



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 04:14 PM EDT

PDB ID : 4W2H / pdb_00004w2h
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with pactamycin (co-crystallized), mRNA and deacylated tRNA in the P site
Authors : Polikanov, Y.S.; Osterman, I.A.; Szal, T.; Tashlitsky, V.N.; Serebryakova, M.V.; Kusochev, P.; Bulkley, D.; Malanicheva, I.A.; Efimenko, T.A.; Efremenkova, O.V.; Konevega, A.L.; Shaw, K.J.; Bogdanov, A.A.; Rodnina, M.V.; Dontsova, O.A.; Mankin, A.S.; Steitz, T.A.; Sergiev, P.V.
Deposited on : 2014-09-12
Resolution : 2.70 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	: 9.0.015 (Gargrove)
Density-Fitness	: 1.0.12
Ideal geometry (proteins)	: Engh & Huber (2001)

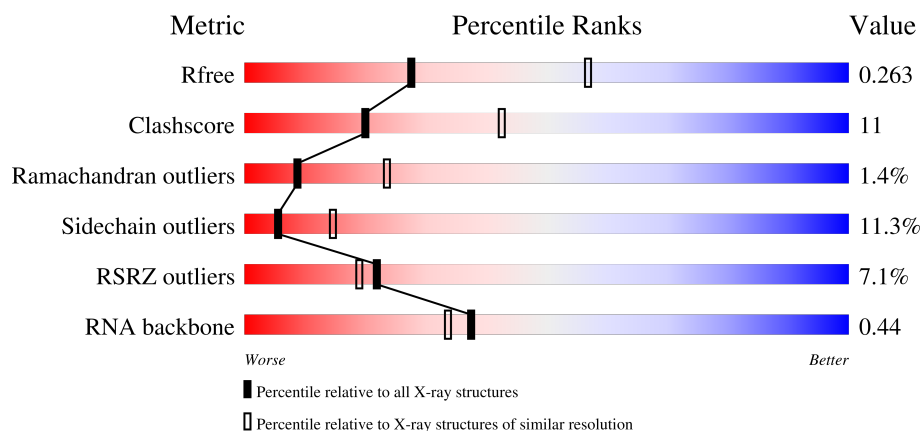
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

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	AA	1521	3% 45% 40% 13% •
1	CA	1521	7% 44% 40% 15% •

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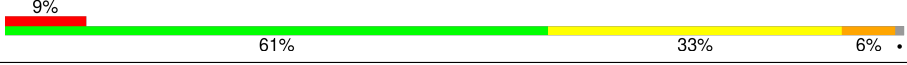
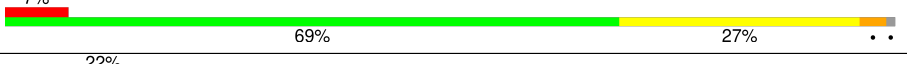
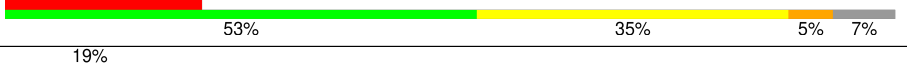
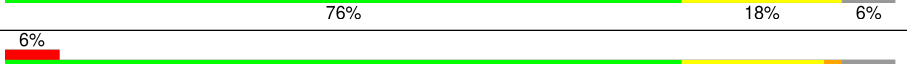
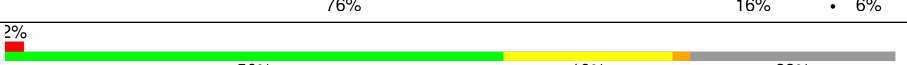
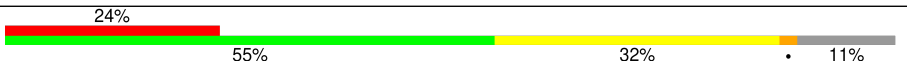
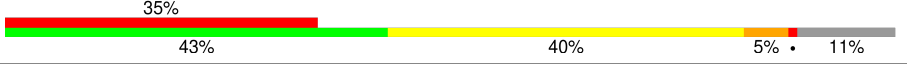
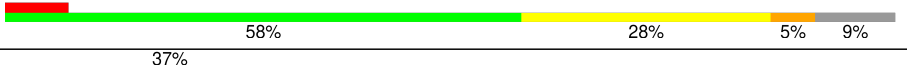
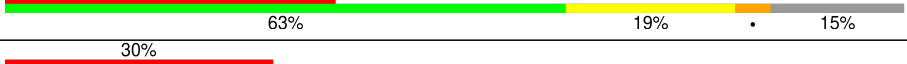
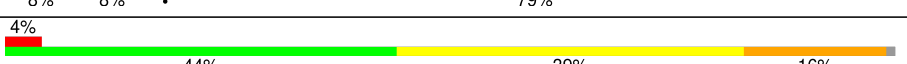
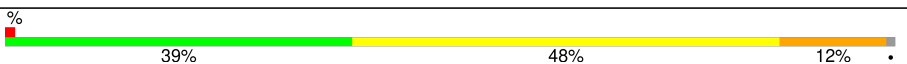
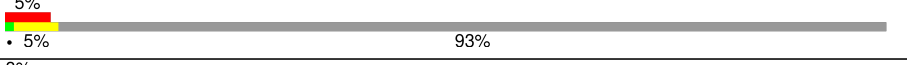
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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Mol	Chain	Length	Quality of chain
2	AB	256	
2	CB	256	
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	

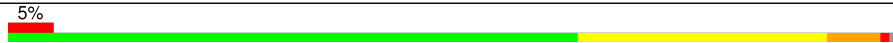
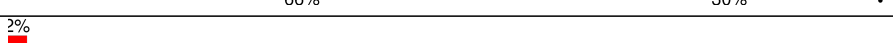
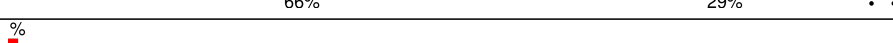
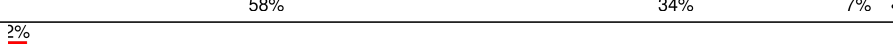
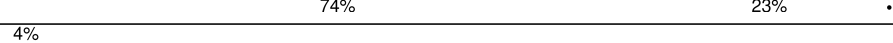
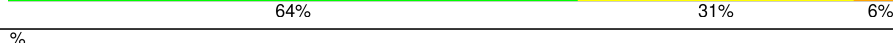
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Mol	Chain	Length	Quality of chain
14	CN	61	
15	AO	89	
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	24	
22	CV	24	
23	AX	77	
23	CX	77	
24	AY	76	
24	CY	76	
25	BA	2915	
25	DA	2915	
26	BB	121	
26	DB	121	

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Mol	Chain	Length	Quality of chain
27	BD	276	
27	DD	276	
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	
38	DS	112	
39	BT	146	

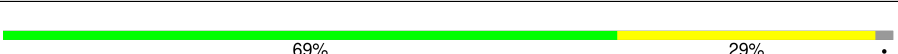
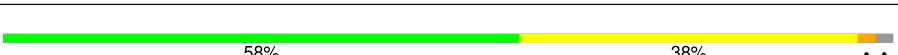
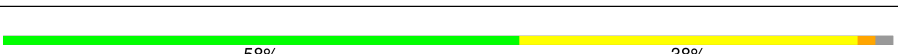
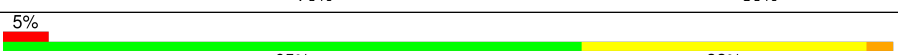
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Mol	Chain	Length	Quality of chain
39	DT	146	
40	BU	118	
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	
51	B5	60	
51	D5	60	

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Mol	Chain	Length	Quality of chain
52	B6	54	
52	D6	54	
53	B7	49	
53	D7	49	
54	B8	65	
54	D8	65	
55	B9	37	
55	D9	37	

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
56	MG	CX	3002	-	-	-	X
56	MG	DA	3655	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 290807 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 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1497	Total	C	N	O	P	0	0	0
			32183	14323	5965	10398	1497			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1552	976	302	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1659	1040	326	286	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			983	623	193	167			
9	CI	127	Total	C	N	O	0	0	0
			978	619	190	169			

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O	0	0	0
			709	440	138	131			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total	C	N	O			
			714	445	138	131	0	0	0

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	AK	114	Total	C	N	O	S		
			829	516	155	155	3	0	0
11	CK	114	Total	C	N	O	S		
			833	519	156	155	3	0	0

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0
12	CL	122	Total	C	N	O	S		
			930	585	185	159	1	0	0

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	AM	120	Total	C	N	O	S		
			937	578	194	163	2	0	0
13	CM	118	Total	C	N	O	S		
			920	566	191	161	2	0	0

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0
14	CN	60	Total	C	N	O	S		
			492	312	104	72	4	0	0

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0
15	CO	88	Total	C	N	O	S		
			728	456	144	126	2	0	0

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	8	Total	C	N	O	P	0	0	0
			169	76	29	56	8			
22	CV	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 23 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
23	CX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 24 is a RNA chain called E-site tRNA Acceptor Stem.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AY	18	Total	C	N	O	P	0	0	0
			385	171	71	125	18			
24	CY	5	Total	C	N	O	P	0	0	0
			104	47	19	33	5			

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2822	Total	C	N	O	P	0	0	0
			60792	27054	11380	19537	2821			
25	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 27 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
27	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 28 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
28	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
29	DF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BG	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
30	DG	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 31 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
31	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 32 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BI	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
32	DI	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 33 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
33	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 34 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
34	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
35	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 36 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
36	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 37 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
37	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 38 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O		0	0	0
			877	553	175	149				
38	DS	110	Total	C	N	O		0	0	0
			870	549	173	148				

- Molecule 39 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
39	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 40 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
40	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 41 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
41	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 42 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 43 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
43	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 44 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
44	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 45 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BZ	171	Total	C	N	O	S	0	0	0
			1349	862	243	242	2			
45	DZ	174	Total	C	N	O	S	0	0	0
			1360	870	243	245	2			

- Molecule 46 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
46	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 47 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
47	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 48 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
48	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 49 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 50 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 51 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
51	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 52 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
52	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 53 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
53	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 54 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B8	64	Total	C	N	O	S	0	0	0
			511	328	99	82	2			
54	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 55 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	190	Total	Mg	0	0
			190	190		
56	AD	1	Total	Mg	0	0
			1	1		
56	AE	3	Total	Mg	0	0
			3	3		
56	AF	1	Total	Mg	0	0
			1	1		
56	AM	1	Total	Mg	0	0
			1	1		
56	AN	1	Total	Mg	0	0
			1	1		
56	AQ	1	Total	Mg	0	0
			1	1		
56	AX	9	Total	Mg	0	0
			9	9		
56	BA	814	Total	Mg	0	0
			814	814		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	BB	22	Total 22	Mg 22	0	0
56	BD	9	Total 9	Mg 9	0	0
56	BE	7	Total 7	Mg 7	0	0
56	BF	9	Total 9	Mg 9	0	0
56	BG	2	Total 2	Mg 2	0	0
56	BN	7	Total 7	Mg 7	0	0
56	BO	1	Total 1	Mg 1	0	0
56	BP	4	Total 4	Mg 4	0	0
56	BQ	4	Total 4	Mg 4	0	0
56	BR	3	Total 3	Mg 3	0	0
56	BU	9	Total 9	Mg 9	0	0
56	BV	4	Total 4	Mg 4	0	0
56	BW	4	Total 4	Mg 4	0	0
56	BX	2	Total 2	Mg 2	0	0
56	BY	3	Total 3	Mg 3	0	0
56	BZ	2	Total 2	Mg 2	0	0
56	B0	5	Total 5	Mg 5	0	0
56	B2	1	Total 1	Mg 1	0	0
56	B3	1	Total 1	Mg 1	0	0
56	B4	1	Total 1	Mg 1	0	0
56	B5	4	Total 4	Mg 4	0	0

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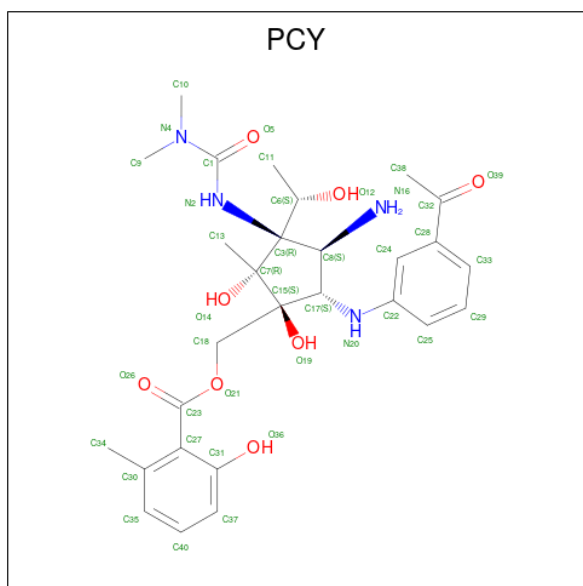
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	B6	2	Total 2	Mg 2	0	0
56	B7	5	Total 5	Mg 5	0	0
56	B8	2	Total 2	Mg 2	0	0
56	B9	1	Total 1	Mg 1	0	0
56	CA	175	Total 175	Mg 175	0	0
56	CE	2	Total 2	Mg 2	0	0
56	CF	1	Total 1	Mg 1	0	0
56	CJ	1	Total 1	Mg 1	0	0
56	CT	1	Total 1	Mg 1	0	0
56	CX	2	Total 2	Mg 2	0	0
56	DA	674	Total 674	Mg 674	0	0
56	DB	10	Total 10	Mg 10	0	0
56	DD	8	Total 8	Mg 8	0	0
56	DE	5	Total 5	Mg 5	0	0
56	DF	5	Total 5	Mg 5	0	0
56	DG	1	Total 1	Mg 1	0	0
56	DN	1	Total 1	Mg 1	0	0
56	DO	1	Total 1	Mg 1	0	0
56	DP	2	Total 2	Mg 2	0	0
56	DQ	3	Total 3	Mg 3	0	0
56	DR	1	Total 1	Mg 1	0	0

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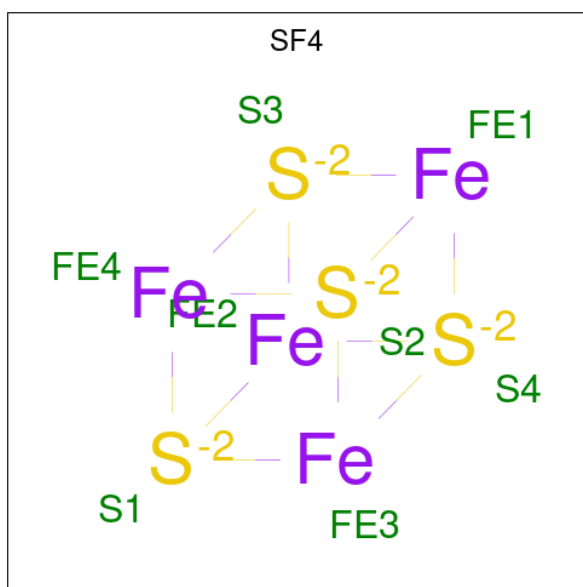
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	DU	4	Total	Mg	0	0
			4	4		
56	DV	3	Total	Mg	0	0
			3	3		
56	DW	2	Total	Mg	0	0
			2	2		
56	DY	1	Total	Mg	0	0
			1	1		
56	D0	2	Total	Mg	0	0
			2	2		
56	D1	1	Total	Mg	0	0
			1	1		
56	D3	1	Total	Mg	0	0
			1	1		
56	D8	1	Total	Mg	0	0
			1	1		

- Molecule 57 is Pactamycin (CCD ID: PCY) (formula: $C_{28}H_{38}N_4O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	AA	1	Total	C	N	O	0	0
			40	28	4	8		
57	CA	1	Total	C	N	O	0	0
			40	28	4	8		

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
58	AD	1	Total	Fe	S	0	0
			8	4	4		
58	CD	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	AN	1	Total	Zn	0	0
			1	1		
59	BY	1	Total	Zn	0	0
			1	1		
59	B4	1	Total	Zn	0	0
			1	1		
59	B5	1	Total	Zn	0	0
			1	1		
59	B6	1	Total	Zn	0	0
			1	1		
59	B9	1	Total	Zn	0	0
			1	1		
59	CN	1	Total	Zn	0	0
			1	1		
59	DY	1	Total	Zn	0	0
			1	1		
59	D4	1	Total	Zn	0	0
			1	1		
59	D5	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	D6	1	Total 1	Zn 1	0	0
59	D9	1	Total 1	Zn 1	0	0

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	AX	1	Total 1	K 1	0	0
60	CX	1	Total 1	K 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AA	175	Total 175	O 175	0	0
61	AJ	2	Total 2	O 2	0	0
61	AL	1	Total 1	O 1	0	0
61	AM	1	Total 1	O 1	0	0
61	AO	1	Total 1	O 1	0	0
61	AV	1	Total 1	O 1	0	0
61	AX	8	Total 8	O 8	0	0
61	BA	1294	Total 1294	O 1294	0	0
61	BB	34	Total 34	O 34	0	0
61	BD	16	Total 16	O 16	0	0
61	BE	12	Total 12	O 12	0	0
61	BF	7	Total 7	O 7	0	0
61	BG	3	Total 3	O 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BI	1	Total 1	O 1	0	0
61	BN	1	Total 1	O 1	0	0
61	BO	4	Total 4	O 4	0	0
61	BP	15	Total 15	O 15	0	0
61	BQ	5	Total 5	O 5	0	0
61	BR	1	Total 1	O 1	0	0
61	BU	2	Total 2	O 2	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	3	Total 3	O 3	0	0
61	BX	5	Total 5	O 5	0	0
61	B0	4	Total 4	O 4	0	0
61	B1	1	Total 1	O 1	0	0
61	B3	1	Total 1	O 1	0	0
61	B5	4	Total 4	O 4	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	1	Total 1	O 1	0	0
61	B8	10	Total 10	O 10	0	0
61	CA	137	Total 137	O 137	0	0
61	CD	1	Total 1	O 1	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CN	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CX	2	Total 2	O 2	0	0
61	DA	924	Total 924	O 924	0	0
61	DB	8	Total 8	O 8	0	0
61	DD	18	Total 18	O 18	0	0
61	DE	9	Total 9	O 9	0	0
61	DF	5	Total 5	O 5	0	0
61	DN	1	Total 1	O 1	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	14	Total 14	O 14	0	0
61	DR	1	Total 1	O 1	0	0
61	DT	1	Total 1	O 1	0	0
61	DU	3	Total 3	O 3	0	0
61	DV	1	Total 1	O 1	0	0
61	DW	1	Total 1	O 1	0	0
61	DX	1	Total 1	O 1	0	0
61	DY	1	Total 1	O 1	0	0
61	D0	7	Total 7	O 7	0	0
61	D1	1	Total 1	O 1	0	0
61	D3	1	Total 1	O 1	0	0

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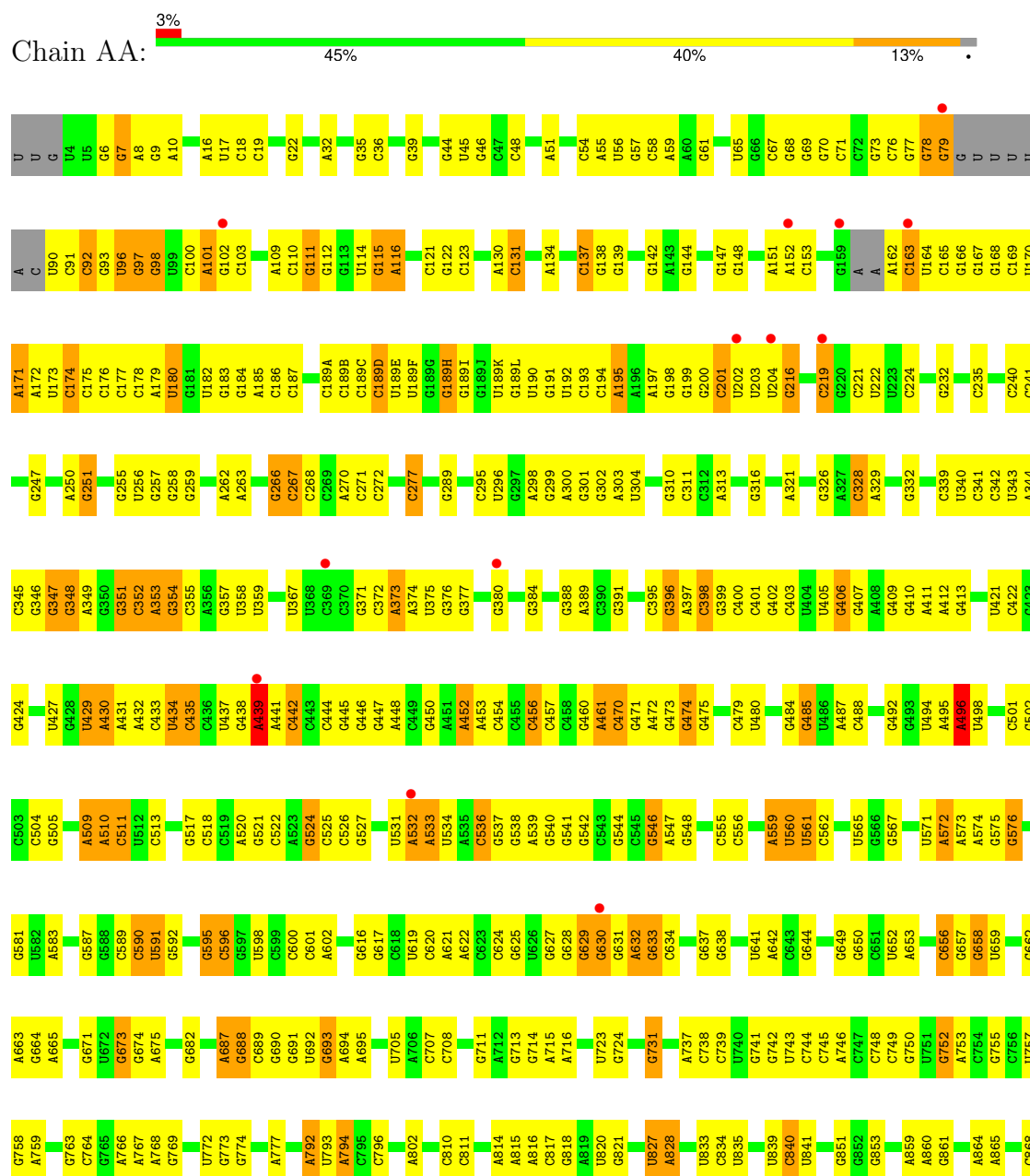
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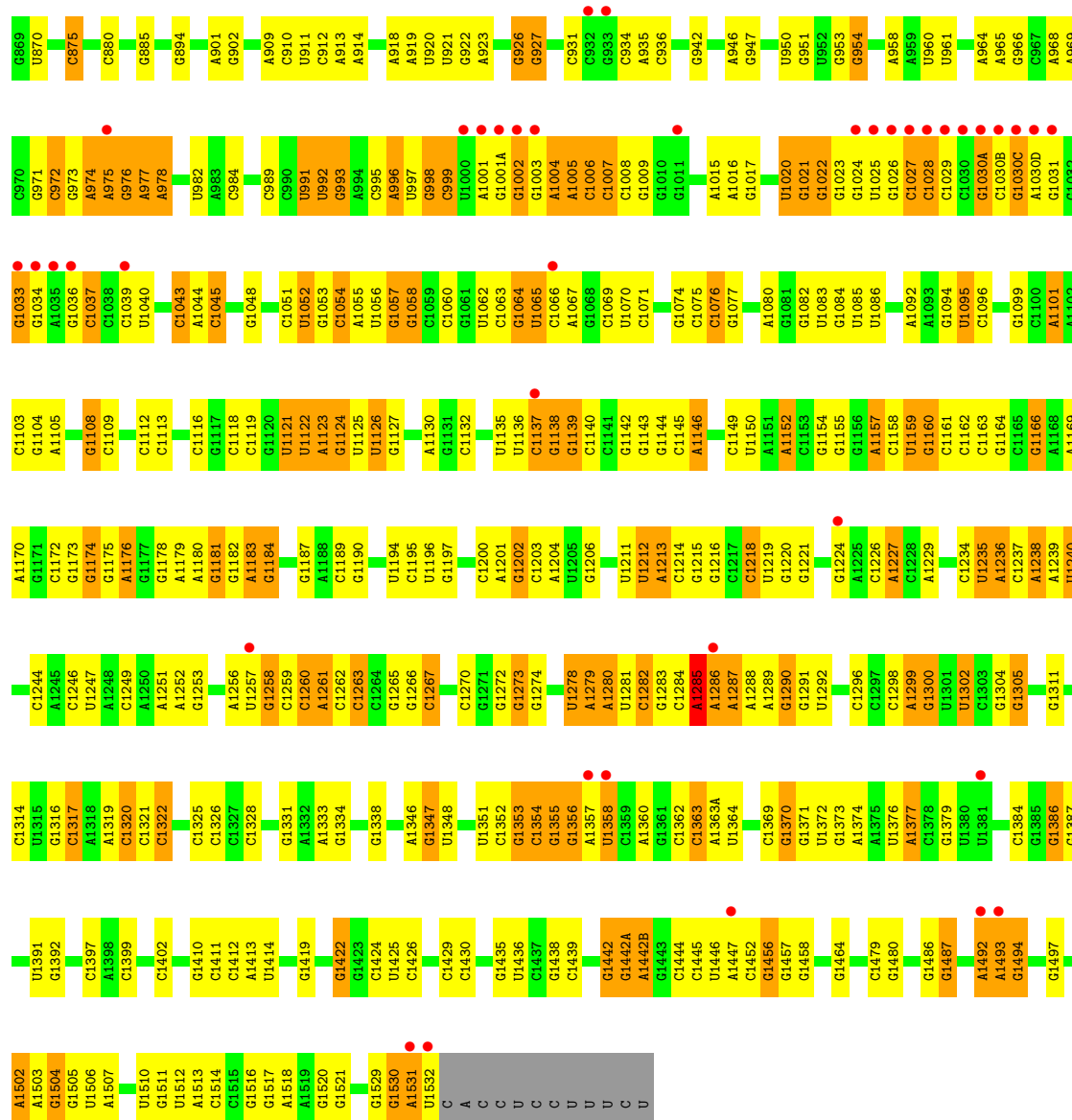
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	D8	4	Total	O	0	0
			4	4		

3 Residue-property plots

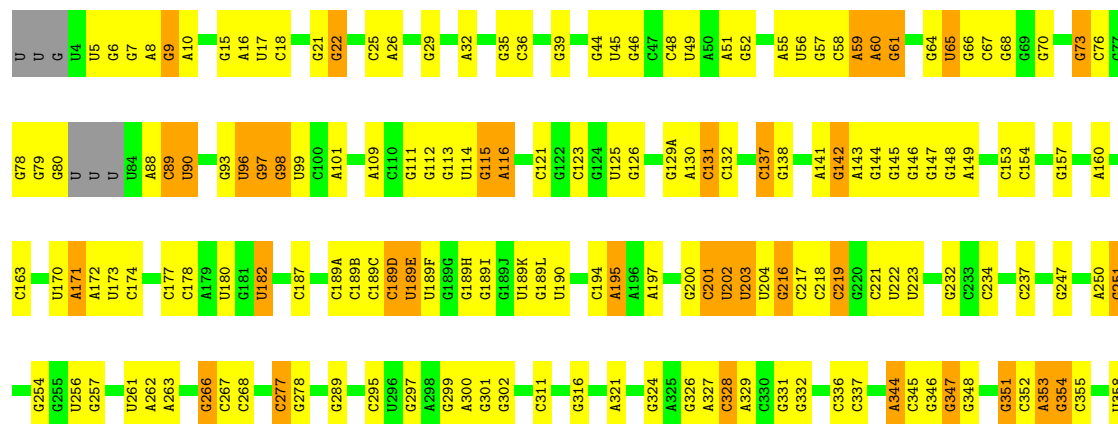
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

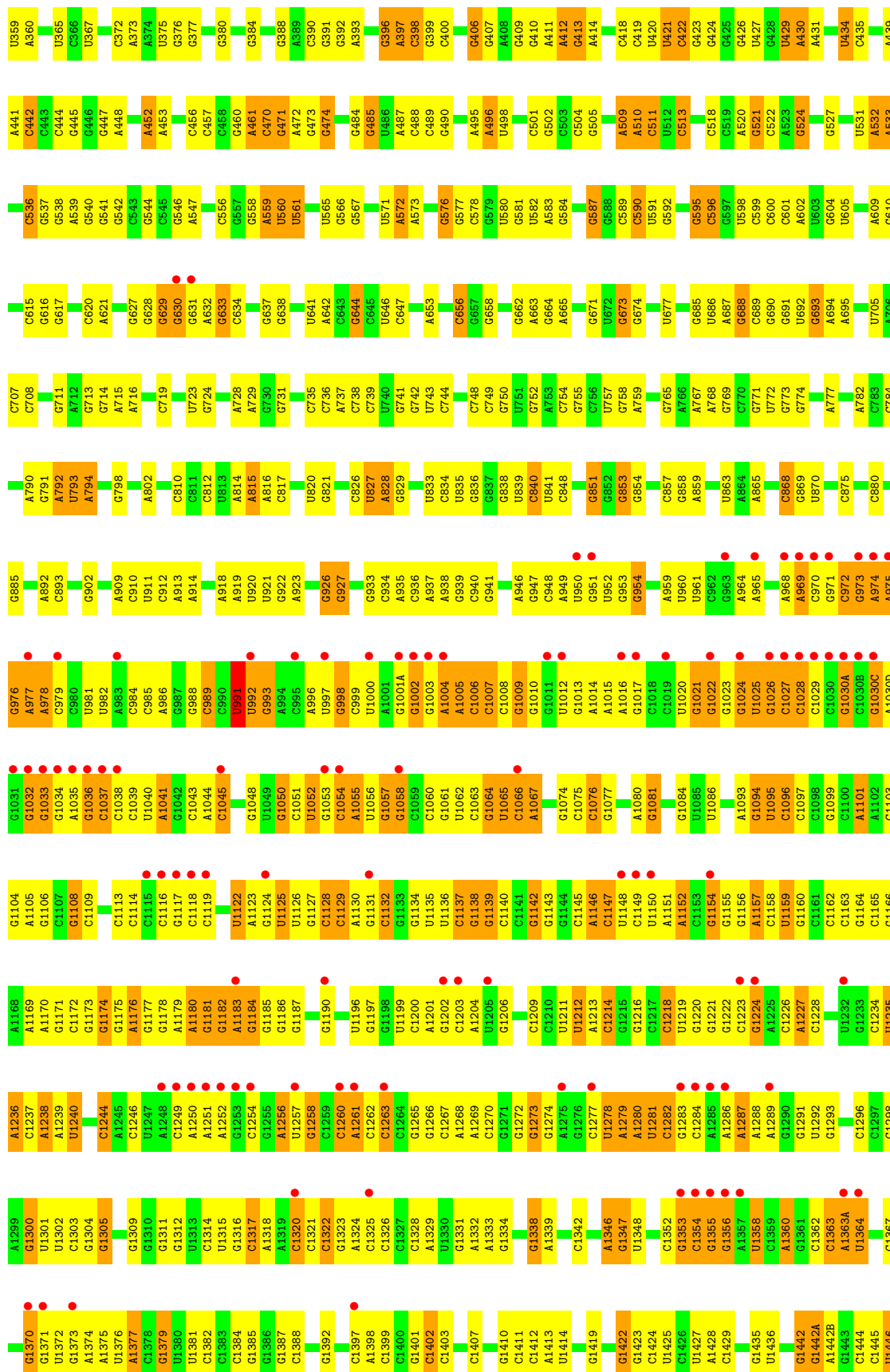
• Molecule 1: 16S Ribosomal RNA

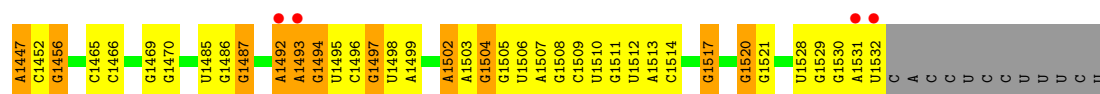




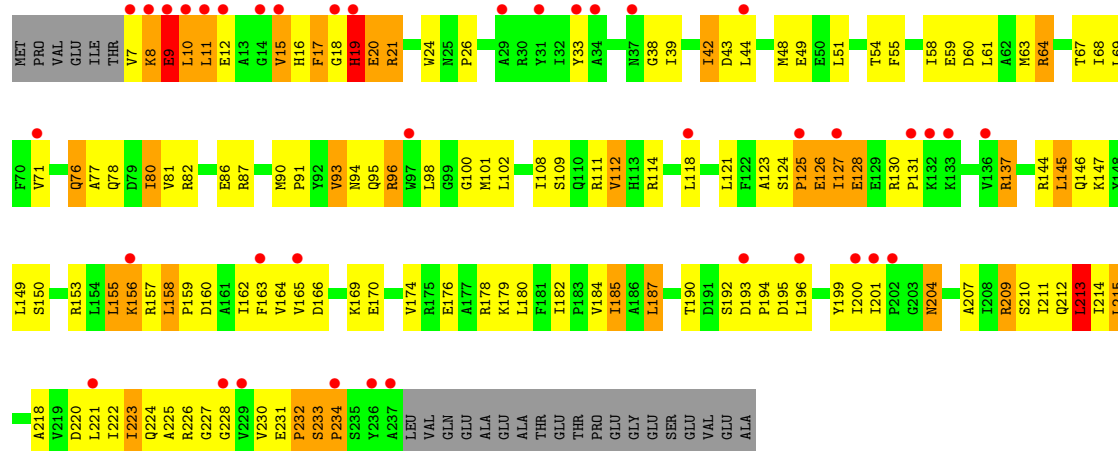
Chain CA: 7% 44% 40% 15%



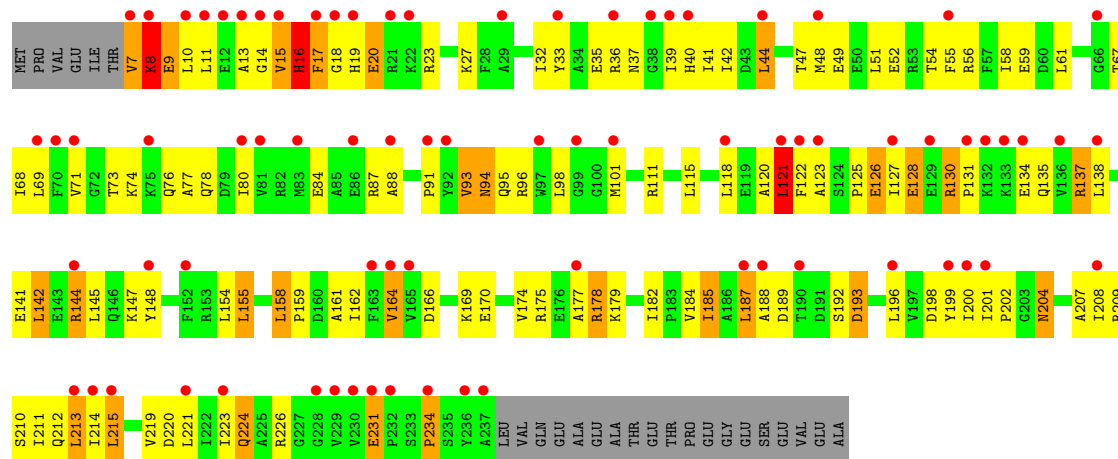




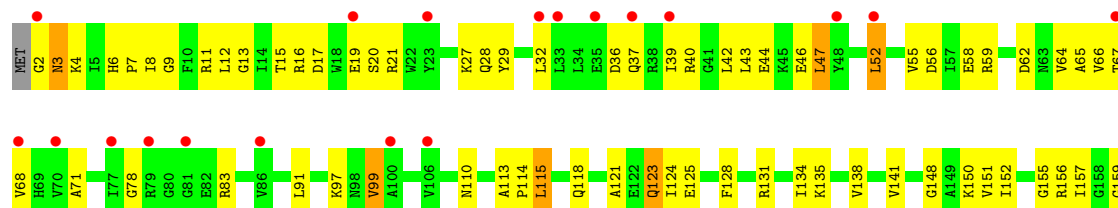
• Molecule 2: 30S Ribosomal Protein S2



• Molecule 2: 30S Ribosomal Protein S2

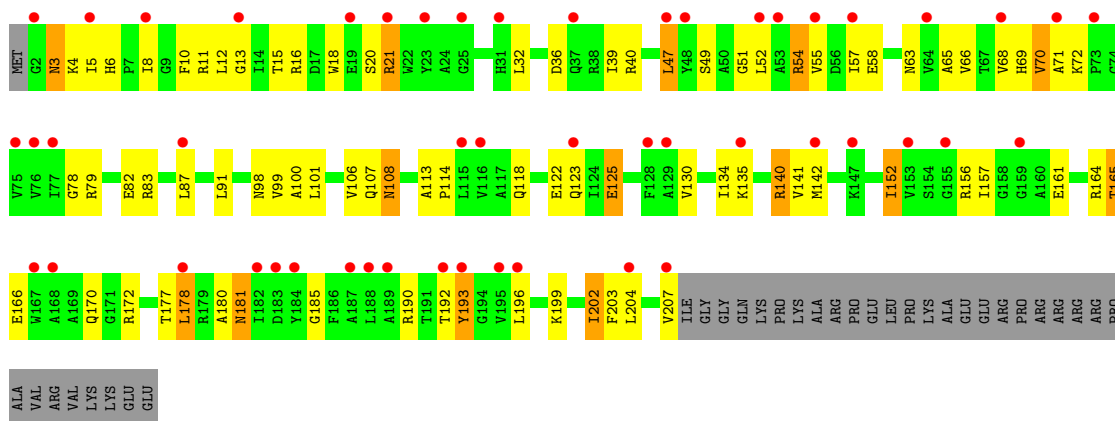


• Molecule 3: 30S Ribosomal Protein S3

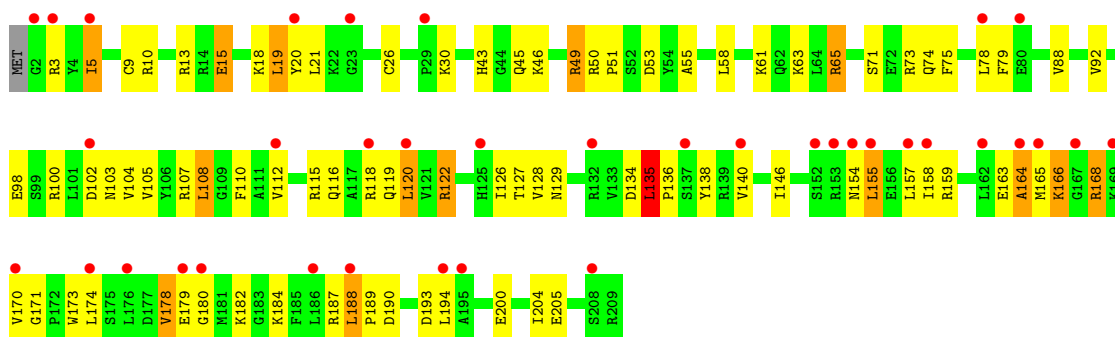




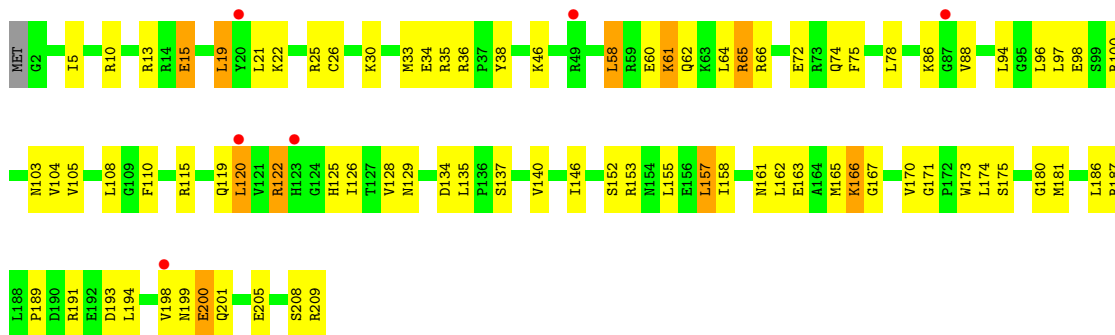
• Molecule 3: 30S Ribosomal Protein S3



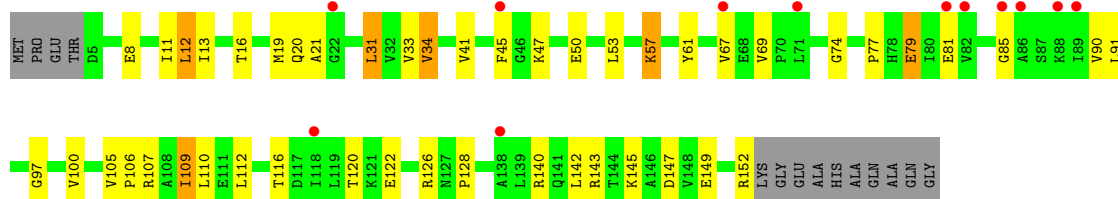
• Molecule 4: 30S Ribosomal Protein S4



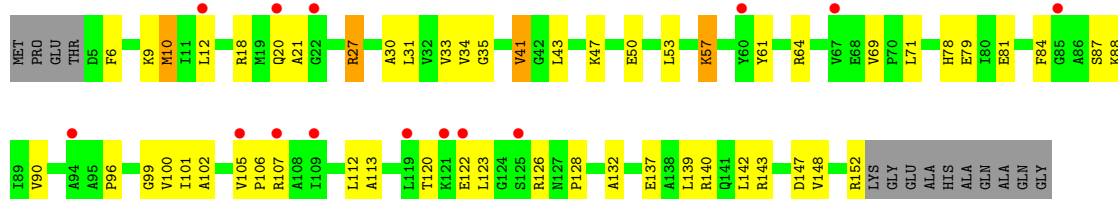
• Molecule 4: 30S Ribosomal Protein S4



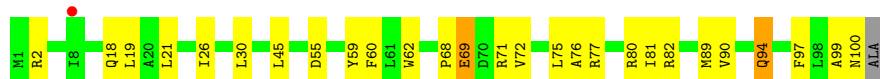
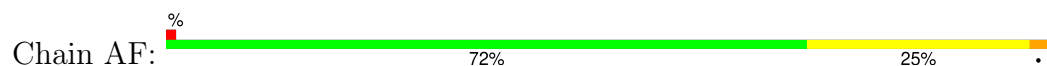
• Molecule 5: 30S Ribosomal Protein S5



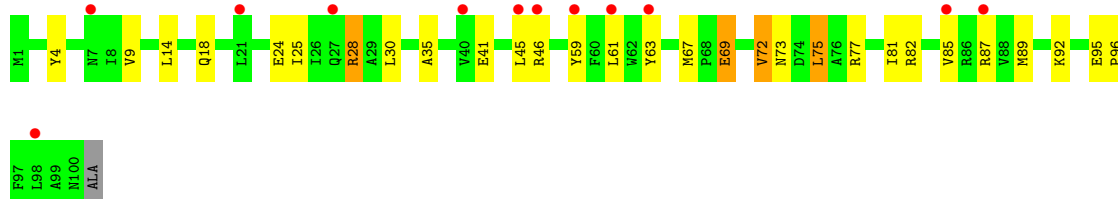
- Molecule 5: 30S Ribosomal Protein S5



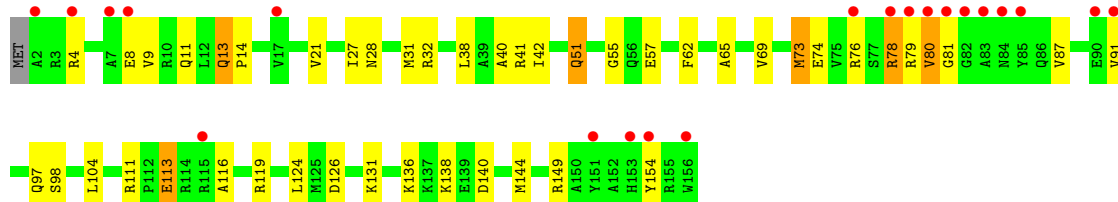
- Molecule 6: 30S Ribosomal Protein S6



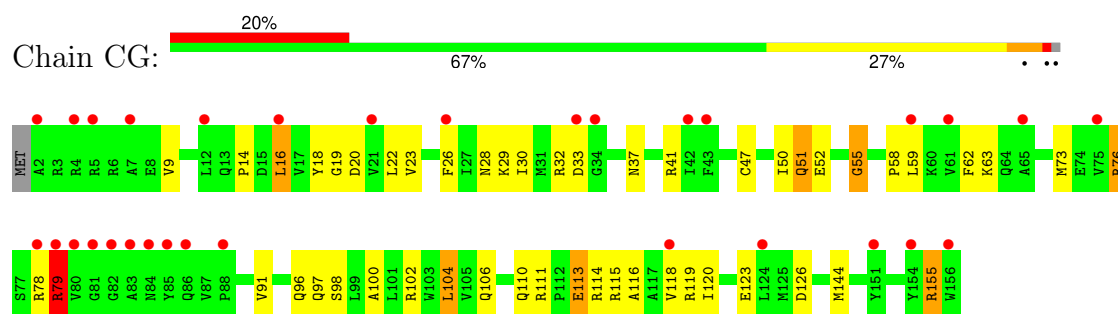
- Molecule 6: 30S Ribosomal Protein S6



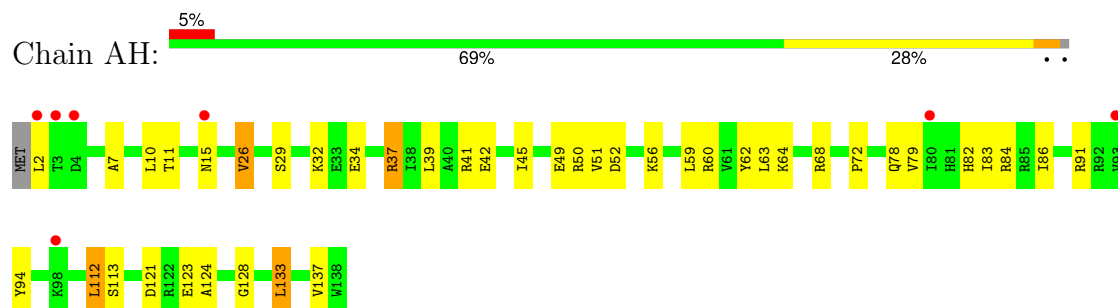
- Molecule 7: 30S Ribosomal Protein S7



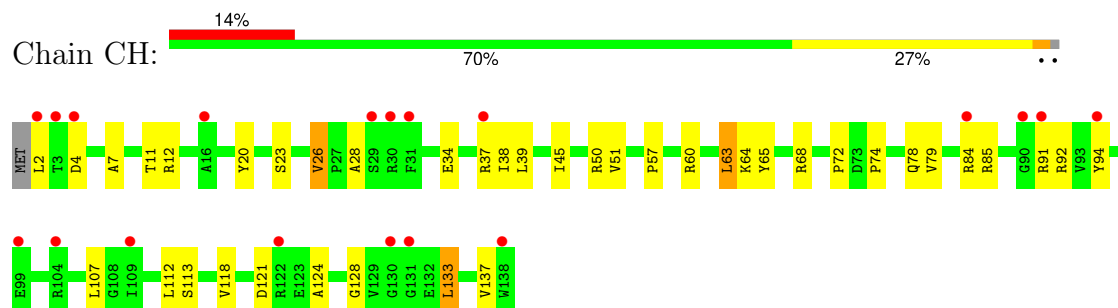
- Molecule 7: 30S Ribosomal Protein S7



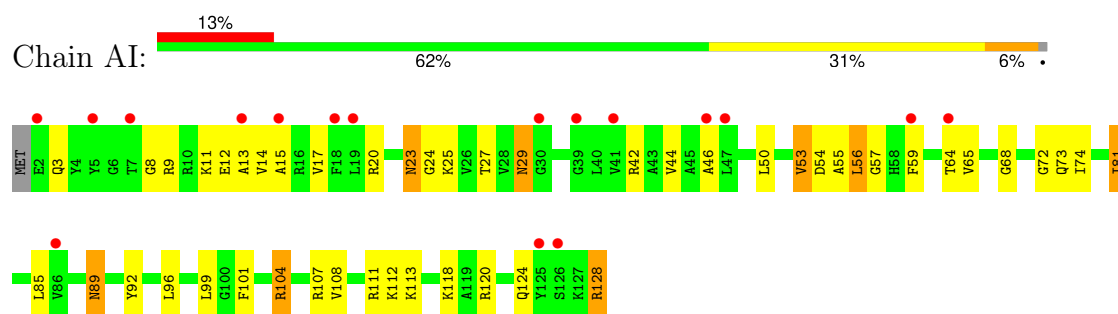
- Molecule 8: 30S Ribosomal Protein S8



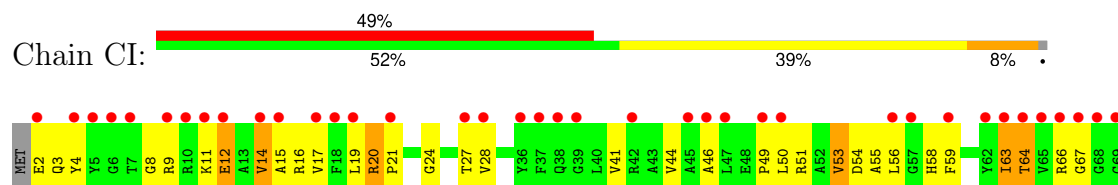
- Molecule 8: 30S Ribosomal Protein S8

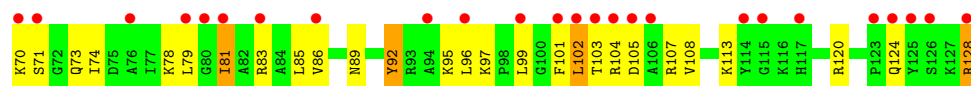


- Molecule 9: 30S Ribosomal Protein S9

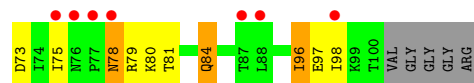
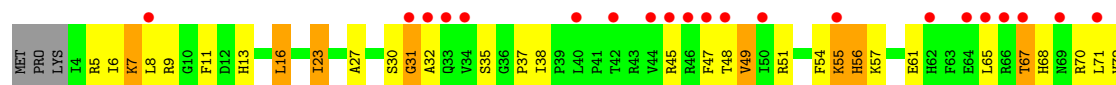


- Molecule 9: 30S Ribosomal Protein S9

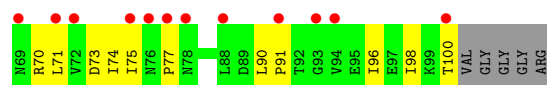
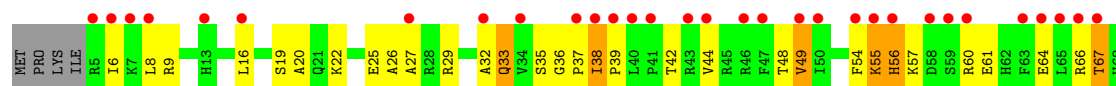
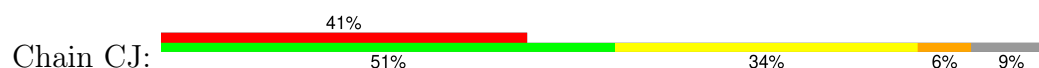




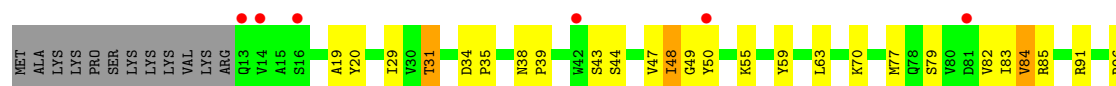
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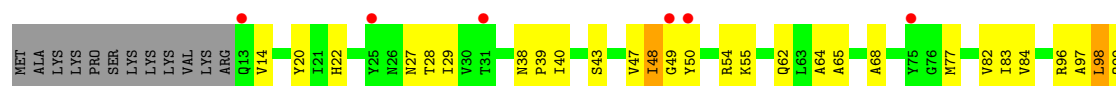
• Molecule 10: 30S Ribosomal Protein S10



• Molecule 11: 30S Ribosomal Protein S11

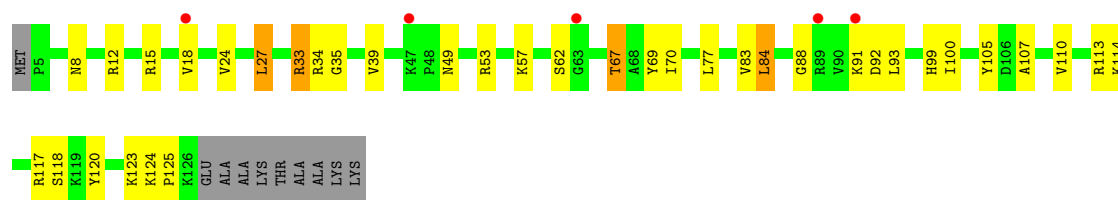


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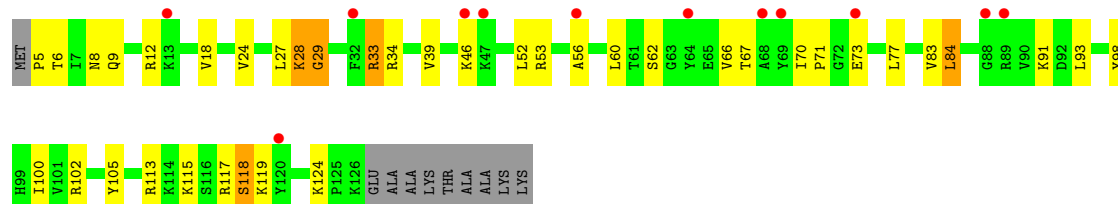


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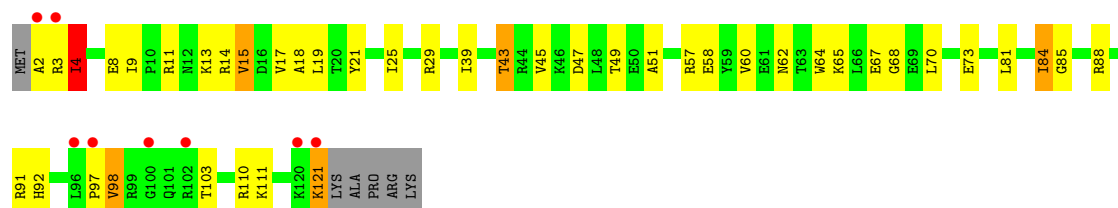




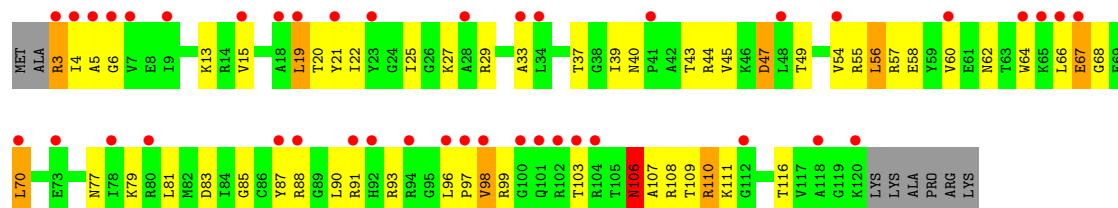
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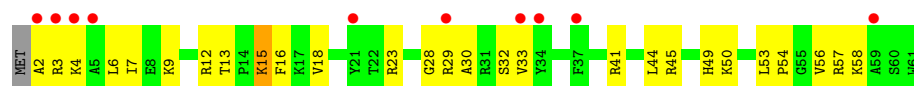
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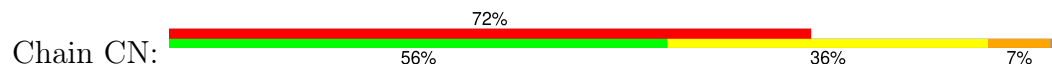
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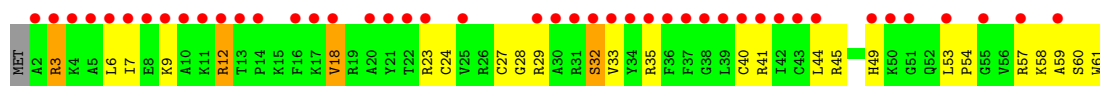


• Molecule 14: 30S Ribosomal Protein S14

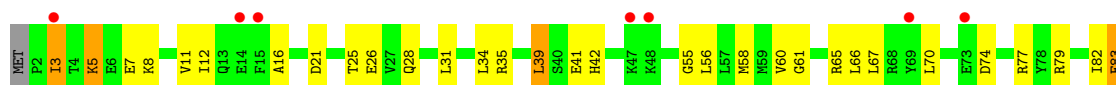


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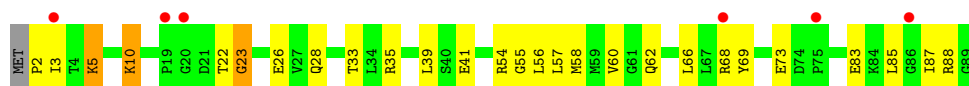




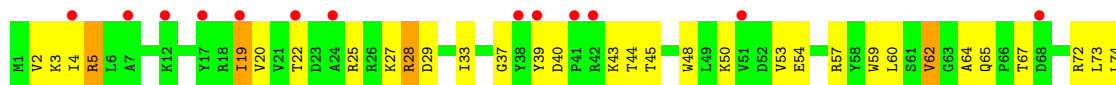
• Molecule 15: 30S Ribosomal Protein S15



• Molecule 15: 30S Ribosomal Protein S15



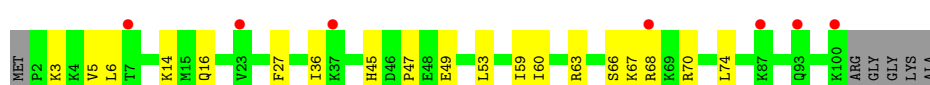
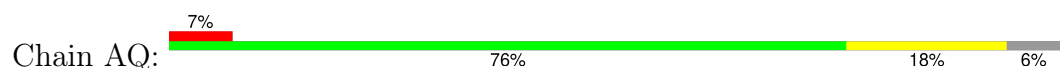
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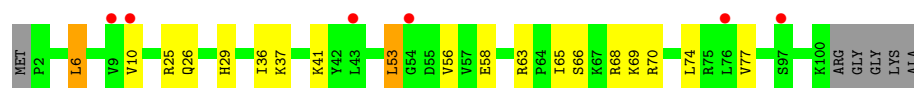
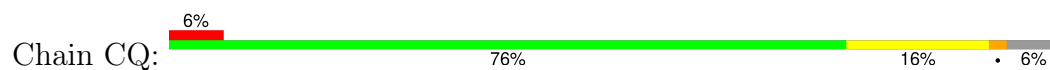
• Molecule 16: 30S Ribosomal Protein S16



• Molecule 17: 30S Ribosomal Protein S17



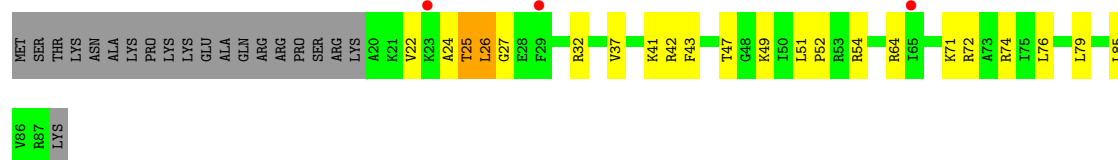
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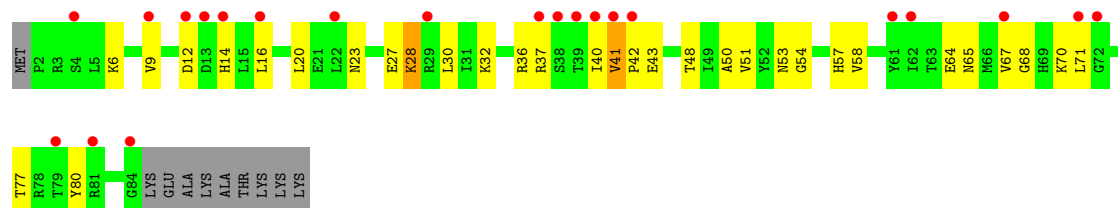
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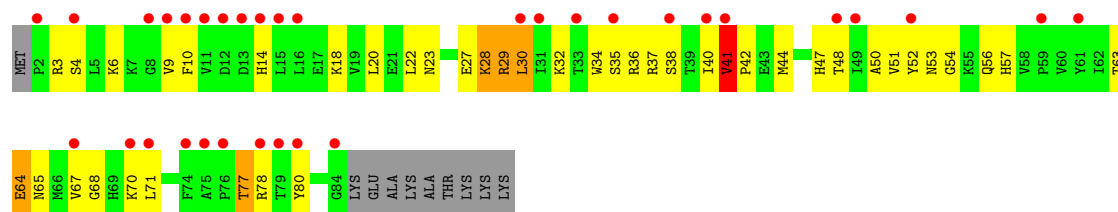
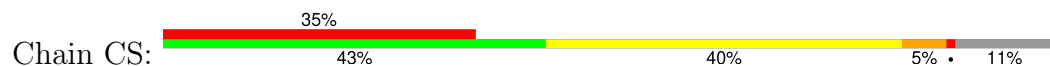
• Molecule 18: 30S Ribosomal Protein S18



• Molecule 19: 30S Ribosomal Protein S19

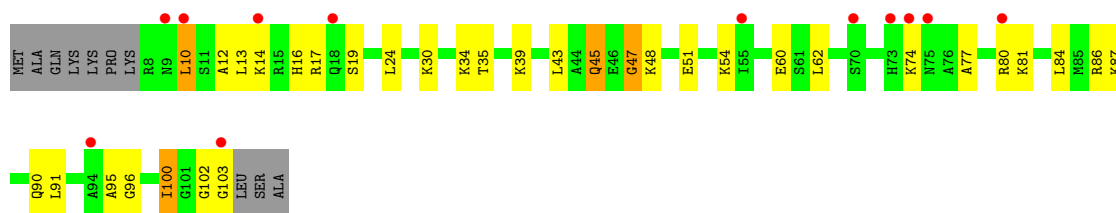


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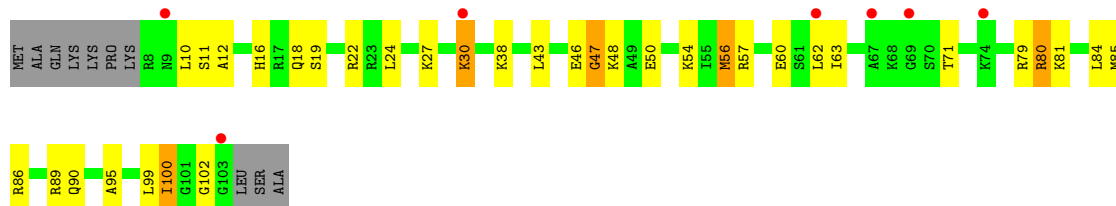


• Molecule 20: 30S Ribosomal Protein S20

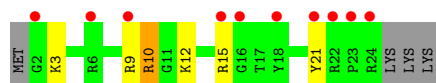
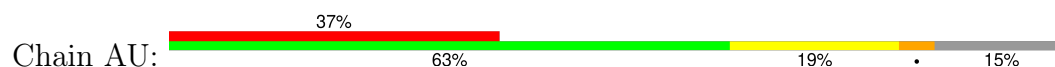




● Molecule 20: 30S Ribosomal Protein S20



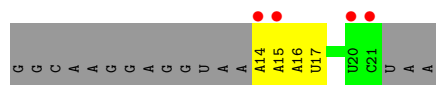
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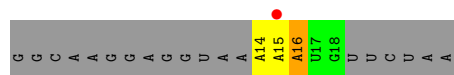
● Molecule 21: 30S Ribosomal Protein THX



● Molecule 22: mRNA

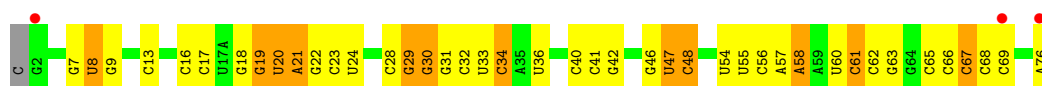


● Molecule 22: mRNA

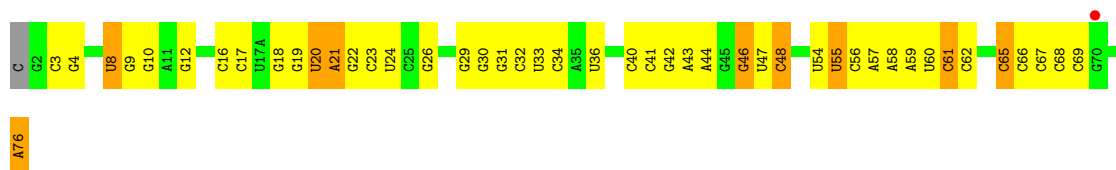


● Molecule 23: P-site tRNA

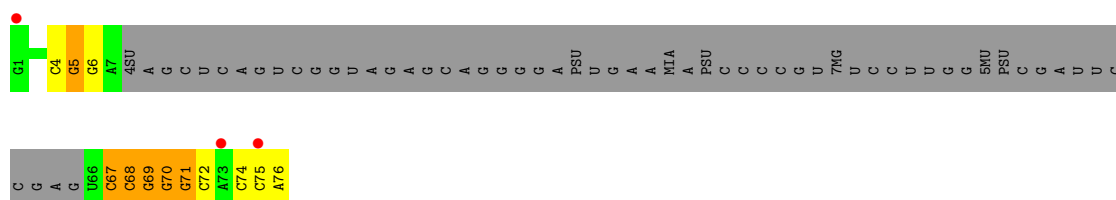




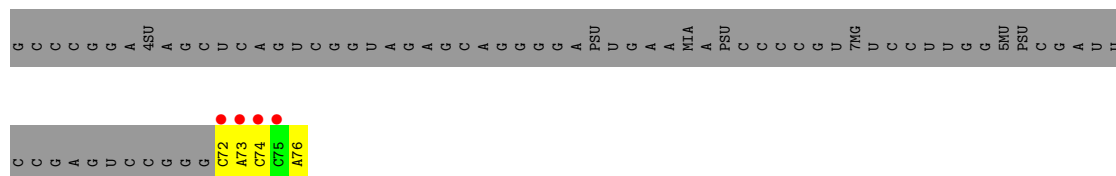
• Molecule 23: P-site tRNA



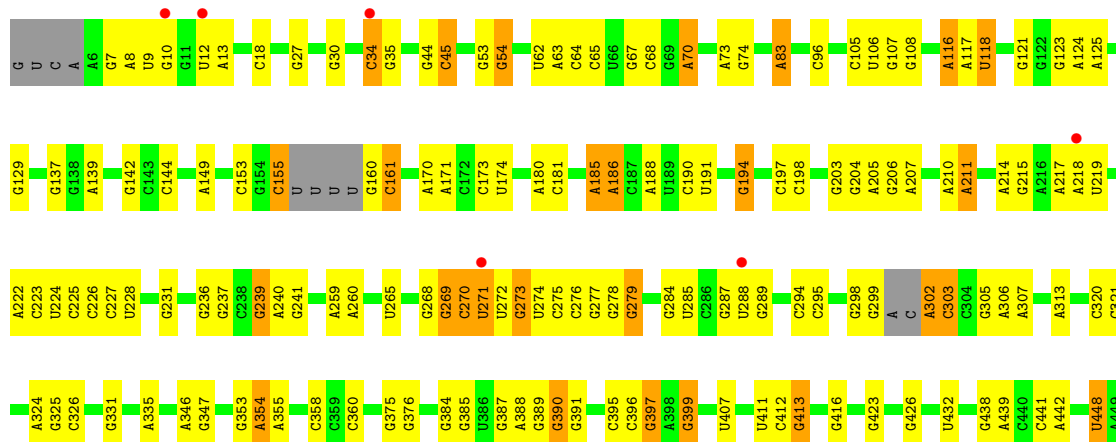
• Molecule 24: E-site tRNA Acceptor Stem



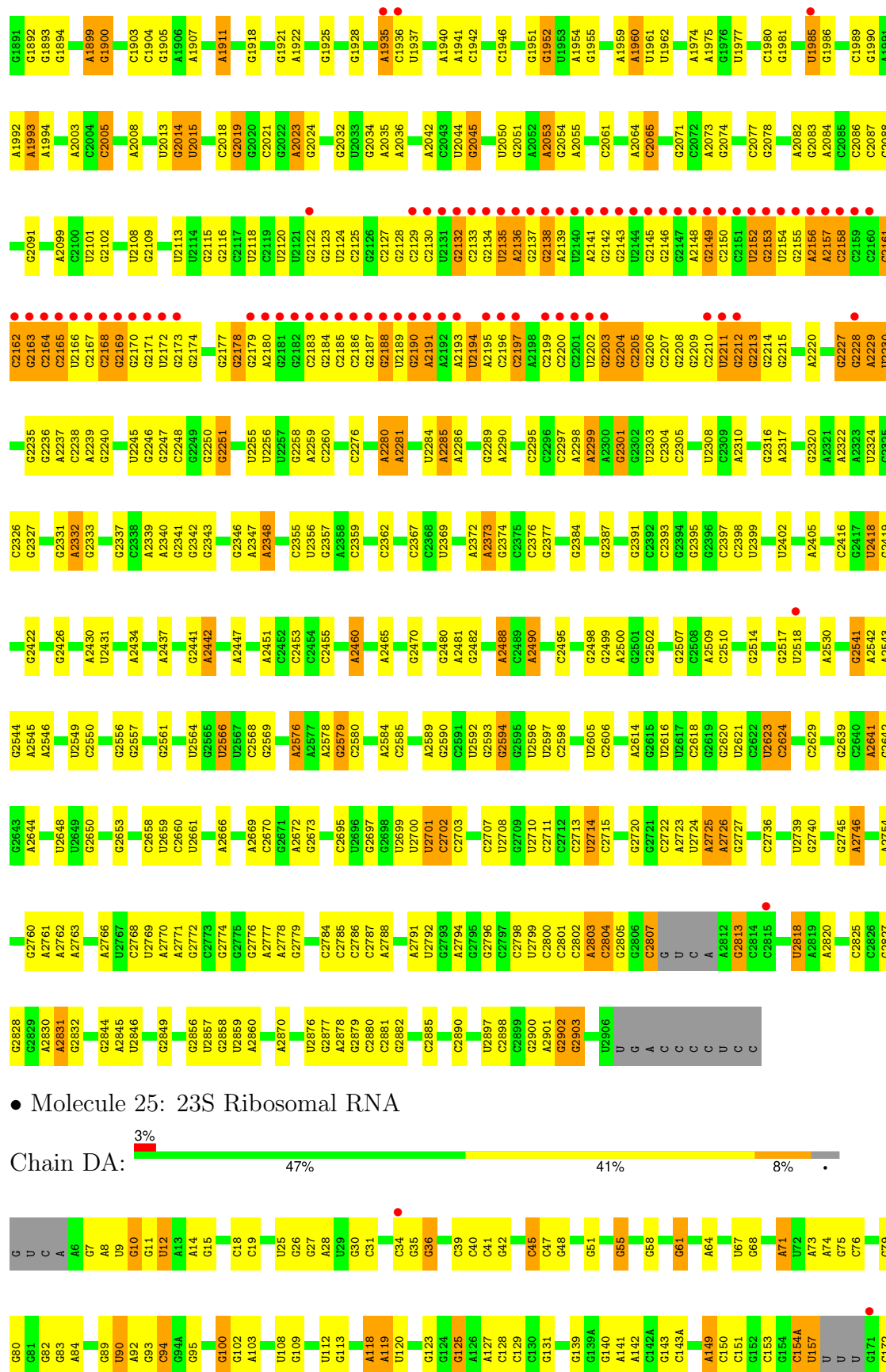
• Molecule 24: E-site tRNA Acceptor Stem

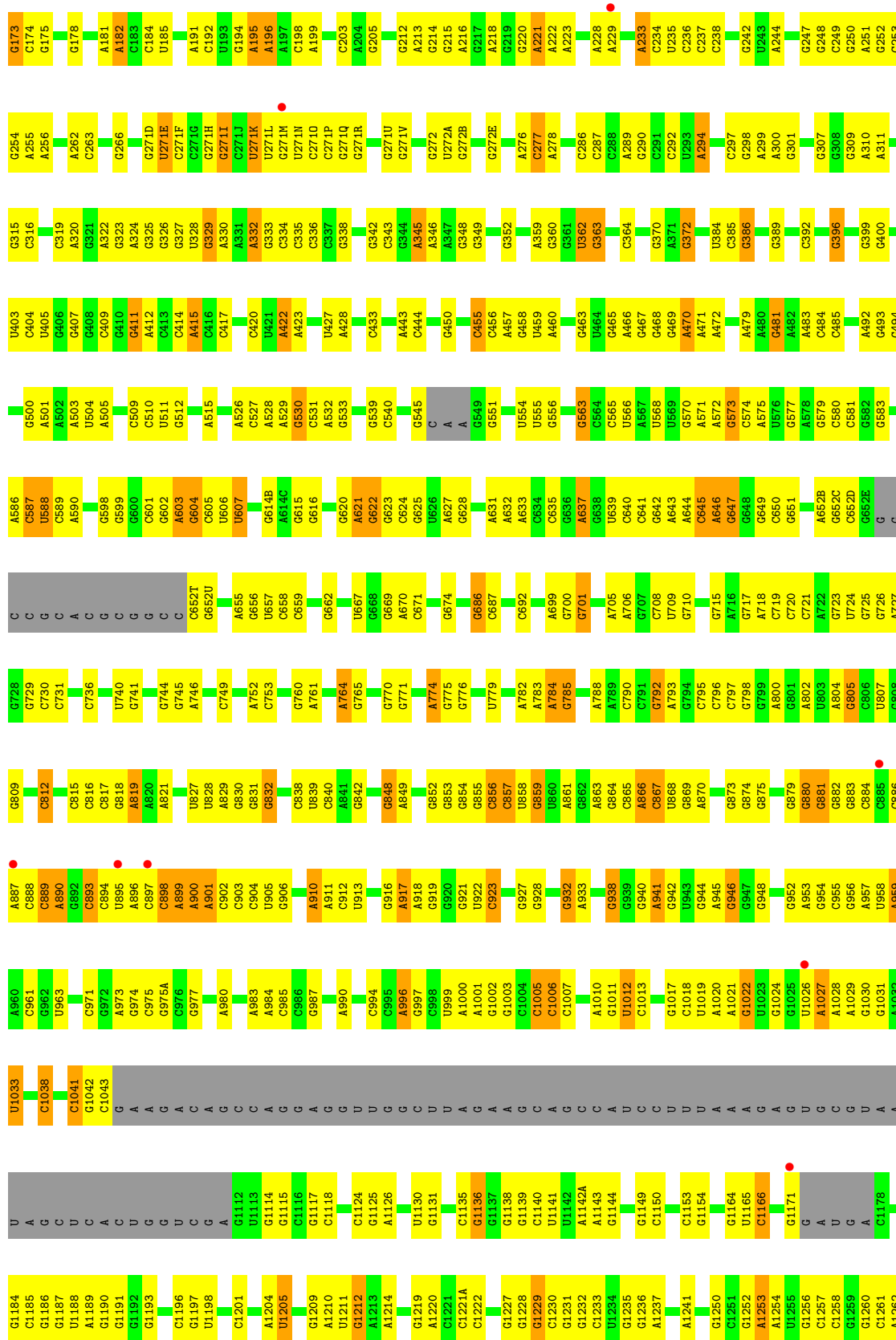


• Molecule 25: 23S Ribosomal RNA

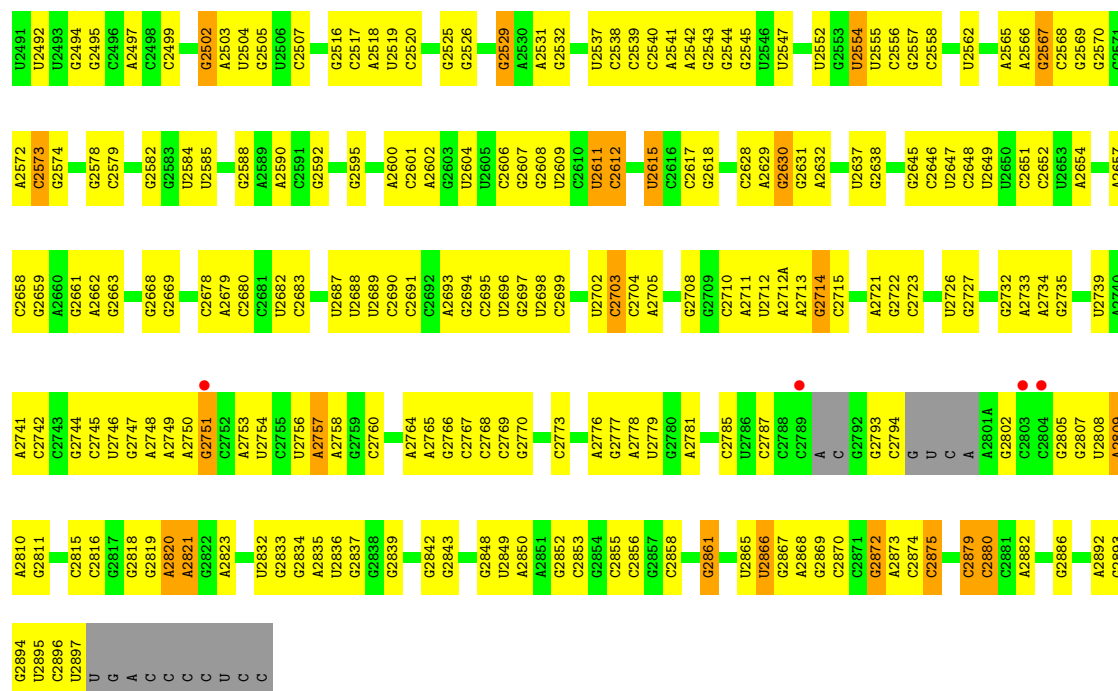


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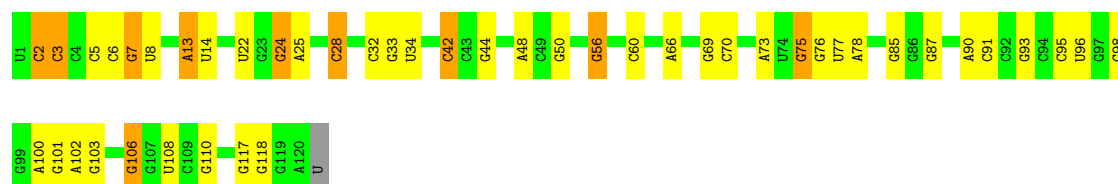


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U2459	G2377	A2298	G2136	A2059	C1982	A1889	A1789	C1670	A1508	G1422	U1341
G2460	A2378	G2302	C2137	A2060	C1983	A1890	C1790	C1671	C1509	G1423	A1342
A2461	G2383	G2303	G2138	G2061	G1984	A1891	A1791	C1672	A1509	G1424	G1343
U2462	C2384	C2304	C2139	C2062	U1992	A1892	A1792	G1674	A1509B	A1427	G1344
G2463	C2385	A2305	G2140	C2063	G1993	A1893	G1792	G1675	G1510	G1428	U1352
G2464	C2386	G2306	G2141	C2064	U1994	A1894	U1796	C1686	U1514	G1429	A1353
U2465	U2387	A2307	G2142	C2065	C1995	A1895	C1797	C1687	G1515	A1354	G1355
A2466	A2388	A2310	U2143	G2066	U1996	A1896	U1798	U1688	U1516	U1431	
U2467	A2389	G2311	G2144	G2067	G1997	A1897	U1799	U1689	U1517		
G2468	A2390	A2312	C2145	U2074	G1998	A1898	G1801	A1689	U1518		
A2469	C2391	U2313	G2146	U2075	G1999	A1899	A1802	U1692	U1519		
U2470	G2392	G2314	G2147	G2076	G2000	A1900	A1803	U1693	U1520		
U2471	C2393	G2315	G2148	C2077	A2001	A1901	A1912	C1696	C1598		
G2472	G2394	G2316	G2149	G2078	G2002	A1913	A1913				
A2473	C2395	G2317	G2150	U2079	C2003	A1914	C1914				
U2474	G2396	G2318	G2151	G2080	C2006						



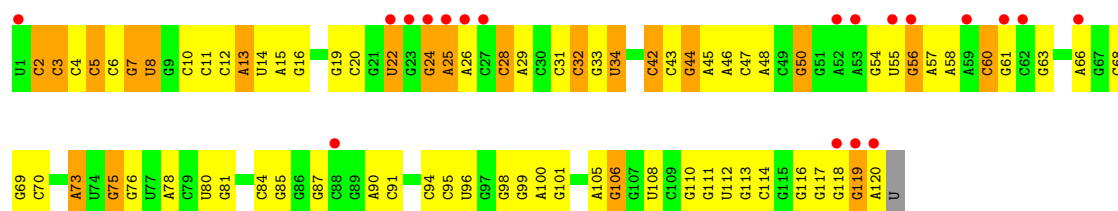
• Molecule 26: 5S Ribosomal RNA

Chain BB: 61% 30% 8% .



• Molecule 26: 5S Ribosomal RNA

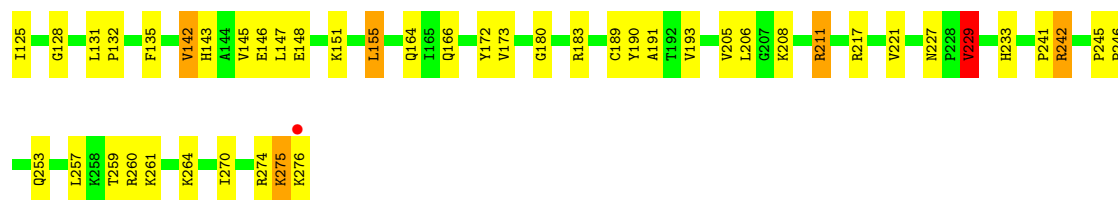
Chain DB: 16% 36% 46% 17% .



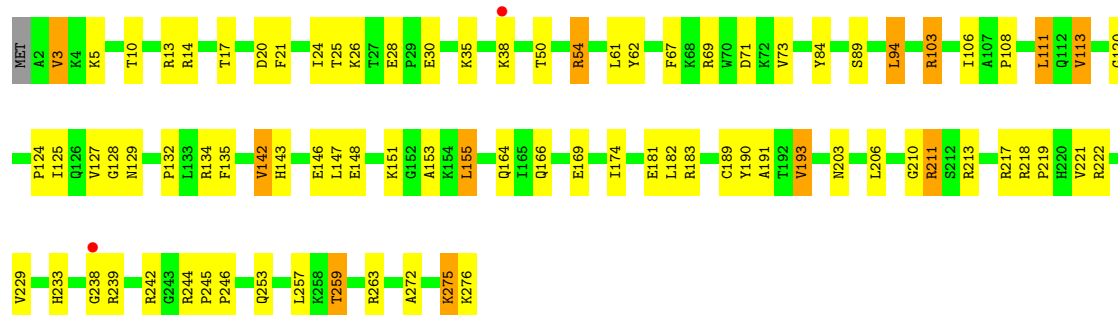
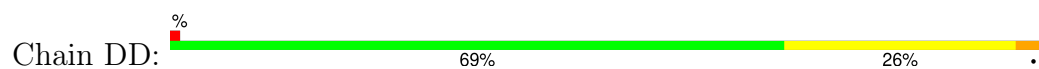
• Molecule 27: 50S Ribosomal Protein L2

Chain BD: 70% 25% .

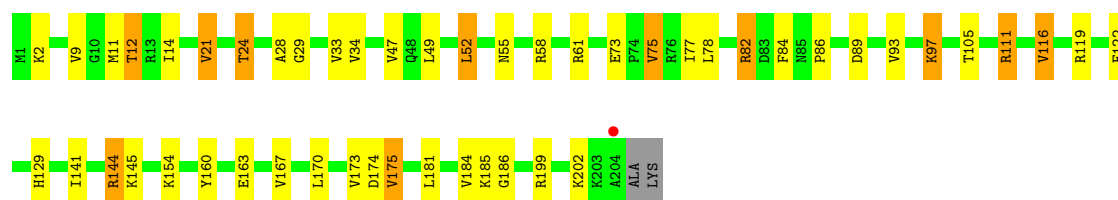
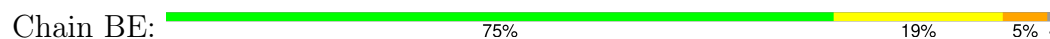




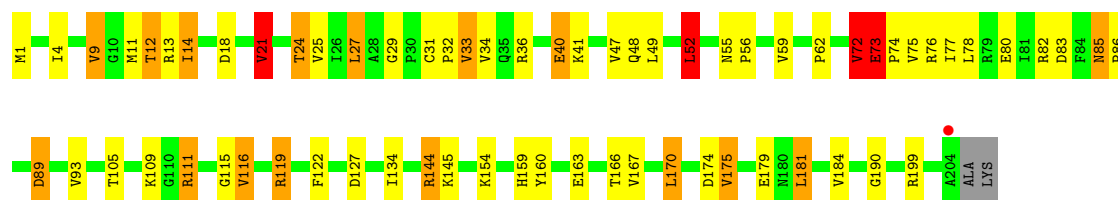
• Molecule 27: 50S Ribosomal Protein L2



• Molecule 28: 50S Ribosomal Protein L3

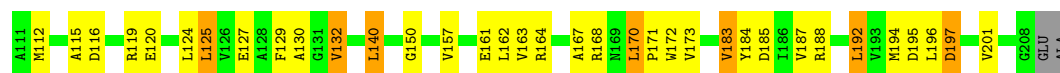


• Molecule 28: 50S Ribosomal Protein L3

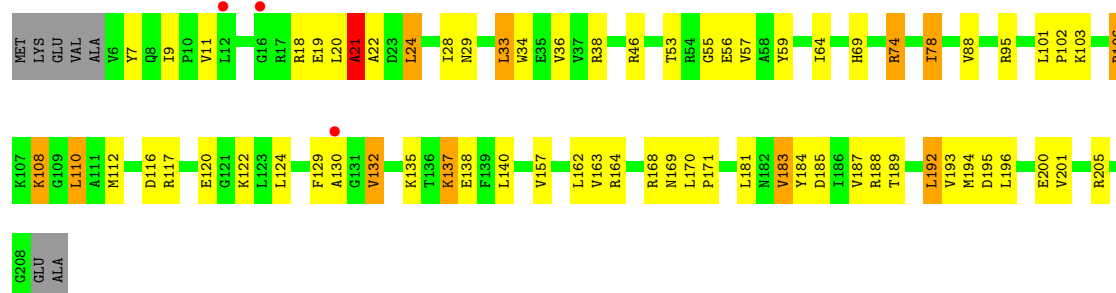


• Molecule 29: 50S Ribosomal Protein L4

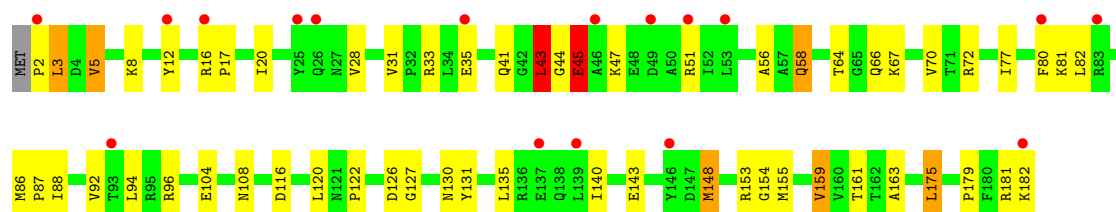




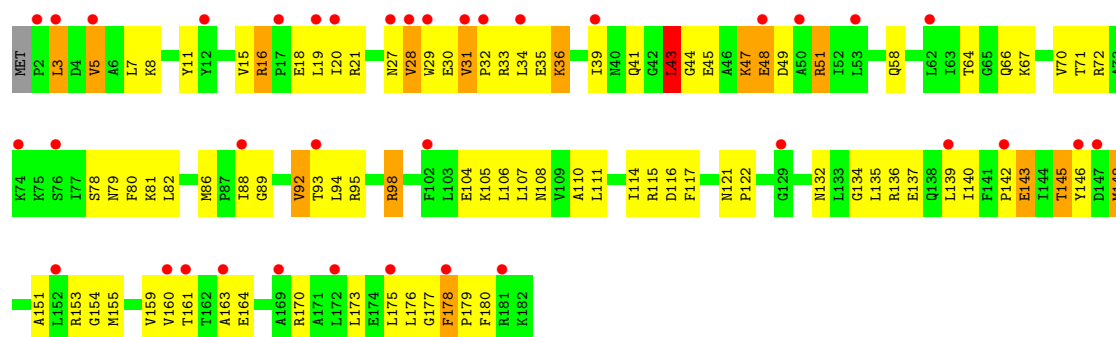
• Molecule 29: 50S Ribosomal Protein L4



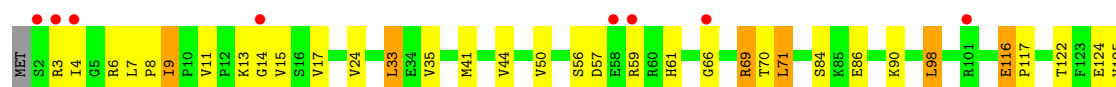
• Molecule 30: 50S Ribosomal Protein L5



• Molecule 30: 50S Ribosomal Protein L5

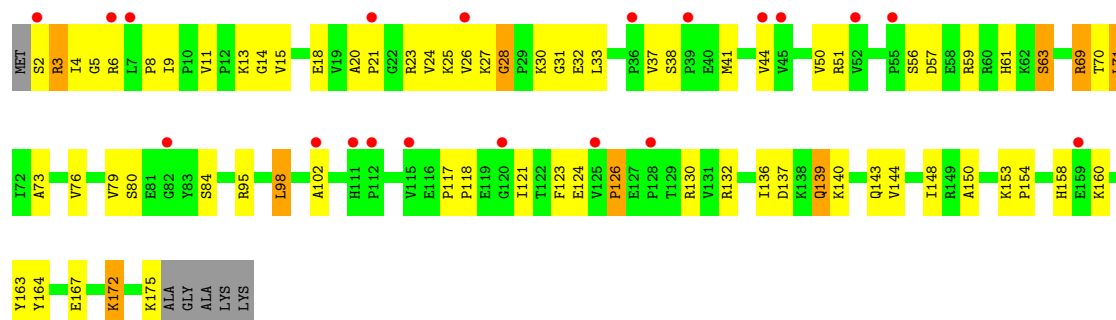


• Molecule 31: 50S Ribosomal Protein L6

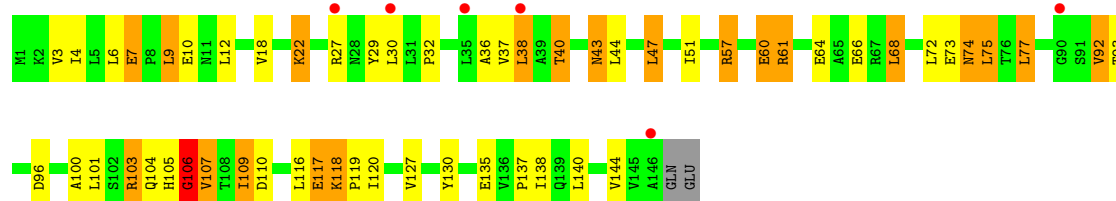




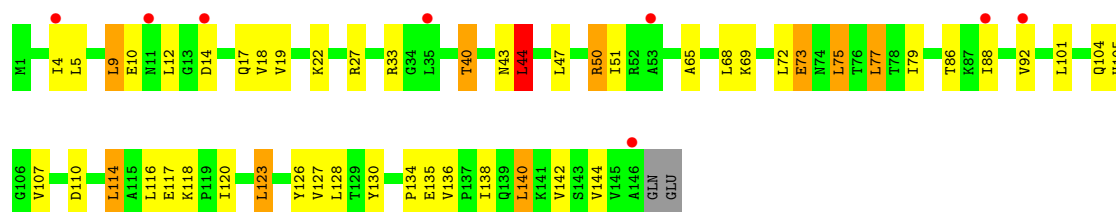
• Molecule 31: 50S Ribosomal Protein L6



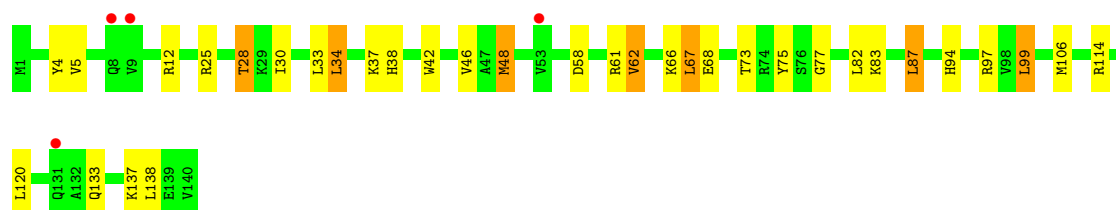
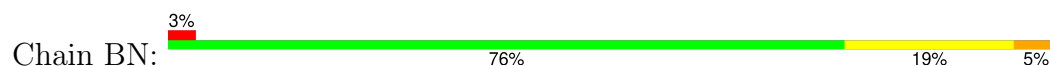
• Molecule 32: 50S Ribosomal Protein L9



• Molecule 32: 50S Ribosomal Protein L9



• Molecule 33: 50S Ribosomal Protein L13



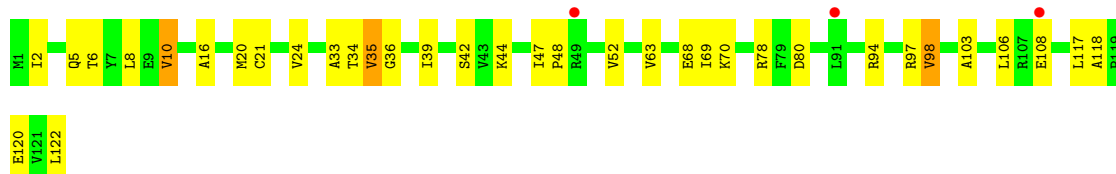
- Molecule 33: 50S Ribosomal Protein L13

Chain DN:  76% 21%



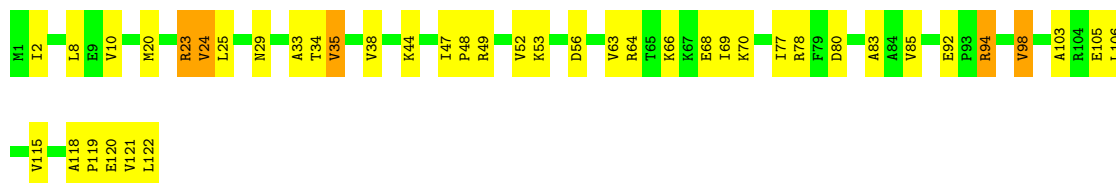
- Molecule 34: 50S Ribosomal Protein L14

Chain BO:  2% 71% 26%



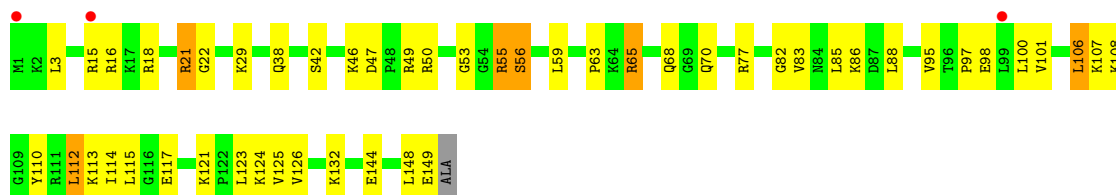
- Molecule 34: 50S Ribosomal Protein L14

Chain DO:  66% 30%



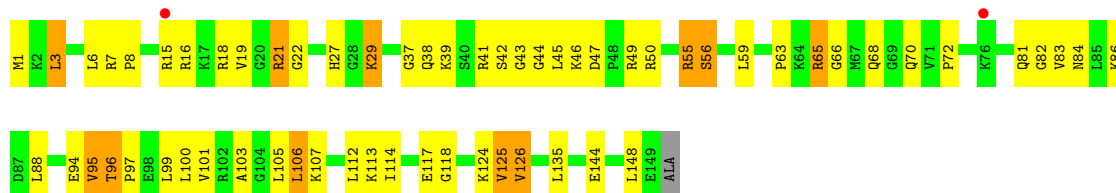
- Molecule 35: 50S Ribosomal Protein L15

Chain BP:  2% 66% 29%



- Molecule 35: 50S Ribosomal Protein L15

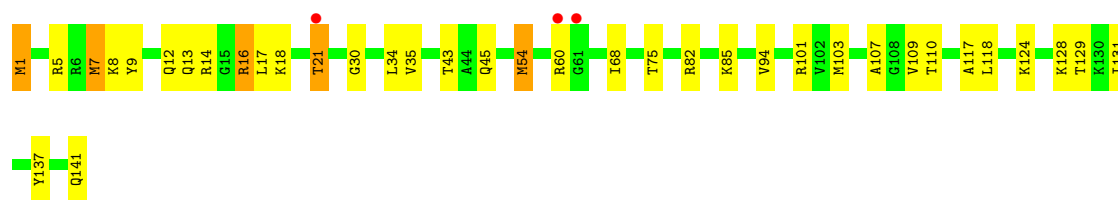
Chain DP:  58% 34% 7%



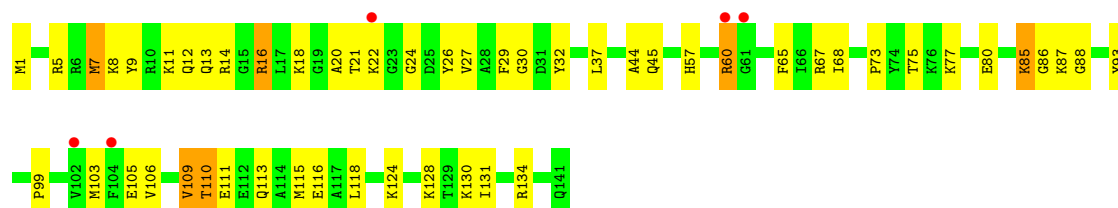
- Molecule 36: 50S Ribosomal Protein L16

Chain BQ:  2% 74% 23%

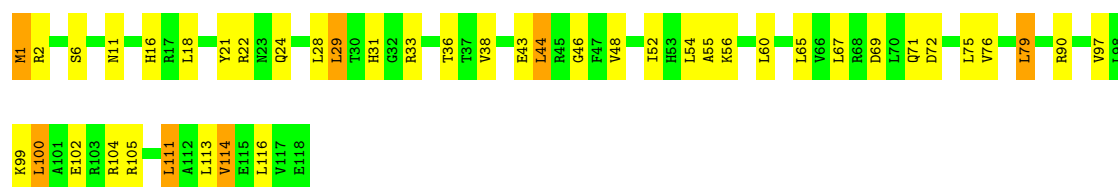




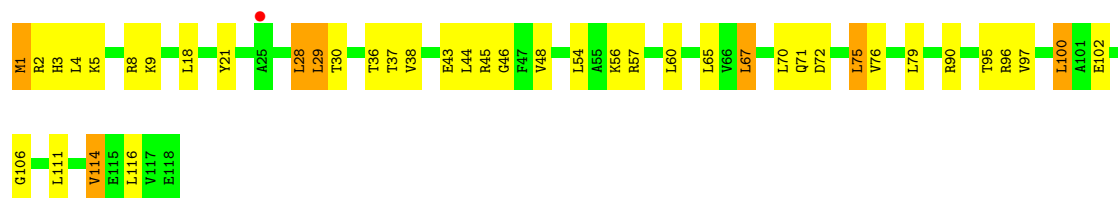
• Molecule 36: 50S Ribosomal Protein L16



• Molecule 37: 50S Ribosomal Protein L17



• Molecule 37: 50S Ribosomal Protein L17

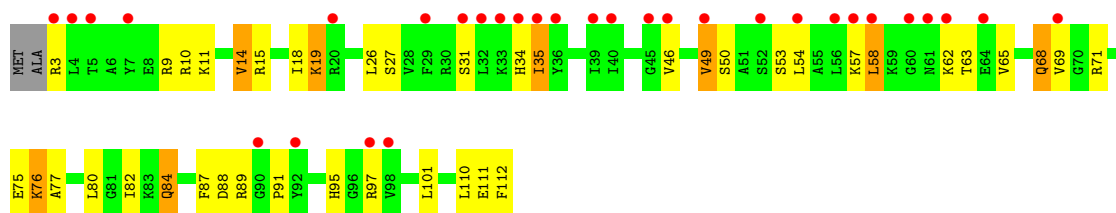


• Molecule 38: 50S Ribosomal Protein L18

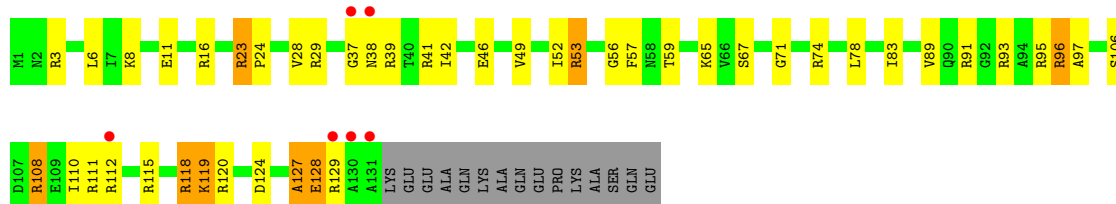


• Molecule 38: 50S Ribosomal Protein L18

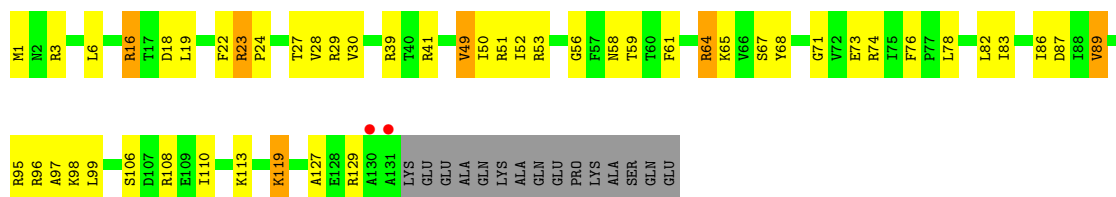




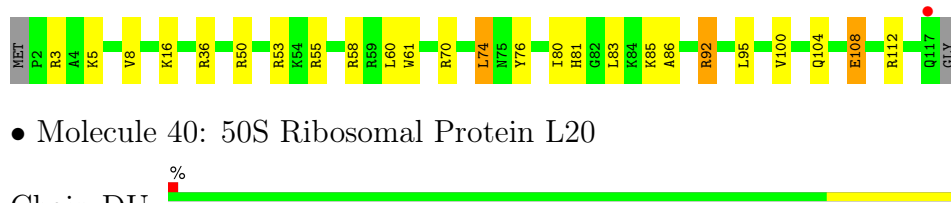
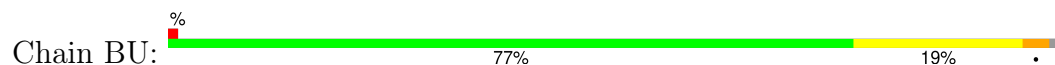
• Molecule 39: 50S Ribosomal Protein L19



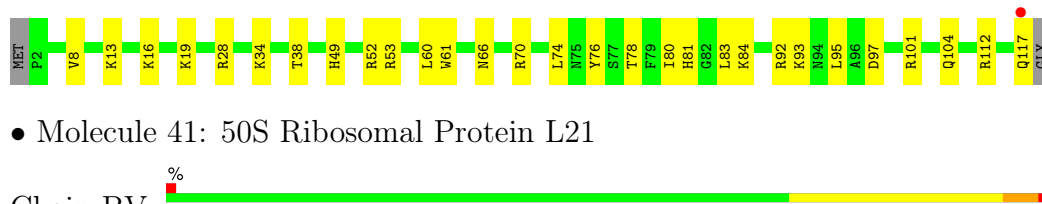
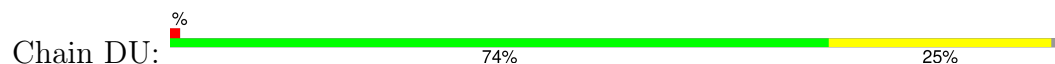
• Molecule 39: 50S Ribosomal Protein L19



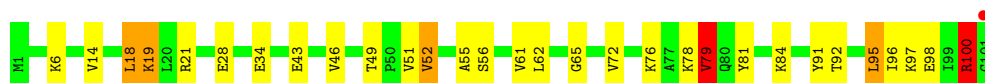
• Molecule 40: 50S Ribosomal Protein L20



• Molecule 40: 50S Ribosomal Protein L20



• Molecule 41: 50S Ribosomal Protein L21



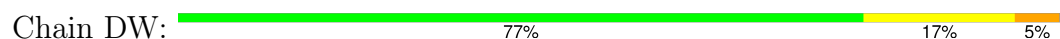
● Molecule 41: 50S Ribosomal Protein L21



● Molecule 42: 50S Ribosomal Protein L22



● Molecule 42: 50S Ribosomal Protein L22



● Molecule 43: 50S Ribosomal Protein L23



● Molecule 43: 50S Ribosomal Protein L23

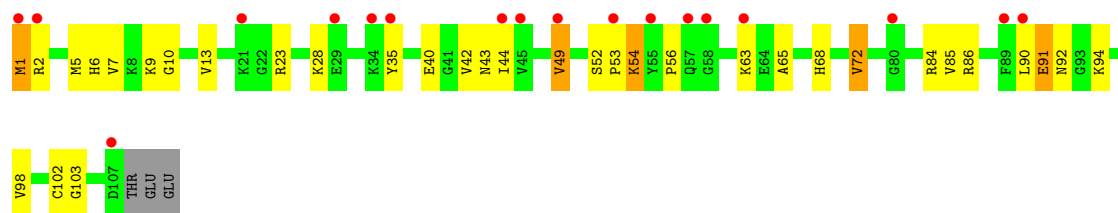


● Molecule 44: 50S Ribosomal Protein L24

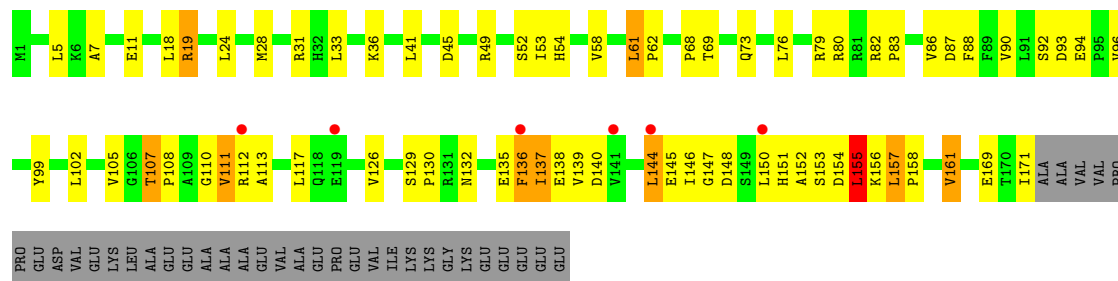


● Molecule 44: 50S Ribosomal Protein L24

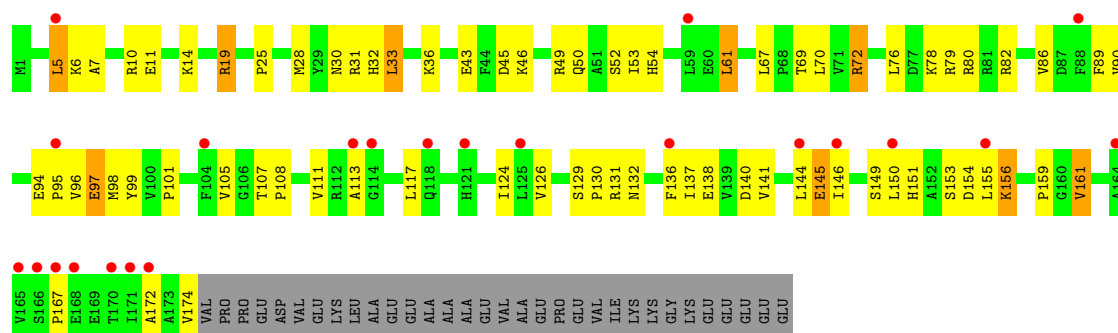




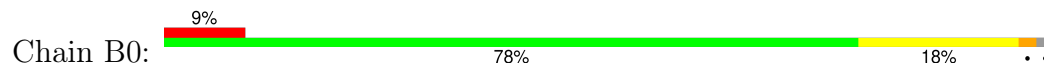
● Molecule 45: 50S Ribosomal Protein L25



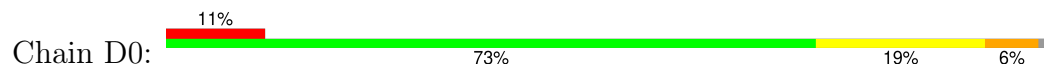
● Molecule 45: 50S Ribosomal Protein L25



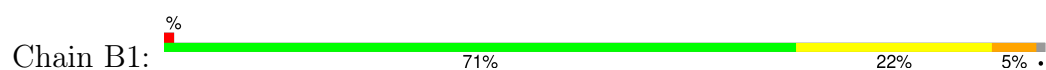
● Molecule 46: 50S Ribosomal Protein L27



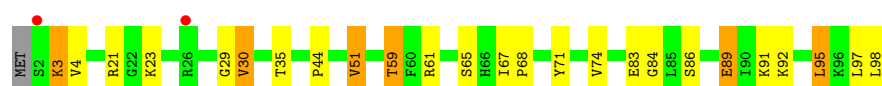
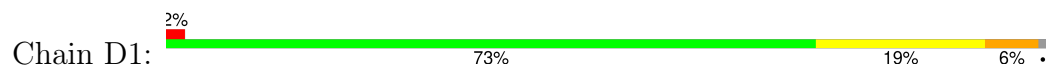
● Molecule 46: 50S Ribosomal Protein L27



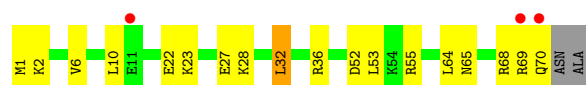
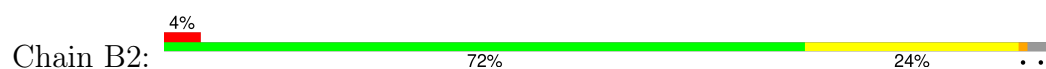
● Molecule 47: 50S Ribosomal Protein L28



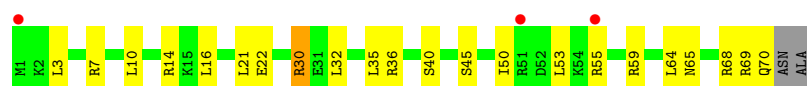
• Molecule 47: 50S Ribosomal Protein L28



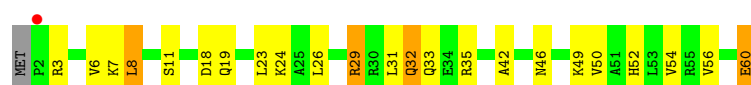
• Molecule 48: 50S Ribosomal Protein L29



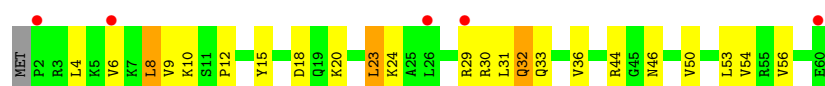
• Molecule 48: 50S Ribosomal Protein L29



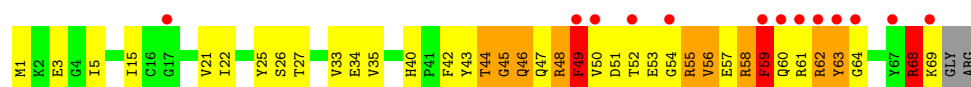
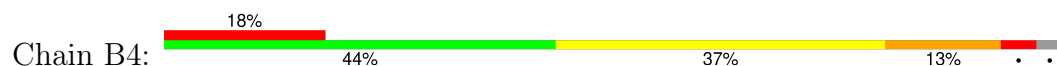
• Molecule 49: 50S Ribosomal Protein L30



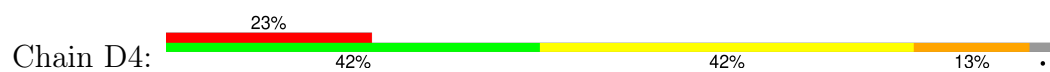
• Molecule 49: 50S Ribosomal Protein L30



• Molecule 50: 50S Ribosomal Protein L31



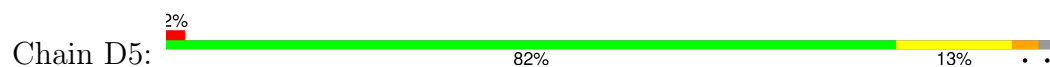
• Molecule 50: 50S Ribosomal Protein L31



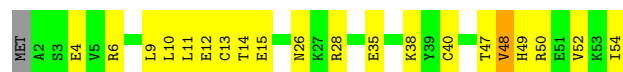
• Molecule 51: 50S Ribosomal Protein L32



• Molecule 51: 50S Ribosomal Protein L32



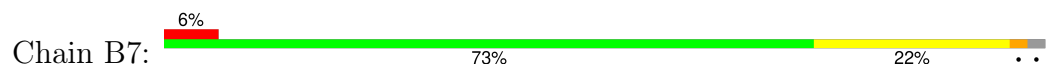
• Molecule 52: 50S Ribosomal Protein L33



• Molecule 52: 50S Ribosomal Protein L33



• Molecule 53: 50S Ribosomal Protein L34

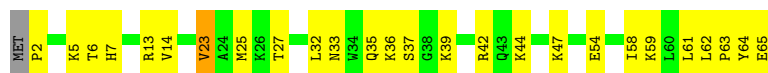


• Molecule 53: 50S Ribosomal Protein L34



• Molecule 54: 50S Ribosomal Protein L35

Chain B8:  58% 38% ..



