



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 02:59 PM EDT

PDB ID : 1VY5 / pdb_00001vy5
Title : Crystal structure of the Thermus thermophilus 70S ribosome in the post-catalysis state of peptide bond formation containing dipeptidyl-tRNA in the A site and deacylated tRNA in the P site.
Authors : Polikanov, Y.S.; Steitz, T.A.; Innis, C.A.
Deposited on : 2014-05-13
Resolution : 2.55 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
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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

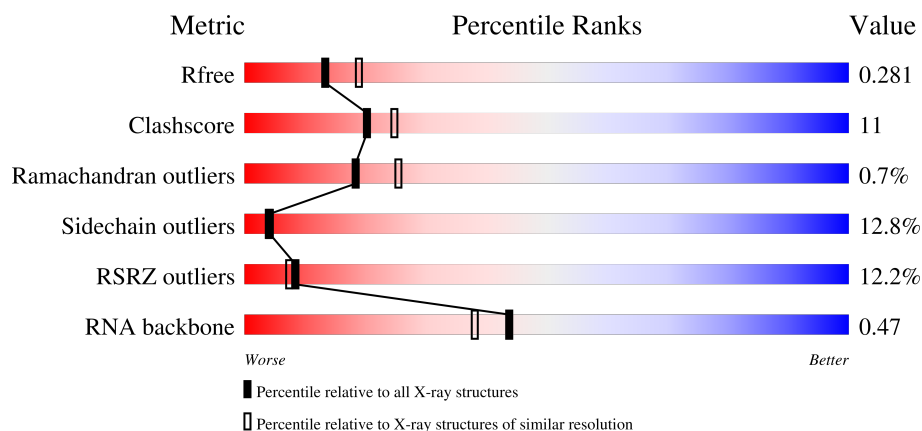
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)
RNA backbone	3983	1112 (2.80-2.28)

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	5% 51% 38% 9%
1	CA	1521	13% 45% 43% 11%
2	AB	256	27% 39% 41% 10% 10%
2	CB	256	43% 35% 41% 13% 10%

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Mol	Chain	Length	Quality of chain
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	
14	CN	61	
15	AO	89	

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Mol	Chain	Length	Quality of chain
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	AW	76	
23	CW	76	
24	AX	77	
24	CX	77	
25	AY	76	
25	CY	76	
26	BA	2915	
26	DA	2915	
27	BB	121	
27	DB	121	

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

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

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

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 297141 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	1498	Total	C	N	O	P	0	0	0
			32205	14333	5970	10404	1498			
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	123	Total	C	N	O	S		
			958	592	198	166	2	0	0
13	CM	122	Total	C	N	O	S		
			950	586	197	165	2	0	0

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

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	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	12	Total	C	N	O	P	0	0	0
			252	115	46	80	11			

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1607	727	288	516	73	3			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1560	702	281	503	72	2			

- Molecule 24 is a RNA chain called P-site tRNA.

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

- Molecule 25 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
25	AY	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
25	CY	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

- Molecule 26 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BA	2819	Total	C	N	O	P	0	0	0
			60729	27026	11370	19515	2818			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	DA	2800	Total	C	N	O	P	0	0	0
			60311	26840	11284	19388	2799			

- Molecule 27 is a RNA chain called 5S Ribosomal RNA.

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

- Molecule 28 is a protein called 50S ribosomal protein L2.

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

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L25.

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

- Molecule 47 is a protein called 50S ribosomal protein L27.

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

- Molecule 48 is a protein called 50S ribosomal protein L28.

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

- Molecule 49 is a protein called 50S ribosomal protein L29.

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

- Molecule 50 is a protein called 50S ribosomal protein L30.

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

- Molecule 51 is a protein called 50S ribosomal protein L31.

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

- Molecule 52 is a protein called 50S ribosomal protein L32.

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

- Molecule 53 is a protein called 50S ribosomal protein L33.

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

- Molecule 54 is a protein called 50S ribosomal protein L34.

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

- Molecule 55 is a protein called 50S ribosomal protein L35.

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

- Molecule 56 is a protein called 50S ribosomal protein L36.

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

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AA	214	Total	Mg	0	0
			214	214		
57	AE	3	Total	Mg	0	0
			3	3		
57	AF	1	Total	Mg	0	0
			1	1		
57	AK	1	Total	Mg	0	0
			1	1		
57	AM	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	AN	2	Total 2	Mg 2	0	0
57	AW	4	Total 4	Mg 4	0	0
57	AX	15	Total 15	Mg 15	0	0
57	AY	3	Total 3	Mg 3	0	0
57	BA	812	Total 812	Mg 812	0	0
57	BB	20	Total 20	Mg 20	0	0
57	BD	9	Total 9	Mg 9	0	0
57	BE	8	Total 8	Mg 8	0	0
57	BF	9	Total 9	Mg 9	0	0
57	BG	3	Total 3	Mg 3	0	0
57	BN	6	Total 6	Mg 6	0	0
57	BO	2	Total 2	Mg 2	0	0
57	BP	5	Total 5	Mg 5	0	0
57	BQ	5	Total 5	Mg 5	0	0
57	BR	2	Total 2	Mg 2	0	0
57	BU	8	Total 8	Mg 8	0	0
57	BV	5	Total 5	Mg 5	0	0
57	BW	4	Total 4	Mg 4	0	0
57	BX	3	Total 3	Mg 3	0	0
57	BY	1	Total 1	Mg 1	0	0
57	BZ	1	Total 1	Mg 1	0	0

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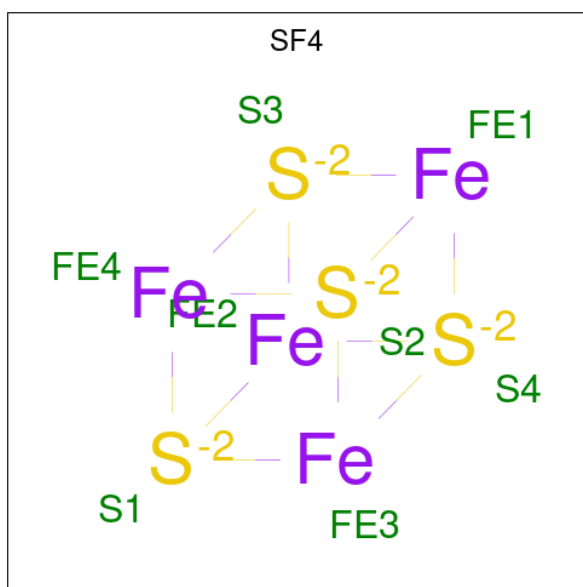
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	B0	3	Total 3	Mg 3	0	0
57	B1	1	Total 1	Mg 1	0	0
57	B2	1	Total 1	Mg 1	0	0
57	B3	2	Total 2	Mg 2	0	0
57	B4	1	Total 1	Mg 1	0	0
57	B5	1	Total 1	Mg 1	0	0
57	B6	2	Total 2	Mg 2	0	0
57	B7	5	Total 5	Mg 5	0	0
57	B8	1	Total 1	Mg 1	0	0
57	B9	1	Total 1	Mg 1	0	0
57	CA	170	Total 170	Mg 170	0	0
57	CD	1	Total 1	Mg 1	0	0
57	CE	1	Total 1	Mg 1	0	0
57	CF	1	Total 1	Mg 1	0	0
57	CJ	1	Total 1	Mg 1	0	0
57	CK	1	Total 1	Mg 1	0	0
57	CT	1	Total 1	Mg 1	0	0
57	CV	1	Total 1	Mg 1	0	0
57	CW	1	Total 1	Mg 1	0	0
57	CX	3	Total 3	Mg 3	0	0
57	DA	677	Total 677	Mg 677	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	DB	13	Total 13	Mg 13	0	0
57	DD	9	Total 9	Mg 9	0	0
57	DE	4	Total 4	Mg 4	0	0
57	DF	4	Total 4	Mg 4	0	0
57	DG	1	Total 1	Mg 1	0	0
57	DN	1	Total 1	Mg 1	0	0
57	DO	1	Total 1	Mg 1	0	0
57	DP	2	Total 2	Mg 2	0	0
57	DQ	4	Total 4	Mg 4	0	0
57	DR	1	Total 1	Mg 1	0	0
57	DU	2	Total 2	Mg 2	0	0
57	DV	3	Total 3	Mg 3	0	0
57	DW	4	Total 4	Mg 4	0	0
57	DX	1	Total 1	Mg 1	0	0
57	DY	1	Total 1	Mg 1	0	0
57	D0	1	Total 1	Mg 1	0	0
57	D3	1	Total 1	Mg 1	0	0
57	D8	1	Total 1	Mg 1	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



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	227	Total 227	O 227	0	0
61	AE	2	Total 2	O 2	0	0
61	AJ	1	Total 1	O 1	0	0
61	AL	1	Total 1	O 1	0	0
61	AM	1	Total 1	O 1	0	0
61	AU	1	Total 1	O 1	0	0
61	AV	3	Total 3	O 3	0	0
61	AW	3	Total 3	O 3	0	0
61	AX	6	Total 6	O 6	0	0
61	AY	1	Total 1	O 1	0	0
61	BA	1383	Total 1383	O 1383	0	0
61	BB	36	Total 36	O 36	0	0
61	BD	12	Total 12	O 12	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	BE	14	Total 14	O 14	0	0
61	BF	8	Total 8	O 8	0	0
61	BG	3	Total 3	O 3	0	0
61	BI	1	Total 1	O 1	0	0
61	BO	4	Total 4	O 4	0	0
61	BP	16	Total 16	O 16	0	0
61	BQ	4	Total 4	O 4	0	0
61	BR	2	Total 2	O 2	0	0
61	BT	2	Total 2	O 2	0	0
61	BU	3	Total 3	O 3	0	0
61	BV	2	Total 2	O 2	0	0
61	BW	1	Total 1	O 1	0	0
61	BX	4	Total 4	O 4	0	0
61	BZ	1	Total 1	O 1	0	0
61	B0	3	Total 3	O 3	0	0
61	B1	1	Total 1	O 1	0	0
61	B3	2	Total 2	O 2	0	0
61	B5	2	Total 2	O 2	0	0
61	B6	1	Total 1	O 1	0	0
61	B7	2	Total 2	O 2	0	0
61	B8	8	Total 8	O 8	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CA	185	Total 185	O 185	0	0
61	CJ	2	Total 2	O 2	0	0
61	CL	1	Total 1	O 1	0	0
61	CT	1	Total 1	O 1	0	0
61	CV	1	Total 1	O 1	0	0
61	CW	2	Total 2	O 2	0	0
61	DA	1025	Total 1025	O 1025	0	0
61	DB	9	Total 9	O 9	0	0
61	DD	19	Total 19	O 19	0	0
61	DE	11	Total 11	O 11	0	0
61	DF	3	Total 3	O 3	0	0
61	DN	2	Total 2	O 2	0	0
61	DO	1	Total 1	O 1	0	0
61	DP	16	Total 16	O 16	0	0
61	DR	1	Total 1	O 1	0	0
61	DT	3	Total 3	O 3	0	0
61	DU	2	Total 2	O 2	0	0
61	DX	3	Total 3	O 3	0	0
61	DY	2	Total 2	O 2	0	0
61	D0	3	Total 3	O 3	0	0
61	D1	1	Total 1	O 1	0	0

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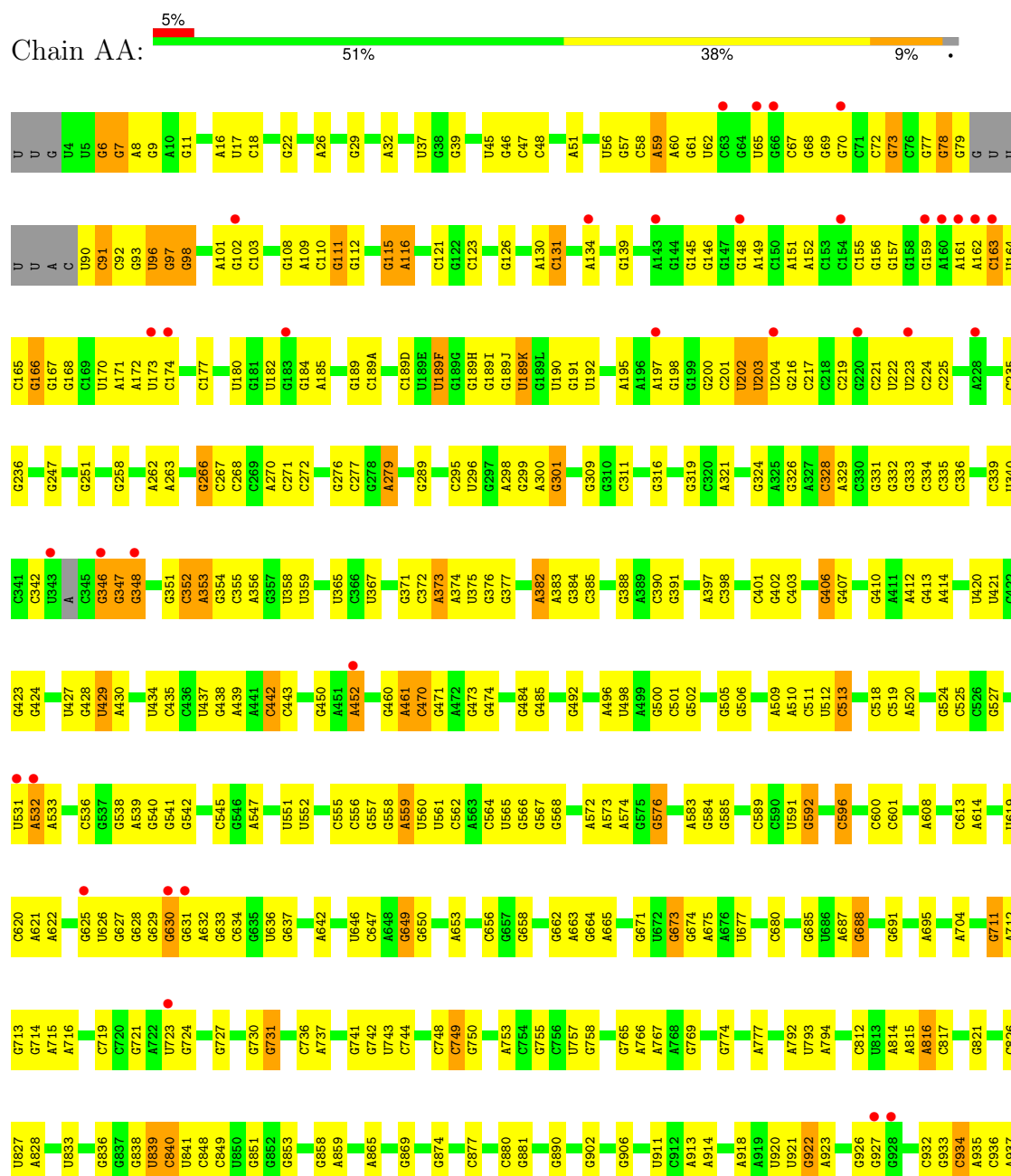
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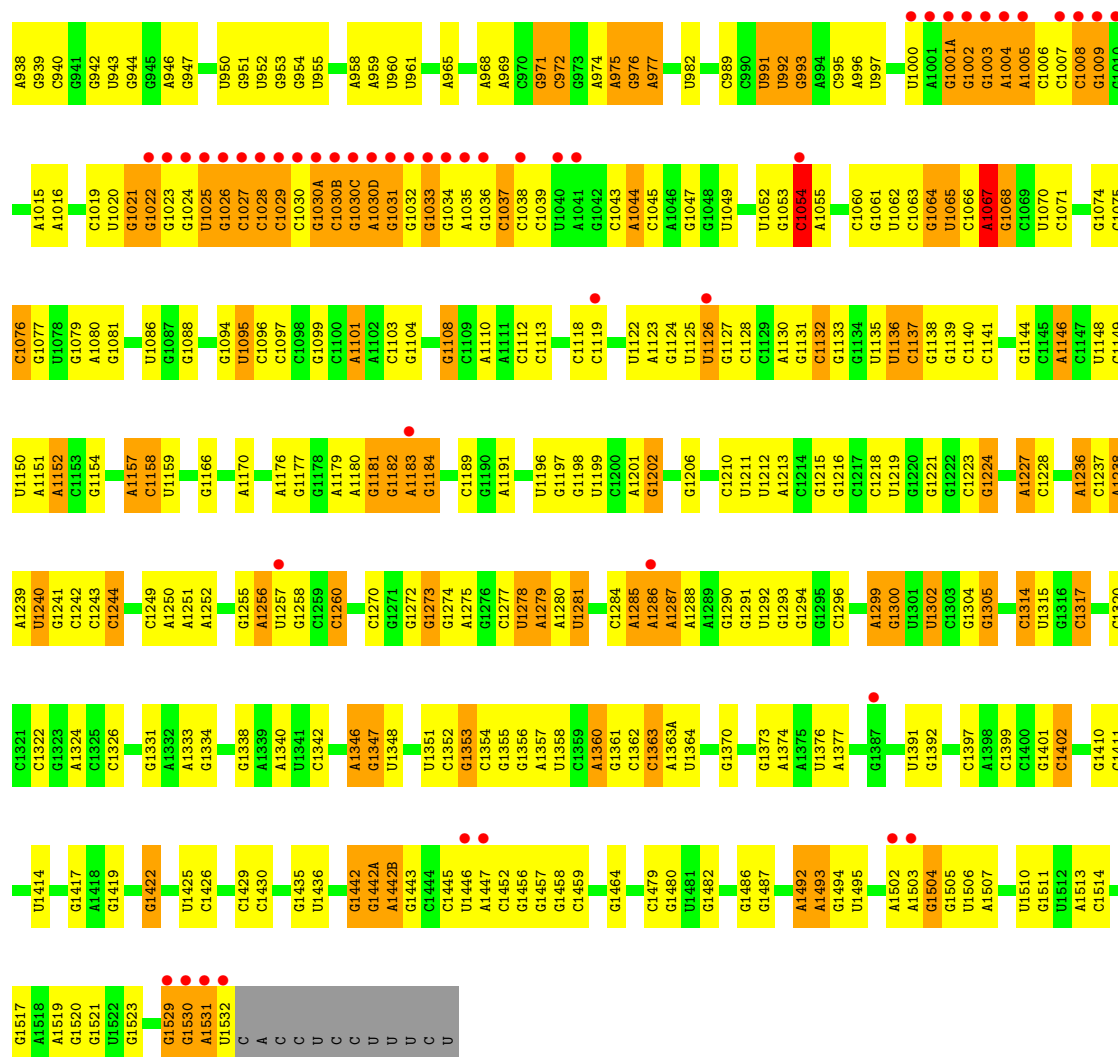
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	D3	1	Total	O	0	0
			1	1		
61	D7	3	Total	O	0	0
			3	3		
61	D8	4	Total	O	0	0
			4	4		

3 Residue-property plots

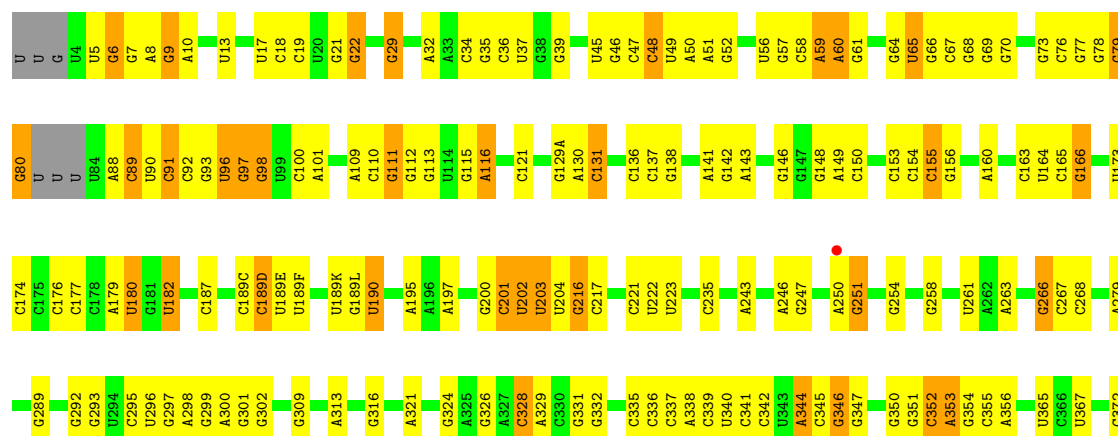
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

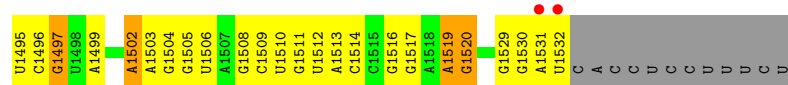




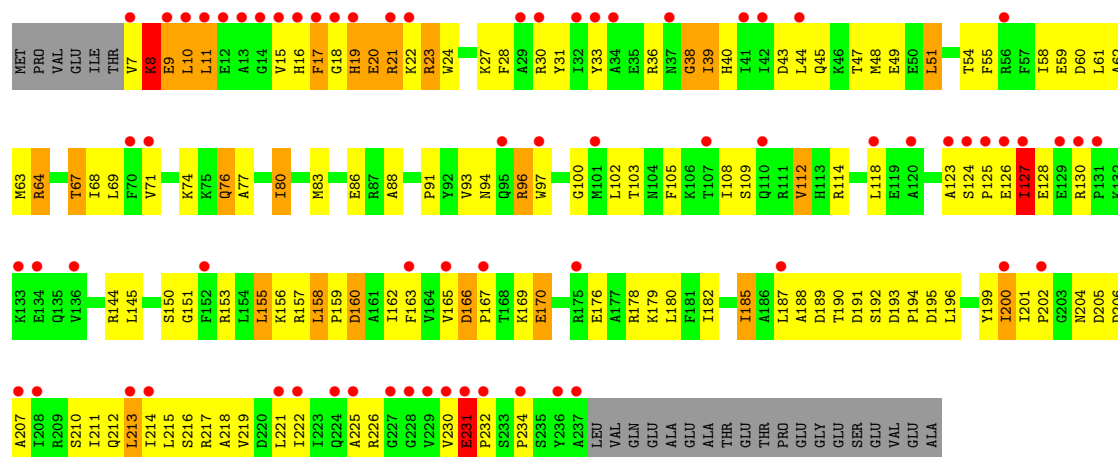
• Molecule 1: 16S Ribosomal RNA



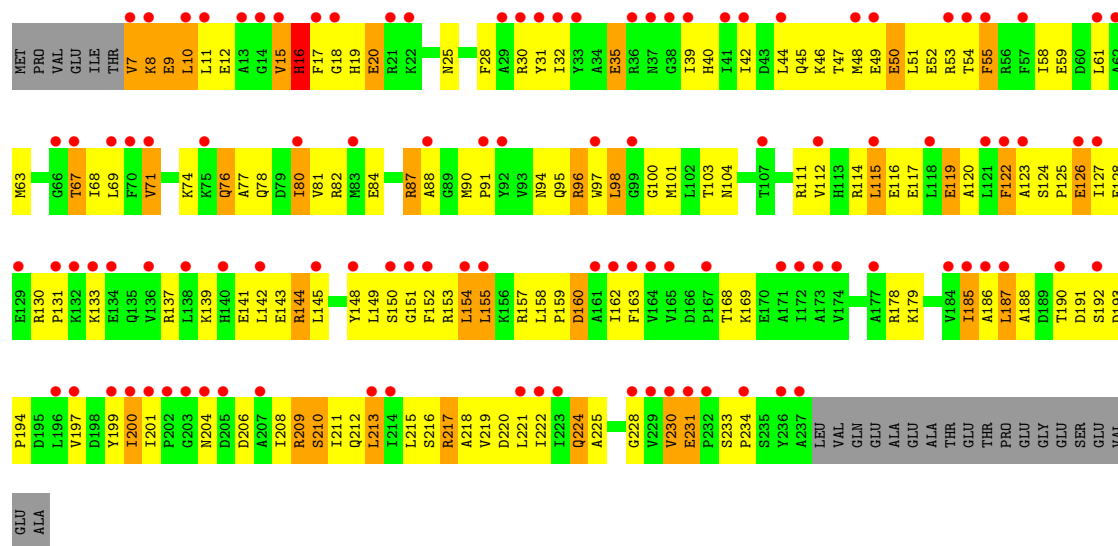
G1378	G1379	C1383	G1386	G1387	G1388	U1391	U1392	C1397	A1398	C1399	C1402	G1410	C1411	A1413	U1414	G1419	G1422	C1423	C1424	U1426	U1427	G1428	U1429	A430	A431	A432	C433	U434	C435	C436	U437	G438	A439	A441	C442	C443	C444	G446																			
C1249	A1250	A1251	A1252	G1253	C1254	G1255	A1256	G1257	G1258	C1259	A1260	A1261	C1262	C1263	A1269	C1270	G1271	G1272	G1273	G1274	A1275	G1276	C1277	U1278	A1279	A1280	U1281	C1282	G1283	C1284	A1285	A1286	A1287	A1288	G1289	G1291	U1292	G1293	G1294	C1297	C1298	A1299	G1300	U1301	U1302	C1303	G1304	G1305	U1308	G1309	G1310	G1311	G1312	C1314			
U1315	G1316	C1317	A1318	C1319	C1320	C1321	C1322	G1323	A1324	C1325	C1326	C1327	C1328	G1331	A1332	A1333	G1334	G1338	A1339	A1340	C1341	C1342	G1343	C1344	U1345	C1346	C1347	C1348	C1349	A1350	U1351	C1352	G1353	C1354	G1355	G1356	A1357	U1358	C1359	A1360	G1361	C1362	C1363	A1363A	U1364	G1365	C1366	C1367	G1370	G1371	U1372	C1373	A1374	A1375	A1492	A1493	A1494
C1116	G1117	C1118	C1119	G1120	U1121	U1122	A1123	G1124	U1125	U1126	G1127	C1128	C1129	A1130	G1131	C1132	G1133	G1134	U1135	U1136	C1137	G1138	C1139	C1140	C1141	G1142	G1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	G1154	G1155	C1156	A1157	C1158	U1159	C1162	C1163	C1164	C1165	A1169	A1170	G1171	G1172	G1173	G1174	G1175	A1176	C1177	G1178
A1179	A1180	G1181	G1182	A1183	G1184	G1190	A1191	A1192	U1196	U1197	G1198	U1199	C1200	A1201	C1203	A1204	U1205	G1206	C1209	C1210	U1211	U1212	A1213	C1214	G1215	C1216	C1217	C1218	U1219	G1220	C1221	A1222	G1223	G1224	C1226	A1227	C1228	G1231	U1232	G1233	C1234	U1235	A1236	G1237	A1238	U1239	U1240	C1243	C1244	A1245	C1246						
C1116	G1117	C1118	C1119	G1120	U1121	U1122	A1123	G1124	U1125	U1126	G1127	C1128	C1129	A1130	G1131	C1132	G1133	G1134	U1135	U1136	C1137	G1138	C1139	C1140	C1141	G1142	G1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	G1154	G1155	C1156	A1157	C1158	U1159	C1162	C1163	C1164	C1165	A1169	A1170	G1171	G1172	G1173	G1174	G1175	A1176	C1177	G1178
C1249	A1250	A1251	A1252	G1253	C1254	G1255	A1256	G1257	G1258	C1259	A1260	A1261	C1262	C1263	A1269	C1270	G1271	G1272	G1273	G1274	A1275	G1276	C1277	U1278	A1279	A1280	U1281	C1282	G1283	C1284	A1285	A1286	A1287	A1288	G1289	G1291	U1292	G1293	G1294	C1297	C1298	A1299	G1300	U1301	U1302	C1303	G1304	G1305	U1308	G1309	G1310	G1311	G1312	C1314			
U1315	G1316	C1317	A1318	C1319	C1320	C1321	C1322	G1323	A1324	C1325	C1326	C1327	C1328	G1331	A1332	A1333	G1334	G1338	A1339	A1340	C1341	C1342	G1343	C1344	U1345	C1346	C1347	C1348	C1349	A1350	U1351	C1352	G1353	C1354	G1355	G1356	A1357	U1358	C1359	A1360	G1361	C1362	C1363	A1363A	U1364	G1365	C1366	C1367	G1370	G1371	U1372	C1373	A1374	A1375	A1492	A1493	A1494
A373	A374	U375	G376	G377	A382	A383	G384	G388	A389	C390	G391	G392	A393	G396	A397	C398	C400	G406	G407	A408	A411	A412	C413	A414	A415	C419	U420	U421	G422	G423	G424	G425	G426	U427	G428	U429	A430	A431	A432	C433	U434	C435	C436	U437	G438	A439	A441	C442	C443	C444	G446						
G447	A448	C449	G450	A451	A452	A453	C460	A461	C470	A471	G472	G473	G474	C484	G485	C488	G492	A496	U498	A499	G500	C501	G502	C503	C504	C505	A509	U510	C511	G512	C513	C514	C518	C521	G522	A523	C528	U529	G530	G531	A532	A533	U534	A535	C536	G537	G538	A539	G540	G541							
G542	C543	G544	C545	G546	A547	U551	U552	C556	A559	U560	C561	C562	U565	G566	A572	A573	G576	U580	G581	U582	G583	C584	G587	G593	G592	C596	A607	A608	A609	C610	U619	C620	G625	U626	G627	G628	G629	G630	G631	A632	G633	U641	A642	C643	C644	C645											
U646	C647	A648	G649	G650	A653	C656	G657	G662	A663	G664	A665	G673	G674	U677	C680	G683	A684	G685	U686	G687	G688	C689	G690	G693	G692	A694	A695	A696	U697	G698	C701	A702	G707	C708	G711	A712	G713	G714	A715	G719	C720	G721	A722	U723	G724	G727											
G730	G731	C736	C737	A741	G742	C748	G749	G750	A753	C754	G755	G756	U757	G758	A766	G768	G769	C770	G771	U772	G773	C774	G775	G776	G777	A778	C784	U789	A790	G791	A792	U793	A794	U804	C805	G808	A813	G815	A816	C817	G821	C826	G827	C831													
A828	U833	G838	U839	C840	U841	G851	G852	G853	C857	G858	A859	A860	G861	G862	C866	G867	G868	G869	G874	C875	G876	C879	C880	G885	G886	G887	G888	G889	G890	G891	G892	G893	A901	A914	A915	G916	U920	U921	G922	A923	G924	G925	G926	G927	C931												
C932	G933	C934	A935	C936	A937	A938	G939	G942	A946	C948	A949	U950	G951	U952	U953	G954	U955	U956	U957	A958	A959	U960	U961	C962	G963	A964	A965	G966	C967	A968	A969	C970	G971	C972	G973	A974	A975	G976	A977	A978	C979	C980	U981	U982	A983	C984	C985	A986	G987	G988	C989	C990	U991	U992	G993	A994	
C995	A996	U997	G998	C999	U1000	A1001	G1001A	G1002	A1003	A1004	A1005	C1006	C1007	C1008	G1009	U1010	G1011	U1012	G1013	A1014	A1015	A1016	G1017	G1018	C1019	U1020	G1021	G1022	G1023	A1024	A1025	U1026	C1027	U1028	C1029	G1030	C1031	G1032	G1033	G1034	A1035	G1036	C1037	C1038	C1039	U1040	A1041	C1042	G1043	G1044	A1045	A1046	G1047	C1048	U1049		
G1050	C1051	U1052	G1053	C1054	U1055	U1056	G1057	C1058	C1059	G1060	G1061	U1062	C1063	G1064	U1065	C1066	G1068	C1069	U1070	C1071	G1072	U1073	G1074	C1075	C1076	G1079	A1080	G1081	U1082	U1083	G1084	U1085	U1086	G1087	G1088	A1092	A1093	C1094	U1095	C1096	C1097	C1098	G1099	C1100	A1101	A1102	C1103	G1104	G1108	C1109	A1110	C1113	C1115				
C1116	G1117	C1118	C1119	G1120	U1121	U1122	A1123	G1124	U1125	U1126	G1127	C1128	C1129	A1130	G1131	C1132	G1133	G1134	U1135	U1136	C1137	G1138	C1139	C1140	C1141	G1142	G1143	C1144	C1145	A1146	C1147	U1148	C1149	U1150	A1151	A1152	C1153	G1154	G1155	C1156	A1157	C1158	U1159	C1162	C1163	C1164	C1165	A1169	A1170	G1171	G1172	G1173	G1174	G1175	A1176	C1177	G1178
A1179	A1180	G1181	G1182	A1183	G1184	G1190	A1191	A1192	U1196	U1197	G1198	U1199	C1200	A1201	C1203	A1204	U1205	G1206	C1209	C1210	U1211	U1212	A1213	C1214	G1215	C1216	C1217	C1218	U1219	G1220	C1221	A1222	G1223	G1224	C1226	A1227	C1228	G1231	U1232	G1233	C1234	U1235	A1236	G1237	A1238	U1239	U1240	C1243	C1244	A1245	C1246						
C1249	A1250	A1251	A1252	G1253	C1254	G1255	A1256	G1257	G1258	C1259	A1260	A1261	C1262	C1263	A1269	C1270	G1271	G1272	G1273	G1274	A1275	G1276	C1277	U1278	A1279	A1280	U1281	C1282	G1283	C1284	A1285	A1286	A1287	A1288	G1289	G1291	U1292	G1293	G1294	C1297	C1298	A1299	G1300	U1301	U1302	C1303	G1304	G1305	U1308	G1309	G1310	G1311	G1312	C1314			
U1315	G1316	C1317	A1318	C1319	C1320	C1321	C1322	G1323	A1324	C1325	C1326	C1327	C1328	G1331	A1332	A1333	G1334	G1338	A1339	A1340	C1341	C1342	G1343	C1344	U1345	C1346	C1347	C1348	C1349	A1350	U1351	C1352	G1353	C1354	G1355	G1356	A1357	U1358	C1359	A1360	G1361	C1362	C1363	A1363A	U1364	G1365	C1366	C1367	G1370	G1371	U1372	C1373	A1374	A1375	A1492	A1493	A1494



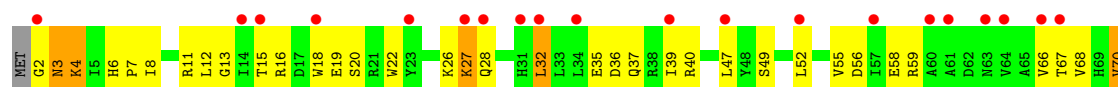
• Molecule 2: 30S ribosomal protein S2

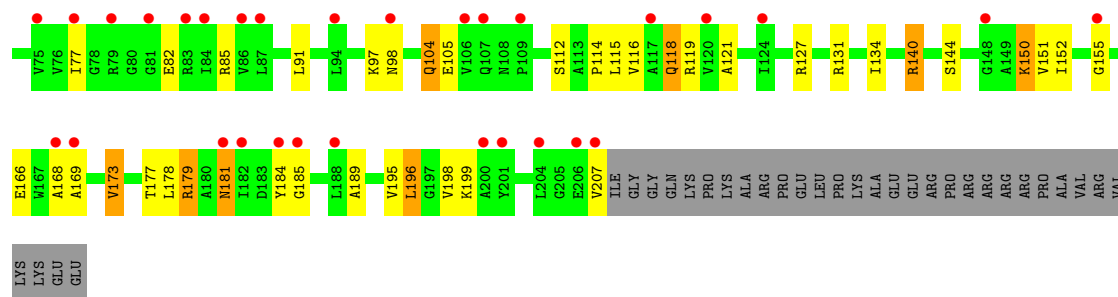


• Molecule 2: 30S ribosomal protein S2

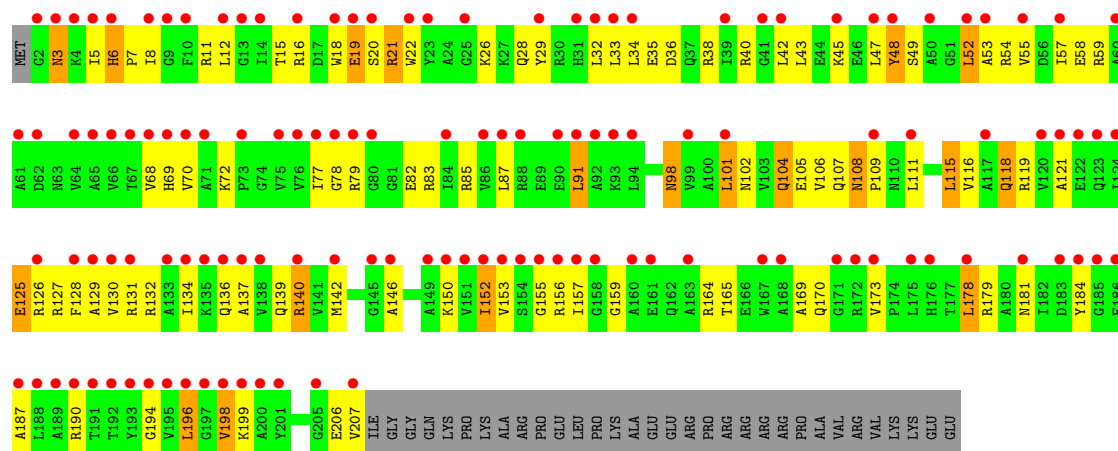
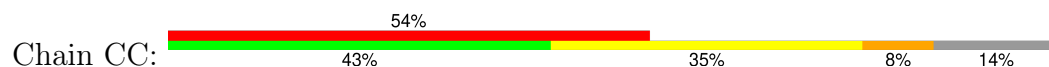


• Molecule 3: 30S ribosomal protein S3

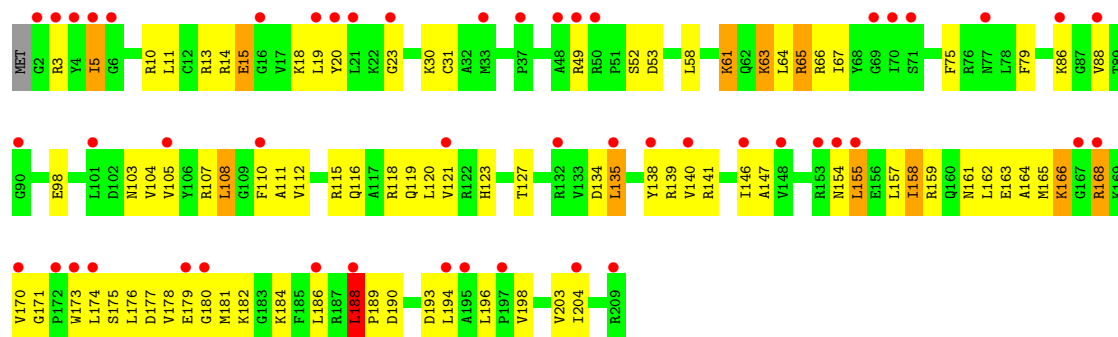




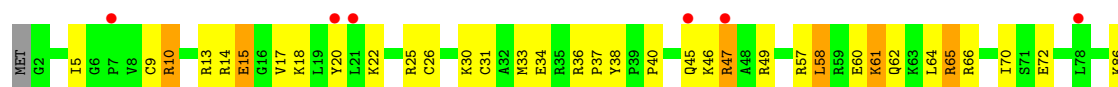
• Molecule 3: 30S ribosomal protein S3

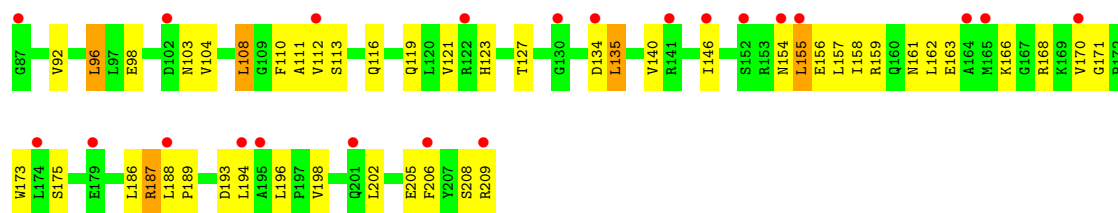


• Molecule 4: 30S ribosomal protein S4

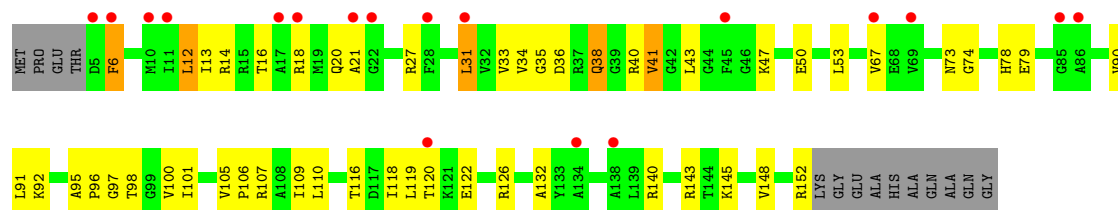


• Molecule 4: 30S ribosomal protein S4

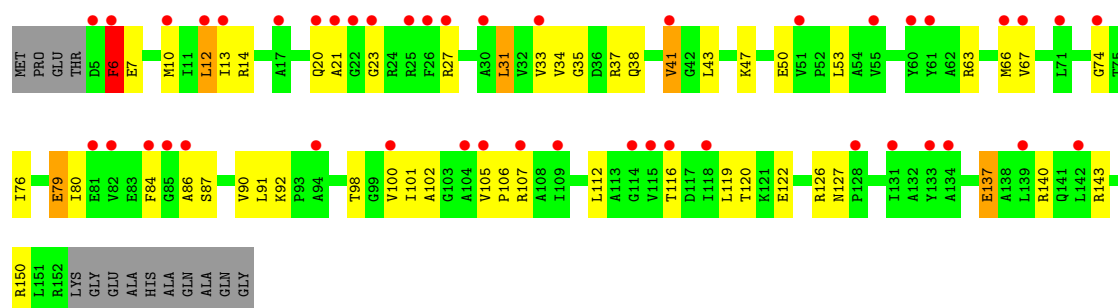




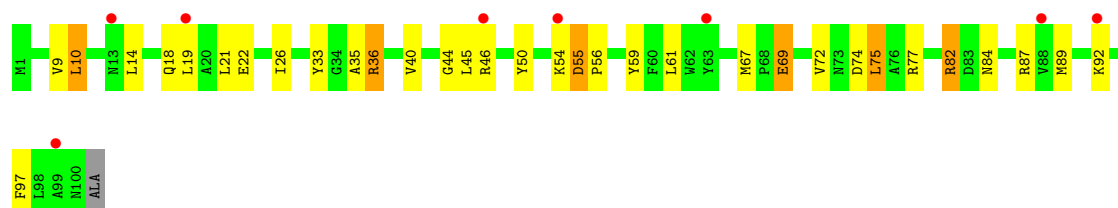
• Molecule 5: 30S ribosomal protein S5



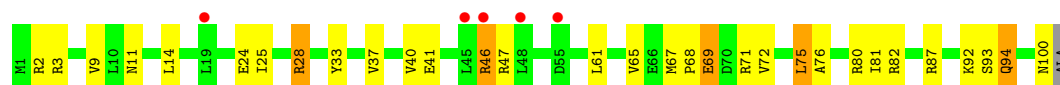
• Molecule 5: 30S ribosomal protein S5



• Molecule 6: 30S ribosomal protein S6

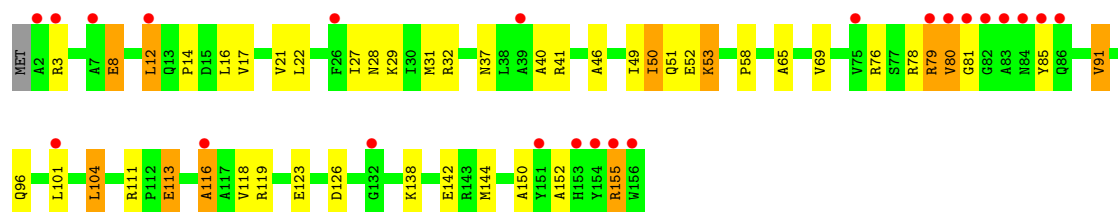


• Molecule 6: 30S ribosomal protein S6



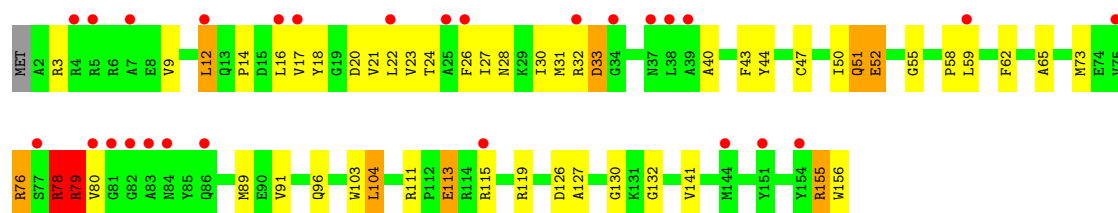
- Molecule 7: 30S ribosomal protein S7

Chain AG: 



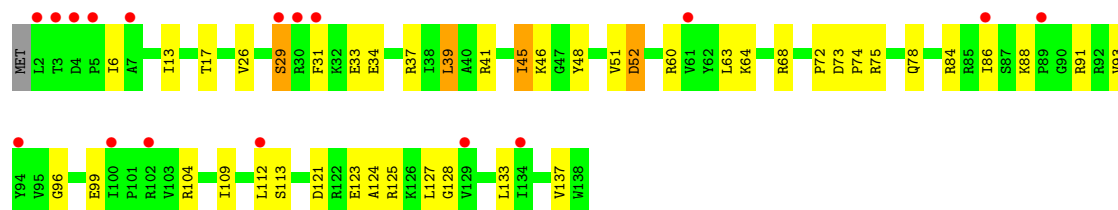
- Molecule 7: 30S ribosomal protein S7

Chain CG: 



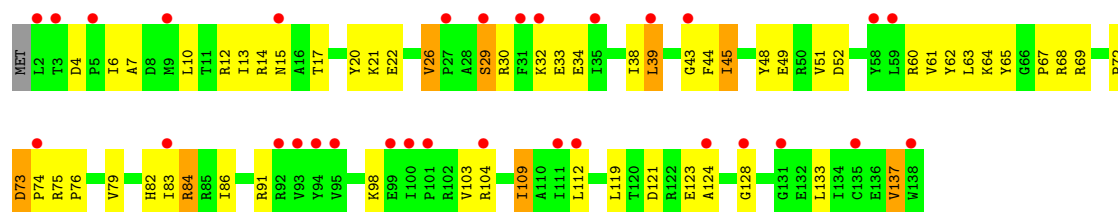
- Molecule 8: 30S ribosomal protein S8

Chain AH: 



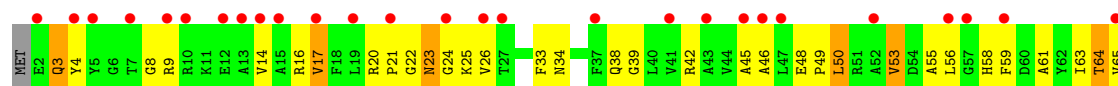
- Molecule 8: 30S ribosomal protein S8

Chain CH: 



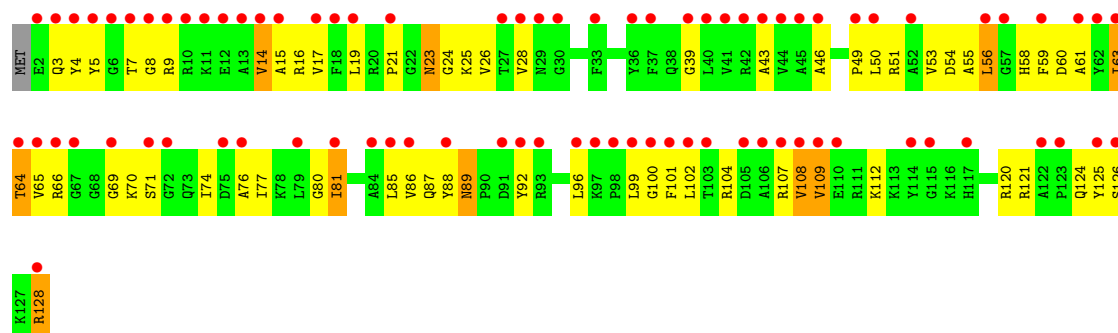
- Molecule 9: 30S ribosomal protein S9

Chain AI: 

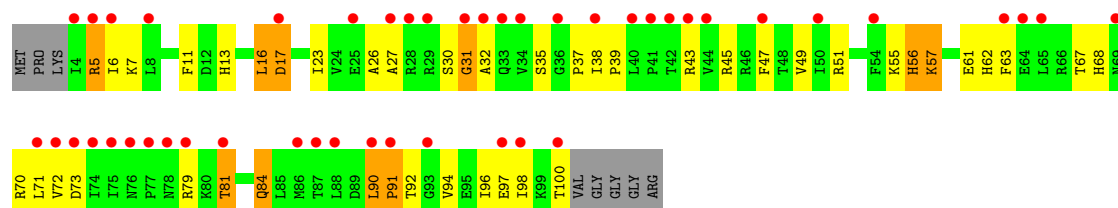




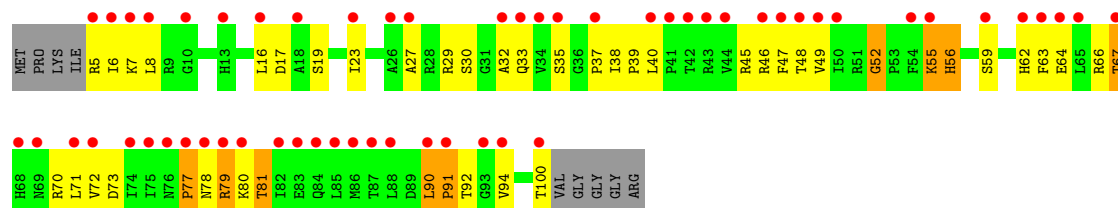
• Molecule 9: 30S ribosomal protein S9



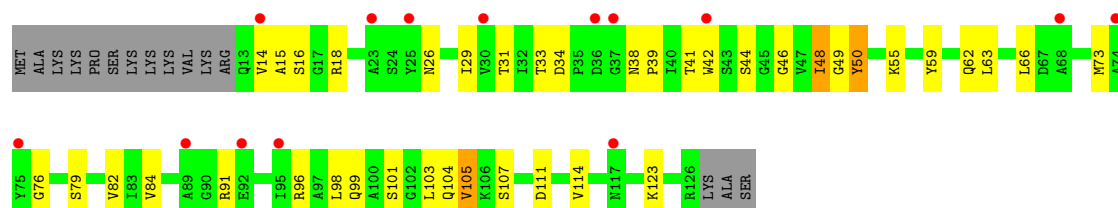
• Molecule 10: 30S ribosomal protein S10



• Molecule 10: 30S ribosomal protein S10

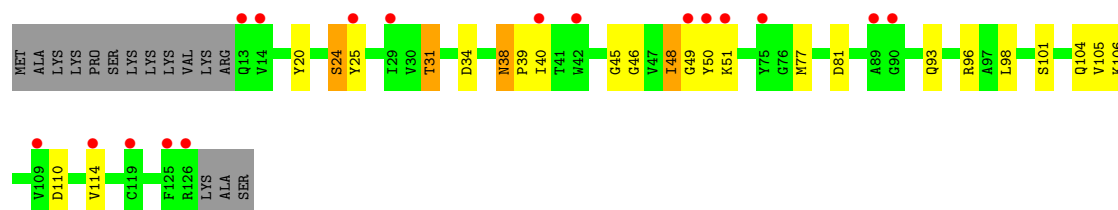


• Molecule 11: 30S ribosomal protein S11



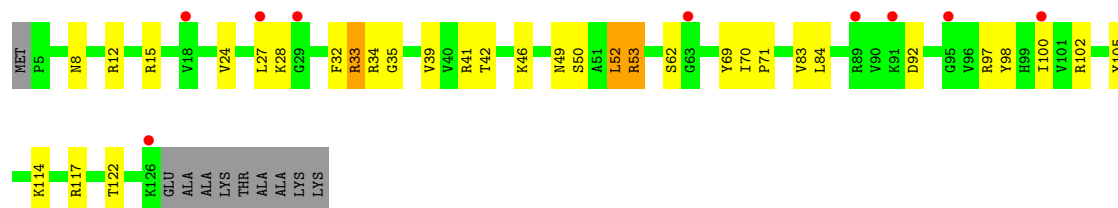
- Molecule 11: 30S ribosomal protein S11

Chain CK: 



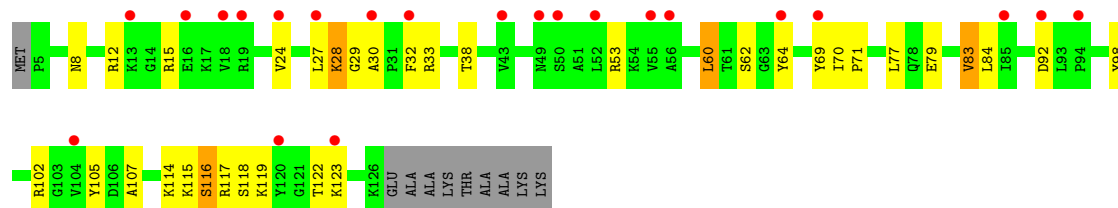
- Molecule 12: 30S ribosomal protein S12

Chain AL: 



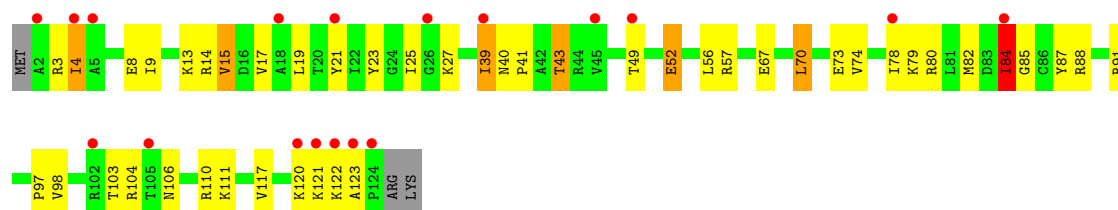
- Molecule 12: 30S ribosomal protein S12

Chain CL: 



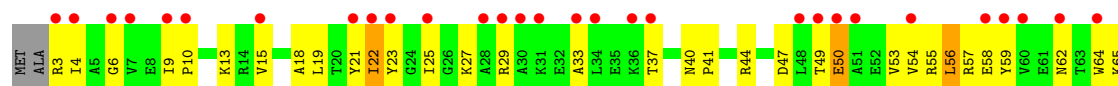
- Molecule 13: 30S ribosomal protein S13

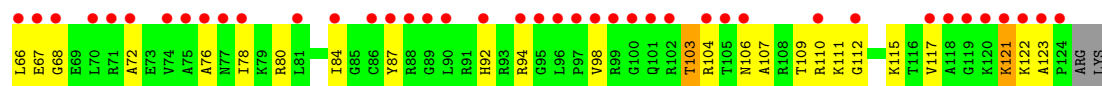
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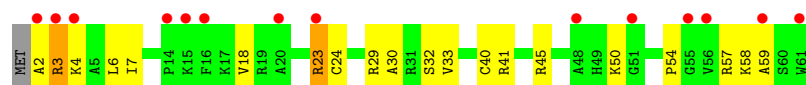
- Molecule 13: 30S ribosomal protein S13

Chain CM: 

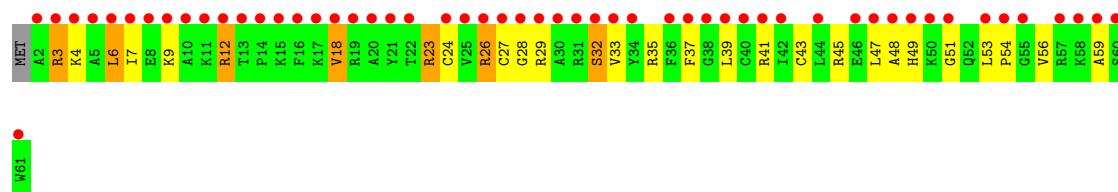
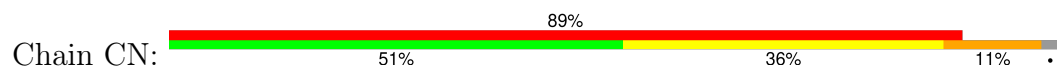




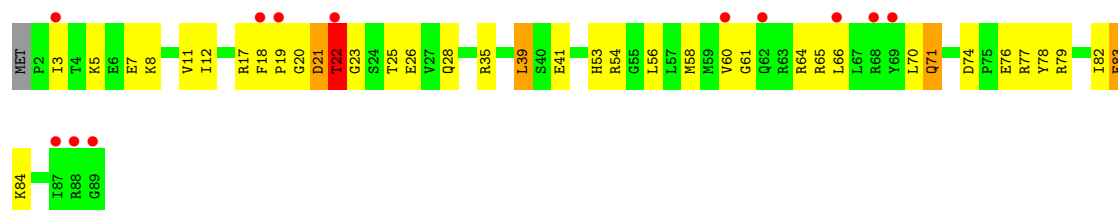
- Molecule 14: 30S ribosomal protein S14 type Z



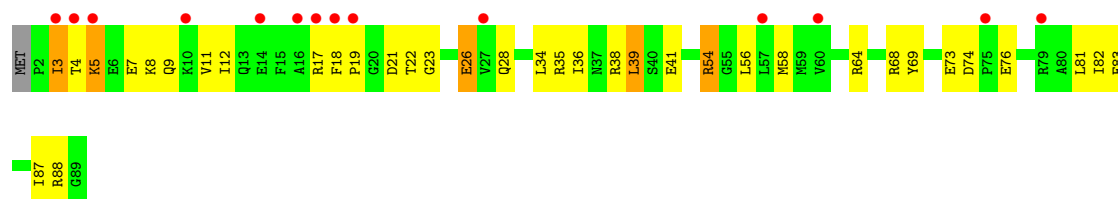
- Molecule 14: 30S ribosomal protein S14 type Z



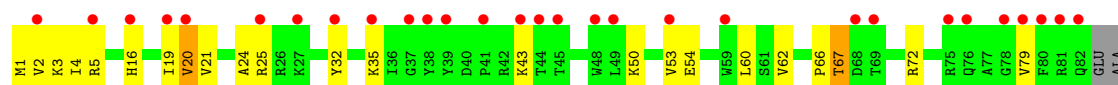
- Molecule 15: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S15

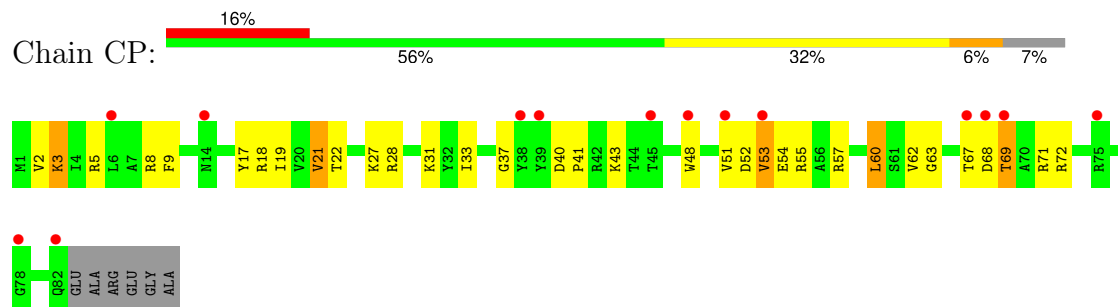


- Molecule 16: 30S ribosomal protein S16

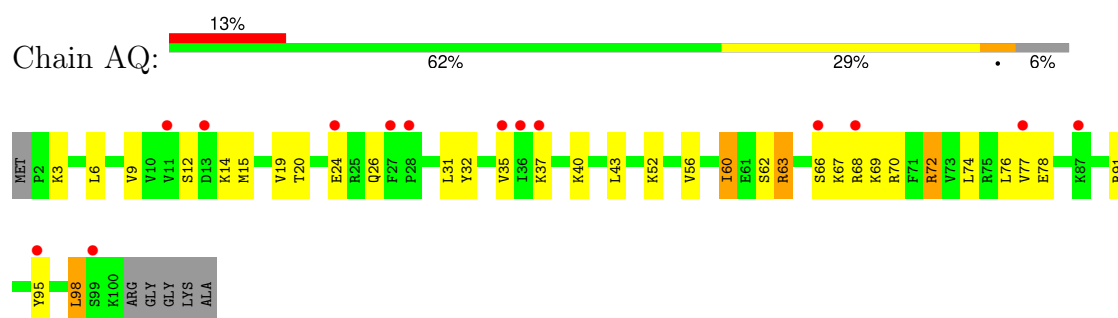


ARG
GLU
GLY
ALA

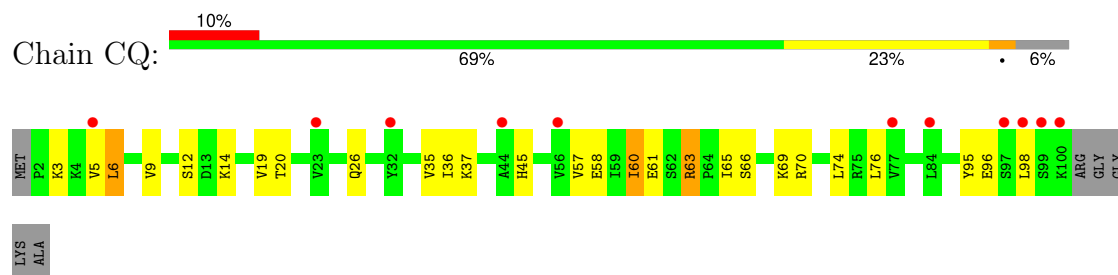
• Molecule 16: 30S ribosomal protein S16



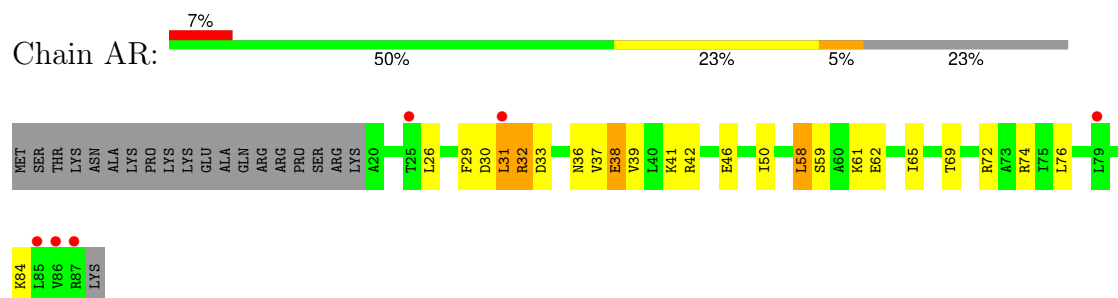
• Molecule 17: 30S ribosomal protein S17



• Molecule 17: 30S ribosomal protein S17

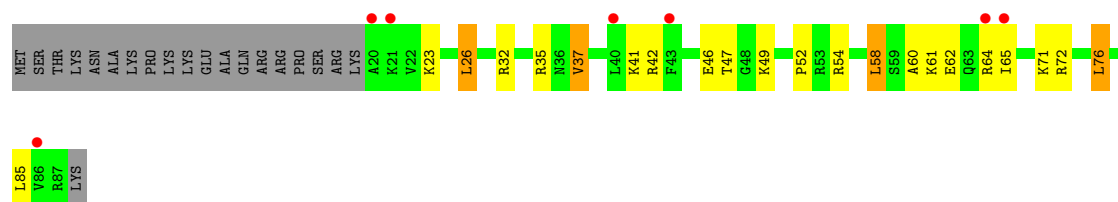


• Molecule 18: 30S ribosomal protein S18

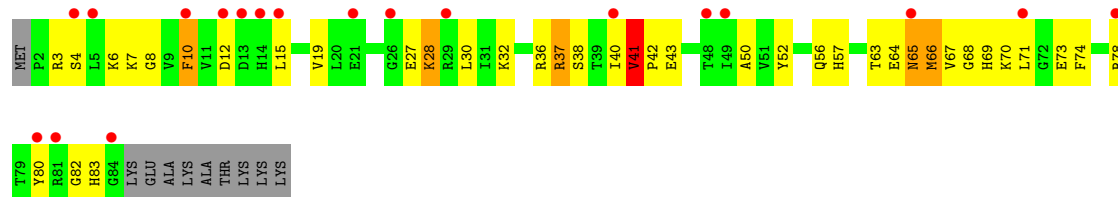


• Molecule 18: 30S ribosomal protein S18

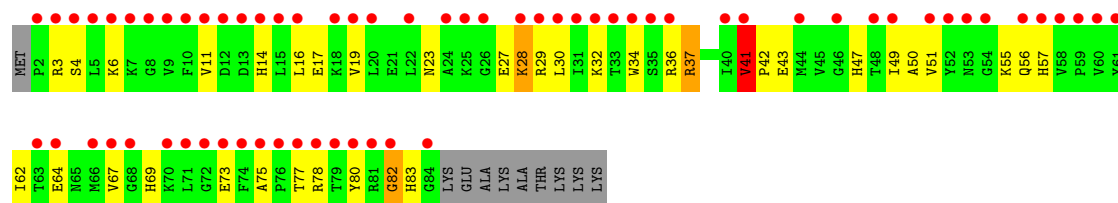
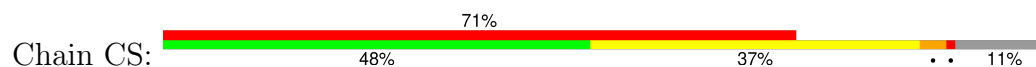




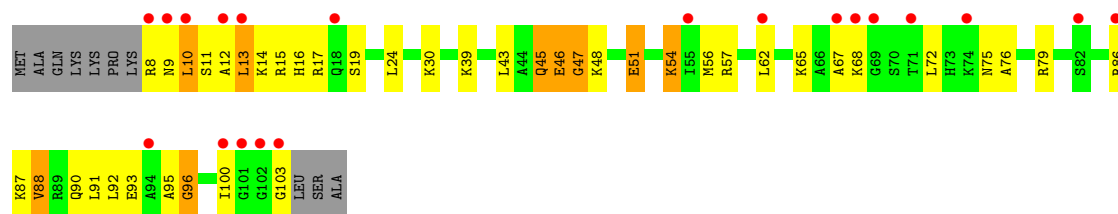
• Molecule 19: 30S ribosomal protein S19



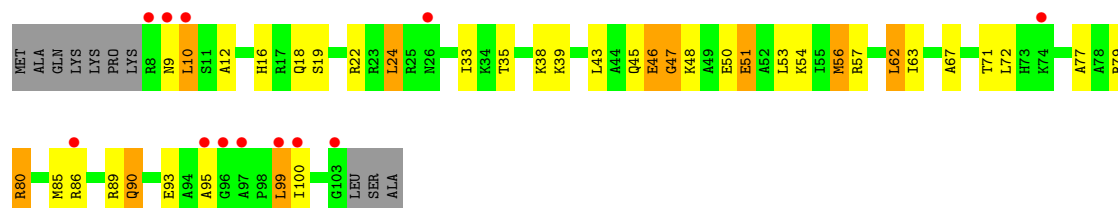
• Molecule 19: 30S ribosomal protein S19



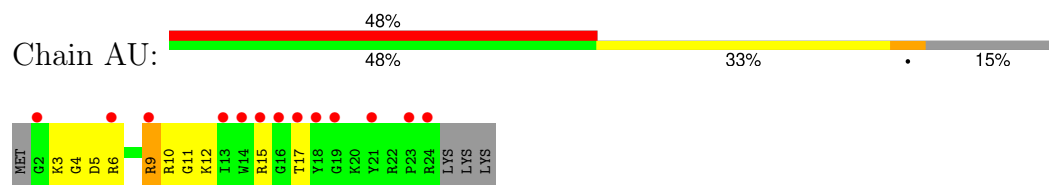
• Molecule 20: 30S ribosomal protein S20



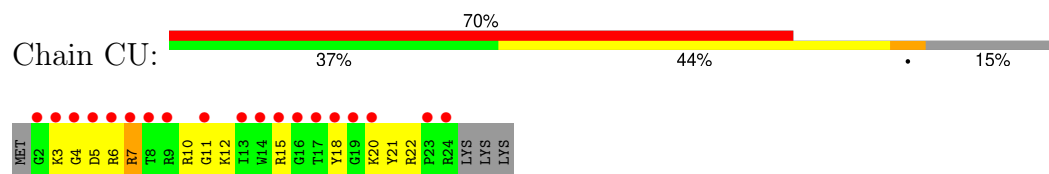
• Molecule 20: 30S ribosomal protein S20



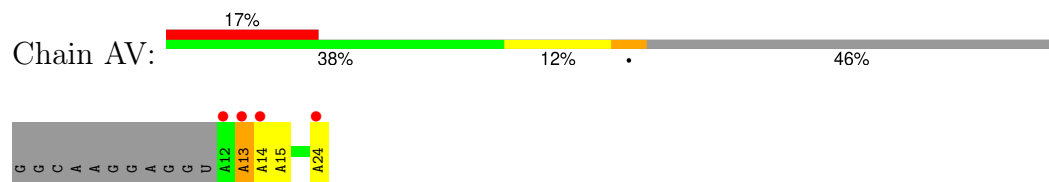
- Molecule 21: 30S ribosomal protein Thx



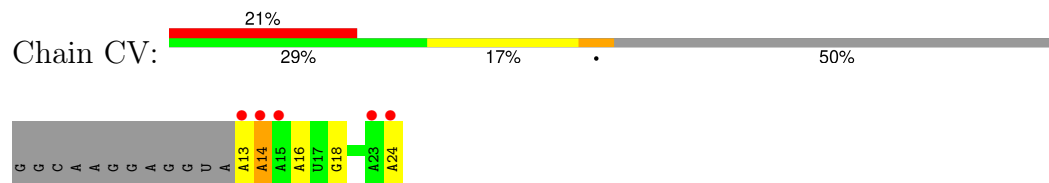
- Molecule 21: 30S ribosomal protein Thx



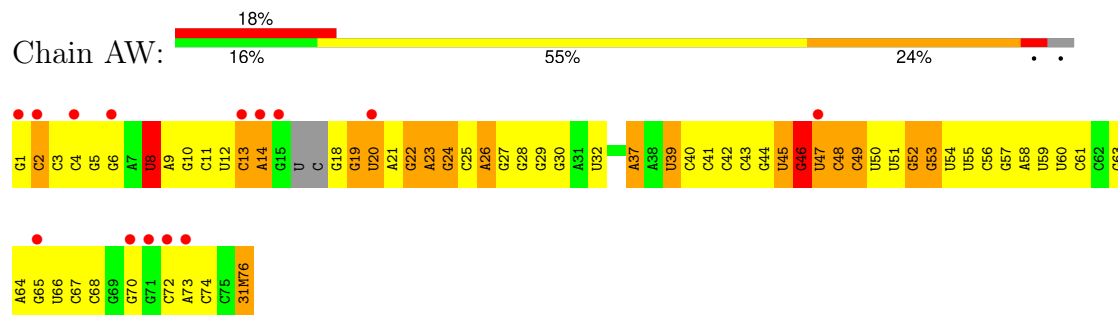
- Molecule 22: mRNA



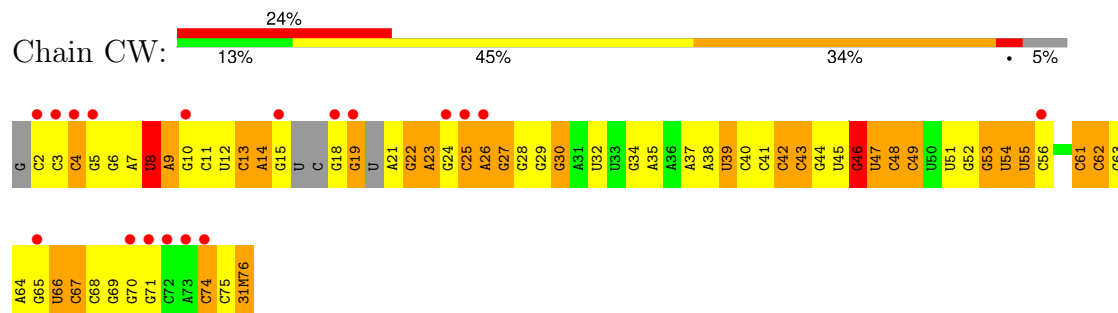
- Molecule 22: mRNA



- Molecule 23: A-site tRNA



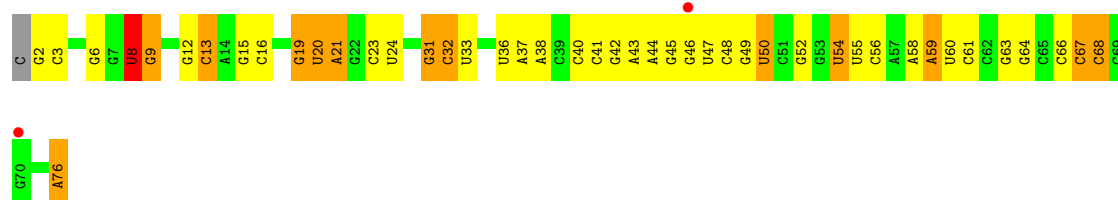
- Molecule 23: A-site tRNA



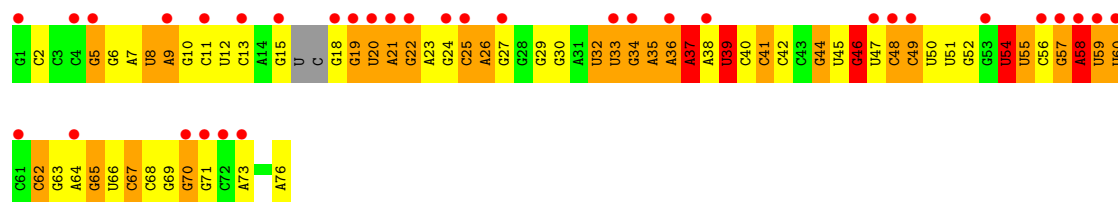
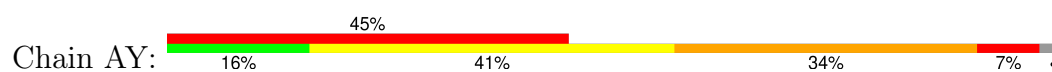
- Molecule 24: P-site tRNA



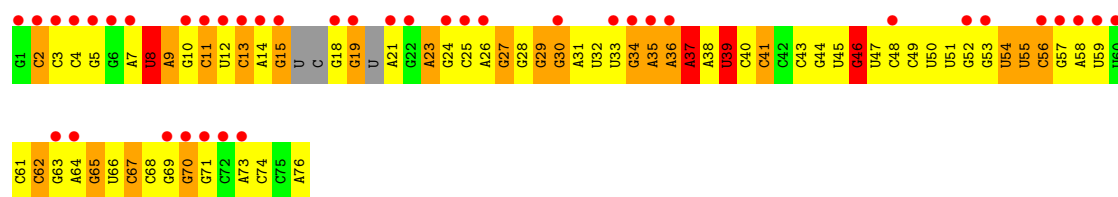
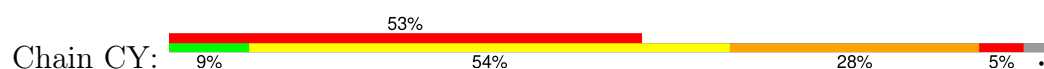
- Molecule 24: P-site tRNA



