



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:32 PM UTC

PDB ID : 8C3A / pdb_00008c3a
Title : Crystal structure of aianthone bound to the Candida albicans 80S ribosome
Authors : Kolosova, O.; Zgadzay, Y.; Yusupov, M.
Deposited on : 2022-12-23
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

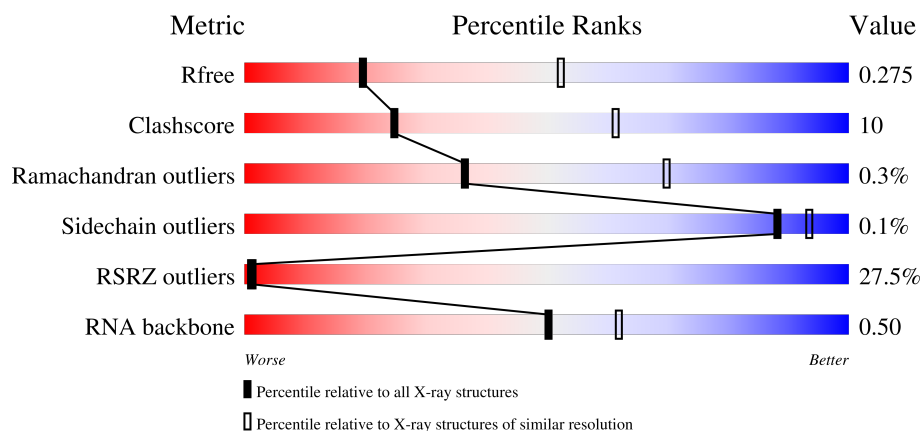
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)
RNA backbone	3983	1109 (3.20-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3359	11% 47% 41% 8% .
1	AS	3359	15% 48% 39% 9% .
2	3	121	2% 67% 31% .
2	AT	121	6% 66% 31% .

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Mol	Chain	Length	Quality of chain
3	4	158	
3	AU	158	
4	AW	254	
4	j	254	
5	AX	389	
5	k	389	
6	AY	363	
6	l	363	
7	AZ	298	
7	m	298	
8	BA	176	
8	n	176	
9	BB	241	
9	o	241	
10	BC	262	
10	p	262	
11	BD	191	
11	q	191	
12	BE	220	
12	r	220	
13	BF	174	
13	s	174	
14	BG	202	
14	t	202	
15	BH	131	

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Mol	Chain	Length	Quality of chain
15	u	131	13% 82% 17% .
16	BI	204	48% 75% 24%
16	v	204	20% 75% 24%
17	BJ	200	18% 82% 18%
17	w	200	10% 82% 17%
18	BK	185	24% 82% 14% 5%
18	x	185	24% 73% 21% 6%
19	BL	186	24% 83% 17% .
19	y	186	27% 78% 22% .
20	BM	190	19% 78% 16% 6%
20	z	190	31% 79% 15% 6%
21	0	172	16% 80% 19% .
21	BN	172	12% 80% 19% .
22	2	160	24% 84% 15% .
22	BO	160	32% 84% 16% .
23	5	124	28% 66% 16% . 17%
23	BP	124	26% 58% 23% . 18%
24	6	137	13% 80% 16% .
24	BQ	137	18% 78% 17% . .
25	7	155	12% 65% 11% 24%
25	BR	155	16% 52% 11% 37%
26	8	142	15% 70% 15% 15%
26	BS	142	23% 74% 10% 16%
27	9	127	24% 82% 17% .
27	BT	127	26% 79% 20% .

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Mol	Chain	Length	Quality of chain
28	AA	136	
28	BU	136	
29	AB	149	
29	BV	149	
30	AC	63	
30	BW	63	
31	AD	106	
31	BX	106	
32	AE	112	
32	BY	112	
33	AF	131	
33	BZ	131	
34	AG	107	
34	CA	107	
35	AH	122	
35	CB	122	
36	AI	120	
36	CC	120	
37	AJ	99	
37	CD	99	
38	AK	87	
38	CE	87	
39	AL	78	
39	CF	78	
40	AM	51	

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Mol	Chain	Length	Quality of chain
40	CG	51	
41	AN	52	
41	CH	52	
42	AO	25	
42	CI	25	
43	AP	106	
43	CJ	106	
44	AQ	92	
44	CK	92	
45	CL	267	
45	i	267	
46	B	1787	
46	CM	1787	
47	C	261	
47	CN	261	
48	CO	256	
48	D	256	
49	CP	249	
49	E	249	
50	CQ	251	
50	F	251	
51	CR	262	
51	G	262	
52	CS	225	
52	H	225	

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Mol	Chain	Length	Quality of chain
53	CT	236	
53	I	236	
54	CU	186	
54	J	186	
55	CV	206	
55	K	206	
56	CW	189	
56	L	189	
57	CX	118	
57	M	118	
58	CY	155	
58	N	155	
59	CZ	143	
59	O	143	
60	DA	151	
60	P	151	
61	DB	132	
61	Q	132	
62	DC	142	
62	R	142	
63	DD	142	
63	S	142	
64	DE	137	
64	T	137	
65	DF	145	

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Mol	Chain	Length	Quality of chain
65	U	145	
66	DG	145	
66	V	145	
67	DH	119	
67	W	119	
68	DI	87	
68	X	87	
69	DJ	130	
69	Y	130	
70	DK	145	
70	Z	145	
71	DL	135	
71	a	135	
72	DM	105	
72	b	105	
73	DN	119	
73	c	119	
74	DO	82	
74	d	82	
75	DP	67	
75	e	67	
76	DQ	56	
76	f	56	
77	DR	63	
77	g	63	

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Mol	Chain	Length	Quality of chain
78	DS	193	
78	h	193	
79	AR	317	
79	DT	317	
80	P0	312	
80	p0	312	
81	12	165	
82	L1	217	
82	l1	217	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
83	MG	1	3405	-	-	-	X
83	MG	1	3406	-	-	-	X
83	MG	1	3415	-	-	-	X
83	MG	1	3464	-	-	-	X
83	MG	1	3514	-	-	-	X
83	MG	1	3561	-	-	-	X
83	MG	1	3567	-	-	-	X
83	MG	1	3600	-	-	-	X
83	MG	1	3657	-	-	-	X
83	MG	1	3663	-	-	-	X
83	MG	1	3788	-	-	-	X
83	MG	AS	3528	-	-	-	X
83	MG	AS	3533	-	-	-	X
83	MG	AS	3542	-	-	-	X
83	MG	AS	3575	-	-	-	X
83	MG	AS	3631	-	-	-	X
83	MG	AS	3701	-	-	-	X
83	MG	AS	3722	-	-	-	X
83	MG	AS	3753	-	-	-	X
83	MG	AT	209	-	-	-	X
83	MG	B	1804	-	-	-	X
83	MG	B	1805	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
83	MG	B	1839	-	-	-	X
83	MG	B	1856	-	-	-	X
83	MG	B	1894	-	-	-	X
83	MG	B	1919	-	-	-	X
83	MG	B	1943	-	-	-	X
83	MG	B	1955	-	-	-	X
83	MG	B	1956	-	-	-	X
83	MG	B	1960	-	-	-	X
83	MG	B	1972	-	-	-	X
83	MG	CL	302	-	-	-	X
83	MG	CM	1836	-	-	-	X
83	MG	CM	1948	-	-	-	X
83	MG	Z	201	-	-	-	X

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 410139 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	3217	Total	C	N	O	P	0	0	0
			68771	30722	12362	22470	3217			
1	AS	3229	Total	C	N	O	P	0	0	0
			69025	30835	12406	22555	3229			

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	3	121	Total	C	N	O	P	0	0	0
			2579	1153	463	842	121			
2	AT	121	Total	C	N	O	P	0	0	0
			2579	1153	463	842	121			

- Molecule 3 is a RNA chain called 5.8S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	157	Total	C	N	O	P	0	0	0
			3333	1491	583	1102	157			
3	AU	158	Total	C	N	O	P	0	0	0
			3353	1500	585	1110	158			

- Molecule 4 is a protein called 60S ribosomal protein L2-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	j	249	Total	C	N	O	S	0	1	0
			1894	1185	377	330	2			
4	AW	249	Total	C	N	O	S	0	1	0
			1894	1185	377	330	2			

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	k	386	Total	C	N	O	S	0	1	0
			3084	1955	584	538	7			
5	AX	386	Total	C	N	O	S	0	0	0
			3077	1950	582	538	7			

- Molecule 6 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	l	361	Total	C	N	O	S	0	0	0
			2751	1729	529	490	3			
6	AY	361	Total	C	N	O	S	0	0	0
			2751	1729	529	490	3			

- Molecule 7 is a protein called Uncharacterized protein CaJ7.0206.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	m	296	Total	C	N	O	S	0	0	0
			2426	1544	422	458	2			
7	AZ	292	Total	C	N	O	S	0	0	0
			2394	1526	416	450	2			

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	n	157	Total	C	N	O	S	0	0	0
			1242	796	226	219	1			
8	BA	153	Total	C	N	O		0	0	0
			1210	777	221	212				

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	o	234	Total	C	N	O	S	0	0	0
			1885	1208	345	331	1			
9	BB	234	Total	C	N	O	S	0	0	0
			1885	1208	345	331	1			

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	p	238	Total	C	N	O	S	0	0	0
			1839	1175	327	334	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	BC	233	Total	C	N	O	S	0	0	0
			1805	1156	321	325	3			

- Molecule 11 is a protein called 60S ribosomal protein L9-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	q	190	Total	C	N	O	S	0	0	0
			1519	958	276	281	4			
11	BD	190	Total	C	N	O	S	0	0	0
			1519	958	276	281	4			

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	r	208	Total	C	N	O	S	0	0	0
			1689	1069	322	291	7			
12	BE	208	Total	C	N	O	S	0	0	0
			1689	1069	322	291	7			

- Molecule 13 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	s	171	Total	C	N	O	S	0	0	0
			1371	857	260	250	4			
13	BF	171	Total	C	N	O	S	0	0	0
			1371	857	260	250	4			

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	t	200	Total	C	N	O	0	0	0
			1610	1009	318	283			
14	BG	200	Total	C	N	O	0	0	0
			1610	1009	318	283			

- Molecule 15 is a protein called 60S ribosomal protein L14-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	u	130	Total	C	N	O	S	0	0	0
			1029	660	193	175	1			
15	BH	130	Total	C	N	O	S	0	0	0
			1029	660	193	175	1			

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	v	203	Total	C	N	O	S	0	0	0
			1713	1075	356	280	2			
16	BI	203	Total	C	N	O	S	0	0	0
			1713	1075	356	280	2			

- Molecule 17 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	w	199	Total	C	N	O	S	0	0	0
			1590	1025	294	269	2			
17	BJ	199	Total	C	N	O	S	0	0	0
			1590	1025	294	269	2			

- Molecule 18 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	x	173	Total	C	N	O	0	0	0
			1387	856	280	251			
18	BK	176	Total	C	N	O	0	0	0
			1406	868	284	254			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	y	185	Total	C	N	O	0	0	0
			1458	916	297	245			
19	BL	185	Total	C	N	O	0	0	0
			1458	916	297	245			

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	z	179	Total	C	N	O	S	0	0	0
			1457	901	310	243	3			
20	BM	179	Total	C	N	O	S	0	0	0
			1457	901	310	243	3			

- Molecule 21 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	0	170	Total	C	N	O	S	0	0	0
			1423	921	258	241	3			
21	BN	170	Total	C	N	O	S	0	0	0
			1423	921	258	241	3			

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	2	159	Total	C	N	O	S	0	0	0
			1262	798	241	221	2			
22	BO	159	Total	C	N	O	S	0	0	0
			1262	798	241	221	2			

- Molecule 23 is a protein called 60S ribosomal protein L22-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	5	103	Total	C	N	O		0	0	0
			831	539	138	154				
23	BP	102	Total	C	N	O		6	2	0
			843	550	138	155				

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	6	131	Total	C	N	O	S	0	0	0
			977	615	183	171	8			
24	BQ	131	Total	C	N	O	S	0	0	0
			977	615	183	171	8			

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	7	118	Total	C	N	O	S	0	0	0
			945	591	192	161	1			
25	BR	98	Total	C	N	O	S	0	0	0
			801	501	162	137	1			

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	8	121	Total	C	N	O	S	0	0	0
			974	622	175	176	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BS	119	Total	C	N	O	S	0	0	0
			960	613	172	174	1			

- Molecule 27 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	9	126	Total	C	N	O		0	0	0
			989	618	190	181				
27	BT	126	Total	C	N	O		0	0	0
			989	618	190	181				

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	AA	135	Total	C	N	O	S	0	0	0
			1087	705	197	183	2			
28	BU	135	Total	C	N	O	S	0	0	0
			1087	705	197	183	2			

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	AB	148	Total	C	N	O	S	0	0	0
			1170	741	231	197	1			
29	BV	148	Total	C	N	O	S	0	0	0
			1170	741	231	197	1			

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	AC	62	Total	C	N	O		0	0	0
			493	307	105	81				
30	BW	61	Total	C	N	O		0	0	0
			488	304	104	80				

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	AD	96	Total	C	N	O	S	0	0	0
			729	469	121	137	2			
31	BX	96	Total	C	N	O	S	0	0	0
			729	469	121	137	2			

- Molecule 32 is a protein called 60S ribosomal protein L31-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	AE	110	Total	C	N	O	S	0	0	0
			894	565	168	159	2			
32	BY	110	Total	C	N	O	S	0	0	0
			894	565	168	159	2			

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	AF	124	Total	C	N	O	S	0	0	0
			1000	638	194	167	1			
33	BZ	124	Total	C	N	O	S	0	0	0
			1004	641	195	167	1			

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	AG	106	Total	C	N	O	S	0	0	0
			847	543	161	142	1			
34	CA	106	Total	C	N	O	S	0	0	0
			847	543	161	142	1			

- Molecule 35 is a protein called 60S ribosomal protein L34-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	AH	112	Total	C	N	O	S	0	0	0
			887	547	182	154	4			
35	CB	112	Total	C	N	O	S	0	0	0
			887	547	182	154	4			

- Molecule 36 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	AI	120	Total	C	N	O	S	0	1	0
			998	634	196	167	1			
36	CC	118	Total	C	N	O		6	1	0
			985	626	194	165				

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	AJ	97	Total	C	N	O	S	0	0	0
			758	471	156	130	1			
37	CD	97	Total	C	N	O	S	0	0	0
			758	471	156	130	1			

- Molecule 38 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	AK	86	Total	C	N	O	S	0	0	0
			677	413	148	110	6			
38	CE	86	Total	C	N	O	S	0	0	0
			677	413	148	110	6			

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
39	AL	77	Total	C	N	O	0	0	0
			617	393	115	109			
39	CF	77	Total	C	N	O	0	0	0
			617	393	115	109			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	AM	50	Total	C	N	O	0	0	0
			438	275	97	66			
40	CG	50	Total	C	N	O	0	1	0
			446	280	100	66			

- Molecule 41 is a protein called 60S ribosomal protein L40-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	AN	52	Total	C	N	O	S	0	0	0
			419	260	86	67	6			
41	CH	51	Total	C	N	O	S	0	0	0
			411	255	85	66	5			

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	AO	25	Total	C	N	O	S	0	0	0
			236	144	63	28	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	CI	24	Total	C	N	O	S	0	0	0
			227	138	61	27	1			

- Molecule 43 is a protein called 60S ribosomal protein L42-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	AP	103	Total	C	N	O	S	0	0	0
			828	521	165	137	5			
43	CJ	103	Total	C	N	O	S	0	0	0
			828	521	165	137	5			

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	AQ	91	Total	C	N	O	S	0	0	0
			698	430	140	124	4			
44	CK	91	Total	C	N	O	S	0	0	0
			698	430	140	124	4			

- Molecule 45 is a protein called 60S ribosomal protein CAALFM_C304810CA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
45	i	121	Total	C	N	O	0	0	0
			930	563	166	201			
45	CL	121	Total	C	N	O	0	0	0
			930	563	166	201			

- Molecule 46 is a RNA chain called 18S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B	1761	Total	C	N	O	P	0	0	0
			37537	16780	6656	12340	1761			
46	CM	1765	Total	C	N	O	P	0	0	0
			37621	16818	6670	12368	1765			

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	C	208	Total	C	N	O	S	0	0	0
			1627	1041	284	297	5			
47	CN	208	Total	C	N	O	S	0	0	0
			1627	1041	284	297	5			

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	D	214	Total	C	N	O	S	0	0	0
			1724	1094	313	313	4			
48	CO	214	Total	C	N	O	S	0	0	0
			1724	1094	313	313	4			

- Molecule 49 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	E	217	Total	C	N	O	S	0	0	0
			1629	1039	289	296	5			
49	CP	217	Total	C	N	O	S	0	0	0
			1629	1039	289	296	5			

- Molecule 50 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	F	223	Total	C	N	O	S	0	0	0
			1707	1087	311	305	4			
50	CQ	223	Total	C	N	O	S	0	0	0
			1707	1087	311	305	4			

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	G	259	Total	C	N	O	S	0	0	0
			2051	1304	385	357	5			
51	CR	260	Total	C	N	O	S	0	0	0
			2055	1306	386	358	5			

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	H	206	Total	C	N	O	S	0	0	0
			1614	1008	301	301	4			
52	CS	206	Total	C	N	O	S	0	0	0
			1614	1008	301	301	4			

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	I	226	Total	C	N	O	S	0	0	0
			1820	1133	351	330	6			
53	CT	236	Total	C	N	O	S	0	0	0
			1904	1184	369	345	6			

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	J	185	Total	C	N	O	S	0	0	0
			1491	953	269	269				
54	CU	183	Total	C	N	O	S	0	0	0
			1475	944	265	266				

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	K	203	Total	C	N	O	S	0	0	0
			1579	973	322	283	1			
55	CV	203	Total	C	N	O	S	0	0	0
			1579	973	322	283	1			

- Molecule 56 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	L	178	Total	C	N	O	S	0	0	0
			1453	918	286	248	1			
56	CW	178	Total	C	N	O	S	0	0	0
			1453	918	286	248	1			

- Molecule 57 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	M	98	Total	C	N	O	S	0	0	0
			817	531	135	150	1			
57	CX	94	Total	C	N	O	S	0	0	0
			791	515	131	144	1			

- Molecule 58 is a protein called 40S ribosomal protein S11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	N	144	Total	C	N	O	S	0	0	0
			1150	734	215	198	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	CY	141	Total	C	N	O	S	0	0	0
			1129	722	212	192	3			

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	O	116	Total	C	N	O	S	0	0	0
			885	550	158	172	5			
59	CZ	119	Total	C	N	O	S	0	0	0
			913	566	163	179	5			

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	P	150	Total	C	N	O	S	0	0	0
			1187	757	219	210	1			
60	DA	150	Total	C	N	O	S	0	0	0
			1187	757	219	210	1			

- Molecule 61 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	Q	127	Total	C	N	O	S	0	0	0
			942	579	186	174	3			
61	DB	127	Total	C	N	O	S	0	0	0
			942	579	186	174	3			

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
62	R	129	Total	C	N	O	S	0	0	0
			1018	649	185	177	7			
62	DC	130	Total	C	N	O	S	0	0	0
			1029	655	189	178	7			

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
63	S	140	Total	C	N	O	S	0	0	0
			1091	700	198	192	1			
63	DD	140	Total	C	N	O	S	0	0	0
			1091	700	198	192	1			

- Molecule 64 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	T	124	Total	C	N	O	S	0	0	0
			997	628	183	185	1			
64	DE	124	Total	C	N	O	S	0	0	0
			997	628	183	185	1			

- Molecule 65 is a protein called 40S ribosomal protein S18-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
65	U	144	Total	C	N	O	S	0	0	0
			1187	744	233	207	3			
65	DF	141	Total	C	N	O	S	0	0	0
			1161	727	227	204	3			

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	V	141	Total	C	N	O	S	0	0	0
			1100	689	210	200	1			
66	DG	141	Total	C	N	O	S	0	0	0
			1100	689	210	200	1			

- Molecule 67 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	W	102	Total	C	N	O	S	0	0	0
			808	509	150	147	2			
67	DH	97	Total	C	N	O	S	0	0	0
			763	481	140	140	2			

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	X	87	Total	C	N	O	S	0	0	0
			676	415	126	133	2			
68	DI	87	Total	C	N	O	S	0	0	0
			676	415	126	133	2			

- Molecule 69 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	Y	129	Total	C	N	O	S	0	0	0
			1032	655	191	183	3			
69	DJ	129	Total	C	N	O	S	0	0	0
			1032	655	191	183	3			

- Molecule 70 is a protein called Ribosomal protein S23 (S12).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	Z	143	Total	C	N	O	S	0	0	0
			1110	701	219	188	2			
70	DK	143	Total	C	N	O	S	0	0	0
			1110	701	219	188	2			

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
71	a	134	Total	C	N	O		0	0	0
			1086	677	218	191				
71	DL	132	Total	C	N	O		0	0	0
			1072	670	216	186				

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	b	72	Total	C	N	O		0	0	0
			578	369	103	106				
72	DM	71	Total	C	N	O		0	0	0
			570	365	102	103				

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	c	98	Total	C	N	O	S	0	0	0
			779	482	163	128	6			
73	DN	98	Total	C	N	O	S	0	0	0
			779	482	163	128	6			

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	d	81	Total	C	N	O	S	0	0	0
			614	383	110	114	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	DO	81	Total	C	N	O	S	0	0	0
			614	383	110	114	7			

- Molecule 75 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	e	62	Total	C	N	O	S	0	0	0
			487	299	98	88	2			
75	DP	61	Total	C	N	O	S	0	0	0
			476	293	94	87	2			

- Molecule 76 is a protein called 40S ribosomal protein S29A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	f	55	Total	C	N	O	S	0	0	0
			454	281	94	75	4			
76	DQ	54	Total	C	N	O	S	0	0	0
			449	278	93	74	4			

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	g	60	Total	C	N	O	S	0	0	0
			474	297	96	79	2			
77	DR	58	Total	C	N	O	S	0	0	0
			461	289	93	77	2			

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S31 fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
78	h	70	Total	C	N	O	S	0	0	0
			574	362	113	93	6			
78	DS	70	Total	C	N	O	S	0	0	0
			574	362	113	93	6			

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	AR	311	Total	C	N	O	S	0	0	0
			2398	1519	412	462	5			
79	DT	311	Total	C	N	O	S	0	0	0
			2398	1519	412	462	5			

- Molecule 80 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	P0	107	Total	C	N	O	S	0	0	0
			845	542	150	150	3			
80	p0	107	Total	C	N	O	S	0	0	0
			845	542	150	150	3			

- Molecule 81 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
81	12	63	Total	C	N	O	S	0	0	0
			480	297	85	96	2			

- Molecule 82 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	L1	217	Total	C	N	O	S	0	0	0
			1711	1096	294	312	9			
82	11	217	Total	C	N	O	S	0	0	0
			1711	1096	294	312	9			

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	1	556	Total	Mg	0	0
			556	556		
83	3	15	Total	Mg	0	0
			15	15		
83	4	11	Total	Mg	0	0
			11	11		
83	j	3	Total	Mg	0	0
			3	3		
83	k	6	Total	Mg	0	0
			6	6		
83	o	4	Total	Mg	0	0
			4	4		
83	r	2	Total	Mg	0	0
			2	2		
83	s	1	Total	Mg	0	0
			1	1		
83	u	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	v	2	Total 2	Mg 2	0	0
83	w	3	Total 3	Mg 3	0	0
83	x	2	Total 2	Mg 2	0	0
83	0	4	Total 4	Mg 4	0	0
83	2	1	Total 1	Mg 1	0	0
83	6	4	Total 4	Mg 4	0	0
83	8	3	Total 3	Mg 3	0	0
83	9	2	Total 2	Mg 2	0	0
83	AB	2	Total 2	Mg 2	0	0
83	AC	1	Total 1	Mg 1	0	0
83	AE	3	Total 3	Mg 3	0	0
83	AF	2	Total 2	Mg 2	0	0
83	AG	3	Total 3	Mg 3	0	0
83	AH	2	Total 2	Mg 2	0	0
83	AK	1	Total 1	Mg 1	0	0
83	AP	2	Total 2	Mg 2	0	0
83	i	1	Total 1	Mg 1	0	0
83	B	172	Total 172	Mg 172	0	0
83	D	1	Total 1	Mg 1	0	0
83	G	2	Total 2	Mg 2	0	0
83	I	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	J	1	Total 1	Mg 1	0	0
83	K	1	Total 1	Mg 1	0	0
83	Q	2	Total 2	Mg 2	0	0
83	R	1	Total 1	Mg 1	0	0
83	V	1	Total 1	Mg 1	0	0
83	Y	3	Total 3	Mg 3	0	0
83	Z	2	Total 2	Mg 2	0	0
83	f	1	Total 1	Mg 1	0	0
83	g	1	Total 1	Mg 1	0	0
83	AR	1	Total 1	Mg 1	0	0
83	AS	380	Total 380	Mg 380	0	0
83	AT	10	Total 10	Mg 10	0	0
83	AU	10	Total 10	Mg 10	0	0
83	AW	4	Total 4	Mg 4	0	0
83	AX	2	Total 2	Mg 2	0	0
83	AY	1	Total 1	Mg 1	0	0
83	AZ	1	Total 1	Mg 1	0	0
83	BB	4	Total 4	Mg 4	0	0
83	BE	2	Total 2	Mg 2	0	0
83	BF	1	Total 1	Mg 1	0	0
83	BH	1	Total 1	Mg 1	0	0

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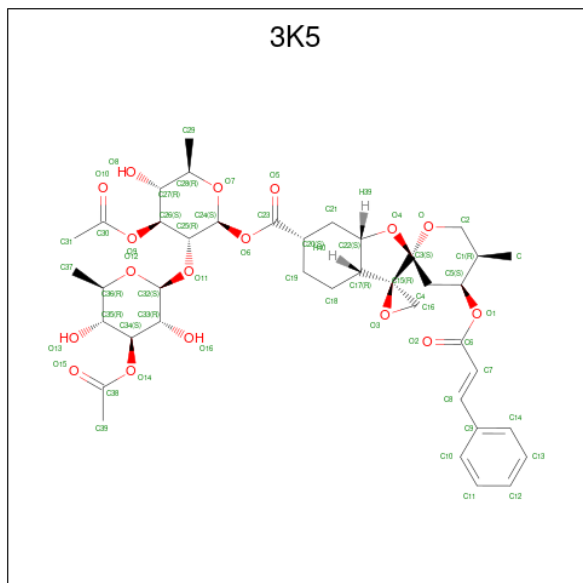
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	BI	1	Total 1	Mg 1	0	0
83	BJ	3	Total 3	Mg 3	0	0
83	BK	2	Total 2	Mg 2	0	0
83	BN	1	Total 1	Mg 1	0	0
83	BO	1	Total 1	Mg 1	0	0
83	BS	1	Total 1	Mg 1	0	0
83	BV	1	Total 1	Mg 1	0	0
83	BZ	4	Total 4	Mg 4	0	0
83	CA	3	Total 3	Mg 3	0	0
83	CJ	1	Total 1	Mg 1	0	0
83	CK	2	Total 2	Mg 2	0	0
83	CL	3	Total 3	Mg 3	0	0
83	CM	148	Total 148	Mg 148	0	0
83	CO	1	Total 1	Mg 1	0	0
83	CP	1	Total 1	Mg 1	0	0
83	CQ	2	Total 2	Mg 2	0	0
83	CY	1	Total 1	Mg 1	0	0
83	DA	1	Total 1	Mg 1	0	0
83	DB	4	Total 4	Mg 4	0	0
83	DG	2	Total 2	Mg 2	0	0
83	DJ	2	Total 2	Mg 2	0	0

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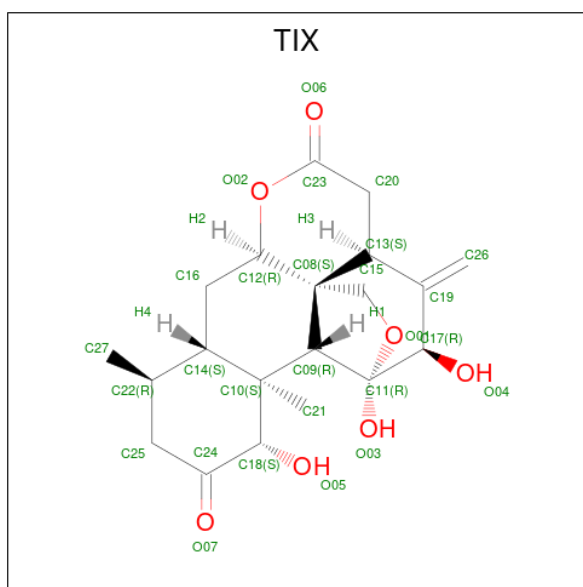
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	DQ	1	Total	Mg	0	0
			1	1		

- Molecule 84 is 3-O-acetyl-2-O-(3-O-acetyl-6-deoxy-beta-D-glucopyranosyl)-6-deoxy-1-O-{[(2R,2'S,3a'R,4''S,5''R,6'S,7a'S)-5''-methyl-4''-{[(2E)-3-phenylprop-2-enoyl]oxy}decahydrodispiro[oxirane-2,3'-[1]benzofuran-2',2''-pyran]-6'-yl]carbonyl}-beta-D-glucopyranose (CCD ID: 3K5) (formula: C₄₀H₅₂O₁₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
84	1	1	Total	C	O	0	0
			57	40	17		
84	AS	1	Total	C	O	0	0
			57	40	17		

- Molecule 85 is aianthone (CCD ID: TIX) (formula: C₂₀H₂₆O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
85	1	1	Total	C	O	0	0
			27	20	7		
85	AS	1	Total	C	O	0	0
			27	20	7		

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	AH	1	Total	Zn	0	0
			1	1		
86	AK	1	Total	Zn	0	0
			1	1		
86	AN	1	Total	Zn	0	0
			1	1		
86	AP	1	Total	Zn	0	0
			1	1		
86	AQ	1	Total	Zn	0	0
			1	1		
86	c	1	Total	Zn	0	0
			1	1		
86	d	1	Total	Zn	0	0
			1	1		
86	f	1	Total	Zn	0	0
			1	1		
86	h	1	Total	Zn	0	0
			1	1		
86	CB	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
86	CE	1	Total 1	Zn 1	0	0
86	CH	1	Total 1	Zn 1	0	0
86	CJ	1	Total 1	Zn 1	0	0
86	CK	1	Total 1	Zn 1	0	0
86	DN	1	Total 1	Zn 1	0	0
86	DO	1	Total 1	Zn 1	0	0
86	DQ	1	Total 1	Zn 1	0	0
86	DS	1	Total 1	Zn 1	0	0

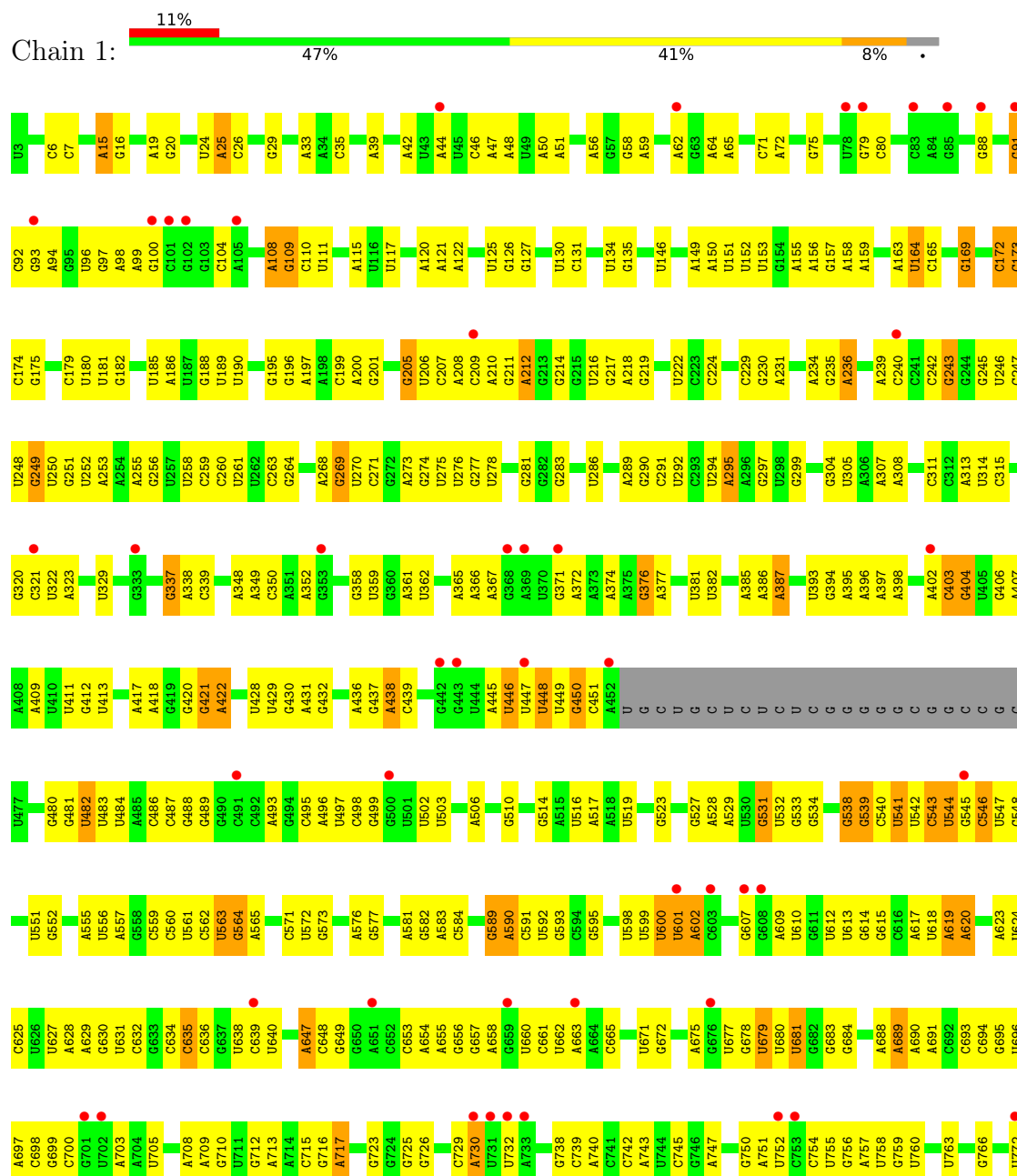
- Molecule 87 is water.

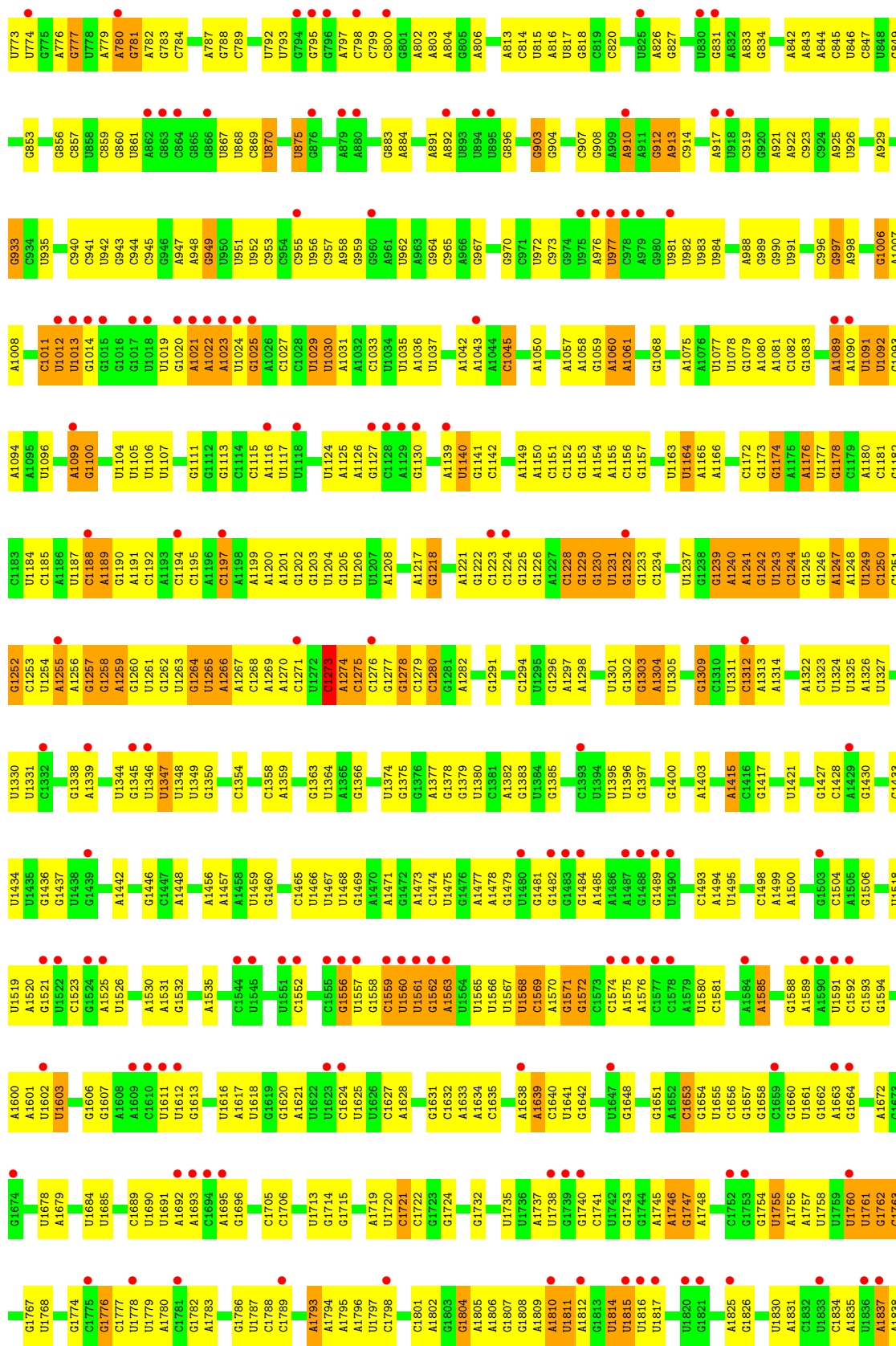
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
87	1	20	Total 20	O 20	0	0
87	4	3	Total 3	O 3	0	0
87	l	1	Total 1	O 1	0	0
87	B	12	Total 12	O 12	0	0
87	AS	26	Total 26	O 26	0	0
87	BQ	3	Total 3	O 3	0	0
87	BV	1	Total 1	O 1	0	0

3 Residue-property plots

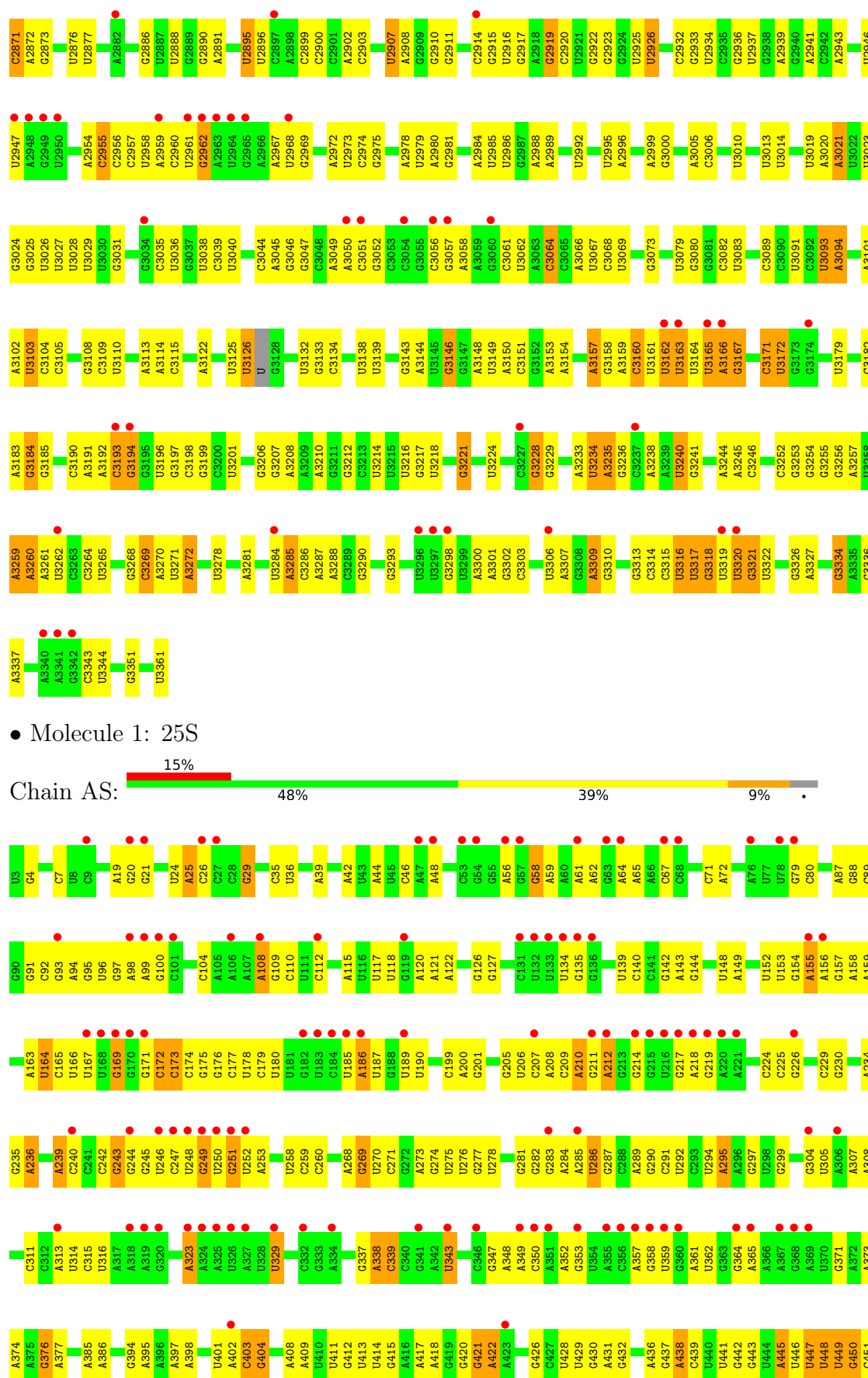
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

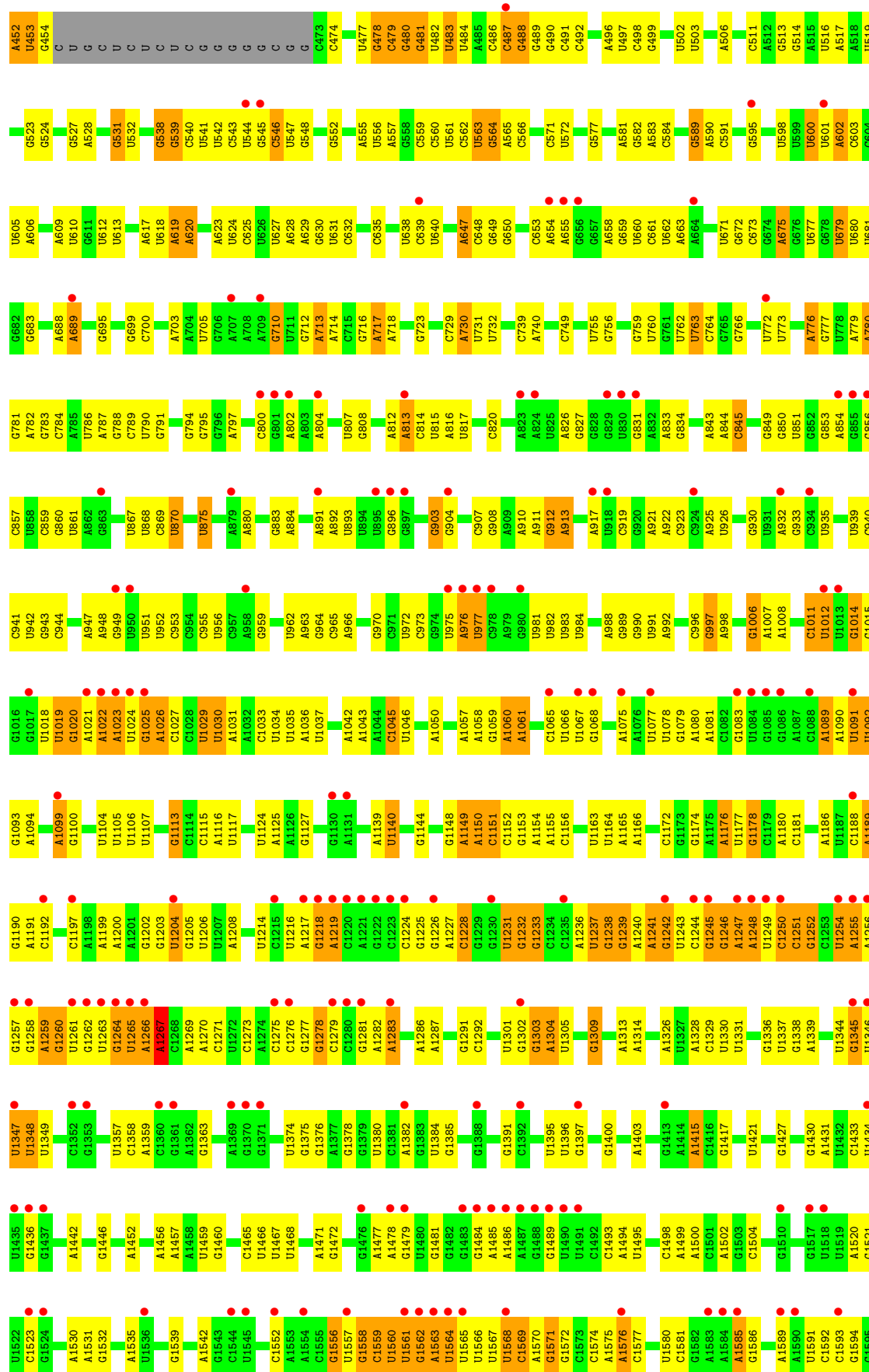
• Molecule 1: 25S



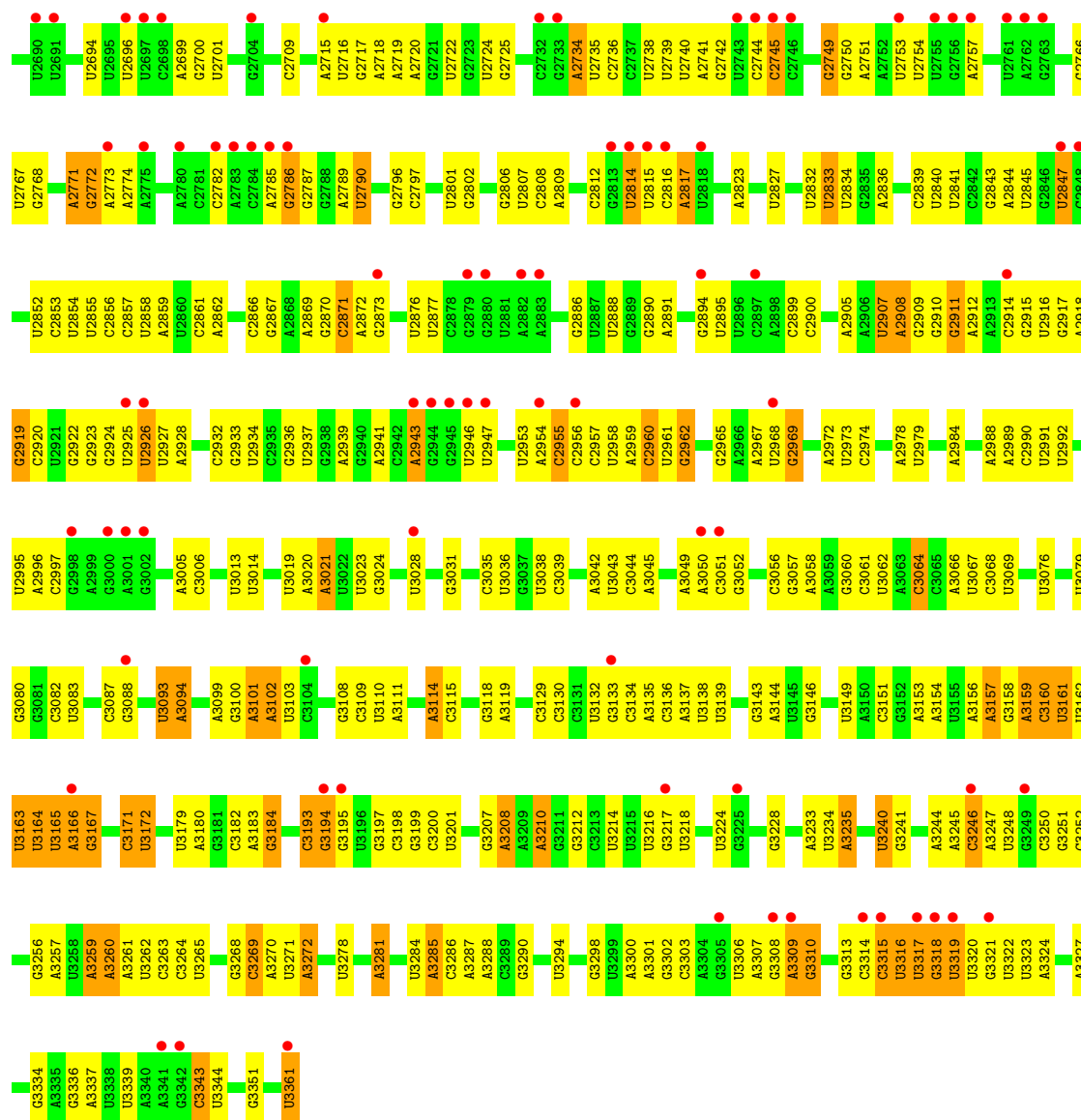


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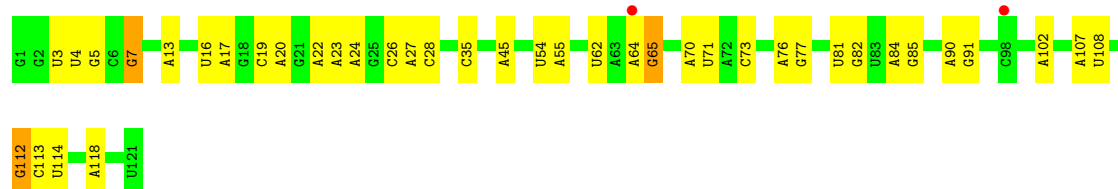






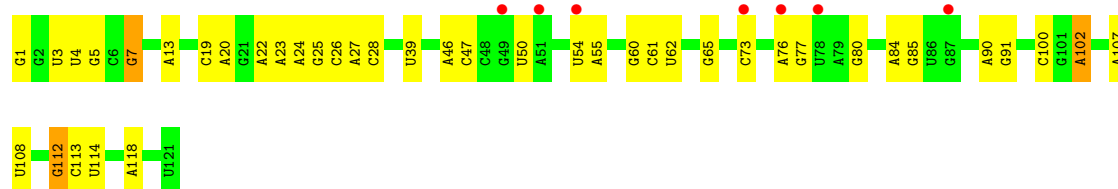


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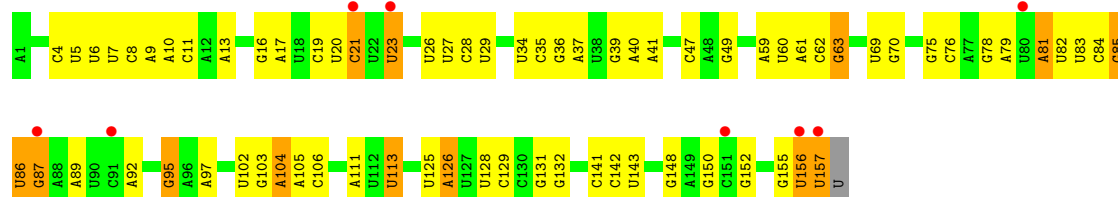


- Molecule 2: 5S

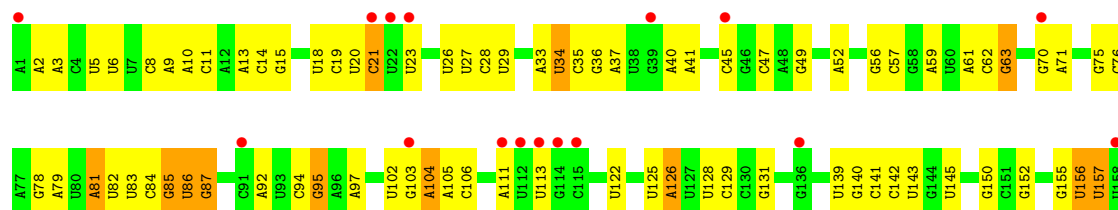




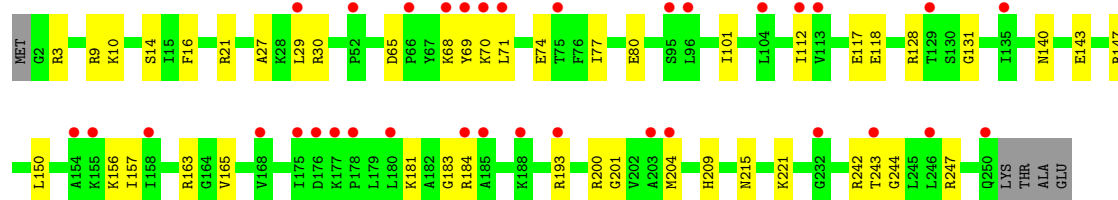
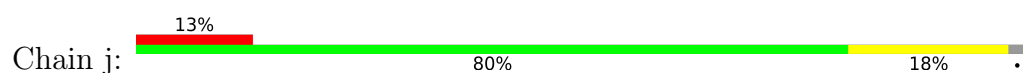
• Molecule 3: 5.8S



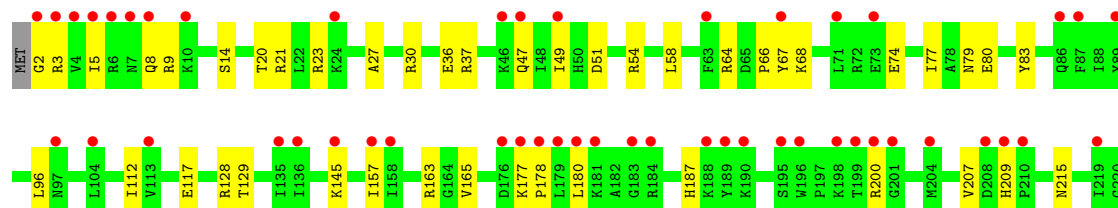
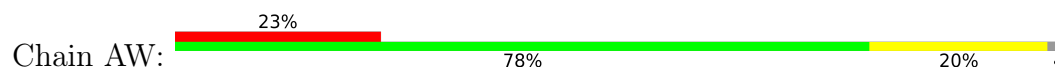
• Molecule 3: 5.8S

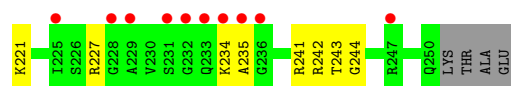


• Molecule 4: 60S ribosomal protein L2-B

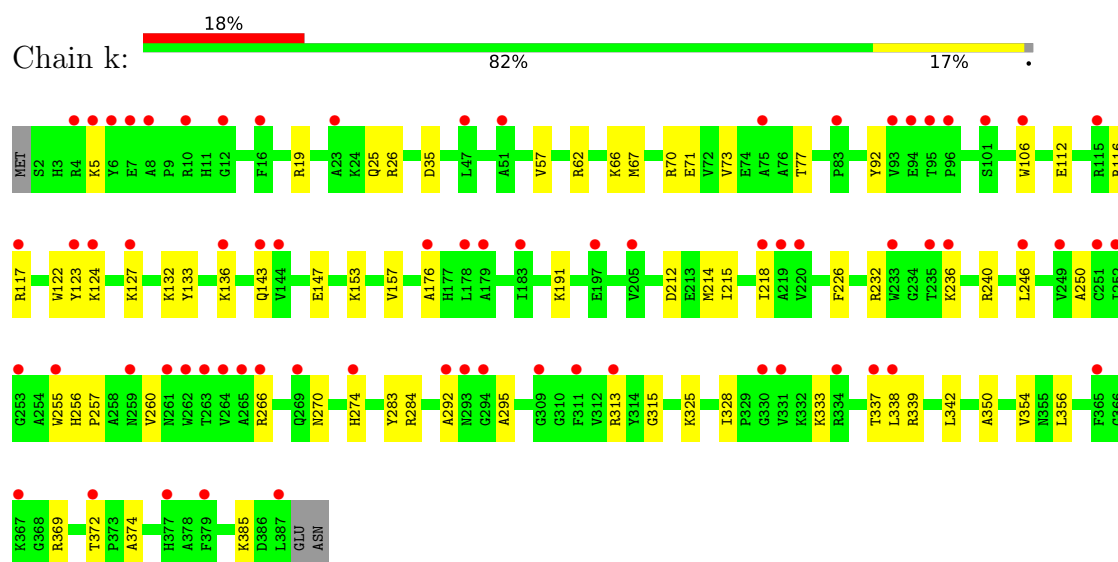


• Molecule 4: 60S ribosomal protein L2-B

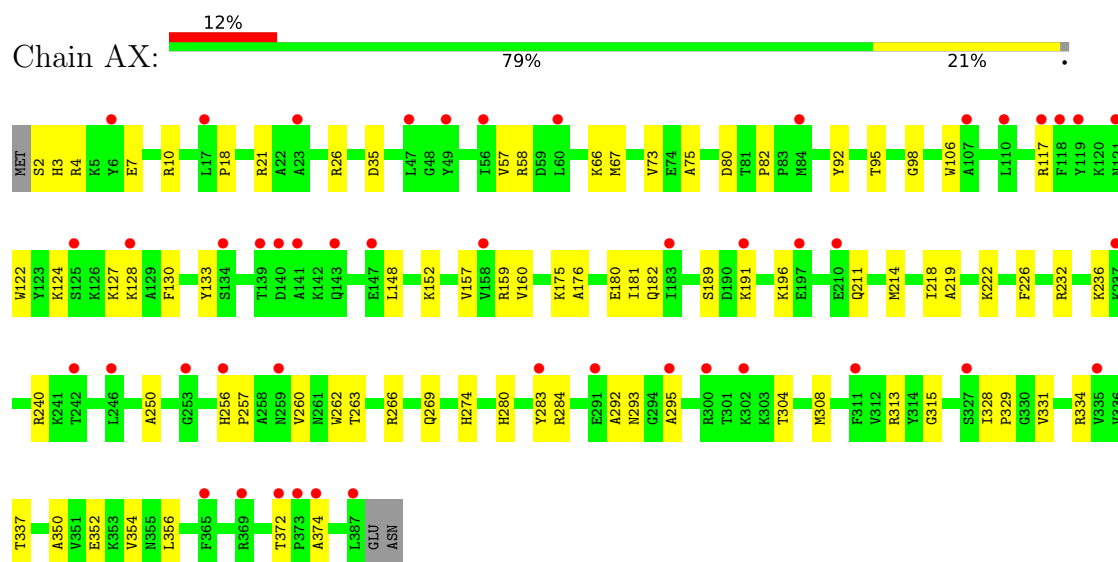




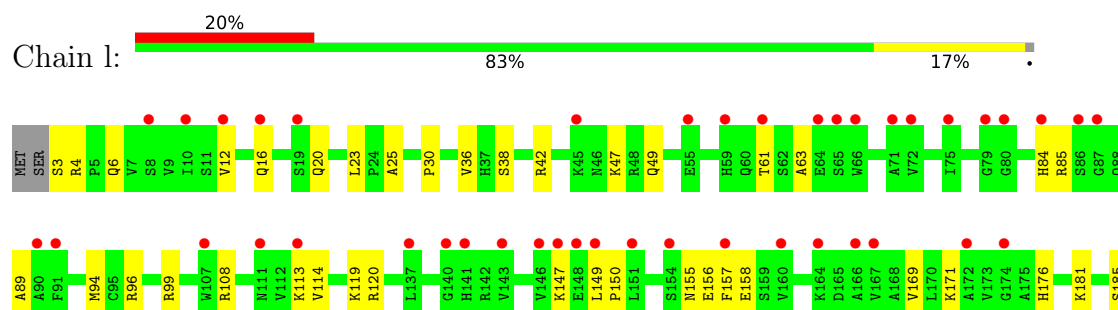
• Molecule 5: 60S ribosomal protein L3

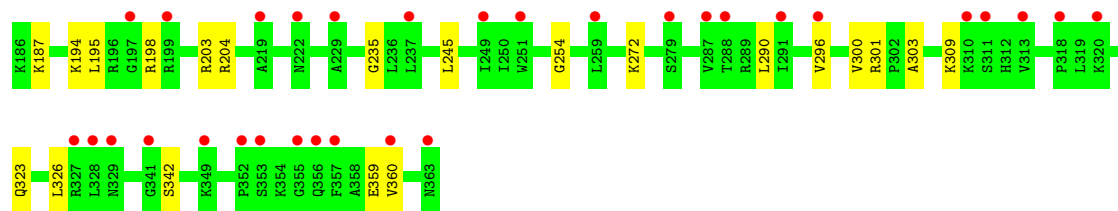


• Molecule 5: 60S ribosomal protein L3

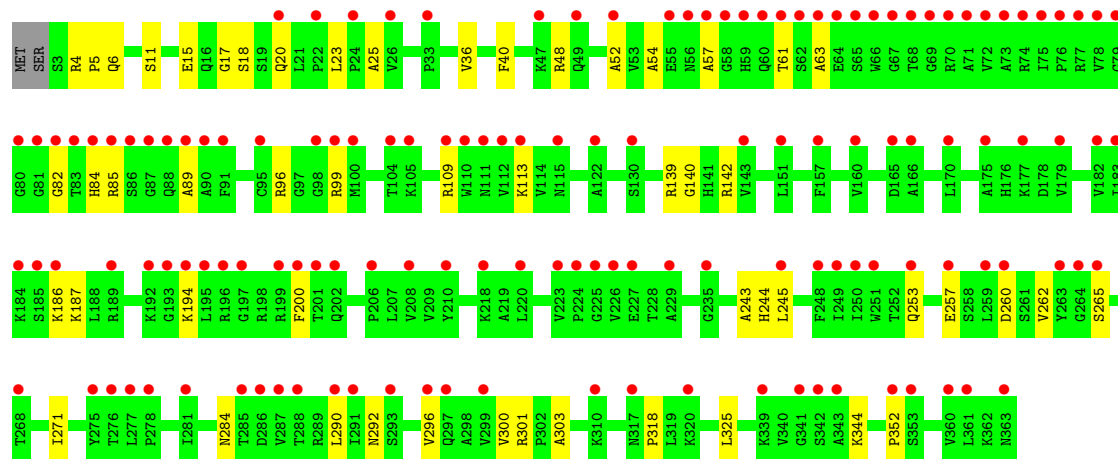
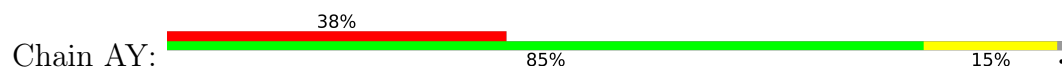


• Molecule 6: 60S ribosomal protein L4-B

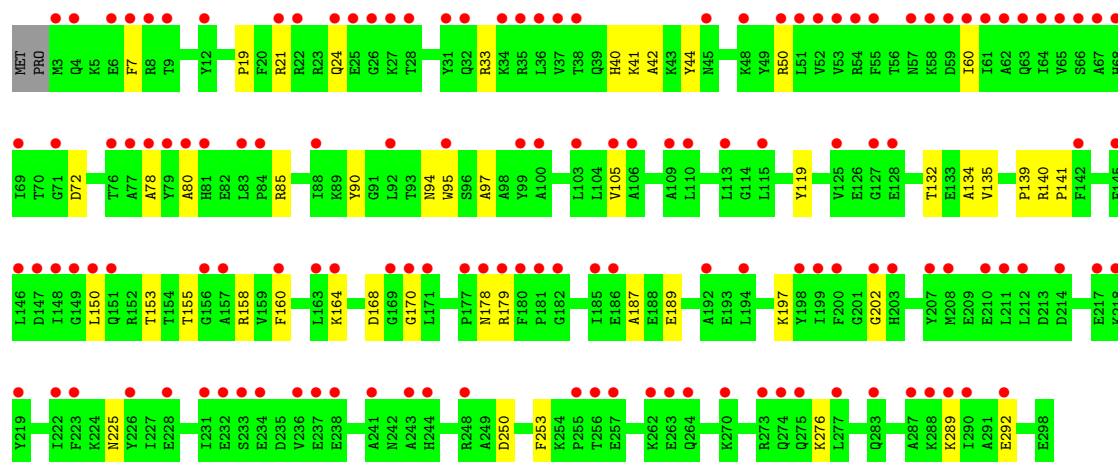
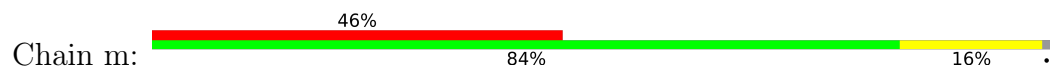




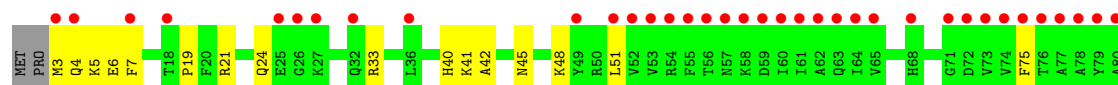
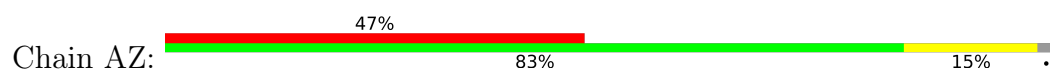
• Molecule 6: 60S ribosomal protein L4-B

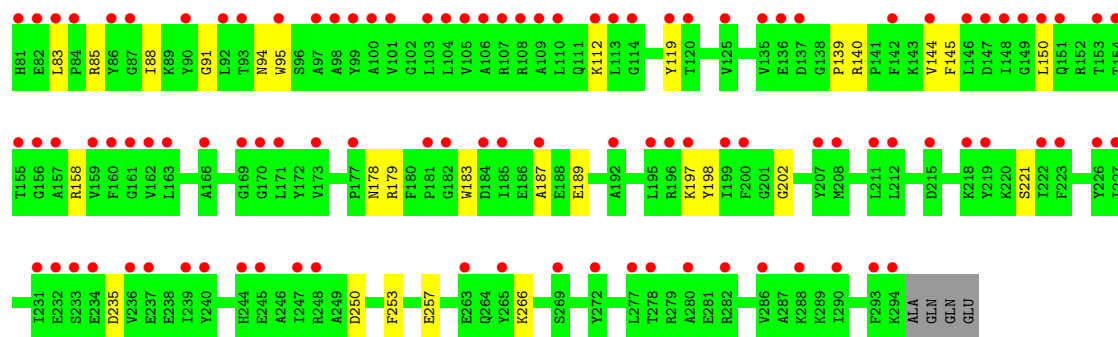


• Molecule 7: Uncharacterized protein CaJ7.0206

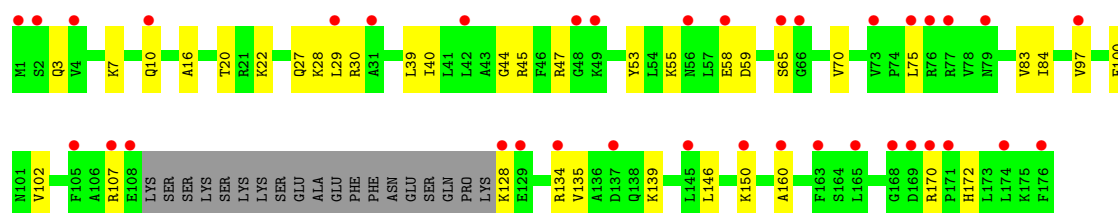


• Molecule 7: Uncharacterized protein CaJ7.0206

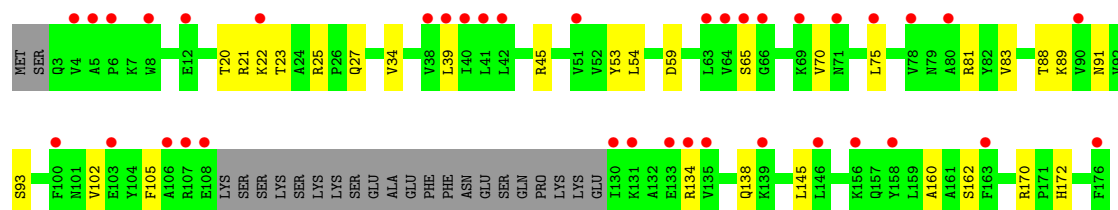
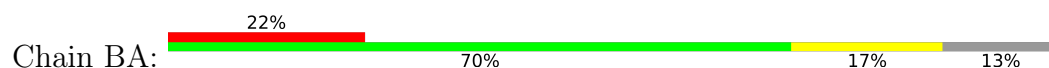




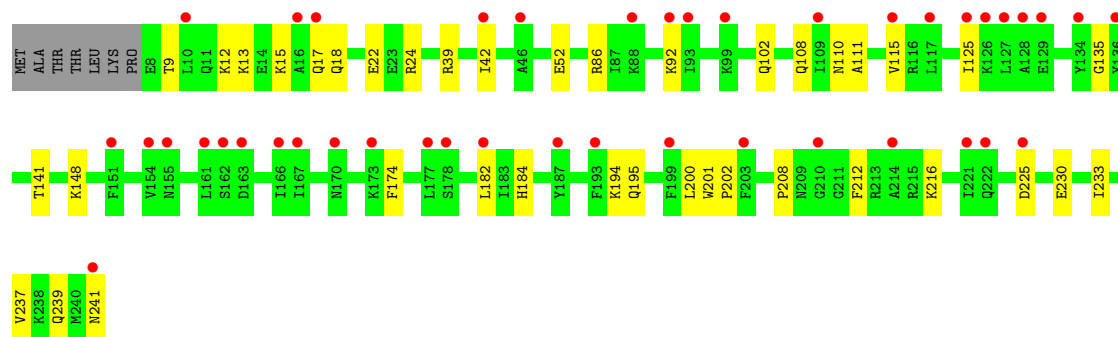
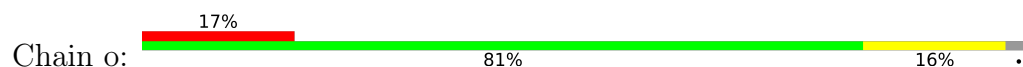
• Molecule 8: 60S ribosomal protein L6



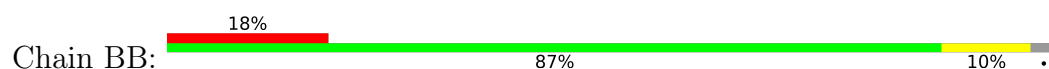
• Molecule 8: 60S ribosomal protein L6

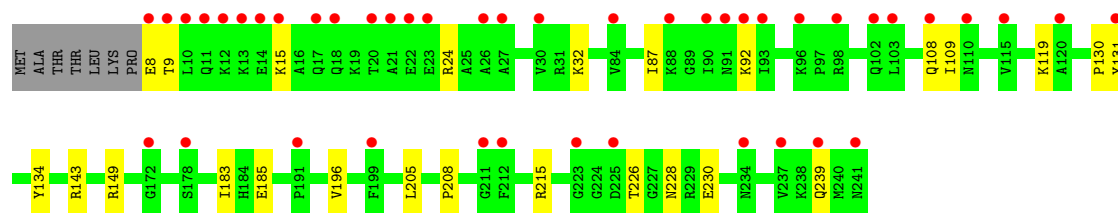


• Molecule 9: 60S ribosomal protein L7-A

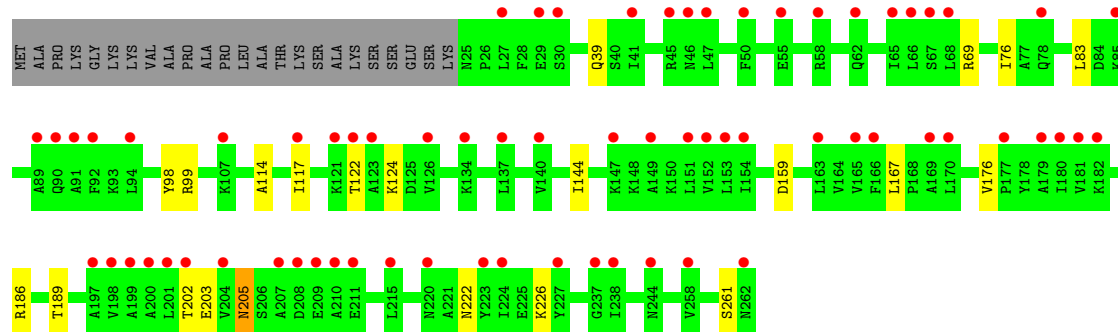
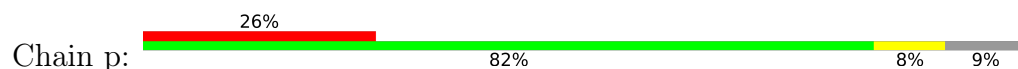


• Molecule 9: 60S ribosomal protein L7-A

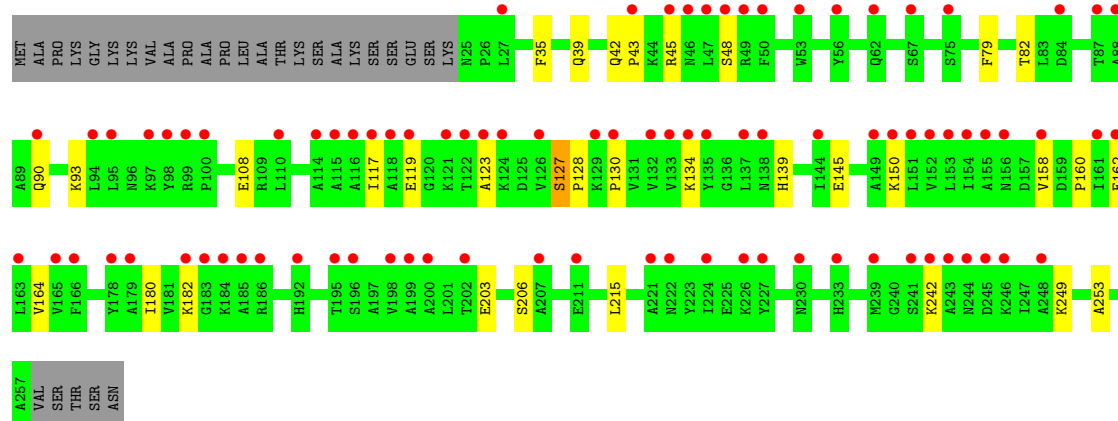
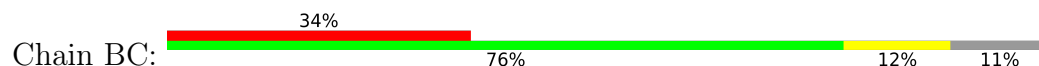




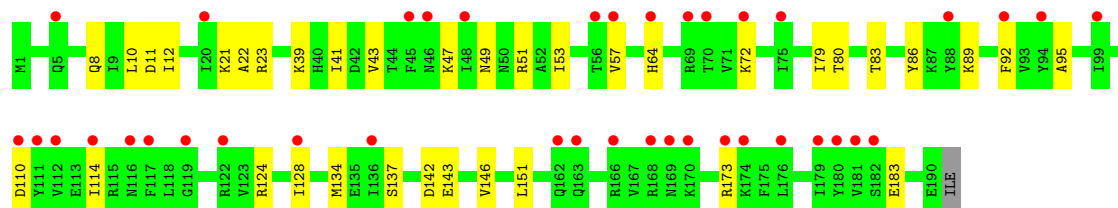
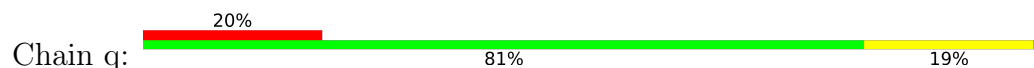
• Molecule 10: 60S ribosomal protein L8



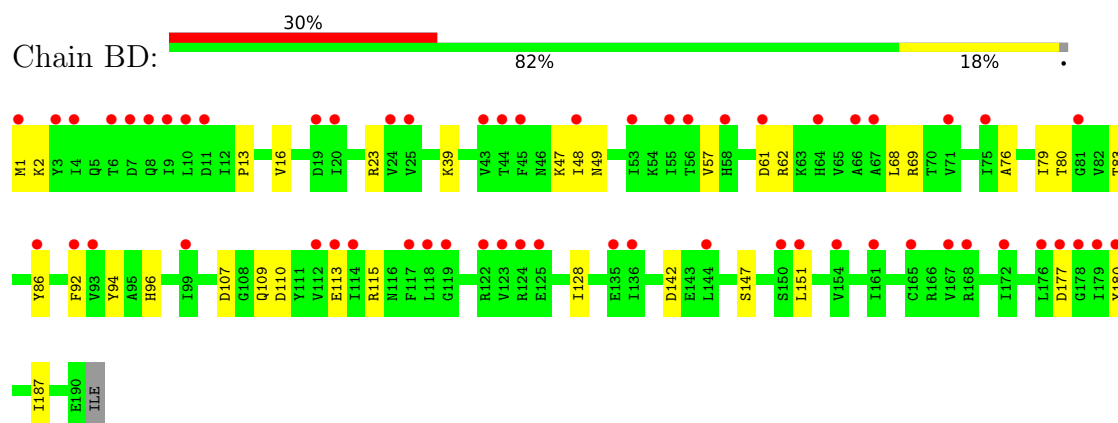
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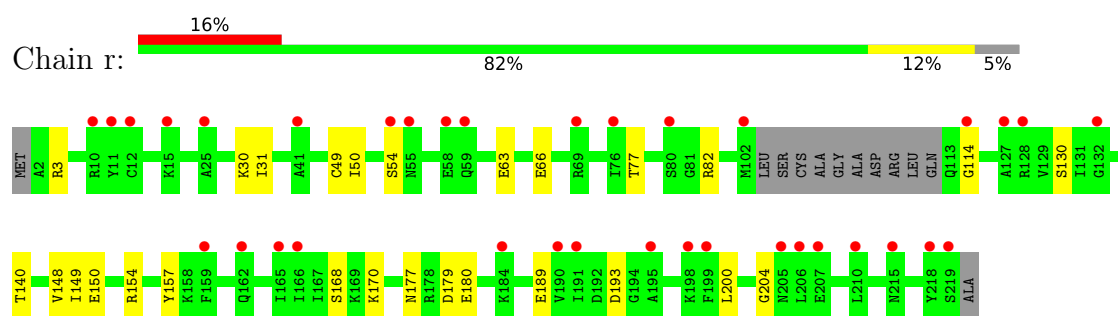
• Molecule 11: 60S ribosomal protein L9-B



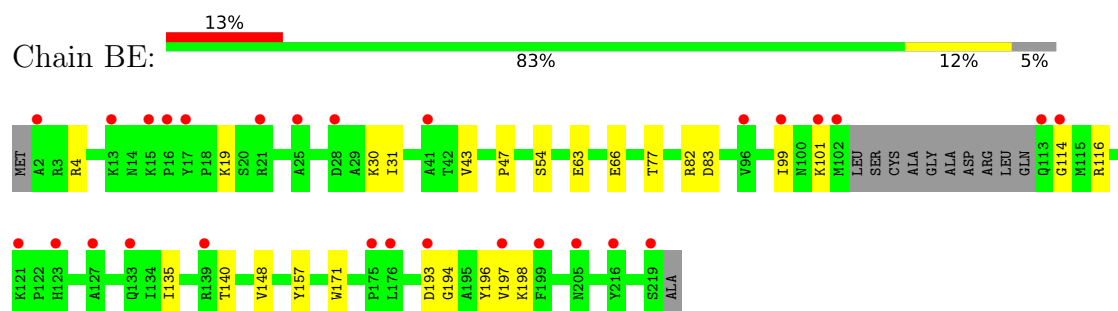
- Molecule 11: 60S ribosomal protein L9-B



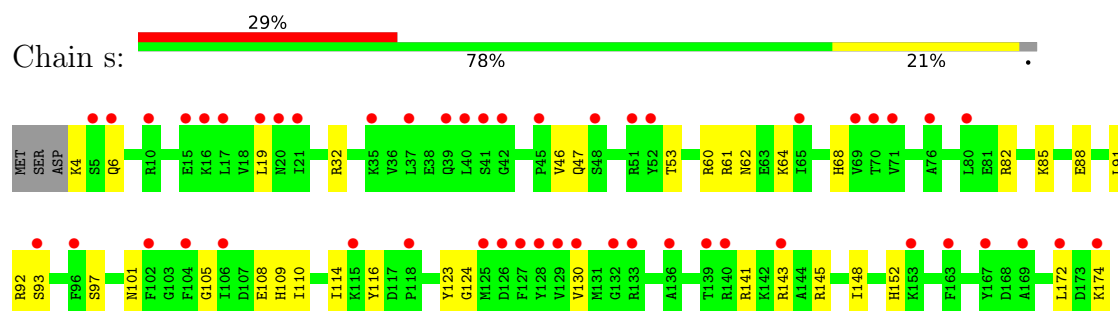
- Molecule 12: 60S ribosomal protein L10



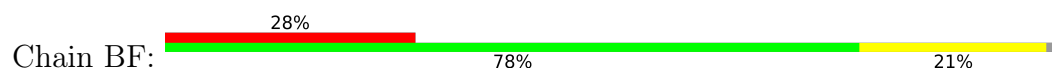
- Molecule 12: 60S ribosomal protein L10

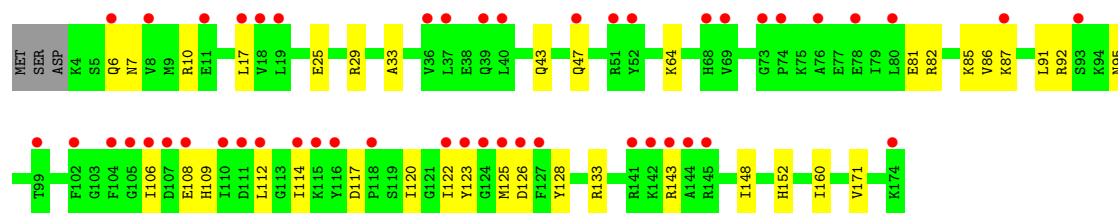


- Molecule 13: 60S ribosomal protein L11-B

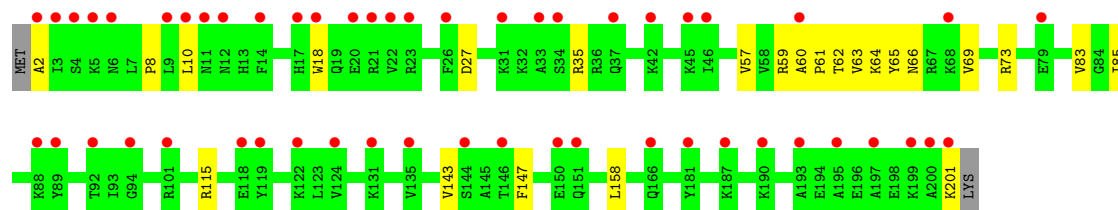
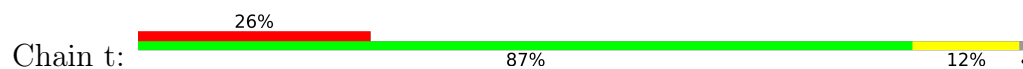


- Molecule 13: 60S ribosomal protein L11-B

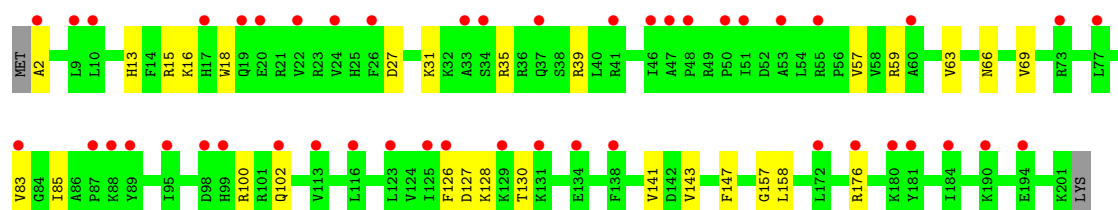
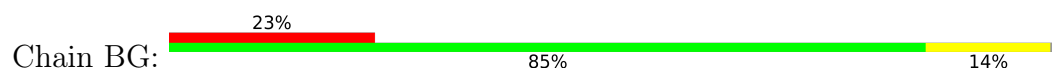




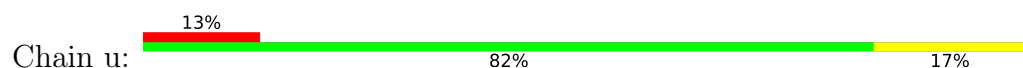
• Molecule 14: 60S ribosomal protein L13



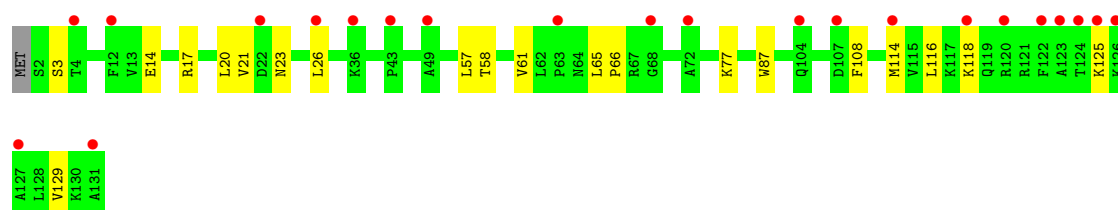
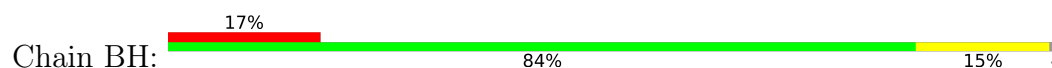
• Molecule 14: 60S ribosomal protein L13



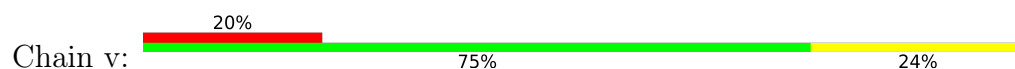
• Molecule 15: 60S ribosomal protein L14-B

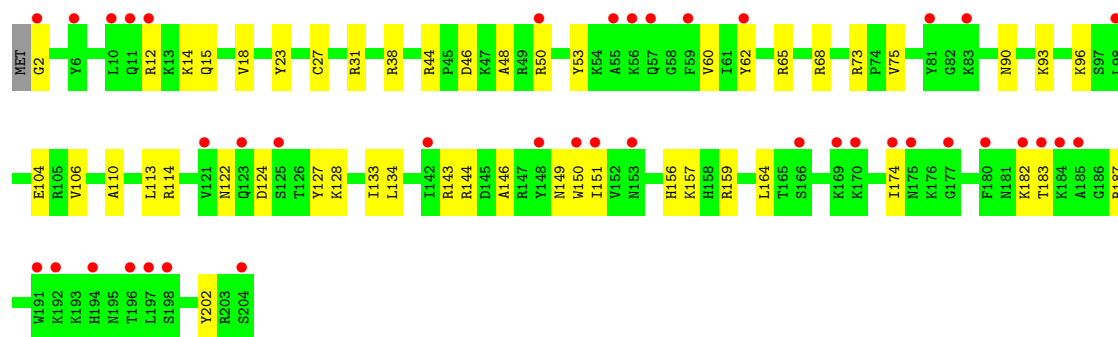


• Molecule 15: 60S ribosomal protein L14-B

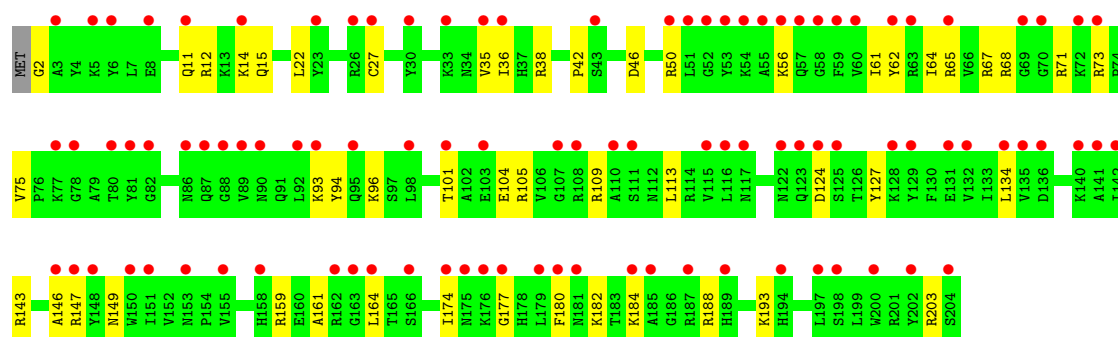


• Molecule 16: 60S ribosomal protein L15-A

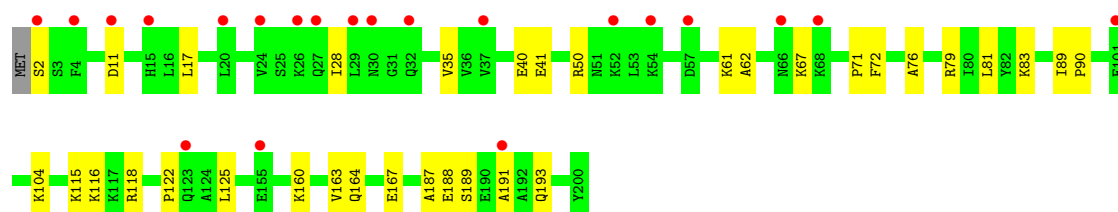
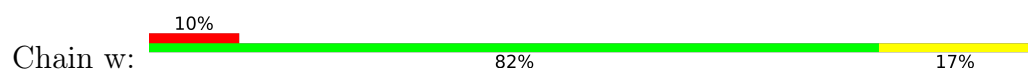




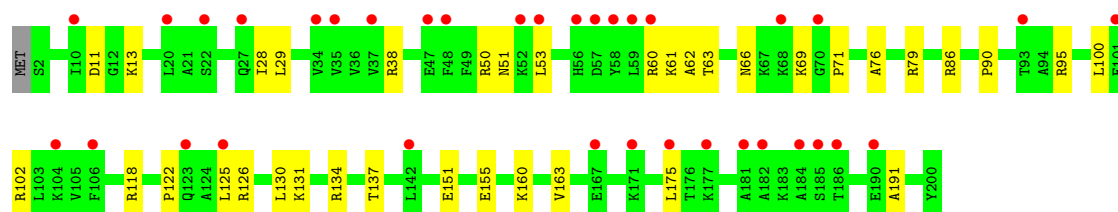
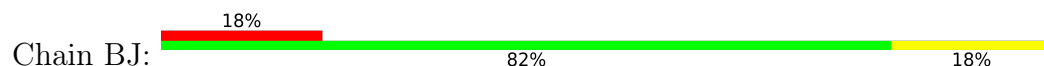
• Molecule 16: 60S ribosomal protein L15-A



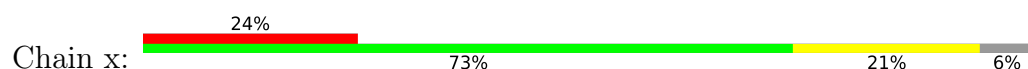
• Molecule 17: Ribosomal protein L13

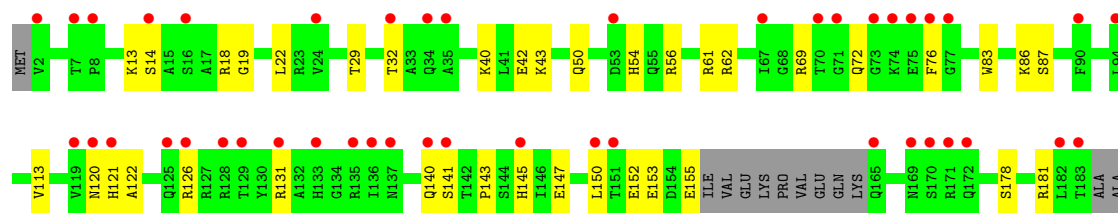


• Molecule 17: Ribosomal protein L13

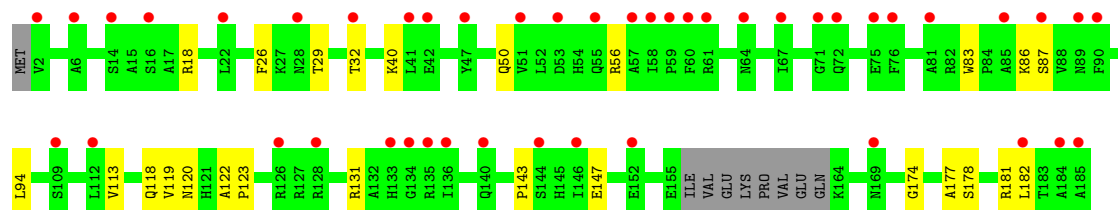
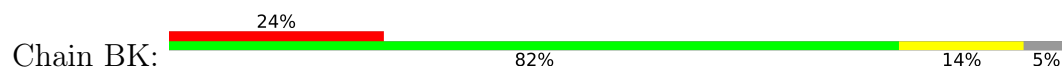


• Molecule 18: Ribosomal protein L22

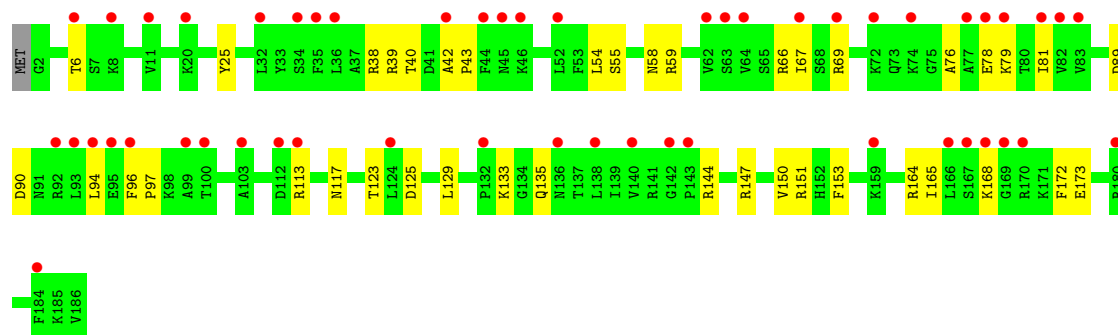
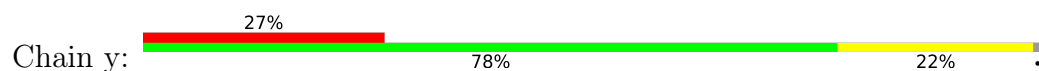




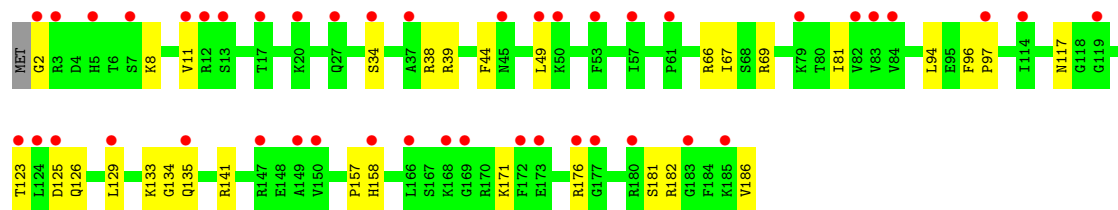
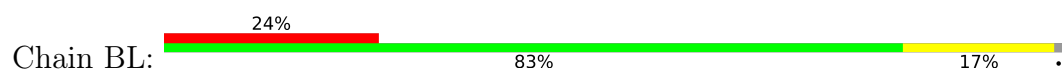
• Molecule 18: Ribosomal protein L22



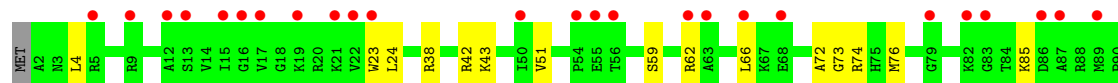
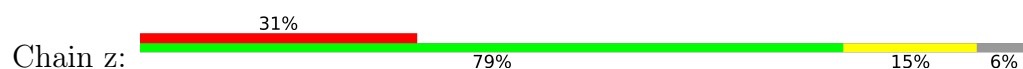
• Molecule 19: 60S ribosomal protein L18-A

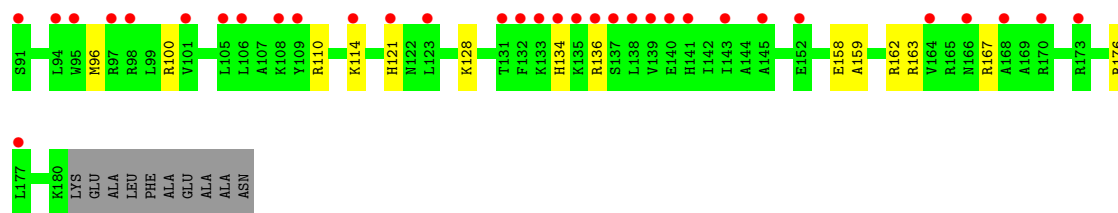


• Molecule 19: 60S ribosomal protein L18-A

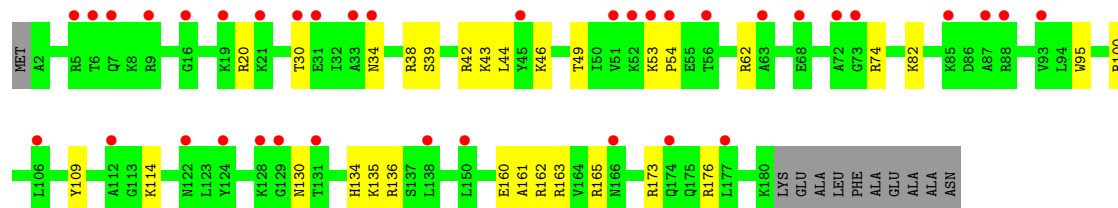
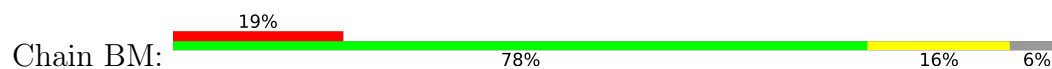


• Molecule 20: 60S ribosomal protein L19-A

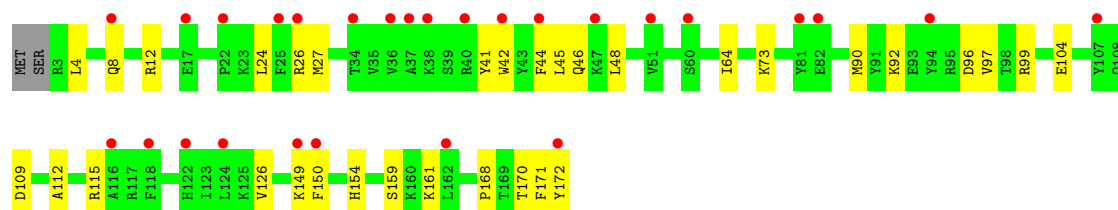
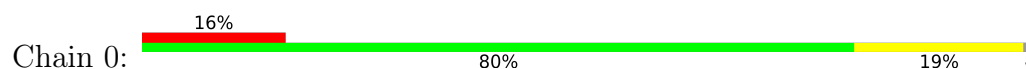




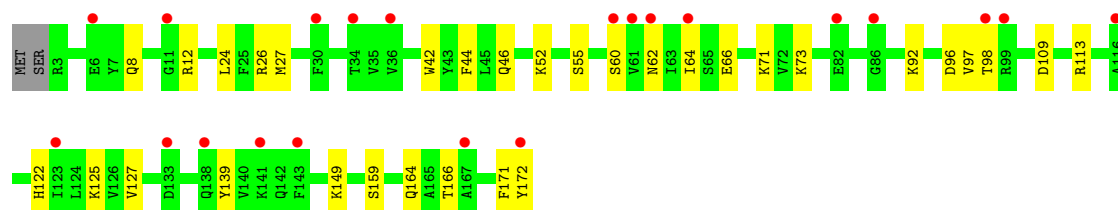
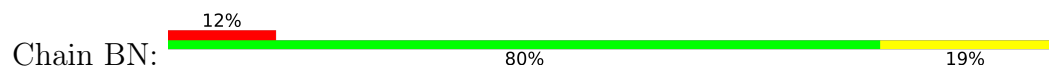
• Molecule 20: 60S ribosomal protein L19-A



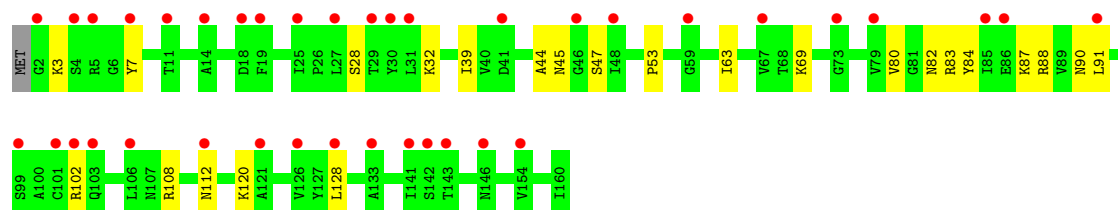
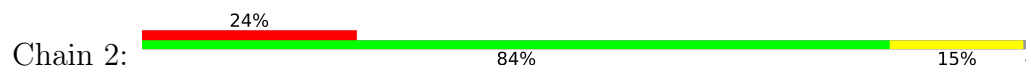
• Molecule 21: 60S ribosomal protein L20



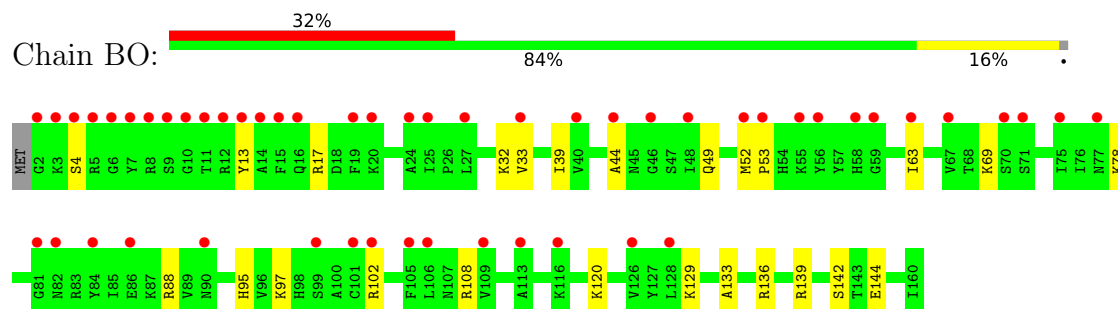
• Molecule 21: 60S ribosomal protein L20



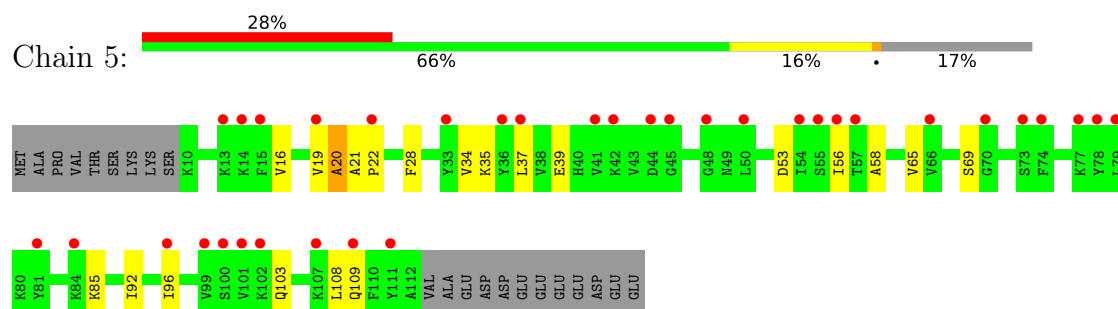
• Molecule 22: 60S ribosomal protein L21-A



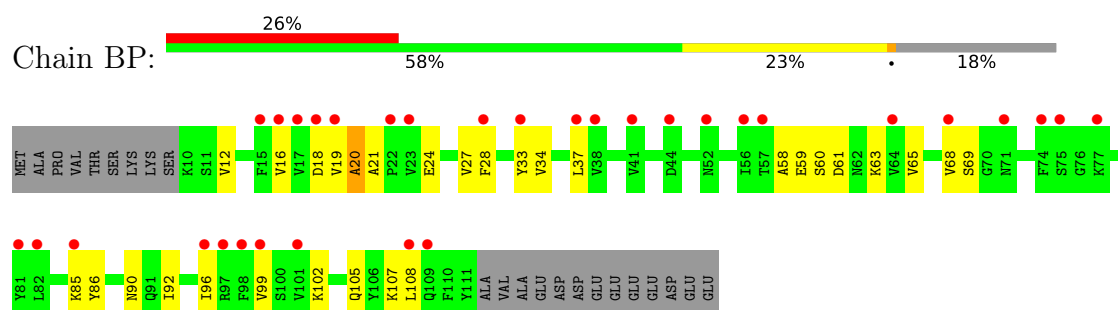
- Molecule 22: 60S ribosomal protein L21-A



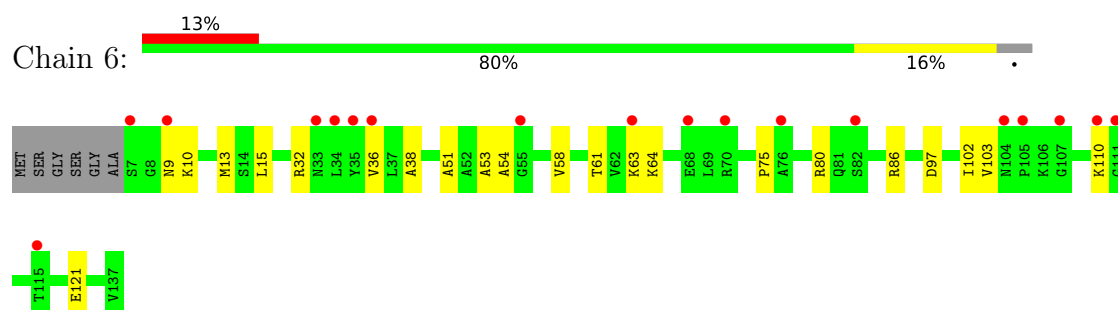
- Molecule 23: 60S ribosomal protein L22-B



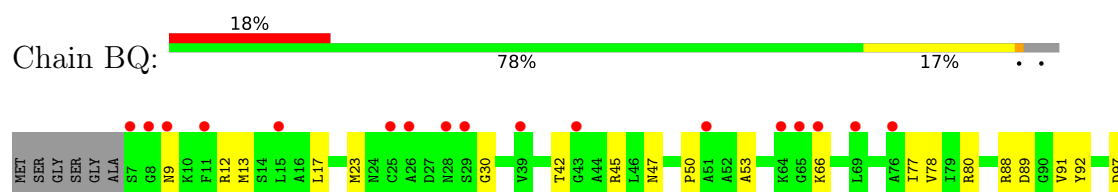
- Molecule 23: 60S ribosomal protein L22-B

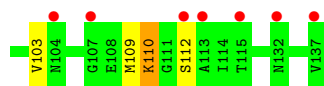


- Molecule 24: 60S ribosomal protein L23-A

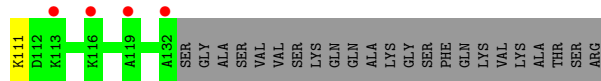
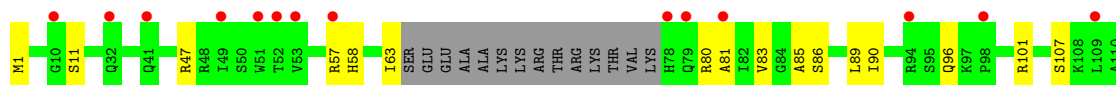


- Molecule 24: 60S ribosomal protein L23-A

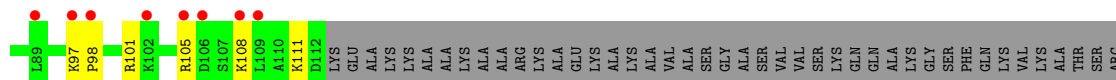
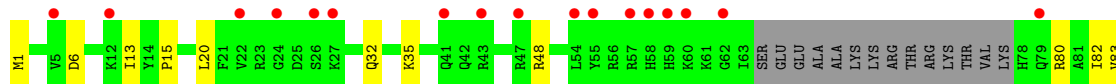




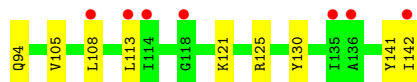
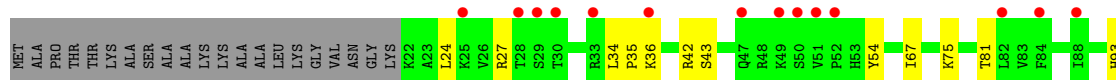
- Molecule 25: 60S ribosomal protein L24-A



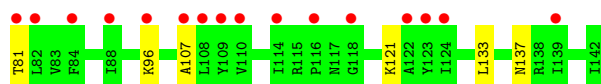
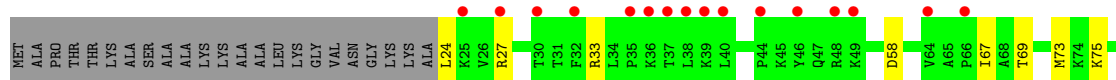
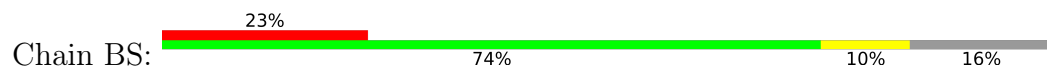
- Molecule 25: 60S ribosomal protein L24-A



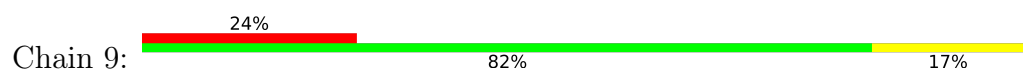
- Molecule 26: 60S ribosomal protein L25

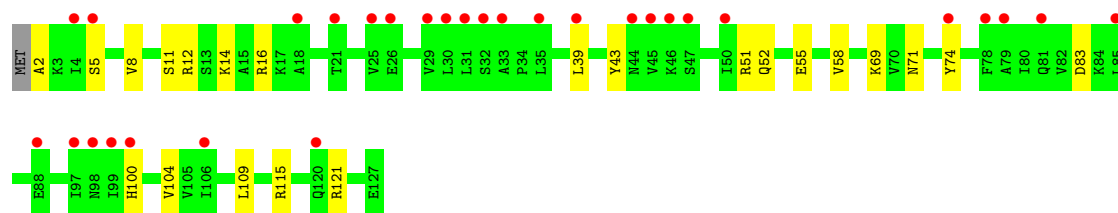


- Molecule 26: 60S ribosomal protein L25

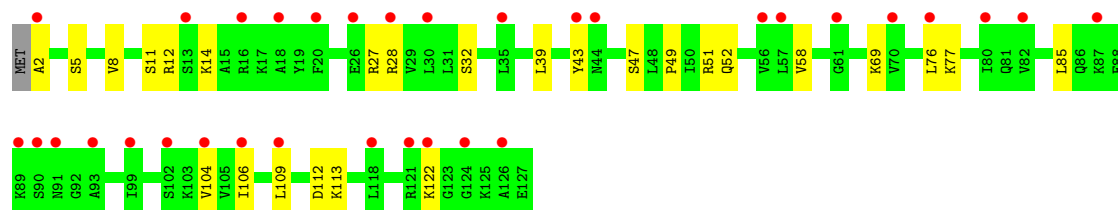
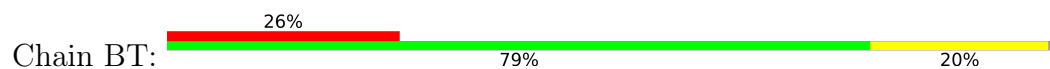


- Molecule 27: Ribosomal protein L24

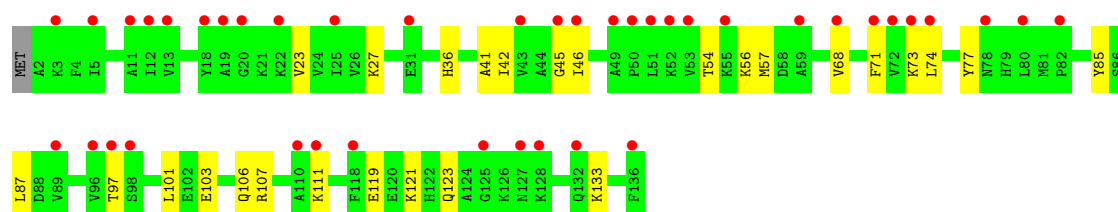
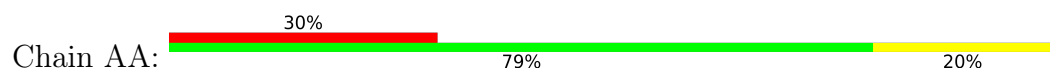




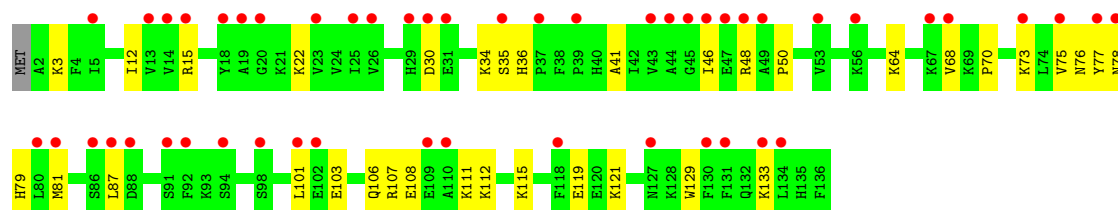
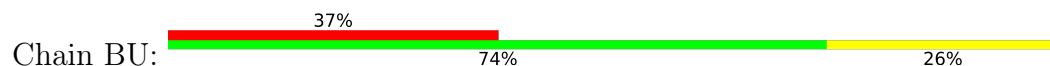
• Molecule 27: Ribosomal protein L24



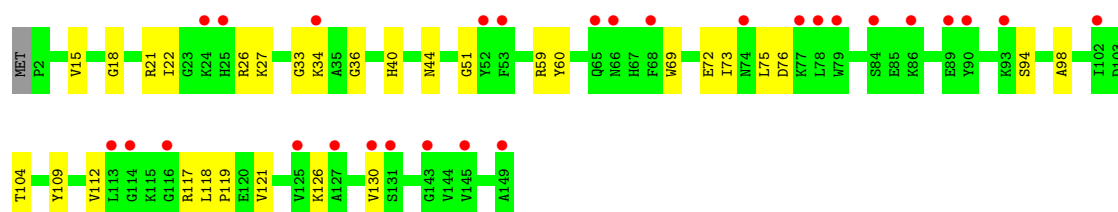
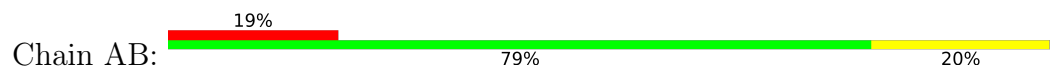
• Molecule 28: 60S ribosomal protein L27



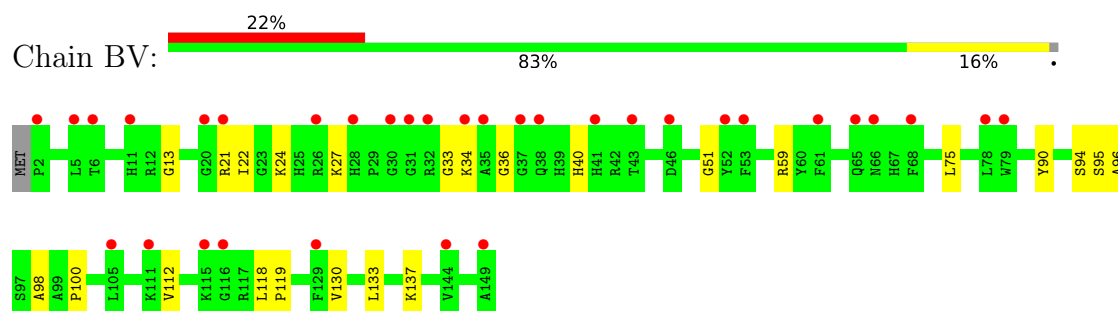
• Molecule 28: 60S ribosomal protein L27



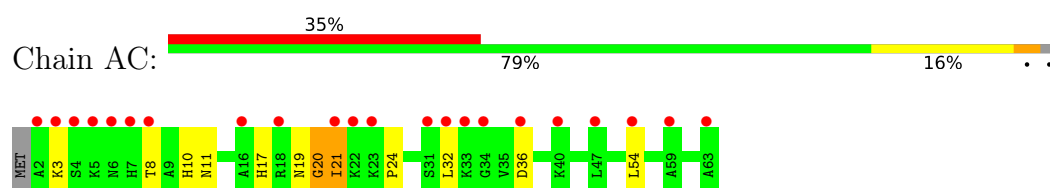
• Molecule 29: 60S ribosomal protein L28



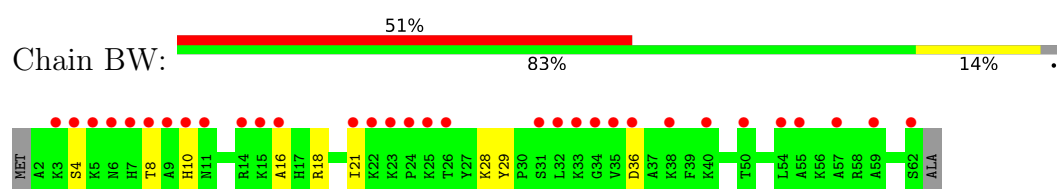
- Molecule 29: 60S ribosomal protein L28



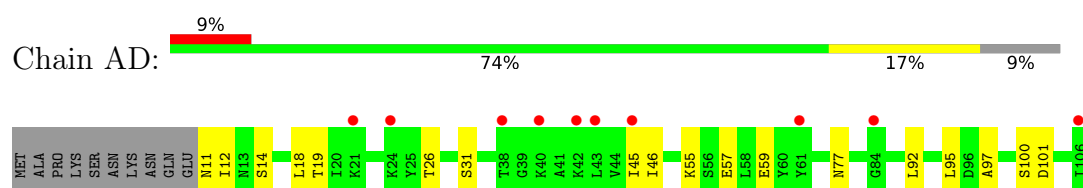
- Molecule 30: 60S ribosomal protein L29



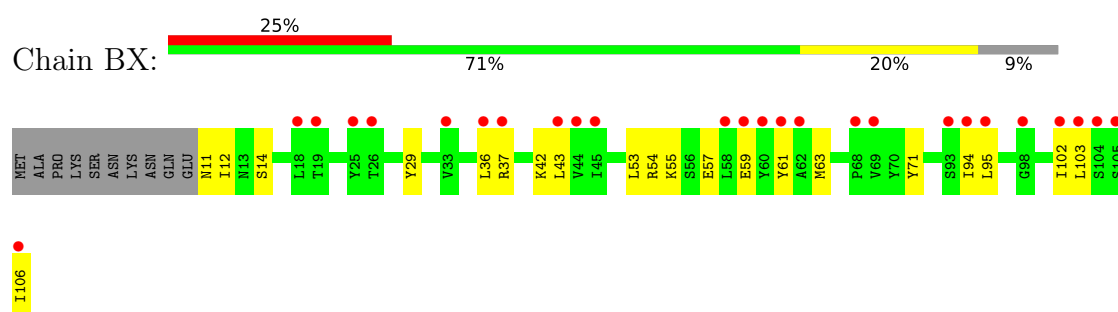
- Molecule 30: 60S ribosomal protein L29



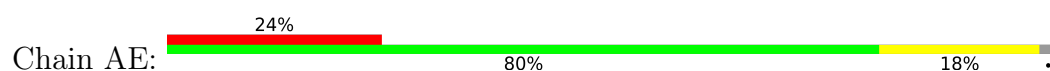
- Molecule 31: 60S ribosomal protein L30

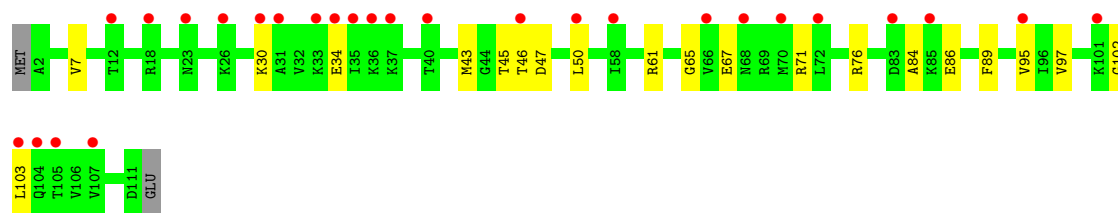


- Molecule 31: 60S ribosomal protein L30

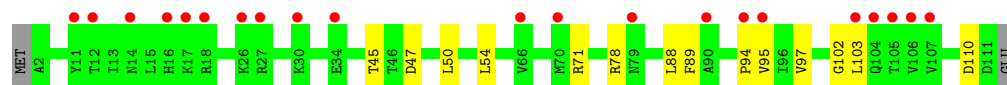
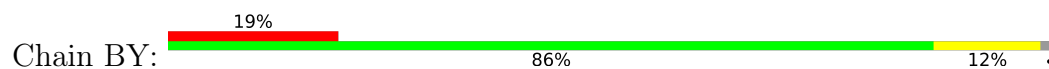


- Molecule 32: 60S ribosomal protein L31-B

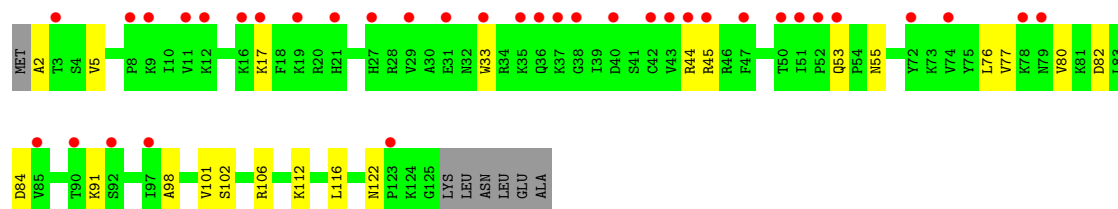
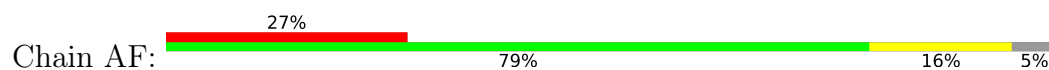




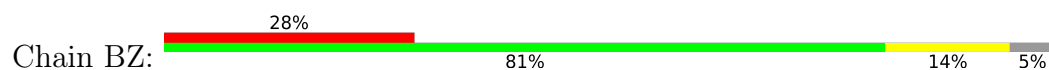
- Molecule 32: 60S ribosomal protein L31-B



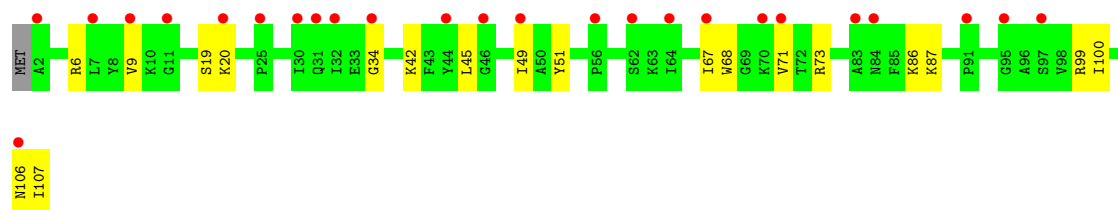
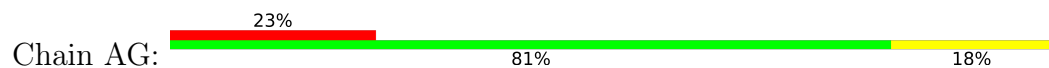
- Molecule 33: 60S ribosomal protein L32



- Molecule 33: 60S ribosomal protein L32

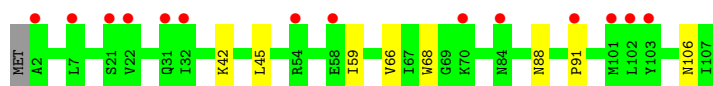


- Molecule 34: 60S ribosomal protein L33-A

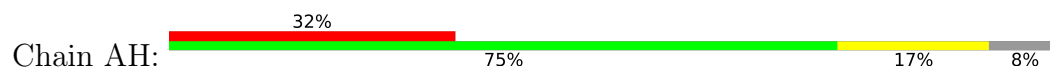


- Molecule 34: 60S ribosomal protein L33-A

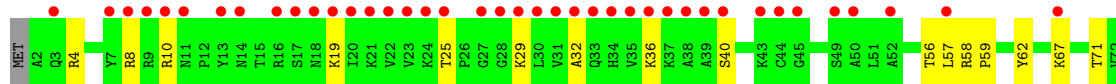
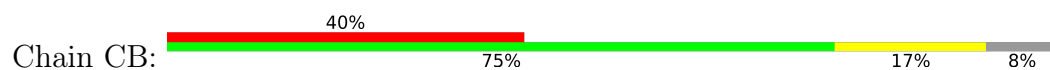




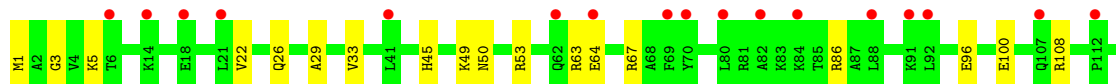
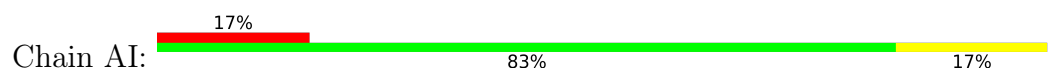
- Molecule 35: 60S ribosomal protein L34-B



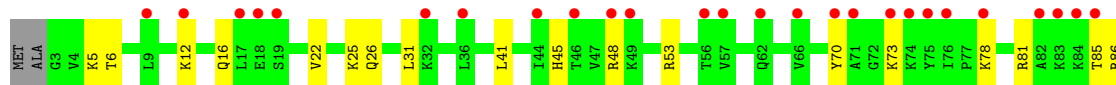
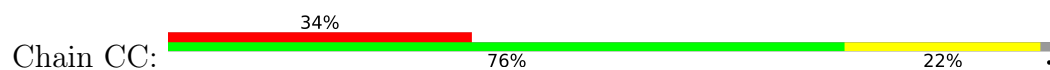
- Molecule 35: 60S ribosomal protein L34-B



- Molecule 36: Ribosomal protein L29

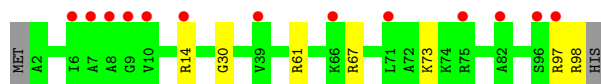


- Molecule 36: Ribosomal protein L29

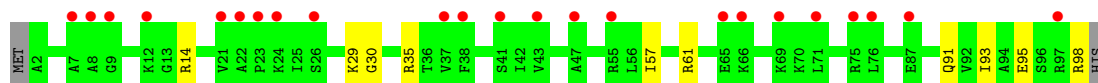
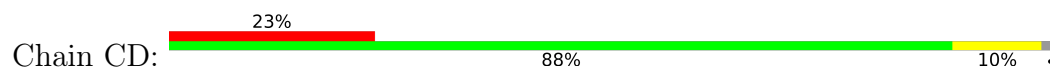


- Molecule 37: 60S ribosomal protein L36

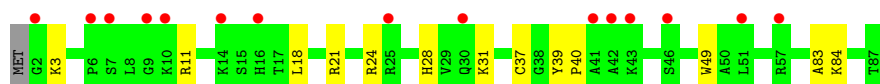
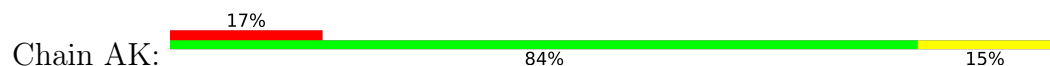




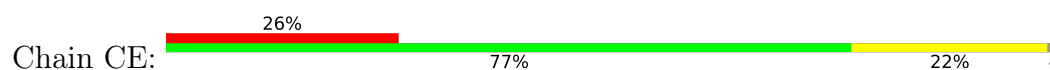
- Molecule 37: 60S ribosomal protein L36



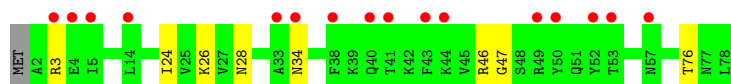
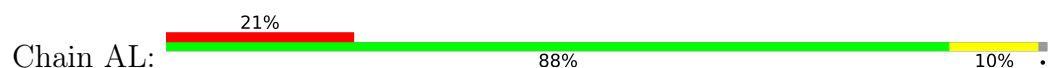
- Molecule 38: 60S ribosomal protein L37-B



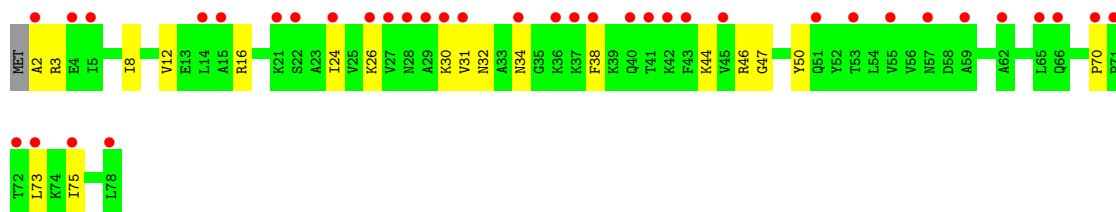
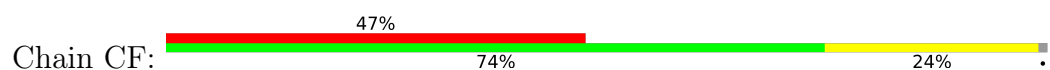
- Molecule 38: 60S ribosomal protein L37-B



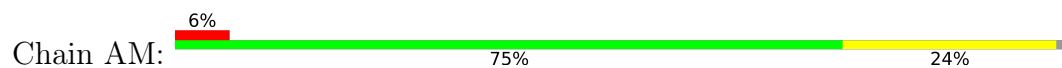
- Molecule 39: 60S ribosomal protein L38

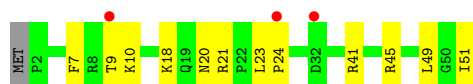


- Molecule 39: 60S ribosomal protein L38

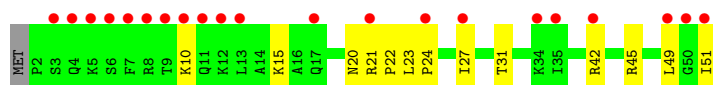
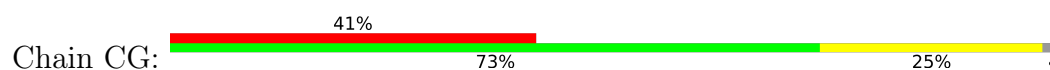


- Molecule 40: 60S ribosomal protein L39

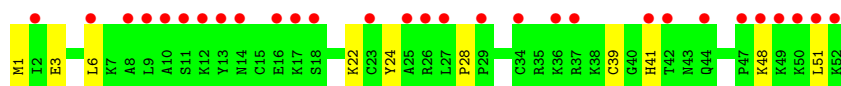
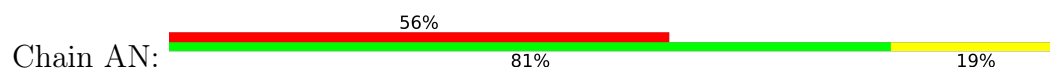




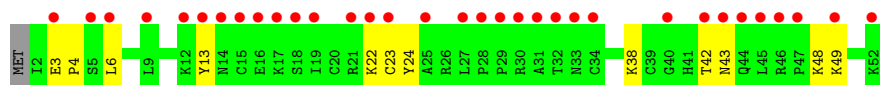
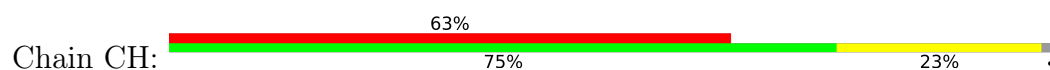
- Molecule 40: 60S ribosomal protein L39



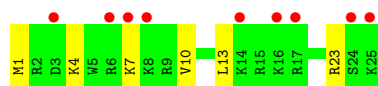
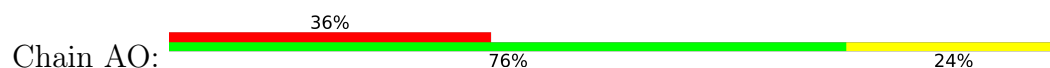
- Molecule 41: 60S ribosomal protein L40-B



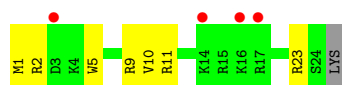
- Molecule 41: 60S ribosomal protein L40-B



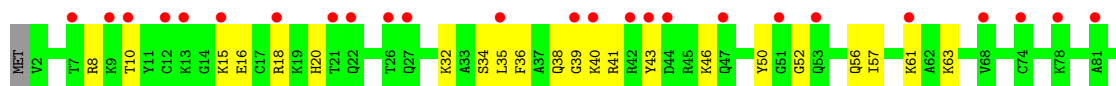
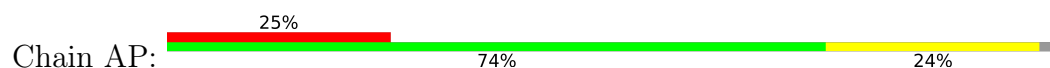
- Molecule 42: 60S ribosomal protein L41

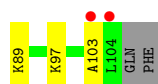


- Molecule 42: 60S ribosomal protein L41

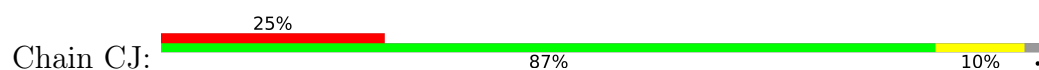


- Molecule 43: 60S ribosomal protein L42-B

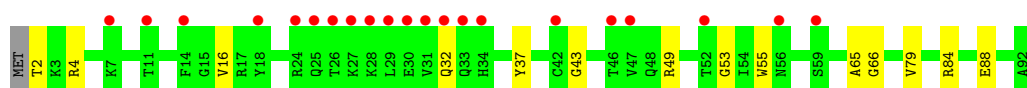
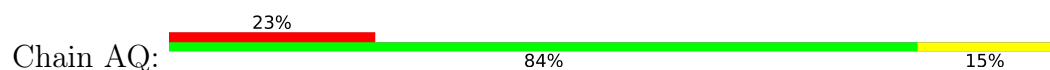




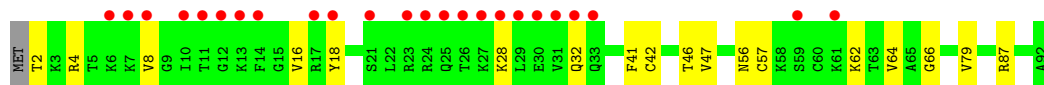
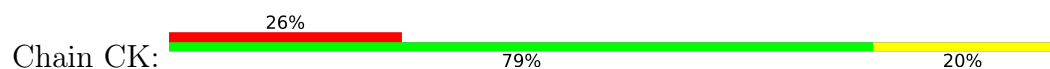
- Molecule 43: 60S ribosomal protein L42-B



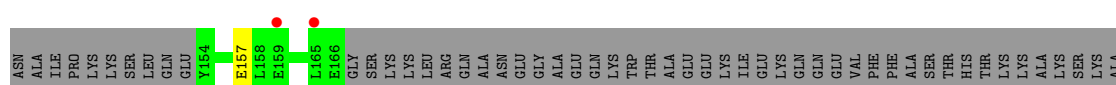
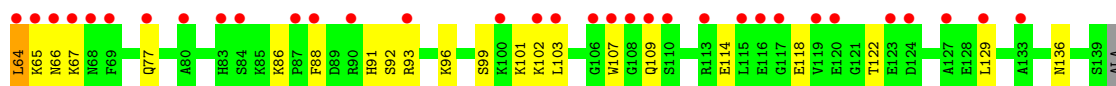
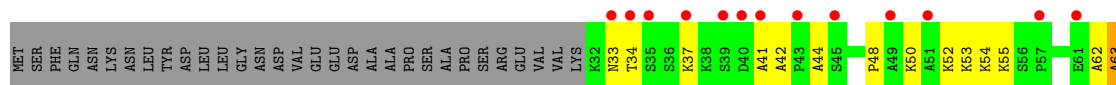
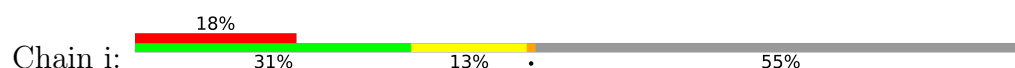
- Molecule 44: 60S ribosomal protein L43-A



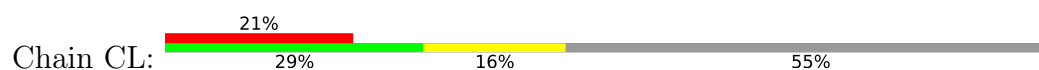
- Molecule 44: 60S ribosomal protein L43-A

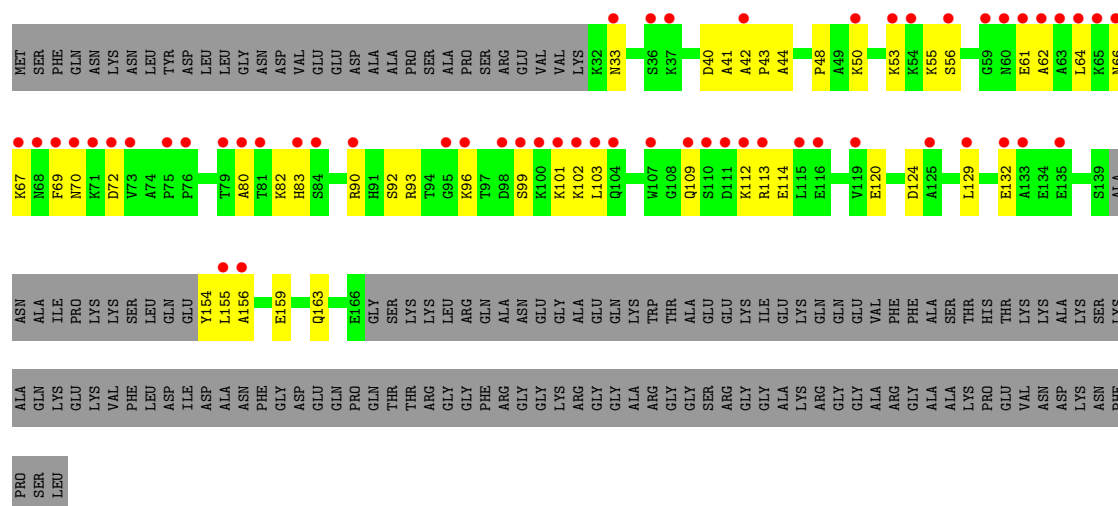


- Molecule 45: 60S ribosomal protein CAALFM_C304810CA

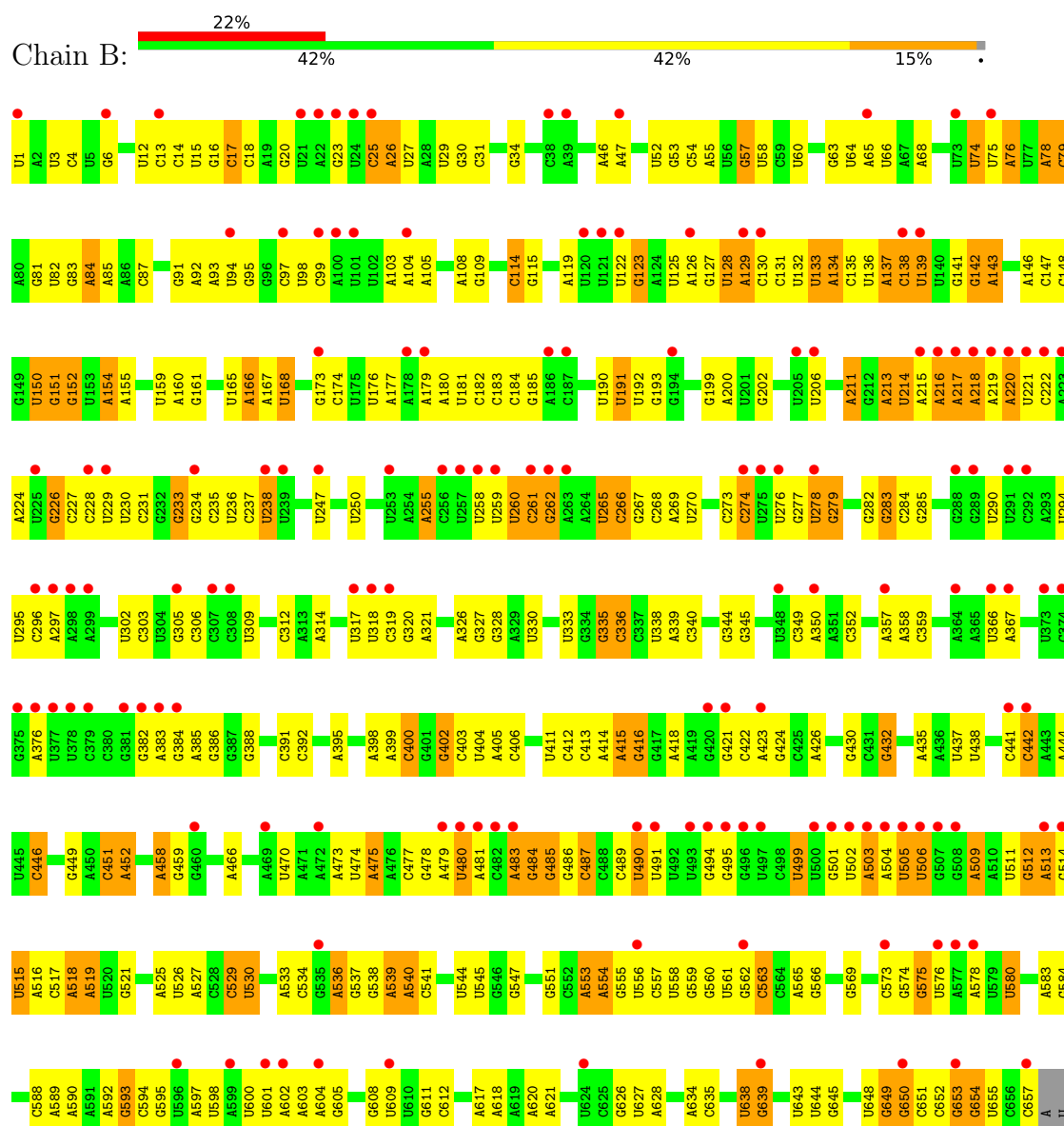


- Molecule 45: 60S ribosomal protein CAALFM_C304810CA

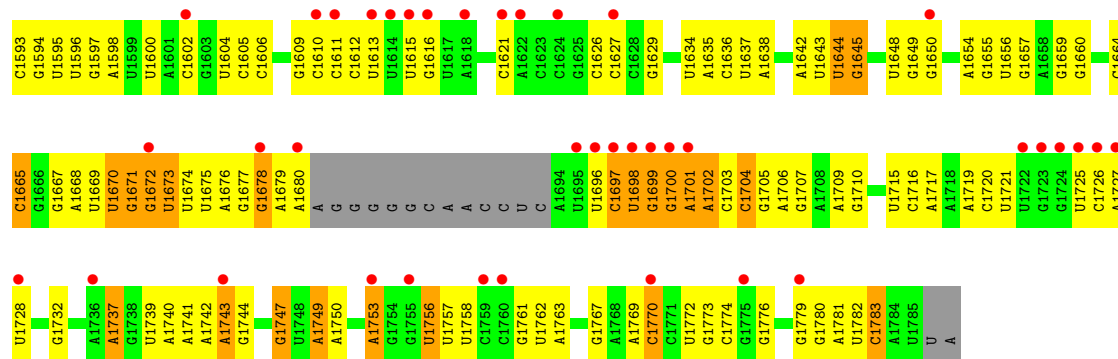




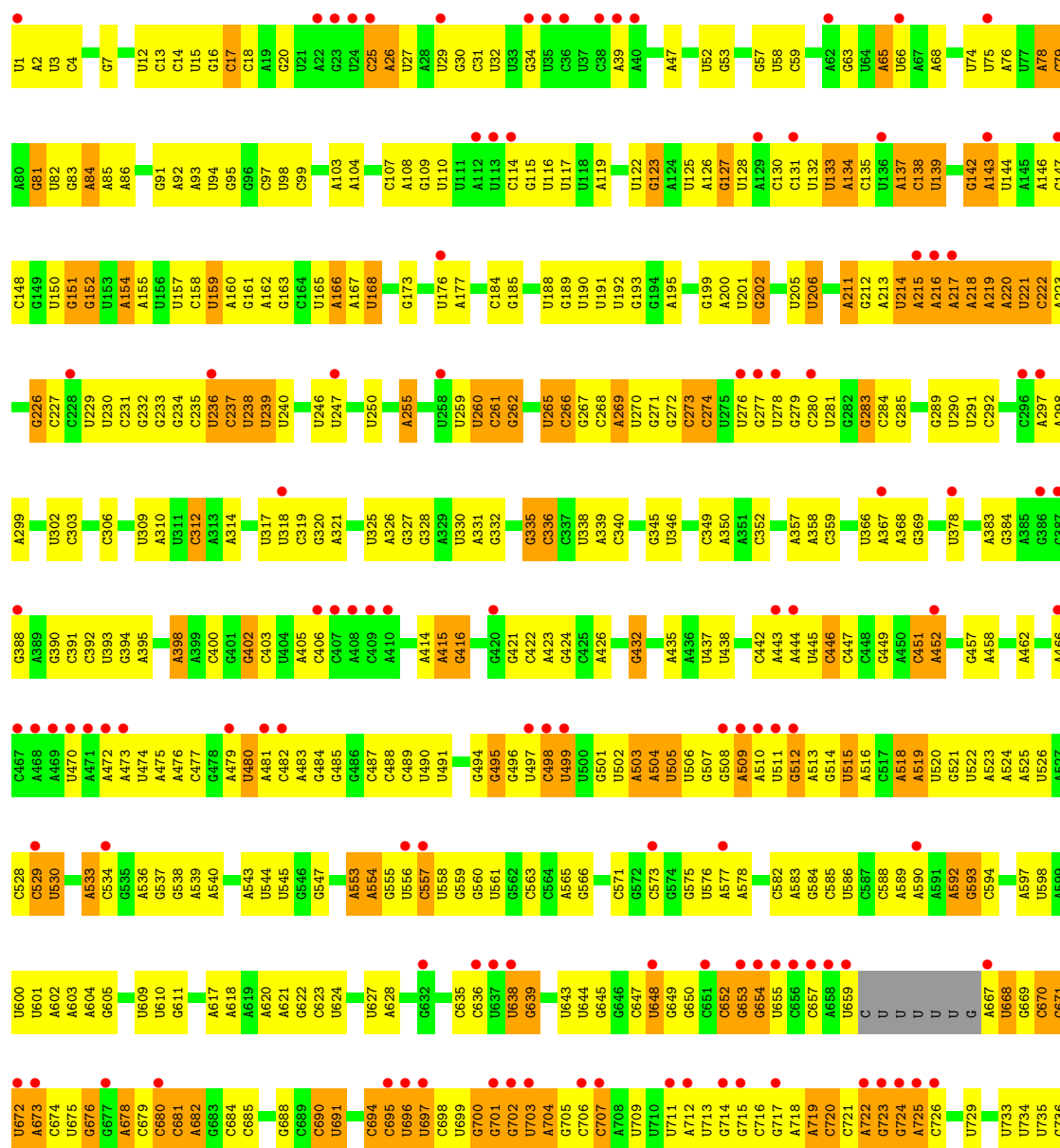
• Molecule 46: 18S



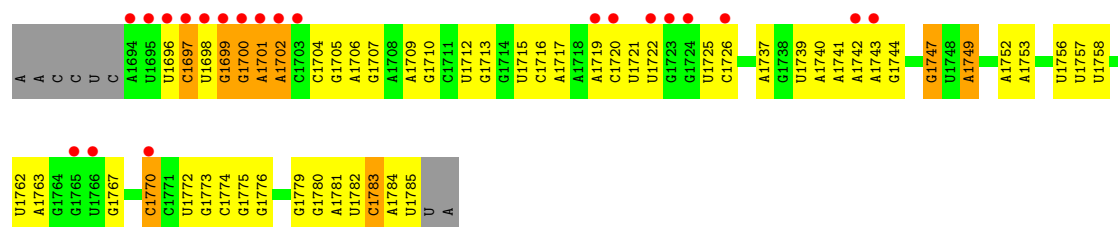
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A1457	U1246	U1247	U1247	G1246	U1170	U1100	C941	A869	A795	U727	U
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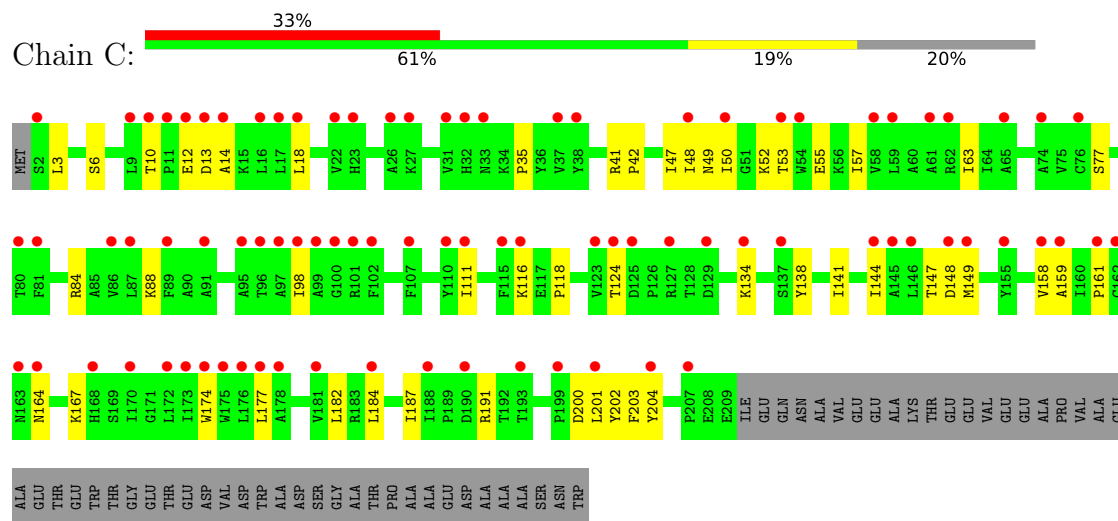
• Molecule 46: 18S



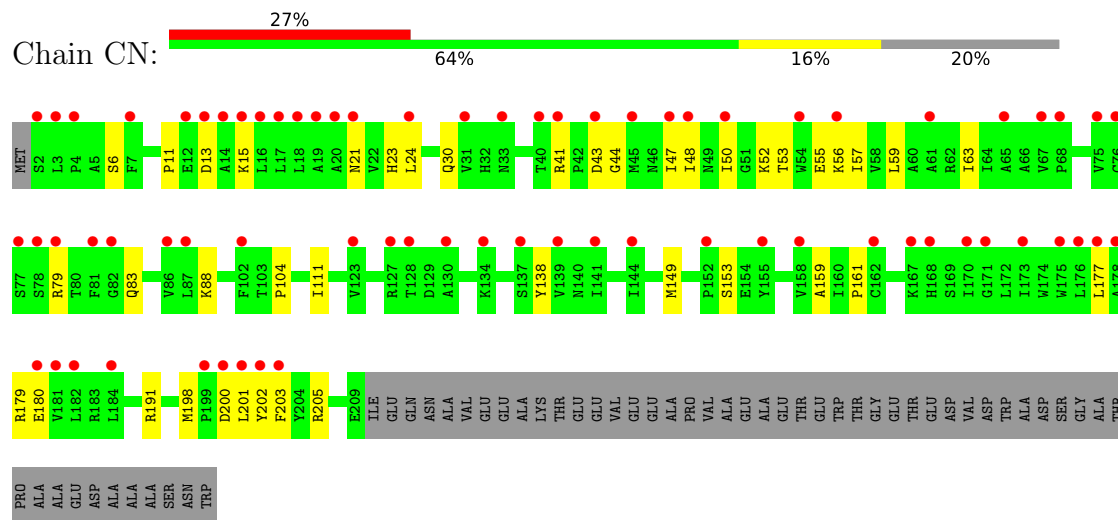
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A1618	U1547	G1479	U1341	C1201	A1127	U1040	U946	C877	U811	A739
G1621	C1412	A1480	A1342	A1202	A1128	C1041	U947	U878	U812	A740
A1622	G1413	U1483	G1343	G1203	U1129	U1042	A948	U879	U813	A741
C1623	G1414	U1484	C1344	A1204	U1130	U1043	A951	G880	A814	U744
G1624	G1415	U1485	A1345	C1205	U1131	U1044	A952	U881	U815	U745
U1625	U1416	G1486	U1346	U1206	G1132	U1045	U953	A885	U816	A746
C1626	C1417	C1487	U1347	C1207	A1133	U1046	C954	C886	U817	A747
G1627	U1418	U1491	G1348	A1211	G1135	U1047	G965	C887	U818	U751
C1628	G1421	U1492	U1349	A1212	G1138	U1048	C970	U888	U820	G750
G1629	U1422	G1493	U1350	G1213	A1142	U1049	G971	A890	G822	U752
U1630	U1423	G1494	G1352	G1214	A1144	A1055	G972	A891	C823	C753
A1635	G1424	U1495	U1285	A1215	G1143	U1056	U973	U824	U825	A756
C1636	C1425	C1496	U1286	U1216	C1144	C1057	U974	U826	U827	A759
U1637	C1426	U1497	A1355	U1217	A1145	U1058	C975	U828	U829	G760
A1638	G1431	G1498	U1356	G1218	C1146	G1059	G976	U830	C762	G761
U1644	U1432	U1500	U1295	A1219	A1147	C1060	U977	U831	C763	C762
G1645	A1433	A1501	U1296	C1220	G1148	A1061	A902	U832	U764	U765
U1648	U1436	A1502	A1297	A1221	G1149	C1062	U903	U833	U766	U766
C1649	U1437	A1503	U1298	A1222	A1150	C1063	A904	U834	C767	G767
G1650	C1438	U1504	U1299	A1223	G1151	U1064	C905	U835	U770	U769
U1651	U1439	C1505	U1300	G1226	A1152	U1065	C985	U836	G771	G771
C1652	G1440	U1508	G1301	A1227	G1155	A1066	A986	U837	A772	A772
U1656	U1441	G1509	C1302	G1228	A1156	C1067	G987	U838	U774	U774
G1657	C1442	A1510	G1303	A1229	G1157	A988	U989	U839	A775	A775
U1658	U1443	G1511	A1306	G1230	C1158	G1068	A911	U840	U778	U778
C1659	C1444	U1512	A1307	C1231	G1159	A1071	C912	U841	U779	U779
G1660	U1445	A1513	C1308	U1232	C1158	A1072	U913	U842	U784	U784
U1663	G1446	C1514	G1309	U1233	G1161	A1073	A914	U843	G785	G785
C1664	U1450	U1515	A1310	U1236	C1162	U1074	U994	U844	G786	G786
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U1671	U1458	G1524	C1317	U1243	U1171	U1083	A926	U851	U804	U804
G1672	C1459	U1525	C1318	U1244	A1174	U1084	C927	U852	U805	U805
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C1674	G1461	U1527	C1323	G1246	U1179	G1086	A929	U854	U807	U807
U1675	C1462	G1528	C1324	U1247	A1181	G1092	U930	U855	U874	U874
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G1679	C1468	U1536	A1328	G1251	G1185	A1101	C934	U859		
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A	G1470	U1538	A1330	G1253	G1187	G1026	A936	U861		
G	U1471	U1539	C1331	G1254	A1187	G1027	A937	U862		
C	G1472	G1540	A1332	G1255	U1189	U1028	G938	U863		
U1541	U1473	U1541	U1333	G1256	C1191	G1105	U939	U869		
A1542	U1474	A1542	U1335	G1262	A1193	U1105	A940	U871		
U1543	U1475	G1402	G1336	C1265	C1192	C1106	C941	U872		
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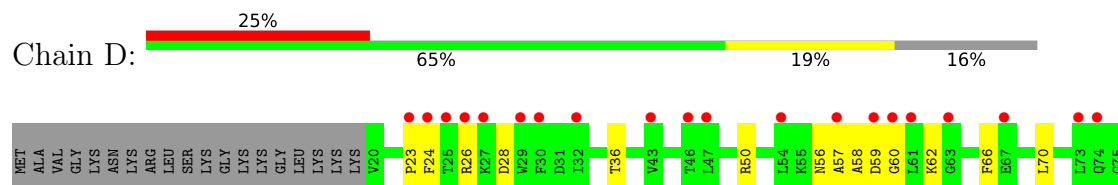
• Molecule 47: 40S ribosomal protein S0

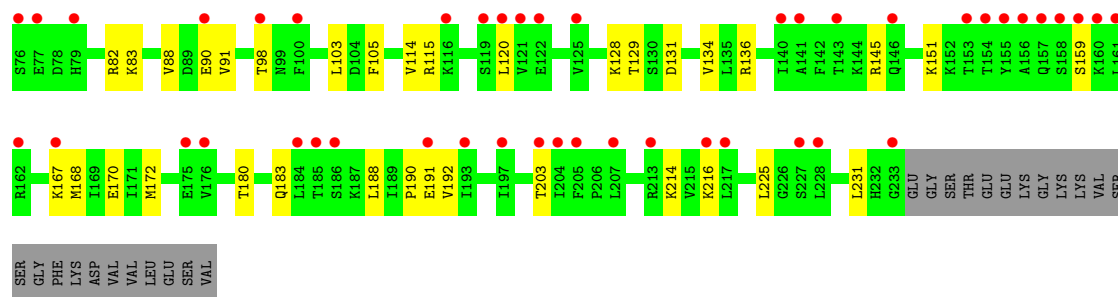


• Molecule 47: 40S ribosomal protein S0

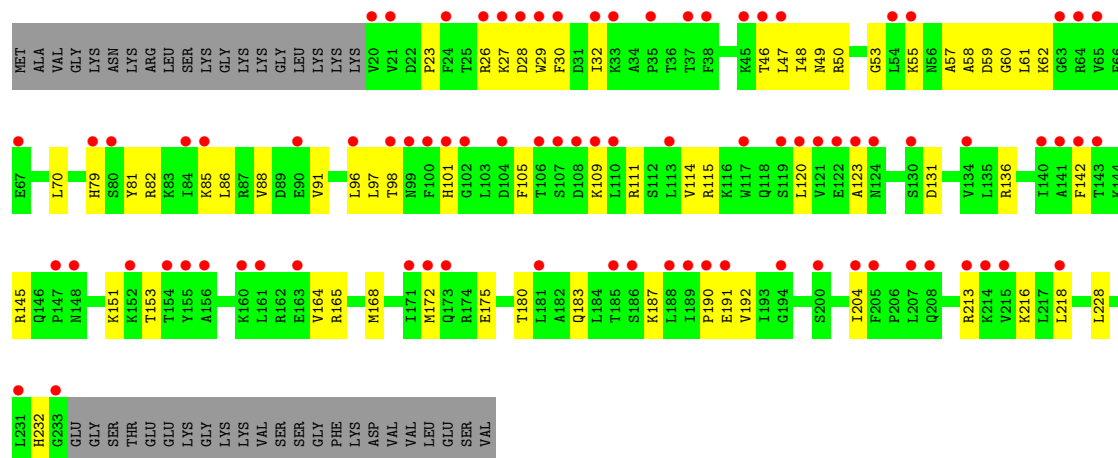


• Molecule 48: 40S ribosomal protein S1

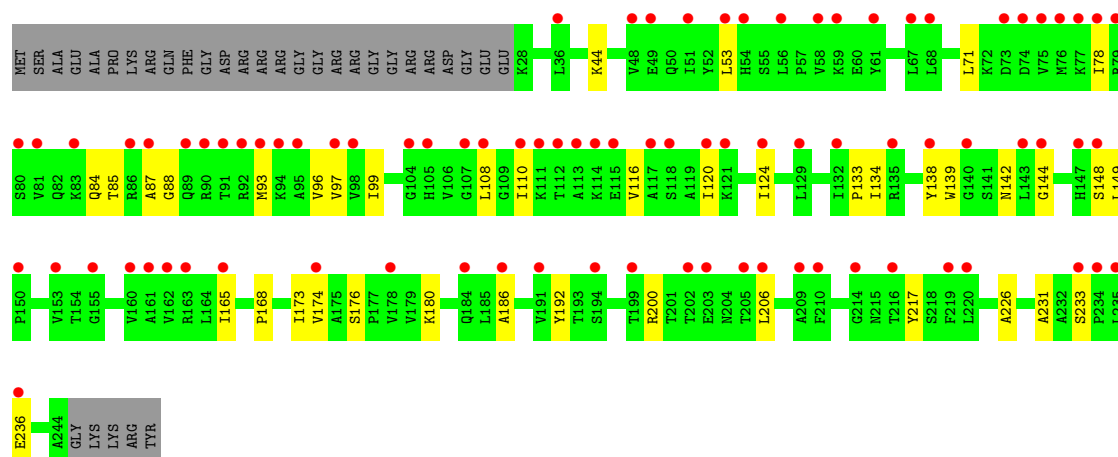




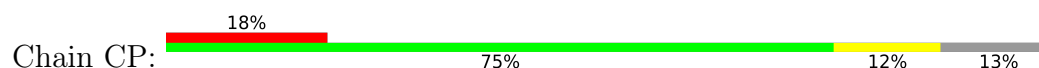
• Molecule 48: 40S ribosomal protein S1

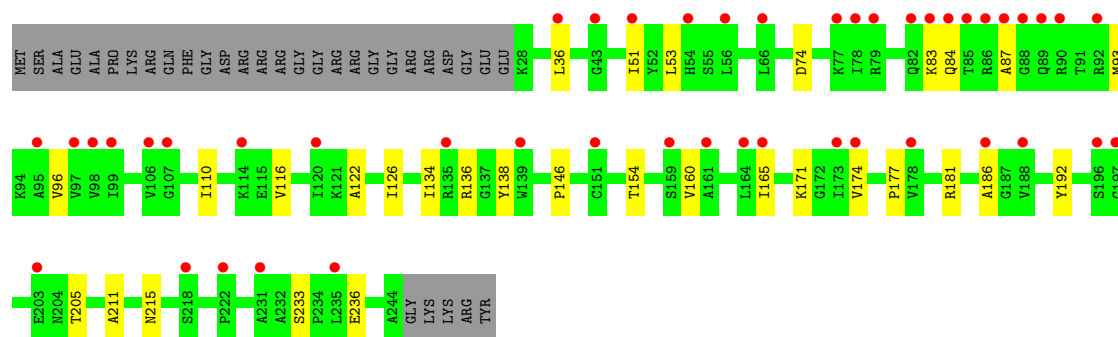


• Molecule 49: Ribosomal protein S5

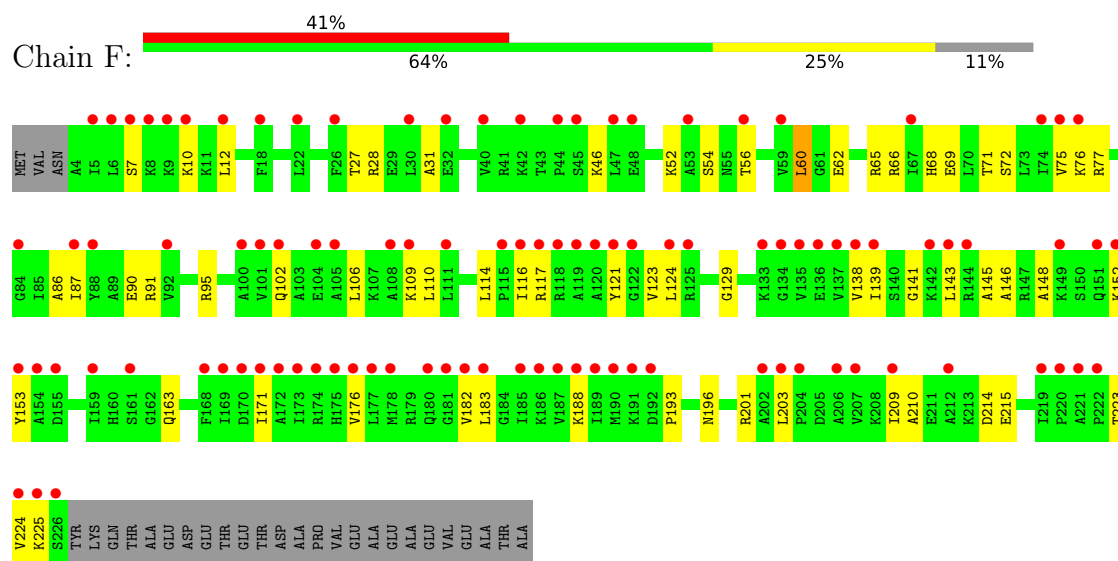


• Molecule 49: Ribosomal protein S5

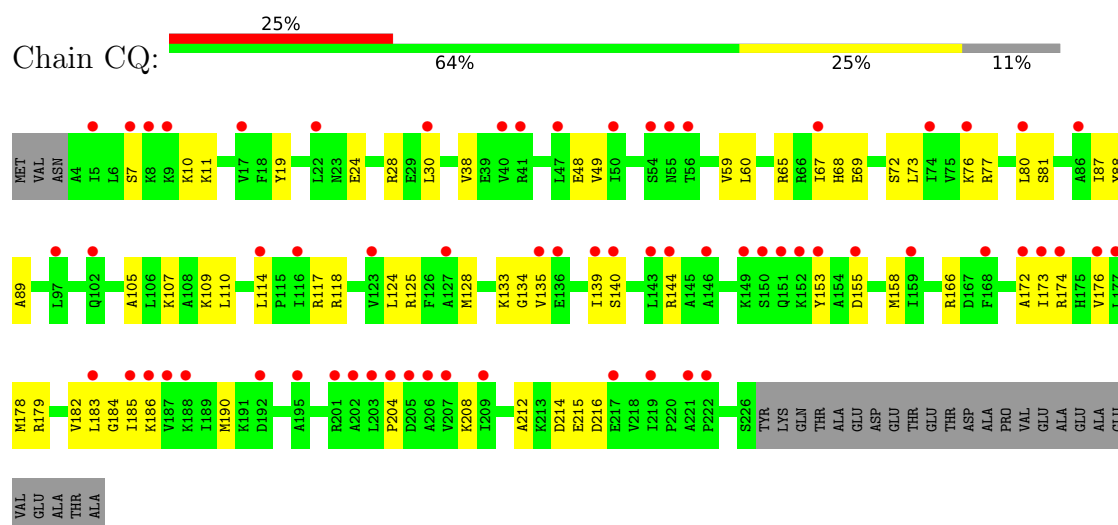




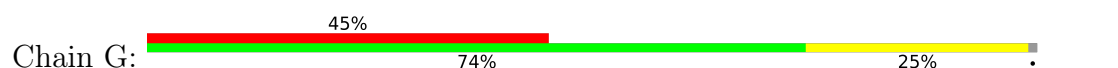
• Molecule 50: Ribosomal protein S3

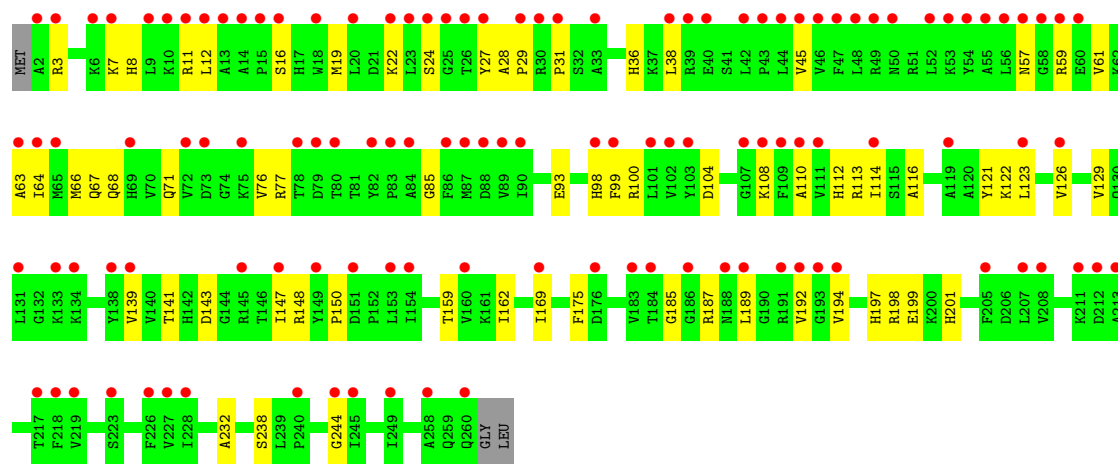


• Molecule 50: Ribosomal protein S3

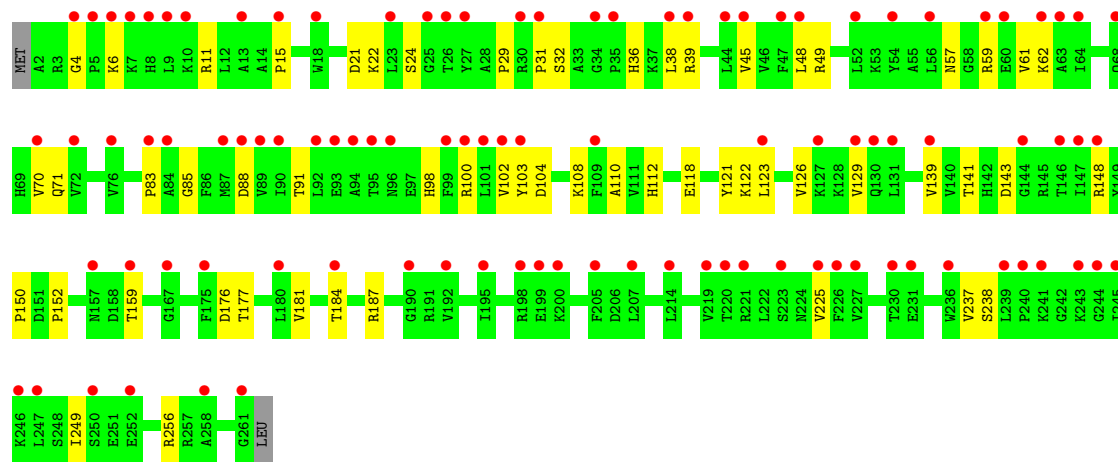
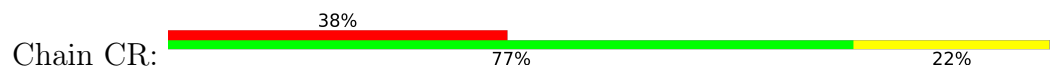