- Molecule 54: 50S Ribosomal Protein L35

Chain D8:  58% 38% ..



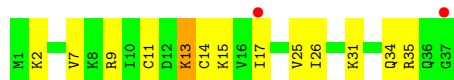
- Molecule 55: 50S Ribosomal Protein L36

Chain B9:  3% 70% 30%



- Molecule 55: 50S Ribosomal Protein L36

Chain D9:  5% 65% 32% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.93Å 446.95Å 619.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	144.86 – 2.70 144.86 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (144.86-2.70) 99.6 (144.86-2.70)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.215 , 0.262 0.216 , 0.263	Depositor DCC
R_{free} test set	78302 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	53.5	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 55.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	290807	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 5MC, PSU, PCY, K, 5MU, SF4, 4SU

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	AA	0.51	14/36024 (0.0%)	0.47	7/56222 (0.0%)
1	CA	0.24	0/36170	0.46	1/56452 (0.0%)
2	AB	0.43	0/1881	1.03	10/2542 (0.4%)
2	CB	0.45	0/1860	1.05	8/2518 (0.3%)
3	AC	0.40	0/1576	0.88	2/2130 (0.1%)
3	CC	0.43	0/1566	0.99	4/2119 (0.2%)
4	AD	0.42	0/1689	0.89	2/2267 (0.1%)
4	CD	0.40	0/1704	0.87	2/2284 (0.1%)
5	AE	0.42	0/1145	0.87	0/1543
5	CE	0.42	0/1149	0.97	3/1548 (0.2%)
6	AF	0.39	0/819	0.80	0/1111
6	CF	0.42	0/829	0.84	0/1123
7	AG	0.39	0/1250	0.86	0/1679
7	CG	0.38	0/1254	0.93	2/1683 (0.1%)
8	AH	0.40	0/1108	0.87	0/1494
8	CH	0.38	0/1108	0.87	0/1494
9	AI	0.37	0/1002	0.87	2/1346 (0.1%)
9	CI	0.43	0/997	0.95	5/1343 (0.4%)
10	AJ	0.42	0/722	0.93	0/982
10	CJ	0.48	0/727	1.02	2/988 (0.2%)
11	AK	0.43	0/844	0.88	0/1145
11	CK	0.39	0/848	0.90	1/1149 (0.1%)
12	AL	0.42	0/946	0.82	0/1274
12	CL	0.41	0/946	0.94	4/1274 (0.3%)
13	AM	0.38	0/947	0.92	1/1272 (0.1%)
13	CM	0.41	0/930	0.87	0/1250
14	AN	0.37	0/501	0.93	2/664 (0.3%)
14	CN	0.38	0/501	0.84	0/664
15	AO	0.41	0/739	0.86	0/985
15	CO	0.37	0/739	0.82	0/985
16	AP	0.41	0/697	0.83	0/939
16	CP	0.42	0/693	0.83	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.39	0/836	0.81	0/1117
17	CQ	0.35	0/836	0.79	2/1117 (0.2%)
18	AR	0.39	0/560	0.83	0/746
18	CR	0.36	0/560	0.78	0/746
19	AS	0.39	0/667	0.86	0/900
19	CS	0.46	0/661	1.03	3/893 (0.3%)
20	AT	0.39	0/730	0.94	0/965
20	CT	0.40	0/729	0.88	1/965 (0.1%)
21	AU	0.36	0/203	0.83	0/266
21	CU	0.42	0/203	0.88	1/266 (0.4%)
22	AV	0.31	0/188	0.52	0/290
22	CV	0.30	0/122	0.48	0/188
23	AX	0.29	0/1725	0.45	0/2689
23	CX	0.29	0/1725	0.47	0/2689
24	AY	0.28	0/428	0.35	0/661
24	CY	0.26	0/115	0.31	0/176
25	BA	0.37	0/68083	0.51	2/106274 (0.0%)
25	DA	0.28	0/67542	0.48	1/105428 (0.0%)
26	BB	0.29	0/2878	0.45	0/4490
26	DB	0.30	0/2878	0.48	0/4490
27	BD	0.57	0/2186	0.92	3/2944 (0.1%)
27	DD	0.49	0/2186	0.92	3/2944 (0.1%)
28	BE	0.60	0/1592	0.93	2/2149 (0.1%)
28	DE	0.49	0/1592	1.02	11/2149 (0.5%)
29	BF	0.55	0/1619	0.88	0/2193
29	DF	0.45	0/1615	0.95	5/2188 (0.2%)
30	BG	0.43	0/1450	0.90	3/1959 (0.2%)
30	DG	0.43	0/1449	0.98	4/1958 (0.2%)
31	BH	0.48	0/1356	0.88	1/1834 (0.1%)
31	DH	0.42	0/1356	0.93	3/1834 (0.2%)
32	BI	0.44	0/1100	0.95	8/1501 (0.5%)
32	DI	0.41	0/1076	0.88	1/1471 (0.1%)
33	BN	0.53	0/1144	0.84	0/1543
33	DN	0.43	0/1144	0.89	0/1543
34	BO	0.59	0/943	0.88	2/1269 (0.2%)
34	DO	0.46	0/943	0.88	2/1269 (0.2%)
35	BP	0.55	0/1152	0.87	2/1533 (0.1%)
35	DP	0.45	0/1152	1.00	8/1533 (0.5%)
36	BQ	0.57	0/1143	0.84	0/1527
36	DQ	0.46	0/1143	0.88	0/1527
37	BR	0.62	1/982 (0.1%)	0.90	0/1312
37	DR	0.46	0/982	0.81	1/1312 (0.1%)
38	BS	0.47	0/887	0.92	0/1180

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DS	0.44	0/880	0.91	0/1172
39	BT	0.49	0/1105	0.87	0/1477
39	DT	0.44	0/1097	0.84	0/1468
40	BU	0.60	0/977	0.86	0/1301
40	DU	0.41	0/977	0.80	0/1301
41	BV	0.55	0/782	0.88	0/1049
41	DV	0.41	0/782	0.84	0/1049
42	BW	0.67	0/897	0.87	0/1205
42	DW	0.47	0/897	0.83	2/1205 (0.2%)
43	BX	0.55	0/764	0.87	1/1025 (0.1%)
43	DX	0.42	0/764	0.82	0/1025
44	BY	0.50	0/819	0.91	0/1095
44	DY	0.39	0/819	0.91	1/1095 (0.1%)
45	BZ	0.49	0/1379	1.01	5/1873 (0.3%)
45	DZ	0.40	0/1390	0.94	4/1890 (0.2%)
46	B0	0.54	0/662	0.91	1/881 (0.1%)
46	D0	0.40	0/662	0.86	3/881 (0.3%)
47	B1	0.50	0/762	0.82	0/1014
47	D1	0.44	0/762	0.86	0/1014
48	B2	0.49	0/590	0.88	0/781
48	D2	0.35	0/590	0.80	0/781
49	B3	0.54	0/474	0.96	2/635 (0.3%)
49	D3	0.40	0/469	0.88	0/630
50	B4	0.46	0/571	1.07	5/768 (0.7%)
50	D4	0.42	0/545	0.99	3/737 (0.4%)
51	B5	0.62	0/469	0.98	0/635
51	D5	0.45	0/469	0.80	0/635
52	B6	0.65	0/460	0.91	0/613
52	D6	0.45	0/456	0.78	0/608
53	B7	0.61	0/426	0.84	0/561
53	D7	0.52	0/426	0.87	2/561 (0.4%)
54	B8	0.59	0/519	0.87	0/684
54	D8	0.47	0/525	0.81	0/691
55	B9	0.58	0/310	0.91	1/407 (0.2%)
55	D9	0.46	0/310	0.90	0/407
All	All	0.39	15/310558 (0.0%)	0.62	157/464586 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	1
7	CG	0	2
38	BS	0	1
50	B4	0	1
50	D4	0	1
All	All	0	6

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	439	A	C5-C4	50.86	2.40	1.38
1	AA	496	A	C6-N1	40.12	2.15	1.35
1	AA	496	A	C2-N3	24.68	1.82	1.33
1	AA	439	A	C5-C6	18.99	1.79	1.41
1	AA	439	A	C6-N1	18.63	1.72	1.35
1	AA	439	A	N1-C2	18.30	1.71	1.34
1	AA	439	A	N3-C4	17.78	1.70	1.34
1	AA	439	A	C2-N3	17.54	1.68	1.33
1	AA	439	A	N9-C4	13.37	1.64	1.37
1	AA	439	A	N9-C8	13.10	1.64	1.37
1	AA	439	A	N7-C5	12.41	1.64	1.39
1	AA	439	A	C8-N7	11.52	1.54	1.31
37	BR	38	VAL	CA-CB	-6.31	1.50	1.54
1	AA	496	A	N3-C4	5.97	1.46	1.34
1	AA	496	A	C5-C4	-5.01	1.28	1.38

All (157) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	496	A	C2-N3-C4	16.17	159.12	110.60
1	AA	496	A	N1-C2-N3	-15.00	84.31	129.30
2	CB	231	GLU	CA-C-N	-12.93	107.23	120.03
2	CB	231	GLU	C-N-CA	-12.93	107.23	120.03
1	AA	496	A	C5-C6-N6	-9.80	94.30	123.70
2	AB	128	GLU	N-CA-C	-8.61	100.75	114.09
2	AB	38	GLY	N-CA-C	-8.51	102.72	115.32
45	BZ	107	THR	CA-C-N	7.98	129.82	119.84
45	BZ	107	THR	C-N-CA	7.98	129.82	119.84
35	DP	43	GLY	N-CA-C	7.89	123.02	113.79
3	CC	72	LYS	CA-C-N	7.56	127.27	119.56
3	CC	72	LYS	C-N-CA	7.56	127.27	119.56
12	CL	28	LYS	N-CA-C	7.37	121.41	111.24
1	AA	439	A	N3-C4-N9	7.28	149.24	127.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	DP	44	GLY	CA-C-N	7.24	134.73	121.70
35	DP	44	GLY	C-N-CA	7.24	134.73	121.70
7	CG	79	ARG	CB-CA-C	-7.12	108.37	116.63
28	DE	21	VAL	CA-C-N	7.09	128.20	119.98
28	DE	21	VAL	C-N-CA	7.09	128.20	119.98
45	DZ	107	THR	CA-C-N	7.01	127.05	119.90
45	DZ	107	THR	C-N-CA	7.01	127.05	119.90
25	BA	2014	G	C2'-C3'-O3'	6.96	119.94	109.50
3	AC	4	LYS	N-CA-C	6.83	119.11	110.24
3	CC	108	ASN	CA-C-N	6.83	126.52	119.56
3	CC	108	ASN	C-N-CA	6.83	126.52	119.56
28	DE	72	VAL	CA-C-N	6.79	133.93	121.70
28	DE	72	VAL	C-N-CA	6.79	133.93	121.70
50	B4	60	GLN	N-CA-C	-6.72	105.41	112.93
7	CG	79	ARG	N-CA-C	6.68	119.38	108.08
11	CK	40	ILE	N-CA-C	-6.64	106.38	111.62
2	AB	9	GLU	N-CA-C	6.63	124.92	110.80
10	CJ	90	LEU	CA-C-N	6.57	128.05	119.84
10	CJ	90	LEU	C-N-CA	6.57	128.05	119.84
3	AC	29	TYR	N-CA-C	-6.51	104.27	112.93
5	CE	6	PHE	N-CA-C	6.42	120.51	110.17
50	B4	40	HIS	CA-C-N	6.36	127.79	119.84
50	B4	40	HIS	C-N-CA	6.36	127.79	119.84
35	DP	144	GLU	CA-C-N	6.36	126.12	119.76
35	DP	144	GLU	C-N-CA	6.36	126.12	119.76
30	DG	48	GLU	N-CA-C	-6.34	106.08	113.88
50	D4	61	ARG	N-CA-C	-6.34	103.63	112.45
13	AM	84	ILE	N-CA-C	6.27	119.84	111.44
46	B0	12	ASN	N-CA-C	6.26	121.08	113.38
5	CE	105	VAL	CA-C-N	-6.24	113.26	119.56
5	CE	105	VAL	C-N-CA	-6.24	113.26	119.56
44	DY	91	GLU	N-CA-C	-6.23	105.64	113.18
32	BI	110	ASP	CA-C-N	6.21	126.41	119.32
32	BI	110	ASP	C-N-CA	6.21	126.41	119.32
28	DE	89	ASP	N-CA-C	-6.21	105.28	112.92
27	DD	275	LYS	N-CA-C	-6.19	99.27	108.99
2	AB	21	ARG	N-CA-C	6.16	119.23	108.52
35	BP	22	GLY	CA-C-N	6.13	125.85	119.05
35	BP	22	GLY	C-N-CA	6.13	125.85	119.05
1	AA	439	A	C6-C5-N7	6.11	150.64	132.30
34	DO	47	ILE	CA-C-N	6.01	126.37	119.93
34	DO	47	ILE	C-N-CA	6.01	126.37	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	DW	13	SER	CA-C-N	6.01	125.49	119.24
42	DW	13	SER	C-N-CA	6.01	125.49	119.24
2	CB	193	ASP	CA-C-N	5.96	126.11	119.32
2	CB	193	ASP	C-N-CA	5.96	126.11	119.32
30	BG	127	GLY	N-CA-C	-5.96	106.51	114.25
20	CT	11	SER	N-CA-C	-5.95	105.60	112.92
29	DF	9	ILE	N-CA-C	5.95	114.38	107.89
25	DA	1992	G	C2'-C3'-O3'	5.94	118.41	109.50
14	AN	13	THR	CA-C-N	5.94	125.91	120.21
14	AN	13	THR	C-N-CA	5.94	125.91	120.21
35	DP	22	GLY	CA-C-N	5.92	125.62	119.05
35	DP	22	GLY	C-N-CA	5.92	125.62	119.05
19	CS	41	VAL	CA-C-N	5.90	126.05	119.32
19	CS	41	VAL	C-N-CA	5.90	126.05	119.32
46	D0	82	ARG	CA-C-N	5.88	125.82	119.76
46	D0	82	ARG	C-N-CA	5.88	125.82	119.76
32	DI	44	LEU	N-CA-C	-5.86	104.85	112.23
27	BD	229	VAL	CB-CA-C	-5.86	103.50	112.05
50	D4	68	ARG	N-CA-C	5.83	118.51	111.40
27	DD	244	ARG	CA-C-N	-5.76	114.45	120.38
27	DD	244	ARG	C-N-CA	-5.76	114.45	120.38
9	CI	89	ASN	CA-C-N	5.75	126.15	119.47
9	CI	89	ASN	C-N-CA	5.75	126.15	119.47
35	DP	44	GLY	N-CA-C	-5.73	102.44	112.53
49	B3	11	SER	CA-C-N	5.70	125.80	119.87
49	B3	11	SER	C-N-CA	5.70	125.80	119.87
27	BD	131	LEU	CA-C-N	-5.66	114.13	119.85
27	BD	131	LEU	C-N-CA	-5.66	114.13	119.85
2	CB	130	ARG	CA-C-N	5.64	126.89	119.84
2	CB	130	ARG	C-N-CA	5.64	126.89	119.84
1	CA	991	U	C2'-C3'-O3'	5.63	117.95	109.50
32	BI	118	LYS	CA-C-N	5.62	126.87	119.84
32	BI	118	LYS	C-N-CA	5.62	126.87	119.84
34	BO	47	ILE	CA-C-N	5.62	126.87	119.84
34	BO	47	ILE	C-N-CA	5.62	126.87	119.84
25	BA	1700	G	C2'-C3'-O3'	5.61	117.91	109.50
2	CB	16	HIS	N-CA-C	5.58	122.68	110.80
30	BG	96	ARG	CB-CA-C	-5.57	110.14	116.54
2	AB	232	PRO	N-CA-C	5.56	119.01	111.22
30	BG	45	GLU	N-CA-C	-5.55	105.77	112.54
50	B4	52	THR	N-CA-C	-5.55	103.81	111.81
31	DH	31	GLY	N-CA-C	5.55	117.49	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	BZ	157	LEU	CA-C-N	5.54	126.08	120.38
45	BZ	157	LEU	C-N-CA	5.54	126.08	120.38
31	BH	9	ILE	N-CA-C	5.49	112.98	107.55
53	D7	6	GLN	CA-C-N	5.47	125.48	119.90
53	D7	6	GLN	C-N-CA	5.47	125.48	119.90
12	CL	29	GLY	N-CA-C	-5.46	97.47	113.30
19	CS	67	VAL	N-CA-C	5.44	115.53	110.42
28	DE	73	GLU	CA-C-N	5.43	125.74	119.93
28	DE	73	GLU	C-N-CA	5.43	125.74	119.93
9	CI	20	ARG	CA-C-N	5.42	125.36	119.78
9	CI	20	ARG	C-N-CA	5.42	125.36	119.78
28	DE	85	ASN	CA-C-N	5.38	125.28	119.85
28	DE	85	ASN	C-N-CA	5.38	125.28	119.85
28	BE	52	LEU	CA-C-N	5.36	125.12	119.76
28	BE	52	LEU	C-N-CA	5.36	125.12	119.76
9	CI	63	ILE	N-CA-C	5.36	115.70	107.77
1	AA	496	A	C5-C6-N1	5.33	133.69	117.70
32	BI	106	GLY	CA-C-N	5.31	131.26	121.70
32	BI	106	GLY	C-N-CA	5.31	131.26	121.70
29	DF	21	ALA	CA-C-N	5.30	131.24	121.70
29	DF	21	ALA	C-N-CA	5.30	131.24	121.70
17	CQ	29	HIS	CA-C-N	5.30	125.36	119.32
17	CQ	29	HIS	C-N-CA	5.30	125.36	119.32
43	BX	69	TYR	N-CA-C	5.28	117.35	108.96
55	B9	28	GLU	N-CA-C	-5.26	105.61	112.23
46	D0	13	GLY	N-CA-C	5.23	121.05	114.25
9	AI	89	ASN	CA-C-N	5.23	125.54	119.47
9	AI	89	ASN	C-N-CA	5.23	125.54	119.47
2	CB	14	GLY	N-CA-C	-5.19	107.21	115.66
32	BI	22	LYS	CA-C-N	5.18	125.23	119.32
32	BI	22	LYS	C-N-CA	5.18	125.23	119.32
4	CD	171	GLY	CA-C-N	5.17	125.46	119.47
4	CD	171	GLY	C-N-CA	5.17	125.46	119.47
2	AB	233	SER	CA-C-N	5.16	126.29	119.84
2	AB	233	SER	C-N-CA	5.16	126.29	119.84
12	CL	118	SER	N-CA-C	-5.15	105.58	111.14
2	AB	123	ALA	N-CA-C	-5.14	107.17	112.93
2	AB	193	ASP	CA-C-N	5.14	125.19	119.32
2	AB	193	ASP	C-N-CA	5.14	125.19	119.32
50	B4	51	ASP	N-CA-C	5.13	117.44	108.52
4	AD	135	LEU	CA-C-N	5.12	126.24	119.84
4	AD	135	LEU	C-N-CA	5.12	126.24	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	CL	119	LYS	N-CA-C	-5.12	104.11	110.41
1	AA	1285	A	P-O3'-C3'	5.11	127.87	120.20
45	DZ	14	LYS	CA-C-N	5.11	125.39	119.47
45	DZ	14	LYS	C-N-CA	5.11	125.39	119.47
30	DG	178	PHE	CA-C-N	5.09	127.41	120.79
30	DG	178	PHE	C-N-CA	5.09	127.41	120.79
28	DE	190	GLY	CA-C-N	5.08	125.29	120.31
28	DE	190	GLY	C-N-CA	5.08	125.29	120.31
37	DR	38	VAL	CB-CA-C	-5.08	108.88	113.70
31	DH	28	GLY	CA-C-N	5.05	124.66	119.05
31	DH	28	GLY	C-N-CA	5.05	124.66	119.05
30	DG	78	SER	N-CA-C	5.04	116.46	111.07
21	CU	18	TYR	N-CA-C	5.03	116.32	109.18
29	DF	24	LEU	CA-C-N	5.02	125.02	119.90
29	DF	24	LEU	C-N-CA	5.02	125.02	119.90
50	D4	36	CYS	N-CA-C	5.01	114.91	108.34
45	BZ	135	GLU	N-CA-C	-5.00	108.92	114.62

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	439	A	Sidechain
50	B4	59	PHE	Peptide
38	BS	58	LEU	Peptide
7	CG	78	ARG	Peptide
7	CG	79	ARG	Peptide
50	D4	67	TYR	Peptide

5.2 Too-close contacts ⓘ

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	AA	32183	0	16244	644	0
1	CA	32312	0	16308	680	0
2	AB	1846	0	1867	91	0
2	CB	1825	0	1828	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AC	1552	0	1546	53	0
3	CC	1542	0	1517	53	0
4	AD	1659	0	1676	75	0
4	CD	1674	0	1714	54	0
5	AE	1129	0	1185	32	0
5	CE	1133	0	1191	37	0
6	AF	806	0	793	19	0
6	CF	816	0	808	17	0
7	AG	1231	0	1238	25	0
7	CG	1235	0	1249	39	0
8	AH	1088	0	1126	28	0
8	CH	1088	0	1126	26	0
9	AI	983	0	986	31	0
9	CI	978	0	966	47	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	34	0
11	AK	829	0	825	21	0
11	CK	833	0	836	18	0
12	AL	930	0	980	25	0
12	CL	930	0	980	28	0
13	AM	937	0	977	28	0
13	CM	920	0	950	37	0
14	AN	492	0	529	22	0
14	CN	492	0	529	24	0
15	AO	728	0	760	23	0
15	CO	728	0	760	23	0
16	AP	681	0	697	23	0
16	CP	677	0	686	17	0
17	AQ	823	0	891	11	0
17	CQ	823	0	891	11	0
18	AR	555	0	618	13	0
18	CR	555	0	618	14	0
19	AS	652	0	662	25	0
19	CS	646	0	644	41	0
20	AT	728	0	798	21	0
20	CT	727	0	796	17	0
21	AU	199	0	208	5	0
21	CU	199	0	208	9	0
22	AV	169	0	86	4	0
22	CV	109	0	55	5	0
23	AX	1625	0	828	20	0
23	CX	1625	0	829	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	AY	385	0	199	11	0
24	CY	104	0	56	6	0
25	BA	60792	0	30653	707	0
25	DA	60311	0	30414	1002	0
26	BB	2573	0	1306	23	0
26	DB	2573	0	1306	73	0
27	BD	2136	0	2218	61	0
27	DD	2136	0	2218	67	0
28	BE	1559	0	1618	26	0
28	DE	1559	0	1618	46	0
29	BF	1584	0	1625	48	0
29	DF	1580	0	1619	52	0
30	BG	1425	0	1443	45	0
30	DG	1424	0	1434	69	0
31	BH	1330	0	1407	24	0
31	DH	1330	0	1407	50	0
32	BI	1085	0	1114	39	0
32	DI	1061	0	1080	30	0
33	BN	1117	0	1183	20	0
33	DN	1117	0	1184	17	0
34	BO	933	0	996	24	0
34	DO	933	0	996	28	0
35	BP	1135	0	1212	34	0
35	DP	1135	0	1212	54	0
36	BQ	1122	0	1179	27	0
36	DQ	1122	0	1179	39	0
37	BR	968	0	1033	22	0
37	DR	968	0	1033	28	0
38	BS	877	0	938	26	0
38	DS	870	0	923	29	0
39	BT	1091	0	1151	38	0
39	DT	1083	0	1136	38	0
40	BU	959	0	1019	18	0
40	DU	959	0	1019	19	0
41	BV	771	0	830	14	0
41	DV	771	0	830	19	0
42	BW	886	0	940	19	0
42	DW	886	0	940	16	0
43	BX	750	0	814	23	0
43	DX	750	0	814	19	0
44	BY	806	0	881	22	0
44	DY	806	0	881	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BZ	1349	0	1355	46	0
45	DZ	1360	0	1363	47	0
46	B0	653	0	674	15	0
46	D0	653	0	674	23	0
47	B1	755	0	826	23	0
47	D1	755	0	826	19	0
48	B2	588	0	643	10	0
48	D2	588	0	643	12	0
49	B3	469	0	518	11	0
49	D3	464	0	514	12	0
50	B4	558	0	544	37	0
50	D4	532	0	503	26	0
51	B5	455	0	465	10	0
51	D5	455	0	465	8	0
52	B6	453	0	473	9	0
52	D6	449	0	469	10	0
53	B7	418	0	467	9	0
53	D7	418	0	467	9	0
54	B8	511	0	571	22	0
54	D8	517	0	582	17	0
55	B9	307	0	335	9	0
55	D9	307	0	335	7	0
56	AA	190	0	0	0	0
56	AD	1	0	0	0	0
56	AE	3	0	0	0	0
56	AF	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AQ	1	0	0	0	0
56	AX	9	0	0	0	0
56	B0	5	0	0	0	0
56	B2	1	0	0	0	0
56	B3	1	0	0	0	0
56	B4	1	0	0	0	0
56	B5	4	0	0	0	0
56	B6	2	0	0	0	0
56	B7	5	0	0	0	0
56	B8	2	0	0	0	0
56	B9	1	0	0	0	0
56	BA	814	0	0	0	0
56	BB	22	0	0	0	0
56	BD	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BE	7	0	0	0	0
56	BF	9	0	0	0	0
56	BG	2	0	0	0	0
56	BN	7	0	0	0	0
56	BO	1	0	0	0	0
56	BP	4	0	0	0	0
56	BQ	4	0	0	0	0
56	BR	3	0	0	0	0
56	BU	9	0	0	0	0
56	BV	4	0	0	0	0
56	BW	4	0	0	0	0
56	BX	2	0	0	0	0
56	BY	3	0	0	0	0
56	BZ	2	0	0	0	0
56	CA	175	0	0	0	0
56	CE	2	0	0	0	0
56	CF	1	0	0	0	0
56	CJ	1	0	0	0	0
56	CT	1	0	0	0	0
56	CX	2	0	0	0	0
56	D0	2	0	0	0	0
56	D1	1	0	0	0	0
56	D3	1	0	0	0	0
56	D8	1	0	0	0	0
56	DA	674	0	0	0	0
56	DB	10	0	0	0	0
56	DD	8	0	0	0	0
56	DE	5	0	0	0	0
56	DF	5	0	0	0	0
56	DG	1	0	0	0	0
56	DN	1	0	0	0	0
56	DO	1	0	0	0	0
56	DP	2	0	0	0	0
56	DQ	3	0	0	0	0
56	DR	1	0	0	0	0
56	DU	4	0	0	0	0
56	DV	3	0	0	0	0
56	DW	2	0	0	0	0
56	DY	1	0	0	0	0
57	AA	40	0	38	6	0
57	CA	40	0	38	4	0
58	AD	8	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	CD	8	0	0	0	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	175	0	0	13	0
61	AJ	2	0	0	0	0
61	AL	1	0	0	0	0
61	AM	1	0	0	0	0
61	AO	1	0	0	0	0
61	AV	1	0	0	0	0
61	AX	8	0	0	0	0
61	B0	4	0	0	0	0
61	B1	1	0	0	0	0
61	B3	1	0	0	0	0
61	B5	4	0	0	1	0
61	B6	1	0	0	0	0
61	B7	1	0	0	0	0
61	B8	10	0	0	1	0
61	BA	1294	0	0	49	0
61	BB	34	0	0	1	0
61	BD	16	0	0	1	0
61	BE	12	0	0	1	0
61	BF	7	0	0	1	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BN	1	0	0	0	0
61	BO	4	0	0	0	0
61	BP	15	0	0	1	0
61	BQ	5	0	0	0	0
61	BR	1	0	0	0	0
61	BU	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	BV	2	0	0	0	0
61	BW	3	0	0	0	0
61	BX	5	0	0	0	0
61	CA	137	0	0	12	0
61	CD	1	0	0	0	0
61	CJ	2	0	0	0	0
61	CL	1	0	0	1	0
61	CN	1	0	0	0	0
61	CT	1	0	0	0	0
61	CX	2	0	0	0	0
61	D0	7	0	0	0	0
61	D1	1	0	0	0	0
61	D3	1	0	0	0	0
61	D8	4	0	0	0	0
61	DA	924	0	0	75	0
61	DB	8	0	0	0	0
61	DD	18	0	0	3	0
61	DE	9	0	0	1	0
61	DF	5	0	0	0	0
61	DN	1	0	0	0	0
61	DO	1	0	0	0	0
61	DP	14	0	0	1	0
61	DR	1	0	0	0	0
61	DT	1	0	0	0	0
61	DU	3	0	0	0	0
61	DV	1	0	0	0	0
61	DW	1	0	0	0	0
61	DX	1	0	0	0	0
61	DY	1	0	0	0	0
All	All	290807	0	193177	5227	0

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 11.