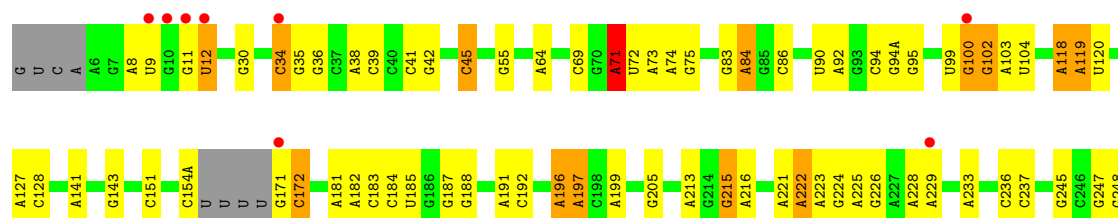
- Molecule 25: E-site tRNA

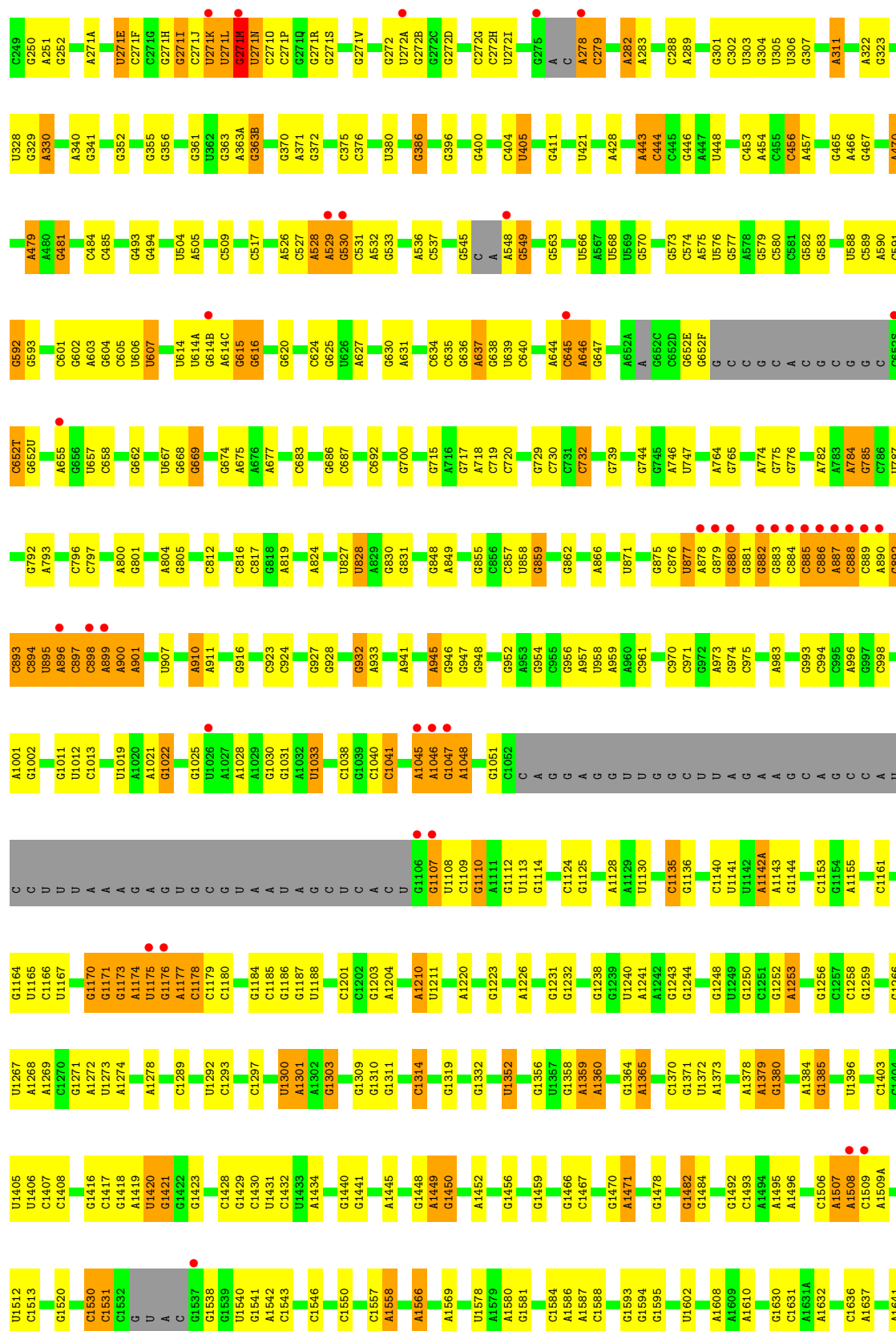


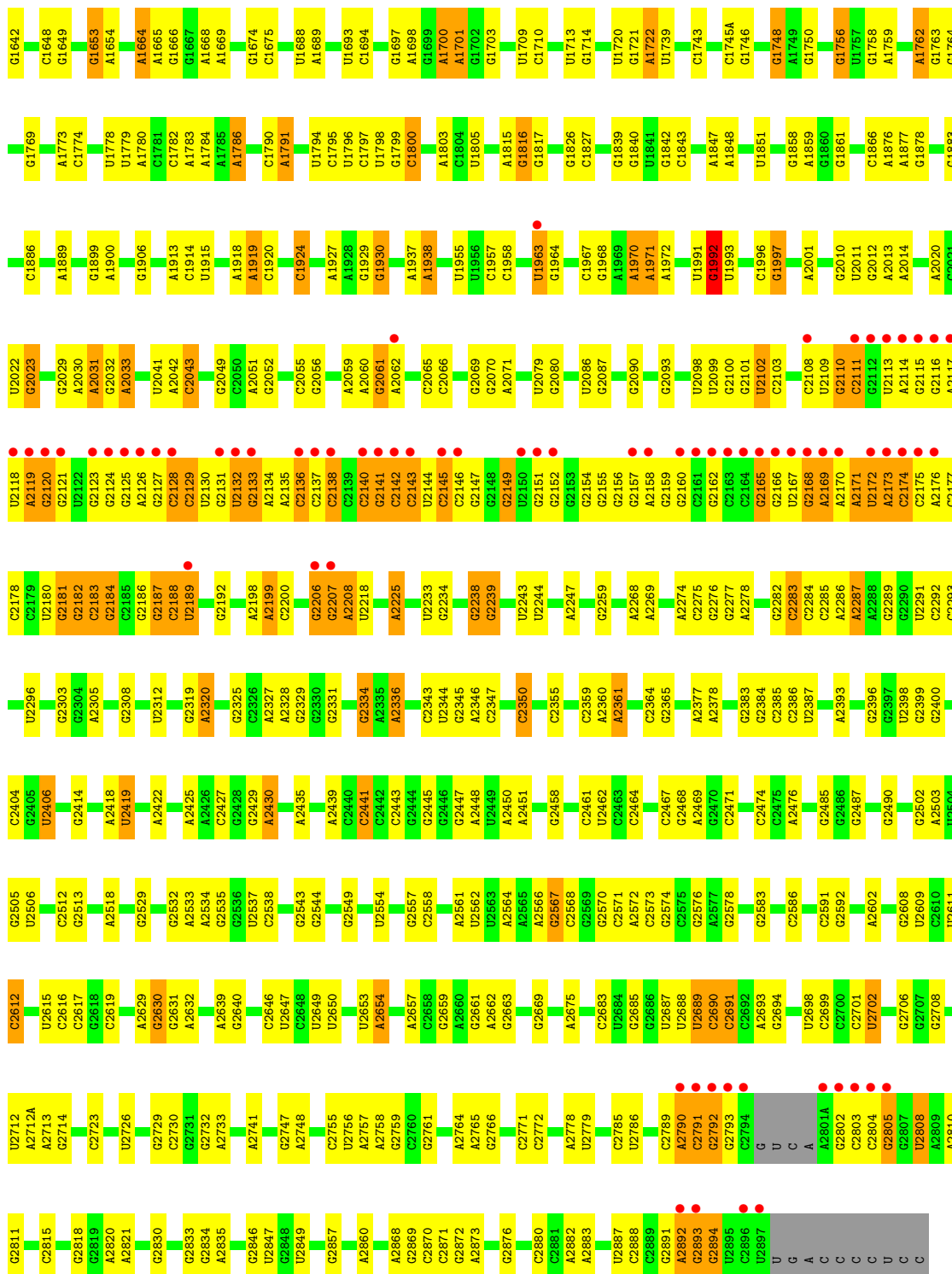
- Molecule 25: E-site tRNA



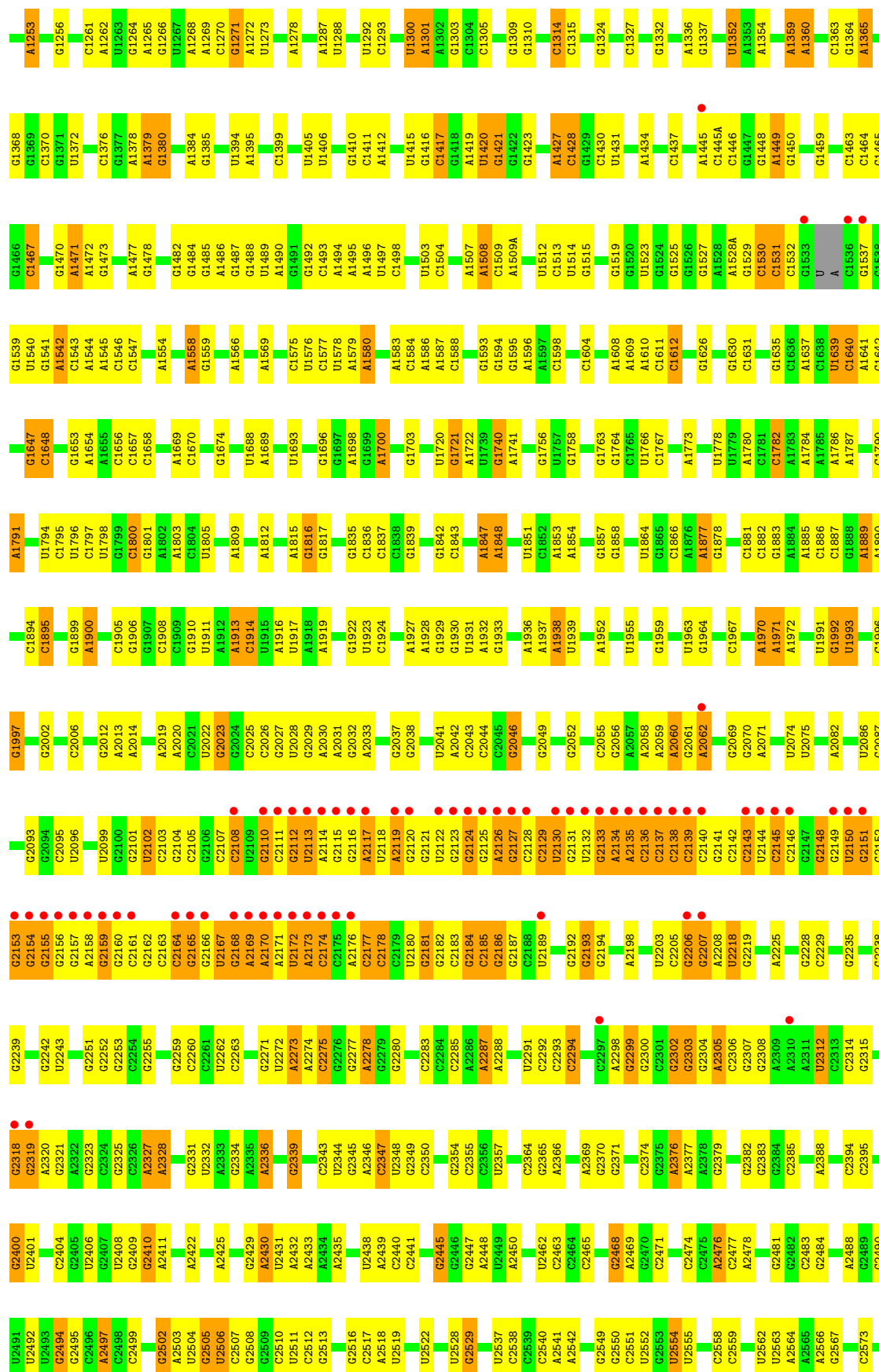
- Molecule 26: 23S Ribosomal RNA

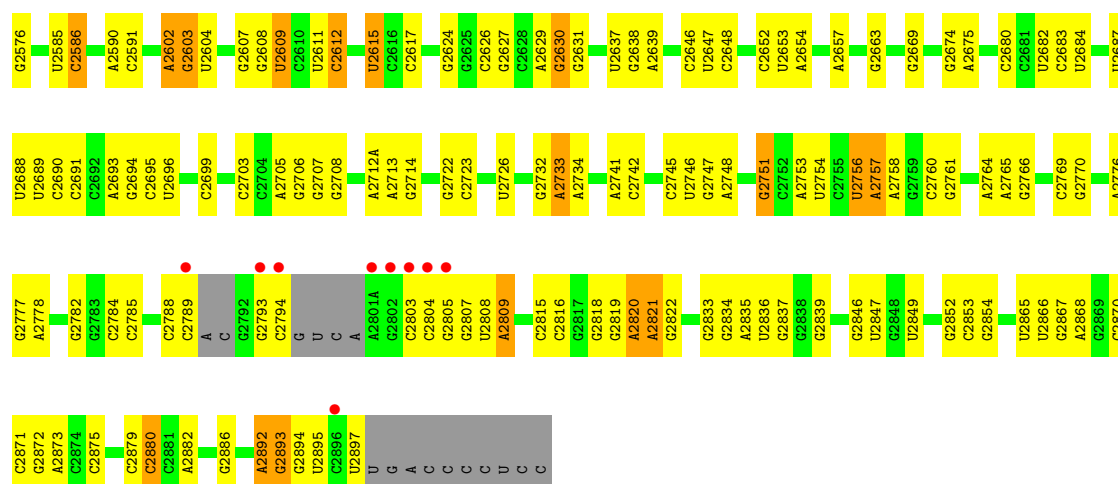




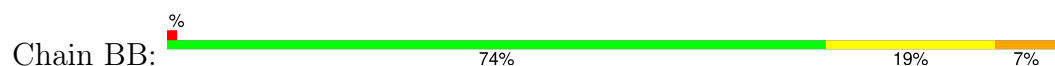


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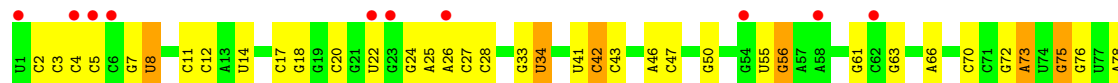




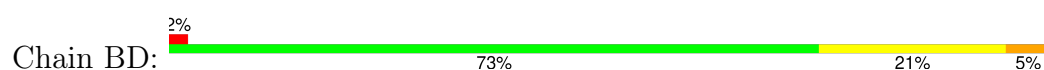
• Molecule 27: 5S Ribosomal RNA



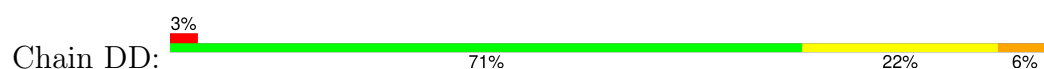
• Molecule 27: 5S Ribosomal RNA



• Molecule 28: 50S ribosomal protein L2

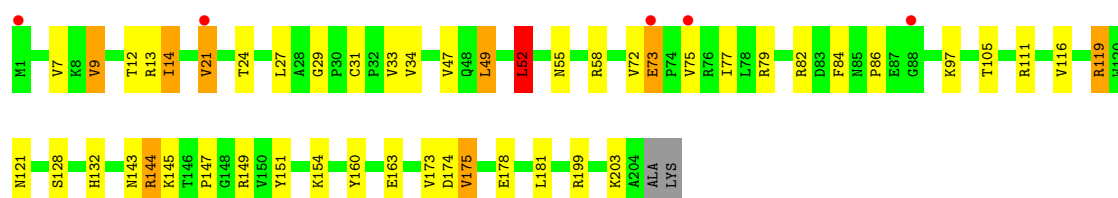
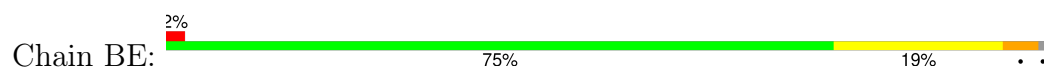


• Molecule 28: 50S ribosomal protein L2

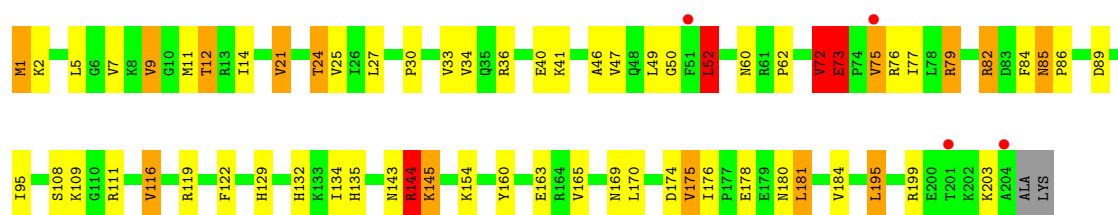




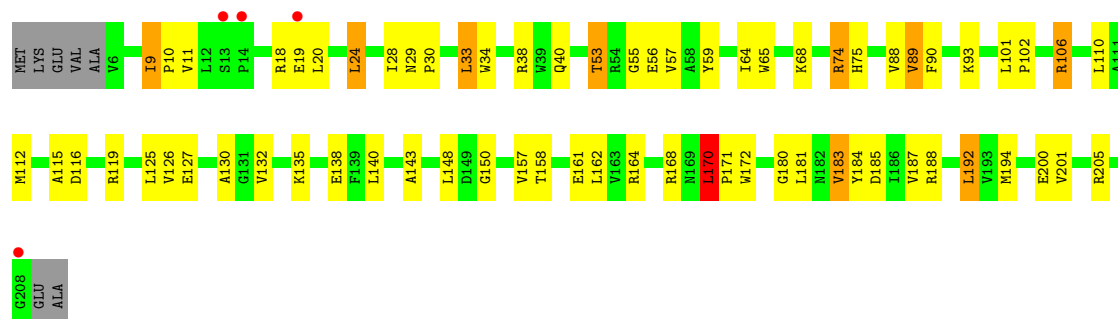
• Molecule 29: 50S ribosomal protein L3



• Molecule 29: 50S ribosomal protein L3

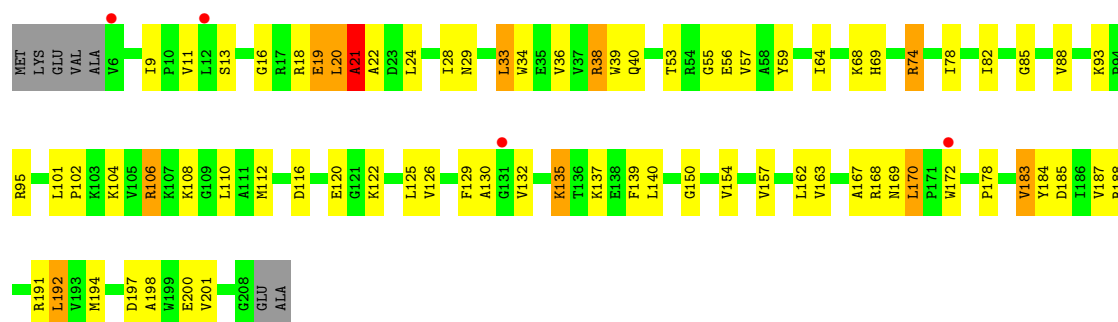


• Molecule 30: 50S ribosomal protein L4

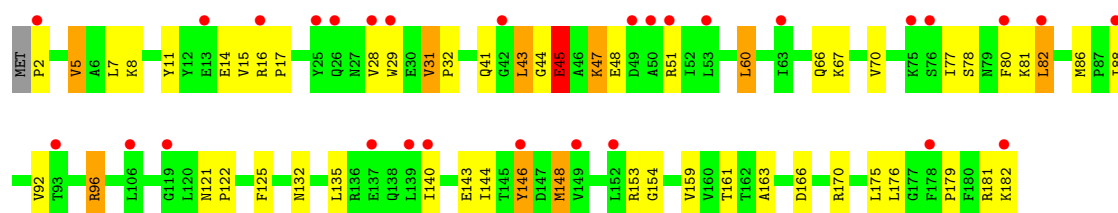


• Molecule 30: 50S ribosomal protein L4

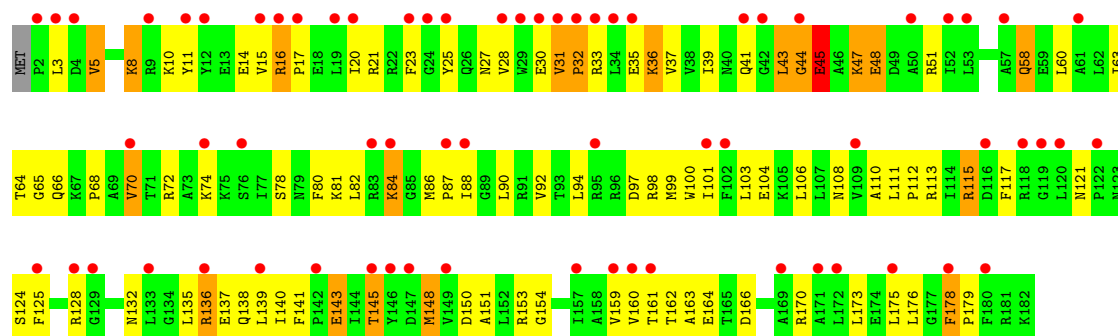
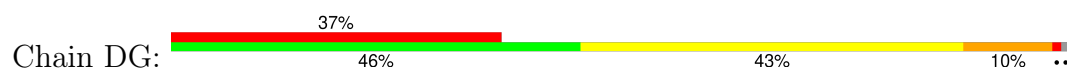




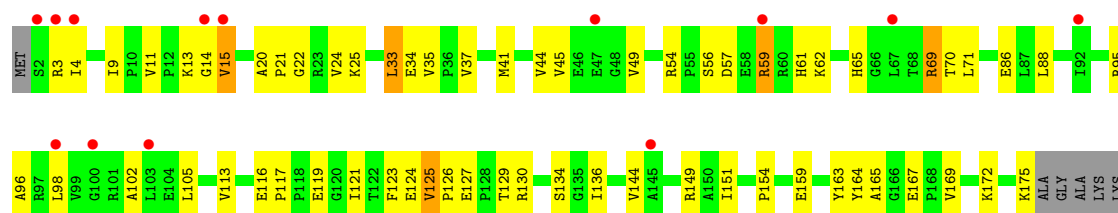
• Molecule 31: 50S ribosomal protein L5



• Molecule 31: 50S ribosomal protein L5

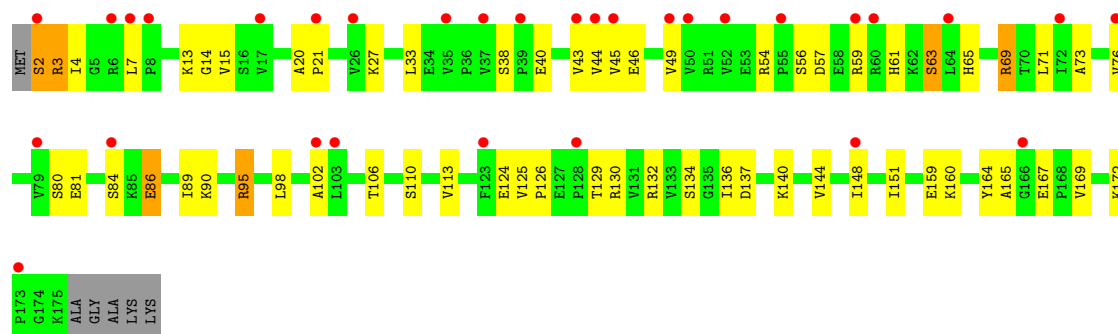


• Molecule 32: 50S ribosomal protein L6

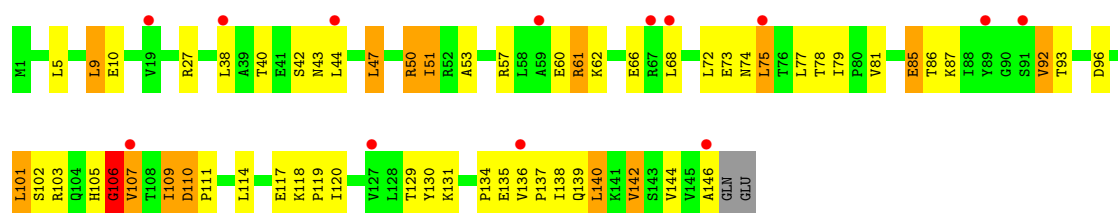


• Molecule 32: 50S ribosomal protein L6

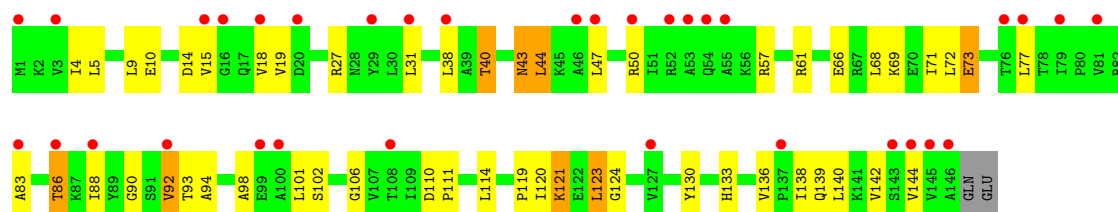




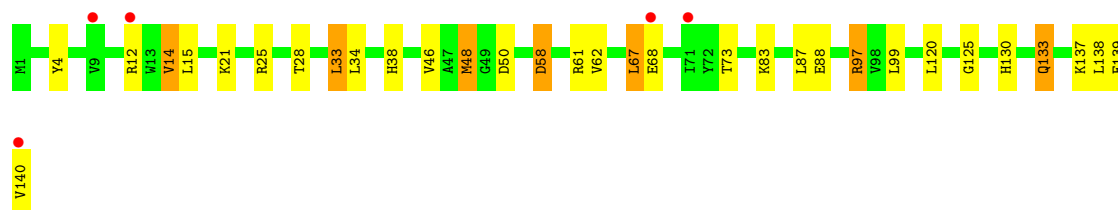
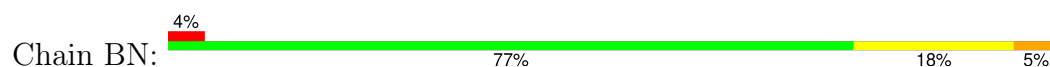
• Molecule 33: 50S ribosomal protein L9



• Molecule 33: 50S ribosomal protein L9



• Molecule 34: 50S ribosomal protein L13

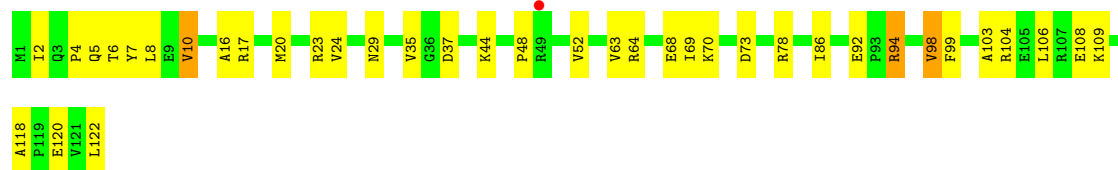


• Molecule 34: 50S ribosomal protein L13

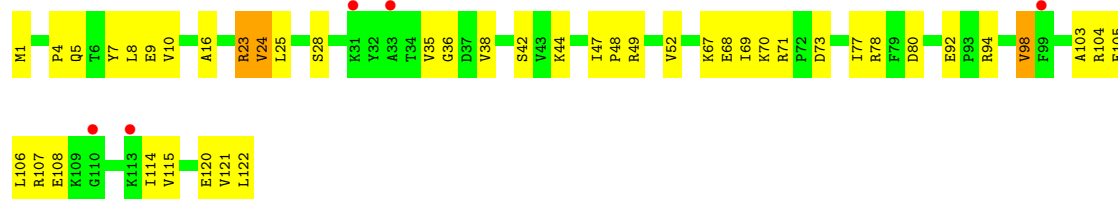




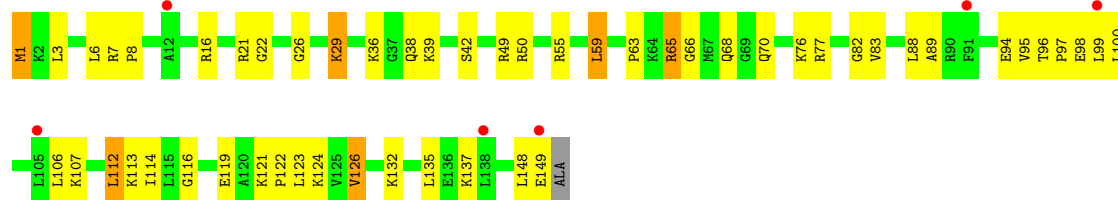
- Molecule 35: 50S ribosomal protein L14



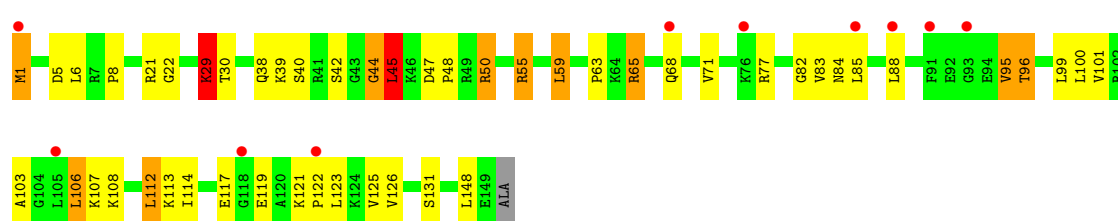
- Molecule 35: 50S ribosomal protein L14



- Molecule 36: 50S ribosomal protein L15

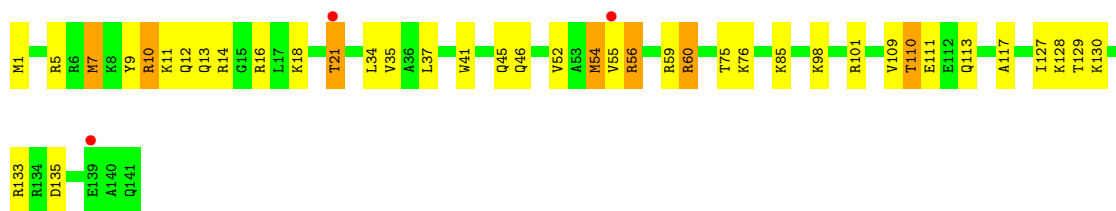


- Molecule 36: 50S ribosomal protein L15

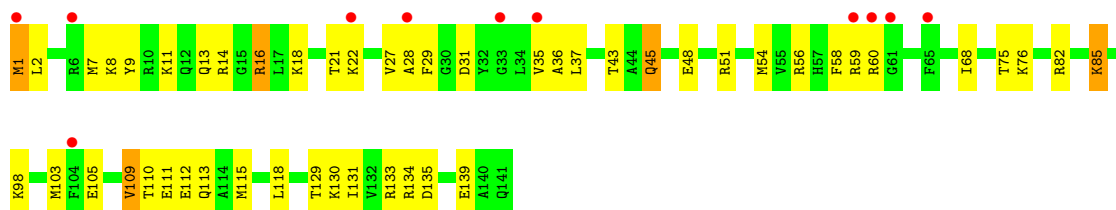


- Molecule 37: 50S ribosomal protein L16

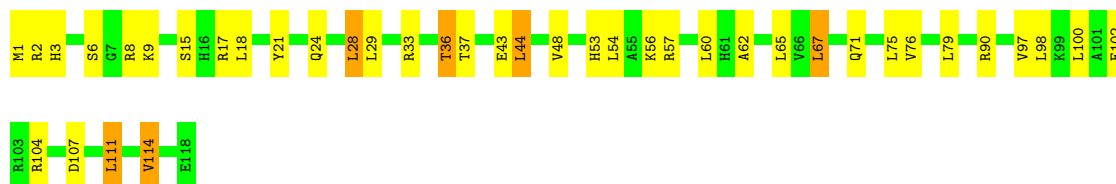




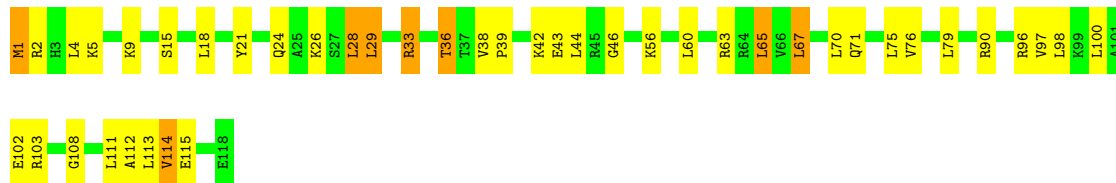
- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17



- Molecule 38: 50S ribosomal protein L17

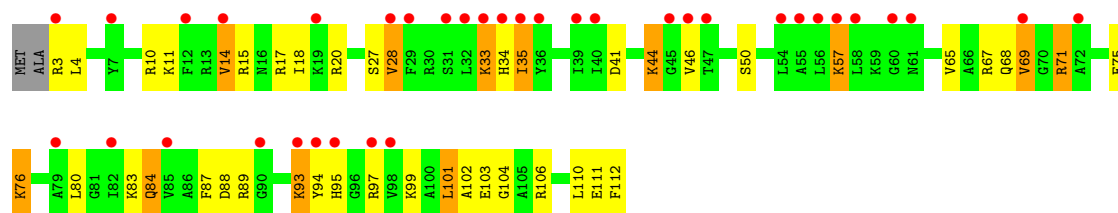


- Molecule 39: 50S ribosomal protein L18

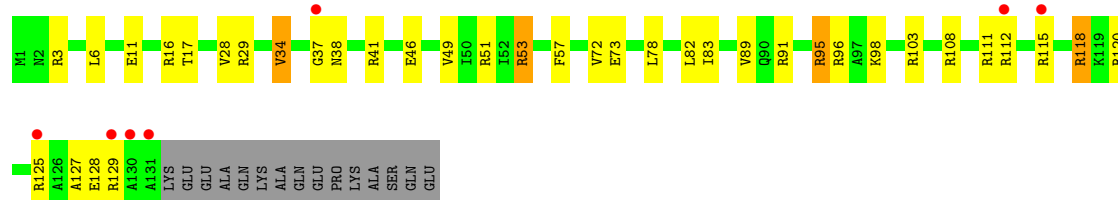


- Molecule 39: 50S ribosomal protein L18

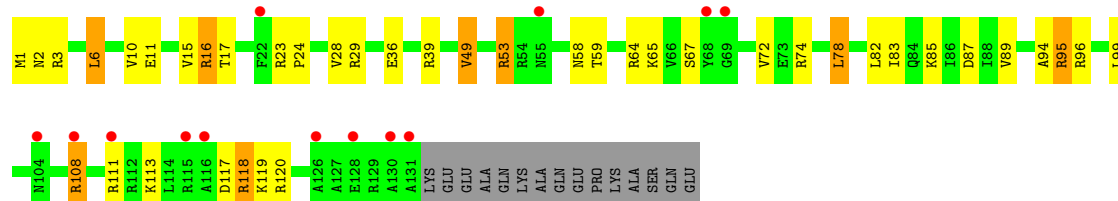




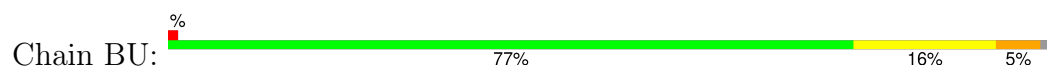
- Molecule 40: 50S ribosomal protein L19



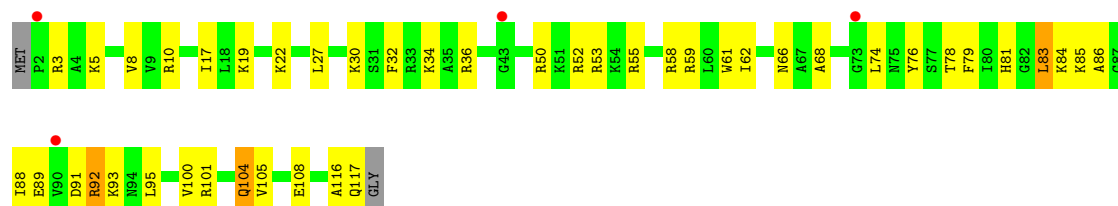
- Molecule 40: 50S ribosomal protein L19



- Molecule 41: 50S ribosomal protein L20

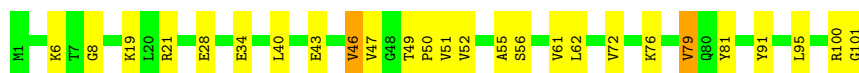


- Molecule 41: 50S ribosomal protein L20

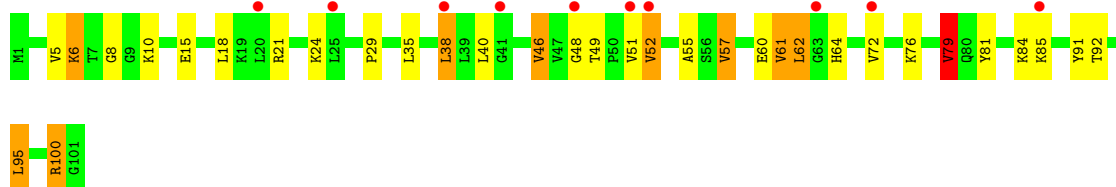


- Molecule 42: 50S ribosomal protein L21

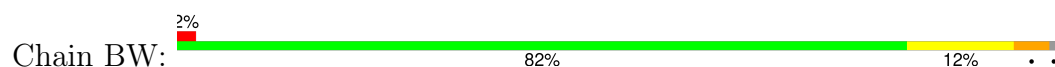




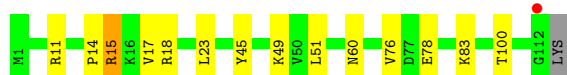
- Molecule 42: 50S ribosomal protein L21



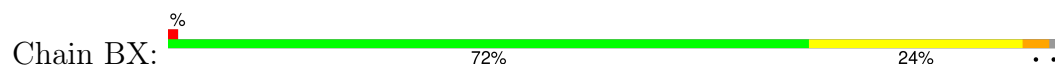
- Molecule 43: 50S ribosomal protein L22



- Molecule 43: 50S ribosomal protein L22



- Molecule 44: 50S ribosomal protein L23

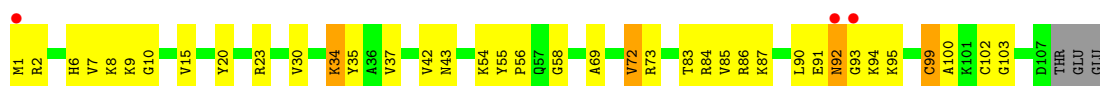


- Molecule 44: 50S ribosomal protein L23

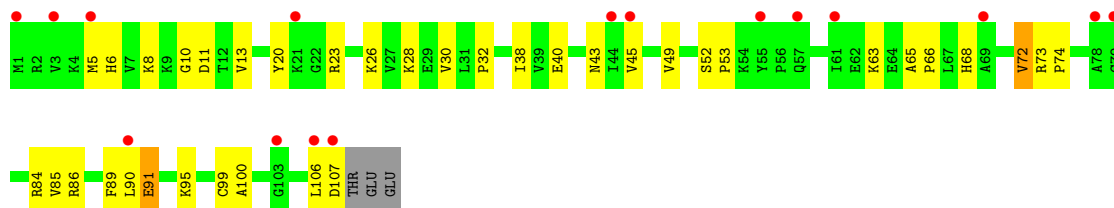


- Molecule 45: 50S ribosomal protein L24

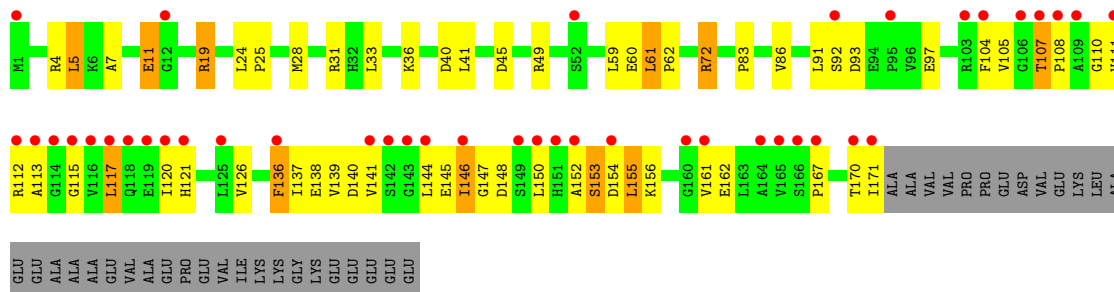




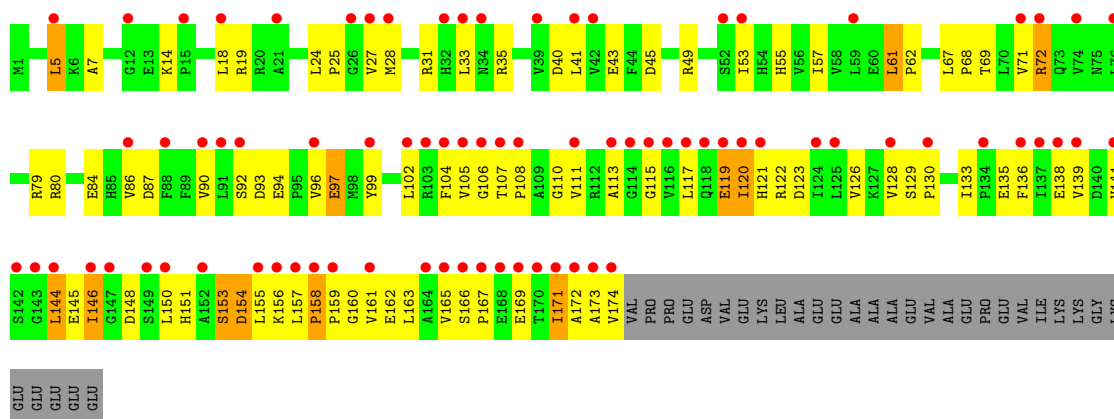
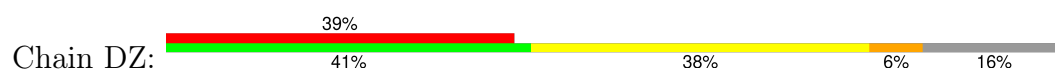
- Molecule 45: 50S ribosomal protein L24



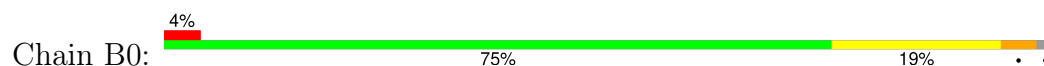
- Molecule 46: 50S ribosomal protein L25



- Molecule 46: 50S ribosomal protein L25



- Molecule 47: 50S ribosomal protein L27

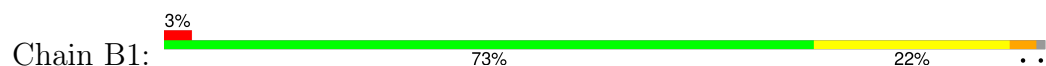




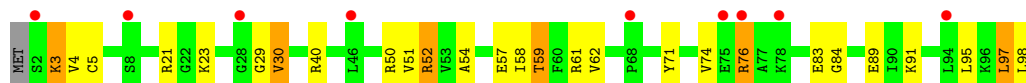
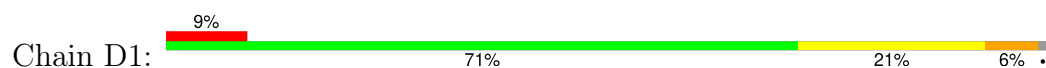
- Molecule 47: 50S ribosomal protein L27



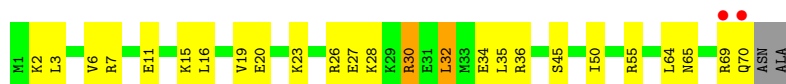
- Molecule 48: 50S ribosomal protein L28



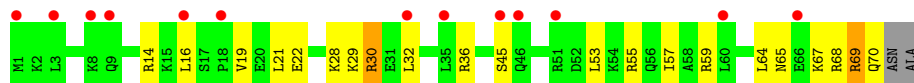
- Molecule 48: 50S ribosomal protein L28



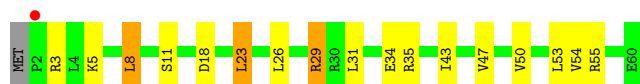
- Molecule 49: 50S ribosomal protein L29



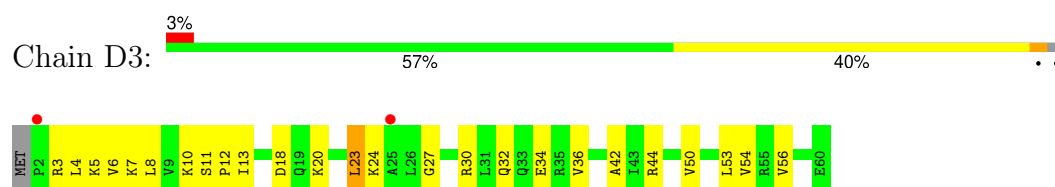
- Molecule 49: 50S ribosomal protein L29



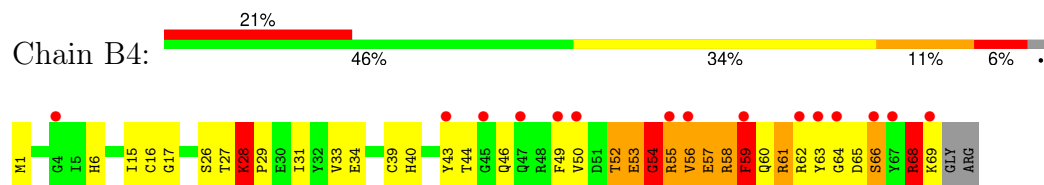
- Molecule 50: 50S ribosomal protein L30



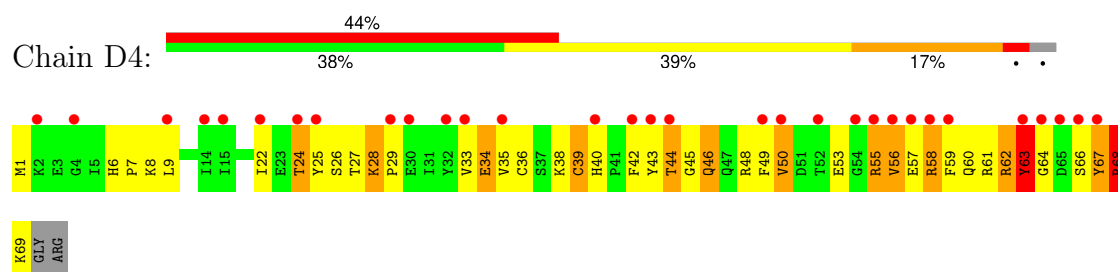
- Molecule 50: 50S ribosomal protein L30



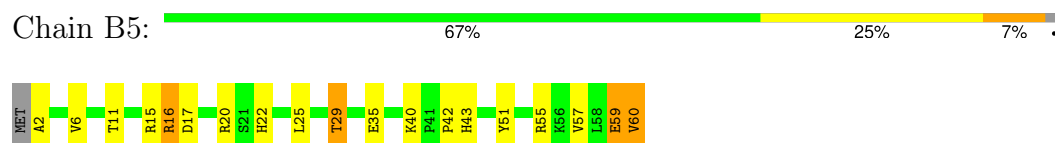
- Molecule 51: 50S ribosomal protein L31



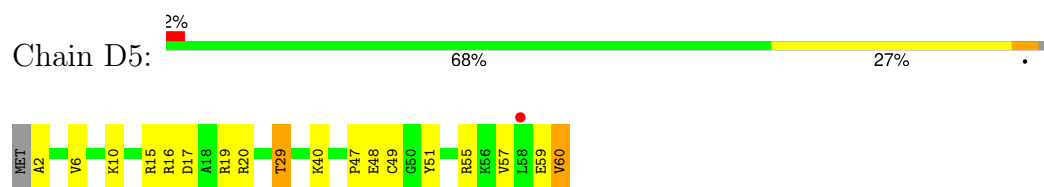
- Molecule 51: 50S ribosomal protein L31



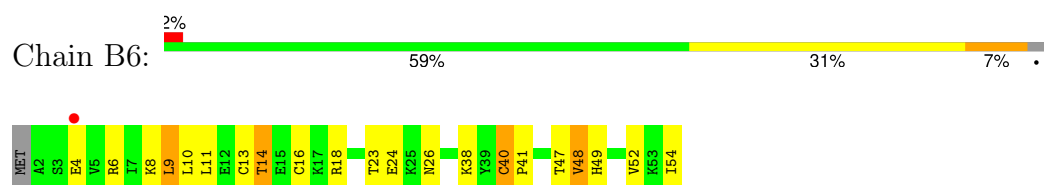
- Molecule 52: 50S ribosomal protein L32



- Molecule 52: 50S ribosomal protein L32

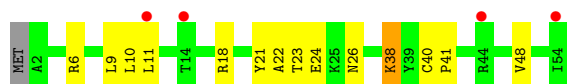


- Molecule 53: 50S ribosomal protein L33

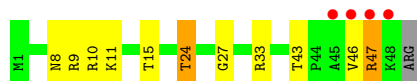
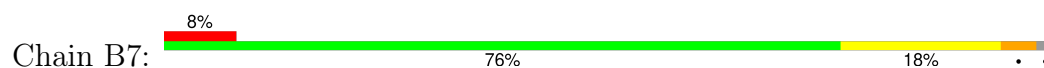


- Molecule 53: 50S ribosomal protein L33

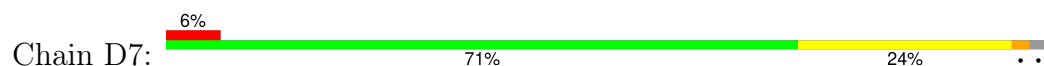




- Molecule 54: 50S ribosomal protein L34



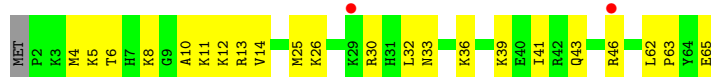
- Molecule 54: 50S ribosomal protein L34



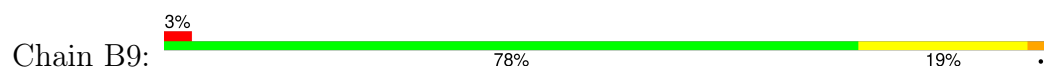
- Molecule 55: 50S ribosomal protein L35



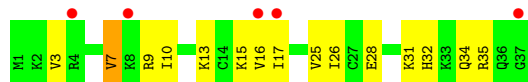
- Molecule 55: 50S ribosomal protein L35



- Molecule 56: 50S ribosomal protein L36



- Molecule 56: 50S ribosomal protein L36



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.32Å 450.06Å 622.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	152.51 – 2.55 152.51 – 2.55	Depositor EDS
% Data completeness (in resolution range)	95.8 (152.51-2.55) 95.8 (152.51-2.55)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.55Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.233 , 0.280 0.235 , 0.281	Depositor DCC
R_{free} test set	90444 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	297141	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.64% 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: MIA, 5MU, SF4, K, 31M, MG, ZN, 5MC, PSU, 7MG, 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	0.21	0/36049	0.44	4/56261 (0.0%)
1	CA	0.22	0/36170	0.47	11/56452 (0.0%)
2	AB	0.40	0/1881	1.01	11/2542 (0.4%)
2	CB	0.44	0/1860	1.04	6/2518 (0.2%)
3	AC	0.39	0/1576	0.87	1/2130 (0.0%)
3	CC	0.43	0/1566	1.01	10/2119 (0.5%)
4	AD	0.39	0/1689	0.90	2/2267 (0.1%)
4	CD	0.38	0/1704	0.87	2/2284 (0.1%)
5	AE	0.42	0/1145	0.92	1/1543 (0.1%)
5	CE	0.43	0/1149	1.05	9/1548 (0.6%)
6	AF	0.36	0/819	0.76	0/1111
6	CF	0.38	0/829	0.81	0/1123
7	AG	0.37	0/1250	0.87	1/1679 (0.1%)
7	CG	0.37	0/1254	0.93	4/1683 (0.2%)
8	AH	0.37	0/1108	0.85	0/1494
8	CH	0.35	0/1108	0.89	2/1494 (0.1%)
9	AI	0.40	0/1002	0.90	2/1346 (0.1%)
9	CI	0.41	0/997	0.92	1/1343 (0.1%)
10	AJ	0.40	0/722	0.99	4/982 (0.4%)
10	CJ	0.44	0/727	1.01	5/988 (0.5%)
11	AK	0.39	0/844	0.90	2/1145 (0.2%)
11	CK	0.39	0/848	0.88	2/1149 (0.2%)
12	AL	0.38	0/946	0.82	1/1274 (0.1%)
12	CL	0.37	0/946	0.88	3/1274 (0.2%)
13	AM	0.39	0/969	0.98	2/1302 (0.2%)
13	CM	0.40	0/961	0.94	4/1291 (0.3%)
14	AN	0.38	0/501	0.80	0/664
14	CN	0.40	0/501	0.87	1/664 (0.2%)
15	AO	0.38	0/739	0.88	2/985 (0.2%)
15	CO	0.38	0/739	0.83	0/985
16	AP	0.38	0/697	0.83	0/939
16	CP	0.40	0/693	0.83	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.36	0/836	0.80	0/1117
17	CQ	0.33	0/836	0.79	0/1117
18	AR	0.36	0/560	0.83	0/746
18	CR	0.36	0/560	0.79	0/746
19	AS	0.39	0/667	0.94	4/900 (0.4%)
19	CS	0.45	0/661	1.05	3/893 (0.3%)
20	AT	0.37	0/730	0.94	2/965 (0.2%)
20	CT	0.38	0/729	0.82	0/965
21	AU	0.33	0/203	0.80	0/266
21	CU	0.38	0/203	0.91	0/266
22	AV	0.21	0/310	0.37	0/480
22	CV	0.25	0/282	0.48	0/437
23	AW	0.28	0/1577	0.52	0/2454
23	CW	0.35	0/1531	0.62	0/2379
24	AX	0.27	0/1725	0.45	0/2689
24	CX	0.24	0/1725	0.43	0/2689
25	AY	0.35	1/1602 (0.1%)	0.65	1/2493 (0.0%)
25	CY	0.35	1/1579 (0.1%)	0.61	0/2455
26	BA	0.27	0/68013	0.46	4/106165 (0.0%)
26	DA	0.23	0/67542	0.45	0/105428
27	BB	0.23	0/2878	0.43	0/4490
27	DB	0.24	0/2878	0.46	0/4490
28	BD	0.48	0/2186	0.92	6/2944 (0.2%)
28	DD	0.43	0/2186	0.89	5/2944 (0.2%)
29	BE	0.49	0/1592	0.90	2/2149 (0.1%)
29	DE	0.45	0/1592	0.98	8/2149 (0.4%)
30	BF	0.46	0/1619	0.85	4/2193 (0.2%)
30	DF	0.41	0/1615	0.92	3/2188 (0.1%)
31	BG	0.41	0/1450	0.90	5/1959 (0.3%)
31	DG	0.42	0/1449	1.03	9/1958 (0.5%)
32	BH	0.43	0/1356	0.86	1/1834 (0.1%)
32	DH	0.41	0/1356	0.93	3/1834 (0.2%)
33	BI	0.40	0/1100	0.95	7/1501 (0.5%)
33	DI	0.40	0/1076	0.91	3/1471 (0.2%)
34	BN	0.43	0/1144	0.89	2/1543 (0.1%)
34	DN	0.39	0/1144	0.98	8/1543 (0.5%)
35	BO	0.46	0/943	0.84	0/1269
35	DO	0.41	0/943	0.82	0/1269
36	BP	0.46	0/1152	0.85	2/1533 (0.1%)
36	DP	0.39	0/1152	0.93	5/1533 (0.3%)
37	BQ	0.44	0/1143	0.81	0/1527
37	DQ	0.40	0/1143	0.84	0/1527
38	BR	0.47	0/982	0.85	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	DR	0.40	0/982	0.78	0/1312
39	BS	0.40	0/887	0.87	1/1180 (0.1%)
39	DS	0.39	0/880	0.96	1/1172 (0.1%)
40	BT	0.41	0/1105	0.79	0/1477
40	DT	0.38	0/1097	0.82	0/1468
41	BU	0.51	0/977	0.82	0/1301
41	DU	0.39	0/977	0.82	0/1301
42	BV	0.49	0/782	0.83	1/1049 (0.1%)
42	DV	0.39	0/782	0.83	0/1049
43	BW	0.51	0/897	0.89	2/1205 (0.2%)
43	DW	0.42	0/897	0.85	0/1205
44	BX	0.47	0/764	0.86	0/1025
44	DX	0.40	0/764	0.85	0/1025
45	BY	0.42	0/819	0.90	1/1095 (0.1%)
45	DY	0.37	0/819	0.87	1/1095 (0.1%)
46	BZ	0.42	0/1379	0.98	5/1873 (0.3%)
46	DZ	0.38	0/1390	0.98	12/1890 (0.6%)
47	B0	0.43	0/662	0.85	2/881 (0.2%)
47	D0	0.34	0/662	0.82	2/881 (0.2%)
48	B1	0.46	0/762	0.87	0/1014
48	D1	0.41	0/762	0.79	0/1014
49	B2	0.42	0/590	0.86	0/781
49	D2	0.35	0/590	0.74	0/781
50	B3	0.46	0/474	0.88	2/635 (0.3%)
50	D3	0.34	0/469	0.85	0/630
51	B4	0.46	0/571	1.19	10/768 (1.3%)
51	D4	0.49	0/545	1.24	8/737 (1.1%)
52	B5	0.52	0/469	0.79	0/635
52	D5	0.43	0/469	0.76	0/635
53	B6	0.45	0/460	0.77	2/613 (0.3%)
53	D6	0.37	0/456	0.72	0/608
54	B7	0.51	0/426	0.82	1/561 (0.2%)
54	D7	0.48	0/426	0.88	0/561
55	B8	0.46	0/519	0.86	0/684
55	D8	0.40	0/525	0.80	0/691
56	B9	0.42	0/310	0.83	0/407
56	D9	0.36	0/310	0.84	0/407
All	All	0.30	2/316594 (0.0%)	0.60	231/473970 (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
2	AB	0	4
7	AG	0	2
7	CG	0	1
20	CT	0	1
28	BD	0	1
39	BS	0	1
51	B4	0	2
51	D4	0	1
All	All	0	13

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	AY	8	4SU	O3'-P	5.64	1.61	1.56
25	CY	8	4SU	O3'-P	5.11	1.61	1.56

All (231) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	B4	60	GLN	N-CA-C	-8.56	103.89	112.97
2	AB	9	GLU	N-CA-C	8.30	123.36	109.76
7	CG	79	ARG	N-CA-C	8.20	122.37	108.67
8	CH	73	ASP	CA-C-N	8.11	128.31	119.87
8	CH	73	ASP	C-N-CA	8.11	128.31	119.87
2	AB	128	GLU	N-CA-C	-7.89	100.72	113.19
7	CG	79	ARG	CB-CA-C	-7.88	106.51	117.23
29	DE	72	VAL	CA-C-N	7.87	135.86	121.70
29	DE	72	VAL	C-N-CA	7.87	135.86	121.70
3	CC	139	GLN	N-CA-C	7.77	119.44	110.97
3	CC	125	GLU	N-CA-C	-7.59	103.02	111.82
51	B4	52	THR	N-CA-C	-7.32	101.52	111.55
31	DG	31	VAL	CA-C-N	7.31	128.98	119.84
31	DG	31	VAL	C-N-CA	7.31	128.98	119.84
28	BD	274	ARG	N-CA-C	7.28	120.79	110.23
5	CE	105	VAL	CA-C-N	-7.22	112.27	119.56
5	CE	105	VAL	C-N-CA	-7.22	112.27	119.56
1	CA	1125	U	O3'-P-O5'	7.21	114.81	104.00
47	B0	13	GLY	N-CA-C	7.15	122.34	114.40
1	CA	1054	C	P-O3'-C3'	7.03	130.75	120.20
34	DN	125	GLY	CA-C-N	7.03	126.66	119.56
34	DN	125	GLY	C-N-CA	7.03	126.66	119.56
2	AB	38	GLY	N-CA-C	-7.02	104.08	114.90
26	BA	1992	G	C2'-C3'-O3'	6.86	119.80	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	CI	63	ILE	N-CA-C	6.78	117.81	107.77
4	AD	188	LEU	CA-C-N	6.77	126.74	119.76
4	AD	188	LEU	C-N-CA	6.77	126.74	119.76
13	AM	84	ILE	N-CA-C	6.76	123.23	113.16
26	BA	271(M)	G	OP1-P-O3'	6.75	120.05	105.20
36	DP	44	GLY	CA-C-N	6.71	133.79	121.70
36	DP	44	GLY	C-N-CA	6.71	133.79	121.70
51	D4	46	GLN	CB-CA-C	-6.71	108.85	116.63
46	DZ	158	PRO	CA-C-N	6.62	126.59	120.03
46	DZ	158	PRO	C-N-CA	6.62	126.59	120.03
1	CA	1154	G	N1-C2-N2	-6.58	96.45	116.20
31	DG	178	PHE	CA-C-N	6.54	127.52	120.13
31	DG	178	PHE	C-N-CA	6.54	127.52	120.13
1	CA	1119	C	N1-C2-O2	6.44	138.21	118.90
13	CM	106	ASN	N-CA-C	6.43	120.29	111.54
5	CE	98	THR	N-CA-C	6.42	117.94	111.07
45	BY	92	ASN	N-CA-C	6.40	118.26	111.28
36	DP	22	GLY	CA-C-N	6.40	125.83	118.85
36	DP	22	GLY	C-N-CA	6.40	125.83	118.85
30	DF	9	ILE	N-CA-C	6.39	115.59	108.05
51	D4	68	ARG	N-CA-C	6.35	118.00	111.14
33	BI	110	ASP	CA-C-N	6.30	125.79	119.24
33	BI	110	ASP	C-N-CA	6.30	125.79	119.24
46	DZ	133	ILE	CA-C-N	6.25	126.71	120.52
46	DZ	133	ILE	C-N-CA	6.25	126.71	120.52
47	D0	82	ARG	CA-C-N	6.25	126.20	119.76
47	D0	82	ARG	C-N-CA	6.25	126.20	119.76
51	B4	68	ARG	N-CA-C	6.24	118.08	110.41
10	AJ	5	ARG	N-CA-C	6.21	119.58	109.59
4	CD	171	GLY	CA-C-N	6.19	126.65	119.47
4	CD	171	GLY	C-N-CA	6.19	126.65	119.47
1	CA	1119	C	C2-N1-C1'	6.17	137.32	118.80
51	B4	28	LYS	CA-C-N	6.16	125.38	118.97
51	B4	28	LYS	C-N-CA	6.16	125.38	118.97
28	BD	85	ASP	CA-C-N	6.14	126.25	119.87
28	BD	85	ASP	C-N-CA	6.14	126.25	119.87
31	DG	48	GLU	N-CA-C	-6.14	106.33	113.88
31	BG	96	ARG	CB-CA-C	-6.13	109.48	116.54
15	AO	20	GLY	N-CA-C	6.12	120.07	112.73
1	CA	1054	C	C2'-C3'-O3'	6.09	118.64	109.50
30	BF	89	VAL	N-CA-C	6.08	116.28	110.74
43	BW	13	SER	CA-C-N	6.04	126.21	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	BW	13	SER	C-N-CA	6.04	126.21	119.32
30	DF	21	ALA	CA-C-N	6.02	132.53	121.70
30	DF	21	ALA	C-N-CA	6.02	132.53	121.70
12	CL	28	LYS	N-CA-C	6.00	119.68	111.39
26	BA	271(M)	G	P-O3'-C3'	5.99	126.89	119.70
12	CL	105	TYR	CB-CA-C	-5.94	109.74	116.63
53	B6	40	CYS	CA-C-N	5.94	125.81	119.28
53	B6	40	CYS	C-N-CA	5.94	125.81	119.28
2	CB	25	ASN	CA-C-N	5.92	125.60	119.56
2	CB	25	ASN	C-N-CA	5.92	125.60	119.56
12	CL	119	LYS	N-CA-C	-5.92	102.15	110.50
51	D4	67	TYR	N-CA-C	-5.92	100.35	109.76
33	BI	51	ILE	N-CA-C	-5.92	104.97	110.53
33	BI	118	LYS	CA-C-N	5.91	125.93	119.90
33	BI	118	LYS	C-N-CA	5.91	125.93	119.90
46	DZ	106	GLY	N-CA-C	-5.90	103.91	112.17
31	BG	45	GLU	N-CA-C	-5.87	105.02	111.82
51	B4	65	ASP	N-CA-C	-5.87	106.36	112.93
31	BG	146	TYR	N-CA-C	-5.84	105.98	113.23
2	AB	166	ASP	CA-C-N	5.81	125.50	119.05
2	AB	166	ASP	C-N-CA	5.81	125.50	119.05
25	AY	58	A	C4'-C3'-O3'	5.79	118.08	109.40
29	DE	85	ASN	CA-C-N	5.78	125.73	119.78
29	DE	85	ASN	C-N-CA	5.78	125.73	119.78
45	DY	91	GLU	N-CA-C	-5.77	106.19	113.18
1	AA	1054	C	P-O3'-C3'	5.74	128.81	120.20
1	CA	1154	G	N3-C2-N2	5.71	137.03	119.90
33	DI	72	LEU	N-CA-C	5.69	118.42	111.82
34	DN	94	HIS	CA-C-N	5.68	125.53	119.28
34	DN	94	HIS	C-N-CA	5.68	125.53	119.28
46	DZ	115	GLY	N-CA-C	5.66	122.49	112.64
28	DD	120	GLY	CA-C-N	5.66	126.03	119.47
28	DD	120	GLY	C-N-CA	5.66	126.03	119.47
15	AO	22	THR	N-CA-C	-5.66	101.02	109.96
7	AG	116	ALA	N-CA-C	5.65	117.44	111.28
32	DH	38	SER	N-CA-C	5.64	116.51	109.57
28	DD	70	TRP	N-CA-C	-5.64	106.48	113.19
31	DG	78	SER	N-CA-C	5.64	117.10	111.07
3	CC	72	LYS	CA-C-N	5.62	125.99	119.47
3	CC	72	LYS	C-N-CA	5.62	125.99	119.47
2	AB	8	LYS	N-CA-C	5.62	120.27	113.41
51	D4	28	LYS	CA-C-N	5.62	124.81	118.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	D4	28	LYS	C-N-CA	5.62	124.81	118.97
12	AL	105	TYR	CB-CA-C	-5.60	110.13	116.63
5	CE	6	PHE	N-CA-C	5.60	118.38	109.81
10	CJ	90	LEU	CA-C-N	5.60	126.84	119.84
10	CJ	90	LEU	C-N-CA	5.60	126.84	119.84
34	DN	10	GLU	CA-C-N	5.60	125.53	119.76
34	DN	10	GLU	C-N-CA	5.60	125.53	119.76
34	BN	125	GLY	CA-C-N	5.58	125.20	119.56
34	BN	125	GLY	C-N-CA	5.58	125.20	119.56
1	CA	1126	U	P-O5'-C5'	5.58	129.27	120.90
2	AB	193	ASP	CA-C-N	5.58	124.77	118.97
2	AB	193	ASP	C-N-CA	5.58	124.77	118.97
3	CC	48	TYR	N-CA-C	-5.57	105.30	111.71
31	DG	45	GLU	N-CA-C	-5.57	105.58	112.38
19	CS	41	VAL	CA-C-N	5.55	126.78	119.84
19	CS	41	VAL	C-N-CA	5.55	126.78	119.84
13	AM	106	ASN	CB-CA-C	-5.55	110.16	116.54
28	DD	275	LYS	N-CA-C	-5.53	100.87	109.72
47	B0	12	ASN	N-CA-C	5.53	120.02	112.88
28	BD	275	LYS	N-CA-C	5.52	122.56	110.80
14	CN	12	ARG	N-CA-C	5.52	118.23	110.23
29	DE	176	ILE	CA-C-N	5.52	125.87	119.47
29	DE	176	ILE	C-N-CA	5.52	125.87	119.47
5	CE	76	ILE	CA-C-N	5.51	125.34	119.28
5	CE	76	ILE	C-N-CA	5.51	125.34	119.28
2	CB	119	GLU	N-CA-C	-5.51	105.43	111.82
46	BZ	107	THR	CA-C-N	5.50	125.77	119.83
46	BZ	107	THR	C-N-CA	5.50	125.77	119.83
10	AJ	57	LYS	N-CA-C	5.49	117.26	111.28
11	CK	38	ASN	CA-C-N	5.49	125.41	119.76
11	CK	38	ASN	C-N-CA	5.49	125.41	119.76
2	AB	123	ALA	N-CA-C	-5.48	106.36	113.16
50	B3	11	SER	CA-C-N	5.48	125.09	119.56
50	B3	11	SER	C-N-CA	5.48	125.09	119.56
51	B4	40	HIS	CA-C-N	5.47	126.68	119.84
51	B4	40	HIS	C-N-CA	5.47	126.68	119.84
13	CM	112	GLY	CA-C-N	5.47	125.48	119.90
13	CM	112	GLY	C-N-CA	5.47	125.48	119.90
20	AT	11	SER	N-CA-C	-5.46	106.20	112.92
31	BG	31	VAL	CA-C-N	5.45	126.66	119.84
31	BG	31	VAL	C-N-CA	5.45	126.66	119.84
30	BF	170	LEU	CA-C-N	5.45	125.10	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	BF	170	LEU	C-N-CA	5.45	125.10	119.05
5	CE	127	ASN	CA-C-N	5.45	124.90	119.24
5	CE	127	ASN	C-N-CA	5.45	124.90	119.24
33	BI	106	GLY	CA-C-N	5.44	131.50	121.70
33	BI	106	GLY	C-N-CA	5.44	131.50	121.70
42	BV	47	VAL	N-CA-C	5.44	115.69	107.75
1	CA	1054	C	C1'-C2'-O2'	-5.43	103.65	111.80
29	BE	52	LEU	CA-C-N	5.42	125.36	119.78
29	BE	52	LEU	C-N-CA	5.42	125.36	119.78
20	AT	88	VAL	N-CA-C	5.41	115.55	110.30
51	B4	54	GLY	CA-C-N	5.40	131.85	121.54
51	B4	54	GLY	C-N-CA	5.40	131.85	121.54
51	D4	49	PHE	CB-CA-C	-5.39	110.34	116.54
46	BZ	115	GLY	N-CA-C	5.38	121.08	112.58
2	AB	11	LEU	N-CA-C	-5.38	106.56	113.02
33	DI	124	GLY	N-CA-C	5.37	118.13	110.46
10	CJ	79	ARG	N-CA-C	5.36	122.22	110.80
10	CJ	52	GLY	CA-C-N	5.33	125.03	119.64
10	CJ	52	GLY	C-N-CA	5.33	125.03	119.64
46	DZ	14	LYS	CA-C-N	5.33	125.65	119.47
46	DZ	14	LYS	C-N-CA	5.33	125.65	119.47
1	CA	1119	C	C6-N1-C1'	-5.32	104.84	120.80
34	DN	110	GLY	CA-C-N	5.31	125.38	119.32
34	DN	110	GLY	C-N-CA	5.31	125.38	119.32
1	AA	1054	C	C2'-C3'-O3'	5.30	117.46	109.50
3	CC	108	ASN	CA-C-N	5.29	124.96	119.56
3	CC	108	ASN	C-N-CA	5.29	124.96	119.56
2	AB	127	ILE	N-CA-C	5.29	116.64	108.44
2	CB	122	PHE	N-CA-C	-5.27	102.21	110.17
46	BZ	117	LEU	N-CA-C	5.27	116.84	108.67
3	CC	6	HIS	CA-C-N	5.27	124.88	119.56
3	CC	6	HIS	C-N-CA	5.27	124.88	119.56
9	AI	48	GLU	CA-C-N	-5.26	113.21	119.05
9	AI	48	GLU	C-N-CA	-5.26	113.21	119.05
19	CS	82	GLY	N-CA-C	5.26	118.44	110.97
3	AC	4	LYS	N-CA-C	5.24	117.63	110.24
33	DI	71	ILE	N-CA-C	5.23	115.45	110.53
7	CG	78	ARG	N-CA-C	5.21	117.50	107.44
3	CC	19	GLU	N-CA-C	-5.21	105.66	112.23
7	CG	132	GLY	N-CA-C	5.19	116.88	111.95
1	AA	1054	C	O3'-P-O5'	5.19	111.78	104.00
11	AK	50	TYR	N-CA-C	5.18	118.14	110.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	BS	67	ARG	NE-CZ-NH1	-5.18	116.32	121.50
10	AJ	90	LEU	CA-C-N	5.16	126.29	119.84
10	AJ	90	LEU	C-N-CA	5.16	126.29	119.84
51	D4	36	CYS	N-CA-C	5.16	114.95	108.45
2	CB	193	ASP	CA-C-N	5.16	124.33	118.97
2	CB	193	ASP	C-N-CA	5.16	124.33	118.97
30	BF	9	ILE	N-CA-C	5.16	113.55	107.77
36	DP	40	SER	N-CA-C	-5.15	106.51	112.89
19	AS	41	VAL	CA-C-N	5.14	126.27	119.84
19	AS	41	VAL	C-N-CA	5.14	126.27	119.84
39	DS	28	VAL	N-CA-C	5.14	115.68	108.17
11	AK	18	ARG	NE-CZ-NH1	-5.14	116.36	121.50
31	DG	65	GLY	N-CA-C	-5.14	108.16	115.30
46	DZ	129	SER	CA-C-N	5.14	125.18	119.32
46	DZ	129	SER	C-N-CA	5.14	125.18	119.32
1	CA	1067	A	C2'-C3'-O3'	5.14	117.20	109.50
28	BD	70	TRP	CA-C-N	5.12	127.09	120.44
28	BD	70	TRP	C-N-CA	5.12	127.09	120.44
32	BH	9	ILE	N-CA-C	5.11	112.61	107.55
19	AS	36	ARG	N-CA-C	-5.11	107.04	113.28
19	AS	10	PHE	N-CA-C	5.10	117.07	108.96
28	DD	256	GLY	N-CA-C	5.10	120.88	114.25
5	AE	98	THR	N-CA-C	5.10	117.23	111.11
1	AA	1067	A	C2'-C3'-O3'	5.09	117.14	109.50
46	DZ	107	THR	CA-C-N	5.09	125.33	119.83
46	DZ	107	THR	C-N-CA	5.09	125.33	119.83
5	CE	23	GLY	N-CA-C	5.08	117.22	112.04
29	DE	144	ARG	CB-CA-C	-5.08	109.06	116.53
13	CM	68	GLY	N-CA-C	5.07	118.38	112.50
29	DE	89	ASP	N-CA-C	-5.07	106.69	112.92
54	B7	47	ARG	N-CA-C	5.06	119.08	113.01
31	DG	44	GLY	N-CA-C	-5.03	108.76	115.40
46	BZ	141	VAL	N-CA-C	5.03	117.00	111.77
32	DH	38	SER	CA-C-N	5.02	124.74	119.82
32	DH	38	SER	C-N-CA	5.02	124.74	119.82
26	BA	71	A	C4'-C3'-O3'	5.02	116.93	109.40
36	BP	22	GLY	CA-C-N	5.01	124.31	118.85
36	BP	22	GLY	C-N-CA	5.01	124.31	118.85
51	D4	39	CYS	N-CA-C	5.01	121.47	110.80