• Molecule 51: 40S ribosomal protein S4

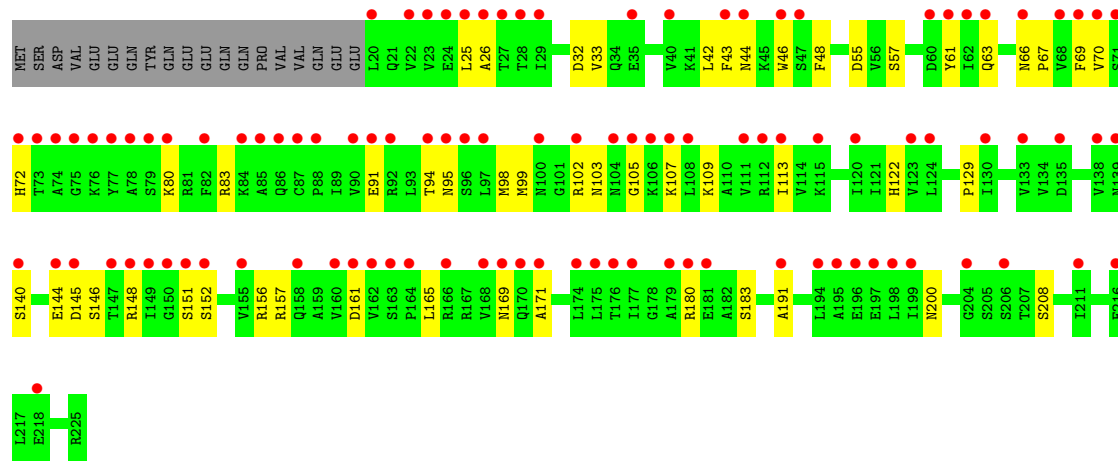




• Molecule 51: 40S ribosomal protein S4

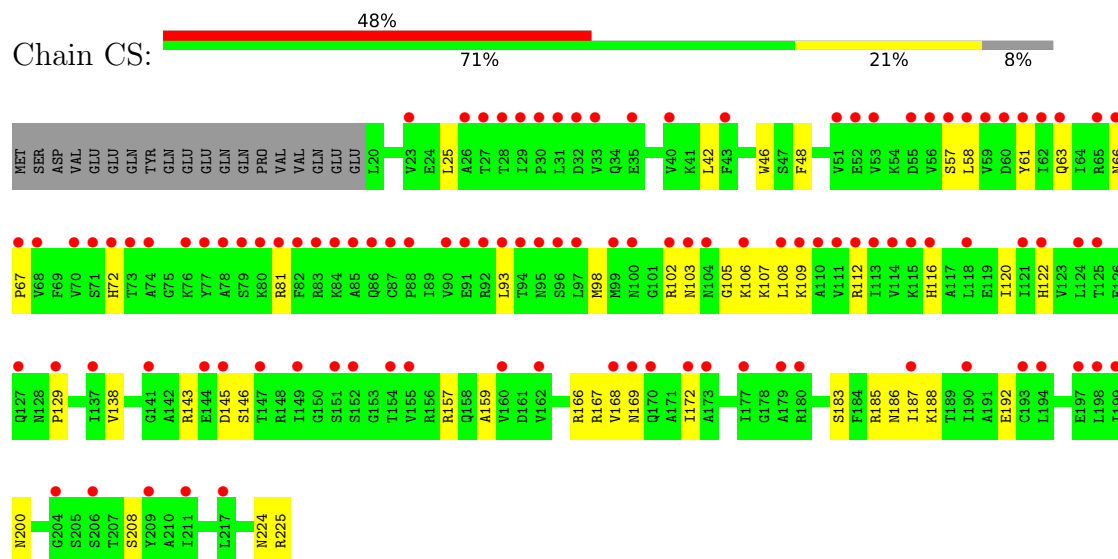


• Molecule 52: Ribosomal protein S7



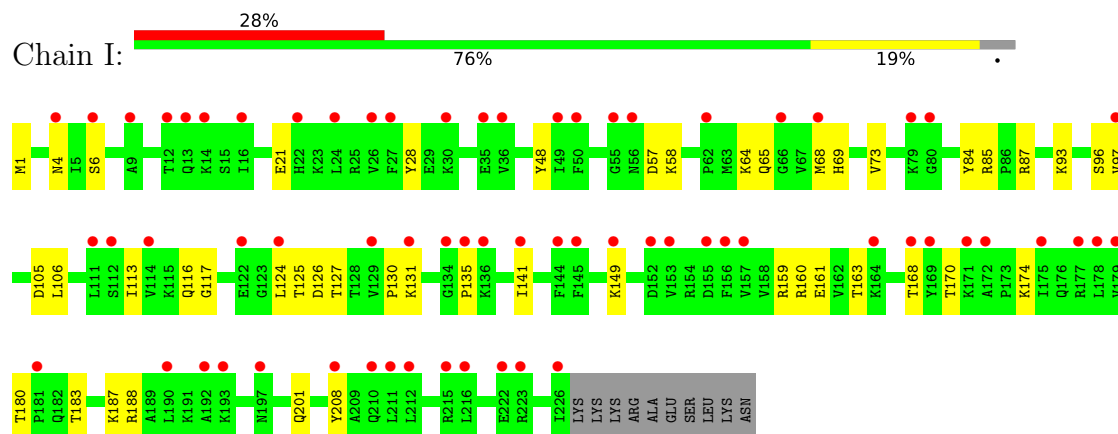
• Molecule 52: Ribosomal protein S7

Chain CS:



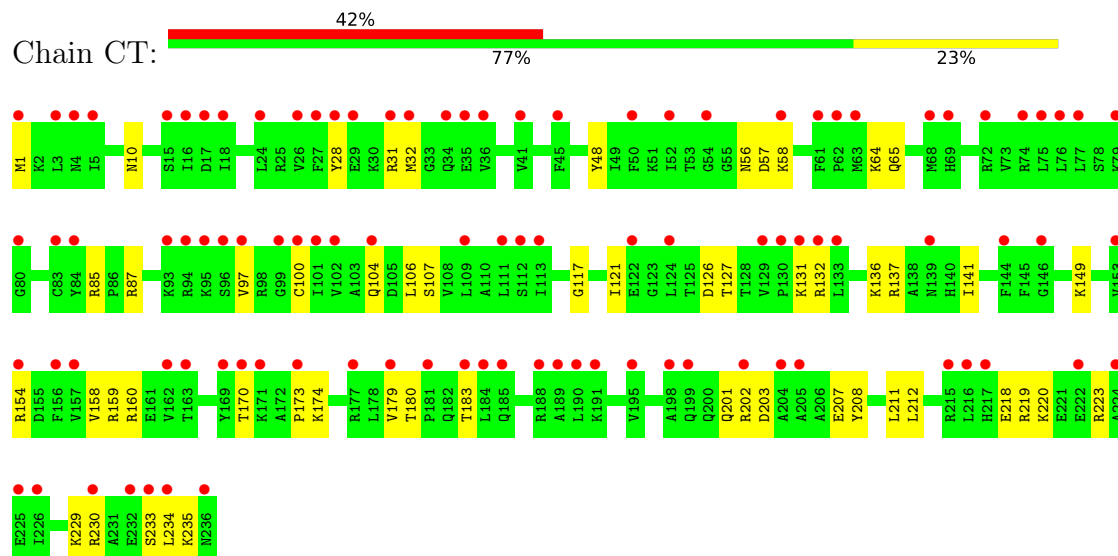
• Molecule 53: 40S ribosomal protein S6

Chain I:

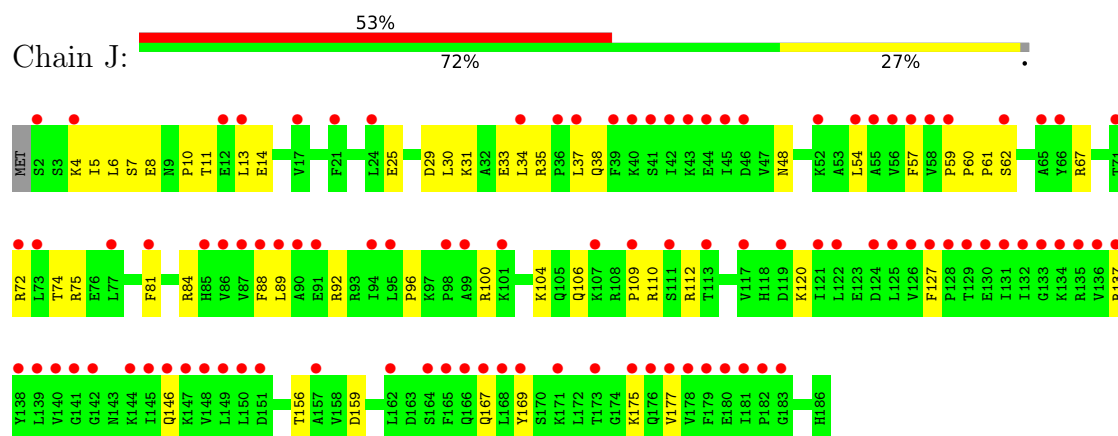


• Molecule 53: 40S ribosomal protein S6

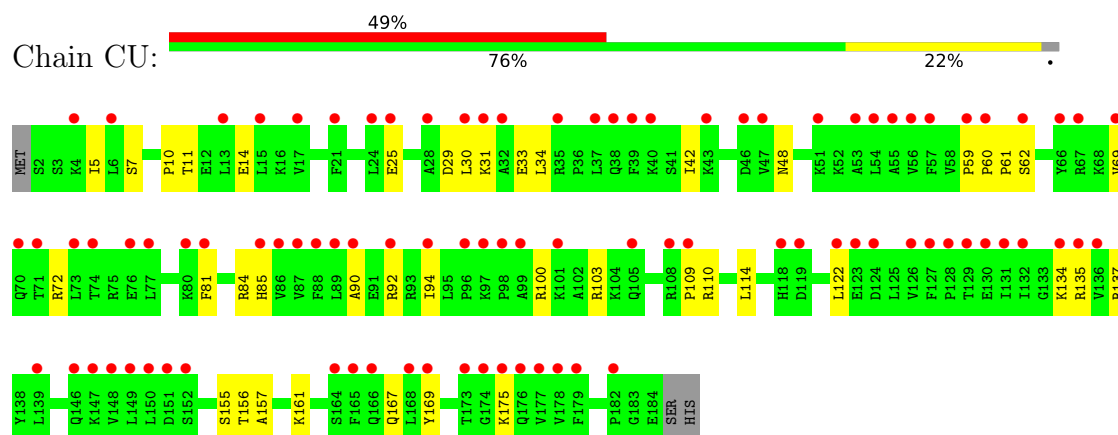
Chain CT:



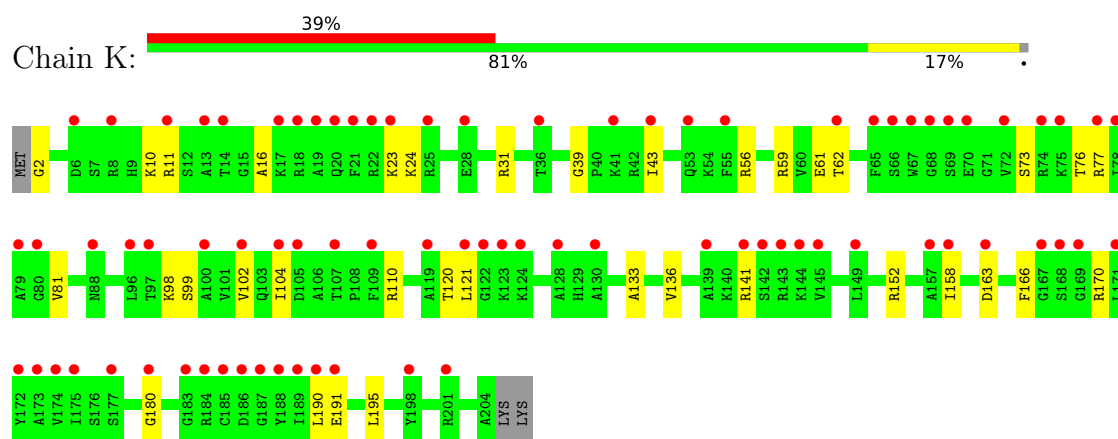
- Molecule 54: 40S ribosomal protein S7



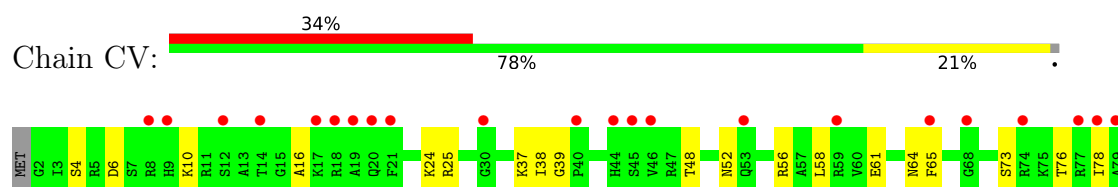
- Molecule 54: 40S ribosomal protein S7

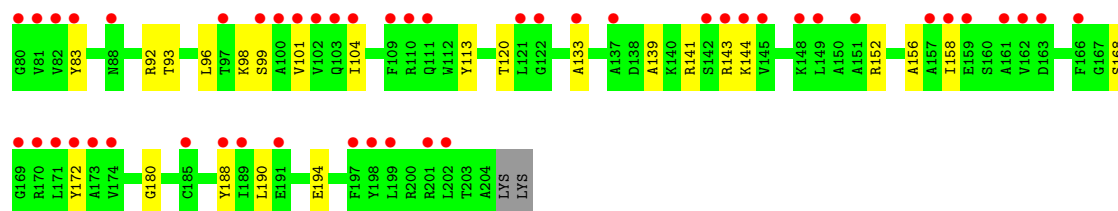


- Molecule 55: 40S ribosomal protein S8

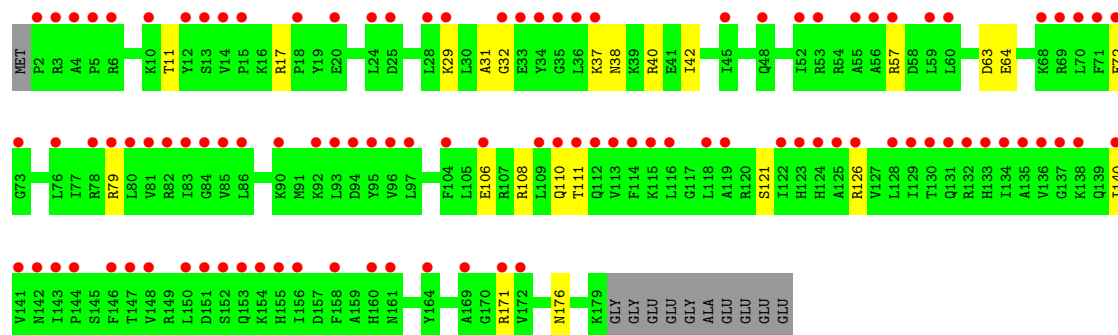
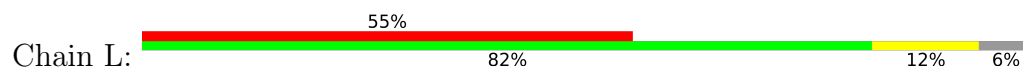


- Molecule 55: 40S ribosomal protein S8

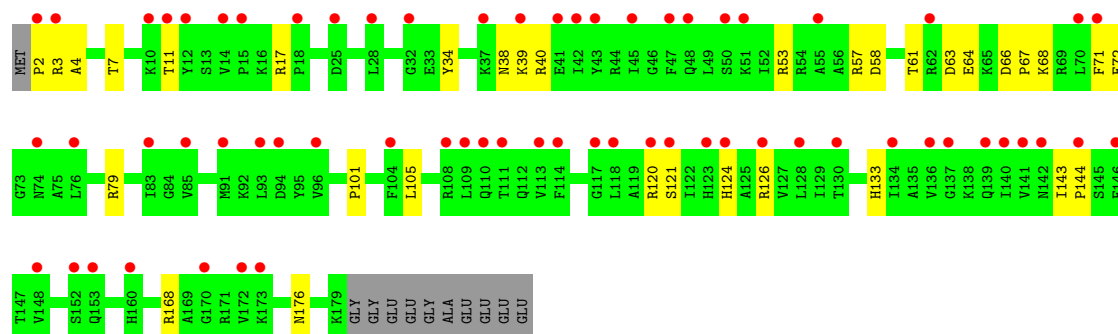
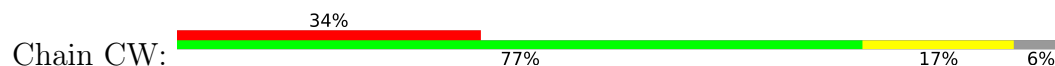




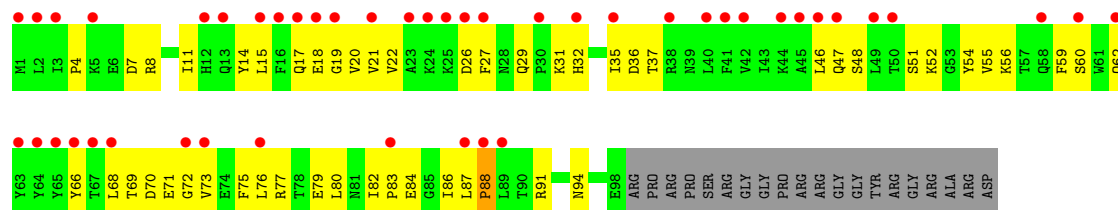
● Molecule 56: Ribosomal protein S4



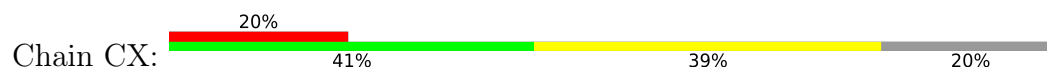
● Molecule 56: Ribosomal protein S4

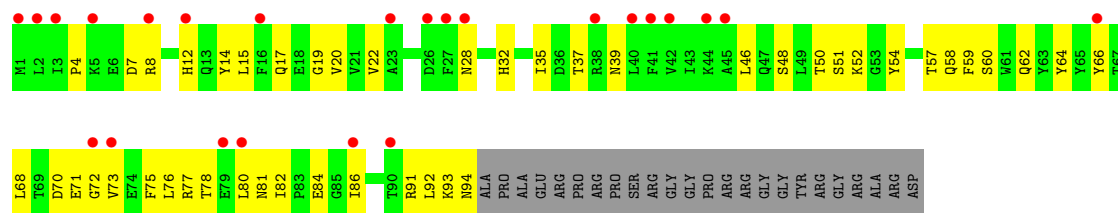


● Molecule 57: 40S ribosomal protein S10-A

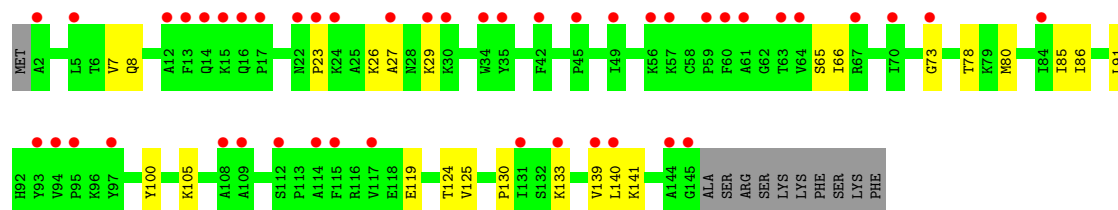
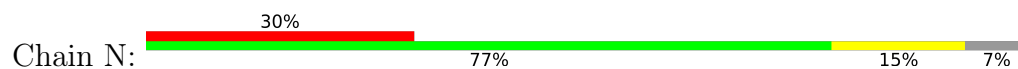


● Molecule 57: 40S ribosomal protein S10-A

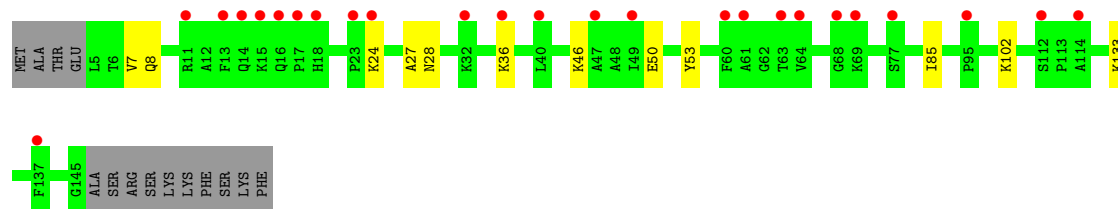
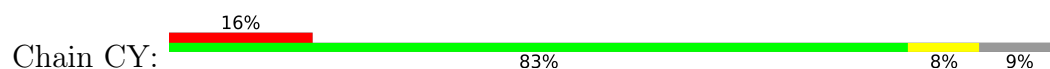




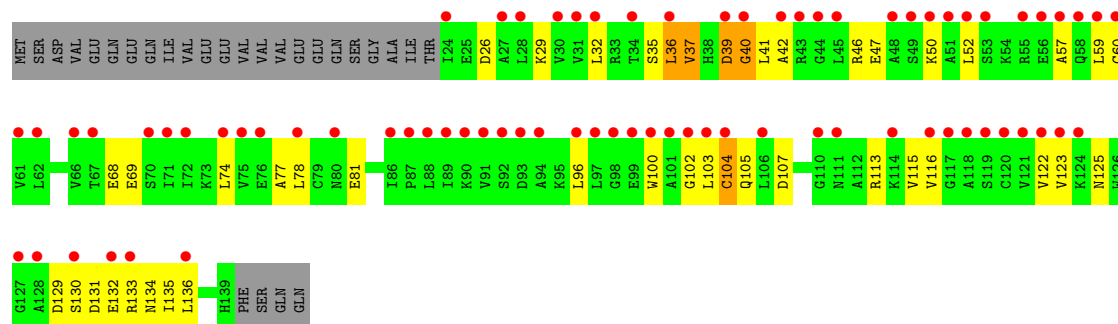
• Molecule 58: 40S ribosomal protein S11A



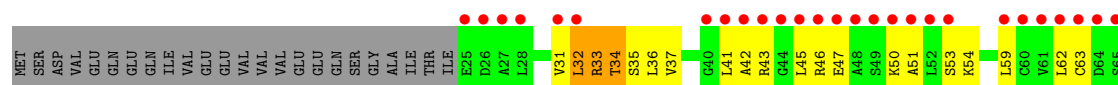
• Molecule 58: 40S ribosomal protein S11A

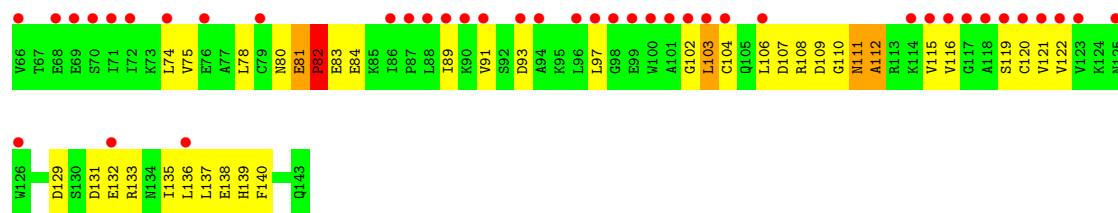


• Molecule 59: 40S ribosomal protein S12

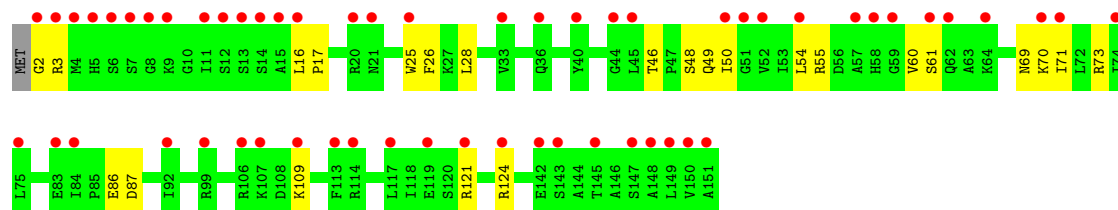
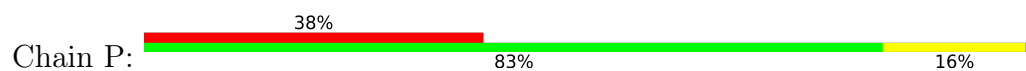


• Molecule 59: 40S ribosomal protein S12

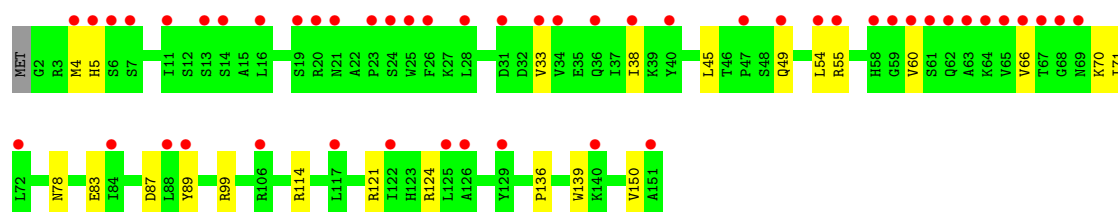
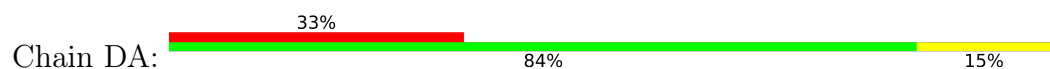




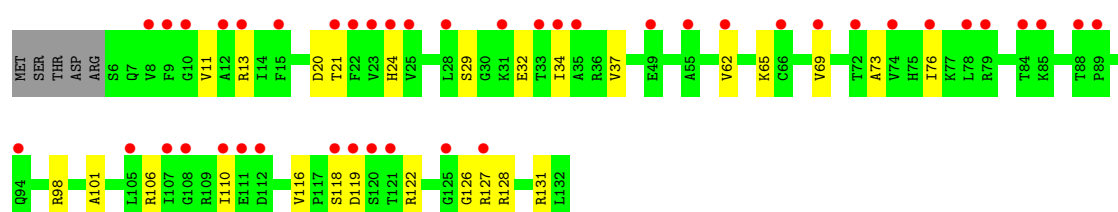
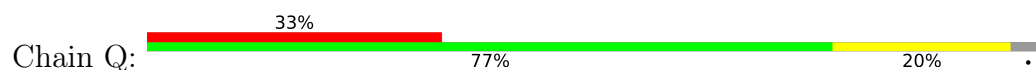
- Molecule 60: 40S ribosomal protein S13



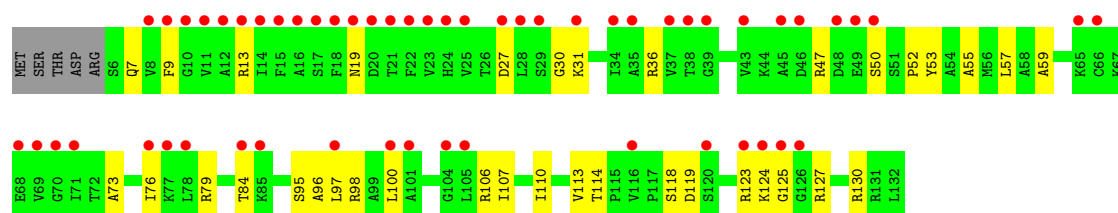
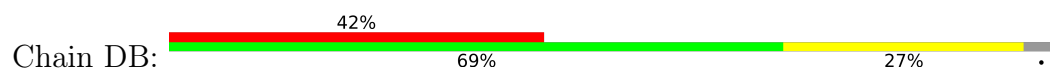
- Molecule 60: 40S ribosomal protein S13



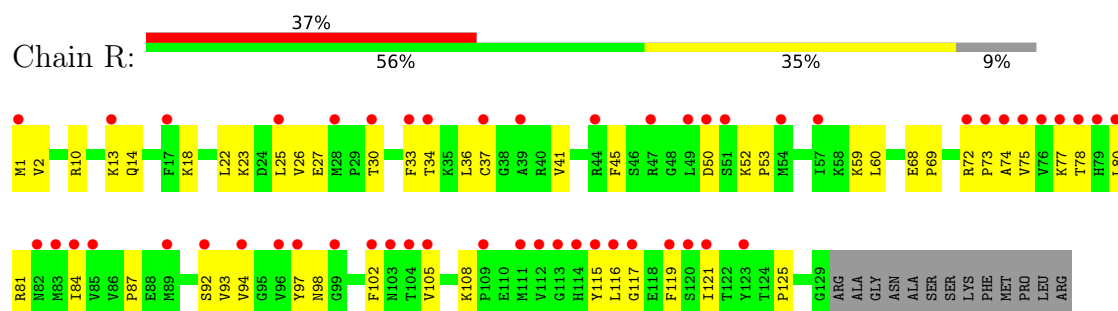
- Molecule 61: 40S ribosomal protein S14-A



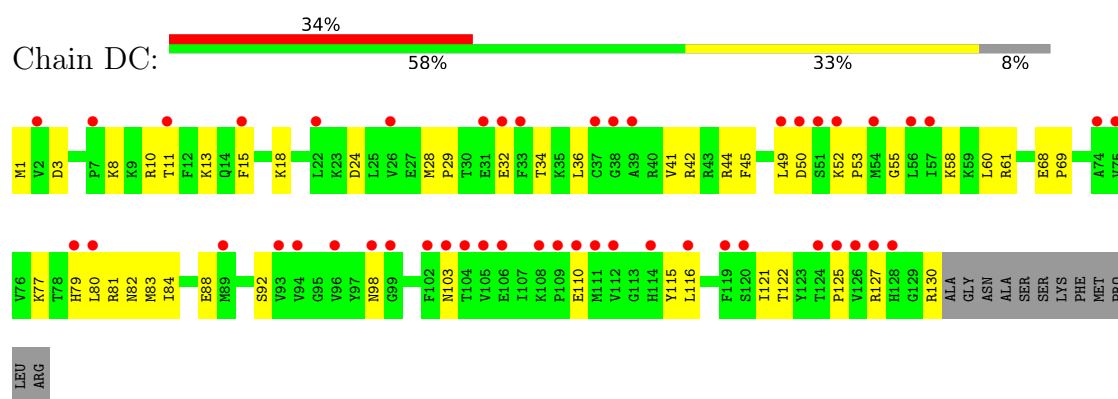
- Molecule 61: 40S ribosomal protein S14-A



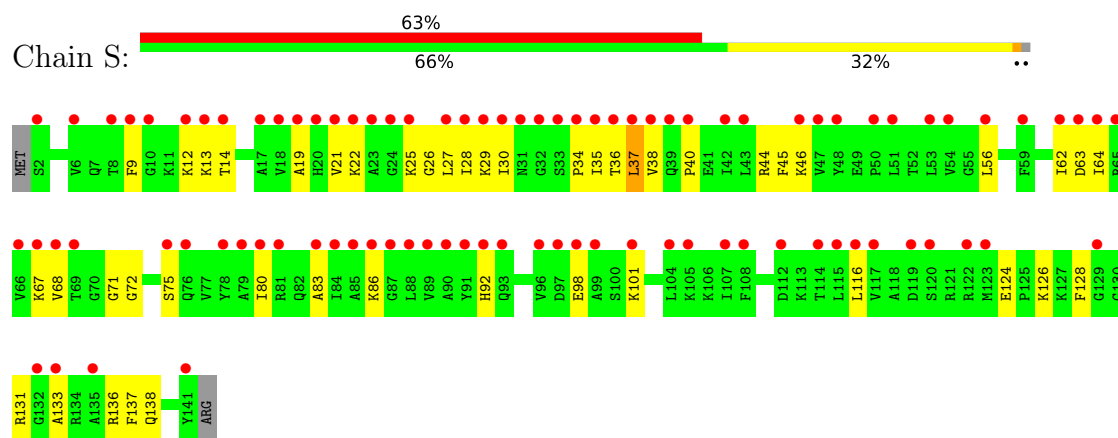
- Molecule 62: 40S ribosomal protein S15



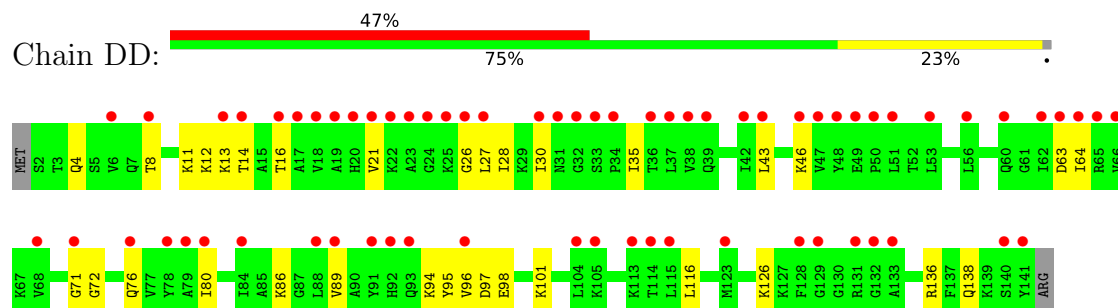
- Molecule 62: 40S ribosomal protein S15



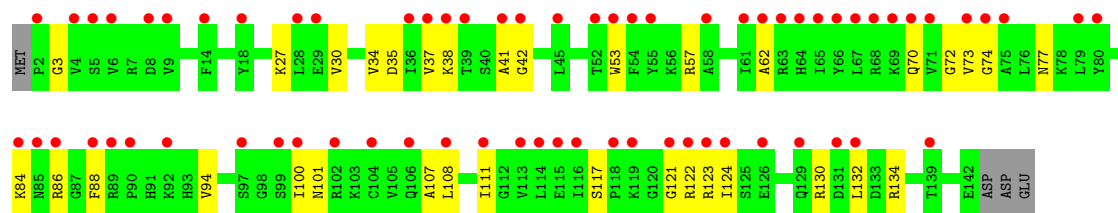
- Molecule 63: 40S ribosomal protein S16



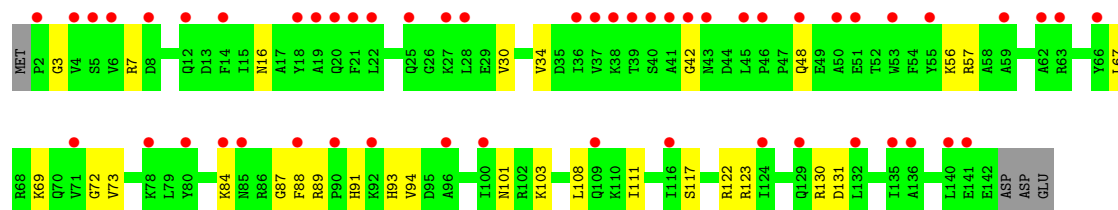
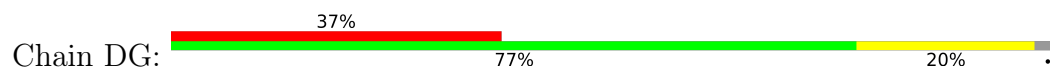
- Molecule 63: 40S ribosomal protein S16



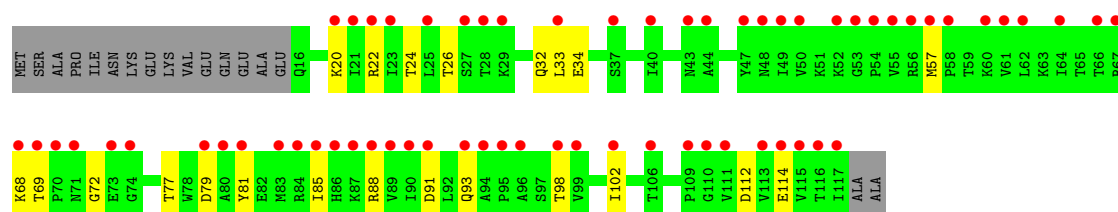
- Molecule 64: 40S ribosomal protein S17-B



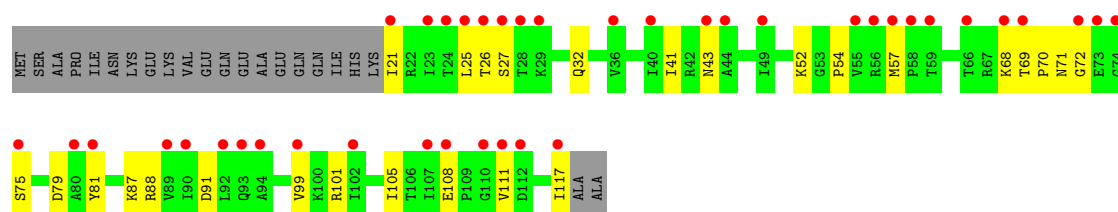
• Molecule 66: 40S ribosomal protein S19-A



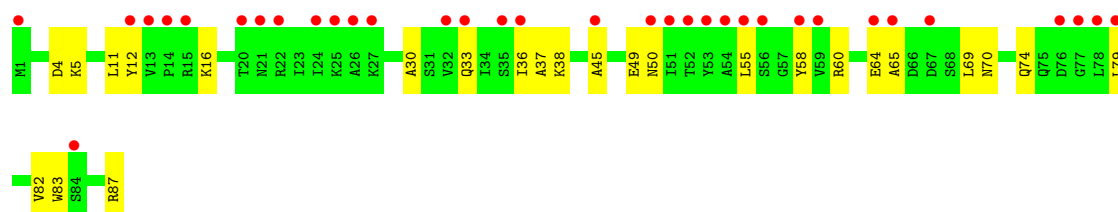
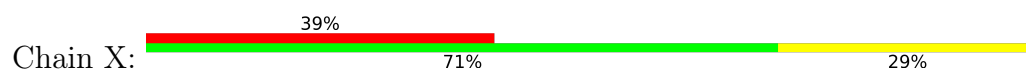
• Molecule 67: Ribosomal protein S10



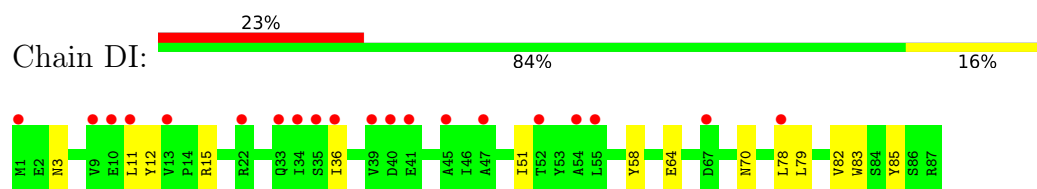
• Molecule 67: Ribosomal protein S10



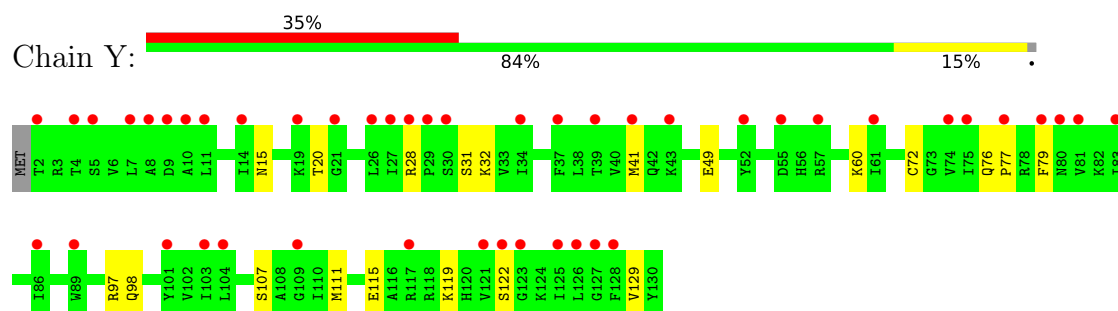
• Molecule 68: 40S ribosomal protein S21



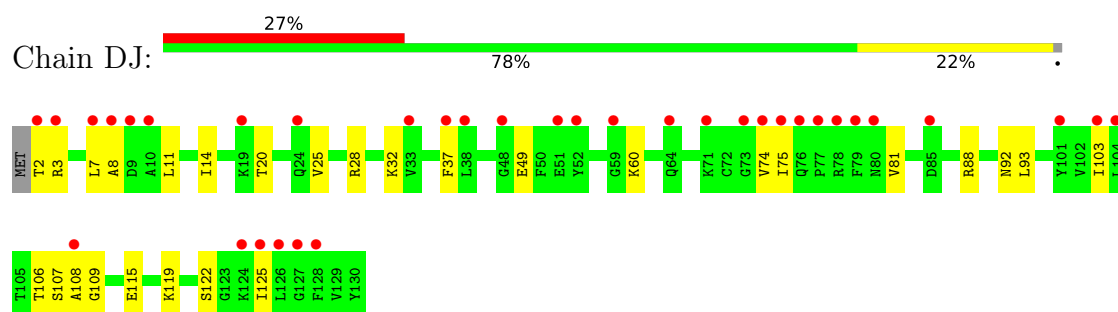
- Molecule 68: 40S ribosomal protein S21



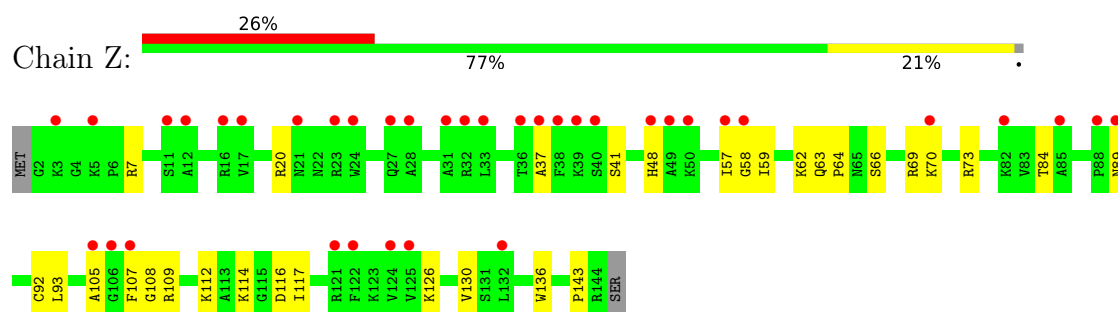
- Molecule 69: 40S ribosomal protein S22-A



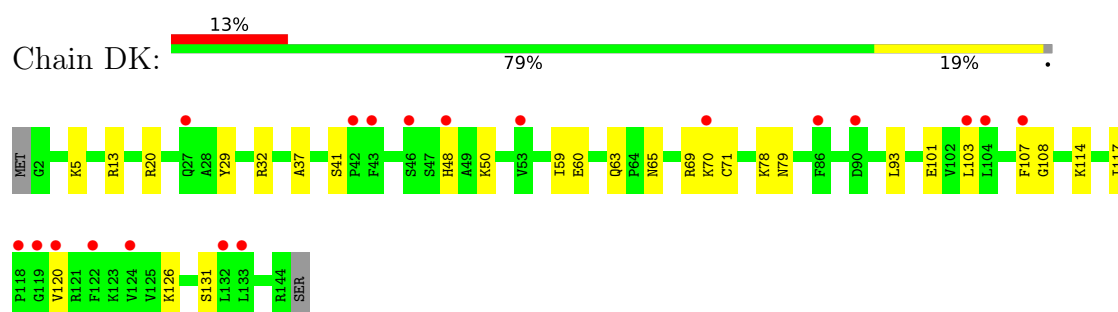
- Molecule 69: 40S ribosomal protein S22-A



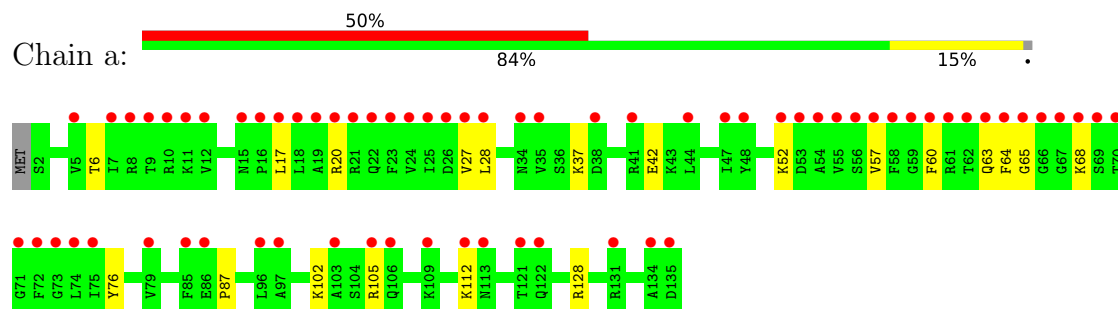
- Molecule 70: Ribosomal protein S23 (S12)



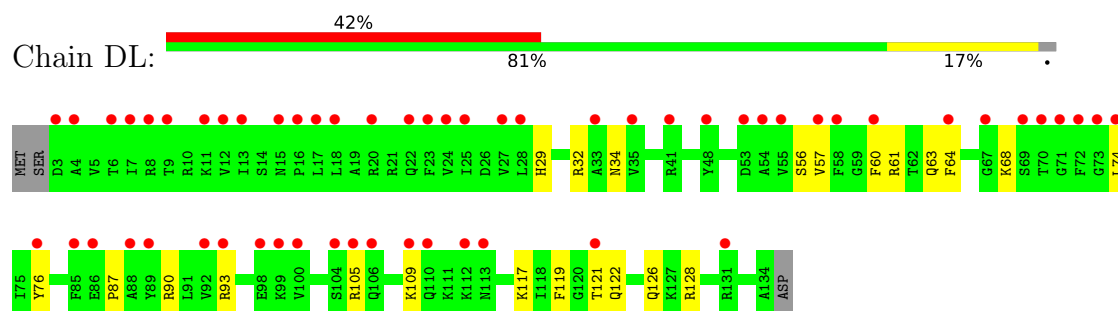
- Molecule 70: Ribosomal protein S23 (S12)



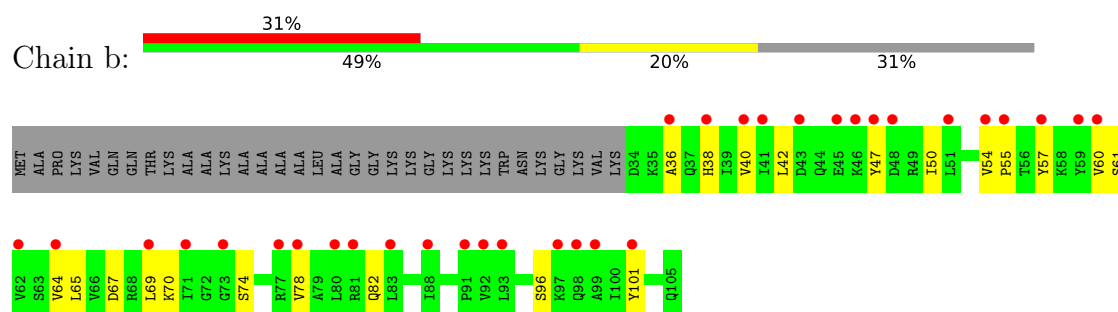
- Molecule 71: 40S ribosomal protein S24



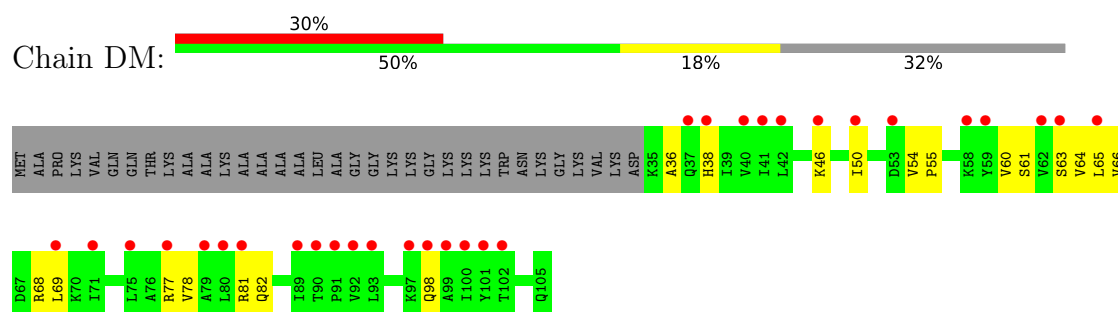
- Molecule 71: 40S ribosomal protein S24



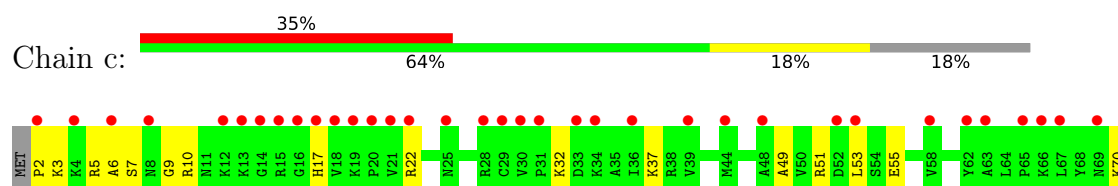
- Molecule 72: 40S ribosomal protein S25

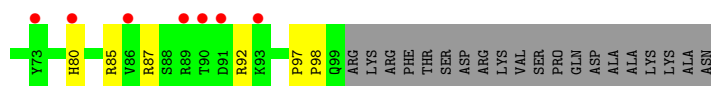


- Molecule 72: 40S ribosomal protein S25

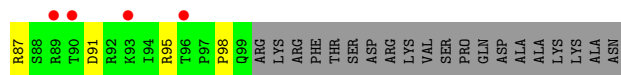
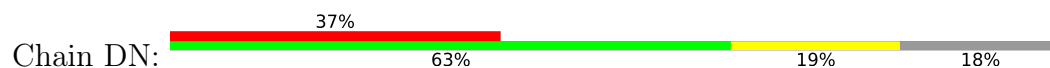


- Molecule 73: 40S ribosomal protein S26

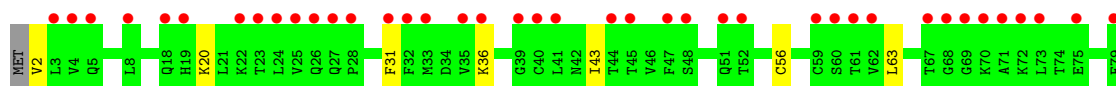
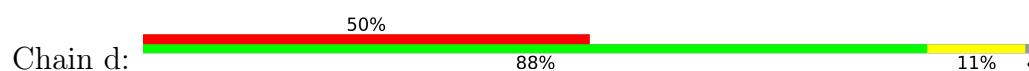




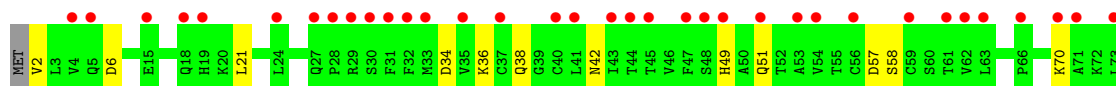
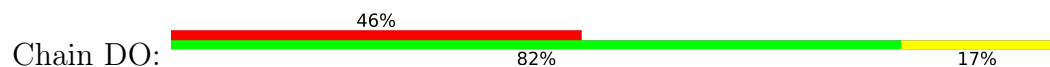
• Molecule 73: 40S ribosomal protein S26



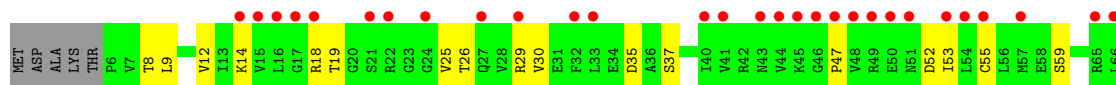
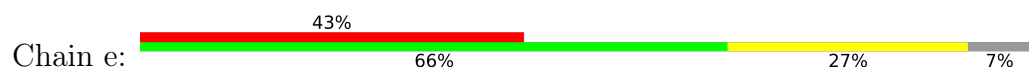
• Molecule 74: 40S ribosomal protein S27



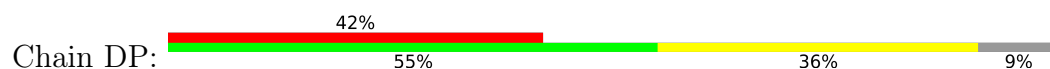
• Molecule 74: 40S ribosomal protein S27

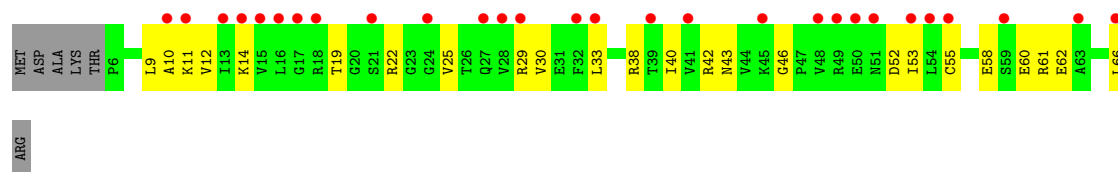


• Molecule 75: 40S ribosomal protein S28-B

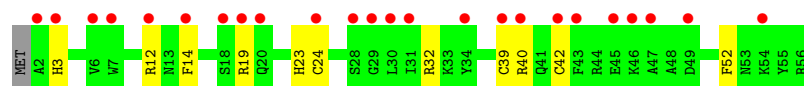
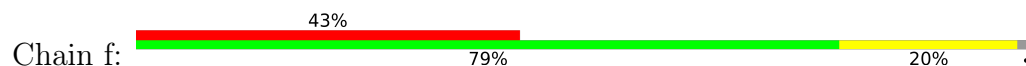


• Molecule 75: 40S ribosomal protein S28-B

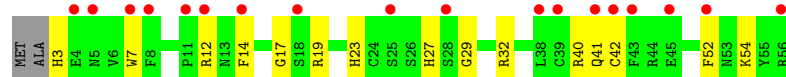
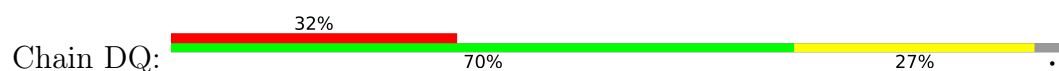




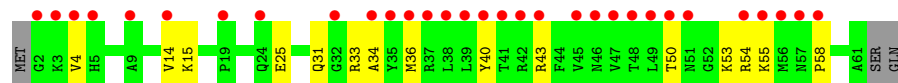
- Molecule 76: 40S ribosomal protein S29A



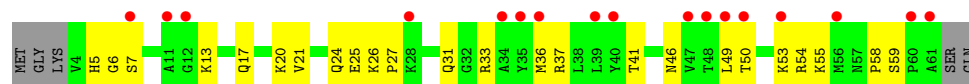
- Molecule 76: 40S ribosomal protein S29A



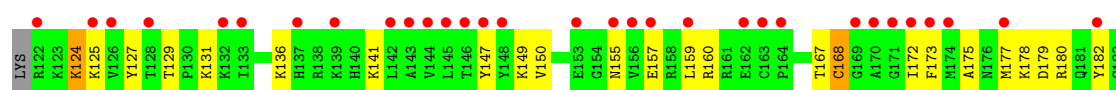
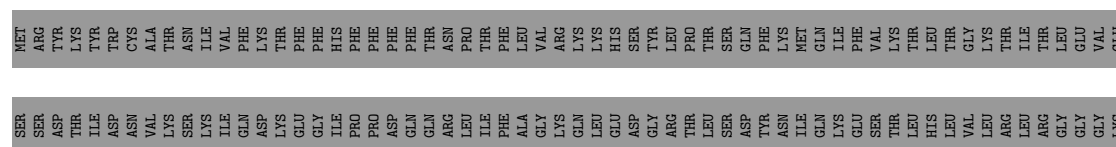
- Molecule 77: 40S ribosomal protein S30

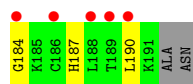


- Molecule 77: 40S ribosomal protein S30

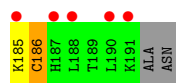
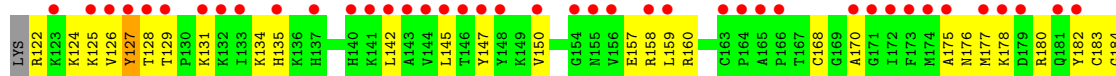
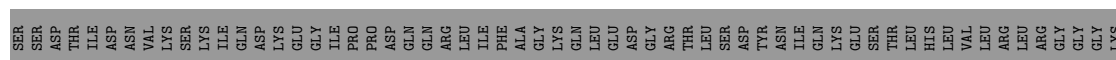
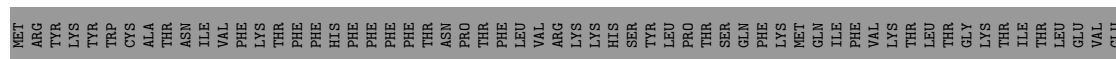


- Molecule 78: Ubiquitin-40S ribosomal protein S31 fusion protein

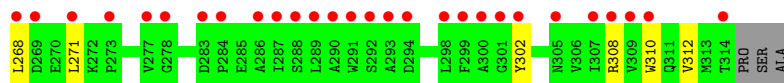
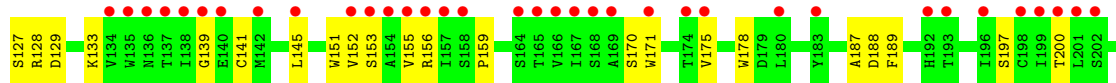
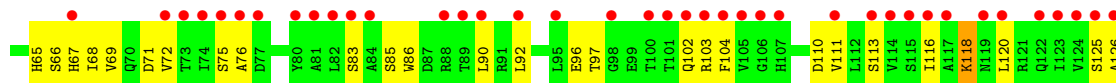
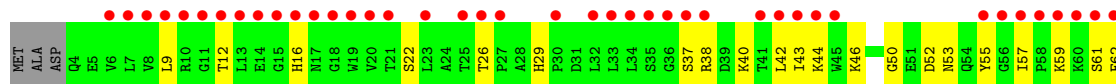
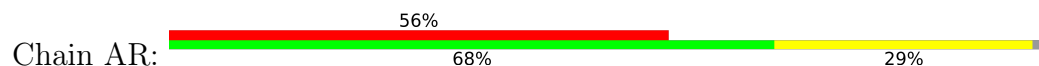




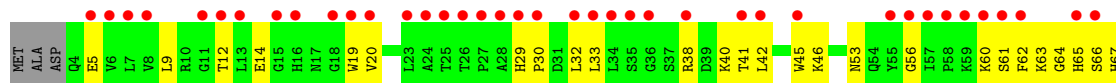
- Molecule 78: Ubiquitin-40S ribosomal protein S31 fusion protein

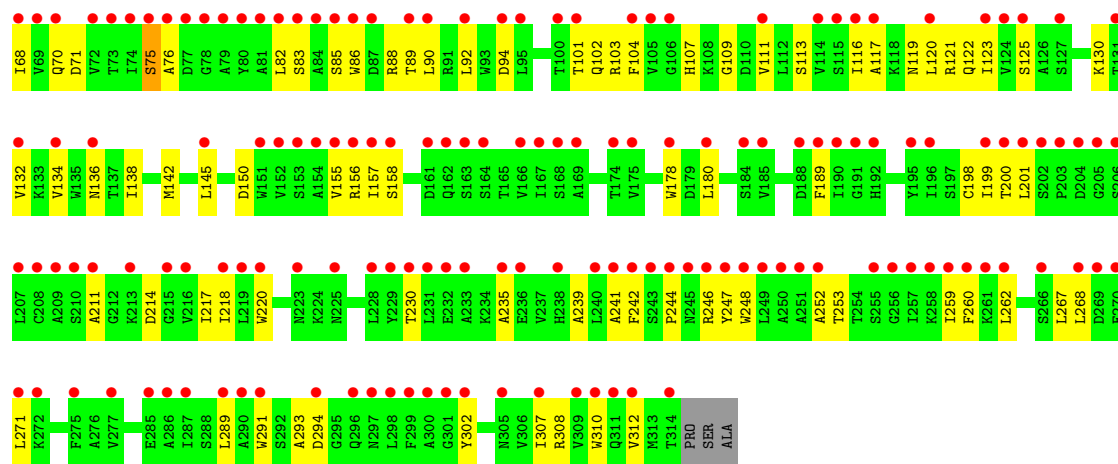


- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

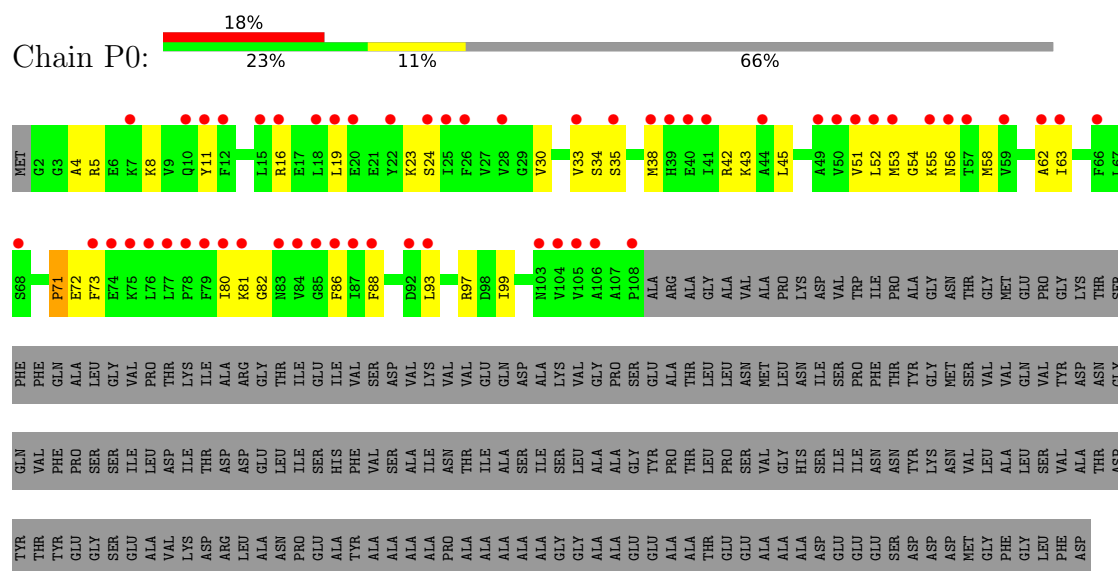


- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

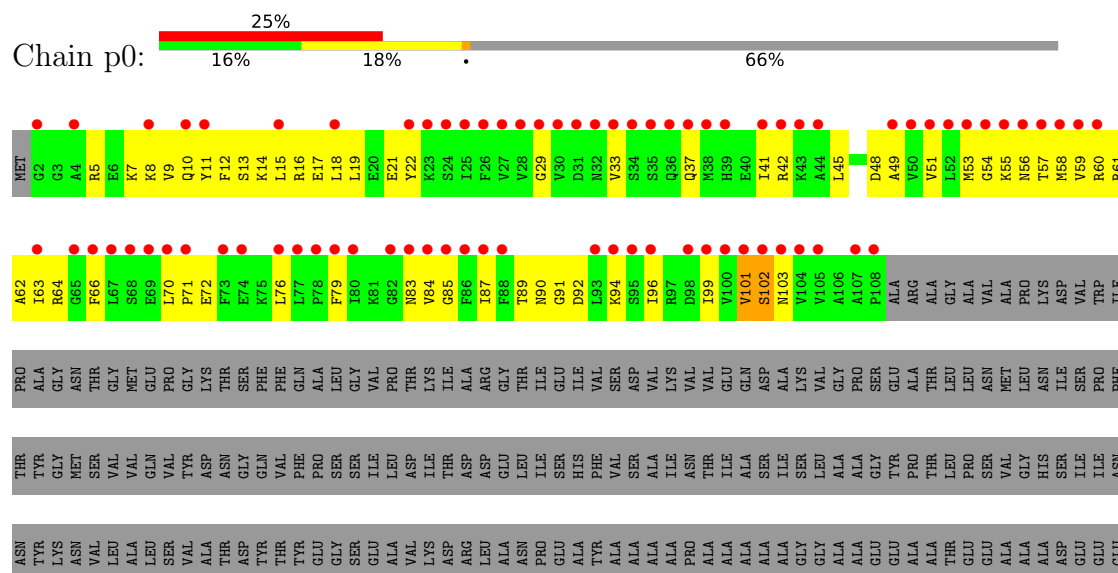




● Molecule 80: 60S acidic ribosomal protein P0



● Molecule 80: 60S acidic ribosomal protein P0



SER
ASP
ASP
ASP
MET
GLY
PHE
GLY
PHE
ASP

• Molecule 81: 60S ribosomal protein L12-A

Chain 12: 13% 20% 18% 62%

MET PRO PRO LYS PHE ASP PRO ASN GLU VAL LYS PHE LEU TYR LEU ARG ALA VAL GLY GLY VAL GLY SER ALA PRO LYS TLE GLY PRO LEU GLY LEU LEU SER PRO LYS VAL GLY ASP ILE ALA LYS THR LYS TYR GLY TLE LYS VAL THR VAL

GLN LEU ARG ILE GLN ASN ARG GLN ALA THR VAL SER PHE LEU VAL VAL PRO SER ARG ALA VAL SER LEU VAL ILE THR VAL ILE THR GLY PRO VAL ARG ASP ARG LYS HIS VAL GLY N103 I104 P105 E108 F110 E111 I112 Q117 M116 K119 S120 F121 M124

L125 A126 S127 V128 K129 S130 E131 I132 L133 T134 G135 Q136 Q137 S138 C141 R142 V143 D144 G145 P148 H149 D150 I151 I152 D153 I155 E159 I160 D161 V162 P163 E164 N165

• Molecule 82: Ribosomal protein

Chain L1: 37% 59% 40%

K1 S2 K3 I4 T5 S6 S7 S8 V9 E11 N12 H13 H14 K15 L16 L17 S20 T21 E22 T23 K24 K25 N27 F28 L29 E30 T31 V32 E33 L34 Q35 V36 G37 L38 K39 M40 Y41 P43 Q44 R45 D46 K47 R48 F49 S50 G51 T52 L53 K54 L55 V58 P59 R60 M63

T64 I65 C66 I67 F68 F69 D70 D73 R76 D83 K84 M85 S86 V87 N96 K97 L98 L99 I100 K101 K102 L103 A104 A109 F110 I111 A112 S113 V115 L116 I117 K118 Q119 I120 L123 L124 G125 P126 T127 S129 G132 K133 F134 G202 P135 S203 T136 P137 D142 L143 L144

K147 V148 P212 D150 S153 T154 I155 K156 F157 Q158 L159 K160 K161 V162 C164 A165 A166 V167 V169 G170 N171 V172 D173 M174 E176 I177 V178 L179 L180 Q182 I183 M184 M185 F189 L190 S192 L193 K195 K196 N197 V198 Q199 N200 V201 G202 S203 L204 V205 I206 K207 S208 T209

R210 C211 P212 S213 T214 R215 I216 Y217

• Molecule 82: Ribosomal protein

Chain I1: 45% 45% 52%

K1 S2 K3 I4 T5 S6 S7 S8 V9 E11 N12 H13 H14 K15 L16 L17 E18 Y19 S20 T21 E22 T23 K24 K25 N27 F28 L29 E30 T31 V32 E33 L34 Q35 V36 G37 L38 K39 M40 Y41 P43 Q44 R45 F49 S50 G51 T52 L53 K54 L55 P56 V58 P59 R60 M63

T64 I65 C66 I67 F68 F69 D70 D73 R76 D83 K84 M85 S86 V87 N96 K97 L98 L99 I100 K101 K102 L103 Q104 A105 K106 I107 N108 A109 F110 I111 A112 S113 V115 L116 I117 K118 Q119 I120 P121 R122 P56 L123 L124 G125 P126 T127 L128

S129 K130 K133 F134 P135 T136 F137 F138 H140 H141 D142 D143 L144 K147 V148 T149 D150 V151 S152 S153 T154 I155 K156 F157 Q158 L159 V162 L163 C164 L165 A166 V167 A168 V169 G170 N171 V172 D173 M174 E175 V178 L179 V180 N181 Q182 I183 F184 F189 L190 L193 L194 K195 K196

H197	H198	N200	N201	S203	L204	V205	T206	K207	S208	T209	K210	G211	F212	S213	F214	R215	T216	Y217

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	298.96Å 294.09Å 450.21Å 90.00° 100.12° 90.00°	Depositor
Resolution (Å)	227.46 – 3.00 227.46 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (227.46-3.00) 89.8 (227.46-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.95 (at 3.01Å)	Xtriage
Refinement program	PHENIX 19.2	Depositor
R, R_{free}	0.268 , 0.299 (Not available) , 0.275	Depositor DCC
R_{free} test set	2000 reflections (0.13%)	wwPDB-VP
Wilson B-factor (Å ²)	53.4	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	410139	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TIX, 3K5, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.18	1/76970 (0.0%)	0.44	7/119993 (0.0%)
1	AS	0.19	0/77254	0.44	10/120438 (0.0%)
2	3	0.14	0/2884	0.32	0/4492
2	AT	0.15	0/2884	0.33	0/4492
3	4	0.15	0/3724	0.39	1/5798 (0.0%)
3	AU	0.14	0/3746	0.38	1/5832 (0.0%)
4	AW	0.14	0/1931	0.38	0/2592
4	j	0.16	0/1931	0.42	0/2592
5	AX	0.16	0/3145	0.41	0/4231
5	k	0.16	0/3156	0.43	0/4246
6	AY	0.13	0/2799	0.39	0/3777
6	l	0.16	0/2799	0.43	0/3777
7	AZ	0.13	0/2447	0.38	0/3294
7	m	0.15	0/2479	0.42	0/3337
8	BA	0.14	0/1231	0.40	0/1662
8	n	0.14	0/1263	0.39	0/1703
9	BB	0.14	0/1918	0.38	0/2575
9	o	0.17	0/1918	0.42	0/2575
10	BC	0.14	0/1835	0.45	0/2472
10	p	0.16	0/1869	0.43	0/2519
11	BD	0.15	0/1537	0.40	0/2067
11	q	0.17	0/1537	0.42	0/2067
12	BE	0.14	0/1724	0.40	0/2314
12	r	0.15	0/1724	0.41	0/2314
13	BF	0.15	0/1390	0.42	0/1861
13	s	0.16	0/1390	0.45	0/1861
14	BG	0.14	0/1637	0.40	0/2195
14	t	0.17	0/1637	0.44	0/2195
15	BH	0.16	0/1044	0.40	0/1407
15	u	0.15	0/1044	0.39	0/1407
16	BI	0.13	0/1753	0.40	0/2347
16	v	0.17	0/1753	0.42	0/2347

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	BJ	0.16	0/1620	0.40	0/2167
17	w	0.16	0/1620	0.39	0/2167
18	BK	0.14	0/1429	0.39	0/1920
18	x	0.14	0/1410	0.41	0/1895
19	BL	0.15	0/1482	0.38	0/1985
19	y	0.14	0/1482	0.41	0/1985
20	BM	0.14	0/1475	0.41	0/1961
20	z	0.14	0/1475	0.38	0/1961
21	0	0.15	0/1457	0.42	0/1962
21	BN	0.15	0/1457	0.37	0/1962
22	2	0.14	0/1285	0.36	0/1723
22	BO	0.14	0/1285	0.37	0/1723
23	5	0.13	0/846	0.40	0/1140
23	BP	0.16	0/866	0.46	0/1168
24	6	0.19	0/993	0.41	0/1339
24	BQ	0.21	0/993	0.50	1/1339 (0.1%)
25	7	0.12	0/958	0.31	0/1267
25	BR	0.12	0/814	0.28	0/1079
26	8	0.15	0/990	0.38	0/1337
26	BS	0.11	0/976	0.35	0/1319
27	9	0.13	0/999	0.36	0/1334
27	BT	0.12	0/999	0.37	0/1334
28	AA	0.13	0/1112	0.34	0/1488
28	BU	0.13	0/1112	0.37	0/1488
29	AB	0.14	0/1199	0.41	0/1607
29	BV	0.15	0/1199	0.38	0/1607
30	AC	0.19	0/503	0.56	2/668 (0.3%)
30	BW	0.14	0/498	0.42	0/661
31	AD	0.12	0/738	0.35	0/994
31	BX	0.11	0/738	0.39	0/994
32	AE	0.13	0/907	0.41	0/1219
32	BY	0.14	0/907	0.44	0/1219
33	AF	0.14	0/1021	0.38	0/1368
33	BZ	0.13	0/1025	0.42	0/1372
34	AG	0.14	0/866	0.37	0/1165
34	CA	0.15	0/866	0.37	0/1165
35	AH	0.14	0/896	0.44	0/1195
35	CB	0.14	0/896	0.47	1/1195 (0.1%)
36	AI	0.13	0/1012	0.39	0/1347
36	CC	0.13	0/999	0.39	0/1330
37	AJ	0.13	0/763	0.36	0/1012
37	CD	0.13	0/763	0.42	0/1012
38	AK	0.16	0/690	0.38	0/916

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	CE	0.13	0/690	0.40	0/916
39	AL	0.13	0/623	0.39	0/831
39	CF	0.17	0/623	0.50	0/831
40	AM	0.13	0/447	0.34	0/594
40	CG	0.14	0/458	0.44	0/609
41	AN	0.15	0/425	0.40	0/563
41	CH	0.16	0/417	0.43	0/553
42	AO	0.17	0/237	0.40	0/304
42	CI	0.16	0/228	0.41	0/293
43	AP	0.24	0/840	0.49	0/1110
43	CJ	0.24	0/840	0.51	0/1110
44	AQ	0.19	0/705	0.40	0/940
44	CK	0.13	0/705	0.38	0/940
45	CL	0.22	0/941	0.76	0/1257
45	i	0.21	0/941	0.77	0/1257
46	B	0.18	0/41987	0.45	4/65427 (0.0%)
46	CM	0.18	0/42081	0.46	6/65573 (0.0%)
47	C	0.13	0/1666	0.36	0/2273
47	CN	0.14	0/1666	0.41	0/2273
48	CO	0.17	0/1750	0.47	0/2354
48	D	0.14	0/1750	0.40	0/2354
49	CP	0.14	0/1657	0.40	0/2248
49	E	0.12	0/1657	0.36	0/2248
50	CQ	0.17	0/1731	0.52	0/2324
50	F	0.17	0/1731	0.51	1/2324 (0.0%)
51	CR	0.13	0/2096	0.39	0/2822
51	G	0.14	0/2092	0.38	0/2817
52	CS	0.14	0/1631	0.40	0/2199
52	H	0.15	0/1631	0.42	0/2199
53	CT	0.13	0/1929	0.42	0/2571
53	I	0.13	0/1845	0.39	0/2464
54	CU	0.17	0/1499	0.43	0/2016
54	J	0.14	0/1516	0.41	0/2039
55	CV	0.15	0/1606	0.40	0/2150
55	K	0.15	0/1606	0.41	0/2150
56	CW	0.13	0/1478	0.37	0/1978
56	L	0.12	0/1478	0.37	0/1978
57	CX	0.19	0/809	0.57	0/1092
57	M	0.18	0/836	0.64	0/1130
58	CY	0.14	0/1154	0.42	0/1553
58	N	0.13	0/1175	0.42	0/1582
59	CZ	0.25	0/921	0.90	7/1240 (0.6%)
59	O	0.30	0/892	0.80	0/1203

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	DA	0.12	0/1210	0.38	0/1631
60	P	0.13	0/1210	0.37	0/1631
61	DB	0.27	0/953	0.53	1/1279 (0.1%)
61	Q	0.23	0/953	0.51	1/1279 (0.1%)
62	DC	0.18	0/1049	0.56	0/1409
62	R	0.18	0/1038	0.52	0/1395
63	DD	0.15	0/1109	0.42	0/1486
63	S	0.23	0/1109	0.51	0/1486
64	DE	0.19	0/1009	0.57	0/1354
64	T	0.15	0/1009	0.48	0/1354
65	DF	0.14	0/1178	0.45	0/1579
65	U	0.21	0/1205	0.51	1/1615 (0.1%)
66	DG	0.15	0/1120	0.44	0/1508
66	V	0.17	0/1120	0.50	0/1508
67	DH	0.16	0/772	0.46	0/1045
67	W	0.14	0/818	0.43	0/1106
68	DI	0.15	0/683	0.46	0/918
68	X	0.14	0/683	0.41	0/918
69	DJ	0.15	0/1049	0.40	0/1412
69	Y	0.13	0/1049	0.36	0/1412
70	DK	0.16	0/1128	0.44	0/1505
70	Z	0.16	0/1128	0.51	0/1505
71	DL	0.13	0/1086	0.36	0/1447
71	a	0.14	0/1100	0.36	0/1466
72	DM	0.14	0/577	0.46	0/778
72	b	0.13	0/585	0.35	0/789
73	DN	0.15	0/791	0.41	0/1060
73	c	0.15	0/791	0.43	0/1060
74	DO	0.17	0/624	0.49	0/843
74	d	0.14	0/624	0.40	0/843
75	DP	0.33	0/478	0.67	0/640
75	e	0.15	0/489	0.46	0/654
76	DQ	0.26	0/461	0.60	0/613
76	f	0.24	0/466	0.62	1/620 (0.2%)
77	DR	0.23	0/469	0.75	1/626 (0.2%)
77	g	0.18	0/482	0.50	0/642
78	DS	0.37	0/585	0.73	0/778
78	h	0.20	0/585	0.63	0/778
79	AR	0.20	0/2451	0.43	0/3337
79	DT	0.19	0/2451	0.55	0/3337
80	P0	0.17	0/857	0.43	0/1148
80	p0	0.22	0/857	0.51	0/1148
81	12	0.19	0/486	0.50	0/653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
82	L1	0.16	0/1737	0.36	0/2335
82	l1	0.20	0/1737	0.49	1/2335 (0.0%)
All	All	0.17	1/438315 (0.0%)	0.44	47/642822 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2482	U	C1'-N1	6.14	1.57	1.48