All (5227) 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)
1:AA:439:A:N3	1:AA:439:A:C2	1.68	1.62
1:AA:439:A:C5	1:AA:439:A:C6	1.79	1.62
1:AA:439:A:N3	1:AA:439:A:C4	1.70	1.56
1:AA:439:A:C6	1:AA:439:A:N1	1.72	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:439:A:C2	1:AA:439:A:N1	1.70	1.54
1:AA:439:A:C4	1:AA:496:A:C6	1.95	1.53
1:AA:439:A:C5	1:AA:496:A:C6	1.97	1.50
1:AA:496:A:N3	1:AA:496:A:C2	1.82	1.47
1:AA:439:A:C2	1:AA:496:A:N3	1.92	1.35
1:AA:439:A:C5	1:AA:496:A:N3	1.94	1.35
1:AA:439:A:C4	1:AA:496:A:N3	1.93	1.35
1:AA:439:A:C6	1:AA:496:A:N3	1.95	1.34
1:AA:439:A:N1	1:AA:496:A:N3	1.82	1.25
1:AA:439:A:C8	1:AA:496:A:C6	2.30	1.19
1:AA:439:A:C6	1:AA:496:A:C2	2.31	1.18
1:AA:496:A:C6	1:AA:496:A:N1	2.15	1.14
1:AA:439:A:N3	1:AA:496:A:N3	1.98	1.11
1:CA:1162:C:N4	1:CA:1174:G:H1	1.49	1.08
1:AA:439:A:N9	1:AA:496:A:C6	2.21	1.07
1:AA:439:A:N7	1:AA:496:A:C6	2.25	1.03
1:AA:439:A:N3	1:AA:496:A:C2	2.28	1.00
1:AA:439:A:C2	1:AA:496:A:C2	2.49	1.00
25:DA:2138:C:N4	25:DA:2153:G:H1	1.61	0.99
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.44	0.97
25:DA:2104:G:H1	25:DA:2185:C:H42	1.12	0.97
25:BA:1065:U:HO2'	25:BA:1067:A:H2	1.01	0.96
1:CA:998:G:H1	1:CA:1043:C:H42	0.98	0.95
1:CA:1029:C:N4	1:CA:1032:G:H1	1.62	0.95
22:CV:16:A:H61	23:CX:36:U:H3	1.05	0.95
1:AA:1161:C:N4	1:AA:1175:G:H1	1.64	0.94
1:CA:1262:C:H42	1:CA:1273:G:H1	1.14	0.94
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.50	0.94
25:DA:1359:A:N1	25:DA:1372:U:N3	2.16	0.93
1:AA:997:U:H3	1:AA:1044:A:H61	1.04	0.93
1:AA:1161:C:H42	1:AA:1175:G:H1	1.04	0.92
1:AA:1162:C:H42	1:AA:1174:G:H1	1.07	0.91
1:AA:439:A:C8	1:AA:496:A:N6	2.39	0.91
1:CA:1025:U:H3	1:CA:1036:G:H1	1.11	0.91
1:AA:78:G:H1	1:AA:91:C:H42	1.17	0.91
1:CA:1162:C:N3	1:CA:1174:G:N2	2.19	0.90
1:AA:984:C:H42	1:AA:1221:G:H1	1.18	0.90
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.51	0.90
25:BA:927:G:N2	25:BA:944:C:N3	2.21	0.89
22:CV:16:A:N6	23:CX:36:U:H3	1.69	0.89
25:DA:620:G:H4'	25:DA:621:A:H5'	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2138:C:H42	25:DA:2153:G:H1	0.92	0.89
1:CA:1029:C:N3	1:CA:1032:G:N2	2.21	0.89
1:AA:496:A:N3	1:AA:496:A:N1	2.21	0.88
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.54	0.88
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.55	0.88
35:DP:126:VAL:HG12	35:DP:148:LEU:HD22	1.56	0.88
1:CA:975:A:H4'	1:CA:976:G:H5''	1.56	0.88
1:CA:998:G:H1	1:CA:1043:C:N4	1.71	0.88
1:CA:1162:C:H42	1:CA:1174:G:H1	0.91	0.87
25:DA:2046:G:H5'	51:D5:19:ARG:HA	1.54	0.87
25:DA:2166:G:H3'	25:DA:2167:U:H5''	1.54	0.87
1:AA:1502:A:H2	1:AA:1505:G:H1	1.21	0.87
1:AA:439:A:C5	1:AA:496:A:C4	2.61	0.87
1:AA:1162:C:N4	1:AA:1174:G:H1	1.73	0.87
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.57	0.86
25:BA:2118:U:H3	25:BA:2215:G:H1	1.20	0.86
4:AD:107:ARG:HH22	4:AD:194:LEU:HD22	1.36	0.86
1:AA:439:A:N1	1:AA:496:A:C2	2.44	0.86
1:AA:439:A:C4	1:AA:496:A:C4	2.63	0.85
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.09	0.85
1:CA:1000:U:H3	1:CA:1041:A:H61	1.19	0.85
25:DA:880:G:N1	25:DA:898:C:O2	2.09	0.85
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.57	0.85
2:AB:16:HIS:CD2	2:AB:17:PHE:H	1.94	0.84
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.10	0.84
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.43	0.84
25:DA:2401:U:H5'	52:D6:18:ARG:HH12	1.41	0.84
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.10	0.84
25:BA:1360:C:OP1	61:BA:4706:HOH:O	1.95	0.83
25:BA:839:G:O6	61:BA:4691:HOH:O	1.95	0.83
10:CJ:8:LEU:HB2	10:CJ:70:ARG:HB2	1.60	0.83
1:AA:201:C:H42	1:AA:216:G:H1	1.27	0.82
25:BA:2163:G:O6	25:BA:2172:U:O2	1.95	0.82
1:CA:1154:G:H2'	1:CA:1155:G:H8	1.44	0.82
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.59	0.82
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.58	0.82
1:AA:1027:C:C2	1:AA:1034:G:N1	2.46	0.82
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.42	0.82
25:DA:740:U:OP2	61:DA:4497:HOH:O	1.96	0.82
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.62	0.82
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:997:U:H3	1:AA:1044:A:N6	1.77	0.81
25:DA:2807:G:N1	25:DA:2893:G:O6	2.10	0.81
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.61	0.81
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.14	0.81
25:DA:1271:G:OP2	61:DA:4489:HOH:O	1.98	0.81
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.61	0.81
1:CA:1007:C:N3	1:CA:1022:G:O6	2.14	0.81
26:DB:2:C:O2	26:DB:119:G:N2	2.13	0.81
25:DA:1153:C:OP2	61:DA:4453:HOH:O	2.00	0.80
25:DA:1721:G:H8	25:DA:1741:A:H62	1.26	0.80
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.63	0.80
25:DA:1602:U:O4	61:DA:4187:HOH:O	2.00	0.80
31:DH:24:VAL:HG13	31:DH:37:VAL:HG21	1.63	0.80
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.46	0.80
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.14	0.80
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.00	0.80
1:AA:1158:C:C4	1:AA:1160:G:H8	1.99	0.80
25:BA:388:A:H2'	25:BA:389:G:H8	1.47	0.80
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.15	0.80
25:DA:1204:A:H2	25:DA:1241:A:H62	1.27	0.79
4:CD:122:ARG:NH1	4:CD:134:ASP:O	2.16	0.79
25:DA:1332:G:OP1	61:DA:4448:HOH:O	1.99	0.79
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.63	0.79
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.47	0.79
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.48	0.79
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.64	0.79
53:B7:24:THR:HG22	53:B7:27:GLY:H	1.48	0.79
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.27	0.79
37:DR:97:VAL:HG22	37:DR:114:VAL:HG13	1.65	0.79
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.00	0.79
25:DA:2502:G:N7	61:DA:4677:HOH:O	2.14	0.79
25:BA:932:C:H3'	25:BA:933:C:H5''	1.65	0.79
1:CA:1422:G:H5'	34:DO:48:PRO:HB3	1.65	0.79
1:AA:642:A:N3	8:AH:113:SER:OG	2.15	0.78
1:CA:953:G:H5'	1:CA:965:A:H61	1.48	0.78
1:CA:1119:C:H42	1:CA:1154:G:H1	1.31	0.78
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.16	0.78
1:AA:894:G:N7	61:AA:4102:HOH:O	2.15	0.78
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.65	0.78
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.66	0.78
25:DA:191:A:N1	61:DA:4501:HOH:O	2.15	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1422:G:H5'	34:BO:48:PRO:HB3	1.65	0.78
1:CA:1028:C:N3	1:CA:1033:G:C6	2.51	0.78
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.17	0.78
25:DA:2104:G:H1	25:DA:2185:C:N4	1.81	0.78
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.63	0.78
1:AA:76:C:H42	1:AA:93:G:H1	1.30	0.78
1:AA:975:A:H4'	1:AA:976:G:H5''	1.65	0.78
1:CA:596:C:O2	1:CA:644:G:N2	2.13	0.78
25:BA:2831:A:OP2	61:BA:5266:HOH:O	2.02	0.78
22:AV:16:A:H61	23:AX:36:U:H3	1.31	0.78
1:AA:78:G:N2	1:AA:91:C:N3	2.33	0.77
2:AB:231:GLU:HB3	2:AB:232:PRO:HD2	1.64	0.77
1:AA:78:G:H1	1:AA:91:C:N4	1.81	0.77
25:DA:602:G:O2'	25:DA:655:A:N6	2.16	0.77
27:DD:238:GLY:O	61:DD:407:HOH:O	2.02	0.77
25:BA:1829:U:H5'	27:BD:259:THR:HG22	1.66	0.77
25:BA:2163:G:H1	25:BA:2171:G:H22	1.29	0.77
1:AA:266:G:H5''	1:AA:268:C:H41	1.48	0.77
1:AA:1007:C:N3	1:AA:1022:G:O6	2.17	0.77
1:CA:664:G:H22	1:CA:741:G:H1	1.31	0.77
1:AA:953:G:H5'	1:AA:965:A:H61	1.48	0.77
25:BA:2251:G:OP2	61:BA:4424:HOH:O	2.02	0.77
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.49	0.77
25:DA:1689:A:H62	25:DA:1698:A:H2	1.31	0.77
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.83	0.77
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.67	0.76
25:BA:1577:C:O2'	25:BA:1578:C:O5'	2.03	0.76
25:BA:2832:G:OP2	61:BA:5266:HOH:O	2.03	0.76
1:CA:771:G:N7	61:CA:4031:HOH:O	2.18	0.76
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.18	0.76
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.34	0.76
25:DA:2114:A:N6	25:DA:2119:A:N7	2.34	0.76
25:BA:894:U:OP2	61:BA:4495:HOH:O	2.02	0.76
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.16	0.76
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.67	0.76
25:BA:2299:A:H62	25:BA:2356:U:H3	1.33	0.76
1:CA:1209:C:O2'	1:CA:1214:C:N4	2.18	0.76
1:CA:504:C:OP1	61:CA:4008:HOH:O	2.04	0.76
1:AA:627:G:H2'	1:AA:628:G:H8	1.51	0.75
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.66	0.75
25:DA:563:G:OP2	61:DA:4452:HOH:O	2.05	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:478:G:OP2	61:BA:5249:HOH:O	2.04	0.75
25:BA:1981:G:N7	61:BA:4103:HOH:O	2.20	0.75
1:CA:1165:C:H42	1:CA:1171:G:H1	1.35	0.75
1:CA:1221:G:OP1	1:CA:1320:C:N4	2.19	0.75
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.69	0.75
13:CM:22:ILE:HG23	13:CM:67:GLU:HG2	1.69	0.75
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.19	0.75
25:BA:591:U:O4	61:BA:4249:HOH:O	2.05	0.75
45:BZ:129:SER:HB2	45:BZ:132:ASN:HB2	1.69	0.75
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.20	0.75
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.20	0.75
25:DA:2268:A:OP1	61:DA:4414:HOH:O	2.05	0.75
25:DA:2312:U:H5'	30:DG:88:ILE:HD11	1.69	0.75
25:DA:2430:A:OP2	61:DA:4569:HOH:O	2.05	0.74
10:AJ:7:LYS:HE2	10:AJ:9:ARG:HH12	1.52	0.74
25:BA:1378:G:OP1	61:BA:4706:HOH:O	2.06	0.74
1:CA:1183:A:O2'	1:CA:1184:G:OP1	2.04	0.74
25:BA:1480:A:H61	25:BA:1605:A:H62	1.33	0.74
25:DA:587:C:OP2	35:DP:21:ARG:NH2	2.20	0.74
1:AA:439:A:C6	1:AA:496:A:C4	2.76	0.74
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.52	0.74
25:DA:1783:A:OP1	61:DA:4497:HOH:O	2.04	0.74
25:BA:2015:U:OP2	61:BA:5270:HOH:O	2.05	0.74
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.35	0.74
9:CI:53:VAL:O	9:CI:55:ALA:N	2.20	0.74
25:DA:64:A:N6	25:DA:90:U:O4	2.19	0.74
25:DA:971:C:OP2	61:DA:4841:HOH:O	2.06	0.74
25:BA:1462:G:N2	25:BA:1629:C:O2	2.17	0.74
25:DA:2308:G:O6	25:DA:2311:A:N6	2.16	0.74
1:AA:652:U:O4	1:AA:752:G:O2'	2.05	0.74
1:CA:1114:C:O2'	14:CN:60:SER:O	2.05	0.74
2:CB:123:ALA:H	2:CB:127:ILE:HD12	1.53	0.74
1:AA:574:A:OP2	61:AA:4007:HOH:O	2.04	0.74
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.68	0.74
25:DA:568:U:O4	61:DA:4154:HOH:O	2.06	0.74
1:AA:1158:C:H5	1:AA:1181:G:H1	1.36	0.73
25:BA:2877:G:OP2	39:BT:119:LYS:NZ	2.21	0.73
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.18	0.73
11:CK:48:ILE:O	11:CK:50:TYR:N	2.17	0.73
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.36	0.73
25:DA:2638:G:P	28:DE:82:ARG:HH22	2.11	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:972:C:OP1	61:AA:4128:HOH:O	2.07	0.73
1:CA:1507:A:N6	1:CA:1528:U:O4	2.16	0.73
35:BP:42:SER:O	61:BP:305:HOH:O	2.06	0.73
1:CA:76:C:H42	1:CA:93:G:H1	1.36	0.73
30:DG:80:PHE:O	30:DG:82:LEU:N	2.21	0.73
1:AA:316:G:OP2	1:AA:351:G:O2'	2.05	0.73
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.22	0.73
25:DA:573:G:OP2	41:DV:78:LYS:NZ	2.21	0.73
25:DA:2867:G:OP2	39:DT:119:LYS:NZ	2.20	0.73
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.70	0.73
9:AI:17:VAL:HG21	9:AI:81:ILE:HG22	1.70	0.73
26:DB:22:U:H3	26:DB:61:G:H1	1.34	0.73
51:D5:16:ARG:NH1	51:D5:17:ASP:OD1	2.21	0.73
1:AA:400:C:H5''	4:AD:73:ARG:HH22	1.53	0.73
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.21	0.73
1:AA:78:G:N1	1:AA:91:C:N4	2.36	0.73
1:CA:419:C:OP1	1:CA:513:C:O2'	2.05	0.73
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.52	0.73
25:BA:2324:U:H5'	30:BG:88:ILE:HD11	1.71	0.73
2:CB:87:ARG:HD3	2:CB:234:PRO:HD2	1.70	0.73
30:DG:7:LEU:HD13	30:DG:104:GLU:HA	1.70	0.73
25:DA:792:G:O6	61:DA:4438:HOH:O	2.06	0.72
25:DA:1327:C:OP2	61:DA:4194:HOH:O	2.06	0.72
1:AA:439:A:C5	1:AA:496:A:C5	2.75	0.72
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.22	0.72
1:CA:1004:A:N6	1:CA:1037:C:N3	2.37	0.72
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.72	0.72
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.70	0.72
35:DP:42:SER:O	61:DP:303:HOH:O	2.06	0.72
39:DT:16:ARG:NH1	39:DT:18:ASP:OD1	2.21	0.72
40:DU:78:THR:O	40:DU:117:GLN:NE2	2.22	0.72
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.15	0.72
1:CA:1048:G:OP1	14:CN:3:ARG:NH2	2.22	0.72
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.54	0.72
1:AA:567:G:N3	61:AA:4097:HOH:O	2.22	0.72
19:AS:68:GLY:H	50:B4:58:ARG:HD3	1.54	0.72
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.22	0.72
1:CA:1183:A:O2'	1:CA:1185:G:OP2	2.08	0.72
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.71	0.72
25:DA:1315:C:OP2	61:DA:4448:HOH:O	2.06	0.72
25:DA:1530:C:O2'	25:DA:1531:C:O5'	2.07	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.25	0.72
51:D5:16:ARG:HG2	51:D5:16:ARG:HH11	1.54	0.72
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.22	0.72
25:DA:2595:G:N7	61:DA:4581:HOH:O	2.22	0.72
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.72	0.72
52:B6:35:GLU:OE2	52:B6:50:ARG:NH1	2.23	0.71
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.23	0.71
1:CA:1123:A:H4'	10:CJ:36:GLY:HA3	1.72	0.71
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.23	0.71
16:AP:22:THR:HA	16:AP:33:ILE:HG12	1.73	0.71
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.08	0.71
1:AA:664:G:H22	1:AA:741:G:H1	1.35	0.71
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.72	0.71
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.72	0.71
25:BA:2162:C:C2	25:BA:2173:G:N1	2.57	0.71
25:DA:131:G:OP1	61:DA:4106:HOH:O	2.07	0.71
25:BA:973:G:N7	61:BA:4494:HOH:O	2.24	0.71
45:BZ:111:VAL:HG12	45:BZ:112:ARG:H	1.55	0.71
49:B3:8:LEU:HD13	49:B3:31:LEU:HD23	1.71	0.71
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.23	0.71
25:BA:2125:C:H42	25:BA:2208:G:H1	1.39	0.71
26:BB:48:A:H4'	38:BS:95:HIS:HD2	1.55	0.71
1:CA:1187:G:H5'	9:CI:113:LYS:HE2	1.71	0.71
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.72	0.71
25:DA:1010:A:OP2	61:DA:4463:HOH:O	2.09	0.71
1:AA:1027:C:O2'	1:AA:1034:G:N2	2.24	0.71
57:AA:3191:PCY:O14	57:AA:3191:PCY:O21	2.08	0.71
25:BA:2343:G:O2'	25:BA:2348:A:N1	2.19	0.71
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.23	0.71
1:CA:798:G:N7	61:CA:4027:HOH:O	2.24	0.71
7:CG:16:LEU:HD23	9:CI:41:VAL:HG12	1.73	0.71
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.23	0.71
25:BA:1370:G:O6	61:BA:4308:HOH:O	2.09	0.71
44:BY:54:LYS:HA	44:BY:56:PRO:HD3	1.72	0.71
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.26	0.71
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.71	0.71
25:DA:2584:U:H2'	25:DA:2585:U:H2'	1.71	0.71
1:CA:1029:C:H42	1:CA:1032:G:H1	0.80	0.70
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.23	0.70
9:CI:95:LYS:HA	9:CI:99:LEU:HD13	1.72	0.70
25:DA:11:G:H2'	25:DA:12:U:H5''	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1114:G:H2'	25:DA:1115:G:H8	1.56	0.70
25:DA:2849:U:O4	39:DT:23:ARG:NH2	2.24	0.70
1:AA:1086:U:H3	1:AA:1099:G:H22	1.38	0.70
25:BA:426:G:OP2	61:BA:5008:HOH:O	2.09	0.70
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.24	0.70
4:CD:61:LYS:NZ	4:CD:72:GLU:OE2	2.22	0.70
32:DI:27:ARG:HD2	47:D1:71:TYR:CE1	2.26	0.70
47:D1:59:THR:O	47:D1:91:LYS:NZ	2.23	0.70
1:AA:1183:A:H8	1:AA:1183:A:H5''	1.55	0.70
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.09	0.70
25:DA:89:G:H3'	25:DA:90:U:H5''	1.73	0.70
25:BA:1296:G:N7	35:BP:18:ARG:NH2	2.39	0.70
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.25	0.70
25:BA:2138:G:N2	25:BA:2184:G:OP1	2.24	0.70
39:BT:95:ARG:HG2	39:BT:95:ARG:HH11	1.54	0.70
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.24	0.70
29:DF:185:ASP:HA	29:DF:188:ARG:HD3	1.72	0.70
43:DX:11:PRO:HB3	43:DX:92:LEU:HD11	1.73	0.70
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.23	0.70
25:DA:71:A:H5''	25:DA:73:A:C8	2.26	0.70
25:DA:2042:A:OP1	61:DA:4176:HOH:O	2.10	0.70
25:DA:2748:A:H5'	31:DH:4:ILE:HD12	1.74	0.70
26:DB:20:C:H42	26:DB:63:G:H1	1.39	0.70
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.73	0.70
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.72	0.70
1:CA:201:C:H42	1:CA:216:G:H1	1.38	0.70
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.72	0.70
14:CN:9:LYS:HG3	14:CN:12:ARG:HH11	1.55	0.70
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.20	0.70
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.26	0.70
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.26	0.70
1:CA:1000:U:H3	1:CA:1041:A:N6	1.90	0.70
25:BA:2802:C:O2	25:BA:2903:G:N2	2.21	0.70
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.25	0.70
25:DA:954:G:H5''	36:DQ:13:GLN:HB3	1.74	0.70
25:DA:2682:U:OP2	61:DA:4144:HOH:O	2.10	0.70
2:AB:16:HIS:CG	2:AB:17:PHE:H	2.09	0.70
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.22	0.70
1:CA:1237:C:HO2'	1:CA:1300:G:H1	1.37	0.70
10:CJ:61:GLU:OE1	14:CN:58:LYS:NZ	2.24	0.70
25:BA:932:C:N3	25:BA:937:A:N6	2.40	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.72	0.70
45:BZ:139:VAL:HG22	45:BZ:155:LEU:HD11	1.74	0.70
1:CA:1262:C:N4	1:CA:1273:G:H1	1.87	0.70
1:AA:46:G:O6	61:AA:4149:HOH:O	2.07	0.69
1:AA:596:C:OP2	61:AA:4065:HOH:O	2.10	0.69
25:DA:2748:A:O2'	31:DH:63:SER:O	2.10	0.69
25:BA:832:G:OP2	61:BA:4267:HOH:O	2.10	0.69
1:CA:673:G:H2'	1:CA:674:G:C8	2.28	0.69
12:AL:33:ARG:HD3	12:AL:62:SER:HB3	1.73	0.69
25:DA:123:G:N7	61:DA:4069:HOH:O	2.24	0.69
25:BA:1249:A:H2	25:BA:1287:A:H62	1.40	0.69
31:BH:98:LEU:HD13	31:BH:125:VAL:HG23	1.74	0.69
34:BO:63:VAL:HG12	34:BO:106:LEU:HD11	1.73	0.69
1:CA:1086:U:H3	1:CA:1099:G:H22	1.40	0.69
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.27	0.69
25:DA:2198:A:OP1	32:DI:33:ARG:NH2	2.24	0.69
25:BA:2145:G:H1	25:BA:2197:C:H42	1.40	0.69
3:CC:58:GLU:HB2	3:CC:65:ALA:HB3	1.75	0.69
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.24	0.69
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.75	0.69
25:BA:1199:C:OP1	40:BU:92:ARG:NH1	2.24	0.69
25:BA:2695:C:O2	34:BO:70:LYS:NZ	2.20	0.69
43:BX:57:LEU:HD11	43:BX:78:LYS:HE2	1.74	0.69
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.75	0.69
25:DA:2504:U:OP2	61:DA:4445:HOH:O	2.09	0.69
1:AA:439:A:C4	1:AA:496:A:C5	2.76	0.69
1:AA:984:C:N4	1:AA:1221:G:H1	1.88	0.69
25:BA:709:G:OP1	61:BA:4721:HOH:O	2.10	0.69
25:BA:1018:A:OP2	61:BA:4249:HOH:O	2.11	0.69
25:BA:1170:C:OP1	61:BA:4957:HOH:O	2.09	0.69
1:CA:1154:G:H2'	1:CA:1155:G:C8	2.27	0.69
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.26	0.69
25:DA:731:C:OP1	61:DA:4606:HOH:O	2.10	0.69
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.74	0.69
45:DZ:28:MET:HE1	45:DZ:61:LEU:HD21	1.75	0.69
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.73	0.69
25:BA:153:C:OP2	47:B1:92:LYS:NZ	2.26	0.69
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.73	0.69
1:CA:1132:C:H42	1:CA:1142:G:H1	1.38	0.69
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.73	0.69
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.07	0.68
1:AA:532:A:O2'	1:AA:533:A:OP1	2.11	0.68
25:BA:96:C:OP1	48:B2:2:LYS:NZ	2.25	0.68
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.41	0.68
25:DA:2820:A:OP2	37:DR:2:ARG:NH2	2.26	0.68
9:AI:53:VAL:O	9:AI:55:ALA:N	2.25	0.68
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.26	0.68
25:BA:1067:A:H62	25:BA:1186:U:H3	1.41	0.68
2:CB:120:ALA:O	2:CB:122:PHE:N	2.26	0.68
9:CI:17:VAL:HG21	9:CI:81:ILE:HG22	1.74	0.68
1:AA:839:U:O2'	1:AA:840:C:OP1	2.09	0.68
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.75	0.68
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.76	0.68
25:BA:2162:C:O2	25:BA:2173:G:N1	2.26	0.68
1:CA:1493:A:H2'	25:DA:1913:A:H61	1.59	0.68
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.75	0.68
25:DA:2121:G:H1	25:DA:2177:C:H42	1.41	0.68
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.10	0.68
1:CA:728:A:H2'	1:CA:729:A:C8	2.29	0.68
24:AY:76:A:N6	25:BA:2434:A:O4'	2.26	0.68
25:BA:303:C:H42	25:BA:385:G:H1	1.41	0.68
25:BA:2465:A:OP1	61:BA:4680:HOH:O	2.10	0.68
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.94	0.68
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.28	0.68
25:BA:129:G:OP1	61:BA:4179:HOH:O	2.12	0.68
31:BH:86:GLU:OE2	31:BH:132:ARG:NH2	2.27	0.68
35:BP:86:LYS:HE3	35:BP:117:GLU:HB3	1.74	0.68
25:DA:2574:G:OP1	61:DA:4879:HOH:O	2.11	0.68
28:DE:36:ARG:HD3	28:DE:85:ASN:HD21	1.59	0.68
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.29	0.68
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.28	0.68
1:CA:768:A:OP2	61:CA:4016:HOH:O	2.10	0.68
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.28	0.68
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.57	0.68
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.76	0.68
1:AA:517:G:N2	1:AA:533:A:OP2	2.25	0.68
1:AA:1069:C:OP2	61:AA:4170:HOH:O	2.10	0.68
1:CA:1007:C:O2	1:CA:1022:G:N1	2.22	0.68
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.75	0.68
31:DH:3:ARG:HH12	31:DH:5:GLY:N	1.91	0.68
2:AB:87:ARG:NH2	2:AB:220:ASP:OD1	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1502:A:H2	1:CA:1505:G:H1	1.42	0.67
25:DA:2138:C:N3	25:DA:2153:G:N2	2.38	0.67
1:AA:67:C:H2'	1:AA:68:G:C8	2.29	0.67
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.27	0.67
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.27	0.67
25:DA:1658:C:OP1	61:DA:4482:HOH:O	2.11	0.67
25:BA:388:A:H2'	25:BA:389:G:C8	2.28	0.67
40:BU:76:TYR:OH	40:BU:92:ARG:NH1	2.27	0.67
3:AC:11:ARG:HB3	3:AC:15:THR:HB	1.74	0.67
1:CA:521:G:H4'	12:CL:73:GLU:HG2	1.77	0.67
25:DA:2010:G:N7	61:DA:4368:HOH:O	2.26	0.67
1:AA:79:G:C2	1:AA:90:U:O2	2.48	0.67
35:BP:65:ARG:HG3	54:B8:25:MET:HG3	1.77	0.67
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.27	0.67
2:AB:212:GLN:NE2	2:AB:234:PRO:O	2.27	0.67
12:AL:70:ILE:HD13	12:AL:77:LEU:HD12	1.75	0.67
25:BA:2367:C:H1'	46:B0:39:ARG:HH21	1.59	0.67
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.27	0.67
1:AA:1172:C:H2'	1:AA:1173:G:H8	1.60	0.67
25:BA:1491:A:N7	61:BA:4087:HOH:O	2.26	0.67
5:CE:148:VAL:HG21	8:CH:107:LEU:HD13	1.75	0.67
25:DA:987:G:O2'	25:DA:1000:A:N3	2.25	0.67
25:DA:1114:G:H2'	25:DA:1115:G:C8	2.29	0.67
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.77	0.67
25:BA:206:G:OP2	61:BA:5041:HOH:O	2.13	0.67
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.59	0.67
25:DA:880:G:H22	25:DA:898:C:H1'	1.59	0.67
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.29	0.67
30:DG:11:TYR:HB2	30:DG:176:LEU:HD21	1.76	0.67
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.22	0.67
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.77	0.67
25:DA:320:A:OP2	29:DF:137:LYS:NZ	2.25	0.67
4:AD:122:ARG:NH2	4:AD:134:ASP:OD1	2.28	0.67
9:AI:9:ARG:HG2	9:AI:14:VAL:HG13	1.77	0.67
26:BB:106:G:H5'	45:BZ:31:ARG:HG2	1.77	0.67
25:DA:956:G:H5''	36:DQ:77:LYS:HD2	1.77	0.67
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.74	0.66
6:AF:69:GLU:O	6:AF:72:VAL:HG12	1.95	0.66
25:DA:2062:A:OP1	61:DA:4140:HOH:O	2.11	0.66
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.10	0.66
25:BA:1431:G:O2'	25:BA:1442:U:O2	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:88:LEU:HD11	35:BP:114:ILE:HD12	1.76	0.66
1:CA:532:A:O2'	1:CA:533:A:OP1	2.12	0.66
1:CA:974:A:OP2	14:CN:29:ARG:NH2	2.28	0.66
1:CA:1005:A:O2'	1:CA:1037:C:O2'	2.12	0.66
9:CI:17:VAL:HG23	9:CI:63:ILE:HG12	1.77	0.66
25:DA:2176:A:H2'	25:DA:2177:C:C6	2.31	0.66
25:DA:2323:G:O6	25:DA:2332:U:N3	2.18	0.66
26:DB:106:G:H5'	45:DZ:31:ARG:HG2	1.76	0.66
1:AA:991:U:O2'	1:AA:992:U:OP2	2.13	0.66
11:AK:48:ILE:HG21	11:AK:63:LEU:HB3	1.78	0.66
29:BF:53:THR:HG22	29:BF:55:GLY:H	1.60	0.66
1:CA:35:G:O2'	12:CL:118:SER:O	2.07	0.66
25:DA:574:C:OP1	61:DA:4132:HOH:O	2.12	0.66
25:DA:2126:A:H62	25:DA:2172:U:H5'	1.61	0.66
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.76	0.66
7:AG:9:VAL:O	7:AG:11:GLN:NE2	2.28	0.66
1:CA:782:A:OP1	61:CA:4023:HOH:O	2.12	0.66
1:CA:794:A:OP2	61:CA:4023:HOH:O	2.14	0.66
25:DA:1189:A:OP2	61:DA:4459:HOH:O	2.14	0.66
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.28	0.66
25:DA:2162:G:H4'	25:DA:2172:U:H2'	1.75	0.66
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.29	0.66
1:AA:974:A:OP2	14:AN:41:ARG:NH1	2.28	0.66
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.29	0.66
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.28	0.66
46:B0:27:GLU:HG3	46:B0:68:GLU:HA	1.77	0.66
25:DA:1648:C:OP1	61:DA:4489:HOH:O	2.14	0.66
26:DB:84:C:OP1	49:D3:15:TYR:OH	2.12	0.66
1:AA:1027:C:C4	1:AA:1034:G:O6	2.49	0.66
28:BE:47:VAL:HG21	28:BE:86:PRO:HD2	1.78	0.66
38:BS:39:ILE:HB	38:BS:49:VAL:HG13	1.78	0.66
1:CA:316:G:OP2	1:CA:351:G:O2'	2.13	0.66
25:DA:2113:U:H3	25:DA:2170:A:H61	1.43	0.66
38:DS:49:VAL:HG23	38:DS:80:LEU:HD22	1.77	0.66
45:BZ:28:MET:HE1	45:BZ:61:LEU:HD21	1.78	0.66
25:DA:1371:G:H2'	25:DA:1372:U:H5	1.60	0.66
28:DE:73:GLU:HG3	28:DE:73:GLU:O	1.95	0.66
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.76	0.66
30:BG:56:ALA:HA	30:BG:153:ARG:HH21	1.61	0.66
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.78	0.66
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.25	0.66
48:D2:22:GLU:OE2	48:D2:68:ARG:NH2	2.29	0.66
2:CB:221:LEU:HD23	2:CB:224:GLN:HE22	1.59	0.65
4:CD:162:LEU:HD13	4:CD:181:MET:HG2	1.79	0.65
25:DA:2296:U:OP2	38:DS:9:ARG:NH2	2.28	0.65
39:DT:65:LYS:HE2	39:DT:67:SER:HB2	1.77	0.65
1:CA:815:A:N7	1:CA:1509:C:O2'	2.27	0.65
1:AA:1003:G:N2	1:AA:1004:A:N3	2.44	0.65
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.29	0.65
25:DA:1418:G:OP2	61:DA:4396:HOH:O	2.13	0.65
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.78	0.65
25:BA:118:U:OP2	61:BA:4118:HOH:O	2.14	0.65
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.96	0.65
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	1.79	0.65
25:DA:2127:G:O6	25:DA:2161:C:N3	2.28	0.65
2:AB:87:ARG:CZ	2:AB:233:SER:HB3	2.27	0.65
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.77	0.65
25:BA:2122:G:H1	25:BA:2211:U:H3	0.73	0.65
25:DA:2638:G:OP2	28:DE:82:ARG:NH2	2.26	0.65
1:AA:1530:G:H2'	1:AA:1531:A:O4'	1.97	0.65
29:BF:51:THR:HB	29:BF:88:VAL:HG11	1.77	0.65
1:CA:1320:C:H5''	19:CS:70:LYS:HG3	1.78	0.65
6:CF:89:MET:HE1	18:CR:72:ARG:HB3	1.78	0.65
2:AB:126:GLU:HG2	2:AB:127:ILE:HG12	1.78	0.65
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	1.78	0.65
38:BS:15:ARG:O	38:BS:19:LYS:HG2	1.97	0.65
43:BX:35:THR:HG22	43:BX:38:GLU:H	1.61	0.65
41:DV:35:LEU:HB2	41:DV:57:VAL:HG23	1.79	0.65
25:BA:872:C:O2	35:BP:55:ARG:NH2	2.25	0.65
25:BA:2495:C:N3	36:BQ:124:LYS:NZ	2.44	0.65
32:BI:3:VAL:HG12	32:BI:38:LEU:HA	1.79	0.65
1:CA:142:G:H2'	1:CA:143:A:C8	2.31	0.65
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.11	0.65
19:CS:28:LYS:HB3	19:CS:28:LYS:HZ3	1.62	0.65
29:DF:103:LYS:HA	29:DF:106:ARG:HG3	1.78	0.65
25:BA:1299:A:OP1	61:BA:4949:HOH:O	2.14	0.65
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.77	0.65
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.77	0.65
25:DA:1237:A:OP1	61:DA:4740:HOH:O	2.14	0.65
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.77	0.65
25:DA:770:G:OP2	61:DA:4536:HOH:O	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DH:9:ILE:HB	31:DH:50:VAL:HB	1.78	0.65
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.27	0.64
57:AA:3191:PCY:H25	57:AA:3191:PCY:H162	1.62	0.64
25:BA:1815:A:OP2	61:BA:4761:HOH:O	2.15	0.64
25:BA:2122:G:O6	25:BA:2211:U:O4	2.15	0.64
50:B4:15:ILE:HG23	50:B4:21:VAL:HG22	1.79	0.64
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.79	0.64
39:DT:95:ARG:HG2	39:DT:95:ARG:HH11	1.60	0.64
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.32	0.64
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.30	0.64
5:CE:10:MET:SD	5:CE:10:MET:N	2.71	0.64
25:DA:2163:C:OP1	25:DA:2165:G:N2	2.30	0.64
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.80	0.64
4:AD:166:LYS:HA	4:AD:178:VAL:HG21	1.79	0.64
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.80	0.64
37:BR:104:ARG:HG3	37:BR:111:LEU:HD21	1.78	0.64
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.79	0.64
25:DA:994:C:O2'	25:DA:996:A:OP1	2.10	0.64
1:AA:79:G:C2	1:AA:90:U:C2	2.85	0.64
25:BA:2239:A:N7	61:BA:4799:HOH:O	2.29	0.64
25:BA:2658:C:OP2	25:BA:2745:G:O2'	2.12	0.64
41:BV:95:LEU:HD13	41:BV:97:LYS:HD3	1.79	0.64
25:BA:30:G:OP2	40:BU:5:LYS:NZ	2.30	0.64
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.45	0.64
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.63	0.64
26:DB:76:G:N2	26:DB:101:G:O6	2.28	0.64
39:DT:16:ARG:NH2	39:DT:83:ILE:O	2.30	0.64
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.80	0.64
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.24	0.64
1:AA:1158:C:C4	1:AA:1160:G:C8	2.85	0.64
4:AD:187:ARG:NH1	4:AD:190:ASP:OD1	2.31	0.64
25:BA:610:C:OP2	35:BP:21:ARG:NH2	2.30	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.28	0.64
25:DA:1278:A:OP1	37:DR:36:THR:HG23	1.97	0.64
25:DA:2125:G:H22	25:DA:2172:U:H5'	1.62	0.64
39:DT:50:ILE:HA	39:DT:99:LEU:HD12	1.79	0.64
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.78	0.64
25:BA:2442:A:N3	25:BA:2442:A:H2'	2.12	0.64
30:BG:41:GLN:HE22	30:BG:153:ARG:HB3	1.63	0.64
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.33	0.64
25:DA:997:G:OP1	40:DU:92:ARG:HG2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1814:G:O3'	27:DD:54:ARG:NH2	2.31	0.64
28:DE:59:VAL:HG21	28:DE:74:PRO:HB3	1.80	0.64
45:DZ:52:SER:OG	45:DZ:53:ILE:N	2.31	0.64
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	1.98	0.64
26:DB:10:C:O2	26:DB:111:G:N2	2.19	0.64
27:DD:3:VAL:HG21	27:DD:203:ASN:HB2	1.80	0.64
13:AM:65:LYS:NZ	50:B4:53:GLU:OE1	2.25	0.64
1:CA:578:C:OP1	61:CA:4043:HOH:O	2.14	0.64
25:DA:2122:U:O4	25:DA:2176:A:N1	2.31	0.64
25:DA:2753:A:N3	55:D9:15:LYS:NZ	2.46	0.64
31:DH:59:ARG:O	31:DH:63:SER:OG	2.16	0.64
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.24	0.63
25:BA:1221:G:H1'	25:BA:1222:A:H5'	1.79	0.63
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.79	0.63
24:CY:76:A:O5'	61:DA:4895:HOH:O	2.14	0.63
25:BA:2113:U:O4	61:BA:4797:HOH:O	2.14	0.63
25:BA:2130:C:H42	25:BA:2203:G:H1	1.44	0.63
1:CA:532:A:H61	3:CC:193:TYR:HB3	1.62	0.63
2:CB:80:ILE:HD13	2:CB:211:ILE:HB	1.80	0.63
25:DA:2364:C:OP1	46:D0:55:ARG:NH1	2.31	0.63
14:CN:3:ARG:HH21	14:CN:3:ARG:HB3	1.63	0.63
25:DA:143:G:H4'	43:DX:35:THR:HG21	1.80	0.63
1:AA:1004:A:N6	1:AA:1036:G:N7	2.46	0.63
13:CM:96:LEU:O	13:CM:110:ARG:NH1	2.31	0.63
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.28	0.63
25:DA:2287:A:H62	25:DA:2344:U:H3	1.46	0.63
25:BA:611:U:H2'	25:BA:612:C:C6	2.34	0.63
20:CT:43:LEU:O	20:CT:47:GLY:N	2.25	0.63
25:BA:902:G:O2'	46:B0:27:GLU:OE2	2.13	0.63
25:BA:1890:A:N6	25:BA:1905:G:O2'	2.32	0.63
25:DA:1889:A:H2'	25:DA:1890:A:C8	2.34	0.63
36:DQ:22:LYS:O	45:DZ:78:LYS:NZ	2.29	0.63
2:AB:95:GLN:HG3	2:AB:147:LYS:HD3	1.81	0.63
1:CA:444:C:H2'	1:CA:445:G:H8	1.62	0.63
1:CA:839:U:O2'	1:CA:840:C:OP1	2.16	0.63
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.34	0.63
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.26	0.63
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.80	0.63
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.81	0.63
37:DR:36:THR:HG22	37:DR:37:THR:H	1.63	0.63
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AV:16:A:N6	23:AX:36:U:H3	1.96	0.63
25:BA:630:U:OP1	29:BF:102:PRO:HA	1.98	0.63
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.81	0.63
42:BW:4:LYS:HD3	42:BW:6:ILE:HD11	1.80	0.63
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.79	0.63
45:BZ:11:GLU:O	45:BZ:36:LYS:NZ	2.20	0.63
1:CA:142:G:H2'	1:CA:143:A:H8	1.63	0.63
38:BS:27:SER:HA	38:BS:88:ASP:HB3	1.80	0.62
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.32	0.62
15:CO:54:ARG:HG2	15:CO:58:MET:HE2	1.81	0.62
26:DB:45:A:O4'	30:DG:95:ARG:NH1	2.32	0.62
36:DQ:109:VAL:HG13	36:DQ:113:GLN:HB3	1.80	0.62
25:BA:591:U:O2'	61:BA:5137:HOH:O	2.15	0.62
25:BA:2162:C:N3	25:BA:2173:G:O6	2.32	0.62
36:BQ:54:MET:HG3	36:BQ:117:ALA:HB1	1.79	0.62
45:BZ:136:PHE:O	45:BZ:137:ILE:HG13	1.99	0.62
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.32	0.62
40:BU:81:HIS:CE1	40:BU:85:LYS:HD2	2.33	0.62
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.32	0.62
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.63	0.62
28:DE:72:VAL:HG13	28:DE:73:GLU:O	1.98	0.62
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.80	0.62
25:BA:2297:C:OP2	52:B6:6:ARG:NH1	2.33	0.62
45:BZ:52:SER:OG	45:BZ:53:ILE:N	2.32	0.62
45:BZ:117:LEU:HD11	45:BZ:144:LEU:HD23	1.81	0.62
1:CA:1023:G:H3'	1:CA:1024:G:C8	2.35	0.62
1:CA:1029:C:N4	1:CA:1032:G:N1	2.33	0.62
1:CA:1127:G:H5'	1:CA:1280:A:O2'	2.00	0.62
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.32	0.62
12:CL:70:ILE:HG12	12:CL:100:ILE:HD12	1.79	0.62
25:DA:322:A:OP2	29:DF:169:ASN:HB2	1.98	0.62
25:DA:2070:G:OP2	61:DA:4726:HOH:O	2.16	0.62
35:DP:86:LYS:HB3	35:DP:118:GLY:HA3	1.81	0.62
1:AA:1145:C:H4'	1:AA:1146:A:H5'	1.80	0.62
1:AA:1521:G:N3	61:AA:4051:HOH:O	2.31	0.62
25:BA:1185:C:O3'	33:BN:25:ARG:NH1	2.32	0.62
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.82	0.62
39:BT:53:ARG:HB3	39:BT:53:ARG:NH1	2.14	0.62
1:CA:998:G:N2	1:CA:1043:C:N3	2.43	0.62
1:CA:1157:A:H4'	1:CA:1158:C:O5'	1.99	0.62
1:CA:1179:A:H4'	9:CI:103:THR:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1321:C:H5''	1:CA:1322:C:H2'	1.80	0.62
2:CB:128:GLU:OE1	2:CB:135:GLN:NE2	2.33	0.62
30:DG:41:GLN:HE22	30:DG:153:ARG:HB3	1.64	0.62
41:DV:5:VAL:HG11	41:DV:57:VAL:HG21	1.81	0.62
1:AA:221:C:H2'	1:AA:222:U:H6	1.63	0.62
15:AO:5:LYS:HE2	15:AO:5:LYS:H	1.63	0.62
25:BA:602:G:H2'	25:BA:603:C:C6	2.34	0.62
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.34	0.62
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.18	0.62
26:DB:14:U:OP2	26:DB:70:C:O2'	2.15	0.62
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.14	0.62
25:BA:1093:G:H2'	25:BA:1156:G:H1	1.65	0.62
30:BG:41:GLN:NE2	30:BG:154:GLY:O	2.33	0.62
1:CA:1392:G:H21	1:CA:1502:A:H8	1.48	0.62
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.82	0.62
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.17	0.62
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.81	0.62
25:DA:2483:C:N3	36:DQ:124:LYS:NZ	2.47	0.62
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.81	0.62
30:DG:108:ASN:HD22	50:D4:22:ILE:HG12	1.64	0.62
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.32	0.62
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.16	0.62
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.32	0.62
25:BA:2369:U:OP1	46:B0:20:ARG:NH1	2.32	0.62
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.79	0.62
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.15	0.62
1:AA:79:G:C6	1:AA:90:U:N3	2.68	0.62
25:BA:271:U:O2'	25:BA:273:G:N2	2.32	0.62
25:BA:2374:G:OP1	54:B8:44:LYS:NZ	2.28	0.62
25:DA:1300:U:H4'	25:DA:1301:A:H5''	1.82	0.62
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.35	0.62
1:AA:1314:C:OP1	19:AS:6:LYS:NZ	2.24	0.62
1:CA:977:A:O2'	1:CA:981:U:N3	2.32	0.62
1:CA:1003:G:H2'	1:CA:1004:A:O4'	2.00	0.62
8:CH:4:ASP:OD2	8:CH:85:ARG:NH1	2.32	0.62
25:DA:2356:C:OP1	46:D0:24:LYS:NZ	2.28	0.62
32:DI:114:LEU:HD11	32:DI:128:LEU:HD13	1.82	0.62
49:D3:8:LEU:HD13	49:D3:31:LEU:HD23	1.82	0.62
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.33	0.61
1:AA:1158:C:N4	1:AA:1160:G:H8	1.97	0.61
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.47	0.61
25:BA:2145:G:H2'	25:BA:2146:G:H8	1.65	0.61
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.32	0.61
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.33	0.61
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.31	0.61
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.15	0.61
25:DA:848:G:H2'	25:DA:849:A:C8	2.35	0.61
1:AA:79:G:N1	1:AA:90:U:C2	2.69	0.61
9:AI:3:GLN:HG2	9:AI:20:ARG:HE	1.65	0.61
2:CB:48:MET:HA	2:CB:51:LEU:HD12	1.82	0.61
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.61
25:DA:1033:U:OP1	55:D9:9:ARG:NH2	2.33	0.61
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.81	0.61
1:AA:1174:G:H2'	1:AA:1175:G:H8	1.63	0.61
25:BA:83:A:H5''	44:BY:8:LYS:HE3	1.82	0.61
25:BA:671:A:H2'	25:BA:672:G:O4'	2.01	0.61
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.35	0.61
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.36	0.61
25:DA:2166:G:N7	25:DA:2168:G:N2	2.45	0.61
25:DA:2314:C:H2'	25:DA:2315:G:C8	2.36	0.61
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.32	0.61
11:AK:48:ILE:HD13	11:AK:48:ILE:H	1.65	0.61
25:BA:2754:A:OP1	55:B9:22:ARG:NH2	2.21	0.61
45:BZ:111:VAL:C	45:BZ:113:ALA:H	2.07	0.61
3:CC:13:GLY:HA3	14:CN:57:ARG:HH21	1.63	0.61
37:DR:21:TYR:CZ	37:DR:43:GLU:HG2	2.35	0.61
1:AA:439:A:C2	1:AA:496:A:C4	2.86	0.61
1:AA:1203:C:H2'	1:AA:1204:A:H8	1.65	0.61
50:B4:48:ARG:NH1	50:B4:48:ARG:HA	2.16	0.61
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.33	0.61
2:CB:125:PRO:O	2:CB:127:ILE:N	2.33	0.61
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	1.82	0.61
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.81	0.61
25:DA:1762:A:N1	61:DA:4564:HOH:O	2.30	0.61
25:DA:2074:U:H2'	25:DA:2075:U:C6	2.35	0.61
25:DA:2114:A:N1	25:DA:2117:A:N6	2.49	0.61
1:AA:946:A:H2'	1:AA:947:G:C8	2.35	0.61
3:AC:62:ASP:HA	3:AC:97:LYS:HD3	1.81	0.61
25:BA:1040:C:OP1	40:BU:53:ARG:NH2	2.34	0.61
25:BA:2348:A:H61	46:B0:43:THR:CG2	2.13	0.61
25:DA:2147:G:C2	25:DA:2148:G:H1'	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1714:G:O2'	25:BA:2013:U:O4	2.14	0.61
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.34	0.61
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.18	0.61
25:BA:929:G:H22	25:BA:940:C:H42	1.48	0.61
1:CA:56:U:H2'	1:CA:57:G:C8	2.36	0.61
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.36	0.61
25:DA:1231:G:H2'	25:DA:1232:G:H8	1.65	0.61
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.15	0.61
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.35	0.61
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.83	0.61
8:AH:112:LEU:HB3	8:AH:133:LEU:HA	1.81	0.61
25:BA:934:A:O2'	25:BA:935:C:OP2	2.18	0.61
25:BA:965:G:N2	25:BA:2281:A:OP2	2.34	0.61
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.36	0.61
27:BD:132:PRO:HD3	27:BD:190:TYR:CZ	2.35	0.61
29:BF:20:LEU:HD22	29:BF:21:ALA:H	1.66	0.61
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.20	0.61
13:CM:33:ALA:O	13:CM:37:THR:OG1	2.15	0.61
31:DH:144:VAL:O	31:DH:148:ILE:HG12	2.00	0.61
25:BA:646:A:OP2	35:BP:108:LYS:NZ	2.33	0.61
25:BA:1076:G:OP2	36:BQ:128:LYS:NZ	2.33	0.61
13:CM:47:ASP:OD2	13:CM:47:ASP:N	2.34	0.61
25:DA:2661:G:H2'	25:DA:2662:A:C8	2.36	0.61
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.33	0.60
25:BA:70:A:N7	43:BX:31:HIS:HE1	1.99	0.60
25:BA:397:G:H5''	25:BA:450:A:N6	2.16	0.60
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.34	0.60
47:B1:50:ARG:HG2	47:B1:59:THR:HB	1.83	0.60
1:CA:1235:U:O2'	1:CA:1305:G:OP1	2.16	0.60
11:CK:82:VAL:HB	11:CK:108:ILE:HG12	1.83	0.60
25:DA:1371:G:H2'	25:DA:1372:U:C5	2.36	0.60
27:DD:108:PRO:HG2	27:DD:111:LEU:HG	1.83	0.60
45:DZ:45:ASP:OD1	45:DZ:49:ARG:NH1	2.34	0.60
1:AA:1161:C:N3	1:AA:1175:G:N2	2.36	0.60
2:AB:163:PHE:HA	2:AB:185:ILE:HG13	1.83	0.60
45:BZ:145:GLU:O	45:BZ:148:ASP:N	2.26	0.60
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.82	0.60
29:DF:101:LEU:O	29:DF:106:ARG:NH1	2.30	0.60
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.34	0.60
25:BA:1338:U:H2'	25:BA:1339:C:C6	2.37	0.60
1:CA:1381:U:H1'	7:CG:79:ARG:HD3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:479:A:N3	25:DA:481:G:H5''	2.15	0.60
25:DA:588:U:H2'	25:DA:589:C:C6	2.35	0.60
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.35	0.60
25:DA:1292:U:H2'	25:DA:1293:C:C6	2.36	0.60
44:DY:43:ASN:CG	44:DY:65:ALA:HB3	2.26	0.60
45:DZ:108:PRO:HG2	45:DZ:117:LEU:HD13	1.83	0.60
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.36	0.60
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.35	0.60
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.31	0.60
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	1.83	0.60
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.82	0.60
8:CH:34:GLU:OE1	8:CH:37:ARG:NH1	2.35	0.60
25:DA:2061:G:H5''	25:DA:2503:A:C2	2.36	0.60
25:DA:2125:G:N1	25:DA:2172:U:O5'	2.35	0.60
1:AA:97:G:HO2'	1:AA:98:G:H8	1.47	0.60
1:AA:954:G:H21	1:AA:1227:A:H62	1.49	0.60
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.83	0.60
25:BA:1781:G:O2'	25:BA:2870:A:N1	2.34	0.60
25:BA:1846:A:N1	61:BA:4015:HOH:O	2.30	0.60
1:CA:977:A:HO2'	1:CA:981:U:H3	1.49	0.60
1:AA:1020:U:H2'	1:AA:1021:G:H8	1.65	0.60
1:AA:1502:A:H2	1:AA:1505:G:N1	1.96	0.60
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.83	0.60
25:BA:997:G:OP1	36:BQ:16:ARG:NH2	2.35	0.60
31:BH:56:SER:OG	31:BH:57:ASP:N	2.35	0.60
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.35	0.60
1:AA:97:G:O2'	1:AA:98:G:H5''	2.01	0.60
1:AA:1052:U:H2'	1:AA:1055:A:OP2	2.01	0.60
23:AX:8:4SU:O5'	23:AX:8:4SU:H6	2.01	0.60
25:BA:1899:A:H5'	25:BA:1900:G:OP2	2.02	0.60
30:BG:77:ILE:HG22	30:BG:80:PHE:H	1.65	0.60
31:BH:159:GLU:HG3	31:BH:169:VAL:HG11	1.84	0.60
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.84	0.60
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.83	0.60
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.34	0.60
25:DA:2109:U:H4'	25:DA:2149:G:H21	1.67	0.60
31:DH:38:SER:HB3	31:DH:41:MET:HG2	1.84	0.60
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.37	0.60
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.37	0.60
5:AE:57:LYS:HD3	5:AE:61:TYR:HE2	1.66	0.60
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:80:ARG:HB3	45:BZ:82:ARG:HG3	1.84	0.60
1:CA:757:U:H2'	1:CA:758:G:O4'	2.02	0.60
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.84	0.60
25:DA:153:C:OP2	47:D1:92:LYS:NZ	2.34	0.60
25:DA:807:U:OP2	35:DP:41:ARG:NH2	2.35	0.60
25:DA:1041:C:OP1	45:DZ:46:LYS:NZ	2.35	0.60
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.35	0.60
28:DE:111:ARG:HD3	37:DR:1:MET:HE1	1.83	0.60
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.83	0.60
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.83	0.60
25:BA:1410:G:OP2	47:B1:3:LYS:HG3	2.02	0.60
26:BB:103:G:O2'	45:BZ:73:GLN:NE2	2.35	0.60
27:BD:12:SER:HB3	27:BD:208:LYS:HB3	1.84	0.60
1:CA:677:U:H3	1:CA:713:G:H22	1.50	0.60
3:CC:130:VAL:O	3:CC:134:ILE:HG12	2.02	0.60
25:DA:1028:A:N6	25:DA:1125:G:H2'	2.16	0.60
30:DG:41:GLN:NE2	30:DG:154:GLY:O	2.35	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.01	0.59
32:BI:103:ARG:HG2	32:BI:104:GLN:N	2.17	0.59
45:BZ:58:VAL:HG12	45:BZ:68:PRO:HA	1.82	0.59
1:CA:123:C:OP1	1:CA:311:C:O2'	2.17	0.59
1:CA:396:G:O2'	1:CA:398:C:OP1	2.16	0.59
1:CA:693:G:O6	57:CA:3176:PCY:N16	2.34	0.59
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.37	0.59
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.85	0.59
1:CA:627:G:H2'	1:CA:628:G:H8	1.66	0.59
25:DA:307:G:N1	25:DA:310:A:OP2	2.35	0.59
25:DA:792:G:OP2	61:DA:4161:HOH:O	2.16	0.59
36:DQ:32:TYR:OH	36:DQ:111:GLU:OE1	2.19	0.59
25:BA:173:C:H2'	25:BA:174:U:C6	2.37	0.59
1:CA:694:A:H62	57:CA:3176:PCY:H93	1.67	0.59
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	1.83	0.59
25:DA:125:G:H5''	53:D7:19:ARG:HD3	1.83	0.59
25:DA:2134:A:H62	25:DA:2157:G:H4'	1.67	0.59
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.37	0.59
25:DA:2648:C:H2'	25:DA:2649:U:C6	2.38	0.59
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.36	0.59
1:AA:629:G:H2'	1:AA:630:G:O4'	2.03	0.59
7:AG:62:PHE:HA	7:AG:124:LEU:HD22	1.84	0.59
10:AJ:27:ALA:HA	10:AJ:81:THR:HG21	1.85	0.59
19:AS:67:VAL:HB	50:B4:58:ARG:HB3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1793:A:H2'	61:BA:5153:HOH:O	2.03	0.59
25:BA:1952:G:O2'	25:BA:1990:G:O6	2.20	0.59
42:BW:69:LEU:HD13	42:BW:107:LEU:HD23	1.84	0.59
1:CA:67:C:H2'	1:CA:68:G:C8	2.37	0.59
1:CA:448:A:P	1:CA:485:G:H22	2.26	0.59
1:CA:959:A:O2'	1:CA:984:C:O2'	2.21	0.59
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.83	0.59
10:CJ:55:LYS:O	10:CJ:57:LYS:N	2.34	0.59
25:DA:1991:U:H2'	25:DA:1992:G:H5''	1.84	0.59
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.17	0.59
42:DW:34:ASN:OD1	42:DW:37:ARG:NH2	2.35	0.59
1:AA:411:A:OP1	4:AD:30:LYS:NZ	2.35	0.59
19:AS:9:VAL:HG21	50:B4:61:ARG:HH12	1.67	0.59
25:BA:1221:G:H1'	25:BA:1222:A:C5'	2.32	0.59
25:BA:2736:C:O3'	37:BR:1:MET:HE3	2.01	0.59
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.66	0.59
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.37	0.59
2:CB:71:VAL:HA	2:CB:93:VAL:HG23	1.85	0.59
2:CB:98:LEU:HB2	2:CB:101:MET:HE3	1.84	0.59
23:CX:8:4SU:O5'	23:CX:8:4SU:H6	2.02	0.59
25:DA:2127:G:N1	25:DA:2161:C:O2	2.28	0.59
26:DB:29:A:O2'	26:DB:58:A:N1	2.32	0.59
43:DX:4:ALA:HB1	43:DX:42:ALA:HA	1.85	0.59
45:DZ:80:ARG:HB3	45:DZ:82:ARG:HG3	1.85	0.59
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.84	0.59
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.84	0.59
10:AJ:30:SER:OG	10:AJ:84:GLN:NE2	2.36	0.59
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.34	0.59
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.84	0.59
25:BA:53:G:O2'	53:B7:35:ARG:HD3	2.03	0.59
25:BA:1219:A:H4'	25:BA:1220:U:OP1	2.01	0.59
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.83	0.59
29:BF:192:LEU:HD13	29:BF:194:MET:HE2	1.83	0.59
6:CF:30:LEU:O	6:CF:35:ALA:HB3	2.03	0.59
25:DA:1803:A:O2'	27:DD:259:THR:HG21	2.02	0.59
26:DB:5:C:H42	26:DB:116:G:H1	1.50	0.59
26:DB:90:A:C5	26:DB:91:C:H1'	2.37	0.59
29:DF:110:LEU:HD21	29:DF:181:LEU:HG	1.84	0.59
1:AA:1414:U:H3	1:AA:1486:G:H1	1.50	0.59
20:AT:60:GLU:HG3	20:AT:81:LYS:HD2	1.83	0.59
25:BA:1613:A:OP1	27:BD:211:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:53:ASN:HB2	19:CS:77:THR:HA	1.84	0.59
25:DA:796:C:H2'	25:DA:797:C:C6	2.38	0.59
25:DA:1600:C:OP1	43:DX:58:HIS:NE2	2.26	0.59
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.36	0.59
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	1.84	0.59
1:AA:1320:C:H5''	19:AS:70:LYS:HG3	1.84	0.59
25:BA:667:G:H21	25:BA:671:A:H2	1.50	0.59
25:BA:2163:G:C6	25:BA:2172:U:O2	2.56	0.59
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.30	0.59
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.38	0.59
25:DA:322:A:OP1	29:DF:168:ARG:HD2	2.02	0.59
25:DA:1021:A:H62	25:DA:1141:U:H3	1.50	0.59
34:DO:77:ILE:HB	39:DT:74:ARG:HD3	1.85	0.59
1:AA:671:G:H5'	6:AF:77:ARG:HH22	1.68	0.59
1:AA:1001:A:N1	1:AA:1040:U:O4	2.36	0.59
1:AA:1005:A:H5''	1:AA:1006:C:OP2	2.03	0.59
3:AC:20:SER:HB2	3:AC:40:ARG:HH12	1.67	0.59
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.18	0.59
40:BU:3:ARG:HH12	40:BU:5:LYS:HD3	1.67	0.59
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.37	0.59
25:DA:1971:A:OP2	27:DD:242:ARG:NH2	2.33	0.59
1:AA:144:G:H1	1:AA:178:C:H42	1.50	0.59
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.28	0.59
2:AB:137:ARG:CZ	2:AB:137:ARG:HB3	2.32	0.59
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.68	0.59
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.29	0.59
48:B2:65:ASN:OD1	48:B2:69:ARG:NH1	2.35	0.59
25:DA:299:A:N1	25:DA:322:A:O2'	2.32	0.59
25:DA:529:A:H62	25:DA:2041:U:H3	1.49	0.59
25:DA:607:U:OP1	29:DF:102:PRO:HA	2.03	0.59
29:DF:64:ILE:HG21	29:DF:78:ILE:HG23	1.85	0.59
25:BA:918:U:OP1	36:BQ:5:ARG:HD3	2.02	0.58
25:BA:1785:C:OP1	39:BT:96:ARG:NH1	2.35	0.58
25:BA:2416:C:O3'	35:BP:77:ARG:NH2	2.36	0.58
1:CA:26:A:N6	1:CA:558:G:O2'	2.35	0.58
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.20	0.58
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.84	0.58
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.37	0.58
37:DR:67:LEU:HD22	37:DR:76:VAL:HG21	1.85	0.58
10:AJ:78:ASN:O	10:AJ:80:LYS:N	2.36	0.58
25:BA:121:G:OP2	61:BA:4119:HOH:O	2.16	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:77:U:OP1	45:BZ:19:ARG:NH2	2.36	0.58
25:DA:1316:U:H2'	25:DA:1317:A:C8	2.38	0.58
31:DH:8:PRO:O	31:DH:69:ARG:NH1	2.36	0.58
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.85	0.58
1:AA:376:G:H4'	16:AP:5:ARG:HE	1.67	0.58
2:AB:15:VAL:O	2:AB:16:HIS:ND1	2.37	0.58
31:BH:11:VAL:HG21	31:BH:50:VAL:HG23	1.85	0.58
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.83	0.58
25:DA:577:G:O2'	25:DA:1254:A:OP1	2.19	0.58
25:DA:1038:C:H42	25:DA:1117:G:H1	1.50	0.58
28:DE:27:LEU:HD22	39:DT:1:MET:HE1	1.85	0.58
28:DE:174:ASP:OD1	28:DE:175:VAL:N	2.36	0.58
1:CA:974:A:P	14:CN:29:ARG:HH21	2.27	0.58
9:CI:49:PRO:HD2	9:CI:81:ILE:HD11	1.85	0.58
9:CI:85:LEU:HB3	9:CI:92:TYR:CD2	2.39	0.58
13:CM:85:GLY:HA2	13:CM:93:ARG:HH22	1.67	0.58
25:DA:1446:C:H42	25:DA:1465:G:H1	1.51	0.58
25:DA:2104:G:N2	25:DA:2185:C:N3	2.42	0.58
25:DA:2126:A:N6	25:DA:2162:G:HO2'	2.02	0.58
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.02	0.58
34:DO:63:VAL:HG12	34:DO:106:LEU:HD11	1.85	0.58
45:DZ:129:SER:HB3	45:DZ:132:ASN:HB2	1.86	0.58
1:AA:139:G:N2	1:AA:224:C:O2	2.30	0.58
1:AA:501:C:OP1	12:AL:117:ARG:NH2	2.24	0.58
25:BA:989:G:O3'	61:BA:4867:HOH:O	2.17	0.58
25:BA:1153:G:N2	25:BA:1154:U:O4	2.37	0.58
32:BI:27:ARG:HD2	47:B1:71:TYR:CE1	2.38	0.58
41:BV:14:VAL:HB	41:BV:96:ILE:HG13	1.84	0.58
47:B1:3:LYS:HB2	47:B1:61:ARG:HH12	1.68	0.58
1:CA:148:G:H2'	1:CA:149:A:H8	1.68	0.58
1:CA:1172:C:H2'	1:CA:1173:G:C8	2.38	0.58
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.33	0.58
27:DD:206:LEU:HD22	27:DD:211:ARG:HG2	1.85	0.58
32:DI:117:GLU:HG3	32:DI:118:LYS:H	1.69	0.58
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.84	0.58
1:AA:693:G:C6	57:AA:3191:PCY:H25	2.39	0.58
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.69	0.58
25:BA:1249:A:H61	25:BA:1286:U:H2'	1.69	0.58
25:DA:247:G:H4'	25:DA:386:G:C5	2.38	0.58
25:DA:539:G:H2'	25:DA:540:C:C6	2.39	0.58
1:AA:262:A:H2'	1:AA:263:A:C8	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.36	0.58
10:AJ:65:LEU:HD13	14:AN:56:VAL:HG22	1.84	0.58
25:BA:313:A:N6	25:BA:375:G:O2'	2.37	0.58
25:BA:1346:U:H4'	25:BA:1347:A:H5''	1.84	0.58
30:BG:16:ARG:NE	30:BG:31:VAL:HG11	2.18	0.58
1:CA:45:U:H2'	1:CA:46:G:C8	2.39	0.58
3:CC:71:ALA:HA	3:CC:106:VAL:HB	1.86	0.58
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.39	0.58
34:DO:120:GLU:HG2	34:DO:122:LEU:HG	1.84	0.58
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.19	0.58
2:AB:18:GLY:HA2	2:AB:42:ILE:HG13	1.85	0.58
12:AL:57:LYS:HD3	12:AL:67:THR:HG23	1.85	0.58
25:BA:139:A:H8	25:BA:1454:C:O2'	1.86	0.58
25:BA:904:C:OP1	46:B0:77:ARG:NH2	2.36	0.58
1:CA:598:U:H4'	8:CH:94:TYR:CD2	2.39	0.58
2:CB:95:GLN:HG3	2:CB:147:LYS:HD3	1.85	0.58
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.84	0.58
16:CP:23:ASP:OD2	16:CP:25:ARG:NH1	2.36	0.58
30:DG:151:ALA:HB3	30:DG:153:ARG:HH11	1.68	0.58
1:AA:1160:G:C5	1:AA:1161:C:H5	2.21	0.58
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.35	0.58
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.04	0.58
32:BI:106:GLY:HA2	32:BI:107:VAL:O	2.03	0.58
1:CA:457:C:H42	1:CA:474:G:H1	1.51	0.58
1:CA:975:A:H5''	1:CA:1363(A):A:N6	2.19	0.58
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.38	0.58
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.84	0.58
25:DA:854:G:H2'	25:DA:855:G:C8	2.39	0.58
29:DF:29:ASN:H	29:DF:112:MET:HE1	1.69	0.58
30:DG:3:LEU:HD13	50:D4:25:TYR:CZ	2.39	0.58
1:AA:589:C:C2'	1:AA:590:C:H5'	2.34	0.58
9:AI:85:LEU:HB3	9:AI:92:TYR:HD2	1.69	0.58
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.37	0.58
25:BA:1154:U:O2'	25:BA:1155:C:O4'	2.22	0.58
1:CA:997:U:H3	1:CA:1044:A:H61	1.52	0.58
1:CA:1074:G:O2'	1:CA:1101:A:N1	2.35	0.58
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.67	0.58
25:DA:492:A:H2'	25:DA:493:G:O4'	2.04	0.58
25:DA:1325:G:OP1	25:DA:1647:G:O2'	2.11	0.58
25:DA:2303:G:O2'	30:DG:132:ASN:HB2	2.04	0.58
2:AB:8:LYS:HG2	2:AB:9:GLU:H	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:187:LEU:HA	2:AB:201:ILE:HB	1.85	0.57
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.86	0.57
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.04	0.57
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.04	0.57
25:BA:1053:C:OP1	33:BN:37:LYS:NZ	2.37	0.57
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.86	0.57
32:BI:68:LEU:HD11	32:BI:109:ILE:HD11	1.86	0.57
1:CA:36:C:O2'	12:CL:117:ARG:NH2	2.37	0.57
25:DA:2723:C:H5''	37:DR:1:MET:HE2	1.86	0.57
4:AD:49:ARG:H	4:AD:49:ARG:HE	1.50	0.57
5:AE:81:GLU:HG2	5:AE:90:VAL:HG13	1.86	0.57
28:BE:14:ILE:HD11	28:BE:173:VAL:HG11	1.86	0.57
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.69	0.57
25:DA:1342:A:O2'	25:DA:1344:G:OP2	2.15	0.57
25:DA:2570:G:O6	61:DA:4792:HOH:O	2.17	0.57
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.37	0.57
28:DE:127:ASP:OD2	61:DE:409:HOH:O	2.17	0.57
1:AA:123:C:OP1	1:AA:311:C:O2'	2.19	0.57
1:AA:964:A:OP1	61:AA:4146:HOH:O	2.17	0.57
4:CD:88:VAL:HG22	5:CE:96:PRO:HB2	1.85	0.57
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.39	0.57
1:AA:649:G:H2'	1:AA:650:G:H8	1.68	0.57
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.39	0.57
1:AA:1173:G:C2'	1:AA:1174:G:H5'	2.34	0.57
1:AA:1239:A:H62	1:AA:1299:A:N6	2.02	0.57
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.40	0.57
2:AB:98:LEU:HB2	2:AB:101:MET:HE3	1.86	0.57
6:AF:99:ALA:HB1	18:AR:23:LYS:HE2	1.86	0.57
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.19	0.57
25:BA:1736:A:H62	25:BA:1745:A:H2	1.51	0.57
25:BA:2701:U:H4'	25:BA:2702:C:H5'	1.85	0.57
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.86	0.57
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.86	0.57
23:CX:23:C:H2'	23:CX:24:U:C6	2.39	0.57
25:DA:566:U:H5''	35:DP:29:LYS:HE3	1.86	0.57
27:DD:142:VAL:HG22	27:DD:193:VAL:HA	1.85	0.57
38:DS:84:GLN:H	38:DS:111:GLU:HB2	1.68	0.57
1:AA:76:C:N4	1:AA:93:G:H1	1.98	0.57
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.85	0.57
25:BA:572:A:O2'	25:BA:573:G:OP1	2.23	0.57
25:BA:2594:G:OP2	61:BA:4493:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BB:102:A:N7	61:BB:315:HOH:O	2.32	0.57
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.38	0.57
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.86	0.57
25:DA:41:C:H2'	25:DA:42:G:H8	1.69	0.57
25:DA:852:G:H2'	25:DA:853:G:C8	2.39	0.57
25:DA:2879:C:OP2	61:DA:4411:HOH:O	2.17	0.57
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.39	0.57
1:AA:1239:A:H62	1:AA:1299:A:H62	1.52	0.57
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.85	0.57
43:BX:2:LYS:NZ	43:BX:38:GLU:OE2	2.27	0.57
1:CA:1150:U:O4	1:CA:1151:A:N6	2.37	0.57
4:CD:30:LYS:HA	4:CD:35:ARG:HD2	1.85	0.57
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.69	0.57
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.87	0.57
25:DA:643:A:N1	25:DA:2369:A:O2'	2.37	0.57
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.70	0.57
25:DA:1588:C:H2'	25:DA:1589:C:C6	2.39	0.57
1:AA:682:G:H1	1:AA:708:C:H42	1.53	0.57
2:AB:18:GLY:O	2:AB:19:HIS:HB3	2.04	0.57
9:AI:13:ALA:HB2	9:AI:68:GLY:HA3	1.86	0.57
47:B1:23:LYS:HB3	47:B1:29:GLY:HA3	1.86	0.57
1:CA:1495:U:O2'	25:DA:1919:A:N1	2.32	0.57
3:CC:180:ALA:HB1	3:CC:203:PHE:HE1	1.69	0.57
13:CM:68:GLY:HA3	30:DG:116:ASP:OD1	2.04	0.57
24:CY:76:A:N3	25:DA:2394:C:N4	2.52	0.57
25:DA:323:G:O2'	25:DA:1205:U:N3	2.35	0.57
25:DA:842:G:N7	61:DA:4699:HOH:O	2.32	0.57
25:DA:2113:U:H3	25:DA:2170:A:N6	2.02	0.57
25:DA:2557:G:H2'	25:DA:2558:C:C6	2.39	0.57
26:DB:44:G:OP1	30:DG:98:ARG:NH2	2.36	0.57
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.86	0.57
2:AB:10:LEU:O	2:AB:12:GLU:N	2.36	0.57
23:AX:23:C:H2'	23:AX:24:U:C6	2.39	0.57
32:BI:93:THR:OG1	32:BI:96:ASP:OD1	2.17	0.57
1:CA:737:A:H1'	6:CF:73:ASN:HD21	1.69	0.57
22:CV:16:A:N1	23:CX:36:U:O2	2.38	0.57
25:DA:2537:U:H2'	25:DA:2538:C:C6	2.40	0.57
15:AO:11:VAL:HG21	15:AO:34:LEU:HD22	1.85	0.57
1:CA:76:C:N4	1:CA:93:G:H1	2.03	0.57
1:CA:1239:A:H4'	1:CA:1240:U:H5''	1.86	0.57
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.86	0.57
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.87	0.57
25:DA:889:C:H2'	25:DA:890:A:O4'	2.04	0.57
25:DA:2079:U:O3'	47:D1:35:THR:OG1	2.23	0.57
25:DA:2721:A:OP1	61:DA:4144:HOH:O	2.16	0.57
27:DD:10:THR:OG1	27:DD:13:ARG:HG2	2.05	0.57
52:D6:10:LEU:HD23	52:D6:22:ALA:HB2	1.87	0.57
1:AA:992:U:O2	1:AA:1043:C:N4	2.38	0.57
1:AA:1162:C:N3	1:AA:1174:G:N2	2.43	0.57
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.87	0.57
25:BA:2825:C:H5'	51:B5:29:THR:HG21	1.87	0.57
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.38	0.57
33:BN:94:HIS:HB3	33:BN:97:ARG:HD3	1.87	0.57
1:CA:583:A:N6	1:CA:758:G:O2'	2.38	0.57
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.70	0.57
2:CB:161:ALA:HB1	2:CB:185:ILE:HD11	1.86	0.57
6:CF:24:GLU:HG3	6:CF:28:ARG:NH1	2.19	0.57
25:DA:2139:C:H42	25:DA:2152:G:H1	1.51	0.57
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.40	0.57
43:DX:32:PRO:HA	43:DX:77:LYS:HD2	1.87	0.57
50:D4:62:ARG:O	50:D4:64:GLY:N	2.38	0.57
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.19	0.56
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.37	0.56
32:BI:72:LEU:C	32:BI:74:ASN:H	2.13	0.56
45:BZ:41:LEU:HD21	45:BZ:83:PRO:HG2	1.85	0.56
1:CA:145:G:H1	1:CA:177:C:H42	1.52	0.56
1:CA:524:G:O5'	1:CA:524:G:H8	1.87	0.56
1:CA:826:C:H2'	1:CA:827:U:C6	2.40	0.56
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	1.85	0.56
13:AM:92:HIS:CE1	13:AM:98:VAL:HG11	2.40	0.56
25:BA:9:U:H3	25:BA:2641:A:H2	1.52	0.56
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.40	0.56
25:BA:1091:A:OP1	25:BA:1091:A:H4'	2.06	0.56
25:BA:1503:G:OP2	61:BA:4135:HOH:O	2.16	0.56
25:BA:2163:G:H1	25:BA:2171:G:N2	2.02	0.56
25:BA:2545:A:H2'	25:BA:2546:A:O4'	2.06	0.56
51:B5:16:ARG:HH11	51:B5:16:ARG:HG2	1.69	0.56
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.37	0.56
1:CA:572:A:OP1	61:CA:4039:HOH:O	2.17	0.56
25:DA:1588:C:H2'	25:DA:1589:C:H6	1.70	0.56
25:DA:2331:G:O2'	25:DA:2336:A:N1	2.28	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DH:3:ARG:HB3	31:DH:3:ARG:HH11	1.71	0.56
37:DR:21:TYR:OH	37:DR:43:GLU:HG2	2.05	0.56
49:D3:46:ASN:O	49:D3:50:VAL:HG22	2.05	0.56
1:AA:167:G:H2'	1:AA:168:G:H8	1.69	0.56
1:AA:707:C:OP1	11:AK:85:ARG:NH1	2.39	0.56
1:AA:1033:G:H2'	1:AA:1034:G:C8	2.35	0.56
1:AA:1053:G:N2	61:AA:4025:HOH:O	2.39	0.56
1:AA:1183:A:H5''	1:AA:1183:A:C8	2.39	0.56
1:AA:1238:A:OP2	61:AA:4121:HOH:O	2.18	0.56
6:AF:60:PHE:HE2	18:AR:76:LEU:HD12	1.70	0.56
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.37	0.56
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.38	0.56
25:BA:1033:G:O2'	25:BA:1046:A:N3	2.36	0.56
25:BA:2023:A:H2'	25:BA:2024:G:C8	2.40	0.56
30:BG:3:LEU:HD12	30:BG:5:VAL:HG12	1.87	0.56
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.20	0.56
51:B5:16:ARG:HD2	51:B5:20:ARG:NH1	2.20	0.56
1:CA:345:C:OP2	39:DT:39:ARG:NH2	2.36	0.56
1:CA:664:G:N2	1:CA:741:G:H1	2.02	0.56
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.06	0.56
25:DA:647:G:H8	25:DA:647:G:O5'	1.88	0.56
25:DA:2744:G:N2	31:DH:143:GLN:OE1	2.39	0.56
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.86	0.56
30:DG:16:ARG:O	30:DG:20:ILE:HG13	2.04	0.56
32:DI:130:TYR:HB3	32:DI:138:ILE:HB	1.87	0.56
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.05	0.56
29:BF:53:THR:CG2	29:BF:55:GLY:H	2.18	0.56
36:BQ:16:ARG:HG3	36:BQ:17:LEU:H	1.71	0.56
37:BR:21:TYR:OH	37:BR:43:GLU:HG2	2.05	0.56
45:BZ:111:VAL:O	45:BZ:113:ALA:N	2.35	0.56
2:CB:8:LYS:HD2	2:CB:9:GLU:H	1.71	0.56
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.38	0.56
7:CG:111:ARG:HD2	7:CG:123:GLU:HB2	1.88	0.56
25:DA:572:A:H5''	25:DA:573:G:OP2	2.05	0.56
25:DA:1946:U:H2'	25:DA:1947:C:C6	2.40	0.56
25:DA:2167:U:O2'	25:DA:2168:G:N3	2.34	0.56
35:DP:50:ARG:HD3	54:D8:7:HIS:CD2	2.39	0.56
39:DT:27:THR:HB	39:DT:89:VAL:HG22	1.88	0.56
43:DX:31:HIS:CD2	43:DX:33:LYS:HB2	2.40	0.56
1:AA:445:G:H2'	1:AA:446:G:C8	2.40	0.56
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:188:LEU:HD23	4:AD:188:LEU:H	1.70	0.56
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.39	0.56
27:BD:132:PRO:HG2	27:BD:135:PHE:CD2	2.41	0.56
1:CA:839:U:H3'	1:CA:840:C:C5	2.41	0.56
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.86	0.56
25:DA:500:G:N1	25:DA:503:A:OP2	2.37	0.56
26:DB:13:A:N1	26:DB:69:G:O2'	2.31	0.56
32:DI:72:LEU:HD21	32:DI:107:VAL:HG11	1.86	0.56
1:AA:814:A:H2'	1:AA:816:A:H5''	1.87	0.56
2:AB:59:GLU:HG2	2:AB:63:MET:HE3	1.86	0.56
25:BA:139:A:C8	25:BA:1454:C:O2'	2.59	0.56
25:BA:287:G:H4'	25:BA:288:U:H5''	1.87	0.56
29:BF:116:ASP:OD1	29:BF:119:ARG:NH2	2.39	0.56
45:BZ:45:ASP:OD2	45:BZ:49:ARG:NH1	2.38	0.56
1:CA:589:C:C2'	1:CA:590:C:H5'	2.36	0.56
1:CA:1028:C:C2	1:CA:1033:G:N1	2.74	0.56
9:CI:97:LYS:HA	9:CI:102:LEU:HG	1.87	0.56
25:DA:1639:U:H2'	25:DA:1640:C:H5''	1.88	0.56
25:DA:2429:G:OP2	61:DA:4569:HOH:O	2.18	0.56
25:DA:2708:G:H1'	37:DR:71:GLN:HE22	1.70	0.56
26:DB:48:A:H4'	38:DS:95:HIS:HD2	1.71	0.56
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.87	0.56
40:DU:97:ASP:OD1	40:DU:101:ARG:HD2	2.05	0.56
1:AA:56:U:H2'	1:AA:57:G:C8	2.41	0.56
25:BA:354:A:H2	25:BA:1255:A:O2'	1.89	0.56
25:BA:934:A:H4'	25:BA:935:C:H5	1.71	0.56
25:BA:1827:U:H2'	25:BA:1828:C:H6	1.70	0.56
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.05	0.56
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.12	0.56
1:CA:1318:A:OP1	19:CS:3:ARG:NH1	2.39	0.56
1:AA:193:C:H2'	1:AA:194:C:H6	1.71	0.56
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.29	0.56
25:BA:805:C:O2'	25:BA:2003:A:N3	2.38	0.56
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.24	0.56
50:B4:44:THR:O	50:B4:46:GLN:N	2.39	0.56
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.21	0.56
1:CA:1367:C:H4'	10:CJ:48:THR:HG21	1.86	0.56
25:DA:299:A:H5''	44:DY:86:ARG:HH21	1.69	0.56
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.39	0.56
25:DA:1316:U:H2'	25:DA:1317:A:H8	1.69	0.56
25:BA:1387:U:OP2	25:BA:1440:U:O2'	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BX:57:LEU:CD1	43:BX:78:LYS:HG2	2.36	0.56
23:CX:40:C:H2'	23:CX:41:C:H6	1.69	0.56
25:DA:635:C:O2'	25:DA:639:U:OP1	2.22	0.56
29:DF:192:LEU:HD22	29:DF:194:MET:HG3	1.87	0.56
47:D1:23:LYS:HB3	47:D1:29:GLY:HA3	1.87	0.56
1:AA:1027:C:N3	1:AA:1034:G:O6	2.38	0.56
25:BA:1500:A:OP2	61:BA:4134:HOH:O	2.18	0.56
25:BA:2331:G:H22	38:BS:3:ARG:NE	2.04	0.56
40:BU:76:TYR:CZ	40:BU:80:ILE:HG13	2.40	0.56
1:CA:160:A:H61	1:CA:347:G:H1'	1.70	0.56
1:CA:489:C:H2'	1:CA:490:G:H8	1.71	0.56
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.05	0.56
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	1.88	0.56
20:CT:16:HIS:O	20:CT:19:SER:OG	2.20	0.56
23:CX:23:C:H2'	23:CX:24:U:H6	1.71	0.56
25:DA:816:C:O2'	25:DA:932:G:O6	2.19	0.56
25:DA:952:G:OP1	36:DQ:16:ARG:NH2	2.39	0.56
25:DA:2165:G:N2	25:DA:2172:U:O4	2.38	0.56
25:BA:191:U:OP1	61:BA:4909:HOH:O	2.18	0.55
25:BA:1541:A:H2'	25:BA:1542:A:C8	2.42	0.55
25:BA:2188:G:N7	25:BA:2190:G:N2	2.54	0.55
30:BG:131:TYR:HB3	30:BG:159:VAL:HG13	1.88	0.55
32:BI:104:GLN:O	32:BI:106:GLY:N	2.34	0.55
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.38	0.55
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.87	0.55
25:DA:1697:G:OP2	25:DA:1698:A:O2'	2.21	0.55
25:DA:1913:A:H4'	25:DA:1914:C:C5'	2.36	0.55
1:AA:757:U:H2'	1:AA:758:G:O4'	2.06	0.55
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.88	0.55
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.40	0.55
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.42	0.55
25:BA:2858:G:C8	39:BT:97:ALA:HB2	2.40	0.55
27:BD:147:LEU:HD13	27:BD:155:LEU:HD21	1.87	0.55
1:CA:646:U:H2'	1:CA:647:C:C6	2.42	0.55
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.87	0.55
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	1.89	0.55
18:CR:26:LEU:HD12	18:CR:27:GLY:H	1.71	0.55
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	1.88	0.55
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.54	0.55
1:AA:439:A:C2	1:AA:496:A:H1'	2.41	0.55
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:553:A:C2	25:BA:2065:C:H4'	2.42	0.55
1:CA:1173:G:H2'	1:CA:1174:G:C8	2.41	0.55
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.88	0.55
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.38	0.55
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.06	0.55
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.41	0.55
34:DO:68:GLU:OE2	34:DO:78:ARG:NH1	2.39	0.55
46:D0:27:GLU:HG3	46:D0:68:GLU:HA	1.89	0.55
25:BA:956:A:H62	36:BQ:12:GLN:HA	1.72	0.55
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.07	0.55
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	1.88	0.55
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	1.88	0.55
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.41	0.55
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.87	0.55
25:DA:194:G:H2'	25:DA:195:A:O4'	2.06	0.55
25:DA:764:A:H5'	27:DD:210:GLY:HA2	1.87	0.55
25:DA:859:G:O2'	25:DA:916:G:O6	2.23	0.55
1:AA:114:U:H1'	1:AA:353:A:H1'	1.89	0.55
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.53	0.55
25:BA:878:G:N2	35:BP:53:GLY:O	2.39	0.55
28:BE:11:MET:HG2	28:BE:24:THR:HB	1.89	0.55
35:BP:59:LEU:HD23	54:B8:58:ILE:HD13	1.88	0.55
44:BY:7:VAL:HG21	44:BY:72:VAL:HG12	1.89	0.55
1:CA:596:C:N3	1:CA:644:G:N1	2.43	0.55
1:CA:833:U:H2'	1:CA:834:C:C6	2.41	0.55
1:CA:1074:G:OP1	5:CE:64:ARG:NH2	2.40	0.55
1:CA:1093:A:H2'	1:CA:1095:U:H5'	1.87	0.55
15:CO:54:ARG:O	15:CO:58:MET:HG3	2.07	0.55
25:DA:41:C:H2'	25:DA:42:G:C8	2.41	0.55
25:DA:2369:A:H2'	25:DA:2370:G:H8	1.71	0.55
30:DG:170:ARG:HH21	30:DG:180:PHE:HB2	1.71	0.55
31:DH:3:ARG:HH12	31:DH:5:GLY:H	1.51	0.55
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.06	0.55
13:AM:49:THR:HG22	13:AM:51:ALA:H	1.70	0.55
25:BA:709:G:H5''	35:BP:16:ARG:HG2	1.89	0.55
28:BE:29:GLY:HA3	61:BE:405:HOH:O	2.06	0.55
27:DD:108:PRO:HB3	27:DD:143:HIS:HE1	1.70	0.55
31:DH:56:SER:OG	31:DH:57:ASP:N	2.38	0.55
51:D5:16:ARG:NH1	51:D5:16:ARG:HG2	2.22	0.55
1:AA:627:G:H2'	1:AA:628:G:C8	2.36	0.55
1:AA:1399:C:C2	1:AA:1502:A:N6	2.74	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:56:ASP:HB2	3:AC:67:THR:HB	1.88	0.55
4:AD:18:LYS:HG2	58:AD:501:SF4:S1	2.47	0.55
25:BA:956:A:N3	25:BA:2276:C:O2'	2.39	0.55
25:BA:1219:A:H1'	25:BA:1220:U:H5''	1.88	0.55
25:BA:2212:G:H2'	25:BA:2213:G:O4'	2.07	0.55
25:BA:2804:C:H2'	25:BA:2805:G:H8	1.70	0.55
39:BT:127:ALA:O	39:BT:129:ARG:N	2.40	0.55
1:CA:1134:G:H1	1:CA:1140:C:H42	1.55	0.55
25:DA:14:A:N1	25:DA:2044:C:O2'	2.34	0.55
25:DA:39:C:O2	29:DF:46:ARG:NH2	2.39	0.55
25:DA:1614:A:P	25:DA:1614:A:H8	2.30	0.55
25:DA:2126:A:H2	25:DA:2127:G:N3	2.05	0.55
25:DA:2184:G:H2'	25:DA:2185:C:H5'	1.88	0.55
31:DH:154:PRO:HB3	31:DH:163:TYR:CZ	2.42	0.55
52:D6:13:CYS:SG	52:D6:47:THR:HG21	2.47	0.55
1:AA:201:C:N4	1:AA:216:G:H1	1.99	0.55
1:AA:621:A:H2'	1:AA:622:A:C8	2.41	0.55
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.54	0.55
1:AA:1258:G:H2'	1:AA:1259:C:C6	2.42	0.55
17:AQ:27:PHE:CZ	17:AQ:36:ILE:HD11	2.42	0.55
25:BA:1269:G:N2	25:BA:1272:A:OP2	2.37	0.55
25:BA:1634:C:H2'	25:BA:1635:C:C6	2.41	0.55
41:BV:21:ARG:HG2	41:BV:91:TYR:CD1	2.41	0.55
1:CA:489:C:H2'	1:CA:490:G:C8	2.42	0.55
1:CA:798:G:O6	61:CA:4029:HOH:O	2.17	0.55
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.42	0.55
29:DF:120:GLU:HB2	29:DF:122:LYS:HG2	1.89	0.55
1:AA:673:G:H2'	1:AA:674:G:C8	2.41	0.55
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.20	0.55
45:BZ:108:PRO:HB2	45:BZ:111:VAL:HG23	1.89	0.55
1:CA:972:C:OP1	61:CA:4116:HOH:O	2.18	0.55
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.39	0.55
25:DA:220:G:O2'	25:DA:233:A:N3	2.38	0.55
25:DA:289:A:H2'	25:DA:290:G:O4'	2.05	0.55
25:DA:1357:U:H2'	25:DA:1358:G:O4'	2.07	0.55
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.22	0.55
1:AA:78:G:C2	1:AA:91:C:N3	2.75	0.55
1:AA:183:G:HO2'	1:AA:224:C:HO2'	1.50	0.55
1:AA:376:G:H5''	16:AP:5:ARG:HB2	1.88	0.55
1:AA:448:A:O5'	1:AA:485:G:N2	2.24	0.55
1:AA:1039:C:H2'	1:AA:1040:U:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1372:U:OP1	9:AI:72:GLY:N	2.40	0.55
13:AM:88:ARG:HG3	13:AM:98:VAL:HG12	1.89	0.55
15:AO:79:ARG:O	15:AO:83:GLU:HB2	2.07	0.55
25:BA:1588:G:H3'	25:BA:1589:A:H2'	1.89	0.55
25:BA:1874:C:H5'	27:BD:253:GLN:NE2	2.22	0.55
25:BA:1961:U:OP1	25:BA:2616:U:O2'	2.23	0.55
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.42	0.55
31:BH:164:TYR:HB2	31:BH:167:GLU:HB2	1.89	0.55
34:BO:2:ILE:HB	34:BO:33:ALA:HB3	1.89	0.55
1:CA:472:A:H2'	1:CA:473:G:O4'	2.06	0.55
25:DA:48:G:O6	61:DA:4033:HOH:O	2.15	0.55
1:AA:537:G:H2'	1:AA:538:G:H8	1.71	0.54
1:AA:1051:C:H2'	1:AA:1052:U:C6	2.42	0.54
4:AD:19:LEU:HB3	4:AD:21:LEU:HD21	1.88	0.54
25:BA:878:G:O2'	35:BP:38:GLN:NE2	2.39	0.54
25:BA:2240:G:OP1	27:BD:261:LYS:NZ	2.34	0.54
1:CA:986:A:H1'	19:CS:54:GLY:O	2.07	0.54
1:CA:1131:G:H2'	1:CA:1132:C:C6	2.42	0.54
3:CC:40:ARG:NH2	3:CC:55:VAL:O	2.39	0.54
4:CD:19:LEU:HB3	4:CD:21:LEU:HD21	1.89	0.54
25:DA:1376:C:OP2	61:DA:4086:HOH:O	2.18	0.54
25:DA:2532:G:O2'	25:DA:2657:A:N1	2.35	0.54
34:DO:2:ILE:HB	34:DO:33:ALA:HB3	1.90	0.54
1:AA:976:G:N2	1:AA:1363:C:OP2	2.35	0.54
1:AA:1007:C:O2	1:AA:1022:G:N1	2.25	0.54
1:AA:1095:U:P	1:AA:1108:G:H1	2.30	0.54
25:BA:1627:A:H8	25:BA:1627:A:OP2	1.90	0.54
25:BA:1829:U:OP2	27:BD:274:ARG:NH2	2.39	0.54
33:BN:67:LEU:HD12	33:BN:87:LEU:HD13	1.89	0.54
1:CA:56:U:H2'	1:CA:57:G:H8	1.71	0.54
25:DA:586:A:N1	25:DA:809:G:O2'	2.34	0.54
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.41	0.54
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.25	0.54
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.54	0.54
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.88	0.54
23:AX:23:C:H2'	23:AX:24:U:H6	1.73	0.54
25:BA:939:C:H2'	25:BA:940:C:C6	2.42	0.54
32:BI:61:ARG:HH11	32:BI:61:ARG:HA	1.72	0.54
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.40	0.54
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.41	0.54
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:571:A:H5'	25:DA:2030:A:N7	2.21	0.54
26:DB:114:C:H4'	38:DS:46:VAL:HG22	1.89	0.54
1:AA:166:G:H2'	1:AA:167:G:H8	1.72	0.54
1:AA:598:U:O4	61:AA:4065:HOH:O	2.17	0.54
26:BB:6:C:H2'	26:BB:7:G:H5''	1.89	0.54
50:B4:47:GLN:HG2	50:B4:49:PHE:H	1.72	0.54
19:CS:44:MET:O	19:CS:47:HIS:HB2	2.08	0.54
25:DA:1010:A:H1'	25:DA:1153:C:H1'	1.90	0.54
25:DA:2180:U:H2'	25:DA:2181:G:O4'	2.08	0.54
25:DA:2747:G:H1	25:DA:2754:U:H2'	1.72	0.54
31:DH:18:GLU:HB3	31:DH:25:LYS:HB2	1.90	0.54
1:AA:1278:U:H5'	1:AA:1279:A:O4'	2.08	0.54
2:AB:55:PHE:HA	2:AB:58:ILE:HB	1.90	0.54
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.28	0.54
24:AY:71:G:H4'	25:BA:1882:U:H4'	1.88	0.54
27:BD:145:VAL:HG12	27:BD:146:GLU:O	2.08	0.54
1:CA:975:A:N1	10:CJ:48:THR:HB	2.21	0.54
1:CA:1028:C:N3	1:CA:1033:G:O6	2.39	0.54
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.06	0.54
7:CG:106:GLN:O	7:CG:110:GLN:HG3	2.08	0.54
25:DA:459:U:H5''	53:D7:40:TRP:CD2	2.43	0.54
25:DA:555:U:O2'	25:DA:556:G:N7	2.41	0.54
25:DA:622:G:H2'	25:DA:623:G:H8	1.72	0.54
25:DA:740:U:H2'	25:DA:741:G:C8	2.43	0.54
25:DA:1011:G:OP2	40:DU:66:ASN:ND2	2.39	0.54
25:DA:1410:G:H2'	25:DA:1411:C:C6	2.42	0.54
25:DA:2820:A:C5	37:DR:4:LEU:HD11	2.43	0.54
26:DB:95:C:H2'	26:DB:96:U:C6	2.42	0.54
34:DO:77:ILE:HG13	39:DT:74:ARG:HG2	1.88	0.54
45:DZ:19:ARG:HG3	45:DZ:25:PRO:HD3	1.88	0.54
1:AA:958:A:N6	19:AS:77:THR:O	2.41	0.54
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.07	0.54
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.42	0.54
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.08	0.54
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.90	0.54
25:BA:34:C:H5''	25:BA:35:G:OP2	2.07	0.54
25:BA:2135:U:N3	25:BA:2136:A:N7	2.56	0.54
40:BU:3:ARG:NH1	40:BU:5:LYS:HD3	2.22	0.54
1:CA:1376:U:OP1	7:CG:98:SER:OG	2.19	0.54
25:DA:603:A:H4'	25:DA:604:G:H5'	1.89	0.54
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1188:U:H4'	41:DV:79:VAL:HG22	1.89	0.54
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.43	0.54
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.07	0.54
25:BA:1014:U:H2'	25:BA:1015:C:C6	2.42	0.54
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.08	0.54
1:CA:89:C:H2'	1:CA:90:U:O4'	2.07	0.54
1:CA:1155:G:N2	1:CA:1156:G:H1'	2.23	0.54
25:DA:857:C:H1'	46:D0:26:TYR:HE1	1.71	0.54
26:DB:6:C:H2'	26:DB:7:G:H5''	1.89	0.54
34:DO:20:MET:HE3	34:DO:44:LYS:HE3	1.90	0.54
39:DT:30:VAL:HG22	39:DT:86:ILE:HG12	1.88	0.54
50:D4:53:GLU:HG2	50:D4:55:ARG:H	1.72	0.54
1:AA:688:G:H2'	1:AA:689:C:H6	1.72	0.54
1:AA:1320:C:H6	1:AA:1320:C:H5'	1.73	0.54
25:BA:1003:U:H5''	36:BQ:14:ARG:HD3	1.90	0.54
25:BA:1249:A:N6	25:BA:1286:U:H2'	2.23	0.54
36:BQ:43:THR:HG22	36:BQ:94:VAL:HG12	1.90	0.54
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.89	0.54
3:CC:180:ALA:HB1	3:CC:203:PHE:CE1	2.42	0.54
9:CI:3:GLN:HG2	9:CI:20:ARG:HE	1.72	0.54
19:CS:32:LYS:HE3	19:CS:57:HIS:CD2	2.43	0.54
25:DA:1341:U:OP1	25:DA:1397:U:N3	2.38	0.54
25:DA:1842:G:O2'	27:DD:253:GLN:NE2	2.41	0.54
25:DA:2126:A:N6	25:DA:2172:U:H5'	2.22	0.54
25:DA:2552:U:H2'	25:DA:2554:U:H5''	1.90	0.54
45:DZ:70:LEU:O	45:DZ:89:PHE:N	2.37	0.54
45:DZ:99:TYR:HA	45:DZ:124:ILE:O	2.08	0.54
1:AA:931:C:H42	1:AA:1386:G:H1	1.54	0.54
20:AT:16:HIS:O	20:AT:19:SER:OG	2.24	0.54
25:BA:331:G:H21	25:BA:354:A:H62	1.55	0.54
25:BA:2340:A:H2'	25:BA:2341:G:H8	1.72	0.54
25:BA:2879:G:H2'	25:BA:2880:C:O4'	2.07	0.54
1:CA:452:A:O2'	1:CA:453:A:OP2	2.23	0.54
25:DA:863:A:H2'	25:DA:864:G:C8	2.43	0.54
35:DP:94:GLU:HG3	35:DP:124:LYS:HD3	1.90	0.54
1:AA:479:C:N4	1:AA:480:U:O4	2.41	0.54
1:AA:1456:G:N2	20:AT:43:LEU:HD11	2.22	0.54
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.42	0.54
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.33	0.54
9:AI:8:GLY:O	9:AI:15:ALA:N	2.41	0.54
32:BI:75:LEU:HD22	32:BI:105:HIS:CG	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:BT:59:THR:HG23	39:BT:78:LEU:HB3	1.90	0.54
48:B2:22:GLU:OE2	48:B2:68:ARG:NH2	2.41	0.54
1:CA:1269:A:H2	1:CA:1312:G:N3	2.06	0.54
25:DA:1827:C:OP2	27:DD:222:ARG:NH1	2.38	0.54
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.07	0.54
26:DB:50:G:OP1	38:DS:63:THR:N	2.40	0.54
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.07	0.53
10:AJ:54:PHE:O	10:AJ:56:HIS:N	2.36	0.53
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.08	0.53
1:CA:922:G:N3	1:CA:1398:A:H2	2.05	0.53
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.72	0.53
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.26	0.53
25:DA:2274:A:O2'	25:DA:2276:G:OP1	2.22	0.53
25:DA:2305:A:H5''	30:DG:134:GLY:HA3	1.91	0.53
38:DS:35:ILE:HD12	38:DS:101:LEU:HD12	1.89	0.53
44:DY:1:MET:HG2	44:DY:2:ARG:H	1.73	0.53
1:AA:56:U:H2'	1:AA:57:G:H8	1.72	0.53
1:AA:1456:G:H22	20:AT:43:LEU:HD11	1.73	0.53
1:AA:1493:A:H5''	1:AA:1494:G:OP2	2.08	0.53
3:AC:71:ALA:HB2	3:AC:115:LEU:HD21	1.90	0.53
10:AJ:5:ARG:HD3	10:AJ:71:LEU:HD11	1.90	0.53
14:AN:4:LYS:C	14:AN:6:LEU:H	2.15	0.53
24:AY:67:C:H2'	24:AY:68:C:C6	2.42	0.53
27:BD:9:TYR:CZ	27:BD:13:ARG:HG2	2.44	0.53
29:BF:197:ASP:N	29:BF:197:ASP:OD1	2.41	0.53
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.26	0.53
45:BZ:7:ALA:HB3	45:BZ:61:LEU:HD12	1.90	0.53
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.17	0.53
1:CA:153:C:H2'	1:CA:154:C:C6	2.43	0.53
1:CA:937:A:H1'	1:CA:1379:G:N2	2.23	0.53
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.09	0.53
1:CA:1338:G:H21	23:CX:41:C:H1'	1.73	0.53
2:CB:73:THR:HB	2:CB:95:GLN:O	2.08	0.53
2:CB:223:ILE:HA	2:CB:226:ARG:HG2	1.89	0.53
25:DA:18:C:H2'	25:DA:19:C:C6	2.44	0.53
25:DA:692:C:O2'	27:DD:38:LYS:NZ	2.41	0.53
25:DA:903:C:H2'	25:DA:904:C:C6	2.43	0.53
31:DH:56:SER:HB3	31:DH:61:HIS:ND1	2.23	0.53
1:AA:1006:C:H42	1:AA:1023:G:H1	1.57	0.53
25:BA:270:C:H4'	25:BA:271:U:OP1	2.08	0.53
25:BA:596:G:OP2	41:BV:78:LYS:NZ	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:92:SER:O	45:BZ:130:PRO:HG2	2.08	0.53
1:CA:278:G:OP2	17:CQ:41:LYS:NZ	2.37	0.53
1:CA:692:U:O2'	1:CA:694:A:N7	2.33	0.53
1:CA:920:U:H2'	1:CA:921:U:C6	2.44	0.53
1:CA:1292:U:OP2	7:CG:41:ARG:NH2	2.42	0.53
7:CG:113:GLU:HG3	7:CG:118:VAL:HG12	1.89	0.53
25:DA:203:C:OP1	61:DA:4577:HOH:O	2.19	0.53
28:DE:82:ARG:HG2	28:DE:83:ASP:N	2.23	0.53
30:DG:114:ILE:HB	30:DG:117:PHE:HB2	1.90	0.53
31:DH:3:ARG:HB3	31:DH:6:ARG:HG2	1.90	0.53
32:DI:104:GLN:O	32:DI:105:HIS:ND1	2.42	0.53
1:AA:96:U:O2'	1:AA:97:G:H5'	2.09	0.53
1:AA:1095:U:H5''	1:AA:1109:C:O2	2.08	0.53
2:AB:77:ALA:HB2	2:AB:165:VAL:HG11	1.90	0.53
25:BA:2130:C:N4	25:BA:2203:G:H1	2.06	0.53
25:BA:2187:G:H1	25:BA:2194:U:H5	1.56	0.53
2:CB:189:ASP:HB3	2:CB:204:ASN:HA	1.90	0.53
23:CX:21:A:H3'	23:CX:46:G:O6	2.08	0.53
25:DA:2184:G:C2'	25:DA:2185:C:H5'	2.39	0.53
25:DA:2364:C:H2'	25:DA:2365:G:O4'	2.07	0.53
38:DS:34:HIS:O	38:DS:97:ARG:NH2	2.41	0.53
1:AA:950:U:H2'	1:AA:951:G:H8	1.73	0.53
1:AA:1137:C:H4'	1:AA:1138:G:C2	2.42	0.53
25:BA:1361:C:OP2	61:BA:4706:HOH:O	2.19	0.53
25:BA:2776:G:OP2	61:BA:4759:HOH:O	2.17	0.53
44:BY:102:CYS:SG	44:BY:103:GLY:N	2.81	0.53
25:DA:154(A):C:H2'	25:DA:157:U:H5'	1.91	0.53
25:DA:493:G:H2'	25:DA:494:G:O4'	2.08	0.53
25:DA:1266:G:O2'	25:DA:2012:G:O6	2.23	0.53
52:D6:9:LEU:HA	52:D6:54:ILE:HB	1.91	0.53
1:AA:17:U:H2'	1:AA:18:C:C6	2.43	0.53
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.43	0.53
2:AB:71:VAL:HA	2:AB:93:VAL:HG23	1.90	0.53
2:AB:145:LEU:HD12	2:AB:149:LEU:HD12	1.91	0.53
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.41	0.53
16:AP:19:ILE:HG23	16:AP:37:GLY:C	2.33	0.53
19:AS:40:ILE:HD11	19:AS:71:LEU:HD23	1.90	0.53
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.89	0.53
25:BA:2101:U:O3'	47:B1:35:THR:OG1	2.27	0.53
1:CA:97:G:O2'	1:CA:98:G:H5''	2.08	0.53
1:CA:221:C:H2'	1:CA:222:U:H6	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:324:G:N7	61:CA:4062:HOH:O	2.33	0.53
1:CA:1095:U:P	1:CA:1108:G:H1	2.32	0.53
13:CM:88:ARG:HG3	13:CM:98:VAL:HG12	1.90	0.53
19:CS:20:LEU:HD23	19:CS:23:ASN:HD22	1.73	0.53
25:DA:191:A:H2'	25:DA:192:C:C6	2.42	0.53
25:DA:644:A:H4'	25:DA:645:C:C5	2.44	0.53
25:DA:646:A:H2'	25:DA:647:G:O4'	2.08	0.53
25:DA:1688:U:O2	25:DA:1700:A:H5'	2.08	0.53
25:DA:1721:G:H2'	25:DA:1740:G:O6	2.09	0.53
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.22	0.53
25:DA:2751:G:H5'	31:DH:2:SER:HA	1.90	0.53
45:DZ:108:PRO:HG3	45:DZ:141:VAL:HB	1.90	0.53
1:AA:1203:C:H2'	1:AA:1204:A:C8	2.43	0.53
1:AA:1376:U:OP1	7:AG:98:SER:OG	2.23	0.53
19:AS:41:VAL:HG13	19:AS:43:GLU:H	1.74	0.53
27:BD:146:GLU:HB2	27:BD:189:CYS:HB3	1.90	0.53
34:BO:16:ALA:HB2	34:BO:52:VAL:HG21	1.89	0.53
1:CA:328:C:H4'	1:CA:329:A:H5'	1.91	0.53
1:CA:532:A:N6	3:CC:193:TYR:HB3	2.24	0.53
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.08	0.53
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.71	0.53
2:CB:68:ILE:HG12	2:CB:161:ALA:HB3	1.90	0.53
25:DA:400:G:N7	61:DA:4657:HOH:O	2.33	0.53
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.08	0.53
25:DA:902:C:H2'	25:DA:903:C:H6	1.74	0.53
25:DA:1996:C:H4'	25:DA:1997:G:OP1	2.09	0.53
25:DA:2283:C:H2'	25:DA:2284:C:O4'	2.09	0.53
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	1.90	0.53
1:AA:347:G:H2'	1:AA:348:G:O4'	2.09	0.53
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.34	0.53
1:AA:617:G:H4'	16:AP:44:THR:O	2.08	0.53
3:AC:44:GLU:HA	3:AC:52:LEU:HD12	1.91	0.53
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.09	0.53
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.44	0.53
35:BP:63:PRO:HG2	54:B8:25:MET:HB2	1.91	0.53
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.38	0.53
39:BT:65:LYS:HE2	39:BT:67:SER:HB2	1.91	0.53
54:B8:42:ARG:HD2	61:B8:206:HOH:O	2.07	0.53
1:CA:991:U:C4	1:CA:1212:U:H1'	2.44	0.53
2:CB:71:VAL:HB	2:CB:164:VAL:HG13	1.89	0.53
25:DA:27:G:O2'	25:DA:28:A:OP2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:465:G:OP1	53:D7:12:ARG:NH2	2.35	0.53
25:DA:910:A:H62	36:DQ:12:GLN:HA	1.74	0.53
26:DB:20:C:N4	26:DB:63:G:H1	2.05	0.53
28:DE:14:ILE:HG13	28:DE:21:VAL:HG13	1.90	0.53
33:DN:43:THR:N	33:DN:48:MET:SD	2.80	0.53
50:D4:60:GLN:HA	50:D4:62:ARG:HG2	1.90	0.53
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.74	0.53
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.91	0.53
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.34	0.53
47:B1:51:VAL:HG11	47:B1:74:VAL:HG21	1.91	0.53
1:CA:452:A:OP1	16:CP:43:LYS:NZ	2.37	0.53
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.44	0.53
2:CB:84:GLU:HB3	2:CB:219:VAL:HG21	1.91	0.53
23:CX:55:PSU:O2'	23:CX:57:A:N7	2.41	0.53
25:DA:1423:G:H2'	25:DA:1424:G:H8	1.74	0.53
25:DA:1802:A:N1	25:DA:1822:G:H1'	2.24	0.53
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.43	0.53
50:D4:15:ILE:HG23	50:D4:21:VAL:HG22	1.90	0.53
1:AA:997:U:H2'	1:AA:998:G:H8	1.74	0.53
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.08	0.53
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.43	0.53
9:AI:50:LEU:HD13	9:AI:56:LEU:HA	1.90	0.53
25:BA:211:A:H5''	25:BA:448:U:OP1	2.09	0.53
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.09	0.53
25:BA:922:G:H2'	25:BA:923:C:O4'	2.09	0.53
25:BA:1742:G:N7	27:BD:14:ARG:NH2	2.56	0.53
32:BI:43:ASN:HD22	32:BI:43:ASN:C	2.17	0.53
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.09	0.53
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.24	0.53
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.23	0.53
1:CA:1288:A:N3	1:CA:1352:C:O2'	2.40	0.53
2:CB:142:LEU:HA	2:CB:145:LEU:HD12	1.91	0.53
4:CD:165:MET:O	4:CD:167:GLY:N	2.42	0.53
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.09	0.53
25:DA:342:G:O6	61:DA:4680:HOH:O	2.15	0.53
25:DA:999:U:OP2	61:DA:4453:HOH:O	2.19	0.53
25:DA:2227:A:OP2	61:DA:4521:HOH:O	2.19	0.53
25:DA:2556:C:H2'	25:DA:2557:G:O4'	2.09	0.53
28:DE:9:VAL:HG13	28:DE:25:VAL:O	2.08	0.53
29:DF:34:TRP:CE2	35:DP:8:PRO:HG3	2.44	0.53
31:DH:98:LEU:HD12	31:DH:102:ALA:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.09	0.53
1:AA:193:C:H2'	1:AA:194:C:C6	2.43	0.52
1:AA:232:G:H1'	1:AA:262:A:N1	2.25	0.52
1:AA:1392:G:N2	1:AA:1502:A:H8	2.06	0.52
1:CA:1028:C:C4	1:CA:1033:G:O6	2.62	0.52
1:CA:1054:C:H4'	1:CA:1055:A:OP1	2.08	0.52
8:CH:7:ALA:O	8:CH:11:THR:OG1	2.22	0.52
25:DA:527:C:H3'	61:DA:4467:HOH:O	2.08	0.52
25:DA:852:G:H2'	25:DA:853:G:H8	1.72	0.52
25:DA:2704:C:H2'	25:DA:2705:A:O4'	2.09	0.52
28:DE:48:GLN:HA	28:DE:80:GLU:HA	1.91	0.52
30:DG:19:LEU:HD22	30:DG:32:PRO:HG2	1.91	0.52
32:DI:120:ILE:HG21	32:DI:126:TYR:CE2	2.44	0.52
32:DI:128:LEU:O	32:DI:140:LEU:N	2.36	0.52
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.45	0.52
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.41	0.52
1:AA:405:U:O2'	1:AA:496:A:O2'	2.25	0.52
2:AB:10:LEU:C	2:AB:12:GLU:H	2.17	0.52
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.74	0.52
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.91	0.52
23:AX:7:G:H1	23:AX:66:C:H42	1.57	0.52
25:BA:801:C:H2'	25:BA:802:C:H6	1.74	0.52
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.42	0.52
25:BA:2145:G:H1	25:BA:2197:C:N4	2.06	0.52
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.44	0.52
7:CG:20:ASP:HB3	7:CG:23:VAL:HB	1.91	0.52
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.40	0.52
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.44	0.52
25:DA:403:U:H4'	25:DA:404:C:H5'	1.91	0.52
25:DA:1467:C:C5	25:DA:1546:C:H2'	2.45	0.52
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.44	0.52
25:DA:1664:A:OP1	61:DA:4762:HOH:O	2.19	0.52
25:DA:2131:G:N7	25:DA:2133:G:N2	2.58	0.52
25:DA:2815:C:C5'	51:D5:29:THR:HG21	2.39	0.52
41:DV:43:GLU:N	41:DV:43:GLU:OE2	2.43	0.52
1:AA:396:G:O2'	1:AA:398:C:OP1	2.16	0.52
25:BA:236:G:H4'	25:BA:413:G:C5	2.44	0.52
25:BA:2740:G:O2'	34:BO:70:LYS:NZ	2.40	0.52
1:CA:17:U:H2'	1:CA:18:C:C6	2.45	0.52
1:CA:460:G:N2	1:CA:471:G:OP2	2.28	0.52
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1174:G:H2'	1:CA:1175:G:H8	1.74	0.52
2:CB:138:LEU:HA	2:CB:141:GLU:HB3	1.92	0.52
9:CI:8:GLY:O	9:CI:15:ALA:N	2.39	0.52
25:DA:223:A:O2'	25:DA:420:C:O2	2.27	0.52
25:DA:2206:G:H5'	25:DA:2207:G:N7	2.23	0.52
28:DE:170:LEU:HB3	28:DE:184:VAL:HG22	1.92	0.52
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.74	0.52
1:AA:192:U:H2'	1:AA:193:C:C6	2.44	0.52
16:AP:3:LYS:HG2	16:AP:65:GLN:HB2	1.92	0.52
25:BA:1848:G:OP1	27:BD:88:ARG:NH2	2.40	0.52
37:BR:100:LEU:HD11	37:BR:113:LEU:HD23	1.92	0.52
5:CE:78:HIS:CE1	5:CE:143:ARG:H	2.27	0.52
25:DA:2309:A:H61	30:DG:79:ASN:ND2	2.08	0.52
31:DH:137:ASP:HB3	31:DH:140:LYS:HB3	1.92	0.52
1:AA:57:G:H2'	1:AA:58:C:C6	2.45	0.52
1:AA:270:A:H2'	1:AA:271:C:C6	2.44	0.52
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	1.90	0.52
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.24	0.52
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.44	0.52
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.36	0.52
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.24	0.52
44:BY:1:MET:HE3	44:BY:2:ARG:H	1.74	0.52
1:CA:954:G:H21	1:CA:1227:A:H62	1.56	0.52
1:CA:1399:C:C2	1:CA:1502:A:N6	2.77	0.52
25:DA:2473:U:O2	25:DA:2473:U:H2'	2.09	0.52
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.38	0.52
30:DG:43:LEU:C	30:DG:45:GLU:H	2.17	0.52
45:DZ:108:PRO:HB2	45:DZ:111:VAL:HG23	1.90	0.52
48:D2:10:LEU:HD13	48:D2:14:ARG:HH12	1.74	0.52
50:D4:16:CYS:HA	50:D4:33:VAL:HB	1.91	0.52
50:D4:59:PHE:HA	50:D4:60:GLN:C	2.34	0.52
4:AD:168:ARG:CD	4:AD:168:ARG:H	2.23	0.52
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.92	0.52
8:AH:49:GLU:HG2	8:AH:62:TYR:HE1	1.74	0.52
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.43	0.52
30:BG:5:VAL:HG23	30:BG:104:GLU:OE2	2.09	0.52
39:BT:96:ARG:CZ	39:BT:96:ARG:HB3	2.38	0.52
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.73	0.52
25:DA:212:G:H2'	25:DA:213:A:O4'	2.10	0.52
25:DA:236:C:H2'	25:DA:237:C:C6	2.45	0.52
25:DA:2134:A:H2'	25:DA:2135:A:O4'	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:18:ASP:HB3	39:DT:82:LEU:HD21	1.91	0.52
30:DG:33:ARG:O	30:DG:34:LEU:HD23	2.10	0.52
42:DW:12:ILE:O	42:DW:101:SER:OG	2.25	0.52
1:AA:1051:C:H2'	1:AA:1052:U:H6	1.74	0.52
25:BA:934:A:H4'	25:BA:935:C:C5	2.44	0.52
25:BA:1233:U:H4'	41:BV:79:VAL:HG22	1.92	0.52
25:BA:1594:C:H2'	25:BA:1595:C:C6	2.44	0.52
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.45	0.52
25:BA:2235:G:OP1	27:BD:172:TYR:OH	2.22	0.52
45:BZ:24:LEU:HB2	45:BZ:41:LEU:HD23	1.92	0.52
1:CA:975:A:C4'	1:CA:976:G:H5''	2.35	0.52
1:CA:1238:A:OP2	61:CA:4060:HOH:O	2.19	0.52
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.92	0.52
13:CM:6:GLY:O	30:DG:115:ARG:NH2	2.42	0.52
25:DA:1636:C:H2'	25:DA:1637:A:C8	2.45	0.52
25:DA:2371:G:O6	61:DA:4325:HOH:O	2.17	0.52
1:AA:520:A:N1	1:AA:536:C:H1'	2.25	0.52
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.35	0.52
1:AA:1256:A:N6	1:AA:1278:U:O4'	2.40	0.52
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.74	0.52
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	1.92	0.52
25:BA:1814:A:H5'	25:BA:2620:G:H4'	1.92	0.52
1:CA:629:G:H2'	1:CA:630:G:O4'	2.10	0.52
8:CH:28:ALA:HB3	8:CH:57:PRO:HB2	1.91	0.52
25:DA:128:C:H2'	25:DA:129:C:H6	1.74	0.52
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.43	0.52
25:DA:902:C:H2'	25:DA:903:C:C6	2.44	0.52
46:D0:68:GLU:HB2	46:D0:82:ARG:HH11	1.75	0.52
1:AA:501:C:H2'	1:AA:502:G:C8	2.45	0.52
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.92	0.52
25:BA:2123:G:H2'	25:BA:2124:U:C6	2.45	0.52
32:BI:4:ILE:HG12	32:BI:18:VAL:HG22	1.91	0.52
39:BT:112:ARG:HG3	39:BT:115:ARG:HH21	1.74	0.52
1:CA:96:U:O2'	1:CA:97:G:H5'	2.09	0.52
1:CA:422:C:H4'	1:CA:423:G:C4	2.43	0.52
1:CA:688:G:H2'	1:CA:689:C:H6	1.74	0.52
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.25	0.52
1:CA:735:C:H2'	1:CA:736:C:H6	1.75	0.52
1:CA:827:U:H5''	1:CA:828:A:OP2	2.10	0.52
1:CA:922:G:H2'	1:CA:923:A:C8	2.45	0.52
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CS:14:HIS:O	19:CS:18:LYS:HG3	2.10	0.52
25:DA:27:G:N2	25:DA:512:G:H1'	2.24	0.52
25:DA:637:A:H5''	35:DP:117:GLU:HG2	1.92	0.52
25:DA:652(T):C:H2'	25:DA:652(U):G:C8	2.45	0.52
25:DA:1530:C:HO2'	25:DA:1531:C:P	2.33	0.52
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.90	0.52
47:D1:3:LYS:HB2	47:D1:61:ARG:HH12	1.74	0.52
1:AA:439:A:C8	1:AA:439:A:H3'	2.45	0.52
1:AA:600:C:H2'	1:AA:601:C:C6	2.45	0.52
9:AI:23:ASN:HD22	9:AI:25:LYS:HG2	1.75	0.52
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.33	0.52
25:BA:1444:C:OP1	43:BX:53:LYS:NZ	2.40	0.52
30:BG:66:GLN:NE2	30:BG:94:LEU:HD23	2.25	0.52
43:BX:57:LEU:HD11	43:BX:78:LYS:HG2	1.92	0.52
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.43	0.52
2:CB:158:LEU:HD23	2:CB:182:ILE:HD11	1.92	0.52
25:DA:526:A:N3	25:DA:2044:C:H1'	2.25	0.52
25:DA:1264:G:H2'	25:DA:2014:A:N6	2.25	0.52
25:DA:1430:C:H2'	25:DA:1431:U:C6	2.44	0.52
25:DA:2110:G:C2	25:DA:2120:G:H1'	2.44	0.52
39:DT:16:ARG:HH12	39:DT:19:LEU:HG	1.75	0.52
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.92	0.51
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.08	0.51
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.93	0.51
11:AK:99:GLN:HG3	11:AK:105:VAL:HG11	1.91	0.51
45:BZ:45:ASP:O	45:BZ:49:ARG:HG3	2.09	0.51
45:BZ:110:GLY:N	45:BZ:144:LEU:O	2.42	0.51
48:B2:1:MET:HE2	48:B2:6:VAL:HG22	1.91	0.51
1:CA:336:C:H2'	1:CA:337:C:C6	2.45	0.51
1:CA:421:U:O2'	1:CA:423:G:N7	2.43	0.51
1:CA:1165:C:N4	1:CA:1171:G:H1	2.04	0.51
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.44	0.51
8:CH:34:GLU:HB3	8:CH:118:VAL:HG21	1.92	0.51
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.90	0.51
30:DG:64:THR:HB	30:DG:94:LEU:HD21	1.91	0.51
1:AA:1063:C:H3'	1:AA:1064:G:H2'	1.93	0.51
27:BD:26:LYS:HE2	27:BD:28:GLU:O	2.10	0.51
28:BE:21:VAL:HG23	28:BE:185:LYS:HD2	1.93	0.51
42:BW:18:ARG:NH1	42:BW:76:VAL:O	2.43	0.51
1:CA:992:U:H4'	1:CA:993:G:O5'	2.10	0.51
2:CB:221:LEU:HD23	2:CB:224:GLN:NE2	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:32:LEU:O	3:CC:36:ASP:HB2	2.10	0.51
5:CE:81:GLU:HG2	5:CE:90:VAL:HG13	1.92	0.51
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.92	0.51
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.36	0.51
25:DA:686:G:N2	25:DA:788:A:H61	2.08	0.51
25:DA:857:C:H4'	46:D0:23:VAL:HG21	1.92	0.51
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.21	0.51
25:DA:2075:U:OP2	25:DA:2238:G:O2'	2.26	0.51
25:DA:2849:U:P	39:DT:95:ARG:HH12	2.34	0.51
26:DB:3:C:H2'	26:DB:4:C:H6	1.75	0.51
30:DG:137:GLU:HB3	30:DG:139:LEU:HG	1.91	0.51
31:DH:20:ALA:HB3	31:DH:23:ARG:HG3	1.92	0.51
1:AA:192:U:H2'	1:AA:193:C:H6	1.76	0.51
1:AA:1003:G:C2	1:AA:1004:A:N3	2.79	0.51
1:AA:1260:C:O5'	1:AA:1284:C:H4'	2.11	0.51
1:AA:1328:C:OP1	21:AU:21:TYR:OH	2.13	0.51
14:AN:23:ARG:HD2	14:AN:28:GLY:O	2.10	0.51
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.10	0.51
25:BA:27:G:N2	25:BA:537:G:H1'	2.26	0.51
25:BA:174:U:H4'	25:BA:207:A:H4'	1.93	0.51
25:BA:395:C:OP2	61:BA:4985:HOH:O	2.19	0.51
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.46	0.51
32:BI:27:ARG:HD2	47:B1:71:TYR:CZ	2.44	0.51
34:BO:98:VAL:HG13	34:BO:117:LEU:HB3	1.92	0.51
36:BQ:85:LYS:HD3	46:B0:7:LEU:HG	1.92	0.51
1:CA:834:C:H2'	1:CA:835:U:C6	2.45	0.51
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.27	0.51
19:CS:40:ILE:HD12	19:CS:71:LEU:HD12	1.91	0.51
25:DA:309:G:N3	25:DA:329:G:O2'	2.41	0.51
25:DA:323:G:C8	29:DF:171:PRO:HG3	2.45	0.51
25:DA:839:U:H1'	25:DA:1191:G:H1'	1.92	0.51
25:DA:1231:G:H2'	25:DA:1232:G:C8	2.46	0.51
25:DA:2552:U:C2	25:DA:2554:U:H5'	2.46	0.51
1:AA:353:A:H8	1:AA:353:A:H5'	1.75	0.51
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.43	0.51
10:AJ:16:LEU:HD22	10:AJ:68:HIS:HB2	1.93	0.51
11:AK:48:ILE:O	11:AK:50:TYR:N	2.36	0.51
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.09	0.51
36:BQ:30:GLY:HA2	36:BQ:107:ALA:HB2	1.92	0.51
47:B1:3:LYS:HB2	47:B1:61:ARG:NH1	2.25	0.51
1:CA:148:G:H2'	1:CA:149:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.76	0.51
1:CA:992:U:H6	1:CA:992:U:H5'	1.76	0.51
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.28	0.51
2:CB:184:VAL:N	2:CB:198:ASP:OD2	2.28	0.51
12:CL:56:ALA:HB2	12:CL:70:ILE:HD11	1.92	0.51
25:DA:571:A:N6	25:DA:2499:C:O3'	2.43	0.51
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.45	0.51
25:DA:2286:A:H4'	25:DA:2287:A:O4'	2.11	0.51
25:DA:2657:A:O3'	31:DH:160:LYS:NZ	2.42	0.51
33:DN:4:TYR:HB2	40:DU:101:ARG:NH1	2.26	0.51
38:DS:77:ALA:HB1	38:DS:82:ILE:HB	1.93	0.51
41:DV:72:VAL:HG22	41:DV:85:LYS:HB3	1.93	0.51
1:AA:1052:U:H5''	1:AA:1053:G:OP2	2.11	0.51
1:AA:1218:C:OP2	14:AN:9:LYS:NZ	2.33	0.51
25:BA:185:A:N3	25:BA:185:A:H2'	2.26	0.51
25:BA:1410:G:P	47:B1:3:LYS:HG3	2.50	0.51
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.46	0.51
5:CE:137:GLU:HA	5:CE:140:ARG:HB3	1.93	0.51
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.92	0.51
25:DA:1499:C:H2'	25:DA:1500:G:H8	1.76	0.51
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.11	0.51
25:DA:2823:A:OP1	28:DE:159:HIS:NE2	2.40	0.51
47:D1:95:LEU:HD12	47:D1:98:LEU:HD12	1.93	0.51
1:AA:395:C:N4	61:AA:4042:HOH:O	2.43	0.51
1:AA:456:C:H2'	1:AA:457:C:C6	2.46	0.51
1:AA:984:C:N3	1:AA:1221:G:N2	2.50	0.51
1:AA:997:U:H2'	1:AA:998:G:C8	2.45	0.51
1:AA:1125:U:H1'	1:AA:1126:U:H6	1.74	0.51
1:AA:1161:C:O2'	1:AA:1162:C:H5'	2.11	0.51
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.76	0.51
1:CA:991:U:H2'	1:CA:1212:U:C4	2.45	0.51
1:CA:997:U:C2'	1:CA:998:G:H5'	2.40	0.51
9:CI:24:GLY:HA2	9:CI:59:PHE:O	2.11	0.51
10:CJ:54:PHE:O	10:CJ:56:HIS:N	2.37	0.51
18:CR:26:LEU:HD22	18:CR:42:ARG:HE	1.76	0.51
25:DA:839:U:H2'	25:DA:840:C:C6	2.45	0.51
26:DB:75:G:O2'	45:DZ:10:ARG:NH2	2.44	0.51
32:DI:92:VAL:HG23	32:DI:120:ILE:HB	1.91	0.51
1:AA:403:C:O2'	4:AD:122:ARG:NH1	2.43	0.51
1:AA:447:G:O6	1:AA:485:G:O2'	2.23	0.51
1:AA:1004:A:N6	1:AA:1036:G:C5	2.77	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.93	0.51
3:AC:64:VAL:HG13	3:AC:99:VAL:HA	1.92	0.51
25:BA:260:A:N3	25:BA:395:C:O2'	2.38	0.51
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.26	0.51
28:BE:47:VAL:HG23	28:BE:84:PHE:O	2.10	0.51
30:BG:16:ARG:HB2	30:BG:17:PRO:HD3	1.92	0.51
32:BI:4:ILE:HD11	32:BI:44:LEU:HD12	1.93	0.51
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.25	0.51
55:B9:15:LYS:HE2	55:B9:17:ILE:HD13	1.92	0.51
1:CA:954:G:H21	1:CA:1227:A:N6	2.09	0.51
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.19	0.51
1:CA:1402:C:H2'	1:CA:1403:C:O4'	2.11	0.51
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.76	0.51
25:DA:30:G:H2'	25:DA:31:C:C6	2.46	0.51
25:DA:1288:U:C2	25:DA:1327:C:O2	2.64	0.51
35:DP:59:LEU:HD21	54:D8:10:ALA:HA	1.91	0.51
36:DQ:11:LYS:NZ	36:DQ:88:GLY:O	2.33	0.51
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.11	0.51
44:DY:102:CYS:SG	44:DY:103:GLY:N	2.83	0.51
1:AA:576:G:O6	1:AA:880:C:O2'	2.25	0.51
1:AA:946:A:O2'	1:AA:1333:A:N3	2.36	0.51
4:AD:3:ARG:HE	4:AD:118:ARG:HD3	1.76	0.51
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	1.92	0.51
25:BA:2021:C:H5''	25:BA:2736:C:O2'	2.11	0.51
25:BA:2157:A:N6	25:BA:2178:G:O2'	2.36	0.51
25:BA:2402:U:P	54:B8:35:GLN:HE22	2.34	0.51
34:BO:20:MET:HE3	34:BO:44:LYS:HE3	1.93	0.51
50:B4:43:TYR:O	50:B4:45:GLY:N	2.44	0.51
1:CA:447:G:O6	1:CA:485:G:O2'	2.19	0.51
1:CA:964:A:N3	1:CA:969:A:O2'	2.44	0.51
5:CE:57:LYS:HD3	5:CE:61:TYR:HE2	1.75	0.51
25:DA:221:A:C4	25:DA:266:G:N7	2.79	0.51
25:DA:2135:A:N7	25:DA:2136:C:N4	2.58	0.51
25:DA:2142:C:H2'	25:DA:2143:C:O4'	2.11	0.51
30:DG:170:ARG:HH21	30:DG:180:PHE:CB	2.23	0.51
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.43	0.51
1:AA:77:G:H2'	1:AA:78:G:H5'	1.93	0.51
1:AA:864:A:H2'	1:AA:865:A:C8	2.46	0.51
1:AA:918:A:H2'	1:AA:919:A:C8	2.46	0.51
1:AA:1530:G:OP1	1:AA:1530:G:H4'	2.10	0.51
12:AL:77:LEU:HD21	12:AL:107:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:2:ALA:N	13:AM:8:GLU:OE1	2.44	0.51
25:BA:441:C:H2'	25:BA:442:A:C8	2.46	0.51
25:BA:624:C:OP1	29:BF:108:LYS:HE3	2.11	0.51
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.25	0.51
25:BA:2125:C:N4	25:BA:2208:G:H1	2.06	0.51
25:BA:2203:G:O2'	25:BA:2204:G:OP1	2.28	0.51
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.45	0.51
30:BG:33:ARG:O	30:BG:161:THR:HG23	2.11	0.51
45:BZ:69:THR:HG22	45:BZ:90:VAL:HA	1.92	0.51
1:CA:565:U:OP2	1:CA:566:G:O2'	2.29	0.51
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.29	0.51
1:CA:1003:G:N2	1:CA:1025:U:O4	2.43	0.51
1:CA:1262:C:N3	1:CA:1273:G:N2	2.54	0.51
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.44	0.51
32:DI:5:LEU:HD12	32:DI:9:LEU:HD23	1.93	0.51
1:AA:267:C:OP1	17:AQ:67:LYS:HD2	2.11	0.51
1:CA:663:A:O3'	18:CR:64:ARG:NH2	2.38	0.51
1:CA:664:G:P	18:CR:64:ARG:HH21	2.34	0.51
10:CJ:25:GLU:O	10:CJ:29:ARG:HG2	2.11	0.51
25:DA:392:C:H5''	25:DA:409:C:H5''	1.93	0.51
25:DA:484:C:H2'	25:DA:485:C:C6	2.47	0.51
25:DA:623:G:H2'	25:DA:624:C:C6	2.46	0.51
25:DA:2141:G:O6	25:DA:2150:U:O2	2.29	0.51
25:DA:2773:C:OP1	28:DE:166:THR:OG1	2.26	0.51
25:DA:2808:U:C2'	25:DA:2809:A:H5'	2.41	0.51
52:D6:10:LEU:HG	52:D6:54:ILE:HG13	1.93	0.51
1:AA:184:G:H2'	1:AA:185:A:H8	1.76	0.50
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.76	0.50
8:AH:121:ASP:OD2	8:AH:121:ASP:N	2.44	0.50
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.91	0.50
25:BA:505:A:N3	25:BA:507:G:H5''	2.25	0.50
44:BY:5:MET:HE1	44:BY:32:PRO:HA	1.93	0.50
44:BY:35:TYR:CE2	44:BY:69:ALA:HB3	2.46	0.50
51:B5:16:ARG:NH1	51:B5:17:ASP:OD1	2.44	0.50
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.93	0.50
1:CA:735:C:H2'	1:CA:736:C:C6	2.45	0.50
24:CY:72:C:H4'	25:DA:1852:C:H5''	1.93	0.50
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.26	0.50
25:BA:1073:A:C2	25:BA:2500:A:H5'	2.47	0.50
25:BA:1320:A:N3	25:BA:1343:C:H1'	2.26	0.50
25:BA:1634:C:H2'	25:BA:1635:C:H6	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.27	0.50
25:BA:2348:A:H61	46:B0:43:THR:HG21	1.74	0.50
25:BA:2724:U:O2'	25:BA:2726:A:H5'	2.10	0.50
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.26	0.50
3:CC:66:VAL:HB	3:CC:101:LEU:HA	1.94	0.50
13:CM:19:LEU:HD21	13:CM:56:LEU:HD11	1.93	0.50
25:DA:195:A:H61	25:DA:198:C:H3'	1.74	0.50
25:DA:539:G:H2'	25:DA:540:C:H6	1.76	0.50
25:DA:1477:A:H2'	25:DA:1478:G:O4'	2.11	0.50
36:DQ:20:ALA:HA	36:DQ:99:PRO:HD2	1.92	0.50
36:DQ:65:PHE:HB2	36:DQ:105:GLU:HB2	1.92	0.50
1:AA:1226:C:P	13:AM:91:ARG:HH12	2.34	0.50
2:AB:19:HIS:NE2	2:AB:20:GLU:OE2	2.45	0.50
5:AE:152:ARG:HD3	8:AH:42:GLU:O	2.12	0.50
10:AJ:78:ASN:C	10:AJ:80:LYS:H	2.20	0.50
16:AP:57:ARG:NH2	16:AP:79:VAL:O	2.43	0.50
25:BA:298:G:H2'	25:BA:299:G:H8	1.77	0.50
25:BA:876:A:N7	25:BA:2259:A:O2'	2.42	0.50
25:BA:2073:A:H4'	28:BE:141:ILE:HG12	1.94	0.50
25:BA:2490:A:OP2	55:B9:2:LYS:NZ	2.35	0.50
27:BD:145:VAL:HB	27:BD:155:LEU:HB2	1.92	0.50
27:BD:180:GLY:HA3	27:BD:275:LYS:HG3	1.92	0.50
30:BG:161:THR:HG22	30:BG:163:ALA:H	1.75	0.50
35:BP:97:PRO:HD3	35:BP:126:VAL:O	2.11	0.50
25:DA:2750:A:H8	25:DA:2750:A:OP1	1.94	0.50
33:DN:34:LEU:O	33:DN:49:GLY:HA3	2.10	0.50
1:AA:1060:C:OP1	14:AN:45:ARG:NH2	2.40	0.50
1:AA:1174:G:H2'	1:AA:1175:G:C8	2.46	0.50
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.10	0.50
25:BA:2132:G:C2	25:BA:2142:G:H1'	2.46	0.50
25:BA:2230:U:O4'	47:B1:52:ARG:NH2	2.45	0.50
25:BA:2807:C:N4	25:BA:2813:G:H1	2.09	0.50
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.26	0.50
52:B6:11:LEU:HB3	52:B6:49:HIS:HB3	1.93	0.50
1:CA:222:U:H2'	1:CA:223:U:C6	2.46	0.50
1:CA:427:U:OP2	4:CD:36:ARG:NH2	2.45	0.50
1:CA:1119:C:OP1	9:CI:83:ARG:NH1	2.44	0.50
1:CA:1244:C:H42	1:CA:1293:G:H1	1.59	0.50
1:CA:1338:G:H2'	1:CA:1339:A:C8	2.47	0.50
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.46	0.50
25:DA:2012:G:OP1	42:DW:11:ARG:NH2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.77	0.50
32:DI:110:ASP:N	32:DI:130:TYR:OH	2.24	0.50
39:DT:106:SER:O	39:DT:110:ILE:HG13	2.12	0.50
40:DU:81:HIS:HD2	40:DU:84:LYS:HD3	1.77	0.50
42:DW:60:ASN:HD22	42:DW:60:ASN:N	2.10	0.50
1:AA:540:G:H2'	1:AA:541:G:O4'	2.12	0.50
1:AA:664:G:N2	1:AA:741:G:H1	2.06	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.09	0.50
3:AC:124:ILE:HD12	3:AC:196:LEU:HD12	1.94	0.50
39:BT:29:ARG:HG3	39:BT:46:GLU:HB2	1.93	0.50
1:CA:1002:G:N1	1:CA:1038:C:O2	2.41	0.50
2:CB:174:VAL:O	2:CB:178:ARG:HB3	2.10	0.50
9:CI:96:LEU:HD22	9:CI:101:PHE:HB2	1.94	0.50
19:CS:41:VAL:HB	19:CS:44:MET:HE3	1.94	0.50
25:DA:601:C:O2	25:DA:605:C:H4'	2.12	0.50
25:DA:2001:A:H2'	25:DA:2002:G:C8	2.46	0.50
26:DB:8:U:H3	26:DB:113:G:H1	1.60	0.50
26:DB:31:C:H4'	30:DG:29:TRP:CZ2	2.47	0.50
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	1.93	0.50
1:AA:950:U:H2'	1:AA:951:G:C8	2.46	0.50
1:AA:1189:C:P	10:AJ:51:ARG:HH22	2.34	0.50
9:AI:29:ASN:OD1	9:AI:65:VAL:N	2.32	0.50
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.92	0.50
25:BA:241:G:OP1	35:BP:50:ARG:NH1	2.45	0.50
25:BA:1002:A:N1	25:BA:2470:G:H4'	2.27	0.50
25:BA:1698:G:N7	37:BR:11:ASN:ND2	2.60	0.50
25:BA:2166:U:H2'	25:BA:2168:C:H5	1.77	0.50
25:BA:2177:G:H2'	25:BA:2178:G:O4'	2.12	0.50
1:CA:716:A:N3	11:CK:118:GLY:HA2	2.25	0.50
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.93	0.50
1:CA:1362:C:C2'	1:CA:1363:C:H5''	2.42	0.50
3:CC:113:ALA:HB2	3:CC:202:ILE:HG13	1.94	0.50
21:CU:15:ARG:HH11	21:CU:15:ARG:HB2	1.77	0.50
25:DA:422:A:H2'	25:DA:423:A:C8	2.46	0.50
25:DA:455:C:N3	25:DA:472:A:H2'	2.26	0.50
25:DA:783:A:O2'	25:DA:785:G:OP1	2.25	0.50
25:DA:821:A:H2'	25:DA:946:G:H5''	1.92	0.50
25:DA:2169:A:H2'	25:DA:2170:A:C8	2.47	0.50
26:DB:15:A:OP2	26:DB:69:G:N2	2.43	0.50
28:DE:1:MET:HE1	28:DE:199:ARG:HD2	1.94	0.50
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:795:G:O6	42:BW:90:ARG:NH1	2.45	0.50
25:BA:2162:C:O2	25:BA:2162:C:H2'	2.10	0.50
50:B4:59:PHE:CD1	50:B4:59:PHE:N	2.80	0.50
1:CA:1132:C:N4	1:CA:1142:G:H1	2.07	0.50
10:CJ:8:LEU:HD23	10:CJ:96:ILE:HG23	1.93	0.50
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.94	0.50
25:DA:921:G:C6	25:DA:922:U:C4	3.00	0.50
25:DA:1354:A:H2'	25:DA:1355:G:O4'	2.11	0.50
25:DA:2869:G:H2'	25:DA:2870:C:O4'	2.12	0.50
1:AA:473:G:C2'	1:AA:474:G:H5'	2.40	0.50
1:AA:504:C:H2'	1:AA:511:C:H5	1.77	0.50
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.94	0.50
24:AY:75:C:H5''	24:AY:76:A:H5'	1.94	0.50
25:BA:2018:C:H4'	25:BA:2019:G:OP1	2.12	0.50
25:BA:2398:C:H2'	25:BA:2399:U:C6	2.47	0.50
29:BF:18:ARG:HG2	29:BF:19:GLU:H	1.75	0.50
50:B4:63:TYR:N	50:B4:63:TYR:CD1	2.80	0.50
51:B5:11:THR:HG23	51:B5:15:ARG:HB3	1.93	0.50
1:CA:707:C:H2'	1:CA:708:C:C6	2.47	0.50
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.44	0.50
25:DA:253:C:OP2	54:D8:5:LYS:NZ	2.30	0.50
25:DA:2059:A:O2'	29:DF:69:HIS:HD2	1.95	0.50
30:DG:28:VAL:O	30:DG:31:VAL:HG12	2.12	0.50
1:AA:438:G:O2'	1:AA:494:U:O4	2.29	0.50
1:AA:461:A:O2'	1:AA:470:C:H5'	2.12	0.50
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.94	0.50
25:BA:559:U:H2'	25:BA:560:C:C6	2.47	0.50
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.27	0.50
25:BA:2169:G:H2'	25:BA:2170:G:O4'	2.12	0.50
39:BT:108:ARG:HH22	39:BT:112:ARG:NH1	2.09	0.50
55:B9:25:VAL:HB	55:B9:34:GLN:HB2	1.92	0.50
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.45	0.50
1:CA:1119:C:N4	1:CA:1154:G:H1	2.05	0.50
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.94	0.50
11:CK:62:GLN:HG3	11:CK:97:ALA:HB2	1.92	0.50
23:CX:48:C:C2	23:CX:59:A:H1'	2.47	0.50
25:DA:61:G:H5'	48:D2:50:ILE:HG21	1.94	0.50
25:DA:817:C:H2'	25:DA:818:G:O4'	2.12	0.50
25:DA:1184:G:OP1	49:D3:30:ARG:HD2	2.11	0.50
25:DA:1528(A):A:H2'	25:DA:1529:G:O4'	2.11	0.50
25:DA:1590:U:H2'	25:DA:1591:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DB:3:C:H2'	26:DB:4:C:C6	2.47	0.50
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.47	0.50
1:AA:598:U:H4'	8:AH:94:TYR:CD2	2.47	0.49
25:BA:1535:U:HO2'	25:BA:1536:A:H8	1.60	0.49
1:CA:429:U:H1'	1:CA:430:A:H5''	1.93	0.49
1:CA:620:C:H2'	1:CA:621:A:O4'	2.12	0.49
1:CA:953:G:H5'	1:CA:965:A:N6	2.23	0.49
1:CA:1037:C:O5'	1:CA:1037:C:H6	1.95	0.49
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	1.93	0.49
19:CS:23:ASN:HA	19:CS:27:GLU:CD	2.37	0.49
23:CX:61:C:H2'	23:CX:62:C:H6	1.76	0.49
25:DA:100:G:O2'	48:D2:7:ARG:NH2	2.43	0.49
25:DA:528:A:C2	25:DA:2042:A:H2'	2.47	0.49
30:DG:173:LEU:HB3	30:DG:178:PHE:CD1	2.47	0.49
31:DH:30:LYS:HG3	31:DH:80:SER:O	2.12	0.49
39:DT:22:PHE:CE2	39:DT:52:ILE:HD11	2.47	0.49
47:D1:3:LYS:HB2	47:D1:61:ARG:NH1	2.26	0.49
1:AA:1213:A:O2'	1:AA:1215:G:N7	2.34	0.49
4:AD:102:ASP:OD2	4:AD:118:ARG:NH1	2.44	0.49
4:AD:107:ARG:NH2	4:AD:194:LEU:HD22	2.17	0.49
25:BA:2549:U:H2'	25:BA:2550:C:C6	2.48	0.49
1:CA:64:G:H4'	1:CA:65:U:H3'	1.94	0.49
1:CA:297:G:N2	1:CA:300:A:OP2	2.43	0.49
1:CA:839:U:H3'	1:CA:840:C:C6	2.46	0.49
1:CA:1407:C:O2'	25:DA:1912:A:N1	2.43	0.49
6:CF:4:TYR:HD1	6:CF:92:LYS:HA	1.77	0.49
25:DA:1667:G:O2'	25:DA:1991:U:O4	2.24	0.49
25:DA:1772:G:OP1	61:DA:4511:HOH:O	2.19	0.49
25:DA:2166:G:H5'	25:DA:2167:U:OP2	2.12	0.49
25:DA:2355:C:O3'	46:D0:24:LYS:HD2	2.11	0.49
45:DZ:54:HIS:CG	45:DZ:101:PRO:HG3	2.46	0.49
1:AA:191:G:N2	20:AT:103:GLY:HA2	2.27	0.49
1:AA:662:G:H2'	1:AA:663:A:C8	2.47	0.49
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.94	0.49
1:AA:818:G:HO2'	1:AA:820:U:H6	1.59	0.49
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.93	0.49
25:BA:768:C:H2'	25:BA:769:A:C8	2.47	0.49
1:CA:420:U:O2'	1:CA:423:G:O6	2.26	0.49
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.48	0.49
1:CA:1258:G:H21	1:CA:1279:A:H62	1.60	0.49
25:DA:1197:G:H2'	25:DA:1198:U:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1363:C:O2'	25:DA:1809:A:N3	2.43	0.49
25:DA:1581:G:H2'	25:DA:1582:C:O4'	2.12	0.49
25:DA:2637:U:H5''	28:DE:82:ARG:NH2	2.27	0.49
32:DI:130:TYR:HD2	32:DI:138:ILE:HD12	1.77	0.49
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.27	0.49
1:AA:16:A:O2'	5:AE:16:THR:HB	2.13	0.49
1:AA:1075:C:H2'	1:AA:1076:C:H5'	1.93	0.49
24:AY:71:G:H2'	24:AY:72:C:C6	2.48	0.49
25:BA:18:C:O2'	25:BA:577:U:OP1	2.26	0.49
25:BA:2152:U:H2'	25:BA:2153:G:N2	2.27	0.49
31:BH:144:VAL:O	31:BH:148:ILE:HG13	2.13	0.49
1:CA:532:A:H61	3:CC:193:TYR:CB	2.24	0.49
1:CA:863:U:O2'	1:CA:865:A:N7	2.39	0.49
1:CA:937:A:H1'	1:CA:1379:G:H22	1.78	0.49
1:CA:1029:C:N3	1:CA:1032:G:C2	2.81	0.49
1:CA:1052:U:H5''	1:CA:1053:G:OP2	2.13	0.49
2:CB:55:PHE:O	2:CB:59:GLU:N	2.35	0.49
2:CB:95:GLN:HB2	2:CB:148:TYR:HD1	1.77	0.49
13:CM:106:ASN:OD1	13:CM:106:ASN:N	2.44	0.49
25:DA:39:C:H2'	25:DA:40:C:C6	2.47	0.49
25:DA:2394:C:OP2	54:D8:30:ARG:NH1	2.45	0.49
27:DD:28:GLU:OE1	61:DD:413:HOH:O	2.19	0.49
36:DQ:37:LEU:HD11	36:DQ:130:LYS:HB2	1.94	0.49
1:AA:713:G:H2'	1:AA:714:G:C8	2.47	0.49
1:AA:1027:C:O2	1:AA:1034:G:N1	2.45	0.49
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.34	0.49
19:AS:41:VAL:HG22	19:AS:42:PRO:HD2	1.95	0.49
25:BA:904:C:N4	25:BA:905:U:O4	2.46	0.49
1:CA:1028:C:O2	1:CA:1033:G:N1	2.45	0.49
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.47	0.49
25:DA:82:G:N1	25:DA:103:A:OP2	2.42	0.49
25:DA:606:U:H4'	25:DA:658:C:H4'	1.95	0.49
25:DA:709:U:H2'	25:DA:710:G:C8	2.47	0.49
25:DA:2035:G:OP1	61:DA:4476:HOH:O	2.19	0.49
26:DB:33:G:C6	26:DB:34:U:C4	3.01	0.49
29:DF:184:TYR:CE1	35:DP:3:LEU:HD21	2.48	0.49
36:DQ:57:HIS:NE2	36:DQ:116:GLU:HB3	2.28	0.49
37:DR:72:ASP:OD2	37:DR:75:LEU:HB2	2.11	0.49
1:AA:741:G:H2'	1:AA:742:G:O4'	2.13	0.49
1:AA:743:U:H2'	1:AA:744:C:C6	2.48	0.49
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:20:GLU:HB3	2:AB:190:THR:OG1	2.12	0.49
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.13	0.49
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.42	0.49
25:BA:305:G:H1'	25:BA:384:G:N2	2.27	0.49
25:BA:1153:G:N3	25:BA:1153:G:H2'	2.28	0.49
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.95	0.49
25:BA:2157:A:H61	25:BA:2178:G:C2'	2.26	0.49
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.47	0.49
1:CA:950:U:H2'	1:CA:951:G:H8	1.78	0.49
10:CJ:38:ILE:HG12	10:CJ:71:LEU:O	2.13	0.49
23:CX:76:A:H3'	25:DA:2585:U:C5	2.47	0.49
25:DA:745:G:O6	61:DA:4342:HOH:O	2.19	0.49
25:DA:2787:C:H1'	28:DE:62:PRO:HG3	1.93	0.49
35:DP:88:LEU:HD11	35:DP:114:ILE:HD12	1.93	0.49
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.49
1:AA:589:C:H2'	1:AA:590:C:H5'	1.95	0.49
1:AA:839:U:H3'	1:AA:840:C:C5	2.47	0.49
1:AA:839:U:HO2'	1:AA:840:C:P	2.32	0.49
3:AC:42:LEU:O	3:AC:46:GLU:HG2	2.13	0.49
25:BA:225:C:H2'	25:BA:226:C:C6	2.48	0.49
25:BA:2008:A:OP1	61:BA:4484:HOH:O	2.20	0.49
25:BA:2202:U:H2'	25:BA:2203:G:O4'	2.12	0.49
25:BA:2624:C:OP2	51:B5:2:ALA:N	2.46	0.49
29:BF:29:ASN:H	29:BF:112:MET:CE	2.24	0.49
44:BY:15:VAL:HG21	44:BY:42:VAL:HG11	1.93	0.49
49:B3:29:ARG:N	49:B3:33:GLN:OE1	2.43	0.49
50:B4:46:GLN:N	50:B4:46:GLN:HE21	2.10	0.49
1:CA:189(K):U:H2'	1:CA:189(L):G:C8	2.47	0.49
1:CA:820:U:H4'	1:CA:821:G:OP2	2.13	0.49
1:CA:1106:G:H5''	3:CC:172:ARG:HG2	1.94	0.49
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.95	0.49
3:CC:125:GLU:HG3	3:CC:190:ARG:O	2.12	0.49
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.12	0.49
25:DA:112:U:H2'	25:DA:113:G:O4'	2.13	0.49
25:DA:297:C:H2'	25:DA:298:G:O4'	2.12	0.49
25:DA:800:A:H8	25:DA:800:A:OP1	1.95	0.49
25:DA:1759:A:H4'	25:DA:2715:C:O4'	2.13	0.49
25:DA:2001:A:OP1	37:DR:9:LYS:NZ	2.45	0.49
25:DA:2329:G:N2	46:D0:41:ARG:HB3	2.28	0.49
31:DH:118:PRO:HG2	31:DH:121:ILE:HG13	1.95	0.49
33:DN:111:PRO:HA	33:DN:114:ARG:NH1	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:258:G:H2'	1:AA:259:G:H8	1.78	0.49
1:AA:454:C:OP1	16:AP:75:ARG:NH2	2.45	0.49
1:AA:1262:C:H2'	1:AA:1263:C:H6	1.78	0.49
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.45	0.49
25:BA:1219:A:H1'	25:BA:1220:U:C5'	2.43	0.49
25:BA:1232:G:H5''	41:BV:81:TYR:CE1	2.48	0.49
25:BA:1553:A:O2'	25:BA:1554:A:O4'	2.31	0.49
25:BA:2860:A:OP2	25:BA:2876:U:H5	1.96	0.49
30:BG:44:GLY:N	30:BG:88:ILE:O	2.45	0.49
36:BQ:118:LEU:HB2	36:BQ:131:ILE:HD13	1.95	0.49
1:CA:441:A:H3'	1:CA:442:C:C6	2.48	0.49
1:CA:627:G:H2'	1:CA:628:G:C8	2.46	0.49
1:CA:1119:C:N3	1:CA:1154:G:N2	2.61	0.49
1:CA:1122:U:H2'	1:CA:1123:A:C8	2.48	0.49
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.48	0.49
3:CC:98:ASN:O	3:CC:100:ALA:N	2.46	0.49
10:CJ:20:ALA:HB1	10:CJ:37:PRO:HB3	1.94	0.49
20:CT:56:MET:HE1	20:CT:85:MET:HA	1.95	0.49
25:DA:1359:A:N1	25:DA:1372:U:C4	2.80	0.49
25:DA:1864:U:OP1	25:DA:2410:G:O2'	2.28	0.49
25:DA:2417:C:OP1	35:DP:65:ARG:NH2	2.44	0.49
32:DI:14:ASP:N	32:DI:17:GLN:OE1	2.43	0.49
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.47	0.49
45:DZ:138:GLU:H	45:DZ:156:LYS:HZ1	1.59	0.49
53:D7:24:THR:O	53:D7:28:ARG:HG3	2.12	0.49
1:AA:792:A:O2'	1:AA:794:A:N7	2.42	0.49
2:AB:24:TRP:CZ3	2:AB:26:PRO:HA	2.48	0.49
6:AF:81:ILE:HD11	27:BD:125:ILE:HB	1.94	0.49
23:AX:47:U:H5'	23:AX:48:C:H5'	1.95	0.49
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.45	0.49
25:BA:1874:C:H5'	27:BD:253:GLN:HE22	1.76	0.49
1:CA:35:G:H2'	1:CA:36:C:C6	2.47	0.49
1:CA:218:C:C2'	1:CA:219:C:H5'	2.43	0.49
1:CA:537:G:H2'	1:CA:538:G:C8	2.47	0.49
1:CA:1427:U:H2'	1:CA:1428:A:C8	2.48	0.49
2:CB:94:ASN:HB3	2:CB:95:GLN:NE2	2.27	0.49
3:CC:54:ARG:HG3	3:CC:69:HIS:HB2	1.95	0.49
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.94	0.49
8:CH:121:ASP:N	8:CH:121:ASP:OD1	2.43	0.49
9:CI:128:ARG:NH2	23:CX:33:U:OP2	2.46	0.49
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:143:G:H2'	25:DA:143(A):C:C6	2.48	0.49
25:DA:468:G:N7	53:D7:39:ARG:NH2	2.56	0.49
25:DA:807:U:O2'	25:DA:2060:A:N1	2.42	0.49
25:DA:1508:A:H5'	25:DA:1509(A):A:N7	2.28	0.49
25:DA:1608:A:H1'	25:DA:1610:A:OP2	2.12	0.49
25:DA:1889:A:N1	25:DA:2234:G:H1'	2.28	0.49
47:D1:91:LYS:HG2	47:D1:95:LEU:HD22	1.95	0.49
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.95	0.49
1:AA:1048:G:OP1	14:AN:3:ARG:HB3	2.13	0.49
1:AA:1095:U:OP1	1:AA:1108:G:N2	2.45	0.49
1:AA:1289:A:N1	1:AA:1371:G:O2'	2.46	0.49
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.27	0.49
1:CA:194:C:H2'	1:CA:195:A:H5''	1.94	0.49
1:CA:520:A:N1	1:CA:536:C:H1'	2.28	0.49
1:CA:742:G:OP1	15:CO:35:ARG:NH2	2.46	0.49
1:CA:838:G:H1	1:CA:848:C:H42	1.60	0.49
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.48	0.49
1:CA:1375:A:O2'	7:CG:29:LYS:NZ	2.44	0.49
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.78	0.49
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.13	0.49
25:DA:1865:G:N2	25:DA:1877:A:OP2	2.43	0.49
25:DA:2094:G:OP1	32:DI:22:LYS:HD2	2.13	0.49
25:DA:2103:C:H2'	25:DA:2104:G:O4'	2.12	0.49
28:DE:179:GLU:HB3	28:DE:181:LEU:HD22	1.94	0.49
31:DH:73:ALA:O	31:DH:76:VAL:HG12	2.13	0.49
32:DI:88:ILE:HG12	32:DI:123:LEU:HD13	1.94	0.49
1:AA:501:C:H2'	1:AA:502:G:H8	1.78	0.48
1:AA:539:A:H2'	1:AA:540:G:C8	2.47	0.48
1:AA:715:A:H2'	1:AA:716:A:C8	2.47	0.48
1:AA:1172:C:H2'	1:AA:1173:G:C8	2.44	0.48
1:AA:1260:C:OP1	1:AA:1284:C:O2'	2.31	0.48
1:AA:1369:C:H2'	1:AA:1370:G:C8	2.48	0.48
2:AB:78:GLN:O	2:AB:94:ASN:ND2	2.46	0.48
24:AY:4:C:H5'	25:BA:1907:A:H5''	1.95	0.48
25:BA:553:A:N1	25:BA:2064:A:H2'	2.28	0.48
25:BA:1272:A:OP1	41:BV:84:LYS:HE2	2.13	0.48
25:BA:2377:G:O6	54:B8:39:LYS:HE3	2.13	0.48
25:BA:2772:G:N7	61:BA:4232:HOH:O	2.35	0.48
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.43	0.48
32:BI:100:ALA:HA	32:BI:103:ARG:HD2	1.95	0.48
1:CA:427:U:O2'	1:CA:541:G:OP1	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:91:PRO:HG2	2:CB:155:LEU:HD23	1.95	0.48
25:DA:880:G:H2'	25:DA:881:G:H5'	1.95	0.48
25:DA:2121:G:H1	25:DA:2177:C:N4	2.08	0.48
3:AC:43:LEU:HD21	3:AC:91:LEU:HD13	1.95	0.48
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.78	0.48
12:AL:84:LEU:HB2	12:AL:105:TYR:CE2	2.48	0.48
25:BA:909:G:H2'	25:BA:910:A:O4'	2.13	0.48
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.78	0.48
25:BA:1879:A:H2'	25:BA:1880:G:H8	1.78	0.48
27:BD:108:PRO:HG2	27:BD:111:LEU:HG	1.94	0.48
50:B4:57:GLU:HB3	50:B4:58:ARG:HA	1.95	0.48
51:B5:5:PRO:O	61:B5:4001:HOH:O	2.20	0.48
1:CA:444:C:H2'	1:CA:445:G:C8	2.47	0.48
25:DA:1591:G:H2'	25:DA:1592:C:C6	2.47	0.48
25:DA:1798:U:H5'	27:DD:259:THR:CG2	2.38	0.48
25:DA:2695:C:H2'	25:DA:2696:U:C6	2.48	0.48
26:DB:73:A:C4	26:DB:105:A:C2	3.00	0.48
29:DF:20:LEU:HA	29:DF:20:LEU:HD23	1.67	0.48
32:DI:77:LEU:HD12	32:DI:140:LEU:HD11	1.94	0.48
38:DS:10:ARG:HH21	38:DS:91:PRO:HB2	1.78	0.48
1:AA:1039:C:H2'	1:AA:1040:U:H6	1.78	0.48
1:AA:1304:G:C6	1:AA:1305:G:N1	2.81	0.48
25:BA:886:U:H2'	25:BA:887:C:C6	2.49	0.48
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.47	0.48
25:BA:2509:A:H5''	61:BA:4109:HOH:O	2.12	0.48
31:BH:24:VAL:HG22	31:BH:35:VAL:HB	1.94	0.48
1:CA:359:U:H2'	1:CA:360:A:C8	2.48	0.48
1:CA:628:G:C2'	1:CA:629:G:H5'	2.42	0.48
3:CC:39:ILE:HG23	3:CC:91:LEU:HD11	1.94	0.48
25:DA:1462:C:H4'	25:DA:2703:C:H5'	1.95	0.48
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.48	0.48
35:DP:38:GLN:O	35:DP:39:LYS:HB3	2.14	0.48
1:AA:166:G:H2'	1:AA:167:G:C8	2.48	0.48
1:AA:977:A:H1'	1:AA:982:U:O4	2.14	0.48
1:AA:1121:U:C2'	1:AA:1122:U:H5'	2.44	0.48
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.78	0.48
13:AM:29:ARG:HD3	13:AM:64:TRP:CD2	2.49	0.48
25:BA:186:A:N6	25:BA:2442:A:O2'	2.46	0.48
25:BA:721:G:O2'	29:BF:74:ARG:HD3	2.14	0.48
25:BA:895:G:O6	25:BA:974:G:H2'	2.14	0.48
25:BA:895:G:N3	25:BA:978:A:H1'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1091:A:OP1	25:BA:1092:A:H3'	2.14	0.48
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.14	0.48
45:BZ:105:VAL:O	45:BZ:140:ASP:HA	2.14	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.02	0.48
1:CA:1262:C:O2'	1:CA:1263:C:H5'	2.13	0.48
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	1.95	0.48
4:CD:78:LEU:HD22	4:CD:96:LEU:HB3	1.96	0.48
25:DA:625:G:N7	35:DP:107:LYS:NZ	2.51	0.48
25:DA:863:A:OP1	36:DQ:22:LYS:HG3	2.13	0.48
25:DA:994:C:H1'	41:DV:10:LYS:HE3	1.94	0.48
25:DA:1364:G:OP2	47:D1:3:LYS:HG3	2.13	0.48
25:DA:2006:C:O5'	25:DA:2006:C:H6	1.95	0.48
25:DA:2276:G:H5'	36:DQ:86:GLY:HA2	1.96	0.48
25:DA:2531:A:N3	25:DA:2658:C:O2'	2.43	0.48
37:DR:2:ARG:NH1	37:DR:5:LYS:O	2.44	0.48
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.51	0.48
54:D8:22:VAL:HG12	54:D8:50:LEU:HD12	1.94	0.48
1:AA:909:A:H2'	1:AA:910:C:O4'	2.14	0.48
3:AC:164:ARG:HD2	3:AC:166:GLU:HG2	1.95	0.48
15:AO:82:ILE:HD11	15:AO:88:ARG:HH11	1.77	0.48
25:BA:1411:A:OP2	47:B1:3:LYS:HG2	2.13	0.48
25:BA:1800:G:O2'	25:BA:1980:C:OP1	2.26	0.48
25:BA:2087:C:H2'	25:BA:2088:C:C6	2.48	0.48
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.13	0.48
50:B4:61:ARG:HG3	50:B4:62:ARG:N	2.27	0.48
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.14	0.48
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.95	0.48
2:CB:27:LYS:HD3	2:CB:193:ASP:OD1	2.14	0.48
25:DA:271(P):C:H2'	25:DA:271(Q):G:O4'	2.13	0.48
25:DA:570:G:H5''	61:DA:4155:HOH:O	2.13	0.48
25:DA:705:A:H2'	25:DA:706:A:O4'	2.14	0.48
25:DA:2161:C:H2'	25:DA:2162:G:C8	2.47	0.48
25:DA:2369:A:H2'	25:DA:2370:G:C8	2.48	0.48
25:DA:2557:G:H2'	25:DA:2558:C:H6	1.79	0.48
29:DF:117:ARG:NH2	29:DF:189:THR:O	2.46	0.48
30:DG:105:LYS:NZ	30:DG:143:GLU:OE2	2.47	0.48
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	1.96	0.48
34:DO:63:VAL:HG11	34:DO:85:VAL:HG23	1.96	0.48
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.46	0.48
36:DQ:68:ILE:HG23	36:DQ:103:MET:HA	1.95	0.48
1:AA:429:U:H1'	1:AA:430:A:H5''	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.79	0.48
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.79	0.48
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.95	0.48
5:AE:11:ILE:HB	5:AE:31:LEU:HB3	1.96	0.48
25:BA:116:A:OP1	53:B7:22:MET:HE2	2.13	0.48
25:BA:287:G:N7	25:BA:448:U:H2'	2.29	0.48
25:BA:354:A:HO2'	25:BA:355:A:H8	1.59	0.48
25:BA:390:G:H2'	25:BA:391:G:C8	2.49	0.48
25:BA:2650:G:OP1	28:BE:82:ARG:NH2	2.46	0.48
25:BA:2858:G:H8	39:BT:97:ALA:HB2	1.78	0.48
27:BD:10:THR:OG1	27:BD:13:ARG:HB2	2.14	0.48
31:BH:124:GLU:HB2	31:BH:132:ARG:HB3	1.95	0.48
1:CA:299:G:H2'	1:CA:300:A:C8	2.49	0.48
1:CA:434:U:H2'	1:CA:435:C:C6	2.49	0.48
7:CG:47:CYS:HA	7:CG:50:ILE:HG12	1.95	0.48
19:CS:20:LEU:HA	19:CS:23:ASN:HB2	1.95	0.48
25:DA:8:A:H2'	25:DA:9:U:H6	1.78	0.48
25:DA:857:C:H1'	46:D0:26:TYR:CE1	2.49	0.48
25:DA:1378:A:OP1	53:D7:10:ARG:NH2	2.47	0.48
25:DA:1429:G:H2'	25:DA:1430:C:C6	2.48	0.48
25:DA:1939:U:OP1	25:DA:2604:U:O2'	2.32	0.48
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.47	0.48
31:DH:27:LYS:NZ	31:DH:32:GLU:OE2	2.41	0.48
53:D7:9:ARG:HE	53:D7:47:ARG:HG3	1.78	0.48
1:AA:97:G:O2'	1:AA:98:G:H8	1.96	0.48
1:AA:175:C:H2'	1:AA:176:C:H6	1.79	0.48
1:AA:389:A:H2'	1:AA:389:A:N3	2.29	0.48
1:AA:688:G:H2'	1:AA:689:C:C6	2.49	0.48
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.02	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.49	0.48
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.13	0.48
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.77	0.48
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.13	0.48
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.28	0.48
23:AX:21:A:H5'	23:AX:22:G:OP1	2.13	0.48
25:BA:223:C:H2'	25:BA:224:U:H6	1.79	0.48
25:BA:927:G:H2'	25:BA:928:G:H8	1.79	0.48
25:BA:1495:G:H4'	25:BA:1589:A:OP1	2.13	0.48
25:BA:2186:C:H5	25:BA:2187:G:N3	2.12	0.48
25:BA:2760:G:O6	25:BA:2768:C:H5''	2.12	0.48
29:BF:164:ARG:O	29:BF:168:ARG:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BZ:150:LEU:O	45:BZ:171:ILE:HG13	2.13	0.48
50:B4:56:VAL:HG23	50:B4:57:GLU:HG3	1.95	0.48
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.48	0.48
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.96	0.48
1:CA:1493:A:H8	25:DA:1913:A:N1	2.12	0.48
1:CA:1494:G:N2	25:DA:1912:A:N3	2.61	0.48
57:CA:3176:PCY:H181	57:CA:3176:PCY:H8	1.55	0.48
3:CC:125:GLU:N	3:CC:125:GLU:OE2	2.46	0.48
25:DA:938:G:OP1	54:D8:52:LYS:HD2	2.14	0.48
25:DA:1288:U:O4	37:DR:106:GLY:HA3	2.14	0.48
25:DA:1637:A:H4'	25:DA:2711:A:O2'	2.14	0.48
25:DA:2776:A:H4'	25:DA:2777:G:H5''	1.95	0.48
25:DA:2809:A:H2'	25:DA:2810:A:C8	2.49	0.48
27:DD:3:VAL:HG13	27:DD:17:THR:HB	1.94	0.48
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.95	0.48
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	1.96	0.48
1:AA:153:C:H42	1:AA:169:C:N4	2.12	0.48
1:AA:495:A:N3	1:AA:496:A:C8	2.82	0.48
2:AB:81:VAL:HG12	2:AB:215:LEU:HD11	1.95	0.48
7:AG:149:ARG:HD2	11:AK:59:TYR:CE1	2.49	0.48
25:BA:155:C:OP2	25:BA:155:C:H6	1.97	0.48
25:BA:715:G:H5'	25:BA:716:G:OP2	2.13	0.48
25:BA:999:G:H5''	36:BQ:13:GLN:HB3	1.95	0.48
26:BB:14:U:OP2	26:BB:70:C:O2'	2.32	0.48
26:BB:28:C:H5''	38:BS:31:SER:HB3	1.95	0.48
37:BR:55:ALA:HB2	37:BR:79:LEU:HD13	1.96	0.48
42:BW:51:LEU:HD23	42:BW:105:VAL:HG11	1.95	0.48
1:CA:302:G:N3	1:CA:556:C:H4'	2.29	0.48
1:CA:918:A:H2'	1:CA:919:A:C8	2.49	0.48
1:CA:1036:G:H3'	1:CA:1037:C:C6	2.49	0.48
2:CB:166:ASP:HB3	2:CB:169:LYS:HB3	1.94	0.48
4:CD:74:GLN:NE2	4:CD:137:SER:OG	2.47	0.48
25:DA:530:G:N1	61:DA:4457:HOH:O	2.17	0.48
25:DA:2815:C:H2'	25:DA:2816:C:C6	2.49	0.48
27:DD:73:VAL:HG13	27:DD:120:GLY:HA3	1.96	0.48
28:DE:11:MET:HG2	28:DE:24:THR:HB	1.95	0.48
37:DR:1:MET:HE3	37:DR:3:HIS:CE1	2.49	0.48
1:AA:921:U:O2	5:AE:19:MET:HB2	2.12	0.48
13:AM:9:ILE:HB	13:AM:18:ALA:HB1	1.96	0.48
25:BA:275:C:H2'	25:BA:276:C:C6	2.48	0.48
25:BA:1954:A:H2'	25:BA:1955:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2818:U:H5''	25:BA:2900:G:O6	2.14	0.48
30:BG:66:GLN:HG3	50:B4:1:MET:CE	2.44	0.48
35:BP:107:LYS:O	35:BP:110:TYR:HB2	2.13	0.48
36:BQ:1:MET:SD	36:BQ:1:MET:N	2.82	0.48
37:BR:22:ARG:NE	37:BR:69:ASP:OD1	2.41	0.48
54:B8:6:THR:HG22	54:B8:63:PRO:HD2	1.95	0.48
1:CA:539:A:H2'	1:CA:540:G:C8	2.48	0.48
1:CA:1057:G:C2'	1:CA:1058:G:H5'	2.44	0.48
1:CA:1095:U:H5''	1:CA:1109:C:O2	2.14	0.48
1:CA:1122:U:C4	1:CA:1123:A:N7	2.81	0.48
3:CC:181:ASN:HD21	3:CC:204:LEU:HD12	1.77	0.48
25:DA:642:G:H21	25:DA:646:A:H2	1.60	0.48
25:DA:1796:U:H2'	25:DA:1797:C:H6	1.78	0.48
25:DA:2745:C:C4	25:DA:2746:U:C4	3.02	0.48
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.79	0.48
2:AB:76:GLN:CD	2:AB:76:GLN:H	2.22	0.48
3:AC:157:ILE:HD12	3:AC:164:ARG:HB3	1.96	0.48
5:AE:77:PRO:HD2	5:AE:142:LEU:HD22	1.95	0.48
25:BA:197:C:H2'	25:BA:198:C:C6	2.49	0.48
25:BA:482:C:H4'	61:BA:4029:HOH:O	2.14	0.48
25:BA:661:G:OP1	35:BP:132:LYS:HE2	2.13	0.48
25:BA:2101:U:OP1	47:B1:21:ARG:NH2	2.47	0.48
48:B2:32:LEU:HD13	48:B2:36:ARG:NH1	2.29	0.48
1:CA:600:C:H2'	1:CA:601:C:C6	2.49	0.48
1:CA:911:U:H2'	1:CA:912:C:C6	2.49	0.48
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.40	0.48
19:CS:3:ARG:HH22	19:CS:10:PHE:HD2	1.61	0.48
25:DA:911:A:H2'	36:DQ:9:TYR:OH	2.13	0.48
25:DA:1290:C:H2'	25:DA:1291:C:H6	1.79	0.48
25:DA:1899:G:O2'	25:DA:1900:A:OP2	2.29	0.48
25:DA:2647:U:H2'	25:DA:2648:C:C6	2.49	0.48
25:DA:2680:C:OP2	28:DE:111:ARG:NH2	2.47	0.48
28:DE:12:THR:HG22	39:DT:58:ASN:OD1	2.14	0.48
30:DG:3:LEU:HD12	30:DG:5:VAL:HG12	1.95	0.48
45:DZ:7:ALA:HB3	45:DZ:61:LEU:HD12	1.96	0.48
1:AA:911:U:H2'	1:AA:912:C:C6	2.49	0.47
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.96	0.47
19:AS:9:VAL:HG11	50:B4:61:ARG:NH2	2.29	0.47
25:BA:83:A:H5'	44:BY:8:LYS:HG2	1.95	0.47
25:BA:207:A:C2	25:BA:224:U:H4'	2.49	0.47
25:BA:1629:C:O2'	25:BA:1632:A:N3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2162:C:N3	25:BA:2173:G:C6	2.82	0.47
30:BG:108:ASN:HD22	50:B4:22:ILE:HG21	1.79	0.47
43:BX:61:GLY:HA3	43:BX:73:ARG:O	2.14	0.47
54:B8:23:VAL:HG11	54:B8:47:LYS:HD3	1.94	0.47
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.14	0.47
1:CA:407:G:O4'	4:CD:119:GLN:NE2	2.47	0.47
1:CA:880:C:OP1	12:CL:8:ASN:ND2	2.45	0.47
1:CA:984:C:H2'	1:CA:985:C:H6	1.78	0.47
1:CA:1028:C:C2	1:CA:1033:G:C6	3.02	0.47
1:CA:1097:C:H1'	1:CA:1170:A:H1'	1.95	0.47
25:DA:467:G:OP1	53:D7:33:ARG:HD2	2.13	0.47
25:DA:2114:A:N6	25:DA:2115:G:H21	2.12	0.47
25:DA:2131:G:C8	25:DA:2133:G:C2	3.02	0.47
25:DA:2734:A:H2'	25:DA:2735:G:O4'	2.13	0.47
26:DB:31:C:C2'	26:DB:32:C:H5'	2.44	0.47
30:DG:7:LEU:HD11	30:DG:107:LEU:HD12	1.95	0.47
32:DI:47:LEU:O	32:DI:51:ILE:HG13	2.14	0.47
42:DW:51:LEU:HD23	42:DW:105:VAL:HG11	1.96	0.47
1:AA:1392:G:H21	1:AA:1502:A:H8	1.59	0.47
25:BA:215:G:H21	25:BA:217:A:H62	1.61	0.47
25:BA:842:C:H2'	25:BA:843:C:C6	2.49	0.47
25:BA:923:C:H2'	25:BA:924:U:O4'	2.14	0.47
25:BA:2798:C:H2'	25:BA:2799:U:O4'	2.14	0.47
25:BA:2804:C:H2'	25:BA:2805:G:C8	2.48	0.47
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.67	0.47
1:CA:739:C:OP1	15:CO:2:PRO:HD3	2.14	0.47
1:CA:814:A:N7	1:CA:816:A:C4	2.82	0.47
1:CA:938:A:C6	1:CA:939:G:C5	3.02	0.47
16:CP:3:LYS:HG2	16:CP:65:GLN:HB2	1.95	0.47
26:DB:2:C:H2'	26:DB:3:C:C6	2.49	0.47
45:DZ:5:LEU:HD13	45:DZ:6:LYS:O	2.14	0.47
1:AA:96:U:H2'	1:AA:97:G:C8	2.50	0.47
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.96	0.47
1:AA:833:U:H2'	1:AA:834:C:C6	2.49	0.47
1:AA:991:U:HO2'	1:AA:992:U:P	2.34	0.47
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.49	0.47
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.33	0.47
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.49	0.47
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.15	0.47
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.32	0.47
25:BA:2183:C:O2'	25:BA:2195:A:H4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.30	0.47
25:BA:2596:U:H2'	25:BA:2597:U:H2'	1.95	0.47
25:BA:2885:C:OP1	39:BT:3:ARG:NH1	2.43	0.47
30:BG:41:GLN:C	30:BG:43:LEU:H	2.22	0.47
1:CA:59:A:H3'	1:CA:331:G:H22	1.79	0.47
1:CA:750:G:H1'	15:CO:22:THR:HG1	1.78	0.47
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.98	0.47
1:CA:1238:A:C2	1:CA:1303:C:H4'	2.50	0.47
1:CA:1309:G:O2'	13:CM:77:ASN:ND2	2.47	0.47
25:DA:898:C:H2'	25:DA:899:A:O4'	2.14	0.47
25:DA:1186:G:C2	25:DA:1187:G:H1'	2.49	0.47
25:DA:2683:C:P	39:DT:53:ARG:HH22	2.36	0.47
26:DB:32:C:H2'	26:DB:33:G:O4'	2.15	0.47
34:DO:119:PRO:HB2	39:DT:68:TYR:CE2	2.48	0.47
45:DZ:31:ARG:HD2	45:DZ:94:GLU:OE2	2.13	0.47
1:AA:144:G:H1	1:AA:178:C:N4	2.11	0.47
1:AA:649:G:H2'	1:AA:650:G:C8	2.47	0.47
1:AA:1005:A:N3	1:AA:1036:G:N2	2.56	0.47
1:AA:1057:G:C2'	1:AA:1058:G:H5'	2.44	0.47
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.49	0.47
1:AA:1464:G:OP2	39:BT:111:ARG:NH2	2.48	0.47
3:AC:9:GLY:N	14:AN:49:HIS:O	2.46	0.47
13:AM:121:LYS:HB2	13:AM:121:LYS:HZ2	1.80	0.47
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.39	0.47
25:BA:302:A:H4'	25:BA:303:C:OP1	2.14	0.47
25:BA:662:A:H8	35:BP:117:GLU:HG3	1.79	0.47
25:BA:2623:U:H5'	25:BA:2623:U:H6	1.79	0.47
41:BV:34:GLU:HB3	41:BV:56:SER:HB2	1.97	0.47
1:CA:1057:G:H2'	1:CA:1058:G:H5'	1.95	0.47
1:CA:1165:C:N3	1:CA:1171:G:N2	2.63	0.47
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.49	0.47
1:CA:1465:C:H2'	1:CA:1466:C:O4'	2.15	0.47
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.14	0.47
2:CB:123:ALA:N	2:CB:127:ILE:HD12	2.27	0.47
15:CO:55:GLY:HA2	15:CO:58:MET:HE3	1.96	0.47
25:DA:875:G:O2'	45:DZ:151:HIS:HE1	1.97	0.47
25:DA:1131:G:C8	25:DA:2025:C:H4'	2.49	0.47
25:DA:2144:U:H1'	25:DA:2148:G:N2	2.29	0.47
29:DF:137:LYS:NZ	29:DF:137:LYS:HB3	2.29	0.47
31:DH:118:PRO:HD2	31:DH:121:ILE:HG21	1.96	0.47
35:DP:39:LYS:HD2	35:DP:45:LEU:HD11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.45	0.47
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.95	0.47
45:DZ:50:GLN:OE1	45:DZ:50:GLN:N	2.47	0.47
1:AA:391:G:P	16:AP:28:ARG:HH12	2.37	0.47
1:AA:542:G:OP1	4:AD:10:ARG:NH2	2.37	0.47
1:AA:630:G:O2'	1:AA:631:G:H5'	2.14	0.47
1:AA:1239:A:H4'	1:AA:1240:U:H5''	1.95	0.47
1:AA:1326:C:OP1	21:AU:12:LYS:NZ	2.41	0.47
10:AJ:13:HIS:HA	10:AJ:16:LEU:HB3	1.97	0.47
26:BB:24:G:N7	26:BB:56:G:H2'	2.29	0.47
38:BS:59:LYS:HB2	38:BS:60:GLY:H	1.51	0.47
40:BU:86:ALA:O	41:BV:49:THR:HG23	2.15	0.47
1:CA:728:A:H2'	1:CA:729:A:H8	1.76	0.47
1:CA:976:G:P	14:CN:32:SER:H	2.38	0.47
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.29	0.47
1:CA:1063:C:P	1:CA:1064:G:HO2'	2.37	0.47
1:CA:1342:C:H1'	9:CI:124:GLN:NE2	2.30	0.47
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.50	0.47
13:CM:81:LEU:HD22	13:CM:88:ARG:HB3	1.96	0.47
14:CN:24:CYS:O	14:CN:28:GLY:N	2.43	0.47
19:CS:64:GLU:HB2	50:D4:59:PHE:CE1	2.49	0.47
25:DA:307:G:N2	25:DA:310:A:O5'	2.39	0.47
25:DA:484:C:H2'	25:DA:485:C:H6	1.80	0.47
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.49	0.47
25:DA:1209:G:O2'	25:DA:1237:A:N1	2.38	0.47
25:DA:1448:G:H4'	25:DA:1542:A:OP1	2.14	0.47
25:DA:1486:A:O2'	25:DA:1487:G:H5'	2.14	0.47
25:DA:1505:C:H2'	25:DA:1506:C:C6	2.50	0.47
25:DA:2106:G:H2'	25:DA:2107:C:O4'	2.15	0.47
25:DA:2137:C:H2'	25:DA:2138:C:C5	2.49	0.47
25:DA:2483:C:H2'	25:DA:2484:G:O4'	2.15	0.47
25:DA:2615:U:OP1	61:DA:4295:HOH:O	2.20	0.47
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.95	0.47