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	18	GLY	Peptide
2	AB	231	GLU	Peptide
2	AB	8	LYS	Peptide
2	AB	9	GLU	Peptide
7	AG	78	ARG	Peptide
7	AG	79	ARG	Peptide
51	B4	52	THR	Peptide
51	B4	59	PHE	Peptide
28	BD	274	ARG	Peptide
39	BS	58	LEU	Peptide
7	CG	78	ARG	Peptide
20	CT	9	ASN	Peptide
51	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	32205	0	16254	503	0
1	CA	32312	0	16307	665	0
2	AB	1846	0	1867	97	0
2	CB	1825	0	1828	105	0
3	AC	1552	0	1546	55	0
3	CC	1542	0	1517	82	0
4	AD	1659	0	1676	73	0
4	CD	1674	0	1714	63	0
5	AE	1129	0	1185	34	0
5	CE	1133	0	1191	34	0
6	AF	806	0	793	26	0
6	CF	816	0	808	20	0
7	AG	1231	0	1238	30	0
7	CG	1235	0	1249	37	0
8	AH	1088	0	1126	27	0
8	CH	1088	0	1126	41	0
9	AI	983	0	986	47	0
9	CI	978	0	966	48	0
10	AJ	709	0	650	35	0
10	CJ	714	0	672	36	0
11	AK	829	0	825	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	CK	833	0	836	17	0
12	AL	930	0	980	24	0
12	CL	930	0	980	27	0
13	AM	958	0	1002	31	0
13	CM	950	0	988	40	0
14	AN	492	0	529	16	0
14	CN	492	0	529	33	0
15	AO	728	0	760	21	0
15	CO	728	0	760	30	0
16	AP	681	0	697	12	0
16	CP	677	0	686	23	0
17	AQ	823	0	891	22	0
17	CQ	823	0	891	15	0
18	AR	555	0	618	19	0
18	CR	555	0	618	16	0
19	AS	652	0	662	31	0
19	CS	646	0	644	39	0
20	AT	728	0	798	33	0
20	CT	727	0	796	27	0
21	AU	199	0	208	9	0
21	CU	199	0	208	10	0
22	AV	277	0	140	2	0
22	CV	252	0	130	7	0
23	AW	1607	0	839	55	0
23	CW	1560	0	803	56	0
24	AX	1625	0	828	31	0
24	CX	1625	0	828	30	0
25	AY	1581	0	805	95	0
25	CY	1561	0	796	79	0
26	BA	60729	0	30621	675	0
26	DA	60311	0	30409	889	0
27	BB	2573	0	1306	21	0
27	DB	2573	0	1306	50	0
28	BD	2136	0	2218	53	0
28	DD	2136	0	2218	63	0
29	BE	1559	0	1618	30	0
29	DE	1559	0	1618	47	0
30	BF	1584	0	1625	51	0
30	DF	1580	0	1619	53	0
31	BG	1425	0	1443	39	0
31	DG	1424	0	1434	68	0
32	BH	1330	0	1407	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	DH	1330	0	1407	30	0
33	BI	1085	0	1114	43	0
33	DI	1061	0	1080	26	0
34	BN	1117	0	1183	16	0
34	DN	1117	0	1184	29	0
35	BO	933	0	996	22	0
35	DO	933	0	996	28	0
36	BP	1135	0	1212	39	0
36	DP	1135	0	1212	43	0
37	BQ	1122	0	1179	32	0
37	DQ	1122	0	1179	36	0
38	BR	968	0	1033	18	0
38	DR	968	0	1033	29	0
39	BS	877	0	938	23	0
39	DS	870	0	923	34	0
40	BT	1091	0	1151	28	0
40	DT	1083	0	1136	31	0
41	BU	959	0	1019	20	0
41	DU	959	0	1019	38	0
42	BV	771	0	830	13	0
42	DV	771	0	830	25	0
43	BW	886	0	939	14	0
43	DW	886	0	940	10	0
44	BX	750	0	814	17	0
44	DX	750	0	814	23	0
45	BY	806	0	881	23	0
45	DY	806	0	881	27	0
46	BZ	1349	0	1355	45	0
46	DZ	1360	0	1363	63	0
47	B0	653	0	674	14	0
47	D0	653	0	674	20	0
48	B1	755	0	826	20	0
48	D1	755	0	826	18	0
49	B2	588	0	643	12	0
49	D2	588	0	643	12	0
50	B3	469	0	518	9	0
50	D3	464	0	514	13	0
51	B4	558	0	544	24	0
51	D4	532	0	503	34	0
52	B5	455	0	465	12	0
52	D5	455	0	465	12	0
53	B6	453	0	473	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	D6	449	0	469	8	0
54	B7	418	0	467	9	0
54	D7	418	0	467	10	0
55	B8	511	0	571	23	0
55	D8	517	0	582	13	0
56	B9	307	0	335	7	0
56	D9	307	0	335	13	0
57	AA	214	0	0	0	0
57	AE	3	0	0	0	0
57	AF	1	0	0	0	0
57	AK	1	0	0	0	0
57	AM	1	0	0	0	0
57	AN	2	0	0	0	0
57	AW	4	0	0	0	0
57	AX	15	0	0	0	0
57	AY	3	0	0	0	0
57	B0	3	0	0	0	0
57	B1	1	0	0	0	0
57	B2	1	0	0	0	0
57	B3	2	0	0	0	0
57	B4	1	0	0	0	0
57	B5	1	0	0	0	0
57	B6	2	0	0	0	0
57	B7	5	0	0	0	0
57	B8	1	0	0	0	0
57	B9	1	0	0	0	0
57	BA	812	0	0	0	0
57	BB	20	0	0	0	0
57	BD	9	0	0	0	0
57	BE	8	0	0	0	0
57	BF	9	0	0	0	0
57	BG	3	0	0	0	0
57	BN	6	0	0	0	0
57	BO	2	0	0	0	0
57	BP	5	0	0	0	0
57	BQ	5	0	0	0	0
57	BR	2	0	0	0	0
57	BU	8	0	0	0	0
57	BV	5	0	0	0	0
57	BW	4	0	0	0	0
57	BX	3	0	0	0	0
57	BY	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	BZ	1	0	0	0	0
57	CA	170	0	0	0	0
57	CD	1	0	0	0	0
57	CE	1	0	0	0	0
57	CF	1	0	0	0	0
57	CJ	1	0	0	0	0
57	CK	1	0	0	0	0
57	CT	1	0	0	0	0
57	CV	1	0	0	0	0
57	CW	1	0	0	0	0
57	CX	3	0	0	1	0
57	D0	1	0	0	0	0
57	D3	1	0	0	0	0
57	D8	1	0	0	0	0
57	DA	677	0	0	0	0
57	DB	13	0	0	0	0
57	DD	9	0	0	0	0
57	DE	4	0	0	0	0
57	DF	4	0	0	0	0
57	DG	1	0	0	0	0
57	DN	1	0	0	0	0
57	DO	1	0	0	0	0
57	DP	2	0	0	0	0
57	DQ	4	0	0	0	0
57	DR	1	0	0	0	0
57	DU	2	0	0	0	0
57	DV	3	0	0	0	0
57	DW	4	0	0	0	0
57	DX	1	0	0	0	0
57	DY	1	0	0	0	0
58	AD	8	0	0	0	0
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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	227	0	0	17	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	1	0	0	1	0
61	AM	1	0	0	0	0
61	AU	1	0	0	1	0
61	AV	3	0	0	0	0
61	AW	3	0	0	0	0
61	AX	6	0	0	2	0
61	AY	1	0	0	0	0
61	B0	3	0	0	0	0
61	B1	1	0	0	0	0
61	B3	2	0	0	0	0
61	B5	2	0	0	0	0
61	B6	1	0	0	0	0
61	B7	2	0	0	0	0
61	B8	8	0	0	1	0
61	BA	1383	0	0	61	0
61	BB	36	0	0	1	0
61	BD	12	0	0	1	0
61	BE	14	0	0	4	0
61	BF	8	0	0	0	0
61	BG	3	0	0	0	0
61	BI	1	0	0	0	0
61	BO	4	0	0	0	0
61	BP	16	0	0	3	0
61	BQ	4	0	0	0	0
61	BR	2	0	0	0	0
61	BT	2	0	0	0	0
61	BU	3	0	0	0	0
61	BV	2	0	0	0	0
61	BW	1	0	0	0	0
61	BX	4	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	185	0	0	17	0
61	CJ	2	0	0	1	0
61	CL	1	0	0	0	0
61	CT	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	CV	1	0	0	0	0
61	CW	2	0	0	0	0
61	D0	3	0	0	0	0
61	D1	1	0	0	0	0
61	D3	1	0	0	1	0
61	D7	3	0	0	0	0
61	D8	4	0	0	0	0
61	DA	1025	0	0	79	0
61	DB	9	0	0	0	0
61	DD	19	0	0	4	0
61	DE	11	0	0	0	0
61	DF	3	0	0	0	0
61	DN	2	0	0	1	0
61	DO	1	0	0	0	0
61	DP	16	0	0	2	0
61	DR	1	0	0	0	0
61	DT	3	0	0	0	0
61	DU	2	0	0	0	0
61	DX	3	0	0	0	0
61	DY	2	0	0	0	0
All	All	297141	0	196251	5318	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 (5318) 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)
25:CY:7:A:N6	25:CY:66:U:H3	1.37	1.21
25:AY:49:C:N4	25:AY:65:G:H1	1.44	1.16
26:DA:2139:C:N4	26:DA:2152:G:H1	1.42	1.16
1:CA:1000:U:H3	1:CA:1041:A:N6	1.44	1.15
1:CA:1002:G:H1	1:CA:1038:C:N4	1.48	1.12
26:BA:2136:C:N4	26:BA:2155:G:H1	1.51	1.08
26:DA:2138:C:N4	26:DA:2153:G:H1	1.54	1.03
26:DA:2121:G:H1	26:DA:2177:C:N4	1.54	1.02
23:AW:26:A:H61	23:AW:44:G:H1	1.04	1.02
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.36	1.01
25:CY:19:G:N2	25:CY:56:C:N3	2.08	1.01
25:CY:19:G:H1	25:CY:56:C:N4	1.58	1.01
1:CA:999:C:H42	1:CA:1042:G:H1	1.07	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:50:U:H3	25:CY:64:A:N6	1.58	1.00
26:BA:1019:U:HO2'	26:BA:1021:A:H2	1.07	1.00
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	1.44	1.00
1:CA:1162:C:H42	1:CA:1174:G:H1	1.01	0.99
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.41	0.98
25:CY:8:4SU:HN3	25:CY:14:A:H62	1.10	0.98
26:DA:2124:G:H1	26:DA:2174:C:N4	1.62	0.97
26:BA:993:G:OP1	41:BU:50:ARG:NH2	1.98	0.97
26:BA:1798:U:H5'	28:BD:259:THR:HG22	1.47	0.97
25:AY:7:A:H61	25:AY:66:U:H3	1.11	0.97
1:CA:1162:C:N4	1:CA:1174:G:H1	1.63	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.10	0.96
7:AG:50:ILE:HD11	7:AG:58:PRO:HA	1.48	0.95
26:BA:2123:G:H1	26:BA:2175:C:H42	1.12	0.95
23:CW:66:U:H3'	23:CW:67:C:H5''	1.49	0.95
25:CY:51:U:H3	25:CY:63:G:H1	1.13	0.95
26:DA:2136:C:HO2'	26:DA:2137:C:H6	1.10	0.94
27:DB:22:U:H3	27:DB:61:G:H1	1.11	0.94
24:AX:5:G:H1	24:AX:68:C:N4	1.65	0.94
25:AY:49:C:N3	25:AY:65:G:N2	2.14	0.94
1:CA:76:C:N4	1:CA:93:G:H1	1.66	0.93
42:DV:100:ARG:HH11	42:DV:100:ARG:HG3	1.33	0.93
23:AW:29:G:H1	23:AW:41:C:H42	1.16	0.93
25:CY:50:U:H3	25:CY:64:A:H61	0.96	0.92
1:CA:76:C:H42	1:CA:93:G:H1	0.97	0.92
46:BZ:153:SER:HB3	46:BZ:167:PRO:HB3	1.49	0.92
26:BA:2136:C:H42	26:BA:2155:G:H1	0.96	0.92
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.02	0.92
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	1.51	0.91
23:AW:50:U:H3	23:AW:64:A:H61	1.02	0.91
26:BA:517:C:OP1	52:B5:16:ARG:NH2	2.04	0.91
26:DA:2124:G:H1	26:DA:2174:C:H42	1.17	0.91
26:DA:1204:A:H2	26:DA:1241:A:H62	1.19	0.90
24:AX:5:G:H1	24:AX:68:C:H42	0.92	0.90
26:DA:2206:G:H3'	26:DA:2207:G:C8	2.07	0.89
25:CY:15:G:N1	25:CY:48:C:N3	2.19	0.89
25:AY:26:A:H61	25:AY:44:G:H1	1.14	0.88
25:CY:9:A:N6	25:CY:23:A:OP2	2.06	0.88
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.56	0.88
1:CA:1000:U:H3	1:CA:1041:A:H61	0.88	0.88
1:CA:1502:A:H2	1:CA:1505:G:H1	1.22	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:664:G:H22	1:AA:741:G:H1	1.19	0.87
1:CA:1002:G:N2	1:CA:1038:C:N3	2.23	0.87
47:B0:11:ARG:O	47:B0:14:ARG:NH2	2.07	0.87
23:AW:50:U:H3	23:AW:64:A:N6	1.71	0.87
26:DA:994:C:OP1	41:DU:53:ARG:NH2	2.08	0.87
29:DE:27:LEU:HD22	40:DT:1:MET:HE1	1.56	0.87
23:AW:76:31M:H8	23:AW:76:31M:H5'	1.56	0.87
26:DA:1689:A:H62	26:DA:1698:A:H2	1.20	0.86
26:DA:1798:U:H5'	28:DD:259:THR:HG22	1.55	0.86
1:AA:1025:U:O2	1:AA:1036:G:O6	1.93	0.86
29:BE:47:VAL:HG21	29:BE:86:PRO:HD2	1.57	0.86
26:DA:397:G:N7	61:DA:4625:HOH:O	2.08	0.86
1:CA:664:G:H22	1:CA:741:G:H1	1.24	0.86
26:DA:827:U:OP1	61:DA:4303:HOH:O	1.91	0.85
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.10	0.85
26:DA:1169:G:H1	26:DA:1180:C:H42	1.23	0.85
26:DA:2130:U:H4'	26:DA:2133:G:H4'	1.58	0.85
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.59	0.85
30:DF:53:THR:HG22	30:DF:56:GLU:HG3	1.58	0.84
26:BA:1689:A:H62	26:BA:1698:A:H2	1.25	0.84
26:DA:2430:A:OP2	61:DA:4303:HOH:O	1.94	0.84
26:BA:631:A:OP1	36:BP:65:ARG:NH1	2.10	0.84
7:CG:79:ARG:HE	7:CG:80:VAL:HG23	1.42	0.84
26:DA:2138:C:N3	26:DA:2153:G:N2	2.24	0.84
26:BA:100:G:O2'	49:B2:7:ARG:NH2	2.10	0.84
26:BA:2287:A:H62	26:BA:2344:U:H3	1.23	0.84
9:CI:51:ARG:HG2	9:CI:56:LEU:HD21	1.60	0.84
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.11	0.84
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.23	0.83
33:BI:92:VAL:HG13	33:BI:120:ILE:HB	1.60	0.83
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.11	0.83
23:AW:26:A:N6	23:AW:44:G:H1	1.75	0.83
30:DF:53:THR:HG23	30:DF:55:GLY:H	1.44	0.83
23:AW:6:G:H1	23:AW:67:C:N4	1.77	0.82
10:CJ:7:LYS:HG3	10:CJ:71:LEU:HD12	1.60	0.82
29:DE:11:MET:HG2	29:DE:24:THR:HB	1.61	0.82
25:AY:50:U:O4	25:AY:64:A:N1	2.13	0.82
26:BA:1176:G:H1'	26:BA:1177:A:H5'	1.59	0.82
35:DO:35:VAL:HG11	35:DO:103:ALA:HB3	1.62	0.82
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.12	0.82
3:CC:58:GLU:HB3	10:CJ:92:THR:HG21	1.59	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:885:C:H3'	26:BA:886:C:H5''	1.61	0.82
25:CY:31:A:N1	25:CY:39:PSU:O2	2.13	0.82
36:DP:100:LEU:HD12	36:DP:112:LEU:HD11	1.60	0.82
26:BA:2100:G:H1	26:BA:2189:U:H3	1.27	0.82
23:CW:4:C:N4	23:CW:69:G:H1	1.77	0.82
25:CY:19:G:H1	25:CY:56:C:H42	0.85	0.82
4:AD:158:ILE:HD13	4:AD:158:ILE:H	1.45	0.81
1:CA:1029:C:N3	1:CA:1032:G:N2	2.28	0.81
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.62	0.81
46:BZ:117:LEU:HD11	46:BZ:144:LEU:HD22	1.61	0.81
1:CA:1029:C:N4	1:CA:1032:G:N1	2.29	0.81
26:DA:2139:C:H42	26:DA:2152:G:H1	0.83	0.81
1:CA:1153:C:H42	1:CA:1154:G:H21	1.28	0.81
26:BA:279:C:H42	26:BA:361:G:H1	1.26	0.81
26:DA:2124:G:N2	26:DA:2174:C:N3	2.28	0.81
46:DZ:126:VAL:HG11	46:DZ:161:VAL:HG23	1.61	0.81
26:BA:1530:C:O2'	26:BA:1531:C:O5'	1.99	0.81
26:DA:2114:A:N6	26:DA:2119:A:N7	2.28	0.81
26:BA:2723:C:OP1	38:BR:3:HIS:ND1	2.12	0.81
1:CA:999:C:N4	1:CA:1042:G:H1	1.77	0.81
26:DA:2121:G:N2	26:DA:2177:C:N3	2.27	0.81
1:CA:201:C:H42	1:CA:216:G:H1	1.28	0.80
32:BH:59:ARG:HB2	32:BH:59:ARG:HH11	1.43	0.80
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.62	0.80
26:DA:2114:A:N1	26:DA:2171:A:N6	2.29	0.80
1:AA:407:G:H5''	4:AD:115:ARG:HG2	1.62	0.80
39:BS:25:ARG:NH1	39:BS:42:ASP:OD1	2.14	0.80
26:DA:1315:C:OP2	61:DA:4172:HOH:O	1.99	0.80
26:DA:529:A:N6	26:DA:2041:U:O2	2.14	0.80
1:CA:985:C:H42	1:CA:1220:G:H1	1.24	0.80
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.12	0.80
1:CA:1317:C:N3	19:CS:37:ARG:NH2	2.30	0.80
26:DA:2819:G:N7	61:DA:4078:HOH:O	2.15	0.80
26:BA:1466:G:HO2'	26:BA:1546:C:HO2'	1.22	0.79
25:CY:53:G:O6	25:CY:61:C:N4	2.16	0.79
26:DA:2139:C:N3	26:DA:2152:G:N2	2.26	0.79
25:AY:19:G:N2	25:AY:56:C:N3	2.30	0.79
25:CY:19:G:N1	25:CY:56:C:N4	2.23	0.79
1:CA:1133:G:H1	1:CA:1141:C:H42	1.26	0.79
25:CY:8:4SU:S4	25:CY:14:A:N7	2.56	0.79
26:DA:2682:U:OP2	61:DA:3832:HOH:O	2.00	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1000:U:O2	1:CA:1041:A:N1	2.15	0.79
26:DA:1530:C:O2'	26:DA:1531:C:O5'	2.01	0.79
26:BA:1506:C:H2'	26:BA:1507:A:H8	1.47	0.79
26:BA:2683:C:O2	35:BO:70:LYS:NZ	2.15	0.79
35:BO:35:VAL:HG11	35:BO:103:ALA:HB3	1.64	0.79
1:CA:1024:G:H2'	1:CA:1025:U:H5''	1.62	0.79
26:DA:2138:C:H42	26:DA:2153:G:H1	0.80	0.79
9:CI:71:SER:HA	9:CI:74:ILE:HD12	1.65	0.78
23:CW:29:G:H1	23:CW:41:C:H42	1.29	0.78
26:BA:2808:U:O2	26:BA:2892:A:N6	2.15	0.78
1:CA:656:C:O2'	15:CO:28:GLN:NE2	2.15	0.78
26:DA:1324:G:N7	61:DA:3887:HOH:O	2.15	0.78
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.16	0.78
26:BA:2141:G:H1	26:BA:2149:G:H22	1.31	0.78
1:CA:975:A:H4'	1:CA:976:G:H5''	1.64	0.78
1:AA:156:G:N2	1:AA:165:C:O2	2.17	0.78
1:AA:1158:C:H5	1:AA:1181:G:H1	1.32	0.78
5:CE:122:GLU:O	5:CE:126:ARG:NH1	2.16	0.78
47:D0:11:ARG:O	47:D0:14:ARG:NH2	2.17	0.78
26:BA:2123:G:H1	26:BA:2175:C:N4	1.81	0.78
51:B4:53:GLU:C	51:B4:55:ARG:H	1.92	0.78
25:CY:15:G:N2	25:CY:48:C:H42	1.82	0.78
26:DA:2608:G:N7	61:DA:4023:HOH:O	2.17	0.78
46:DZ:19:ARG:NH1	46:DZ:84:GLU:O	2.17	0.78
26:DA:1648:C:OP1	61:DA:4215:HOH:O	2.01	0.78
9:AI:50:LEU:HD23	9:AI:81:ILE:HD11	1.67	0.77
25:CY:62:C:H2'	25:CY:63:G:H8	1.49	0.77
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.18	0.77
26:DA:2287:A:H62	26:DA:2344:U:H3	1.30	0.77
1:CA:985:C:N4	1:CA:1220:G:H1	1.81	0.77
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.65	0.77
26:BA:2136:C:N3	26:BA:2155:G:N2	2.27	0.77
1:CA:1255:G:OP1	10:CJ:45:ARG:NH2	2.17	0.77
26:BA:998:C:OP1	61:BA:4663:HOH:O	2.02	0.77
46:BZ:72:ARG:NH2	46:BZ:97:GLU:O	2.18	0.77
3:CC:129:ALA:HB3	3:CC:132:ARG:HB2	1.67	0.77
25:CY:25:C:H2'	25:CY:26:A:H8	1.47	0.77
1:AA:1260:C:O2	1:AA:1275:A:N6	2.17	0.77
33:BI:129:THR:HG22	33:BI:139:GLN:HE22	1.48	0.77
23:CW:19:G:H1	23:CW:56:C:H42	1.33	0.77
23:AW:53:G:OP1	37:BQ:60:ARG:NH2	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:7:A:N6	25:AY:66:U:H3	1.82	0.77
1:AA:1422:G:H5''	35:BO:48:PRO:HB3	1.67	0.76
26:BA:927:G:N7	61:BA:4413:HOH:O	2.17	0.76
1:CA:1025:U:H3	1:CA:1036:G:H1	1.32	0.76
37:DQ:135:ASP:OD2	46:DZ:49:ARG:NH2	2.18	0.76
26:BA:400:G:N7	61:BA:5004:HOH:O	2.17	0.76
1:CA:838:G:H1	1:CA:848:C:N4	1.84	0.76
26:BA:1452:A:OP2	61:BA:4011:HOH:O	2.02	0.76
42:BV:40:LEU:HB2	42:BV:46:VAL:HG13	1.67	0.76
30:BF:18:ARG:NH2	30:BF:127:GLU:OE1	2.18	0.76
1:CA:1422:G:H5''	35:DO:48:PRO:HB3	1.67	0.76
23:CW:4:C:N3	23:CW:69:G:N2	2.34	0.76
26:DA:143:G:H4'	44:DX:35:THR:HG21	1.68	0.76
1:AA:975:A:H4'	1:AA:976:G:H5''	1.67	0.76
26:BA:2103:C:H42	26:BA:2186:G:H1	1.30	0.76
28:DD:238:GLY:O	61:DD:408:HOH:O	2.03	0.76
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.18	0.76
1:CA:1054:C:O2'	1:CA:1055:A:O5'	2.02	0.76
56:D9:25:VAL:HB	56:D9:34:GLN:HB2	1.66	0.76
3:CC:98:ASN:N	3:CC:98:ASN:OD1	2.19	0.76
26:BA:11:G:H2'	26:BA:12:U:H5''	1.68	0.76
26:DA:880:G:N1	26:DA:898:C:O2	2.18	0.76
51:D4:38:LYS:O	51:D4:40:HIS:N	2.17	0.76
13:CM:25:ILE:HD11	13:CM:66:LEU:HD13	1.68	0.75
36:BP:126:VAL:HG12	36:BP:148:LEU:HD22	1.66	0.75
2:CB:17:PHE:HB2	2:CB:44:LEU:HD11	1.66	0.75
26:DA:792:G:O6	61:DA:4162:HOH:O	2.03	0.75
29:DE:14:ILE:HG13	29:DE:21:VAL:HG13	1.68	0.75
36:DP:29:LYS:HG3	36:DP:30:THR:N	2.01	0.75
1:AA:532:A:H2	1:AA:1206:G:H21	1.35	0.75
24:AX:6:G:H1	24:AX:67:C:H42	1.34	0.75
26:BA:1332:G:OP1	61:BA:4653:HOH:O	2.03	0.75
42:BV:76:LYS:HB2	42:BV:81:TYR:HB3	1.68	0.75
23:CW:4:C:H42	23:CW:69:G:H1	1.33	0.75
23:CW:49:C:N4	23:CW:65:G:O6	2.20	0.75
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.68	0.75
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.20	0.75
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.19	0.75
26:DA:631:A:OP1	36:DP:65:ARG:NH1	2.20	0.75
1:CA:1456:G:O6	20:CT:54:LYS:NZ	2.16	0.75
26:DA:2638:G:OP2	29:DE:82:ARG:NH2	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1183:A:H3'	1:AA:1184:G:H5''	1.69	0.75
26:BA:271(R):G:OP1	48:B1:76:ARG:NH1	2.19	0.75
26:BA:307:G:H21	26:BA:330:A:H62	1.35	0.75
1:CA:1149:C:O2'	1:CA:1280:A:N1	2.18	0.75
1:AA:78:G:N2	1:AA:91:C:N3	2.35	0.75
1:AA:574:A:OP2	61:AA:4005:HOH:O	2.05	0.75
23:AW:6:G:N2	23:AW:67:C:N3	2.34	0.75
23:AW:29:G:H1	23:AW:41:C:N4	1.84	0.75
35:BO:64:ARG:NH2	35:BO:99:PHE:O	2.20	0.75
3:CC:179:ARG:HD2	3:CC:206:GLU:HB2	1.68	0.75
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.59	0.75
1:AA:642:A:N3	8:AH:113:SER:OG	2.20	0.74
1:AA:1314:C:OP2	19:AS:4:SER:OG	2.05	0.74
26:BA:301:G:OP2	45:BY:84:ARG:NH2	2.19	0.74
1:AA:1036:G:H21	1:AA:1037:C:H1'	1.51	0.74
26:BA:2741:A:OP1	56:B9:22:ARG:NH2	2.17	0.74
19:CS:42:PRO:HG3	51:D4:61:ARG:HG2	1.69	0.74
26:DA:1189:A:OP2	61:DA:4184:HOH:O	2.04	0.74
4:CD:104:VAL:HG11	4:CD:146:ILE:HD13	1.68	0.74
27:DB:76:G:N2	27:DB:101:G:O6	2.19	0.74
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.52	0.74
28:DD:148:GLU:HB2	28:DD:151:LYS:HD2	1.68	0.74
46:DZ:72:ARG:NH2	46:DZ:97:GLU:O	2.21	0.74
26:BA:2467:C:OP2	61:BA:5096:HOH:O	2.05	0.74
1:CA:958:A:N6	19:CS:77:THR:O	2.20	0.74
4:CD:154:ASN:HA	4:CD:159:ARG:HH21	1.53	0.74
26:DA:449:A:OP2	61:DA:4657:HOH:O	2.05	0.74
26:DA:1815:A:OP2	28:DD:54:ARG:NH2	2.19	0.74
1:CA:811:C:N4	61:CA:4023:HOH:O	2.20	0.74
25:AY:50:U:H3	25:AY:64:A:H2	1.35	0.74
23:CW:2:C:N3	23:CW:71:G:O6	2.21	0.74
23:CW:7:A:N1	23:CW:66:U:O4	2.19	0.74
26:DA:2169:A:O2'	26:DA:2170:A:O5'	2.06	0.74
27:DB:75:G:N2	46:DZ:87:ASP:OD1	2.21	0.74
26:BA:1840:G:N7	61:BA:4332:HOH:O	2.20	0.74
26:DA:884:C:N4	26:DA:892:G:O6	2.20	0.74
26:DA:2049:G:N7	61:DA:3798:HOH:O	2.19	0.74
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.21	0.74
28:BD:17:THR:O	28:BD:211:ARG:NH2	2.21	0.74
1:CA:1226:C:O2'	13:CM:111:LYS:NZ	2.20	0.74
3:CC:150:LYS:HG3	3:CC:169:ALA:HB2	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1314:C:OP1	61:DA:4172:HOH:O	2.04	0.74
4:AD:104:VAL:HG11	4:AD:146:ILE:HD13	1.69	0.74
26:BA:568:U:O4	61:BA:4141:HOH:O	2.05	0.74
36:DP:96:THR:H	36:DP:99:LEU:HD21	1.53	0.74
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.21	0.73
3:AC:15:THR:HG21	3:AC:181:ASN:HA	1.69	0.73
25:CY:62:C:H2'	25:CY:63:G:C8	2.23	0.73
49:D2:22:GLU:OE2	49:D2:68:ARG:NH2	2.21	0.73
1:AA:1505:G:O2'	22:AV:13:A:O2'	2.05	0.73
26:BA:1602:U:O4	61:BA:4228:HOH:O	2.06	0.73
26:BA:2187:G:O2'	26:BA:2188:C:OP1	2.07	0.73
1:CA:1291:G:H4'	9:CI:39:GLY:HA3	1.68	0.73
25:CY:31:A:C6	25:CY:39:PSU:O2	2.41	0.73
26:DA:2121:G:H1	26:DA:2177:C:H42	0.80	0.73
29:DE:77:ILE:HD13	29:DE:195:LEU:HD13	1.70	0.73
51:D4:40:HIS:O	51:D4:44:THR:N	2.17	0.73
51:D4:40:HIS:HB3	51:D4:43:TYR:HB2	1.71	0.73
5:CE:80:ILE:HG22	5:CE:91:LEU:HB2	1.71	0.73
27:DB:20:C:N4	27:DB:63:G:O6	2.19	0.73
26:DA:1959:G:N7	61:DA:4503:HOH:O	2.21	0.73
26:DA:2815:C:H5'	52:D5:29:THR:HG21	1.71	0.73
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.21	0.73
26:DA:1352:U:OP2	61:DA:3767:HOH:O	2.06	0.73
4:CD:187:ARG:NH2	4:CD:193:ASP:OD2	2.22	0.73
25:CY:18:G:N2	25:CY:55:PSU:N3	2.37	0.73
1:AA:972:C:O2'	10:AJ:55:LYS:O	2.05	0.73
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.71	0.73
11:CK:20:TYR:HB2	11:CK:31:THR:HG22	1.69	0.73
26:DA:11:G:N7	61:DA:4280:HOH:O	2.20	0.73
27:DB:24:G:N2	27:DB:27:C:N3	2.32	0.73
4:AD:15:GLU:HG2	4:AD:63:LYS:HB3	1.71	0.73
51:B4:59:PHE:HD1	51:B4:59:PHE:H	1.35	0.73
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.69	0.73
23:AW:52:G:H4'	37:BQ:56:ARG:HH22	1.54	0.72
25:AY:26:A:N6	25:AY:44:G:H1	1.85	0.72
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.22	0.72
12:CL:24:VAL:HG13	12:CL:98:TYR:HE1	1.53	0.72
25:CY:36:A:H2'	25:CY:37:MIA:O4'	1.89	0.72
26:DA:2562:U:H1'	35:DO:23:ARG:HH11	1.53	0.72
31:DG:136:ARG:HD2	31:DG:137:GLU:HG3	1.70	0.72
36:BP:94:GLU:OE2	36:BP:124:LYS:NZ	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:741:G:OP2	61:DA:4224:HOH:O	2.05	0.72
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.72	0.72
45:BY:92:ASN:HB3	45:BY:94:LYS:H	1.52	0.72
25:CY:31:A:N1	25:CY:39:PSU:C2	2.57	0.72
26:BA:1507:A:O2'	26:BA:1508:A:O4'	2.06	0.72
1:CA:976:G:H5'	1:CA:1358:U:O2'	1.89	0.72
26:DA:1449:A:O2'	26:DA:1529:G:N2	2.22	0.72
36:DP:126:VAL:HG12	36:DP:148:LEU:HD22	1.71	0.72
42:DV:6:LYS:HB2	42:DV:38:LEU:HD21	1.69	0.72
1:AA:266:G:H5''	1:AA:268:C:H41	1.53	0.72
25:AY:56:C:H2'	25:AY:57:G:O4'	1.88	0.72
25:AY:76:A:N6	26:BA:2422:A:O4'	2.22	0.72
26:BA:1019:U:H3	26:BA:1142(A):A:H62	1.35	0.72
26:BA:2810:A:N6	26:BA:2891:G:O2'	2.21	0.72
1:CA:1055:A:N7	1:CA:1200:C:N4	2.37	0.72
25:CY:26:A:N1	25:CY:44:G:O6	2.23	0.72
26:DA:2683:C:O2	35:DO:70:LYS:NZ	2.23	0.72
1:AA:347:G:O2'	1:AA:348:G:OP1	2.08	0.72
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.06	0.72
26:BA:739:G:OP1	61:BA:5196:HOH:O	2.06	0.72
1:CA:324:G:N7	61:CA:4089:HOH:O	2.23	0.72
25:CY:5:G:H1	25:CY:68:C:H42	1.36	0.72
25:AY:62:C:H2'	25:AY:63:G:H8	1.55	0.72
47:B0:10:THR:HG22	47:B0:12:ASN:H	1.54	0.72
5:CE:102:ALA:O	5:CE:107:ARG:NH1	2.22	0.72
26:DA:2166:G:H3'	26:DA:2167:U:H5''	1.70	0.72
1:CA:977:A:N6	1:CA:1224:G:OP1	2.21	0.72
1:CA:1009:G:N2	1:CA:1021:G:H1'	2.04	0.72
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.07	0.72
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.23	0.72
26:BA:1714:G:H1	26:BA:1745(A):C:H42	1.38	0.72
9:CI:53:VAL:O	9:CI:55:ALA:N	2.22	0.72
25:CY:71:G:H4'	26:DA:1851:U:H4'	1.71	0.72
26:DA:1670:C:OP1	61:DA:3752:HOH:O	2.06	0.72
28:DD:28:GLU:OE1	61:DD:416:HOH:O	2.06	0.72
1:AA:1445:C:O2	1:AA:1457:G:N2	2.20	0.72
2:AB:59:GLU:HG2	2:AB:63:MET:HE2	1.70	0.72
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.14	0.72
26:DA:1604:C:OP2	61:DA:4546:HOH:O	2.08	0.72
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.07	0.71
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1162:C:N3	1:CA:1174:G:N2	2.34	0.71
48:B1:86:SER:OG	48:B1:89:GLU:OE1	2.07	0.71
26:DA:2134:A:N3	26:DA:2159:G:O2'	2.21	0.71
1:AA:1086:U:H3	1:AA:1099:G:H22	1.37	0.71
26:BA:957:A:H5'	37:BQ:76:LYS:HG3	1.72	0.71
26:DA:1890:A:OP2	61:DA:4472:HOH:O	2.08	0.71
25:CY:15:G:N2	25:CY:48:C:N4	2.38	0.71
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.37	0.71
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.73	0.71
17:AQ:3:LYS:HD2	17:AQ:60:ILE:HD11	1.71	0.71
25:AY:25:C:O2'	25:AY:26:A:O5'	2.09	0.71
1:CA:1054:C:C4	23:CW:34:G:H1'	2.25	0.71
10:CJ:5:ARG:N	61:CJ:5101:HOH:O	2.22	0.71
23:CW:29:G:H1	23:CW:41:C:N4	1.87	0.71
26:DA:370:G:N7	61:DA:3786:HOH:O	2.23	0.71
46:DZ:144:LEU:HD11	46:DZ:172:ALA:HB1	1.72	0.71
26:BA:528:A:H2'	26:BA:529:A:H5''	1.72	0.71
36:BP:116:GLY:O	36:BP:137:LYS:NZ	2.22	0.71
44:BX:53:LYS:HB3	44:BX:82:GLN:HB3	1.73	0.71
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.72	0.71
26:BA:2124:G:H1	26:BA:2174:C:H42	1.37	0.71
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.73	0.71
26:BA:2130:U:H4'	26:BA:2133:G:H4'	1.72	0.71
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.24	0.71
23:CW:27:G:H1	23:CW:43:C:H42	1.37	0.71
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.73	0.71
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.71	0.71
12:CL:24:VAL:HG13	12:CL:98:TYR:CE1	2.24	0.71
46:DZ:92:SER:O	46:DZ:130:PRO:HG2	1.91	0.71
9:AI:46:ALA:HB2	9:AI:74:ILE:HG23	1.72	0.70
26:BA:1022:G:H22	26:BA:1142(A):A:H2	1.39	0.70
26:BA:1815:A:OP2	28:BD:54:ARG:NH2	2.22	0.70
40:BT:95:ARG:HG2	40:BT:95:ARG:HH11	1.54	0.70
26:DA:643:A:N1	26:DA:2369:A:O2'	2.22	0.70
26:DA:731:C:OP1	61:DA:4348:HOH:O	2.08	0.70
31:DG:63:ILE:HA	31:DG:143:GLU:HG3	1.72	0.70
46:DZ:145:GLU:H	46:DZ:148:ASP:HB2	1.57	0.70
1:AA:972:C:OP1	61:AA:4173:HOH:O	2.09	0.70
26:BA:2239:G:OP2	61:BA:4335:HOH:O	2.08	0.70
30:BF:185:ASP:HA	30:BF:188:ARG:HD3	1.70	0.70
40:BT:16:ARG:NH2	40:BT:83:ILE:O	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:986:A:O2'	19:CS:55:LYS:O	2.08	0.70
38:BR:67:LEU:HD13	38:BR:76:VAL:HG21	1.72	0.70
26:DA:1637:A:OP2	61:DA:4569:HOH:O	2.09	0.70
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.73	0.70
1:AA:1492:A:O2'	1:AA:1493:A:O5'	2.08	0.70
26:BA:1310:G:OP2	54:B7:9:ARG:NH1	2.25	0.70
1:CA:771:G:N7	61:CA:4042:HOH:O	2.24	0.70
46:DZ:119:GLU:O	46:DZ:122:ARG:NH1	2.24	0.70
12:AL:70:ILE:HG12	12:AL:100:ILE:HD12	1.74	0.70
23:AW:6:G:H1	23:AW:67:C:H42	1.32	0.70
1:CA:1256:A:H61	1:CA:1278:U:H1'	1.56	0.70
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.21	0.70
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.56	0.70
2:CB:87:ARG:NH2	2:CB:220:ASP:OD1	2.24	0.70
25:CY:51:U:O2	25:CY:63:G:N2	2.23	0.70
26:BA:2102:U:O2	26:BA:2187:G:N2	2.25	0.70
26:BA:2108:C:H2'	26:BA:2109:U:H6	1.57	0.70
31:BG:41:GLN:NE2	31:BG:154:GLY:O	2.24	0.70
1:CA:1277:C:HO2'	1:CA:1279:A:H8	1.40	0.70
1:AA:134:A:H61	16:AP:25:ARG:HH12	1.39	0.70
26:BA:2102:U:H3	26:BA:2187:G:H1	1.40	0.70
26:DA:2820:A:OP2	38:DR:2:ARG:NH2	2.24	0.70
1:AA:1027:C:O2	1:AA:1034:G:C2	2.45	0.70
1:AA:1076:C:H6	1:AA:1076:C:H5'	1.57	0.70
23:AW:47:U:H6	23:AW:47:U:H5'	1.57	0.70
26:BA:729:G:OP2	28:BD:13:ARG:NH1	2.24	0.70
7:CG:113:GLU:HG2	7:CG:119:ARG:HG2	1.73	0.70
26:DA:2138:C:N4	26:DA:2153:G:N1	2.27	0.70
18:AR:26:LEU:HD21	18:AR:39:VAL:HG13	1.74	0.69
26:DA:987:G:O2'	26:DA:1000:A:N3	2.23	0.69
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.25	0.69
26:BA:1250:G:OP2	36:BP:21:ARG:NH1	2.26	0.69
46:BZ:11:GLU:O	46:BZ:36:LYS:NZ	2.23	0.69
6:CF:81:ILE:HD11	28:DD:125:ILE:HB	1.73	0.69
48:D1:59:THR:O	48:D1:91:LYS:NZ	2.24	0.69
26:BA:2285:C:OP2	53:B6:6:ARG:NH1	2.25	0.69
36:BP:59:LEU:HD21	55:B8:10:ALA:HA	1.75	0.69
26:DA:2504:U:OP2	61:DA:4169:HOH:O	2.11	0.69
44:DX:8:ILE:O	49:D2:36:ARG:NH2	2.25	0.69
44:DX:53:LYS:HB3	44:DX:82:GLN:HB3	1.74	0.69
1:AA:1414:U:H3	1:AA:1486:G:H1	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BD:147:LEU:HD13	28:BD:155:LEU:HD21	1.73	0.69
1:CA:76:C:N3	1:CA:93:G:N2	2.34	0.69
26:DA:1011:G:OP2	41:DU:66:ASN:ND2	2.24	0.69
30:DF:33:LEU:HD13	30:DF:112:MET:HE2	1.74	0.69
54:B7:24:THR:HG22	54:B7:27:GLY:H	1.57	0.69
1:CA:664:G:OP1	18:CR:64:ARG:NH2	2.26	0.69
26:DA:993:G:OP1	41:DU:50:ARG:NH2	2.25	0.69
35:DO:80:ASP:OD1	40:DT:64:ARG:NH2	2.25	0.69
28:BD:148:GLU:HB2	28:BD:151:LYS:HD2	1.75	0.69
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.74	0.69
1:CA:200:G:H1	1:CA:217:C:H42	1.40	0.69
3:CC:18:TRP:O	3:CC:21:ARG:NH1	2.23	0.69
26:DA:2323:G:O6	26:DA:2332:U:N3	2.18	0.69
30:DF:184:TYR:CE2	30:DF:188:ARG:HD2	2.28	0.69
1:AA:78:G:N1	1:AA:91:C:N4	2.40	0.69
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	1.73	0.69
27:BB:106:G:H5'	46:BZ:31:ARG:HG2	1.75	0.69
10:CJ:49:VAL:HG23	14:CN:41:ARG:HD2	1.75	0.69
26:DA:2060:A:N3	61:DA:4112:HOH:O	2.25	0.69
26:DA:2206:G:H3'	26:DA:2207:G:H8	1.57	0.69
39:DS:93:LYS:HD2	39:DS:95:HIS:HB2	1.74	0.69
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.26	0.69
26:BA:527:C:OP1	61:BA:4682:HOH:O	2.11	0.69
37:BQ:21:THR:HG21	37:BQ:101:ARG:HD3	1.75	0.69
46:BZ:145:GLU:O	46:BZ:148:ASP:N	2.26	0.69
1:AA:96:U:HO2'	1:AA:97:G:H8	1.41	0.68
1:CA:1119:C:H2'	1:CA:1120:G:C8	2.28	0.68
29:DE:1:MET:HE1	29:DE:199:ARG:HD2	1.76	0.68
2:AB:20:GLU:HG2	2:AB:191:ASP:HB3	1.74	0.68
26:BA:1352:U:OP1	61:BA:4087:HOH:O	2.11	0.68
1:CA:560:U:OP2	61:CA:4161:HOH:O	2.11	0.68
26:DA:882:G:N2	26:DA:894:C:O2	2.18	0.68
26:BA:1140:C:O3'	34:BN:25:ARG:NH1	2.27	0.68
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.08	0.68
31:DG:161:THR:HG22	31:DG:163:ALA:H	1.59	0.68
5:CE:20:GLN:NE2	5:CE:21:ALA:O	2.26	0.68
31:DG:41:GLN:HB3	31:DG:43:LEU:HD22	1.76	0.68
1:CA:1129:C:OP1	9:CI:16:ARG:NH1	2.26	0.68
26:DA:1223:G:N2	26:DA:1226:A:OP2	2.23	0.68
29:DE:72:VAL:HG13	29:DE:73:GLU:O	1.93	0.68
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2612:C:OP2	52:B5:2:ALA:N	2.27	0.68
1:CA:1004:A:H8	1:CA:1005:A:H4'	1.58	0.68
5:CE:7:GLU:OE1	5:CE:37:ARG:NH2	2.26	0.68
26:DA:89:G:H3'	26:DA:90:U:H5''	1.76	0.68
26:DA:880:G:H22	26:DA:898:C:H1'	1.59	0.68
1:AA:538:G:H5''	12:AL:114:LYS:HB2	1.73	0.68
26:BA:1843:C:H5'	28:BD:253:GLN:NE2	2.09	0.68
26:DA:2127:G:O6	26:DA:2161:C:N3	2.26	0.68
26:DA:2139:C:N4	26:DA:2152:G:N1	2.16	0.68
26:BA:1045:A:OP1	26:BA:1045:A:H4'	1.92	0.68
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.26	0.68
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.76	0.68
24:CX:8:4SU:O5'	24:CX:8:4SU:H6	1.93	0.68
26:DA:194:G:N7	61:DA:4296:HOH:O	2.26	0.68
33:DI:4:ILE:HG12	33:DI:18:VAL:HG22	1.76	0.68
43:DW:18:ARG:NH1	43:DW:76:VAL:O	2.27	0.68
3:AC:3:ASN:OD1	3:AC:3:ASN:N	2.26	0.68
26:BA:2110:G:O2'	26:BA:2120:G:OP2	2.12	0.68
26:DA:2165:G:H22	26:DA:2172:U:H5	1.40	0.68
1:AA:235:C:H5'	17:AQ:70:ARG:HG2	1.76	0.68
1:CA:952:U:O2'	1:CA:965:A:N6	2.27	0.68
1:CA:1442:G:O2'	1:CA:1442(A):G:OP1	2.11	0.68
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.10	0.68
26:DA:1647:G:OP1	61:DA:4215:HOH:O	2.12	0.68
30:DF:157:VAL:HB	30:DF:194:MET:HG2	1.76	0.68
1:AA:1027:C:N3	1:AA:1034:G:C6	2.63	0.67
23:AW:66:U:H2'	23:AW:67:C:C6	2.29	0.67
26:BA:271(L):U:OP1	33:BI:50:ARG:NH1	2.26	0.67
1:CA:446:G:H1	1:CA:488:C:H42	1.39	0.67
26:DA:857:C:OP2	47:D0:77:ARG:NH2	2.26	0.67
26:BA:2312:U:H5'	31:BG:88:ILE:HD11	1.75	0.67
51:B4:55:ARG:HB2	51:B4:56:VAL:O	1.94	0.67
15:CO:22:THR:OG1	15:CO:23:GLY:N	2.24	0.67
25:CY:25:C:H2'	25:CY:26:A:C8	2.30	0.67
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.94	0.67
1:CA:1133:G:H1	1:CA:1141:C:N4	1.92	0.67
2:AB:91:PRO:HG2	2:AB:155:LEU:HD23	1.75	0.67
30:BF:53:THR:HG23	30:BF:55:GLY:H	1.58	0.67
2:CB:88:ALA:HB2	2:CB:219:VAL:HG13	1.76	0.67
49:D2:29:LYS:HE2	49:D2:57:ILE:HG21	1.74	0.67
1:AA:324:G:N7	61:AA:4166:HOH:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.77	0.67
25:AY:66:U:H2'	25:AY:67:C:C6	2.29	0.67
26:BA:692:C:O2'	28:BD:38:LYS:NZ	2.26	0.67
15:CO:54:ARG:HD3	15:CO:58:MET:HE2	1.76	0.67
1:AA:1075:C:OP1	2:AB:179:LYS:NZ	2.24	0.67
5:AE:100:VAL:O	5:AE:107:ARG:NH2	2.27	0.67
26:BA:1783:A:N7	61:BA:5061:HOH:O	2.26	0.67
23:CW:43:C:H2'	23:CW:44:G:C8	2.29	0.67
26:BA:662:G:H5''	36:BP:16:ARG:HG2	1.75	0.67
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.28	0.67
24:AX:5:G:N2	24:AX:68:C:N3	2.40	0.67
25:AY:22:G:H2'	25:AY:23:A:C8	2.29	0.67
26:BA:994:C:OP1	41:BU:53:ARG:NH2	2.28	0.67
1:CA:999:C:N3	1:CA:1042:G:N2	2.38	0.67
10:CJ:35:SER:HB3	10:CJ:73:ASP:HB2	1.77	0.67
26:DA:307:G:N1	26:DA:310:A:OP2	2.26	0.67
26:DA:2886:G:N7	61:DA:4141:HOH:O	2.26	0.67
28:DD:28:GLU:OE2	61:DD:417:HOH:O	2.13	0.67
31:DG:41:GLN:NE2	31:DG:154:GLY:O	2.27	0.67
1:CA:1492:A:O2'	1:CA:1493:A:O5'	2.13	0.67
13:CM:80:ARG:HH22	19:CS:69:HIS:CE1	2.12	0.67
37:DQ:1:MET:SD	37:DQ:1:MET:N	2.66	0.67
26:BA:2759:G:N7	61:BA:4124:HOH:O	2.28	0.67
29:BE:149:ARG:O	61:BE:406:HOH:O	2.12	0.67
1:CA:316:G:OP2	1:CA:351:G:O2'	2.12	0.67
26:DA:600:G:O6	61:DA:4398:HOH:O	2.11	0.67
26:DA:2639:A:OP2	61:DA:3839:HOH:O	2.12	0.67
30:DF:178:PRO:HB3	30:DF:198:ALA:HA	1.77	0.67
1:AA:1238:A:OP2	61:AA:4160:HOH:O	2.12	0.66
1:CA:664:G:P	18:CR:64:ARG:HH22	2.18	0.66
1:CA:1125:U:O2'	1:CA:1126:U:H2'	1.95	0.66
3:CC:34:LEU:HG	3:CC:38:ARG:HH12	1.59	0.66
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.77	0.66
23:CW:51:U:H3	23:CW:63:G:H1	1.41	0.66
26:DA:692:C:O2'	28:DD:38:LYS:NZ	2.28	0.66
26:DA:1993:U:OP2	61:DA:4714:HOH:O	2.13	0.66
1:AA:437:U:H5'	4:AD:155:LEU:HD21	1.75	0.66
26:BA:568:U:O2'	61:BA:5168:HOH:O	2.13	0.66
26:BA:1238:G:OP2	61:BA:5012:HOH:O	2.14	0.66
26:DA:2499:C:OP2	61:DA:4653:HOH:O	2.12	0.66
26:DA:2805:G:H2'	26:DA:2807:G:C8	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:192:LEU:HD13	30:BF:194:MET:HE2	1.78	0.66
13:CM:3:ARG:NH2	13:CM:9:ILE:O	2.28	0.66
26:DA:1019:U:H3	26:DA:1142(A):A:H62	1.41	0.66
1:AA:410:G:OP1	4:AD:30:LYS:NZ	2.23	0.66
25:AY:9:A:H5'	25:AY:46:7MG:HN22	1.60	0.66
26:BA:84:A:H5'	45:BY:8:LYS:HG2	1.76	0.66
37:BQ:111:GLU:OE1	37:BQ:133:ARG:NH2	2.26	0.66
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.42	0.66
26:DA:20:C:OP1	41:DU:22:LYS:NZ	2.25	0.66
26:DA:2148:G:H2'	26:DA:2149:G:H8	1.60	0.66
24:AX:8:4SU:O2	24:AX:21:A:H2	1.79	0.66
25:AY:35:A:H2'	25:AY:36:A:C8	2.30	0.66
26:BA:278:A:H2'	26:BA:279:C:C6	2.30	0.66
25:CY:2:C:H2'	25:CY:3:C:H6	1.61	0.66
26:DA:307:G:H21	26:DA:330:A:H62	1.44	0.66
26:DA:770:G:OP2	61:DA:4267:HOH:O	2.12	0.66
26:DA:2552:U:H2'	26:DA:2554:U:OP2	1.95	0.66
36:DP:39:LYS:HB2	36:DP:45:LEU:HG	1.77	0.66
51:D4:24:THR:OG1	51:D4:25:TYR:N	2.24	0.66
26:BA:250:G:OP2	55:B8:13:ARG:NH2	2.28	0.66
30:BF:53:THR:HG22	30:BF:56:GLU:HG3	1.78	0.66
1:CA:972:C:OP1	61:CA:4167:HOH:O	2.13	0.66
13:CM:6:GLY:H	13:CM:67:GLU:HG3	1.61	0.66
32:DH:46:GLU:HB2	32:DH:49:VAL:HG12	1.76	0.66
41:DU:83:LEU:HD12	41:DU:88:ILE:HD12	1.78	0.66
1:AA:1278:U:H5'	1:AA:1279:A:O4'	1.96	0.66
9:AI:71:SER:HA	9:AI:74:ILE:HD12	1.78	0.66
10:AJ:61:GLU:OE2	14:AN:45:ARG:NE	2.29	0.66
2:CB:125:PRO:O	2:CB:127:ILE:N	2.27	0.66
18:CR:52:PRO:HB2	18:CR:54:ARG:HG2	1.77	0.66
1:AA:165:C:H2'	1:AA:166:G:C8	2.31	0.66
1:AA:567:G:N3	61:AA:4131:HOH:O	2.28	0.66
25:AY:9:A:O2'	25:AY:10:G:N7	2.28	0.66
26:BA:624:C:O2'	26:BA:657:U:OP1	2.12	0.66
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.19	0.66
2:CB:122:PHE:HD1	2:CB:123:ALA:H	1.43	0.66
52:D5:16:ARG:NH1	52:D5:17:ASP:OD1	2.29	0.66
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.77	0.66
20:AT:43:LEU:HD13	20:AT:51:GLU:HB3	1.78	0.66
26:DA:2169:A:HO2'	26:DA:2170:A:P	2.19	0.66
40:DT:108:ARG:HG2	40:DT:111:ARG:HH12	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:97:PHE:N	18:AR:30:ASP:OD1	2.29	0.66
26:DA:2171:A:N3	26:DA:2172:U:N3	2.44	0.66
27:DB:4:C:H42	27:DB:117:G:H1	1.45	0.66
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.64	0.65
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.27	0.65
3:CC:137:ALA:HA	3:CC:140:ARG:HH12	1.61	0.65
10:CJ:78:ASN:O	10:CJ:80:LYS:N	2.28	0.65
25:CY:28:G:N2	25:CY:43:C:H1'	2.10	0.65
26:DA:740:U:OP2	61:DA:4223:HOH:O	2.13	0.65
4:AD:140:VAL:HG11	4:AD:146:ILE:HD11	1.78	0.65
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.29	0.65
26:BA:84:A:H5''	45:BY:8:LYS:HE3	1.77	0.65
1:CA:673:G:H2'	1:CA:674:G:C8	2.31	0.65
3:CC:15:THR:HG21	3:CC:181:ASN:HA	1.78	0.65
26:DA:299:A:N1	26:DA:322:A:O2'	2.25	0.65
26:DA:2336:A:H61	47:D0:43:THR:HG22	1.60	0.65
31:DG:15:VAL:HG22	31:DG:175:LEU:HB3	1.78	0.65
51:D4:62:ARG:O	51:D4:64:GLY:N	2.29	0.65
9:AI:53:VAL:HG11	9:AI:92:TYR:CZ	2.31	0.65
20:AT:9:ASN:O	20:AT:10:LEU:HB2	1.95	0.65
46:BZ:108:PRO:HB3	46:BZ:117:LEU:HD13	1.79	0.65
1:CA:460:G:O6	1:CA:470:C:H5''	1.96	0.65
2:CB:178:ARG:HH22	8:CH:68:ARG:HH22	1.43	0.65
26:DA:1140:C:O3'	34:DN:25:ARG:NH1	2.29	0.65
26:DA:2492:U:OP1	61:DA:4150:HOH:O	2.15	0.65
26:BA:744:G:OP1	61:BA:4704:HOH:O	2.14	0.65
37:BQ:110:THR:HG23	37:BQ:113:GLN:HB2	1.78	0.65
1:CA:974:A:OP2	14:CN:41:ARG:NH1	2.29	0.65
1:CA:1015:A:N3	1:CA:1218:C:O2'	2.24	0.65
26:DA:422:A:OP2	61:DA:3787:HOH:O	2.15	0.65
26:DA:1246:A:OP1	30:DF:38:ARG:NH1	2.30	0.65
26:DA:2260:C:OP1	61:DA:4688:HOH:O	2.14	0.65
26:BA:1267:U:OP1	61:BA:5106:HOH:O	2.14	0.65
40:BT:118:ARG:HH11	40:BT:118:ARG:HG3	1.60	0.65
1:CA:396:G:O2'	1:CA:398:C:OP1	2.05	0.65
29:DE:72:VAL:HG22	29:DE:73:GLU:HG3	1.78	0.65
10:AJ:5:ARG:NE	10:AJ:73:ASP:OD1	2.30	0.65
27:BB:66:A:H61	27:BB:108:U:H2'	1.62	0.65
26:DA:2404:C:O3'	36:DP:77:ARG:NH2	2.26	0.65
31:DG:36:LYS:HG2	31:DG:160:VAL:HB	1.78	0.65
51:B4:63:TYR:N	51:B4:64:GLY:HA2	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1402:C:N4	22:CV:18:G:OP2	2.28	0.65
27:DB:5:C:H42	27:DB:116:G:H1	1.43	0.65
1:AA:1028:C:H42	1:AA:1033:G:H1	1.45	0.65
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.77	0.65
8:CH:29:SER:HB2	8:CH:32:LYS:HG3	1.78	0.65
30:DF:101:LEU:O	30:DF:106:ARG:NH1	2.29	0.65
30:DF:140:LEU:HD21	30:DF:170:LEU:HD11	1.79	0.65
36:DP:42:SER:O	61:DP:304:HOH:O	2.14	0.65
26:BA:1314:C:OP1	61:BA:4653:HOH:O	2.14	0.65
26:BA:2079:U:OP1	48:B1:21:ARG:NH2	2.29	0.65
29:BE:105:THR:OG1	29:BE:199:ARG:NH2	2.29	0.65
1:CA:1011:G:N2	1:CA:1019:C:H1'	2.12	0.65
1:CA:1132:C:H2'	1:CA:1133:G:H8	1.61	0.65
8:CH:45:ILE:HD13	8:CH:61:VAL:HG13	1.79	0.65
26:DA:1642:G:N7	61:DA:4099:HOH:O	2.28	0.65
26:DA:2355:C:H4'	47:D0:24:LYS:HD3	1.79	0.65
29:DE:111:ARG:HD3	38:DR:1:MET:HE1	1.79	0.65
1:AA:1502:A:H2	1:AA:1505:G:N1	1.91	0.64
4:AD:64:LEU:HA	4:AD:67:ILE:HD12	1.77	0.64
1:AA:166:G:H2'	1:AA:167:G:C8	2.32	0.64
26:BA:568:U:H5'	26:BA:945:A:N1	2.12	0.64
26:BA:2287:A:N6	26:BA:2344:U:H3	1.93	0.64
6:CF:67:MET:HE1	6:CF:75:LEU:HD12	1.79	0.64
30:DF:116:ASP:OD2	36:DP:1:MET:N	2.24	0.64
2:AB:16:HIS:HE1	2:AB:214:ILE:HD11	1.63	0.64
26:BA:1113:U:H2'	26:BA:1114:G:H8	1.62	0.64
26:BA:1300:U:H4'	26:BA:1301:A:C5'	2.27	0.64
26:BA:2608:G:N7	61:BA:4411:HOH:O	2.29	0.64
33:BI:130:TYR:HB3	33:BI:138:ILE:HB	1.78	0.64
1:CA:35:G:O2'	12:CL:118:SER:O	2.15	0.64
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.29	0.64
31:DG:80:PHE:O	31:DG:82:LEU:N	2.30	0.64
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.27	0.64
26:BA:956:G:OP2	37:BQ:14:ARG:NH2	2.25	0.64
26:BA:1434:A:H61	26:BA:1558:A:H62	1.44	0.64
26:BA:2131:G:H5''	26:BA:2132:U:H3'	1.80	0.64
47:B0:27:GLU:HG3	47:B0:68:GLU:HA	1.80	0.64
1:CA:187:C:O2'	20:CT:89:ARG:NH2	2.28	0.64
1:CA:1024:G:C2'	1:CA:1025:U:H5''	2.27	0.64
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.79	0.64
25:AY:19:G:N1	25:AY:56:C:N4	2.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:607:U:OP1	30:BF:102:PRO:HA	1.98	0.64
26:BA:1557:C:OP2	26:BA:1558:A:O2'	2.10	0.64
30:BF:157:VAL:HB	30:BF:194:MET:HG2	1.79	0.64
1:CA:96:U:O2'	1:CA:97:G:H5'	1.97	0.64
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.98	0.64
12:CL:117:ARG:HB3	12:CL:122:THR:HB	1.80	0.64
20:CT:16:HIS:O	20:CT:19:SER:OG	2.13	0.64
26:DA:2624:G:N7	61:DA:4478:HOH:O	2.29	0.64
41:DU:76:TYR:OH	41:DU:92:ARG:NH1	2.30	0.64
46:DZ:28:MET:HE1	46:DZ:61:LEU:HD21	1.79	0.64
1:AA:159:G:O2'	1:AA:161:A:N7	2.30	0.64
4:AD:154:ASN:HA	4:AD:159:ARG:HH21	1.63	0.64
26:BA:887:A:O2'	26:BA:888:C:OP2	2.13	0.64
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.79	0.64
25:CY:12:U:O4	25:CY:23:A:N1	2.31	0.64
1:CA:1118:C:C2	1:CA:1119:C:H5	2.16	0.64
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.63	0.64
26:DA:2646:C:OP2	26:DA:2732:G:O2'	2.15	0.64
37:DQ:18:LYS:O	37:DQ:98:LYS:NZ	2.26	0.64
39:DS:84:GLN:H	39:DS:111:GLU:HB2	1.62	0.64
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.33	0.64
22:CV:16:A:H61	24:CX:36:U:H3	1.46	0.64
31:DG:5:VAL:HG22	31:DG:8:LYS:H	1.62	0.64
2:AB:83:MET:HB3	2:AB:234:PRO:HG2	1.80	0.64
26:BA:187:G:OP2	61:BA:4468:HOH:O	2.14	0.64
26:BA:1047:G:H2'	26:BA:1110:G:H1	1.62	0.64
26:DA:2161:C:H2'	26:DA:2162:G:C8	2.33	0.64
37:DQ:85:LYS:HG2	47:D0:7:LEU:HB3	1.80	0.64
28:BD:69:ARG:NH2	28:BD:128:GLY:O	2.30	0.64
35:BO:37:ASP:OD1	35:BO:109:LYS:NZ	2.30	0.64
26:DA:568:U:H5'	26:DA:945:A:N1	2.13	0.64
40:DT:95:ARG:HG2	40:DT:95:ARG:HH11	1.62	0.64
1:AA:11:G:O2'	1:AA:506:G:N2	2.31	0.63
25:AY:26:A:N6	25:AY:44:G:N1	2.43	0.63
32:BH:149:ARG:NH1	32:BH:167:GLU:OE2	2.32	0.63
53:B6:6:ARG:NH1	53:B6:26:ASN:HB2	2.12	0.63
1:CA:1318:A:OP1	19:CS:3:ARG:NH2	2.31	0.63
26:DA:918:A:N3	27:DB:80:U:O2'	2.28	0.63
31:DG:33:ARG:NH2	31:DG:162:THR:HG21	2.13	0.63
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.79	0.63
11:AK:98:LEU:O	11:AK:101:SER:OG	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:526:A:OP1	61:BA:4682:HOH:O	2.15	0.63
26:BA:700:G:O2'	26:BA:1632:A:N3	2.29	0.63
26:BA:2328:A:H2'	26:BA:2329:G:C8	2.33	0.63
1:CA:148:G:H2'	1:CA:149:A:H8	1.63	0.63
1:CA:1157:A:H4'	1:CA:1158:C:O5'	1.98	0.63
26:DA:2893:G:H5'	26:DA:2893:G:H8	1.63	0.63
48:D1:51:VAL:HG11	48:D1:74:VAL:HG21	1.80	0.63
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.78	0.63
2:AB:178:ARG:HH21	8:AH:74:PRO:HB3	1.62	0.63
11:AK:79:SER:HA	11:AK:104:GLN:HB2	1.80	0.63
26:BA:2632:A:HO2'	26:BA:2811:G:HO2'	1.43	0.63
27:BB:105:A:OP1	46:BZ:72:ARG:NH1	2.30	0.63
1:CA:683:G:O6	61:CA:4143:HOH:O	2.14	0.63
3:CC:12:LEU:HD23	3:CC:16:ARG:HB3	1.80	0.63
26:DA:248:G:OP1	61:DA:4415:HOH:O	2.16	0.63
26:DA:1022:G:H22	26:DA:1142(A):A:H2	1.42	0.63
1:AA:1157:A:H4'	1:AA:1158:C:O5'	1.98	0.63
12:AL:49:ASN:ND2	12:AL:92:ASP:OD2	2.25	0.63
26:BA:2022:U:OP1	61:BA:4666:HOH:O	2.15	0.63
55:B8:23:VAL:HG11	55:B8:47:LYS:HD3	1.80	0.63
1:CA:991:U:O2'	1:CA:992:U:O5'	2.14	0.63
26:DA:2143:C:H2'	26:DA:2144:U:O4'	1.98	0.63
1:AA:1030(D):A:H2'	1:AA:1031:G:O4'	1.99	0.63
25:AY:55:PSU:C2	25:AY:57:G:H5'	2.34	0.63
26:BA:625:G:O6	36:BP:107:LYS:NZ	2.31	0.63
1:CA:406:G:H21	4:CD:119:GLN:HE22	1.46	0.63
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.80	0.63
21:CU:5:ASP:O	21:CU:11:GLY:HA3	1.98	0.63
29:DE:111:ARG:HG3	29:DE:160:TYR:CD2	2.33	0.63
1:CA:266:G:H5''	1:CA:268:C:H41	1.64	0.63
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.81	0.63
26:DA:662:G:OP1	61:DA:4188:HOH:O	2.15	0.63
31:DG:113:ARG:NH1	31:DG:141:PHE:O	2.32	0.63
1:AA:557:G:OP1	61:AA:4076:HOH:O	2.16	0.63
55:B8:62:LEU:HB3	55:B8:65:GLU:HG3	1.80	0.63
3:CC:125:GLU:HG3	3:CC:190:ARG:O	1.99	0.63
1:CA:1347:G:H5''	9:CI:107:ARG:HB3	1.81	0.63
26:DA:852:G:H2'	26:DA:853:G:H8	1.63	0.63
26:DA:2148:G:H2'	26:DA:2149:G:C8	2.34	0.63
26:DA:2537:U:H2'	26:DA:2538:C:C6	2.33	0.63
26:DA:2839:G:H5'	38:DR:46:GLY:HA2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:352:C:OP2	61:AA:4116:HOH:O	2.15	0.63
1:AA:1003:G:C2	1:AA:1004:A:H1'	2.34	0.63
2:AB:127:ILE:HD12	2:AB:130:ARG:HD3	1.80	0.63
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.80	0.63
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.81	0.63
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.79	0.63
26:BA:1371:G:O6	61:BA:4345:HOH:O	2.12	0.63
1:CA:1256:A:N6	1:CA:1278:U:H1'	2.13	0.63
25:CY:27:G:O6	25:CY:43:C:N3	2.32	0.63
32:DH:159:GLU:HG3	32:DH:169:VAL:HG11	1.80	0.63
1:AA:346:G:C4	1:AA:347:G:H1'	2.33	0.62
1:AA:1047:G:H5''	14:AN:4:LYS:HD2	1.81	0.62
26:BA:1174:A:H4'	26:BA:1175:U:OP1	1.98	0.62
26:BA:1364:G:OP2	48:B1:3:LYS:HG3	1.99	0.62
28:BD:12:SER:HB3	28:BD:208:LYS:HB3	1.80	0.62
29:BE:121:ASN:ND2	61:BE:411:HOH:O	2.22	0.62
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.81	0.62
3:CC:22:TRP:CG	3:CC:59:ARG:HD2	2.34	0.62
25:CY:50:U:O2	25:CY:64:A:N1	2.32	0.62
26:DA:1803:A:O2'	28:DD:259:THR:HG21	1.98	0.62
26:DA:2183:C:H2'	26:DA:2184:G:H8	1.63	0.62
31:DG:113:ARG:NH1	31:DG:139:LEU:O	2.32	0.62
49:D2:65:ASN:OD1	49:D2:69:ARG:NH1	2.32	0.62
1:AA:157:G:H1	1:AA:164:U:H3	1.47	0.62
1:AA:1030(A):G:O2'	1:AA:1030(C):G:N7	2.27	0.62
33:BI:92:VAL:HG11	33:BI:144:VAL:HG11	1.82	0.62
46:BZ:117:LEU:HD21	46:BZ:144:LEU:HD13	1.80	0.62
1:CA:1029:C:N4	1:CA:1032:G:H1	1.96	0.62
1:CA:1076:C:H5'	1:CA:1076:C:H6	1.62	0.62
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.13	0.62
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.64	0.62
26:DA:2273:A:H2'	26:DA:2274:A:C8	2.33	0.62
1:AA:1347:G:H5''	9:AI:107:ARG:HB3	1.81	0.62
26:BA:2689:U:H4'	26:BA:2690:C:H5'	1.82	0.62
38:BR:97:VAL:HG22	38:BR:114:VAL:HG13	1.82	0.62
1:CA:473:G:H2'	1:CA:474:G:H8	1.62	0.62
2:CB:19:HIS:HB2	2:CB:204:ASN:HB2	1.80	0.62
15:CO:11:VAL:HG21	15:CO:34:LEU:HD22	1.81	0.62
23:CW:47:U:O2'	23:CW:48:C:OP1	2.16	0.62
1:AA:56:U:H2'	1:AA:57:G:C8	2.34	0.62
7:AG:37:ASN:ND2	9:AI:39:GLY:O	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:AO:22:THR:OG1	15:AO:23:GLY:N	2.31	0.62
26:BA:1143:A:OP1	34:BN:25:ARG:NH2	2.32	0.62
26:BA:2830:G:O6	61:BA:5189:HOH:O	2.13	0.62
26:DA:1842:G:O2'	28:DD:253:GLN:NE2	2.32	0.62
38:DR:97:VAL:HG22	38:DR:114:VAL:HG13	1.80	0.62
1:CA:983:A:N1	1:CA:1222:G:N2	2.47	0.62
1:CA:1054:C:N4	23:CW:34:G:H1'	2.14	0.62
1:CA:1244:C:H42	1:CA:1293:G:H1	1.47	0.62
26:DA:880:G:N2	26:DA:898:C:H1'	2.14	0.62
1:AA:202:U:O2'	1:AA:203:U:O5'	2.16	0.62
1:AA:277:C:H5''	17:AQ:68:ARG:NH2	2.15	0.62
25:AY:22:G:N7	25:AY:46:7MG:O6	2.32	0.62
3:CC:20:SER:HB2	3:CC:40:ARG:HH12	1.65	0.62
12:CL:60:LEU:N	12:CL:64:TYR:O	2.25	0.62
23:CW:19:G:N2	23:CW:56:C:N3	2.45	0.62
1:AA:406:G:OP2	61:AA:4123:HOH:O	2.15	0.62
3:AC:12:LEU:HD23	3:AC:16:ARG:HB3	1.81	0.62
26:BA:2893:G:O2'	26:BA:2894:G:OP2	2.14	0.62
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.81	0.62
15:CO:5:LYS:H	15:CO:5:LYS:HD3	1.64	0.62
25:CY:9:A:O2'	25:CY:10:G:N7	2.32	0.62
27:DB:106:G:H5'	46:DZ:31:ARG:HG2	1.82	0.62
8:AH:121:ASP:OD1	8:AH:125:ARG:NH2	2.32	0.62
23:AW:56:C:H5	26:BA:897:C:O4'	1.83	0.62
26:BA:2572:A:N7	29:BE:144:ARG:HD2	2.15	0.62
34:BN:15:LEU:HD12	34:BN:137:LYS:HG2	1.82	0.62
1:CA:959:A:O2'	1:CA:984:C:O2'	2.17	0.62
1:CA:1067:A:N3	1:CA:1068:G:H1'	2.15	0.62
2:CB:50:GLU:HG3	2:CB:200:ILE:O	1.98	0.62
13:CM:4:ILE:HG23	13:CM:22:ILE:HD11	1.82	0.62
1:AA:92:C:H2'	1:AA:93:G:C8	2.35	0.62
26:BA:30:G:OP2	41:BU:5:LYS:NZ	2.29	0.62
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.82	0.62
13:CM:121:LYS:NZ	13:CM:121:LYS:H	1.97	0.62
1:AA:1007:C:H2'	1:AA:1008:C:H5''	1.81	0.62
2:AB:231:GLU:HB3	2:AB:232:PRO:CD	2.30	0.62
18:AR:38:GLU:HA	18:AR:41:LYS:HD3	1.82	0.62
30:BF:101:LEU:O	30:BF:106:ARG:NH1	2.32	0.62
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.65	0.62
26:DA:882:G:N1	26:DA:894:C:N3	2.46	0.62
26:DA:900:A:H2'	26:DA:901:A:H8	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:179:PRO:HB2	51:D4:42:PHE:HE1	1.64	0.62
9:AI:53:VAL:HG11	9:AI:92:TYR:CE1	2.35	0.61
26:BA:732:C:OP2	61:BA:4004:HOH:O	2.16	0.61
1:CA:977:A:O2'	1:CA:981:U:N3	2.33	0.61
26:DA:509:C:OP1	61:DA:4324:HOH:O	2.16	0.61
28:DD:132:PRO:HD3	28:DD:190:TYR:CZ	2.35	0.61
30:DF:192:LEU:HD13	30:DF:194:MET:HE2	1.82	0.61
1:AA:953:G:H5'	1:AA:965:A:H61	1.65	0.61
1:AA:1027:C:C2	1:AA:1034:G:N1	2.67	0.61
2:AB:17:PHE:HD2	2:AB:44:LEU:HD21	1.65	0.61
24:AX:6:G:H1	24:AX:67:C:N4	1.97	0.61
26:BA:2168:G:C6	26:BA:2171:A:H8	2.18	0.61
27:BB:45:A:OP2	31:BG:96:ARG:NH2	2.28	0.61
1:CA:345:C:OP2	40:DT:39:ARG:NH2	2.30	0.61
25:CY:8:4SU:HN3	25:CY:14:A:N6	1.91	0.61
26:DA:373:U:H2'	26:DA:374:A:H8	1.65	0.61
27:DB:24:G:N7	27:DB:56:G:H2'	2.15	0.61
27:DB:24:G:N3	27:DB:26:A:N6	2.48	0.61
28:DD:206:LEU:HD22	28:DD:211:ARG:HG2	1.81	0.61
1:AA:976:G:H5'	1:AA:1358:U:O2'	1.99	0.61
26:BA:2049:G:N7	61:BA:5165:HOH:O	2.31	0.61
26:DA:1261:C:OP2	43:DW:83:LYS:NZ	2.33	0.61
26:DA:2022:U:O2'	26:DA:2617:C:H5'	2.00	0.61
29:DE:52:LEU:O	29:DE:76:ARG:N	2.25	0.61
1:AA:677:U:H3	1:AA:713:G:H22	1.47	0.61
2:AB:74:LYS:NZ	2:AB:205:ASP:OD2	2.33	0.61
15:AO:79:ARG:O	15:AO:83:GLU:HB2	1.99	0.61
26:BA:1800:C:OP2	28:BD:183:ARG:NH2	2.32	0.61
1:CA:757:U:H2'	1:CA:758:G:O4'	1.99	0.61
25:CY:26:A:N1	25:CY:44:G:C6	2.69	0.61
36:DP:99:LEU:O	36:DP:103:ALA:N	2.32	0.61
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.61
1:AA:1005:A:H1'	1:AA:1036:G:H22	1.65	0.61
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.36	0.61
8:AH:51:VAL:HG11	8:AH:60:ARG:HH12	1.66	0.61
26:BA:1816:G:O6	28:BD:35:LYS:NZ	2.28	0.61
26:BA:2206:G:H5'	26:BA:2207:G:N7	2.14	0.61
29:BE:111:ARG:HG3	29:BE:160:TYR:CD2	2.34	0.61
1:CA:1120:G:O6	1:CA:1154:G:N2	2.33	0.61
2:CB:55:PHE:HA	2:CB:58:ILE:HB	1.82	0.61
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:52:LEU:HD21	3:CC:55:VAL:HG23	1.80	0.61
12:CL:24:VAL:HG11	12:CL:27:LEU:HD22	1.81	0.61
26:DA:2074:U:H2'	26:DA:2075:U:C6	2.36	0.61
26:DA:2431:U:OP1	61:DA:3906:HOH:O	2.16	0.61
50:D3:12:PRO:HB2	50:D3:20:LYS:HG2	1.81	0.61
1:AA:189:G:H1	1:AA:189(K):U:H3	1.48	0.61
1:AA:1027:C:H2'	1:AA:1028:C:C5	2.35	0.61
26:BA:1385:G:O2'	26:BA:1396:U:O2	2.14	0.61
1:CA:985:C:N3	1:CA:1220:G:N2	2.46	0.61
1:CA:1148:U:H1'	9:CI:66:ARG:HH12	1.66	0.61
3:CC:18:TRP:HE3	3:CC:18:TRP:H	1.47	0.61
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.33	0.61
44:DX:46:ALA:O	49:D2:30:ARG:NH2	2.33	0.61
46:DZ:117:LEU:HD12	46:DZ:174:VAL:HG22	1.80	0.61
50:D3:6:VAL:HG13	50:D3:56:VAL:HG22	1.81	0.61
26:BA:2350:C:OP2	61:BA:4049:HOH:O	2.16	0.61
41:BU:76:TYR:OH	41:BU:92:ARG:NH1	2.33	0.61
50:D3:5:LYS:NZ	50:D3:34:GLU:OE2	2.18	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.35	0.61
3:AC:39:ILE:HG23	3:AC:91:LEU:HD11	1.83	0.61
26:BA:2714:G:OP1	61:BA:4546:HOH:O	2.16	0.61
1:CA:952:U:H2'	1:CA:953:G:C8	2.36	0.61
10:CJ:27:ALA:HA	10:CJ:81:THR:HG22	1.83	0.61
25:CY:5:G:H1	25:CY:68:C:N4	1.99	0.61
26:DA:301:G:OP2	45:DY:84:ARG:NH2	2.33	0.61
26:DA:952:G:OP1	37:DQ:16:ARG:NH2	2.33	0.61
26:DA:958:U:OP2	37:DQ:14:ARG:NH1	2.33	0.61
26:DA:1220:A:OP2	41:DU:19:LYS:NZ	2.29	0.61
38:DR:33:ARG:NH1	38:DR:115:GLU:OE2	2.29	0.61
1:AA:166:G:H2'	1:AA:167:G:H8	1.65	0.61
1:AA:562:C:H1'	12:AL:15:ARG:HB3	1.82	0.61
37:BQ:85:LYS:HG2	47:B0:7:LEU:HB3	1.83	0.61
1:CA:692:U:O2'	1:CA:694:A:N7	2.31	0.61
1:CA:920:U:H2'	1:CA:921:U:C6	2.35	0.61
1:CA:1317:C:O2	19:CS:37:ARG:NH1	2.33	0.61
11:CK:34:ASP:HB3	11:CK:40:ILE:HD11	1.83	0.61
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.64	0.61
26:DA:526:A:OP1	61:DA:4194:HOH:O	2.16	0.61
26:DA:1939:U:OP1	26:DA:2604:U:O2'	2.19	0.61
27:DB:110:G:H2'	27:DB:111:G:C8	2.36	0.61
26:BA:528:A:C2'	26:BA:529:A:H5''	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BW:14:PRO:HG2	43:BW:78:GLU:HG2	1.82	0.61
1:CA:957:U:H2'	1:CA:959:A:OP2	2.01	0.61
1:CA:1067:A:O2'	1:CA:1068:G:OP2	2.17	0.61
26:DA:2126:A:N3	26:DA:2127:G:H1'	2.16	0.61
40:DT:85:LYS:NZ	40:DT:87:ASP:OD2	2.28	0.61
2:AB:55:PHE:HA	2:AB:58:ILE:HB	1.83	0.60
26:BA:2791:C:H2'	26:BA:2792:G:C8	2.36	0.60
1:CA:646:U:H2'	1:CA:647:C:C6	2.36	0.60
2:CB:47:THR:O	2:CB:51:LEU:N	2.32	0.60
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.82	0.60
26:DA:1005:C:H2'	26:DA:1006:C:C6	2.36	0.60
26:DA:2046:G:H5'	52:D5:19:ARG:HA	1.83	0.60
26:DA:2708:G:H1'	38:DR:71:GLN:HE22	1.65	0.60
26:DA:2785:C:OP1	29:DE:41:LYS:NZ	2.34	0.60
13:AM:80:ARG:HH22	19:AS:69:HIS:HE1	1.48	0.60
26:BA:1204:A:H2	26:BA:1241:A:H62	1.49	0.60
29:BE:9:VAL:HB	40:BT:3:ARG:HG2	1.82	0.60
30:BF:143:ALA:HB1	30:BF:148:LEU:HB2	1.82	0.60
39:BS:56:LEU:HD12	39:BS:69:VAL:HG12	1.82	0.60
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.36	0.60
26:DA:1816:G:O6	28:DD:35:LYS:NZ	2.25	0.60
2:AB:80:ILE:HD11	2:AB:212:GLN:HA	1.82	0.60
19:AS:3:ARG:NH1	19:AS:8:GLY:O	2.35	0.60
27:BB:33:G:H5'	31:BG:2:PRO:HD3	1.83	0.60
48:B1:51:VAL:HG11	48:B1:74:VAL:HG21	1.84	0.60
1:CA:148:G:H2'	1:CA:149:A:C8	2.37	0.60
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.36	0.60
38:DR:56:LYS:NZ	38:DR:90:ARG:O	2.33	0.60
46:DZ:7:ALA:HB3	46:DZ:61:LEU:HD12	1.81	0.60
1:AA:413:G:N2	1:AA:428:G:H1'	2.16	0.60
12:AL:24:VAL:HG12	12:AL:27:LEU:HB2	1.83	0.60
17:AQ:67:LYS:HA	17:AQ:70:ARG:HH12	1.66	0.60
29:BE:29:GLY:HA3	61:BE:408:HOH:O	2.01	0.60
31:BG:47:LYS:HG3	31:BG:48:GLU:H	1.66	0.60
44:BX:2:LYS:NZ	44:BX:38:GLU:OE2	2.30	0.60
45:BY:92:ASN:N	45:BY:93:GLY:HA2	2.16	0.60
51:B4:57:GLU:HB3	51:B4:58:ARG:HA	1.83	0.60
9:CI:23:ASN:ND2	9:CI:60:ASP:OD2	2.33	0.60
26:DA:954:G:H5''	37:DQ:13:GLN:HB3	1.83	0.60
1:AA:865:A:H2	1:AA:918:A:H4'	1.67	0.60
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:59:U:H3'	25:AY:60:U:C6	2.35	0.60
28:BD:71:ASP:HB3	28:BD:103:ARG:NH2	2.16	0.60
36:BP:26:GLY:O	61:BP:311:HOH:O	2.16	0.60
1:CA:1120:G:C6	1:CA:1154:G:N2	2.69	0.60
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.02	0.60
1:CA:1157:A:H5'	1:CA:1158:C:C6	2.35	0.60
46:DZ:159:PRO:HA	46:DZ:161:VAL:HG12	1.84	0.60
51:D4:59:PHE:HA	51:D4:60:GLN:C	2.27	0.60
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.82	0.60
1:CA:9:G:H2'	1:CA:10:A:H8	1.66	0.60
26:DA:2400:G:O3'	53:D6:18:ARG:NH1	2.34	0.60
46:DZ:53:ILE:HG22	46:DZ:71:VAL:O	2.02	0.60
48:D1:23:LYS:HB3	48:D1:29:GLY:HA3	1.84	0.60
1:AA:1026:G:O6	1:AA:1034:G:N2	2.32	0.60
4:AD:108:LEU:HD13	4:AD:174:LEU:HD13	1.83	0.60
25:AY:19:G:H1	25:AY:56:C:N4	2.00	0.60
26:BA:2870:C:H2'	26:BA:2871:C:O4'	2.02	0.60
51:B4:53:GLU:O	51:B4:55:ARG:N	2.34	0.60
1:CA:1075:C:H2'	1:CA:1076:C:H5''	1.84	0.60
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.67	0.60
26:DA:1007:C:OP1	34:DN:35:ARG:NH1	2.34	0.60
26:DA:1226:A:OP1	42:DV:84:LYS:HE2	2.01	0.60
1:AA:662:G:H2'	1:AA:663:A:C8	2.37	0.60
1:AA:1025:U:O2'	1:AA:1026:G:O4'	2.19	0.60
26:BA:2033:A:OP1	61:BA:4308:HOH:O	2.17	0.60
26:BA:2447:G:OP2	61:BA:4563:HOH:O	2.16	0.60
1:CA:662:G:H2'	1:CA:663:A:H8	1.67	0.60
26:DA:774:A:N6	61:DA:3733:HOH:O	2.35	0.60
26:DA:1693:U:O2'	28:DD:14:ARG:NH2	2.35	0.60
26:DA:2291:U:H2'	26:DA:2292:C:C6	2.37	0.60
26:DA:2747:G:H1	26:DA:2754:U:H2'	1.66	0.60
23:AW:56:C:P	26:BA:897:C:H5'	2.42	0.60
26:BA:880:G:N2	26:BA:898:C:O2	2.35	0.60
32:BH:25:LYS:HG2	32:BH:34:GLU:HG2	1.84	0.60
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.34	0.60
18:CR:60:ALA:O	18:CR:64:ARG:HG3	2.02	0.60
26:DA:2808:U:C2'	26:DA:2809:A:H5'	2.32	0.60
32:DH:20:ALA:HB1	32:DH:21:PRO:HD2	1.84	0.60
36:DP:38:GLN:O	36:DP:39:LYS:HB3	2.02	0.60
19:AS:28:LYS:HB3	19:AS:28:LYS:HZ2	1.67	0.60
26:BA:1048:A:OP2	26:BA:1109:C:N4	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:542:G:OP1	4:CD:10:ARG:NH2	2.27	0.60
1:CA:1505:G:HO2'	22:CV:13:A:H2	1.49	0.60
26:DA:1247:A:OP1	30:DF:95:ARG:NH2	2.32	0.60
26:DA:2499:C:N3	61:DA:3930:HOH:O	2.31	0.60
36:DP:59:LEU:HD21	55:D8:10:ALA:HA	1.82	0.60
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.35	0.59
26:BA:1418:G:OP2	61:BA:4580:HOH:O	2.16	0.59
26:BA:2155:G:H2'	26:BA:2156:G:O4'	2.01	0.59
26:BA:2206:G:H3'	26:BA:2207:G:C8	2.37	0.59
26:BA:2871:C:N3	61:BA:4781:HOH:O	2.31	0.59
28:BD:132:PRO:HG2	28:BD:135:PHE:CD2	2.37	0.59
33:BI:72:LEU:C	33:BI:74:ASN:H	2.10	0.59
40:BT:118:ARG:HH22	40:BT:125:ARG:HH12	1.50	0.59
46:BZ:139:VAL:HG22	46:BZ:155:LEU:HD11	1.84	0.59
5:CE:102:ALA:HB1	5:CE:106:PRO:HG2	1.84	0.59
14:CN:6:LEU:HB3	14:CN:23:ARG:HH21	1.67	0.59
26:DA:247:G:H4'	26:DA:386:G:C5	2.36	0.59
26:DA:2638:G:P	29:DE:82:ARG:HH22	2.25	0.59
51:D4:46:GLN:C	51:D4:48:ARG:H	2.10	0.59
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.67	0.59
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.84	0.59
26:BA:898:C:H2'	26:BA:899:A:C8	2.37	0.59
26:BA:1173:G:O2'	26:BA:1174:A:O5'	2.20	0.59
31:BG:5:VAL:HG22	31:BG:8:LYS:H	1.67	0.59
32:BH:56:SER:HB3	32:BH:61:HIS:ND1	2.17	0.59
9:CI:53:VAL:C	9:CI:55:ALA:H	2.10	0.59
22:CV:14:A:C4	25:CY:34:G:C6	2.90	0.59
26:DA:1434:A:H61	26:DA:1558:A:H62	1.49	0.59
26:DA:2846:G:N7	61:DA:4073:HOH:O	2.32	0.59
31:DG:151:ALA:HB3	31:DG:153:ARG:HH11	1.66	0.59
42:DV:76:LYS:HB2	42:DV:81:TYR:HB3	1.83	0.59
1:AA:200:G:H1	1:AA:217:C:H42	1.51	0.59
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.25	0.59
31:BG:15:VAL:HG21	31:BG:176:LEU:HD23	1.82	0.59
46:BZ:150:LEU:O	46:BZ:171:ILE:HG13	2.03	0.59
1:CA:113:G:OP1	61:CA:4148:HOH:O	2.17	0.59
1:CA:539:A:H2'	1:CA:540:G:C8	2.37	0.59
1:CA:596:C:O2	1:CA:644:G:N2	2.17	0.59
3:CC:134:ILE:HD11	3:CC:153:VAL:HG21	1.83	0.59
13:CM:65:LYS:N	51:D4:50:VAL:HG21	2.18	0.59
23:CW:14:A:H61	23:CW:21:A:H2	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:61:C:O2'	23:CW:62:C:O5'	2.14	0.59
26:DA:1800:C:OP2	28:DD:183:ARG:NH2	2.35	0.59
36:DP:85:LEU:HA	36:DP:88:LEU:HD12	1.85	0.59
37:DQ:85:LYS:HB2	47:D0:7:LEU:HD12	1.83	0.59
46:DZ:105:VAL:N	46:DZ:139:VAL:O	2.35	0.59
1:AA:428:G:OP2	4:AD:10:ARG:NH1	2.35	0.59
3:AC:19:GLU:HB3	3:AC:40:ARG:HH22	1.67	0.59
25:AY:59:U:H3'	25:AY:60:U:H6	1.68	0.59
26:BA:2103:C:N4	26:BA:2186:G:H1	1.98	0.59
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.17	0.59
1:CA:538:G:H5''	12:CL:114:LYS:HB2	1.82	0.59
1:CA:769:G:H4'	1:CA:1513:A:H4'	1.85	0.59
26:DA:1446:C:H42	26:DA:1465:G:H1	1.50	0.59
30:DF:185:ASP:HA	30:DF:188:ARG:HD3	1.84	0.59
34:DN:58:ASP:OD1	34:DN:58:ASP:N	2.34	0.59
36:DP:84:ASN:CG	36:DP:117:GLU:HB2	2.27	0.59
46:DZ:108:PRO:HG3	46:DZ:141:VAL:HB	1.84	0.59
51:D4:33:VAL:HG12	51:D4:35:VAL:H	1.66	0.59
1:AA:189(A):C:H42	1:AA:189(J):G:H1	1.51	0.59
1:AA:736:C:H2'	1:AA:737:A:C8	2.37	0.59
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.20	0.59
3:AC:8:ILE:HD13	3:AC:184:TYR:HB3	1.84	0.59
3:AC:82:GLU:HG2	3:AC:85:ARG:NH2	2.17	0.59
26:BA:271(M):G:H4'	26:BA:271(N):U:OP1	2.01	0.59
26:DA:2023:G:H5'	26:DA:2617:C:H4'	1.83	0.59
3:AC:114:PRO:O	3:AC:118:GLN:NE2	2.35	0.59
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.85	0.59
15:AO:18:PHE:HB2	15:AO:19:PRO:HD2	1.85	0.59
23:AW:22:G:O2'	23:AW:23:A:OP1	2.18	0.59
26:BA:1025:G:C4	26:BA:1135:C:H1'	2.37	0.59
26:BA:1040:C:H2'	26:BA:1041:C:O4'	2.01	0.59
26:BA:1649:G:O2'	38:BR:107:ASP:OD2	2.17	0.59
50:B3:23:LEU:HD13	50:B3:50:VAL:HG11	1.85	0.59
26:DA:2002:G:OP2	38:DR:9:LYS:NZ	2.35	0.59
26:DA:2140:C:H1'	26:DA:2152:G:N2	2.18	0.59
1:AA:1002:G:H3'	1:AA:1003:G:C8	2.38	0.59
19:AS:32:LYS:HA	19:AS:50:ALA:HB3	1.84	0.59
26:BA:652(E):G:O6	26:BA:652(T):C:N4	2.30	0.59
36:BP:89:ALA:O	36:BP:121:LYS:NZ	2.27	0.59
39:BS:15:ARG:O	39:BS:19:LYS:HG2	2.03	0.59
23:CW:11:C:H42	23:CW:24:G:H1	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CY:18:G:N2	25:CY:55:PSU:C4	2.71	0.59
26:DA:2176:A:H2'	26:DA:2177:C:C6	2.37	0.59
37:DQ:31:ASP:OD1	37:DQ:134:ARG:NH1	2.32	0.59
25:AY:58:A:H3'	25:AY:58:A:P	2.43	0.59
26:BA:1405:U:H2'	26:BA:1406:U:C6	2.38	0.59
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.36	0.59
11:CK:98:LEU:O	11:CK:101:SER:OG	2.19	0.59
26:DA:271(R):G:H5''	48:D1:97:LEU:HD21	1.84	0.59
26:DA:2062:A:OP1	61:DA:3829:HOH:O	2.17	0.59
31:DG:101:ILE:HD13	51:D4:25:TYR:HB2	1.84	0.59
1:AA:1239:A:H62	1:AA:1299:A:N6	2.01	0.59
2:AB:212:GLN:O	2:AB:216:SER:OG	2.19	0.59
23:AW:5:G:H2'	23:AW:6:G:H8	1.67	0.59
1:CA:1010:G:C2	1:CA:1011:G:C8	2.91	0.59
1:CA:1182:G:H4'	1:CA:1183:A:H3'	1.84	0.59
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.02	0.59
26:DA:2173:A:H2'	26:DA:2174:C:O4'	2.03	0.59
1:AA:1030(D):A:H62	1:AA:1031:G:H21	1.49	0.59
19:AS:30:LEU:HD11	19:AS:50:ALA:HB2	1.85	0.59
26:BA:322:A:OP1	30:BF:168:ARG:HD2	2.03	0.59
26:BA:1913:A:H4'	26:BA:1914:C:H5''	1.83	0.59
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.14	0.59
15:CO:18:PHE:HB2	15:CO:19:PRO:HD2	1.85	0.59
26:DA:249:C:O2	55:D8:12:LYS:NZ	2.29	0.59
26:DA:2112:G:C5	26:DA:2113:U:H1'	2.37	0.59
31:DG:64:THR:HB	31:DG:94:LEU:HD21	1.85	0.59
46:DZ:55:HIS:HE1	46:DZ:135:GLU:HG3	1.68	0.59
21:AU:5:ASP:OD2	61:AU:101:HOH:O	2.17	0.58
26:BA:2789:C:O2	26:BA:2894:G:N2	2.35	0.58
1:CA:1220:G:O3'	19:CS:36:ARG:HD3	2.03	0.58
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.37	0.58
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.36	0.58
8:CH:4:ASP:OD1	8:CH:7:ALA:N	2.23	0.58
26:DA:848:G:N3	26:DA:933:A:H1'	2.18	0.58
26:DA:2151:G:H2'	26:DA:2152:G:H8	1.67	0.58
1:AA:17:U:H2'	1:AA:18:C:C6	2.38	0.58
1:AA:1202:G:O4'	14:AN:29:ARG:NH1	2.35	0.58
2:AB:162:ILE:O	2:AB:185:ILE:HG12	2.03	0.58
6:AF:50:TYR:OH	18:AR:74:ARG:O	2.18	0.58
20:AT:45:GLN:HB2	20:AT:91:LEU:HD13	1.85	0.58
26:BA:526:A:O2'	26:BA:2043:C:O2	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:636:G:OP1	36:BP:132:LYS:HE2	2.02	0.58
1:CA:1338:G:H21	24:CX:41:C:H1'	1.68	0.58
4:CD:64:LEU:HB2	4:CD:198:VAL:HG11	1.84	0.58
26:DA:2849:U:OP2	40:DT:95:ARG:NH1	2.37	0.58
37:DQ:111:GLU:O	37:DQ:115:MET:HG2	2.02	0.58
53:B6:6:ARG:NE	53:B6:24:GLU:OE1	2.22	0.58
1:CA:1204:A:OP1	14:CN:3:ARG:NH1	2.36	0.58
17:CQ:57:VAL:HG12	17:CQ:76:LEU:HA	1.84	0.58
37:DQ:48:GLU:OE1	37:DQ:51:ARG:NH2	2.33	0.58
39:DS:14:VAL:O	39:DS:18:ILE:HG12	2.03	0.58
1:AA:46:G:O6	61:AA:4200:HOH:O	2.15	0.58
23:AW:66:U:H2'	23:AW:67:C:H6	1.66	0.58
26:BA:1021:A:H62	26:BA:1141:U:H3	1.51	0.58
1:CA:504:C:OP1	61:CA:4008:HOH:O	2.17	0.58
12:CL:70:ILE:HD13	12:CL:77:LEU:HD12	1.85	0.58
35:DO:115:VAL:HG13	35:DO:121:VAL:HG21	1.86	0.58
9:AI:99:LEU:HB3	9:AI:101:PHE:CE1	2.38	0.58
23:AW:47:U:O2'	23:AW:48:C:OP1	2.20	0.58
26:BA:2336:A:H61	47:B0:43:THR:CG2	2.16	0.58
26:BA:2485:G:OP1	37:BQ:46:GLN:NE2	2.35	0.58
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.84	0.58
5:CE:31:LEU:HD22	5:CE:43:LEU:HD11	1.85	0.58
24:CX:50:U:H3	24:CX:64:G:H1	1.51	0.58
26:DA:2365:G:O6	55:D8:43:GLN:NE2	2.36	0.58
30:DF:21:ALA:HB3	30:DF:22:ALA:HA	1.84	0.58
1:AA:1302:U:C5	13:AM:17:VAL:HG21	2.38	0.58
26:BA:184:C:H2'	26:BA:185:U:C6	2.38	0.58
1:CA:48:C:OP2	61:CA:4100:HOH:O	2.16	0.58
1:CA:420:U:O2'	1:CA:423:G:O6	2.18	0.58
26:DA:900:A:H2'	26:DA:901:A:C8	2.39	0.58
32:DH:3:ARG:NH1	32:DH:3:ARG:HB3	2.18	0.58
32:DH:73:ALA:O	32:DH:76:VAL:HG12	2.03	0.58
1:AA:473:G:H2'	1:AA:474:G:C8	2.39	0.58
1:AA:1125:U:H1'	1:AA:1126:U:H2'	1.86	0.58
46:BZ:24:LEU:HB2	46:BZ:41:LEU:HD23	1.85	0.58
2:CB:178:ARG:HE	8:CH:74:PRO:HG3	1.68	0.58
6:CF:24:GLU:HG3	6:CF:28:ARG:NH1	2.19	0.58
26:DA:1952:A:OP1	35:DO:42:SER:OG	2.21	0.58
26:DA:2137:C:H2'	26:DA:2138:C:C6	2.38	0.58
26:BA:871:U:OP1	37:BQ:5:ARG:HD3	2.04	0.58
26:BA:2144:U:O2'	26:BA:2145:C:H2'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2659:G:O2'	32:BH:175:LYS:NZ	2.37	0.58
1:CA:473:G:H2'	1:CA:474:G:C8	2.39	0.58
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.19	0.58
15:CO:3:ILE:HD13	15:CO:3:ILE:H	1.67	0.58
15:CO:69:TYR:O	15:CO:73:GLU:HG2	2.04	0.58
26:DA:1300:U:H4'	26:DA:1301:A:H5''	1.86	0.58
26:DA:2318:G:H21	39:DS:3:ARG:HD2	1.69	0.58
26:DA:2438:U:O2'	26:DA:2440:C:OP1	2.20	0.58
46:DZ:117:LEU:HA	46:DZ:174:VAL:HA	1.86	0.58
1:AA:473:G:H2'	1:AA:474:G:H8	1.69	0.58
2:AB:16:HIS:HB3	2:AB:210:SER:CB	2.33	0.58
4:AD:111:ALA:HB2	4:AD:120:LEU:HD12	1.86	0.58
23:AW:28:G:H2'	23:AW:29:G:H8	1.67	0.58
26:BA:801:G:O6	30:BF:53:THR:OG1	2.20	0.58
38:BR:56:LYS:NZ	38:BR:90:ARG:O	2.36	0.58
4:CD:61:LYS:HZ1	4:CD:72:GLU:CD	2.11	0.58
26:DA:997:G:OP1	41:DU:92:ARG:HG2	2.04	0.58
26:DA:1253:A:N6	61:DA:3721:HOH:O	2.33	0.58
1:AA:347:G:H2'	1:AA:348:G:O4'	2.03	0.58
1:AA:727:G:N2	1:AA:730:G:OP2	2.36	0.58
12:AL:24:VAL:HG11	12:AL:27:LEU:HD22	1.86	0.58
13:AM:40:ASN:O	13:AM:43:THR:OG1	2.21	0.58
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.03	0.58
26:BA:303:U:O4	61:BA:4677:HOH:O	2.13	0.58
1:CA:971:G:OP2	1:CA:1231:G:N2	2.26	0.58
1:CA:1277:C:O2'	1:CA:1279:A:H8	1.86	0.58
1:CA:1422:G:O3'	35:DO:49:ARG:NH1	2.33	0.58
9:CI:5:TYR:O	9:CI:87:GLN:NE2	2.37	0.58
25:CY:40:C:C2'	25:CY:41:C:H5'	2.34	0.58
48:D1:76:ARG:HH11	48:D1:97:LEU:HD22	1.67	0.58
26:BA:566:U:H5''	36:BP:29:LYS:HE3	1.86	0.57
33:BI:129:THR:HG22	33:BI:139:GLN:NE2	2.17	0.57
46:BZ:138:GLU:H	46:BZ:156:LYS:HD3	1.69	0.57
50:B3:18:ASP:OD1	50:B3:18:ASP:N	2.37	0.57
51:B4:54:GLY:C	51:B4:56:VAL:HA	2.28	0.57
1:CA:995:C:O2	14:CN:4:LYS:NZ	2.28	0.57
1:CA:1153:C:H42	1:CA:1154:G:N2	2.01	0.57
26:DA:465:G:OP1	54:D7:12:ARG:NH2	2.37	0.57
7:AG:113:GLU:HG2	7:AG:119:ARG:HG2	1.86	0.57
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	1.85	0.57
25:AY:38:A:H2'	25:AY:39:PSU:O4'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1166:C:H2'	26:BA:1167:U:C6	2.39	0.57
26:BA:2430:A:H2'	26:BA:2430:A:N3	2.18	0.57
27:BB:75:G:H5''	27:BB:75:G:H8	1.69	0.57
1:CA:34:C:H2'	1:CA:35:G:H8	1.69	0.57
9:CI:21:PRO:HA	9:CI:59:PHE:HA	1.85	0.57
16:CP:43:LYS:HA	16:CP:48:TRP:HB3	1.86	0.57
19:CS:64:GLU:O	19:CS:67:VAL:HG23	2.04	0.57
23:AW:5:G:H2'	23:AW:6:G:C8	2.39	0.57
26:BA:859:G:O2'	26:BA:916:G:O6	2.21	0.57
33:BI:140:LEU:HD22	33:BI:142:VAL:HG13	1.86	0.57
1:CA:890:G:O2'	1:CA:906:G:O6	2.20	0.57
26:DA:322:A:OP2	30:DF:169:ASN:HB2	2.04	0.57
26:DA:399:G:OP2	61:DA:4406:HOH:O	2.17	0.57
26:DA:2110:G:OP1	26:DA:2118:U:N3	2.33	0.57
34:DN:17:ASP:HB2	34:DN:137:LYS:HZ1	1.69	0.57
38:DR:33:ARG:NH2	52:D5:57:VAL:O	2.29	0.57
1:AA:224:C:H2'	1:AA:225:C:C6	2.38	0.57
1:AA:757:U:H2'	1:AA:758:G:O4'	2.04	0.57
2:AB:16:HIS:HD2	2:AB:17:PHE:N	2.00	0.57
5:AE:78:HIS:HD1	8:AH:104:ARG:HD2	1.68	0.57
10:AJ:5:ARG:O	10:AJ:98:ILE:HA	2.05	0.57
25:AY:63:G:H2'	25:AY:64:A:O4'	2.04	0.57
26:BA:893:C:H2'	26:BA:894:C:C6	2.39	0.57
41:BU:89:GLU:HG3	42:BV:50:PRO:HB3	1.86	0.57
1:CA:975:A:N1	10:CJ:48:THR:HB	2.19	0.57
1:CA:1026:G:O6	1:CA:1036:G:N2	2.37	0.57
5:CE:137:GLU:HG2	5:CE:140:ARG:HH11	1.68	0.57
15:CO:82:ILE:HB	15:CO:87:ILE:HB	1.87	0.57
26:DA:1359:A:H61	26:DA:1372:U:H3	1.52	0.57
26:DA:1448:G:H4'	26:DA:1542:A:OP1	2.05	0.57
26:DA:2630:G:H2'	26:DA:2631:G:C8	2.39	0.57
28:DD:132:PRO:HG2	28:DD:135:PHE:CD2	2.40	0.57
1:AA:191:G:H21	20:AT:103:GLY:HA2	1.69	0.57
1:AA:1392:G:N2	1:AA:1502:A:H8	2.01	0.57
26:BA:1423:G:OP1	26:BA:1492:G:O2'	2.23	0.57
26:BA:2165:G:O2'	26:BA:2166:G:O4'	2.21	0.57
26:BA:2334:G:H5'	39:BS:9:ARG:HG2	1.85	0.57
31:BG:170:ARG:NH2	31:BG:182:LYS:O	2.37	0.57
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.01	0.57
26:DA:531:C:H4'	26:DA:532:A:H5''	1.86	0.57
26:DA:903:C:H2'	26:DA:904:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1264:G:OP1	52:D5:19:ARG:NH2	2.35	0.57
26:DA:1593:G:H2'	26:DA:1594:G:C8	2.40	0.57
26:DA:1853:A:H2'	26:DA:1854:A:C8	2.40	0.57
27:DB:3:C:H2'	27:DB:4:C:C6	2.40	0.57
47:D0:10:THR:HG22	47:D0:12:ASN:H	1.70	0.57
27:BB:14:U:OP2	27:BB:70:C:O2'	2.20	0.57
48:B1:3:LYS:HB2	48:B1:61:ARG:HH12	1.69	0.57
49:B2:65:ASN:OD1	49:B2:69:ARG:NH1	2.35	0.57
1:CA:1099:G:OP2	2:CB:144:ARG:NH2	2.34	0.57
2:CB:63:MET:HG3	2:CB:225:ALA:HB1	1.86	0.57
10:CJ:64:GLU:OE2	10:CJ:66:ARG:NH1	2.37	0.57
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.70	0.57
26:BA:878:A:H61	26:BA:899:A:H1'	1.70	0.57
32:BH:113:VAL:HG11	32:BH:151:ILE:HD13	1.86	0.57
4:CD:173:TRP:HB3	4:CD:187:ARG:HE	1.70	0.57
25:CY:2:C:H2'	25:CY:3:C:C6	2.39	0.57
27:DB:41:U:H5	31:DG:70:VAL:H	1.51	0.57
46:DZ:7:ALA:O	46:DZ:62:PRO:HD3	2.05	0.57
26:BA:579:G:H2'	26:BA:580:C:C6	2.40	0.57
26:BA:2207:G:O2'	26:BA:2208:A:OP1	2.21	0.57
1:CA:992:U:H3	1:CA:1044:A:H62	1.53	0.57
26:DA:658:C:H2'	26:DA:659:C:C6	2.40	0.57
26:DA:1013:C:H2'	26:DA:1014:U:H6	1.69	0.57
26:DA:1209:G:O2'	26:DA:1237:A:N1	2.32	0.57
26:DA:1857:G:O2'	26:DA:1885:A:N6	2.35	0.57
1:AA:69:G:H2'	1:AA:70:G:C8	2.39	0.57
1:AA:450:G:OP1	16:AP:43:LYS:NZ	2.37	0.57
1:AA:993:G:H2'	1:AA:995:C:H41	1.69	0.57
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.40	0.57
26:BA:576:U:H2'	26:BA:577:G:C8	2.39	0.57
30:BF:24:LEU:HD23	30:BF:115:ALA:HA	1.87	0.57
31:BG:161:THR:HG22	31:BG:163:ALA:H	1.70	0.57
45:BY:54:LYS:H	45:BY:56:PRO:HD3	1.70	0.57
1:CA:1000:U:N3	1:CA:1041:A:N6	2.22	0.57
6:CF:25:ILE:HD13	6:CF:82:ARG:HE	1.70	0.57
11:CK:48:ILE:O	11:CK:50:TYR:N	2.37	0.57
14:CN:24:CYS:O	14:CN:28:GLY:N	2.30	0.57
24:CX:67:C:H2'	24:CX:68:C:H5'	1.86	0.57
25:CY:27:G:N1	25:CY:43:C:O2	2.38	0.57
26:DA:197:A:O2'	61:DA:3732:HOH:O	2.16	0.57
36:DP:44:GLY:CA	36:DP:45:LEU:HB2	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DR:67:LEU:HD13	38:DR:76:VAL:HG21	1.86	0.57
14:AN:3:ARG:HB3	14:AN:3:ARG:HH21	1.70	0.57
25:AY:59:U:H5'	25:AY:60:U:H5	1.70	0.57
37:BQ:135:ASP:OD2	46:BZ:49:ARG:NH2	2.38	0.57
1:CA:1086:U:H3	1:CA:1099:G:H22	1.53	0.57
2:CB:178:ARG:NE	8:CH:74:PRO:HG3	2.20	0.57
26:DA:2875:C:O2'	40:DT:2:ASN:OD1	2.21	0.57
32:DH:80:SER:OG	32:DH:81:GLU:OE1	2.17	0.57
46:DZ:45:ASP:OD1	46:DZ:49:ARG:NH1	2.31	0.57
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.38	0.56
26:BA:880:G:H2'	26:BA:881:G:H8	1.69	0.56
40:BT:112:ARG:HG3	40:BT:115:ARG:HH21	1.70	0.56
44:BX:43:VAL:HG21	44:BX:81:VAL:HG11	1.86	0.56
46:BZ:137:ILE:HA	46:BZ:156:LYS:HZ2	1.70	0.56
1:CA:1321:C:H4'	13:CM:87:TYR:CE2	2.40	0.56
19:CS:28:LYS:HB2	19:CS:29:ARG:HA	1.87	0.56
26:DA:2808:U:H2'	26:DA:2809:A:H5'	1.87	0.56
44:DX:31:HIS:CD2	44:DX:33:LYS:H	2.22	0.56
1:AA:977:A:N6	1:AA:1224:G:OP1	2.29	0.56
7:AG:22:LEU:HD11	7:AG:101:LEU:HD21	1.85	0.56
46:BZ:45:ASP:OD2	46:BZ:49:ARG:NH1	2.38	0.56
1:CA:953:G:H5'	1:CA:965:A:N6	2.20	0.56
3:CC:11:ARG:HB3	3:CC:15:THR:HB	1.87	0.56
25:CY:9:A:OP2	25:CY:13:C:N4	2.38	0.56
26:DA:1864:U:OP1	26:DA:2410:G:O2'	2.17	0.56
40:DT:53:ARG:HB3	40:DT:53:ARG:HH11	1.70	0.56
46:DZ:69:THR:HG22	46:DZ:90:VAL:HA	1.88	0.56
1:AA:333:G:H4'	20:AT:16:HIS:CE1	2.41	0.56
13:AM:23:TYR:HB3	13:AM:67:GLU:HA	1.87	0.56
46:BZ:137:ILE:HA	46:BZ:156:LYS:NZ	2.20	0.56
1:CA:426:G:OP1	4:CD:36:ARG:HD2	2.05	0.56
1:CA:923:A:O2'	1:CA:1399:C:OP2	2.21	0.56
1:CA:1154:G:N7	1:CA:1155:G:C8	2.73	0.56
1:CA:1502:A:H2	1:CA:1505:G:N1	1.99	0.56
3:CC:126:ARG:HB3	3:CC:128:PHE:CE1	2.40	0.56
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.87	0.56
23:CW:30:G:H1	23:CW:40:C:H42	1.51	0.56
26:DA:866:A:H2	26:DA:867:C:C4	2.23	0.56
26:DA:2167:U:H2'	26:DA:2168:G:H21	1.68	0.56
33:DI:110:ASP:N	33:DI:130:TYR:OH	2.34	0.56
1:AA:952:U:H2'	1:AA:953:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:17:PHE:HB2	2:AB:44:LEU:HD21	1.88	0.56
4:AD:155:LEU:HD22	4:AD:157:LEU:H	1.70	0.56
24:AX:8:4SU:O5'	24:AX:8:4SU:H6	2.05	0.56
26:BA:453:C:O2	26:BA:457:A:O2'	2.22	0.56
26:BA:1252:G:OP1	41:BU:36:ARG:NH2	2.39	0.56
44:BX:5:TYR:CZ	49:B2:30:ARG:HB2	2.40	0.56
1:CA:222:U:H2'	1:CA:223:U:C6	2.39	0.56
20:CT:63:ILE:HD13	20:CT:80:ARG:HB3	1.88	0.56
26:DA:1405:U:H2'	26:DA:1406:U:C6	2.40	0.56
27:DB:110:G:H2'	27:DB:111:G:H8	1.70	0.56
46:DZ:141:VAL:HG12	46:DZ:144:LEU:HD12	1.87	0.56
1:AA:96:U:O2'	1:AA:97:G:H8	1.88	0.56
13:AM:84:ILE:HD12	19:AS:74:PHE:HE2	1.70	0.56
33:BI:135:GLU:C	33:BI:137:PRO:HD3	2.31	0.56
46:BZ:111:VAL:HG21	46:BZ:117:LEU:HB2	1.88	0.56
9:CI:49:PRO:HG2	9:CI:81:ILE:HG23	1.87	0.56
26:DA:534:U:H2'	26:DA:535:C:C6	2.41	0.56
26:DA:1579:A:H2'	26:DA:1580:A:C8	2.41	0.56
26:DA:1805:U:O2	28:DD:50:THR:HB	2.05	0.56
5:AE:6:PHE:HB2	5:AE:34:VAL:HG22	1.88	0.56
26:BA:2708:G:H1'	38:BR:71:GLN:HE22	1.70	0.56
31:BG:16:ARG:HB2	31:BG:17:PRO:HD3	1.88	0.56
46:BZ:121:HIS:HB2	46:BZ:171:ILE:HG22	1.88	0.56
1:CA:9:G:H2'	1:CA:10:A:C8	2.41	0.56
1:CA:1392:G:N2	1:CA:1502:A:H8	2.03	0.56
8:CH:12:ARG:HD2	8:CH:26:VAL:HG12	1.88	0.56
12:CL:24:VAL:HG12	12:CL:27:LEU:HB2	1.88	0.56
26:DA:323:G:O2'	26:DA:1205:U:N3	2.35	0.56
26:DA:1507:A:O2'	26:DA:1508:A:O5'	2.20	0.56
26:DA:1639:U:H2'	26:DA:1640:C:H5''	1.88	0.56
31:DG:16:ARG:O	31:DG:20:ILE:HG13	2.05	0.56
1:AA:671:G:H5'	6:AF:77:ARG:HH22	1.70	0.56
1:AA:976:G:N2	1:AA:1363:C:OP2	2.38	0.56
26:BA:171:G:O2'	26:BA:172:C:H5'	2.06	0.56
26:BA:588:U:H2'	26:BA:589:C:C6	2.41	0.56
26:BA:668:G:H5'	26:BA:669:G:OP2	2.06	0.56
26:BA:2022:U:O2'	26:BA:2617:C:H5'	2.06	0.56
26:BA:2869:G:H2'	26:BA:2870:C:O4'	2.04	0.56
30:BF:161:GLU:HG2	30:BF:164:ARG:NH2	2.20	0.56
31:BG:41:GLN:HG3	31:BG:60:LEU:HD21	1.88	0.56
26:DA:125:G:O2'	54:D7:48:LYS:NZ	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:245:G:O6	55:D8:8:LYS:NZ	2.31	0.56
26:DA:912:C:OP1	37:DQ:8:LYS:NZ	2.25	0.56
26:DA:1787:A:N3	61:DA:3727:HOH:O	2.33	0.56
26:DA:2167:U:O2'	26:DA:2168:G:O4'	2.23	0.56
26:DA:2327:A:H2'	26:DA:2328:A:C8	2.41	0.56
45:DY:99:CYS:HB2	45:DY:106:LEU:HD21	1.88	0.56
1:AA:58:C:O2'	1:AA:388:G:N7	2.33	0.56
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.41	0.56
20:AT:9:ASN:HD22	20:AT:10:LEU:H	1.53	0.56
26:BA:71:A:OP2	26:BA:71:A:H3'	2.06	0.56
26:BA:2023:G:H5'	26:BA:2617:C:H4'	1.88	0.56
44:BX:35:THR:HG22	44:BX:38:GLU:HB2	1.87	0.56
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.06	0.56
21:CU:7:ARG:HD2	21:CU:21:TYR:HE2	1.69	0.56
28:DD:4:LYS:HB3	28:DD:18:VAL:HG23	1.88	0.56
45:DY:20:TYR:CE1	45:DY:43:ASN:HA	2.41	0.56
47:D0:17:GLN:O	47:D0:19:LYS:NZ	2.38	0.56
25:AY:7:A:O2'	25:AY:49:C:OP2	2.21	0.56
26:BA:2124:G:H1	26:BA:2174:C:N4	2.04	0.56
26:BA:2151:G:H2'	26:BA:2152:G:C8	2.41	0.56
31:BG:77:ILE:HG22	31:BG:80:PHE:H	1.69	0.56
44:BX:31:HIS:CD2	44:BX:33:LYS:H	2.24	0.56
1:CA:1047:G:H5''	14:CN:4:LYS:HD2	1.87	0.56
2:CB:219:VAL:HA	2:CB:222:ILE:HG12	1.88	0.56
8:CH:39:LEU:HD12	8:CH:44:PHE:HB2	1.88	0.56
10:CJ:47:PHE:N	10:CJ:63:PHE:O	2.33	0.56
26:DA:783:A:O2'	26:DA:785:G:OP1	2.24	0.56
26:DA:2138:C:H2'	26:DA:2139:C:H5''	1.87	0.56
1:AA:139:G:N2	1:AA:224:C:O2	2.35	0.56
4:AD:173:TRP:CZ3	4:AD:174:LEU:HG	2.41	0.56
26:BA:784:A:H5'	26:BA:785:G:OP1	2.06	0.56
26:BA:2646:C:OP2	26:BA:2732:G:O2'	2.19	0.56
26:DA:1265:A:OP2	61:DA:4004:HOH:O	2.18	0.56
32:DH:113:VAL:HG11	32:DH:151:ILE:HD13	1.87	0.56
34:DN:4:TYR:HB2	41:DU:101:ARG:NH1	2.21	0.56
1:AA:736:C:H2'	1:AA:737:A:H8	1.71	0.55
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.71	0.55
1:CA:1120:G:C6	1:CA:1121:U:C4	2.94	0.55
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.88	0.55
27:DB:28:C:OP2	39:DS:33:LYS:NZ	2.32	0.55
30:DF:21:ALA:CB	30:DF:22:ALA:HA	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DN:39:ARG:HE	34:DN:48:MET:HE3	1.72	0.55
1:AA:1392:G:H21	1:AA:1502:A:H8	1.54	0.55
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.53	0.55
4:AD:175:SER:HB3	4:AD:186:LEU:HD11	1.88	0.55
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.06	0.55
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.87	0.55
26:BA:592:G:O6	61:BA:4937:HOH:O	2.16	0.55
26:BA:1309:G:O6	61:BA:4912:HOH:O	2.17	0.55
33:BI:27:ARG:HD2	48:B1:71:TYR:CE1	2.41	0.55
1:CA:442:C:H42	1:CA:492:G:H1	1.53	0.55
1:CA:450:G:OP1	16:CP:43:LYS:NZ	2.38	0.55
2:CB:8:LYS:HG3	2:CB:9:GLU:HG3	1.87	0.55
24:CX:40:C:H2'	24:CX:41:C:H6	1.71	0.55
26:DA:1039:G:O6	26:DA:1116:C:N4	2.37	0.55
2:AB:231:GLU:HB3	2:AB:232:PRO:HD3	1.88	0.55
7:AG:16:LEU:HD11	9:AI:45:ALA:HB2	1.87	0.55
12:AL:24:VAL:HG13	12:AL:98:TYR:CE1	2.41	0.55
25:AY:19:G:H3'	25:AY:20:U:C6	2.41	0.55
26:BA:2238:G:H2'	26:BA:2238:G:N3	2.20	0.55
26:BA:2662:A:H2'	26:BA:2663:G:O4'	2.07	0.55
1:CA:572:A:HO2'	1:CA:916:G:HO2'	1.54	0.55
5:CE:50:GLU:HB2	5:CE:53:LEU:HD12	1.88	0.55
19:CS:28:LYS:HB2	19:CS:29:ARG:CA	2.36	0.55
26:DA:140:G:N2	26:DA:1596:A:H4'	2.21	0.55
26:DA:2135:A:H2'	26:DA:2136:C:C6	2.41	0.55
1:AA:442:C:H42	1:AA:492:G:H1	1.53	0.55
11:AK:34:ASP:OD1	11:AK:38:ASN:N	2.40	0.55
20:AT:9:ASN:ND2	20:AT:10:LEU:H	2.05	0.55
26:BA:2791:C:H2'	26:BA:2792:G:H8	1.71	0.55
30:BF:158:THR:O	30:BF:164:ARG:NH1	2.38	0.55
1:CA:1065:U:OP2	1:CA:1190:G:N2	2.39	0.55
3:CC:6:HIS:CD2	3:CC:8:ILE:H	2.23	0.55
9:CI:125:TYR:HD1	9:CI:126:SER:N	2.03	0.55
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.40	0.55
13:CM:65:LYS:HA	51:D4:50:VAL:HG11	1.87	0.55
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.41	0.55
26:DA:253:C:OP2	55:D8:5:LYS:NZ	2.30	0.55
26:DA:1378:A:OP1	54:D7:10:ARG:NH2	2.39	0.55
26:DA:2169:A:H2'	26:DA:2170:A:C8	2.41	0.55
33:DI:38:LEU:HB2	33:DI:40:THR:HG22	1.89	0.55
1:AA:1445:C:N3	1:AA:1457:G:N1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:222:A:H5''	26:BA:421:U:OP1	2.07	0.55
1:CA:1154:G:N7	1:CA:1155:G:N9	2.55	0.55
3:CC:33:LEU:HD21	14:CN:53:LEU:HD23	1.88	0.55
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.88	0.55
26:DA:320:A:OP2	30:DF:137:LYS:NZ	2.33	0.55
26:DA:859:G:N2	26:DA:917:A:OP2	2.39	0.55
26:DA:1239:G:H2'	26:DA:1240:U:O4'	2.06	0.55
26:DA:2400:G:H2'	26:DA:2401:U:H6	1.70	0.55
26:DA:2882:A:H5'	38:DR:96:ARG:HG3	1.87	0.55
46:DZ:111:VAL:HG21	46:DZ:117:LEU:HB2	1.88	0.55
1:AA:123:C:OP1	1:AA:311:C:O2'	2.20	0.55
26:BA:2110:G:C2	26:BA:2120:G:H1'	2.42	0.55
26:BA:2171:A:H1'	26:BA:2172:U:O4'	2.07	0.55
27:BB:91:C:H5'	37:BQ:18:LYS:HA	1.87	0.55
55:B8:62:LEU:HB3	55:B8:65:GLU:CG	2.36	0.55
1:CA:129(A):G:C6	1:CA:189(E):U:H4'	2.41	0.55
2:CB:48:MET:HA	2:CB:51:LEU:HB2	1.89	0.55
3:CC:22:TRP:CD2	3:CC:59:ARG:HD2	2.41	0.55
11:CK:24:SER:OG	11:CK:25:TYR:N	2.38	0.55
26:DA:84:A:H5''	45:DY:8:LYS:HE3	1.88	0.55
26:DA:833:U:O2	36:DP:55:ARG:NH2	2.37	0.55
26:DA:848:G:C2	26:DA:933:A:H1'	2.42	0.55
36:DP:121:LYS:HG2	36:DP:122:PRO:HD2	1.89	0.55
1:AA:353:A:H8	1:AA:353:A:H5'	1.72	0.55
1:AA:923:A:O2'	1:AA:1399:C:OP2	2.23	0.55
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.21	0.55
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.72	0.55
20:AT:65:LYS:HA	20:AT:68:LYS:HD3	1.88	0.55
26:BA:330:A:H2	26:BA:1210:A:HO2'	1.54	0.55
26:BA:1566:A:OP1	28:BD:211:ARG:NH1	2.40	0.55
33:BI:106:GLY:HA2	33:BI:107:VAL:O	2.06	0.55
1:CA:235:C:H5'	17:CQ:70:ARG:HG2	1.88	0.55
1:CA:1002:G:H1	1:CA:1038:C:H42	0.70	0.55
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.07	0.55
10:CJ:55:LYS:HG3	10:CJ:56:HIS:CD2	2.42	0.55
26:DA:994:C:O2'	26:DA:996:A:OP1	2.16	0.55
26:DA:1530:C:HO2'	26:DA:1531:C:P	2.29	0.55
26:DA:1803:A:H4'	28:DD:259:THR:HG23	1.89	0.55
27:DB:24:G:H4'	27:DB:25:A:C8	2.41	0.55
3:AC:13:GLY:HA3	14:AN:57:ARG:HH21	1.72	0.55
8:AH:51:VAL:HG11	8:AH:60:ARG:NH1	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:64:G:H4'	37:BQ:10:ARG:HH21	1.71	0.55
26:BA:898:C:H2'	26:BA:899:A:H8	1.70	0.55
1:CA:328:C:H4'	1:CA:329:A:H5'	1.89	0.55
1:CA:947:G:O3'	13:CM:109:THR:OG1	2.25	0.55
1:CA:1376:U:H2'	1:CA:1377:A:H8	1.70	0.55
2:CB:45:GLN:O	2:CB:49:GLU:HB2	2.06	0.55
26:DA:1796:U:H2'	26:DA:1797:C:C6	2.42	0.55
31:DG:179:PRO:HB2	51:D4:42:PHE:CE1	2.41	0.55
1:AA:1255:G:N7	10:AJ:43:ARG:NH2	2.55	0.55
1:AA:1290:G:H2'	1:AA:1291:G:H8	1.71	0.55
2:AB:16:HIS:O	2:AB:17:PHE:HD1	1.89	0.55
25:AY:50:U:N3	25:AY:64:A:C2	2.69	0.55
26:BA:2141:G:H1	26:BA:2149:G:N2	2.02	0.55
26:BA:2336:A:H61	47:B0:43:THR:HG22	1.71	0.55
36:BP:36:LYS:O	61:BP:306:HOH:O	2.18	0.55
39:BS:15:ARG:HE	39:BS:88:ASP:CG	2.14	0.55
1:CA:1023:G:C4	1:CA:1024:G:C8	2.94	0.55
1:CA:1035:A:H2'	1:CA:1036:G:H8	1.71	0.55
1:CA:1104:G:H4'	2:CB:111:ARG:NH1	2.22	0.55
4:CD:196:LEU:O	4:CD:198:VAL:N	2.36	0.55
26:DA:900:A:O2'	26:DA:901:A:OP1	2.24	0.55
30:DF:150:GLY:HA2	30:DF:172:TRP:CD2	2.41	0.55
34:DN:128:HIS:O	34:DN:131:GLN:NE2	2.40	0.55
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.88	0.55
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.06	0.55
35:BO:63:VAL:HG12	35:BO:106:LEU:HD11	1.88	0.55
7:CG:78:ARG:HB2	7:CG:156:TRP:HZ3	1.72	0.55
7:CG:91:VAL:HB	7:CG:96:GLN:HG2	1.88	0.55
26:DA:2349:G:OP1	61:DA:3781:HOH:O	2.18	0.55
41:DU:85:LYS:HB2	41:DU:116:ALA:HB1	1.89	0.55
1:AA:109:A:OP1	61:AA:4215:HOH:O	2.18	0.54
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.07	0.54
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.89	0.54
25:AY:33:U:H2'	25:AY:35:A:OP2	2.07	0.54
26:BA:1371:G:H2'	26:BA:1372:U:H5	1.70	0.54
1:CA:136:C:O2'	16:CP:63:GLY:O	2.24	0.54
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	1.89	0.54
25:CY:29:G:H1	25:CY:41:C:N4	2.05	0.54
26:DA:223:A:O2'	26:DA:420:C:O2	2.25	0.54
26:DA:1399:C:OP1	44:DX:25:LYS:NZ	2.40	0.54
26:DA:1467:C:C5	26:DA:1546:C:H2'	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:163:LEU:HG	46:DZ:165:VAL:HG22	1.88	0.54
1:AA:1179:A:O3'	9:AI:103:THR:HB	2.06	0.54
2:AB:109:SER:HA	2:AB:112:VAL:HG13	1.87	0.54
26:BA:1253:A:OP1	61:BA:4931:HOH:O	2.18	0.54
26:BA:1693:U:O2'	28:BD:14:ARG:NH2	2.40	0.54
26:BA:2532:G:O2'	26:BA:2657:A:N1	2.39	0.54
1:CA:419:C:OP1	1:CA:513:C:O2'	2.23	0.54
4:CD:98:GLU:HG2	4:CD:189:PRO:HG2	1.89	0.54
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.90	0.54
15:CO:5:LYS:HD3	15:CO:5:LYS:N	2.23	0.54
16:CP:8:ARG:HG3	16:CP:17:TYR:CE1	2.42	0.54
25:CY:39:PSU:C2	25:CY:40:C:C2	2.95	0.54
26:DA:191:A:N1	61:DA:4228:HOH:O	2.34	0.54
26:DA:637:A:H2'	36:DP:117:GLU:OE2	2.08	0.54
26:DA:1014:U:H2'	26:DA:1015:G:H8	1.72	0.54
26:DA:1300:U:H4'	26:DA:1301:A:C5'	2.37	0.54
26:DA:2150:U:H2'	26:DA:2151:G:C8	2.41	0.54
26:DA:2155:G:H2'	26:DA:2156:G:H5'	1.89	0.54
30:DF:150:GLY:HA2	30:DF:172:TRP:CE3	2.42	0.54
39:DS:93:LYS:HD3	39:DS:94:TYR:N	2.22	0.54
48:D1:54:ALA:HB1	48:D1:83:GLU:HG3	1.88	0.54
1:AA:103:C:O2'	1:AA:172:A:N1	2.34	0.54
1:AA:501:C:H2'	1:AA:502:G:C8	2.43	0.54
1:AA:1007:C:N3	1:AA:1022:G:O6	2.41	0.54
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.31	0.54
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.42	0.54
2:AB:20:GLU:HA	2:AB:21:ARG:NH2	2.22	0.54
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.89	0.54
7:AG:152:ALA:HB1	7:AG:155:ARG:HH21	1.72	0.54
26:BA:69:C:O2	26:BA:73:A:O2'	2.23	0.54
26:BA:226:G:H21	26:BA:228:A:H62	1.54	0.54
26:BA:404:C:H4'	26:BA:405:U:H5'	1.89	0.54
26:BA:2180:U:H2'	26:BA:2181:G:O4'	2.08	0.54
39:BS:34:HIS:ND1	39:BS:53:SER:OG	2.36	0.54
43:BW:25:ARG:NH2	43:BW:74:ALA:O	2.35	0.54
46:BZ:4:ARG:NE	46:BZ:60:GLU:OE1	2.28	0.54
26:DA:276:A:H5''	26:DA:277:C:H5'	1.88	0.54
26:DA:586:A:N1	26:DA:809:G:O2'	2.35	0.54
26:DA:2136:C:O2'	26:DA:2137:C:O5'	2.25	0.54
26:DA:2612:C:OP2	52:D5:2:ALA:N	2.41	0.54
26:DA:2753:A:N3	56:D9:15:LYS:NZ	2.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:DG:23:PHE:HB2	31:DG:25:TYR:CZ	2.42	0.54
1:AA:890:G:O2'	1:AA:906:G:O6	2.24	0.54
25:AY:51:U:H3	25:AY:63:G:H1	1.55	0.54
26:BA:1113:U:H2'	26:BA:1114:G:C8	2.41	0.54
26:BA:2129:C:H2'	26:BA:2130:U:C6	2.42	0.54
26:BA:2445:G:OP1	30:BF:74:ARG:NH2	2.38	0.54
29:BE:55:ASN:HB3	29:BE:58:ARG:HG3	1.88	0.54
1:CA:859:A:OP2	1:CA:869:G:N1	2.34	0.54
1:CA:1378:C:H5	1:CA:1379:G:C4	2.25	0.54
1:CA:1495:U:O2'	26:DA:1919:A:N1	2.31	0.54
3:CC:20:SER:OG	3:CC:22:TRP:NE1	2.40	0.54
4:CD:60:GLU:HG2	4:CD:202:LEU:HB2	1.90	0.54
26:DA:300:A:P	45:DY:86:ARG:HH22	2.30	0.54
26:DA:796:C:H2'	26:DA:797:C:C6	2.42	0.54
26:DA:2733:A:N1	29:DE:203:LYS:HA	2.23	0.54
40:DT:24:PRO:HA	40:DT:49:VAL:HG22	1.89	0.54
1:AA:576:G:O6	1:AA:880:C:O2'	2.25	0.54
1:AA:848:C:H2'	1:AA:849:C:C6	2.43	0.54
1:AA:1033:G:H2'	1:AA:1034:G:H8	1.72	0.54
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.24	0.54
2:AB:105:PHE:CE1	2:AB:155:LEU:HD12	2.43	0.54
3:AC:104:GLN:HE21	3:AC:105:GLU:N	2.05	0.54
5:AE:91:LEU:HB3	5:AE:118:ILE:HD11	1.89	0.54
5:AE:140:ARG:O	5:AE:143:ARG:NH2	2.41	0.54
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.41	0.54
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.06	0.54
26:BA:1721:G:H3'	26:BA:1722:A:H5''	1.88	0.54
26:BA:2116:G:N1	26:BA:2162:G:OP1	2.41	0.54
26:DA:641:C:H42	26:DA:647:G:H1	1.56	0.54
32:DH:56:SER:OG	32:DH:57:ASP:N	2.41	0.54
1:AA:1292:U:H5'	9:AI:38:GLN:NE2	2.22	0.54
3:AC:150:LYS:HB2	3:AC:173:VAL:HG21	1.88	0.54
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.90	0.54
23:AW:52:G:H4'	37:BQ:56:ARG:NH2	2.22	0.54
25:AY:67:C:H2'	25:AY:68:C:O4'	2.08	0.54
26:BA:1971:A:N1	61:BA:4352:HOH:O	2.33	0.54
29:BE:174:ASP:OD1	29:BE:175:VAL:N	2.40	0.54
36:BP:100:LEU:HD12	36:BP:112:LEU:HD11	1.90	0.54
1:CA:701:C:OP1	1:CA:702:A:O2'	2.14	0.54
1:CA:1301:U:O2'	1:CA:1302:U:H5'	2.08	0.54
2:CB:61:LEU:HD23	2:CB:68:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CD:57:ARG:HH22	5:CE:107:ARG:HD3	1.72	0.54
6:CF:46:ARG:HG3	6:CF:47:ARG:N	2.21	0.54
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.88	0.54
18:CR:61:LYS:O	18:CR:65:ILE:HG12	2.07	0.54
26:DA:1183:G:H5'	50:D3:30:ARG:HH12	1.73	0.54
33:DI:14:ASP:OD1	33:DI:15:VAL:N	2.38	0.54
1:AA:45:U:H2'	1:AA:46:G:C8	2.42	0.54
1:AA:171:A:H2'	1:AA:172:A:C8	2.42	0.54
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	1.88	0.54
19:AS:67:VAL:HG21	51:B4:59:PHE:HB3	1.88	0.54
24:AX:19:G:H4'	24:AX:20:U:OP2	2.06	0.54
26:BA:443:A:H1'	26:BA:1201:C:O4'	2.07	0.54
26:BA:2327:A:H2'	26:BA:2328:A:C8	2.42	0.54
1:CA:1003:G:N2	1:CA:1025:U:O4	2.40	0.54
3:CC:6:HIS:CG	14:CN:49:HIS:HB3	2.43	0.54
24:CX:58:A:H4'	24:CX:59:A:OP1	2.08	0.54
26:DA:252:G:P	36:DP:50:ARG:HH12	2.31	0.54
26:DA:855:G:H2'	26:DA:856:C:C6	2.43	0.54
26:DA:1527:G:HO2'	26:DA:1544:A:H62	1.56	0.54
26:DA:2206:G:H3'	26:DA:2207:G:N7	2.23	0.54
1:AA:524:G:H2'	1:AA:525:C:C6	2.43	0.54
1:AA:539:A:H2'	1:AA:540:G:C8	2.43	0.54
1:AA:934:C:OP1	61:AA:4110:HOH:O	2.18	0.54
1:AA:1347:G:N2	1:AA:1373:G:H2'	2.23	0.54
4:AD:188:LEU:HD23	4:AD:188:LEU:H	1.73	0.54
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.40	0.54
26:BA:271(E):U:H2'	26:BA:271(F):C:C6	2.43	0.54
26:BA:784:A:C6	28:BD:229:VAL:HG11	2.43	0.54
26:BA:2243:U:OP1	61:BA:4017:HOH:O	2.17	0.54
1:CA:399:G:H2'	1:CA:400:C:C6	2.43	0.54
1:CA:441:A:H3'	1:CA:442:C:C6	2.43	0.54
3:CC:29:TYR:OH	14:CN:54:PRO:O	2.20	0.54
26:DA:879:G:H3'	26:DA:880:G:H8	1.72	0.54
26:DA:971:C:OP2	61:DA:4647:HOH:O	2.18	0.54
26:DA:1153:C:H2'	26:DA:1154:G:O4'	2.07	0.54
26:DA:2591:C:OP1	28:DD:239:ARG:HD2	2.08	0.54
28:DD:3:VAL:HG13	28:DD:17:THR:HB	1.89	0.54
31:DG:48:GLU:O	31:DG:51:ARG:HG3	2.07	0.54
42:DV:35:LEU:HB2	42:DV:57:VAL:HG23	1.90	0.54
1:AA:222:U:H2'	1:AA:223:U:C6	2.43	0.54
1:AA:316:G:OP2	1:AA:351:G:O2'	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:11:ARG:NH2	3:AC:177:THR:O	2.41	0.54
3:AC:58:GLU:HB3	10:AJ:92:THR:HG21	1.89	0.54
23:AW:9:A:O2'	23:AW:10:G:N7	2.40	0.54
26:BA:272:G:O2'	26:BA:421:U:OP2	2.22	0.54
26:BA:887:A:H4'	26:BA:888:C:C5	2.43	0.54
26:BA:1174:A:H1'	26:BA:1175:U:H5''	1.89	0.54
26:BA:1796:U:H2'	26:BA:1797:C:C6	2.43	0.54
1:CA:428:G:OP2	4:CD:10:ARG:NH1	2.41	0.54
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.08	0.54
1:CA:1490:C:H2'	1:CA:1491:G:H8	1.72	0.54
3:CC:55:VAL:HG22	3:CC:68:VAL:HG22	1.88	0.54
3:CC:157:ILE:HD12	3:CC:164:ARG:HB3	1.90	0.54
26:DA:391:G:O2'	26:DA:410:G:OP1	2.19	0.54
26:DA:1013:C:H2'	26:DA:1014:U:C6	2.43	0.54
1:AA:26:A:N6	1:AA:558:G:O2'	2.39	0.54
1:AA:880:C:OP1	12:AL:8:ASN:ND2	2.39	0.54
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.41	0.54
25:AY:6:G:O6	25:AY:7:A:N6	2.40	0.54
26:BA:271(H):G:O2'	26:BA:271(I):G:H8	1.90	0.54
26:BA:1470:G:N2	26:BA:1520:G:OP2	2.34	0.54
26:BA:2630:G:H2'	26:BA:2631:G:C8	2.43	0.54
36:BP:97:PRO:HD3	36:BP:126:VAL:O	2.08	0.54
1:CA:59:A:H5''	1:CA:60:A:H5''	1.89	0.54
1:CA:411:A:OP1	4:CD:30:LYS:NZ	2.40	0.54
2:CB:16:HIS:CB	2:CB:210:SER:HB2	2.28	0.54
13:CM:64:TRP:HB2	13:CM:66:LEU:HD21	1.89	0.54
26:DA:2102:U:H3	26:DA:2187:G:H1	1.56	0.54
26:DA:2182:G:H2'	26:DA:2183:C:C6	2.42	0.54
26:DA:2723:C:OP2	29:DE:109:LYS:NZ	2.41	0.54
1:AA:940:C:OP1	7:AG:29:LYS:NZ	2.41	0.53
1:AA:1005:A:H1'	1:AA:1036:G:N2	2.23	0.53
9:AI:17:VAL:HG11	9:AI:81:ILE:HA	1.90	0.53
25:AY:9:A:H5''	25:AY:46:7MG:N2	2.23	0.53
26:BA:2693:A:H2'	26:BA:2694:G:H8	1.72	0.53
54:B7:24:THR:CG2	54:B7:27:GLY:H	2.20	0.53
1:CA:93:G:O2'	1:CA:96:U:H5'	2.08	0.53
1:CA:299:G:H2'	1:CA:300:A:C8	2.43	0.53
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.43	0.53
1:CA:1206:G:O4'	3:CC:194:GLY:HA2	2.08	0.53
2:CB:15:VAL:HG12	2:CB:16:HIS:H	1.73	0.53
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.89	0.53
18:CR:58:LEU:HB3	18:CR:62:GLU:HG3	1.89	0.53
19:CS:49:ILE:HD13	19:CS:62:ILE:HD13	1.90	0.53
23:CW:66:U:C3'	23:CW:67:C:H5''	2.32	0.53
26:DA:203:C:OP2	61:DA:4309:HOH:O	2.19	0.53
26:DA:625:G:O6	36:DP:107:LYS:NZ	2.36	0.53
45:DY:28:LYS:HD2	45:DY:40:GLU:HG3	1.89	0.53
1:AA:159:G:N2	1:AA:162:A:OP2	2.37	0.53
26:BA:1406:U:H2'	26:BA:1407:C:C6	2.44	0.53
26:BA:2142:C:H2'	26:BA:2143:C:C6	2.43	0.53
26:BA:2441:C:OP2	26:BA:2586:C:O2'	2.26	0.53
37:BQ:85:LYS:HB2	47:B0:7:LEU:HD12	1.91	0.53
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.90	0.53
1:CA:1011:G:C6	1:CA:1012:U:C2	2.97	0.53
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.43	0.53