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	DR	6	GLY	N-CA-C	-8.23	105.28	115.08
1	AS	2431	U	C2'-C3'-O3'	8.08	121.61	109.50
1	1	1738	U	P-O3'-C3'	-8.05	108.12	120.20
1	AS	1738	U	P-O3'-C3'	-7.91	108.34	120.20
1	1	1737	A	P-O3'-C3'	-7.30	109.24	120.20
59	CZ	81	GLU	C-N-CD	-7.08	95.95	125.00
1	AS	1247	A	O3'-P-O5'	6.77	114.16	104.00
1	AS	1737	A	P-O3'-C3'	-6.74	110.09	120.20
46	B	676	G	N9-C1'-C2'	6.23	121.34	112.00
59	CZ	82	PRO	CA-C-N	6.17	133.32	121.54
59	CZ	82	PRO	C-N-CA	6.17	133.32	121.54
46	B	676	G	O4'-C1'-N9	5.97	117.45	108.50
1	1	446	U	O3'-P-O5'	-5.92	95.11	104.00
46	CM	970	G	O3'-P-O5'	5.89	112.83	104.00
24	BQ	110	LYS	N-CA-C	-5.87	105.61	112.89
46	CM	725	A	O5'-C5'-C4'	-5.86	102.70	111.50
1	AS	2449	U	C2'-C3'-O3'	5.83	118.25	109.50
76	f	39	CYS	CB-CA-C	-5.79	100.05	110.36
61	DB	118	SER	N-CA-C	-5.75	104.43	112.25
46	CM	725	A	C5'-C4'-C3'	-5.74	107.39	116.00
46	B	721	C	N1-C1'-C2'	5.66	120.49	112.00
46	CM	1672	G	O3'-P-O5'	5.61	112.41	104.00
1	AS	2468	C	C2'-C3'-O3'	-5.56	101.16	109.50
61	Q	118	SER	N-CA-C	-5.52	103.86	111.81
35	CB	111	LYS	CB-CA-C	-5.49	109.17	117.07
82	l1	209	THR	N-CA-C	-5.48	106.91	113.21
1	AS	2449	U	C4'-C3'-O3'	5.46	117.58	109.40
65	U	138	THR	CA-CB-OG1	-5.43	101.46	109.60
1	AS	2455	G	C4'-C3'-O3'	5.28	120.92	113.00
1	1	1273	C	C4'-C3'-O3'	5.26	120.89	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	CM	823	G	P-O5'-C5'	-5.24	113.04	120.90
1	AS	2455	G	C2'-C3'-O3'	5.23	121.55	113.70
1	1	3165	U	P-O5'-C5'	5.22	128.73	120.90
3	AU	21	C	N1-C1'-C2'	5.22	119.82	112.00
1	AS	1267	A	O5'-P-OP2	-5.21	92.38	108.00
59	CZ	111	ASN	CA-C-N	5.20	131.46	121.54
59	CZ	111	ASN	C-N-CA	5.20	131.46	121.54
46	CM	814	A	P-O3'-C3'	5.18	127.97	120.20
50	F	60	LEU	CA-CB-CG	5.17	134.41	116.30
30	AC	20	GLY	CA-C-N	5.15	131.25	121.97
30	AC	20	GLY	C-N-CA	5.15	131.25	121.97
3	4	21	C	N1-C1'-C2'	5.14	119.72	112.00
1	1	1218	G	O3'-P-O5'	-5.12	96.32	104.00
1	1	1218	G	O5'-C5'-C4'	5.12	119.38	111.70
59	CZ	33	ARG	CA-C-N	5.08	131.24	121.54
59	CZ	33	ARG	C-N-CA	5.08	131.24	121.54
46	B	824	U	O4'-C1'-N1	-5.05	100.92	108.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68771	0	34562	1183	1
1	AS	69025	0	34689	1160	0
2	3	2579	0	1303	30	0
2	AT	2579	0	1304	31	0
3	4	3333	0	1684	65	0
3	AU	3353	0	1694	65	0
4	AW	1894	0	1975	45	0
4	j	1894	0	1975	44	0
5	AX	3077	0	3166	63	0
5	k	3084	0	3173	51	0
6	AY	2751	0	2879	41	0
6	l	2751	0	2879	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	AZ	2394	0	2361	40	0
7	m	2426	0	2389	33	0
8	BA	1210	0	1285	24	0
8	n	1242	0	1321	28	0
9	BB	1885	0	1977	16	0
9	o	1885	0	1977	25	0
10	BC	1805	0	1925	25	1
10	p	1839	0	1957	15	0
11	BD	1519	0	1588	27	0
11	q	1519	0	1588	21	0
12	BE	1689	0	1731	18	0
12	r	1689	0	1731	18	0
13	BF	1371	0	1410	27	0
13	s	1371	0	1410	30	0
14	BG	1610	0	1686	25	0
14	t	1610	0	1686	21	0
15	BH	1029	0	1116	23	0
15	u	1029	0	1116	24	0
16	BI	1713	0	1763	44	0
16	v	1713	0	1764	39	0
17	BJ	1590	0	1705	25	0
17	w	1590	0	1705	27	0
18	BK	1406	0	1431	19	0
18	x	1387	0	1408	26	0
19	BL	1458	0	1556	24	0
19	y	1458	0	1556	37	0
20	BM	1457	0	1564	27	0
20	z	1457	0	1564	27	0
21	0	1423	0	1480	30	0
21	BN	1423	0	1480	29	0
22	2	1262	0	1314	17	0
22	BO	1262	0	1314	21	0
23	5	831	0	848	15	0
23	BP	843	0	859	22	0
24	6	977	0	1026	19	0
24	BQ	977	0	1026	14	0
25	7	945	0	1010	13	0
25	BR	801	0	840	15	0
26	8	974	0	1032	18	0
26	BS	960	0	1014	9	0
27	9	989	0	1064	19	0
27	BT	989	0	1064	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	AA	1087	0	1154	19	0
28	BU	1087	0	1154	27	0
29	AB	1170	0	1203	26	0
29	BV	1170	0	1203	19	0
30	AC	493	0	520	11	0
30	BW	488	0	515	7	0
31	AD	729	0	775	13	0
31	BX	729	0	775	16	0
32	AE	894	0	941	17	0
32	BY	894	0	941	9	0
33	AF	1000	0	1069	17	0
33	BZ	1004	0	1077	13	0
34	AG	847	0	893	16	0
34	CA	847	0	893	8	0
35	AH	887	0	947	22	0
35	CB	887	0	947	20	0
36	AI	998	0	1106	18	0
36	CC	985	0	1089	21	0
37	AJ	758	0	838	10	0
37	CD	758	0	838	9	0
38	AK	677	0	697	11	0
38	CE	677	0	697	19	0
39	AL	617	0	675	6	0
39	CF	617	0	675	15	0
40	AM	438	0	475	9	0
40	CG	446	0	488	13	0
41	AN	419	0	460	9	0
41	CH	411	0	448	7	0
42	AO	236	0	285	6	0
42	CI	227	0	272	8	0
43	AP	828	0	893	30	0
43	CJ	828	0	893	8	0
44	AQ	698	0	734	11	0
44	CK	698	0	734	16	0
45	CL	930	0	905	48	0
45	i	930	0	905	42	0
46	B	37537	0	18884	805	0
46	CM	37621	0	18926	885	1
47	C	1627	0	1644	41	0
47	CN	1627	0	1644	33	0
48	CO	1724	0	1805	52	0
48	D	1724	0	1805	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	CP	1629	0	1728	28	0
49	E	1629	0	1728	31	0
50	CQ	1707	0	1807	60	0
50	F	1707	0	1807	51	0
51	CR	2055	0	2137	45	0
51	G	2051	0	2134	50	0
52	CS	1614	0	1688	43	0
52	H	1614	0	1688	45	0
53	CT	1904	0	1994	50	0
53	I	1820	0	1896	41	0
54	CU	1475	0	1567	35	0
54	J	1491	0	1579	35	0
55	CV	1579	0	1602	38	0
55	K	1579	0	1602	32	0
56	CW	1453	0	1532	37	0
56	L	1453	0	1532	21	0
57	CX	791	0	805	45	0
57	M	817	0	828	47	0
58	CY	1129	0	1183	14	0
58	N	1150	0	1201	16	0
59	CZ	913	0	934	54	0
59	O	885	0	915	37	0
60	DA	1187	0	1249	19	0
60	P	1187	0	1249	19	0
61	DB	942	0	981	28	0
61	Q	942	0	981	18	0
62	DC	1029	0	1078	37	0
62	R	1018	0	1065	43	0
63	DD	1091	0	1155	25	0
63	S	1091	0	1155	45	0
64	DE	997	0	1053	35	0
64	T	997	0	1053	40	0
65	DF	1161	0	1205	44	0
65	U	1187	0	1237	35	0
66	DG	1100	0	1114	23	0
66	V	1100	0	1114	27	0
67	DH	763	0	824	20	0
67	W	808	0	871	15	0
68	DI	676	0	677	18	0
68	X	676	0	677	24	0
69	DJ	1032	0	1066	29	0
69	Y	1032	0	1066	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	DK	1110	0	1182	25	0
70	Z	1110	0	1182	25	0
71	DL	1072	0	1123	21	0
71	a	1086	0	1132	18	0
72	DM	570	0	609	17	0
72	b	578	0	613	15	0
73	DN	779	0	833	22	0
73	c	779	0	832	18	0
74	DO	614	0	630	10	0
74	d	614	0	627	6	0
75	DP	476	0	510	22	0
75	e	487	0	523	14	0
76	DQ	449	0	426	12	0
76	f	454	0	432	8	0
77	DR	461	0	499	27	0
77	g	474	0	515	16	0
78	DS	574	0	606	24	0
78	h	574	0	606	24	0
79	AR	2398	0	2374	64	0
79	DT	2398	0	2374	79	1
80	P0	845	0	884	33	0
80	p0	845	0	884	54	0
81	12	480	0	477	30	0
82	L1	1711	0	1817	62	0
82	l1	1711	0	1817	109	0
83	0	4	0	0	0	0
83	1	556	0	0	0	0
83	2	1	0	0	0	0
83	3	15	0	0	0	0
83	4	11	0	0	0	0
83	6	4	0	0	0	0
83	8	3	0	0	0	0
83	9	2	0	0	0	0
83	AB	2	0	0	0	0
83	AC	1	0	0	0	0
83	AE	3	0	0	0	0
83	AF	2	0	0	0	0
83	AG	3	0	0	0	0
83	AH	2	0	0	0	0
83	AK	1	0	0	0	0
83	AP	2	0	0	0	0
83	AR	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	AS	380	0	0	0	0
83	AT	10	0	0	0	0
83	AU	10	0	0	0	0
83	AW	4	0	0	0	0
83	AX	2	0	0	0	0
83	AY	1	0	0	0	0
83	AZ	1	0	0	0	0
83	B	172	0	0	0	0
83	BB	4	0	0	0	0
83	BE	2	0	0	0	0
83	BF	1	0	0	0	0
83	BH	1	0	0	0	0
83	BI	1	0	0	0	0
83	BJ	3	0	0	0	0
83	BK	2	0	0	0	0
83	BN	1	0	0	0	0
83	BO	1	0	0	0	0
83	BS	1	0	0	0	0
83	BV	1	0	0	0	0
83	BZ	4	0	0	0	0
83	CA	3	0	0	0	0
83	CJ	1	0	0	0	0
83	CK	2	0	0	0	0
83	CL	3	0	0	0	0
83	CM	148	0	0	0	0
83	CO	1	0	0	0	0
83	CP	1	0	0	0	0
83	CQ	2	0	0	0	0
83	CY	1	0	0	0	0
83	D	1	0	0	0	0
83	DA	1	0	0	0	0
83	DB	4	0	0	0	0
83	DG	2	0	0	0	0
83	DJ	2	0	0	0	0
83	DQ	1	0	0	0	0
83	G	2	0	0	0	0
83	I	1	0	0	0	0
83	J	1	0	0	0	0
83	K	1	0	0	0	0
83	Q	2	0	0	0	0
83	R	1	0	0	0	0
83	V	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	Y	3	0	0	0	0
83	Z	2	0	0	0	0
83	f	1	0	0	0	0
83	g	1	0	0	0	0
83	i	1	0	0	0	0
83	j	3	0	0	0	0
83	k	6	0	0	0	0
83	o	4	0	0	0	0
83	r	2	0	0	0	0
83	s	1	0	0	0	0
83	u	2	0	0	0	0
83	v	2	0	0	0	0
83	w	3	0	0	0	0
83	x	2	0	0	0	0
84	1	57	0	52	4	0
84	AS	57	0	52	1	0
85	1	27	0	0	2	0
85	AS	27	0	0	1	0
86	AH	1	0	0	0	0
86	AK	1	0	0	0	0
86	AN	1	0	0	0	0
86	AP	1	0	0	0	0
86	AQ	1	0	0	0	0
86	CB	1	0	0	0	0
86	CE	1	0	0	0	0
86	CH	1	0	0	0	0
86	CJ	1	0	0	0	0
86	CK	1	0	0	0	0
86	DN	1	0	0	0	0
86	DO	1	0	0	0	0
86	DQ	1	0	0	0	0
86	DS	1	0	0	0	0
86	c	1	0	0	0	0
86	d	1	0	0	0	0
86	f	1	0	0	0	0
86	h	1	0	0	0	0
87	1	20	0	0	0	0
87	4	3	0	0	1	0
87	AS	26	0	0	3	0
87	B	12	0	0	0	0
87	BQ	3	0	0	1	0
87	BV	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	1	1	0	0	1	0
All	All	410139	0	305114	6944	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (6944) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:6:102:ILE:CG2	24:6:110:LYS:HD2	1.77	1.13
1:1:1233:G:H1	1:1:1247:A:N6	1.46	1.13
24:6:102:ILE:HG21	24:6:110:LYS:HD2	1.38	1.05
46:B:671:G:H3'	46:B:672:U:H5'	1.39	1.03
77:g:50:THR:OG1	77:g:53:LYS:HB2	1.58	1.01
59:O:132:GLU:OE2	59:O:136:LEU:HD13	1.63	0.96
46:CM:271:G:H1	46:CM:281:U:H3	1.12	0.95
54:CU:25:GLU:HB2	54:CU:31:LYS:HG3	1.47	0.95
46:CM:543:A:OP1	77:DR:31:GLN:NE2	2.00	0.95
66:V:117:SER:HB2	66:V:123:ARG:HB2	1.47	0.94
69:DJ:2:THR:HG22	69:DJ:3:ARG:H	1.31	0.94
80:p0:33:VAL:HG22	80:p0:37:GLN:HB3	1.48	0.94
70:Z:107:PHE:HE2	70:Z:114:LYS:HD3	1.33	0.94
1:AS:1870:A:N7	20:BM:20:ARG:NH2	2.16	0.94
1:AS:538:G:H1	1:AS:547:U:H3	0.97	0.94
1:AS:185:U:H3	1:AS:229:C:N4	1.65	0.93
46:B:701:G:H2'	46:B:702:G:H2'	1.51	0.93
46:CM:694:C:H3'	46:CM:695:C:H5''	1.48	0.92
1:AS:1014:G:H1	1:AS:1030:U:H3	0.95	0.92
46:CM:1410:A:H2'	49:CP:87:ALA:HB3	1.51	0.92
70:Z:107:PHE:CE2	70:Z:114:LYS:HD3	2.05	0.91
46:CM:218:A:H3'	46:CM:219:A:H5''	1.53	0.90
1:AS:437:G:H22	1:AS:620:A:H61	1.19	0.90
79:DT:75:SER:HA	79:DT:116:ILE:HD13	1.54	0.90
24:6:102:ILE:HG22	24:6:110:LYS:HD2	1.52	0.89
48:CO:97:LEU:HD22	48:CO:232:HIS:CD2	2.08	0.89
43:AP:34:SER:O	43:AP:40:LYS:CD	2.21	0.88
1:AS:1575:A:OP1	1:AS:2500:G:N2	2.05	0.88
46:CM:272:G:N2	46:CM:280:C:O2	2.04	0.88
35:CB:58:ARG:HD3	35:CB:59:PRO:HD2	1.53	0.88
82:11:59:PRO:HB3	82:11:169:VAL:HB	1.52	0.87
35:AH:58:ARG:HD3	35:AH:59:PRO:HD2	1.56	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:2233:A:HO2'	46:CM:1744:G:HO2'	1.20	0.87
1:1:2420:G:H1	1:1:2483:U:H3	1.22	0.87
1:AS:3313:G:H1	1:AS:3322:U:H3	1.21	0.87
1:AS:3162:U:H3	1:AS:3166:A:H2	1.23	0.86
78:DS:157:GLU:HG2	78:DS:159:LEU:HG	1.56	0.86
46:CM:95:G:OP1	51:CR:6:LYS:NZ	2.09	0.86
77:DR:50:THR:OG1	77:DR:53:LYS:HB2	1.74	0.86
46:B:880:G:H1	46:B:902:U:H3	1.24	0.86
1:AS:447:U:H2'	1:AS:448:U:H5''	1.55	0.86
50:CQ:215:GLU:HG3	50:CQ:216:ASP:H	1.39	0.86
46:CM:272:G:N1	46:CM:280:C:N3	2.23	0.86
59:CZ:80:ASN:O	59:CZ:82:PRO:HD3	1.73	0.86
43:AP:35:LEU:HA	43:AP:40:LYS:HD3	1.58	0.85
1:AS:617:A:H5'	1:AS:619:A:H1'	1.57	0.85
46:CM:474:U:H2'	77:DR:31:GLN:HE21	1.41	0.85
79:DT:42:LEU:HB2	79:DT:62:PHE:HB2	1.59	0.85
46:CM:701:G:H5'	53:CT:230:ARG:HH12	1.42	0.84
82:l1:26:ARG:NH1	82:l1:210:MET:SD	2.50	0.84
1:1:572:U:H2'	1:1:573:G:H8	1.42	0.84
46:CM:880:G:H1	46:CM:902:U:H3	1.25	0.84
1:1:2070:A:O2'	20:z:114:LYS:NZ	2.11	0.84
18:BK:50:GLN:OE1	18:BK:56:ARG:NH2	2.11	0.83
52:H:95:ASN:OD1	52:H:107:LYS:NZ	2.11	0.83
46:CM:1236:U:O2'	46:CM:1237:C:O2	1.95	0.83
13:s:61:ARG:NH1	45:i:42:ALA:O	2.12	0.83
46:B:512:G:H1	46:B:541:C:H5	1.27	0.83
46:B:871:U:OP1	48:D:214:LYS:NZ	2.12	0.83
45:i:103:LEU:HB3	45:i:109:GLN:HG3	1.61	0.82
6:l:359:GLU:O	21:0:26:ARG:NH1	2.11	0.82
80:P0:8:LYS:HG2	80:P0:58:MET:HE1	1.61	0.82
46:CM:697:U:H3	46:CM:724:G:H1	1.27	0.82
46:CM:484:G:H1	46:CM:499:U:H3	0.86	0.82
46:B:1042:U:H3'	46:B:1043:U:H2'	1.61	0.82
59:O:68:GLU:O	59:O:69:GLU:HG3	1.80	0.82
46:CM:271:G:N2	46:CM:281:U:O2	2.12	0.82
46:B:853:G:H1	46:B:945:U:H3	1.24	0.82
32:AE:45:THR:HG21	32:AE:89:PHE:HA	1.62	0.82
1:1:1231:U:H4'	1:1:1232:G:H5'	1.60	0.81
46:B:721:C:O2'	46:B:722:A:H5'	1.80	0.81
46:B:1198:G:H1	46:B:1436:U:H3	1.26	0.81
46:B:1431:G:N2	78:h:129:THR:O	2.12	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BF:7:ASN:OD1	13:BF:10:ARG:HG3	1.80	0.81
1:1:2086:C:H1'	1:1:3309:A:C8	2.14	0.81
46:B:1334:G:N3	46:B:1365:C:N4	2.28	0.81
46:B:1218:G:H1	46:B:1237:C:H5	1.29	0.81
20:BM:160:GLU:OE2	20:BM:163:ARG:NH1	2.13	0.81
46:CM:1067:C:H4'	68:DI:58:TYR:HE1	1.45	0.81
69:DJ:75:ILE:HD11	69:DJ:93:LEU:HD11	1.63	0.81
54:CU:94:ILE:HD13	54:CU:114:LEU:HD12	1.63	0.81
80:p0:57:THR:HA	80:p0:60:ARG:HD2	1.63	0.81
54:CU:81:PHE:HB3	54:CU:84:ARG:HD2	1.62	0.80
69:DJ:11:LEU:HD11	69:DJ:37:PHE:HE2	1.45	0.80
46:CM:216:A:N6	46:CM:829:A:O2'	2.13	0.80
46:B:1236:U:O2'	46:B:1237:C:O2	2.00	0.80
1:1:2530:C:N4	31:AD:59:GLU:OE2	2.14	0.80
46:B:1753:A:N1	73:c:80:HIS:ND1	2.30	0.80
1:1:581:A:H5''	34:AG:106:ASN:HD21	1.46	0.80
1:AS:185:U:H3	1:AS:229:C:H42	0.82	0.80
46:CM:151:G:O6	71:DL:128:ARG:NH2	2.14	0.79
70:DK:107:PHE:HD2	70:DK:114:LYS:HD3	1.46	0.79
46:CM:538:G:N2	77:DR:25:GLU:OE2	2.14	0.79
1:AS:1561:U:O2'	1:AS:1562:G:OP1	2.00	0.79
1:1:3235:A:N7	8:n:45:ARG:NH1	2.30	0.79
1:AS:850:G:O2'	20:BM:130:ASN:OD1	2.00	0.79
1:AS:1657:G:H2'	1:AS:1658:G:C8	2.18	0.79
46:CM:504:A:H62	77:DR:27:PRO:HB3	1.47	0.79
46:B:696:U:H3'	46:B:697:U:H5''	1.65	0.79
54:J:48:ASN:OD1	54:J:167:GLN:NE2	2.14	0.79
30:AC:8:THR:HG22	30:AC:10:HIS:H	1.47	0.79
50:F:56:THR:O	50:F:60:LEU:HG	1.83	0.79
46:B:217:A:N6	46:B:828:U:O2	2.16	0.79
51:CR:45:VAL:HG23	51:CR:61:VAL:HG11	1.64	0.79
1:1:617:A:H5'	1:1:619:A:H1'	1.64	0.78
1:1:1481:G:N2	35:AH:4:ARG:HD2	1.98	0.78
1:1:2200:A:H2'	1:1:2201:A:C8	2.17	0.78
46:B:696:U:H3'	46:B:697:U:C5'	2.13	0.78
46:CM:148:C:H42	46:CM:162:A:H61	1.30	0.78
50:F:65:ARG:HD2	57:M:91:ARG:HH11	1.48	0.78
51:G:11:ARG:HH12	51:G:24:SER:HB3	1.47	0.78
3:AU:103:G:OP2	3:AU:105:A:O2'	2.01	0.78
46:B:509:A:OP2	56:L:176:ASN:ND2	2.14	0.78
65:DF:49:LYS:NZ	65:DF:80:LYS:O	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:DG:117:SER:HB2	66:DG:123:ARG:HB2	1.65	0.78
1:1:3199:G:H1	1:1:3218:U:H3	1.29	0.78
59:O:107:ASP:HB3	59:O:113:ARG:HG3	1.65	0.78
5:AX:10:ARG:NH2	5:AX:263:THR:O	2.17	0.78
30:BW:8:THR:HG22	30:BW:10:HIS:H	1.49	0.78
18:x:50:GLN:OE1	18:x:56:ARG:NH2	2.16	0.77
43:AP:34:SER:O	43:AP:40:LYS:HD2	1.84	0.77
1:AS:2836:A:H5'	12:BE:114:GLY:HA2	1.67	0.77
58:CY:46:LYS:NZ	58:CY:50:GLU:OE1	2.17	0.77
65:DF:69:ILE:HG22	65:DF:73:MET:HE2	1.66	0.77
82:l1:73:ASP:O	82:l1:75:ASP:N	2.17	0.77
1:1:447:U:H3	1:1:483:U:H3	1.29	0.77
50:F:138:VAL:HG22	50:F:152:LYS:HG2	1.66	0.77
4:AW:54:ARG:HH21	4:AW:58:LEU:HD11	1.48	0.77
23:BP:19:VAL:HG23	23:BP:20:ALA:H	1.49	0.77
59:O:104:CYS:SG	59:O:115:VAL:HA	2.23	0.77
43:AP:34:SER:O	43:AP:40:LYS:HD3	1.83	0.77
1:AS:1631:G:N2	1:AS:1634:A:OP2	2.16	0.77
45:i:63:ALA:O	45:i:65:LYS:N	2.18	0.77
46:CM:586:U:OP2	77:DR:26:LYS:NZ	2.17	0.77
46:B:593:G:H5'	56:L:40:ARG:HH22	1.49	0.76
46:B:553:A:N3	46:B:588:C:O2'	2.18	0.76
79:DT:158:SER:HA	79:DT:201:LEU:HD12	1.67	0.76
1:1:2191:A:H2'	1:1:2192:A:C8	2.19	0.76
3:AU:122:U:H3	3:AU:131:G:H1	1.32	0.76
1:1:653:C:H2'	1:1:654:A:H8	1.50	0.76
1:1:1233:G:N2	1:1:1247:A:N1	2.30	0.76
11:q:8:GLN:HB3	11:q:72:LYS:HD2	1.67	0.76
57:M:17:GLN:H	57:M:88:PRO:HB3	1.50	0.76
11:BD:92:PHE:HB2	11:BD:142:ASP:HB3	1.68	0.76
1:1:3021:A:N1	24:6:86:ARG:NH2	2.33	0.76
65:U:29:MET:HB2	65:U:54:LEU:HD22	1.68	0.76
1:1:1519:U:H5'	26:8:113:LEU:HD13	1.67	0.76
46:CM:1445:C:OP2	65:DF:138:THR:OG1	2.02	0.76
43:AP:35:LEU:HA	43:AP:40:LYS:CE	2.16	0.76
45:CL:67:LYS:HG2	65:DF:129:TRP:HZ2	1.51	0.76
66:V:27:LYS:HG2	66:V:111:ILE:HD12	1.68	0.76
1:AS:1279:C:OP1	80:p0:60:ARG:NH1	2.19	0.76
1:AS:3165:U:H2'	1:AS:3166:A:O4'	1.86	0.76
1:1:800:C:OP1	6:l:99:ARG:NH2	2.19	0.76
23:5:19:VAL:HG23	23:5:20:ALA:H	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:I:159:ARG:NH1	53:I:170:THR:OG1	2.19	0.76
80:p0:41:ILE:HG22	80:p0:51:VAL:HG21	1.68	0.76
46:B:1242:U:O2'	57:M:8:ARG:NH2	2.19	0.75
1:AS:1436:G:OP1	6:AY:84:HIS:NE2	2.20	0.75
1:AS:2199:G:N2	1:AS:2202:A:OP2	2.19	0.75
46:CM:853:G:H1	46:CM:945:U:H3	1.31	0.75
65:DF:134:ARG:HB2	65:DF:136:GLN:HE22	1.49	0.75
72:DM:78:VAL:HG12	72:DM:81:ARG:HH21	1.50	0.75
19:BL:96:PHE:O	19:BL:117:ASN:ND2	2.20	0.75
1:1:2163:G:O2'	1:1:2292:U:OP2	2.05	0.75
46:CM:1598:A:OP1	52:CS:107:LYS:NZ	2.18	0.75
46:B:869:A:H62	46:B:913:U:H3	1.33	0.75
50:F:54:SER:O	50:F:95:ARG:NH1	2.19	0.75
55:K:2:GLY:O	55:K:24:LYS:NZ	2.14	0.75
3:4:89:A:OP1	36:AI:1:MET:N	2.19	0.75
24:6:102:ILE:HG22	24:6:110:LYS:CD	2.16	0.75
46:B:1675:U:O2	46:B:1701:A:N6	2.14	0.75
47:CN:200:ASP:HB2	64:DE:85:VAL:HG23	1.67	0.75
1:AS:449:U:H2'	1:AS:450:G:C8	2.21	0.75
6:AY:290:LEU:HD22	19:BL:129:LEU:HD11	1.69	0.75
1:1:831:G:O2'	1:1:853:G:N2	2.19	0.75
24:BQ:80:ARG:NH1	24:BQ:97:ASP:OD1	2.20	0.75
46:CM:345:G:H5''	58:CY:85:ILE:HD11	1.68	0.75
46:B:961:G:H1	46:B:1008:A:HO2'	0.75	0.74
5:AX:21:ARG:HE	5:AX:269:GLN:HG3	1.52	0.74
46:CM:1410:A:H2'	49:CP:87:ALA:CB	2.17	0.74
1:1:1091:U:H4'	1:1:1092:U:H5'	1.69	0.74
1:AS:3259:A:OP1	5:AX:128:LYS:NZ	2.21	0.74
82:l1:49:PHE:HB2	82:l1:193:LEU:HD22	1.67	0.74
1:1:1248:A:H2'	1:1:1249:U:H5'	1.67	0.74
1:1:1653:C:O2'	1:1:1793:A:OP2	2.05	0.74
1:AS:1091:U:H4'	1:AS:1092:U:H5'	1.67	0.74
54:J:25:GLU:HG3	54:J:35:ARG:HH12	1.52	0.74
46:CM:829:A:H2'	46:CM:830:G:H8	1.52	0.74
15:u:17:ARG:NH2	15:u:58:THR:O	2.20	0.74
1:1:1672:A:O2'	23:5:103:GLN:OE1	2.04	0.74
43:AP:36:PHE:O	43:AP:41:ARG:NH1	2.20	0.74
46:CM:847:A:O2'	46:CM:948:A:N1	2.19	0.74
12:BE:43:VAL:HG21	12:BE:197:VAL:HG13	1.69	0.74
16:BI:42:PRO:HD3	16:BI:61:ILE:HG13	1.69	0.74
79:DT:102:GLN:NE2	79:DT:138:ILE:O	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:P0:71:PRO:O	80:P0:73:PHE:N	2.18	0.74
1:AS:831:G:O2'	1:AS:853:G:N2	2.20	0.74
46:CM:127:G:N7	53:CT:202:ARG:NH2	2.35	0.74
46:B:1511:A:H2'	46:B:1512:A:C8	2.23	0.74
47:C:124:THR:HG22	47:C:174:TRP:HE1	1.52	0.74
69:DJ:37:PHE:HE1	69:DJ:103:ILE:HG13	1.53	0.74
82:l1:93:LEU:HD21	82:l1:100:ILE:HG23	1.70	0.74
12:BE:30:LYS:HG3	12:BE:63:GLU:HG3	1.69	0.74
84:1:3403:3K5:H47	84:1:3403:3K5:H15	1.70	0.73
52:H:156:ARG:HH12	75:e:67:ARG:HG3	1.53	0.73
46:CM:1353:G:H5''	66:DG:69:LYS:HE3	1.70	0.73
82:l1:76:ARG:HG2	82:l1:144:LEU:HD21	1.70	0.73
82:l1:76:ARG:NH1	82:l1:140:HIS:O	2.20	0.73
46:B:1543:A:OP1	62:R:115:TYR:OH	2.04	0.73
1:1:1631:G:N2	1:1:1634:A:OP2	2.18	0.73
43:AP:35:LEU:HA	43:AP:40:LYS:CD	2.18	0.73
46:B:1181:A:OP2	46:B:1450:G:N2	2.18	0.73
59:O:74:LEU:HA	78:h:150:VAL:HG11	1.68	0.73
1:AS:3161:U:H2'	1:AS:3162:U:C6	2.22	0.73
1:AS:1089:A:OP2	22:BO:120:LYS:NZ	2.20	0.73
25:7:80:ARG:HH21	53:I:131:LYS:HG2	1.54	0.73
46:B:766:U:H4'	46:B:767:G:H5''	1.71	0.73
1:AS:564:G:H2'	1:AS:565:A:C8	2.24	0.73
46:CM:122:U:H2'	46:CM:123:G:H5''	1.70	0.73
55:CV:139:ALA:HB3	55:CV:141:ARG:HH12	1.52	0.73
1:1:1202:G:OP1	12:r:157:TYR:OH	2.06	0.73
46:B:635:C:O2	54:J:110:ARG:NH2	2.21	0.73
82:L1:194:LEU:HD13	82:L1:200:ASN:HD22	1.53	0.73
24:6:102:ILE:CG2	24:6:110:LYS:CD	2.63	0.73
1:AS:2936:G:N2	1:AS:2939:A:OP2	2.20	0.73
45:CL:156:ALA:HB1	57:CX:17:GLN:HG2	1.71	0.73
46:CM:79:C:OP1	53:CT:159:ARG:NH2	2.20	0.73
46:CM:1042:U:H3'	46:CM:1043:U:H2'	1.70	0.73
1:1:1436:G:OP1	6:l:84:HIS:NE2	2.20	0.73
1:AS:2334:A:N3	18:BK:131:ARG:NH2	2.37	0.73
2:AT:39:U:H5'	45:CL:33:ASN:HD22	1.52	0.73
1:1:1657:G:H2'	1:1:1658:G:C8	2.23	0.73
18:x:122:ALA:HB3	18:x:143:PRO:HB2	1.70	0.73
46:B:1579:A:H2'	46:B:1580:A:H8	1.54	0.73
68:X:38:LYS:HD2	68:X:49:GLU:HG3	1.71	0.73
1:AS:1562:G:N2	1:AS:1564:U:O4	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DT:117:ALA:HB2	79:DT:122:GLN:HB2	1.70	0.73
82:l1:26:ARG:H	82:l1:26:ARG:HD3	1.52	0.73
1:1:3157:A:OP1	11:q:23:ARG:NH1	2.22	0.72
1:AS:3318:G:H5''	1:AS:3319:U:H4'	1.70	0.72
46:CM:1156:A:H2'	46:CM:1157:G:C8	2.23	0.72
64:DE:27:ASP:OD2	79:DT:38:ARG:NH2	2.19	0.72
46:B:1375:C:O5'	64:T:48:ASN:ND2	2.21	0.72
1:1:2470:C:H1'	82:l1:207:LYS:HE3	1.69	0.72
46:B:1043:U:O2'	46:B:1045:U:OP2	2.06	0.72
1:AS:437:G:N2	1:AS:620:A:H61	1.88	0.72
28:BU:78:ASN:OD1	31:BX:37:ARG:NH2	2.22	0.72
46:CM:814:A:O2'	46:CM:815:U:OP2	2.06	0.72
1:1:3194:G:H4'	15:u:129:VAL:HG11	1.71	0.72
46:B:1665:C:OP1	55:K:59:ARG:NH2	2.22	0.72
55:K:11:ARG:O	58:N:133:LYS:NZ	2.23	0.72
66:DG:130:ARG:NH1	66:DG:131:ASP:OD1	2.21	0.72
13:s:101:ASN:HD22	13:s:130:VAL:HA	1.55	0.72
79:AR:16:HIS:CE1	79:AR:37:SER:HB2	2.24	0.72
1:AS:316:U:O2'	37:CD:29:LYS:NZ	2.21	0.72
26:8:75:LYS:HB3	26:8:81:THR:HG23	1.71	0.72
46:B:1400:U:H5''	64:T:3:ARG:HE	1.54	0.72
1:AS:653:C:H2'	1:AS:654:A:H8	1.53	0.72
1:AS:2086:C:H1'	1:AS:3309:A:C8	2.25	0.72
17:BJ:63:THR:HG21	17:BJ:69:LYS:HB2	1.71	0.72
18:BK:122:ALA:HB3	18:BK:143:PRO:HB2	1.72	0.72
1:AS:2867:G:O2'	41:CH:24:TYR:O	2.07	0.72
1:1:2428:G:H22	1:1:2475:U:H3	1.38	0.72
1:AS:153:U:OP2	36:CC:103:LYS:NZ	2.19	0.72
1:AS:740:A:OP1	19:BL:66:ARG:NH2	2.23	0.72
8:BA:34:VAL:HB	8:BA:89:LYS:HE3	1.72	0.72
55:K:136:VAL:O	55:K:141:ARG:NH2	2.23	0.71
1:AS:2492:U:OP2	1:AS:2558:G:N2	2.23	0.71
1:1:627:U:H2'	1:1:628:A:C8	2.25	0.71
1:AS:3165:U:C2	1:AS:3166:A:H1'	2.25	0.71
31:BX:57:GLU:HB2	35:CB:94:LEU:HD11	1.71	0.71
48:CO:30:PHE:CE1	48:CO:46:THR:HB	2.25	0.71
46:B:945:U:H5'	60:P:55:ARG:HD3	1.71	0.71
1:1:1936:G:H21	1:1:3327:A:H8	1.38	0.71
46:B:139:U:OP1	53:I:149:LYS:NZ	2.22	0.71
46:B:1422:A:OP2	50:F:28:ARG:NH2	2.23	0.71
3:AU:29:U:H5''	14:BG:27:ASP:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:CP:211:ALA:O	49:CP:215:ASN:ND2	2.22	0.71
1:1:1279:C:H2'	1:1:1280:C:H6	1.55	0.71
1:1:1400:G:N2	1:1:1403:A:OP2	2.16	0.71
63:S:21:VAL:HG22	63:S:64:ILE:HG12	1.73	0.71
33:BZ:106:ARG:NH2	33:BZ:122:ASN:O	2.24	0.71
80:p0:101:VAL:O	80:p0:103:ASN:N	2.22	0.71
65:U:140:THR:HA	65:U:143:ARG:HH21	1.54	0.71
16:v:183:THR:HG22	16:v:187:ARG:HB2	1.72	0.71
19:y:96:PHE:O	19:y:117:ASN:ND2	2.22	0.71
46:B:480:U:H2'	46:B:481:A:C8	2.26	0.71
15:BH:17:ARG:NH2	15:BH:58:THR:O	2.24	0.71
46:CM:553:A:N3	46:CM:588:C:O2'	2.23	0.71
1:1:2155:G:OP2	4:j:128:ARG:NH1	2.24	0.71
1:AS:1020:G:N2	1:AS:1023:A:OP2	2.24	0.70
1:AS:1034:U:H1'	7:AZ:3:MET:HE3	1.72	0.70
1:AS:1761:U:C5	20:BM:43:LYS:HE3	2.26	0.70
80:p0:45:LEU:HD12	80:p0:49:ALA:HB3	1.72	0.70
1:AS:2163:G:O2'	1:AS:2292:U:OP2	2.09	0.70
1:AS:2191:A:H2'	1:AS:2192:A:C8	2.25	0.70
23:BP:68:VAL:HG12	23:BP:69:SER:H	1.55	0.70
46:CM:1520:C:OP2	72:DM:77:ARG:NH1	2.22	0.70
46:CM:1529:G:N2	46:CM:1556:A:OP2	2.25	0.70
1:1:572:U:H2'	1:1:573:G:C8	2.24	0.70
1:AS:662:U:H2'	1:AS:663:A:C8	2.27	0.70
1:AS:834:G:O6	44:CK:4:ARG:NH2	2.25	0.70
1:AS:2638:C:O2'	45:CL:40:ASP:OD2	2.08	0.70
11:q:80:THR:HA	11:q:83:THR:HG22	1.72	0.70
46:B:856:G:H2'	46:B:857:G:C8	2.26	0.70
1:AS:538:G:N2	1:AS:547:U:O2	2.22	0.70
1:AS:833:A:OP2	44:CK:4:ARG:NH1	2.24	0.70
1:AS:1735:U:HO2'	35:CB:56:THR:HG1	1.33	0.70
1:1:2899:C:H2'	1:1:2900:C:C6	2.27	0.70
1:1:3179:U:OP2	15:u:121:ARG:NH2	2.25	0.70
1:AS:1384:U:OP1	33:BZ:105:LYS:NZ	2.25	0.70
20:BM:165:ARG:NE	46:CM:835:A:OP1	2.25	0.70
46:CM:477:C:OP1	56:CW:121:SER:OG	2.07	0.70
1:1:564:G:H2'	1:1:565:A:C8	2.26	0.70
1:1:1251:C:H2'	1:1:1252:G:H8	1.56	0.70
13:s:46:VAL:HG12	45:i:33:ASN:HB3	1.73	0.70
37:AJ:97:ARG:H	82:l:215:ARG:HH22	1.40	0.70
1:AS:1542:A:N7	16:BI:71:ARG:NH1	2.38	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BQ:30:GLY:HA3	24:BQ:66:LYS:HE2	1.72	0.70
45:CL:124:ASP:OD2	50:CQ:118:ARG:NH1	2.24	0.70
46:CM:63:G:O2'	46:CM:168:U:OP1	2.10	0.70
46:CM:78:A:H8	53:CT:154:ARG:HG3	1.54	0.70
82:l1:34:LEU:HD11	82:l1:183:ILE:HG21	1.72	0.70
1:l:1479:G:O6	35:AH:4:ARG:NH2	2.24	0.70
12:r:30:LYS:HG3	12:r:63:GLU:HG3	1.74	0.70
46:B:903:U:H2'	46:B:904:A:C8	2.27	0.70
80:p0:16:ARG:NH2	80:p0:62:ALA:O	2.24	0.70
14:t:115:ARG:NH2	14:t:147:PHE:O	2.25	0.70
4:AW:36:GLU:OE1	4:AW:163:ARG:NH1	2.25	0.70
46:CM:1339:G:O6	46:CM:1354:U:O2	2.08	0.70
1:l:1172:C:H4'	17:w:90:PRO:HD3	1.74	0.70
46:B:1354:U:N3	46:B:1355:A:N7	2.39	0.70
1:AS:976:A:H2'	1:AS:977:U:H5'	1.74	0.70
13:s:109:HIS:HD2	13:s:123:TYR:H	1.38	0.70
28:BU:3:LYS:NZ	28:BU:30:ASP:OD1	2.19	0.70
32:AE:45:THR:HG22	32:AE:47:ASP:H	1.57	0.69
1:AS:429:U:H2'	1:AS:430:G:H8	1.56	0.69
16:BI:159:ARG:HB2	16:BI:164:LEU:HB2	1.73	0.69
50:CQ:128:MET:HE2	50:CQ:135:VAL:HG12	1.74	0.69
1:l:2736:C:O2	84:l:3403:3K5:H36	1.92	0.69
25:BR:97:LYS:HG3	25:BR:98:PRO:HD3	1.74	0.69
46:B:1460:G:H2'	46:B:1461:A:H8	1.57	0.69
63:S:37:LEU:HA	63:S:44:ARG:HH21	1.56	0.69
1:l:496:A:H4'	8:n:27:GLN:HG3	1.74	0.69
50:F:214:ASP:OD1	50:F:215:GLU:N	2.18	0.69
6:AY:109:ARG:HG2	16:BI:203:ARG:HG3	1.73	0.69
59:CZ:59:LEU:HD11	59:CZ:89:ILE:HD11	1.73	0.69
46:CM:636:C:OP2	69:DJ:32:LYS:NZ	2.24	0.69
46:CM:829:A:H2'	46:CM:830:G:C8	2.28	0.69
1:l:2370:C:H1'	5:k:266:ARG:HH21	1.56	0.69
46:B:1026:G:H2'	46:B:1027:G:C8	2.27	0.69
65:U:110:ARG:NH2	65:U:111:ASP:OD1	2.26	0.69
46:CM:139:U:OP1	53:CT:149:LYS:NZ	2.23	0.69
54:CU:48:ASN:OD1	54:CU:167:GLN:NE2	2.24	0.69
82:l1:44:GLN:HB3	82:l1:45:ARG:HE	1.57	0.69
11:q:92:PHE:HB2	11:q:142:ASP:HB3	1.74	0.69
16:v:159:ARG:HB2	16:v:164:LEU:HB2	1.73	0.69
46:B:853:G:OP1	60:P:121:ARG:NH1	2.24	0.69
57:M:80:LEU:HB3	57:M:82:ILE:HG23	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:T:103:ASP:OD1	64:T:104:ALA:N	2.26	0.69
1:AS:412:G:H21	18:BK:118:GLN:HE22	1.40	0.69
46:CM:1698:U:H2'	46:CM:1699:G:H4'	1.74	0.69
79:DT:19:TRP:HB2	79:DT:38:ARG:HD2	1.75	0.69
63:S:12:LYS:HG3	63:S:13:LYS:H	1.58	0.69
46:CM:1145:A:H2'	46:CM:1146:C:H6	1.58	0.69
46:CM:1669:U:O4	46:CM:1707:G:N2	2.26	0.69
59:CZ:129:ASP:HA	59:CZ:133:ARG:HD3	1.75	0.69
69:DJ:88:ARG:O	69:DJ:92:ASN:ND2	2.25	0.69
46:B:122:U:H2'	46:B:123:G:H5''	1.75	0.69
46:B:702:G:H1'	46:B:703:U:H1'	1.75	0.69
52:H:109:LYS:O	52:H:113:ILE:HD12	1.91	0.69
1:AS:2545:C:O2'	1:AS:2547:G:N3	2.26	0.69
46:CM:690:C:H2'	46:CM:691:U:C6	2.27	0.69
57:CX:15:LEU:O	57:CX:19:GLY:HA2	1.93	0.69
79:DT:247:TYR:HB3	79:DT:262:LEU:HD12	1.75	0.69
1:1:662:U:H2'	1:1:663:A:C8	2.28	0.68
1:1:680:U:H5''	1:1:681:U:H5	1.56	0.68
1:1:3014:U:OP2	1:1:3064:C:N4	2.26	0.68
46:CM:1511:A:H2'	46:CM:1512:A:C8	2.28	0.68
1:1:2867:G:O2'	41:AN:24:TYR:O	2.11	0.68
20:z:73:GLY:HA2	20:z:76:MET:HE2	1.75	0.68
46:B:477:C:OP1	56:L:121:SER:OG	2.11	0.68
46:B:540:A:N6	77:g:25:GLU:OE2	2.26	0.68
46:B:681:C:H3'	46:B:682:A:C8	2.29	0.68
46:B:1131:G:H2'	46:B:1132:A:C8	2.28	0.68
54:J:25:GLU:HB2	54:J:31:LYS:HG3	1.75	0.68
55:K:56:ARG:NH1	55:K:180:GLY:O	2.26	0.68
1:AS:71:C:O2'	14:BG:66:ASN:OD1	2.11	0.68
46:CM:336:C:H5''	55:CV:10:LYS:HD2	1.75	0.68
46:CM:515:U:H2'	46:CM:516:A:H8	1.58	0.68
1:1:2334:A:N3	18:x:131:ARG:NH2	2.40	0.68
15:u:14:GLU:HG2	15:u:17:ARG:HG2	1.76	0.68
46:B:1452:G:O2'	46:B:1589:C:OP1	2.11	0.68
1:AS:496:A:OP1	8:BA:81:ARG:NH1	2.26	0.68
22:BO:49:GLN:HA	22:BO:52:MET:HE3	1.75	0.68
82:l:19:TYR:HD2	82:l:210:MET:HB3	1.57	0.68
46:B:944:U:OP2	74:d:20:LYS:NZ	2.27	0.68
46:B:1087:G:OP2	70:Z:7:ARG:NH1	2.24	0.68
46:B:1239:U:OP2	59:O:46:ARG:NH1	2.26	0.68
1:AS:628:A:H2'	1:AS:629:A:C8	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1663:A:H2'	1:AS:1664:G:C8	2.28	0.68
1:AS:2557:G:O6	10:BC:48:SER:OG	2.11	0.68
54:CU:5:ILE:HG21	54:CU:10:PRO:HB3	1.74	0.68
46:B:1410:A:H2'	49:E:87:ALA:HB3	1.75	0.68
51:G:104:ASP:HB3	51:G:110:ALA:HB2	1.76	0.68
50:CQ:48:GLU:HG2	50:CQ:88:TYR:HE2	1.58	0.68
67:DH:26:THR:HG22	67:DH:87:LYS:HG3	1.74	0.68
1:1:1251:C:H2'	1:1:1252:G:C8	2.28	0.68
4:j:27:ALA:O	4:j:128:ARG:NH2	2.24	0.68
1:AS:1662:G:H2'	1:AS:1663:A:H8	1.58	0.68
46:CM:482:C:H2'	46:CM:483:A:C8	2.28	0.68
46:CM:652:C:H5'	46:CM:653:G:OP2	1.93	0.68
46:CM:1156:A:H2'	46:CM:1157:G:H8	1.58	0.68
82:l1:36:VAL:HA	82:l1:204:LEU:HA	1.75	0.68
1:1:653:C:H2'	1:1:654:A:C8	2.28	0.68
1:1:660:U:H2'	1:1:661:C:C6	2.29	0.68
16:v:96:LYS:NZ	16:v:104:GLU:OE2	2.26	0.68
47:C:84:ARG:NH1	47:C:203:PHE:O	2.26	0.68
15:BH:23:ASN:ND2	15:BH:23:ASN:O	2.26	0.68
46:CM:65:A:H2	46:CM:84:A:H62	1.39	0.68
82:L1:44:GLN:O	82:L1:46:ASP:N	2.27	0.68
1:1:3287:A:H2'	1:1:3288:A:C8	2.28	0.68
46:B:814:A:O2'	46:B:815:U:OP2	2.11	0.68
45:CL:42:ALA:O	45:CL:44:ALA:N	2.26	0.68
1:1:2932:C:H2'	1:1:2933:G:C8	2.29	0.68
50:F:224:VAL:HG23	79:AR:188:ASP:HB2	1.75	0.68
1:AS:595:G:OP2	9:BB:32:LYS:NZ	2.27	0.68
14:BG:126:PHE:O	14:BG:130:THR:OG1	2.12	0.68
20:BM:30:THR:O	20:BM:34:ASN:ND2	2.27	0.68
1:1:627:U:H2'	1:1:628:A:H8	1.59	0.68
1:1:2191:A:H2'	1:1:2192:A:H8	1.57	0.68
59:O:129:ASP:O	59:O:131:ASP:N	2.27	0.68
1:AS:2669:A:H2'	1:AS:2670:G:C8	2.29	0.68
46:CM:533:A:OP1	56:CW:168:ARG:NH2	2.25	0.68
1:1:1253:C:H42	1:1:1257:G:N2	1.92	0.67
1:1:1789:C:H2'	4:j:184:ARG:HH22	1.57	0.67
21:0:73:LYS:NZ	21:0:97:VAL:O	2.25	0.67
46:B:784:U:H2'	46:B:785:G:H8	1.59	0.67
1:AS:2139:G:H5''	4:AW:227:ARG:HH12	1.57	0.67
46:CM:1485:G:H5''	66:DG:72:GLY:HA3	1.76	0.67
46:CM:1487:C:OP1	66:DG:122:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:365:A:OP1	6:l:85:ARG:NH1	2.27	0.67
1:1:2808:C:H5	1:1:2824:C:H42	1.42	0.67
46:B:1673:U:H2'	46:B:1674:U:O4'	1.94	0.67
46:B:1698:U:H2'	46:B:1699:G:O4'	1.94	0.67
13:BF:85:LYS:HE3	62:DC:11:THR:HA	1.75	0.67
58:CY:102:LYS:O	70:DK:13:ARG:NH1	2.18	0.67
75:DP:42:ARG:NH1	75:DP:58:GLU:O	2.28	0.67
46:B:987:G:N2	46:B:1747:G:O3'	2.27	0.67
46:B:1431:G:O2'	78:h:127:TYR:OH	2.12	0.67
64:T:71:PHE:HD1	64:T:72:LYS:H	1.41	0.67
46:CM:952:A:OP2	60:DA:124:ARG:NH2	2.26	0.67
48:D:190:PRO:HG2	48:D:192:VAL:HG23	1.74	0.67
51:G:45:VAL:HG23	51:G:61:VAL:HG11	1.76	0.67
60:P:54:LEU:HB3	60:P:60:VAL:HB	1.75	0.67
46:CM:222:C:N3	46:CM:823:G:N2	2.43	0.67
48:CO:190:PRO:HG2	48:CO:192:VAL:HG23	1.76	0.67
69:DJ:2:THR:HG22	69:DJ:3:ARG:N	2.09	0.67
1:1:115:A:OP2	16:v:2:GLY:N	2.27	0.67
1:1:833:A:OP2	44:AQ:4:ARG:NH1	2.27	0.67
7:m:289:LYS:HA	7:m:292:GLU:HG2	1.77	0.67
1:AS:2194:G:H22	1:AS:2207:A:H2	1.42	0.67
11:BD:47:LYS:HE3	11:BD:49:ASN:O	1.94	0.67
46:CM:821:U:H2'	46:CM:822:G:C8	2.29	0.67
46:CM:903:U:H2'	46:CM:904:A:C8	2.29	0.67
82:L1:175:GLU:HG3	82:L1:177:ASP:H	1.60	0.67
1:1:1782:G:H2'	1:1:1783:A:C8	2.30	0.67
55:K:158:ILE:HD11	55:K:163:ASP:OD1	1.95	0.67
1:AS:339:C:OP1	1:AS:1376:G:O2'	2.12	0.67
1:AS:447:U:O2'	1:AS:448:U:OP1	2.13	0.67
48:CO:28:ASP:HB3	48:CO:50:ARG:CD	2.25	0.67
70:DK:107:PHE:CD2	70:DK:114:LYS:HD3	2.30	0.67
79:DT:132:VAL:HB	79:DT:145:LEU:HD22	1.76	0.67
1:1:3039:C:H3'	20:z:62:ARG:HH22	1.59	0.67
16:v:143:ARG:O	16:v:149:ASN:ND2	2.28	0.67
46:CM:482:C:H2'	46:CM:483:A:H8	1.58	0.67
53:CT:57:ASP:HA	53:CT:106:LEU:HA	1.74	0.67
73:DN:74:CYS:SG	73:DN:75:VAL:N	2.67	0.67
1:1:739:C:H5''	19:y:69:ARG:HH22	1.59	0.67
46:B:1578:C:H2'	46:B:1579:A:H8	1.60	0.67
46:CM:869:A:H62	46:CM:913:U:H3	1.40	0.67
46:CM:1460:G:H2'	46:CM:1461:A:H8	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CR:11:ARG:HH12	51:CR:24:SER:HB2	1.59	0.67
1:1:1188:C:N4	1:1:1297:A:O2'	2.28	0.67
46:B:236:U:O2'	46:B:238:U:OP2	2.13	0.67
51:G:100:ARG:NH2	51:G:121:TYR:O	2.27	0.67
1:AS:1124:U:OP1	12:BE:4:ARG:NH1	2.27	0.67
1:AS:1217:A:N7	80:p0:9:VAL:HA	2.10	0.67
46:CM:784:U:H2'	46:CM:785:G:H8	1.56	0.67
1:1:480:G:H2'	1:1:481:G:H8	1.60	0.67
79:AR:42:LEU:HB2	79:AR:62:PHE:HB2	1.75	0.67
79:AR:52:ASP:O	79:AR:53:ASN:ND2	2.28	0.67
79:AR:200:THR:HG21	79:AR:241:ALA:HA	1.77	0.67
16:BI:143:ARG:O	16:BI:149:ASN:ND2	2.27	0.67
54:CU:5:ILE:HG22	54:CU:7:SER:H	1.60	0.67
62:DC:52:LYS:HB3	62:DC:80:LEU:HD13	1.76	0.67
70:DK:69:ARG:HG3	70:DK:117:ILE:HG12	1.77	0.67
1:1:429:U:H2'	1:1:430:G:H8	1.58	0.66
16:BI:113:LEU:HB2	16:BI:134:LEU:HD23	1.77	0.66
46:CM:1043:U:O2'	46:CM:1045:U:OP2	2.13	0.66
55:CV:139:ALA:HB3	55:CV:141:ARG:NH1	2.10	0.66
63:DD:86:LYS:HG2	63:DD:116:LEU:HD13	1.76	0.66
64:DE:78:ARG:HH11	64:DE:81:LYS:HD3	1.60	0.66
80:p0:5:ARG:O	80:p0:9:VAL:N	2.25	0.66
1:AS:600:U:C2	1:AS:602:A:H1'	2.30	0.66
1:AS:2932:C:H2'	1:AS:2933:G:H8	1.60	0.66
47:CN:205:ARG:NH2	64:DE:82:ASP:OD1	2.28	0.66
1:1:294:U:OP2	16:v:15:GLN:NE2	2.23	0.66
46:B:345:G:H5''	58:N:85:ILE:HD11	1.76	0.66
51:G:199:GLU:OE2	51:G:201:HIS:NE2	2.22	0.66
59:O:105:GLN:HG3	59:O:113:ARG:HD3	1.77	0.66
71:a:6:THR:HB	71:a:28:LEU:HB2	1.78	0.66
1:AS:3233:A:OP1	8:BA:45:ARG:NH2	2.29	0.66
63:DD:12:LYS:HG3	63:DD:13:LYS:H	1.60	0.66
75:DP:19:THR:HG23	75:DP:25:VAL:HG13	1.78	0.66
1:1:307:A:H2'	1:1:308:A:C8	2.29	0.66
13:s:47:GLN:HB2	45:i:34:THR:HG22	1.75	0.66
45:i:129:LEU:HD21	50:F:129:GLY:HA3	1.78	0.66
46:B:1276:G:H22	46:B:1309:G:N2	1.93	0.66
46:B:1282:G:N2	46:B:1285:A:OP2	2.23	0.66
46:B:1719:A:H2'	46:B:1720:C:C6	2.31	0.66
49:E:231:ALA:O	68:X:33:GLN:NE2	2.29	0.66
1:AS:437:G:H22	1:AS:620:A:N6	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:660:U:H2'	1:AS:661:C:C6	2.30	0.66
1:AS:3162:U:N3	1:AS:3166:A:H2	1.92	0.66
22:BO:142:SER:OG	22:BO:144:GLU:OE1	2.13	0.66
46:CM:824:U:OP2	58:CY:28:ASN:HB2	1.96	0.66
46:CM:826:U:H2'	46:CM:827:C:H5'	1.76	0.66
1:1:2138:G:H2'	1:1:2139:G:H8	1.60	0.66
1:1:2836:A:H5''	12:r:114:GLY:HA2	1.77	0.66
1:1:3254:G:H2'	1:1:3255:G:H8	1.61	0.66
46:B:211:A:H62	46:B:250:U:H3	1.41	0.66
49:E:78:ILE:HD11	49:E:120:ILE:HD11	1.75	0.66
1:AS:627:U:H2'	1:AS:628:A:C8	2.29	0.66
46:CM:1463:G:H2'	46:CM:1464:G:H8	1.61	0.66
48:CO:26:ARG:NH1	48:CO:49:ASN:OD1	2.28	0.66
57:CX:54:TYR:HD1	57:CX:72:GLY:HA2	1.60	0.66
60:DA:54:LEU:HB3	60:DA:60:VAL:HB	1.76	0.66
1:1:2932:C:H2'	1:1:2933:G:H8	1.59	0.66
6:l:38:SER:HG	6:l:42:ARG:HH21	1.42	0.66
1:AS:2196:G:H2'	1:AS:2197:A:H8	1.60	0.66
7:AZ:41:LYS:NZ	22:BO:32:LYS:O	2.29	0.66
25:BR:1:MET:HE2	25:BR:15:PRO:HG2	1.76	0.66
46:CM:812:C:O2'	58:CY:50:GLU:OE2	2.14	0.66
46:CM:1276:G:H22	46:CM:1309:G:N2	1.93	0.66
1:1:2669:A:H2'	1:1:2670:G:C8	2.30	0.66
84:1:3403:3K5:H13	43:AP:57:ILE:HG23	1.76	0.66
46:B:1715:U:H2'	46:B:1716:C:C6	2.30	0.66
69:Y:28:ARG:HD3	69:Y:60:LYS:HE2	1.78	0.66
46:CM:700:G:O2'	46:CM:701:G:O5'	2.12	0.66
1:1:2171:U:O4	1:1:2221:A:N6	2.29	0.66
59:O:132:GLU:HG3	59:O:133:ARG:H	1.59	0.66
7:AZ:91:GLY:O	7:AZ:94:ASN:ND2	2.28	0.66
67:DH:41:ILE:HD11	67:DH:54:PRO:HD3	1.78	0.66
1:1:92:C:OP2	1:1:2736:C:O2'	2.14	0.66
46:B:700:G:H5''	46:B:717:G:H22	1.59	0.66
1:AS:654:A:H2'	1:AS:655:A:C8	2.30	0.66
1:AS:2530:C:OP1	35:CB:102:LYS:NZ	2.22	0.66
46:CM:747:A:OP1	56:CW:79:ARG:NH2	2.28	0.66
46:CM:856:G:H2'	46:CM:857:G:C8	2.31	0.66
82:L1:160:LYS:H	82:L1:162:VAL:HG12	1.61	0.66
1:1:581:A:H5''	34:AG:106:ASN:ND2	2.11	0.66
46:B:79:C:OP1	53:I:159:ARG:NH2	2.28	0.66
57:M:88:PRO:HD2	57:M:91:ARG:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:U:92:GLN:OE1	65:U:115:ARG:NH2	2.29	0.66
1:AS:1760:U:OP1	20:BM:43:LYS:HE2	1.94	0.66
1:1:1230:G:H2'	1:1:1231:U:C6	2.31	0.65
35:AH:81:CYS:SG	35:AH:82:ALA:N	2.69	0.65
46:B:1463:G:H2'	46:B:1464:G:H8	1.60	0.65
47:C:147:THR:HG21	47:C:159:ALA:HB1	1.77	0.65
48:D:180:THR:HG22	48:D:183:GLN:OE1	1.96	0.65
1:AS:2932:C:H2'	1:AS:2933:G:C8	2.32	0.65
3:AU:21:C:OP1	6:AY:194:LYS:NZ	2.27	0.65
46:CM:921:G:OP1	46:CM:1059:G:N2	2.27	0.65
1:1:1663:A:H2'	1:1:1664:G:C8	2.31	0.65
3:4:20:U:OP1	87:4:301:HOH:O	2.13	0.65
36:AI:1:MET:HB3	36:AI:45:HIS:HE1	1.61	0.65
54:J:5:ILE:HG21	54:J:10:PRO:HB3	1.78	0.65
1:AS:1662:G:H2'	1:AS:1663:A:C8	2.31	0.65
1:AS:2634:G:H2'	1:AS:2635:A:C8	2.31	0.65
23:BP:59:GLU:HG2	23:BP:60:SER:H	1.61	0.65
46:CM:518:A:H2'	46:CM:519:A:C8	2.30	0.65
46:CM:739:A:H5''	46:CM:740:A:H5'	1.79	0.65
46:CM:1578:C:H2'	46:CM:1579:A:H8	1.61	0.65
48:CO:57:ALA:O	48:CO:61:LEU:HD13	1.96	0.65
79:DT:145:LEU:HD21	79:DT:178:TRP:CE2	2.31	0.65
1:1:628:A:H2'	1:1:629:A:H8	1.61	0.65
1:1:2322:U:H2'	1:1:2323:A:C8	2.31	0.65
1:1:2458:G:H4'	82:11:102:LYS:HZ1	1.61	0.65
1:1:3207:G:OP1	17:w:160:LYS:NZ	2.17	0.65
46:B:1470:G:H21	46:B:1593:C:H1'	1.60	0.65
46:B:1678:G:O6	46:B:1698:U:O4	2.14	0.65
48:D:82:ARG:NH2	48:D:188:LEU:O	2.29	0.65
49:E:96:VAL:HG22	49:E:110:ILE:HG12	1.78	0.65
46:CM:696:U:H6	46:CM:696:U:OP1	1.79	0.65
48:CO:151:LYS:NZ	48:CO:153:THR:O	2.28	0.65
55:CV:4:SER:OG	55:CV:6:ASP:OD1	2.14	0.65
67:DH:21:ILE:HG12	67:DH:117:ILE:HG12	1.79	0.65
1:1:3236:G:O6	8:n:128:LYS:NZ	2.28	0.65
46:B:85:A:N3	46:B:146:A:O2'	2.29	0.65
71:DL:87:PRO:HD2	71:DL:90:ARG:HD2	1.77	0.65
79:DT:107:HIS:HE2	79:DT:125:SER:HG	1.42	0.65
80:P0:53:MET:HE3	80:P0:54:GLY:H	1.61	0.65
1:1:628:A:H2'	1:1:629:A:C8	2.31	0.65
1:1:1199:A:H2'	1:1:1200:A:C8	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Y:15:ASN:ND2	69:Y:72:CYS:O	2.23	0.65
1:AS:1251:C:H2'	1:AS:1252:G:C8	2.32	0.65
32:BY:45:THR:HG21	32:BY:89:PHE:HA	1.78	0.65
46:CM:1334:G:N3	46:CM:1365:C:N4	2.44	0.65
46:CM:1668:A:H8	53:CT:65:GLN:HG3	1.61	0.65
82:L1:23:THR:HG22	82:L1:24:LYS:H	1.62	0.65
1:AS:907:C:OP1	4:AW:14:SER:OG	2.15	0.65
1:AS:2694:U:O2'	22:BO:88:ARG:O	2.12	0.65
1:AS:2988:A:H2'	1:AS:2989:A:H8	1.61	0.65
26:BS:58:ASP:OD2	36:CC:25:LYS:NZ	2.27	0.65
46:CM:85:A:N3	46:CM:146:A:O2'	2.29	0.65
46:CM:994:U:OP2	61:DB:124:LYS:NZ	2.21	0.65
46:CM:1235:U:O2'	78:DS:177:MET:HE2	1.97	0.65
52:CS:157:ARG:HG3	52:CS:224:ASN:OD1	1.97	0.65
13:s:61:ARG:HH22	45:i:42:ALA:HA	1.61	0.65
75:e:8:THR:HG21	75:e:59:SER:HB2	1.76	0.65
1:AS:294:U:OP2	16:BI:15:GLN:NE2	2.27	0.65
1:AS:307:A:H2'	1:AS:308:A:C8	2.31	0.65
46:CM:349:C:OP1	46:CM:628:A:O2'	2.13	0.65
46:CM:820:U:H2'	46:CM:821:U:C6	2.31	0.65
46:CM:1596:U:O2'	52:CS:105:GLY:O	2.11	0.65
48:CO:48:ILE:HG21	48:CO:61:LEU:HD11	1.79	0.65
52:CS:159:ALA:O	75:DP:61:ARG:NH2	2.25	0.65
79:DT:90:LEU:HD11	79:DT:125:SER:HB3	1.78	0.65
1:1:654:A:H2'	1:1:655:A:C8	2.32	0.65
1:1:2974:C:OP1	5:k:26:ARG:NH1	2.30	0.65
46:B:305:G:OP2	58:N:105:LYS:NZ	2.29	0.65
46:B:738:A:OP1	51:G:187:ARG:N	2.29	0.65
46:B:944:U:O2	60:P:61:SER:OG	2.12	0.65
46:CM:352:C:H5''	55:CV:16:ALA:HB2	1.79	0.65
46:CM:647:C:HO2'	46:CM:648:U:H6	1.45	0.65
1:1:1903:C:O2	5:k:240:ARG:NH2	2.30	0.65
18:x:32:THR:HG21	18:x:87:SER:HB3	1.79	0.65
43:AP:15:LYS:HD3	43:AP:18:ARG:HH21	1.62	0.65
52:H:43:PHE:HE1	52:H:70:VAL:HG23	1.61	0.65
46:CM:390:G:OP1	55:CV:24:LYS:NZ	2.19	0.65
46:CM:578:A:H5''	50:CQ:144:ARG:HH21	1.62	0.65
46:CM:653:G:O2'	46:CM:655:U:O4	2.15	0.65
46:CM:1472:G:N2	46:CM:1580:A:OP1	2.27	0.65
65:DF:126:ARG:HB2	65:DF:133:VAL:HG12	1.79	0.65
1:1:1231:U:OP2	81:12:119:LYS:NZ	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2171:U:H5'	1:1:2172:G:H5'	1.80	0.64
46:B:515:U:H2'	46:B:516:A:H8	1.63	0.64
46:B:747:A:OP1	56:L:79:ARG:NH2	2.30	0.64
1:AS:1058:A:O2'	22:BO:108:ARG:NH2	2.30	0.64
45:CL:82:LYS:HZ2	45:CL:83:HIS:H	1.43	0.64
1:1:1115:C:H2'	1:1:1116:A:H8	1.61	0.64
46:B:1324:C:O2'	46:B:1326:A:N7	2.30	0.64
46:CM:766:U:H4'	46:CM:767:G:H5''	1.79	0.64
46:CM:1275:U:H2'	46:CM:1276:G:C8	2.32	0.64
49:CP:96:VAL:HG22	49:CP:110:ILE:HG12	1.78	0.64
50:CQ:107:LYS:HB2	50:CQ:176:VAL:HG22	1.79	0.64
64:DE:20:PHE:O	64:DE:24:LEU:HD12	1.96	0.64
21:O:8:GLN:HB2	21:O:64:ILE:HD11	1.80	0.64
46:B:518:A:H2'	46:B:519:A:C8	2.33	0.64
47:C:184:LEU:HB3	68:X:45:ALA:HB2	1.79	0.64
59:O:36:LEU:HD21	59:O:102:GLY:HA3	1.77	0.64
1:AS:448:U:O2'	1:AS:483:U:OP1	2.16	0.64
1:AS:1283:A:OP2	1:AS:1283:A:H8	1.80	0.64
1:AS:2740:U:H2'	1:AS:2741:A:H8	1.62	0.64
3:AU:122:U:O2	3:AU:131:G:N2	2.28	0.64
46:CM:1679:A:H2	46:CM:1696:U:H3	1.45	0.64
1:1:716:G:OP1	29:AB:117:ARG:NH2	2.30	0.64
5:k:372:THR:HG22	5:k:374:ALA:H	1.61	0.64
46:B:1156:A:H2'	46:B:1157:G:C8	2.33	0.64
58:N:7:VAL:HG23	58:N:8:GLN:HG2	1.78	0.64
1:AS:1199:A:H2'	1:AS:1200:A:C8	2.31	0.64
46:CM:1592:G:OP2	63:DD:126:LYS:NZ	2.28	0.64
1:1:252:U:H5'	1:1:253:A:C8	2.32	0.64
1:1:602:A:H8	1:1:602:A:OP1	1.80	0.64
1:1:1481:G:H21	35:AH:4:ARG:HD2	1.63	0.64
17:w:76:ALA:HB3	17:w:79:ARG:HG2	1.80	0.64
1:AS:92:C:OP2	1:AS:2736:C:O2'	2.11	0.64
15:BH:14:GLU:HG2	15:BH:17:ARG:HG2	1.78	0.64
46:CM:78:A:C8	53:CT:154:ARG:HG3	2.32	0.64
50:CQ:49:VAL:HB	50:CQ:87:ILE:HD13	1.80	0.64
55:CV:120:THR:HG21	55:CV:133:ALA:HA	1.79	0.64
1:1:3254:G:H2'	1:1:3255:G:C8	2.32	0.64
46:B:700:G:O2'	46:B:701:G:O4'	2.16	0.64
73:c:7:SER:OG	73:c:10:ARG:O	2.15	0.64
1:AS:358:G:N2	1:AS:361:A:OP2	2.28	0.64
46:CM:2:A:OP1	49:CP:171:LYS:NZ	2.24	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:605:G:H5'	46:CM:611:G:N2	2.11	0.64
69:DJ:81:VAL:O	69:DJ:122:SER:OG	2.14	0.64
1:1:1057:A:O2'	22:2:102:ARG:NH2	2.31	0.64
7:m:155:THR:HG22	7:m:179:ARG:HD3	1.80	0.64
45:i:77:GLN:OE1	46:B:1446:A:N6	2.30	0.64
46:B:418:A:OP1	53:I:96:SER:OG	2.15	0.64
63:S:26:GLY:HA2	63:S:62:ILE:O	1.98	0.64
79:AR:90:LEU:HB2	79:AR:104:PHE:HB2	1.79	0.64
1:AS:289:A:H2'	1:AS:290:G:H8	1.63	0.64
1:AS:1744:G:OP1	39:CF:44:LYS:NZ	2.25	0.64
1:AS:2634:G:H2'	1:AS:2635:A:H8	1.62	0.64
17:BJ:11:ASP:HB2	17:BJ:118:ARG:HB3	1.78	0.64
46:CM:12:U:H2'	46:CM:13:C:C6	2.32	0.64
46:CM:142:G:O2'	46:CM:143:A:O5'	2.16	0.64
46:CM:573:C:N4	70:DK:65:ASN:OD1	2.29	0.64
11:q:22:ALA:O	11:q:39:LYS:NZ	2.28	0.64
46:B:1275:U:H2'	46:B:1276:G:C8	2.32	0.64
59:O:132:GLU:CD	59:O:136:LEU:HD13	2.23	0.64
53:CT:159:ARG:NH1	53:CT:170:THR:OG1	2.30	0.64
81:12:149:HIS:H	81:12:152:ILE:HD12	1.61	0.64
1:1:1611:U:H2'	1:1:1612:U:C6	2.33	0.64
6:l:42:ARG:HD2	6:l:114:VAL:HG22	1.81	0.64
11:BD:110:ASP:HB3	11:BD:128:ILE:HD12	1.80	0.64
23:BP:16:VAL:HG12	23:BP:65:VAL:HG22	1.80	0.64
45:CL:64:LEU:O	45:CL:66:ASN:N	2.25	0.64
46:CM:855:C:O2	74:DO:51:GLN:NE2	2.31	0.64
56:CW:68:LYS:HE3	56:CW:72:GLU:HG3	1.80	0.64
80:p0:8:LYS:HA	80:p0:11:TYR:HB3	1.80	0.64
10:p:144:ILE:HG23	10:p:176:VAL:HG21	1.80	0.63
23:5:92:ILE:HD12	23:5:96:ILE:HD12	1.81	0.63
42:AO:7:LYS:NZ	46:B:1761:G:OP1	2.30	0.63
1:AS:93:G:H2'	1:AS:94:A:C8	2.33	0.63
1:AS:1202:G:OP1	12:BE:157:TYR:OH	2.12	0.63
1:AS:1653:C:O2'	1:AS:1793:A:OP2	2.15	0.63
1:AS:2516:U:O2'	1:AS:2519:A:N1	2.30	0.63
1:AS:2684:U:HO2'	1:AS:2715:A:HO2'	1.46	0.63
5:AX:372:THR:HG22	5:AX:374:ALA:H	1.63	0.63
82:L1:50:SER:HA	82:L1:158:GLN:HA	1.80	0.63
82:l1:33:GLU:HA	82:l1:168:ALA:HB3	1.80	0.63
1:1:169:G:N2	1:1:248:U:O2	2.30	0.63
45:i:93:ARG:H	46:B:1259:C:H5	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:960:C:H5''	60:P:109:LYS:HD3	1.80	0.63
46:B:1240:G:N7	59:O:46:ARG:NH2	2.43	0.63
52:H:72:HIS:CD2	52:H:107:LYS:HD3	2.33	0.63
62:R:41:VAL:HG13	62:R:84:ILE:HD13	1.79	0.63
23:BP:28:PHE:HE1	23:BP:33:TYR:HB2	1.63	0.63
39:CF:32:ASN:C	39:CF:34:ASN:H	2.04	0.63
2:3:64:A:H61	12:r:200:LEU:HD21	1.63	0.63
46:B:778:U:O2'	46:B:779:U:O2	2.16	0.63
63:S:124:GLU:HG2	63:S:133:ALA:HB1	1.81	0.63
1:AS:1208:A:O3'	21:BN:92:LYS:NZ	2.31	0.63
2:AT:4:U:H2'	2:AT:5:G:H8	1.62	0.63
3:AU:36:G:C5	36:CC:86:ARG:HD3	2.33	0.63
28:BU:115:LYS:NZ	28:BU:119:GLU:OE2	2.30	0.63
46:CM:238:U:H3'	46:CM:239:U:O4'	1.97	0.63
81:12:142:ARG:NH1	81:12:145:GLY:O	2.31	0.63
1:1:2424:U:H5''	37:AJ:97:ARG:HH12	1.62	0.63
1:AS:589:G:N2	1:AS:610:U:OP1	2.31	0.63
1:AS:827:G:O2'	1:AS:1860:A:N3	2.30	0.63
1:AS:1344:U:OP1	19:BL:39:ARG:NH2	2.31	0.63
5:AX:284:ARG:NH2	5:AX:295:ALA:O	2.32	0.63
5:AX:331:VAL:HG22	5:AX:334:ARG:HG3	1.80	0.63
35:CB:57:LEU:HB2	35:CB:62:TYR:CE1	2.34	0.63
79:DT:92:LEU:O	79:DT:101:THR:N	2.31	0.63
46:B:1410:A:H2'	49:E:87:ALA:CB	2.28	0.63
48:D:128:LYS:HG2	48:D:134:VAL:HG22	1.80	0.63
46:CM:738:A:OP1	51:CR:187:ARG:N	2.32	0.63
46:CM:778:U:O2'	46:CM:779:U:O2	2.16	0.63
46:CM:1400:U:H5''	64:DE:3:ARG:HE	1.63	0.63
46:CM:1579:A:H2'	46:CM:1580:A:H8	1.64	0.63
65:DF:134:ARG:HB2	65:DF:136:GLN:NE2	2.13	0.63
20:z:23:TRP:HB3	20:z:51:VAL:HG12	1.81	0.63
46:B:330:U:P	55:K:56:ARG:HH22	2.22	0.63
46:CM:1459:U:OP1	52:CS:183:SER:OG	2.16	0.63
55:CV:113:TYR:OH	55:CV:156:ALA:O	2.16	0.63
1:1:541:U:H3	1:1:543:C:HO2'	1.47	0.63
46:B:1460:G:H2'	46:B:1461:A:C8	2.34	0.63
78:h:124:LYS:NZ	78:h:125:LYS:O	2.31	0.63
1:AS:628:A:H2'	1:AS:629:A:H8	1.64	0.63
1:AS:2244:U:H2'	1:AS:2245:C:C6	2.34	0.63
1:AS:3014:U:OP2	1:AS:3064:C:N4	2.28	0.63
17:BJ:62:ALA:HA	17:BJ:71:PRO:HD2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:211:A:H62	46:CM:250:U:H3	1.46	0.63
46:CM:405:A:H2'	46:CM:406:C:C6	2.34	0.63
46:CM:1239:U:OP2	59:CZ:46:ARG:NH2	2.32	0.63
59:CZ:36:LEU:HD11	59:CZ:43:ARG:HH21	1.62	0.63
60:DA:55:ARG:NH2	74:DO:51:GLN:OE1	2.30	0.63
82:l1:138:VAL:HG13	82:l1:147:LYS:HZ1	1.64	0.63
1:l:1230:G:H5''	81:12:119:LYS:HE2	1.80	0.63
8:n:30:ARG:NE	34:AG:107:ILE:O	2.31	0.63
46:B:219:A:H5''	46:B:818:U:H1'	1.80	0.63
46:B:511:U:H2'	46:B:512:G:C8	2.34	0.63
46:B:1578:C:H2'	46:B:1579:A:C8	2.33	0.63
1:AS:653:C:H2'	1:AS:654:A:C8	2.32	0.63
21:BN:8:GLN:HB2	21:BN:64:ILE:HD11	1.81	0.63
21:BN:71:LYS:O	21:BN:73:LYS:NZ	2.27	0.63
32:BY:45:THR:HG22	32:BY:47:ASP:H	1.62	0.63
45:CL:80:ALA:O	46:CM:1163:G:O2'	2.12	0.63
65:DF:22:ILE:HD11	65:DF:35:ILE:HG13	1.80	0.63
78:DS:175:ALA:N	78:DS:182:TYR:O	2.32	0.63
1:l:2668:A:H2'	1:l:2669:A:C8	2.34	0.63
1:l:3318:G:P	55:K:77:ARG:HH22	2.22	0.63
36:AI:1:MET:N	36:AI:1:MET:SD	2.71	0.63
46:B:480:U:H2'	46:B:481:A:H8	1.62	0.63
53:I:161:GLU:HB3	53:I:170:THR:HG22	1.80	0.63
63:S:98:GLU:HG3	63:S:101:LYS:HE3	1.81	0.63
64:T:36:SER:OG	64:T:47:ARG:NH1	2.32	0.63
77:g:55:LYS:HB2	77:g:58:PRO:HG3	1.81	0.63
1:AS:2580:G:OP1	4:AW:2:GLY:N	2.32	0.63
7:AZ:85:ARG:NH2	7:AZ:250:ASP:OD2	2.32	0.63
27:BT:39:LEU:HD22	27:BT:43:TYR:HE2	1.64	0.63
1:l:2244:U:H2'	1:l:2245:C:C6	2.33	0.62
1:l:3260:A:H2'	1:l:3261:A:C8	2.34	0.62
3:4:29:U:H5''	14:t:27:ASP:HB3	1.81	0.62
10:p:99:ARG:NH2	10:p:189:THR:O	2.31	0.62
42:AO:1:MET:HB3	46:B:1629:G:H5'	1.80	0.62
46:B:479:A:H2'	46:B:480:U:C6	2.34	0.62
46:B:915:A:H2'	48:D:114:VAL:HG11	1.81	0.62
46:B:1130:U:O2'	49:E:84:GLN:O	2.16	0.62
46:B:1395:G:N2	46:B:1398:G:OP2	2.32	0.62
46:B:1592:G:OP2	63:S:126:LYS:NZ	2.24	0.62
50:F:91:ARG:HD2	50:F:95:ARG:NH2	2.14	0.62
5:AX:4:ARG:HD3	5:AX:7:GLU:HG2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:CJ:61:LYS:NZ	43:CJ:63:LYS:O	2.32	0.62
46:CM:452:A:H4'	51:CR:62:LYS:HE3	1.80	0.62
46:CM:870:G:H2'	46:CM:871:U:C6	2.34	0.62
31:AD:46:ILE:HG21	31:AD:55:LYS:HG3	1.81	0.62
43:AP:61:LYS:NZ	43:AP:63:LYS:O	2.31	0.62
46:B:784:U:H2'	46:B:785:G:C8	2.34	0.62
1:AS:2138:G:H2'	1:AS:2139:G:H8	1.64	0.62
18:BK:118:GLN:OE1	18:BK:120:ASN:ND2	2.31	0.62
46:CM:218:A:H3'	46:CM:219:A:C5'	2.27	0.62
46:CM:784:U:H2'	46:CM:785:G:C8	2.34	0.62
48:CO:28:ASP:HB3	48:CO:50:ARG:HD2	1.81	0.62
59:CZ:82:PRO:HB2	59:CZ:84:GLU:H	1.63	0.62
67:DH:52:LYS:HB3	67:DH:91:ASP:HB2	1.79	0.62
82:L1:191:VAL:HG11	82:L1:198:TRP:CD1	2.34	0.62
1:1:842:A:N6	46:B:956:A:N1	2.46	0.62
28:AA:54:THR:HG23	28:AA:56:LYS:HG3	1.81	0.62
46:B:1138:G:OP1	73:c:85:ARG:NH1	2.32	0.62
46:CM:1138:G:OP1	73:DN:85:ARG:NH1	2.32	0.62
82:L1:10:ARG:HG2	82:L1:180:VAL:HG21	1.81	0.62
1:1:976:A:H2'	1:1:977:U:H5'	1.79	0.62
46:CM:68:A:OP1	53:CT:160:ARG:NH2	2.28	0.62
1:1:654:A:H2'	1:1:655:A:H8	1.65	0.62
1:1:1713:U:H2'	1:1:1714:G:C8	2.34	0.62
1:1:1801:C:H2'	1:1:1802:A:H8	1.63	0.62
46:B:1487:C:P	66:V:122:ARG:HH22	2.21	0.62
1:AS:479:C:H2'	1:AS:480:G:C8	2.35	0.62
46:CM:52:U:H2'	46:CM:53:G:H8	1.65	0.62
46:CM:1245:U:H2'	46:CM:1246:G:H8	1.65	0.62
1:1:289:A:H2'	1:1:290:G:H8	1.65	0.62
1:1:1662:G:H2'	1:1:1663:A:C8	2.35	0.62
1:1:1662:G:H2'	1:1:1663:A:H8	1.65	0.62
46:B:216:A:H4'	46:B:217:A:OP1	2.00	0.62
49:E:168:PRO:HG3	56:L:57:ARG:HD3	1.80	0.62
54:J:146:GLN:HB2	54:J:177:VAL:HG23	1.80	0.62
79:AR:152:VAL:HG12	79:AR:170:SER:HB2	1.80	0.62
1:AS:239:A:OP1	36:CC:94:LYS:NZ	2.23	0.62
25:BR:108:LYS:HA	25:BR:111:LYS:HD2	1.82	0.62
46:CM:255:A:N3	55:CV:64:ASN:ND2	2.47	0.62
46:CM:1715:U:H2'	46:CM:1716:C:C6	2.33	0.62
59:CZ:80:ASN:C	59:CZ:82:PRO:HD3	2.24	0.62
1:1:2244:U:H2'	1:1:2245:C:H6	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2347:G:H2'	1:1:2348:G:C8	2.35	0.62
1:1:2820:G:OP1	41:AN:24:TYR:OH	2.16	0.62
48:D:180:THR:HG22	48:D:183:GLN:CD	2.25	0.62
75:e:19:THR:HG23	75:e:25:VAL:HG13	1.82	0.62
1:AS:1801:C:H2'	1:AS:1802:A:H8	1.65	0.62
46:CM:1026:G:H2'	46:CM:1027:G:C8	2.33	0.62
79:DT:65:HIS:CG	79:DT:85:SER:HG	2.17	0.62
79:DT:211:ALA:HB2	79:DT:217:ILE:HG12	1.80	0.62
79:DT:252:ALA:HB2	79:DT:289:LEU:HD11	1.81	0.62
80:P0:45:LEU:HD21	80:P0:99:ILE:HB	1.81	0.62
82:l1:14:HIS:O	82:l1:18:GLU:N	2.32	0.62
1:1:417:A:H2'	1:1:418:A:C8	2.34	0.62
1:1:3318:G:OP1	55:K:170:ARG:NH2	2.32	0.62
21:0:12:ARG:HB3	21:0:24:LEU:HD23	1.82	0.62
46:B:1326:A:H1'	79:AR:66:SER:HB2	1.82	0.62
1:AS:581:A:H5''	34:CA:106:ASN:HD21	1.63	0.62
1:AS:2335:A:H2'	1:AS:2336:A:H8	1.64	0.62
5:AX:211:GLN:NE2	5:AX:283:TYR:O	2.31	0.62
21:BN:52:LYS:HG2	21:BN:55:SER:HB3	1.82	0.62
25:BR:98:PRO:HA	25:BR:101:ARG:HD2	1.82	0.62
46:CM:721:C:H42	46:CM:722:A:H62	1.48	0.62
46:CM:972:G:N2	46:CM:998:A:OP1	2.32	0.62
69:DJ:37:PHE:CE1	69:DJ:103:ILE:HG13	2.33	0.62
73:DN:12:LYS:HA	73:DN:15:ARG:HH12	1.64	0.62
1:1:2888:U:H5	1:1:2907:U:HO2'	1.48	0.62
46:B:1600:U:OP1	52:H:169:ASN:HB2	1.99	0.62
48:D:83:LYS:NZ	48:D:105:PHE:O	2.33	0.62
53:I:163:THR:HA	53:I:168:THR:HG22	1.81	0.62
1:AS:591:C:O2	9:BB:24:ARG:NH1	2.33	0.62
8:BA:39:LEU:HD11	8:BA:53:TYR:HB2	1.81	0.62
23:BP:28:PHE:CE1	23:BP:33:TYR:HB2	2.35	0.62
46:CM:1066:A:O2'	46:CM:1068:G:N7	2.32	0.62
46:CM:1282:G:N2	46:CM:1285:A:OP2	2.21	0.62
57:CX:50:THR:HG21	57:CX:57:THR:HG22	1.82	0.62
82:l1:194:LEU:HD13	82:l1:200:ASN:HB2	1.81	0.62
1:1:935:U:OP2	29:AB:26:ARG:NH2	2.33	0.62
1:1:2789:A:H4'	1:1:2790:U:OP2	2.00	0.62
1:AS:647:A:OP2	1:AS:2840:U:O2'	2.18	0.62
13:BF:117:ASP:HB3	13:BF:120:ILE:HD12	1.82	0.62
1:1:3133:G:H2'	1:1:3134:C:C6	2.35	0.61
2:3:13:A:H2	7:m:21:ARG:HB2	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:F:210:ALA:O	64:T:19:ARG:NH1	2.33	0.61
53:I:21:GLU:OE2	53:I:28:TYR:OH	2.18	0.61
64:T:27:ASP:O	64:T:31:ASN:ND2	2.31	0.61
72:b:67:ASP:O	72:b:70:LYS:NZ	2.32	0.61
1:AS:1144:G:OP2	87:AS:3801:HOH:O	2.16	0.61
1:AS:1782:G:H2'	1:AS:1783:A:C8	2.35	0.61
1:AS:2086:C:H1'	1:AS:3309:A:H8	1.62	0.61
46:CM:267:G:H2'	46:CM:268:C:C6	2.35	0.61
46:CM:1543:A:OP1	62:DC:115:TYR:OH	2.18	0.61
57:CX:77:ARG:HD2	57:CX:84:GLU:HA	1.81	0.61
61:DB:124:LYS:HG3	61:DB:125:GLY:N	2.15	0.61
81:12:116:MET:HB3	81:12:119:LYS:HG2	1.80	0.61
1:1:2442:U:O2'	1:1:2443:G:N7	2.33	0.61
32:AE:43:MET:HE3	32:AE:76:ARG:HB2	1.81	0.61
1:AS:2873:G:O2'	1:AS:2996:A:N1	2.32	0.61
46:CM:16:G:H2'	46:CM:17:C:C6	2.35	0.61
46:CM:881:U:H5'	48:CO:23:PRO:HG2	1.82	0.61
2:3:81:U:H2'	2:3:82:G:H8	1.65	0.61
46:B:52:U:H2'	46:B:53:G:C8	2.35	0.61
65:U:16:ARG:NH1	65:U:21:ASN:OD1	2.34	0.61
6:AY:253:GLN:NE2	6:AY:257:GLU:OE2	2.34	0.61
46:CM:272:G:O6	46:CM:280:C:N4	2.31	0.61
63:DD:98:GLU:HG3	63:DD:101:LYS:HE3	1.82	0.61
79:DT:235:ALA:HB3	79:DT:253:THR:HB	1.82	0.61
1:1:358:G:N2	1:1:361:A:OP2	2.33	0.61
1:1:1735:U:HO2'	35:AH:56:THR:HG1	1.46	0.61
1:1:2669:A:H2'	1:1:2670:G:H8	1.65	0.61
9:o:52:GLU:OE2	9:o:184:HIS:NE2	2.34	0.61
11:q:95:ALA:O	41:AN:1:MET:N	2.33	0.61
46:B:1230:G:H1	46:B:1235:U:H3	1.47	0.61
46:B:1783:C:OP2	73:c:5:ARG:NH2	2.33	0.61
1:AS:1489:G:N2	1:AS:1489:G:OP2	2.30	0.61
6:AY:301:ARG:NH2	19:BL:38:ARG:O	2.33	0.61
37:CD:91:GLN:HG3	82:L1:3:LYS:HE3	1.82	0.61
46:CM:1548:U:H4'	46:CM:1586:C:H4'	1.82	0.61
47:CN:59:LEU:HD22	68:DI:79:LEU:HD11	1.83	0.61
51:CR:148:ARG:NH2	53:CT:201:GLN:OE1	2.33	0.61
1:1:1774:G:O2'	1:1:1776:G:OP2	2.19	0.61
1:1:2395:U:H5''	4:j:221:LYS:HE3	1.80	0.61
1:1:2451:C:OP1	1:1:2452:G:N2	2.33	0.61
6:l:359:GLU:OE2	21:0:8:GLN:NE2	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1144:C:N4	46:B:1270:U:OP1	2.33	0.61
46:B:1741:A:H2'	46:B:1742:A:C8	2.36	0.61
63:S:86:LYS:HG2	63:S:116:LEU:HD13	1.81	0.61
66:V:62:ALA:HB2	66:V:108:LEU:HD21	1.82	0.61
5:AX:35:ASP:OD2	5:AX:191:LYS:NZ	2.24	0.61
46:CM:405:A:H2'	46:CM:406:C:H6	1.66	0.61
46:CM:511:U:H2'	46:CM:512:G:C8	2.35	0.61
47:CN:15:LYS:HZ1	64:DE:93:LEU:HD13	1.65	0.61
1:1:1152:C:OP2	9:o:92:LYS:NZ	2.32	0.61
1:1:3287:A:H2'	1:1:3288:A:H8	1.65	0.61
3:4:103:G:OP2	3:4:105:A:O2'	2.18	0.61
4:j:101:ILE:HG12	4:j:165:VAL:HG22	1.82	0.61
46:B:57:G:OP1	71:a:112:LYS:NZ	2.34	0.61
68:X:55:LEU:HD11	68:X:69:LEU:HD21	1.81	0.61
1:AS:498:C:H5''	8:BA:25:ARG:NH2	2.15	0.61
1:AS:1255:A:H61	80:p0:33:VAL:HG12	1.65	0.61
2:AT:23:A:H2'	2:AT:24:A:C8	2.36	0.61
46:CM:702:G:H4'	46:CM:703:U:OP1	2.01	0.61
46:CM:1463:G:H2'	46:CM:1464:G:C8	2.35	0.61
56:CW:38:ASN:HA	77:DR:36:MET:HE3	1.82	0.61
1:1:740:A:OP1	19:y:66:ARG:NH2	2.33	0.61
15:u:34:ASP:OD2	15:u:37:ARG:NH2	2.33	0.61
17:w:2:SER:N	21:0:161:LYS:HZ3	1.98	0.61
47:C:200:ASP:HB2	64:T:85:VAL:HG23	1.83	0.61
51:G:148:ARG:NH2	53:I:201:GLN:OE1	2.34	0.61
54:J:72:ARG:HG2	54:J:75:ARG:HH21	1.66	0.61
1:AS:1758:U:H5	1:AS:1759:U:HO2'	1.49	0.61
23:BP:34:VAL:HG21	23:BP:58:ALA:HB2	1.81	0.61
1:1:1080:A:H2'	1:1:1081:A:C8	2.36	0.61
1:1:1931:G:HO2'	46:B:1654:A:HO2'	1.49	0.61
1:1:2655:U:H2'	1:1:2656:C:C6	2.35	0.61
13:s:93:SER:N	13:s:172:LEU:O	2.34	0.61
46:B:150:U:O2	53:I:4:ASN:ND2	2.27	0.61
1:AS:2655:U:H2'	1:AS:2656:C:C6	2.36	0.61
64:DE:61:ILE:HD11	64:DE:69:ILE:HD11	1.83	0.61
31:AD:57:GLU:HB2	35:AH:94:LEU:HD11	1.83	0.61
46:B:952:A:OP2	60:P:124:ARG:NH2	2.34	0.61
1:AS:1774:G:O2'	1:AS:1776:G:OP2	2.17	0.61
24:BQ:47:ASN:OD1	87:BQ:201:HOH:O	2.16	0.61
46:CM:1719:A:H2'	46:CM:1720:C:C6	2.36	0.61
59:CZ:31:VAL:O	59:CZ:35:SER:HB3	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1560:U:H3	1:1:1571:G:H1	1.48	0.61
1:1:1592:C:H2'	1:1:1593:C:C6	2.36	0.61
1:1:2199:G:N2	1:1:2202:A:OP2	2.28	0.61
1:1:2941:A:N7	4:j:215:ASN:ND2	2.49	0.61
21:0:161:LYS:HB3	21:0:161:LYS:HZ2	1.66	0.61
46:B:515:U:H2'	46:B:516:A:C8	2.35	0.61
54:J:92:ARG:NH1	54:J:120:LYS:HB3	2.16	0.61
1:AS:2669:A:H2'	1:AS:2670:G:H8	1.65	0.61
1:AS:3260:A:H2'	1:AS:3261:A:C8	2.36	0.61
23:BP:19:VAL:O	23:BP:21:ALA:N	2.34	0.61
79:DT:30:PRO:HB3	79:DT:293:ALA:HB3	1.82	0.61
1:1:1255:A:C8	80:P0:53:MET:HB3	2.36	0.60
46:B:728:U:OP1	54:J:104:LYS:N	2.34	0.60
46:B:985:C:H5	46:B:988:A:H5''	1.66	0.60
68:X:70:ASN:HB3	68:X:83:TRP:HB2	1.83	0.60
1:AS:1635:C:OP2	35:CB:74:ARG:NH1	2.31	0.60
1:AS:2347:G:H2'	1:AS:2348:G:C8	2.36	0.60
1:AS:3136:C:H2'	1:AS:3137:A:C8	2.36	0.60
29:BV:75:LEU:HD22	29:BV:118:LEU:HD11	1.83	0.60
46:CM:1265:C:H2'	46:CM:1266:G:H8	1.66	0.60
82:L1:66:CYS:HB2	82:L1:83:ASP:HB2	1.83	0.60
1:1:2936:G:N2	1:1:2939:A:OP2	2.31	0.60
46:B:29:U:H2'	46:B:30:G:H8	1.65	0.60
50:F:141:GLY:HA3	50:F:183:LEU:HD23	1.82	0.60
62:R:97:TYR:HE1	62:R:102:PHE:CZ	2.19	0.60
1:AS:2191:A:H2'	1:AS:2192:A:H8	1.65	0.60
46:CM:52:U:H2'	46:CM:53:G:C8	2.35	0.60
77:DR:55:LYS:HB2	77:DR:58:PRO:HG3	1.83	0.60
80:p0:53:MET:HE3	80:p0:54:GLY:H	1.65	0.60
1:1:827:G:O2'	1:1:1860:A:N3	2.33	0.60
1:1:3162:U:H2'	1:1:3163:U:H4'	1.82	0.60
8:n:3:GLN:NE2	33:AF:76:LEU:O	2.35	0.60
46:B:504:A:H5''	46:B:505:U:O5'	2.00	0.60
46:B:1127:A:H5''	73:c:2:PRO:HB3	1.82	0.60
46:B:1463:G:H2'	46:B:1464:G:C8	2.36	0.60
1:AS:1199:A:H2'	1:AS:1200:A:H8	1.66	0.60
1:AS:3262:U:O4	5:AX:124:LYS:NZ	2.34	0.60
46:CM:1131:G:H2'	46:CM:1132:A:C8	2.36	0.60
46:CM:1668:A:O3'	53:CT:31:ARG:NH2	2.35	0.60
64:DE:75:GLU:HG3	64:DE:76:GLU:OE1	2.01	0.60
65:DF:27:LYS:HA	65:DF:57:ARG:HA	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:p0:9:VAL:O	80:p0:13:SER:N	2.34	0.60
80:p0:10:GLN:HA	80:p0:13:SER:HB2	1.84	0.60
1:1:1217:A:H1'	80:P0:8:LYS:HZ1	1.66	0.60
1:1:1489:G:OP2	1:1:1489:G:N2	2.29	0.60
1:1:2331:G:H5''	18:x:86:LYS:HB2	1.83	0.60
1:1:2634:G:H2'	1:1:2635:A:C8	2.37	0.60
46:B:521:G:OP2	71:a:37:LYS:NZ	2.32	0.60
46:B:1635:A:H2'	46:B:1636:C:C6	2.37	0.60
7:AZ:197:LYS:HG2	7:AZ:202:GLY:HA3	1.83	0.60
46:CM:518:A:H2'	46:CM:519:A:H8	1.66	0.60
46:CM:589:A:H2'	46:CM:590:A:C8	2.37	0.60
62:DC:18:LYS:NZ	65:DF:90:LYS:O	2.27	0.60
80:p0:45:LEU:HD22	80:p0:99:ILE:HG22	1.84	0.60
1:1:482:U:H2'	1:1:483:U:C6	2.37	0.60
8:n:65:SER:HB2	8:n:75:LEU:HD23	1.82	0.60
23:5:34:VAL:HG13	23:5:56:ILE:HG22	1.83	0.60
46:B:108:A:H2'	46:B:109:G:C8	2.37	0.60
46:B:444:A:H5''	51:G:57:ASN:HD22	1.65	0.60
46:B:589:A:H2'	46:B:590:A:C8	2.37	0.60
46:B:876:A:H2'	46:B:877:G:H8	1.66	0.60
46:B:1245:U:H2'	46:B:1246:G:H8	1.65	0.60
50:F:124:LEU:HD11	50:F:153:TYR:HB3	1.82	0.60
54:J:5:ILE:HG22	54:J:7:SER:H	1.66	0.60
66:V:107:ALA:O	66:V:111:ILE:HG12	2.01	0.60
68:X:64:GLU:OE2	74:d:2:VAL:N	2.34	0.60
1:AS:1011:C:H4'	1:AS:1012:U:H6	1.67	0.60
1:AS:1695:A:O2'	39:CF:3:ARG:NH1	2.33	0.60
1:AS:2244:U:H2'	1:AS:2245:C:H6	1.66	0.60
1:AS:3256:G:H2'	1:AS:3257:A:C8	2.37	0.60
46:CM:787:A:O2'	54:CU:100:ARG:NE	2.34	0.60
52:CS:72:HIS:CD2	52:CS:107:LYS:HD3	2.36	0.60
56:CW:101:PRO:O	56:CW:105:LEU:HD12	2.01	0.60
1:1:2937:U:O2	4:j:221:LYS:NZ	2.28	0.60
1:AS:62:A:H5''	16:BI:174:ILE:HG21	1.83	0.60
1:AS:1795:A:H2'	1:AS:1796:A:C8	2.37	0.60
34:AG:51:TYR:HD2	34:AG:67:ILE:HD12	1.67	0.60
46:B:671:G:H5'	46:B:672:U:H2'	1.83	0.60
46:B:921:G:OP1	46:B:1059:G:N2	2.31	0.60
58:N:26:LYS:HZ2	58:N:29:LYS:HB3	1.67	0.60
62:R:26:VAL:HG23	62:R:27:GLU:HG3	1.84	0.60
1:AS:1302:G:C5	17:BJ:63:THR:HA	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BX:29:TYR:OH	31:BX:57:GLU:OE2	2.20	0.60
45:CL:40:ASP:O	45:CL:42:ALA:N	2.30	0.60
80:p0:56:ASN:ND2	80:p0:84:VAL:O	2.35	0.60
1:1:510:G:O2'	6:1:342:SER:HB3	2.02	0.60
46:B:336:C:H5''	55:K:10:LYS:HD2	1.84	0.60
1:AS:112:C:OP1	16:BI:147:ARG:NH2	2.35	0.60
1:AS:2520:A:H1'	1:AS:2521:C:H5	1.65	0.60
3:AU:34:U:H4'	36:CC:85:THR:HG21	1.82	0.60
4:AW:51:ASP:OD2	4:AW:54:ARG:NH2	2.34	0.60
59:CZ:42:ALA:HB1	59:CZ:47:GLU:HB3	1.84	0.60
1:1:2079:C:HO2'	1:1:2080:U:H6	1.49	0.60
4:j:29:LEU:HD22	4:j:101:ILE:HD13	1.84	0.60
51:G:175:PHE:HE2	51:G:198:ARG:HD2	1.66	0.60
5:AX:152:LYS:HG2	5:AX:189:SER:HA	1.84	0.60
15:BH:14:GLU:HB3	21:BN:149:LYS:HG2	1.84	0.60
46:CM:530:U:OP1	71:DL:64:PHE:HA	2.01	0.60
46:CM:1600:U:OP1	52:CS:169:ASN:HB2	2.02	0.60
82:L1:67:ILE:HG22	82:L1:68:PHE:H	1.67	0.60
1:1:429:U:H5''	34:AG:87:LYS:HE3	1.83	0.60
36:AI:1:MET:HG2	36:AI:53:ARG:HH22	1.65	0.60
46:B:317:U:H4'	46:B:321:A:C8	2.37	0.60
46:B:626:G:N1	46:B:955:A:OP2	2.25	0.60
46:B:881:U:H5'	48:D:23:PRO:HG2	1.83	0.60
1:AS:411:U:H2'	1:AS:412:G:H8	1.66	0.60
1:AS:449:U:H2'	1:AS:450:G:H8	1.66	0.60
1:AS:654:A:H2'	1:AS:655:A:H8	1.67	0.60
1:AS:2322:U:H2'	1:AS:2323:A:C8	2.37	0.60
1:AS:3287:A:H2'	1:AS:3288:A:C8	2.36	0.60
20:BM:162:ARG:NH1	46:CM:835:A:OP1	2.34	0.60
47:CN:57:ILE:HG23	47:CN:177:LEU:HD23	1.84	0.60
79:DT:218:ILE:HG23	79:DT:230:THR:HG22	1.84	0.60
1:1:483:U:H2'	1:1:484:U:C6	2.37	0.59
1:1:907:C:OP1	4:j:14:SER:OG	2.20	0.59
1:1:2233:A:O2'	46:B:1744:G:O2'	2.09	0.59
1:1:2679:U:O2'	45:i:37:LYS:O	2.20	0.59
1:AS:1241:A:N7	1:AS:1267:A:O2'	2.31	0.59
1:AS:1242:G:O2'	1:AS:1260:G:OP2	2.19	0.59
1:AS:1692:A:H2'	1:AS:1693:A:C8	2.36	0.59
1:AS:1899:U:OP1	87:AS:3802:HOH:O	2.16	0.59
1:AS:2171:U:H5'	1:AS:2172:G:H5'	1.83	0.59
1:AS:2937:U:O2'	4:AW:221:LYS:HD3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:481:G:H2'	1:1:482:U:C6	2.37	0.59
27:9:51:ARG:HG2	27:9:52:GLN:H	1.67	0.59
46:B:1579:A:H2'	46:B:1580:A:C8	2.34	0.59
1:AS:1218:G:H4'	1:AS:1219:A:H5''	1.84	0.59
11:BD:107:ASP:O	11:BD:109:GLN:NE2	2.34	0.59
26:BS:75:LYS:HB3	26:BS:81:THR:HB	1.84	0.59
46:CM:515:U:H2'	46:CM:516:A:C8	2.36	0.59
46:CM:723:G:C4	46:CM:724:G:H1'	2.37	0.59
48:CO:62:LYS:HA	48:CO:88:VAL:HG13	1.84	0.59
82:11:59:PRO:HA	82:11:170:GLY:HA2	1.83	0.59
46:B:1160:U:H2'	46:B:1161:G:H8	1.67	0.59
46:B:1596:U:O2'	52:H:105:GLY:O	2.16	0.59
62:R:1:MET:HB3	65:U:17:LEU:HA	1.83	0.59
79:AR:90:LEU:HD11	79:AR:125:SER:HB3	1.84	0.59
1:AS:72:A:N7	14:BG:66:ASN:HB3	2.18	0.59
1:AS:480:G:H2'	1:AS:480:G:N3	2.14	0.59
46:CM:948:A:N7	60:DA:70:LYS:NZ	2.51	0.59
47:CN:48:ILE:HG12	47:CN:149:MET:HE3	1.85	0.59
79:DT:65:HIS:CE1	79:DT:85:SER:HG	2.21	0.59
82:11:41:TYR:HB3	82:11:163:LEU:HD11	1.83	0.59
46:B:92:A:OP1	51:G:7:LYS:NZ	2.35	0.59
52:H:148:ARG:HB3	52:H:157:ARG:HH11	1.68	0.59
63:S:131:ARG:HG3	63:S:137:PHE:HE1	1.67	0.59
1:AS:362:U:O4	38:CE:24:ARG:NH2	2.35	0.59
1:AS:2530:C:N4	31:BX:59:GLU:OE2	2.36	0.59
10:BC:249:LYS:HE3	10:BC:253:ALA:HB2	1.85	0.59
27:BT:11:SER:HB3	27:BT:14:LYS:HB2	1.84	0.59
46:CM:1421:G:O6	57:CX:64:TYR:OH	2.14	0.59
46:CM:1578:C:H2'	46:CM:1579:A:C8	2.38	0.59
46:CM:1659:G:H2'	46:CM:1660:G:C8	2.37	0.59
67:DH:32:GLN:HB3	67:DH:108:GLU:HG2	1.84	0.59
75:DP:12:VAL:HG22	75:DP:52:ASP:H	1.66	0.59
6:l:290:LEU:HD22	19:y:129:LEU:HD11	1.84	0.59
18:x:126:ARG:HG3	18:x:140:GLN:HG2	1.83	0.59
75:e:12:VAL:HG12	75:e:30:VAL:HG12	1.83	0.59
79:AR:102:GLN:NE2	79:AR:103:ARG:O	2.36	0.59
1:AS:1018:U:H2'	1:AS:1019:U:H5''	1.84	0.59
1:AS:1663:A:H2'	1:AS:1664:G:H8	1.66	0.59
5:AX:293:ASN:HB2	5:AX:304:THR:HA	1.84	0.59
46:CM:924:A:H2'	46:CM:925:A:C8	2.37	0.59
46:CM:1145:A:H2'	46:CM:1146:C:C6	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CR:48:LEU:HD11	51:CR:70:VAL:HG21	1.84	0.59
51:CR:126:VAL:HG13	51:CR:139:VAL:HG13	1.85	0.59
1:1:756:G:O2'	1:1:766:G:N2	2.27	0.59
1:1:1921:U:O4	1:1:2297:U:O2'	2.18	0.59
46:B:839:U:O4	46:B:840:A:N6	2.36	0.59
46:B:1156:A:H2'	46:B:1157:G:H8	1.65	0.59
1:AS:662:U:H2'	1:AS:663:A:H8	1.66	0.59
1:AS:880:A:HO2'	38:CE:2:GLY:N	2.00	0.59
20:BM:162:ARG:HA	20:BM:165:ARG:HD3	1.83	0.59
46:CM:521:G:H5'	71:DL:60:PHE:O	2.02	0.59
46:CM:1458:C:OP1	52:CS:102:ARG:NH2	2.32	0.59
79:DT:14:GLU:CD	79:DT:53:ASN:HD21	2.10	0.59
1:1:1106:U:H2'	1:1:1107:U:C6	2.37	0.59
1:1:1199:A:H2'	1:1:1200:A:H8	1.66	0.59
1:1:1265:U:H5'	1:1:1266:A:OP2	2.02	0.59
1:1:1600:A:H4'	1:1:1831:A:H4'	1.85	0.59
46:B:813:U:H2'	46:B:814:A:C8	2.37	0.59
49:E:97:VAL:HG11	49:E:124:ILE:HG12	1.85	0.59
63:S:128:PHE:O	63:S:136:ARG:NH1	2.31	0.59
1:AS:1479:G:O6	35:CB:4:ARG:NH2	2.35	0.59
1:AS:2196:G:H2'	1:AS:2197:A:C8	2.38	0.59
10:BC:79:PHE:HA	10:BC:180:ILE:HD13	1.85	0.59
33:BZ:97:ILE:HG21	33:BZ:106:ARG:HG3	1.84	0.59
46:CM:1615:U:H2'	46:CM:1616:G:C8	2.38	0.59
50:CQ:212:ALA:HB2	64:DE:19:ARG:HG3	1.83	0.59
68:DI:70:ASN:HB3	68:DI:83:TRP:HB2	1.85	0.59
1:1:252:U:H5'	1:1:253:A:H8	1.67	0.59
1:1:782:A:H4'	1:1:783:G:H5'	1.85	0.59
25:7:81:ALA:HB3	53:I:130:PRO:HB3	1.83	0.59
45:i:64:LEU:H	45:i:64:LEU:HD12	1.68	0.59
46:B:681:C:H3'	46:B:682:A:H8	1.66	0.59
52:H:42:LEU:HB3	52:H:46:TRP:HB2	1.83	0.59
57:M:14:TYR:HD2	57:M:21:VAL:HG22	1.67	0.59
1:AS:627:U:H2'	1:AS:628:A:H8	1.67	0.59
31:BX:42:LYS:HB3	31:BX:103:LEU:HD21	1.85	0.59
46:CM:1230:G:H1	46:CM:1235:U:H3	1.51	0.59
46:CM:1579:A:H2'	46:CM:1580:A:C8	2.37	0.59
59:CZ:132:GLU:O	59:CZ:136:LEU:HB2	2.03	0.59
65:DF:79:TYR:O	65:DF:81:ILE:N	2.35	0.59
79:DT:155:VAL:O	79:DT:156:ARG:NH1	2.33	0.59
82:L1:28:PHE:HD1	82:L1:29:LEU:H	1.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:834:G:O6	44:AQ:4:ARG:NH2	2.35	0.59
1:1:1591:U:O2'	1:1:1602:U:O2	2.20	0.59
46:B:217:A:H2'	46:B:218:A:O4'	2.03	0.59
46:B:558:U:H2'	46:B:559:G:H8	1.68	0.59
48:D:180:THR:N	48:D:183:GLN:OE1	2.36	0.59
1:AS:172:C:O2'	1:AS:173:C:OP1	2.21	0.59
1:AS:2503:G:OP2	4:AW:37:ARG:NH2	2.36	0.59
8:BA:39:LEU:HD13	8:BA:83:VAL:HG11	1.85	0.59
16:BI:177:GLY:H	16:BI:184:LYS:NZ	2.01	0.59
31:BX:43:LEU:HD23	31:BX:94:ILE:HD12	1.85	0.59
37:CD:57:ILE:HG23	37:CD:93:ILE:HD11	1.84	0.59
46:CM:509:A:OP2	56:CW:176:ASN:ND2	2.36	0.59
46:CM:1152:G:H21	63:DD:138:GLN:HE22	1.51	0.59
50:CQ:24:GLU:OE1	76:DQ:23:HIS:HE1	1.85	0.59
1:1:783:G:H2'	1:1:784:C:C6	2.37	0.59
1:1:1692:A:H2'	1:1:1693:A:C8	2.38	0.59
1:1:2527:G:N2	1:1:2527:G:OP2	2.35	0.59
10:p:222:ASN:HA	10:p:226:LYS:HE2	1.85	0.59
46:B:703:U:H2'	46:B:704:A:N7	2.18	0.59
46:B:940:A:H4'	46:B:1058:G:O2'	2.03	0.59
46:B:1349:G:H21	66:V:3:GLY:H	1.51	0.59
64:T:75:GLU:HA	64:T:78:ARG:HB2	1.85	0.59
27:BT:51:ARG:HG2	27:BT:52:GLN:H	1.67	0.59
52:CS:116:HIS:HD2	72:DM:98:GLN:HB3	1.68	0.59
81:12:124:ASN:O	81:12:126:ALA:N	2.30	0.59
1:1:1240:A:O2'	1:1:1244:C:N4	2.35	0.58
1:1:2206:A:H2'	1:1:2207:A:C8	2.38	0.58
1:1:3269:C:O2	5:k:25:GLN:NE2	2.36	0.58
4:j:204:MET:SD	4:j:209:HIS:HB2	2.44	0.58
5:k:106:TRP:HB2	5:k:133:TYR:CE2	2.38	0.58
31:AD:19:THR:HG23	31:AD:97:ALA:HA	1.84	0.58
46:B:871:U:H2'	46:B:872:A:H8	1.68	0.58
46:B:1048:U:O2'	48:D:203:THR:OG1	2.19	0.58
46:B:1593:C:H2'	46:B:1594:G:C8	2.37	0.58
64:T:96:THR:HG23	64:T:98:GLY:H	1.68	0.58
70:Z:109:ARG:HB3	70:Z:112:LYS:HG3	1.85	0.58
1:AS:941:C:H2'	1:AS:942:U:C6	2.37	0.58
1:AS:1259:A:H4'	1:AS:1260:G:H5''	1.84	0.58
1:AS:2958:U:H2'	1:AS:2959:A:H8	1.68	0.58
1:AS:3194:G:H4'	15:BH:129:VAL:HG11	1.83	0.58
45:CL:90:ARG:HG3	46:CM:1624:C:C2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:261:C:O2'	46:CM:262:G:N2	2.34	0.58
46:CM:1536:C:OP1	62:DC:42:ARG:NH1	2.36	0.58
54:CU:137:ARG:NH2	69:DJ:49:GLU:OE2	2.36	0.58
57:CX:70:ASP:OD1	57:CX:71:GLU:N	2.36	0.58
1:1:480:G:H2'	1:1:481:G:C8	2.38	0.58
1:1:907:C:H42	4:j:3:ARG:HD3	1.67	0.58
1:1:1079:G:H2'	1:1:1080:A:C8	2.38	0.58
1:1:1237:U:O2'	1:1:1239:G:N7	2.32	0.58
1:1:1273:C:H2'	1:1:1274:A:H8	1.69	0.58
1:1:2634:G:H2'	1:1:2635:A:H8	1.66	0.58
3:4:36:G:C5	36:AI:86:ARG:HD3	2.38	0.58
46:B:309:U:OP2	70:Z:20:ARG:HD3	2.03	0.58
46:B:671:G:H5''	46:B:672:U:C6	2.38	0.58
46:B:1478:A:O2'	46:B:1479:A:O4'	2.20	0.58
1:AS:2645:A:O2'	13:BF:126:ASP:OD1	2.11	0.58
1:AS:2672:G:H5''	22:BO:17:ARG:HG2	1.84	0.58
2:AT:3:U:H2'	2:AT:4:U:C6	2.39	0.58
82:l1:93:LEU:C	82:l1:95:LYS:H	2.09	0.58
1:1:1115:C:H2'	1:1:1116:A:C8	2.38	0.58
46:B:12:U:H2'	46:B:13:C:C6	2.38	0.58
63:S:30:ILE:HG12	63:S:35:ILE:HG22	1.84	0.58
3:AU:36:G:OP1	38:CE:66:TYR:OH	2.15	0.58
46:CM:17:C:H2'	46:CM:18:C:C6	2.38	0.58
46:CM:1495:U:H2'	46:CM:1496:C:C6	2.38	0.58
59:CZ:63:CYS:HB2	59:CZ:97:LEU:HD11	1.85	0.58
65:DF:29:MET:HB2	65:DF:54:LEU:HD23	1.85	0.58
82:l1:41:TYR:HE1	82:l1:195:LYS:H	1.50	0.58
1:1:662:U:H2'	1:1:663:A:H8	1.67	0.58
1:1:1230:G:H5'	81:12:119:LYS:HB3	1.84	0.58
55:K:191:GLU:HB3	58:N:23:PRO:HG3	1.85	0.58
1:AS:908:G:N7	4:AW:9:ARG:NH2	2.51	0.58
1:AS:1795:A:H2'	1:AS:1796:A:H8	1.67	0.58
2:AT:4:U:H2'	2:AT:5:G:C8	2.38	0.58
11:BD:80:THR:HA	11:BD:83:THR:HG22	1.85	0.58
46:CM:472:A:H5''	56:CW:144:PRO:HD2	1.86	0.58
46:CM:592:A:OP1	56:CW:40:ARG:NH1	2.33	0.58
46:CM:940:A:H4'	46:CM:1058:G:O2'	2.03	0.58
46:CM:970:G:H2'	46:CM:971:G:C8	2.38	0.58
46:CM:1335:U:H2'	46:CM:1336:G:C8	2.39	0.58
50:CQ:114:LEU:HD23	50:CQ:118:ARG:HD3	1.84	0.58
65:DF:63:GLN:O	65:DF:67:GLU:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:997:G:O2'	1:1:1037:U:OP2	2.19	0.58
1:1:2093:G:H22	1:1:2098:A:H1'	1.68	0.58
3:4:63:G:O2'	36:AI:49:LYS:NZ	2.37	0.58
46:B:653:G:N2	46:B:654:G:O6	2.33	0.58
46:B:1265:C:O2'	67:W:69:THR:HG22	2.03	0.58
46:B:1468:C:H5''	46:B:1508:G:H22	1.66	0.58
70:Z:57:ILE:HG23	70:Z:58:GLY:H	1.69	0.58
1:AS:477:U:H2'	1:AS:478:G:H8	1.68	0.58
1:AS:1106:U:H2'	1:AS:1107:U:C6	2.39	0.58
1:AS:1580:U:H2'	1:AS:1581:C:H6	1.68	0.58
41:CH:22:LYS:HG3	41:CH:42:THR:HG21	1.84	0.58
46:CM:965:G:H4'	46:CM:1763:A:H4'	1.85	0.58
1:1:730:A:H4'	1:1:730:A:OP1	2.04	0.58
1:1:1642:G:O2'	1:1:1804:G:N2	2.31	0.58
46:B:405:A:H2'	46:B:406:C:H6	1.68	0.58
62:R:81:ARG:NH2	62:R:117:GLY:O	2.37	0.58
1:AS:1903:C:O2	5:AX:240:ARG:NH2	2.35	0.58
1:AS:2925:U:H2'	1:AS:2926:U:H2'	1.86	0.58
3:AU:9:A:H2'	3:AU:10:A:C8	2.38	0.58
23:BP:16:VAL:HG21	23:BP:105:GLN:HE21	1.68	0.58
46:CM:815:U:O2'	46:CM:816:U:O5'	2.22	0.58
46:CM:1192:C:N3	46:CM:1442:C:H5	2.02	0.58
46:CM:1460:G:H2'	46:CM:1461:A:C8	2.37	0.58
50:CQ:166:ARG:NH2	76:DQ:54:LYS:O	2.35	0.58
63:DD:28:ILE:HG22	63:DD:64:ILE:HB	1.85	0.58
1:1:208:A:H4'	1:1:210:A:C8	2.39	0.58
1:1:896:G:H1'	1:1:1585:A:N6	2.18	0.58
1:1:2429:G:H2'	1:1:2430:G:C8	2.39	0.58
8:n:7:LYS:H	8:n:10:GLN:HG3	1.68	0.58
43:AP:35:LEU:HA	43:AP:40:LYS:HE2	1.86	0.58
1:AS:1239:G:N2	1:AS:1266:A:O2'	2.32	0.58
46:CM:79:C:H1'	53:CT:174:LYS:HB2	1.85	0.58
46:CM:1610:C:H2'	46:CM:1611:C:H6	1.69	0.58
47:CN:50:ILE:HA	47:CN:53:THR:HB	1.86	0.58
48:CO:145:ARG:NH2	48:CO:151:LYS:O	2.37	0.58
49:CP:134:ILE:HD13	49:CP:186:ALA:HB1	1.84	0.58
50:CQ:28:ARG:HB3	57:CX:58:GLN:HE21	1.68	0.58
58:CY:7:VAL:HG23	58:CY:8:GLN:HG2	1.84	0.58
81:12:137:GLN:HB2	81:12:148:PRO:HB2	1.85	0.58
1:1:249:G:N2	1:1:251:G:N7	2.52	0.58
1:1:1571:G:H2'	1:1:1572:G:C8	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:i:63:ALA:O	45:i:66:ASN:N	2.36	0.58
46:B:1265:C:H2'	46:B:1266:G:H8	1.68	0.58
59:O:81:GLU:HG3	78:h:155:ASN:HB2	1.86	0.58
1:AS:638:U:H2'	1:AS:639:C:C6	2.38	0.58
1:AS:1564:U:N3	1:AS:1568:U:O4	2.36	0.58
1:AS:2853:C:H2'	1:AS:2854:U:C6	2.39	0.58
15:BH:65:LEU:HD12	15:BH:77:LYS:HD2	1.85	0.58
46:CM:1551:U:H2'	46:CM:1552:C:C6	2.38	0.58
46:CM:1739:U:H2'	46:CM:1740:A:H8	1.68	0.58
66:DG:7:ARG:NH2	66:DG:67:LEU:O	2.36	0.58
1:1:1079:G:H2'	1:1:1080:A:H8	1.69	0.58
1:1:2453:G:OP2	1:1:2454:C:N4	2.35	0.58
1:1:2470:C:O2	82:l1:35:GLN:NE2	2.36	0.58
1:1:3196:U:H2'	1:1:3197:G:H8	1.67	0.58
16:v:27:CYS:HB2	16:v:122:ASN:ND2	2.18	0.58
46:B:1301:G:OP1	64:T:7:LYS:N	2.35	0.58
46:B:1575:G:H1	46:B:1595:U:H3	1.50	0.58
1:AS:394:G:N1	1:AS:397:A:OP2	2.34	0.58
1:AS:1481:G:N2	35:CB:4:ARG:HD2	2.19	0.58
1:AS:1530:A:H2'	1:AS:1531:A:C8	2.39	0.58
1:AS:1713:U:H2'	1:AS:1714:G:C8	2.38	0.58
45:CL:67:LYS:HD2	62:DC:125:PRO:HG3	1.86	0.58
46:CM:327:G:H5''	55:CV:98:LYS:HB3	1.84	0.58
46:CM:504:A:N6	77:DR:27:PRO:HB3	2.18	0.58
50:CQ:215:GLU:HG3	50:CQ:216:ASP:N	2.16	0.58
82:L1:36:VAL:HG13	82:L1:204:LEU:HG	1.86	0.58
82:l1:53:LEU:HB3	82:l1:189:PHE:CZ	2.38	0.58
1:1:2428:G:N2	1:1:2475:U:H3	2.01	0.58
1:1:2718:A:H5'	7:m:178:ASN:OD1	2.04	0.58
19:y:94:LEU:HD22	29:AB:119:PRO:HG3	1.85	0.58
46:B:442:C:OP1	71:a:102:LYS:NZ	2.36	0.58
46:B:483:A:H2'	46:B:484:G:C8	2.39	0.58
46:B:1205:C:O3'	57:M:52:LYS:NZ	2.26	0.58
64:T:14:LYS:HB2	64:T:69:ILE:HD11	1.86	0.58
23:BP:99:VAL:HG12	23:BP:107:LYS:O	2.04	0.58
46:CM:474:U:C2'	77:DR:31:GLN:HE21	2.16	0.58
46:CM:487:C:O2	46:CM:496:G:N2	2.36	0.58
46:CM:1300:U:OP1	46:CM:1313:G:N2	2.31	0.58
46:CM:1469:A:H2'	46:CM:1470:G:C8	2.39	0.58
46:CM:1670:U:H3	46:CM:1705:G:H1	1.52	0.58
51:CR:100:ARG:HG2	51:CR:102:VAL:HG13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CR:123:LEU:HD13	51:CR:237:VAL:HG13	1.86	0.58
3:4:141:C:O3'	16:v:62:TYR:OH	2.21	0.57
7:m:85:ARG:NH2	7:m:250:ASP:OD2	2.37	0.57
46:B:605:G:H5'	46:B:611:G:N2	2.19	0.57
46:B:673:A:H2'	46:B:674:C:O4'	2.04	0.57
46:B:871:U:C2	46:B:872:A:C8	2.92	0.57
46:B:924:A:H2'	46:B:925:A:C8	2.39	0.57
46:B:1237:C:O2'	78:h:184:GLY:N	2.34	0.57
62:R:121:ILE:HD11	65:U:125:ILE:HD13	1.85	0.57
65:U:69:ILE:HG22	65:U:73:MET:HE2	1.85	0.57
79:AR:302:TYR:CE2	79:AR:308:ARG:HD2	2.39	0.57
1:AS:1400:G:N2	1:AS:1403:A:OP2	2.33	0.57
45:CL:67:LYS:HG2	65:DF:129:TRP:CZ2	2.35	0.57
46:CM:29:U:H2'	46:CM:30:G:H8	1.69	0.57
50:CQ:128:MET:HE1	50:CQ:134:GLY:HA2	1.86	0.57
50:CQ:214:ASP:CG	50:CQ:215:GLU:H	2.11	0.57
82:L1:116:LEU:HA	82:L1:119:GLN:HB2	1.86	0.57
80:p0:92:ASP:HB3	80:p0:94:LYS:HG2	1.86	0.57
1:1:638:U:H2'	1:1:639:C:C6	2.39	0.57
1:1:907:C:N4	4:j:3:ARG:HD3	2.18	0.57
1:1:1225:G:H2'	1:1:1226:G:C8	2.39	0.57
1:1:2625:C:OP1	43:AP:89:LYS:HB2	2.04	0.57
1:1:2975:G:O2'	5:k:92:TYR:OH	2.20	0.57
17:w:122:PRO:HA	17:w:125:LEU:HD12	1.85	0.57
64:T:72:LYS:NZ	64:T:76:GLU:OE2	2.37	0.57
1:AS:2520:A:H1'	1:AS:2521:C:C5	2.39	0.57
2:AT:3:U:H2'	2:AT:4:U:H6	1.68	0.57
46:CM:1701:A:H2'	46:CM:1702:A:C8	2.40	0.57
64:DE:25:THR:HG23	64:DE:27:ASP:H	1.67	0.57
80:p0:18:LEU:HA	80:p0:21:GLU:HB3	1.84	0.57
1:1:2958:U:H2'	1:1:2959:A:H8	1.68	0.57
6:l:96:ARG:NH2	87:l:401:HOH:O	2.37	0.57
46:B:932:U:H2'	46:B:933:A:H8	1.68	0.57
64:T:17:ILE:HB	64:T:69:ILE:HD12	1.86	0.57
1:AS:1115:C:H2'	1:AS:1116:A:H8	1.67	0.57
1:AS:1217:A:H4'	1:AS:1218:G:OP2	2.04	0.57
1:1:1265:U:N3	1:1:1268:C:OP2	2.32	0.57
1:1:2405:U:H2'	1:1:2406:U:C6	2.39	0.57
1:1:2826:U:P	12:r:3:ARG:HH22	2.27	0.57
46:B:578:A:O2'	46:B:580:U:OP1	2.22	0.57
55:K:120:THR:HG21	55:K:133:ALA:HA	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:M:77:ARG:NH1	57:M:83:PRO:O	2.37	0.57
14:BG:158:LEU:HB3	29:BV:98:ALA:HB1	1.86	0.57
46:CM:816:U:H2'	46:CM:817:U:C6	2.39	0.57
46:CM:1266:G:O3'	67:DH:75:SER:OG	2.21	0.57
82:11:113:SER:OG	82:11:114:GLU:N	2.34	0.57
1:1:93:G:H2'	1:1:94:A:C8	2.40	0.57
1:1:2384:C:H2'	1:1:2385:C:C6	2.40	0.57
1:1:3133:G:H2'	1:1:3134:C:H6	1.69	0.57
46:B:68:A:OP1	53:I:160:ARG:NH2	2.29	0.57
46:B:1487:C:OP1	66:V:122:ARG:NH2	2.36	0.57
46:B:1649:G:H2'	46:B:1650:G:H8	1.69	0.57
50:F:193:PRO:HG3	50:F:203:LEU:HD12	1.86	0.57
32:BY:71:ARG:HH11	32:BY:103:LEU:HD13	1.70	0.57
1:1:683:G:OP2	14:t:35:ARG:NH1	2.38	0.57
11:q:110:ASP:HB3	11:q:128:ILE:HD12	1.86	0.57
15:u:19:VAL:HG12	15:u:57:LEU:HA	1.86	0.57
18:x:54:HIS:O	18:x:72:GLN:NE2	2.34	0.57
29:AB:36:GLY:HA3	29:AB:40:HIS:CE1	2.40	0.57
46:B:768:C:H2'	46:B:769:U:O4'	2.05	0.57
62:R:72:ARG:HH21	62:R:93:VAL:HG11	1.70	0.57
67:W:34:GLU:OE2	67:W:88:ARG:NH2	2.38	0.57
1:AS:3256:G:H2'	1:AS:3257:A:H8	1.67	0.57
2:AT:112:G:H2'	2:AT:113:C:C6	2.39	0.57
16:BI:177:GLY:H	16:BI:184:LYS:HZ2	1.51	0.57
46:CM:768:C:H2'	46:CM:769:U:O4'	2.05	0.57
46:CM:1383:U:O2'	46:CM:1386:A:N6	2.31	0.57
52:CS:122:HIS:HB2	52:CS:129:PRO:HG3	1.86	0.57
57:CX:81:ASN:HB3	59:CZ:37:VAL:HG13	1.85	0.57
61:DB:107:ILE:HG13	73:DN:53:LEU:HD12	1.87	0.57
3:4:150:G:OP1	26:8:27:ARG:NH2	2.37	0.57
66:V:53:TRP:HH2	66:V:100:ILE:HD12	1.70	0.57
1:AS:1841:G:H5''	1:AS:1842:C:H5'	1.86	0.57
1:AS:1949:G:H1	1:AS:2070:A:H2'	1.68	0.57
46:CM:39:A:OP1	56:CW:3:ARG:NH2	2.37	0.57
67:DH:25:LEU:HD23	67:DH:88:ARG:O	2.05	0.57
67:DH:70:PRO:HA	76:DQ:41:GLN:HG2	1.86	0.57
80:P0:55:LYS:HD3	80:P0:58:MET:HG3	1.86	0.57
1:1:158:A:H2'	1:1:159:A:H8	1.70	0.57
1:1:268:A:C4	16:v:12:ARG:HG2	2.40	0.57
1:1:1174:G:N3	1:1:1324:U:O2'	2.38	0.57
1:1:2342:G:H22	1:1:2374:G:H1'	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:t:158:LEU:HB3	29:AB:98:ALA:HB1	1.86	0.57
46:B:739:A:H5''	46:B:740:A:H5'	1.86	0.57
46:B:1486:G:OP2	66:V:73:VAL:HG12	2.04	0.57
54:J:13:LEU:HD21	54:J:54:LEU:HD11	1.87	0.57
1:AS:252:U:H5'	1:AS:253:A:C8	2.40	0.57
1:AS:2206:A:H2'	1:AS:2207:A:C8	2.40	0.57
1:AS:3060:G:OP1	5:AX:313:ARG:NH1	2.38	0.57
28:BU:15:ARG:HD2	28:BU:79:HIS:CD2	2.40	0.57
46:CM:1486:G:OP2	66:DG:73:VAL:HG12	2.04	0.57
46:CM:1649:G:H2'	46:CM:1650:G:H8	1.69	0.57
62:DC:121:ILE:HD11	65:DF:125:ILE:HD13	1.87	0.57
82:L1:60:ARG:HB2	82:L1:63:MET:HE3	1.86	0.57
1:1:269:G:H5''	16:v:14:LYS:HE2	1.85	0.57
2:3:81:U:H2'	2:3:82:G:C8	2.40	0.57
3:4:9:A:H2'	3:4:10:A:C8	2.40	0.57
46:B:1719:A:H2'	46:B:1720:C:H6	1.69	0.57
53:I:68:MET:O	53:I:69:HIS:ND1	2.38	0.57
1:AS:1216:U:H5''	1:AS:1218:G:C4	2.39	0.57
1:AS:1627:C:H3'	28:BU:48:ARG:HH12	1.69	0.57
46:CM:669:G:H2'	46:CM:671:G:C8	2.39	0.57
68:DI:36:ILE:HD12	68:DI:78:LEU:HD13	1.85	0.57
69:DJ:7:LEU:HD11	69:DJ:37:PHE:HD2	1.70	0.57
80:P0:30:VAL:HB	80:P0:33:VAL:HG21	1.87	0.57
46:B:213:A:C2'	46:B:214:U:H5'	2.35	0.57
46:B:965:G:H4'	46:B:1763:A:H4'	1.87	0.57
47:C:52:LYS:HD3	68:X:82:VAL:HG23	1.87	0.57
1:AS:208:A:H4'	1:AS:210:A:N7	2.20	0.57
1:AS:896:G:H1'	1:AS:1585:A:N6	2.20	0.57
1:AS:1030:U:H2'	1:AS:1031:A:C8	2.40	0.57
1:AS:3300:A:H2'	1:AS:3301:A:C8	2.40	0.57
3:AU:8:C:H2'	3:AU:9:A:H8	1.70	0.57
46:CM:1637:U:H2'	46:CM:1638:A:C8	2.40	0.57
1:1:1794:A:H2'	1:1:1795:A:C8	2.40	0.56
1:1:3316:U:H3	55:K:110:ARG:NH1	2.02	0.56
46:B:1276:G:H22	46:B:1309:G:H22	1.50	0.56
1:AS:447:U:C2'	1:AS:448:U:H5''	2.34	0.56
1:AS:1014:G:N2	1:AS:1030:U:O2	2.28	0.56
1:AS:1275:C:H2'	1:AS:1276:C:C6	2.39	0.56
1:AS:1434:U:H4'	6:AY:89:ALA:HB3	1.85	0.56
1:AS:2335:A:H2'	1:AS:2336:A:C8	2.40	0.56
5:AX:218:ILE:HB	5:AX:337:THR:HB	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:733:U:O2'	69:DJ:122:SER:O	2.21	0.56
46:CM:1410:A:C2'	49:CP:87:ALA:HB3	2.30	0.56
1:1:2872:A:H5'	41:AN:51:LEU:HD21	1.87	0.56
2:3:4:U:H2'	2:3:5:G:H8	1.70	0.56
46:B:352:C:H5''	55:K:16:ALA:HB2	1.87	0.56
46:B:405:A:H2'	46:B:406:C:C6	2.41	0.56
46:B:1012:A:OP1	46:B:1776:G:O2'	2.14	0.56
5:AX:284:ARG:HH11	5:AX:356:LEU:HD12	1.70	0.56
28:BU:103:GLU:HB2	28:BU:106:GLN:HB2	1.87	0.56
31:BX:42:LYS:NZ	31:BX:95:LEU:O	2.29	0.56
48:CO:32:ILE:HG22	48:CO:96:LEU:HD11	1.87	0.56
1:1:35:C:H41	1:1:46:C:H6	1.53	0.56
1:1:173:C:H2'	1:1:174:C:C6	2.41	0.56
1:1:386:A:C5	1:1:387:A:H1'	2.41	0.56
1:1:438:A:N1	1:1:489:G:O2'	2.34	0.56
1:1:647:A:H2'	1:1:648:C:C6	2.39	0.56
1:1:1060:A:H4'	1:1:1061:A:O5'	2.05	0.56
1:1:1232:G:N2	1:1:1241:A:N7	2.53	0.56
1:1:2107:U:H2'	1:1:2108:G:C8	2.40	0.56
1:1:2583:U:H2'	1:1:2584:U:C6	2.40	0.56
1:1:2740:U:H2'	1:1:2741:A:H8	1.70	0.56
5:k:218:ILE:HB	5:k:337:THR:HB	1.87	0.56
8:n:39:LEU:HB3	8:n:83:VAL:HG13	1.86	0.56
46:B:458:A:O2'	51:G:27:TYR:OH	2.13	0.56
46:B:1193:A:H4'	46:B:1255:G:P	2.45	0.56
46:B:1672:G:N2	46:B:1704:C:C2	2.74	0.56
46:B:1701:A:H2'	46:B:1702:A:H1'	1.87	0.56
50:F:60:LEU:HD12	50:F:60:LEU:O	2.06	0.56
59:O:77:ALA:HB1	78:h:155:ASN:HA	1.87	0.56
67:W:24:THR:HB	67:W:114:GLU:HG3	1.88	0.56
79:AR:152:VAL:HA	79:AR:170:SER:HA	1.88	0.56
1:AS:115:A:OP2	16:BI:2:GLY:N	2.39	0.56
1:AS:831:G:HO2'	1:AS:853:G:H22	1.51	0.56
1:AS:2281:A:OP1	42:CI:23:ARG:NE	2.34	0.56
1:AS:2391:A:H2'	1:AS:2392:G:H8	1.70	0.56
8:BA:39:LEU:HB3	8:BA:83:VAL:HG13	1.87	0.56
19:BL:181:SER:OG	19:BL:182:ARG:NH1	2.38	0.56
29:BV:36:GLY:HA3	29:BV:40:HIS:CE1	2.40	0.56
45:CL:61:GLU:OE1	45:CL:61:GLU:N	2.37	0.56
45:CL:92:SER:HB2	46:CM:1413:A:H62	1.70	0.56
46:CM:786:G:H21	69:DJ:107:SER:HB3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1064:U:H2'	46:CM:1065:U:C6	2.40	0.56
46:CM:1083:U:OP1	49:CP:154:THR:OG1	2.21	0.56
46:CM:1549:G:OP1	66:DG:89:ARG:NH1	2.38	0.56
59:CZ:106:LEU:HB3	59:CZ:110:GLY:HA2	1.87	0.56
65:DF:87:ASN:HB2	65:DF:99:HIS:CE1	2.41	0.56
1:1:172:C:O2'	1:1:173:C:OP1	2.22	0.56
1:1:788:G:H2'	1:1:789:C:C6	2.41	0.56
46:B:255:A:H1'	55:K:73:SER:HB2	1.87	0.56
46:B:1024:A:O2'	46:B:1025:G:O5'	2.24	0.56
46:B:1277:G:H21	47:C:111:ILE:HD11	1.69	0.56
60:P:46:THR:O	60:P:50:ILE:HD12	2.04	0.56
1:AS:1493:C:H2'	1:AS:1494:A:H8	1.69	0.56
4:AW:96:LEU:O	44:CK:87:ARG:HD3	2.05	0.56
46:CM:1302:C:H2'	46:CM:1303:G:O4'	2.06	0.56
63:DD:21:VAL:HG22	63:DD:64:ILE:HG12	1.88	0.56
69:DJ:11:LEU:HD11	69:DJ:37:PHE:CE2	2.35	0.56
71:DL:29:HIS:HB2	71:DL:32:ARG:HB3	1.87	0.56
1:1:631:U:H2'	1:1:632:C:C6	2.40	0.56
1:1:1456:A:H2'	1:1:1457:A:C8	2.41	0.56
1:1:2334:A:H61	1:1:2955:C:H5	1.49	0.56
1:1:2854:U:H2'	1:1:2855:U:C6	2.40	0.56
5:k:35:ASP:OD2	5:k:191:LYS:NZ	2.28	0.56
46:B:4:C:H4'	49:E:176:SER:HB3	1.88	0.56
46:B:1276:G:H1	46:B:1309:G:H22	1.52	0.56
46:B:1300:U:HO2'	46:B:1301:G:H8	1.53	0.56
64:T:99:GLN:OE1	64:T:99:GLN:N	2.38	0.56
79:AR:257:ILE:HB	79:AR:271:LEU:HB2	1.88	0.56
20:BM:53:LYS:HG2	20:BM:54:PRO:HD2	1.87	0.56
45:CL:103:LEU:HB3	45:CL:109:GLN:HG3	1.87	0.56
46:CM:874:U:H2'	46:CM:875:C:H6	1.70	0.56
46:CM:1149:G:O2'	46:CM:1599:U:O2	2.17	0.56
49:CP:36:LEU:HD21	49:CP:51:ILE:HD12	1.86	0.56
51:CR:152:PRO:HG3	53:CT:212:LEU:HD23	1.87	0.56
81:12:104:ILE:HD12	81:12:109:ILE:HD13	1.87	0.56
1:1:2138:G:H2'	1:1:2139:G:C8	2.39	0.56
7:m:95:TRP:CD1	7:m:158:ARG:HA	2.41	0.56
46:B:1469:A:N3	46:B:1594:G:O2'	2.31	0.56
49:E:53:LEU:HA	68:X:12:TYR:HE1	1.69	0.56
65:U:4:VAL:HG22	72:b:82:GLN:OE1	2.06	0.56
1:AS:782:A:H4'	1:AS:783:G:H5'	1.86	0.56
1:AS:1059:G:N7	1:AS:1093:G:O2'	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1642:G:O2'	1:AS:1804:G:N2	2.35	0.56
1:AS:1655:U:H2'	1:AS:1656:C:C6	2.41	0.56
1:AS:2628:A:H4'	43:CJ:98:LYS:HE3	1.87	0.56
46:CM:165:U:H2'	46:CM:166:A:H5''	1.88	0.56
1:1:1611:U:H5''	35:AH:64:GLN:OE1	2.05	0.56
1:1:3256:G:H2'	1:1:3257:A:H8	1.69	0.56
46:B:125:U:OP1	53:I:201:GLN:NE2	2.33	0.56
46:B:219:A:H2'	46:B:220:A:C8	2.41	0.56
46:B:1413:A:O2'	46:B:1414:G:OP1	2.24	0.56
1:AS:619:A:H2'	1:AS:620:A:C8	2.40	0.56
1:AS:1060:A:H4'	1:AS:1061:A:O5'	2.05	0.56
4:AW:27:ALA:O	4:AW:128:ARG:NH2	2.33	0.56
16:BI:73:ARG:HG2	16:BI:75:VAL:HG13	1.88	0.56
46:CM:970:G:H2'	46:CM:971:G:H8	1.71	0.56
46:CM:1160:U:H2'	46:CM:1161:G:H8	1.69	0.56
46:CM:1453:C:O2'	66:DG:88:PHE:O	2.15	0.56
48:CO:30:PHE:CD1	48:CO:96:LEU:HD21	2.40	0.56
79:DT:14:GLU:OE2	79:DT:53:ASN:ND2	2.37	0.56
82:l1:12:ASN:HB3	82:l1:206:ILE:HG21	1.86	0.56
1:1:3309:A:H2	1:1:3326:G:H21	1.52	0.56
38:AK:21:ARG:HD2	38:AK:37:CYS:SG	2.46	0.56
46:B:52:U:H2'	46:B:53:G:H8	1.71	0.56
46:B:213:A:H2'	46:B:214:U:H5'	1.87	0.56
46:B:1131:G:H2'	46:B:1132:A:H8	1.71	0.56
46:B:1192:C:N3	46:B:1442:C:H5	2.04	0.56
59:O:26:ASP:HA	59:O:29:LYS:HG2	1.88	0.56
67:W:81:TYR:HB3	76:f:52:PHE:HB3	1.88	0.56
78:h:157:GLU:CG	78:h:159:LEU:HG	2.36	0.56
1:AS:2718:A:H5'	7:AZ:178:ASN:OD1	2.06	0.56
4:AW:54:ARG:NH2	4:AW:58:LEU:HD11	2.19	0.56
41:CH:23:CYS:HB2	41:CH:38:LYS:HD2	1.88	0.56
45:CL:99:SER:OG	46:CM:573:C:OP1	2.23	0.56
46:CM:151:G:H2'	46:CM:152:G:C8	2.41	0.56
46:CM:876:A:H2'	46:CM:877:G:H8	1.71	0.56
79:DT:9:LEU:HB2	79:DT:310:TRP:CZ3	2.41	0.56
82:L1:104:ALA:HB2	82:L1:128:LEU:HD12	1.88	0.56
1:1:1021:A:C2	62:R:75:VAL:HB	2.41	0.56
1:1:3194:G:H5'	15:u:129:VAL:HG21	1.88	0.56
4:j:77:ILE:HD13	4:j:128:ARG:HB3	1.86	0.56
16:v:90:ASN:O	43:AP:50:TYR:OH	2.22	0.56
46:B:413:C:O2'	46:B:416:G:O6	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1020:G:OP1	60:P:2:GLY:N	2.38	0.56
46:B:1399:U:O2'	46:B:1400:U:OP1	2.23	0.56
63:S:34:PRO:HB2	63:S:36:THR:HG22	1.88	0.56
1:AS:447:U:O2	1:AS:483:U:N3	2.39	0.56
1:AS:730:A:H4'	1:AS:730:A:OP1	2.06	0.56
1:AS:1214:U:H5''	80:p0:5:ARG:HH22	1.71	0.56
1:AS:1456:A:H2'	1:AS:1457:A:C8	2.41	0.56
1:AS:2345:A:H2'	1:AS:2346:A:C8	2.40	0.56
1:AS:2587:G:H2'	1:AS:2588:C:H6	1.69	0.56
1:AS:2933:G:H2'	1:AS:2934:U:C6	2.41	0.56
1:AS:3088:G:H4'	11:BD:69:ARG:NH1	2.21	0.56
1:AS:3240:U:OP2	34:CA:66:VAL:HG21	2.05	0.56
45:CL:69:PHE:CE1	62:DC:127:ARG:HD3	2.41	0.56
46:CM:189:G:N7	55:CV:143:ARG:NH2	2.53	0.56
46:CM:1218:G:H1	46:CM:1237:C:H5	1.52	0.56
46:CM:1245:U:H2'	46:CM:1246:G:C8	2.41	0.56
46:CM:1551:U:H2'	46:CM:1552:C:H6	1.71	0.56
54:CU:69:VAL:HG12	54:CU:72:ARG:HH21	1.70	0.56
77:DR:50:THR:HG1	77:DR:53:LYS:HB2	1.66	0.56
23:5:37:LEU:HB3	23:5:56:ILE:HD13	1.88	0.56
46:B:518:A:H2'	46:B:519:A:H8	1.70	0.56
46:B:829:A:H2'	46:B:830:G:H8	1.70	0.56
46:B:878:U:H5'	46:B:879:U:OP2	2.06	0.56
46:B:1672:G:O2'	46:B:1673:U:H5'	2.06	0.56
47:C:41:ARG:HD3	47:C:47:ILE:HD11	1.88	0.56
1:AS:2876:U:H2'	1:AS:2877:U:C6	2.41	0.56
10:BC:150:LYS:HE3	10:BC:203:GLU:HA	1.88	0.56
57:CX:78:THR:O	57:CX:81:ASN:ND2	2.38	0.56
62:DC:10:ARG:NH1	62:DC:13:LYS:HE3	2.20	0.56
1:1:1493:C:H2'	1:1:1494:A:H8	1.71	0.55
12:r:54:SER:OG	12:r:130:SER:O	2.25	0.55
45:i:77:GLN:HE22	46:B:1165:C:H5'	1.71	0.55
46:B:1459:U:OP1	52:H:183:SER:OG	2.24	0.55
53:I:159:ARG:HB2	53:I:170:THR:HB	1.87	0.55
57:M:11:ILE:HD11	57:M:37:THR:HG21	1.87	0.55
79:AR:127:SER:OG	79:AR:129:ASP:OD1	2.20	0.55
1:AS:932:A:OP2	29:BV:27:LYS:HE2	2.07	0.55
1:AS:1949:G:O2'	1:AS:2066:G:N2	2.39	0.55
5:AX:95:THR:OG1	5:AX:98:GLY:O	2.24	0.55
46:CM:32:U:O2'	46:CM:592:A:N1	2.39	0.55
46:CM:119:A:H1'	46:CM:395:A:C5	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1067:C:H4'	68:DI:58:TYR:CE1	2.34	0.55
52:CS:98:MET:HB2	52:CS:103:ASN:O	2.07	0.55
81:12:132:ILE:HA	81:12:135:THR:HG22	1.87	0.55
1:1:1456:A:H2'	1:1:1457:A:H8	1.71	0.55
1:1:1795:A:H2'	1:1:1796:A:H8	1.70	0.55
1:1:2385:C:H2'	1:1:2386:U:H6	1.71	0.55
1:1:2444:G:OP2	82:l1:60:ARG:NH1	2.39	0.55
16:v:113:LEU:HB2	16:v:134:LEU:HD23	1.88	0.55
50:F:209:ILE:HD12	64:T:16:LEU:HD21	1.87	0.55
52:H:200:ASN:HB3	52:H:208:SER:HB3	1.87	0.55
57:M:87:LEU:HD22	57:M:91:ARG:O	2.05	0.55
63:S:37:LEU:HA	63:S:44:ARG:NH2	2.20	0.55
18:BK:32:THR:HG21	18:BK:87:SER:HB3	1.88	0.55
24:BQ:17:LEU:HD13	24:BQ:23:MET:HE2	1.88	0.55
46:CM:987:G:N2	46:CM:1747:G:O3'	2.39	0.55
46:CM:1147:C:H4'	75:DP:22:ARG:HD3	1.88	0.55
50:CQ:65:ARG:HD2	57:CX:91:ARG:HE	1.70	0.55
1:1:612:U:H2'	1:1:613:U:C6	2.42	0.55
2:3:16:U:H2'	2:3:17:A:C8	2.41	0.55
2:3:19:C:H2'	2:3:20:A:H8	1.71	0.55
13:s:108:GLU:OE1	65:U:110:ARG:NH1	2.40	0.55
23:5:19:VAL:O	23:5:21:ALA:N	2.38	0.55
24:6:32:ARG:HH21	24:6:64:LYS:HD3	1.70	0.55
46:B:703:U:H2'	46:B:704:A:C5	2.42	0.55
46:B:874:U:H2'	46:B:875:C:H6	1.71	0.55
47:C:124:THR:O	47:C:164:ASN:ND2	2.39	0.55
63:S:98:GLU:OE1	79:AR:61:SER:N	2.39	0.55
75:e:12:VAL:HG22	75:e:52:ASP:H	1.72	0.55
1:AS:1779:U:H2'	1:AS:1780:A:C8	2.41	0.55
1:AS:2158:A:H2'	1:AS:2159:C:C6	2.42	0.55
1:AS:2862:A:O2'	1:AS:2905:A:N3	2.30	0.55
1:AS:2869:A:H2'	1:AS:2871:C:H5''	1.88	0.55
1:AS:3294:U:H5''	5:AX:308:MET:HE2	1.88	0.55
31:BX:53:LEU:HD13	35:CB:91:ARG:HD3	1.89	0.55
46:CM:157:U:H5'	71:DL:117:LYS:HB3	1.88	0.55
46:CM:834:C:H2'	46:CM:835:A:C8	2.42	0.55
46:CM:1393:U:H2'	46:CM:1394:G:C8	2.41	0.55
46:CM:1635:A:H2'	46:CM:1636:C:C6	2.42	0.55
53:CT:218:GLU:HG2	53:CT:219:ARG:NH2	2.21	0.55
79:DT:157:ILE:O	79:DT:201:LEU:HD11	2.05	0.55
1:1:158:A:H2'	1:1:159:A:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1279:C:H2'	1:1:1280:C:C6	2.39	0.55
1:1:2469:A:N3	82:11:209:THR:HA	2.22	0.55
1:1:3153:A:H2	1:1:3158:G:H4'	1.70	0.55
18:x:120:ASN:HB2	18:x:145:HIS:HB2	1.88	0.55
21:0:96:ASP:OD1	21:0:97:VAL:N	2.39	0.55
46:B:1566:U:H2'	46:B:1567:C:C6	2.41	0.55
51:G:11:ARG:HA	51:G:28:ALA:HB2	1.89	0.55
28:BU:12:ILE:HB	28:BU:81:MET:HB3	1.88	0.55
46:CM:233:G:H2'	46:CM:234:G:C8	2.41	0.55
46:CM:1129:U:H2'	46:CM:1130:U:C6	2.41	0.55
61:DB:59:ALA:HB1	61:DB:100:LEU:HG	1.88	0.55
1:1:231:A:O2'	1:AS:246:U:OP1	2.19	0.55
1:1:647:A:OP2	1:1:2840:U:O2'	2.24	0.55
1:1:1493:C:H2'	1:1:1494:A:C8	2.42	0.55
1:1:2391:A:H2'	1:1:2392:G:H8	1.71	0.55
1:1:2876:U:H2'	1:1:2877:U:C6	2.40	0.55
3:4:49:G:OP1	36:AI:45:HIS:HB2	2.06	0.55
46:B:338:U:H2'	46:B:339:A:H8	1.72	0.55
50:F:65:ARG:HD2	57:M:91:ARG:NH1	2.17	0.55
1:AS:487:C:O2'	1:AS:488:G:OP1	2.20	0.55
1:AS:1256:A:H1'	1:AS:1276:C:H1'	1.87	0.55
1:AS:1794:A:H2'	1:AS:1795:A:C8	2.42	0.55
1:AS:2709:C:O2'	30:BW:36:ASP:OD1	2.23	0.55
1:AS:2740:U:H2'	1:AS:2741:A:C8	2.41	0.55
11:BD:147:SER:HB2	11:BD:187:ILE:HD11	1.89	0.55
39:CF:24:ILE:HB	39:CF:44:LYS:HB2	1.89	0.55
45:CL:64:LEU:HB2	62:DC:103:ASN:HD21	1.72	0.55
46:CM:635:C:O2	54:CU:110:ARG:NH2	2.35	0.55
46:CM:1155:G:C2	46:CM:1156:A:C8	2.94	0.55
46:CM:1212:A:H2	59:CZ:43:ARG:HB3	1.71	0.55
49:CP:171:LYS:HE2	56:CW:57:ARG:CZ	2.35	0.55
59:CZ:74:LEU:HD23	78:DS:150:VAL:HG13	1.87	0.55
65:DF:36:ARG:NH1	65:DF:105:LEU:HD22	2.22	0.55
65:DF:67:GLU:HA	65:DF:70:VAL:HG22	1.89	0.55
67:DH:32:GLN:OE1	67:DH:32:GLN:N	2.39	0.55
76:DQ:19:ARG:HD2	76:DQ:32:ARG:HD3	1.87	0.55
15:u:116:LEU:HD22	17:w:191:ALA:HA	1.89	0.55
16:v:23:TYR:O	16:v:122:ASN:ND2	2.40	0.55
29:AB:104:THR:OG1	29:AB:126:LYS:O	2.23	0.55
46:B:345:G:H5''	58:N:80:MET:HE2	1.88	0.55
46:B:932:U:H2'	46:B:933:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:236:A:OP1	3:AU:95:G:N2	2.30	0.55
1:AS:2197:A:H2'	1:AS:2198:A:C8	2.42	0.55
1:AS:3195:G:H5''	15:BH:125:LYS:HE2	1.89	0.55
16:BI:46:ASP:OD2	16:BI:50:ARG:NH2	2.34	0.55
21:BN:60:SER:OG	21:BN:62:ASN:OD1	2.24	0.55
32:BY:78:ARG:HA	32:BY:88:LEU:HD23	1.89	0.55
46:CM:1597:G:N7	63:DD:13:LYS:NZ	2.54	0.55
46:CM:1719:A:H2'	46:CM:1720:C:H6	1.71	0.55
1:1:1795:A:H2'	1:1:1796:A:C8	2.42	0.55
1:1:2196:G:H2'	1:1:2197:A:H8	1.71	0.55
1:1:3199:G:N2	1:1:3218:U:O2	2.31	0.55
46:B:452:A:O4'	51:G:66:MET:HG3	2.07	0.55
46:B:1315:G:H21	64:T:8:THR:HG21	1.71	0.55
51:G:126:VAL:HG13	51:G:139:VAL:HG13	1.87	0.55
72:b:50:ILE:HG12	72:b:69:LEU:HD13	1.88	0.55
1:AS:538:G:H2'	1:AS:539:G:C8	2.42	0.55
1:AS:1591:U:OP2	35:CB:36:LYS:NZ	2.38	0.55
1:AS:2126:U:H2'	1:AS:2127:A:C8	2.41	0.55
1:AS:2988:A:H2'	1:AS:2989:A:C8	2.41	0.55
21:BN:73:LYS:NZ	21:BN:97:VAL:O	2.40	0.55
21:BN:96:ASP:OD1	21:BN:97:VAL:N	2.39	0.55
23:BP:33:TYR:O	23:BP:37:LEU:HD23	2.06	0.55
61:DB:52:PRO:HB3	61:DB:95:SER:OG	2.07	0.55
82:l1:92:LYS:HG3	82:l1:93:LEU:H	1.72	0.55
1:1:25:A:H2'	1:1:26:C:H6	1.72	0.55
1:1:314:U:H2'	1:1:315:C:C6	2.42	0.55
1:1:431:A:H2'	1:1:432:G:C8	2.41	0.55
1:1:527:G:H2'	1:1:528:A:C8	2.42	0.55
1:1:1241:A:H3'	1:1:1242:G:C5'	2.37	0.55
36:AI:1:MET:HB3	36:AI:45:HIS:CE1	2.42	0.55
46:B:17:C:H2'	46:B:18:C:C6	2.42	0.55
59:O:26:ASP:HA	59:O:29:LYS:CG	2.37	0.55
3:AU:52:A:H62	40:CG:27:ILE:HD13	1.70	0.55
46:CM:1417:C:O2'	46:CM:1423:U:O4	2.14	0.55
46:CM:1474:G:H3'	46:CM:1502:A:H61	1.71	0.55
79:DT:90:LEU:HB2	79:DT:104:PHE:HB2	1.89	0.55
1:1:374:A:N3	1:1:376:G:H5''	2.22	0.55
1:1:589:G:N2	1:1:610:U:OP1	2.37	0.55
5:k:284:ARG:HH11	5:k:356:LEU:HD12	1.72	0.55
46:B:583:A:OP1	77:g:15:LYS:NZ	2.40	0.55
48:D:62:LYS:NZ	48:D:90:GLU:HA	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:F:62:GLU:HB3	50:F:65:ARG:NH2	2.22	0.55
1:AS:496:A:H4'	8:BA:27:GLN:HG3	1.87	0.55
1:AS:1939:C:O2'	55:CV:92:ARG:NH1	2.40	0.55
1:AS:2869:A:OP2	41:CH:48:LYS:NZ	2.38	0.55
1:AS:3285:A:H2'	1:AS:3286:C:C6	2.42	0.55
3:AU:63:G:H22	3:AU:97:A:H2	1.54	0.55
59:CZ:75:VAL:HA	59:CZ:78:LEU:HG	1.88	0.55
1:1:362:U:O4	38:AK:24:ARG:NH2	2.40	0.55
1:1:1593:C:P	35:AH:8:ARG:HH22	2.29	0.55
1:1:2370:C:H1'	5:k:266:ARG:NH2	2.22	0.55
2:3:112:G:H2'	2:3:113:C:C6	2.42	0.55
25:7:83:VAL:HG11	46:B:68:A:C2	2.42	0.55
30:AC:17:HIS:CD2	30:AC:21:ILE:HG13	2.41	0.55
59:O:52:LEU:HD21	59:O:60:CYS:SG	2.47	0.55
1:AS:1245:G:O2'	1:AS:1246:G:OP1	2.24	0.55
1:AS:1493:C:H2'	1:AS:1494:A:C8	2.42	0.55
4:AW:180:LEU:HD23	44:CK:18:TYR:CD2	2.41	0.55
16:BI:36:ILE:HG12	16:BI:64:ILE:HG13	1.89	0.55
46:CM:327:G:H5'	55:CV:99:SER:HB3	1.89	0.55
46:CM:701:G:H5'	53:CT:230:ARG:NH1	2.19	0.55
46:CM:874:U:H2'	46:CM:875:C:C6	2.42	0.55
46:CM:1216:U:H3	46:CM:1239:U:H3	1.55	0.55
46:CM:1399:U:O2'	46:CM:1400:U:OP1	2.24	0.55
66:DG:16:ASN:OD1	66:DG:56:LYS:NZ	2.39	0.55
1:1:1302:G:O6	1:1:2344:C:O2'	2.23	0.54
1:1:1518:U:O2'	26:8:113:LEU:HD11	2.06	0.54
1:1:1556:G:N7	26:8:36:LYS:HE2	2.23	0.54
1:1:1561:U:H2'	1:1:1562:G:C8	2.41	0.54
1:1:1580:U:H2'	1:1:1581:C:H6	1.72	0.54
46:B:870:G:P	48:D:136:ARG:HH11	2.30	0.54
64:T:25:THR:HG23	64:T:27:ASP:H	1.72	0.54
1:AS:46:C:H5''	14:BG:16:LYS:HG2	1.88	0.54
1:AS:1007:A:H2'	1:AS:1008:A:C8	2.42	0.54
1:AS:1943:G:O2'	1:AS:1944:G:OP1	2.21	0.54
1:AS:2139:G:H5''	4:AW:227:ARG:NH1	2.19	0.54
1:AS:2974:C:OP1	5:AX:26:ARG:NH1	2.40	0.54
13:BF:160:ILE:HG23	13:BF:171:VAL:HG21	1.88	0.54
46:CM:108:A:H2'	46:CM:109:G:C8	2.42	0.54
46:CM:560:G:H2'	46:CM:561:U:O2	2.07	0.54
46:CM:1219:A:HO2'	78:DS:182:TYR:HH	1.50	0.54
62:DC:68:GLU:OE1	62:DC:68:GLU:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:P0:4:ALA:HB3	80:P0:5:ARG:NH1	2.22	0.54
1:1:662:U:H5'	6:l:108:ARG:HA	1.89	0.54
1:1:1021:A:N6	62:R:74:ALA:HA	2.22	0.54
1:1:1197:C:N4	1:1:2829:C:OP1	2.40	0.54
1:1:1241:A:H3'	1:1:1242:G:H5''	1.89	0.54
1:1:2345:A:H2'	1:1:2346:A:C8	2.42	0.54
1:1:2408:A:H2'	1:1:2409:C:C6	2.42	0.54
3:4:75:G:OP2	27:9:74:TYR:OH	2.23	0.54
21:0:92:LYS:HE2	21:0:109:ASP:OD1	2.08	0.54
36:AI:64:GLU:HA	36:AI:67:ARG:HB2	1.89	0.54
46:B:79:C:H1'	53:I:174:LYS:HB2	1.88	0.54
46:B:123:G:OP1	51:G:77:ARG:NH2	2.32	0.54
46:B:1453:C:O2'	66:V:88:PHE:O	2.19	0.54
48:D:82:ARG:NH2	48:D:191:GLU:OE2	2.40	0.54
53:I:57:ASP:HA	53:I:106:LEU:HA	1.90	0.54
56:L:110:GLN:NE2	56:L:126:ARG:HB2	2.23	0.54
1:AS:527:G:H2'	1:AS:528:A:C8	2.42	0.54
1:AS:800:C:OP1	6:AY:99:ARG:NH2	2.41	0.54
1:AS:1610:C:OP1	39:CF:50:TYR:OH	2.22	0.54
1:AS:2384:C:H2'	1:AS:2385:C:C6	2.42	0.54
14:BG:59:ARG:NH1	14:BG:66:ASN:O	2.39	0.54
46:CM:1301:G:HO2'	46:CM:1387:A:HO2'	1.55	0.54
46:CM:1696:U:H2'	46:CM:1697:C:C5	2.43	0.54
46:CM:1772:U:H2'	46:CM:1773:G:H8	1.71	0.54
55:CV:76:THR:HG21	55:CV:104:ILE:HD12	1.90	0.54
62:DC:13:LYS:H	62:DC:13:LYS:HD2	1.70	0.54
64:DE:16:LEU:HD12	64:DE:54:THR:HG21	1.89	0.54
66:DG:42:GLY:HA2	66:DG:84:LYS:HG3	1.88	0.54
82:L1:15:LYS:HB2	82:L1:214:PHE:CZ	2.42	0.54
80:p0:101:VAL:HG23	80:p0:102:SER:H	1.72	0.54
3:4:21:C:OP1	6:l:194:LYS:NZ	2.31	0.54
11:q:12:ILE:HD11	11:q:53:ILE:HG13	1.88	0.54
46:B:296:C:H5''	51:G:38:LEU:HB2	1.90	0.54
50:F:223:THR:HG21	79:AR:225:ASN:HB3	1.89	0.54
1:AS:1345:G:N2	6:AY:292:ASN:O	2.41	0.54
1:AS:2090:U:H4'	1:AS:2091:A:O5'	2.07	0.54
1:AS:2583:U:H2'	1:AS:2584:U:C6	2.42	0.54
1:AS:2587:G:H2'	1:AS:2588:C:C6	2.43	0.54
1:AS:3193:C:H4'	1:AS:3194:G:O5'	2.06	0.54
46:CM:1324:C:O2'	46:CM:1326:A:N7	2.38	0.54
46:CM:1672:G:O2'	46:CM:1673:U:H5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1716:C:H2'	46:CM:1717:A:O4'	2.06	0.54
82:11:49:PHE:CG	82:11:193:LEU:HB3	2.42	0.54
1:1:185:U:H3	1:1:229:C:H42	1.56	0.54
1:1:248:U:H2'	1:1:249:G:H4'	1.89	0.54
1:1:1841:G:H5''	1:1:1842:C:H5'	1.88	0.54
6:1:6:GLN:HB3	6:1:20:GLN:HB3	1.88	0.54
43:AP:8:ARG:HG2	43:AP:10:THR:HG23	1.88	0.54
46:B:669:G:H2'	46:B:671:G:C8	2.42	0.54
46:B:948:A:N7	60:P:70:LYS:NZ	2.56	0.54
46:B:1335:U:H2'	46:B:1336:G:C8	2.42	0.54
46:B:1669:U:HO2'	46:B:1670:U:H6	1.55	0.54
52:H:55:ASP:OD1	52:H:57:SER:OG	2.23	0.54
52:H:98:MET:O	52:H:99:MET:HE2	2.07	0.54
57:M:70:ASP:OD1	57:M:71:GLU:N	2.41	0.54
65:U:91:ASP:OD1	65:U:92:GLN:N	2.39	0.54
79:AR:216:VAL:HA	79:AR:232:GLU:HA	1.89	0.54
1:AS:710:G:OP1	14:BG:176:ARG:NH1	2.40	0.54
1:AS:907:C:N4	4:AW:3:ARG:HD3	2.22	0.54
1:AS:1163:U:OP1	87:AS:3803:HOH:O	2.19	0.54
1:AS:1592:C:H2'	1:AS:1593:C:C6	2.42	0.54
1:AS:2183:U:O2'	1:AS:2184:G:OP1	2.23	0.54
1:AS:3019:U:OP1	5:AX:222:LYS:N	2.40	0.54
46:CM:214:U:H4'	46:CM:215:A:OP2	2.06	0.54
46:CM:1043:U:O2	46:CM:1045:U:N3	2.40	0.54
67:DH:68:LYS:HE2	67:DH:79:ASP:OD1	2.07	0.54
59:O:74:LEU:O	59:O:78:LEU:HD13	2.07	0.54
1:AS:582:G:H2'	1:AS:583:A:H8	1.73	0.54
1:AS:1830:U:OP2	40:CG:10:LYS:NZ	2.37	0.54
1:AS:3261:A:H2'	1:AS:3262:U:H6	1.73	0.54
13:BF:86:VAL:HG21	13:BF:112:LEU:HD22	1.88	0.54
46:CM:1024:A:O2'	46:CM:1025:G:O5'	2.25	0.54
52:CS:61:TYR:OH	75:DP:52:ASP:OD1	2.23	0.54
1:1:403:C:O2'	1:1:404:G:OP1	2.22	0.54
1:1:2418:A:H2'	1:1:2419:A:C8	2.43	0.54
1:1:2978:A:H2'	1:1:2979:U:O4'	2.08	0.54
1:1:2981:G:OP1	17:w:67:LYS:HD2	2.08	0.54
40:AM:9:THR:HG23	40:AM:51:ILE:HG21	1.88	0.54
46:B:870:G:H2'	46:B:871:U:C6	2.43	0.54
46:B:1245:U:H2'	46:B:1246:G:C8	2.43	0.54
46:B:1656:U:H2'	46:B:1657:G:O4'	2.07	0.54
54:J:4:LYS:NZ	54:J:34:LEU:O	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:J:137:ARG:NH2	69:Y:49:GLU:OE1	2.38	0.54
57:M:86:ILE:HG13	57:M:87:LEU:HG	1.89	0.54
63:S:14:THR:HB	63:S:71:GLY:HA2	1.90	0.54
1:AS:252:U:H5'	1:AS:253:A:H8	1.71	0.54
1:AS:411:U:H2'	1:AS:412:G:C8	2.42	0.54
1:AS:647:A:H2'	1:AS:648:C:C6	2.43	0.54
5:AX:58:ARG:NH1	5:AX:352:GLU:OE2	2.30	0.54
46:CM:290:U:H2'	46:CM:291:U:C6	2.42	0.54
46:CM:1300:U:HO2'	46:CM:1301:G:H8	1.56	0.54
48:CO:26:ARG:O	48:CO:50:ARG:N	2.40	0.54
79:DT:189:PHE:HD2	79:DT:220:TRP:CE3	2.26	0.54
82:l1:19:TYR:CD2	82:l1:210:MET:HB3	2.40	0.54
1:1:648:C:H2'	1:1:649:G:C8	2.43	0.54
1:1:1530:A:H2'	1:1:1531:A:C8	2.42	0.54
1:1:2587:G:H2'	1:1:2588:C:H6	1.72	0.54
1:1:2958:U:H2'	1:1:2959:A:C8	2.42	0.54
1:1:3046:G:H4'	32:AE:61:ARG:HD2	1.88	0.54
5:k:339:ARG:NH2	5:k:342:LEU:HD11	2.23	0.54
27:9:39:LEU:HD22	27:9:43:TYR:HE2	1.71	0.54
32:AE:7:VAL:HG13	32:AE:43:MET:HE1	1.90	0.54
41:AN:22:LYS:HG3	41:AN:39:CYS:HB2	1.90	0.54
43:AP:35:LEU:CA	43:AP:40:LYS:HD3	2.33	0.54
46:B:30:G:H2'	46:B:31:C:C6	2.43	0.54
46:B:103:A:H4'	46:B:105:A:C8	2.43	0.54
46:B:786:G:H21	69:Y:107:SER:HB3	1.72	0.54
52:H:98:MET:HB2	52:H:103:ASN:O	2.08	0.54
57:M:4:PRO:HG2	57:M:7:ASP:HB2	1.90	0.54
64:T:89:SER:C	64:T:91:LEU:H	2.16	0.54
1:AS:200:A:H2'	1:AS:201:G:H8	1.73	0.54
1:AS:438:A:N1	1:AS:489:G:O2'	2.35	0.54
1:AS:3156:A:O2'	11:BD:23:ARG:NH1	2.34	0.54
6:AY:300:VAL:HB	19:BL:39:ARG:HG2	1.88	0.54
46:CM:476:A:OP1	77:DR:37:ARG:NH1	2.34	0.54
46:CM:739:A:H5''	46:CM:740:A:C5'	2.37	0.54
46:CM:1436:U:H2'	46:CM:1437:C:C6	2.43	0.54
62:DC:50:ASP:C	62:DC:52:LYS:H	2.14	0.54
82:l1:208:SER:C	82:l1:210:MET:H	2.15	0.54
80:p0:76:LEU:HD22	80:p0:79:PHE:HZ	1.72	0.54
1:1:538:G:H2'	1:1:539:G:C8	2.42	0.54
1:1:948:A:H4'	1:1:964:G:N2	2.23	0.54
1:1:1253:C:H42	1:1:1257:G:H22	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3039:C:H3'	20:z:62:ARG:NH2	2.22	0.54
17:w:28:ILE:HD11	17:w:89:ILE:HD11	1.90	0.54
21:0:161:LYS:HB3	21:0:161:LYS:NZ	2.21	0.54
46:B:653:G:O2'	46:B:672:U:N3	2.38	0.54
46:B:789:U:O4	54:J:100:ARG:NH2	2.39	0.54
46:B:1337:C:H2'	46:B:1338:U:O4'	2.08	0.54
46:B:1350:C:H5''	63:S:27:LEU:HD22	1.89	0.54
79:AR:68:ILE:O	79:AR:86:TRP:N	2.32	0.54
1:AS:431:A:H2'	1:AS:432:G:C8	2.42	0.54
1:AS:1580:U:H2'	1:AS:1581:C:C6	2.43	0.54
1:AS:2961:U:O2'	5:AX:232:ARG:NH1	2.40	0.54
1:AS:3260:A:H2'	1:AS:3261:A:H8	1.73	0.54
5:AX:280:HIS:HD1	5:AX:328:ILE:HG22	1.72	0.54
7:AZ:119:TYR:OH	7:AZ:139:PRO:O	2.26	0.54
10:BC:42:GLN:OE1	10:BC:45:ARG:NH2	2.34	0.54
18:BK:40:LYS:HD2	18:BK:113:VAL:HG22	1.90	0.54
46:CM:238:U:O2'	46:CM:239:U:OP1	2.24	0.54
50:CQ:65:ARG:HD2	57:CX:91:ARG:NE	2.23	0.54
52:CS:58:LEU:HD12	52:CS:138:VAL:HG12	1.90	0.54
62:DC:24:ASP:O	62:DC:28:MET:HG3	2.07	0.54
62:DC:130:ARG:HD3	62:DC:130:ARG:H	1.73	0.54
69:DJ:2:THR:CG2	69:DJ:3:ARG:H	2.14	0.54
1:1:563:U:H2'	1:1:564:G:C8	2.43	0.54
1:1:1617:A:H2'	1:1:1618:U:C6	2.43	0.54
1:1:1663:A:H2'	1:1:1664:G:H8	1.71	0.54
1:1:2270:U:HO2'	46:B:1643:U:HO2'	1.53	0.54
13:s:92:ARG:HD3	13:s:174:LYS:HE3	1.89	0.54
38:AK:39:TYR:CD1	38:AK:40:PRO:HA	2.43	0.54
46:B:219:A:H3'	46:B:818:U:O2	2.08	0.54
46:B:1145:A:H2'	46:B:1146:C:C6	2.43	0.54
46:B:1670:U:O2'	46:B:1671:G:O5'	2.24	0.54
51:G:71:GLN:NE2	51:G:93:GLU:OE2	2.41	0.54
1:AS:429:U:H2'	1:AS:430:G:C8	2.40	0.54
1:AS:565:A:H2'	1:AS:566:C:O4'	2.08	0.54
1:AS:2687:A:O2'	43:CJ:8:ARG:NH2	2.35	0.54
1:AS:2853:C:H2'	1:AS:2854:U:H6	1.72	0.54
1:AS:3310:G:OP1	55:CV:92:ARG:HG2	2.07	0.54
8:BA:20:THR:HG22	8:BA:22:LYS:H	1.71	0.54
12:BE:101:LYS:HE2	12:BE:101:LYS:HA	1.89	0.54
14:BG:126:PHE:HB3	14:BG:130:THR:OG1	2.07	0.54
36:CC:85:THR:O	36:CC:89:ARG:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1593:C:H2'	46:CM:1594:G:C8	2.43	0.54
53:CT:180:THR:HG23	53:CT:183:THR:H	1.72	0.54
57:CX:81:ASN:CB	59:CZ:37:VAL:HG13	2.37	0.54
61:DB:76:ILE:HD13	61:DB:97:LEU:HD11	1.88	0.54
1:1:15:A:OP1	26:8:42:ARG:HG2	2.08	0.54
1:1:1383:G:O6	6:l:187:LYS:HD3	2.08	0.54
1:1:2628:A:OP2	43:AP:97:LYS:HD3	2.08	0.54
1:1:2933:G:H2'	1:1:2934:U:C6	2.42	0.54
46:B:1235:U:O2'	78:h:177:MET:HE2	2.08	0.54
46:B:1669:U:O4	46:B:1707:G:N2	2.40	0.54
47:C:14:ALA:O	47:C:18:LEU:HD12	2.08	0.54
47:C:88:LYS:HG3	47:C:201:LEU:HD11	1.89	0.54
54:J:29:ASP:OD1	54:J:30:LEU:HD23	2.08	0.54
1:AS:1611:U:H2'	1:AS:1612:U:C6	2.42	0.54
1:AS:2107:U:H2'	1:AS:2108:G:C8	2.43	0.54
1:AS:2385:C:H2'	1:AS:2386:U:H6	1.73	0.54
1:AS:3164:U:H1'	1:AS:3165:U:C5	2.42	0.54
13:BF:92:ARG:HB3	13:BF:95:ASN:OD1	2.08	0.54
46:CM:222:C:C2	46:CM:823:G:N2	2.75	0.54
46:CM:1072:A:H2'	46:CM:1073:A:C8	2.43	0.54
46:CM:1276:G:H22	46:CM:1309:G:H22	1.54	0.54
46:CM:1609:G:H2'	46:CM:1610:C:C6	2.43	0.54
59:CZ:82:PRO:HB2	59:CZ:84:GLU:N	2.23	0.54
1:1:780:A:C2	19:y:69:ARG:HD3	2.43	0.53
1:1:1575:A:OP1	1:1:2500:G:N2	2.34	0.53
2:3:65:G:O3'	12:r:204:GLY:HA2	2.08	0.53
12:r:49:CYS:HB3	12:r:168:SER:HB3	1.88	0.53
16:v:31:ARG:NH1	16:v:124:ASP:OD2	2.39	0.53
46:B:216:A:N6	46:B:829:A:O2'	2.40	0.53
46:B:335:G:O2'	55:K:10:LYS:NZ	2.40	0.53
62:R:81:ARG:NH1	62:R:98:ASN:HA	2.23	0.53
78:h:157:GLU:HG2	78:h:159:LEU:HG	1.90	0.53
1:AS:605:U:OP2	8:BA:21:ARG:HG2	2.08	0.53
4:AW:80:GLU:HG3	44:CK:66:GLY:HA2	1.90	0.53
44:CK:28:LYS:O	44:CK:32:GLN:HG3	2.06	0.53
46:CM:15:U:H2'	46:CM:16:G:O4'	2.08	0.53
46:CM:676:G:OP1	46:CM:676:G:H4'	2.08	0.53
67:DH:43:ASN:HD21	67:DH:105:ILE:HG21	1.74	0.53
71:DL:57:VAL:HB	71:DL:60:PHE:HE1	1.73	0.53
1:1:624:U:H2'	1:1:625:C:C6	2.43	0.53
1:1:1006:G:N2	12:r:193:ASP:O	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2210:A:H2'	1:1:2211:A:C8	2.43	0.53
24:6:15:LEU:HD13	24:6:51:ALA:HB3	1.91	0.53
46:B:563:C:O3'	70:Z:66:SER:OG	2.26	0.53
46:B:746:G:O2'	56:L:72:GLU:OE2	2.20	0.53
46:B:1129:U:H2'	46:B:1130:U:C6	2.43	0.53
46:B:1615:U:H2'	46:B:1616:G:C8	2.43	0.53
51:G:123:LEU:HD23	51:G:159:THR:HG21	1.90	0.53
1:AS:29:G:H5''	16:BI:188:ARG:HH12	1.72	0.53
1:AS:563:U:H2'	1:AS:564:G:C8	2.43	0.53
1:AS:629:A:C2	34:CA:91:PRO:HG2	2.43	0.53
1:AS:981:U:H2'	1:AS:982:U:H6	1.73	0.53
1:AS:2469:A:H4'	82:L1:212:PRO:HA	1.90	0.53
1:AS:2470:C:H5'	82:L1:213:SER:HB3	1.89	0.53
1:AS:2854:U:H2'	1:AS:2855:U:C6	2.43	0.53
9:BB:119:LYS:HB2	22:BO:133:ALA:HB3	1.89	0.53
72:DM:61:SER:H	72:DM:64:VAL:HB	1.73	0.53
79:DT:20:VAL:HG11	79:DT:307:ILE:HG12	1.90	0.53
82:L1:58:VAL:HA	82:L1:153:SER:HB3	1.90	0.53
82:l1:26:ARG:HD3	82:l1:26:ARG:N	2.21	0.53
1:1:1448:A:N3	1:1:2324:C:O2'	2.41	0.53
1:1:1559:C:O2'	1:1:1560:U:OP1	2.26	0.53
1:1:2158:A:H2'	1:1:2159:C:C6	2.42	0.53
1:1:2492:U:OP2	1:1:2558:G:N2	2.41	0.53
2:3:3:U:H2'	2:3:4:U:C6	2.44	0.53
2:3:3:U:H2'	2:3:4:U:H6	1.72	0.53
7:m:119:TYR:OH	7:m:139:PRO:O	2.14	0.53
45:i:64:LEU:HA	45:i:67:LYS:HE2	1.90	0.53
46:B:218:A:OP2	46:B:817:U:H5'	2.07	0.53
47:C:48:ILE:HD12	47:C:149:MET:HE3	1.90	0.53
48:D:103:LEU:HD13	48:D:188:LEU:HD13	1.90	0.53
63:S:27:LEU:HB3	63:S:63:ASP:HB2	1.89	0.53
77:g:43:ARG:HG2	77:g:54:ARG:HH22	1.73	0.53
1:AS:21:G:H5''	38:CE:43:LYS:HG2	1.89	0.53
1:AS:430:G:H2'	1:AS:431:A:C8	2.43	0.53
1:AS:675:A:N6	1:AS:782:A:O4'	2.41	0.53
3:AU:126:A:O2'	3:AU:129:C:N4	2.42	0.53
5:AX:292:ALA:HB1	5:AX:295:ALA:HB3	1.90	0.53
10:BC:134:LYS:HD2	10:BC:139:HIS:HE1	1.73	0.53
28:BU:70:PRO:O	28:BU:111:LYS:HE3	2.09	0.53
46:CM:870:G:OP1	48:CO:216:LYS:NZ	2.33	0.53
46:CM:878:U:H5'	46:CM:879:U:OP2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1143:C:O2'	46:CM:1568:C:OP2	2.23	0.53
46:CM:1183:G:O3'	76:DQ:40:ARG:NH2	2.39	0.53
46:CM:1265:C:H2'	46:CM:1266:G:C8	2.42	0.53
46:CM:1265:C:O2'	67:DH:69:THR:HG22	2.09	0.53
55:CV:172:TYR:HB3	55:CV:190:LEU:HD12	1.89	0.53
65:DF:4:VAL:N	72:DM:82:GLN:OE1	2.42	0.53
70:DK:70:LYS:HB3	70:DK:93:LEU:HD22	1.90	0.53
82:L1:205:VAL:HG11	82:L1:213:SER:HB2	1.89	0.53
1:1:715:C:OP1	1:1:747:A:O2'	2.24	0.53
1:1:1239:G:O2'	1:1:1240:A:H5'	2.07	0.53
1:1:2196:G:H2'	1:1:2197:A:C8	2.43	0.53
1:1:2528:U:O4'	10:p:39:GLN:NE2	2.39	0.53
4:j:117:GLU:OE2	4:j:163:ARG:NE	2.42	0.53
9:o:13:LYS:HE3	9:o:17:GLN:NE2	2.24	0.53
28:AA:41:ALA:HB2	28:AA:77:TYR:HE1	1.73	0.53
40:AM:23:LEU:HD12	40:AM:24:PRO:HD2	1.90	0.53
46:B:142:G:O2'	46:B:143:A:O5'	2.21	0.53
57:M:77:ARG:HD2	57:M:84:GLU:HA	1.90	0.53
62:R:60:LEU:HD21	62:R:94:VAL:HG12	1.89	0.53
1:AS:268:A:C4	16:BI:12:ARG:HG2	2.43	0.53
1:AS:1456:A:H2'	1:AS:1457:A:H8	1.73	0.53
1:AS:2197:A:H2'	1:AS:2198:A:H8	1.74	0.53
1:AS:2210:A:H2'	1:AS:2211:A:C8	2.44	0.53
1:AS:2958:U:H2'	1:AS:2959:A:C8	2.44	0.53
1:AS:2995:U:H2'	1:AS:2996:A:H8	1.74	0.53
4:AW:242:ARG:NH2	4:AW:243:THR:O	2.42	0.53
5:AX:117:ARG:HD2	5:AX:176:ALA:O	2.07	0.53
46:CM:852:G:H5''	60:DA:4:MET:HE2	1.90	0.53
46:CM:915:A:H2'	48:CO:114:VAL:HG11	1.89	0.53
46:CM:1026:G:H2'	46:CM:1027:G:H8	1.73	0.53
49:CP:53:LEU:O	68:DI:15:ARG:NE	2.40	0.53
54:CU:33:GLU:HG3	54:CU:69:VAL:HG11	1.90	0.53
59:CZ:102:GLY:C	59:CZ:104:CYS:H	2.15	0.53
71:DL:122:GLN:HG2	71:DL:126:GLN:HE22	1.73	0.53
79:DT:117:ALA:HA	79:DT:157:ILE:HD13	1.90	0.53
1:1:33:A:N3	1:1:806:A:O2'	2.39	0.53
1:1:547:U:H2'	1:1:548:G:H8	1.72	0.53
1:1:1807:G:H2'	1:1:1808:G:O4'	2.08	0.53
1:1:2651:A:H1'	45:i:50:LYS:HE2	1.91	0.53
1:1:2853:C:H2'	1:1:2854:U:C6	2.44	0.53
46:B:349:C:OP1	46:B:628:A:O2'	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1648:U:H2'	46:B:1649:G:H8	1.74	0.53
1:AS:430:G:H2'	1:AS:431:A:H8	1.73	0.53
1:AS:783:G:H2'	1:AS:784:C:C6	2.43	0.53
1:AS:1303:G:H5'	17:BJ:61:LYS:HE3	1.89	0.53
1:AS:1937:C:O2'	1:AS:3309:A:N6	2.42	0.53
6:AY:4:ARG:HH22	6:AY:25:ALA:HA	1.74	0.53
12:BE:82:ARG:NH1	12:BE:83:ASP:OD1	2.41	0.53
16:BI:38:ARG:HD2	16:BI:62:TYR:HE1	1.74	0.53
46:CM:623:C:H2'	46:CM:624:U:C6	2.43	0.53
46:CM:1281:A:OP1	47:CN:138:TYR:OH	2.27	0.53
46:CM:1354:U:N3	46:CM:1355:A:N7	2.56	0.53
46:CM:1512:A:H2'	46:CM:1513:A:C8	2.43	0.53
50:CQ:128:MET:HE3	50:CQ:155:ASP:HB3	1.89	0.53
82:l1:33:GLU:H	82:l1:208:SER:HA	1.73	0.53
82:l1:68:PHE:H	82:l1:111:ILE:HG12	1.73	0.53
80:p0:61:ARG:HG2	80:p0:64:ARG:HG3	1.91	0.53
1:1:624:U:H2'	1:1:625:C:H6	1.74	0.53
1:1:1184:U:OP1	1:1:1206:U:O2'	2.23	0.53
1:1:1255:A:N3	1:1:1276:C:O2'	2.39	0.53
1:1:1691:U:O2'	1:1:1745:A:N1	2.37	0.53
1:1:1779:U:H2'	1:1:1780:A:C8	2.43	0.53
1:1:2126:U:H2'	1:1:2127:A:C8	2.44	0.53
1:1:2995:U:H2'	1:1:2996:A:H8	1.74	0.53
1:1:3313:G:H1	1:1:3322:U:H3	1.56	0.53
15:u:14:GLU:HB3	21:0:149:LYS:HG2	1.90	0.53
19:y:67:ILE:HG12	19:y:81:ILE:HG21	1.89	0.53
28:AA:54:THR:CG2	28:AA:56:LYS:HG3	2.39	0.53
29:AB:76:ASP:OD1	29:AB:76:ASP:N	2.42	0.53
46:B:1260:A:O2'	50:F:146:ALA:O	2.25	0.53
46:B:1354:U:C2	46:B:1355:A:N7	2.77	0.53
46:B:1469:A:H2'	46:B:1470:G:C8	2.44	0.53
46:B:1637:U:H2'	46:B:1638:A:C8	2.44	0.53
72:b:61:SER:H	72:b:64:VAL:HB	1.74	0.53
1:AS:294:U:P	16:BI:15:GLN:HE22	2.32	0.53
1:AS:437:G:O2'	1:AS:438:A:OP1	2.24	0.53
1:AS:523:G:H1	1:AS:563:U:H3	1.56	0.53
1:AS:1050:A:H5''	1:AS:2609:A:H61	1.73	0.53
1:AS:1617:A:H2'	1:AS:1618:U:C6	2.44	0.53
46:CM:1369:G:O2'	46:CM:1370:A:H8	1.91	0.53
46:CM:1740:A:H2'	46:CM:1741:A:H8	1.73	0.53
46:CM:1742:A:OP1	70:DK:63:GLN:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:DG:42:GLY:HA3	66:DG:94:VAL:HG21	1.91	0.53
80:p0:15:LEU:O	80:p0:19:LEU:HB2	2.09	0.53
1:1:208:A:H4'	1:1:210:A:N7	2.23	0.53
1:1:1035:U:H2'	1:1:1036:A:C8	2.44	0.53
1:1:1762:G:O2'	1:1:1763:C:OP1	2.25	0.53
1:1:1801:C:O2'	35:AH:76:TYR:HA	2.09	0.53
1:1:2869:A:H2'	1:1:2871:C:H5''	1.90	0.53
1:1:3082:C:H2'	1:1:3083:U:C6	2.43	0.53
7:m:40:HIS:CE1	7:m:42:ALA:HB3	2.43	0.53
9:o:86:ARG:O	9:o:110:ASN:N	2.40	0.53
15:u:62:LEU:HD21	15:u:77:LYS:HB3	1.91	0.53
32:AE:84:ALA:C	32:AE:86:GLU:H	2.17	0.53
46:B:1398:G:H4'	46:B:1399:U:O5'	2.08	0.53
46:B:1548:U:H2'	46:B:1549:G:H8	1.72	0.53
46:B:1659:G:H2'	46:B:1660:G:C8	2.42	0.53
48:D:56:ASN:OD1	48:D:57:ALA:N	2.42	0.53
51:G:139:VAL:HG23	51:G:150:PRO:HG3	1.89	0.53
1:AS:989:G:N3	1:AS:2609:A:H2'	2.24	0.53
1:AS:1067:U:H3	1:AS:1083:G:H1	1.57	0.53
1:AS:1625:U:H3	28:BU:111:LYS:HE2	1.74	0.53
1:AS:3287:A:H2'	1:AS:3288:A:H8	1.72	0.53
23:BP:96:ILE:HG21	23:BP:108:LEU:HD13	1.90	0.53
46:CM:680:C:HO2'	46:CM:681:C:H6	1.55	0.53
48:CO:97:LEU:HD22	48:CO:232:HIS:CG	2.43	0.53
50:CQ:208:LYS:HB3	64:DE:40:VAL:HB	1.90	0.53
54:CU:29:ASP:OD1	54:CU:30:LEU:HD23	2.09	0.53
54:CU:169:TYR:HE2	54:CU:175:LYS:HB2	1.74	0.53
78:DS:178:LYS:O	78:DS:180:ARG:HG2	2.08	0.53
80:p0:89:THR:HG22	80:p0:91:GLY:H	1.74	0.53
1:1:428:U:H2'	1:1:429:U:C6	2.43	0.53
1:1:1187:U:OP2	17:w:50:ARG:HD2	2.09	0.53
1:1:1810:A:H4'	1:1:1811:U:O4'	2.09	0.53
1:1:2130:A:H2'	1:1:2131:U:H6	1.74	0.53
6:l:12:VAL:HG21	10:BC:119:GLU:HB3	1.91	0.53
31:AD:26:THR:HG23	31:AD:95:LEU:HD11	1.91	0.53
39:AL:34:ASN:ND2	39:AL:34:ASN:O	2.42	0.53
46:B:16:G:H2'	46:B:17:C:C6	2.44	0.53
46:B:1417:C:O2'	46:B:1423:U:O4	2.17	0.53
46:CM:1160:U:H2'	46:CM:1161:G:C8	2.44	0.53
82:l1:64:THR:HB	82:l1:108:ASN:HB2	1.90	0.53
1:1:941:C:H2'	1:1:942:U:C6	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2680:C:H2'	1:1:2681:C:H6	1.73	0.53
1:1:2813:G:H1	1:1:2816:C:H2'	1.74	0.53
1:1:2876:U:H2'	1:1:2877:U:H6	1.73	0.53
1:1:3216:U:H2'	1:1:3217:G:C8	2.43	0.53
3:4:8:C:H2'	3:4:9:A:H8	1.73	0.53
8:n:20:THR:HG22	8:n:22:LYS:H	1.74	0.53
46:B:801:A:O4'	54:J:106:GLN:NE2	2.42	0.53
46:B:1007:C:H4'	46:B:1110:A:H61	1.73	0.53
46:B:1026:G:H2'	46:B:1027:G:H8	1.70	0.53
46:B:1219:A:O2'	78:h:187:HIS:ND1	2.42	0.53
46:B:1642:A:N6	46:B:1732:G:O2'	2.41	0.53
62:R:26:VAL:HA	62:R:87:PRO:HB2	1.90	0.53
67:W:26:THR:OG1	67:W:112:ASP:OD1	2.24	0.53
79:AR:42:LEU:HD11	79:AR:83:SER:HB3	1.91	0.53
79:AR:96:GLU:HG2	79:AR:97:THR:HG23	1.91	0.53
1:AS:1116:A:H2'	1:AS:1117:U:H6	1.74	0.53
1:AS:1755:U:H2'	1:AS:1756:A:H5''	1.90	0.53
1:AS:3339:U:H2'	1:AS:3343:C:H41	1.74	0.53
3:AU:49:G:OP2	36:CC:48:ARG:NH1	2.41	0.53
20:BM:39:SER:HA	20:BM:42:ARG:HH11	1.73	0.53
28:BU:87:LEU:HD11	28:BU:121:LYS:HD2	1.91	0.53
32:BY:54:LEU:HA	32:BY:94:PRO:HG3	1.91	0.53
46:CM:449:G:H2'	46:CM:451:C:C5	2.44	0.53
46:CM:834:C:H2'	46:CM:835:A:H8	1.74	0.53
46:CM:1277:G:H2'	46:CM:1278:U:C6	2.44	0.53
46:CM:1315:G:H2'	46:CM:1316:A:O4'	2.08	0.53
46:CM:1452:G:O2'	46:CM:1589:C:OP1	2.26	0.53
48:CO:123:ALA:HB2	48:CO:165:ARG:HG3	1.91	0.53
57:CX:76:LEU:O	57:CX:80:LEU:HB2	2.09	0.53
64:DE:7:LYS:O	64:DE:11:ARG:HG2	2.09	0.53
82:I:93:LEU:HG	82:I:94:ASN:H	1.74	0.53
1:1:1059:G:N7	1:1:1093:G:O2'	2.32	0.53
1:1:1116:A:H2'	1:1:1117:U:H6	1.73	0.53
1:1:2335:A:H2'	1:1:2336:A:H8	1.74	0.53
1:1:3171:C:H5''	1:1:3172:U:O5'	2.08	0.53
9:o:182:LEU:HD21	9:o:200:LEU:HD11	1.90	0.53
46:B:55:A:OP1	71:a:112:LYS:NZ	2.41	0.53
46:B:136:U:O2'	53:I:149:LYS:NZ	2.42	0.53
46:B:826:U:H2'	46:B:827:C:O4'	2.09	0.53
46:B:1145:A:H2'	46:B:1146:C:H6	1.73	0.53
46:B:1187:A:H1'	46:B:1192:C:N4	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:422:A:C2	1:AS:2341:A:H4'	2.44	0.53
1:AS:583:A:H2'	1:AS:584:C:C6	2.44	0.53
1:AS:856:G:O2'	1:AS:891:A:H4'	2.09	0.53
1:AS:1023:A:N6	1:AS:1025:G:N3	2.57	0.53
1:AS:1596:U:H5''	20:BM:42:ARG:NH2	2.24	0.53
1:AS:1799:C:H4'	35:CB:62:TYR:HB3	1.90	0.53
1:AS:3244:A:O2'	1:AS:3245:A:H5'	2.09	0.53
3:AU:150:G:OP1	26:BS:27:ARG:NH2	2.42	0.53
19:BL:67:ILE:HG12	19:BL:81:ILE:HG21	1.91	0.53
38:CE:21:ARG:HD2	38:CE:37:CYS:SG	2.49	0.53
46:CM:1218:G:N1	46:CM:1238:U:O2	2.42	0.53
46:CM:1237:C:H2'	46:CM:1238:U:O4'	2.09	0.53
79:DT:198:CYS:O	79:DT:199:ILE:HG12	2.09	0.53
1:1:599:U:C6	1:1:600:U:H5	2.28	0.52
1:1:1222:G:H5'	1:1:3089:C:H1'	1.91	0.52
1:1:2407:G:H2'	1:1:2408:A:H8	1.74	0.52
1:1:3150:A:C4	17:w:115:LYS:HA	2.44	0.52
45:i:99:SER:OG	46:B:574:G:OP2	2.21	0.52
46:B:444:A:N6	46:B:459:G:H21	2.07	0.52
46:B:1479:A:H4'	46:B:1480:G:O5'	2.09	0.52
47:C:47:ILE:HD12	64:T:106:THR:HG22	1.91	0.52
63:S:67:LYS:O	63:S:67:LYS:HG2	2.09	0.52
73:c:5:ARG:HD3	73:c:9:GLY:N	2.23	0.52
1:AS:314:U:H2'	1:AS:315:C:C6	2.44	0.52
1:AS:797:A:OP1	29:BV:27:LYS:HE3	2.08	0.52
1:AS:2130:A:H2'	1:AS:2131:U:H6	1.74	0.52
1:AS:2408:A:H2'	1:AS:2409:C:C6	2.43	0.52
13:BF:6:GLN:OE1	13:BF:6:GLN:N	2.42	0.52
17:BJ:126:ARG:HG2	17:BJ:130:LEU:HD12	1.91	0.52
19:BL:94:LEU:HD22	29:BV:119:PRO:HG3	1.91	0.52
46:CM:813:U:O2'	46:CM:814:A:H5'	2.08	0.52
46:CM:818:U:H5'	46:CM:819:G:H5'	1.90	0.52
46:CM:1302:C:O2'	46:CM:1386:A:N3	2.38	0.52
46:CM:1548:U:H2'	46:CM:1549:G:H8	1.74	0.52
51:CR:123:LEU:HD23	51:CR:159:THR:HG21	1.90	0.52
1:1:348:A:N3	1:1:352:A:O2'	2.42	0.52
1:1:630:G:H2'	1:1:631:U:C6	2.45	0.52
1:1:1256:A:N6	80:P0:38:MET:SD	2.82	0.52
1:1:2354:G:H2'	1:1:2355:G:C8	2.44	0.52
1:1:2899:C:H2'	1:1:2900:C:H6	1.71	0.52
23:5:22:PRO:HB2	23:5:28:PHE:HB2	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1335:U:H5'	63:S:67:LYS:HZ3	1.74	0.52
46:B:1740:A:H2'	46:B:1741:A:H8	1.75	0.52
51:G:129:VAL:HG22	51:G:139:VAL:HG22	1.90	0.52
57:M:55:VAL:HG12	57:M:68:LEU:HA	1.89	0.52
1:AS:25:A:H2'	1:AS:26:C:H6	1.74	0.52
1:AS:290:G:H1'	16:BI:93:LYS:HD2	1.91	0.52
1:AS:1301:U:C2	5:AX:257:PRO:HG3	2.44	0.52
1:AS:1561:U:H6	1:AS:1561:U:H5''	1.75	0.52
1:AS:2876:U:H2'	1:AS:2877:U:H6	1.74	0.52
1:AS:2919:G:OP1	1:AS:2954:A:N6	2.33	0.52
3:AU:8:C:H2'	3:AU:9:A:C8	2.43	0.52
6:AY:36:VAL:HG21	6:AY:245:LEU:HD21	1.90	0.52
23:BP:19:VAL:C	23:BP:21:ALA:H	2.16	0.52
46:CM:17:C:H2'	46:CM:18:C:H6	1.74	0.52
46:CM:226:G:C6	46:CM:819:G:C4	2.97	0.52
46:CM:1258:G:N7	46:CM:1416:U:H3'	2.24	0.52
46:CM:1306:A:H4'	46:CM:1307:A:O5'	2.09	0.52
51:CR:21:ASP:OD2	51:CR:24:SER:OG	2.26	0.52
60:DA:4:MET:HE1	60:DA:121:ARG:HG3	1.89	0.52
65:DF:91:ASP:OD1	65:DF:92:GLN:N	2.42	0.52
72:DM:65:LEU:HD13	72:DM:69:LEU:HD12	1.90	0.52
73:DN:51:ARG:NH2	75:DP:60:GLU:HG3	2.24	0.52
1:1:634:C:O2	1:1:2355:G:O2'	2.20	0.52
1:1:1278:G:OP1	80:P0:55:LYS:HB2	2.09	0.52
1:1:2090:U:H4'	1:1:2091:A:O5'	2.09	0.52
1:1:2709:C:O2'	30:AC:36:ASP:OD1	2.27	0.52
46:B:1205:C:H2'	46:B:1206:A:C8	2.45	0.52
64:T:77:GLU:O	64:T:81:LYS:HB2	2.09	0.52
70:Z:69:ARG:HG3	70:Z:117:ILE:HG12	1.90	0.52
1:AS:281:G:N7	16:BI:182:LYS:NZ	2.48	0.52
1:AS:631:U:H2'	1:AS:632:C:C6	2.44	0.52
1:AS:907:C:H42	4:AW:3:ARG:HD3	1.73	0.52
1:AS:1021:A:C6	1:AS:1022:A:H1'	2.45	0.52
1:AS:1945:A:OP2	20:BM:135:LYS:NZ	2.35	0.52
46:CM:904:A:H2'	46:CM:905:C:C6	2.44	0.52
46:CM:1387:A:OP1	64:DE:56:HIS:NE2	2.27	0.52
61:DB:76:ILE:HD12	61:DB:110:ILE:HG13	1.91	0.52
81:12:155:ILE:HG13	81:12:159:GLU:HB3	1.91	0.52
1:1:754:C:OP1	43:AP:15:LYS:NZ	2.42	0.52
35:AH:58:ARG:CD	35:AH:59:PRO:HD2	2.36	0.52
46:B:1265:C:H2'	46:B:1266:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:T:71:PHE:HZ	64:T:74:GLN:HG3	1.75	0.52
79:AR:69:VAL:HA	79:AR:85:SER:HA	1.90	0.52
1:AS:224:C:OP1	27:BT:47:SER:OG	2.27	0.52
1:AS:297:G:OP2	1:AS:297:G:N2	2.32	0.52
1:AS:421:G:O6	1:AS:2361:C:O2'	2.20	0.52
8:BA:54:LEU:HD21	8:BA:145:LEU:HD11	1.92	0.52
46:CM:338:U:H2'	46:CM:339:A:H8	1.73	0.52
46:CM:1068:G:HO2'	46:CM:1079:G:HO2'	1.57	0.52
59:CZ:63:CYS:HA	59:CZ:91:VAL:O	2.09	0.52
75:DP:40:ILE:HG23	75:DP:62:GLU:HG3	1.90	0.52
82:l1:3:LYS:HG3	82:l1:217:TYR:CE1	2.45	0.52
82:l1:189:PHE:O	82:l1:193:LEU:HG	2.09	0.52
1:1:582:G:H2'	1:1:583:A:H8	1.74	0.52
1:1:629:A:H2'	1:1:630:G:C8	2.45	0.52
1:1:1593:C:H2'	1:1:1594:G:C8	2.44	0.52
1:1:1656:C:H2'	1:1:1657:G:H8	1.75	0.52
1:1:2196:G:OP1	37:AJ:67:ARG:NH2	2.40	0.52
1:1:2498:A:H2'	1:1:2499:U:C6	2.44	0.52
1:1:2988:A:H2'	1:1:2989:A:H8	1.73	0.52
46:B:1220:C:H3'	46:B:1221:A:H8	1.73	0.52
46:B:1772:U:P	61:Q:128:ARG:HH22	2.32	0.52
53:I:180:THR:HG23	53:I:183:THR:H	1.75	0.52
62:R:14:GLN:OE1	62:R:22:LEU:N	2.42	0.52
1:AS:1593:C:H2'	1:AS:1594:G:C8	2.44	0.52
1:AS:1756:A:C2	1:AS:1759:U:H5	2.26	0.52
1:AS:2097:A:H2	20:BM:82:LYS:HZ1	1.57	0.52
14:BG:63:VAL:HA	14:BG:66:ASN:ND2	2.25	0.52
46:CM:384:G:OP2	55:CV:25:ARG:NH2	2.43	0.52
46:CM:1470:G:H5'	63:DD:14:THR:HG21	1.90	0.52
46:CM:1776:G:OP2	61:DB:127:ARG:NH2	2.34	0.52
64:DE:89:SER:C	64:DE:91:LEU:H	2.17	0.52
79:DT:70:GLN:OE1	79:DT:86:TRP:NE1	2.41	0.52
82:L1:67:ILE:HB	82:L1:84:ALA:HA	1.91	0.52
1:1:299:G:C8	37:AJ:30:GLY:HA3	2.44	0.52
1:1:437:G:O2'	1:1:438:A:OP1	2.28	0.52
1:1:623:A:H2'	1:1:624:U:C6	2.45	0.52
1:1:3166:A:H2'	1:1:3167:G:H8	1.74	0.52
24:6:10:LYS:NZ	24:6:54:ALA:O	2.42	0.52
46:B:638:U:H2'	46:B:639:G:O4'	2.08	0.52
46:B:874:U:H2'	46:B:875:C:C6	2.45	0.52
46:B:1672:G:H2'	46:B:1673:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:X:79:LEU:HD13	68:X:82:VAL:HG11	1.90	0.52
1:AS:2668:A:H2'	1:AS:2669:A:C8	2.44	0.52
1:AS:3079:U:H2'	1:AS:3080:G:C8	2.45	0.52
6:AY:40:PHE:CD2	6:AY:243:ALA:HB2	2.44	0.52
11:BD:23:ARG:NH2	11:BD:39:LYS:O	2.42	0.52
36:CC:105:ARG:HG3	36:CC:108:ARG:HH21	1.74	0.52
46:CM:4:C:H5	46:CM:20:G:H1	1.57	0.52
46:CM:504:A:H5''	46:CM:505:U:OP1	2.09	0.52
50:CQ:28:ARG:HD2	57:CX:60:SER:HB2	1.92	0.52
51:CR:104:ASP:HB3	51:CR:110:ALA:HB2	1.91	0.52
82:l1:87:VAL:HG23	82:l1:88:ASP:H	1.73	0.52
82:l1:174:MET:HB3	82:l1:178:VAL:HB	1.92	0.52
1:1:964:G:H2'	1:1:965:C:C6	2.45	0.52
1:1:964:G:H2'	1:1:965:C:H6	1.75	0.52
1:1:1249:U:H3'	1:1:1250:C:H5'	1.92	0.52
8:n:170:ARG:HB3	8:n:172:HIS:CE1	2.45	0.52
25:7:85:ALA:HB1	25:7:89:LEU:HD22	1.92	0.52
46:B:184:C:OP1	55:K:152:ARG:NH2	2.36	0.52
46:B:788:A:C8	69:Y:107:SER:HA	2.44	0.52
46:B:1323:C:H1'	46:B:1396:A:C5	2.44	0.52
46:B:1343:G:H4'	66:V:130:ARG:HA	1.90	0.52
71:a:42:GLU:HG3	71:a:52:LYS:HE3	1.90	0.52
1:AS:401:U:H1'	1:AS:403:C:C4	2.44	0.52
1:AS:1576:A:H5''	1:AS:1577:C:H5	1.75	0.52
1:AS:2405:U:H2'	1:AS:2406:U:C6	2.45	0.52
1:AS:3208:A:OP1	17:BJ:160:LYS:NZ	2.28	0.52
45:CL:62:ALA:C	45:CL:64:LEU:H	2.16	0.52
46:CM:457:G:OP1	71:DL:109:LYS:NZ	2.31	0.52
46:CM:672:U:H1'	46:CM:673:A:C5	2.44	0.52
46:CM:938:G:H2'	46:CM:939:G:C8	2.45	0.52
46:CM:1220:C:H5	78:DS:180:ARG:HE	1.57	0.52
46:CM:1237:C:OP1	78:DS:160:ARG:NH1	2.41	0.52
46:CM:1595:U:O3'	63:DD:72:GLY:HA3	2.09	0.52
47:CN:13:ASP:CG	47:CN:179:ARG:HH22	2.17	0.52
48:CO:23:PRO:HB3	48:CO:26:ARG:HH21	1.73	0.52
79:DT:121:ARG:O	79:DT:121:ARG:HG2	2.08	0.52
82:L1:48:ARG:NH1	82:L1:161:LYS:H	2.08	0.52
5:k:19:ARG:NH2	5:k:270:ASN:OD1	2.42	0.52
7:m:95:TRP:HD1	7:m:158:ARG:HA	1.73	0.52
46:B:1582:U:H5'	46:B:1583:C:OP2	2.09	0.52
46:B:1678:G:O6	46:B:1698:U:C4	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:AR:155:VAL:O	79:AR:156:ARG:NH1	2.38	0.52
1:AS:148:U:H4'	16:BI:56:LYS:HG2	1.91	0.52
1:AS:1391:G:O2'	3:AU:18:U:O2	2.28	0.52
1:AS:1936:G:H21	1:AS:3327:A:H8	1.58	0.52
35:CB:8:ARG:HD2	35:CB:32:ALA:O	2.10	0.52
46:CM:78:A:H2'	46:CM:79:C:H6	1.73	0.52
46:CM:157:U:O2'	53:CT:87:ARG:NE	2.42	0.52
46:CM:234:G:H2'	46:CM:235:C:C6	2.45	0.52
46:CM:398:A:H5''	55:CV:25:ARG:HA	1.91	0.52
46:CM:1341:U:H2'	46:CM:1342:A:C8	2.45	0.52
46:CM:1610:C:H2'	46:CM:1611:C:C6	2.45	0.52
46:CM:1636:C:H2'	46:CM:1637:U:C6	2.45	0.52
46:CM:1677:G:H3'	46:CM:1679:A:N6	2.24	0.52
48:CO:82:ARG:NH1	48:CO:191:GLU:OE2	2.43	0.52
50:CQ:60:LEU:HD11	50:CQ:89:ALA:HB3	1.91	0.52
53:CT:1:MET:HE2	53:CT:106:LEU:HB2	1.90	0.52
76:DQ:17:GLY:HA2	76:DQ:27:HIS:ND1	2.25	0.52
77:DR:13:LYS:O	77:DR:17:GLN:HG2	2.09	0.52
80:p0:45:LEU:HB3	80:p0:49:ALA:O	2.09	0.52
1:1:79:G:H2'	1:1:80:C:H6	1.75	0.52
1:1:1250:C:H2'	1:1:1251:C:C6	2.45	0.52
1:1:1385:G:H5''	33:AF:102:SER:HB3	1.90	0.52
1:1:1715:G:OP1	20:z:110:ARG:NH1	2.36	0.52
1:1:2084:A:H2'	1:1:2085:A:C8	2.45	0.52
46:B:854:A:H61	46:B:943:U:H5	1.55	0.52
46:B:1149:G:H2'	46:B:1150:G:C8	2.45	0.52
62:R:10:ARG:HG2	62:R:13:LYS:HE2	1.90	0.52
62:R:77:LYS:HB3	62:R:102:PHE:CE1	2.45	0.52
65:U:140:THR:HA	65:U:143:ARG:NH2	2.25	0.52
70:Z:62:LYS:H	70:Z:116:ASP:HB2	1.75	0.52
1:AS:1302:G:C6	17:BJ:63:THR:HA	2.45	0.52
1:AS:2155:G:OP2	4:AW:128:ARG:NH1	2.42	0.52
1:AS:2331:G:H5''	18:BK:86:LYS:HB2	1.91	0.52
1:AS:2351:A:N3	1:AS:2796:G:O2'	2.38	0.52
1:AS:2370:C:H1'	5:AX:266:ARG:NH2	2.24	0.52
1:AS:3171:C:H5''	1:AS:3172:U:O5'	2.10	0.52
39:CF:46:ARG:HD2	39:CF:47:GLY:O	2.10	0.52
46:CM:29:U:H2'	46:CM:30:G:C8	2.44	0.52
46:CM:78:A:H2'	46:CM:79:C:C6	2.44	0.52
46:CM:391:C:H2'	46:CM:392:C:C6	2.45	0.52
46:CM:638:U:H2'	46:CM:639:G:O4'	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1262:G:O3'	50:CQ:184:GLY:HA3	2.10	0.52
46:CM:1566:U:H2'	46:CM:1567:C:C6	2.45	0.52
46:CM:1774:C:H2'	46:CM:1775:G:C8	2.45	0.52
57:CX:15:LEU:HD21	57:CX:68:LEU:HD13	1.92	0.52
68:DI:11:LEU:HD23	68:DI:11:LEU:H	1.74	0.52
78:DS:184:GLY:O	78:DS:186:CYS:N	2.43	0.52
1:1:559:C:H2'	1:1:560:C:H6	1.74	0.52
1:1:592:U:O2'	6:l:309:LYS:NZ	2.36	0.52
1:1:797:A:OP1	29:AB:27:LYS:HE3	2.10	0.52
1:1:1301:U:C2	5:k:257:PRO:HG3	2.44	0.52
1:1:2420:G:H2'	1:1:2421:A:C8	2.45	0.52
1:1:2832:U:O2	1:1:2910:G:H4'	2.10	0.52
1:1:3159:A:H2'	1:1:3160:C:C6	2.44	0.52
1:1:3285:A:H2'	1:1:3286:C:C6	2.44	0.52
12:r:179:ASP:OD1	12:r:180:GLU:N	2.43	0.52
14:t:8:PRO:HD3	19:y:164:ARG:HB3	1.92	0.52
33:AF:77:VAL:HG13	33:AF:82:ASP:HB2	1.92	0.52
33:AF:84:ASP:OD1	33:AF:112:LYS:NZ	2.42	0.52
50:F:77:ARG:HB2	57:M:22:VAL:HG11	1.92	0.52
53:I:84:TYR:HE1	53:I:93:LYS:HE3	1.75	0.52
54:J:156:THR:HA	54:J:159:ASP:OD2	2.10	0.52
1:AS:278:U:H3	1:AS:287:G:H1	1.58	0.52
1:AS:612:U:H2'	1:AS:613:U:C6	2.45	0.52
1:AS:671:U:H2'	1:AS:672:G:C8	2.46	0.52
46:CM:220:A:C8	46:CM:221:U:H5	2.28	0.52
46:CM:1659:G:H2'	46:CM:1660:G:H8	1.74	0.52
79:DT:67:HIS:CG	79:DT:68:ILE:H	2.28	0.52
80:p0:19:LEU:HB3	80:p0:66:PHE:CE2	2.45	0.52
1:1:236:A:OP1	3:4:95:G:N2	2.37	0.51
1:1:277:G:H2'	1:1:278:U:C6	2.44	0.51
1:1:2469:A:H2'	82:l:207:LYS:HE2	1.91	0.51
1:1:3317:U:O2	55:K:170:ARG:NH1	2.43	0.51
9:o:39:ARG:HA	9:o:42:ILE:HG12	1.91	0.51
46:B:654:G:H3'	46:B:655:U:C6	2.45	0.51
49:E:108:LEU:HD11	49:E:206:LEU:HB3	1.92	0.51
51:G:67:GLN:NE2	71:a:17:LEU:O	2.42	0.51
79:AR:218:ILE:HG23	79:AR:230:THR:HG22	1.92	0.51
1:AS:72:A:C4	37:CD:14:ARG:HD2	2.45	0.51
1:AS:169:G:H5''	36:CC:109:ILE:HD13	1.92	0.51
1:AS:481:G:P	1:AS:481:G:O4'	2.68	0.51
1:AS:1007:A:H2'	1:AS:1008:A:H8	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:3013:U:H2'	1:AS:3014:U:C6	2.45	0.51
46:CM:103:A:O3'	46:CM:306:C:N4	2.43	0.51
46:CM:116:U:H2'	46:CM:117:U:C6	2.45	0.51
46:CM:723:G:H2'	46:CM:724:G:C4'	2.39	0.51
57:CX:8:ARG:O	57:CX:12:HIS:ND1	2.43	0.51
1:1:359:U:OP1	38:AK:11:ARG:NH1	2.43	0.51
1:1:619:A:H2'	1:1:620:A:C8	2.45	0.51
1:1:1344:U:OP1	19:y:39:ARG:NH2	2.43	0.51
1:1:1469:G:H5''	20:z:23:TRP:CD1	2.46	0.51
1:1:3256:G:H2'	1:1:3257:A:C8	2.45	0.51
6:l:4:ARG:HH12	6:l:25:ALA:HA	1.75	0.51
46:B:64:U:O2'	46:B:166:A:N3	2.30	0.51
46:B:233:G:H2'	46:B:234:G:C8	2.45	0.51
46:B:736:G:H2'	46:B:737:A:H8	1.75	0.51
46:B:822:G:H3'	46:B:823:G:C5'	2.40	0.51
46:B:1029:U:H2'	46:B:1030:C:C6	2.45	0.51
46:B:1216:U:H3	46:B:1239:U:H3	1.58	0.51
46:B:1423:U:O2'	50:F:182:VAL:HG23	2.11	0.51
1:AS:1218:G:OP1	80:p0:58:MET:HA	2.11	0.51
1:AS:1434:U:H4'	6:AY:89:ALA:CB	2.40	0.51
1:AS:2174:C:H2'	1:AS:2220:A:H61	1.75	0.51
1:AS:2342:G:H22	1:AS:2374:G:H1'	1.74	0.51
1:AS:3093:U:H1'	1:AS:3094:A:H5''	1.92	0.51
14:BG:141:VAL:HG21	36:CC:118:ILE:HB	1.93	0.51
26:BS:96:LYS:HG3	26:BS:107:ALA:HB3	1.92	0.51
46:CM:122:U:C2'	46:CM:123:G:H5''	2.39	0.51
46:CM:1582:U:H5'	46:CM:1583:C:OP2	2.09	0.51
47:CN:11:PRO:O	47:CN:15:LYS:HG3	2.10	0.51
82:l:49:PHE:CZ	82:l:159:LEU:HB2	2.45	0.51
82:l:112:ALA:O	82:l:116:LEU:HB2	2.10	0.51
1:1:1229:G:N2	81:12:131:GLU:OE2	2.30	0.51
1:1:2649:G:H2'	1:1:2649:G:N3	2.25	0.51
2:3:19:C:H2'	2:3:20:A:C8	2.45	0.51
46:B:415:A:H4'	46:B:416:G:O5'	2.10	0.51
46:B:679:C:O2'	46:B:680:C:H4'	2.09	0.51
46:B:1064:U:H2'	46:B:1065:U:C6	2.44	0.51
46:B:1219:A:OP2	46:B:1230:G:O2'	2.21	0.51
47:C:49:ASN:ND2	47:C:52:LYS:HG3	2.25	0.51
61:Q:20:ASP:OD1	61:Q:21:THR:N	2.42	0.51
76:f:12:ARG:HB2	76:f:12:ARG:HH11	1.74	0.51
79:AR:40:LYS:HD2	79:AR:65:HIS:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:164:U:H2'	1:AS:165:C:C6	2.44	0.51
1:AS:547:U:H2'	1:AS:548:G:H8	1.75	0.51
1:AS:964:G:H2'	1:AS:965:C:H6	1.75	0.51
4:AW:112:ILE:HG13	44:CK:79:VAL:HG22	1.92	0.51
11:BD:57:VAL:HG23	11:BD:68:LEU:HD13	1.91	0.51
46:CM:1354:U:H2'	46:CM:1355:A:H8	1.76	0.51
46:CM:1648:U:H2'	46:CM:1649:G:C8	2.45	0.51
57:CX:15:LEU:HD23	57:CX:76:LEU:HD11	1.92	0.51
1:1:779:A:H5''	1:1:780:A:H5''	1.91	0.51
1:1:1058:A:O2'	22:2:108:ARG:NH2	2.44	0.51
1:1:1611:U:H2'	1:1:1612:U:H6	1.76	0.51
1:1:3344:U:H4'	5:k:315:GLY:HA2	1.91	0.51
3:4:8:C:H2'	3:4:9:A:C8	2.45	0.51
12:r:50:ILE:HD13	12:r:149:ILE:HG13	1.92	0.51
46:B:1516:C:H2'	46:B:1517:C:C6	2.45	0.51
46:B:1701:A:H2'	46:B:1702:A:C1'	2.40	0.51
48:D:58:ALA:O	48:D:62:LYS:HG3	2.10	0.51
49:E:217:TYR:OH	68:X:11:LEU:O	2.27	0.51
49:E:226:ALA:O	68:X:16:LYS:NZ	2.38	0.51
59:O:36:LEU:HA	59:O:41:LEU:HD22	1.93	0.51
1:AS:2183:U:O4	1:AS:2216:G:N1	2.43	0.51
1:AS:2233:A:O2'	46:CM:1744:G:O2'	2.07	0.51
1:AS:2941:A:N7	4:AW:215:ASN:ND2	2.59	0.51
1:AS:3290:G:O3'	32:BY:102:GLY:HA2	2.10	0.51
3:AU:94:C:OP1	38:CE:75:LYS:NZ	2.36	0.51
13:BF:82:ARG:HH22	13:BF:114:ILE:HD11	1.75	0.51
17:BJ:76:ALA:HB3	17:BJ:79:ARG:HG2	1.93	0.51
30:BW:16:ALA:HB1	30:BW:21:ILE:HD11	1.93	0.51
46:CM:740:A:H2'	46:CM:741:A:H8	1.76	0.51
46:CM:1211:A:O2'	46:CM:1241:A:N1	2.40	0.51
46:CM:1212:A:C2	59:CZ:43:ARG:HB3	2.45	0.51
50:CQ:124:LEU:HD11	50:CQ:153:TYR:HB3	1.91	0.51
50:CQ:133:LYS:HB3	50:CQ:190:MET:HE2	1.92	0.51
1:1:780:A:H2'	1:1:780:A:N3	2.26	0.51
1:1:788:G:H2'	1:1:789:C:H6	1.76	0.51
1:1:1580:U:H2'	1:1:1581:C:C6	2.46	0.51
1:1:2221:A:H3'	4:j:244:GLY:HA2	1.92	0.51
19:y:165:ILE:HD11	19:y:172:PHE:HB3	1.91	0.51
21:O:42:TRP:O	21:O:46:GLN:HG3	2.10	0.51
46:B:1716:C:H2'	46:B:1717:A:O4'	2.10	0.51
1:AS:779:A:H5''	1:AS:780:A:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1172:C:H4'	17:BJ:90:PRO:HD3	1.92	0.51
1:AS:2138:G:H2'	1:AS:2139:G:C8	2.44	0.51
1:AS:2525:A:H2'	1:AS:2526:C:O4'	2.10	0.51
1:AS:3153:A:H2	1:AS:3158:G:H4'	1.74	0.51
8:BA:65:SER:HB3	8:BA:75:LEU:HD23	1.92	0.51
12:BE:194:GLY:C	12:BE:196:TYR:H	2.18	0.51
19:BL:96:PHE:CD1	19:BL:97:PRO:HD2	2.45	0.51
28:BU:34:LYS:C	28:BU:36:HIS:H	2.18	0.51
46:CM:217:A:N6	46:CM:828:U:O2'	2.43	0.51
46:CM:671:G:H5'	46:CM:672:U:OP2	2.10	0.51
46:CM:701:G:N2	46:CM:721:C:C2	2.79	0.51
46:CM:1741:A:H2'	46:CM:1742:A:C8	2.46	0.51
55:CV:38:ILE:HG12	55:CV:96:LEU:HD11	1.93	0.51
82:L1:124:LEU:HD22	82:L1:128:LEU:HD13	1.92	0.51
1:1:2174:C:H2'	1:1:2220:A:H61	1.74	0.51
1:1:2407:G:H2'	1:1:2408:A:C8	2.45	0.51
13:s:109:HIS:ND1	13:s:114:ILE:HD11	2.25	0.51
14:t:63:VAL:HA	14:t:66:ASN:ND2	2.25	0.51
28:AA:103:GLU:HB2	28:AA:106:GLN:HB2	1.92	0.51
46:B:1086:G:H4'	69:Y:76:GLN:HG3	1.92	0.51
46:B:1317:C:O2'	50:F:163:GLN:HB3	2.10	0.51
46:B:1341:U:H2'	46:B:1342:A:C8	2.45	0.51
46:B:1445:C:C4	65:U:139:LYS:HB3	2.45	0.51
46:B:1609:G:H2'	46:B:1610:C:C6	2.46	0.51
47:C:167:LYS:NZ	47:C:204:TYR:O	2.44	0.51
50:F:68:HIS:CE1	57:M:94:ASN:HB3	2.46	0.51
52:H:57:SER:HB2	75:e:53:ILE:O	2.11	0.51
73:c:32:LYS:O	73:c:37:LYS:NZ	2.41	0.51
78:h:167:THR:HG23	78:h:168:CYS:SG	2.51	0.51
1:AS:623:A:H2'	1:AS:624:U:C6	2.45	0.51
6:AY:140:GLY:O	6:AY:142:ARG:NH1	2.44	0.51
9:BB:108:GLN:HG2	9:BB:109:ILE:N	2.26	0.51
19:BL:133:LYS:HB2	19:BL:135:GLN:NE2	2.26	0.51
45:CL:129:LEU:HA	45:CL:132:GLU:OE1	2.11	0.51
46:CM:110:U:OP1	46:CM:738:A:O2'	2.27	0.51
46:CM:1127:A:H2'	46:CM:1128:A:C8	2.46	0.51
46:CM:1227:A:O2'	46:CM:1229:A:OP1	2.24	0.51
46:CM:1479:A:H4'	46:CM:1480:G:O5'	2.10	0.51
48:CO:111:ARG:HB3	73:DN:68:TYR:HB2	1.92	0.51
49:CP:171:LYS:HE3	49:CP:192:TYR:OH	2.11	0.51
1:1:164:U:H2'	1:1:165:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:430:G:H2'	1:1:431:A:H8	1.76	0.51
1:1:792:U:H2'	1:1:793:U:C6	2.45	0.51
1:1:1099:A:N6	1:1:1359:A:H1'	2.26	0.51
1:1:1863:A:H2'	1:1:1864:G:H8	1.76	0.51
1:1:2433:U:C2	1:1:2434:A:C8	2.99	0.51
13:s:32:ARG:NH1	13:s:123:TYR:OH	2.44	0.51
46:B:1512:A:N3	46:B:1576:C:O2'	2.36	0.51
46:B:1644:U:O5'	46:B:1645:G:H5''	2.11	0.51
57:M:70:ASP:O	57:M:73:VAL:HG22	2.10	0.51
1:AS:258:U:H2'	1:AS:259:C:C6	2.45	0.51
1:AS:289:A:H2'	1:AS:290:G:C8	2.43	0.51
1:AS:477:U:H2'	1:AS:478:G:C8	2.45	0.51
5:AX:58:ARG:HD2	5:AX:354:VAL:HG13	1.92	0.51
14:BG:100:ARG:O	14:BG:102:GLN:NE2	2.43	0.51
46:CM:137:A:O4'	46:CM:139:U:H5'	2.11	0.51
46:CM:335:G:H3'	58:CY:133:LYS:HB2	1.91	0.51
46:CM:473:A:OP1	56:CW:126:ARG:HD3	2.10	0.51
46:CM:938:G:H2'	46:CM:939:G:H8	1.76	0.51
82:l1:70:ASP:OD1	82:l1:87:VAL:N	2.44	0.51
1:1:591:C:O2	9:o:24:ARG:NH1	2.44	0.51
1:1:679:U:O2'	1:1:695:G:O6	2.20	0.51
1:1:1837:A:H1'	40:AM:45:ARG:HH22	1.75	0.51
1:1:2902:A:H2'	1:1:2903:C:C6	2.45	0.51
1:1:2919:G:OP1	1:1:2954:A:N6	2.38	0.51
7:m:60:ILE:HB	7:m:80:ALA:HB2	1.93	0.51
46:B:151:G:H2'	46:B:152:G:C8	2.46	0.51
46:B:338:U:H2'	46:B:339:A:C8	2.46	0.51
1:AS:36:U:OP1	1:AS:930:G:N2	2.41	0.51
1:AS:428:U:H2'	1:AS:429:U:C6	2.45	0.51
1:AS:538:G:O6	1:AS:547:U:O4	2.28	0.51
1:AS:1225:G:H2'	1:AS:1226:G:C8	2.46	0.51
1:AS:1863:A:H2'	1:AS:1864:G:C8	2.46	0.51
2:AT:13:A:H2	7:AZ:21:ARG:HB2	1.76	0.51
19:BL:157:PRO:HB3	19:BL:186:VAL:HB	1.93	0.51
21:BN:109:ASP:OD1	21:BN:113:ARG:NH1	2.39	0.51
46:CM:638:U:O2	54:CU:175:LYS:HE3	2.11	0.51
46:CM:849:U:OP1	69:DJ:28:ARG:NH1	2.44	0.51
46:CM:1231:C:O3'	78:DS:134:LYS:NZ	2.44	0.51
46:CM:1279:G:O2'	46:CM:1306:A:N1	2.37	0.51
51:CR:100:ARG:NH1	51:CR:118:GLU:OE2	2.43	0.51
51:CR:100:ARG:NH2	51:CR:121:TYR:O	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:CS:25:LEU:HD12	63:DD:26:GLY:HA3	1.92	0.51
60:DA:33:VAL:HG21	60:DA:66:VAL:HG11	1.92	0.51
1:1:1230:G:H2'	1:1:1231:U:C5	2.46	0.51
1:1:2201:A:H2'	1:1:2202:A:C8	2.45	0.51
3:4:75:G:H2'	3:4:76:C:C6	2.44	0.51
14:t:143:VAL:HG13	14:t:147:PHE:HD2	1.75	0.51
28:AA:119:GLU:O	28:AA:123:GLN:HG2	2.11	0.51
46:B:265:U:H2'	46:B:266:C:H6	1.75	0.51
46:B:717:G:H4'	46:B:719:A:N1	2.25	0.51
46:B:859:C:OP1	48:D:159:SER:OG	2.25	0.51
46:B:1668:A:H8	53:I:65:GLN:HG3	1.75	0.51
79:AR:76:ALA:HB3	79:AR:120:LEU:HD11	1.92	0.51
79:AR:214:ASP:OD1	79:AR:214:ASP:N	2.43	0.51
1:AS:437:G:O2'	1:AS:438:A:H5''	2.11	0.51
1:AS:1035:U:H2'	1:AS:1036:A:C8	2.46	0.51
1:AS:1180:A:H2'	1:AS:1181:C:C6	2.45	0.51
1:AS:2498:A:H2'	1:AS:2499:U:C6	2.45	0.51
1:AS:3066:A:H2'	1:AS:3067:U:C6	2.45	0.51
3:AU:47:C:H1'	3:AU:61:A:H2'	1.92	0.51
12:BE:77:THR:HG22	12:BE:82:ARG:HA	1.93	0.51
15:BH:57:LEU:HG	21:BN:172:TYR:OH	2.11	0.51
21:BN:8:GLN:HG3	21:BN:26:ARG:HD2	1.93	0.51
23:BP:18:ASP:HA	23:BP:63:LYS:HG2	1.93	0.51
42:CI:1:MET:HB3	46:CM:1629:G:H5'	1.93	0.51
46:CM:476:A:O2'	56:CW:124:HIS:ND1	2.42	0.51
46:CM:479:A:H2'	46:CM:480:U:H6	1.76	0.51
47:CN:198:MET:HB3	64:DE:85:VAL:HG21	1.93	0.51
62:DC:44:ARG:NH2	62:DC:82:ASN:OD1	2.44	0.51
79:DT:214:ASP:N	79:DT:214:ASP:OD1	2.43	0.51
1:1:3233:A:OP1	8:n:45:ARG:NH2	2.44	0.51
46:B:302:U:H2'	46:B:303:C:C6	2.45	0.51
46:B:526:U:H2'	46:B:527:A:O4'	2.11	0.51
46:B:1636:C:H2'	46:B:1637:U:C6	2.46	0.51
46:B:1749:A:H1'	46:B:1770:C:H5'	1.93	0.51
66:V:38:LYS:NZ	66:V:41:ALA:HA	2.26	0.51
1:AS:814:C:H2'	1:AS:815:U:O4'	2.11	0.51
1:AS:1539:G:OP1	16:BI:35:VAL:N	2.43	0.51
1:AS:1651:G:OP1	35:CB:40:SER:OG	2.27	0.51
1:AS:2236:U:C2	1:AS:2237:A:C8	3.00	0.51
1:AS:2603:U:OP2	22:BO:4:SER:OG	2.28	0.51
44:CK:46:THR:OG1	44:CK:57:CYS:SG	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1029:U:H2'	46:CM:1030:C:C6	2.46	0.51
46:CM:1413:A:O2'	46:CM:1414:G:OP1	2.22	0.51
46:CM:1455:A:H2'	46:CM:1456:C:C6	2.46	0.51
52:CS:109:LYS:HG2	52:CS:112:ARG:NH2	2.26	0.51
53:CT:104:GLN:OE1	53:CT:104:GLN:N	2.44	0.51
79:DT:239:ALA:HB3	79:DT:289:LEU:HD12	1.92	0.51
82:L1:30:GLU:H	82:L1:172:VAL:HB	1.75	0.51
1:1:249:G:H2'	1:1:251:G:OP2	2.11	0.50
1:1:449:U:H2'	1:1:450:G:C8	2.46	0.50
1:1:1248:A:C2'	1:1:1249:U:H5'	2.40	0.50
1:1:1249:U:OP2	1:1:1249:U:H2'	2.11	0.50
1:1:2084:A:H2'	1:1:2085:A:H8	1.76	0.50
1:1:2197:A:H2'	1:1:2198:A:C8	2.46	0.50
1:1:2335:A:H2'	1:1:2336:A:C8	2.46	0.50
1:1:3244:A:O2'	1:1:3245:A:H5'	2.11	0.50
13:s:141:ARG:O	13:s:145:ARG:HG2	2.11	0.50
39:AL:24:ILE:HD13	39:AL:76:THR:HB	1.92	0.50
46:B:1470:G:H5'	63:S:14:THR:HG21	1.92	0.50
49:E:138:TYR:OH	49:E:144:GLY:O	2.28	0.50
50:F:143:LEU:O	50:F:145:ALA:N	2.37	0.50
51:G:197:HIS:CE1	51:G:199:GLU:HB2	2.46	0.50
53:I:48:TYR:CD2	53:I:117:GLY:HA3	2.47	0.50
54:J:8:GLU:H	54:J:8:GLU:CD	2.19	0.50
70:Z:73:ARG:NH1	70:Z:84:THR:OG1	2.37	0.50
1:AS:179:C:H2'	1:AS:180:U:H6	1.76	0.50
1:AS:843:A:H2'	1:AS:844:A:C8	2.46	0.50
1:AS:1275:C:H2'	1:AS:1276:C:H6	1.75	0.50
1:AS:1561:U:H5''	1:AS:1561:U:C6	2.46	0.50
10:BC:158:VAL:HG21	10:BC:164:VAL:CG2	2.41	0.50
25:BR:82:ILE:HG21	53:CT:158:VAL:HG11	1.93	0.50
46:CM:583:A:H2'	46:CM:584:G:C8	2.46	0.50
46:CM:971:G:H2'	46:CM:972:G:O4'	2.10	0.50
46:CM:1133:C:O2'	46:CM:1752:A:N1	2.43	0.50
46:CM:1193:A:H4'	46:CM:1255:G:P	2.51	0.50
46:CM:1298:A:N3	46:CM:1300:U:H5'	2.26	0.50
56:CW:38:ASN:HD21	56:CW:40:ARG:NH1	2.09	0.50
64:DE:69:ILE:O	64:DE:69:ILE:HG13	2.10	0.50
66:DG:108:LEU:HA	66:DG:111:ILE:HG22	1.92	0.50
81:12:133:LEU:HB3	81:12:152:ILE:HG12	1.93	0.50
82:l1:37:GLY:HA3	82:l1:203:SER:HB3	1.93	0.50
1:1:72:A:N7	14:t:66:ASN:HB3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3138:U:H2'	1:1:3139:U:C6	2.46	0.50
5:k:123:TYR:CZ	5:k:124:LYS:HG3	2.45	0.50
5:k:369:ARG:HD2	25:7:11:SER:HB3	1.94	0.50
16:v:62:TYR:HD2	16:v:106:VAL:HG13	1.76	0.50
23:5:19:VAL:C	23:5:21:ALA:H	2.20	0.50
45:i:107:TRP:HA	50:F:116:ILE:HD11	1.92	0.50
46:B:634:A:H5''	69:Y:31:SER:HB3	1.92	0.50
46:B:1149:G:H2'	46:B:1150:G:H8	1.75	0.50
57:M:54:TYR:HD1	57:M:72:GLY:HA2	1.75	0.50
69:Y:111:MET:SD	69:Y:115:GLU:HG2	2.52	0.50
79:AR:126:ALA:HB1	79:AR:152:VAL:HG23	1.93	0.50
1:AS:277:G:H2'	1:AS:278:U:C6	2.45	0.50
1:AS:417:A:H2'	1:AS:418:A:C8	2.46	0.50
1:AS:1556:G:O2'	1:AS:1557:U:H5'	2.11	0.50
1:AS:2063:C:H3'	1:AS:2064:A:C8	2.46	0.50
1:AS:2992:U:H2'	1:AS:3005:A:N6	2.27	0.50
7:AZ:150:LEU:HD12	13:BF:143:ARG:HG3	1.93	0.50
20:BM:162:ARG:HD3	20:BM:165:ARG:HD3	1.92	0.50
46:CM:873:U:H2'	46:CM:874:U:C6	2.46	0.50
46:CM:932:U:H2'	46:CM:933:A:H8	1.76	0.50
46:CM:1016:U:H4'	46:CM:1017:G:OP2	2.11	0.50
46:CM:1254:U:H5'	46:CM:1418:U:OP2	2.10	0.50
46:CM:1326:A:H1'	79:DT:66:SER:OG	2.11	0.50
46:CM:1604:U:H2'	46:CM:1605:C:C6	2.46	0.50
47:CN:52:LYS:HD3	68:DI:82:VAL:HG23	1.93	0.50
81:12:154:ALA:HB1	81:12:159:GLU:HB2	1.93	0.50
1:1:394:G:N1	1:1:397:A:OP2	2.44	0.50
1:1:531:G:O2'	1:1:552:G:N1	2.43	0.50
1:1:1374:U:H2'	1:1:1375:G:H8	1.75	0.50
1:1:3261:A:H2'	1:1:3262:U:H6	1.77	0.50
3:4:142:C:H2'	3:4:143:U:C6	2.45	0.50
31:AD:55:LYS:O	31:AD:59:GLU:HG2	2.12	0.50
43:AP:38:GLN:OE1	43:AP:41:ARG:NH2	2.44	0.50
46:B:139:U:P	53:I:149:LYS:HZ1	2.33	0.50
46:B:180:A:H2'	46:B:181:U:C6	2.46	0.50
46:B:1648:U:H2'	46:B:1649:G:C8	2.46	0.50
59:O:29:LYS:HE2	59:O:100:TRP:CE3	2.45	0.50
59:O:135:ILE:O	59:O:136:LEU:HD12	2.12	0.50
70:Z:59:ILE:HD11	70:Z:84:THR:HG21	1.93	0.50
1:AS:1743:G:H21	39:CF:2:ALA:HB3	1.75	0.50
1:AS:2186:A:O2'	1:AS:2187:U:H5'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AZ:75:PHE:O	7:AZ:112:LYS:NZ	2.42	0.50
28:BU:41:ALA:HB2	28:BU:77:TYR:HE1	1.76	0.50
46:CM:585:C:H5'	77:DR:24:GLN:NE2	2.26	0.50
46:CM:695:C:O2'	46:CM:696:U:OP1	2.21	0.50
46:CM:1187:A:H1'	46:CM:1192:C:N4	2.26	0.50
46:CM:1301:G:OP1	64:DE:7:LYS:N	2.30	0.50
52:CS:225:ARG:HD2	75:DP:58:GLU:CD	2.36	0.50
59:CZ:97:LEU:HD13	59:CZ:119:SER:HA	1.93	0.50
73:DN:35:ALA:O	73:DN:37:LYS:HD3	2.12	0.50
79:DT:200:THR:HG21	79:DT:242:PHE:H	1.77	0.50
80:P0:19:LEU:HD21	80:P0:73:PHE:HZ	1.77	0.50
1:1:294:U:P	16:v:15:GLN:HE22	2.31	0.50
1:1:1660:G:H2'	1:1:1661:U:C6	2.46	0.50
1:1:3260:A:H2'	1:1:3261:A:H8	1.75	0.50
4:j:112:ILE:HG13	44:AQ:79:VAL:HG22	1.93	0.50
45:i:96:LYS:HA	46:B:575:G:C6	2.47	0.50
46:B:1039:U:H2'	46:B:1040:U:C6	2.47	0.50
46:B:1127:A:H2'	46:B:1128:A:C8	2.47	0.50
52:H:91:GLU:HA	52:H:94:THR:HG22	1.93	0.50
79:AR:200:THR:OG1	79:AR:240:LEU:O	2.29	0.50
1:AS:1616:U:H2'	1:AS:1617:A:C8	2.47	0.50
1:AS:1863:A:H2'	1:AS:1864:G:H8	1.75	0.50
9:BB:149:ARG:HD2	9:BB:205:LEU:HD23	1.91	0.50
40:CG:21[B]:ARG:HG3	40:CG:22:PRO:O	2.11	0.50
46:CM:1511:A:N3	46:CM:1577:G:O2'	2.38	0.50
82:L1:17:LEU:O	82:L1:21:THR:HG22	2.11	0.50
82:L1:53:LEU:HD23	82:L1:155:ILE:HD11	1.93	0.50
1:1:179:C:H2'	1:1:180:U:H6	1.75	0.50
1:1:1029:U:H2'	1:1:1030:U:C6	2.46	0.50
1:1:1482:G:N2	35:AH:6:THR:HG22	2.26	0.50
1:1:1642:G:H1'	1:1:1805:A:N6	2.26	0.50
1:1:2959:A:H2'	1:1:2960:C:H6	1.77	0.50
13:s:82:ARG:HA	13:s:85:LYS:HE2	1.94	0.50
18:x:29:THR:HA	18:x:32:THR:HG22	1.93	0.50
46:B:128:U:H1'	46:B:129:A:N7	2.27	0.50
46:B:739:A:H5''	46:B:740:A:C5'	2.42	0.50
46:B:1160:U:H2'	46:B:1161:G:C8	2.45	0.50
46:B:1344:C:O2	66:V:3:GLY:HA3	2.11	0.50
47:C:10:THR:OG1	47:C:12:GLU:OE1	2.29	0.50
53:I:116:GLN:NE2	53:I:125:THR:HB	2.26	0.50
62:R:14:GLN:HE22	62:R:23:LYS:HB2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:W:32:GLN:OE1	67:W:32:GLN:N	2.44	0.50
1:AS:357:A:O4'	6:AY:82:GLY:HA3	2.11	0.50
1:AS:1199:A:N3	1:AS:2827:U:O2'	2.40	0.50
1:AS:2978:A:H2'	1:AS:2979:U:O4'	2.11	0.50
46:CM:1127:A:H5''	73:DN:2:PRO:HB3	1.93	0.50
46:CM:1174:A:N3	46:CM:1179:A:O2'	2.44	0.50
46:CM:1218:G:N2	46:CM:1238:U:H1'	2.27	0.50
59:CZ:137:LEU:HA	59:CZ:140:PHE:CZ	2.46	0.50
62:DC:53:PRO:HB3	62:DC:83:MET:SD	2.51	0.50
82:L1:195:LYS:HD3	82:L1:196:LYS:HD3	1.92	0.50
82:l1:21:THR:HA	82:l1:25:LYS:HE3	1.93	0.50
1:1:412:G:OP1	18:x:62:ARG:NH1	2.37	0.50
1:1:783:G:H2'	1:1:784:C:H6	1.76	0.50
1:1:1277:G:OP1	80:P0:55:LYS:HD2	2.12	0.50
1:1:1473:A:OP1	1:1:3047:G:O2'	2.17	0.50
1:1:1569:C:H2'	1:1:1570:A:C8	2.47	0.50
13:s:47:GLN:OE1	13:s:64:LYS:HD3	2.11	0.50
45:i:52:LYS:C	45:i:54:LYS:H	2.19	0.50
57:M:15:LEU:O	57:M:19:GLY:HA2	2.12	0.50
66:V:35:ASP:OD1	66:V:35:ASP:N	2.43	0.50
1:AS:118:U:O2'	10:BC:134:LYS:NZ	2.44	0.50
1:AS:169:G:C6	1:AS:249:G:H1'	2.46	0.50
1:AS:307:A:H2'	1:AS:308:A:H8	1.75	0.50
1:AS:602:A:H2'	1:AS:603:C:C6	2.47	0.50
1:AS:2943:A:H2'	1:AS:2943:A:N3	2.27	0.50
1:AS:3019:U:O2'	1:AS:3020:A:H5'	2.12	0.50
11:BD:47:LYS:NZ	15:BH:3:SER:HA	2.26	0.50
15:BH:17:ARG:HD2	15:BH:61:VAL:HG22	1.93	0.50
28:BU:34:LYS:O	28:BU:35:SER:OG	2.21	0.50
33:BZ:10:ILE:HG12	33:BZ:64:THR:HB	1.93	0.50
46:CM:107:C:H2'	46:CM:108:A:H8	1.77	0.50
46:CM:470:U:H5''	56:CW:11:THR:HG23	1.94	0.50
46:CM:1335:U:O2'	46:CM:1336:G:OP1	2.29	0.50
59:CZ:135:ILE:HA	59:CZ:138:GLU:OE2	2.12	0.50
65:DF:25:ARG:NH1	65:DF:25:ARG:HB3	2.26	0.50
1:1:739:C:H5''	19:y:69:ARG:NH2	2.25	0.50
1:1:1325:U:O3'	34:AG:19:SER:OG	2.29	0.50
1:1:1684:U:H2'	1:1:1685:U:C6	2.47	0.50
3:4:60:U:OP1	26:8:54:TYR:OH	2.25	0.50
46:B:15:U:H2'	46:B:16:G:O4'	2.11	0.50
46:B:871:U:O2'	61:Q:116:VAL:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1485:G:H4'	66:V:121:GLY:H	1.75	0.50
56:L:38:ASN:HA	77:g:36:MET:HE3	1.94	0.50
62:R:60:LEU:HD22	62:R:92:SER:OG	2.12	0.50
65:U:33:THR:HA	65:U:38:VAL:O	2.12	0.50
1:AS:35:C:H4'	1:AS:804:A:C2	2.46	0.50
1:AS:97:G:OP1	14:BG:16:LYS:NZ	2.41	0.50
1:AS:142:G:H4'	3:AU:145:U:OP1	2.12	0.50
1:AS:487:C:HO2'	1:AS:488:G:P	2.34	0.50
1:AS:997:G:O2'	1:AS:1037:U:OP2	2.27	0.50
1:AS:1079:G:H2'	1:AS:1080:A:H8	1.75	0.50
1:AS:1080:A:H2'	1:AS:1081:A:C8	2.47	0.50
1:AS:2404:U:H2'	1:AS:2405:U:C6	2.46	0.50
1:AS:3259:A:H2'	1:AS:3260:A:O4'	2.12	0.50
1:AS:3344:U:H4'	5:AX:315:GLY:HA2	1.94	0.50
46:CM:317:U:H4'	46:CM:321:A:C8	2.46	0.50
46:CM:643:U:H2'	46:CM:644:U:O4'	2.11	0.50
46:CM:673:A:H2'	46:CM:674:C:C6	2.47	0.50
46:CM:771:G:H4'	51:CR:256:ARG:HH22	1.76	0.50
46:CM:824:U:C5	46:CM:825:U:H5	2.30	0.50
46:CM:886:G:H2'	46:CM:887:G:C8	2.47	0.50
46:CM:1199:U:HO2'	76:DQ:3:HIS:HD1	1.59	0.50
46:CM:1672:G:H2'	46:CM:1673:U:H6	1.77	0.50
49:CP:177:PRO:HD3	56:CW:17:ARG:HH22	1.76	0.50
50:CQ:179:ARG:H	50:CQ:179:ARG:HD2	1.76	0.50
56:CW:53:ARG:O	56:CW:57:ARG:HG3	2.10	0.50
57:CX:54:TYR:CE1	57:CX:75:PHE:HB2	2.47	0.50
65:DF:112:ASP:OD1	65:DF:115:ARG:NH2	2.44	0.50
82:l1:128:LEU:O	82:l1:130:LYS:N	2.45	0.50
1:1:1568:U:C4	1:1:1569:C:H1'	2.46	0.50
1:1:1656:C:H2'	1:1:1657:G:C8	2.46	0.50
1:1:2385:C:H2'	1:1:2386:U:C6	2.47	0.50
1:1:2985:U:H2'	1:1:2986:U:C6	2.46	0.50
1:1:3300:A:H2'	1:1:3301:A:C8	2.47	0.50
2:3:16:U:H2'	2:3:17:A:H8	1.76	0.50
12:r:189:GLU:HG3	12:r:200:LEU:HB3	1.94	0.50
45:i:48:PRO:C	45:i:50:LYS:H	2.18	0.50
46:B:82:U:H2'	46:B:83:G:O4'	2.12	0.50
46:B:133:U:H4'	46:B:134:A:OP2	2.11	0.50
50:F:143:LEU:C	50:F:145:ALA:H	2.17	0.50
62:R:94:VAL:HG21	62:R:116:LEU:HD11	1.92	0.50
79:AR:38:ARG:HG2	79:AR:68:ILE:HG23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:620:A:OP1	34:CA:59:ILE:HD11	2.12	0.50
1:AS:951:U:H2'	1:AS:952:U:C6	2.46	0.50
1:AS:1115:C:H2'	1:AS:1116:A:C8	2.46	0.50
1:AS:1254:U:OP1	80:p0:42:ARG:HB3	2.11	0.50
9:BB:143:ARG:HG3	9:BB:183:ILE:HD13	1.93	0.50
26:BS:133:LEU:O	26:BS:137:ASN:ND2	2.43	0.50
46:CM:151:G:H2'	46:CM:152:G:H8	1.76	0.50
46:CM:1332:U:C4	67:DH:57:MET:HE1	2.47	0.50
51:CR:15:PRO:HG3	51:CR:39:ARG:HD3	1.94	0.50
80:P0:16:ARG:NH2	80:P0:62:ALA:O	2.37	0.50
1:1:169:G:C6	1:1:249:G:H1'	2.47	0.50
1:1:1116:A:H2'	1:1:1117:U:C6	2.47	0.50
1:1:1303:G:C4	17:w:61:LYS:HD3	2.47	0.50
1:1:2992:U:H2'	1:1:3005:A:N6	2.27	0.50
1:1:3132:U:H2'	1:1:3133:G:C8	2.47	0.50
33:AF:112:LYS:HE2	33:AF:116:LEU:HD11	1.94	0.50
46:B:119:A:H1'	46:B:395:A:C5	2.47	0.50
46:B:684:C:H2'	46:B:685:C:C6	2.47	0.50
51:G:141:THR:OG1	51:G:143:ASP:OD1	2.24	0.50
51:G:150:PRO:O	53:I:208:TYR:HE1	1.95	0.50
52:H:80:LYS:HB2	52:H:83:ARG:NH1	2.27	0.50
66:V:37:VAL:HG21	66:V:100:ILE:HD11	1.94	0.50
1:AS:249:G:H2'	1:AS:251:G:OP2	2.11	0.50
1:AS:347:G:O6	38:CE:55:ARG:NH1	2.44	0.50
1:AS:1011:C:H4'	1:AS:1012:U:C6	2.46	0.50
1:AS:1632:C:H5''	28:BU:73:LYS:NZ	2.27	0.50
1:AS:3261:A:H2'	1:AS:3262:U:C6	2.47	0.50
7:AZ:95:TRP:CD1	7:AZ:158:ARG:HA	2.47	0.50
7:AZ:187:ALA:O	7:AZ:189:GLU:N	2.43	0.50
46:CM:291:U:H2'	46:CM:292:C:C6	2.47	0.50
46:CM:908:A:H2'	46:CM:909:A:C8	2.47	0.50
51:CR:139:VAL:HG23	51:CR:150:PRO:HG3	1.93	0.50
54:CU:122:LEU:HD11	54:CU:169:TYR:CD1	2.47	0.50
57:CX:12:HIS:HB3	57:CX:80:LEU:HD21	1.94	0.50
82:L1:73:ASP:CG	82:L1:113:SER:HB2	2.37	0.50
80:p0:45:LEU:HD13	80:p0:99:ILE:HB	1.94	0.50
1:1:109:G:OP2	14:t:73:ARG:NH2	2.43	0.49
1:1:498:C:H2'	1:1:499:G:C8	2.46	0.49
1:1:1153:G:H2'	1:1:1154:A:O4'	2.12	0.49
1:1:1239:G:N2	1:1:1266:A:O2'	2.29	0.49
1:1:1825:A:H5''	1:1:1826:G:H5'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:l:300:VAL:HB	19:y:39:ARG:HG2	1.92	0.49
8:n:55:LYS:NZ	8:n:100:PHE:O	2.41	0.49
46:B:829:A:H2'	46:B:830:G:C8	2.47	0.49
46:B:988:A:H2'	46:B:990:A:N7	2.27	0.49
46:B:1515:U:OP1	52:H:109:LYS:HB2	2.12	0.49
46:B:1529:G:N2	46:B:1555:C:H1'	2.28	0.49
50:F:52:LYS:NZ	50:F:90:GLU:OE1	2.41	0.49
78:h:175:ALA:O	78:h:177:MET:HG3	2.11	0.49
79:AR:263:GLN:O	79:AR:264:GLU:HG2	2.12	0.49
1:AS:117:U:O2	1:AS:120:A:H5''	2.11	0.49
1:AS:1203:G:OP1	41:CH:43:ASN:ND2	2.41	0.49
1:AS:1593:C:H2'	1:AS:1594:G:H8	1.76	0.49
1:AS:1762:G:O2'	1:AS:1763:C:OP1	2.27	0.49
1:AS:2888:U:H5	1:AS:2907:U:HO2'	1.58	0.49
1:AS:3302:G:H2'	1:AS:3303:C:C6	2.47	0.49
17:BJ:28:ILE:O	17:BJ:102:ARG:NH1	2.43	0.49
45:CL:155:LEU:HA	57:CX:92:LEU:HD21	1.94	0.49
46:CM:474:U:O2	77:DR:31:GLN:NE2	2.45	0.49
46:CM:726:C:O2	54:CU:103:ARG:NH2	2.39	0.49
46:CM:1344:C:O2	66:DG:3:GLY:HA3	2.12	0.49
46:CM:1725:U:H2'	46:CM:1726:C:C6	2.47	0.49
51:CR:91:THR:HG23	51:CR:98:HIS:CE1	2.47	0.49
1:1:534:G:H1	1:1:551:U:H3	1.60	0.49
1:1:657:G:H2'	1:1:1428:C:H42	1.76	0.49
1:1:951:U:H2'	1:1:952:U:C6	2.47	0.49
1:1:1863:A:H2'	1:1:1864:G:C8	2.47	0.49
6:l:114:VAL:HB	6:l:119:LYS:HE3	1.94	0.49
8:n:135:VAL:O	8:n:139:LYS:HD3	2.13	0.49
46:B:151:G:H2'	46:B:152:G:H8	1.76	0.49
46:B:180:A:H2'	46:B:181:U:H6	1.77	0.49
46:B:518:A:O2'	46:B:519:A:OP1	2.26	0.49
46:B:1573:A:H2'	46:B:1574:A:O4'	2.12	0.49
46:B:1598:A:OP1	52:H:107:LYS:NZ	2.42	0.49
49:E:165:ILE:HB	49:E:192:TYR:HB2	1.94	0.49
54:J:6:LEU:HG	54:J:38:GLN:HB3	1.94	0.49
63:S:68:VAL:HG11	63:S:80:ILE:HD11	1.94	0.49
76:f:12:ARG:HB2	76:f:12:ARG:NH1	2.27	0.49
7:AZ:235:ASP:OD1	7:AZ:235:ASP:N	2.45	0.49
36:CC:78:LYS:HA	36:CC:81:ARG:HD2	1.93	0.49
46:CM:302:U:H2'	46:CM:303:C:C6	2.48	0.49
46:CM:871:U:C2	46:CM:872:A:C8	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1183:G:OP1	46:CM:1184:G:O2'	2.21	0.49
46:CM:1226:G:C8	62:DC:79:HIS:CE1	2.99	0.49
46:CM:1398:G:H4'	46:CM:1399:U:O5'	2.12	0.49
46:CM:1457:A:H5'	52:CS:185:ARG:HG2	1.93	0.49
46:CM:1477:U:H4'	46:CM:1478:A:H5'	1.95	0.49
46:CM:1672:G:H2'	46:CM:1673:U:C6	2.47	0.49
47:CN:200:ASP:O	47:CN:203:PHE:HB2	2.11	0.49
52:CS:159:ALA:HB3	52:CS:225:ARG:HB3	1.95	0.49
59:CZ:41:LEU:HD13	59:CZ:121:VAL:HG11	1.94	0.49
59:CZ:53:SER:HB2	78:DS:158:ARG:HH21	1.76	0.49
62:DC:41:VAL:HG13	62:DC:84:ILE:HD13	1.94	0.49
69:DJ:106:THR:HG23	69:DJ:108:ALA:H	1.76	0.49
1:1:407:A:C2	3:4:17:A:H1'	2.48	0.49
1:1:925:A:O2'	38:AK:49:TRP:O	2.26	0.49
1:1:1225:G:H2'	1:1:1226:G:H8	1.76	0.49
1:1:2680:C:H2'	1:1:2681:C:C6	2.48	0.49
16:v:46:ASP:OD2	16:v:50:ARG:NH2	2.45	0.49
46:B:706:C:H2'	46:B:708:A:OP2	2.12	0.49
46:B:1336:G:H2'	46:B:1337:C:O4'	2.13	0.49
46:B:1432:A:O2'	46:B:1433:C:H3'	2.12	0.49
52:H:80:LYS:HB2	52:H:83:ARG:HH11	1.76	0.49
79:AR:50:GLY:H	79:AR:55:TYR:HA	1.77	0.49
1:AS:164:U:H2'	1:AS:165:C:H6	1.76	0.49
1:AS:581:A:H5''	34:CA:106:ASN:ND2	2.27	0.49
1:AS:964:G:H2'	1:AS:965:C:C6	2.47	0.49
1:AS:1227:A:H5''	1:AS:1228:C:C5'	2.43	0.49
1:AS:1678:U:O2	23:BP:85:LYS:HG2	2.12	0.49
1:AS:2956:C:H2'	1:AS:2957:C:H6	1.77	0.49
2:AT:7:G:O3'	7:AZ:33:ARG:NH2	2.45	0.49
3:AU:26:U:H2'	3:AU:27:U:C6	2.47	0.49
18:BK:18:ARG:NH1	18:BK:147:GLU:OE1	2.43	0.49
21:BN:92:LYS:HE2	21:BN:109:ASP:OD2	2.13	0.49
27:BT:51:ARG:HG2	27:BT:52:GLN:N	2.27	0.49
46:CM:246:U:H5'	58:CY:36:LYS:HG3	1.94	0.49
46:CM:875:C:H2'	46:CM:876:A:H8	1.75	0.49
46:CM:1105:U:H2'	46:CM:1106:C:C6	2.47	0.49
46:CM:1436:U:H2'	46:CM:1437:C:H6	1.77	0.49
46:CM:1478:A:O2'	46:CM:1479:A:O4'	2.27	0.49
46:CM:1635:A:H2'	46:CM:1636:C:H6	1.78	0.49
69:DJ:14:ILE:HG12	69:DJ:25:VAL:HG11	1.95	0.49
75:DP:11:LYS:HA	75:DP:52:ASP:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:DP:58:GLU:OE2	75:DP:61:ARG:NE	2.40	0.49
82:L1:126:PRO:HA	82:L1:129:SER:HB2	1.94	0.49
1:1:91:G:O5'	43:AP:46:LYS:NZ	2.44	0.49
1:1:559:C:H2'	1:1:560:C:C6	2.47	0.49
1:1:601:U:H4'	1:1:602:A:OP1	2.10	0.49
1:1:1239:G:OP2	1:1:1239:G:H8	1.95	0.49
1:1:1678:U:O2	23:5:85:LYS:HG2	2.12	0.49
6:l:38:SER:OG	6:l:42:ARG:NH2	2.27	0.49
14:t:61:PRO:C	14:t:62:THR:HG23	2.37	0.49
46:B:503:A:H2'	46:B:505:U:C6	2.48	0.49
46:B:560:G:H2'	46:B:561:U:O2	2.12	0.49
46:B:635:C:OP1	69:Y:32:LYS:N	2.31	0.49
46:B:1094:G:H1	46:B:1121:U:H3	1.60	0.49
46:B:1659:G:H2'	46:B:1660:G:H8	1.77	0.49
64:T:89:SER:HB3	64:T:92:ASP:HB2	1.93	0.49
72:b:42:LEU:HD21	72:b:47:TYR:HD1	1.78	0.49
1:AS:385:A:H2'	1:AS:386:A:C8	2.47	0.49
1:AS:511:C:H5''	6:AY:344:LYS:HD2	1.94	0.49
1:AS:1116:A:H2'	1:AS:1117:U:C6	2.47	0.49
1:AS:2739:U:H2'	1:AS:2740:U:C6	2.47	0.49
1:AS:3336:G:H2'	1:AS:3337:A:H8	1.77	0.49
46:CM:544:U:H2'	46:CM:545:U:C6	2.48	0.49
46:CM:815:U:HO2'	46:CM:816:U:H6	1.57	0.49
46:CM:1181:A:OP2	46:CM:1450:G:N2	2.37	0.49
46:CM:1399:U:O2'	46:CM:1402:G:OP1	2.30	0.49
46:CM:1571:G:O2'	46:CM:1597:G:O6	2.26	0.49
48:CO:59:ASP:OD1	48:CO:60:GLY:N	2.45	0.49
49:CP:165:ILE:HB	49:CP:192:TYR:HB2	1.94	0.49
54:CU:69:VAL:HG12	54:CU:72:ARG:NH2	2.27	0.49
79:DT:42:LEU:HD11	79:DT:83:SER:HB3	1.94	0.49
80:P0:52:LEU:HB3	80:P0:86:PHE:HB2	1.93	0.49
80:P0:52:LEU:HD22	80:P0:88:PHE:HE2	1.77	0.49
1:1:1029:U:O2'	1:1:1030:U:OP1	2.29	0.49
1:1:1104:U:H2'	1:1:1105:U:C6	2.47	0.49
1:1:1761:U:C5	20:z:43:LYS:HE3	2.47	0.49
1:1:1852:C:H2'	1:1:1853:C:H6	1.78	0.49
36:AI:118:ILE:HG22	36:AI:119:LYS:N	2.27	0.49
45:i:86:LYS:HG3	45:i:93:ARG:NH1	2.27	0.49
46:B:4:C:H5	46:B:20:G:H1	1.60	0.49
46:B:94:U:O2'	51:G:8:HIS:ND1	2.44	0.49
46:B:511:U:O4	56:L:171:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:D:26:ARG:HA	48:D:50:ARG:HH12	1.77	0.49
79:AR:75:SER:HA	79:AR:116:ILE:HD11	1.94	0.49
1:AS:359:U:OP1	38:CE:11:ARG:NH1	2.45	0.49
1:AS:1329:C:OP1	19:BL:2:GLY:N	2.45	0.49
1:AS:1628:A:OP1	28:BU:48:ARG:NH1	2.44	0.49
1:AS:3038:U:H2'	1:AS:3039:C:C6	2.47	0.49
3:AU:26:U:O2'	6:AY:52:ALA:O	2.28	0.49
25:BR:82:ILE:HD13	53:CT:131:LYS:HG3	1.93	0.49
40:CG:49:LEU:O	40:CG:51:ILE:N	2.41	0.49
46:CM:215:A:H4'	46:CM:216:A:OP2	2.13	0.49
46:CM:338:U:H2'	46:CM:339:A:C8	2.46	0.49
46:CM:654:G:H8	46:CM:654:G:O5'	1.96	0.49
46:CM:815:U:O2'	46:CM:816:U:H6	1.94	0.49
46:CM:953:U:H2'	46:CM:954:C:O4'	2.12	0.49
46:CM:1277:G:H21	47:CN:111:ILE:HD11	1.77	0.49
46:CM:1523:G:O2'	46:CM:1524:C:OP1	2.26	0.49
50:CQ:214:ASP:OD1	50:CQ:215:GLU:N	2.30	0.49
62:DC:60:LEU:HD22	62:DC:92:SER:HB3	1.94	0.49
80:P0:8:LYS:NZ	80:P0:58:MET:SD	2.84	0.49
80:P0:42:ARG:HB3	80:P0:51:VAL:HG21	1.93	0.49
1:1:496:A:H2'	1:1:497:U:C6	2.47	0.49
1:1:1007:A:H2'	1:1:1008:A:C8	2.48	0.49
2:3:62:U:OP2	7:m:276:LYS:NZ	2.46	0.49
3:4:126:A:O2'	3:4:129:C:N4	2.45	0.49
5:k:117:ARG:HD2	5:k:176:ALA:O	2.11	0.49
8:n:146:LEU:O	8:n:150:LYS:HG2	2.12	0.49
13:s:61:ARG:HG2	13:s:62:ASN:ND2	2.28	0.49
16:v:68:ARG:HG2	16:v:128:LYS:HG3	1.94	0.49
17:w:62:ALA:HA	17:w:71:PRO:HD2	1.93	0.49
19:y:96:PHE:CD1	19:y:97:PRO:HD2	2.48	0.49
46:B:17:C:H2'	46:B:18:C:H6	1.78	0.49
46:B:473:A:OP1	56:L:126:ARG:HD3	2.12	0.49
46:B:733:U:O2'	69:Y:122:SER:O	2.24	0.49
46:B:1218:G:N1	46:B:1237:C:H5	2.05	0.49
1:AS:158:A:H2'	1:AS:159:A:H8	1.77	0.49
1:AS:343:U:H1'	6:AY:96:ARG:HG3	1.94	0.49
1:AS:1777:C:H2'	1:AS:1778:U:C6	2.46	0.49
1:AS:2370:C:H1'	5:AX:266:ARG:HH21	1.78	0.49
21:BN:42:TRP:O	21:BN:46:GLN:HG3	2.13	0.49
50:CQ:140:SER:O	50:CQ:184:GLY:N	2.40	0.49
59:CZ:139:HIS:ND1	59:CZ:139:HIS:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:DF:24:GLY:HA2	65:DF:58:ALA:HB3	1.94	0.49
80:P0:43:LYS:HD3	81:12:121:PHE:HB3	1.95	0.49
82:L1:10:ARG:O	82:L1:14:HIS:ND1	2.45	0.49
1:1:716:G:O2'	1:1:717:A:OP1	2.24	0.49
1:1:1396:U:H2'	1:1:1397:G:O4'	2.12	0.49
1:1:1777:C:H2'	1:1:1778:U:C6	2.47	0.49
1:1:2322:U:H2'	1:1:2323:A:H8	1.73	0.49
1:1:2853:C:H2'	1:1:2854:U:H6	1.78	0.49
5:k:122:TRP:CE2	5:k:127:LYS:HE3	2.48	0.49
28:AA:85:TYR:OH	35:AH:97:GLU:OE2	2.25	0.49
38:AK:28:HIS:HB3	38:AK:31:LYS:HB2	1.93	0.49
63:S:38:VAL:HB	63:S:44:ARG:HG3	1.95	0.49
1:AS:1256:A:O2'	1:AS:1275:C:O2	2.30	0.49
1:AS:1949:G:N1	1:AS:2070:A:H2'	2.28	0.49
7:AZ:6:GLU:OE1	7:AZ:7:PHE:N	2.45	0.49
33:BZ:33:TRP:CH2	33:BZ:53:GLN:HG2	2.47	0.49
46:CM:7:G:H4'	46:CM:571:C:H4'	1.94	0.49
46:CM:983:A:N6	46:CM:989:U:OP2	2.45	0.49
50:CQ:60:LEU:HD23	50:CQ:67:ILE:HG21	1.94	0.49
59:CZ:50:LYS:HE3	59:CZ:54:LYS:HE3	1.93	0.49
80:p0:59:VAL:HA	80:p0:62:ALA:HB3	1.94	0.49
1:1:393:U:H2'	1:1:394:G:O4'	2.12	0.49
1:1:1233:G:H2'	1:1:1234:C:H6	1.77	0.49
1:1:1949:G:H22	20:z:114:LYS:CE	2.26	0.49
5:k:283:TYR:CE1	5:k:354:VAL:HG21	2.48	0.49
7:m:164:LYS:NZ	7:m:168:ASP:OD1	2.39	0.49
27:9:11:SER:HB3	27:9:14:LYS:HB2	1.93	0.49
46:B:65:A:H2	46:B:84:A:H62	1.60	0.49
46:B:78:A:H2'	46:B:79:C:H6	1.78	0.49
46:B:261:C:H4'	46:B:290:U:H5'	1.94	0.49
46:B:938:G:H2'	46:B:939:G:C8	2.48	0.49
46:B:1485:G:H2'	46:B:1486:G:H8	1.78	0.49
56:L:108:ARG:NH1	56:L:110:GLN:OE1	2.45	0.49
1:AS:19:A:H2'	1:AS:20:G:C8	2.48	0.49
1:AS:120:A:C2	10:BC:130:PRO:HB3	2.48	0.49
1:AS:1079:G:H2'	1:AS:1080:A:C8	2.48	0.49
1:AS:1176:A:C4	1:AS:1178:G:C8	3.01	0.49
1:AS:1632:C:OP1	28:BU:36:HIS:NE2	2.41	0.49
1:AS:2134:U:OP1	4:AW:241:ARG:NH2	2.46	0.49
1:AS:2696:U:OP1	22:BO:78:LYS:NZ	2.40	0.49
1:AS:3035:C:H2'	1:AS:3036:U:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AX:92:TYR:HB2	5:AX:157:VAL:HB	1.94	0.49
10:BC:160:PRO:HB2	10:BC:162:GLU:OE1	2.13	0.49
22:BO:136:ARG:HD3	22:BO:139:ARG:NH2	2.28	0.49
25:BR:83:VAL:HG11	46:CM:68:A:N1	2.28	0.49
46:CM:68:A:N6	53:CT:132:ARG:HG3	2.27	0.49
46:CM:291:U:H2'	46:CM:292:C:H6	1.78	0.49
46:CM:415:A:H4'	46:CM:416:G:O5'	2.11	0.49
46:CM:1656:U:H2'	46:CM:1657:G:O4'	2.13	0.49
49:CP:177:PRO:HG3	56:CW:17:ARG:HH12	1.77	0.49
51:CR:141:THR:OG1	51:CR:143:ASP:OD1	2.25	0.49
55:CV:78:ILE:HD13	55:CV:104:ILE:HG22	1.95	0.49
60:DA:83:GLU:OE1	60:DA:83:GLU:N	2.46	0.49
63:DD:89:VAL:HG13	63:DD:101:LYS:HG2	1.95	0.49
82:L1:43:PRO:HB3	82:L1:161:LYS:HA	1.95	0.49
1:1:234:A:H2'	1:1:235:G:O4'	2.13	0.49
1:1:281:G:N7	16:v:182:LYS:HE2	2.28	0.49
1:1:693:C:H5''	6:l:272:LYS:HD3	1.94	0.49
1:1:2086:C:H1'	1:1:3309:A:H8	1.72	0.49
1:1:2117:A:C4	38:AK:3:LYS:HE2	2.47	0.49
1:1:2681:C:H2'	1:1:2682:C:C6	2.47	0.49
16:v:73:ARG:HG2	16:v:75:VAL:HG13	1.94	0.49
32:AE:30:LYS:NZ	32:AE:34:GLU:OE2	2.45	0.49
46:B:217:A:H5''	46:B:816:U:O2	2.13	0.49
46:B:1306:A:H4'	46:B:1307:A:O5'	2.12	0.49
46:B:1515:U:H2'	46:B:1516:C:C6	2.48	0.49
50:F:171:ILE:HG12	50:F:188:LYS:HG3	1.95	0.49
65:U:57:ARG:NH1	72:b:40:VAL:HB	2.28	0.49
79:AR:12:THR:O	79:AR:53:ASN:HA	2.13	0.49
1:AS:158:A:H2'	1:AS:159:A:C8	2.48	0.49
1:AS:353:G:O6	38:CE:55:ARG:NH2	2.46	0.49
1:AS:1278:G:H5''	80:p0:83:ASN:H	1.77	0.49
1:AS:1895:G:O2'	1:AS:2312:U:O4	2.24	0.49
1:AS:3023:U:C2	1:AS:3024:G:C8	3.00	0.49
1:AS:3136:C:H2'	1:AS:3137:A:H8	1.77	0.49
10:BC:158:VAL:HG21	10:BC:164:VAL:HG21	1.93	0.49
24:BQ:77:ILE:HD12	24:BQ:103:VAL:HG11	1.95	0.49
28:BU:46:ILE:HG23	28:BU:68:VAL:HG13	1.95	0.49
39:CF:73:LEU:HD12	39:CF:75:ILE:HG23	1.95	0.49
45:CL:120:GLU:HG2	50:CQ:118:ARG:HE	1.78	0.49
46:CM:214:U:H5'	46:CM:815:U:H4'	1.93	0.49
46:CM:814:A:H2'	46:CM:814:A:OP2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:CO:180:THR:HG23	48:CO:183:GLN:H	1.78	0.49
55:CV:65:PHE:CZ	55:CV:78:ILE:HD11	2.48	0.49
82:L1:16:LEU:HD11	82:L1:208:SER:H	1.77	0.49
82:l1:57:GLN:O	82:l1:59:PRO:HD3	2.11	0.49
80:p0:41:ILE:O	80:p0:45:LEU:HD23	2.11	0.49
1:1:583:A:H2'	1:1:584:C:C6	2.48	0.49
1:1:1157:G:O2'	33:AF:55:ASN:OD1	2.28	0.49
1:1:1466:U:H2'	1:1:1467:U:C6	2.47	0.49
1:1:2239:G:O2'	1:1:2241:C:N4	2.46	0.49
1:1:2470:C:H2'	1:1:2471:U:O4'	2.13	0.49
1:1:2516:U:O2'	1:1:2519:A:N1	2.44	0.49
1:1:2902:A:H2'	1:1:2903:C:H6	1.78	0.49
1:1:3293:G:OP1	5:k:385:LYS:HE3	2.13	0.49
6:l:157:PHE:CD1	6:l:169:VAL:HG11	2.47	0.49
14:t:57:VAL:HG22	14:t:69:VAL:HG22	1.95	0.49
15:u:21:VAL:HG22	15:u:55:ILE:HG22	1.95	0.49
20:z:158:GLU:OE2	20:z:162:ARG:NH2	2.45	0.49
24:6:121:GLU:OE1	24:6:121:GLU:N	2.45	0.49
32:AE:95:VAL:HG12	32:AE:97:VAL:HG13	1.93	0.49
33:AF:106:ARG:NH2	33:AF:122:ASN:O	2.46	0.49
45:i:77:GLN:NE2	46:B:1165:C:H5'	2.28	0.49
60:P:69:ASN:HB3	60:P:73:ARG:HD2	1.93	0.49
64:T:100:LEU:HB3	64:T:102:ILE:HG23	1.95	0.49
79:AR:175:VAL:HB	79:AR:189:PHE:HB2	1.94	0.49
1:AS:1560:U:H3	1:AS:1571:G:H1	1.61	0.49
1:AS:2679:U:H2'	1:AS:2680:C:C6	2.48	0.49
1:AS:3166:A:C2	1:AS:3167:G:N7	2.81	0.49
19:BL:125:ASP:OD1	19:BL:126:GLN:N	2.46	0.49
25:BR:13:ILE:HG12	25:BR:32:GLN:HB2	1.94	0.49
46:CM:147:C:C2	46:CM:148:C:C5	3.01	0.49
46:CM:577:A:H2'	50:CQ:144:ARG:HH22	1.78	0.49
1:1:99:A:H3'	1:1:100:G:H21	1.78	0.48
1:1:169:G:N1	1:1:249:G:H1'	2.28	0.48
1:1:590:A:H5'	8:n:16:ALA:O	2.12	0.48
1:1:2535:A:OP1	4:j:69:TYR:OH	2.26	0.48
1:1:2854:U:H2'	1:1:2855:U:H6	1.77	0.48
2:3:23:A:H2'	2:3:24:A:C8	2.47	0.48
2:3:27:A:H2'	2:3:28:C:C6	2.48	0.48
3:4:37:A:H5''	3:4:39:G:O4'	2.13	0.48
46:B:220:A:H2'	46:B:221:U:C2	2.48	0.48
46:B:583:A:H2'	46:B:584:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1067:C:H4'	68:X:58:TYR:CE2	2.48	0.48
46:B:1369:G:O2'	46:B:1370:A:H8	1.96	0.48
46:B:1635:A:H2'	46:B:1636:C:H6	1.74	0.48
48:D:62:LYS:HZ2	48:D:90:GLU:HA	1.76	0.48
52:H:151:SER:OG	52:H:156:ARG:NH2	2.43	0.48
56:L:110:GLN:HE21	56:L:126:ARG:HB2	1.77	0.48
1:AS:1661:U:H2'	1:AS:1662:G:H8	1.78	0.48
1:AS:2354:G:H2'	1:AS:2355:G:C8	2.48	0.48
1:AS:2719:A:H2'	1:AS:2720:A:C8	2.47	0.48
16:BI:38:ARG:HA	16:BI:62:TYR:CD1	2.48	0.48
46:CM:480:U:H2'	46:CM:481:A:C8	2.48	0.48
46:CM:723:G:H2'	46:CM:724:G:H4'	1.94	0.48
46:CM:1092:G:O2'	46:CM:1093:G:H5'	2.13	0.48
1:1:307:A:H2'	1:1:308:A:H8	1.74	0.48
1:1:431:A:H2'	1:1:432:G:H8	1.78	0.48
1:1:1011:C:O2'	1:1:1012:U:OP2	2.30	0.48
1:1:1130:G:O2'	1:1:2614:A:N3	2.43	0.48
1:1:1260:G:H21	1:1:1273:C:H42	1.61	0.48
1:1:1380:U:OP2	6:l:203:ARG:HA	2.12	0.48
1:1:1434:U:H4'	6:l:89:ALA:HB3	1.94	0.48
1:1:2236:U:C2	1:1:2237:A:C8	3.01	0.48
1:1:2540:G:P	28:AA:54:THR:OG1	2.71	0.48
1:1:2583:U:H2'	1:1:2584:U:H6	1.77	0.48
1:1:3019:U:O2'	1:1:3020:A:H5'	2.13	0.48
4:j:140:ASN:ND2	4:j:143:GLU:OE1	2.46	0.48
5:k:212:ASP:OD2	5:k:354:VAL:N	2.23	0.48
19:y:123:THR:OG1	19:y:125:ASP:OD1	2.21	0.48
46:B:25:C:H4'	46:B:26:A:O5'	2.13	0.48
46:B:441:C:OP2	71:a:105:ARG:HB2	2.13	0.48
46:B:718:A:H4'	46:B:719:A:C6	2.48	0.48
46:B:846:U:H5'	46:B:847:A:OP2	2.12	0.48
46:B:1141:C:H2'	46:B:1142:A:C8	2.48	0.48
54:J:29:ASP:OD1	54:J:30:LEU:N	2.46	0.48
1:AS:431:A:H2'	1:AS:432:G:H8	1.78	0.48
1:AS:496:A:H2'	1:AS:497:U:C6	2.47	0.48
1:AS:516:U:OP1	6:AY:352:PRO:HD2	2.12	0.48
1:AS:648:C:H2'	1:AS:649:G:C8	2.48	0.48
1:AS:976:A:C2'	1:AS:977:U:H5'	2.43	0.48
1:AS:1153:G:O2'	1:AS:1165:A:N3	2.44	0.48
1:AS:1251:C:H2'	1:AS:1252:G:H8	1.77	0.48
1:AS:2330:A:H5''	18:BK:83:TRP:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:3138:U:H2'	1:AS:3139:U:C6	2.48	0.48
3:AU:5:U:H2'	3:AU:6:U:C6	2.49	0.48
11:BD:86:TYR:CE2	11:BD:151:LEU:HB2	2.49	0.48
46:CM:477:C:H5'	56:CW:124:HIS:HD1	1.79	0.48
1:1:381:U:H2'	1:1:382:U:C6	2.48	0.48
1:1:599:U:H6	1:1:600:U:H5	1.61	0.48
1:1:1140:U:OP1	1:1:1363:G:O2'	2.29	0.48
1:1:1190:G:H2'	1:1:1191:A:C8	2.48	0.48
1:1:1255:A:N7	80:P0:53:MET:HB3	2.27	0.48
1:1:1911:A:H2'	1:1:1912:U:C6	2.47	0.48
1:1:2482:U:H2'	1:1:2483:U:H5'	1.95	0.48
28:AA:23:VAL:HG12	28:AA:45:GLY:HA3	1.95	0.48
46:B:946:U:H5''	60:P:71:ILE:HD12	1.96	0.48
47:C:6:SER:O	47:C:191:ARG:NH1	2.46	0.48
52:H:113:ILE:HG23	52:H:191:ALA:HA	1.94	0.48
57:M:47:GLN:O	57:M:51:SER:HB3	2.12	0.48
70:Z:37:ALA:HA	70:Z:41:SER:HB3	1.93	0.48
1:AS:1104:U:H2'	1:AS:1105:U:C6	2.47	0.48
1:AS:2557:G:C6	26:BS:24:LEU:HD21	2.47	0.48
1:AS:2899:C:H2'	1:AS:2900:C:C6	2.48	0.48
1:AS:3082:C:H2'	1:AS:3083:U:C6	2.48	0.48
1:AS:3162:U:C4	1:AS:3163:U:C2	3.01	0.48
9:BB:8:GLU:HG3	9:BB:9:THR:H	1.77	0.48
40:CG:23:LEU:HD12	40:CG:24:PRO:HD2	1.95	0.48
45:CL:80:ALA:HA	46:CM:1164:G:H4'	1.96	0.48
46:CM:78:A:H2	53:CT:174:LYS:HG3	1.78	0.48
46:CM:1183:G:O4'	67:DH:72:GLY:HA3	2.12	0.48
46:CM:1543:A:H1'	46:CM:1547:U:OP2	2.13	0.48
47:CN:79:ARG:O	47:CN:83:GLN:HG3	2.13	0.48
47:CN:88:LYS:HD2	47:CN:201:LEU:HD11	1.95	0.48
50:CQ:28:ARG:HB3	57:CX:58:GLN:NE2	2.28	0.48
55:CV:83:TYR:HB3	55:CV:101:VAL:HB	1.94	0.48
61:DB:79:ARG:HB3	61:DB:113:VAL:HG23	1.94	0.48
64:DE:93:LEU:HD12	64:DE:98:GLY:O	2.13	0.48
82:I:1:75:ASP:HA	82:I:1:78:LYS:HD2	1.95	0.48
1:1:870:U:H5''	1:1:2922:G:OP1	2.13	0.48
1:1:1042:A:H2'	1:1:1045:C:C5	2.48	0.48
1:1:1176:A:C4	1:1:1178:G:C8	3.01	0.48
1:1:2740:U:H2'	1:1:2741:A:C8	2.48	0.48
46:B:432:G:N1	46:B:435:A:OP2	2.46	0.48
46:B:538:G:N2	77:g:25:GLU:OE2	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1375:C:O2'	64:T:52:GLY:HA3	2.13	0.48
46:B:1597:G:N7	63:S:13:LYS:NZ	2.61	0.48
46:B:1757:U:H2'	46:B:1758:U:C6	2.48	0.48
1:AS:171:G:H1	1:AS:246:U:H3	1.61	0.48
1:AS:268:A:H61	1:AS:295:A:H3'	1.79	0.48
1:AS:487:C:H2'	1:AS:488:G:O4'	2.13	0.48
1:AS:1046:U:OP2	22:BO:13:TYR:OH	2.26	0.48
1:AS:1277:G:OP1	80:p0:55:LYS:HG2	2.12	0.48
1:AS:1563:A:H2	1:AS:1569:C:C4	2.32	0.48
1:AS:2854:U:H2'	1:AS:2855:U:H6	1.78	0.48
1:AS:3067:U:H2'	1:AS:3068:C:H6	1.78	0.48
4:AW:20:THR:HA	4:AW:23:ARG:HG3	1.94	0.48
8:BA:170:ARG:HB3	8:BA:172:HIS:CE1	2.48	0.48
23:BP:19:VAL:HG12	23:BP:108:LEU:HG	1.94	0.48
46:CM:1218:G:H22	46:CM:1238:U:H1'	1.77	0.48
54:CU:134:LYS:C	54:CU:135:ARG:HD2	2.38	0.48
63:DD:27:LEU:HB3	63:DD:63:ASP:HB2	1.96	0.48
64:DE:66:VAL:HG13	64:DE:69:ILE:HG12	1.94	0.48
68:DI:64:GLU:OE2	74:DO:2:VAL:N	2.46	0.48
75:DP:10:ALA:HB1	75:DP:30:VAL:HB	1.94	0.48
82:L1:180:VAL:O	82:L1:184:MET:HG2	2.13	0.48
82:l1:196:LYS:HD2	82:l1:200:ASN:HD21	1.78	0.48
1:1:200:A:H2'	1:1:201:G:H8	1.77	0.48
1:1:538:G:O2'	1:1:539:G:OP1	2.29	0.48
1:1:547:U:H2'	1:1:548:G:C8	2.48	0.48
1:1:1309:G:O2'	1:1:1314:A:N1	2.45	0.48
1:1:1330:U:H2'	1:1:1331:U:C6	2.49	0.48
1:1:2477:U:H2'	1:1:2478:A:H8	1.77	0.48
1:1:3044:C:H2'	1:1:3045:A:O4'	2.14	0.48
2:3:4:U:H2'	2:3:5:G:C8	2.48	0.48
5:k:66:LYS:NZ	24:6:9:ASN:H	2.10	0.48
9:o:208:PRO:HB3	9:o:239:GLN:HB3	1.94	0.48
15:u:57:LEU:HG	21:0:172:TYR:OH	2.13	0.48
45:i:101:LYS:HD3	46:B:573:C:H4'	1.96	0.48
46:B:479:A:H2'	46:B:480:U:H6	1.77	0.48
46:B:1486:G:OP1	66:V:122:ARG:NH1	2.42	0.48
47:C:50:ILE:HA	47:C:53:THR:HB	1.94	0.48
67:W:20:LYS:HD3	67:W:93:GLN:HG2	1.95	0.48
1:AS:1140:U:OP1	1:AS:1363:G:O2'	2.26	0.48
1:AS:1246:G:H2'	1:AS:1247:A:C8	2.49	0.48
1:AS:1810:A:H4'	1:AS:1811:U:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:2334:A:H61	1:AS:2955:C:H5	1.54	0.48
10:BC:117:ILE:HG12	10:BC:123:ALA:HA	1.95	0.48
36:CC:118:ILE:HG22	36:CC:119:LYS:N	2.28	0.48
46:CM:558:U:H2'	46:CM:559:G:H8	1.77	0.48
46:CM:1663:U:H5''	55:CV:58:LEU:HD21	1.96	0.48
46:CM:1783:C:OP1	73:DN:87:ARG:NE	2.46	0.48
50:CQ:69:GLU:O	57:CX:20:VAL:HG11	2.13	0.48
51:CR:112:HIS:NE2	51:CR:238:SER:O	2.46	0.48
59:CZ:62:LEU:HG	59:CZ:63:CYS:N	2.28	0.48
62:DC:55:GLY:O	62:DC:58:LYS:HG2	2.13	0.48
65:DF:72:ILE:HD13	65:DF:79:TYR:CG	2.49	0.48
1:1:371:G:N1	1:1:374:A:OP2	2.38	0.48
1:1:883:G:H2'	1:1:884:A:C8	2.48	0.48
1:1:1182:G:N3	21:0:112:ALA:HB1	2.29	0.48
1:1:2391:A:H2'	1:1:2392:G:C8	2.49	0.48
1:1:2404:U:H2'	1:1:2405:U:C6	2.48	0.48
2:3:118:A:H5''	7:m:253:PHE:CZ	2.48	0.48
6:l:3:SER:OG	6:l:4:ARG:N	2.36	0.48
6:l:113:LYS:HE3	16:v:202:TYR:HB3	1.94	0.48
45:i:99:SER:OG	45:i:102:LYS:HD2	2.13	0.48
46:B:366:U:H2'	46:B:367:A:O4'	2.13	0.48
46:B:551:G:N2	46:B:569:G:N7	2.59	0.48
46:B:786:G:H2'	46:B:787:A:C8	2.48	0.48
46:B:1277:G:H2'	46:B:1278:U:C6	2.49	0.48
46:B:1469:A:OP2	46:B:1508:G:N2	2.42	0.48
46:B:1704:C:C2	46:B:1705:G:C8	3.02	0.48
1:AS:1057:A:O2'	22:BO:102:ARG:NH2	2.47	0.48
1:AS:1250:C:H41	1:AS:1259:A:P	2.35	0.48
1:AS:1254:U:N3	1:AS:1257:G:OP2	2.46	0.48
1:AS:2201:A:H2'	1:AS:2202:A:C8	2.49	0.48
1:AS:2407:G:H2'	1:AS:2408:A:C8	2.49	0.48
1:AS:2812:C:N4	1:AS:2817:A:O2'	2.45	0.48
1:AS:3184:G:H1	8:BA:162:SER:HG	1.61	0.48
10:BC:145:GLU:OE2	37:CD:35:ARG:NH1	2.46	0.48
14:BG:31:LYS:O	14:BG:35:ARG:HB2	2.13	0.48
17:BJ:160:LYS:O	17:BJ:163:VAL:HG12	2.13	0.48
45:CL:155:LEU:HD13	57:CX:92:LEU:HD13	1.95	0.48
46:CM:445:U:OP1	51:CR:49:ARG:NH1	2.47	0.48
46:CM:1132:A:H2'	46:CM:1133:C:C6	2.49	0.48
46:CM:1243:U:C6	46:CM:1244:U:H5	2.31	0.48
46:CM:1395:G:N2	46:CM:1398:G:OP2	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1423:U:O2'	50:CQ:182:VAL:HG23	2.13	0.48
48:CO:27:LYS:HD2	48:CO:47:LEU:HD13	1.95	0.48
52:CS:93:LEU:HD12	52:CS:172:ILE:HG23	1.96	0.48
82:l1:179:LEU:O	82:l1:181:ASN:N	2.45	0.48
1:1:268:A:N1	1:1:295:A:H5'	2.29	0.48
1:1:712:G:H1	29:AB:72:GLU:CD	2.22	0.48
1:1:1937:C:H2'	1:1:1938:U:C6	2.49	0.48
1:1:2472:A:H3'	1:1:2473:C:H5''	1.95	0.48
1:1:2785:A:H2'	1:1:2786:G:O4'	2.14	0.48
1:1:2956:C:H2'	1:1:2957:C:H6	1.78	0.48
1:1:3024:G:H2'	1:1:3025:G:H8	1.79	0.48
1:1:3290:G:O3'	32:AE:102:GLY:HA2	2.14	0.48
4:j:147:ARG:HG2	4:j:157:ILE:HG12	1.96	0.48
23:5:19:VAL:HG12	23:5:108:LEU:HG	1.94	0.48
46:B:29:U:H2'	46:B:30:G:C8	2.45	0.48
46:B:78:A:H2	53:I:174:LYS:HG3	1.79	0.48
46:B:558:U:H2'	46:B:559:G:C8	2.49	0.48
46:B:875:C:H2'	46:B:876:A:H8	1.79	0.48
55:K:76:THR:HG21	55:K:104:ILE:HD12	1.95	0.48
63:S:37:LEU:CA	63:S:44:ARG:HH21	2.26	0.48
79:AR:145:LEU:HD13	79:AR:178:TRP:CD2	2.48	0.48
1:AS:99:A:H3'	1:AS:100:G:H21	1.79	0.48
1:AS:729:C:H3'	1:AS:730:A:H5''	1.95	0.48
1:AS:948:A:H4'	1:AS:964:G:N2	2.28	0.48
1:AS:1034:U:H5''	7:AZ:5:LYS:HG2	1.96	0.48
1:AS:1632:C:H5''	28:BU:73:LYS:HZ1	1.78	0.48
1:AS:2385:C:H2'	1:AS:2386:U:C6	2.48	0.48
1:AS:2433:U:H2'	1:AS:2434:A:C8	2.49	0.48
1:AS:2449:U:N3	1:AS:2452:G:H2'	2.29	0.48
1:AS:2919:G:N3	5:AX:250:ALA:HB1	2.28	0.48
2:AT:77:G:H3'	21:BN:46:GLN:O	2.13	0.48
46:CM:1785:U:C4	73:DN:98:PRO:HG2	2.48	0.48
48:CO:97:LEU:CD1	48:CO:228:LEU:HD11	2.44	0.48
54:CU:14:GLU:HA	54:CU:42:ILE:HD12	1.94	0.48
67:DH:101:ARG:O	67:DH:105:ILE:HG12	2.13	0.48
1:1:71:C:O2'	14:t:66:ASN:OD1	2.18	0.48
1:1:164:U:H2'	1:1:165:C:H6	1.77	0.48
1:1:411:U:H2'	1:1:412:G:C8	2.49	0.48
1:1:1231:U:H1'	1:1:1233:G:OP2	2.14	0.48
1:1:1468:U:H5'	20:z:4:LEU:HB2	1.95	0.48
1:1:1485:A:OP1	35:AH:10:ARG:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:AA:71:PHE:HA	28:AA:111:LYS:HE2	1.96	0.48
46:B:138:C:OP2	53:I:187:LYS:NZ	2.32	0.48
46:B:1376:U:C5	64:T:3:ARG:HG3	2.49	0.48
46:B:1458:C:OP1	52:H:102:ARG:NH2	2.46	0.48
46:B:1551:U:H2'	46:B:1552:C:H6	1.79	0.48
46:B:1669:U:O2'	46:B:1670:U:H6	1.96	0.48
46:B:1774:C:OP1	61:Q:122:ARG:NH2	2.44	0.48
49:E:71:LEU:HB3	49:E:99:ILE:HD11	1.95	0.48
50:F:72:SER:O	50:F:76:LYS:HD2	2.13	0.48
52:H:26:ALA:HB2	63:S:25:LYS:HG3	1.96	0.48
1:AS:7:C:H42	3:AU:150:G:H1	1.60	0.48
1:AS:941:C:H2'	1:AS:942:U:H6	1.76	0.48
1:AS:2639:A:N6	1:AS:2659:G:O2'	2.47	0.48
1:AS:3165:U:N3	1:AS:3166:A:N3	2.62	0.48
1:AS:3339:U:H2'	1:AS:3343:C:N4	2.28	0.48
2:AT:50:U:O2'	7:AZ:221:SER:O	2.26	0.48
13:BF:106:ILE:HD11	13:BF:125:MET:HB3	1.94	0.48
45:CL:154:TYR:HB2	57:CX:86:ILE:HG22	1.95	0.48
46:CM:696:U:OP1	46:CM:696:U:C6	2.65	0.48
46:CM:1494:G:H2'	46:CM:1495:U:C6	2.49	0.48
46:CM:1668:A:H2'	46:CM:1669:U:H5'	1.94	0.48
51:CR:88:ASP:OD1	51:CR:122:LYS:NZ	2.47	0.48
82:L1:143:ASP:O	82:L1:147:LYS:N	2.39	0.48
80:p0:19:LEU:HD23	80:p0:66:PHE:CD2	2.49	0.48
1:1:291:C:H2'	1:1:292:U:C6	2.49	0.48
1:1:665:C:H1'	14:t:10:LEU:HD21	1.95	0.48
1:1:1252:G:O2'	81:12:120:SER:OG	2.27	0.48
1:1:2729:U:H4'	22:2:7:TYR:HB3	1.96	0.48
1:1:2847:U:OP2	1:1:2917:G:N1	2.39	0.48
16:v:38:ARG:HA	16:v:62:TYR:CD1	2.49	0.48
20:z:167:ARG:NH1	46:B:798:A:OP1	2.47	0.48
37:AJ:97:ARG:N	82:l1:215:ARG:HH22	2.11	0.48
45:i:62:ALA:O	45:i:63:ALA:C	2.56	0.48
46:B:6:G:OP2	49:E:200:ARG:NE	2.34	0.48
46:B:114:C:O2'	58:N:65:SER:OG	2.24	0.48
46:B:470:U:H5''	56:L:11:THR:HG23	1.96	0.48
46:B:671:G:H3'	46:B:672:U:C5'	2.28	0.48
46:B:1551:U:H2'	46:B:1552:C:C6	2.48	0.48
46:B:1596:U:OP1	63:S:75:SER:N	2.39	0.48
46:B:1750:A:H5''	46:B:1758:U:H5''	1.96	0.48
50:F:71:THR:HB	50:F:87:ILE:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:W:33:LEU:HG	67:W:88:ARG:HH21	1.79	0.48
67:W:68:LYS:HE2	67:W:79:ASP:OD1	2.13	0.48
68:X:58:TYR:OH	69:Y:20:THR:HA	2.14	0.48
79:AR:261:LYS:HZ2	79:AR:268:LEU:HD13	1.79	0.48
1:AS:559:C:H2'	1:AS:560:C:H6	1.79	0.48
1:AS:912:G:N1	4:AW:207:VAL:HG11	2.29	0.48
1:AS:1385:G:O6	6:AY:187:LYS:NZ	2.38	0.48
4:AW:64:ARG:NH2	10:BC:39:GLN:O	2.47	0.48
7:AZ:178:ASN:HA	7:AZ:183:TRP:CD2	2.49	0.48
17:BJ:86:ARG:HG3	17:BJ:100:LEU:HD11	1.95	0.48
19:BL:123:THR:OG1	19:BL:125:ASP:OD1	2.30	0.48
46:CM:17:C:O2'	46:CM:1122:A:N1	2.41	0.48
46:CM:496:G:H2'	46:CM:497:U:O4'	2.14	0.48
46:CM:799:G:H8	46:CM:799:G:OP1	1.97	0.48
46:CM:1648:U:H2'	46:CM:1649:G:H8	1.77	0.48
49:CP:74:ASP:OD2	49:CP:181:ARG:NE	2.45	0.48
50:CQ:183:LEU:HD23	50:CQ:183:LEU:H	1.78	0.48
53:CT:136:LYS:HG3	53:CT:173:PRO:HB2	1.96	0.48
82:11:87:VAL:HG12	82:11:90:LEU:HD12	1.95	0.48
1:1:125:U:OP1	16:v:144:ARG:NH1	2.39	0.48
1:1:716:G:H3'	1:1:717:A:H5''	1.96	0.48
1:1:892:A:H5'	4:j:183:GLY:HA2	1.96	0.48
1:1:1298:A:N7	1:1:2829:C:O2'	2.45	0.48
1:1:1593:C:H2'	1:1:1594:G:H8	1.79	0.48
1:1:2351:A:N3	1:1:2796:G:O2'	2.43	0.48
1:1:2408:A:H2'	1:1:2409:C:H6	1.78	0.48
1:1:2423:A:O2'	37:AJ:61:ARG:NH1	2.47	0.48
2:3:26:C:H2'	2:3:27:A:O4'	2.14	0.48
13:s:88:GLU:HB3	62:R:10:ARG:NH1	2.29	0.48
16:v:65:ARG:HG2	16:v:127:TYR:CD1	2.48	0.48
19:y:150:VAL:HA	19:y:153:PHE:CD2	2.49	0.48
26:8:75:LYS:HB3	26:8:81:THR:CG2	2.43	0.48
27:9:51:ARG:HG2	27:9:52:GLN:N	2.28	0.48
46:B:1227:A:O2'	46:B:1229:A:OP1	2.28	0.48