44:DY:28:LYS:HD2	44:DY:40:GLU:HG3	1.95	0.47
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.66	0.47
1:AA:407:G:OP1	4:AD:115:ARG:HD3	2.15	0.47
1:AA:620:C:H2'	1:AA:621:A:O4'	2.13	0.47
4:AD:61:LYS:O	4:AD:65:ARG:HB2	2.15	0.47
4:AD:166:LYS:HD3	4:AD:178:VAL:HG11	1.96	0.47
8:AH:26:VAL:HG22	8:AH:59:LEU:HB2	1.97	0.47
24:AY:69:G:C2	24:AY:70:G:H1'	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:777:C:H3'	61:BA:4849:HOH:O	2.15	0.47
25:BA:895:G:N9	25:BA:978:A:H8	2.12	0.47
25:BA:1189:A:OP1	33:BN:25:ARG:NH2	2.48	0.47
25:BA:1258:A:N3	25:BA:1284:G:O2'	2.46	0.47
45:BZ:138:GLU:N	45:BZ:156:LYS:HD3	2.28	0.47
49:B3:26:LEU:O	49:B3:35:ARG:NE	2.46	0.47
1:CA:359:U:H2'	1:CA:360:A:H8	1.78	0.47
1:CA:642:A:N3	8:CH:113:SER:OG	2.45	0.47
10:CJ:42:THR:HG21	10:CJ:66:ARG:HB3	1.96	0.47
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.54	0.47
25:DA:797:C:H2'	25:DA:798:G:O4'	2.15	0.47
25:DA:1131:G:H8	25:DA:2025:C:H4'	1.78	0.47
25:DA:2320:A:H2'	25:DA:2320:A:N3	2.30	0.47
25:DA:2562:U:H1'	34:DO:23:ARG:HH11	1.80	0.47
25:DA:2579:C:H4'	28:DE:134:ILE:HG12	1.97	0.47
29:DF:29:ASN:H	29:DF:112:MET:CE	2.26	0.47
29:DF:164:ARG:O	29:DF:168:ARG:HB2	2.13	0.47
38:DS:62:LYS:HA	38:DS:65:VAL:HB	1.96	0.47
1:AA:221:C:H2'	1:AA:222:U:C6	2.48	0.47
1:AA:373:A:H2'	1:AA:374:A:H8	1.79	0.47
1:AA:439:A:N3	1:AA:496:A:C4	2.82	0.47
1:AA:472:A:H2'	1:AA:473:G:O4'	2.15	0.47
1:AA:745:C:H2'	1:AA:746:A:C8	2.49	0.47
1:AA:811:C:O2'	1:AA:901:A:N1	2.43	0.47
1:AA:1442(B):A:C4	39:BT:118:ARG:NH2	2.83	0.47
2:AB:170:GLU:O	2:AB:174:VAL:HG23	2.15	0.47
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.47	0.47
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.70	0.47
25:BA:484:G:C8	53:B7:37:LYS:HG2	2.49	0.47
25:BA:762:G:H2'	25:BA:763:A:O4'	2.15	0.47
25:BA:831:A:C6	27:BD:229:VAL:HG11	2.50	0.47
25:BA:1604:C:OP2	25:BA:1605:A:O2'	2.21	0.47
25:BA:1974:A:C6	25:BA:1975:A:N1	2.83	0.47
25:BA:2156:A:HO2'	25:BA:2157:A:P	2.38	0.47
25:BA:2204:G:H2'	25:BA:2205:C:C6	2.49	0.47
25:BA:2639:G:O2'	25:BA:2794:A:N1	2.37	0.47
30:BG:16:ARG:CZ	30:BG:31:VAL:HG11	2.44	0.47
45:BZ:111:VAL:C	45:BZ:113:ALA:N	2.72	0.47
49:B3:18:ASP:N	49:B3:18:ASP:OD1	2.46	0.47
54:B8:61:LEU:C	54:B8:63:PRO:HD3	2.40	0.47
1:CA:58:C:O2'	1:CA:388:G:N7	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:300:A:H1'	1:CA:565:U:O2	2.15	0.47
1:CA:390:C:H2'	1:CA:391:G:C8	2.50	0.47
1:CA:509:A:O2'	1:CA:510:A:OP1	2.26	0.47
1:CA:662:G:H2'	1:CA:663:A:C8	2.49	0.47
1:CA:750:G:H1'	15:CO:22:THR:OG1	2.14	0.47
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.29	0.47
1:CA:1118:C:OP1	9:CI:9:ARG:HD2	2.15	0.47
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.80	0.47
1:CA:1493:A:H3'	25:DA:1913:A:N1	2.29	0.47
57:CA:3176:PCY:O21	57:CA:3176:PCY:N20	2.48	0.47
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.79	0.47
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.78	0.47
7:CG:111:ARG:NH2	7:CG:126:ASP:OD2	2.46	0.47
13:CM:91:ARG:NE	13:CM:97:PRO:O	2.48	0.47
15:CO:62:GLN:HE21	15:CO:66:LEU:HD13	1.79	0.47
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.96	0.47
23:CX:4:G:H1	23:CX:69:C:H42	1.62	0.47
25:DA:10:G:H2'	25:DA:11:G:C8	2.50	0.47
25:DA:325:G:H2'	25:DA:326:G:O4'	2.15	0.47
25:DA:818:G:O2'	25:DA:838:C:O2'	2.23	0.47
25:DA:864:G:N2	25:DA:913:U:C2	2.83	0.47
25:DA:948:G:H21	25:DA:985:C:P	2.37	0.47
25:DA:1509(B):A:H2'	25:DA:1510:G:H8	1.79	0.47
25:DA:1639:U:C2'	25:DA:1640:C:H5''	2.44	0.47
25:DA:2019:A:H4'	40:DU:34:LYS:HD2	1.97	0.47
25:DA:2261:C:O2'	25:DA:2262:U:H5'	2.15	0.47
25:DA:2332:U:O2'	25:DA:2335:A:N3	2.40	0.47
25:DA:2617:C:H2'	25:DA:2618:G:O4'	2.15	0.47
26:DB:31:C:H2'	26:DB:32:C:H5'	1.95	0.47
30:DG:106:LEU:O	30:DG:111:LEU:HG	2.15	0.47
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	1.96	0.47
38:DS:11:LYS:HD3	38:DS:91:PRO:HD3	1.95	0.47
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.95	0.47
47:D1:67:ILE:N	47:D1:68:PRO:HD2	2.30	0.47
49:D3:29:ARG:N	49:D3:33:GLN:OE1	2.36	0.47
1:AA:240:C:H2'	1:AA:241:C:C6	2.50	0.47
1:AA:250:A:H4'	1:AA:251:G:O5'	2.15	0.47
1:AA:1112:C:H1'	3:AC:179:ARG:HG2	1.95	0.47
4:AD:170:VAL:HG12	4:AD:171:GLY:H	1.80	0.47
6:AF:62:TRP:CD1	18:AR:35:ARG:HD2	2.50	0.47
6:AF:76:ALA:O	6:AF:80:ARG:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AJ:5:ARG:HB3	10:AJ:73:ASP:OD1	2.14	0.47
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.96	0.47
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.95	0.47
25:BA:756:U:H2'	25:BA:757:G:C8	2.50	0.47
25:BA:801:C:H2'	25:BA:802:C:C6	2.50	0.47
25:BA:1552:C:H2'	25:BA:1553:A:H8	1.79	0.47
25:BA:1831:C:OP1	27:BD:264:LYS:NZ	2.38	0.47
26:BB:87:G:N2	26:BB:90:A:OP2	2.32	0.47
29:BF:51:THR:HB	29:BF:88:VAL:CG1	2.45	0.47
1:CA:232:G:H1'	1:CA:262:A:N1	2.29	0.47
1:CA:690:G:C6	1:CA:691:G:C6	3.03	0.47
2:CB:207:ALA:O	2:CB:210:SER:HB3	2.15	0.47
4:CD:65:ARG:HG2	4:CD:75:PHE:CD1	2.50	0.47
4:CD:128:VAL:HG12	4:CD:129:ASN:ND2	2.29	0.47
25:DA:172:C:H2'	25:DA:173:G:C8	2.50	0.47
25:DA:528:A:C2'	25:DA:529:A:H5''	2.44	0.47
25:DA:579:G:H2'	25:DA:580:C:C6	2.50	0.47
25:DA:761:A:OP2	61:DA:4073:HOH:O	2.20	0.47
25:DA:1686:C:H2'	25:DA:1687:G:O4'	2.14	0.47
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.29	0.47
25:DA:2590:A:OP2	27:DD:238:GLY:HA2	2.14	0.47
25:DA:2785:C:OP1	28:DE:41:LYS:NZ	2.47	0.47
26:DB:119:G:H2'	26:DB:120:A:C8	2.50	0.47
27:DD:124:PRO:HG2	27:DD:129:ASN:HD21	1.79	0.47
32:DI:86:THR:O	32:DI:123:LEU:HD22	2.14	0.47
34:DO:34:THR:OG1	34:DO:35:VAL:N	2.47	0.47
38:DS:34:HIS:ND1	38:DS:53:SER:OG	2.41	0.47
44:DY:44:ILE:HA	44:DY:63:LYS:O	2.13	0.47
45:DZ:145:GLU:HG3	45:DZ:146:ILE:H	1.79	0.47
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.50	0.47
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.97	0.47
8:AH:11:THR:HG22	8:AH:15:ASN:ND2	2.30	0.47
25:BA:895:G:C4	25:BA:978:A:H8	2.33	0.47
25:BA:1857:G:H4'	27:BD:242:ARG:CZ	2.45	0.47
31:BH:17:VAL:HG21	31:BH:50:VAL:HG21	1.97	0.47
37:BR:29:LEU:HD12	37:BR:116:LEU:HD11	1.97	0.47
48:B2:23:LYS:O	48:B2:27:GLU:HG3	2.14	0.47
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.14	0.47
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.15	0.47
4:CD:100:ARG:NH1	4:CD:137:SER:OG	2.48	0.47
25:DA:67:U:H2'	25:DA:68:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:579:G:O2'	25:DA:2019:A:OP1	2.28	0.47
25:DA:628:G:HO2'	25:DA:651:G:HO2'	1.63	0.47
26:DB:11:C:OP2	26:DB:12:C:N4	2.36	0.47
1:AA:189(K):U:H2'	1:AA:189(L):G:C8	2.50	0.47
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.50	0.47
1:AA:1160:G:C6	1:AA:1161:C:C5	3.03	0.47
2:AB:223:ILE:HA	2:AB:226:ARG:HG2	1.97	0.47
3:AC:131:ARG:NH1	3:AC:135:LYS:HE3	2.30	0.47
5:AE:105:VAL:HG21	5:AE:128:PRO:HB3	1.97	0.47
7:AG:144:MET:HE2	7:AG:144:MET:HB3	1.85	0.47
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.50	0.47
13:AM:4:ILE:HG13	13:AM:57:ARG:HA	1.97	0.47
25:BA:555:G:C5	25:BA:2044:U:H5''	2.50	0.47
25:BA:1074:A:H61	25:BA:1171:G:H2'	1.80	0.47
26:BB:48:A:H4'	38:BS:95:HIS:CD2	2.43	0.47
50:B4:68:ARG:HD2	50:B4:68:ARG:HA	1.62	0.47
1:CA:114:U:H2'	1:CA:115:G:C8	2.50	0.47
1:CA:266:G:H5''	1:CA:268:C:H41	1.79	0.47
1:CA:609:A:C5	1:CA:610:G:C8	3.03	0.47
1:CA:838:G:H1	1:CA:848:C:N4	2.13	0.47
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.15	0.47
1:CA:1075:C:H2'	1:CA:1076:C:H5'	1.96	0.47
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.47	0.47
1:CA:1279:A:OP2	10:CJ:9:ARG:NH1	2.48	0.47
25:DA:784:A:C8	25:DA:792:G:C5	3.02	0.47
25:DA:1266:G:O4'	42:DW:15:ARG:NH2	2.46	0.47
25:DA:1593:G:H2'	25:DA:1594:G:H8	1.79	0.47
25:DA:2065:C:H2'	25:DA:2066:C:C6	2.50	0.47
25:DA:2408:U:H2'	25:DA:2409:G:C8	2.49	0.47
25:DA:2687:U:H2'	25:DA:2688:U:O4'	2.14	0.47
29:DF:18:ARG:HG2	29:DF:19:GLU:H	1.80	0.47
30:DG:72:ARG:HA	30:DG:86:MET:O	2.15	0.47
32:DI:14:ASP:O	32:DI:17:GLN:HB3	2.15	0.47
38:DS:84:GLN:HA	38:DS:111:GLU:O	2.14	0.47
45:DZ:31:ARG:HB2	45:DZ:32:HIS:CD2	2.49	0.47
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.50	0.46
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.97	0.46
25:BA:561:A:H2'	25:BA:562:C:C6	2.50	0.46
25:BA:600:G:O2'	25:BA:1300:A:OP1	2.30	0.46
25:BA:1217:G:H3'	25:BA:1218:G:H5'	1.98	0.46
25:BA:2298:A:H4'	25:BA:2299:A:O5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.77	0.46
25:BA:2707:C:H2'	25:BA:2708:U:C6	2.50	0.46
43:BX:47:PHE:O	43:BX:49:VAL:HG13	2.15	0.46
1:CA:25:C:H5'	1:CA:524:G:H1'	1.97	0.46
1:CA:838:G:H3'	1:CA:840:C:H41	1.78	0.46
1:CA:948:C:H2'	1:CA:949:A:H8	1.80	0.46
25:DA:55:G:O2'	25:DA:127:A:N1	2.41	0.46
25:DA:71:A:H5''	25:DA:73:A:N9	2.31	0.46
25:DA:128:C:H2'	25:DA:129:C:C6	2.50	0.46
25:DA:774:A:N3	25:DA:774:A:H2'	2.30	0.46
25:DA:2171:A:H1'	25:DA:2172:U:C6	2.50	0.46
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.47	0.46
45:DZ:61:LEU:HD22	45:DZ:67:LEU:HG	1.97	0.46
45:DZ:95:PRO:HA	45:DZ:130:PRO:HD3	1.97	0.46
1:AA:8:A:N6	4:AD:205:GLU:O	2.48	0.46
1:AA:67:C:O2'	1:AA:171:A:N3	2.34	0.46
1:AA:165:C:H2'	1:AA:166:G:C8	2.50	0.46
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.48	0.46
1:AA:429:U:H3'	4:AD:9:CYS:SG	2.55	0.46
1:AA:452:A:O2'	1:AA:453:A:OP2	2.26	0.46
1:AA:546:G:O2'	1:AA:548:G:O2'	2.27	0.46
1:AA:1003:G:N2	1:AA:1004:A:H1'	2.31	0.46
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.16	0.46
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.46	0.46
2:AB:146:GLN:O	2:AB:150:SER:HB3	2.15	0.46
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.81	0.46
6:AF:100:ASN:HB2	18:AR:28:GLU:HA	1.96	0.46
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.80	0.46
25:BA:142:G:H1'	43:BX:37:THR:HG21	1.97	0.46
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.50	0.46
25:BA:1171:G:H5'	55:B9:37:GLY:HA2	1.97	0.46
25:BA:1577:C:HO2'	25:BA:1578:C:P	2.37	0.46
25:BA:2158:C:H42	25:BA:2177:G:H1	1.63	0.46
29:BF:129:PHE:CD2	29:BF:163:VAL:HG21	2.50	0.46
1:CA:234:C:H5''	17:CQ:70:ARG:HH21	1.81	0.46
1:CA:1173:G:C2'	1:CA:1174:G:H5'	2.44	0.46
2:CB:52:GLU:HG2	2:CB:56:ARG:NH2	2.31	0.46
23:CX:20:U:O2	23:CX:20:U:H2'	2.16	0.46
25:DA:90:U:H1'	25:DA:92:A:C8	2.51	0.46
25:DA:262:A:H2'	25:DA:263:C:O4'	2.14	0.46
25:DA:873:G:N2	25:DA:905:U:C2	2.82	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1499:C:H2'	25:DA:1500:G:C8	2.50	0.46
25:DA:2147:G:H2'	25:DA:2148:G:H4'	1.96	0.46
25:DA:2322:A:H2'	25:DA:2323:G:O4'	2.16	0.46
25:DA:2848:G:C8	39:DT:97:ALA:HB2	2.51	0.46
27:DD:71:ASP:HB3	27:DD:103:ARG:NH2	2.30	0.46
42:DW:45:TYR:CZ	42:DW:49:LYS:HE3	2.50	0.46
1:AA:300:A:H1'	1:AA:565:U:O2	2.15	0.46
1:AA:328:C:H4'	1:AA:329:A:H5'	1.97	0.46
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.34	0.46
1:AA:1362:C:H2'	1:AA:1363:C:H5''	1.97	0.46
7:AG:136:LYS:O	7:AG:140:ASP:HB2	2.15	0.46
13:AM:97:PRO:HG2	13:AM:103:THR:HG22	1.97	0.46
25:BA:105:C:H2'	25:BA:106:U:H6	1.79	0.46
25:BA:843:C:H2'	25:BA:844:C:C6	2.51	0.46
25:BA:932:C:H3'	25:BA:933:C:C5'	2.42	0.46
25:BA:956:A:C5	36:BQ:13:GLN:HG3	2.51	0.46
25:BA:2482:G:O6	25:BA:2488:A:O2'	2.25	0.46
26:BB:76:G:N2	26:BB:101:G:O6	2.45	0.46
28:BE:116:VAL:HG13	28:BE:122:PHE:HB2	1.97	0.46
32:BI:6:LEU:C	32:BI:7:GLU:HG2	2.40	0.46
34:BO:35:VAL:HG11	34:BO:103:ALA:CB	2.41	0.46
1:CA:853:G:H2'	1:CA:854:G:H8	1.80	0.46
4:CD:105:VAL:HG13	4:CD:110:PHE:HB2	1.98	0.46
9:CI:20:ARG:HA	9:CI:21:PRO:HD3	1.82	0.46
25:DA:1710:C:H2'	25:DA:1711:C:C6	2.50	0.46
25:DA:2110:G:OP1	25:DA:2118:U:N3	2.40	0.46
28:DE:13:ARG:HG2	39:DT:58:ASN:HD21	1.81	0.46
30:DG:41:GLN:C	30:DG:43:LEU:H	2.22	0.46
31:DH:164:TYR:HB2	31:DH:167:GLU:HB2	1.97	0.46
1:AA:103:C:P	20:AT:17:ARG:HH21	2.37	0.46
1:AA:342:C:C2	1:AA:348:G:N2	2.83	0.46
1:AA:926:G:C6	1:AA:1505:G:C6	3.03	0.46
1:AA:975:A:N1	10:AJ:48:THR:HB	2.30	0.46
1:AA:1302:U:H5	13:AM:17:VAL:HG21	1.81	0.46
4:AD:164:ALA:O	4:AD:168:ARG:HD3	2.15	0.46
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.51	0.46
25:BA:1715:A:H4'	25:BA:1716:A:O5'	2.16	0.46
25:BA:1841:A:H2'	25:BA:1842:G:O4'	2.15	0.46
25:BA:2308:U:OP2	38:BS:9:ARG:NH2	2.45	0.46
27:BD:61:LEU:O	27:BD:63:ARG:NH1	2.48	0.46
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1005:A:OP2	1:CA:1006:C:N4	2.49	0.46
1:CA:1286:A:H2	21:CU:18:TYR:OH	1.99	0.46
11:CK:99:GLN:O	11:CK:101:SER:N	2.37	0.46
15:CO:5:LYS:NZ	15:CO:5:LYS:H	2.14	0.46
25:DA:18:C:H2'	25:DA:19:C:H6	1.79	0.46
25:DA:861:A:C2	25:DA:917:A:C4	3.03	0.46
25:DA:910:A:N3	25:DA:2264:C:O2'	2.44	0.46
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.15	0.46
30:DG:15:VAL:HG13	30:DG:175:LEU:HD23	1.97	0.46
30:DG:148:MET:H	30:DG:148:MET:HG3	1.47	0.46
1:AA:79:G:N1	1:AA:90:U:N3	2.63	0.46
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.50	0.46
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.16	0.46
4:AD:178:VAL:C	4:AD:180:GLY:H	2.22	0.46
25:BA:217:A:H2'	25:BA:219:U:O4'	2.16	0.46
25:BA:287:G:O2'	25:BA:448:U:OP2	2.23	0.46
25:BA:664:U:H2'	25:BA:665:C:C6	2.51	0.46
25:BA:904:C:H4'	46:B0:23:VAL:HG21	1.97	0.46
25:BA:1074:A:N3	25:BA:2498:G:O2'	2.44	0.46
25:BA:2372:A:H2'	25:BA:2373:A:O4'	2.15	0.46
25:BA:2859:U:H4'	25:BA:2878:A:C2	2.50	0.46
28:BE:12:THR:HG21	39:BT:11:GLU:HG2	1.98	0.46
30:BG:126:ASP:OD2	30:BG:130:ASN:ND2	2.48	0.46
32:BI:75:LEU:HD22	32:BI:105:HIS:ND1	2.30	0.46
1:CA:984:C:O5'	1:CA:984:C:H6	1.98	0.46
1:CA:1203:C:H2'	1:CA:1204:A:O4'	2.15	0.46
2:CB:127:ILE:O	2:CB:128:GLU:HB2	2.14	0.46
19:CS:30:LEU:HD11	19:CS:32:LYS:HG3	1.98	0.46
25:DA:570:G:H2'	25:DA:2030:A:C5	2.50	0.46
25:DA:784:A:OP1	25:DA:2588:G:H5''	2.15	0.46
25:DA:912:C:N4	25:DA:913:U:O4	2.48	0.46
25:DA:2727:G:O2'	34:DO:70:LYS:NZ	2.48	0.46
30:DG:173:LEU:HB3	30:DG:178:PHE:CG	2.51	0.46
35:DP:135:LEU:HD23	35:DP:135:LEU:HA	1.73	0.46
1:AA:189(C):C:H2'	1:AA:189(D):C:O4'	2.15	0.46
1:AA:401:C:H2'	1:AA:402:G:C8	2.50	0.46
1:AA:433:C:C2'	1:AA:434:U:H5'	2.46	0.46
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.50	0.46
2:AB:156:LYS:HB3	2:AB:156:LYS:HE2	1.72	0.46
10:AJ:5:ARG:HB3	10:AJ:5:ARG:HE	1.53	0.46
20:AT:45:GLN:HE21	20:AT:45:GLN:HB3	1.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1067:A:H3'	25:BA:1067:A:H8	1.81	0.46
25:BA:1081:U:H2'	25:BA:1082:G:C8	2.50	0.46
25:BA:2332:A:N3	25:BA:2332:A:H2'	2.31	0.46
53:B7:1:MET:HE3	53:B7:3:ARG:NH2	2.31	0.46
1:CA:397:A:H3'	1:CA:397:A:N3	2.29	0.46
1:CA:615:C:H2'	1:CA:616:G:O4'	2.16	0.46
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.16	0.46
1:CA:814:A:H2'	1:CA:816:A:H5''	1.97	0.46
1:CA:1227:A:H3'	1:CA:1227:A:C8	2.51	0.46
1:CA:1401:G:C2	1:CA:1402:C:H1'	2.51	0.46
5:CE:88:LYS:HB3	5:CE:123:LEU:HB2	1.97	0.46
6:CF:45:LEU:HD12	6:CF:59:TYR:HD2	1.81	0.46
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.16	0.46
7:CG:116:ALA:O	7:CG:120:ILE:HG13	2.15	0.46
18:CR:24:ALA:C	18:CR:26:LEU:H	2.23	0.46
25:DA:271(K):U:O2	32:DI:50:ARG:NE	2.49	0.46
25:DA:1131:G:O6	25:DA:2040:C:H1'	2.15	0.46
25:DA:1638:C:H4'	25:DA:2710:C:O2	2.16	0.46
25:DA:2308:G:H5''	25:DA:2310:A:OP2	2.15	0.46
25:DA:2395:C:O2'	47:D1:30:VAL:HG13	2.15	0.46
38:DS:27:SER:HA	38:DS:88:ASP:HB3	1.98	0.46
1:AA:109:A:H2'	1:AA:326:G:N2	2.31	0.46
17:AQ:5:VAL:HA	17:AQ:59:ILE:O	2.15	0.46
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.48	0.46
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.81	0.46
25:BA:1790:A:H1'	25:BA:2723:A:C2	2.51	0.46
25:BA:2786:C:H2'	25:BA:2787:C:H6	1.80	0.46
25:BA:2856:G:H2'	25:BA:2857:U:O4'	2.16	0.46
32:BI:6:LEU:HD11	32:BI:37:VAL:HG23	1.98	0.46
33:BN:12:ARG:HH12	33:BN:38:HIS:HE2	1.64	0.46
33:BN:138:LEU:HD23	33:BN:138:LEU:HA	1.72	0.46
49:B3:19:GLN:OE1	49:B3:52:HIS:NE2	2.40	0.46
52:B6:50:ARG:HE	52:B6:50:ARG:HB2	1.53	0.46
1:CA:421:U:H6	1:CA:421:U:H5'	1.81	0.46
1:CA:688:G:H2'	1:CA:689:C:C6	2.49	0.46
1:CA:951:G:N3	1:CA:970:C:O2'	2.39	0.46
1:CA:1256:A:N6	1:CA:1278:U:O2'	2.48	0.46
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.46	0.46
1:CA:1298:C:H2'	7:CG:114:ARG:HH12	1.81	0.46
2:CB:16:HIS:CB	2:CB:210:SER:HB2	2.37	0.46
8:CH:38:ILE:HD12	8:CH:118:VAL:HG12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:658:C:H2'	25:DA:659:C:C6	2.50	0.46
25:DA:662:G:H5''	35:DP:16:ARG:HG2	1.96	0.46
25:DA:1651:G:H2'	25:DA:1652:A:O4'	2.15	0.46
26:DB:19:G:H2'	26:DB:20:C:O4'	2.16	0.46
1:AA:820:U:H4'	1:AA:821:G:OP2	2.16	0.46
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.80	0.46
2:AB:162:ILE:HD11	2:AB:184:VAL:HG22	1.97	0.46
9:AI:24:GLY:HA3	9:AI:57:GLY:HA2	1.97	0.46
25:BA:223:C:H2'	25:BA:224:U:C6	2.51	0.46
25:BA:555:G:O4'	25:BA:555:G:N3	2.46	0.46
25:BA:794:U:O2	25:BA:2036:A:H1'	2.15	0.46
25:BA:831:A:O4'	27:BD:227:ASN:ND2	2.49	0.46
25:BA:1159:U:H2'	25:BA:1160:G:C8	2.50	0.46
25:BA:1417:G:H2'	25:BA:1418:U:H5	1.79	0.46
34:BO:120:GLU:HG2	34:BO:122:LEU:HG	1.98	0.46
36:BQ:68:ILE:HG23	36:BQ:103:MET:HA	1.98	0.46
1:CA:171:A:H2'	1:CA:172:A:C8	2.51	0.46
1:CA:978:A:O2'	1:CA:1321:C:N4	2.49	0.46
1:CA:1151:A:N3	10:CJ:39:PRO:HG3	2.31	0.46
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.16	0.46
1:CA:1374:A:O2'	7:CG:28:ASN:HB3	2.16	0.46
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.98	0.46
25:DA:656:G:H2'	25:DA:657:U:O4'	2.14	0.46
26:DB:28:C:H5''	38:DS:31:SER:HB3	1.97	0.46
31:DH:118:PRO:O	31:DH:121:ILE:HB	2.16	0.46
32:DI:134:PRO:C	32:DI:136:VAL:H	2.24	0.46
33:DN:99:LEU:HD23	33:DN:99:LEU:HA	1.82	0.46
37:DR:95:THR:HG22	37:DR:116:LEU:HD23	1.98	0.46
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.98	0.46
53:D7:18:PHE:CE1	53:D7:22:MET:HG3	2.51	0.46
1:AA:130:A:O2'	1:AA:131:C:O5'	2.31	0.46
1:AA:148:G:H1	1:AA:174:C:N4	2.14	0.46
1:AA:189(D):C:O2	1:AA:189(H):G:C6	2.69	0.46
1:AA:542:G:P	4:AD:10:ARG:HH22	2.39	0.46
1:AA:833:U:H2'	1:AA:834:C:H6	1.80	0.46
1:AA:1125:U:H1'	1:AA:1126:U:C6	2.50	0.46
25:BA:553:A:OP2	33:BN:114:ARG:NH1	2.49	0.46
25:BA:624:C:O2'	25:BA:628:C:OP1	2.29	0.46
25:BA:936:C:H2'	25:BA:936:C:OP2	2.15	0.46
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.51	0.46
25:BA:1633:A:H2'	25:BA:1634:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1823:G:H5'	27:BD:205:VAL:HG13	1.98	0.46
25:BA:1904:C:H2'	25:BA:1905:G:O4'	2.16	0.46
25:BA:2165:C:H2'	25:BA:2166:U:O4'	2.16	0.46
25:BA:2177:G:C2	25:BA:2178:G:H1'	2.51	0.46
25:BA:2236:G:H4'	25:BA:2238:C:C2	2.51	0.46
34:BO:68:GLU:HB3	34:BO:78:ARG:HB2	1.97	0.46
35:BP:55:ARG:HG2	35:BP:56:SER:N	2.30	0.46
48:B2:32:LEU:HD13	48:B2:36:ARG:HH11	1.81	0.46
50:B4:33:VAL:HG12	50:B4:35:VAL:H	1.81	0.46
1:CA:947:G:H2'	1:CA:948:C:O4'	2.16	0.46
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.15	0.46
1:CA:1289:A:OP1	21:CU:9:ARG:NH2	2.48	0.46
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.31	0.46
1:CA:1509:C:H2'	1:CA:1510:U:O4'	2.15	0.46
5:CE:35:GLY:HA3	5:CE:112:LEU:HB3	1.98	0.46
7:CG:100:ALA:O	7:CG:104:LEU:HD13	2.15	0.46
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.98	0.46
25:DA:195:A:H2'	25:DA:198:C:N4	2.30	0.46
25:DA:2156:G:H3'	25:DA:2157:G:C5	2.51	0.46
25:DA:2632:A:O2'	25:DA:2811:G:O2'	2.21	0.46
26:DB:16:G:N2	26:DB:68:C:O2	2.49	0.46
26:DB:46:A:C5	26:DB:47:C:C4	3.04	0.46
34:DO:23:ARG:HG3	34:DO:24:VAL:N	2.31	0.46
35:DP:96:THR:HG23	35:DP:99:LEU:HD23	1.98	0.46
49:D3:24:LYS:HE3	49:D3:24:LYS:HB2	1.63	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.03	0.46
6:AF:68:PRO:HB2	6:AF:71:ARG:HG3	1.97	0.46
9:AI:92:TYR:O	9:AI:96:LEU:HB2	2.16	0.46
25:BA:211:A:H3'	25:BA:448:U:H5'	1.98	0.46
25:BA:2186:C:H5	25:BA:2187:G:C4	2.34	0.46
31:BH:90:LYS:HD3	31:BH:159:GLU:HG2	1.97	0.46
33:BN:73:THR:OG1	33:BN:82:LEU:HD11	2.16	0.46
39:BT:8:LYS:HD3	39:BT:8:LYS:HA	1.77	0.46
1:CA:202:U:H3'	1:CA:203:U:C6	2.51	0.46
1:CA:502:G:OP1	12:CL:118:SER:HB3	2.16	0.46
1:CA:1186:G:H21	14:CN:61:TRP:C	2.23	0.46
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.15	0.46
7:CG:22:LEU:HD23	7:CG:63:LYS:HG2	1.98	0.46
20:CT:54:LYS:HA	20:CT:57:ARG:NH2	2.31	0.46
23:CX:10:G:N2	23:CX:26:G:H1'	2.31	0.46
25:DA:832:G:H5'	35:DP:45:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1547:C:H2'	25:DA:1548:C:H6	1.81	0.46
25:DA:2712:U:OP1	25:DA:2714:G:H4'	2.16	0.46
30:DG:71:THR:N	30:DG:89:GLY:O	2.42	0.46
30:DG:108:ASN:HA	50:D4:37:SER:HB2	1.96	0.46
30:DG:151:ALA:O	30:DG:153:ARG:HD3	2.16	0.46
1:AA:7:G:H5''	1:AA:298:A:O4'	2.16	0.45
1:AA:153:C:H42	1:AA:169:C:H42	1.63	0.45
1:AA:524:G:H2'	1:AA:525:C:C6	2.52	0.45
1:AA:1236:A:H4'	1:AA:1304:G:H4'	1.98	0.45
1:AA:1320:C:H2'	1:AA:1321:C:O4'	2.16	0.45
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.50	0.45
57:AA:3191:PCY:H112	57:AA:3191:PCY:C1	2.46	0.45
2:AB:82:ARG:NH1	2:AB:86:GLU:OE2	2.49	0.45
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.16	0.45
25:BA:670:C:H5''	25:BA:671:A:OP2	2.16	0.45
25:BA:1759:C:H2'	25:BA:1760:U:O4'	2.16	0.45
25:BA:2301:G:OP1	61:BA:4230:HOH:O	2.21	0.45
25:BA:2331:G:H22	38:BS:3:ARG:CZ	2.27	0.45
25:BA:2418:U:H2'	25:BA:2418:U:OP2	2.16	0.45
25:BA:2541:G:H5''	25:BA:2542:A:H5''	1.98	0.45
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.51	0.45
50:B4:26:SER:OG	50:B4:27:THR:N	2.49	0.45
1:CA:9:G:H2'	1:CA:10:A:H8	1.81	0.45
1:CA:324:G:N1	1:CA:327:A:OP2	2.48	0.45
1:CA:461:A:O2'	1:CA:470:C:H5'	2.15	0.45
1:CA:909:A:H2'	1:CA:910:C:O4'	2.17	0.45
25:DA:637:A:H2'	35:DP:117:GLU:OE2	2.16	0.45
25:DA:1789:A:H2'	25:DA:1790:C:C6	2.51	0.45
25:DA:1913:A:H4'	25:DA:1914:C:O5'	2.15	0.45
25:DA:2238:G:H2'	25:DA:2238:G:N3	2.31	0.45
25:DA:2432:A:H5''	25:DA:2433:A:OP2	2.15	0.45
25:DA:2850:A:N7	25:DA:2868:A:O2'	2.31	0.45
25:DA:2865:U:C4	25:DA:2866:U:C4	3.04	0.45
30:DG:44:GLY:N	30:DG:88:ILE:O	2.48	0.45
30:DG:105:LYS:HB3	30:DG:142:PRO:HG3	1.99	0.45
1:AA:175:C:H2'	1:AA:176:C:C6	2.51	0.45
1:AA:437:U:OP1	4:AD:155:LEU:HD21	2.16	0.45
18:AR:26:LEU:HD23	18:AR:29:PHE:CD2	2.50	0.45
25:BA:636:G:O2'	25:BA:640:A:N1	2.45	0.45
25:BA:1580:G:H3'	25:BA:1581:U:O2	2.15	0.45
25:BA:2556:G:H1'	25:BA:2658:C:H4'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BN:62:VAL:CG1	33:BN:66:LYS:HB2	2.46	0.45
39:BT:37:GLY:HA2	39:BT:38:ASN:HA	1.64	0.45
39:BT:127:ALA:C	39:BT:129:ARG:N	2.74	0.45
40:BU:112:ARG:H	40:BU:112:ARG:HG2	1.57	0.45
45:BZ:158:PRO:HG2	45:BZ:161:VAL:HG11	1.98	0.45
1:CA:137:C:H2'	1:CA:138:G:H8	1.82	0.45
1:CA:392:G:H2'	1:CA:393:A:C8	2.51	0.45
1:CA:637:G:H2'	1:CA:638:G:C8	2.51	0.45
1:CA:1030(C):G:H2'	1:CA:1030(D):A:C8	2.51	0.45
1:CA:1353:G:H2'	1:CA:1354:C:C6	2.51	0.45
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.97	0.45
3:CC:10:PHE:O	3:CC:178:LEU:HD11	2.16	0.45
4:CD:60:GLU:OE1	4:CD:199:ASN:N	2.34	0.45
25:DA:108:U:H2'	25:DA:109:G:C8	2.51	0.45
25:DA:854:G:H2'	25:DA:855:G:H8	1.78	0.45
25:DA:1547:C:H2'	25:DA:1548:C:C6	2.52	0.45
25:DA:1970:A:OP1	61:DA:4253:HOH:O	2.21	0.45
32:DI:72:LEU:HA	32:DI:75:LEU:HD22	1.96	0.45
50:D4:62:ARG:H	50:D4:62:ARG:HD3	1.81	0.45
1:AA:1054:C:H4'	1:AA:1055:A:OP1	2.16	0.45
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.16	0.45
5:AE:79:GLU:H	5:AE:79:GLU:HG3	1.47	0.45
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.98	0.45
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.96	0.45
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.41	0.45
25:BA:185:A:O2'	25:BA:852:G:O6	2.29	0.45
25:BA:552:C:C5	25:BA:2792:U:H2'	2.51	0.45
25:BA:1985:U:H4'	25:BA:1986:G:OP1	2.16	0.45
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.44	0.45
30:BG:58:GLN:HE21	30:BG:58:GLN:HA	1.81	0.45
50:B4:68:ARG:HB3	50:B4:69:LYS:H	1.51	0.45
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.45
1:CA:1353:G:H2'	1:CA:1354:C:H6	1.80	0.45
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.56	0.45
5:CE:43:LEU:HD21	5:CE:132:ALA:HB1	1.98	0.45
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.39	0.45
11:CK:27:ASN:OD1	11:CK:28:THR:N	2.44	0.45
16:CP:19:ILE:HG22	16:CP:36:ILE:HG13	1.98	0.45
18:CR:22:VAL:HA	18:CR:25:THR:HG22	1.98	0.45
25:DA:234:C:H2'	25:DA:235:U:C6	2.51	0.45
25:DA:286:C:H2'	25:DA:287:C:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:315:G:H2'	25:DA:316:C:C6	2.52	0.45
25:DA:362:U:O2'	25:DA:363:G:H5'	2.16	0.45
25:DA:727:A:OP1	25:DA:1431:U:O2'	2.34	0.45
25:DA:729:G:OP2	27:DD:13:ARG:HD3	2.17	0.45
25:DA:819:A:C4	25:DA:1189:A:C2	3.05	0.45
25:DA:923:C:O5'	25:DA:923:C:H6	1.99	0.45
25:DA:973:A:C8	25:DA:1188:U:C2	3.04	0.45
25:DA:1214:A:N6	25:DA:1235:G:H1'	2.32	0.45
25:DA:1268:A:OP1	61:DA:4293:HOH:O	2.21	0.45
25:DA:1592:C:H2'	25:DA:1593:G:H8	1.82	0.45
25:DA:1816:G:H3'	27:DD:62:TYR:CE1	2.51	0.45
25:DA:2645:G:N2	25:DA:2767:C:OP2	2.48	0.45
25:DA:2722:G:H2'	25:DA:2723:C:C6	2.51	0.45
1:AA:441:A:H3'	1:AA:442:C:C6	2.51	0.45
1:AA:509:A:H5''	4:AD:55:ALA:HB2	1.99	0.45
1:AA:691:G:H2'	1:AA:692:U:C6	2.52	0.45
1:AA:834:C:H2'	1:AA:835:U:C6	2.52	0.45
1:AA:1285:A:O2'	1:AA:1286:A:OP2	2.34	0.45
5:AE:105:VAL:O	5:AE:109:ILE:HD12	2.17	0.45
7:AG:78:ARG:NE	7:AG:154:TYR:O	2.48	0.45
25:BA:397:G:H8	25:BA:397:G:OP2	1.98	0.45
25:BA:734:C:H5''	53:B7:2:LYS:HE2	1.98	0.45
25:BA:1087:C:H42	25:BA:1160:G:H1	1.63	0.45
26:BB:13:A:N1	26:BB:69:G:O2'	2.42	0.45
27:BD:111:LEU:HD23	27:BD:111:LEU:HA	1.86	0.45
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.41	0.45
30:BG:64:THR:HB	30:BG:94:LEU:HD21	1.99	0.45
32:BI:40:THR:O	32:BI:44:LEU:HB2	2.17	0.45
32:BI:57:ARG:HA	32:BI:60:GLU:HB3	1.97	0.45
46:B0:36:ILE:HD13	46:B0:58:THR:HG21	1.98	0.45
52:B6:12:GLU:OE2	52:B6:52:VAL:HG21	2.15	0.45
1:CA:8:A:N6	4:CD:205:GLU:O	2.47	0.45
1:CA:1222:G:H5'	19:CS:77:THR:HG21	1.99	0.45
2:CB:121:LEU:H	2:CB:125:PRO:HG2	1.80	0.45
3:CC:122:GLU:HA	3:CC:125:GLU:OE1	2.15	0.45
4:CD:108:LEU:HD13	4:CD:174:LEU:HD13	1.98	0.45
5:CE:84:PHE:N	5:CE:87:SER:O	2.48	0.45
25:DA:271(D):G:H2'	25:DA:271(E):U:C6	2.51	0.45
25:DA:300:A:OP1	44:DY:86:ARG:NH2	2.40	0.45
25:DA:307:G:H2'	25:DA:309:G:OP2	2.17	0.45
25:DA:687:C:N3	25:DA:788:A:H5'	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:900:A:O2'	25:DA:901:A:OP1	2.30	0.45
25:DA:1509(A):A:H3'	25:DA:1509(B):A:H8	1.82	0.45
26:DB:16:G:H1	26:DB:68:C:H42	1.63	0.45
26:DB:87:G:N2	26:DB:90:A:OP2	2.45	0.45
1:AA:162:A:H3'	1:AA:163:C:O4'	2.17	0.45
1:AA:171:A:H2'	1:AA:172:A:C8	2.51	0.45
1:AA:345:C:OP2	39:BT:39:ARG:NH2	2.46	0.45
1:AA:473:G:O2'	1:AA:474:G:H5'	2.17	0.45
1:AA:693:G:H2'	1:AA:694:A:C8	2.51	0.45
1:AA:1371:G:C6	1:AA:1372:U:C4	3.05	0.45
2:AB:55:PHE:HD1	2:AB:58:ILE:HD12	1.80	0.45
4:AD:88:VAL:O	4:AD:92:VAL:HG23	2.16	0.45
4:AD:116:GLN:NE2	4:AD:157:LEU:HD11	2.32	0.45
9:AI:55:ALA:HB1	9:AI:59:PHE:CD2	2.52	0.45
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.84	0.45
11:AK:70:LYS:HE2	11:AK:70:LYS:HB2	1.71	0.45
25:BA:354:A:H2	25:BA:1255:A:C2'	2.29	0.45
25:BA:1057:G:OP2	40:BU:70:ARG:NH2	2.49	0.45
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.17	0.45
25:BA:1845:G:H4'	27:BD:51:VAL:HG21	1.97	0.45
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.32	0.45
25:BA:2564:U:C2	25:BA:2566:U:H5'	2.51	0.45
38:BS:87:PHE:HB2	38:BS:112:PHE:CE2	2.52	0.45
48:B2:10:LEU:HD23	48:B2:10:LEU:HA	1.86	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.51	0.45
1:CA:587:G:N2	1:CA:754:C:OP2	2.48	0.45
1:CA:1005:A:H3'	1:CA:1006:C:H5''	1.98	0.45
3:CC:79:ARG:H	3:CC:82:GLU:HB3	1.81	0.45
5:CE:12:LEU:O	5:CE:30:ALA:HA	2.17	0.45
25:DA:1999:C:H4'	25:DA:2723:C:O2	2.17	0.45
25:DA:2436:G:C6	25:DA:2437:U:C4	3.05	0.45
25:DA:2497:A:H5''	61:DA:4062:HOH:O	2.16	0.45
25:DA:2836:U:H2'	25:DA:2837:G:C8	2.51	0.45
26:DB:42:C:O2	30:DG:93:THR:N	2.27	0.45
36:DQ:118:LEU:HB2	36:DQ:131:ILE:HD13	1.99	0.45
1:AA:444:C:H2'	1:AA:445:G:C8	2.52	0.45
1:AA:537:G:H2'	1:AA:538:G:C8	2.49	0.45
1:AA:581:G:OP1	15:AO:65:ARG:NH2	2.49	0.45
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.81	0.45
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.16	0.45
12:AL:124:LYS:HA	12:AL:125:PRO:HD3	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:776:G:OP2	27:BD:13:ARG:NH1	2.49	0.45
25:BA:2507:G:H5''	36:BQ:82:ARG:HG2	1.98	0.45
28:BE:24:THR:HG23	28:BE:184:VAL:HG12	1.98	0.45
37:BR:56:LYS:NZ	37:BR:90:ARG:O	2.50	0.45
1:CA:70:G:H1	1:CA:99:U:H3	1.65	0.45
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.49	0.45
1:CA:537:G:H5''	12:CL:113:ARG:NH1	2.32	0.45
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.50	0.45
1:CA:693:G:H2'	1:CA:694:A:C8	2.52	0.45
1:CA:1142:G:H3'	1:CA:1143:G:H8	1.81	0.45
2:CB:161:ALA:HB1	2:CB:185:ILE:CD1	2.47	0.45
2:CB:169:LYS:O	2:CB:169:LYS:HD3	2.17	0.45
21:CU:2:GLY:O	21:CU:4:GLY:N	2.49	0.45
25:DA:414:C:H2'	25:DA:415:A:C8	2.52	0.45
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.17	0.45
25:DA:603:A:N1	25:DA:625:G:O2'	2.44	0.45
25:DA:1197:G:H2'	25:DA:1198:U:C6	2.52	0.45
25:DA:1638:C:H5''	25:DA:2710:C:O2'	2.15	0.45
25:DA:1799:G:O2'	27:DD:181:GLU:OE2	2.22	0.45
31:DH:126:PRO:HD2	31:DH:130:ARG:O	2.17	0.45
31:DH:175:LYS:HB2	31:DH:175:LYS:HE3	1.76	0.45
50:D4:40:HIS:O	50:D4:44:THR:N	2.43	0.45
1:AA:19:C:O2'	1:AA:572:A:N1	2.49	0.45
25:BA:240:A:C5	25:BA:241:G:H1'	2.51	0.45
25:BA:2132:G:O2'	25:BA:2142:G:OP2	2.35	0.45
25:BA:2902:G:H4'	25:BA:2903:G:O5'	2.17	0.45
29:BF:33:LEU:HD13	29:BF:112:MET:HE2	1.97	0.45
1:CA:1125:U:C2	10:CJ:38:ILE:HD12	2.52	0.45
1:CA:1174:G:H2'	1:CA:1175:G:C8	2.51	0.45
2:CB:33:TYR:N	2:CB:41:ILE:O	2.41	0.45
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.98	0.45
25:DA:906:G:O2'	36:DQ:67:ARG:NH2	2.39	0.45
25:DA:1002:G:H22	25:DA:1154:G:H1'	1.82	0.45
25:DA:1262:A:H2	51:D5:10:LYS:HD2	1.80	0.45
25:DA:1452:A:O2'	25:DA:1453:U:H2'	2.17	0.45
25:DA:1688:U:H2'	25:DA:1698:A:N6	2.32	0.45
25:DA:1779:U:H2'	61:DA:4760:HOH:O	2.15	0.45
25:DA:2114:A:C2	25:DA:2115:G:H1'	2.52	0.45
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.51	0.45
25:DA:2741:A:H2'	25:DA:2742:C:O4'	2.16	0.45
26:DB:42:C:O2'	30:DG:66:GLN:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DG:15:VAL:HG12	30:DG:19:LEU:HD12	1.98	0.45
32:DI:65:ALA:O	32:DI:69:LYS:N	2.49	0.45
37:DR:28:LEU:HD12	37:DR:48:VAL:HG11	1.99	0.45
1:AA:116:A:H61	1:AA:313:A:H1'	1.81	0.45
1:AA:303:A:H2'	1:AA:304:U:O4'	2.17	0.45
1:AA:624:C:H2'	1:AA:625:G:H8	1.82	0.45
1:AA:1221:G:H4'	19:AS:53:ASN:O	2.16	0.45
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.97	0.45
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.32	0.45
13:AM:3:ARG:HD2	13:AM:9:ILE:CG1	2.46	0.45
25:BA:144:C:H5'	43:BX:2:LYS:HE2	1.99	0.45
25:BA:537:G:OP1	25:BA:1280:U:O2'	2.30	0.45
25:BA:950:C:H4'	45:BZ:169:GLU:OE2	2.17	0.45
25:BA:1388:A:O2'	25:BA:1390:G:OP2	2.26	0.45
25:BA:1405:A:N1	25:BA:1418:U:C4	2.85	0.45
25:BA:2660:C:H2'	25:BA:2661:U:C6	2.52	0.45
34:BO:34:THR:OG1	34:BO:35:VAL:N	2.50	0.45
1:CA:113:G:O4'	1:CA:354:G:H4'	2.16	0.45
1:CA:501:C:H2'	1:CA:502:G:C8	2.51	0.45
1:CA:576:G:O6	1:CA:880:C:O2'	2.31	0.45
1:CA:637:G:H2'	1:CA:638:G:H8	1.82	0.45
1:CA:792:A:H4'	1:CA:793:U:H5''	1.99	0.45
1:CA:993:G:H1	1:CA:1045:C:H42	1.64	0.45
1:CA:1142:G:C2	1:CA:1143:G:H1'	2.52	0.45
1:CA:1228:C:P	13:CM:108:ARG:HH12	2.39	0.45
1:CA:1268:A:N3	1:CA:1326:C:O2'	2.47	0.45
1:CA:1353:G:O2'	1:CA:1354:C:H5'	2.15	0.45
3:CC:3:ASN:OD1	3:CC:3:ASN:N	2.49	0.45
7:CG:144:MET:HE2	7:CG:144:MET:HB3	1.81	0.45
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.98	0.45
10:CJ:22:LYS:O	10:CJ:26:ALA:N	2.50	0.45
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.82	0.45
13:CM:97:PRO:HG2	13:CM:103:THR:HG22	1.99	0.45
25:DA:345:A:OP2	25:DA:345:A:H8	1.99	0.45
25:DA:528:A:H2'	25:DA:529:A:H5''	1.98	0.45
25:DA:631:A:H1'	35:DP:66:GLY:HA2	1.99	0.45
25:DA:1399:C:C2'	25:DA:1400:G:H5'	2.47	0.45
25:DA:1913:A:H4'	25:DA:1914:C:H5''	1.99	0.45
26:DB:60:C:O5'	26:DB:60:C:H6	2.00	0.45
26:DB:98:G:H2'	26:DB:99:G:O4'	2.17	0.45
35:DP:38:GLN:HG2	35:DP:45:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.85	0.45
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.15	0.45
1:AA:1178:G:N2	1:AA:1181:G:OP2	2.47	0.45
2:AB:220:ASP:O	2:AB:223:ILE:HG12	2.17	0.45
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.99	0.45
5:AE:45:PHE:CE2	5:AE:47:LYS:HE3	2.52	0.45
18:AR:74:ARG:HG2	18:AR:80:PRO:O	2.16	0.45
22:AV:16:A:H2'	22:AV:17:U:O4'	2.17	0.45
25:BA:933:C:N3	25:BA:934:A:H8	2.15	0.45
26:BB:66:A:H61	26:BB:108:U:H2'	1.82	0.45
31:BH:3:ARG:HH22	31:BH:66:GLY:HA3	1.82	0.45
39:BT:112:ARG:HG3	39:BT:115:ARG:NH2	2.31	0.45
1:CA:848:C:O5'	1:CA:848:C:H6	2.00	0.45
1:CA:953:G:C2	1:CA:954:G:H1'	2.52	0.45
1:CA:1492:A:H4'	1:CA:1493:A:OP1	2.17	0.45
2:CB:44:LEU:HD22	2:CB:44:LEU:H	1.81	0.45
3:CC:140:ARG:HH22	3:CC:141:VAL:HG23	1.82	0.45
5:CE:78:HIS:CD2	5:CE:142:LEU:HD23	2.52	0.45
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.52	0.45
25:DA:510:C:H2'	25:DA:511:U:O4'	2.17	0.45
25:DA:515:A:H1'	25:DA:581:C:H1'	1.99	0.45
25:DA:565:C:H2'	25:DA:566:U:O4'	2.17	0.45
25:DA:1003:G:O2'	25:DA:1010:A:N1	2.39	0.45
25:DA:1846:G:H1	25:DA:1894:C:H42	1.65	0.45
25:DA:2135:A:H61	25:DA:2157:G:H21	1.65	0.45
25:DA:2155:G:C5	25:DA:2156:G:H1'	2.52	0.45
25:DA:2207:G:H3'	25:DA:2208:A:H5''	1.98	0.45
26:DB:24:G:H5''	26:DB:25:A:N7	2.32	0.45
26:DB:112:U:H2'	26:DB:113:G:H8	1.81	0.45
35:DP:101:VAL:HA	35:DP:106:LEU:O	2.17	0.45
39:DT:16:ARG:HB3	39:DT:16:ARG:HH11	1.81	0.45
50:D4:48:ARG:O	50:D4:50:VAL:N	2.50	0.45
1:AA:70:G:H2'	1:AA:71:C:C6	2.52	0.45
1:AA:110:C:H2'	1:AA:111:G:O4'	2.16	0.45
1:AA:1084:G:C5	1:AA:1085:U:C4	3.05	0.45
1:AA:1267:C:O5'	1:AA:1267:C:H6	1.99	0.45
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.17	0.45
16:AP:28:ARG:HG2	16:AP:29:ASP:OD1	2.16	0.45
25:BA:1077:G:H21	55:B9:36:GLN:HE22	1.65	0.45
25:BA:1846:A:P	27:BD:54:ARG:HH22	2.39	0.45
27:BD:233:HIS:HA	61:BD:3406:HOH:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BF:7:TYR:CD2	29:BF:24:LEU:HB2	2.52	0.45
29:BF:125:LEU:HD12	29:BF:194:MET:HB2	1.99	0.45
32:BI:9:LEU:HB3	32:BI:12:LEU:HB2	1.99	0.45
44:BY:56:PRO:C	44:BY:58:GLY:H	2.25	0.45
1:CA:130:A:O2'	1:CA:131:C:O5'	2.26	0.45
1:CA:250:A:H4'	1:CA:251:G:O5'	2.16	0.45
1:CA:302:G:O2'	1:CA:556:C:H5''	2.17	0.45
1:CA:375:U:C4	1:CA:376:G:N7	2.85	0.45
1:CA:411:A:H2'	1:CA:412:A:H4'	1.99	0.45
1:CA:1002:G:O6	1:CA:1038:C:N3	2.50	0.45
1:CA:1005:A:O2'	1:CA:1006:C:OP1	2.35	0.45
6:CF:82:ARG:HB2	6:CF:85:VAL:HG23	1.99	0.45
12:CL:113:ARG:NH2	61:CL:201:HOH:O	2.50	0.45
19:CS:41:VAL:HG22	19:CS:42:PRO:HD2	1.99	0.45
23:CX:40:C:H2'	23:CX:41:C:C6	2.51	0.45
25:DA:25:U:C4	25:DA:26:G:C6	3.05	0.45
25:DA:940:G:H2'	25:DA:941:A:O4'	2.17	0.45
25:DA:1539:G:H2'	25:DA:1540:U:O4'	2.17	0.45
25:DA:1922:G:H2'	25:DA:1923:U:O4'	2.17	0.45
25:DA:2529:G:OP1	31:DH:172:LYS:HE2	2.17	0.45
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.41	0.45
29:DF:7:TYR:O	29:DF:22:ALA:N	2.50	0.45
37:DR:29:LEU:HD23	37:DR:70:LEU:HD11	1.98	0.45
54:D8:54:GLU:O	54:D8:58:ILE:HG13	2.17	0.45
1:AA:54:C:H2'	1:AA:352:C:H41	1.81	0.44
1:AA:137:C:H2'	1:AA:138:G:C8	2.52	0.44
1:AA:538:G:H2'	1:AA:539:A:H8	1.82	0.44
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.43	0.44
2:AB:102:LEU:HD23	2:AB:182:ILE:HD12	1.99	0.44
2:AB:224:GLN:HA	2:AB:228:GLY:O	2.17	0.44
16:AP:5:ARG:HH11	16:AP:22:THR:HG23	1.82	0.44
25:BA:1480:A:N6	25:BA:1605:A:H62	2.09	0.44
25:BA:1577:C:O2'	25:BA:1578:C:P	2.75	0.44
25:BA:2163:G:O6	25:BA:2172:U:C2	2.67	0.44
29:BF:161:GLU:HG2	29:BF:164:ARG:NH2	2.32	0.44
34:BO:80:ASP:OD2	39:BT:71:GLY:HA3	2.17	0.44
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.18	0.44
51:B5:36:CYS:C	51:B5:38:ALA:H	2.25	0.44
1:CA:495:A:H4'	1:CA:496:A:OP1	2.16	0.44
1:CA:1050:G:H1'	1:CA:1214:C:O2	2.17	0.44
1:CA:1347:G:O2'	1:CA:1348:U:OP2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:63:ASN:HB3	3:CC:98:ASN:HD22	1.82	0.44
8:CH:51:VAL:HG21	8:CH:60:ARG:HH11	1.81	0.44
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.98	0.44
25:DA:530:G:O4'	25:DA:530:G:N3	2.48	0.44
25:DA:2064:C:H2'	25:DA:2065:C:C6	2.51	0.44
25:DA:2318:G:H22	38:DS:3:ARG:NH1	2.15	0.44
25:DA:2569:G:C2	25:DA:2570:G:C8	3.05	0.44
34:DO:53:LYS:HG2	34:DO:56:ASP:OD1	2.16	0.44
38:DS:84:GLN:HG3	38:DS:111:GLU:OE2	2.17	0.44
1:AA:358:U:H2'	1:AA:359:U:C6	2.52	0.44
1:AA:445:G:H2'	1:AA:446:G:H8	1.82	0.44
1:AA:600:C:O2'	1:AA:601:C:H5'	2.17	0.44
3:AC:123:GLN:HG2	3:AC:128:PHE:CD2	2.53	0.44
5:AE:8:GLU:HG3	5:AE:34:VAL:HG23	1.99	0.44
7:AG:73:MET:HE2	7:AG:73:MET:HB2	1.81	0.44
12:AL:53:ARG:HB3	12:AL:93:LEU:HD11	1.98	0.44
25:BA:44:G:H5''	25:BA:45:C:OP1	2.17	0.44
25:BA:227:C:H2'	25:BA:228:U:O4'	2.18	0.44
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.41	0.44
25:BA:1555:C:H4'	25:BA:1556:A:OP2	2.17	0.44
27:BD:142:VAL:HG13	27:BD:191:ALA:HB1	1.98	0.44
32:BI:135:GLU:C	32:BI:137:PRO:HD3	2.43	0.44
36:BQ:7:MET:HE3	36:BQ:7:MET:HB2	1.86	0.44
54:B8:61:LEU:O	54:B8:63:PRO:HD3	2.17	0.44
1:CA:595:G:H1'	1:CA:596:C:H5	1.82	0.44
1:CA:691:G:H2'	1:CA:692:U:C6	2.52	0.44
1:CA:1066:C:H2'	1:CA:1067:A:C8	2.52	0.44
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.17	0.44
1:CA:1206:G:H4'	3:CC:192:THR:O	2.18	0.44
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.17	0.44
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.16	0.44
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.33	0.44
7:CG:18:TYR:CD1	7:CG:59:LEU:HB2	2.52	0.44
12:CL:60:LEU:HD21	12:CL:66:VAL:HG22	1.99	0.44
14:CN:29:ARG:HD3	14:CN:40:CYS:HB2	1.99	0.44
23:CX:21:A:H5'	23:CX:22:G:OP1	2.17	0.44
25:DA:26:G:C6	25:DA:27:G:N1	2.86	0.44
25:DA:641:C:O2'	25:DA:2350:C:OP1	2.22	0.44
25:DA:821:A:N1	61:DA:4375:HOH:O	2.36	0.44
25:DA:866:A:H2'	25:DA:866:A:N3	2.32	0.44
25:DA:1038:C:N4	25:DA:1117:G:H1	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1411:C:H2'	25:DA:1412:A:C8	2.52	0.44
25:DA:1592:C:H2'	25:DA:1593:G:C8	2.53	0.44
25:DA:1983:C:H4'	25:DA:2606:C:H4'	1.99	0.44
25:DA:2126:A:N3	25:DA:2127:G:H1'	2.32	0.44
25:DA:2134:A:H3'	25:DA:2135:A:C8	2.52	0.44
25:DA:2144:U:H1'	25:DA:2148:G:H22	1.81	0.44
1:AA:442:C:H42	1:AA:492:G:H1	1.64	0.44
1:AA:1479:C:H2'	1:AA:1480:G:C8	2.52	0.44
1:AA:1494:G:H4'	25:BA:1935:A:C8	2.52	0.44
57:AA:3191:PCY:O5	57:AA:3191:PCY:N16	2.48	0.44
4:AD:168:ARG:H	4:AD:168:ARG:HD2	1.80	0.44
11:AK:19:ALA:HB3	11:AK:82:VAL:HA	1.99	0.44
25:BA:181:C:O2'	25:BA:849:A:N3	2.46	0.44
25:BA:609:A:N1	25:BA:856:G:O2'	2.44	0.44
25:BA:1398:U:OP1	61:BA:4203:HOH:O	2.21	0.44
25:BA:1517:G:N2	25:BA:1568:G:OP2	2.30	0.44
25:BA:2543:A:N3	25:BA:2670:C:O2'	2.48	0.44
27:BD:75:ILE:HD13	27:BD:99:ASP:OD2	2.17	0.44
30:BG:45:GLU:H	30:BG:45:GLU:HG2	1.52	0.44
40:BU:74:LEU:H	40:BU:74:LEU:HD12	1.81	0.44
50:B4:46:GLN:O	50:B4:46:GLN:HG2	2.16	0.44
1:CA:520:A:C2	1:CA:536:C:H1'	2.52	0.44
1:CA:743:U:H2'	1:CA:744:C:C6	2.52	0.44
1:CA:1058:G:H1	1:CA:1199:U:H3	1.65	0.44
1:CA:1157:A:C6	1:CA:1180:A:C5	3.05	0.44
1:CA:1309:G:N7	13:CM:99:ARG:NH2	2.65	0.44
3:CC:20:SER:HB2	3:CC:40:ARG:NH1	2.32	0.44
3:CC:83:ARG:O	3:CC:87:LEU:HG	2.18	0.44
23:CX:61:C:H2'	23:CX:62:C:C6	2.52	0.44
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.53	0.44
25:DA:526:A:OP1	61:DA:4468:HOH:O	2.21	0.44
25:DA:1165:U:H2'	25:DA:1166:C:C6	2.53	0.44
25:DA:1221(A):C:C2	25:DA:1229:G:C2	3.05	0.44
25:DA:1288:U:O2'	25:DA:1647:G:N2	2.50	0.44
25:DA:2332:U:H5'	25:DA:2336:A:N6	2.32	0.44
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.16	0.44
25:DA:2832:U:OP2	61:DA:4417:HOH:O	2.20	0.44
29:DF:116:ASP:O	29:DF:120:GLU:HG3	2.17	0.44
34:DO:80:ASP:OD2	39:DT:71:GLY:HA3	2.18	0.44
41:DV:85:LYS:HE3	41:DV:85:LYS:HB2	1.72	0.44
44:DY:1:MET:HG2	44:DY:2:ARG:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:DZ:150:LEU:HD12	45:DZ:150:LEU:HA	1.79	0.44
1:AA:346:G:OP1	39:BT:41:ARG:NH1	2.49	0.44
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.51	0.44
1:AA:495:A:N3	1:AA:496:A:H8	2.16	0.44
1:AA:993:G:H1	1:AA:1045:C:H42	1.65	0.44
1:AA:997:U:O2	1:AA:1044:A:N1	2.51	0.44
1:AA:1159:U:O2	1:AA:1160:G:N1	2.50	0.44
1:AA:1220:G:N2	19:AS:54:GLY:O	2.41	0.44
1:AA:1325:C:O2'	1:AA:1326:C:H5'	2.17	0.44
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.99	0.44
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.33	0.44
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.48	0.44
18:AR:24:ALA:C	18:AR:26:LEU:H	2.25	0.44
25:BA:510:C:H2'	25:BA:511:C:C6	2.53	0.44
25:BA:659:C:H2'	25:BA:660:C:C6	2.53	0.44
25:BA:1314:A:H2'	25:BA:1315:A:O4'	2.17	0.44
25:BA:1911:A:N1	25:BA:2246:G:H1'	2.33	0.44
29:BF:89:VAL:O	61:BF:403:HOH:O	2.21	0.44
1:CA:501:C:H2'	1:CA:502:G:H8	1.81	0.44
1:CA:600:C:O2'	1:CA:601:C:H5'	2.17	0.44
1:CA:926:G:H5''	1:CA:927:G:O5'	2.17	0.44
1:CA:1157:A:H5'	1:CA:1158:C:N1	2.31	0.44
1:CA:1227:A:H3'	1:CA:1227:A:H8	1.83	0.44
2:CB:32:ILE:HD13	2:CB:40:HIS:CD2	2.52	0.44
15:CO:33:THR:HG21	15:CO:85:LEU:HD22	1.98	0.44
23:CX:12:G:H4'	25:DA:1908:C:O2	2.17	0.44
25:DA:792:G:H5''	25:DA:793:A:H5'	2.00	0.44
25:DA:1270:C:O2'	25:DA:1325:G:H2'	2.17	0.44
25:DA:1815:A:H8	25:DA:1815:A:OP1	2.01	0.44
25:DA:2023:G:H5'	25:DA:2617:C:H4'	1.98	0.44
25:DA:2126:A:N1	25:DA:2162:G:H1'	2.33	0.44
25:DA:2154:G:H2'	25:DA:2154:G:N3	2.33	0.44
25:DA:2274:A:C5	25:DA:2276:G:C8	3.05	0.44
39:DT:24:PRO:HA	39:DT:49:VAL:HG22	1.98	0.44
40:DU:28:ARG:NH1	40:DU:38:THR:OG1	2.49	0.44
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.99	0.44
1:AA:58:C:O2'	1:AA:388:G:N7	2.39	0.44
1:AA:194:C:H2'	1:AA:195:A:H5''	2.00	0.44
5:AE:152:ARG:HA	8:AH:64:LYS:HE2	1.99	0.44
11:AK:77:MET:HE2	11:AK:77:MET:HB2	1.92	0.44
19:AS:28:LYS:HB3	19:AS:28:LYS:HE3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:331:G:N7	61:BA:4427:HOH:O	2.36	0.44
25:BA:347:G:C8	29:BF:171:PRO:HG3	2.53	0.44
25:BA:471:C:O2'	25:BA:472:G:H5'	2.17	0.44
25:BA:611:U:H2'	25:BA:612:C:H6	1.82	0.44
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.83	0.44
27:BD:206:LEU:HD22	27:BD:211:ARG:HG2	1.98	0.44
34:BO:36:GLY:HA2	34:BO:106:LEU:HD23	2.00	0.44
35:BP:47:ASP:OD2	35:BP:49:ARG:NH2	2.50	0.44
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.98	0.44
47:B1:94:LEU:O	47:B1:97:LEU:HB2	2.18	0.44
50:B4:54:GLY:O	50:B4:56:VAL:HA	2.18	0.44
1:CA:1027:C:O2'	1:CA:1034:G:N2	2.51	0.44
2:CB:118:LEU:O	2:CB:122:PHE:HB3	2.17	0.44
4:CD:13:ARG:NH1	4:CD:38:TYR:O	2.50	0.44
5:CE:139:LEU:HA	5:CE:142:LEU:HD12	1.99	0.44
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.83	0.44
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.89	0.44
24:CY:76:A:H3'	61:DA:4895:HOH:O	2.17	0.44
25:DA:1029:A:N1	25:DA:2465:C:O2'	2.47	0.44
25:DA:2313:C:H2'	25:DA:2314:C:C6	2.52	0.44
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.51	0.44
39:DT:29:ARG:HB3	39:DT:87:ASP:HB2	1.99	0.44
50:D4:33:VAL:HG12	50:D4:35:VAL:H	1.83	0.44
1:AA:352:C:H4'	1:AA:354:G:OP1	2.18	0.44
1:AA:431:A:H2'	1:AA:432:A:O4'	2.18	0.44
2:AB:78:GLN:C	2:AB:94:ASN:HD21	2.25	0.44
2:AB:114:ARG:O	2:AB:118:LEU:HG	2.18	0.44
3:AC:134:ILE:O	3:AC:138:VAL:HG23	2.17	0.44
14:AN:9:LYS:HG3	14:AN:12:ARG:HH12	1.83	0.44
15:AO:55:GLY:HA2	15:AO:58:MET:CE	2.48	0.44
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.18	0.44
25:BA:27:G:C2	25:BA:537:G:N3	2.86	0.44
25:BA:416:G:N1	35:BP:70:GLN:HG3	2.33	0.44
25:BA:776:G:C6	27:BD:208:LYS:HB2	2.52	0.44
25:BA:821:A:N3	25:BA:821:A:H2'	2.33	0.44
25:BA:1893:G:H2'	25:BA:1894:G:H8	1.81	0.44
25:BA:2129:C:H2'	25:BA:2130:C:C6	2.53	0.44
25:BA:2162:C:C4	25:BA:2173:G:O6	2.71	0.44
36:BQ:85:LYS:HG2	46:B0:7:LEU:HB3	1.97	0.44
39:BT:106:SER:O	39:BT:110:ILE:HG13	2.17	0.44
43:BX:31:HIS:HA	43:BX:32:PRO:HD3	1.87	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:946:A:H2'	1:CA:947:G:C8	2.53	0.44
1:CA:1137:C:O2'	1:CA:1138:G:N2	2.51	0.44
1:CA:1304:G:N2	1:CA:1332:A:OP2	2.41	0.44
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.99	0.44
4:CD:163:GLU:C	4:CD:165:MET:H	2.24	0.44
25:DA:602:G:H4'	25:DA:604:G:H4'	2.00	0.44
25:DA:941:A:H2'	25:DA:942:G:O4'	2.18	0.44
25:DA:1927:A:H2'	25:DA:1928:A:C8	2.52	0.44
25:DA:2058:A:N7	61:DA:4182:HOH:O	2.36	0.44
25:DA:2697:G:H2'	25:DA:2698:U:O4'	2.18	0.44
61:DA:4920:HOH:O	46:D0:4:LYS:NZ	2.50	0.44
26:DB:7:G:H3'	26:DB:8:U:H5''	2.00	0.44
27:DD:169:GLU:OE2	27:DD:174:ILE:HD11	2.18	0.44
30:DG:177:GLY:O	30:DG:179:PRO:HD3	2.18	0.44
31:DH:71:LEU:HD12	31:DH:71:LEU:HA	1.85	0.44
45:DZ:136:PHE:O	45:DZ:137:ILE:HG13	2.17	0.44
49:D3:18:ASP:OD1	49:D3:18:ASP:N	2.51	0.44
1:AA:44:G:H2'	1:AA:45:U:O4'	2.18	0.44
1:AA:406:G:H21	4:AD:119:GLN:HE22	1.64	0.44
1:AA:714:G:H2'	1:AA:715:A:C8	2.53	0.44
1:AA:745:C:H2'	1:AA:746:A:H8	1.83	0.44
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.44
1:AA:1082:G:H2'	1:AA:1083:U:O4'	2.18	0.44
1:AA:1160:G:C5	1:AA:1161:C:C5	3.05	0.44
1:AA:1166:G:N2	1:AA:1169:A:H3'	2.33	0.44
1:AA:1187:G:H5'	9:AI:113:LYS:HE2	1.98	0.44
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.53	0.44
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.53	0.44
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.49	0.44
4:AD:50:ARG:HA	4:AD:51:PRO:HD3	1.86	0.44
13:AM:3:ARG:NH2	13:AM:11:ARG:HH21	2.16	0.44
25:BA:950:C:H2'	25:BA:951:U:C6	2.53	0.44
25:BA:1052:C:O2'	33:BN:106:MET:HB3	2.18	0.44
25:BA:1513:G:O2'	25:BA:1593:C:O2'	2.26	0.44
25:BA:1925:G:OP1	27:BD:241:PRO:HB2	2.17	0.44
25:BA:2145:G:H2'	25:BA:2146:G:C8	2.49	0.44
25:BA:2228:G:H2'	25:BA:2229:A:C2	2.53	0.44
28:BE:55:ASN:HB3	28:BE:58:ARG:HG3	2.00	0.44
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.53	0.44
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.50	0.44
52:B6:14:THR:HG21	52:B6:48:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1034:G:H5''	1:CA:1035:A:OP2	2.18	0.44
1:CA:1381:U:C2'	1:CA:1382:C:H5'	2.48	0.44
2:CB:121:LEU:N	2:CB:125:PRO:HG2	2.33	0.44
16:CP:51:VAL:HG12	16:CP:53:VAL:N	2.31	0.44
25:DA:67:U:H2'	25:DA:68:G:C8	2.53	0.44
25:DA:815:C:C2	25:DA:1193:G:C2	3.05	0.44
25:DA:1314:C:OP1	61:DA:4448:HOH:O	2.20	0.44
25:DA:2207:G:P	25:DA:2207:G:H8	2.41	0.44
25:DA:2356:C:H2'	25:DA:2357:U:O4'	2.18	0.44
25:DA:2607:G:H2'	25:DA:2608:G:O4'	2.18	0.44
29:DF:36:VAL:HG11	29:DF:183:VAL:HG11	1.99	0.44
29:DF:183:VAL:O	29:DF:187:VAL:HG23	2.17	0.44
35:DP:19:VAL:HG12	35:DP:27:HIS:HB3	1.99	0.44
41:DV:56:SER:OG	41:DV:100:ARG:HD2	2.17	0.44
44:DY:94:LYS:HD3	44:DY:94:LYS:HA	1.81	0.44
45:DZ:131:ARG:H	45:DZ:131:ARG:HD2	1.83	0.44
1:AA:346:G:H3'	1:AA:346:G:N3	2.33	0.44
1:AA:371:G:O2'	1:AA:373:A:N7	2.46	0.44
1:AA:926:G:H5''	1:AA:927:G:O5'	2.18	0.44
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.99	0.44
3:AC:58:GLU:HB2	3:AC:65:ALA:HB3	1.99	0.44
3:AC:155:GLY:HA3	3:AC:196:LEU:HD22	1.99	0.44
4:AD:173:TRP:CD1	4:AD:173:TRP:H	2.36	0.44
13:AM:68:GLY:HA3	30:BG:116:ASP:OD1	2.17	0.44
25:BA:502:G:H4'	25:BA:527:A:N1	2.33	0.44
25:BA:596:G:O2'	25:BA:597:C:H3'	2.18	0.44
25:BA:1594:C:H2'	25:BA:1595:C:H6	1.83	0.44
25:BA:2156:A:O2'	25:BA:2157:A:OP1	2.29	0.44
25:BA:2316:G:H22	25:BA:2324:U:H3	1.65	0.44
27:BD:79:VAL:O	27:BD:114:GLY:N	2.45	0.44
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.18	0.44
30:BG:67:LYS:HD3	50:B4:5:ILE:HB	1.99	0.44
36:BQ:16:ARG:HG2	36:BQ:18:LYS:HG3	2.00	0.44
38:BS:3:ARG:HA	38:BS:3:ARG:HE	1.82	0.44
45:BZ:73:GLN:HB3	45:BZ:87:ASP:HB2	2.00	0.44
53:B7:24:THR:O	53:B7:28:ARG:HG3	2.18	0.44
1:CA:542:G:P	4:CD:10:ARG:HH22	2.40	0.44
1:CA:1134:G:H1	1:CA:1140:C:N4	2.15	0.44
1:CA:1392:G:N2	1:CA:1502:A:H8	2.13	0.44
25:DA:458:G:O2'	25:DA:469:G:O6	2.32	0.44
25:DA:1344:G:O2'	25:DA:1385:G:H2'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1531:C:H42	25:DA:1538:G:H1	1.66	0.44
25:DA:2280:G:N7	61:DA:4535:HOH:O	2.36	0.44
25:DA:2525:G:C2	25:DA:2539:C:C2	3.06	0.44
26:DB:2:C:H3'	26:DB:2:C:OP2	2.18	0.44
26:DB:45:A:C6	26:DB:46:A:C5	3.05	0.44
26:DB:57:A:O4'	30:DG:30:GLU:HG3	2.18	0.44
28:DE:105:THR:HG1	28:DE:199:ARG:HH21	1.61	0.44
34:DO:64:ARG:HB2	34:DO:83:ALA:HB3	1.99	0.44
1:AA:1127:G:H5'	1:AA:1280:A:O2'	2.17	0.44
1:AA:1511:G:H2'	1:AA:1512:U:O4'	2.18	0.44
4:AD:15:GLU:HG3	4:AD:63:LYS:HE2	1.99	0.44
4:AD:71:SER:OG	4:AD:74:GLN:HB2	2.18	0.44
11:AK:84:VAL:HG11	11:AK:91:ARG:HH11	1.83	0.44
13:AM:14:ARG:H	13:AM:14:ARG:HG3	1.62	0.44
14:AN:53:LEU:HA	14:AN:54:PRO:HD2	1.88	0.44
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.18	0.44
15:AO:74:ASP:HB3	15:AO:77:ARG:HB2	2.00	0.44
19:AS:51:VAL:HG22	19:AS:71:LEU:HD22	1.99	0.44
19:AS:71:LEU:HD23	19:AS:71:LEU:HA	1.89	0.44
25:BA:1405:A:C2	25:BA:1418:U:O4	2.71	0.44
25:BA:2163:G:C6	25:BA:2164:C:C2	3.05	0.44
25:BA:2710:U:H2'	25:BA:2711:C:C6	2.53	0.44
25:BA:2784:C:H2'	25:BA:2785:C:H6	1.82	0.44
25:BA:2859:U:OP2	39:BT:95:ARG:NH1	2.50	0.44
25:BA:2880:C:H2'	25:BA:2881:C:O4'	2.18	0.44
29:BF:29:ASN:H	29:BF:112:MET:HE1	1.83	0.44
31:BH:7:LEU:HA	31:BH:8:PRO:HD3	1.83	0.44
1:CA:344:A:H4'	1:CA:345:C:OP2	2.18	0.44
1:CA:589:C:H2'	1:CA:590:C:H5'	1.99	0.44
1:CA:714:G:H2'	1:CA:715:A:C8	2.52	0.44
1:CA:1023:G:C4	1:CA:1024:G:C8	3.05	0.44
1:CA:1254:C:O4'	1:CA:1356:G:H5''	2.18	0.44
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.52	0.44
4:CD:201:GLN:HE22	5:CE:99:GLY:HA2	1.83	0.44
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.18	0.44
10:CJ:67:THR:O	10:CJ:67:THR:OG1	2.33	0.44
13:CM:79:LYS:NZ	13:CM:83:ASP:OD2	2.39	0.44
19:CS:22:LEU:HB3	19:CS:27:GLU:HG3	1.99	0.44
25:DA:570:G:H2'	25:DA:2030:A:N7	2.33	0.44
25:DA:918:A:H5''	26:DB:98:G:O2'	2.17	0.44
25:DA:2029:G:H2'	25:DA:2031:A:OP1	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2080:G:O2'	25:DA:2081:C:H5'	2.17	0.44
25:DA:2117:A:O2'	25:DA:2118:U:H5''	2.18	0.44
25:DA:2236:C:H2'	25:DA:2237:G:O4'	2.18	0.44
25:DA:2376:A:N1	38:DS:87:PHE:HB3	2.33	0.44
35:DP:7:ARG:HA	35:DP:8:PRO:HD3	1.90	0.44
36:DQ:29:PHE:HB2	36:DQ:105:GLU:OE2	2.18	0.44
54:D8:4:MET:HE3	54:D8:63:PRO:HG3	1.99	0.44
1:AA:67:C:H2'	1:AA:68:G:H8	1.78	0.43
1:AA:767:A:H2'	1:AA:768:A:O4'	2.18	0.43
2:AB:51:LEU:HD21	2:AB:201:ILE:HG23	1.99	0.43
3:AC:156:ARG:NH2	3:AC:159:GLY:O	2.51	0.43
11:AK:44:SER:O	11:AK:48:ILE:HD13	2.18	0.43
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.18	0.43
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.18	0.43
25:BA:320:C:H2'	25:BA:321:C:H6	1.81	0.43
25:BA:515:G:H2'	25:BA:516:G:O4'	2.18	0.43
25:BA:898:U:O2'	49:B3:42:ALA:O	2.36	0.43
25:BA:1056:A:N3	25:BA:1199:C:H1'	2.32	0.43
25:BA:1067:A:H8	25:BA:1068:G:H5''	1.82	0.43
25:BA:1338:U:H2'	25:BA:1339:C:H6	1.83	0.43
25:BA:2762:A:OP2	25:BA:2763:A:O2'	2.32	0.43
26:BB:2:C:H2'	26:BB:3:C:C6	2.53	0.43
29:BF:18:ARG:NH2	29:BF:127:GLU:OE1	2.50	0.43
30:BG:66:GLN:HG3	50:B4:1:MET:HE1	2.00	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CZ	2.53	0.43
41:BV:98:GLU:CD	41:BV:100:ARG:HH11	2.26	0.43
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.21	0.43
1:CA:353:A:H5'	1:CA:353:A:H8	1.82	0.43
1:CA:741:G:H2'	1:CA:742:G:O4'	2.18	0.43
1:CA:1177:G:H3'	1:CA:1178:G:H8	1.83	0.43
1:CA:1234:C:H1'	1:CA:1364:U:O2	2.18	0.43
8:CH:39:LEU:HB3	8:CH:45:ILE:HG12	1.99	0.43
11:CK:99:GLN:C	11:CK:101:SER:H	2.24	0.43
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.43
18:CR:74:ARG:HG3	18:CR:79:LEU:HB2	2.00	0.43
25:DA:18:C:O2'	25:DA:554:U:OP1	2.36	0.43
25:DA:411:G:C5	35:DP:72:PRO:HB3	2.53	0.43
25:DA:471:A:H2'	25:DA:472:A:O4'	2.17	0.43
25:DA:1021:A:H3'	25:DA:1021:A:H8	1.83	0.43
25:DA:1550:C:H2'	25:DA:1551:C:C6	2.53	0.43
25:DA:2469:A:H2'	25:DA:2470:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2678:C:H2'	25:DA:2679:A:O4'	2.18	0.43
25:DA:2760:C:H1'	31:DH:139:GLN:HE22	1.83	0.43
25:DA:2815:C:H5''	51:D5:29:THR:HG21	2.00	0.43
26:DB:54:G:H21	30:DG:29:TRP:HE1	1.66	0.43
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.51	0.43
31:DH:5:GLY:HA2	31:DH:69:ARG:HB3	2.00	0.43
44:DY:6:HIS:H	44:DY:6:HIS:CD2	2.36	0.43
45:DZ:33:LEU:HD21	45:DZ:90:VAL:HG21	1.99	0.43
49:D3:4:LEU:O	49:D3:36:VAL:HA	2.17	0.43
1:AA:537:G:OP1	12:AL:113:ARG:NH2	2.37	0.43
1:AA:657:G:C2	1:AA:750:G:C5	3.06	0.43
1:AA:860:A:H2'	1:AA:861:G:O4'	2.18	0.43
1:AA:1152:A:H5'	10:AJ:13:HIS:CG	2.54	0.43
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.46	0.43
25:BA:1810:U:H2'	61:BA:5050:HOH:O	2.18	0.43
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.99	0.43
28:BE:173:VAL:CG2	28:BE:185:LYS:HB2	2.47	0.43
30:BG:17:PRO:HA	30:BG:20:ILE:HD12	2.01	0.43
37:BR:16:HIS:O	37:BR:16:HIS:HD2	2.00	0.43
50:B4:49:PHE:HD1	50:B4:49:PHE:HA	1.69	0.43
1:CA:8:A:H5'	5:CE:101:ILE:HG22	2.01	0.43
1:CA:685:G:C2	1:CA:686:U:C4	3.06	0.43
1:CA:940:C:H2'	1:CA:941:G:C8	2.53	0.43
1:CA:977:A:H1'	1:CA:982:U:O4	2.18	0.43
1:CA:1256:A:H61	1:CA:1278:U:C1'	2.31	0.43
1:CA:1304:G:C6	1:CA:1305:G:N1	2.85	0.43
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.52	0.43
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.99	0.43
25:DA:601:C:O2'	25:DA:605:C:H5''	2.18	0.43
25:DA:1021:A:H3'	25:DA:1021:A:C8	2.53	0.43
25:DA:1190:G:O2'	25:DA:1191:G:H5'	2.18	0.43
25:DA:1214:A:H61	25:DA:1235:G:H1'	1.83	0.43
25:DA:1227:G:OP2	40:DU:16:LYS:NZ	2.46	0.43
25:DA:2128:C:H2'	25:DA:2129:C:O4'	2.17	0.43
25:DA:2882:A:OP1	37:DR:96:ARG:NE	2.51	0.43
30:DG:98:ARG:H	30:DG:98:ARG:HG2	1.40	0.43
31:DH:11:VAL:HG21	31:DH:50:VAL:HG23	2.00	0.43
33:DN:115:ARG:HA	33:DN:118:LYS:HE3	1.99	0.43
45:DZ:10:ARG:NH1	45:DZ:36:LYS:HD2	2.33	0.43
50:D4:40:HIS:HB3	50:D4:43:TYR:HB2	2.00	0.43
1:AA:628:G:C2'	1:AA:629:G:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.16	0.43
1:AA:1229:A:O2'	23:AX:30:G:OP1	2.36	0.43
1:AA:1247:U:H3	1:AA:1290:G:H1	1.65	0.43
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.53	0.43
1:AA:1422:G:C5'	34:BO:48:PRO:HB3	2.43	0.43
2:AB:174:VAL:O	2:AB:178:ARG:HB2	2.18	0.43
3:AC:15:THR:HG23	3:AC:181:ASN:HD22	1.84	0.43
4:AD:18:LYS:NZ	4:AD:26:CYS:O	2.32	0.43
4:AD:43:HIS:HA	4:AD:46:LYS:HD3	1.99	0.43
7:AG:51:GLN:O	7:AG:55:GLY:HA2	2.18	0.43
16:AP:75:ARG:O	16:AP:78:GLY:N	2.46	0.43
25:BA:1199:C:H2'	25:BA:1200:G:O4'	2.19	0.43
25:BA:1451:U:H2'	25:BA:1452:U:H6	1.83	0.43
25:BA:1576:G:C2'	25:BA:1577:C:H5'	2.48	0.43
25:BA:1576:G:O2'	25:BA:1577:C:H5'	2.17	0.43
25:BA:1756:U:H2'	25:BA:1757:C:C6	2.53	0.43
25:BA:2005:C:H4'	25:BA:2618:C:H4'	1.99	0.43
25:BA:2331:G:C2	38:BS:3:ARG:HA	2.53	0.43
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.52	0.43
28:BE:75:VAL:HG13	28:BE:77:ILE:H	1.83	0.43
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.54	0.43
30:BG:122:PRO:HG3	30:BG:182:LYS:H	1.83	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CE2	2.53	0.43
33:BN:30:ILE:HG22	33:BN:34:LEU:HD22	1.99	0.43
35:BP:85:LEU:HG	35:BP:115:LEU:O	2.18	0.43
45:BZ:137:ILE:HA	45:BZ:156:LYS:NZ	2.34	0.43
48:B2:28:LYS:HG3	48:B2:53:LEU:HD21	1.99	0.43
52:B6:15:GLU:HG3	52:B6:47:THR:HG23	1.99	0.43
1:CA:560:U:H4'	1:CA:561:U:O5'	2.18	0.43
1:CA:833:U:H2'	1:CA:834:C:H6	1.82	0.43
1:CA:1138:G:C5	1:CA:1140:C:H1'	2.53	0.43
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.47	0.43
1:CA:1485:U:H2'	1:CA:1486:G:C8	2.53	0.43
23:CX:65:C:H2'	23:CX:66:C:C6	2.54	0.43
24:CY:76:A:H5'	47:D1:30:VAL:HG21	1.99	0.43
25:DA:632:A:H2'	25:DA:633:A:C8	2.53	0.43
25:DA:674:G:O2'	29:DF:74:ARG:HD3	2.19	0.43
25:DA:746:A:H2'	25:DA:2612:C:H5''	2.00	0.43
25:DA:1027:A:C6	25:DA:1126:A:C4	3.06	0.43
25:DA:1260:G:C6	25:DA:1261:C:C4	3.07	0.43
25:DA:1530:C:H1'	25:DA:1531:C:OP1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1654:A:H1'	25:DA:2823:A:H5'	2.00	0.43
25:DA:2136:C:N3	25:DA:2155:G:O6	2.52	0.43
27:DD:164:GLN:NE2	27:DD:166:GLN:OE1	2.47	0.43
29:DF:116:ASP:OD2	35:DP:1:MET:N	2.44	0.43
35:DP:95:VAL:HG13	35:DP:125:VAL:HA	2.00	0.43
36:DQ:1:MET:HE2	36:DQ:1:MET:HB3	1.92	0.43
39:DT:64:ARG:HB2	39:DT:73:GLU:HG2	2.01	0.43
49:D3:10:LYS:HB3	49:D3:53:LEU:HA	2.00	0.43
1:AA:1057:G:H2'	1:AA:1058:G:H5'	1.99	0.43
4:AD:187:ARG:NH2	4:AD:193:ASP:OD1	2.46	0.43
7:AG:78:ARG:NH1	7:AG:79:ARG:HD2	2.33	0.43
20:AT:77:ALA:O	20:AT:81:LYS:HG3	2.19	0.43
22:AV:14:A:H2'	22:AV:15:A:H8	1.82	0.43
25:BA:1314:A:C2	25:BA:2035:A:C4	3.07	0.43
30:BG:16:ARG:O	30:BG:20:ILE:HG13	2.18	0.43
39:BT:23:ARG:HG3	39:BT:120:ARG:NH1	2.33	0.43
44:BY:99:CYS:HB2	44:BY:106:LEU:HD21	2.00	0.43
45:BZ:7:ALA:O	45:BZ:62:PRO:HD3	2.19	0.43
47:B1:64:ALA:HA	47:B1:67:ILE:HG13	2.00	0.43
49:B3:7:LYS:HE3	49:B3:32:GLN:HE21	1.83	0.43
50:B4:58:ARG:O	50:B4:61:ARG:HB3	2.18	0.43
54:B8:62:LEU:HB3	54:B8:65:GLU:CG	2.48	0.43
1:CA:141:A:H1'	1:CA:182:U:O2	2.19	0.43
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.19	0.43
1:CA:950:U:H2'	1:CA:951:G:C8	2.54	0.43
1:CA:1145:C:H4'	1:CA:1146:A:H5'	2.01	0.43
1:CA:1314:C:OP1	19:CS:6:LYS:NZ	2.30	0.43
2:CB:144:ARG:NH2	2:CB:148:TYR:OH	2.49	0.43
3:CC:11:ARG:HB3	3:CC:15:THR:HB	2.00	0.43
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.51	0.43
12:CL:46:LYS:NZ	12:CL:91:LYS:O	2.42	0.43
25:DA:320:A:H4'	25:DA:322:A:C8	2.52	0.43
25:DA:720:C:H2'	25:DA:721:C:C6	2.54	0.43
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.35	0.43
25:DA:1257:C:H2'	25:DA:1258:C:C6	2.53	0.43
25:DA:1614:A:C2	42:DW:93:ALA:HB2	2.53	0.43
25:DA:2349:G:OP1	61:DA:4097:HOH:O	2.21	0.43
25:DA:2695:C:H2'	25:DA:2696:U:H6	1.83	0.43
30:DG:121:ASN:HA	30:DG:122:PRO:HD3	1.80	0.43
36:DQ:111:GLU:O	36:DQ:115:MET:HG2	2.18	0.43
38:DS:58:LEU:HD11	38:DS:65:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:DU:61:TRP:CH2	40:DU:93:LYS:HB2	2.54	0.43
45:DZ:5:LEU:HD21	45:DZ:43:GLU:HB3	1.99	0.43
1:AA:522:C:H41	12:AL:53:ARG:NH2	2.16	0.43
1:AA:526:C:OP2	12:AL:91:LYS:HE3	2.19	0.43
1:AA:737:A:H2'	1:AA:738:C:C6	2.53	0.43
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.17	0.43
5:AE:145:LYS:O	5:AE:149:GLU:HG2	2.18	0.43
13:AM:11:ARG:HA	13:AM:45:VAL:HB	2.01	0.43
25:BA:599:U:H2'	25:BA:600:G:C8	2.54	0.43
25:BA:847:A:H8	25:BA:847:A:OP1	2.00	0.43
25:BA:964:A:H5''	26:BB:98:G:O2'	2.18	0.43
25:BA:1373:C:O2'	37:BR:105:ARG:NH1	2.43	0.43
25:BA:1553:A:O2'	25:BA:1554:A:O5'	2.25	0.43
25:BA:1686:U:O2'	25:BA:1687:C:H5'	2.19	0.43
25:BA:2761:A:H5'	31:BH:4:ILE:HD12	2.01	0.43
45:BZ:54:HIS:HD2	45:BZ:99:TYR:O	2.01	0.43
1:CA:598:U:H2'	1:CA:599:C:C6	2.52	0.43
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	2.01	0.43
1:CA:1492:A:H2'	1:CA:1493:A:C4	2.53	0.43
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	2.00	0.43
13:CM:13:LYS:O	13:CM:45:VAL:HG23	2.19	0.43
14:CN:59:ALA:HB1	14:CN:61:TRP:HZ3	1.82	0.43
25:DA:149:A:H2'	25:DA:150:C:O4'	2.19	0.43
25:DA:234:C:H2'	25:DA:235:U:H6	1.84	0.43
25:DA:298:G:H5''	25:DA:299:A:OP1	2.18	0.43
25:DA:417:C:H1'	25:DA:2407:G:N2	2.33	0.43
25:DA:1041:C:H42	25:DA:1114:G:H1	1.66	0.43
25:DA:1153:C:H2'	25:DA:1154:G:O4'	2.19	0.43
25:DA:1292:U:H2'	25:DA:1293:C:H6	1.83	0.43
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.99	0.43
25:DA:1932:A:H2'	25:DA:1933:G:O4'	2.18	0.43
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.19	0.43
25:DA:2516:G:C6	25:DA:2517:C:C4	3.07	0.43
25:DA:2572:A:N7	28:DE:145:LYS:HB2	2.34	0.43
35:DP:38:GLN:HG2	35:DP:45:LEU:N	2.33	0.43
42:DW:18:ARG:HG2	42:DW:76:VAL:HB	2.01	0.43
43:DX:20:GLY:HA2	43:DX:23:GLU:OE2	2.19	0.43
49:D3:9:VAL:HG12	49:D3:32:GLN:HE22	1.83	0.43
1:AA:100:C:H2'	1:AA:101:A:C8	2.54	0.43
1:AA:162:A:H5''	1:AA:163:C:OP2	2.18	0.43
1:AA:430:A:OP1	4:AD:9:CYS:N	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:534:U:O5'	1:AA:534:U:H6	2.02	0.43
1:AA:560:U:H4'	1:AA:561:U:O5'	2.18	0.43
1:AA:796:C:H1'	57:AA:3191:PCY:H92	2.00	0.43
1:AA:1015:A:O3'	14:AN:15:LYS:NZ	2.52	0.43
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.56	0.43
24:AY:5:G:N2	24:AY:6:G:H1'	2.33	0.43
25:BA:160:G:O2'	25:BA:161:C:H5'	2.18	0.43
25:BA:197:C:H2'	25:BA:198:C:H6	1.84	0.43
25:BA:504:A:N1	25:BA:525:G:H4'	2.33	0.43
25:BA:1302:G:O2'	29:BF:75:HIS:HE1	2.02	0.43
25:BA:1685:C:H5''	25:BA:2722:C:O2'	2.19	0.43
25:BA:2827:G:OP1	37:BR:99:LYS:HE2	2.19	0.43
26:BB:75:G:H5''	26:BB:75:G:H8	1.82	0.43
27:BD:71:ASP:HB3	27:BD:103:ARG:NH2	2.27	0.43
30:BG:72:ARG:NH1	30:BG:87:PRO:HG3	2.33	0.43
38:BS:59:LYS:HB2	38:BS:59:LYS:HE3	1.83	0.43
45:BZ:93:ASP:OD1	45:BZ:94:GLU:N	2.51	0.43
1:CA:473:G:C2'	1:CA:474:G:H5'	2.48	0.43
1:CA:1002:G:H3'	1:CA:1003:G:C8	2.53	0.43
1:CA:1055:A:N3	3:CC:156:ARG:HD2	2.34	0.43
1:CA:1371:G:C6	1:CA:1372:U:C4	3.06	0.43
1:CA:1446:U:H4'	1:CA:1447:A:C5	2.52	0.43
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.19	0.43
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.48	0.43
11:CK:43:SER:HB3	11:CK:68:ALA:HB2	2.01	0.43
14:CN:24:CYS:HB3	14:CN:29:ARG:H	1.83	0.43
19:CS:20:LEU:HA	19:CS:23:ASN:HD22	1.83	0.43
25:DA:93:G:H2'	25:DA:94:C:C6	2.54	0.43
25:DA:649:G:H2'	25:DA:650:C:O4'	2.18	0.43
25:DA:893:C:H5'	25:DA:894:C:OP2	2.19	0.43
25:DA:959:A:N3	25:DA:2457:U:O2'	2.45	0.43
25:DA:1415:U:O2'	25:DA:1417:C:OP1	2.37	0.43
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.53	0.43
25:DA:2135:A:H61	25:DA:2157:G:N2	2.17	0.43
25:DA:2545:G:N3	25:DA:2565:A:H2	2.16	0.43
25:DA:2819:G:H2'	25:DA:2821:A:N7	2.34	0.43
26:DB:26:A:O5'	26:DB:26:A:H8	2.02	0.43
26:DB:33:G:C2	26:DB:50:G:C2	3.07	0.43
34:DO:98:VAL:HG22	34:DO:118:ALA:HA	2.00	0.43
35:DP:99:LEU:O	35:DP:103:ALA:N	2.50	0.43
36:DQ:24:GLY:HA2	36:DQ:67:ARG:NH2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:68:G:C2	1:AA:69:G:H1'	2.54	0.43
1:AA:164:U:H2'	1:AA:165:C:C6	2.54	0.43
1:AA:479:C:C4	1:AA:480:U:C4	3.06	0.43
1:AA:1028:C:H2'	1:AA:1029:C:H4'	2.00	0.43
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.34	0.43
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.19	0.43
2:AB:71:VAL:HG12	2:AB:170:GLU:HG3	2.01	0.43
4:AD:128:VAL:HG12	4:AD:129:ASN:ND2	2.33	0.43
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.33	0.43
6:AF:2:ARG:NE	6:AF:69:GLU:HG2	2.34	0.43
25:BA:553:A:C2	25:BA:2064:A:H2'	2.53	0.43
25:BA:1093:G:O2'	25:BA:1094:A:H8	2.01	0.43
26:BB:78:A:C2	26:BB:100:A:C4	3.06	0.43
29:BF:132:VAL:HG22	29:BF:163:VAL:HG22	2.01	0.43
30:BG:179:PRO:HG3	50:B4:43:TYR:OH	2.18	0.43
36:BQ:21:THR:HG21	36:BQ:101:ARG:HD3	2.00	0.43
42:BW:88:ARG:HG3	42:BW:92:ARG:HH21	1.83	0.43
1:CA:399:G:H2'	1:CA:400:C:C6	2.53	0.43
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.52	0.43
1:CA:1228:C:H4'	13:CM:116:THR:HA	2.01	0.43
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.16	0.43
6:CF:61:LEU:HD23	6:CF:63:TYR:HE1	1.84	0.43
9:CI:67:GLY:O	9:CI:73:GLN:NE2	2.43	0.43
9:CI:99:LEU:HB3	9:CI:101:PHE:HE2	1.83	0.43
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.87	0.43
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.83	0.43
24:CY:73:A:H2'	24:CY:74:C:O4'	2.18	0.43
25:DA:1579:A:H2'	25:DA:1580:A:C8	2.54	0.43
25:DA:2025:C:H2'	25:DA:2026:C:C6	2.54	0.43
25:DA:2031:A:N3	25:DA:2455:G:O2'	2.35	0.43
25:DA:2037:G:O2'	25:DA:2038:G:H5'	2.18	0.43
25:DA:2628:C:H1'	25:DA:2781:A:H2'	2.00	0.43
26:DB:13:A:O2'	26:DB:14:U:H3'	2.19	0.43
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	2.01	0.43
29:DF:34:TRP:CZ2	35:DP:8:PRO:HG3	2.53	0.43
39:DT:56:GLY:O	39:DT:59:THR:HG22	2.18	0.43
43:DX:18:TYR:C	43:DX:20:GLY:H	2.26	0.43
50:D4:57:GLU:HA	50:D4:58:ARG:HA	1.82	0.43
54:D8:63:PRO:HG2	54:D8:64:TYR:CD2	2.54	0.43
1:AA:922:G:H2'	1:AA:923:A:C8	2.54	0.43
1:AA:993:G:H2'	1:AA:995:C:H41	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1092:A:H8	1:AA:1092:A:O5'	2.01	0.43
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.51	0.43
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.65	0.43
2:AB:196:LEU:HD12	2:AB:196:LEU:HA	1.90	0.43
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.19	0.43
3:AC:113:ALA:HB3	3:AC:114:PRO:HD3	2.01	0.43
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.48	0.43
5:AE:90:VAL:O	5:AE:91:LEU:HD13	2.19	0.43
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.34	0.43
14:AN:3:ARG:HA	14:AN:3:ARG:HD2	1.58	0.43
16:AP:4:ILE:N	16:AP:65:GLN:O	2.30	0.43
20:AT:43:LEU:O	20:AT:47:GLY:N	2.44	0.43
25:BA:1440:U:H2'	25:BA:1441:A:O4'	2.19	0.43
25:BA:1587:U:H2'	25:BA:1588:G:O4'	2.18	0.43
25:BA:1797:U:H2'	25:BA:1798:C:H6	1.84	0.43
25:BA:2166:U:H2'	25:BA:2168:C:C5	2.53	0.43
25:BA:2897:U:H2'	25:BA:2898:C:C6	2.52	0.43
29:BF:183:VAL:O	29:BF:187:VAL:HG23	2.19	0.43
32:BI:6:LEU:HG	32:BI:36:ALA:HA	2.01	0.43
42:BW:14:PRO:HG2	42:BW:78:GLU:CG	2.48	0.43
1:CA:406:G:H4'	4:CD:5:ILE:HD11	2.00	0.43
1:CA:582:U:OP1	15:CO:68:ARG:NH1	2.51	0.43
1:CA:617:G:H4'	16:CP:44:THR:O	2.17	0.43
1:CA:790:A:N6	1:CA:1498:U:OP1	2.52	0.43
1:CA:1039:C:H2'	1:CA:1040:U:C6	2.54	0.43
2:CB:187:LEU:HD23	2:CB:201:ILE:HB	2.00	0.43
3:CC:51:GLY:O	3:CC:70:VAL:HA	2.19	0.43
6:CF:67:MET:HE1	6:CF:75:LEU:HD12	2.00	0.43
9:CI:99:LEU:HB3	9:CI:101:PHE:CE2	2.54	0.43
11:CK:48:ILE:HD11	11:CK:64:ALA:HA	2.01	0.43
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.18	0.43
17:CQ:56:VAL:O	17:CQ:77:VAL:HB	2.19	0.43
20:CT:86:ARG:O	20:CT:90:GLN:NE2	2.49	0.43
25:DA:28:A:O2'	25:DA:583:G:H5'	2.18	0.43
25:DA:151:C:H42	25:DA:175:G:H1	1.67	0.43
25:DA:237:C:H2'	25:DA:238:C:C6	2.53	0.43
25:DA:764:A:H5'	27:DD:210:GLY:CA	2.49	0.43
25:DA:864:G:C6	25:DA:865:C:N4	2.86	0.43
25:DA:1301:A:H2	25:DA:1626:G:N3	2.17	0.43
25:DA:1508:A:H4'	25:DA:1509(A):A:C4	2.54	0.43
25:DA:2872:G:O2'	25:DA:2873:A:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:52:LEU:O	28:DE:76:ARG:N	2.34	0.43
36:DQ:20:ALA:HB2	45:DZ:79:ARG:HG2	1.99	0.43
38:DS:68:GLN:HE21	38:DS:68:GLN:HA	1.83	0.43
45:DZ:144:LEU:HA	45:DZ:144:LEU:HD23	1.76	0.43
1:AA:575:G:O2'	1:AA:821:G:OP2	2.28	0.43
1:AA:590:C:H2'	1:AA:591:U:C6	2.54	0.43
1:AA:931:C:N4	1:AA:1386:G:H1	2.16	0.43
1:AA:1290:G:C4	1:AA:1291:G:C8	3.06	0.43
10:AJ:8:LEU:HD23	10:AJ:96:ILE:HA	2.01	0.43
19:AS:30:LEU:HD21	19:AS:32:LYS:HG3	2.01	0.43
25:BA:354:A:H2	25:BA:1255:A:H2'	1.83	0.43
25:BA:844:C:OP1	29:BF:60:SER:OG	2.29	0.43
27:BD:5:LYS:HB3	27:BD:5:LYS:HE3	1.57	0.43
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.84	0.43
40:BU:58:ARG:HA	40:BU:61:TRP:CE3	2.54	0.43
44:BY:5:MET:HE2	44:BY:5:MET:HB2	1.59	0.43
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	2.01	0.43
1:CA:9:G:H2'	1:CA:10:A:C8	2.54	0.43
1:CA:153:C:H2'	1:CA:154:C:H6	1.83	0.43
1:CA:418:C:H2'	1:CA:419:C:C6	2.53	0.43
1:CA:1009:G:C2	1:CA:1010:G:C4	3.07	0.43
1:CA:1493:A:C8	25:DA:1913:A:N1	2.86	0.43
7:CG:14:PRO:HB3	7:CG:19:GLY:C	2.43	0.43
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.19	0.43
13:CM:90:LEU:HD23	13:CM:93:ARG:HE	1.84	0.43
25:DA:1188:U:C4'	41:DV:79:VAL:HG22	2.49	0.43
25:DA:1505:C:H2'	25:DA:1506:C:H6	1.84	0.43
25:DA:2257:U:O2'	25:DA:2258:C:H5'	2.18	0.43
25:DA:2815:C:H2'	25:DA:2816:C:H6	1.82	0.43
43:DX:35:THR:HB	43:DX:38:GLU:HB2	2.01	0.43
47:D1:86:SER:OG	47:D1:89:GLU:OE2	2.27	0.43
1:AA:271:C:H2'	1:AA:272:C:C6	2.54	0.43
1:AA:299:G:C6	1:AA:300:A:C6	3.07	0.43
1:AA:444:C:H2'	1:AA:445:G:H8	1.84	0.43
1:AA:920:U:H2'	1:AA:921:U:C6	2.54	0.43
3:AC:138:VAL:HG22	3:AC:151:VAL:HG23	2.00	0.43
4:AD:184:LYS:HE2	4:AD:184:LYS:HB3	1.80	0.43
8:AH:29:SER:HB2	8:AH:32:LYS:HG3	2.01	0.43
20:AT:51:GLU:HG3	20:AT:54:LYS:NZ	2.34	0.43
23:AX:61:C:H2'	23:AX:62:C:H6	1.84	0.43
25:BA:411:U:H2'	25:BA:412:C:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:543:G:H2'	25:BA:544:U:C6	2.54	0.43
25:BA:2021:C:H4'	25:BA:2736:C:O2	2.18	0.43
25:BA:2116:G:OP1	32:BI:22:LYS:HD2	2.19	0.43
25:BA:2172:U:N3	25:BA:2173:G:N7	2.66	0.43
25:BA:2193:A:H1'	25:BA:2194:U:C6	2.54	0.43
32:BI:12:LEU:HD23	32:BI:12:LEU:HA	1.71	0.43
32:BI:72:LEU:O	32:BI:74:ASN:N	2.52	0.43
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	2.00	0.43
39:BT:24:PRO:HD3	39:BT:52:ILE:HD12	2.00	0.43
46:B0:43:THR:HG23	46:B0:43:THR:O	2.19	0.43
51:B5:35:GLU:HG3	51:B5:51:TYR:CD2	2.53	0.43
1:CA:1008:C:H42	1:CA:1021:G:H1	1.67	0.43
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.99	0.43
8:CH:51:VAL:HG11	8:CH:60:ARG:HH12	1.84	0.43
10:CJ:6:ILE:O	10:CJ:71:LEU:HD12	2.18	0.43
20:CT:57:ARG:HH22	20:CT:100:ILE:HD12	1.84	0.43
25:DA:80:G:O2'	25:DA:294:A:N1	2.47	0.43
25:DA:749:C:O2	25:DA:1618:A:H2'	2.19	0.43
25:DA:829:A:N7	25:DA:2248:C:H5'	2.33	0.43
25:DA:1022:G:C6	25:DA:1140:C:C4	3.06	0.43
25:DA:1185:C:H5''	25:DA:1186:G:OP1	2.18	0.43
25:DA:1790:C:H5''	25:DA:1791:A:OP1	2.19	0.43
25:DA:1791:A:H3'	25:DA:1792:G:H8	1.84	0.43
25:DA:2377:A:H2'	25:DA:2378:A:C8	2.54	0.43
32:DI:77:LEU:HD11	32:DI:101:LEU:HB2	2.00	0.43
45:DZ:53:ILE:H	45:DZ:53:ILE:HG13	1.73	0.43
45:DZ:146:ILE:H	45:DZ:146:ILE:HG13	1.62	0.43
1:AA:240:C:H2'	1:AA:241:C:H6	1.84	0.42
1:AA:302:G:O2'	1:AA:556:C:H5''	2.19	0.42
1:AA:739:C:O2'	15:AO:42:HIS:ND1	2.51	0.42
1:AA:996:A:H2'	1:AA:997:U:O4'	2.19	0.42
11:AK:20:TYR:CZ	11:AK:83:ILE:HD12	2.54	0.42
25:BA:284:G:C2	25:BA:285:U:O4	2.72	0.42
25:BA:399:G:H8	47:B1:65:SER:O	2.02	0.42
25:BA:1653:C:H4'	25:BA:1654:A:O5'	2.19	0.42
25:BA:2258:G:H2'	25:BA:2259:A:C8	2.54	0.42
30:BG:43:LEU:HD11	30:BG:153:ARG:HG2	2.01	0.42
39:BT:11:GLU:OE1	39:BT:57:PHE:HB3	2.19	0.42
49:B3:46:ASN:O	49:B3:50:VAL:HG22	2.19	0.42
54:B8:54:GLU:O	54:B8:58:ILE:HG13	2.19	0.42
1:CA:630:G:O2'	1:CA:631:G:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:742:G:P	15:CO:35:ARG:HH21	2.42	0.42
1:CA:1118:C:H1'	1:CA:1179:A:C6	2.54	0.42
1:CA:1240:U:O2	7:CG:32:ARG:HB2	2.19	0.42
2:CB:170:GLU:O	2:CB:174:VAL:HG23	2.19	0.42
4:CD:153:ARG:NH2	4:CD:180:GLY:O	2.51	0.42
25:DA:272(E):G:C2	25:DA:364:C:C2	3.07	0.42
25:DA:699:A:C2	25:DA:1633:G:N3	2.87	0.42
25:DA:818:G:H4'	25:DA:838:C:O3'	2.19	0.42
25:DA:956:G:OP2	36:DQ:14:ARG:NH2	2.50	0.42
25:DA:977:G:N3	25:DA:1001:A:H2	2.16	0.42
25:DA:980:A:C4	25:DA:1136:G:O4'	2.72	0.42
25:DA:1227:G:OP1	40:DU:13:LYS:HG2	2.19	0.42
25:DA:1721:G:N3	25:DA:1721:G:H5''	2.34	0.42
25:DA:1878:G:H2'	25:DA:1879:C:C6	2.54	0.42
25:DA:2128:C:H5'	25:DA:2173:A:C2	2.54	0.42
25:DA:2261:C:H1'	25:DA:2388:A:N3	2.34	0.42
25:DA:2330:G:H2'	25:DA:2331:G:O4'	2.18	0.42
26:DB:16:G:C6	26:DB:69:G:C2	3.07	0.42
27:DD:276:LYS:H	27:DD:276:LYS:HG2	1.63	0.42
29:DF:132:VAL:HA	29:DF:138:GLU:HB3	2.00	0.42
32:DI:69:LYS:O	32:DI:73:GLU:HB2	2.19	0.42
34:DO:52:VAL:HG12	34:DO:94:ARG:HH22	1.84	0.42
50:D4:14:ILE:HG23	50:D4:31:ILE:HB	2.01	0.42
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	2.00	0.42
1:AA:35:G:O2'	12:AL:118:SER:O	2.32	0.42
1:AA:198:G:O6	1:AA:219:C:N4	2.52	0.42
1:AA:690:G:C6	1:AA:691:G:C6	3.07	0.42
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.55	0.42
1:AA:1252:A:H2'	1:AA:1253:G:O4'	2.19	0.42
2:AB:209:ARG:HB2	2:AB:209:ARG:HH11	1.84	0.42
7:AG:13:GLN:HA	7:AG:14:PRO:HD3	1.90	0.42
10:AJ:27:ALA:HA	10:AJ:81:THR:CG2	2.49	0.42
12:AL:110:VAL:HG23	12:AL:120:TYR:HB3	2.01	0.42
25:BA:194:G:O6	47:B1:39:LYS:NZ	2.42	0.42
25:BA:1903:C:H2'	25:BA:1904:C:H6	1.83	0.42
25:BA:2320:G:O2'	25:BA:2322:A:N7	2.51	0.42
25:BA:2339:A:H2'	25:BA:2340:A:H8	1.82	0.42
29:BF:53:THR:HB	29:BF:56:GLU:OE2	2.19	0.42
30:BG:120:LEU:HD23	30:BG:120:LEU:HA	1.88	0.42
34:BO:98:VAL:HG22	34:BO:118:ALA:HA	2.01	0.42
35:BP:121:LYS:O	35:BP:123:LEU:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BR:31:HIS:C	37:BR:33:ARG:H	2.28	0.42
37:BR:72:ASP:O	37:BR:76:VAL:HG23	2.19	0.42
41:BV:18:LEU:HD22	41:BV:19:LYS:N	2.34	0.42
50:B4:62:ARG:HB2	50:B4:63:TYR:CD1	2.54	0.42
1:CA:411:A:C6	1:CA:429:U:C4	3.07	0.42
1:CA:857:C:H2'	1:CA:858:G:O4'	2.18	0.42
1:CA:982:U:N3	1:CA:1223:C:N3	2.67	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.19	0.42
1:CA:1183:A:H3'	1:CA:1184:G:H5''	2.01	0.42
1:CA:1355:G:C2'	1:CA:1356:G:H5'	2.48	0.42
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.33	0.42
3:CC:107:GLN:O	3:CC:108:ASN:C	2.63	0.42
7:CG:16:LEU:HD22	7:CG:16:LEU:H	1.84	0.42
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	2.01	0.42
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	2.01	0.42
15:CO:10:LYS:HB2	15:CO:10:LYS:HE2	1.72	0.42
25:DA:271(U):G:H2'	25:DA:271(V):G:H8	1.82	0.42
25:DA:1007:C:OP1	33:DN:35:ARG:NH1	2.49	0.42
25:DA:1337:G:H2'	25:DA:1338:G:O4'	2.19	0.42
25:DA:2335:A:O2'	25:DA:2336:A:H5''	2.20	0.42
25:DA:2647:U:O2'	25:DA:2648:C:H5'	2.19	0.42
25:DA:2768:C:C4	25:DA:2769:C:C5	3.07	0.42
26:DB:80:U:H2'	26:DB:81:G:C8	2.54	0.42
28:DE:4:ILE:HD11	28:DE:29:GLY:HA2	2.02	0.42
31:DH:28:GLY:HA3	31:DH:79:VAL:HB	2.00	0.42
33:DN:91:LEU:HA	33:DN:95:PRO:HA	2.00	0.42
35:DP:84:ASN:HB3	35:DP:117:GLU:O	2.19	0.42
36:DQ:7:MET:HB3	36:DQ:7:MET:HE3	1.82	0.42
36:DQ:75:THR:HG21	36:DQ:87:LYS:HZ3	1.83	0.42
42:DW:80:PRO:O	42:DW:100:THR:HB	2.19	0.42
48:D2:10:LEU:HB3	48:D2:14:ARG:NH1	2.34	0.42
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.82	0.42
1:AA:657:G:C2	1:AA:658:G:C8	3.07	0.42
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.54	0.42
14:AN:4:LYS:C	14:AN:6:LEU:N	2.78	0.42
25:BA:298:G:H2'	25:BA:299:G:C8	2.54	0.42
25:BA:518:G:H2'	25:BA:519:G:O4'	2.19	0.42
25:BA:895:G:H2'	25:BA:896:A:C8	2.54	0.42
25:BA:1615:G:H5'	27:BD:60:ARG:HA	2.01	0.42
25:BA:2023:A:H5''	25:BA:2701:U:H2'	2.00	0.42
25:BA:2034:G:OP1	42:BW:11:ARG:NH2	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BE:111:ARG:HA	37:BR:1:MET:SD	2.59	0.42
29:BF:116:ASP:O	29:BF:120:GLU:HG3	2.18	0.42
31:BH:9:ILE:HG12	31:BH:69:ARG:HH11	1.82	0.42
37:BR:97:VAL:HG22	37:BR:114:VAL:HG13	2.00	0.42
44:BY:1:MET:H1	44:BY:1:MET:HG3	1.43	0.42
44:BY:55:TYR:CE1	44:BY:61:ILE:HG21	2.55	0.42
45:BZ:79:ARG:HB3	45:BZ:80:ARG:NH1	2.34	0.42
50:B4:54:GLY:O	50:B4:55:ARG:HB2	2.19	0.42
1:CA:392:G:H2'	1:CA:393:A:H8	1.83	0.42
1:CA:487:A:H2'	1:CA:488:C:O4'	2.19	0.42
1:CA:1003:G:H2'	1:CA:1004:A:C1'	2.49	0.42
1:CA:1204:A:P	14:CN:3:ARG:HH11	2.42	0.42
2:CB:147:LYS:HD2	2:CB:148:TYR:CE1	2.54	0.42
2:CB:213:LEU:HD22	2:CB:214:ILE:HD13	2.02	0.42
3:CC:11:ARG:NH2	3:CC:177:THR:O	2.52	0.42
6:CF:14:LEU:HD22	6:CF:18:GLN:HB3	2.02	0.42
9:CI:46:ALA:HA	9:CI:78:LYS:HB2	2.01	0.42
11:CK:65:ALA:HB1	11:CK:98:LEU:HD23	2.02	0.42
12:CL:6:THR:HG23	12:CL:9:GLN:OE1	2.20	0.42
14:CN:6:LEU:HD12	14:CN:6:LEU:HA	1.90	0.42
18:CR:43:PHE:C	18:CR:51:LEU:HD12	2.45	0.42
25:DA:185:U:H4'	25:DA:218:A:H4'	2.00	0.42
25:DA:332:A:O2'	25:DA:334:C:OP2	2.28	0.42
25:DA:1272:A:H3'	25:DA:1273:U:H5''	2.00	0.42
25:DA:1896:G:H2'	25:DA:1897:G:H8	1.84	0.42
25:DA:2651:C:H2'	25:DA:2652:C:C6	2.54	0.42
27:DD:24:ILE:HD13	27:DD:84:TYR:HB2	2.01	0.42
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.76	0.42
35:DP:46:LYS:HE3	35:DP:46:LYS:HB3	1.76	0.42
35:DP:55:ARG:HG2	35:DP:56:SER:O	2.19	0.42
43:DX:35:THR:HG22	43:DX:37:THR:N	2.34	0.42
44:DY:54:LYS:O	44:DY:56:PRO:HD3	2.19	0.42
1:AA:102:G:O2'	1:AA:151:A:N3	2.42	0.42
1:AA:110:C:C2'	1:AA:111:G:H5'	2.48	0.42
1:AA:348:G:C2'	1:AA:349:A:H5'	2.49	0.42
1:AA:460:G:H21	1:AA:472:A:H62	1.68	0.42
1:AA:595:G:H1'	1:AA:596:C:H5	1.84	0.42
1:AA:978:A:O2'	1:AA:1322:C:N3	2.41	0.42
2:AB:166:ASP:OD2	2:AB:169:LYS:HB2	2.19	0.42
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.34	0.42
3:AC:110:ASN:O	3:AC:141:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:118:GLN:H	3:AC:118:GLN:HG2	1.62	0.42
4:AD:138:TYR:CE1	4:AD:140:VAL:HA	2.54	0.42
4:AD:188:LEU:H	4:AD:188:LEU:CD2	2.31	0.42
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.01	0.42
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	2.00	0.42
25:BA:515:G:N7	42:BW:49:LYS:NZ	2.64	0.42
25:BA:704:U:H2'	25:BA:705:C:C6	2.54	0.42
25:BA:990:A:C4	25:BA:2460:A:C2	3.07	0.42
25:BA:992:G:H2'	25:BA:993:G:C8	2.54	0.42
25:BA:2032:G:H5''	42:BW:42:ARG:HB2	2.00	0.42
25:BA:2589:A:H5''	25:BA:2590:G:H5'	2.01	0.42
32:BI:93:THR:H	32:BI:96:ASP:CG	2.27	0.42
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.55	0.42
1:CA:15:G:C4	1:CA:16:A:C8	3.07	0.42
1:CA:143:A:O3'	1:CA:144:G:H8	2.02	0.42
1:CA:532:A:H5'	3:CC:161:GLU:OE2	2.20	0.42
1:CA:767:A:H2'	1:CA:768:A:O4'	2.19	0.42
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.54	0.42
1:CA:1261:A:C5	1:CA:1262:C:C4	3.06	0.42
1:CA:1442:G:HO2'	1:CA:1442(A):G:P	2.38	0.42
8:CH:23:SER:HA	8:CH:63:LEU:HD22	2.00	0.42
14:CN:53:LEU:HA	14:CN:54:PRO:HD2	1.92	0.42
16:CP:14:ASN:OD1	16:CP:42:ARG:NH2	2.53	0.42
25:DA:251:A:C5	25:DA:252:G:H1'	2.54	0.42
25:DA:348:G:H2'	25:DA:349:G:C8	2.54	0.42
25:DA:372:G:H8	47:D1:65:SER:O	2.02	0.42
25:DA:652(D):C:H42	25:DA:652(U):G:H1	1.66	0.42
25:DA:921:G:H4'	25:DA:2269:A:C5	2.54	0.42
25:DA:954:G:C5	25:DA:955:C:C5	3.07	0.42
25:DA:984:A:H5''	25:DA:985:C:H5	1.85	0.42
25:DA:1524:G:N2	25:DA:1525:G:H1'	2.34	0.42
25:DA:2376:A:H3'	25:DA:2377:A:H8	1.84	0.42
27:DD:147:LEU:HD13	27:DD:155:LEU:HD21	2.01	0.42
28:DE:115:GLY:O	28:DE:119:ARG:HB2	2.20	0.42
29:DF:196:LEU:HD23	29:DF:196:LEU:HA	1.79	0.42
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.75	0.42
45:DZ:117:LEU:HD12	45:DZ:174:VAL:HG22	2.00	0.42
1:AA:406:G:N2	4:AD:119:GLN:HE22	2.18	0.42
1:AA:439:A:N1	1:AA:496:A:C4	2.78	0.42
1:AA:1353:G:O2'	1:AA:1354:C:H5'	2.20	0.42
1:AA:1362:C:C2'	1:AA:1363:C:H5''	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:11:THR:HG22	8:AH:15:ASN:HD21	1.83	0.42
25:BA:324:A:H2'	25:BA:358:C:H1'	2.02	0.42
25:BA:496:A:H2'	25:BA:497:A:O4'	2.20	0.42
25:BA:672:G:H8	25:BA:672:G:O5'	2.03	0.42
25:BA:1077:G:H5''	55:B9:8:LYS:HE3	2.01	0.42
25:BA:1576:G:C6	25:BA:1577:C:N4	2.88	0.42
25:BA:2247:G:H2'	25:BA:2248:C:C6	2.54	0.42
25:BA:2556:G:H2'	25:BA:2557:G:O4'	2.19	0.42
25:BA:2849:G:H5'	37:BR:46:GLY:HA2	2.01	0.42
30:BG:155:MET:HE2	30:BG:155:MET:HB3	1.88	0.42
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.33	0.42
39:BT:53:ARG:O	39:BT:59:THR:HA	2.20	0.42
39:BT:108:ARG:HH22	39:BT:112:ARG:HH11	1.67	0.42
43:BX:31:HIS:CD2	43:BX:33:LYS:H	2.37	0.42
47:B1:89:GLU:H	47:B1:89:GLU:HG2	1.47	0.42
1:CA:407:G:OP1	4:CD:115:ARG:HD3	2.19	0.42
1:CA:1095:U:C4	1:CA:1096:C:C4	3.07	0.42
1:CA:1124:G:H5''	10:CJ:35:SER:OG	2.20	0.42
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.85	0.42
8:CH:124:ALA:O	8:CH:128:GLY:N	2.51	0.42
10:CJ:70:ARG:HA	10:CJ:70:ARG:HD3	1.91	0.42
13:CM:57:ARG:NH1	50:D4:34:GLU:HA	2.34	0.42
19:CS:68:GLY:H	50:D4:58:ARG:NH1	2.18	0.42
25:DA:58:G:O2'	25:DA:73:A:N1	2.44	0.42
25:DA:236:C:H2'	25:DA:237:C:H6	1.85	0.42
25:DA:271(R):G:H5''	47:D1:97:LEU:HD21	2.00	0.42
25:DA:463:G:N2	25:DA:466:A:OP2	2.38	0.42
25:DA:1212:G:C2	25:DA:1236:G:C4	3.07	0.42
25:DA:1262:A:C5	25:DA:1263:U:C5	3.07	0.42
25:DA:1514:U:H2'	25:DA:1515:G:C8	2.55	0.42
25:DA:2365:G:O6	54:D8:39:LYS:HE3	2.19	0.42
25:DA:2365:G:O6	54:D8:43:GLN:NE2	2.52	0.42
28:DE:181:LEU:HD12	28:DE:181:LEU:HA	1.86	0.42
29:DF:135:LYS:HB2	29:DF:138:GLU:CD	2.44	0.42
30:DG:67:LYS:HE2	50:D4:5:ILE:HD12	2.01	0.42
36:DQ:110:THR:HG23	36:DQ:113:GLN:OE1	2.20	0.42
42:DW:13:SER:HA	42:DW:14:PRO:HD3	1.91	0.42
43:DX:5:TYR:CE1	48:D2:30:ARG:HB2	2.55	0.42
45:DZ:98:MET:HE2	45:DZ:98:MET:HB2	1.84	0.42
46:D0:82:ARG:HA	46:D0:83:PRO:HD3	1.79	0.42
55:D9:7:VAL:HG12	55:D9:34:GLN:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:176:C:H2'	1:AA:177:C:C6	2.54	0.42
1:AA:186:C:H2'	1:AA:187:C:C6	2.54	0.42
1:AA:555:C:H2'	1:AA:556:C:C6	2.55	0.42
1:AA:687:A:N3	1:AA:688:G:H1'	2.34	0.42
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.50	0.42
4:AD:134:ASP:O	4:AD:136:PRO:HD3	2.19	0.42
8:AH:82:HIS:CE1	8:AH:84:ARG:HD2	2.55	0.42
25:BA:180:A:H2'	25:BA:181:C:C6	2.55	0.42
25:BA:278:G:H2'	25:BA:279:G:H5''	2.02	0.42
25:BA:876:A:N7	25:BA:2260:C:H5'	2.35	0.42
25:BA:1220:U:O3'	25:BA:1221:G:H4'	2.19	0.42
25:BA:1940:A:O2'	25:BA:1942:C:N4	2.53	0.42
25:BA:2170:G:OP2	25:BA:2170:G:H8	2.02	0.42
25:BA:2787:C:H2'	25:BA:2788:A:O4'	2.20	0.42
29:BF:140:LEU:HD21	29:BF:170:LEU:HD11	2.01	0.42
31:BH:116:GLU:HA	31:BH:117:PRO:HD3	1.95	0.42
39:BT:124:ASP:O	39:BT:128:GLU:HG3	2.19	0.42
42:BW:2:GLU:OE2	42:BW:72:LYS:NZ	2.36	0.42
54:B8:6:THR:HG23	54:B8:64:TYR:HD2	1.84	0.42
1:CA:26:A:O2'	4:CD:209:ARG:NH2	2.52	0.42
1:CA:988:G:C2	1:CA:989:C:H1'	2.55	0.42
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.55	0.42
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.37	0.42
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.55	0.42
9:CI:50:LEU:HD21	9:CI:81:ILE:HD12	2.01	0.42
25:DA:858:U:H1'	25:DA:2268:A:H2'	2.01	0.42
25:DA:1005:C:H2'	25:DA:1006:C:H6	1.84	0.42
25:DA:1751:C:O2'	25:DA:2861:G:O2'	2.34	0.42
25:DA:1810:A:H2'	25:DA:1811:G:O4'	2.19	0.42
25:DA:2114:A:O2'	25:DA:2167:U:H1'	2.20	0.42
25:DA:2294:C:P	38:DS:89:ARG:HH22	2.43	0.42
25:DA:2820:A:C6	37:DR:4:LEU:HD11	2.55	0.42
27:DD:142:VAL:CG1	27:DD:191:ALA:HB1	2.49	0.42
31:DH:8:PRO:HB3	31:DH:51:ARG:HG2	2.02	0.42
44:DY:90:LEU:HB2	44:DY:92:ASN:HB3	2.01	0.42
54:D8:23:VAL:HG11	54:D8:47:LYS:HD3	2.00	0.42
1:AA:10:A:OP2	5:AE:126:ARG:HD2	2.20	0.42
1:AA:590:C:H2'	1:AA:591:U:H6	1.85	0.42
1:AA:1125:U:H5''	10:AJ:5:ARG:HH22	1.85	0.42
2:AB:55:PHE:CD1	2:AB:58:ILE:HD12	2.55	0.42
14:AN:2:ALA:HB1	14:AN:6:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:82:ILE:O	15:AO:86:GLY:N	2.51	0.42
16:AP:39:TYR:CG	16:AP:73:LEU:HD13	2.54	0.42
25:BA:484:G:O2'	25:BA:495:G:O6	2.28	0.42
25:BA:764:G:H2'	25:BA:765:A:O4'	2.20	0.42
25:BA:898:U:OP1	49:B3:49:LYS:NZ	2.51	0.42
25:BA:1583:C:H2'	25:BA:1584:G:O4'	2.19	0.42
25:BA:1597:C:OP1	25:BA:1765:U:O2'	2.23	0.42
25:BA:2050:U:H2'	25:BA:2051:G:O4'	2.19	0.42
25:BA:2127:C:H2'	25:BA:2128:G:C8	2.54	0.42
25:BA:2430:A:H2'	25:BA:2431:U:C6	2.54	0.42
25:BA:2648:U:H1'	25:BA:2796:G:N2	2.34	0.42
25:BA:2736:C:H4'	37:BR:1:MET:HG3	2.02	0.42
29:BF:150:GLY:HA2	29:BF:172:TRP:CD2	2.55	0.42
30:BG:148:MET:HE3	30:BG:148:MET:HB2	1.79	0.42
33:BN:42:TRP:HD1	33:BN:48:MET:HE1	1.85	0.42
38:BS:63:THR:HG23	38:BS:100:ALA:HB2	2.01	0.42
44:BY:7:VAL:HG21	44:BY:72:VAL:CG1	2.50	0.42
47:B1:89:GLU:O	47:B1:93:GLU:HG2	2.20	0.42
48:B2:2:LYS:O	48:B2:6:VAL:HG23	2.18	0.42
1:CA:1502:A:H2	1:CA:1505:G:N1	2.13	0.42
2:CB:13:ALA:C	2:CB:15:VAL:H	2.25	0.42
2:CB:179:LYS:HG3	8:CH:72:PRO:HG3	2.02	0.42
7:CG:26:PHE:O	7:CG:30:ILE:HG13	2.19	0.42
22:CV:16:A:N1	23:CX:36:U:C2	2.88	0.42
23:CX:65:C:H2'	23:CX:66:C:H6	1.84	0.42
25:DA:805:G:H5''	35:DP:38:GLN:HG3	2.02	0.42
25:DA:1124:C:H2'	25:DA:1125:G:O4'	2.19	0.42
25:DA:1628:G:H2'	25:DA:1629:U:C6	2.55	0.42
25:DA:2137:C:C2	25:DA:2138:C:H5	2.38	0.42
25:DA:2567:G:H2'	25:DA:2568:C:C6	2.54	0.42
26:DB:94:C:H2'	26:DB:95:C:C6	2.55	0.42
27:DD:25:THR:HG21	27:DD:113:VAL:HG11	2.01	0.42
27:DD:146:GLU:HB2	27:DD:189:CYS:HB3	2.02	0.42
36:DQ:73:PRO:HA	36:DQ:93:TYR:CD1	2.54	0.42
41:DV:39:LEU:HD12	41:DV:47:VAL:HA	2.02	0.42
51:D5:35:GLU:HG3	51:D5:51:TYR:CD2	2.54	0.42
52:D6:40:CYS:HA	52:D6:41:PRO:HD3	1.82	0.42
1:AA:91:C:H2'	1:AA:92:C:C6	2.54	0.42
1:AA:179:A:H2'	1:AA:180:U:C6	2.54	0.42
1:AA:1438:G:H2'	1:AA:1439:C:C6	2.55	0.42
24:AY:5:G:C2	24:AY:69:G:C4	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1387:U:O4'	43:BX:57:LEU:HD23	2.19	0.42
25:BA:1432:C:H2'	25:BA:1433:C:C6	2.54	0.42
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.19	0.42
25:BA:2284:U:H5''	25:BA:2285:A:OP1	2.20	0.42
25:BA:2699:U:H2'	25:BA:2700:U:O4'	2.19	0.42
29:BF:24:LEU:HB3	29:BF:115:ALA:HB2	2.00	0.42
34:BO:21:CYS:HB2	34:BO:39:ILE:HD12	2.02	0.42
43:BX:43:VAL:HG21	43:BX:81:VAL:HG11	2.02	0.42
49:B3:24:LYS:HB2	49:B3:24:LYS:HE2	1.83	0.42
53:B7:18:PHE:CE2	53:B7:22:MET:HG3	2.55	0.42
1:CA:868:C:H2'	1:CA:869:G:O4'	2.20	0.42
4:CD:125:HIS:HD2	4:CD:152:SER:OG	2.03	0.42
13:CM:20:THR:HA	13:CM:25:ILE:HG22	2.01	0.42
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.19	0.42
19:CS:51:VAL:O	19:CS:57:HIS:HA	2.20	0.42
22:CV:14:A:H3'	22:CV:15:A:H8	1.85	0.42
25:DA:7:G:H2'	25:DA:8:A:H8	1.85	0.42
25:DA:266:G:N2	25:DA:427:U:H1'	2.34	0.42
25:DA:300:A:N3	25:DA:319:C:H1'	2.34	0.42
25:DA:631:A:N3	25:DA:2415:G:O2'	2.42	0.42
25:DA:927:G:H2'	25:DA:928:G:O4'	2.20	0.42
25:DA:1138:G:O2'	33:DN:105:GLY:HA3	2.19	0.42
25:DA:1978:A:H2'	25:DA:1979:C:O4'	2.20	0.42
25:DA:2298:A:N6	25:DA:2318:G:C8	2.88	0.42
25:DA:2852:G:H2'	25:DA:2853:C:O4'	2.20	0.42
26:DB:78:A:C2	26:DB:100:A:C4	3.08	0.42
29:DF:124:LEU:HB3	29:DF:193:VAL:HG22	2.02	0.42
36:DQ:1:MET:HG3	36:DQ:44:ALA:HB1	2.02	0.42
41:DV:62:LEU:HD21	41:DV:95:LEU:HB2	2.01	0.42
43:DX:31:HIS:HA	43:DX:32:PRO:HD3	1.85	0.42
50:D4:40:HIS:HA	50:D4:41:PRO:HD2	1.82	0.42
1:AA:92:C:H2'	1:AA:93:G:C8	2.55	0.42
1:AA:122:G:H2'	1:AA:123:C:O4'	2.20	0.42
1:AA:763:G:H2'	1:AA:764:C:C6	2.55	0.42
1:AA:997:U:C2'	1:AA:998:G:H5'	2.49	0.42
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.55	0.42
1:AA:1234:C:C2'	1:AA:1235:U:H5'	2.50	0.42
2:AB:124:SER:HA	2:AB:125:PRO:HA	1.77	0.42
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	2.01	0.42
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.54	0.42
6:AF:72:VAL:HG23	6:AF:90:VAL:HG11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2161:C:H6	25:BA:2161:C:O5'	2.02	0.42
25:BA:2800:C:H2'	25:BA:2801:C:C6	2.55	0.42
26:BB:91:C:OP1	36:BQ:16:ARG:HG3	2.20	0.42
27:BD:79:VAL:HG12	27:BD:113:VAL:HA	2.01	0.42
31:BH:33:LEU:HD23	31:BH:136:ILE:HG13	2.02	0.42
43:BX:12:VAL:HG21	43:BX:27:THR:HG22	2.02	0.42
43:BX:60:ARG:NH1	53:B7:47:ARG:HH22	2.17	0.42
1:CA:93:G:O2'	1:CA:96:U:H5'	2.20	0.42
1:CA:115:G:H1'	1:CA:116:A:N7	2.34	0.42
1:CA:131:C:H2'	1:CA:132:C:C6	2.54	0.42
1:CA:411:A:C4	1:CA:413:G:O4'	2.72	0.42
1:CA:765:G:N1	1:CA:812:C:O2'	2.40	0.42
1:CA:933:G:C6	1:CA:1385:G:C6	3.08	0.42
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.20	0.42
1:CA:1328:C:H2'	1:CA:1329:A:O4'	2.19	0.42
2:CB:177:ALA:HB1	2:CB:182:ILE:HB	2.01	0.42
6:CF:35:ALA:HB2	6:CF:67:MET:HB3	2.01	0.42
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	2.01	0.42
12:CL:117:ARG:NH2	12:CL:124:LYS:HB2	2.35	0.42
13:CM:25:ILE:HD12	13:CM:66:LEU:HD22	2.02	0.42
25:DA:172:C:H2'	25:DA:173:G:H8	1.84	0.42
25:DA:271(H):G:N3	25:DA:271(I):G:C8	2.88	0.42
25:DA:601:C:OP1	29:DF:108:LYS:NZ	2.38	0.42
25:DA:900:A:H2'	25:DA:901:A:C8	2.54	0.42
25:DA:1359:A:C2	25:DA:1372:U:O4	2.72	0.42
25:DA:1434:A:H61	25:DA:1558:A:H62	1.66	0.42
25:DA:1607:C:H4'	25:DA:1608:A:O5'	2.19	0.42
25:DA:1823:G:OP1	27:DD:54:ARG:NH1	2.53	0.42
25:DA:1849:G:H2'	25:DA:1850:G:H8	1.85	0.42
25:DA:2386:C:H2'	25:DA:2387:U:C6	2.54	0.42
25:DA:2410:G:C2	25:DA:2411:A:H1'	2.54	0.42
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.54	0.42
27:DD:5:LYS:HB3	27:DD:5:LYS:HE3	1.55	0.42
30:DG:164:GLU:N	30:DG:164:GLU:OE2	2.53	0.42
36:DQ:30:GLY:O	36:DQ:134:ARG:HD3	2.19	0.42
48:D2:16:LEU:HB2	48:D2:21:LEU:HD22	2.02	0.42
1:AA:16:A:N1	1:AA:919:A:H2	2.16	0.42
1:AA:1160:G:C6	1:AA:1161:C:H5	2.37	0.42
1:AA:1261:A:H5''	1:AA:1262:C:OP2	2.20	0.42
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.26	0.42
6:AF:94:GLN:HE21	6:AF:94:GLN:HB2	1.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:78:ARG:HB3	7:AG:87:VAL:HG21	2.02	0.42
25:BA:276:C:H2'	25:BA:277:G:O4'	2.20	0.42
25:BA:629:U:H4'	25:BA:705:C:H4'	2.01	0.42
25:BA:1249:A:H2	25:BA:1287:A:N6	2.12	0.42
25:BA:2149:G:H2'	25:BA:2150:C:O4'	2.20	0.42
25:BA:2605:U:H2'	25:BA:2606:C:C6	2.55	0.42
29:BF:63:LYS:HE2	29:BF:67:GLN:HB2	2.02	0.42
29:BF:167:ALA:HB1	29:BF:173:VAL:HG11	2.02	0.42
42:BW:27:LYS:HD2	42:BW:31:GLU:CD	2.44	0.42
1:CA:262:A:H2'	1:CA:263:A:C8	2.55	0.42
1:CA:977:A:O2'	1:CA:979:C:OP2	2.38	0.42
1:CA:1074:G:C6	1:CA:1075:C:C4	3.08	0.42
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	2.02	0.42
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.20	0.42
5:CE:9:LYS:HB2	5:CE:112:LEU:HD11	2.02	0.42
11:CK:43:SER:HA	11:CK:47:VAL:HG21	2.02	0.42
17:CQ:10:VAL:O	17:CQ:53:LEU:HD12	2.19	0.42
25:DA:622:G:H2'	25:DA:623:G:C8	2.52	0.42
25:DA:700:G:H2'	25:DA:701:G:O4'	2.20	0.42
25:DA:736:C:H6	25:DA:736:C:O5'	2.03	0.42
25:DA:1410:G:H2'	25:DA:1411:C:H6	1.84	0.42
25:DA:1514:U:H2'	25:DA:1515:G:H8	1.85	0.42
25:DA:2133:G:N2	25:DA:2157:G:H1'	2.35	0.42
25:DA:2227:A:OP1	27:DD:263:ARG:HD2	2.20	0.42
25:DA:2337:G:C2	25:DA:2338:G:C8	3.08	0.42
25:DA:2355:C:H1'	46:D0:36:ILE:HD12	2.02	0.42
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.34	0.42
27:DD:275:LYS:HA	27:DD:275:LYS:HD3	1.65	0.42
29:DF:29:ASN:O	29:DF:33:LEU:HD22	2.20	0.42
34:DO:29:ASN:N	34:DO:29:ASN:OD1	2.49	0.42
39:DT:127:ALA:C	39:DT:129:ARG:N	2.78	0.42
48:D2:35:LEU:HD12	48:D2:53:LEU:HD12	2.01	0.42
1:AA:374:A:C6	1:AA:375:U:C4	3.08	0.41
1:AA:1137:C:H4'	1:AA:1138:G:N3	2.35	0.41
1:AA:1187:G:H4'	9:AI:111:ARG:HH11	1.85	0.41
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.87	0.41
6:AF:60:PHE:CE2	18:AR:76:LEU:HD12	2.52	0.41
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.19	0.41
23:AX:13:C:O2'	25:BA:1946:C:H4'	2.20	0.41
25:BA:390:G:H2'	25:BA:391:G:H8	1.84	0.41
25:BA:1549:U:H2'	25:BA:1550:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1821:C:H5''	25:BA:1822:A:OP1	2.20	0.41
25:BA:2255:U:H2'	25:BA:2256:U:H6	1.83	0.41
33:BN:48:MET:C	33:BN:48:MET:HE3	2.45	0.41
39:BT:91:ARG:HD2	39:BT:120:ARG:NH1	2.35	0.41
1:CA:510:A:H5''	1:CA:511:C:P	2.59	0.41
1:CA:690:G:O5'	1:CA:690:G:H8	2.03	0.41
1:CA:707:C:H2'	1:CA:708:C:H6	1.83	0.41
1:CA:736:C:H2'	1:CA:737:A:C8	2.55	0.41
1:CA:1007:C:N3	1:CA:1022:G:C6	2.85	0.41
1:CA:1023:G:C3'	1:CA:1024:G:H8	2.31	0.41
1:CA:1224:G:O2'	1:CA:1322:C:OP1	2.30	0.41
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.34	0.41
18:CR:26:LEU:HD13	18:CR:42:ARG:HH11	1.84	0.41
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	2.02	0.41
25:DA:774:A:N6	61:DA:4022:HOH:O	2.52	0.41
25:DA:1297:C:H5''	61:DA:4283:HOH:O	2.19	0.41
25:DA:2114:A:H2'	25:DA:2114:A:N3	2.35	0.41
25:DA:2494:G:C4	25:DA:2495:G:C8	3.08	0.41
25:DA:2611:U:H3'	25:DA:2611:U:OP2	2.20	0.41
25:DA:2659:G:P	31:DH:158:HIS:HE2	2.43	0.41
30:DG:145:THR:OG1	30:DG:146:TYR:N	2.52	0.41
31:DH:26:VAL:HG12	31:DH:79:VAL:HG11	2.00	0.41
31:DH:124:GLU:HB2	31:DH:132:ARG:HB3	2.02	0.41
41:DV:14:VAL:HB	41:DV:96:ILE:HG13	2.02	0.41
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.35	0.41
45:DZ:45:ASP:CG	45:DZ:49:ARG:HH11	2.27	0.41
45:DZ:105:VAL:O	45:DZ:140:ASP:HA	2.20	0.41
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.35	0.41
1:AA:399:G:H2'	1:AA:400:C:C6	2.55	0.41
1:AA:875:C:H1'	8:AH:15:ASN:OD1	2.19	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5'	2.50	0.41
1:AA:1226:C:H4'	19:AS:80:TYR:OH	2.21	0.41
1:AA:1424:C:H2'	1:AA:1425:U:O4'	2.20	0.41
1:AA:1492:A:H4'	1:AA:1493:A:OP1	2.20	0.41
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.20	0.41
7:AG:51:GLN:HE21	7:AG:51:GLN:HB3	1.69	0.41
11:AK:34:ASP:HB2	11:AK:35:PRO:HD2	2.02	0.41
13:AM:81:LEU:HD22	13:AM:88:ARG:HB3	2.02	0.41
23:AX:28:C:C2'	23:AX:29:G:H5'	2.50	0.41
23:AX:47:U:H5'	23:AX:48:C:C5'	2.50	0.41
25:BA:738:C:H2'	25:BA:739:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1563:G:H2'	25:BA:1564:C:C6	2.55	0.41
25:BA:2149:G:N2	25:BA:2195:A:H1'	2.35	0.41
25:BA:2245:U:H2'	25:BA:2246:G:C8	2.55	0.41
25:BA:2342:G:H2'	25:BA:2343:G:O4'	2.20	0.41
28:BE:2:LYS:H	28:BE:2:LYS:HG2	1.61	0.41
29:BF:170:LEU:HA	29:BF:171:PRO:HD3	1.91	0.41
29:BF:172:TRP:CD1	29:BF:172:TRP:H	2.38	0.41
30:BG:66:GLN:HE21	30:BG:92:VAL:CG2	2.33	0.41
35:BP:124:LYS:HA	35:BP:144:GLU:HB3	2.01	0.41
39:BT:56:GLY:O	39:BT:59:THR:HG22	2.20	0.41
50:B4:59:PHE:H	50:B4:59:PHE:HD1	1.64	0.41
1:CA:8:A:C6	4:CD:209:ARG:HG3	2.55	0.41
1:CA:644:G:H4'	8:CH:92:ARG:NH2	2.35	0.41
1:CA:952:U:H2'	1:CA:953:G:H8	1.84	0.41
2:CB:162:ILE:O	2:CB:185:ILE:HG12	2.20	0.41
3:CC:114:PRO:HA	3:CC:185:GLY:HA3	2.01	0.41
10:CJ:35:SER:CB	10:CJ:73:ASP:HB2	2.45	0.41
15:CO:56:LEU:O	15:CO:60:VAL:HG23	2.20	0.41
19:CS:9:VAL:HG11	50:D4:61:ARG:HH21	1.84	0.41
25:DA:7:G:H2'	25:DA:8:A:C8	2.56	0.41
25:DA:255:A:C6	25:DA:256:A:C5	3.08	0.41
25:DA:598:G:H2'	25:DA:599:G:O4'	2.20	0.41
25:DA:616:G:H5'	29:DF:205:ARG:HD2	2.01	0.41
25:DA:628:G:O2'	25:DA:651:G:O2'	2.33	0.41
25:DA:855:G:C6	25:DA:856:C:N4	2.89	0.41
25:DA:1278:A:H2'	25:DA:1279:G:C8	2.55	0.41
25:DA:1319:G:C6	25:DA:1320:C:N4	2.88	0.41
25:DA:1389:G:C2	25:DA:1390:U:C2	3.08	0.41
25:DA:1704:G:H2'	25:DA:1705:G:O4'	2.21	0.41
25:DA:1791:A:H5'	25:DA:1792:G:OP2	2.20	0.41
25:DA:2019:A:C4'	40:DU:34:LYS:HD2	2.51	0.41
25:DA:2065:C:H2'	25:DA:2066:C:H6	1.84	0.41
25:DA:2139:C:N4	25:DA:2152:G:H1	2.16	0.41
25:DA:2370:G:H2'	25:DA:2371:G:C8	2.55	0.41
34:DO:103:ALA:HB1	34:DO:105:GLU:OE1	2.19	0.41
52:D6:23:THR:OG1	52:D6:24:GLU:N	2.52	0.41
1:AA:152:A:N6	1:AA:170:U:C2	2.88	0.41
1:AA:266:G:H5'	1:AA:266:G:C8	2.56	0.41
1:AA:616:G:O2'	1:AA:617:G:H5'	2.19	0.41
1:AA:658:G:H2'	1:AA:659:U:H6	1.85	0.41
1:AA:954:G:H21	1:AA:1227:A:N6	2.17	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:993:G:C2'	1:AA:995:C:H41	2.33	0.41
1:AA:1139:G:N2	1:AA:1143:G:C6	2.89	0.41
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.35	0.41
3:AC:178:LEU:HD12	3:AC:178:LEU:HA	1.82	0.41
9:AI:96:LEU:HD23	9:AI:96:LEU:HA	1.94	0.41
15:AO:39:LEU:O	15:AO:42:HIS:N	2.54	0.41
25:BA:67:G:H2'	25:BA:68:C:O4'	2.19	0.41
25:BA:1044:C:H2'	25:BA:1045:U:O4'	2.20	0.41
25:BA:2697:G:H5'	34:BO:68:GLU:OE1	2.21	0.41
25:BA:2800:C:H2'	25:BA:2801:C:H6	1.85	0.41
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.80	0.41
32:BI:30:LEU:HA	32:BI:30:LEU:HD23	1.80	0.41
45:BZ:28:MET:HA	45:BZ:88:PHE:O	2.20	0.41
45:BZ:137:ILE:HA	45:BZ:156:LYS:HZ1	1.85	0.41
45:BZ:150:LEU:HD12	45:BZ:150:LEU:HA	1.88	0.41
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.51	0.41
1:CA:922:G:C6	1:CA:923:A:C6	3.09	0.41
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.21	0.41
1:CA:1428:A:H2'	1:CA:1429:C:O4'	2.20	0.41
1:CA:1446:U:O2'	1:CA:1447:A:O5'	2.22	0.41
1:CA:1517:G:H1'	25:DA:1919:A:O3'	2.20	0.41
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.20	0.41
7:CG:115:ARG:O	7:CG:119:ARG:HG3	2.20	0.41
7:CG:155:ARG:CZ	7:CG:155:ARG:HB3	2.48	0.41
9:CI:104:ARG:HG2	9:CI:105:ASP:N	2.35	0.41
15:CO:57:LEU:HD23	15:CO:57:LEU:HA	1.86	0.41
25:DA:242:G:N2	25:DA:254:G:H2'	2.35	0.41
25:DA:276:A:H5''	25:DA:277:C:H5'	2.02	0.41
25:DA:396:G:O3'	47:D1:44:PRO:HA	2.20	0.41
25:DA:483:A:O2'	44:DY:49:VAL:O	2.27	0.41
25:DA:1142(A):A:C4	25:DA:1144:G:C8	3.07	0.41
25:DA:1420:U:O2'	25:DA:1421:G:OP1	2.34	0.41
25:DA:2054:A:OP1	25:DA:2055:C:O2'	2.24	0.41
25:DA:2547:U:O2	34:DO:23:ARG:NH2	2.53	0.41
26:DB:5:C:N4	26:DB:116:G:H1	2.16	0.41
26:DB:11:C:H3'	26:DB:12:C:C6	2.56	0.41
26:DB:47:C:C4	26:DB:48:A:N7	2.88	0.41
30:DG:18:GLU:OE2	30:DG:21:ARG:NH1	2.53	0.41
30:DG:45:GLU:C	30:DG:47:LYS:H	2.28	0.41
31:DH:27:LYS:HZ1	31:DH:32:GLU:CD	2.28	0.41
39:DT:19:LEU:HD22	39:DT:86:ILE:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D4:46:GLN:HG3	50:D4:48:ARG:CZ	2.50	0.41
1:AA:376:G:O2'	1:AA:377:G:H5'	2.19	0.41
1:AA:624:C:H2'	1:AA:625:G:C8	2.56	0.41
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.21	0.41
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.55	0.41
4:AD:45:GLN:HE21	4:AD:45:GLN:HB3	1.63	0.41
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.85	0.41
8:AH:34:GLU:OE1	8:AH:37:ARG:NH2	2.53	0.41
23:AX:66:C:H2'	23:AX:67:C:O4'	2.21	0.41
25:BA:54:G:O2'	25:BA:125:A:N1	2.41	0.41
25:BA:738:C:H2'	25:BA:739:C:H6	1.86	0.41
25:BA:782:A:N7	25:BA:808:A:H2	2.19	0.41
25:BA:1312:G:O2'	25:BA:2034:G:O6	2.37	0.41
25:BA:2405:A:O2'	54:B8:13:ARG:NH1	2.51	0.41
26:BB:42:C:O2'	30:BG:66:GLN:HG2	2.21	0.41
32:BI:96:ASP:OD1	32:BI:96:ASP:N	2.53	0.41
39:BT:6:LEU:HA	39:BT:6:LEU:HD13	1.86	0.41
39:BT:118:ARG:HD2	39:BT:118:ARG:HA	1.57	0.41
44:BY:90:LEU:HD21	44:BY:96:ILE:HG12	2.02	0.41
54:B8:62:LEU:HB3	54:B8:65:GLU:HG3	2.01	0.41
1:CA:202:U:H3'	1:CA:203:U:C5	2.56	0.41
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.02	0.41
1:CA:836:G:C6	1:CA:851:G:C6	3.09	0.41
1:CA:1077:G:N1	1:CA:1081:G:C6	2.88	0.41
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.69	0.41
1:CA:1314:C:H2'	1:CA:1315:U:C6	2.55	0.41
1:CA:1316:G:H4'	14:CN:18:VAL:HG13	2.02	0.41
1:CA:1342:C:O2'	9:CI:124:GLN:HG3	2.21	0.41
3:CC:181:ASN:ND2	3:CC:204:LEU:HD12	2.34	0.41
5:CE:12:LEU:HD12	5:CE:128:PRO:HB2	2.02	0.41
9:CI:96:LEU:HD23	9:CI:96:LEU:HA	1.98	0.41
10:CJ:57:LYS:HE2	10:CJ:60:ARG:NH2	2.35	0.41
13:CM:29:ARG:HD3	13:CM:64:TRP:CE2	2.56	0.41
25:DA:76:C:O3'	48:D2:59:ARG:HG3	2.20	0.41
25:DA:118:A:H1'	25:DA:178:G:O4'	2.20	0.41
25:DA:335:C:H2'	25:DA:336:C:H6	1.84	0.41
25:DA:1282:U:H2'	25:DA:1283:G:O4'	2.21	0.41
25:DA:1652:A:OP1	37:DR:8:ARG:NH1	2.49	0.41
25:DA:2134:A:H4'	25:DA:2159:G:H21	1.84	0.41
25:DA:2153:G:H3'	25:DA:2154:G:H8	1.85	0.41
25:DA:2350:C:H2'	25:DA:2351:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2721:A:O2'	25:DA:2874:C:H5'	2.20	0.41
27:DD:67:PHE:CD1	27:DD:153:ALA:HB3	2.55	0.41
28:DE:33:VAL:HG13	28:DE:89:ASP:HA	2.02	0.41
28:DE:40:GLU:H	28:DE:40:GLU:HG2	1.46	0.41
33:DN:138:LEU:HD23	33:DN:138:LEU:HA	1.74	0.41
39:DT:61:PHE:CE1	39:DT:76:PHE:HB2	2.55	0.41
40:DU:76:TYR:CZ	40:DU:80:ILE:HG13	2.56	0.41
1:AA:537:G:H5''	12:AL:113:ARG:NH1	2.35	0.41
1:AA:633:G:H2'	1:AA:634:C:C6	2.56	0.41
1:AA:637:G:H2'	1:AA:638:G:H8	1.85	0.41
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.20	0.41
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.55	0.41
1:AA:1279:A:O2'	1:AA:1282:C:N4	2.53	0.41
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.84	0.41
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	2.01	0.41
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.85	0.41
4:AD:120:LEU:HB3	4:AD:126:ILE:HD11	2.03	0.41
7:AG:74:GLU:HG2	7:AG:91:VAL:HG22	2.02	0.41
8:AH:56:LYS:HA	8:AH:56:LYS:HD3	1.89	0.41
9:AI:11:LYS:C	9:AI:13:ALA:H	2.29	0.41
11:AK:43:SER:HA	11:AK:47:VAL:HG21	2.02	0.41
16:AP:40:ASP:O	16:AP:48:TRP:HB2	2.20	0.41
19:AS:36:ARG:NH1	19:AS:53:ASN:HA	2.35	0.41
20:AT:100:ILE:H	20:AT:100:ILE:HG12	1.69	0.41
25:BA:1765:U:H2'	25:BA:1766:G:O4'	2.21	0.41
26:BB:95:C:H2'	26:BB:96:U:C6	2.54	0.41
29:BF:7:TYR:O	29:BF:21:ALA:HA	2.20	0.41
30:BG:12:TYR:HA	30:BG:16:ARG:HG2	2.02	0.41
31:BH:71:LEU:HD12	31:BH:71:LEU:HA	1.82	0.41
32:BI:77:LEU:HD23	32:BI:77:LEU:HA	1.68	0.41
33:BN:34:LEU:HD12	33:BN:34:LEU:HA	1.94	0.41
37:BR:52:ILE:HD11	37:BR:116:LEU:HD22	2.00	0.41
39:BT:95:ARG:HH11	39:BT:95:ARG:CG	2.28	0.41
42:BW:9:TYR:HA	42:BW:100:THR:CG2	2.51	0.41
45:BZ:157:LEU:HA	45:BZ:158:PRO:HD2	1.85	0.41
1:CA:44:G:H2'	1:CA:45:U:O4'	2.20	0.41
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	2.02	0.41
4:CD:94:LEU:HD23	4:CD:97:LEU:HD12	2.01	0.41
4:CD:191:ARG:HE	4:CD:200:GLU:CD	2.28	0.41
5:CE:78:HIS:ND1	8:CH:107:LEU:HD12	2.35	0.41
9:CI:16:ARG:HD3	9:CI:64:THR:HG21	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:27:ALA:HB1	10:CJ:74:ILE:HD13	2.02	0.41
25:DA:328:U:H4'	44:DY:68:HIS:CG	2.55	0.41
25:DA:460:A:C2	25:DA:470:A:C4	3.09	0.41
25:DA:804:A:H5''	25:DA:805:G:OP1	2.20	0.41
25:DA:1230:C:H2'	25:DA:1231:G:C8	2.54	0.41
25:DA:1710:C:H4'	25:DA:2858:C:O2	2.20	0.41
25:DA:2118:U:C2	25:DA:2149:G:H1'	2.55	0.41
27:DD:124:PRO:HG2	27:DD:129:ASN:ND2	2.35	0.41
37:DR:100:LEU:HD12	37:DR:100:LEU:HA	1.86	0.41
38:DS:15:ARG:O	38:DS:19:LYS:HG2	2.21	0.41
1:AA:339:C:H2'	1:AA:340:U:C6	2.56	0.41
4:AD:163:GLU:C	4:AD:165:MET:H	2.28	0.41
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.42	0.41
17:AQ:45:HIS:NE2	17:AQ:47:PRO:HG3	2.36	0.41
25:BA:1188:A:C4	25:BA:1190:G:C8	3.09	0.41
25:BA:1343:C:O2'	25:BA:1348:A:N1	2.48	0.41
25:BA:2191:A:H2'	25:BA:2191:A:N3	2.36	0.41
25:BA:2544:G:O2'	25:BA:2669:A:N1	2.49	0.41
25:BA:2568:C:H2'	25:BA:2569:G:O4'	2.21	0.41
25:BA:2592:U:C5	25:BA:2593:G:C6	3.09	0.41
27:BD:35:LYS:HB2	27:BD:36:PRO:HD2	2.02	0.41
28:BE:97:LYS:NZ	28:BE:97:LYS:HB3	2.36	0.41
30:BG:3:LEU:HD13	50:B4:25:TYR:CZ	2.55	0.41
32:BI:29:TYR:C	32:BI:32:PRO:HD2	2.46	0.41
40:BU:16:LYS:HE2	40:BU:16:LYS:HB3	1.89	0.41
40:BU:108:GLU:O	40:BU:112:ARG:HG2	2.21	0.41
1:CA:93:G:H2'	1:CA:96:U:O4'	2.20	0.41
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.48	0.41
1:CA:991:U:O2'	1:CA:992:U:P	2.79	0.41
1:CA:1424:C:H2'	1:CA:1425:U:O4'	2.20	0.41
2:CB:16:HIS:O	2:CB:18:GLY:N	2.53	0.41
4:CD:191:ARG:NE	4:CD:200:GLU:OE2	2.52	0.41
13:CM:40:ASN:HB3	13:CM:43:THR:HG23	2.02	0.41
19:CS:38:SER:HB2	19:CS:71:LEU:HD13	2.03	0.41
25:DA:389:G:N1	35:DP:70:GLN:HG3	2.36	0.41
25:DA:984:A:H5''	25:DA:985:C:C5	2.56	0.41
25:DA:2360:A:H8	25:DA:2360:A:O5'	2.04	0.41
25:DA:2519:U:C6	25:DA:2542:A:N6	2.89	0.41
25:DA:2698:U:H2'	25:DA:2699:C:C6	2.56	0.41
26:DB:45:A:C4	26:DB:46:A:C8	3.09	0.41
26:DB:66:A:H61	26:DB:108:U:H3'	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:127:VAL:HA	27:DD:193:VAL:HG22	2.03	0.41
30:DG:155:MET:HE2	30:DG:155:MET:HB3	1.86	0.41
35:DP:47:ASP:OD2	35:DP:49:ARG:NH2	2.53	0.41
49:D3:12:PRO:HB2	49:D3:20:LYS:HG2	2.03	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.21	0.41
1:AA:266:G:O3'	17:AQ:67:LYS:HB2	2.20	0.41
1:AA:583:A:N6	1:AA:758:G:O2'	2.53	0.41
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.77	0.41
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.35	0.41
8:AH:7:ALA:O	8:AH:11:THR:OG1	2.28	0.41
23:AX:19:G:H4'	23:AX:20:U:OP2	2.20	0.41
25:BA:7:G:H2'	25:BA:8:A:O4'	2.21	0.41
25:BA:645:G:N3	25:BA:645:G:H5'	2.35	0.41
25:BA:1293:A:OP1	29:BF:95:ARG:NH2	2.50	0.41
25:BA:1467:G:C2	25:BA:1468:G:C8	3.09	0.41
27:BD:245:PRO:HA	27:BD:246:PRO:HD3	1.90	0.41
29:BF:102:PRO:HB2	29:BF:105:VAL:HG23	2.02	0.41
30:BG:41:GLN:NE2	30:BG:153:ARG:HB3	2.32	0.41
42:BW:25:ARG:NH2	42:BW:74:ALA:O	2.47	0.41
50:B4:61:ARG:O	50:B4:62:ARG:C	2.64	0.41
1:CA:144:G:H1	1:CA:178:C:H42	1.68	0.41
1:CA:170:U:O2'	1:CA:171:A:H5'	2.21	0.41
1:CA:952:U:H2'	1:CA:953:G:C8	2.56	0.41
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.85	0.41
1:CA:1486:G:H2'	1:CA:1487:G:O4'	2.20	0.41
7:CG:114:ARG:O	7:CG:119:ARG:NH1	2.54	0.41
25:DA:173:G:C2	25:DA:174:C:C2	3.09	0.41
25:DA:724:U:H2'	25:DA:725:G:O4'	2.21	0.41
25:DA:1297:C:H2'	25:DA:1298:C:C6	2.55	0.41
25:DA:1859:A:N6	25:DA:1883:G:O2'	2.54	0.41
25:DA:2167:U:H2'	25:DA:2168:G:H21	1.85	0.41
25:DA:2330:G:O2'	46:D0:41:ARG:O	2.25	0.41
25:DA:2371:G:C2	25:DA:2372:G:C8	3.09	0.41
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.21	0.41
29:DF:59:TYR:CD2	29:DF:78:ILE:HG13	2.56	0.41
30:DG:39:ILE:HB	30:DG:92:VAL:HG13	2.03	0.41
36:DQ:32:TYR:HB2	36:DQ:106:VAL:HG23	2.02	0.41
42:DW:18:ARG:NH1	42:DW:76:VAL:O	2.52	0.41
43:DX:47:PHE:O	43:DX:49:VAL:HG13	2.21	0.41
1:AA:357:G:O2'	1:AA:358:U:H5'	2.21	0.41
1:AA:400:C:H5''	4:AD:73:ARG:NH2	2.30	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:632:A:C3'	1:AA:633:G:H5'	2.51	0.41
1:AA:731:G:OP1	1:AA:766:A:H1'	2.20	0.41
1:AA:1064:G:N2	1:AA:1190:G:O2'	2.54	0.41
1:AA:1206:G:O4'	3:AC:194:GLY:HA2	2.21	0.41
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.20	0.41
3:AC:181:ASN:OD1	3:AC:204:LEU:HB2	2.21	0.41
5:AE:106:PRO:O	5:AE:110:LEU:HG	2.20	0.41
7:AG:38:LEU:O	7:AG:42:ILE:HG13	2.20	0.41
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.20	0.41
8:AH:124:ALA:O	8:AH:128:GLY:N	2.51	0.41
12:AL:8:ASN:O	12:AL:12:ARG:HG3	2.21	0.41
13:AM:29:ARG:HD3	13:AM:64:TRP:CE2	2.56	0.41
14:AN:15:LYS:HD2	14:AN:16:PHE:CZ	2.56	0.41
15:AO:7:GLU:H	15:AO:7:GLU:HG3	1.70	0.41
24:AY:4:C:N3	24:AY:70:G:N2	2.69	0.41
25:BA:354:A:O2'	25:BA:355:A:H8	2.03	0.41
25:BA:865:G:H4'	25:BA:885:C:O3'	2.20	0.41
25:BA:1219:A:N3	25:BA:1220:U:H5''	2.35	0.41
25:BA:2184:G:H4'	25:BA:2194:U:H3'	2.02	0.41
25:BA:2227:G:H5'	25:BA:2228:G:N7	2.36	0.41
25:BA:2326:C:H2'	25:BA:2327:G:C8	2.56	0.41
25:BA:2724:U:H1'	25:BA:2725:A:C8	2.56	0.41
32:BI:117:GLU:H	32:BI:117:GLU:HG3	1.55	0.41
33:BN:99:LEU:HD23	33:BN:99:LEU:HA	1.84	0.41
55:B9:17:ILE:HD12	55:B9:17:ILE:HA	1.91	0.41
1:CA:567:G:O6	12:CL:5:PRO:HD3	2.21	0.41
1:CA:633:G:H2'	1:CA:634:C:C6	2.55	0.41
1:CA:690:G:H2'	1:CA:691:G:O4'	2.20	0.41
1:CA:737:A:H2'	1:CA:738:C:C6	2.56	0.41
1:CA:1002:G:N2	1:CA:1039:C:C2	2.89	0.41
2:CB:47:THR:HA	2:CB:202:PRO:HG2	2.02	0.41
2:CB:134:GLU:O	2:CB:137:ARG:HB2	2.21	0.41
4:CD:120:LEU:HB3	4:CD:126:ILE:HD11	2.02	0.41
7:CG:76:ARG:HB2	7:CG:76:ARG:HH11	1.86	0.41
7:CG:102:ARG:O	7:CG:106:GLN:HG3	2.20	0.41
12:CL:53:ARG:HB3	12:CL:93:LEU:HD11	2.03	0.41
13:CM:70:LEU:HD23	13:CM:70:LEU:HA	1.83	0.41
15:CO:39:LEU:HD23	15:CO:39:LEU:HA	1.83	0.41
25:DA:359:A:H2'	25:DA:360:G:O4'	2.20	0.41
25:DA:590:A:OP1	29:DF:95:ARG:NH1	2.53	0.41
25:DA:718:A:H3'	25:DA:719:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1472:A:N6	25:DA:1519:G:H1'	2.36	0.41
25:DA:1526:G:H2'	25:DA:1527:G:O4'	2.21	0.41
25:DA:1659:U:C4	25:DA:1660:C:C5	3.09	0.41
25:DA:1805:U:O2	27:DD:50:THR:HB	2.20	0.41
25:DA:1957:C:H2'	25:DA:1958:C:C6	2.56	0.41
25:DA:2055:C:OP1	25:DA:2056:G:H4'	2.20	0.41
25:DA:2277:G:OP2	46:D0:10:THR:HG21	2.21	0.41
25:DA:2280:G:O6	46:D0:14:ARG:HD2	2.21	0.41
25:DA:2751:G:H8	31:DH:2:SER:N	2.19	0.41
25:DA:2855:C:H2'	25:DA:2856:C:C6	2.56	0.41
27:DD:26:LYS:NZ	27:DD:30:GLU:OE1	2.53	0.41
29:DF:184:TYR:HE1	35:DP:3:LEU:HD21	1.84	0.41
34:DO:25:LEU:HD12	34:DO:38:VAL:HG12	2.02	0.41
35:DP:3:LEU:HD12	35:DP:3:LEU:HA	1.88	0.41
44:DY:7:VAL:HG21	44:DY:72:VAL:HG12	2.03	0.41
44:DY:13:VAL:HB	44:DY:72:VAL:HG13	2.03	0.41
45:DZ:30:ASN:HA	45:DZ:89:PHE:HE1	1.85	0.41
55:D9:11:CYS:SG	55:D9:13:LYS:HB2	2.60	0.41
1:AA:341:C:H2'	1:AA:342:C:C6	2.56	0.41
1:AA:674:G:O2'	1:AA:675:A:H5'	2.21	0.41
1:AA:827:U:H5''	1:AA:828:A:OP2	2.20	0.41
1:AA:972:C:O2'	10:AJ:57:LYS:HB2	2.20	0.41
1:AA:991:U:O2'	1:AA:992:U:P	2.78	0.41
1:AA:991:U:C4	1:AA:1212:U:H1'	2.55	0.41
1:AA:1002:G:C6	1:AA:1003:G:C2	3.09	0.41
1:AA:1112:C:O2	3:AC:179:ARG:N	2.51	0.41
1:AA:1161:C:N4	1:AA:1176:A:C6	2.88	0.41
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.85	0.41
3:AC:181:ASN:OD1	3:AC:204:LEU:HD12	2.21	0.41
4:AD:20:TYR:HA	4:AD:26:CYS:SG	2.60	0.41
5:AE:50:GLU:HB2	5:AE:53:LEU:CD1	2.51	0.41
23:AX:57:A:H2'	23:AX:58:A:H5'	2.02	0.41
25:BA:64:C:H2'	25:BA:65:C:H6	1.86	0.41
25:BA:259:A:N1	25:BA:396:C:H4'	2.36	0.41
25:BA:789:G:H4'	25:BA:1723:A:H5'	2.03	0.41
25:BA:905:U:O2	25:BA:2280:A:H2'	2.20	0.41
25:BA:1086:C:H2'	25:BA:1087:C:O4'	2.21	0.41
25:BA:1387:U:O4	43:BX:16:LYS:HE2	2.19	0.41
25:BA:1616:A:H2'	25:BA:1617:A:O4'	2.21	0.41
25:BA:1797:U:H2'	25:BA:1798:C:C6	2.56	0.41
25:BA:1820:A:H2'	25:BA:1821:C:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2086:C:H2'	25:BA:2087:C:C6	2.56	0.41
25:BA:2134:G:N2	25:BA:2135:U:H1'	2.36	0.41
25:BA:2148:A:H4'	25:BA:2149:G:OP1	2.21	0.41
25:BA:2162:C:H2'	25:BA:2173:G:H22	1.85	0.41
25:BA:2172:U:C2	25:BA:2173:G:N7	2.89	0.41
27:BD:25:THR:HG21	27:BD:113:VAL:HG11	2.02	0.41
27:BD:102:LYS:C	27:BD:103:ARG:HG2	2.45	0.41
33:BN:58:ASP:OD1	33:BN:58:ASP:N	2.42	0.41
35:BP:148:LEU:H	35:BP:148:LEU:HD23	1.85	0.41
38:BS:34:HIS:O	38:BS:97:ARG:NH2	2.54	0.41
42:BW:9:TYR:HA	42:BW:100:THR:HG23	2.03	0.41
45:BZ:144:LEU:HG	45:BZ:148:ASP:HB2	2.03	0.41
47:B1:67:ILE:N	47:B1:68:PRO:HD2	2.35	0.41
1:CA:237:C:H5''	17:CQ:25:ARG:NE	2.36	0.41
1:CA:358:U:H2'	1:CA:359:U:C6	2.56	0.41
1:CA:604:G:H2'	1:CA:605:U:O4'	2.21	0.41
1:CA:765:G:H1	1:CA:812:C:HO2'	1.64	0.41
1:CA:892:A:H2'	1:CA:893:C:C6	2.56	0.41
1:CA:1014:A:N3	1:CA:1219:U:H1'	2.36	0.41
1:CA:1028:C:O2	1:CA:1033:G:C2	2.73	0.41
1:CA:1057:G:C4	1:CA:1204:A:C2	3.08	0.41
1:CA:1067:A:H3'	1:CA:1094:G:OP1	2.21	0.41
1:CA:1076:C:H5'	1:CA:1076:C:H6	1.85	0.41
1:CA:1123:A:C2	10:CJ:39:PRO:HD2	2.55	0.41
1:CA:1221:G:O3'	19:CS:77:THR:HG21	2.20	0.41
1:CA:1291:G:OP1	7:CG:37:ASN:ND2	2.53	0.41
1:CA:1372:U:H2'	1:CA:1373:G:O4'	2.21	0.41
1:CA:1414:U:H3	1:CA:1486:G:H1	1.69	0.41
1:CA:1423:G:OP1	34:DO:49:ARG:NH2	2.50	0.41
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.56	0.41
1:CA:1508:G:H2'	1:CA:1509:C:O4'	2.20	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.21	0.41
3:CC:5:ILE:HG12	3:CC:6:HIS:N	2.36	0.41
3:CC:140:ARG:H	3:CC:140:ARG:HG3	1.47	0.41
5:CE:57:LYS:HD3	5:CE:61:TYR:CE2	2.55	0.41
5:CE:78:HIS:HE2	5:CE:142:LEU:HA	1.85	0.41
11:CK:22:HIS:O	11:CK:29:ILE:N	2.33	0.41
11:CK:27:ASN:ND2	11:CK:55:LYS:HD2	2.35	0.41
16:CP:74:LEU:HG	16:CP:79:VAL:HG21	2.02	0.41
25:DA:36:G:N3	25:DA:450:G:O2'	2.53	0.41
25:DA:45:C:H2'	25:DA:47:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:336:C:O2'	44:DY:35:TYR:OH	2.36	0.41
25:DA:466:A:N1	25:DA:795:C:O2'	2.49	0.41
25:DA:624:C:O2'	25:DA:657:U:H5''	2.20	0.41
25:DA:708:C:H42	25:DA:723:G:H1	1.69	0.41
25:DA:900:A:H2'	25:DA:901:A:H8	1.85	0.41
25:DA:975(A):G:C2	25:DA:990:A:C8	3.08	0.41
25:DA:1002:G:N2	25:DA:1154:G:H1'	2.36	0.41
25:DA:1596:A:H2'	25:DA:1597:A:O4'	2.21	0.41
25:DA:1668:A:N3	25:DA:1670:C:C4	2.88	0.41
25:DA:1894:C:H2'	25:DA:1895:C:H6	1.85	0.41
25:DA:1991:U:C2'	25:DA:1992:G:H5''	2.50	0.41
25:DA:2165:G:H2'	25:DA:2166:G:C8	2.56	0.41
25:DA:2490:G:H8	25:DA:2490:G:OP2	2.03	0.41
25:DA:2540:C:H2'	25:DA:2541:A:O4'	2.21	0.41
25:DA:2658:C:H2'	25:DA:2659:G:O4'	2.20	0.41
25:DA:2747:G:H1'	25:DA:2757:A:H61	1.84	0.41
25:DA:2808:U:O2'	25:DA:2809:A:H5'	2.21	0.41
25:DA:2875:C:OP1	39:DT:3:ARG:NH1	2.52	0.41
26:DB:33:G:C6	26:DB:34:U:N3	2.89	0.41
26:DB:68:C:H2'	26:DB:69:G:H8	1.86	0.41
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.53	0.41
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.44	0.41
30:DG:48:GLU:O	30:DG:51:ARG:HG3	2.21	0.41
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.86	0.41
30:DG:179:PRO:HG3	50:D4:43:TYR:OH	2.20	0.41
35:DP:6:LEU:HD23	35:DP:6:LEU:HA	1.83	0.41
35:DP:84:ASN:OD1	35:DP:117:GLU:HB2	2.21	0.41
37:DR:36:THR:HG22	37:DR:37:THR:N	2.31	0.41
38:DS:26:LEU:HD22	38:DS:87:PHE:CE1	2.56	0.41
38:DS:57:LYS:HE2	38:DS:57:LYS:HB2	1.89	0.41
40:DU:112:ARG:H	40:DU:112:ARG:HG2	1.65	0.41
41:DV:12:TYR:CG	41:DV:20:LEU:HD21	2.56	0.41
44:DY:52:SER:HB2	44:DY:53:PRO:HD2	2.02	0.41
45:DZ:159:PRO:HA	45:DZ:161:VAL:N	2.36	0.41
55:D9:2:LYS:HE2	55:D9:31:LYS:O	2.20	0.41
1:AA:35:G:H2'	1:AA:36:C:C6	2.56	0.41
1:AA:93:G:O2'	1:AA:96:U:H5'	2.21	0.41
1:AA:434:U:H2'	1:AA:435:C:C6	2.56	0.41
1:AA:509:A:O2'	1:AA:510:A:OP1	2.23	0.41
1:AA:658:G:H5''	15:AO:31:LEU:HD11	2.03	0.41
10:AJ:23:ILE:HD12	10:AJ:23:ILE:HA	1.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:30:LYS:O	20:AT:34:LYS:HG3	2.21	0.41
25:BA:732:A:C8	25:BA:821:A:C6	3.09	0.41
25:BA:1067:A:C8	25:BA:1067:A:C3'	3.04	0.41
25:BA:1214:G:H1	25:BA:1226:C:H42	1.69	0.41
25:BA:1468:G:H1'	25:BA:1542:A:N1	2.35	0.41
25:BA:2387:G:O6	61:BA:4806:HOH:O	2.22	0.41
25:BA:2766:A:N3	55:B9:15:LYS:NZ	2.64	0.41
29:BF:12:LEU:HB2	29:BF:124:LEU:HD11	2.03	0.41
30:BG:175:LEU:HD12	30:BG:175:LEU:HA	1.96	0.41
34:BO:35:VAL:HG21	34:BO:69:ILE:HD13	2.02	0.41
41:BV:52:VAL:HG22	41:BV:55:ALA:HB3	2.03	0.41
1:CA:49:U:O4	1:CA:365:U:H5	2.04	0.41
1:CA:125:U:H2'	1:CA:126:G:C8	2.56	0.41
1:CA:1222:G:H5''	19:CS:78:ARG:NH2	2.36	0.41
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.20	0.41
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.56	0.41
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.36	0.41
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.36	0.41
25:DA:140:G:N3	25:DA:142:A:N6	2.63	0.41
25:DA:184:C:H2'	25:DA:185:U:C6	2.56	0.41
25:DA:342:G:H2'	25:DA:343:C:H6	1.86	0.41
25:DA:760:G:H2'	25:DA:761:A:O4'	2.20	0.41
25:DA:869:G:C4	25:DA:870:A:C8	3.10	0.41
25:DA:918:A:C5	25:DA:919:G:H1'	2.56	0.41
25:DA:1196:C:C4	25:DA:1197:G:N7	2.89	0.41
25:DA:1826:G:H4'	27:DD:242:ARG:NH1	2.36	0.41
25:DA:2078:C:C4	25:DA:2079:U:C4	3.08	0.41
25:DA:2134:A:C8	25:DA:2158:A:N3	2.89	0.41
25:DA:2365:G:P	46:D0:55:ARG:HG2	2.61	0.41
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.56	0.41
29:DF:29:ASN:N	29:DF:112:MET:HE1	2.36	0.41
29:DF:195:ASP:OD1	29:DF:196:LEU:N	2.54	0.41
30:DG:36:LYS:HG2	30:DG:160:VAL:HB	2.02	0.41
31:DH:117:PRO:HG3	31:DH:123:PHE:CD2	2.56	0.41
31:DH:150:ALA:HA	31:DH:153:LYS:HG3	2.03	0.41
32:DI:101:LEU:O	32:DI:105:HIS:HB2	2.21	0.41
35:DP:37:GLY:C	35:DP:38:GLN:O	2.64	0.41
38:DS:54:LEU:O	38:DS:57:LYS:HD3	2.20	0.41
1:AA:251:G:C6	1:AA:266:G:C6	3.09	0.40
1:AA:353:A:H5'	1:AA:353:A:C8	2.53	0.40
1:AA:526:C:P	12:AL:91:LYS:HE3	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1015:A:C6	1:AA:1016:A:C6	3.09	0.40
2:AB:160:ASP:OD2	2:AB:160:ASP:N	2.52	0.40
2:AB:169:LYS:HD3	2:AB:169:LYS:O	2.21	0.40
7:AG:79:ARG:HB3	7:AG:80:VAL:H	1.59	0.40
10:AJ:67:THR:O	10:AJ:67:THR:OG1	2.38	0.40
15:AO:3:ILE:H	15:AO:3:ILE:HD13	1.86	0.40
19:AS:12:ASP:HB3	19:AS:14:HIS:CD2	2.56	0.40
23:AX:20:U:H5''	23:AX:21:A:OP2	2.21	0.40
24:AY:70:G:C2'	24:AY:71:G:H5'	2.51	0.40
25:BA:160:G:C2'	25:BA:161:C:H5'	2.50	0.40
25:BA:556:C:H4'	25:BA:557:A:H5''	2.01	0.40
25:BA:795:G:C8	42:BW:89:ALA:HB1	2.56	0.40
25:BA:2713:C:H2'	25:BA:2714:U:H2'	2.03	0.40
25:BA:2801:C:OP1	28:BE:61:ARG:NH2	2.37	0.40
25:BA:2803:A:N3	25:BA:2803:A:H2'	2.36	0.40
29:BF:196:LEU:HD23	29:BF:196:LEU:HA	1.90	0.40
32:BI:38:LEU:HD11	47:B1:75:GLU:CD	2.45	0.40
36:BQ:34:LEU:HD11	36:BQ:129:THR:HB	2.02	0.40
36:BQ:137:TYR:O	36:BQ:141:GLN:HG2	2.20	0.40
44:BY:34:LYS:O	44:BY:34:LYS:HG2	2.21	0.40
45:BZ:129:SER:O	45:BZ:132:ASN:N	2.51	0.40
1:CA:60:A:H4'	1:CA:61:G:O5'	2.20	0.40
1:CA:397:A:H5'	1:CA:398:C:OP1	2.21	0.40
1:CA:448:A:O5'	1:CA:485:G:N2	2.50	0.40
1:CA:991:U:O2'	1:CA:992:U:OP2	2.36	0.40
1:CA:1222:G:H5''	19:CS:78:ARG:HH21	1.85	0.40
1:CA:1237:C:O2'	1:CA:1300:G:N1	2.34	0.40
2:CB:54:THR:HG21	2:CB:201:ILE:HD11	2.04	0.40
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.36	0.40
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.21	0.40
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.40
5:CE:41:VAL:HG22	5:CE:113:ALA:HA	2.02	0.40
11:CK:77:MET:HE2	11:CK:77:MET:HB2	1.95	0.40
16:CP:4:ILE:HA	16:CP:20:VAL:O	2.21	0.40
16:CP:15:PRO:O	16:CP:16:HIS:ND1	2.54	0.40
20:CT:27:LYS:HA	20:CT:30:LYS:HE2	2.03	0.40
23:CX:3:C:H5'	25:DA:2255:G:O2'	2.21	0.40
25:DA:182:A:H2	25:DA:433:C:O2	2.05	0.40
25:DA:830:G:H4'	25:DA:831:G:OP2	2.21	0.40
25:DA:940:G:N3	25:DA:1191:G:H4'	2.35	0.40
25:DA:1164:G:H2'	25:DA:1165:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1654:A:C1'	25:DA:2823:A:H5'	2.50	0.40
25:DA:1666:G:OP1	34:DO:66:LYS:HD3	2.20	0.40
25:DA:2038:G:H2'	25:DA:2039:C:O4'	2.20	0.40
25:DA:2135:A:C5	25:DA:2136:C:N4	2.88	0.40
25:DA:2302:G:C2	25:DA:2303:G:C8	3.09	0.40
25:DA:2507:C:H5''	25:DA:2573:C:N4	2.36	0.40
27:DD:26:LYS:HE2	27:DD:28:GLU:O	2.21	0.40
27:DD:206:LEU:HD23	27:DD:206:LEU:HA	1.83	0.40
28:DE:31:CYS:HA	28:DE:32:PRO:HD2	1.80	0.40
31:DH:98:LEU:HD12	31:DH:98:LEU:HA	1.93	0.40
33:DN:133:GLN:H	33:DN:133:GLN:HG2	1.64	0.40
40:DU:66:ASN:HD21	40:DU:70:ARG:HH21	1.68	0.40
46:D0:36:ILE:HD13	46:D0:58:THR:HG21	2.02	0.40
52:D6:16:CYS:SG	52:D6:18:ARG:HD2	2.61	0.40
1:AA:432:A:H3'	1:AA:433:C:H6	1.86	0.40
1:AA:1104:G:H2'	1:AA:1105:A:O4'	2.21	0.40
1:AA:1194:U:H2'	1:AA:1195:C:C6	2.56	0.40
2:AB:16:HIS:CE1	2:AB:214:ILE:HD11	2.56	0.40
2:AB:90:MET:HA	2:AB:91:PRO:HD3	1.96	0.40
2:AB:166:ASP:HB3	2:AB:169:LYS:HB3	2.03	0.40
3:AC:37:GLN:HE21	3:AC:40:ARG:HD2	1.85	0.40
3:AC:118:GLN:HA	3:AC:121:ALA:HB3	2.04	0.40
4:AD:100:ARG:HH22	4:AD:118:ARG:HH22	1.69	0.40
4:AD:159:ARG:O	4:AD:163:GLU:HG3	2.21	0.40
5:AE:33:VAL:HG13	5:AE:112:LEU:HD12	2.03	0.40
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.87	0.40
15:AO:67:LEU:HA	15:AO:67:LEU:HD23	1.88	0.40
16:AP:59:TRP:HA	16:AP:62:VAL:HG12	2.02	0.40
19:AS:50:ALA:HA	19:AS:58:VAL:O	2.22	0.40
21:AU:15:ARG:HB2	21:AU:15:ARG:HH11	1.86	0.40
25:BA:1676:G:H2'	25:BA:1677:C:C6	2.57	0.40
25:BA:1699:A:C2'	25:BA:1700:G:H5'	2.51	0.40
25:BA:1974:A:OP1	34:BO:42:SER:OG	2.34	0.40
25:BA:2199:C:H2'	25:BA:2200:C:O4'	2.21	0.40
25:BA:2455:C:OP1	29:BF:68:LYS:HD3	2.21	0.40
25:BA:2672:A:H2'	25:BA:2673:G:O4'	2.20	0.40
29:BF:33:LEU:HD12	29:BF:33:LEU:HA	1.89	0.40
41:BV:65:GLY:HA3	41:BV:91:TYR:CZ	2.56	0.40
1:CA:277:C:H5''	17:CQ:68:ARG:NH2	2.37	0.40
1:CA:393:A:OP1	16:CP:13:HIS:HE1	2.04	0.40
1:CA:414:A:C5	1:CA:431:A:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:583:A:H2'	1:CA:584:G:O4'	2.21	0.40
1:CA:791:G:C6	1:CA:792:A:N7	2.88	0.40
1:CA:1125:U:H5''	1:CA:1127:G:O6	2.21	0.40
1:CA:1172:C:H2'	1:CA:1173:G:H8	1.86	0.40
1:CA:1499:A:H1'	1:CA:1520:G:H5'	2.03	0.40
7:CG:115:ARG:HG2	7:CG:118:VAL:HG23	2.03	0.40
17:CQ:65:ILE:HB	17:CQ:69:LYS:HB3	2.02	0.40
19:CS:22:LEU:HB3	19:CS:27:GLU:CG	2.51	0.40
25:DA:244:A:C2	25:DA:255:A:C4	3.09	0.40
25:DA:527:C:C4	25:DA:2779:U:H2'	2.56	0.40
25:DA:645:C:O2	25:DA:645:C:H2'	2.21	0.40
25:DA:901:A:H2'	25:DA:902:C:O4'	2.21	0.40
25:DA:1270:C:H5''	25:DA:1271:G:O5'	2.22	0.40
25:DA:1449:A:HO2'	25:DA:1529:G:H21	1.56	0.40
25:DA:1692:U:O2'	25:DA:1693:U:H2'	2.21	0.40
25:DA:2328:A:H2'	25:DA:2329:G:C8	2.55	0.40
25:DA:2397:G:N2	25:DA:2420:C:H1'	2.36	0.40
25:DA:2600:A:C6	25:DA:2601:C:N4	2.89	0.40
26:DB:94:C:H2'	26:DB:95:C:H6	1.85	0.40
30:DG:43:LEU:C	30:DG:45:GLU:N	2.80	0.40
33:DN:38:HIS:CE1	33:DN:39:ARG:HG3	2.56	0.40
38:DS:87:PHE:HB2	38:DS:112:PHE:CE2	2.56	0.40
1:AA:148:G:H1	1:AA:174:C:H42	1.68	0.40
1:AA:194:C:C2'	1:AA:195:A:H5''	2.52	0.40
1:AA:487:A:H2'	1:AA:488:C:O4'	2.22	0.40
1:AA:966:G:C2	23:AX:34:C:H5'	2.56	0.40
1:AA:998:G:H2'	1:AA:999:C:O4'	2.22	0.40
1:AA:1004:A:C5	1:AA:1037:C:N3	2.89	0.40
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.40
4:AD:108:LEU:HD12	4:AD:108:LEU:HA	1.64	0.40
10:AJ:49:VAL:HG21	14:AN:41:ARG:O	2.22	0.40
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	2.03	0.40
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	2.03	0.40
25:BA:325:G:H1'	25:BA:326:C:C6	2.56	0.40
25:BA:908:A:C2	25:BA:963:A:C4	3.10	0.40
25:BA:1540:A:H2'	25:BA:1541:A:C8	2.56	0.40
25:BA:1787:G:H4'	25:BA:1789:G:O4'	2.21	0.40
25:BA:2598:C:OP2	25:BA:2620:G:N1	2.49	0.40
25:BA:2720:G:H1'	37:BR:71:GLN:HE22	1.87	0.40
27:BD:183:ARG:HG3	27:BD:270:ILE:HG12	2.03	0.40
30:BG:179:PRO:HB2	50:B4:42:PHE:HE2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:46:LYS:HE3	35:BP:46:LYS:HB3	1.76	0.40
43:BX:1:MET:HE3	43:BX:1:MET:HB2	1.89	0.40
1:CA:16:A:N1	1:CA:919:A:H2	2.20	0.40
1:CA:109:A:C6	1:CA:326:G:C6	3.10	0.40
1:CA:376:G:O2'	1:CA:377:G:H5'	2.21	0.40
1:CA:577:G:C8	1:CA:816:A:C6	3.10	0.40
1:CA:794:A:H4'	1:CA:1521:G:O2'	2.21	0.40
1:CA:1004:A:N7	1:CA:1037:C:O2	2.54	0.40
1:CA:1148:U:H1'	9:CI:66:ARG:HH12	1.86	0.40
1:CA:1250:A:H2	1:CA:1370:G:H1'	1.87	0.40
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.50	0.40
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.91	0.40
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.57	0.40
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	2.03	0.40
9:CI:2:GLU:O	9:CI:20:ARG:HG2	2.21	0.40
9:CI:71:SER:HA	9:CI:74:ILE:HD12	2.04	0.40
12:CL:34:ARG:HE	12:CL:34:ARG:HB3	1.64	0.40
14:CN:45:ARG:O	14:CN:49:HIS:HD2	2.04	0.40
25:DA:551:G:O2'	25:DA:1220:A:N3	2.51	0.40
25:DA:589:C:H2'	25:DA:590:A:C8	2.56	0.40
25:DA:670:A:H4'	25:DA:671:C:O5'	2.20	0.40
25:DA:839:U:H2'	25:DA:840:C:H6	1.87	0.40
25:DA:956:G:H2'	25:DA:957:A:H2'	2.03	0.40
25:DA:1222:C:N3	25:DA:1228:G:C2	2.90	0.40
25:DA:2228:G:C5	25:DA:2229:C:C4	3.09	0.40
25:DA:2445:G:OP1	29:DF:74:ARG:NH2	2.47	0.40
25:DA:2842:G:H2'	25:DA:2843:G:O4'	2.22	0.40
26:DB:33:G:N3	26:DB:50:G:N2	2.69	0.40
27:DD:20:ASP:OD1	27:DD:21:PHE:N	2.55	0.40
28:DE:55:ASN:HA	28:DE:56:PRO:HD3	1.88	0.40
30:DG:49:ASP:OD1	30:DG:49:ASP:N	2.54	0.40
44:DY:86:ARG:HB2	44:DY:98:VAL:CG2	2.51	0.40
45:DZ:149:SER:HB2	45:DZ:172:ALA:O	2.22	0.40
49:D3:23:LEU:HD13	49:D3:50:VAL:HG11	2.02	0.40
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.56	0.40
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.29	0.40
3:AC:47:LEU:HD12	3:AC:68:VAL:HG11	2.02	0.40
4:AD:78:LEU:HA	4:AD:78:LEU:HD23	1.86	0.40
9:AI:128:ARG:NH2	23:AX:33:U:OP2	2.54	0.40
15:AO:16:ALA:HB1	15:AO:21:ASP:HB3	2.02	0.40
25:BA:268:G:HO2'	25:BA:269:G:H8	1.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:922:G:O3'	45:BZ:151:HIS:HE1	2.05	0.40
25:BA:2289:G:P	46:B0:10:THR:HG21	2.62	0.40
25:BA:2304:C:H2'	25:BA:2305:C:C6	2.56	0.40
27:BD:68:LYS:HD3	27:BD:70:TRP:CZ2	2.57	0.40
27:BD:164:GLN:NE2	27:BD:166:GLN:OE1	2.53	0.40
30:BG:122:PRO:HD3	30:BG:181:ARG:HG2	2.02	0.40
32:BI:47:LEU:O	32:BI:51:ILE:HG13	2.22	0.40
32:BI:118:LYS:HA	32:BI:119:PRO:HD3	1.93	0.40
34:BO:10:VAL:HG21	34:BO:16:ALA:HB3	2.03	0.40
36:BQ:54:MET:HE2	36:BQ:54:MET:HB2	1.74	0.40
38:BS:58:LEU:HD23	38:BS:58:LEU:HA	1.81	0.40
43:BX:57:LEU:HD12	43:BX:78:LYS:HG2	2.03	0.40
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.61	0.40
52:B6:10:LEU:HG	52:B6:54:ILE:HG13	2.02	0.40
1:CA:29:G:HO2'	1:CA:295:C:H4'	1.86	0.40
1:CA:790:A:C6	1:CA:791:G:C6	3.10	0.40
1:CA:1105:A:H2'	1:CA:1106:G:H8	1.87	0.40
1:CA:1251:A:H5''	9:CI:12:GLU:OE1	2.22	0.40
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.36	0.40
1:CA:1320:C:H5'	1:CA:1320:C:H6	1.85	0.40
1:CA:1325:C:C2'	1:CA:1326:C:H5'	2.51	0.40
2:CB:36:ARG:O	2:CB:37:ASN:HB2	2.21	0.40
4:CD:25:ARG:NH1	4:CD:30:LYS:HB3	2.36	0.40
4:CD:64:LEU:HB2	4:CD:198:VAL:HG11	2.04	0.40
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	2.01	0.40
13:CM:87:TYR:HA	13:CM:90:LEU:HD12	2.04	0.40
19:CS:35:SER:O	19:CS:71:LEU:HD22	2.21	0.40
23:CX:43:A:H2'	23:CX:44:A:C8	2.56	0.40
25:DA:192:C:O2'	25:DA:802:A:N3	2.52	0.40
25:DA:196:A:N3	25:DA:196:A:H2'	2.37	0.40
25:DA:384:U:H2'	25:DA:385:C:H6	1.85	0.40
25:DA:528:A:C2	25:DA:2043:C:H4'	2.57	0.40
25:DA:639:U:H2'	25:DA:640:C:C6	2.57	0.40
25:DA:764:A:O4'	27:DD:213:ARG:HG3	2.22	0.40
25:DA:1005:C:C2	25:DA:1143:A:C5	3.10	0.40
25:DA:1291:C:O2'	25:DA:1292:U:H5'	2.21	0.40
25:DA:2080:G:N2	25:DA:2241:A:C4	2.89	0.40
25:DA:2182:G:H2'	25:DA:2183:C:C6	2.56	0.40
25:DA:2494:G:O2'	36:DQ:80:GLU:HA	2.22	0.40
25:DA:2748:A:C4	25:DA:2749:A:C8	3.10	0.40
26:DB:43:C:C4	26:DB:45:A:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:38:LYS:HA	27:DD:38:LYS:HD2	1.99	0.40
27:DD:94:LEU:HD23	27:DD:94:LEU:HA	1.95	0.40
27:DD:245:PRO:HA	27:DD:246:PRO:HD3	1.94	0.40
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.40
1:AA:1286:A:H2'	1:AA:1287:A:H4'	2.02	0.40
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.51	0.40
4:AD:18:LYS:HE2	4:AD:20:TYR:CZ	2.56	0.40
4:AD:88:VAL:HA	5:AE:97:GLY:HA2	2.03	0.40
4:AD:178:VAL:C	4:AD:180:GLY:N	2.79	0.40
6:AF:26:ILE:O	6:AF:30:LEU:HG	2.22	0.40
11:AK:19:ALA:HB3	11:AK:82:VAL:HG22	2.04	0.40
16:AP:59:TRP:HB3	16:AP:64:ALA:HB2	2.03	0.40
23:AX:40:C:H2'	23:AX:41:C:H6	1.87	0.40
25:BA:107:G:H2'	25:BA:108:G:O4'	2.22	0.40
25:BA:470:C:H4'	29:BF:49:ALA:HB2	2.03	0.40
25:BA:1052:C:C2	25:BA:1183:G:N2	2.89	0.40
25:BA:1058:U:C5	33:BN:28:THR:HG21	2.56	0.40
25:BA:1066:A:N1	25:BA:1186:U:O2'	2.50	0.40
25:BA:1717:C:O2	28:BE:129:HIS:NE2	2.52	0.40
25:BA:2102:G:OP1	47:B1:35:THR:HG21	2.20	0.40
30:BG:43:LEU:C	30:BG:45:GLU:H	2.29	0.40
35:BP:101:VAL:HG22	35:BP:106:LEU:O	2.21	0.40
38:BS:3:ARG:HE	38:BS:3:ARG:CA	2.34	0.40
38:BS:68:GLN:HG2	38:BS:71:ARG:HH12	1.86	0.40
42:BW:13:SER:HA	42:BW:14:PRO:HD3	1.94	0.40
50:B4:55:ARG:HB3	50:B4:56:VAL:O	2.22	0.40
1:CA:973:G:H3'	1:CA:974:A:H5''	2.03	0.40
1:CA:1262:C:O2'	1:CA:1263:C:C5'	2.69	0.40
1:CA:1325:C:H4'	21:CU:17:THR:HG21	2.02	0.40
1:CA:1502:A:H5''	1:CA:1504:G:N7	2.37	0.40
2:CB:7:VAL:HB	2:CB:8:LYS:H	1.66	0.40
2:CB:74:LYS:H	2:CB:74:LYS:HG2	1.52	0.40
2:CB:96:ARG:CZ	2:CB:98:LEU:HD13	2.52	0.40
10:CJ:16:LEU:HD23	10:CJ:16:LEU:HA	1.93	0.40
12:CL:84:LEU:HB2	12:CL:105:TYR:CD2	2.56	0.40
25:DA:71:A:H3'	25:DA:71:A:OP2	2.21	0.40
25:DA:118:A:OP2	25:DA:119:A:H2'	2.21	0.40
25:DA:812:C:H5''	25:DA:1250:G:O2'	2.22	0.40
25:DA:867:C:H2'	25:DA:868:U:H6	1.86	0.40
25:DA:1024:G:H21	25:DA:1144:G:C4'	2.35	0.40
25:DA:1252:G:C2	25:DA:1253:A:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1297:C:H2'	25:DA:1298:C:H6	1.87	0.40
25:DA:1423:G:H2'	25:DA:1424:G:C8	2.56	0.40
25:DA:1448:G:H21	25:DA:1528(A):A:H2	1.69	0.40
25:DA:2023:G:H4'	25:DA:2617:C:O3'	2.22	0.40
25:DA:2240:C:O2'	25:DA:2241:A:H5'	2.21	0.40
25:DA:2648:C:H2'	25:DA:2649:U:H6	1.85	0.40
26:DB:56:G:OP1	30:DG:27:ASN:ND2	2.54	0.40
26:DB:57:A:N3	30:DG:29:TRP:HB3	2.36	0.40
27:DD:71:ASP:HB3	27:DD:103:ARG:HH22	1.87	0.40
27:DD:233:HIS:HA	61:DD:406:HOH:O	2.20	0.40
29:DF:36:VAL:HG11	29:DF:183:VAL:CG1	2.51	0.40
30:DG:135:LEU:HB2	30:DG:155:MET:HG2	2.03	0.40
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.90	0.40
35:DP:81:GLN:NE2	35:DP:105:LEU:O	2.55	0.40
48:D2:3:LEU:HD23	48:D2:3:LEU:HA	1.88	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	
2	AB	229/256 (90%)	194 (85%)	24 (10%)	11 (5%)	2	3
2	CB	229/256 (90%)	195 (85%)	24 (10%)	10 (4%)	2	4
3	AC	204/239 (85%)	179 (88%)	23 (11%)	2 (1%)	12	32
3	CC	204/239 (85%)	178 (87%)	23 (11%)	3 (2%)	8	22
4	AD	206/209 (99%)	189 (92%)	15 (7%)	2 (1%)	12	32
4	CD	206/209 (99%)	190 (92%)	14 (7%)	2 (1%)	12	32
5	AE	146/162 (90%)	139 (95%)	5 (3%)	2 (1%)	9	23
5	CE	146/162 (90%)	136 (93%)	8 (6%)	2 (1%)	9	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AF	98/101 (97%)	88 (90%)	10 (10%)	0	100	100
6	CF	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
7	AG	153/156 (98%)	139 (91%)	11 (7%)	3 (2%)	6	16
7	CG	153/156 (98%)	137 (90%)	15 (10%)	1 (1%)	18	41
8	AH	135/138 (98%)	130 (96%)	5 (4%)	0	100	100
8	CH	135/138 (98%)	129 (96%)	5 (4%)	1 (1%)	18	41
9	AI	125/128 (98%)	107 (86%)	14 (11%)	4 (3%)	3	7
9	CI	125/128 (98%)	109 (87%)	12 (10%)	4 (3%)	3	7
10	AJ	95/105 (90%)	80 (84%)	9 (10%)	6 (6%)	1	2
10	CJ	94/105 (90%)	83 (88%)	6 (6%)	5 (5%)	1	3
11	AK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	6	18
11	CK	112/129 (87%)	101 (90%)	8 (7%)	3 (3%)	4	10
12	AL	120/132 (91%)	111 (92%)	9 (8%)	0	100	100
12	CL	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
13	AM	118/126 (94%)	103 (87%)	13 (11%)	2 (2%)	7	19
13	CM	116/126 (92%)	101 (87%)	11 (10%)	4 (3%)	3	7
14	AN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
14	CN	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
15	AO	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
15	CO	86/89 (97%)	78 (91%)	7 (8%)	1 (1%)	10	27
16	AP	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
16	CP	80/88 (91%)	74 (92%)	5 (6%)	1 (1%)	9	25
17	AQ	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
17	CQ	97/105 (92%)	90 (93%)	7 (7%)	0	100	100
18	AR	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
18	CR	66/88 (75%)	64 (97%)	1 (2%)	1 (2%)	8	22
19	AS	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
19	CS	81/93 (87%)	68 (84%)	11 (14%)	2 (2%)	4	11
20	AT	94/106 (89%)	82 (87%)	6 (6%)	6 (6%)	1	1
20	CT	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	1	3
21	AU	21/27 (78%)	17 (81%)	4 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	CU	21/27 (78%)	16 (76%)	4 (19%)	1 (5%)	2	3
27	BD	273/276 (99%)	258 (94%)	14 (5%)	1 (0%)	30	54
27	DD	273/276 (99%)	257 (94%)	14 (5%)	2 (1%)	18	41
28	BE	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	48
28	DE	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	12	32
29	BF	201/210 (96%)	196 (98%)	4 (2%)	1 (0%)	24	48
29	DF	201/210 (96%)	195 (97%)	4 (2%)	2 (1%)	12	32
30	BG	179/182 (98%)	165 (92%)	11 (6%)	3 (2%)	7	19
30	DG	179/182 (98%)	161 (90%)	14 (8%)	4 (2%)	5	14
31	BH	172/180 (96%)	161 (94%)	10 (6%)	1 (1%)	21	44
31	DH	172/180 (96%)	160 (93%)	11 (6%)	1 (1%)	21	44
32	BI	144/148 (97%)	129 (90%)	12 (8%)	3 (2%)	5	15
32	DI	144/148 (97%)	130 (90%)	12 (8%)	2 (1%)	9	23
33	BN	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
33	DN	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	18	41
34	BO	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	16	37
34	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
35	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	18	41
35	DP	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18	41
36	BQ	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	18	41
36	DQ	139/141 (99%)	132 (95%)	5 (4%)	2 (1%)	9	23
37	BR	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
37	DR	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	14	35
38	BS	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	14	35
38	DS	108/112 (96%)	98 (91%)	9 (8%)	1 (1%)	14	35
39	BT	129/146 (88%)	122 (95%)	5 (4%)	2 (2%)	7	20
39	DT	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
40	BU	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
40	DU	114/118 (97%)	112 (98%)	2 (2%)	0	100	100
41	BV	99/101 (98%)	92 (93%)	5 (5%)	2 (2%)	6	16
41	DV	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
42	DW	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
43	BX	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	11	29
43	DX	93/96 (97%)	88 (95%)	3 (3%)	2 (2%)	5	14
44	BY	105/110 (96%)	97 (92%)	6 (6%)	2 (2%)	6	17
44	DY	105/110 (96%)	99 (94%)	5 (5%)	1 (1%)	12	32
45	BZ	169/206 (82%)	147 (87%)	18 (11%)	4 (2%)	4	12
45	DZ	172/206 (84%)	154 (90%)	17 (10%)	1 (1%)	21	44
46	B0	81/85 (95%)	76 (94%)	4 (5%)	1 (1%)	10	27
46	D0	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
47	B1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	29
47	D1	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	29
48	B2	68/72 (94%)	68 (100%)	0	0	100	100
48	D2	68/72 (94%)	68 (100%)	0	0	100	100
49	B3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
49	D3	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
50	B4	67/71 (94%)	50 (75%)	10 (15%)	7 (10%)	0	0
50	D4	67/71 (94%)	53 (79%)	7 (10%)	7 (10%)	0	0
51	B5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
51	D5	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
52	B6	51/54 (94%)	49 (96%)	1 (2%)	1 (2%)	6	16
52	D6	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
53	B7	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
53	D7	46/49 (94%)	45 (98%)	0	1 (2%)	5	14
54	B8	62/65 (95%)	62 (100%)	0	0	100	100
54	D8	62/65 (95%)	62 (100%)	0	0	100	100
55	B9	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
55	D9	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
All	All	11402/12128 (94%)	10561 (93%)	687 (6%)	154 (1%)	9	23