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.23	0.53
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.72	0.53
26:DA:500:G:N1	26:DA:503:A:OP2	2.40	0.53
29:DE:174:ASP:OD1	29:DE:175:VAL:N	2.40	0.53
33:DI:27:ARG:HD2	48:D1:71:TYR:CE1	2.43	0.53
1:AA:1191:A:H5''	3:AC:4:LYS:NZ	2.23	0.53
2:AB:204:ASN:OD1	2:AB:206:ASP:N	2.29	0.53
10:AJ:13:HIS:O	10:AJ:17:ASP:HB2	2.09	0.53
12:AL:32:PHE:HB3	12:AL:84:LEU:HD11	1.89	0.53
19:AS:65:ASN:ND2	19:AS:66:MET:HG2	2.23	0.53
38:BR:44:LEU:HD22	38:BR:48:VAL:HG23	1.90	0.53
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.74	0.53
2:CB:95:GLN:HG3	2:CB:148:TYR:HA	1.90	0.53
4:CD:61:LYS:HD2	4:CD:206:PHE:CE2	2.43	0.53
5:CE:92:LYS:HB3	5:CE:119:LEU:HB2	1.90	0.53
26:DA:957:A:H5'	37:DQ:76:LYS:HG3	1.90	0.53
26:DA:1021:A:H3'	26:DA:1021:A:H8	1.72	0.53
27:DB:90:A:C5	27:DB:91:C:H1'	2.44	0.53
36:DP:121:LYS:O	36:DP:123:LEU:N	2.40	0.53
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.24	0.53
13:AM:80:ARG:HH22	19:AS:69:HIS:CE1	2.25	0.53
17:AQ:95:TYR:HA	17:AQ:98:LEU:HD22	1.89	0.53
26:BA:910:A:H62	37:BQ:12:GLN:HA	1.73	0.53
26:BA:2115:G:H21	26:BA:2171:A:H61	1.57	0.53
28:BD:132:PRO:HD3	28:BD:190:TYR:CZ	2.44	0.53
51:B4:15:ILE:O	51:B4:33:VAL:N	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:382:A:H2'	1:CA:383:A:C8	2.43	0.53
1:CA:1272:G:C2	1:CA:1273:G:H1'	2.43	0.53
2:CB:186:ALA:O	2:CB:201:ILE:N	2.40	0.53
3:CC:125:GLU:OE2	3:CC:125:GLU:N	2.36	0.53
7:CG:26:PHE:CE1	7:CG:30:ILE:HD11	2.44	0.53
8:CH:86:ILE:HG13	8:CH:133:LEU:HD22	1.91	0.53
23:CW:8:4SU:H1'	23:CW:48:C:H1'	1.89	0.53
23:CW:27:G:H1	23:CW:43:C:N4	2.03	0.53
26:DA:1203:G:O2'	26:DA:1242:A:N6	2.39	0.53
29:DE:36:ARG:HD3	29:DE:85:ASN:HD21	1.73	0.53
51:D4:59:PHE:HA	51:D4:61:ARG:N	2.23	0.53
1:AA:198:G:O6	1:AA:219:C:N4	2.42	0.53
1:AA:346:G:OP1	40:BT:41:ARG:NH2	2.41	0.53
1:AA:715:A:H2'	1:AA:716:A:C8	2.44	0.53
26:BA:2537:U:H2'	26:BA:2538:C:C6	2.44	0.53
26:BA:2557:G:H2'	26:BA:2558:C:C6	2.44	0.53
33:BI:61:ARG:HH11	33:BI:61:ARG:HA	1.73	0.53
36:BP:42:SER:O	61:BP:305:HOH:O	2.18	0.53
1:CA:543:C:OP1	4:CD:14:ARG:NE	2.36	0.53
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.74	0.53
3:CC:155:GLY:HA3	3:CC:196:LEU:HD13	1.90	0.53
13:CM:22:ILE:HG23	13:CM:67:GLU:HG2	1.91	0.53
26:DA:1266:G:O5'	43:DW:15:ARG:NH2	2.41	0.53
26:DA:2070:G:OP2	61:DA:4495:HOH:O	2.18	0.53
27:DB:95:C:H2'	27:DB:96:U:C6	2.44	0.53
39:DS:67:ARG:HG3	39:DS:104:GLY:HA3	1.90	0.53
47:D0:27:GLU:HG3	47:D0:68:GLU:HA	1.91	0.53
1:AA:69:G:H2'	1:AA:70:G:H8	1.74	0.53
1:AA:848:C:H2'	1:AA:849:C:H6	1.74	0.53
1:AA:1112:C:O2	3:AC:179:ARG:HG3	2.09	0.53
3:AC:19:GLU:HB3	3:AC:40:ARG:NH2	2.23	0.53
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.09	0.53
23:AW:18:G:H4'	23:AW:60:U:C5	2.43	0.53
25:AY:49:C:H42	25:AY:65:G:H1	0.68	0.53
26:BA:548:A:H61	42:BV:19:LYS:H	1.56	0.53
26:BA:2693:A:H2'	26:BA:2694:G:C8	2.44	0.53
29:BE:31:CYS:HB3	29:BE:49:LEU:HG	1.90	0.53
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.24	0.53
26:DA:922:U:H2'	26:DA:923:C:C6	2.43	0.53
31:DG:106:LEU:HA	31:DG:110:ALA:HB3	1.90	0.53
35:DO:16:ALA:HB2	35:DO:52:VAL:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.08	0.53
26:BA:1778:U:H2'	26:BA:1784:A:N6	2.23	0.53
26:BA:2116:G:H2'	26:BA:2117:A:C6	2.44	0.53
26:BA:2137:C:H2'	26:BA:2138:C:C6	2.43	0.53
26:BA:2690:C:OP1	38:BR:17:ARG:NH1	2.33	0.53
46:BZ:111:VAL:C	46:BZ:113:ALA:H	2.17	0.53
1:CA:895:G:N7	61:CA:4069:HOH:O	2.34	0.53
1:CA:1120:G:C6	1:CA:1154:G:C2	2.96	0.53
2:CB:46:LYS:O	2:CB:50:GLU:N	2.42	0.53
26:DA:644:A:H4'	26:DA:645:C:C5	2.43	0.53
26:DA:1364:G:OP2	48:D1:3:LYS:HG3	2.09	0.53
26:DA:1423:G:OP1	26:DA:1492:G:O2'	2.26	0.53
26:DA:1658:C:OP1	61:DA:4209:HOH:O	2.18	0.53
26:DA:2177:C:H2'	26:DA:2178:C:O4'	2.08	0.53
26:DA:2630:G:H2'	26:DA:2631:G:H8	1.74	0.53
42:DV:24:LYS:HG3	42:DV:64:HIS:HD2	1.73	0.53
1:AA:946:A:H2'	1:AA:947:G:C8	2.43	0.53
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.44	0.53
4:AD:15:GLU:CG	4:AD:63:LYS:HB3	2.39	0.53
12:AL:39:VAL:HG11	12:AL:41:ARG:NH1	2.24	0.53
23:AW:1:G:H2'	23:AW:2:C:C6	2.44	0.53
23:AW:9:A:H1'	23:AW:45:U:O2'	2.09	0.53
26:BA:2115:G:N2	26:BA:2171:A:H61	2.06	0.53
46:BZ:126:VAL:HG11	46:BZ:161:VAL:HG23	1.89	0.53
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.27	0.53
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.90	0.53
8:CH:30:ARG:O	8:CH:34:GLU:HG2	2.08	0.53
23:CW:75:C:H2'	23:CW:76:31M:C4	2.39	0.53
26:DA:875:G:O2'	46:DZ:151:HIS:HE1	1.92	0.53
39:DS:11:LYS:O	39:DS:15:ARG:HG3	2.08	0.53
1:AA:270:A:H2'	1:AA:271:C:C6	2.44	0.53
1:AA:520:A:N1	1:AA:536:C:H1'	2.23	0.53
2:AB:76:GLN:CD	2:AB:76:GLN:H	2.16	0.53
6:AF:9:VAL:HB	6:AF:87:ARG:HB2	1.90	0.53
24:AX:7:G:H1	24:AX:66:C:H42	1.56	0.53
29:BE:12:THR:HG22	29:BE:13:ARG:H	1.73	0.53
26:DA:144:C:H2'	26:DA:145:G:H8	1.73	0.53
26:DA:1379:A:H4'	26:DA:1380:G:OP2	2.07	0.53
26:DA:1420:U:O2'	26:DA:1421:G:OP1	2.25	0.53
39:DS:87:PHE:CZ	39:DS:102:ALA:HB2	2.44	0.53
1:AA:97:G:O2'	1:AA:98:G:H5''	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:262:A:H2'	1:AA:263:A:C8	2.44	0.53
6:AF:69:GLU:CD	6:AF:69:GLU:H	2.16	0.53
26:BA:639:U:H2'	26:BA:640:C:C6	2.44	0.53
33:BI:40:THR:O	33:BI:44:LEU:HB2	2.09	0.53
46:BZ:111:VAL:HG12	46:BZ:112:ARG:H	1.73	0.53
1:CA:1122:U:C4	1:CA:1123:A:N7	2.76	0.53
1:CA:1125:U:C3'	1:CA:1126:U:H5''	2.38	0.53
5:CE:6:PHE:HB3	5:CE:35:GLY:C	2.34	0.53
6:CF:69:GLU:CD	6:CF:69:GLU:H	2.17	0.53
17:CQ:12:SER:HB3	17:CQ:20:THR:HB	1.89	0.53
26:DA:1415:U:O2'	26:DA:1417:C:OP1	2.25	0.53
26:DA:1532:C:N4	26:DA:1537:G:O6	2.20	0.53
26:DA:2112:G:N7	26:DA:2169:A:N6	2.57	0.53
46:DZ:53:ILE:HD13	46:DZ:99:TYR:HB2	1.91	0.53
1:AA:942:G:H21	9:AI:124:GLN:NE2	2.08	0.52
26:BA:252:G:OP1	36:BP:50:ARG:NH1	2.42	0.52
28:BD:10:THR:OG1	28:BD:13:ARG:HB2	2.08	0.52
49:B2:11:GLU:O	49:B2:15:LYS:HG3	2.09	0.52
1:CA:437:U:H5'	4:CD:155:LEU:HD21	1.91	0.52
1:CA:620:C:C2	4:CD:135:LEU:HG	2.43	0.52
1:CA:1125:U:O2	10:CJ:38:ILE:HG21	2.09	0.52
2:CB:91:PRO:HD3	2:CB:154:LEU:HD12	1.91	0.52
3:CC:54:ARG:HH11	3:CC:54:ARG:HB3	1.74	0.52
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.45	0.52
16:CP:52:ASP:O	16:CP:54:GLU:N	2.33	0.52
26:DA:857:C:H4'	47:D0:23:VAL:HG21	1.91	0.52
26:DA:878:A:N6	26:DA:899:A:O2'	2.43	0.52
26:DA:2646:C:H2'	26:DA:2647:U:O4'	2.09	0.52
26:DA:2684:U:O2'	35:DO:68:GLU:OE1	2.28	0.52
28:DD:85:ASP:OD2	28:DD:88:ARG:NH1	2.40	0.52
1:AA:167:G:H2'	1:AA:168:G:H8	1.75	0.52
24:AX:56:C:O5'	24:AX:56:C:H6	1.92	0.52
25:AY:67:C:H2'	25:AY:68:C:C6	2.44	0.52
26:BA:330:A:H2	26:BA:1210:A:O2'	1.92	0.52
26:BA:1359:A:H2'	26:BA:1360:A:H5'	1.91	0.52
32:BH:159:GLU:HG3	32:BH:169:VAL:HG11	1.91	0.52
1:CA:164:U:H2'	1:CA:165:C:C6	2.44	0.52
1:CA:1119:C:N3	1:CA:1154:G:O6	2.42	0.52
1:CA:1125:U:C2	10:CJ:38:ILE:HD13	2.44	0.52
1:CA:1260:C:O5'	1:CA:1284:C:H4'	2.09	0.52
26:DA:1790:C:H5''	26:DA:1791:A:OP1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2180:U:H2'	26:DA:2181:G:O4'	2.09	0.52
1:AA:67:C:H2'	1:AA:68:G:C8	2.44	0.52
1:AA:1027:C:N3	1:AA:1028:C:N4	2.57	0.52
3:AC:22:TRP:CZ2	14:AN:54:PRO:HG3	2.44	0.52
3:AC:152:ILE:HB	3:AC:199:LYS:HB2	1.91	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:CD1	2.39	0.52
17:AQ:56:VAL:HB	17:AQ:78:GLU:HB3	1.91	0.52
20:AT:16:HIS:O	20:AT:19:SER:OG	2.25	0.52
34:BN:21:LYS:HE3	34:BN:140:VAL:OXT	2.09	0.52
50:B3:50:VAL:HB	50:B3:53:LEU:HD12	1.90	0.52
1:CA:625:G:H2'	1:CA:626:U:H6	1.74	0.52
1:CA:1278:U:H5'	1:CA:1279:A:O4'	2.08	0.52
3:CC:3:ASN:OD1	3:CC:3:ASN:N	2.42	0.52
26:DA:1188:U:H4'	42:DV:79:VAL:HG22	1.91	0.52
30:DF:120:GLU:HB2	30:DF:122:LYS:HG2	1.90	0.52
34:DN:67:LEU:O	34:DN:88:GLU:HG3	2.10	0.52
40:DT:11:GLU:O	40:DT:15:VAL:HG23	2.10	0.52
1:AA:1053:G:C3'	1:AA:1054:C:H5'	2.39	0.52
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.92	0.52
12:AL:24:VAL:HG13	12:AL:98:TYR:HE1	1.73	0.52
26:BA:1429:G:H2'	26:BA:1430:C:C6	2.44	0.52
26:BA:1482:G:O6	26:BA:1507:A:N6	2.42	0.52
26:BA:1843:C:H5'	28:BD:253:GLN:HE22	1.74	0.52
27:BB:7:G:H8	27:BB:7:G:H5''	1.75	0.52
28:BD:108:PRO:HB3	28:BD:143:HIS:CE1	2.45	0.52
31:BG:179:PRO:HG3	51:B4:43:TYR:OH	2.10	0.52
32:BH:56:SER:OG	32:BH:57:ASP:N	2.42	0.52
37:BQ:54:MET:HG3	37:BQ:117:ALA:HB1	1.92	0.52
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.42	0.52
1:CA:1158:C:O3'	2:CB:133:LYS:NZ	2.43	0.52
3:CC:111:LEU:HD22	3:CC:146:ALA:HB2	1.92	0.52
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.44	0.52
26:DA:1021:A:H3'	26:DA:1021:A:C8	2.45	0.52
26:DA:2176:A:H2'	26:DA:2177:C:C5	2.44	0.52
26:DA:2748:A:H5'	32:DH:4:ILE:HD12	1.92	0.52
26:DA:2803:C:H2'	26:DA:2804:C:H6	1.74	0.52
28:DD:276:LYS:HD3	28:DD:276:LYS:H	1.74	0.52
33:DI:40:THR:O	33:DI:44:LEU:HB2	2.09	0.52
44:DX:11:PRO:HB3	44:DX:92:LEU:HD11	1.90	0.52
44:DX:44:GLU:O	44:DX:48:LYS:N	2.42	0.52
55:D8:6:THR:HG22	55:D8:63:PRO:HD2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.45	0.52
23:AW:1:G:O6	23:AW:72:C:N3	2.42	0.52
26:BA:1187:G:H5''	42:BV:81:TYR:CE1	2.43	0.52
26:BA:1750:G:O2'	26:BA:2860:A:N1	2.38	0.52
26:BA:2136:C:N4	26:BA:2155:G:N1	2.32	0.52
36:BP:49:ARG:NH1	55:B8:61:LEU:HD23	2.24	0.52
1:CA:1243:C:H42	1:CA:1294:G:H1	1.58	0.52
1:CA:1490:C:H2'	1:CA:1491:G:C8	2.44	0.52
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.41	0.52
26:DA:77:C:O2'	49:D2:14:ARG:NH2	2.42	0.52
26:DA:1839:G:C8	26:DA:1927:A:H1'	2.44	0.52
36:DP:95:VAL:HG13	36:DP:125:VAL:HA	1.91	0.52
45:DY:5:MET:HE1	45:DY:32:PRO:HA	1.92	0.52
50:D3:13:ILE:O	61:D3:3101:HOH:O	2.19	0.52
1:AA:685:G:N2	1:AA:704:A:OP2	2.33	0.52
1:AA:1131:G:H2'	1:AA:1132:C:H6	1.74	0.52
1:AA:1320:C:OP1	19:AS:70:LYS:HE3	2.09	0.52
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.43	0.52
1:AA:1464:G:OP2	40:BT:111:ARG:NH2	2.43	0.52
1:AA:1530:G:H2'	1:AA:1531:A:O4'	2.09	0.52
4:AD:79:PHE:HE1	4:AD:204:ILE:HD13	1.75	0.52
7:AG:49:ILE:O	7:AG:53:LYS:HG3	2.10	0.52
24:AX:4:G:H2'	24:AX:5:G:C8	2.44	0.52
26:BA:141:A:H8	26:BA:1408:C:HO2'	1.54	0.52
26:BA:957:A:N1	26:BA:2458:G:H4'	2.25	0.52
1:CA:876:G:O5'	8:CH:14:ARG:NH1	2.43	0.52
1:CA:1469:G:N7	61:CA:4124:HOH:O	2.34	0.52
2:CB:141:GLU:O	2:CB:145:LEU:HG	2.09	0.52
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.10	0.52
15:CO:39:LEU:HD13	15:CO:56:LEU:HB2	1.91	0.52
25:CY:61:C:H2'	25:CY:62:C:C6	2.45	0.52
26:DA:821:A:N1	61:DA:4093:HOH:O	2.34	0.52
26:DA:1899:G:O2'	26:DA:1900:A:OP2	2.24	0.52
41:DU:81:HIS:HB3	41:DU:117:GLN:HE22	1.74	0.52
1:AA:838:G:H2'	1:AA:839:U:H2'	1.92	0.52
4:AD:107:ARG:HH22	4:AD:194:LEU:HD21	1.74	0.52
6:AF:22:GLU:OE2	6:AF:82:ARG:HG2	2.10	0.52
26:BA:1803:A:O2'	28:BD:259:THR:HG21	2.09	0.52
26:BA:2243:U:H2'	26:BA:2244:U:C6	2.45	0.52
39:BS:106:ARG:O	39:BS:109:GLY:N	2.40	0.52
1:CA:189(L):G:H2'	1:CA:190:U:H6	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:296:U:O2'	1:CA:556:C:O2	2.27	0.52
1:CA:1075:C:C2'	1:CA:1076:C:H5''	2.40	0.52
1:CA:1154:G:N7	1:CA:1155:G:C4	2.78	0.52
2:CB:53:ARG:HB3	2:CB:53:ARG:NH1	2.25	0.52
5:CE:6:PHE:HB2	5:CE:34:VAL:HG22	1.91	0.52
7:CG:28:ASN:HA	7:CG:31:MET:HE2	1.92	0.52
8:CH:49:GLU:HG2	8:CH:62:TYR:HE1	1.75	0.52
17:CQ:5:VAL:HG22	17:CQ:60:ILE:HG12	1.91	0.52
20:CT:43:LEU:O	20:CT:47:GLY:N	2.42	0.52
26:DA:593:G:H4'	55:D8:4:MET:HE2	1.92	0.52
26:DA:2171:A:C4	26:DA:2172:U:C4	2.98	0.52
31:DG:17:PRO:HA	31:DG:20:ILE:HD12	1.92	0.52
1:AA:346:G:H3'	1:AA:347:G:H4'	1.92	0.52
1:AA:649:G:H2'	1:AA:650:G:H8	1.74	0.52
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.91	0.52
4:AD:155:LEU:HB3	4:AD:158:ILE:HD11	1.92	0.52
11:AK:15:ALA:HA	11:AK:76:GLY:O	2.09	0.52
26:BA:2051:A:H5'	26:BA:2578:G:O4'	2.10	0.52
26:BA:2747:G:O6	26:BA:2755:C:H5''	2.10	0.52
1:CA:1070:U:H2'	1:CA:1071:C:H6	1.75	0.52
3:CC:126:ARG:HB3	3:CC:128:PHE:HE1	1.75	0.52
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.43	0.52
9:CI:15:ALA:HB2	9:CI:65:VAL:HG23	1.91	0.52
13:CM:121:LYS:H	13:CM:121:LYS:HZ1	1.56	0.52
14:CN:32:SER:O	14:CN:32:SER:OG	2.19	0.52
26:DA:657:U:H2'	26:DA:658:C:C6	2.44	0.52
26:DA:2203:U:H2'	26:DA:2205:C:C6	2.45	0.52
31:DG:68:PRO:HB3	31:DG:92:VAL:HB	1.92	0.52
36:DP:44:GLY:HA3	36:DP:45:LEU:HB2	1.92	0.52
51:D4:1:MET:HE2	51:D4:6:HIS:CD2	2.44	0.52
1:AA:428:G:H4'	1:AA:429:U:O5'	2.10	0.52
20:AT:14:LYS:HG3	20:AT:17:ARG:NH2	2.25	0.52
25:AY:5:G:H1'	25:AY:69:G:N2	2.25	0.52
26:BA:1177:A:H3'	26:BA:1178:C:C6	2.44	0.52
26:BA:2404:C:O3'	36:BP:77:ARG:NH2	2.43	0.52
40:BT:118:ARG:HG3	40:BT:118:ARG:NH1	2.22	0.52
1:CA:768:A:OP2	61:CA:4019:HOH:O	2.19	0.52
7:CG:50:ILE:HD11	7:CG:58:PRO:HA	1.92	0.52
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.74	0.52
23:CW:19:G:H1	23:CW:56:C:N4	2.04	0.52
26:DA:942:G:OP2	36:DP:39:LYS:NZ	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:1033:U:OP1	56:D9:9:ARG:NH2	2.43	0.52
40:DT:16:ARG:NH2	40:DT:83:ILE:O	2.42	0.52
1:AA:1131:G:H2'	1:AA:1132:C:C6	2.45	0.52
7:AG:12:LEU:H	7:AG:12:LEU:HD12	1.74	0.52
32:BH:88:LEU:HD13	32:BH:130:ARG:HG2	1.92	0.52
39:BS:11:LYS:O	39:BS:15:ARG:HG3	2.09	0.52
39:BS:46:VAL:HG12	39:BS:48:LEU:HD12	1.91	0.52
1:CA:261:U:OP2	20:CT:79:ARG:NH2	2.43	0.52
1:CA:551:U:H2'	1:CA:552:U:C6	2.44	0.52
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.38	0.52
1:CA:1006:C:OP1	1:CA:1037:C:O2'	2.27	0.52
2:CB:76:GLN:HB2	2:CB:208:ILE:HG12	1.92	0.52
26:DA:81:G:N7	61:DA:4166:HOH:O	2.33	0.52
26:DA:171:G:H2'	26:DA:172:C:H6	1.75	0.52
26:DA:373:U:H2'	26:DA:374:A:C8	2.44	0.52
26:DA:1266:G:O2'	26:DA:2012:G:O6	2.26	0.52
26:DA:2590:A:OP2	28:DD:238:GLY:HA2	2.10	0.52
30:DF:20:LEU:HD12	30:DF:125:LEU:HD13	1.91	0.52
36:DP:29:LYS:HG3	36:DP:30:THR:H	1.75	0.52
43:DW:45:TYR:CZ	43:DW:49:LYS:HE3	2.45	0.52
1:AA:664:G:N2	1:AA:741:G:H1	2.00	0.51
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.56	0.51
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.92	0.51
8:AH:73:ASP:OD1	8:AH:75:ARG:HD3	2.10	0.51
19:AS:65:ASN:HD22	19:AS:66:MET:N	2.09	0.51
26:BA:1858:G:N2	26:BA:1883:G:H2'	2.24	0.51
29:BE:143:ASN:HD22	29:BE:147:PRO:HD3	1.76	0.51
33:BI:93:THR:HG22	33:BI:119:PRO:HB3	1.91	0.51
1:CA:565:U:OP2	1:CA:566:G:O2'	2.27	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.45	0.51
1:CA:1304:G:C6	1:CA:1305:G:N1	2.78	0.51
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.45	0.51
15:CO:8:LYS:O	15:CO:12:ILE:HG13	2.10	0.51
26:DA:2299:G:H2'	26:DA:2300:G:H8	1.75	0.51
29:DE:12:THR:HG22	40:DT:58:ASN:OD1	2.10	0.51
41:DU:58:ARG:HA	41:DU:61:TRP:CE3	2.45	0.51
1:AA:78:G:C2	1:AA:91:C:N3	2.78	0.51
1:AA:1036:G:H5'	1:AA:1037:C:OP2	2.09	0.51
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.74	0.51
15:AO:74:ASP:CG	15:AO:77:ARG:HG3	2.35	0.51
25:AY:7:A:N1	25:AY:66:U:O2	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:793:A:OP2	26:BA:2071:A:O2'	2.27	0.51
26:BA:1593:G:H2'	26:BA:1594:G:C8	2.45	0.51
26:BA:2001:A:OP1	38:BR:9:LYS:NZ	2.36	0.51
26:BA:2361:A:OP1	55:B8:27:THR:OG1	2.13	0.51
29:BE:47:VAL:HG23	29:BE:84:PHE:O	2.10	0.51
49:B2:2:LYS:O	49:B2:6:VAL:HG23	2.09	0.51
1:CA:17:U:H2'	1:CA:18:C:C6	2.44	0.51
1:CA:1118:C:C2	1:CA:1119:C:C5	2.96	0.51
1:CA:1129:C:P	9:CI:16:ARG:HH12	2.33	0.51
1:CA:1305:G:H5'	21:CU:4:GLY:C	2.36	0.51
1:CA:1327:C:H5''	21:CU:20:LYS:HB3	1.93	0.51
8:CH:67:PRO:O	8:CH:69:ARG:HG3	2.10	0.51
26:DA:1006:C:OP2	61:DA:4190:HOH:O	2.19	0.51
26:DA:1803:A:HO2'	28:DD:259:THR:HG21	1.76	0.51
29:DE:50:GLY:HA3	29:DE:75:VAL:HG11	1.91	0.51
31:DG:39:ILE:HB	31:DG:92:VAL:HG13	1.92	0.51
32:DH:81:GLU:OE1	32:DH:81:GLU:N	2.44	0.51
33:DI:110:ASP:H	33:DI:130:TYR:HH	1.57	0.51
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.44	0.51
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.30	0.51
26:BA:8:A:H2'	26:BA:9:U:H6	1.74	0.51
26:BA:2277:G:OP2	47:B0:10:THR:HG21	2.10	0.51
46:BZ:28:MET:HE1	46:BZ:61:LEU:HD21	1.92	0.51
1:CA:955:U:O2'	19:CS:83:HIS:HD2	1.93	0.51
1:CA:1226:C:H2'	13:CM:103:THR:HB	1.93	0.51
1:CA:1360:A:O5'	1:CA:1360:A:H8	1.93	0.51
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.92	0.51
2:CB:168:THR:OG1	2:CB:192:SER:HA	2.09	0.51
4:CD:38:TYR:CE1	4:CD:45:GLN:HG2	2.45	0.51
9:CI:85:LEU:HB3	9:CI:92:TYR:HD2	1.75	0.51
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.24	0.51
18:CR:47:THR:HG23	18:CR:49:LYS:HG3	1.92	0.51
26:DA:62:C:H42	26:DA:93:G:H1	1.57	0.51
26:DA:867:C:H2'	26:DA:868:U:H5'	1.92	0.51
44:DX:88:LYS:HG2	44:DX:93:GLU:HG3	1.92	0.51
1:AA:1004:A:O2'	1:AA:1038:C:O2	2.28	0.51
1:AA:1035:A:H2	1:AA:1036:G:N7	2.09	0.51
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.10	0.51
26:BA:602:G:O2'	26:BA:655:A:N6	2.43	0.51
26:BA:637:A:H4'	26:BA:638:G:O5'	2.11	0.51
26:BA:1164:G:H2'	26:BA:1165:U:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1420:U:O2'	26:BA:1421:G:OP1	2.22	0.51
26:BA:2687:U:H2'	26:BA:2688:U:O4'	2.10	0.51
50:B3:8:LEU:HD13	50:B3:31:LEU:HD23	1.90	0.51
1:CA:34:C:H2'	1:CA:35:G:C8	2.45	0.51
1:CA:179:A:H2'	1:CA:180:U:C6	2.46	0.51
1:CA:352:C:N3	1:CA:356:A:N6	2.58	0.51
1:CA:784:C:H4'	26:DA:1837:C:OP1	2.10	0.51
1:CA:1004:A:H62	1:CA:1037:C:H3'	1.76	0.51
1:CA:1362:C:H2'	1:CA:1363:C:H5''	1.92	0.51
3:CC:118:GLN:HA	3:CC:121:ALA:HB3	1.92	0.51
3:CC:187:ALA:O	3:CC:198:VAL:HG23	2.11	0.51
9:CI:96:LEU:O	9:CI:100:GLY:N	2.43	0.51
13:CM:3:ARG:HA	51:D4:34:GLU:HG2	1.92	0.51
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD13	1.91	0.51
23:CW:74:C:N4	26:DA:2507:C:O2'	2.44	0.51
26:DA:607:U:OP1	30:DF:102:PRO:HA	2.10	0.51
26:DA:710:G:H1	26:DA:721:C:H42	1.56	0.51
26:DA:832:G:OP1	61:DA:4285:HOH:O	2.19	0.51
26:DA:1155:A:H5''	41:DU:55:ARG:HD3	1.93	0.51
26:DA:2019:A:H4'	41:DU:34:LYS:HD2	1.92	0.51
29:DE:52:LEU:HB2	29:DE:76:ARG:HB2	1.92	0.51
1:AA:997:U:H3	1:AA:1044:A:H61	1.59	0.51
26:BA:34:C:H5''	26:BA:35:G:OP2	2.09	0.51
26:BA:45:C:OP2	26:BA:215:G:H2'	2.10	0.51
30:BF:53:THR:CG2	30:BF:55:GLY:H	2.24	0.51
1:CA:448:A:P	1:CA:485:G:H22	2.33	0.51
1:CA:1050:G:H1'	1:CA:1214:C:O2	2.10	0.51
1:CA:1155:G:H2'	1:CA:1156:G:O4'	2.11	0.51
19:CS:11:VAL:HB	19:CS:16:LEU:HD12	1.93	0.51
23:CW:47:U:H3'	23:CW:48:C:H5'	1.92	0.51
26:DA:621:A:OP2	36:DP:108:LYS:NZ	2.43	0.51
26:DA:652(T):C:H2'	26:DA:652(U):G:C8	2.46	0.51
26:DA:1593:G:H2'	26:DA:1594:G:H8	1.76	0.51
30:DF:154:VAL:HG22	30:DF:191:ARG:HB2	1.92	0.51
45:DY:6:HIS:H	45:DY:6:HIS:CD2	2.28	0.51
51:D4:7:PRO:HB2	51:D4:27:THR:HG21	1.93	0.51
1:AA:1002:G:N3	1:AA:1003:G:H1'	2.26	0.51
1:AA:1025:U:C2	1:AA:1036:G:O6	2.63	0.51
1:AA:1221:G:OP1	1:AA:1320:C:N4	2.43	0.51
2:AB:67:THR:N	2:AB:160:ASP:OD1	2.44	0.51
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:77:ILE:O	9:AI:81:ILE:HG22	2.10	0.51
18:AR:33:ASP:OD2	18:AR:36:ASN:HB2	2.11	0.51
26:BA:2123:G:N2	26:BA:2175:C:N3	2.48	0.51
33:BI:72:LEU:O	33:BI:74:ASN:N	2.44	0.51
1:CA:1057:G:H2'	1:CA:1058:G:O4'	2.11	0.51
1:CA:1227:A:OP2	13:CM:111:LYS:HE3	2.09	0.51
1:CA:1392:G:H21	1:CA:1502:A:H8	1.57	0.51
4:CD:65:ARG:HD3	4:CD:70:ILE:O	2.11	0.51
24:CX:31:G:H3'	24:CX:32:5MC:HM53	1.93	0.51
31:DG:37:VAL:HG23	31:DG:99:MET:HG3	1.92	0.51
36:DP:82:GLY:HA2	36:DP:113:LYS:O	2.10	0.51
37:DQ:36:ALA:HA	37:DQ:129:THR:HG22	1.92	0.51
46:DZ:138:GLU:H	46:DZ:156:LYS:HZ1	1.58	0.51
1:AA:164:U:H2'	1:AA:165:C:C6	2.46	0.51
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.40	0.51
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	1.91	0.51
23:AW:28:G:H2'	23:AW:29:G:C8	2.46	0.51
26:BA:848:G:C4	26:BA:933:A:H8	2.29	0.51
26:BA:1506:C:H2'	26:BA:1507:A:C8	2.36	0.51
26:BA:1790:C:H5''	26:BA:1791:A:OP1	2.11	0.51
33:BI:75:LEU:HD22	33:BI:105:HIS:ND1	2.25	0.51
34:BN:12:ARG:NH1	34:BN:50:ASP:OD2	2.43	0.51
1:CA:662:G:H2'	1:CA:663:A:C8	2.46	0.51
15:CO:64:ARG:HD3	15:CO:68:ARG:NH2	2.25	0.51
26:DA:10:G:H2'	26:DA:11:G:H8	1.76	0.51
26:DA:1023:U:OP2	61:DA:4648:HOH:O	2.20	0.51
26:DA:1639:U:H4'	26:DA:2699:C:H4'	1.92	0.51
26:DA:1670:C:O2	29:DE:129:HIS:NE2	2.42	0.51
26:DA:2218:U:O4'	48:D1:52:ARG:NH2	2.44	0.51
1:AA:145:G:H1	1:AA:177:C:H42	1.59	0.51
1:AA:954:G:H21	1:AA:1227:A:H62	1.59	0.51
24:AX:61:C:H2'	24:AX:62:C:H6	1.75	0.51
24:AX:76:A:O3'	61:AX:3101:HOH:O	2.19	0.51
25:AY:54:5MU:H72	25:AY:55:PSU:O2	2.11	0.51
26:BA:271(K):U:C2	33:BI:50:ARG:HD3	2.46	0.51
26:BA:529:A:H62	26:BA:2041:U:H3	1.59	0.51
26:BA:1011:G:OP1	41:BU:77:SER:OG	2.26	0.51
26:BA:1930:G:O2'	26:BA:1968:G:O6	2.28	0.51
26:BA:2331:G:O2'	26:BA:2336:A:N1	2.42	0.51
26:BA:2691:C:O3'	26:BA:2871:C:H4'	2.10	0.51
1:CA:375:U:O4	61:CA:4093:HOH:O	2.17	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:950:U:H2'	1:CA:951:G:H8	1.76	0.51
1:CA:1004:A:C6	1:CA:1037:C:C2	2.98	0.51
1:CA:1062:U:H2'	1:CA:1063:C:C6	2.45	0.51
1:CA:1457:G:H5''	20:CT:35:THR:HG21	1.93	0.51
7:CG:78:ARG:HG2	7:CG:79:ARG:HB2	1.93	0.51
26:DA:82:G:N1	26:DA:103:A:OP2	2.37	0.51
26:DA:2364:C:OP1	47:D0:55:ARG:NH1	2.41	0.51
26:DA:2769:C:H2'	26:DA:2770:G:O4'	2.11	0.51
28:DD:134:ARG:NH1	28:DD:188:GLU:OE2	2.44	0.51
28:DD:218:ARG:HB3	28:DD:219:PRO:HD2	1.93	0.51
32:DH:90:LYS:HD3	32:DH:159:GLU:HG2	1.92	0.51
1:AA:600:C:H2'	1:AA:601:C:C6	2.45	0.51
1:AA:1004:A:N7	1:AA:1036:G:C2	2.79	0.51
1:AA:1067:A:O2'	1:AA:1068:G:OP2	2.21	0.51
25:AY:19:G:H1	25:AY:56:C:H42	1.48	0.51
26:BA:467:G:OP1	54:B7:33:ARG:NH1	2.44	0.51
26:BA:952:G:OP1	37:BQ:16:ARG:NH2	2.44	0.51
1:CA:69:G:H2'	1:CA:70:G:H8	1.76	0.51
1:CA:429:U:H3'	4:CD:9:CYS:SG	2.51	0.51
1:CA:587:G:N1	1:CA:754:C:OP2	2.41	0.51
1:CA:1120:G:N1	1:CA:1154:G:N3	2.59	0.51
1:CA:1169:A:H2'	1:CA:1170:A:C8	2.46	0.51
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.45	0.51
3:CC:53:ALA:HB3	3:CC:106:VAL:HG21	1.93	0.51
9:CI:8:GLY:HA3	9:CI:76:ALA:O	2.10	0.51
26:DA:1688:U:O2	26:DA:1700:A:H5'	2.11	0.51
26:DA:2121:G:O6	26:DA:2176:A:N6	2.44	0.51
26:DA:2357:U:OP1	47:D0:20:ARG:NH1	2.35	0.51
44:DX:5:TYR:CE1	49:D2:30:ARG:HB2	2.46	0.51
1:AA:460:G:O5'	1:AA:460:G:H8	1.93	0.51
1:AA:1227:A:P	13:AM:111:LYS:HZ2	2.33	0.51
8:AH:124:ALA:O	8:AH:128:GLY:N	2.43	0.51
9:AI:128:ARG:NH1	24:AX:35:A:OP2	2.44	0.51
20:AT:76:ALA:HA	20:AT:79:ARG:NH1	2.26	0.51
26:BA:1365:A:OP2	48:B1:3:LYS:HG2	2.10	0.51
26:BA:2168:G:C6	26:BA:2171:A:C8	2.99	0.51
44:BX:1:MET:HE1	49:B2:26:ARG:NH2	2.26	0.51
1:CA:1358:U:H2'	1:CA:1359:C:O4'	2.11	0.51
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.46	0.51
3:CC:130:VAL:O	3:CC:134:ILE:HD13	2.11	0.51
7:CG:22:LEU:HG	7:CG:62:PHE:HE2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:309:G:N3	26:DA:329:G:O2'	2.43	0.51
26:DA:1028:A:N6	26:DA:1125:G:H2'	2.26	0.51
26:DA:2142:C:H2'	26:DA:2143:C:C6	2.46	0.51
41:DU:52:ARG:HA	41:DU:55:ARG:HE	1.74	0.51
41:DU:104:GLN:OE1	41:DU:105:VAL:N	2.34	0.51
1:AA:749:C:H2'	1:AA:750:G:H8	1.76	0.50
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.11	0.50
4:AD:108:LEU:HD12	4:AD:176:LEU:HB2	1.93	0.50
17:AQ:12:SER:HB3	17:AQ:20:THR:HB	1.92	0.50
19:AS:3:ARG:HH21	19:AS:7:LYS:HE2	1.76	0.50
25:AY:8:4SU:H4'	25:AY:48:C:H4'	1.93	0.50
25:AY:40:C:H2'	25:AY:41:C:H6	1.76	0.50
26:BA:1817:G:OP1	28:BD:88:ARG:NH2	2.40	0.50
28:BD:72:LYS:NZ	28:BD:99:ASP:OD2	2.37	0.50
31:BG:43:LEU:HD11	31:BG:153:ARG:HG2	1.93	0.50
1:CA:719:C:N4	18:CR:71:LYS:HE2	2.26	0.50
1:CA:1014:A:H4'	19:CS:14:HIS:CE1	2.46	0.50
3:CC:42:LEU:HA	3:CC:45:LYS:HZ3	1.76	0.50
20:CT:56:MET:HG3	20:CT:57:ARG:N	2.27	0.50
25:CY:7:A:H61	25:CY:66:U:H3	0.60	0.50
26:DA:1916:A:H2'	26:DA:1917:U:O4'	2.12	0.50
31:DG:97:ASP:HA	31:DG:100:TRP:HD1	1.75	0.50
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.11	0.50
1:AA:1144:G:N2	1:AA:1146:A:H62	2.10	0.50
3:AC:35:GLU:OE2	3:AC:59:ARG:NH2	2.43	0.50
24:AX:61:C:H2'	24:AX:62:C:C6	2.46	0.50
36:BP:88:LEU:HD11	36:BP:114:ILE:HD12	1.93	0.50
45:BY:87:LYS:HB3	45:BY:95:LYS:HD3	1.93	0.50
48:B1:3:LYS:HB2	48:B1:61:ARG:NH1	2.26	0.50
56:B9:25:VAL:HB	56:B9:34:GLN:HB2	1.92	0.50
1:CA:160:A:H61	1:CA:347:G:H1'	1.76	0.50
1:CA:431:A:H2'	1:CA:432:A:C8	2.46	0.50
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.44	0.50
25:CY:11:C:N3	25:CY:24:G:O6	2.44	0.50
26:DA:376:C:OP1	61:DA:4418:HOH:O	2.19	0.50
26:DA:479:A:N3	26:DA:481:G:H5''	2.26	0.50
29:DE:116:VAL:HG13	29:DE:122:PHE:HB2	1.92	0.50
44:DX:43:VAL:HG21	44:DX:81:VAL:HG11	1.93	0.50
51:D4:62:ARG:H	51:D4:62:ARG:HD3	1.77	0.50
1:AA:1277:C:O2'	1:AA:1279:A:H1'	2.10	0.50
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:62:C:H2'	25:AY:63:G:C8	2.40	0.50
26:BA:1030:G:OP2	37:BQ:128:LYS:NZ	2.44	0.50
26:BA:1274:A:N3	26:BA:1297:C:H1'	2.26	0.50
37:BQ:18:LYS:O	37:BQ:98:LYS:NZ	2.25	0.50
1:CA:1176:A:H2'	1:CA:1177:G:C8	2.47	0.50
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.46	0.50
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.46	0.50
7:CG:26:PHE:HE2	7:CG:104:LEU:HD23	1.76	0.50
27:DB:17:C:H2'	27:DB:18:G:O4'	2.11	0.50
29:DE:2:LYS:HB2	29:DE:95:ILE:HD12	1.93	0.50
29:DE:7:VAL:HG12	29:DE:27:LEU:HB3	1.92	0.50
31:DG:70:VAL:HA	31:DG:90:LEU:HD23	1.92	0.50
45:DY:38:ILE:HD11	45:DY:66:PRO:HG3	1.92	0.50
53:D6:23:THR:OG1	53:D6:24:GLU:N	2.43	0.50
1:AA:619:U:C2	4:AD:135:LEU:HD22	2.45	0.50
1:AA:1176:A:H2'	1:AA:1177:G:C8	2.46	0.50
26:BA:796:C:H2'	26:BA:797:C:C6	2.46	0.50
27:BB:2:C:H2'	27:BB:3:C:C6	2.46	0.50
45:BY:20:TYR:CE1	45:BY:43:ASN:HA	2.46	0.50
1:CA:1119:C:H2'	1:CA:1120:G:H8	1.75	0.50
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.94	0.50
16:CP:68:ASP:O	16:CP:71:ARG:HG2	2.11	0.50
26:DA:2153:G:C2	26:DA:2154:G:C4	2.99	0.50
32:DH:56:SER:HB3	32:DH:61:HIS:ND1	2.26	0.50
38:DR:2:ARG:NH1	38:DR:5:LYS:O	2.44	0.50
1:AA:78:G:H1	1:AA:91:C:N4	2.07	0.50
1:AA:1521:G:N3	61:AA:4065:HOH:O	2.35	0.50
2:AB:60:ASP:O	2:AB:64:ARG:HB2	2.12	0.50
4:AD:147:ALA:HB2	4:AD:182:LYS:HA	1.94	0.50
9:AI:4:TYR:CD2	9:AI:88:TYR:HA	2.47	0.50
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.26	0.50
24:AX:55:PSU:O2'	24:AX:57:A:N7	2.33	0.50
26:BA:2512:C:H2'	26:BA:2513:G:O4'	2.12	0.50
43:BW:79:GLY:HA3	43:BW:100:THR:HG22	1.93	0.50
1:CA:67:C:H2'	1:CA:68:G:C8	2.47	0.50
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.11	0.50
1:CA:1030:C:N4	1:CA:1032:G:O6	2.44	0.50
2:CB:233:SER:HB2	2:CB:234:PRO:HD2	1.93	0.50
8:CH:43:GLY:O	8:CH:64:LYS:NZ	2.42	0.50
10:CJ:55:LYS:HG3	10:CJ:56:HIS:H	1.75	0.50
26:DA:286:C:H2'	26:DA:287:C:H6	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:443:A:H1'	26:DA:1201:C:O4'	2.10	0.50
26:DA:483:A:O2'	45:DY:49:VAL:O	2.25	0.50
26:DA:1020:A:N1	26:DA:1141:U:O2'	2.41	0.50
26:DA:2318:G:N2	39:DS:3:ARG:HH11	2.09	0.50
27:DB:11:C:OP2	27:DB:12:C:N4	2.32	0.50
34:DN:4:TYR:HB2	41:DU:101:ARG:HH12	1.76	0.50
50:D3:7:LYS:NZ	50:D3:32:GLN:O	2.29	0.50
4:AD:15:GLU:HG2	4:AD:63:LYS:CB	2.41	0.50
6:AF:67:MET:HE1	6:AF:75:LEU:HD12	1.93	0.50
11:AK:29:ILE:HG23	11:AK:44:SER:HB3	1.94	0.50
12:AL:28:LYS:HG3	12:AL:62:SER:HB2	1.94	0.50
18:AR:42:ARG:HH21	18:AR:42:ARG:HA	1.75	0.50
23:AW:58:A:O2'	23:AW:60:U:OP2	2.24	0.50
26:BA:456:C:H4'	61:BA:3946:HOH:O	2.11	0.50
26:BA:1045:A:H1'	26:BA:1047:G:N3	2.26	0.50
26:BA:1448:G:H4'	26:BA:1542:A:OP1	2.11	0.50
26:BA:1449:A:H5'	26:BA:1450:G:OP2	2.12	0.50
55:B8:6:THR:HG22	55:B8:63:PRO:HD2	1.93	0.50
3:CC:142:MET:HG3	3:CC:170:GLN:HB3	1.93	0.50
17:CQ:45:HIS:HA	17:CQ:69:LYS:HE3	1.94	0.50
23:CW:14:A:H2'	23:CW:15:G:O4'	2.11	0.50
25:CY:23:A:O5'	25:CY:23:A:H8	1.94	0.50
26:DA:885:C:H2'	26:DA:886:C:H4'	1.94	0.50
26:DA:1266:G:O4'	43:DW:15:ARG:NH2	2.45	0.50
26:DA:2136:C:O2'	26:DA:2137:C:H6	1.85	0.50
33:DI:130:TYR:HB3	33:DI:138:ILE:HB	1.94	0.50
1:AA:376:G:P	16:AP:67:THR:HG21	2.51	0.50
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.11	0.50
5:AE:78:HIS:HD1	8:AH:104:ARG:CD	2.24	0.50
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.92	0.50
14:AN:33:VAL:HA	14:AN:40:CYS:HA	1.94	0.50
15:AO:8:LYS:O	15:AO:12:ILE:HG13	2.11	0.50
23:AW:37:MIA:O2'	26:BA:1913:A:N1	2.44	0.50
25:AY:69:G:C2	25:AY:70:G:H1'	2.47	0.50
26:BA:1379:A:H4'	26:BA:1380:G:OP2	2.10	0.50
26:BA:1688:U:O2	26:BA:1700:A:H5'	2.12	0.50
1:CA:677:U:H3	1:CA:713:G:H22	1.58	0.50
20:CT:67:ALA:HB2	20:CT:77:ALA:HB2	1.92	0.50
23:CW:9:A:O2'	23:CW:10:G:N7	2.43	0.50
24:CX:6:G:H1	24:CX:67:C:H42	1.58	0.50
26:DA:854:G:H2'	26:DA:855:G:H8	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2139:C:N4	26:DA:2153:G:C2	2.79	0.50
27:DB:75:G:H1'	46:DZ:27:VAL:HG11	1.94	0.50
31:DG:11:TYR:HB2	31:DG:176:LEU:HD21	1.93	0.50
39:DS:50:SER:O	39:DS:76:LYS:NZ	2.45	0.50
1:AA:714:G:H2'	1:AA:715:A:C8	2.47	0.50
1:AA:1132:C:H2'	1:AA:1133:G:H8	1.76	0.50
1:AA:1181:G:O2'	1:AA:1182:G:N7	2.45	0.50
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.46	0.50
6:AF:36:ARG:HB3	6:AF:36:ARG:HH11	1.77	0.50
19:AS:68:GLY:H	51:B4:58:ARG:HH11	1.59	0.50
23:AW:49:C:H42	23:AW:65:G:H1	1.60	0.50
26:BA:272(H):C:H42	26:BA:363(B):G:H1	1.58	0.50
26:BA:1866:C:H2'	26:BA:1876:A:O4'	2.11	0.50
26:BA:2319:G:H22	39:BS:3:ARG:NE	2.09	0.50
45:BY:6:HIS:H	45:BY:6:HIS:CD2	2.30	0.50
52:B5:11:THR:HG23	52:B5:15:ARG:HB3	1.93	0.50
1:CA:952:U:H2'	1:CA:953:G:H8	1.77	0.50
1:CA:1411:C:H2'	1:CA:1412:C:H6	1.76	0.50
3:CC:136:GLN:O	3:CC:140:ARG:NH1	2.45	0.50
6:CF:37:VAL:HA	6:CF:65:VAL:HG12	1.93	0.50
26:DA:11:G:H2'	26:DA:12:U:H5''	1.93	0.50
26:DA:1021:A:H62	26:DA:1141:U:H3	1.59	0.50
26:DA:1187:G:H5'	42:DV:81:TYR:CE1	2.47	0.50
26:DA:1894:C:H2'	26:DA:1895:C:H6	1.77	0.50
39:DS:93:LYS:CD	39:DS:95:HIS:HB2	2.40	0.50
46:DZ:93:ASP:OD1	46:DZ:94:GLU:HG3	2.12	0.50
1:AA:279:A:C5	17:AQ:98:LEU:HD23	2.47	0.50
1:AA:673:G:H2'	1:AA:674:G:C8	2.47	0.50
1:AA:1131:G:O2'	1:AA:1132:C:H5'	2.12	0.50
1:AA:1249:C:O2'	9:AI:73:GLN:NE2	2.45	0.50
3:AC:181:ASN:C	3:AC:181:ASN:HD22	2.20	0.50
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.45	0.50
16:AP:4:ILE:HB	16:AP:66:PRO:HA	1.94	0.50
23:AW:11:C:H42	23:AW:24:G:H1	1.58	0.50
25:AY:33:U:C3'	25:AY:34:G:H5''	2.41	0.50
26:BA:548:A:N6	42:BV:19:LYS:H	2.09	0.50
26:BA:2712:U:H2'	26:BA:2714:G:H5''	1.93	0.50
30:BF:64:ILE:HD11	30:BF:75:HIS:HB2	1.94	0.50
40:BT:29:ARG:HG3	40:BT:46:GLU:HB2	1.93	0.50
44:BX:61:GLY:HA3	44:BX:73:ARG:O	2.11	0.50
1:CA:406:G:N2	4:CD:119:GLN:HE22	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:933:G:N2	1:CA:935:A:O4'	2.45	0.50
1:CA:936:C:H2'	1:CA:937:A:O4'	2.10	0.50
1:CA:950:U:H2'	1:CA:951:G:C8	2.47	0.50
1:CA:1244:C:N4	1:CA:1293:G:H1	2.10	0.50
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.46	0.50
2:CB:186:ALA:HB3	2:CB:197:VAL:HG11	1.93	0.50
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.12	0.50
7:CG:76:ARG:HB3	7:CG:156:TRP:CH2	2.47	0.50
12:CL:117:ARG:CZ	12:CL:117:ARG:HB2	2.41	0.50
26:DA:1300:U:O2'	26:DA:1635:G:OP1	2.27	0.50
26:DA:1996:C:H4'	26:DA:1997:G:OP1	2.11	0.50
26:DA:2302:G:C2'	26:DA:2303:G:H5'	2.41	0.50
26:DA:2657:A:O3'	32:DH:160:LYS:NZ	2.45	0.50
34:DN:73:THR:OG1	34:DN:82:LEU:HD11	2.11	0.50
1:AA:376:G:H5''	16:AP:5:ARG:HB3	1.92	0.49
1:AA:991:U:O2'	1:AA:992:U:OP2	2.23	0.49
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.47	0.49
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.47	0.49
4:AD:196:LEU:O	4:AD:198:VAL:N	2.41	0.49
6:AF:89:MET:HE1	18:AR:72:ARG:HB3	1.94	0.49
9:AI:49:PRO:HG2	9:AI:81:ILE:HG23	1.93	0.49
26:BA:282:A:H2'	26:BA:282:A:N3	2.27	0.49
26:BA:646:A:H2'	26:BA:647:G:O4'	2.12	0.49
26:BA:747:U:O2	26:BA:2014:A:H1'	2.12	0.49
26:BA:1779:U:H2'	61:BA:5061:HOH:O	2.11	0.49
26:BA:2128:C:O2'	26:BA:2129:C:H5'	2.12	0.49
26:BA:2278:A:OP2	47:B0:12:ASN:ND2	2.45	0.49
26:BA:2396:G:OP1	48:B1:25:LYS:NZ	2.39	0.49
28:BD:9:TYR:CZ	28:BD:13:ARG:HG2	2.47	0.49
38:BR:28:LEU:HD12	38:BR:48:VAL:HG21	1.94	0.49
41:BU:74:LEU:H	41:BU:74:LEU:HD12	1.77	0.49
44:BX:35:THR:HG22	44:BX:38:GLU:H	1.77	0.49
48:B1:85:LEU:HB3	48:B1:89:GLU:HG2	1.94	0.49
51:B4:61:ARG:HG3	51:B4:62:ARG:N	2.26	0.49
1:CA:1039:C:H2'	1:CA:1040:U:O4'	2.11	0.49
1:CA:1387:G:H2'	1:CA:1388:C:C6	2.47	0.49
10:CJ:67:THR:O	10:CJ:67:THR:OG1	2.30	0.49
20:CT:50:GLU:HG3	20:CT:100:ILE:HD13	1.94	0.49
26:DA:1037:G:H2'	26:DA:1038:C:O4'	2.12	0.49
26:DA:1278:A:OP1	38:DR:36:THR:HG23	2.12	0.49
26:DA:1359:A:N6	26:DA:1372:U:H3	2.08	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2128:C:H5'	26:DA:2173:A:C2	2.47	0.49
35:DO:1:MET:HG3	35:DO:67:LYS:HG2	1.93	0.49
36:DP:99:LEU:HD23	36:DP:99:LEU:H	1.77	0.49
46:DZ:117:LEU:HD11	46:DZ:144:LEU:HD13	1.93	0.49
47:D0:37:LEU:HD13	47:D0:79:VAL:HG11	1.94	0.49
1:AA:1053:G:O2'	61:AA:4100:HOH:O	2.19	0.49
1:AA:1095:U:P	1:AA:1108:G:H1	2.35	0.49
1:AA:1125:U:O2'	1:AA:1127:G:N7	2.24	0.49
1:AA:1399:C:C2	1:AA:1502:A:N6	2.80	0.49
2:AB:103:THR:HA	2:AB:180:LEU:HD11	1.93	0.49
26:BA:1774:C:O5'	26:BA:1774:C:H6	1.95	0.49
26:BA:2259:G:C8	26:BA:2427:C:C4	3.00	0.49
39:BS:14:VAL:O	39:BS:18:ILE:HG12	2.11	0.49
45:BY:92:ASN:HB3	45:BY:94:LYS:N	2.25	0.49
46:BZ:7:ALA:HB3	46:BZ:61:LEU:HD12	1.93	0.49
1:CA:137:C:H2'	1:CA:138:G:H8	1.76	0.49
1:CA:155:C:H2'	1:CA:156:G:O4'	2.11	0.49
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.95	0.49
14:CN:48:ALA:HB2	14:CN:53:LEU:HD12	1.94	0.49
26:DA:996:A:C2	26:DA:997:G:C8	3.00	0.49
26:DA:1359:A:H2'	26:DA:1360:A:H5'	1.94	0.49
26:DA:1721:G:H8	26:DA:1741:A:H62	1.60	0.49
26:DA:2294:C:H5''	39:DS:10:ARG:HD2	1.94	0.49
26:DA:2483:C:H2'	26:DA:2484:G:O4'	2.11	0.49
26:DA:2849:U:P	40:DT:95:ARG:HH12	2.35	0.49
34:DN:30:ILE:HG23	34:DN:52:VAL:HG11	1.94	0.49
1:AA:1008:C:H2'	1:AA:1009:G:O4'	2.12	0.49
2:AB:20:GLU:HA	2:AB:21:ARG:HH21	1.78	0.49
26:BA:271(K):U:H1'	33:BI:50:ARG:CZ	2.43	0.49
26:BA:1155:A:OP1	41:BU:55:ARG:HD3	2.12	0.49
26:BA:2345:G:H4'	26:BA:2346:A:H5''	1.94	0.49
28:BD:70:TRP:HB3	28:BD:190:TYR:CE1	2.46	0.49
38:BR:21:TYR:OH	38:BR:43:GLU:HG2	2.12	0.49
46:BZ:117:LEU:CD1	46:BZ:144:LEU:HD22	2.39	0.49
1:CA:110:C:H2'	1:CA:111:G:O4'	2.12	0.49
1:CA:984:C:O5'	1:CA:984:C:H6	1.94	0.49
4:CD:57:ARG:NE	4:CD:205:GLU:OE2	2.44	0.49
15:CO:3:ILE:O	15:CO:3:ILE:HG12	2.13	0.49
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.12	0.49
26:DA:286:C:H2'	26:DA:287:C:C6	2.47	0.49
26:DA:335:C:H4'	45:DY:73:ARG:CZ	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2805:G:H2'	26:DA:2807:G:H8	1.75	0.49
30:DF:129:PHE:CD2	30:DF:163:VAL:HG21	2.48	0.49
32:DH:89:ILE:O	32:DH:129:THR:HG23	2.13	0.49
34:DN:38:HIS:CE1	34:DN:39:ARG:HG3	2.46	0.49
39:DS:68:GLN:O	39:DS:71:ARG:HG3	2.13	0.49
42:DV:62:LEU:HD11	42:DV:95:LEU:HB2	1.93	0.49
44:DX:31:HIS:CD2	44:DX:33:LYS:HB2	2.47	0.49
44:DX:92:LEU:C	44:DX:94:GLY:H	2.18	0.49
46:DZ:104:PHE:HA	46:DZ:139:VAL:HB	1.95	0.49
1:AA:110:C:H2'	1:AA:111:G:O4'	2.12	0.49
1:AA:920:U:H2'	1:AA:921:U:C6	2.48	0.49
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.92	0.49
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.45	0.49
23:AW:63:G:H2'	23:AW:64:A:O4'	2.13	0.49
26:BA:83:G:N2	26:BA:103:A:OP2	2.44	0.49
26:BA:831:G:O2'	36:BP:38:GLN:NE2	2.44	0.49
26:BA:2815:C:H5'	52:B5:29:THR:HG21	1.94	0.49
37:BQ:16:ARG:HG2	37:BQ:18:LYS:HE2	1.94	0.49
1:CA:875:C:H1'	8:CH:15:ASN:HD21	1.77	0.49
10:CJ:62:HIS:HB3	14:CN:59:ALA:HB3	1.93	0.49
26:DA:10:G:H2'	26:DA:11:G:C8	2.47	0.49
26:DA:528:A:C2	26:DA:2042:A:H2'	2.47	0.49
26:DA:1264:G:H2'	26:DA:2014:A:N6	2.27	0.49
30:DF:11:VAL:HG22	30:DF:125:LEU:HB2	1.94	0.49
30:DF:13:SER:OG	30:DF:16:GLY:O	2.26	0.49
34:DN:67:LEU:HD13	34:DN:87:LEU:HD13	1.94	0.49
35:DO:73:ASP:HB2	40:DT:82:LEU:HD13	1.93	0.49
1:AA:1523:G:OP1	11:AK:123:LYS:NZ	2.30	0.49
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.94	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:NH1	2.26	0.49
12:AL:33:ARG:HH11	12:AL:62:SER:HB3	1.77	0.49
25:AY:50:U:N3	25:AY:64:A:H2	2.05	0.49
26:BA:8:A:H2'	26:BA:9:U:C6	2.47	0.49
26:BA:956:G:P	37:BQ:14:ARG:HH22	2.36	0.49
26:BA:2029:G:H2'	26:BA:2031:A:OP1	2.12	0.49
36:BP:50:ARG:HG2	55:B8:61:LEU:HD11	1.95	0.49
1:CA:91:C:H2'	1:CA:92:C:C6	2.48	0.49
1:CA:444:C:H2'	1:CA:445:G:H8	1.78	0.49
1:CA:528:C:H5'	1:CA:529:G:OP2	2.13	0.49
1:CA:923:A:OP1	5:CE:21:ALA:HB2	2.11	0.49
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.94	0.49
26:DA:1778:U:H2'	26:DA:1784:A:N6	2.28	0.49
26:DA:2408:U:H2'	26:DA:2409:G:C8	2.46	0.49
26:DA:2471:C:N4	26:DA:2476:A:O2'	2.43	0.49
26:DA:2558:C:H2'	26:DA:2559:C:O4'	2.13	0.49
27:DB:41:U:H5	31:DG:70:VAL:N	2.09	0.49
31:DG:43:LEU:HD11	31:DG:153:ARG:HG2	1.93	0.49
42:DV:100:ARG:HG3	42:DV:100:ARG:NH1	2.10	0.49
46:DZ:157:LEU:C	46:DZ:161:VAL:HG11	2.37	0.49
1:AA:630:G:O2'	1:AA:631:G:H5'	2.13	0.49
1:AA:674:G:OP1	6:AF:87:ARG:NH2	2.43	0.49
1:AA:1244:C:OP1	21:AU:9:ARG:HB2	2.13	0.49
1:AA:1492:A:H2'	1:AA:1493:A:C8	2.48	0.49
4:AD:166:LYS:HB2	4:AD:168:ARG:CZ	2.42	0.49
10:AJ:16:LEU:HD21	10:AJ:70:ARG:HG2	1.93	0.49
26:BA:55:G:O2'	26:BA:127:A:N1	2.39	0.49
26:BA:1292:U:H2'	26:BA:1293:C:C6	2.47	0.49
26:BA:1356:G:OP1	61:BA:5239:HOH:O	2.20	0.49
26:BA:1794:U:H2'	26:BA:1795:C:H6	1.78	0.49
26:BA:2319:G:N1	39:BS:3:ARG:HA	2.28	0.49
1:CA:45:U:H2'	1:CA:46:G:C8	2.47	0.49
1:CA:576:G:O6	1:CA:880:C:O2'	2.30	0.49
1:CA:1287:A:N3	1:CA:1353:G:O2'	2.42	0.49
2:CB:77:ALA:HB2	2:CB:211:ILE:HD13	1.94	0.49
12:CL:33:ARG:HG2	12:CL:60:LEU:HD12	1.94	0.49
23:CW:76:31M:O	24:CX:76:A:O2'	2.19	0.49
26:DA:300:A:H3'	45:DY:84:ARG:HH22	1.77	0.49
26:DA:639:U:H2'	26:DA:640:C:C6	2.48	0.49
26:DA:1153:C:OP1	41:DU:92:ARG:NH1	2.42	0.49
26:DA:2058:A:N7	61:DA:3876:HOH:O	2.34	0.49
26:DA:2123:G:H2'	26:DA:2124:G:C8	2.47	0.49
28:DD:275:LYS:HG3	28:DD:276:LYS:HA	1.94	0.49
31:DG:16:ARG:HB2	31:DG:17:PRO:HD3	1.94	0.49
31:DG:103:LEU:HD22	31:DG:178:PHE:HZ	1.77	0.49
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.78	0.49
24:AX:66:C:H2'	24:AX:67:C:O4'	2.13	0.49
25:AY:51:U:H2'	25:AY:52:G:C8	2.48	0.49
26:BA:548:A:O2'	26:BA:549:G:OP1	2.27	0.49
26:BA:1278:A:OP1	38:BR:36:THR:HG23	2.12	0.49
26:BA:2291:U:H2'	26:BA:2292:C:C6	2.48	0.49
1:CA:8:A:H5'	5:CE:101:ILE:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.45	0.49
1:CA:838:G:N2	1:CA:848:C:N3	2.58	0.49
1:CA:1002:G:N3	1:CA:1003:G:H8	2.10	0.49
6:CF:11:ASN:HB3	6:CF:14:LEU:HG	1.95	0.49
26:DA:588:U:H2'	26:DA:589:C:C6	2.46	0.49
26:DA:764:A:H5'	28:DD:210:GLY:HA2	1.94	0.49
26:DA:989:G:H4'	26:DA:990:A:OP1	2.12	0.49
44:DX:12:VAL:HG22	44:DX:29:TRP:CE2	2.47	0.49
49:D2:32:LEU:HD23	49:D2:53:LEU:HB3	1.94	0.49
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.48	0.49
1:AA:865:A:C2	1:AA:918:A:H4'	2.45	0.49
1:AA:1030(D):A:N6	1:AA:1031:G:H21	2.10	0.49
3:AC:114:PRO:HA	3:AC:185:GLY:HA3	1.94	0.49
24:AX:21:A:N6	24:AX:46:G:H2'	2.27	0.49
25:AY:22:G:H2'	25:AY:23:A:H8	1.75	0.49
61:BA:4985:HOH:O	36:BP:39:LYS:HE3	2.12	0.49
31:BG:28:VAL:O	31:BG:31:VAL:HG12	2.13	0.49
1:CA:539:A:H2'	1:CA:540:G:H8	1.76	0.49
1:CA:815:A:N7	1:CA:1509:C:O2'	2.41	0.49
1:CA:1479:C:H2'	1:CA:1480:G:H8	1.77	0.49
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD22	1.94	0.49
26:DA:25:U:C4	26:DA:26:G:C6	3.00	0.49
41:DU:86:ALA:O	42:DV:49:THR:HG23	2.13	0.49
7:AG:152:ALA:O	7:AG:155:ARG:HB3	2.13	0.49
19:AS:41:VAL:O	19:AS:43:GLU:N	2.45	0.49
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.46	0.49
26:BA:885:C:H3'	26:BA:886:C:C5'	2.40	0.49
26:BA:1899:G:H2'	26:BA:1899:G:N3	2.28	0.49
26:BA:2140:C:H1'	26:BA:2152:G:H22	1.77	0.49
36:BP:50:ARG:HH21	55:B8:7:HIS:HD2	1.59	0.49
44:BX:31:HIS:HD2	44:BX:33:LYS:H	1.59	0.49
1:CA:376:G:H5''	16:CP:5:ARG:HB2	1.94	0.49
1:CA:1029:C:N4	1:CA:1033:G:O6	2.46	0.49
1:CA:1217:C:H2'	1:CA:1218:C:O4'	2.13	0.49
1:CA:1494:G:H4'	26:DA:1913:A:N7	2.28	0.49
3:CC:48:TYR:HE1	3:CC:118:GLN:HG3	1.78	0.49
5:CE:34:VAL:HG11	5:CE:63:ARG:HG3	1.94	0.49
7:CG:126:ASP:O	7:CG:130:GLY:N	2.46	0.49
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.27	0.49
26:DA:812:C:H2'	26:DA:813:U:H6	1.77	0.49
26:DA:2154:G:C2	26:DA:2155:G:C8	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:DZ:5:LEU:HD21	46:DZ:43:GLU:HB3	1.94	0.49
1:AA:72:C:H2'	1:AA:73:G:O4'	2.13	0.49
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.13	0.49
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.47	0.49
12:AL:117:ARG:HB3	12:AL:122:THR:HB	1.95	0.49
24:AX:57:A:O4'	31:BG:78:SER:OG	2.31	0.49
26:BA:183:C:N4	26:BA:213:A:H61	2.10	0.49
26:BA:1165:U:H2'	26:BA:1166:C:C6	2.48	0.49
26:BA:2042:A:OP1	61:BA:5120:HOH:O	2.20	0.49
26:BA:2319:G:C2	39:BS:3:ARG:HA	2.48	0.49
28:BD:26:LYS:HB3	28:BD:83:GLU:HG2	1.94	0.49
30:BF:116:ASP:OD1	30:BF:119:ARG:NH2	2.46	0.49
46:BZ:41:LEU:HD21	46:BZ:83:PRO:HG2	1.94	0.49
1:CA:78:G:H2'	1:CA:79:G:H5''	1.95	0.49
1:CA:1411:C:H2'	1:CA:1412:C:C6	2.47	0.49
8:CH:83:ILE:HB	8:CH:137:VAL:HG13	1.94	0.49
24:CX:9:G:N2	24:CX:46:G:OP2	2.46	0.49
25:CY:18:G:C2	25:CY:55:PSU:C4	3.00	0.49
26:DA:1268:A:H2'	26:DA:1269:A:O4'	2.12	0.49
26:DA:1512:U:H2'	26:DA:1513:C:C6	2.48	0.49
28:DD:132:PRO:HG2	28:DD:135:PHE:HD2	1.78	0.49
35:DO:122:LEU:HD13	40:DT:72:VAL:HG11	1.94	0.49
36:DP:1:MET:HE2	36:DP:5:ASP:HB3	1.95	0.49
1:AA:236:G:OP1	17:AQ:40:LYS:NZ	2.45	0.48
2:AB:24:TRP:CD1	2:AB:24:TRP:H	2.31	0.48
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.95	0.48
23:AW:25:C:C2'	23:AW:26:A:H5'	2.43	0.48
24:AX:47:U:H5''	24:AX:48:C:OP1	2.13	0.48
27:BB:102:A:N7	61:BB:318:HOH:O	2.35	0.48
1:CA:1118:C:H1'	1:CA:1179:A:C4	2.48	0.48
25:CY:29:G:N2	25:CY:41:C:N3	2.61	0.48
26:DA:131:G:OP1	61:DA:3791:HOH:O	2.19	0.48
26:DA:1007:C:P	34:DN:37:LYS:HZ1	2.36	0.48
26:DA:2037:G:H2'	26:DA:2038:G:C8	2.48	0.48
26:DA:2278:A:OP1	37:DQ:11:LYS:HD2	2.12	0.48
26:DA:2376:A:N3	39:DS:106:ARG:NH2	2.52	0.48
55:D8:33:ASN:HA	55:D8:36:LYS:HD2	1.94	0.48
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.14	0.48
26:BA:1364:G:P	48:B1:3:LYS:HG3	2.53	0.48
30:BF:164:ARG:O	30:BF:168:ARG:HB2	2.12	0.48
53:B6:8:LYS:HG2	55:B8:34:TRP:CG	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:50:A:H1'	1:CA:52:G:C8	2.48	0.48
1:CA:189(L):G:H2'	1:CA:190:U:C6	2.48	0.48
1:CA:392:G:H2'	1:CA:393:A:H8	1.77	0.48
1:CA:976:G:OP1	14:CN:32:SER:N	2.34	0.48
1:CA:1138:G:C6	1:CA:1140:C:H1'	2.48	0.48
2:CB:119:GLU:OE2	2:CB:153:ARG:NH2	2.41	0.48
3:CC:78:GLY:HA3	3:CC:83:ARG:H	1.76	0.48
9:CI:86:VAL:HA	9:CI:89:ASN:O	2.13	0.48
23:CW:21:A:O2'	23:CW:22:G:OP1	2.28	0.48
26:DA:222:A:H5''	26:DA:421:U:OP1	2.13	0.48
26:DA:652(B):A:N1	26:DA:655:A:H1'	2.29	0.48
26:DA:2137:C:H42	26:DA:2154:G:H1	1.59	0.48
26:DA:2206:G:H5'	26:DA:2207:G:N7	2.28	0.48
33:DI:40:THR:HG23	33:DI:43:ASN:HD21	1.77	0.48
39:DS:41:ASP:OD2	39:DS:44:LYS:HE2	2.13	0.48
43:DW:60:ASN:HD22	43:DW:60:ASN:N	2.11	0.48
56:D9:10:ILE:HD12	56:D9:32:HIS:HA	1.94	0.48
1:AA:621:A:H2'	1:AA:622:A:C8	2.48	0.48
1:AA:1284:C:OP2	1:AA:1285:A:O2'	2.29	0.48
1:AA:1302:U:OP1	13:AM:13:LYS:HE3	2.13	0.48
2:AB:163:PHE:CD2	2:AB:185:ILE:HG13	2.48	0.48
3:AC:6:HIS:CD2	3:AC:8:ILE:HB	2.48	0.48
7:AG:80:VAL:HB	7:AG:85:TYR:HE2	1.77	0.48
8:AH:13:ILE:O	8:AH:17:THR:HG23	2.13	0.48
25:AY:32:PSU:C2	25:AY:33:U:H5	2.32	0.48
26:BA:247:G:H4'	26:BA:386:G:C5	2.48	0.48
26:BA:2138:C:C2	26:BA:2154:G:C2	3.02	0.48
34:BN:4:TYR:CD2	41:BU:100:VAL:HG11	2.48	0.48
34:BN:58:ASP:OD1	34:BN:58:ASP:N	2.40	0.48
37:BQ:52:VAL:HA	37:BQ:55:VAL:HG12	1.94	0.48
1:CA:73:G:C6	1:CA:97:G:C6	3.01	0.48
7:CG:20:ASP:HB3	7:CG:23:VAL:HB	1.95	0.48
8:CH:20:TYR:CE1	8:CH:76:PRO:HG2	2.48	0.48
8:CH:64:LYS:HG2	8:CH:79:VAL:HG21	1.94	0.48
11:CK:98:LEU:C	11:CK:101:SER:HG	2.20	0.48
25:CY:7:A:N6	25:CY:66:U:N3	2.17	0.48
26:DA:1127:A:N7	26:DA:2488:A:O2'	2.47	0.48
26:DA:1309:G:H3'	54:D7:9:ARG:HH12	1.78	0.48
26:DA:1922:G:H2'	26:DA:1923:U:O4'	2.13	0.48
32:DH:164:TYR:HB2	32:DH:167:GLU:HB2	1.95	0.48
1:AA:627:G:H2'	1:AA:628:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.42	0.48
1:AA:1425:U:H2'	1:AA:1426:C:C6	2.48	0.48
23:AW:26:A:N1	23:AW:44:G:N2	2.61	0.48
26:BA:630:G:OP1	55:B8:47:LYS:NZ	2.41	0.48
26:BA:800:A:H8	26:BA:800:A:OP1	1.96	0.48
26:BA:1786:A:H1'	26:BA:1938:A:N6	2.28	0.48
26:BA:2119:A:C2	26:BA:2170:A:H2'	2.48	0.48
26:BA:2640:G:OP1	34:BN:97:ARG:NH2	2.46	0.48
26:BA:2771:C:H2'	26:BA:2772:C:C6	2.48	0.48
35:BO:98:VAL:HG22	35:BO:118:ALA:HA	1.96	0.48
36:BP:63:PRO:HD3	55:B8:27:THR:HG22	1.94	0.48
39:BS:3:ARG:HE	39:BS:4:LEU:N	2.11	0.48
55:B8:23:VAL:CG1	55:B8:47:LYS:HD3	2.43	0.48
56:B9:7:VAL:HG12	56:B9:34:GLN:HB3	1.94	0.48
1:CA:339:C:H2'	1:CA:340:U:C6	2.49	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:H8	2.11	0.48
1:CA:1035:A:H2'	1:CA:1036:G:C8	2.48	0.48
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.13	0.48
15:CO:26:GLU:HB3	15:CO:81:LEU:HD13	1.96	0.48
25:CY:35:A:H2'	25:CY:36:A:O4'	2.13	0.48
26:DA:2126:A:H4'	26:DA:2127:G:OP1	2.13	0.48
26:DA:2331:G:O2'	26:DA:2336:A:N1	2.40	0.48
26:DA:2602:A:H4'	26:DA:2603:G:O5'	2.14	0.48
26:DA:2853:C:H2'	26:DA:2854:G:H8	1.77	0.48
28:DD:137:PRO:O	28:DD:140:THR:HG23	2.14	0.48
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.27	0.48
7:AG:150:ALA:HB2	11:AK:50:TYR:OH	2.13	0.48
26:BA:323:G:C8	30:BF:171:PRO:HG3	2.48	0.48
26:BA:1405:U:H2'	26:BA:1406:U:H6	1.78	0.48
33:BI:85:GLU:HB3	33:BI:86:THR:H	1.52	0.48
51:B4:26:SER:OG	51:B4:27:THR:N	2.45	0.48
1:CA:141:A:H1'	1:CA:182:U:O2	2.13	0.48
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.78	0.48
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.49	0.48
2:CB:71:VAL:HG23	2:CB:163:PHE:O	2.14	0.48
5:CE:12:LEU:HB3	5:CE:31:LEU:HB2	1.95	0.48
19:CS:17:GLU:O	19:CS:17:GLU:HG2	2.14	0.48
25:CY:69:G:C2	25:CY:70:G:H1'	2.48	0.48
26:DA:2203:U:H4'	28:DD:151:LYS:HG2	1.95	0.48
31:DG:43:LEU:HD12	31:DG:45:GLU:HG3	1.96	0.48
34:DN:38:HIS:ND1	34:DN:39:ARG:HG3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:DR:103:ARG:NH1	38:DR:108:GLY:O	2.42	0.48
41:DU:78:THR:O	41:DU:117:GLN:NE2	2.46	0.48
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.94	0.48
26:BA:184:C:H2'	26:BA:185:U:H6	1.78	0.48
26:BA:893:C:H2'	26:BA:894:C:H6	1.79	0.48
26:BA:1540:U:H2'	26:BA:1541:G:O4'	2.13	0.48
26:BA:1668:A:H4'	26:BA:1669:A:O5'	2.14	0.48
26:BA:2141:G:N3	26:BA:2142:C:H1'	2.29	0.48
29:BE:178:GLU:N	29:BE:178:GLU:OE2	2.46	0.48
33:BI:47:LEU:O	33:BI:51:ILE:HG13	2.13	0.48
33:BI:61:ARG:N	33:BI:61:ARG:HD2	2.28	0.48
48:B1:72:GLU:O	48:B1:76:ARG:HG3	2.13	0.48
1:CA:189(C):C:H2'	1:CA:189(D):C:O4'	2.14	0.48
1:CA:428:G:H4'	1:CA:429:U:O5'	2.12	0.48
1:CA:1029:C:N4	1:CA:1032:G:C6	2.77	0.48
1:CA:1190:G:OP1	3:CC:5:ILE:N	2.38	0.48
1:CA:1262:C:H2'	1:CA:1263:C:H6	1.79	0.48
2:CB:178:ARG:NH2	8:CH:68:ARG:HH12	2.10	0.48
9:CI:16:ARG:HH11	9:CI:66:ARG:HH11	1.62	0.48
26:DA:184:C:H2'	26:DA:185:U:C6	2.48	0.48
26:DA:861:A:N3	27:DB:79:C:O2'	2.41	0.48
26:DA:1364:G:P	48:D1:3:LYS:HG3	2.53	0.48
30:DF:183:VAL:O	30:DF:187:VAL:HG23	2.13	0.48
40:DT:59:THR:HG23	40:DT:78:LEU:HB3	1.96	0.48
1:AA:62:U:OP1	1:AA:385:C:O2'	2.26	0.48
1:AA:1429:C:H2'	1:AA:1430:C:C6	2.48	0.48
8:AH:51:VAL:HG12	8:AH:52:ASP:N	2.28	0.48
25:AY:63:G:C2	25:AY:64:A:H1'	2.48	0.48
26:BA:288:C:H2'	26:BA:289:A:H8	1.79	0.48
26:BA:1231:G:H2'	26:BA:1232:G:C8	2.48	0.48
26:BA:1996:C:H4'	26:BA:1997:G:OP1	2.12	0.48
26:BA:2129:C:H2'	26:BA:2130:U:H6	1.77	0.48
26:BA:2140:C:C2	26:BA:2151:G:N2	2.82	0.48
26:BA:2386:C:H2'	26:BA:2387:U:C6	2.49	0.48
1:CA:408:A:H4'	4:CD:112:VAL:HG21	1.96	0.48
1:CA:742:G:P	15:CO:35:ARG:HH22	2.36	0.48
1:CA:1060:C:H2'	1:CA:1061:G:H8	1.77	0.48
1:CA:1119:C:C4	1:CA:1154:G:O6	2.66	0.48
1:CA:1135:U:H2'	1:CA:1137:C:O2	2.14	0.48
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.28	0.48
26:DA:952:G:H5''	26:DA:953:A:OP2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:DA:4209:HOH:O	29:DE:135:HIS:NE2	2.24	0.48
31:DG:125:PHE:HB3	31:DG:166:ASP:OD1	2.14	0.48
35:DO:4:PRO:O	35:DO:5:GLN:HB2	2.14	0.48
44:DX:20:GLY:HA2	44:DX:23:GLU:OE2	2.14	0.48
1:AA:300:A:O2'	1:AA:564:C:N3	2.39	0.48
1:AA:1158:C:H5	1:AA:1181:G:N1	2.06	0.48
7:AG:111:ARG:HD2	7:AG:123:GLU:HB2	1.95	0.48
10:AJ:11:PHE:CE1	10:AJ:67:THR:HG22	2.49	0.48
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.14	0.48
26:BA:196:A:N3	26:BA:196:A:H2'	2.27	0.48
26:BA:1665:A:H2'	26:BA:1666:G:O4'	2.14	0.48
26:BA:2328:A:H2'	26:BA:2329:G:H8	1.75	0.48
28:BD:70:TRP:HB3	28:BD:190:TYR:CZ	2.49	0.48
31:BG:11:TYR:CZ	31:BG:16:ARG:HD3	2.48	0.48
31:BG:66:GLN:HB3	31:BG:92:VAL:HG21	1.94	0.48
39:BS:59:LYS:HE3	39:BS:60:GLY:H	1.79	0.48
1:CA:1125:U:H3'	1:CA:1126:U:H5''	1.96	0.48
1:CA:1228:C:OP1	13:CM:115:LYS:N	2.23	0.48
1:CA:1255:G:O2'	1:CA:1258:G:O2'	2.24	0.48
2:CB:81:VAL:HB	2:CB:94:ASN:HD21	1.78	0.48
7:CG:12:LEU:H	7:CG:12:LEU:HD12	1.78	0.48
14:CN:27:CYS:SG	14:CN:29:ARG:HB2	2.53	0.48
26:DA:171:G:H2'	26:DA:172:C:C6	2.49	0.48
26:DA:1472:A:H2'	26:DA:1473:G:O4'	2.13	0.48
26:DA:2162:G:H4'	26:DA:2172:U:O2'	2.13	0.48
26:DA:2695:C:H2'	26:DA:2696:U:C6	2.49	0.48
29:DE:108:SER:HB3	29:DE:165:VAL:HG21	1.96	0.48
30:DF:120:GLU:CB	30:DF:122:LYS:HG2	2.44	0.48
46:DZ:110:GLY:HA3	46:DZ:145:GLU:HA	1.96	0.48
53:D6:11:LEU:HB2	53:D6:21:TYR:HB2	1.95	0.48
1:AA:328:C:H4'	1:AA:329:A:H5'	1.96	0.48
1:AA:1149:C:H2'	1:AA:1150:U:H6	1.77	0.48
4:AD:3:ARG:HD3	4:AD:118:ARG:CD	2.44	0.48
5:AE:36:ASP:OD1	5:AE:38:GLN:N	2.38	0.48
26:BA:582:G:H2'	26:BA:583:G:C8	2.49	0.48
26:BA:848:G:H2'	26:BA:849:A:C8	2.48	0.48
26:BA:2116:G:N2	26:BA:2162:G:OP1	2.46	0.48
26:BA:2183:C:H2'	26:BA:2184:G:H8	1.78	0.48
26:BA:2791:C:H6	26:BA:2791:C:OP2	1.96	0.48
39:BS:15:ARG:NE	39:BS:88:ASP:OD2	2.45	0.48
47:B0:53:MET:HG3	47:B0:59:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:10:A:OP2	5:CE:126:ARG:HD2	2.14	0.48
1:CA:707:C:H2'	1:CA:708:C:C6	2.49	0.48
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.78	0.48
1:CA:1133:G:N2	1:CA:1141:C:N3	2.58	0.48
2:CB:46:LYS:O	2:CB:50:GLU:HB2	2.14	0.48
3:CC:32:LEU:HD12	3:CC:59:ARG:HH22	1.79	0.48
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.96	0.48
5:CE:84:PHE:N	5:CE:87:SER:O	2.45	0.48
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.95	0.48
26:DA:77:C:H42	26:DA:109:G:H1	1.61	0.48
26:DA:390:A:H4'	26:DA:391:G:H5'	1.94	0.48
26:DA:828:U:H2'	26:DA:829:A:C8	2.49	0.48
26:DA:1363:C:O2'	26:DA:1809:A:N3	2.37	0.48
26:DA:1434:A:H61	26:DA:1558:A:N6	2.12	0.48
26:DA:2118:U:C4	26:DA:2149:G:H1'	2.48	0.48
26:DA:2293:C:H42	26:DA:2339:G:H1	1.61	0.48
26:DA:2540:C:H2'	26:DA:2541:A:O4'	2.14	0.48
28:DD:108:PRO:HB3	28:DD:143:HIS:CE1	2.49	0.48
31:DG:15:VAL:HG13	31:DG:175:LEU:HD23	1.96	0.48
34:DN:34:LEU:O	34:DN:49:GLY:HA3	2.13	0.48
37:DQ:36:ALA:HB2	37:DQ:103:MET:SD	2.54	0.48
1:AA:501:C:H2'	1:AA:502:G:H8	1.78	0.48
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.49	0.48
9:AI:99:LEU:HB3	9:AI:101:PHE:CD1	2.49	0.48
10:AJ:49:VAL:HG23	14:AN:41:ARG:HD2	1.96	0.48
12:AL:34:ARG:NH2	61:AL:201:HOH:O	2.25	0.48
23:AW:47:U:H5'	23:AW:47:U:C6	2.45	0.48
26:BA:493:G:O6	61:BA:4550:HOH:O	2.19	0.48
26:BA:2099:U:H2'	26:BA:2100:G:C8	2.49	0.48
26:BA:2286:A:H4'	26:BA:2287:A:O4'	2.14	0.48
26:BA:2572:A:C8	29:BE:144:ARG:HD2	2.49	0.48
32:BH:154:PRO:HB3	32:BH:163:TYR:CE2	2.49	0.48
35:BO:16:ALA:HB2	35:BO:52:VAL:HG21	1.96	0.48
51:B4:59:PHE:C	51:B4:61:ARG:H	2.21	0.48
1:CA:93:G:C2'	1:CA:96:U:H5'	2.44	0.48
1:CA:1030(A):G:N3	1:CA:1030(C):G:C8	2.81	0.48
1:CA:1058:G:H1	1:CA:1199:U:H3	1.62	0.48
1:CA:1063:C:H3'	1:CA:1064:G:H2'	1.96	0.48
1:CA:1179:A:H2'	1:CA:1180:A:O4'	2.13	0.48
1:CA:1333:A:H2'	1:CA:1334:G:O4'	2.14	0.48
3:CC:87:LEU:O	3:CC:91:LEU:N	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:33:TYR:CD2	6:CF:75:LEU:HD23	2.49	0.48
12:CL:53:ARG:HH12	12:CL:92:ASP:HB2	1.79	0.48
26:DA:272(E):G:C2	26:DA:364:C:C2	3.02	0.48
26:DA:1889:A:H2'	26:DA:1890:A:C8	2.49	0.48
26:DA:2586:C:OP2	26:DA:2608:G:N1	2.42	0.48
26:DA:2820:A:OP1	38:DR:4:LEU:HD23	2.14	0.48
27:DB:5:C:OP1	27:DB:61:G:O2'	2.31	0.48
28:DD:73:VAL:HG13	28:DD:120:GLY:HA3	1.95	0.48
53:D6:6:ARG:NH1	53:D6:26:ASN:HB2	2.28	0.48
1:AA:1137:C:H3'	1:AA:1137:C:H6	1.77	0.47
25:AY:5:G:C2	25:AY:6:G:C4	3.02	0.47
25:AY:58:A:H4'	25:AY:59:U:OP1	2.14	0.47
26:BA:527:C:C5	26:BA:2779:U:H2'	2.49	0.47
30:BF:150:GLY:HA2	30:BF:172:TRP:CD2	2.49	0.47
31:BG:16:ARG:HE	31:BG:31:VAL:HG11	1.79	0.47
36:BP:50:ARG:HD3	55:B8:7:HIS:CD2	2.49	0.47
1:CA:89:C:H2'	1:CA:90:U:O4'	2.14	0.47
1:CA:130:A:O2'	1:CA:131:C:O5'	2.28	0.47
1:CA:933:G:O6	7:CG:3:ARG:NH2	2.47	0.47
1:CA:1121:U:C4	1:CA:1122:U:C4	3.01	0.47
1:CA:1371:G:O3'	9:CI:69:GLY:HA3	2.14	0.47
2:CB:139:LYS:O	2:CB:143:GLU:HG3	2.14	0.47
2:CB:212:GLN:NE2	2:CB:234:PRO:O	2.46	0.47
3:CC:101:LEU:HD12	3:CC:102:ASN:N	2.29	0.47
26:DA:196:A:O2'	26:DA:805:G:O6	2.27	0.47
26:DA:1365:A:OP2	48:D1:3:LYS:HG2	2.14	0.47
26:DA:2564:A:C2	26:DA:2647:U:H4'	2.49	0.47
27:DB:14:U:H5'	27:DB:70:C:O2	2.13	0.47
1:AA:950:U:H2'	1:AA:951:G:H8	1.80	0.47
5:AE:90:VAL:O	5:AE:120:THR:HA	2.14	0.47
13:AM:123:ALA:HB2	23:AW:39:PSU:H1'	1.95	0.47
19:AS:40:ILE:HD11	19:AS:74:PHE:HE1	1.78	0.47
26:BA:667:U:O2	55:B8:2:PRO:HD2	2.14	0.47
32:BH:117:PRO:HG3	32:BH:123:PHE:CD2	2.49	0.47
33:BI:130:TYR:N	33:BI:138:ILE:O	2.42	0.47
35:BO:4:PRO:O	35:BO:5:GLN:HB2	2.14	0.47
36:BP:82:GLY:HA2	36:BP:113:LYS:O	2.13	0.47
1:CA:392:G:H2'	1:CA:393:A:C8	2.48	0.47
1:CA:646:U:H2'	1:CA:647:C:H6	1.75	0.47
1:CA:657:G:H4'	15:CO:28:GLN:HG2	1.96	0.47
1:CA:1125:U:C2'	1:CA:1126:U:H5''	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1298:C:H4'	1:CA:1299:A:H5'	1.96	0.47
20:CT:24:LEU:HD13	20:CT:24:LEU:HA	1.69	0.47
23:CW:8:4SU:S4	23:CW:14:A:N7	2.88	0.47
24:CX:67:C:C2'	24:CX:68:C:H5'	2.43	0.47
26:DA:93:G:H2'	26:DA:94:C:C6	2.49	0.47
26:DA:817:C:H2'	26:DA:818:G:O4'	2.14	0.47
26:DA:1449:A:HO2'	26:DA:1529:G:H21	1.58	0.47
26:DA:1641:A:H2'	26:DA:1642:G:O4'	2.14	0.47
26:DA:2141:G:H2'	26:DA:2142:C:O4'	2.14	0.47
26:DA:2304:G:H22	26:DA:2312:U:H3	1.61	0.47
26:DA:2776:A:H4'	26:DA:2777:G:H5''	1.96	0.47
1:AA:165:C:H2'	1:AA:166:G:H8	1.79	0.47
1:AA:371:G:O2'	1:AA:373:A:N7	2.47	0.47
1:AA:596:C:OP2	61:AA:4083:HOH:O	2.20	0.47
1:AA:950:U:H2'	1:AA:951:G:C8	2.49	0.47
3:AC:118:GLN:H	3:AC:118:GLN:HG2	1.45	0.47
26:BA:446:G:OP1	41:BU:3:ARG:NH1	2.42	0.47
26:BA:900:A:H2'	26:BA:901:A:O4'	2.14	0.47
26:BA:1709:U:H2'	26:BA:1710:C:C6	2.48	0.47
33:BI:114:LEU:HD13	33:BI:130:TYR:HD1	1.78	0.47
37:BQ:34:LEU:HD11	37:BQ:129:THR:HB	1.95	0.47
55:B8:42:ARG:HD2	61:B8:205:HOH:O	2.15	0.47
1:CA:934:C:OP1	61:CA:4164:HOH:O	2.20	0.47
1:CA:1128:C:H1'	1:CA:1147:C:N4	2.25	0.47
1:CA:1320:C:O4'	19:CS:73:GLU:HG3	2.13	0.47
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.96	0.47
10:CJ:8:LEU:HB3	10:CJ:16:LEU:HD22	1.95	0.47
21:CU:12:LYS:HD3	21:CU:22:ARG:HB3	1.96	0.47
26:DA:39:C:H2'	26:DA:40:C:C6	2.49	0.47
26:DA:322:A:OP1	30:DF:168:ARG:HD2	2.14	0.47
26:DA:615:G:OP1	30:DF:40:GLN:HG2	2.14	0.47
26:DA:2723:C:H5''	38:DR:1:MET:HE2	1.97	0.47
28:DD:71:ASP:HB3	28:DD:103:ARG:NH2	2.28	0.47
29:DE:144:ARG:HB3	29:DE:145:LYS:H	1.48	0.47
29:DE:178:GLU:OE2	29:DE:178:GLU:N	2.42	0.47
31:DG:43:LEU:C	31:DG:45:GLU:H	2.22	0.47
32:DH:7:LEU:O	32:DH:69:ARG:NH1	2.40	0.47
37:DQ:37:LEU:HD21	37:DQ:130:LYS:HE2	1.96	0.47
42:DV:5:VAL:HG11	42:DV:57:VAL:HG21	1.96	0.47
44:DX:4:ALA:HB1	44:DX:42:ALA:HA	1.95	0.47
1:AA:461:A:O2'	1:AA:470:C:H5'	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:134:ILE:HG22	3:AC:168:ALA:HB3	1.96	0.47
7:AG:111:ARG:HB3	7:AG:113:GLU:OE2	2.14	0.47
10:AJ:47:PHE:HB2	10:AJ:63:PHE:HB2	1.96	0.47
26:BA:616:G:H5'	30:BF:205:ARG:HD2	1.96	0.47
26:BA:899:A:HO2'	26:BA:900:A:H8	1.60	0.47
26:BA:1701:A:OP2	61:BA:5017:HOH:O	2.20	0.47
26:BA:2712:U:OP1	26:BA:2714:G:H4'	2.14	0.47
27:BB:66:A:N6	27:BB:108:U:H2'	2.28	0.47
41:BU:86:ALA:O	42:BV:49:THR:HG23	2.14	0.47
1:CA:736:C:H2'	1:CA:737:A:C8	2.49	0.47
1:CA:1030(A):G:N2	1:CA:1030(C):G:H3'	2.30	0.47
1:CA:1057:G:H5'	3:CC:155:GLY:HA2	1.95	0.47
1:CA:1181:G:O2'	1:CA:1182:G:N7	2.47	0.47
19:CS:32:LYS:HE3	19:CS:57:HIS:CD2	2.49	0.47
26:DA:816:C:OP1	26:DA:1185:C:O2'	2.22	0.47
26:DA:851:U:O2'	50:D3:42:ALA:O	2.30	0.47
35:DO:7:TYR:CZ	35:DO:44:LYS:HG3	2.50	0.47
42:DV:21:ARG:HG2	42:DV:91:TYR:CD2	2.49	0.47
1:AA:1027:C:H2'	1:AA:1028:C:C6	2.49	0.47
2:AB:36:ARG:C	2:AB:38:GLY:H	2.21	0.47
12:AL:97:ARG:HB2	12:AL:98:TYR:CE2	2.49	0.47
23:AW:76:31M:HNH1	26:BA:2061:G:H22	1.62	0.47
25:AY:32:PSU:C2	25:AY:33:U:C5	3.02	0.47
25:AY:50:U:H2'	25:AY:51:U:C6	2.48	0.47
26:BA:302:C:OP2	45:BY:73:ARG:NH2	2.46	0.47
26:BA:1031:G:H21	56:B9:36:GLN:HE22	1.62	0.47
32:BH:20:ALA:HB1	32:BH:21:PRO:HD2	1.97	0.47
35:BO:120:GLU:HG2	35:BO:122:LEU:HG	1.97	0.47
1:CA:727:G:P	1:CA:742:G:H21	2.38	0.47
1:CA:1328:C:O2'	13:CM:29:ARG:NH2	2.45	0.47
2:CB:120:ALA:O	2:CB:122:PHE:N	2.43	0.47
3:CC:69:HIS:CD2	3:CC:104:GLN:HB3	2.49	0.47
4:CD:173:TRP:NE1	4:CD:189:PRO:HG3	2.29	0.47
8:CH:33:GLU:HG2	8:CH:48:TYR:CE1	2.49	0.47
21:CU:15:ARG:HH11	21:CU:15:ARG:HB2	1.79	0.47
26:DA:709:U:H2'	26:DA:710:G:C8	2.50	0.47
28:DD:4:LYS:HB3	28:DD:18:VAL:CG2	2.44	0.47
33:DI:31:LEU:HD21	33:DI:38:LEU:HG	1.96	0.47
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.97	0.47
1:AA:1191:A:H5''	3:AC:4:LYS:HZ2	1.79	0.47
1:AA:1210:C:N4	1:AA:1211:U:O4	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:166:ASP:O	2:AB:170:GLU:N	2.39	0.47
4:AD:175:SER:OG	4:AD:184:LYS:HB2	2.14	0.47
25:AY:18:G:H1	25:AY:55:PSU:H1'	1.80	0.47
25:AY:36:A:N6	25:AY:37:MIA:C6	2.78	0.47
26:BA:143:G:H1'	44:BX:37:THR:HG21	1.97	0.47
26:BA:1178:C:O5'	26:BA:1178:C:H6	1.96	0.47
30:BF:172:TRP:H	30:BF:172:TRP:CD1	2.32	0.47
1:CA:952:U:H4'	1:CA:964:A:N1	2.30	0.47
4:CD:57:ARG:NH2	5:CE:107:ARG:HD3	2.28	0.47
7:CG:89:MET:SD	7:CG:155:ARG:HB2	2.55	0.47
14:CN:26:ARG:HB3	14:CN:43:CYS:SG	2.54	0.47
24:CX:23:C:H2'	24:CX:24:U:C6	2.49	0.47
26:DA:310:A:H1'	26:DA:311:A:H2'	1.95	0.47
26:DA:1410:G:H2'	26:DA:1411:C:C6	2.49	0.47
26:DA:1528(A):A:H2'	26:DA:1529:G:O4'	2.15	0.47
26:DA:2528:U:H5''	56:D9:31:LYS:HE2	1.97	0.47
61:DA:3829:HOH:O	30:DF:68:LYS:HE2	2.14	0.47
30:DF:29:ASN:O	30:DF:112:MET:HE1	2.13	0.47
32:DH:86:GLU:OE2	32:DH:132:ARG:NH2	2.47	0.47
1:AA:46:G:O2'	1:AA:365:U:O2	2.31	0.47
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.20	0.47
1:AA:1346:A:N1	1:AA:1374:A:H5''	2.30	0.47
1:AA:1360:A:H2'	1:AA:1361:G:O4'	2.15	0.47
2:AB:63:MET:HB3	2:AB:225:ALA:HB1	1.97	0.47
2:AB:102:LEU:HB3	2:AB:180:LEU:HD12	1.96	0.47
2:AB:188:ALA:HB1	2:AB:192:SER:OG	2.15	0.47
3:AC:32:LEU:HD13	3:AC:59:ARG:HD3	1.97	0.47
25:AY:27:G:N2	25:AY:44:G:N3	2.63	0.47
25:AY:58:A:O2'	25:AY:60:U:OP2	2.29	0.47
26:BA:1045:A:OP1	26:BA:1046:A:H3'	2.15	0.47
26:BA:1173:G:N2	26:BA:1177:A:OP2	2.31	0.47
26:BA:2110:G:H4'	26:BA:2111:C:OP2	2.15	0.47
26:BA:2117:A:O2'	26:BA:2118:U:H5''	2.15	0.47
26:BA:2701:C:H2'	26:BA:2702:U:H2'	1.96	0.47
31:BG:28:VAL:HG23	31:BG:29:TRP:CD1	2.50	0.47
32:BH:69:ARG:HG3	32:BH:70:THR:N	2.30	0.47
40:BT:53:ARG:HB3	40:BT:53:ARG:NH1	2.30	0.47
41:BU:85:LYS:HE2	41:BU:117:GLN:HA	1.97	0.47
45:BY:30:VAL:HG13	45:BY:37:VAL:HG12	1.97	0.47
53:B6:16:CYS:SG	53:B6:18:ARG:HD3	2.54	0.47
1:CA:109:A:C6	1:CA:326:G:C6	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:627:G:H2'	1:CA:628:G:H8	1.78	0.47
1:CA:988:G:C4'	1:CA:1014:A:H61	2.28	0.47
1:CA:1133:G:H2'	1:CA:1134:G:C8	2.49	0.47
2:CB:54:THR:HG23	2:CB:199:TYR:HB3	1.96	0.47
2:CB:115:LEU:HD11	2:CB:153:ARG:CZ	2.44	0.47
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.14	0.47
9:CI:88:TYR:CD1	9:CI:89:ASN:HB2	2.49	0.47
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.97	0.47
10:CJ:46:ARG:HG2	10:CJ:64:GLU:HB3	1.97	0.47
13:CM:10:PRO:HD2	13:CM:18:ALA:HB1	1.95	0.47
13:CM:92:HIS:CE1	13:CM:98:VAL:HG11	2.49	0.47
22:CV:14:A:H8	22:CV:14:A:OP1	1.97	0.47
26:DA:118:A:N3	26:DA:178:G:H1'	2.30	0.47
26:DA:855:G:O2'	47:D0:27:GLU:OE2	2.31	0.47
26:DA:897:C:H3'	26:DA:898:C:C6	2.50	0.47
26:DA:1196:C:H2'	26:DA:1197:G:H8	1.79	0.47
26:DA:1514:U:H2'	26:DA:1515:G:H8	1.80	0.47
26:DA:1877:A:H5'	26:DA:1878:G:OP2	2.15	0.47
26:DA:2086:U:H2'	26:DA:2087:G:C8	2.49	0.47
26:DA:2364:C:H2'	26:DA:2365:G:O4'	2.14	0.47
26:DA:2751:G:C8	32:DH:2:SER:HA	2.49	0.47
26:DA:2788:C:H2'	26:DA:2789:C:C6	2.50	0.47
28:DD:5:LYS:HE3	28:DD:5:LYS:HB3	1.52	0.47
29:DE:5:LEU:HD11	29:DE:79:ARG:HB2	1.96	0.47
31:DG:121:ASN:HB3	31:DG:124:SER:HB2	1.97	0.47
32:DH:144:VAL:O	32:DH:148:ILE:HG12	2.15	0.47
46:DZ:108:PRO:HB2	46:DZ:111:VAL:HG23	1.96	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:NH1	2.30	0.47
48:D1:3:LYS:HB2	48:D1:61:ARG:HH12	1.80	0.47
1:AA:407:G:OP1	4:AD:115:ARG:NH2	2.48	0.47
1:AA:1293:G:H2'	1:AA:1294:G:C8	2.49	0.47
26:BA:41:C:H2'	26:BA:42:G:O4'	2.15	0.47
26:BA:1311:G:O2'	54:B7:47:ARG:NH2	2.47	0.47
46:BZ:107:THR:HA	46:BZ:108:PRO:HD3	1.77	0.47
1:CA:337:C:H2'	1:CA:338:A:H8	1.79	0.47
1:CA:1027:C:OP1	1:CA:1027:C:H4'	2.14	0.47
1:CA:1179:A:C6	1:CA:1180:A:C4	3.03	0.47
1:CA:1343:G:H2'	1:CA:1344:C:C6	2.50	0.47
3:CC:6:HIS:HB3	14:CN:49:HIS:ND1	2.30	0.47
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.15	0.47
24:CX:44:A:C6	24:CX:45:G:C6	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:121:G:H4'	26:DA:149:A:H5'	1.97	0.47
26:DA:797:C:H2'	26:DA:798:G:O4'	2.14	0.47
26:DA:1025:G:C4	26:DA:1135:C:H1'	2.49	0.47
26:DA:1270:C:H5''	26:DA:1271:G:O5'	2.15	0.47
26:DA:2306:C:H3'	26:DA:2307:G:H2'	1.97	0.47
26:DA:2506:U:OP1	29:DE:144:ARG:NH2	2.48	0.47
26:DA:2522:U:O2'	26:DA:2647:U:OP1	2.25	0.47
26:DA:2722:G:H2'	26:DA:2723:C:C6	2.50	0.47
43:DW:14:PRO:HG2	43:DW:78:GLU:HG2	1.97	0.47
51:D4:53:GLU:HG2	51:D4:55:ARG:N	2.29	0.47
1:AA:299:G:O6	61:AA:4081:HOH:O	2.14	0.47
1:AA:1028:C:H2'	1:AA:1029:C:H4'	1.96	0.47
1:AA:1132:C:H2'	1:AA:1133:G:C8	2.50	0.47
1:AA:1443:G:N2	1:AA:1459:C:O2	2.37	0.47
2:AB:17:PHE:CD2	2:AB:44:LEU:HD21	2.48	0.47
26:BA:1243:G:O2'	36:BP:7:ARG:NH2	2.47	0.47
26:BA:1799:G:O2'	28:BD:181:GLU:OE2	2.22	0.47
28:BD:72:LYS:HB3	28:BD:75:ILE:HD12	1.97	0.47
1:CA:1118:C:H1'	1:CA:1179:A:C5	2.50	0.47
1:CA:1139:G:H4'	1:CA:1140:C:OP1	2.14	0.47
9:CI:16:ARG:HH11	9:CI:64:THR:HG21	1.80	0.47
19:CS:32:LYS:HA	19:CS:50:ALA:HB3	1.96	0.47
24:CX:19:G:H4'	24:CX:20:U:OP2	2.15	0.47
26:DA:77:C:OP1	49:D2:59:ARG:HD3	2.14	0.47
26:DA:315:G:H2'	26:DA:316:C:C6	2.50	0.47
26:DA:601:C:O2'	30:DF:104:LYS:NZ	2.44	0.47
26:DA:2166:G:H3'	26:DA:2167:U:C5'	2.40	0.47
26:DA:2563:U:H4'	35:DO:28:SER:HA	1.97	0.47
40:DT:29:ARG:HB3	40:DT:87:ASP:HB2	1.97	0.47
1:AA:156:G:N1	1:AA:165:C:N3	2.55	0.47
1:AA:1030(B):C:H2'	1:AA:1030(B):C:O2	2.15	0.47
2:AB:19:HIS:O	2:AB:39:ILE:HG23	2.15	0.47
31:BG:144:ILE:HA	31:BG:148:MET:HE1	1.97	0.47
36:BP:59:LEU:HD11	55:B8:10:ALA:HB2	1.97	0.47
43:BW:2:GLU:OE2	43:BW:72:LYS:NZ	2.38	0.47
2:CB:185:ILE:HG22	2:CB:199:TYR:HD2	1.79	0.47
4:CD:140:VAL:HG11	4:CD:146:ILE:HD11	1.95	0.47
7:CG:44:TYR:O	7:CG:47:CYS:HB2	2.15	0.47
8:CH:124:ALA:O	8:CH:128:GLY:N	2.48	0.47
13:CM:54:VAL:HA	13:CM:57:ARG:HB3	1.97	0.47
23:CW:29:G:N2	23:CW:41:C:N3	2.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:511:U:H4'	26:DA:1235:G:H4'	1.96	0.47
26:DA:571:A:N6	26:DA:2499:C:O3'	2.47	0.47
26:DA:1514:U:H2'	26:DA:1515:G:C8	2.50	0.47
26:DA:2298:A:C8	26:DA:2299:G:C8	3.03	0.47
26:DA:2319:G:N2	39:DS:3:ARG:HA	2.30	0.47
26:DA:2477:C:N4	56:D9:10:ILE:HG23	2.30	0.47
27:DB:115:G:H2'	27:DB:116:G:O4'	2.15	0.47
31:DG:143:GLU:H	31:DG:143:GLU:HG2	1.41	0.47
46:DZ:57:ILE:HD12	46:DZ:71:VAL:HG23	1.97	0.47
1:AA:161:A:H2'	1:AA:162:A:C8	2.50	0.46
1:AA:163:C:H2'	1:AA:164:U:C6	2.49	0.46
1:AA:346:G:C3'	1:AA:347:G:H4'	2.45	0.46
1:AA:625:G:H2'	1:AA:626:U:H6	1.79	0.46
1:AA:953:G:N7	13:AM:104:ARG:NH2	2.63	0.46
1:AA:1028:C:N4	1:AA:1033:G:H1	2.10	0.46
1:AA:1183:A:HO2'	1:AA:1184:G:P	2.35	0.46
1:AA:1530:G:OP1	1:AA:1530:G:H4'	2.14	0.46
2:AB:30:ARG:HG3	2:AB:31:TYR:CD1	2.50	0.46
23:AW:52:G:H4'	37:BQ:56:ARG:HH12	1.80	0.46
26:BA:303:U:H2'	26:BA:304:G:H8	1.80	0.46
26:BA:620:G:N3	26:BA:620:G:H5'	2.30	0.46
26:BA:1587:A:H2'	26:BA:1588:C:C6	2.50	0.46
26:BA:1641:A:H2'	26:BA:1642:G:O4'	2.14	0.46
38:BR:104:ARG:HG3	38:BR:111:LEU:HD21	1.97	0.46
1:CA:309:G:O2'	1:CA:607:A:N1	2.48	0.46
1:CA:1456:G:N1	20:CT:51:GLU:OE1	2.45	0.46
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.48	0.46
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	1.96	0.46
26:DA:854:G:H2'	26:DA:855:G:C8	2.50	0.46
26:DA:1116:C:H2'	26:DA:1117:G:H8	1.79	0.46
26:DA:1169:G:H8	26:DA:1169:G:O5'	1.98	0.46
26:DA:1430:C:H2'	26:DA:1431:U:C6	2.49	0.46
26:DA:1797:C:H4'	28:DD:257:LEU:O	2.15	0.46
26:DA:2059:A:O2'	30:DF:69:HIS:HD2	1.98	0.46
26:DA:2516:G:O6	26:DA:2517:C:N4	2.48	0.46
26:DA:2846:G:H2'	26:DA:2847:U:O4'	2.14	0.46
37:DQ:45:GLN:H	37:DQ:45:GLN:CD	2.23	0.46
42:DV:40:LEU:HB2	42:DV:46:VAL:HG13	1.96	0.46
1:AA:382:A:H2'	1:AA:383:A:C8	2.49	0.46
1:AA:1002:G:H3'	1:AA:1003:G:H8	1.81	0.46
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:17:PHE:HB2	2:AB:44:LEU:HD11	1.96	0.46
2:AB:21:ARG:H	2:AB:21:ARG:HD2	1.80	0.46
2:AB:102:LEU:HD23	2:AB:182:ILE:HD12	1.98	0.46
5:AE:43:LEU:HD21	5:AE:132:ALA:HB1	1.97	0.46
23:AW:6:G:N1	23:AW:67:C:N4	2.39	0.46
26:BA:744:G:OP1	29:BE:132:HIS:ND1	2.43	0.46
26:BA:1028:A:N6	26:BA:1125:G:H2'	2.30	0.46
26:BA:1179:C:H2'	26:BA:1180:C:H6	1.80	0.46
26:BA:2010:G:H5''	43:BW:42:ARG:HB2	1.98	0.46
26:BA:2887:U:H2'	26:BA:2888:C:C6	2.49	0.46
30:BF:93:LYS:HD3	30:BF:93:LYS:HA	1.68	0.46
31:BG:146:TYR:O	31:BG:146:TYR:HD1	1.98	0.46
1:CA:772:U:H2'	1:CA:773:G:O4'	2.15	0.46
2:CB:76:GLN:HG3	2:CB:206:ASP:O	2.15	0.46
7:CG:76:ARG:HB3	7:CG:156:TRP:HH2	1.80	0.46
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.30	0.46
10:CJ:23:ILE:HD13	10:CJ:23:ILE:HA	1.77	0.46
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.16	0.46
23:CW:76:31M:N	24:CX:76:A:O3'	2.49	0.46
25:CY:74:C:H4'	48:D1:23:LYS:HE3	1.97	0.46
26:DA:229:A:H5''	26:DA:230:U:H5'	1.96	0.46
26:DA:528:A:OP2	34:DN:114:ARG:NH1	2.48	0.46
26:DA:1630:G:H2'	26:DA:1631:C:C6	2.51	0.46
26:DA:1786:A:H1'	26:DA:1938:A:N6	2.31	0.46
26:DA:1932:A:H2'	26:DA:1933:G:O4'	2.15	0.46
26:DA:2141:G:C8	26:DA:2151:G:N2	2.83	0.46
26:DA:2318:G:H4'	26:DA:2319:G:OP1	2.14	0.46
26:DA:2516:G:C6	26:DA:2517:C:C4	3.03	0.46
26:DA:2647:U:H2'	26:DA:2648:C:C6	2.51	0.46
26:DA:2836:U:H2'	26:DA:2837:G:C8	2.50	0.46
37:DQ:133:ARG:HG2	37:DQ:134:ARG:N	2.30	0.46
40:DT:16:ARG:HB3	40:DT:16:ARG:HH11	1.80	0.46
42:DV:60:GLU:HB3	42:DV:95:LEU:HB3	1.97	0.46
1:AA:406:G:H4'	4:AD:3:ARG:HH22	1.80	0.46
1:AA:688:G:H5'	11:AK:46:GLY:C	2.40	0.46
1:AA:743:U:H2'	1:AA:744:C:C6	2.51	0.46
2:AB:59:GLU:HG3	2:AB:225:ALA:HB2	1.96	0.46
4:AD:163:GLU:O	4:AD:165:MET:N	2.48	0.46
15:AO:18:PHE:CZ	15:AO:21:ASP:HB3	2.50	0.46
18:AR:58:LEU:HB3	18:AR:62:GLU:HG3	1.98	0.46
25:AY:12:U:C2	25:AY:24:G:C2	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:69:G:C5	25:AY:70:G:C8	3.03	0.46
26:BA:278:A:O2'	26:BA:279:C:OP1	2.23	0.46
26:BA:527:C:C4	26:BA:2779:U:H2'	2.50	0.46
26:BA:615:G:OP1	30:BF:40:GLN:HG2	2.15	0.46
26:BA:1107:G:H2'	26:BA:1107:G:N3	2.29	0.46
26:BA:1653:G:H3'	38:BR:2:ARG:HD3	1.96	0.46
45:BY:55:TYR:CD2	45:BY:55:TYR:N	2.84	0.46
46:BZ:5:LEU:O	46:BZ:59:LEU:HA	2.15	0.46
1:CA:1492:A:H2'	1:CA:1493:A:C8	2.51	0.46
8:CH:44:PHE:CE2	8:CH:109:ILE:HG12	2.51	0.46
22:CV:16:A:N6	24:CX:36:U:H3	2.12	0.46
24:CX:13:C:O2'	26:DA:1924:C:H4'	2.15	0.46
25:CY:69:G:C6	25:CY:70:G:C8	3.04	0.46
26:DA:8:A:H2'	26:DA:9:U:H6	1.81	0.46
26:DA:724:U:H2'	26:DA:725:G:O4'	2.15	0.46
26:DA:2263:C:N4	47:D0:15:ASP:OD1	2.47	0.46
26:DA:2510:C:C4	26:DA:2511:U:C4	3.03	0.46
29:DE:50:GLY:HA2	29:DE:77:ILE:O	2.14	0.46
56:D9:13:LYS:HD3	56:D9:28:GLU:OE2	2.15	0.46
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.15	0.46
2:AB:210:SER:O	2:AB:214:ILE:HG12	2.16	0.46
4:AD:178:VAL:C	4:AD:180:GLY:H	2.23	0.46
5:AE:6:PHE:HB3	5:AE:35:GLY:C	2.40	0.46
7:AG:113:GLU:HG3	7:AG:118:VAL:HG12	1.96	0.46
7:AG:138:LYS:NZ	7:AG:142:GLU:OE2	2.49	0.46
23:AW:8:4SU:O2'	23:AW:46:7MG:N2	2.49	0.46
23:AW:19:G:H4'	23:AW:20:U:OP1	2.16	0.46
24:AX:17:C:H5'	24:AX:61:C:OP1	2.16	0.46
26:BA:2792:G:N2	26:BA:2805:G:H1'	2.31	0.46
29:BE:149:ARG:N	61:BE:406:HOH:O	2.38	0.46
37:BQ:37:LEU:HD21	37:BQ:130:LYS:HB2	1.98	0.46
43:BW:9:TYR:HA	43:BW:100:THR:HG23	1.98	0.46
1:CA:1318:A:H5''	19:CS:3:ARG:HH22	1.80	0.46
1:CA:1499:A:H1'	1:CA:1520:G:H5'	1.96	0.46
24:CX:37:A:H2'	24:CX:38:A:O4'	2.16	0.46
25:CY:15:G:C2	25:CY:48:C:N3	2.82	0.46
26:DA:28:A:C2	26:DA:513:A:C8	3.03	0.46
26:DA:647:G:H8	26:DA:647:G:O5'	1.98	0.46
26:DA:995:C:N3	34:DN:2:LYS:HA	2.31	0.46
26:DA:1359:A:N1	26:DA:1372:U:O4	2.47	0.46
26:DA:2745:C:C4	26:DA:2746:U:C4	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2870:C:H5''	38:DR:65:LEU:HD21	1.97	0.46
1:AA:224:C:H2'	1:AA:225:C:H6	1.81	0.46
1:AA:1003:G:C2	1:AA:1004:A:N3	2.84	0.46
9:AI:8:GLY:HA3	9:AI:76:ALA:O	2.15	0.46
10:AJ:70:ARG:HA	10:AJ:70:ARG:HD3	1.83	0.46
11:AK:82:VAL:N	11:AK:107:SER:O	2.45	0.46
25:AY:36:A:H2'	25:AY:37:MIA:O4'	2.15	0.46
26:BA:236:C:H2'	26:BA:237:C:C6	2.50	0.46
26:BA:2130:U:H2'	26:BA:2131:G:N2	2.31	0.46
26:BA:2748:A:H5'	32:BH:4:ILE:HD12	1.97	0.46
30:BF:28:ILE:O	30:BF:30:PRO:HD3	2.15	0.46
49:B2:32:LEU:HD13	49:B2:36:ARG:NH1	2.30	0.46
1:CA:69:G:H2'	1:CA:70:G:C8	2.51	0.46
1:CA:90:U:O2'	1:CA:91:C:H5'	2.15	0.46
1:CA:992:U:H6	1:CA:992:U:H5''	1.80	0.46
2:CB:149:LEU:HD22	2:CB:152:PHE:HD2	1.80	0.46
19:CS:27:GLU:HB2	19:CS:28:LYS:NZ	2.31	0.46
26:DA:195:A:H2'	26:DA:198:C:N4	2.31	0.46
26:DA:383:U:H2'	26:DA:385:C:H5	1.81	0.46
26:DA:811:U:H2'	36:DP:21:ARG:HA	1.96	0.46
26:DA:2502:G:H5''	26:DA:2503:A:H5''	1.98	0.46
27:DB:55:U:O3'	31:DG:27:ASN:ND2	2.49	0.46
29:DE:1:MET:O	29:DE:84:PHE:HB2	2.15	0.46
32:DH:86:GLU:CD	32:DH:130:ARG:HD3	2.40	0.46
32:DH:86:GLU:HB3	32:DH:165:ALA:HB2	1.97	0.46
48:D1:83:GLU:HA	48:D1:84:GLY:HA2	1.62	0.46
1:AA:1025:U:O2	1:AA:1036:G:C6	2.66	0.46
1:AA:1136:U:H5''	1:AA:1137:C:N3	2.30	0.46
1:AA:1351:U:O4	9:AI:118:LYS:NZ	2.49	0.46
2:AB:61:LEU:HD23	2:AB:68:ILE:HD11	1.96	0.46
4:AD:110:PHE:HE1	4:AD:176:LEU:HD13	1.80	0.46
18:AR:65:ILE:O	18:AR:69:THR:HG23	2.16	0.46
26:BA:191:A:H2'	26:BA:192:C:C6	2.51	0.46
26:BA:484:C:H2'	26:BA:485:C:C6	2.51	0.46
26:BA:1021:A:H3'	26:BA:1021:A:C8	2.50	0.46
26:BA:1176:G:H1'	26:BA:1177:A:C5'	2.38	0.46
26:BA:1495:A:H2'	26:BA:1496:A:C8	2.51	0.46
26:BA:1697:G:OP2	26:BA:1698:A:O2'	2.14	0.46
26:BA:1859:A:N6	26:BA:1883:G:O2'	2.48	0.46
26:BA:2128:C:H2'	26:BA:2129:C:C6	2.50	0.46
40:BT:51:ARG:HG3	40:BT:98:LYS:HD2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:BW:13:SER:HA	43:BW:14:PRO:HD3	1.84	0.46
1:CA:630:G:H2'	1:CA:631:G:H8	1.81	0.46
1:CA:1002:G:N3	1:CA:1003:G:C8	2.84	0.46
1:CA:1095:U:C4	1:CA:1096:C:C4	3.03	0.46
1:CA:1134:G:H2'	1:CA:1135:U:H5'	1.98	0.46
1:CA:1291:G:C6	1:CA:1292:U:C4	3.04	0.46
14:CN:6:LEU:HB3	14:CN:23:ARG:NH2	2.30	0.46
18:CR:26:LEU:CD2	18:CR:42:ARG:HD2	2.46	0.46
25:CY:35:A:N6	25:CY:36:A:N1	2.63	0.46
26:DA:191:A:H2'	26:DA:192:C:C6	2.50	0.46
26:DA:740:U:H2'	26:DA:741:G:C8	2.51	0.46
26:DA:1310:G:OP2	54:D7:9:ARG:NH1	2.49	0.46
26:DA:1611:C:H2'	26:DA:1612:C:H5'	1.98	0.46
52:D5:16:ARG:HD2	52:D5:20:ARG:NH1	2.31	0.46
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.39	0.46
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.98	0.46
4:AD:3:ARG:HD3	4:AD:118:ARG:HD2	1.97	0.46
26:BA:882:G:H2'	26:BA:883:G:O4'	2.15	0.46
26:BA:1204:A:N6	26:BA:1240:U:H2'	2.30	0.46
26:BA:1300:U:H4'	26:BA:1301:A:H5'	1.97	0.46
26:BA:2086:U:H2'	26:BA:2087:G:C8	2.51	0.46
26:BA:2141:G:N7	26:BA:2151:G:C2	2.84	0.46
26:BA:2199:A:OP2	26:BA:2200:C:H5	1.99	0.46
26:BA:2630:G:H2'	26:BA:2631:G:H8	1.80	0.46
31:BG:47:LYS:O	31:BG:51:ARG:HG2	2.16	0.46
37:BQ:14:ARG:HG2	37:BQ:41:TRP:HH2	1.79	0.46
1:CA:937:A:H1'	1:CA:1379:G:N2	2.30	0.46
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.16	0.46
10:CJ:30:SER:O	10:CJ:81:THR:HG23	2.16	0.46
25:CY:50:U:C2	25:CY:64:A:N1	2.84	0.46
26:DA:195:A:H2'	26:DA:198:C:H41	1.80	0.46
26:DA:999:U:O2'	26:DA:1000:A:H5'	2.16	0.46
26:DA:1913:A:H4'	26:DA:1914:C:O5'	2.15	0.46
26:DA:2291:U:O2'	26:DA:2374:C:H1'	2.16	0.46
26:DA:2821:A:H2'	26:DA:2822:G:C8	2.51	0.46
31:DG:10:LYS:HG3	31:DG:14:GLU:OE1	2.16	0.46
33:DI:77:LEU:HD11	33:DI:101:LEU:HB2	1.98	0.46
39:DS:27:SER:HA	39:DS:88:ASP:HB3	1.96	0.46
1:AA:93:G:O2'	1:AA:96:U:H5'	2.16	0.46
1:AA:1429:C:H2'	1:AA:1430:C:H6	1.80	0.46
3:AC:20:SER:OG	3:AC:40:ARG:NH1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AK:73:MET:HG2	11:AK:103:LEU:HD21	1.98	0.46
26:BA:271(V):G:O6	61:BA:4948:HOH:O	2.20	0.46
26:BA:536:A:H2'	26:BA:537:C:C6	2.50	0.46
26:BA:2533:A:H2'	26:BA:2534:A:O4'	2.16	0.46
61:BA:5273:HOH:O	47:B0:41:ARG:HA	2.15	0.46
33:BI:85:GLU:OE1	33:BI:85:GLU:HA	2.16	0.46
50:B3:26:LEU:O	50:B3:35:ARG:NE	2.49	0.46
51:B4:68:ARG:HD2	51:B4:69:LYS:H	1.81	0.46
1:CA:450:G:H4'	16:CP:41:PRO:HB2	1.98	0.46
1:CA:1220:G:H5'	19:CS:34:TRP:O	2.15	0.46
1:CA:1457:G:OP1	20:CT:39:LYS:NZ	2.37	0.46
2:CB:28:PHE:HD1	2:CB:194:PRO:HG3	1.81	0.46
2:CB:30:ARG:HG3	2:CB:31:TYR:CD1	2.50	0.46
7:CG:79:ARG:HB3	7:CG:80:VAL:H	1.37	0.46
26:DA:774:A:N3	26:DA:774:A:H2'	2.30	0.46
31:DG:25:TYR:HB3	31:DG:30:GLU:HB3	1.98	0.46
33:DI:43:ASN:HD22	33:DI:43:ASN:C	2.24	0.46
1:AA:6:G:O2'	1:AA:7:G:H5'	2.16	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.03	0.46
1:AA:1237:C:O2'	1:AA:1300:G:N2	2.43	0.46
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.24	0.46
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.48	0.46
26:BA:857:C:N4	26:BA:858:U:O4	2.49	0.46
26:BA:2141:G:C4	26:BA:2142:C:H1'	2.51	0.46
30:BF:29:ASN:H	30:BF:112:MET:CE	2.28	0.46
38:BR:36:THR:HG22	38:BR:37:THR:H	1.81	0.46
52:B5:42:PRO:HB2	52:B5:43:HIS:ND1	2.31	0.46
1:CA:202:U:O2'	1:CA:203:U:O5'	2.31	0.46
1:CA:1004:A:N7	1:CA:1037:C:H2'	2.31	0.46
1:CA:1006:C:H2'	1:CA:1007:C:O4'	2.16	0.46
1:CA:1317:C:H5	14:CN:18:VAL:HG21	1.80	0.46
1:CA:1516:G:N2	1:CA:1519:A:OP2	2.49	0.46
2:CB:100:GLY:HA2	2:CB:103:THR:OG1	2.15	0.46
2:CB:218:ALA:O	2:CB:222:ILE:HG23	2.15	0.46
4:CD:92:VAL:O	4:CD:96:LEU:HD22	2.16	0.46
25:CY:76:A:O2'	26:DA:2394:C:N3	2.44	0.46
26:DA:307:G:H22	26:DA:310:A:P	2.38	0.46
26:DA:1032:A:H2	26:DA:1122:G:H22	1.61	0.46
26:DA:1484:G:C6	26:DA:1485:G:N7	2.84	0.46
26:DA:2687:U:H2'	26:DA:2688:U:O4'	2.16	0.46
31:DG:44:GLY:O	31:DG:47:LYS:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:DX:92:LEU:HD12	44:DX:92:LEU:HA	1.83	0.46
46:DZ:150:LEU:HD12	46:DZ:150:LEU:HA	1.78	0.46
1:AA:93:G:C2'	1:AA:96:U:H5'	2.46	0.46
1:AA:1273:G:H3'	1:AA:1274:G:C8	2.51	0.46
1:AA:1457:G:H2'	1:AA:1458:G:C8	2.51	0.46
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.98	0.46
13:AM:4:ILE:HD12	13:AM:57:ARG:HA	1.97	0.46
26:BA:271(P):C:O3'	33:BI:42:SER:OG	2.27	0.46
26:BA:2011:U:OP1	43:BW:42:ARG:HD3	2.16	0.46
26:BA:2359:C:H2'	26:BA:2360:A:O4'	2.16	0.46
26:BA:2675:A:H5'	35:BO:29:ASN:O	2.15	0.46
26:BA:2803:C:H2'	26:BA:2804:C:C6	2.51	0.46
33:BI:93:THR:H	33:BI:96:ASP:CG	2.23	0.46
1:CA:533:A:O2'	1:CA:535:A:OP2	2.25	0.46
1:CA:664:G:H5''	18:CR:64:ARG:NH2	2.31	0.46
1:CA:994:A:C5	1:CA:1216:G:H4'	2.51	0.46
2:CB:96:ARG:HD2	2:CB:98:LEU:HD22	1.97	0.46
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.16	0.46
3:CC:121:ALA:HB2	3:CC:198:VAL:HG21	1.98	0.46
26:DA:517:C:O2'	43:DW:18:ARG:NH2	2.49	0.46
26:DA:1477:A:H2'	26:DA:1478:G:O4'	2.14	0.46
26:DA:1539:G:H2'	26:DA:1540:U:O4'	2.16	0.46
26:DA:1857:G:C6	26:DA:1858:G:N1	2.84	0.46
26:DA:1913:A:H4'	26:DA:1914:C:C5'	2.46	0.46
26:DA:2119:A:H2	26:DA:2171:A:H5'	1.81	0.46
27:DB:5:C:N4	27:DB:116:G:H1	2.13	0.46
27:DB:80:U:H2'	27:DB:81:G:C8	2.51	0.46
33:DI:90:GLY:O	33:DI:121:LYS:HE3	2.16	0.46
38:DR:98:LEU:HB2	38:DR:113:LEU:HD11	1.98	0.46
47:D0:82:ARG:HA	47:D0:83:PRO:HD3	1.78	0.46
1:AA:691:G:OP2	11:AK:26:ASN:ND2	2.38	0.45
1:AA:1075:C:H2'	1:AA:1076:C:H5''	1.98	0.45
2:AB:45:GLN:O	2:AB:49:GLU:HB2	2.16	0.45
26:BA:271(O):C:H2'	26:BA:271(P):C:C6	2.51	0.45
26:BA:1178:C:H2'	26:BA:1179:C:C6	2.51	0.45
33:BI:77:LEU:HB2	33:BI:142:VAL:HG12	1.97	0.45
42:BV:21:ARG:HG2	42:BV:91:TYR:CD1	2.51	0.45
50:B3:43:ILE:O	50:B3:47:VAL:HG23	2.16	0.45
1:CA:59:A:H3'	1:CA:331:G:H22	1.81	0.45
1:CA:345:C:O2'	1:CA:346:G:OP2	2.33	0.45
1:CA:689:C:P	11:CK:46:GLY:HA3	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:920:U:H2'	1:CA:921:U:H6	1.77	0.45
1:CA:976:G:C8	1:CA:1362:C:N4	2.84	0.45
1:CA:1084:G:C5	1:CA:1085:U:C4	3.04	0.45
1:CA:1423:G:H2'	1:CA:1424:C:H6	1.80	0.45
7:CG:111:ARG:HB3	7:CG:113:GLU:OE2	2.16	0.45
12:CL:8:ASN:O	12:CL:12:ARG:HG3	2.16	0.45
15:CO:74:ASP:OD1	15:CO:76:GLU:HB2	2.16	0.45
19:CS:27:GLU:HB3	19:CS:28:LYS:HA	1.96	0.45
26:DA:385:C:O2	36:DP:71:VAL:HG21	2.16	0.45
26:DA:754:C:H2'	26:DA:755:C:C6	2.50	0.45
26:DA:1300:U:H4'	26:DA:1301:A:O5'	2.16	0.45
28:DD:72:LYS:HB3	28:DD:75:ILE:HD12	1.98	0.45
33:DI:102:SER:O	33:DI:106:GLY:N	2.37	0.45
1:AA:59:A:H3'	1:AA:331:G:H22	1.81	0.45
1:AA:1034:G:H3'	1:AA:1035:A:C8	2.51	0.45
2:AB:16:HIS:CB	2:AB:204:ASN:HB3	2.31	0.45
3:AC:155:GLY:HA3	3:AC:196:LEU:HD22	1.97	0.45
4:AD:162:LEU:CD1	4:AD:181:MET:HG2	2.46	0.45
5:AE:27:ARG:HE	5:AE:27:ARG:HB2	1.48	0.45
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.16	0.45
26:BA:911:A:H2'	37:BQ:9:TYR:OH	2.16	0.45
26:BA:1803:A:H4'	28:BD:259:THR:HG23	1.98	0.45
26:BA:1842:G:O2'	28:BD:253:GLN:NE2	2.49	0.45
26:BA:2567:G:H2'	26:BA:2568:C:C6	2.51	0.45
26:BA:2846:G:H2'	26:BA:2847:U:O4'	2.16	0.45
31:BG:16:ARG:NE	31:BG:31:VAL:HG11	2.30	0.45
53:B6:11:LEU:HB3	53:B6:49:HIS:HB3	1.98	0.45
1:CA:775:G:N2	1:CA:804:U:O4	2.48	0.45
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.51	0.45
2:CB:178:ARG:NH2	8:CH:68:ARG:HH22	2.12	0.45
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.81	0.45
9:CI:53:VAL:C	9:CI:55:ALA:N	2.72	0.45
9:CI:99:LEU:HB3	9:CI:101:PHE:CE2	2.51	0.45
13:CM:37:THR:HG21	13:CM:56:LEU:HA	1.97	0.45
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.16	0.45
20:CT:56:MET:HE1	20:CT:85:MET:HA	1.99	0.45
26:DA:698:C:O2'	26:DA:734:A:N6	2.49	0.45
26:DA:752:A:P	54:D7:3:ARG:HH22	2.39	0.45
26:DA:1027:A:C6	26:DA:1126:A:C4	3.04	0.45
26:DA:1991:U:H2'	26:DA:1992:G:H5''	1.97	0.45
26:DA:2379:G:O2'	39:DS:17:ARG:NH2	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DD:96:HIS:CD2	28:DD:102:LYS:HG2	2.52	0.45
33:DI:93:THR:HG22	33:DI:119:PRO:HB3	1.97	0.45
38:DR:29:LEU:HD12	38:DR:29:LEU:HA	1.78	0.45
47:D0:53:MET:HG2	47:D0:57:PHE:HA	1.98	0.45
1:AA:1243:C:H2'	1:AA:1244:C:C6	2.50	0.45
2:AB:16:HIS:CE1	2:AB:214:ILE:HD11	2.46	0.45
10:AJ:31:GLY:HA2	10:AJ:32:ALA:HA	1.44	0.45
26:BA:90:U:H4'	26:BA:92:A:H5'	1.99	0.45
26:BA:1301:A:C8	26:BA:1303:G:C8	3.04	0.45
26:BA:2141:G:C6	26:BA:2142:C:C2	3.04	0.45
28:BD:52:ARG:NH2	61:BD:411:HOH:O	2.22	0.45
31:BG:45:GLU:H	31:BG:45:GLU:HG2	1.36	0.45
34:BN:38:HIS:NE2	34:BN:50:ASP:OD2	2.50	0.45
1:CA:21:G:H2'	1:CA:22:G:C8	2.51	0.45
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.45
1:CA:1053:G:C3'	1:CA:1054:C:H5'	2.45	0.45
2:CB:97:TRP:CZ3	2:CB:101:MET:HB2	2.52	0.45
11:CK:81:ASP:OD1	11:CK:106:LYS:HB2	2.17	0.45
16:CP:19:ILE:N	16:CP:37:GLY:O	2.49	0.45
19:CS:41:VAL:HG12	19:CS:43:GLU:H	1.80	0.45
26:DA:2127:G:N1	26:DA:2161:C:O2	2.34	0.45
26:DA:2468:G:C2	26:DA:2481:G:N3	2.85	0.45
26:DA:2653:U:O2'	32:DH:110:SER:HB3	2.15	0.45
39:DS:3:ARG:HE	39:DS:4:LEU:N	2.15	0.45
1:AA:356:A:N7	61:AA:4035:HOH:O	2.36	0.45
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.52	0.45
1:AA:1273:G:H3'	1:AA:1274:G:H8	1.81	0.45
4:AD:138:TYR:HE1	4:AD:140:VAL:HA	1.81	0.45
5:AE:18:ARG:HE	5:AE:27:ARG:HH21	1.64	0.45
7:AG:91:VAL:HB	7:AG:96:GLN:HG2	1.99	0.45
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.17	0.45
31:BG:14:GLU:C	31:BG:17:PRO:HD2	2.42	0.45
31:BG:31:VAL:HA	31:BG:32:PRO:HD2	1.79	0.45
36:BP:121:LYS:O	36:BP:123:LEU:N	2.45	0.45
1:CA:56:U:H2'	1:CA:57:G:C8	2.52	0.45
1:CA:991:U:H3'	1:CA:1212:U:N3	2.32	0.45
3:CC:79:ARG:H	3:CC:82:GLU:HB3	1.82	0.45
5:CE:90:VAL:O	5:CE:120:THR:HA	2.17	0.45
6:CF:28:ARG:HB2	6:CF:28:ARG:HH11	1.82	0.45
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.17	0.45
26:DA:94(A):G:H2'	26:DA:95:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:241:A:H8	26:DA:241:A:OP1	2.00	0.45
26:DA:583:G:OP2	41:DU:10:ARG:NH1	2.49	0.45
26:DA:2019:A:C4'	41:DU:34:LYS:HD2	2.47	0.45
29:DE:9:VAL:HG13	29:DE:25:VAL:O	2.16	0.45
45:DY:86:ARG:HD2	45:DY:100:ALA:HA	1.98	0.45
50:D3:4:LEU:O	50:D3:36:VAL:HA	2.17	0.45
1:AA:1305:G:H5''	21:AU:4:GLY:HA3	1.98	0.45
2:AB:22:LYS:H	2:AB:40:HIS:CE1	2.35	0.45
2:AB:150:SER:OG	2:AB:151:GLY:N	2.49	0.45
4:AD:170:VAL:HG12	4:AD:171:GLY:N	2.32	0.45
5:AE:12:LEU:HD22	5:AE:13:ILE:N	2.32	0.45
6:AF:44:GLY:HA2	6:AF:59:TYR:CE2	2.52	0.45
18:AR:31:LEU:HD11	18:AR:62:GLU:HB2	1.98	0.45
32:BH:11:VAL:HG13	32:BH:15:VAL:HG22	1.98	0.45
35:BO:7:TYR:CZ	35:BO:44:LYS:HG3	2.52	0.45
46:BZ:105:VAL:N	46:BZ:139:VAL:O	2.41	0.45
1:CA:22:G:H4'	1:CA:885:G:C8	2.52	0.45
1:CA:189(F):U:O2	17:CQ:63:ARG:NH2	2.50	0.45
1:CA:1097:C:O2'	1:CA:1169:A:N3	2.41	0.45
1:CA:1218:C:OP2	14:CN:9:LYS:NZ	2.49	0.45
6:CF:46:ARG:HH21	18:CR:37:VAL:HG11	1.81	0.45
12:CL:69:TYR:CE2	12:CL:71:PRO:HA	2.52	0.45
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.82	0.45
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.98	0.45
20:CT:53:LEU:O	20:CT:57:ARG:HG3	2.16	0.45
26:DA:25:U:H5'	43:DW:78:GLU:O	2.16	0.45
26:DA:468:G:N7	54:D7:39:ARG:NH2	2.63	0.45
26:DA:2287:A:N1	26:DA:2346:A:N7	2.65	0.45
26:DA:2447:G:N2	26:DA:2450:A:OP2	2.46	0.45
30:DF:172:TRP:CD1	30:DF:172:TRP:H	2.33	0.45
31:DG:125:PHE:HB3	31:DG:166:ASP:CG	2.42	0.45
36:DP:63:PRO:HG2	55:D8:25:MET:HB2	1.99	0.45
42:DV:5:VAL:CG1	42:DV:57:VAL:HG21	2.47	0.45
1:AA:836:G:OP1	18:AR:61:LYS:NZ	2.49	0.45
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.81	0.45
10:AJ:55:LYS:O	10:AJ:57:LYS:N	2.50	0.45
11:AK:41:THR:OG1	11:AK:42:TRP:N	2.50	0.45
26:BA:528:A:N1	26:BA:2042:A:H2'	2.31	0.45
26:BA:1300:U:H4'	26:BA:1301:A:H5''	1.99	0.45
26:BA:2544:G:H1'	26:BA:2646:C:H4'	1.99	0.45
29:BE:7:VAL:HG12	29:BE:27:LEU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:102:SER:OG	33:BI:103:ARG:N	2.50	0.45
46:BZ:138:GLU:N	46:BZ:156:LYS:HD3	2.30	0.45
1:CA:93:G:C6	1:CA:96:U:C4	3.05	0.45
1:CA:97:G:O2'	1:CA:98:G:H5''	2.17	0.45
1:CA:1009:G:C2	1:CA:1010:G:C4	3.04	0.45
1:CA:1054:C:O2'	1:CA:1055:A:C5'	2.64	0.45
25:CY:21:A:N6	25:CY:46:7MG:H81	2.32	0.45
26:DA:93:G:H2'	26:DA:94:C:H6	1.82	0.45
26:DA:251:A:H5''	36:DP:50:ARG:HH11	1.81	0.45
26:DA:686:G:H21	26:DA:788:A:H61	1.65	0.45
26:DA:1463:C:H2'	26:DA:1464:C:H6	1.81	0.45
26:DA:1782:C:H1'	26:DA:2609:U:H5''	1.98	0.45
26:DA:2450:A:OP1	26:DA:2497:A:O2'	2.35	0.45
28:DD:17:THR:O	28:DD:211:ARG:NH2	2.45	0.45
41:DU:27:LEU:HD23	41:DU:30:LYS:HB2	1.98	0.45
42:DV:100:ARG:HH11	42:DV:100:ARG:CG	2.17	0.45
45:DY:13:VAL:HG12	45:DY:74:PRO:HA	1.99	0.45
46:DZ:113:ALA:HB3	46:DZ:146:ILE:HD11	1.97	0.45
55:D8:62:LEU:HB3	55:D8:65:GLU:HG3	1.97	0.45
1:AA:78:G:C6	1:AA:91:C:N4	2.83	0.45
1:AA:565:U:OP2	1:AA:566:G:O2'	2.29	0.45
1:AA:1047:G:O2'	1:AA:1215:G:O2'	2.32	0.45
2:AB:158:LEU:HA	2:AB:159:PRO:HD3	1.83	0.45
4:AD:61:LYS:HA	4:AD:203:VAL:HG22	1.98	0.45
16:AP:5:ARG:NH1	16:AP:24:ALA:HA	2.31	0.45
25:AY:50:U:C4	25:AY:64:A:N1	2.84	0.45
26:BA:141:A:H8	26:BA:1408:C:O2'	2.00	0.45
26:BA:1794:U:H2'	26:BA:1795:C:C6	2.50	0.45
28:BD:5:LYS:HE3	28:BD:5:LYS:HB3	1.56	0.45
33:BI:136:VAL:N	33:BI:137:PRO:HD3	2.32	0.45
36:BP:135:LEU:HD23	36:BP:135:LEU:HA	1.77	0.45
37:BQ:18:LYS:HE3	37:BQ:18:LYS:HB2	1.72	0.45
53:B6:13:CYS:SG	53:B6:47:THR:HG21	2.56	0.45
1:CA:297:G:N2	1:CA:300:A:OP2	2.49	0.45
1:CA:335:C:H2'	1:CA:336:C:C6	2.51	0.45
1:CA:1000:U:C2	1:CA:1041:A:N1	2.83	0.45
2:CB:55:PHE:O	2:CB:59:GLU:N	2.33	0.45
3:CC:156:ARG:NH2	3:CC:159:GLY:O	2.27	0.45
23:CW:47:U:H3'	23:CW:48:C:C5'	2.47	0.45
25:CY:70:G:H2'	25:CY:71:G:H5'	1.99	0.45
26:DA:30:G:H2'	26:DA:31:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:864:G:C6	26:DA:865:C:N4	2.85	0.45
26:DA:2348:U:O4	26:DA:2382:G:N1	2.50	0.45
31:DG:74:LYS:O	31:DG:84:LYS:HD2	2.16	0.45
35:DO:107:ARG:CZ	40:DT:36:GLU:HG2	2.46	0.45
1:AA:279:A:C4	17:AQ:98:LEU:HD23	2.51	0.45
1:AA:300:A:H2'	1:AA:301:G:O4'	2.17	0.45
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.47	0.45
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.33	0.45
4:AD:121:VAL:O	4:AD:134:ASP:HA	2.15	0.45
26:BA:1783:A:H5'	26:BA:2608:G:H4'	1.98	0.45
1:CA:58:C:O2'	1:CA:388:G:N7	2.40	0.45
1:CA:1048:G:OP1	14:CN:3:ARG:HD2	2.17	0.45
11:CK:34:ASP:OD2	11:CK:38:ASN:HB2	2.17	0.45
26:DA:94(A):G:C6	26:DA:95:G:C5	3.05	0.45
26:DA:270:A:N1	26:DA:366:C:H4'	2.32	0.45
26:DA:443:A:OP2	26:DA:614(B):G:N2	2.38	0.45
26:DA:848:G:C4	26:DA:933:A:H8	2.35	0.45
26:DA:1027:A:C2	26:DA:2488:A:H5'	2.52	0.45
26:DA:1740:G:H2'	26:DA:1741:A:C8	2.51	0.45
26:DA:2637:U:H1'	26:DA:2782:G:N2	2.32	0.45
30:DF:64:ILE:HG21	30:DF:78:ILE:HG23	1.99	0.45
37:DQ:118:LEU:HB3	37:DQ:131:ILE:HD12	1.97	0.45
40:DT:65:LYS:HE2	40:DT:67:SER:HB2	1.98	0.45
1:AA:189(A):C:N4	1:AA:189(J):G:H1	2.15	0.45
1:AA:662:G:H2'	1:AA:663:A:H8	1.79	0.45
3:AC:35:GLU:CD	3:AC:59:ARG:HH22	2.24	0.45
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.98	0.45
11:AK:38:ASN:HA	11:AK:39:PRO:HD3	1.86	0.45
23:AW:18:G:O2'	23:AW:57:G:N2	2.39	0.45
26:BA:729:G:C6	28:BD:208:LYS:HB2	2.52	0.45
26:BA:897:C:C4	26:BA:898:C:N4	2.85	0.45
26:BA:1957:C:H2'	26:BA:1958:C:C6	2.52	0.45
26:BA:2080:G:OP1	48:B1:35:THR:HG21	2.17	0.45
27:BB:42:C:OP1	31:BG:67:LYS:NZ	2.44	0.45
31:BG:11:TYR:O	31:BG:16:ARG:HG2	2.17	0.45
34:BN:14:VAL:HG11	34:BN:138:LEU:HD12	1.99	0.45
45:BY:34:LYS:HG3	45:BY:34:LYS:O	2.15	0.45
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.82	0.45
1:CA:1374:A:O2'	7:CG:28:ASN:HB3	2.16	0.45
2:CB:15:VAL:HG21	2:CB:213:LEU:HD12	1.98	0.45
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:150:SER:OG	2:CB:151:GLY:N	2.48	0.45
9:CI:4:TYR:HB2	9:CI:19:LEU:HB2	1.99	0.45
13:CM:33:ALA:HA	13:CM:59:TYR:CE2	2.51	0.45
23:CW:18:G:O6	23:CW:55:PSU:H1'	2.17	0.45
23:CW:76:31M:HA	23:CW:76:31M:HD1	1.41	0.45
26:DA:263:C:H2'	26:DA:264:C:O4'	2.17	0.45
26:DA:1116:C:H2'	26:DA:1117:G:C8	2.52	0.45
26:DA:1395:A:OP1	61:DA:4546:HOH:O	2.21	0.45
26:DA:2052:G:H4'	29:DE:143:ASN:O	2.16	0.45
26:DA:2305:A:H2'	26:DA:2306:C:O4'	2.17	0.45
27:DB:11:C:H3'	27:DB:12:C:C6	2.52	0.45
27:DB:66:A:N6	27:DB:108:U:H3'	2.32	0.45
28:DD:10:THR:OG1	28:DD:13:ARG:HG2	2.16	0.45
28:DD:96:HIS:HD2	28:DD:102:LYS:HG2	1.81	0.45
40:DT:117:ASP:OD2	40:DT:120:ARG:NE	2.41	0.45
42:DV:40:LEU:HB2	42:DV:46:VAL:HG22	1.99	0.45
45:DY:5:MET:HE2	45:DY:5:MET:HB2	1.63	0.45
1:AA:1442(B):A:N3	40:BT:118:ARG:NH2	2.65	0.45
17:AQ:15:MET:HE1	17:AQ:43:LEU:HD22	1.99	0.45
26:BA:250:G:P	55:B8:13:ARG:HH22	2.39	0.45
26:BA:899:A:O2'	26:BA:900:A:H8	2.00	0.45
26:BA:973:A:OP2	61:BA:4141:HOH:O	2.20	0.45
26:BA:2168:G:O6	26:BA:2171:A:H8	1.99	0.45
26:BA:2576:G:H1'	61:BA:4454:HOH:O	2.17	0.45