56:L:29:LYS:HA	77:g:40:TYR:CE1	2.48	0.48
62:R:52:LYS:HB2	62:R:53:PRO:HD3	1.96	0.48
78:h:168:CYS:HB2	78:h:172:ILE:HB	1.96	0.48
1:AS:154:G:H5''	1:AS:155:A:H2'	1.95	0.48
1:AS:243:G:H2'	1:AS:244:G:H8	1.78	0.48
1:AS:408:A:N3	1:AS:653:C:O2'	2.44	0.48
1:AS:714:A:OP1	29:BV:137:LYS:NZ	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1655:U:H2'	1:AS:1656:C:H6	1.78	0.48
1:AS:1911:A:H2'	1:AS:1912:U:C6	2.49	0.48
1:AS:2108:G:O4'	1:AS:2122:A:H4'	2.14	0.48
9:BB:8:GLU:HG3	9:BB:9:THR:N	2.28	0.48
43:CJ:8:ARG:HG2	43:CJ:10:THR:HG23	1.95	0.48
45:CL:53:LYS:C	45:CL:55:LYS:H	2.21	0.48
46:CM:25:C:H4'	46:CM:26:A:O5'	2.14	0.48
46:CM:165:U:C2'	46:CM:166:A:H5''	2.44	0.48
46:CM:267:G:H2'	46:CM:268:C:H6	1.77	0.48
46:CM:583:A:H2'	46:CM:584:G:H8	1.78	0.48
46:CM:822:G:H8	46:CM:822:G:O5'	1.97	0.48
46:CM:1567:C:H4'	63:DD:136:ARG:HB2	1.94	0.48
59:CZ:103:LEU:HD13	59:CZ:116:VAL:O	2.12	0.48
59:CZ:139:HIS:O	59:CZ:139:HIS:CG	2.67	0.48
64:DE:72:LYS:HD2	64:DE:72:LYS:HA	1.73	0.48
64:DE:89:SER:HB3	64:DE:92:ASP:HB2	1.96	0.48
81:12:143:VAL:HG11	81:12:148:PRO:HG3	1.96	0.48
1:1:1456:A:H5'	32:AE:50:LEU:O	2.14	0.47
1:1:2202:A:H5'	37:AJ:73:LYS:NZ	2.29	0.47
26:8:105:VAL:HG23	26:8:130:TYR:CG	2.49	0.47
29:AB:73:ILE:HB	29:AB:109:TYR:CD2	2.49	0.47
46:B:711:U:O2'	46:B:713:U:OP1	2.31	0.47
46:B:1241:A:H5'	46:B:1242:U:C6	2.49	0.47
46:B:1396:A:O2'	46:B:1397:A:OP1	2.28	0.47
46:B:1546:G:C5	65:U:134:ARG:HD3	2.49	0.47
1:AS:126:G:H2'	1:AS:127:G:H8	1.79	0.47
1:AS:365:A:OP1	6:AY:85:ARG:NH1	2.47	0.47
1:AS:755:U:H2'	1:AS:756:G:O4'	2.14	0.47
1:AS:1214:U:H5''	80:p0:5:ARG:HH12	1.79	0.47
1:AS:1494:A:H2'	1:AS:1495:U:C6	2.49	0.47
1:AS:1725:A:O4'	31:BX:54:ARG:NH1	2.46	0.47
1:AS:1852:C:H2'	1:AS:1853:C:H6	1.78	0.47
25:BR:6:ASP:HA	25:BR:13:ILE:HD11	1.96	0.47
27:BT:58:VAL:HA	27:BT:104:VAL:HG12	1.95	0.47
39:CF:30:LYS:HB3	39:CF:38:PHE:CE2	2.48	0.47
46:CM:309:U:OP2	70:DK:20:ARG:HD3	2.13	0.47
46:CM:821:U:H2'	46:CM:822:G:H8	1.76	0.47
46:CM:1609:G:H2'	46:CM:1610:C:H6	1.79	0.47
51:CR:103:TYR:HE2	51:CR:184:THR:HG23	1.79	0.47
52:CS:108:LEU:HD21	63:DD:43:LEU:HD11	1.95	0.47
59:CZ:103:LEU:O	59:CZ:115:VAL:HG13	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:DC:68:GLU:N	62:DC:69:PRO:HD3	2.29	0.47
79:DT:260:PHE:CE2	79:DT:267:LEU:HD13	2.49	0.47
82:L1:63:MET:HG2	82:L1:65:ILE:HG12	1.96	0.47
82:l1:53:LEU:HB3	82:l1:189:PHE:HZ	1.76	0.47
82:l1:206:ILE:HG12	82:l1:216:ILE:HG13	1.94	0.47
1:1:1249:U:H5''	1:1:1259:A:H2	1.79	0.47
1:1:2234:A:H62	46:B:1742:A:H1'	1.79	0.47
1:1:2857:C:O2'	1:1:2858:U:H5'	2.14	0.47
5:k:133:TYR:O	5:k:136:LYS:HB2	2.14	0.47
24:6:102:ILE:HG21	24:6:110:LYS:CD	2.28	0.47
45:i:41:ALA:HB1	45:i:44:ALA:HB2	1.96	0.47
46:B:94:U:O2'	51:G:7:LYS:HB2	2.14	0.47
46:B:583:A:H2'	46:B:584:G:C8	2.48	0.47
46:B:627:U:C2	46:B:628:A:C8	3.02	0.47
46:B:1148:A:H2'	46:B:1149:G:O4'	2.13	0.47
46:B:1318:C:H2'	46:B:1319:U:H6	1.78	0.47
46:B:1602:C:N4	52:H:80:LYS:O	2.47	0.47
52:H:32:ASP:OD1	52:H:33:VAL:N	2.47	0.47
56:L:37:LYS:HA	77:g:33:ARG:HA	1.95	0.47
1:AS:547:U:H2'	1:AS:548:G:C8	2.49	0.47
1:AS:1708:G:N2	1:AS:1729:G:O6	2.48	0.47
1:AS:1738:U:H2'	1:AS:1739:G:C8	2.49	0.47
1:AS:2220:A:H5''	4:AW:244:GLY:HA3	1.95	0.47
1:AS:2339:A:H2'	1:AS:2340:C:H6	1.79	0.47
1:AS:3021:A:C5	5:AX:75:ALA:HB2	2.49	0.47
3:AU:141:C:O3'	16:BI:62:TYR:OH	2.32	0.47
21:BN:12:ARG:HB3	21:BN:24:LEU:HD23	1.96	0.47
27:BT:32:SER:HA	27:BT:49:PRO:HA	1.96	0.47
28:BU:101:LEU:HB3	28:BU:107:ARG:NH2	2.29	0.47
46:CM:3:U:O2	56:CW:17:ARG:NH2	2.47	0.47
46:CM:477:C:H4'	56:CW:120:ARG:HG3	1.95	0.47
55:CV:188:TYR:OH	55:CV:194:GLU:OE2	2.26	0.47
59:CZ:131:ASP:O	59:CZ:135:ILE:HB	2.14	0.47
61:DB:79:ARG:HB2	61:DB:114:THR:HA	1.96	0.47
82:L1:59:PRO:HD3	82:L1:153:SER:HA	1.95	0.47
82:l1:126:PRO:HA	82:l1:130:LYS:HE2	1.96	0.47
1:1:1358:C:H2'	1:1:1359:A:C8	2.49	0.47
1:1:1571:G:H2'	1:1:1572:G:H8	1.80	0.47
1:1:1639:A:H2'	1:1:1640:C:C2	2.49	0.47
1:1:2584:U:H2'	1:1:2585:U:O4'	2.15	0.47
1:1:2690:U:H2'	1:1:2691:U:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3316:U:H3	55:K:110:ARG:CZ	2.26	0.47
2:3:7:G:OP1	7:m:33:ARG:NH1	2.47	0.47
3:4:9:A:H2'	3:4:10:A:H8	1.77	0.47
9:o:135:GLY:HA3	9:o:233:ILE:HB	1.96	0.47
17:w:160:LYS:O	17:w:164:GLN:HG3	2.14	0.47
30:AC:11:ASN:O	30:AC:11:ASN:ND2	2.47	0.47
46:B:1238:U:H2'	46:B:1239:U:H6	1.79	0.47
46:B:1495:U:H2'	46:B:1496:C:C6	2.49	0.47
46:B:1543:A:H1'	46:B:1547:U:OP2	2.13	0.47
50:F:109:LYS:HE3	50:F:114:LEU:HD22	1.95	0.47
79:AR:71:ASP:HB3	79:AR:113:SER:HA	1.95	0.47
1:AS:1020:G:H4'	1:AS:1020:G:OP1	2.14	0.47
1:AS:1338:G:H2'	1:AS:1339:A:O4'	2.14	0.47
1:AS:2376:A:OP1	1:AS:2845:U:H4'	2.14	0.47
30:BW:28:LYS:HG2	30:BW:29:TYR:CE1	2.49	0.47
46:CM:788:A:C8	69:DJ:107:SER:HA	2.50	0.47
46:CM:1219:A:O2'	78:DS:182:TYR:OH	2.21	0.47
46:CM:1573:A:H2'	46:CM:1574:A:O4'	2.13	0.47
48:CO:46:THR:HG23	61:DB:27:ASP:HB2	1.97	0.47
68:DI:58:TYR:OH	69:DJ:20:THR:HA	2.15	0.47
73:DN:12:LYS:HA	73:DN:15:ARG:NH1	2.28	0.47
77:DR:50:THR:HG21	77:DR:55:LYS:NZ	2.29	0.47
78:DS:142:LEU:HB3	78:DS:145:LEU:HG	1.95	0.47
79:DT:40:LYS:HD3	79:DT:66:SER:C	2.40	0.47
82:l1:66:CYS:HB2	82:l1:107:TYR:CG	2.48	0.47
1:1:385:A:H2'	1:1:386:A:C8	2.49	0.47
1:1:498:C:H2'	1:1:499:G:H8	1.79	0.47
1:1:671:U:H2'	1:1:672:G:C8	2.49	0.47
1:1:689:A:N1	3:4:28:C:O2'	2.42	0.47
1:1:2484:U:H2'	1:1:2485:U:C6	2.49	0.47
1:1:2644:G:H1'	13:s:97:SER:HB3	1.96	0.47
1:1:3038:U:H2'	1:1:3039:C:C6	2.49	0.47
1:1:3193:C:H4'	1:1:3194:G:O5'	2.13	0.47
2:3:64:A:N6	12:r:200:LEU:HD21	2.28	0.47
3:4:155:G:H5'	10:p:186:ARG:HD2	1.95	0.47
17:w:2:SER:HB2	34:AG:34:GLY:HA2	1.96	0.47
46:B:810:U:H2'	46:B:811:U:O4'	2.14	0.47
46:B:975:C:H2'	46:B:976:G:O4'	2.15	0.47
46:B:1318:C:H2'	46:B:1319:U:C6	2.50	0.47
46:B:1512:A:H2'	46:B:1513:A:C8	2.50	0.47
1:AS:1152:C:OP2	9:BB:92:LYS:NZ	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:3088:G:H4'	11:BD:69:ARG:HH12	1.79	0.47
1:AS:3285:A:H2'	1:AS:3286:C:H6	1.80	0.47
46:CM:86:A:H5'	71:DL:119:PHE:CE1	2.49	0.47
46:CM:1354:U:C2	46:CM:1355:A:N7	2.83	0.47
47:CN:63:ILE:HG12	68:DI:36:ILE:HG22	1.96	0.47
79:DT:145:LEU:HD11	79:DT:178:TRP:CG	2.49	0.47
82:L1:76:ARG:HH22	82:L1:142:ASP:HB2	1.78	0.47
1:1:297:G:OP2	1:1:297:G:N2	2.30	0.47
1:1:815:U:H2'	1:1:816:A:H8	1.80	0.47
1:1:1249:U:OP1	81:12:137:GLN:NE2	2.48	0.47
1:1:1713:U:H2'	1:1:1714:G:H8	1.79	0.47
1:1:2206:A:H2'	1:1:2207:A:H8	1.76	0.47
1:1:2557:G:H2'	1:1:2557:G:N3	2.30	0.47
5:k:284:ARG:NH2	5:k:295:ALA:O	2.47	0.47
46:B:217:A:N7	46:B:218:A:C8	2.83	0.47
46:B:226:G:H2'	46:B:227:C:C6	2.50	0.47
46:B:391:C:H2'	46:B:392:C:C6	2.49	0.47
46:B:871:U:OP2	48:D:216:LYS:NZ	2.48	0.47
54:J:169:TYR:OH	54:J:175:LYS:HE3	2.15	0.47
1:AS:477:U:O5'	1:AS:477:U:H6	1.97	0.47
1:AS:939:U:H3'	29:BV:13:GLY:HA2	1.96	0.47
1:AS:1225:G:H2'	1:AS:1226:G:H8	1.79	0.47
1:AS:1739:G:H2'	1:AS:1740:G:H8	1.79	0.47
1:AS:2232:U:H2'	1:AS:2239:G:N2	2.29	0.47
1:AS:2785:A:H2'	1:AS:2786:G:O4'	2.15	0.47
3:AU:9:A:H2'	3:AU:10:A:H8	1.79	0.47
11:BD:86:TYR:CZ	11:BD:151:LEU:HB2	2.49	0.47
19:BL:176:ARG:N	29:BV:51:GLY:HA2	2.29	0.47
20:BM:44:LEU:HB3	20:BM:49:THR:HB	1.97	0.47
46:CM:479:A:H2'	46:CM:480:U:C6	2.49	0.47
46:CM:559:G:H2'	46:CM:560:G:H8	1.80	0.47
46:CM:840:A:O2'	46:CM:841:A:H3'	2.14	0.47
46:CM:1774:C:H2'	46:CM:1775:G:H8	1.79	0.47
48:CO:70:LEU:HD23	48:CO:79:HIS:HB3	1.97	0.47
79:DT:82:LEU:HD11	79:DT:123:ILE:HG12	1.97	0.47
82:l1:12:ASN:ND2	82:l1:216:ILE:HD12	2.29	0.47
1:1:705:U:OP2	19:y:168:LYS:NZ	2.40	0.47
1:1:780:A:H2	19:y:69:ARG:HD3	1.80	0.47
1:1:1377:A:H2'	1:1:1378:G:H8	1.80	0.47
1:1:2136:A:O2'	4:j:118:GLU:OE1	2.24	0.47
1:1:2443:G:H5''	1:1:2443:G:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2474:C:H5'	1:1:2475:U:OP2	2.15	0.47
1:1:2694:U:O2'	22:2:88:ARG:O	2.28	0.47
1:1:3240:U:O2'	34:AG:99:ARG:NH1	2.48	0.47
2:3:113:C:H2'	2:3:114:U:O4'	2.14	0.47
5:k:260:VAL:HG11	5:k:266:ARG:HH11	1.80	0.47
9:o:174:PHE:CZ	9:o:195:GLN:HG2	2.50	0.47
10:p:202:THR:O	10:p:203:GLU:HG2	2.15	0.47
13:s:148:ILE:HG23	13:s:152:HIS:HB3	1.96	0.47
45:i:88:PHE:HD2	45:i:91:HIS:CE1	2.33	0.47
46:B:480:U:C2	46:B:481:A:C8	3.03	0.47
46:B:840:A:O2'	46:B:841:A:H3'	2.14	0.47
46:B:1425:C:H2'	46:B:1426:C:H6	1.79	0.47
46:B:1626:C:H2'	46:B:1627:C:O4'	2.15	0.47
46:B:1776:G:OP2	61:Q:127:ARG:NH2	2.37	0.47
48:D:145:ARG:NH2	48:D:151:LYS:O	2.47	0.47
49:E:85:THR:OG1	49:E:88:GLY:O	2.26	0.47
1:AS:1303:G:OP1	17:BJ:60:ARG:NH2	2.47	0.47
1:AS:1921:U:O4	1:AS:2297:U:O2'	2.32	0.47
1:AS:1923:G:N7	44:CK:16:VAL:HG13	2.30	0.47
1:AS:2063:C:H3'	1:AS:2064:A:H8	1.79	0.47
3:AU:37:A:OP2	36:CC:86:ARG:HD2	2.14	0.47
5:AX:106:TRP:HB2	5:AX:133:TYR:CE1	2.50	0.47
9:BB:185:GLU:HG2	9:BB:196:VAL:HG21	1.96	0.47
9:BB:208:PRO:HB3	9:BB:239:GLN:HB3	1.97	0.47
29:BV:95:SER:OG	29:BV:96:ALA:N	2.47	0.47
36:CC:70:TYR:HA	36:CC:73:LYS:HG3	1.97	0.47
46:CM:1332:U:C5	67:DH:57:MET:HE1	2.49	0.47
46:CM:1636:C:H2'	46:CM:1637:U:H6	1.79	0.47
49:CP:171:LYS:HE2	56:CW:57:ARG:NH1	2.30	0.47
50:CQ:172:ALA:HB1	50:CQ:174:ARG:NH1	2.30	0.47
65:DF:36:ARG:HH12	65:DF:105:LEU:HD22	1.80	0.47
79:DT:41:THR:CG2	79:DT:61:SER:HB2	2.45	0.47
79:DT:46:LYS:O	79:DT:56:GLY:HA2	2.15	0.47
79:DT:302:TYR:CE2	79:DT:308:ARG:HD2	2.49	0.47
82:11:205:VAL:HG13	82:11:213:SER:HB3	1.96	0.47
1:1:429:U:H2'	1:1:430:G:C8	2.46	0.47
1:1:859:C:H2'	1:1:860:G:O4'	2.14	0.47
1:1:1256:A:H2'	1:1:1257:G:C8	2.50	0.47
1:1:1258:G:O6	1:1:1260:G:N2	2.47	0.47
1:1:2204:U:H2'	1:1:2205:C:C6	2.49	0.47
1:1:2587:G:H2'	1:1:2588:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2925:U:H2'	1:1:2926:U:H2'	1.97	0.47
1:1:2959:A:H2'	1:1:2960:C:C6	2.49	0.47
1:1:3066:A:H2'	1:1:3067:U:C6	2.49	0.47
1:1:3190:C:C2	1:1:3191:A:C8	3.02	0.47
6:l:181:LYS:O	6:l:185:SER:HB3	2.15	0.47
7:m:40:HIS:CE1	22:2:69:LYS:HA	2.49	0.47
12:r:140:THR:HG21	12:r:148:VAL:HG21	1.96	0.47
16:v:114:ARG:NH2	16:v:157:LYS:HG2	2.30	0.47
46:B:474:U:H2'	77:g:31:GLN:HB2	1.97	0.47
46:B:553:A:H2'	46:B:554:A:C8	2.50	0.47
46:B:670:C:H3'	46:B:671:G:H4'	1.97	0.47
46:B:685:C:H5''	69:Y:119:LYS:HG2	1.96	0.47
46:B:876:A:H2'	46:B:877:G:C8	2.48	0.47
46:B:1132:A:H2'	46:B:1133:C:C6	2.50	0.47
46:B:1399:U:O2'	46:B:1402:G:OP1	2.33	0.47
46:B:1469:A:C2	46:B:1594:G:H1'	2.50	0.47
46:B:1676:A:H2	46:B:1699:G:H22	1.63	0.47
46:B:1739:U:H2'	46:B:1740:A:H8	1.79	0.47
47:C:98:ILE:HG12	47:C:116:LYS:NZ	2.29	0.47
53:I:84:TYR:CE1	53:I:93:LYS:HB2	2.49	0.47
54:J:81:PHE:HB3	54:J:84:ARG:HG3	1.97	0.47
58:N:125:VAL:HG12	58:N:139:VAL:HA	1.97	0.47
71:a:27:VAL:O	71:a:68:LYS:HA	2.15	0.47
1:AS:180:U:H4'	38:CE:75:LYS:CG	2.45	0.47
1:AS:248:U:H2'	1:AS:249:G:H4'	1.96	0.47
1:AS:966:A:OP1	30:BW:18:ARG:HD2	2.15	0.47
1:AS:1151:C:H2'	1:AS:1152:C:H6	1.80	0.47
1:AS:1637:U:O2'	1:AS:1638:A:H3'	2.13	0.47
1:AS:1937:C:OP2	20:BM:74:ARG:HB3	2.15	0.47
1:AS:2391:A:H2'	1:AS:2392:G:C8	2.48	0.47
1:AS:2590:G:OP1	12:BE:116:ARG:HG3	2.15	0.47
1:AS:2915:G:H2'	1:AS:2916:U:O4'	2.15	0.47
1:AS:2972:A:H2'	1:AS:2973:U:C6	2.50	0.47
1:AS:3166:A:C2'	1:AS:3167:G:H5'	2.45	0.47
5:AX:122:TRP:CE2	5:AX:127:LYS:HE3	2.50	0.47
37:CD:95:GLU:O	37:CD:98:ARG:NH1	2.47	0.47
45:CL:120:GLU:HG2	50:CQ:118:ARG:NE	2.30	0.47
46:CM:222:C:H2'	46:CM:223:A:C8	2.50	0.47
46:CM:446:C:OP1	51:CR:29:PRO:HD3	2.14	0.47
46:CM:696:U:C2'	46:CM:697:U:H5'	2.44	0.47
46:CM:897:U:OP1	46:CM:898:G:O2'	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1445:C:OP1	65:DF:126:ARG:NH1	2.46	0.47
46:CM:1546:G:C5	65:DF:134:ARG:HD3	2.50	0.47
62:DC:1:MET:HE1	62:DC:3:ASP:HB3	1.97	0.47
64:DE:93:LEU:HD23	64:DE:93:LEU:H	1.80	0.47
70:DK:107:PHE:CE1	70:DK:120:VAL:HG12	2.50	0.47
78:DS:177:MET:SD	78:DS:180:ARG:NH2	2.87	0.47
82:L1:60:ARG:HE	82:L1:63:MET:HE3	1.78	0.47
82:l1:5:THR:O	82:l1:9:VAL:HG23	2.15	0.47
1:1:745:C:H5''	30:AC:32:LEU:HD12	1.96	0.47
1:1:814:C:H2'	1:1:815:U:O4'	2.15	0.47
1:1:1253:C:N4	1:1:1257:G:H22	2.11	0.47
1:1:1278:G:OP1	80:P0:55:LYS:HE3	2.15	0.47
1:1:2719:A:H2'	1:1:2720:A:C8	2.50	0.47
1:1:3261:A:H2'	1:1:3262:U:C6	2.50	0.47
10:p:261:SER:HB3	48:D:225:LEU:HD23	1.97	0.47
13:s:101:ASN:ND2	13:s:130:VAL:HG13	2.30	0.47
46:B:569:G:H5''	70:Z:114:LYS:HD2	1.96	0.47
46:B:1302:C:O2'	46:B:1386:A:N3	2.42	0.47
46:B:1347:U:H1'	46:B:1348:U:O2	2.15	0.47
46:B:1727:A:H2'	46:B:1728:U:C6	2.50	0.47
46:B:1776:G:OP1	73:c:17:HIS:NE2	2.42	0.47
52:H:48:PHE:CD1	52:H:67:PRO:HB3	2.49	0.47
70:Z:48:HIS:CD2	70:Z:105:ALA:HB2	2.50	0.47
1:AS:211:G:OP2	27:BT:2:ALA:N	2.48	0.47
1:AS:807:U:H2'	1:AS:808:G:C8	2.50	0.47
1:AS:2645:A:H5''	13:BF:95:ASN:HD22	1.80	0.47
3:AU:85:G:N1	27:BT:112:ASP:OD2	2.45	0.47
3:AU:139:U:H2'	3:AU:140:G:H8	1.80	0.47
13:BF:47:GLN:OE1	13:BF:64:LYS:HD3	2.14	0.47
35:CB:25:THR:OG1	35:CB:29:LYS:HG2	2.15	0.47
38:CE:28:HIS:HB3	38:CE:31:LYS:HB2	1.96	0.47
46:CM:184:C:H2'	46:CM:185:G:O4'	2.14	0.47
46:CM:484:G:H2'	46:CM:485:G:C8	2.50	0.47
46:CM:610:U:OP2	70:DK:5:LYS:NZ	2.46	0.47
46:CM:947:C:H2'	46:CM:948:A:O4'	2.15	0.47
62:DC:61:ARG:NH1	62:DC:88:GLU:OE2	2.47	0.47
65:DF:83:ALA:HB1	65:DF:97:ASP:OD2	2.15	0.47
72:DM:64:VAL:HG13	72:DM:68:ARG:HH21	1.79	0.47
1:1:2381:G:N2	85:1:3958:TIX:O06	2.47	0.47
2:3:77:G:H3'	21:0:46:GLN:O	2.15	0.47
7:m:197:LYS:HG2	7:m:202:GLY:HA3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:AE:71:ARG:HH11	32:AE:103:LEU:HD13	1.79	0.47
46:B:1016:U:H4'	46:B:1017:G:OP2	2.13	0.47
46:B:1072:A:H2'	46:B:1073:A:C8	2.50	0.47
46:B:1566:U:H1'	63:S:138:GLN:HG3	1.96	0.47
49:E:133:PRO:HB2	49:E:217:TYR:HE2	1.78	0.47
52:H:63:GLN:HE22	52:H:66:ASN:HB2	1.79	0.47
69:Y:77:PRO:HD2	69:Y:79:PHE:CZ	2.50	0.47
1:AS:1808:G:N7	28:BU:64:LYS:NZ	2.51	0.47
1:AS:1909:A:N3	1:AS:2098:A:H2'	2.29	0.47
1:AS:2734:A:H2'	1:AS:2735:U:H6	1.79	0.47
1:AS:3039:C:OP2	20:BM:62:ARG:NH2	2.48	0.47
2:AT:77:G:N2	2:AT:102:A:OP2	2.33	0.47
15:BH:26:LEU:HD11	15:BH:87:TRP:CG	2.50	0.47
16:BI:101:THR:O	16:BI:105:ARG:HD2	2.15	0.47
40:CG:24:PRO:HG2	40:CG:27:ILE:HD12	1.95	0.47
45:CL:93:ARG:HG2	46:CM:1259:C:N3	2.29	0.47
46:CM:30:G:H2'	46:CM:31:C:C6	2.50	0.47
46:CM:335:G:O2'	55:CV:10:LYS:NZ	2.48	0.47
46:CM:339:A:H2'	46:CM:340:C:C6	2.50	0.47
46:CM:826:U:C2'	46:CM:827:C:H5'	2.43	0.47
46:CM:876:A:H2'	46:CM:877:G:C8	2.48	0.47
46:CM:985:C:H5	46:CM:988:A:H5''	1.79	0.47
46:CM:1161:G:C6	46:CM:1450:G:C6	3.03	0.47
46:CM:1238:U:H2'	46:CM:1239:U:H6	1.79	0.47
48:CO:85:LYS:HB2	48:CO:101:HIS:HB3	1.96	0.47
50:CQ:173:ILE:HG12	50:CQ:186:LYS:HZ3	1.80	0.47
75:DP:60:GLU:H	75:DP:60:GLU:CD	2.22	0.47
82:l1:63:MET:HB2	82:l1:152:LYS:HG2	1.97	0.47
82:l1:212:PRO:HD2	82:l1:214:PHE:CE1	2.50	0.47
1:1:269:G:N2	1:1:295:A:OP2	2.29	0.47
1:1:867:U:H2'	1:1:868:U:C6	2.50	0.47
1:1:1243:U:H2'	1:1:1264:G:O6	2.14	0.47
1:1:1350:G:N1	1:1:1354:C:H5'	2.30	0.47
1:1:1754:G:OP1	23:5:109:GLN:NE2	2.47	0.47
1:1:1834:C:H4'	1:1:1835:A:O4'	2.14	0.47
1:1:2197:A:H2'	1:1:2198:A:H8	1.80	0.47
1:1:2332:C:H2'	1:1:2333:G:O4'	2.14	0.47
3:4:142:C:H2'	3:4:143:U:H6	1.80	0.47
7:m:119:TYR:OH	7:m:135:VAL:HG22	2.15	0.47
7:m:132:THR:HG21	7:m:170:GLY:O	2.14	0.47
11:q:47:LYS:HB2	15:u:5:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:q:134:MET:SD	11:q:146:VAL:HG22	2.54	0.47
46:B:4:C:O2'	56:L:17:ARG:NH2	2.45	0.47
46:B:1445:C:H2'	65:U:138:THR:OG1	2.15	0.47
46:B:1610:C:H2'	46:B:1611:C:C6	2.50	0.47
50:F:12:LEU:HD12	67:W:85:ILE:HG12	1.97	0.47
66:V:30:VAL:HG13	66:V:34:VAL:HG11	1.96	0.47
68:X:30:ALA:O	68:X:60:ARG:NE	2.43	0.47
73:c:3:LYS:NZ	73:c:6:ALA:HA	2.29	0.47
75:e:9:LEU:HA	75:e:55:CYS:HA	1.96	0.47
1:AS:972:U:H2'	1:AS:973:C:O4'	2.15	0.47
1:AS:1023:A:C6	1:AS:1025:G:H1'	2.50	0.47
1:AS:2290:A:OP1	1:AS:2292:U:H5	1.98	0.47
1:AS:2628:A:C8	1:AS:2630:G:C8	3.03	0.47
3:AU:87:G:OP2	36:CC:5:LYS:HD2	2.14	0.47
11:BD:76:ALA:O	11:BD:79:ILE:HG22	2.15	0.47
23:BP:12:VAL:HB	23:BP:68:VAL:O	2.15	0.47
27:BT:5:SER:HB3	27:BT:8:VAL:HG23	1.97	0.47
39:CF:16:ARG:HG3	39:CF:70:PRO:HG3	1.96	0.47
46:CM:154:A:H2'	46:CM:155:A:O4'	2.15	0.47
46:CM:1220:C:H5	78:DS:180:ARG:NE	2.12	0.47
46:CM:1740:A:H2'	46:CM:1741:A:C8	2.50	0.47
70:DK:107:PHE:HE1	70:DK:120:VAL:HG12	1.80	0.47
71:DL:63:GLN:CD	71:DL:68:LYS:HD3	2.39	0.47
79:DT:63:LYS:NZ	79:DT:64:GLY:H	2.13	0.47
82:l:120:ILE:HB	82:l:121:PRO:HD3	1.96	0.47
1:1:981:U:H2'	1:1:982:U:H6	1.79	0.46
1:1:1030:U:H2'	1:1:1031:A:C8	2.50	0.46
1:1:1228:C:C2	1:1:1229:G:C8	3.03	0.46
1:1:1746:A:OP2	39:AL:28:ASN:ND2	2.48	0.46
1:1:2116:A:C4	38:AK:3:LYS:HB3	2.50	0.46
1:1:2429:G:O2'	1:1:2430:G:O4'	2.30	0.46
1:1:2546:U:H5'	1:1:2547:G:O4'	2.14	0.46
1:1:2739:U:H2'	1:1:2740:U:C6	2.51	0.46
3:4:5:U:H2'	3:4:6:U:H6	1.80	0.46
34:AG:20:LYS:HE2	34:AG:20:LYS:HB2	1.58	0.46
45:i:118:GLU:O	45:i:122:THR:N	2.37	0.46
46:B:217:A:N1	46:B:828:U:O2'	2.38	0.46
46:B:1092:G:O2'	46:B:1093:G:H5'	2.15	0.46
46:B:1241:A:H5'	46:B:1242:U:C5	2.51	0.46
46:B:1455:A:H2'	46:B:1456:C:C6	2.50	0.46
48:D:62:LYS:HA	48:D:88:VAL:HG13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:G:63:ALA:O	51:G:67:GLN:HG2	2.15	0.46
59:O:32:LEU:HA	59:O:35:SER:HB3	1.97	0.46
78:h:180:ARG:HA	78:h:190:LEU:O	2.15	0.46
1:AS:2869:A:H5''	41:CH:49:LYS:HB2	1.97	0.46
1:AS:3323:U:H2'	1:AS:3324:A:H8	1.78	0.46
2:AT:27:A:H2'	2:AT:28:C:C6	2.50	0.46
3:AU:140:G:O3'	16:BI:109:ARG:NH1	2.48	0.46
45:CL:70:ASN:OD1	45:CL:70:ASN:N	2.48	0.46
45:CL:159:GLU:OE2	45:CL:163:GLN:NE2	2.35	0.46
46:CM:518:A:O2'	46:CM:519:A:OP1	2.28	0.46
46:CM:520:U:O3'	71:DL:60:PHE:HB2	2.15	0.46
46:CM:1739:U:H2'	46:CM:1740:A:C8	2.49	0.46
52:CS:116:HIS:O	52:CS:120:ILE:HG13	2.15	0.46
53:CT:48:TYR:CD2	53:CT:117:GLY:HA3	2.50	0.46
64:DE:90:ALA:HA	64:DE:95:HIS:CD2	2.50	0.46
80:P0:55:LYS:HD3	80:P0:58:MET:CG	2.45	0.46
1:1:236:A:P	3:4:95:G:H22	2.37	0.46
1:1:1761:U:C6	20:z:43:LYS:HE3	2.50	0.46
1:1:2679:U:H2'	1:1:2680:C:C6	2.49	0.46
1:1:2915:G:H2'	1:1:2916:U:O4'	2.15	0.46
3:4:95:G:N7	38:AK:83:ALA:HB2	2.30	0.46
11:q:10:LEU:HD23	11:q:11:ASP:N	2.30	0.46
26:8:141:TYR:HB3	36:AI:33:VAL:HG13	1.96	0.46
46:B:137:A:O4'	46:B:139:U:H5'	2.15	0.46
46:B:827:C:H5''	46:B:828:U:OP2	2.16	0.46
46:B:857:G:H2'	46:B:858:U:O4'	2.15	0.46
47:C:88:LYS:HD3	47:C:88:LYS:HA	1.76	0.46
1:AS:629:A:H2'	1:AS:630:G:C8	2.50	0.46
1:AS:673:C:O2'	1:AS:677:U:OP1	2.27	0.46
1:AS:813:A:H8	38:CE:15:SER:HG	1.62	0.46
1:AS:943:G:H2'	1:AS:944:C:C6	2.51	0.46
1:AS:1790:U:C2	4:AW:187:HIS:CD2	3.03	0.46
1:AS:2560:U:OP1	10:BC:242:LYS:NZ	2.44	0.46
5:AX:260:VAL:HG11	5:AX:266:ARG:HH11	1.81	0.46
8:BA:70:VAL:HG13	8:BA:160:ALA:HB2	1.96	0.46
45:CL:112:LYS:HG3	45:CL:113:ARG:H	1.79	0.46
46:CM:1:U:H1'	49:CP:174:VAL:HG13	1.97	0.46
46:CM:504:A:H5''	46:CM:505:U:P	2.55	0.46
46:CM:740:A:O2'	46:CM:741:A:OP1	2.32	0.46
46:CM:1276:G:H1	46:CM:1309:G:H22	1.63	0.46
51:CR:11:ARG:NH1	51:CR:21:ASP:O	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:CV:37:LYS:NZ	55:CV:93:THR:HB	2.29	0.46
59:CZ:82:PRO:HB2	59:CZ:83:GLU:H	1.15	0.46
78:DS:160:ARG:NH1	78:DS:176:ASN:H	2.14	0.46
81:12:120:SER:HB2	81:12:131:GLU:CD	2.40	0.46
82:L1:174:MET:HE3	82:L1:178:VAL:HG21	1.96	0.46
82:I1:35:GLN:HA	82:I1:166:ALA:HB1	1.97	0.46
80:p0:76:LEU:HD22	80:p0:79:PHE:CZ	2.50	0.46
1:1:483:U:H2'	1:1:484:U:H6	1.76	0.46
1:1:849:G:OP2	44:AQ:2:THR:HG21	2.14	0.46
1:1:2458:G:H4'	82:I1:102:LYS:NZ	2.29	0.46
1:1:2895:U:H2'	1:1:2896:U:C6	2.51	0.46
1:1:3023:U:C2	1:1:3024:G:C8	3.03	0.46
4:j:77:ILE:CD1	4:j:128:ARG:HB3	2.46	0.46
6:l:4:ARG:HH21	6:l:23:LEU:HD23	1.80	0.46
6:l:156:GLU:HB3	10:BC:119:GLU:O	2.15	0.46
8:n:70:VAL:HG13	8:n:160:ALA:HB2	1.97	0.46
22:2:28:SER:O	22:2:32:LYS:HG3	2.14	0.46
27:9:58:VAL:HA	27:9:104:VAL:HG12	1.97	0.46
46:B:593:G:H2'	46:B:594:C:C6	2.50	0.46
46:B:697:U:H3	46:B:724:G:H1	1.63	0.46
46:B:1474:G:H3'	46:B:1502:A:H61	1.79	0.46
57:M:77:ARG:NE	57:M:86:ILE:HG22	2.30	0.46
57:M:77:ARG:CZ	57:M:86:ILE:HG22	2.45	0.46
59:O:32:LEU:HA	59:O:32:LEU:HD23	1.70	0.46
59:O:74:LEU:HA	78:h:150:VAL:CG1	2.43	0.46
1:AS:173:C:H2'	1:AS:174:C:C6	2.51	0.46
1:AS:185:U:N3	1:AS:229:C:N4	2.41	0.46
1:AS:662:U:H3	1:AS:794:G:H1	1.64	0.46
1:AS:1329:C:C2	1:AS:1330:U:C5	3.03	0.46
1:AS:1945:A:H2'	1:AS:1946:U:C6	2.51	0.46
1:AS:2435:G:H3'	1:AS:2436:A:C5'	2.45	0.46
1:AS:2959:A:H2'	1:AS:2960:C:H6	1.79	0.46
2:AT:84:A:H2'	2:AT:85:G:C8	2.51	0.46
12:BE:47:PRO:HB3	12:BE:171:TRP:CZ2	2.50	0.46
15:BH:20:LEU:HD23	15:BH:21:VAL:N	2.30	0.46
35:CB:58:ARG:CD	35:CB:59:PRO:HD2	2.36	0.46
46:CM:487:C:O2	46:CM:496:G:C2	2.69	0.46
46:CM:690:C:H4'	46:CM:691:U:OP1	2.15	0.46
46:CM:770:C:OP1	46:CM:770:C:H6	1.98	0.46
46:CM:903:U:H2'	46:CM:904:A:H8	1.73	0.46
48:CO:131:ASP:OD1	48:CO:131:ASP:N	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:CP:53:LEU:HA	68:DI:12:TYR:HE1	1.79	0.46
54:CU:30:LEU:HD12	54:CU:34:LEU:HD21	1.97	0.46
82:l1:175:GLU:HB3	82:l1:178:VAL:HG23	1.96	0.46
1:1:179:C:H2'	1:1:180:U:C6	2.50	0.46
1:1:777:G:OP1	19:y:151:ARG:HD2	2.15	0.46
1:1:1023:A:C6	1:1:1025:G:H1'	2.50	0.46
1:1:2186:A:O2'	1:1:2187:U:H5'	2.16	0.46
1:1:3093:U:H1'	1:1:3094:A:H5''	1.97	0.46
2:3:84:A:H2'	2:3:85:G:C8	2.50	0.46
3:4:5:U:H2'	3:4:6:U:C6	2.50	0.46
3:4:63:G:H1	3:4:97:A:H61	1.62	0.46
4:j:70[A]:LYS:HG3	4:j:71:LEU:N	2.30	0.46
5:k:71:GLU:OE2	25:7:1:MET:N	2.44	0.46
5:k:92:TYR:HB2	5:k:157:VAL:HB	1.97	0.46
7:m:150:LEU:HD12	13:s:143:ARG:HG3	1.98	0.46
8:n:39:LEU:HD11	8:n:53:TYR:HB2	1.97	0.46
14:t:2:ALA:HB1	29:AB:33:GLY:O	2.16	0.46
21:0:171:PHE:O	21:0:172:TYR:HB2	2.14	0.46
34:AG:42:LYS:HA	34:AG:45:LEU:HG	1.98	0.46
46:B:258:U:H5	55:K:43:ILE:H	1.64	0.46
46:B:598:U:P	70:Z:108:GLY:HA2	2.56	0.46
46:B:654:G:H3'	46:B:655:U:H6	1.79	0.46
46:B:1143:C:O2'	46:B:1568:C:OP2	2.30	0.46
46:B:1254:U:H5'	46:B:1418:U:OP2	2.14	0.46
46:B:1604:U:H2'	46:B:1605:C:C6	2.51	0.46
60:P:46:THR:OG1	60:P:49:GLN:HG3	2.16	0.46
62:R:80:LEU:HD12	62:R:80:LEU:O	2.15	0.46
75:e:14:LYS:HB3	75:e:29:ARG:HB3	1.97	0.46
79:AR:151:TRP:O	79:AR:171:TRP:N	2.40	0.46
1:AS:269:G:H5''	16:BI:14:LYS:HE2	1.98	0.46
1:AS:659:G:H4'	1:AS:660:U:C6	2.50	0.46
1:AS:867:U:H2'	1:AS:868:U:C6	2.50	0.46
1:AS:983:U:H2'	1:AS:984:U:C6	2.50	0.46
1:AS:1124:U:H2'	1:AS:1125:A:O4'	2.15	0.46
1:AS:1241:A:H3'	1:AS:1242:G:C5'	2.45	0.46
1:AS:1486:A:O2'	38:CE:12:HIS:O	2.27	0.46
1:AS:2871:C:O2'	1:AS:2873:G:OP2	2.30	0.46
1:AS:3135:A:H2'	1:AS:3136:C:C6	2.51	0.46
6:AY:260:ASP:OD1	6:AY:265:SER:HB3	2.15	0.46
7:AZ:40:HIS:CE1	22:BO:69:LYS:HA	2.51	0.46
46:CM:107:C:H2'	46:CM:108:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:125:U:H5''	51:CR:148:ARG:CZ	2.45	0.46
46:CM:378:U:H4'	56:CW:2:PRO:HD2	1.97	0.46
46:CM:507:G:H2'	46:CM:508:G:C8	2.50	0.46
46:CM:698:C:H2'	46:CM:699:U:C6	2.51	0.46
46:CM:839:U:O4	46:CM:840:A:N6	2.48	0.46
46:CM:1529:G:N2	46:CM:1555:C:H1'	2.30	0.46
47:CN:205:ARG:NH2	64:DE:84:TYR:HB3	2.30	0.46
49:CP:93:MET:HG3	49:CP:116:VAL:HG23	1.97	0.46
49:CP:138:TYR:OH	68:DI:3:ASN:HB3	2.16	0.46
66:DG:30:VAL:HG13	66:DG:34:VAL:HG11	1.97	0.46
1:1:712:G:N2	29:AB:72:GLU:OE1	2.47	0.46
1:1:831:G:HO2'	1:1:853:G:H22	1.59	0.46
1:1:875:U:O2'	18:x:131:ARG:HD2	2.16	0.46
1:1:1804:G:OP2	28:AA:133:LYS:NZ	2.47	0.46
1:1:2632:G:OP1	1:1:2722:U:O2'	2.34	0.46
1:1:2700:G:N7	22:2:87:LYS:NZ	2.60	0.46
1:1:2753:U:H2'	1:1:2754:U:C6	2.50	0.46
4:j:117:GLU:OE2	4:j:163:ARG:HB2	2.16	0.46
5:k:260:VAL:HG11	5:k:266:ARG:NH1	2.31	0.46
31:AD:18:LEU:HB3	31:AD:100:SER:HB2	1.97	0.46
46:B:696:U:H5''	46:B:697:U:H5''	1.96	0.46
47:C:18:LEU:HD22	64:T:102:ILE:HG21	1.97	0.46
47:C:77:SER:HB2	47:C:124:THR:HG21	1.98	0.46
55:K:121:LEU:HD13	55:K:166:PHE:CE2	2.50	0.46
79:AR:67:HIS:CG	79:AR:68:ILE:H	2.33	0.46
1:AS:374:A:N3	1:AS:376:G:H5''	2.31	0.46
1:AS:1291:G:H2'	1:AS:1292:C:C6	2.50	0.46
1:AS:2239:G:O2'	1:AS:2241:C:N4	2.48	0.46
1:AS:2407:G:H2'	1:AS:2408:A:H8	1.81	0.46
1:AS:2584:U:H2'	1:AS:2585:U:O4'	2.16	0.46
1:AS:2958:U:C2	1:AS:2959:A:C8	3.03	0.46
4:AW:5:ILE:HG12	4:AW:8:GLN:HG3	1.98	0.46
6:AY:6:GLN:HB2	6:AY:20:GLN:OE1	2.14	0.46
10:BC:82:THR:HG21	10:BC:182:LYS:HE3	1.96	0.46
46:CM:502:U:H2'	46:CM:503:A:H8	1.81	0.46
46:CM:1205:C:OP1	57:CX:48:SER:HB2	2.15	0.46
46:CM:1255:G:OP2	78:DS:122:ARG:NH2	2.49	0.46
57:CX:46:LEU:HD23	57:CX:66:TYR:CG	2.51	0.46
79:DT:29:HIS:CD2	79:DT:32:LEU:HD23	2.51	0.46
80:p0:61:ARG:HG2	80:p0:64:ARG:CG	2.46	0.46
1:1:50:A:C4	1:1:51:A:C8	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:436:A:H2'	1:1:437:G:C8	2.51	0.46
1:1:942:U:H2'	1:1:943:G:H8	1.80	0.46
1:1:1312:C:H5'	1:1:1313:A:C2	2.51	0.46
1:1:1338:G:H2'	1:1:1339:A:O4'	2.15	0.46
1:1:1632:C:H4'	28:AA:74:LEU:O	2.15	0.46
1:1:2330:A:H5''	18:x:83:TRP:O	2.15	0.46
1:1:2946:U:H2'	1:1:2947:U:C6	2.51	0.46
1:1:3228:G:H2'	1:1:3229:G:H8	1.80	0.46
3:4:19:C:H2'	3:4:20:U:C6	2.51	0.46
18:x:14:SER:HA	18:x:150:LEU:O	2.16	0.46
35:AH:16:ARG:HG2	35:AH:37:LYS:HD3	1.97	0.46
36:AI:22:VAL:O	36:AI:26:GLN:HG3	2.16	0.46
46:B:261:C:O2'	46:B:262:G:H5'	2.16	0.46
46:B:400:C:OP1	51:G:3:ARG:NH1	2.49	0.46
46:B:597:A:H2'	46:B:598:U:C6	2.51	0.46
46:B:1167:U:H2'	46:B:1168:A:O3'	2.15	0.46
46:B:1436:U:H2'	46:B:1437:C:C6	2.51	0.46
46:B:1668:A:H2'	46:B:1669:U:H5'	1.96	0.46
47:C:57:ILE:HG23	47:C:177:LEU:HD23	1.97	0.46
63:S:98:GLU:N	79:AR:59:LYS:O	2.29	0.46
79:AR:38:ARG:HB3	79:AR:68:ILE:HG12	1.97	0.46
1:AS:1656:C:H2'	1:AS:1657:G:H8	1.81	0.46
1:AS:3035:C:H2'	1:AS:3036:U:C6	2.50	0.46
3:AU:40:A:H2'	3:AU:41:A:C8	2.51	0.46
7:AZ:40:HIS:CE1	7:AZ:42:ALA:HB3	2.50	0.46
46:CM:12:U:H2'	46:CM:13:C:H6	1.79	0.46
46:CM:82:U:H2'	46:CM:83:G:O4'	2.15	0.46
46:CM:703:U:H2'	46:CM:704:A:N7	2.30	0.46
46:CM:744:U:C2	46:CM:745:A:C8	3.03	0.46
46:CM:977:A:O2'	46:CM:1772:U:O2	2.33	0.46
47:CN:53:THR:OG1	47:CN:161:PRO:HG2	2.16	0.46
48:CO:28:ASP:O	48:CO:29:TRP:HB2	2.15	0.46
79:DT:33:LEU:O	79:DT:45:TRP:HD1	1.99	0.46
82:l1:9:VAL:HB	82:l1:180:VAL:HG13	1.97	0.46
82:l1:95:LYS:HA	82:l1:95:LYS:HD3	1.82	0.46
1:1:72:A:C4	37:AJ:14:ARG:HD2	2.51	0.46
1:1:169:G:H1	1:1:248:U:H3	1.63	0.46
1:1:269:G:OP2	16:v:44:ARG:NH1	2.49	0.46
1:1:289:A:H2'	1:1:290:G:C8	2.49	0.46
1:1:2384:C:H2'	1:1:2385:C:H6	1.79	0.46
1:1:3259:A:H2'	1:1:3260:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:142:C:H4'	16:v:60:VAL:HG21	1.96	0.46
6:l:326:LEU:O	9:o:39:ARG:NH2	2.45	0.46
32:AE:45:THR:HG22	32:AE:47:ASP:N	2.27	0.46
46:B:536:A:H1'	46:B:539:A:C8	2.51	0.46
46:B:1227:A:OP1	62:R:59:LYS:NZ	2.38	0.46
46:B:1242:U:O2	46:B:1242:U:H2'	2.14	0.46
46:B:1498:G:H2'	46:B:1499:G:H8	1.80	0.46
51:G:19:MET:HE2	51:G:108:LYS:HG2	1.97	0.46
51:G:112:HIS:NE2	51:G:238:SER:O	2.49	0.46
51:G:185:GLY:HA2	51:G:189:LEU:HD12	1.96	0.46
54:J:57:PHE:HE1	54:J:89:LEU:HD12	1.79	0.46
62:R:68:GLU:N	62:R:69:PRO:HD3	2.31	0.46
75:e:18:ARG:HD2	75:e:26:THR:HG22	1.96	0.46
1:AS:683:G:OP1	14:BG:39:ARG:NH2	2.49	0.46
1:AS:762:U:H4'	1:AS:763:U:O4'	2.15	0.46
1:AS:786:U:H5''	6:AY:113:LYS:HD3	1.97	0.46
1:AS:1206:U:H5''	11:BD:62:ARG:HD3	1.96	0.46
1:AS:1286:A:H2'	1:AS:1287:A:C8	2.50	0.46
1:AS:1396:U:H2'	1:AS:1397:G:O4'	2.15	0.46
16:BI:67:ARG:HG2	16:BI:127:TYR:CE1	2.51	0.46
16:BI:104:GLU:OE2	16:BI:161:ALA:HA	2.15	0.46
25:BR:80:ARG:HH12	53:CT:10:ASN:C	2.24	0.46
27:BT:47:SER:O	27:BT:122:LYS:HE2	2.16	0.46
27:BT:85:LEU:HD23	27:BT:85:LEU:HA	1.81	0.46
45:CL:112:LYS:C	45:CL:114:GLU:H	2.23	0.46
46:CM:226:G:H2'	46:CM:227:C:O4'	2.15	0.46
46:CM:903:U:H4'	61:DB:13:ARG:HD3	1.97	0.46
46:CM:1307:A:O2'	47:CN:104:PRO:HG2	2.15	0.46
46:CM:1339:G:O6	46:CM:1354:U:C2	2.69	0.46
46:CM:1425:C:H2'	46:CM:1426:C:H6	1.80	0.46
48:CO:115:ARG:HA	48:CO:115:ARG:HD3	1.78	0.46
61:DB:53:TYR:CE2	61:DB:57:LEU:HD11	2.51	0.46
71:DL:74:LEU:HD13	71:DL:76:TYR:CE1	2.51	0.46
1:1:411:U:H2'	1:1:412:G:H8	1.81	0.46
1:1:430:G:H2'	1:1:431:A:C8	2.50	0.46
1:1:546:C:H2'	1:1:547:U:O4'	2.16	0.46
1:1:972:U:H2'	1:1:973:C:O4'	2.15	0.46
1:1:1172:C:H2'	1:1:1173:G:N2	2.30	0.46
1:1:1478:A:H4'	1:1:1479:G:OP2	2.16	0.46
1:1:1689:C:O2'	1:1:1768:U:O2'	2.23	0.46
1:1:1882:A:O2'	5:k:226:PHE:O	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:l:2961:U:O2'	5:k:232:ARG:NH1	2.48	0.46
1:l:3298:G:N2	1:l:3334:G:O2'	2.48	0.46
33:AF:5:VAL:N	33:AF:91:LYS:O	2.48	0.46
45:i:157:GLU:H	45:i:157:GLU:CD	2.24	0.46
46:B:385:A:OP1	55:K:23:LYS:HE3	2.16	0.46
46:B:904:A:H2'	46:B:905:C:C6	2.51	0.46
46:B:945:U:H5'	60:P:55:ARG:CD	2.41	0.46
52:H:148:ARG:HB3	52:H:157:ARG:NH1	2.30	0.46
66:V:84:LYS:HZ2	66:V:86:ARG:HG3	1.81	0.46
67:W:98:THR:O	67:W:102:ILE:HG13	2.16	0.46
73:c:51:ARG:O	73:c:55:GLU:HG3	2.16	0.46
1:AS:178:U:H2'	1:AS:179:C:H6	1.80	0.46
1:AS:206:U:H2'	1:AS:207:C:C6	2.50	0.46
1:AS:859:C:H2'	1:AS:860:G:O4'	2.15	0.46
1:AS:1569:C:H2'	1:AS:1570:A:C8	2.51	0.46
1:AS:3061:C:H2'	1:AS:3062:U:O4'	2.15	0.46
3:AU:156:U:O2'	3:AU:157:U:P	2.74	0.46
12:BE:54:SER:HB2	12:BE:135:ILE:HD11	1.98	0.46
22:BO:97:LYS:HB3	22:BO:97:LYS:HE2	1.69	0.46
24:BQ:42:THR:HG21	24:BQ:50:PRO:HG3	1.98	0.46
45:CL:48:PRO:O	45:CL:50:LYS:N	2.47	0.46
46:CM:218:A:N6	46:CM:827:C:O2	2.46	0.46
46:CM:695:C:H1'	46:CM:696:U:P	2.56	0.46
46:CM:1220:C:H41	78:DS:180:ARG:HH21	1.62	0.46
46:CM:1325:U:O4	63:DD:8:THR:HA	2.16	0.46
53:CT:64:LYS:HB2	53:CT:97:VAL:HG21	1.98	0.46
62:DC:83:MET:HB3	62:DC:116:LEU:HD22	1.98	0.46
64:DE:80:ARG:HA	64:DE:83:GLN:NE2	2.30	0.46
67:DH:81:TYR:HB3	76:DQ:52:PHE:HB3	1.97	0.46
79:DT:259:ILE:HG13	79:DT:268:LEU:HB3	1.98	0.46
82:l:201:VAL:HB	82:l:217:TYR:HE2	1.81	0.46
1:l:337:G:O4'	6:l:49:GLN:NE2	2.49	0.46
1:l:1273:C:H2'	1:l:1274:A:C8	2.48	0.46
1:l:2183:U:O2'	1:l:2184:G:OP1	2.27	0.46
1:l:3234:U:H3	8:n:134:ARG:NH1	2.14	0.46
3:4:69:U:H3	3:4:89:A:H61	1.63	0.46
3:4:75:G:H2'	3:4:76:C:H6	1.81	0.46
3:4:126:A:O2'	3:4:128:U:OP2	2.19	0.46
4:j:70[B]:LYS:HG3	4:j:71:LEU:N	2.31	0.46
18:x:40:LYS:HD2	18:x:113:VAL:HG22	1.98	0.46
19:y:147:ARG:HB3	19:y:150:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AD:101:ASP:OD1	31:AD:101:ASP:N	2.49	0.46
46:B:267:G:H2'	46:B:268:C:C6	2.51	0.46
46:B:700:G:C2	46:B:701:G:C5	3.04	0.46
46:B:1216:U:OP1	78:h:136:LYS:NZ	2.36	0.46
46:B:1709:A:H2'	46:B:1710:G:O4'	2.16	0.46
58:N:66:ILE:HG13	58:N:140:LEU:HD21	1.97	0.46
61:Q:76:ILE:HB	61:Q:110:ILE:HG12	1.98	0.46
65:U:4:VAL:HG12	72:b:78:VAL:HG23	1.97	0.46
79:AR:240:LEU:HD22	79:AR:249:LEU:HD11	1.98	0.46
1:AS:270:U:H2'	1:AS:271:C:H6	1.81	0.46
1:AS:619:A:H2'	1:AS:620:A:N7	2.31	0.46
1:AS:663:A:OP1	16:BI:203:ARG:HD2	2.16	0.46
1:AS:783:G:H2'	1:AS:784:C:H6	1.80	0.46
1:AS:870:U:H5''	1:AS:2922:G:OP1	2.16	0.46
1:AS:1099:A:H62	1:AS:1359:A:H1'	1.79	0.46
1:AS:1231:U:H1'	1:AS:1233:G:OP2	2.16	0.46
1:AS:1264:G:H21	1:AS:1269:A:H62	1.63	0.46
1:AS:2206:A:H2'	1:AS:2207:A:H8	1.80	0.46
1:AS:2370:C:O2'	5:AX:266:ARG:NH2	2.49	0.46
1:AS:2742:G:H5''	43:CJ:79:THR:HG23	1.97	0.46
1:AS:2957:C:H2'	1:AS:2958:U:H6	1.81	0.46
15:BH:23:ASN:HD22	15:BH:23:ASN:C	2.17	0.46
15:BH:66:PRO:HD3	15:BH:77:LYS:HE3	1.98	0.46
21:BN:27:MET:HE2	21:BN:27:MET:HB3	1.83	0.46
22:BO:52:MET:HA	22:BO:95:HIS:CE1	2.51	0.46
33:BZ:33:TRP:HH2	33:BZ:53:GLN:HG2	1.80	0.46
36:CC:22:VAL:O	36:CC:26:GLN:HG3	2.16	0.46
38:CE:69:HIS:O	38:CE:73:ARG:HG3	2.16	0.46
46:CM:561:U:H4'	77:DR:17:GLN:OE1	2.16	0.46
46:CM:1468:C:H5''	46:CM:1508:G:H22	1.79	0.46
52:CS:166:ARG:HB2	75:DP:46:GLY:HA3	1.98	0.46
56:CW:58:ASP:O	56:CW:61:THR:OG1	2.34	0.46
60:DA:89:TYR:CE2	60:DA:150:VAL:HG12	2.51	0.46
65:DF:49:LYS:HA	65:DF:49:LYS:HD3	1.71	0.46
82:L1:3:LYS:HD3	82:L1:3:LYS:HA	1.66	0.46
1:1:514:G:H2'	1:1:516:U:H5'	1.98	0.46
1:1:787:A:H2'	1:1:788:G:H8	1.80	0.46
1:1:1099:A:N3	1:1:1099:A:H2'	2.31	0.46
1:1:1165:A:H4'	9:o:216:LYS:HD2	1.98	0.46
1:1:1255:A:N6	80:P0:53:MET:HE2	2.31	0.46
1:1:1617:A:H2'	1:1:1618:U:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2771:A:H5''	1:1:2772:G:O5'	2.16	0.46
1:1:2873:G:O2'	1:1:2996:A:N1	2.49	0.46
3:4:81:A:H2'	3:4:82:U:C6	2.51	0.46
18:x:13:LYS:HB3	18:x:152:GLU:HB2	1.98	0.46
23:5:16:VAL:HG12	23:5:65:VAL:HG22	1.97	0.46
29:AB:94:SER:HB3	29:AB:121:VAL:HG13	1.97	0.46
46:B:1:U:C2	46:B:3:U:C4	3.03	0.46
46:B:99:C:H2'	46:B:376:A:H4'	1.98	0.46
46:B:267:G:H2'	46:B:268:C:H6	1.80	0.46
46:B:702:G:H1'	46:B:703:U:C1'	2.44	0.46
46:B:1099:G:O2'	46:B:1115:G:O6	2.29	0.46
46:B:1140:G:H2'	46:B:1141:C:C6	2.50	0.46
46:B:1611:C:H2'	46:B:1612:C:H6	1.81	0.46
50:F:46:LYS:HD2	50:F:86:ALA:HB2	1.98	0.46
52:H:200:ASN:CB	52:H:208:SER:HB3	2.45	0.46
53:I:69:HIS:HD2	53:I:73:VAL:HG11	1.81	0.46
1:AS:67:C:N4	1:AS:314:U:O2'	2.47	0.46
1:AS:206:U:H2'	1:AS:207:C:H6	1.80	0.46
1:AS:208:A:H4'	1:AS:210:A:C8	2.50	0.46
1:AS:1029:U:O2'	1:AS:1030:U:OP1	2.27	0.46
1:AS:2627:U:H4'	1:AS:2628:A:O4'	2.16	0.46
1:AS:2655:U:H2'	1:AS:2656:C:H6	1.79	0.46
1:AS:2852:U:H1'	5:AX:250:ALA:HB3	1.98	0.46
1:AS:2912:A:OP2	5:AX:2:SER:N	2.49	0.46
1:AS:2959:A:H2'	1:AS:2960:C:C6	2.50	0.46
1:AS:3314:C:H2'	1:AS:3315:C:C6	2.51	0.46
3:AU:155:G:C5	3:AU:156:U:C4	3.03	0.46
4:AW:30:ARG:HG2	4:AW:74:GLU:HG3	1.98	0.46
46:CM:14:C:H2'	46:CM:15:U:C6	2.50	0.46
46:CM:151:G:N2	53:CT:56:ASN:OD1	2.44	0.46
46:CM:444:A:H5''	51:CR:57:ASN:HD22	1.81	0.46
46:CM:756:A:H4'	56:CW:7:THR:O	2.16	0.46
46:CM:819:G:C5	46:CM:820:U:C5	3.04	0.46
46:CM:1529:G:H5''	66:DG:87:GLY:C	2.41	0.46
46:CM:1669:U:HO2'	46:CM:1670:U:H6	1.64	0.46
48:CO:168:MET:O	48:CO:172:MET:HG3	2.16	0.46
52:CS:57:SER:OG	52:CS:167:ARG:NH2	2.49	0.46
59:CZ:33:ARG:O	59:CZ:34:THR:HG23	2.15	0.46
61:DB:73:ALA:HB2	61:DB:106:ARG:HB2	1.97	0.46
62:DC:81:ARG:HH12	62:DC:122:THR:HG22	1.81	0.46
74:DO:36:LYS:HZ1	74:DO:42:ASN:C	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
79:DT:244:PRO:HD3	79:DT:291:TRP:HB3	1.98	0.46
1:1:117:U:O2	1:1:120:A:H5''	2.16	0.45
1:1:533:G:H2'	1:1:534:G:O4'	2.16	0.45
1:1:795:G:O2'	14:t:18:TRP:NE1	2.46	0.45
1:1:1050:A:H5''	1:1:2609:A:H61	1.81	0.45
1:1:1189:A:H4'	1:1:1294:C:OP1	2.15	0.45
1:1:1705:C:H2'	1:1:1706:C:H6	1.81	0.45
1:1:1852:C:H2'	1:1:1853:C:C6	2.51	0.45
1:1:2367:C:O2'	1:1:3272:A:N1	2.42	0.45
1:1:2469:A:H5'	1:1:2470:C:OP2	2.15	0.45
1:1:3104:C:H2'	1:1:3105:C:C6	2.52	0.45
1:1:3172:U:O4	21:0:159:SER:HB3	2.16	0.45
3:4:131:G:H4'	26:8:93:HIS:ND1	2.31	0.45
4:j:80:GLU:HG3	44:AQ:66:GLY:HA2	1.98	0.45
17:w:35:VAL:HG22	17:w:104:LYS:HB2	1.98	0.45
44:AQ:84:ARG:O	44:AQ:88:GLU:HG2	2.16	0.45
46:B:681:C:H5''	46:B:682:A:OP2	2.15	0.45
46:B:974:U:H2'	46:B:975:C:C6	2.51	0.45
46:B:1042:U:O4	46:B:1045:U:H3'	2.16	0.45
46:B:1571:G:H22	46:B:1598:A:P	2.39	0.45
46:B:1649:G:H2'	46:B:1650:G:C8	2.49	0.45
46:B:1772:U:H2'	46:B:1773:G:H8	1.81	0.45
48:D:58:ALA:HB1	48:D:91:VAL:HG11	1.98	0.45
49:E:138:TYR:CD1	49:E:142:ASN:HA	2.51	0.45
66:V:74:GLY:HA2	66:V:77:ASN:HD22	1.80	0.45
70:Z:70:LYS:HB3	70:Z:93:LEU:HD22	1.98	0.45
1:AS:414:U:H2'	1:AS:415:G:H8	1.82	0.45
1:AS:820:C:H5''	4:AW:21:ARG:HD3	1.97	0.45
1:AS:1478:A:H4'	1:AS:1479:G:OP2	2.16	0.45
1:AS:2455:G:H21	1:AS:2466:A:H2	1.64	0.45
1:AS:2557:G:N3	1:AS:2557:G:H2'	2.32	0.45
1:AS:2832:U:O2	1:AS:2910:G:H4'	2.15	0.45
2:AT:118:A:H5''	7:AZ:253:PHE:CZ	2.51	0.45
3:AU:71:A:N1	3:AU:82:U:O2'	2.44	0.45
18:BK:29:THR:HA	18:BK:32:THR:HG22	1.97	0.45
42:CI:10:VAL:HG11	46:CM:1100:U:H5''	1.98	0.45
46:CM:78:A:H5'	53:CT:154:ARG:O	2.16	0.45
46:CM:533:A:P	56:CW:168:ARG:HH22	2.37	0.45
47:CN:41:ARG:CD	47:CN:47:ILE:HD11	2.46	0.45
50:CQ:139:ILE:HG12	50:CQ:185:ILE:HG22	1.97	0.45
53:CT:220:LYS:HD2	53:CT:223:ARG:HH21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:CU:85:HIS:ND1	54:CU:161:LYS:HG2	2.31	0.45
66:DG:57:ARG:NH2	66:DG:101:ASN:OD1	2.46	0.45
67:DH:27:SER:OG	67:DH:111:VAL:HA	2.16	0.45
75:DP:30:VAL:HG22	75:DP:40:ILE:O	2.16	0.45
76:DQ:29:GLY:O	76:DQ:40:ARG:N	2.44	0.45
79:DT:200:THR:HG21	79:DT:241:ALA:HA	1.98	0.45
1:1:290:G:H2'	1:1:291:C:C6	2.51	0.45
1:1:582:G:H2'	1:1:583:A:C8	2.51	0.45
1:1:2394:U:H2'	1:1:2395:U:C6	2.52	0.45
1:1:2646:A:H5''	13:s:105:GLY:HA3	1.98	0.45
1:1:2919:G:N3	5:k:250:ALA:HB1	2.30	0.45
6:l:36:VAL:HG21	6:l:245:LEU:HD21	1.96	0.45
30:AC:17:HIS:NE2	30:AC:21:ILE:HG13	2.32	0.45
31:AD:26:THR:HB	31:AD:31:SER:HB3	1.98	0.45
42:AO:13:LEU:HD11	46:B:1737:A:O5'	2.16	0.45
46:B:78:A:H2'	46:B:79:C:C6	2.51	0.45
46:B:940:A:OP1	60:P:3:ARG:HD2	2.15	0.45
49:E:233:SER:HB3	49:E:236:GLU:HG3	1.98	0.45
65:U:63:GLN:O	65:U:67:GLU:HG3	2.16	0.45
79:AR:44:LYS:O	79:AR:59:LYS:N	2.48	0.45
1:AS:214:G:OP1	27:BT:12:ARG:NH1	2.46	0.45
1:AS:242:C:O2'	1:AS:243:G:H8	1.99	0.45
1:AS:371:G:N1	1:AS:374:A:OP2	2.43	0.45
1:AS:479:C:H2'	1:AS:480:G:H8	1.81	0.45
1:AS:925:A:H2'	1:AS:926:U:C6	2.52	0.45
1:AS:1586:G:O2'	1:AS:1793:A:N6	2.49	0.45
1:AS:1691:U:O2'	1:AS:1745:A:N1	2.40	0.45
84:AS:3401:3K5:H16	84:AS:3401:3K5:H39	1.98	0.45
3:AU:10:A:H2'	3:AU:11:C:C6	2.51	0.45
17:BJ:29:LEU:HD22	17:BJ:95:ARG:CZ	2.47	0.45
20:BM:161:ALA:O	20:BM:165:ARG:HG3	2.15	0.45
23:BP:27:VAL:HG12	23:BP:92:ILE:HD13	1.98	0.45
23:BP:86:TYR:O	23:BP:90:ASN:ND2	2.49	0.45
46:CM:261:C:O2'	46:CM:262:G:H5'	2.16	0.45
46:CM:432:G:OP1	70:DK:78:LYS:HA	2.16	0.45
46:CM:857:G:N2	46:CM:1032:G:H4'	2.30	0.45
46:CM:1074:U:O2'	46:CM:1078:A:N1	2.44	0.45
46:CM:1396:A:O2'	46:CM:1397:A:OP1	2.28	0.45
59:CZ:62:LEU:HD22	59:CZ:75:VAL:HG21	1.98	0.45
62:DC:49:LEU:HB3	62:DC:50:ASP:H	1.52	0.45
68:DI:36:ILE:HG13	68:DI:51:ILE:HB	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:DS:168:CYS:SG	78:DS:186:CYS:HB3	2.55	0.45
82:L1:96:ASN:C	82:L1:98:LYS:H	2.23	0.45
80:p0:87:ILE:HG21	80:p0:96:ILE:HD12	1.97	0.45
1:1:173:C:H2'	1:1:174:C:H6	1.81	0.45
1:1:868:U:H2'	1:1:869:C:C6	2.51	0.45
1:1:2183:U:O4	1:1:2216:G:N1	2.49	0.45
1:1:2233:A:HO2'	46:B:1744:G:HO2'	1.35	0.45
1:1:3027:U:H1'	1:1:3029:U:OP2	2.16	0.45
6:l:12:VAL:CG2	10:BC:119:GLU:HB3	2.47	0.45
8:n:39:LEU:HD13	8:n:83:VAL:HG11	1.97	0.45
11:q:49:ASN:ND2	11:q:51:ARG:H	2.15	0.45
15:u:87:TRP:CE2	15:u:93:ALA:HB2	2.50	0.45
46:B:74:U:O2'	46:B:76:A:OP1	2.31	0.45
46:B:494:G:H2'	46:B:495:G:O4'	2.16	0.45
46:B:741:A:H5'	51:G:16:SER:OG	2.15	0.45
46:B:824:U:OP2	58:N:27:ALA:HA	2.17	0.45
46:B:1595:U:O3'	63:S:72:GLY:HA3	2.16	0.45
46:B:1654:A:H2'	46:B:1655:G:C8	2.51	0.45
48:D:59:ASP:OD1	48:D:60:GLY:N	2.48	0.45
57:M:54:TYR:CE1	57:M:75:PHE:HB2	2.51	0.45
1:AS:1747:G:H5'	39:CF:26:LYS:HE2	1.98	0.45
1:AS:2269:A:H2'	1:AS:2270:U:C6	2.51	0.45
1:AS:2965:G:H2'	1:AS:3114:A:N6	2.31	0.45
1:AS:3207:G:N2	1:AS:3210:A:OP2	2.49	0.45
5:AX:159:ARG:HG2	5:AX:182:GLN:HA	1.98	0.45
5:AX:260:VAL:HG11	5:AX:266:ARG:NH1	2.32	0.45
8:BA:39:LEU:HB3	8:BA:83:VAL:CG1	2.46	0.45
13:BF:25:GLU:OE2	13:BF:29:ARG:HD3	2.17	0.45
16:BI:65:ARG:HG2	16:BI:127:TYR:CD1	2.51	0.45
46:CM:283:G:H2'	46:CM:284:C:C6	2.51	0.45
46:CM:510:A:O2'	56:CW:133:HIS:NE2	2.44	0.45
46:CM:1062:C:OP1	73:DN:13:LYS:NZ	2.48	0.45
46:CM:1200:C:OP1	78:DS:134:LYS:NZ	2.40	0.45
46:CM:1230:G:N2	46:CM:1235:U:O4	2.44	0.45
46:CM:1375:C:O2'	64:DE:52:GLY:HA3	2.15	0.45
46:CM:1577:G:OP1	66:DG:91:HIS:HB2	2.16	0.45
46:CM:1584:A:C8	76:DQ:14:PHE:HB2	2.51	0.45
56:CW:63:ASP:OD1	56:CW:64:GLU:N	2.50	0.45
57:CX:4:PRO:HG2	57:CX:7:ASP:HB2	1.98	0.45
62:DC:81:ARG:NH1	62:DC:98:ASN:HA	2.31	0.45
79:DT:75:SER:OG	79:DT:76:ALA:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:l1:26:ARG:HH21	82:l1:29:LEU:C	2.24	0.45
1:1:212:A:O4'	27:9:2:ALA:HA	2.16	0.45
1:1:640:U:OP1	29:AB:22:ILE:HG23	2.16	0.45
1:1:846:U:H2'	1:1:847:C:H6	1.81	0.45
1:1:1124:U:H2'	1:1:1125:A:O4'	2.17	0.45
1:1:1140:U:OP2	33:AF:44:ARG:NH1	2.46	0.45
1:1:1141:G:OP1	33:AF:45:ARG:HD2	2.17	0.45
1:1:1651:G:H5''	35:AH:58:ARG:NH1	2.32	0.45
1:1:1900:C:H2'	1:1:1901:G:O4'	2.17	0.45
1:1:2130:A:H2'	1:1:2131:U:C6	2.51	0.45
1:1:2869:A:OP2	41:AN:48:LYS:NZ	2.43	0.45
1:1:3192:A:O3'	15:u:126:LYS:NZ	2.42	0.45
2:3:13:A:C2	7:m:21:ARG:HB2	2.47	0.45
5:k:292:ALA:HB1	5:k:295:ALA:HB3	1.98	0.45
6:l:301:ARG:NH2	19:y:38:ARG:O	2.50	0.45
11:q:41:ILE:HG22	11:q:43:VAL:HG13	1.98	0.45
22:2:45:ASN:OD1	22:2:47:SER:OG	2.27	0.45
32:AE:61:ARG:HH12	32:AE:67:GLU:CD	2.24	0.45
34:AG:68:TRP:O	34:AG:86:LYS:HG2	2.16	0.45
38:AK:84:LYS:HE3	38:AK:84:LYS:HB2	1.76	0.45
43:AP:16:GLU:H	43:AP:16:GLU:CD	2.23	0.45
46:B:1457:A:H2	46:B:1460:G:N3	2.15	0.45
51:G:192:VAL:HG23	51:G:244:GLY:HA3	1.99	0.45
59:O:39:ASP:O	59:O:40:GLY:C	2.59	0.45
66:V:108:LEU:HD12	66:V:108:LEU:HA	1.84	0.45
79:AR:156:ARG:HD3	79:AR:156:ARG:HA	1.85	0.45
1:AS:89:C:OP1	29:BV:59:ARG:NH1	2.49	0.45
1:AS:139:U:H2'	1:AS:140:C:C6	2.51	0.45
1:AS:716:G:H3'	1:AS:717:A:H5''	1.97	0.45
1:AS:1937:C:H2'	1:AS:1938:U:C6	2.51	0.45
1:AS:2771:A:H5''	1:AS:2772:G:O5'	2.16	0.45
1:AS:2814:U:H2'	1:AS:2814:U:O2	2.15	0.45
1:AS:2967:A:H2'	1:AS:2968:U:O4'	2.16	0.45
1:AS:3038:U:H2'	1:AS:3039:C:H6	1.81	0.45
5:AX:256:HIS:HA	5:AX:257:PRO:C	2.42	0.45
10:BC:35:PHE:CD1	10:BC:43:PRO:HD3	2.52	0.45
46:CM:557:C:OP1	77:DR:59:SER:OG	2.24	0.45
46:CM:1012:A:OP1	46:CM:1776:G:O2'	2.34	0.45
55:CV:158:ILE:HA	58:CY:24:LYS:HD3	1.99	0.45
1:1:222:U:OP1	1:1:224:C:N4	2.40	0.45
1:1:258:U:H2'	1:1:259:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:684:G:C2	1:1:693:C:C2	3.04	0.45
1:1:892:A:H5'	4:j:183:GLY:CA	2.47	0.45
1:1:1612:U:H2'	1:1:1613:G:H8	1.80	0.45
1:1:1797:U:H2'	1:1:1798:C:C6	2.52	0.45
1:1:3010:U:H5''	5:k:62:ARG:HG2	1.97	0.45
1:1:3236:G:O2'	8:n:107:ARG:NH1	2.49	0.45
1:1:3314:C:H2'	1:1:3315:C:C6	2.52	0.45
3:4:10:A:H2'	3:4:11:C:C6	2.52	0.45
18:x:122:ALA:HA	18:x:145:HIS:CE1	2.51	0.45
24:6:13:MET:HE2	24:6:53:ALA:HB1	1.98	0.45
46:B:330:U:H5''	55:K:31:ARG:NH1	2.32	0.45
46:B:1206:A:H2'	46:B:1207:C:O4'	2.17	0.45
49:E:138:TYR:O	69:Y:98:GLN:NE2	2.39	0.45
79:AR:104:PHE:CE2	79:AR:139:GLY:HA2	2.51	0.45
1:AS:299:G:C8	37:CD:30:GLY:HA3	2.51	0.45
1:AS:348:A:N3	1:AS:352:A:O2'	2.50	0.45
1:AS:481:G:H2'	1:AS:481:G:N3	2.31	0.45
1:AS:716:G:O2'	1:AS:717:A:OP1	2.29	0.45
1:AS:883:G:H2'	1:AS:884:A:C8	2.52	0.45
1:AS:903:G:H2'	1:AS:922:A:H62	1.82	0.45
1:AS:2739:U:H2'	1:AS:2740:U:H6	1.82	0.45
1:AS:2796:G:H2'	1:AS:2797:C:H6	1.81	0.45
2:AT:26:C:H2'	2:AT:27:A:O4'	2.16	0.45
3:AU:83:U:O2	27:BT:51:ARG:NH2	2.50	0.45
17:BJ:131:LYS:HB3	17:BJ:134:ARG:HG2	1.98	0.45
34:CA:42:LYS:HA	34:CA:45:LEU:HG	1.97	0.45
42:CI:11:ARG:NH2	46:CM:1762:U:OP1	2.39	0.45
44:CK:41:PHE:CG	44:CK:62:LYS:HD2	2.51	0.45
46:CM:269:A:C2	46:CM:283:G:C6	3.04	0.45
46:CM:932:U:H2'	46:CM:933:A:C8	2.50	0.45
46:CM:1315:G:H2'	46:CM:1316:A:H8	1.81	0.45
52:CS:63:GLN:HE22	52:CS:66:ASN:HB2	1.82	0.45
52:CS:116:HIS:CD2	72:DM:98:GLN:HB3	2.50	0.45
53:CT:149:LYS:HB3	53:CT:149:LYS:HE2	1.68	0.45
54:CU:14:GLU:HG2	54:CU:42:ILE:HG13	1.98	0.45
60:DA:45:LEU:HD22	60:DA:49:GLN:CD	2.41	0.45
80:P0:56:ASN:ND2	80:P0:82:GLY:O	2.41	0.45
81:12:159:GLU:HG3	81:12:160:ILE:HG12	1.98	0.45
1:1:6:C:H2'	1:1:7:C:C6	2.52	0.45
1:1:88:G:H21	1:1:281:G:C4'	2.30	0.45
1:1:406:G:H1'	3:4:16:G:N2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:593:G:C8	1:1:607:G:C6	3.04	0.45
1:1:725:G:O6	1:1:738:G:O2'	2.34	0.45
1:1:729:C:H3'	1:1:730:A:H5''	1.99	0.45
1:1:817:U:H2'	1:1:818:G:H8	1.81	0.45
1:1:1721:C:H2'	1:1:1722:C:C6	2.51	0.45
1:1:1944:G:H2'	1:1:1945:A:H8	1.81	0.45
1:1:2108:G:O4'	1:1:2122:A:H4'	2.15	0.45
1:1:2434:A:N1	1:1:2464:A:N6	2.65	0.45
1:1:2492:U:H5'	10:p:69:ARG:HG3	1.98	0.45
4:j:242:ARG:NH2	4:j:243:THR:O	2.50	0.45
9:o:115:VAL:HG11	9:o:125:ILE:HD11	1.98	0.45
11:q:10:LEU:HD21	11:q:79:ILE:CD1	2.46	0.45
16:v:53:TYR:HB2	16:v:133:ILE:HD13	1.99	0.45
46:B:327:G:H5''	55:K:98:LYS:HB3	1.99	0.45
46:B:1477:U:H4'	46:B:1478:A:H5'	1.98	0.45
46:B:1610:C:H2'	46:B:1611:C:H6	1.80	0.45
51:G:31:PRO:HD2	51:G:38:LEU:HD11	1.99	0.45
52:H:57:SER:HA	75:e:53:ILE:HB	1.99	0.45
58:N:78:THR:HG23	58:N:119:GLU:HG2	1.98	0.45
62:R:18:LYS:N	65:U:92:GLN:O	2.39	0.45
69:Y:41:MET:HG2	69:Y:129:VAL:HG21	1.99	0.45
71:a:63:GLN:CD	71:a:68:LYS:HD3	2.42	0.45
78:h:178:LYS:HB3	78:h:179:ASP:H	1.48	0.45
1:AS:1591:U:O2'	1:AS:1602:U:O2	2.34	0.45
1:AS:2116:A:C4	38:CE:3:LYS:HB3	2.52	0.45
1:AS:2332:C:H2'	1:AS:2333:G:O4'	2.17	0.45
1:AS:2428:G:H1	1:AS:2475:U:H3	1.65	0.45
1:AS:2449:U:H4'	1:AS:2450:U:OP1	2.17	0.45
1:AS:2919:G:C2	5:AX:250:ALA:HB1	2.52	0.45
1:AS:3269:C:O2	5:AX:334:ARG:HG2	2.17	0.45
11:BD:1:MET:HE3	21:BN:139:TYR:HD2	1.82	0.45
20:BM:38:ARG:O	20:BM:42:ARG:HG3	2.16	0.45
28:BU:50:PRO:HD3	28:BU:68:VAL:HG22	1.99	0.45
35:CB:57:LEU:HB2	35:CB:62:TYR:HE1	1.80	0.45
46:CM:94:U:H2'	46:CM:95:G:O4'	2.16	0.45
46:CM:445:U:H2'	46:CM:446:C:O4'	2.17	0.45
46:CM:565:A:H5''	70:DK:70:LYS:NZ	2.31	0.45
46:CM:1555:C:H4'	46:CM:1556:A:O5'	2.17	0.45
46:CM:1602:C:H5''	46:CM:1603:G:O5'	2.17	0.45
48:CO:53:GLY:O	48:CO:55:LYS:N	2.42	0.45
51:CR:36:HIS:CG	51:CR:85:GLY:HA3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:DK:29:TYR:HA	70:DK:32:ARG:HH12	1.82	0.45
1:1:1011:C:O5'	1:1:1011:C:H6	2.00	0.45
1:1:2545:C:O2'	1:1:2547:G:H1'	2.17	0.45
1:1:2871:C:N3	11:q:173:ARG:NH2	2.64	0.45
3:4:97:A:OP1	36:AI:63:ARG:NH2	2.50	0.45
20:z:176:ARG:NH2	46:B:838:G:OP2	2.46	0.45
34:AG:9:VAL:HB	34:AG:100:ILE:HB	1.98	0.45
46:B:221:U:C4	46:B:823:G:N2	2.85	0.45
46:B:1302:C:H2'	46:B:1303:G:O4'	2.16	0.45
58:N:124:THR:HB	58:N:141:LYS:HB3	1.99	0.45
59:O:47:GLU:HG2	59:O:50:LYS:HE2	1.98	0.45
66:V:57:ARG:NH2	66:V:101:ASN:OD1	2.42	0.45
70:Z:59:ILE:HG23	77:g:4:VAL:HG22	1.99	0.45
72:b:65:LEU:O	72:b:69:LEU:HB2	2.16	0.45
1:AS:122:A:C6	1:AS:149:A:C5	3.04	0.45
1:AS:283:G:O6	1:AS:304:G:H1'	2.17	0.45
1:AS:438:A:C8	33:BZ:3:THR:HG23	2.52	0.45
1:AS:638:U:OP1	29:BV:21:ARG:NH1	2.48	0.45
1:AS:992:A:N3	2:AT:80:G:O2'	2.49	0.45
1:AS:1255:A:H5'	80:p0:53:MET:O	2.16	0.45
1:AS:1632:C:H1'	28:BU:76:ASN:HB2	1.99	0.45
1:AS:1705:C:H2'	1:AS:1706:C:H6	1.80	0.45
1:AS:1767:G:H2'	1:AS:1768:U:O4'	2.16	0.45
1:AS:2130:A:H2'	1:AS:2131:U:C6	2.52	0.45
1:AS:2449:U:H2'	1:AS:2452:G:H21	1.82	0.45
1:AS:2514:G:N7	1:AS:2515:G:N1	2.65	0.45
1:AS:3298:G:N7	25:BR:35:LYS:NZ	2.63	0.45
1:AS:3336:G:H2'	1:AS:3337:A:C8	2.51	0.45
21:BN:171:PHE:O	21:BN:172:TYR:HB2	2.16	0.45
27:BT:27:ARG:NH1	27:BT:76:LEU:HA	2.32	0.45
46:CM:627:U:C2	46:CM:628:A:C8	3.04	0.45
46:CM:690:C:H2'	46:CM:691:U:H6	1.78	0.45
46:CM:845:U:O4'	54:CU:110:ARG:HG3	2.17	0.45
46:CM:1148:A:H2'	46:CM:1149:G:O4'	2.16	0.45
46:CM:1623:C:O2	46:CM:1752:A:N6	2.50	0.45
46:CM:1678:G:H3'	46:CM:1679:A:H8	1.81	0.45
59:CZ:93:ASP:OD1	59:CZ:93:ASP:N	2.49	0.45
79:DT:40:LYS:HG2	79:DT:67:HIS:O	2.17	0.45
79:DT:88:ARG:HA	79:DT:111:VAL:HG23	1.99	0.45
1:1:541:U:N3	1:1:543:C:O2'	2.44	0.45
1:1:1012:U:H4'	1:1:1013:U:H4'	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2339:A:H2'	1:1:2340:C:H6	1.82	0.45
1:1:2397:A:H2'	1:1:2398:C:C6	2.51	0.45
1:1:3197:G:H2'	1:1:3198:C:C6	2.52	0.45
2:3:7:G:OP1	7:m:33:ARG:HD2	2.17	0.45
6:l:155:ASN:O	6:l:158:GLU:HB2	2.17	0.45
6:l:296:VAL:O	6:l:300:VAL:HG13	2.16	0.45
7:m:41:LYS:HD3	7:m:41:LYS:HA	1.80	0.45
19:y:90:ASP:O	19:y:113:ARG:NH1	2.50	0.45
22:2:44:ALA:HB2	22:2:53:PRO:HG2	1.98	0.45
46:B:384:G:H2'	46:B:385:A:C8	2.52	0.45
46:B:700:G:H2'	46:B:701:G:H8	1.82	0.45
46:B:1183:G:OP1	46:B:1184:G:O2'	2.29	0.45
67:W:22:ARG:NE	67:W:91:ASP:OD1	2.50	0.45
1:AS:489:G:C2	1:AS:490:G:C8	3.05	0.45
1:AS:1363:G:OP1	33:BZ:46:ARG:NH2	2.50	0.45
1:AS:1882:A:O2'	5:AX:226:PHE:O	2.31	0.45
1:AS:2079:C:HO2'	1:AS:2080:U:H6	1.62	0.45
1:AS:2787:G:N2	1:AS:2790:U:O2	2.46	0.45
1:AS:2857:C:O2'	1:AS:2858:U:H5'	2.17	0.45
1:AS:2957:C:H2'	1:AS:2958:U:C6	2.51	0.45
1:AS:3315:C:O2'	1:AS:3316:U:O5'	2.29	0.45
4:AW:47:GLN:HG2	4:AW:49:ILE:HG23	1.98	0.45
7:AZ:48:LYS:HG2	7:AZ:145:PHE:HE2	1.82	0.45
42:CI:9:ARG:HH12	46:CM:1630:U:P	2.40	0.45
46:CM:1062:C:H2'	46:CM:1063:C:H6	1.81	0.45
46:CM:1105:U:H2'	46:CM:1106:C:H6	1.81	0.45
46:CM:1239:U:OP1	59:CZ:50:LYS:NZ	2.49	0.45
46:CM:1342:A:H3'	46:CM:1343:G:H8	1.81	0.45
46:CM:1396:A:HO2'	46:CM:1397:A:P	2.39	0.45
59:CZ:132:GLU:OE1	59:CZ:132:GLU:N	2.47	0.45
77:DR:49:LEU:HD22	77:DR:54:ARG:HG2	1.97	0.45
82:L1:115:VAL:O	82:L1:119:GLN:HG2	2.16	0.45
1:1:130:U:H2'	1:1:131:C:C6	2.52	0.45
1:1:726:G:H5''	19:y:43:PRO:HB2	1.98	0.45
1:1:1165:A:H2'	1:1:1166:A:C8	2.52	0.45
1:1:1199:A:N3	1:1:2827:U:O2'	2.47	0.45
1:1:1250:C:H2'	1:1:1251:C:H6	1.81	0.45
1:1:1313:A:O2'	1:1:1314:A:H3'	2.17	0.45
1:1:1830:U:OP2	40:AM:10:LYS:NZ	2.35	0.45
1:1:2260:U:O2	1:1:2288:U:H4'	2.17	0.45
1:1:2520:A:H1'	1:1:2521:C:C5	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2957:C:H2'	1:1:2958:U:C6	2.52	0.45
6:l:171:LYS:HA	6:l:176:HIS:HB2	1.98	0.45
6:l:303:ALA:HB2	19:y:39:ARG:HH12	1.81	0.45
19:y:78:GLU:OE1	19:y:78:GLU:N	2.50	0.45
26:8:43:SER:O	26:8:43:SER:OG	2.32	0.45
35:AH:109:GLN:OE1	35:AH:113:LYS:NZ	2.50	0.45
46:B:94:U:H2'	46:B:95:G:O4'	2.17	0.45
46:B:151:G:C6	46:B:160:A:C6	3.05	0.45
46:B:167:A:H8	46:B:167:A:OP2	2.00	0.45
46:B:489:C:N4	46:B:490:U:O2	2.49	0.45
46:B:671:G:H5'	46:B:672:U:OP2	2.17	0.45
46:B:885:A:H2'	46:B:886:G:H8	1.82	0.45
46:B:1335:U:H5'	63:S:67:LYS:NZ	2.31	0.45
46:B:1472:G:N2	46:B:1580:A:OP1	2.37	0.45
46:B:1675:U:O2'	46:B:1700:G:O6	2.34	0.45
51:G:45:VAL:HA	51:G:61:VAL:HG21	1.99	0.45
52:H:42:LEU:HD12	52:H:69:PHE:O	2.17	0.45
52:H:122:HIS:HB2	52:H:129:PRO:HG3	1.98	0.45
59:O:96:LEU:HD12	59:O:100:TRP:CZ3	2.51	0.45
1:AS:412:G:H5'	18:BK:26:PHE:HZ	1.82	0.45
1:AS:624:U:H2'	1:AS:625:C:C6	2.52	0.45
1:AS:624:U:H2'	1:AS:625:C:H6	1.82	0.45
1:AS:1021:A:C5	1:AS:1022:A:H1'	2.51	0.45
1:AS:2384:C:H2'	1:AS:2385:C:H6	1.82	0.45
1:AS:2872:A:N3	1:AS:2997:C:O2'	2.42	0.45
1:AS:3056:C:H2'	1:AS:3057:G:O4'	2.17	0.45
1:AS:3166:A:H2'	1:AS:3167:G:H8	1.82	0.45
10:BC:162:GLU:OE2	16:BI:22:LEU:HD13	2.16	0.45
10:BC:215:LEU:HD23	10:BC:215:LEU:HA	1.82	0.45
21:BN:44:PHE:HE1	21:BN:122:HIS:ND1	2.15	0.45
40:CG:20:ASN:OD1	40:CG:42:ARG:HG2	2.17	0.45
46:CM:703:U:OP2	53:CT:234:LEU:HD13	2.17	0.45
46:CM:885:A:H2'	46:CM:886:G:H8	1.81	0.45
46:CM:1337:C:H2'	46:CM:1338:U:O4'	2.16	0.45
46:CM:1649:G:H2'	46:CM:1650:G:C8	2.51	0.45
53:CT:229:LYS:O	53:CT:233:SER:OG	2.33	0.45
63:DD:4:GLN:HG2	63:DD:95:TYR:CE1	2.52	0.45
72:DM:46:LYS:NZ	72:DM:69:LEU:O	2.40	0.45
74:DO:38:GLN:HB2	74:DO:76:GLY:O	2.17	0.45
79:DT:88:ARG:HG2	79:DT:109:GLY:C	2.42	0.45
82:L1:194:LEU:HD13	82:L1:200:ASN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:976:A:N6	1:1:1100:G:O2'	2.39	0.45
1:1:1208:A:O3'	21:0:92:LYS:NZ	2.49	0.45
1:1:1226:G:H4'	80:P0:34:SER:HA	1.99	0.45
1:1:1240:A:H5''	1:1:1241:A:N7	2.32	0.45
1:1:1377:A:OP1	6:l:198:ARG:NE	2.41	0.45
1:1:1562:G:C4	1:1:1563:A:H1'	2.52	0.45
1:1:2478:A:N3	1:1:2478:A:H2'	2.32	0.45
1:1:2666:A:H2'	1:1:2667:A:C8	2.51	0.45
1:1:3302:G:H2'	1:1:3303:C:C6	2.52	0.45
12:r:150:GLU:O	12:r:154:ARG:HG3	2.17	0.45
15:u:19:VAL:HG11	15:u:55:ILE:HD12	1.98	0.45
24:6:13:MET:HE1	24:6:54:ALA:HB3	1.99	0.45
24:6:36:VAL:HG22	24:6:58:VAL:HG11	1.99	0.45
32:AE:61:ARG:HB2	32:AE:65:GLY:HA3	1.99	0.45
41:AN:3:GLU:HG3	41:AN:6:LEU:H	1.82	0.45
44:AQ:49:ARG:HB2	44:AQ:55:TRP:CZ3	2.52	0.45
46:B:530:U:OP1	71:a:64:PHE:HA	2.17	0.45
46:B:1341:U:H2'	46:B:1342:A:H8	1.82	0.45
46:B:1469:A:H2	46:B:1594:G:H1'	1.82	0.45
56:L:31:ALA:HB2	56:L:42:ILE:HD11	1.99	0.45
1:AS:169:G:N1	1:AS:249:G:H1'	2.32	0.45
1:AS:868:U:H2'	1:AS:869:C:C6	2.52	0.45
1:AS:1692:A:H2'	1:AS:1693:A:H8	1.81	0.45
1:AS:2210:A:N3	1:AS:2406:U:O2'	2.45	0.45
1:AS:2484:U:H2'	1:AS:2485:U:C6	2.52	0.45
1:AS:3199:G:H2'	1:AS:3200:C:C6	2.52	0.45
2:AT:7:G:OP1	7:AZ:33:ARG:NH1	2.50	0.45
3:AU:75:G:H2'	3:AU:76:C:C6	2.52	0.45
7:AZ:83:LEU:HD13	7:AZ:88:ILE:HD12	1.99	0.45
7:AZ:95:TRP:HD1	7:AZ:158:ARG:HA	1.82	0.45
12:BE:31:ILE:HA	12:BE:66:GLU:OE1	2.16	0.45
17:BJ:53:LEU:HD23	17:BJ:53:LEU:HA	1.84	0.45
31:BX:59:GLU:OE1	31:BX:71:TYR:OH	2.34	0.45
42:CI:1:MET:N	46:CM:1628:C:O3'	2.49	0.45
46:CM:586:U:P	77:DR:26:LYS:HZ1	2.40	0.45
46:CM:850:A:OP1	69:DJ:28:ARG:NH2	2.50	0.45
46:CM:946:U:C2	46:CM:947:C:C5	3.05	0.45
46:CM:1205:C:H5'	57:CX:51:SER:HB3	1.99	0.45
46:CM:1345:A:N1	46:CM:1349:G:C6	2.85	0.45
51:CR:176:ASP:OD1	51:CR:177:THR:N	2.47	0.45
54:CU:169:TYR:CE2	54:CU:175:LYS:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:DC:83:MET:HB3	62:DC:116:LEU:HD13	1.98	0.45
70:DK:103:LEU:HD22	70:DK:126:LYS:NZ	2.32	0.45
77:DR:20:LYS:NZ	77:DR:21:VAL:O	2.50	0.45
82:L1:26:ARG:HB3	82:L1:27:ASN:H	1.64	0.45
1:1:149:A:C4	1:1:150:A:C8	3.05	0.44
1:1:486:C:H2'	1:1:487:C:C6	2.52	0.44
1:1:1233:G:H1	1:1:1247:A:H61	0.65	0.44
1:1:2455:G:O2'	1:1:2456:C:OP1	2.30	0.44
1:1:3038:U:H2'	1:1:3039:C:H6	1.82	0.44
1:1:3047:G:H5''	32:AE:61:ARG:O	2.18	0.44
14:t:83:VAL:HG23	14:t:85:ILE:HG13	1.98	0.44
21:0:99:ARG:NH1	21:0:126:VAL:O	2.48	0.44
21:0:154:HIS:HA	21:0:170:THR:HB	1.98	0.44
46:B:151:G:O6	71:a:128:ARG:NH1	2.49	0.44
46:B:382:G:H2'	46:B:383:A:C8	2.52	0.44
46:B:1248:G:H2'	46:B:1249:G:O4'	2.17	0.44
46:B:1298:A:N3	46:B:1300:U:H5'	2.32	0.44
46:B:1419:G:O2'	76:f:24:CYS:SG	2.67	0.44
46:B:1553:U:H5''	65:U:39:GLY:H	1.83	0.44
47:C:10:THR:HG23	47:C:13:ASP:H	1.82	0.44
54:J:92:ARG:HH12	54:J:120:LYS:HB3	1.80	0.44
61:Q:98:ARG:HD2	73:c:49:ALA:HB2	1.98	0.44
1:AS:413:U:H2'	1:AS:414:U:H6	1.82	0.44
1:AS:640:U:OP1	29:BV:22:ILE:HG23	2.17	0.44
1:AS:718:A:H5''	19:BL:69:ARG:HH12	1.81	0.44
1:AS:739:C:N3	19:BL:141:ARG:NH2	2.65	0.44
1:AS:2583:U:H2'	1:AS:2584:U:H6	1.82	0.44
1:AS:3067:U:H2'	1:AS:3068:C:C6	2.51	0.44
6:AY:262:VAL:HA	6:AY:271:ILE:HG12	1.98	0.44
11:BD:48:ILE:HG22	11:BD:49:ASN:HD22	1.82	0.44
20:BM:134:HIS:CD2	20:BM:136:ARG:HB3	2.52	0.44
45:CL:82:LYS:HG3	45:CL:83:HIS:N	2.31	0.44
46:CM:1706:A:H2'	46:CM:1707:G:O4'	2.17	0.44
53:CT:28:TYR:CZ	53:CT:104:GLN:HG3	2.52	0.44
57:CX:73:VAL:HG21	57:CX:91:ARG:NH1	2.32	0.44
57:CX:77:ARG:NH1	57:CX:86:ILE:O	2.48	0.44
61:DB:55:ALA:HB1	61:DB:96:ALA:HB2	1.99	0.44
65:DF:77:THR:HG23	65:DF:86:LEU:HD11	1.98	0.44
69:DJ:28:ARG:HD2	69:DJ:60:LYS:HE2	1.99	0.44
1:1:283:G:O6	1:1:304:G:H1'	2.17	0.44
1:1:394:G:N2	1:1:396:A:H3'	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:445:A:C2	1:1:446:U:C2	3.04	0.44
1:1:544:U:H5'	1:1:546:C:H5''	1.99	0.44
1:1:629:A:H2'	1:1:630:G:H8	1.82	0.44
1:1:1895:G:O2'	1:1:2312:U:O4	2.27	0.44
1:1:2176:A:C2	1:1:2177:G:C8	3.05	0.44
1:1:2404:U:H2'	1:1:2405:U:H6	1.83	0.44
1:1:2615:A:OP2	22:2:3:LYS:HE2	2.17	0.44
3:4:40:A:H2'	3:4:41:A:C8	2.52	0.44
20:z:72:ALA:O	20:z:74:ARG:NH1	2.50	0.44
28:AA:27:LYS:HE3	28:AA:97:THR:HG22	1.99	0.44
40:AM:18:LYS:HG2	40:AM:21:ARG:NH2	2.32	0.44
46:B:23:G:O2'	46:B:366:U:OP1	2.35	0.44
46:B:484:G:H2'	46:B:485:G:C8	2.52	0.44
46:B:671:G:C5'	46:B:672:U:H2'	2.45	0.44
46:B:935:C:H2'	46:B:936:A:C8	2.52	0.44
46:B:1344:C:OP1	66:V:134:ARG:NH2	2.50	0.44
46:B:1345:A:N1	46:B:1349:G:C6	2.86	0.44
46:B:1606:C:O3'	52:H:152:SER:OG	2.36	0.44
46:B:1706:A:H2'	46:B:1707:G:O4'	2.18	0.44
57:M:46:LEU:HD23	57:M:66:TYR:CG	2.52	0.44
61:Q:13:ARG:N	61:Q:24:HIS:O	2.46	0.44
61:Q:73:ALA:HB2	61:Q:106:ARG:HB2	2.00	0.44
63:S:25:LYS:H	63:S:25:LYS:HG2	1.60	0.44
70:Z:63:GLN:OE1	70:Z:64:PRO:HA	2.17	0.44
75:e:35:ASP:O	75:e:37:SER:N	2.49	0.44
1:AS:816:A:H2'	1:AS:817:U:C6	2.53	0.44
1:AS:1042:A:H2'	1:AS:1045:C:C5	2.52	0.44
1:AS:1217:A:H62	80:p0:9:VAL:HG13	1.83	0.44
1:AS:1558:G:H5'	1:AS:1559:C:OP2	2.18	0.44
1:AS:1617:A:H2'	1:AS:1618:U:H6	1.81	0.44
1:AS:3281:A:C6	5:AX:124:LYS:HG2	2.52	0.44
14:BG:127:ASP:OD1	14:BG:128:LYS:N	2.37	0.44
15:BH:14:GLU:HG2	15:BH:17:ARG:CG	2.45	0.44
26:BS:67:ILE:HD12	26:BS:121:LYS:HG3	1.98	0.44
32:BY:95:VAL:HG12	32:BY:97:VAL:HG13	1.99	0.44
46:CM:59:C:H5''	46:CM:449:G:N2	2.33	0.44
46:CM:366:U:H2'	46:CM:367:A:O4'	2.17	0.44
46:CM:524:A:P	71:DL:93:ARG:HH21	2.39	0.44
46:CM:854:A:H61	46:CM:943:U:H5	1.65	0.44
46:CM:1187:A:N6	46:CM:1443:C:O5'	2.50	0.44
50:CQ:77:ARG:HB2	57:CX:22:VAL:HG11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:CR:129:VAL:HG22	51:CR:139:VAL:HG22	2.00	0.44
52:CS:58:LEU:HD22	52:CS:168:VAL:HG23	1.99	0.44
53:CT:57:ASP:O	53:CT:107:SER:OG	2.19	0.44
62:DC:18:LYS:HB2	62:DC:36:LEU:HD12	2.00	0.44
64:DE:81:LYS:N	64:DE:83:GLN:OE1	2.50	0.44
70:DK:59:ILE:HD12	70:DK:71:CYS:SG	2.57	0.44
80:P0:55:LYS:HB2	80:P0:55:LYS:HE3	1.72	0.44
80:P0:80:ILE:C	80:P0:81:LYS:HD2	2.41	0.44
82:L1:181:ASN:O	82:L1:185:MET:HG3	2.17	0.44
82:l1:156:LYS:HG2	82:l1:157:PHE:H	1.82	0.44
82:l1:179:LEU:HB3	82:l1:180:VAL:H	1.52	0.44
1:1:561:U:H2'	1:1:562:C:C6	2.52	0.44
1:1:1125:A:H2'	1:1:1126:A:C8	2.52	0.44
1:1:3013:U:H2'	1:1:3014:U:C6	2.53	0.44
22:2:80:VAL:O	22:2:83:ARG:NH1	2.50	0.44
46:B:30:G:H2'	46:B:31:C:H6	1.80	0.44
46:B:63:G:O2'	46:B:168:U:OP1	2.35	0.44
46:B:857:G:N2	46:B:1032:G:H4'	2.31	0.44
46:B:1199:U:O2'	76:f:3:HIS:ND1	2.50	0.44
53:I:1:MET:HE2	53:I:106:LEU:O	2.17	0.44
54:J:25:GLU:CD	54:J:35:ARG:HH22	2.26	0.44
65:U:50:ALA:HB2	65:U:72:ILE:HD12	1.99	0.44
74:d:36:LYS:HZ1	74:d:43:ILE:HD13	1.82	0.44
1:AS:364:G:OP1	6:AY:61:THR:HG23	2.17	0.44
1:AS:589:G:H22	1:AS:610:U:P	2.39	0.44
1:AS:925:A:O2'	38:CE:49:TRP:O	2.34	0.44
1:AS:1239:G:O2'	1:AS:1240:A:H5'	2.17	0.44
1:AS:2084:A:H2'	1:AS:2085:A:H8	1.82	0.44
1:AS:2117:A:C4	38:CE:3:LYS:HE2	2.52	0.44
1:AS:3172:U:C4	21:BN:159:SER:HB2	2.52	0.44
1:AS:3199:G:H2'	1:AS:3200:C:H6	1.83	0.44
10:BC:108:GLU:OE1	10:BC:108:GLU:N	2.51	0.44
12:BE:4:ARG:NH1	12:BE:99:ILE:HG13	2.32	0.44
19:BL:8:LYS:HB3	19:BL:11:VAL:HG21	1.99	0.44
33:BZ:112:LYS:HE2	33:BZ:116:LEU:HD11	1.99	0.44
36:CC:31:LEU:HD22	36:CC:41:LEU:HD21	1.99	0.44
46:CM:415:A:H5'	46:CM:416:G:C4	2.53	0.44
46:CM:723:G:H2'	46:CM:724:G:O4'	2.17	0.44
46:CM:724:G:C4	46:CM:725:A:C8	3.05	0.44
46:CM:810:U:H2'	46:CM:811:U:O4'	2.18	0.44
46:CM:849:U:O2	74:DO:21:LEU:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:1248:G:H2'	46:CM:1249:G:O4'	2.17	0.44
46:CM:1335:U:H2'	46:CM:1336:G:H8	1.79	0.44
48:CO:23:PRO:O	48:CO:27:LYS:NZ	2.50	0.44
51:CR:181:VAL:HG11	51:CR:225:VAL:HG13	1.99	0.44
53:CT:126:ASP:OD1	53:CT:127:THR:N	2.50	0.44
63:DD:76:GLN:O	63:DD:80:ILE:HG13	2.17	0.44
81:12:105:PRO:O	81:12:108:GLU:HG2	2.17	0.44
82:l1:118:LYS:HB3	82:l1:118:LYS:HE3	1.80	0.44
1:1:130:U:H2'	1:1:131:C:H6	1.83	0.44
1:1:599:U:H6	1:1:600:U:C5	2.35	0.44
1:1:952:U:H2'	1:1:953:C:C6	2.52	0.44
1:1:989:G:N3	1:1:2609:A:H2'	2.31	0.44
1:1:1153:G:O2'	1:1:1165:A:N3	2.42	0.44
1:1:2079:C:O2'	1:1:2080:U:H6	2.00	0.44
1:1:2115:U:C6	1:1:2119:U:C4	3.05	0.44
1:1:2333:G:OP1	18:x:141:SER:OG	2.33	0.44
1:1:2367:C:H2'	1:1:2368:A:C8	2.53	0.44
1:1:2658:A:H2'	1:1:2659:G:O4'	2.16	0.44
1:1:3005:A:H2'	1:1:3006:C:H6	1.82	0.44
1:1:3313:G:H2'	1:1:3314:C:C6	2.53	0.44
7:m:187:ALA:O	7:m:189:GLU:N	2.47	0.44
8:n:44:GLY:O	8:n:47:ARG:NH1	2.43	0.44
18:x:153:GLU:HG3	18:x:155:GLU:HG3	1.99	0.44
21:0:44:PHE:O	21:0:48:LEU:HD12	2.18	0.44
27:9:71:ASN:ND2	27:9:83:ASP:HA	2.33	0.44
46:B:191:U:H4'	46:B:192:U:H5'	1.99	0.44
46:B:415:A:H5'	46:B:416:G:C4	2.53	0.44
46:B:872:A:H2'	46:B:873:U:H6	1.83	0.44
49:E:44:LYS:HA	49:E:44:LYS:HD3	1.80	0.44
51:G:59:ARG:HH12	71:a:87:PRO:HG3	1.81	0.44
53:I:64:LYS:HB2	53:I:97:VAL:HG21	1.99	0.44
54:J:59:PRO:HG2	54:J:62:SER:HB3	1.99	0.44
70:Z:130:VAL:HG21	70:Z:143:PRO:HD3	1.99	0.44
1:AS:157:G:H2'	1:AS:158:A:H8	1.82	0.44
1:AS:179:C:H2'	1:AS:180:U:C6	2.51	0.44
1:AS:1231:U:O3'	1:AS:1232:G:H3'	2.17	0.44
1:AS:1807:G:H2'	1:AS:1808:G:O4'	2.17	0.44
1:AS:2649:G:H2'	1:AS:2649:G:N3	2.31	0.44
3:AU:126:A:O2'	3:AU:128:U:OP2	2.27	0.44
6:AY:11:SER:OG	6:AY:15:GLU:OE1	2.34	0.44
8:BA:59:ASP:HB2	8:BA:102:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:BG:143:VAL:HG13	14:BG:147:PHE:HD2	1.83	0.44
16:BI:56:LYS:HE3	16:BI:56:LYS:HB3	1.85	0.44
46:CM:273:C:H2'	46:CM:274:C:O4'	2.17	0.44
46:CM:426:A:N3	46:CM:438:U:O2'	2.35	0.44
46:CM:584:G:H2'	46:CM:585:C:H6	1.83	0.44
46:CM:931:U:H2'	46:CM:932:U:C6	2.52	0.44
46:CM:1102:U:H2'	46:CM:1103:G:C8	2.53	0.44
46:CM:1308:C:H2'	46:CM:1309:G:O4'	2.17	0.44
46:CM:1500:G:H1'	46:CM:1505:C:O2	2.17	0.44
54:CU:60:PRO:N	54:CU:61:PRO:HD2	2.33	0.44
82:L1:116:LEU:HD23	82:L1:119:GLN:HB2	1.98	0.44
80:p0:12:PHE:HZ	80:p0:16:ARG:HH21	1.64	0.44
80:p0:33:VAL:CG2	80:p0:37:GLN:HB3	2.35	0.44
1:1:216:U:H4'	27:9:100:HIS:CD2	2.52	0.44
1:1:656:G:N2	6:l:94:MET:HB2	2.32	0.44
1:1:699:G:H2'	1:1:700:C:C6	2.53	0.44
1:1:1021:A:C2	1:1:1022:A:H1'	2.53	0.44
1:1:1591:U:C2	1:1:1592:C:C5	3.06	0.44
1:1:1616:U:H2'	1:1:1617:A:C8	2.53	0.44
1:1:1721:C:H2'	1:1:1722:C:H6	1.82	0.44
1:1:2646:A:C2	13:s:124:GLY:HA3	2.52	0.44
1:1:2796:G:H2'	1:1:2797:C:H6	1.82	0.44
1:1:3061:C:H2'	1:1:3062:U:O4'	2.17	0.44
1:1:3240:U:H5''	34:AG:68:TRP:HZ2	1.83	0.44
1:1:3320:U:H5''	1:1:3321:G:OP1	2.18	0.44
19:y:76:ALA:HA	19:y:79:LYS:HG3	1.99	0.44
22:2:90:ASN:O	22:2:91:LEU:HD23	2.17	0.44
27:9:109:LEU:HD22	27:9:115:ARG:NH2	2.32	0.44
45:i:65:LYS:HB3	62:R:119:PHE:O	2.18	0.44
46:B:122:U:C2'	46:B:123:G:H5''	2.44	0.44
46:B:757:G:OP1	51:G:22:LYS:NZ	2.33	0.44
46:B:875:C:H2'	46:B:876:A:C8	2.53	0.44
1:AS:680:U:H5''	1:AS:681:U:H5	1.83	0.44
1:AS:988:A:O2'	1:AS:989:G:H5'	2.17	0.44
1:AS:1568:U:C4	1:AS:1569:C:H1'	2.53	0.44
1:AS:1656:C:H2'	1:AS:1657:G:C8	2.53	0.44
1:AS:2504:C:H2'	1:AS:2505:G:H8	1.83	0.44
1:AS:2687:A:HO2'	43:CJ:8:ARG:HH22	1.59	0.44
1:AS:3179:U:H2'	15:BH:114:MET:HE1	2.00	0.44
3:AU:78:G:H2'	3:AU:79:A:N3	2.33	0.44
30:BW:28:LYS:HG2	30:BW:29:TYR:CD1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BX:11:ASN:O	31:BX:14:SER:OG	2.34	0.44
40:CG:49:LEU:C	40:CG:51:ILE:H	2.25	0.44
46:CM:133:U:H4'	46:CM:134:A:OP2	2.11	0.44
46:CM:528:C:O2	71:DL:61:ARG:NH1	2.30	0.44
46:CM:820:U:C2	46:CM:821:U:C5	3.06	0.44
46:CM:871:U:H2'	46:CM:872:A:H8	1.83	0.44
52:CS:57:SER:HB2	75:DP:53:ILE:O	2.17	0.44
54:CU:29:ASP:OD1	54:CU:30:LEU:N	2.49	0.44
59:CZ:106:LEU:HD23	59:CZ:112:ALA:HB2	1.98	0.44
64:DE:18:GLU:HA	64:DE:71:PHE:HB3	2.00	0.44
82:L1:174:MET:HB3	82:L1:178:VAL:HB	1.99	0.44
82:l1:6:SER:O	82:l1:10:ARG:HG3	2.18	0.44
82:l1:26:ARG:NH2	82:l1:28:PHE:O	2.50	0.44
82:l1:93:LEU:CG	82:l1:94:ASN:H	2.30	0.44
1:l:694:C:OP2	6:l:120:ARG:NH2	2.45	0.44
1:l:755:U:H2'	1:l:756:G:O4'	2.18	0.44
1:l:1237:U:H2'	1:l:1239:G:OP2	2.16	0.44
1:l:2136:A:O4'	1:l:2138:G:C8	2.71	0.44
1:l:2655:U:H2'	1:l:2656:C:H6	1.81	0.44
1:l:2734:A:H2'	1:l:2735:U:H6	1.81	0.44
1:l:2855:U:H2'	1:l:2856:C:C6	2.53	0.44
1:l:3196:U:H2'	1:l:3197:G:C8	2.48	0.44
14:t:59:ARG:NH1	14:t:66:ASN:O	2.45	0.44
24:6:75:PRO:HG2	24:6:103:VAL:O	2.17	0.44
46:B:404:U:H2'	46:B:405:A:C8	2.53	0.44
46:B:470:U:O2'	46:B:754:A:N3	2.43	0.44
46:B:873:U:O2	46:B:973:A:O2'	2.36	0.44
46:B:1161:G:C6	46:B:1450:G:C6	3.06	0.44
46:B:1654:A:H2'	46:B:1655:G:H8	1.83	0.44
47:C:84:ARG:NE	64:T:82:ASP:OD1	2.49	0.44
50:F:196:ASN:O	50:F:201:ARG:NH1	2.51	0.44
57:M:14:TYR:CD2	57:M:21:VAL:HG22	2.50	0.44
59:O:105:GLN:HG3	59:O:113:ARG:CD	2.47	0.44
60:P:25:TRP:CE3	74:d:82:LYS:HE3	2.52	0.44
72:b:36:ALA:HB1	72:b:38:HIS:CE1	2.52	0.44
77:g:43:ARG:HG2	77:g:54:ARG:NH2	2.32	0.44
1:AS:186:A:H2'	1:AS:187:U:C6	2.51	0.44
1:AS:2345:A:H2'	1:AS:2346:A:H8	1.82	0.44
1:AS:2753:U:H2'	1:AS:2754:U:C6	2.52	0.44
1:AS:3005:A:H2'	1:AS:3006:C:H6	1.83	0.44
1:AS:3079:U:H2'	1:AS:3080:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AU:27:U:H2'	3:AU:28:C:H6	1.83	0.44
6:AY:54:ALA:HB3	6:AY:57:ALA:HB2	1.99	0.44
16:BI:177:GLY:O	16:BI:184:LYS:NZ	2.51	0.44
21:BN:66:GLU:HB2	21:BN:98:THR:HG23	1.98	0.44
46:CM:1039:U:H2'	46:CM:1040:U:C6	2.53	0.44
46:CM:1064:U:H2'	46:CM:1065:U:H6	1.82	0.44
46:CM:1527:G:OP2	65:DF:40:ARG:NH2	2.51	0.44
59:CZ:54:LYS:HA	78:DS:170:ALA:HB3	2.00	0.44
64:DE:27:ASP:CG	79:DT:38:ARG:HH22	2.21	0.44
66:DG:103:LYS:HA	66:DG:103:LYS:HD3	1.78	0.44
71:DL:56:SER:HB3	71:DL:74:LEU:CD1	2.47	0.44
73:DN:12:LYS:HB2	73:DN:33:ASP:OD2	2.18	0.44
1:1:111:U:C2	1:1:320:G:C2	3.06	0.44
1:1:157:G:H2'	1:1:158:A:H8	1.82	0.44
1:1:1012:U:C4'	1:1:1013:U:H4'	2.48	0.44
1:1:1239:G:C2'	1:1:1240:A:H5'	2.48	0.44
1:1:1606:G:H2'	1:1:1607:G:O4'	2.18	0.44
1:1:1724:G:N3	1:1:1724:G:H5'	2.32	0.44
1:1:2957:C:H2'	1:1:2958:U:H6	1.81	0.44
1:1:3184:G:H4'	1:1:3185:G:H5'	2.00	0.44
13:s:91:LEU:O	13:s:172:LEU:N	2.34	0.44
13:s:110:ILE:HG21	13:s:116:TYR:HD2	1.82	0.44
13:s:141:ARG:O	13:s:145:ARG:NE	2.46	0.44
15:u:14:GLU:HG2	15:u:17:ARG:CG	2.45	0.44
31:AD:77:ASN:ND2	44:AQ:43:GLY:O	2.41	0.44
36:AI:3:GLY:HA3	36:AI:50:ASN:OD1	2.18	0.44
46:B:283:G:H2'	46:B:284:C:C6	2.53	0.44
46:B:404:U:H2'	46:B:405:A:H8	1.83	0.44
46:B:736:G:H2'	46:B:737:A:C8	2.53	0.44
46:B:761:G:N2	46:B:769:U:H1'	2.33	0.44
46:B:918:A:OP1	73:c:70:LYS:NZ	2.46	0.44
49:E:173:ILE:HG21	49:E:180:LYS:HA	1.99	0.44
62:R:77:LYS:HD2	62:R:102:PHE:CZ	2.53	0.44
64:T:77:GLU:O	64:T:80:ARG:NH1	2.51	0.44
65:U:6:GLN:OE1	65:U:6:GLN:N	2.50	0.44
79:AR:235:ALA:HB3	79:AR:253:THR:HB	2.00	0.44
1:AS:4:G:C6	3:AU:155:G:O6	2.71	0.44
1:AS:166:U:H2'	1:AS:167:U:H6	1.83	0.44
1:AS:290:G:H2'	1:AS:291:C:C6	2.53	0.44
1:AS:911:A:H8	1:AS:2114:C:O2'	2.00	0.44
1:AS:2415:G:C6	1:AS:2489:A:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:2502:A:H1'	1:AS:2503:G:C8	2.53	0.44
29:BV:90:TYR:O	29:BV:94:SER:HB2	2.18	0.44
45:CL:90:ARG:HG3	46:CM:1624:C:N3	2.33	0.44
46:CM:261:C:H4'	46:CM:290:U:H5'	1.99	0.44
46:CM:806:A:OP1	46:CM:806:A:H3'	2.18	0.44
46:CM:1323:C:H1'	46:CM:1396:A:C5	2.53	0.44
46:CM:1512:A:H5'	66:DG:93:HIS:HB2	2.00	0.44
48:CO:53:GLY:C	48:CO:55:LYS:H	2.24	0.44
61:DB:27:ASP:OD1	61:DB:30:GLY:N	2.48	0.44
62:DC:29:PRO:HG2	62:DC:32:GLU:HG2	1.99	0.44
69:DJ:8:ALA:HB2	69:DJ:74:VAL:HG21	2.00	0.44
82:l1:93:LEU:HD22	82:l1:99:LEU:HD13	1.99	0.44
80:p0:64:ARG:HA	80:p0:64:ARG:HD2	1.86	0.44
1:1:94:A:H5''	29:AB:34:LYS:HB2	1.99	0.44
1:1:150:A:C5	1:1:151:U:C5	3.05	0.44
1:1:856:G:N7	4:j:181:LYS:HB3	2.33	0.44
1:1:948:A:H4'	1:1:964:G:H21	1.83	0.44
1:1:1474:C:H2'	1:1:1475:U:C6	2.53	0.44
1:1:1621:A:H4'	1:1:1639:A:C5	2.53	0.44
1:1:2972:A:H2'	1:1:2973:U:C6	2.52	0.44
1:1:3206:G:OP2	5:k:153:LYS:NZ	2.37	0.44
1:1:3316:U:H3	55:K:110:ARG:HH12	1.66	0.44
3:4:7:U:H2'	3:4:8:C:C6	2.53	0.44
3:4:23:U:OP1	27:9:16:ARG:NH1	2.50	0.44
17:w:11:ASP:HB2	17:w:118:ARG:HB3	1.98	0.44
20:z:159:ALA:HB1	20:z:163:ARG:HH22	1.81	0.44
46:B:221:U:O4	46:B:823:G:N2	2.50	0.44
46:B:600:U:H2'	46:B:601:U:C6	2.53	0.44
46:B:809:G:H2'	46:B:810:U:C6	2.53	0.44
46:B:1152:G:N2	63:S:138:GLN:OE1	2.51	0.44
50:F:106:LEU:HD21	50:F:139:ILE:HD11	2.00	0.44
51:G:99:PHE:HE1	51:G:113:ARG:HG2	1.82	0.44
57:M:70:ASP:OD1	57:M:71:GLU:HG3	2.18	0.44
62:R:1:MET:HB2	65:U:18:LEU:H	1.82	0.44
71:a:57:VAL:HB	71:a:60:PHE:HE2	1.83	0.44
1:AS:25:A:H4'	1:AS:329:U:H2'	2.00	0.44
1:AS:96:U:H2'	1:AS:97:G:C8	2.52	0.44
1:AS:2650:A:H8	45:CL:56:SER:OG	2.01	0.44
1:AS:2680:C:H2'	1:AS:2681:C:H6	1.83	0.44
1:AS:2814:U:OP1	1:AS:2816:C:N4	2.50	0.44
1:AS:2956:C:H2'	1:AS:2957:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:BQ:89:ASP:OD1	24:BQ:91:VAL:HG12	2.18	0.44
33:BZ:98:ALA:HB3	33:BZ:101:VAL:HG23	1.99	0.44
45:CL:114:GLU:OE2	50:CQ:117:ARG:NH2	2.51	0.44
46:CM:191:U:H4'	46:CM:192:U:H5'	2.00	0.44
46:CM:201:U:H3'	46:CM:202:G:H5'	1.99	0.44
46:CM:415:A:H5'	46:CM:416:G:C5	2.52	0.44
46:CM:1519:U:OP2	72:DM:77:ARG:HD2	2.18	0.44
46:CM:1709:A:H2'	46:CM:1710:G:O4'	2.17	0.44
61:DB:19:ASN:C	61:DB:50:SER:HB3	2.43	0.44
65:DF:6:GLN:OE1	65:DF:6:GLN:N	2.51	0.44
73:DN:87:ARG:NH2	73:DN:91:ASP:O	2.50	0.44
82:L1:5:THR:O	82:L1:9:VAL:HG23	2.17	0.44
1:1:62:A:H5''	16:v:174:ILE:HG21	2.00	0.44
1:1:2424:U:OP1	37:AJ:97:ARG:NH2	2.50	0.44
1:1:3056:C:H2'	1:1:3057:G:O4'	2.18	0.44
1:1:3122:A:OP1	5:k:132:LYS:HB2	2.18	0.44
5:k:214:MET:HE2	5:k:350:ALA:HA	1.98	0.44
8:n:59:ASP:HB2	8:n:102:VAL:HG22	2.00	0.44
11:q:89:LYS:HB2	11:q:183:GLU:HB3	2.00	0.44
21:0:27:MET:HE2	21:0:27:MET:HB3	1.82	0.44
24:6:38:ALA:O	24:6:58:VAL:HG13	2.17	0.44
33:AF:80:VAL:CG1	33:AF:112:LYS:HD2	2.48	0.44
48:D:26:ARG:HA	48:D:50:ARG:NH1	2.33	0.44
48:D:70:LEU:HD23	48:D:82:ARG:HD3	1.99	0.44
53:I:85:ARG:O	53:I:87:ARG:NH1	2.51	0.44
55:K:81:VAL:HG22	55:K:102:VAL:HG12	2.00	0.44
59:O:105:GLN:H	59:O:105:GLN:HG2	1.61	0.44
62:R:125:PRO:HB3	65:U:129:TRP:CH2	2.53	0.44
68:X:4:ASP:OD1	68:X:5:LYS:N	2.51	0.44
1:AS:1075:A:H4'	7:AZ:140:ARG:O	2.18	0.44
1:AS:1241:A:H3'	1:AS:1242:G:H5''	2.00	0.44
1:AS:2236:U:H2'	1:AS:2237:A:H8	1.83	0.44
1:AS:2738:U:H2'	1:AS:2739:U:C6	2.53	0.44
1:AS:3180:A:OP2	15:BH:118:LYS:NZ	2.47	0.44
1:AS:3247:A:H2'	1:AS:3248:U:C6	2.53	0.44
3:AU:156:U:H2'	3:AU:157:U:C6	2.53	0.44
20:BM:109:TYR:CD1	20:BM:114:LYS:HD2	2.52	0.44
31:BX:102:ILE:O	31:BX:106:ILE:HG23	2.18	0.44
46:CM:327:G:H2'	46:CM:328:G:H8	1.83	0.44
46:CM:584:G:H2'	46:CM:585:C:C6	2.52	0.44
46:CM:736:G:H2'	46:CM:737:A:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:740:A:H2'	46:CM:741:A:C8	2.53	0.44
46:CM:852:G:H1	46:CM:946:U:H3	1.65	0.44
47:CN:56:LYS:NZ	47:CN:159:ALA:O	2.49	0.44
48:CO:26:ARG:O	48:CO:50:ARG:HG2	2.18	0.44
48:CO:136:ARG:HG3	48:CO:218:LEU:HD11	2.00	0.44
50:CQ:72:SER:O	50:CQ:76:LYS:HD2	2.17	0.44
52:CS:192:GLU:OE1	72:DM:63:SER:OG	2.36	0.44
52:CS:200:ASN:CB	52:CS:208:SER:HB3	2.47	0.44
73:DN:13:LYS:H	73:DN:15:ARG:NH2	2.16	0.44
79:DT:94:ASP:OD1	79:DT:101:THR:OG1	2.36	0.44
82:l1:59:PRO:HG2	82:l1:153:SER:HA	1.99	0.44
80:p0:22:TYR:HD1	80:p0:90:ASN:HB2	1.82	0.44
1:1:438:A:N7	33:AF:2:ALA:N	2.65	0.43
1:1:949:G:O2'	1:1:1111:G:H4'	2.18	0.43
1:1:1089:A:OP2	22:2:120:LYS:NZ	2.41	0.43
1:1:1592:C:O2'	1:1:1692:A:N3	2.49	0.43
1:1:3040:U:OP1	20:z:59:SER:N	2.33	0.43
1:1:3079:U:H2'	1:1:3080:G:C8	2.52	0.43
7:m:94:ASN:HB2	7:m:97:ALA:H	1.83	0.43
29:AB:75:LEU:HD22	29:AB:118:LEU:HD11	2.00	0.43
33:AF:33:TRP:HH2	33:AF:53:GLN:HG2	1.82	0.43
45:i:114:GLU:HG3	50:F:117:ARG:NH2	2.32	0.43
46:B:569:G:H5''	70:Z:114:LYS:CE	2.48	0.43
46:B:886:G:H2'	46:B:887:G:C8	2.53	0.43
46:B:1032:G:H2'	46:B:1033:U:H6	1.83	0.43
46:B:1181:A:H4'	46:B:1182:C:H5''	1.99	0.43
49:E:134:ILE:HD13	49:E:186:ALA:HB1	2.00	0.43
51:G:100:ARG:HB2	51:G:114:ILE:HD13	2.00	0.43
51:G:147:ILE:HG21	51:G:169:ILE:HG13	2.00	0.43
55:K:62:THR:HA	55:K:77:ARG:HA	2.00	0.43
65:U:49:LYS:HD3	65:U:49:LYS:HA	1.74	0.43
1:AS:314:U:H2'	1:AS:315:C:H6	1.82	0.43
1:AS:502:U:H2'	1:AS:503:U:C6	2.53	0.43
1:AS:705:U:OP1	1:AS:776:A:O2'	2.23	0.43
1:AS:1029:U:H2'	1:AS:1030:U:C6	2.53	0.43
1:AS:1151:C:H2'	1:AS:1152:C:C6	2.53	0.43
1:AS:1247:A:H3'	1:AS:1248:A:H5''	2.00	0.43
1:AS:1852:C:C2	1:AS:1853:C:C5	3.06	0.43
1:AS:2461:G:H1	1:AS:2464:A:H5''	1.83	0.43
1:AS:2632:G:OP1	1:AS:2722:U:O2'	2.35	0.43
2:AT:39:U:H5'	45:CL:33:ASN:ND2	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AW:117:GLU:OE2	4:AW:163:ARG:NH2	2.51	0.43
4:AW:145:LYS:HD2	4:AW:157:ILE:HG22	2.00	0.43
45:CL:112:LYS:HG3	45:CL:113:ARG:N	2.32	0.43
46:CM:236:U:O2'	46:CM:237:C:H5''	2.17	0.43
46:CM:255:A:H1'	55:CV:73:SER:HB2	1.99	0.43
46:CM:498:C:O2'	46:CM:499:U:H5'	2.18	0.43
46:CM:857:G:H2'	46:CM:858:U:O4'	2.18	0.43
46:CM:869:A:OP1	48:CO:136:ARG:NH2	2.51	0.43
46:CM:879:U:H1'	61:DB:31:LYS:NZ	2.32	0.43
46:CM:1475:U:OP1	50:CQ:10:LYS:NZ	2.30	0.43
46:CM:1518:G:H21	66:DG:48:GLN:CD	2.26	0.43
48:CO:175:GLU:OE1	48:CO:187:LYS:NZ	2.43	0.43
50:CQ:73:LEU:CD2	57:CX:20:VAL:HB	2.48	0.43
52:CS:186:ASN:HD21	52:CS:188:LYS:HD2	1.83	0.43
56:CW:68:LYS:HE2	56:CW:68:LYS:HB3	1.80	0.43
73:DN:3:LYS:NZ	73:DN:6:ALA:HA	2.33	0.43
79:DT:145:LEU:HD11	79:DT:178:TRP:CD2	2.53	0.43
80:P0:23:LYS:HB3	80:P0:24:SER:H	1.50	0.43
82:L1:100:ILE:HB	82:L1:124:LEU:HD23	2.00	0.43
82:L1:207:LYS:HD2	82:L1:208:SER:O	2.17	0.43
80:p0:13:SER:O	80:p0:17:GLU:HG3	2.18	0.43
1:1:480:G:C4	1:1:481:G:C8	3.07	0.43
1:1:1379:G:OP1	6:l:204:ARG:HD3	2.19	0.43
1:1:1499:A:C4	1:1:1500:A:C8	3.06	0.43
1:1:1556:G:O2'	1:1:1557:U:H5'	2.18	0.43
1:1:1746:A:H1'	1:1:1748:A:N7	2.33	0.43
1:1:2164:U:OP2	4:j:200:ARG:HD2	2.18	0.43
1:1:2232:U:H2'	1:1:2239:G:N2	2.32	0.43
1:1:2737:C:O3'	43:AP:39:GLY:HA3	2.18	0.43
1:1:3132:U:H3	1:1:3253:G:H1	1.66	0.43
7:m:19:PRO:HG2	7:m:24:GLN:HB2	2.00	0.43
7:m:78:ALA:HB3	7:m:105:VAL:HB	2.00	0.43
7:m:90:TYR:CZ	7:m:225:ASN:HB3	2.53	0.43
15:u:62:LEU:HD22	15:u:65:LEU:HB2	1.99	0.43
17:w:187:ALA:O	17:w:188:GLU:HG2	2.18	0.43
46:B:12:U:H2'	46:B:13:C:H6	1.80	0.43
46:B:46:A:N1	46:B:430:G:O2'	2.47	0.43
46:B:333:U:O2'	58:N:130:PRO:O	2.28	0.43
46:B:1067:C:H4'	68:X:58:TYR:HE2	1.83	0.43
46:B:1200:C:H2'	46:B:1201:C:C6	2.53	0.43
46:B:1219:A:H3'	46:B:1230:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1364:U:HO2'	63:S:9:PHE:HD2	1.63	0.43
46:B:1575:G:O6	46:B:1595:U:O4	2.36	0.43
50:F:66:ARG:HA	50:F:69:GLU:HG2	2.00	0.43
50:F:176:VAL:HB	50:F:183:LEU:HB2	1.99	0.43
50:F:225:LYS:HG3	79:AR:187:ALA:HB2	2.00	0.43
51:G:64:ILE:O	51:G:67:GLN:HG3	2.18	0.43
57:M:35:ILE:O	57:M:37:THR:N	2.50	0.43
1:AS:212:A:O4'	27:BT:2:ALA:HA	2.18	0.43
1:AS:249:G:N2	1:AS:251:G:N7	2.66	0.43
1:AS:291:C:H2'	1:AS:292:U:C6	2.53	0.43
1:AS:373:A:N1	1:AS:394:G:H4'	2.33	0.43
1:AS:602:A:H2'	1:AS:603:C:H6	1.82	0.43
1:AS:1065:C:H2'	1:AS:1066:U:H6	1.83	0.43
1:AS:1560:U:H2'	1:AS:1561:U:C6	2.53	0.43
1:AS:2404:U:H2'	1:AS:2405:U:H6	1.83	0.43
1:AS:2802:G:H1'	1:AS:2833:U:C2	2.53	0.43
1:AS:2927:U:H2'	1:AS:2928:A:O4'	2.18	0.43
1:AS:3313:G:H2'	1:AS:3314:C:C6	2.53	0.43
6:AY:186:LYS:HE3	6:AY:200:PHE:HB3	1.99	0.43
14:BG:157:GLY:O	29:BV:100:PRO:HA	2.19	0.43
21:BN:66:GLU:OE2	21:BN:73:LYS:HE2	2.18	0.43
23:BP:60:SER:OG	23:BP:61:ASP:OD1	2.20	0.43
24:BQ:92:TYR:O	25:BR:20:LEU:N	2.50	0.43
27:BT:69:LYS:HE2	27:BT:69:LYS:HB3	1.86	0.43
33:BZ:3:THR:O	33:BZ:91:LYS:HE2	2.18	0.43
39:CF:30:LYS:HG3	39:CF:31:VAL:H	1.83	0.43
46:CM:30:G:H4'	70:DK:131:SER:HB2	2.00	0.43
46:CM:488:C:O2	46:CM:495:G:N2	2.51	0.43
46:CM:501:G:O2'	77:DR:46:ASN:ND2	2.50	0.43
57:CX:32:HIS:HB2	57:CX:39:ASN:HA	2.00	0.43
79:DT:89:THR:HG21	79:DT:103:ARG:NH1	2.33	0.43
79:DT:102:GLN:HG2	79:DT:103:ARG:N	2.32	0.43
81:12:129:SER:O	81:12:133:LEU:HG	2.17	0.43
82:L1:117:ILE:HD11	82:L1:137:PRO:HB3	1.99	0.43
80:p0:48:ASP:OD1	80:p0:48:ASP:N	2.42	0.43
1:1:843:A:H2'	1:1:844:A:C8	2.53	0.43
1:1:1921:U:O2'	1:1:1923:G:N7	2.51	0.43
1:1:2958:U:C2	1:1:2959:A:C8	3.06	0.43
3:4:155:G:C5	3:4:156:U:C4	3.06	0.43
7:m:50:ARG:NH2	7:m:72:ASP:OD2	2.50	0.43
9:o:102:GLN:HG2	19:y:6:THR:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:o:148:LYS:HD3	9:o:241:ASN:OD1	2.19	0.43
15:u:52:LEU:HD23	15:u:55:ILE:HD11	2.00	0.43
16:v:146:ALA:HA	16:v:149:ASN:OD1	2.18	0.43
16:v:151:ILE:HD12	16:v:156:HIS:HB3	1.99	0.43
25:7:107:SER:O	25:7:111:LYS:HG2	2.19	0.43
37:AJ:98:ARG:HB3	82:l1:215:ARG:NE	2.34	0.43
46:B:1187:A:N6	46:B:1443:C:O5'	2.51	0.43
46:B:1431:G:N7	78:h:131:LYS:NZ	2.66	0.43
46:B:1485:G:H5''	66:V:72:GLY:HA3	2.01	0.43
62:R:50:ASP:N	62:R:50:ASP:OD1	2.50	0.43
1:AS:498:C:H2'	1:AS:499:G:C8	2.53	0.43
1:AS:582:G:H2'	1:AS:583:A:C8	2.52	0.43
1:AS:1245:G:HO2'	1:AS:1246:G:P	2.41	0.43
1:AS:1720:U:H1'	1:AS:1721:C:C6	2.53	0.43
1:AS:1725:A:C6	44:CK:42:CYS:HA	2.53	0.43
1:AS:1804:G:OP2	28:BU:133:LYS:NZ	2.51	0.43
1:AS:2933:G:H2'	1:AS:2934:U:H6	1.81	0.43
9:BB:15:LYS:HE3	9:BB:15:LYS:HB3	1.88	0.43
12:BE:193:ASP:OD2	12:BE:198:LYS:HE3	2.17	0.43
28:BU:73:LYS:CD	28:BU:75:VAL:HG22	2.48	0.43
32:BY:45:THR:HG22	32:BY:47:ASP:N	2.31	0.43
38:CE:14:LYS:NZ	40:CG:51:ILE:HG22	2.33	0.43
39:CF:16:ARG:HG3	39:CF:70:PRO:CG	2.48	0.43
46:CM:81:G:H2'	46:CM:82:U:C6	2.53	0.43
46:CM:93:A:O2'	51:CR:4:GLY:HA3	2.17	0.43
46:CM:652:C:C5	46:CM:676:G:N1	2.84	0.43
46:CM:721:C:N4	46:CM:722:A:H62	2.15	0.43
46:CM:904:A:H2'	46:CM:905:C:H6	1.84	0.43
46:CM:992:C:OP1	61:DB:130:ARG:HA	2.19	0.43
46:CM:1464:G:O2'	66:DG:56:LYS:HD2	2.18	0.43
46:CM:1515:U:OP1	52:CS:109:LYS:HG3	2.17	0.43
47:CN:48:ILE:CG2	47:CN:161:PRO:HB2	2.48	0.43
54:CU:90:ALA:HB3	54:CU:92:ARG:NH1	2.33	0.43
56:CW:126:ARG:HE	77:DR:33:ARG:HD3	1.82	0.43
59:CZ:45:LEU:HA	59:CZ:120:CYS:SG	2.58	0.43
61:DB:107:ILE:HG21	73:DN:53:LEU:HD11	2.01	0.43
65:DF:72:ILE:HD13	65:DF:79:TYR:CD2	2.53	0.43
69:DJ:106:THR:HG22	69:DJ:109:GLY:O	2.17	0.43
79:DT:246:ARG:HH12	79:DT:312:VAL:HG11	1.83	0.43
80:P0:16:ARG:HE	80:P0:63:ILE:HD13	1.82	0.43
81:12:116:MET:HB3	81:12:119:LYS:CG	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:l1:8:GLY:O	82:l1:12:ASN:ND2	2.51	0.43
1:1:200:A:H2'	1:1:201:G:C8	2.54	0.43
1:1:263:C:H2'	1:1:264:G:O4'	2.18	0.43
1:1:412:G:H2'	1:1:413:U:C6	2.54	0.43
1:1:528:A:O2'	1:1:529:A:H5'	2.18	0.43
1:1:742:C:H2'	1:1:743:A:C8	2.53	0.43
1:1:781:G:N2	1:1:782:A:H62	2.17	0.43
1:1:903:G:H2'	1:1:922:A:H62	1.83	0.43
1:1:943:G:H2'	1:1:944:C:C6	2.54	0.43
1:1:1030:U:H2'	1:1:1031:A:H8	1.83	0.43
1:1:1852:C:C2	1:1:1853:C:C5	3.06	0.43
1:1:2361:C:H5'	17:w:72:PHE:CE2	2.53	0.43
1:1:3146:G:OP1	34:AG:6:ARG:HB2	2.17	0.43
1:1:3264:C:H2'	1:1:3265:U:C6	2.54	0.43
9:o:141:THR:HG23	9:o:237:VAL:HG11	1.99	0.43
23:5:34:VAL:HG21	23:5:58:ALA:HB2	2.01	0.43
46:B:182:C:H2'	46:B:183:C:H6	1.84	0.43
46:B:643:U:H2'	46:B:644:U:O4'	2.18	0.43
46:B:795:A:N6	54:J:109:PRO:HD3	2.34	0.43
46:B:809:G:H2'	46:B:810:U:H6	1.83	0.43
46:B:1155:G:C2	46:B:1156:A:C8	3.07	0.43
46:B:1174:A:N3	46:B:1179:A:O2'	2.48	0.43
46:B:1238:U:C2	46:B:1239:U:C5	3.07	0.43
46:B:1335:U:O2'	46:B:1336:G:OP1	2.32	0.43
46:B:1597:G:H5''	52:H:107:LYS:HD2	2.00	0.43
47:C:41:ARG:HG2	47:C:42:PRO:HD2	1.99	0.43
48:D:66:PHE:CE1	61:Q:29:SER:HB3	2.53	0.43
52:H:140:SER:OG	52:H:171:ALA:HB1	2.18	0.43
56:L:106:GLU:HA	56:L:111:THR:HG21	1.98	0.43
59:O:57:ALA:HB1	59:O:125:ASN:OD1	2.18	0.43
62:R:81:ARG:HB2	62:R:117:GLY:HA3	2.00	0.43
62:R:108:LYS:NZ	65:U:118:LYS:HG2	2.34	0.43
1:AS:246:U:H2'	1:AS:247:C:C6	2.53	0.43
1:AS:630:G:H2'	1:AS:631:U:C6	2.54	0.43
1:AS:1014:G:H2'	1:AS:1015:G:H8	1.84	0.43
1:AS:2251:G:H22	1:AS:2290:A:P	2.41	0.43
1:AS:2515:G:H1'	1:AS:2516:U:O4'	2.18	0.43
1:AS:2790:U:H6	1:AS:2790:U:H5'	1.83	0.43
1:AS:2996:A:H5''	11:BD:96:HIS:CE1	2.53	0.43
3:AU:13:A:C6	3:AU:14:C:C4	3.07	0.43
5:AX:106:TRP:CG	5:AX:130:PHE:HE2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BD:13:PRO:HG2	11:BD:16:VAL:HG21	2.00	0.43
16:BI:11:GLN:O	16:BI:14:LYS:NZ	2.46	0.43
21:BN:164:GLN:HG2	21:BN:166:THR:H	1.84	0.43
35:CB:67:LYS:O	35:CB:71:THR:HG22	2.18	0.43
36:CC:6:THR:HG22	36:CC:53:ARG:HD3	2.00	0.43
46:CM:246:U:H4'	58:CY:36:LYS:HD3	2.00	0.43
46:CM:260:U:O2'	46:CM:261:C:H5'	2.19	0.43
46:CM:346:U:P	58:CY:85:ILE:HD13	2.58	0.43
46:CM:451:C:O2	46:CM:451:C:H2'	2.17	0.43
46:CM:1539:U:O2'	46:CM:1584:A:N3	2.47	0.43
46:CM:1700:G:H5'	46:CM:1701:A:OP2	2.18	0.43
46:CM:1712:U:H2'	46:CM:1713:G:C8	2.53	0.43
48:CO:58:ALA:CB	48:CO:91:VAL:HG11	2.49	0.43
58:CY:7:VAL:HG12	58:CY:53:TYR:HA	2.00	0.43
75:DP:14:LYS:HB3	75:DP:29:ARG:HB3	1.99	0.43
1:1:188:G:C6	1:1:205:G:C5	3.06	0.43
1:1:421:G:O6	1:1:2361:C:O2'	2.31	0.43
1:1:1201:A:C6	1:1:1296:G:N2	2.87	0.43
1:1:1303:G:H5'	17:w:61:LYS:HE3	2.00	0.43
1:1:1434:U:H4'	6:l:89:ALA:CB	2.48	0.43
1:1:2181:U:H2'	1:1:2182:C:C6	2.54	0.43
3:4:113:U:H5''	40:AM:7:PHE:CB	2.49	0.43
5:k:57:VAL:HG22	5:k:73:VAL:HG22	2.01	0.43
17:w:83:LYS:HE2	17:w:83:LYS:HB3	1.67	0.43
19:y:67:ILE:HG23	19:y:81:ILE:HG13	2.01	0.43
45:i:63:ALA:C	45:i:65:LYS:H	2.25	0.43
46:B:426:A:N3	46:B:438:U:O2'	2.34	0.43
46:B:649:G:C5	46:B:650:G:H1'	2.53	0.43
46:B:953:U:H2'	46:B:954:C:O4'	2.17	0.43
46:B:1219:A:O2'	78:h:182:TYR:OH	2.29	0.43
46:B:1259:C:O2	46:B:1413:A:O2'	2.23	0.43
46:B:1452:G:H2'	46:B:1453:C:C6	2.52	0.43
46:B:1503:A:H8	67:W:57:MET:HE1	1.83	0.43
50:F:110:LEU:HD21	50:F:116:ILE:HG22	1.99	0.43
1:AS:679:U:O2'	1:AS:695:G:O6	2.35	0.43
1:AS:712:G:O2'	1:AS:749:C:O2'	2.35	0.43
1:AS:1153:G:H2'	1:AS:1154:A:O4'	2.19	0.43
1:AS:1502:A:H1'	1:AS:1844:G:O6	2.19	0.43
1:AS:2065:C:H5'	1:AS:2066:G:OP2	2.18	0.43
1:AS:2164:U:OP2	4:AW:200:ARG:HD2	2.18	0.43
1:AS:2581:A:H2'	1:AS:2582:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:2990:C:C4	1:AS:2991:U:C4	3.07	0.43
1:AS:3153:A:H2'	1:AS:3154:A:C8	2.53	0.43
3:AU:56:G:H2'	3:AU:57:C:O4'	2.17	0.43
46:CM:246:U:C4'	58:CY:36:LYS:HD3	2.49	0.43
46:CM:383:A:H2'	46:CM:384:G:C8	2.53	0.43
46:CM:582:C:C4	46:CM:583:A:N7	2.87	0.43
46:CM:588:C:H2'	46:CM:589:A:C8	2.52	0.43
46:CM:1579:A:O2'	46:CM:1580:A:OP1	2.34	0.43
46:CM:1677:G:H2'	46:CM:1678:G:N7	2.33	0.43
47:CN:23:HIS:O	47:CN:48:ILE:HD12	2.19	0.43
48:CO:30:PHE:HE1	48:CO:46:THR:HB	1.80	0.43
52:CS:42:LEU:HB3	52:CS:46:TRP:HB2	2.01	0.43
52:CS:103:ASN:HA	52:CS:106:LYS:HD3	2.00	0.43
53:CT:203:ASP:O	53:CT:207:GLU:HG3	2.18	0.43
55:CV:48:THR:HG22	55:CV:52:ASN:C	2.42	0.43
62:DC:8:LYS:HA	62:DC:8:LYS:HD3	1.79	0.43
69:DJ:11:LEU:HD12	69:DJ:74:VAL:HG13	2.01	0.43
69:DJ:75:ILE:HD12	69:DJ:125:ILE:CD1	2.49	0.43
74:DO:49:HIS:HA	74:DO:70:LYS:HA	2.01	0.43
79:DT:102:GLN:HE22	79:DT:138:ILE:C	2.16	0.43
80:P0:11:TYR:OH	80:P0:54:GLY:HA3	2.18	0.43
82:l1:98:LYS:HA	82:l1:101:LYS:HB3	2.00	0.43
1:1:242:C:O2'	1:1:243:G:H8	2.02	0.43
1:1:908:G:N7	4:j:9:ARG:NH2	2.66	0.43
1:1:1588:G:OP2	35:AH:37:LYS:NZ	2.40	0.43
1:1:2199:G:H2'	1:1:2201:A:OP2	2.19	0.43
1:1:2257:A:C8	1:1:2266:G:C8	3.06	0.43
1:1:3285:A:H2'	1:1:3286:C:H6	1.82	0.43
1:1:3336:G:H2'	1:1:3337:A:H8	1.83	0.43
5:k:77:THR:HG21	5:k:328:ILE:HG12	2.01	0.43
5:k:313:ARG:O	5:k:333:LYS:HE3	2.19	0.43
9:o:108:GLN:HG3	9:o:111:ALA:HB2	2.00	0.43
11:q:137:SER:HB3	11:q:143:GLU:HB3	2.01	0.43
25:7:96:GLN:NE2	25:7:101:ARG:HE	2.17	0.43
46:B:30:G:OP1	70:Z:126:LYS:NZ	2.51	0.43
46:B:165:U:H2'	46:B:166:A:H5''	1.99	0.43
46:B:217:A:C5	46:B:218:A:C8	3.06	0.43
46:B:282:G:N7	53:I:188:ARG:NH2	2.55	0.43
46:B:485:G:C2	46:B:486:G:C8	3.06	0.43
46:B:880:G:H4'	61:Q:32:GLU:OE1	2.18	0.43
48:D:28:ASP:OD2	48:D:50:ARG:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:H:61:TYR:OH	75:e:52:ASP:OD1	2.17	0.43
57:M:56:LYS:HZ2	57:M:69:THR:HG22	1.83	0.43
64:T:7:LYS:O	64:T:11:ARG:HG2	2.18	0.43
78:h:157:GLU:HG3	78:h:159:LEU:HG	2.00	0.43
1:AS:152:U:H4'	1:AS:157:G:H4'	2.00	0.43
1:AS:282:G:H2'	1:AS:286:U:O4'	2.18	0.43
1:AS:403:C:O2'	1:AS:404:G:OP1	2.26	0.43
1:AS:1600:A:H4'	1:AS:1831:A:H4'	1.99	0.43
1:AS:1905:A:H2'	1:AS:1906:A:C8	2.53	0.43
1:AS:2128:G:O2'	1:AS:2167:U:OP1	2.30	0.43
1:AS:2339:A:H2'	1:AS:2340:C:C6	2.53	0.43
7:AZ:4:GLN:HG3	7:AZ:5:LYS:N	2.32	0.43
11:BD:94:TYR:HA	11:BD:177:ASP:OD1	2.18	0.43
13:BF:108:GLU:HB3	13:BF:122:ILE:HD11	2.01	0.43
20:BM:176:ARG:NH2	46:CM:838:G:OP2	2.51	0.43
45:CL:82:LYS:HD3	46:CM:1175:C:N4	2.33	0.43
46:CM:1226:G:H4'	62:DC:77:LYS:O	2.18	0.43
46:CM:1276:G:N2	46:CM:1309:G:H22	2.14	0.43
46:CM:1282:G:N2	46:CM:1284:G:H3'	2.33	0.43
46:CM:1518:G:N2	66:DG:48:GLN:OE1	2.50	0.43
46:CM:1637:U:H2'	46:CM:1638:A:H8	1.82	0.43
47:CN:55:GLU:HB3	68:DI:79:LEU:HD22	2.01	0.43
80:P0:43:LYS:HD2	80:P0:43:LYS:HA	1.76	0.43
82:l:1:93:LEU:C	82:l:1:95:LYS:N	2.75	0.43
1:1:35:C:H4'	1:1:804:A:C2	2.54	0.43
1:1:273:A:H2'	1:1:274:G:H8	1.82	0.43
1:1:321:C:H4'	16:v:150:TRP:CG	2.54	0.43
1:1:493:A:O2'	1:1:3238:A:N1	2.47	0.43
1:1:929:A:C2	6:l:99:ARG:NH2	2.86	0.43
1:1:1075:A:H4'	7:m:140:ARG:O	2.18	0.43
1:1:1747:G:H5'	39:AL:26:LYS:HE2	2.01	0.43
1:1:1754:G:H2'	1:1:1755:U:O4'	2.18	0.43
1:1:2220:A:H5''	4:j:244:GLY:HA3	2.01	0.43
1:1:2222:A:H5''	4:j:243:THR:HB	2.01	0.43
1:1:2376:A:OP1	1:1:2845:U:H4'	2.18	0.43
1:1:2557:G:C6	26:8:24:LEU:HD21	2.53	0.43
3:4:85:G:H4'	3:4:86:U:OP1	2.19	0.43
7:m:153:THR:HG22	7:m:179:ARG:HE	1.83	0.43
22:2:82:ASN:HB2	30:AC:20:GLY:HA3	1.99	0.43
25:7:86:SER:O	25:7:90:ILE:HG12	2.18	0.43
27:9:109:LEU:HD22	27:9:115:ARG:HH22	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:60:U:H4'	46:B:452:A:OP1	2.18	0.43
46:B:265:U:H2'	46:B:266:C:C6	2.53	0.43
46:B:475:A:H5'	77:g:34:ALA:CB	2.48	0.43
46:B:486:G:H2'	46:B:487:C:O4'	2.18	0.43
46:B:1142:A:H2'	46:B:1145:A:N7	2.33	0.43
46:B:1303:G:H5''	64:T:67:ARG:NH1	2.34	0.43
46:B:1634:U:H2'	46:B:1635:A:H8	1.83	0.43
46:B:1678:G:H1	46:B:1698:U:H3	1.66	0.43
47:C:53:THR:OG1	47:C:161:PRO:HG2	2.19	0.43
48:D:88:VAL:HA	48:D:98:THR:HA	2.00	0.43
51:G:36:HIS:CG	51:G:85:GLY:HA3	2.54	0.43
51:G:59:ARG:NH1	71:a:87:PRO:HG3	2.33	0.43
72:b:54:VAL:HA	72:b:57:TYR:CD2	2.53	0.43
1:AS:409:A:H61	3:AU:15:G:H1'	1.83	0.43
1:AS:659:G:H4'	1:AS:660:U:H6	1.84	0.43
1:AS:1113:G:OP1	30:BW:4:SER:HB2	2.18	0.43
1:AS:1452:A:N1	1:AS:1472:G:O2'	2.50	0.43
1:AS:1780:A:OP1	35:CB:19:LYS:NZ	2.52	0.43
1:AS:2078:A:H3'	1:AS:2078:A:N3	2.34	0.43
1:AS:2420:G:H1	1:AS:2483:U:H3	1.67	0.43
1:AS:2641:G:P	45:CL:50:LYS:HZ2	2.42	0.43
1:AS:2855:U:H2'	1:AS:2856:C:C6	2.54	0.43
1:AS:3118:G:H2'	1:AS:3119:A:C8	2.54	0.43
11:BD:13:PRO:HG2	11:BD:16:VAL:CG2	2.49	0.43
46:CM:166:A:H2'	46:CM:167:A:C8	2.53	0.43
46:CM:310:A:C2	46:CM:312:C:H2'	2.53	0.43
46:CM:704:A:N1	46:CM:719:A:C5	2.87	0.43
46:CM:862:G:H22	46:CM:936:A:H2	1.67	0.43
46:CM:974:U:H2'	46:CM:975:C:C6	2.54	0.43
46:CM:1157:G:H2'	46:CM:1158:C:C6	2.54	0.43
46:CM:1544:U:OP2	46:CM:1546:G:O2'	2.29	0.43
46:CM:1670:U:O2'	46:CM:1671:G:O5'	2.31	0.43
51:CR:22:LYS:HB3	56:CW:4:ALA:HB3	1.99	0.43
57:CX:35:ILE:HG22	57:CX:37:THR:HG22	2.00	0.43
57:CX:59:PHE:CZ	57:CX:62:GLN:HA	2.54	0.43
59:CZ:62:LEU:HA	59:CZ:119:SER:O	2.18	0.43
75:DP:9:LEU:C	75:DP:33:LEU:HD23	2.44	0.43
79:DT:294:ASP:N	79:DT:294:ASP:OD1	2.51	0.43
82:l1:156:LYS:HB3	82:l1:156:LYS:HE2	1.72	0.43
1:1:277:G:H2'	1:1:278:U:H6	1.83	0.43
1:1:757:A:H2'	1:1:758:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1163:U:P	34:AG:73:ARG:HH12	2.41	0.43
1:1:1258:G:H3'	1:1:1258:G:OP2	2.19	0.43
1:1:2345:A:H2'	1:1:2346:A:H8	1.82	0.43
1:1:2738:U:H2'	1:1:2739:U:C6	2.53	0.43
1:1:2961:U:H2'	1:1:2962:G:O4'	2.18	0.43
1:1:3148:A:C2	17:w:116:LYS:HD2	2.54	0.43
1:1:3201:U:H1'	1:1:3217:G:N2	2.34	0.43
1:1:3264:C:H2'	1:1:3265:U:H6	1.84	0.43
3:4:6:U:H2'	3:4:7:U:H6	1.84	0.43
5:k:215:ILE:HD12	5:k:338:LEU:HB3	2.00	0.43
11:q:114:ILE:HB	11:q:124:ARG:HB2	2.01	0.43
19:y:54:LEU:HD22	19:y:58:ASN:HB3	2.01	0.43
40:AM:41:ARG:HA	40:AM:41:ARG:HD2	1.76	0.43
42:AO:10:VAL:HG11	46:B:1100:U:H5''	2.00	0.43
46:B:963:A:H2'	46:B:964:A:O4'	2.17	0.43
46:B:1183:G:O4'	67:W:72:GLY:HA3	2.19	0.43
46:B:1243:U:C6	46:B:1244:U:H5	2.37	0.43
46:B:1276:G:N2	46:B:1309:G:H22	2.15	0.43
46:B:1305:U:O2	46:B:1307:A:H5'	2.19	0.43
46:B:1387:A:OP1	64:T:56:HIS:NE2	2.39	0.43
46:B:1636:C:H2'	46:B:1637:U:H6	1.84	0.43
46:B:1727:A:H2'	46:B:1728:U:H6	1.84	0.43
59:O:68:GLU:C	59:O:69:GLU:HG3	2.40	0.43
66:V:70:GLN:HB3	66:V:121:GLY:HA3	2.00	0.43
66:V:124:ILE:HD11	66:V:132:LEU:HD12	2.01	0.43
1:AS:278:U:OP2	43:CJ:49:GLY:HA3	2.19	0.43
1:AS:795:G:O2'	14:BG:18:TRP:NE1	2.45	0.43
1:AS:1011:C:N4	1:AS:1031:A:H61	2.16	0.43
1:AS:3111:A:O4'	5:AX:18:PRO:HD2	2.18	0.43
3:AU:139:U:H2'	3:AU:140:G:C8	2.53	0.43
4:AW:178:PRO:O	4:AW:180:LEU:HD12	2.18	0.43
46:CM:393:U:H2'	46:CM:394:G:O4'	2.18	0.43
46:CM:804:U:H2'	46:CM:805:U:H5	1.84	0.43
46:CM:824:U:C5	46:CM:825:U:C5	3.07	0.43
46:CM:849:U:H3'	69:DJ:28:ARG:HH22	1.84	0.43
46:CM:933:A:H2'	46:CM:934:C:C6	2.54	0.43
46:CM:1308:C:H2'	46:CM:1309:G:C8	2.54	0.43
52:CS:187:ILE:HD13	72:DM:66:VAL:HG21	2.01	0.43
55:CV:39:GLY:O	55:CV:61:GLU:HG3	2.18	0.43
79:DT:41:THR:HG22	79:DT:42:LEU:H	1.82	0.43
80:p0:19:LEU:HD21	80:p0:63:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:211:G:OP2	27:9:2:ALA:N	2.52	0.43
1:1:696:U:H2'	1:1:697:A:O4'	2.18	0.43
1:1:798:C:H2'	1:1:799:C:C6	2.54	0.43
1:1:947:A:H5''	1:1:1139:A:N1	2.34	0.43
1:1:1466:U:H2'	1:1:1467:U:H6	1.83	0.43
1:1:1923:G:C8	44:AQ:16:VAL:HG12	2.54	0.43
1:1:2096:C:H2'	1:1:2097:A:O4'	2.19	0.43
1:1:2855:U:H2'	1:1:2856:C:H6	1.84	0.43
1:1:3233:A:OP1	18:x:181:ARG:NH2	2.44	0.43
2:3:107:A:H2'	2:3:108:U:C6	2.53	0.43
5:k:256:HIS:HA	5:k:257:PRO:C	2.44	0.43
12:r:31:ILE:HA	12:r:66:GLU:OE1	2.19	0.43
18:x:18:ARG:NH1	18:x:147:GLU:OE1	2.52	0.43
23:5:35:LYS:HZ3	23:5:39:GLU:CD	2.27	0.43
24:6:80:ARG:HD2	24:6:97:ASP:OD1	2.19	0.43
25:7:47:ARG:HD2	25:7:58:HIS:CD2	2.53	0.43
27:9:5:SER:HB3	27:9:8:VAL:HG23	2.00	0.43
35:AH:9:ARG:HD2	35:AH:34:HIS:CE1	2.54	0.43
43:AP:10:THR:O	43:AP:20:HIS:HA	2.19	0.43
45:i:63:ALA:C	45:i:65:LYS:N	2.75	0.43
47:C:63:ILE:HG12	68:X:36:ILE:HG12	2.00	0.43
47:C:182:LEU:HB3	47:C:187:ILE:HB	2.00	0.43
47:C:184:LEU:HB3	68:X:45:ALA:CB	2.49	0.43
47:C:201:LEU:O	47:C:202:TYR:HB2	2.18	0.43
50:F:102:GLN:OE1	50:F:123:VAL:HG23	2.19	0.43
50:F:193:PRO:HG3	50:F:203:LEU:CD1	2.48	0.43
62:R:25:LEU:HG	62:R:87:PRO:HB3	2.00	0.43
63:S:92:HIS:HB3	63:S:101:LYS:HB2	2.00	0.43
1:AS:571:C:H2'	1:AS:572:U:C6	2.54	0.43
1:AS:671:U:H2'	1:AS:672:G:H8	1.83	0.43
1:AS:689:A:N1	3:AU:28:C:O2'	2.49	0.43
1:AS:947:A:H5''	1:AS:1139:A:N1	2.34	0.43
1:AS:1330:U:H2'	1:AS:1331:U:C6	2.54	0.43
1:AS:1456:A:H5'	32:BY:50:LEU:O	2.18	0.43
1:AS:1618:U:H2'	1:AS:1619:G:C8	2.54	0.43
1:AS:1713:U:H2'	1:AS:1714:G:H8	1.81	0.43
1:AS:2156:A:H5''	4:AW:129:THR:OG1	2.19	0.43
1:AS:2257:A:C8	1:AS:2266:G:C8	3.07	0.43
1:AS:3195:G:H4'	15:BH:125:LYS:HE2	2.01	0.43
3:AU:156:U:H2'	3:AU:157:U:C5	2.53	0.43
5:AX:283:TYR:CE1	5:AX:354:VAL:HG21	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AY:303:ALA:CA	19:BL:39:ARG:HH12	2.31	0.43
16:BI:180:PHE:O	16:BI:184:LYS:HG3	2.18	0.43
36:CC:12:LYS:HD3	36:CC:16:GLN:HB3	2.00	0.43
46:CM:265:U:H2'	46:CM:266:C:H6	1.84	0.43
46:CM:402:G:H2'	46:CM:403:C:C6	2.53	0.43
46:CM:654:G:H5''	46:CM:655:U:OP2	2.18	0.43
46:CM:890:A:H5''	61:DB:47:ARG:HB2	2.01	0.43
46:CM:946:U:H5''	60:DA:71:ILE:HD12	2.01	0.43
47:CN:201:LEU:O	47:CN:202:TYR:HB2	2.19	0.43
57:CX:80:LEU:HB3	57:CX:82:ILE:HG23	2.01	0.43
61:DB:84:THR:O	61:DB:123:ARG:HD2	2.18	0.43
74:DO:34:ASP:OD1	74:DO:82:LYS:NZ	2.43	0.43
79:DT:41:THR:HG22	79:DT:42:LEU:N	2.33	0.43
1:1:122:A:C6	1:1:149:A:C5	3.07	0.43
1:1:671:U:H2'	1:1:672:G:H8	1.83	0.43
1:1:691:A:O2'	6:l:235:GLY:HA3	2.18	0.43
1:1:1022:A:H8	1:1:1022:A:OP2	2.01	0.43
1:1:1180:A:H2'	1:1:1181:C:C6	2.54	0.43
1:1:1494:A:H2'	1:1:1495:U:C6	2.54	0.43
1:1:1612:U:H2'	1:1:1613:G:C8	2.54	0.43
1:1:1802:A:H4'	35:AH:76:TYR:CZ	2.53	0.43
1:1:2285:G:O2'	1:1:2288:U:OP2	2.31	0.43
1:1:2686:G:H4'	1:1:2687:A:H5''	2.01	0.43
1:1:2995:U:H2'	1:1:2996:A:C8	2.54	0.43
1:1:3197:G:C6	1:1:3221:G:C6	3.07	0.43
3:4:21:C:H5''	6:l:195:LEU:HD21	2.00	0.43
3:4:47:C:H1'	3:4:61:A:H2'	2.01	0.43
4:j:150:LEU:HD11	4:j:156:LYS:HD2	2.01	0.43
7:m:134:ALA:HA	7:m:141:PRO:HD3	2.01	0.43
15:u:65:LEU:HD12	15:u:77:LYS:HD2	2.00	0.43
17:w:17:LEU:HD11	17:w:81:LEU:HA	2.01	0.43
46:B:451:C:O2	46:B:451:C:H2'	2.19	0.43
46:B:818:U:H3'	46:B:819:G:H5'	1.99	0.43
46:B:1151:A:H2'	46:B:1152:G:O4'	2.19	0.43
57:M:17:GLN:O	57:M:18:GLU:HB2	2.18	0.43
61:Q:101:ALA:HB2	73:c:53:LEU:CD2	2.49	0.43
1:AS:200:A:H2'	1:AS:201:G:C8	2.52	0.43
1:AS:426:G:H4'	33:BZ:52:PRO:HD3	2.01	0.43
1:AS:623:A:H2'	1:AS:624:U:H6	1.83	0.43
1:AS:912:G:H5'	1:AS:913:A:OP1	2.19	0.43
1:AS:1328:A:H2'	1:AS:1329:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1357:U:H2'	1:AS:1358:C:C6	2.53	0.43
1:AS:1865:C:H4'	1:AS:3049:A:O2'	2.18	0.43
1:AS:2140:U:OP1	4:AW:234:LYS:NZ	2.43	0.43
1:AS:3153:A:H2'	1:AS:3154:A:H8	1.84	0.43
3:AU:49:G:OP1	36:CC:45:HIS:HB2	2.18	0.43
5:AX:219:ALA:HB3	5:AX:329:PRO:HG2	2.01	0.43
7:AZ:19:PRO:HG2	7:AZ:24:GLN:HB2	2.01	0.43
9:BB:87:ILE:HD11	9:BB:226:THR:HG22	2.00	0.43
17:BJ:151:GLU:O	17:BJ:155:GLU:HG2	2.19	0.43
21:BN:125:LYS:HG2	21:BN:127:VAL:HG23	2.00	0.43
27:BT:113:LYS:HE2	27:BT:113:LYS:HB2	1.79	0.43
29:BV:112:VAL:HB	29:BV:130:VAL:HG12	2.00	0.43
31:BX:36:LEU:HD13	31:BX:61:TYR:HB3	2.00	0.43
46:CM:98:U:H2'	46:CM:99:C:C6	2.54	0.43
46:CM:289:G:H2'	46:CM:290:U:C6	2.53	0.43
46:CM:481:A:H2'	46:CM:482:C:C6	2.54	0.43
46:CM:483:A:H2'	46:CM:484:G:O4'	2.19	0.43
46:CM:1071:A:H2'	46:CM:1072:A:C8	2.53	0.43
46:CM:1452:G:H2'	46:CM:1453:C:C6	2.54	0.43
46:CM:1485:G:H2'	46:CM:1486:G:H8	1.83	0.43
46:CM:1552:C:OP1	65:DF:41:ARG:HD3	2.19	0.43
60:DA:136:PRO:HG2	60:DA:139:TRP:HB2	2.01	0.43
79:DT:12:THR:O	79:DT:53:ASN:HA	2.19	0.43
1:1:270:U:H2'	1:1:271:C:H6	1.84	0.42
1:1:291:C:C2	1:1:292:U:C5	3.07	0.42
1:1:595:G:H21	6:l:323:GLN:CD	2.27	0.42
1:1:798:C:H2'	1:1:799:C:H6	1.84	0.42
1:1:1268:C:H3'	1:1:1269:A:H8	1.83	0.42
1:1:1519:U:OP1	1:1:1603:U:N3	2.43	0.42
1:1:1949:G:H1	1:1:2070:A:H2'	1.84	0.42
1:1:2525:A:H2'	1:1:2526:C:O4'	2.18	0.42
1:1:2627:U:H4'	1:1:2628:A:O4'	2.19	0.42
1:1:2812:C:N4	1:1:2817:A:O2'	2.52	0.42
5:k:240:ARG:HA	5:k:246:LEU:HD13	2.00	0.42
15:u:14:GLU:OE2	15:u:17:ARG:HD3	2.18	0.42
17:w:125:LEU:HD13	21:0:168:PRO:HG3	2.00	0.42
20:z:38:ARG:O	20:z:42:ARG:HG3	2.19	0.42
46:B:521:G:H5'	71:a:60:PHE:O	2.20	0.42
46:B:701:G:C2'	46:B:702:G:H2'	2.34	0.42
46:B:715:G:H3'	46:B:715:G:N3	2.33	0.42
46:B:989:U:H3'	46:B:990:A:H5''	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1594:G:C2	46:B:1595:U:C5	3.07	0.42
47:C:55:GLU:HB3	68:X:79:LEU:HD22	2.00	0.42
48:D:168:MET:O	48:D:172:MET:HG3	2.19	0.42
51:G:122:LYS:HG2	51:G:162:ILE:HB	2.00	0.42
51:G:194:VAL:HG11	51:G:232:ALA:HB2	2.00	0.42
57:M:32:HIS:O	57:M:32:HIS:CG	2.72	0.42
61:Q:11:VAL:HG12	61:Q:13:ARG:HG3	2.01	0.42
61:Q:37:VAL:HB	61:Q:62:VAL:HG23	2.01	0.42
62:R:33:PHE:O	62:R:36:LEU:HG	2.19	0.42
71:a:20:ARG:HB3	71:a:76:TYR:CD2	2.54	0.42
79:AR:9:LEU:HB2	79:AR:310:TRP:CZ3	2.53	0.42
1:AS:291:C:H2'	1:AS:292:U:H6	1.84	0.42
1:AS:699:G:H2'	1:AS:700:C:C6	2.54	0.42
1:AS:922:A:H2'	1:AS:923:C:C6	2.54	0.42
1:AS:942:U:H2'	1:AS:943:G:H8	1.84	0.42
1:AS:1265:U:H5'	1:AS:1266:A:OP2	2.18	0.42
1:AS:1660:G:H2'	1:AS:1661:U:C6	2.54	0.42
1:AS:2089:G:H5''	25:BR:48:ARG:CZ	2.49	0.42
1:AS:2276:U:O2'	1:AS:2277:A:H5'	2.19	0.42
1:AS:2367:C:H2'	1:AS:2368:A:C8	2.54	0.42
1:AS:2408:A:H2'	1:AS:2409:C:H6	1.82	0.42
1:AS:2681:C:H2'	1:AS:2682:C:C6	2.54	0.42
3:AU:2:A:C4	3:AU:3:A:C8	3.06	0.42
8:BA:145:LEU:HD23	8:BA:145:LEU:HA	1.88	0.42
10:BC:90:GLN:O	10:BC:93:LYS:HG2	2.19	0.42
37:CD:91:GLN:OE1	82:L1:3:LYS:HG3	2.19	0.42
46:CM:553:A:H2'	46:CM:554:A:C8	2.54	0.42
46:CM:593:G:H2'	46:CM:594:C:C6	2.54	0.42
46:CM:1533:G:OP1	65:DF:123:ARG:NH1	2.51	0.42
46:CM:1721:U:H2'	46:CM:1722:U:C6	2.54	0.42
59:CZ:32:LEU:O	59:CZ:35:SER:OG	2.26	0.42
65:DF:25:ARG:H	65:DF:25:ARG:HG2	1.60	0.42
79:DT:259:ILE:HD12	79:DT:268:LEU:HD23	2.00	0.42
1:1:146:U:N3	10:p:159:ASP:O	2.38	0.42
1:1:212:A:OP1	27:9:2:ALA:N	2.52	0.42
1:1:291:C:H2'	1:1:292:U:H6	1.82	0.42
1:1:1415:A:OP1	3:4:20:U:O2'	2.37	0.42
1:1:1655:U:H3	1:1:1786:G:H1	1.67	0.42
1:1:2406:U:H2'	1:1:2407:G:H8	1.84	0.42
3:4:70:G:P	27:9:121:ARG:HH22	2.42	0.42
3:4:104:A:OP2	3:4:105:A:H2'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:k:112:GLU:O	5:k:116:ARG:HG3	2.20	0.42
6:l:155:ASN:OD1	6:l:254:GLY:N	2.33	0.42
8:n:40:ILE:HB	8:n:84:ILE:HB	1.99	0.42
10:p:76:ILE:HD11	16:v:18:VAL:HG13	2.00	0.42
15:u:32:ILE:HG21	21:0:150:PHE:HE1	1.83	0.42
18:x:61:ARG:HH22	18:x:76:PHE:HB3	1.85	0.42
33:AF:17:LYS:HE2	33:AF:17:LYS:HB3	1.79	0.42
46:B:14:C:H2'	46:B:15:U:C6	2.54	0.42
46:B:87:C:O2'	46:B:167:A:N1	2.48	0.42
46:B:103:A:O3'	46:B:306:C:N4	2.52	0.42
46:B:147:C:C2	46:B:148:C:C5	3.07	0.42
46:B:415:A:H5'	46:B:416:G:C5	2.54	0.42
46:B:693:U:H4'	54:J:96:PRO:HG3	2.01	0.42
46:B:740:A:O2'	46:B:741:A:OP1	2.30	0.42
46:B:744:U:C2	46:B:745:A:C8	3.06	0.42
46:B:1202:A:C2	57:M:27:PHE:HD2	2.37	0.42
46:B:1238:U:H2'	46:B:1239:U:C6	2.55	0.42
46:B:1300:U:O2'	46:B:1301:G:H8	2.00	0.42
49:E:93:MET:HG3	49:E:116:VAL:HG23	2.01	0.42
52:H:156:ARG:NH1	75:e:67:ARG:HG3	2.29	0.42
57:M:26:ASP:OD2	57:M:29:GLN:NE2	2.49	0.42
57:M:59:PHE:CZ	57:M:62:GLN:HA	2.54	0.42
57:M:79:GLU:OE1	57:M:80:LEU:HD22	2.19	0.42
58:N:91:LEU:HB3	58:N:100:TYR:HB3	2.00	0.42
60:P:16:LEU:HG	60:P:17:PRO:HD2	2.01	0.42
60:P:26:PHE:CE1	60:P:28:LEU:HB2	2.53	0.42
63:S:28:ILE:HA	63:S:64:ILE:O	2.19	0.42
68:X:74:GLN:NE2	68:X:83:TRP:O	2.49	0.42
73:c:87:ARG:NH2	73:c:92:ARG:O	2.52	0.42
79:AR:110:ASP:HB2	79:AR:128:ARG:HD2	2.00	0.42
1:AS:546:C:H2'	1:AS:547:U:O4'	2.18	0.42
1:AS:1852:C:H2'	1:AS:1853:C:C6	2.53	0.42
1:AS:2195:U:H2'	1:AS:2196:G:H8	1.84	0.42
1:AS:2394:U:H2'	1:AS:2395:U:C6	2.54	0.42
3:AU:52:A:OP1	40:CG:21[A]:ARG:NH1	2.52	0.42
3:AU:104:A:OP2	3:AU:105:A:H2'	2.19	0.42
7:AZ:179:ARG:HA	7:AZ:179:ARG:HD3	1.82	0.42
11:BD:180:TYR:CD1	41:CH:13:TYR:HD2	2.38	0.42
13:BF:17:LEU:HD12	13:BF:128:TYR:O	2.20	0.42
13:BF:81:GLU:O	13:BF:85:LYS:HG3	2.20	0.42
25:BR:80:ARG:HH21	46:CM:163:G:H4'	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BU:22:LYS:NZ	28:BU:129:TRP:O	2.41	0.42
46:CM:701:G:N2	46:CM:721:C:O2	2.52	0.42
46:CM:875:C:H2'	46:CM:876:A:C8	2.53	0.42
46:CM:908:A:H2'	46:CM:909:A:H8	1.82	0.42
46:CM:1437:C:OP1	76:DQ:12:ARG:NH1	2.40	0.42
50:CQ:68:HIS:NE2	57:CX:94:ASN:HB3	2.33	0.42
55:CV:56:ARG:NH1	55:CV:180:GLY:O	2.52	0.42
58:CY:36:LYS:HE2	58:CY:36:LYS:HB3	1.90	0.42
59:CZ:78:LEU:HA	59:CZ:81:GLU:HG2	2.00	0.42
79:DT:271:LEU:HD21	79:DT:310:TRP:CD2	2.54	0.42
1:1:246:U:H2'	1:1:247:C:C6	2.54	0.42
1:1:304:G:H3'	1:1:304:G:OP2	2.20	0.42
1:1:1632:C:OP1	28:AA:36:HIS:NE2	2.48	0.42
1:1:1714:G:OP2	20:z:121:HIS:ND1	2.52	0.42
1:1:2458:G:H2'	1:1:2458:G:N3	2.34	0.42
1:1:2641:G:H2'	1:1:2642:G:H8	1.84	0.42
1:1:2716:U:H2'	1:1:2717:G:C8	2.55	0.42
1:1:2717:G:N2	1:1:2720:A:OP2	2.39	0.42
1:1:3110:U:OP1	5:k:274:HIS:ND1	2.47	0.42
9:o:233:ILE:HD12	9:o:233:ILE:HA	1.90	0.42
18:x:42:GLU:HG2	18:x:43:LYS:N	2.33	0.42
31:AD:45:ILE:HD12	31:AD:92:LEU:HD11	2.01	0.42
36:AI:100:GLU:OE1	36:AI:108:ARG:NE	2.53	0.42
46:B:474:U:OP1	46:B:475:A:O2'	2.36	0.42
46:B:544:U:H2'	46:B:545:U:C6	2.54	0.42
46:B:873:U:H2'	46:B:874:U:C6	2.54	0.42
53:I:161:GLU:HA	53:I:170:THR:HA	2.01	0.42
56:L:63:ASP:OD1	56:L:64:GLU:N	2.52	0.42
59:O:47:GLU:O	59:O:50:LYS:HG2	2.19	0.42
79:AR:26:THR:HG23	79:AR:29:HIS:H	1.82	0.42
1:AS:1166:A:OP1	9:BB:215:ARG:HA	2.20	0.42
1:AS:1615:A:H2'	1:AS:1616:U:O4'	2.18	0.42
1:AS:1797:U:H2'	1:AS:1798:C:C6	2.54	0.42
1:AS:2645:A:H5''	13:BF:95:ASN:ND2	2.34	0.42
1:AS:2801:U:C2	1:AS:2802:G:C8	3.07	0.42
1:AS:2894:G:C2	1:AS:2924:G:H1'	2.54	0.42
2:AT:113:C:H2'	2:AT:114:U:O4'	2.19	0.42
8:BA:75:LEU:N	8:BA:138:GLN:OE1	2.31	0.42
9:BB:130:PRO:HG2	9:BB:131:TYR:CE2	2.54	0.42
17:BJ:122:PRO:HA	17:BJ:125:LEU:HD12	2.01	0.42
46:CM:205:U:H2'	46:CM:206:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:598:U:P	70:DK:108:GLY:HA2	2.59	0.42
46:CM:600:U:H2'	46:CM:601:U:C6	2.54	0.42
46:CM:746:G:H4'	56:CW:72:GLU:OE1	2.20	0.42
46:CM:852:G:H21	60:DA:87:ASP:CG	2.27	0.42
46:CM:1678:G:H3'	46:CM:1679:A:C8	2.54	0.42
46:CM:1721:U:H2'	46:CM:1722:U:H6	1.83	0.42
52:CS:225:ARG:O	61:DB:98:ARG:NH2	2.50	0.42
53:CT:234:LEU:HB3	53:CT:235:LYS:HE2	2.01	0.42
59:CZ:51:ALA:HB3	59:CZ:122:VAL:HG11	2.00	0.42
60:DA:38:ILE:HD11	60:DA:78:ASN:ND2	2.34	0.42
70:DK:29:TYR:HA	70:DK:32:ARG:NH1	2.34	0.42
81:12:119:LYS:HD2	81:12:119:LYS:N	2.35	0.42
1:1:79:G:H2'	1:1:80:C:C6	2.53	0.42
1:1:152:U:O2'	1:1:153:U:H5'	2.20	0.42
1:1:820:C:O2'	1:1:1530:A:N3	2.51	0.42
1:1:1912:U:H5''	20:z:85:LYS:HB2	2.01	0.42
8:n:58:GLU:H	8:n:58:GLU:CD	2.26	0.42
11:q:86:TYR:CE2	11:q:151:LEU:HB2	2.54	0.42
15:u:14:GLU:CB	21:0:149:LYS:HG2	2.49	0.42
22:2:39:ILE:HG12	22:2:63:ILE:CD1	2.49	0.42
30:AC:19:ASN:OD1	30:AC:19:ASN:N	2.53	0.42
46:B:695:C:H1'	46:B:696:U:P	2.60	0.42
46:B:792:U:H2'	46:B:793:A:C8	2.55	0.42
46:B:1128:A:OP2	73:c:2:PRO:HG3	2.20	0.42
47:C:118:PRO:HG2	47:C:141:ILE:HD13	2.02	0.42
48:D:36:THR:HG23	48:D:231:LEU:O	2.19	0.42
48:D:129:THR:OG1	48:D:131:ASP:OD1	2.34	0.42
54:J:33:GLU:O	54:J:37:LEU:HG	2.20	0.42
57:M:56:LYS:NZ	57:M:69:THR:HG22	2.34	0.42
79:AR:145:LEU:HD23	79:AR:145:LEU:HA	1.87	0.42
1:AS:523:G:H2'	1:AS:524:G:H8	1.84	0.42
1:AS:661:C:H2'	1:AS:662:U:C6	2.54	0.42
1:AS:1245:G:H2'	1:AS:1246:G:H8	1.84	0.42
1:AS:2322:U:H2'	1:AS:2323:A:H8	1.81	0.42
1:AS:2744:C:H4'	1:AS:2745:C:H5'	2.02	0.42
1:AS:3308:G:O2'	1:AS:3327:A:N6	2.51	0.42
5:AX:148:LEU:CD1	5:AX:196:LYS:HD2	2.50	0.42
6:AY:296:VAL:O	6:AY:300:VAL:HG13	2.19	0.42
7:AZ:178:ASN:HA	7:AZ:183:TRP:CG	2.54	0.42
11:BD:47:LYS:HE2	15:BH:3:SER:HB3	2.02	0.42
46:CM:138:C:O4'	53:CT:179:VAL:HG11	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:272:G:C2	46:CM:281:U:H1'	2.54	0.42
46:CM:495:G:H2'	46:CM:496:G:C8	2.54	0.42
46:CM:824:U:C4	46:CM:825:U:C5	3.08	0.42
46:CM:872:A:H2'	46:CM:873:U:H6	1.82	0.42
46:CM:1377:A:H2'	46:CM:1378:U:C6	2.55	0.42
47:CN:180:GLU:OE2	47:CN:191:ARG:NH2	2.52	0.42
48:CO:86:LEU:HB3	48:CO:98:THR:HB	2.00	0.42
51:CR:31:PRO:HG2	51:CR:38:LEU:HG	2.01	0.42
75:DP:43:ASN:ND2	75:DP:66:LEU:HD13	2.34	0.42
79:DT:76:ALA:H	79:DT:120:LEU:HD21	1.84	0.42
82:l1:41:TYR:CE1	82:l1:195:LYS:HG2	2.54	0.42
82:l1:67:ILE:N	82:l1:83:ASP:OD2	2.51	0.42
82:l1:93:LEU:O	82:l1:95:LYS:N	2.52	0.42
82:l1:215:ARG:C	82:l1:216:ILE:HD13	2.45	0.42
1:1:19:A:H2'	1:1:20:G:C8	2.55	0.42
1:1:602:A:OP1	1:1:602:A:C8	2.66	0.42
1:1:635:C:C2	1:1:636:C:C5	3.07	0.42
1:1:750:G:H1	1:1:774:U:H3	1.68	0.42
1:1:856:G:O2'	1:1:891:A:H4'	2.19	0.42
1:1:1467:U:H2'	1:1:1468:U:C6	2.55	0.42
1:1:1633:A:OP1	28:AA:73:LYS:HE2	2.18	0.42
1:1:2564:G:H4'	1:1:2566:C:C2	2.54	0.42
1:1:3067:U:H2'	1:1:3068:C:H6	1.84	0.42
1:1:3153:A:H2'	1:1:3154:A:C8	2.54	0.42
4:j:65:ASP:HB3	4:j:68:LYS:O	2.19	0.42
19:y:173:GLU:HA	29:AB:51:GLY:C	2.45	0.42
22:2:112:ASN:HB3	22:2:128:LEU:HD13	2.01	0.42
27:9:55:GLU:HA	27:9:69:LYS:HA	2.02	0.42
32:AE:43:MET:CE	32:AE:76:ARG:HB2	2.48	0.42
33:AF:98:ALA:HB3	33:AF:101:VAL:HG23	2.01	0.42
44:AQ:32:GLN:O	44:AQ:37:TYR:OH	2.34	0.42
45:i:92:SER:HA	46:B:1259:C:C5	2.54	0.42
46:B:1:U:H1'	49:E:174:VAL:HG13	2.02	0.42
46:B:294:U:H2'	46:B:295:U:C6	2.54	0.42
46:B:740:A:HO2'	46:B:741:A:P	2.41	0.42
46:B:770:C:H6	46:B:770:C:OP1	2.02	0.42
46:B:871:U:H2'	46:B:872:A:C8	2.51	0.42
46:B:953:U:H5''	46:B:1018:C:O2'	2.20	0.42
46:B:1191:U:OP2	46:B:1192:C:O2'	2.18	0.42
46:B:1609:G:H2'	46:B:1610:C:H6	1.84	0.42
46:B:1634:U:H2'	46:B:1635:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:1756:U:H1'	61:Q:131:ARG:HB3	2.01	0.42
54:J:11:THR:HG23	54:J:14:GLU:H	1.84	0.42
57:M:11:ILE:HA	57:M:35:ILE:HD13	2.02	0.42
57:M:70:ASP:HB3	57:M:91:ARG:NH2	2.34	0.42
63:S:22:LYS:HB3	63:S:63:ASP:OD1	2.20	0.42
70:Z:89:ASN:HB2	70:Z:92:CYS:SG	2.59	0.42
79:AR:246:ARG:NH2	79:AR:312:VAL:HG21	2.34	0.42
1:AS:88:G:N7	19:BL:171:LYS:NZ	2.67	0.42
1:AS:225:C:H2'	1:AS:226:G:O4'	2.19	0.42
1:AS:277:G:H2'	1:AS:278:U:H6	1.83	0.42
1:AS:935:U:O2'	1:AS:2380:A:N1	2.50	0.42
1:AS:1190:G:H2'	1:AS:1191:A:C8	2.55	0.42
1:AS:1837:A:H1'	40:CG:45:ARG:HH22	1.84	0.42
1:AS:2310:A:H2'	1:AS:2311:C:O4'	2.20	0.42
1:AS:2855:U:H2'	1:AS:2856:C:H6	1.84	0.42
1:AS:3201:U:H1'	1:AS:3217:G:N2	2.35	0.42
17:BJ:51:ASN:ND2	17:BJ:137:THR:OG1	2.44	0.42
18:BK:94:LEU:HD23	18:BK:94:LEU:HA	1.87	0.42
18:BK:177:ALA:O	18:BK:181:ARG:HG3	2.19	0.42
31:BX:63:MET:HE3	31:BX:63:MET:HB3	1.83	0.42
46:CM:233:G:H8	46:CM:233:G:OP2	2.02	0.42
46:CM:260:U:C2'	46:CM:261:C:H5'	2.49	0.42
46:CM:496:G:C6	46:CM:497:U:C2	3.07	0.42
46:CM:518:A:HO2'	46:CM:519:A:P	2.42	0.42
46:CM:652:C:N4	46:CM:654:G:C6	2.88	0.42
46:CM:671:G:N2	46:CM:672:U:O2	2.53	0.42
46:CM:720:C:O2'	46:CM:721:C:OP2	2.38	0.42
46:CM:1130:U:O2'	49:CP:84:GLN:O	2.35	0.42
46:CM:1237:C:H5'	78:DS:147:TYR:OH	2.19	0.42
46:CM:1354:U:C2'	46:CM:1355:A:H5'	2.49	0.42
46:CM:1784:A:H5'	73:DN:95:ARG:HG2	2.00	0.42
47:CN:43:ASP:OD1	47:CN:44:GLY:N	2.52	0.42
50:CQ:176:VAL:HB	50:CQ:183:LEU:CD2	2.50	0.42
52:CS:57:SER:HA	75:DP:53:ILE:HB	2.00	0.42
52:CS:143:ARG:HG2	75:DP:55:CYS:SG	2.60	0.42
62:DC:34:THR:HG21	62:DC:45:PHE:CD2	2.54	0.42
64:DE:89:SER:C	64:DE:91:LEU:N	2.78	0.42
68:DI:85:TYR:O	74:DO:6:ASP:N	2.52	0.42
69:DJ:75:ILE:HD12	69:DJ:125:ILE:HD13	2.01	0.42
82:L1:24:LYS:H	82:L1:24:LYS:HG2	1.65	0.42
1:1:96:U:H2'	1:1:97:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:623:A:H2'	1:1:624:U:H6	1.82	0.42
1:1:677:U:H2'	1:1:678:G:C8	2.55	0.42
1:1:787:A:H2'	1:1:788:G:C8	2.55	0.42
1:1:1139:A:H5'	1:1:1364:U:H1'	2.01	0.42
1:1:2159:C:H5''	4:j:193:ARG:CZ	2.50	0.42
1:1:2293:G:C2	1:1:2294:G:N7	2.88	0.42
1:1:2367:C:H1'	18:x:69:ARG:CZ	2.49	0.42
1:1:2814:U:O2	1:1:2814:U:H2'	2.19	0.42
1:1:2956:C:H2'	1:1:2957:C:C6	2.54	0.42
6:l:16:GLN:NE2	6:l:147:LYS:HD2	2.35	0.42
13:s:62:ASN:HB2	43:AP:103:ALA:HA	2.02	0.42
19:y:55:SER:O	19:y:59:ARG:HG2	2.19	0.42
46:B:234:G:H2'	46:B:235:C:C6	2.54	0.42
46:B:327:G:H5'	55:K:99:SER:OG	2.20	0.42
46:B:769:U:O2'	46:B:770:C:OP2	2.34	0.42
46:B:1230:G:N2	46:B:1235:U:O4	2.44	0.42
47:C:144:ILE:HG12	47:C:158:VAL:HB	2.01	0.42
59:O:60:CYS:SG	59:O:122:VAL:HG22	2.59	0.42
59:O:103:LEU:HD13	59:O:116:VAL:HB	2.01	0.42
70:Z:107:PHE:CD2	70:Z:114:LYS:HD3	2.51	0.42
79:AR:133:LYS:HD3	79:AR:141:CYS:SG	2.59	0.42
1:AS:108:A:O2'	1:AS:323:A:N6	2.52	0.42
1:AS:831:G:H1'	1:AS:854:A:N6	2.35	0.42
1:AS:1303:G:H4'	1:AS:1304:A:O5'	2.20	0.42
1:AS:2062:G:H2'	1:AS:2063:C:H5	1.83	0.42
1:AS:2279:U:H2'	1:AS:2280:G:H8	1.84	0.42
1:AS:2623:G:H5''	1:AS:2624:U:O4'	2.19	0.42
1:AS:3013:U:OP1	24:BQ:12:ARG:NE	2.51	0.42
3:AU:142:C:H2'	3:AU:143:U:C6	2.54	0.42
7:AZ:41:LYS:HD3	7:AZ:41:LYS:HA	1.81	0.42
13:BF:87:LYS:HG2	13:BF:91:LEU:HD23	2.02	0.42
13:BF:108:GLU:OE2	65:DF:110:ARG:NH2	2.46	0.42
28:BU:12:ILE:O	28:BU:81:MET:N	2.47	0.42
39:CF:8:ILE:O	39:CF:12:VAL:HG23	2.19	0.42
46:CM:58:U:O2'	46:CM:449:G:N3	2.49	0.42
46:CM:325:U:H2'	46:CM:326:A:C8	2.54	0.42
46:CM:529:C:O2'	46:CM:530:U:OP1	2.33	0.42
46:CM:1416:U:H1'	67:DH:71:ASN:HB3	2.00	0.42
47:CN:21:ASN:HB3	47:CN:24:LEU:HD12	2.02	0.42
50:CQ:105:ALA:O	50:CQ:109:LYS:HG2	2.19	0.42
53:CT:48:TYR:OH	53:CT:121:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:CT:159:ARG:HB2	53:CT:170:THR:HB	2.01	0.42
61:DB:9:PHE:HA	61:DB:73:ALA:O	2.18	0.42
63:DD:11:LYS:HG2	63:DD:16:THR:HG22	2.01	0.42
63:DD:46:LYS:HA	63:DD:46:LYS:HD2	1.71	0.42
79:DT:134:VAL:HG23	79:DT:142:MET:HE2	2.02	0.42
81:12:103:ASN:O	81:12:104:ILE:HG12	2.19	0.42
80:p0:7:LYS:HA	80:p0:7:LYS:HD3	1.84	0.42
1:1:195:G:N2	1:1:197:A:H3'	2.35	0.42
1:1:259:C:H2'	1:1:260:C:C6	2.54	0.42
1:1:260:C:H2'	1:1:261:U:C6	2.54	0.42
1:1:922:A:H2'	1:1:923:C:C6	2.55	0.42
1:1:2400:C:O5'	43:AP:52:GLY:HA2	2.18	0.42
1:1:2401:U:H2'	1:1:2402:A:C8	2.54	0.42
1:1:2459:G:H3'	82:l1:98:LYS:NZ	2.34	0.42
1:1:2933:G:H2'	1:1:2934:U:H6	1.82	0.42
1:1:3316:U:H3	55:K:110:ARG:NH2	2.18	0.42
1:1:3336:G:H2'	1:1:3337:A:C8	2.54	0.42
85:1:3958:TIX:O05	85:1:3958:TIX:O03	2.38	0.42
3:4:13:A:O2'	18:x:121:HIS:O	2.35	0.42
4:j:247:ARG:HB3	46:B:997:U:H4'	2.02	0.42
6:l:30:PRO:HB3	19:y:25:TYR:HE2	1.84	0.42
13:s:19:LEU:O	13:s:68:HIS:HA	2.19	0.42
26:8:67:ILE:HD12	26:8:121:LYS:HG3	2.01	0.42
31:AD:12:ILE:H	31:AD:12:ILE:HD12	1.85	0.42
34:AG:49:ILE:HD11	34:AG:71:VAL:HG22	2.02	0.42
45:i:64:LEU:HD22	62:R:98:ASN:ND2	2.34	0.42
45:i:118:GLU:HG2	50:F:121:TYR:CE2	2.55	0.42
46:B:182:C:H2'	46:B:183:C:C6	2.55	0.42
46:B:1163:G:H5'	46:B:1175:C:H42	1.84	0.42
46:B:1219:A:H5'	46:B:1220:C:OP1	2.19	0.42
46:B:1350:C:O3'	63:S:29:LYS:HE2	2.19	0.42
46:B:1464:G:C4	46:B:1465:A:C8	3.07	0.42
48:D:115:ARG:HD3	48:D:115:ARG:HA	1.64	0.42
52:H:43:PHE:CE1	52:H:70:VAL:HG23	2.47	0.42
76:f:19:ARG:HD2	76:f:32:ARG:HD3	2.00	0.42
79:AR:118:LYS:HD2	79:AR:159:PRO:HA	2.01	0.42
1:AS:259:C:H2'	1:AS:260:C:C6	2.54	0.42
1:AS:649:G:C6	1:AS:650:G:C6	3.07	0.42
1:AS:976:A:H8	1:AS:976:A:H3'	1.85	0.42
1:AS:1255:A:H61	80:p0:33:VAL:CG1	2.31	0.42
1:AS:1559:C:O2'	1:AS:1560:U:OP1	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:1619:G:H2'	1:AS:1620:G:O4'	2.19	0.42
1:AS:1737:A:H2'	1:AS:1738:U:O4'	2.18	0.42
1:AS:1922:C:H5''	44:CK:8:VAL:CG1	2.50	0.42
1:AS:2115:U:C6	1:AS:2119:U:C4	3.07	0.42
1:AS:2451:C:H3'	1:AS:2452:G:H4'	2.01	0.42
1:AS:2658:A:H2'	1:AS:2659:G:O4'	2.20	0.42
1:AS:3199:G:H1	1:AS:3218:U:H3	1.68	0.42
15:BH:116:LEU:HD22	17:BJ:191:ALA:HA	2.01	0.42
46:CM:825:U:O2'	46:CM:826:U:H5''	2.19	0.42
46:CM:1575:G:O2'	52:CS:106:LYS:NZ	2.52	0.42
46:CM:1581:G:H2'	46:CM:1582:U:O4'	2.19	0.42
49:CP:160:VAL:HG11	49:CP:205:THR:HA	2.01	0.42
50:CQ:110:LEU:HD13	50:CQ:183:LEU:HD11	2.01	0.42
50:CQ:158:MET:HE2	50:CQ:158:MET:HB2	1.91	0.42
51:CR:152:PRO:HD2	53:CT:211:LEU:HD22	2.02	0.42
53:CT:32:MET:HE2	53:CT:100:CYS:HB2	2.01	0.42
54:CU:85:HIS:HD1	54:CU:161:LYS:HG2	1.85	0.42
59:CZ:107:ASP:C	59:CZ:109:ASP:H	2.27	0.42
68:DI:36:ILE:HG12	68:DI:51:ILE:O	2.19	0.42
72:DM:50:ILE:HG12	72:DM:69:LEU:HD13	2.02	0.42
1:1:619:A:H8	1:1:619:A:OP2	2.02	0.42
1:1:1221:A:H2'	1:1:1222:G:H8	1.84	0.42
1:1:1268:C:H2'	1:1:1269:A:O4'	2.20	0.42
1:1:1620:G:O2'	1:1:1639:A:N1	2.50	0.42
1:1:1714:G:H2'	1:1:1715:G:H8	1.84	0.42
1:1:2329:U:H2'	1:1:2330:A:H8	1.85	0.42
1:1:2632:G:O3'	1:1:2721:G:N2	2.53	0.42
1:1:3067:U:H2'	1:1:3068:C:C6	2.54	0.42
3:4:83:U:H4'	3:4:85:G:N3	2.35	0.42
10:p:83:LEU:HD23	10:p:83:LEU:HA	1.82	0.42
45:i:64:LEU:HA	45:i:67:LYS:CE	2.49	0.42
46:B:538:G:H22	77:g:25:GLU:CD	2.28	0.42
46:B:962:A:H2'	46:B:963:A:O4'	2.19	0.42
46:B:1537:A:C6	46:B:1549:G:C6	3.07	0.42
52:H:44:ASN:HB2	63:S:45:PHE:CZ	2.54	0.42
59:O:59:LEU:HD22	59:O:123:VAL:CG2	2.50	0.42
65:U:57:ARG:NH2	72:b:74:SER:OG	2.43	0.42
79:AR:153:SER:OG	79:AR:197:SER:O	2.28	0.42
1:AS:273:A:H2'	1:AS:274:G:H8	1.84	0.42
1:AS:291:C:C2	1:AS:292:U:C5	3.08	0.42
1:AS:452:A:HO2'	1:AS:453:U:P	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:713:A:OP1	29:BV:133:LEU:HB3	2.19	0.42
1:AS:1576:A:H3'	1:AS:1577:C:H6	1.85	0.42
1:AS:1618:U:H2'	1:AS:1619:G:H8	1.84	0.42
1:AS:1754:G:H2'	1:AS:1755:U:O4'	2.20	0.42
1:AS:2718:A:H2'	1:AS:2719:A:O4'	2.20	0.42
1:AS:2807:U:C2	1:AS:2808:C:C5	3.08	0.42
13:BF:117:ASP:CB	13:BF:120:ILE:HD12	2.49	0.42
14:BG:2:ALA:HB1	29:BV:33:GLY:O	2.20	0.42
45:CL:101:LYS:HD3	46:CM:573:C:H4'	2.02	0.42
46:CM:188:U:O4	55:CV:143:ARG:HB2	2.19	0.42
46:CM:1238:U:H2'	46:CM:1239:U:C6	2.55	0.42
46:CM:1757:U:H2'	46:CM:1758:U:C6	2.55	0.42
47:CN:88:LYS:HG3	47:CN:201:LEU:HD11	2.02	0.42
49:CP:122:ALA:O	49:CP:126:ILE:HG13	2.20	0.42
65:DF:16:ARG:NH1	65:DF:21:ASN:OD1	2.52	0.42
65:DF:25:ARG:HB3	65:DF:25:ARG:HH11	1.85	0.42
70:DK:79:ASN:OD1	70:DK:79:ASN:N	2.51	0.42
74:DO:57:ASP:OD1	74:DO:58:SER:N	2.52	0.42
77:DR:37:ARG:O	77:DR:41:THR:HG23	2.20	0.42
82:I1:21:THR:CA	82:I1:25:LYS:HE3	2.50	0.42
1:1:196:G:N2	1:1:372:A:C8	2.88	0.42
1:1:571:C:H2'	1:1:572:U:C6	2.55	0.42
1:1:638:U:OP1	29:AB:15:VAL:HG21	2.19	0.42
1:1:708:A:H2'	1:1:709:A:C8	2.55	0.42
1:1:945:C:O2'	1:1:967:G:OP1	2.36	0.42
1:1:1163:U:H2'	1:1:1164:U:O4'	2.20	0.42
1:1:1232:G:O3'	1:1:1241:A:H4'	2.19	0.42
1:1:1275:C:H2'	1:1:1276:C:C6	2.55	0.42
1:1:1627:C:H5''	1:1:1628:A:H5''	2.02	0.42
1:1:1767:G:H2'	1:1:1768:U:O4'	2.20	0.42
1:1:2183:U:HO2'	1:1:2184:G:P	2.42	0.42
1:1:2471:U:H3'	1:1:2472:A:H5''	2.02	0.42
1:1:2988:A:H2'	1:1:2989:A:C8	2.53	0.42
1:1:3079:U:H2'	1:1:3080:G:H8	1.85	0.42
1:1:3270:A:H2'	1:1:3271:U:O4'	2.20	0.42
3:4:4:C:H2'	3:4:5:U:C6	2.55	0.42
8:n:29:LEU:HD23	8:n:29:LEU:HA	1.89	0.42
8:n:59:ASP:HB2	8:n:102:VAL:CG2	2.50	0.42
16:v:62:TYR:HE2	16:v:110:ALA:HB2	1.85	0.42
16:v:143:ARG:HB3	36:AI:96:GLU:OE1	2.19	0.42
26:8:108:LEU:N	26:8:125:ARG:O	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:B:141:G:H2'	46:B:142:G:C8	2.55	0.42
46:B:517:C:H6	46:B:517:C:H2'	1.69	0.42
46:B:1484:U:C4	46:B:1498:G:C2	3.07	0.42
48:D:167:LYS:HD3	48:D:170:GLU:OE2	2.20	0.42
50:F:7:SER:HB3	50:F:10:LYS:HG3	2.02	0.42
56:L:140:ILE:HD12	71:a:65:GLY:HA3	2.02	0.42
58:N:73:GLY:HA3	58:N:86:ILE:HD12	2.02	0.42
59:O:132:GLU:C	59:O:134:ASN:H	2.27	0.42
64:T:71:PHE:CZ	64:T:74:GLN:HG3	2.54	0.42
68:X:37:ALA:HA	68:X:50:ASN:OD1	2.20	0.42
1:AS:46:C:OP1	14:BG:16:LYS:HE2	2.20	0.42
1:AS:284:A:N6	1:AS:2757:A:O4'	2.52	0.42
1:AS:292:U:OP2	16:BI:68:ARG:NH2	2.40	0.42
1:AS:790:U:H2'	1:AS:791:G:H8	1.85	0.42
1:AS:952:U:H2'	1:AS:953:C:C6	2.55	0.42
1:AS:1705:C:H2'	1:AS:1706:C:C6	2.54	0.42
1:AS:1756:A:C6	1:AS:1762:G:C5	3.08	0.42
1:AS:2193:A:C4	1:AS:2194:G:C8	3.07	0.42
1:AS:2442:U:H1'	82:L1:162:VAL:HG23	2.02	0.42
1:AS:2467:C:H3'	1:AS:2468:C:H2'	2.02	0.42
1:AS:3172:U:N3	21:BN:164:GLN:OE1	2.42	0.42
1:AS:3322:U:H2'	1:AS:3323:U:C6	2.55	0.42
5:AX:66:LYS:NZ	24:BQ:9:ASN:H	2.18	0.42
11:BD:2:LYS:HD3	11:BD:61:ASP:OD2	2.19	0.42
13:BF:87:LYS:HB2	13:BF:87:LYS:HE2	1.82	0.42
16:BI:146:ALA:HA	16:BI:149:ASN:OD1	2.20	0.42
17:BJ:63:THR:HG23	17:BJ:66:ASN:O	2.20	0.42
18:BK:123:PRO:O	18:BK:143:PRO:HG2	2.20	0.42
46:CM:144:U:H5	46:CM:166:A:N7	2.17	0.42
46:CM:331:A:H2'	46:CM:332:G:C8	2.55	0.42
46:CM:840:A:C2	46:CM:842:U:H1'	2.54	0.42
46:CM:1158:C:H2'	46:CM:1159:C:H6	1.85	0.42
46:CM:1233:C:C2	46:CM:1234:U:C5	3.08	0.42
46:CM:1311:A:H2'	46:CM:1312:C:H6	1.84	0.42
48:CO:105:PHE:CE1	48:CO:213:ARG:HA	2.54	0.42
48:CO:136:ARG:NE	48:CO:218:LEU:HD11	2.34	0.42
50:CQ:30:LEU:HD22	50:CQ:59:VAL:HG22	2.00	0.42
57:CX:14:TYR:CD2	57:CX:35:ILE:HD11	2.55	0.42
59:CZ:80:ASN:O	59:CZ:82:PRO:CD	2.57	0.42
59:CZ:111:ASN:O	59:CZ:112:ALA:O	2.37	0.42
72:DM:36:ALA:HB1	72:DM:38:HIS:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:L1:55:LEU:HB2	82:L1:153:SER:HB2	2.01	0.42
1:1:126:G:H2'	1:1:127:G:H8	1.85	0.42
1:1:214:G:OP1	27:9:12:ARG:NH1	2.51	0.42
1:1:1593:C:OP1	35:AH:8:ARG:NH2	2.49	0.42
1:1:1908:U:O2'	1:1:2099:G:N7	2.33	0.42
1:1:2850:G:H5''	5:k:5:LYS:HE2	2.01	0.42
3:4:4:C:H2'	3:4:5:U:H6	1.85	0.42
4:j:201:GLY:O	4:j:204:MET:HG3	2.20	0.42
18:x:19:GLY:HA3	18:x:22:LEU:HD11	2.02	0.42
29:AB:59:ARG:HH22	43:AP:38:GLN:HG2	1.84	0.42
45:i:52:LYS:HG3	45:i:53:LYS:N	2.35	0.42
46:B:154:A:H2'	46:B:155:A:O4'	2.20	0.42
46:B:218:A:N1	46:B:219:A:C5	2.88	0.42
46:B:885:A:O4'	46:B:900:A:H2	2.02	0.42
46:B:1144:C:H4'	46:B:1567:C:OP1	2.20	0.42
46:B:1410:A:C2'	49:E:87:ALA:HB3	2.47	0.42
52:H:145:ASP:OD1	52:H:146:SER:N	2.53	0.42
63:S:30:ILE:CG1	63:S:35:ILE:HG22	2.49	0.42
64:T:89:SER:C	64:T:91:LEU:N	2.76	0.42
65:U:126:ARG:HB2	65:U:133:VAL:HG12	2.02	0.42
1:AS:1093:G:H4'	22:BO:129:LYS:HG2	2.01	0.42
1:AS:1328:A:H2'	1:AS:1329:C:H6	1.85	0.42
1:AS:1696:G:H2'	1:AS:1697:C:C6	2.55	0.42
1:AS:1714:G:H2'	1:AS:1715:G:H8	1.85	0.42
1:AS:2096:C:H2'	1:AS:2097:A:O4'	2.19	0.42
1:AS:2401:U:H2'	1:AS:2402:A:C8	2.55	0.42
1:AS:2749:G:H5'	1:AS:2751:A:OP2	2.20	0.42
2:AT:46:A:OP1	7:AZ:158:ARG:N	2.47	0.42
3:AU:19:C:H2'	3:AU:20:U:C6	2.54	0.42
7:AZ:95:TRP:CE3	7:AZ:198:TYR:HB3	2.55	0.42
13:BF:148:ILE:HG22	13:BF:152:HIS:HB3	2.01	0.42
16:BI:94:TYR:OH	16:BI:96:LYS:HE2	2.20	0.42
19:BL:44:PHE:CD2	19:BL:134:GLY:HA3	2.55	0.42
23:BP:102:LYS:HE3	23:BP:102:LYS:HB2	1.86	0.42
46:CM:91:G:H2'	46:CM:92:A:O4'	2.20	0.42
46:CM:588:C:H2'	46:CM:589:A:H8	1.84	0.42
46:CM:647:C:O2'	46:CM:648:U:H6	2.02	0.42
46:CM:881:U:O2	61:DB:36:ARG:NH1	2.53	0.42
46:CM:891:A:H2'	46:CM:892:A:C8	2.55	0.42
46:CM:1020:G:C2	46:CM:1086:G:C6	3.08	0.42
50:CQ:68:HIS:CE1	57:CX:93:LYS:HG2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:DA:5:HIS:HB2	60:DA:121:ARG:HH21	1.85	0.42
61:DB:98:ARG:HD2	73:DN:49:ALA:HB2	2.02	0.42
65:DF:84:TRP:C	65:DF:89:GLN:HE22	2.28	0.42
79:DT:145:LEU:HD21	79:DT:178:TRP:CZ2	2.55	0.42
81:12:116:MET:O	81:12:119:LYS:HG2	2.20	0.42
82:l1:73:ASP:OD1	82:l1:113:SER:HB2	2.19	0.42
1:1:163:A:H2'	1:1:164:U:O4'	2.20	0.41
1:1:276:U:O2	16:v:93:LYS:HE2	2.20	0.41
1:1:313:A:H2'	1:1:314:U:C6	2.54	0.41
1:1:798:C:C2	1:1:799:C:C5	3.08	0.41
1:1:962:U:OP1	29:AB:44:ASN:ND2	2.53	0.41
1:1:1291:G:H4'	21:0:115:ARG:HG2	2.02	0.41
1:1:1660:G:H2'	1:1:1661:U:H6	1.85	0.41
1:1:2157:C:C4	4:j:131:GLY:HA3	2.55	0.41
1:1:2383:C:O2	1:1:2791:A:N1	2.53	0.41
1:1:2497:A:C6	1:1:2561:G:C6	3.08	0.41
6:l:61:THR:HG22	6:l:63:ALA:N	2.34	0.41
7:m:160:PHE:CE2	7:m:179:ARG:HB3	2.55	0.41
13:s:88:GLU:HB3	62:R:10:ARG:HH11	1.83	0.41
46:B:53:G:H2'	46:B:54:C:C6	2.55	0.41
46:B:411:U:H2'	46:B:412:C:C6	2.55	0.41
46:B:512:G:N3	46:B:513:A:C8	2.88	0.41
46:B:1198:G:N2	46:B:1436:U:O2	2.41	0.41
46:B:1293:G:H2'	46:B:1294:C:C6	2.55	0.41
46:B:1517:C:O5'	72:b:96:SER:OG	2.37	0.41
46:B:1700:G:N3	46:B:1700:G:H2'	2.35	0.41
46:B:1783:C:H6	73:c:7:SER:HB3	1.84	0.41
54:J:60:PRO:N	54:J:61:PRO:HD2	2.34	0.41
61:Q:126:GLY:O	73:c:22:ARG:NH2	2.53	0.41
74:d:56:CYS:HB3	74:d:63:LEU:HD11	2.01	0.41
79:AR:118:LYS:HD2	79:AR:159:PRO:C	2.45	0.41
1:AS:58:G:H2'	3:AU:33:A:O2'	2.20	0.41
1:AS:787:A:H2'	1:AS:788:G:H8	1.85	0.41
1:AS:807:U:H2'	1:AS:808:G:H8	1.85	0.41
1:AS:1236:A:H3'	1:AS:1237:U:C5	2.54	0.41
1:AS:1347:U:O2'	1:AS:1348:U:OP2	2.33	0.41
1:AS:1737:A:H3'	1:AS:1738:U:H6	1.85	0.41
1:AS:2242:U:H2'	1:AS:2243:C:H6	1.85	0.41
1:AS:2423:A:O3'	37:CD:61:ARG:HD3	2.20	0.41
1:AS:2660:U:O4	7:AZ:19:PRO:HD3	2.20	0.41
1:AS:3110:U:OP1	5:AX:274:HIS:ND1	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:3264:C:H2'	1:AS:3265:U:C6	2.54	0.41
2:AT:61:C:H2'	2:AT:62:U:H6	1.85	0.41
2:AT:107:A:H2'	2:AT:108:U:C6	2.54	0.41
6:AY:5:PRO:O	6:AY:23:LEU:HB2	2.20	0.41
46:CM:158:C:H2'	46:CM:159:U:O4'	2.20	0.41
46:CM:233:G:H2'	46:CM:234:G:H8	1.82	0.41
46:CM:368:A:H2'	46:CM:369:G:C8	2.55	0.41
46:CM:598:U:OP2	70:DK:108:GLY:HA2	2.19	0.41
46:CM:1205:C:H2'	46:CM:1206:A:C8	2.54	0.41
46:CM:1206:A:H2'	46:CM:1207:C:O4'	2.19	0.41
48:CO:81:TYR:HB2	48:CO:109:LYS:HG2	2.00	0.41
48:CO:120:LEU:HD13	48:CO:142:PHE:CE2	2.55	0.41
50:CQ:7:SER:O	50:CQ:11:LYS:N	2.53	0.41
50:CQ:80:LEU:HD23	50:CQ:81:SER:H	1.84	0.41
56:CW:34:TYR:CD2	56:CW:105:LEU:HD22	2.55	0.41
65:DF:33:THR:HA	65:DF:38:VAL:O	2.20	0.41
75:DP:38:ARG:O	75:DP:40:ILE:HG12	2.20	0.41
82:l1:35:GLN:HB2	82:l1:205:VAL:HB	2.02	0.41
82:l1:111:ILE:HA	82:l1:136:THR:HB	2.02	0.41
80:p0:45:LEU:CD1	80:p0:49:ALA:HB3	2.48	0.41
1:1:259:C:H2'	1:1:260:C:H6	1.86	0.41
1:1:538:G:C6	1:1:548:G:C6	3.08	0.41
1:1:933:G:N2	1:1:957:C:OP1	2.51	0.41
1:1:1083:G:O2'	30:AC:54:LEU:HD11	2.19	0.41
1:1:1142:C:H4'	1:1:1327:U:C4	2.54	0.41
1:1:1194:C:OP2	1:1:1195:C:O2'	2.32	0.41
1:1:1221:A:H2'	1:1:1222:G:C8	2.55	0.41
1:1:1233:G:C4	1:1:1234:C:C5	3.08	0.41
1:1:1696:G:H5'	39:AL:3:ARG:NH1	2.35	0.41
1:1:1945:A:H2'	1:1:1946:U:C6	2.54	0.41
1:1:2642:G:H2'	1:1:2643:A:C8	2.55	0.41
1:1:2979:U:H2'	1:1:2980:A:C8	2.56	0.41
1:1:3228:G:H2'	1:1:3229:G:C8	2.55	0.41
35:AH:67:LYS:HA	35:AH:70:LYS:HE2	2.02	0.41
46:B:684:C:H2'	46:B:685:C:H6	1.82	0.41
46:B:1258:G:N7	46:B:1416:U:H3'	2.35	0.41
46:B:1743:A:OP2	46:B:1743:A:H8	2.03	0.41
47:C:147:THR:CG2	47:C:159:ALA:HB1	2.47	0.41
47:C:200:ASP:O	47:C:203:PHE:HB2	2.20	0.41
55:K:39:GLY:O	55:K:61:GLU:HG3	2.20	0.41
57:M:35:ILE:HG22	57:M:37:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:R:34:THR:HA	62:R:37:CYS:SG	2.60	0.41
63:S:19:ALA:HB2	63:S:83:ALA:HB1	2.01	0.41
63:S:72:GLY:H	63:S:75:SER:HB3	1.85	0.41
65:U:22:ILE:HD11	65:U:35:ILE:HD11	2.01	0.41
66:V:42:GLY:HA3	66:V:94:VAL:HG21	2.02	0.41
73:c:97:PRO:HA	73:c:98:PRO:HD3	1.97	0.41
79:AR:90:LEU:HD21	79:AR:111:VAL:HG11	2.02	0.41
1:AS:429:U:H4'	34:CA:88:ASN:O	2.20	0.41
1:AS:787:A:H2'	1:AS:788:G:C8	2.55	0.41
1:AS:975:U:H4'	1:AS:976:A:O4'	2.20	0.41
1:AS:1825:A:H5''	1:AS:1826:G:H5'	2.01	0.41
1:AS:2659:G:H4'	7:AZ:7:PHE:CE2	2.55	0.41
1:AS:3014:U:O3'	24:BQ:45:ARG:HD3	2.20	0.41
1:AS:3101:A:H2'	1:AS:3102:A:H5''	2.02	0.41
85:AS:3782:TIX:O03	85:AS:3782:TIX:O05	2.37	0.41
2:AT:19:C:H2'	2:AT:20:A:C8	2.55	0.41
2:AT:60:G:H2'	2:AT:61:C:C6	2.55	0.41
5:AX:160:VAL:HG12	5:AX:181:ILE:O	2.19	0.41
6:AY:17:GLY:O	6:AY:18:SER:OG	2.33	0.41
8:BA:91:ASN:OD1	8:BA:93:SER:OG	2.32	0.41
12:BE:19:LYS:HB3	12:BE:19:LYS:HE2	1.70	0.41
17:BJ:13:LYS:HD2	17:BJ:38:ARG:NH2	2.34	0.41
25:BR:101:ARG:O	25:BR:105:ARG:HG3	2.20	0.41
46:CM:272:G:N2	46:CM:281:U:H1'	2.35	0.41
46:CM:402:G:H2'	46:CM:403:C:H6	1.85	0.41
46:CM:474:U:H2'	77:DR:31:GLN:NE2	2.23	0.41
46:CM:494:G:H3'	46:CM:495:G:H5''	2.02	0.41
46:CM:520:U:H2'	46:CM:521:G:O4'	2.20	0.41
46:CM:1149:G:H2'	46:CM:1150:G:C8	2.55	0.41
46:CM:1293:G:H2'	46:CM:1294:C:C6	2.55	0.41
46:CM:1296:U:C2	46:CM:1300:U:C4	3.08	0.41
46:CM:1503:A:O2'	46:CM:1504:U:H5'	2.19	0.41
51:CR:249:ILE:HD12	56:CW:71:PHE:CD2	2.55	0.41
53:CT:229:LYS:HE3	53:CT:229:LYS:HB3	1.61	0.41
54:CU:33:GLU:HG3	54:CU:69:VAL:CG1	2.50	0.41
59:CZ:74:LEU:O	59:CZ:78:LEU:HD23	2.20	0.41
62:DC:15:PHE:CE1	62:DC:110:GLU:HG3	2.55	0.41
72:DM:54:VAL:HG13	72:DM:60:VAL:HG11	2.02	0.41
79:DT:121:ARG:O	79:DT:121:ARG:CG	2.68	0.41
82:l1:208:SER:C	82:l1:210:MET:N	2.78	0.41
1:l:972:U:OP1	19:y:144:ARG:NH2	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1303:G:H4'	1:1:1304:A:O5'	2.19	0.41
1:1:2077:A:O2'	1:1:2078:A:H5'	2.20	0.41
1:1:2145:A:H2'	1:1:2146:A:C8	2.55	0.41
1:1:2256:C:OP1	42:AO:23:ARG:NH2	2.53	0.41
1:1:2628:A:C8	1:1:2630:G:C8	3.08	0.41
1:1:3103:U:H2'	1:1:3104:C:C6	2.55	0.41
3:4:6:U:H2'	3:4:7:U:C6	2.55	0.41
4:j:30:ARG:HG2	4:j:74:GLU:HG3	2.02	0.41
10:p:122:THR:C	10:p:124:LYS:H	2.29	0.41
20:z:62:ARG:O	20:z:66:LEU:HD23	2.20	0.41
21:0:4:LEU:HD12	21:0:104:GLU:HG3	2.02	0.41
33:AF:33:TRP:CH2	33:AF:53:GLN:HG2	2.56	0.41
45:i:136:ASN:CG	50:F:91:ARG:HH12	2.28	0.41
46:B:97:C:H2'	46:B:98:U:C6	2.55	0.41
46:B:227:C:H2'	46:B:228:C:O4'	2.20	0.41
46:B:260:U:O2'	46:B:261:C:H5'	2.20	0.41
46:B:339:A:H2'	46:B:340:C:C6	2.55	0.41
46:B:1503:A:O2'	46:B:1504:U:H5'	2.20	0.41
46:B:1546:G:N7	65:U:134:ARG:HD3	2.35	0.41
46:B:1725:U:H2'	46:B:1726:C:C6	2.55	0.41
47:C:3:LEU:HD12	47:C:3:LEU:HA	1.96	0.41
69:Y:77:PRO:HD3	70:Z:7:ARG:O	2.20	0.41
72:b:60:VAL:HG23	72:b:101:TYR:HB2	2.01	0.41
79:AR:213:LYS:HA	79:AR:236:GLU:HB2	2.03	0.41
1:AS:94:A:H5''	29:BV:34:LYS:HB2	2.02	0.41
1:AS:452:A:O2'	1:AS:453:U:P	2.78	0.41
1:AS:531:G:HO2'	1:AS:552:G:H1	1.66	0.41
1:AS:606:A:C5	8:BA:21:ARG:HD3	2.55	0.41
1:AS:849:G:N7	44:CK:2:THR:HG23	2.35	0.41
1:AS:1499:A:C4	1:AS:1500:A:C8	3.08	0.41
1:AS:1661:U:H2'	1:AS:1662:G:C8	2.56	0.41
1:AS:1706:C:H2'	1:AS:1707:U:H6	1.85	0.41
1:AS:1789:C:OP1	4:AW:177:LYS:NZ	2.49	0.41
1:AS:3135:A:H2'	1:AS:3136:C:H6	1.85	0.41
1:AS:3159:A:O2'	1:AS:3160:C:OP1	2.31	0.41
8:BA:105:PHE:HA	8:BA:134:ARG:HH22	1.85	0.41
19:BL:34:SER:HA	19:BL:49:LEU:HD22	2.02	0.41
26:BS:69:THR:O	26:BS:73:MET:HG2	2.20	0.41
46:CM:195:A:N6	55:CV:144:LYS:HD3	2.35	0.41
46:CM:212:G:N2	46:CM:250:U:O4	2.53	0.41
46:CM:223:A:C6	46:CM:822:G:N1	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:578:A:H5''	50:CQ:144:ARG:NH2	2.32	0.41
46:CM:667:A:H2'	46:CM:668:U:C6	2.55	0.41
46:CM:1102:U:H2'	46:CM:1103:G:H8	1.85	0.41
46:CM:1537:A:H2'	46:CM:1538:U:C6	2.55	0.41
46:CM:1602:C:P	52:CS:81:ARG:HE	2.43	0.41
53:CT:220:LYS:HD2	53:CT:220:LYS:HA	1.79	0.41
54:CU:155:SER:O	54:CU:157:ALA:N	2.45	0.41
60:DA:99:ARG:NH1	60:DA:99:ARG:HB2	2.36	0.41
70:DK:60:GLU:HG3	77:DR:5:HIS:NE2	2.34	0.41
79:DT:5:GLU:HB3	79:DT:248:TRP:HH2	1.86	0.41
82:L1:14:HIS:CE1	82:L1:176:GLU:HB2	2.55	0.41
1:1:941:C:H2'	1:1:942:U:H6	1.84	0.41
1:1:1695:A:C6	1:1:1743:G:C6	3.08	0.41
1:1:2182:C:H2'	1:1:2183:U:H6	1.84	0.41
5:k:283:TYR:CZ	5:k:325:LYS:HB2	2.55	0.41
12:r:77:THR:HG22	12:r:82:ARG:HA	2.02	0.41
25:7:83:VAL:HG11	46:B:68:A:H2	1.82	0.41
29:AB:119:PRO:O	29:AB:121:VAL:N	2.52	0.41
46:B:91:G:H2'	46:B:92:A:O4'	2.20	0.41
46:B:160:A:H3'	46:B:161:G:H21	1.86	0.41
46:B:326:A:H2'	46:B:327:G:O4'	2.21	0.41
46:B:399:A:O2'	46:B:400:C:H4'	2.20	0.41
46:B:478:G:H1	46:B:506:U:H3	1.68	0.41
46:B:1612:C:H2'	46:B:1613:U:H6	1.86	0.41
50:F:28:ARG:HD2	57:M:60:SER:HB2	2.02	0.41
51:G:12:LEU:HD23	51:G:12:LEU:HA	1.90	0.41
57:M:22:VAL:O	57:M:32:HIS:NE2	2.27	0.41
61:Q:65:LYS:O	61:Q:69:VAL:HG23	2.21	0.41
62:R:77:LYS:HD2	62:R:102:PHE:CE1	2.55	0.41
1:AS:29:G:H5''	16:BI:188:ARG:NH1	2.36	0.41
1:AS:95:G:H5'	14:BG:15:ARG:CZ	2.50	0.41
1:AS:187:U:O2'	1:AS:206:U:O2	2.31	0.41
1:AS:605:U:OP1	8:BA:23:THR:HB	2.20	0.41
1:AS:756:G:O2'	1:AS:766:G:N2	2.45	0.41
1:AS:962:U:H2'	1:AS:963:A:C8	2.55	0.41
1:AS:1237:U:H5''	1:AS:1238:G:OP2	2.20	0.41
1:AS:1459:U:H2'	1:AS:1460:G:O4'	2.21	0.41
1:AS:2393:C:H5''	4:AW:207:VAL:HG12	2.03	0.41
1:AS:2806:G:C4	1:AS:2807:U:C5	3.09	0.41
1:AS:2890:G:C2	1:AS:2891:A:N7	2.88	0.41
4:AW:68:LYS:HE3	4:AW:68:LYS:HB2	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AX:67:MET:HE2	24:BQ:88:ARG:HB2	2.02	0.41
11:BD:113:GLU:CD	11:BD:115:ARG:HE	2.28	0.41
13:BF:109:HIS:ND1	13:BF:122:ILE:HD12	2.35	0.41
46:CM:97:C:H2'	46:CM:98:U:C6	2.55	0.41
46:CM:484:G:O6	46:CM:499:U:O4	2.38	0.41
46:CM:976:G:P	61:DB:124:LYS:HD2	2.60	0.41
46:CM:1357:A:H4'	46:CM:1358:G:OP1	2.21	0.41
48:CO:164:VAL:HG23	48:CO:204:ILE:HG21	2.03	0.41
49:CP:233:SER:OG	49:CP:236:GLU:HG2	2.21	0.41
52:CS:48:PHE:CD1	52:CS:67:PRO:HB3	2.55	0.41
57:CX:28:ASN:HD21	76:DQ:7:TRP:HE1	1.69	0.41
59:CZ:78:LEU:O	59:CZ:81:GLU:HG3	2.20	0.41
67:DH:21:ILE:HD13	67:DH:99:VAL:HG21	2.02	0.41
82:II:98:LYS:O	82:II:100:ILE:N	2.51	0.41
1:1:314:U:H2'	1:1:315:C:H6	1.84	0.41
1:1:613:U:H2'	1:1:614:G:C8	2.56	0.41
1:1:820:C:H5''	4:j:21:ARG:HD3	2.02	0.41
1:1:1814:U:O2'	1:1:1815:U:O5'	2.35	0.41
1:1:1937:C:H42	1:1:2085:A:H61	1.67	0.41
1:1:2397:A:H1'	1:1:2776:A:O4'	2.21	0.41
1:1:2482:U:C2'	1:1:2483:U:H5'	2.51	0.41
1:1:3190:C:H2'	1:1:3191:A:H8	1.85	0.41
84:1:3403:3K5:H27	43:AP:43:TYR:CD2	2.56	0.41
9:o:9:THR:HA	9:o:12:LYS:HE3	2.02	0.41
9:o:22:GLU:OE1	9:o:22:GLU:HA	2.19	0.41
14:t:201:LYS:HE2	82:II:51:GLY:HA2	2.03	0.41
17:w:163:VAL:O	17:w:167:GLU:HG3	2.21	0.41
22:2:84:TYR:HB2	30:AC:24:PRO:HD3	2.03	0.41
25:7:57:ARG:HH21	25:7:63:ILE:HG13	1.85	0.41
39:AL:46:ARG:HD3	39:AL:47:GLY:O	2.20	0.41
46:B:795:A:H62	54:J:109:PRO:HD3	1.85	0.41
46:B:1027:G:H22	46:B:1061:A:H2	1.67	0.41
46:B:1219:A:H5''	46:B:1230:G:H2'	2.01	0.41
46:B:1502:A:O2'	46:B:1505:C:N4	2.54	0.41
46:B:1584:A:C8	76:f:14:PHE:HD1	2.39	0.41
50:F:110:LEU:HD23	50:F:110:LEU:HA	1.92	0.41
51:G:98:HIS:ND1	51:G:116:ALA:HA	2.35	0.41
52:H:165:LEU:HD23	75:e:47:PRO:HG2	2.02	0.41
53:I:6:SER:O	53:I:113:ILE:HG13	2.20	0.41
54:J:67:ARG:HD2	54:J:127:PHE:CD1	2.56	0.41
59:O:132:GLU:CG	59:O:133:ARG:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:P:87:ASP:N	60:P:87:ASP:OD1	2.52	0.41
62:R:34:THR:HG21	62:R:45:PHE:CG	2.56	0.41
63:S:46:LYS:HD2	63:S:46:LYS:HA	1.76	0.41
1:AS:243:G:H2'	1:AS:244:G:C8	2.54	0.41
1:AS:276:U:O2	16:BI:93:LYS:HE2	2.20	0.41
1:AS:436:A:H2'	1:AS:437:G:C8	2.56	0.41
1:AS:498:C:H2'	1:AS:499:G:H8	1.85	0.41
1:AS:1575:A:H3'	26:BS:33:ARG:HH22	1.84	0.41
1:AS:1900:C:H2'	1:AS:1901:G:O4'	2.20	0.41
1:AS:2918:A:H1'	1:AS:2953:U:C4	2.55	0.41
1:AS:3139:U:N3	1:AS:3247:A:C2	2.89	0.41
2:AT:47:C:OP2	7:AZ:158:ARG:HD3	2.20	0.41
3:AU:81:A:H2'	3:AU:82:U:C6	2.55	0.41
4:AW:209:HIS:CE1	4:AW:235:ALA:HB1	2.55	0.41
6:AY:318:PRO:O	6:AY:325:LEU:HB2	2.21	0.41
19:BL:158:HIS:NE2	19:BL:186:VAL:HG12	2.35	0.41
22:BO:39:ILE:HG12	22:BO:63:ILE:CD1	2.50	0.41
22:BO:44:ALA:HB2	22:BO:53:PRO:HG2	2.03	0.41
23:BP:90:ASN:O	23:BP:92:ILE:HG13	2.21	0.41
24:BQ:13:MET:HE2	24:BQ:53:ALA:HB1	2.01	0.41
45:CL:156:ALA:N	57:CX:92:LEU:HD11	2.36	0.41
46:CM:119:A:H1'	46:CM:395:A:C4	2.55	0.41
46:CM:638:U:HO2'	46:CM:639:G:P	2.41	0.41
46:CM:681:C:O2'	46:CM:682:A:OP1	2.34	0.41
46:CM:937:A:O2'	60:DA:114:ARG:HG3	2.20	0.41
46:CM:975:C:H2'	46:CM:976:G:O4'	2.20	0.41
46:CM:1472:G:N2	46:CM:1509:U:O4	2.54	0.41
46:CM:1484:U:C4	46:CM:1498:G:C2	3.08	0.41
46:CM:1520:C:H4'	46:CM:1526:G:O6	2.20	0.41
46:CM:1611:C:H2'	46:CM:1612:C:H6	1.85	0.41
46:CM:1720:C:H2'	46:CM:1721:U:H6	1.85	0.41
52:CS:145:ASP:OD1	52:CS:146:SER:N	2.54	0.41
59:CZ:41:LEU:HA	59:CZ:122:VAL:O	2.20	0.41
63:DD:14:THR:HB	63:DD:71:GLY:HA2	2.01	0.41
64:DE:47:ARG:O	64:DE:50:ILE:HG22	2.20	0.41
82:L1:7:SER:HA	82:L1:10:ARG:HH21	1.85	0.41
82:l1:26:ARG:HG2	82:l1:27:ASN:N	2.36	0.41
82:l1:53:LEU:HB3	82:l1:189:PHE:CE1	2.56	0.41
1:1:846:U:H2'	1:1:847:C:C6	2.55	0.41
1:1:983:U:H2'	1:1:984:U:C6	2.55	0.41
1:1:988:A:O2'	1:1:989:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1714:G:H2'	1:1:1715:G:C8	2.56	0.41
1:1:1787:U:H2'	1:1:1788:C:C6	2.55	0.41
1:1:1805:A:H2'	1:1:1806:A:O4'	2.21	0.41
1:1:1865:C:H4'	1:1:3049:A:O2'	2.21	0.41
1:1:2205:C:OP1	43:AP:32:LYS:NZ	2.53	0.41
1:1:2486:U:H2'	1:1:2487:U:H6	1.84	0.41
2:3:35:C:N3	2:3:45:A:O2'	2.48	0.41
3:4:26:U:H2'	3:4:27:U:C6	2.56	0.41
6:l:84:HIS:ND1	6:l:84:HIS:O	2.54	0.41
8:n:28:LYS:HE3	8:n:28:LYS:HB3	1.82	0.41
9:o:201:TRP:CD1	9:o:202:PRO:HD2	2.56	0.41
9:o:212:PHE:HB3	9:o:225:ASP:OD2	2.21	0.41
26:8:34:LEU:HD12	26:8:35:PRO:HD2	2.02	0.41
28:AA:42:ILE:HD11	28:AA:74:LEU:HD12	2.03	0.41
45:i:65:LYS:HD3	62:R:105:VAL:HG12	2.02	0.41
46:B:58:U:O2'	46:B:449:G:N3	2.52	0.41
46:B:767:G:O2'	46:B:768:C:H6	2.03	0.41
46:B:1130:U:H2'	46:B:1131:G:O4'	2.21	0.41
46:B:1377:A:H2'	46:B:1378:U:C6	2.55	0.41
46:B:1669:U:O2'	46:B:1670:U:O5'	2.38	0.41
53:I:149:LYS:HB3	53:I:149:LYS:HE2	1.80	0.41
62:R:73:PRO:CG	62:R:92:SER:HA	2.51	0.41
79:AR:71:ASP:CB	79:AR:113:SER:HA	2.49	0.41
1:AS:120:A:N6	10:BC:127:SER:OG	2.53	0.41
1:AS:649:G:O2'	1:AS:1431:A:OP1	2.38	0.41
1:AS:730:A:H2'	1:AS:731:U:H2'	2.02	0.41
1:AS:1025:G:N2	1:AS:1026:A:H1'	2.35	0.41
1:AS:2084:A:H2'	1:AS:2085:A:C8	2.55	0.41
1:AS:2809:A:H2	1:AS:2823:A:N7	2.18	0.41
1:AS:2872:A:C4	1:AS:2873:G:C8	3.09	0.41
1:AS:3044:C:H2'	1:AS:3045:A:O4'	2.21	0.41
1:AS:3270:A:H2'	1:AS:3271:U:O4'	2.21	0.41
1:AS:3300:A:H2'	1:AS:3301:A:H8	1.83	0.41
3:AU:57:C:H4'	3:AU:63:G:N7	2.36	0.41
4:AW:79:ASN:ND2	4:AW:165:VAL:HG12	2.36	0.41
5:AX:57:VAL:HG22	5:AX:73:VAL:HG22	2.01	0.41
5:AX:80:ASP:OD1	5:AX:82:PRO:HD3	2.21	0.41
7:AZ:51:LEU:HB2	7:AZ:144:VAL:CG1	2.50	0.41
14:BG:57:VAL:HG22	14:BG:69:VAL:HG22	2.02	0.41
17:BJ:175:LEU:O	17:BJ:175:LEU:HD23	2.21	0.41
31:BX:12:ILE:H	31:BX:12:ILE:HD12	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:CI:2:ARG:HB3	42:CI:5:TRP:CD1	2.56	0.41
46:CM:302:U:H2'	46:CM:303:C:H6	1.85	0.41
46:CM:330:U:P	55:CV:56:ARG:HH22	2.43	0.41
46:CM:521:G:N2	46:CM:526:U:OP2	2.49	0.41
46:CM:590:A:OP1	56:CW:39:LYS:NZ	2.45	0.41
46:CM:597:A:H2'	46:CM:598:U:C6	2.55	0.41
46:CM:670:C:H3'	46:CM:671:G:O4'	2.21	0.41
46:CM:680:C:O2'	46:CM:681:C:H6	2.04	0.41
46:CM:1626:C:H2'	46:CM:1627:C:O4'	2.20	0.41
50:CQ:178:MET:HG3	50:CQ:183:LEU:CD2	2.51	0.41
62:DC:81:ARG:NH1	62:DC:122:THR:HG22	2.35	0.41
63:DD:30:ILE:HG12	63:DD:35:ILE:HD13	2.02	0.41
69:DJ:115:GLU:O	69:DJ:119:LYS:HG2	2.21	0.41
82:L1:31:THR:O	82:L1:209:THR:N	2.52	0.41
80:p0:70:LEU:HD13	80:p0:72:GLU:CD	2.45	0.41
1:1:495:C:H2'	1:1:496:A:H8	1.86	0.41
1:1:908:G:C2	1:1:910:A:C2	3.09	0.41
1:1:925:A:H2'	1:1:926:U:C6	2.55	0.41
1:1:1377:A:H2'	1:1:1378:G:C8	2.54	0.41
1:1:2079:C:O2'	1:1:2080:U:H5''	2.21	0.41
1:1:2397:A:H2'	1:1:2398:C:H6	1.85	0.41
1:1:2979:U:H2'	1:1:2980:A:H8	1.86	0.41
1:1:3091:U:H4'	41:AN:28:PRO:HG2	2.02	0.41
1:1:3235:A:N6	18:x:178:SER:OG	2.42	0.41
3:4:87:G:OP2	36:AI:5:LYS:HD2	2.19	0.41
10:p:167:LEU:HD23	10:p:167:LEU:HA	1.91	0.41
11:q:21:LYS:HD2	15:u:6:LYS:HD3	2.02	0.41
14:t:60:ALA:HB3	14:t:65:TYR:O	2.20	0.41
20:z:163:ARG:NH2	46:B:799:G:N7	2.68	0.41
46:B:446:C:OP1	51:G:29:PRO:HD3	2.21	0.41
46:B:767:G:HO2'	46:B:768:C:H6	1.69	0.41
46:B:1325:U:O4'	46:B:1364:U:H5''	2.20	0.41
46:B:1532:A:H2'	46:B:1533:G:H8	1.84	0.41
52:H:144:GLU:HG2	52:H:161:ASP:HA	2.03	0.41
53:I:58:LYS:HG2	53:I:105:ASP:O	2.20	0.41
57:M:77:ARG:NH2	57:M:86:ILE:HA	2.35	0.41
62:R:78:THR:OG1	62:R:80:LEU:HG	2.21	0.41
64:T:34:LEU:O	64:T:38:ILE:HG12	2.21	0.41
64:T:99:GLN:HB2	64:T:118:PRO:O	2.21	0.41
76:f:23:HIS:HB3	76:f:42:CYS:SG	2.61	0.41
1:AS:169:G:N2	1:AS:248:U:O2	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:338:A:OP1	6:AY:48:ARG:HA	2.21	0.41
1:AS:445:A:H2'	1:AS:446:U:C6	2.55	0.41
1:AS:491:C:H2'	1:AS:492:C:C6	2.56	0.41
1:AS:1165:A:H2'	1:AS:1166:A:C8	2.55	0.41
1:AS:1347:U:O2	1:AS:1347:U:H2'	2.20	0.41
1:AS:1614:G:O2'	3:AU:126:A:N1	2.53	0.41
1:AS:1690:U:O2'	1:AS:1691:U:H5'	2.20	0.41
1:AS:2545:C:H6	1:AS:2545:C:H2'	1.71	0.41
1:AS:3068:C:H2'	1:AS:3069:U:C6	2.56	0.41
1:AS:3157:A:OP1	11:BD:23:ARG:HG3	2.21	0.41
1:AS:3165:U:O2	1:AS:3166:A:H1'	2.20	0.41
1:AS:3194:G:H5'	15:BH:129:VAL:HG21	2.03	0.41
12:BE:140:THR:HG21	12:BE:148:VAL:HG21	2.02	0.41
13:BF:10:ARG:O	13:BF:133:ARG:HD3	2.20	0.41
18:BK:29:THR:HG22	18:BK:119:VAL:HG21	2.01	0.41
42:CI:2:ARG:HD3	42:CI:5:TRP:NE1	2.35	0.41
46:CM:160:A:H3'	46:CM:161:G:H21	1.85	0.41
46:CM:1220:C:H6	46:CM:1220:C:H2'	1.67	0.41
46:CM:1222:G:H2'	46:CM:1223:A:H8	1.85	0.41
46:CM:1317:C:H4'	50:CQ:204:PRO:HB3	2.02	0.41
46:CM:1628:C:H2'	46:CM:1629:G:C8	2.55	0.41
50:CQ:125:ARG:HA	50:CQ:125:ARG:HD3	1.88	0.41
51:CR:59:ARG:HH22	71:DL:87:PRO:HG3	1.85	0.41
59:CZ:33:ARG:HD2	59:CZ:33:ARG:C	2.46	0.41
64:DE:103:ASP:OD2	64:DE:105:ASP:HB2	2.21	0.41
65:DF:30:TYR:O	65:DF:33:THR:OG1	2.37	0.41
70:DK:48:HIS:HB3	70:DK:103:LEU:HD11	2.03	0.41
78:DS:134:LYS:HB3	78:DS:135:HIS:H	1.58	0.41
1:1:15:A:H2'	1:1:16:G:O4'	2.21	0.41
1:1:206:U:H2'	1:1:207:C:C6	2.56	0.41
1:1:409:A:N1	1:1:1437:G:O2'	2.49	0.41
1:1:638:U:OP1	29:AB:21:ARG:NH1	2.52	0.41
1:1:1521:G:N3	1:1:1521:G:H2'	2.36	0.41
1:1:1632:C:N3	1:1:1706:C:H4'	2.36	0.41
1:1:1719:A:OP1	20:z:128:LYS:NZ	2.48	0.41
1:1:2262:C:C4	1:1:2286:C:O4'	2.74	0.41
1:1:2486:U:H2'	1:1:2487:U:C6	2.55	0.41
1:1:2601:U:O2	1:1:2621:G:N2	2.43	0.41
1:1:2749:G:C2	29:AB:60:TYR:CE2	3.08	0.41
1:1:3035:C:H2'	1:1:3036:U:H6	1.86	0.41
1:1:3068:C:H2'	1:1:3069:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:6:61:THR:OG1	24:6:63:LYS:NZ	2.53	0.41
28:AA:54:THR:HG22	28:AA:57:MET:HE3	2.02	0.41
29:AB:112:VAL:HB	29:AB:130:VAL:HG12	2.02	0.41
44:AQ:53:GLY:O	44:AQ:65:ALA:HA	2.21	0.41
45:i:102:LYS:HE3	46:B:574:G:OP1	2.20	0.41
46:B:30:G:C6	46:B:595:G:C6	3.08	0.41
46:B:673:A:H8	46:B:673:A:O5'	2.04	0.41
53:I:126:ASP:OD1	53:I:127:THR:N	2.52	0.41
60:P:48:SER:OG	60:P:86:GLU:OE2	2.27	0.41
62:R:30:THR:O	62:R:34:THR:HG23	2.21	0.41
64:T:5:ARG:O	64:T:10:LYS:HE3	2.21	0.41
65:U:88:ARG:HH21	65:U:92:GLN:HG2	1.85	0.41
1:AS:169:G:H1	1:AS:248:U:H3	1.68	0.41
1:AS:313:A:H2'	1:AS:314:U:C6	2.55	0.41
1:AS:414:U:H2'	1:AS:415:G:C8	2.55	0.41
1:AS:561:U:H2'	1:AS:562:C:C6	2.55	0.41
1:AS:1018:U:C2'	1:AS:1019:U:H5''	2.51	0.41
1:AS:1149:A:O2'	1:AS:1150:A:H5'	2.21	0.41
1:AS:1336:G:H2'	1:AS:1337:U:H6	1.86	0.41
1:AS:1521:G:N3	1:AS:1521:G:H2'	2.35	0.41
1:AS:1639:A:H2'	1:AS:1640:C:C2	2.56	0.41
1:AS:2650:A:C2	45:CL:53:LYS:HG2	2.56	0.41
1:AS:2911:G:OP2	5:AX:3:HIS:HD2	2.04	0.41
1:AS:3240:U:H5''	34:CA:68:TRP:HZ2	1.86	0.41
1:AS:3317:U:H2'	55:CV:168:SER:O	2.20	0.41
2:AT:100:C:OP2	21:BN:52:LYS:NZ	2.54	0.41
3:AU:70:G:H5''	27:BT:28:ARG:CZ	2.51	0.41
45:CL:67:LYS:HG3	45:CL:69:PHE:HD2	1.84	0.41
46:CM:623:C:H2'	46:CM:624:U:H6	1.85	0.41
46:CM:678:A:OP1	46:CM:678:A:H4'	2.21	0.41
46:CM:795:A:H62	54:CU:109:PRO:HD3	1.85	0.41
46:CM:1131:G:H2'	46:CM:1132:A:H8	1.82	0.41
46:CM:1132:A:O2'	46:CM:1623:C:OP2	2.34	0.41
46:CM:1167:U:H2'	46:CM:1168:A:O3'	2.19	0.41
46:CM:1286:U:H5'	49:CP:83:LYS:CD	2.51	0.41
46:CM:1378:U:H2'	46:CM:1379:C:C6	2.56	0.41
46:CM:1394:G:H2'	46:CM:1395:G:O4'	2.20	0.41
46:CM:1699:G:C6	46:CM:1700:G:C8	3.09	0.41
47:CN:6:SER:O	47:CN:191:ARG:NH1	2.54	0.41
48:CO:26:ARG:HG3	48:CO:49:ASN:OD1	2.20	0.41
52:CS:200:ASN:HB2	52:CS:208:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:CT:137:ARG:O	53:CT:141:ILE:HG13	2.20	0.41
57:CX:52:LYS:HE2	57:CX:54:TYR:HE2	1.86	0.41
70:DK:50:LYS:HD3	70:DK:101:GLU:OE2	2.20	0.41
73:DN:41:ILE:HG12	73:DN:68:TYR:CD2	2.56	0.41
79:DT:130:LYS:HG2	79:DT:150:ASP:C	2.46	0.41
80:P0:93:LEU:O	80:P0:97:ARG:HD2	2.21	0.41
82:L1:189:PHE:O	82:L1:193:LEU:HD12	2.20	0.41
1:1:25:A:H2'	1:1:26:C:C6	2.55	0.41
1:1:275:U:H2'	1:1:276:U:C6	2.56	0.41
1:1:290:G:H1'	16:v:93:LYS:HD2	2.03	0.41
1:1:366:A:H2'	1:1:367:A:O4'	2.21	0.41
1:1:437:G:O2'	1:1:438:A:H5''	2.21	0.41
1:1:502:U:H2'	1:1:503:U:C6	2.55	0.41
1:1:551:U:H3'	1:1:552:G:C8	2.55	0.41
1:1:690:A:C4	1:1:691:A:C8	3.09	0.41
1:1:816:A:H2'	1:1:817:U:C6	2.56	0.41
1:1:910:A:C2	4:j:204:MET:HE2	2.55	0.41
1:1:1506:G:H8	1:1:1506:G:O5'	2.04	0.41
1:1:1690:U:O2'	1:1:1691:U:H5'	2.21	0.41
1:1:2070:A:H5''	1:1:2072:C:H1'	2.01	0.41
1:1:2290:A:OP1	1:1:2292:U:H5	2.04	0.41
1:1:2296:U:H2'	1:1:2297:U:O4'	2.21	0.41
1:1:2406:U:H2'	1:1:2407:G:C8	2.56	0.41
1:1:2777:G:C6	1:1:2778:U:C4	3.09	0.41
1:1:2801:U:C2	1:1:2802:G:C8	3.09	0.41
1:1:2992:U:H2'	1:1:3005:A:H61	1.85	0.41
1:1:3025:G:H2'	1:1:3026:U:H6	1.86	0.41
1:1:3108:G:C5	1:1:3109:C:C5	3.09	0.41
1:1:3133:G:H2'	1:1:3134:C:O4'	2.21	0.41
1:1:3264:C:C2	1:1:3265:U:C5	3.08	0.41
3:4:27:U:H2'	3:4:28:C:C6	2.55	0.41
4:j:10:LYS:HA	4:j:16:PHE:CD2	2.56	0.41
5:k:236:LYS:HB2	5:k:236:LYS:HE2	1.86	0.41
6:l:360:VAL:HG22	21:0:64:ILE:HG12	2.03	0.41
7:m:7:PHE:CD1	7:m:7:PHE:C	2.99	0.41
12:r:170:LYS:NZ	12:r:177:ASN:OD1	2.54	0.41
13:s:4:LYS:HG3	13:s:6:GLN:H	1.86	0.41
13:s:53:THR:HG23	13:s:60:ARG:HA	2.03	0.41
17:w:189:SER:O	17:w:193:GLN:HG2	2.20	0.41
19:y:40:THR:C	19:y:42:ALA:H	2.28	0.41
19:y:133:LYS:HB2	19:y:135:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:z:134:HIS:CE1	20:z:136:ARG:HB2	2.56	0.41
20:z:162:ARG:HD2	46:B:799:G:O4'	2.20	0.41
21:0:90:MET:HE3	21:0:90:MET:HB2	1.89	0.41
30:AC:21:ILE:O	30:AC:21:ILE:HG22	2.20	0.41
32:AE:46:THR:OG1	32:AE:86:GLU:OE1	2.38	0.41
42:AO:4:LYS:NZ	46:B:1762:U:O4	2.38	0.41
46:B:260:U:C2'	46:B:261:C:H5'	2.50	0.41
46:B:261:C:O2'	46:B:262:G:N2	2.46	0.41
46:B:327:G:H2'	46:B:328:G:H8	1.86	0.41
46:B:386:G:OP1	46:B:400:C:H5	2.03	0.41
46:B:562:G:O2'	46:B:575:G:H4'	2.20	0.41
46:B:608:G:H2'	46:B:612:C:C5	2.56	0.41
46:B:931:U:H2'	46:B:932:U:C6	2.56	0.41
46:B:1071:A:H2'	46:B:1072:A:C8	2.55	0.41
46:B:1159:C:C4	46:B:1160:U:C4	3.09	0.41
46:B:1664:C:H2'	46:B:1665:C:C6	2.55	0.41
48:D:24:PHE:HZ	61:Q:34:ILE:HA	1.86	0.41
50:F:72:SER:O	50:F:75:VAL:HG22	2.21	0.41
50:F:72:SER:HB2	57:M:20:VAL:HG21	2.02	0.41
51:G:64:ILE:HA	51:G:67:GLN:HE21	1.86	0.41
52:H:25:LEU:HD22	63:S:56:LEU:HD22	2.03	0.41
53:I:135:PRO:HB2	53:I:141:ILE:HG12	2.03	0.41
56:L:32:GLY:HA3	77:g:40:TYR:CG	2.56	0.41
57:M:76:LEU:O	57:M:80:LEU:HB2	2.21	0.41
65:U:11:PHE:CZ	65:U:25:ARG:HG2	2.56	0.41
74:d:31:PHE:CD1	74:d:81:ARG:HG3	2.56	0.41
78:h:147:TYR:HD2	78:h:173:PHE:CD2	2.39	0.41
78:h:160:ARG:HG3	78:h:160:ARG:O	2.21	0.41
79:AR:46:LYS:N	79:AR:57:ILE:O	2.47	0.41
79:AR:104:PHE:CD2	79:AR:139:GLY:HA2	2.56	0.41
1:AS:61:A:H2'	1:AS:62:A:C8	2.56	0.41
1:AS:234:A:H2'	1:AS:235:G:O4'	2.21	0.41
1:AS:268:A:N1	1:AS:295:A:H5'	2.35	0.41
1:AS:629:A:H2'	1:AS:630:G:H8	1.85	0.41
1:AS:1467:U:H2'	1:AS:1468:U:C6	2.56	0.41
1:AS:1494:A:H2'	1:AS:1495:U:H6	1.83	0.41
1:AS:1562:G:OP1	1:AS:1562:G:O4'	2.38	0.41
1:AS:1762:G:N7	20:BM:46:LYS:HE2	2.35	0.41
1:AS:2961:U:H2'	1:AS:2962:G:O4'	2.20	0.41
1:AS:2974:C:O2'	5:AX:180:GLU:OE2	2.30	0.41
1:AS:3108:G:C5	1:AS:3109:C:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:3172:U:O4	21:BN:159:SER:HB2	2.21	0.41
1:AS:3250:C:H2'	1:AS:3251:G:H8	1.86	0.41
1:AS:3262:U:H2'	1:AS:3263:C:H6	1.85	0.41
2:AT:1:G:C8	7:AZ:266:LYS:HB2	2.56	0.41
3:AU:40:A:H2'	3:AU:41:A:H8	1.85	0.41
3:AU:45:C:H3'	40:CG:15:LYS:NZ	2.36	0.41
5:AX:117:ARG:NH2	5:AX:175:LYS:HD3	2.36	0.41
5:AX:214:MET:HE2	5:AX:350:ALA:HA	2.02	0.41
7:AZ:45:ASN:OD1	22:BO:33:VAL:HG21	2.21	0.41
9:BB:134:TYR:CZ	9:BB:228:ASN:HB2	2.55	0.41
36:CC:114:ARG:HD2	36:CC:114:ARG:HA	1.83	0.41
38:CE:79:GLN:HE21	38:CE:79:GLN:HB2	1.74	0.41
44:CK:47:VAL:HA	44:CK:56:ASN:O	2.20	0.41
46:CM:443:A:H1'	46:CM:523:A:H5'	2.01	0.41
46:CM:484:G:N2	46:CM:499:U:O2	2.38	0.41
46:CM:707:C:N4	46:CM:715:G:H2'	2.36	0.41
46:CM:940:A:H2'	46:CM:941:C:H6	1.86	0.41
46:CM:1262:G:C5	46:CM:1422:A:C2	3.09	0.41
46:CM:1325:U:O4'	46:CM:1364:U:H5''	2.20	0.41
46:CM:1438:U:H2'	46:CM:1439:G:C8	2.56	0.41
46:CM:1470:G:H21	46:CM:1593:C:H1'	1.86	0.41
46:CM:1698:U:C2'	46:CM:1699:G:H4'	2.45	0.41
46:CM:1720:C:H2'	46:CM:1721:U:C6	2.56	0.41
47:CN:23:HIS:HD2	64:DE:106:THR:HG21	1.86	0.41
48:CO:29:TRP:HA	48:CO:46:THR:O	2.20	0.41
48:CO:97:LEU:HD11	48:CO:228:LEU:HD21	2.02	0.41
50:CQ:124:LEU:HD21	50:CQ:153:TYR:O	2.21	0.41
51:CR:112:HIS:NE2	51:CR:238:SER:OG	2.50	0.41
51:CR:150:PRO:O	53:CT:208:TYR:HE1	2.04	0.41
53:CT:85:ARG:NH2	53:CT:87:ARG:HH12	2.18	0.41
55:CV:37:LYS:HA	55:CV:37:LYS:HD2	1.91	0.41
60:DA:4:MET:HE2	60:DA:4:MET:HB3	1.97	0.41
63:DD:96:VAL:HG12	63:DD:97:ASP:N	2.36	0.41
65:DF:89:GLN:HA	65:DF:97:ASP:HA	2.02	0.41
71:DL:57:VAL:HB	71:DL:60:PHE:CE1	2.53	0.41
81:12:149:HIS:H	81:12:152:ILE:CD1	2.31	0.41
82:L1:116:LEU:HA	82:L1:116:LEU:HD23	1.95	0.41
82:L1:158:GLN:H	82:L1:158:GLN:CD	2.28	0.41
82:l1:4:ILE:HD13	82:l1:4:ILE:HA	1.90	0.41
82:l1:55:LEU:HD23	82:l1:55:LEU:HA	1.87	0.41
82:l1:140:HIS:O	82:l1:142:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:l1:144:LEU:HD23	82:l1:144:LEU:HA	1.81	0.41
80:p0:29:GLY:HA2	80:p0:84:VAL:HA	2.03	0.41
1:1:75:G:H3'	14:t:73:ARG:HD2	2.03	0.41
1:1:447:U:H3'	1:1:448:U:H5''	2.03	0.41
1:1:725:G:H2'	1:1:726:G:O4'	2.21	0.41
1:1:751:A:C5	1:1:752:U:C5	3.09	0.41
1:1:976:A:C2'	1:1:977:U:H5'	2.48	0.41
1:1:1203:G:H4'	41:AN:41:HIS:O	2.21	0.41
1:1:1459:U:H2'	1:1:1460:G:O4'	2.21	0.41
1:1:2132:U:H2'	1:1:2133:G:H8	1.86	0.41
1:1:2396:G:N3	1:1:2396:G:H2'	2.36	0.41
1:1:2713:C:O2	43:AP:20:HIS:HE1	2.04	0.41
28:AA:87:LEU:HD11	28:AA:121:LYS:HD2	2.03	0.41
36:AI:29:ALA:O	36:AI:33:VAL:HG23	2.21	0.41
46:B:219:A:C6	46:B:220:A:N6	2.89	0.41
46:B:722:A:O2'	46:B:723:G:H8	2.03	0.41
46:B:821:U:H2'	46:B:822:G:H8	1.86	0.41
46:B:1062:C:H2'	46:B:1063:C:H6	1.85	0.41
46:B:1342:A:H3'	46:B:1343:G:H8	1.85	0.41
55:K:190:LEU:HB3	55:K:195:LEU:HB2	2.03	0.41
57:M:31:LYS:NZ	57:M:36:ASP:OD1	2.35	0.41
70:Z:92:CYS:HG	70:Z:136:TRP:CD1	2.39	0.41
79:AR:22:SER:OG	79:AR:72:VAL:N	2.54	0.41
1:AS:87:A:H2'	1:AS:88:G:O4'	2.20	0.41
1:AS:413:U:H2'	1:AS:414:U:C6	2.56	0.41
1:AS:763:U:C2	1:AS:764:C:C5	3.09	0.41
1:AS:875:U:O2'	18:BK:131:ARG:HD2	2.20	0.41
1:AS:1006:G:N2	12:BE:193:ASP:O	2.36	0.41
1:AS:1309:G:O2'	1:AS:1314:A:N1	2.50	0.41
1:AS:2603:U:H2'	1:AS:2604:G:C8	2.56	0.41
1:AS:3042:A:C5	1:AS:3043:U:C5	3.09	0.41
1:AS:3129:C:H2'	1:AS:3130:C:H6	1.86	0.41
1:AS:3235:A:O4'	18:BK:174:GLY:HA3	2.21	0.41
3:AU:85:G:H4'	3:AU:86:U:OP1	2.20	0.41
4:AW:66:PRO:HG2	4:AW:67:TYR:CE2	2.56	0.41
6:AY:61:THR:HG22	6:AY:63:ALA:N	2.36	0.41
13:BF:33:ALA:HB2	13:BF:123:TYR:CE2	2.56	0.41
16:BI:27:CYS:SG	16:BI:124:ASP:HB3	2.61	0.41
27:BT:77:LYS:HE3	40:CG:31:THR:HG21	2.03	0.41
33:BZ:43:VAL:HG22	33:BZ:50:THR:HB	2.02	0.41
45:CL:102:LYS:HB3	50:CQ:144:ARG:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:CM:298:A:H2'	46:CM:299:A:C8	2.56	0.41
46:CM:432:G:N2	46:CM:435:A:OP2	2.52	0.41
46:CM:761:G:N2	46:CM:769:U:H1'	2.36	0.41
46:CM:824:U:C4	46:CM:825:U:H5	2.39	0.41
46:CM:1149:G:H2'	46:CM:1150:G:H8	1.86	0.41
46:CM:1749:A:H1'	46:CM:1770:C:H5'	2.02	0.41
47:CN:30:GLN:OE1	47:CN:153:SER:OG	2.31	0.41
48:CO:26:ARG:C	48:CO:50:ARG:HG2	2.46	0.41
49:CP:36:LEU:HD12	49:CP:36:LEU:HA	1.88	0.41
50:CQ:19:TYR:HE1	50:CQ:38:VAL:HG13	1.86	0.41
51:CR:45:VAL:HA	51:CR:61:VAL:HG21	2.03	0.41
65:DF:41:ARG:HG2	65:DF:85:PHE:CE1	2.56	0.41
70:DK:37:ALA:HA	70:DK:41:SER:HB3	2.03	0.41
1:1:35:C:H4'	1:1:804:A:N1	2.35	0.40
1:1:255:A:H2'	1:1:256:G:C8	2.57	0.40
1:1:273:A:H2'	1:1:274:G:C8	2.55	0.40
1:1:1081:A:H2'	1:1:1082:C:C6	2.56	0.40
1:1:1096:U:OP2	9:o:194:LYS:NZ	2.50	0.40
1:1:1740:G:H2'	1:1:1741:C:C6	2.57	0.40
1:1:1760:U:C5	1:1:1761:U:H1'	2.56	0.40
1:1:2641:G:H2'	1:1:2642:G:C8	2.57	0.40
1:1:2686:G:OP2	43:AP:10:THR:HG22	2.22	0.40
2:3:90:A:H2'	2:3:91:G:O4'	2.21	0.40
3:4:27:U:H2'	3:4:28:C:H6	1.86	0.40
3:4:78:G:H2'	3:4:79:A:N3	2.36	0.40
3:4:132:G:H5''	26:8:94:GLN:HE21	1.85	0.40
3:4:156:U:O2'	3:4:157:U:P	2.79	0.40
5:k:67:MET:SD	5:k:70:ARG:HD2	2.60	0.40
14:t:64:LYS:HA	29:AB:69:TRP:CE3	2.56	0.40
26:8:142:ILE:HD12	26:8:142:ILE:HA	1.89	0.40
27:9:69:LYS:HE3	27:9:69:LYS:HB3	1.94	0.40
28:AA:46:ILE:HG23	28:AA:68:VAL:HG13	2.03	0.40
46:B:273:C:H2'	46:B:274:C:O4'	2.22	0.40
46:B:602:A:H2'	46:B:603:A:O4'	2.21	0.40
46:B:1311:A:H2'	46:B:1312:C:H6	1.86	0.40
46:B:1489:G:N2	46:B:1492:A:OP2	2.52	0.40
46:B:1720:C:H2'	46:B:1721:U:C6	2.56	0.40
46:B:1740:A:H2'	46:B:1741:A:C8	2.54	0.40
49:E:148:SER:OG	49:E:149:LEU:N	2.54	0.40
54:J:74:THR:HG22	54:J:88:PHE:HE1	1.87	0.40
63:S:12:LYS:O	63:S:13:LYS:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:T:93:LEU:O	64:T:93:LEU:HD12	2.21	0.40
68:X:65:ALA:O	68:X:69:LEU:HD23	2.21	0.40
1:AS:79:G:H2'	1:AS:80:C:H6	1.84	0.40
1:AS:163:A:H2'	1:AS:164:U:O4'	2.20	0.40
1:AS:176:G:C5	1:AS:177:C:C5	3.09	0.40
1:AS:1313:A:O2'	1:AS:1314:A:H3'	2.21	0.40
1:AS:1336:G:H2'	1:AS:1337:U:C6	2.56	0.40
1:AS:1374:U:H2'	1:AS:1375:G:H8	1.86	0.40
1:AS:1415:A:H5''	6:AY:194:LYS:HE2	2.01	0.40
1:AS:1485:A:OP1	35:CB:10:ARG:HD2	2.21	0.40
1:AS:1853:C:O2	35:CB:4:ARG:HB3	2.21	0.40
1:AS:2716:U:H2'	1:AS:2717:G:C8	2.56	0.40
1:AS:2766:G:O2'	1:AS:2767:U:OP2	2.39	0.40
1:AS:2841:U:O2'	1:AS:2845:U:OP1	2.38	0.40
1:AS:2908:A:H2'	1:AS:2909:G:C8	2.56	0.40
1:AS:2946:U:H2'	1:AS:2947:U:C6	2.56	0.40
1:AS:3023:U:H2'	1:AS:3024:G:H8	1.86	0.40
7:AZ:257:GLU:H	7:AZ:257:GLU:CD	2.28	0.40
15:BH:57:LEU:HG	21:BN:172:TYR:CZ	2.57	0.40
24:BQ:23:MET:HE1	24:BQ:78:VAL:HG22	2.02	0.40
27:BT:106:ILE:HG21	27:BT:109:LEU:HD23	2.04	0.40
46:CM:392:C:H2'	46:CM:393:U:C6	2.55	0.40
46:CM:457:G:OP2	71:DL:105:ARG:NH2	2.44	0.40
46:CM:684:C:H2'	46:CM:685:C:H6	1.85	0.40
46:CM:1204:A:N3	57:CX:51:SER:OG	2.44	0.40
46:CM:1226:G:C8	62:DC:79:HIS:HE1	2.40	0.40
46:CM:1678:G:H1	46:CM:1698:U:H3	1.69	0.40
51:CR:32:SER:O	51:CR:83:PRO:HG3	2.22	0.40
53:CT:58:LYS:HA	53:CT:107:SER:HB3	2.03	0.40
59:CZ:36:LEU:HD21	59:CZ:43:ARG:HH21	1.86	0.40
63:DD:12:LYS:O	63:DD:13:LYS:C	2.64	0.40
73:DN:3:LYS:NZ	73:DN:5:ARG:O	2.53	0.40
82:11:49:PHE:CD1	82:11:193:LEU:HD13	2.56	0.40
1:1:108:A:N1	1:1:322:U:O2'	2.54	0.40
1:1:206:U:H2'	1:1:207:C:H6	1.87	0.40
1:1:487:C:H2'	1:1:488:G:O4'	2.21	0.40
1:1:1322:A:H2'	1:1:1323:C:O4'	2.21	0.40
1:1:2195:U:H2'	1:1:2196:G:H8	1.85	0.40
1:1:2956:C:C2	1:1:2957:C:C5	3.09	0.40
1:1:2978:A:C2	1:1:3113:A:C4	3.09	0.40
1:1:3138:U:C2	1:1:3139:U:C5	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:j:68:LYS:HE3	4:j:68:LYS:HB2	1.96	0.40
6:l:301:ARG:HG2	19:y:39:ARG:O	2.20	0.40
10:p:114:ALA:HA	10:p:117:ILE:HG22	2.03	0.40
11:q:57:VAL:HG13	11:q:64:HIS:CE1	2.57	0.40
16:v:27:CYS:HB2	16:v:122:ASN:HD21	1.84	0.40
16:v:48:ALA:HA	16:v:133:ILE:HD11	2.04	0.40
21:0:41:TYR:O	21:0:45:LEU:HD23	2.21	0.40
33:AF:80:VAL:HG12	33:AF:112:LYS:HD2	2.03	0.40
38:AK:18:LEU:HD11	40:AM:51:ILE:HD12	2.03	0.40
46:B:103:A:H4'	46:B:105:A:N7	2.37	0.40
46:B:217:A:H61	46:B:828:U:H1'	1.87	0.40
46:B:220:A:H8	46:B:220:A:OP2	2.04	0.40
46:B:485:G:N2	46:B:499:U:C2	2.89	0.40
46:B:515:U:C2	46:B:516:A:C8	3.09	0.40
46:B:635:C:OP1	69:Y:32:LYS:HG3	2.20	0.40
46:B:916:C:H1'	48:D:120:LEU:HB3	2.03	0.40
46:B:1389:U:H2'	46:B:1390:C:C6	2.55	0.40
49:E:217:TYR:CE2	68:X:12:TYR:HD2	2.39	0.40
54:J:109:PRO:HG2	54:J:112:ARG:HD3	2.03	0.40
65:U:3:LEU:HB2	72:b:82:GLN:CD	2.46	0.40
1:AS:143:A:H2'	1:AS:144:G:O4'	2.21	0.40
1:AS:275:U:H2'	1:AS:276:U:C6	2.57	0.40
1:AS:448:U:H2'	1:AS:481:G:N1	2.36	0.40
1:AS:559:C:H2'	1:AS:560:C:C6	2.56	0.40
1:AS:788:G:H2'	1:AS:789:C:C6	2.55	0.40
1:AS:851:U:H5''	20:BM:95:TRP:CG	2.56	0.40
1:AS:1148:G:OP2	1:AS:1148:G:N2	2.55	0.40
1:AS:1186:A:N3	1:AS:1186:A:H2'	2.37	0.40
1:AS:1378:G:N2	6:AY:244:HIS:HE1	2.19	0.40
1:AS:1466:U:H2'	1:AS:1467:U:C6	2.56	0.40
1:AS:1721:C:H2'	1:AS:1722:C:C6	2.56	0.40
1:AS:1725:A:N6	44:CK:42:CYS:HA	2.36	0.40
1:AS:2192:A:H2'	1:AS:2193:A:O4'	2.21	0.40
1:AS:2504:C:H2'	1:AS:2505:G:C8	2.56	0.40
1:AS:2833:U:H2'	1:AS:2834:U:O4'	2.21	0.40
1:AS:2847:U:OP2	1:AS:2917:G:N1	2.41	0.40
1:AS:2969:G:C6	1:AS:3361:U:C4	3.09	0.40
1:AS:3197:G:H2'	1:AS:3198:C:C6	2.56	0.40
1:AS:3245:A:O2'	1:AS:3246:C:H6	2.04	0.40
1:AS:3313:G:H2'	1:AS:3314:C:H6	1.86	0.40
3:AU:156:U:O2'	3:AU:157:U:OP1	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AX:236:LYS:HE2	5:AX:236:LYS:HB2	1.94	0.40
20:BM:173:ARG:HH22	46:CM:839:U:H5	1.69	0.40
46:CM:147:C:OP1	71:DL:121:THR:OG1	2.29	0.40
46:CM:498:C:C2	46:CM:499:U:C5	3.09	0.40
46:CM:622:G:H2'	46:CM:623:C:C6	2.56	0.40
46:CM:734:U:H2'	46:CM:735:U:C6	2.55	0.40
46:CM:753:C:C2	56:CW:143:ILE:HG21	2.55	0.40
46:CM:1142:A:H2'	46:CM:1145:A:N7	2.36	0.40
46:CM:1220:C:H3'	46:CM:1221:A:H8	1.85	0.40
46:CM:1239:U:H5'	78:DS:185:LYS:HG3	2.02	0.40
46:CM:1318:C:H2'	46:CM:1319:U:C6	2.56	0.40
46:CM:1584:A:C5	46:CM:1585:U:C5	3.09	0.40
46:CM:1669:U:O2'	46:CM:1670:U:O5'	2.39	0.40
46:CM:1672:G:C2'	46:CM:1673:U:H5'	2.50	0.40
49:CP:136:ARG:HB3	49:CP:146:PRO:HB2	2.03	0.40
61:DB:7:GLN:NE2	73:DN:58:VAL:HG12	2.36	0.40
79:DT:71:ASP:HB3	79:DT:113:SER:HA	2.04	0.40
79:DT:180:LEU:HD23	79:DT:180:LEU:HA	1.95	0.40
81:12:103:ASN:HB2	81:12:142:ARG:O	2.21	0.40
82:11:32:VAL:HB	82:11:169:VAL:O	2.21	0.40
82:11:65:ILE:HD12	82:11:109:ALA:HB3	2.03	0.40
82:11:129:SER:HA	82:11:133:LYS:HB2	2.04	0.40
80:p0:53:MET:SD	80:p0:85:GLY:HA2	2.61	0.40
1:1:181:U:H2'	1:1:182:G:H8	1.85	0.40
1:1:614:G:H2'	1:1:615:G:C8	2.57	0.40
1:1:803:A:C2	1:1:804:A:C8	3.10	0.40
1:1:1233:G:N2	81:12:138:SER:HB2	2.36	0.40
1:1:1468:U:H5''	20:z:24:LEU:HD12	2.02	0.40
1:1:1908:U:H2'	1:1:1909:A:O4'	2.22	0.40
1:1:2081:U:H2'	1:1:2082:A:C8	2.57	0.40
1:1:2504:C:H2'	1:1:2505:G:C8	2.57	0.40
1:1:2509:C:C4	1:1:2510:U:C4	3.09	0.40
1:1:2540:G:H2'	1:1:2541:C:H6	1.87	0.40
1:1:2601:U:H3	1:1:2621:G:H1	1.69	0.40
1:1:2890:G:C2	1:1:2891:A:N7	2.89	0.40
1:1:3197:G:H2'	1:1:3198:C:H6	1.85	0.40
6:l:149:LEU:HA	6:l:150:PRO:C	2.45	0.40
17:w:40:GLU:HG2	17:w:41:GLU:HG2	2.03	0.40
20:z:96:MET:HE3	20:z:100:ARG:NH1	2.36	0.40
25:7:80:ARG:HE	53:I:131:LYS:HE2	1.86	0.40
40:AM:20:ASN:O	40:AM:41:ARG:NE	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:AP:10:THR:HA	43:AP:20:HIS:HD2	1.87	0.40
45:i:101:LYS:HD3	46:B:573:C:O3'	2.22	0.40
46:B:151:G:HO2'	46:B:152:G:P	2.44	0.40
46:B:278:U:H4'	46:B:279:G:O5'	2.21	0.40
46:B:501:G:H2'	46:B:502:U:C6	2.55	0.40
46:B:1261:U:H4'	50:F:148:ALA:HB2	2.02	0.40
47:C:35:PRO:HG3	68:X:87:ARG:CZ	2.51	0.40
47:C:148:ASP:N	47:C:164:ASN:OD1	2.55	0.40
50:F:27:THR:O	50:F:31:ALA:HB2	2.22	0.40
51:G:68:GLN:OE1	51:G:76:VAL:HG11	2.21	0.40
65:U:11:PHE:CE1	65:U:59:GLY:HA3	2.57	0.40
72:b:54:VAL:N	72:b:55:PRO:HD2	2.37	0.40
78:h:149:LYS:O	78:h:157:GLU:HB2	2.22	0.40
1:AS:981:U:H2'	1:AS:982:U:C6	2.55	0.40
1:AS:1380:U:H5'	6:AY:139:ARG:NH1	2.36	0.40
1:AS:1642:G:H1'	1:AS:1805:A:N6	2.36	0.40
1:AS:1695:A:C6	1:AS:1743:G:C6	3.09	0.40
1:AS:1814:U:O2'	1:AS:1815:U:O5'	2.38	0.40
1:AS:2680:C:H2'	1:AS:2681:C:C6	2.55	0.40
1:AS:2888:U:H5	1:AS:2907:U:O2'	2.05	0.40
1:AS:2972:A:H2'	1:AS:2973:U:H6	1.85	0.40
1:AS:3099:A:H2'	1:AS:3100:G:O4'	2.22	0.40
1:AS:3132:U:H2'	1:AS:3133:G:C8	2.56	0.40
1:AS:3216:U:H2'	1:AS:3217:G:C8	2.57	0.40
1:AS:3271:U:H2'	1:AS:3272:A:H5''	2.04	0.40
1:AS:3315:C:H4'	1:AS:3316:U:OP1	2.22	0.40
2:AT:39:U:O2'	13:BF:43:GLN:HB3	2.21	0.40
4:AW:83:TYR:HB3	44:CK:64:VAL:HG23	2.03	0.40
6:AY:284:ASN:HB3	6:AY:290:LEU:HD11	2.02	0.40
18:BK:178:SER:O	18:BK:182:LEU:HG	2.21	0.40
22:BO:102:ARG:HA	22:BO:102:ARG:NE	2.37	0.40
28:BU:108:GLU:O	28:BU:112:LYS:HG2	2.21	0.40
43:CJ:47:GLN:HE22	43:CJ:53:GLN:CD	2.29	0.40
46:CM:184:C:OP1	55:CV:152:ARG:NH2	2.43	0.40
46:CM:522:U:O2'	46:CM:524:A:N7	2.49	0.40
46:CM:801:A:H2'	46:CM:802:C:H6	1.87	0.40
46:CM:945:U:H5'	60:DA:55:ARG:HD3	2.04	0.40
46:CM:1238:U:C2	46:CM:1239:U:C5	3.09	0.40
46:CM:1367:U:O4	46:CM:1368:A:N6	2.54	0.40
52:CS:109:LYS:HB3	52:CS:109:LYS:HE2	1.80	0.40
54:CU:11:THR:HG23	54:CU:14:GLU:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:CU:59:PRO:HG2	54:CU:62:SER:HB3	2.03	0.40
55:CV:65:PHE:HZ	55:CV:78:ILE:HD11	1.86	0.40
63:DD:94:LYS:O	79:DT:60:LYS:NZ	2.36	0.40
72:DM:69:LEU:HD23	72:DM:69:LEU:HA	1.94	0.40
77:DR:24:GLN:O	77:DR:26:LYS:HG3	2.21	0.40
82:l1:99:LEU:O	82:l1:103:LEU:HB2	2.21	0.40
1:1:523:G:C6	1:1:564:G:C6	3.10	0.40
1:1:698:C:H2'	1:1:699:G:H8	1.86	0.40
1:1:912:G:H5'	1:1:913:A:OP1	2.21	0.40
1:1:1347:U:O2	1:1:1347:U:H2'	2.22	0.40
1:1:1366:G:H5''	29:AB:18:GLY:C	2.45	0.40
1:1:2192:A:H2	1:1:2408:A:O4'	2.04	0.40
1:1:2373:G:H5''	5:k:255:TRP:CD1	2.57	0.40
1:1:3150:A:C6	17:w:115:LYS:HG2	2.56	0.40
2:3:70:A:H2'	2:3:71:U:C6	2.56	0.40
3:4:40:A:H2'	3:4:41:A:H8	1.87	0.40
5:k:143:GLN:O	5:k:147:GLU:HG2	2.22	0.40
6:l:303:ALA:CA	19:y:39:ARG:HH12	2.33	0.40
9:o:15:LYS:HE2	9:o:15:LYS:HB3	1.96	0.40
19:y:89:ASP:OD1	19:y:90:ASP:N	2.53	0.40
23:5:53:ASP:HA	23:5:69:SER:HB3	2.02	0.40
28:AA:101:LEU:HB3	28:AA:107:ARG:HH21	1.85	0.40
46:B:119:A:H1'	46:B:395:A:C4	2.56	0.40
46:B:344:G:C2	46:B:345:G:C8	3.10	0.40
46:B:529:C:O2'	46:B:530:U:OP1	2.36	0.40
46:B:824:U:H2'	46:B:825:U:C6	2.56	0.40
46:B:903:U:H2'	46:B:904:A:H8	1.79	0.40
46:B:1234:U:C4	46:B:1235:U:C4	3.10	0.40
46:B:1256:G:C2	46:B:1426:C:C2	3.10	0.40
46:B:1301:G:O2'	64:T:10:LYS:NZ	2.49	0.40
46:B:1637:U:H2'	46:B:1638:A:H8	1.85	0.40
46:B:1670:U:O2'	46:B:1671:G:H8	2.05	0.40
46:B:1696:U:H2'	46:B:1697:C:C5	2.56	0.40
47:C:124:THR:HG22	47:C:174:TRP:NE1	2.29	0.40
47:C:134:LYS:HE3	47:C:138:TYR:HE1	1.86	0.40
49:E:139:TRP:CE2	69:Y:97:ARG:HD2	2.56	0.40
52:H:99:MET:HB2	52:H:180:ARG:CZ	2.52	0.40
53:I:113:ILE:HD11	53:I:124:LEU:HD21	2.02	0.40
64:T:6:THR:OG1	64:T:7:LYS:N	2.54	0.40
1:AS:97:G:N7	14:BG:13:HIS:NE2	2.66	0.40
1:AS:815:U:H2'	1:AS:816:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:844:A:C5	1:AS:845:C:H1'	2.56	0.40
1:AS:1180:A:H2'	1:AS:1181:C:H6	1.86	0.40
1:AS:1204:U:O2	1:AS:3087:C:N4	2.54	0.40
1:AS:1216:U:H5''	1:AS:1218:G:C5	2.57	0.40
1:AS:1743:G:N2	39:CF:2:ALA:HB3	2.36	0.40
1:AS:2074:A:H2'	1:AS:2075:U:C6	2.56	0.40
1:AS:3159:A:H2'	1:AS:3160:C:C6	2.57	0.40
2:AT:90:A:H2'	2:AT:91:G:O4'	2.22	0.40
27:BT:39:LEU:HD22	27:BT:43:TYR:CE2	2.51	0.40
31:BX:55:LYS:O	31:BX:59:GLU:HG2	2.22	0.40
45:CL:96:LYS:HA	46:CM:575:G:C6	2.57	0.40
46:CM:1:U:C2	46:CM:3:U:C4	3.09	0.40
46:CM:446:C:H2'	46:CM:447:C:H6	1.87	0.40
46:CM:449:G:H3'	46:CM:451:C:H41	1.87	0.40
46:CM:769:U:O2'	46:CM:770:C:OP2	2.31	0.40
46:CM:789:U:O4	54:CU:100:ARG:NH2	2.52	0.40
50:CQ:107:LYS:HB2	50:CQ:176:VAL:CG2	2.50	0.40
51:CR:71:GLN:HB3	51:CR:91:THR:HB	2.02	0.40
51:CR:108:LYS:HE3	51:CR:108:LYS:HB2	1.83	0.40
57:CX:77:ARG:HH12	57:CX:86:ILE:H	1.70	0.40
68:DI:79:LEU:HD13	68:DI:82:VAL:HG11	2.03	0.40
71:DL:34:ASN:N	71:DL:34:ASN:OD1	2.54	0.40
79:DT:116:ILE:O	79:DT:157:ILE:HG21	2.22	0.40
80:P0:34:SER:OG	80:P0:35:SER:N	2.54	0.40
81:12:162:VAL:N	81:12:163:PRO:HD3	2.37	0.40
82:l1:49:PHE:CE1	82:l1:159:LEU:HB2	2.56	0.40
1:1:422:A:N1	1:1:2340:C:O2'	2.50	0.40
1:1:690:A:O4'	6:l:47:LYS:HG3	2.21	0.40
1:1:1185:C:N4	1:1:1311:U:H1'	2.36	0.40
1:1:2078:A:H3'	1:1:2078:A:N3	2.37	0.40
1:1:2094:G:OP1	1:1:2096:C:N4	2.49	0.40
1:1:2967:A:H2'	1:1:2968:U:O4'	2.22	0.40
1:1:2999:A:H2'	1:1:3000:G:O4'	2.22	0.40
8:n:97:VAL:HA	8:n:100:PHE:CD2	2.56	0.40
9:o:18:GLN:O	9:o:22:GLU:HG2	2.22	0.40
10:p:98:TYR:OH	10:p:205:ASN:OD1	2.39	0.40
31:AD:11:ASN:O	31:AD:14:SER:OG	2.40	0.40
46:B:184:C:H2'	46:B:185:G:O4'	2.21	0.40
46:B:402:G:H2'	46:B:403:C:C6	2.57	0.40
46:B:565:A:N3	77:g:14:VAL:HG21	2.36	0.40
46:B:1204:A:O2'	57:M:48:SER:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:S:128:PHE:CE2	67:W:77:THR:HA	2.56	0.40
79:AR:16:HIS:CD2	79:AR:43:ILE:HD12	2.55	0.40
79:AR:92:LEU:HB2	79:AR:104:PHE:HE1	1.85	0.40
1:AS:95:G:H2'	1:AS:96:U:O4'	2.22	0.40
1:AS:283:G:OP2	1:AS:285:A:O2'	2.29	0.40
1:AS:513:G:O2'	1:AS:514:G:H5'	2.22	0.40
1:AS:560:C:O3'	21:BN:71:LYS:NZ	2.49	0.40
1:AS:1189:A:OP1	17:BJ:50:ARG:NH2	2.52	0.40
1:AS:1718:U:OP1	20:BM:100:ARG:NE	2.54	0.40
1:AS:1802:A:H2'	1:AS:1803:G:C8	2.56	0.40
2:AT:24:A:H2'	2:AT:25:G:C8	2.57	0.40
4:AW:77:ILE:HD13	4:AW:128:ARG:HB3	2.03	0.40
5:AX:262:TRP:H	5:AX:262:TRP:CD1	2.39	0.40
8:BA:88:THR:HG21	15:BH:108:PHE:HB2	2.04	0.40
14:BG:83:VAL:HG23	14:BG:85:ILE:HG13	2.02	0.40
16:BI:193:LYS:HB3	16:BI:193:LYS:HE2	1.83	0.40
46:CM:602:A:H2'	46:CM:603:A:O4'	2.22	0.40
46:CM:787:A:N3	54:CU:100:ARG:NH1	2.69	0.40
46:CM:1219:A:H5'	46:CM:1220:C:OP1	2.22	0.40
46:CM:1232:U:H2'	46:CM:1233:C:C6	2.57	0.40
56:CW:66:ASP:OD1	56:CW:67:PRO:HD2	2.21	0.40
72:DM:54:VAL:N	72:DM:55:PRO:HD2	2.37	0.40
79:DT:136:ASN:OD1	79:DT:136:ASN:N	2.47	0.40
80:p0:14:LYS:HA	80:p0:14:LYS:HD3	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3126:U:OP2	79:DT:119:ASN:ND2[2_545]	2.02	0.18
10:BC:206:SER:OG	46:CM:221:U:O2'[2_555]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AW	248/254 (98%)	240 (97%)	8 (3%)	0	100	100
4	j	248/254 (98%)	240 (97%)	8 (3%)	0	100	100
5	AX	384/389 (99%)	372 (97%)	12 (3%)	0	100	100
5	k	385/389 (99%)	371 (96%)	14 (4%)	0	100	100
6	AY	359/363 (99%)	349 (97%)	10 (3%)	0	100	100
6	l	359/363 (99%)	348 (97%)	11 (3%)	0	100	100
7	AZ	290/298 (97%)	279 (96%)	11 (4%)	0	100	100
7	m	294/298 (99%)	282 (96%)	11 (4%)	1 (0%)	36	70
8	BA	149/176 (85%)	147 (99%)	2 (1%)	0	100	100
8	n	153/176 (87%)	149 (97%)	4 (3%)	0	100	100
9	BB	232/241 (96%)	226 (97%)	5 (2%)	1 (0%)	30	65
9	o	232/241 (96%)	226 (97%)	5 (2%)	1 (0%)	30	65
10	BC	231/262 (88%)	219 (95%)	10 (4%)	2 (1%)	14	48
10	p	236/262 (90%)	227 (96%)	8 (3%)	1 (0%)	30	65
11	BD	188/191 (98%)	183 (97%)	5 (3%)	0	100	100
11	q	188/191 (98%)	183 (97%)	5 (3%)	0	100	100
12	BE	204/220 (93%)	199 (98%)	5 (2%)	0	100	100
12	r	204/220 (93%)	201 (98%)	3 (2%)	0	100	100
13	BF	169/174 (97%)	163 (96%)	6 (4%)	0	100	100
13	s	169/174 (97%)	161 (95%)	8 (5%)	0	100	100
14	BG	198/202 (98%)	194 (98%)	4 (2%)	0	100	100
14	t	198/202 (98%)	196 (99%)	2 (1%)	0	100	100
15	BH	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
15	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
16	BI	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
16	v	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	BJ	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
17	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
18	BK	172/185 (93%)	168 (98%)	4 (2%)	0	100	100
18	x	169/185 (91%)	166 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	BL	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
19	y	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
20	BM	177/190 (93%)	173 (98%)	4 (2%)	0	100	100
20	z	177/190 (93%)	174 (98%)	3 (2%)	0	100	100
21	0	168/172 (98%)	166 (99%)	2 (1%)	0	100	100
21	BN	168/172 (98%)	166 (99%)	2 (1%)	0	100	100
22	2	157/160 (98%)	155 (99%)	2 (1%)	0	100	100
22	BO	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
23	5	101/124 (82%)	95 (94%)	5 (5%)	1 (1%)	12	45
23	BP	102/124 (82%)	89 (87%)	11 (11%)	2 (2%)	6	28
24	6	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
24	BQ	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
25	7	114/155 (74%)	103 (90%)	11 (10%)	0	100	100
25	BR	94/155 (61%)	91 (97%)	3 (3%)	0	100	100
26	8	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
26	BS	117/142 (82%)	115 (98%)	2 (2%)	0	100	100
27	9	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
27	BT	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
28	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
28	BU	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
29	AB	146/149 (98%)	139 (95%)	7 (5%)	0	100	100
29	BV	146/149 (98%)	139 (95%)	6 (4%)	1 (1%)	18	53
30	AC	60/63 (95%)	56 (93%)	2 (3%)	2 (3%)	3	17
30	BW	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
31	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
31	BX	94/106 (89%)	92 (98%)	2 (2%)	0	100	100
32	AE	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
32	BY	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	14	48
33	AF	122/131 (93%)	122 (100%)	0	0	100	100
33	BZ	122/131 (93%)	122 (100%)	0	0	100	100
34	AG	104/107 (97%)	101 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	CA	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
35	AH	110/122 (90%)	108 (98%)	2 (2%)	0	100	100
35	CB	110/122 (90%)	107 (97%)	3 (3%)	0	100	100
36	AI	119/120 (99%)	114 (96%)	5 (4%)	0	100	100
36	CC	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
37	AJ	95/99 (96%)	94 (99%)	1 (1%)	0	100	100
37	CD	95/99 (96%)	94 (99%)	1 (1%)	0	100	100
38	AK	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
38	CE	84/87 (97%)	81 (96%)	3 (4%)	0	100	100
39	AL	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
39	CF	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
40	AM	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	27
40	CG	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
41	AN	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
41	CH	49/52 (94%)	46 (94%)	0	3 (6%)	1	7
42	AO	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
42	CI	22/25 (88%)	22 (100%)	0	0	100	100
43	AP	101/106 (95%)	99 (98%)	2 (2%)	0	100	100
43	CJ	101/106 (95%)	99 (98%)	2 (2%)	0	100	100
44	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
44	CK	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	CL	117/267 (44%)	92 (79%)	22 (19%)	3 (3%)	4	23
45	i	117/267 (44%)	95 (81%)	19 (16%)	3 (3%)	4	23
47	C	206/261 (79%)	201 (98%)	5 (2%)	0	100	100
47	CN	206/261 (79%)	198 (96%)	8 (4%)	0	100	100
48	CO	212/256 (83%)	204 (96%)	8 (4%)	0	100	100
48	D	212/256 (83%)	207 (98%)	5 (2%)	0	100	100
49	CP	215/249 (86%)	210 (98%)	5 (2%)	0	100	100
49	E	215/249 (86%)	210 (98%)	5 (2%)	0	100	100
50	CQ	221/251 (88%)	211 (96%)	10 (4%)	0	100	100
50	F	221/251 (88%)	213 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	CR	258/262 (98%)	254 (98%)	4 (2%)	0	100	100
51	G	257/262 (98%)	253 (98%)	4 (2%)	0	100	100
52	CS	204/225 (91%)	197 (97%)	7 (3%)	0	100	100
52	H	204/225 (91%)	193 (95%)	11 (5%)	0	100	100
53	CT	234/236 (99%)	230 (98%)	4 (2%)	0	100	100
53	I	224/236 (95%)	220 (98%)	4 (2%)	0	100	100
54	CU	181/186 (97%)	171 (94%)	9 (5%)	1 (1%)	21	56
54	J	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
55	CV	201/206 (98%)	199 (99%)	2 (1%)	0	100	100
55	K	201/206 (98%)	200 (100%)	1 (0%)	0	100	100
56	CW	176/189 (93%)	174 (99%)	2 (1%)	0	100	100
56	L	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
57	CX	92/118 (78%)	85 (92%)	7 (8%)	0	100	100
57	M	96/118 (81%)	82 (85%)	13 (14%)	1 (1%)	12	45
58	CY	139/155 (90%)	133 (96%)	5 (4%)	1 (1%)	18	53
58	N	142/155 (92%)	137 (96%)	5 (4%)	0	100	100
59	CZ	117/143 (82%)	90 (77%)	21 (18%)	6 (5%)	1	10
59	O	114/143 (80%)	89 (78%)	20 (18%)	5 (4%)	2	12
60	DA	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
60	P	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
61	DB	125/132 (95%)	120 (96%)	4 (3%)	1 (1%)	16	50
61	Q	125/132 (95%)	119 (95%)	6 (5%)	0	100	100
62	DC	128/142 (90%)	111 (87%)	17 (13%)	0	100	100
62	R	127/142 (89%)	115 (91%)	11 (9%)	1 (1%)	16	50
63	DD	138/142 (97%)	134 (97%)	4 (3%)	0	100	100
63	S	138/142 (97%)	132 (96%)	5 (4%)	1 (1%)	18	53
64	DE	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
64	T	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
65	DF	139/145 (96%)	134 (96%)	3 (2%)	2 (1%)	9	36
65	U	142/145 (98%)	137 (96%)	5 (4%)	0	100	100
66	DG	139/145 (96%)	134 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	V	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
67	DH	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
67	W	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
68	DI	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
68	X	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
69	DJ	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
69	Y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
70	DK	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
70	Z	141/145 (97%)	138 (98%)	3 (2%)	0	100	100
71	DL	130/135 (96%)	130 (100%)	0	0	100	100
71	a	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
72	DM	69/105 (66%)	66 (96%)	3 (4%)	0	100	100
72	b	70/105 (67%)	69 (99%)	1 (1%)	0	100	100
73	DN	96/119 (81%)	94 (98%)	2 (2%)	0	100	100
73	c	96/119 (81%)	94 (98%)	2 (2%)	0	100	100
74	DO	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
74	d	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
75	DP	59/67 (88%)	53 (90%)	6 (10%)	0	100	100
75	e	60/67 (90%)	57 (95%)	3 (5%)	0	100	100
76	DQ	52/56 (93%)	50 (96%)	2 (4%)	0	100	100
76	f	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
77	DR	56/63 (89%)	50 (89%)	5 (9%)	1 (2%)	6	31
77	g	58/63 (92%)	54 (93%)	4 (7%)	0	100	100
78	DS	68/193 (35%)	57 (84%)	10 (15%)	1 (2%)	8	35
78	h	68/193 (35%)	56 (82%)	10 (15%)	2 (3%)	3	20
79	AR	309/317 (98%)	292 (94%)	16 (5%)	1 (0%)	36	70
79	DT	309/317 (98%)	287 (93%)	21 (7%)	1 (0%)	36	70
80	P0	105/312 (34%)	87 (83%)	16 (15%)	2 (2%)	6	30
80	p0	105/312 (34%)	74 (70%)	28 (27%)	3 (3%)	3	20
81	12	61/165 (37%)	36 (59%)	25 (41%)	0	100	100
82	L1	215/217 (99%)	173 (80%)	40 (19%)	2 (1%)	14	48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
82	l1	215/217 (99%)	132 (61%)	74 (34%)	9 (4%)	2	13
All	All	22818/25493 (90%)	21825 (96%)	929 (4%)	64 (0%)	36	70