All (154) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	9	GLU
2	AB	10	LEU
2	AB	125	PRO
4	AD	166	LYS
7	AG	80	VAL
9	AI	44	VAL
9	AI	54	ASP
10	AJ	56	HIS
10	AJ	79	ARG
27	BD	275	LYS
29	BF	130	ALA
30	BG	43	LEU
31	BH	126	PRO
32	BI	107	VAL
39	BT	127	ALA
39	BT	128	GLU
47	B1	3	LYS
50	B4	44	THR
50	B4	45	GLY
50	B4	68	ARG
2	CB	16	HIS
2	CB	17	PHE
2	CB	126	GLU
2	CB	231	GLU
3	CC	99	VAL
4	CD	46	LYS
4	CD	166	LYS
9	CI	44	VAL
9	CI	54	ASP
10	CJ	55	LYS
10	CJ	56	HIS
13	CM	67	GLU
13	CM	106	ASN
20	CT	95	ALA
20	CT	99	LEU
29	DF	130	ALA
30	DG	43	LEU
30	DG	47	LYS
30	DG	81	LYS
31	DH	126	PRO
32	DI	10	GLU
36	DQ	60	ARG
41	DV	79	VAL

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Mol	Chain	Res	Type
50	D4	45	GLY
50	D4	49	PHE
50	D4	62	ARG
50	D4	63	TYR
53	D7	46	VAL
2	AB	11	LEU
2	AB	19	HIS
5	AE	85	GLY
7	AG	81	GLY
10	AJ	31	GLY
10	AJ	55	LYS
11	AK	49	GLY
13	AM	67	GLU
20	AT	47	GLY
30	BG	47	LYS
30	BG	51	ARG
32	BI	106	GLY
36	BQ	60	ARG
41	BV	79	VAL
41	BV	100	ARG
43	BX	94	GLY
45	BZ	137	ILE
46	B0	13	GLY
50	B4	49	PHE
52	B6	13	CYS
2	CB	8	LYS
2	CB	10	LEU
2	CB	20	GLU
2	CB	121	LEU
3	CC	4	LYS
3	CC	181	ASN
7	CG	55	GLY
8	CH	133	LEU
10	CJ	75	ILE
10	CJ	77	PRO
11	CK	49	GLY
11	CK	100	ALA
19	CS	30	LEU
20	CT	47	GLY
21	CU	3	LYS
27	DD	239	ARG
29	DF	21	ALA