26:BA:2893:G:HO2'	26:BA:2894:G:P	2.38	0.45
61:BA:4103:HOH:O	30:BF:68:LYS:HE2	2.17	0.45
30:BF:184:TYR:O	30:BF:188:ARG:HG3	2.17	0.45
32:BH:98:LEU:HD12	32:BH:102:ALA:O	2.16	0.45
42:BV:55:ALA:HB2	42:BV:101:GLY:HA2	1.99	0.45
53:B6:40:CYS:HA	53:B6:41:PRO:HD3	1.78	0.45
1:CA:200:G:H1	1:CA:217:C:N4	2.09	0.45
1:CA:582:U:OP2	1:CA:758:G:N1	2.45	0.45
1:CA:986:A:H2'	1:CA:987:G:O4'	2.17	0.45
1:CA:1028:C:N3	1:CA:1033:G:C6	2.84	0.45
1:CA:1133:G:C4	1:CA:1134:G:C8	3.04	0.45
1:CA:1191:A:OP2	3:CC:3:ASN:ND2	2.49	0.45
1:CA:1338:G:C6	1:CA:1339:A:C6	3.05	0.45
5:CE:79:GLU:OE1	8:CH:104:ARG:HA	2.17	0.45
26:DA:492:A:H2'	26:DA:493:G:O4'	2.17	0.45
26:DA:1427:A:H4'	26:DA:1428:C:O5'	2.15	0.45
26:DA:2303:G:O2'	31:DG:132:ASN:ND2	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:2607:G:O6	61:DA:4661:HOH:O	2.20	0.45
30:DF:36:VAL:HG11	30:DF:183:VAL:HG11	1.99	0.45
34:DN:37:LYS:NZ	61:DN:5101:HOH:O	2.49	0.45
39:DS:106:ARG:HG3	39:DS:112:PHE:CZ	2.51	0.45
45:DY:5:MET:HG2	45:DY:30:VAL:HG11	1.99	0.45
1:AA:6:G:H4'	1:AA:298:A:H4'	1.99	0.44
1:AA:636:U:H2'	1:AA:637:G:C8	2.52	0.44
6:AF:18:GLN:HA	6:AF:21:LEU:HD12	1.99	0.44
26:BA:1371:G:H2'	26:BA:1372:U:C5	2.50	0.44
26:BA:2615:U:H2'	26:BA:2616:C:H6	1.82	0.44
36:BP:50:ARG:NH2	55:B8:7:HIS:HD2	2.15	0.44
1:CA:353:A:H5'	1:CA:353:A:H8	1.82	0.44
1:CA:501:C:H2'	1:CA:502:G:C8	2.52	0.44
1:CA:866:C:C4	1:CA:867:G:H1'	2.52	0.44
1:CA:1070:U:H2'	1:CA:1071:C:C6	2.52	0.44
1:CA:1249:C:O4'	9:CI:70:LYS:HE2	2.17	0.44
1:CA:1326:C:H5''	21:CU:18:TYR:O	2.17	0.44
1:CA:1386:G:C2	1:CA:1387:G:C8	3.04	0.44
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.98	0.44
17:CQ:6:LEU:O	17:CQ:58:GLU:HA	2.16	0.44
20:CT:46:GLU:O	20:CT:46:GLU:HG2	2.16	0.44
25:CY:66:U:H2'	25:CY:67:C:O4'	2.17	0.44
26:DA:182:A:H2	26:DA:433:C:O2	2.00	0.44
26:DA:307:G:H21	26:DA:330:A:N6	2.10	0.44
26:DA:321:G:OP1	30:DF:135:LYS:NZ	2.49	0.44
26:DA:1794:U:H2'	26:DA:1795:C:C6	2.53	0.44
26:DA:2203:U:H2'	26:DA:2205:C:H6	1.81	0.44
26:DA:2298:A:H2'	26:DA:2299:G:O4'	2.16	0.44
27:DB:66:A:H61	27:DB:109:C:H5'	1.82	0.44
37:DQ:58:PHE:CE2	37:DQ:109:VAL:HG21	2.52	0.44
1:AA:767:A:N7	61:AA:4048:HOH:O	2.36	0.44
1:AA:923:A:OP1	5:AE:21:ALA:HB2	2.17	0.44
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.40	0.44
16:AP:20:VAL:HG21	16:AP:32:TYR:CD2	2.52	0.44
20:AT:47:GLY:HA2	20:AT:48:LYS:C	2.41	0.44
25:AY:41:C:H2'	25:AY:42:C:C6	2.53	0.44
26:BA:305:U:H2'	26:BA:306:U:C6	2.52	0.44
26:BA:470:A:OP1	30:BF:59:TYR:HE1	1.99	0.44
26:BA:1019:U:H3	26:BA:1142(A):A:N6	2.10	0.44
26:BA:1630:G:H2'	26:BA:1631:C:C6	2.53	0.44
26:BA:2649:U:H2'	26:BA:2650:U:C6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:153:C:H2'	1:CA:154:C:C6	2.52	0.44
2:CB:213:LEU:O	2:CB:217:ARG:HB2	2.17	0.44
8:CH:44:PHE:HE2	8:CH:109:ILE:HG12	1.82	0.44
9:CI:99:LEU:HB3	9:CI:101:PHE:CD2	2.52	0.44
26:DA:55:G:O2'	26:DA:127:A:N1	2.47	0.44
26:DA:686:G:N2	26:DA:788:A:H61	2.14	0.44
26:DA:727:A:OP1	26:DA:1431:U:O2'	2.35	0.44
27:DB:72:G:H1'	27:DB:105:A:H61	1.82	0.44
31:DG:138:GLN:OE1	31:DG:138:GLN:N	2.43	0.44
33:DI:133:HIS:HD2	33:DI:136:VAL:HG23	1.82	0.44
39:DS:34:HIS:O	39:DS:97:ARG:NH2	2.50	0.44
45:DY:52:SER:HB2	45:DY:53:PRO:HD2	1.99	0.44
56:D9:3:VAL:HA	56:D9:35:ARG:O	2.18	0.44
1:AA:620:C:H2'	1:AA:621:A:O4'	2.16	0.44
3:AC:52:LEU:HA	3:AC:70:VAL:HG23	1.99	0.44
9:AI:99:LEU:HB3	9:AI:101:PHE:HE1	1.80	0.44
26:BA:245:G:O6	55:B8:8:LYS:NZ	2.33	0.44
26:BA:675:A:C8	26:BA:804:A:C6	3.05	0.44
26:BA:1378:A:OP1	54:B7:10:ARG:NH2	2.51	0.44
26:BA:2661:G:H2'	26:BA:2662:A:C8	2.51	0.44
26:BA:2849:U:H4'	26:BA:2868:A:C2	2.52	0.44
29:BE:79:ARG:HD3	29:BE:79:ARG:HA	1.82	0.44
32:BH:54:ARG:HD3	32:BH:65:HIS:ND1	2.32	0.44
46:BZ:108:PRO:CG	46:BZ:117:LEU:HD22	2.47	0.44
51:B4:64:GLY:C	51:B4:66:SER:H	2.25	0.44
1:CA:1273:G:H3'	1:CA:1274:G:C8	2.51	0.44
1:CA:1318:A:H5''	19:CS:3:ARG:NH2	2.32	0.44
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.32	0.44
4:CD:47:ARG:HH11	4:CD:49:ARG:HH21	1.65	0.44
4:CD:173:TRP:CE2	4:CD:189:PRO:HG3	2.53	0.44
12:CL:33:ARG:HD3	12:CL:62:SER:HB3	1.99	0.44
15:CO:54:ARG:HD3	15:CO:58:MET:CE	2.47	0.44
19:CS:30:LEU:CD1	19:CS:50:ALA:HB2	2.48	0.44
26:DA:2153:G:N2	26:DA:2154:G:N3	2.65	0.44
31:DG:28:VAL:O	31:DG:31:VAL:HG12	2.18	0.44
31:DG:173:LEU:HB3	31:DG:178:PHE:CG	2.53	0.44
36:DP:88:LEU:HD11	36:DP:114:ILE:HD12	1.99	0.44
46:DZ:128:VAL:HG23	46:DZ:160:GLY:O	2.17	0.44
51:D4:57:GLU:HA	51:D4:58:ARG:HA	1.71	0.44
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.99	0.44
3:AC:27:LYS:HA	3:AC:27:LYS:NZ	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HD23	1.98	0.44
23:AW:51:U:H2'	23:AW:52:G:H8	1.83	0.44
25:AY:40:C:H2'	25:AY:41:C:C6	2.52	0.44
26:BA:141:A:C8	26:BA:1408:C:O2'	2.69	0.44
26:BA:311:A:C6	26:BA:328:U:C4	3.06	0.44
26:BA:1184:G:H5'	50:B3:29:ARG:NH1	2.32	0.44
26:BA:1268:A:C2	26:BA:2013:A:C4	3.05	0.44
26:BA:2384:G:OP2	47:B0:55:ARG:NH1	2.51	0.44
27:BB:4:C:H2'	27:BB:5:C:C6	2.52	0.44
30:BF:30:PRO:HB3	36:BP:1:MET:HE1	2.00	0.44
33:BI:101:LEU:HD13	33:BI:107:VAL:O	2.16	0.44
40:BT:37:GLY:HA2	40:BT:38:ASN:HA	1.69	0.44
1:CA:142:G:H2'	1:CA:143:A:O4'	2.16	0.44
1:CA:551:U:H2'	1:CA:552:U:H6	1.81	0.44
1:CA:1054:C:HO2'	1:CA:1055:A:P	2.36	0.44
1:CA:1084:G:OP1	1:CA:1086:U:C2	2.70	0.44
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.99	0.44
1:CA:1324:A:O4'	1:CA:1362:C:H4'	2.17	0.44
2:CB:80:ILE:HD11	2:CB:212:GLN:CA	2.48	0.44
4:CD:163:GLU:O	4:CD:166:LYS:N	2.44	0.44
10:CJ:5:ARG:HA	10:CJ:73:ASP:HA	2.00	0.44
17:CQ:66:SER:H	17:CQ:69:LYS:HB3	1.82	0.44
25:CY:7:A:N1	25:CY:66:U:O2	2.50	0.44
26:DA:593:G:C4'	55:D8:4:MET:HE2	2.48	0.44
26:DA:1035:U:H2'	26:DA:1036:G:C8	2.52	0.44
26:DA:1219:G:H1	26:DA:1230:C:H42	1.64	0.44
26:DA:2370:G:C6	26:DA:2371:G:C6	3.06	0.44
29:DE:181:LEU:HA	29:DE:181:LEU:HD12	1.84	0.44
35:DO:71:ARG:NE	35:DO:105:GLU:OE2	2.40	0.44
44:DX:59:VAL:HB	44:DX:76:ARG:HB2	1.99	0.44
1:AA:102:G:O2'	1:AA:151:A:N3	2.44	0.44
1:AA:162:A:H8	1:AA:162:A:O5'	2.01	0.44
1:AA:420:U:O2'	1:AA:423:G:O6	2.34	0.44
1:AA:1028:C:H2'	1:AA:1029:C:C4'	2.47	0.44
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.53	0.44
2:AB:21:ARG:H	2:AB:21:ARG:CD	2.30	0.44
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	2.00	0.44
3:AC:12:LEU:O	14:AN:57:ARG:NH2	2.50	0.44
4:AD:105:VAL:HG13	4:AD:110:PHE:HB2	1.99	0.44
4:AD:177:ASP:HB3	4:AD:182:LYS:HG2	2.00	0.44
8:AH:6:ILE:HD11	8:AH:31:PHE:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	2.00	0.44
13:AM:79:LYS:HA	13:AM:82:MET:HE2	1.99	0.44
26:BA:848:G:O6	26:BA:928:G:H2'	2.17	0.44
26:BA:1001:A:H2'	26:BA:1002:G:O4'	2.18	0.44
26:BA:1047:G:HO2'	26:BA:1048:A:H8	1.66	0.44
26:BA:2052:G:H4'	29:BE:143:ASN:O	2.17	0.44
26:BA:2849:U:OP2	40:BT:95:ARG:NH1	2.50	0.44
28:BD:232:PRO:HB3	28:BD:244:ARG:CZ	2.48	0.44
33:BI:27:ARG:HD2	48:B1:71:TYR:CZ	2.51	0.44
50:B3:31:LEU:HD23	50:B3:31:LEU:HA	1.69	0.44
1:CA:537:G:H2'	1:CA:538:G:C8	2.53	0.44
1:CA:789:U:O2'	1:CA:791:G:N7	2.32	0.44
1:CA:938:A:C6	1:CA:939:G:C5	3.06	0.44
1:CA:1226:C:H4'	19:CS:80:TYR:OH	2.17	0.44
1:CA:1441:G:H8	1:CA:1441:G:O5'	2.00	0.44
2:CB:74:LYS:HB3	2:CB:169:LYS:HE2	1.98	0.44
3:CC:33:LEU:HD12	3:CC:36:ASP:HB3	1.99	0.44
7:CG:51:GLN:O	7:CG:55:GLY:HA2	2.16	0.44
26:DA:250:G:C6	26:DA:251:A:C6	3.05	0.44
26:DA:900:A:HO2'	26:DA:901:A:P	2.40	0.44
26:DA:1153:C:H5''	41:DU:62:ILE:HD13	2.00	0.44
26:DA:1463:C:H2'	26:DA:1464:C:C6	2.53	0.44
26:DA:1472:A:N6	26:DA:1519:G:H1'	2.32	0.44
26:DA:1894:C:H2'	26:DA:1895:C:C6	2.53	0.44
26:DA:2156:G:H8	26:DA:2156:G:O5'	1.99	0.44
26:DA:2892:A:N6	26:DA:2893:G:O6	2.51	0.44
28:DD:79:VAL:HG21	28:DD:111:LEU:HD11	1.99	0.44
35:DO:103:ALA:HB1	35:DO:105:GLU:OE1	2.16	0.44
37:DQ:35:VAL:HG12	37:DQ:130:LYS:O	2.18	0.44
1:AA:92:C:H2'	1:AA:93:G:H8	1.80	0.44
1:AA:636:U:H2'	1:AA:637:G:H8	1.83	0.44
1:AA:1513:A:H2'	1:AA:1514:C:C6	2.53	0.44
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.53	0.44
9:AI:4:TYR:CE1	9:AI:88:TYR:HD1	2.36	0.44
23:AW:56:C:OP1	26:BA:897:C:H5'	2.18	0.44
26:BA:910:A:N1	26:BA:2277:G:H1'	2.32	0.44
26:BA:1153:C:OP1	41:BU:92:ARG:NH1	2.50	0.44
26:BA:1178:C:H2'	26:BA:1179:C:H6	1.82	0.44
26:BA:2093:G:C6	26:BA:2225:A:C8	3.06	0.44
26:BA:2115:G:C2	26:BA:2117:A:N7	2.86	0.44
26:BA:2303:G:O2'	31:BG:132:ASN:ND2	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:BF:135:LYS:HB2	30:BF:138:GLU:CD	2.42	0.44
45:BY:102:CYS:SG	45:BY:103:GLY:N	2.91	0.44
1:CA:37:U:O2'	1:CA:500:G:H4'	2.17	0.44
1:CA:826:C:H2'	1:CA:827:U:C6	2.53	0.44
1:CA:1493:A:H5''	1:CA:1494:G:OP2	2.18	0.44
1:CA:1508:G:H2'	1:CA:1509:C:C6	2.52	0.44
4:CD:161:ASN:HD22	4:CD:161:ASN:N	2.16	0.44
8:CH:51:VAL:HG11	8:CH:60:ARG:NH1	2.33	0.44
11:CK:77:MET:HE2	11:CK:77:MET:HB2	1.90	0.44
12:CL:24:VAL:HG12	12:CL:24:VAL:O	2.17	0.44
16:CP:9:PHE:CE1	16:CP:18:ARG:HD2	2.52	0.44
23:CW:39:PSU:H2'	23:CW:40:C:H6	1.83	0.44
26:DA:556:G:H2'	26:DA:557:U:C6	2.52	0.44
26:DA:2336:A:H61	47:D0:43:THR:CG2	2.29	0.44
26:DA:2880:C:O3'	38:DR:90:ARG:NH1	2.51	0.44
27:DB:3:C:H2'	27:DB:4:C:H6	1.83	0.44
27:DB:46:A:H2'	27:DB:47:C:C6	2.52	0.44
29:DE:77:ILE:CD1	29:DE:195:LEU:HD13	2.46	0.44
31:DG:128:ARG:HE	31:DG:128:ARG:HB2	1.67	0.44
35:DO:77:ILE:HB	40:DT:74:ARG:HD3	2.00	0.44
1:AA:346:G:N3	1:AA:347:G:H1'	2.33	0.44
1:AA:434:U:H2'	1:AA:435:C:C6	2.52	0.44
1:AA:630:G:H2'	1:AA:631:G:H8	1.83	0.44
1:AA:658:G:O4'	15:AO:22:THR:OG1	2.35	0.44
1:AA:674:G:H2'	1:AA:675:A:H8	1.83	0.44
1:AA:952:U:H2'	1:AA:953:G:H8	1.80	0.44
1:AA:1326:C:OP1	21:AU:12:LYS:NZ	2.50	0.44
3:AC:140:ARG:HE	3:AC:140:ARG:HB2	1.51	0.44
7:AG:46:ALA:O	7:AG:50:ILE:HG23	2.18	0.44
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.99	0.44
15:AO:53:HIS:O	15:AO:56:LEU:HB3	2.18	0.44
23:AW:22:G:H2'	23:AW:23:A:C8	2.53	0.44
26:BA:251:A:C5	26:BA:252:G:H1'	2.52	0.44
26:BA:530:G:O4'	26:BA:530:G:N3	2.50	0.44
26:BA:2319:G:N2	39:BS:3:ARG:HA	2.33	0.44
32:BH:24:VAL:HG22	32:BH:35:VAL:HB	1.99	0.44
32:BH:125:VAL:HG12	32:BH:127:GLU:O	2.18	0.44
32:BH:164:TYR:HB2	32:BH:167:GLU:HB2	1.99	0.44
33:BI:79:ILE:HB	33:BI:144:VAL:HG12	2.00	0.44
39:BS:58:LEU:HA	39:BS:58:LEU:HD23	1.70	0.44
46:BZ:155:LEU:HD12	46:BZ:156:LYS:H	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:B2:30:ARG:O	49:B2:34:GLU:HG3	2.17	0.44
51:B4:53:GLU:C	51:B4:55:ARG:N	2.65	0.44
54:B7:11:LYS:HE3	54:B7:15:THR:OG1	2.18	0.44
1:CA:79:G:N2	1:CA:80:G:C4	2.86	0.44
1:CA:684:A:O2'	11:CK:39:PRO:O	2.34	0.44
1:CA:696:A:H8	1:CA:696:A:O5'	2.01	0.44
1:CA:1134:G:C2'	1:CA:1135:U:H5'	2.48	0.44
1:CA:1170:A:H2'	1:CA:1171:G:O4'	2.17	0.44
2:CB:74:LYS:HG3	2:CB:77:ALA:HB3	1.99	0.44
2:CB:224:GLN:HA	2:CB:228:GLY:O	2.18	0.44
8:CH:68:ARG:NH1	8:CH:74:PRO:HB3	2.32	0.44
11:CK:48:ILE:C	11:CK:50:TYR:H	2.26	0.44
13:CM:40:ASN:ND2	13:CM:41:PRO:HD2	2.33	0.44
23:CW:14:A:N6	23:CW:21:A:H2	2.15	0.44
23:CW:38:A:H2'	23:CW:39:PSU:O4'	2.18	0.44
23:CW:76:31M:H4'	26:DA:2506:U:O2'	2.17	0.44
26:DA:192:C:O2'	26:DA:802:A:N3	2.46	0.44
26:DA:582:G:H2'	26:DA:583:G:C8	2.53	0.44
26:DA:656:G:H2'	26:DA:657:U:O4'	2.18	0.44
26:DA:828:U:H4'	26:DA:831:G:N1	2.32	0.44
26:DA:1016:G:H2'	26:DA:1017:G:O4'	2.18	0.44
26:DA:2144:U:O3'	26:DA:2145:C:H2'	2.17	0.44
26:DA:2242:G:H2'	26:DA:2243:U:O4'	2.18	0.44
28:DD:108:PRO:HG2	28:DD:111:LEU:HB2	1.99	0.44
28:DD:164:GLN:NE2	28:DD:166:GLN:OE1	2.46	0.44
30:DF:39:TRP:HB3	30:DF:101:LEU:HD22	2.00	0.44
50:D3:18:ASP:OD1	50:D3:18:ASP:N	2.44	0.44
1:AA:68:G:C2	1:AA:69:G:H1'	2.53	0.44
1:AA:184:G:H2'	1:AA:185:A:H8	1.81	0.44
1:AA:299:G:H2'	1:AA:300:A:C8	2.53	0.44
1:AA:406:G:N3	4:AD:119:GLN:NE2	2.60	0.44
1:AA:731:G:H5'	1:AA:766:A:H4'	2.00	0.44
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.53	0.44
1:AA:1118:C:H2'	1:AA:1119:C:H6	1.83	0.44
1:AA:1250:A:H4'	9:AI:68:GLY:N	2.33	0.44
15:AO:54:ARG:O	15:AO:58:MET:HG3	2.18	0.44
16:AP:53:VAL:HG13	16:AP:79:VAL:HG22	1.99	0.44
20:AT:72:LEU:HD23	20:AT:72:LEU:HA	1.84	0.44
21:AU:15:ARG:HB2	21:AU:15:ARG:HH11	1.82	0.44
23:AW:51:U:H2'	23:AW:52:G:C8	2.53	0.44
26:BA:875:G:H2'	26:BA:876:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2030:A:H4'	26:BA:2031:A:C8	2.53	0.44
26:BA:2059:A:OP2	61:BA:4337:HOH:O	2.21	0.44
29:BE:73:GLU:H	29:BE:73:GLU:HG3	1.63	0.44
48:B1:86:SER:H	48:B1:89:GLU:CD	2.26	0.44
1:CA:408:A:OP1	4:CD:113:SER:OG	2.28	0.44
1:CA:1040:U:C4	1:CA:1041:A:C8	3.05	0.44
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.17	0.44
4:CD:47:ARG:NH1	4:CD:49:ARG:HH21	2.16	0.44
9:CI:4:TYR:CZ	9:CI:88:TYR:HD2	2.36	0.44
14:CN:26:ARG:HD2	14:CN:43:CYS:HB3	2.00	0.44
19:CS:19:VAL:O	19:CS:23:ASN:ND2	2.50	0.44
25:CY:65:G:H2'	25:CY:66:U:C6	2.53	0.44
26:DA:330:A:H2	26:DA:1210:A:H2'	1.83	0.44
26:DA:888:C:H5''	26:DA:889:C:OP2	2.18	0.44
26:DA:1288:U:C2	26:DA:1327:C:O2	2.71	0.44
26:DA:2680:C:OP2	29:DE:111:ARG:NH2	2.50	0.44
28:DD:13:ARG:HA	28:DD:13:ARG:HD2	1.71	0.44
28:DD:237:GLU:OE2	61:DD:401:HOH:O	2.21	0.44
30:DF:11:VAL:HB	30:DF:18:ARG:HB3	1.99	0.44
34:DN:15:LEU:HD12	34:DN:137:LYS:HG2	1.99	0.44
50:D3:23:LEU:O	50:D3:27:GLY:N	2.50	0.44
51:D4:40:HIS:ND1	51:D4:43:TYR:HD2	2.15	0.44
1:AA:958:A:C6	1:AA:959:A:N1	2.86	0.44
8:AH:96:GLY:N	8:AH:99:GLU:OE2	2.28	0.44
11:AK:33:THR:HA	11:AK:39:PRO:HA	2.00	0.44
16:AP:20:VAL:HG23	16:AP:35:LYS:HA	2.00	0.44
26:BA:574:C:N3	29:BE:145:LYS:NZ	2.63	0.44
26:BA:876:C:H2'	26:BA:877:U:O4'	2.18	0.44
26:BA:1636:C:H2'	26:BA:1637:A:C8	2.53	0.44
26:BA:2364:C:H2'	26:BA:2365:G:O4'	2.18	0.44
28:BD:83:GLU:OE1	28:BD:104:TYR:OH	2.28	0.44
29:BE:143:ASN:HD22	29:BE:147:PRO:CD	2.31	0.44
32:BH:3:ARG:HH12	32:BH:65:HIS:HB3	1.83	0.44
34:BN:67:LEU:O	34:BN:88:GLU:HG3	2.17	0.44
35:BO:2:ILE:HD12	35:BO:6:THR:HG21	1.99	0.44
44:BX:88:LYS:NZ	44:BX:90:GLU:OE1	2.33	0.44
1:CA:35:G:H2'	1:CA:36:C:C6	2.53	0.44
1:CA:292:G:N7	1:CA:293:G:H1'	2.33	0.44
2:CB:192:SER:O	2:CB:194:PRO:HD3	2.17	0.44
6:CF:3:ARG:HB3	6:CF:93:SER:HB2	2.00	0.44
8:CH:39:LEU:HA	8:CH:39:LEU:HD13	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:CL:69:TYR:HE2	12:CL:71:PRO:HA	1.83	0.44
25:CY:30:G:C2	25:CY:31:A:C8	3.06	0.44
26:DA:26:G:C6	26:DA:27:G:N1	2.86	0.44
26:DA:265:A:C8	26:DA:266:G:H1'	2.53	0.44
26:DA:328:U:H4'	45:DY:68:HIS:CG	2.52	0.44
26:DA:911:A:H2'	37:DQ:9:TYR:OH	2.18	0.44
26:DA:927:G:H2'	26:DA:928:G:O4'	2.17	0.44
26:DA:1032:A:H4'	56:D9:16:VAL:HG11	2.00	0.44
26:DA:1301:A:H2	26:DA:1626:G:N3	2.14	0.44
26:DA:2070:G:H2'	26:DA:2071:A:H8	1.83	0.44
26:DA:2615:U:OP1	61:DA:4004:HOH:O	2.21	0.44
31:DG:111:LEU:HB3	31:DG:117:PHE:CE2	2.53	0.44
39:DS:35:ILE:HD11	39:DS:101:LEU:HD12	1.99	0.44
1:AA:276:G:O3'	17:AQ:68:ARG:NH1	2.51	0.43
1:AA:401:C:H2'	1:AA:402:G:C8	2.53	0.43
1:AA:858:G:O6	1:AA:869:G:H3'	2.18	0.43
1:AA:1001(A):G:C6	1:AA:1002:G:C5	3.06	0.43
1:AA:1118:C:H2'	1:AA:1119:C:C6	2.53	0.43
2:AB:16:HIS:HD2	2:AB:17:PHE:H	1.56	0.43
4:AD:11:LEU:HD23	4:AD:66:ARG:HB3	1.99	0.43
6:AF:14:LEU:HD11	6:AF:84:ASN:CG	2.43	0.43
9:AI:22:GLY:N	9:AI:58:HIS:O	2.39	0.43
26:BA:970:C:H2'	26:BA:971:C:C6	2.53	0.43
26:BA:1440:G:H2'	26:BA:1441:G:O4'	2.18	0.43
26:BA:1826:G:H2'	26:BA:1827:C:O4'	2.17	0.43
26:BA:2685:G:H5'	35:BO:68:GLU:OE1	2.18	0.43
30:BF:140:LEU:HD21	30:BF:170:LEU:HD11	2.00	0.43
39:BS:3:ARG:HE	39:BS:4:LEU:H	1.66	0.43
46:BZ:7:ALA:O	46:BZ:62:PRO:HD3	2.18	0.43
46:BZ:111:VAL:CG2	46:BZ:117:LEU:HB2	2.48	0.43
1:CA:1095:U:H2'	1:CA:1096:C:O4'	2.18	0.43
1:CA:1118:C:N1	1:CA:1119:C:H5	2.16	0.43
1:CA:1136:U:H5''	1:CA:1137:C:C5	2.53	0.43
1:CA:1423:G:H2'	1:CA:1424:C:C6	2.53	0.43
2:CB:7:VAL:HG12	2:CB:8:LYS:HG2	2.00	0.43
3:CC:6:HIS:HA	3:CC:7:PRO:HD3	1.71	0.43
7:CG:18:TYR:HB3	7:CG:59:LEU:HD13	2.00	0.43
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.99	0.43
13:CM:72:ALA:O	13:CM:76:ALA:N	2.42	0.43
25:CY:37:MIA:H3'	25:CY:38:A:H8	1.82	0.43
26:DA:458:G:O2'	26:DA:469:G:O6	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DA:668:G:H5'	26:DA:669:G:OP2	2.18	0.43
26:DA:2164:C:H5	26:DA:2165:G:N3	2.16	0.43
26:DA:2347:C:H2'	26:DA:2348:U:C6	2.53	0.43
26:DA:2732:G:OP1	29:DE:203:LYS:NZ	2.43	0.43
26:DA:2742:C:OP1	56:D9:35:ARG:HD3	2.18	0.43
33:DI:57:ARG:O	33:DI:61:ARG:HG2	2.18	0.43
33:DI:88:ILE:HD11	33:DI:144:VAL:HG11	2.00	0.43
34:DN:4:TYR:CD2	41:DU:100:VAL:HG11	2.52	0.43
37:DQ:27:VAL:O	37:DQ:29:PHE:N	2.51	0.43
37:DQ:29:PHE:O	46:DZ:122:ARG:NH2	2.51	0.43
37:DQ:139:GLU:HG2	46:DZ:122:ARG:HG3	2.00	0.43
45:DY:10:GLY:O	45:DY:26:LYS:HD3	2.18	0.43
51:D4:46:GLN:C	51:D4:48:ARG:N	2.74	0.43
1:AA:339:C:H2'	1:AA:340:U:C6	2.54	0.43
1:AA:646:U:H2'	1:AA:647:C:C6	2.53	0.43
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.82	0.43
4:AD:65:ARG:HG2	4:AD:75:PHE:CD2	2.53	0.43
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.18	0.43
4:AD:188:LEU:HA	4:AD:189:PRO:HD3	1.80	0.43
9:AI:23:ASN:ND2	9:AI:25:LYS:HG2	2.33	0.43
23:AW:76:31M:N1	26:BA:2583:G:O2'	2.51	0.43
25:AY:57:G:C2	25:AY:58:A:H5'	2.53	0.43
26:BA:94:C:H2'	26:BA:94(A):G:O4'	2.19	0.43
26:BA:127:A:H5''	26:BA:128:C:C6	2.53	0.43
26:BA:363(A):A:H2'	26:BA:363(B):G:C8	2.53	0.43
26:BA:1358:G:N2	26:BA:1372:U:C5	2.86	0.43
26:BA:1769:G:O2'	26:BA:1958:C:OP1	2.25	0.43
26:BA:2320:A:N3	26:BA:2320:A:H2'	2.34	0.43
26:BA:2447:G:N2	26:BA:2450:A:OP2	2.51	0.43
35:BO:78:ARG:NH2	40:BT:73:GLU:OE2	2.49	0.43
41:BU:117:GLN:H	41:BU:117:GLN:HG2	1.42	0.43
46:BZ:150:LEU:HA	46:BZ:150:LEU:HD12	1.78	0.43
1:CA:766:A:OP2	61:CA:4021:HOH:O	2.21	0.43
1:CA:1115:C:H2'	1:CA:1116:C:C6	2.53	0.43
1:CA:1152:A:C6	1:CA:1153:C:C4	3.06	0.43
2:CB:20:GLU:HG3	2:CB:191:ASP:HB3	1.99	0.43
3:CC:18:TRP:N	3:CC:18:TRP:CE3	2.85	0.43
3:CC:47:LEU:HD12	3:CC:68:VAL:HG11	2.00	0.43
7:CG:26:PHE:CD2	7:CG:62:PHE:HE1	2.36	0.43
9:CI:108:VAL:HG12	9:CI:109:VAL:H	1.84	0.43
10:CJ:16:LEU:HD23	10:CJ:94:VAL:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:CM:50:GLU:O	13:CM:54:VAL:HG22	2.18	0.43
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.53	0.43
26:DA:124:G:OP1	26:DA:1376:C:O2'	2.30	0.43
26:DA:288:C:H2'	26:DA:289:A:H8	1.82	0.43
26:DA:601:C:O2	26:DA:605:C:H4'	2.18	0.43
26:DA:817:C:OP2	61:DA:4676:HOH:O	2.21	0.43
26:DA:903:C:H2'	26:DA:904:C:H6	1.81	0.43
26:DA:910:A:N1	26:DA:2277:G:H1'	2.32	0.43
26:DA:2006:C:O5'	26:DA:2006:C:H6	2.00	0.43
26:DA:2172:U:O2'	26:DA:2173:A:OP1	2.30	0.43
26:DA:2626:C:H2'	26:DA:2627:G:O4'	2.18	0.43
37:DQ:68:ILE:HD13	37:DQ:103:MET:HG2	2.00	0.43
38:DR:21:TYR:CZ	38:DR:43:GLU:HG2	2.52	0.43
46:DZ:154:ASP:OD1	46:DZ:154:ASP:N	2.39	0.43
1:AA:335:C:H2'	1:AA:336:C:C6	2.54	0.43
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.44	0.43
3:AC:52:LEU:HD11	3:AC:55:VAL:CG2	2.48	0.43
5:AE:41:VAL:HG23	5:AE:67:VAL:HG12	2.00	0.43
9:AI:61:ALA:HB1	9:AI:63:ILE:HD11	2.01	0.43
14:AN:24:CYS:HB2	14:AN:33:VAL:HG12	2.01	0.43
20:AT:92:LEU:HD23	20:AT:92:LEU:HA	1.84	0.43
26:BA:1594:G:H2'	26:BA:1595:G:O4'	2.18	0.43
26:BA:1970:A:H4'	26:BA:1971:A:OP1	2.18	0.43
26:BA:2406:U:H2'	26:BA:2406:U:OP2	2.19	0.43
43:BW:14:PRO:HG2	43:BW:78:GLU:CG	2.45	0.43
52:B5:20:ARG:C	52:B5:22:HIS:H	2.26	0.43
1:CA:757:U:O2'	1:CA:879:C:O2	2.31	0.43
1:CA:1002:G:N2	1:CA:1039:C:C4	2.86	0.43
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.18	0.43
1:CA:1080:A:H5''	1:CA:1081:G:OP2	2.19	0.43
4:CD:111:ALA:HB1	4:CD:116:GLN:HB3	2.00	0.43
6:CF:94:GLN:NE2	18:CR:72:ARG:HH12	2.16	0.43
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	2.00	0.43
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.18	0.43
16:CP:60:LEU:HD13	16:CP:60:LEU:HA	1.84	0.43
20:CT:90:GLN:O	20:CT:93:GLU:HB3	2.18	0.43
26:DA:324:A:H2'	26:DA:325:G:O4'	2.19	0.43
26:DA:623:G:H2'	26:DA:624:C:C6	2.54	0.43
26:DA:2674:G:H2'	26:DA:2675:A:C8	2.53	0.43
35:DO:25:LEU:HD12	35:DO:38:VAL:HG12	1.99	0.43
51:D4:56:VAL:HG13	51:D4:57:GLU:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:374:A:C6	1:AA:375:U:C4	3.05	0.43
1:AA:814:A:H2'	1:AA:816:A:H5''	1.99	0.43
1:AA:1302:U:H5	13:AM:17:VAL:HG21	1.83	0.43
2:AB:204:ASN:OD1	2:AB:204:ASN:C	2.61	0.43
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	2.00	0.43
3:AC:6:HIS:HA	3:AC:7:PRO:HD3	1.83	0.43
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.17	0.43
13:AM:70:LEU:O	13:AM:74:VAL:HG23	2.19	0.43
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.18	0.43
23:AW:76:31M:HE1	26:BA:2451:A:C6	2.53	0.43
26:BA:590:A:H2'	26:BA:591:C:O4'	2.18	0.43
26:BA:886:C:OP1	26:BA:886:C:H4'	2.17	0.43
26:BA:2168:G:H5'	26:BA:2169:A:H5''	2.00	0.43
26:BA:2377:A:H2'	26:BA:2378:A:C8	2.53	0.43
26:BA:2543:G:H2'	26:BA:2544:G:C8	2.53	0.43
30:BF:64:ILE:HD12	30:BF:65:TRP:CZ3	2.54	0.43
44:BX:50:LYS:N	44:BX:87:GLN:OE1	2.48	0.43
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.53	0.43
1:CA:1399:C:C2	1:CA:1502:A:N6	2.87	0.43
3:CC:34:LEU:HG	3:CC:38:ARG:NH1	2.31	0.43
14:CN:37:PHE:HZ	14:CN:56:VAL:HG21	1.83	0.43
20:CT:47:GLY:HA2	20:CT:48:LYS:C	2.43	0.43
26:DA:540:C:H2'	26:DA:541:C:C6	2.53	0.43
26:DA:627:A:H4'	26:DA:628:G:H5'	2.00	0.43
26:DA:1881:C:H2'	26:DA:1882:C:O4'	2.19	0.43
26:DA:2410:G:H2'	26:DA:2411:A:O4'	2.19	0.43
26:DA:2820:A:C5	38:DR:4:LEU:HD11	2.53	0.43
30:DF:33:LEU:HB3	36:DP:6:LEU:HD21	2.01	0.43
34:DN:57:ALA:HB1	34:DN:96:GLU:HA	2.01	0.43
45:DY:89:PHE:CE2	45:DY:95:LYS:HB2	2.53	0.43
1:AA:262:A:H4'	20:AT:75:ASN:HB2	2.00	0.43
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.52	0.43
5:AE:105:VAL:O	5:AE:109:ILE:HD12	2.19	0.43
6:AF:10:LEU:HB2	6:AF:59:TYR:HB3	2.01	0.43
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.53	0.43
23:AW:56:C:H5'	26:BA:896:A:H1'	2.00	0.43
26:BA:1171:G:H3'	26:BA:1173:G:H5'	2.01	0.43
26:BA:1177:A:N3	26:BA:1177:A:H2'	2.33	0.43
26:BA:1431:U:H2'	26:BA:1432:C:C6	2.54	0.43
26:BA:1918:A:O2'	26:BA:1920:C:N4	2.51	0.43
31:BG:122:PRO:HD3	31:BG:181:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BH:33:LEU:HD21	32:BH:136:ILE:HG13	2.00	0.43
33:BI:81:VAL:O	33:BI:146:ALA:HA	2.19	0.43
1:CA:324:G:O2'	1:CA:326:G:N7	2.50	0.43
1:CA:722:A:N6	1:CA:724:G:C2	2.87	0.43
1:CA:1279:A:O2'	1:CA:1282:C:N4	2.51	0.43
2:CB:35:GLU:HB2	2:CB:40:HIS:HD2	1.82	0.43
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	2.01	0.43
16:CP:55:ARG:HD2	16:CP:55:ARG:HA	1.88	0.43
25:CY:4:C:H2'	25:CY:5:G:H5'	2.00	0.43
26:DA:1817:G:OP1	28:DD:88:ARG:NH2	2.48	0.43
26:DA:2134:A:C2	26:DA:2159:G:H4'	2.53	0.43
26:DA:2134:A:H3'	26:DA:2135:A:C8	2.53	0.43
26:DA:2516:G:C6	26:DA:2517:C:N4	2.86	0.43
28:DD:182:LEU:HB2	28:DD:272:ALA:HB3	2.01	0.43
31:DG:45:GLU:H	31:DG:45:GLU:HG2	1.43	0.43
32:DH:98:LEU:HD12	32:DH:102:ALA:O	2.18	0.43
41:DU:79:PHE:CZ	41:DU:83:LEU:HD21	2.54	0.43
45:DY:43:ASN:OD1	45:DY:65:ALA:HB3	2.19	0.43
49:D2:16:LEU:O	49:D2:67:LYS:NZ	2.47	0.43
1:AA:1061:G:H1'	10:AJ:56:HIS:CE1	2.53	0.43
13:AM:120:LYS:HE3	23:AW:40:C:O2'	2.19	0.43
19:AS:52:TYR:HA	19:AS:56:GLN:O	2.18	0.43
25:AY:33:U:H2'	25:AY:34:G:H5''	2.00	0.43
25:AY:71:G:H4'	26:BA:1851:U:H4'	2.00	0.43
26:BA:1258:C:H2'	26:BA:1259:G:O4'	2.19	0.43
26:BA:1720:U:H2'	26:BA:1721:G:O4'	2.18	0.43
26:BA:2183:C:O2'	26:BA:2184:G:OP1	2.35	0.43
26:BA:2591:C:H2'	26:BA:2592:G:C8	2.54	0.43
26:BA:2791:C:H5'	26:BA:2893:G:N2	2.34	0.43
28:BD:137:PRO:O	28:BD:140:THR:HG23	2.18	0.43
31:BG:43:LEU:HB3	31:BG:44:GLY:H	1.55	0.43
34:BN:67:LEU:HD12	34:BN:67:LEU:HA	1.80	0.43
40:BT:118:ARG:HD2	40:BT:118:ARG:HA	1.61	0.43
51:B4:1:MET:HE2	51:B4:6:HIS:CD2	2.53	0.43
1:CA:447:G:O6	1:CA:485:G:O2'	2.19	0.43
1:CA:693:G:H2'	1:CA:694:A:C8	2.53	0.43
1:CA:750:G:N2	15:CO:23:GLY:O	2.48	0.43
1:CA:1009:G:N2	1:CA:1010:G:H1'	2.33	0.43
1:CA:1030(A):G:C2	1:CA:1030(C):G:H8	2.36	0.43
9:CI:17:VAL:HG11	9:CI:80:GLY:C	2.44	0.43
9:CI:43:ALA:HB2	9:CI:74:ILE:CD1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CN:47:LEU:O	14:CN:51:GLY:N	2.51	0.43
23:CW:76:31M:HAM	24:CX:76:A:O3'	2.19	0.43
24:CX:15:G:H2'	24:CX:59:A:N1	2.34	0.43
26:DA:69:C:N4	61:DA:4335:HOH:O	2.52	0.43
26:DA:782:A:H5'	26:DA:783:A:N7	2.34	0.43
26:DA:2695:C:H2'	26:DA:2696:U:H6	1.84	0.43
28:DD:142:VAL:HG13	28:DD:191:ALA:HB1	2.00	0.43
46:DZ:153:SER:HB3	46:DZ:167:PRO:HA	2.00	0.43
51:D4:68:ARG:O	51:D4:69:LYS:HB3	2.18	0.43
1:AA:90:U:O2'	1:AA:91:C:H5'	2.19	0.43
1:AA:1198:G:H2'	1:AA:1199:U:C6	2.54	0.43
2:AB:200:ILE:H	2:AB:200:ILE:HD13	1.84	0.43
7:AG:46:ALA:HA	7:AG:49:ILE:HD12	2.01	0.43
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.51	0.43
19:AS:27:GLU:HB3	19:AS:28:LYS:HB3	2.01	0.43
26:BA:1045:A:H1'	26:BA:1047:G:C2	2.53	0.43
26:BA:2292:C:H2'	26:BA:2293:C:H6	1.83	0.43
26:BA:2706:G:N7	61:BA:4733:HOH:O	2.37	0.43
33:BI:50:ARG:HA	33:BI:53:ALA:HB3	2.01	0.43
41:BU:104:GLN:CD	41:BU:104:GLN:H	2.26	0.43
42:BV:34:GLU:HB3	42:BV:56:SER:HB2	2.00	0.43
43:BW:19:LEU:HB3	52:B5:25:LEU:HD11	2.01	0.43
48:B1:50:ARG:HG2	48:B1:59:THR:HB	2.00	0.43
53:B6:10:LEU:HG	53:B6:54:ILE:HG13	2.00	0.43
1:CA:503:C:OP2	12:CL:116:SER:HB3	2.19	0.43
1:CA:572:A:O2'	1:CA:916:G:O2'	2.31	0.43
1:CA:935:A:O2'	1:CA:1383:C:N3	2.44	0.43
1:CA:1011:G:C2	1:CA:1012:U:H1'	2.54	0.43
1:CA:1014:A:H2'	1:CA:1015:A:C8	2.54	0.43
1:CA:1110:A:OP2	61:CA:4091:HOH:O	2.21	0.43
1:CA:1442(A):G:O2'	40:DT:118:ARG:HG2	2.18	0.43
13:CM:50:GLU:HA	13:CM:53:VAL:HB	2.01	0.43
19:CS:28:LYS:HB2	19:CS:29:ARG:CB	2.48	0.43
25:CY:8:4SU:C2	25:CY:14:A:H62	2.30	0.43
26:DA:991:C:OP2	26:DA:1186:G:H5'	2.18	0.43
26:DA:1503:U:H2'	26:DA:1504:C:C6	2.54	0.43
26:DA:2805:G:C6	26:DA:2807:G:C6	3.07	0.43
26:DA:2870:C:H2'	26:DA:2871:C:O4'	2.19	0.43
30:DF:18:ARG:HG2	30:DF:19:GLU:H	1.84	0.43
32:DH:59:ARG:O	32:DH:63:SER:OG	2.36	0.43
33:DI:73:GLU:HG3	33:DI:139:GLN:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:DV:8:GLY:O	42:DV:10:LYS:NZ	2.51	0.43
1:AA:1151:A:O4'	10:AJ:39:PRO:HB2	2.19	0.43
2:AB:54:THR:HG21	2:AB:201:ILE:HD11	1.99	0.43
4:AD:64:LEU:HB2	4:AD:198:VAL:HG21	2.00	0.43
5:AE:148:VAL:O	5:AE:152:ARG:HG3	2.18	0.43
8:AH:34:GLU:CD	8:AH:37:ARG:HH12	2.26	0.43
12:AL:24:VAL:HG12	12:AL:24:VAL:O	2.18	0.43
15:AO:56:LEU:HD21	26:BA:715:G:C2	2.54	0.43
26:BA:11:G:C2'	26:BA:12:U:H5''	2.45	0.43
26:BA:197:A:N6	26:BA:2430:A:O2'	2.51	0.43
26:BA:848:G:N9	26:BA:933:A:H8	2.17	0.43
26:BA:2233:U:H2'	26:BA:2234:G:C8	2.54	0.43
26:BA:2790:A:N3	26:BA:2790:A:H2'	2.34	0.43
27:BB:48:A:H4'	39:BS:95:HIS:HD2	1.83	0.43
38:BR:53:HIS:O	38:BR:56:LYS:HB2	2.18	0.43
40:BT:127:ALA:C	40:BT:129:ARG:H	2.27	0.43
49:B2:16:LEU:HB3	49:B2:20:GLU:HB2	1.99	0.43
1:CA:165:C:H2'	1:CA:166:G:C8	2.54	0.43
1:CA:302:G:N3	1:CA:556:C:H4'	2.33	0.43
1:CA:664:G:N2	1:CA:741:G:H1	2.04	0.43
1:CA:1320:C:C1'	19:CS:73:GLU:HG3	2.49	0.43
2:CB:84:GLU:OE1	2:CB:216:SER:HA	2.18	0.43
4:CD:38:TYR:CZ	4:CD:45:GLN:HG2	2.54	0.43
7:CG:78:ARG:CZ	7:CG:79:ARG:HH12	2.32	0.43
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.49	0.43
20:CT:86:ARG:O	20:CT:90:GLN:HB2	2.19	0.43
23:CW:61:C:O2'	23:CW:62:C:H6	2.02	0.43
26:DA:265:A:H1'	26:DA:266:G:O4'	2.19	0.43
26:DA:644:A:H5''	26:DA:645:C:OP1	2.19	0.43
26:DA:974:G:C4	26:DA:989:G:C2	3.07	0.43
26:DA:1487:G:H2'	26:DA:1488:G:O4'	2.18	0.43
26:DA:1656:C:H2'	26:DA:1657:C:H6	1.84	0.43
26:DA:2494:G:C4	26:DA:2495:G:C8	3.07	0.43
26:DA:2602:A:H4'	26:DA:2603:G:C5'	2.48	0.43
31:DG:37:VAL:O	31:DG:94:LEU:N	2.50	0.43
31:DG:164:GLU:N	31:DG:164:GLU:OE2	2.51	0.43
36:DP:101:VAL:HA	36:DP:106:LEU:O	2.18	0.43
37:DQ:7:MET:HE2	37:DQ:7:MET:HB3	1.90	0.43
45:DY:13:VAL:HB	45:DY:72:VAL:HG13	2.00	0.43
49:D2:53:LEU:HD23	49:D2:53:LEU:HA	1.89	0.43
1:AA:402:G:C6	1:AA:403:C:C4	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1529:G:H4'	1:AA:1530:G:OP2	2.19	0.43
2:AB:88:ALA:O	2:AB:226:ARG:NH1	2.51	0.43
3:AC:6:HIS:HD2	3:AC:8:ILE:N	2.11	0.43
25:AY:49:C:N4	25:AY:65:G:N1	2.28	0.43
26:BA:288:C:H2'	26:BA:289:A:C8	2.53	0.43
26:BA:1175:U:O3'	26:BA:1176:G:H4'	2.17	0.43
26:BA:1372:U:H2'	26:BA:1373:A:O4'	2.18	0.43
26:BA:2176:A:H2'	26:BA:2177:C:C6	2.54	0.43
26:BA:2296:U:OP2	39:BS:9:ARG:NH2	2.52	0.43
26:BA:2653:U:H2'	26:BA:2654:A:C8	2.53	0.43
28:BD:69:ARG:C	28:BD:71:ASP:H	2.26	0.43
28:BD:71:ASP:HB3	28:BD:103:ARG:HH22	1.83	0.43
32:BH:121:ILE:HG13	32:BH:144:VAL:HG21	2.01	0.43
35:BO:104:ARG:NH1	40:BT:34:VAL:HG21	2.34	0.43
46:BZ:144:LEU:HD21	46:BZ:148:ASP:O	2.19	0.43
1:CA:397:A:H3'	1:CA:397:A:N3	2.34	0.43
1:CA:607:A:C2	16:CP:31:LYS:HG3	2.54	0.43
1:CA:1133:G:H2'	1:CA:1134:G:H8	1.84	0.43
1:CA:1289:A:H2	1:CA:1372:U:O4'	2.01	0.43
15:CO:87:ILE:HG22	15:CO:88:ARG:N	2.33	0.43
24:CX:54:5MU:H6	24:CX:54:5MU:O5'	2.02	0.43
26:DA:208:C:H2'	26:DA:209:C:C6	2.54	0.43
26:DA:224:G:N7	26:DA:420:C:H4'	2.33	0.43
26:DA:380:U:H2'	26:DA:381:G:H8	1.83	0.43
26:DA:1262:A:H2	52:D5:10:LYS:HD2	1.83	0.43
26:DA:2228:G:C5	26:DA:2229:C:C4	3.07	0.43
26:DA:2400:G:H2'	26:DA:2401:U:C6	2.50	0.43
28:DD:68:LYS:O	28:DD:69:ARG:HB2	2.19	0.43
33:DI:14:ASP:OD1	33:DI:15:VAL:HG12	2.19	0.43
36:DP:39:LYS:CB	36:DP:45:LEU:HG	2.47	0.43
46:DZ:156:LYS:HE3	46:DZ:158:PRO:HD3	2.01	0.43
52:D5:48:GLU:O	52:D5:60:VAL:HG11	2.18	0.43
1:AA:130:A:N3	1:AA:263:A:O2'	2.38	0.43
1:AA:584:G:H2'	1:AA:585:G:C8	2.54	0.43
1:AA:943:U:H2'	1:AA:944:G:H5'	2.00	0.43
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.54	0.43
1:AA:1342:C:H4'	9:AI:125:TYR:HB3	2.01	0.43
4:AD:63:LYS:HG3	4:AD:64:LEU:N	2.33	0.43
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.54	0.43
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	2.01	0.43
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:6:G:H2'	25:AY:7:A:H5'	2.01	0.43
26:BA:224:G:H2'	26:BA:225:A:O4'	2.18	0.43
26:BA:340:A:H2'	26:BA:341:G:O4'	2.19	0.43
26:BA:657:U:H2'	26:BA:658:C:C6	2.53	0.43
26:BA:881:G:H2'	26:BA:881:G:N3	2.34	0.43
26:BA:882:G:N2	26:BA:895:U:O2	2.52	0.43
26:BA:892:G:C5	26:BA:893:C:C4	3.07	0.43
26:BA:1380:G:OP2	61:BA:5152:HOH:O	2.22	0.43
26:BA:1664:A:H1'	26:BA:2685:G:O2'	2.19	0.43
26:BA:1826:G:H4'	28:BD:242:ARG:CZ	2.49	0.43
26:BA:2292:C:P	39:BS:17:ARG:HH12	2.41	0.43
26:BA:2646:C:H2'	26:BA:2647:U:O4'	2.18	0.43
27:BB:110:G:H2'	27:BB:111:G:H8	1.84	0.43
28:BD:206:LEU:HD22	28:BD:211:ARG:HG2	2.00	0.43
30:BF:29:ASN:H	30:BF:112:MET:HE3	1.83	0.43
31:BG:77:ILE:HD12	31:BG:82:LEU:HD12	2.00	0.43
36:BP:96:THR:OG1	36:BP:99:LEU:HG	2.18	0.43
41:BU:66:ASN:O	41:BU:70:ARG:HG3	2.19	0.43
44:BX:66:LEU:HD23	44:BX:66:LEU:HA	1.73	0.43
52:B5:59:GLU:HG2	52:B5:60:VAL:H	1.83	0.43
1:CA:92:C:H2'	1:CA:93:G:O4'	2.19	0.43
1:CA:337:C:H2'	1:CA:338:A:C8	2.53	0.43
1:CA:1144:G:C6	1:CA:1145:C:N4	2.87	0.43
7:CG:33:ASP:OD1	7:CG:33:ASP:N	2.51	0.43
10:CJ:90:LEU:HA	10:CJ:91:PRO:HD3	1.83	0.43
25:CY:34:G:C6	25:CY:35:A:C6	3.07	0.43
26:DA:140:G:H22	26:DA:1596:A:H4'	1.83	0.43
26:DA:816:C:O2'	26:DA:932:G:O6	2.37	0.43
26:DA:855:G:C6	26:DA:856:C:N4	2.86	0.43
26:DA:2028:U:H2'	26:DA:2029:G:O4'	2.19	0.43
26:DA:2529:G:O6	56:D9:31:LYS:NZ	2.52	0.43
27:DB:114:C:H4'	39:DS:46:VAL:HG22	2.01	0.43
28:DD:69:ARG:C	28:DD:71:ASP:H	2.25	0.43
31:DG:44:GLY:N	31:DG:88:ILE:O	2.52	0.43
35:DO:104:ARG:NH2	35:DO:121:VAL:O	2.52	0.43
42:DV:55:ALA:HA	42:DV:100:ARG:O	2.19	0.43
48:D1:50:ARG:HD2	48:D1:57:GLU:OE1	2.19	0.43
54:D7:26:GLY:O	54:D7:30:VAL:HG23	2.19	0.43
1:AA:96:U:H6	1:AA:96:U:OP2	2.02	0.42
1:AA:839:U:H3'	1:AA:840:C:C5	2.53	0.42
1:AA:1288:A:N3	1:AA:1352:C:O2'	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1353:G:H2'	1:AA:1354:C:H6	1.84	0.42
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.19	0.42
2:AB:21:ARG:HB3	2:AB:39:ILE:HA	2.00	0.42
2:AB:28:PHE:CD1	2:AB:190:THR:HG22	2.54	0.42
3:AC:104:GLN:HE21	3:AC:105:GLU:H	1.66	0.42
6:AF:45:LEU:HD12	6:AF:59:TYR:HD2	1.84	0.42
13:AM:19:LEU:HB3	13:AM:25:ILE:HG21	2.01	0.42
17:AQ:62:SER:OG	17:AQ:72:ARG:HD2	2.19	0.42
20:AT:13:LEU:HD12	20:AT:14:LYS:N	2.33	0.42
24:AX:19:G:H3'	24:AX:20:U:H6	1.84	0.42
26:BA:614(C):A:C4	30:BF:180:GLY:HA2	2.54	0.42
26:BA:1796:U:H2'	26:BA:1797:C:H6	1.84	0.42
26:BA:2173:A:H2'	26:BA:2174:C:O4'	2.18	0.42
26:BA:2561:A:H2'	26:BA:2562:U:O4'	2.18	0.42
28:BD:145:VAL:HG12	28:BD:146:GLU:O	2.18	0.42
37:BQ:7:MET:HB2	37:BQ:7:MET:HE3	1.69	0.42
40:BT:95:ARG:HH11	40:BT:95:ARG:CG	2.26	0.42
1:CA:130:A:N3	1:CA:263:A:O2'	2.49	0.42
1:CA:532:A:N6	3:CC:156:ARG:HH22	2.16	0.42
1:CA:580:U:H5''	15:CO:58:MET:HG2	2.00	0.42
1:CA:608:A:H2'	1:CA:609:A:O4'	2.18	0.42
1:CA:1286:A:C8	1:CA:1286:A:H3'	2.54	0.42
24:CX:8:4SU:H5''	24:CX:49:G:H5'	2.01	0.42
24:CX:21:A:N6	24:CX:46:G:H2'	2.34	0.42
26:DA:140:G:H1'	26:DA:141:A:H2	1.84	0.42
26:DA:325:G:H2'	26:DA:326:G:O4'	2.20	0.42
26:DA:414:C:O2'	26:DA:415:A:H5'	2.19	0.42
26:DA:827:U:H4'	26:DA:828:U:C6	2.53	0.42
26:DA:1161:C:H2'	26:DA:1162:G:C8	2.53	0.42
26:DA:2137:C:O2'	26:DA:2138:C:H5'	2.19	0.42
26:DA:2865:U:C4	26:DA:2866:U:C4	3.07	0.42
28:DD:36:PRO:HA	28:DD:61:LEU:HD13	2.01	0.42
28:DD:69:ARG:C	28:DD:71:ASP:N	2.77	0.42
28:DD:121:PRO:HB3	28:DD:135:PHE:CE2	2.53	0.42
30:DF:53:THR:HG23	30:DF:55:GLY:N	2.22	0.42
31:DG:125:PHE:CZ	31:DG:170:ARG:HA	2.54	0.42
33:DI:94:ALA:O	33:DI:98:ALA:N	2.44	0.42
37:DQ:31:ASP:HA	37:DQ:134:ARG:HH11	1.83	0.42
46:DZ:55:HIS:CE1	46:DZ:135:GLU:HG3	2.51	0.42
1:AA:126:G:H4'	1:AA:634:C:O2	2.19	0.42
1:AA:346:G:H2'	1:AA:347:G:H4'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.35	0.42
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.41	0.42
17:AQ:76:LEU:HD12	17:AQ:77:VAL:H	1.83	0.42
24:AX:7:G:O2'	24:AX:49:G:H5'	2.19	0.42
26:BA:38:A:H2'	26:BA:39:C:C6	2.54	0.42
26:BA:528:A:C2	26:BA:2043:C:H4'	2.53	0.42
26:BA:1713:U:H2'	26:BA:1714:G:H8	1.84	0.42
26:BA:1991:U:H2'	26:BA:1992:G:H5''	2.00	0.42
29:BE:12:THR:HG22	29:BE:13:ARG:N	2.33	0.42
33:BI:72:LEU:C	33:BI:74:ASN:N	2.77	0.42
33:BI:106:GLY:HA2	33:BI:107:VAL:C	2.44	0.42
35:BO:122:LEU:HD13	40:BT:72:VAL:HG11	2.01	0.42
40:BT:118:ARG:HH11	40:BT:118:ARG:CG	2.30	0.42
44:BX:92:LEU:C	44:BX:94:GLY:H	2.27	0.42
45:BY:35:TYR:CE2	45:BY:69:ALA:HB3	2.53	0.42
48:B1:8:SER:HB3	48:B1:66:HIS:CD2	2.55	0.42
51:B4:39:CYS:HA	51:B4:44:THR:HG21	2.01	0.42
1:CA:49:U:O4	1:CA:365:U:H5	2.01	0.42
1:CA:684:A:H1'	11:CK:39:PRO:HD2	2.01	0.42
1:CA:1051:C:N4	61:CA:4001:HOH:O	2.51	0.42
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.19	0.42
3:CC:6:HIS:HD2	3:CC:8:ILE:N	2.14	0.42
4:CD:155:LEU:HD23	4:CD:156:GLU:H	1.84	0.42
7:CG:103:TRP:CH2	7:CG:141:VAL:HG21	2.54	0.42
21:CU:6:ARG:O	21:CU:12:LYS:NZ	2.37	0.42
26:DA:212:G:H2'	26:DA:213:A:O4'	2.18	0.42
26:DA:452:G:O2'	26:DA:457:A:N1	2.49	0.42
26:DA:746:A:H2'	26:DA:2612:C:H5''	2.00	0.42
26:DA:760:G:H2'	26:DA:761:A:O4'	2.18	0.42
26:DA:1235:G:C6	26:DA:1236:G:N1	2.87	0.42
26:DA:1292:U:H2'	26:DA:1293:C:C6	2.54	0.42
26:DA:1471:A:OP2	26:DA:1519:G:N1	2.42	0.42
26:DA:1587:A:H2'	26:DA:1588:C:C6	2.54	0.42
26:DA:2345:G:OP2	53:D6:38:LYS:NZ	2.42	0.42
29:DE:170:LEU:HB3	29:DE:184:VAL:CG2	2.49	0.42
35:DO:23:ARG:HG3	35:DO:24:VAL:N	2.33	0.42
51:D4:62:ARG:HB2	51:D4:63:TYR:CD1	2.54	0.42
53:D6:40:CYS:HA	53:D6:41:PRO:HD3	1.90	0.42
1:AA:8:A:H5'	5:AE:101:ILE:HG22	2.00	0.42
1:AA:16:A:O2'	5:AE:16:THR:HB	2.19	0.42
1:AA:540:G:H2'	1:AA:541:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:568:G:O2'	1:AA:574:A:N1	2.49	0.42
1:AA:1236:A:O2'	1:AA:1304:G:H4'	2.19	0.42
1:AA:1299:A:H5''	1:AA:1299:A:N3	2.35	0.42
1:AA:1317:C:N3	19:AS:37:ARG:NH2	2.63	0.42
1:AA:1410:G:H2'	1:AA:1411:C:C6	2.53	0.42
2:AB:166:ASP:HA	2:AB:167:PRO:HD3	1.81	0.42
4:AD:107:ARG:HA	4:AD:107:ARG:HD2	1.79	0.42
8:AH:86:ILE:HG22	8:AH:93:VAL:HG21	2.01	0.42
13:AM:39:ILE:HD12	13:AM:52:GLU:HG2	2.00	0.42
24:AX:13:C:O2'	26:BA:1924:C:H4'	2.20	0.42
25:AY:55:PSU:N3	25:AY:57:G:H5'	2.33	0.42
26:BA:192:C:OP1	61:BA:4017:HOH:O	2.21	0.42
26:BA:226:G:N2	26:BA:228:A:H62	2.15	0.42
26:BA:644:A:H4'	26:BA:645:C:H5	1.83	0.42
26:BA:1188:U:H4'	42:BV:79:VAL:HG22	2.01	0.42
26:BA:1797:C:H4'	28:BD:257:LEU:O	2.18	0.42
30:BF:9:ILE:HA	30:BF:10:PRO:HD2	1.82	0.42
30:BF:24:LEU:HB3	30:BF:115:ALA:HB2	2.02	0.42
30:BF:89:VAL:HG12	30:BF:90:PHE:CD2	2.55	0.42
31:BG:48:GLU:HA	31:BG:51:ARG:HG3	2.00	0.42
35:BO:7:TYR:HE1	35:BO:20:MET:HE3	1.84	0.42
46:BZ:136:PHE:O	46:BZ:137:ILE:HG13	2.20	0.42
51:B4:59:PHE:N	51:B4:59:PHE:CD1	2.77	0.42
1:CA:922:G:C6	1:CA:923:A:C6	3.07	0.42
4:CD:13:ARG:HB2	4:CD:40:PRO:HD3	2.01	0.42
12:CL:71:PRO:O	12:CL:102:ARG:HD2	2.18	0.42
19:CS:51:VAL:HB	19:CS:75:ALA:HB2	2.00	0.42
23:CW:74:C:C4	23:CW:75:C:C2	3.07	0.42
25:CY:9:A:C8	25:CY:11:C:N4	2.87	0.42
26:DA:39:C:H2'	26:DA:40:C:H6	1.83	0.42
26:DA:699:A:H2'	26:DA:700:G:O4'	2.19	0.42
26:DA:1545:A:H2'	26:DA:1546:C:O4'	2.20	0.42
26:DA:1575:C:H2'	26:DA:1576:U:O4'	2.19	0.42
26:DA:1656:C:H2'	26:DA:1657:C:C6	2.54	0.42
26:DA:1970:A:H4'	26:DA:1971:A:OP1	2.19	0.42
26:DA:2168:G:O3'	26:DA:2169:A:H8	2.02	0.42
26:DA:2272:U:H5''	26:DA:2273:A:OP1	2.18	0.42
26:DA:2745:C:H2'	26:DA:2746:U:O4'	2.19	0.42
30:DF:33:LEU:HD12	30:DF:33:LEU:HA	1.75	0.42
32:DH:137:ASP:HB3	32:DH:140:LYS:HB3	1.99	0.42
35:DO:68:GLU:HB3	35:DO:78:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DQ:43:THR:OG1	37:DQ:45:GLN:HG2	2.19	0.42
39:DS:67:ARG:HG3	39:DS:104:GLY:CA	2.49	0.42
41:DU:17:ILE:HG13	41:DU:32:PHE:HE1	1.83	0.42
46:DZ:138:GLU:H	46:DZ:156:LYS:NZ	2.16	0.42
53:D6:10:LEU:HD23	53:D6:22:ALA:HB2	2.01	0.42
1:AA:741:G:H2'	1:AA:742:G:O4'	2.19	0.42
1:AA:1479:C:H2'	1:AA:1480:G:H8	1.84	0.42
2:AB:207:ALA:O	2:AB:210:SER:HB3	2.19	0.42
3:AC:36:ASP:C	3:AC:40:ARG:HG3	2.44	0.42
20:AT:67:ALA:HA	20:AT:72:LEU:O	2.18	0.42
22:AV:15:A:O5'	22:AV:15:A:H8	2.02	0.42
24:AX:9:G:O2'	24:AX:10:G:N7	2.47	0.42
25:AY:50:U:H2'	25:AY:51:U:O4'	2.20	0.42
26:BA:466:A:N3	26:BA:683:C:H1'	2.34	0.42
26:BA:1142(A):A:C4	26:BA:1144:G:C8	3.06	0.42
26:BA:1530:C:H1'	26:BA:1531:C:OP1	2.19	0.42
26:BA:2116:G:H2'	26:BA:2117:A:C5	2.54	0.42
33:BI:93:THR:H	33:BI:96:ASP:HB2	1.84	0.42
34:BN:130:HIS:O	34:BN:133:GLN:HG2	2.19	0.42
38:BR:98:LEU:HD12	52:B5:57:VAL:HG11	2.01	0.42
46:BZ:19:ARG:HD3	46:BZ:25:PRO:CD	2.49	0.42
1:CA:583:A:N6	1:CA:758:G:O2'	2.52	0.42
1:CA:898:G:N2	1:CA:901:A:OP2	2.50	0.42
1:CA:924:C:O2'	1:CA:1502:A:N6	2.49	0.42
1:CA:1122:U:N3	1:CA:1123:A:N7	2.67	0.42
1:CA:1410:G:H2'	1:CA:1411:C:H6	1.84	0.42
2:CB:160:ASP:N	2:CB:160:ASP:OD1	2.52	0.42
4:CD:112:VAL:HG22	4:CD:116:GLN:OE1	2.20	0.42
4:CD:121:VAL:O	4:CD:134:ASP:HA	2.20	0.42
23:CW:11:C:N4	23:CW:24:G:H1	2.14	0.42
25:C'Y:50:U:H2'	25:C'Y:51:U:C6	2.53	0.42
26:DA:729:G:O2'	26:DA:763:G:H4'	2.19	0.42
26:DA:910:A:C5	37:DQ:13:GLN:HG3	2.55	0.42
26:DA:989:G:OP2	50:D3:11:SER:OG	2.37	0.42
26:DA:996:A:C6	26:DA:1160:G:N1	2.87	0.42
26:DA:1847:A:H3'	26:DA:1848:A:H5'	2.00	0.42
26:DA:2110:G:C2	26:DA:2120:G:H1'	2.55	0.42
26:DA:2114:A:H2'	26:DA:2114:A:N3	2.34	0.42
26:DA:2251:G:OP1	37:DQ:82:ARG:NH1	2.52	0.42
26:DA:2376:A:H3'	26:DA:2377:A:H8	1.85	0.42
27:DB:33:G:N3	27:DB:50:G:N2	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:DP:6:LEU:HA	36:DP:6:LEU:HD23	1.78	0.42
41:DU:76:TYR:HH	41:DU:92:ARG:HH11	1.64	0.42
42:DV:48:GLY:HA2	42:DV:52:VAL:HG12	2.01	0.42
51:D4:33:VAL:HG12	51:D4:34:GLU:N	2.34	0.42
1:AA:109:A:C6	1:AA:326:G:C6	3.07	0.42
1:AA:1079:G:O3'	5:AE:14:ARG:NH2	2.52	0.42
1:AA:1125:U:H4'	1:AA:1126:U:OP1	2.19	0.42
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.55	0.42
5:AE:20:GLN:NE2	5:AE:21:ALA:O	2.52	0.42
8:AH:46:LYS:HG3	8:AH:64:LYS:HB2	2.02	0.42
24:AX:2:G:N3	24:AX:2:G:H2'	2.34	0.42
26:BA:375:C:H2'	26:BA:376:C:C6	2.54	0.42
26:BA:1124:C:H1'	56:B9:36:GLN:NE2	2.34	0.42
28:BD:218:ARG:HB3	28:BD:219:PRO:HD2	2.01	0.42
31:BG:121:ASN:HA	31:BG:122:PRO:HD3	1.87	0.42
32:BH:22:GLY:HA2	32:BH:37:VAL:O	2.20	0.42
53:B6:11:LEU:HD23	53:B6:11:LEU:HA	1.82	0.42
1:CA:1173:G:H2'	1:CA:1174:G:H8	1.84	0.42
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.55	0.42
1:CA:1297:C:P	13:CM:44:ARG:HH22	2.42	0.42
2:CB:67:THR:HA	2:CB:90:MET:HE2	2.02	0.42
4:CD:158:ILE:HG22	4:CD:162:LEU:HD12	2.02	0.42
6:CF:68:PRO:HB2	6:CF:71:ARG:HG3	2.01	0.42
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HA	2.00	0.42
26:DA:352:G:N2	61:DA:3734:HOH:O	2.32	0.42
26:DA:744:G:OP1	29:DE:132:HIS:ND1	2.47	0.42
26:DA:864:G:N2	26:DA:913:U:C2	2.87	0.42
26:DA:2171:A:OP1	26:DA:2171:A:H3'	2.19	0.42
30:DF:139:PHE:CD2	30:DF:167:ALA:HB2	2.55	0.42
30:DF:184:TYR:CZ	30:DF:188:ARG:HD2	2.54	0.42
39:DS:57:LYS:HB2	39:DS:57:LYS:HE3	1.80	0.42
46:DZ:144:LEU:CD1	46:DZ:172:ALA:HB1	2.47	0.42
1:AA:60:A:OP1	1:AA:111:G:N2	2.51	0.42
1:AA:299:G:H8	1:AA:299:G:O5'	2.02	0.42
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.55	0.42
1:AA:1326:C:OP1	21:AU:17:THR:OG1	2.33	0.42
2:AB:24:TRP:H	2:AB:24:TRP:HD1	1.68	0.42
4:AD:163:GLU:C	4:AD:165:MET:H	2.28	0.42
4:AD:166:LYS:HA	4:AD:166:LYS:HD3	1.79	0.42
25:AY:52:G:H1	25:AY:62:C:H42	1.67	0.42
26:BA:606:U:H4'	26:BA:658:C:H4'	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1675:C:O2	29:BE:128:SER:OG	2.37	0.42
27:BB:110:G:H2'	27:BB:111:G:C8	2.54	0.42
28:BD:242:ARG:N	28:BD:242:ARG:HD3	2.33	0.42
30:BF:33:LEU:HD13	30:BF:112:MET:HE2	2.00	0.42
30:BF:34:TRP:CH2	36:BP:8:PRO:HB3	2.54	0.42
31:BG:77:ILE:N	31:BG:82:LEU:O	2.48	0.42
1:CA:444:C:H2'	1:CA:445:G:C8	2.55	0.42
1:CA:715:A:H5''	1:CA:805:C:H1'	2.02	0.42
1:CA:792:A:H4'	1:CA:793:U:H5''	2.01	0.42
1:CA:971:G:OP1	1:CA:971:G:H3'	2.19	0.42
1:CA:979:C:H2'	1:CA:980:C:H5'	2.01	0.42
1:CA:1057:G:C5	1:CA:1204:A:C2	3.07	0.42
1:CA:1079:G:O3'	5:CE:14:ARG:NH2	2.53	0.42
1:CA:1092:A:C6	1:CA:1093:A:C6	3.07	0.42
2:CB:133:LYS:O	2:CB:137:ARG:HG3	2.20	0.42
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	2.01	0.42
13:CM:65:LYS:CA	51:D4:50:VAL:HG11	2.49	0.42
23:CW:25:C:C2'	23:CW:26:A:H5'	2.49	0.42
25:CY:18:G:C2	25:CY:55:PSU:O4	2.72	0.42
26:DA:29:U:OP1	41:DU:5:LYS:NZ	2.52	0.42
26:DA:251:A:C5	26:DA:252:G:H1'	2.55	0.42
26:DA:608:A:C6	26:DA:609:A:C6	3.08	0.42
26:DA:896:A:N6	46:DZ:146:ILE:HD13	2.34	0.42
26:DA:1151:G:C2	26:DA:1152:C:C2	3.07	0.42
26:DA:1354:A:H5''	28:DD:38:LYS:HD3	2.01	0.42
26:DA:1488:G:H5'	26:DA:1489:U:OP2	2.20	0.42
26:DA:2128:C:H2'	26:DA:2129:C:O4'	2.18	0.42
26:DA:2271:G:OP1	47:D0:18:ALA:HB1	2.19	0.42
26:DA:2365:G:O6	55:D8:39:LYS:HE3	2.19	0.42
27:DB:33:G:C6	27:DB:34:U:C4	3.07	0.42
27:DB:73:A:C4	27:DB:105:A:C2	3.07	0.42
28:DD:264:LYS:HA	28:DD:265:PRO:HD3	1.88	0.42
29:DE:72:VAL:HA	29:DE:73:GLU:CB	2.50	0.42
31:DG:136:ARG:HH11	31:DG:136:ARG:H	1.68	0.42
33:DI:66:GLU:OE2	33:DI:69:LYS:HD3	2.18	0.42
35:DO:36:GLY:HA2	35:DO:106:LEU:HD23	2.01	0.42
1:AA:877:C:OP1	8:AH:88:LYS:NZ	2.33	0.42
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.45	0.42
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.54	0.42
7:AG:144:MET:HB3	7:AG:144:MET:HE2	1.69	0.42
11:AK:111:ASP:HB2	18:AR:84:LYS:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:118:A:H3'	26:BA:119:A:H5''	2.02	0.42
26:BA:493:G:H2'	26:BA:494:G:O4'	2.19	0.42
26:BA:1268:A:H2'	26:BA:1269:A:O4'	2.18	0.42
26:BA:1748:G:H5''	26:BA:1748:G:H8	1.85	0.42
29:BE:14:ILE:HD11	29:BE:173:VAL:HG11	2.01	0.42
40:BT:91:ARG:HD2	40:BT:120:ARG:NH1	2.35	0.42
46:BZ:110:GLY:CA	46:BZ:145:GLU:HA	2.50	0.42
46:BZ:145:GLU:H	46:BZ:148:ASP:HB2	1.84	0.42
47:B0:38:VAL:HG12	47:B0:40:GLN:HG2	2.01	0.42
1:CA:116:A:H61	1:CA:313:A:H1'	1.84	0.42
1:CA:779:C:H2'	1:CA:780:A:O4'	2.19	0.42
1:CA:1053:G:C4'	1:CA:1054:C:H5'	2.50	0.42
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.18	0.42
1:CA:1446:U:H4'	1:CA:1447:A:C5	2.54	0.42
2:CB:69:LEU:HB3	2:CB:162:ILE:HG22	2.01	0.42
6:CF:2:ARG:HH11	6:CF:92:LYS:HZ3	1.66	0.42
26:DA:698:C:H5''	26:DA:699:A:OP1	2.20	0.42
26:DA:868:U:C4	26:DA:869:G:N7	2.88	0.42
26:DA:937:U:H2'	26:DA:938:G:O4'	2.20	0.42
26:DA:1167:U:C2	26:DA:1168:G:C8	3.07	0.42
26:DA:2285:C:OP2	53:D6:6:ARG:NH1	2.52	0.42
28:DD:37:LEU:HD13	28:DD:87:ASN:ND2	2.34	0.42
30:DF:34:TRP:CE2	36:DP:8:PRO:HG3	2.55	0.42
44:DX:12:VAL:HG21	44:DX:27:THR:HG22	2.02	0.42
1:AA:938:A:C6	1:AA:939:G:C5	3.07	0.42
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.55	0.42
1:AA:1287:A:H2	1:AA:1353:G:N3	2.18	0.42
4:AD:107:ARG:HH22	4:AD:194:LEU:CD2	2.33	0.42
6:AF:35:ALA:HA	6:AF:67:MET:HB3	2.02	0.42
12:AL:53:ARG:HG2	12:AL:69:TYR:HE1	1.84	0.42
13:AM:84:ILE:HD12	19:AS:74:PHE:CE2	2.51	0.42
25:AY:52:G:H1	25:AY:62:C:N4	2.17	0.42
26:BA:570:G:H2'	26:BA:2030:A:C5	2.55	0.42
26:BA:717:G:H2'	26:BA:718:A:O4'	2.20	0.42
26:BA:1512:U:O2'	26:BA:1513:C:H5'	2.20	0.42
26:BA:1714:G:H1	26:BA:1745(A):C:N4	2.13	0.42
31:BG:77:ILE:HG21	31:BG:80:PHE:CD2	2.55	0.42
35:BO:73:ASP:HB2	40:BT:82:LEU:HD13	2.00	0.42
49:B2:32:LEU:HD13	49:B2:36:ARG:HH11	1.85	0.42
56:B9:27:CYS:SG	56:B9:28:GLU:N	2.93	0.42
1:CA:583:A:H2'	1:CA:584:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:685:G:C2	1:CA:686:U:C4	3.08	0.42
1:CA:1067:A:H1'	1:CA:1068:G:O4'	2.20	0.42
1:CA:1072:G:C6	1:CA:1073:U:C4	3.08	0.42
1:CA:1233:G:H2'	1:CA:1234:C:C6	2.55	0.42
2:CB:137:ARG:O	2:CB:141:GLU:N	2.36	0.42
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.19	0.42
15:CO:36:ILE:HG23	15:CO:56:LEU:HD11	2.01	0.42
26:DA:536:A:H2'	26:DA:537:C:C6	2.55	0.42
26:DA:1198:U:H2'	26:DA:1199:U:C6	2.55	0.42
26:DA:2107:C:H2'	26:DA:2108:C:O4'	2.20	0.42
28:DD:145:VAL:HB	28:DD:155:LEU:HB2	2.02	0.42
29:DE:9:VAL:HB	40:DT:3:ARG:HG2	2.02	0.42
34:DN:40:PRO:HB3	41:DU:68:ALA:HB2	2.01	0.42
45:DY:45:VAL:N	45:DY:63:LYS:O	2.45	0.42
46:DZ:24:LEU:HA	46:DZ:25:PRO:HD3	1.90	0.42
51:D4:9:LEU:HD23	51:D4:9:LEU:HA	1.90	0.42
56:D9:7:VAL:HG12	56:D9:34:GLN:HB3	2.01	0.42
1:AA:108:G:O6	20:AT:15:ARG:HD2	2.19	0.42
1:AA:130:A:O2'	1:AA:131:C:O5'	2.32	0.42
1:AA:152:A:N6	1:AA:170:U:C2	2.88	0.42
1:AA:583:A:N6	1:AA:758:G:O2'	2.53	0.42
1:AA:1006:C:H2'	1:AA:1007:C:C6	2.55	0.42
1:AA:1029:C:N3	1:AA:1032:G:O6	2.53	0.42
1:AA:1182:G:C3'	1:AA:1183:A:H5'	2.50	0.42
1:AA:1495:U:O2'	26:BA:1919:A:N1	2.40	0.42
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.84	0.42
15:AO:78:TYR:CZ	15:AO:82:ILE:HD13	2.55	0.42
17:AQ:66:SER:H	17:AQ:69:LYS:HB3	1.85	0.42
20:AT:56:MET:HE3	20:AT:88:VAL:HG21	2.01	0.42
25:AY:56:C:C2	25:AY:57:G:C8	3.08	0.42
26:BA:222:A:H3'	26:BA:421:U:H5'	2.00	0.42
26:BA:1858:G:H21	26:BA:1883:G:H2'	1.84	0.42
26:BA:2090:G:O6	61:BA:4756:HOH:O	2.19	0.42
26:BA:2111:C:OP2	26:BA:2145:C:N4	2.51	0.42
26:BA:2461:C:H2'	26:BA:2462:U:C6	2.55	0.42
29:BE:14:ILE:HG12	29:BE:21:VAL:HG13	2.00	0.42
33:BI:131:LYS:HA	33:BI:137:PRO:HA	2.02	0.42
40:BT:53:ARG:HB3	40:BT:53:ARG:CZ	2.50	0.42
45:BY:54:LYS:HA	45:BY:55:TYR:HA	1.85	0.42
1:CA:6:G:H4'	1:CA:298:A:H4'	2.00	0.42
1:CA:344:A:H5''	1:CA:345:C:H5	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1269:A:H2	1:CA:1312:G:N3	2.17	0.42
1:CA:1357:A:N6	1:CA:1363(A):A:N1	2.67	0.42
2:CB:120:ALA:C	2:CB:122:PHE:H	2.25	0.42
3:CC:19:GLU:HB3	3:CC:55:VAL:O	2.20	0.42
11:CK:38:ASN:HA	11:CK:39:PRO:HD3	1.80	0.42
23:CW:29:G:N2	23:CW:42:C:C2	2.88	0.42
24:CX:3:C:H5'	26:DA:2255:G:O2'	2.20	0.42
26:DA:234:C:H2'	26:DA:235:U:C6	2.54	0.42
26:DA:839:U:H2'	26:DA:840:C:C6	2.55	0.42
26:DA:863:A:P	37:DQ:22:LYS:HG3	2.60	0.42
26:DA:1231:G:H2'	26:DA:1232:G:C8	2.55	0.42
26:DA:1470:G:HO2'	26:DA:1471:A:H8	1.63	0.42
26:DA:1794:U:H2'	26:DA:1795:C:H6	1.85	0.42
28:DD:73:VAL:O	28:DD:75:ILE:HG13	2.19	0.42
31:DG:72:ARG:NH1	31:DG:87:PRO:HG3	2.35	0.42
34:DN:138:LEU:HD23	34:DN:138:LEU:HA	1.73	0.42
44:DX:84:ALA:HB3	44:DX:87:GLN:NE2	2.35	0.42
46:DZ:146:ILE:H	46:DZ:146:ILE:HG13	1.62	0.42
1:AA:881:G:P	12:AL:12:ARG:HH22	2.42	0.42
1:AA:922:G:C6	1:AA:923:A:C6	3.08	0.42
1:AA:1314:C:H2'	1:AA:1315:U:C6	2.54	0.42
2:AB:62:ALA:HB3	2:AB:225:ALA:HB3	2.02	0.42
3:AC:56:ASP:HB2	3:AC:67:THR:HB	2.02	0.42
3:AC:112:SER:O	3:AC:116:VAL:HG23	2.20	0.42
3:AC:131:ARG:NE	3:AC:166:GLU:OE2	2.53	0.42
4:AD:170:VAL:HG11	4:AD:174:LEU:HB2	2.02	0.42
9:AI:16:ARG:HB2	9:AI:64:THR:HB	2.01	0.42
13:AM:14:ARG:NH2	13:AM:41:PRO:O	2.53	0.42
18:AR:26:LEU:HD23	18:AR:29:PHE:CE2	2.55	0.42
25:AY:38:A:C5	25:AY:39:PSU:C6	3.08	0.42
25:AY:68:C:N3	25:AY:69:G:C8	2.88	0.42
26:BA:1047:G:O2'	26:BA:1048:A:H8	2.03	0.42
26:BA:1419:A:O2'	26:BA:1421:G:N7	2.49	0.42
26:BA:1762:A:H2'	61:BA:5184:HOH:O	2.19	0.42
26:BA:2101:G:H2'	26:BA:2102:U:C6	2.55	0.42
26:BA:2443:C:OP1	30:BF:68:LYS:HD3	2.20	0.42
26:BA:2619:C:H4'	29:BE:151:TYR:O	2.20	0.42
27:BB:55:U:H2'	27:BB:56:G:O4'	2.20	0.42
45:BY:9:LYS:HA	45:BY:10:GLY:HA2	1.71	0.42
50:B3:5:LYS:NZ	50:B3:34:GLU:OE2	2.40	0.42
51:B4:62:ARG:HB2	51:B4:63:TYR:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:340:U:H2'	1:CA:341:C:C6	2.54	0.42
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.20	0.42
1:CA:641:U:O3'	1:CA:642:A:H8	2.03	0.42
1:CA:1154:G:C8	1:CA:1155:G:C8	3.07	0.42
2:CB:87:ARG:HH22	2:CB:220:ASP:CG	2.27	0.42
3:CC:107:GLN:O	3:CC:108:ASN:C	2.63	0.42
3:CC:115:LEU:HD12	3:CC:115:LEU:HA	1.80	0.42
4:CD:57:ARG:HD3	4:CD:205:GLU:HB2	2.00	0.42
10:CJ:56:HIS:CD2	10:CJ:56:HIS:H	2.38	0.42
11:CK:110:ASP:HB3	18:CR:85:LEU:HB3	2.02	0.42
13:CM:94:ARG:CZ	19:CS:80:TYR:HD2	2.33	0.42
20:CT:33:ILE:HG13	20:CT:62:LEU:HD22	2.02	0.42
25:CY:15:G:H22	25:CY:48:C:N4	2.15	0.42
26:DA:300:A:H3'	45:DY:84:ARG:NH2	2.35	0.42
26:DA:526:A:N3	26:DA:2044:C:H1'	2.35	0.42
26:DA:1015:G:O2'	26:DA:1016:G:H5'	2.20	0.42
26:DA:1019:U:H3	26:DA:1142(A):A:N6	2.13	0.42
26:DA:2252:G:H2'	26:DA:2253:G:O4'	2.19	0.42
26:DA:2262:U:H4'	26:DA:2328:A:H2	1.84	0.42
26:DA:2307:G:H8	26:DA:2307:G:OP1	2.03	0.42
26:DA:2853:C:H2'	26:DA:2854:G:C8	2.54	0.42
39:DS:80:LEU:HD12	39:DS:80:LEU:HA	1.84	0.42
46:DZ:5:LEU:HD22	46:DZ:5:LEU:HA	1.82	0.42
1:AA:78:G:N2	1:AA:91:C:C2	2.88	0.41
1:AA:555:C:H2'	1:AA:556:C:C6	2.55	0.41
1:AA:591:U:H2'	1:AA:592:G:C8	2.54	0.41
1:AA:1003:G:N3	1:AA:1004:A:H1'	2.34	0.41
1:AA:1035:A:H8	1:AA:1035:A:O5'	2.02	0.41
2:AB:71:VAL:HG13	2:AB:93:VAL:CG2	2.50	0.41
3:AC:47:LEU:CD1	3:AC:68:VAL:HG11	2.50	0.41
7:AG:28:ASN:HA	7:AG:31:MET:HE2	2.02	0.41
9:AI:93:ARG:NH1	9:AI:93:ARG:HB2	2.35	0.41
33:BI:110:ASP:HA	33:BI:111:PRO:HD2	1.78	0.41
36:BP:63:PRO:HG2	55:B8:25:MET:HB2	2.02	0.41
36:BP:121:LYS:HG2	36:BP:122:PRO:HD2	2.02	0.41
40:BT:11:GLU:OE1	40:BT:57:PHE:HB3	2.19	0.41
40:BT:73:GLU:OE1	40:BT:103:ARG:NE	2.41	0.41
40:BT:127:ALA:O	40:BT:128:GLU:HB2	2.18	0.41
45:BY:7:VAL:HG21	45:BY:72:VAL:HG12	2.02	0.41
45:BY:86:ARG:HH11	45:BY:100:ALA:HB1	1.85	0.41
51:B4:63:TYR:N	51:B4:63:TYR:CD1	2.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:998:G:C6	1:CA:999:C:C4	3.08	0.41
1:CA:1039:C:C4	1:CA:1040:U:C4	3.07	0.41
4:CD:17:VAL:HG12	4:CD:18:LYS:N	2.35	0.41
23:CW:76:31M:N3'	26:DA:2585:U:O4	2.53	0.41
26:DA:569:U:H5''	61:DA:4096:HOH:O	2.20	0.41
26:DA:776:G:C8	26:DA:793:A:C2	3.08	0.41
26:DA:867:C:C2'	26:DA:868:U:H5'	2.50	0.41
26:DA:1720:U:H2'	26:DA:1721:G:O4'	2.20	0.41
26:DA:1843:C:H5'	28:DD:253:GLN:NE2	2.34	0.41
26:DA:2505:G:O6	26:DA:2576:G:H2'	2.20	0.41
26:DA:2512:C:H2'	26:DA:2513:G:O4'	2.20	0.41
26:DA:2788:C:C4	26:DA:2789:C:N4	2.88	0.41
26:DA:2815:C:H2'	26:DA:2816:C:H6	1.85	0.41
29:DE:60:ASN:CG	29:DE:62:PRO:HD2	2.45	0.41
44:DX:88:LYS:NZ	44:DX:90:GLU:HG2	2.34	0.41
46:DZ:67:LEU:HA	46:DZ:68:PRO:HD3	1.93	0.41
46:DZ:166:SER:O	46:DZ:169:GLU:HB2	2.20	0.41
1:AA:309:G:H1'	1:AA:608:A:C2	2.55	0.41
1:AA:765:G:N1	1:AA:812:C:O2'	2.43	0.41
1:AA:1128:C:H4'	1:AA:1148:U:O2	2.19	0.41
1:AA:1296:C:H4'	1:AA:1302:U:C4	2.55	0.41
1:AA:1417:G:H22	1:AA:1482:G:H2'	1.84	0.41
2:AB:27:LYS:HB2	2:AB:194:PRO:HD2	2.01	0.41
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.21	0.41
11:AK:59:TYR:CZ	11:AK:63:LEU:HD11	2.55	0.41
12:AL:42:THR:OG1	12:AL:52:LEU:HD13	2.20	0.41
19:AS:3:ARG:NH1	19:AS:10:PHE:HB2	2.35	0.41
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	2.01	0.41
19:AS:38:SER:HB2	19:AS:71:LEU:HD12	2.01	0.41
23:AW:25:C:H2'	23:AW:26:A:H5'	2.02	0.41
25:AY:22:G:C2	25:AY:23:A:C5	3.08	0.41
25:AY:39:PSU:H6	25:AY:39:PSU:H5'	1.86	0.41
26:BA:355:G:H2'	26:BA:356:G:O4'	2.20	0.41
26:BA:479:A:N3	26:BA:481:G:H5''	2.35	0.41
26:BA:954:G:H5''	37:BQ:13:GLN:HB3	2.01	0.41
26:BA:1530:C:HO2'	26:BA:1531:C:P	2.37	0.41
26:BA:2012:G:OP1	43:BW:11:ARG:NH2	2.45	0.41
32:BH:96:ALA:HB2	32:BH:105:LEU:HD13	2.02	0.41
34:BN:33:LEU:HD12	34:BN:33:LEU:HA	1.84	0.41
39:BS:10:ARG:HG3	39:BS:13:ARG:NH2	2.35	0.41
41:BU:17:ILE:HG13	41:BU:32:PHE:HE1	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:BZ:104:PHE:CD2	46:BZ:139:VAL:HB	2.55	0.41
1:CA:434:U:H2'	1:CA:435:C:C6	2.55	0.41
1:CA:657:G:H1'	1:CA:750:G:N2	2.35	0.41
1:CA:791:G:N2	1:CA:1497:G:O3'	2.50	0.41
1:CA:814:A:N7	1:CA:816:A:C4	2.88	0.41
1:CA:971:G:H22	1:CA:1363(A):A:P	2.42	0.41
1:CA:1178:G:N2	1:CA:1181:G:OP2	2.49	0.41
1:CA:1346:A:N1	1:CA:1374:A:H5''	2.34	0.41
3:CC:82:GLU:O	3:CC:85:ARG:HB2	2.20	0.41
3:CC:116:VAL:HG13	3:CC:119:ARG:HD3	2.02	0.41
4:CD:112:VAL:HG13	4:CD:161:ASN:OD1	2.20	0.41
8:CH:72:PRO:O	8:CH:73:ASP:HB3	2.20	0.41
13:CM:56:LEU:HD23	13:CM:57:ARG:N	2.35	0.41
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.55	0.41
17:CQ:65:ILE:HB	17:CQ:69:LYS:HB3	2.03	0.41
25:CY:5:G:N2	25:CY:68:C:N3	2.63	0.41
26:DA:27:G:O2'	26:DA:28:A:OP2	2.36	0.41
26:DA:1885:A:H2'	26:DA:1886:C:O4'	2.20	0.41
26:DA:1905:C:H1'	26:DA:1928:A:H2	1.85	0.41
26:DA:2124:G:N1	26:DA:2174:C:N4	2.34	0.41
26:DA:2519:U:C4	26:DA:2542:A:C5	3.08	0.41
27:DB:108:U:H2'	27:DB:109:C:H5''	2.03	0.41
31:DG:86:MET:HA	31:DG:87:PRO:HD3	1.97	0.41
32:DH:40:GLU:OE1	32:DH:61:HIS:NE2	2.52	0.41
38:DR:26:LYS:HE2	38:DR:70:LEU:O	2.20	0.41
46:DZ:158:PRO:HA	46:DZ:159:PRO:HD3	1.69	0.41
1:AA:295:C:H2'	1:AA:296:U:O4'	2.21	0.41
1:AA:589:C:H5''	8:AH:29:SER:OG	2.20	0.41
1:AA:663:A:H5'	1:AA:836:G:OP1	2.19	0.41
1:AA:977:A:H1'	1:AA:982:U:O4	2.20	0.41
1:AA:1027:C:C2	1:AA:1034:G:C6	3.07	0.41
2:AB:48:MET:HA	2:AB:51:LEU:HD12	2.03	0.41
4:AD:190:ASP:H	4:AD:193:ASP:HB2	1.86	0.41
9:AI:127:LYS:O	9:AI:128:ARG:HG2	2.20	0.41
10:AJ:47:PHE:N	10:AJ:63:PHE:O	2.47	0.41
17:AQ:31:LEU:HD23	17:AQ:32:TYR:CZ	2.56	0.41
23:AW:76:31M:HD2	26:BA:2506:U:O4'	2.20	0.41
24:AX:15:G:H21	24:AX:21:A:H1'	1.84	0.41
25:AY:19:G:C4'	25:AY:57:G:H22	2.33	0.41
26:BA:303:U:H2'	26:BA:304:G:C8	2.55	0.41
26:BA:528:A:C8	26:BA:528:A:H3'	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:615:G:OP1	30:BF:40:GLN:NE2	2.53	0.41
26:BA:1963:U:H4'	26:BA:1964:G:OP1	2.20	0.41
26:BA:2698:U:H2'	26:BA:2699:C:C6	2.55	0.41
27:BB:110:G:O2'	27:BB:111:G:H5'	2.20	0.41
32:BH:88:LEU:HD23	32:BH:165:ALA:HA	2.01	0.41
38:BR:57:ARG:HH21	38:BR:62:ALA:HB2	1.85	0.41
45:BY:56:PRO:C	45:BY:58:GLY:H	2.28	0.41
46:BZ:105:VAL:O	46:BZ:140:ASP:HA	2.20	0.41
52:B5:35:GLU:HG3	52:B5:51:TYR:CG	2.55	0.41
1:CA:250:A:H4'	1:CA:251:G:O5'	2.18	0.41
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.41
1:CA:741:G:H2'	1:CA:742:G:O4'	2.20	0.41
1:CA:1118:C:H2'	1:CA:1119:C:C6	2.56	0.41
1:CA:1240:U:OP2	7:CG:115:ARG:HA	2.19	0.41
5:CE:41:VAL:O	5:CE:66:MET:HA	2.20	0.41
9:CI:77:ILE:O	9:CI:81:ILE:HG22	2.21	0.41
17:CQ:3:LYS:HD3	17:CQ:61:GLU:O	2.20	0.41
26:DA:275:G:H2'	26:DA:276:A:O4'	2.20	0.41
26:DA:784:A:N6	28:DD:229:VAL:HG11	2.35	0.41
26:DA:1008:C:H4'	41:DU:59:ARG:NH2	2.35	0.41
26:DA:1248:G:C5	41:DU:3:ARG:HB2	2.55	0.41
26:DA:1372:U:O5'	26:DA:1372:U:H6	2.03	0.41
26:DA:2172:U:O2'	26:DA:2173:A:P	2.78	0.41
26:DA:2541:A:N7	61:DA:3999:HOH:O	2.37	0.41
32:DH:13:LYS:HA	32:DH:14:GLY:HA2	1.67	0.41
39:DS:83:LYS:HE2	39:DS:83:LYS:HB3	1.90	0.41
42:DV:46:VAL:HG23	42:DV:52:VAL:HG11	2.01	0.41
46:DZ:126:VAL:HG11	46:DZ:161:VAL:CG2	2.41	0.41
51:D4:26:SER:OG	51:D4:27:THR:N	2.51	0.41
1:AA:103:C:OP2	20:AT:14:LYS:NZ	2.44	0.41
1:AA:382:A:H2'	1:AA:383:A:H8	1.85	0.41
1:AA:826:C:H2'	1:AA:827:U:C6	2.56	0.41
1:AA:1122:U:H2'	1:AA:1123:A:O4'	2.21	0.41
2:AB:218:ALA:O	2:AB:222:ILE:HG13	2.20	0.41
4:AD:64:LEU:HB2	4:AD:198:VAL:HG11	2.03	0.41
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.54	0.41
10:AJ:81:THR:HA	10:AJ:84:GLN:HB3	2.02	0.41
11:AK:62:GLN:O	11:AK:66:LEU:HG	2.21	0.41
13:AM:91:ARG:HB2	13:AM:98:VAL:HG13	2.03	0.41
18:AR:58:LEU:HD12	18:AR:62:GLU:CD	2.46	0.41
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:AY:19:G:H4'	25:AY:20:U:OP2	2.19	0.41
25:AY:57:G:N3	25:AY:58:A:H5'	2.35	0.41
26:BA:443:A:H5''	26:BA:444:C:OP1	2.21	0.41
26:BA:601:C:O2'	26:BA:605:C:H5''	2.20	0.41
26:BA:816:C:H2'	26:BA:817:C:C6	2.55	0.41
26:BA:1011:G:P	41:BU:77:SER:HG	2.43	0.41
26:BA:1266:G:O4'	43:BW:15:ARG:NH2	2.50	0.41
26:BA:1403:C:H5''	26:BA:1471:A:H1'	2.01	0.41
26:BA:2119:A:C5	26:BA:2171:A:C6	3.08	0.41
26:BA:2564:A:C2	26:BA:2647:U:H4'	2.55	0.41
26:BA:2785:C:H2'	26:BA:2786:U:O4'	2.20	0.41
29:BE:119:ARG:HG2	29:BE:160:TYR:CG	2.56	0.41
45:BY:15:VAL:HG21	45:BY:42:VAL:HG11	2.02	0.41
49:B2:35:LEU:HB3	49:B2:50:ILE:HG12	2.01	0.41
1:CA:336:C:H2'	1:CA:337:C:C6	2.55	0.41
1:CA:501:C:H2'	1:CA:502:G:H8	1.84	0.41
1:CA:562:C:H1'	12:CL:15:ARG:HB3	2.02	0.41
1:CA:1041:A:H2'	1:CA:1042:G:O4'	2.20	0.41
2:CB:12:GLU:O	2:CB:15:VAL:N	2.50	0.41
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.76	0.41
3:CC:28:GLN:HE21	3:CC:28:GLN:HB2	1.59	0.41
7:CG:23:VAL:HG13	7:CG:43:PHE:CE2	2.55	0.41
8:CH:51:VAL:HG12	8:CH:52:ASP:N	2.35	0.41
14:CN:45:ARG:O	14:CN:49:HIS:HD2	2.04	0.41
26:DA:8:A:H2'	26:DA:9:U:C6	2.55	0.41
26:DA:752:A:OP1	54:D7:3:ARG:NH2	2.50	0.41
26:DA:2867:G:OP2	40:DT:119:LYS:NZ	2.50	0.41
32:DH:27:LYS:HB3	32:DH:27:LYS:HE3	1.82	0.41
33:DI:110:ASP:OD1	33:DI:111:PRO:HD2	2.21	0.41
34:DN:39:ARG:HA	34:DN:40:PRO:HD3	1.80	0.41
35:DO:120:GLU:HG2	35:DO:122:LEU:HG	2.02	0.41
38:DR:21:TYR:OH	38:DR:43:GLU:HG2	2.21	0.41
41:DU:81:HIS:O	41:DU:84:LYS:HB3	2.20	0.41
42:DV:29:PRO:HA	42:DV:61:VAL:HG22	2.02	0.41
46:DZ:120:ILE:HD12	46:DZ:171:ILE:C	2.45	0.41
47:D0:50:ASN:HB3	47:D0:63:VAL:HG22	2.03	0.41
1:AA:103:C:OP2	20:AT:17:ARG:NH2	2.53	0.41
26:BA:465:G:H2'	26:BA:466:A:C8	2.55	0.41
26:BA:634:C:H2'	26:BA:635:C:C6	2.56	0.41
26:BA:1456:G:OP2	61:BA:4012:HOH:O	2.21	0.41
26:BA:2283:C:H2'	26:BA:2284:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:BB:13:A:N1	27:BB:69:G:O2'	2.52	0.41
33:BI:109:ILE:HG23	33:BI:110:ASP:N	2.35	0.41
51:B4:28:LYS:HA	51:B4:29:PRO:HD3	1.84	0.41
1:CA:29:G:O2'	1:CA:295:C:H4'	2.20	0.41
1:CA:730:G:C5	1:CA:731:G:H1'	2.55	0.41
1:CA:971:G:N2	1:CA:1363(A):A:OP2	2.51	0.41
1:CA:978:A:C6	1:CA:1319:A:C5	3.08	0.41
1:CA:1173:G:H2'	1:CA:1174:G:C8	2.55	0.41
6:CF:94:GLN:HE22	18:CR:72:ARG:HH12	1.69	0.41
20:CT:72:LEU:HD23	20:CT:72:LEU:HA	1.84	0.41
26:DA:324:A:N6	26:DA:338:G:O2'	2.49	0.41
26:DA:932:G:H4'	26:DA:933:A:O5'	2.19	0.41
26:DA:996:A:H4'	41:DU:91:ASP:OD2	2.19	0.41
26:DA:1024:G:C6	26:DA:1025:G:C6	3.08	0.41
26:DA:1127:A:C2'	26:DA:1128:A:H5''	2.50	0.41
26:DA:1580:A:H8	26:DA:1580:A:OP2	2.03	0.41
26:DA:1882:C:H3'	26:DA:1883:G:H8	1.85	0.41
26:DA:2169:A:C2	26:DA:2170:A:C2	3.08	0.41
26:DA:2550:G:C6	26:DA:2551:C:C4	3.08	0.41
26:DA:2683:C:OP1	40:DT:53:ARG:NH2	2.49	0.41
26:DA:2693:A:H2'	26:DA:2694:G:H8	1.85	0.41
29:DE:169:ASN:HB2	29:DE:203:LYS:HG3	2.03	0.41
30:DF:135:LYS:HE2	30:DF:135:LYS:HA	2.02	0.41
37:DQ:109:VAL:HG13	37:DQ:113:GLN:HB3	2.02	0.41
40:DT:6:LEU:O	40:DT:10:VAL:HG23	2.20	0.41
1:AA:600:C:H2'	1:AA:601:C:H6	1.85	0.41
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	2.02	0.41
2:AB:77:ALA:CB	2:AB:165:VAL:HG11	2.51	0.41
3:AC:27:LYS:HA	3:AC:27:LYS:HD2	1.76	0.41
4:AD:138:TYR:CE1	4:AD:140:VAL:HA	2.56	0.41
8:AH:33:GLU:HG2	8:AH:48:TYR:CZ	2.56	0.41
10:AJ:27:ALA:HA	10:AJ:81:THR:HG21	2.03	0.41
20:AT:57:ARG:HH22	20:AT:100:ILE:HD12	1.86	0.41
21:AU:6:ARG:O	21:AU:12:LYS:HD2	2.21	0.41
26:BA:719:C:H2'	26:BA:720:C:H6	1.85	0.41
26:BA:1756:G:H4'	26:BA:1758:G:O4'	2.21	0.41
26:BA:2639:A:OP2	61:BA:4129:HOH:O	2.22	0.41
27:BB:6:C:H2'	27:BB:7:G:H5''	2.02	0.41
28:BD:142:VAL:HG13	28:BD:191:ALA:HB1	2.01	0.41
30:BF:183:VAL:O	30:BF:187:VAL:HG23	2.21	0.41
32:BH:13:LYS:HA	32:BH:14:GLY:HA2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:BI:103:ARG:HE	33:BI:103:ARG:HB3	1.53	0.41
34:BN:48:MET:H	34:BN:48:MET:HG3	1.78	0.41
53:B6:9:LEU:HD11	53:B6:23:THR:HG23	2.03	0.41
1:CA:513:C:H2'	1:CA:514:C:O4'	2.19	0.41
1:CA:619:U:H3	4:CD:134:ASP:CG	2.27	0.41
1:CA:722:A:C8	1:CA:724:G:H1'	2.55	0.41
1:CA:857:C:H2'	1:CA:858:G:O4'	2.21	0.41
1:CA:942:G:C2	1:CA:1342:C:C2	3.09	0.41
1:CA:983:A:O2'	1:CA:1050:G:OP2	2.33	0.41
1:CA:998:G:H2'	1:CA:999:C:O4'	2.20	0.41
2:CB:130:ARG:HA	2:CB:131:PRO:HD3	1.88	0.41
4:CD:163:GLU:O	4:CD:166:LYS:HG2	2.21	0.41
4:CD:208:SER:OG	5:CE:101:ILE:HD12	2.20	0.41
14:CN:37:PHE:HB3	14:CN:39:LEU:HG	2.03	0.41
20:CT:86:ARG:HB3	20:CT:86:ARG:CZ	2.49	0.41
23:CW:23:A:H2'	23:CW:24:G:C8	2.56	0.41
26:DA:775:G:O3'	61:DA:4253:HOH:O	2.21	0.41
26:DA:869:G:C6	26:DA:870:A:C5	3.08	0.41
26:DA:1021:A:C8	26:DA:1021:A:C3'	3.02	0.41
26:DA:1766:U:H2'	26:DA:1767:C:H6	1.85	0.41
26:DA:2114:A:N1	26:DA:2117:A:N6	2.69	0.41
26:DA:2154:G:N1	26:DA:2155:G:N7	2.69	0.41
27:DB:8:U:H3	27:DB:113:G:H1	1.69	0.41
30:DF:184:TYR:O	30:DF:188:ARG:HG3	2.21	0.41
31:DG:145:THR:HG23	31:DG:148:MET:HE3	2.02	0.41
32:DH:54:ARG:HD3	32:DH:65:HIS:ND1	2.34	0.41
39:DS:65:VAL:O	39:DS:69:VAL:HG12	2.20	0.41
1:AA:37:U:O2'	1:AA:500:G:H4'	2.20	0.41
1:AA:161:A:H8	1:AA:161:A:O5'	2.02	0.41
1:AA:719:C:O2'	18:AR:50:ILE:O	2.30	0.41
1:AA:993:G:H2'	1:AA:993:G:N3	2.36	0.41
1:AA:1286:A:H2'	1:AA:1287:A:H4'	2.01	0.41
3:AC:15:THR:CG2	3:AC:181:ASN:HA	2.44	0.41
9:AI:26:VAL:HG22	9:AI:61:ALA:HB3	2.02	0.41
20:AT:46:GLU:O	20:AT:46:GLU:HG2	2.20	0.41
23:AW:13:C:O2'	23:AW:14:A:O5'	2.37	0.41
25:AY:38:A:H3'	25:AY:39:PSU:H5'	2.02	0.41
26:BA:271(A):A:N1	26:BA:272(D):G:O2'	2.47	0.41
30:BF:101:LEU:HD12	30:BF:101:LEU:HA	1.84	0.41
30:BF:157:VAL:HG21	30:BF:181:LEU:HD13	2.02	0.41
33:BI:9:LEU:HD22	33:BI:9:LEU:HA	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BP:6:LEU:HD23	36:BP:6:LEU:HA	1.80	0.41
52:B5:16:ARG:NH1	52:B5:17:ASP:OD1	2.50	0.41
1:CA:176:C:H2'	1:CA:177:C:C6	2.55	0.41
3:CC:26:LYS:HB3	3:CC:26:LYS:HE3	1.88	0.41
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.56	0.41
16:CP:17:TYR:HE2	16:CP:41:PRO:HG3	1.86	0.41
23:CW:34:G:H2'	23:CW:35:A:C8	2.56	0.41
26:DA:62:C:N4	26:DA:93:G:H1	2.19	0.41
26:DA:340:A:H2'	26:DA:341:G:O4'	2.20	0.41
26:DA:1498:C:O4'	26:DA:1577:C:H4'	2.21	0.41
26:DA:2025:C:H2'	26:DA:2026:C:C6	2.56	0.41
26:DA:2026:C:H2'	26:DA:2027:G:O4'	2.21	0.41
26:DA:2152:G:C2	26:DA:2153:G:H1'	2.54	0.41
26:DA:2228:G:C6	26:DA:2229:C:C4	3.09	0.41
26:DA:2314:C:H2'	26:DA:2315:G:C8	2.56	0.41
26:DA:2432:A:C6	26:DA:2433:A:C6	3.09	0.41
26:DA:2445:G:OP1	30:DF:74:ARG:NH2	2.45	0.41
27:DB:33:G:C2	27:DB:50:G:C2	3.08	0.41
27:DB:42:C:C4	27:DB:43:C:C4	3.09	0.41
27:DB:119:G:C6	27:DB:120:A:C6	3.09	0.41
31:DG:3:LEU:HD12	31:DG:5:VAL:HG12	2.02	0.41
36:DP:55:ARG:HA	61:DP:309:HOH:O	2.21	0.41
39:DS:28:VAL:HG13	39:DS:35:ILE:HD11	2.03	0.41
39:DS:67:ARG:HG2	39:DS:71:ARG:HH11	1.85	0.41
45:DY:65:ALA:HA	45:DY:66:PRO:HD3	1.92	0.41
46:DZ:121:HIS:HB3	46:DZ:123:ASP:O	2.20	0.41
1:AA:109:A:H2'	1:AA:326:G:N2	2.35	0.41
1:AA:358:U:H2'	1:AA:359:U:C6	2.56	0.41
1:AA:519:C:OP2	12:AL:50:SER:OG	2.26	0.41
1:AA:1256:A:N6	1:AA:1278:U:O4'	2.52	0.41
1:AA:1376:U:H2'	1:AA:1377:A:H8	1.86	0.41
2:AB:19:HIS:O	2:AB:20:GLU:C	2.64	0.41
2:AB:103:THR:HG23	2:AB:176:GLU:OE1	2.21	0.41
6:AF:97:PHE:HB3	18:AR:32:ARG:HD3	2.01	0.41
15:AO:7:GLU:H	15:AO:7:GLU:HG3	1.65	0.41
15:AO:71:GLN:HA	15:AO:71:GLN:HE21	1.85	0.41
20:AT:54:LYS:HB2	20:AT:100:ILE:HD11	2.03	0.41
25:AY:20:U:H4'	25:AY:21:A:OP1	2.20	0.41
25:AY:59:U:H3'	25:AY:60:U:C5	2.56	0.41
25:AY:70:G:C6	25:AY:71:G:C5	3.09	0.41
26:BA:1203:G:OP2	26:BA:1204:A:O2'	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:2061:G:H5''	26:BA:2503:A:C2	2.56	0.41
26:BA:2418:A:H2'	26:BA:2419:U:C6	2.55	0.41
31:BG:14:GLU:O	31:BG:17:PRO:HD2	2.21	0.41
32:BH:3:ARG:HD3	32:BH:54:ARG:HH12	1.85	0.41
33:BI:134:PRO:C	33:BI:136:VAL:H	2.28	0.41
36:BP:65:ARG:HD3	36:BP:66:GLY:N	2.36	0.41
48:B1:23:LYS:HB3	48:B1:29:GLY:HA3	2.02	0.41
48:B1:64:ALA:HA	48:B1:67:ILE:HG13	2.02	0.41
54:B7:24:THR:HG22	54:B7:27:GLY:N	2.30	0.41
1:CA:8:A:C6	4:CD:209:ARG:HG3	2.56	0.41
1:CA:811:C:O2'	1:CA:901:A:N1	2.48	0.41
1:CA:1102:A:O3'	2:CB:96:ARG:NH1	2.47	0.41
1:CA:1315:U:H2'	1:CA:1316:G:O4'	2.21	0.41
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.54	0.41
2:CB:145:LEU:O	2:CB:149:LEU:HB2	2.21	0.41
5:CE:12:LEU:C	5:CE:13:ILE:HD12	2.46	0.41
10:CJ:77:PRO:O	10:CJ:81:THR:OG1	2.39	0.41
18:CR:76:LEU:HA	18:CR:76:LEU:HD12	1.81	0.41
23:CW:21:A:N6	23:CW:46:7MG:C4	2.89	0.41
25:CY:64:A:H2'	25:CY:65:G:C8	2.56	0.41
26:DA:24:G:O2'	43:DW:78:GLU:O	2.28	0.41
26:DA:117:G:C6	26:DA:119:A:C6	3.09	0.41
26:DA:674:G:H1'	30:DF:74:ARG:HD3	2.03	0.41
26:DA:1449:A:C2	26:DA:1529:G:H1'	2.55	0.41
26:DA:2070:G:H2'	26:DA:2071:A:C8	2.56	0.41
26:DA:2185:C:H2'	26:DA:2186:G:O4'	2.20	0.41
26:DA:2395:C:O2'	48:D1:30:VAL:HG22	2.21	0.41
31:DG:58:GLN:HA	31:DG:58:GLN:OE1	2.21	0.41
31:DG:150:ASP:CG	31:DG:153:ARG:HH12	2.29	0.41
37:DQ:58:PHE:CZ	37:DQ:109:VAL:HG21	2.55	0.41
41:DU:85:LYS:HB3	41:DU:85:LYS:HE2	1.77	0.41
51:D4:62:ARG:HB2	51:D4:63:TYR:CE1	2.55	0.41
52:D5:47:PRO:HG2	52:D5:48:GLU:OE1	2.21	0.41
1:AA:115:G:H4'	1:AA:116:A:O5'	2.20	0.41
1:AA:192:U:O3'	20:AT:57:ARG:HD2	2.20	0.41
1:AA:277:C:H5''	17:AQ:68:ARG:HH22	1.86	0.41
1:AA:551:U:H2'	1:AA:552:U:C6	2.55	0.41
1:AA:1278:U:H3'	1:AA:1278:U:H6	1.85	0.41
1:AA:1324:A:O4'	1:AA:1362:C:H4'	2.21	0.41
1:AA:1422:G:C5'	35:BO:48:PRO:HB3	2.44	0.41
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AD:157:LEU:HD23	4:AD:161:ASN:HD21	1.85	0.41
6:AF:36:ARG:HB3	6:AF:36:ARG:NH1	2.36	0.41
6:AF:97:PHE:CB	18:AR:32:ARG:HD3	2.51	0.41
7:AG:104:LEU:HD13	7:AG:104:LEU:HA	1.96	0.41
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.86	0.41
12:AL:34:ARG:HG2	12:AL:35:GLY:N	2.34	0.41
20:AT:10:LEU:HD13	20:AT:12:ALA:HB2	2.01	0.41
24:AX:76:A:OP2	61:AX:3106:HOH:O	2.20	0.41
25:AY:21:A:H4'	25:AY:22:G:OP1	2.21	0.41
25:AY:58:A:H8	25:AY:58:A:H2'	1.72	0.41
25:AY:69:G:H2'	25:AY:70:G:O4'	2.21	0.41
26:BA:86:C:H4'	26:BA:104:U:H1'	2.03	0.41
26:BA:100:G:H3'	26:BA:102:G:C5'	2.50	0.41
26:BA:528:A:C3'	26:BA:529:A:H5''	2.51	0.41
26:BA:687:C:H42	26:BA:787:U:H4'	1.86	0.41
26:BA:947:G:H2'	26:BA:948:G:C8	2.56	0.41
26:BA:1033:U:OP1	56:B9:9:ARG:NH2	2.54	0.41
26:BA:1170:G:C2	26:BA:1171:G:H1'	2.55	0.41
26:BA:1550:C:H4'	26:BA:1743:C:O2	2.21	0.41
26:BA:2065:C:H2'	26:BA:2066:C:C6	2.56	0.41
26:BA:2114:A:H2'	26:BA:2115:G:O4'	2.20	0.41
26:BA:2570:G:H2'	26:BA:2571:C:O4'	2.21	0.41
26:BA:2729:G:H2'	26:BA:2730:C:O4'	2.21	0.41
26:BA:2857:G:N2	26:BA:2860:A:OP2	2.43	0.41
28:BD:121:PRO:HB3	28:BD:135:PHE:CE2	2.56	0.41
28:BD:264:LYS:HA	28:BD:265:PRO:HD3	1.92	0.41
30:BF:11:VAL:HB	30:BF:18:ARG:HB3	2.03	0.41
35:BO:86:ILE:HG22	35:BO:94:ARG:HG3	2.03	0.41
41:BU:58:ARG:HA	41:BU:61:TRP:CE3	2.56	0.41
1:CA:429:U:H1'	1:CA:430:A:H5''	2.03	0.41
1:CA:1002:G:C2	1:CA:1003:G:C8	3.09	0.41
1:CA:1003:G:C6	1:CA:1004:A:C2	3.09	0.41
1:CA:1015:A:H2'	1:CA:1016:A:C8	2.56	0.41
1:CA:1029:C:N3	1:CA:1032:G:C2	2.89	0.41
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.20	0.41
1:CA:1198:G:H2'	1:CA:1199:U:C6	2.56	0.41
1:CA:1243:C:H2'	1:CA:1244:C:H6	1.85	0.41
1:CA:1492:A:H2'	1:CA:1493:A:C5	2.55	0.41
1:CA:1511:G:H2'	1:CA:1512:U:O4'	2.21	0.41
2:CB:48:MET:O	2:CB:52:GLU:N	2.37	0.41
2:CB:100:GLY:O	2:CB:104:ASN:N	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:112:VAL:O	2:CB:116:GLU:HB2	2.21	0.41
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.21	0.41
3:CC:77:ILE:HG13	3:CC:78:GLY:N	2.35	0.41
9:CI:56:LEU:HD23	9:CI:56:LEU:HA	1.86	0.41
23:CW:53:G:H3'	23:CW:54:5MU:H73	2.03	0.41
25:CY:8:4SU:S4	25:CY:14:A:C8	3.13	0.41
26:DA:80:G:O2'	26:DA:294:A:N1	2.52	0.41
26:DA:298:G:O2'	26:DA:322:A:N1	2.46	0.41
26:DA:446:G:OP1	41:DU:3:ARG:NH1	2.52	0.41
26:DA:516:C:H1'	26:DA:1261:C:O2'	2.21	0.41
26:DA:571:A:H5'	26:DA:2030:A:N7	2.36	0.41
26:DA:821:A:H2'	26:DA:946:G:H5''	2.02	0.41
26:DA:921:G:C6	26:DA:922:U:C4	3.09	0.41
26:DA:1268:A:C2	26:DA:2013:A:C4	3.09	0.41
26:DA:1910:G:H2'	26:DA:1911:U:H6	1.85	0.41
26:DA:2113:U:N3	26:DA:2114:A:N7	2.69	0.41
26:DA:2133:G:O2'	26:DA:2134:A:P	2.79	0.41
26:DA:2275:C:H6	26:DA:2275:C:H5'	1.86	0.41
26:DA:2761:G:H2'	26:DA:2761:G:N3	2.35	0.41
26:DA:2803:C:H2'	26:DA:2804:C:C6	2.53	0.41
27:DB:24:G:H4'	27:DB:25:A:N7	2.36	0.41
29:DE:46:ALA:HB2	29:DE:82:ARG:HA	2.02	0.41
31:DG:101:ILE:O	31:DG:104:GLU:HB3	2.20	0.41
31:DG:108:ASN:O	31:DG:112:PRO:HG2	2.21	0.41
32:DH:95:ARG:HE	32:DH:95:ARG:HB3	1.77	0.41
37:DQ:29:PHE:HB2	37:DQ:105:GLU:OE2	2.21	0.41
38:DR:28:LEU:HD23	38:DR:28:LEU:HA	1.93	0.41
39:DS:4:LEU:HA	39:DS:4:LEU:HD23	1.76	0.41
41:DU:61:TRP:CH2	41:DU:93:LYS:HB2	2.56	0.41
44:DX:57:LEU:HD22	44:DX:78:LYS:HG2	2.03	0.41
46:DZ:138:GLU:H	46:DZ:156:LYS:HE2	1.85	0.41
1:AA:1003:G:N2	1:AA:1004:A:N3	2.69	0.41
1:AA:1075:C:C2'	1:AA:1076:C:H5''	2.51	0.41
6:AF:19:LEU:HD11	6:AF:59:TYR:CZ	2.56	0.41
25:AY:21:A:H8	25:AY:21:A:OP2	2.04	0.41
26:BA:593:G:H4'	55:B8:4:MET:HE2	2.02	0.41
26:BA:719:C:H2'	26:BA:720:C:C6	2.56	0.41
26:BA:887:A:H4'	26:BA:888:C:H5	1.82	0.41
26:BA:1359:A:C2	26:BA:1372:U:O4	2.74	0.41
26:BA:2893:G:H4'	26:BA:2894:G:O5'	2.21	0.41
31:BG:125:PHE:HB3	31:BG:166:ASP:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:BN:138:LEU:HA	34:BN:138:LEU:HD23	1.81	0.41
44:BX:88:LYS:HB3	44:BX:88:LYS:HE3	1.87	0.41
1:CA:344:A:H4'	1:CA:345:C:OP2	2.21	0.41
1:CA:436:C:H2'	1:CA:437:U:H6	1.86	0.41
1:CA:609:A:C5	1:CA:610:G:C8	3.09	0.41
1:CA:946:A:H2'	1:CA:947:G:C8	2.56	0.41
1:CA:1030(A):G:N2	1:CA:1030(C):G:H8	2.19	0.41
1:CA:1030(A):G:H2'	1:CA:1030(C):G:OP2	2.20	0.41
1:CA:1053:G:H4'	1:CA:1054:C:H5'	2.03	0.41
4:CD:18:LYS:HE3	4:CD:20:TYR:CE1	2.55	0.41
4:CD:33:MET:O	4:CD:37:PRO:HB3	2.20	0.41
6:CF:100:ASN:ND2	18:CR:23:LYS:HE3	2.36	0.41
7:CG:24:THR:O	7:CG:27:ILE:HB	2.21	0.41
10:CJ:6:ILE:N	10:CJ:72:VAL:O	2.36	0.41
14:CN:37:PHE:CE2	14:CN:53:LEU:HD22	2.56	0.41
26:DA:41:C:H2'	26:DA:42:G:C8	2.56	0.41
26:DA:649:G:H4'	55:D8:46:ARG:HH22	1.86	0.41
26:DA:753:C:OP2	26:DA:753:C:H6	2.03	0.41
26:DA:966:G:H2'	26:DA:967:C:C6	2.55	0.41
26:DA:1161:C:H2'	26:DA:1162:G:H8	1.86	0.41
26:DA:2193:G:H2'	26:DA:2194:G:C8	2.56	0.41
26:DA:2706:G:H2'	26:DA:2707:G:O4'	2.21	0.41
33:DI:83:ALA:CB	33:DI:123:LEU:HD21	2.50	0.41
33:DI:86:THR:O	33:DI:123:LEU:HD23	2.21	0.41
35:DO:98:VAL:HG11	35:DO:114:ILE:HG23	2.02	0.41
36:DP:47:ASP:HA	36:DP:48:PRO:HD3	1.85	0.41
38:DR:38:VAL:HG12	38:DR:42:LYS:HE3	2.03	0.41
38:DR:38:VAL:HB	38:DR:39:PRO:HD3	2.03	0.41
44:DX:35:THR:HG22	44:DX:37:THR:N	2.36	0.41
46:DZ:120:ILE:HD11	46:DZ:173:ALA:CB	2.51	0.41
51:D4:64:GLY:C	51:D4:66:SER:N	2.78	0.41
56:D9:17:ILE:HD12	56:D9:17:ILE:HA	1.92	0.41
1:AA:319:G:H1	1:AA:334:C:H42	1.69	0.40
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.56	0.40
1:AA:1152:A:OP1	10:AJ:68:HIS:ND1	2.52	0.40
2:AB:21:ARG:NH2	2:AB:23:ARG:HE	2.19	0.40
3:AC:52:LEU:HD11	3:AC:55:VAL:HG23	2.02	0.40
4:AD:120:LEU:HD23	4:AD:120:LEU:HA	1.82	0.40
4:AD:178:VAL:HG12	4:AD:179:GLU:H	1.86	0.40
25:AY:6:G:C6	25:AY:7:A:C5	3.08	0.40
26:BA:614:U:H5'	26:BA:614(C):A:N6	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:BA:1185:C:H5''	26:BA:1186:G:OP1	2.20	0.40
26:BA:1266:G:O5'	43:BW:15:ARG:NH2	2.54	0.40
26:BA:2113:U:C4	26:BA:2114:A:N7	2.89	0.40
26:BA:2282:G:OP1	26:BA:2283:C:H1'	2.21	0.40
26:BA:2804:C:H2'	26:BA:2805:G:O4'	2.21	0.40
43:BW:14:PRO:HG2	43:BW:78:GLU:CD	2.46	0.40
46:BZ:92:SER:OG	46:BZ:93:ASP:N	2.55	0.40
46:BZ:146:ILE:HA	46:BZ:147:GLY:HA2	1.77	0.40
1:CA:19:C:H5''	5:CE:86:ALA:HB3	2.03	0.40
1:CA:64:G:H4'	1:CA:65:U:H3'	2.02	0.40
1:CA:690:G:O5'	1:CA:690:G:H8	2.04	0.40
1:CA:861:G:OP1	8:CH:75:ARG:NH2	2.54	0.40
1:CA:1134:G:H2'	1:CA:1134:G:N3	2.35	0.40
1:CA:1243:C:H2'	1:CA:1244:C:C6	2.56	0.40
5:CE:31:LEU:HD23	5:CE:31:LEU:HA	1.86	0.40
7:CG:14:PRO:HG3	7:CG:21:VAL:HG13	2.03	0.40
11:CK:93:GLN:HA	11:CK:93:GLN:HE21	1.86	0.40
23:CW:27:G:H2'	23:CW:28:G:C8	2.56	0.40
26:DA:225:A:N6	26:DA:226:G:C2	2.89	0.40
26:DA:299:A:H5''	45:DY:86:ARG:NH2	2.36	0.40
26:DA:478:A:N1	26:DA:500:G:H4'	2.35	0.40
26:DA:1309:G:H3'	54:D7:9:ARG:NH1	2.36	0.40
26:DA:1336:A:H2'	26:DA:1337:G:C8	2.56	0.40
26:DA:1853:A:N1	26:DA:2087:G:H1'	2.37	0.40
26:DA:2262:U:H4'	26:DA:2328:A:C2	2.57	0.40
26:DA:2849:U:O4	40:DT:23:ARG:NH2	2.43	0.40
26:DA:2849:U:H4'	26:DA:2868:A:C2	2.55	0.40
27:DB:78:A:C2	27:DB:100:A:C4	3.09	0.40
34:DN:67:LEU:C	34:DN:88:GLU:HG3	2.45	0.40
34:DN:96:GLU:H	34:DN:96:GLU:CD	2.29	0.40
40:DT:108:ARG:HG2	40:DT:111:ARG:NH1	2.32	0.40
42:DV:52:VAL:CG2	42:DV:55:ALA:HB3	2.51	0.40
46:DZ:161:VAL:O	46:DZ:161:VAL:HG13	2.20	0.40
1:AA:613:C:H2'	1:AA:614:A:C8	2.55	0.40
1:AA:955:U:O2'	19:AS:83:HIS:HD2	2.03	0.40
1:AA:1223:C:P	19:AS:78:ARG:HH21	2.44	0.40
2:AB:118:LEU:HD23	2:AB:118:LEU:HA	1.84	0.40
8:AH:39:LEU:HA	8:AH:39:LEU:HD12	1.86	0.40
9:AI:50:LEU:HB2	9:AI:55:ALA:HB3	2.04	0.40
15:AO:7:GLU:O	15:AO:11:VAL:HG23	2.21	0.40
18:AR:59:SER:OG	18:AR:62:GLU:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AT:92:LEU:O	20:AT:96:GLY:HA2	2.22	0.40
25:AY:36:A:C6	25:AY:37:MIA:C5	3.03	0.40
26:BA:817:C:H4'	26:BA:932:G:C5	2.56	0.40
26:BA:828:U:C5	26:BA:2247:A:H4'	2.56	0.40
26:BA:1161:C:O2'	42:BV:8:GLY:HA2	2.21	0.40
26:BA:1223:G:N2	26:BA:1226:A:OP2	2.47	0.40
26:BA:1805:U:O2	28:BD:50:THR:HB	2.21	0.40
26:BA:2278:A:OP1	37:BQ:11:LYS:HD2	2.22	0.40
28:BD:180:GLY:HA3	28:BD:275:LYS:HB2	2.03	0.40
30:BF:150:GLY:HA2	30:BF:172:TRP:CE3	2.56	0.40
49:B2:23:LYS:O	49:B2:27:GLU:HG3	2.21	0.40
51:B4:16:CYS:SG	51:B4:17:GLY:N	2.94	0.40
53:B6:14:THR:HB	53:B6:48:VAL:O	2.22	0.40
54:B7:8:ASN:HB3	54:B7:11:LYS:HB3	2.02	0.40
1:CA:149:A:H2'	1:CA:150:C:C6	2.56	0.40
1:CA:993:G:O2'	1:CA:994:A:N7	2.51	0.40
1:CA:1277:C:O2'	1:CA:1279:A:C8	2.66	0.40
1:CA:1414:U:H3	1:CA:1486:G:H1	1.68	0.40
2:CB:219:VAL:O	2:CB:222:ILE:HG12	2.21	0.40
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.60	0.40
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.02	0.40
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.53	0.40
14:CN:23:ARG:HG3	14:CN:28:GLY:O	2.21	0.40
19:CS:69:HIS:HD2	19:CS:73:GLU:OE1	2.05	0.40
22:CV:14:A:C2	25:CY:34:G:C2	3.10	0.40
23:CW:9:A:OP2	23:CW:13:C:N4	2.47	0.40
24:CX:2:G:H5'	57:CX:3002:MG:MG	1.46	0.40
24:CX:43:A:H2'	24:CX:44:A:C8	2.56	0.40
26:DA:214:G:O2'	26:DA:215:G:O4'	2.34	0.40
26:DA:565:C:H2'	26:DA:566:U:O4'	2.20	0.40
26:DA:820:A:N3	26:DA:943:U:H4'	2.36	0.40
26:DA:1394:U:C4	26:DA:1395:A:C5	3.10	0.40
27:DB:33:G:C6	27:DB:34:U:N3	2.89	0.40
27:DB:42:C:O2'	31:DG:66:GLN:HG2	2.21	0.40
27:DB:110:G:O2'	27:DB:111:G:H5'	2.21	0.40
29:DE:30:PRO:HD3	29:DE:180:ASN:ND2	2.35	0.40
30:DF:59:TYR:HE2	30:DF:85:GLY:O	2.04	0.40
30:DF:93:LYS:HA	30:DF:93:LYS:HD3	1.86	0.40
35:DO:47:ILE:HB	35:DO:48:PRO:HD2	2.04	0.40
38:DR:38:VAL:HG22	38:DR:112:ALA:HB2	2.03	0.40
38:DR:63:ARG:O	38:DR:67:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:DS:95:HIS:C	39:DS:99:LYS:HB3	2.45	0.40
1:AA:189(F):U:C2	17:AQ:72:ARG:NH2	2.90	0.40
1:AA:271:C:H2'	1:AA:272:C:H6	1.87	0.40
1:AA:542:G:O3'	4:AD:14:ARG:NH2	2.53	0.40
1:AA:936:C:H2'	1:AA:937:A:O4'	2.20	0.40
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.22	0.40
3:AC:121:ALA:HB1	3:AC:189:ALA:HB2	2.04	0.40
4:AD:11:LEU:HG	4:AD:66:ARG:HD3	2.03	0.40
9:AI:33:PHE:HD1	9:AI:34:ASN:ND2	2.20	0.40
10:AJ:90:LEU:HA	10:AJ:91:PRO:HD3	1.92	0.40
26:BA:570:G:H2'	26:BA:2030:A:N7	2.37	0.40
26:BA:923:C:H2'	26:BA:924:C:C6	2.56	0.40
26:BA:1174:A:H1'	26:BA:1175:U:C5'	2.50	0.40
26:BA:2274:A:C5	26:BA:2276:G:C8	3.10	0.40
26:BA:2615:U:H2'	26:BA:2616:C:C6	2.56	0.40
28:BD:4:LYS:HB3	28:BD:18:VAL:HG23	2.04	0.40
35:BO:10:VAL:HG13	35:BO:17:ARG:C	2.46	0.40
47:B0:50:ASN:HB3	47:B0:63:VAL:HG22	2.02	0.40
1:CA:453:A:H4'	16:CP:72:ARG:HG3	2.02	0.40
1:CA:630:G:O2'	1:CA:631:G:H5'	2.21	0.40
1:CA:697:U:H2'	1:CA:698:G:H5'	2.04	0.40
1:CA:828:A:OP1	1:CA:828:A:H4'	2.21	0.40
1:CA:1084:G:H1'	1:CA:1102:A:N7	2.36	0.40
1:CA:1286:A:H3'	1:CA:1286:A:H8	1.85	0.40
2:CB:28:PHE:O	2:CB:32:ILE:HG13	2.21	0.40
3:CC:29:TYR:CZ	14:CN:54:PRO:HG2	2.57	0.40
4:CD:108:LEU:HB3	4:CD:110:PHE:CE1	2.56	0.40
7:CG:26:PHE:HE1	7:CG:30:ILE:HD11	1.87	0.40
12:CL:27:LEU:HD23	12:CL:30:ALA:O	2.22	0.40
26:DA:234:C:H2'	26:DA:235:U:H6	1.87	0.40
26:DA:856:C:H2'	26:DA:857:C:C6	2.56	0.40
26:DA:866:A:C6	26:DA:914:C:C5	3.10	0.40
26:DA:1014:U:H2'	26:DA:1015:G:C8	2.55	0.40
26:DA:1611:C:C2'	26:DA:1612:C:H5'	2.50	0.40
26:DA:1669:A:H5''	26:DA:2550:G:OP1	2.21	0.40
26:DA:2022:U:OP2	52:D5:15:ARG:NH2	2.54	0.40
26:DA:2155:G:C2'	26:DA:2156:G:H5'	2.52	0.40
26:DA:2705:A:O2'	26:DA:2852:G:OP1	2.37	0.40
29:DE:85:ASN:HA	29:DE:86:PRO:HD2	1.84	0.40
31:DG:115:ARG:HG2	31:DG:136:ARG:HH21	1.85	0.40
33:DI:92:VAL:HG22	33:DI:120:ILE:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DN:60:ILE:HG13	34:DN:61:ARG:N	2.36	0.40
42:DV:24:LYS:HA	42:DV:92:THR:OG1	2.21	0.40
46:DZ:79:ARG:HB2	46:DZ:80:ARG:NH1	2.36	0.40
51:D4:62:ARG:HD3	51:D4:62:ARG:N	2.35	0.40
52:D5:49:CYS:SG	52:D5:51:TYR:HB2	2.61	0.40
1:AA:148:G:H2'	1:AA:149:A:C8	2.50	0.40
1:AA:390:C:H2'	1:AA:391:G:C8	2.56	0.40
1:AA:933:G:O6	7:AG:3:ARG:NH2	2.52	0.40
1:AA:1024:G:H2'	1:AA:1025:U:H5'	2.04	0.40
2:AB:8:LYS:H	2:AB:8:LYS:HG2	1.51	0.40
2:AB:19:HIS:CG	2:AB:20:GLU:H	2.39	0.40
7:AG:14:PRO:HG3	7:AG:21:VAL:HG13	2.03	0.40
10:AJ:26:ALA:O	10:AJ:30:SER:OG	2.39	0.40
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.52	0.40
13:AM:97:PRO:HG2	13:AM:103:THR:HG22	2.04	0.40
19:AS:15:LEU:O	19:AS:19:VAL:HG23	2.21	0.40
19:AS:69:HIS:HD2	19:AS:73:GLU:OE1	2.05	0.40
24:AX:19:G:H5''	24:AX:60:U:O4	2.21	0.40
26:BA:589:C:H2'	26:BA:590:A:C8	2.56	0.40
26:BA:1406:U:H2'	26:BA:1407:C:H6	1.86	0.40
26:BA:2070:G:H2'	26:BA:2071:A:C8	2.57	0.40
26:BA:2181:G:O2'	26:BA:2182:G:OP1	2.34	0.40
26:BA:2355:C:H5'	61:BA:3944:HOH:O	2.22	0.40
26:BA:2398:U:H2'	26:BA:2399:G:C8	2.57	0.40
28:BD:19:ALA:HB3	28:BD:21:PHE:CE1	2.56	0.40
30:BF:64:ILE:HG13	30:BF:65:TRP:N	2.37	0.40
42:BV:49:THR:O	42:BV:49:THR:HG22	2.21	0.40
44:BX:94:GLY:N	44:BX:95:LEU:HA	2.36	0.40
45:BY:83:THR:HG21	45:BY:99:CYS:HB2	2.02	0.40
52:B5:35:GLU:HG3	52:B5:51:TYR:CD2	2.57	0.40
1:CA:57:G:H2'	1:CA:58:C:C6	2.57	0.40
1:CA:1075:C:H42	1:CA:1082:G:H1	1.68	0.40
1:CA:1164:G:O2'	1:CA:1165:C:H5'	2.22	0.40
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.57	0.40
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.21	0.40
1:CA:1429:C:H2'	1:CA:1430:C:C6	2.57	0.40
1:CA:1479:C:H2'	1:CA:1480:G:C8	2.56	0.40
2:CB:16:HIS:ND1	2:CB:17:PHE:N	2.68	0.40
2:CB:53:ARG:HB3	2:CB:53:ARG:CZ	2.50	0.40
3:CC:109:PRO:HB3	3:CC:115:LEU:HD23	2.03	0.40
3:CC:178:LEU:HD13	3:CC:178:LEU:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:119:LEU:HB3	8:CH:123:GLU:CB	2.51	0.40
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.20	0.40
24:CX:12:G:H4'	26:DA:1908:C:O2	2.21	0.40
26:DA:335:C:H4'	45:DY:73:ARG:NE	2.37	0.40
26:DA:428:A:H3'	26:DA:429:A:H8	1.87	0.40
26:DA:443:A:H5''	26:DA:444:C:OP1	2.21	0.40
26:DA:570:G:H2'	26:DA:2030:A:C5	2.56	0.40
26:DA:892:G:H2'	26:DA:893:C:C4'	2.52	0.40
26:DA:971:C:O2'	26:DA:983:A:N3	2.50	0.40
26:DA:996:A:O3'	41:DU:91:ASP:HB2	2.22	0.40
26:DA:1486:A:O2'	26:DA:1487:G:H5'	2.21	0.40
26:DA:2174:C:O2	26:DA:2174:C:H2'	2.21	0.40
26:DA:2462:U:H2'	26:DA:2463:C:C6	2.56	0.40
26:DA:2741:A:H2'	26:DA:2742:C:O4'	2.21	0.40
26:DA:2756:U:H1'	26:DA:2757:A:H5''	2.02	0.40
31:DG:31:VAL:HA	31:DG:32:PRO:HD2	1.72	0.40
36:DP:84:ASN:OD1	36:DP:117:GLU:HB2	2.20	0.40
40:DT:94:ALA:HB1	40:DT:99:LEU:HD21	2.02	0.40
48:D1:5:CYS:SG	48:D1:62:VAL:HG23	2.62	0.40
49:D2:64:LEU:O	49:D2:68:ARG:HG3	2.22	0.40
50:D3:23:LEU:HD13	50:D3:50:VAL:HG11	2.02	0.40
1:AA:512:U:H2'	1:AA:513:C:C6	2.56	0.40
1:AA:1002:G:C6	1:AA:1003:G:C2	3.10	0.40
1:AA:1151:A:O2'	1:AA:1152:A:H8	2.05	0.40
2:AB:215:LEU:HD23	2:AB:215:LEU:HA	1.79	0.40
3:AC:82:GLU:HA	3:AC:85:ARG:CZ	2.51	0.40
4:AD:18:LYS:HE3	4:AD:20:TYR:CZ	2.56	0.40
6:AF:22:GLU:O	6:AF:26:ILE:HG13	2.22	0.40
6:AF:55:ASP:HA	6:AF:56:PRO:HD2	1.98	0.40
13:AM:39:ILE:HG13	13:AM:56:LEU:HD12	2.03	0.40
25:AY:26:A:N1	25:AY:44:G:N2	2.54	0.40
26:BA:370:G:H4'	26:BA:371:A:OP2	2.21	0.40
26:BA:674:G:O2'	30:BF:74:ARG:HD3	2.22	0.40
30:BF:106:ARG:H	30:BF:106:ARG:HG2	1.70	0.40
1:CA:243:A:C2	1:CA:246:A:C8	3.10	0.40
1:CA:1154:G:O6	1:CA:1155:G:C6	2.75	0.40
1:CA:1350:A:OP1	9:CI:121:ARG:HD3	2.21	0.40
1:CA:1367:C:O2'	10:CJ:62:HIS:HE1	2.04	0.40
1:CA:1496:C:H2'	1:CA:1497:G:O4'	2.20	0.40
2:CB:28:PHE:CD2	2:CB:190:THR:HA	2.56	0.40
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.62	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CN:9:LYS:HG3	14:CN:12:ARG:HH11	1.86	0.40
24:CX:66:C:H2'	24:CX:67:C:O4'	2.22	0.40
25:CY:29:G:N1	25:CY:41:C:N4	2.69	0.40
26:DA:56:A:H2'	26:DA:57:C:O4'	2.22	0.40
26:DA:305:U:H2'	26:DA:306:U:C6	2.56	0.40
26:DA:832:G:H5'	36:DP:45:LEU:HD21	2.04	0.40
26:DA:933:A:H2'	26:DA:934:G:O4'	2.22	0.40
26:DA:1001:A:H2'	26:DA:1002:G:O4'	2.21	0.40
26:DA:1221(A):C:C2	26:DA:1229:G:C2	3.09	0.40
26:DA:1241:A:O2'	26:DA:1242:A:H5'	2.21	0.40
26:DA:2294:C:P	39:DS:89:ARG:HH22	2.44	0.40
26:DA:2507:C:H2'	26:DA:2508:G:O4'	2.22	0.40
34:DN:115:ARG:HA	34:DN:118:LYS:HE3	2.02	0.40
46:DZ:171:ILE:H	46:DZ:171:ILE:HG13	1.65	0.40
50:D3:10:LYS:HB3	50:D3:53:LEU:HA	2.02	0.40
51:D4:28:LYS:HA	51:D4:29:PRO:HD3	1.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	229/256 (90%)	208 (91%)	14 (6%)	7 (3%)	3	2
2	CB	229/256 (90%)	206 (90%)	16 (7%)	7 (3%)	3	2
3	AC	204/239 (85%)	195 (96%)	8 (4%)	1 (0%)	24	34
3	CC	204/239 (85%)	189 (93%)	15 (7%)	0	100	100
4	AD	206/209 (99%)	197 (96%)	7 (3%)	2 (1%)	12	17
4	CD	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	24	34
5	AE	146/162 (90%)	142 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CE	146/162 (90%)	140 (96%)	6 (4%)	0	100	100
6	AF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
6	CF	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
7	AG	153/156 (98%)	144 (94%)	5 (3%)	4 (3%)	4	3
7	CG	153/156 (98%)	144 (94%)	8 (5%)	1 (1%)	18	25
8	AH	135/138 (98%)	134 (99%)	1 (1%)	0	100	100
8	CH	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
9	AI	125/128 (98%)	117 (94%)	8 (6%)	0	100	100
9	CI	125/128 (98%)	119 (95%)	5 (4%)	1 (1%)	16	22
10	AJ	95/105 (90%)	85 (90%)	6 (6%)	4 (4%)	2	1
10	CJ	94/105 (90%)	85 (90%)	4 (4%)	5 (5%)	1	0
11	AK	112/129 (87%)	104 (93%)	6 (5%)	2 (2%)	6	7
11	CK	112/129 (87%)	103 (92%)	7 (6%)	2 (2%)	6	7
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100	100
12	CL	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
13	AM	121/126 (96%)	116 (96%)	5 (4%)	0	100	100
13	CM	120/126 (95%)	113 (94%)	7 (6%)	0	100	100
14	AN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	AP	80/88 (91%)	79 (99%)	1 (1%)	0	100	100
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	9	12
17	AQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
17	CQ	97/105 (92%)	93 (96%)	4 (4%)	0	100	100
18	AR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
19	AS	81/93 (87%)	73 (90%)	7 (9%)	1 (1%)	10	13
19	CS	81/93 (87%)	72 (89%)	9 (11%)	0	100	100
20	AT	94/106 (89%)	87 (93%)	3 (3%)	4 (4%)	2	1
20	CT	94/106 (89%)	88 (94%)	3 (3%)	3 (3%)	3	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
21	CU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
28	BD	273/276 (99%)	264 (97%)	8 (3%)	1 (0%)	30	39
28	DD	273/276 (99%)	263 (96%)	8 (3%)	2 (1%)	18	25
29	BE	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24	34
29	DE	202/206 (98%)	196 (97%)	4 (2%)	2 (1%)	12	17
30	BF	201/210 (96%)	200 (100%)	0	1 (0%)	24	34
30	DF	201/210 (96%)	199 (99%)	0	2 (1%)	12	17
31	BG	179/182 (98%)	170 (95%)	8 (4%)	1 (1%)	21	29
31	DG	179/182 (98%)	171 (96%)	5 (3%)	3 (2%)	7	8
32	BH	172/180 (96%)	168 (98%)	3 (2%)	1 (1%)	21	29
32	DH	172/180 (96%)	166 (96%)	5 (3%)	1 (1%)	21	29
33	BI	144/148 (97%)	130 (90%)	11 (8%)	3 (2%)	5	5
33	DI	144/148 (97%)	133 (92%)	10 (7%)	1 (1%)	18	25
34	BN	138/140 (99%)	136 (99%)	2 (1%)	0	100	100
34	DN	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	18	25
35	BO	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	DO	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
36	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	18	25
36	DP	147/150 (98%)	138 (94%)	7 (5%)	2 (1%)	9	11
37	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
37	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	25
38	BR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
38	DR	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
39	BS	108/112 (96%)	104 (96%)	3 (3%)	1 (1%)	14	20
39	DS	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	14	20
40	BT	129/146 (88%)	122 (95%)	7 (5%)	0	100	100
40	DT	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
41	BU	114/118 (97%)	114 (100%)	0	0	100	100
41	DU	114/118 (97%)	114 (100%)	0	0	100	100
42	BV	99/101 (98%)	93 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	DV	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	17
43	BW	110/113 (97%)	110 (100%)	0	0	100	100
43	DW	110/113 (97%)	110 (100%)	0	0	100	100
44	BX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
44	DX	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
45	BY	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
45	DY	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
46	BZ	169/206 (82%)	153 (90%)	15 (9%)	1 (1%)	21	29
46	DZ	172/206 (84%)	161 (94%)	11 (6%)	0	100	100
47	B0	81/85 (95%)	81 (100%)	0	0	100	100
47	D0	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
48	B1	95/98 (97%)	94 (99%)	0	1 (1%)	11	15
48	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	15
49	B2	68/72 (94%)	68 (100%)	0	0	100	100
49	D2	68/72 (94%)	68 (100%)	0	0	100	100
50	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
50	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
51	B4	67/71 (94%)	53 (79%)	11 (16%)	3 (4%)	2	1
51	D4	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	1	0
52	B5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
52	D5	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
53	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
53	D6	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
54	B7	46/49 (94%)	46 (100%)	0	0	100	100
54	D7	46/49 (94%)	45 (98%)	0	1 (2%)	5	5
55	B8	62/65 (95%)	62 (100%)	0	0	100	100
55	D8	62/65 (95%)	62 (100%)	0	0	100	100
56	B9	35/37 (95%)	35 (100%)	0	0	100	100
56	D9	35/37 (95%)	35 (100%)	0	0	100	100
All	All	11409/12128 (94%)	10908 (96%)	416 (4%)	85 (1%)	18	25