All (64) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	AC	21	ILE
40	AM	49	LEU
45	i	55	LYS
45	i	64	LEU
59	O	130	SER
41	CH	3	GLU
41	CH	4	PRO
45	CL	41	ALA
45	CL	43	PRO
45	CL	72	ASP
59	CZ	82	PRO
59	CZ	112	ALA
65	DF	57	ARG
65	DF	80	LYS
79	DT	75	SER
80	P0	71	PRO
80	P0	72	GLU
82	L1	45	ARG
82	l1	71	ALA
82	l1	74	VAL
82	l1	87	VAL
82	l1	129	SER
82	l1	157	PHE
82	l1	212	PRO
80	p0	71	PRO
80	p0	102	SER
10	p	205	ASN
45	i	63	ALA
57	M	88	PRO
62	R	2	VAL
59	CZ	34	THR
59	CZ	108	ARG
78	DS	127	TYR
82	L1	212	PRO
82	l1	27	ASN
82	l1	59	PRO

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Mol	Chain	Res	Type
59	O	42	ALA
9	BB	230	GLU
23	BP	20	ALA
58	CY	27	ALA
61	DB	119	ASP
9	o	230	GLU
23	5	20	ALA
10	BC	127	SER
7	m	44	TYR
59	O	37	VAL
59	O	104	CYS
32	BY	110	ASP
54	CU	156	THR
59	CZ	103	LEU
30	AC	3	LYS
78	h	124	LYS
78	h	141	LYS
79	AR	118	LYS
23	BP	24	GLU
29	BV	24	LYS
41	CH	6	LEU
59	CZ	32	LEU
77	DR	7	SER
82	ll	179	LEU
59	O	40	GLY
80	p0	101	VAL
63	S	40	PRO
10	BC	128	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AW	191/194 (98%)	191 (100%)	0	100	100
4	j	191/194 (98%)	191 (100%)	0	100	100
5	AX	325/328 (99%)	325 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	k	326/328 (99%)	326 (100%)	0	100	100
6	AY	290/292 (99%)	290 (100%)	0	100	100
6	l	290/292 (99%)	290 (100%)	0	100	100
7	AZ	247/252 (98%)	247 (100%)	0	100	100
7	m	250/252 (99%)	250 (100%)	0	100	100
8	BA	132/154 (86%)	132 (100%)	0	100	100
8	n	136/154 (88%)	136 (100%)	0	100	100
9	BB	198/204 (97%)	198 (100%)	0	100	100
9	o	198/204 (97%)	198 (100%)	0	100	100
10	BC	193/216 (89%)	193 (100%)	0	100	100
10	p	198/216 (92%)	198 (100%)	0	100	100
11	BD	169/170 (99%)	169 (100%)	0	100	100
11	q	169/170 (99%)	169 (100%)	0	100	100
12	BE	178/186 (96%)	178 (100%)	0	100	100
12	r	178/186 (96%)	178 (100%)	0	100	100
13	BF	146/149 (98%)	146 (100%)	0	100	100
13	s	146/149 (98%)	146 (100%)	0	100	100
14	BG	166/168 (99%)	166 (100%)	0	100	100
14	t	166/168 (99%)	166 (100%)	0	100	100
15	BH	108/109 (99%)	108 (100%)	0	100	100
15	u	108/109 (99%)	108 (100%)	0	100	100
16	BI	177/178 (99%)	177 (100%)	0	100	100
16	v	177/178 (99%)	177 (100%)	0	100	100
17	BJ	166/167 (99%)	166 (100%)	0	100	100
17	w	166/167 (99%)	166 (100%)	0	100	100
18	BK	145/154 (94%)	145 (100%)	0	100	100
18	x	144/154 (94%)	144 (100%)	0	100	100
19	BL	153/154 (99%)	153 (100%)	0	100	100
19	y	153/154 (99%)	153 (100%)	0	100	100
20	BM	146/153 (95%)	146 (100%)	0	100	100
20	z	146/153 (95%)	146 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	0	155/157 (99%)	155 (100%)	0	100	100
21	BN	155/157 (99%)	155 (100%)	0	100	100
22	2	133/134 (99%)	133 (100%)	0	100	100
22	BO	133/134 (99%)	133 (100%)	0	100	100
23	5	93/112 (83%)	93 (100%)	0	100	100
23	BP	95/112 (85%)	95 (100%)	0	100	100
24	6	101/104 (97%)	101 (100%)	0	100	100
24	BQ	101/104 (97%)	98 (97%)	3 (3%)	36	69
25	7	97/127 (76%)	97 (100%)	0	100	100
25	BR	86/127 (68%)	86 (100%)	0	100	100
26	8	108/121 (89%)	108 (100%)	0	100	100
26	BS	107/121 (88%)	107 (100%)	0	100	100
27	9	111/112 (99%)	111 (100%)	0	100	100
27	BT	111/112 (99%)	111 (100%)	0	100	100
28	AA	117/118 (99%)	117 (100%)	0	100	100
28	BU	117/118 (99%)	117 (100%)	0	100	100
29	AB	120/121 (99%)	120 (100%)	0	100	100
29	BV	120/121 (99%)	120 (100%)	0	100	100
30	AC	48/49 (98%)	48 (100%)	0	100	100
30	BW	48/49 (98%)	48 (100%)	0	100	100
31	AD	81/90 (90%)	81 (100%)	0	100	100
31	BX	81/90 (90%)	81 (100%)	0	100	100
32	AE	98/100 (98%)	98 (100%)	0	100	100
32	BY	98/100 (98%)	98 (100%)	0	100	100
33	AF	109/115 (95%)	109 (100%)	0	100	100
33	BZ	110/115 (96%)	110 (100%)	0	100	100
34	AG	91/92 (99%)	91 (100%)	0	100	100
34	CA	91/92 (99%)	91 (100%)	0	100	100
35	AH	95/102 (93%)	95 (100%)	0	100	100
35	CB	95/102 (93%)	95 (100%)	0	100	100
36	AI	107/106 (101%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	CC	106/106 (100%)	106 (100%)	0	100	100
37	AJ	77/79 (98%)	77 (100%)	0	100	100
37	CD	77/79 (98%)	77 (100%)	0	100	100
38	AK	70/71 (99%)	70 (100%)	0	100	100
38	CE	70/71 (99%)	70 (100%)	0	100	100
39	AL	68/69 (99%)	68 (100%)	0	100	100
39	CF	68/69 (99%)	68 (100%)	0	100	100
40	AM	46/47 (98%)	46 (100%)	0	100	100
40	CG	47/47 (100%)	47 (100%)	0	100	100
41	AN	47/47 (100%)	47 (100%)	0	100	100
41	CH	46/47 (98%)	46 (100%)	0	100	100
42	AO	24/24 (100%)	24 (100%)	0	100	100
42	CI	23/24 (96%)	23 (100%)	0	100	100
43	AP	88/91 (97%)	87 (99%)	1 (1%)	65	83
43	CJ	88/91 (97%)	86 (98%)	2 (2%)	44	74
44	AQ	72/73 (99%)	72 (100%)	0	100	100
44	CK	72/73 (99%)	72 (100%)	0	100	100
45	CL	99/212 (47%)	99 (100%)	0	100	100
45	i	99/212 (47%)	99 (100%)	0	100	100
47	C	176/215 (82%)	176 (100%)	0	100	100
47	CN	176/215 (82%)	176 (100%)	0	100	100
48	CO	194/229 (85%)	194 (100%)	0	100	100
48	D	194/229 (85%)	194 (100%)	0	100	100
49	CP	175/198 (88%)	175 (100%)	0	100	100
49	E	175/198 (88%)	175 (100%)	0	100	100
50	CQ	174/196 (89%)	174 (100%)	0	100	100
50	F	174/196 (89%)	174 (100%)	0	100	100
51	CR	218/220 (99%)	218 (100%)	0	100	100
51	G	218/220 (99%)	218 (100%)	0	100	100
52	CS	178/197 (90%)	178 (100%)	0	100	100
52	H	178/197 (90%)	178 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	CT	204/204 (100%)	204 (100%)	0	100	100
53	I	195/204 (96%)	195 (100%)	0	100	100
54	CU	164/167 (98%)	164 (100%)	0	100	100
54	J	166/167 (99%)	166 (100%)	0	100	100
55	CV	157/160 (98%)	157 (100%)	0	100	100
55	K	157/160 (98%)	157 (100%)	0	100	100
56	CW	153/160 (96%)	153 (100%)	0	100	100
56	L	153/160 (96%)	153 (100%)	0	100	100
57	CX	88/104 (85%)	88 (100%)	0	100	100
57	M	90/104 (86%)	90 (100%)	0	100	100
58	CY	122/134 (91%)	122 (100%)	0	100	100
58	N	124/134 (92%)	124 (100%)	0	100	100
59	CZ	101/123 (82%)	101 (100%)	0	100	100
59	O	98/123 (80%)	95 (97%)	3 (3%)	35	68
60	DA	129/130 (99%)	129 (100%)	0	100	100
60	P	129/130 (99%)	129 (100%)	0	100	100
61	DB	97/102 (95%)	97 (100%)	0	100	100
61	Q	97/102 (95%)	96 (99%)	1 (1%)	68	84
62	DC	112/121 (93%)	112 (100%)	0	100	100
62	R	111/121 (92%)	111 (100%)	0	100	100
63	DD	114/116 (98%)	114 (100%)	0	100	100
63	S	114/116 (98%)	113 (99%)	1 (1%)	70	85
64	DE	112/122 (92%)	112 (100%)	0	100	100
64	T	112/122 (92%)	112 (100%)	0	100	100
65	DF	125/129 (97%)	125 (100%)	0	100	100
65	U	128/129 (99%)	125 (98%)	3 (2%)	44	74
66	DG	113/117 (97%)	113 (100%)	0	100	100
66	V	113/117 (97%)	113 (100%)	0	100	100
67	DH	87/105 (83%)	87 (100%)	0	100	100
67	W	92/105 (88%)	92 (100%)	0	100	100
68	DI	71/71 (100%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	X	71/71 (100%)	71 (100%)	0	100	100
69	DJ	112/113 (99%)	112 (100%)	0	100	100
69	Y	112/113 (99%)	112 (100%)	0	100	100
70	DK	116/118 (98%)	116 (100%)	0	100	100
70	Z	116/118 (98%)	116 (100%)	0	100	100
71	DL	109/112 (97%)	109 (100%)	0	100	100
71	a	111/112 (99%)	111 (100%)	0	100	100
72	DM	63/85 (74%)	63 (100%)	0	100	100
72	b	64/85 (75%)	64 (100%)	0	100	100
73	DN	84/102 (82%)	84 (100%)	0	100	100
73	c	84/102 (82%)	84 (100%)	0	100	100
74	DO	72/73 (99%)	72 (100%)	0	100	100
74	d	72/73 (99%)	72 (100%)	0	100	100
75	DP	53/58 (91%)	53 (100%)	0	100	100
75	e	54/58 (93%)	54 (100%)	0	100	100
76	DQ	47/48 (98%)	46 (98%)	1 (2%)	47	75
76	f	47/48 (98%)	46 (98%)	1 (2%)	47	75
77	DR	50/54 (93%)	50 (100%)	0	100	100
77	g	51/54 (94%)	51 (100%)	0	100	100
78	DS	62/175 (35%)	53 (86%)	9 (14%)	3	15
78	h	62/175 (35%)	61 (98%)	1 (2%)	55	79
79	AR	259/263 (98%)	259 (100%)	0	100	100
79	DT	259/263 (98%)	259 (100%)	0	100	100
80	P0	92/247 (37%)	92 (100%)	0	100	100
80	p0	92/247 (37%)	92 (100%)	0	100	100
81	12	53/137 (39%)	53 (100%)	0	100	100
82	L1	196/196 (100%)	196 (100%)	0	100	100
82	l1	196/196 (100%)	196 (100%)	0	100	100
All	All	19588/21467 (91%)	19562 (100%)	26 (0%)	88	93

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	AP	56	GLN
59	O	36	LEU
59	O	37	VAL
59	O	39	ASP
61	Q	119	ASP
63	S	37	LEU
65	U	139	LYS
65	U	140	THR
65	U	141	THR
76	f	40	ARG
78	h	168	CYS
24	BQ	109	MET
24	BQ	110	LYS
24	BQ	112	SER
43	CJ	40	LYS
43	CJ	56	GLN
76	DQ	42	CYS
78	DS	124	LYS
78	DS	125	LYS
78	DS	126	VAL
78	DS	127	TYR
78	DS	128	THR
78	DS	129	THR
78	DS	131	LYS
78	DS	183	CYS
78	DS	186	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (165) such sidechains are listed below:

Mol	Chain	Res	Type
4	j	97	ASN
4	j	205	ASN
4	j	218	HIS
5	k	182	GLN
5	k	316	ASN
6	l	6	GLN
6	l	49	GLN
6	l	56	ASN
6	l	214	ASN
6	l	321	ASN
7	m	17	GLN
7	m	45	ASN
7	m	151	GLN

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Mol	Chain	Res	Type
9	o	91	ASN
9	o	192	ASN
9	o	239	GLN
10	p	192	HIS
11	q	102	ASN
11	q	116	ASN
12	r	59	GLN
12	r	100	ASN
13	s	101	ASN
16	v	123	GLN
18	x	125	GLN
18	x	179	GLN
20	z	166	ASN
22	2	54	HIS
22	2	103	GLN
25	7	42	GLN
27	9	81	GLN
27	9	86	GLN
28	AA	122	HIS
29	AB	40	HIS
30	AC	48	HIS
31	AD	73	GLN
33	AF	32	ASN
33	AF	36	GLN
34	AG	24	ASN
34	AG	31	GLN
35	AH	33	GLN
36	AI	20	GLN
36	AI	45	HIS
36	AI	59	ASN
36	AI	107	GLN
36	AI	113	GLN
39	AL	40	GLN
39	AL	51	GLN
39	AL	57	ASN
41	AN	41	HIS
43	AP	59	HIS
45	i	66	ASN
47	C	21	ASN
47	C	30	GLN
47	C	33	ASN
48	D	74	GLN

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Mol	Chain	Res	Type
48	D	79	HIS
49	E	54	HIS
49	E	84	GLN
50	F	57	GLN
51	G	17	HIS
51	G	57	ASN
52	H	37	GLN
54	J	19	GLN
54	J	146	GLN
56	L	131	GLN
56	L	153	GLN
57	M	58	GLN
57	M	94	ASN
58	N	14	GLN
60	P	105	ASN
63	S	7	GLN
63	S	60	GLN
63	S	76	GLN
64	T	42	GLN
65	U	74	GLN
66	V	23	GLN
66	V	85	ASN
67	W	35	ASN
69	Y	12	ASN
69	Y	42	GLN
70	Z	94	ASN
71	a	22	GLN
71	a	106	GLN
74	d	26	GLN
79	AR	53	ASN
79	AR	102	GLN
5	AX	25	GLN
5	AX	182	GLN
5	AX	259	ASN
5	AX	316	ASN
6	AY	117	ASN
6	AY	321	ASN
6	AY	363	ASN
7	AZ	151	GLN
8	BA	56	ASN
8	BA	60	ASN
9	BB	50	GLN

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Mol	Chain	Res	Type
9	BB	78	GLN
9	BB	144	GLN
9	BB	155	ASN
10	BC	146	ASN
11	BD	129	HIS
12	BE	55	ASN
12	BE	100	ASN
12	BE	162	GLN
12	BE	187	ASN
13	BF	43	GLN
13	BF	161	GLN
16	BI	175	ASN
18	BK	125	GLN
18	BK	137	ASN
19	BL	58	ASN
20	BM	174	GLN
21	BN	8	GLN
21	BN	46	GLN
22	BO	77	ASN
29	BV	11	HIS
29	BV	40	HIS
30	BW	6	ASN
30	BW	12	GLN
30	BW	48	HIS
31	BX	73	GLN
33	BZ	36	GLN
34	CA	24	ASN
37	CD	79	HIS
38	CE	69	HIS
39	CF	34	ASN
39	CF	51	GLN
41	CH	33	ASN
43	CJ	22	GLN
45	CL	33	ASN
47	CN	21	ASN
47	CN	33	ASN
48	CO	40	ASN
48	CO	101	HIS
48	CO	232	HIS
49	CP	105	HIS
51	CR	98	HIS
51	CR	188	ASN

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Mol	Chain	Res	Type
51	CR	197	HIS
51	CR	260	GLN
52	CS	116	HIS
53	CT	81	HIS
53	CT	139	ASN
54	CU	176	GLN
55	CV	116	HIS
56	CW	38	ASN
57	CX	17	GLN
57	CX	58	GLN
58	CY	18	HIS
61	DB	75	HIS
63	DD	138	GLN
64	DE	120	GLN
66	DG	93	HIS
68	DI	21	ASN
70	DK	18	HIS
72	DM	38	HIS
74	DO	9	HIS
76	DQ	23	HIS
77	DR	24	GLN
79	DT	4	GLN
79	DT	53	ASN
79	DT	311	GLN
80	P0	83	ASN
80	P0	103	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3213/3359 (95%)	614 (19%)	43 (1%)
1	AS	3226/3359 (96%)	634 (19%)	53 (1%)
2	3	120/121 (99%)	9 (7%)	0
2	AT	120/121 (99%)	9 (7%)	0
3	4	156/158 (98%)	23 (14%)	3 (1%)
3	AU	157/158 (99%)	22 (14%)	3 (1%)
46	B	1758/1787 (98%)	446 (25%)	45 (2%)
46	CM	1762/1787 (98%)	451 (25%)	52 (2%)
All	All	10512/10850 (96%)	2208 (21%)	199 (1%)

All (2208) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	15	A
1	1	24	U
1	1	25	A
1	1	29	G
1	1	39	A
1	1	42	A
1	1	44	A
1	1	47	A
1	1	48	A
1	1	56	A
1	1	58	G
1	1	59	A
1	1	64	A
1	1	65	A
1	1	91	G
1	1	98	A
1	1	104	C
1	1	108	A
1	1	109	G
1	1	110	C
1	1	121	A
1	1	134	U
1	1	135	G
1	1	155	A
1	1	156	A
1	1	164	U
1	1	169	G
1	1	172	C
1	1	173	C
1	1	175	G
1	1	186	A
1	1	189	U
1	1	190	U
1	1	199	C
1	1	205	G
1	1	209	C
1	1	212	A
1	1	217	G
1	1	218	A
1	1	219	G
1	1	230	G
1	1	236	A
1	1	239	A

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Mol	Chain	Res	Type
1	1	240	C
1	1	243	G
1	1	245	G
1	1	249	G
1	1	250	U
1	1	269	G
1	1	286	U
1	1	295	A
1	1	305	U
1	1	311	C
1	1	323	A
1	1	329	U
1	1	337	G
1	1	338	A
1	1	339	C
1	1	349	A
1	1	350	C
1	1	376	G
1	1	377	A
1	1	387	A
1	1	395	A
1	1	398	A
1	1	402	A
1	1	403	C
1	1	404	G
1	1	420	G
1	1	421	G
1	1	422	A
1	1	438	A
1	1	439	C
1	1	448	U
1	1	450	G
1	1	451	C
1	1	482	U
1	1	506	A
1	1	517	A
1	1	519	U
1	1	531	G
1	1	532	U
1	1	538	G
1	1	539	G
1	1	540	C

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Mol	Chain	Res	Type
1	1	541	U
1	1	542	U
1	1	543	C
1	1	544	U
1	1	545	G
1	1	546	C
1	1	555	A
1	1	556	U
1	1	557	A
1	1	564	G
1	1	576	A
1	1	577	G
1	1	589	G
1	1	590	A
1	1	598	U
1	1	600	U
1	1	601	U
1	1	602	A
1	1	609	A
1	1	618	U
1	1	619	A
1	1	620	A
1	1	635	C
1	1	647	A
1	1	658	A
1	1	675	A
1	1	679	U
1	1	681	U
1	1	688	A
1	1	689	A
1	1	703	A
1	1	710	G
1	1	713	A
1	1	717	A
1	1	723	G
1	1	730	A
1	1	732	U
1	1	760	U
1	1	763	U
1	1	772	U
1	1	773	U
1	1	776	A

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Mol	Chain	Res	Type
1	1	777	G
1	1	780	A
1	1	781	G
1	1	802	A
1	1	813	A
1	1	826	A
1	1	845	C
1	1	857	C
1	1	861	U
1	1	870	U
1	1	875	U
1	1	903	G
1	1	904	G
1	1	910	A
1	1	912	G
1	1	913	A
1	1	914	C
1	1	917	A
1	1	919	C
1	1	921	A
1	1	933	G
1	1	940	C
1	1	949	G
1	1	955	C
1	1	956	U
1	1	958	A
1	1	959	G
1	1	970	G
1	1	977	U
1	1	990	G
1	1	991	U
1	1	996	C
1	1	997	G
1	1	998	A
1	1	1006	G
1	1	1011	C
1	1	1012	U
1	1	1013	U
1	1	1014	G
1	1	1019	U
1	1	1020	G
1	1	1021	A

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Mol	Chain	Res	Type
1	1	1022	A
1	1	1023	A
1	1	1024	U
1	1	1025	G
1	1	1027	C
1	1	1030	U
1	1	1033	C
1	1	1043	A
1	1	1045	C
1	1	1060	A
1	1	1061	A
1	1	1068	G
1	1	1077	U
1	1	1078	U
1	1	1089	A
1	1	1090	A
1	1	1091	U
1	1	1092	U
1	1	1094	A
1	1	1099	A
1	1	1100	G
1	1	1113	G
1	1	1127	G
1	1	1140	U
1	1	1149	A
1	1	1150	A
1	1	1151	C
1	1	1155	A
1	1	1156	C
1	1	1164	U
1	1	1174	G
1	1	1176	A
1	1	1177	U
1	1	1178	G
1	1	1188	C
1	1	1189	A
1	1	1192	C
1	1	1197	C
1	1	1204	U
1	1	1205	G
1	1	1218	G
1	1	1223	C

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Mol	Chain	Res	Type
1	1	1224	C
1	1	1228	C
1	1	1229	G
1	1	1230	G
1	1	1231	U
1	1	1232	G
1	1	1239	G
1	1	1240	A
1	1	1241	A
1	1	1242	G
1	1	1243	U
1	1	1244	C
1	1	1245	G
1	1	1246	G
1	1	1247	A
1	1	1249	U
1	1	1250	C
1	1	1252	G
1	1	1254	U
1	1	1255	A
1	1	1257	G
1	1	1258	G
1	1	1259	A
1	1	1261	U
1	1	1262	G
1	1	1263	U
1	1	1264	G
1	1	1265	U
1	1	1266	A
1	1	1267	A
1	1	1270	A
1	1	1271	C
1	1	1273	C
1	1	1274	A
1	1	1275	C
1	1	1278	G
1	1	1280	C
1	1	1282	A
1	1	1303	G
1	1	1304	A
1	1	1305	U
1	1	1309	G

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Mol	Chain	Res	Type
1	1	1312	C
1	1	1326	A
1	1	1345	G
1	1	1346	U
1	1	1347	U
1	1	1348	U
1	1	1349	U
1	1	1382	A
1	1	1395	U
1	1	1415	A
1	1	1417	G
1	1	1421	U
1	1	1427	G
1	1	1430	G
1	1	1433	C
1	1	1442	A
1	1	1446	G
1	1	1465	C
1	1	1471	A
1	1	1477	A
1	1	1484	G
1	1	1498	C
1	1	1504	C
1	1	1520	A
1	1	1523	C
1	1	1525	A
1	1	1526	U
1	1	1532	G
1	1	1535	A
1	1	1552	C
1	1	1556	G
1	1	1558	G
1	1	1559	C
1	1	1560	U
1	1	1561	U
1	1	1562	G
1	1	1563	A
1	1	1565	U
1	1	1566	U
1	1	1567	U
1	1	1568	U
1	1	1569	C