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Mol	Chain	Res	Type
36	DQ	27	VAL
43	DX	94	GLY
2	AB	126	GLU
10	AJ	75	ILE
10	AJ	78	ASN
20	AT	96	GLY
20	AT	100	ILE
20	AT	102	GLY
28	BE	52	LEU
45	BZ	155	LEU
50	B4	55	ARG
50	B4	62	ARG
2	CB	9	GLU
2	CB	234	PRO
10	CJ	91	PRO
13	CM	5	ALA
18	CR	25	THR
28	DE	52	LEU
38	DS	84	GLN
50	D4	46	GLN
2	AB	131	PRO
4	AD	164	ALA
9	AI	12	GLU
20	AT	10	LEU
20	AT	95	ALA
32	BI	73	GLU
34	BO	5	GLN
44	BY	54	LYS
45	BZ	152	ALA
50	B4	56	VAL
9	CI	11	LYS
13	CM	4	ILE
19	CS	29	ARG
30	DG	51	ARG
32	DI	135	GLU
35	DP	29	LYS
44	DY	54	LYS
47	D1	3	LYS
2	AB	20	GLU
2	AB	213	LEU
2	AB	227	GLY
2	AB	234	PRO

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Mol	Chain	Res	Type
9	AI	29	ASN
13	AM	4	ILE
35	BP	29	LYS
5	CE	27	ARG
9	CI	12	GLU
20	CT	102	GLY
27	DD	3	VAL
33	DN	2	LYS
37	DR	45	ARG
43	DX	2	LYS
45	DZ	113	ALA
50	D4	55	ARG
3	AC	99	VAL
7	AG	4	ARG
16	CP	81	ARG
20	CT	100	ILE
38	BS	60	GLY
15	CO	23	GLY
28	DE	73	GLU
3	AC	66	VAL
44	BY	53	PRO
45	BZ	111	VAL
5	AE	69	VAL
11	AK	105	VAL
50	D4	29	PRO
5	CE	69	VAL
11	CK	105	VAL

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	
2	AB	192/220 (87%)	152 (79%)	40 (21%)	1	3
2	CB	187/220 (85%)	154 (82%)	33 (18%)	2	5
3	AC	143/188 (76%)	128 (90%)	15 (10%)	6	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CC	140/188 (74%)	121 (86%)	19 (14%)	3	9
4	AD	170/181 (94%)	150 (88%)	20 (12%)	5	13
4	CD	173/181 (96%)	156 (90%)	17 (10%)	7	19
5	AE	113/123 (92%)	103 (91%)	10 (9%)	9	23
5	CE	114/123 (93%)	102 (90%)	12 (10%)	6	17
6	AF	83/90 (92%)	78 (94%)	5 (6%)	17	41
6	CF	85/90 (94%)	79 (93%)	6 (7%)	13	33
7	AG	119/127 (94%)	105 (88%)	14 (12%)	5	13
7	CG	120/127 (94%)	108 (90%)	12 (10%)	7	19
8	AH	114/119 (96%)	104 (91%)	10 (9%)	9	23
8	CH	114/119 (96%)	104 (91%)	10 (9%)	9	23
9	AI	90/99 (91%)	78 (87%)	12 (13%)	4	10
9	CI	89/99 (90%)	79 (89%)	10 (11%)	6	15
10	AJ	66/92 (72%)	58 (88%)	8 (12%)	5	12
10	CJ	69/92 (75%)	62 (90%)	7 (10%)	7	18
11	AK	82/99 (83%)	75 (92%)	7 (8%)	10	25
11	CK	83/99 (84%)	74 (89%)	9 (11%)	6	16
12	AL	97/109 (89%)	89 (92%)	8 (8%)	10	27
12	CL	97/109 (89%)	90 (93%)	7 (7%)	13	32
13	AM	91/101 (90%)	78 (86%)	13 (14%)	3	8
13	CM	89/101 (88%)	76 (85%)	13 (15%)	3	8
14	AN	49/50 (98%)	42 (86%)	7 (14%)	3	8
14	CN	49/50 (98%)	41 (84%)	8 (16%)	2	6
15	AO	78/80 (98%)	69 (88%)	9 (12%)	5	14
15	CO	78/80 (98%)	72 (92%)	6 (8%)	12	30
16	AP	69/74 (93%)	58 (84%)	11 (16%)	2	7
16	CP	68/74 (92%)	58 (85%)	10 (15%)	3	8
17	AQ	94/97 (97%)	88 (94%)	6 (6%)	16	38
17	CQ	94/97 (97%)	89 (95%)	5 (5%)	20	46
18	AR	59/77 (77%)	53 (90%)	6 (10%)	7	18
18	CR	59/77 (77%)	53 (90%)	6 (10%)	7	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AS	69/80 (86%)	64 (93%)	5 (7%)	13	32
19	CS	67/80 (84%)	59 (88%)	8 (12%)	5	13
20	AT	70/82 (85%)	63 (90%)	7 (10%)	7	19
20	CT	70/82 (85%)	61 (87%)	9 (13%)	4	10
21	AU	18/22 (82%)	16 (89%)	2 (11%)	6	15
21	CU	18/22 (82%)	18 (100%)	0	100	100
27	BD	215/218 (99%)	195 (91%)	20 (9%)	8	21
27	DD	215/218 (99%)	197 (92%)	18 (8%)	10	26
28	BE	164/166 (99%)	140 (85%)	24 (15%)	3	8
28	DE	164/166 (99%)	137 (84%)	27 (16%)	2	6
29	BF	160/166 (96%)	139 (87%)	21 (13%)	4	10
29	DF	159/166 (96%)	139 (87%)	20 (13%)	4	11
30	BG	143/156 (92%)	126 (88%)	17 (12%)	5	13
30	DG	142/156 (91%)	124 (87%)	18 (13%)	4	11
31	BH	144/148 (97%)	130 (90%)	14 (10%)	8	20
31	DH	144/148 (97%)	131 (91%)	13 (9%)	9	23
32	BI	110/124 (89%)	86 (78%)	24 (22%)	1	3
32	DI	104/124 (84%)	87 (84%)	17 (16%)	2	6
33	BN	118/119 (99%)	102 (86%)	16 (14%)	3	9
33	DN	118/119 (99%)	105 (89%)	13 (11%)	6	15
34	BO	100/100 (100%)	93 (93%)	7 (7%)	14	34
34	DO	100/100 (100%)	91 (91%)	9 (9%)	9	23
35	BP	115/116 (99%)	101 (88%)	14 (12%)	5	12
35	DP	115/116 (99%)	102 (89%)	13 (11%)	5	14
36	BQ	111/111 (100%)	100 (90%)	11 (10%)	7	19
36	DQ	111/111 (100%)	101 (91%)	10 (9%)	9	23
37	BR	101/101 (100%)	83 (82%)	18 (18%)	2	5
37	DR	101/101 (100%)	84 (83%)	17 (17%)	2	6
38	BS	87/88 (99%)	79 (91%)	8 (9%)	8	22
38	DS	85/88 (97%)	74 (87%)	11 (13%)	4	10
39	BT	115/127 (91%)	103 (90%)	12 (10%)	7	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	DT	113/127 (89%)	102 (90%)	11 (10%)	8	20
40	BU	93/94 (99%)	84 (90%)	9 (10%)	8	20
40	DU	93/94 (99%)	87 (94%)	6 (6%)	15	37
41	BV	80/82 (98%)	65 (81%)	15 (19%)	1	4
41	DV	80/82 (98%)	64 (80%)	16 (20%)	1	4
42	BW	90/92 (98%)	84 (93%)	6 (7%)	15	36
42	DW	90/92 (98%)	83 (92%)	7 (8%)	11	29
43	BX	77/78 (99%)	72 (94%)	5 (6%)	15	37
43	DX	77/78 (99%)	72 (94%)	5 (6%)	15	37
44	BY	85/91 (93%)	77 (91%)	8 (9%)	8	21
44	DY	85/91 (93%)	79 (93%)	6 (7%)	13	33
45	BZ	145/179 (81%)	129 (89%)	16 (11%)	6	15
45	DZ	145/179 (81%)	129 (89%)	16 (11%)	6	15
46	B0	65/67 (97%)	61 (94%)	4 (6%)	16	39
46	D0	65/67 (97%)	60 (92%)	5 (8%)	12	30
47	B1	80/83 (96%)	72 (90%)	8 (10%)	7	19
47	D1	80/83 (96%)	73 (91%)	7 (9%)	9	23
48	B2	65/67 (97%)	60 (92%)	5 (8%)	12	30
48	D2	65/67 (97%)	58 (89%)	7 (11%)	6	16
49	B3	51/52 (98%)	43 (84%)	8 (16%)	2	7
49	D3	50/52 (96%)	43 (86%)	7 (14%)	3	9
50	B4	60/63 (95%)	50 (83%)	10 (17%)	2	6
50	D4	53/63 (84%)	45 (85%)	8 (15%)	3	7
51	B5	50/52 (96%)	41 (82%)	9 (18%)	2	5
51	D5	50/52 (96%)	45 (90%)	5 (10%)	7	19
52	B6	51/52 (98%)	45 (88%)	6 (12%)	5	13
52	D6	50/52 (96%)	46 (92%)	4 (8%)	11	28
53	B7	41/42 (98%)	39 (95%)	2 (5%)	22	49
53	D7	41/42 (98%)	41 (100%)	0	100	100
54	B8	53/55 (96%)	48 (91%)	5 (9%)	8	21
54	D8	54/55 (98%)	48 (89%)	6 (11%)	6	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	B9	34/34 (100%)	33 (97%)	1 (3%)	37	67
55	D9	34/34 (100%)	30 (88%)	4 (12%)	5	13
All	All	9315/10066 (92%)	8264 (89%)	1051 (11%)	5	14

All (1051) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	8	LYS
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	19	HIS
2	AB	21	ARG
2	AB	39	ILE
2	AB	42	ILE
2	AB	49	GLU
2	AB	64	ARG
2	AB	67	THR
2	AB	76	GLN
2	AB	80	ILE
2	AB	93	VAL
2	AB	96	ARG
2	AB	108	ILE
2	AB	112	VAL
2	AB	121	LEU
2	AB	127	ILE
2	AB	128	GLU
2	AB	137	ARG
2	AB	144	ARG
2	AB	145	LEU
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	158	LEU
2	AB	164	VAL
2	AB	185	ILE
2	AB	187	LEU
2	AB	200	ILE
2	AB	204	ASN

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Mol	Chain	Res	Type
2	AB	209	ARG
2	AB	213	LEU
2	AB	215	LEU
2	AB	221	LEU
2	AB	223	ILE
2	AB	230	VAL
3	AC	3	ASN
3	AC	17	ASP
3	AC	21	ARG
3	AC	27	LYS
3	AC	28	GLN
3	AC	47	LEU
3	AC	52	LEU
3	AC	115	LEU
3	AC	123	GLN
3	AC	150	LYS
3	AC	165	THR
3	AC	178	LEU
3	AC	196	LEU
3	AC	202	ILE
3	AC	207	VAL
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	49	ARG
4	AD	53	ASP
4	AD	58	LEU
4	AD	65	ARG
4	AD	108	LEU
4	AD	112	VAL
4	AD	120	LEU
4	AD	122	ARG
4	AD	127	THR
4	AD	135	LEU
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	178	VAL
4	AD	182	LYS
4	AD	188	LEU
4	AD	200	GLU
5	AE	12	LEU

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Mol	Chain	Res	Type
5	AE	31	LEU
5	AE	34	VAL
5	AE	41	VAL
5	AE	57	LYS
5	AE	67	VAL
5	AE	79	GLU
5	AE	109	ILE
5	AE	120	THR
5	AE	147	ASP
6	AF	55	ASP
6	AF	69	GLU
6	AF	75	LEU
6	AF	82	ARG
6	AF	94	GLN
7	AG	8	GLU
7	AG	13	GLN
7	AG	21	VAL
7	AG	32	ARG
7	AG	51	GLN
7	AG	57	GLU
7	AG	73	MET
7	AG	76	ARG
7	AG	78	ARG
7	AG	97	GLN
7	AG	104	LEU
7	AG	113	GLU
7	AG	131	LYS
7	AG	138	LYS
8	AH	2	LEU
8	AH	26	VAL
8	AH	37	ARG
8	AH	50	ARG
8	AH	63	LEU
8	AH	78	GLN
8	AH	91	ARG
8	AH	112	LEU
8	AH	133	LEU
8	AH	137	VAL
9	AI	23	ASN
9	AI	27	THR
9	AI	42	ARG
9	AI	53	VAL

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Mol	Chain	Res	Type
9	AI	56	LEU
9	AI	64	THR
9	AI	81	ILE
9	AI	89	ASN
9	AI	104	ARG
9	AI	108	VAL
9	AI	112	LYS
9	AI	128	ARG
10	AJ	7	LYS
10	AJ	16	LEU
10	AJ	23	ILE
10	AJ	49	VAL
10	AJ	67	THR
10	AJ	84	GLN
10	AJ	96	ILE
10	AJ	98	ILE
11	AK	31	THR
11	AK	48	ILE
11	AK	55	LYS
11	AK	84	VAL
11	AK	96	ARG
11	AK	109	VAL
11	AK	114	VAL
12	AL	18	VAL
12	AL	27	LEU
12	AL	33	ARG
12	AL	39	VAL
12	AL	67	THR
12	AL	83	VAL
12	AL	84	LEU
12	AL	123	LYS
13	AM	4	ILE
13	AM	15	VAL
13	AM	19	LEU
13	AM	25	ILE
13	AM	39	ILE
13	AM	43	THR
13	AM	47	ASP
13	AM	60	VAL
13	AM	70	LEU
13	AM	73	GLU
13	AM	98	VAL

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Mol	Chain	Res	Type
13	AM	110	ARG
13	AM	121	LYS
14	AN	7	ILE
14	AN	15	LYS
14	AN	18	VAL
14	AN	32	SER
14	AN	33	VAL
14	AN	44	LEU
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	66	LEU
15	AO	83	GLU
15	AO	84	LYS
15	AO	88	ARG
16	AP	2	VAL
16	AP	5	ARG
16	AP	19	ILE
16	AP	20	VAL
16	AP	28	ARG
16	AP	45	THR
16	AP	50	LYS
16	AP	54	GLU
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
17	AQ	6	LEU
17	AQ	14	LYS
17	AQ	49	GLU
17	AQ	53	LEU
17	AQ	63	ARG
17	AQ	74	LEU
18	AR	31	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	38	GLU
18	AR	47	THR
18	AR	76	LEU
19	AS	16	LEU

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Mol	Chain	Res	Type
19	AS	28	LYS
19	AS	41	VAL
19	AS	48	THR
19	AS	65	ASN
20	AT	13	LEU
20	AT	24	LEU
20	AT	45	GLN
20	AT	62	LEU
20	AT	74	LYS
20	AT	80	ARG
20	AT	84	LEU
21	AU	9	ARG
21	AU	10	ARG
27	BD	3	VAL
27	BD	54	ARG
27	BD	61	LEU
27	BD	89	SER
27	BD	94	LEU
27	BD	103	ARG
27	BD	106	ILE
27	BD	111	LEU
27	BD	113	VAL
27	BD	142	VAL
27	BD	155	LEU
27	BD	173	VAL
27	BD	193	VAL
27	BD	211	ARG
27	BD	217	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	242	ARG
27	BD	257	LEU
27	BD	260	ARG
28	BE	9	VAL
28	BE	12	THR
28	BE	21	VAL
28	BE	24	THR
28	BE	33	VAL
28	BE	34	VAL
28	BE	49	LEU
28	BE	73	GLU
28	BE	75	VAL

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Mol	Chain	Res	Type
28	BE	78	LEU
28	BE	82	ARG
28	BE	89	ASP
28	BE	97	LYS
28	BE	111	ARG
28	BE	116	VAL
28	BE	119	ARG
28	BE	144	ARG
28	BE	154	LYS
28	BE	163	GLU
28	BE	167	VAL
28	BE	170	LEU
28	BE	175	VAL
28	BE	181	LEU
28	BE	202	LYS
29	BF	24	LEU
29	BF	28	ILE
29	BF	33	LEU
29	BF	38	ARG
29	BF	53	THR
29	BF	57	VAL
29	BF	74	ARG
29	BF	78	ILE
29	BF	88	VAL
29	BF	106	ARG
29	BF	110	LEU
29	BF	125	LEU
29	BF	132	VAL
29	BF	140	LEU
29	BF	162	LEU
29	BF	170	LEU
29	BF	183	VAL
29	BF	192	LEU
29	BF	195	ASP
29	BF	197	ASP
29	BF	201	VAL
30	BG	3	LEU
30	BG	5	VAL
30	BG	28	VAL
30	BG	35	GLU
30	BG	43	LEU
30	BG	45	GLU

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Mol	Chain	Res	Type
30	BG	58	GLN
30	BG	70	VAL
30	BG	81	LYS
30	BG	82	LEU
30	BG	86	MET
30	BG	135	LEU
30	BG	140	ILE
30	BG	143	GLU
30	BG	148	MET
30	BG	159	VAL
30	BG	175	LEU
31	BH	6	ARG
31	BH	15	VAL
31	BH	33	LEU
31	BH	41	MET
31	BH	44	VAL
31	BH	59	ARG
31	BH	69	ARG
31	BH	71	LEU
31	BH	84	SER
31	BH	98	LEU
31	BH	116	GLU
31	BH	122	THR
31	BH	130	ARG
31	BH	175	LYS
32	BI	7	GLU
32	BI	9	LEU
32	BI	10	GLU
32	BI	38	LEU
32	BI	40	THR
32	BI	43	ASN
32	BI	47	LEU
32	BI	57	ARG
32	BI	60	GLU
32	BI	61	ARG
32	BI	64	GLU
32	BI	66	GLU
32	BI	68	LEU
32	BI	74	ASN
32	BI	75	LEU
32	BI	77	LEU
32	BI	92	VAL

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Mol	Chain	Res	Type
32	BI	101	LEU
32	BI	103	ARG
32	BI	109	ILE
32	BI	116	LEU
32	BI	117	GLU
32	BI	127	VAL
32	BI	140	LEU
33	BN	5	VAL
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL
33	BN	67	LEU
33	BN	68	GLU
33	BN	83	LYS
33	BN	87	LEU
33	BN	99	LEU
33	BN	120	LEU
33	BN	133	GLN
33	BN	137	LYS
34	BO	8	LEU
34	BO	10	VAL
34	BO	24	VAL
34	BO	35	VAL
34	BO	94	ARG
34	BO	98	VAL
34	BO	108	GLU
35	BP	3	LEU
35	BP	15	ARG
35	BP	21	ARG
35	BP	55	ARG
35	BP	56	SER
35	BP	65	ARG
35	BP	68	GLN
35	BP	83	VAL
35	BP	95	VAL
35	BP	98	GLU
35	BP	106	LEU
35	BP	112	LEU

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Mol	Chain	Res	Type
35	BP	125	VAL
35	BP	149	GLU
36	BQ	1	MET
36	BQ	7	MET
36	BQ	8	LYS
36	BQ	16	ARG
36	BQ	21	THR
36	BQ	35	VAL
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	75	THR
36	BQ	109	VAL
36	BQ	110	THR
37	BR	1	MET
37	BR	6	SER
37	BR	18	LEU
37	BR	24	GLN
37	BR	28	LEU
37	BR	29	LEU
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	60	LEU
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	100	LEU
37	BR	102	GLU
37	BR	111	LEU
37	BR	114	VAL
38	BS	14	VAL
38	BS	19	LYS
38	BS	20	ARG
38	BS	49	VAL
38	BS	59	LYS
38	BS	69	VAL
38	BS	76	LYS
38	BS	110	LEU
39	BT	23	ARG
39	BT	28	VAL
39	BT	42	ILE

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Mol	Chain	Res	Type
39	BT	49	VAL
39	BT	53	ARG
39	BT	74	ARG
39	BT	89	VAL
39	BT	93	ARG
39	BT	96	ARG
39	BT	108	ARG
39	BT	118	ARG
39	BT	119	LYS
40	BU	8	VAL
40	BU	36	ARG
40	BU	60	LEU
40	BU	74	LEU
40	BU	83	LEU
40	BU	92	ARG
40	BU	95	LEU
40	BU	104	GLN
40	BU	108	GLU
41	BV	6	LYS
41	BV	18	LEU
41	BV	19	LYS
41	BV	28	GLU
41	BV	43	GLU
41	BV	46	VAL
41	BV	51	VAL
41	BV	52	VAL
41	BV	61	VAL
41	BV	62	LEU
41	BV	72	VAL
41	BV	79	VAL
41	BV	92	THR
41	BV	95	LEU
41	BV	100	ARG
42	BW	11	ARG
42	BW	17	VAL
42	BW	19	LEU
42	BW	23	LEU
42	BW	51	LEU
42	BW	107	LEU
43	BX	35	THR
43	BX	66	LEU
43	BX	76	ARG

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Mol	Chain	Res	Type
43	BX	88	LYS
43	BX	92	LEU
44	BY	1	MET
44	BY	5	MET
44	BY	23	ARG
44	BY	43	ASN
44	BY	49	VAL
44	BY	72	VAL
44	BY	85	VAL
44	BY	90	LEU
45	BZ	5	LEU
45	BZ	18	LEU
45	BZ	19	ARG
45	BZ	33	LEU
45	BZ	61	LEU
45	BZ	76	LEU
45	BZ	86	VAL
45	BZ	96	VAL
45	BZ	102	LEU
45	BZ	107	THR
45	BZ	126	VAL
45	BZ	136	PHE
45	BZ	144	LEU
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	161	VAL
46	B0	14	ARG
46	B0	36	ILE
46	B0	49	LYS
46	B0	55	ARG
47	B1	21	ARG
47	B1	30	VAL
47	B1	40	ARG
47	B1	46	LEU
47	B1	51	VAL
47	B1	59	THR
47	B1	89	GLU
47	B1	95	LEU
48	B2	32	LEU
48	B2	52	ASP
48	B2	55	ARG
48	B2	64	LEU

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Mol	Chain	Res	Type
48	B2	70	GLN
49	B3	6	VAL
49	B3	8	LEU
49	B3	23	LEU
49	B3	29	ARG
49	B3	32	GLN
49	B3	54	VAL
49	B3	56	VAL
49	B3	60	GLU
50	B4	3	GLU
50	B4	34	GLU
50	B4	46	GLN
50	B4	48	ARG
50	B4	49	PHE
50	B4	50	VAL
50	B4	58	ARG
50	B4	59	PHE
50	B4	63	TYR
50	B4	68	ARG
51	B5	6	VAL
51	B5	16	ARG
51	B5	26	THR
51	B5	29	THR
51	B5	36	CYS
51	B5	40	LYS
51	B5	49	CYS
51	B5	59	GLU
51	B5	60	VAL
52	B6	4	GLU
52	B6	9	LEU
52	B6	28	ARG
52	B6	38	LYS
52	B6	40	CYS
52	B6	48	VAL
53	B7	24	THR
53	B7	43	THR
54	B8	14	VAL
54	B8	23	VAL
54	B8	32	LEU
54	B8	37	SER
54	B8	59	LYS
55	B9	27	CYS

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Mol	Chain	Res	Type
2	CB	7	VAL
2	CB	8	LYS
2	CB	11	LEU
2	CB	15	VAL
2	CB	23	ARG
2	CB	35	GLU
2	CB	39	ILE
2	CB	44	LEU
2	CB	49	GLU
2	CB	67	THR
2	CB	93	VAL
2	CB	94	ASN
2	CB	115	LEU
2	CB	121	LEU
2	CB	126	GLU
2	CB	128	GLU
2	CB	137	ARG
2	CB	142	LEU
2	CB	144	ARG
2	CB	154	LEU
2	CB	155	LEU
2	CB	158	LEU
2	CB	164	VAL
2	CB	175	ARG
2	CB	178	ARG
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	204	ASN
2	CB	209	ARG
2	CB	213	LEU
2	CB	215	LEU
2	CB	224	GLN
3	CC	3	ASN
3	CC	21	ARG
3	CC	47	LEU
3	CC	49	SER
3	CC	54	ARG
3	CC	57	ILE
3	CC	70	VAL
3	CC	118	GLN
3	CC	123	GLN

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Mol	Chain	Res	Type
3	CC	125	GLU
3	CC	135	LYS
3	CC	140	ARG
3	CC	152	ILE
3	CC	165	THR
3	CC	178	LEU
3	CC	193	TYR
3	CC	196	LEU
3	CC	202	ILE
3	CC	207	VAL
4	CD	15	GLU
4	CD	19	LEU
4	CD	33	MET
4	CD	34	GLU
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	86	LYS
4	CD	120	LEU
4	CD	122	ARG
4	CD	135	LEU
4	CD	155	LEU
4	CD	157	LEU
4	CD	170	VAL
4	CD	194	LEU
4	CD	200	GLU
4	CD	208	SER
5	CE	10	MET
5	CE	18	ARG
5	CE	27	ARG
5	CE	34	VAL
5	CE	41	VAL
5	CE	47	LYS
5	CE	57	LYS
5	CE	71	LEU
5	CE	79	GLU
5	CE	120	THR
5	CE	147	ASP
5	CE	152	ARG
6	CF	28	ARG
6	CF	41	GLU
6	CF	46	ARG

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Mol	Chain	Res	Type
6	CF	69	GLU
6	CF	72	VAL
6	CF	75	LEU
7	CG	9	VAL
7	CG	16	LEU
7	CG	33	ASP
7	CG	51	GLN
7	CG	52	GLU
7	CG	73	MET
7	CG	76	ARG
7	CG	79	ARG
7	CG	97	GLN
7	CG	104	LEU
7	CG	113	GLU
7	CG	155	ARG
8	CH	2	LEU
8	CH	26	VAL
8	CH	50	ARG
8	CH	63	LEU
8	CH	78	GLN
8	CH	84	ARG
8	CH	91	ARG
8	CH	112	LEU
8	CH	133	LEU
8	CH	137	VAL
9	CI	14	VAL
9	CI	27	THR
9	CI	53	VAL
9	CI	64	THR
9	CI	81	ILE
9	CI	86	VAL
9	CI	92	TYR
9	CI	102	LEU
9	CI	108	VAL
9	CI	128	ARG
10	CJ	19	SER
10	CJ	33	GLN
10	CJ	38	ILE
10	CJ	49	VAL
10	CJ	67	THR
10	CJ	98	ILE
10	CJ	100	THR

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Mol	Chain	Res	Type
11	CK	14	VAL
11	CK	48	ILE
11	CK	54	ARG
11	CK	84	VAL
11	CK	96	ARG
11	CK	98	LEU
11	CK	109	VAL
11	CK	114	VAL
11	CK	126	ARG
12	CL	18	VAL
12	CL	33	ARG
12	CL	39	VAL
12	CL	52	LEU
12	CL	67	THR
12	CL	83	VAL
12	CL	84	LEU
13	CM	3	ARG
13	CM	15	VAL
13	CM	19	LEU
13	CM	27	LYS
13	CM	39	ILE
13	CM	47	ASP
13	CM	49	THR
13	CM	56	LEU
13	CM	60	VAL
13	CM	70	LEU
13	CM	98	VAL
13	CM	106	ASN
13	CM	110	ARG
14	CN	3	ARG
14	CN	7	ILE
14	CN	12	ARG
14	CN	18	VAL
14	CN	23	ARG
14	CN	32	SER
14	CN	33	VAL
14	CN	44	LEU
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	26	GLU
15	CO	41	GLU

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Mol	Chain	Res	Type
15	CO	83	GLU
16	CP	2	VAL
16	CP	5	ARG
16	CP	20	VAL
16	CP	21	VAL
16	CP	27	LYS
16	CP	45	THR
16	CP	60	LEU
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	36	ILE
17	CQ	53	LEU
17	CQ	63	ARG
17	CQ	74	LEU
18	CR	26	LEU
18	CR	32	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	47	THR
18	CR	76	LEU
19	CS	28	LYS
19	CS	41	VAL
19	CS	48	THR
19	CS	56	GLN
19	CS	63	THR
19	CS	64	GLU
19	CS	65	ASN
19	CS	77	THR
20	CT	24	LEU
20	CT	30	LYS
20	CT	38	LYS
20	CT	46	GLU
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	84	LEU
27	DD	54	ARG
27	DD	61	LEU
27	DD	89	SER

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Mol	Chain	Res	Type
27	DD	94	LEU
27	DD	103	ARG
27	DD	106	ILE
27	DD	111	LEU
27	DD	113	VAL
27	DD	134	ARG
27	DD	142	VAL
27	DD	155	LEU
27	DD	193	VAL
27	DD	211	ARG
27	DD	217	ARG
27	DD	221	VAL
27	DD	229	VAL
27	DD	257	LEU
27	DD	259	THR
28	DE	9	VAL
28	DE	12	THR
28	DE	14	ILE
28	DE	21	VAL
28	DE	24	THR
28	DE	27	LEU
28	DE	33	VAL
28	DE	34	VAL
28	DE	40	GLU
28	DE	49	LEU
28	DE	52	LEU
28	DE	72	VAL
28	DE	73	GLU
28	DE	75	VAL
28	DE	77	ILE
28	DE	78	LEU
28	DE	93	VAL
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	144	ARG
28	DE	154	LYS
28	DE	163	GLU
28	DE	167	VAL
28	DE	170	LEU
28	DE	175	VAL
28	DE	181	LEU

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Mol	Chain	Res	Type
29	DF	24	LEU
29	DF	28	ILE
29	DF	33	LEU
29	DF	38	ARG
29	DF	57	VAL
29	DF	74	ARG
29	DF	78	ILE
29	DF	88	VAL
29	DF	106	ARG
29	DF	108	LYS
29	DF	110	LEU
29	DF	132	VAL
29	DF	137	LYS
29	DF	140	LEU
29	DF	162	LEU
29	DF	170	LEU
29	DF	183	VAL
29	DF	192	LEU
29	DF	200	GLU
29	DF	201	VAL
30	DG	3	LEU
30	DG	5	VAL
30	DG	16	ARG
30	DG	28	VAL
30	DG	31	VAL
30	DG	35	GLU
30	DG	36	LYS
30	DG	43	LEU
30	DG	58	GLN
30	DG	70	VAL
30	DG	92	VAL
30	DG	98	ARG
30	DG	136	ARG
30	DG	140	ILE
30	DG	143	GLU
30	DG	145	THR
30	DG	148	MET
30	DG	159	VAL
31	DH	3	ARG
31	DH	15	VAL
31	DH	33	LEU
31	DH	44	VAL

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Mol	Chain	Res	Type
31	DH	63	SER
31	DH	69	ARG
31	DH	71	LEU
31	DH	84	SER
31	DH	95	ARG
31	DH	98	LEU
31	DH	136	ILE
31	DH	139	GLN
31	DH	172	LYS
32	DI	9	LEU
32	DI	40	THR
32	DI	43	ASN
32	DI	44	LEU
32	DI	50	ARG
32	DI	68	LEU
32	DI	73	GLU
32	DI	75	LEU
32	DI	77	LEU
32	DI	79	ILE
32	DI	114	LEU
32	DI	116	LEU
32	DI	123	LEU
32	DI	127	VAL
32	DI	140	LEU
32	DI	142	VAL
32	DI	144	VAL
33	DN	5	VAL
33	DN	28	THR
33	DN	33	LEU
33	DN	34	LEU
33	DN	46	VAL
33	DN	62	VAL
33	DN	85	ILE
33	DN	87	LEU
33	DN	97	ARG
33	DN	99	LEU
33	DN	120	LEU
33	DN	133	GLN
33	DN	137	LYS
34	DO	8	LEU
34	DO	10	VAL
34	DO	23	ARG

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Mol	Chain	Res	Type
34	DO	24	VAL
34	DO	35	VAL
34	DO	69	ILE
34	DO	92	GLU
34	DO	94	ARG
34	DO	98	VAL
35	DP	3	LEU
35	DP	15	ARG
35	DP	21	ARG
35	DP	55	ARG
35	DP	56	SER
35	DP	65	ARG
35	DP	68	GLN
35	DP	83	VAL
35	DP	95	VAL
35	DP	96	THR
35	DP	106	LEU
35	DP	125	VAL
35	DP	126	VAL
36	DQ	5	ARG
36	DQ	7	MET
36	DQ	8	LYS
36	DQ	16	ARG
36	DQ	21	THR
36	DQ	45	GLN
36	DQ	60	ARG
36	DQ	85	LYS
36	DQ	109	VAL
36	DQ	110	THR
37	DR	1	MET
37	DR	18	LEU
37	DR	28	LEU
37	DR	29	LEU
37	DR	30	THR
37	DR	44	LEU
37	DR	54	LEU
37	DR	57	ARG
37	DR	60	LEU
37	DR	65	LEU
37	DR	67	LEU
37	DR	75	LEU
37	DR	79	LEU

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Mol	Chain	Res	Type
37	DR	100	LEU
37	DR	102	GLU
37	DR	111	LEU
37	DR	114	VAL
38	DS	14	VAL
38	DS	19	LYS
38	DS	35	ILE
38	DS	49	VAL
38	DS	58	LEU
38	DS	68	GLN
38	DS	69	VAL
38	DS	71	ARG
38	DS	75	GLU
38	DS	76	LYS
38	DS	110	LEU
39	DT	6	LEU
39	DT	16	ARG
39	DT	23	ARG
39	DT	28	VAL
39	DT	49	VAL
39	DT	64	ARG
39	DT	89	VAL
39	DT	96	ARG
39	DT	108	ARG
39	DT	113	LYS
39	DT	119	LYS
40	DU	8	VAL
40	DU	60	LEU
40	DU	74	LEU
40	DU	83	LEU
40	DU	95	LEU
40	DU	104	GLN
41	DV	6	LYS
41	DV	15	GLU
41	DV	18	LEU
41	DV	19	LYS
41	DV	24	LYS
41	DV	28	GLU
41	DV	38	LEU
41	DV	46	VAL
41	DV	52	VAL
41	DV	57	VAL

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Mol	Chain	Res	Type
41	DV	61	VAL
41	DV	62	LEU
41	DV	72	VAL
41	DV	79	VAL
41	DV	85	LYS
41	DV	95	LEU
42	DW	11	ARG
42	DW	17	VAL
42	DW	23	LEU
42	DW	51	LEU
42	DW	60	ASN
42	DW	100	THR
42	DW	107	LEU
43	DX	57	LEU
43	DX	76	ARG
43	DX	88	LYS
43	DX	90	GLU
43	DX	92	LEU
44	DY	1	MET
44	DY	5	MET
44	DY	49	VAL
44	DY	72	VAL
44	DY	85	VAL
44	DY	91	GLU
45	DZ	5	LEU
45	DZ	11	GLU
45	DZ	19	ARG
45	DZ	33	LEU
45	DZ	61	LEU
45	DZ	72	ARG
45	DZ	76	LEU
45	DZ	86	VAL
45	DZ	96	VAL
45	DZ	97	GLU
45	DZ	126	VAL
45	DZ	145	GLU
45	DZ	154	ASP
45	DZ	155	LEU
45	DZ	156	LYS
45	DZ	161	VAL
46	D0	10	THR
46	D0	14	ARG

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Mol	Chain	Res	Type
46	D0	20	ARG
46	D0	36	ILE
46	D0	49	LYS
47	D1	4	VAL
47	D1	21	ARG
47	D1	30	VAL
47	D1	51	VAL
47	D1	59	THR
47	D1	89	GLU
47	D1	95	LEU
48	D2	30	ARG
48	D2	32	LEU
48	D2	40	SER
48	D2	45	SER
48	D2	55	ARG
48	D2	64	LEU
48	D2	70	GLN
49	D3	6	VAL
49	D3	8	LEU
49	D3	23	LEU
49	D3	32	GLN
49	D3	44	ARG
49	D3	54	VAL
49	D3	56	VAL
50	D4	3	GLU
50	D4	8	LYS
50	D4	24	THR
50	D4	50	VAL
50	D4	53	GLU
50	D4	58	ARG
50	D4	63	TYR
50	D4	69	LYS
51	D5	6	VAL
51	D5	16	ARG
51	D5	29	THR
51	D5	40	LYS
51	D5	59	GLU
52	D6	6	ARG
52	D6	9	LEU
52	D6	38	LYS
52	D6	48	VAL
54	D8	14	VAL

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Mol	Chain	Res	Type
54	D8	23	VAL
54	D8	26	LYS
54	D8	37	SER
54	D8	41	ILE
54	D8	59	LYS
55	D9	13	LYS
55	D9	14	CYS
55	D9	26	ILE
55	D9	35	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (184) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	78	GLN
2	AB	94	ASN
2	AB	212	GLN
3	AC	28	GLN
3	AC	37	GLN
3	AC	104	GLN
3	AC	136	GLN
4	AD	43	HIS
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
5	AE	20	GLN
5	AE	38	GLN
5	AE	56	GLN
5	AE	141	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	51	GLN
7	AG	56	GLN
7	AG	64	GLN
7	AG	97	GLN
7	AG	148	ASN
9	AI	23	ASN
9	AI	58	HIS
9	AI	73	GLN
9	AI	124	GLN

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Mol	Chain	Res	Type
10	AJ	56	HIS
10	AJ	84	GLN
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
15	AO	9	GLN
15	AO	28	GLN
15	AO	46	HIS
15	AO	62	GLN
16	AP	13	HIS
16	AP	76	GLN
17	AQ	16	GLN
19	AS	23	ASN
19	AS	47	HIS
19	AS	65	ASN
19	AS	83	HIS
20	AT	45	GLN
27	BD	87	ASN
27	BD	253	GLN
28	BE	121	ASN
29	BF	69	HIS
29	BF	169	ASN
29	BF	203	GLN
30	BG	41	GLN
30	BG	58	GLN
30	BG	108	ASN
32	BI	43	ASN
32	BI	54	GLN
32	BI	105	HIS
33	BN	56	ASN
33	BN	94	HIS
33	BN	101	HIS
34	BO	3	GLN
34	BO	90	GLN
35	BP	38	GLN
36	BQ	45	GLN
37	BR	13	HIS
37	BR	71	GLN
38	BS	95	HIS
39	BT	43	GLN
39	BT	84	GLN

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Mol	Chain	Res	Type
39	BT	123	GLN
40	BU	81	HIS
40	BU	94	ASN
42	BW	40	ASN
42	BW	60	ASN
42	BW	111	HIS
43	BX	31	HIS
43	BX	82	GLN
44	BY	43	ASN
44	BY	68	HIS
45	BZ	73	GLN
45	BZ	151	HIS
46	B0	3	HIS
47	B1	16	ASN
48	B2	70	GLN
49	B3	32	GLN
50	B4	46	GLN
52	B6	20	ASN
52	B6	49	HIS
54	B8	43	GLN
55	B9	36	GLN
2	CB	40	HIS
2	CB	76	GLN
2	CB	146	GLN
2	CB	224	GLN
3	CC	28	GLN
3	CC	37	GLN
3	CC	98	ASN
3	CC	104	GLN
3	CC	118	GLN
3	CC	136	GLN
4	CD	74	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	129	ASN
4	CD	160	GLN
4	CD	161	ASN
4	CD	201	GLN
5	CE	38	GLN
5	CE	56	GLN
5	CE	78	HIS

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Mol	Chain	Res	Type
5	CE	141	GLN
6	CF	64	GLN
6	CF	73	ASN
7	CG	28	ASN
7	CG	37	ASN
7	CG	51	GLN
7	CG	64	GLN
7	CG	86	GLN
7	CG	148	ASN
8	CH	82	HIS
9	CI	31	GLN
9	CI	58	HIS
9	CI	89	ASN
9	CI	124	GLN
10	CJ	13	HIS
11	CK	22	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	77	ASN
14	CN	49	HIS
15	CO	9	GLN
15	CO	28	GLN
15	CO	62	GLN
16	CP	13	HIS
17	CQ	16	GLN
19	CS	23	ASN
19	CS	47	HIS
19	CS	57	HIS
19	CS	83	HIS
27	DD	87	ASN
27	DD	164	GLN
27	DD	166	GLN
27	DD	253	GLN
28	DE	85	ASN
28	DE	180	ASN
28	DE	192	ASN
29	DF	40	GLN
29	DF	69	HIS
29	DF	133	ASN
29	DF	169	ASN
29	DF	203	GLN

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Mol	Chain	Res	Type
30	DG	40	ASN
30	DG	41	GLN
30	DG	79	ASN
30	DG	108	ASN
31	DH	139	GLN
32	DI	43	ASN
33	DN	94	HIS
33	DN	101	HIS
34	DO	3	GLN
35	DP	38	GLN
37	DR	13	HIS
37	DR	50	HIS
37	DR	71	GLN
38	DS	68	GLN
39	DT	58	ASN
40	DU	94	ASN
41	DV	87	HIS
42	DW	60	ASN
43	DX	31	HIS
44	DY	43	ASN
45	DZ	32	HIS
45	DZ	55	HIS
45	DZ	151	HIS
48	D2	56	GLN
49	D3	32	GLN
50	D4	60	GLN
51	D5	4	HIS
51	D5	23	HIS
55	D9	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	367 (24%)	26 (1%)
1	CA	1501/1521 (98%)	374 (24%)	32 (2%)
22	AV	7/24 (29%)	0	0
22	CV	4/24 (16%)	1 (25%)	0
23	AX	75/77 (97%)	25 (33%)	0
23	CX	75/77 (97%)	23 (30%)	0
24	AY	16/76 (21%)	7 (43%)	0
24	CY	4/76 (5%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	BA	2814/2915 (96%)	477 (16%)	31 (1%)
25	DA	2791/2915 (95%)	524 (18%)	27 (0%)
26	BB	119/121 (98%)	24 (20%)	0
26	DB	119/121 (98%)	25 (21%)	0
All	All	9019/9468 (95%)	1847 (20%)	116 (1%)

All (1847) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	7	G
1	AA	9	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	48	C
1	AA	51	A
1	AA	55	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	73	G
1	AA	78	G
1	AA	79	G
1	AA	92	C
1	AA	96	U
1	AA	97	G
1	AA	98	G
1	AA	101	A
1	AA	111	G
1	AA	112	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	137	C
1	AA	142	G
1	AA	147	G
1	AA	163	C
1	AA	171	A
1	AA	173	U
1	AA	174	C

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Mol	Chain	Res	Type
1	AA	180	U
1	AA	182	U
1	AA	189(A)	C
1	AA	189(B)	C
1	AA	189(D)	C
1	AA	189(E)	U
1	AA	189(F)	U
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	199	G
1	AA	200	G
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	219	C
1	AA	247	G
1	AA	251	G
1	AA	256	U
1	AA	257	G
1	AA	266	G
1	AA	267	C
1	AA	277	C
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	343	U
1	AA	344	A
1	AA	347	G
1	AA	348	G
1	AA	351	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U

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Mol	Chain	Res	Type
1	AA	372	C
1	AA	373	A
1	AA	380	G
1	AA	384	G
1	AA	396	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	421	U
1	AA	422	C
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	434	U
1	AA	435	C
1	AA	439	A
1	AA	442	C
1	AA	452	A
1	AA	456	C
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	474	G
1	AA	475	G
1	AA	484	G
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	513	C
1	AA	518	C
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	531	U
1	AA	532	A

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Mol	Chain	Res	Type
1	AA	533	A
1	AA	536	C
1	AA	544	G
1	AA	546	G
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	571	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	587	G
1	AA	590	C
1	AA	591	U
1	AA	592	G
1	AA	595	G
1	AA	596	C
1	AA	602	A
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G
1	AA	641	U
1	AA	644	G
1	AA	653	A
1	AA	656	C
1	AA	658	G
1	AA	665	A
1	AA	673	G
1	AA	687	A
1	AA	688	G
1	AA	693	G
1	AA	695	A
1	AA	705	U
1	AA	711	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	753	A

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Mol	Chain	Res	Type
1	AA	755	G
1	AA	759	A
1	AA	772	U
1	AA	773	G
1	AA	774	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	802	A
1	AA	810	C
1	AA	815	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	868	C
1	AA	870	U
1	AA	875	C
1	AA	885	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	936	C
1	AA	954	G
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	973	G
1	AA	974	A
1	AA	975	A

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Mol	Chain	Res	Type
1	AA	976	G
1	AA	977	A
1	AA	978	A
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	998	G
1	AA	999	C
1	AA	1002	G
1	AA	1004	A
1	AA	1005	A
1	AA	1006	C
1	AA	1007	C
1	AA	1008	C
1	AA	1009	G
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1030(A)	G
1	AA	1030(C)	G
1	AA	1033	G
1	AA	1037	C
1	AA	1043	C
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1056	U
1	AA	1057	G
1	AA	1058	G
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1076	C
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C

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Mol	Chain	Res	Type
1	AA	1101	A
1	AA	1108	G
1	AA	1113	C
1	AA	1116	C
1	AA	1121	U
1	AA	1122	U
1	AA	1123	A
1	AA	1124	G
1	AA	1126	U
1	AA	1130	A
1	AA	1132	C
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1142	G
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1155	G
1	AA	1157	A
1	AA	1159	U
1	AA	1160	G
1	AA	1163	C
1	AA	1164	G
1	AA	1166	G
1	AA	1174	G
1	AA	1176	A
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1200	C
1	AA	1201	A
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C

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Mol	Chain	Res	Type
1	AA	1216	G
1	AA	1218	C
1	AA	1224	G
1	AA	1227	A
1	AA	1235	U
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1246	C
1	AA	1257	U
1	AA	1258	G
1	AA	1260	C
1	AA	1261	A
1	AA	1263	C
1	AA	1265	G
1	AA	1266	G
1	AA	1267	C
1	AA	1270	C
1	AA	1273	G
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1282	C
1	AA	1283	G
1	AA	1286	A
1	AA	1287	A
1	AA	1290	G
1	AA	1296	C
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1311	G
1	AA	1317	C
1	AA	1320	C
1	AA	1322	C
1	AA	1338	G
1	AA	1347	G
1	AA	1353	G
1	AA	1354	C

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Mol	Chain	Res	Type
1	AA	1355	G
1	AA	1356	G
1	AA	1358	U
1	AA	1360	A
1	AA	1363	C
1	AA	1363(A)	A
1	AA	1364	U
1	AA	1370	G
1	AA	1377	A
1	AA	1379	G
1	AA	1384	C
1	AA	1386	G
1	AA	1387	G
1	AA	1397	C
1	AA	1402	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1444	C
1	AA	1445	C
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1497	G
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
23	AX	9	G
23	AX	16	C

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Mol	Chain	Res	Type
23	AX	17	C
23	AX	18	G
23	AX	19	G
23	AX	20	U
23	AX	21	A
23	AX	29	G
23	AX	30	G
23	AX	31	G
23	AX	34	C
23	AX	42	G
23	AX	46	G
23	AX	47	U
23	AX	48	C
23	AX	56	C
23	AX	58	A
23	AX	60	U
23	AX	61	C
23	AX	63	G
23	AX	65	C
23	AX	67	C
23	AX	68	C
23	AX	69	C
23	AX	76	A
24	AY	5	G
24	AY	67	C
24	AY	68	C
24	AY	69	G
24	AY	70	G
24	AY	71	G
24	AY	74	C
25	BA	10	G
25	BA	12	U
25	BA	13	A
25	BA	34	C
25	BA	45	C
25	BA	54	G
25	BA	62	U
25	BA	70	A
25	BA	73	A
25	BA	74	G
25	BA	83	A
25	BA	116	A

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Mol	Chain	Res	Type
25	BA	117	A
25	BA	118	U
25	BA	123	G
25	BA	124	A
25	BA	137	G
25	BA	149	A
25	BA	155	C
25	BA	161	C
25	BA	170	A
25	BA	171	A
25	BA	185	A
25	BA	186	A
25	BA	188	A
25	BA	190	C
25	BA	194	G
25	BA	203	G
25	BA	204	G
25	BA	205	A
25	BA	210	A
25	BA	211	A
25	BA	214	A
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	239	G
25	BA	265	U
25	BA	269	G
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	279	G
25	BA	289	G
25	BA	294	C
25	BA	295	C
25	BA	303	C
25	BA	306	A
25	BA	307	A
25	BA	335	A
25	BA	353	G
25	BA	354	A
25	BA	360	C

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Mol	Chain	Res	Type
25	BA	376	G
25	BA	387	G
25	BA	390	G
25	BA	397	G
25	BA	399	G
25	BA	407	U
25	BA	413	G
25	BA	423	G
25	BA	432	U
25	BA	438	G
25	BA	439	A
25	BA	448	U
25	BA	455	A
25	BA	469	A
25	BA	470	C
25	BA	474	U
25	BA	477	C
25	BA	480	A
25	BA	496	A
25	BA	507	G
25	BA	529	U
25	BA	530	A
25	BA	533	G
25	BA	534	C
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	573	G
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	625	G
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	639	G
25	BA	641	G
25	BA	642	G
25	BA	652	A
25	BA	662	A
25	BA	670	C

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Mol	Chain	Res	Type
25	BA	692	C
25	BA	693	G
25	BA	694	G
25	BA	697	C
25	BA	698	G
25	BA	715	G
25	BA	716	G
25	BA	724	A
25	BA	733	G
25	BA	777	C
25	BA	787	U
25	BA	793	A
25	BA	794	U
25	BA	811	A
25	BA	812	G
25	BA	822	G
25	BA	823	G
25	BA	829	A
25	BA	831	A
25	BA	832	G
25	BA	837	C
25	BA	839	G
25	BA	852	G
25	BA	858	U
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	906	G
25	BA	908	A
25	BA	913	A
25	BA	924	U
25	BA	927	G
25	BA	929	G
25	BA	930	G
25	BA	931	C
25	BA	932	C
25	BA	933	C
25	BA	934	A
25	BA	935	C
25	BA	936	C
25	BA	937	A

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Mol	Chain	Res	Type
25	BA	938	G
25	BA	940	C
25	BA	942	A
25	BA	943	C
25	BA	946	A
25	BA	953	U
25	BA	956	A
25	BA	957	A
25	BA	961	C
25	BA	977	G
25	BA	986	A
25	BA	990	A
25	BA	991	G
25	BA	1003	U
25	BA	1004	A
25	BA	1006	C
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1035	G
25	BA	1042	A
25	BA	1045	U
25	BA	1051	C
25	BA	1054	C
25	BA	1058	U
25	BA	1059	C
25	BA	1068	G
25	BA	1072	U
25	BA	1073	A
25	BA	1079	U
25	BA	1084	C
25	BA	1087	C
25	BA	1090	G
25	BA	1091	A
25	BA	1092	A
25	BA	1093	G
25	BA	1094	A
25	BA	1097	G
25	BA	1153	G
25	BA	1156	G
25	BA	1158	G
25	BA	1175	A

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Mol	Chain	Res	Type
25	BA	1176	U
25	BA	1180	C
25	BA	1181	G
25	BA	1184	G
25	BA	1186	U
25	BA	1195	G
25	BA	1216	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1255	A
25	BA	1256	U
25	BA	1263	C
25	BA	1265	A
25	BA	1287	A
25	BA	1290	G
25	BA	1296	G
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G
25	BA	1318	A
25	BA	1319	U
25	BA	1346	U
25	BA	1347	A
25	BA	1349	G
25	BA	1360	C
25	BA	1366	C
25	BA	1391	C
25	BA	1398	U
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1416	C
25	BA	1426	G
25	BA	1430	A
25	BA	1431	G
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U

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Mol	Chain	Res	Type
25	BA	1467	G
25	BA	1474	C
25	BA	1491	A
25	BA	1497	G
25	BA	1501	U
25	BA	1502	G
25	BA	1507	A
25	BA	1514	C
25	BA	1518	A
25	BA	1525	G
25	BA	1529	G
25	BA	1539	C
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1577	C
25	BA	1578	C
25	BA	1580	G
25	BA	1581	U
25	BA	1586	G
25	BA	1589	A
25	BA	1601	A
25	BA	1605	A
25	BA	1613	A
25	BA	1616	A
25	BA	1625	U
25	BA	1627	A
25	BA	1628	G
25	BA	1631	C
25	BA	1632	A
25	BA	1654	A
25	BA	1655	A
25	BA	1656	A
25	BA	1694	G
25	BA	1695	C
25	BA	1700	G
25	BA	1701	A
25	BA	1711	A
25	BA	1721	G
25	BA	1742	G
25	BA	1743	G
25	BA	1747	A

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Mol	Chain	Res	Type
25	BA	1748	A
25	BA	1750	G
25	BA	1767	A
25	BA	1768	U
25	BA	1776	G
25	BA	1787	G
25	BA	1794	G
25	BA	1795	G
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1822	A
25	BA	1831	C
25	BA	1832	G
25	BA	1847	G
25	BA	1848	G
25	BA	1859	G
25	BA	1878	A
25	BA	1879	A
25	BA	1892	G
25	BA	1899	A
25	BA	1900	G
25	BA	1911	A
25	BA	1918	G
25	BA	1922	A
25	BA	1928	G
25	BA	1935	A
25	BA	1936	C
25	BA	1937	U
25	BA	1941	A
25	BA	1951	G
25	BA	1952	G
25	BA	1959	A
25	BA	1960	A
25	BA	1962	U
25	BA	1977	U
25	BA	1985	U
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2005	C

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Mol	Chain	Res	Type
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2023	A
25	BA	2042	A
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2061	C
25	BA	2065	C
25	BA	2071	G
25	BA	2074	G
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A
25	BA	2091	G
25	BA	2099	A
25	BA	2115	G
25	BA	2120	U
25	BA	2132	G
25	BA	2133	C
25	BA	2135	U
25	BA	2136	A
25	BA	2137	G
25	BA	2138	G
25	BA	2139	A
25	BA	2141	A
25	BA	2143	G
25	BA	2149	G
25	BA	2152	U
25	BA	2153	G
25	BA	2154	U
25	BA	2155	G
25	BA	2156	A
25	BA	2157	A
25	BA	2158	C
25	BA	2161	C
25	BA	2162	C
25	BA	2163	G

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Mol	Chain	Res	Type
25	BA	2164	C
25	BA	2165	C
25	BA	2167	C
25	BA	2168	C
25	BA	2169	G
25	BA	2174	G
25	BA	2178	G
25	BA	2179	G
25	BA	2180	A
25	BA	2185	C
25	BA	2188	G
25	BA	2189	U
25	BA	2190	G
25	BA	2191	A
25	BA	2194	U
25	BA	2196	C
25	BA	2197	C
25	BA	2203	G
25	BA	2204	G
25	BA	2206	G
25	BA	2207	C
25	BA	2209	G
25	BA	2210	C
25	BA	2211	U
25	BA	2212	G
25	BA	2213	G
25	BA	2214	G
25	BA	2220	A
25	BA	2227	G
25	BA	2228	G
25	BA	2229	A
25	BA	2230	U
25	BA	2237	A
25	BA	2250	G
25	BA	2251	G
25	BA	2280	A
25	BA	2281	A
25	BA	2285	A
25	BA	2290	A
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G

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Mol	Chain	Res	Type
25	BA	2310	A
25	BA	2317	A
25	BA	2332	A
25	BA	2333	G
25	BA	2337	G
25	BA	2346	G
25	BA	2347	A
25	BA	2348	A
25	BA	2355	C
25	BA	2359	C
25	BA	2362	C
25	BA	2373	A
25	BA	2384	G
25	BA	2391	G
25	BA	2395	G
25	BA	2397	C
25	BA	2418	U
25	BA	2419	G
25	BA	2422	G
25	BA	2426	G
25	BA	2437	A
25	BA	2441	G
25	BA	2442	A
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C
25	BA	2460	A
25	BA	2480	G
25	BA	2481	A
25	BA	2488	A
25	BA	2490	A
25	BA	2499	G
25	BA	2502	G
25	BA	2514	G
25	BA	2517	G
25	BA	2518	U
25	BA	2530	A
25	BA	2541	G
25	BA	2561	G
25	BA	2566	U
25	BA	2576	A
25	BA	2578	A

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Mol	Chain	Res	Type
25	BA	2579	G
25	BA	2585	C
25	BA	2594	G
25	BA	2614	A
25	BA	2621	U
25	BA	2623	U
25	BA	2624	C
25	BA	2641	A
25	BA	2642	G
25	BA	2644	A
25	BA	2653	G
25	BA	2666	A
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2714	U
25	BA	2715	C
25	BA	2725	A
25	BA	2726	A
25	BA	2727	G
25	BA	2739	U
25	BA	2746	A
25	BA	2770	A
25	BA	2771	A
25	BA	2774	G
25	BA	2777	A
25	BA	2778	A
25	BA	2779	G
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2807	C
25	BA	2813	G
25	BA	2818	U
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2844	G
25	BA	2845	A
25	BA	2846	U
25	BA	2882	G
25	BA	2890	C

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Mol	Chain	Res	Type
25	BA	2901	A
25	BA	2902	G
25	BA	2903	G
26	BB	2	C
26	BB	3	C
26	BB	5	C
26	BB	7	G
26	BB	13	A
26	BB	22	U
26	BB	24	G
26	BB	25	A
26	BB	28	C
26	BB	32	C
26	BB	34	U
26	BB	42	C
26	BB	44	G
26	BB	50	G
26	BB	56	G
26	BB	60	C
26	BB	73	A
26	BB	75	G
26	BB	85	G
26	BB	93	G
26	BB	106	G
26	BB	110	G
26	BB	117	G
26	BB	118	G
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	22	G
1	CA	32	A
1	CA	39	G
1	CA	48	C
1	CA	51	A
1	CA	52	G
1	CA	55	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G

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Mol	Chain	Res	Type
1	CA	73	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	90	U
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	101	A
1	CA	111	G
1	CA	112	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	137	C
1	CA	142	G
1	CA	146	G
1	CA	147	G
1	CA	157	G
1	CA	163	C
1	CA	171	A
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(A)	C
1	CA	189(B)	C
1	CA	189(D)	C
1	CA	189(E)	U
1	CA	189(F)	U
1	CA	189(H)	G
1	CA	189(I)	G
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	200	G
1	CA	201	C
1	CA	202	U
1	CA	203	U

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Mol	Chain	Res	Type
1	CA	204	U
1	CA	216	G
1	CA	217	C
1	CA	219	C
1	CA	247	G
1	CA	251	G
1	CA	256	U
1	CA	257	G
1	CA	266	G
1	CA	267	C
1	CA	277	C
1	CA	289	G
1	CA	301	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	344	A
1	CA	347	G
1	CA	348	G
1	CA	351	G
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	380	G
1	CA	384	G
1	CA	396	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	409	G
1	CA	412	A
1	CA	413	G
1	CA	421	U
1	CA	422	C
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	434	U

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Mol	Chain	Res	Type
1	CA	439	A
1	CA	442	C
1	CA	452	A
1	CA	456	C
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	474	G
1	CA	484	G
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	513	C
1	CA	518	C
1	CA	521	G
1	CA	524	G
1	CA	527	G
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	536	C
1	CA	544	G
1	CA	546	G
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	571	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	587	G
1	CA	590	C
1	CA	591	U
1	CA	592	G
1	CA	595	G
1	CA	596	C
1	CA	602	A

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Mol	Chain	Res	Type
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	641	U
1	CA	644	G
1	CA	653	A
1	CA	656	C
1	CA	658	G
1	CA	665	A
1	CA	673	G
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	705	U
1	CA	711	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A
1	CA	772	U
1	CA	773	G
1	CA	774	G
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	802	A
1	CA	810	C
1	CA	815	A
1	CA	817	C
1	CA	827	U
1	CA	828	A
1	CA	829	G
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	853	G

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Mol	Chain	Res	Type
1	CA	859	A
1	CA	868	C
1	CA	870	U
1	CA	875	C
1	CA	885	G
1	CA	902	G
1	CA	913	A
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	934	C
1	CA	935	A
1	CA	936	C
1	CA	954	G
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	973	G
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	978	A
1	CA	989	C
1	CA	991	U
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	998	G
1	CA	999	C
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1007	C
1	CA	1009	G
1	CA	1020	U
1	CA	1021	G

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Mol	Chain	Res	Type
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1032	G
1	CA	1033	G
1	CA	1036	G
1	CA	1037	C
1	CA	1041	A
1	CA	1045	C
1	CA	1050	G
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1056	U
1	CA	1057	G
1	CA	1058	G
1	CA	1065	U
1	CA	1066	C
1	CA	1067	A
1	CA	1076	C
1	CA	1081	G
1	CA	1084	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1101	A
1	CA	1108	G
1	CA	1113	C
1	CA	1116	C
1	CA	1117	G
1	CA	1122	U
1	CA	1125	U
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U

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Mol	Chain	Res	Type
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1142	G
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1159	U
1	CA	1160	G
1	CA	1163	C
1	CA	1164	G
1	CA	1174	G
1	CA	1176	A
1	CA	1180	A
1	CA	1181	G
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1196	U
1	CA	1197	G
1	CA	1200	C
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1214	C
1	CA	1216	G
1	CA	1218	C
1	CA	1224	G
1	CA	1227	A
1	CA	1235	U
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1246	C
1	CA	1252	A
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G

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Mol	Chain	Res	Type
1	CA	1260	C
1	CA	1261	A
1	CA	1263	C
1	CA	1265	G
1	CA	1266	G
1	CA	1267	C
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1283	G
1	CA	1287	A
1	CA	1296	C
1	CA	1300	G
1	CA	1305	G
1	CA	1311	G
1	CA	1317	C
1	CA	1320	C
1	CA	1322	C
1	CA	1338	G
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1354	C
1	CA	1355	G
1	CA	1356	G
1	CA	1358	U
1	CA	1360	A
1	CA	1363	C
1	CA	1363(A)	A
1	CA	1364	U
1	CA	1370	G
1	CA	1377	A
1	CA	1379	G
1	CA	1384	C
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G

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Mol	Chain	Res	Type
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1444	C
1	CA	1445	C
1	CA	1447	A
1	CA	1452	C
1	CA	1456	G
1	CA	1487	G
1	CA	1492	A
1	CA	1493	A
1	CA	1494	G
1	CA	1497	G
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	16	A
23	CX	9	G
23	CX	16	C
23	CX	17	C
23	CX	18	G
23	CX	19	G
23	CX	20	U
23	CX	21	A
23	CX	29	G
23	CX	30	G
23	CX	31	G
23	CX	34	C
23	CX	42	G
23	CX	46	G
23	CX	47	U
23	CX	48	C
23	CX	56	C
23	CX	58	A
23	CX	60	U

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Mol	Chain	Res	Type
23	CX	61	C
23	CX	65	C
23	CX	67	C
23	CX	68	C
23	CX	76	A
25	DA	10	G
25	DA	12	U
25	DA	15	G
25	DA	34	C
25	DA	35	G
25	DA	36	G
25	DA	45	C
25	DA	51	G
25	DA	55	G
25	DA	61	G
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	79	G
25	DA	83	G
25	DA	84	A
25	DA	90	U
25	DA	94	C
25	DA	95	G
25	DA	100	G
25	DA	102	G
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	125	G
25	DA	139	G
25	DA	141	A
25	DA	149	A
25	DA	154(A)	C
25	DA	157	U
25	DA	173	G
25	DA	181	A
25	DA	182	A
25	DA	196	A
25	DA	199	A
25	DA	205	G
25	DA	214	G

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Mol	Chain	Res	Type
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	228	A
25	DA	229	A
25	DA	233	A
25	DA	248	G
25	DA	250	G
25	DA	271(E)	U
25	DA	271(I)	G
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	271(O)	C
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	277	C
25	DA	278	A
25	DA	292	C
25	DA	294	A
25	DA	311	A
25	DA	324	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	332	A
25	DA	333	G
25	DA	338	G
25	DA	345	A
25	DA	346	A
25	DA	352	G
25	DA	362	U
25	DA	363	G
25	DA	370	G
25	DA	372	G
25	DA	386	G
25	DA	396	G
25	DA	399	G
25	DA	405	U

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Mol	Chain	Res	Type
25	DA	407	G
25	DA	411	G
25	DA	412	A
25	DA	415	A
25	DA	422	A
25	DA	428	A
25	DA	444	C
25	DA	455	C
25	DA	456	C
25	DA	457	A
25	DA	470	A
25	DA	481	G
25	DA	501	A
25	DA	504	U
25	DA	505	A
25	DA	509	C
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	545	G
25	DA	563	G
25	DA	573	G
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	614(B)	G
25	DA	615	G
25	DA	621	A
25	DA	622	G
25	DA	627	A
25	DA	637	A
25	DA	645	C
25	DA	646	A
25	DA	647	G
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	669	G
25	DA	686	G

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Mol	Chain	Res	Type
25	DA	701	G
25	DA	715	G
25	DA	717	G
25	DA	726	G
25	DA	730	C
25	DA	744	G
25	DA	752	A
25	DA	753	C
25	DA	764	A
25	DA	765	G
25	DA	771	G
25	DA	774	A
25	DA	775	G
25	DA	776	G
25	DA	779	U
25	DA	782	A
25	DA	784	A
25	DA	785	G
25	DA	790	C
25	DA	792	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	828	U
25	DA	832	G
25	DA	848	G
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	867	C
25	DA	874	G
25	DA	879	G
25	DA	880	G
25	DA	881	G
25	DA	882	G
25	DA	883	G
25	DA	884	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C

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Mol	Chain	Res	Type
25	DA	890	A
25	DA	893	C
25	DA	895	U
25	DA	896	A
25	DA	897	C
25	DA	898	C
25	DA	899	A
25	DA	900	A
25	DA	901	A
25	DA	910	A
25	DA	917	A
25	DA	923	C
25	DA	932	G
25	DA	933	A
25	DA	938	G
25	DA	941	A
25	DA	944	G
25	DA	945	A
25	DA	946	G
25	DA	953	A
25	DA	959	A
25	DA	961	C
25	DA	963	U
25	DA	974	G
25	DA	975	C
25	DA	983	A
25	DA	996	A
25	DA	1005	C
25	DA	1006	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1018	C
25	DA	1020	A
25	DA	1022	G
25	DA	1026	U
25	DA	1027	A
25	DA	1031	G
25	DA	1033	U
25	DA	1038	C
25	DA	1041	C
25	DA	1042	G

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Mol	Chain	Res	Type
25	DA	1043	C
25	DA	1118	C
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1166	C
25	DA	1171	G
25	DA	1205	U
25	DA	1210	A
25	DA	1211	U
25	DA	1212	G
25	DA	1219	G
25	DA	1229	G
25	DA	1233	C
25	DA	1253	A
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1300	U
25	DA	1301	A
25	DA	1312	U
25	DA	1314	C
25	DA	1321	A
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1368	G
25	DA	1370	C
25	DA	1373	A
25	DA	1379	A
25	DA	1384	A
25	DA	1385	G
25	DA	1391	U
25	DA	1393	A
25	DA	1400	G
25	DA	1416	G
25	DA	1417	C
25	DA	1419	A
25	DA	1420	U

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Mol	Chain	Res	Type
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1435	G
25	DA	1437	C
25	DA	1445	A
25	DA	1449	A
25	DA	1450	G
25	DA	1455	G
25	DA	1459	G
25	DA	1460	A
25	DA	1467	C
25	DA	1471	A
25	DA	1478	G
25	DA	1482	G
25	DA	1492	G
25	DA	1493	C
25	DA	1494	A
25	DA	1496	A
25	DA	1497	U
25	DA	1508	A
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1524	G
25	DA	1528(A)	A
25	DA	1531	C
25	DA	1541	G
25	DA	1542	A
25	DA	1543	C
25	DA	1547	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1583	A
25	DA	1584	C
25	DA	1586	A
25	DA	1598	C
25	DA	1608	A
25	DA	1609	A

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Mol	Chain	Res	Type
25	DA	1610	A
25	DA	1616	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1669	A
25	DA	1674	G
25	DA	1696	G
25	DA	1700	A
25	DA	1701	A
25	DA	1703	G
25	DA	1721	G
25	DA	1722	A
25	DA	1743	C
25	DA	1746	G
25	DA	1756	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A
25	DA	1791	A
25	DA	1800	C
25	DA	1801	G
25	DA	1812	A
25	DA	1816	G
25	DA	1828	G
25	DA	1835	G
25	DA	1847	A
25	DA	1848	A
25	DA	1852	C
25	DA	1877	A
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1929	G
25	DA	1930	G
25	DA	1936	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U

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Mol	Chain	Res	Type
25	DA	1964	G
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1981	A
25	DA	1984	G
25	DA	1993	U
25	DA	1997	G
25	DA	2020	A
25	DA	2023	G
25	DA	2031	A
25	DA	2033	A
25	DA	2043	C
25	DA	2046	G
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2069	G
25	DA	2099	U
25	DA	2102	U
25	DA	2105	C
25	DA	2108	C
25	DA	2109	U
25	DA	2110	G
25	DA	2111	C
25	DA	2112	G
25	DA	2115	G
25	DA	2116	G
25	DA	2119	A
25	DA	2122	U
25	DA	2125	G
25	DA	2126	A
25	DA	2127	G
25	DA	2129	C
25	DA	2131	G
25	DA	2132	U
25	DA	2133	G
25	DA	2135	A
25	DA	2136	C

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Mol	Chain	Res	Type
25	DA	2137	C
25	DA	2138	C
25	DA	2140	C
25	DA	2142	C
25	DA	2146	C
25	DA	2148	G
25	DA	2150	U
25	DA	2151	G
25	DA	2153	G
25	DA	2154	G
25	DA	2155	G
25	DA	2157	G
25	DA	2158	A
25	DA	2159	G
25	DA	2163	C
25	DA	2164	C
25	DA	2165	G
25	DA	2166	G
25	DA	2167	U
25	DA	2168	G
25	DA	2169	A
25	DA	2170	A
25	DA	2172	U
25	DA	2173	A
25	DA	2176	A
25	DA	2178	C
25	DA	2181	G
25	DA	2182	G
25	DA	2185	C
25	DA	2186	G
25	DA	2188	C
25	DA	2189	U
25	DA	2192	G
25	DA	2198	A
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2218	U
25	DA	2219	G
25	DA	2225	A
25	DA	2238	G
25	DA	2239	G

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Mol	Chain	Res	Type
25	DA	2268	A
25	DA	2275	C
25	DA	2279	G
25	DA	2283	C
25	DA	2287	A
25	DA	2288	A
25	DA	2305	A
25	DA	2308	G
25	DA	2309	A
25	DA	2312	U
25	DA	2319	G
25	DA	2320	A
25	DA	2325	G
25	DA	2328	A
25	DA	2336	A
25	DA	2343	C
25	DA	2347	C
25	DA	2350	C
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C
25	DA	2388	A
25	DA	2400	G
25	DA	2402	C
25	DA	2406	U
25	DA	2410	G
25	DA	2417	C
25	DA	2419	U
25	DA	2422	A
25	DA	2423	U
25	DA	2425	A
25	DA	2429	G
25	DA	2430	A
25	DA	2432	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2442	C
25	DA	2445	G
25	DA	2448	A
25	DA	2458	G
25	DA	2465	C

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Mol	Chain	Res	Type
25	DA	2474	C
25	DA	2476	A
25	DA	2490	G
25	DA	2492	U
25	DA	2502	G
25	DA	2505	G
25	DA	2518	A
25	DA	2520	C
25	DA	2529	G
25	DA	2554	U
25	DA	2555	U
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2582	G
25	DA	2592	G
25	DA	2602	A
25	DA	2609	U
25	DA	2611	U
25	DA	2612	C
25	DA	2615	U
25	DA	2629	A
25	DA	2630	G
25	DA	2654	A
25	DA	2663	G
25	DA	2668	G
25	DA	2669	G
25	DA	2689	U
25	DA	2690	C
25	DA	2691	C
25	DA	2702	U
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2726	U
25	DA	2733	A
25	DA	2739	U
25	DA	2751	G
25	DA	2757	A
25	DA	2758	A
25	DA	2764	A

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Mol	Chain	Res	Type
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2793	G
25	DA	2794	C
25	DA	2802	G
25	DA	2809	A
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2834	G
25	DA	2835	A
25	DA	2861	G
25	DA	2866	U
25	DA	2872	G
25	DA	2875	C
25	DA	2879	C
25	DA	2880	C
25	DA	2886	G
25	DA	2892	A
25	DA	2894	G
25	DA	2895	U
25	DA	2896	C
25	DA	2897	U
26	DB	2	C
26	DB	3	C
26	DB	5	C
26	DB	7	G
26	DB	8	U
26	DB	13	A
26	DB	22	U
26	DB	24	G
26	DB	25	A
26	DB	28	C
26	DB	32	C
26	DB	34	U
26	DB	42	C
26	DB	44	G
26	DB	50	G
26	DB	56	G
26	DB	60	C

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Mol	Chain	Res	Type
26	DB	73	A
26	DB	75	G
26	DB	85	G
26	DB	106	G
26	DB	110	G
26	DB	117	G
26	DB	118	G
26	DB	119	G

All (116) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	115	G
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	532	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	793	U
1	AA	840	C
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1064	G
1	AA	1065	U
1	AA	1183	A
1	AA	1201	A
1	AA	1211	U
1	AA	1281	U
1	AA	1285	A
1	AA	1299	A
1	AA	1442	G
1	AA	1446	U
1	AA	1492	A
1	AA	1493	A
25	BA	185	A
25	BA	270	C
25	BA	302	A
25	BA	793	A

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Mol	Chain	Res	Type
25	BA	874	U
25	BA	1019	G
25	BA	1093	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1286	U
25	BA	1425	A
25	BA	1466	U
25	BA	1577	C
25	BA	1654	A
25	BA	1700	G
25	BA	1710	C
25	BA	2014	G
25	BA	2132	G
25	BA	2156	A
25	BA	2164	C
25	BA	2203	G
25	BA	2205	C
25	BA	2209	G
25	BA	2418	U
25	BA	2442	A
25	BA	2623	U
25	BA	2701	U
25	BA	2769	U
25	BA	2902	G
1	CA	60	A
1	CA	65	U
1	CA	115	G
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	532	A
1	CA	560	U
1	CA	687	A
1	CA	748	C
1	CA	793	U
1	CA	840	C
1	CA	913	A
1	CA	991	U
1	CA	992	U

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Mol	Chain	Res	Type
1	CA	1005	A
1	CA	1064	G
1	CA	1065	U
1	CA	1128	C
1	CA	1129	C
1	CA	1183	A
1	CA	1201	A
1	CA	1211	U
1	CA	1212	U
1	CA	1256	A
1	CA	1279	A
1	CA	1281	U
1	CA	1442	G
1	CA	1446	U
1	CA	1492	A
1	CA	1493	A
1	CA	1531	A
25	DA	195	A
25	DA	249	C
25	DA	271(K)	U
25	DA	277	C
25	DA	530	G
25	DA	587	C
25	DA	646	A
25	DA	752	A
25	DA	774	A
25	DA	827	U
25	DA	856	C
25	DA	900	A
25	DA	1026	U
25	DA	1210	A
25	DA	1420	U
25	DA	1530	C
25	DA	1558	A
25	DA	1653	G
25	DA	1913	A
25	DA	1992	G
25	DA	2110	G
25	DA	2126	A
25	DA	2134	A
25	DA	2156	G
25	DA	2406	U

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Mol	Chain	Res	Type
25	DA	2689	U
25	DA	2756	U

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

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$
23	PSU	CX	55	23	18,21,22	1.39	2 (11%)	21,30,33	1.94	5 (23%)
23	PSU	AX	55	23	18,21,22	1.36	2 (11%)	21,30,33	2.05	4 (19%)
23	4SU	AX	8	23	18,21,22	2.29	5 (27%)	25,30,33	1.69	4 (16%)
23	5MU	AX	54	23	19,22,23	1.51	4 (21%)	27,32,35	1.63	5 (18%)
23	5MU	CX	54	23	19,22,23	1.42	4 (21%)	27,32,35	2.00	6 (22%)
23	5MC	CX	32	23	19,22,23	1.54	3 (15%)	26,32,35	1.22	4 (15%)
23	5MC	AX	32	23	19,22,23	1.79	3 (15%)	26,32,35	1.38	4 (15%)
23	4SU	CX	8	23	18,21,22	1.99	5 (27%)	25,30,33	1.36	4 (16%)

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
23	PSU	CX	55	23	-	0/7/25/26	0/2/2/2
23	PSU	AX	55	23	-	0/7/25/26	0/2/2/2
23	4SU	AX	8	23	-	0/7/25/26	0/2/2/2
23	5MU	AX	54	23	-	0/7/25/26	0/2/2/2
23	5MU	CX	54	23	-	0/7/25/26	0/2/2/2
23	5MC	CX	32	23	-	0/7/25/26	0/2/2/2
23	5MC	AX	32	23	-	0/7/25/26	0/2/2/2
23	4SU	CX	8	23	-	0/7/25/26	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AX	32	5MC	C5-C4	6.40	1.49	1.44
23	AX	8	4SU	C4-N3	-5.59	1.31	1.37
23	CX	32	5MC	C5-C4	5.41	1.48	1.44
23	AX	8	4SU	C4-S4	-4.96	1.59	1.68
23	CX	8	4SU	C4-N3	-4.63	1.32	1.37
23	CX	8	4SU	C4-S4	-4.15	1.61	1.68
23	CX	55	PSU	C6-C5	4.09	1.39	1.35
23	AX	8	4SU	C2-N3	-3.75	1.31	1.38
23	AX	8	4SU	C5-C4	-3.52	1.38	1.42
23	AX	55	PSU	C6-C5	3.46	1.39	1.35
23	CX	8	4SU	C5-C4	-3.29	1.38	1.42
23	AX	54	5MU	C4-N3	-3.23	1.32	1.38
23	AX	32	5MC	C6-C5	3.18	1.39	1.34
23	AX	54	5MU	C6-C5	3.16	1.39	1.34
23	CX	54	5MU	C6-C5	3.10	1.39	1.34
23	CX	54	5MU	C4-N3	-2.80	1.33	1.38
23	CX	32	5MC	C6-C5	2.62	1.38	1.34
23	CX	8	4SU	C2-N3	-2.55	1.33	1.38
23	CX	54	5MU	C4-C5	2.52	1.48	1.44
23	AX	54	5MU	C2-N3	-2.51	1.33	1.38
23	CX	8	4SU	O2-C2	2.41	1.27	1.23
23	AX	32	5MC	C6-N1	-2.40	1.33	1.38
23	CX	55	PSU	C4-N3	-2.37	1.34	1.38
23	CX	54	5MU	C2-N3	-2.33	1.33	1.38
23	AX	54	5MU	C4-C5	2.32	1.48	1.44
23	AX	55	PSU	C4-N3	-2.29	1.34	1.38
23	CX	32	5MC	C6-N1	-2.23	1.34	1.38
23	AX	8	4SU	O2-C2	2.21	1.27	1.23

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AX	55	PSU	N1-C2-N3	6.18	121.68	115.17
23	CX	55	PSU	N1-C2-N3	6.13	121.63	115.17
23	CX	54	5MU	N3-C2-N1	5.12	121.56	114.89
23	AX	8	4SU	C6-C5-C4	-5.10	115.54	119.95
23	CX	54	5MU	C4-N3-C2	-4.63	121.27	127.34
23	AX	54	5MU	N3-C2-N1	4.26	120.44	114.89
23	AX	32	5MC	C5-C6-N1	-4.22	118.72	123.31
23	AX	55	PSU	C4-N3-C2	-3.98	120.89	126.37
23	CX	55	PSU	C4-N3-C2	-3.95	120.93	126.37
23	CX	54	5MU	C5-C4-N3	3.87	118.69	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AX	55	PSU	O2-C2-N1	-3.79	118.88	122.79
23	AX	8	4SU	C5-C4-N3	3.73	118.22	114.75
23	CX	8	4SU	C1'-N1-C2	3.58	124.02	117.59
23	CX	54	5MU	C5-C6-N1	-3.57	119.43	123.31
23	AX	54	5MU	C4-N3-C2	-3.51	122.74	127.34
23	CX	54	5MU	O2-C2-N1	-3.41	118.36	122.80
23	AX	54	5MU	C5-C4-N3	3.41	118.28	115.32
23	CX	32	5MC	C5-C6-N1	-3.39	119.63	123.31
23	AX	54	5MU	C5-C6-N1	-3.34	119.69	123.31
23	CX	54	5MU	O4-C4-C5	-3.31	121.13	124.92
23	AX	32	5MC	C5-C4-N3	-3.16	118.51	121.75
23	AX	8	4SU	S4-C4-N3	-3.15	116.90	120.20
23	CX	8	4SU	C6-C5-C4	-3.00	117.35	119.95
23	AX	8	4SU	O2-C2-N1	2.75	126.37	122.80
23	AX	32	5MC	O2-C2-N3	-2.62	118.20	122.33
23	CX	8	4SU	C6-N1-C2	-2.49	117.96	121.00
23	CX	55	PSU	O2-C2-N1	-2.48	120.23	122.79
23	CX	32	5MC	C5-C4-N3	-2.44	119.25	121.75
23	AX	54	5MU	O4-C4-C5	-2.44	122.13	124.92
23	CX	8	4SU	C5-C4-N3	2.39	116.97	114.75
23	CX	55	PSU	C5-C6-N1	-2.32	118.92	122.14
23	CX	32	5MC	C1'-N1-C6	-2.23	117.48	121.15
23	AX	55	PSU	C5-C6-N1	-2.16	119.14	122.14
23	CX	32	5MC	O2-C2-N3	-2.12	118.99	122.33
23	CX	55	PSU	O2-C2-N3	-2.10	118.14	121.86
23	AX	32	5MC	N1-C2-N3	2.04	122.35	118.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	CX	55	PSU	1	0
23	AX	8	4SU	1	0
23	CX	8	4SU	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2061 ligands modelled in this entry, 2057 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$
57	PCY	CA	3176	-	34,42,42	1.77	5 (14%)	41,65,65	0.95	3 (7%)
58	SF4	AD	501	4	0,12,12	-	-	-	-	-
57	PCY	AA	3191	-	34,42,42	1.94	5 (14%)	41,65,65	1.51	8 (19%)
58	SF4	CD	501	4	0,12,12	-	-	-	-	-

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
57	PCY	CA	3176	-	-	6/33/67/67	0/3/3/3
58	SF4	AD	501	4	-	-	0/6/5/5
57	PCY	AA	3191	-	-	18/33/67/67	0/3/3/3
58	SF4	CD	501	4	-	-	0/6/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AA	3191	PCY	C34-C30	-6.06	1.39	1.51
57	CA	3176	PCY	C34-C30	-5.75	1.40	1.51
57	AA	3191	PCY	C28-C32	-5.38	1.39	1.49
57	AA	3191	PCY	C17-N20	4.78	1.51	1.45
57	CA	3176	PCY	C28-C32	-4.73	1.40	1.49
57	CA	3176	PCY	C27-C23	-4.63	1.39	1.50
57	AA	3191	PCY	C27-C23	-4.19	1.40	1.50
57	CA	3176	PCY	C17-N20	2.82	1.48	1.45
57	CA	3176	PCY	C22-N20	-2.74	1.34	1.39
57	AA	3191	PCY	C22-N20	-2.69	1.34	1.39

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	AA	3191	PCY	O21-C18-C15	4.06	115.29	107.79
57	AA	3191	PCY	O21-C23-C27	4.04	121.35	112.35
57	AA	3191	PCY	C18-O21-C23	-2.84	110.93	116.55
57	AA	3191	PCY	C30-C27-C23	2.45	127.43	120.47
57	CA	3176	PCY	C18-O21-C23	-2.35	111.90	116.55
57	CA	3176	PCY	C10-N4-C9	2.35	123.39	115.87
57	AA	3191	PCY	C22-N20-C17	2.34	128.18	123.01
57	AA	3191	PCY	C10-N4-C9	2.32	123.27	115.87
57	AA	3191	PCY	O36-C31-C27	-2.30	116.88	121.14
57	CA	3176	PCY	O36-C31-C27	-2.23	117.01	121.14
57	AA	3191	PCY	C34-C30-C35	-2.02	116.38	120.28

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	AA	3191	PCY	N2-C3-C6-C11
57	AA	3191	PCY	N2-C3-C6-O12
57	AA	3191	PCY	C7-C3-C6-C11
57	AA	3191	PCY	C7-C3-C6-O12
57	AA	3191	PCY	C8-C3-C6-C11
57	AA	3191	PCY	C8-C3-C6-O12
57	AA	3191	PCY	C7-C15-C18-O21
57	AA	3191	PCY	C17-C15-C18-O21
57	AA	3191	PCY	O19-C15-C18-O21
57	AA	3191	PCY	C8-C17-N20-C22
57	CA	3176	PCY	C27-C23-O21-C18
57	CA	3176	PCY	O26-C23-O21-C18
57	CA	3176	PCY	C24-C28-C32-C38
57	CA	3176	PCY	C24-C28-C32-O39
57	AA	3191	PCY	C24-C22-N20-C17
57	CA	3176	PCY	C33-C28-C32-C38
57	CA	3176	PCY	C33-C28-C32-O39
57	AA	3191	PCY	C24-C28-C32-O39
57	AA	3191	PCY	C25-C22-N20-C17
57	AA	3191	PCY	C33-C28-C32-O39
57	AA	3191	PCY	C33-C28-C32-C38
57	AA	3191	PCY	C24-C28-C32-C38
57	AA	3191	PCY	O26-C23-C27-C30
57	AA	3191	PCY	O21-C23-C27-C30

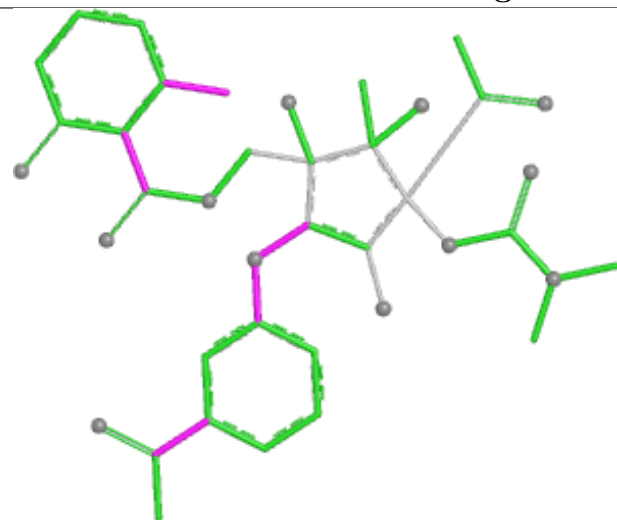
There are no ring outliers.

3 monomers are involved in 11 short contacts:

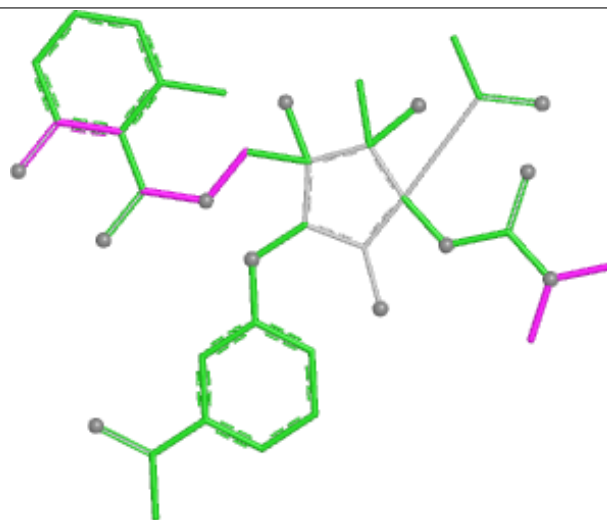
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	CA	3176	PCY	4	0
58	AD	501	SF4	1	0
57	AA	3191	PCY	6	0

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.

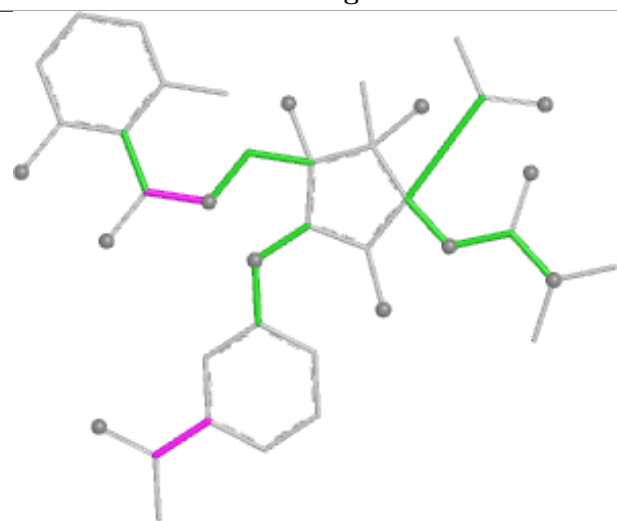
Ligand PCY CA 3176



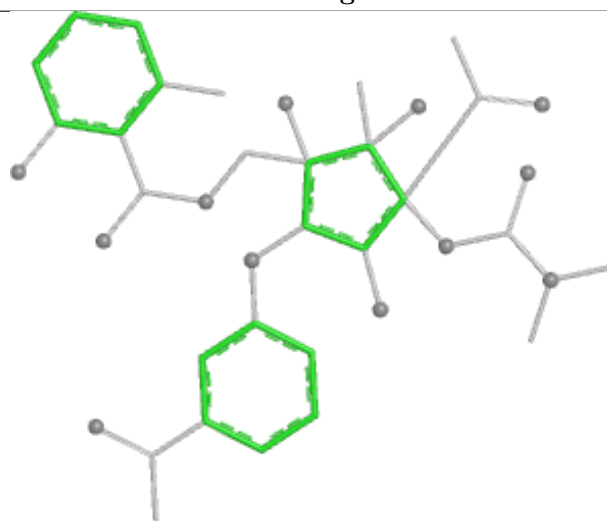
Bond lengths



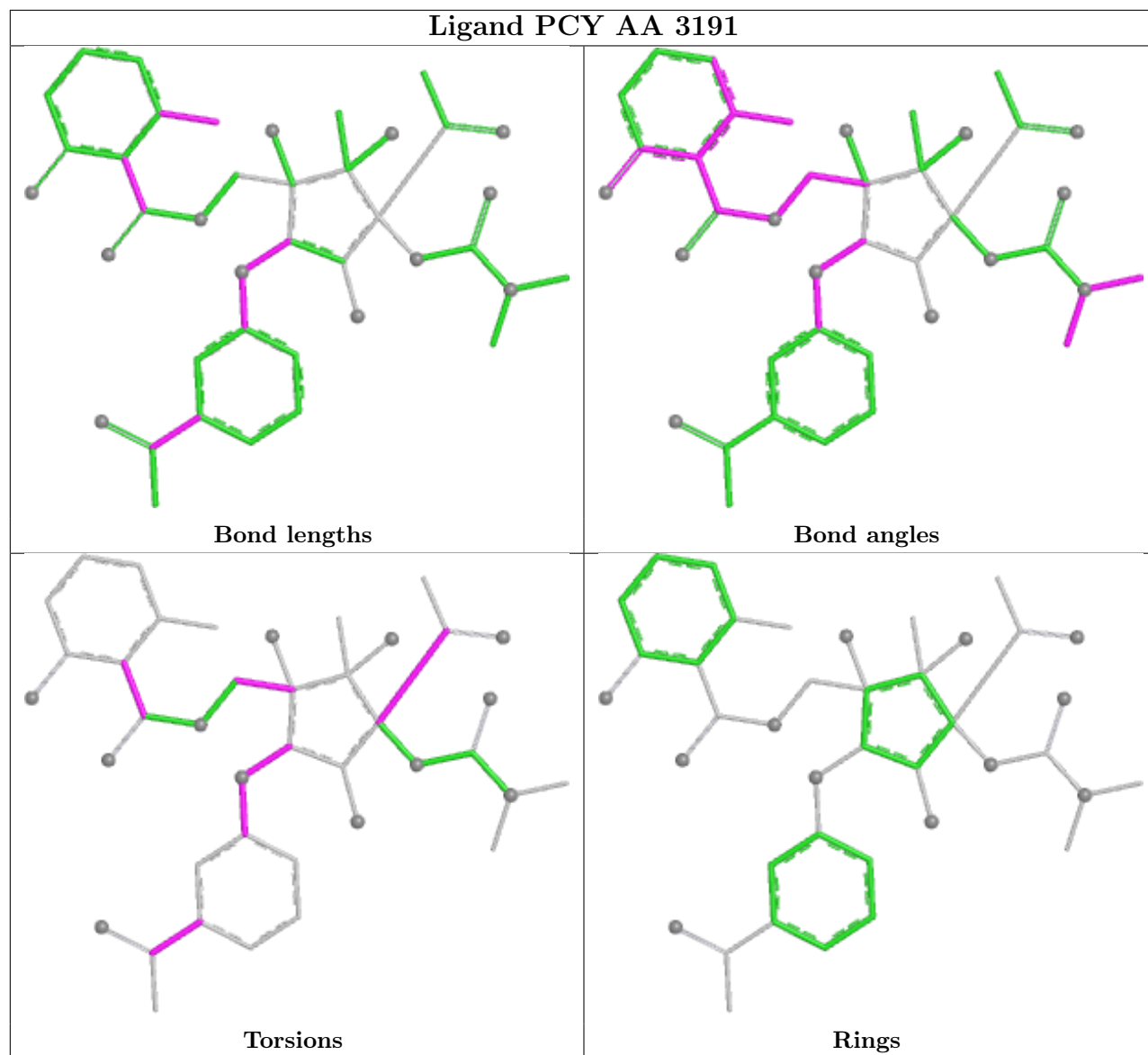
Bond angles



Torsions



Rings



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	AA	1497/1521 (98%)	0.50	52 (3%)	47	43	40, 76, 97, 113	0
1	CA	1503/1521 (98%)	0.57	106 (7%)	22	19	42, 77, 97, 113	0
2	AB	231/256 (90%)	1.24	39 (16%)	4	3	71, 85, 93, 98	0
2	CB	231/256 (90%)	1.71	77 (33%)	1	1	71, 86, 94, 98	0
3	AC	206/239 (86%)	1.06	23 (11%)	10	8	69, 83, 91, 95	0
3	CC	206/239 (86%)	1.55	50 (24%)	2	1	69, 84, 92, 96	0
4	AD	208/209 (99%)	1.30	37 (17%)	4	3	60, 76, 86, 91	0
4	CD	208/209 (99%)	0.77	6 (2%)	53	50	60, 76, 84, 89	0
5	AE	148/162 (91%)	0.86	12 (8%)	18	15	56, 72, 81, 88	0
5	CE	148/162 (91%)	1.04	14 (9%)	14	11	58, 74, 83, 89	0
6	AF	100/101 (99%)	0.71	1 (1%)	79	78	61, 74, 82, 85	0
6	CF	100/101 (99%)	1.05	12 (12%)	9	7	62, 75, 83, 86	0
7	AG	155/156 (99%)	1.00	21 (13%)	7	6	69, 79, 89, 98	0
7	CG	155/156 (99%)	1.42	31 (20%)	3	2	70, 80, 90, 99	0
8	AH	137/138 (99%)	0.81	7 (5%)	33	29	61, 74, 81, 85	0
8	CH	137/138 (99%)	1.19	19 (13%)	6	5	63, 75, 83, 88	0
9	AI	127/128 (99%)	1.21	17 (13%)	7	6	63, 85, 91, 94	0
9	CI	127/128 (99%)	2.05	63 (49%)	0	0	70, 86, 92, 96	0
10	AJ	97/105 (92%)	1.57	28 (28%)	1	1	73, 87, 94, 97	0
10	CJ	96/105 (91%)	2.02	43 (44%)	0	0	76, 89, 95, 96	0
11	AK	114/129 (88%)	0.79	6 (5%)	32	28	52, 72, 84, 87	0
11	CK	114/129 (88%)	0.85	9 (7%)	18	16	54, 74, 84, 87	0
12	AL	122/132 (92%)	0.78	5 (4%)	41	37	52, 67, 77, 81	0
12	CL	122/132 (92%)	0.92	12 (9%)	13	11	53, 67, 76, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	120/126 (95%)	1.03	8 (6%) 24 21	53, 75, 85, 93	0
13	CM	118/126 (93%)	1.74	42 (35%) 1 1	71, 88, 94, 98	0
14	AN	60/61 (98%)	1.26	10 (16%) 4 3	74, 80, 88, 90	0
14	CN	60/61 (98%)	2.63	44 (73%) 0 0	75, 83, 88, 92	0
15	AO	88/89 (98%)	0.99	8 (9%) 15 12	55, 69, 81, 85	0
15	CO	88/89 (98%)	0.82	6 (6%) 23 20	58, 71, 82, 86	0
16	AP	82/88 (93%)	1.54	19 (23%) 2 2	64, 75, 84, 91	0
16	CP	82/88 (93%)	1.39	17 (20%) 2 2	63, 73, 83, 89	0
17	AQ	99/105 (94%)	0.86	7 (7%) 22 19	55, 70, 79, 81	0
17	CQ	99/105 (94%)	1.07	6 (6%) 27 24	58, 71, 80, 84	0
18	AR	68/88 (77%)	0.74	2 (2%) 53 50	62, 74, 84, 89	0
18	CR	68/88 (77%)	0.83	3 (4%) 39 35	64, 74, 84, 91	0
19	AS	83/93 (89%)	1.65	22 (26%) 1 1	75, 85, 93, 94	0
19	CS	83/93 (89%)	1.95	33 (39%) 1 0	78, 87, 93, 96	0
20	AT	96/106 (90%)	1.01	12 (12%) 8 7	63, 72, 82, 87	0
20	CT	96/106 (90%)	1.06	7 (7%) 21 18	61, 73, 82, 87	0
21	AU	23/27 (85%)	1.79	10 (43%) 0 0	71, 77, 79, 81	0
21	CU	23/27 (85%)	1.88	8 (34%) 1 1	72, 79, 81, 83	0
22	AV	8/24 (33%)	1.70	4 (50%) 0 0	62, 89, 94, 97	0
22	CV	5/24 (20%)	1.40	1 (20%) 3 2	65, 73, 91, 96	0
23	AX	72/77 (93%)	0.54	3 (4%) 40 37	40, 71, 88, 98	0
23	CX	72/77 (93%)	0.39	1 (1%) 73 72	43, 74, 90, 97	0
24	AY	18/76 (23%)	1.35	3 (16%) 4 3	62, 104, 109, 109	0
24	CY	5/76 (6%)	2.61	4 (80%) 0 0	74, 101, 102, 106	0
25	BA	2822/2915 (96%)	-0.29	97 (3%) 48 44	18, 41, 91, 109	0
25	DA	2800/2915 (96%)	-0.29	79 (2%) 55 51	22, 45, 91, 112	0
26	BB	120/121 (99%)	0.17	0 100 100	31, 63, 75, 88	0
26	DB	120/121 (99%)	1.07	19 (15%) 5 4	38, 69, 81, 91	0
27	BD	275/276 (99%)	0.02	2 (0%) 84 83	20, 39, 58, 77	0
27	DD	275/276 (99%)	-0.07	2 (0%) 84 83	22, 42, 60, 78	0
28	BE	204/206 (99%)	0.11	1 (0%) 87 86	19, 44, 64, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DE	204/206 (99%)	0.13	1 (0%) 87 86	22, 48, 66, 86	0
29	BF	203/210 (96%)	0.19	1 (0%) 87 86	21, 50, 74, 91	0
29	DF	203/210 (96%)	0.16	3 (1%) 72 70	24, 55, 77, 90	0
30	BG	181/182 (99%)	0.94	17 (9%) 14 12	55, 71, 83, 96	0
30	DG	181/182 (99%)	1.32	37 (20%) 3 2	60, 75, 84, 95	0
31	BH	174/180 (96%)	0.82	10 (5%) 29 26	45, 64, 75, 84	0
31	DH	174/180 (96%)	1.14	20 (11%) 9 8	53, 68, 79, 86	0
32	BI	146/148 (98%)	0.65	6 (4%) 41 37	48, 75, 84, 88	0
32	DI	146/148 (98%)	0.87	8 (5%) 30 27	51, 75, 84, 88	0
33	BN	140/140 (100%)	0.44	4 (2%) 53 50	28, 45, 69, 79	0
33	DN	140/140 (100%)	0.37	0 100 100	33, 49, 71, 81	0
34	BO	122/122 (100%)	0.06	3 (2%) 58 55	31, 45, 63, 70	0
34	DO	122/122 (100%)	0.00	0 100 100	34, 48, 64, 70	0
35	BP	149/150 (99%)	0.36	3 (2%) 65 62	18, 53, 74, 82	0
35	DP	149/150 (99%)	0.32	2 (1%) 75 73	20, 56, 76, 84	0
36	BQ	141/141 (100%)	0.26	3 (2%) 63 61	29, 48, 65, 77	0
36	DQ	141/141 (100%)	0.41	5 (3%) 47 43	32, 52, 69, 78	0
37	BR	118/118 (100%)	-0.34	0 100 100	19, 32, 49, 62	0
37	DR	118/118 (100%)	0.20	1 (0%) 82 81	35, 53, 66, 78	0
38	BS	110/112 (98%)	0.01	0 100 100	30, 47, 65, 70	0
38	DS	110/112 (98%)	1.50	31 (28%) 1 1	63, 77, 88, 93	0
39	BT	131/146 (89%)	0.03	6 (4%) 37 34	30, 43, 71, 85	0
39	DT	131/146 (89%)	0.44	2 (1%) 72 70	43, 59, 78, 88	0
40	BU	116/118 (98%)	-0.45	1 (0%) 81 80	15, 27, 48, 62	0
40	DU	116/118 (98%)	0.38	1 (0%) 81 80	38, 59, 76, 87	0
41	BV	101/101 (100%)	-0.46	1 (0%) 79 78	14, 35, 57, 76	0
41	DV	101/101 (100%)	0.48	1 (0%) 79 78	43, 71, 84, 90	0
42	BW	112/113 (99%)	-0.49	1 (0%) 81 80	17, 28, 50, 75	0
42	DW	112/113 (99%)	0.04	0 100 100	34, 50, 68, 92	0
43	BX	95/96 (98%)	-0.20	1 (1%) 78 76	17, 35, 65, 78	0
43	DX	95/96 (98%)	0.88	9 (9%) 14 11	44, 62, 77, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BY	107/110 (97%)	0.18	1 (0%) 81 80	28, 47, 67, 85	0
44	DY	107/110 (97%)	1.16	18 (16%) 4 3	51, 72, 83, 88	0
45	BZ	171/206 (83%)	0.50	6 (3%) 47 43	36, 62, 81, 90	0
45	DZ	174/206 (84%)	1.28	23 (13%) 7 6	66, 83, 93, 96	0
46	B0	83/85 (97%)	0.02	8 (9%) 13 11	12, 33, 66, 84	0
46	D0	83/85 (97%)	0.87	9 (10%) 11 9	34, 64, 78, 91	0
47	B1	97/98 (98%)	0.01	1 (1%) 79 78	19, 43, 69, 72	0
47	D1	97/98 (98%)	0.45	2 (2%) 63 61	37, 57, 78, 82	0
48	B2	70/72 (97%)	0.08	3 (4%) 40 36	30, 46, 63, 77	0
48	D2	70/72 (97%)	0.83	3 (4%) 40 36	56, 71, 80, 85	0
49	B3	59/60 (98%)	-0.31	1 (1%) 69 67	20, 31, 56, 83	0
49	D3	59/60 (98%)	0.58	5 (8%) 16 14	47, 62, 77, 91	0
50	B4	69/71 (97%)	1.02	13 (18%) 3 3	55, 77, 92, 99	0
50	D4	69/71 (97%)	1.41	16 (23%) 2 2	77, 91, 99, 105	0
51	B5	59/60 (98%)	-0.47	0 100 100	11, 28, 53, 67	0
51	D5	59/60 (98%)	-0.02	1 (1%) 69 67	27, 52, 68, 81	0
52	B6	53/54 (98%)	-0.17	0 100 100	27, 39, 56, 66	0
52	D6	53/54 (98%)	0.66	4 (7%) 20 17	45, 62, 73, 79	0
53	B7	48/49 (97%)	-0.09	3 (6%) 26 23	16, 23, 52, 68	0
53	D7	48/49 (97%)	-0.13	0 100 100	29, 40, 64, 77	0
54	B8	64/65 (98%)	-0.27	0 100 100	24, 31, 43, 61	0
54	D8	64/65 (98%)	0.41	0 100 100	44, 53, 63, 72	0
55	B9	37/37 (100%)	0.27	1 (2%) 56 53	28, 45, 67, 72	0
55	D9	37/37 (100%)	0.72	2 (5%) 31 27	44, 55, 68, 75	0
All	All	20640/21596 (95%)	0.41	1468 (7%) 22 19	11, 64, 91, 113	0