All (85) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	126	GLU
7	AG	80	VAL
20	AT	10	LEU
20	AT	96	GLY
28	BD	275	LYS
29	BE	52	LEU
30	BF	130	ALA
33	BI	107	VAL
51	B4	55	ARG
2	CB	16	HIS
2	CB	20	GLU
2	CB	126	GLU
4	CD	46	LYS
9	CI	54	ASP
10	CJ	79	ARG
20	CT	99	LEU
30	DF	21	ALA
30	DF	130	ALA
33	DI	10	GLU
36	DP	29	LYS
51	D4	39	CYS
51	D4	63	TYR
54	D7	46	VAL
2	AB	10	LEU
2	AB	19	HIS
4	AD	166	LYS
7	AG	8	GLU
7	AG	81	GLY
10	AJ	31	GLY
10	AJ	56	HIS
11	AK	49	GLY
20	AT	47	GLY
33	BI	106	GLY
48	B1	3	LYS
51	B4	54	GLY
51	B4	57	GLU
2	CB	8	LYS
2	CB	9	GLU
10	CJ	56	HIS
10	CJ	77	PRO
11	CK	49	GLY
20	CT	47	GLY
20	CT	95	ALA

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Mol	Chain	Res	Type
29	DE	52	LEU
31	DG	81	LYS
32	DH	126	PRO
37	DQ	28	ALA
51	D4	45	GLY
2	AB	20	GLU
4	AD	164	ALA
10	AJ	79	ARG
19	AS	42	PRO
20	AT	95	ALA
31	BG	47	LYS
32	BH	126	PRO
39	BS	60	GLY
46	BZ	152	ALA
11	CK	105	VAL
28	DD	239	ARG
34	DN	2	LYS
39	DS	84	GLN
33	BI	73	GLU
36	BP	29	LYS
2	CB	10	LEU
10	CJ	55	LYS
28	DD	3	VAL
31	DG	32	PRO
31	DG	47	LYS
36	DP	45	LEU
48	D1	3	LYS
51	D4	55	ARG
10	AJ	91	PRO
29	DE	73	GLU
51	D4	62	ARG
2	AB	231	GLU
3	AC	66	VAL
2	CB	231	GLU
7	CG	17	VAL
16	CP	53	VAL
11	AK	105	VAL
2	AB	124	SER
10	CJ	91	PRO
42	DV	79	VAL
7	AG	17	VAL
2	AB	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	192/220 (87%)	153 (80%)	39 (20%)	1	1
2	CB	187/220 (85%)	148 (79%)	39 (21%)	1	1
3	AC	143/188 (76%)	116 (81%)	27 (19%)	1	1
3	CC	140/188 (74%)	119 (85%)	21 (15%)	3	2
4	AD	170/181 (94%)	149 (88%)	21 (12%)	4	4
4	CD	173/181 (96%)	153 (88%)	20 (12%)	5	6
5	AE	113/123 (92%)	104 (92%)	9 (8%)	11	15
5	CE	114/123 (93%)	102 (90%)	12 (10%)	6	8
6	AF	83/90 (92%)	72 (87%)	11 (13%)	4	4
6	CF	85/90 (94%)	77 (91%)	8 (9%)	8	10
7	AG	119/127 (94%)	106 (89%)	13 (11%)	6	7
7	CG	120/127 (94%)	107 (89%)	13 (11%)	6	7
8	AH	114/119 (96%)	101 (89%)	13 (11%)	5	6
8	CH	114/119 (96%)	99 (87%)	15 (13%)	4	4
9	AI	90/99 (91%)	72 (80%)	18 (20%)	1	1
9	CI	89/99 (90%)	75 (84%)	14 (16%)	2	2
10	AJ	66/92 (72%)	57 (86%)	9 (14%)	3	3
10	CJ	69/92 (75%)	63 (91%)	6 (9%)	9	13
11	AK	82/99 (83%)	75 (92%)	7 (8%)	10	13
11	CK	83/99 (84%)	76 (92%)	7 (8%)	10	14
12	AL	97/109 (89%)	92 (95%)	5 (5%)	21	32
12	CL	97/109 (89%)	92 (95%)	5 (5%)	21	32
13	AM	93/101 (92%)	79 (85%)	14 (15%)	3	2
13	CM	92/101 (91%)	77 (84%)	15 (16%)	2	2
14	AN	49/50 (98%)	42 (86%)	7 (14%)	3	3
14	CN	49/50 (98%)	41 (84%)	8 (16%)	2	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AO	78/80 (98%)	65 (83%)	13 (17%)	2	2
15	CO	78/80 (98%)	70 (90%)	8 (10%)	7	8
16	AP	69/74 (93%)	59 (86%)	10 (14%)	3	2
16	CP	68/74 (92%)	60 (88%)	8 (12%)	5	5
17	AQ	94/97 (97%)	81 (86%)	13 (14%)	3	3
17	CQ	94/97 (97%)	84 (89%)	10 (11%)	6	7
18	AR	59/77 (77%)	52 (88%)	7 (12%)	5	5
18	CR	59/77 (77%)	51 (86%)	8 (14%)	3	3
19	AS	69/80 (86%)	62 (90%)	7 (10%)	7	8
19	CS	67/80 (84%)	61 (91%)	6 (9%)	9	11
20	AT	70/82 (85%)	61 (87%)	9 (13%)	4	4
20	CT	70/82 (85%)	58 (83%)	12 (17%)	2	1
21	AU	18/22 (82%)	16 (89%)	2 (11%)	6	6
21	CU	18/22 (82%)	16 (89%)	2 (11%)	6	6
28	BD	215/218 (99%)	193 (90%)	22 (10%)	7	8
28	DD	215/218 (99%)	191 (89%)	24 (11%)	6	6
29	BE	164/166 (99%)	142 (87%)	22 (13%)	4	3
29	DE	164/166 (99%)	138 (84%)	26 (16%)	2	2
30	BF	160/166 (96%)	140 (88%)	20 (12%)	4	4
30	DF	159/166 (96%)	136 (86%)	23 (14%)	3	2
31	BG	143/156 (92%)	128 (90%)	15 (10%)	6	8
31	DG	142/156 (91%)	121 (85%)	21 (15%)	3	2
32	BH	144/148 (97%)	125 (87%)	19 (13%)	4	4
32	DH	144/148 (97%)	125 (87%)	19 (13%)	4	4
33	BI	110/124 (89%)	87 (79%)	23 (21%)	1	1
33	DI	104/124 (84%)	87 (84%)	17 (16%)	2	2
34	BN	118/119 (99%)	99 (84%)	19 (16%)	2	2
34	DN	118/119 (99%)	102 (86%)	16 (14%)	3	3
35	BO	100/100 (100%)	91 (91%)	9 (9%)	9	11
35	DO	100/100 (100%)	90 (90%)	10 (10%)	7	9
36	BP	115/116 (99%)	99 (86%)	16 (14%)	3	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	DP	115/116 (99%)	100 (87%)	15 (13%)	4	4
37	BQ	111/111 (100%)	97 (87%)	14 (13%)	4	4
37	DQ	111/111 (100%)	97 (87%)	14 (13%)	4	4
38	BR	101/101 (100%)	80 (79%)	21 (21%)	1	1
38	DR	101/101 (100%)	83 (82%)	18 (18%)	2	1
39	BS	87/88 (99%)	77 (88%)	10 (12%)	5	6
39	DS	85/88 (97%)	71 (84%)	14 (16%)	2	2
40	BT	115/127 (91%)	103 (90%)	12 (10%)	7	8
40	DT	113/127 (89%)	100 (88%)	13 (12%)	5	6
41	BU	93/94 (99%)	84 (90%)	9 (10%)	8	9
41	DU	93/94 (99%)	84 (90%)	9 (10%)	8	9
42	BV	80/82 (98%)	68 (85%)	12 (15%)	3	2
42	DV	80/82 (98%)	65 (81%)	15 (19%)	1	1
43	BW	90/92 (98%)	81 (90%)	9 (10%)	7	9
43	DW	90/92 (98%)	84 (93%)	6 (7%)	15	21
44	BX	77/78 (99%)	70 (91%)	7 (9%)	9	11
44	DX	77/78 (99%)	69 (90%)	8 (10%)	7	8
45	BY	85/91 (93%)	76 (89%)	9 (11%)	6	7
45	DY	85/91 (93%)	78 (92%)	7 (8%)	10	14
46	BZ	145/179 (81%)	128 (88%)	17 (12%)	5	6
46	DZ	145/179 (81%)	123 (85%)	22 (15%)	3	2
47	B0	65/67 (97%)	61 (94%)	4 (6%)	16	24
47	D0	65/67 (97%)	61 (94%)	4 (6%)	16	24
48	B1	80/83 (96%)	74 (92%)	6 (8%)	12	17
48	D1	80/83 (96%)	68 (85%)	12 (15%)	3	2
49	B2	65/67 (97%)	56 (86%)	9 (14%)	3	3
49	D2	65/67 (97%)	57 (88%)	8 (12%)	4	4
50	B3	51/52 (98%)	45 (88%)	6 (12%)	5	5
50	D3	50/52 (96%)	44 (88%)	6 (12%)	5	5
51	B4	60/63 (95%)	47 (78%)	13 (22%)	1	1
51	D4	53/63 (84%)	43 (81%)	10 (19%)	1	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	B5	50/52 (96%)	43 (86%)	7 (14%)	3	3
52	D5	50/52 (96%)	44 (88%)	6 (12%)	5	5
53	B6	51/52 (98%)	45 (88%)	6 (12%)	5	5
53	D6	50/52 (96%)	47 (94%)	3 (6%)	17	26
54	B7	41/42 (98%)	38 (93%)	3 (7%)	13	18
54	D7	41/42 (98%)	36 (88%)	5 (12%)	5	4
55	B8	53/55 (96%)	47 (89%)	6 (11%)	5	6
55	D8	54/55 (98%)	47 (87%)	7 (13%)	4	4
56	B9	34/34 (100%)	33 (97%)	1 (3%)	37	55
56	D9	34/34 (100%)	32 (94%)	2 (6%)	18	27
All	All	9320/10066 (93%)	8123 (87%)	1197 (13%)	4	4