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Mol	Chain	Res	Type
1	1	1571	G
1	1	1572	G
1	1	1574	C
1	1	1576	A
1	1	1585	A
1	1	1589	A
1	1	1601	A
1	1	1603	U
1	1	1624	C
1	1	1625	U
1	1	1635	C
1	1	1638	A
1	1	1639	A
1	1	1641	U
1	1	1648	G
1	1	1653	C
1	1	1654	G
1	1	1679	A
1	1	1720	U
1	1	1721	C
1	1	1732	G
1	1	1746	A
1	1	1747	G
1	1	1755	U
1	1	1756	A
1	1	1757	A
1	1	1758	U
1	1	1760	U
1	1	1761	U
1	1	1762	G
1	1	1763	C
1	1	1776	G
1	1	1793	A
1	1	1804	G
1	1	1809	A
1	1	1810	A
1	1	1811	U
1	1	1812	A
1	1	1814	U
1	1	1815	U
1	1	1816	U
1	1	1817	U

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Mol	Chain	Res	Type
1	1	1837	A
1	1	1838	A
1	1	1842	C
1	1	1845	C
1	1	1862	C
1	1	1874	G
1	1	1882	A
1	1	1889	A
1	1	1902	G
1	1	1944	G
1	1	1949	G
1	1	2068	U
1	1	2069	U
1	1	2070	A
1	1	2071	A
1	1	2078	A
1	1	2088	G
1	1	2089	G
1	1	2091	A
1	1	2092	C
1	1	2099	G
1	1	2100	G
1	1	2109	A
1	1	2118	U
1	1	2122	A
1	1	2136	A
1	1	2147	G
1	1	2149	G
1	1	2183	U
1	1	2184	G
1	1	2185	A
1	1	2186	A
1	1	2187	U
1	1	2188	G
1	1	2222	A
1	1	2227	G
1	1	2233	A
1	1	2234	A
1	1	2235	C
1	1	2250	G
1	1	2251	G
1	1	2259	A

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Mol	Chain	Res	Type
1	1	2260	U
1	1	2276	U
1	1	2285	G
1	1	2286	C
1	1	2288	U
1	1	2291	A
1	1	2292	U
1	1	2293	G
1	1	2312	U
1	1	2313	G
1	1	2314	U
1	1	2341	A
1	1	2351	A
1	1	2352	C
1	1	2353	G
1	1	2363	G
1	1	2366	U
1	1	2371	G
1	1	2372	G
1	1	2375	A
1	1	2380	A
1	1	2381	G
1	1	2382	A
1	1	2389	U
1	1	2396	G
1	1	2397	A
1	1	2413	G
1	1	2415	G
1	1	2420	G
1	1	2421	A
1	1	2422	C
1	1	2423	A
1	1	2426	G
1	1	2427	A
1	1	2430	G
1	1	2431	U
1	1	2432	G
1	1	2433	U
1	1	2437	A
1	1	2438	U
1	1	2439	A
1	1	2441	G

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Mol	Chain	Res	Type
1	1	2442	U
1	1	2443	G
1	1	2444	G
1	1	2445	G
1	1	2446	A
1	1	2448	C
1	1	2449	U
1	1	2450	U
1	1	2451	C
1	1	2452	G
1	1	2454	C
1	1	2455	G
1	1	2456	C
1	1	2457	C
1	1	2459	G
1	1	2460	U
1	1	2464	A
1	1	2465	U
1	1	2466	A
1	1	2467	C
1	1	2468	C
1	1	2470	C
1	1	2471	U
1	1	2472	A
1	1	2473	C
1	1	2474	C
1	1	2475	U
1	1	2476	C
1	1	2477	U
1	1	2480	A
1	1	2482	U
1	1	2483	U
1	1	2484	U
1	1	2489	A
1	1	2492	U
1	1	2493	A
1	1	2511	G
1	1	2513	A
1	1	2515	G
1	1	2516	U
1	1	2517	C
1	1	2518	A

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Mol	Chain	Res	Type
1	1	2519	A
1	1	2520	A
1	1	2521	C
1	1	2529	U
1	1	2530	C
1	1	2533	G
1	1	2536	U
1	1	2538	A
1	1	2545	C
1	1	2546	U
1	1	2554	C
1	1	2557	G
1	1	2565	A
1	1	2566	C
1	1	2578	G
1	1	2579	G
1	1	2586	G
1	1	2598	A
1	1	2623	G
1	1	2624	U
1	1	2628	A
1	1	2644	G
1	1	2646	A
1	1	2649	G
1	1	2661	A
1	1	2662	G
1	1	2663	A
1	1	2664	A
1	1	2666	A
1	1	2668	A
1	1	2676	A
1	1	2677	A
1	1	2686	G
1	1	2691	U
1	1	2699	A
1	1	2700	G
1	1	2701	U
1	1	2724	U
1	1	2725	G
1	1	2734	A
1	1	2745	C
1	1	2749	G

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Mol	Chain	Res	Type
1	1	2750	G
1	1	2768	G
1	1	2771	A
1	1	2772	G
1	1	2773	A
1	1	2774	A
1	1	2782	C
1	1	2786	G
1	1	2789	A
1	1	2790	U
1	1	2814	U
1	1	2815	U
1	1	2817	A
1	1	2833	U
1	1	2839	C
1	1	2843	G
1	1	2844	A
1	1	2847	U
1	1	2859	A
1	1	2861	C
1	1	2866	C
1	1	2870	G
1	1	2871	C
1	1	2886	G
1	1	2895	U
1	1	2907	U
1	1	2908	A
1	1	2911	G
1	1	2914	C
1	1	2919	G
1	1	2920	C
1	1	2923	G
1	1	2926	U
1	1	2943	A
1	1	2955	C
1	1	2962	G
1	1	2969	G
1	1	2984	A
1	1	3021	A
1	1	3028	U
1	1	3031	G
1	1	3050	A

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Mol	Chain	Res	Type
1	1	3051	C
1	1	3052	G
1	1	3058	A
1	1	3064	C
1	1	3073	G
1	1	3094	A
1	1	3101	A
1	1	3102	A
1	1	3103	U
1	1	3114	A
1	1	3115	C
1	1	3125	U
1	1	3126	U
1	1	3143	G
1	1	3144	A
1	1	3146	G
1	1	3149	U
1	1	3151	C
1	1	3157	A
1	1	3160	C
1	1	3161	U
1	1	3162	U
1	1	3163	U
1	1	3164	U
1	1	3165	U
1	1	3166	A
1	1	3167	G
1	1	3171	C
1	1	3172	U
1	1	3182	C
1	1	3183	A
1	1	3184	G
1	1	3194	G
1	1	3208	A
1	1	3210	A
1	1	3212	G
1	1	3214	U
1	1	3221	G
1	1	3224	U
1	1	3228	G
1	1	3235	A
1	1	3241	G

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Mol	Chain	Res	Type
1	1	3246	C
1	1	3252	C
1	1	3259	A
1	1	3260	A
1	1	3268	G
1	1	3269	C
1	1	3272	A
1	1	3278	U
1	1	3281	A
1	1	3284	U
1	1	3285	A
1	1	3306	U
1	1	3307	A
1	1	3309	A
1	1	3310	G
1	1	3316	U
1	1	3317	U
1	1	3318	G
1	1	3319	U
1	1	3320	U
1	1	3321	G
1	1	3334	G
1	1	3343	C
1	1	3351	G
1	1	3361	U
2	3	7	G
2	3	22	A
2	3	54	U
2	3	55	A
2	3	65	G
2	3	73	C
2	3	76	A
2	3	102	A
2	3	112	G
3	4	23	U
3	4	34	U
3	4	35	C
3	4	59	A
3	4	62	C
3	4	63	G
3	4	81	A
3	4	84	C

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Mol	Chain	Res	Type
3	4	85	G
3	4	86	U
3	4	87	G
3	4	92	A
3	4	95	G
3	4	102	U
3	4	104	A
3	4	106	C
3	4	111	A
3	4	113	U
3	4	125	U
3	4	126	A
3	4	148	G
3	4	152	G
3	4	157	U
46	B	17	C
46	B	25	C
46	B	26	A
46	B	27	U
46	B	34	G
46	B	47	A
46	B	57	G
46	B	66	U
46	B	74	U
46	B	75	U
46	B	76	A
46	B	78	A
46	B	79	C
46	B	81	G
46	B	84	A
46	B	93	A
46	B	104	A
46	B	114	C
46	B	115	G
46	B	123	G
46	B	126	A
46	B	127	G
46	B	128	U
46	B	129	A
46	B	130	C
46	B	131	C
46	B	132	U

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Mol	Chain	Res	Type
46	B	133	U
46	B	134	A
46	B	135	C
46	B	138	C
46	B	139	U
46	B	142	G
46	B	143	A
46	B	150	U
46	B	151	G
46	B	152	G
46	B	154	A
46	B	159	U
46	B	166	A
46	B	168	U
46	B	173	G
46	B	174	C
46	B	176	U
46	B	177	A
46	B	179	A
46	B	190	U
46	B	191	U
46	B	193	G
46	B	199	G
46	B	200	A
46	B	202	G
46	B	206	U
46	B	211	A
46	B	213	A
46	B	214	U
46	B	215	A
46	B	216	A
46	B	217	A
46	B	218	A
46	B	220	A
46	B	222	C
46	B	224	A
46	B	226	G
46	B	229	U
46	B	230	U
46	B	231	C
46	B	233	G
46	B	237	C

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Mol	Chain	Res	Type
46	B	238	U
46	B	247	U
46	B	255	A
46	B	259	U
46	B	260	U
46	B	261	C
46	B	262	G
46	B	266	C
46	B	269	A
46	B	270	U
46	B	274	C
46	B	276	U
46	B	277	G
46	B	278	U
46	B	279	G
46	B	283	G
46	B	285	G
46	B	297	A
46	B	312	C
46	B	314	A
46	B	318	U
46	B	319	C
46	B	320	G
46	B	335	G
46	B	336	C
46	B	350	A
46	B	357	A
46	B	358	A
46	B	359	C
46	B	388	G
46	B	398	A
46	B	400	C
46	B	402	G
46	B	414	A
46	B	416	G
46	B	421	G
46	B	422	C
46	B	423	A
46	B	424	G
46	B	432	G
46	B	437	U
46	B	442	C

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Mol	Chain	Res	Type
46	B	446	C
46	B	452	A
46	B	458	A
46	B	466	A
46	B	475	A
46	B	480	U
46	B	483	A
46	B	484	G
46	B	485	G
46	B	487	C
46	B	490	U
46	B	491	U
46	B	499	U
46	B	503	A
46	B	505	U
46	B	506	U
46	B	509	A
46	B	512	G
46	B	513	A
46	B	515	U
46	B	518	A
46	B	519	A
46	B	525	A
46	B	530	U
46	B	534	C
46	B	536	A
46	B	537	G
46	B	539	A
46	B	540	A
46	B	547	G
46	B	553	A
46	B	554	A
46	B	555	G
46	B	556	U
46	B	557	C
46	B	563	C
46	B	566	G
46	B	575	G
46	B	576	U
46	B	580	U
46	B	592	A
46	B	593	G

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Mol	Chain	Res	Type
46	B	604	A
46	B	609	U
46	B	617	A
46	B	618	A
46	B	620	A
46	B	621	A
46	B	639	G
46	B	645	G
46	B	648	U
46	B	649	G
46	B	650	G
46	B	651	C
46	B	652	C
46	B	653	G
46	B	654	G
46	B	657	C
46	B	670	C
46	B	671	G
46	B	672	U
46	B	673	A
46	B	674	C
46	B	675	U
46	B	677	G
46	B	678	A
46	B	679	C
46	B	680	C
46	B	681	C
46	B	688	G
46	B	695	C
46	B	696	U
46	B	697	U
46	B	698	C
46	B	700	G
46	B	701	G
46	B	702	G
46	B	703	U
46	B	704	A
46	B	705	G
46	B	706	C
46	B	707	C
46	B	708	A
46	B	709	U

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Mol	Chain	Res	Type
46	B	710	U
46	B	711	U
46	B	712	A
46	B	713	U
46	B	714	G
46	B	715	G
46	B	716	C
46	B	717	G
46	B	718	A
46	B	719	A
46	B	723	G
46	B	729	U
46	B	739	A
46	B	740	A
46	B	741	A
46	B	750	G
46	B	751	U
46	B	756	A
46	B	759	A
46	B	760	G
46	B	762	C
46	B	764	U
46	B	765	U
46	B	766	U
46	B	767	G
46	B	768	C
46	B	770	C
46	B	771	G
46	B	773	A
46	B	775	A
46	B	778	U
46	B	779	U
46	B	796	A
46	B	798	A
46	B	799	G
46	B	802	C
46	B	803	G
46	B	804	U
46	B	805	U
46	B	807	U
46	B	808	G
46	B	813	U

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Mol	Chain	Res	Type
46	B	815	U
46	B	817	U
46	B	819	G
46	B	820	U
46	B	821	U
46	B	822	G
46	B	823	G
46	B	824	U
46	B	825	U
46	B	826	U
46	B	828	U
46	B	829	A
46	B	831	G
46	B	840	A
46	B	842	U
46	B	847	A
46	B	848	A
46	B	856	G
46	B	857	G
46	B	869	A
46	B	871	U
46	B	875	C
46	B	877	G
46	B	878	U
46	B	879	U
46	B	881	U
46	B	891	A
46	B	909	A
46	B	910	G
46	B	911	A
46	B	918	A
46	B	920	U
46	B	927	G
46	B	945	U
46	B	951	A
46	B	973	A
46	B	975	C
46	B	977	A
46	B	988	A
46	B	989	U
46	B	990	A
46	B	997	U

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Mol	Chain	Res	Type
46	B	998	A
46	B	1004	A
46	B	1005	A
46	B	1011	A
46	B	1013	C
46	B	1017	G
46	B	1024	A
46	B	1025	G
46	B	1039	U
46	B	1042	U
46	B	1043	U
46	B	1044	U
46	B	1047	U
46	B	1055	A
46	B	1056	U
46	B	1057	C
46	B	1058	G
46	B	1059	G
46	B	1060	C
46	B	1061	A
46	B	1067	C
46	B	1077	A
46	B	1081	C
46	B	1085	G
46	B	1123	A
46	B	1135	G
46	B	1143	C
46	B	1145	A
46	B	1152	G
46	B	1168	A
46	B	1169	A
46	B	1170	U
46	B	1179	A
46	B	1181	A
46	B	1184	G
46	B	1185	G
46	B	1187	A
46	B	1193	A
46	B	1202	A
46	B	1203	G
46	B	1206	A
46	B	1207	C

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Mol	Chain	Res	Type
46	B	1212	A
46	B	1215	A
46	B	1219	A
46	B	1220	C
46	B	1221	A
46	B	1229	A
46	B	1230	G
46	B	1231	C
46	B	1236	U
46	B	1243	U
46	B	1250	G
46	B	1270	U
46	B	1284	G
46	B	1299	U
46	B	1300	U
46	B	1301	G
46	B	1306	A
46	B	1325	U
46	B	1330	A
46	B	1336	G
46	B	1339	G
46	B	1342	A
46	B	1343	G
46	B	1345	A
46	B	1346	U
46	B	1348	U
46	B	1349	G
46	B	1352	G
46	B	1355	A
46	B	1356	U
46	B	1357	A
46	B	1359	U
46	B	1360	C
46	B	1364	U
46	B	1369	G
46	B	1370	A
46	B	1376	U
46	B	1380	G
46	B	1381	A
46	B	1382	U
46	B	1384	U
46	B	1385	C

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Mol	Chain	Res	Type
46	B	1392	A
46	B	1397	A
46	B	1398	G
46	B	1399	U
46	B	1400	U
46	B	1401	U
46	B	1410	A
46	B	1413	A
46	B	1414	G
46	B	1415	G
46	B	1422	A
46	B	1431	G
46	B	1433	C
46	B	1445	C
46	B	1446	A
46	B	1455	A
46	B	1457	A
46	B	1458	C
46	B	1461	A
46	B	1462	C
46	B	1463	G
46	B	1468	C
46	B	1476	A
46	B	1477	U
46	B	1480	G
46	B	1483	U
46	B	1485	G
46	B	1491	G
46	B	1502	A
46	B	1503	A
46	B	1508	G
46	B	1510	G
46	B	1511	A
46	B	1523	G
46	B	1524	C
46	B	1529	G
46	B	1530	A
46	B	1541	U
46	B	1544	U
46	B	1546	G
46	B	1560	A
46	B	1561	G

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Mol	Chain	Res	Type
46	B	1571	G
46	B	1574	A
46	B	1575	G
46	B	1577	G
46	B	1580	A
46	B	1582	U
46	B	1584	A
46	B	1588	G
46	B	1621	C
46	B	1644	U
46	B	1645	G
46	B	1665	C
46	B	1667	G
46	B	1670	U
46	B	1671	G
46	B	1672	G
46	B	1673	U
46	B	1678	G
46	B	1679	A
46	B	1680	A
46	B	1697	C
46	B	1698	U
46	B	1699	G
46	B	1700	G
46	B	1701	A
46	B	1702	A
46	B	1704	C
46	B	1737	A
46	B	1743	A
46	B	1747	G
46	B	1749	A
46	B	1753	A
46	B	1756	U
46	B	1767	G
46	B	1769	A
46	B	1770	C
46	B	1779	G
46	B	1780	G
46	B	1781	A
46	B	1782	U
46	B	1783	C
1	AS	24	U

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Mol	Chain	Res	Type
1	AS	25	A
1	AS	29	G
1	AS	39	A
1	AS	42	A
1	AS	44	A
1	AS	48	A
1	AS	56	A
1	AS	58	G
1	AS	59	A
1	AS	64	A
1	AS	65	A
1	AS	91	G
1	AS	98	A
1	AS	104	C
1	AS	108	A
1	AS	109	G
1	AS	110	C
1	AS	121	A
1	AS	134	U
1	AS	135	G
1	AS	155	A
1	AS	156	A
1	AS	164	U
1	AS	169	G
1	AS	172	C
1	AS	173	C
1	AS	175	G
1	AS	186	A
1	AS	189	U
1	AS	190	U
1	AS	199	C
1	AS	205	G
1	AS	209	C
1	AS	210	A
1	AS	212	A
1	AS	217	G
1	AS	218	A
1	AS	219	G
1	AS	230	G
1	AS	236	A
1	AS	239	A
1	AS	240	C

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Mol	Chain	Res	Type
1	AS	243	G
1	AS	245	G
1	AS	249	G
1	AS	250	U
1	AS	251	G
1	AS	269	G
1	AS	286	U
1	AS	295	A
1	AS	305	U
1	AS	311	C
1	AS	323	A
1	AS	329	U
1	AS	337	G
1	AS	338	A
1	AS	339	C
1	AS	343	U
1	AS	349	A
1	AS	350	C
1	AS	376	G
1	AS	377	A
1	AS	395	A
1	AS	398	A
1	AS	402	A
1	AS	403	C
1	AS	404	G
1	AS	420	G
1	AS	421	G
1	AS	422	A
1	AS	438	A
1	AS	439	C
1	AS	441	U
1	AS	442	G
1	AS	443	G
1	AS	445	A
1	AS	447	U
1	AS	448	U
1	AS	449	U
1	AS	450	G
1	AS	451	C
1	AS	453	U
1	AS	454	G
1	AS	474	C

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Mol	Chain	Res	Type
1	AS	478	G
1	AS	479	C
1	AS	480	G
1	AS	481	G
1	AS	482	U
1	AS	483	U
1	AS	484	U
1	AS	486	C
1	AS	488	G
1	AS	506	A
1	AS	517	A
1	AS	519	U
1	AS	531	G
1	AS	532	U
1	AS	538	G
1	AS	539	G
1	AS	540	C
1	AS	541	U
1	AS	542	U
1	AS	543	C
1	AS	544	U
1	AS	545	G
1	AS	546	C
1	AS	555	A
1	AS	556	U
1	AS	557	A
1	AS	564	G
1	AS	577	G
1	AS	589	G
1	AS	590	A
1	AS	598	U
1	AS	600	U
1	AS	601	U
1	AS	602	A
1	AS	609	A
1	AS	618	U
1	AS	619	A
1	AS	620	A
1	AS	635	C
1	AS	647	A
1	AS	658	A
1	AS	675	A

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Mol	Chain	Res	Type
1	AS	679	U
1	AS	688	A
1	AS	689	A
1	AS	703	A
1	AS	710	G
1	AS	713	A
1	AS	717	A
1	AS	723	G
1	AS	730	A
1	AS	732	U
1	AS	760	U
1	AS	763	U
1	AS	772	U
1	AS	773	U
1	AS	776	A
1	AS	777	G
1	AS	780	A
1	AS	781	G
1	AS	802	A
1	AS	812	A
1	AS	813	A
1	AS	826	A
1	AS	845	C
1	AS	857	C
1	AS	861	U
1	AS	870	U
1	AS	875	U
1	AS	892	A
1	AS	893	U
1	AS	903	G
1	AS	904	G
1	AS	910	A
1	AS	912	G
1	AS	913	A
1	AS	917	A
1	AS	919	C
1	AS	921	A
1	AS	933	G
1	AS	940	C
1	AS	949	G
1	AS	955	C
1	AS	956	U

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Mol	Chain	Res	Type
1	AS	959	G
1	AS	970	G
1	AS	976	A
1	AS	977	U
1	AS	990	G
1	AS	991	U
1	AS	996	C
1	AS	997	G
1	AS	998	A
1	AS	1006	G
1	AS	1011	C
1	AS	1012	U
1	AS	1014	G
1	AS	1019	U
1	AS	1020	G
1	AS	1022	A
1	AS	1023	A
1	AS	1024	U
1	AS	1025	G
1	AS	1026	A
1	AS	1027	C
1	AS	1030	U
1	AS	1033	C
1	AS	1043	A
1	AS	1045	C
1	AS	1060	A
1	AS	1061	A
1	AS	1068	G
1	AS	1077	U
1	AS	1078	U
1	AS	1089	A
1	AS	1090	A
1	AS	1091	U
1	AS	1092	U
1	AS	1094	A
1	AS	1099	A
1	AS	1100	G
1	AS	1113	G
1	AS	1127	G
1	AS	1140	U
1	AS	1149	A
1	AS	1150	A

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Mol	Chain	Res	Type
1	AS	1151	C
1	AS	1155	A
1	AS	1156	C
1	AS	1164	U
1	AS	1174	G
1	AS	1176	A
1	AS	1177	U
1	AS	1178	G
1	AS	1188	C
1	AS	1189	A
1	AS	1192	C
1	AS	1197	C
1	AS	1204	U
1	AS	1205	G
1	AS	1218	G
1	AS	1219	A
1	AS	1224	C
1	AS	1228	C
1	AS	1231	U
1	AS	1232	G
1	AS	1233	G
1	AS	1237	U
1	AS	1238	G
1	AS	1239	G
1	AS	1241	A
1	AS	1242	G
1	AS	1243	U
1	AS	1244	C
1	AS	1246	G
1	AS	1248	A
1	AS	1249	U
1	AS	1250	C
1	AS	1251	C
1	AS	1252	G
1	AS	1254	U
1	AS	1255	A
1	AS	1258	G
1	AS	1259	A
1	AS	1260	G
1	AS	1261	U
1	AS	1262	G
1	AS	1263	U

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Mol	Chain	Res	Type
1	AS	1264	G
1	AS	1265	U
1	AS	1266	A
1	AS	1267	A
1	AS	1270	A
1	AS	1271	C
1	AS	1273	C
1	AS	1278	G
1	AS	1281	G
1	AS	1282	A
1	AS	1283	A
1	AS	1303	G
1	AS	1304	A
1	AS	1305	U
1	AS	1309	G
1	AS	1326	A
1	AS	1345	G
1	AS	1346	U
1	AS	1347	U
1	AS	1348	U
1	AS	1349	U
1	AS	1382	A
1	AS	1395	U
1	AS	1415	A
1	AS	1417	G
1	AS	1421	U
1	AS	1427	G
1	AS	1430	G
1	AS	1433	C
1	AS	1442	A
1	AS	1446	G
1	AS	1465	C
1	AS	1471	A
1	AS	1477	A
1	AS	1484	G
1	AS	1498	C
1	AS	1504	C
1	AS	1520	A
1	AS	1523	C
1	AS	1532	G
1	AS	1535	A
1	AS	1552	C

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Mol	Chain	Res	Type
1	AS	1556	G
1	AS	1558	G
1	AS	1559	C
1	AS	1560	U
1	AS	1561	U
1	AS	1562	G
1	AS	1563	A
1	AS	1564	U
1	AS	1565	U
1	AS	1566	U
1	AS	1567	U
1	AS	1568	U
1	AS	1569	C
1	AS	1571	G
1	AS	1572	G
1	AS	1574	C
1	AS	1576	A
1	AS	1585	A
1	AS	1589	A
1	AS	1601	A
1	AS	1603	U
1	AS	1624	C
1	AS	1625	U
1	AS	1635	C
1	AS	1638	A
1	AS	1639	A
1	AS	1641	U
1	AS	1648	G
1	AS	1654	G
1	AS	1679	A
1	AS	1720	U
1	AS	1721	C
1	AS	1732	G
1	AS	1746	A
1	AS	1747	G
1	AS	1755	U
1	AS	1756	A
1	AS	1757	A
1	AS	1758	U
1	AS	1759	U
1	AS	1761	U
1	AS	1762	G

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Mol	Chain	Res	Type
1	AS	1763	C
1	AS	1776	G
1	AS	1793	A
1	AS	1804	G
1	AS	1809	A
1	AS	1810	A
1	AS	1811	U
1	AS	1812	A
1	AS	1814	U
1	AS	1815	U
1	AS	1816	U
1	AS	1817	U
1	AS	1835	A
1	AS	1838	A
1	AS	1842	C
1	AS	1845	C
1	AS	1862	C
1	AS	1874	G
1	AS	1882	A
1	AS	1889	A
1	AS	1902	G
1	AS	1944	G
1	AS	1949	G
1	AS	2063	C
1	AS	2064	A
1	AS	2065	C
1	AS	2066	G
1	AS	2067	U
1	AS	2068	U
1	AS	2069	U
1	AS	2070	A
1	AS	2071	A
1	AS	2078	A
1	AS	2088	G
1	AS	2089	G
1	AS	2091	A
1	AS	2092	C
1	AS	2099	G
1	AS	2100	G
1	AS	2109	A
1	AS	2118	U
1	AS	2122	A

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Mol	Chain	Res	Type
1	AS	2136	A
1	AS	2147	G
1	AS	2149	G
1	AS	2183	U
1	AS	2184	G
1	AS	2185	A
1	AS	2186	A
1	AS	2187	U
1	AS	2188	G
1	AS	2201	A
1	AS	2222	A
1	AS	2227	G
1	AS	2233	A
1	AS	2234	A
1	AS	2250	G
1	AS	2251	G
1	AS	2259	A
1	AS	2260	U
1	AS	2276	U
1	AS	2285	G
1	AS	2286	C
1	AS	2288	U
1	AS	2291	A
1	AS	2292	U
1	AS	2293	G
1	AS	2312	U
1	AS	2313	G
1	AS	2314	U
1	AS	2341	A
1	AS	2351	A
1	AS	2352	C
1	AS	2353	G
1	AS	2363	G
1	AS	2366	U
1	AS	2371	G
1	AS	2372	G
1	AS	2375	A
1	AS	2380	A
1	AS	2381	G
1	AS	2382	A
1	AS	2389	U
1	AS	2396	G

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Mol	Chain	Res	Type
1	AS	2397	A
1	AS	2413	G
1	AS	2420	G
1	AS	2421	A
1	AS	2422	C
1	AS	2425	G
1	AS	2426	G
1	AS	2427	A
1	AS	2428	G
1	AS	2429	G
1	AS	2430	G
1	AS	2431	U
1	AS	2432	G
1	AS	2433	U
1	AS	2436	A
1	AS	2437	A
1	AS	2438	U
1	AS	2439	A
1	AS	2440	A
1	AS	2441	G
1	AS	2442	U
1	AS	2443	G
1	AS	2445	G
1	AS	2446	A
1	AS	2447	G
1	AS	2448	C
1	AS	2449	U
1	AS	2450	U
1	AS	2451	C
1	AS	2452	G
1	AS	2453	G
1	AS	2455	G
1	AS	2456	C
1	AS	2457	C
1	AS	2458	G
1	AS	2459	G
1	AS	2460	U
1	AS	2464	A
1	AS	2465	U
1	AS	2466	A
1	AS	2467	C
1	AS	2468	C

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Mol	Chain	Res	Type
1	AS	2469	A
1	AS	2471	U
1	AS	2472	A
1	AS	2473	C
1	AS	2474	C
1	AS	2475	U
1	AS	2476	C
1	AS	2477	U
1	AS	2478	A
1	AS	2480	A
1	AS	2481	G
1	AS	2482	U
1	AS	2483	U
1	AS	2484	U
1	AS	2486	U
1	AS	2489	A
1	AS	2492	U
1	AS	2493	A
1	AS	2510	U
1	AS	2511	G
1	AS	2513	A
1	AS	2515	G
1	AS	2516	U
1	AS	2517	C
1	AS	2518	A
1	AS	2519	A
1	AS	2520	A
1	AS	2521	C
1	AS	2529	U
1	AS	2530	C
1	AS	2533	G
1	AS	2536	U
1	AS	2538	A
1	AS	2545	C
1	AS	2546	U
1	AS	2554	C
1	AS	2557	G
1	AS	2565	A
1	AS	2566	C
1	AS	2578	G
1	AS	2579	G
1	AS	2586	G

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Mol	Chain	Res	Type
1	AS	2598	A
1	AS	2623	G
1	AS	2624	U
1	AS	2628	A
1	AS	2646	A
1	AS	2649	G
1	AS	2661	A
1	AS	2662	G
1	AS	2663	A
1	AS	2666	A
1	AS	2668	A
1	AS	2676	A
1	AS	2677	A
1	AS	2686	G
1	AS	2699	A
1	AS	2700	G
1	AS	2701	U
1	AS	2724	U
1	AS	2725	G
1	AS	2734	A
1	AS	2745	C
1	AS	2749	G
1	AS	2750	G
1	AS	2768	G
1	AS	2771	A
1	AS	2772	G
1	AS	2773	A
1	AS	2774	A
1	AS	2782	C
1	AS	2786	G
1	AS	2789	A
1	AS	2790	U
1	AS	2814	U
1	AS	2815	U
1	AS	2817	A
1	AS	2833	U
1	AS	2839	C
1	AS	2843	G
1	AS	2844	A
1	AS	2847	U
1	AS	2859	A
1	AS	2861	C

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Mol	Chain	Res	Type
1	AS	2866	C
1	AS	2870	G
1	AS	2871	C
1	AS	2886	G
1	AS	2895	U
1	AS	2907	U
1	AS	2908	A
1	AS	2911	G
1	AS	2914	C
1	AS	2919	G
1	AS	2920	C
1	AS	2923	G
1	AS	2926	U
1	AS	2943	A
1	AS	2955	C
1	AS	2960	C
1	AS	2962	G
1	AS	2969	G
1	AS	2984	A
1	AS	3021	A
1	AS	3028	U
1	AS	3031	G
1	AS	3050	A
1	AS	3051	C
1	AS	3052	G
1	AS	3058	A
1	AS	3064	C
1	AS	3076	U
1	AS	3094	A
1	AS	3101	A
1	AS	3102	A
1	AS	3103	U
1	AS	3114	A
1	AS	3115	C
1	AS	3134	C
1	AS	3143	G
1	AS	3144	A
1	AS	3146	G
1	AS	3149	U
1	AS	3151	C
1	AS	3157	A
1	AS	3160	C

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Mol	Chain	Res	Type
1	AS	3161	U
1	AS	3163	U
1	AS	3164	U
1	AS	3165	U
1	AS	3166	A
1	AS	3167	G
1	AS	3171	C
1	AS	3172	U
1	AS	3182	C
1	AS	3183	A
1	AS	3184	G
1	AS	3194	G
1	AS	3208	A
1	AS	3210	A
1	AS	3212	G
1	AS	3214	U
1	AS	3224	U
1	AS	3228	G
1	AS	3235	A
1	AS	3241	G
1	AS	3246	C
1	AS	3252	C
1	AS	3259	A
1	AS	3260	A
1	AS	3268	G
1	AS	3269	C
1	AS	3272	A
1	AS	3278	U
1	AS	3281	A
1	AS	3284	U
1	AS	3285	A
1	AS	3306	U
1	AS	3307	A
1	AS	3309	A
1	AS	3310	G
1	AS	3316	U
1	AS	3317	U
1	AS	3318	G
1	AS	3319	U
1	AS	3320	U
1	AS	3321	G
1	AS	3334	G

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Mol	Chain	Res	Type
1	AS	3343	C
1	AS	3351	G
1	AS	3361	U
2	AT	7	G
2	AT	22	A
2	AT	54	U
2	AT	55	A
2	AT	65	G
2	AT	73	C
2	AT	76	A
2	AT	102	A
2	AT	112	G
3	AU	23	U
3	AU	34	U
3	AU	35	C
3	AU	59	A
3	AU	62	C
3	AU	63	G
3	AU	81	A
3	AU	84	C
3	AU	85	G
3	AU	86	U
3	AU	87	G
3	AU	92	A
3	AU	95	G
3	AU	102	U
3	AU	104	A
3	AU	106	C
3	AU	111	A
3	AU	113	U
3	AU	125	U
3	AU	126	A
3	AU	152	G
3	AU	157	U
46	CM	17	C
46	CM	25	C
46	CM	26	A
46	CM	27	U
46	CM	34	G
46	CM	47	A
46	CM	57	G
46	CM	65	A

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Mol	Chain	Res	Type
46	CM	66	U
46	CM	74	U
46	CM	75	U
46	CM	76	A
46	CM	78	A
46	CM	79	C
46	CM	81	G
46	CM	84	A
46	CM	104	A
46	CM	114	C
46	CM	115	G
46	CM	123	G
46	CM	126	A
46	CM	127	G
46	CM	128	U
46	CM	130	C
46	CM	131	C
46	CM	132	U
46	CM	133	U
46	CM	134	A
46	CM	135	C
46	CM	138	C
46	CM	139	U
46	CM	142	G
46	CM	143	A
46	CM	150	U
46	CM	151	G
46	CM	152	G
46	CM	154	A
46	CM	159	U
46	CM	166	A
46	CM	168	U
46	CM	173	G
46	CM	176	U
46	CM	177	A
46	CM	190	U
46	CM	193	G
46	CM	199	G
46	CM	200	A
46	CM	202	G
46	CM	206	U
46	CM	211	A

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Mol	Chain	Res	Type
46	CM	213	A
46	CM	214	U
46	CM	215	A
46	CM	216	A
46	CM	217	A
46	CM	218	A
46	CM	219	A
46	CM	220	A
46	CM	221	U
46	CM	222	C
46	CM	226	G
46	CM	229	U
46	CM	230	U
46	CM	231	C
46	CM	232	G
46	CM	236	U
46	CM	237	C
46	CM	238	U
46	CM	239	U
46	CM	240	U
46	CM	247	U
46	CM	255	A
46	CM	259	U
46	CM	260	U
46	CM	261	C
46	CM	262	G
46	CM	266	C
46	CM	269	A
46	CM	270	U
46	CM	273	C
46	CM	274	C
46	CM	276	U
46	CM	277	G
46	CM	278	U
46	CM	279	G
46	CM	283	G
46	CM	285	G
46	CM	297	A
46	CM	312	C
46	CM	314	A
46	CM	318	U
46	CM	319	C

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Mol	Chain	Res	Type
46	CM	320	G
46	CM	335	G
46	CM	336	C
46	CM	350	A
46	CM	357	A
46	CM	358	A
46	CM	359	C
46	CM	388	G
46	CM	398	A
46	CM	400	C
46	CM	402	G
46	CM	414	A
46	CM	416	G
46	CM	421	G
46	CM	422	C
46	CM	423	A
46	CM	424	G
46	CM	432	G
46	CM	437	U
46	CM	442	C
46	CM	446	C
46	CM	452	A
46	CM	458	A
46	CM	462	A
46	CM	466	A
46	CM	475	A
46	CM	480	U
46	CM	489	C
46	CM	490	U
46	CM	491	U
46	CM	495	G
46	CM	498	C
46	CM	499	U
46	CM	503	A
46	CM	504	A
46	CM	505	U
46	CM	506	U
46	CM	509	A
46	CM	512	G
46	CM	513	A
46	CM	515	U
46	CM	518	A

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Mol	Chain	Res	Type
46	CM	519	A
46	CM	525	A
46	CM	530	U
46	CM	534	C
46	CM	536	A
46	CM	537	G
46	CM	539	A
46	CM	540	A
46	CM	547	G
46	CM	553	A
46	CM	554	A
46	CM	555	G
46	CM	556	U
46	CM	557	C
46	CM	563	C
46	CM	566	G
46	CM	576	U
46	CM	592	A
46	CM	593	G
46	CM	604	A
46	CM	609	U
46	CM	617	A
46	CM	618	A
46	CM	620	A
46	CM	621	A
46	CM	639	G
46	CM	645	G
46	CM	648	U
46	CM	649	G
46	CM	650	G
46	CM	652	C
46	CM	653	G
46	CM	654	G
46	CM	657	C
46	CM	659	U
46	CM	668	U
46	CM	670	C
46	CM	671	G
46	CM	672	U
46	CM	673	A
46	CM	675	U
46	CM	676	G

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Mol	Chain	Res	Type
46	CM	678	A
46	CM	679	C
46	CM	680	C
46	CM	681	C
46	CM	682	A
46	CM	688	G
46	CM	691	U
46	CM	694	C
46	CM	695	C
46	CM	696	U
46	CM	697	U
46	CM	700	G
46	CM	701	G
46	CM	702	G
46	CM	703	U
46	CM	704	A
46	CM	705	G
46	CM	706	C
46	CM	707	C
46	CM	709	U
46	CM	711	U
46	CM	712	A
46	CM	713	U
46	CM	714	G
46	CM	716	C
46	CM	717	G
46	CM	718	A
46	CM	719	A
46	CM	720	C
46	CM	722	A
46	CM	723	G
46	CM	724	G
46	CM	729	U
46	CM	739	A
46	CM	740	A
46	CM	741	A
46	CM	750	G
46	CM	751	U
46	CM	756	A
46	CM	759	A
46	CM	760	G
46	CM	762	C

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Mol	Chain	Res	Type
46	CM	764	U
46	CM	765	U
46	CM	766	U
46	CM	767	G
46	CM	768	C
46	CM	770	C
46	CM	771	G
46	CM	773	A
46	CM	775	A
46	CM	778	U
46	CM	779	U
46	CM	796	A
46	CM	798	A
46	CM	799	G
46	CM	802	C
46	CM	803	G
46	CM	804	U
46	CM	805	U
46	CM	807	U
46	CM	808	G
46	CM	812	C
46	CM	814	A
46	CM	815	U
46	CM	816	U
46	CM	818	U
46	CM	819	G
46	CM	820	U
46	CM	821	U
46	CM	823	G
46	CM	824	U
46	CM	825	U
46	CM	826	U
46	CM	827	C
46	CM	828	U
46	CM	829	A
46	CM	840	A
46	CM	842	U
46	CM	848	A
46	CM	856	G
46	CM	857	G
46	CM	869	A
46	CM	871	U

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Mol	Chain	Res	Type
46	CM	875	C
46	CM	877	G
46	CM	878	U
46	CM	879	U
46	CM	881	U
46	CM	891	A
46	CM	909	A
46	CM	910	G
46	CM	911	A
46	CM	918	A
46	CM	920	U
46	CM	927	G
46	CM	945	U
46	CM	951	A
46	CM	973	A
46	CM	975	C
46	CM	977	A
46	CM	988	A
46	CM	989	U
46	CM	990	A
46	CM	997	U
46	CM	998	A
46	CM	1004	A
46	CM	1005	A
46	CM	1011	A
46	CM	1013	C
46	CM	1017	G
46	CM	1024	A
46	CM	1025	G
46	CM	1039	U
46	CM	1042	U
46	CM	1043	U
46	CM	1044	U
46	CM	1047	U
46	CM	1055	A
46	CM	1056	U
46	CM	1057	C
46	CM	1058	G
46	CM	1059	G
46	CM	1060	C
46	CM	1061	A
46	CM	1067	C

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Mol	Chain	Res	Type
46	CM	1074	U
46	CM	1077	A
46	CM	1081	C
46	CM	1085	G
46	CM	1123	A
46	CM	1135	G
46	CM	1143	C
46	CM	1145	A
46	CM	1152	G
46	CM	1168	A
46	CM	1169	A
46	CM	1170	U
46	CM	1179	A
46	CM	1181	A
46	CM	1184	G
46	CM	1185	G
46	CM	1186	G
46	CM	1187	A
46	CM	1193	A
46	CM	1202	A
46	CM	1203	G
46	CM	1206	A
46	CM	1207	C
46	CM	1212	A
46	CM	1215	A
46	CM	1219	A
46	CM	1220	C
46	CM	1221	A
46	CM	1229	A
46	CM	1230	G
46	CM	1231	C
46	CM	1234	U
46	CM	1236	U
46	CM	1243	U
46	CM	1250	G
46	CM	1270	U
46	CM	1284	G
46	CM	1299	U
46	CM	1300	U
46	CM	1301	G
46	CM	1306	A
46	CM	1325	U

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Mol	Chain	Res	Type
46	CM	1330	A
46	CM	1336	G
46	CM	1339	G
46	CM	1342	A
46	CM	1343	G
46	CM	1345	A
46	CM	1346	U
46	CM	1348	U
46	CM	1349	G
46	CM	1352	G
46	CM	1355	A
46	CM	1356	U
46	CM	1357	A
46	CM	1359	U
46	CM	1360	C
46	CM	1364	U
46	CM	1365	C
46	CM	1369	G
46	CM	1370	A
46	CM	1376	U
46	CM	1380	G
46	CM	1381	A
46	CM	1382	U
46	CM	1384	U
46	CM	1385	C
46	CM	1392	A
46	CM	1397	A
46	CM	1398	G
46	CM	1399	U
46	CM	1400	U
46	CM	1401	U
46	CM	1410	A
46	CM	1413	A
46	CM	1414	G
46	CM	1415	G
46	CM	1422	A
46	CM	1431	G
46	CM	1433	C
46	CM	1445	C
46	CM	1446	A
46	CM	1455	A
46	CM	1457	A

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Mol	Chain	Res	Type
46	CM	1458	C
46	CM	1461	A
46	CM	1462	C
46	CM	1463	G
46	CM	1468	C
46	CM	1476	A
46	CM	1477	U
46	CM	1480	G
46	CM	1483	U
46	CM	1491	G
46	CM	1502	A
46	CM	1503	A
46	CM	1508	G
46	CM	1510	G
46	CM	1511	A
46	CM	1523	G
46	CM	1524	C
46	CM	1529	G
46	CM	1530	A
46	CM	1541	U
46	CM	1544	U
46	CM	1546	G
46	CM	1556	A
46	CM	1560	A
46	CM	1561	G
46	CM	1571	G
46	CM	1574	A
46	CM	1575	G
46	CM	1577	G
46	CM	1580	A
46	CM	1582	U
46	CM	1584	A
46	CM	1588	G
46	CM	1621	C
46	CM	1644	U
46	CM	1645	G
46	CM	1665	C
46	CM	1667	G
46	CM	1670	U
46	CM	1671	G
46	CM	1672	G
46	CM	1673	U

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Mol	Chain	Res	Type
46	CM	1675	U
46	CM	1677	G
46	CM	1678	G
46	CM	1680	A
46	CM	1697	C
46	CM	1699	G
46	CM	1700	G
46	CM	1701	A
46	CM	1702	A
46	CM	1704	C
46	CM	1737	A
46	CM	1743	A
46	CM	1747	G
46	CM	1749	A
46	CM	1753	A
46	CM	1756	U
46	CM	1767	G
46	CM	1770	C
46	CM	1779	G
46	CM	1780	G
46	CM	1781	A
46	CM	1782	U
46	CM	1783	C

All (199) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	172	C
1	1	403	C
1	1	538	G
1	1	563	U
1	1	601	U
1	1	759	G
1	1	912	G
1	1	1011	C
1	1	1012	U
1	1	1029	U
1	1	1060	A
1	1	1099	A
1	1	1273	C
1	1	1274	A
1	1	1346	U

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Mol	Chain	Res	Type
1	1	1347	U
1	1	1559	C
1	1	1561	U
1	1	1762	G
1	1	1815	U
1	1	1943	G
1	1	2090	U
1	1	2182	C
1	1	2183	U
1	1	2441	G
1	1	2442	U
1	1	2447	G
1	1	2455	G
1	1	2465	U
1	1	2515	G
1	1	2519	A
1	1	2545	C
1	1	2663	A
1	1	2789	A
1	1	3093	U
1	1	3164	U
1	1	3165	U
1	1	3193	C
1	1	3234	U
1	1	3240	U
1	1	3284	U
1	1	3309	A
1	1	3317	U
3	4	85	G
3	4	125	U
3	4	156	U
46	B	25	C
46	B	78	A
46	B	133	U
46	B	137	A
46	B	151	G
46	B	176	U
46	B	215	A
46	B	216	A
46	B	259	U
46	B	265	U
46	B	278	U

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Mol	Chain	Res	Type
46	B	415	A
46	B	451	C
46	B	505	U
46	B	514	G
46	B	518	A
46	B	529	C
46	B	533	A
46	B	553	A
46	B	556	U
46	B	638	U
46	B	695	C
46	B	711	U
46	B	740	A
46	B	763	C
46	B	769	U
46	B	814	A
46	B	855	C
46	B	874	U
46	B	876	A
46	B	1168	A
46	B	1335	U
46	B	1369	G
46	B	1396	A
46	B	1398	G
46	B	1457	A
46	B	1467	C
46	B	1479	A
46	B	1484	U
46	B	1523	G
46	B	1573	A
46	B	1579	A
46	B	1581	G
46	B	1677	G
46	B	1703	C
1	AS	172	C
1	AS	403	C
1	AS	447	U
1	AS	452	A
1	AS	453	U
1	AS	487	C
1	AS	538	G
1	AS	563	U

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Mol	Chain	Res	Type
1	AS	601	U
1	AS	759	G
1	AS	912	G
1	AS	1029	U
1	AS	1060	A
1	AS	1099	A
1	AS	1238	G
1	AS	1245	G
1	AS	1346	U
1	AS	1347	U
1	AS	1559	C
1	AS	1762	G
1	AS	1815	U
1	AS	1943	G
1	AS	2090	U
1	AS	2182	C
1	AS	2183	U
1	AS	2430	G
1	AS	2431	U
1	AS	2438	U
1	AS	2442	U
1	AS	2448	C
1	AS	2449	U
1	AS	2450	U
1	AS	2455	G
1	AS	2458	G
1	AS	2464	A
1	AS	2465	U
1	AS	2468	C
1	AS	2480	A
1	AS	2515	G
1	AS	2519	A
1	AS	2545	C
1	AS	2789	A
1	AS	2790	U
1	AS	3093	U
1	AS	3159	A
1	AS	3160	C
1	AS	3193	C
1	AS	3234	U
1	AS	3240	U
1	AS	3284	U

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Mol	Chain	Res	Type
1	AS	3309	A
1	AS	3315	C
1	AS	3317	U
3	AU	85	G
3	AU	125	U
3	AU	156	U
46	CM	25	C
46	CM	78	A
46	CM	133	U
46	CM	137	A
46	CM	151	G
46	CM	176	U
46	CM	214	U
46	CM	216	A
46	CM	237	C
46	CM	238	U
46	CM	259	U
46	CM	265	U
46	CM	278	U
46	CM	415	A
46	CM	451	C
46	CM	504	A
46	CM	505	U
46	CM	514	G
46	CM	518	A
46	CM	529	C
46	CM	533	A
46	CM	553	A
46	CM	556	U
46	CM	638	U
46	CM	680	C
46	CM	681	C
46	CM	690	C
46	CM	695	C
46	CM	702	G
46	CM	711	U
46	CM	740	A
46	CM	763	C
46	CM	769	U
46	CM	814	A
46	CM	817	U
46	CM	855	C

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Mol	Chain	Res	Type
46	CM	874	U
46	CM	876	A
46	CM	1168	A
46	CM	1335	U
46	CM	1359	U
46	CM	1369	G
46	CM	1396	A
46	CM	1398	G
46	CM	1457	A
46	CM	1467	C
46	CM	1479	A
46	CM	1523	G
46	CM	1555	C
46	CM	1573	A
46	CM	1579	A
46	CM	1581	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1452 ligands modelled in this entry, 1448 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
84	3K5	1	3403	-	63,63,63	2.84	29 (46%)	84,95,95	1.63	15 (17%)
85	TIX	AS	3782	-	30,31,31	3.69	15 (50%)	35,54,54	2.98	18 (51%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
84	3K5	AS	3401	-	63,63,63	0.36	0	84,95,95	0.82	4 (4%)
85	TIX	1	3958	-	30,31,31	3.29	15 (50%)	35,54,54	2.97	18 (51%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	3K5	1	3403	-	-	10/29/121/121	0/7/7/7
85	TIX	AS	3782	-	-	-	0/6/5/5
84	3K5	AS	3401	-	-	5/29/121/121	0/7/7/7
85	TIX	1	3958	-	-	-	0/6/5/5

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	AS	3782	TIX	C15-C08	10.23	1.66	1.54
84	1	3403	3K5	C17-C22	-8.14	1.36	1.53
85	AS	3782	TIX	C08-C12	8.14	1.65	1.53
85	1	3958	TIX	C15-C08	7.88	1.63	1.54
85	1	3958	TIX	C08-C12	7.40	1.63	1.53
84	1	3403	3K5	O4-C22	7.28	1.59	1.43
85	AS	3782	TIX	C10-C18	7.04	1.63	1.55
85	1	3958	TIX	C25-C22	-6.34	1.36	1.53
85	AS	3782	TIX	C25-C22	-6.17	1.36	1.53
84	1	3403	3K5	C21-C22	5.96	1.63	1.52
85	1	3958	TIX	C10-C18	5.95	1.62	1.55
85	1	3958	TIX	O01-C11	-5.77	1.35	1.44
85	AS	3782	TIX	O01-C11	-5.64	1.35	1.44
84	1	3403	3K5	O6-C23	5.20	1.46	1.34
84	1	3403	3K5	O12-C36	4.59	1.55	1.44
84	1	3403	3K5	O1-C6	4.59	1.44	1.34
84	1	3403	3K5	C20-C23	4.35	1.62	1.51
84	1	3403	3K5	C37-C36	-4.21	1.41	1.51
85	AS	3782	TIX	C11-C17	4.13	1.58	1.52
84	1	3403	3K5	O7-C28	3.95	1.53	1.44
84	1	3403	3K5	C29-C28	-3.95	1.42	1.51
84	1	3403	3K5	O-C2	3.95	1.49	1.43
85	AS	3782	TIX	C17-C19	3.95	1.57	1.52
84	1	3403	3K5	C18-C17	3.80	1.60	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	1	3403	3K5	O4-C3	-3.77	1.33	1.42
84	1	3403	3K5	C7-C6	3.68	1.56	1.48
85	AS	3782	TIX	O07-C24	3.61	1.27	1.21
84	1	3403	3K5	O9-C30	3.48	1.42	1.35
85	1	3958	TIX	C25-C24	-3.44	1.44	1.50
85	1	3958	TIX	O07-C24	3.43	1.27	1.21
84	1	3403	3K5	O9-C26	3.36	1.49	1.44
84	1	3403	3K5	O14-C38	3.36	1.42	1.35
85	AS	3782	TIX	C26-C19	3.22	1.37	1.32
84	1	3403	3K5	C26-C25	-3.20	1.45	1.52
85	1	3958	TIX	C26-C19	3.19	1.37	1.32
85	1	3958	TIX	O02-C12	-2.99	1.42	1.46
84	1	3403	3K5	C21-C20	-2.99	1.47	1.53
84	1	3403	3K5	C9-C8	2.96	1.55	1.47
85	1	3958	TIX	C17-C19	2.94	1.55	1.52
85	AS	3782	TIX	C16-C12	2.93	1.58	1.52
85	AS	3782	TIX	C10-C09	2.93	1.63	1.57
85	1	3958	TIX	C16-C12	2.92	1.58	1.52
85	AS	3782	TIX	C13-C19	2.86	1.56	1.51
85	AS	3782	TIX	C20-C13	2.83	1.57	1.53
84	1	3403	3K5	O14-C34	2.75	1.48	1.44
84	1	3403	3K5	C4-C3	2.70	1.57	1.52
85	1	3958	TIX	C11-C17	2.69	1.56	1.52
85	AS	3782	TIX	O02-C12	-2.60	1.43	1.46
84	1	3403	3K5	C15-C3	2.56	1.61	1.52
85	1	3958	TIX	C20-C13	2.48	1.57	1.53
84	1	3403	3K5	O-C3	2.40	1.45	1.42
84	1	3403	3K5	C1-C5	-2.39	1.47	1.52
85	AS	3782	TIX	C08-C13	2.15	1.58	1.55
84	1	3403	3K5	C27-C28	2.13	1.57	1.52
84	1	3403	3K5	O12-C32	2.10	1.47	1.41
85	1	3958	TIX	C10-C09	2.10	1.61	1.57
85	1	3958	TIX	C13-C19	2.08	1.55	1.51
84	1	3403	3K5	O11-C25	2.03	1.49	1.43
84	1	3403	3K5	C35-C36	2.01	1.57	1.52

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	AS	3782	TIX	C15-C08-C12	7.63	125.77	112.86
85	1	3958	TIX	C15-C08-C12	6.61	124.05	112.86
85	AS	3782	TIX	C27-C22-C25	5.79	118.95	110.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	1	3958	TIX	O05-C18-C10	-5.65	104.67	112.28
85	AS	3782	TIX	C16-C14-C10	-5.48	105.90	112.18
84	1	3403	3K5	O-C3-C4	5.35	115.90	110.75
84	1	3403	3K5	O14-C38-C39	5.26	120.47	111.09
85	1	3958	TIX	O02-C23-O06	-5.17	112.09	117.86
85	AS	3782	TIX	O05-C18-C10	-5.12	105.39	112.28
85	1	3958	TIX	C27-C22-C25	4.96	117.78	110.75
85	1	3958	TIX	C16-C14-C10	-4.96	106.50	112.18
85	1	3958	TIX	C27-C22-C14	4.85	121.60	112.14
84	1	3403	3K5	O9-C30-C31	4.58	119.25	111.09
85	AS	3782	TIX	O02-C23-O06	-4.50	112.84	117.86
85	1	3958	TIX	C17-C19-C26	-4.49	118.10	123.03
85	AS	3782	TIX	C27-C22-C14	4.48	120.90	112.14
85	1	3958	TIX	C13-C19-C17	4.48	121.13	114.47
85	AS	3782	TIX	C17-C19-C26	-4.25	118.35	123.03
85	AS	3782	TIX	O07-C24-C18	-4.24	115.73	120.58
85	AS	3782	TIX	C13-C19-C17	4.18	120.69	114.47
84	1	3403	3K5	O1-C6-C7	3.79	119.62	111.39
85	1	3958	TIX	O07-C24-C18	-3.78	116.26	120.58
84	1	3403	3K5	C32-O11-C25	-3.45	109.79	117.98
85	1	3958	TIX	O02-C23-C20	3.24	125.43	118.97
84	1	3403	3K5	O6-C23-C20	3.12	117.58	111.79
85	1	3958	TIX	C20-C13-C19	-2.96	111.22	114.41
85	AS	3782	TIX	O02-C23-C20	2.93	124.80	118.97
84	AS	3401	3K5	C4-C3-C15	-2.92	109.37	114.34
85	1	3958	TIX	O05-C18-C24	-2.88	105.92	111.75
85	AS	3782	TIX	C25-C24-C18	2.88	122.92	115.19
85	1	3958	TIX	C25-C22-C14	2.86	117.68	110.85
84	AS	3401	3K5	O14-C34-C35	2.76	114.10	107.76
85	1	3958	TIX	C25-C24-C18	2.70	122.43	115.19
84	1	3403	3K5	C3-C4-C5	2.66	117.03	112.29
84	1	3403	3K5	O4-C22-C21	2.66	118.46	111.53
84	1	3403	3K5	C9-C8-C7	-2.64	121.15	126.92
84	1	3403	3K5	O1-C5-C4	2.63	114.25	108.43
84	1	3403	3K5	C26-C27-C28	2.52	115.58	110.12
85	AS	3782	TIX	C25-C22-C14	2.50	116.83	110.85
85	1	3958	TIX	O02-C12-C08	2.46	114.90	109.30
84	1	3403	3K5	C4-C3-C15	-2.42	110.22	114.34
84	AS	3401	3K5	C34-O14-C38	2.38	121.41	117.72
85	AS	3782	TIX	C15-O01-C11	-2.37	106.00	108.78
85	AS	3782	TIX	C20-C13-C19	-2.25	111.98	114.41
85	1	3958	TIX	O01-C15-C08	2.25	108.43	105.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	AS	3782	TIX	O02-C12-C08	2.25	114.42	109.30
84	1	3403	3K5	C5-O1-C6	2.22	120.77	117.50
84	1	3403	3K5	C34-O14-C38	-2.19	114.31	117.72
85	1	3958	TIX	C15-O01-C11	-2.19	106.22	108.78
84	1	3403	3K5	C-C1-C5	-2.18	108.97	112.62
85	AS	3782	TIX	C22-C25-C24	2.16	119.73	113.98
85	1	3958	TIX	C22-C25-C24	2.13	119.64	113.98
84	AS	3401	3K5	C20-C21-C22	-2.13	107.41	111.93
85	AS	3782	TIX	O01-C15-C08	2.09	108.24	105.72
85	AS	3782	TIX	O05-C18-C24	-2.07	107.57	111.75

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	1	3403	3K5	C4-C5-O1-C6
84	1	3403	3K5	C7-C6-O1-C5
84	1	3403	3K5	C39-C38-O14-C34
84	1	3403	3K5	O7-C24-O6-C23
84	AS	3401	3K5	C39-C38-O14-C34
84	AS	3401	3K5	C35-C34-O14-C38
84	1	3403	3K5	O15-C38-O14-C34
84	1	3403	3K5	C31-C30-O9-C26
84	AS	3401	3K5	O15-C38-O14-C34
84	1	3403	3K5	O10-C30-O9-C26
84	AS	3401	3K5	C31-C30-O9-C26
84	1	3403	3K5	O2-C6-O1-C5
84	AS	3401	3K5	O10-C30-O9-C26
84	1	3403	3K5	C20-C23-O6-C24
84	1	3403	3K5	O5-C23-O6-C24

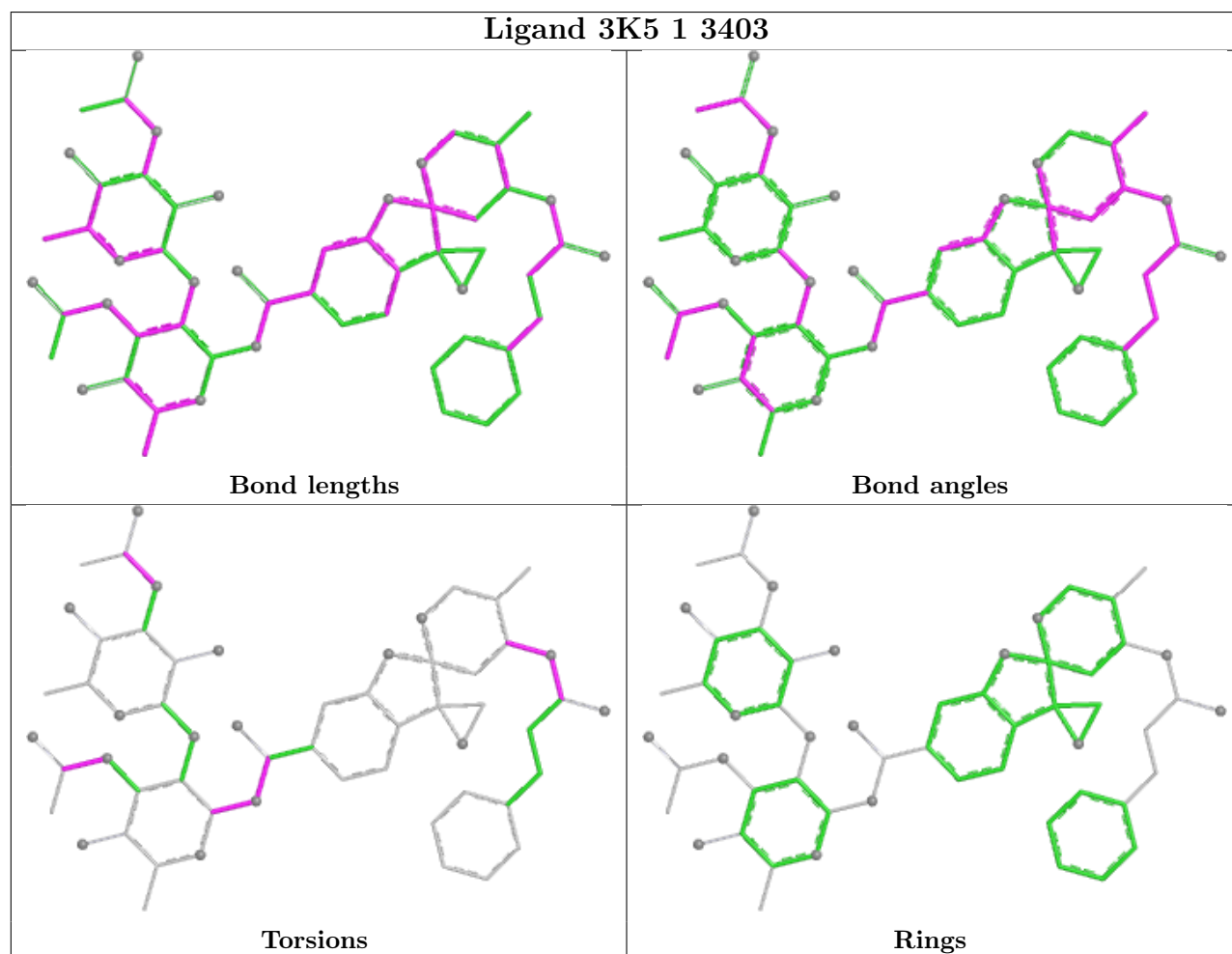
There are no ring outliers.

4 monomers are involved in 8 short contacts:

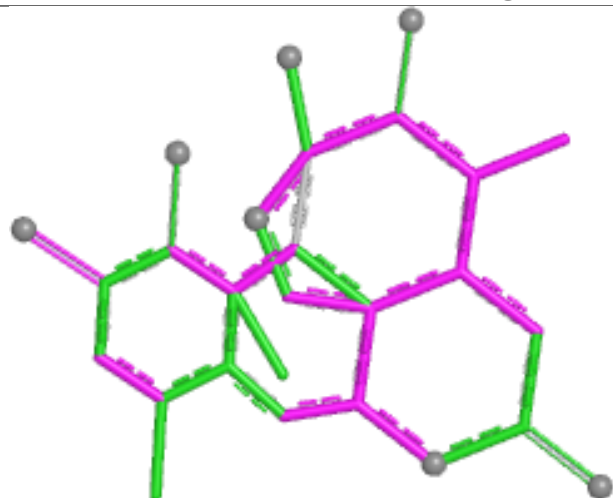
Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	1	3403	3K5	4	0
85	AS	3782	TIX	1	0
84	AS	3401	3K5	1	0
85	1	3958	TIX	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

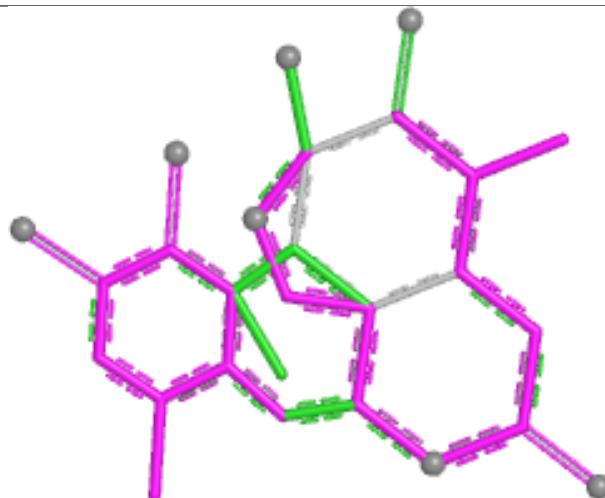
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



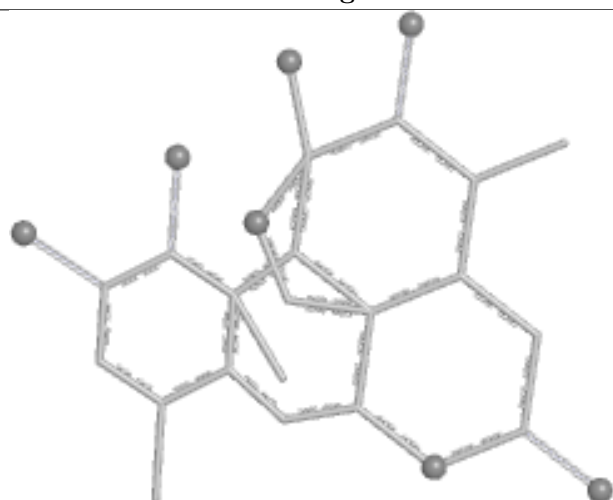
Ligand TIX AS 3782



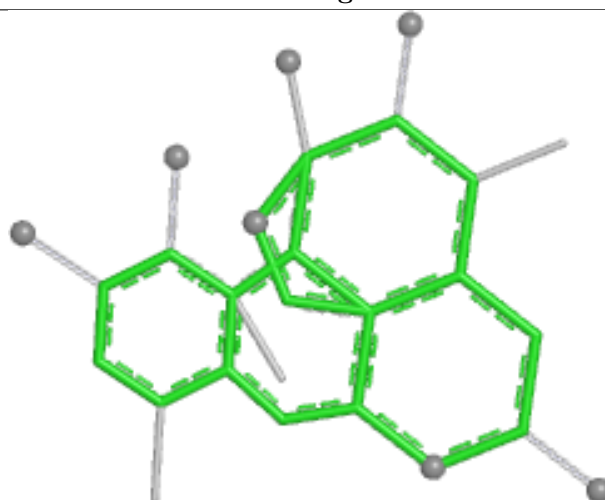
Bond lengths



Bond angles

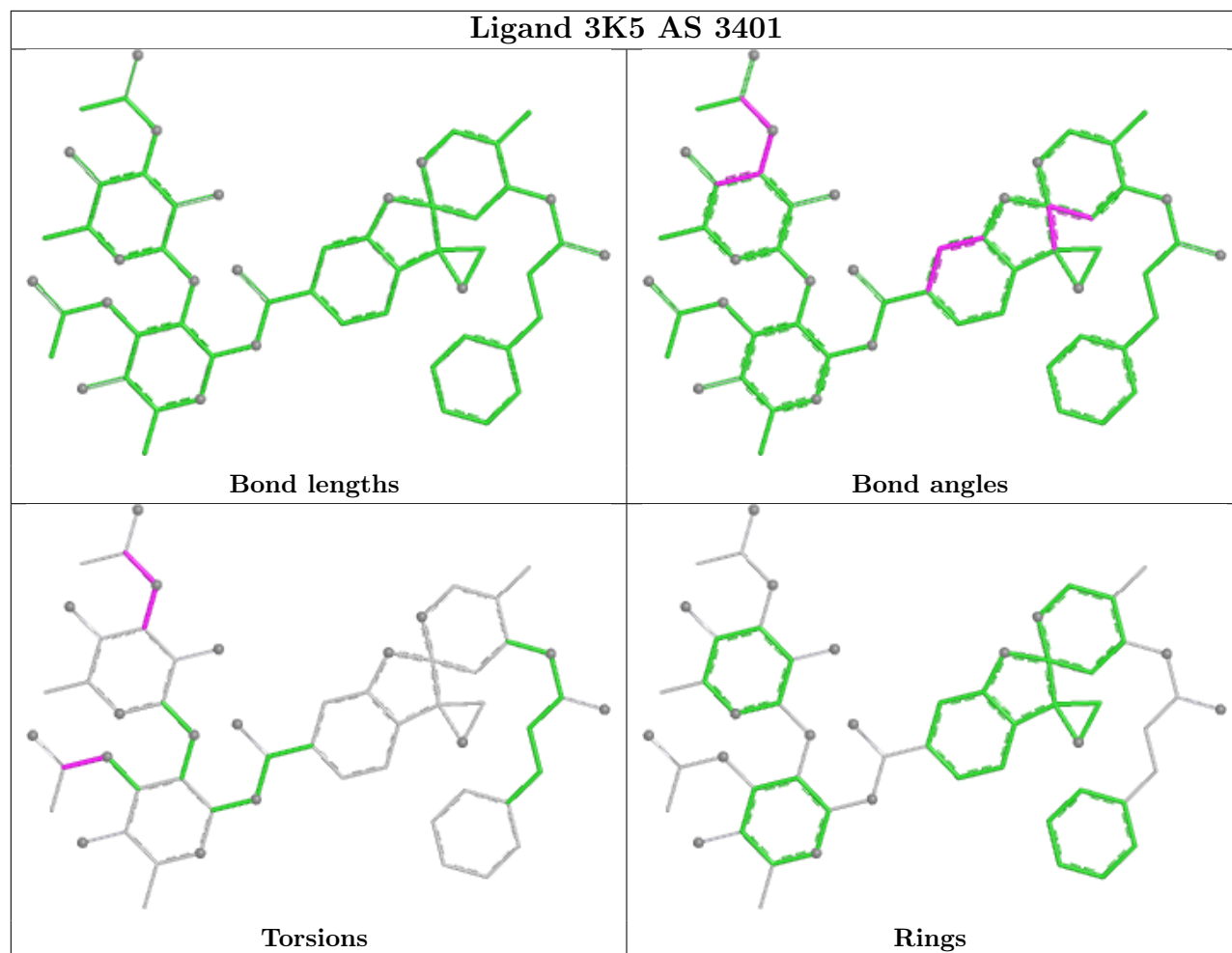


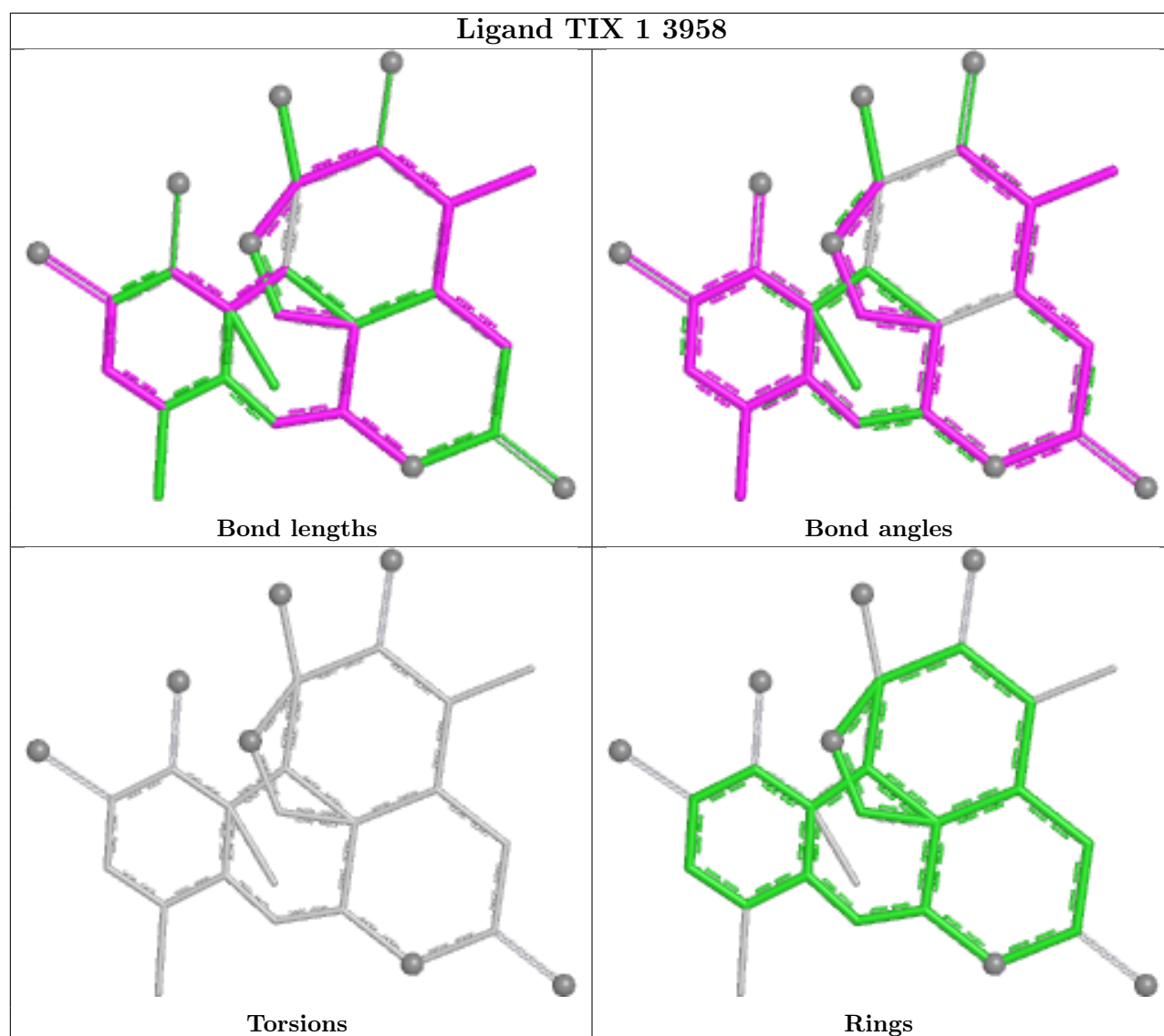
Torsions



Rings

Ligand 3K5 AS 3401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1	3217/3359 (95%)	0.91	384 (11%) 9 5	32, 63, 177, 378	0
1	AS	3229/3359 (96%)	1.07	513 (15%) 5 3	35, 70, 206, 323	0
2	3	121/121 (100%)	0.64	2 (1%) 69 45	41, 76, 96, 129	0
2	AT	121/121 (100%)	0.71	7 (5%) 29 15	37, 71, 94, 142	0
3	4	157/158 (99%)	0.43	8 (5%) 33 17	48, 66, 113, 171	0
3	AU	158/158 (100%)	0.89	16 (10%) 12 7	55, 92, 141, 221	0
4	AW	249/254 (98%)	1.55	59 (23%) 2 1	41, 74, 99, 109	1 (0%)
4	j	249/254 (98%)	1.12	34 (13%) 6 4	27, 53, 77, 105	1 (0%)
5	AX	386/389 (99%)	0.99	47 (12%) 8 5	34, 58, 89, 152	0
5	k	386/389 (99%)	1.15	71 (18%) 3 2	34, 58, 78, 128	1 (0%)
6	AY	361/363 (99%)	2.17	137 (37%) 1 1	47, 75, 106, 143	0
6	l	361/363 (99%)	1.35	73 (20%) 3 2	37, 70, 104, 140	0
7	AZ	292/298 (97%)	2.12	139 (47%) 0 0	47, 93, 127, 143	0
7	m	296/298 (99%)	2.12	138 (46%) 0 0	48, 87, 119, 145	0
8	BA	153/176 (86%)	1.35	38 (24%) 2 1	47, 70, 103, 132	0
8	n	157/176 (89%)	1.56	37 (23%) 2 1	57, 77, 110, 146	0
9	BB	234/241 (97%)	1.18	44 (18%) 3 2	35, 58, 106, 166	0
9	o	234/241 (97%)	1.26	42 (17%) 3 2	35, 64, 126, 166	0
10	BC	233/262 (88%)	1.91	89 (38%) 1 1	86, 123, 162, 183	0
10	p	238/262 (90%)	1.62	69 (28%) 1 1	55, 79, 131, 167	0
11	BD	190/191 (99%)	1.56	58 (30%) 1 1	56, 75, 105, 150	0
11	q	190/191 (99%)	1.30	39 (20%) 2 2	54, 75, 97, 138	0
12	BE	208/220 (94%)	1.20	28 (13%) 7 4	34, 53, 100, 140	0
12	r	208/220 (94%)	1.27	35 (16%) 4 3	37, 61, 102, 115	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	BF	171/174 (98%)	1.61	48 (28%)	1	1	58, 83, 115, 131	0
13	s	171/174 (98%)	1.65	50 (29%)	1	1	58, 90, 113, 125	0
14	BG	200/202 (99%)	1.46	47 (23%)	2	1	49, 96, 130, 153	0
14	t	200/202 (99%)	1.50	52 (26%)	1	1	43, 76, 114, 142	0
15	BH	130/131 (99%)	1.15	22 (16%)	4	3	47, 68, 95, 124	0
15	u	130/131 (99%)	1.07	17 (13%)	7	4	53, 72, 89, 110	0
16	BI	203/204 (99%)	2.03	98 (48%)	0	0	57, 87, 109, 116	0
16	v	203/204 (99%)	1.39	40 (19%)	3	2	35, 57, 73, 83	0
17	BJ	199/200 (99%)	1.09	35 (17%)	4	3	35, 51, 89, 125	0
17	w	199/200 (99%)	1.02	21 (10%)	11	6	36, 55, 85, 113	0
18	BK	176/185 (95%)	1.57	45 (25%)	1	1	45, 65, 95, 130	0
18	x	173/185 (93%)	1.46	44 (25%)	1	1	41, 62, 96, 125	0
19	BL	185/186 (99%)	1.53	44 (23%)	2	1	47, 71, 88, 99	0
19	y	185/186 (99%)	1.54	51 (27%)	1	1	46, 66, 85, 99	0
20	BM	179/190 (94%)	1.38	37 (20%)	2	2	54, 82, 142, 169	0
20	z	179/190 (94%)	1.74	58 (32%)	1	1	52, 71, 127, 143	0
21	0	170/172 (98%)	1.14	27 (15%)	5	3	44, 63, 87, 138	0
21	BN	170/172 (98%)	0.99	21 (12%)	8	5	40, 59, 83, 113	0
22	2	159/160 (99%)	1.34	38 (23%)	2	1	43, 60, 116, 152	0
22	BO	159/160 (99%)	1.69	52 (32%)	1	1	44, 61, 116, 145	0
23	5	103/124 (83%)	1.77	35 (33%)	1	1	84, 111, 142, 162	0
23	BP	102/124 (82%)	1.86	32 (31%)	1	1	92, 128, 149, 165	2 (1%)
24	6	131/137 (95%)	1.11	18 (13%)	6	4	38, 56, 78, 90	0
24	BQ	131/137 (95%)	1.14	24 (18%)	3	2	34, 54, 77, 98	0
25	7	118/155 (76%)	1.19	18 (15%)	5	3	38, 77, 126, 140	0
25	BR	98/155 (63%)	1.52	25 (25%)	1	1	42, 65, 130, 139	0
26	8	121/142 (85%)	1.25	21 (17%)	4	3	60, 73, 91, 127	0
26	BS	119/142 (83%)	1.52	32 (26%)	1	1	65, 98, 115, 129	0
27	9	126/127 (99%)	1.44	30 (23%)	2	1	58, 78, 99, 117	0
27	BT	126/127 (99%)	1.44	33 (26%)	1	1	65, 93, 131, 147	0
28	AA	135/136 (99%)	1.74	41 (30%)	1	1	64, 88, 109, 143	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
28	BU	135/136 (99%)	1.81	50 (37%)	1	1	93, 120, 141, 167	0
29	AB	148/149 (99%)	1.25	28 (18%)	3	2	37, 62, 87, 126	0
29	BV	148/149 (99%)	1.49	33 (22%)	2	1	47, 74, 100, 114	0
30	AC	62/63 (98%)	1.97	22 (35%)	1	1	42, 75, 123, 147	0
30	BW	61/63 (96%)	2.73	32 (52%)	0	0	46, 81, 120, 140	0
31	AD	96/106 (90%)	1.08	10 (10%)	11	6	57, 76, 100, 111	0
31	BX	96/106 (90%)	1.55	26 (27%)	1	1	86, 109, 132, 149	0
32	AE	110/112 (98%)	1.31	27 (24%)	2	1	48, 67, 110, 148	0
32	BY	110/112 (98%)	1.31	21 (19%)	3	2	47, 75, 121, 151	0
33	AF	124/131 (94%)	1.62	36 (29%)	1	1	35, 66, 83, 106	0
33	BZ	124/131 (94%)	1.58	37 (29%)	1	1	34, 63, 90, 112	0
34	AG	106/107 (99%)	1.35	25 (23%)	2	1	47, 60, 76, 93	0
34	CA	106/107 (99%)	1.01	14 (13%)	7	4	40, 54, 74, 87	0
35	AH	112/122 (91%)	2.08	39 (34%)	1	1	52, 70, 118, 140	0
35	CB	112/122 (91%)	2.68	49 (43%)	0	1	62, 98, 137, 159	0
36	AI	120/120 (100%)	1.31	20 (16%)	4	3	58, 82, 109, 124	1 (0%)
36	CC	118/120 (98%)	1.87	41 (34%)	1	1	81, 104, 126, 132	1 (0%)
37	AJ	97/99 (97%)	1.16	13 (13%)	7	4	54, 72, 100, 168	0
37	CD	97/99 (97%)	1.58	23 (23%)	2	1	83, 99, 128, 152	0
38	AK	86/87 (98%)	1.19	15 (17%)	4	3	41, 55, 95, 111	0
38	CE	86/87 (98%)	1.55	23 (26%)	1	1	47, 74, 115, 128	0
39	AL	77/78 (98%)	1.53	16 (20%)	2	2	77, 98, 133, 165	0
39	CF	77/78 (98%)	2.45	37 (48%)	0	0	90, 118, 156, 165	0
40	AM	50/51 (98%)	1.04	3 (6%)	27	14	47, 64, 83, 92	0
40	CG	50/51 (98%)	2.30	21 (42%)	0	1	58, 79, 94, 103	1 (2%)
41	AN	52/52 (100%)	2.60	29 (55%)	0	0	75, 101, 116, 132	0
41	CH	51/52 (98%)	2.65	33 (64%)	0	0	73, 105, 122, 126	0
42	AO	25/25 (100%)	1.55	9 (36%)	1	1	55, 67, 76, 85	0
42	CI	24/25 (96%)	1.11	4 (16%)	4	3	48, 60, 68, 73	0
43	AP	103/106 (97%)	1.48	27 (26%)	1	1	31, 61, 98, 121	0
43	CJ	103/106 (97%)	1.72	26 (25%)	1	1	40, 73, 115, 122	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
44	AQ	91/92 (98%)	1.43	21 (23%)	2	1	40, 58, 101, 116	0
44	CK	91/92 (98%)	1.85	24 (26%)	1	1	48, 78, 110, 121	0
45	CL	121/267 (45%)	2.17	56 (46%)	0	0	59, 92, 127, 139	0
45	i	121/267 (45%)	1.93	48 (39%)	1	1	63, 106, 136, 143	0
46	B	1761/1787 (98%)	1.36	401 (22%)	2	1	46, 87, 178, 458	0
46	CM	1765/1787 (98%)	1.12	263 (14%)	5	3	40, 79, 182, 465	0
47	C	208/261 (79%)	2.03	86 (41%)	0	1	80, 114, 140, 154	0
47	CN	208/261 (79%)	1.81	71 (34%)	1	1	62, 101, 130, 165	0
48	CO	214/256 (83%)	2.07	84 (39%)	1	1	76, 118, 139, 166	0
48	D	214/256 (83%)	1.78	65 (30%)	1	1	67, 92, 115, 127	0
49	CP	217/249 (87%)	1.46	46 (21%)	2	1	46, 71, 98, 118	0
49	E	217/249 (87%)	1.96	86 (39%)	1	1	71, 95, 121, 144	0
50	CQ	223/251 (88%)	1.54	64 (28%)	1	1	53, 77, 136, 169	0
50	F	223/251 (88%)	2.22	102 (45%)	0	0	73, 106, 152, 173	0
51	CR	260/262 (99%)	1.95	100 (38%)	1	1	62, 87, 111, 146	0
51	G	259/262 (98%)	2.17	119 (45%)	0	0	68, 96, 119, 143	0
52	CS	206/225 (91%)	2.48	108 (52%)	0	0	68, 101, 146, 194	0
52	H	206/225 (91%)	2.28	105 (50%)	0	0	76, 102, 142, 162	0
53	CT	236/236 (100%)	2.05	100 (42%)	0	1	52, 98, 139, 158	0
53	I	226/236 (95%)	1.73	66 (29%)	1	1	60, 98, 147, 179	0
54	CU	183/186 (98%)	2.29	92 (50%)	0	0	68, 127, 165, 179	0
54	J	185/186 (99%)	2.34	99 (53%)	0	0	80, 129, 156, 164	0
55	CV	203/206 (98%)	1.84	70 (34%)	1	1	41, 71, 122, 150	0
55	K	203/206 (98%)	1.96	80 (39%)	1	1	37, 80, 124, 156	0
56	CW	178/189 (94%)	1.87	65 (36%)	1	1	65, 94, 119, 140	0
56	L	178/189 (94%)	2.53	104 (58%)	0	0	74, 108, 126, 147	0
57	CX	94/118 (79%)	1.50	24 (25%)	1	1	54, 86, 128, 142	0
57	M	98/118 (83%)	2.09	46 (46%)	0	0	83, 117, 143, 161	0
58	CY	141/155 (90%)	1.18	25 (17%)	4	2	45, 67, 93, 145	0
58	N	144/155 (92%)	1.67	46 (31%)	1	1	45, 78, 114, 156	0
59	CZ	119/143 (83%)	2.47	68 (57%)	0	0	130, 159, 176, 180	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
59	O	116/143 (81%)	2.96	75 (64%)	0	0	151, 178, 195, 200	0
60	DA	150/151 (99%)	1.84	50 (33%)	1	1	58, 92, 121, 136	0
60	P	150/151 (99%)	1.89	57 (38%)	1	1	55, 92, 112, 120	0
61	DB	127/132 (96%)	2.00	55 (43%)	0	1	55, 99, 125, 132	0
61	Q	127/132 (96%)	1.69	43 (33%)	1	1	51, 79, 98, 111	0
62	DC	130/142 (91%)	1.74	48 (36%)	1	1	58, 91, 128, 145	0
62	R	129/142 (90%)	2.13	52 (40%)	0	1	63, 98, 136, 151	0
63	DD	140/142 (98%)	2.15	67 (47%)	0	0	61, 98, 133, 145	0
63	S	140/142 (98%)	2.94	90 (64%)	0	0	70, 110, 145, 155	0
64	DE	124/137 (90%)	2.03	50 (40%)	0	1	62, 112, 160, 169	0
64	T	124/137 (90%)	2.46	74 (59%)	0	0	87, 122, 167, 171	0
65	DF	141/145 (97%)	2.00	56 (39%)	1	1	59, 93, 124, 154	0
65	U	144/145 (99%)	2.02	59 (40%)	0	1	60, 86, 114, 150	0
66	DG	141/145 (97%)	1.84	53 (37%)	1	1	58, 93, 117, 153	0
66	V	141/145 (97%)	2.33	68 (48%)	0	0	79, 101, 135, 147	0
67	DH	97/119 (81%)	1.85	40 (41%)	0	1	46, 96, 125, 144	0
67	W	102/119 (85%)	2.37	64 (62%)	0	0	72, 122, 147, 157	0
68	DI	87/87 (100%)	1.43	20 (22%)	2	1	61, 86, 120, 144	0
68	X	87/87 (100%)	1.76	34 (39%)	1	1	83, 102, 123, 127	0
69	DJ	129/130 (99%)	1.54	35 (27%)	1	1	49, 67, 87, 93	0
69	Y	129/130 (99%)	1.91	46 (35%)	1	1	67, 84, 103, 121	0
70	DK	143/145 (98%)	0.96	19 (13%)	7	4	43, 64, 88, 113	0
70	Z	143/145 (98%)	1.59	37 (25%)	1	1	52, 73, 92, 106	0
71	DL	132/135 (97%)	1.98	57 (43%)	0	1	77, 112, 132, 174	0
71	a	134/135 (99%)	2.47	68 (50%)	0	0	74, 113, 126, 156	0
72	DM	71/105 (67%)	1.97	31 (43%)	0	1	93, 124, 143, 149	0
72	b	72/105 (68%)	2.00	33 (45%)	0	0	87, 109, 132, 143	0
73	DN	98/119 (82%)	2.21	44 (44%)	0	1	56, 77, 136, 143	0
73	c	98/119 (82%)	2.22	42 (42%)	0	1	60, 83, 128, 139	0
74	DO	81/82 (98%)	2.18	38 (46%)	0	0	71, 105, 166, 173	0
74	d	81/82 (98%)	2.13	41 (50%)	0	0	80, 101, 155, 169	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
75	DP	61/67 (91%)	2.26	28 (45%)	0	0	78, 108, 132, 152	0
75	e	62/67 (92%)	2.26	29 (46%)	0	0	90, 110, 134, 143	0
76	DQ	54/56 (96%)	1.56	18 (33%)	1	1	49, 67, 89, 109	0
76	f	55/56 (98%)	1.98	24 (43%)	0	1	71, 89, 114, 136	0
77	DR	58/63 (92%)	1.71	17 (29%)	1	1	69, 99, 156, 178	0
77	g	60/63 (95%)	2.36	31 (51%)	0	0	76, 105, 151, 167	0
78	DS	70/193 (36%)	3.05	46 (65%)	0	0	92, 164, 183, 195	0
78	h	70/193 (36%)	2.46	36 (51%)	0	0	117, 163, 189, 191	0
79	AR	311/317 (98%)	2.56	179 (57%)	0	0	118, 156, 178, 192	0
79	DT	311/317 (98%)	2.52	192 (61%)	0	0	107, 150, 175, 192	0
80	P0	107/312 (34%)	2.47	56 (52%)	0	0	113, 127, 146, 154	0
80	p0	107/312 (34%)	3.26	77 (71%)	0	0	116, 139, 156, 164	0
81	12	63/165 (38%)	1.88	22 (34%)	1	1	111, 130, 149, 158	0
82	L1	217/217 (100%)	1.78	80 (36%)	1	1	99, 128, 165, 231	0
82	l1	217/217 (100%)	2.08	98 (45%)	0	0	110, 137, 163, 196	0
All	All	33669/36343 (92%)	1.54	9265 (27%)	1	1	27, 81, 155, 465	8 (0%)

All (9265) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
80	p0	28	VAL	19.3
60	P	7	SER	16.6
63	S	31	ASN	14.7
6	AY	66	TRP	14.5
12	BE	102	MET	13.9
49	CP	86	ARG	13.1
66	V	69	LYS	13.1
65	DF	120	ARG	12.9
79	AR	208	CYS	12.7
7	AZ	82	GLU	12.5
80	P0	26	PHE	12.4
1	1	2453	G	12.3
35	CB	8	ARG	12.0
79	AR	105	VAL	11.9
80	p0	27	VAL	11.8
1	1	2454	C	11.7
56	L	116	LEU	11.5

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Mol	Chain	Res	Type	RSRZ
47	CN	19	ALA	11.4
56	L	35	GLY	11.4
80	P0	85	GLY	11.3
4	AW	235	ALA	11.2
71	a	69	SER	11.0
59	O	89	ILE	11.0
78	DS	127	TYR	11.0
50	F	153	TYR	11.0
1	1	2157	C	10.9
1	AS	1489	G	10.9
1	1	2436	A	10.8
48	CO	156	ALA	10.7
49	E	86	ARG	10.5
56	L	138	LYS	10.5
63	S	67	LYS	10.4
3	AU	111	A	10.2
64	DE	91	LEU	10.2
1	AS	2943	A	10.0
50	F	122	GLY	10.0
14	BG	2	ALA	9.9
46	CM	1698	U	9.8
51	G	39	ARG	9.8
55	K	20	GLN	9.8
50	F	151	GLN	9.6
52	H	70	VAL	9.6
63	S	65	ARG	9.6
41	AN	12	LYS	9.6
6	AY	65	SER	9.4
41	AN	16	GLU	9.3
35	CB	30	LEU	9.3
63	S	68	VAL	9.3
80	p0	29	GLY	9.3
59	O	48	ALA	9.2
1	AS	1487	A	9.1
6	AY	61	THR	9.1
45	CL	59	GLY	9.1
79	AR	106	GLY	9.1
79	DT	260	PHE	9.1
12	r	114	GLY	9.0
1	AS	356	C	9.0
59	CZ	48	ALA	9.0
79	AR	260	PHE	9.0

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Mol	Chain	Res	Type	RSRZ
1	AS	1488	G	8.9
79	DT	208	CYS	8.9
46	B	1339	G	8.9
78	h	171	GLY	8.9
30	BW	10	HIS	8.9
40	CG	12	LYS	8.9
40	CG	9	THR	8.9
51	G	110	ALA	8.8
54	J	179	PHE	8.8
7	m	150	LEU	8.8
44	CK	13	LYS	8.8
71	a	72	PHE	8.7
79	AR	201	LEU	8.7
8	n	169	ASP	8.7
80	p0	41	ILE	8.6
18	x	128	ARG	8.6
66	V	66	TYR	8.6
1	AS	601	U	8.6
38	CE	18	LEU	8.6
51	CR	56	LEU	8.5
35	CB	28	GLY	8.5
35	AH	33	GLN	8.5
6	AY	361	LEU	8.5
51	CR	9	LEU	8.5
52	H	72	HIS	8.5
35	CB	10	ARG	8.5
47	C	99	ALA	8.5
78	DS	145	LEU	8.5
35	CB	29	LYS	8.5
78	DS	128	THR	8.4
79	DT	210	SER	8.4
62	R	80	LEU	8.4
1	AS	1024	U	8.4
79	AR	138	ILE	8.4
78	DS	146	THR	8.3
44	CK	12	GLY	8.3
64	T	68	GLY	8.3
73	c	29	CYS	8.3
52	H	71	SER	8.2
51	CR	39	ARG	8.2
18	x	136	ILE	8.2
1	AS	132	U	8.1

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Mol	Chain	Res	Type	RSRZ
1	AS	2472	A	8.1
53	CT	96	SER	8.1
59	O	111	ASN	8.1
52	CS	86	GLN	8.1
52	CS	59	VAL	8.1
74	DO	30	SER	8.0
6	AY	64	GLU	8.0
46	B	715	G	8.0
22	BO	10	GLY	8.0
60	DA	62	GLN	8.0
48	D	156	ALA	8.0
47	CN	16	LEU	8.0
78	DS	171	GLY	8.0
53	I	114	VAL	8.0
66	V	18	TYR	8.0
22	BO	2	GLY	8.0
56	CW	12	TYR	7.9
43	CJ	51	GLY	7.9
50	F	154	ALA	7.9
1	AS	357	A	7.9
52	CS	82	PHE	7.9
54	J	87	VAL	7.9
79	DT	262	LEU	7.9
39	CF	57	ASN	7.8
1	AS	1584	A	7.8
33	AF	53	GLN	7.8
51	G	56	LEU	7.8
46	CM	1679	A	7.7
35	AH	61	GLN	7.7
54	CU	87	VAL	7.7
67	W	81	TYR	7.7
59	O	120	CYS	7.7
48	CO	102	GLY	7.7
63	S	50	PRO	7.7
45	i	116	GLU	7.7
15	u	131	ALA	7.6
45	CL	65	LYS	7.6
46	B	374	C	7.6
45	CL	75	PRO	7.6
69	Y	127	GLY	7.6
20	z	136	ARG	7.6
61	DB	85	LYS	7.6

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Mol	Chain	Res	Type	RSRZ
6	AY	73	ALA	7.6
1	AS	1829	G	7.5
46	B	1135	G	7.5
43	AP	40	LYS	7.5
49	E	115	GLU	7.5
71	a	68	LYS	7.5
59	CZ	72	ILE	7.5
65	U	54	LEU	7.5
35	AH	32	ALA	7.5
1	AS	545	G	7.5
18	BK	126	ARG	7.5
71	a	63	GLN	7.5
52	CS	53	VAL	7.5
39	CF	30	LYS	7.5
35	CB	20	ILE	7.4
46	CM	1680	A	7.4
55	CV	159	GLU	7.4
48	D	157	GLN	7.4
71	a	70	THR	7.4
7	AZ	59	ASP	7.4
14	t	2	ALA	7.4
40	CG	50	GLY	7.4
65	U	29	MET	7.4
1	1	2500	G	7.4
43	CJ	44	ASP	7.4
77	DR	34	ALA	7.4
51	G	49	ARG	7.3
45	CL	62	ALA	7.3
35	CB	3	GLN	7.3
5	k	5	LYS	7.3
75	DP	49	ARG	7.3
54	J	146	GLN	7.3
18	BK	128	ARG	7.3
59	O	59	LEU	7.3
53	I	135	PRO	7.3
7	AZ	151	GLN	7.3
6	AY	105	LYS	7.2
16	v	184	LYS	7.2
35	AH	21	LYS	7.2
12	BE	114	GLY	7.2
51	G	43	PRO	7.2
30	BW	14	ARG	7.2

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Mol	Chain	Res	Type	RSRZ
6	AY	80	GLY	7.2
30	AC	4	SER	7.2
73	DN	21	VAL	7.2
48	CO	155	TYR	7.2
46	B	1359	U	7.2
50	F	206	ALA	7.2
52	CS	60	ASP	7.2
30	BW	33	LYS	7.2
30	BW	11	ASN	7.1
63	S	66	VAL	7.1
73	c	20	PRO	7.1
7	AZ	80	ALA	7.1
10	BC	199	ALA	7.1
75	DP	53	ILE	7.1
4	AW	2	GLY	7.1
54	CU	55	ALA	7.1
52	CS	57	SER	7.1
79	AR	75	SER	7.1
69	DJ	127	GLY	7.1
1	AS	1021	A	7.1
78	DS	142	LEU	7.1
79	AR	262	LEU	7.1
20	z	133	LYS	7.0
59	O	119	SER	7.0
57	M	45	ALA	7.0
79	AR	122	GLN	7.0
48	CO	120	LEU	7.0
1	1	1610	C	7.0
60	DA	61	SER	7.0
6	AY	55	GLU	7.0
73	c	18	VAL	7.0
73	c	19	LYS	7.0
6	AY	67	GLY	7.0
80	p0	38	MET	7.0
54	J	141	GLY	6.9
79	DT	154	ALA	6.9
55	CV	20	GLN	6.9
52	CS	112	ARG	6.9
80	p0	84	VAL	6.9
31	BX	106	ILE	6.8
66	DG	92	LYS	6.8
50	F	119	ALA	6.8

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Mol	Chain	Res	Type	RSRZ
51	G	60	GLU	6.8
46	CM	659	U	6.8
52	CS	26	ALA	6.8
74	d	24	LEU	6.8
6	AY	87	GLY	6.8
6	AY	86	SER	6.8
10	BC	47	LEU	6.8
6	AY	186	LYS	6.8
51	G	47	PHE	6.8
80	P0	25	ILE	6.8
82	ll	69	GLY	6.8
54	CU	146	GLN	6.8
80	p0	85	GLY	6.8
73	c	90	THR	6.8
46	CM	1697	C	6.8
46	B	1348	U	6.7
71	a	23	PHE	6.7
6	AY	79	GLY	6.7
35	AH	19	LYS	6.7
35	CB	19	LYS	6.7
49	E	114	LYS	6.7
53	I	131	LYS	6.7
20	z	63	ALA	6.7
79	AR	137	THR	6.7
1	1	1590	A	6.7
78	DS	125	LYS	6.7
6	AY	91	PHE	6.6
62	R	116	LEU	6.6
79	AR	82	LEU	6.6
53	I	49	ILE	6.6
16	BI	146	ALA	6.6
73	DN	18	VAL	6.6
61	Q	88	THR	6.6
56	L	151	ASP	6.6
5	k	253	GLY	6.6
7	m	24	GLN	6.6
7	AZ	113	LEU	6.6
7	m	52	VAL	6.6
7	m	149	GLY	6.6
54	CU	88	PHE	6.6
35	CB	31	VAL	6.6
65	DF	114	GLU	6.6

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Mol	Chain	Res	Type	RSRZ
71	a	71	GLY	6.6
80	p0	74	GLU	6.6
8	n	165	LEU	6.5
30	BW	5	LYS	6.5
44	AQ	29	LEU	6.5
65	DF	117	LYS	6.5
71	DL	25	ILE	6.5
55	K	62	THR	6.5
56	L	172	VAL	6.5
79	AR	157	ILE	6.5
1	1	1789	C	6.5
49	E	118	SER	6.5
35	AH	35	VAL	6.5
18	BK	57	ALA	6.5
63	S	43	LEU	6.5
80	P0	86	PHE	6.5
51	G	78	THR	6.5
30	BW	23	LYS	6.5
63	S	32	GLY	6.5
46	CM	469	A	6.5
56	L	14	VAL	6.5
49	E	77	LYS	6.5
54	J	55	ALA	6.4
1	AS	2847	U	6.4
62	R	113	GLY	6.4
48	CO	100	PHE	6.4
50	F	155	ASP	6.4
51	G	45	VAL	6.4
1	1	732	U	6.4
80	p0	100	VAL	6.4
35	CB	34	HIS	6.4
45	i	115	LEU	6.4
46	CM	1678	G	6.4
1	AS	2450	U	6.4
61	DB	35	ALA	6.4
75	e	16	LEU	6.4
44	CK	28	LYS	6.4
79	AR	155	VAL	6.4
6	l	87	GLY	6.4
50	F	149	LYS	6.4
49	E	210	PHE	6.4
64	T	9	VAL	6.4

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Mol	Chain	Res	Type	RSRZ
80	p0	30	VAL	6.4
45	i	64	LEU	6.3
79	DT	209	ALA	6.3
14	t	17	HIS	6.3
50	F	188	LYS	6.3
44	CK	14	PHE	6.3
7	AZ	92	LEU	6.3
44	AQ	28	LYS	6.3
30	AC	21	ILE	6.3
40	CG	51	ILE	6.3
23	BP	98	PHE	6.3
48	CO	24	PHE	6.3
55	K	65	PHE	6.3
74	DO	32	PHE	6.3
1	1	1576	A	6.3
57	M	46	LEU	6.3
79	DT	249	LEU	6.3
73	DN	15	ARG	6.3
46	CM	1081	C	6.3
59	O	118	ALA	6.3
46	B	318	U	6.3
46	B	750	G	6.3
21	BN	138	GLN	6.3
60	P	121	ARG	6.3
4	j	176	ASP	6.3
45	CL	61	GLU	6.3
52	H	79	SER	6.3
79	AR	135	TRP	6.3
55	CV	201	ARG	6.3
1	AS	1490	U	6.3
46	CM	658	A	6.3
52	H	86	GLN	6.3
60	DA	65	VAL	6.3
77	g	41	THR	6.2
7	m	63	GLN	6.2
71	DL	74	LEU	6.2
72	DM	37	GLN	6.2
38	CE	17	THR	6.2
36	CC	75	TYR	6.2
26	BS	48	ARG	6.2
56	L	118	LEU	6.2
7	m	151	GLN	6.2

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Mol	Chain	Res	Type	RSRZ
35	AH	36	LYS	6.2
54	J	43	LYS	6.2
19	y	95	GLU	6.2
4	AW	232	GLY	6.2
54	CU	57	PHE	6.2
79	AR	124	VAL	6.2
5	k	4	ARG	6.2
47	C	14	ALA	6.2
65	U	2	PRO	6.2
6	AY	184	LYS	6.2
59	CZ	62	LEU	6.2
53	CT	179	VAL	6.2
21	0	116	ALA	6.2
67	DH	81	TYR	6.2
6	AY	245	LEU	6.2
59	O	100	TRP	6.1
57	CX	12	HIS	6.1
46	CM	944	U	6.1
54	CU	176	GLN	6.1
77	g	37	ARG	6.1
52	H	74	ALA	6.1
78	DS	172	ILE	6.1
8	BA	108	GLU	6.1
43	CJ	35	LEU	6.1
52	CS	61	TYR	6.1
79	DT	207	LEU	6.1
54	CU	179	PHE	6.1
74	DO	47	PHE	6.1
82	ll	148	VAL	6.1
64	T	12	ALA	6.1
16	v	198	SER	6.1
59	CZ	119	SER	6.1
82	ll	110	PHE	6.1
46	CM	278	U	6.1
1	AS	655	A	6.1
7	AZ	77	ALA	6.1
55	K	17	LYS	6.1
51	CR	245	ILE	6.1
64	DE	11	ARG	6.1
73	c	16	GLY	6.1
48	D	29	TRP	6.1
60	DA	28	LEU	6.1

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Mol	Chain	Res	Type	RSRZ
75	DP	51	ASN	6.1
18	x	135	ARG	6.0
46	B	504	A	6.0
52	CS	62	ILE	6.0
62	R	83	MET	6.0
41	CH	16	GLU	6.0
52	CS	94	THR	6.0
54	CU	134	LYS	6.0
49	CP	78	ILE	6.0
1	AS	1602	U	6.0
51	G	54	TYR	6.0
35	CB	33	GLN	6.0
44	CK	25	GLN	6.0
39	CF	22	SER	6.0
56	L	15	PRO	6.0
56	L	32	GLY	6.0
7	AZ	109	ALA	6.0
79	DT	202	SER	6.0
36	CC	91	LYS	5.9
59	O	123	VAL	5.9
80	p0	51	VAL	5.9
6	AY	70	ARG	5.9
48	D	26	ARG	5.9
10	BC	67	SER	5.9
7	m	92	LEU	5.9
71	a	9	THR	5.9
50	F	137	VAL	5.9
60	DA	33	VAL	5.9
5	k	330	GLY	5.9
45	i	120	GLU	5.9
5	k	6	TYR	5.9
51	G	2	ALA	5.9
7	AZ	269	SER	5.9
52	CS	170	GLN	5.9
48	D	54	LEU	5.9
46	CM	472	A	5.9
54	J	178	VAL	5.9
62	R	102	PHE	5.9
10	BC	45	ARG	5.9
19	y	94	LEU	5.9
7	m	226	TYR	5.8
48	D	25	THR	5.8

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Mol	Chain	Res	Type	RSRZ
6	AY	200	PHE	5.8
55	K	67	TRP	5.8
54	J	149	LEU	5.8
46	B	1571	G	5.8
64	DE	42	GLN	5.8
59	CZ	120	CYS	5.8
13	s	125	MET	5.8
46	B	25	C	5.8
51	CR	8	HIS	5.8
46	B	357	A	5.8
1	AS	1833	U	5.8
22	BO	16	GLN	5.8
46	B	258	U	5.8
7	AZ	78	ALA	5.8
70	Z	28	ALA	5.8
7	AZ	55	PHE	5.8
15	BH	4	THR	5.8
44	CK	11	THR	5.8
4	j	71	LEU	5.8
1	l	1099	A	5.8
46	B	1410	A	5.8
78	h	144	VAL	5.8
43	AP	43	TYR	5.8
80	p0	88	PHE	5.8
36	AI	91	LYS	5.8
62	DC	52	LYS	5.8
52	CS	97	LEU	5.8
47	C	98	ILE	5.8
10	p	237	GLY	5.8
63	S	54	VAL	5.8
64	T	66	VAL	5.8
27	BT	26	GLU	5.8
1	AS	1352	C	5.8
32	AE	33	LYS	5.8
36	CC	88	LEU	5.8
79	DT	32	LEU	5.8
63	S	69	THR	5.8
43	CJ	84	PRO	5.8
54	CU	119	ASP	5.7
25	7	41	GLN	5.7
75	DP	50	GLU	5.7
80	p0	73	PHE	5.7

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Mol	Chain	Res	Type	RSRZ
28	AA	20	GLY	5.7
46	CM	498	C	5.7
1	AS	1486	A	5.7
1	AS	2382	A	5.7
23	5	66	VAL	5.7
45	i	88	PHE	5.7
80	p0	79	PHE	5.7
60	P	6	SER	5.7
60	DA	7	SER	5.7
49	E	161	ALA	5.7
55	CV	102	VAL	5.7
59	CZ	90	LYS	5.7
51	G	44	LEU	5.7
54	J	77	LEU	5.7
77	g	39	LEU	5.7
27	9	32	SER	5.7
50	F	116	ILE	5.7
6	AY	199	ARG	5.7
7	AZ	170	GLY	5.7
60	P	5	HIS	5.7
39	CF	2	ALA	5.7
79	AR	209	ALA	5.7
7	m	37	VAL	5.7
75	DP	15	VAL	5.7
40	CG	49	LEU	5.7
45	CL	115	LEU	5.7
50	F	203	LEU	5.7
53	CT	77	LEU	5.7
71	DL	72	PHE	5.7
79	AR	32	LEU	5.7
10	BC	119	GLU	5.7
57	M	19	GLY	5.7
7	AZ	62	ALA	5.7
55	K	19	ALA	5.7
69	Y	41	MET	5.7
75	e	15	VAL	5.7
78	h	156	VAL	5.7
57	CX	2	LEU	5.7
44	CK	17	ARG	5.7
20	BM	52	LYS	5.6
30	AC	33	LYS	5.6
6	AY	68	THR	5.6

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Mol	Chain	Res	Type	RSRZ
7	m	38	THR	5.6
1	AS	2396	G	5.6
82	l1	1	MET	5.6
79	DT	218	ILE	5.6
66	V	84	LYS	5.6
58	N	59	PRO	5.6
10	BC	152	VAL	5.6
52	H	23	VAL	5.6
73	DN	35	ALA	5.6
12	r	102	MET	5.6
20	z	141	HIS	5.6
82	l1	165	LEU	5.6
47	C	115	PHE	5.6
7	m	25	GLU	5.6
50	F	136	GLU	5.6
53	CT	83	CYS	5.6
56	L	18	PRO	5.6
4	AW	236	GLY	5.6
71	a	67	GLY	5.6
79	AR	80	TYR	5.6
59	O	116	VAL	5.6
71	a	24	VAL	5.6
48	D	162	ARG	5.6
65	DF	119	ILE	5.6
46	CM	657	C	5.6
1	1	1589	A	5.6
61	Q	12	ALA	5.6
65	U	30	TYR	5.6
59	O	103	LEU	5.6
23	5	74	PHE	5.6
82	L1	111	ILE	5.6
52	H	170	GLN	5.6
1	AS	3319	U	5.6
12	BE	199	PHE	5.6
50	CQ	186	LYS	5.6
71	a	7	ILE	5.6
4	AW	233	GLN	5.5
13	BF	78	GLU	5.5
52	H	181	GLU	5.5
18	x	2	VAL	5.5
38	AK	51	LEU	5.5
54	CU	89	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
82	L1	69	GLY	5.5
52	H	28	THR	5.5
16	BI	198	SER	5.5
56	L	152	SER	5.5
46	B	22	A	5.5
51	G	40	GLU	5.5
21	0	162	LEU	5.5
8	n	168	GLY	5.5
71	a	73	GLY	5.5
65	DF	118	LYS	5.5
35	CB	7	TYR	5.5
52	H	145	ASP	5.5
52	H	177	ILE	5.5
46	B	1356	U	5.5
52	CS	71	SER	5.5
41	CH	22	LYS	5.5
73	DN	20	PRO	5.5
79	DT	299	PHE	5.5
53	CT	16	ILE	5.5
59	CZ	104	CYS	5.5
1	AS	855	G	5.5
35	AH	31	VAL	5.5
52	CS	70	VAL	5.5
75	e	50	GLU	5.5
79	AR	290	ALA	5.5
22	BO	19	PHE	5.5
76	DQ	8	PHE	5.5
3	4	91	C	5.5
33	BZ	27	HIS	5.5
79	DT	230	THR	5.5
6	AY	195	LEU	5.5
78	h	148	TYR	5.5
7	AZ	58	LYS	5.4
51	CR	246	LYS	5.4
54	J	86	VAL	5.4
78	DS	126	VAL	5.4
32	BY	26	LYS	5.4
35	AH	57	LEU	5.4
59	O	97	LEU	5.4
6	AY	63	ALA	5.4
53	I	35	GLU	5.4
55	K	70	GLU	5.4

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Mol	Chain	Res	Type	RSRZ
1	AS	1918	A	5.4
52	CS	102	ARG	5.4
5	AX	302	LYS	5.4
1	1	977	U	5.4
46	CM	1644	U	5.4
4	AW	47	GLN	5.4
47	C	13	ASP	5.4
63	S	39	GLN	5.4
22	BO	12	ARG	5.4
6	AY	220	LEU	5.4
79	AR	34	LEU	5.4
82	ll	124	LEU	5.4
1	1	1552	C	5.4
46	B	1624	C	5.4
79	DT	24	ALA	5.4
14	BG	37	GLN	5.4
19	BL	180	ARG	5.4
52	H	161	ASP	5.4
73	c	12	LYS	5.4
55	CV	188	TYR	5.4
10	BC	243	ALA	5.4
62	R	82	ASN	5.4
65	U	44	ASN	5.4
46	B	1621	C	5.4
53	CT	54	GLY	5.4
6	AY	76	PRO	5.4
7	m	27	LYS	5.4
10	p	62	GLN	5.4
25	BR	27	LYS	5.4
36	AI	84[A]	LYS	5.4
46	B	1	U	5.3
46	CM	1359	U	5.3
6	AY	226	VAL	5.3
77	DR	35	TYR	5.3
64	DE	90	ALA	5.3
20	z	98	ARG	5.3
35	CB	9	ARG	5.3
58	CY	32	LYS	5.3
45	CL	60	ASN	5.3
80	P0	79	PHE	5.3
47	CN	184	LEU	5.3
1	AS	1842	C	5.3

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Mol	Chain	Res	Type	RSRZ
48	CO	119	SER	5.3
10	p	179	ALA	5.3
39	CF	43	PHE	5.3
54	CU	105	GLN	5.3
74	d	27	GLN	5.3
82	L1	40	ASN	5.3
53	I	212	LEU	5.3
59	O	93	ASP	5.3
35	CB	16	ARG	5.3
1	1	2456	C	5.3
52	CS	110	ALA	5.3
58	CY	15	LYS	5.3
46	B	708	A	5.3
4	j	175	ILE	5.3
79	DT	201	LEU	5.3
23	BP	17	VAL	5.3
43	AP	42	ARG	5.3
56	L	154	LYS	5.3
48	CO	205	PHE	5.3
53	I	50	PHE	5.3
57	CX	41	PHE	5.3
62	R	92	SER	5.3
6	AY	82	GLY	5.3
55	K	68	GLY	5.3
52	H	94	THR	5.3
1	1	1562	G	5.3
46	CM	1700	G	5.3
49	CP	174	VAL	5.3
35	CB	36	LYS	5.3
38	CE	23	GLY	5.2
79	AR	207	LEU	5.2
64	T	8	THR	5.2
6	l	64	GLU	5.2
56	CW	14	VAL	5.2
59	O	61	VAL	5.2
18	BK	89	ASN	5.2
1	AS	1249	U	5.2
71	DL	88	ALA	5.2
66	V	64	HIS	5.2
59	O	52	LEU	5.2
79	DT	228	LEU	5.2
77	DR	60	PRO	5.2

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Mol	Chain	Res	Type	RSRZ
6	AY	77	ARG	5.2
79	DT	73	THR	5.2
82	L1	136	THR	5.2
12	r	162	GLN	5.2
44	AQ	27	LYS	5.2
48	CO	121	VAL	5.2
73	DN	19	LYS	5.2
79	AR	20	VAL	5.2
70	Z	31	ALA	5.2
27	9	78	PHE	5.2
47	C	173	ILE	5.2
69	Y	75	ILE	5.2
7	AZ	169	GLY	5.2
15	u	130	LYS	5.2
46	B	23	G	5.2
74	d	45	THR	5.2
41	CH	44	GLN	5.2
22	BO	86	GLU	5.2
63	S	19	ALA	5.2
65	DF	128	PHE	5.2
4	AW	190	LYS	5.2
77	g	3	LYS	5.2
7	AZ	105	VAL	5.2
79	DT	155	VAL	5.2
1	1	1197	C	5.2
61	DB	84	THR	5.2
21	BN	60	SER	5.2
33	BZ	36	GLN	5.2
56	L	13	SER	5.2
54	CU	123	GLU	5.2
54	CU	132	ILE	5.2
63	S	80	ILE	5.2
23	5	15	PHE	5.2
31	BX	61	TYR	5.2
5	k	331	VAL	5.2
52	CS	168	VAL	5.2
45	CL	98	ASP	5.2
79	DT	290	ALA	5.2
1	1	2466	A	5.1
1	1	2474	C	5.1
53	CT	226	ILE	5.1
66	V	124	ILE	5.1

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Mol	Chain	Res	Type	RSRZ
4	AW	184	ARG	5.1
60	DA	26	PHE	5.1
7	AZ	81	HIS	5.1
54	J	126	VAL	5.1
63	DD	36	THR	5.1
71	DL	86	GLU	5.1
23	5	73	SER	5.1
50	F	185	ILE	5.1
65	U	58	ALA	5.1
1	1	1816	U	5.1
25	BR	60	LYS	5.1
46	CM	25	C	5.1
49	E	178	VAL	5.1
13	BF	74	PRO	5.1
49	E	91	THR	5.1
82	l1	136	THR	5.1
47	C	177	LEU	5.1
77	g	34	ALA	5.1
33	AF	35	LYS	5.1
38	CE	14	LYS	5.1
35	CB	17	SER	5.1
76	f	43	PHE	5.1
78	h	173	PHE	5.1
1	1	2455	G	5.1
6	AY	225	GLY	5.1
55	K	102	VAL	5.1
53	I	181	PRO	5.1
1	AS	402	A	5.1
1	AS	2745	C	5.1
51	CR	198	ARG	5.1
82	L1	68	PHE	5.1
6	l	352	PRO	5.1
1	1	1127	G	5.1
1	AS	801	G	5.1
1	1	1591	U	5.1
6	AY	109	ARG	5.1
54	J	125	LEU	5.1
28	AA	71	PHE	5.1
7	m	147	ASP	5.1
31	BX	44	VAL	5.1
80	p0	35	SER	5.1
79	AR	142	MET	5.1

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Mol	Chain	Res	Type	RSRZ
45	i	33	ASN	5.1
49	E	113	ALA	5.0
59	CZ	42	ALA	5.0
82	L1	112	ALA	5.0
46	B	764	U	5.0
62	R	104	THR	5.0
63	DD	39	GLN	5.0
76	f	20	GLN	5.0
46	CM	1480	G	5.0
7	AZ	156	GLY	5.0
1	1	1781	C	5.0
29	BV	52	TYR	5.0
57	CX	8	ARG	5.0
46	B	763	C	5.0
73	c	17	HIS	5.0
79	DT	190	ILE	5.0
50	F	172	ALA	5.0
6	AY	202	GLN	5.0
37	CD	65	GLU	5.0
1	1	1561	U	5.0
67	W	79	ASP	5.0
17	BJ	171	LYS	5.0
30	AC	5	LYS	5.0
56	CW	10	LYS	5.0
61	DB	124	LYS	5.0
24	6	35	TYR	5.0
63	S	27	LEU	5.0
1	1	2089	G	5.0
22	BO	101	CYS	5.0
66	DG	50	ALA	5.0
74	DO	31	PHE	5.0
46	B	706	C	5.0
46	CM	468	A	5.0
52	CS	27	THR	5.0
64	T	42	GLN	5.0
74	DO	27	GLN	5.0
79	DT	220	TRP	5.0
6	AY	78	VAL	5.0
52	CS	76	LYS	5.0
53	I	79	LYS	5.0
66	V	119	LYS	5.0
10	p	201	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
51	CR	94	ALA	5.0
52	H	191	ALA	5.0
73	DN	6	ALA	5.0
50	F	168	PHE	5.0
20	z	19	LYS	5.0
39	CF	41	THR	5.0
46	CM	701	G	5.0
49	CP	89	GLN	5.0
50	F	9	LYS	5.0
55	CV	82	VAL	5.0
82	ll	167	VAL	5.0
66	V	42	GLY	5.0
1	AS	1197	C	5.0
80	P0	87	ILE	5.0
79	AR	35	SER	5.0
51	G	109	PHE	5.0
26	8	36	LYS	5.0
10	p	152	VAL	5.0
36	CC	36	LEU	5.0
45	i	103	LEU	5.0
49	E	206	LEU	5.0
50	F	171	ILE	4.9
80	p0	87	ILE	4.9
1	AS	813	A	4.9
1	AS	1023	A	4.9
59	CZ	118	ALA	4.9
69	Y	37	PHE	4.9
18	BK	135	ARG	4.9
49	CP	90	ARG	4.9
65	U	115	ARG	4.9
63	DD	38	VAL	4.9
1	1	1817	U	4.9
53	CT	139	ASN	4.9
53	CT	80	GLY	4.9
79	DT	240	LEU	4.9
7	AZ	219	TYR	4.9
79	AR	81	ALA	4.9
43	AP	44	ASP	4.9
44	CK	24	ARG	4.9
63	DD	33	SER	4.9
1	AS	802	A	4.9
46	B	139	U	4.9

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Mol	Chain	Res	Type	RSRZ
18	BK	185	ALA	4.9
35	CB	39	ALA	4.9
54	CU	40	LYS	4.9
55	K	11	ARG	4.9
71	a	10	ARG	4.9
73	c	89	ARG	4.9
48	D	158	SER	4.9
14	t	20	GLU	4.9
55	CV	103	GLN	4.9
48	CO	185	THR	4.9
51	G	6	LYS	4.9
1	AS	320	G	4.9
46	B	1349	G	4.9
46	CM	723	G	4.9
46	B	238	U	4.9
63	S	51	LEU	4.9
59	O	49	SER	4.9
79	AR	113	SER	4.9
51	G	154	ILE	4.9
54	J	145	ILE	4.9
61	Q	76	ILE	4.9
6	l	310	LYS	4.9
14	BG	41	ARG	4.9
16	v	153	ASN	4.9
50	CQ	149	LYS	4.9
53	CT	236	ASN	4.9
7	AZ	7	PHE	4.9
1	AS	1917	A	4.9
7	AZ	226	TYR	4.9
38	CE	29	VAL	4.9
54	J	136	VAL	4.9
59	O	91	VAL	4.9
51	G	9	LEU	4.9
74	DO	24	LEU	4.9
46	CM	1696	U	4.9
71	a	26	ASP	4.9
10	BC	48	SER	4.8
50	F	191	LYS	4.8
52	CS	109	LYS	4.8
56	CW	48	GLN	4.8
18	BK	184	ALA	4.8
66	V	62	ALA	4.8

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Mol	Chain	Res	Type	RSRZ
23	BP	15	PHE	4.8
71	DL	58	PHE	4.8
73	DN	31	PRO	4.8
79	AR	104	PHE	4.8
80	p0	33	VAL	4.8
50	F	178	MET	4.8
64	T	53	TYR	4.8
78	h	145	LEU	4.8
44	CK	27	LYS	4.8
45	CL	95	GLY	4.8
46	CM	1703	C	4.8
73	c	33	ASP	4.8
10	BC	162	GLU	4.8
1	AS	1557	U	4.8
46	CM	724	G	4.8
55	CV	121	LEU	4.8
22	BO	5	ARG	4.8
53	CT	72	ARG	4.8
6	AY	89	ALA	4.8
20	z	13	SER	4.8
27	9	79	ALA	4.8
47	C	97	ALA	4.8
46	B	307	C	4.8
18	BK	51	VAL	4.8
51	G	48	LEU	4.8
51	CR	44	LEU	4.8
53	I	190	LEU	4.8
53	CT	97	VAL	4.8
59	O	122	VAL	4.8
44	CK	18	TYR	4.8
55	CV	83	TYR	4.8
70	Z	39	LYS	4.8
59	O	60	CYS	4.8
46	B	381	G	4.8
7	AZ	60	ILE	4.8
80	P0	80	ILE	4.8
71	a	58	PHE	4.8
30	BW	8	THR	4.8
23	BP	64	VAL	4.8
36	AI	88	LEU	4.8
39	CF	45	VAL	4.8
62	DC	49	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
9	BB	96	LYS	4.8
32	AE	26	LYS	4.8
14	t	21	ARG	4.8
46	CM	39	A	4.8
52	CS	92	ARG	4.8
74	DO	29	ARG	4.8
59	CZ	44	GLY	4.8
8	n	58	GLU	4.8
54	CU	130	GLU	4.8
10	p	197	ALA	4.8
5	k	96	PRO	4.8
6	AY	72	VAL	4.8
39	CF	27	VAL	4.8
17	w	2	SER	4.8
79	AR	136	ASN	4.7
13	BF	124	GLY	4.7
56	L	137	GLY	4.7
46	B	1400	U	4.7
13	BF	76	ALA	4.7
19	BL	53	PHE	4.7
35	CB	57	LEU	4.7
66	DG	132	LEU	4.7
10	BC	133	VAL	4.7
63	S	18	VAL	4.7
6	l	353	SER	4.7
6	AY	59	HIS	4.7
7	AZ	119	TYR	4.7
45	CL	66	ASN	4.7
52	CS	137	ILE	4.7
79	AR	116	ILE	4.7
82	ll	117	ILE	4.7
79	DT	81	ALA	4.7
75	e	45	LYS	4.7
1	AS	1849	U	4.7
7	m	8	ARG	4.7
54	J	176	GLN	4.7
1	AS	1478	A	4.7
30	BW	4	SER	4.7
79	AR	74	ILE	4.7
79	AR	139	GLY	4.7
9	BB	88	LYS	4.7
12	BE	15	LYS	4.7

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Mol	Chain	Res	Type	RSRZ
16	v	185	ALA	4.7
37	CD	8	ALA	4.7
39	CF	78	LEU	4.7
52	CS	84	LYS	4.7
53	CT	27	PHE	4.7
57	CX	40	LEU	4.7
70	DK	107	PHE	4.7
13	BF	108	GLU	4.7
54	CU	56	VAL	4.7
1	AS	1484	G	4.7
16	v	57	GLN	4.7
73	DN	29	CYS	4.7
6	AY	110	TRP	4.7
53	CT	62	PRO	4.7
52	H	27	THR	4.7
46	B	1081	C	4.7
58	N	15	LYS	4.7
79	DT	261	LYS	4.7
43	CJ	70	LEU	4.7
48	D	161	LEU	4.7
63	S	53	LEU	4.7
10	BC	200	ALA	4.7
73	DN	22	ARG	4.7
82	ll	68	PHE	4.7
67	W	115	VAL	4.7
11	BD	165	CYS	4.7
67	W	69	THR	4.7
26	8	49	LYS	4.7
65	U	48	LYS	4.7
46	B	259	U	4.7
55	CV	171	LEU	4.7
60	P	15	ALA	4.7
77	g	51	ASN	4.7
78	h	170	ALA	4.7
1	1	1129	A	4.7
25	7	79	GLN	4.6
29	AB	65	GLN	4.6
41	CH	15	CYS	4.6
50	CQ	173	ILE	4.6
65	U	26	ILE	4.6
49	E	92	ARG	4.6
71	DL	20	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
79	DT	34	LEU	4.6
16	v	6	TYR	4.6
50	CQ	150	SER	4.6
52	H	160	VAL	4.6
55	K	66	SER	4.6
69	DJ	128	PHE	4.6
53	CT	63	MET	4.6
56	L	153	GLN	4.6
47	CN	173	ILE	4.6
59	O	72	ILE	4.6
1	1	2476	C	4.6
1	AS	2284	C	4.6
46	CM	296	C	4.6
62	DC	104	THR	4.6
79	AR	101	THR	4.6
41	CH	27	LEU	4.6
54	CU	6	LEU	4.6
30	AC	34	GLY	4.6
13	BF	8	VAL	4.6
24	6	76	ALA	4.6
80	P0	28	VAL	4.6
79	AR	210	SER	4.6
73	DN	25	ASN	4.6
17	w	68	LYS	4.6
50	F	189	ILE	4.6
41	CH	30	ARG	4.6
65	U	41	ARG	4.6
26	8	108	LEU	4.6
67	W	66	THR	4.6
80	p0	18	LEU	4.6
1	1	2341	A	4.6
1	AS	355	A	4.6
46	B	714	G	4.6
46	B	1038	G	4.6
46	CM	408	A	4.6
55	K	55	PHE	4.6
59	CZ	91	VAL	4.6
55	CV	163	ASP	4.6
10	p	107	LYS	4.6
51	CR	7	LYS	4.6
6	AY	75	ILE	4.6
18	BK	58	ILE	4.6

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Mol	Chain	Res	Type	RSRZ
66	DG	46	PRO	4.6
10	p	151	LEU	4.6
51	G	38	LEU	4.6
57	M	2	LEU	4.6
65	DF	113	LEU	4.6
46	B	1292	U	4.6
61	DB	10	GLY	4.6
57	M	16	PHE	4.6
59	O	31	VAL	4.6
72	b	40	VAL	4.6
47	CN	15	LYS	4.6
52	H	76	LYS	4.6
1	AS	1262	G	4.6
46	CM	34	G	4.6
6	AY	85	ARG	4.6
76	f	18	SER	4.6
57	CX	79	GLU	4.6
80	p0	71	PRO	4.6
7	AZ	212	LEU	4.6
59	CZ	136	LEU	4.6
38	CE	2	GLY	4.6
48	CO	46	THR	4.6
64	T	121	THR	4.6
20	z	12	ALA	4.6
22	2	121	ALA	4.6
56	L	113	VAL	4.6
59	O	30	VAL	4.6
78	DS	173	PHE	4.6
82	ll	36	VAL	4.6
46	B	1335	U	4.5
55	CV	172	TYR	4.5
59	O	133	ARG	4.5
6	l	154	SER	4.5
1	1	2437	A	4.5
46	B	383	A	4.5
1	1	2337	C	4.5
15	BH	122	PHE	4.5
46	CM	1546	G	4.5
47	CN	171	GLY	4.5
50	F	176	VAL	4.5
70	Z	124	VAL	4.5
48	D	57	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
78	DS	129	THR	4.5
78	DS	174	MET	4.5
40	CG	8	ARG	4.5
41	AN	26	ARG	4.5
82	L1	41	TYR	4.5
52	CS	190	ILE	4.5
81	12	141	CYS	4.5
46	B	278	U	4.5
11	BD	7	ASP	4.5
31	BX	43	LEU	4.5
56	CW	128	LEU	4.5
63	DD	43	LEU	4.5
82	l1	2	SER	4.5
27	9	29	VAL	4.5
59	CZ	121	VAL	4.5
82	L1	202	GLY	4.5
7	m	34	LYS	4.5
80	P0	38	MET	4.5
1	AS	2474	C	4.5
46	B	482	C	4.5
36	CC	44	ILE	4.5
47	C	76	CYS	4.5
54	CU	96	PRO	4.5
62	DC	116	LEU	4.5
69	DJ	77	PRO	4.5
42	AO	3	ASP	4.5
65	U	51	ASP	4.5
52	CS	63	GLN	4.5
75	e	27	GLN	4.5
65	U	133	VAL	4.5
80	p0	59	VAL	4.5
48	D	24	PHE	4.5
82	l1	104	ALA	4.5
19	BL	17	THR	4.5
56	L	83	ILE	4.5
72	DM	101	TYR	4.5
20	z	94	LEU	4.5
59	O	78	LEU	4.5
1	1	2675	A	4.5
46	CM	1743	A	4.5
1	AS	350	C	4.5
73	c	2	PRO	4.5

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Mol	Chain	Res	Type	RSRZ
11	q	174	LYS	4.5
48	D	121	VAL	4.5
50	F	182	VAL	4.5
64	DE	9	VAL	4.5
79	DT	241	ALA	4.5
1	1	2964	U	4.5
46	CM	1459	U	4.5
18	BK	136	ILE	4.5
8	n	171	PRO	4.5
22	BO	3	LYS	4.5
52	CS	115	LYS	4.5
53	CT	95	LYS	4.5
47	CN	76	CYS	4.5
70	Z	122	PHE	4.5
73	c	28	ARG	4.5
3	AU	45	C	4.4
6	AY	90	ALA	4.4
10	p	200	ALA	4.4
28	AA	49	ALA	4.4
29	BV	20	GLY	4.4
77	g	2	GLY	4.4
48	CO	29	TRP	4.4
82	ll	213	SER	4.4
16	BI	175	ASN	4.4
7	m	231	ILE	4.4
19	BL	5	HIS	4.4
35	AH	20	ILE	4.4
45	CL	81	THR	4.4
58	N	63	THR	4.4
69	Y	61	ILE	4.4
51	CR	60	GLU	4.4
57	M	42	VAL	4.4
23	BP	74	PHE	4.4
7	m	283	GLN	4.4
36	AI	120	ALA	4.4
45	i	117	GLY	4.4
62	DC	50	ASP	4.4
50	F	139	ILE	4.4
54	J	131	ILE	4.4
63	S	120	SER	4.4
7	m	68	HIS	4.4
30	BW	32	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
35	AH	34	HIS	4.4
46	B	1136	A	4.4
61	DB	28	LEU	4.4
46	CM	114	C	4.4
46	CM	482	C	4.4
54	J	134	LYS	4.4
62	DC	108	LYS	4.4
4	AW	178	PRO	4.4
30	BW	35	VAL	4.4
46	CM	1	U	4.4
20	z	132	PHE	4.4
71	a	60	PHE	4.4
71	a	59	GLY	4.4
33	AF	42	CYS	4.4
52	CS	55	ASP	4.4
56	CW	118	LEU	4.4
70	Z	57	ILE	4.4
30	BW	50	THR	4.4
60	P	109	LYS	4.4
71	a	34	ASN	4.4
7	m	65	VAL	4.4
1	l	2467	C	4.4
1	AS	2784	C	4.4
46	B	762	C	4.4
7	AZ	75	PHE	4.4
62	DC	110	GLU	4.4
74	d	33	MET	4.4
7	m	77	ALA	4.4
1	AS	1204	U	4.4
25	BR	41	GLN	4.4
46	B	766	U	4.4
10	p	137	LEU	4.4
47	C	16	LEU	4.4
59	CZ	89	ILE	4.4
18	BK	53	ASP	4.4
7	m	54	ARG	4.4
7	m	76	THR	4.4
23	BP	57	THR	4.4
28	AA	98	SER	4.4
54	J	135	ARG	4.4
79	DT	168	SER	4.4
10	p	165	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
66	V	2	PRO	4.4
79	AR	302	TYR	4.4
49	E	76	MET	4.4
7	AZ	166	ALA	4.4
20	z	140	GLU	4.4
1	AS	1283	A	4.4
7	m	115	LEU	4.4
46	CM	1702	A	4.4
47	C	170	ILE	4.4
78	h	142	LEU	4.4
4	AW	198	LYS	4.4
73	DN	12	LYS	4.4
82	ll	111	ILE	4.4
46	B	319	C	4.4
46	CM	407	C	4.4
1	AS	1830	U	4.4
8	BA	65	SER	4.4
52	CS	151	SER	4.4
61	DB	37	VAL	4.4
58	N	93	TYR	4.4
54	J	21	PHE	4.3
80	P0	88	PHE	4.3
64	DE	12	ALA	4.3
6	AY	197	GLY	4.3
55	K	180	GLY	4.3
30	BW	25	LYS	4.3
59	CZ	97	LEU	4.3
80	P0	19	LEU	4.3
55	CV	189	ILE	4.3
62	R	84	ILE	4.3
67	DH	23	ILE	4.3
39	CF	40	GLN	4.3
1	1	369	A	4.3
46	CM	1701	A	4.3
7	AZ	147	ASP	4.3
65	DF	111	ASP	4.3
67	DH	27	SER	4.3
66	DG	18	TYR	4.3
77	g	35	TYR	4.3
30	AC	2	ALA	4.3
16	BI	92	LEU	4.3
7	m	210	GLU	4.3

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Mol	Chain	Res	Type	RSRZ
11	BD	178	GLY	4.3
47	C	87	LEU	4.3
48	CO	161	LEU	4.3
50	F	181	GLY	4.3
52	H	20	LEU	4.3
47	C	174	TRP	4.3
1	1	2441	G	4.3
61	Q	25	VAL	4.3
80	p0	57	THR	4.3
54	J	88	PHE	4.3
63	S	119	ASP	4.3
80	P0	53	MET	4.3
1	AS	2480	A	4.3
4	AW	145	LYS	4.3
6	AY	57	ALA	4.3
16	BI	43	SER	4.3
16	BI	204	SER	4.3
6	AY	259	LEU	4.3
12	r	55	ASN	4.3
46	CM	473	A	4.3
48	D	119	SER	4.3
50	F	121	TYR	4.3
50	CQ	188	LYS	4.3
79	DT	247	TYR	4.3
59	O	88	LEU	4.3
46	CM	38	C	4.3
3	AU	113	U	4.3
32	BY	18	ARG	4.3
52	CS	83	ARG	4.3
6	AY	88	GLN	4.3
7	AZ	53	VAL	4.3
28	BU	13	VAL	4.3
57	M	12	HIS	4.3
72	DM	40	VAL	4.3
7	m	223	PHE	4.3
33	AF	50	THR	4.3
36	CC	78	LYS	4.3
54	J	171	LYS	4.3
6	l	71	ALA	4.3
58	N	140	LEU	4.3
59	O	62	LEU	4.3
65	U	15	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
22	2	101	CYS	4.3
25	BR	47	ARG	4.3
26	8	50	SER	4.3
26	BS	27	ARG	4.3
60	DA	20	ARG	4.3
65	U	28	ILE	4.3
76	f	12	ARG	4.3
46	B	1213	G	4.3
46	B	741	A	4.3
1	1	1560	U	4.3
1	AS	2926	U	4.3
9	BB	17	GLN	4.3
14	t	22	VAL	4.3
33	AF	43	VAL	4.3
53	CT	36	VAL	4.3
56	L	141	VAL	4.3
79	AR	220	TRP	4.3
5	k	274	HIS	4.3
13	BF	104	PHE	4.3
28	AA	118	PHE	4.3
57	M	15	LEU	4.3
10	BC	155	ALA	4.3
24	BQ	113	ALA	4.3
16	BI	148	TYR	4.3
41	AN	13	TYR	4.3
64	T	102	ILE	4.3
69	Y	52	TYR	4.3
79	DT	116	ILE	4.3
6	AY	264	GLY	4.3
22	BO	6	GLY	4.3
49	CP	218	SER	4.3
65	U	87	ASN	4.3
16	v	182	LYS	4.2
61	DB	23	VAL	4.3
63	S	96	VAL	4.3
74	d	22	LYS	4.2
1	AS	218	A	4.2
46	B	711	U	4.2
46	CM	814	A	4.2
1	AS	3051	C	4.2
17	BJ	181	ALA	4.2
32	BY	105	THR	4.2

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Mol	Chain	Res	Type	RSRZ
49	E	117	ALA	4.2
55	K	189	ILE	4.2
64	DE	117	ILE	4.2
79	AR	89	THR	4.2
79	AR	200	THR	4.2
63	DD	32	GLY	4.2
66	DG	55	TYR	4.2
80	P0	11	TYR	4.2
30	AC	6	ASN	4.2
41	CH	14	ASN	4.2
9	BB	15	LYS	4.2
10	BC	182	LYS	4.2
68	X	27	LYS	4.2
20	z	101	VAL	4.2
50	F	135	VAL	4.2
71	DL	106	GLN	4.2
53	CT	3	LEU	4.2
60	P	3	ARG	4.2
64	T	28	PHE	4.2
74	d	31	PHE	4.2
4	AW	210	PRO	4.2
15	BH	131	ALA	4.2
55	K	175	ILE	4.2
63	S	30	ILE	4.2
79	AR	43	ILE	4.2
80	p0	80	ILE	4.2
46	B	752	U	4.2
46	B	217	A	4.2
1	1	91	G	4.2
1	1	1130	G	4.2
46	B	716	C	4.2
48	CO	67	GLU	4.2
71	DL	3	ASP	4.2
14	t	4	SER	4.2
19	y	11	VAL	4.2
55	CV	185	CYS	4.2
63	S	21	VAL	4.2
13	s	39	GLN	4.2
40	CG	4	GLN	4.2
5	k	334	ARG	4.2
7	AZ	54	ARG	4.2
19	BL	49	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
35	AH	16	ARG	4.2
64	T	91	LEU	4.2
66	V	63	ARG	4.2
10	p	123	ALA	4.2
10	p	180	ILE	4.2
18	BK	85	ALA	4.2
52	H	179	ALA	4.2
63	DD	23	ALA	4.2
6	l	140	GLY	4.2
37	CD	9	GLY	4.2
54	CU	129	THR	4.2
60	DA	59	GLY	4.2
28	AA	111	LYS	4.2
65	U	139	LYS	4.2
3	AU	23	U	4.2
46	B	21	U	4.2
46	B	1047	U	4.2
59	CZ	68	GLU	4.2
1	AS	325	A	4.2
1	AS	2783	A	4.2
18	BK	87	SER	4.2
24	BQ	28	ASN	4.2
46	CM	22	A	4.2
54	CU	151	ASP	4.2
61	DB	25	VAL	4.2
66	DG	71	VAL	4.2
81	12	162	VAL	4.2
82	11	169	VAL	4.2
79	DT	83	SER	4.2
1	AS	249	G	4.2
1	AS	2387	G	4.2
1	AS	2458	G	4.2
10	p	166	PHE	4.2
58	CY	13	PHE	4.2
13	s	21	ILE	4.2
50	CQ	202	ALA	4.2
55	CV	173	ALA	4.2
64	DE	102	ILE	4.2
66	V	90	PRO	4.2
79	AR	251	ALA	4.2
79	DT	169	ALA	4.2
57	M	72	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
4	AW	234	LYS	4.2
32	BY	30	LYS	4.2
80	P0	57	THR	4.2
4	AW	73	GLU	4.2
5	k	264	VAL	4.2
6	l	360	VAL	4.2
14	BG	134	GLU	4.2
50	F	118	ARG	4.2
27	BT	30	LEU	4.2
41	CH	45	LEU	4.2
53	CT	75	LEU	4.2
59	CZ	59	LEU	4.2
63	DD	53	LEU	4.2
66	V	67	LEU	4.2
80	p0	70	LEU	4.2
1	AS	1091	U	4.2
46	B	765	U	4.2
46	CM	1270	U	4.2
53	I	144	PHE	4.2
45	i	41	ALA	4.2
64	T	50	ILE	4.2
66	V	116	ILE	4.2
6	AY	84	HIS	4.2
41	AN	29	PRO	4.2
46	B	215	A	4.2
46	B	1005	A	4.2
46	CM	443	A	4.2
1	AS	184	C	4.2
3	AU	21	C	4.2
9	o	126	LYS	4.2
54	J	147	LYS	4.2
63	S	8	THR	4.2
74	DO	45	THR	4.2
1	AS	1747	G	4.2
46	B	1700	G	4.2
51	G	82	TYR	4.2
10	p	198	VAL	4.1
73	DN	89	ARG	4.2
75	DP	48	VAL	4.1
79	DT	216	VAL	4.1
7	m	212	LEU	4.1
10	BC	153	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
13	s	127	PHE	4.1
63	S	63	ASP	4.1
65	DF	94	ASP	4.1
75	e	43	ASN	4.1
11	BD	48	ILE	4.1
19	y	63	SER	4.1
27	9	33	ALA	4.1
50	CQ	172	ALA	4.1
79	AR	167	ILE	4.1
33	AF	21	HIS	4.1
46	CM	1652	U	4.1
54	CU	109	PRO	4.1
1	1	733	A	4.1
1	1	1609	A	4.1
47	C	127	ARG	4.1
51	CR	146	THR	4.1
52	CS	154	THR	4.1
13	BF	116	TYR	4.1
72	b	59	TYR	4.1
1	1	1694	C	4.1
1	AS	1275	C	4.1
45	CL	103	LEU	4.1
46	B	753	C	4.1
47	C	17	LEU	4.1
65	DF	54	LEU	4.1
51	CR	93	GLU	4.1
51	CR	99	PHE	4.1
80	P0	73	PHE	4.1
1	AS	1524	G	4.1
60	DA	36	GLN	4.1
63	DD	80	ILE	4.1
24	6	63	LYS	4.1
35	CB	38	ALA	4.1
41	AN	14	ASN	4.1
56	L	68	LYS	4.1
60	DA	64	LYS	4.1
64	DE	14	LYS	4.1
70	Z	3	LYS	4.1
47	CN	68	PRO	4.1
48	D	159	SER	4.1
65	U	23	ASP	4.1
65	DF	121	SER	4.1

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Mol	Chain	Res	Type	RSRZ
72	b	55	PRO	4.1
74	DO	49	HIS	4.1
49	CP	79	ARG	4.1
1	1	2968	U	4.1
35	AH	22	VAL	4.1
47	CN	128	THR	4.1
54	J	148	VAL	4.1
7	AZ	171	LEU	4.1
54	J	66	TYR	4.1
54	CU	66	TYR	4.1
60	P	40	TYR	4.1
63	S	56	LEU	4.1
66	V	79	LEU	4.1
80	p0	15	LEU	4.1
20	z	68	GLU	4.1
67	W	114	GLU	4.1
1	1	2419	A	4.1
1	1	2948	A	4.1
1	AS	1248	A	4.1
11	BD	45	PHE	4.1
46	CM	1411	A	4.1
56	L	146	PHE	4.1
81	12	110	PHE	4.1
16	BI	174	ILE	4.1
32	AE	36	LYS	4.1
49	E	120	ILE	4.1
66	DG	36	ILE	4.1
67	W	52	LYS	4.1
1	AS	2476	C	4.1
1	AS	2732	C	4.1
12	BE	2	ALA	4.1
30	BW	6	ASN	4.1
36	CC	48	ARG	4.1
45	i	107	TRP	4.1
78	h	164	PRO	4.1
66	V	123	ARG	4.1
79	DT	94	ASP	4.1
1	AS	2570	G	4.1
4	j	180	LEU	4.1
6	l	12	VAL	4.1
62	R	76	VAL	4.1
77	g	47	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
39	AL	53	THR	4.1
64	DE	8	THR	4.1
80	p0	58	MET	4.1
11	BD	135	GLU	4.1
8	n	163	PHE	4.1
14	t	88	LYS	4.1
46	B	378	U	4.1
59	O	99	GLU	4.1
50	F	159	ILE	4.1
10	BC	179	ALA	4.1
45	i	80	ALA	4.1
48	CO	141	ALA	4.1
50	CQ	206	ALA	4.1
1	AS	155	A	4.1
7	AZ	95	TRP	4.1
7	AZ	26	GLY	4.1
14	t	11	ASN	4.1
16	v	194	HIS	4.1
22	2	59	GLY	4.1
74	d	19	HIS	4.1
1	AS	2470	C	4.1
23	5	100	SER	4.1
59	O	70	SER	4.1
13	s	129	VAL	4.1
49	E	58	VAL	4.1
54	CU	86	VAL	4.1
62	R	94	VAL	4.1
64	DE	46	LEU	4.1
80	p0	52	LEU	4.1
82	ll	127	THR	4.1
79	DT	258	LYS	4.1
53	CT	5	ILE	4.1
79	AR	140	GLU	4.1
3	AU	114	G	4.1
20	BM	87	ALA	4.1
55	CV	137	ALA	4.1
7	m	21	ARG	4.1
64	T	67	ARG	4.1
10	p	90	GLN	4.1
41	CH	29	PRO	4.1
19	BL	177	GLY	4.1
48	CO	101	HIS	4.1

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Mol	Chain	Res	Type	RSRZ
23	5	101	VAL	4.0
53	I	36	VAL	4.0
72	b	54	VAL	4.0
81	12	133	LEU	4.0
8	n	1	MET	4.0
13	BF	125	MET	4.0
20	z	89	MET	4.0
37	CD	24	LYS	4.0
56	L	115	LYS	4.0
63	DD	105	LYS	4.0
30	AC	8	THR	4.0
39	AL	52	TYR	4.0
1	AS	2744	C	4.0
28	BU	46	ILE	4.0
55	K	21	PHE	4.0
58	N	60	PHE	4.0
14	BG	20	GLU	4.0
20	z	145	ALA	4.0
79	AR	103	ARG	4.0
55	K	53	GLN	4.0
66	V	118	PRO	4.0
10	BC	94	LEU	4.0
50	F	183	LEU	4.0
54	CU	77	LEU	4.0
79	DT	291	TRP	4.0
80	P0	76	LEU	4.0
1	AS	1436	G	4.0
35	CB	24	LYS	4.0
46	B	1352	G	4.0
46	CM	1431	G	4.0
55	K	168	SER	4.0
5	AX	372	THR	4.0
28	AA	25	ILE	4.0
48	CO	38	PHE	4.0
54	CU	169	TYR	4.0
82	L1	28	PHE	4.0
13	BF	145	ARG	4.0
29	BV	21	ARG	4.0
56	L	171	ARG	4.0
64	T	11	ARG	4.0
12	r	58	GLU	4.0
33	BZ	31	GLU	4.0

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Mol	Chain	Res	Type	RSRZ
49	E	203	GLU	4.0
53	CT	100	CYS	4.0
54	J	65	ALA	4.0
55	CV	161	ALA	4.0
56	L	33	GLU	4.0
63	S	85	ALA	4.0
1	AS	891	A	4.0
1	AS	932	A	4.0
46	CM	1410	A	4.0
72	b	69	LEU	4.0
82	L1	190	LEU	4.0
19	y	169	GLY	4.0
19	BL	168	LYS	4.0
19	BL	185	LYS	4.0
28	BU	75	VAL	4.0
29	AB	79	TRP	4.0
41	AN	50	LYS	4.0
47	C	134	LYS	4.0
51	CR	4	GLY	4.0
59	O	121	VAL	4.0
71	a	27	VAL	4.0
72	DM	97	LYS	4.0
73	DN	16	GLY	4.0
79	AR	60	LYS	4.0
49	E	93	MET	4.0
78	h	155	ASN	4.0
37	CD	26	SER	4.0
62	R	17	PHE	4.0
71	a	135	ASP	4.0
80	p0	24	SER	4.0
35	CB	25	THR	4.0
62	R	97	TYR	4.0
79	DT	80	TYR	4.0
8	BA	103	GLU	4.0
10	p	211	GLU	4.0
56	L	20	GLU	4.0
46	CM	939	G	4.0
28	BU	39	PRO	4.0
35	AH	30	LEU	4.0
41	AN	51	LEU	4.0
82	L1	16	LEU	4.0
55	K	41	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
7	AZ	161	GLY	4.0
1	1	2338	C	4.0
59	CZ	43	ARG	4.0
13	s	102	PHE	4.0
57	CX	3	ILE	4.0
63	S	35	ILE	4.0
6	l	90	ALA	4.0
6	AY	104	THR	4.0
22	2	30	TYR	4.0
22	2	99	SER	4.0
29	BV	46	ASP	4.0
49	E	202	THR	4.0
63	S	114	THR	4.0
39	AL	4	GLU	4.0
64	DE	101	GLU	4.0
1	1	1611	U	4.0
1	AS	2743	U	4.0
44	CK	29	LEU	4.0
63	DD	13	LYS	4.0
67	W	87	LYS	4.0
78	DS	141	LYS	4.0
7	m	105	VAL	4.0
18	BK	2	VAL	4.0
30	BW	24	PRO	4.0
66	V	129	GLN	4.0
79	AR	134	VAL	4.0
34	AG	11	GLY	4.0
79	AR	11	GLY	4.0
1	1	1556	G	4.0
53	CT	69	HIS	4.0
62	R	44	ARG	4.0
65	U	145	ARG	4.0
51	CR	205	PHE	4.0
55	K	43	ILE	4.0
58	N	13	PHE	4.0
64	T	69	ILE	4.0
46	CM	481	A	4.0
46	CM	509	A	4.0
46	CM	725	A	4.0
1	1	2114	C	4.0
1	AS	1192	C	4.0
5	AX	6	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
63	DD	48	TYR	4.0
68	DI	54	ALA	4.0
46	CM	695	C	4.0
79	DT	12	THR	4.0
79	DT	229	TYR	4.0
52	CS	52	GLU	4.0
7	AZ	104	LEU	4.0
48	D	47	LEU	4.0
18	BK	59	PRO	3.9
63	S	89	VAL	3.9
79	DT	277	VAL	3.9
1	AS	1013	U	3.9
4	j	250	GLN	3.9
55	K	80	GLY	3.9
62	R	114	HIS	3.9
73	c	80	HIS	3.9
69	Y	27	ILE	3.9
79	DT	248	TRP	3.9
6	AY	157	PHE	3.9
5	k	265	ALA	3.9
12	BE	25	ALA	3.9
39	CF	15	ALA	3.9
47	CN	14	ALA	3.9
55	CV	79	ALA	3.9
13	BF	115	LYS	3.9
19	BL	20	LYS	3.9
22	2	112	ASN	3.9
9	o	161	LEU	3.9
54	CU	54	LEU	3.9
55	CV	198	TYR	3.9
57	M	87	LEU	3.9
63	S	78	TYR	3.9
79	DT	42	LEU	3.9
1	1	3342	G	3.9
9	o	115	VAL	3.9
44	AQ	31	VAL	3.9
50	CQ	207	VAL	3.9
51	G	227	VAL	3.9
51	G	15	PRO	3.9
1	AS	26	C	3.9
3	4	21	C	3.9
46	B	1340	C	3.9

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Mol	Chain	Res	Type	RSRZ
46	CM	467	C	3.9
49	CP	88	GLY	3.9
52	H	92	ARG	3.9
71	a	66	GLY	3.9
43	CJ	47	GLN	3.9
68	X	51	ILE	3.9
82	ll	66	CYS	3.9
73	DN	17	HIS	3.9
53	CT	144	PHE	3.9
22	BO	55	LYS	3.9
50	F	8	LYS	3.9
79	DT	251	ALA	3.9
20	z	123	LEU	3.9
48	CO	47	LEU	3.9
56	L	36	LEU	3.9
60	P	117	LEU	3.9
67	DH	25	LEU	3.9
12	r	207	GLU	3.9
18	x	7	THR	3.9
48	CO	191	GLU	3.9
64	T	101	GLU	3.9
65	U	55	THR	3.9
76	DQ	5	ASN	3.9
52	CS	111	VAL	3.9
62	R	85	VAL	3.9
68	DI	39	VAL	3.9
13	s	41	SER	3.9
51	G	65	MET	3.9
51	CR	167	GLY	3.9
16	BI	57	GLN	3.9
79	AR	102	GLN	3.9
1	1	866	G	3.9
1	1	2452	G	3.9
1	AS	829	G	3.9
46	B	1480	G	3.9
46	CM	702	G	3.9
46	CM	1213	G	3.9
46	CM	1699	G	3.9
82	ll	155	ILE	3.9
57	M	27	PHE	3.9
1	1	2470	C	3.9
1	AS	2448	C	3.9

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Mol	Chain	Res	Type	RSRZ
19	y	168	LYS	3.9
73	DN	3	LYS	3.9
50	F	47	LEU	3.9
51	G	23	LEU	3.9
78	h	143	ALA	3.9
79	AR	169	ALA	3.9
1	AS	133	U	3.9
2	AT	78	U	3.9
46	B	94	U	3.9
4	AW	200	ARG	3.9
16	BI	81	TYR	3.9
53	I	179	VAL	3.9
54	J	56	VAL	3.9
62	R	115	TYR	3.9
75	e	41	VAL	3.9
80	p0	11	TYR	3.9
6	AY	363	ASN	3.9
52	H	66	ASN	3.9
61	DB	49	GLU	3.9
68	X	76	ASP	3.9
6	AY	49	GLN	3.9
47	CN	48	ILE	3.9
14	BG	131	LYS	3.9
71	DL	109	LYS	3.9
72	b	38	HIS	3.9
8	n	42	LEU	3.9
13	s	136	ALA	3.9
41	CH	6	LEU	3.9
51	CR	92	LEU	3.9
53	CT	198	ALA	3.9
58	N	114	ALA	3.9
63	DD	27	LEU	3.9
74	DO	53	ALA	3.9
79	AR	117	ALA	3.9
11	q	168	ARG	3.9
46	B	216	A	3.9
46	B	481	A	3.9
46	B	1329	A	3.9
65	DF	115	ARG	3.9
66	V	68	ARG	3.9
1	1	2447	G	3.9
1	AS	1483	G	3.9

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Mol	Chain	Res	Type	RSRZ
46	B	296	C	3.9
46	B	421	G	3.9
47	C	181	VAL	3.9
50	F	187	VAL	3.9
77	g	14	VAL	3.9
20	z	109	TYR	3.9
41	CH	32	THR	3.9
44	CK	30	GLU	3.9
67	W	98	THR	3.9
68	DI	41	GLU	3.9
16	BI	181	ASN	3.9
35	AH	14	ASN	3.9
46	B	713	U	3.9
7	m	156	GLY	3.9
72	b	91	PRO	3.9
33	AF	19	LYS	3.9
50	CQ	116	ILE	3.9
52	H	96	SER	3.9
52	H	140	SER	3.9
52	CS	79	SER	3.9
53	I	152	ASP	3.9
56	CW	140	ILE	3.9
59	O	71	ILE	3.9
72	DM	50	ILE	3.9
81	12	112	ILE	3.9
56	L	109	LEU	3.9
59	CZ	74	LEU	3.9
4	j	154	ALA	3.9
36	CC	71	ALA	3.9
51	G	14	ALA	3.9
51	G	84	ALA	3.9
58	N	61	ALA	3.9
8	n	170	ARG	3.8
6	AY	112	VAL	3.8
50	CQ	40	VAL	3.8
53	CT	102	VAL	3.8
79	AR	175	VAL	3.8
23	5	33	TYR	3.8
48	CO	122	GLU	3.8
1	AS	1554	A	3.8
6	AY	352	PRO	3.8
46	B	297	A	3.8

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Mol	Chain	Res	Type	RSRZ
46	B	1618	A	3.8
46	CM	667	A	3.8
49	CP	197	GLY	3.8
68	X	14	PRO	3.8
79	AR	58	PRO	3.8
7	AZ	61	ILE	3.8
50	F	173	ILE	3.8
51	CR	64	ILE	3.8
59	CZ	86	ILE	3.8
79	DT	167	ILE	3.8
1	AS	2473	C	3.8
46	B	222	C	3.8
44	AQ	25	GLN	3.8
49	CP	84	GLN	3.8
59	CZ	70	SER	3.8
74	d	32	PHE	3.8
79	AR	83	SER	3.8
5	k	47	LEU	3.8
25	BR	54	LEU	3.8
27	9	31	LEU	3.8
50	F	143	LEU	3.8
66	DG	62	ALA	3.8
6	AY	208	VAL	3.8
33	BZ	43	VAL	3.8
55	CV	101	VAL	3.8
56	CW	113	VAL	3.8
63	S	38	VAL	3.8
59	CZ	60	CYS	3.8
75	e	55	CYS	3.8
7	AZ	79	TYR	3.8
18	BK	47	TYR	3.8
51	CR	127	LYS	3.8
52	H	91	GLU	3.8
74	d	72	LYS	3.8
80	P0	40	GLU	3.8
4	AW	199	THR	3.8
17	BJ	186	THR	3.8
14	t	46	ILE	3.8
48	CO	63	GLY	3.8
49	E	110	ILE	3.8
55	K	158	ILE	3.8
61	DB	125	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
79	DT	244	PRO	3.8
6	l	111	ASN	3.8
17	w	30	ASN	3.8
73	c	69	ASN	3.8
63	DD	37	LEU	3.8
64	T	46	LEU	3.8
65	U	45	LEU	3.8
1	AS	824	A	3.8
6	AY	62	SER	3.8
8	n	77	ARG	3.8
18	x	126	ARG	3.8
20	BM	5	ARG	3.8
38	CE	57	ARG	3.8
46	CM	367	A	3.8
49	E	79	ARG	3.8
51	G	59	ARG	3.8
64	T	5	ARG	3.8
63	S	90	ALA	3.8
1	AS	2309	C	3.8
46	B	257	U	3.8
66	V	9	VAL	3.8
67	W	113	VAL	3.8
70	Z	17	VAL	3.8
1	AS	1130	G	3.8
38	AK	10	LYS	3.8
46	CM	1135	G	3.8
66	V	55	TYR	3.8
14	t	94	GLY	3.8
20	BM	54	PRO	3.8
47	CN	144	ILE	3.8
48	D	23	PRO	3.8
52	CS	113	ILE	3.8
65	U	22	ILE	3.8
74	d	68	GLY	3.8
4	AW	6	ARG	3.8
6	AY	74	ARG	3.8
22	2	31	LEU	3.8
56	L	142	ASN	3.8
35	AH	64	GLN	3.8
29	AB	127	ALA	3.8
10	BC	241	SER	3.8
79	DT	115	SER	3.8

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Mol	Chain	Res	Type	RSRZ
67	W	111	VAL	3.8
79	AR	8	VAL	3.8
59	CZ	50	LYS	3.8
66	DG	84	LYS	3.8
46	CM	444	A	3.8
46	CM	258	U	3.8
7	m	12	TYR	3.8
7	m	292	GLU	3.8
14	t	3	ILE	3.8
26	BS	109	TYR	3.8
47	C	204	TYR	3.8
47	CN	155	TYR	3.8
54	J	180	GLU	3.8
55	K	169	GLY	3.8
59	O	87	PRO	3.8
7	AZ	150	LEU	3.8
8	n	174	LEU	3.8
13	s	139	THR	3.8
21	BN	30	PHE	3.8
33	BZ	3	THR	3.8
50	F	177	LEU	3.8
56	L	71	PHE	3.8
58	N	115	PHE	3.8
61	DB	21	THR	3.8
63	DD	8	THR	3.8
77	g	38	LEU	3.8
46	CM	938	G	3.8
33	AF	36	GLN	3.8
47	C	74	ALA	3.8
68	X	26	ALA	3.8
10	BC	192	HIS	3.8
22	BO	109	VAL	3.8
36	CC	57	VAL	3.8
59	CZ	122	VAL	3.8
60	DA	5	HIS	3.8
45	CL	36	SER	3.8
65	U	27	LYS	3.8
80	p0	55	LYS	3.8
82	l1	138	VAL	3.8
74	DO	33	MET	3.8
82	L1	85	MET	3.8
16	v	151	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
51	G	64	ILE	3.8
6	I	318	PRO	3.8
16	BI	8	GLU	3.8
53	CT	169	TYR	3.8
54	J	138	TYR	3.8
65	U	60	GLU	3.8
10	p	153	LEU	3.8
73	c	31	PRO	3.8
26	BS	84	PHE	3.8
54	CU	21	PHE	3.8
63	S	59	PHE	3.8
79	DT	242	PHE	3.8
1	AS	76	A	3.8
1	AS	2186	A	3.8
46	B	1680	A	3.8
46	CM	497	U	3.8
69	Y	2	THR	3.8
1	1	1544	C	3.7
35	AH	63	ALA	3.7
39	CF	29	ALA	3.7
49	E	209	ALA	3.7
50	F	105	ALA	3.7
59	O	101	ALA	3.7
79	AR	154	ALA	3.7
43	AP	27	GLN	3.7
7	AZ	65	VAL	3.7
16	BI	117	ASN	3.7
27	9	44	ASN	3.7
33	BZ	80	VAL	3.7
53	I	56	ASN	3.7
53	I	171	LYS	3.7
69	DJ	74	VAL	3.7
72	b	78	VAL	3.7
76	f	6	VAL	3.7
16	v	150	TRP	3.7
49	CP	139	TRP	3.7
51	CR	18	TRP	3.7
1	AS	2455	G	3.7
1	AS	2577	G	3.7
1	AS	2756	G	3.7
13	BF	107	ASP	3.7
4	AW	49	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
79	AR	257	ILE	3.7
79	DT	199	ILE	3.7
14	BG	73	ARG	3.7
65	U	120	ARG	3.7
13	s	19	LEU	3.7
14	t	9	LEU	3.7
40	CG	13	LEU	3.7
43	AP	35	LEU	3.7
59	O	102	GLY	3.7
80	p0	93	LEU	3.7
9	BB	23	GLU	3.7
11	q	117	PHE	3.7
82	L1	43	PRO	3.7
7	AZ	98	ALA	3.7
32	AE	85	LYS	3.7
53	CT	79	LYS	3.7
71	DL	54	ALA	3.7
35	AH	65	VAL	3.7
46	B	221	U	3.7
46	B	749	U	3.7
63	DD	68	VAL	3.7
73	c	21	VAL	3.7
74	d	26	GLN	3.7
1	1	1021	A	3.7
1	AS	854	A	3.7
1	AS	1382	A	3.7
46	B	712	A	3.7
35	CB	18	ASN	3.7
63	DD	92	HIS	3.7
76	f	3	HIS	3.7
1	1	1188	C	3.7
1	AS	1834	C	3.7
46	B	1375	C	3.7
46	CM	1720	C	3.7
13	s	48	SER	3.7
16	v	125	SER	3.7
59	O	43	ARG	3.7
63	S	33	SER	3.7
79	AR	202	SER	3.7
82	L1	120	ILE	3.7
45	CL	72	ASP	3.7
51	G	88	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
43	CJ	83	LEU	3.7
51	G	107	GLY	3.7
51	CR	38	LEU	3.7
54	CU	122	LEU	3.7
33	AF	52	PRO	3.7
57	M	41	PHE	3.7
62	R	119	PHE	3.7
50	F	104	GLU	3.7
62	DC	109	PRO	3.7
63	DD	50	PRO	3.7
56	L	34	TYR	3.7
79	DT	5	GLU	3.7
10	BC	97	LYS	3.7
14	t	146	THR	3.7
25	7	119	ALA	3.7
56	CW	172	VAL	3.7
63	DD	47	VAL	3.7
79	DT	114	VAL	3.7
43	CJ	27	GLN	3.7
63	S	20	HIS	3.7
20	z	166	ASN	3.7
39	AL	49	ARG	3.7
44	CK	23	ARG	3.7
52	CS	65	ARG	3.7
1	1	1916	U	3.7
1	1	2465	U	3.7
1	1	2471	U	3.7
1	AS	544	U	3.7
46	B	490	U	3.7
46	CM	470	U	3.7
46	B	503	A	3.7
46	B	795	A	3.7
52	H	194	LEU	3.7
78	DS	190	LEU	3.7
49	CP	43	GLY	3.7
62	R	51	SER	3.7
69	Y	30	SER	3.7
70	Z	40	SER	3.7
79	AR	168	SER	3.7
73	DN	33	ASP	3.7
80	p0	26	PHE	3.7
2	AT	73	C	3.7

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Mol	Chain	Res	Type	RSRZ
25	7	98	PRO	3.7
41	AN	47	PRO	3.7
8	BA	139	LYS	3.7
12	BE	101	LYS	3.7
36	CC	49	LYS	3.7
46	B	1697	C	3.7
46	CM	1651	C	3.7
17	BJ	101	GLU	3.7
60	P	83	GLU	3.7
68	X	58	TYR	3.7
82	ll	107	TYR	3.7
10	BC	114	ALA	3.7
13	s	70	THR	3.7
16	BI	55	ALA	3.7
58	CY	63	THR	3.7
64	T	6	THR	3.7
66	V	139	THR	3.7
73	DN	90	THR	3.7
79	AR	73	THR	3.7
59	CZ	66	VAL	3.7
61	Q	74	VAL	3.7
71	DL	55	VAL	3.7
15	u	119	GLN	3.7
22	BO	8	ARG	3.7
28	AA	132	GLN	3.7
47	CN	45	MET	3.7
60	DA	55	ARG	3.7
66	V	70	GLN	3.7
70	Z	32	ARG	3.7
71	a	106	GLN	3.7
75	e	29	ARG	3.7
48	D	197	ILE	3.7
60	P	84	ILE	3.7
67	DH	107	ILE	3.7
80	p0	96	ILE	3.7
1	AS	341	G	3.7
1	AS	2429	G	3.7
75	e	66	LEU	3.7
82	L1	123	LEU	3.7
82	ll	163	LEU	3.7
4	AW	201	GLY	3.7
6	l	79	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
26	BS	36	LYS	3.7
28	AA	45	GLY	3.7
36	CC	74	LYS	3.7
48	CO	85	LYS	3.7
55	CV	80	GLY	3.7
73	c	93	LYS	3.7
79	DT	191	GLY	3.7
1	AS	2486	U	3.7
35	CB	40	SER	3.7
43	CJ	34	SER	3.7
46	B	206	U	3.7
58	N	23	PRO	3.7
74	DO	28	PRO	3.7
28	BU	31	GLU	3.7
59	CZ	25	GLU	3.7
59	CZ	47	GLU	3.7
61	DB	46	ASP	3.7
72	b	101	TYR	3.7
1	1	2439	A	3.7
7	m	157	ALA	3.7
79	DT	6	VAL	3.7
1	AS	2451	C	3.7
1	AS	2454	C	3.7
38	CE	25	ARG	3.7
43	CJ	87	ARG	3.7
82	ll	158	GLN	3.7
4	AW	209	HIS	3.7
10	p	65	ILE	3.7
54	J	132	ILE	3.7
4	AW	180	LEU	3.7
13	s	40	LEU	3.7
59	O	45	LEU	3.7
14	t	68	LYS	3.7
16	BI	122	ASN	3.7
35	CB	11	ASN	3.7
41	AN	48	LYS	3.7
56	CW	142	ASN	3.7
71	DL	99	LYS	3.7
22	BO	81	GLY	3.7
62	R	117	GLY	3.7
70	Z	107	PHE	3.7
73	DN	14	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
54	CU	59	PRO	3.6
56	CW	144	PRO	3.6
69	Y	77	PRO	3.6
1	1	545	G	3.6
1	1	2458	G	3.6
1	1	3298	G	3.6
7	m	62	ALA	3.6
8	n	108	GLU	3.6
49	CP	159	SER	3.6
79	AR	115	SER	3.6
35	AH	23	VAL	3.6
43	CJ	81	ALA	3.6
46	B	1672	G	3.6
47	CN	127	ARG	3.6
66	V	86	ARG	3.6
79	DT	38	ARG	3.6
1	1	1638	A	3.6
1	AS	2379	A	3.6
11	BD	114	ILE	3.6
15	u	32	ILE	3.6
16	BI	151	ILE	3.6
53	CT	52	ILE	3.6
54	CU	131	ILE	3.6
56	L	48	GLN	3.6
57	M	13	GLN	3.6
75	DP	13	ILE	3.6
78	h	188	LEU	3.6
33	AF	9	LYS	3.6
33	BZ	35	LYS	3.6
57	M	25	LYS	3.6
3	AU	91	C	3.6
54	J	57	PHE	3.6
81	12	121	PHE	3.6
6	l	143	VAL	3.6
6	l	199	ARG	3.6
22	BO	99	SER	3.6
28	AA	96	VAL	3.6
49	CP	87	ALA	3.6
55	K	28	GLU	3.6
55	K	74	ARG	3.6
60	P	151	ALA	3.6
62	R	74	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
51	G	223	SER	3.6
60	DA	6	SER	3.6
60	DA	19	SER	3.6
67	W	67	ARG	3.6
79	AR	308	ARG	3.6
52	H	147	THR	3.6
4	AW	225	ILE	3.6
10	BC	151	LEU	3.6
11	q	75	ILE	3.6
11	q	179	ILE	3.6
11	BD	10	LEU	3.6
51	CR	247	LEU	3.6
59	CZ	45	LEU	3.6
69	DJ	7	LEU	3.6
79	DT	68	ILE	3.6
82	ll	120	ILE	3.6
1	1	1018	U	3.6
1	1	1545	U	3.6
1	AS	2442	U	3.6
14	BG	129	LYS	3.6
17	BJ	52	LYS	3.6
39	CF	21	LYS	3.6
44	CK	61	LYS	3.6
59	O	90	LYS	3.6
1	1	2373	G	3.6
1	AS	2944	G	3.6
46	CM	1649	G	3.6
7	m	7	PHE	3.6
54	J	127	PHE	3.6
65	U	37	GLY	3.6
1	AS	917	A	3.6
55	K	18	ARG	3.6
69	DJ	3	ARG	3.6
1	AS	101	C	3.6
1	AS	1853	C	3.6
6	AY	52	ALA	3.6
36	CC	120	ALA	3.6
47	C	65	ALA	3.6
52	CS	173	ALA	3.6
54	CU	178	VAL	3.6
64	T	15	VAL	3.6
64	DE	15	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
66	DG	4	VAL	3.6
7	m	237	GLU	3.6
63	S	91	TYR	3.6
40	CG	3	SER	3.6
55	K	142	SER	3.6
59	CZ	49	SER	3.6
69	Y	122	SER	3.6
50	CQ	192	ASP	3.6
51	G	42	LEU	3.6
59	CZ	64	ASP	3.6
66	V	8	ASP	3.6
20	BM	53	LYS	3.6
36	CC	76	ILE	3.6
36	CC	118	ILE	3.6
58	N	24	LYS	3.6
63	DD	84	ILE	3.6
65	U	56	LYS	3.6
67	W	102	ILE	3.6
68	X	78	LEU	3.6
73	DN	32	LYS	3.6
79	AR	249	LEU	3.6
79	DT	82	LEU	3.6
82	l1	90	LEU	3.6
9	BB	11	GLN	3.6
64	T	120	GLN	3.6
78	DS	137	HIS	3.6
45	CL	69	PHE	3.6
71	DL	23	PHE	3.6
82	L1	110	PHE	3.6
19	BL	169	GLY	3.6
20	z	5	ARG	3.6
71	a	41	ARG	3.6
73	DN	28	ARG	3.6
29	BV	66	ASN	3.6
30	BW	57	ALA	3.6
35	CB	22	VAL	3.6
50	F	202	ALA	3.6
51	G	55	ALA	3.6
63	S	23	ALA	3.6
71	DL	27	VAL	3.6
79	DT	124	VAL	3.6
51	CR	157	ASN	3.6