All (1468) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
20	CT	9	ASN	7.6
25	BA	2143	G	7.5
14	CN	2	ALA	6.6
2	CB	165	VAL	6.3
25	BA	2135	U	6.1

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Mol	Chain	Res	Type	RSRZ
25	BA	2200	C	6.1
31	BH	2	SER	6.0
7	CG	82	GLY	6.0
13	AM	2	ALA	6.0
9	AI	126	SER	5.9
14	CN	5	ALA	5.6
25	BA	2192	A	5.6
25	BA	2142	G	5.6
10	CJ	47	PHE	5.5
13	CM	102	ARG	5.5
25	BA	2133	C	5.5
25	BA	2201	C	5.4
9	CI	9	ARG	5.4
25	BA	2137	G	5.3
13	AM	121	LYS	5.3
25	BA	1221	G	5.3
7	AG	79	ARG	5.3
9	CI	2	GLU	5.2
46	B0	5	LYS	5.2
19	CS	84	GLY	5.2
25	BA	2191	A	5.2
25	DA	2111	C	5.2
9	CI	15	ALA	5.1
25	BA	2144	U	5.1
14	CN	7	ILE	5.1
1	CA	1202	G	5.1
2	AB	7	VAL	5.1
25	BA	2134	G	5.0
1	CA	1030(B)	C	5.0
25	BA	2190	G	5.0
25	BA	2131	U	5.0
25	BA	2141	A	4.9
25	BA	2145	G	4.9
25	DA	2160	G	4.9
25	BA	2132	G	4.9
1	CA	1149	C	4.8
16	AP	68	ASP	4.8
9	CI	126	SER	4.7
2	CB	10	LEU	4.7
1	CA	1036	G	4.7
14	CN	25	VAL	4.7
25	BA	2151	C	4.7

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Mol	Chain	Res	Type	RSRZ
1	CA	1492	A	4.6
13	CM	7	VAL	4.6
16	AP	82	GLN	4.6
25	BA	2152	U	4.6
25	DA	2147	G	4.6
39	BT	131	ALA	4.6
10	CJ	65	LEU	4.6
2	CB	83	MET	4.6
46	B0	3	HIS	4.6
50	D4	56	VAL	4.5
14	CN	4	LYS	4.5
14	CN	33	VAL	4.5
1	CA	1033	G	4.5
25	BA	2182	G	4.5
20	AT	74	LYS	4.4
25	BA	2165	C	4.4
46	B0	7	LEU	4.4
7	CG	16	LEU	4.4
39	DT	131	ALA	4.4
36	BQ	61	GLY	4.4
21	CU	6	ARG	4.3
2	CB	232	PRO	4.3
1	CA	1286	A	4.3
31	DH	2	SER	4.3
25	BA	2150	C	4.3
25	BA	2167	C	4.3
48	B2	70	GLN	4.3
25	DA	2135	A	4.3
1	AA	1257	U	4.3
7	CG	80	VAL	4.3
25	BA	2147	G	4.3
25	BA	2155	G	4.3
19	CS	71	LEU	4.2
9	CI	10	ARG	4.2
9	AI	19	LEU	4.2
25	BA	2196	C	4.2
19	AS	4	SER	4.2
25	DA	2144	U	4.2
39	BT	130	ALA	4.2
25	BA	2139	A	4.2
25	DA	2159	G	4.2
26	DB	23	G	4.2

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Mol	Chain	Res	Type	RSRZ
30	DG	28	VAL	4.2
10	CJ	59	SER	4.2
1	CA	1116	C	4.2
25	DA	2145	C	4.2
25	DA	2146	C	4.2
4	AD	195	ALA	4.1
46	D0	5	LYS	4.1
2	CB	7	VAL	4.1
25	BA	935	C	4.1
26	DB	118	G	4.1
2	CB	22	LYS	4.1
2	CB	21	ARG	4.1
25	BA	2187	G	4.1
3	AC	207	VAL	4.1
9	CI	64	THR	4.1
25	BA	2154	U	4.1
44	DY	1	MET	4.1
2	AB	200	ILE	4.1
2	CB	237	ALA	4.0
25	DA	2116	G	4.0
1	CA	1150	U	4.0
7	CG	83	ALA	4.0
25	BA	2166	U	4.0
46	D0	7	LEU	4.0
7	AG	78	ARG	4.0
50	B4	64	GLY	4.0
4	AD	157	LEU	4.0
25	BA	2153	G	4.0
1	CA	1035	A	4.0
1	CA	1251	A	4.0
38	DS	3	ARG	4.0
14	AN	2	ALA	4.0
20	CT	69	GLY	4.0
2	AB	237	ALA	3.9
43	DX	92	LEU	3.9
25	BA	2130	C	3.9
14	CN	50	LYS	3.9
45	DZ	150	LEU	3.9
50	D4	49	PHE	3.9
3	CC	207	VAL	3.9
50	B4	52	THR	3.9
10	CJ	40	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
36	DQ	61	GLY	3.9
25	BA	2168	C	3.9
10	CJ	32	ALA	3.9
46	D0	2	ALA	3.9
50	B4	59	PHE	3.9
25	DA	2112	G	3.8
19	AS	71	LEU	3.8
43	DX	91	ALA	3.8
10	AJ	31	GLY	3.8
10	CJ	64	GLU	3.8
14	CN	3	ARG	3.8
25	BA	2199	C	3.8
10	AJ	8	LEU	3.8
30	DG	53	LEU	3.8
14	CN	30	ALA	3.8
16	AP	42	ARG	3.8
4	AD	169	LYS	3.8
27	BD	276	LYS	3.8
38	DS	57	LYS	3.8
8	CH	4	ASP	3.8
25	DA	2174	C	3.8
43	DX	86	GLY	3.8
19	CS	49	ILE	3.7
32	DI	146	ALA	3.7
25	DA	2128	C	3.7
25	DA	2136	C	3.7
9	CI	14	VAL	3.7
19	CS	13	ASP	3.7
13	CM	78	ILE	3.7
1	AA	1036	G	3.7
1	CA	973	G	3.7
1	CA	1003	G	3.7
10	CJ	49	VAL	3.7
2	CB	200	ILE	3.7
12	AL	91	LYS	3.7
20	CT	74	LYS	3.7
50	B4	50	VAL	3.7
1	CA	1034	G	3.7
25	BA	2188	G	3.7
38	DS	32	LEU	3.7
1	CA	1354	C	3.7
24	CY	72	C	3.7

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Mol	Chain	Res	Type	RSRZ
25	BA	2164	C	3.7
25	BA	2210	C	3.7
21	CU	14	TRP	3.7
16	CP	12	LYS	3.7
2	CB	234	PRO	3.7
25	BA	2136	A	3.6
13	AM	120	LYS	3.6
1	AA	1026	G	3.6
7	CG	156	TRP	3.6
25	DA	2133	G	3.6
9	CI	5	TYR	3.6
9	CI	6	GLY	3.6
19	CS	9	VAL	3.6
19	CS	33	THR	3.6
1	AA	1532	U	3.6
9	CI	36	TYR	3.6
10	AJ	32	ALA	3.6
14	CN	21	TYR	3.6
39	DT	130	ALA	3.6
1	CA	1224	G	3.6
13	CM	73	GLU	3.6
19	CS	16	LEU	3.6
14	CN	29	ARG	3.6
13	CM	6	GLY	3.6
7	AG	85	TYR	3.6
2	AB	165	VAL	3.6
7	AG	80	VAL	3.6
9	CI	102	LEU	3.6
3	CC	57	ILE	3.6
25	BA	2169	G	3.6
3	CC	48	TYR	3.6
10	CJ	54	PHE	3.6
2	CB	11	LEU	3.6
20	AT	55	ILE	3.5
25	DA	1536	C	3.5
1	CA	1002	G	3.5
10	CJ	63	PHE	3.5
38	DS	58	LEU	3.5
24	CY	73	A	3.5
9	CI	106	ALA	3.5
25	DA	2161	C	3.5
2	CB	236	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
16	AP	17	TYR	3.5
25	DA	2134	A	3.5
4	AD	102	ASP	3.5
7	AG	156	TRP	3.5
14	CN	34	TYR	3.5
26	DB	88	C	3.5
25	BA	2163	G	3.5
14	CN	13	THR	3.5
7	CG	33	ASP	3.5
21	AU	2	GLY	3.5
50	D4	65	ASP	3.5
2	AB	12	GLU	3.5
4	AD	80	GLU	3.5
30	BG	2	PRO	3.5
7	CG	154	TYR	3.4
14	CN	42	ILE	3.4
44	DY	35	TYR	3.4
25	BA	2197	C	3.4
9	CI	7	THR	3.4
14	CN	11	LYS	3.4
1	CA	1356	G	3.4
13	CM	5	ALA	3.4
19	CS	2	PRO	3.4
45	DZ	114	GLY	3.4
38	DS	54	LEU	3.4
10	CJ	46	ARG	3.4
25	BA	2148	A	3.4
13	CM	67	GLU	3.4
2	CB	70	PHE	3.4
9	CI	65	VAL	3.4
25	BA	2181	G	3.4
2	CB	92	TYR	3.4
30	DG	146	TYR	3.4
38	DS	33	LYS	3.4
43	BX	95	LEU	3.4
19	AS	13	ASP	3.4
25	BA	2189	U	3.4
15	AO	69	TYR	3.4
38	DS	7	TYR	3.4
25	BA	2184	G	3.4
25	DA	1171	G	3.4
5	CE	85	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
9	CI	99	LEU	3.4
19	AS	84	GLY	3.4
10	AJ	78	ASN	3.4
2	AB	229	VAL	3.4
10	CJ	72	VAL	3.4
16	AP	80	PHE	3.4
1	CA	1027	C	3.3
7	CG	85	TYR	3.3
19	CS	79	THR	3.3
4	AD	153	ARG	3.3
14	CN	38	GLY	3.3
31	BH	59	ARG	3.3
46	B0	8	GLY	3.3
1	CA	1253	G	3.3
25	DA	171	G	3.3
14	CN	36	PHE	3.3
19	CS	31	ILE	3.3
11	CK	50	TYR	3.3
19	AS	39	THR	3.3
2	CB	44	LEU	3.3
4	AD	155	LEU	3.3
7	AG	83	ALA	3.3
50	D4	50	VAL	3.3
1	AA	1492	A	3.3
1	CA	1289	A	3.3
9	CI	21	PRO	3.3
50	B4	63	TYR	3.3
25	BA	34	C	3.3
25	DA	2140	C	3.3
1	CA	1001(A)	G	3.3
1	CA	1032	G	3.3
4	AD	179	GLU	3.3
23	CX	70	G	3.3
30	BG	53	LEU	3.3
9	CI	125	TYR	3.3
16	CP	82	GLN	3.3
9	AI	59	PHE	3.3
10	CJ	76	ASN	3.3
25	DA	2189	U	3.3
32	DI	14	ASP	3.3
25	BA	2183	C	3.2
48	D2	51	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
10	AJ	65	LEU	3.2
25	BA	1935	A	3.2
5	AE	85	GLY	3.2
27	BD	2	ALA	3.2
3	CC	77	ILE	3.2
25	BA	1072	U	3.2
1	CA	1037	C	3.2
2	CB	221	LEU	3.2
3	CC	47	LEU	3.2
25	DA	2138	C	3.2
38	DS	31	SER	3.2
46	B0	6	GLY	3.2
25	BA	572	A	3.2
2	CB	152	PHE	3.2
2	CB	163	PHE	3.2
1	CA	1030(A)	G	3.2
16	CP	8	ARG	3.2
25	BA	2203	G	3.2
2	CB	187	LEU	3.2
10	AJ	77	PRO	3.2
10	AJ	33	GLN	3.2
1	CA	1038	C	3.2
9	CI	76	ALA	3.2
26	DB	27	C	3.2
28	DE	204	ALA	3.2
38	DS	29	PHE	3.2
10	CJ	77	PRO	3.2
1	CA	1283	G	3.2
1	CA	1532	U	3.2
2	CB	190	THR	3.2
10	AJ	42	THR	3.2
25	DA	2120	G	3.2
12	CL	88	GLY	3.2
2	AB	29	ALA	3.2
2	CB	122	PHE	3.2
19	CS	52	TYR	3.2
19	CS	80	TYR	3.2
50	D4	67	TYR	3.2
25	DA	2129	C	3.1
8	AH	4	ASP	3.1
49	D3	29	ARG	3.1
1	AA	1531	A	3.1

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Mol	Chain	Res	Type	RSRZ
10	CJ	37	PRO	3.1
2	CB	123	ALA	3.1
3	CC	129	ALA	3.1
25	BA	2172	U	3.1
2	CB	201	ILE	3.1
10	CJ	38	ILE	3.1
19	AS	40	ILE	3.1
19	CS	35	SER	3.1
45	DZ	166	SER	3.1
45	DZ	171	ILE	3.1
38	DS	36	TYR	3.1
6	CF	46	ARG	3.1
30	DG	74	LYS	3.1
9	CI	105	ASP	3.1
1	AA	369	C	3.1
1	CA	1254	C	3.1
2	AB	10	LEU	3.1
18	AR	79	LEU	3.1
25	BA	2186	C	3.1
2	CB	97	TRP	3.1
7	AG	91	VAL	3.1
7	CG	79	ARG	3.1
25	BA	2518	U	3.1
25	DA	1533	G	3.1
1	CA	1030	C	3.1
1	CA	1249	C	3.1
7	AG	82	GLY	3.1
9	CI	67	GLY	3.1
30	DG	129	GLY	3.1
1	CA	1363(A)	A	3.1
13	CM	64	TRP	3.1
31	DH	102	ALA	3.1
12	CL	73	GLU	3.1
1	AA	1001(A)	G	3.1
1	AA	1002	G	3.1
1	CA	1190	G	3.1
3	CC	2	GLY	3.1
9	CI	39	GLY	3.1
20	AT	103	GLY	3.1
21	CU	11	GLY	3.1
25	BA	2138	G	3.1
25	DA	2110	G	3.1

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Mol	Chain	Res	Type	RSRZ
25	DA	2115	G	3.1
4	AD	118	ARG	3.1
47	B1	2	SER	3.1
1	CA	1357	A	3.0
30	DG	139	LEU	3.0
10	AJ	76	ASN	3.0
14	CN	8	GLU	3.0
13	CM	97	PRO	3.0
10	CJ	55	LYS	3.0
2	CB	99	GLY	3.0
7	CG	2	ALA	3.0
12	CL	56	ALA	3.0
48	D2	1	MET	3.0
1	AA	1224	G	3.0
1	CA	1030(C)	G	3.0
7	CG	12	LEU	3.0
9	AI	2	GLU	3.0
19	CS	14	HIS	3.0
10	CJ	41	PRO	3.0
1	CA	1250	A	3.0
1	AA	1000	U	3.0
25	DA	2109	U	3.0
45	DZ	146	ILE	3.0
48	B2	69	ARG	3.0
9	CI	17	VAL	3.0
10	CJ	34	VAL	3.0
11	AK	14	VAL	3.0
31	DH	52	VAL	3.0
3	AC	52	LEU	3.0
18	AR	78	LEU	3.0
7	AG	153	HIS	3.0
38	DS	34	HIS	3.0
25	DA	2148	G	3.0
1	AA	163	C	3.0
1	CA	1493	A	3.0
9	AI	64	THR	3.0
16	CP	69	THR	3.0
50	B4	54	GLY	3.0
25	BA	1581	U	3.0
2	AB	196	LEU	3.0
4	AD	162	LEU	3.0
19	CS	30	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
7	CG	84	ASN	3.0
19	CS	12	ASP	3.0
13	CM	9	ILE	3.0
25	DA	2156	G	3.0
1	AA	1027	C	3.0
1	CA	1285	A	3.0
2	CB	136	VAL	3.0
14	CN	39	LEU	2.9
26	DB	1	U	2.9
13	CM	120	LYS	2.9
20	AT	9	ASN	2.9
7	AG	76	ARG	2.9
7	CG	78	ARG	2.9
19	AS	29	ARG	2.9
17	CQ	54	GLY	2.9
32	BI	90	GLY	2.9
8	CH	2	LEU	2.9
17	AQ	100	LYS	2.9
22	AV	21	C	2.9
25	BA	639	G	2.9
25	BA	2195	A	2.9
45	DZ	167	PRO	2.9
25	DA	2118	U	2.9
9	CI	66	ARG	2.9
10	CJ	69	ASN	2.9
14	CN	35	ARG	2.9
9	CI	63	ILE	2.9
3	CC	159	GLY	2.9
4	CD	87	GLY	2.9
38	DS	45	GLY	2.9
50	D4	45	GLY	2.9
16	AP	22	THR	2.9
4	AD	164	ALA	2.9
2	CB	71	VAL	2.9
5	AE	45	PHE	2.9
33	BN	9	VAL	2.9
14	CN	49	HIS	2.9
14	CN	23	ARG	2.9
20	AT	80	ARG	2.9
1	AA	159	G	2.9
25	DA	2155	G	2.9
7	AG	154	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
16	AP	19	ILE	2.9
16	CP	19	ILE	2.9
20	CT	103	GLY	2.9
46	D0	6	GLY	2.9
8	CH	3	THR	2.9
3	AC	33	LEU	2.9
3	CC	204	LEU	2.9
4	AD	194	LEU	2.9
10	CJ	71	LEU	2.9
13	CM	34	LEU	2.9
14	CN	6	LEU	2.9
19	CS	41	VAL	2.9
2	AB	9	GLU	2.9
2	CB	19	HIS	2.9
2	CB	134	GLU	2.9
19	CS	38	SER	2.9
8	CH	109	ILE	2.9
10	CJ	75	ILE	2.9
19	CS	40	ILE	2.9
1	AA	1447	A	2.9
1	CA	950	U	2.9
1	CA	1119	C	2.9
2	CB	18	GLY	2.9
25	DA	2137	C	2.9
30	BG	146	TYR	2.9
50	D4	52	THR	2.9
3	CC	52	LEU	2.9
3	CC	187	ALA	2.9
9	CI	56	LEU	2.9
10	AJ	34	VAL	2.9
25	BA	2173	G	2.9
25	DA	2104	G	2.9
25	DA	2751	G	2.9
2	CB	48	MET	2.8
9	CI	123	PRO	2.8
8	CH	30	ARG	2.8
14	CN	41	ARG	2.8
3	CC	167	TRP	2.8
4	AD	5	ILE	2.8
4	AD	154	ASN	2.8
9	CI	62	TYR	2.8
10	CJ	93	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
4	AD	174	LEU	2.8
4	AD	188	LEU	2.8
20	AT	10	LEU	2.8
50	D4	44	THR	2.8
2	CB	15	VAL	2.8
45	DZ	165	VAL	2.8
1	CA	968	A	2.8
13	CM	88	ARG	2.8
13	CM	91	ARG	2.8
15	CO	68	ARG	2.8
25	BA	2149	G	2.8
25	DA	2154	G	2.8
26	DB	119	G	2.8
3	CC	5	ILE	2.8
20	CT	30	LYS	2.8
6	CF	45	LEU	2.8
14	AN	5	ALA	2.8
16	CP	7	ALA	2.8
31	BH	58	GLU	2.8
1	CA	1257	U	2.8
31	DH	36	PRO	2.8
1	CA	974	A	2.8
33	BN	8	GLN	2.8
1	AA	1030(B)	C	2.8
25	BA	2160	C	2.8
25	DA	34	C	2.8
27	DD	38	LYS	2.8
30	DG	20	ILE	2.8
1	AA	630	G	2.8
1	AA	1024	G	2.8
25	DA	2121	G	2.8
2	AB	221	LEU	2.8
2	CB	215	LEU	2.8
9	AI	47	LEU	2.8
30	BG	25	TYR	2.8
30	DG	160	VAL	2.8
3	CC	73	PRO	2.8
10	AJ	66	ARG	2.8
1	CA	1364	U	2.8
1	AA	1029	C	2.8
8	AH	15	ASN	2.8
39	BT	38	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
4	AD	180	GLY	2.8
11	CK	49	GLY	2.8
44	DY	90	LEU	2.8
45	BZ	150	LEU	2.8
30	BG	49	ASP	2.8
3	AC	86	VAL	2.8
3	CC	19	GLU	2.8
3	CC	195	VAL	2.8
9	CI	37	PHE	2.8
10	CJ	44	VAL	2.8
45	DZ	172	ALA	2.8
50	B4	49	PHE	2.8
1	CA	1031	G	2.8
7	CG	4	ARG	2.8
9	CI	4	TYR	2.8
25	BA	2146	G	2.8
25	DA	2149	G	2.8
50	B4	62	ARG	2.8
2	CB	39	ILE	2.7
25	BA	12	U	2.7
2	CB	118	LEU	2.7
32	DI	35	LEU	2.7
1	AA	1035	A	2.7
1	CA	1252	A	2.7
22	AV	15	A	2.7
26	DB	26	A	2.7
1	AA	932	C	2.7
1	CA	1223	C	2.7
4	AD	170	VAL	2.7
9	CI	59	PHE	2.7
10	AJ	87	THR	2.7
34	BO	108	GLU	2.7
21	AU	24	ARG	2.7
1	AA	1003	G	2.7
26	DB	24	G	2.7
18	CR	65	ILE	2.7
13	CM	19	LEU	2.7
43	DX	95	LEU	2.7
2	AB	18	GLY	2.7
3	CC	155	GLY	2.7
38	DS	60	GLY	2.7
43	DX	1	MET	2.7

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Mol	Chain	Res	Type	RSRZ
3	CC	75	VAL	2.7
7	AG	7	ALA	2.7
16	AP	75	ARG	2.7
30	BG	93	THR	2.7
45	DZ	113	ALA	2.7
10	AJ	47	PHE	2.7
25	BA	2157	A	2.7
25	DA	2169	A	2.7
25	DA	2173	A	2.7
13	CM	87	TYR	2.7
14	CN	9	LYS	2.7
30	BG	26	GLN	2.7
46	B0	4	LYS	2.7
50	B4	60	GLN	2.7
50	B4	67	TYR	2.7
10	AJ	98	ILE	2.7
2	CB	196	LEU	2.7
38	DS	56	LEU	2.7
1	CA	1117	G	2.7
38	DS	64	GLU	2.7
2	AB	193	ASP	2.7
9	CI	103	THR	2.7
14	CN	10	ALA	2.7
32	DI	92	VAL	2.7
50	D4	51	ASP	2.7
1	AA	204	U	2.7
25	BA	288	U	2.7
26	DB	22	U	2.7
26	DB	55	U	2.7
49	D3	2	PRO	2.7
9	CI	114	TYR	2.7
13	CM	23	TYR	2.7
16	AP	39	TYR	2.7
43	DX	69	TYR	2.7
1	AA	439	A	2.7
22	CV	15	A	2.7
26	DB	25	A	2.7
2	CB	214	ILE	2.7
7	CG	42	ILE	2.7
1	AA	1028	C	2.7
1	CA	995	C	2.7
1	CA	1019	C	2.7

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Mol	Chain	Res	Type	RSRZ
25	BA	1555	C	2.7
2	CB	138	LEU	2.7
3	CC	142	MET	2.7
9	CI	19	LEU	2.7
30	DG	19	LEU	2.7
32	BI	35	LEU	2.7
46	D0	3	HIS	2.7
3	AC	79	ARG	2.7
4	AD	23	GLY	2.7
5	CE	22	GLY	2.7
34	BO	49	ARG	2.7
43	DX	68	ARG	2.7
19	CS	4	SER	2.7
2	AB	133	LYS	2.7
3	CC	189	ALA	2.7
12	AL	18	VAL	2.7
9	CI	27	THR	2.7
9	CI	46	ALA	2.7
11	CK	31	THR	2.7
45	BZ	136	PHE	2.7
45	DZ	164	ALA	2.7
46	D0	4	LYS	2.7
31	DH	21	PRO	2.7
1	CA	1017	G	2.6
8	CH	94	TYR	2.6
12	CL	120	TYR	2.6
25	DA	1026	U	2.6
1	AA	1001	A	2.6
1	CA	1261	A	2.6
6	CF	61	LEU	2.6
25	BA	218	A	2.6
45	DZ	5	LEU	2.6
3	CC	21	ARG	2.6
9	CI	57	GLY	2.6
1	AA	1030	C	2.6
1	CA	1054	C	2.6
9	CI	11	LYS	2.6
18	CR	23	LYS	2.6
3	CC	168	ALA	2.6
17	CQ	97	SER	2.6
12	CL	32	PHE	2.6
38	DS	98	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
31	DH	112	PRO	2.6
45	DZ	170	THR	2.6
11	AK	81	ASP	2.6
2	AB	31	TYR	2.6
38	DS	35	ILE	2.6
1	CA	951	G	2.6
1	CA	963	G	2.6
1	CA	1232	U	2.6
25	DA	2123	G	2.6
3	CC	87	LEU	2.6
2	CB	14	GLY	2.6
44	BY	91	GLU	2.6
1	AA	1286	A	2.6
25	DA	2117	A	2.6
2	CB	188	ALA	2.6
3	AC	68	VAL	2.6
3	CC	55	VAL	2.6
10	AJ	44	VAL	2.6
2	AB	97	TRP	2.6
14	CN	32	SER	2.6
30	DG	50	ALA	2.6
45	DZ	88	PHE	2.6
1	CA	1029	C	2.6
19	AS	12	ASP	2.6
30	DG	147	ASP	2.6
10	CJ	50	ILE	2.6
2	AB	33	TYR	2.6
13	CM	66	LEU	2.6
1	CA	992	U	2.6
1	CA	1148	U	2.6
2	CB	133	LYS	2.6
14	AN	4	LYS	2.6
44	DY	34	LYS	2.6
2	CB	12	GLU	2.6
13	CM	112	GLY	2.6
15	AO	89	GLY	2.6
1	AA	1030(A)	G	2.6
2	AB	136	VAL	2.6
3	AC	70	VAL	2.6
2	CB	55	PHE	2.6
14	CN	59	ALA	2.6
11	AK	42	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	CA	970	C	2.6
3	CC	188	LEU	2.6
19	CS	15	LEU	2.6
29	DF	12	LEU	2.6
10	AJ	46	ARG	2.6
31	DH	6	ARG	2.6
13	CM	92	HIS	2.6
15	AO	47	LYS	2.6
8	CH	99	GLU	2.6
3	AC	81	GLY	2.6
5	AE	22	GLY	2.6
55	D9	37	GLY	2.6
14	CN	14	PRO	2.6
17	CQ	9	VAL	2.6
22	AV	20	U	2.6
30	DG	31	VAL	2.6
51	D5	60	VAL	2.6
9	CI	18	PHE	2.6
10	CJ	78	ASN	2.6
10	AJ	67	THR	2.5
19	AS	38	SER	2.5
19	CS	48	THR	2.5
1	AA	1031	G	2.5
1	CA	1026	G	2.5
24	AY	1	G	2.5
8	AH	80	ILE	2.5
9	CI	81	ILE	2.5
1	AA	1493	A	2.5
1	CA	1183	A	2.5
9	CI	79	LEU	2.5
30	DG	34	LEU	2.5
38	DS	4	LEU	2.5
14	AN	3	ARG	2.5
15	AO	48	LYS	2.5
36	DQ	60	ARG	2.5
39	BT	129	ARG	2.5
3	CC	31	HIS	2.5
2	CB	33	TYR	2.5
30	DG	48	GLU	2.5
1	AA	1066	C	2.5
25	BA	933	C	2.5
25	DA	2188	C	2.5

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Mol	Chain	Res	Type	RSRZ
8	CH	130	GLY	2.5
31	BH	66	GLY	2.5
44	DY	80	GLY	2.5
2	AB	131	PRO	2.5
19	CS	59	PRO	2.5
31	BH	169	VAL	2.5
31	DH	128	PRO	2.5
7	CG	65	ALA	2.5
10	AJ	75	ILE	2.5
15	CO	3	ILE	2.5
38	DS	39	ILE	2.5
4	CD	120	LEU	2.5
10	CJ	16	LEU	2.5
13	AM	96	LEU	2.5
17	AQ	68	ARG	2.5
21	AU	9	ARG	2.5
53	B7	48	LYS	2.5
7	AG	90	GLU	2.5
11	CK	75	TYR	2.5
25	DA	2158	A	2.5
19	AS	72	GLY	2.5
14	CN	18	VAL	2.5
9	CI	124	GLN	2.5
13	CM	118	ALA	2.5
14	CN	16	PHE	2.5
14	CN	37	PHE	2.5
25	DA	2139	C	2.5
3	AC	67	THR	2.5
19	AS	79	THR	2.5
38	DS	61	ASN	2.5
30	DG	39	ILE	2.5
36	DQ	22	LYS	2.5
5	CE	119	LEU	2.5
9	CI	96	LEU	2.5
13	CM	94	ARG	2.5
5	AE	81	GLU	2.5
3	CC	23	TYR	2.5
30	DG	12	TYR	2.5
9	CI	68	GLY	2.5
4	AD	112	VAL	2.5
17	CQ	10	VAL	2.5
25	BA	1152	G	2.5

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Mol	Chain	Res	Type	RSRZ
25	BA	2228	G	2.5
25	DA	229	A	2.5
25	DA	2131	G	2.5
2	CB	177	ALA	2.5
3	CC	71	ALA	2.5
29	DF	130	ALA	2.5
13	CM	65	LYS	2.5
30	DG	76	SER	2.5
38	DS	20	ARG	2.5
21	CU	5	ASP	2.5
23	AX	69	C	2.5
44	DY	107	ASP	2.5
2	CB	40	HIS	2.5
1	CA	1205	U	2.5
48	B2	11	GLU	2.5
2	CB	148	TYR	2.5
13	CM	41	PRO	2.5
16	CP	38	TYR	2.5
2	CB	230	VAL	2.5
3	CC	116	VAL	2.5
31	DH	115	VAL	2.5
3	AC	100	ALA	2.5
9	CI	101	PHE	2.5
16	AP	7	ALA	2.5
2	CB	132	LYS	2.4
12	AL	47	LYS	2.4
14	CN	22	THR	2.4
11	CK	117	ASN	2.4
11	CK	126	ARG	2.4
2	AB	118	LEU	2.4
4	AD	158	ILE	2.4
6	CF	21	LEU	2.4
10	AJ	50	ILE	2.4
13	CM	96	LEU	2.4
10	CJ	13	HIS	2.4
2	CB	231	GLU	2.4
24	AY	75	C	2.4
25	DA	2108	C	2.4
2	AB	228	GLY	2.4
21	AU	23	PRO	2.4
2	CB	164	VAL	2.4
2	CB	229	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
10	CJ	94	VAL	2.4
19	CS	11	VAL	2.4
40	BU	117	GLN	2.4
3	CC	128	PHE	2.4
30	DG	102	PHE	2.4
43	DX	28	PHE	2.4
14	CN	57	ARG	2.4
19	CS	78	ARG	2.4
30	DG	93	THR	2.4
52	D6	44	ARG	2.4
6	AF	8	ILE	2.4
10	AJ	69	ASN	2.4
32	DI	11	ASN	2.4
45	DZ	155	LEU	2.4
10	CJ	56	HIS	2.4
22	AV	14	A	2.4
25	BA	2180	A	2.4
31	DH	159	GLU	2.4
1	CA	1353	G	2.4
1	CA	1373	G	2.4
25	DA	2157	G	2.4
25	DA	2166	G	2.4
26	DB	56	G	2.4
3	CC	13	GLY	2.4
3	CC	25	GLY	2.4
30	DG	17	PRO	2.4
30	DG	142	PRO	2.4
31	BH	14	GLY	2.4
50	B4	69	LYS	2.4
3	AC	23	TYR	2.4
5	CE	67	VAL	2.4
7	AG	17	VAL	2.4
13	CM	101	GLN	2.4
16	CP	79	VAL	2.4
24	CY	74	C	2.4
24	CY	75	C	2.4
7	AG	2	ALA	2.4
7	AG	4	ARG	2.4
8	CH	122	ARG	2.4
35	BP	15	ARG	2.4
3	AC	77	ILE	2.4
10	AJ	48	THR	2.4

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Mol	Chain	Res	Type	RSRZ
45	DZ	59	LEU	2.4
19	AS	14	HIS	2.4
50	D4	66	SER	2.4
7	AG	8	GLU	2.4
16	CP	29	ASP	2.4
1	AA	1030(D)	A	2.4
2	AB	125	PRO	2.4
5	AE	88	LYS	2.4
12	CL	13	LYS	2.4
25	DA	2119	A	2.4
30	DG	2	PRO	2.4
35	DP	76	LYS	2.4
12	AL	63	GLY	2.4
3	CC	64	VAL	2.4
13	CM	98	VAL	2.4
16	CP	51	VAL	2.4
1	AA	380	G	2.4
1	CA	1355	G	2.4
4	AD	3	ARG	2.4
9	CI	42	ARG	2.4
11	CK	25	TYR	2.4
13	CM	18	ALA	2.4
16	CP	42	ARG	2.4
19	AS	37	ARG	2.4
30	BG	12	TYR	2.4
31	BH	3	ARG	2.4
52	D6	2	ALA	2.4
5	AE	89	ILE	2.4
8	AH	2	LEU	2.4
25	BA	2202	U	2.4
25	DA	2113	U	2.4
44	DY	44	ILE	2.4
55	D9	17	ILE	2.4
1	CA	1277	C	2.4
50	D4	40	HIS	2.4
50	D4	57	GLU	2.4
8	AH	98	LYS	2.4
30	BG	182	LYS	2.4
19	AS	42	PRO	2.4
19	CS	76	PRO	2.4
16	AP	76	GLN	2.4
2	AB	15	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
9	CI	86	VAL	2.4
9	CI	128	ARG	2.4
13	CM	3	ARG	2.4
13	CM	60	VAL	2.4
44	DY	49	VAL	2.4
2	CB	17	PHE	2.4
26	DB	66	A	2.4
2	CB	88	ALA	2.4
9	AI	15	ALA	2.4
3	CC	184	TYR	2.3
10	CJ	8	LEU	2.3
17	CQ	76	LEU	2.3
19	AS	16	LEU	2.3
3	CC	182	ILE	2.3
5	CE	109	ILE	2.3
3	CC	192	THR	2.3
9	CI	117	HIS	2.3
2	AB	37	ASN	2.3
20	AT	75	ASN	2.3
15	AO	14	GLU	2.3
25	DA	2132	U	2.3
30	BG	35	GLU	2.3
1	CA	979	C	2.3
1	CA	1260	C	2.3
1	CA	1325	C	2.3
3	CC	135	LYS	2.3
3	CC	147	LYS	2.3
11	AK	16	SER	2.3
25	DA	885	C	2.3
38	DS	52	SER	2.3
47	D1	2	SER	2.3
53	B7	1	MET	2.3
25	DA	2175	C	2.3
16	AP	41	PRO	2.3
7	CG	34	GLY	2.3
7	CG	81	GLY	2.3
8	CH	131	GLY	2.3
21	AU	15	ARG	2.3
30	DG	181	ARG	2.3
2	CB	81	VAL	2.3
31	DH	45	VAL	2.3
9	AI	18	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
7	CG	124	LEU	2.3
32	BI	146	ALA	2.3
10	CJ	6	ILE	2.3
3	CC	193	TYR	2.3
9	AI	125	TYR	2.3
21	AU	21	TYR	2.3
10	CJ	100	THR	2.3
13	CM	103	THR	2.3
25	BA	1092	A	2.3
25	DA	2114	A	2.3
9	CI	70	LYS	2.3
1	AA	1358	U	2.3
25	BA	1220	U	2.3
25	BA	2211	U	2.3
1	AA	1033	G	2.3
1	CA	1124	G	2.3
25	DA	2127	G	2.3
31	DH	55	PRO	2.3
1	CA	1118	C	2.3
6	CF	27	GLN	2.3
9	CI	80	GLY	2.3
12	AL	89	ARG	2.3
21	CU	16	GLY	2.3
25	BA	932	C	2.3
38	DS	97	ARG	2.3
44	DY	57	GLN	2.3
50	B4	17	GLY	2.3
9	AI	41	VAL	2.3
19	AS	41	VAL	2.3
7	CG	26	PHE	2.3
3	CC	53	ALA	2.3
34	BO	91	LEU	2.3
2	AB	236	TYR	2.3
3	AC	201	TYR	2.3
13	CM	21	TYR	2.3
2	CB	101	MET	2.3
3	AC	19	GLU	2.3
17	AQ	87	LYS	2.3
45	DZ	168	GLU	2.3
46	D0	68	GLU	2.3
1	AA	532	A	2.3
1	CA	1531	A	2.3

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Mol	Chain	Res	Type	RSRZ
8	CH	29	SER	2.3
14	CN	12	ARG	2.3
14	CN	31	ARG	2.3
29	BF	17	ARG	2.3
15	CO	20	GLY	2.3
3	CC	153	VAL	2.3
14	CN	40	CYS	2.3
16	AP	79	VAL	2.3
4	AD	78	LEU	2.3
5	AE	71	LEU	2.3
7	CG	43	PHE	2.3
8	CH	31	PHE	2.3
10	AJ	88	LEU	2.3
43	DX	9	LEU	2.3
1	AA	933	G	2.3
1	AA	1011	G	2.3
5	AE	118	ILE	2.3
7	CG	7	ALA	2.3
12	CL	68	ALA	2.3
1	CA	1028	C	2.3
1	CA	1058	G	2.3
2	AB	127	ILE	2.3
21	CU	13	ILE	2.3
46	B0	2	ALA	2.3
25	BA	2815	C	2.3
31	DH	111	HIS	2.3
5	CE	121	LYS	2.3
8	AH	3	THR	2.3
20	AT	14	LYS	2.3
6	CF	63	TYR	2.3
38	DS	92	TYR	2.3
2	CB	86	GLU	2.3
7	AG	84	ASN	2.3
3	CC	183	ASP	2.3
9	CI	83	ARG	2.3
12	CL	89	ARG	2.3
13	CM	104	ARG	2.3
30	BG	83	ARG	2.3
45	DZ	95	PRO	2.3
47	D1	26	ARG	2.3
1	AA	152	A	2.3
20	AT	18	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
4	AD	167	GLY	2.3
14	CN	51	GLY	2.3
39	BT	37	GLY	2.3
42	BW	112	GLY	2.3
2	CB	69	LEU	2.3
10	AJ	71	LEU	2.3
16	CP	2	VAL	2.3
19	AS	9	VAL	2.3
30	DG	3	LEU	2.3
31	DH	44	VAL	2.3
45	BZ	141	VAL	2.3
50	D4	35	VAL	2.3
16	CP	9	PHE	2.3
30	BG	80	PHE	2.3
1	CA	997	U	2.2
2	AB	201	ILE	2.2
9	AI	13	ALA	2.2
10	CJ	27	ALA	2.2
14	CN	20	ALA	2.2
30	DG	88	ILE	2.2
30	DG	163	ALA	2.2
32	DI	4	ILE	2.2
38	DS	5	THR	2.2
3	AC	35	GLU	2.2
25	BA	1936	C	2.2
25	BA	2159	C	2.2
6	CF	7	ASN	2.2
25	BA	2179	G	2.2
25	DA	2168	G	2.2
26	DB	61	G	2.2
13	CM	80	ARG	2.2
32	BI	27	ARG	2.2
9	CI	49	PRO	2.2
10	CJ	39	PRO	2.2
44	DY	53	PRO	2.2
49	B3	2	PRO	2.2
3	CC	37	GLN	2.2
4	AD	208	SER	2.2
45	DZ	118	GLN	2.2
2	CB	66	GLY	2.2
21	AU	16	GLY	2.2
4	AD	140	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
5	AE	82	VAL	2.2
5	CE	105	VAL	2.2
9	CI	47	LEU	2.2
30	DG	29	TRP	2.2
1	AA	975	A	2.2
1	CA	977	A	2.2
1	CA	1004	A	2.2
2	CB	208	ILE	2.2
3	AC	39	ILE	2.2
3	CC	8	ILE	2.2
5	AE	138	ALA	2.2
16	AP	12	LYS	2.2
16	CP	3	LYS	2.2
23	AX	76	A	2.2
25	BA	2156	A	2.2
44	DY	29	GLU	2.2
45	BZ	119	GLU	2.2
3	AC	48	TYR	2.2
10	AJ	45	ARG	2.2
1	CA	1115	C	2.2
1	CA	1203	C	2.2
1	CA	1320	C	2.2
25	BA	2185	C	2.2
25	DA	897	C	2.2
25	DA	2142	C	2.2
1	CA	630	G	2.2
1	CA	1131	G	2.2
4	AD	2	GLY	2.2
15	CO	86	GLY	2.2
3	AC	32	LEU	2.2
3	AC	188	LEU	2.2
3	CC	115	LEU	2.2
5	CE	12	LEU	2.2
17	CQ	43	LEU	2.2
23	AX	2	G	2.2
25	DA	2100	G	2.2
25	DA	2153	G	2.2
32	BI	38	LEU	2.2
10	AJ	55	LYS	2.2
12	CL	46	LYS	2.2
12	CL	47	LYS	2.2
17	AQ	23	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
44	DY	21	LYS	2.2
13	CM	4	ILE	2.2
36	DQ	104	PHE	2.2
55	B9	17	ILE	2.2
2	AB	34	ALA	2.2
16	AP	24	ALA	2.2
30	BG	137	GLU	2.2
24	AY	73	A	2.2
26	DB	120	A	2.2
52	D6	14	THR	2.2
10	CJ	43	ARG	2.2
16	AP	81	ARG	2.2
25	BA	1985	U	2.2
25	DA	895	U	2.2
25	DA	2150	U	2.2
30	BG	16	ARG	2.2
45	BZ	112	ARG	2.2
2	CB	199	TYR	2.2
12	CL	69	TYR	2.2
30	DG	27	ASN	2.2
44	DY	55	TYR	2.2
2	AB	202	PRO	2.2
2	CB	91	PRO	2.2
4	AD	29	PRO	2.2
7	CG	88	PRO	2.2
13	AM	100	GLY	2.2
13	CM	100	GLY	2.2
19	CS	70	LYS	2.2
20	CT	62	LEU	2.2
30	DG	62	LEU	2.2
30	DG	172	LEU	2.2
32	BI	30	LEU	2.2
38	DS	90	GLY	2.2
5	AE	67	VAL	2.2
1	CA	1263	C	2.2
2	AB	163	PHE	2.2
2	CB	223	ILE	2.2
4	CD	123	HIS	2.2
8	CH	138	TRP	2.2
15	AO	3	ILE	2.2
16	AP	4	ILE	2.2
16	CP	13	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
25	BA	696	C	2.2
25	DA	2789	C	2.2
2	CB	13	ALA	2.2
28	BE	204	ALA	2.2
1	AA	1030(C)	G	2.2
1	CA	1024	G	2.2
1	CA	1371	G	2.2
2	CB	129	GLU	2.2
5	CE	122	GLU	2.2
9	CI	12	GLU	2.2
25	BA	2171	G	2.2
7	AG	115	ARG	2.2
8	CH	91	ARG	2.2
13	AM	102	ARG	2.2
30	BG	51	ARG	2.2
39	BT	112	ARG	2.2
46	B0	11	ARG	2.2
53	B7	47	ARG	2.2
1	AA	1357	A	2.2
7	AG	151	TYR	2.2
7	CG	151	TYR	2.2
13	AM	97	PRO	2.2
14	AN	34	TYR	2.2
15	CO	19	PRO	2.2
25	BA	2193	A	2.2
25	DA	887	A	2.2
31	DH	39	PRO	2.2
50	D4	63	TYR	2.2
1	CA	1000	U	2.2
5	CE	20	GLN	2.2
11	CK	13	GLN	2.2
14	CN	17	LYS	2.2
25	BA	271	U	2.2
2	AB	44	LEU	2.2
2	CB	38	GLY	2.2
9	CI	115	GLY	2.2
41	BV	101	GLY	2.2
44	DY	58	GLY	2.2
45	BZ	144	LEU	2.2
45	DZ	125	LEU	2.2
6	CF	85	VAL	2.2
9	CI	28	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
13	CM	54	VAL	2.2
30	DG	178	PHE	2.2
20	AT	94	ALA	2.1
20	CT	67	ALA	2.1
30	DG	169	ALA	2.1
1	CA	1045	C	2.1
1	CA	1066	C	2.1
1	CA	1397	C	2.1
7	CG	5	ARG	2.1
10	CJ	5	ARG	2.1
10	CJ	66	ARG	2.1
25	BA	2162	C	2.1
25	DA	2178	C	2.1
31	BH	101	ARG	2.1
1	CA	971	G	2.1
1	CA	1154	G	2.1
2	CB	131	PRO	2.1
25	BA	2170	G	2.1
25	DA	271(M)	G	2.1
3	AC	193	TYR	2.1
3	CC	123	GLN	2.1
16	AP	38	TYR	2.1
2	CB	121	LEU	2.1
3	CC	178	LEU	2.1
13	CM	48	LEU	2.1
19	AS	22	LEU	2.1
1	CA	1248	A	2.1
9	AI	39	GLY	2.1
1	AA	1381	U	2.1
4	CD	198	VAL	2.1
9	CI	71	SER	2.1
13	CM	15	VAL	2.1
20	AT	73	HIS	2.1
25	BA	2140	U	2.1
20	AT	70	SER	2.1
13	CM	28	ALA	2.1
30	BG	46	ALA	2.1
31	BH	145	ALA	2.1
16	CP	48	TRP	2.1
4	AD	132	ARG	2.1
10	CJ	60	ARG	2.1
2	AB	234	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
10	CJ	91	PRO	2.1
30	DG	32	PRO	2.1
1	AA	1137	C	2.1
11	CK	119	CYS	2.1
25	BA	2129	C	2.1
2	AB	11	LEU	2.1
2	CB	213	LEU	2.1
3	CC	196	LEU	2.1
6	CF	59	TYR	2.1
6	CF	98	LEU	2.1
10	CJ	88	LEU	2.1
12	CL	64	TYR	2.1
30	BG	139	LEU	2.1
2	AB	14	GLY	2.1
2	CB	228	GLY	2.1
8	CH	90	GLY	2.1
14	CN	55	GLY	2.1
31	DH	120	GLY	2.1
41	DV	65	GLY	2.1
1	AA	79	G	2.1
1	AA	1034	G	2.1
1	CA	631	G	2.1
1	CA	1011	G	2.1
1	CA	1022	G	2.1
2	CB	80	ILE	2.1
7	CG	75	VAL	2.1
8	AH	93	VAL	2.1
14	AN	33	VAL	2.1
16	AP	51	VAL	2.1
25	BA	2122	G	2.1
25	BA	2212	G	2.1
25	DA	2125	G	2.1
30	DG	5	VAL	2.1
31	BH	4	ILE	2.1
31	DH	26	VAL	2.1
36	DQ	102	VAL	2.1
38	DS	46	VAL	2.1
38	DS	69	VAL	2.1
46	D0	71	ASP	2.1
52	D6	52	VAL	2.1
4	AD	137	SER	2.1
19	CS	10	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
45	DZ	104	PHE	2.1
50	D4	42	PHE	2.1
50	D4	59	PHE	2.1
9	AI	46	ALA	2.1
13	CM	33	ALA	2.1
26	DB	52	A	2.1
26	DB	53	A	2.1
15	AO	73	GLU	2.1
8	CH	37	ARG	2.1
13	AM	3	ARG	2.1
14	AN	29	ARG	2.1
36	BQ	60	ARG	2.1
17	AQ	7	THR	2.1
30	DG	161	THR	2.1
2	AB	8	LYS	2.1
2	AB	132	LYS	2.1
2	CB	75	LYS	2.1
17	AQ	37	LYS	2.1
11	AK	13	GLN	2.1
35	BP	1	MET	2.1
9	CI	50	LEU	2.1
13	CM	70	LEU	2.1
35	BP	99	LEU	2.1
14	CN	43	CYS	2.1
3	AC	2	GLY	2.1
5	CE	60	TYR	2.1
16	CP	39	TYR	2.1
1	CA	1284	C	2.1
2	AB	71	VAL	2.1
2	CB	127	ILE	2.1
7	CG	21	VAL	2.1
9	AI	86	VAL	2.1
25	DA	2179	C	2.1
4	AD	152	SER	2.1
5	CE	94	ALA	2.1
5	CE	107	ARG	2.1
9	CI	45	ALA	2.1
9	CI	94	ALA	2.1
10	AJ	64	GLU	2.1
19	CS	75	ALA	2.1
49	D3	60	GLU	2.1
1	AA	102	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1053	G	2.1
1	AA	1025	U	2.1
1	CA	969	A	2.1
1	CA	1012	U	2.1
1	CA	1016	A	2.1
10	CJ	7	LYS	2.1
25	BA	10	G	2.1
25	DA	2182	G	2.1
9	AI	7	THR	2.1
4	AD	165	MET	2.1
9	CI	38	GLN	2.1
40	DU	117	GLN	2.1
4	AD	186	LEU	2.1
7	CG	59	LEU	2.1
30	DG	175	LEU	2.1
31	DH	7	LEU	2.1
49	D3	26	LEU	2.1
2	AB	19	HIS	2.1
27	DD	238	GLY	2.1
45	DZ	121	HIS	2.1
4	CD	20	TYR	2.1
9	AI	5	TYR	2.1
11	AK	50	TYR	2.1
19	AS	62	ILE	2.1
38	DS	40	ILE	2.1
3	CC	68	VAL	2.1
7	CG	61	VAL	2.1
19	AS	67	VAL	2.1
19	CS	67	VAL	2.1
33	BN	53	VAL	2.1
4	CD	49	ARG	2.0
10	CJ	58	ASP	2.0
15	AO	15	PHE	2.1
19	CS	74	PHE	2.1
45	DZ	136	PHE	2.1
21	CU	24	ARG	2.0
50	B4	61	ARG	2.0
2	CB	29	ALA	2.0
5	CE	125	SER	2.0
14	AN	59	ALA	2.0
1	AA	219	C	2.0
21	CU	3	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
25	BA	2158	C	2.0
25	DA	2803	C	2.0
25	DA	2804	C	2.0
26	DB	62	C	2.0
38	DS	62	LYS	2.0
44	DY	63	LYS	2.0
3	AC	37	GLN	2.0
4	AD	120	LEU	2.0
4	AD	176	LEU	2.0
33	BN	131	GLN	2.0
45	DZ	144	LEU	2.0
46	D0	75	LEU	2.0
1	CA	975	A	2.0
1	CA	983	A	2.0
1	CA	1275	A	2.0
1	CA	1370	G	2.0
4	AD	125	HIS	2.0
10	AJ	62	HIS	2.0
7	AG	81	GLY	2.0
19	CS	8	GLY	2.0
31	DH	82	GLY	2.0
3	AC	106	VAL	2.0
3	CC	76	VAL	2.0
14	AN	21	TYR	2.0
19	AS	61	TYR	2.0
21	AU	18	TYR	2.0
31	DH	125	VAL	2.0
38	DS	49	VAL	2.0
49	D3	6	VAL	2.0
8	CH	104	ARG	2.0
14	AN	37	PHE	2.0
18	CR	29	PHE	2.0
19	AS	81	ARG	2.0
44	DY	2	ARG	2.0
44	DY	89	PHE	2.0
48	D2	55	ARG	2.0
2	AB	156	LYS	2.0
2	CB	8	LYS	2.0
5	AE	86	ALA	2.0
8	CH	16	ALA	2.0
32	DI	53	ALA	2.0
37	DR	25	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
10	CJ	67	THR	2.0
15	CO	75	PRO	2.0
36	BQ	21	THR	2.0
1	AA	1039	C	2.0
7	CG	86	GLN	2.0
10	AJ	40	LEU	2.0
14	CN	44	LEU	2.0
14	CN	53	LEU	2.0
17	AQ	93	GLN	2.0
25	BA	670	C	2.0
25	DA	2143	C	2.0
30	DG	152	LEU	2.0
1	AA	202	U	2.0
25	DA	2122	U	2.0
9	AI	30	GLY	2.0
9	CI	69	GLY	2.0
29	DF	16	GLY	2.0
32	DI	88	ILE	2.0
1	CA	965	A	2.0
2	CB	36	ARG	2.0
2	CB	144	ARG	2.0
6	CF	40	VAL	2.0
6	CF	87	ARG	2.0
7	CG	118	VAL	2.0
8	CH	84	ARG	2.0
9	CI	104	ARG	2.0
21	AU	6	ARG	2.0
21	AU	22	ARG	2.0
25	DA	2126	A	2.0
25	DA	2171	A	2.0
26	DB	59	A	2.0
35	DP	15	ARG	2.0
44	DY	45	VAL	2.0
4	AD	20	TYR	2.0
19	CS	61	TYR	2.0