All (1197) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	7	VAL
2	AB	8	LYS
2	AB	10	LEU
2	AB	11	LEU
2	AB	15	VAL
2	AB	17	PHE
2	AB	21	ARG
2	AB	23	ARG
2	AB	39	ILE
2	AB	51	LEU
2	AB	64	ARG
2	AB	67	THR
2	AB	76	GLN
2	AB	80	ILE
2	AB	86	GLU
2	AB	94	ASN
2	AB	96	ARG
2	AB	108	ILE
2	AB	112	VAL
2	AB	114	ARG
2	AB	127	ILE
2	AB	144	ARG
2	AB	145	LEU

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Mol	Chain	Res	Type
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	157	ARG
2	AB	158	LEU
2	AB	160	ASP
2	AB	169	LYS
2	AB	170	GLU
2	AB	185	ILE
2	AB	187	LEU
2	AB	196	LEU
2	AB	200	ILE
2	AB	213	LEU
2	AB	217	ARG
2	AB	221	LEU
2	AB	230	VAL
3	AC	3	ASN
3	AC	26	LYS
3	AC	27	LYS
3	AC	28	GLN
3	AC	32	LEU
3	AC	37	GLN
3	AC	49	SER
3	AC	70	VAL
3	AC	77	ILE
3	AC	97	LYS
3	AC	98	ASN
3	AC	104	GLN
3	AC	115	LEU
3	AC	118	GLN
3	AC	119	ARG
3	AC	127	ARG
3	AC	140	ARG
3	AC	144	SER
3	AC	150	LYS
3	AC	173	VAL
3	AC	178	LEU
3	AC	179	ARG
3	AC	181	ASN
3	AC	195	VAL
3	AC	196	LEU
3	AC	198	VAL