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Mol	Chain	Res	Type	RSRZ
82	l1	12	ASN	3.6
1	1	1503	G	3.6
1	AS	3001	A	3.6
11	BD	3	TYR	3.6
17	BJ	68	LYS	3.6
36	AI	119	LYS	3.6
37	CD	69	LYS	3.6
41	AN	52	LYS	3.6
41	CH	52	LYS	3.6
46	CM	40	A	3.6
46	CM	712	A	3.6
46	CM	1476	A	3.6
75	DP	45	LYS	3.6
78	DS	148	TYR	3.6
4	j	135	ILE	3.6
11	BD	176	LEU	3.6
13	s	37	LEU	3.6
47	C	184	LEU	3.6
59	O	28	LEU	3.6
59	CZ	32	LEU	3.6
50	CQ	140	SER	3.6
59	O	130	SER	3.6
64	T	70	SER	3.6
79	AR	287	ILE	3.6
9	BB	20	THR	3.6
29	BV	6	THR	3.6
48	CO	28	ASP	3.6
48	CO	143	THR	3.6
61	Q	119	ASP	3.6
66	V	39	THR	3.6
5	k	377[A]	HIS	3.6
39	CF	38	PHE	3.6
55	CV	166	PHE	3.6
63	S	9	PHE	3.6
39	AL	3	ARG	3.6
47	C	100	GLY	3.6
56	CW	3	ARG	3.6
59	O	117	GLY	3.6
7	m	100	ALA	3.6
30	BW	59	ALA	3.6
52	CS	88	PRO	3.6
55	CV	145	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
59	CZ	116	VAL	3.6
68	DI	47	ALA	3.6
1	1	1557	U	3.6
7	m	99	TYR	3.6
7	AZ	163	LEU	3.6
9	o	129	GLU	3.6
50	CQ	9	LYS	3.6
51	G	134	LYS	3.6
49	E	56	LEU	3.6
52	CS	99	MET	3.6
54	J	150	LEU	3.6
56	L	72	GLU	3.6
64	T	31	ASN	3.6
65	DF	116	LEU	3.6
82	L1	165	LEU	3.6
7	m	185	ILE	3.6
34	AG	32	ILE	3.6
50	F	67	ILE	3.6
30	AC	31	SER	3.6
1	1	371	G	3.5
1	1	1563	A	3.5
1	1	2336	A	3.5
1	1	2469	A	3.5
1	AS	211	G	3.5
1	AS	2813	G	3.5
46	B	724	G	3.5
46	B	929	A	3.5
46	B	1755	G	3.5
61	DB	9	PHE	3.5
6	l	84	HIS	3.5
63	DD	20	HIS	3.5
45	i	108	GLY	3.5
79	DT	185	VAL	3.5
10	BC	115	ALA	3.5
37	CD	7	ALA	3.5
24	BQ	66	LYS	3.5
11	q	176	LEU	3.5
17	w	20	LEU	3.5
26	BS	40	LEU	3.5
11	BD	125	GLU	3.5
16	BI	62	TYR	3.5
16	BI	90	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
24	BQ	9	ASN	3.5
53	I	175	ILE	3.5
54	J	45	ILE	3.5
56	CW	42	ILE	3.5
79	DT	74	ILE	3.5
53	CT	28	TYR	3.5
1	1	3284	U	3.5
44	CK	26	THR	3.5
68	X	84	SER	3.5
80	p0	86	PHE	3.5
41	AN	44	GLN	3.5
6	l	80	GLY	3.5
25	7	78	HIS	3.5
29	BV	30	GLY	3.5
6	AY	320	LYS	3.5
11	q	181	VAL	3.5
21	0	36	VAL	3.5
15	BH	123	ALA	3.5
25	BR	102	LYS	3.5
28	BU	133	LYS	3.5
48	CO	55	LYS	3.5
60	P	150	VAL	3.5
80	P0	51	VAL	3.5
82	L1	201	VAL	3.5
51	G	18	TRP	3.5
67	W	80	ALA	3.5
71	a	134	ALA	3.5
1	1	1022	A	3.5
4	j	246	LEU	3.5
13	s	17	LEU	3.5
14	t	10	LEU	3.5
54	CU	149	LEU	3.5
56	L	93	LEU	3.5
1	AS	1345	G	3.5
1	AS	1370	G	3.5
1	AS	2704	G	3.5
46	B	761	G	3.5
46	CM	23	G	3.5
46	CM	1650	G	3.5
1	AS	247	C	3.5
10	BC	161	ILE	3.5
11	BD	113	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
52	H	196	GLU	3.5
54	J	42	ILE	3.5
79	DT	157	ILE	3.5
80	p0	32	ASN	3.5
47	C	162	CYS	3.5
19	y	96	PHE	3.5
57	M	67	THR	3.5
57	CX	90	THR	3.5
62	DC	119	PHE	3.5
82	ll	23	THR	3.5
1	1	2477	U	3.5
1	1	2950	U	3.5
1	AS	248	U	3.5
46	CM	29	U	3.5
46	CM	764	U	3.5
46	CM	989	U	3.5
66	V	5	SER	3.5
78	DS	181	GLN	3.5
6	l	146	VAL	3.5
36	CC	83	LYS	3.5
51	CR	25	GLY	3.5
53	I	80	GLY	3.5
55	K	183	GLY	3.5
51	G	46	VAL	3.5
66	DG	38	LYS	3.5
69	Y	121	VAL	3.5
35	CB	50	ALA	3.5
37	CD	71	LEU	3.5
64	T	34	LEU	3.5
26	BS	124	ILE	3.5
56	CW	45	ILE	3.5
69	Y	103	ILE	3.5
50	F	174	ARG	3.5
56	CW	41	GLU	3.5
1	AS	2519	A	3.5
10	BC	98	TYR	3.5
52	H	61	TYR	3.5
52	CS	77	TYR	3.5
68	X	21	ASN	3.5
80	p0	56	ASN	3.5
1	1	2451	C	3.5
6	AY	248	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
46	B	308	C	3.5
46	CM	131	C	3.5
1	1	863	G	3.5
1	AS	1085	G	3.5
1	AS	2443	G	3.5
1	AS	3002	G	3.5
46	B	1353	G	3.5
48	CO	45	LYS	3.5
25	BR	62	GLY	3.5
44	CK	21	SER	3.5
48	CO	130	SER	3.5
52	H	105	GLY	3.5
70	DK	120	VAL	3.5
78	h	137	HIS	3.5
79	AR	107	HIS	3.5
7	m	287	ALA	3.5
41	AN	8	ALA	3.5
69	Y	9	ASP	3.5
1	1	2068	U	3.5
56	CW	18	PRO	3.5
58	N	95	PRO	3.5
25	7	51	TRP	3.5
49	E	78	ILE	3.5
50	CQ	219	ILE	3.5
63	S	28	ILE	3.5
64	T	38	ILE	3.5
54	CU	108	ARG	3.5
10	BC	184	LYS	3.5
14	BG	180	LYS	3.5
24	BQ	64	LYS	3.5
36	CC	32	LYS	3.5
39	CF	28	ASN	3.5
40	CG	5	LYS	3.5
40	CG	10	LYS	3.5
54	J	144	LYS	3.5
71	DL	60	PHE	3.5
45	i	68	ASN	3.5
74	d	70	LYS	3.5
1	1	2480	A	3.5
1	AS	365	A	3.5
7	AZ	125	VAL	3.5
22	2	154	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
22	BO	59	GLY	3.5
54	CU	148	VAL	3.5
63	S	24	GLY	3.5
71	a	35	VAL	3.5
78	h	163	CYS	3.5
7	AZ	100	ALA	3.5
8	n	2	SER	3.5
21	BN	116	ALA	3.5
26	BS	38	LEU	3.5
30	BW	54	LEU	3.5
45	CL	84	SER	3.5
55	CV	99	SER	3.5
56	L	119	ALA	3.5
75	e	54	LEU	3.5
10	BC	100	PRO	3.5
46	B	707	C	3.5
17	BJ	57	ASP	3.5
52	CS	177	ILE	3.5
54	J	119	ASP	3.5
1	AS	2444	G	3.5
15	BH	120	ARG	3.5
62	R	121	ILE	3.5
46	CM	632	G	3.5
67	W	88	ARG	3.5
71	a	8	ARG	3.5
1	1	2475	U	3.5
1	1	2847	U	3.5
1	AS	216	U	3.5
45	i	61	GLU	3.4
46	B	276	U	3.5
46	B	609	U	3.5
53	CT	29	GLU	3.4
14	t	42	LYS	3.4
16	v	192	LYS	3.4
20	BM	45	TYR	3.4
60	P	70	LYS	3.4
76	f	46	LYS	3.4
36	CC	116	PHE	3.4
45	i	69	PHE	3.4
69	DJ	37	PHE	3.4
78	DS	147	TYR	3.4
22	BO	90	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
39	CF	31	VAL	3.4
6	AY	83	THR	3.4
10	p	215	LEU	3.4
10	BC	122	THR	3.4
11	BD	6	THR	3.4
12	r	132	GLY	3.4
7	AZ	146	LEU	3.4
20	BM	177	LEU	3.4
32	AE	40	THR	3.4
63	DD	71	GLY	3.4
72	b	73	GLY	3.4
39	CF	14	LEU	3.4
7	AZ	244	HIS	3.4
11	q	162	GLN	3.4
15	BH	127	ALA	3.4
39	CF	51	GLN	3.4
52	H	171	ALA	3.4
56	L	110	GLN	3.4
72	DM	75	LEU	3.4
75	e	33	LEU	3.4
65	DF	73	MET	3.4
4	AW	157	ILE	3.4
16	BI	108	ARG	3.4
39	CF	24	ILE	3.4
44	AQ	24	ARG	3.4
47	C	50	ILE	3.4
50	F	125	ARG	3.4
50	CQ	209	ILE	3.4
51	G	147	ILE	3.4
55	K	8	ARG	3.4
68	X	35	SER	3.4
60	P	25	TRP	3.4
1	1	1128	C	3.4
1	1	2897	C	3.4
1	AS	67	C	3.4
18	x	74	LYS	3.4
43	CJ	67	LYS	3.4
72	b	46	LYS	3.4
64	DE	79	GLU	3.4
78	h	153	GLU	3.4
79	DT	55	TYR	3.4
1	1	2832	U	3.4

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Mol	Chain	Res	Type	RSRZ
1	AS	134	U	3.4
1	AS	977	U	3.4
6	AY	223	VAL	3.4
12	BE	96	VAL	3.4
46	B	373	U	3.4
46	B	500	U	3.4
46	B	676	G	3.4
46	B	717	G	3.4
46	CM	511	U	3.4
49	E	48	VAL	3.4
28	AA	80	LEU	3.4
48	CO	37	THR	3.4
51	CR	184	THR	3.4
52	H	169	ASN	3.4
52	CS	100	ASN	3.4
61	Q	78	LEU	3.4
82	L1	179	LEU	3.4
7	m	9	THR	3.4
21	BN	34	THR	3.4
56	CW	11	THR	3.4
57	CX	45	ALA	3.4
75	DP	10	ALA	3.4
79	AR	211	ALA	3.4
79	DT	89	THR	3.4
25	BR	58	HIS	3.4
24	6	105	PRO	3.4
79	DT	57	ILE	3.4
79	DT	203	PRO	3.4
31	BX	105	SER	3.4
4	AW	46	LYS	3.4
25	BR	108	LYS	3.4
56	L	37	LYS	3.4
63	S	13	LYS	3.4
63	S	22	LYS	3.4
75	DP	11	LYS	3.4
78	DS	132	LYS	3.4
70	DK	90	ASP	3.4
52	H	144	GLU	3.4
52	CS	197	GLU	3.4
54	J	81	PHE	3.4
55	K	109	PHE	3.4
82	l1	33	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	1	2117	A	3.4
1	1	2502	A	3.4
46	CM	847	A	3.4
7	AZ	162	VAL	3.4
15	u	5	VAL	3.4
19	BL	82	VAL	3.4
19	BL	83	VAL	3.4
78	DS	144	VAL	3.4
79	DT	8	VAL	3.4
23	BP	108	LEU	3.4
48	D	120	LEU	3.4
66	V	132	LEU	3.4
79	DT	231	LEU	3.4
1	1	1577	C	3.4
6	AY	69	GLY	3.4
4	AW	229	ALA	3.4
7	AZ	196	ARG	3.4
1	AS	1012	U	3.4
21	0	34	THR	3.4
22	BO	52	MET	3.4
48	D	153	THR	3.4
51	G	50	ASN	3.4
52	CS	66	ASN	3.4
68	DI	1	MET	3.4
7	m	290	ILE	3.4
33	BZ	53	GLN	3.4
63	S	92	HIS	3.4
71	a	25	ILE	3.4
45	i	43	PRO	3.4
62	R	109	PRO	3.4
43	AP	15	LYS	3.4
45	i	67	LYS	3.4
51	G	53	LYS	3.4
54	CU	31	LYS	3.4
76	f	54	LYS	3.4
1	1	1740	G	3.4
1	AS	2453	G	3.4
46	CM	1460	G	3.4
79	AR	164	SER	3.4
80	p0	95	SER	3.4
6	l	91	PHE	3.4
33	AF	31	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
6	AY	287	VAL	3.4
7	AZ	52	VAL	3.4
23	BP	99	VAL	3.4
51	G	12	LEU	3.4
51	G	52	LEU	3.4
65	DF	4	VAL	3.4
66	V	4	VAL	3.4
66	V	80	TYR	3.4
73	c	30	VAL	3.4
74	d	4	VAL	3.4
75	e	44	VAL	3.4
77	g	49	LEU	3.4
79	AR	166	VAL	3.4
80	P0	18	LEU	3.4
80	P0	77	LEU	3.4
71	DL	8	ARG	3.4
6	l	166	ALA	3.4
7	m	67	ALA	3.4
22	BO	113	ALA	3.4
53	I	66	GLY	3.4
50	F	190	MET	3.4
54	J	90	ALA	3.4
56	CW	55	ALA	3.4
57	M	1	MET	3.4
59	CZ	101	ALA	3.4
1	1	2382	A	3.4
1	AS	56	A	3.4
6	AY	183	ILE	3.4
6	AY	250	ILE	3.4
9	o	42	ILE	3.4
11	BD	9	ILE	3.4
49	E	199	THR	3.4
53	CT	18	ILE	3.4
69	DJ	75	ILE	3.4
82	L1	117	ILE	3.4
14	t	151	GLN	3.4
6	AY	224	PRO	3.4
7	AZ	84	PRO	3.4
45	i	65	LYS	3.4
54	CU	97	LYS	3.4
56	CW	37	LYS	3.4
71	a	109	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
71	DL	22	GLN	3.4
79	AR	273	PRO	3.4
1	AS	189	U	3.4
1	AS	830	U	3.4
1	AS	1261	U	3.4
46	B	1354	U	3.4
46	B	1615	U	3.4
79	AR	291	TRP	3.4
35	AH	79	SER	3.4
47	C	102	PHE	3.4
51	G	24	SER	3.4
57	CX	27	PHE	3.4
61	Q	22	PHE	3.4
61	DB	50	SER	3.4
80	P0	24	SER	3.4
9	o	117	LEU	3.4
10	p	66	LEU	3.4
11	q	69	ARG	3.4
13	BF	19	LEU	3.4
16	BI	51	LEU	3.4
19	y	140	VAL	3.4
21	0	124	LEU	3.4
31	BX	103	LEU	3.4
33	BZ	76	LEU	3.4
37	CD	76	LEU	3.4
45	i	40	ASP	3.4
47	C	158	VAL	3.4
49	E	162	VAL	3.4
49	E	163	ARG	3.4
53	CT	26	VAL	3.4
60	P	106	ARG	3.4
64	T	110	VAL	3.4
67	DH	92	LEU	3.4
70	DK	124	VAL	3.4
74	DO	35	VAL	3.4
79	AR	298	LEU	3.4
80	P0	92	ASP	3.4
82	ll	73	ASP	3.4
1	1	2443	G	3.4
1	AS	1901	G	3.4
1	AS	2880	G	3.4
16	BI	6	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
43	CJ	43	TYR	3.4
7	m	208	MET	3.4
13	BF	105	GLY	3.4
52	H	26	ALA	3.4
55	K	173	ALA	3.4
56	L	73	GLY	3.4
67	DH	74	GLY	3.4
77	DR	56	MET	3.4
79	AR	250	ALA	3.4
79	DT	78	GLY	3.4
82	L1	211	GLY	3.4
7	AZ	148	ILE	3.4
11	BD	20	ILE	3.4
16	BI	36	ILE	3.4
16	BI	184	LYS	3.4
25	7	49	ILE	3.4
26	BS	49	LYS	3.4
39	CF	75	ILE	3.4
43	CJ	40	LYS	3.4
48	D	193	ILE	3.4
52	H	84	LYS	3.4
68	X	24	ILE	3.4
5	AX	139	THR	3.4
13	s	6	GLN	3.4
51	CR	68	GLN	3.4
61	Q	21	THR	3.4
66	DG	39	THR	3.4
27	9	98	ASN	3.3
41	CH	33	ASN	3.3
75	e	51	ASN	3.3
1	AS	2259	A	3.3
46	B	1386	A	3.3
46	B	1411	A	3.3
46	CM	410	A	3.3
46	CM	1694	A	3.3
66	DG	88	PHE	3.3
1	1	1574	C	3.3
16	BI	65	ARG	3.3
16	BI	164	LEU	3.3
1	AS	2925	U	3.3
4	j	168	VAL	3.3
6	AY	293	SER	3.3

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Mol	Chain	Res	Type	RSRZ
7	m	186	GLU	3.3
7	AZ	236	VAL	3.3
22	BO	9	SER	3.3
26	BS	110	VAL	3.3
35	AH	8	ARG	3.3
45	i	123	GLU	3.3
46	B	1406	C	3.3
46	CM	1467	C	3.3
50	F	7	SER	3.3
52	CS	96	SER	3.3
56	L	82	ARG	3.3
56	CW	148	VAL	3.3
60	P	114	ARG	3.3
61	Q	23	VAL	3.3
62	R	112	VAL	3.3
63	S	47	VAL	3.3
67	W	56	ARG	3.3
71	a	28	LEU	3.3
79	DT	7	LEU	3.3
80	p0	67	LEU	3.3
46	B	1541	U	3.3
14	BG	98	ASP	3.3
63	DD	63	ASP	3.3
6	AY	71	ALA	3.3
9	o	46	ALA	3.3
12	r	195	ALA	3.3
16	BI	185	ALA	3.3
22	BO	13	TYR	3.3
51	G	103	TYR	3.3
51	CR	190	GLY	3.3
62	DC	111	MET	3.3
64	T	21	TYR	3.3
20	z	135	LYS	3.3
78	h	184	GLY	3.3
78	DS	143	ALA	3.3
80	P0	62	ALA	3.3
56	CW	134	ILE	3.3
65	DF	22	ILE	3.3
6	AY	24	PRO	3.3
7	m	244	HIS	3.3
26	8	30	THR	3.3
50	F	115	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
53	I	210	GLN	3.3
54	CU	98	PRO	3.3
54	CU	118	HIS	3.3
57	M	88	PRO	3.3
60	DA	58	HIS	3.3
75	DP	27	GLN	3.3
79	AR	25	THR	3.3
79	AR	284	PRO	3.3
1	1	1489	G	3.3
1	AS	57	G	3.3
1	AS	1222	G	3.3
39	AL	57	ASN	3.3
46	B	1293	G	3.3
46	B	1508	G	3.3
53	I	197	ASN	3.3
63	DD	65	ARG	3.3
74	DO	81	ARG	3.3
23	5	37	LEU	3.3
47	CN	175	TRP	3.3
27	9	45	VAL	3.3
48	CO	113	LEU	3.3
51	CR	123	LEU	3.3
62	DC	80	LEU	3.3
68	X	55	LEU	3.3
73	c	86	VAL	3.3
7	m	6	GLU	3.3
1	1	1090	A	3.3
1	1	1693	A	3.3
7	AZ	27	LYS	3.3
20	BM	19	LYS	3.3
27	BT	90	SER	3.3
33	AF	37	LYS	3.3
44	AQ	59	SER	3.3
45	CL	71	LYS	3.3
46	B	578	A	3.3
46	B	1202	A	3.3
53	I	193	LYS	3.3
82	L1	39	LYS	3.3
82	l1	113	SER	3.3
7	m	169	GLY	3.3
11	BD	99	ILE	3.3
11	BD	161	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
19	BL	37	ALA	3.3
25	7	81	ALA	3.3
31	BX	45	ILE	3.3
36	CC	82	ALA	3.3
37	AJ	6	ILE	3.3
61	DB	14	ILE	3.3
63	DD	133	ALA	3.3
78	DS	133	ILE	3.3
79	DT	56	GLY	3.3
1	1	2483	U	3.3
1	1	2486	U	3.3
1	AS	2946	U	3.3
46	B	505	U	3.3
46	B	556	U	3.3
46	B	1338	U	3.3
1	AS	934	C	3.3
7	AZ	76	THR	3.3
15	BH	104	GLN	3.3
18	x	133	HIS	3.3
35	CB	73	GLN	3.3
50	CQ	222	PRO	3.3
51	CR	15	PRO	3.3
58	N	45	PRO	3.3
68	DI	33	GLN	3.3
80	P0	78	PRO	3.3
79	AR	41	THR	3.3
55	CV	8	ARG	3.3
6	AY	56	ASN	3.3
7	AZ	142	PHE	3.3
7	AZ	160	PHE	3.3
10	BC	137	LEU	3.3
10	BC	222	ASN	3.3
23	BP	52	ASN	3.3
45	CL	70	ASN	3.3
59	O	106	LEU	3.3
59	CZ	28	LEU	3.3
60	P	16	LEU	3.3
75	DP	66	LEU	3.3
82	l1	157	PHE	3.3
19	BL	150	VAL	3.3
32	AE	66	VAL	3.3
37	CD	43	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
47	CN	181	VAL	3.3
6	l	147	LYS	3.3
28	AA	22	LYS	3.3
45	CL	101	LYS	3.3
41	CH	3	GLU	3.3
48	CO	163	GLU	3.3
63	DD	49	GLU	3.3
1	AS	904	G	3.3
1	AS	1874	G	3.3
4	AW	231	SER	3.3
7	m	233	SER	3.3
7	AZ	247	ILE	3.3
10	BC	118	ALA	3.3
19	y	99	ALA	3.3
49	CP	196	SER	3.3
71	a	54	ALA	3.3
78	DS	154	GLY	3.3
80	P0	44	ALA	3.3
80	p0	65	GLY	3.3
4	AW	189	TYR	3.3
47	C	110	TYR	3.3
79	AR	55	TYR	3.3
1	l	1043	A	3.3
1	l	2963	A	3.3
1	AS	2475	U	3.3
19	y	170	ARG	3.3
46	B	944	U	3.3
47	C	80	THR	3.3
49	E	90	ARG	3.3
50	F	102	GLN	3.3
52	H	63	GLN	3.3
1	AS	27	C	3.3
10	BC	95	LEU	3.3
7	m	289	LYS	3.3
10	p	126	VAL	3.3
19	BL	50	LYS	3.3
42	CI	16	LYS	3.3
45	CL	100	LYS	3.3
47	CN	21	ASN	3.3
49	CP	83	LYS	3.3
52	H	106	LYS	3.3
54	J	175	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
55	CV	162	VAL	3.3
56	L	148	VAL	3.3
61	DB	11	VAL	3.3
74	DO	62	VAL	3.3
80	p0	104	VAL	3.3
61	DB	19	ASN	3.3
4	AW	204	MET	3.3
6	l	249	ILE	3.3
12	r	165	ILE	3.3
50	F	221	ALA	3.3
52	H	24	GLU	3.3
81	12	109	ILE	3.3
82	l1	100	ILE	3.3
62	R	99	GLY	3.3
30	BW	31	SER	3.3
51	CR	223	SER	3.3
57	M	64	TYR	3.3
74	d	48	SER	3.3
75	e	21	SER	3.3
9	o	163	ASP	3.3
61	DB	66	CYS	3.3
31	BX	68	PRO	3.3
50	CQ	174	ARG	3.3
52	H	112	ARG	3.3
55	K	25	ARG	3.3
66	DG	63	ARG	3.3
1	AS	2578	G	3.3
5	k	337	THR	3.3
6	AY	290	LEU	3.3
25	7	32	GLN	3.3
46	B	1724	G	3.3
46	CM	1723	G	3.3
52	CS	116	HIS	3.3
7	m	55	PHE	3.3
10	p	92	PHE	3.3
47	C	124	THR	3.3
47	C	201	LEU	3.3
48	D	203	THR	3.3
55	CV	197	PHE	3.3
56	CW	104	PHE	3.3
79	AR	9	LEU	3.3
15	BH	126	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
24	6	36	VAL	3.3
28	BU	14	VAL	3.3
47	C	123	VAL	3.3
55	K	75	LYS	3.3
60	DA	60	VAL	3.3
67	W	61	VAL	3.3
1	AS	2260	U	3.3
46	B	101	U	3.3
46	CM	637	U	3.3
16	BI	153	ASN	3.3
56	CW	74	ASN	3.3
59	CZ	100	TRP	3.3
67	W	83	MET	3.3
7	m	241	ALA	3.3
28	AA	5	ILE	3.3
47	C	48	ILE	3.3
56	L	56	ALA	3.3
63	S	133	ALA	3.3
67	W	64	ILE	3.3
67	DH	40	ILE	3.3
67	DH	90	ILE	3.3
78	h	162	GLU	3.3
48	CO	233	GLY	3.3
82	L1	170	GLY	3.3
12	BE	21	ARG	3.2
73	c	15	ARG	3.2
68	X	56	SER	3.2
12	BE	175	PRO	3.2
13	s	45	PRO	3.2
10	BC	245	ASP	3.2
19	y	166	LEU	3.2
55	CV	199	LEU	3.2
15	u	12	PHE	3.2
37	CD	12	LYS	3.2
40	CG	11	GLN	3.2
43	AP	53	GLN	3.2
53	CT	34	GLN	3.2
56	L	112	GLN	3.2
63	DD	25	LYS	3.2
10	BC	165	VAL	3.2
29	BV	144	VAL	3.2
52	CS	125	THR	3.2

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Mol	Chain	Res	Type	RSRZ
53	CT	157	VAL	3.2
62	R	75	VAL	3.2
82	L1	87	VAL	3.2
13	BF	122	ILE	3.2
63	S	64	ILE	3.2
79	AR	57	ILE	3.2
79	DT	178	TRP	3.2
24	BQ	26	ALA	3.2
51	CR	63	ALA	3.2
79	AR	76	ALA	3.2
82	l1	206	ILE	3.2
1	1	1815	U	3.2
1	1	2428	G	3.2
1	1	2743	U	3.2
1	AS	1890	U	3.2
1	AS	2162	U	3.2
46	B	596	U	3.2
61	Q	10	GLY	3.2
63	S	87	GLY	3.2
1	AS	156	A	3.2
1	AS	1485	A	3.2
1	AS	2419	A	3.2
46	B	1469	A	3.2
68	X	15	ARG	3.2
1	1	2468	C	3.2
1	AS	1224	C	3.2
30	BW	40	LYS	3.2
33	BZ	119	LYS	3.2
46	B	1610	C	3.2
48	D	61	LEU	3.2
51	CR	48	LEU	3.2
54	J	107	LYS	3.2
55	CV	17	LYS	3.2
55	CV	142	SER	3.2
56	CW	2	PRO	3.2
60	DA	16	LEU	3.2
68	DI	35	SER	3.2
79	AR	42	LEU	3.2
11	BD	117	PHE	3.2
10	p	204	VAL	3.2
23	BP	19	VAL	3.2
50	F	175	HIS	3.2

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Mol	Chain	Res	Type	RSRZ
50	CQ	151	GLN	3.2
56	L	25	ASP	3.2
58	CY	16	GLN	3.2
58	CY	18	HIS	3.2
63	S	93	GLN	3.2
66	V	113	VAL	3.2
52	CS	28	THR	3.2
62	R	78	THR	3.2
71	DL	6	THR	3.2
79	DT	41	THR	3.2
15	BH	114	MET	3.2
27	9	4	ILE	3.2
66	V	61	ILE	3.2
66	DG	124	ILE	3.2
69	Y	83	ILE	3.2
66	DG	41	ALA	3.2
19	BL	45	ASN	3.2
34	AG	84	ASN	3.2
63	S	129	GLY	3.2
75	DP	17	GLY	3.2
76	f	40	ARG	3.2
10	BC	135	TYR	3.2
10	BC	150	LYS	3.2
13	s	16	LYS	3.2
16	BI	197	LEU	3.2
39	CF	26	LYS	3.2
43	CJ	72	LEU	3.2
50	F	186	LYS	3.2
56	L	12	TYR	3.2
63	S	29	LYS	3.2
64	T	14	LYS	3.2
1	AS	3028	U	3.2
3	4	157	U	3.2
46	B	506	U	3.2
46	B	751	U	3.2
10	BC	43	PRO	3.2
26	BS	66	PRO	3.2
54	J	109	PRO	3.2
54	CU	128	PRO	3.2
77	g	58	PRO	3.2
1	1	960	G	3.2
1	1	2374	G	3.2

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Mol	Chain	Res	Type	RSRZ
1	1	2434	A	3.2
1	1	2459	G	3.2
1	AS	369	A	3.2
1	AS	2502	A	3.2
1	AS	3000	G	3.2
1	AS	3341	A	3.2
4	AW	4	VAL	3.2
19	y	62	VAL	3.2
46	B	1215	A	3.2
46	CM	1618	A	3.2
50	CQ	176	VAL	3.2
71	a	64	PHE	3.2
71	DL	24	VAL	3.2
78	DS	150	VAL	3.2
80	P0	35	SER	3.2
82	L1	50	SER	3.2
82	l1	162	VAL	3.2
13	BF	39	GLN	3.2
14	BG	102	GLN	3.2
15	u	35	GLN	3.2
19	BL	27	GLN	3.2
32	BY	16	HIS	3.2
54	CU	85	HIS	3.2
67	W	93	GLN	3.2
74	d	51	GLN	3.2
46	B	726	C	3.2
48	D	143	THR	3.2
56	L	147	THR	3.2
68	X	67	ASP	3.2
71	a	121	THR	3.2
76	DQ	42	CYS	3.2
82	L1	70	ASP	3.2
7	AZ	231	ILE	3.2
10	p	154	ILE	3.2
23	5	54	ILE	3.2
5	k	117	ARG	3.2
45	CL	80	ALA	3.2
49	CP	92	ARG	3.2
55	K	157	ALA	3.2
59	O	27	ALA	3.2
70	Z	23	ARG	3.2
75	DP	63	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
26	BS	118	GLY	3.2
64	DE	68	GLY	3.2
69	Y	89	TRP	3.2
79	AR	18	GLY	3.2
79	AR	310	TRP	3.2
16	v	175	ASN	3.2
30	BW	38	LYS	3.2
58	N	57	LYS	3.2
67	W	60	LYS	3.2
14	BG	77	LEU	3.2
17	BJ	53	LEU	3.2
19	y	138	LEU	3.2
29	BV	5	LEU	3.2
41	AN	6	LEU	3.2
49	E	220	LEU	3.2
52	CS	124	LEU	3.2
65	DF	17	LEU	3.2
78	h	190	LEU	3.2
28	BU	77	TYR	3.2
31	BX	60	TYR	3.2
71	DL	76	TYR	3.2
8	n	176	PHE	3.2
37	CD	23	PRO	3.2
9	BB	30	VAL	3.2
13	BF	127	PHE	3.2
47	C	107	PHE	3.2
50	F	204	PRO	3.2
79	AR	30	PRO	3.2
1	1	825	U	3.2
1	1	2482	U	3.2
46	B	1614	U	3.2
46	CM	75	U	3.2
49	E	80	SER	3.2
53	CT	104	GLN	3.2
74	DO	48	SER	3.2
5	k	263	THR	3.2
4	AW	176	ASP	3.2
5	AX	369	ARG	3.2
7	m	61	ILE	3.2
50	CQ	56	THR	3.2
52	H	29	ILE	3.2
53	CT	32	MET	3.2

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Mol	Chain	Res	Type	RSRZ
11	q	122	ARG	3.2
64	T	103	ASP	3.2
64	DE	82	ASP	3.2
78	h	133	ILE	3.2
79	AR	38	ARG	3.2
1	1	1116	A	3.2
15	BH	49	ALA	3.2
39	CF	59	ALA	3.2
46	B	1407	A	3.2
46	CM	988	A	3.2
49	CP	186	ALA	3.2
66	DG	96	ALA	3.2
79	DT	84	ALA	3.2
1	AS	1086	G	3.2
23	5	70	GLY	3.2
30	AC	3	LYS	3.2
30	BW	3	LYS	3.2
46	B	1472	G	3.2
46	CM	1240	G	3.2
80	P0	7	LYS	3.2
1	1	2309	C	3.2
46	B	1505	C	3.2
46	CM	656	C	3.2
45	CL	64	LEU	3.2
53	CT	4	ASN	3.2
68	X	50	ASN	3.2
12	r	218	TYR	3.2
26	BS	46	TYR	3.2
53	I	208	TYR	3.2
69	DJ	101	TYR	3.2
71	a	48	TYR	3.2
16	v	121	VAL	3.2
49	E	81	VAL	3.2
54	CU	69	VAL	3.2
63	DD	34	PRO	3.2
64	T	122	VAL	3.2
72	DM	91	PRO	3.2
79	DT	20	VAL	3.2
79	DT	104	PHE	3.2
79	DT	166	VAL	3.2
25	BR	57	ARG	3.2
48	D	204	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
48	CO	213	ARG	3.2
56	L	6	ARG	3.2
62	R	111	MET	3.2
65	DF	110	ARG	3.2
6	l	19	SER	3.2
37	AJ	96	SER	3.2
67	W	57	MET	3.2
67	DH	75	SER	3.2
77	g	56	MET	3.2
82	ll	119	GLN	3.2
10	p	89	ALA	3.2
10	p	199	ALA	3.2
65	DF	58	ALA	3.2
79	DT	200	THR	3.2
1	1	2450	U	3.1
1	1	2660	U	3.1
1	AS	1263	U	3.1
8	BA	156	LYS	3.1
47	CN	167	LYS	3.1
51	G	211	LYS	3.1
51	CR	10	LYS	3.1
57	CX	44	LYS	3.1
29	BV	116	GLY	3.1
41	AN	34	CYS	3.1
79	DT	11	GLY	3.1
8	BA	75	LEU	3.1
27	BT	76	LEU	3.1
48	CO	188	LEU	3.1
49	E	108	LEU	3.1
54	J	139	LEU	3.1
79	DT	180	LEU	3.1
82	L1	99	LEU	3.1
45	CL	116	GLU	3.1
1	1	3050	A	3.1
1	AS	323	A	3.1
46	B	298	A	3.1
5	k	365	PHE	3.1
9	o	170	ASN	3.1
18	BK	76	PHE	3.1
22	BO	15	PHE	3.1
23	BP	28	PHE	3.1
28	BU	118	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
29	AB	125	VAL	3.1
29	BV	61	PHE	3.1
43	CJ	36	PHE	3.1
49	E	219	PHE	3.1
49	CP	97	VAL	3.1
56	CW	141	VAL	3.1
58	N	42	PHE	3.1
63	S	48	TYR	3.1
71	a	79	VAL	3.1
71	DL	57	VAL	3.1
39	CF	71	PRO	3.1
1	1	240	C	3.1
1	1	795	G	3.1
46	B	1360	C	3.1
46	B	1471	C	3.1
46	CM	1472	G	3.1
46	CM	1671	G	3.1
60	P	124	ARG	3.1
66	V	89	ARG	3.1
27	9	99	ILE	3.1
45	i	83	HIS	3.1
47	C	149	MET	3.1
50	F	87	ILE	3.1
62	R	57	ILE	3.1
69	DJ	103	ILE	3.1
80	P0	39	HIS	3.1
17	w	123	GLN	3.1
34	CA	31	GLN	3.1
6	AY	201	THR	3.1
16	BI	3	ALA	3.1
22	BO	116	LYS	3.1
30	BW	22	LYS	3.1
47	C	91	ALA	3.1
47	CN	134	LYS	3.1
48	D	141	ALA	3.1
58	CY	24	LYS	3.1
79	AR	193	THR	3.1
79	DT	300	ALA	3.1
17	BJ	125	LEU	3.1
18	x	71	GLY	3.1
49	E	68	LEU	3.1
53	CT	17	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
57	M	68	LEU	3.1
69	Y	11	LEU	3.1
71	DL	18	LEU	3.1
75	e	46	GLY	3.1
82	L1	124	LEU	3.1
82	l1	89	ASP	3.1
1	1	78	U	3.1
1	AS	329	U	3.1
1	AS	1916	U	3.1
1	AS	2471	U	3.1
46	B	816	U	3.1
46	CM	1363	U	3.1
7	AZ	159	VAL	3.1
10	BC	198	VAL	3.1
11	BD	167	VAL	3.1
12	r	199	PHE	3.1
13	s	69	VAL	3.1
22	BO	67	VAL	3.1
35	CB	35	VAL	3.1
51	G	183	VAL	3.1
52	CS	56	VAL	3.1
55	CV	46	VAL	3.1
55	CV	109	PHE	3.1
64	DE	66	VAL	3.1
11	q	116	ASN	3.1
12	r	10	ARG	3.1
56	CW	120	ARG	3.1
69	Y	80	ASN	3.1
72	DM	77	ARG	3.1
82	l1	217	TYR	3.1
13	s	106	ILE	3.1
14	t	5	LYS	3.1
23	BP	56	ILE	3.1
46	B	682	A	3.1
35	CB	43	LYS	3.1
52	H	80	LYS	3.1
55	CV	144	LYS	3.1
78	DS	135	HIS	3.1
78	DS	191	LYS	3.1
82	l1	67	ILE	3.1
10	BC	149	ALA	3.1
10	BC	185	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
11	BD	8	GLN	3.1
14	BG	33	ALA	3.1
29	BV	38	GLN	3.1
52	H	85	ALA	3.1
56	L	4	ALA	3.1
56	L	169	ALA	3.1
66	V	41	ALA	3.1
10	p	163	LEU	3.1
20	z	131	THR	3.1
27	BT	109	LEU	3.1
31	BX	19	THR	3.1
46	CM	409	C	3.1
54	CU	150	LEU	3.1
57	M	49	LEU	3.1
63	DD	51	LEU	3.1
67	W	25	LEU	3.1
79	DT	13	LEU	3.1
82	L1	103	LEU	3.1
1	AS	1257	G	3.1
1	AS	2686	G	3.1
5	k	12	GLY	3.1
46	B	650	G	3.1
46	B	1441	G	3.1
46	B	1510	G	3.1
59	CZ	117	GLY	3.1
82	l1	211	GLY	3.1
33	AF	40	ASP	3.1
79	AR	248	TRP	3.1
7	m	273	ARG	3.1
13	BF	141	ARG	3.1
53	I	27	PHE	3.1
55	CV	18	ARG	3.1
56	L	132	ARG	3.1
56	CW	146	PHE	3.1
77	g	42	ARG	3.1
7	m	219	TYR	3.1
13	BF	123	TYR	3.1
35	CB	13	TYR	3.1
80	P0	22	TYR	3.1
1	1	2424	U	3.1
1	1	3320	U	3.1
1	AS	2691	U	3.1

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Mol	Chain	Res	Type	RSRZ
7	m	148	ILE	3.1
9	BB	93	ILE	3.1
10	p	46	ASN	3.1
10	p	121	LYS	3.1
14	t	122	LYS	3.1
20	z	15	ILE	3.1
30	AC	22	LYS	3.1
30	AC	40	LYS	3.1
50	F	5	ILE	3.1
52	CS	169	ASN	3.1
54	J	181	ILE	3.1
60	P	9	LYS	3.1
63	DD	30	ILE	3.1
71	a	112	LYS	3.1
8	n	31	ALA	3.1
16	BI	87	GLN	3.1
43	AP	47	GLN	3.1
51	CR	13	ALA	3.1
54	CU	32	ALA	3.1
58	CY	114	ALA	3.1
63	S	99	ALA	3.1
6	AY	151	LEU	3.1
19	BL	166	LEU	3.1
27	9	35	LEU	3.1
56	L	59	LEU	3.1
59	O	96	LEU	3.1
63	S	115	LEU	3.1
63	DD	56	LEU	3.1
72	DM	93	LEU	3.1
1	AS	2104	A	3.1
6	AY	81	GLY	3.1
10	BC	183	GLY	3.1
24	6	107	GLY	3.1
46	CM	1329	A	3.1
58	N	145	GLY	3.1
59	O	110	GLY	3.1
77	g	48	THR	3.1
23	5	55	SER	3.1
35	CB	49	SER	3.1
54	J	164	SER	3.1
64	T	13	SER	3.1
79	DT	163	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	AS	2782	C	3.1
13	s	143	ARG	3.1
25	BR	5	VAL	3.1
46	CM	1621	C	3.1
48	CO	30	PHE	3.1
51	G	194	VAL	3.1
53	I	153	VAL	3.1
53	CT	74	ARG	3.1
51	G	226	PHE	3.1
54	J	140	VAL	3.1
63	S	6	VAL	3.1
79	DT	152	VAL	3.1
5	k	136	LYS	3.1
6	AY	113	LYS	3.1
10	BC	246	LYS	3.1
56	L	2	PRO	3.1
62	R	37	CYS	3.1
66	V	38	LYS	3.1
78	DS	178	LYS	3.1
79	DT	27	PRO	3.1
1	1	1488	G	3.1
1	1	1664	G	3.1
1	1	2420	G	3.1
1	AS	656	G	3.1
46	B	1131	G	3.1
46	B	1650	G	3.1
49	CP	173	ILE	3.1
51	G	90	ILE	3.1
54	J	169	TYR	3.1
62	DC	54	MET	3.1
63	S	84	ILE	3.1
67	W	23	ILE	3.1
81	12	104	ILE	3.1
82	11	216	ILE	3.1
70	Z	89	ASN	3.1
60	DA	63	ALA	3.1
1	1	981	U	3.1
1	1	1522	U	3.1
1	AS	250	U	3.1
10	BC	163	LEU	3.1
17	w	27	GLN	3.1
18	x	34	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
21	0	8	GLN	3.1
26	8	47	GLN	3.1
28	BU	134	LEU	3.1
37	AJ	71	LEU	3.1
51	CR	23	LEU	3.1
54	J	162	LEU	3.1
54	CU	166	GLN	3.1
63	DD	88	LEU	3.1
65	U	12	GLN	3.1
70	DK	104	LEU	3.1
70	DK	133	LEU	3.1
71	DL	28	LEU	3.1
82	ll	123	LEU	3.1
4	j	75	THR	3.1
10	p	202	THR	3.1
22	BO	11	THR	3.1
33	BZ	125	GLY	3.1
49	CP	85	THR	3.1
79	DT	205	GLY	3.1
53	I	223	ARG	3.1
67	W	84	ARG	3.1
13	s	71	VAL	3.1
16	BI	132	VAL	3.1
50	F	207	VAL	3.1
54	J	41	SER	3.1
82	ll	151	VAL	3.1
54	J	165	PHE	3.1
66	DG	53	TRP	3.1
79	DT	45	TRP	3.1
4	j	177	LYS	3.1
23	5	77	LYS	3.1
43	CJ	9	LYS	3.1
46	CM	471	A	3.1
56	CW	51	LYS	3.1
63	S	101	LYS	3.1
25	BR	98	PRO	3.1
51	CR	147	ILE	3.1
75	e	47	PRO	3.1
10	p	223	TYR	3.1
66	V	104	CYS	3.1
1	1	1393	C	3.0
1	AS	2897	C	3.0

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Mol	Chain	Res	Type	RSRZ
46	CM	557	C	3.0
6	AY	277	LEU	3.0
17	BJ	59	LEU	3.0
45	CL	68	ASN	3.0
52	CS	85	ALA	3.0
60	P	75	LEU	3.0
71	a	15	ASN	3.0
72	DM	42	LEU	3.0
73	c	25	ASN	3.0
79	AR	222	LEU	3.0
82	L1	29	LEU	3.0
82	l1	190	LEU	3.0
5	AX	143	GLN	3.0
64	T	74	GLN	3.0
82	L1	199	GLN	3.0
1	AS	3342	G	3.0
23	5	48	GLY	3.0
28	BU	45	GLY	3.0
45	i	90	ARG	3.0
46	B	1470	G	3.0
46	CM	1724	G	3.0
55	K	143	ARG	3.0
55	CV	122	GLY	3.0
60	DA	68	GLY	3.0
79	AR	256	GLY	3.0
11	q	56	THR	3.0
71	DL	9	THR	3.0
1	AS	2477	U	3.0
6	l	313	VAL	3.0
10	BC	126	VAL	3.0
14	BG	22	VAL	3.0
46	B	778	U	3.0
48	CO	134	VAL	3.0
53	CT	195	VAL	3.0
60	P	52	VAL	3.0
62	DC	94	VAL	3.0
64	T	40	VAL	3.0
81	12	128	VAL	3.0
31	AD	24	LYS	3.0
8	n	129	GLU	3.0
36	AI	64	GLU	3.0
63	S	75	SER	3.0

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Mol	Chain	Res	Type	RSRZ
80	p0	34	SER	3.0
7	AZ	222	ILE	3.0
13	BF	114	ILE	3.0
49	CP	51	ILE	3.0
52	H	130	ILE	3.0
65	DF	76	PRO	3.0
78	DS	177	MET	3.0
79	AR	123	ILE	3.0
80	p0	25	ILE	3.0
82	L1	137	PRO	3.0
34	AG	44	TYR	3.0
8	n	75	LEU	3.0
15	BH	26	LEU	3.0
25	7	109	LEU	3.0
1	AS	313	A	3.0
1	AS	2535	A	3.0
28	BU	19	ALA	3.0
56	L	128	LEU	3.0
64	T	26	LEU	3.0
69	Y	126	LEU	3.0
73	DN	74	CYS	3.0
74	DO	71	ALA	3.0
80	P0	52	LEU	3.0
82	l1	34	LEU	3.0
46	B	956	A	3.0
46	CM	1719	A	3.0
4	AW	8	GLN	3.0
16	BI	73	ARG	3.0
23	BP	71	ASN	3.0
52	CS	122	HIS	3.0
56	L	155	HIS	3.0
73	DN	72	HIS	3.0
78	DS	187	HIS	3.0
33	AF	44	ARG	3.0
64	DE	5	ARG	3.0
71	a	105	ARG	3.0
79	DT	223	ASN	3.0
1	1	2797	C	3.0
16	BI	107	GLY	3.0
19	BL	183	GLY	3.0
35	AH	3	GLN	3.0
55	K	187	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
58	CY	68	GLY	3.0
71	a	122	GLN	3.0
46	B	1467	C	3.0
9	BB	12	LYS	3.0
23	BP	23	VAL	3.0
28	BU	23	VAL	3.0
37	CD	66	LYS	3.0
41	CH	17	LYS	3.0
48	CO	98	THR	3.0
49	E	153	VAL	3.0
51	G	217	THR	3.0
52	H	68	VAL	3.0
55	K	14	THR	3.0
56	L	130	THR	3.0
77	g	55	LYS	3.0
79	DT	174	THR	3.0
10	p	41	ILE	3.0
12	BE	99	ILE	3.0
28	AA	46	ILE	3.0
52	H	120	ILE	3.0
56	L	134	ILE	3.0
60	DA	84	ILE	3.0
72	DM	71	ILE	3.0
81	12	132	ILE	3.0
34	AG	91	PRO	3.0
46	B	480	U	3.0
46	CM	648	U	3.0
48	CO	190	PRO	3.0
53	CT	181	PRO	3.0
63	S	34	PRO	3.0
82	11	135	PRO	3.0
1	1	2425	G	3.0
1	AS	980	G	3.0
46	B	514	G	3.0
5	AX	47	LEU	3.0
7	m	211	LEU	3.0
9	BB	10	LEU	3.0
27	BT	35	LEU	3.0
36	CC	92	LEU	3.0
48	CO	54	LEU	3.0
51	G	101	LEU	3.0
53	CT	111	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
54	J	73	LEU	3.0
54	CU	124	ASP	3.0
65	U	32	LEU	3.0
70	Z	33	LEU	3.0
5	AX	107	ALA	3.0
9	o	134	TYR	3.0
9	o	187	TYR	3.0
16	v	62	TYR	3.0
21	0	81	TYR	3.0
45	CL	156	ALA	3.0
69	DJ	10	ALA	3.0
73	c	6	ALA	3.0
9	BB	98	ARG	3.0
38	CE	11	ARG	3.0
35	AH	69	HIS	3.0
43	CJ	88	CYS	3.0
6	l	222	ASN	3.0
8	n	128	LYS	3.0
27	9	81	GLN	3.0
32	AE	30	LYS	3.0
39	AL	40	GLN	3.0
51	G	193	GLY	3.0
54	J	166	GLN	3.0
58	N	22	ASN	3.0
80	P0	10	GLN	3.0
1	1	2427	A	3.0
46	B	423	A	3.0
46	CM	215	A	3.0
80	P0	84	VAL	3.0
28	AA	97	THR	3.0
45	CL	79	THR	3.0
49	E	205	THR	3.0
61	Q	33	THR	3.0
63	S	36	THR	3.0
64	DE	30	THR	3.0
66	DG	14	PHE	3.0
79	AR	299	PHE	3.0
82	l1	209	THR	3.0
11	BD	179	ILE	3.0
22	2	141	ILE	3.0
44	AQ	30	GLU	3.0
64	DE	50	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
29	BV	2	PRO	3.0
64	DE	22	PRO	3.0
5	AX	125	SER	3.0
7	AZ	103	LEU	3.0
26	8	29	SER	3.0
29	AB	78	LEU	3.0
33	BZ	92	SER	3.0
34	AG	97	SER	3.0
59	CZ	88	LEU	3.0
60	P	61	SER	3.0
63	S	104	LEU	3.0
72	b	51	LEU	3.0
79	AR	206	SER	3.0
80	P0	93	LEU	3.0
80	p0	77	LEU	3.0
5	AX	300	ARG	3.0
47	C	101	ARG	3.0
48	D	213	ARG	3.0
65	U	36	ARG	3.0
72	b	99	ALA	3.0
1	1	601	U	3.0
1	1	3162	U	3.0
13	s	126	ASP	3.0
46	B	1696	U	3.0
10	p	134	LYS	3.0
12	BE	123	HIS	3.0
20	BM	21	LYS	3.0
51	CR	62	LYS	3.0
61	DB	24	HIS	3.0
79	DT	192	HIS	3.0
1	1	659	G	3.0
1	1	1020	G	3.0
1	1	2128	G	3.0
1	AS	217	G	3.0
1	AS	283	G	3.0
1	AS	1510	G	3.0
6	l	356	GLN	3.0
49	E	214	GLY	3.0
59	CZ	102	GLY	3.0
61	Q	108	GLY	3.0
11	BD	25	VAL	3.0
26	BS	64	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
31	BX	33	VAL	3.0
32	BY	106	VAL	3.0
46	B	382	G	3.0
46	B	1214	G	3.0
46	B	1526	G	3.0
46	CM	387	G	3.0
46	CM	1500	G	3.0
49	E	191	VAL	3.0
63	S	76	GLN	3.0
65	U	89	GLN	3.0
75	DP	55	CYS	3.0
79	AR	114	VAL	3.0
10	p	262	ASN	3.0
20	BM	122	ASN	3.0
52	H	95	ASN	3.0
13	s	104	PHE	3.0
15	BH	12	PHE	3.0
69	Y	79	PHE	3.0
79	DT	275	PHE	3.0
51	G	26	THR	3.0
65	U	138	THR	3.0
67	DH	66	THR	3.0
68	DI	52	THR	3.0
79	DT	100	THR	3.0
7	m	60	ILE	3.0
12	r	166	ILE	3.0
65	U	14	ILE	3.0
71	a	75	ILE	3.0
9	BB	22	GLU	3.0
20	z	95	TRP	3.0
1	1	2158	A	3.0
1	AS	2436	A	3.0
22	2	128	LEU	3.0
25	BR	109	LEU	3.0
51	G	31	PRO	3.0
51	G	153	LEU	3.0
54	J	44	GLU	3.0
54	J	89	LEU	3.0
56	CW	70	LEU	3.0
76	DQ	4	GLU	3.0
46	B	1316	A	3.0
46	CM	297	A	3.0

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Mol	Chain	Res	Type	RSRZ
46	CM	577	A	3.0
79	DT	33	LEU	3.0
50	CQ	41	ARG	3.0
56	L	126	ARG	3.0
28	BU	98	SER	3.0
36	AI	82	ALA	3.0
48	CO	186	SER	3.0
54	CU	164	SER	3.0
67	DH	44	ALA	3.0
69	DJ	108	ALA	3.0
78	DS	170	ALA	3.0
1	1	2914	C	3.0
12	r	11	TYR	3.0
36	AI	70	TYR	3.0
46	B	1568	C	3.0
46	CM	763	C	3.0
51	CR	243	LYS	3.0
53	CT	171	LYS	3.0
71	DL	89	TYR	3.0
82	L1	217	TYR	3.0
13	s	132	GLY	3.0
16	BI	189	HIS	3.0
28	AA	68	VAL	3.0
52	CS	162	VAL	3.0
55	K	174	VAL	3.0
1	1	1778	U	3.0
1	AS	1623	U	3.0
1	AS	2613	U	3.0
46	B	1270	U	3.0
46	CM	35	U	3.0
5	AX	311	PHE	3.0
51	G	99	PHE	3.0
24	6	104	ASN	3.0
24	BQ	104	ASN	3.0
47	C	164	ASN	3.0
49	CP	151	CYS	3.0
59	CZ	79	CYS	3.0
60	P	21	ASN	3.0
62	DC	37	CYS	3.0
79	DT	297	ASN	3.0
13	BF	106	ILE	3.0
50	CQ	67	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
66	DG	116	ILE	3.0
72	DM	100	ILE	3.0
81	12	155	ILE	3.0
7	m	110	LEU	2.9
27	9	85	LEU	2.9
28	AA	74	LEU	2.9
47	C	18	LEU	2.9
48	CO	231	LEU	2.9
64	T	16	LEU	2.9
66	V	108	LEU	2.9
69	Y	26	LEU	2.9
6	AY	257	GLU	2.9
1	1	2686	G	2.9
1	AS	1218	G	2.9
1	AS	2184	G	2.9
1	AS	2447	G	2.9
1	AS	3225	G	2.9
33	AF	123	PRO	2.9
40	CG	24	PRO	2.9
56	CW	62	ARG	2.9
46	CM	1099	G	2.9
58	CY	23	PRO	2.9
65	DF	41	ARG	2.9
46	B	1723	G	2.9
79	AR	45	TRP	2.9
5	AX	237	LYS	2.9
10	p	147	LYS	2.9
11	q	72	LYS	2.9
16	v	55	ALA	2.9
16	BI	176	LYS	2.9
39	CF	37	LYS	2.9
63	DD	46	LYS	2.9
64	T	90	ALA	2.9
69	Y	43	LYS	2.9
70	Z	49	ALA	2.9
27	BT	43	TYR	2.9
45	i	39	SER	2.9
51	CR	54	TYR	2.9
57	M	60	SER	2.9
79	DT	195	TYR	2.9
1	1	1339	A	2.9
1	1	2462	A	2.9

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Mol	Chain	Res	Type	RSRZ
46	CM	479	A	2.9
46	CM	1473	A	2.9
64	DE	119	VAL	2.9
64	T	27	ASP	2.9
66	V	74	GLY	2.9
69	DJ	48	GLY	2.9
73	DN	50	VAL	2.9
77	g	4	VAL	2.9
77	g	5	HIS	2.9
79	AR	309	VAL	2.9
11	BD	61	ASP	2.9
55	K	163	ASP	2.9
79	DT	161	ASP	2.9
80	p0	98	ASP	2.9
50	CQ	168	PHE	2.9
52	CS	43	PHE	2.9
56	CW	71	PHE	2.9
63	DD	93	GLN	2.9
1	AS	487	C	2.9
4	j	112	ILE	2.9
33	AF	51	ILE	2.9
61	DB	34	ILE	2.9
61	DB	76	ILE	2.9
77	g	36	MET	2.9
82	L1	216	ILE	2.9
82	l1	4	ILE	2.9
1	1	1551	U	2.9
1	1	1836	U	2.9
1	1	2153	U	2.9
3	AU	22	U	2.9
4	AW	3	ARG	2.9
15	BH	124	THR	2.9
17	BJ	142	LEU	2.9
46	CM	1722	U	2.9
48	CO	106	THR	2.9
50	F	111	LEU	2.9
52	H	25	LEU	2.9
52	H	87	CYS	2.9
29	BV	43	THR	2.9
32	AE	105	THR	2.9
53	CT	109	LEU	2.9
56	L	80	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
57	CX	80	LEU	2.9
60	P	99	ARG	2.9
71	a	96	LEU	2.9
79	AR	268	LEU	2.9
4	AW	10	LYS	2.9
13	s	15	GLU	2.9
14	BG	48	PRO	2.9
24	6	68	GLU	2.9
41	AN	17	LYS	2.9
47	C	116	LYS	2.9
51	CR	31	PRO	2.9
62	DC	106	GLU	2.9
82	l1	137	PRO	2.9
28	AA	110	ALA	2.9
37	AJ	82	ALA	2.9
55	CV	19	ALA	2.9
82	l1	71	ALA	2.9
48	CO	80	SER	2.9
52	H	151	SER	2.9
53	I	169	TYR	2.9
55	CV	12	SER	2.9
78	h	147	TYR	2.9
5	k	220	VAL	2.9
26	8	51	VAL	2.9
77	g	45	VAL	2.9
82	L1	162	VAL	2.9
7	m	182	GLY	2.9
7	AZ	114	GLY	2.9
19	BL	2	GLY	2.9
64	T	2	GLY	2.9
1	1	2435	G	2.9
1	1	2444	G	2.9
1	AS	2579	G	2.9
29	BV	129	PHE	2.9
46	B	843	G	2.9
46	B	1373	G	2.9
54	CU	165	PHE	2.9
56	CW	123	HIS	2.9
62	DC	33	PHE	2.9
6	AY	165	ASP	2.9
7	AZ	32	GLN	2.9
8	n	10	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
9	o	167	ILE	2.9
18	x	140	GLN	2.9
19	BL	135	GLN	2.9
20	BM	174	GLN	2.9
23	5	44	ASP	2.9
71	a	22	GLN	2.9
82	L1	173	ASP	2.9
22	BO	48	ILE	2.9
28	AA	12	ILE	2.9
28	BU	25	ILE	2.9
49	CP	99	ILE	2.9
50	CQ	185	ILE	2.9
62	R	54	MET	2.9
1	1	1089	A	2.9
1	1	1575	A	2.9
1	1	2310	A	2.9
1	AS	351	A	2.9
4	AW	104	LEU	2.9
9	o	10	LEU	2.9
16	BI	162	ARG	2.9
26	8	33	ARG	2.9
46	B	364	A	2.9
46	B	367	A	2.9
46	CM	129	A	2.9
46	CM	929	A	2.9
48	CO	26	ARG	2.9
49	CP	56	LEU	2.9
52	H	108	LEU	2.9
56	L	150	LEU	2.9
60	DA	117	LEU	2.9
62	R	25	LEU	2.9
72	b	83	LEU	2.9
72	DM	80	LEU	2.9
72	DM	81	ARG	2.9
75	DP	33	LEU	2.9
78	DS	188	LEU	2.9
80	p0	76	LEU	2.9
4	j	243	THR	2.9
6	l	320	LYS	2.9
23	BP	85	LYS	2.9
26	BS	39	LYS	2.9
36	CC	73	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
41	CH	34	CYS	2.9
42	AO	16	LYS	2.9
45	CL	96	LYS	2.9
51	G	22	LYS	2.9
67	DH	69	THR	2.9
79	AR	174	THR	2.9
80	P0	103	ASN	2.9
82	ll	31	THR	2.9
1	1	83	C	2.9
1	1	1194	C	2.9
1	1	2448	C	2.9
1	AS	3104	C	2.9
7	m	257	GLU	2.9
9	BB	8	GLU	2.9
6	l	66	TRP	2.9
20	z	168	ALA	2.9
20	BM	63	ALA	2.9
33	BZ	94	ALA	2.9
35	CB	32	ALA	2.9
38	AK	41	ALA	2.9
41	CH	25	ALA	2.9
46	B	187	C	2.9
46	B	274	C	2.9
54	J	182	PRO	2.9
66	V	58	ALA	2.9
67	W	44	ALA	2.9
67	W	73	GLU	2.9
46	B	121	U	2.9
46	B	703	U	2.9
46	B	1091	U	2.9
46	B	1695	U	2.9
46	CM	655	U	2.9
13	s	130	VAL	2.9
17	w	24	VAL	2.9
29	AB	145	VAL	2.9
69	Y	101	TYR	2.9
71	a	12	VAL	2.9
80	P0	104	VAL	2.9
80	P0	105	VAL	2.9
9	o	162	SER	2.9
11	BD	92	PHE	2.9
45	CL	110	SER	2.9

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Mol	Chain	Res	Type	RSRZ
55	K	167	GLY	2.9
79	AR	36	GLY	2.9
80	p0	2	GLY	2.9
69	Y	128	PHE	2.9
19	BL	114	ILE	2.9
4	AW	179	LEU	2.9
8	n	29	LEU	2.9
9	BB	239	GLN	2.9
23	BP	109	GLN	2.9
34	CA	101	MET	2.9
37	CD	55	ARG	2.9
47	C	188	ILE	2.9
50	F	219	ILE	2.9
52	CS	172	ILE	2.9
60	P	71	ILE	2.9
61	Q	34	ILE	2.9
62	DC	89	MET	2.9
67	W	85	ILE	2.9
68	X	36	ILE	2.9
69	Y	34	ILE	2.9
50	CQ	47	LEU	2.9
54	CU	139	LEU	2.9
55	K	121	LEU	2.9
65	DF	131	LEU	2.9
69	Y	7	LEU	2.9
79	DT	246	ARG	2.9
82	ll	38	LEU	2.9
7	AZ	137	ASP	2.9
14	t	131	LYS	2.9
51	G	79	ASP	2.9
52	CS	106	LYS	2.9
54	CU	80	LYS	2.9
59	O	124	LYS	2.9
66	V	131	ASP	2.9
79	AR	44	LYS	2.9
80	p0	43	LYS	2.9
7	m	28	THR	2.9
1	1	102	G	2.9
1	1	2432	G	2.9
1	1	2548	G	2.9
1	AS	169	G	2.9
1	AS	1281	G	2.9

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Mol	Chain	Res	Type	RSRZ
1	AS	1479	G	2.9
1	AS	2998	G	2.9
7	AZ	157	ALA	2.9
10	BC	116	ALA	2.9
10	BC	221	ALA	2.9
13	BF	144	ALA	2.9
14	t	195	ALA	2.9
22	BO	77	ASN	2.9
26	BS	81	THR	2.9
47	C	96	THR	2.9
47	C	199	PRO	2.9
53	I	4	ASN	2.9
67	W	48	ASN	2.9
74	d	23	THR	2.9
77	g	50	THR	2.9
41	CH	31	ALA	2.9
46	B	494	G	2.9
46	B	683	G	2.9
46	B	702	G	2.9
46	B	939	G	2.9
46	B	1230	G	2.9
46	CM	653	G	2.9
49	E	49	GLU	2.9
66	V	115	GLU	2.9
68	X	54	ALA	2.9
74	DO	56	CYS	2.9
79	DT	28	ALA	2.9
1	1	1584	A	2.9
1	AS	99	A	2.9
1	AS	108	A	2.9
1	AS	707	A	2.9
1	AS	1255	A	2.9
1	AS	1589	A	2.9
1	AS	2439	A	2.9
1	AS	2581	A	2.9
46	B	179	A	2.9
46	B	350	A	2.9
46	CM	1050	A	2.9
10	BC	132	VAL	2.9
17	BJ	37	VAL	2.9
52	H	133	VAL	2.9
67	W	55	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
69	DJ	33	VAL	2.9
80	P0	50	VAL	2.9
1	AS	1244	C	2.9
1	AS	1832	C	2.9
1	1	731	U	2.9
1	AS	183	U	2.9
1	AS	326	U	2.9
1	AS	359	U	2.9
1	AS	772	U	2.9
5	k	379	PHE	2.9
6	AY	58	GLY	2.9
7	m	71	GLY	2.9
7	AZ	293	PHE	2.9
18	x	76	PHE	2.9
20	z	16	GLY	2.9
24	6	111	GLY	2.9
35	AH	48	GLY	2.9
41	CH	13	TYR	2.9
46	B	1351	U	2.9
46	B	1725	U	2.9
46	CM	556	U	2.9
47	C	38	TYR	2.9
57	M	66	TYR	2.9
64	DE	53	TYR	2.9
19	BL	3	ARG	2.9
20	z	97	ARG	2.9
52	H	82	PHE	2.9
75	DP	29	ARG	2.9
6	l	279	SER	2.9
8	n	65	SER	2.9
11	q	182	SER	2.9
11	BD	53	ILE	2.9
12	r	219	SER	2.9
8	BA	131	LYS	2.9
10	BC	242	LYS	2.9
16	v	169	LYS	2.9
20	z	106	LEU	2.9
20	z	143	ILE	2.9
26	8	88	ILE	2.9
27	9	97	ILE	2.9
30	AC	7	HIS	2.9
31	BX	102	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
45	i	84	SER	2.9
49	E	105	HIS	2.9
49	CP	66	LEU	2.9
50	CQ	139	ILE	2.9
50	CQ	183	LEU	2.9
52	CS	194	LEU	2.9
56	CW	39	LYS	2.9
59	O	36	LEU	2.9
59	CZ	106	LEU	2.9
60	P	147	SER	2.9
64	T	17	ILE	2.9
64	T	112	SER	2.9
67	W	49	ILE	2.9
78	DS	159	LEU	2.9
79	AR	16	HIS	2.9
79	AR	33	LEU	2.9
79	AR	307	ILE	2.9
79	DT	206	SER	2.9
24	6	110	LYS	2.9
44	CK	7	LYS	2.9
53	I	30	LYS	2.9
64	T	23	LYS	2.9
66	V	92	LYS	2.9
73	DN	37	LYS	2.9
17	w	32	GLN	2.9
32	BY	104	GLN	2.9
36	AI	62	GLN	2.9
70	Z	27	GLN	2.9
82	L1	35	GLN	2.9
22	2	41	ASP	2.9
28	BU	30	ASP	2.9
40	AM	32	ASP	2.9
50	F	170	ASP	2.9
55	K	6	ASP	2.9
57	M	26	ASP	2.9
7	AZ	18	THR	2.9
37	CD	22	ALA	2.9
43	AP	103	ALA	2.9
51	G	213	ALA	2.9
52	CS	67	PRO	2.9
53	CT	205	ALA	2.9
79	DT	131	THR	2.9

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Mol	Chain	Res	Type	RSRZ
10	BC	230	ASN	2.9
11	q	169	ASN	2.9
12	r	205	ASN	2.9
18	x	75	GLU	2.9
24	6	9	ASN	2.9
36	CC	102	GLU	2.9
50	CQ	136	GLU	2.9
51	G	188	ASN	2.9
52	H	104	ASN	2.9
82	L1	114	GLU	2.9
18	x	24	VAL	2.9
51	CR	76	VAL	2.9
66	DG	6	VAL	2.9
66	DG	37	VAL	2.9
7	AZ	71	GLY	2.9
1	1	1487	A	2.9
4	AW	89	TYR	2.9
11	q	92	PHE	2.9
13	BF	143	ARG	2.9
16	BI	59	PHE	2.9
26	BS	32	PHE	2.9
27	BT	28	ARG	2.9
35	AH	7	TYR	2.9
38	AK	2	GLY	2.9
38	CE	39	TYR	2.9
50	F	26	PHE	2.9
50	F	84	GLY	2.9
51	CR	221	ARG	2.9
53	CT	84	TYR	2.9
54	J	39	PHE	2.9
60	P	59	GLY	2.9
61	DB	123	ARG	2.9
77	g	54	ARG	2.9
1	1	2547	G	2.9
1	AS	215	G	2.9
1	AS	1025	G	2.9
1	AS	1219	A	2.9
1	AS	2432	G	2.9
1	AS	3194	G	2.9
5	AX	84	MET	2.9
16	v	142	ILE	2.9
35	AH	37	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
36	AI	14	LYS	2.9
46	B	479	A	2.9
39	CF	65	LEU	2.9
41	CH	9	LEU	2.9
45	i	102	LYS	2.9
46	B	639	G	2.9
46	B	723	G	2.9
46	B	1183	G	2.9
46	B	1736	A	2.9
46	CM	216	A	2.9
26	BS	82	LEU	2.9
31	BX	95	LEU	2.9
6	l	59	HIS	2.8
17	BJ	56	HIS	2.8
32	AE	70	MET	2.9
50	F	12	LEU	2.9
50	CQ	203	LEU	2.9
51	G	245	ILE	2.9
54	CU	37	LEU	2.9
55	CV	158	ILE	2.9
62	R	49	LEU	2.9
63	S	123	MET	2.9
64	DE	7	LYS	2.9
68	DI	34	ILE	2.9
72	b	88	ILE	2.9
72	DM	46	LYS	2.9
72	DM	69	LEU	2.9
78	h	172	ILE	2.9
79	AR	199	ILE	2.9
1	1	321	C	2.8
1	1	978	C	2.8
1	1	2457	C	2.8
1	AS	2465	U	2.8
18	x	165	GLN	2.8
19	y	34	SER	2.8
21	0	60	SER	2.8
46	B	377	U	2.8
46	B	493	U	2.8
46	B	502	U	2.8
46	B	1364	U	2.8
46	B	1698	U	2.8
46	CM	825	U	2.8

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Mol	Chain	Res	Type	RSRZ
46	CM	1328	U	2.8
52	CS	152	SER	2.8
46	CM	1462	C	2.8
50	F	220	PRO	2.8
51	G	63	ALA	2.8
59	CZ	93	ASP	2.8
45	i	34	THR	2.8
45	i	87	PRO	2.8
56	L	111	THR	2.8
68	X	52	THR	2.8
71	DL	16	PRO	2.8
79	AR	12	THR	2.8
27	9	88	GLU	2.8
36	AI	18	GLU	2.8
49	CP	203	GLU	2.8
51	CR	199	GLU	2.8
57	M	18	GLU	2.8
74	DO	15	GLU	2.8
5	k	259	ASN	2.8
16	BI	86	ASN	2.8
47	CN	31	VAL	2.8
51	CR	70	VAL	2.8
52	CS	114	VAL	2.8
58	CY	64	VAL	2.8
71	a	57	VAL	2.8
7	m	35	ARG	2.8
38	CE	24	ARG	2.8
80	p0	60	ARG	2.8
14	t	187	LYS	2.8
23	5	13	LYS	2.8
38	AK	43	LYS	2.8
51	G	7	LYS	2.8
65	U	49	LYS	2.8
4	AW	71	LEU	2.8
48	D	140	ILE	2.8
48	CO	110	LEU	2.8
48	CO	189	ILE	2.8
51	CR	90	ILE	2.8
52	H	77	TYR	2.8
53	I	141	ILE	2.8
59	O	32	LEU	2.8
66	DG	21	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
78	h	169	GLY	2.8
7	m	199	ILE	2.8
12	BE	17	TYR	2.8
14	BG	184	ILE	2.8
16	v	174	ILE	2.8
16	BI	30	TYR	2.8
21	0	107	TYR	2.8
34	CA	103	TYR	2.8
77	DR	36	MET	2.8
79	DT	302	TYR	2.8
82	L1	210	MET	2.8
11	BD	64	HIS	2.8
1	1	62	A	2.8
1	1	3340	A	2.8
1	AS	324	A	2.8
1	AS	1854	A	2.8
1	AS	2954	A	2.8
24	BQ	29	SER	2.8
34	AG	62	SER	2.8
40	CG	6	SER	2.8
43	CJ	82	GLN	2.8
46	B	1357	A	2.8
53	CT	233	SER	2.8
79	DT	75	SER	2.8
5	k	23	ALA	2.8
14	BG	53	ALA	2.8
29	AB	149	ALA	2.8
35	AH	75	ALA	2.8
45	i	51	ALA	2.8
79	DT	117	ALA	2.8
79	DT	252	ALA	2.8
1	1	333	G	2.8
1	1	1521	G	2.8
1	1	1848	G	2.8
1	AS	2763	G	2.8
46	B	779	U	2.8
46	B	1240	G	2.8
46	CM	277	G	2.8
46	CM	654	G	2.8
62	R	73	PRO	2.8
22	2	29	THR	2.8
41	CH	42	THR	2.8

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Mol	Chain	Res	Type	RSRZ
48	CO	154	THR	2.8
50	CQ	205	ASP	2.8
52	CS	145	ASP	2.8
1	1	1853	C	2.8
5	k	197	GLU	2.8
16	BI	155	VAL	2.8
31	BX	37	ARG	2.8
33	BZ	74	VAL	2.8
46	B	1006	C	2.8
46	CM	529	C	2.8
51	CR	252	GLU	2.8
53	I	222	GLU	2.8
58	N	139	VAL	2.8
73	c	39	VAL	2.8
79	AR	171	TRP	2.8
10	BC	124	LYS	2.8
20	BM	34	ASN	2.8
28	BU	127	ASN	2.8
29	AB	74	ASN	2.8
29	BV	34	LYS	2.8
6	AY	98	GLY	2.8
7	AZ	87	GLY	2.8
19	BL	119	GLY	2.8
21	BN	64	ILE	2.8
22	2	48	ILE	2.8
28	AA	51	LEU	2.8
28	BU	20	GLY	2.8
31	AD	45	ILE	2.8
34	CA	32	ILE	2.8
49	E	51	ILE	2.8
50	CQ	22	LEU	2.8
52	CS	199	ILE	2.8
54	J	13	LEU	2.8
54	J	34	LEU	2.8
55	CV	30	GLY	2.8
59	O	44	GLY	2.8
61	Q	28	LEU	2.8
64	DE	58	MET	2.8
66	V	65	ILE	2.8
74	d	73	LEU	2.8
74	d	79	PHE	2.8
75	e	53	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
79	AR	56	GLY	2.8
79	AR	218	ILE	2.8
7	AZ	99	TYR	2.8
28	BU	18	TYR	2.8
22	BO	58	HIS	2.8
38	CE	16	HIS	2.8
56	L	123	HIS	2.8
10	p	78	GLN	2.8
10	BC	90	GLN	2.8
55	CV	53	GLN	2.8
65	U	63	GLN	2.8
7	AZ	187	ALA	2.8
24	BQ	112	SER	2.8
27	BT	2	ALA	2.8
28	BU	35	SER	2.8
28	BU	49	ALA	2.8
34	AG	83	ALA	2.8
77	DR	7	SER	2.8
7	m	84	PRO	2.8
8	BA	6	PRO	2.8
13	BF	51	ARG	2.8
16	BI	26	ARG	2.8
19	y	180	ARG	2.8
36	CC	112	PRO	2.8
56	CW	108	ARG	2.8
64	T	60	ARG	2.8
69	Y	29	PRO	2.8
71	a	20	ARG	2.8
20	z	139	VAL	2.8
23	5	41	VAL	2.8
48	CO	20	VAL	2.8
51	CR	102	VAL	2.8
69	Y	74	VAL	2.8
63	S	46	LYS	2.8
64	T	29	GLU	2.8
70	Z	36	THR	2.8
79	DT	132	VAL	2.8
6	AY	194	LYS	2.8
7	m	217	GLU	2.8
9	o	173	LYS	2.8
16	BI	14	LYS	2.8
21	0	47	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
26	BS	25	LYS	2.8
1	1	1525	A	2.8
1	1	1695	A	2.8
1	1	2078	A	2.8
1	AS	318	A	2.8
1	AS	367	A	2.8
1	AS	1563	A	2.8
1	AS	2518	A	2.8
11	BD	11	ASP	2.8
14	t	79	GLU	2.8
49	CP	77	LYS	2.8
53	CT	225	GLU	2.8
54	CU	76	GLU	2.8
79	AR	258	LYS	2.8
46	B	129	A	2.8
46	B	814	A	2.8
46	B	968	A	2.8
46	B	1370	A	2.8
79	DT	188	ASP	2.8
1	1	1833	U	2.8
1	1	2305	U	2.8
1	1	2479	U	2.8
1	AS	78	U	2.8
1	AS	343	U	2.8
10	p	94	LEU	2.8
20	z	66	LEU	2.8
29	BV	53	PHE	2.8
36	CC	17	LEU	2.8
60	DA	25	TRP	2.8
46	CM	24	U	2.8
4	AW	228	GLY	2.8
6	l	363	ASN	2.8
11	q	46	ASN	2.8
14	t	14	PHE	2.8
14	BG	126	PHE	2.8
46	CM	1243	U	2.8
46	CM	1766	U	2.8
62	DC	56	LEU	2.8
63	DD	104	LEU	2.8
65	U	17	LEU	2.8
66	DG	28	LEU	2.8
66	DG	45	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
74	DO	73	LEU	2.8
49	E	132	ILE	2.8
65	DF	87	ASN	2.8
76	DQ	43	PHE	2.8
79	AR	119	ASN	2.8
79	AR	242	PHE	2.8
79	DT	257	ILE	2.8
80	p0	99	ILE	2.8
82	l1	214	PHE	2.8
20	BM	16	GLY	2.8
25	7	10	GLY	2.8
33	AF	38	GLY	2.8
34	AG	34	GLY	2.8
54	J	142	GLY	2.8
69	Y	123	GLY	2.8
1	1	753	C	2.8
1	1	1852	C	2.8
1	AS	79	G	2.8
1	AS	219	G	2.8
1	AS	978	C	2.8
1	AS	1223	C	2.8
1	AS	3246	C	2.8
46	B	562	G	2.8
46	B	1115	G	2.8
46	B	1276	G	2.8
46	B	1350	C	2.8
46	CM	1339	G	2.8
46	CM	1765	G	2.8
47	C	155	TYR	2.8
51	G	27	TYR	2.8
71	DL	48	TYR	2.8
18	x	121	HIS	2.8
67	W	86	HIS	2.8
79	DT	29	HIS	2.8
7	m	109	ALA	2.8
17	w	191	ALA	2.8
17	BJ	182	ALA	2.8
36	CC	107	GLN	2.8
45	CL	109	GLN	2.8
47	C	95	ALA	2.8
49	CP	161	ALA	2.8
54	CU	70	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
55	K	13	ALA	2.8
55	CV	100	ALA	2.8
63	S	17	ALA	2.8
76	DQ	12	ARG	2.8
4	AW	195	SER	2.8
6	AY	185	SER	2.8
9	o	178	SER	2.8
12	r	190	VAL	2.8
18	BK	109	SER	2.8
20	z	21	LYS	2.8
33	AF	8	PRO	2.8
33	BZ	29	VAL	2.8
49	E	75	VAL	2.8
49	E	160	VAL	2.8
50	F	226	SER	2.8
54	J	59	PRO	2.8
59	CZ	61	VAL	2.8
62	R	96	VAL	2.8
62	DC	51	SER	2.8
67	DH	29	LYS	2.8
73	DN	57	SER	2.8
79	AR	266	SER	2.8
79	DT	69	VAL	2.8
79	DT	266	SER	2.8
7	m	36	LEU	2.8
7	m	146	LEU	2.8
29	AB	113	LEU	2.8
36	CC	46	THR	2.8
43	AP	7	THR	2.8
45	CL	129	LEU	2.8
47	C	172	LEU	2.8
48	CO	90	GLU	2.8
51	G	189	LEU	2.8
53	CT	184	LEU	2.8
59	O	34	THR	2.8
63	DD	16	THR	2.8
64	T	30	THR	2.8
66	DG	51	GLU	2.8
71	a	62	THR	2.8
71	a	74	LEU	2.8
80	P0	74	GLU	2.8
9	o	125	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
10	BC	50	PHE	2.8
11	q	110	ASP	2.8
14	t	26	PHE	2.8
14	BG	51	ILE	2.8
27	BT	99	ILE	2.8
52	H	43	PHE	2.8
53	I	156	PHE	2.8
56	L	129	ILE	2.8
58	N	34	TRP	2.8
62	R	50	ASP	2.8
63	DD	42	ILE	2.8
63	DD	62	ILE	2.8
64	T	41	ILE	2.8
80	P0	41	ILE	2.8
52	H	204	GLY	2.8
54	J	133	GLY	2.8
58	N	73	GLY	2.8
69	DJ	73	GLY	2.8
71	DL	73	GLY	2.8
18	x	137	ASN	2.8
21	BN	62	ASN	2.8
70	Z	21	ASN	2.8
1	1	2137	U	2.8
1	1	2536	U	2.8
1	AS	2487	U	2.8
3	4	23	U	2.8
7	AZ	272	TYR	2.8
46	B	376	A	2.8
46	B	604	A	2.8
46	B	847	A	2.8
46	B	1511	A	2.8
46	CM	62	A	2.8
46	CM	1236	U	2.8
47	CN	202	TYR	2.8
48	D	155	TYR	2.8
73	c	73	TYR	2.8
6	AY	196	ARG	2.8
1	1	1775	C	2.8
18	BK	81	ALA	2.8
28	BU	44	ALA	2.8
6	l	45	LYS	2.8
7	m	274	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
9	o	222	GLN	2.8
9	BB	26	ALA	2.8
11	BD	66	ALA	2.8
12	BE	121	LYS	2.8
27	BT	87	LYS	2.8
32	AE	37	LYS	2.8
46	B	1412	C	2.8
46	CM	1520	C	2.8
47	CN	20	ALA	2.8
59	CZ	46	ARG	2.8
63	DD	17	ALA	2.8
54	CU	175	LYS	2.8
73	DN	93	LYS	2.8
1	1	85	G	2.8
1	1	3194	G	2.8
1	AS	896	G	2.8
1	AS	2611	G	2.8
6	AY	22	PRO	2.8
6	AY	182	VAL	2.8
21	0	22	PRO	2.8
28	AA	43	VAL	2.8
33	BZ	52	PRO	2.8
35	AH	26	PRO	2.8
46	B	305	G	2.8
46	B	705	G	2.8
46	B	1466	G	2.8
46	B	1678	G	2.8
51	CR	72	VAL	2.8
51	CR	227	VAL	2.8
52	CS	33	VAL	2.8
66	V	71	VAL	2.8
66	V	73	VAL	2.8
67	DH	99	VAL	2.8
71	a	55	VAL	2.8
71	DL	92	VAL	2.8
74	DO	4	VAL	2.8
78	DS	164	PRO	2.8
82	L1	148	VAL	2.8
6	l	151	LEU	2.8
6	AY	353	SER	2.8
7	AZ	233	SER	2.8
12	BE	176	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
12	BE	219	SER	2.8
16	BI	111	SER	2.8
18	BK	22	LEU	2.8
30	BW	62	SER	2.8
47	CN	177	LEU	2.8
49	E	235	LEU	2.8
56	CW	93	LEU	2.8
63	S	37	LEU	2.8
69	Y	104	LEU	2.8
79	DT	243	SER	2.8
82	L1	144	LEU	2.8
12	r	76	ILE	2.8
22	2	25	ILE	2.8
24	BQ	115	THR	2.8
32	AE	12	THR	2.8
32	BY	12	THR	2.8
47	C	81	PHE	2.7
50	F	18	PHE	2.7
51	CR	26	THR	2.8
51	CR	95	THR	2.8
59	CZ	76	GLU	2.8
56	L	140	ILE	2.8
69	Y	86	ILE	2.8
69	DJ	125	ILE	2.8
74	DO	79	PHE	2.7
79	AR	253	THR	2.8
79	DT	259	ILE	2.8
5	AX	140	ASP	2.7
16	BI	88	GLY	2.7
47	CN	13	ASP	2.7
50	F	134	GLY	2.7
51	CR	144	GLY	2.7
48	CO	148	ASN	2.7
67	W	71	ASN	2.7
7	m	31	TYR	2.7
16	v	148	TYR	2.7
33	AF	72	TYR	2.7
33	BZ	72	TYR	2.7
25	BR	59	HIS	2.7
51	G	69	HIS	2.7
71	a	131	ARG	2.7
7	m	270	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
10	BC	248	ALA	2.7
34	CA	2	ALA	2.7
41	CH	12	LYS	2.7
45	CL	37	LYS	2.7
45	CL	102	LYS	2.7
79	DT	272	LYS	2.7
80	p0	44	ALA	2.7
82	l1	109	ALA	2.7
1	1	402	A	2.7
1	1	2156	A	2.7
1	1	3319	U	2.7
1	AS	823	A	2.7
1	AS	2780	A	2.7
16	BI	115	VAL	2.7
34	AG	9	VAL	2.7
46	B	75	U	2.7
46	B	599	A	2.7
46	CM	236	U	2.7
46	CM	703	U	2.7
46	CM	815	U	2.7
49	E	174	VAL	2.7
50	CQ	135	VAL	2.7
52	CS	40	VAL	2.7
53	I	26	VAL	2.7
55	K	72	VAL	2.7
57	M	21	VAL	2.7
79	DT	175	VAL	2.7
80	P0	108	PRO	2.7
5	AX	60	LEU	2.7
9	o	182	LEU	2.7
14	BG	10	LEU	2.7
54	CU	30	LEU	2.7
55	K	190	LEU	2.7
56	L	97	LEU	2.7
59	CZ	41	LEU	2.7
66	DG	22	LEU	2.7
69	DJ	104	LEU	2.7
82	L1	163	LEU	2.7
19	BL	172	PHE	2.7
16	v	183	THR	2.7
21	0	82	GLU	2.7
29	AB	68	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
41	CH	18	SER	2.7
44	CK	59	SER	2.7
56	L	114	PHE	2.7
60	DA	24	SER	2.7
61	Q	9	PHE	2.7
61	DB	71	ILE	2.7
62	R	120	SER	2.7
64	T	117	ILE	2.7
65	U	35	ILE	2.7
82	L1	157	PHE	2.7
64	DE	96	THR	2.7
79	DT	26	THR	2.7
16	v	2	GLY	2.7
43	CJ	49	GLY	2.7
60	P	2	GLY	2.7
60	P	8	GLY	2.7
62	DC	99	GLY	2.7
71	a	65	GLY	2.7
1	1	442	G	2.7
1	1	2965	G	2.7
1	AS	358	G	2.7
1	AS	1226	G	2.7
1	AS	1264	G	2.7
1	AS	2441	G	2.7
1	AS	2527	G	2.7
46	B	1134	G	2.7
46	B	1301	G	2.7
46	CM	1085	G	2.7
13	s	10	ARG	2.7
36	CC	105	ARG	2.7
55	K	201	ARG	2.7
55	CV	110	ARG	2.7
65	U	57	ARG	2.7
8	n	56	ASN	2.7
10	p	227	TYR	2.7
18	x	169	ASN	2.7
22	BO	20	LYS	2.7
23	BP	81	TYR	2.7
29	AB	77	LYS	2.7
38	CE	10	LYS	2.7
45	CL	67	LYS	2.7
58	N	133	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
68	X	53	TYR	2.7
5	AX	374	ALA	2.7
10	p	169	ALA	2.7
19	y	42	ALA	2.7
28	AA	19	ALA	2.7
34	AG	2	ALA	2.7
41	AN	10	ALA	2.7
50	F	108	ALA	2.7
52	CS	72	HIS	2.7
53	CT	224	ALA	2.7
58	N	12	ALA	2.7
69	Y	8	ALA	2.7
72	b	36	ALA	2.7
7	m	275	GLN	2.7
20	z	164	VAL	2.7
22	2	79	VAL	2.7
49	CP	82	GLN	2.7
50	F	180	GLN	2.7
51	G	89	VAL	2.7
53	CT	41	VAL	2.7
53	CT	153	VAL	2.7
54	CU	126	VAL	2.7
57	CX	42	VAL	2.7
7	m	103	LEU	2.7
7	m	171	LEU	2.7
15	BH	43	PRO	2.7
16	BI	116	LEU	2.7
23	BP	22	PRO	2.7
30	AC	54	LEU	2.7
34	CA	102	LEU	2.7
47	CN	162	CYS	2.7
50	CQ	97	LEU	2.7
50	CQ	114	LEU	2.7
52	H	175	LEU	2.7
53	I	178	LEU	2.7
60	P	45	LEU	2.7
60	P	54	LEU	2.7
67	W	33	LEU	2.7
1	1	1012	U	2.7
1	AS	950	U	2.7
1	AS	1435	U	2.7
1	AS	2697	U	2.7

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Mol	Chain	Res	Type	RSRZ
3	4	156	U	2.7
3	AU	158	U	2.7
5	k	252	ILE	2.7
7	m	69	ILE	2.7
9	o	199	PHE	2.7
11	BD	172	ILE	2.7
51	G	228	ILE	2.7
53	I	145	PHE	2.7
54	CU	81	PHE	2.7
66	V	100	ILE	2.7
80	p0	53	MET	2.7
14	BG	194	GLU	2.7
20	z	152	GLU	2.7
79	DT	270	GLU	2.7
1	1	1663	A	2.7
1	1	2130	A	2.7
1	AS	1700	A	2.7
1	AS	2462	A	2.7
9	BB	178	SER	2.7
29	BV	31	GLY	2.7
35	CB	79	SER	2.7
46	B	186	A	2.7
46	B	796	A	2.7
53	I	134	GLY	2.7
54	J	71	THR	2.7
55	K	177	SER	2.7
56	CW	117	GLY	2.7
60	P	51	GLY	2.7
61	Q	121	THR	2.7
64	T	35	THR	2.7
79	AR	301	GLY	2.7
79	DT	255	SER	2.7
41	AN	37	ARG	2.7
56	L	78	ARG	2.7
56	L	79	ARG	2.7
70	Z	16	ARG	2.7
10	BC	121	LYS	2.7
10	BC	134	LYS	2.7
19	y	79	LYS	2.7
33	BZ	73	LYS	2.7
34	AG	20	LYS	2.7
50	F	152	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
73	DN	4	LYS	2.7
1	1	864	C	2.7
1	AS	1523	C	2.7
1	AS	2848	C	2.7
11	BD	177	ASP	2.7
12	BE	193	ASP	2.7
15	u	34	ASP	2.7
46	B	292	C	2.7
46	B	1317	C	2.7
46	CM	1237	C	2.7
23	BP	33	TYR	2.7
55	K	188	TYR	2.7
73	DN	59	TYR	2.7
80	p0	22	TYR	2.7
6	AY	111	ASN	2.7
7	AZ	97	ALA	2.7
22	BO	82	ASN	2.7
39	AL	33	ALA	2.7
47	C	32	HIS	2.7
51	G	57	ASN	2.7
51	CR	84	ALA	2.7
54	CU	99	ALA	2.7
58	N	109	ALA	2.7
73	c	63	ALA	2.7
79	DT	211	ALA	2.7
9	BB	237	VAL	2.7
23	5	19	VAL	2.7
52	H	40	VAL	2.7
56	L	85	VAL	2.7
6	l	328	LEU	2.7
10	BC	110	LEU	2.7
16	v	197	LEU	2.7
34	AG	7	LEU	2.7
36	CC	9	LEU	2.7
51	CR	239	LEU	2.7
65	U	105	LEU	2.7
79	DT	271	LEU	2.7
1	1	1524	G	2.7
1	1	1949	G	2.7
1	1	2445	G	2.7
1	AS	54	G	2.7
1	AS	100	G	2.7

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Mol	Chain	Res	Type	RSRZ
1	AS	214	G	2.7
1	AS	2374	G	2.7
7	m	32	GLN	2.7
7	m	255	PRO	2.7
16	BI	11	GLN	2.7
46	B	701	G	2.7
46	B	942	G	2.7
46	B	1184	G	2.7
56	CW	15	PRO	2.7
58	CY	17	PRO	2.7
64	DE	62	GLN	2.7
70	Z	88	PRO	2.7
72	b	98	GLN	2.7
6	l	157	PHE	2.7
7	AZ	64	ILE	2.7
7	AZ	223	PHE	2.7
7	AZ	290	ILE	2.7
8	n	105	PHE	2.7
18	BK	146	ILE	2.7
23	5	56	ILE	2.7
33	AF	47	PHE	2.7
55	CV	104	ILE	2.7
64	DE	28	PHE	2.7
81	12	160	ILE	2.7
82	L1	206	ILE	2.7
41	AN	23	CYS	2.7
44	AQ	42	CYS	2.7
52	CS	87	CYS	2.7
62	R	89	MET	2.7
4	j	232	GLY	2.7
6	l	55	GLU	2.7
7	m	170	GLY	2.7
16	BI	177	GLY	2.7
21	BN	82	GLU	2.7
82	L1	30	GLU	2.7
6	AY	177	LYS	2.7
22	BO	71	SER	2.7
29	AB	86	LYS	2.7
33	AF	78	LYS	2.7
35	AH	6	THR	2.7
35	AH	25	THR	2.7
48	D	185	THR	2.7

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Mol	Chain	Res	Type	RSRZ
50	F	144	ARG	2.7
53	CT	230	ARG	2.7
35	CB	21	LYS	2.7
55	K	97	THR	2.7
57	CX	38	ARG	2.7
52	CS	80	LYS	2.7
63	S	86	LYS	2.7
63	DD	114	THR	2.7
1	1	1647	U	2.7
1	AS	1265	U	2.7
6	l	107	TRP	2.7
64	T	123	SER	2.7
72	DM	63	SER	2.7
76	DQ	7	TRP	2.7
79	AR	292	SER	2.7
79	DT	59	LYS	2.7
81	12	120	SER	2.7
82	l1	147	LYS	2.7
46	B	1274	U	2.7
46	B	1399	U	2.7
1	1	2464	A	2.7
1	1	2478	A	2.7
46	CM	112	A	2.7
46	CM	1479	A	2.7
7	m	192	ALA	2.7
10	p	207	ALA	2.7
13	s	169	ALA	2.7
18	BK	6	ALA	2.7
22	BO	7	TYR	2.7
36	CC	110	ALA	2.7
49	CP	95	ALA	2.7
51	CR	27	TYR	2.7
56	L	94	ASP	2.7
62	DC	74	ALA	2.7
17	w	15	HIS	2.7
19	y	82	VAL	2.7
21	0	122	HIS	2.7
45	CL	73	VAL	2.7
7	m	178	ASN	2.7
8	BA	63	LEU	2.7
8	BA	78	VAL	2.7
11	BD	43	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
47	C	59	LEU	2.7
47	CN	139	VAL	2.7
51	CR	101	LEU	2.7
52	CS	51	VAL	2.7
55	CV	174	VAL	2.7
59	CZ	115	VAL	2.7
60	P	58	HIS	2.7
62	DC	96	VAL	2.7
65	DF	105	LEU	2.7
67	DH	111	VAL	2.7
72	DM	38	HIS	2.7
28	AA	78	ASN	2.7
77	DR	49	LEU	2.7
79	AR	289	LEU	2.7
79	DT	95	LEU	2.7
82	l1	55	LEU	2.7
1	1	1559	C	2.7
1	1	3193	C	2.7
1	AS	68	C	2.7
1	AS	1593	C	2.7
3	AU	115	C	2.7
11	q	20	ILE	2.7
14	t	37	GLN	2.7
26	BS	116	PRO	2.7
46	B	99	C	2.7
46	CM	1412	C	2.7
48	CO	84	ILE	2.7
48	CO	204	ILE	2.7
54	J	121	ILE	2.7
56	CW	153	GLN	2.7
60	DA	122	ILE	2.7
67	DH	93	GLN	2.7
79	DT	58	PRO	2.7
82	L1	212	PRO	2.7
26	8	84	PHE	2.7
33	BZ	47	PHE	2.7
12	r	128	ARG	2.7
27	BT	121	ARG	2.7
55	CV	74	ARG	2.7
80	p0	42	ARG	2.7
7	AZ	112	LYS	2.7
7	AZ	197	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
9	BB	14	GLU	2.7
9	BB	223	GLY	2.7
16	v	177	GLY	2.7
20	z	108	LYS	2.7
33	AF	16	LYS	2.7
41	CH	23	CYS	2.7
45	i	106	GLY	2.7
53	CT	99	GLY	2.7
56	L	92	LYS	2.7
60	P	119	GLU	2.7
61	Q	49	GLU	2.7
61	DB	39	GLY	2.7
73	DN	70	LYS	2.7
75	DP	14	LYS	2.7
77	g	32	GLY	2.7
79	AR	198	CYS	2.7
4	j	129	THR	2.7
44	AQ	26	THR	2.7
63	DD	14	THR	2.7
79	AR	26	THR	2.7
1	1	1923	G	2.7
1	1	2429	G	2.7
1	AS	1302	G	2.7
1	AS	2089	G	2.7
46	B	501	G	2.7
46	B	1405	G	2.7
46	B	1421	G	2.7
46	B	1521	G	2.7
46	CM	1086	G	2.7
42	AO	24	SER	2.7
52	CS	206	SER	2.7
55	CV	45	SER	2.7
60	P	12	SER	2.7
71	DL	69	SER	2.7
79	AR	61	SER	2.7
79	DT	153	SER	2.7
80	p0	68	SER	2.7
51	G	33	ALA	2.7
1	1	1013	U	2.7
1	1	3297	U	2.7
6	AY	26	VAL	2.7
14	BG	83	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
19	y	93	LEU	2.7
23	BP	101	VAL	2.7
28	BU	53	VAL	2.7
31	AD	61	TYR	2.7
31	BX	69	VAL	2.7
39	CF	73	LEU	2.7
51	G	111	VAL	2.7
51	G	160	VAL	2.7
52	CS	90	VAL	2.7
53	I	211	LEU	2.7
54	CU	168	LEU	2.7
55	K	145	VAL	2.7
56	L	70	LEU	2.7
61	DB	78	LEU	2.7
63	DD	78	TYR	2.7
67	W	99	VAL	2.7
73	DN	58	VAL	2.7
79	DT	298	LEU	2.7
51	G	212	ASP	2.7
74	DO	19	HIS	2.7
79	DT	294	ASP	2.7
6	AY	115	ASN	2.7
12	r	215	ASN	2.7
13	s	20	ASN	2.7
1	1	1255	A	2.6
1	1	1837	A	2.6
1	AS	1022	A	2.6
1	AS	1221	A	2.6
6	AY	100	MET	2.6
6	AY	297	GLN	2.6
11	q	163	GLN	2.6
16	BI	180	PHE	2.6
18	BK	55	GLN	2.6
39	CF	70	PRO	2.6
45	CL	76	PRO	2.6
46	B	178	A	2.6
46	B	1297	A	2.6
46	CM	841	A	2.6
52	CS	127	GLN	2.6
55	K	104	ILE	2.6
55	CV	111	GLN	2.6
64	T	115	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
69	DJ	64	GLN	2.6
79	DT	196	ILE	2.6
50	F	117	ARG	2.6
56	L	3	ARG	2.6
28	AA	3	LYS	2.6
58	CY	69	LYS	2.6
71	a	11	LYS	2.6
11	BD	119	GLY	2.6
16	BI	82	GLY	2.6
49	E	144	GLY	2.6
46	CM	1505	C	2.6
52	H	216	GLU	2.6
64	T	98	GLY	2.6
69	Y	21	GLY	2.6
1	1	1592	C	2.6
1	AS	1279	C	2.6
46	B	657	C	2.6
46	B	1323	C	2.6
46	CM	280	C	2.6
6	AY	288	THR	2.6
10	BC	195	THR	2.6
26	BS	37	THR	2.6
44	AQ	52	THR	2.6
51	G	80	THR	2.6
52	H	73	THR	2.6
54	J	129	THR	2.6
64	DE	55	THR	2.6
71	DL	121	THR	2.6
74	DO	44	THR	2.6
76	f	39	CYS	2.6
76	DQ	39	CYS	2.6
5	AX	387	LEU	2.6
11	BD	112	VAL	2.6
13	BF	80	LEU	2.6
14	t	135	VAL	2.6
15	u	61	VAL	2.6
17	BJ	175	LEU	2.6
20	BM	33	ALA	2.6
20	BM	150	LEU	2.6
28	AA	72	VAL	2.6
43	CJ	85	LEU	2.6
45	i	45	SER	2.6

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Mol	Chain	Res	Type	RSRZ
45	i	119	VAL	2.6
45	i	127	ALA	2.6
47	C	178	ALA	2.6
49	CP	231	ALA	2.6
50	F	75	VAL	2.6
54	CU	28	ALA	2.6
61	DB	69	VAL	2.6
63	DD	21	VAL	2.6
64	T	4	VAL	2.6
64	DE	123	SER	2.6
71	a	18	LEU	2.6
75	DP	54	LEU	2.6
79	AR	37	SER	2.6
79	AR	92	LEU	2.6
6	AY	263	TYR	2.6
23	5	111	TYR	2.6
55	K	172	TYR	2.6
7	AZ	68	HIS	2.6
49	E	54	HIS	2.6
56	L	160	HIS	2.6
79	AR	67	HIS	2.6
1	1	79	G	2.6
1	1	368	G	2.6
1	1	1483	G	2.6
1	1	2962	G	2.6
1	AS	2251	G	2.6
1	AS	2313	G	2.6
1	AS	2452	G	2.6
50	CQ	50	ILE	2.6
60	P	50	ILE	2.6
72	b	43	ASP	2.6
1	1	1738	U	2.6
1	1	2484	U	2.6
1	AS	2660	U	2.6
5	k	311	PHE	2.6
16	v	180	PHE	2.6
17	w	66	ASN	2.6
19	y	69	ARG	2.6
46	B	822	G	2.6
46	B	970	G	2.6
21	0	25	PHE	2.6
29	BV	111	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
33	AF	17	LYS	2.6
39	AL	38	PHE	2.6
41	AN	36	LYS	2.6
50	CQ	204	PRO	2.6
51	G	83	PRO	2.6
46	CM	1242	U	2.6
52	H	139	ASN	2.6
52	H	166	ARG	2.6
53	I	164	LYS	2.6
53	CT	154	ARG	2.6
54	CU	60	PRO	2.6
54	CU	182	PRO	2.6
55	CV	148	LYS	2.6
57	CX	28	ASN	2.6
60	P	64	LYS	2.6
60	P	113	PHE	2.6
61	Q	13	ARG	2.6
62	DC	103	ASN	2.6
64	DE	31	ASN	2.6
69	Y	57	ARG	2.6
46	B	821	U	2.6
46	B	1459	U	2.6
46	CM	318	U	2.6
74	d	18	GLN	2.6
1	1	2520	A	2.6
45	i	159	GLU	2.6
46	B	577	A	2.6
46	B	740	A	2.6
46	CM	510	A	2.6
46	CM	1357	A	2.6
55	K	191	GLU	2.6
59	CZ	132	GLU	2.6
79	DT	285	GLU	2.6
5	k	251	CYS	2.6
6	AY	268	THR	2.6
18	x	183	THR	2.6
19	y	6	THR	2.6
21	BN	98	THR	2.6
60	P	145	THR	2.6
66	V	52	THR	2.6
6	AY	143	VAL	2.6
9	o	177	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
11	BD	71	VAL	2.6
14	t	197	ALA	2.6
14	BG	24	VAL	2.6
21	0	51	VAL	2.6
30	AC	32	LEU	2.6
45	CL	133	ALA	2.6
47	CN	182	LEU	2.6
50	CQ	177	LEU	2.6
53	I	111	LEU	2.6
56	CW	28	LEU	2.6
61	Q	35	ALA	2.6
63	S	83	ALA	2.6
63	DD	6	VAL	2.6
72	DM	79	ALA	2.6
73	DN	24	LEU	2.6
79	AR	6	VAL	2.6
79	AR	267	LEU	2.6
79	AR	271	LEU	2.6
81	12	125	LEU	2.6
1	AS	639	C	2.6
46	CM	753	C	2.6
61	DB	17	SER	2.6
67	W	37	SER	2.6
60	DA	40	TYR	2.6
63	DD	91	TYR	2.6
14	t	31	LYS	2.6
14	BG	46	ILE	2.6
16	v	83	LYS	2.6
23	BP	97	ARG	2.6
29	AB	102	ILE	2.6
34	AG	49	ILE	2.6
35	CB	67	LYS	2.6
42	AO	25	LYS	2.6
49	E	121	LYS	2.6
54	CU	94	ILE	2.6
55	K	23	LYS	2.6
60	P	107	LYS	2.6
60	DA	38	ILE	2.6
61	Q	127	ARG	2.6
63	S	25	LYS	2.6
70	Z	5	LYS	2.6
73	c	13	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
79	AR	10	ARG	2.6
79	AR	261	LYS	2.6
14	BG	138	PHE	2.6
34	AG	56	PRO	2.6
41	CH	28	PRO	2.6
51	CR	226	PHE	2.6
56	L	5	PRO	2.6
9	o	225	ASP	2.6
48	CO	208	GLN	2.6
61	DB	27	ASP	2.6
65	DF	23	ASP	2.6
18	x	120	ASN	2.6
18	BK	64	ASN	2.6
34	AG	106	ASN	2.6
69	DJ	80	ASN	2.6
51	CR	244	GLY	2.6
1	AS	975	U	2.6
1	AS	1254	U	2.6
1	AS	1778	U	2.6
1	AS	1817	U	2.6
46	B	1613	U	2.6
46	CM	1348	U	2.6
60	P	142	GLU	2.6
78	h	157	GLU	2.6
1	1	443	G	2.6
1	1	1901	G	2.6
1	AS	226	G	2.6
1	AS	304	G	2.6
1	AS	360	G	2.6
46	B	1500	G	2.6
46	CM	860	G	2.6
46	CM	1474	G	2.6
27	BT	118	LEU	2.6
5	k	233	TRP	2.6
7	AZ	155	THR	2.6
10	p	47	LEU	2.6
47	C	176	LEU	2.6
49	E	53	LEU	2.6
57	M	76	LEU	2.6
71	a	44	LEU	2.6
71	DL	17	LEU	2.6
73	c	53	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
82	l1	194	LEU	2.6
8	BA	8	TRP	2.6
16	BI	110	ALA	2.6
19	y	64	VAL	2.6
19	BL	11	VAL	2.6
29	BV	149	ALA	2.6
47	C	175	TRP	2.6
54	CU	53	ALA	2.6
66	DG	136	ALA	2.6
79	DT	76	ALA	2.6
1	1	910	A	2.6
1	1	979	A	2.6
1	AS	1835	A	2.6
1	AS	2762	A	2.6
20	BM	9	ARG	2.6
7	AZ	185	ILE	2.6
8	n	49	LYS	2.6
13	s	133	ARG	2.6
14	t	23	ARG	2.6
14	BG	176	ARG	2.6
14	BG	190	LYS	2.6
20	BM	85	LYS	2.6
41	AN	49	LYS	2.6
46	B	126	A	2.6
46	B	472	A	2.6
46	B	1322	A	2.6
54	CU	4	LYS	2.6
55	K	77	ARG	2.6
57	M	44	LYS	2.6
57	CX	5	LYS	2.6
6	l	141	HIS	2.6
7	AZ	240	TYR	2.6
17	BJ	58	TYR	2.6
27	BT	102	SER	2.6
51	CR	250	SER	2.6
60	P	11	ILE	2.6
63	S	62	ILE	2.6
76	f	31	ILE	2.6
70	DK	48	HIS	2.6
77	DR	40	TYR	2.6
7	AZ	3	MET	2.6
10	p	50	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
17	BJ	106	PHE	2.6
21	0	118	PHE	2.6
53	CT	68	MET	2.6
28	AA	82	PRO	2.6
51	CR	5	PRO	2.6
51	CR	240	PRO	2.6
71	DL	64	PHE	2.6
74	d	28	PRO	2.6
79	DT	62	PHE	2.6
80	p0	78	PRO	2.6
7	m	264	GLN	2.6
10	BC	62	GLN	2.6
16	v	11	GLN	2.6
46	B	1468	C	2.6
48	CO	108	ASP	2.6
79	DT	162	GLN	2.6
79	DT	311	GLN	2.6
81	12	161	ASP	2.6
9	BB	234	ASN	2.6
11	BD	81	GLY	2.6
39	CF	34	ASN	2.6
48	D	63	GLY	2.6
63	S	10	GLY	2.6
73	c	14	GLY	2.6
79	AR	15	GLY	2.6
18	x	150	LEU	2.6
31	BX	36	LEU	2.6
35	CB	105	LEU	2.6
47	CN	87	LEU	2.6
48	D	90	GLU	2.6
55	K	149	LEU	2.6
60	DA	54	LEU	2.6
65	U	65	GLU	2.6
73	c	67	LEU	2.6
74	d	75	GLU	2.6
6	l	287	VAL	2.6
6	AY	175	ALA	2.6
6	AY	360	VAL	2.6
12	r	127	ALA	2.6
23	BP	38	VAL	2.6
33	AF	29	VAL	2.6
37	AJ	8	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
44	CK	31	VAL	2.6
1	1	2544	U	2.6
1	AS	2389	U	2.6
1	AS	2488	U	2.6
1	AS	2536	U	2.6
6	AY	189	ARG	2.6
7	AZ	108	ARG	2.6
11	BD	122	ARG	2.6
38	CE	5	THR	2.6
45	CL	42	ALA	2.6
45	CL	119	VAL	2.6
47	CN	86	VAL	2.6
62	DC	93	VAL	2.6
67	DH	55	VAL	2.6
75	DP	41	VAL	2.6
78	h	126	VAL	2.6
80	p0	50	VAL	2.6
19	BL	123	THR	2.6
25	BR	43	ARG	2.6
26	BS	96	LYS	2.6
32	BY	17	LYS	2.6
45	CL	90	ARG	2.6
46	B	601	U	2.6
46	B	842	U	2.6
46	CM	1695	U	2.6
47	C	54	TRP	2.6
47	CN	40	THR	2.6
48	D	154	THR	2.6
53	CT	132	ARG	2.6
55	CV	14	THR	2.6
47	CN	56	LYS	2.6
48	D	27	LYS	2.6
62	R	47	ARG	2.6
67	DH	24	THR	2.6
79	AR	19	TRP	2.6
79	AR	156	ARG	2.6
79	DT	25	THR	2.6
65	DF	80	LYS	2.6
80	P0	55	LYS	2.6
82	l1	198	TRP	2.6
8	BA	40	ILE	2.6
10	p	224	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
12	r	191	ILE	2.6
14	BG	95	ILE	2.6
16	BI	142	ILE	2.6
22	BO	63	ILE	2.6
33	AF	97	ILE	2.6
47	CN	170	ILE	2.6
50	F	74	ILE	2.6
55	K	185	CYS	2.6
1	AS	1437	G	2.6
1	AS	2445	G	2.6
1	AS	2580	G	2.6
1	AS	2894	G	2.6
1	AS	3249	G	2.6
2	AT	87	G	2.6
3	AU	136	G	2.6
11	q	180	TYR	2.6
18	x	90	PHE	2.6
4	j	178	PRO	2.6
5	AX	373	PRO	2.6
25	BR	26	SER	2.6
30	BW	7	HIS	2.6
46	B	384	G	2.6
46	B	748	G	2.6
46	B	1358	G	2.6
47	CN	203	PHE	2.6
51	CR	47	PHE	2.6
51	CR	109	PHE	2.6
53	CT	61	PHE	2.6
57	M	65	TYR	2.6
48	CO	147	PRO	2.6
56	L	144	PRO	2.6
60	P	14	SER	2.6
1	1	2423	A	2.6
1	1	2773	A	2.6
1	AS	423	A	2.6
1	AS	664	A	2.6
1	AS	2437	A	2.6
1	AS	2440	A	2.6
1	AS	2464	A	2.6
7	AZ	4	GLN	2.6
12	BE	113	GLN	2.6
46	CM	466	A	2.6

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Mol	Chain	Res	Type	RSRZ
46	CM	590	A	2.6
53	CT	199	GLN	2.6
79	AR	263	GLN	2.6
79	DT	296	GLN	2.6
82	L1	158	GLN	2.6
6	l	341	GLY	2.6
6	AY	286	ASP	2.6
7	m	26	GLY	2.6
8	n	66	GLY	2.6
29	BV	37	GLY	2.6
9	o	155	ASN	2.6
33	BZ	84	ASP	2.6
78	DS	179	ASP	2.6
79	AR	98	GLY	2.6
65	DF	104	ASN	2.6
71	DL	15	ASN	2.6
79	DT	245	ASN	2.6
5	k	338	LEU	2.6
11	BD	151	LEU	2.6
16	BI	134	LEU	2.6
28	BU	87	LEU	2.6
48	CO	207	LEU	2.6
59	CZ	52	LEU	2.6
59	CZ	96	LEU	2.6
77	DR	39	LEU	2.6
1	AS	924	C	2.6
1	AS	2321	C	2.6
1	AS	2468	C	2.6
49	E	236	GLU	2.6
50	F	48	GLU	2.6
53	CT	222	GLU	2.6
54	J	130	GLU	2.6
72	b	45	GLU	2.6
4	j	188	LYS	2.6
4	AW	247	ARG	2.6
10	p	91	ALA	2.6
11	q	112	VAL	2.6
6	l	349	LYS	2.6
7	AZ	288	LYS	2.6
8	BA	69	LYS	2.6
17	BJ	184	ALA	2.6
21	BN	99	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
24	BQ	76	ALA	2.6
28	BU	26	VAL	2.6
35	CB	104	VAL	2.6
46	B	1611	C	2.6
27	9	46	LYS	2.6
39	CF	36	LYS	2.6
45	CL	125	ALA	2.6
51	CR	192	VAL	2.6
54	J	177	VAL	2.6
54	CU	90	ALA	2.6
55	CV	81	VAL	2.6
58	N	27	ALA	2.6
60	DA	126	ALA	2.6
61	DB	45	ALA	2.6
78	h	139	LYS	2.6
79	AR	252	ALA	2.6
79	DT	72	VAL	2.6
47	C	10	THR	2.6
49	E	216	THR	2.6
50	F	56	THR	2.6
59	O	67	THR	2.6
61	DB	38	THR	2.6
73	DN	96	THR	2.6
74	d	61	THR	2.6
82	L1	209	THR	2.6
6	l	291	ILE	2.5
9	BB	90	ILE	2.5
10	BC	224	ILE	2.5
30	BW	21	ILE	2.5
52	H	62	ILE	2.5
52	CS	149	ILE	2.5
65	U	119	ILE	2.5
66	V	111	ILE	2.5
68	DI	36	ILE	2.5
1	1	1623	U	2.5
16	BI	27	CYS	2.5
46	B	491	U	2.5
46	B	1102	U	2.5
46	B	1114	U	2.5
46	CM	176	U	2.5
46	CM	765	U	2.5
55	K	198	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
59	O	104	CYS	2.5
62	R	123	TYR	2.5
41	CH	47	PRO	2.5
67	W	95	PRO	2.5
76	f	24	CYS	2.5
6	AY	265	SER	2.5
12	r	54	SER	2.5
17	BJ	185	SER	2.5
29	AB	84	SER	2.5
41	AN	18	SER	2.5
70	DK	46	SER	2.5
76	DQ	28	SER	2.5
79	AR	243	SER	2.5
79	AR	288	SER	2.5
7	m	127	GLY	2.5
18	x	73	GLY	2.5
56	L	131	GLN	2.5
57	M	47	GLN	2.5
65	DF	124	GLY	2.5
66	DG	109	GLN	2.5
20	z	105	LEU	2.5
24	6	34	LEU	2.5
32	AE	72	LEU	2.5
36	AI	21	LEU	2.5
51	CR	131	LEU	2.5
53	CT	216	LEU	2.5
79	AR	23	LEU	2.5
79	DT	289	LEU	2.5
1	1	607	G	2.5
1	1	1844	G	2.5
1	1	2481	G	2.5
1	AS	93	G	2.5
1	AS	1413	G	2.5
4	AW	97	ASN	2.5
11	q	57	VAL	2.5
12	BE	139	ARG	2.5
13	BF	18	VAL	2.5
13	BF	36	VAL	2.5
20	z	9	ARG	2.5
21	0	38	LYS	2.5
1	1	2376	A	2.5
1	AS	654	A	2.5

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Mol	Chain	Res	Type	RSRZ
1	AS	879	A	2.5
1	AS	2185	A	2.5
1	AS	3166	A	2.5
9	BB	21	ALA	2.5
29	AB	89	GLU	2.5
33	AF	11	VAL	2.5
46	B	375	G	2.5
46	B	535	G	2.5
46	CM	388	G	2.5
46	CM	714	G	2.5
48	D	77	GLU	2.5
49	CP	178	VAL	2.5
51	G	139	VAL	2.5
52	H	100	ASN	2.5
46	CM	1331	A	2.5
52	CS	144	GLU	2.5
53	I	14	LYS	2.5
53	CT	177	ARG	2.5
56	CW	173	LYS	2.5
63	DD	31	ASN	2.5
64	T	49	LYS	2.5
64	T	92	ASP	2.5
66	V	6	VAL	2.5
67	W	68	LYS	2.5
71	DL	35	VAL	2.5
75	e	49	ARG	2.5
79	AR	88	ARG	2.5
19	y	103	ALA	2.5
22	BO	14	ALA	2.5
45	CL	63	ALA	2.5
46	B	1132	A	2.5
46	CM	217	A	2.5
46	CM	722	A	2.5
58	N	2	ALA	2.5
59	O	94	ALA	2.5
61	Q	55	ALA	2.5
61	Q	111	GLU	2.5
76	f	45	GLU	2.5
7	m	256	THR	2.5
20	z	50	ILE	2.5
40	AM	9	THR	2.5
52	CS	147	THR	2.5

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Mol	Chain	Res	Type	RSRZ
64	DE	124	ILE	2.5
67	W	116	THR	2.5
79	AR	21	THR	2.5
82	L1	155	ILE	2.5
1	1	2159	C	2.5
1	AS	1828	C	2.5
1	AS	3315	C	2.5
4	AW	87	PHE	2.5
46	B	1113	C	2.5
46	B	1237	C	2.5
46	CM	706	C	2.5
46	CM	707	C	2.5
48	D	30	PHE	2.5
75	e	32	PHE	2.5
80	P0	66	PHE	2.5
10	BC	178	TYR	2.5
22	BO	56	TYR	2.5
23	5	81	TYR	2.5
29	AB	52	TYR	2.5
35	CB	76	TYR	2.5
70	DK	42	PRO	2.5
76	DQ	11	PRO	2.5
77	g	40	TYR	2.5
1	AS	1518	U	2.5
1	AS	1568	U	2.5
1	AS	2755	U	2.5
1	AS	3361	U	2.5
16	BI	123	GLN	2.5
18	x	172	GLN	2.5
20	z	138	LEU	2.5
27	BT	57	LEU	2.5
33	BZ	103	SER	2.5
47	C	9	LEU	2.5
48	D	73	LEU	2.5
49	E	148	SER	2.5
48	D	146	GLN	2.5
48	CO	218	LEU	2.5
52	CS	141	GLY	2.5
55	CV	68	GLY	2.5
56	L	76	LEU	2.5
60	P	13	SER	2.5
62	DC	120	SER	2.5

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Mol	Chain	Res	Type	RSRZ
66	DG	40	SER	2.5
46	B	275	U	2.5
46	B	624	U	2.5
72	DM	65	LEU	2.5
72	DM	98	GLN	2.5
79	AR	90	LEU	2.5
79	DT	301	GLY	2.5
4	AW	188	LYS	2.5
7	m	50	ARG	2.5
12	r	15	LYS	2.5
14	t	45	LYS	2.5
17	BJ	104	LYS	2.5
19	y	74	LYS	2.5
28	AA	55	LYS	2.5
28	BU	15	ARG	2.5
30	AC	18	ARG	2.5
43	AP	9	LYS	2.5
45	i	93	ARG	2.5
48	D	116	LYS	2.5
56	L	57	ARG	2.5
59	CZ	114	LYS	2.5
73	c	22	ARG	2.5
35	CB	85	VAL	2.5
39	CF	55	VAL	2.5
58	N	117	VAL	2.5
6	AY	260	ASP	2.5
45	i	66	ASN	2.5
50	F	32	GLU	2.5
51	G	151	ASP	2.5
52	H	197	GLU	2.5
60	DA	69	ASN	2.5
60	DA	151	ALA	2.5
68	DI	45	ALA	2.5
78	DS	165	ALA	2.5
80	p0	4	ALA	2.5
23	5	96	ILE	2.5
28	BU	5	ILE	2.5
52	H	211	ILE	2.5
52	CS	211	ILE	2.5
56	L	143	ILE	2.5
58	N	84	ILE	2.5
5	k	95	THR	2.5

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Mol	Chain	Res	Type	RSRZ
43	CJ	10	THR	2.5
45	CL	107	TRP	2.5
53	CT	1	MET	2.5
79	AR	165	THR	2.5
8	BA	100	PHE	2.5
22	BO	105	PHE	2.5
82	L1	49	PHE	2.5
82	l1	28	PHE	2.5
1	1	780	A	2.5
1	AS	221	A	2.5
46	B	719	A	2.5
1	1	100	G	2.5
1	1	2342	G	2.5
1	AS	1562	G	2.5
2	AT	49	G	2.5
46	B	1111	G	2.5
4	j	66	PRO	2.5
7	m	81	HIS	2.5
7	AZ	86	TYR	2.5
10	BC	56	TYR	2.5
14	t	119	TYR	2.5
16	BI	23	TYR	2.5
26	8	52	PRO	2.5
33	AF	27	HIS	2.5
63	S	40	PRO	2.5
67	W	47	TYR	2.5
5	AX	246	LEU	2.5
20	z	177	LEU	2.5
1	1	3051	C	2.5
1	AS	800	C	2.5
1	AS	1689	C	2.5
7	m	262	LYS	2.5
7	AZ	218	LYS	2.5
10	BC	49	ARG	2.5
11	BD	118	LEU	2.5
16	BI	70	GLY	2.5
17	w	52	LYS	2.5
27	9	39	LEU	2.5
21	BN	86	GLY	2.5
30	AC	23	LYS	2.5
45	CL	155	LEU	2.5
47	CN	18	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
48	D	184	LEU	2.5
49	E	59	LYS	2.5
53	CT	191	LYS	2.5
54	CU	24	LEU	2.5
54	CU	92	ARG	2.5
57	M	40	LEU	2.5
65	DF	61	LEU	2.5
71	DL	41	ARG	2.5
71	DL	67	GLY	2.5
71	DL	71	GLY	2.5
71	DL	131	ARG	2.5
76	f	30	LEU	2.5
46	CM	36	C	2.5
78	DS	123	LYS	2.5
80	P0	16	ARG	2.5
5	k	101	SER	2.5
13	s	5	SER	2.5
22	2	4	SER	2.5
28	BU	91	SER	2.5
38	AK	7	SER	2.5
56	CW	50	SER	2.5
58	N	14	GLN	2.5
76	DQ	25	SER	2.5
11	BD	93	VAL	2.5
22	2	126	VAL	2.5
32	BY	107	VAL	2.5
33	AF	74	VAL	2.5
48	CO	21	VAL	2.5
50	CQ	123	VAL	2.5
51	CR	219	VAL	2.5
54	CU	47	VAL	2.5
80	p0	101	VAL	2.5
14	t	193	ALA	2.5
52	H	78	ALA	2.5
59	O	128	ALA	2.5
70	Z	105	ALA	2.5
72	DM	99	ALA	2.5
1	1	702	U	2.5
1	AS	1622	U	2.5
1	AS	2753	U	2.5
16	BI	103	GLU	2.5
17	w	155	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
4	AW	5	ILE	2.5
10	p	220	ASN	2.5
11	BD	75	ILE	2.5
20	BM	166	ASN	2.5
27	BT	80	ILE	2.5
42	CI	3	ASP	2.5
47	C	163	ASN	2.5
47	CN	50	ILE	2.5
50	CQ	5	ILE	2.5
52	H	199	ILE	2.5
52	CS	95	ASN	2.5
52	CS	121	ILE	2.5
64	T	124	ILE	2.5
68	DI	40	ASP	2.5
79	AR	17	ASN	2.5
80	p0	83	ASN	2.5
60	DA	4	MET	2.5
65	DF	29	MET	2.5
75	e	57	MET	2.5
11	BD	56	THR	2.5
29	BV	79	TRP	2.5
52	CS	73	THR	2.5
53	CT	50	PHE	2.5
53	CT	170	THR	2.5
61	Q	84	THR	2.5
62	R	34	THR	2.5
62	DC	124	THR	2.5
80	P0	12	PHE	2.5
82	l1	154	THR	2.5
4	AW	67	TYR	2.5
5	AX	191	LYS	2.5
7	AZ	277	LEU	2.5
11	BD	168	ARG	2.5
13	BF	17	LEU	2.5
13	BF	68	HIS	2.5
19	BL	129	LEU	2.5
22	2	27	LEU	2.5
24	6	70	ARG	2.5
24	BQ	15	LEU	2.5
25	7	113	LYS	2.5
32	AE	101	LYS	2.5
45	CL	83	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
48	D	79	HIS	2.5
48	D	167	LYS	2.5
48	CO	64	ARG	2.5
53	I	22	HIS	2.5
57	M	83	PRO	2.5
62	DC	128	HIS	2.5
63	S	105	LYS	2.5
63	DD	22	LYS	2.5
64	T	84	TYR	2.5
65	DF	32	LEU	2.5
66	V	114	LEU	2.5
66	DG	66	TYR	2.5
75	e	14	LYS	2.5
76	f	34	TYR	2.5
82	ll	212	PRO	2.5
54	J	122	LEU	2.5
58	N	5	LEU	2.5
79	AR	13	LEU	2.5
79	AR	59	LYS	2.5
79	AR	219	LEU	2.5
79	DT	90	LEU	2.5
79	DT	120	LEU	2.5
1	AS	349	A	2.5
1	AS	1838	A	2.5
1	AS	2785	A	2.5
1	AS	3050	A	2.5
6	AY	341	GLY	2.5
16	BI	52	GLY	2.5
35	AH	78	GLY	2.5
43	AP	39	GLY	2.5
46	B	756	A	2.5
46	CM	1407	A	2.5
59	O	98	GLY	2.5
61	DB	104	GLY	2.5
63	DD	129	GLY	2.5
75	e	24	GLY	2.5
75	DP	24	GLY	2.5
79	AR	212	GLY	2.5
6	AY	20	GLN	2.5
13	BF	6	GLN	2.5
44	AQ	33	GLN	2.5
45	CL	104	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
48	CO	65	VAL	2.5
52	H	168	VAL	2.5
63	DD	18	VAL	2.5
79	DT	70	GLN	2.5
82	ll	9	VAL	2.5
1	1	796	G	2.5
1	1	831	G	2.5
1	1	1345	G	2.5
1	1	1739	G	2.5
1	1	2461	G	2.5
1	1	3060	G	2.5
1	AS	135	G	2.5
1	AS	1258	G	2.5
1	AS	1902	G	2.5
1	AS	2879	G	2.5
4	j	185	ALA	2.5
15	u	7	ALA	2.5
16	BI	166	SER	2.5
19	y	77	ALA	2.5
20	z	91	SER	2.5
21	0	37	ALA	2.5
43	AP	81	ALA	2.5
46	CM	750	G	2.5
46	CM	1228	G	2.5
47	C	2	SER	2.5
47	C	26	ALA	2.5
47	CN	65	ALA	2.5
48	CO	107	SER	2.5
49	E	233	SER	2.5
52	CS	74	ALA	2.5
66	DG	5	SER	2.5
78	DS	163	CYS	2.5
79	AR	84	ALA	2.5
79	DT	250	ALA	2.5
80	P0	49	ALA	2.5
7	m	64	ILE	2.5
1	1	639	C	2.5
1	AS	1552	C	2.5
1	AS	2467	C	2.5
7	m	238	GLU	2.5
10	BC	154	ILE	2.5
11	q	128	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
17	w	101	GLU	2.5
19	y	81	ILE	2.5
26	8	114	ILE	2.5
26	BS	139	ILE	2.5
50	F	209	ILE	2.5
51	G	249	ILE	2.5
56	L	106	GLU	2.5
57	M	3	ILE	2.5
60	DA	11	ILE	2.5
69	Y	14	ILE	2.5
71	DL	7	ILE	2.5
76	DQ	45	GLU	2.5
79	DT	123	ILE	2.5
46	B	256	C	2.5
46	B	1090	C	2.5
46	CM	1051	C	2.5
5	AX	365	PHE	2.5
9	BB	91	ASN	2.5
11	BD	19	ASP	2.5
12	BE	28	ASP	2.5
19	y	44	PHE	2.5
28	BU	131	PHE	2.5
52	CS	103	ASN	2.5
54	CU	39	PHE	2.5
59	O	39	ASP	2.5
61	Q	15	PHE	2.5
67	DH	43	ASN	2.5
1	1	894	U	2.5
1	1	2637	U	2.5
1	AS	2571	U	2.5
1	AS	3317	U	2.5
3	AU	112	U	2.5
5	k	235	THR	2.5
6	AY	251	TRP	2.5
11	BD	44	THR	2.5
46	B	1044	U	2.5
46	B	1216	U	2.5
46	CM	247	U	2.5
46	CM	817	U	2.5
5	k	367	LYS	2.5
9	BB	92	LYS	2.5
13	s	115	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
16	BI	56	LYS	2.5
7	AZ	195	LEU	2.5
10	p	170	LEU	2.5
16	BI	98	LEU	2.5
18	x	182	LEU	2.5
19	y	92	ARG	2.5
28	AA	52	LYS	2.5
48	D	216	LYS	2.5
47	CN	17	LEU	2.5
47	CN	176	LEU	2.5
49	E	135	ARG	2.5
47	CN	199	PRO	2.5
49	E	143	LEU	2.5
50	F	124	LEU	2.5
51	G	123	LEU	2.5
51	CR	148	ARG	2.5
53	CT	93	LYS	2.5
54	J	4	LYS	2.5
55	K	22	ARG	2.5
56	L	29	LYS	2.5
56	L	90	LYS	2.5
58	N	67	ARG	2.5
62	R	77	LYS	2.5
63	S	116	LEU	2.5
65	U	126	ARG	2.5
82	L1	102	LYS	2.5
28	BU	37	PRO	2.5
55	CV	149	LEU	2.5
66	DG	140	LEU	2.5
78	h	159	LEU	2.5
79	DT	92	LEU	2.5
82	L1	194	LEU	2.5
82	l1	43	PRO	2.5
82	l1	128	LEU	2.5
14	BG	99	HIS	2.5
38	AK	16	HIS	2.5
73	DN	68	TYR	2.5
30	BW	34	GLY	2.5
63	DD	26	GLY	2.5
7	AZ	173	VAL	2.5
23	5	99	VAL	2.5
49	CP	106	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
52	H	162	VAL	2.5
56	L	81	VAL	2.5
59	CZ	31	VAL	2.5
61	Q	62	VAL	2.5
78	DS	156	VAL	2.5
80	p0	105	VAL	2.5
82	l1	172	VAL	2.5
49	E	89	GLN	2.5
51	G	260	GLN	2.5
74	DO	5	GLN	2.5
80	p0	36	GLN	2.5
33	BZ	30	ALA	2.4
37	CD	47	ALA	2.4
61	DB	12	ALA	2.4
73	DN	49	ALA	2.4
79	DT	79	ALA	2.4
80	P0	106	ALA	2.4
5	AX	183	ILE	2.4
6	l	86	SER	2.4
12	r	12	CYS	2.4
13	s	65	ILE	2.4
31	AD	106	ILE	2.4
47	C	144	ILE	2.4
54	J	62	SER	2.4
56	CW	83	ILE	2.4
59	CZ	63	CYS	2.4
67	W	21	ILE	2.4
72	DM	89	ILE	2.4
74	DO	77	CYS	2.4
75	DP	21	SER	2.4
76	DQ	18	SER	2.4
79	DT	127	SER	2.4
79	DT	164	SER	2.4
1	1	2185	A	2.4
1	AS	1369	A	2.4
1	AS	2434	A	2.4
1	AS	2882	A	2.4
16	BI	131	GLU	2.4
36	CC	18	GLU	2.4
43	CJ	73	GLU	2.4
46	B	1502	A	2.4
46	B	1701	A	2.4

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Mol	Chain	Res	Type	RSRZ
52	CS	35	GLU	2.4
57	CX	1	MET	2.4
60	P	4	MET	2.4
69	DJ	51	GLU	2.4
79	AR	14	GLU	2.4
6	l	357	PHE	2.4
7	m	200	PHE	2.4
17	BJ	48	PHE	2.4
56	L	158	PHE	2.4
70	DK	86	PHE	2.4
80	p0	66	PHE	2.4
4	AW	7	ASN	2.4
6	AY	47	LYS	2.4
6	AY	218	LYS	2.4
33	BZ	104	ARG	2.4
34	AG	70	LYS	2.4
43	AP	18	ARG	2.4
45	CL	54	LYS	2.4
1	1	491	C	2.4
1	1	1015	G	2.4
1	1	1232	G	2.4
1	1	2129	C	2.4
1	AS	595	G	2.4
1	AS	863	G	2.4
1	AS	1068	G	2.4
1	AS	1813	G	2.4
1	AS	2428	G	2.4
3	AU	70	G	2.4
7	AZ	51	LEU	2.4
7	AZ	154	THR	2.4
8	n	137	ASP	2.4
47	C	125	ASP	2.4
49	E	83	LYS	2.4
52	CS	180	ARG	2.4
55	K	144	LYS	2.4
56	CW	25	ASP	2.4
56	CW	126	ARG	2.4
46	CM	1349	G	2.4
46	CM	1518	G	2.4
47	C	193	THR	2.4
60	DA	31	ASP	2.4
65	U	68	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
66	DG	27	LYS	2.4
68	X	22	ARG	2.4
64	DE	35	THR	2.4
71	DL	70	THR	2.4
73	c	91	ASP	2.4
77	DR	53	LYS	2.4
78	DS	155	ASN	2.4
79	DT	60	LYS	2.4
10	p	27	LEU	2.4
13	s	172	LEU	2.4
14	BG	172	LEU	2.4
19	y	124	LEU	2.4
22	BO	128	LEU	2.4
25	7	52	THR	2.4
33	BZ	90	THR	2.4
43	AP	21	THR	2.4
79	DT	310	TRP	2.4
82	L1	150	ASP	2.4
46	B	38	C	2.4
46	B	234	G	2.4
46	B	799	G	2.4
46	B	803	G	2.4
46	B	1185	G	2.4
49	CP	235	LEU	2.4
54	J	54	LEU	2.4
55	K	171	LEU	2.4
68	DI	11	LEU	2.4
82	L1	154	THR	2.4
46	CM	573	C	2.4
34	CA	91	PRO	2.4
77	g	19	PRO	2.4
1	1	2546	U	2.4
16	BI	53	TYR	2.4
20	z	134	HIS	2.4
46	B	122	U	2.4
46	B	291	U	2.4
46	B	917	U	2.4
46	CM	499	U	2.4
47	CN	168	HIS	2.4
6	AY	235	GLY	2.4
7	m	53	VAL	2.4
9	BB	84	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
10	p	181	VAL	2.4
19	BL	84	VAL	2.4
31	BX	98	GLY	2.4
47	C	31	VAL	2.4
47	CN	75	VAL	2.4
50	F	92	VAL	2.4
51	G	219	VAL	2.4
56	CW	137	GLY	2.4
56	CW	170	GLY	2.4
61	DB	8	VAL	2.4
63	S	132	GLY	2.4
67	DH	110	GLY	2.4
70	Z	58	GLY	2.4
72	b	62	VAL	2.4
72	DM	92	VAL	2.4
75	e	48	VAL	2.4
79	AR	278	GLY	2.4
79	DT	36	GLY	2.4
82	L1	167	VAL	2.4
7	m	78	ALA	2.4
19	BL	149	ALA	2.4
30	AC	63	ALA	2.4
35	CB	52	ALA	2.4
50	CQ	127	ALA	2.4
53	I	192	ALA	2.4
66	V	75	ALA	2.4
70	Z	85	ALA	2.4
80	p0	10	GLN	2.4
27	BT	106	ILE	2.4
53	I	16	ILE	2.4
66	V	36	ILE	2.4
74	DO	43	ILE	2.4
11	BD	1	MET	2.4
10	p	55	GLU	2.4
17	BJ	47	GLU	2.4
24	BQ	25	CYS	2.4
28	AA	31	GLU	2.4
39	CF	4	GLU	2.4
48	D	76	SER	2.4
68	X	64	GLU	2.4
71	DL	104	SER	2.4
79	DT	158	SER	2.4

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Mol	Chain	Res	Type	RSRZ
4	AW	177	LYS	2.4
7	m	160	PHE	2.4
7	m	180	PHE	2.4
5	k	10	ARG	2.4
5	k	236	LYS	2.4
6	AY	99	ARG	2.4
6	AY	192	LYS	2.4
10	p	182	LYS	2.4
15	u	111	PHE	2.4
16	v	59	PHE	2.4
16	BI	77	LYS	2.4
21	0	149	LYS	2.4
33	BZ	45	ARG	2.4
37	AJ	75	ARG	2.4
45	CL	112	LYS	2.4
51	CR	175	PHE	2.4
53	CT	131	LYS	2.4
64	T	7	LYS	2.4
71	DL	105	ARG	2.4
72	b	97	LYS	2.4
82	L1	207	LYS	2.4
82	l1	134	PHE	2.4
76	DQ	56	ARG	2.4
7	AZ	110	LEU	2.4
11	BD	144	LEU	2.4
22	2	91	LEU	2.4
22	BO	106	LEU	2.4
23	5	79	LEU	2.4
28	BU	101	LEU	2.4
41	AN	27	LEU	2.4
49	E	67	LEU	2.4
50	CQ	143	LEU	2.4
54	CU	73	LEU	2.4
60	DA	88	LEU	2.4
61	DB	97	LEU	2.4
65	U	109	LEU	2.4
68	X	79	LEU	2.4
68	DI	55	LEU	2.4
70	DK	103	LEU	2.4
75	DP	16	LEU	2.4
5	k	106	TRP	2.4
5	k	262	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
7	m	95	TRP	2.4
8	BA	71	ASN	2.4
19	y	45	ASN	2.4
1	1	2440	A	2.4
1	AS	98	A	2.4
1	AS	1583	A	2.4
1	AS	2142	A	2.4
17	w	57	ASP	2.4
20	BM	131	THR	2.4
22	2	143	THR	2.4
32	BY	14	ASN	2.4
50	CQ	55	ASN	2.4
30	AC	36	ASP	2.4
14	BG	87	PRO	2.4
46	B	1753	A	2.4
46	CM	1046	A	2.4
46	CM	1478	A	2.4
48	D	46	THR	2.4
56	L	161	ASN	2.4
56	CW	111	THR	2.4
77	DR	48	THR	2.4
79	DT	101	THR	2.4
80	p0	103	ASN	2.4
72	DM	53	ASP	2.4
47	C	207	PRO	2.4
60	DA	23	PRO	2.4
16	BI	129	TYR	2.4
21	0	172	TYR	2.4
26	8	118	GLY	2.4
38	CE	12	HIS	2.4
49	E	138	TYR	2.4
51	G	58	GLY	2.4
52	CS	68	VAL	2.4
53	I	129	VAL	2.4
59	O	66	VAL	2.4
61	Q	8	VAL	2.4
61	DB	116	VAL	2.4
62	DC	105	VAL	2.4
67	W	74	GLY	2.4
74	d	39	GLY	2.4
79	DT	105	VAL	2.4
82	L1	13	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
82	l1	115	VAL	2.4
1	1	1900	C	2.4
1	AS	1235	C	2.4
5	AX	23	ALA	2.4
6	AY	229	ALA	2.4
8	BA	106	ALA	2.4
1	1	918	U	2.4
1	1	1017	G	2.4
1	1	1484	G	2.4
1	1	2485	U	2.4
1	1	2487	U	2.4
1	1	2947	U	2.4
1	1	3174	G	2.4
1	AS	21	G	2.4
1	AS	251	G	2.4
1	AS	353	G	2.4
1	AS	1346	U	2.4
3	4	80	U	2.4
9	BB	108	GLN	2.4
10	BC	117	ILE	2.4
33	BZ	97	ILE	2.4
46	CM	228	C	2.4
50	F	120	ALA	2.4
51	G	13	ALA	2.4
46	CM	1358	G	2.4
51	G	169	ILE	2.4
52	CS	78	ALA	2.4
58	CY	61	ALA	2.4
67	W	117	ILE	2.4
67	DH	49	ILE	2.4
70	Z	12	ALA	2.4
25	BR	79	GLN	2.4
43	AP	22	GLN	2.4
46	B	507	G	2.4
46	B	1099	G	2.4
46	B	1474	G	2.4
46	B	1728	U	2.4
46	CM	378	U	2.4
61	Q	94	GLN	2.4
74	DO	18	GLN	2.4
53	I	68	MET	2.4
56	CW	91	MET	2.4

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Mol	Chain	Res	Type	RSRZ
4	j	70[A]	LYS	2.4
4	j	193	ARG	2.4
7	m	58	LYS	2.4
7	m	248	ARG	2.4
10	p	45	ARG	2.4
11	BD	124	ARG	2.4
13	s	35	LYS	2.4
15	BH	125	LYS	2.4
17	w	54	LYS	2.4
18	BK	61	ARG	2.4
19	BL	12	ARG	2.4
19	BL	147	ARG	2.4
20	z	82	LYS	2.4
28	BU	56	LYS	2.4
33	BZ	44	ARG	2.4
42	AO	8	LYS	2.4
47	C	27	LYS	2.4
50	F	42	LYS	2.4
53	CT	188	ARG	2.4
54	J	40	LYS	2.4
57	M	38	ARG	2.4
59	CZ	69	GLU	2.4
60	DA	106	ARG	2.4
61	DB	31	LYS	2.4
47	CN	81	PHE	2.4
48	D	175	GLU	2.4
48	D	191	GLU	2.4
51	G	205	PHE	2.4
52	H	35	GLU	2.4
62	R	72	ARG	2.4
71	DL	11	LYS	2.4
22	2	19	PHE	2.4
66	V	29	GLU	2.4
69	DJ	79	PHE	2.4
82	l1	114	GLU	2.4
18	x	170	SER	2.4
45	i	35	SER	2.4
48	D	227	SER	2.4
55	K	69	SER	2.4
64	T	89	SER	2.4
82	L1	208	SER	2.4
12	r	206	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
14	BG	116	LEU	2.4
16	BI	179	LEU	2.4
47	CN	3	LEU	2.4
53	CT	24	LEU	2.4
55	K	96	LEU	2.4
60	P	149	LEU	2.4
79	AR	145	LEU	2.4
82	l1	53	LEU	2.4
14	t	18	TRP	2.4
21	0	42	TRP	2.4
22	BO	53	PRO	2.4
31	BX	26	THR	2.4
33	AF	79	ASN	2.4
43	AP	26	THR	2.4
45	CL	33	ASN	2.4
52	H	164	PRO	2.4
54	CU	173	THR	2.4
56	CW	130	THR	2.4
58	CY	95	PRO	2.4
60	DA	21	ASN	2.4
62	R	30	THR	2.4
62	DC	7	PRO	2.4
66	DG	85	ASN	2.4
67	W	70	PRO	2.4
77	g	46	ASN	2.4
7	AZ	72	ASP	2.4
7	AZ	144	VAL	2.4
8	BA	4	VAL	2.4
15	BH	107	ASP	2.4
17	BJ	34	VAL	2.4
22	2	18	ASP	2.4
23	BP	44	ASP	2.4
32	BY	95	VAL	2.4
45	i	124	ASP	2.4
47	CN	200	ASP	2.4
52	H	22	VAL	2.4
62	DC	126	VAL	2.4
65	U	5	VAL	2.4
79	AR	283	ASP	2.4
79	DT	111	VAL	2.4
82	l1	70	ASP	2.4
5	k	123	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
9	BB	211	GLY	2.4
11	q	64	HIS	2.4
16	v	81	TYR	2.4
22	2	73	GLY	2.4
27	9	74	TYR	2.4
52	H	150	GLY	2.4
57	M	63	TYR	2.4
59	CZ	98	GLY	2.4
65	U	24	GLY	2.4
68	X	12	TYR	2.4
69	DJ	59	GLY	2.4
72	b	47	TYR	2.4
78	h	182	TYR	2.4
82	L1	51	GLY	2.4
7	m	106	ALA	2.4
10	p	149	ALA	2.4
28	BU	110	ALA	2.4
47	CN	61	ALA	2.4
46	CM	1316	A	2.4
48	D	32	ILE	2.4
51	CR	195	ILE	2.4
56	L	55	ALA	2.4
56	L	125	ALA	2.4
57	M	35	ILE	2.4
59	O	57	ALA	2.4
73	c	48	ALA	2.4
76	f	2	ALA	2.4
79	AR	286	ALA	2.4
1	1	917	A	2.4
1	1	1854	A	2.4
1	AS	1256	A	2.4
1	AS	1889	A	2.4
3	AU	1	A	2.4
11	q	136	ILE	2.4
46	CM	452	A	2.4
7	m	4	GLN	2.4
10	BC	239	MET	2.4
16	BI	93	LYS	2.4
27	BT	122	LYS	2.4
38	CE	30	GLN	2.4
40	CG	17	GLN	2.4
44	CK	6	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
45	i	109	GLN	2.4
48	CO	27	LYS	2.4
51	CR	100	ARG	2.4
54	J	72	ARG	2.4
54	CU	51	LYS	2.4
63	DD	76	GLN	2.4
67	DH	57	MET	2.4
54	CU	67	ARG	2.4
60	P	20	ARG	2.4
75	DP	18	ARG	2.4
9	o	151	PHE	2.4
9	BB	212	PHE	2.4
13	BF	102	PHE	2.4
21	0	150	PHE	2.4
64	T	71	PHE	2.4
1	1	1851	U	2.4
1	1	1890	U	2.4
1	1	2606	U	2.4
1	AS	1215	C	2.4
1	AS	2482	U	2.4
1	AS	2761	U	2.4
7	AZ	232	GLU	2.4
7	AZ	234	GLU	2.4
13	BF	11	GLU	2.4
13	BF	37	LEU	2.4
19	BL	173	GLU	2.4
26	8	82	LEU	2.4
28	BU	80	LEU	2.4
46	B	1080	U	2.4
46	B	1083	U	2.4
46	B	1627	C	2.4
46	B	1722	U	2.4
46	CM	636	C	2.4
46	CM	1477	U	2.4
47	C	12	GLU	2.4
52	H	97	LEU	2.4
53	I	24	LEU	2.4
53	I	122	GLU	2.4
54	CU	25	GLU	2.4
65	U	3	LEU	2.4
65	DF	18	LEU	2.4
69	DJ	38	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
6	l	8	SER	2.4
6	l	311	SER	2.4
19	y	167	SER	2.4
24	6	82	SER	2.4
38	AK	46	SER	2.4
47	CN	77	SER	2.4
48	CO	200	SER	2.4
59	O	53	SER	2.4
60	DA	13	SER	2.4
61	DB	120	SER	2.4
1	1	608	G	2.4
1	1	701	G	2.4
1	1	3034	G	2.4
1	AS	119	G	2.4
1	AS	170	G	2.4
1	AS	1230	G	2.4
46	B	289	G	2.4
46	B	1444	G	2.4
46	CM	512	G	2.4
46	CM	1441	G	2.4
76	f	42	CYS	2.4
20	z	23	TRP	2.4
6	l	160	VAL	2.4
7	AZ	278	THR	2.4
8	BA	64	VAL	2.4
18	x	70	THR	2.4
27	BT	82	VAL	2.4
38	AK	6	PRO	2.4
39	CF	72	THR	2.4
52	H	123	VAL	2.4
52	CS	23	VAL	2.4
53	CT	129	VAL	2.4
53	CT	173	PRO	2.4
54	CU	177	VAL	2.4
62	DC	75	VAL	2.4
63	DD	66	VAL	2.4
64	T	54	THR	2.4
69	Y	81	VAL	2.4
79	AR	27	PRO	2.4
9	o	210	GLY	2.4
9	BB	110	ASN	2.4
9	BB	241	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
16	BI	58	GLY	2.4
18	x	53	ASP	2.4
18	x	77	GLY	2.4
20	z	79	GLY	2.4
21	BN	11	GLY	2.4
22	2	2	GLY	2.4
24	BQ	65	GLY	2.4
32	BY	79	ASN	2.4
53	I	55	GLY	2.4
57	CX	72	GLY	2.4
65	DF	144	GLY	2.4
67	W	53	GLY	2.4
69	Y	55	ASP	2.4
71	a	53	ASP	2.4
74	d	69	GLY	2.4
79	DT	136	ASN	2.4
79	DT	256	GLY	2.4
80	p0	54	GLY	2.4
6	AY	122	ALA	2.4
6	AY	275	TYR	2.4
7	AZ	239	ILE	2.4
13	BF	110	ILE	2.4
23	5	78	TYR	2.4
24	BQ	51	ALA	2.4
26	BS	88	ILE	2.4
28	AA	18	TYR	2.4
32	AE	31	ALA	2.4
50	F	169	ILE	2.4
50	CQ	74	ILE	2.4
55	CV	78	ILE	2.4
63	S	107	ILE	2.4
65	DF	42	TYR	2.4
71	DL	13	ILE	2.4
9	BB	13	LYS	2.4
23	BP	77	LYS	2.4
28	BU	67	LYS	2.4
29	AB	34	LYS	2.4
29	AB	93	LYS	2.4
51	CR	200	LYS	2.4
54	J	52	LYS	2.4
61	DB	65	LYS	2.4
61	DB	77	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
64	DE	32	LYS	2.4
80	p0	8	LYS	2.4
8	n	134	ARG	2.4
10	p	58	ARG	2.4
16	v	50	ARG	2.4
19	BL	176	ARG	2.4
37	AJ	97	ARG	2.4
47	CN	41	ARG	2.4
55	CV	77	ARG	2.4
74	d	81	ARG	2.4
17	BJ	123	GLN	2.4
22	2	103	GLN	2.4
54	CU	127	PHE	2.4
56	L	104	PHE	2.4
61	DB	22	PHE	2.4
63	S	108	PHE	2.4
66	V	14	PHE	2.4
70	Z	38	PHE	2.4
17	BJ	20	LEU	2.4
52	CS	31	LEU	2.4
52	CS	58	LEU	2.4
53	CT	234	LEU	2.4
64	DE	24	LEU	2.4
82	ll	99	LEU	2.4
1	1	452	A	2.4
1	1	892	A	2.4
1	AS	689	A	2.4
1	AS	1247	A	2.4
1	AS	1831	A	2.4
1	AS	2302	A	2.4
28	BU	109	GLU	2.4
46	B	1574	A	2.4
46	CM	832	A	2.4
48	D	122	GLU	2.4
59	O	56	GLU	2.4
61	DB	68	GLU	2.4
80	p0	69	GLU	2.4
11	BD	150	SER	2.4
18	x	14	SER	2.4
29	AB	131	SER	2.4
31	BX	104	SER	2.4
48	D	186	SER	2.4

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Mol	Chain	Res	Type	RSRZ
54	J	111	SER	2.4
1	1	830	U	2.4
1	1	975	U	2.4
1	AS	252	U	2.4
7	m	177	PRO	2.4
7	m	236	VAL	2.4
8	BA	51	VAL	2.4
10	BC	53	TRP	2.4
10	BC	158	VAL	2.4
11	BD	24	VAL	2.4
15	u	115	VAL	2.4
22	BO	126	VAL	2.4
46	CM	276	U	2.4
46	CM	1674	U	2.4
47	C	11	PRO	2.4
47	CN	158	VAL	2.4
51	CR	83	PRO	2.4
56	CW	96	VAL	2.4
66	DG	2	PRO	2.4
1	1	1659	C	2.3
1	1	2311	C	2.3
1	1	2473	C	2.3
1	AS	131	C	2.3
1	AS	1280	C	2.3
1	AS	2457	C	2.3
1	AS	2746	C	2.3
5	k	309	GLY	2.3
20	BM	6	THR	2.3
24	BQ	8	GLY	2.3
32	AE	46	THR	2.3
46	B	1487	C	2.3
46	CM	651	C	2.3
35	AH	53	GLY	2.3
55	K	107	THR	2.3
63	S	14	THR	2.3
65	U	140	THR	2.3
74	d	67	THR	2.3
79	AR	205	GLY	2.3
5	k	261	ASN	2.3
10	BC	46	ASN	2.3
15	BH	36	LYS	2.3
16	BI	54	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
16	BI	140	LYS	2.3
19	y	8	LYS	2.3
20	z	121	HIS	2.3
4	j	184	ARG	2.3
4	j	203	ALA	2.3
5	k	115	ARG	2.3
7	AZ	207	TYR	2.3
9	BB	225	ASP	2.3
10	BC	227	TYR	2.3
11	q	88	TYR	2.3
16	v	12	ARG	2.3
20	z	170	ARG	2.3
20	BM	72	ALA	2.3
28	BU	29	HIS	2.3
29	BV	32	ARG	2.3
30	BW	16	ALA	2.3
33	BZ	68	ASN	2.3
36	AI	115	LYS	2.3
41	CH	43	ASN	2.3
49	E	87	ALA	2.3
58	N	49	ILE	2.3
59	CZ	27	ALA	2.3
59	CZ	125	ASN	2.3
67	W	22	ARG	2.3
67	DH	56	ARG	2.3
67	DH	117	ILE	2.3
71	a	97	ALA	2.3
72	DM	41	ILE	2.3
73	DN	13	LYS	2.3
21	BN	133	ASP	2.3
37	CD	75	ARG	2.3
51	G	149	TYR	2.3
52	H	148	ARG	2.3
52	CS	81	ARG	2.3
71	a	21	ARG	2.3
79	AR	293	ALA	2.3
80	p0	63	ILE	2.3
82	L1	109	ALA	2.3
82	L1	174	MET	2.3
1	1	2313	G	2.3
1	AS	856	G	2.3
1	AS	1353	G	2.3

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Mol	Chain	Res	Type	RSRZ
1	AS	1397	G	2.3
1	AS	1767	G	2.3
1	AS	1888	G	2.3
1	AS	3318	G	2.3
46	B	173	G	2.3
46	B	508	G	2.3
46	B	808	G	2.3
46	B	831	G	2.3
46	CM	830	G	2.3
46	CM	1672	G	2.3
9	o	193	PHE	2.3
30	AC	47	LEU	2.3
47	C	146	LEU	2.3
51	G	131	LEU	2.3
52	CS	118	LEU	2.3
55	CV	21	PHE	2.3
56	L	24	LEU	2.3
60	DA	125	LEU	2.3
61	DB	105	LEU	2.3
64	T	57	LEU	2.3
6	AY	227	GLU	2.3
7	m	234	GLU	2.3
20	BM	68	GLU	2.3
79	DT	232	GLU	2.3
7	m	125	VAL	2.3
7	AZ	74	VAL	2.3
28	BU	43	VAL	2.3
49	CP	188	VAL	2.3
51	G	102	VAL	2.3
60	DA	66	VAL	2.3
71	DL	12	VAL	2.3
82	L1	205	VAL	2.3
6	AY	278	PRO	2.3
20	z	54	PRO	2.3
23	5	22	PRO	2.3
50	F	44	PRO	2.3
1	1	730	A	2.3
1	1	3166	A	2.3
1	1	3341	A	2.3
10	p	30	SER	2.3
16	v	166	SER	2.3
24	6	7	SER	2.3

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Mol	Chain	Res	Type	RSRZ
41	CH	5	SER	2.3
10	p	122	THR	2.3
15	u	4	THR	2.3
15	BH	118	LYS	2.3
16	v	170	LYS	2.3
16	BI	80	THR	2.3
19	y	159	LYS	2.3
46	B	39	A	2.3
46	B	513	A	2.3
46	B	798	A	2.3
46	B	1169	A	2.3
46	B	1743	A	2.3
50	F	161	SER	2.3
50	F	222	PRO	2.3
60	P	143	SER	2.3
65	U	121	SER	2.3
74	d	60	SER	2.3
79	AR	125	SER	2.3
48	CO	32	ILE	2.3
49	CP	135	ARG	2.3
51	G	184	THR	2.3
54	J	113	THR	2.3
56	L	10	LYS	2.3
18	x	131	ARG	2.3
18	x	171	ARG	2.3
19	y	113	ARG	2.3
20	BM	30	THR	2.3
21	0	40	ARG	2.3
5	k	51	ALA	2.3
6	AY	249	ILE	2.3
6	AY	281	ILE	2.3
7	m	88	ILE	2.3
10	p	238	ILE	2.3
11	q	173	ARG	2.3
14	t	200	ALA	2.3
29	BV	28	HIS	2.3
35	CB	44	CYS	2.3
55	K	78	ILE	2.3
55	CV	170	ARG	2.3
59	CZ	40	GLY	2.3
63	DD	24	GLY	2.3
63	DD	132	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
64	T	25	THR	2.3
73	c	34	LYS	2.3
82	l1	39	LYS	2.3
47	C	145	ALA	2.3
47	CN	178	ALA	2.3
49	E	186	ALA	2.3
50	CQ	146	ALA	2.3
50	CQ	159	ILE	2.3
59	O	24	ILE	2.3
59	CZ	94	ALA	2.3
60	P	74	ILE	2.3
65	DF	88	ARG	2.3
63	DD	79	ALA	2.3
65	DF	125	ILE	2.3
67	W	96	ALA	2.3
69	Y	125	ILE	2.3
71	a	61	ARG	2.3
72	b	71	ILE	2.3
78	DS	158	ARG	2.3
62	R	79	HIS	2.3
77	DR	61	ALA	2.3
1	1	2438	U	2.3
1	1	2449	U	2.3
1	1	3163	U	2.3
1	AS	1545	U	2.3
1	AS	1561	U	2.3
1	AS	1564	U	2.3
1	AS	2947	U	2.3
5	AX	259	ASN	2.3
5	AX	283	TYR	2.3
7	m	3	MET	2.3
11	q	111	TYR	2.3
39	AL	34	ASN	2.3
39	AL	50	TYR	2.3
46	B	229	U	2.3
46	B	943	U	2.3
46	B	1363	U	2.3
51	CR	87	MET	2.3
55	K	88	ASN	2.3
67	W	43	ASN	2.3
1	AS	1220	C	2.3
1	AS	1250	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	AS	1392	C	2.3
1	AS	2816	C	2.3
9	BB	103	LEU	2.3
9	BB	199	PHE	2.3
13	s	163	PHE	2.3
17	w	29	LEU	2.3
46	B	130	C	2.3
46	B	1365	C	2.3
46	B	1726	C	2.3
46	B	1760	C	2.3
50	CQ	155	ASP	2.3
54	J	151	ASP	2.3
59	CZ	26	ASP	2.3
61	DB	48	ASP	2.3
71	DL	53	ASP	2.3
48	D	205	PHE	2.3
51	CR	180	LEU	2.3
53	CT	76	LEU	2.3
56	CW	76	LEU	2.3
70	DK	132	LEU	2.3
74	DO	63	LEU	2.3
17	BJ	27	GLN	2.3
32	AE	104	GLN	2.3
44	CK	32	GLN	2.3
69	DJ	76	GLN	2.3
70	DK	27	GLN	2.3
17	BJ	167	GLU	2.3
28	BU	102	GLU	2.3
71	DL	98	GLU	2.3
1	1	2426	G	2.3
1	AS	136	G	2.3
1	AS	1658	G	2.3
1	AS	1923	G	2.3
1	AS	2373	G	2.3
16	BI	60	VAL	2.3
25	7	53	VAL	2.3
35	CB	23	VAL	2.3
46	B	420	G	2.3
46	B	495	G	2.3
46	B	819	G	2.3
46	B	969	G	2.3
46	B	1528	G	2.3

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Mol	Chain	Res	Type	RSRZ
46	B	1775	G	2.3
46	CM	831	G	2.3
50	CQ	17	VAL	2.3
73	c	58	VAL	2.3
74	d	25	VAL	2.3
79	DT	134	VAL	2.3
9	o	92	LYS	2.3
14	t	199	LYS	2.3
16	BI	33	LYS	2.3
20	BM	128	LYS	2.3
23	5	42	LYS	2.3
34	CA	70	LYS	2.3
39	AL	44	LYS	2.3
42	AO	14	LYS	2.3
80	p0	23	LYS	2.3
7	m	181	PRO	2.3
7	AZ	181	PRO	2.3
10	BC	130	PRO	2.3
19	y	143	PRO	2.3
19	BL	61	PRO	2.3
25	7	94	ARG	2.3
29	BV	26	ARG	2.3
51	G	145	ARG	2.3
54	J	128	PRO	2.3
64	T	3	ARG	2.3
65	U	82	PRO	2.3
65	DF	123	ARG	2.3
66	V	102	ARG	2.3
71	DL	93	ARG	2.3
6	l	75	ILE	2.3
7	AZ	199	ILE	2.3
10	p	210	ALA	2.3
18	x	141	SER	2.3
22	BO	75	ILE	2.3
27	BT	61	GLY	2.3
33	AF	33	TRP	2.3
35	CB	89	ILE	2.3
44	CK	10	ILE	2.3
20	z	87	ALA	2.3
21	BN	167	ALA	2.3
41	AN	42	THR	2.3
45	CL	56	SER	2.3

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Mol	Chain	Res	Type	RSRZ
49	CP	120	ILE	2.3
49	CP	165	ILE	2.3
51	G	186	GLY	2.3
52	H	149	ILE	2.3
52	CS	187	ILE	2.3
53	I	112	SER	2.3
53	CT	15	SER	2.3
59	O	40	GLY	2.3
54	CU	74	THR	2.3
58	N	144	ALA	2.3
61	Q	120	SER	2.3
74	DO	61	THR	2.3
75	DP	59	SER	2.3
79	AR	255	SER	2.3
79	DT	151	TRP	2.3
79	DT	307	ILE	2.3
82	ll	51	GLY	2.3
65	U	50	ALA	2.3
65	U	83	ALA	2.3
82	ll	112	ALA	2.3
10	BC	233	HIS	2.3
32	BY	70	MET	2.3
51	G	98	HIS	2.3
82	ll	14	HIS	2.3
82	ll	184	MET	2.3
5	AX	49	TYR	2.3
20	BM	124	TYR	2.3
29	AB	90	TYR	2.3
49	E	61	TYR	2.3
64	DE	84	TYR	2.3
73	c	62	TYR	2.3
74	DO	37	CYS	2.3
4	j	96	LEU	2.3
7	m	45	ASN	2.3
8	n	145	LEU	2.3
12	BE	205	ASN	2.3
13	BF	40	LEU	2.3
19	y	52	LEU	2.3
24	BQ	69	LEU	2.3
48	D	207	LEU	2.3
48	CO	181	LEU	2.3
53	I	124	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
53	CT	133	LEU	2.3
59	O	136	LEU	2.3
59	CZ	103	LEU	2.3
66	V	28	LEU	2.3
72	b	80	LEU	2.3
73	DN	53	LEU	2.3
74	d	3	LEU	2.3
74	d	8	LEU	2.3
1	1	880	A	2.3
1	1	2446	A	2.3
1	AS	1266	A	2.3
1	AS	1585	A	2.3
1	AS	1907	A	2.3
1	AS	2773	A	2.3
1	AS	2775	A	2.3
2	AT	51	A	2.3
29	BV	68	PHE	2.3
36	AI	69	PHE	2.3
46	B	104	A	2.3
46	B	219	A	2.3
46	B	915	A	2.3
46	CM	918	A	2.3
47	C	89	PHE	2.3
51	G	86	PHE	2.3
53	CT	156	PHE	2.3
71	DL	85	PHE	2.3
20	z	86	ASP	2.3
33	BZ	40	ASP	2.3
47	CN	43	ASP	2.3
61	DB	20	ASP	2.3
71	a	38	ASP	2.3
79	AR	77	ASP	2.3
79	DT	77	ASP	2.3
1	1	895	U	2.3
1	1	1602	U	2.3
1	AS	895	U	2.3
1	AS	1434	U	2.3
1	AS	1536	U	2.3
1	AS	2818	U	2.3
1	AS	2968	U	2.3
9	o	17	GLN	2.3
9	BB	18	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
23	5	109	GLN	2.3
46	B	497	U	2.3
46	B	1332	U	2.3
46	CM	1217	U	2.3
63	DD	60	GLN	2.3
55	CV	191	GLU	2.3
67	DH	73	GLU	2.3
79	DT	236	GLU	2.3
1	1	2190	C	2.3
1	AS	240	C	2.3
1	AS	2315	C	2.3
1	AS	2610	C	2.3
4	AW	181	LYS	2.3
5	AX	335	VAL	2.3
8	n	4	VAL	2.3
8	BA	135	VAL	2.3
22	2	67	VAL	2.3
24	BQ	137	VAL	2.3
25	BR	22	VAL	2.3
42	CI	14	LYS	2.3
46	B	97	C	2.3
47	C	58	VAL	2.3
47	CN	67	VAL	2.3
50	F	59	VAL	2.3
51	G	133	LYS	2.3
51	CR	225	VAL	2.3
52	H	107	LYS	2.3
52	H	138	VAL	2.3
52	H	155	VAL	2.3
63	DD	89	VAL	2.3
68	DI	9	VAL	2.3
69	DJ	71	LYS	2.3
71	a	52	LYS	2.3
72	DM	58	LYS	2.3
74	DO	54	VAL	2.3
81	12	143	VAL	2.3
82	11	105	LYS	2.3
6	l	327	ARG	2.3
13	s	140	ARG	2.3
32	AE	18	ARG	2.3
33	AF	45	ARG	2.3
35	AH	58	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
37	AJ	14	ARG	2.3
53	CT	215	ARG	2.3
68	DI	22	ARG	2.3
4	AW	219	ILE	2.3
7	m	222	ILE	2.3
9	BB	172	GLY	2.3
20	z	83	GLY	2.3
34	AG	64	ILE	2.3
54	J	98	PRO	2.3
70	DK	118	PRO	2.3
81	12	163	PRO	2.3
51	CR	236	TRP	2.3
64	DE	2	GLY	2.3
65	U	124	GLY	2.3
79	DT	18	GLY	2.3
5	k	219	ALA	2.3
27	9	18	ALA	2.3
28	AA	11	ALA	2.3
32	BY	90	ALA	2.3
63	S	79	ALA	2.3
69	Y	10	ALA	2.3
74	d	71	ALA	2.3
81	12	136	ALA	2.3
5	AX	134	SER	2.3
6	l	288	THR	2.3
7	m	83	LEU	2.3
8	BA	146	LEU	2.3
18	x	145	HIS	2.3
22	2	142	SER	2.3
23	5	57	THR	2.3
31	AD	38	THR	2.3
33	AF	92	SER	2.3
44	AQ	11	THR	2.3
52	H	152	SER	2.3
53	CT	112	SER	2.3
53	I	216	LEU	2.3
53	CT	217	HIS	2.3
54	J	37	LEU	2.3
56	L	133	HIS	2.3
56	CW	160	HIS	2.3
59	O	92	SER	2.3
61	DB	29	SER	2.3

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Mol	Chain	Res	Type	RSRZ
64	T	106	THR	2.3
67	W	28	THR	2.3
78	h	189	THR	2.3
62	DC	79	HIS	2.3
79	AR	158	SER	2.3
80	P0	68	SER	2.3
36	AI	80	LEU	2.3
51	G	207	LEU	2.3
59	O	74	LEU	2.3
66	V	45	LEU	2.3
80	p0	39	HIS	2.3
1	1	353	G	2.3
1	1	1915	G	2.3
1	1	3057	G	2.3
1	AS	3305	G	2.3
4	j	69	TYR	2.3
21	0	94	TYR	2.3
26	BS	123	TYR	2.3
46	CM	923	G	2.3
46	CM	1038	G	2.3
50	CQ	153	TYR	2.3
51	CR	103	TYR	2.3
63	S	141	TYR	2.3
65	U	42	TYR	2.3
4	AW	63	PHE	2.3
5	AX	118	PHE	2.3
58	CY	60	PHE	2.3
76	DQ	52	PHE	2.3
9	o	241	ASN	2.3
10	BC	244	ASN	2.3
35	CB	14	ASN	2.3
51	CR	96	ASN	2.3
82	L1	12	ASN	2.3
82	l1	108	ASN	2.3
7	AZ	63	GLN	2.3
13	BF	111	ASP	2.3
30	BW	36	ASP	2.3
53	CT	185	GLN	2.3
55	K	105	ASP	2.3
80	p0	37	GLN	2.3
5	k	124	LYS	2.3
5	k	127	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
8	n	150	LYS	2.3
16	BI	128	LYS	2.3
17	w	26	LYS	2.3
17	BJ	177	LYS	2.3
33	BZ	91	LYS	2.3
36	CC	12	LYS	2.3
49	E	94	LYS	2.3
78	h	132	LYS	2.3
1	1	879	A	2.3
1	1	2116	A	2.3
1	1	2123	A	2.3
1	1	2304	A	2.3
1	AS	64	A	2.3
1	AS	1217	A	2.3
1	AS	1897	A	2.3
7	AZ	135	VAL	2.3
10	p	29	GLU	2.3
11	BD	123	VAL	2.3
18	BK	42	GLU	2.3
18	BK	152	GLU	2.3
19	y	78	GLU	2.3
22	BO	102	ARG	2.3
25	7	57	ARG	2.3
32	BY	66	VAL	2.3
45	CL	135	GLU	2.3
46	B	988	A	2.3
47	CN	180	GLU	2.3
51	CR	59	ARG	2.3
62	DC	26	VAL	2.3
63	S	98	GLU	2.3
65	DF	60	GLU	2.3
66	V	126	GLU	2.3
71	a	86	GLU	2.3
72	b	60	VAL	2.3
72	b	92	VAL	2.3
79	AR	152	VAL	2.3
1	1	1760	U	2.3
1	AS	185	U	2.3
1	AS	2814	U	2.3
46	B	1065	U	2.3
10	BC	144	ILE	2.3
26	8	142	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
27	9	106	ILE	2.3
40	AM	24	PRO	2.3
53	I	226	ILE	2.3
57	CX	86	ILE	2.3
65	DF	28	ILE	2.3
67	W	58	PRO	2.3
67	W	90	ILE	2.3
73	c	65	PRO	2.3
81	12	152	ILE	2.3
5	k	294	GLY	2.3
6	AY	166	ALA	2.3
7	AZ	106	ALA	2.3
9	BB	120	ALA	2.3
10	BC	88	ALA	2.3
13	s	42	GLY	2.3
15	BH	68	GLY	2.3
22	2	133	ALA	2.3
29	AB	114	GLY	2.3
29	AB	116	GLY	2.3
39	CF	62	ALA	2.3
47	C	159	ALA	2.3
49	E	95	ALA	2.3
49	CP	107	GLY	2.3
55	K	128	ALA	2.3
56	L	135	ALA	2.3
57	CX	23	ALA	2.3
59	CZ	51	ALA	2.3
65	DF	83	ALA	2.3
69	DJ	8	ALA	2.3
77	DR	11	ALA	2.3
78	DS	175	ALA	2.3
79	AR	300	ALA	2.3
79	DT	15	GLY	2.3
1	1	101	C	2.3
1	1	1798	C	2.3
1	1	3054	C	2.3
1	AS	1276	C	2.3
1	AS	1823	C	2.3
4	j	204	MET	2.3
46	B	1018	C	2.3
46	B	1182	C	2.3
46	B	1602	C	2.3