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

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($\text{\AA}^2$)	Q<0.9
23	4SU	CX	8	20/21	0.81	0.11	73,81,98,100	0
23	PSU	CX	55	20/21	0.82	0.13	56,73,80,86	0
23	5MU	CX	54	21/22	0.84	0.13	69,80,93,106	0
23	PSU	AX	55	20/21	0.91	0.11	56,70,78,80	0
23	5MC	CX	32	21/22	0.91	0.12	66,75,83,86	0
23	5MU	AX	54	21/22	0.92	0.11	60,72,80,91	0
23	4SU	AX	8	20/21	0.94	0.10	47,67,77,84	0
23	5MC	AX	32	21/22	0.95	0.13	38,59,69,83	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
56	MG	AA	3147	1/1	0.56	0.18	72,72,72,72	0
56	MG	CJ	5001	1/1	0.58	0.14	94,94,94,94	0
56	MG	DB	3001	1/1	0.58	0.13	77,77,77,77	0
56	MG	AA	3177	1/1	0.62	0.23	80,80,80,80	0
56	MG	DA	3640	1/1	0.64	0.19	64,64,64,64	0
56	MG	DA	3533	1/1	0.64	0.14	52,52,52,52	0
56	MG	DA	3655	1/1	0.67	0.54	74,74,74,74	0
56	MG	DA	3612	1/1	0.67	0.21	58,58,58,58	0
56	MG	BA	3447	1/1	0.68	0.21	59,59,59,59	0
56	MG	CA	3124	1/1	0.68	0.20	75,75,75,75	0
56	MG	DA	3607	1/1	0.69	0.22	63,63,63,63	0
56	MG	BE	306	1/1	0.69	0.28	93,93,93,93	0
56	MG	DA	3634	1/1	0.69	0.19	61,61,61,61	0
56	MG	DA	3657	1/1	0.70	0.20	56,56,56,56	0
56	MG	CA	3174	1/1	0.70	0.15	80,80,80,80	0
56	MG	CA	3054	1/1	0.72	0.39	70,70,70,70	0
56	MG	BA	3657	1/1	0.72	0.27	52,52,52,52	0
56	MG	AA	3171	1/1	0.72	0.18	67,67,67,67	0
56	MG	CA	3131	1/1	0.73	0.35	81,81,81,81	0
56	MG	CX	3002	1/1	0.73	0.43	81,81,81,81	0
56	MG	CA	3084	1/1	0.74	0.28	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	AA	3067	1/1	0.74	0.40	72,72,72,72	0
57	PCY	CA	3176	40/40	0.74	0.22	72,89,98,102	0
56	MG	BA	3703	1/1	0.75	0.14	57,57,57,57	0
56	MG	DA	3562	1/1	0.75	0.19	72,72,72,72	0
56	MG	BA	3598	1/1	0.75	0.24	53,53,53,53	0
56	MG	AA	3059	1/1	0.75	0.27	64,64,64,64	0
56	MG	DA	3466	1/1	0.75	0.24	66,66,66,66	0
56	MG	AA	3040	1/1	0.76	0.16	72,72,72,72	0
56	MG	BA	3659	1/1	0.76	0.32	67,67,67,67	0
56	MG	BA	3671	1/1	0.76	0.23	59,59,59,59	0
56	MG	AA	3163	1/1	0.76	0.24	58,58,58,58	0
56	MG	CE	201	1/1	0.76	0.30	73,73,73,73	0
56	MG	BA	3555	1/1	0.76	0.11	61,61,61,61	0
56	MG	AA	3043	1/1	0.76	0.32	76,76,76,76	0
56	MG	DA	3211	1/1	0.76	0.15	53,53,53,53	0
56	MG	CA	3082	1/1	0.76	0.32	73,73,73,73	0
56	MG	DA	3484	1/1	0.76	0.16	32,32,32,32	0
56	MG	AA	3153	1/1	0.77	0.19	81,81,81,81	0
56	MG	BA	3692	1/1	0.77	0.15	51,51,51,51	0
56	MG	BA	3521	1/1	0.77	0.19	29,29,29,29	0
56	MG	BA	3768	1/1	0.77	0.12	61,61,61,61	0
56	MG	AA	3179	1/1	0.77	0.26	61,61,61,61	0
57	PCY	AA	3191	40/40	0.77	0.21	59,86,97,99	0
56	MG	DA	3319	1/1	0.77	0.15	52,52,52,52	0
56	MG	BA	3737	1/1	0.78	0.16	70,70,70,70	0
56	MG	BA	3498	1/1	0.78	0.21	43,43,43,43	0
56	MG	BA	3505	1/1	0.78	0.18	33,33,33,33	0
56	MG	AA	3125	1/1	0.78	0.14	72,72,72,72	0
56	MG	CA	3063	1/1	0.78	0.32	70,70,70,70	0
56	MG	BA	3384	1/1	0.78	0.22	63,63,63,63	0
56	MG	AA	3100	1/1	0.78	0.26	66,66,66,66	0
56	MG	DA	3110	1/1	0.79	0.33	64,64,64,64	0
56	MG	CA	3144	1/1	0.79	0.26	68,68,68,68	0
56	MG	CA	3171	1/1	0.79	0.24	65,65,65,65	0
56	MG	CA	3100	1/1	0.79	0.17	69,69,69,69	0
56	MG	AA	3184	1/1	0.79	0.13	66,66,66,66	0
56	MG	DA	3527	1/1	0.79	0.15	61,61,61,61	0
56	MG	AA	3034	1/1	0.79	0.21	70,70,70,70	0
56	MG	DA	3537	1/1	0.79	0.25	58,58,58,58	0
56	MG	CA	3142	1/1	0.79	0.17	81,81,81,81	0
56	MG	DA	3567	1/1	0.80	0.19	57,57,57,57	0
56	MG	BA	3514	1/1	0.80	0.11	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3341	1/1	0.80	0.20	67,67,67,67	0
56	MG	DA	3435	1/1	0.80	0.30	55,55,55,55	0
56	MG	BA	3512	1/1	0.80	0.23	47,47,47,47	0
56	MG	BA	3626	1/1	0.80	0.17	43,43,43,43	0
56	MG	BA	3650	1/1	0.80	0.21	48,48,48,48	0
56	MG	DA	3103	1/1	0.80	0.15	71,71,71,71	0
56	MG	CA	3149	1/1	0.80	0.31	74,74,74,74	0
56	MG	B4	502	1/1	0.80	0.21	77,77,77,77	0
56	MG	BA	3592	1/1	0.81	0.22	64,64,64,64	0
56	MG	AA	3169	1/1	0.81	0.18	73,73,73,73	0
56	MG	AA	3170	1/1	0.81	0.25	73,73,73,73	0
56	MG	DA	3559	1/1	0.81	0.21	61,61,61,61	0
56	MG	CA	3091	1/1	0.81	0.24	70,70,70,70	0
56	MG	BA	3760	1/1	0.81	0.14	43,43,43,43	0
56	MG	CA	3107	1/1	0.81	0.12	77,77,77,77	0
56	MG	DA	3175	1/1	0.81	0.18	51,51,51,51	0
56	MG	AX	3002	1/1	0.81	0.18	69,69,69,69	0
56	MG	BB	205	1/1	0.81	0.29	76,76,76,76	0
56	MG	AA	3127	1/1	0.81	0.17	79,79,79,79	0
56	MG	BA	3437	1/1	0.81	0.20	61,61,61,61	0
56	MG	DA	3438	1/1	0.81	0.15	55,55,55,55	0
56	MG	CA	3043	1/1	0.81	0.31	67,67,67,67	0
56	MG	AA	3094	1/1	0.81	0.29	66,66,66,66	0
56	MG	CA	3019	1/1	0.82	0.29	62,62,62,62	0
56	MG	CT	3001	1/1	0.82	0.31	59,59,59,59	0
56	MG	BA	3725	1/1	0.82	0.17	44,44,44,44	0
56	MG	AA	3049	1/1	0.82	0.15	64,64,64,64	0
56	MG	DA	3109	1/1	0.82	0.30	68,68,68,68	0
56	MG	AA	3105	1/1	0.82	0.23	71,71,71,71	0
56	MG	BA	3663	1/1	0.82	0.26	65,65,65,65	0
56	MG	DA	3202	1/1	0.82	0.19	52,52,52,52	0
56	MG	BA	3108	1/1	0.82	0.27	64,64,64,64	0
56	MG	DA	3222	1/1	0.82	0.12	46,46,46,46	0
56	MG	CA	3159	1/1	0.82	0.25	71,71,71,71	0
56	MG	DA	3324	1/1	0.82	0.15	32,32,32,32	0
56	MG	BA	3288	1/1	0.82	0.14	44,44,44,44	0
56	MG	DA	3402	1/1	0.82	0.14	56,56,56,56	0
56	MG	DA	3426	1/1	0.82	0.12	39,39,39,39	0
56	MG	DB	3008	1/1	0.82	0.17	64,64,64,64	0
56	MG	DD	308	1/1	0.82	0.33	72,72,72,72	0
56	MG	DV	3003	1/1	0.82	0.09	55,55,55,55	0
56	MG	CA	3096	1/1	0.82	0.17	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3525	1/1	0.82	0.13	23,23,23,23	0
56	MG	BA	3579	1/1	0.83	0.17	43,43,43,43	0
56	MG	DA	3469	1/1	0.83	0.11	53,53,53,53	0
56	MG	CA	3083	1/1	0.83	0.29	72,72,72,72	0
56	MG	DA	3488	1/1	0.83	0.16	51,51,51,51	0
56	MG	DA	3499	1/1	0.83	0.23	61,61,61,61	0
56	MG	BA	3583	1/1	0.83	0.14	56,56,56,56	0
56	MG	BA	3518	1/1	0.83	0.17	65,65,65,65	0
56	MG	AA	3185	1/1	0.83	0.15	61,61,61,61	0
56	MG	BP	203	1/1	0.83	0.16	49,49,49,49	0
56	MG	DA	3150	1/1	0.83	0.22	52,52,52,52	0
56	MG	B0	101	1/1	0.83	0.15	55,55,55,55	0
56	MG	DA	3606	1/1	0.83	0.12	48,48,48,48	0
56	MG	DA	3185	1/1	0.83	0.16	55,55,55,55	0
56	MG	CA	3122	1/1	0.83	0.26	65,65,65,65	0
56	MG	DA	3626	1/1	0.83	0.18	56,56,56,56	0
56	MG	BA	3607	1/1	0.83	0.22	51,51,51,51	0
56	MG	BA	3693	1/1	0.83	0.16	74,74,74,74	0
56	MG	CA	3025	1/1	0.83	0.31	61,61,61,61	0
56	MG	BA	3617	1/1	0.83	0.17	44,44,44,44	0
56	MG	CA	3053	1/1	0.83	0.27	55,55,55,55	0
56	MG	DA	3400	1/1	0.83	0.18	56,56,56,56	0
56	MG	BA	3265	1/1	0.83	0.15	49,49,49,49	0
56	MG	BA	3389	1/1	0.83	0.16	56,56,56,56	0
56	MG	CA	3067	1/1	0.83	0.24	72,72,72,72	0
56	MG	CA	3078	1/1	0.83	0.28	64,64,64,64	0
56	MG	AX	3007	1/1	0.84	0.20	69,69,69,69	0
56	MG	DA	3221	1/1	0.84	0.17	52,52,52,52	0
56	MG	BA	3677	1/1	0.84	0.18	56,56,56,56	0
56	MG	DA	3257	1/1	0.84	0.37	57,57,57,57	0
56	MG	BA	3296	1/1	0.84	0.17	47,47,47,47	0
56	MG	DA	3599	1/1	0.84	0.15	47,47,47,47	0
56	MG	BA	3066	1/1	0.84	0.23	52,52,52,52	0
56	MG	CA	3090	1/1	0.84	0.27	67,67,67,67	0
56	MG	CA	3011	1/1	0.84	0.27	69,69,69,69	0
56	MG	BA	3097	1/1	0.84	0.26	52,52,52,52	0
56	MG	AA	3157	1/1	0.84	0.19	84,84,84,84	0
56	MG	BA	3112	1/1	0.84	0.11	42,42,42,42	0
56	MG	DA	3437	1/1	0.84	0.12	36,36,36,36	0
56	MG	BA	3558	1/1	0.84	0.28	57,57,57,57	0
56	MG	BA	3221	1/1	0.84	0.10	39,39,39,39	0
56	MG	AA	3020	1/1	0.84	0.44	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	CA	3134	1/1	0.84	0.18	65,65,65,65	0
56	MG	CA	3138	1/1	0.84	0.24	65,65,65,65	0
56	MG	CA	3139	1/1	0.84	0.28	69,69,69,69	0
56	MG	BB	211	1/1	0.84	0.13	81,81,81,81	0
56	MG	DA	3229	1/1	0.85	0.28	64,64,64,64	0
56	MG	DA	3249	1/1	0.85	0.29	65,65,65,65	0
56	MG	CA	3030	1/1	0.85	0.11	56,56,56,56	0
56	MG	DA	3268	1/1	0.85	0.20	56,56,56,56	0
56	MG	BA	3420	1/1	0.85	0.22	46,46,46,46	0
56	MG	BA	3605	1/1	0.85	0.14	44,44,44,44	0
56	MG	DA	3059	1/1	0.85	0.09	40,40,40,40	0
56	MG	DA	3583	1/1	0.85	0.09	56,56,56,56	0
56	MG	DA	3364	1/1	0.85	0.16	57,57,57,57	0
56	MG	DA	3389	1/1	0.85	0.12	50,50,50,50	0
56	MG	BA	3506	1/1	0.85	0.10	31,31,31,31	0
56	MG	B5	105	1/1	0.85	0.14	66,66,66,66	0
56	MG	DA	3412	1/1	0.85	0.14	56,56,56,56	0
56	MG	DA	3629	1/1	0.85	0.13	61,61,61,61	0
56	MG	DA	3631	1/1	0.85	0.20	57,57,57,57	0
56	MG	DA	3417	1/1	0.85	0.19	62,62,62,62	0
56	MG	DA	3418	1/1	0.85	0.12	44,44,44,44	0
56	MG	CA	3007	1/1	0.85	0.21	42,42,42,42	0
56	MG	CA	3158	1/1	0.85	0.15	75,75,75,75	0
56	MG	CA	3116	1/1	0.85	0.13	54,54,54,54	0
56	MG	CA	3164	1/1	0.85	0.19	73,73,73,73	0
56	MG	CA	3169	1/1	0.85	0.15	52,52,52,52	0
56	MG	BA	3392	1/1	0.85	0.15	41,41,41,41	0
56	MG	BA	3721	1/1	0.85	0.08	9,9,9,9	0
56	MG	BA	3503	1/1	0.85	0.22	64,64,64,64	0
56	MG	AA	3141	1/1	0.86	0.20	50,50,50,50	0
56	MG	AA	3080	1/1	0.86	0.42	71,71,71,71	0
56	MG	BA	3455	1/1	0.86	0.10	32,32,32,32	0
56	MG	B7	104	1/1	0.86	0.19	64,64,64,64	0
56	MG	CA	3151	1/1	0.86	0.20	60,60,60,60	0
56	MG	DA	3423	1/1	0.86	0.11	56,56,56,56	0
56	MG	CA	3152	1/1	0.86	0.12	54,54,54,54	0
56	MG	DA	3433	1/1	0.86	0.13	34,34,34,34	0
56	MG	CA	3155	1/1	0.86	0.22	76,76,76,76	0
56	MG	BA	3458	1/1	0.86	0.38	66,66,66,66	0
56	MG	BA	3109	1/1	0.86	0.35	56,56,56,56	0
56	MG	AA	3150	1/1	0.86	0.18	66,66,66,66	0
56	MG	BA	3165	1/1	0.86	0.24	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3479	1/1	0.86	0.18	35,35,35,35	0
56	MG	BA	3175	1/1	0.86	0.20	57,57,57,57	0
56	MG	BA	3199	1/1	0.86	0.18	51,51,51,51	0
56	MG	CA	3052	1/1	0.86	0.16	69,69,69,69	0
56	MG	DA	3502	1/1	0.86	0.08	48,48,48,48	0
56	MG	BA	3216	1/1	0.86	0.13	62,62,62,62	0
56	MG	AA	3122	1/1	0.86	0.14	80,80,80,80	0
56	MG	CA	3061	1/1	0.86	0.16	64,64,64,64	0
56	MG	BA	3698	1/1	0.86	0.16	50,50,50,50	0
56	MG	BA	3699	1/1	0.86	0.14	48,48,48,48	0
56	MG	AA	3183	1/1	0.86	0.22	73,73,73,73	0
56	MG	DA	3569	1/1	0.86	0.13	59,59,59,59	0
56	MG	BA	3274	1/1	0.86	0.18	51,51,51,51	0
56	MG	AA	3138	1/1	0.86	0.10	73,73,73,73	0
56	MG	DA	3603	1/1	0.86	0.23	55,55,55,55	0
56	MG	AA	3139	1/1	0.86	0.13	72,72,72,72	0
56	MG	BA	3744	1/1	0.86	0.14	61,61,61,61	0
56	MG	BA	3381	1/1	0.86	0.12	45,45,45,45	0
56	MG	DA	3621	1/1	0.86	0.33	50,50,50,50	0
56	MG	BA	3767	1/1	0.86	0.20	57,57,57,57	0
56	MG	CA	3099	1/1	0.86	0.14	58,58,58,58	0
56	MG	AA	3166	1/1	0.86	0.16	74,74,74,74	0
56	MG	CA	3103	1/1	0.86	0.11	79,79,79,79	0
56	MG	BA	3770	1/1	0.86	0.20	47,47,47,47	0
56	MG	DA	3648	1/1	0.86	0.09	31,31,31,31	0
56	MG	DA	3650	1/1	0.86	0.14	46,46,46,46	0
56	MG	BA	3813	1/1	0.86	0.13	58,58,58,58	0
56	MG	AA	3167	1/1	0.86	0.19	61,61,61,61	0
56	MG	DA	3670	1/1	0.86	0.13	49,49,49,49	0
56	MG	BB	209	1/1	0.86	0.29	69,69,69,69	0
56	MG	CA	3129	1/1	0.86	0.19	69,69,69,69	0
56	MG	DD	302	1/1	0.86	0.17	73,73,73,73	0
56	MG	BA	3595	1/1	0.86	0.46	43,43,43,43	0
56	MG	AA	3140	1/1	0.86	0.22	36,36,36,36	0
56	MG	DY	502	1/1	0.86	0.16	58,58,58,58	0
56	MG	DA	3377	1/1	0.86	0.19	62,62,62,62	0
56	MG	BA	3083	1/1	0.86	0.12	51,51,51,51	0
56	MG	BA	3711	1/1	0.87	0.22	51,51,51,51	0
56	MG	BA	3044	1/1	0.87	0.14	61,61,61,61	0
56	MG	AA	3173	1/1	0.87	0.25	60,60,60,60	0
56	MG	BA	3728	1/1	0.87	0.12	60,60,60,60	0
56	MG	BA	3082	1/1	0.87	0.30	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3455	1/1	0.87	0.23	46,46,46,46	0
56	MG	DA	3458	1/1	0.87	0.12	57,57,57,57	0
56	MG	AA	3098	1/1	0.87	0.24	71,71,71,71	0
56	MG	BA	3745	1/1	0.87	0.17	58,58,58,58	0
56	MG	BA	3755	1/1	0.87	0.14	52,52,52,52	0
56	MG	BA	3759	1/1	0.87	0.10	36,36,36,36	0
56	MG	DA	3044	1/1	0.87	0.13	49,49,49,49	0
56	MG	AA	3016	1/1	0.87	0.30	55,55,55,55	0
56	MG	BA	3294	1/1	0.87	0.24	67,67,67,67	0
56	MG	DA	3525	1/1	0.87	0.17	44,44,44,44	0
56	MG	BA	3612	1/1	0.87	0.19	58,58,58,58	0
56	MG	AA	3102	1/1	0.87	0.17	64,64,64,64	0
56	MG	CA	3093	1/1	0.87	0.28	65,65,65,65	0
56	MG	DA	3547	1/1	0.87	0.12	45,45,45,45	0
56	MG	BA	3793	1/1	0.87	0.19	52,52,52,52	0
56	MG	BA	3359	1/1	0.87	0.21	40,40,40,40	0
56	MG	BA	3648	1/1	0.87	0.18	65,65,65,65	0
56	MG	BA	3371	1/1	0.87	0.14	40,40,40,40	0
56	MG	DA	3575	1/1	0.87	0.16	51,51,51,51	0
56	MG	AA	3073	1/1	0.87	0.20	71,71,71,71	0
56	MG	BB	220	1/1	0.87	0.09	51,51,51,51	0
56	MG	CA	3117	1/1	0.87	0.20	58,58,58,58	0
56	MG	BB	221	1/1	0.87	0.12	43,43,43,43	0
56	MG	AA	3038	1/1	0.87	0.20	61,61,61,61	0
56	MG	DA	3266	1/1	0.87	0.31	56,56,56,56	0
56	MG	AA	3084	1/1	0.87	0.31	62,62,62,62	0
56	MG	DA	3276	1/1	0.87	0.14	54,54,54,54	0
56	MG	DA	3290	1/1	0.87	0.12	46,46,46,46	0
56	MG	AA	3012	1/1	0.87	0.11	50,50,50,50	0
56	MG	DA	3632	1/1	0.87	0.12	50,50,50,50	0
56	MG	BA	3673	1/1	0.87	0.11	28,28,28,28	0
56	MG	DA	3330	1/1	0.87	0.20	54,54,54,54	0
56	MG	DA	3339	1/1	0.87	0.16	60,60,60,60	0
56	MG	BA	3027	1/1	0.87	0.09	45,45,45,45	0
56	MG	DA	3347	1/1	0.87	0.09	46,46,46,46	0
56	MG	BA	3690	1/1	0.87	0.11	52,52,52,52	0
56	MG	BA	3427	1/1	0.87	0.14	52,52,52,52	0
56	MG	CA	3009	1/1	0.87	0.31	66,66,66,66	0
56	MG	CA	3148	1/1	0.87	0.12	88,88,88,88	0
56	MG	BA	3561	1/1	0.87	0.18	55,55,55,55	0
56	MG	CA	3013	1/1	0.87	0.16	54,54,54,54	0
56	MG	BA	3571	1/1	0.87	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3575	1/1	0.87	0.13	27,27,27,27	0
56	MG	DA	3419	1/1	0.87	0.15	45,45,45,45	0
56	MG	BA	3434	1/1	0.87	0.16	40,40,40,40	0
56	MG	BA	3624	1/1	0.88	0.14	37,37,37,37	0
56	MG	DA	3420	1/1	0.88	0.14	40,40,40,40	0
56	MG	AA	3078	1/1	0.88	0.13	72,72,72,72	0
56	MG	BA	3644	1/1	0.88	0.15	50,50,50,50	0
56	MG	DA	3431	1/1	0.88	0.12	64,64,64,64	0
56	MG	CA	3062	1/1	0.88	0.26	67,67,67,67	0
56	MG	BA	3766	1/1	0.88	0.13	59,59,59,59	0
56	MG	BA	3378	1/1	0.88	0.11	47,47,47,47	0
56	MG	CA	3075	1/1	0.88	0.29	67,67,67,67	0
56	MG	DA	3446	1/1	0.88	0.15	44,44,44,44	0
56	MG	AA	3180	1/1	0.88	0.14	49,49,49,49	0
56	MG	CA	3081	1/1	0.88	0.25	58,58,58,58	0
56	MG	DA	3465	1/1	0.88	0.21	49,49,49,49	0
56	MG	DA	3034	1/1	0.88	0.12	45,45,45,45	0
56	MG	BA	3185	1/1	0.88	0.13	52,52,52,52	0
56	MG	DA	3478	1/1	0.88	0.20	67,67,67,67	0
56	MG	BA	3772	1/1	0.88	0.17	56,56,56,56	0
56	MG	DA	3062	1/1	0.88	0.25	51,51,51,51	0
56	MG	DA	3083	1/1	0.88	0.23	63,63,63,63	0
56	MG	DA	3098	1/1	0.88	0.11	57,57,57,57	0
56	MG	BA	3194	1/1	0.88	0.22	62,62,62,62	0
56	MG	DA	3524	1/1	0.88	0.22	59,59,59,59	0
56	MG	CA	3086	1/1	0.88	0.33	76,76,76,76	0
56	MG	CA	3087	1/1	0.88	0.14	62,62,62,62	0
56	MG	DA	3124	1/1	0.88	0.16	50,50,50,50	0
56	MG	DA	3534	1/1	0.88	0.11	67,67,67,67	0
56	MG	DA	3131	1/1	0.88	0.18	52,52,52,52	0
56	MG	DA	3541	1/1	0.88	0.14	40,40,40,40	0
56	MG	CA	3088	1/1	0.88	0.23	66,66,66,66	0
56	MG	AA	3124	1/1	0.88	0.21	71,71,71,71	0
56	MG	BB	201	1/1	0.88	0.21	65,65,65,65	0
56	MG	DA	3563	1/1	0.88	0.23	61,61,61,61	0
56	MG	CA	3092	1/1	0.88	0.30	61,61,61,61	0
56	MG	AA	3047	1/1	0.88	0.24	63,63,63,63	0
56	MG	BA	3096	1/1	0.88	0.25	61,61,61,61	0
56	MG	DA	3582	1/1	0.88	0.13	64,64,64,64	0
56	MG	BA	3566	1/1	0.88	0.17	50,50,50,50	0
56	MG	DA	3589	1/1	0.88	0.12	53,53,53,53	0
56	MG	DA	3590	1/1	0.88	0.14	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3241	1/1	0.88	0.09	45,45,45,45	0
56	MG	BA	3259	1/1	0.88	0.19	59,59,59,59	0
56	MG	DA	3255	1/1	0.88	0.26	62,62,62,62	0
56	MG	BA	3440	1/1	0.88	0.12	29,29,29,29	0
56	MG	DA	3609	1/1	0.88	0.24	61,61,61,61	0
56	MG	BO	5001	1/1	0.88	0.12	55,55,55,55	0
56	MG	BA	3580	1/1	0.88	0.15	48,48,48,48	0
56	MG	DA	3623	1/1	0.88	0.22	66,66,66,66	0
56	MG	BA	3262	1/1	0.88	0.34	54,54,54,54	0
56	MG	DA	3286	1/1	0.88	0.15	54,54,54,54	0
56	MG	AA	3048	1/1	0.88	0.27	59,59,59,59	0
56	MG	CA	3128	1/1	0.88	0.24	68,68,68,68	0
56	MG	DA	3321	1/1	0.88	0.06	30,30,30,30	0
56	MG	AA	3136	1/1	0.88	0.18	62,62,62,62	0
56	MG	BA	3716	1/1	0.88	0.20	39,39,39,39	0
56	MG	DA	3649	1/1	0.88	0.17	53,53,53,53	0
56	MG	CA	3005	1/1	0.88	0.36	73,73,73,73	0
56	MG	BA	3477	1/1	0.88	0.17	59,59,59,59	0
56	MG	DA	3656	1/1	0.88	0.09	57,57,57,57	0
56	MG	BA	3604	1/1	0.88	0.16	46,46,46,46	0
56	MG	DA	3666	1/1	0.88	0.20	47,47,47,47	0
56	MG	AA	3074	1/1	0.88	0.25	51,51,51,51	0
56	MG	BA	3111	1/1	0.88	0.17	57,57,57,57	0
56	MG	BA	3738	1/1	0.88	0.16	60,60,60,60	0
56	MG	DA	3392	1/1	0.88	0.09	50,50,50,50	0
56	MG	AA	3109	1/1	0.88	0.21	67,67,67,67	0
56	MG	BA	3135	1/1	0.88	0.08	61,61,61,61	0
56	MG	CA	3042	1/1	0.88	0.30	70,70,70,70	0
56	MG	BA	3747	1/1	0.88	0.14	33,33,33,33	0
56	MG	BA	3748	1/1	0.88	0.15	69,69,69,69	0
56	MG	BA	3028	1/1	0.89	0.26	52,52,52,52	0
56	MG	CA	3006	1/1	0.89	0.11	59,59,59,59	0
56	MG	BA	3697	1/1	0.89	0.10	46,46,46,46	0
56	MG	BA	3161	1/1	0.89	0.21	46,46,46,46	0
56	MG	BA	3029	1/1	0.89	0.13	30,30,30,30	0
56	MG	BA	3040	1/1	0.89	0.15	52,52,52,52	0
56	MG	CA	3014	1/1	0.89	0.14	57,57,57,57	0
56	MG	BA	3704	1/1	0.89	0.24	36,36,36,36	0
56	MG	CA	3021	1/1	0.89	0.24	65,65,65,65	0
56	MG	BA	3567	1/1	0.89	0.11	45,45,45,45	0
56	MG	CA	3168	1/1	0.89	0.27	60,60,60,60	0
56	MG	BA	3387	1/1	0.89	0.12	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	CA	3036	1/1	0.89	0.34	72,72,72,72	0
56	MG	DA	3445	1/1	0.89	0.15	50,50,50,50	0
56	MG	BA	3717	1/1	0.89	0.17	54,54,54,54	0
56	MG	DA	3454	1/1	0.89	0.13	56,56,56,56	0
56	MG	AA	3004	1/1	0.89	0.14	66,66,66,66	0
56	MG	CA	3045	1/1	0.89	0.31	68,68,68,68	0
56	MG	DA	3459	1/1	0.89	0.12	44,44,44,44	0
56	MG	CA	3047	1/1	0.89	0.13	59,59,59,59	0
56	MG	CA	3049	1/1	0.89	0.12	71,71,71,71	0
56	MG	DA	3017	1/1	0.89	0.15	56,56,56,56	0
56	MG	DA	3472	1/1	0.89	0.20	60,60,60,60	0
56	MG	BA	3576	1/1	0.89	0.13	36,36,36,36	0
56	MG	BA	3055	1/1	0.89	0.31	55,55,55,55	0
56	MG	DA	3057	1/1	0.89	0.09	55,55,55,55	0
56	MG	BA	3396	1/1	0.89	0.09	41,41,41,41	0
56	MG	DA	3494	1/1	0.89	0.20	57,57,57,57	0
56	MG	CA	3058	1/1	0.89	0.19	59,59,59,59	0
56	MG	BA	3059	1/1	0.89	0.15	49,49,49,49	0
56	MG	DA	3510	1/1	0.89	0.09	55,55,55,55	0
56	MG	DA	3512	1/1	0.89	0.10	48,48,48,48	0
56	MG	BA	3740	1/1	0.89	0.10	35,35,35,35	0
56	MG	BA	3741	1/1	0.89	0.12	50,50,50,50	0
56	MG	BA	3584	1/1	0.89	0.14	34,34,34,34	0
56	MG	AA	3162	1/1	0.89	0.14	59,59,59,59	0
56	MG	DA	3115	1/1	0.89	0.17	46,46,46,46	0
56	MG	DA	3118	1/1	0.89	0.20	43,43,43,43	0
56	MG	AA	3104	1/1	0.89	0.33	70,70,70,70	0
56	MG	DA	3542	1/1	0.89	0.23	58,58,58,58	0
56	MG	BA	3225	1/1	0.89	0.13	31,31,31,31	0
56	MG	DA	3132	1/1	0.89	0.12	54,54,54,54	0
56	MG	DA	3146	1/1	0.89	0.18	49,49,49,49	0
56	MG	AA	3097	1/1	0.89	0.41	71,71,71,71	0
56	MG	BA	3242	1/1	0.89	0.09	47,47,47,47	0
56	MG	BA	3606	1/1	0.89	0.19	67,67,67,67	0
56	MG	BA	3452	1/1	0.89	0.18	55,55,55,55	0
56	MG	BA	3255	1/1	0.89	0.14	41,41,41,41	0
56	MG	DA	3218	1/1	0.89	0.14	30,30,30,30	0
56	MG	BA	3457	1/1	0.89	0.17	47,47,47,47	0
56	MG	BA	3092	1/1	0.89	0.13	53,53,53,53	0
56	MG	DA	3225	1/1	0.89	0.12	49,49,49,49	0
56	MG	BA	3464	1/1	0.89	0.10	46,46,46,46	0
56	MG	DA	3240	1/1	0.89	0.09	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3634	1/1	0.89	0.21	47,47,47,47	0
56	MG	BA	3639	1/1	0.89	0.11	54,54,54,54	0
56	MG	AA	3142	1/1	0.89	0.14	46,46,46,46	0
56	MG	DA	3264	1/1	0.89	0.24	50,50,50,50	0
56	MG	AA	3130	1/1	0.89	0.15	56,56,56,56	0
56	MG	AA	3055	1/1	0.89	0.40	69,69,69,69	0
56	MG	AX	3003	1/1	0.89	0.29	66,66,66,66	0
56	MG	DA	3630	1/1	0.89	0.16	51,51,51,51	0
56	MG	BA	3292	1/1	0.89	0.17	40,40,40,40	0
56	MG	AA	3001	1/1	0.89	0.16	77,77,77,77	0
56	MG	DA	3309	1/1	0.89	0.13	46,46,46,46	0
56	MG	DA	3637	1/1	0.89	0.06	70,70,70,70	0
56	MG	BA	3666	1/1	0.89	0.09	47,47,47,47	0
56	MG	CA	3118	1/1	0.89	0.19	60,60,60,60	0
56	MG	DA	3322	1/1	0.89	0.17	53,53,53,53	0
56	MG	BF	304	1/1	0.89	0.12	35,35,35,35	0
56	MG	DA	3654	1/1	0.89	0.14	50,50,50,50	0
56	MG	BA	3295	1/1	0.89	0.18	49,49,49,49	0
56	MG	CA	3127	1/1	0.89	0.32	65,65,65,65	0
56	MG	AA	3156	1/1	0.89	0.13	67,67,67,67	0
56	MG	DA	3665	1/1	0.89	0.14	48,48,48,48	0
56	MG	BA	3315	1/1	0.89	0.21	59,59,59,59	0
56	MG	B0	105	1/1	0.89	0.13	64,64,64,64	0
56	MG	DA	3673	1/1	0.89	0.18	68,68,68,68	0
56	MG	DA	3365	1/1	0.89	0.11	56,56,56,56	0
56	MG	DA	3376	1/1	0.89	0.15	51,51,51,51	0
56	MG	CA	3132	1/1	0.89	0.24	55,55,55,55	0
56	MG	DA	3388	1/1	0.89	0.10	52,52,52,52	0
56	MG	DG	3001	1/1	0.89	0.15	57,57,57,57	0
56	MG	DP	202	1/1	0.89	0.23	55,55,55,55	0
56	MG	DV	3002	1/1	0.89	0.20	48,48,48,48	0
56	MG	BA	3682	1/1	0.89	0.19	39,39,39,39	0
56	MG	DW	201	1/1	0.89	0.12	67,67,67,67	0
56	MG	BA	3125	1/1	0.89	0.15	49,49,49,49	0
56	MG	DA	3399	1/1	0.89	0.12	55,55,55,55	0
56	MG	BA	3547	1/1	0.89	0.09	64,64,64,64	0
60	K	CX	3001	1/1	0.89	0.14	77,77,77,77	0
56	MG	BA	3290	1/1	0.90	0.23	50,50,50,50	0
56	MG	AA	3025	1/1	0.90	0.30	69,69,69,69	0
56	MG	CA	3163	1/1	0.90	0.10	78,78,78,78	0
56	MG	BA	3121	1/1	0.90	0.14	45,45,45,45	0
56	MG	AA	3026	1/1	0.90	0.18	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	AA	3008	1/1	0.90	0.07	56,56,56,56	0
56	MG	BA	3529	1/1	0.90	0.15	25,25,25,25	0
56	MG	BA	3310	1/1	0.90	0.10	42,42,42,42	0
56	MG	CA	3032	1/1	0.90	0.11	57,57,57,57	0
56	MG	BA	3312	1/1	0.90	0.12	35,35,35,35	0
56	MG	BA	3706	1/1	0.90	0.08	63,63,63,63	0
56	MG	BA	3039	1/1	0.90	0.22	58,58,58,58	0
56	MG	BA	3319	1/1	0.90	0.12	39,39,39,39	0
56	MG	DA	3442	1/1	0.90	0.10	37,37,37,37	0
56	MG	DA	3443	1/1	0.90	0.17	38,38,38,38	0
56	MG	DA	3032	1/1	0.90	0.08	47,47,47,47	0
56	MG	DA	3033	1/1	0.90	0.11	54,54,54,54	0
56	MG	DA	3453	1/1	0.90	0.18	56,56,56,56	0
56	MG	BA	3356	1/1	0.90	0.19	52,52,52,52	0
56	MG	BA	3162	1/1	0.90	0.15	53,53,53,53	0
56	MG	BA	3363	1/1	0.90	0.10	66,66,66,66	0
56	MG	AA	3149	1/1	0.90	0.12	68,68,68,68	0
56	MG	BA	3733	1/1	0.90	0.08	46,46,46,46	0
56	MG	DA	3076	1/1	0.90	0.11	39,39,39,39	0
56	MG	BA	3377	1/1	0.90	0.17	48,48,48,48	0
56	MG	DA	3089	1/1	0.90	0.14	47,47,47,47	0
56	MG	CA	3059	1/1	0.90	0.15	75,75,75,75	0
56	MG	DA	3100	1/1	0.90	0.29	66,66,66,66	0
56	MG	BA	3578	1/1	0.90	0.13	20,20,20,20	0
56	MG	AA	3174	1/1	0.90	0.11	54,54,54,54	0
56	MG	DA	3489	1/1	0.90	0.12	45,45,45,45	0
56	MG	DA	3493	1/1	0.90	0.25	63,63,63,63	0
56	MG	BA	3048	1/1	0.90	0.21	47,47,47,47	0
56	MG	BA	3193	1/1	0.90	0.27	62,62,62,62	0
56	MG	CA	3072	1/1	0.90	0.34	62,62,62,62	0
56	MG	AA	3091	1/1	0.90	0.13	40,40,40,40	0
56	MG	BA	3587	1/1	0.90	0.09	54,54,54,54	0
56	MG	BA	3590	1/1	0.90	0.20	60,60,60,60	0
56	MG	DA	3135	1/1	0.90	0.24	46,46,46,46	0
56	MG	BA	3195	1/1	0.90	0.26	52,52,52,52	0
56	MG	DA	3531	1/1	0.90	0.14	62,62,62,62	0
56	MG	BA	3056	1/1	0.90	0.08	50,50,50,50	0
56	MG	BA	3204	1/1	0.90	0.13	55,55,55,55	0
56	MG	DA	3184	1/1	0.90	0.15	49,49,49,49	0
56	MG	CA	3085	1/1	0.90	0.23	73,73,73,73	0
56	MG	DA	3194	1/1	0.90	0.18	54,54,54,54	0
56	MG	DA	3201	1/1	0.90	0.31	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3548	1/1	0.90	0.12	55,55,55,55	0
56	MG	DA	3549	1/1	0.90	0.12	32,32,32,32	0
56	MG	BA	3399	1/1	0.90	0.15	61,61,61,61	0
56	MG	BA	3211	1/1	0.90	0.18	41,41,41,41	0
56	MG	DA	3212	1/1	0.90	0.17	54,54,54,54	0
56	MG	DA	3214	1/1	0.90	0.27	51,51,51,51	0
56	MG	BA	3422	1/1	0.90	0.15	53,53,53,53	0
56	MG	DA	3570	1/1	0.90	0.11	59,59,59,59	0
56	MG	AA	3057	1/1	0.90	0.43	66,66,66,66	0
56	MG	BA	3219	1/1	0.90	0.12	62,62,62,62	0
56	MG	BA	3789	1/1	0.90	0.16	37,37,37,37	0
56	MG	DA	3226	1/1	0.90	0.17	57,57,57,57	0
56	MG	AA	3096	1/1	0.90	0.39	60,60,60,60	0
56	MG	DA	3233	1/1	0.90	0.14	40,40,40,40	0
56	MG	DA	3234	1/1	0.90	0.22	56,56,56,56	0
56	MG	DA	3239	1/1	0.90	0.20	51,51,51,51	0
56	MG	BA	3806	1/1	0.90	0.32	33,33,33,33	0
56	MG	BA	3618	1/1	0.90	0.11	56,56,56,56	0
56	MG	AA	3010	1/1	0.90	0.13	63,63,63,63	0
56	MG	DA	3616	1/1	0.90	0.10	43,43,43,43	0
56	MG	BA	3237	1/1	0.90	0.37	63,63,63,63	0
56	MG	DA	3260	1/1	0.90	0.30	55,55,55,55	0
56	MG	DA	3624	1/1	0.90	0.23	46,46,46,46	0
56	MG	BA	3631	1/1	0.90	0.21	49,49,49,49	0
56	MG	AA	3158	1/1	0.90	0.12	71,71,71,71	0
56	MG	BA	3636	1/1	0.90	0.14	52,52,52,52	0
56	MG	BA	3453	1/1	0.90	0.21	52,52,52,52	0
56	MG	DA	3278	1/1	0.90	0.12	37,37,37,37	0
56	MG	DA	3282	1/1	0.90	0.19	42,42,42,42	0
56	MG	AA	3066	1/1	0.90	0.23	58,58,58,58	0
56	MG	DA	3639	1/1	0.90	0.15	52,52,52,52	0
56	MG	CA	3123	1/1	0.90	0.16	67,67,67,67	0
56	MG	DA	3643	1/1	0.90	0.18	49,49,49,49	0
56	MG	DA	3305	1/1	0.90	0.13	45,45,45,45	0
56	MG	BA	3250	1/1	0.90	0.22	42,42,42,42	0
56	MG	CA	3125	1/1	0.90	0.08	63,63,63,63	0
56	MG	DA	3652	1/1	0.90	0.18	53,53,53,53	0
56	MG	DA	3320	1/1	0.90	0.12	34,34,34,34	0
56	MG	AD	502	1/1	0.90	0.28	56,56,56,56	0
56	MG	BA	3654	1/1	0.90	0.13	49,49,49,49	0
56	MG	BU	201	1/1	0.90	0.12	36,36,36,36	0
56	MG	BU	206	1/1	0.90	0.42	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BZ	301	1/1	0.90	0.13	58,58,58,58	0
56	MG	AA	3017	1/1	0.90	0.34	69,69,69,69	0
56	MG	DA	3343	1/1	0.90	0.14	42,42,42,42	0
56	MG	DA	3344	1/1	0.90	0.13	46,46,46,46	0
56	MG	DB	3002	1/1	0.90	0.20	58,58,58,58	0
56	MG	DA	3345	1/1	0.90	0.13	38,38,38,38	0
56	MG	BA	3103	1/1	0.90	0.11	44,44,44,44	0
56	MG	BA	3479	1/1	0.90	0.11	53,53,53,53	0
56	MG	DE	302	1/1	0.90	0.10	33,33,33,33	0
56	MG	BA	3495	1/1	0.90	0.11	58,58,58,58	0
56	MG	DP	201	1/1	0.90	0.24	58,58,58,58	0
56	MG	CA	3143	1/1	0.90	0.24	77,77,77,77	0
56	MG	AA	3019	1/1	0.90	0.14	66,66,66,66	0
56	MG	AX	3006	1/1	0.90	0.17	71,71,71,71	0
56	MG	BA	3277	1/1	0.90	0.20	54,54,54,54	0
56	MG	BA	3678	1/1	0.90	0.28	35,35,35,35	0
56	MG	DA	3398	1/1	0.90	0.29	52,52,52,52	0
56	MG	AA	3011	1/1	0.90	0.20	56,56,56,56	0
56	MG	CA	3010	1/1	0.90	0.24	57,57,57,57	0
56	MG	BA	3019	1/1	0.91	0.11	39,39,39,39	0
56	MG	CA	3160	1/1	0.91	0.20	61,61,61,61	0
56	MG	CA	3162	1/1	0.91	0.08	42,42,42,42	0
56	MG	BA	3318	1/1	0.91	0.08	25,25,25,25	0
56	MG	DA	3391	1/1	0.91	0.07	44,44,44,44	0
56	MG	BA	3020	1/1	0.91	0.13	36,36,36,36	0
56	MG	BA	3685	1/1	0.91	0.14	51,51,51,51	0
56	MG	BA	3687	1/1	0.91	0.18	53,53,53,53	0
56	MG	BA	3321	1/1	0.91	0.11	21,21,21,21	0
56	MG	BA	3534	1/1	0.91	0.12	44,44,44,44	0
56	MG	DA	3405	1/1	0.91	0.10	41,41,41,41	0
56	MG	BA	3355	1/1	0.91	0.14	28,28,28,28	0
56	MG	AA	3095	1/1	0.91	0.17	50,50,50,50	0
56	MG	BA	3180	1/1	0.91	0.24	46,46,46,46	0
56	MG	AA	3168	1/1	0.91	0.10	57,57,57,57	0
56	MG	CX	3003	1/1	0.91	0.14	58,58,58,58	0
56	MG	DA	3014	1/1	0.91	0.07	43,43,43,43	0
56	MG	DA	3424	1/1	0.91	0.12	41,41,41,41	0
56	MG	DA	3015	1/1	0.91	0.21	48,48,48,48	0
56	MG	BA	3700	1/1	0.91	0.11	53,53,53,53	0
56	MG	DA	3019	1/1	0.91	0.11	48,48,48,48	0
56	MG	BA	3368	1/1	0.91	0.12	35,35,35,35	0
56	MG	BA	3186	1/1	0.91	0.13	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	AA	3033	1/1	0.91	0.30	58,58,58,58	0
56	MG	DA	3037	1/1	0.91	0.09	34,34,34,34	0
56	MG	AA	3021	1/1	0.91	0.19	62,62,62,62	0
56	MG	DA	3046	1/1	0.91	0.21	56,56,56,56	0
56	MG	CA	3041	1/1	0.91	0.34	62,62,62,62	0
56	MG	BA	3715	1/1	0.91	0.13	51,51,51,51	0
56	MG	AA	3070	1/1	0.91	0.18	65,65,65,65	0
56	MG	DA	3066	1/1	0.91	0.21	47,47,47,47	0
56	MG	DA	3068	1/1	0.91	0.14	47,47,47,47	0
56	MG	AA	3022	1/1	0.91	0.07	54,54,54,54	0
56	MG	BA	3719	1/1	0.91	0.11	36,36,36,36	0
56	MG	DA	3087	1/1	0.91	0.10	50,50,50,50	0
56	MG	BA	3720	1/1	0.91	0.12	45,45,45,45	0
56	MG	DA	3091	1/1	0.91	0.15	46,46,46,46	0
56	MG	AA	3054	1/1	0.91	0.15	62,62,62,62	0
56	MG	BA	3724	1/1	0.91	0.09	25,25,25,25	0
56	MG	DA	3482	1/1	0.91	0.12	42,42,42,42	0
56	MG	BA	3050	1/1	0.91	0.15	46,46,46,46	0
56	MG	CA	3057	1/1	0.91	0.16	52,52,52,52	0
56	MG	AA	3076	1/1	0.91	0.08	56,56,56,56	0
56	MG	BA	3731	1/1	0.91	0.07	26,26,26,26	0
56	MG	DA	3116	1/1	0.91	0.13	48,48,48,48	0
56	MG	BA	3395	1/1	0.91	0.14	36,36,36,36	0
56	MG	BA	3735	1/1	0.91	0.08	20,20,20,20	0
56	MG	DA	3128	1/1	0.91	0.23	57,57,57,57	0
56	MG	DA	3511	1/1	0.91	0.15	54,54,54,54	0
56	MG	DA	3129	1/1	0.91	0.14	42,42,42,42	0
56	MG	DA	3517	1/1	0.91	0.09	57,57,57,57	0
56	MG	BA	3736	1/1	0.91	0.10	42,42,42,42	0
56	MG	BA	3585	1/1	0.91	0.08	58,58,58,58	0
56	MG	CA	3068	1/1	0.91	0.30	64,64,64,64	0
56	MG	AA	3077	1/1	0.91	0.25	54,54,54,54	0
56	MG	CA	3073	1/1	0.91	0.16	55,55,55,55	0
56	MG	DA	3168	1/1	0.91	0.07	47,47,47,47	0
56	MG	DA	3536	1/1	0.91	0.08	44,44,44,44	0
56	MG	AA	3039	1/1	0.91	0.09	46,46,46,46	0
56	MG	DA	3181	1/1	0.91	0.27	54,54,54,54	0
56	MG	DA	3182	1/1	0.91	0.07	43,43,43,43	0
56	MG	CA	3077	1/1	0.91	0.31	61,61,61,61	0
56	MG	BA	3411	1/1	0.91	0.17	30,30,30,30	0
56	MG	DA	3186	1/1	0.91	0.27	54,54,54,54	0
56	MG	DA	3556	1/1	0.91	0.14	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3187	1/1	0.91	0.27	51,51,51,51	0
56	MG	AA	3181	1/1	0.91	0.19	63,63,63,63	0
56	MG	DA	3200	1/1	0.91	0.21	57,57,57,57	0
56	MG	DA	3565	1/1	0.91	0.18	45,45,45,45	0
56	MG	BA	3596	1/1	0.91	0.20	68,68,68,68	0
56	MG	BA	3597	1/1	0.91	0.13	40,40,40,40	0
56	MG	DA	3210	1/1	0.91	0.14	53,53,53,53	0
56	MG	DA	3574	1/1	0.91	0.12	55,55,55,55	0
56	MG	BA	3229	1/1	0.91	0.13	44,44,44,44	0
56	MG	BA	3754	1/1	0.91	0.17	60,60,60,60	0
56	MG	AA	3182	1/1	0.91	0.25	64,64,64,64	0
56	MG	BA	3431	1/1	0.91	0.10	63,63,63,63	0
56	MG	AA	3155	1/1	0.91	0.15	49,49,49,49	0
56	MG	AA	3056	1/1	0.91	0.29	54,54,54,54	0
56	MG	AA	3002	1/1	0.91	0.15	63,63,63,63	0
56	MG	BA	3615	1/1	0.91	0.13	60,60,60,60	0
56	MG	BA	3254	1/1	0.91	0.22	55,55,55,55	0
56	MG	DA	3608	1/1	0.91	0.07	47,47,47,47	0
56	MG	CA	3094	1/1	0.91	0.40	68,68,68,68	0
56	MG	BA	3771	1/1	0.91	0.19	52,52,52,52	0
56	MG	AA	3187	1/1	0.91	0.14	54,54,54,54	0
56	MG	BA	3778	1/1	0.91	0.14	41,41,41,41	0
56	MG	DA	3242	1/1	0.91	0.28	68,68,68,68	0
56	MG	BA	3781	1/1	0.91	0.14	47,47,47,47	0
56	MG	BA	3622	1/1	0.91	0.10	29,29,29,29	0
56	MG	DA	3627	1/1	0.91	0.11	64,64,64,64	0
56	MG	DA	3256	1/1	0.91	0.13	46,46,46,46	0
56	MG	CA	3112	1/1	0.91	0.16	56,56,56,56	0
56	MG	AA	3085	1/1	0.91	0.26	66,66,66,66	0
56	MG	BA	3800	1/1	0.91	0.09	41,41,41,41	0
56	MG	AE	202	1/1	0.91	0.09	74,74,74,74	0
56	MG	DA	3635	1/1	0.91	0.19	47,47,47,47	0
56	MG	AF	3001	1/1	0.91	0.16	56,56,56,56	0
56	MG	AA	3087	1/1	0.91	0.34	53,53,53,53	0
56	MG	BA	3461	1/1	0.91	0.08	62,62,62,62	0
56	MG	DA	3279	1/1	0.91	0.27	54,54,54,54	0
56	MG	DA	3646	1/1	0.91	0.15	54,54,54,54	0
56	MG	DA	3280	1/1	0.91	0.28	62,62,62,62	0
56	MG	BB	206	1/1	0.91	0.18	58,58,58,58	0
56	MG	AA	3018	1/1	0.91	0.17	50,50,50,50	0
56	MG	BA	3280	1/1	0.91	0.08	32,32,32,32	0
56	MG	DA	3293	1/1	0.91	0.20	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3294	1/1	0.91	0.08	36,36,36,36	0
56	MG	BB	216	1/1	0.91	0.21	63,63,63,63	0
56	MG	BB	219	1/1	0.91	0.11	74,74,74,74	0
56	MG	DA	3664	1/1	0.91	0.25	50,50,50,50	0
56	MG	DA	3310	1/1	0.91	0.10	49,49,49,49	0
56	MG	DA	3316	1/1	0.91	0.08	34,34,34,34	0
56	MG	BA	3646	1/1	0.91	0.12	57,57,57,57	0
56	MG	BA	3120	1/1	0.91	0.09	50,50,50,50	0
56	MG	BA	3649	1/1	0.91	0.09	44,44,44,44	0
56	MG	BE	307	1/1	0.91	0.08	31,31,31,31	0
56	MG	BA	3492	1/1	0.91	0.09	47,47,47,47	0
56	MG	DB	3009	1/1	0.91	0.21	58,58,58,58	0
56	MG	DB	3010	1/1	0.91	0.23	53,53,53,53	0
56	MG	DA	3326	1/1	0.91	0.15	47,47,47,47	0
56	MG	AA	3165	1/1	0.91	0.16	49,49,49,49	0
56	MG	DA	3338	1/1	0.91	0.13	43,43,43,43	0
56	MG	AA	3061	1/1	0.91	0.19	54,54,54,54	0
56	MG	CA	3147	1/1	0.91	0.24	70,70,70,70	0
56	MG	BA	3133	1/1	0.91	0.12	48,48,48,48	0
56	MG	AX	3009	1/1	0.91	0.18	74,74,74,74	0
56	MG	BA	3137	1/1	0.91	0.21	40,40,40,40	0
56	MG	BA	3147	1/1	0.91	0.09	41,41,41,41	0
56	MG	AX	3010	1/1	0.91	0.11	59,59,59,59	0
56	MG	BA	3674	1/1	0.91	0.14	55,55,55,55	0
56	MG	DA	3369	1/1	0.91	0.09	37,37,37,37	0
56	MG	DA	3370	1/1	0.91	0.08	50,50,50,50	0
56	MG	DA	3415	1/1	0.92	0.13	59,59,59,59	0
56	MG	BA	3632	1/1	0.92	0.21	43,43,43,43	0
56	MG	DA	3079	1/1	0.92	0.08	32,32,32,32	0
56	MG	BA	3633	1/1	0.92	0.14	59,59,59,59	0
56	MG	AA	3029	1/1	0.92	0.17	43,43,43,43	0
56	MG	AA	3144	1/1	0.92	0.19	59,59,59,59	0
56	MG	AA	3189	1/1	0.92	0.32	62,62,62,62	0
56	MG	BA	3643	1/1	0.92	0.13	58,58,58,58	0
56	MG	DA	3430	1/1	0.92	0.10	52,52,52,52	0
56	MG	BA	3360	1/1	0.92	0.09	21,21,21,21	0
56	MG	BA	3645	1/1	0.92	0.09	50,50,50,50	0
56	MG	DA	3106	1/1	0.92	0.07	52,52,52,52	0
56	MG	DA	3107	1/1	0.92	0.12	43,43,43,43	0
56	MG	BA	3222	1/1	0.92	0.08	48,48,48,48	0
56	MG	BA	3779	1/1	0.92	0.09	45,45,45,45	0
56	MG	CA	3079	1/1	0.92	0.48	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3122	1/1	0.92	0.23	46,46,46,46	0
56	MG	AA	3146	1/1	0.92	0.23	53,53,53,53	0
56	MG	DA	3450	1/1	0.92	0.12	41,41,41,41	0
56	MG	BA	3792	1/1	0.92	0.11	52,52,52,52	0
56	MG	BA	3231	1/1	0.92	0.12	51,51,51,51	0
56	MG	BA	3795	1/1	0.92	0.18	43,43,43,43	0
56	MG	BA	3796	1/1	0.92	0.15	47,47,47,47	0
56	MG	AA	3041	1/1	0.92	0.14	64,64,64,64	0
56	MG	BA	3656	1/1	0.92	0.14	64,64,64,64	0
56	MG	CA	3089	1/1	0.92	0.28	67,67,67,67	0
56	MG	DA	3147	1/1	0.92	0.17	53,53,53,53	0
56	MG	BA	3807	1/1	0.92	0.18	66,66,66,66	0
56	MG	DA	3152	1/1	0.92	0.10	62,62,62,62	0
56	MG	BA	3054	1/1	0.92	0.18	43,43,43,43	0
56	MG	DA	3170	1/1	0.92	0.20	46,46,46,46	0
56	MG	BA	3537	1/1	0.92	0.12	21,21,21,21	0
56	MG	BA	3538	1/1	0.92	0.10	26,26,26,26	0
56	MG	BA	3545	1/1	0.92	0.07	36,36,36,36	0
56	MG	AA	3030	1/1	0.92	0.12	63,63,63,63	0
56	MG	BA	3551	1/1	0.92	0.16	49,49,49,49	0
56	MG	BA	3246	1/1	0.92	0.09	47,47,47,47	0
56	MG	DA	3501	1/1	0.92	0.08	46,46,46,46	0
56	MG	BA	3247	1/1	0.92	0.18	50,50,50,50	0
56	MG	DA	3504	1/1	0.92	0.12	41,41,41,41	0
56	MG	DA	3192	1/1	0.92	0.08	57,57,57,57	0
56	MG	BA	3559	1/1	0.92	0.08	59,59,59,59	0
56	MG	BA	3144	1/1	0.92	0.12	43,43,43,43	0
56	MG	DA	3513	1/1	0.92	0.08	30,30,30,30	0
56	MG	BA	3251	1/1	0.92	0.32	52,52,52,52	0
56	MG	BA	3252	1/1	0.92	0.17	44,44,44,44	0
56	MG	AA	3064	1/1	0.92	0.07	54,54,54,54	0
56	MG	CA	3120	1/1	0.92	0.18	65,65,65,65	0
56	MG	BF	306	1/1	0.92	0.20	30,30,30,30	0
56	MG	DA	3213	1/1	0.92	0.09	46,46,46,46	0
56	MG	BG	3002	1/1	0.92	0.08	50,50,50,50	0
56	MG	DA	3215	1/1	0.92	0.31	49,49,49,49	0
56	MG	BN	3002	1/1	0.92	0.12	57,57,57,57	0
56	MG	BA	3572	1/1	0.92	0.10	52,52,52,52	0
56	MG	BA	3401	1/1	0.92	0.15	34,34,34,34	0
56	MG	DA	3545	1/1	0.92	0.11	51,51,51,51	0
56	MG	BA	3151	1/1	0.92	0.08	37,37,37,37	0
56	MG	BA	3417	1/1	0.92	0.13	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3419	1/1	0.92	0.09	25,25,25,25	0
56	MG	DA	3554	1/1	0.92	0.13	47,47,47,47	0
56	MG	DA	3230	1/1	0.92	0.21	52,52,52,52	0
56	MG	BZ	302	1/1	0.92	0.23	56,56,56,56	0
56	MG	BA	3256	1/1	0.92	0.13	54,54,54,54	0
56	MG	DA	3236	1/1	0.92	0.10	42,42,42,42	0
56	MG	DA	3564	1/1	0.92	0.08	50,50,50,50	0
56	MG	BA	3157	1/1	0.92	0.39	36,36,36,36	0
56	MG	DA	3566	1/1	0.92	0.11	62,62,62,62	0
56	MG	AA	3129	1/1	0.92	0.14	70,70,70,70	0
56	MG	DA	3568	1/1	0.92	0.08	66,66,66,66	0
56	MG	B5	101	1/1	0.92	0.25	39,39,39,39	0
56	MG	DA	3243	1/1	0.92	0.10	47,47,47,47	0
56	MG	DA	3244	1/1	0.92	0.30	59,59,59,59	0
56	MG	BA	3062	1/1	0.92	0.09	48,48,48,48	0
56	MG	DA	3577	1/1	0.92	0.11	49,49,49,49	0
56	MG	AA	3154	1/1	0.92	0.18	50,50,50,50	0
56	MG	CA	3002	1/1	0.92	0.14	62,62,62,62	0
56	MG	DA	3584	1/1	0.92	0.12	31,31,31,31	0
56	MG	BA	3168	1/1	0.92	0.10	39,39,39,39	0
56	MG	DA	3258	1/1	0.92	0.32	51,51,51,51	0
56	MG	DA	3594	1/1	0.92	0.11	54,54,54,54	0
56	MG	DA	3597	1/1	0.92	0.07	49,49,49,49	0
56	MG	DA	3259	1/1	0.92	0.30	53,53,53,53	0
56	MG	BA	3439	1/1	0.92	0.10	71,71,71,71	0
56	MG	DA	3605	1/1	0.92	0.10	54,54,54,54	0
56	MG	BA	3172	1/1	0.92	0.12	52,52,52,52	0
56	MG	CA	3008	1/1	0.92	0.40	60,60,60,60	0
56	MG	CA	3153	1/1	0.92	0.13	52,52,52,52	0
56	MG	AA	3176	1/1	0.92	0.14	57,57,57,57	0
56	MG	CA	3157	1/1	0.92	0.19	61,61,61,61	0
56	MG	AA	3046	1/1	0.92	0.27	56,56,56,56	0
56	MG	AA	3134	1/1	0.92	0.10	65,65,65,65	0
56	MG	AA	3103	1/1	0.92	0.20	48,48,48,48	0
56	MG	BA	3192	1/1	0.92	0.10	53,53,53,53	0
56	MG	DA	3625	1/1	0.92	0.15	56,56,56,56	0
56	MG	CA	3016	1/1	0.92	0.21	53,53,53,53	0
56	MG	DA	3291	1/1	0.92	0.11	41,41,41,41	0
56	MG	BA	3726	1/1	0.92	0.17	65,65,65,65	0
56	MG	AA	3092	1/1	0.92	0.36	54,54,54,54	0
56	MG	CA	3024	1/1	0.92	0.23	58,58,58,58	0
56	MG	BA	3100	1/1	0.92	0.27	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	CA	3026	1/1	0.92	0.18	55,55,55,55	0
56	MG	CA	3029	1/1	0.92	0.15	58,58,58,58	0
56	MG	BA	3611	1/1	0.92	0.09	45,45,45,45	0
56	MG	DA	3638	1/1	0.92	0.10	42,42,42,42	0
56	MG	BA	3026	1/1	0.92	0.17	49,49,49,49	0
56	MG	BA	3613	1/1	0.92	0.19	55,55,55,55	0
56	MG	CA	3039	1/1	0.92	0.20	55,55,55,55	0
56	MG	DA	3645	1/1	0.92	0.08	38,38,38,38	0
56	MG	DA	3002	1/1	0.92	0.19	55,55,55,55	0
56	MG	DA	3325	1/1	0.92	0.08	37,37,37,37	0
56	MG	DA	3006	1/1	0.92	0.40	58,58,58,58	0
56	MG	CA	3040	1/1	0.92	0.15	45,45,45,45	0
56	MG	BA	3614	1/1	0.92	0.30	59,59,59,59	0
56	MG	BA	3197	1/1	0.92	0.25	51,51,51,51	0
56	MG	BA	3739	1/1	0.92	0.12	46,46,46,46	0
56	MG	DA	3026	1/1	0.92	0.11	52,52,52,52	0
56	MG	BA	3616	1/1	0.92	0.13	51,51,51,51	0
56	MG	BA	3478	1/1	0.92	0.13	59,59,59,59	0
56	MG	AA	3015	1/1	0.92	0.07	65,65,65,65	0
56	MG	DA	3360	1/1	0.92	0.14	37,37,37,37	0
56	MG	DA	3036	1/1	0.92	0.14	46,46,46,46	0
56	MG	CA	3051	1/1	0.92	0.32	55,55,55,55	0
56	MG	DA	3367	1/1	0.92	0.14	55,55,55,55	0
56	MG	DA	3043	1/1	0.92	0.12	52,52,52,52	0
56	MG	DB	3003	1/1	0.92	0.10	56,56,56,56	0
56	MG	DB	3004	1/1	0.92	0.20	53,53,53,53	0
56	MG	DB	3006	1/1	0.92	0.26	60,60,60,60	0
56	MG	AA	3106	1/1	0.92	0.09	61,61,61,61	0
56	MG	DA	3372	1/1	0.92	0.09	24,24,24,24	0
56	MG	AA	3079	1/1	0.92	0.33	55,55,55,55	0
56	MG	DA	3052	1/1	0.92	0.05	26,26,26,26	0
56	MG	DD	306	1/1	0.92	0.46	48,48,48,48	0
56	MG	DA	3385	1/1	0.92	0.06	32,32,32,32	0
56	MG	DA	3054	1/1	0.92	0.08	39,39,39,39	0
56	MG	BA	3496	1/1	0.92	0.14	59,59,59,59	0
56	MG	DO	5001	1/1	0.92	0.18	55,55,55,55	0
56	MG	CA	3055	1/1	0.92	0.23	55,55,55,55	0
56	MG	DA	3061	1/1	0.92	0.06	41,41,41,41	0
56	MG	DR	5001	1/1	0.92	0.12	51,51,51,51	0
56	MG	DU	3001	1/1	0.92	0.21	55,55,55,55	0
56	MG	DU	3004	1/1	0.92	0.18	59,59,59,59	0
56	MG	DA	3393	1/1	0.92	0.07	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3750	1/1	0.92	0.16	42,42,42,42	0
56	MG	BA	3629	1/1	0.92	0.20	57,57,57,57	0
56	MG	DW	202	1/1	0.92	0.15	46,46,46,46	0
56	MG	BA	3344	1/1	0.92	0.23	55,55,55,55	0
56	MG	D1	101	1/1	0.92	0.13	50,50,50,50	0
56	MG	D8	5001	1/1	0.92	0.18	52,52,52,52	0
56	MG	DA	3070	1/1	0.92	0.14	51,51,51,51	0
56	MG	DA	3073	1/1	0.92	0.25	55,55,55,55	0
56	MG	DA	3074	1/1	0.92	0.14	56,56,56,56	0
56	MG	BA	3485	1/1	0.93	0.09	55,55,55,55	0
56	MG	DA	3148	1/1	0.93	0.17	43,43,43,43	0
56	MG	DA	3444	1/1	0.93	0.09	46,46,46,46	0
56	MG	CA	3121	1/1	0.93	0.09	81,81,81,81	0
56	MG	BA	3366	1/1	0.93	0.09	42,42,42,42	0
56	MG	DA	3163	1/1	0.93	0.21	54,54,54,54	0
56	MG	DA	3166	1/1	0.93	0.17	35,35,35,35	0
56	MG	BA	3190	1/1	0.93	0.19	50,50,50,50	0
56	MG	BA	3191	1/1	0.93	0.18	43,43,43,43	0
56	MG	DA	3457	1/1	0.93	0.11	43,43,43,43	0
56	MG	DA	3172	1/1	0.93	0.11	31,31,31,31	0
56	MG	CA	3001	1/1	0.93	0.08	59,59,59,59	0
56	MG	DA	3180	1/1	0.93	0.12	58,58,58,58	0
56	MG	BA	3375	1/1	0.93	0.12	38,38,38,38	0
56	MG	DA	3467	1/1	0.93	0.25	48,48,48,48	0
56	MG	AA	3006	1/1	0.93	0.10	71,71,71,71	0
56	MG	DA	3470	1/1	0.93	0.15	31,31,31,31	0
56	MG	BA	3257	1/1	0.93	0.24	54,54,54,54	0
56	MG	BA	3002	1/1	0.93	0.14	57,57,57,57	0
56	MG	BA	3018	1/1	0.93	0.19	63,63,63,63	0
56	MG	AA	3101	1/1	0.93	0.18	49,49,49,49	0
56	MG	DA	3191	1/1	0.93	0.18	46,46,46,46	0
56	MG	DA	3485	1/1	0.93	0.11	43,43,43,43	0
56	MG	DA	3486	1/1	0.93	0.11	50,50,50,50	0
56	MG	CA	3135	1/1	0.93	0.16	63,63,63,63	0
56	MG	DA	3193	1/1	0.93	0.20	46,46,46,46	0
56	MG	DA	3491	1/1	0.93	0.07	42,42,42,42	0
56	MG	CA	3136	1/1	0.93	0.09	55,55,55,55	0
56	MG	DA	3195	1/1	0.93	0.14	58,58,58,58	0
56	MG	DA	3497	1/1	0.93	0.12	36,36,36,36	0
56	MG	DA	3198	1/1	0.93	0.10	49,49,49,49	0
56	MG	BA	3065	1/1	0.93	0.19	41,41,41,41	0
56	MG	BA	3519	1/1	0.93	0.20	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3276	1/1	0.93	0.07	42,42,42,42	0
56	MG	DA	3508	1/1	0.93	0.12	41,41,41,41	0
56	MG	DA	3509	1/1	0.93	0.14	55,55,55,55	0
56	MG	DA	3203	1/1	0.93	0.11	50,50,50,50	0
56	MG	BA	3523	1/1	0.93	0.17	47,47,47,47	0
56	MG	AA	3014	1/1	0.93	0.25	62,62,62,62	0
56	MG	CA	3146	1/1	0.93	0.18	65,65,65,65	0
56	MG	BA	3025	1/1	0.93	0.19	48,48,48,48	0
56	MG	DA	3518	1/1	0.93	0.15	58,58,58,58	0
56	MG	BA	3398	1/1	0.93	0.11	51,51,51,51	0
56	MG	CA	3022	1/1	0.93	0.30	60,60,60,60	0
56	MG	CA	3023	1/1	0.93	0.05	39,39,39,39	0
56	MG	DA	3220	1/1	0.93	0.09	50,50,50,50	0
56	MG	BA	3536	1/1	0.93	0.11	36,36,36,36	0
56	MG	BA	3637	1/1	0.93	0.14	54,54,54,54	0
56	MG	CA	3154	1/1	0.93	0.17	54,54,54,54	0
56	MG	BA	3638	1/1	0.93	0.18	56,56,56,56	0
56	MG	CA	3028	1/1	0.93	0.27	55,55,55,55	0
56	MG	AA	3044	1/1	0.93	0.34	55,55,55,55	0
56	MG	DA	3544	1/1	0.93	0.09	39,39,39,39	0
56	MG	DA	3231	1/1	0.93	0.17	38,38,38,38	0
56	MG	BA	3640	1/1	0.93	0.11	42,42,42,42	0
56	MG	CA	3031	1/1	0.93	0.14	59,59,59,59	0
56	MG	BA	3150	1/1	0.93	0.13	56,56,56,56	0
56	MG	CA	3034	1/1	0.93	0.18	51,51,51,51	0
56	MG	BA	3539	1/1	0.93	0.12	29,29,29,29	0
56	MG	DA	3241	1/1	0.93	0.10	48,48,48,48	0
56	MG	DA	3561	1/1	0.93	0.11	58,58,58,58	0
56	MG	CA	3165	1/1	0.93	0.10	60,60,60,60	0
56	MG	CA	3038	1/1	0.93	0.12	63,63,63,63	0
56	MG	BA	3764	1/1	0.93	0.13	44,44,44,44	0
56	MG	DA	3248	1/1	0.93	0.16	49,49,49,49	0
56	MG	BA	3541	1/1	0.93	0.15	55,55,55,55	0
56	MG	DA	3250	1/1	0.93	0.21	40,40,40,40	0
56	MG	BA	3544	1/1	0.93	0.16	45,45,45,45	0
56	MG	CA	3175	1/1	0.93	0.20	46,46,46,46	0
56	MG	BA	3410	1/1	0.93	0.16	31,31,31,31	0
56	MG	AA	3081	1/1	0.93	0.22	51,51,51,51	0
56	MG	AE	203	1/1	0.93	0.24	73,73,73,73	0
56	MG	DA	3576	1/1	0.93	0.17	50,50,50,50	0
56	MG	BA	3651	1/1	0.93	0.07	52,52,52,52	0
56	MG	DA	3580	1/1	0.93	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3262	1/1	0.93	0.14	46,46,46,46	0
56	MG	CA	3048	1/1	0.93	0.13	77,77,77,77	0
56	MG	AA	3062	1/1	0.93	0.21	67,67,67,67	0
56	MG	DA	3586	1/1	0.93	0.09	39,39,39,39	0
56	MG	CA	3050	1/1	0.93	0.19	52,52,52,52	0
56	MG	DA	3011	1/1	0.93	0.12	51,51,51,51	0
56	MG	DA	3593	1/1	0.93	0.07	50,50,50,50	0
56	MG	AQ	3001	1/1	0.93	0.20	52,52,52,52	0
56	MG	BA	3780	1/1	0.93	0.12	54,54,54,54	0
56	MG	BA	3297	1/1	0.93	0.22	46,46,46,46	0
56	MG	BA	3786	1/1	0.93	0.14	58,58,58,58	0
56	MG	DA	3285	1/1	0.93	0.25	52,52,52,52	0
56	MG	DA	3024	1/1	0.93	0.37	37,37,37,37	0
56	MG	BA	3787	1/1	0.93	0.20	57,57,57,57	0
56	MG	BA	3307	1/1	0.93	0.20	50,50,50,50	0
56	MG	DA	3292	1/1	0.93	0.12	40,40,40,40	0
56	MG	BA	3660	1/1	0.93	0.18	51,51,51,51	0
56	MG	DA	3615	1/1	0.93	0.09	50,50,50,50	0
56	MG	BA	3662	1/1	0.93	0.10	52,52,52,52	0
56	MG	BA	3430	1/1	0.93	0.11	31,31,31,31	0
56	MG	AA	3032	1/1	0.93	0.26	59,59,59,59	0
56	MG	DA	3039	1/1	0.93	0.11	44,44,44,44	0
56	MG	BA	3668	1/1	0.93	0.21	48,48,48,48	0
56	MG	DA	3318	1/1	0.93	0.10	33,33,33,33	0
56	MG	BA	3166	1/1	0.93	0.16	46,46,46,46	0
56	MG	BA	3233	1/1	0.93	0.16	61,61,61,61	0
56	MG	AA	3135	1/1	0.93	0.10	60,60,60,60	0
56	MG	DA	3053	1/1	0.93	0.19	37,37,37,37	0
56	MG	BA	3238	1/1	0.93	0.14	41,41,41,41	0
56	MG	DA	3056	1/1	0.93	0.21	60,60,60,60	0
56	MG	BA	3445	1/1	0.93	0.13	48,48,48,48	0
56	MG	BA	3446	1/1	0.93	0.10	31,31,31,31	0
56	MG	DA	3060	1/1	0.93	0.10	48,48,48,48	0
56	MG	BA	3169	1/1	0.93	0.14	50,50,50,50	0
56	MG	BA	3340	1/1	0.93	0.06	40,40,40,40	0
56	MG	BA	3342	1/1	0.93	0.06	33,33,33,33	0
56	MG	DA	3644	1/1	0.93	0.10	40,40,40,40	0
56	MG	DA	3067	1/1	0.93	0.14	45,45,45,45	0
56	MG	BA	3046	1/1	0.93	0.15	34,34,34,34	0
56	MG	DA	3069	1/1	0.93	0.16	55,55,55,55	0
56	MG	BA	3586	1/1	0.93	0.11	60,60,60,60	0
56	MG	DA	3362	1/1	0.93	0.20	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3071	1/1	0.93	0.09	48,48,48,48	0
56	MG	DA	3653	1/1	0.93	0.18	32,32,32,32	0
56	MG	BA	3696	1/1	0.93	0.08	45,45,45,45	0
56	MG	BA	3351	1/1	0.93	0.12	59,59,59,59	0
56	MG	BA	3588	1/1	0.93	0.06	29,29,29,29	0
56	MG	DA	3077	1/1	0.93	0.08	47,47,47,47	0
56	MG	DA	3659	1/1	0.93	0.18	39,39,39,39	0
56	MG	DA	3662	1/1	0.93	0.11	38,38,38,38	0
56	MG	BF	302	1/1	0.93	0.27	56,56,56,56	0
56	MG	BF	303	1/1	0.93	0.17	43,43,43,43	0
56	MG	BA	3353	1/1	0.93	0.12	49,49,49,49	0
56	MG	DA	3379	1/1	0.93	0.10	50,50,50,50	0
56	MG	DA	3672	1/1	0.93	0.12	59,59,59,59	0
56	MG	BA	3459	1/1	0.93	0.08	47,47,47,47	0
56	MG	DA	3387	1/1	0.93	0.13	39,39,39,39	0
56	MG	BF	309	1/1	0.93	0.07	45,45,45,45	0
56	MG	DA	3094	1/1	0.93	0.22	52,52,52,52	0
56	MG	DA	3097	1/1	0.93	0.14	57,57,57,57	0
56	MG	DB	3005	1/1	0.93	0.22	48,48,48,48	0
56	MG	BA	3460	1/1	0.93	0.14	58,58,58,58	0
56	MG	AA	3107	1/1	0.93	0.19	63,63,63,63	0
56	MG	DA	3102	1/1	0.93	0.12	49,49,49,49	0
56	MG	BN	3007	1/1	0.93	0.18	50,50,50,50	0
56	MG	BA	3178	1/1	0.93	0.33	42,42,42,42	0
56	MG	CA	3097	1/1	0.93	0.12	64,64,64,64	0
56	MG	BA	3473	1/1	0.93	0.17	52,52,52,52	0
56	MG	DA	3411	1/1	0.93	0.13	46,46,46,46	0
56	MG	BR	201	1/1	0.93	0.16	40,40,40,40	0
56	MG	DA	3113	1/1	0.93	0.20	50,50,50,50	0
56	MG	BA	3712	1/1	0.93	0.21	29,29,29,29	0
56	MG	CA	3104	1/1	0.93	0.08	60,60,60,60	0
56	MG	CA	3105	1/1	0.93	0.13	51,51,51,51	0
56	MG	DA	3122	1/1	0.93	0.22	53,53,53,53	0
56	MG	DU	3003	1/1	0.93	0.15	53,53,53,53	0
56	MG	BA	3714	1/1	0.93	0.12	41,41,41,41	0
56	MG	DA	3126	1/1	0.93	0.09	46,46,46,46	0
56	MG	BA	3603	1/1	0.93	0.19	42,42,42,42	0
56	MG	CA	3113	1/1	0.93	0.16	49,49,49,49	0
56	MG	CA	3115	1/1	0.93	0.15	60,60,60,60	0
56	MG	AA	3027	1/1	0.93	0.16	46,46,46,46	0
56	MG	BA	3119	1/1	0.93	0.13	29,29,29,29	0
56	MG	DA	3436	1/1	0.93	0.10	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3142	1/1	0.93	0.14	50,50,50,50	0
56	MG	AA	3113	1/1	0.93	0.18	67,67,67,67	0
59	ZN	B5	104	1/1	0.93	0.10	82,82,82,82	0
56	MG	DA	3440	1/1	0.93	0.12	51,51,51,51	0
56	MG	DA	3023	1/1	0.94	0.07	44,44,44,44	0
56	MG	CA	3069	1/1	0.94	0.17	59,59,59,59	0
56	MG	DA	3025	1/1	0.94	0.26	52,52,52,52	0
56	MG	CA	3071	1/1	0.94	0.15	57,57,57,57	0
56	MG	AA	3005	1/1	0.94	0.37	77,77,77,77	0
56	MG	AN	502	1/1	0.94	0.08	56,56,56,56	0
56	MG	CA	3074	1/1	0.94	0.22	57,57,57,57	0
56	MG	DA	3035	1/1	0.94	0.06	40,40,40,40	0
56	MG	BA	3308	1/1	0.94	0.15	49,49,49,49	0
56	MG	BA	3099	1/1	0.94	0.21	67,67,67,67	0
56	MG	BA	3412	1/1	0.94	0.18	19,19,19,19	0
56	MG	DA	3041	1/1	0.94	0.21	56,56,56,56	0
56	MG	BF	305	1/1	0.94	0.06	45,45,45,45	0
56	MG	DA	3506	1/1	0.94	0.06	40,40,40,40	0
56	MG	BA	3620	1/1	0.94	0.17	62,62,62,62	0
56	MG	BA	3621	1/1	0.94	0.10	39,39,39,39	0
56	MG	DA	3252	1/1	0.94	0.08	38,38,38,38	0
56	MG	DA	3051	1/1	0.94	0.07	45,45,45,45	0
56	MG	BA	3034	1/1	0.94	0.09	34,34,34,34	0
56	MG	BA	3101	1/1	0.94	0.09	39,39,39,39	0
56	MG	DA	3514	1/1	0.94	0.07	45,45,45,45	0
56	MG	AA	3178	1/1	0.94	0.12	59,59,59,59	0
56	MG	DA	3055	1/1	0.94	0.09	54,54,54,54	0
56	MG	BA	3106	1/1	0.94	0.11	44,44,44,44	0
56	MG	BA	3630	1/1	0.94	0.15	43,43,43,43	0
56	MG	DA	3263	1/1	0.94	0.17	44,44,44,44	0
56	MG	AA	3112	1/1	0.94	0.13	60,60,60,60	0
56	MG	BA	3327	1/1	0.94	0.11	37,37,37,37	0
56	MG	BU	204	1/1	0.94	0.09	43,43,43,43	0
56	MG	DA	3269	1/1	0.94	0.21	54,54,54,54	0
56	MG	DA	3271	1/1	0.94	0.21	51,51,51,51	0
56	MG	DA	3540	1/1	0.94	0.08	56,56,56,56	0
56	MG	DA	3274	1/1	0.94	0.11	54,54,54,54	0
56	MG	BA	3331	1/1	0.94	0.14	38,38,38,38	0
56	MG	BV	204	1/1	0.94	0.18	47,47,47,47	0
56	MG	BW	201	1/1	0.94	0.19	45,45,45,45	0
56	MG	BA	3336	1/1	0.94	0.17	50,50,50,50	0
56	MG	DA	3281	1/1	0.94	0.11	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	AA	3133	1/1	0.94	0.08	66,66,66,66	0
56	MG	BA	3548	1/1	0.94	0.10	40,40,40,40	0
56	MG	B0	103	1/1	0.94	0.11	38,38,38,38	0
56	MG	DA	3557	1/1	0.94	0.10	44,44,44,44	0
56	MG	DA	3558	1/1	0.94	0.08	43,43,43,43	0
56	MG	DA	3072	1/1	0.94	0.23	52,52,52,52	0
56	MG	DA	3560	1/1	0.94	0.07	47,47,47,47	0
56	MG	AA	3068	1/1	0.94	0.34	62,62,62,62	0
56	MG	B2	3001	1/1	0.94	0.08	49,49,49,49	0
56	MG	BA	3047	1/1	0.94	0.11	43,43,43,43	0
56	MG	BA	3187	1/1	0.94	0.21	48,48,48,48	0
56	MG	DA	3296	1/1	0.94	0.07	35,35,35,35	0
56	MG	DA	3300	1/1	0.94	0.11	41,41,41,41	0
56	MG	BA	3642	1/1	0.94	0.08	36,36,36,36	0
56	MG	DA	3308	1/1	0.94	0.12	49,49,49,49	0
56	MG	DA	3080	1/1	0.94	0.09	49,49,49,49	0
56	MG	CA	3108	1/1	0.94	0.13	52,52,52,52	0
56	MG	BA	3113	1/1	0.94	0.14	39,39,39,39	0
56	MG	B8	101	1/1	0.94	0.12	36,36,36,36	0
56	MG	DA	3090	1/1	0.94	0.20	48,48,48,48	0
56	MG	AA	3115	1/1	0.94	0.22	45,45,45,45	0
56	MG	DA	3578	1/1	0.94	0.08	40,40,40,40	0
56	MG	BA	3562	1/1	0.94	0.11	44,44,44,44	0
56	MG	AA	3119	1/1	0.94	0.06	65,65,65,65	0
56	MG	BA	3647	1/1	0.94	0.12	49,49,49,49	0
56	MG	CA	3119	1/1	0.94	0.14	51,51,51,51	0
56	MG	DA	3585	1/1	0.94	0.16	43,43,43,43	0
56	MG	BA	3751	1/1	0.94	0.08	55,55,55,55	0
56	MG	BA	3358	1/1	0.94	0.09	40,40,40,40	0
56	MG	DA	3333	1/1	0.94	0.09	51,51,51,51	0
56	MG	DA	3337	1/1	0.94	0.07	44,44,44,44	0
56	MG	DA	3104	1/1	0.94	0.09	39,39,39,39	0
56	MG	BA	3454	1/1	0.94	0.07	29,29,29,29	0
56	MG	DA	3340	1/1	0.94	0.07	30,30,30,30	0
56	MG	AA	3009	1/1	0.94	0.08	24,24,24,24	0
56	MG	BA	3258	1/1	0.94	0.28	61,61,61,61	0
56	MG	BA	3761	1/1	0.94	0.21	53,53,53,53	0
56	MG	DA	3111	1/1	0.94	0.07	53,53,53,53	0
56	MG	CA	3126	1/1	0.94	0.08	57,57,57,57	0
56	MG	DA	3357	1/1	0.94	0.06	38,38,38,38	0
56	MG	DA	3610	1/1	0.94	0.09	49,49,49,49	0
56	MG	DA	3611	1/1	0.94	0.13	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3358	1/1	0.94	0.08	28,28,28,28	0
56	MG	BA	3763	1/1	0.94	0.10	39,39,39,39	0
56	MG	CA	3015	1/1	0.94	0.17	58,58,58,58	0
56	MG	DA	3617	1/1	0.94	0.07	45,45,45,45	0
56	MG	DA	3619	1/1	0.94	0.12	54,54,54,54	0
56	MG	BA	3361	1/1	0.94	0.11	61,61,61,61	0
56	MG	DA	3622	1/1	0.94	0.10	35,35,35,35	0
56	MG	CA	3017	1/1	0.94	0.12	76,76,76,76	0
56	MG	BA	3765	1/1	0.94	0.11	53,53,53,53	0
56	MG	CA	3133	1/1	0.94	0.08	45,45,45,45	0
56	MG	BA	3577	1/1	0.94	0.17	18,18,18,18	0
56	MG	AA	3082	1/1	0.94	0.33	51,51,51,51	0
56	MG	DA	3628	1/1	0.94	0.07	47,47,47,47	0
56	MG	BA	3006	1/1	0.94	0.10	52,52,52,52	0
56	MG	BA	3264	1/1	0.94	0.22	45,45,45,45	0
56	MG	BA	3582	1/1	0.94	0.12	19,19,19,19	0
56	MG	DA	3381	1/1	0.94	0.07	34,34,34,34	0
56	MG	DA	3141	1/1	0.94	0.17	46,46,46,46	0
56	MG	BA	3016	1/1	0.94	0.07	37,37,37,37	0
56	MG	BA	3372	1/1	0.94	0.08	56,56,56,56	0
56	MG	BA	3476	1/1	0.94	0.12	48,48,48,48	0
56	MG	BA	3373	1/1	0.94	0.07	42,42,42,42	0
56	MG	AA	3093	1/1	0.94	0.23	51,51,51,51	0
56	MG	BA	3785	1/1	0.94	0.13	81,81,81,81	0
56	MG	DA	3156	1/1	0.94	0.25	50,50,50,50	0
56	MG	DA	3158	1/1	0.94	0.16	30,30,30,30	0
56	MG	CA	3033	1/1	0.94	0.16	60,60,60,60	0
56	MG	DA	3647	1/1	0.94	0.09	53,53,53,53	0
56	MG	DA	3164	1/1	0.94	0.24	47,47,47,47	0
56	MG	BA	3376	1/1	0.94	0.11	43,43,43,43	0
56	MG	DA	3408	1/1	0.94	0.10	51,51,51,51	0
56	MG	DA	3651	1/1	0.94	0.09	40,40,40,40	0
56	MG	DA	3409	1/1	0.94	0.20	55,55,55,55	0
56	MG	BA	3480	1/1	0.94	0.07	50,50,50,50	0
56	MG	CA	3037	1/1	0.94	0.18	46,46,46,46	0
56	MG	AA	3172	1/1	0.94	0.09	55,55,55,55	0
56	MG	DA	3173	1/1	0.94	0.12	51,51,51,51	0
56	MG	BA	3593	1/1	0.94	0.12	47,47,47,47	0
56	MG	DA	3177	1/1	0.94	0.12	46,46,46,46	0
56	MG	DA	3179	1/1	0.94	0.10	57,57,57,57	0
56	MG	CA	3156	1/1	0.94	0.13	41,41,41,41	0
56	MG	BA	3683	1/1	0.94	0.09	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3425	1/1	0.94	0.19	52,52,52,52	0
56	MG	DA	3668	1/1	0.94	0.55	51,51,51,51	0
56	MG	BA	3489	1/1	0.94	0.25	44,44,44,44	0
56	MG	DA	3183	1/1	0.94	0.07	40,40,40,40	0
56	MG	BA	3206	1/1	0.94	0.10	37,37,37,37	0
56	MG	DA	3674	1/1	0.94	0.23	43,43,43,43	0
56	MG	BA	3798	1/1	0.94	0.07	51,51,51,51	0
56	MG	BA	3799	1/1	0.94	0.27	50,50,50,50	0
56	MG	AA	3050	1/1	0.94	0.09	77,77,77,77	0
56	MG	DA	3189	1/1	0.94	0.12	41,41,41,41	0
56	MG	BA	3801	1/1	0.94	0.15	39,39,39,39	0
56	MG	DA	3439	1/1	0.94	0.15	46,46,46,46	0
56	MG	BA	3382	1/1	0.94	0.10	41,41,41,41	0
56	MG	BA	3599	1/1	0.94	0.12	45,45,45,45	0
56	MG	BA	3281	1/1	0.94	0.12	56,56,56,56	0
56	MG	BA	3071	1/1	0.94	0.10	40,40,40,40	0
56	MG	DA	3197	1/1	0.94	0.20	55,55,55,55	0
56	MG	DD	307	1/1	0.94	0.10	50,50,50,50	0
56	MG	BA	3217	1/1	0.94	0.13	47,47,47,47	0
56	MG	BA	3080	1/1	0.94	0.26	51,51,51,51	0
56	MG	DE	304	1/1	0.94	0.16	40,40,40,40	0
56	MG	BA	3509	1/1	0.94	0.07	39,39,39,39	0
56	MG	CE	202	1/1	0.94	0.08	74,74,74,74	0
56	MG	CA	3056	1/1	0.94	0.15	60,60,60,60	0
56	MG	BB	210	1/1	0.94	0.23	55,55,55,55	0
56	MG	DQ	3003	1/1	0.94	0.09	52,52,52,52	0
56	MG	BA	3702	1/1	0.94	0.15	53,53,53,53	0
56	MG	AE	201	1/1	0.94	0.34	64,64,64,64	0
56	MG	DA	3461	1/1	0.94	0.16	57,57,57,57	0
56	MG	DA	3463	1/1	0.94	0.06	32,32,32,32	0
56	MG	BB	217	1/1	0.94	0.10	41,41,41,41	0
56	MG	DA	3003	1/1	0.94	0.18	48,48,48,48	0
56	MG	AA	3128	1/1	0.94	0.10	67,67,67,67	0
56	MG	DA	3468	1/1	0.94	0.12	37,37,37,37	0
56	MG	AA	3160	1/1	0.94	0.18	54,54,54,54	0
56	MG	CA	3064	1/1	0.94	0.18	59,59,59,59	0
56	MG	CA	3066	1/1	0.94	0.15	47,47,47,47	0
56	MG	BA	3707	1/1	0.94	0.09	43,43,43,43	0
56	MG	DA	3018	1/1	0.94	0.13	51,51,51,51	0
56	MG	DA	3481	1/1	0.94	0.07	24,24,24,24	0
59	ZN	D4	501	1/1	0.94	0.07	151,151,151,151	0
56	MG	BD	3306	1/1	0.94	0.19	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3367	1/1	0.95	0.09	34,34,34,34	0
56	MG	BB	218	1/1	0.95	0.07	31,31,31,31	0
56	MG	DA	3434	1/1	0.95	0.07	27,27,27,27	0
56	MG	DA	3143	1/1	0.95	0.27	36,36,36,36	0
56	MG	BA	3077	1/1	0.95	0.21	29,29,29,29	0
56	MG	BA	3369	1/1	0.95	0.11	40,40,40,40	0
56	MG	CA	3106	1/1	0.95	0.07	58,58,58,58	0
56	MG	BA	3526	1/1	0.95	0.11	35,35,35,35	0
56	MG	DA	3151	1/1	0.95	0.09	33,33,33,33	0
56	MG	DA	3441	1/1	0.95	0.06	30,30,30,30	0
56	MG	BD	3304	1/1	0.95	0.07	25,25,25,25	0
56	MG	DA	3153	1/1	0.95	0.12	38,38,38,38	0
56	MG	DA	3154	1/1	0.95	0.20	52,52,52,52	0
56	MG	BA	3153	1/1	0.95	0.07	50,50,50,50	0
56	MG	DA	3157	1/1	0.95	0.13	42,42,42,42	0
56	MG	DA	3447	1/1	0.95	0.11	41,41,41,41	0
56	MG	BD	3307	1/1	0.95	0.27	56,56,56,56	0
56	MG	DA	3160	1/1	0.95	0.20	38,38,38,38	0
56	MG	BA	3530	1/1	0.95	0.12	25,25,25,25	0
56	MG	BA	3532	1/1	0.95	0.16	30,30,30,30	0
56	MG	DA	3165	1/1	0.95	0.17	42,42,42,42	0
56	MG	BF	301	1/1	0.95	0.18	32,32,32,32	0
56	MG	BA	3533	1/1	0.95	0.09	38,38,38,38	0
56	MG	DA	3169	1/1	0.95	0.21	44,44,44,44	0
56	MG	BA	3670	1/1	0.95	0.12	47,47,47,47	0
56	MG	AA	3110	1/1	0.95	0.17	46,46,46,46	0
56	MG	BA	3024	1/1	0.95	0.17	45,45,45,45	0
56	MG	AA	3190	1/1	0.95	0.11	48,48,48,48	0
56	MG	DA	3176	1/1	0.95	0.12	44,44,44,44	0
56	MG	BF	308	1/1	0.95	0.14	45,45,45,45	0
56	MG	DA	3178	1/1	0.95	0.07	53,53,53,53	0
56	MG	DA	3471	1/1	0.95	0.18	54,54,54,54	0
56	MG	BA	3675	1/1	0.95	0.15	29,29,29,29	0
56	MG	DA	3474	1/1	0.95	0.07	30,30,30,30	0
56	MG	DA	3477	1/1	0.95	0.06	30,30,30,30	0
56	MG	BG	3001	1/1	0.95	0.21	51,51,51,51	0
56	MG	BA	3676	1/1	0.95	0.12	37,37,37,37	0
56	MG	BA	3088	1/1	0.95	0.14	49,49,49,49	0
56	MG	BN	3004	1/1	0.95	0.20	61,61,61,61	0
56	MG	BN	3006	1/1	0.95	0.17	47,47,47,47	0
56	MG	AA	3148	1/1	0.95	0.12	58,58,58,58	0
56	MG	BA	3679	1/1	0.95	0.29	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3093	1/1	0.95	0.17	48,48,48,48	0
56	MG	DA	3188	1/1	0.95	0.07	26,26,26,26	0
56	MG	BP	204	1/1	0.95	0.09	54,54,54,54	0
56	MG	BA	3380	1/1	0.95	0.05	36,36,36,36	0
56	MG	BA	3094	1/1	0.95	0.17	44,44,44,44	0
56	MG	BU	202	1/1	0.95	0.06	29,29,29,29	0
56	MG	BA	3171	1/1	0.95	0.17	54,54,54,54	0
56	MG	BU	205	1/1	0.95	0.11	43,43,43,43	0
56	MG	AA	3088	1/1	0.95	0.18	42,42,42,42	0
56	MG	BV	203	1/1	0.95	0.20	31,31,31,31	0
56	MG	CA	3145	1/1	0.95	0.10	68,68,68,68	0
56	MG	DA	3507	1/1	0.95	0.09	57,57,57,57	0
56	MG	BA	3549	1/1	0.95	0.10	36,36,36,36	0
56	MG	BA	3385	1/1	0.95	0.20	41,41,41,41	0
56	MG	BY	202	1/1	0.95	0.17	48,48,48,48	0
56	MG	DA	3209	1/1	0.95	0.12	46,46,46,46	0
56	MG	BY	204	1/1	0.95	0.26	52,52,52,52	0
56	MG	BA	3695	1/1	0.95	0.11	37,37,37,37	0
56	MG	BA	3554	1/1	0.95	0.09	24,24,24,24	0
56	MG	DA	3516	1/1	0.95	0.07	52,52,52,52	0
56	MG	BA	3386	1/1	0.95	0.16	47,47,47,47	0
56	MG	B0	102	1/1	0.95	0.15	50,50,50,50	0
56	MG	DA	3519	1/1	0.95	0.10	32,32,32,32	0
56	MG	DA	3520	1/1	0.95	0.05	44,44,44,44	0
56	MG	DA	3521	1/1	0.95	0.14	55,55,55,55	0
56	MG	BA	3557	1/1	0.95	0.14	37,37,37,37	0
56	MG	BA	3260	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3219	1/1	0.95	0.10	36,36,36,36	0
56	MG	DA	3530	1/1	0.95	0.12	47,47,47,47	0
56	MG	AA	3089	1/1	0.95	0.28	57,57,57,57	0
56	MG	BA	3176	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3394	1/1	0.95	0.05	20,20,20,20	0
56	MG	DA	3535	1/1	0.95	0.09	59,59,59,59	0
56	MG	DA	3224	1/1	0.95	0.10	47,47,47,47	0
56	MG	B5	102	1/1	0.95	0.15	45,45,45,45	0
56	MG	B5	103	1/1	0.95	0.06	41,41,41,41	0
56	MG	BA	3563	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3098	1/1	0.95	0.15	38,38,38,38	0
56	MG	BA	3269	1/1	0.95	0.22	42,42,42,42	0
56	MG	CA	3166	1/1	0.95	0.09	52,52,52,52	0
56	MG	DA	3546	1/1	0.95	0.07	47,47,47,47	0
56	MG	CA	3167	1/1	0.95	0.06	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3709	1/1	0.95	0.20	28,28,28,28	0
56	MG	DA	3237	1/1	0.95	0.05	43,43,43,43	0
56	MG	BA	3569	1/1	0.95	0.20	56,56,56,56	0
56	MG	AA	3152	1/1	0.95	0.07	48,48,48,48	0
56	MG	BA	3032	1/1	0.95	0.17	42,42,42,42	0
56	MG	BA	3573	1/1	0.95	0.08	24,24,24,24	0
56	MG	AA	3090	1/1	0.95	0.19	41,41,41,41	0
56	MG	AA	3065	1/1	0.95	0.09	55,55,55,55	0
56	MG	DA	3245	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3105	1/1	0.95	0.10	39,39,39,39	0
56	MG	BA	3282	1/1	0.95	0.23	41,41,41,41	0
56	MG	CA	3012	1/1	0.95	0.17	51,51,51,51	0
56	MG	BA	3283	1/1	0.95	0.07	30,30,30,30	0
56	MG	DA	3254	1/1	0.95	0.18	35,35,35,35	0
56	MG	DA	3001	1/1	0.95	0.07	40,40,40,40	0
56	MG	BA	3722	1/1	0.95	0.07	17,17,17,17	0
56	MG	BA	3286	1/1	0.95	0.26	41,41,41,41	0
56	MG	AA	3013	1/1	0.95	0.12	57,57,57,57	0
56	MG	BA	3041	1/1	0.95	0.12	35,35,35,35	0
56	MG	BA	3424	1/1	0.95	0.11	55,55,55,55	0
56	MG	CA	3020	1/1	0.95	0.18	46,46,46,46	0
56	MG	DA	3016	1/1	0.95	0.10	42,42,42,42	0
56	MG	AA	3123	1/1	0.95	0.12	51,51,51,51	0
56	MG	AA	3003	1/1	0.95	0.12	63,63,63,63	0
56	MG	DA	3267	1/1	0.95	0.14	41,41,41,41	0
56	MG	AX	3005	1/1	0.95	0.24	64,64,64,64	0
56	MG	AA	3023	1/1	0.95	0.27	48,48,48,48	0
56	MG	DA	3270	1/1	0.95	0.39	56,56,56,56	0
56	MG	BA	3114	1/1	0.95	0.13	34,34,34,34	0
56	MG	DA	3273	1/1	0.95	0.12	39,39,39,39	0
56	MG	BA	3300	1/1	0.95	0.20	28,28,28,28	0
56	MG	DA	3592	1/1	0.95	0.10	40,40,40,40	0
56	MG	BA	3200	1/1	0.95	0.14	41,41,41,41	0
56	MG	DA	3277	1/1	0.95	0.25	54,54,54,54	0
56	MG	DA	3030	1/1	0.95	0.07	46,46,46,46	0
56	MG	DA	3031	1/1	0.95	0.24	44,44,44,44	0
56	MG	DA	3600	1/1	0.95	0.09	43,43,43,43	0
56	MG	DA	3602	1/1	0.95	0.08	51,51,51,51	0
56	MG	BA	3117	1/1	0.95	0.22	35,35,35,35	0
56	MG	AA	3159	1/1	0.95	0.10	59,59,59,59	0
56	MG	BA	3742	1/1	0.95	0.15	21,21,21,21	0
56	MG	DA	3283	1/1	0.95	0.11	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3207	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3449	1/1	0.95	0.11	32,32,32,32	0
56	MG	DA	3287	1/1	0.95	0.06	39,39,39,39	0
56	MG	AA	3028	1/1	0.95	0.20	49,49,49,49	0
56	MG	BA	3214	1/1	0.95	0.14	44,44,44,44	0
56	MG	DA	3614	1/1	0.95	0.16	61,61,61,61	0
56	MG	AA	3161	1/1	0.95	0.19	59,59,59,59	0
56	MG	AA	3143	1/1	0.95	0.09	57,57,57,57	0
56	MG	BA	3323	1/1	0.95	0.09	43,43,43,43	0
56	MG	DA	3618	1/1	0.95	0.06	64,64,64,64	0
56	MG	BA	3324	1/1	0.95	0.15	42,42,42,42	0
56	MG	DA	3620	1/1	0.95	0.15	59,59,59,59	0
56	MG	DA	3297	1/1	0.95	0.11	24,24,24,24	0
56	MG	DA	3047	1/1	0.95	0.05	39,39,39,39	0
56	MG	DA	3304	1/1	0.95	0.07	40,40,40,40	0
56	MG	DA	3048	1/1	0.95	0.21	51,51,51,51	0
56	MG	DA	3049	1/1	0.95	0.17	53,53,53,53	0
56	MG	BA	3756	1/1	0.95	0.11	56,56,56,56	0
56	MG	BA	3758	1/1	0.95	0.11	44,44,44,44	0
56	MG	DA	3313	1/1	0.95	0.06	46,46,46,46	0
56	MG	BA	3610	1/1	0.95	0.08	39,39,39,39	0
56	MG	AA	3086	1/1	0.95	0.19	48,48,48,48	0
56	MG	BA	3330	1/1	0.95	0.10	52,52,52,52	0
56	MG	BA	3127	1/1	0.95	0.07	36,36,36,36	0
56	MG	DA	3633	1/1	0.95	0.07	56,56,56,56	0
56	MG	BA	3128	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3467	1/1	0.95	0.09	49,49,49,49	0
56	MG	DA	3636	1/1	0.95	0.19	52,52,52,52	0
56	MG	BA	3472	1/1	0.95	0.13	38,38,38,38	0
56	MG	BA	3337	1/1	0.95	0.10	46,46,46,46	0
56	MG	BA	3338	1/1	0.95	0.21	43,43,43,43	0
56	MG	DA	3327	1/1	0.95	0.09	47,47,47,47	0
56	MG	DA	3642	1/1	0.95	0.06	48,48,48,48	0
56	MG	DA	3328	1/1	0.95	0.10	41,41,41,41	0
56	MG	BA	3769	1/1	0.95	0.07	24,24,24,24	0
56	MG	DA	3332	1/1	0.95	0.11	50,50,50,50	0
56	MG	BA	3224	1/1	0.95	0.22	50,50,50,50	0
56	MG	BA	3130	1/1	0.95	0.22	41,41,41,41	0
56	MG	BA	3227	1/1	0.95	0.08	34,34,34,34	0
56	MG	BA	3777	1/1	0.95	0.17	44,44,44,44	0
56	MG	BA	3346	1/1	0.95	0.08	29,29,29,29	0
56	MG	BA	3483	1/1	0.95	0.14	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3348	1/1	0.95	0.07	24,24,24,24	0
56	MG	BA	3014	1/1	0.95	0.07	38,38,38,38	0
56	MG	BA	3783	1/1	0.95	0.06	43,43,43,43	0
56	MG	CA	3065	1/1	0.95	0.21	64,64,64,64	0
56	MG	DA	3353	1/1	0.95	0.12	42,42,42,42	0
56	MG	DA	3355	1/1	0.95	0.12	35,35,35,35	0
56	MG	DA	3078	1/1	0.95	0.09	35,35,35,35	0
56	MG	BA	3490	1/1	0.95	0.10	60,60,60,60	0
56	MG	BA	3491	1/1	0.95	0.12	45,45,45,45	0
56	MG	DA	3081	1/1	0.95	0.10	48,48,48,48	0
56	MG	BA	3352	1/1	0.95	0.10	45,45,45,45	0
56	MG	BA	3494	1/1	0.95	0.05	47,47,47,47	0
56	MG	CA	3070	1/1	0.95	0.13	49,49,49,49	0
56	MG	DA	3671	1/1	0.95	0.08	37,37,37,37	0
56	MG	BA	3790	1/1	0.95	0.17	29,29,29,29	0
56	MG	BA	3635	1/1	0.95	0.10	51,51,51,51	0
56	MG	BA	3134	1/1	0.95	0.16	36,36,36,36	0
56	MG	DA	3096	1/1	0.95	0.17	48,48,48,48	0
56	MG	AA	3164	1/1	0.95	0.10	51,51,51,51	0
56	MG	BA	3234	1/1	0.95	0.19	32,32,32,32	0
56	MG	BA	3499	1/1	0.95	0.10	19,19,19,19	0
56	MG	DA	3382	1/1	0.95	0.06	31,31,31,31	0
56	MG	BA	3501	1/1	0.95	0.07	43,43,43,43	0
56	MG	BA	3502	1/1	0.95	0.05	20,20,20,20	0
56	MG	BA	3357	1/1	0.95	0.09	46,46,46,46	0
56	MG	DA	3105	1/1	0.95	0.06	41,41,41,41	0
56	MG	AA	3145	1/1	0.95	0.12	65,65,65,65	0
56	MG	DD	303	1/1	0.95	0.17	51,51,51,51	0
56	MG	AA	3072	1/1	0.95	0.21	45,45,45,45	0
56	MG	BA	3808	1/1	0.95	0.08	40,40,40,40	0
56	MG	BA	3507	1/1	0.95	0.18	35,35,35,35	0
56	MG	BA	3814	1/1	0.95	0.16	42,42,42,42	0
56	MG	DE	303	1/1	0.95	0.13	62,62,62,62	0
56	MG	BA	3240	1/1	0.95	0.06	30,30,30,30	0
56	MG	DE	305	1/1	0.95	0.14	38,38,38,38	0
56	MG	DF	301	1/1	0.95	0.26	47,47,47,47	0
56	MG	DF	303	1/1	0.95	0.05	52,52,52,52	0
56	MG	DF	305	1/1	0.95	0.17	44,44,44,44	0
56	MG	DA	3114	1/1	0.95	0.12	55,55,55,55	0
56	MG	DN	5001	1/1	0.95	0.06	54,54,54,54	0
56	MG	DA	3403	1/1	0.95	0.08	56,56,56,56	0
56	MG	DA	3404	1/1	0.95	0.08	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BB	202	1/1	0.95	0.14	45,45,45,45	0
56	MG	BB	203	1/1	0.95	0.16	44,44,44,44	0
56	MG	BA	3072	1/1	0.95	0.08	58,58,58,58	0
56	MG	DA	3410	1/1	0.95	0.06	46,46,46,46	0
56	MG	BA	3362	1/1	0.95	0.10	40,40,40,40	0
56	MG	BB	207	1/1	0.95	0.17	39,39,39,39	0
56	MG	DV	3001	1/1	0.95	0.10	61,61,61,61	0
56	MG	BA	3073	1/1	0.95	0.23	45,45,45,45	0
56	MG	DA	3416	1/1	0.95	0.06	22,22,22,22	0
56	MG	BA	3245	1/1	0.95	0.14	61,61,61,61	0
56	MG	CA	3095	1/1	0.95	0.11	56,56,56,56	0
56	MG	DA	3130	1/1	0.95	0.21	54,54,54,54	0
56	MG	BA	3520	1/1	0.95	0.09	50,50,50,50	0
56	MG	D3	3001	1/1	0.95	0.13	60,60,60,60	0
56	MG	BB	212	1/1	0.95	0.09	42,42,42,42	0
56	MG	DA	3133	1/1	0.95	0.14	52,52,52,52	0
56	MG	DA	3134	1/1	0.95	0.08	48,48,48,48	0
56	MG	BA	3655	1/1	0.95	0.12	54,54,54,54	0
59	ZN	B6	103	1/1	0.95	0.06	62,62,62,62	0
59	ZN	CN	501	1/1	0.95	0.07	103,103,103,103	0
56	MG	DA	3429	1/1	0.95	0.07	45,45,45,45	0
56	MG	DA	3140	1/1	0.95	0.13	44,44,44,44	0
56	MG	BQ	201	1/1	0.96	0.15	35,35,35,35	0
56	MG	CA	3141	1/1	0.96	0.14	53,53,53,53	0
56	MG	BQ	203	1/1	0.96	0.11	36,36,36,36	0
56	MG	BQ	204	1/1	0.96	0.15	43,43,43,43	0
56	MG	AA	3058	1/1	0.96	0.12	61,61,61,61	0
56	MG	DA	3451	1/1	0.96	0.10	20,20,20,20	0
56	MG	BA	3035	1/1	0.96	0.11	42,42,42,42	0
56	MG	BA	3390	1/1	0.96	0.08	25,25,25,25	0
56	MG	BA	3701	1/1	0.96	0.10	20,20,20,20	0
56	MG	DA	3456	1/1	0.96	0.15	54,54,54,54	0
56	MG	BA	3391	1/1	0.96	0.06	26,26,26,26	0
56	MG	BA	3267	1/1	0.96	0.14	45,45,45,45	0
56	MG	CA	3150	1/1	0.96	0.12	47,47,47,47	0
56	MG	BU	208	1/1	0.96	0.15	28,28,28,28	0
56	MG	BA	3268	1/1	0.96	0.29	57,57,57,57	0
56	MG	BA	3705	1/1	0.96	0.18	28,28,28,28	0
56	MG	BA	3170	1/1	0.96	0.35	52,52,52,52	0
56	MG	BW	202	1/1	0.96	0.13	41,41,41,41	0
56	MG	BY	201	1/1	0.96	0.07	52,52,52,52	0
56	MG	BA	3271	1/1	0.96	0.17	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3196	1/1	0.96	0.20	45,45,45,45	0
56	MG	BA	3565	1/1	0.96	0.04	43,43,43,43	0
56	MG	BA	3038	1/1	0.96	0.14	40,40,40,40	0
56	MG	DA	3199	1/1	0.96	0.21	55,55,55,55	0
56	MG	AA	3069	1/1	0.96	0.06	52,52,52,52	0
56	MG	BA	3713	1/1	0.96	0.13	26,26,26,26	0
56	MG	BA	3568	1/1	0.96	0.12	26,26,26,26	0
56	MG	DA	3480	1/1	0.96	0.05	38,38,38,38	0
56	MG	BA	3174	1/1	0.96	0.08	50,50,50,50	0
56	MG	DA	3204	1/1	0.96	0.10	50,50,50,50	0
56	MG	DA	3483	1/1	0.96	0.11	32,32,32,32	0
56	MG	DA	3205	1/1	0.96	0.18	34,34,34,34	0
56	MG	DA	3207	1/1	0.96	0.23	36,36,36,36	0
56	MG	DA	3208	1/1	0.96	0.12	44,44,44,44	0
56	MG	BA	3403	1/1	0.96	0.04	22,22,22,22	0
56	MG	AX	3008	1/1	0.96	0.10	37,37,37,37	0
56	MG	AA	3045	1/1	0.96	0.31	54,54,54,54	0
56	MG	AA	3083	1/1	0.96	0.19	53,53,53,53	0
56	MG	BA	3416	1/1	0.96	0.12	36,36,36,36	0
56	MG	DA	3496	1/1	0.96	0.15	35,35,35,35	0
56	MG	BA	3179	1/1	0.96	0.08	41,41,41,41	0
56	MG	CA	3173	1/1	0.96	0.12	58,58,58,58	0
56	MG	DA	3500	1/1	0.96	0.16	51,51,51,51	0
56	MG	DA	3217	1/1	0.96	0.09	34,34,34,34	0
56	MG	BA	3418	1/1	0.96	0.09	34,34,34,34	0
56	MG	DA	3503	1/1	0.96	0.09	31,31,31,31	0
56	MG	B6	102	1/1	0.96	0.20	51,51,51,51	0
56	MG	BA	3284	1/1	0.96	0.20	33,33,33,33	0
56	MG	BA	3285	1/1	0.96	0.20	54,54,54,54	0
56	MG	CF	3001	1/1	0.96	0.12	55,55,55,55	0
56	MG	DA	3223	1/1	0.96	0.20	41,41,41,41	0
56	MG	B9	502	1/1	0.96	0.10	47,47,47,47	0
56	MG	BA	3102	1/1	0.96	0.30	61,61,61,61	0
56	MG	BA	3045	1/1	0.96	0.10	38,38,38,38	0
56	MG	DA	3227	1/1	0.96	0.07	49,49,49,49	0
56	MG	BA	3001	1/1	0.96	0.11	31,31,31,31	0
56	MG	DA	3515	1/1	0.96	0.06	39,39,39,39	0
56	MG	BA	3291	1/1	0.96	0.10	50,50,50,50	0
56	MG	AA	3071	1/1	0.96	0.13	51,51,51,51	0
56	MG	DA	3232	1/1	0.96	0.14	45,45,45,45	0
56	MG	BA	3004	1/1	0.96	0.09	26,26,26,26	0
56	MG	BA	3435	1/1	0.96	0.09	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3235	1/1	0.96	0.15	35,35,35,35	0
56	MG	DA	3522	1/1	0.96	0.12	53,53,53,53	0
56	MG	DA	3007	1/1	0.96	0.11	43,43,43,43	0
56	MG	DA	3010	1/1	0.96	0.10	45,45,45,45	0
56	MG	BA	3049	1/1	0.96	0.15	34,34,34,34	0
56	MG	BA	3438	1/1	0.96	0.06	21,21,21,21	0
56	MG	AA	3060	1/1	0.96	0.11	52,52,52,52	0
56	MG	BA	3051	1/1	0.96	0.14	18,18,18,18	0
56	MG	BA	3443	1/1	0.96	0.10	27,27,27,27	0
56	MG	BA	3444	1/1	0.96	0.17	43,43,43,43	0
56	MG	BA	3746	1/1	0.96	0.09	55,55,55,55	0
56	MG	DA	3247	1/1	0.96	0.07	34,34,34,34	0
56	MG	BA	3010	1/1	0.96	0.12	41,41,41,41	0
56	MG	BA	3305	1/1	0.96	0.07	46,46,46,46	0
56	MG	BA	3749	1/1	0.96	0.07	29,29,29,29	0
56	MG	DA	3543	1/1	0.96	0.15	52,52,52,52	0
56	MG	BA	3600	1/1	0.96	0.11	50,50,50,50	0
56	MG	DA	3253	1/1	0.96	0.14	47,47,47,47	0
56	MG	BA	3602	1/1	0.96	0.12	32,32,32,32	0
56	MG	BA	3753	1/1	0.96	0.08	27,27,27,27	0
56	MG	AA	3117	1/1	0.96	0.16	34,34,34,34	0
56	MG	AA	3118	1/1	0.96	0.10	39,39,39,39	0
56	MG	BA	3450	1/1	0.96	0.07	10,10,10,10	0
56	MG	CA	3027	1/1	0.96	0.29	61,61,61,61	0
56	MG	BA	3757	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3198	1/1	0.96	0.13	28,28,28,28	0
56	MG	DA	3038	1/1	0.96	0.12	28,28,28,28	0
56	MG	BA	3057	1/1	0.96	0.06	53,53,53,53	0
56	MG	DA	3040	1/1	0.96	0.14	58,58,58,58	0
56	MG	BA	3314	1/1	0.96	0.14	44,44,44,44	0
56	MG	DA	3042	1/1	0.96	0.21	46,46,46,46	0
56	MG	BA	3017	1/1	0.96	0.14	52,52,52,52	0
56	MG	BA	3762	1/1	0.96	0.15	53,53,53,53	0
56	MG	BA	3317	1/1	0.96	0.08	41,41,41,41	0
56	MG	DA	3272	1/1	0.96	0.16	45,45,45,45	0
56	MG	BA	3201	1/1	0.96	0.18	41,41,41,41	0
56	MG	BA	3202	1/1	0.96	0.06	38,38,38,38	0
56	MG	DA	3275	1/1	0.96	0.22	58,58,58,58	0
56	MG	DA	3571	1/1	0.96	0.10	51,51,51,51	0
56	MG	DA	3573	1/1	0.96	0.10	27,27,27,27	0
56	MG	BA	3320	1/1	0.96	0.07	55,55,55,55	0
56	MG	BA	3203	1/1	0.96	0.18	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3322	1/1	0.96	0.21	48,48,48,48	0
56	MG	BA	3061	1/1	0.96	0.24	49,49,49,49	0
56	MG	BA	3468	1/1	0.96	0.08	45,45,45,45	0
56	MG	AA	3051	1/1	0.96	0.18	60,60,60,60	0
56	MG	BA	3325	1/1	0.96	0.13	51,51,51,51	0
56	MG	CA	3046	1/1	0.96	0.17	50,50,50,50	0
56	MG	DA	3284	1/1	0.96	0.19	37,37,37,37	0
56	MG	BA	3774	1/1	0.96	0.07	37,37,37,37	0
56	MG	BA	3776	1/1	0.96	0.09	48,48,48,48	0
56	MG	BA	3623	1/1	0.96	0.04	33,33,33,33	0
56	MG	DA	3289	1/1	0.96	0.06	39,39,39,39	0
56	MG	BA	3475	1/1	0.96	0.10	45,45,45,45	0
56	MG	DA	3063	1/1	0.96	0.21	54,54,54,54	0
56	MG	DA	3064	1/1	0.96	0.14	56,56,56,56	0
56	MG	DA	3065	1/1	0.96	0.10	41,41,41,41	0
56	MG	BA	3326	1/1	0.96	0.07	22,22,22,22	0
56	MG	BA	3627	1/1	0.96	0.19	57,57,57,57	0
56	MG	BA	3628	1/1	0.96	0.06	34,34,34,34	0
56	MG	DA	3299	1/1	0.96	0.10	40,40,40,40	0
56	MG	DA	3604	1/1	0.96	0.08	47,47,47,47	0
56	MG	BA	3124	1/1	0.96	0.09	35,35,35,35	0
56	MG	DA	3303	1/1	0.96	0.08	55,55,55,55	0
56	MG	BA	3328	1/1	0.96	0.09	11,11,11,11	0
56	MG	BA	3064	1/1	0.96	0.10	33,33,33,33	0
56	MG	BA	3213	1/1	0.96	0.07	35,35,35,35	0
56	MG	BA	3335	1/1	0.96	0.14	42,42,42,42	0
56	MG	BA	3126	1/1	0.96	0.12	47,47,47,47	0
56	MG	DA	3312	1/1	0.96	0.06	41,41,41,41	0
56	MG	DA	3075	1/1	0.96	0.07	43,43,43,43	0
56	MG	DA	3314	1/1	0.96	0.07	45,45,45,45	0
56	MG	DA	3315	1/1	0.96	0.06	44,44,44,44	0
56	MG	AA	3121	1/1	0.96	0.08	33,33,33,33	0
56	MG	DA	3317	1/1	0.96	0.06	38,38,38,38	0
56	MG	AA	3175	1/1	0.96	0.09	66,66,66,66	0
56	MG	BA	3067	1/1	0.96	0.16	49,49,49,49	0
56	MG	BA	3131	1/1	0.96	0.17	39,39,39,39	0
56	MG	BA	3797	1/1	0.96	0.09	19,19,19,19	0
56	MG	BA	3132	1/1	0.96	0.16	49,49,49,49	0
56	MG	DA	3082	1/1	0.96	0.06	40,40,40,40	0
56	MG	BA	3223	1/1	0.96	0.06	39,39,39,39	0
56	MG	BA	3641	1/1	0.96	0.06	54,54,54,54	0
56	MG	BA	3347	1/1	0.96	0.09	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3804	1/1	0.96	0.06	35,35,35,35	0
56	MG	BA	3805	1/1	0.96	0.16	30,30,30,30	0
56	MG	DA	3331	1/1	0.96	0.09	49,49,49,49	0
56	MG	DA	3093	1/1	0.96	0.14	54,54,54,54	0
56	MG	BA	3068	1/1	0.96	0.25	46,46,46,46	0
56	MG	DA	3335	1/1	0.96	0.07	43,43,43,43	0
56	MG	DA	3095	1/1	0.96	0.07	43,43,43,43	0
56	MG	BA	3349	1/1	0.96	0.16	49,49,49,49	0
56	MG	BA	3350	1/1	0.96	0.10	28,28,28,28	0
56	MG	BA	3810	1/1	0.96	0.08	43,43,43,43	0
56	MG	DA	3099	1/1	0.96	0.13	45,45,45,45	0
56	MG	DA	3342	1/1	0.96	0.06	46,46,46,46	0
56	MG	BA	3811	1/1	0.96	0.24	41,41,41,41	0
56	MG	DA	3641	1/1	0.96	0.08	49,49,49,49	0
56	MG	DA	3101	1/1	0.96	0.13	55,55,55,55	0
56	MG	AA	3052	1/1	0.96	0.17	49,49,49,49	0
56	MG	AM	201	1/1	0.96	0.04	59,59,59,59	0
56	MG	DA	3349	1/1	0.96	0.09	31,31,31,31	0
56	MG	DA	3350	1/1	0.96	0.06	53,53,53,53	0
56	MG	CA	3080	1/1	0.96	0.13	56,56,56,56	0
56	MG	DA	3354	1/1	0.96	0.07	48,48,48,48	0
56	MG	AA	3075	1/1	0.96	0.32	49,49,49,49	0
56	MG	BA	3139	1/1	0.96	0.08	53,53,53,53	0
56	MG	BA	3232	1/1	0.96	0.10	51,51,51,51	0
56	MG	DA	3359	1/1	0.96	0.11	39,39,39,39	0
56	MG	BB	204	1/1	0.96	0.07	42,42,42,42	0
56	MG	BA	3508	1/1	0.96	0.05	34,34,34,34	0
56	MG	DA	3363	1/1	0.96	0.13	49,49,49,49	0
56	MG	BA	3652	1/1	0.96	0.09	61,61,61,61	0
56	MG	DA	3112	1/1	0.96	0.18	37,37,37,37	0
56	MG	DA	3658	1/1	0.96	0.08	55,55,55,55	0
56	MG	DA	3366	1/1	0.96	0.05	38,38,38,38	0
56	MG	DA	3661	1/1	0.96	0.09	54,54,54,54	0
56	MG	BA	3653	1/1	0.96	0.09	39,39,39,39	0
56	MG	BA	3140	1/1	0.96	0.16	34,34,34,34	0
56	MG	BA	3141	1/1	0.96	0.16	42,42,42,42	0
56	MG	BA	3236	1/1	0.96	0.11	34,34,34,34	0
56	MG	DA	3117	1/1	0.96	0.10	42,42,42,42	0
56	MG	BA	3142	1/1	0.96	0.15	29,29,29,29	0
56	MG	DA	3121	1/1	0.96	0.10	40,40,40,40	0
56	MG	BB	214	1/1	0.96	0.17	53,53,53,53	0
56	MG	AA	3024	1/1	0.96	0.26	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	DA	3383	1/1	0.96	0.08	31,31,31,31	0
56	MG	DA	3125	1/1	0.96	0.08	40,40,40,40	0
56	MG	DA	3386	1/1	0.96	0.06	23,23,23,23	0
56	MG	BA	3239	1/1	0.96	0.16	40,40,40,40	0
56	MG	BA	3079	1/1	0.96	0.25	49,49,49,49	0
56	MG	BA	3522	1/1	0.96	0.10	16,16,16,16	0
56	MG	DA	3390	1/1	0.96	0.06	19,19,19,19	0
56	MG	BA	3365	1/1	0.96	0.13	37,37,37,37	0
56	MG	AA	3042	1/1	0.96	0.20	55,55,55,55	0
56	MG	BA	3669	1/1	0.96	0.09	36,36,36,36	0
56	MG	DA	3396	1/1	0.96	0.07	47,47,47,47	0
56	MG	BD	3305	1/1	0.96	0.09	31,31,31,31	0
56	MG	DD	305	1/1	0.96	0.36	39,39,39,39	0
56	MG	AA	3007	1/1	0.96	0.13	54,54,54,54	0
56	MG	BA	3527	1/1	0.96	0.06	27,27,27,27	0
56	MG	DA	3138	1/1	0.96	0.07	63,63,63,63	0
56	MG	BD	3308	1/1	0.96	0.20	60,60,60,60	0
56	MG	BD	3309	1/1	0.96	0.09	40,40,40,40	0
56	MG	BE	301	1/1	0.96	0.10	27,27,27,27	0
56	MG	BE	302	1/1	0.96	0.20	40,40,40,40	0
56	MG	BE	303	1/1	0.96	0.33	32,32,32,32	0
56	MG	DF	302	1/1	0.96	0.09	44,44,44,44	0
56	MG	BE	304	1/1	0.96	0.12	43,43,43,43	0
56	MG	DF	304	1/1	0.96	0.16	40,40,40,40	0
56	MG	BA	3672	1/1	0.96	0.07	62,62,62,62	0
56	MG	DA	3149	1/1	0.96	0.26	37,37,37,37	0
56	MG	BA	3152	1/1	0.96	0.16	42,42,42,42	0
56	MG	BA	3030	1/1	0.96	0.09	40,40,40,40	0
56	MG	BA	3531	1/1	0.96	0.09	43,43,43,43	0
56	MG	BA	3154	1/1	0.96	0.17	37,37,37,37	0
56	MG	DQ	3001	1/1	0.96	0.07	45,45,45,45	0
56	MG	BA	3248	1/1	0.96	0.30	52,52,52,52	0
56	MG	BA	3155	1/1	0.96	0.26	30,30,30,30	0
56	MG	DA	3422	1/1	0.96	0.07	51,51,51,51	0
56	MG	BA	3087	1/1	0.96	0.32	40,40,40,40	0
56	MG	BF	307	1/1	0.96	0.18	40,40,40,40	0
56	MG	DA	3159	1/1	0.96	0.06	42,42,42,42	0
56	MG	BA	3158	1/1	0.96	0.10	40,40,40,40	0
56	MG	DA	3161	1/1	0.96	0.13	37,37,37,37	0
56	MG	DA	3162	1/1	0.96	0.06	37,37,37,37	0
56	MG	BA	3159	1/1	0.96	0.11	40,40,40,40	0
56	MG	BA	3160	1/1	0.96	0.17	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	D0	102	1/1	0.96	0.13	51,51,51,51	0
56	MG	BA	3379	1/1	0.96	0.11	39,39,39,39	0
56	MG	BN	3001	1/1	0.96	0.34	52,52,52,52	0
56	MG	BA	3688	1/1	0.96	0.06	16,16,16,16	0
56	MG	BA	3031	1/1	0.96	0.13	28,28,28,28	0
56	MG	BA	3090	1/1	0.96	0.07	27,27,27,27	0
56	MG	DA	3171	1/1	0.96	0.13	53,53,53,53	0
56	MG	BA	3163	1/1	0.96	0.11	34,34,34,34	0
56	MG	BA	3164	1/1	0.96	0.25	35,35,35,35	0
56	MG	AA	3036	1/1	0.96	0.40	69,69,69,69	0
60	K	AX	3001	1/1	0.96	0.12	65,65,65,65	0
56	MG	BA	3033	1/1	0.96	0.28	42,42,42,42	0
56	MG	AA	3099	1/1	0.97	0.25	47,47,47,47	0
56	MG	CA	3140	1/1	0.97	0.11	75,75,75,75	0
56	MG	DA	3295	1/1	0.97	0.06	30,30,30,30	0
56	MG	DA	3123	1/1	0.97	0.13	52,52,52,52	0
56	MG	B7	105	1/1	0.97	0.12	46,46,46,46	0
56	MG	BA	3095	1/1	0.97	0.11	30,30,30,30	0
56	MG	BA	3661	1/1	0.97	0.09	48,48,48,48	0
56	MG	DA	3301	1/1	0.97	0.09	51,51,51,51	0
56	MG	BA	3279	1/1	0.97	0.27	45,45,45,45	0
56	MG	BA	3167	1/1	0.97	0.14	43,43,43,43	0
56	MG	CA	3004	1/1	0.97	0.05	67,67,67,67	0
56	MG	DA	3307	1/1	0.97	0.06	27,27,27,27	0
56	MG	BA	3782	1/1	0.97	0.29	30,30,30,30	0
56	MG	BA	3015	1/1	0.97	0.19	50,50,50,50	0
56	MG	DA	3523	1/1	0.97	0.06	52,52,52,52	0
56	MG	BA	3784	1/1	0.97	0.08	23,23,23,23	0
56	MG	BA	3667	1/1	0.97	0.13	39,39,39,39	0
56	MG	BA	3129	1/1	0.97	0.30	38,38,38,38	0
56	MG	DA	3136	1/1	0.97	0.26	43,43,43,43	0
56	MG	BA	3564	1/1	0.97	0.13	50,50,50,50	0
56	MG	DA	3532	1/1	0.97	0.08	61,61,61,61	0
56	MG	DA	3139	1/1	0.97	0.06	41,41,41,41	0
56	MG	BA	3456	1/1	0.97	0.05	32,32,32,32	0
56	MG	AA	3114	1/1	0.97	0.09	45,45,45,45	0
56	MG	AA	3053	1/1	0.97	0.13	46,46,46,46	0
56	MG	BA	3070	1/1	0.97	0.16	39,39,39,39	0
56	MG	DA	3538	1/1	0.97	0.06	44,44,44,44	0
56	MG	DA	3144	1/1	0.97	0.06	39,39,39,39	0
56	MG	DA	3145	1/1	0.97	0.13	38,38,38,38	0
56	MG	DA	3323	1/1	0.97	0.09	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3173	1/1	0.97	0.25	41,41,41,41	0
56	MG	BA	3570	1/1	0.97	0.11	35,35,35,35	0
56	MG	BA	3287	1/1	0.97	0.16	28,28,28,28	0
56	MG	BA	3462	1/1	0.97	0.10	49,49,49,49	0
56	MG	BA	3226	1/1	0.97	0.16	25,25,25,25	0
56	MG	DA	3329	1/1	0.97	0.13	47,47,47,47	0
56	MG	BA	3466	1/1	0.97	0.10	44,44,44,44	0
56	MG	DA	3552	1/1	0.97	0.07	36,36,36,36	0
56	MG	BA	3681	1/1	0.97	0.12	50,50,50,50	0
56	MG	DA	3555	1/1	0.97	0.05	56,56,56,56	0
56	MG	BA	3803	1/1	0.97	0.13	33,33,33,33	0
56	MG	AA	3116	1/1	0.97	0.06	32,32,32,32	0
56	MG	BA	3228	1/1	0.97	0.30	56,56,56,56	0
56	MG	DA	3336	1/1	0.97	0.05	39,39,39,39	0
56	MG	BA	3684	1/1	0.97	0.13	51,51,51,51	0
56	MG	BA	3469	1/1	0.97	0.10	41,41,41,41	0
56	MG	BA	3686	1/1	0.97	0.07	41,41,41,41	0
56	MG	BA	3809	1/1	0.97	0.06	41,41,41,41	0
56	MG	BA	3471	1/1	0.97	0.07	27,27,27,27	0
56	MG	AA	3037	1/1	0.97	0.20	46,46,46,46	0
56	MG	BA	3812	1/1	0.97	0.09	31,31,31,31	0
56	MG	BA	3689	1/1	0.97	0.09	53,53,53,53	0
56	MG	BA	3581	1/1	0.97	0.05	37,37,37,37	0
56	MG	DA	3346	1/1	0.97	0.10	48,48,48,48	0
56	MG	CA	3035	1/1	0.97	0.13	52,52,52,52	0
56	MG	DA	3167	1/1	0.97	0.14	38,38,38,38	0
56	MG	DA	3572	1/1	0.97	0.06	68,68,68,68	0
56	MG	BA	3691	1/1	0.97	0.08	68,68,68,68	0
56	MG	DA	3352	1/1	0.97	0.06	27,27,27,27	0
56	MG	BA	3293	1/1	0.97	0.09	40,40,40,40	0
56	MG	BA	3053	1/1	0.97	0.09	23,23,23,23	0
56	MG	BA	3694	1/1	0.97	0.15	54,54,54,54	0
56	MG	DA	3356	1/1	0.97	0.14	37,37,37,37	0
56	MG	DA	3579	1/1	0.97	0.06	52,52,52,52	0
56	MG	BA	3075	1/1	0.97	0.10	21,21,21,21	0
56	MG	BA	3104	1/1	0.97	0.13	23,23,23,23	0
56	MG	DA	3005	1/1	0.97	0.12	26,26,26,26	0
56	MG	BA	3076	1/1	0.97	0.12	34,34,34,34	0
56	MG	DA	3361	1/1	0.97	0.05	25,25,25,25	0
56	MG	BA	3298	1/1	0.97	0.24	49,49,49,49	0
56	MG	DA	3588	1/1	0.97	0.05	65,65,65,65	0
56	MG	DA	3008	1/1	0.97	0.09	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	CA	3044	1/1	0.97	0.10	44,44,44,44	0
56	MG	DA	3591	1/1	0.97	0.05	59,59,59,59	0
56	MG	BA	3299	1/1	0.97	0.05	44,44,44,44	0
56	MG	DA	3012	1/1	0.97	0.04	39,39,39,39	0
56	MG	BA	3481	1/1	0.97	0.13	44,44,44,44	0
56	MG	DA	3595	1/1	0.97	0.08	39,39,39,39	0
56	MG	BA	3181	1/1	0.97	0.11	26,26,26,26	0
56	MG	DA	3598	1/1	0.97	0.08	30,30,30,30	0
56	MG	BB	213	1/1	0.97	0.09	30,30,30,30	0
56	MG	DA	3371	1/1	0.97	0.07	22,22,22,22	0
56	MG	BA	3484	1/1	0.97	0.10	51,51,51,51	0
56	MG	DA	3374	1/1	0.97	0.05	31,31,31,31	0
56	MG	DA	3375	1/1	0.97	0.06	37,37,37,37	0
56	MG	BA	3301	1/1	0.97	0.06	48,48,48,48	0
56	MG	BA	3302	1/1	0.97	0.12	24,24,24,24	0
56	MG	DA	3020	1/1	0.97	0.05	32,32,32,32	0
56	MG	DA	3021	1/1	0.97	0.18	40,40,40,40	0
56	MG	DA	3190	1/1	0.97	0.10	41,41,41,41	0
56	MG	BA	3304	1/1	0.97	0.05	37,37,37,37	0
56	MG	BA	3182	1/1	0.97	0.07	21,21,21,21	0
56	MG	AA	3186	1/1	0.97	0.11	42,42,42,42	0
56	MG	DA	3613	1/1	0.97	0.04	55,55,55,55	0
56	MG	BA	3708	1/1	0.97	0.20	36,36,36,36	0
56	MG	DA	3028	1/1	0.97	0.14	45,45,45,45	0
56	MG	BB	222	1/1	0.97	0.14	50,50,50,50	0
56	MG	BD	3301	1/1	0.97	0.11	37,37,37,37	0
56	MG	BD	3302	1/1	0.97	0.05	46,46,46,46	0
56	MG	BA	3021	1/1	0.97	0.07	22,22,22,22	0
56	MG	CA	3060	1/1	0.97	0.08	47,47,47,47	0
56	MG	AA	3126	1/1	0.97	0.14	57,57,57,57	0
56	MG	BA	3388	1/1	0.97	0.05	27,27,27,27	0
56	MG	BA	3311	1/1	0.97	0.08	23,23,23,23	0
56	MG	BA	3188	1/1	0.97	0.15	46,46,46,46	0
56	MG	DA	3401	1/1	0.97	0.04	43,43,43,43	0
56	MG	BA	3189	1/1	0.97	0.17	46,46,46,46	0
56	MG	DA	3206	1/1	0.97	0.16	46,46,46,46	0
56	MG	BA	3243	1/1	0.97	0.12	56,56,56,56	0
56	MG	BA	3609	1/1	0.97	0.07	54,54,54,54	0
56	MG	BA	3718	1/1	0.97	0.13	53,53,53,53	0
56	MG	BA	3244	1/1	0.97	0.25	39,39,39,39	0
56	MG	BA	3146	1/1	0.97	0.06	19,19,19,19	0
56	MG	DA	3045	1/1	0.97	0.32	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3110	1/1	0.97	0.06	46,46,46,46	0
56	MG	DA	3413	1/1	0.97	0.04	34,34,34,34	0
56	MG	DA	3414	1/1	0.97	0.06	38,38,38,38	0
56	MG	BA	3148	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3081	1/1	0.97	0.09	33,33,33,33	0
56	MG	BA	3249	1/1	0.97	0.09	40,40,40,40	0
56	MG	DA	3050	1/1	0.97	0.08	37,37,37,37	0
56	MG	BA	3510	1/1	0.97	0.07	42,42,42,42	0
56	MG	CA	3076	1/1	0.97	0.17	35,35,35,35	0
56	MG	BA	3511	1/1	0.97	0.16	43,43,43,43	0
56	MG	BA	3729	1/1	0.97	0.04	27,27,27,27	0
56	MG	BA	3402	1/1	0.97	0.06	25,25,25,25	0
56	MG	BA	3732	1/1	0.97	0.06	41,41,41,41	0
56	MG	BA	3619	1/1	0.97	0.07	33,33,33,33	0
56	MG	DA	3427	1/1	0.97	0.04	45,45,45,45	0
56	MG	DA	3428	1/1	0.97	0.05	26,26,26,26	0
56	MG	DA	3058	1/1	0.97	0.07	50,50,50,50	0
56	MG	AA	3188	1/1	0.97	0.19	49,49,49,49	0
56	MG	DA	3228	1/1	0.97	0.14	46,46,46,46	0
56	MG	BA	3517	1/1	0.97	0.08	49,49,49,49	0
56	MG	BA	3406	1/1	0.97	0.06	32,32,32,32	0
56	MG	BA	3408	1/1	0.97	0.05	21,21,21,21	0
56	MG	BA	3058	1/1	0.97	0.09	27,27,27,27	0
56	MG	BA	3196	1/1	0.97	0.07	40,40,40,40	0
56	MG	BA	3086	1/1	0.97	0.17	49,49,49,49	0
56	MG	BA	3115	1/1	0.97	0.07	33,33,33,33	0
56	MG	DA	3660	1/1	0.97	0.04	28,28,28,28	0
56	MG	BA	3116	1/1	0.97	0.05	35,35,35,35	0
56	MG	BA	3156	1/1	0.97	0.08	32,32,32,32	0
56	MG	AA	3111	1/1	0.97	0.15	61,61,61,61	0
56	MG	BQ	202	1/1	0.97	0.14	37,37,37,37	0
56	MG	BA	3528	1/1	0.97	0.10	46,46,46,46	0
56	MG	DA	3667	1/1	0.97	0.10	66,66,66,66	0
56	MG	BA	3332	1/1	0.97	0.12	36,36,36,36	0
56	MG	DA	3669	1/1	0.97	0.12	38,38,38,38	0
56	MG	BA	3421	1/1	0.97	0.14	48,48,48,48	0
56	MG	BR	202	1/1	0.97	0.15	42,42,42,42	0
56	MG	DA	3449	1/1	0.97	0.05	33,33,33,33	0
56	MG	CA	3098	1/1	0.97	0.10	44,44,44,44	0
56	MG	BR	203	1/1	0.97	0.16	34,34,34,34	0
56	MG	DA	3452	1/1	0.97	0.05	37,37,37,37	0
56	MG	BA	3060	1/1	0.97	0.18	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	CA	3102	1/1	0.97	0.12	49,49,49,49	0
56	MG	BA	3089	1/1	0.97	0.14	42,42,42,42	0
56	MG	BA	3752	1/1	0.97	0.07	32,32,32,32	0
56	MG	BA	3042	1/1	0.97	0.09	41,41,41,41	0
56	MG	DB	3007	1/1	0.97	0.10	42,42,42,42	0
56	MG	BA	3263	1/1	0.97	0.28	56,56,56,56	0
56	MG	BA	3205	1/1	0.97	0.14	40,40,40,40	0
56	MG	DA	3460	1/1	0.97	0.07	42,42,42,42	0
56	MG	DA	3084	1/1	0.97	0.07	47,47,47,47	0
56	MG	DA	3462	1/1	0.97	0.05	31,31,31,31	0
56	MG	DD	304	1/1	0.97	0.10	33,33,33,33	0
56	MG	DA	3086	1/1	0.97	0.17	36,36,36,36	0
56	MG	DA	3464	1/1	0.97	0.04	24,24,24,24	0
56	MG	BA	3091	1/1	0.97	0.22	40,40,40,40	0
56	MG	DA	3088	1/1	0.97	0.11	30,30,30,30	0
56	MG	CA	3109	1/1	0.97	0.17	41,41,41,41	0
56	MG	DA	3261	1/1	0.97	0.14	36,36,36,36	0
56	MG	CA	3110	1/1	0.97	0.21	48,48,48,48	0
56	MG	BA	3343	1/1	0.97	0.06	30,30,30,30	0
56	MG	DA	3092	1/1	0.97	0.11	48,48,48,48	0
56	MG	DA	3265	1/1	0.97	0.13	37,37,37,37	0
56	MG	DA	3473	1/1	0.97	0.07	30,30,30,30	0
56	MG	BA	3266	1/1	0.97	0.12	27,27,27,27	0
56	MG	DA	3475	1/1	0.97	0.08	38,38,38,38	0
56	MG	DA	3476	1/1	0.97	0.11	53,53,53,53	0
56	MG	CA	3114	1/1	0.97	0.09	52,52,52,52	0
56	MG	BA	3540	1/1	0.97	0.07	57,57,57,57	0
56	MG	BX	101	1/1	0.97	0.07	36,36,36,36	0
56	MG	BA	3345	1/1	0.97	0.05	28,28,28,28	0
56	MG	BA	3542	1/1	0.97	0.09	20,20,20,20	0
56	MG	BA	3543	1/1	0.97	0.15	23,23,23,23	0
56	MG	BA	3123	1/1	0.97	0.14	28,28,28,28	0
56	MG	BA	3210	1/1	0.97	0.06	43,43,43,43	0
56	MG	DU	3002	1/1	0.97	0.28	52,52,52,52	0
56	MG	BA	3442	1/1	0.97	0.06	36,36,36,36	0
56	MG	AA	3031	1/1	0.97	0.21	54,54,54,54	0
56	MG	DA	3487	1/1	0.97	0.09	37,37,37,37	0
56	MG	BA	3270	1/1	0.97	0.24	40,40,40,40	0
56	MG	B0	104	1/1	0.97	0.10	41,41,41,41	0
56	MG	DA	3490	1/1	0.97	0.07	43,43,43,43	0
56	MG	BA	3550	1/1	0.97	0.06	25,25,25,25	0
56	MG	BA	3212	1/1	0.97	0.10	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	D0	101	1/1	0.97	0.07	50,50,50,50	0
56	MG	DA	3108	1/1	0.97	0.07	46,46,46,46	0
56	MG	B3	3001	1/1	0.97	0.09	38,38,38,38	0
56	MG	BA	3552	1/1	0.97	0.06	46,46,46,46	0
56	MG	CA	3130	1/1	0.97	0.15	51,51,51,51	0
56	MG	BA	3553	1/1	0.97	0.09	53,53,53,53	0
56	MG	BA	3273	1/1	0.97	0.24	41,41,41,41	0
59	ZN	B4	501	1/1	0.97	0.04	99,99,99,99	0
56	MG	AX	3004	1/1	0.97	0.12	53,53,53,53	0
56	MG	DA	3288	1/1	0.97	0.08	48,48,48,48	0
59	ZN	B9	501	1/1	0.97	0.04	49,49,49,49	0
56	MG	BA	3775	1/1	0.97	0.05	34,34,34,34	0
56	MG	B6	101	1/1	0.97	0.08	47,47,47,47	0
56	MG	BA	3658	1/1	0.97	0.08	51,51,51,51	0
56	MG	B7	103	1/1	0.97	0.07	35,35,35,35	0
56	MG	DA	3119	1/1	0.98	0.12	40,40,40,40	0
56	MG	BA	3215	1/1	0.98	0.09	47,47,47,47	0
56	MG	BA	3601	1/1	0.98	0.09	49,49,49,49	0
56	MG	BA	3451	1/1	0.98	0.09	31,31,31,31	0
56	MG	BA	3383	1/1	0.98	0.08	20,20,20,20	0
56	MG	CA	3101	1/1	0.98	0.14	54,54,54,54	0
56	MG	DA	3022	1/1	0.98	0.04	29,29,29,29	0
56	MG	DA	3127	1/1	0.98	0.13	36,36,36,36	0
56	MG	BD	3303	1/1	0.98	0.04	33,33,33,33	0
56	MG	DA	3348	1/1	0.98	0.04	32,32,32,32	0
56	MG	BA	3333	1/1	0.98	0.04	23,23,23,23	0
56	MG	BA	3334	1/1	0.98	0.07	26,26,26,26	0
56	MG	DA	3351	1/1	0.98	0.11	32,32,32,32	0
56	MG	AA	3137	1/1	0.98	0.06	42,42,42,42	0
56	MG	DA	3238	1/1	0.98	0.09	54,54,54,54	0
56	MG	AA	3035	1/1	0.98	0.09	26,26,26,26	0
56	MG	DA	3029	1/1	0.98	0.06	36,36,36,36	0
56	MG	BA	3608	1/1	0.98	0.11	34,34,34,34	0
56	MG	BA	3218	1/1	0.98	0.10	34,34,34,34	0
56	MG	BA	3253	1/1	0.98	0.21	47,47,47,47	0
56	MG	DA	3137	1/1	0.98	0.22	43,43,43,43	0
56	MG	BA	3535	1/1	0.98	0.15	31,31,31,31	0
56	MG	DA	3246	1/1	0.98	0.08	31,31,31,31	0
56	MG	CA	3111	1/1	0.98	0.10	56,56,56,56	0
56	MG	BA	3074	1/1	0.98	0.09	31,31,31,31	0
56	MG	CA	3018	1/1	0.98	0.06	52,52,52,52	0
56	MG	DA	3492	1/1	0.98	0.05	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3220	1/1	0.98	0.15	40,40,40,40	0
56	MG	DA	3251	1/1	0.98	0.11	46,46,46,46	0
56	MG	BE	305	1/1	0.98	0.07	19,19,19,19	0
56	MG	AA	3120	1/1	0.98	0.07	49,49,49,49	0
56	MG	DA	3498	1/1	0.98	0.05	44,44,44,44	0
56	MG	BA	3136	1/1	0.98	0.07	42,42,42,42	0
56	MG	BA	3043	1/1	0.98	0.05	35,35,35,35	0
56	MG	BA	3465	1/1	0.98	0.06	47,47,47,47	0
56	MG	BA	3138	1/1	0.98	0.20	40,40,40,40	0
56	MG	BA	3397	1/1	0.98	0.06	25,25,25,25	0
56	MG	AA	3063	1/1	0.98	0.09	42,42,42,42	0
56	MG	DA	3505	1/1	0.98	0.07	45,45,45,45	0
56	MG	BA	3261	1/1	0.98	0.04	46,46,46,46	0
56	MG	DA	3378	1/1	0.98	0.05	34,34,34,34	0
56	MG	BA	3470	1/1	0.98	0.11	37,37,37,37	0
56	MG	DA	3380	1/1	0.98	0.05	35,35,35,35	0
56	MG	BA	3400	1/1	0.98	0.05	34,34,34,34	0
56	MG	BA	3118	1/1	0.98	0.27	37,37,37,37	0
56	MG	DA	3155	1/1	0.98	0.25	38,38,38,38	0
56	MG	DA	3384	1/1	0.98	0.09	39,39,39,39	0
56	MG	BA	3625	1/1	0.98	0.04	31,31,31,31	0
56	MG	BA	3078	1/1	0.98	0.06	15,15,15,15	0
56	MG	BA	3474	1/1	0.98	0.04	20,20,20,20	0
56	MG	BA	3303	1/1	0.98	0.17	37,37,37,37	0
56	MG	BN	3003	1/1	0.98	0.09	44,44,44,44	0
56	MG	BA	3404	1/1	0.98	0.10	23,23,23,23	0
56	MG	BN	3005	1/1	0.98	0.10	35,35,35,35	0
56	MG	BA	3005	1/1	0.98	0.06	33,33,33,33	0
56	MG	BA	3143	1/1	0.98	0.05	39,39,39,39	0
56	MG	DA	3395	1/1	0.98	0.04	33,33,33,33	0
56	MG	BA	3354	1/1	0.98	0.04	20,20,20,20	0
56	MG	DA	3397	1/1	0.98	0.03	30,30,30,30	0
56	MG	BP	202	1/1	0.98	0.06	27,27,27,27	0
56	MG	DA	3528	1/1	0.98	0.04	39,39,39,39	0
56	MG	DA	3663	1/1	0.98	0.05	37,37,37,37	0
56	MG	DA	3529	1/1	0.98	0.06	57,57,57,57	0
56	MG	BA	3230	1/1	0.98	0.21	36,36,36,36	0
56	MG	BA	3788	1/1	0.98	0.07	10,10,10,10	0
56	MG	AA	3151	1/1	0.98	0.05	56,56,56,56	0
56	MG	BA	3414	1/1	0.98	0.11	33,33,33,33	0
56	MG	BA	3791	1/1	0.98	0.05	18,18,18,18	0
56	MG	BA	3710	1/1	0.98	0.16	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3415	1/1	0.98	0.09	34,34,34,34	0
56	MG	DA	3174	1/1	0.98	0.23	50,50,50,50	0
56	MG	BA	3309	1/1	0.98	0.05	50,50,50,50	0
56	MG	DA	3539	1/1	0.98	0.08	38,38,38,38	0
56	MG	BA	3145	1/1	0.98	0.08	41,41,41,41	0
56	MG	BA	3008	1/1	0.98	0.08	26,26,26,26	0
56	MG	BA	3063	1/1	0.98	0.32	54,54,54,54	0
56	MG	BA	3313	1/1	0.98	0.08	34,34,34,34	0
56	MG	AA	3132	1/1	0.98	0.10	36,36,36,36	0
56	MG	BA	3272	1/1	0.98	0.09	22,22,22,22	0
56	MG	BA	3802	1/1	0.98	0.19	23,23,23,23	0
56	MG	BU	209	1/1	0.98	0.21	27,27,27,27	0
56	MG	BV	202	1/1	0.98	0.20	33,33,33,33	0
56	MG	BA	3423	1/1	0.98	0.06	31,31,31,31	0
56	MG	DD	301	1/1	0.98	0.06	43,43,43,43	0
56	MG	DA	3550	1/1	0.98	0.09	22,22,22,22	0
56	MG	DA	3551	1/1	0.98	0.04	47,47,47,47	0
56	MG	BA	3497	1/1	0.98	0.03	44,44,44,44	0
56	MG	DA	3553	1/1	0.98	0.04	46,46,46,46	0
56	MG	BA	3364	1/1	0.98	0.15	29,29,29,29	0
56	MG	BA	3425	1/1	0.98	0.08	48,48,48,48	0
56	MG	BW	204	1/1	0.98	0.19	31,31,31,31	0
56	MG	DE	301	1/1	0.98	0.07	35,35,35,35	0
56	MG	CA	3161	1/1	0.98	0.10	51,51,51,51	0
56	MG	BA	3316	1/1	0.98	0.11	25,25,25,25	0
56	MG	DA	3302	1/1	0.98	0.07	32,32,32,32	0
56	MG	BX	102	1/1	0.98	0.08	36,36,36,36	0
56	MG	BA	3149	1/1	0.98	0.21	36,36,36,36	0
56	MG	BA	3085	1/1	0.98	0.12	23,23,23,23	0
56	MG	DA	3306	1/1	0.98	0.19	35,35,35,35	0
56	MG	DA	3432	1/1	0.98	0.05	37,37,37,37	0
56	MG	BA	3504	1/1	0.98	0.05	40,40,40,40	0
56	MG	BA	3432	1/1	0.98	0.07	35,35,35,35	0
56	MG	BA	3433	1/1	0.98	0.08	31,31,31,31	0
56	MG	BA	3275	1/1	0.98	0.17	34,34,34,34	0
56	MG	DA	3311	1/1	0.98	0.06	19,19,19,19	0
56	MG	CA	3170	1/1	0.98	0.11	53,53,53,53	0
56	MG	BA	3022	1/1	0.98	0.03	25,25,25,25	0
56	MG	DQ	3002	1/1	0.98	0.10	41,41,41,41	0
56	MG	CA	3172	1/1	0.98	0.08	50,50,50,50	0
56	MG	BA	3436	1/1	0.98	0.09	17,17,17,17	0
56	MG	BA	3177	1/1	0.98	0.06	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3278	1/1	0.98	0.21	30,30,30,30	0
56	MG	BA	3023	1/1	0.98	0.09	35,35,35,35	0
56	MG	BA	3374	1/1	0.98	0.04	21,21,21,21	0
56	MG	BA	3036	1/1	0.98	0.12	19,19,19,19	0
56	MG	BA	3589	1/1	0.98	0.07	42,42,42,42	0
56	MG	DA	3448	1/1	0.98	0.06	45,45,45,45	0
56	MG	BB	208	1/1	0.98	0.08	36,36,36,36	0
56	MG	BA	3208	1/1	0.98	0.13	19,19,19,19	0
56	MG	BA	3743	1/1	0.98	0.07	43,43,43,43	0
56	MG	BA	3664	1/1	0.98	0.10	17,17,17,17	0
56	MG	BA	3665	1/1	0.98	0.06	40,40,40,40	0
56	MG	DA	3587	1/1	0.98	0.12	52,52,52,52	0
56	MG	B7	101	1/1	0.98	0.06	47,47,47,47	0
56	MG	B7	102	1/1	0.98	0.10	28,28,28,28	0
56	MG	BA	3052	1/1	0.98	0.12	23,23,23,23	0
56	MG	BA	3011	1/1	0.98	0.04	33,33,33,33	0
58	SF4	AD	501	8/8	0.98	0.05	62,74,91,95	0
58	SF4	CD	501	8/8	0.98	0.04	64,77,89,111	0
59	ZN	AN	501	1/1	0.98	0.05	86,86,86,86	0
56	MG	BA	3012	1/1	0.98	0.18	33,33,33,33	0
56	MG	BA	3183	1/1	0.98	0.08	35,35,35,35	0
56	MG	B8	102	1/1	0.98	0.07	41,41,41,41	0
56	MG	DA	3334	1/1	0.98	0.05	45,45,45,45	0
56	MG	BA	3448	1/1	0.98	0.08	23,23,23,23	0
56	MG	BA	3524	1/1	0.98	0.10	53,53,53,53	0
56	MG	BA	3184	1/1	0.98	0.17	37,37,37,37	0
56	MG	CA	3003	1/1	0.98	0.09	51,51,51,51	0
56	MG	DA	3407	1/1	0.99	0.02	28,28,28,28	0
56	MG	BA	3429	1/1	0.99	0.03	23,23,23,23	0
56	MG	DA	3009	1/1	0.99	0.07	29,29,29,29	0
56	MG	BA	3546	1/1	0.99	0.05	38,38,38,38	0
56	MG	DA	3120	1/1	0.99	0.07	34,34,34,34	0
56	MG	BP	201	1/1	0.99	0.24	28,28,28,28	0
56	MG	BA	3513	1/1	0.99	0.03	43,43,43,43	0
56	MG	DA	3013	1/1	0.99	0.04	32,32,32,32	0
56	MG	BB	215	1/1	0.99	0.04	35,35,35,35	0
56	MG	BA	3341	1/1	0.99	0.03	43,43,43,43	0
56	MG	BA	3515	1/1	0.99	0.06	35,35,35,35	0
56	MG	BA	3482	1/1	0.99	0.08	42,42,42,42	0
56	MG	DA	3298	1/1	0.99	0.04	55,55,55,55	0
56	MG	BA	3407	1/1	0.99	0.09	40,40,40,40	0
56	MG	DA	3421	1/1	0.99	0.02	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	BA	3007	1/1	0.99	0.06	35,35,35,35	0
56	MG	BA	3409	1/1	0.99	0.07	21,21,21,21	0
56	MG	BA	3486	1/1	0.99	0.05	22,22,22,22	0
56	MG	BA	3591	1/1	0.99	0.08	48,48,48,48	0
56	MG	BA	3289	1/1	0.99	0.30	35,35,35,35	0
56	MG	BA	3556	1/1	0.99	0.06	48,48,48,48	0
56	MG	BU	203	1/1	0.99	0.13	27,27,27,27	0
56	MG	BA	3594	1/1	0.99	0.11	33,33,33,33	0
56	MG	DA	3027	1/1	0.99	0.15	42,42,42,42	0
56	MG	DA	3495	1/1	0.99	0.12	39,39,39,39	0
56	MG	BA	3037	1/1	0.99	0.31	29,29,29,29	0
56	MG	DA	3368	1/1	0.99	0.06	24,24,24,24	0
56	MG	BA	3235	1/1	0.99	0.12	26,26,26,26	0
56	MG	BU	207	1/1	0.99	0.24	29,29,29,29	0
56	MG	DA	3085	1/1	0.99	0.12	38,38,38,38	0
56	MG	BA	3413	1/1	0.99	0.08	27,27,27,27	0
56	MG	DA	3373	1/1	0.99	0.06	39,39,39,39	0
56	MG	BA	3560	1/1	0.99	0.10	38,38,38,38	0
56	MG	BV	201	1/1	0.99	0.19	27,27,27,27	0
56	MG	BA	3493	1/1	0.99	0.06	49,49,49,49	0
56	MG	BA	3463	1/1	0.99	0.03	10,10,10,10	0
56	MG	BA	3393	1/1	0.99	0.05	22,22,22,22	0
56	MG	BA	3003	1/1	0.99	0.05	30,30,30,30	0
56	MG	BA	3107	1/1	0.99	0.18	50,50,50,50	0
56	MG	BW	203	1/1	0.99	0.10	37,37,37,37	0
56	MG	BA	3680	1/1	0.99	0.05	53,53,53,53	0
56	MG	BA	3441	1/1	0.99	0.08	32,32,32,32	0
56	MG	BA	3306	1/1	0.99	0.14	18,18,18,18	0
56	MG	BA	3500	1/1	0.99	0.08	32,32,32,32	0
56	MG	BA	3723	1/1	0.99	0.04	25,25,25,25	0
56	MG	BA	3069	1/1	0.99	0.14	39,39,39,39	0
56	MG	BA	3084	1/1	0.99	0.11	33,33,33,33	0
56	MG	BA	3209	1/1	0.99	0.07	35,35,35,35	0
56	MG	BA	3013	1/1	0.99	0.10	26,26,26,26	0
56	MG	DA	3216	1/1	0.99	0.13	41,41,41,41	0
56	MG	BA	3009	1/1	0.99	0.04	25,25,25,25	0
56	MG	BA	3730	1/1	0.99	0.08	13,13,13,13	0
56	MG	DA	3394	1/1	0.99	0.04	40,40,40,40	0
56	MG	BA	3773	1/1	0.99	0.04	38,38,38,38	0
56	MG	BA	3574	1/1	0.99	0.04	28,28,28,28	0
56	MG	DA	3526	1/1	0.99	0.17	28,28,28,28	0
56	MG	BA	3339	1/1	0.99	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
56	MG	BA	3370	1/1	0.99	0.04	27,27,27,27	0
56	MG	DA	3596	1/1	0.99	0.03	65,65,65,65	0
59	ZN	BY	203	1/1	0.99	0.02	54,54,54,54	0
56	MG	BA	3734	1/1	0.99	0.07	18,18,18,18	0
56	MG	AA	3108	1/1	0.99	0.08	58,58,58,58	0
56	MG	BA	3426	1/1	0.99	0.10	20,20,20,20	0
56	MG	DA	3004	1/1	0.99	0.12	25,25,25,25	0
56	MG	BA	3405	1/1	0.99	0.09	22,22,22,22	0
59	ZN	DY	501	1/1	0.99	0.05	97,97,97,97	0
56	MG	CA	3137	1/1	0.99	0.09	50,50,50,50	0
59	ZN	D6	501	1/1	0.99	0.05	66,66,66,66	0
59	ZN	D9	501	1/1	0.99	0.03	65,65,65,65	0
56	MG	BA	3428	1/1	0.99	0.12	36,36,36,36	0
56	MG	DA	3406	1/1	0.99	0.04	33,33,33,33	0
56	MG	AA	3131	1/1	1.00	0.07	29,29,29,29	0
56	MG	DA	3601	1/1	1.00	0.02	26,26,26,26	0
56	MG	BA	3487	1/1	1.00	0.07	23,23,23,23	0
56	MG	BA	3516	1/1	1.00	0.09	28,28,28,28	0
56	MG	BA	3727	1/1	1.00	0.02	34,34,34,34	0
59	ZN	D5	501	1/1	1.00	0.03	52,52,52,52	0
56	MG	BA	3794	1/1	1.00	0.07	29,29,29,29	0
56	MG	DA	3581	1/1	1.00	0.03	35,35,35,35	0
56	MG	BA	3488	1/1	1.00	0.06	16,16,16,16	0
56	MG	BA	3329	1/1	1.00	0.06	24,24,24,24	0

6.5 Other polymers

There are no such residues in this entry.