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Mol	Chain	Res	Type	RSRZ
59	CZ	126	TRP	2.3
79	DT	86	TRP	2.3
4	j	29	LEU	2.3
4	j	104	LEU	2.3
5	k	372	THR	2.3
6	l	237	LEU	2.3
7	m	277	LEU	2.3
7	AZ	36	LEU	2.3
10	BC	27	LEU	2.3
14	t	92	THR	2.3
18	x	151	THR	2.3
19	y	32	LEU	2.3
22	BO	27	LEU	2.3
23	BP	82	LEU	2.3
31	AD	43	LEU	2.3
33	AF	3	THR	2.3
47	CN	201	LEU	2.3
48	D	98	THR	2.3
64	DE	25	THR	2.3
64	DE	34	LEU	2.3
64	DE	54	THR	2.3
79	AR	100	THR	2.3
79	DT	23	LEU	2.3
19	y	184	PHE	2.3
22	BO	70	SER	2.3
24	BQ	7	SER	2.3
21	BN	172	TYR	2.3
24	BQ	11	PHE	2.3
44	AQ	14	PHE	2.3
50	CQ	7	SER	2.3
58	N	112	SER	2.3
58	CY	77	SER	2.3
60	DA	14	SER	2.3
61	DB	15	PHE	2.3
64	T	125	SER	2.3
72	b	57	TYR	2.3
76	DQ	14	PHE	2.3
79	DT	189	PHE	2.3
10	BC	138	ASN	2.3
5	k	269	GLN	2.3
6	l	164	LYS	2.3
6	AY	253	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
12	BE	13	LYS	2.3
26	8	25	LYS	2.3
28	AA	128	LYS	2.3
31	AD	42	LYS	2.3
32	AE	68	ASN	2.3
43	AP	61	LYS	2.3
7	m	22	ARG	2.3
12	r	69	ARG	2.3
38	AK	25	ARG	2.3
40	CG	42	ARG	2.3
44	CK	33	GLN	2.3
48	CO	109	LYS	2.3
49	E	184	GLN	2.3
50	F	225	LYS	2.3
50	CQ	152	LYS	2.3
53	I	149	LYS	2.3
51	G	11	ARG	2.3
51	G	191	ARG	2.3
53	I	177	ARG	2.3
54	J	167	GLN	2.3
64	T	33	ARG	2.3
65	DF	136	GLN	2.3
66	V	122	ARG	2.3
69	Y	28	ARG	2.3
69	DJ	24	GLN	2.3
71	DL	112	LYS	2.3
58	CY	11	ARG	2.3
74	DO	51	GLN	2.3
4	AW	208	ASP	2.3
10	BC	84	ASP	2.3
11	BD	154	VAL	2.3
16	BI	135	VAL	2.3
17	w	11	ASP	2.3
19	BL	125	ASP	2.3
23	BP	16	VAL	2.3
25	BR	106	ASP	2.3
28	BU	68	VAL	2.3
54	J	17	VAL	2.3
61	Q	112	ASP	2.3
64	DE	40	VAL	2.3
67	W	50	VAL	2.3
74	d	62	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
82	l1	74	VAL	2.3
5	k	94	GLU	2.2
7	m	263	GLU	2.2
7	AZ	237	GLU	2.2
8	BA	133	GLU	2.2
65	DF	7	GLU	2.2
67	DH	108	GLU	2.2
1	1	1014	G	2.2
1	AS	244	G	2.2
1	AS	364	G	2.2
1	AS	897	G	2.2
1	AS	1371	G	2.2
46	B	1334	G	2.2
46	CM	717	G	2.2
46	CM	1369	G	2.2
46	CM	1499	G	2.2
19	y	67	ILE	2.2
22	BO	25	ILE	2.2
31	BX	94	ILE	2.2
32	AE	35	ILE	2.2
53	CT	113	ILE	2.2
81	12	151	ILE	2.2
14	BG	50	PRO	2.2
15	BH	63	PRO	2.2
19	BL	97	PRO	2.2
6	l	219	ALA	2.2
14	BG	47	ALA	2.2
22	2	14	ALA	2.2
26	BS	122	ALA	2.2
27	BT	126	ALA	2.2
28	AA	125	GLY	2.2
34	AG	25	PRO	2.2
53	I	62	PRO	2.2
56	L	84	GLY	2.2
61	Q	125	GLY	2.2
64	T	65	PRO	2.2
67	W	54	PRO	2.2
28	BU	81	MET	2.2
30	BW	9	ALA	2.2
38	AK	42	ALA	2.2
62	R	39	ALA	2.2
66	DG	19	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
70	Z	106	GLY	2.2
73	c	44	MET	2.2
1	1	1612	U	2.2
1	1	2379	A	2.2
1	1	2433	U	2.2
1	1	3262	U	2.2
1	1	3296	U	2.2
1	AS	186	A	2.2
1	AS	220	A	2.2
1	AS	334	A	2.2
1	AS	804	A	2.2
1	AS	1099	A	2.2
1	AS	1590	A	2.2
1	AS	1692	A	2.2
1	AS	1843	A	2.2
1	AS	2305	U	2.2
1	AS	2431	U	2.2
1	AS	2463	A	2.2
1	AS	2696	U	2.2
14	BG	9	LEU	2.2
5	k	255	TRP	2.2
46	B	469	A	2.2
46	B	739	A	2.2
46	B	1361	A	2.2
46	CM	113	U	2.2
46	CM	711	U	2.2
46	CM	1102	U	2.2
46	CM	1670	U	2.2
46	CM	1673	U	2.2
55	CV	202	LEU	2.2
56	CW	109	LEU	2.2
57	M	89	LEU	2.2
64	DE	57	LEU	2.2
68	DI	78	LEU	2.2
71	a	17	LEU	2.2
79	AR	7	LEU	2.2
9	BB	9	THR	2.2
10	BC	166	PHE	2.2
14	BG	26	PHE	2.2
16	BI	158	HIS	2.2
19	y	35	PHE	2.2
27	BT	20	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
28	AA	136	PHE	2.2
47	C	23	HIS	2.2
51	CR	220	THR	2.2
53	CT	163	THR	2.2
54	CU	71	THR	2.2
61	Q	72	THR	2.2
62	DC	11	THR	2.2
62	DC	114	HIS	2.2
72	DM	90	THR	2.2
74	d	47	PHE	2.2
75	DP	39	THR	2.2
4	j	95	SER	2.2
10	p	67	SER	2.2
23	5	107	LYS	2.2
35	CB	37	LYS	2.2
37	CD	41	SER	2.2
39	CF	42	LYS	2.2
47	CN	78	SER	2.2
52	H	115	LYS	2.2
57	M	24	LYS	2.2
57	CX	66	TYR	2.2
58	N	29	LYS	2.2
69	Y	5	SER	2.2
78	DS	182	TYR	2.2
79	AR	153	SER	2.2
80	p0	94	LYS	2.2
1	1	3056	C	2.2
1	AS	1188	C	2.2
1	AS	2698	C	2.2
14	t	101	ARG	2.2
35	AH	9	ARG	2.2
46	B	442	C	2.2
46	B	1759	C	2.2
46	CM	1770	C	2.2
50	CQ	201	ARG	2.2
61	Q	79	ARG	2.2
65	U	88	ARG	2.2
77	g	43	ARG	2.2
5	k	143	GLN	2.2
5	AX	121	ASN	2.2
6	l	167	VAL	2.2
6	AY	160	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
6	AY	299	VAL	2.2
7	AZ	286	VAL	2.2
10	p	140	VAL	2.2
14	t	6	ASN	2.2
16	BI	89	VAL	2.2
18	BK	72	GLN	2.2
23	BP	41	VAL	2.2
27	BT	70	VAL	2.2
32	AE	95	VAL	2.2
32	AE	107	VAL	2.2
37	AJ	10	VAL	2.2
37	AJ	39	VAL	2.2
48	CO	173	GLN	2.2
50	F	224	VAL	2.2
50	CQ	187	VAL	2.2
52	CS	155	VAL	2.2
52	CS	160	VAL	2.2
52	CS	193	CYS	2.2
56	CW	136	VAL	2.2
65	DF	93	VAL	2.2
66	DG	25	GLN	2.2
67	W	89	VAL	2.2
68	X	59	VAL	2.2
70	Z	125	VAL	2.2
77	g	57	ASN	2.2
74	DO	40	CYS	2.2
82	ll	201	VAL	2.2
5	AX	291	GLU	2.2
7	m	232	GLU	2.2
7	AZ	25	GLU	2.2
20	z	55	GLU	2.2
23	BP	18	ASP	2.2
35	CB	87	GLU	2.2
45	CL	132	GLU	2.2
51	CR	88	ASP	2.2
54	CU	46	ASP	2.2
59	O	132	GLU	2.2
66	DG	8	ASP	2.2
79	DT	87	ASP	2.2
5	k	218	ILE	2.2
11	BD	55	ILE	2.2
17	BJ	10	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
27	9	50	ILE	2.2
53	CT	101	ILE	2.2
63	DD	64	ILE	2.2
82	ll	183	ILE	2.2
6	AY	170	LEU	2.2
6	AY	193	GLY	2.2
18	BK	112	LEU	2.2
22	2	106	LEU	2.2
22	BO	46	GLY	2.2
24	BQ	107	GLY	2.2
25	7	132	ALA	2.2
25	BR	24	GLY	2.2
26	BS	35	PRO	2.2
26	BS	107	ALA	2.2
34	AG	46	GLY	2.2
34	AG	95	GLY	2.2
35	AH	45	GLY	2.2
35	AH	59	PRO	2.2
35	CB	27	GLY	2.2
38	CE	42	ALA	2.2
39	AL	14	LEU	2.2
41	AN	25	ALA	2.2
45	i	165	LEU	2.2
47	CN	130	ALA	2.2
48	CO	96	LEU	2.2
49	CP	164	LEU	2.2
50	CQ	86	ALA	2.2
51	G	240	PRO	2.2
51	CR	214	LEU	2.2
52	H	174	LEU	2.2
52	CS	198	LEU	2.2
52	CS	204	GLY	2.2
53	CT	124	LEU	2.2
53	CT	189	ALA	2.2
54	J	99	ALA	2.2
55	K	119	ALA	2.2
55	CV	169	GLY	2.2
60	P	57	ALA	2.2
60	DA	47	PRO	2.2
61	DB	16	ALA	2.2
65	U	66	LEU	2.2
66	V	121	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
71	a	103	ALA	2.2
71	DL	33	ALA	2.2
76	f	47	ALA	2.2
78	DS	166	PRO	2.2
79	AR	244	PRO	2.2
79	DT	30	PRO	2.2
73	DN	67	LEU	2.2
80	P0	15	LEU	2.2
82	ll	166	ALA	2.2
70	Z	24	TRP	2.2
79	DT	19	TRP	2.2
1	1	93	G	2.2
1	1	500	G	2.2
1	1	794	G	2.2
1	1	1674	G	2.2
1	AS	1388	G	2.2
1	AS	2378	G	2.2
1	AS	2420	G	2.2
1	AS	2430	G	2.2
1	AS	2547	G	2.2
1	AS	2945	G	2.2
1	AS	3088	G	2.2
6	AY	339	LYS	2.2
7	m	142	PHE	2.2
10	BC	87	THR	2.2
13	BF	87	LYS	2.2
13	BF	174	LYS	2.2
23	5	102	LYS	2.2
33	AF	12	LYS	2.2
43	AP	10	THR	2.2
45	i	37	LYS	2.2
48	CO	142	PHE	2.2
46	B	262	G	2.2
46	B	677	G	2.2
46	B	1499	G	2.2
46	B	1699	G	2.2
48	CO	152	LYS	2.2
51	G	10	LYS	2.2
51	G	218	PHE	2.2
51	CR	230	THR	2.2
54	CU	43	LYS	2.2
64	DE	95	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
69	DJ	19	LYS	2.2
70	DK	122	PHE	2.2
55	CV	9	HIS	2.2
57	M	32	HIS	2.2
57	M	50	THR	2.2
67	DH	59	THR	2.2
77	DR	50	THR	2.2
82	L1	156	LYS	2.2
1	AS	1491	U	2.2
1	AS	1768	U	2.2
1	AS	2314	U	2.2
1	AS	2546	U	2.2
5	AX	117	ARG	2.2
7	m	207	TYR	2.2
7	AZ	248	ARG	2.2
8	BA	158	TYR	2.2
9	o	136	TYR	2.2
9	BB	131	TYR	2.2
11	BD	86	TYR	2.2
13	s	51	ARG	2.2
14	t	181	TYR	2.2
16	BI	187	ARG	2.2
22	BO	84	TYR	2.2
32	BY	11	TYR	2.2
41	CH	21	ARG	2.2
46	B	239	U	2.2
46	CM	1338	U	2.2
47	CN	79	ARG	2.2
54	J	137	ARG	2.2
62	DC	127	ARG	2.2
69	DJ	52	TYR	2.2
75	e	18	ARG	2.2
75	e	65	ARG	2.2
1	1	1812	A	2.2
1	1	2463	A	2.2
1	AS	1891	A	2.2
5	AX	327	SER	2.2
14	t	34	SER	2.2
14	t	144	SER	2.2
17	BJ	22	SER	2.2
22	BO	4	SER	2.2
31	BX	93	SER	2.2

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Mol	Chain	Res	Type	RSRZ
46	B	100	A	2.2
46	B	299	A	2.2
46	B	602	A	2.2
46	B	1501	A	2.2
46	CM	143	A	2.2
46	CM	1502	A	2.2
49	E	194	SER	2.2
51	G	16	SER	2.2
73	DN	54	SER	2.2
8	n	73	VAL	2.2
8	BA	38	VAL	2.2
22	BO	33	VAL	2.2
34	AG	71	VAL	2.2
52	H	90	VAL	2.2
53	I	97	VAL	2.2
57	CX	73	VAL	2.2
6	AY	60	GLN	2.2
14	BG	19	GLN	2.2
39	CF	66	GLN	2.2
56	CW	110	GLN	2.2
58	N	16	GLN	2.2
71	DL	110	GLN	2.2
6	l	329	ASN	2.2
10	p	244	ASN	2.2
52	H	44	ASN	2.2
55	CV	88	ASN	2.2
59	O	80	ASN	2.2
73	c	8	ASN	2.2
79	DT	225	ASN	2.2
80	P0	83	ASN	2.2
5	AX	147	GLU	2.2
6	l	148	GLU	2.2
6	AY	95	CYS	2.2
9	o	109	ILE	2.2
19	BL	57	ILE	2.2
22	2	86	GLU	2.2
27	9	26	GLU	2.2
28	BU	47	GLU	2.2
35	AH	81	CYS	2.2
35	CB	100	ILE	2.2
40	CG	35	ILE	2.2
48	CO	171	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
51	G	114	ILE	2.2
54	J	12	GLU	2.2
67	W	40	ILE	2.2
78	h	186	CYS	2.2
82	L1	67	ILE	2.2
82	l1	30	GLU	2.2
1	1	955	C	2.2
1	1	1223	C	2.2
1	1	3237	C	2.2
1	AS	1840	C	2.2
5	k	246	LEU	2.2
7	AZ	83	LEU	2.2
8	n	48	GLY	2.2
8	BA	80	ALA	2.2
18	x	35	ALA	2.2
18	BK	71	GLY	2.2
26	8	113	LEU	2.2
28	AA	50	PRO	2.2
29	BV	78	LEU	2.2
34	CA	7	LEU	2.2
36	AI	92	LEU	2.2
37	AJ	7	ALA	2.2
38	AK	9	GLY	2.2
41	AN	9	LEU	2.2
48	CO	172	MET	2.2
50	F	30	LEU	2.2
50	CQ	195	ALA	2.2
51	G	29	PRO	2.2
51	G	87	MET	2.2
53	I	155	ASP	2.2
54	J	46	ASP	2.2
56	CW	94	ASP	2.2
79	AR	269	ASP	2.2
79	AR	294	ASP	2.2
79	DT	204	ASP	2.2
79	DT	269	ASP	2.2
53	I	172	ALA	2.2
58	N	17	PRO	2.2
59	O	51	ALA	2.2
61	DB	70	GLY	2.2
61	DB	126	GLY	2.2
68	X	77	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
70	Z	37	ALA	2.2
73	DN	2	PRO	2.2
80	p0	82	GLY	2.2
7	m	288	LYS	2.2
11	q	170	LYS	2.2
19	BL	79	LYS	2.2
28	AA	73	LYS	2.2
31	AD	21	LYS	2.2
45	i	100	LYS	2.2
50	F	142	LYS	2.2
51	CR	241	LYS	2.2
53	CT	58	LYS	2.2
58	N	30	LYS	2.2
64	DE	49	LYS	2.2
70	DK	70	LYS	2.2
7	m	145	PHE	2.2
40	CG	7	PHE	2.2
5	k	266	ARG	2.2
15	u	10	TRP	2.2
62	R	33	PHE	2.2
62	DC	15	PHE	2.2
63	DD	128	PHE	2.2
64	DE	71	PHE	2.2
21	0	26	ARG	2.2
42	AO	6	ARG	2.2
56	L	69	ARG	2.2
63	S	122	ARG	2.2
70	Z	121	ARG	2.2
13	BF	99	THR	2.2
16	BI	194	HIS	2.2
18	x	129	THR	2.2
22	2	11	THR	2.2
29	BV	41	HIS	2.2
33	BZ	89	HIS	2.2
56	CW	124	HIS	2.2
64	T	56	HIS	2.2
65	DF	62	THR	2.2
67	W	106	THR	2.2
6	AY	210	TYR	2.2
13	s	52	TYR	2.2
33	BZ	93	TYR	2.2
9	o	154	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
15	u	13	VAL	2.2
18	x	119	VAL	2.2
48	CO	215	VAL	2.2
49	E	98	VAL	2.2
50	F	101	VAL	2.2
51	G	208	VAL	2.2
57	M	73	VAL	2.2
61	DB	43	VAL	2.2
67	DH	36	VAL	2.2
71	a	5	VAL	2.2
79	AR	72	VAL	2.2
79	AR	111	VAL	2.2
6	l	65	SER	2.2
6	AY	342	SER	2.2
16	v	204	SER	2.2
27	BT	13	SER	2.2
47	CN	2	SER	2.2
47	CN	137	SER	2.2
52	H	206	SER	2.2
79	DT	66	SER	2.2
82	ll	208	SER	2.2
1	1	1480	U	2.2
1	1	2961	U	2.2
1	1	3306	U	2.2
1	AS	167	U	2.2
1	AS	1077	U	2.2
1	AS	1881	U	2.2
1	AS	1908	U	2.2
1	AS	2438	U	2.2
14	t	166	GLN	2.2
16	v	123	GLN	2.2
16	BI	95	GLN	2.2
34	AG	31	GLN	2.2
44	AQ	32	GLN	2.2
46	B	815	U	2.2
46	B	1043	U	2.2
46	CM	672	U	2.2
46	CM	1048	U	2.2
50	CQ	102	GLN	2.2
60	DA	49	GLN	2.2
77	g	24	GLN	2.2
4	AW	136	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
6	l	10	ILE	2.2
8	BA	130	ILE	2.2
11	q	99	ILE	2.2
18	x	67	ILE	2.2
40	CG	27	ILE	2.2
41	AN	2	ILE	2.2
41	CH	19	ILE	2.2
49	E	124	ILE	2.2
66	DG	100	ILE	2.2
72	b	41	ILE	2.2
79	AR	259	ILE	2.2
18	BK	28	ASN	2.2
1	1	1429	A	2.2
1	1	1753	G	2.2
1	AS	182	G	2.2
1	AS	976	A	2.2
1	AS	2567	A	2.2
1	AS	2582	G	2.2
1	AS	2733	G	2.2
1	AS	3195	G	2.2
3	AU	39	G	2.2
6	l	149	LEU	2.2
6	l	259	LEU	2.2
7	m	163	LEU	2.2
7	m	228	GLU	2.2
12	r	210	LEU	2.2
18	BK	182	LEU	2.2
31	BX	59	GLU	2.2
32	BY	34	GLU	2.2
46	B	725	A	2.2
46	B	923	G	2.2
46	B	1149	G	2.2
46	B	1498	G	2.2
46	CM	420	G	2.2
46	CM	677	G	2.2
46	CM	1276	G	2.2
46	CM	1677	G	2.2
47	CN	24	LEU	2.2
51	CR	207	LEU	2.2
52	CS	217	LEU	2.2
69	DJ	126	LEU	2.2
80	P0	20	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
5	AX	253	GLY	2.2
6	l	229	ALA	2.2
7	m	243	ALA	2.2
10	BC	207	ALA	2.2
15	BH	72	ALA	2.2
19	y	142	GLY	2.2
23	5	45	GLY	2.2
27	BT	124	GLY	2.2
36	CC	87	ALA	2.2
47	C	61	ALA	2.2
47	C	161	PRO	2.2
48	CO	123	ALA	2.2
52	H	195	ALA	2.2
55	K	100	ALA	2.2
55	K	130	ALA	2.2
57	M	23	ALA	2.2
60	P	148	ALA	2.2
61	DB	101	ALA	2.2
62	R	28	MET	2.2
43	AP	12	CYS	2.2
43	AP	74	CYS	2.2
66	DG	42	GLY	2.2
66	DG	59	ALA	2.2
71	DL	4	ALA	2.2
82	ll	164	CYS	2.2
7	AZ	294	LYS	2.2
8	BA	22	LYS	2.2
10	p	85	LYS	2.2
36	CC	84[A]	LYS	2.2
43	AP	13	LYS	2.2
43	AP	78	LYS	2.2
54	J	124	ASP	2.2
57	CX	26	ASP	2.2
58	CY	36	LYS	2.2
63	DD	113	LYS	2.2
73	c	4	LYS	2.2
82	L1	97	LYS	2.2
7	m	179	ARG	2.2
10	BC	186	ARG	2.2
12	r	159	PHE	2.2
21	BN	143	PHE	2.2
29	AB	53	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
66	V	54	PHE	2.2
1	AS	53	C	2.2
1	AS	332	C	2.2
1	AS	2914	C	2.2
2	3	98	C	2.2
16	v	191	TRP	2.2
46	B	138	C	2.2
46	B	1770	C	2.2
46	CM	406	C	2.2
46	CM	1340	C	2.2
46	CM	1362	C	2.2
66	V	53	TRP	2.2
5	AX	256	HIS	2.2
6	AY	276	THR	2.2
19	BL	158	HIS	2.2
20	z	56	THR	2.2
20	BM	56	THR	2.2
44	AQ	34	HIS	2.2
47	C	53	THR	2.2
53	CT	183	THR	2.2
56	L	124	HIS	2.2
69	Y	4	THR	2.2
78	DS	140	HIS	2.2
79	AR	314	THR	2.2
79	DT	65	HIS	2.2
5	k	93	VAL	2.2
7	AZ	49	TYR	2.2
7	AZ	73	VAL	2.2
8	n	97	VAL	2.2
10	p	258	VAL	2.2
13	BF	69	VAL	2.2
14	BG	89	TYR	2.2
19	y	83	VAL	2.2
20	BM	51	VAL	2.2
23	5	36	TYR	2.2
43	AP	68	VAL	2.2
44	AQ	18	TYR	2.2
48	D	176	VAL	2.2
54	J	58	VAL	2.2
64	T	119	VAL	2.2
4	AW	158	ILE	2.2
5	k	183	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
6	AY	130	SER	2.2
10	p	117	ILE	2.2
10	BC	196	SER	2.2
18	BK	16	SER	2.2
18	BK	140	GLN	2.2
27	9	5	SER	2.2
28	BU	86	SER	2.2
38	AK	30	GLN	2.2
48	D	74	GLN	2.2
50	CQ	54	SER	2.2
52	H	113	ILE	2.2
52	CS	29	ILE	2.2
53	I	13	GLN	2.2
59	O	58	GLN	2.2
63	DD	140	SER	2.2
66	V	106	GLN	2.2
68	X	33	GLN	2.2
75	e	40	ILE	2.2
76	f	28	SER	2.2
79	DT	85	SER	2.2
9	o	127	LEU	2.2
27	9	30	LEU	2.2
32	BY	103	LEU	2.2
33	BZ	88	LEU	2.2
43	AP	104	LEU	2.2
45	i	129	LEU	2.2
53	CT	190	LEU	2.2
54	CU	13	LEU	2.2
54	CU	15	LEU	2.2
56	L	28	LEU	2.2
63	DD	115	LEU	2.2
79	DT	145	LEU	2.2
5	AX	197	GLU	2.2
5	AX	210	GLU	2.2
9	o	16	ALA	2.2
9	BB	27	ALA	2.2
14	t	60	ALA	2.2
17	BJ	190	GLU	2.2
1	1	772	U	2.2
1	1	1346	U	2.2
1	AS	1067	U	2.2
1	AS	1851	U	2.2

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Mol	Chain	Res	Type	RSRZ
1	AS	2690	U	2.2
7	AZ	182	GLY	2.2
17	BJ	70	GLY	2.2
19	y	132	PRO	2.2
20	z	114	LYS	2.2
20	BM	73	GLY	2.2
21	BN	141	LYS	2.2
22	BO	44	ALA	2.2
32	AE	23	ASN	2.2
36	CC	117	ALA	2.2
44	AQ	56	ASN	2.2
51	CR	231	GLU	2.2
49	E	150	PRO	2.2
50	F	76	LYS	2.2
51	CR	6	LYS	2.2
52	CS	104	ASN	2.2
53	I	9	ALA	2.2
58	CY	47	ALA	2.2
63	DD	19	ALA	2.2
66	DG	78	LYS	2.2
67	W	94	ALA	2.2
67	DH	80	ALA	2.2
73	DN	69	ASN	2.2
79	AR	241	ALA	2.2
79	AR	305	ASN	2.2
79	DT	305	ASN	2.2
46	B	348	U	2.2
46	CM	696	U	2.2
46	CM	943	U	2.2
52	CS	30	PRO	2.2
57	M	30	PRO	2.2
59	O	127	GLY	2.2
67	DH	72	GLY	2.2
82	ll	126	PRO	2.2
7	AZ	107	ARG	2.2
27	BT	16	ARG	2.2
28	BU	48	ARG	2.2
38	CE	45	ARG	2.2
41	CH	46	ARG	2.2
63	DD	131	ARG	2.2
76	f	19	ARG	2.2
47	C	190	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
48	CO	104	ASP	2.2
51	G	176	ASP	2.2
56	CW	47	PHE	2.2
62	DC	102	PHE	2.2
66	V	88	PHE	2.2
76	f	14	PHE	2.2
1	1	663	A	2.2
1	1	1692	A	2.2
1	1	2518	A	2.2
1	1	2774	A	2.2
1	AS	2446	A	2.2
1	AS	2469	A	2.2
46	CM	673	A	2.2
1	1	2430	G	2.2
1	AS	20	G	2.2
1	AS	949	G	2.2
1	AS	1017	G	2.2
1	AS	1361	G	2.2
6	l	251	TRP	2.2
46	B	823	G	2.2
46	B	1371	G	2.2
46	B	1486	G	2.2
48	CO	117	TRP	2.2
47	C	168	HIS	2.2
79	DT	238	HIS	2.2
82	L1	14	HIS	2.2
14	t	124	VAL	2.1
16	BI	101	THR	2.1
18	x	32	THR	2.1
18	BK	32	THR	2.1
27	BT	104	VAL	2.1
36	AI	6	THR	2.1
36	CC	85	THR	2.1
48	D	125	VAL	2.1
54	J	173	THR	2.1
54	CU	17	VAL	2.1
55	K	36	THR	2.1
58	N	64	VAL	2.1
63	DD	96	VAL	2.1
67	DH	28	THR	2.1
79	DT	314	THR	2.1
80	P0	33	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
82	L1	172	VAL	2.1
82	l1	52	THR	2.1
82	l1	149	THR	2.1
7	AZ	90	TYR	2.1
11	q	94	TYR	2.1
16	BI	202	TYR	2.1
25	BR	55	TYR	2.1
35	AH	62	TYR	2.1
52	CS	209	TYR	2.1
1	1	1332	C	2.1
1	1	1578	C	2.1
1	1	2545	C	2.1
1	AS	1788	C	2.1
9	o	166	ILE	2.1
11	BD	136	ILE	2.1
21	BN	123	ILE	2.1
23	BP	96	ILE	2.1
26	8	135	ILE	2.1
46	B	441	C	2.1
46	B	1294	C	2.1
46	B	1555	C	2.1
46	CM	1516	C	2.1
56	L	45	ILE	2.1
61	Q	110	ILE	2.1
73	c	36	ILE	2.1
5	k	178	LEU	2.1
5	AX	17	LEU	2.1
12	r	59	GLN	2.1
13	s	80	LEU	2.1
23	5	50	LEU	2.1
45	i	77	GLN	2.1
54	J	168	LEU	2.1
54	CU	38	GLN	2.1
56	L	86	LEU	2.1
57	M	17	GLN	2.1
62	DC	22	LEU	2.1
66	DG	20	GLN	2.1
72	b	93	LEU	2.1
79	AR	120	LEU	2.1
4	j	155	LYS	2.1
10	BC	226	LYS	2.1
12	r	184	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
13	s	153	LYS	2.1
48	CO	214	LYS	2.1
5	AX	141	ALA	2.1
6	l	172	ALA	2.1
8	BA	5	ALA	2.1
16	BI	125	SER	2.1
18	x	16	SER	2.1
18	BK	14	SER	2.1
25	BR	12	LYS	2.1
38	CE	43	LYS	2.1
14	t	118	GLU	2.1
14	t	150	GLU	2.1
4	AW	183	GLY	2.1
6	AY	206	PRO	2.1
10	p	177	PRO	2.1
16	BI	63	ARG	2.1
18	BK	75	GLU	2.1
21	BN	6	GLU	2.1
27	BT	18	ALA	2.1
38	CE	41	ALA	2.1
45	i	49	ALA	2.1
50	F	45	SER	2.1
50	F	100	ALA	2.1
52	H	47	SER	2.1
53	I	6	SER	2.1
55	K	124	LYS	2.1
63	S	2	SER	2.1
64	T	94	SER	2.1
64	T	111	LYS	2.1
66	V	97	SER	2.1
68	X	65	ALA	2.1
79	DT	125	SER	2.1
27	BT	91	ASN	2.1
32	BY	94	PRO	2.1
41	CH	40	GLY	2.1
45	CL	113	ARG	2.1
50	CQ	217	GLU	2.1
51	CR	30	ARG	2.1
52	H	218	GLU	2.1
82	L1	33	GLU	2.1
82	l1	84	ALA	2.1
48	CO	99	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
49	CP	222	PRO	2.1
55	CV	40	PRO	2.1
62	DC	98	ASN	2.1
67	W	109	PRO	2.1
67	DH	58	PRO	2.1
71	a	16	PRO	2.1
13	s	96	PHE	2.1
28	BU	92	PHE	2.1
37	CD	38	PHE	2.1
70	DK	43	PHE	2.1
79	AR	62	PHE	2.1
1	1	447	U	2.1
1	1	1118	U	2.1
1	AS	168	U	2.1
1	AS	246	U	2.1
1	AS	1814	U	2.1
1	AS	2131	U	2.1
16	BI	124	ASP	2.1
32	AE	83	ASP	2.1
46	B	253	U	2.1
46	B	849	U	2.1
46	CM	66	U	2.1
46	CM	888	U	2.1
49	E	73	ASP	2.1
63	S	112	ASP	2.1
67	W	91	ASP	2.1
67	DH	112	ASP	2.1
12	BE	197	VAL	2.1
16	BI	150	TRP	2.1
18	BK	133	HIS	2.1
20	z	22	VAL	2.1
44	AQ	47	VAL	2.1
44	CK	8	VAL	2.1
47	C	37	VAL	2.1
47	CN	54	TRP	2.1
51	CR	139	VAL	2.1
52	H	46	TRP	2.1
53	I	157	VAL	2.1
54	J	85	HIS	2.1
59	O	75	VAL	2.1
61	Q	24	HIS	2.1
61	Q	69	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
65	U	99	HIS	2.1
72	b	64	VAL	2.1
79	AR	238	HIS	2.1
81	12	118	HIS	2.1
39	CF	53	THR	2.1
60	DA	67	THR	2.1
68	X	20	THR	2.1
78	h	146	THR	2.1
1	AS	2070	A	2.1
4	j	158	ILE	2.1
4	AW	135	ILE	2.1
7	AZ	265	TYR	2.1
11	BD	180	TYR	2.1
14	t	89	TYR	2.1
36	CC	109	ILE	2.1
46	B	263	A	2.1
46	B	1476	A	2.1
46	CM	915	A	2.1
46	CM	1122	A	2.1
46	CM	1326	A	2.1
46	CM	1355	A	2.1
47	CN	47	ILE	2.1
56	L	156	ILE	2.1
58	CY	49	ILE	2.1
63	S	42	ILE	2.1
63	DD	141	TYR	2.1
4	j	68	LYS	2.1
6	l	113	LYS	2.1
7	m	48	LYS	2.1
7	m	51	LEU	2.1
7	m	164	LYS	2.1
7	m	194	LEU	2.1
7	m	218	LYS	2.1
8	BA	42	LEU	2.1
12	r	198	LYS	2.1
18	x	94	LEU	2.1
19	y	72	LYS	2.1
23	5	14	LYS	2.1
23	5	84	LYS	2.1
25	BR	97	LYS	2.1
26	BS	108	LEU	2.1
48	CO	33	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
50	F	10	LYS	2.1
50	CQ	76	LYS	2.1
52	H	124	LEU	2.1
52	CS	108	LEU	2.1
59	O	50	LYS	2.1
61	Q	105	LEU	2.1
67	DH	68	LYS	2.1
73	c	66	LYS	2.1
74	DO	41	LEU	2.1
82	L1	38	LEU	2.1
1	1	1902	G	2.1
1	1	2101	G	2.1
1	AS	171	G	2.1
1	AS	831	G	2.1
1	AS	2461	G	2.1
1	AS	2786	G	2.1
3	4	87	G	2.1
5	k	313	ARG	2.1
7	AZ	280	ALA	2.1
8	BA	134	ARG	2.1
13	BF	47	GLN	2.1
9	o	128	ALA	2.1
12	BE	41	ALA	2.1
29	BV	35	ALA	2.1
33	BZ	25	ARG	2.1
46	B	194	G	2.1
46	B	653	G	2.1
46	B	838	G	2.1
46	B	1581	G	2.1
46	B	1588	G	2.1
46	CM	887	G	2.1
46	CM	1571	G	2.1
51	G	30	ARG	2.1
51	G	119	ALA	2.1
53	I	215	ARG	2.1
55	K	139	ALA	2.1
71	a	19	ALA	2.1
79	AR	126	ALA	2.1
79	DT	233	ALA	2.1
80	p0	49	ALA	2.1
5	k	7	GLU	2.1
16	BI	69	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
20	z	137	SER	2.1
21	0	17	GLU	2.1
28	BU	94	SER	2.1
29	AB	143	GLY	2.1
1	1	1276	C	2.1
1	AS	112	C	2.1
1	AS	3314	C	2.1
6	AY	33	PRO	2.1
7	AZ	136	GLU	2.1
14	BG	34	SER	2.1
47	CN	82	GLY	2.1
48	D	60	GLY	2.1
49	E	107	GLY	2.1
49	E	140	GLY	2.1
49	E	155	GLY	2.1
52	CS	91	GLU	2.1
59	CZ	53	SER	2.1
59	CZ	87	PRO	2.1
62	DC	32	GLU	2.1
76	f	29	GLY	2.1
79	DT	35	SER	2.1
79	DT	215	GLY	2.1
80	p0	102	SER	2.1
80	p0	108	PRO	2.1
82	L1	132	GLY	2.1
46	B	1458	C	2.1
5	k	293	ASN	2.1
6	AY	317	ASN	2.1
8	BA	176	PHE	2.1
9	o	203	PHE	2.1
34	CA	84	ASN	2.1
47	CN	33	ASN	2.1
55	CV	65	PHE	2.1
71	a	85	PHE	2.1
80	P0	56	ASN	2.1
4	j	113	VAL	2.1
7	m	214	ASP	2.1
13	BF	126	ASP	2.1
15	BH	22	ASP	2.1
16	BI	35	VAL	2.1
17	w	37	VAL	2.1
21	BN	61	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
29	AB	130	VAL	2.1
51	G	73	ASP	2.1
52	H	60	ASP	2.1
53	CT	162	VAL	2.1
55	K	186	ASP	2.1
58	N	94	VAL	2.1
67	DH	89	VAL	2.1
68	DI	13	VAL	2.1
69	DJ	9	ASP	2.1
75	DP	28	VAL	2.1
76	f	7	TRP	2.1
29	BV	11	HIS	2.1
43	CJ	20	HIS	2.1
49	CP	54	HIS	2.1
70	Z	48	HIS	2.1
1	1	752	U	2.1
1	1	1490	U	2.1
1	1	1881	U	2.1
1	1	3165	U	2.1
1	AS	918	U	2.1
1	AS	2815	U	2.1
4	AW	24	LYS	2.1
5	AX	56	ILE	2.1
6	l	61	THR	2.1
6	l	137	LEU	2.1
6	AY	291	ILE	2.1
7	AZ	56	THR	2.1
7	AZ	120	THR	2.1
9	o	88	LYS	2.1
9	o	221	ILE	2.1
10	p	68	LEU	2.1
10	BC	202	THR	2.1
11	q	48	ILE	2.1
18	BK	41	LEU	2.1
19	BL	124	LEU	2.1
20	BM	106	LEU	2.1
26	8	28	THR	2.1
28	BU	73	LYS	2.1
33	AF	90	THR	2.1
33	BZ	105	LYS	2.1
35	AH	70	LYS	2.1
36	AI	41	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
36	CC	56	THR	2.1
22	2	7	TYR	2.1
36	CC	70	TYR	2.1
40	CG	34	LYS	2.1
45	CL	53	LYS	2.1
46	B	205	U	2.1
46	B	727	U	2.1
46	B	1199	U	2.1
46	CM	697	U	2.1
46	CM	778	U	2.1
46	CM	1191	U	2.1
46	CM	1515	U	2.1
46	CM	1669	U	2.1
48	D	217	LEU	2.1
49	E	36	LEU	2.1
49	E	112	THR	2.1
52	H	176	THR	2.1
52	H	198	LEU	2.1
54	J	95	LEU	2.1
54	CU	147	LYS	2.1
55	K	123	LYS	2.1
56	L	52	ILE	2.1
58	N	97	TYR	2.1
61	Q	85	LYS	2.1
61	Q	107	ILE	2.1
63	S	12	LYS	2.1
69	Y	39	THR	2.1
70	Z	50	LYS	2.1
74	d	36	LYS	2.1
76	DQ	38	LEU	2.1
79	AR	240	LEU	2.1
79	DT	268	LEU	2.1
80	P0	63	ILE	2.1
56	L	95	TYR	2.1
82	l1	116	LEU	2.1
8	n	76	ARG	2.1
10	BC	99	ARG	2.1
16	BI	50	ARG	2.1
16	BI	147	ARG	2.1
40	CG	21[A]	ARG	2.1
54	CU	135	ARG	2.1
55	CV	143	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
63	DD	123	MET	2.1
79	DT	156	ARG	2.1
5	k	75	ALA	2.1
6	l	16	GLN	2.1
7	m	80	ALA	2.1
12	r	41	ALA	2.1
14	BG	60	ALA	2.1
27	9	120	GLN	2.1
38	CE	79	GLN	2.1
50	CQ	221	ALA	2.1
55	K	79	ALA	2.1
55	CV	151	ALA	2.1
57	M	62	GLN	2.1
58	N	108	ALA	2.1
59	O	42	ALA	2.1
60	P	62	GLN	2.1
63	S	135	ALA	2.1
64	DE	74	GLN	2.1
79	DT	286	ALA	2.1
80	p0	107	ALA	2.1
1	1	976	A	2.1
1	1	1896	A	2.1
1	1	2121	A	2.1
1	1	2273	A	2.1
1	1	2959	A	2.1
1	AS	106	A	2.1
1	AS	212	A	2.1
1	AS	327	A	2.1
1	AS	2675	A	2.1
2	3	64	A	2.1
6	l	174	GLY	2.1
7	AZ	263	GLU	2.1
12	BE	16	PRO	2.1
13	BF	118	PRO	2.1
24	6	55	GLY	2.1
37	CD	87	GLU	2.1
46	B	223	A	2.1
46	B	718	A	2.1
46	B	844	A	2.1
47	CN	152	PRO	2.1
49	E	234	PRO	2.1
53	CT	35	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
53	CT	146	GLY	2.1
53	CT	232	GLU	2.1
54	J	36	PRO	2.1
66	DG	90	PRO	2.1
68	DI	10	GLU	2.1
75	e	17	GLY	2.1
8	BA	163	PHE	2.1
10	BC	75	SER	2.1
11	q	45	PHE	2.1
13	BF	93	SER	2.1
17	w	4	PHE	2.1
18	BK	144	SER	2.1
34	CA	21	SER	2.1
45	i	110	SER	2.1
47	CN	7	PHE	2.1
59	CZ	65	SER	2.1
66	V	99	SER	2.1
82	L1	20	SER	2.1
82	L1	113	SER	2.1
14	t	12	ASN	2.1
18	BK	169	ASN	2.1
24	6	33	ASN	2.1
27	BT	44	ASN	2.1
28	AA	127	ASN	2.1
38	CE	13	ASN	2.1
48	CO	124	ASN	2.1
66	DG	43	ASN	2.1
1	1	1439	G	2.1
1	1	2261	G	2.1
1	AS	368	G	2.1
1	AS	1476	G	2.1
1	AS	1517	G	2.1
1	AS	1762	G	2.1
1	AS	2342	G	2.1
1	AS	3133	G	2.1
1	AS	3321	G	2.1
5	AX	158	VAL	2.1
17	BJ	35	VAL	2.1
21	BN	36	VAL	2.1
22	BO	40	VAL	2.1
33	AF	85	VAL	2.1
36	CC	66	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
46	B	6	G	2.1
46	B	496	G	2.1
46	B	861	G	2.1
46	CM	508	G	2.1
46	CM	1155	G	2.1
46	CM	1659	G	2.1
48	D	43	VAL	2.1
49	E	97	VAL	2.1
62	R	105	VAL	2.1
62	DC	2	VAL	2.1
65	DF	133	VAL	2.1
79	DT	309	VAL	2.1
82	ll	13	VAL	2.1
1	1	1624	C	2.1
1	1	2308	C	2.1
1	AS	346	C	2.1
1	AS	1544	C	2.1
46	B	1051	C	2.1
46	B	1119	C	2.1
46	CM	534	C	2.1
5	AX	128	LYS	2.1
14	BG	88	LYS	2.1
16	BI	5	LYS	2.1
7	m	113	LEU	2.1
11	BD	4	ILE	2.1
14	BG	123	LEU	2.1
18	BK	67	ILE	2.1
19	y	36	LEU	2.1
19	y	112	ASP	2.1
25	7	116	LYS	2.1
37	AJ	66	LYS	2.1
44	AQ	7	LYS	2.1
45	CL	50	LYS	2.1
22	2	85	ILE	2.1
25	BR	89	LEU	2.1
29	BV	105	LEU	2.1
31	BX	58	LEU	2.1
45	CL	111	ASP	2.1
47	C	148	ASP	2.1
49	E	74	ASP	2.1
50	CQ	8	LYS	2.1
52	H	135	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
58	N	56	LYS	2.1
52	CS	93	LEU	2.1
59	O	86	ILE	2.1
61	Q	66	CYS	2.1
61	DB	100	LEU	2.1
65	DF	112	ASP	2.1
68	DI	67	ASP	2.1
72	b	48	ASP	2.1
73	c	52	ASP	2.1
74	d	59	CYS	2.1
79	AR	180	LEU	2.1
79	AR	192	HIS	2.1
79	DT	219	LEU	2.1
5	AX	242	THR	2.1
7	AZ	282	ARG	2.1
8	n	107	ARG	2.1
11	q	70	THR	2.1
12	BE	216	TYR	2.1
14	BG	181	TYR	2.1
16	v	196	THR	2.1
20	z	173	ARG	2.1
22	2	5	ARG	2.1
22	2	102	ARG	2.1
30	BW	26	THR	2.1
42	AO	17	ARG	2.1
45	i	113	ARG	2.1
47	C	62	ARG	2.1
51	G	3	ARG	2.1
52	H	102	ARG	2.1
51	G	138	TYR	2.1
53	I	12	THR	2.1
55	K	184	ARG	2.1
59	O	55	ARG	2.1
67	DH	26	THR	2.1
69	DJ	2	THR	2.1
82	ll	5	THR	2.1
78	h	177	MET	2.1
82	L1	185	MET	2.1
5	AX	295	ALA	2.1
14	t	33	ALA	2.1
22	BO	24	ALA	2.1
30	BW	55	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
51	G	258	ALA	2.1
52	CS	179	ALA	2.1
62	DC	39	ALA	2.1
73	DN	48	ALA	2.1
1	1	2442	U	2.1
1	1	2537	U	2.1
1	1	2690	U	2.1
1	AS	1084	U	2.1
1	AS	1347	U	2.1
1	AS	1565	U	2.1
9	BB	102	GLN	2.1
20	BM	7	GLN	2.1
46	B	225	U	2.1
46	B	576	U	2.1
46	B	696	U	2.1
58	CY	14	GLN	2.1
76	DQ	41	GLN	2.1
11	q	119	GLY	2.1
13	BF	73	GLY	2.1
20	BM	129	GLY	2.1
35	CB	45	GLY	2.1
43	CJ	52	GLY	2.1
55	K	122	GLY	2.1
60	P	44	GLY	2.1
67	W	110	GLY	2.1
70	DK	119	GLY	2.1
79	DT	106	GLY	2.1
7	AZ	177	PRO	2.1
8	BA	12	GLU	2.1
9	BB	191	PRO	2.1
10	BC	211	GLU	2.1
26	BS	44	PRO	2.1
28	BU	130	PHE	2.1
52	CS	129	PRO	2.1
56	CW	114	PHE	2.1
57	CX	16	PHE	2.1
59	O	76	GLU	2.1
61	Q	89	PRO	2.1
74	DO	66	PRO	2.1
75	DP	32	PHE	2.1
82	L1	134	PHE	2.1
7	m	66	SER	2.1

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Mol	Chain	Res	Type	RSRZ
19	BL	7	SER	2.1
19	BL	34	SER	2.1
38	CE	36	SER	2.1
47	C	137	SER	2.1
54	J	2	SER	2.1
54	CU	62	SER	2.1
54	CU	152	SER	2.1
56	CW	121	SER	2.1
56	CW	152	SER	2.1
79	DT	61	SER	2.1
79	DT	184	SER	2.1
6	l	72	VAL	2.1
6	AY	296	VAL	2.1
8	BA	90	VAL	2.1
28	AA	13	VAL	2.1
28	AA	53	VAL	2.1
28	AA	89	VAL	2.1
34	CA	22	VAL	2.1
47	CN	123	VAL	2.1
51	G	126	VAL	2.1
51	CR	45	VAL	2.1
51	CR	89	VAL	2.1
51	CR	129	VAL	2.1
52	H	111	VAL	2.1
56	L	96	VAL	2.1
56	L	136	VAL	2.1
56	CW	85	VAL	2.1
62	DC	112	VAL	2.1
65	DF	100	VAL	2.1
66	V	37	VAL	2.1
73	DN	30	VAL	2.1
1	1	651	A	2.1
1	1	1023	A	2.1
1	1	1139	A	2.1
1	1	1825	A	2.1
1	AS	319	A	2.1
1	AS	958	A	2.1
1	AS	1075	A	2.1
1	AS	1576	A	2.1
1	AS	2612	A	2.1
7	AZ	57	ASN	2.1
13	s	174	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
15	u	126	LYS	2.1
19	y	136	ASN	2.1
31	AD	40	LYS	2.1
38	AK	14	LYS	2.1
46	B	47	A	2.1
46	B	218	A	2.1
46	B	1241	A	2.1
46	CM	1370	A	2.1
47	C	33	ASN	2.1
51	G	108	LYS	2.1
67	W	20	LYS	2.1
68	X	25	LYS	2.1
70	Z	70	LYS	2.1
70	Z	82	LYS	2.1
71	a	113	ASN	2.1
78	h	125	LYS	2.1
79	DT	213	LYS	2.1
80	P0	81	LYS	2.1
4	AW	196	TRP	2.1
7	AZ	211	LEU	2.1
8	BA	39	LEU	2.1
16	v	98	LEU	2.1
7	m	203	HIS	2.1
14	BG	17	HIS	2.1
16	BI	200	TRP	2.1
20	BM	88	ARG	2.1
20	BM	138	LEU	2.1
23	BP	37	LEU	2.1
26	BS	114	ILE	2.1
32	AE	58	ILE	2.1
34	CA	54	ARG	2.1
36	CC	114	ARG	2.1
42	CI	17	ARG	2.1
48	D	228	LEU	2.1
49	E	165	ILE	2.1
49	CP	36	LEU	2.1
53	CT	202	ARG	2.1
55	K	141	ARG	2.1
59	CZ	71	ILE	2.1
64	DE	26	LEU	2.1
66	DG	135	ILE	2.1
65	DF	13	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
69	DJ	78	ARG	2.1
70	Z	132	LEU	2.1
72	b	81	ARG	2.1
75	e	22	ARG	2.1
79	AR	95	LEU	2.1
82	ll	103	LEU	2.1
79	DT	16	HIS	2.1
7	AZ	184	ASP	2.1
7	AZ	215	ASP	2.1
10	p	208	ASP	2.1
63	S	97	ASP	2.1
7	m	79	TYR	2.1
13	s	128	TYR	2.1
17	BJ	93	THR	2.1
19	y	100	THR	2.1
31	BX	25	TYR	2.1
39	AL	41	THR	2.1
44	AQ	46	THR	2.1
68	X	1	MET	2.1
69	DJ	85	ASP	2.1
51	CR	159	THR	2.1
53	I	168	THR	2.1
56	L	164	TYR	2.1
58	N	35	TYR	2.1
60	DA	129	TYR	2.1
72	DM	102	THR	2.1
74	DO	59	CYS	2.1
79	AR	227	THR	2.1
82	L1	164	CYS	2.1
1	1	1224	C	2.1
1	1	1752	C	2.1
1	1	2072	C	2.1
1	1	2745	C	2.1
1	AS	1065	C	2.1
1	AS	1088	C	2.1
1	AS	1775	C	2.1
1	AS	2521	C	2.1
3	4	151	C	2.1
1	1	88	G	2.1
1	1	676	G	2.1
1	1	876	G	2.1
1	1	1025	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	1	1482	G	2.1
1	1	2726	G	2.1
1	1	2949	G	2.1
1	AS	63	G	2.1
1	AS	1245	G	2.1
1	AS	1649	G	2.1
1	AS	3217	G	2.1
3	AU	103	G	2.1
7	AZ	192	ALA	2.1
10	BC	123	ALA	2.1
12	r	25	ALA	2.1
13	s	76	ALA	2.1
27	BT	93	ALA	2.1
46	B	228	C	2.1
46	B	261	C	2.1
46	B	912	C	2.1
46	B	1442	C	2.1
46	CM	726	C	2.1
46	CM	928	C	2.1
46	CM	1269	C	2.1
46	CM	1471	C	2.1
46	CM	1726	C	2.1
46	B	288	G	2.1
46	B	460	G	2.1
46	B	794	G	2.1
46	B	971	G	2.1
46	B	1093	G	2.1
46	B	1273	G	2.1
46	B	1369	G	2.1
46	B	1616	G	2.1
46	CM	386	G	2.1
46	CM	715	G	2.1
46	CM	863	G	2.1
46	CM	1103	G	2.1
46	CM	1115	G	2.1
50	F	212	ALA	2.1
51	CR	258	ALA	2.1
54	J	157	ALA	2.1
55	CV	133	ALA	2.1
55	CV	157	ALA	2.1
67	DH	94	ALA	2.1
79	DT	235	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
4	AW	86	GLN	2.1
7	m	202	GLY	2.1
11	q	5	GLN	2.1
24	BQ	43	GLY	2.1
29	BV	65	GLN	2.1
31	AD	84	GLY	2.1
36	AI	107	GLN	2.1
51	CR	130	GLN	2.1
54	J	183	GLY	2.1
56	CW	32	GLY	2.1
56	CW	139	GLN	2.1
65	DF	89	GLN	2.1
66	DG	12	GLN	2.1
66	DG	48	GLN	2.1
66	DG	129	GLN	2.1
77	DR	12	GLY	2.1
82	ll	202	GLY	2.1
5	k	16	PHE	2.1
7	m	128	GLU	2.1
7	AZ	200	PHE	2.1
10	p	209	GLU	2.1
18	BK	60	PHE	2.1
18	BK	90	PHE	2.1
32	AE	34	GLU	2.1
34	CA	58	GLU	2.1
45	i	57	PRO	2.1
47	CN	102	PHE	2.1
53	CT	45	PHE	2.1
53	CT	122	GLU	2.1
53	CT	130	PRO	2.1
54	J	91	GLU	2.1
62	DC	125	PRO	2.1
66	DG	141	GLU	2.1
82	ll	121	PRO	2.1
1	1	1024	U	2.0
1	1	1820	U	2.0
5	k	205	VAL	2.0
5	k	249	VAL	2.0
10	BC	129	LYS	2.0
14	t	190	LYS	2.0
27	9	25	VAL	2.0
27	BT	56	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
33	BZ	78	LYS	2.0
41	CH	49	LYS	2.0
42	AO	7	LYS	2.0
43	CJ	13	LYS	2.0
46	B	73	U	2.0
46	B	675	U	2.0
46	CM	136	U	2.0
46	CM	638	U	2.0
46	CM	1351	U	2.0
48	D	160	LYS	2.0
49	CP	98	VAL	2.0
50	F	109	LYS	2.0
51	G	75	LYS	2.0
54	CU	101	LYS	2.0
59	CZ	123	VAL	2.0
60	DA	34	VAL	2.0
60	DA	140	LYS	2.0
65	U	52	VAL	2.0
67	W	29	LYS	2.0
68	X	13	VAL	2.0
68	X	32	VAL	2.0
71	DL	100	VAL	2.0
78	DS	131	LYS	2.0
13	s	93	SER	2.0
19	BL	13	SER	2.0
23	BP	75	SER	2.0
36	CC	19	SER	2.0
41	AN	11	SER	2.0
45	CL	99	SER	2.0
71	a	56	SER	2.0
5	k	387	LEU	2.0
5	AX	110	LEU	2.0
8	n	79	ASN	2.0
14	BG	125	ILE	2.0
16	v	10	LEU	2.0
20	z	62	ARG	2.0
22	2	146	ASN	2.0
25	BR	105	ARG	2.0
28	BU	78	ASN	2.0
29	AB	66	ASN	2.0
31	BX	18	LEU	2.0
33	BZ	48	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
37	CD	97	ARG	2.0
39	AL	5	ILE	2.0
50	F	22	LEU	2.0
52	H	180	ARG	2.0
54	J	24	LEU	2.0
54	J	94	ILE	2.0
60	P	92	ILE	2.0
61	DB	13	ARG	2.0
62	R	103	ASN	2.0
62	DC	57	ILE	2.0
63	S	81	ARG	2.0
65	DF	35	ILE	2.0
65	DF	66	LEU	2.0
66	V	85	ASN	2.0
67	W	62	LEU	2.0
67	DH	21	ILE	2.0
71	DL	113	ASN	2.0
74	d	41	LEU	2.0
79	DT	287	ILE	2.0
82	L1	159	LEU	2.0
27	9	100	HIS	2.0
48	CO	79	HIS	2.0
78	h	174	MET	2.0
1	1	44	A	2.0
1	1	862	A	2.0
1	1	2350	A	2.0
1	AS	47	A	2.0
1	AS	709	A	2.0
1	AS	1608	A	2.0
1	AS	2427	A	2.0
5	k	8	ALA	2.0
5	k	176	ALA	2.0
5	k	179	ALA	2.0
5	k	292	ALA	2.0
7	m	198	TYR	2.0
9	o	214	ALA	2.0
13	s	167	TYR	2.0
20	BM	112	ALA	2.0
24	6	115	THR	2.0
31	BX	62	ALA	2.0
45	i	133	ALA	2.0
46	B	65	A	2.0

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Mol	Chain	Res	Type	RSRZ
46	B	220	A	2.0
46	B	1212	A	2.0
46	B	1622	A	2.0
46	CM	829	A	2.0
46	CM	850	A	2.0
47	C	129	ASP	2.0
48	D	59	ASP	2.0
50	F	88	TYR	2.0
52	CS	32	ASP	2.0
56	CW	43	TYR	2.0
68	X	45	ALA	2.0
72	DM	59	TYR	2.0
74	d	44	THR	2.0
76	f	49	ASP	2.0
74	d	40	CYS	2.0
6	l	197	GLY	2.0
7	AZ	149	GLY	2.0
12	BE	133	GLN	2.0
16	BI	163	GLY	2.0
18	x	125	GLN	2.0
36	CC	62	GLN	2.0
13	s	118	PRO	2.0
36	AI	112	PRO	2.0
39	AL	43	PHE	2.0
48	D	100	PHE	2.0
48	D	233	GLY	2.0
51	G	244	GLY	2.0
51	CR	261	GLY	2.0
52	H	75	GLY	2.0
52	H	158	GLN	2.0
54	CU	174	GLY	2.0
57	M	58	GLN	2.0
58	CY	137	PHE	2.0
60	P	36	GLN	2.0
69	Y	109	GLY	2.0
82	ll	35	GLN	2.0
52	H	88	PRO	2.0
7	AZ	245	GLU	2.0
1	1	798	C	2.0
1	1	800	C	2.0
1	1	1271	C	2.0
1	1	3227	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	AS	207	C	2.0
1	AS	1360	C	2.0
1	AS	1752	C	2.0
1	AS	1766	C	2.0
13	BF	142	LYS	2.0
16	v	56	LYS	2.0
19	y	46	LYS	2.0
27	BT	89	LYS	2.0
29	BV	115	LYS	2.0
30	BW	15	LYS	2.0
48	D	67	GLU	2.0
4	AW	113	VAL	2.0
6	AY	179	VAL	2.0
7	AZ	101	VAL	2.0
20	BM	93	VAL	2.0
23	BP	68	VAL	2.0
24	BQ	39	VAL	2.0
37	CD	37	VAL	2.0
46	B	13	C	2.0
46	B	1190	C	2.0
46	CM	147	C	2.0
46	CM	680	C	2.0
46	CM	1220	C	2.0
50	F	133	LYS	2.0
53	I	136	LYS	2.0
59	CZ	99	GLU	2.0
61	Q	31	LYS	2.0
62	DC	31	GLU	2.0
65	U	64	GLU	2.0
69	Y	19	LYS	2.0
74	DO	70	LYS	2.0
77	DR	28	LYS	2.0
82	l1	195	LYS	2.0
47	C	22	VAL	2.0
50	F	40	VAL	2.0
51	G	72	VAL	2.0
54	J	117	VAL	2.0
54	CU	136	VAL	2.0
63	S	117	VAL	2.0
64	DE	110	VAL	2.0
65	U	4	VAL	2.0
72	DM	62	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
74	d	35	VAL	2.0
77	DR	47	VAL	2.0
79	AR	277	VAL	2.0
79	DT	312	VAL	2.0
80	P0	59	VAL	2.0
1	1	1821	G	2.0
1	AS	1083	G	2.0
1	AS	1242	G	2.0
1	AS	2662	G	2.0
1	AS	2873	G	2.0
1	AS	3308	G	2.0
8	BA	41	LEU	2.0
8	BA	107	ARG	2.0
11	q	166	ARG	2.0
17	BJ	60	ARG	2.0
38	AK	57	ARG	2.0
46	B	1533	G	2.0
46	B	1779	G	2.0
46	CM	1059	G	2.0
50	F	6	LEU	2.0
51	CR	52	LEU	2.0
53	CT	31	ARG	2.0
53	CT	94	ARG	2.0
54	CU	35	ARG	2.0
55	CV	59	ARG	2.0
56	L	60	LEU	2.0
63	S	88	LEU	2.0
64	T	45	ARG	2.0
65	DF	25	ARG	2.0
69	Y	117	ARG	2.0
78	h	122	ARG	2.0
7	AZ	227	ILE	2.0
9	o	93	ILE	2.0
11	q	114	ILE	2.0
12	r	80	SER	2.0
27	9	47	SER	2.0
34	AG	30	ILE	2.0
47	C	111	ILE	2.0
47	CN	141	ILE	2.0
52	H	163	SER	2.0
56	L	122	ILE	2.0
58	N	70	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
58	CY	112	SER	2.0
61	Q	118	SER	2.0
64	DE	41	ILE	2.0
67	W	27	SER	2.0
67	DH	102	ILE	2.0
70	Z	11	SER	2.0
71	a	47	ILE	2.0
79	AR	196	ILE	2.0
81	12	129	SER	2.0
1	1	774	U	2.0
1	1	2499	U	2.0
1	AS	2483	U	2.0
2	AT	54	U	2.0
7	m	57	ASN	2.0
7	AZ	208	MET	2.0
10	BC	156	ASN	2.0
24	BQ	132	ASN	2.0
46	B	24	U	2.0
46	B	120	U	2.0
46	B	247	U	2.0
46	B	317	U	2.0
46	B	366	U	2.0
46	B	1244	U	2.0
11	BD	58	HIS	2.0
29	AB	25	HIS	2.0
41	AN	41	HIS	2.0
49	E	147	HIS	2.0
55	CV	44	HIS	2.0
62	R	1	MET	2.0
16	BI	141	ALA	2.0
26	8	136	ALA	2.0
5	AX	119	TYR	2.0
6	AY	285	THR	2.0
6	AY	343	ALA	2.0
7	AZ	93	THR	2.0
7	AZ	153	THR	2.0
8	n	160	ALA	2.0
11	BD	67	ALA	2.0
12	BE	127	ALA	2.0
13	BF	52	TYR	2.0
26	BS	30	THR	2.0
27	9	21	THR	2.0

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Mol	Chain	Res	Type	RSRZ
28	AA	59	ALA	2.0
30	AC	16	ALA	2.0
30	AC	59	ALA	2.0
50	F	53	ALA	2.0
53	CT	204	ALA	2.0
55	CV	97	THR	2.0
73	DN	60	ALA	2.0
66	DG	80	TYR	2.0
74	d	52	THR	2.0
77	g	9	ALA	2.0
78	h	128	THR	2.0
82	L1	168	ALA	2.0
60	DA	89	TYR	2.0
79	AR	183	TYR	2.0
7	m	59	ASP	2.0
16	BI	136	ASP	2.0
28	BU	88	ASP	2.0
50	F	192	ASP	2.0
80	p0	31	ASP	2.0
6	l	355	GLY	2.0
8	BA	66	GLY	2.0
16	BI	78	GLY	2.0
18	BK	134	GLY	2.0
21	0	44	PHE	2.0
22	2	46	GLY	2.0
37	AJ	9	GLY	2.0
43	AP	51	GLY	2.0
48	CO	194	GLY	2.0
49	E	104	GLY	2.0
51	G	25	GLY	2.0
51	CR	34	GLY	2.0
52	H	69	PHE	2.0
61	DB	18	PHE	2.0
62	DC	38	GLY	2.0
64	T	52	GLY	2.0
65	DF	37	GLY	2.0
4	j	52	PRO	2.0
5	k	83	PRO	2.0
6	AY	310	LYS	2.0
9	o	99	LYS	2.0
14	t	201	LYS	2.0
16	BI	72	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
18	x	8	PRO	2.0
19	y	20	LYS	2.0
29	AB	24	LYS	2.0
47	CN	4	PRO	2.0
48	CO	35	PRO	2.0
48	CO	160	LYS	2.0
49	E	111	LYS	2.0
49	CP	114	LYS	2.0
51	CR	35	PRO	2.0
54	J	101	LYS	2.0
57	M	5	LYS	2.0
59	O	114	LYS	2.0
62	R	13	LYS	2.0
64	T	59	LYS	2.0
65	DF	6	GLN	2.0
65	DF	82	PRO	2.0
69	DJ	124	LYS	2.0
74	d	5	GLN	2.0
78	DS	185	LYS	2.0
80	P0	75	LYS	2.0
82	L1	15	LYS	2.0
82	L1	182	GLN	2.0
1	1	105	A	2.0
1	1	1810	A	2.0
1	1	2186	A	2.0
1	1	2472	A	2.0
1	1	2715	A	2.0
1	1	2882	A	2.0
1	AS	48	A	2.0
1	AS	61	A	2.0
1	AS	285	A	2.0
1	AS	306	A	2.0
1	AS	1131	A	2.0
1	AS	1905	A	2.0
1	AS	1926	A	2.0
1	AS	2715	A	2.0
1	AS	2757	A	2.0
1	AS	2883	A	2.0
1	AS	3309	A	2.0
2	AT	76	A	2.0
5	k	144	VAL	2.0
6	l	296	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
9	BB	115	VAL	2.0
14	BG	55	ARG	2.0
14	BG	113	VAL	2.0
15	u	110	ARG	2.0
20	z	17	VAL	2.0
20	BM	31	GLU	2.0
37	CD	21	VAL	2.0
46	B	483	A	2.0
46	B	742	A	2.0
46	B	1298	A	2.0
46	B	1727	A	2.0
46	CM	1676	A	2.0
46	CM	1742	A	2.0
47	C	86	VAL	2.0
47	CN	12	GLU	2.0
50	F	138	VAL	2.0
50	CQ	144	ARG	2.0
51	G	192	VAL	2.0
56	L	53	ARG	2.0
60	P	33	VAL	2.0
64	DE	122	VAL	2.0
70	DK	53	VAL	2.0
82	ll	22	GLU	2.0
32	BY	27	ARG	2.0
72	b	77	ARG	2.0
13	BF	112	LEU	2.0
32	AE	50	LEU	2.0
32	AE	103	LEU	2.0
49	E	129	LEU	2.0
50	CQ	30	LEU	2.0
50	CQ	80	LEU	2.0
51	G	20	LEU	2.0
58	CY	40	LEU	2.0
60	DA	72	LEU	2.0
64	T	93	LEU	2.0
65	DF	86	LEU	2.0
82	ll	16	LEU	2.0
34	AG	67	ILE	2.0
39	CF	5	ILE	2.0
48	CO	140	ILE	2.0
58	N	131	ILE	2.0
1	1	209	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	1	603	C	2.0
1	1	1312	C	2.0
1	1	1555	C	2.0
1	1	1842	C	2.0
1	AS	9	C	2.0
1	AS	2956	C	2.0
46	B	379	C	2.0
46	B	573	C	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
83	MG	1	3629	1/1	0.03	0.32	156,156,156,156	0
83	MG	1	3934	1/1	0.11	0.31	89,89,89,89	0
83	MG	B	1929	1/1	0.11	0.34	112,112,112,112	0
83	MG	AS	3630	1/1	0.28	0.23	87,87,87,87	0
83	MG	B	1956	1/1	0.30	0.49	74,74,74,74	0
83	MG	B	1919	1/1	0.33	0.54	83,83,83,83	0
83	MG	B	1805	1/1	0.33	0.46	91,91,91,91	0
83	MG	B	1943	1/1	0.34	0.40	94,94,94,94	0
83	MG	AS	3775	1/1	0.34	0.25	66,66,66,66	0
83	MG	1	3518	1/1	0.35	0.24	79,79,79,79	0
83	MG	1	3920	1/1	0.37	0.32	69,69,69,69	0
83	MG	B	1960	1/1	0.37	0.45	75,75,75,75	0
83	MG	B	1899	1/1	0.38	0.30	73,73,73,73	0
83	MG	AS	3598	1/1	0.39	0.15	129,129,129,129	0
83	MG	1	3798	1/1	0.40	0.27	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1914	1/1	0.40	0.37	87,87,87,87	0
83	MG	3	208	1/1	0.42	0.16	64,64,64,64	0
83	MG	1	3940	1/1	0.42	0.22	77,77,77,77	0
83	MG	AS	3528	1/1	0.43	0.45	64,64,64,64	0
83	MG	1	3862	1/1	0.44	0.19	72,72,72,72	0
83	MG	CM	1948	1/1	0.44	0.44	76,76,76,76	0
83	MG	AS	3643	1/1	0.45	0.23	56,56,56,56	0
83	MG	AS	3753	1/1	0.45	0.42	75,75,75,75	0
83	MG	AE	203	1/1	0.45	0.20	84,84,84,84	0
83	MG	1	3650	1/1	0.45	0.23	82,82,82,82	0
83	MG	AS	3732	1/1	0.47	0.12	56,56,56,56	0
83	MG	AS	3463	1/1	0.48	0.28	65,65,65,65	0
83	MG	B	1923	1/1	0.49	0.18	62,62,62,62	0
83	MG	1	3926	1/1	0.49	0.14	63,63,63,63	0
83	MG	DJ	202	1/1	0.49	0.33	74,74,74,74	0
83	MG	1	3925	1/1	0.50	0.33	75,75,75,75	0
83	MG	4	201	1/1	0.51	0.28	72,72,72,72	0
83	MG	AS	3733	1/1	0.51	0.19	79,79,79,79	0
83	MG	1	3514	1/1	0.52	0.46	79,79,79,79	0
83	MG	1	3604	1/1	0.52	0.26	70,70,70,70	0
83	MG	AS	3724	1/1	0.52	0.24	69,69,69,69	0
83	MG	B	1959	1/1	0.53	0.23	73,73,73,73	0
83	MG	AS	3700	1/1	0.53	0.22	46,46,46,46	0
83	MG	1	3464	1/1	0.53	0.40	58,58,58,58	0
83	MG	J	201	1/1	0.54	0.15	121,121,121,121	0
83	MG	1	3690	1/1	0.54	0.14	57,57,57,57	0
83	MG	AS	3649	1/1	0.54	0.31	66,66,66,66	0
83	MG	AS	3673	1/1	0.54	0.20	65,65,65,65	0
83	MG	B	1958	1/1	0.55	0.16	76,76,76,76	0
83	MG	AS	3768	1/1	0.56	0.17	74,74,74,74	0
83	MG	1	3883	1/1	0.56	0.24	76,76,76,76	0
83	MG	1	3845	1/1	0.56	0.27	78,78,78,78	0
83	MG	1	3657	1/1	0.56	0.40	62,62,62,62	0
83	MG	AS	3776	1/1	0.57	0.31	72,72,72,72	0
83	MG	1	3929	1/1	0.57	0.32	77,77,77,77	0
83	MG	1	3600	1/1	0.57	0.41	81,81,81,81	0
83	MG	CM	1897	1/1	0.58	0.17	69,69,69,69	0
83	MG	1	3588	1/1	0.58	0.15	73,73,73,73	0
83	MG	1	3722	1/1	0.58	0.17	51,51,51,51	0
83	MG	CO	301	1/1	0.59	0.26	46,46,46,46	0
83	MG	1	3642	1/1	0.59	0.16	41,41,41,41	0
83	MG	CM	1822	1/1	0.60	0.21	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3447	1/1	0.60	0.28	41,41,41,41	0
83	MG	AS	3556	1/1	0.60	0.21	56,56,56,56	0
83	MG	B	1955	1/1	0.60	0.42	60,60,60,60	0
83	MG	CM	1808	1/1	0.60	0.34	81,81,81,81	0
83	MG	B	1837	1/1	0.61	0.24	321,321,321,321	0
83	MG	B	1817	1/1	0.61	0.32	82,82,82,82	0
83	MG	g	101	1/1	0.62	0.35	78,78,78,78	0
83	MG	AS	3602	1/1	0.62	0.33	44,44,44,44	0
83	MG	1	3857	1/1	0.62	0.20	64,64,64,64	0
83	MG	1	3861	1/1	0.62	0.17	85,85,85,85	0
83	MG	1	3719	1/1	0.62	0.22	90,90,90,90	0
83	MG	AS	3654	1/1	0.62	0.21	66,66,66,66	0
83	MG	1	3567	1/1	0.62	0.40	64,64,64,64	0
83	MG	B	1942	1/1	0.63	0.32	75,75,75,75	0
83	MG	CM	1864	1/1	0.63	0.28	68,68,68,68	0
83	MG	1	3841	1/1	0.63	0.32	72,72,72,72	0
83	MG	B	1804	1/1	0.63	0.41	70,70,70,70	0
83	MG	AS	3614	1/1	0.63	0.23	57,57,57,57	0
83	MG	AS	3670	1/1	0.63	0.19	73,73,73,73	0
83	MG	B	1936	1/1	0.64	0.40	98,98,98,98	0
83	MG	CM	1945	1/1	0.64	0.20	61,61,61,61	0
83	MG	i	301	1/1	0.64	0.32	69,69,69,69	0
83	MG	B	1957	1/1	0.64	0.31	82,82,82,82	0
83	MG	1	3957	1/1	0.64	0.10	59,59,59,59	0
83	MG	1	3816	1/1	0.65	0.24	51,51,51,51	0
83	MG	1	3683	1/1	0.65	0.20	67,67,67,67	0
83	MG	1	3814	1/1	0.65	0.16	56,56,56,56	0
83	MG	B	1857	1/1	0.65	0.29	57,57,57,57	0
83	MG	CM	1912	1/1	0.65	0.30	58,58,58,58	0
83	MG	1	3877	1/1	0.65	0.14	49,49,49,49	0
83	MG	B	1908	1/1	0.65	0.17	49,49,49,49	0
83	MG	3	204	1/1	0.65	0.26	58,58,58,58	0
83	MG	AY	401	1/1	0.65	0.15	62,62,62,62	0
83	MG	1	3756	1/1	0.66	0.36	57,57,57,57	0
83	MG	B	1898	1/1	0.66	0.18	49,49,49,49	0
83	MG	AS	3757	1/1	0.66	0.24	80,80,80,80	0
83	MG	AS	3451	1/1	0.66	0.33	67,67,67,67	0
83	MG	CM	1915	1/1	0.66	0.28	62,62,62,62	0
83	MG	1	3508	1/1	0.66	0.27	42,42,42,42	0
83	MG	AS	3722	1/1	0.66	0.56	69,69,69,69	0
83	MG	B	1924	1/1	0.66	0.40	74,74,74,74	0
83	MG	1	3709	1/1	0.66	0.20	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3548	1/1	0.67	0.34	48,48,48,48	0
83	MG	1	3566	1/1	0.67	0.16	61,61,61,61	0
83	MG	B	1816	1/1	0.67	0.35	52,52,52,52	0
83	MG	AS	3764	1/1	0.67	0.27	76,76,76,76	0
83	MG	1	3806	1/1	0.67	0.23	54,54,54,54	0
83	MG	1	3414	1/1	0.67	0.33	56,56,56,56	0
83	MG	1	3896	1/1	0.67	0.19	64,64,64,64	0
83	MG	AS	3634	1/1	0.67	0.28	79,79,79,79	0
83	MG	1	3909	1/1	0.67	0.19	45,45,45,45	0
83	MG	u	201	1/1	0.68	0.17	56,56,56,56	0
83	MG	1	3826	1/1	0.68	0.13	57,57,57,57	0
83	MG	3	209	1/1	0.68	0.20	60,60,60,60	0
83	MG	Z	201	1/1	0.68	0.94	72,72,72,72	0
83	MG	AU	208	1/1	0.68	0.14	74,74,74,74	0
83	MG	AS	3632	1/1	0.68	0.19	51,51,51,51	0
83	MG	CA	203	1/1	0.68	0.38	68,68,68,68	0
83	MG	CM	1806	1/1	0.68	0.30	52,52,52,52	0
83	MG	1	3495	1/1	0.68	0.18	54,54,54,54	0
86	ZN	d	101	1/1	0.68	0.17	273,273,273,273	0
83	MG	1	3879	1/1	0.69	0.12	62,62,62,62	0
83	MG	1	3805	1/1	0.69	0.30	85,85,85,85	0
83	MG	B	1913	1/1	0.69	0.26	58,58,58,58	0
83	MG	R	201	1/1	0.69	0.32	78,78,78,78	0
83	MG	B	1889	1/1	0.69	0.09	73,73,73,73	0
83	MG	AS	3592	1/1	0.69	0.32	71,71,71,71	0
83	MG	CM	1836	1/1	0.69	0.53	76,76,76,76	0
83	MG	1	3947	1/1	0.69	0.22	55,55,55,55	0
83	MG	B	1814	1/1	0.70	0.26	57,57,57,57	0
83	MG	B	1941	1/1	0.70	0.23	75,75,75,75	0
83	MG	CM	1852	1/1	0.70	0.35	85,85,85,85	0
83	MG	CM	1859	1/1	0.70	0.38	59,59,59,59	0
83	MG	B	1850	1/1	0.70	0.15	53,53,53,53	0
83	MG	B	1900	1/1	0.70	0.23	56,56,56,56	0
83	MG	1	3695	1/1	0.70	0.24	184,184,184,184	0
83	MG	AS	3470	1/1	0.70	0.31	44,44,44,44	0
83	MG	AB	202	1/1	0.70	0.18	54,54,54,54	0
83	MG	AS	3533	1/1	0.70	0.40	60,60,60,60	0
83	MG	CL	302	1/1	0.70	0.55	77,77,77,77	0
83	MG	AS	3636	1/1	0.70	0.32	71,71,71,71	0
83	MG	AS	3540	1/1	0.70	0.23	41,41,41,41	0
83	MG	1	3419	1/1	0.71	0.26	69,69,69,69	0
83	MG	AS	3769	1/1	0.71	0.37	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3772	1/1	0.71	0.18	45,45,45,45	0
83	MG	AS	3542	1/1	0.71	0.42	66,66,66,66	0
83	MG	B	1972	1/1	0.71	0.44	84,84,84,84	0
83	MG	AS	3455	1/1	0.71	0.31	65,65,65,65	0
83	MG	AU	209	1/1	0.71	0.23	72,72,72,72	0
83	MG	1	3619	1/1	0.71	0.17	50,50,50,50	0
83	MG	1	3599	1/1	0.71	0.25	60,60,60,60	0
83	MG	1	3432	1/1	0.71	0.24	65,65,65,65	0
83	MG	AS	3758	1/1	0.71	0.19	61,61,61,61	0
83	MG	1	3691	1/1	0.71	0.18	80,80,80,80	0
83	MG	CM	1821	1/1	0.71	0.18	57,57,57,57	0
83	MG	1	3660	1/1	0.72	0.23	31,31,31,31	0
83	MG	1	3860	1/1	0.72	0.22	51,51,51,51	0
83	MG	B	1856	1/1	0.72	0.45	84,84,84,84	0
83	MG	r	302	1/1	0.72	0.13	56,56,56,56	0
83	MG	AS	3575	1/1	0.72	0.43	58,58,58,58	0
83	MG	1	3577	1/1	0.72	0.11	53,53,53,53	0
83	MG	D	301	1/1	0.72	0.24	60,60,60,60	0
83	MG	1	3726	1/1	0.72	0.30	47,47,47,47	0
83	MG	1	3872	1/1	0.72	0.27	58,58,58,58	0
83	MG	DB	204	1/1	0.72	0.28	57,57,57,57	0
83	MG	AS	3707	1/1	0.72	0.28	70,70,70,70	0
83	MG	AS	3529	1/1	0.72	0.35	60,60,60,60	0
83	MG	AS	3749	1/1	0.73	0.31	44,44,44,44	0
83	MG	1	3402	1/1	0.73	0.33	20,20,20,20	0
83	MG	CM	1916	1/1	0.73	0.13	57,57,57,57	0
83	MG	1	3754	1/1	0.73	0.37	67,67,67,67	0
83	MG	AS	3714	1/1	0.73	0.23	35,35,35,35	0
83	MG	1	3835	1/1	0.73	0.29	66,66,66,66	0
83	MG	DA	201	1/1	0.73	0.13	62,62,62,62	0
83	MG	DB	203	1/1	0.73	0.33	61,61,61,61	0
83	MG	AS	3493	1/1	0.73	0.26	49,49,49,49	0
83	MG	1	3415	1/1	0.73	0.41	36,36,36,36	0
83	MG	1	3771	1/1	0.73	0.13	39,39,39,39	0
83	MG	1	3779	1/1	0.74	0.27	51,51,51,51	0
83	MG	1	3922	1/1	0.74	0.22	75,75,75,75	0
83	MG	AS	3633	1/1	0.74	0.24	80,80,80,80	0
83	MG	1	3923	1/1	0.74	0.13	59,59,59,59	0
83	MG	CM	1853	1/1	0.74	0.32	57,57,57,57	0
83	MG	1	3844	1/1	0.74	0.24	70,70,70,70	0
83	MG	B	1841	1/1	0.74	0.20	46,46,46,46	0
83	MG	CM	1875	1/1	0.74	0.19	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3666	1/1	0.74	0.37	45,45,45,45	0
83	MG	I	301	1/1	0.74	0.19	113,113,113,113	0
83	MG	AS	3659	1/1	0.74	0.38	69,69,69,69	0
83	MG	1	3849	1/1	0.74	0.21	59,59,59,59	0
83	MG	1	3931	1/1	0.74	0.37	62,62,62,62	0
83	MG	AS	3681	1/1	0.74	0.25	53,53,53,53	0
83	MG	B	1862	1/1	0.74	0.19	67,67,67,67	0
83	MG	1	3526	1/1	0.74	0.19	43,43,43,43	0
83	MG	1	3884	1/1	0.74	0.18	53,53,53,53	0
83	MG	1	3654	1/1	0.74	0.39	70,70,70,70	0
83	MG	AS	3608	1/1	0.74	0.25	40,40,40,40	0
83	MG	1	3840	1/1	0.74	0.28	60,60,60,60	0
86	ZN	DO	101	1/1	0.74	0.16	225,225,225,225	0
83	MG	1	3424	1/1	0.75	0.24	45,45,45,45	0
83	MG	1	3663	1/1	0.75	0.46	61,61,61,61	0
83	MG	1	3622	1/1	0.75	0.17	52,52,52,52	0
83	MG	CL	301	1/1	0.75	0.09	41,41,41,41	0
83	MG	1	3863	1/1	0.75	0.26	67,67,67,67	0
83	MG	1	3547	1/1	0.75	0.13	49,49,49,49	0
83	MG	AS	3688	1/1	0.75	0.18	29,29,29,29	0
83	MG	AS	3534	1/1	0.75	0.24	64,64,64,64	0
83	MG	AS	3701	1/1	0.75	0.56	97,97,97,97	0
83	MG	1	3928	1/1	0.75	0.21	74,74,74,74	0
83	MG	AS	3711	1/1	0.75	0.20	50,50,50,50	0
83	MG	B	1894	1/1	0.75	0.48	61,61,61,61	0
83	MG	1	3597	1/1	0.75	0.21	61,61,61,61	0
83	MG	1	3466	1/1	0.75	0.31	37,37,37,37	0
83	MG	AF	202	1/1	0.75	0.17	71,71,71,71	0
83	MG	CM	1876	1/1	0.75	0.20	50,50,50,50	0
83	MG	1	3788	1/1	0.75	0.41	56,56,56,56	0
83	MG	CM	1900	1/1	0.75	0.27	54,54,54,54	0
83	MG	AS	3744	1/1	0.75	0.22	68,68,68,68	0
83	MG	B	1802	1/1	0.75	0.20	71,71,71,71	0
83	MG	1	3936	1/1	0.75	0.12	61,61,61,61	0
83	MG	1	3467	1/1	0.75	0.34	37,37,37,37	0
83	MG	1	3943	1/1	0.75	0.17	40,40,40,40	0
83	MG	AS	3446	1/1	0.75	0.19	45,45,45,45	0
83	MG	1	3656	1/1	0.75	0.21	60,60,60,60	0
83	MG	1	3951	1/1	0.75	0.22	48,48,48,48	0
83	MG	1	3483	1/1	0.75	0.28	56,56,56,56	0
83	MG	AS	3638	1/1	0.75	0.13	56,56,56,56	0
83	MG	AS	3456	1/1	0.75	0.20	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1839	1/1	0.75	0.47	55,55,55,55	0
83	MG	AX	401	1/1	0.76	0.27	59,59,59,59	0
83	MG	3	214	1/1	0.76	0.14	61,61,61,61	0
83	MG	B	1917	1/1	0.76	0.37	54,54,54,54	0
83	MG	G	302	1/1	0.76	0.17	62,62,62,62	0
83	MG	1	3890	1/1	0.76	0.28	76,76,76,76	0
83	MG	CM	1801	1/1	0.76	0.21	51,51,51,51	0
83	MG	4	203	1/1	0.76	0.20	56,56,56,56	0
83	MG	1	3497	1/1	0.76	0.26	39,39,39,39	0
83	MG	1	3581	1/1	0.76	0.09	37,37,37,37	0
83	MG	w	303	1/1	0.76	0.20	73,73,73,73	0
83	MG	AS	3434	1/1	0.76	0.32	55,55,55,55	0
83	MG	CM	1846	1/1	0.76	0.30	53,53,53,53	0
83	MG	1	3919	1/1	0.76	0.20	69,69,69,69	0
83	MG	1	3702	1/1	0.76	0.12	46,46,46,46	0
83	MG	AS	3621	1/1	0.76	0.26	72,72,72,72	0
83	MG	1	3561	1/1	0.76	0.45	62,62,62,62	0
83	MG	AS	3631	1/1	0.76	0.40	54,54,54,54	0
83	MG	AS	3746	1/1	0.76	0.30	62,62,62,62	0
83	MG	CM	1896	1/1	0.76	0.13	42,42,42,42	0
83	MG	1	3716	1/1	0.76	0.30	70,70,70,70	0
83	MG	1	3541	1/1	0.76	0.35	60,60,60,60	0
83	MG	1	3687	1/1	0.76	0.24	68,68,68,68	0
83	MG	3	207	1/1	0.76	0.18	66,66,66,66	0
83	MG	1	3521	1/1	0.76	0.32	52,52,52,52	0
83	MG	AS	3765	1/1	0.76	0.35	65,65,65,65	0
83	MG	AS	3507	1/1	0.76	0.37	63,63,63,63	0
83	MG	AS	3522	1/1	0.76	0.25	40,40,40,40	0
83	MG	1	3733	1/1	0.76	0.14	61,61,61,61	0
83	MG	B	1965	1/1	0.76	0.23	61,61,61,61	0
83	MG	AS	3660	1/1	0.76	0.22	70,70,70,70	0
83	MG	AU	204	1/1	0.76	0.08	70,70,70,70	0
83	MG	AS	3665	1/1	0.76	0.11	29,29,29,29	0
83	MG	AS	3669	1/1	0.76	0.38	64,64,64,64	0
83	MG	B	1844	1/1	0.77	0.20	72,72,72,72	0
83	MG	1	3873	1/1	0.77	0.29	46,46,46,46	0
83	MG	AS	3766	1/1	0.77	0.36	53,53,53,53	0
83	MG	1	3539	1/1	0.77	0.32	73,73,73,73	0
83	MG	AS	3691	1/1	0.77	0.20	70,70,70,70	0
83	MG	1	3603	1/1	0.77	0.17	52,52,52,52	0
83	MG	1	3423	1/1	0.77	0.30	38,38,38,38	0
83	MG	1	3406	1/1	0.77	0.40	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3780	1/1	0.77	0.30	59,59,59,59	0
83	MG	1	3530	1/1	0.77	0.35	58,58,58,58	0
83	MG	B	1834	1/1	0.77	0.27	35,35,35,35	0
83	MG	1	3942	1/1	0.77	0.16	54,54,54,54	0
83	MG	AS	3560	1/1	0.77	0.18	34,34,34,34	0
83	MG	AS	3728	1/1	0.77	0.30	57,57,57,57	0
83	MG	AS	3646	1/1	0.77	0.12	65,65,65,65	0
83	MG	AS	3564	1/1	0.77	0.22	45,45,45,45	0
83	MG	3	213	1/1	0.77	0.29	62,62,62,62	0
83	MG	AS	3468	1/1	0.77	0.25	58,58,58,58	0
83	MG	1	3730	1/1	0.77	0.26	34,34,34,34	0
83	MG	B	1951	1/1	0.77	0.12	79,79,79,79	0
83	MG	CM	1818	1/1	0.77	0.21	43,43,43,43	0
83	MG	AS	3503	1/1	0.77	0.29	45,45,45,45	0
83	MG	AS	3612	1/1	0.77	0.27	40,40,40,40	0
83	MG	AS	3637	1/1	0.78	0.22	51,51,51,51	0
83	MG	AS	3736	1/1	0.78	0.29	48,48,48,48	0
83	MG	1	3700	1/1	0.78	0.10	44,44,44,44	0
83	MG	3	206	1/1	0.78	0.13	57,57,57,57	0
83	MG	B	1937	1/1	0.78	0.23	52,52,52,52	0
83	MG	1	3484	1/1	0.78	0.25	39,39,39,39	0
83	MG	B	1868	1/1	0.78	0.29	68,68,68,68	0
83	MG	CM	1848	1/1	0.78	0.29	62,62,62,62	0
83	MG	B	1881	1/1	0.78	0.28	40,40,40,40	0
83	MG	B	1947	1/1	0.78	0.20	55,55,55,55	0
83	MG	1	3897	1/1	0.78	0.13	66,66,66,66	0
83	MG	1	3901	1/1	0.78	0.14	49,49,49,49	0
83	MG	CM	1868	1/1	0.78	0.34	73,73,73,73	0
83	MG	CM	1870	1/1	0.78	0.17	54,54,54,54	0
83	MG	1	3851	1/1	0.78	0.21	63,63,63,63	0
83	MG	AS	3459	1/1	0.78	0.21	47,47,47,47	0
83	MG	CM	1885	1/1	0.78	0.31	47,47,47,47	0
83	MG	1	3914	1/1	0.78	0.26	75,75,75,75	0
83	MG	AS	3609	1/1	0.78	0.12	45,45,45,45	0
83	MG	AS	3690	1/1	0.78	0.15	68,68,68,68	0
83	MG	1	3917	1/1	0.78	0.18	64,64,64,64	0
83	MG	AT	203	1/1	0.78	0.24	52,52,52,52	0
83	MG	AT	209	1/1	0.78	0.45	53,53,53,53	0
83	MG	CM	1944	1/1	0.78	0.14	75,75,75,75	0
83	MG	1	3876	1/1	0.78	0.30	61,61,61,61	0
83	MG	4	207	1/1	0.78	0.20	52,52,52,52	0
83	MG	AS	3628	1/1	0.78	0.23	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3501	1/1	0.78	0.37	55,55,55,55	0
83	MG	j	303	1/1	0.78	0.16	22,22,22,22	0
83	MG	1	3559	1/1	0.78	0.24	51,51,51,51	0
83	MG	1	3664	1/1	0.78	0.36	53,53,53,53	0
83	MG	1	3429	1/1	0.78	0.32	45,45,45,45	0
83	MG	1	3670	1/1	0.78	0.37	52,52,52,52	0
83	MG	1	3405	1/1	0.79	0.41	59,59,59,59	0
83	MG	B	1861	1/1	0.79	0.23	86,86,86,86	0
83	MG	B	1927	1/1	0.79	0.14	49,49,49,49	0
83	MG	AS	3625	1/1	0.79	0.20	52,52,52,52	0
83	MG	1	3601	1/1	0.79	0.29	56,56,56,56	0
83	MG	AS	3512	1/1	0.79	0.31	60,60,60,60	0
83	MG	AS	3779	1/1	0.79	0.24	59,59,59,59	0
83	MG	B	1864	1/1	0.79	0.16	68,68,68,68	0
83	MG	1	3735	1/1	0.79	0.36	25,25,25,25	0
83	MG	B	1809	1/1	0.79	0.32	46,46,46,46	0
83	MG	AU	203	1/1	0.79	0.24	54,54,54,54	0
83	MG	Z	202	1/1	0.79	0.28	67,67,67,67	0
83	MG	1	3485	1/1	0.79	0.09	36,36,36,36	0
83	MG	AS	3431	1/1	0.79	0.29	42,42,42,42	0
83	MG	1	3950	1/1	0.79	0.12	39,39,39,39	0
83	MG	1	3820	1/1	0.79	0.11	34,34,34,34	0
83	MG	CM	1914	1/1	0.79	0.10	55,55,55,55	0
83	MG	BB	303	1/1	0.79	0.33	48,48,48,48	0
83	MG	BZ	203	1/1	0.79	0.22	74,74,74,74	0
83	MG	AS	3558	1/1	0.79	0.17	34,34,34,34	0
83	MG	1	3952	1/1	0.79	0.20	59,59,59,59	0
83	MG	1	3549	1/1	0.79	0.35	59,59,59,59	0
83	MG	B	1904	1/1	0.79	0.22	90,90,90,90	0
83	MG	CM	1803	1/1	0.79	0.19	31,31,31,31	0
83	MG	1	3830	1/1	0.79	0.13	48,48,48,48	0
83	MG	1	3651	1/1	0.79	0.23	55,55,55,55	0
83	MG	1	3720	1/1	0.79	0.09	42,42,42,42	0
83	MG	1	3448	1/1	0.79	0.21	23,23,23,23	0
83	MG	1	3697	1/1	0.79	0.20	38,38,38,38	0
83	MG	1	3525	1/1	0.80	0.39	53,53,53,53	0
83	MG	CM	1827	1/1	0.80	0.43	38,38,38,38	0
83	MG	AS	3667	1/1	0.80	0.12	54,54,54,54	0
83	MG	AS	3478	1/1	0.80	0.32	73,73,73,73	0
83	MG	B	1806	1/1	0.80	0.38	53,53,53,53	0
83	MG	1	3715	1/1	0.80	0.08	38,38,38,38	0
83	MG	1	3944	1/1	0.80	0.16	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3921	1/1	0.80	0.12	69,69,69,69	0
83	MG	V	201	1/1	0.80	0.20	46,46,46,46	0
83	MG	AS	3624	1/1	0.80	0.14	42,42,42,42	0
83	MG	1	3848	1/1	0.80	0.14	45,45,45,45	0
83	MG	CM	1873	1/1	0.80	0.20	80,80,80,80	0
83	MG	AT	204	1/1	0.80	0.16	74,74,74,74	0
83	MG	1	3750	1/1	0.80	0.18	56,56,56,56	0
83	MG	CM	1881	1/1	0.80	0.24	72,72,72,72	0
83	MG	1	3434	1/1	0.80	0.31	42,42,42,42	0
83	MG	AS	3709	1/1	0.80	0.15	60,60,60,60	0
83	MG	B	1949	1/1	0.80	0.17	61,61,61,61	0
83	MG	1	3694	1/1	0.80	0.30	26,26,26,26	0
83	MG	CM	1907	1/1	0.80	0.34	59,59,59,59	0
83	MG	CM	1909	1/1	0.80	0.15	74,74,74,74	0
83	MG	1	3627	1/1	0.80	0.23	66,66,66,66	0
83	MG	1	3428	1/1	0.80	0.23	25,25,25,25	0
83	MG	AS	3550	1/1	0.80	0.33	37,37,37,37	0
83	MG	1	3781	1/1	0.80	0.33	78,78,78,78	0
83	MG	CM	1917	1/1	0.80	0.10	59,59,59,59	0
83	MG	CM	1926	1/1	0.80	0.36	58,58,58,58	0
83	MG	AH	202	1/1	0.80	0.20	58,58,58,58	0
83	MG	AS	3642	1/1	0.80	0.34	58,58,58,58	0
83	MG	1	3836	1/1	0.80	0.19	56,56,56,56	0
83	MG	AS	3645	1/1	0.80	0.13	47,47,47,47	0
83	MG	B	1920	1/1	0.80	0.28	62,62,62,62	0
83	MG	AS	3571	1/1	0.80	0.14	60,60,60,60	0
83	MG	1	3605	1/1	0.80	0.24	34,34,34,34	0
83	MG	CM	1817	1/1	0.80	0.28	42,42,42,42	0
83	MG	AS	3581	1/1	0.80	0.26	36,36,36,36	0
83	MG	1	3644	1/1	0.80	0.24	24,24,24,24	0
83	MG	k	405	1/1	0.81	0.24	54,54,54,54	0
83	MG	1	3623	1/1	0.81	0.34	51,51,51,51	0
83	MG	1	3885	1/1	0.81	0.12	42,42,42,42	0
83	MG	1	3810	1/1	0.81	0.32	54,54,54,54	0
83	MG	0	201	1/1	0.81	0.17	49,49,49,49	0
83	MG	1	3954	1/1	0.81	0.14	51,51,51,51	0
83	MG	1	3811	1/1	0.81	0.12	50,50,50,50	0
83	MG	CM	1866	1/1	0.81	0.16	74,74,74,74	0
83	MG	1	3705	1/1	0.81	0.23	47,47,47,47	0
83	MG	AS	3704	1/1	0.81	0.19	56,56,56,56	0
83	MG	AT	208	1/1	0.81	0.21	44,44,44,44	0
83	MG	AH	201	1/1	0.81	0.10	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1939	1/1	0.81	0.35	77,77,77,77	0
83	MG	CM	1879	1/1	0.81	0.31	61,61,61,61	0
83	MG	3	205	1/1	0.81	0.21	46,46,46,46	0
83	MG	CM	1882	1/1	0.81	0.17	49,49,49,49	0
83	MG	AS	3412	1/1	0.81	0.12	29,29,29,29	0
83	MG	AS	3425	1/1	0.81	0.25	49,49,49,49	0
83	MG	AW	301	1/1	0.81	0.14	38,38,38,38	0
83	MG	AW	303	1/1	0.81	0.16	46,46,46,46	0
83	MG	1	3418	1/1	0.81	0.23	46,46,46,46	0
83	MG	AS	3727	1/1	0.81	0.36	69,69,69,69	0
83	MG	1	3628	1/1	0.81	0.28	61,61,61,61	0
83	MG	CM	1913	1/1	0.81	0.17	70,70,70,70	0
83	MG	BI	301	1/1	0.81	0.14	61,61,61,61	0
83	MG	AS	3445	1/1	0.81	0.28	39,39,39,39	0
83	MG	1	3910	1/1	0.81	0.09	24,24,24,24	0
83	MG	1	3912	1/1	0.81	0.22	56,56,56,56	0
83	MG	1	3470	1/1	0.81	0.23	34,34,34,34	0
83	MG	CM	1935	1/1	0.81	0.16	48,48,48,48	0
83	MG	AS	3647	1/1	0.81	0.15	76,76,76,76	0
83	MG	1	3476	1/1	0.81	0.17	59,59,59,59	0
83	MG	1	3570	1/1	0.81	0.13	48,48,48,48	0
83	MG	AS	3756	1/1	0.81	0.38	59,59,59,59	0
83	MG	CQ	302	1/1	0.81	0.10	67,67,67,67	0
83	MG	AS	3585	1/1	0.81	0.17	49,49,49,49	0
83	MG	1	3882	1/1	0.81	0.25	61,61,61,61	0
83	MG	1	3946	1/1	0.81	0.12	41,41,41,41	0
83	MG	B	1826	1/1	0.81	0.26	49,49,49,49	0
83	MG	1	3859	1/1	0.81	0.22	67,67,67,67	0
83	MG	CM	1834	1/1	0.81	0.30	54,54,54,54	0
83	MG	BJ	301	1/1	0.82	0.28	64,64,64,64	0
83	MG	BZ	202	1/1	0.82	0.20	71,71,71,71	0
83	MG	1	3797	1/1	0.82	0.34	58,58,58,58	0
83	MG	1	3589	1/1	0.82	0.33	49,49,49,49	0
83	MG	1	3801	1/1	0.82	0.08	62,62,62,62	0
83	MG	1	3891	1/1	0.82	0.17	65,65,65,65	0
83	MG	B	1970	1/1	0.82	0.29	59,59,59,59	0
83	MG	1	3839	1/1	0.82	0.13	39,39,39,39	0
83	MG	1	3615	1/1	0.82	0.12	62,62,62,62	0
83	MG	1	3871	1/1	0.82	0.09	66,66,66,66	0
83	MG	CM	1811	1/1	0.82	0.26	42,42,42,42	0
83	MG	1	3757	1/1	0.82	0.43	50,50,50,50	0
83	MG	1	3596	1/1	0.82	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1892	1/1	0.82	0.19	46,46,46,46	0
83	MG	1	3774	1/1	0.82	0.07	26,26,26,26	0
83	MG	1	3587	1/1	0.82	0.17	49,49,49,49	0
83	MG	1	3544	1/1	0.82	0.31	57,57,57,57	0
83	MG	1	3624	1/1	0.82	0.20	56,56,56,56	0
83	MG	AT	210	1/1	0.82	0.34	50,50,50,50	0
83	MG	B	1948	1/1	0.82	0.12	69,69,69,69	0
83	MG	AS	3617	1/1	0.82	0.31	44,44,44,44	0
83	MG	B	1902	1/1	0.82	0.32	74,74,74,74	0
83	MG	AG	201	1/1	0.82	0.15	67,67,67,67	0
83	MG	CY	201	1/1	0.82	0.15	71,71,71,71	0
83	MG	AG	202	1/1	0.82	0.10	43,43,43,43	0
83	MG	DB	201	1/1	0.82	0.19	38,38,38,38	0
83	MG	AS	3752	1/1	0.82	0.17	62,62,62,62	0
83	MG	B	1843	1/1	0.82	0.15	37,37,37,37	0
83	MG	AS	3755	1/1	0.82	0.28	63,63,63,63	0
83	MG	1	3796	1/1	0.82	0.27	67,67,67,67	0
83	MG	AS	3685	1/1	0.82	0.28	41,41,41,41	0
83	MG	AS	3426	1/1	0.83	0.14	20,20,20,20	0
83	MG	1	3773	1/1	0.83	0.13	38,38,38,38	0
83	MG	CM	1858	1/1	0.83	0.11	55,55,55,55	0
83	MG	1	3903	1/1	0.83	0.13	48,48,48,48	0
83	MG	CM	1861	1/1	0.83	0.13	43,43,43,43	0
83	MG	B	1940	1/1	0.83	0.09	73,73,73,73	0
83	MG	AT	207	1/1	0.83	0.27	49,49,49,49	0
83	MG	B	1866	1/1	0.83	0.33	47,47,47,47	0
83	MG	1	3749	1/1	0.83	0.18	59,59,59,59	0
83	MG	CM	1871	1/1	0.83	0.25	45,45,45,45	0
83	MG	B	1869	1/1	0.83	0.16	71,71,71,71	0
83	MG	B	1946	1/1	0.83	0.20	59,59,59,59	0
83	MG	B	1880	1/1	0.83	0.27	52,52,52,52	0
83	MG	1	3728	1/1	0.83	0.28	46,46,46,46	0
83	MG	AS	3461	1/1	0.83	0.27	23,23,23,23	0
83	MG	AS	3619	1/1	0.83	0.32	42,42,42,42	0
83	MG	B	1883	1/1	0.83	0.29	39,39,39,39	0
83	MG	1	3842	1/1	0.83	0.14	54,54,54,54	0
83	MG	1	3753	1/1	0.83	0.35	52,52,52,52	0
83	MG	1	3783	1/1	0.83	0.15	49,49,49,49	0
83	MG	j	302	1/1	0.83	0.10	59,59,59,59	0
83	MG	AS	3496	1/1	0.83	0.08	20,20,20,20	0
83	MG	1	3846	1/1	0.83	0.43	64,64,64,64	0
83	MG	AS	3502	1/1	0.83	0.20	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	k	402	1/1	0.83	0.14	57,57,57,57	0
83	MG	k	404	1/1	0.83	0.34	72,72,72,72	0
83	MG	l	3637	1/1	0.83	0.14	47,47,47,47	0
83	MG	k	406	1/1	0.83	0.57	62,62,62,62	0
83	MG	B	1910	1/1	0.83	0.19	37,37,37,37	0
83	MG	l	3789	1/1	0.83	0.20	41,41,41,41	0
83	MG	l	3557	1/1	0.83	0.09	35,35,35,35	0
83	MG	B	1840	1/1	0.83	0.30	59,59,59,59	0
83	MG	CM	1814	1/1	0.83	0.23	39,39,39,39	0
83	MG	AS	3535	1/1	0.83	0.23	58,58,58,58	0
83	MG	l	3655	1/1	0.83	0.15	47,47,47,47	0
83	MG	CM	1820	1/1	0.83	0.29	33,33,33,33	0
83	MG	l	3834	1/1	0.83	0.14	65,65,65,65	0
83	MG	l	3758	1/1	0.83	0.13	41,41,41,41	0
83	MG	l	3927	1/1	0.83	0.27	55,55,55,55	0
83	MG	B	1925	1/1	0.83	0.28	54,54,54,54	0
83	MG	l	3742	1/1	0.83	0.26	36,36,36,36	0
83	MG	l	3838	1/1	0.83	0.12	54,54,54,54	0
86	ZN	h	201	1/1	0.83	0.14	216,216,216,216	0
83	MG	l	3930	1/1	0.83	0.21	51,51,51,51	0
83	MG	AS	3719	1/1	0.84	0.48	74,74,74,74	0
83	MG	AS	3588	1/1	0.84	0.33	74,74,74,74	0
83	MG	CM	1813	1/1	0.84	0.40	46,46,46,46	0
83	MG	l	3489	1/1	0.84	0.13	44,44,44,44	0
83	MG	l	3717	1/1	0.84	0.23	51,51,51,51	0
83	MG	B	1801	1/1	0.84	0.18	38,38,38,38	0
83	MG	f	102	1/1	0.84	0.15	59,59,59,59	0
83	MG	l	3784	1/1	0.84	0.23	63,63,63,63	0
83	MG	B	1912	1/1	0.84	0.31	55,55,55,55	0
83	MG	AS	3737	1/1	0.84	0.20	18,18,18,18	0
83	MG	CM	1828	1/1	0.84	0.31	50,50,50,50	0
83	MG	l	3460	1/1	0.84	0.22	39,39,39,39	0
83	MG	AS	3616	1/1	0.84	0.23	48,48,48,48	0
83	MG	3	202	1/1	0.84	0.17	57,57,57,57	0
83	MG	l	3602	1/1	0.84	0.18	51,51,51,51	0
83	MG	l	3721	1/1	0.84	0.08	26,26,26,26	0
83	MG	l	3634	1/1	0.84	0.22	68,68,68,68	0
83	MG	l	3852	1/1	0.84	0.28	49,49,49,49	0
83	MG	l	3918	1/1	0.84	0.14	59,59,59,59	0
83	MG	B	1822	1/1	0.84	0.22	45,45,45,45	0
83	MG	l	3673	1/1	0.84	0.17	37,37,37,37	0
83	MG	3	210	1/1	0.84	0.25	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1931	1/1	0.84	0.17	44,44,44,44	0
83	MG	B	1934	1/1	0.84	0.10	86,86,86,86	0
83	MG	B	1835	1/1	0.84	0.24	62,62,62,62	0
83	MG	AS	3771	1/1	0.84	0.28	47,47,47,47	0
83	MG	1	3679	1/1	0.84	0.22	66,66,66,66	0
83	MG	1	3579	1/1	0.84	0.08	32,32,32,32	0
83	MG	AS	3639	1/1	0.84	0.15	40,40,40,40	0
83	MG	CM	1880	1/1	0.84	0.12	33,33,33,33	0
83	MG	1	3496	1/1	0.84	0.19	55,55,55,55	0
83	MG	1	3527	1/1	0.84	0.42	48,48,48,48	0
83	MG	4	204	1/1	0.84	0.18	32,32,32,32	0
83	MG	CM	1891	1/1	0.84	0.28	27,27,27,27	0
83	MG	1	3646	1/1	0.84	0.10	33,33,33,33	0
83	MG	1	3866	1/1	0.84	0.31	86,86,86,86	0
83	MG	1	3693	1/1	0.84	0.17	51,51,51,51	0
83	MG	1	3608	1/1	0.84	0.11	57,57,57,57	0
83	MG	1	3818	1/1	0.84	0.18	40,40,40,40	0
83	MG	1	3421	1/1	0.84	0.22	12,12,12,12	0
83	MG	1	3560	1/1	0.84	0.34	79,79,79,79	0
83	MG	o	302	1/1	0.84	0.17	37,37,37,37	0
83	MG	1	3878	1/1	0.84	0.15	57,57,57,57	0
83	MG	1	3935	1/1	0.84	0.10	76,76,76,76	0
83	MG	1	3698	1/1	0.84	0.30	41,41,41,41	0
83	MG	CM	1919	1/1	0.84	0.30	52,52,52,52	0
83	MG	AS	3539	1/1	0.84	0.30	50,50,50,50	0
83	MG	CM	1927	1/1	0.84	0.23	56,56,56,56	0
83	MG	CM	1933	1/1	0.84	0.10	53,53,53,53	0
83	MG	1	3451	1/1	0.84	0.12	41,41,41,41	0
83	MG	CM	1942	1/1	0.84	0.12	62,62,62,62	0
83	MG	0	203	1/1	0.84	0.13	63,63,63,63	0
83	MG	BB	304	1/1	0.84	0.33	63,63,63,63	0
83	MG	B	1967	1/1	0.84	0.30	70,70,70,70	0
83	MG	1	3454	1/1	0.84	0.07	42,42,42,42	0
83	MG	BS	201	1/1	0.84	0.16	76,76,76,76	0
83	MG	B	1971	1/1	0.84	0.15	63,63,63,63	0
83	MG	B	1890	1/1	0.84	0.20	38,38,38,38	0
83	MG	1	3468	1/1	0.84	0.29	55,55,55,55	0
83	MG	1	3706	1/1	0.84	0.26	47,47,47,47	0
83	MG	1	3625	1/1	0.84	0.20	57,57,57,57	0
83	MG	1	3777	1/1	0.84	0.24	32,32,32,32	0
83	MG	CM	1802	1/1	0.84	0.39	34,34,34,34	0
83	MG	1	3661	1/1	0.84	0.33	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3715	1/1	0.84	0.29	66,66,66,66	0
83	MG	1	3609	1/1	0.85	0.14	72,72,72,72	0
83	MG	B	1945	1/1	0.85	0.12	71,71,71,71	0
83	MG	1	3800	1/1	0.85	0.14	44,44,44,44	0
83	MG	AS	3419	1/1	0.85	0.09	38,38,38,38	0
83	MG	AS	3421	1/1	0.85	0.09	28,28,28,28	0
83	MG	k	401	1/1	0.85	0.12	63,63,63,63	0
83	MG	1	3408	1/1	0.85	0.31	33,33,33,33	0
83	MG	B	1853	1/1	0.85	0.07	32,32,32,32	0
83	MG	1	3802	1/1	0.85	0.20	49,49,49,49	0
83	MG	1	3718	1/1	0.85	0.09	39,39,39,39	0
83	MG	CM	1884	1/1	0.85	0.17	44,44,44,44	0
83	MG	AS	3738	1/1	0.85	0.10	62,62,62,62	0
83	MG	AS	3739	1/1	0.85	0.15	54,54,54,54	0
83	MG	B	1859	1/1	0.85	0.08	59,59,59,59	0
83	MG	1	3407	1/1	0.85	0.35	35,35,35,35	0
83	MG	AS	3747	1/1	0.85	0.13	69,69,69,69	0
83	MG	1	3938	1/1	0.85	0.14	25,25,25,25	0
83	MG	AS	3750	1/1	0.85	0.22	43,43,43,43	0
83	MG	AS	3561	1/1	0.85	0.15	45,45,45,45	0
83	MG	AS	3453	1/1	0.85	0.25	39,39,39,39	0
83	MG	1	3786	1/1	0.85	0.28	43,43,43,43	0
83	MG	1	3546	1/1	0.85	0.24	56,56,56,56	0
83	MG	AS	3458	1/1	0.85	0.36	40,40,40,40	0
83	MG	B	1811	1/1	0.85	0.15	24,24,24,24	0
83	MG	1	3812	1/1	0.85	0.21	69,69,69,69	0
83	MG	B	1870	1/1	0.85	0.27	42,42,42,42	0
83	MG	B	1928	1/1	0.85	0.07	39,39,39,39	0
83	MG	AS	3599	1/1	0.85	0.14	79,79,79,79	0
83	MG	1	3674	1/1	0.85	0.16	49,49,49,49	0
83	MG	AS	3471	1/1	0.85	0.21	43,43,43,43	0
83	MG	AS	3686	1/1	0.85	0.25	36,36,36,36	0
83	MG	1	3793	1/1	0.85	0.19	57,57,57,57	0
83	MG	2	201	1/1	0.85	0.33	43,43,43,43	0
83	MG	9	202	1/1	0.85	1.09	72,72,72,72	0
83	MG	AS	3693	1/1	0.85	0.15	43,43,43,43	0
83	MG	AS	3694	1/1	0.85	0.18	39,39,39,39	0
83	MG	1	3576	1/1	0.85	0.07	50,50,50,50	0
83	MG	AC	101	1/1	0.85	0.25	57,57,57,57	0
83	MG	1	3550	1/1	0.85	0.32	33,33,33,33	0
83	MG	1	3847	1/1	0.85	0.26	37,37,37,37	0
83	MG	DG	201	1/1	0.85	0.35	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3908	1/1	0.85	0.17	70,70,70,70	0
83	MG	CM	1863	1/1	0.85	0.13	64,64,64,64	0
83	MG	AS	3520	1/1	0.85	0.31	44,44,44,44	0
83	MG	AS	3521	1/1	0.85	0.34	45,45,45,45	0
83	MG	AS	3444	1/1	0.86	0.21	34,34,34,34	0
83	MG	1	3586	1/1	0.86	0.18	35,35,35,35	0
83	MG	CM	1810	1/1	0.86	0.17	43,43,43,43	0
83	MG	B	1860	1/1	0.86	0.10	36,36,36,36	0
83	MG	AS	3730	1/1	0.86	0.08	49,49,49,49	0
83	MG	1	3955	1/1	0.86	0.14	32,32,32,32	0
83	MG	1	3732	1/1	0.86	0.39	58,58,58,58	0
83	MG	AS	3734	1/1	0.86	0.13	40,40,40,40	0
83	MG	B	1863	1/1	0.86	0.23	59,59,59,59	0
83	MG	1	3524	1/1	0.86	0.25	43,43,43,43	0
83	MG	1	3607	1/1	0.86	0.16	42,42,42,42	0
83	MG	B	1867	1/1	0.86	0.20	56,56,56,56	0
83	MG	1	3442	1/1	0.86	0.31	50,50,50,50	0
83	MG	1	3501	1/1	0.86	0.29	31,31,31,31	0
83	MG	CM	1835	1/1	0.86	0.33	49,49,49,49	0
83	MG	1	3590	1/1	0.86	0.28	46,46,46,46	0
83	MG	1	3799	1/1	0.86	0.20	65,65,65,65	0
83	MG	1	3648	1/1	0.86	0.22	35,35,35,35	0
83	MG	B	1954	1/1	0.86	0.14	34,34,34,34	0
83	MG	1	3843	1/1	0.86	0.10	27,27,27,27	0
83	MG	CM	1854	1/1	0.86	0.14	29,29,29,29	0
83	MG	1	3507	1/1	0.86	0.21	45,45,45,45	0
83	MG	1	3710	1/1	0.86	0.10	21,21,21,21	0
83	MG	1	3681	1/1	0.86	0.20	30,30,30,30	0
83	MG	B	1893	1/1	0.86	0.14	58,58,58,58	0
83	MG	1	3682	1/1	0.86	0.15	47,47,47,47	0
83	MG	CM	1865	1/1	0.86	0.09	38,38,38,38	0
83	MG	AS	3640	1/1	0.86	0.16	48,48,48,48	0
83	MG	B	1963	1/1	0.86	0.26	55,55,55,55	0
83	MG	AS	3767	1/1	0.86	0.14	30,30,30,30	0
83	MG	AS	3511	1/1	0.86	0.17	39,39,39,39	0
83	MG	1	3888	1/1	0.86	0.19	43,43,43,43	0
83	MG	1	3933	1/1	0.86	0.33	62,62,62,62	0
83	MG	4	210	1/1	0.86	0.11	58,58,58,58	0
83	MG	1	3575	1/1	0.86	0.12	26,26,26,26	0
83	MG	1	3686	1/1	0.86	0.07	88,88,88,88	0
83	MG	AS	3656	1/1	0.86	0.18	44,44,44,44	0
83	MG	1	3850	1/1	0.86	0.21	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AT	202	1/1	0.86	0.23	34,34,34,34	0
83	MG	1	3471	1/1	0.86	0.22	39,39,39,39	0
83	MG	B	1832	1/1	0.86	0.19	46,46,46,46	0
83	MG	1	3898	1/1	0.86	0.17	66,66,66,66	0
83	MG	Q	202	1/1	0.86	0.24	52,52,52,52	0
83	MG	1	3688	1/1	0.86	0.10	33,33,33,33	0
83	MG	AS	3672	1/1	0.86	0.16	42,42,42,42	0
83	MG	AU	202	1/1	0.86	0.26	46,46,46,46	0
83	MG	B	1916	1/1	0.86	0.15	37,37,37,37	0
83	MG	AS	3548	1/1	0.86	0.35	40,40,40,40	0
83	MG	1	3902	1/1	0.86	0.18	60,60,60,60	0
83	MG	1	3854	1/1	0.86	0.09	32,32,32,32	0
83	MG	1	3945	1/1	0.86	0.10	28,28,28,28	0
83	MG	1	3475	1/1	0.86	0.28	9,9,9,9	0
83	MG	AW	304	1/1	0.86	0.11	67,67,67,67	0
83	MG	CM	1924	1/1	0.86	0.26	43,43,43,43	0
83	MG	v	301	1/1	0.86	0.11	31,31,31,31	0
83	MG	AS	3413	1/1	0.86	0.33	55,55,55,55	0
83	MG	AZ	301	1/1	0.86	0.25	27,27,27,27	0
83	MG	1	3462	1/1	0.86	0.17	18,18,18,18	0
83	MG	CM	1940	1/1	0.86	0.31	59,59,59,59	0
83	MG	AS	3573	1/1	0.86	0.09	39,39,39,39	0
83	MG	BE	302	1/1	0.86	0.21	45,45,45,45	0
83	MG	B	1847	1/1	0.86	0.28	41,41,41,41	0
83	MG	AS	3580	1/1	0.86	0.23	33,33,33,33	0
83	MG	BO	201	1/1	0.86	0.16	57,57,57,57	0
83	MG	AS	3706	1/1	0.86	0.28	44,44,44,44	0
83	MG	1	3422	1/1	0.86	0.19	43,43,43,43	0
83	MG	1	3584	1/1	0.86	0.21	42,42,42,42	0
83	MG	CA	201	1/1	0.86	0.18	40,40,40,40	0
83	MG	AS	3427	1/1	0.86	0.26	32,32,32,32	0
83	MG	CK	101	1/1	0.86	0.38	67,67,67,67	0
83	MG	0	204	1/1	0.86	0.23	59,59,59,59	0
83	MG	1	3913	1/1	0.86	0.16	28,28,28,28	0
83	MG	DQ	101	1/1	0.86	0.17	63,63,63,63	0
83	MG	AS	3441	1/1	0.86	0.16	28,28,28,28	0
83	MG	AS	3721	1/1	0.86	0.36	64,64,64,64	0
86	ZN	CB	201	1/1	0.86	0.11	180,180,180,180	0
83	MG	AS	3601	1/1	0.86	0.32	55,55,55,55	0
83	MG	BB	301	1/1	0.87	0.11	29,29,29,29	0
83	MG	1	3477	1/1	0.87	0.17	25,25,25,25	0
83	MG	1	3738	1/1	0.87	0.10	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3500	1/1	0.87	0.25	31,31,31,31	0
83	MG	BF	201	1/1	0.87	0.17	58,58,58,58	0
83	MG	AS	3590	1/1	0.87	0.13	38,38,38,38	0
83	MG	1	3675	1/1	0.87	0.08	39,39,39,39	0
83	MG	AS	3595	1/1	0.87	0.23	52,52,52,52	0
83	MG	1	3645	1/1	0.87	0.29	30,30,30,30	0
83	MG	1	3874	1/1	0.87	0.23	49,49,49,49	0
83	MG	1	3680	1/1	0.87	0.25	30,30,30,30	0
83	MG	1	3631	1/1	0.87	0.09	42,42,42,42	0
83	MG	AS	3440	1/1	0.87	0.19	28,28,28,28	0
83	MG	AS	3680	1/1	0.87	0.19	33,33,33,33	0
83	MG	CK	102	1/1	0.87	0.29	48,48,48,48	0
83	MG	AS	3516	1/1	0.87	0.26	27,27,27,27	0
83	MG	AS	3759	1/1	0.87	0.11	50,50,50,50	0
83	MG	1	3633	1/1	0.87	0.09	41,41,41,41	0
83	MG	AS	3443	1/1	0.87	0.11	49,49,49,49	0
83	MG	s	201	1/1	0.87	0.20	35,35,35,35	0
83	MG	1	3792	1/1	0.87	0.20	51,51,51,51	0
83	MG	1	3503	1/1	0.87	0.17	44,44,44,44	0
83	MG	AS	3620	1/1	0.87	0.13	44,44,44,44	0
83	MG	1	3723	1/1	0.87	0.24	36,36,36,36	0
83	MG	AS	3622	1/1	0.87	0.27	62,62,62,62	0
83	MG	B	1812	1/1	0.87	0.22	33,33,33,33	0
83	MG	1	3412	1/1	0.87	0.35	25,25,25,25	0
83	MG	AS	3777	1/1	0.87	0.23	38,38,38,38	0
83	MG	AS	3626	1/1	0.87	0.14	50,50,50,50	0
83	MG	K	301	1/1	0.87	0.16	52,52,52,52	0
83	MG	B	1911	1/1	0.87	0.12	61,61,61,61	0
83	MG	CM	1941	1/1	0.87	0.15	59,59,59,59	0
83	MG	AS	3710	1/1	0.87	0.16	47,47,47,47	0
83	MG	1	3766	1/1	0.87	0.15	34,34,34,34	0
83	MG	1	3652	1/1	0.87	0.37	44,44,44,44	0
83	MG	1	3837	1/1	0.87	0.26	41,41,41,41	0
83	MG	1	3772	1/1	0.87	0.08	35,35,35,35	0
83	MG	CP	301	1/1	0.87	0.27	36,36,36,36	0
83	MG	AS	3467	1/1	0.87	0.30	73,73,73,73	0
83	MG	CM	1847	1/1	0.87	0.22	44,44,44,44	0
83	MG	1	3640	1/1	0.87	0.11	49,49,49,49	0
83	MG	4	209	1/1	0.87	0.11	29,29,29,29	0
83	MG	AS	3725	1/1	0.87	0.20	55,55,55,55	0
83	MG	1	3671	1/1	0.87	0.24	73,73,73,73	0
83	MG	AS	3570	1/1	0.87	0.07	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	DJ	201	1/1	0.87	0.12	29,29,29,29	0
83	MG	1	3578	1/1	0.87	0.28	50,50,50,50	0
83	MG	AS	3486	1/1	0.87	0.28	43,43,43,43	0
83	MG	AS	3644	1/1	0.87	0.07	27,27,27,27	0
83	MG	AS	3574	1/1	0.87	0.34	47,47,47,47	0
83	MG	AS	3487	1/1	0.87	0.22	70,70,70,70	0
83	MG	AS	3489	1/1	0.87	0.28	32,32,32,32	0
83	MG	1	3858	1/1	0.88	0.18	41,41,41,41	0
83	MG	AS	3438	1/1	0.88	0.30	43,43,43,43	0
83	MG	CM	1838	1/1	0.88	0.22	44,44,44,44	0
83	MG	CM	1842	1/1	0.88	0.06	36,36,36,36	0
83	MG	B	1803	1/1	0.88	0.30	39,39,39,39	0
83	MG	AS	3563	1/1	0.88	0.08	38,38,38,38	0
83	MG	1	3825	1/1	0.88	0.10	31,31,31,31	0
83	MG	AS	3668	1/1	0.88	0.14	64,64,64,64	0
83	MG	AS	3569	1/1	0.88	0.16	37,37,37,37	0
83	MG	B	1944	1/1	0.88	0.07	67,67,67,67	0
83	MG	CM	1857	1/1	0.88	0.11	44,44,44,44	0
83	MG	B	1878	1/1	0.88	0.29	64,64,64,64	0
83	MG	1	3941	1/1	0.88	0.25	46,46,46,46	0
83	MG	1	3643	1/1	0.88	0.41	46,46,46,46	0
83	MG	CM	1862	1/1	0.88	0.18	62,62,62,62	0
83	MG	B	1807	1/1	0.88	0.15	43,43,43,43	0
83	MG	B	1887	1/1	0.88	0.12	91,91,91,91	0
83	MG	AS	3781	1/1	0.88	0.28	54,54,54,54	0
83	MG	1	3904	1/1	0.88	0.29	61,61,61,61	0
83	MG	B	1953	1/1	0.88	0.09	57,57,57,57	0
83	MG	1	3536	1/1	0.88	0.10	17,17,17,17	0
83	MG	1	3479	1/1	0.88	0.29	42,42,42,42	0
83	MG	1	3794	1/1	0.88	0.27	32,32,32,32	0
83	MG	1	3795	1/1	0.88	0.12	39,39,39,39	0
83	MG	AS	3695	1/1	0.88	0.26	46,46,46,46	0
83	MG	AS	3696	1/1	0.88	0.08	38,38,38,38	0
83	MG	AS	3698	1/1	0.88	0.09	41,41,41,41	0
83	MG	AS	3699	1/1	0.88	0.26	71,71,71,71	0
83	MG	1	3725	1/1	0.88	0.06	33,33,33,33	0
83	MG	o	303	1/1	0.88	0.32	41,41,41,41	0
83	MG	B	1823	1/1	0.88	0.21	31,31,31,31	0
83	MG	AS	3705	1/1	0.88	0.18	51,51,51,51	0
83	MG	B	1961	1/1	0.88	0.12	74,74,74,74	0
83	MG	B	1962	1/1	0.88	0.14	65,65,65,65	0
83	MG	AS	3708	1/1	0.88	0.21	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	CM	1905	1/1	0.88	0.19	82,82,82,82	0
83	MG	AS	3477	1/1	0.88	0.19	46,46,46,46	0
83	MG	1	3684	1/1	0.88	0.43	69,69,69,69	0
83	MG	1	3763	1/1	0.88	0.18	60,60,60,60	0
83	MG	B	1906	1/1	0.88	0.07	29,29,29,29	0
83	MG	B	1968	1/1	0.88	0.26	61,61,61,61	0
83	MG	AS	3718	1/1	0.88	0.10	76,76,76,76	0
83	MG	BH	201	1/1	0.88	0.11	35,35,35,35	0
83	MG	1	3953	1/1	0.88	0.32	62,62,62,62	0
83	MG	1	3554	1/1	0.88	0.11	51,51,51,51	0
83	MG	w	302	1/1	0.88	0.10	40,40,40,40	0
83	MG	1	3768	1/1	0.88	0.14	36,36,36,36	0
83	MG	1	3457	1/1	0.88	0.12	28,28,28,28	0
83	MG	1	3630	1/1	0.88	0.22	23,23,23,23	0
83	MG	CM	1934	1/1	0.88	0.11	40,40,40,40	0
83	MG	1	3543	1/1	0.88	0.29	32,32,32,32	0
83	MG	CM	1936	1/1	0.88	0.24	67,67,67,67	0
83	MG	1	3416	1/1	0.88	0.27	27,27,27,27	0
83	MG	Q	201	1/1	0.88	0.20	60,60,60,60	0
83	MG	AS	3515	1/1	0.88	0.26	33,33,33,33	0
83	MG	B	1845	1/1	0.88	0.21	42,42,42,42	0
83	MG	1	3808	1/1	0.88	0.07	70,70,70,70	0
83	MG	1	3736	1/1	0.88	0.23	25,25,25,25	0
83	MG	1	3737	1/1	0.88	0.28	41,41,41,41	0
83	MG	1	3887	1/1	0.88	0.14	46,46,46,46	0
83	MG	AS	3741	1/1	0.88	0.09	46,46,46,46	0
83	MG	AF	201	1/1	0.88	0.10	54,54,54,54	0
83	MG	AS	3745	1/1	0.88	0.21	63,63,63,63	0
83	MG	1	3426	1/1	0.88	0.09	38,38,38,38	0
83	MG	1	3565	1/1	0.88	0.28	51,51,51,51	0
83	MG	1	3748	1/1	0.88	0.19	51,51,51,51	0
83	MG	1	3893	1/1	0.88	0.15	55,55,55,55	0
83	MG	B	1935	1/1	0.88	0.18	71,71,71,71	0
83	MG	1	3534	1/1	0.88	0.07	37,37,37,37	0
83	MG	AS	3544	1/1	0.88	0.11	46,46,46,46	0
84	3K5	AS	3401	57/57	0.88	0.18	42,64,91,93	0
83	MG	AK	101	1/1	0.88	0.09	32,32,32,32	0
83	MG	1	3819	1/1	0.88	0.19	63,63,63,63	0
83	MG	1	3535	1/1	0.88	0.19	34,34,34,34	0
83	MG	AS	3655	1/1	0.88	0.09	48,48,48,48	0
83	MG	1	3531	1/1	0.89	0.25	37,37,37,37	0
83	MG	B	1897	1/1	0.89	0.14	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AE	201	1/1	0.89	0.15	33,33,33,33	0
83	MG	AE	202	1/1	0.89	0.16	87,87,87,87	0
83	MG	BJ	302	1/1	0.89	0.21	37,37,37,37	0
83	MG	AS	3751	1/1	0.89	0.10	74,74,74,74	0
83	MG	AS	3683	1/1	0.89	0.12	47,47,47,47	0
83	MG	4	205	1/1	0.89	0.16	40,40,40,40	0
83	MG	AS	3513	1/1	0.89	0.23	26,26,26,26	0
83	MG	AS	3610	1/1	0.89	0.06	34,34,34,34	0
83	MG	1	3401	1/1	0.89	0.27	20,20,20,20	0
83	MG	B	1903	1/1	0.89	0.21	82,82,82,82	0
83	MG	CM	1894	1/1	0.89	0.33	40,40,40,40	0
83	MG	1	3665	1/1	0.89	0.23	54,54,54,54	0
83	MG	AS	3761	1/1	0.89	0.19	53,53,53,53	0
83	MG	1	3892	1/1	0.89	0.24	39,39,39,39	0
83	MG	CM	1904	1/1	0.89	0.22	34,34,34,34	0
83	MG	1	3492	1/1	0.89	0.18	47,47,47,47	0
83	MG	AS	3439	1/1	0.89	0.38	29,29,29,29	0
83	MG	1	3924	1/1	0.89	0.31	36,36,36,36	0
83	MG	1	3668	1/1	0.89	0.11	32,32,32,32	0
83	MG	CM	1807	1/1	0.89	0.26	35,35,35,35	0
83	MG	1	3761	1/1	0.89	0.11	27,27,27,27	0
83	MG	1	3618	1/1	0.89	0.18	37,37,37,37	0
83	MG	1	3900	1/1	0.89	0.21	56,56,56,56	0
83	MG	CM	1812	1/1	0.89	0.11	42,42,42,42	0
83	MG	1	3714	1/1	0.89	0.08	25,25,25,25	0
83	MG	CM	1920	1/1	0.89	0.22	45,45,45,45	0
83	MG	1	3443	1/1	0.89	0.23	50,50,50,50	0
83	MG	1	3458	1/1	0.89	0.21	18,18,18,18	0
83	MG	1	3553	1/1	0.89	0.13	47,47,47,47	0
83	MG	CM	1930	1/1	0.89	0.20	35,35,35,35	0
83	MG	AS	3549	1/1	0.89	0.12	41,41,41,41	0
83	MG	1	3511	1/1	0.89	0.17	16,16,16,16	0
83	MG	B	1865	1/1	0.89	0.30	61,61,61,61	0
83	MG	1	3831	1/1	0.89	0.16	42,42,42,42	0
83	MG	CM	1937	1/1	0.89	0.24	50,50,50,50	0
83	MG	1	3880	1/1	0.89	0.21	46,46,46,46	0
83	MG	AT	205	1/1	0.89	0.10	57,57,57,57	0
83	MG	1	3465	1/1	0.89	0.08	24,24,24,24	0
83	MG	1	3939	1/1	0.89	0.16	52,52,52,52	0
83	MG	x	202	1/1	0.89	0.07	32,32,32,32	0
83	MG	CM	1840	1/1	0.89	0.34	51,51,51,51	0
83	MG	1	3744	1/1	0.89	0.20	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3696	1/1	0.89	0.11	45,45,45,45	0
83	MG	3	215	1/1	0.89	0.22	65,65,65,65	0
83	MG	1	3515	1/1	0.89	0.27	41,41,41,41	0
83	MG	6	203	1/1	0.89	0.17	43,43,43,43	0
83	MG	B	1888	1/1	0.89	0.22	53,53,53,53	0
83	MG	B	1831	1/1	0.89	0.19	39,39,39,39	0
83	MG	AS	3488	1/1	0.89	0.18	31,31,31,31	0
83	MG	AS	3583	1/1	0.89	0.34	45,45,45,45	0
83	MG	8	203	1/1	0.89	0.07	38,38,38,38	0
83	MG	AX	402	1/1	0.89	0.26	25,25,25,25	0
83	MG	AS	3587	1/1	0.89	0.19	38,38,38,38	0
83	MG	4	202	1/1	0.89	0.29	43,43,43,43	0
83	MG	1	3593	1/1	0.89	0.15	45,45,45,45	0
83	MG	AS	3404	1/1	0.89	0.32	26,26,26,26	0
83	MG	AS	3406	1/1	0.89	0.50	34,34,34,34	0
83	MG	AS	3597	1/1	0.89	0.22	54,54,54,54	0
83	MG	1	3853	1/1	0.90	0.07	49,49,49,49	0
83	MG	1	3762	1/1	0.90	0.06	52,52,52,52	0
83	MG	AS	3506	1/1	0.90	0.09	39,39,39,39	0
83	MG	1	3540	1/1	0.90	0.13	37,37,37,37	0
83	MG	AS	3509	1/1	0.90	0.27	32,32,32,32	0
83	MG	B	1808	1/1	0.90	0.10	75,75,75,75	0
83	MG	AS	3615	1/1	0.90	0.21	35,35,35,35	0
83	MG	u	202	1/1	0.90	0.15	30,30,30,30	0
83	MG	1	3635	1/1	0.90	0.22	36,36,36,36	0
83	MG	AU	206	1/1	0.90	0.06	45,45,45,45	0
83	MG	AU	207	1/1	0.90	0.12	73,73,73,73	0
83	MG	1	3610	1/1	0.90	0.08	57,57,57,57	0
83	MG	1	3594	1/1	0.90	0.28	55,55,55,55	0
83	MG	1	3894	1/1	0.90	0.24	45,45,45,45	0
83	MG	CM	1872	1/1	0.90	0.17	65,65,65,65	0
83	MG	AS	3424	1/1	0.90	0.34	45,45,45,45	0
83	MG	1	3404	1/1	0.90	0.29	28,28,28,28	0
83	MG	AS	3525	1/1	0.90	0.18	60,60,60,60	0
83	MG	B	1821	1/1	0.90	0.30	37,37,37,37	0
83	MG	1	3486	1/1	0.90	0.19	29,29,29,29	0
83	MG	1	3741	1/1	0.90	0.18	28,28,28,28	0
83	MG	1	3864	1/1	0.90	0.12	49,49,49,49	0
83	MG	BB	302	1/1	0.90	0.35	32,32,32,32	0
83	MG	B	1827	1/1	0.90	0.11	30,30,30,30	0
83	MG	AS	3536	1/1	0.90	0.23	31,31,31,31	0
83	MG	1	3803	1/1	0.90	0.08	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3635	1/1	0.90	0.14	37,37,37,37	0
83	MG	8	201	1/1	0.90	0.21	52,52,52,52	0
83	MG	CM	1899	1/1	0.90	0.16	50,50,50,50	0
83	MG	1	3937	1/1	0.90	0.12	53,53,53,53	0
83	MG	AS	3543	1/1	0.90	0.19	54,54,54,54	0
83	MG	AS	3735	1/1	0.90	0.09	44,44,44,44	0
83	MG	AS	3442	1/1	0.90	0.28	32,32,32,32	0
83	MG	9	201	1/1	0.90	0.17	45,45,45,45	0
83	MG	1	3869	1/1	0.90	0.23	58,58,58,58	0
83	MG	B	1901	1/1	0.90	0.26	69,69,69,69	0
83	MG	BZ	204	1/1	0.90	0.12	49,49,49,49	0
83	MG	AS	3551	1/1	0.90	0.26	32,32,32,32	0
83	MG	AS	3743	1/1	0.90	0.17	40,40,40,40	0
83	MG	1	3444	1/1	0.90	0.20	40,40,40,40	0
83	MG	1	3427	1/1	0.90	0.31	26,26,26,26	0
83	MG	1	3583	1/1	0.90	0.08	38,38,38,38	0
83	MG	CM	1921	1/1	0.90	0.10	28,28,28,28	0
83	MG	B	1905	1/1	0.90	0.15	46,46,46,46	0
83	MG	AS	3651	1/1	0.90	0.26	28,28,28,28	0
83	MG	1	3562	1/1	0.90	0.15	51,51,51,51	0
83	MG	1	3875	1/1	0.90	0.24	33,33,33,33	0
83	MG	AS	3566	1/1	0.90	0.28	32,32,32,32	0
83	MG	1	3461	1/1	0.90	0.25	28,28,28,28	0
83	MG	B	1966	1/1	0.90	0.13	41,41,41,41	0
83	MG	AS	3664	1/1	0.90	0.17	23,23,23,23	0
83	MG	1	3482	1/1	0.90	0.25	28,28,28,28	0
83	MG	B	1849	1/1	0.90	0.16	43,43,43,43	0
83	MG	1	3439	1/1	0.90	0.22	28,28,28,28	0
83	MG	B	1852	1/1	0.90	0.25	65,65,65,65	0
83	MG	AS	3577	1/1	0.90	0.21	40,40,40,40	0
83	MG	1	3677	1/1	0.90	0.13	55,55,55,55	0
83	MG	B	1855	1/1	0.90	0.12	49,49,49,49	0
83	MG	1	3791	1/1	0.90	0.08	28,28,28,28	0
83	MG	k	403	1/1	0.90	0.25	60,60,60,60	0
83	MG	CQ	301	1/1	0.90	0.14	42,42,42,42	0
83	MG	CM	1824	1/1	0.90	0.15	28,28,28,28	0
83	MG	1	3881	1/1	0.90	0.15	26,26,26,26	0
83	MG	AP	201	1/1	0.90	0.11	31,31,31,31	0
83	MG	CM	1831	1/1	0.90	0.26	25,25,25,25	0
83	MG	1	3606	1/1	0.90	0.15	47,47,47,47	0
83	MG	AS	3774	1/1	0.90	0.17	50,50,50,50	0
83	MG	AS	3687	1/1	0.90	0.30	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	DG	202	1/1	0.90	0.12	45,45,45,45	0
83	MG	1	3500	1/1	0.90	0.26	36,36,36,36	0
83	MG	CM	1839	1/1	0.90	0.12	40,40,40,40	0
83	MG	o	301	1/1	0.90	0.23	33,33,33,33	0
84	3K5	1	3403	57/57	0.90	0.15	36,53,77,93	0
83	MG	1	3823	1/1	0.90	0.17	36,36,36,36	0
83	MG	AS	3499	1/1	0.90	0.32	39,39,39,39	0
83	MG	Y	203	1/1	0.90	0.21	61,61,61,61	0
83	MG	AS	3600	1/1	0.90	0.14	50,50,50,50	0
83	MG	1	3430	1/1	0.90	0.31	30,30,30,30	0
83	MG	1	3611	1/1	0.91	0.21	23,23,23,23	0
83	MG	o	304	1/1	0.91	0.29	56,56,56,56	0
83	MG	AS	3591	1/1	0.91	0.16	41,41,41,41	0
83	MG	1	3916	1/1	0.91	0.08	73,73,73,73	0
83	MG	1	3537	1/1	0.91	0.18	43,43,43,43	0
83	MG	1	3617	1/1	0.91	0.26	25,25,25,25	0
83	MG	AS	3697	1/1	0.91	0.06	32,32,32,32	0
83	MG	1	3455	1/1	0.91	0.29	26,26,26,26	0
83	MG	AS	3498	1/1	0.91	0.32	36,36,36,36	0
83	MG	1	3563	1/1	0.91	0.15	29,29,29,29	0
83	MG	1	3564	1/1	0.91	0.16	39,39,39,39	0
83	MG	1	3456	1/1	0.91	0.05	7,7,7,7	0
83	MG	AS	3603	1/1	0.91	0.48	49,49,49,49	0
83	MG	1	3473	1/1	0.91	0.29	23,23,23,23	0
83	MG	AU	210	1/1	0.91	0.08	33,33,33,33	0
83	MG	1	3519	1/1	0.91	0.36	60,60,60,60	0
83	MG	B	1875	1/1	0.91	0.21	47,47,47,47	0
83	MG	AS	3405	1/1	0.91	0.18	26,26,26,26	0
83	MG	CM	1877	1/1	0.91	0.12	42,42,42,42	0
83	MG	B	1876	1/1	0.91	0.24	50,50,50,50	0
83	MG	B	1938	1/1	0.91	0.17	35,35,35,35	0
83	MG	1	3598	1/1	0.91	0.18	33,33,33,33	0
83	MG	B	1879	1/1	0.91	0.24	27,27,27,27	0
83	MG	AS	3420	1/1	0.91	0.20	42,42,42,42	0
83	MG	1	3498	1/1	0.91	0.16	26,26,26,26	0
83	MG	1	3572	1/1	0.91	0.16	52,52,52,52	0
83	MG	1	3522	1/1	0.91	0.10	32,32,32,32	0
83	MG	B	1884	1/1	0.91	0.21	41,41,41,41	0
83	MG	1	3413	1/1	0.91	0.23	21,21,21,21	0
83	MG	AS	3430	1/1	0.91	0.26	26,26,26,26	0
83	MG	1	3889	1/1	0.91	0.09	38,38,38,38	0
83	MG	AS	3729	1/1	0.91	0.23	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3532	1/1	0.91	0.10	55,55,55,55	0
83	MG	BN	201	1/1	0.91	0.09	56,56,56,56	0
83	MG	CM	1908	1/1	0.91	0.15	45,45,45,45	0
83	MG	B	1828	1/1	0.91	0.25	47,47,47,47	0
83	MG	AS	3437	1/1	0.91	0.24	61,61,61,61	0
83	MG	B	1830	1/1	0.91	0.26	42,42,42,42	0
83	MG	1	3727	1/1	0.91	0.28	40,40,40,40	0
83	MG	1	3450	1/1	0.91	0.17	33,33,33,33	0
83	MG	AB	201	1/1	0.91	0.13	37,37,37,37	0
83	MG	1	3729	1/1	0.91	0.17	50,50,50,50	0
83	MG	1	3436	1/1	0.91	0.12	28,28,28,28	0
83	MG	1	3855	1/1	0.91	0.18	32,32,32,32	0
83	MG	1	3776	1/1	0.91	0.21	51,51,51,51	0
83	MG	1	3731	1/1	0.91	0.17	20,20,20,20	0
83	MG	1	3504	1/1	0.91	0.16	22,22,22,22	0
83	MG	1	3505	1/1	0.91	0.13	41,41,41,41	0
83	MG	AS	3552	1/1	0.91	0.21	20,20,20,20	0
83	MG	CM	1805	1/1	0.91	0.24	31,31,31,31	0
83	MG	AS	3553	1/1	0.91	0.16	21,21,21,21	0
83	MG	AS	3452	1/1	0.91	0.26	28,28,28,28	0
83	MG	1	3782	1/1	0.91	0.20	58,58,58,58	0
83	MG	AS	3559	1/1	0.91	0.27	41,41,41,41	0
83	MG	1	3490	1/1	0.91	0.23	53,53,53,53	0
83	MG	1	3445	1/1	0.91	0.32	36,36,36,36	0
83	MG	B	1907	1/1	0.91	0.10	29,29,29,29	0
83	MG	AS	3658	1/1	0.91	0.09	37,37,37,37	0
83	MG	1	3827	1/1	0.91	0.15	47,47,47,47	0
83	MG	AS	3565	1/1	0.91	0.19	22,22,22,22	0
83	MG	1	3703	1/1	0.91	0.30	43,43,43,43	0
83	MG	AS	3567	1/1	0.91	0.22	22,22,22,22	0
83	MG	1	3510	1/1	0.91	0.19	24,24,24,24	0
83	MG	AS	3465	1/1	0.91	0.22	22,22,22,22	0
83	MG	CM	1825	1/1	0.91	0.10	39,39,39,39	0
83	MG	B	1854	1/1	0.91	0.26	29,29,29,29	0
83	MG	AP	202	1/1	0.91	0.32	85,85,85,85	0
83	MG	AS	3469	1/1	0.91	0.15	26,26,26,26	0
83	MG	1	3493	1/1	0.91	0.14	33,33,33,33	0
83	MG	AS	3679	1/1	0.91	0.05	37,37,37,37	0
83	MG	AS	3773	1/1	0.91	0.18	53,53,53,53	0
83	MG	AS	3576	1/1	0.91	0.06	44,44,44,44	0
83	MG	B	1915	1/1	0.91	0.14	46,46,46,46	0
83	MG	AS	3472	1/1	0.91	0.24	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3684	1/1	0.91	0.21	36,36,36,36	0
83	MG	AS	3476	1/1	0.91	0.07	20,20,20,20	0
83	MG	1	3708	1/1	0.91	0.10	36,36,36,36	0
83	MG	1	3743	1/1	0.91	0.30	29,29,29,29	0
83	MG	CM	1850	1/1	0.91	0.17	42,42,42,42	0
83	MG	AS	3480	1/1	0.91	0.07	45,45,45,45	0
83	MG	1	3523	1/1	0.92	0.08	31,31,31,31	0
83	MG	AS	3497	1/1	0.92	0.20	26,26,26,26	0
83	MG	B	1858	1/1	0.92	0.10	38,38,38,38	0
83	MG	AS	3572	1/1	0.92	0.26	35,35,35,35	0
83	MG	CM	1867	1/1	0.92	0.17	60,60,60,60	0
83	MG	AS	3428	1/1	0.92	0.30	35,35,35,35	0
83	MG	1	3425	1/1	0.92	0.16	19,19,19,19	0
83	MG	1	3509	1/1	0.92	0.22	44,44,44,44	0
83	MG	1	3790	1/1	0.92	0.25	31,31,31,31	0
83	MG	3	212	1/1	0.92	0.27	41,41,41,41	0
83	MG	CM	1874	1/1	0.92	0.29	49,49,49,49	0
83	MG	AS	3578	1/1	0.92	0.22	31,31,31,31	0
83	MG	AS	3740	1/1	0.92	0.06	69,69,69,69	0
83	MG	1	3638	1/1	0.92	0.13	32,32,32,32	0
83	MG	AS	3742	1/1	0.92	0.06	57,57,57,57	0
83	MG	BJ	303	1/1	0.92	0.17	24,24,24,24	0
83	MG	1	3755	1/1	0.92	0.19	35,35,35,35	0
83	MG	AS	3582	1/1	0.92	0.17	51,51,51,51	0
83	MG	CM	1883	1/1	0.92	0.23	65,65,65,65	0
83	MG	1	3453	1/1	0.92	0.13	23,23,23,23	0
83	MG	BV	201	1/1	0.92	0.22	45,45,45,45	0
83	MG	CM	1887	1/1	0.92	0.09	38,38,38,38	0
83	MG	CM	1889	1/1	0.92	0.20	39,39,39,39	0
83	MG	AS	3661	1/1	0.92	0.08	87,87,87,87	0
83	MG	AS	3584	1/1	0.92	0.20	42,42,42,42	0
83	MG	CM	1895	1/1	0.92	0.14	32,32,32,32	0
83	MG	AS	3510	1/1	0.92	0.19	23,23,23,23	0
83	MG	1	3833	1/1	0.92	0.09	32,32,32,32	0
83	MG	6	204	1/1	0.92	0.07	20,20,20,20	0
83	MG	1	3478	1/1	0.92	0.21	22,22,22,22	0
83	MG	CM	1902	1/1	0.92	0.23	33,33,33,33	0
83	MG	AS	3514	1/1	0.92	0.15	36,36,36,36	0
83	MG	AS	3671	1/1	0.92	0.11	38,38,38,38	0
83	MG	1	3669	1/1	0.92	0.07	45,45,45,45	0
83	MG	B	1825	1/1	0.92	0.28	58,58,58,58	0
83	MG	AS	3517	1/1	0.92	0.16	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3867	1/1	0.92	0.21	28,28,28,28	0
83	MG	CM	1804	1/1	0.92	0.42	42,42,42,42	0
83	MG	1	3759	1/1	0.92	0.23	37,37,37,37	0
83	MG	AS	3448	1/1	0.92	0.17	34,34,34,34	0
83	MG	1	3760	1/1	0.92	0.38	37,37,37,37	0
83	MG	1	3906	1/1	0.92	0.15	38,38,38,38	0
83	MG	CM	1809	1/1	0.92	0.29	86,86,86,86	0
83	MG	1	3569	1/1	0.92	0.06	27,27,27,27	0
83	MG	AS	3606	1/1	0.92	0.08	41,41,41,41	0
83	MG	CM	1922	1/1	0.92	0.22	43,43,43,43	0
83	MG	AS	3607	1/1	0.92	0.16	37,37,37,37	0
83	MG	CM	1925	1/1	0.92	0.11	47,47,47,47	0
83	MG	AS	3531	1/1	0.92	0.09	29,29,29,29	0
83	MG	4	211	1/1	0.92	0.21	51,51,51,51	0
83	MG	j	301	1/1	0.92	0.06	19,19,19,19	0
83	MG	CM	1931	1/1	0.92	0.19	42,42,42,42	0
83	MG	1	3528	1/1	0.92	0.20	39,39,39,39	0
83	MG	CM	1819	1/1	0.92	0.18	56,56,56,56	0
83	MG	1	3571	1/1	0.92	0.15	37,37,37,37	0
83	MG	1	3529	1/1	0.92	0.10	40,40,40,40	0
83	MG	AS	3462	1/1	0.92	0.22	34,34,34,34	0
83	MG	1	3488	1/1	0.92	0.26	26,26,26,26	0
83	MG	AS	3464	1/1	0.92	0.31	47,47,47,47	0
83	MG	1	3649	1/1	0.92	0.24	41,41,41,41	0
83	MG	CM	1943	1/1	0.92	0.34	38,38,38,38	0
83	MG	AT	201	1/1	0.92	0.19	17,17,17,17	0
83	MG	B	1891	1/1	0.92	0.13	49,49,49,49	0
83	MG	CM	1947	1/1	0.92	0.18	44,44,44,44	0
83	MG	1	3552	1/1	0.92	0.09	45,45,45,45	0
83	MG	1	3446	1/1	0.92	0.09	82,82,82,82	0
83	MG	1	3517	1/1	0.92	0.18	36,36,36,36	0
83	MG	AR	401	1/1	0.92	0.12	60,60,60,60	0
83	MG	AS	3627	1/1	0.92	0.19	55,55,55,55	0
83	MG	1	3653	1/1	0.92	0.22	34,34,34,34	0
83	MG	AS	3474	1/1	0.92	0.18	29,29,29,29	0
83	MG	1	3480	1/1	0.92	0.18	21,21,21,21	0
83	MG	DB	202	1/1	0.92	0.25	67,67,67,67	0
83	MG	1	3481	1/1	0.92	0.17	31,31,31,31	0
83	MG	B	1851	1/1	0.92	0.14	63,63,63,63	0
83	MG	1	3520	1/1	0.92	0.25	41,41,41,41	0
83	MG	AS	3482	1/1	0.92	0.16	29,29,29,29	0
83	MG	1	3474	1/1	0.92	0.26	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3817	1/1	0.92	0.14	31,31,31,31	0
83	MG	CM	1855	1/1	0.92	0.19	41,41,41,41	0
83	MG	CM	1856	1/1	0.92	0.12	25,25,25,25	0
83	MG	B	1952	1/1	0.92	0.18	49,49,49,49	0
85	TIX	1	3958	27/27	0.92	0.27	51,60,85,184	0
85	TIX	AS	3782	27/27	0.92	0.18	48,60,73,150	0
83	MG	1	3746	1/1	0.92	0.29	42,42,42,42	0
83	MG	AS	3726	1/1	0.92	0.17	56,56,56,56	0
83	MG	1	3469	1/1	0.92	0.33	42,42,42,42	0
83	MG	AS	3641	1/1	0.92	0.12	38,38,38,38	0
83	MG	B	1969	1/1	0.93	0.05	28,28,28,28	0
83	MG	CM	1869	1/1	0.93	0.13	40,40,40,40	0
83	MG	AS	3720	1/1	0.93	0.17	43,43,43,43	0
83	MG	AS	3629	1/1	0.93	0.09	38,38,38,38	0
83	MG	1	3452	1/1	0.93	0.20	23,23,23,23	0
83	MG	1	3621	1/1	0.93	0.19	40,40,40,40	0
83	MG	1	3895	1/1	0.93	0.09	71,71,71,71	0
83	MG	B	1848	1/1	0.93	0.17	33,33,33,33	0
83	MG	1	3513	1/1	0.93	0.28	32,32,32,32	0
83	MG	AS	3555	1/1	0.93	0.16	36,36,36,36	0
83	MG	1	3659	1/1	0.93	0.17	23,23,23,23	0
83	MG	1	3707	1/1	0.93	0.16	31,31,31,31	0
83	MG	1	3438	1/1	0.93	0.18	28,28,28,28	0
83	MG	1	3865	1/1	0.93	0.10	77,77,77,77	0
83	MG	1	3417	1/1	0.93	0.19	30,30,30,30	0
83	MG	BK	202	1/1	0.93	0.07	30,30,30,30	0
83	MG	1	3734	1/1	0.93	0.08	28,28,28,28	0
83	MG	1	3868	1/1	0.93	0.15	41,41,41,41	0
83	MG	1	3905	1/1	0.93	0.19	38,38,38,38	0
83	MG	1	3516	1/1	0.93	0.31	33,33,33,33	0
83	MG	CM	1893	1/1	0.93	0.32	30,30,30,30	0
83	MG	1	3907	1/1	0.93	0.17	39,39,39,39	0
83	MG	1	3870	1/1	0.93	0.05	46,46,46,46	0
83	MG	1	3948	1/1	0.93	0.07	40,40,40,40	0
83	MG	1	3713	1/1	0.93	0.24	39,39,39,39	0
83	MG	CM	1898	1/1	0.93	0.29	38,38,38,38	0
83	MG	CA	202	1/1	0.93	0.16	53,53,53,53	0
83	MG	1	3447	1/1	0.93	0.26	21,21,21,21	0
83	MG	CJ	201	1/1	0.93	0.09	49,49,49,49	0
83	MG	1	3420	1/1	0.93	0.20	33,33,33,33	0
83	MG	AS	3491	1/1	0.93	0.28	42,42,42,42	0
83	MG	AS	3492	1/1	0.93	0.16	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	r	301	1/1	0.93	0.21	23,23,23,23	0
83	MG	CL	303	1/1	0.93	0.09	41,41,41,41	0
83	MG	CM	1911	1/1	0.93	0.29	30,30,30,30	0
83	MG	AS	3494	1/1	0.93	0.11	45,45,45,45	0
83	MG	AS	3407	1/1	0.93	0.15	23,23,23,23	0
83	MG	AS	3409	1/1	0.93	0.24	20,20,20,20	0
83	MG	AS	3663	1/1	0.93	0.25	56,56,56,56	0
83	MG	1	3740	1/1	0.93	0.23	35,35,35,35	0
83	MG	1	3804	1/1	0.93	0.17	31,31,31,31	0
83	MG	CM	1918	1/1	0.93	0.14	51,51,51,51	0
83	MG	AS	3418	1/1	0.93	0.19	30,30,30,30	0
83	MG	B	1810	1/1	0.93	0.24	43,43,43,43	0
83	MG	1	3915	1/1	0.93	0.11	71,71,71,71	0
83	MG	1	3647	1/1	0.93	0.10	26,26,26,26	0
83	MG	CM	1923	1/1	0.93	0.13	39,39,39,39	0
83	MG	B	1874	1/1	0.93	0.18	53,53,53,53	0
83	MG	1	3775	1/1	0.93	0.20	38,38,38,38	0
83	MG	v	302	1/1	0.93	0.08	69,69,69,69	0
83	MG	AS	3675	1/1	0.93	0.05	20,20,20,20	0
83	MG	AS	3678	1/1	0.93	0.07	43,43,43,43	0
83	MG	w	301	1/1	0.93	0.20	29,29,29,29	0
83	MG	AS	3593	1/1	0.93	0.09	48,48,48,48	0
83	MG	AS	3770	1/1	0.93	0.14	31,31,31,31	0
83	MG	AS	3594	1/1	0.93	0.14	35,35,35,35	0
83	MG	AS	3682	1/1	0.93	0.14	43,43,43,43	0
83	MG	B	1818	1/1	0.93	0.26	24,24,24,24	0
83	MG	CM	1939	1/1	0.93	0.18	64,64,64,64	0
83	MG	B	1820	1/1	0.93	0.12	38,38,38,38	0
83	MG	3	203	1/1	0.93	0.33	47,47,47,47	0
83	MG	AS	3432	1/1	0.93	0.21	23,23,23,23	0
83	MG	1	3435	1/1	0.93	0.18	23,23,23,23	0
83	MG	CM	1833	1/1	0.93	0.24	36,36,36,36	0
83	MG	x	201	1/1	0.93	0.23	23,23,23,23	0
83	MG	B	1885	1/1	0.93	0.12	78,78,78,78	0
83	MG	1	3612	1/1	0.93	0.33	34,34,34,34	0
83	MG	1	3778	1/1	0.93	0.15	43,43,43,43	0
83	MG	1	3613	1/1	0.93	0.28	32,32,32,32	0
83	MG	AS	3523	1/1	0.93	0.12	33,33,33,33	0
83	MG	1	3632	1/1	0.93	0.13	42,42,42,42	0
83	MG	B	1829	1/1	0.93	0.14	56,56,56,56	0
83	MG	1	3672	1/1	0.93	0.06	33,33,33,33	0
83	MG	AS	3613	1/1	0.93	0.06	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3499	1/1	0.93	0.21	24,24,24,24	0
83	MG	3	211	1/1	0.93	0.14	52,52,52,52	0
83	MG	AS	3703	1/1	0.93	0.23	18,18,18,18	0
83	MG	1	3545	1/1	0.93	0.33	34,34,34,34	0
83	MG	1	3751	1/1	0.93	0.17	37,37,37,37	0
83	MG	AU	205	1/1	0.93	0.11	40,40,40,40	0
83	MG	B	1836	1/1	0.93	0.27	27,27,27,27	0
83	MG	1	3724	1/1	0.93	0.21	35,35,35,35	0
83	MG	AS	3538	1/1	0.93	0.22	37,37,37,37	0
83	MG	1	3822	1/1	0.93	0.31	32,32,32,32	0
83	MG	AS	3623	1/1	0.93	0.08	62,62,62,62	0
83	MG	1	3856	1/1	0.93	0.09	36,36,36,36	0
83	MG	AW	302	1/1	0.93	0.13	35,35,35,35	0
83	MG	1	3411	1/1	0.93	0.22	24,24,24,24	0
83	MG	B	1842	1/1	0.93	0.27	29,29,29,29	0
83	MG	1	3676	1/1	0.93	0.13	67,67,67,67	0
83	MG	Y	201	1/1	0.94	0.05	39,39,39,39	0
83	MG	B	1846	1/1	0.94	0.06	58,58,58,58	0
83	MG	B	1877	1/1	0.94	0.18	53,53,53,53	0
83	MG	B	1950	1/1	0.94	0.20	49,49,49,49	0
83	MG	AS	3568	1/1	0.94	0.18	24,24,24,24	0
83	MG	AS	3450	1/1	0.94	0.17	35,35,35,35	0
83	MG	1	3824	1/1	0.94	0.11	47,47,47,47	0
83	MG	1	3787	1/1	0.94	0.12	34,34,34,34	0
83	MG	AS	3508	1/1	0.94	0.23	25,25,25,25	0
83	MG	1	3752	1/1	0.94	0.12	29,29,29,29	0
83	MG	1	3573	1/1	0.94	0.13	27,27,27,27	0
83	MG	4	206	1/1	0.94	0.12	27,27,27,27	0
83	MG	1	3911	1/1	0.94	0.09	39,39,39,39	0
83	MG	4	208	1/1	0.94	0.17	27,27,27,27	0
83	MG	AT	206	1/1	0.94	0.25	39,39,39,39	0
83	MG	AS	3460	1/1	0.94	0.14	24,24,24,24	0
83	MG	AS	3579	1/1	0.94	0.26	46,46,46,46	0
83	MG	AS	3408	1/1	0.94	0.11	45,45,45,45	0
83	MG	B	1886	1/1	0.94	0.16	61,61,61,61	0
83	MG	AS	3411	1/1	0.94	0.28	29,29,29,29	0
83	MG	CM	1826	1/1	0.94	0.21	48,48,48,48	0
83	MG	B	1922	1/1	0.94	0.06	38,38,38,38	0
83	MG	1	3956	1/1	0.94	0.17	38,38,38,38	0
83	MG	CM	1829	1/1	0.94	0.30	33,33,33,33	0
83	MG	CM	1830	1/1	0.94	0.20	42,42,42,42	0
83	MG	AS	3723	1/1	0.94	0.07	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3648	1/1	0.94	0.05	22,22,22,22	0
83	MG	AS	3466	1/1	0.94	0.07	44,44,44,44	0
83	MG	AS	3650	1/1	0.94	0.09	27,27,27,27	0
83	MG	AS	3586	1/1	0.94	0.20	20,20,20,20	0
83	MG	AS	3652	1/1	0.94	0.12	31,31,31,31	0
83	MG	1	3828	1/1	0.94	0.22	35,35,35,35	0
83	MG	3	201	1/1	0.94	0.15	21,21,21,21	0
83	MG	AS	3731	1/1	0.94	0.08	35,35,35,35	0
83	MG	CM	1845	1/1	0.94	0.20	28,28,28,28	0
83	MG	CM	1932	1/1	0.94	0.10	52,52,52,52	0
83	MG	1	3829	1/1	0.94	0.08	44,44,44,44	0
83	MG	AS	3657	1/1	0.94	0.21	30,30,30,30	0
83	MG	1	3658	1/1	0.94	0.23	31,31,31,31	0
83	MG	AS	3423	1/1	0.94	0.24	22,22,22,22	0
83	MG	1	3574	1/1	0.94	0.07	36,36,36,36	0
83	MG	1	3437	1/1	0.94	0.24	19,19,19,19	0
83	MG	AS	3475	1/1	0.94	0.21	29,29,29,29	0
83	MG	B	1833	1/1	0.94	0.16	45,45,45,45	0
83	MG	B	1895	1/1	0.94	0.20	40,40,40,40	0
83	MG	1	3532	1/1	0.94	0.28	31,31,31,31	0
83	MG	1	3685	1/1	0.94	0.26	76,76,76,76	0
83	MG	AS	3481	1/1	0.94	0.07	25,25,25,25	0
83	MG	AS	3541	1/1	0.94	0.36	25,25,25,25	0
83	MG	1	3813	1/1	0.94	0.19	44,44,44,44	0
83	MG	AS	3605	1/1	0.94	0.16	21,21,21,21	0
83	MG	AS	3483	1/1	0.94	0.21	22,22,22,22	0
83	MG	BK	201	1/1	0.94	0.17	22,22,22,22	0
83	MG	AS	3484	1/1	0.94	0.26	23,23,23,23	0
83	MG	AS	3545	1/1	0.94	0.30	29,29,29,29	0
83	MG	AS	3546	1/1	0.94	0.18	21,21,21,21	0
83	MG	AS	3485	1/1	0.94	0.11	42,42,42,42	0
83	MG	1	3699	1/1	0.94	0.16	23,23,23,23	0
83	MG	BZ	201	1/1	0.94	0.16	38,38,38,38	0
83	MG	G	301	1/1	0.94	0.08	82,82,82,82	0
83	MG	AS	3435	1/1	0.94	0.12	23,23,23,23	0
83	MG	1	3502	1/1	0.94	0.20	39,39,39,39	0
83	MG	1	3780	1/1	0.94	0.27	29,29,29,29	0
83	MG	AS	3554	1/1	0.94	0.09	45,45,45,45	0
83	MG	1	3555	1/1	0.94	0.05	41,41,41,41	0
83	MG	1	3542	1/1	0.94	0.14	39,39,39,39	0
83	MG	AS	3557	1/1	0.94	0.22	29,29,29,29	0
83	MG	1	3551	1/1	0.94	0.17	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3692	1/1	0.94	0.28	25,25,25,25	0
86	ZN	AH	203	1/1	0.94	0.13	122,122,122,122	0
83	MG	AS	3495	1/1	0.94	0.15	37,37,37,37	0
83	MG	B	1871	1/1	0.94	0.16	53,53,53,53	0
83	MG	1	3582	1/1	0.94	0.20	52,52,52,52	0
83	MG	1	3692	1/1	0.94	0.22	38,38,38,38	0
83	MG	CM	1841	1/1	0.95	0.13	38,38,38,38	0
83	MG	1	3616	1/1	0.95	0.10	34,34,34,34	0
83	MG	CM	1843	1/1	0.95	0.16	34,34,34,34	0
83	MG	CM	1910	1/1	0.95	0.15	65,65,65,65	0
83	MG	1	3770	1/1	0.95	0.06	31,31,31,31	0
83	MG	1	3580	1/1	0.95	0.26	32,32,32,32	0
83	MG	B	1896	1/1	0.95	0.15	54,54,54,54	0
83	MG	1	3639	1/1	0.95	0.04	34,34,34,34	0
83	MG	CM	1849	1/1	0.95	0.15	41,41,41,41	0
83	MG	1	3662	1/1	0.95	0.24	32,32,32,32	0
83	MG	1	3441	1/1	0.95	0.29	33,33,33,33	0
83	MG	AS	3677	1/1	0.95	0.16	27,27,27,27	0
83	MG	1	3494	1/1	0.95	0.23	24,24,24,24	0
83	MG	1	3689	1/1	0.95	0.17	63,63,63,63	0
83	MG	1	3533	1/1	0.95	0.18	22,22,22,22	0
83	MG	1	3556	1/1	0.95	0.06	42,42,42,42	0
83	MG	1	3667	1/1	0.95	0.23	37,37,37,37	0
83	MG	1	3585	1/1	0.95	0.17	38,38,38,38	0
83	MG	CM	1860	1/1	0.95	0.10	31,31,31,31	0
83	MG	1	3431	1/1	0.95	0.06	31,31,31,31	0
83	MG	1	3558	1/1	0.95	0.10	49,49,49,49	0
83	MG	CM	1928	1/1	0.95	0.08	52,52,52,52	0
83	MG	CM	1929	1/1	0.95	0.16	32,32,32,32	0
83	MG	B	1838	1/1	0.95	0.14	35,35,35,35	0
83	MG	B	1909	1/1	0.95	0.26	30,30,30,30	0
83	MG	1	3626	1/1	0.95	0.26	30,30,30,30	0
83	MG	0	202	1/1	0.95	0.07	47,47,47,47	0
83	MG	1	3487	1/1	0.95	0.11	38,38,38,38	0
83	MG	1	3449	1/1	0.95	0.26	24,24,24,24	0
83	MG	1	3463	1/1	0.95	0.17	22,22,22,22	0
83	MG	6	202	1/1	0.95	0.15	40,40,40,40	0
83	MG	CM	1938	1/1	0.95	0.18	44,44,44,44	0
83	MG	1	3591	1/1	0.95	0.24	23,23,23,23	0
83	MG	1	3592	1/1	0.95	0.12	29,29,29,29	0
83	MG	AS	3504	1/1	0.95	0.08	38,38,38,38	0
83	MG	1	3538	1/1	0.95	0.13	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	8	202	1/1	0.95	0.12	59,59,59,59	0
83	MG	AS	3415	1/1	0.95	0.07	46,46,46,46	0
83	MG	AS	3417	1/1	0.95	0.29	22,22,22,22	0
83	MG	CM	1878	1/1	0.95	0.12	34,34,34,34	0
83	MG	1	3678	1/1	0.95	0.08	32,32,32,32	0
83	MG	AS	3754	1/1	0.95	0.08	35,35,35,35	0
83	MG	1	3932	1/1	0.95	0.13	35,35,35,35	0
83	MG	1	3821	1/1	0.95	0.10	63,63,63,63	0
83	MG	CM	1823	1/1	0.95	0.07	37,37,37,37	0
83	MG	B	1964	1/1	0.95	0.08	57,57,57,57	0
83	MG	1	3433	1/1	0.95	0.12	80,80,80,80	0
83	MG	AS	3611	1/1	0.95	0.26	50,50,50,50	0
83	MG	CM	1888	1/1	0.95	0.15	51,51,51,51	0
83	MG	AS	3760	1/1	0.95	0.10	70,70,70,70	0
83	MG	CM	1890	1/1	0.95	0.20	30,30,30,30	0
83	MG	B	1819	1/1	0.95	0.18	44,44,44,44	0
83	MG	AS	3762	1/1	0.95	0.14	38,38,38,38	0
83	MG	1	3491	1/1	0.95	0.18	24,24,24,24	0
83	MG	1	3459	1/1	0.95	0.12	27,27,27,27	0
83	MG	CM	1832	1/1	0.95	0.18	32,32,32,32	0
83	MG	AS	3712	1/1	0.95	0.14	32,32,32,32	0
83	MG	AS	3713	1/1	0.95	0.05	28,28,28,28	0
83	MG	AS	3518	1/1	0.95	0.15	26,26,26,26	0
83	MG	AS	3519	1/1	0.95	0.18	26,26,26,26	0
83	MG	CM	1901	1/1	0.95	0.19	14,14,14,14	0
83	MG	1	3636	1/1	0.95	0.07	38,38,38,38	0
83	MG	CM	1903	1/1	0.95	0.14	43,43,43,43	0
83	MG	B	1932	1/1	0.95	0.06	24,24,24,24	0
83	MG	B	1933	1/1	0.95	0.11	60,60,60,60	0
83	MG	1	3765	1/1	0.96	0.15	43,43,43,43	0
83	MG	1	3641	1/1	0.96	0.14	21,21,21,21	0
83	MG	AS	3702	1/1	0.96	0.25	31,31,31,31	0
83	MG	1	3886	1/1	0.96	0.13	29,29,29,29	0
83	MG	B	1918	1/1	0.96	0.11	32,32,32,32	0
83	MG	AS	3505	1/1	0.96	0.14	41,41,41,41	0
83	MG	1	3815	1/1	0.96	0.05	42,42,42,42	0
83	MG	1	3949	1/1	0.96	0.05	49,49,49,49	0
83	MG	AS	3604	1/1	0.96	0.05	37,37,37,37	0
83	MG	1	3747	1/1	0.96	0.15	26,26,26,26	0
83	MG	1	3769	1/1	0.96	0.16	22,22,22,22	0
83	MG	AU	201	1/1	0.96	0.06	21,21,21,21	0
83	MG	CM	1886	1/1	0.96	0.29	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3674	1/1	0.96	0.22	27,27,27,27	0
83	MG	AS	3454	1/1	0.96	0.19	22,22,22,22	0
83	MG	AS	3676	1/1	0.96	0.23	15,15,15,15	0
83	MG	1	3568	1/1	0.96	0.19	24,24,24,24	0
83	MG	CM	1844	1/1	0.96	0.12	32,32,32,32	0
83	MG	CM	1892	1/1	0.96	0.14	28,28,28,28	0
83	MG	1	3739	1/1	0.96	0.20	19,19,19,19	0
83	MG	AS	3716	1/1	0.96	0.07	44,44,44,44	0
83	MG	AS	3717	1/1	0.96	0.10	52,52,52,52	0
83	MG	AS	3457	1/1	0.96	0.21	31,31,31,31	0
83	MG	CM	1946	1/1	0.96	0.03	43,43,43,43	0
83	MG	AS	3547	1/1	0.96	0.11	36,36,36,36	0
83	MG	AS	3403	1/1	0.96	0.17	17,17,17,17	0
83	MG	CM	1851	1/1	0.96	0.14	27,27,27,27	0
83	MG	B	1926	1/1	0.96	0.09	46,46,46,46	0
83	MG	1	3704	1/1	0.96	0.07	34,34,34,34	0
83	MG	AS	3763	1/1	0.96	0.12	41,41,41,41	0
83	MG	AS	3433	1/1	0.96	0.09	38,38,38,38	0
83	MG	AS	3490	1/1	0.96	0.24	39,39,39,39	0
83	MG	B	1815	1/1	0.96	0.08	86,86,86,86	0
83	MG	CM	1906	1/1	0.96	0.09	64,64,64,64	0
83	MG	AS	3618	1/1	0.96	0.29	35,35,35,35	0
83	MG	1	3807	1/1	0.96	0.06	32,32,32,32	0
83	MG	AS	3689	1/1	0.96	0.12	59,59,59,59	0
83	MG	1	3711	1/1	0.96	0.18	27,27,27,27	0
83	MG	CM	1815	1/1	0.96	0.08	32,32,32,32	0
83	MG	CM	1816	1/1	0.96	0.17	25,25,25,25	0
83	MG	AS	3653	1/1	0.96	0.15	40,40,40,40	0
83	MG	BE	301	1/1	0.96	0.19	25,25,25,25	0
83	MG	1	3809	1/1	0.96	0.10	37,37,37,37	0
83	MG	1	3614	1/1	0.96	0.26	31,31,31,31	0
83	MG	AS	3524	1/1	0.96	0.12	50,50,50,50	0
83	MG	B	1872	1/1	0.96	0.12	56,56,56,56	0
86	ZN	AP	203	1/1	0.96	0.12	147,147,147,147	0
83	MG	B	1873	1/1	0.96	0.15	44,44,44,44	0
83	MG	1	3506	1/1	0.96	0.13	22,22,22,22	0
83	MG	AS	3416	1/1	0.96	0.22	25,25,25,25	0
83	MG	1	3701	1/1	0.96	0.17	51,51,51,51	0
83	MG	B	1930	1/1	0.97	0.23	48,48,48,48	0
83	MG	AS	3537	1/1	0.97	0.12	39,39,39,39	0
83	MG	1	3595	1/1	0.97	0.10	42,42,42,42	0
83	MG	1	3899	1/1	0.97	0.16	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3778	1/1	0.97	0.05	32,32,32,32	0
83	MG	1	3785	1/1	0.97	0.16	32,32,32,32	0
83	MG	1	3767	1/1	0.97	0.14	24,24,24,24	0
83	MG	1	3620	1/1	0.97	0.07	27,27,27,27	0
83	MG	B	1921	1/1	0.97	0.06	55,55,55,55	0
83	MG	AS	3429	1/1	0.97	0.24	23,23,23,23	0
83	MG	B	1882	1/1	0.97	0.16	63,63,63,63	0
83	MG	AS	3589	1/1	0.97	0.15	33,33,33,33	0
83	MG	1	3472	1/1	0.97	0.09	23,23,23,23	0
83	MG	1	3764	1/1	0.97	0.12	34,34,34,34	0
83	MG	AS	3526	1/1	0.97	0.11	30,30,30,30	0
83	MG	AS	3662	1/1	0.97	0.10	76,76,76,76	0
83	MG	AS	3527	1/1	0.97	0.11	55,55,55,55	0
83	MG	B	1824	1/1	0.97	0.19	30,30,30,30	0
83	MG	B	1813	1/1	0.97	0.14	46,46,46,46	0
83	MG	AS	3666	1/1	0.97	0.06	39,39,39,39	0
83	MG	AS	3596	1/1	0.97	0.20	29,29,29,29	0
83	MG	1	3832	1/1	0.97	0.21	34,34,34,34	0
83	MG	AS	3436	1/1	0.97	0.06	50,50,50,50	0
83	MG	AG	203	1/1	0.97	0.06	39,39,39,39	0
86	ZN	f	101	1/1	0.97	0.14	80,80,80,80	0
83	MG	1	3512	1/1	0.97	0.20	33,33,33,33	0
83	MG	CM	1837	1/1	0.97	0.07	29,29,29,29	0
86	ZN	DN	201	1/1	0.97	0.05	69,69,69,69	0
83	MG	AS	3402	1/1	0.97	0.08	42,42,42,42	0
86	ZN	DQ	102	1/1	0.97	0.17	55,55,55,55	0
83	MG	AS	3530	1/1	0.98	0.19	29,29,29,29	0
83	MG	1	3712	1/1	0.98	0.22	23,23,23,23	0
83	MG	1	3409	1/1	0.98	0.06	61,61,61,61	0
83	MG	1	3410	1/1	0.98	0.04	18,18,18,18	0
83	MG	AS	3748	1/1	0.98	0.15	33,33,33,33	0
83	MG	AS	3414	1/1	0.98	0.28	28,28,28,28	0
86	ZN	AQ	101	1/1	0.98	0.07	65,65,65,65	0
83	MG	AS	3473	1/1	0.98	0.14	25,25,25,25	0
83	MG	AS	3422	1/1	0.98	0.05	55,55,55,55	0
83	MG	Y	202	1/1	0.98	0.12	66,66,66,66	0
83	MG	1	3745	1/1	0.98	0.14	31,31,31,31	0
86	ZN	CJ	202	1/1	0.98	0.08	173,173,173,173	0
83	MG	AS	3449	1/1	0.98	0.05	12,12,12,12	0
83	MG	AS	3562	1/1	0.98	0.10	35,35,35,35	0
83	MG	6	201	1/1	0.98	0.04	37,37,37,37	0
86	ZN	DS	201	1/1	0.98	0.09	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
86	ZN	CE	101	1/1	0.99	0.05	66,66,66,66	0
86	ZN	CH	101	1/1	0.99	0.05	63,63,63,63	0
86	ZN	c	201	1/1	0.99	0.03	71,71,71,71	0
86	ZN	CK	103	1/1	0.99	0.04	87,87,87,87	0
83	MG	1	3440	1/1	0.99	0.05	32,32,32,32	0
86	ZN	AN	101	1/1	0.99	0.08	71,71,71,71	0
83	MG	AS	3410	1/1	0.99	0.07	54,54,54,54	0
83	MG	AS	3479	1/1	0.99	0.03	21,21,21,21	0
86	ZN	AK	102	1/1	1.00	0.04	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.