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Mol	Chain	Res	Type
3	AC	207	VAL
4	AD	5	ILE
4	AD	15	GLU
4	AD	19	LEU
4	AD	31	CYS
4	AD	49	ARG
4	AD	52	SER
4	AD	53	ASP
4	AD	58	LEU
4	AD	61	LYS
4	AD	63	LYS
4	AD	65	ARG
4	AD	86	LYS
4	AD	108	LEU
4	AD	127	THR
4	AD	135	LEU
4	AD	139	ARG
4	AD	141	ARG
4	AD	155	LEU
4	AD	158	ILE
4	AD	168	ARG
4	AD	188	LEU
5	AE	6	PHE
5	AE	12	LEU
5	AE	31	LEU
5	AE	38	GLN
5	AE	41	VAL
5	AE	47	LYS
5	AE	73	ASN
5	AE	79	GLU
5	AE	145	LYS
6	AF	10	LEU
6	AF	36	ARG
6	AF	40	VAL
6	AF	46	ARG
6	AF	55	ASP
6	AF	61	LEU
6	AF	69	GLU
6	AF	74	ASP
6	AF	75	LEU
6	AF	82	ARG
6	AF	92	LYS

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Mol	Chain	Res	Type
7	AG	8	GLU
7	AG	12	LEU
7	AG	32	ARG
7	AG	50	ILE
7	AG	51	GLN
7	AG	52	GLU
7	AG	53	LYS
7	AG	76	ARG
7	AG	79	ARG
7	AG	91	VAL
7	AG	104	LEU
7	AG	113	GLU
7	AG	155	ARG
8	AH	26	VAL
8	AH	29	SER
8	AH	39	LEU
8	AH	45	ILE
8	AH	52	ASP
8	AH	63	LEU
8	AH	78	GLN
8	AH	84	ARG
8	AH	91	ARG
8	AH	109	ILE
8	AH	112	LEU
8	AH	127	LEU
8	AH	137	VAL
9	AI	3	GLN
9	AI	14	VAL
9	AI	17	VAL
9	AI	23	ASN
9	AI	42	ARG
9	AI	50	LEU
9	AI	53	VAL
9	AI	56	LEU
9	AI	64	THR
9	AI	65	VAL
9	AI	81	ILE
9	AI	86	VAL
9	AI	103	THR
9	AI	108	VAL
9	AI	109	VAL
9	AI	121	ARG

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Mol	Chain	Res	Type
9	AI	127	LYS
9	AI	128	ARG
10	AJ	7	LYS
10	AJ	16	LEU
10	AJ	17	ASP
10	AJ	23	ILE
10	AJ	81	THR
10	AJ	84	GLN
10	AJ	94	VAL
10	AJ	96	ILE
10	AJ	100	THR
11	AK	14	VAL
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	55	LYS
11	AK	96	ARG
11	AK	114	VAL
12	AL	33	ARG
12	AL	46	LYS
12	AL	52	LEU
12	AL	53	ARG
12	AL	83	VAL
13	AM	4	ILE
13	AM	15	VAL
13	AM	27	LYS
13	AM	39	ILE
13	AM	43	THR
13	AM	49	THR
13	AM	52	GLU
13	AM	70	LEU
13	AM	73	GLU
13	AM	78	ILE
13	AM	84	ILE
13	AM	110	ARG
13	AM	117	VAL
13	AM	121	LYS
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	18	VAL
14	AN	23	ARG

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Mol	Chain	Res	Type
14	AN	32	SER
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	21	ASP
15	AO	22	THR
15	AO	26	GLU
15	AO	39	LEU
15	AO	41	GLU
15	AO	64	ARG
15	AO	66	LEU
15	AO	71	GLN
15	AO	76	GLU
15	AO	83	GLU
15	AO	84	LYS
16	AP	1	MET
16	AP	2	VAL
16	AP	19	ILE
16	AP	20	VAL
16	AP	21	VAL
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	9	VAL
17	AQ	14	LYS
17	AQ	19	VAL
17	AQ	24	GLU
17	AQ	35	VAL
17	AQ	52	LYS
17	AQ	60	ILE
17	AQ	63	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	98	LEU
18	AR	31	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	38	GLU

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Mol	Chain	Res	Type
18	AR	46	GLU
18	AR	58	LEU
18	AR	76	LEU
19	AS	6	LYS
19	AS	12	ASP
19	AS	28	LYS
19	AS	37	ARG
19	AS	41	VAL
19	AS	65	ASN
19	AS	66	MET
20	AT	8	ARG
20	AT	13	LEU
20	AT	24	LEU
20	AT	30	LYS
20	AT	45	GLN
20	AT	46	GLU
20	AT	51	GLU
20	AT	54	LYS
20	AT	62	LEU
21	AU	9	ARG
21	AU	10	ARG
28	BD	5	LYS
28	BD	12	SER
28	BD	13	ARG
28	BD	61	LEU
28	BD	88	ARG
28	BD	94	LEU
28	BD	103	ARG
28	BD	113	VAL
28	BD	126	GLN
28	BD	138	VAL
28	BD	140	THR
28	BD	142	VAL
28	BD	155	LEU
28	BD	193	VAL
28	BD	211	ARG
28	BD	217	ARG
28	BD	221	VAL
28	BD	229	VAL
28	BD	257	LEU
28	BD	259	THR
28	BD	260	ARG

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Mol	Chain	Res	Type
28	BD	276	LYS
29	BE	9	VAL
29	BE	14	ILE
29	BE	21	VAL
29	BE	24	THR
29	BE	33	VAL
29	BE	34	VAL
29	BE	49	LEU
29	BE	52	LEU
29	BE	72	VAL
29	BE	73	GLU
29	BE	75	VAL
29	BE	77	ILE
29	BE	82	ARG
29	BE	97	LYS
29	BE	116	VAL
29	BE	119	ARG
29	BE	144	ARG
29	BE	154	LYS
29	BE	163	GLU
29	BE	175	VAL
29	BE	181	LEU
29	BE	203	LYS
30	BF	19	GLU
30	BF	20	LEU
30	BF	24	LEU
30	BF	33	LEU
30	BF	38	ARG
30	BF	53	THR
30	BF	57	VAL
30	BF	74	ARG
30	BF	88	VAL
30	BF	106	ARG
30	BF	110	LEU
30	BF	125	LEU
30	BF	126	VAL
30	BF	132	VAL
30	BF	162	LEU
30	BF	170	LEU
30	BF	183	VAL
30	BF	192	LEU
30	BF	200	GLU

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Mol	Chain	Res	Type
30	BF	201	VAL
31	BG	5	VAL
31	BG	7	LEU
31	BG	43	LEU
31	BG	45	GLU
31	BG	60	LEU
31	BG	70	VAL
31	BG	81	LYS
31	BG	82	LEU
31	BG	86	MET
31	BG	135	LEU
31	BG	140	ILE
31	BG	143	GLU
31	BG	148	MET
31	BG	159	VAL
31	BG	175	LEU
32	BH	15	VAL
32	BH	33	LEU
32	BH	41	MET
32	BH	44	VAL
32	BH	45	VAL
32	BH	49	VAL
32	BH	59	ARG
32	BH	62	LYS
32	BH	69	ARG
32	BH	71	LEU
32	BH	86	GLU
32	BH	95	ARG
32	BH	116	GLU
32	BH	119	GLU
32	BH	124	GLU
32	BH	125	VAL
32	BH	129	THR
32	BH	134	SER
32	BH	172	LYS
33	BI	5	LEU
33	BI	9	LEU
33	BI	10	GLU
33	BI	38	LEU
33	BI	43	ASN
33	BI	47	LEU
33	BI	50	ARG

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Mol	Chain	Res	Type
33	BI	57	ARG
33	BI	60	GLU
33	BI	61	ARG
33	BI	62	LYS
33	BI	66	GLU
33	BI	68	LEU
33	BI	75	LEU
33	BI	78	THR
33	BI	85	GLU
33	BI	87	LYS
33	BI	92	VAL
33	BI	101	LEU
33	BI	109	ILE
33	BI	117	GLU
33	BI	140	LEU
33	BI	142	VAL
34	BN	14	VAL
34	BN	28	THR
34	BN	33	LEU
34	BN	34	LEU
34	BN	46	VAL
34	BN	48	MET
34	BN	58	ASP
34	BN	61	ARG
34	BN	62	VAL
34	BN	67	LEU
34	BN	68	GLU
34	BN	73	THR
34	BN	83	LYS
34	BN	87	LEU
34	BN	97	ARG
34	BN	99	LEU
34	BN	120	LEU
34	BN	133	GLN
34	BN	139	GLU
35	BO	8	LEU
35	BO	10	VAL
35	BO	23	ARG
35	BO	24	VAL
35	BO	69	ILE
35	BO	92	GLU
35	BO	94	ARG

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Mol	Chain	Res	Type
35	BO	98	VAL
35	BO	108	GLU
36	BP	1	MET
36	BP	3	LEU
36	BP	55	ARG
36	BP	59	LEU
36	BP	65	ARG
36	BP	68	GLN
36	BP	70	GLN
36	BP	76	LYS
36	BP	83	VAL
36	BP	95	VAL
36	BP	98	GLU
36	BP	106	LEU
36	BP	112	LEU
36	BP	119	GLU
36	BP	126	VAL
36	BP	149	GLU
37	BQ	1	MET
37	BQ	7	MET
37	BQ	10	ARG
37	BQ	21	THR
37	BQ	35	VAL
37	BQ	45	GLN
37	BQ	54	MET
37	BQ	56	ARG
37	BQ	59	ARG
37	BQ	60	ARG
37	BQ	75	THR
37	BQ	109	VAL
37	BQ	110	THR
37	BQ	127	ILE
38	BR	1	MET
38	BR	6	SER
38	BR	8	ARG
38	BR	15	SER
38	BR	18	LEU
38	BR	24	GLN
38	BR	28	LEU
38	BR	29	LEU
38	BR	33	ARG
38	BR	36	THR

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Mol	Chain	Res	Type
38	BR	44	LEU
38	BR	54	LEU
38	BR	60	LEU
38	BR	65	LEU
38	BR	67	LEU
38	BR	75	LEU
38	BR	79	LEU
38	BR	100	LEU
38	BR	102	GLU
38	BR	111	LEU
38	BR	114	VAL
39	BS	14	VAL
39	BS	19	LYS
39	BS	20	ARG
39	BS	33	LYS
39	BS	57	LYS
39	BS	59	LYS
39	BS	67	ARG
39	BS	83	LYS
39	BS	103	GLU
39	BS	110	LEU
40	BT	6	LEU
40	BT	17	THR
40	BT	28	VAL
40	BT	34	VAL
40	BT	49	VAL
40	BT	53	ARG
40	BT	78	LEU
40	BT	89	VAL
40	BT	95	ARG
40	BT	96	ARG
40	BT	108	ARG
40	BT	118	ARG
41	BU	8	VAL
41	BU	36	ARG
41	BU	74	LEU
41	BU	77	SER
41	BU	83	LEU
41	BU	92	ARG
41	BU	95	LEU
41	BU	104	GLN
41	BU	117	GLN

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Mol	Chain	Res	Type
42	BV	6	LYS
42	BV	28	GLU
42	BV	43	GLU
42	BV	46	VAL
42	BV	51	VAL
42	BV	52	VAL
42	BV	61	VAL
42	BV	62	LEU
42	BV	72	VAL
42	BV	79	VAL
42	BV	95	LEU
42	BV	100	ARG
43	BW	4	LYS
43	BW	11	ARG
43	BW	15	ARG
43	BW	17	VAL
43	BW	19	LEU
43	BW	23	LEU
43	BW	51	LEU
43	BW	100	THR
43	BW	107	LEU
44	BX	35	THR
44	BX	45	THR
44	BX	57	LEU
44	BX	66	LEU
44	BX	72	LYS
44	BX	76	ARG
44	BX	88	LYS
45	BY	1	MET
45	BY	2	ARG
45	BY	23	ARG
45	BY	34	LYS
45	BY	72	VAL
45	BY	85	VAL
45	BY	90	LEU
45	BY	91	GLU
45	BY	99	CYS
46	BZ	5	LEU
46	BZ	11	GLU
46	BZ	19	ARG
46	BZ	33	LEU
46	BZ	40	ASP

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Mol	Chain	Res	Type
46	BZ	61	LEU
46	BZ	72	ARG
46	BZ	86	VAL
46	BZ	91	LEU
46	BZ	120	ILE
46	BZ	136	PHE
46	BZ	146	ILE
46	BZ	153	SER
46	BZ	154	ASP
46	BZ	155	LEU
46	BZ	162	GLU
46	BZ	170	THR
47	B0	10	THR
47	B0	20	ARG
47	B0	55	ARG
47	B0	82	ARG
48	B1	21	ARG
48	B1	40	ARG
48	B1	59	THR
48	B1	78	LYS
48	B1	95	LEU
48	B1	98	LEU
49	B2	3	LEU
49	B2	19	VAL
49	B2	28	LYS
49	B2	30	ARG
49	B2	32	LEU
49	B2	45	SER
49	B2	55	ARG
49	B2	64	LEU
49	B2	70	GLN
50	B3	3	ARG
50	B3	8	LEU
50	B3	23	LEU
50	B3	29	ARG
50	B3	54	VAL
50	B3	55	ARG
51	B4	28	LYS
51	B4	31	ILE
51	B4	34	GLU
51	B4	46	GLN
51	B4	49	PHE

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Mol	Chain	Res	Type
51	B4	50	VAL
51	B4	53	GLU
51	B4	56	VAL
51	B4	58	ARG
51	B4	59	PHE
51	B4	61	ARG
51	B4	66	SER
51	B4	68	ARG
52	B5	6	VAL
52	B5	16	ARG
52	B5	29	THR
52	B5	40	LYS
52	B5	55	ARG
52	B5	59	GLU
52	B5	60	VAL
53	B6	4	GLU
53	B6	9	LEU
53	B6	14	THR
53	B6	38	LYS
53	B6	48	VAL
53	B6	52	VAL
54	B7	24	THR
54	B7	43	THR
54	B7	46	VAL
55	B8	11	LYS
55	B8	13	ARG
55	B8	14	VAL
55	B8	26	LYS
55	B8	30	ARG
55	B8	32	LEU
56	B9	7	VAL
2	CB	7	VAL
2	CB	10	LEU
2	CB	11	LEU
2	CB	15	VAL
2	CB	16	HIS
2	CB	35	GLU
2	CB	39	ILE
2	CB	50	GLU
2	CB	55	PHE
2	CB	67	THR
2	CB	71	VAL

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Mol	Chain	Res	Type
2	CB	76	GLN
2	CB	80	ILE
2	CB	82	ARG
2	CB	87	ARG
2	CB	96	ARG
2	CB	98	LEU
2	CB	114	ARG
2	CB	115	LEU
2	CB	117	GLU
2	CB	124	SER
2	CB	126	GLU
2	CB	128	GLU
2	CB	142	LEU
2	CB	144	ARG
2	CB	154	LEU
2	CB	155	LEU
2	CB	157	ARG
2	CB	160	ASP
2	CB	185	ILE
2	CB	187	LEU
2	CB	200	ILE
2	CB	209	ARG
2	CB	210	SER
2	CB	213	LEU
2	CB	217	ARG
2	CB	221	LEU
2	CB	224	GLN
2	CB	230	VAL
3	CC	3	ASN
3	CC	21	ARG
3	CC	35	GLU
3	CC	49	SER
3	CC	52	LEU
3	CC	57	ILE
3	CC	70	VAL
3	CC	91	LEU
3	CC	98	ASN
3	CC	101	LEU
3	CC	104	GLN
3	CC	105	GLU
3	CC	115	LEU
3	CC	118	GLN

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Mol	Chain	Res	Type
3	CC	140	ARG
3	CC	152	ILE
3	CC	173	VAL
3	CC	178	LEU
3	CC	196	LEU
3	CC	198	VAL
3	CC	207	VAL
4	CD	10	ARG
4	CD	15	GLU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	86	LYS
4	CD	96	LEU
4	CD	108	LEU
4	CD	127	THR
4	CD	135	LEU
4	CD	155	LEU
4	CD	157	LEU
4	CD	168	ARG
4	CD	170	VAL
4	CD	187	ARG
4	CD	188	LEU
4	CD	194	LEU
5	CE	6	PHE
5	CE	10	MET
5	CE	12	LEU
5	CE	27	ARG
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	67	VAL
5	CE	79	GLU
5	CE	137	GLU
5	CE	150	ARG
6	CF	28	ARG
6	CF	40	VAL
6	CF	41	GLU

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Mol	Chain	Res	Type
6	CF	46	ARG
6	CF	61	LEU
6	CF	69	GLU
6	CF	75	LEU
6	CF	94	GLN
7	CG	9	VAL
7	CG	12	LEU
7	CG	16	LEU
7	CG	32	ARG
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	104	LEU
7	CG	113	GLU
7	CG	155	ARG
8	CH	21	LYS
8	CH	22	GLU
8	CH	26	VAL
8	CH	29	SER
8	CH	38	ILE
8	CH	39	LEU
8	CH	45	ILE
8	CH	63	LEU
8	CH	84	ARG
8	CH	91	ARG
8	CH	98	LYS
8	CH	103	VAL
8	CH	109	ILE
8	CH	112	LEU
8	CH	137	VAL
9	CI	3	GLN
9	CI	7	THR
9	CI	14	VAL
9	CI	23	ASN
9	CI	50	LEU
9	CI	56	LEU
9	CI	64	THR
9	CI	81	ILE
9	CI	89	ASN

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Mol	Chain	Res	Type
9	CI	102	LEU
9	CI	108	VAL
9	CI	109	VAL
9	CI	112	LYS
9	CI	128	ARG
10	CJ	19	SER
10	CJ	29	ARG
10	CJ	59	SER
10	CJ	67	THR
10	CJ	81	THR
10	CJ	100	THR
11	CK	24	SER
11	CK	31	THR
11	CK	48	ILE
11	CK	51	LYS
11	CK	96	ARG
11	CK	104	GLN
11	CK	114	VAL
12	CL	38	THR
12	CL	60	LEU
12	CL	79	GLU
12	CL	83	VAL
12	CL	116	SER
13	CM	15	VAL
13	CM	19	LEU
13	CM	22	ILE
13	CM	27	LYS
13	CM	47	ASP
13	CM	49	THR
13	CM	50	GLU
13	CM	56	LEU
13	CM	78	ILE
13	CM	84	ILE
13	CM	103	THR
13	CM	104	ARG
13	CM	110	ARG
13	CM	117	VAL
13	CM	121	LYS
14	CN	3	ARG
14	CN	6	LEU
14	CN	7	ILE
14	CN	18	VAL

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Mol	Chain	Res	Type
14	CN	23	ARG
14	CN	26	ARG
14	CN	32	SER
14	CN	33	VAL
15	CO	3	ILE
15	CO	5	LYS
15	CO	26	GLU
15	CO	38	ARG
15	CO	39	LEU
15	CO	41	GLU
15	CO	54	ARG
15	CO	83	GLU
16	CP	2	VAL
16	CP	3	LYS
16	CP	21	VAL
16	CP	27	LYS
16	CP	60	LEU
16	CP	62	VAL
16	CP	67	THR
16	CP	69	THR
17	CQ	6	LEU
17	CQ	9	VAL
17	CQ	14	LYS
17	CQ	19	VAL
17	CQ	35	VAL
17	CQ	36	ILE
17	CQ	60	ILE
17	CQ	63	ARG
17	CQ	74	LEU
17	CQ	96	GLU
18	CR	26	LEU
18	CR	32	ARG
18	CR	35	ARG
18	CR	37	VAL
18	CR	41	LYS
18	CR	46	GLU
18	CR	58	LEU
18	CR	76	LEU
19	CS	6	LYS
19	CS	28	LYS
19	CS	37	ARG
19	CS	41	VAL

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Mol	Chain	Res	Type
19	CS	56	GLN
19	CS	78	ARG
20	CT	10	LEU
20	CT	24	LEU
20	CT	38	LYS
20	CT	45	GLN
20	CT	46	GLU
20	CT	51	GLU
20	CT	56	MET
20	CT	62	LEU
20	CT	71	THR
20	CT	80	ARG
20	CT	90	GLN
20	CT	99	LEU
21	CU	7	ARG
21	CU	10	ARG
28	DD	3	VAL
28	DD	5	LYS
28	DD	54	ARG
28	DD	61	LEU
28	DD	78	LYS
28	DD	88	ARG
28	DD	94	LEU
28	DD	103	ARG
28	DD	106	ILE
28	DD	113	VAL
28	DD	134	ARG
28	DD	140	THR
28	DD	142	VAL
28	DD	155	LEU
28	DD	162	SER
28	DD	193	VAL
28	DD	211	ARG
28	DD	217	ARG
28	DD	221	VAL
28	DD	229	VAL
28	DD	257	LEU
28	DD	259	THR
28	DD	260	ARG
28	DD	276	LYS
29	DE	1	MET
29	DE	9	VAL

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Mol	Chain	Res	Type
29	DE	12	THR
29	DE	21	VAL
29	DE	24	THR
29	DE	33	VAL
29	DE	34	VAL
29	DE	40	GLU
29	DE	47	VAL
29	DE	49	LEU
29	DE	52	LEU
29	DE	72	VAL
29	DE	73	GLU
29	DE	75	VAL
29	DE	79	ARG
29	DE	82	ARG
29	DE	116	VAL
29	DE	119	ARG
29	DE	134	ILE
29	DE	144	ARG
29	DE	145	LYS
29	DE	154	LYS
29	DE	163	GLU
29	DE	175	VAL
29	DE	181	LEU
29	DE	195	LEU
30	DF	19	GLU
30	DF	20	LEU
30	DF	24	LEU
30	DF	28	ILE
30	DF	33	LEU
30	DF	38	ARG
30	DF	57	VAL
30	DF	74	ARG
30	DF	82	ILE
30	DF	88	VAL
30	DF	106	ARG
30	DF	108	LYS
30	DF	110	LEU
30	DF	126	VAL
30	DF	132	VAL
30	DF	135	LYS
30	DF	162	LEU
30	DF	170	LEU

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Mol	Chain	Res	Type
30	DF	183	VAL
30	DF	192	LEU
30	DF	197	ASP
30	DF	200	GLU
30	DF	201	VAL
31	DG	5	VAL
31	DG	8	LYS
31	DG	16	ARG
31	DG	21	ARG
31	DG	35	GLU
31	DG	36	LYS
31	DG	43	LEU
31	DG	45	GLU
31	DG	58	GLN
31	DG	60	LEU
31	DG	70	VAL
31	DG	84	LYS
31	DG	98	ARG
31	DG	115	ARG
31	DG	135	LEU
31	DG	136	ARG
31	DG	140	ILE
31	DG	143	GLU
31	DG	145	THR
31	DG	148	MET
31	DG	159	VAL
32	DH	2	SER
32	DH	3	ARG
32	DH	15	VAL
32	DH	33	LEU
32	DH	43	VAL
32	DH	44	VAL
32	DH	45	VAL
32	DH	63	SER
32	DH	69	ARG
32	DH	71	LEU
32	DH	84	SER
32	DH	86	GLU
32	DH	95	ARG
32	DH	106	THR
32	DH	124	GLU
32	DH	125	VAL

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Mol	Chain	Res	Type
32	DH	134	SER
32	DH	136	ILE
32	DH	172	LYS
33	DI	5	LEU
33	DI	9	LEU
33	DI	19	VAL
33	DI	40	THR
33	DI	43	ASN
33	DI	44	LEU
33	DI	47	LEU
33	DI	50	ARG
33	DI	68	LEU
33	DI	73	GLU
33	DI	86	THR
33	DI	92	VAL
33	DI	114	LEU
33	DI	121	LYS
33	DI	123	LEU
33	DI	140	LEU
33	DI	142	VAL
34	DN	14	VAL
34	DN	28	THR
34	DN	33	LEU
34	DN	34	LEU
34	DN	38	HIS
34	DN	46	VAL
34	DN	58	ASP
34	DN	61	ARG
34	DN	62	VAL
34	DN	85	ILE
34	DN	87	LEU
34	DN	97	ARG
34	DN	99	LEU
34	DN	120	LEU
34	DN	137	LYS
34	DN	139	GLU
35	DO	8	LEU
35	DO	9	GLU
35	DO	10	VAL
35	DO	23	ARG
35	DO	24	VAL
35	DO	69	ILE

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Mol	Chain	Res	Type
35	DO	92	GLU
35	DO	94	ARG
35	DO	98	VAL
35	DO	108	GLU
36	DP	1	MET
36	DP	29	LYS
36	DP	45	LEU
36	DP	50	ARG
36	DP	55	ARG
36	DP	59	LEU
36	DP	65	ARG
36	DP	68	GLN
36	DP	83	VAL
36	DP	95	VAL
36	DP	96	THR
36	DP	106	LEU
36	DP	112	LEU
36	DP	119	GLU
36	DP	131	SER
37	DQ	1	MET
37	DQ	2	LEU
37	DQ	16	ARG
37	DQ	21	THR
37	DQ	45	GLN
37	DQ	54	MET
37	DQ	56	ARG
37	DQ	59	ARG
37	DQ	60	ARG
37	DQ	75	THR
37	DQ	85	LYS
37	DQ	109	VAL
37	DQ	110	THR
37	DQ	112	GLU
38	DR	1	MET
38	DR	15	SER
38	DR	18	LEU
38	DR	24	GLN
38	DR	28	LEU
38	DR	29	LEU
38	DR	33	ARG
38	DR	36	THR
38	DR	44	LEU

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Mol	Chain	Res	Type
38	DR	60	LEU
38	DR	65	LEU
38	DR	67	LEU
38	DR	75	LEU
38	DR	79	LEU
38	DR	100	LEU
38	DR	102	GLU
38	DR	111	LEU
38	DR	114	VAL
39	DS	14	VAL
39	DS	20	ARG
39	DS	33	LYS
39	DS	35	ILE
39	DS	44	LYS
39	DS	57	LYS
39	DS	69	VAL
39	DS	71	ARG
39	DS	75	GLU
39	DS	76	LYS
39	DS	93	LYS
39	DS	101	LEU
39	DS	103	GLU
39	DS	110	LEU
40	DT	6	LEU
40	DT	16	ARG
40	DT	17	THR
40	DT	28	VAL
40	DT	49	VAL
40	DT	53	ARG
40	DT	78	LEU
40	DT	89	VAL
40	DT	95	ARG
40	DT	96	ARG
40	DT	108	ARG
40	DT	113	LYS
40	DT	118	ARG
41	DU	8	VAL
41	DU	36	ARG
41	DU	74	LEU
41	DU	83	LEU
41	DU	89	GLU
41	DU	92	ARG

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Mol	Chain	Res	Type
41	DU	95	LEU
41	DU	104	GLN
41	DU	108	GLU
42	DV	6	LYS
42	DV	15	GLU
42	DV	18	LEU
42	DV	38	LEU
42	DV	46	VAL
42	DV	51	VAL
42	DV	52	VAL
42	DV	57	VAL
42	DV	61	VAL
42	DV	62	LEU
42	DV	72	VAL
42	DV	79	VAL
42	DV	85	LYS
42	DV	95	LEU
42	DV	100	ARG
43	DW	11	ARG
43	DW	15	ARG
43	DW	17	VAL
43	DW	23	LEU
43	DW	51	LEU
43	DW	100	THR
44	DX	23	GLU
44	DX	57	LEU
44	DX	70	LEU
44	DX	72	LYS
44	DX	76	ARG
44	DX	88	LYS
44	DX	90	GLU
44	DX	92	LEU
45	DY	11	ASP
45	DY	23	ARG
45	DY	72	VAL
45	DY	85	VAL
45	DY	90	LEU
45	DY	91	GLU
45	DY	107	ASP
46	DZ	5	LEU
46	DZ	18	LEU
46	DZ	33	LEU

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Mol	Chain	Res	Type
46	DZ	35	ARG
46	DZ	40	ASP
46	DZ	41	LEU
46	DZ	61	LEU
46	DZ	72	ARG
46	DZ	86	VAL
46	DZ	96	VAL
46	DZ	97	GLU
46	DZ	102	LEU
46	DZ	119	GLU
46	DZ	120	ILE
46	DZ	136	PHE
46	DZ	144	LEU
46	DZ	146	ILE
46	DZ	153	SER
46	DZ	154	ASP
46	DZ	155	LEU
46	DZ	162	GLU
46	DZ	171	ILE
47	D0	10	THR
47	D0	19	LYS
47	D0	20	ARG
47	D0	24	LYS
48	D1	4	VAL
48	D1	21	ARG
48	D1	30	VAL
48	D1	40	ARG
48	D1	52	ARG
48	D1	58	ILE
48	D1	59	THR
48	D1	76	ARG
48	D1	89	GLU
48	D1	95	LEU
48	D1	97	LEU
48	D1	98	LEU
49	D2	19	VAL
49	D2	21	LEU
49	D2	28	LYS
49	D2	30	ARG
49	D2	45	SER
49	D2	55	ARG
49	D2	69	ARG

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Mol	Chain	Res	Type
49	D2	70	GLN
50	D3	3	ARG
50	D3	8	LEU
50	D3	23	LEU
50	D3	24	LYS
50	D3	44	ARG
50	D3	54	VAL
51	D4	8	LYS
51	D4	22	ILE
51	D4	24	THR
51	D4	34	GLU
51	D4	44	THR
51	D4	50	VAL
51	D4	56	VAL
51	D4	58	ARG
51	D4	63	TYR
51	D4	68	ARG
52	D5	6	VAL
52	D5	29	THR
52	D5	40	LYS
52	D5	55	ARG
52	D5	59	GLU
52	D5	60	VAL
53	D6	9	LEU
53	D6	38	LYS
53	D6	48	VAL
54	D7	1	MET
54	D7	14	LYS
54	D7	23	ARG
54	D7	43	THR
54	D7	46	VAL
55	D8	11	LYS
55	D8	13	ARG
55	D8	14	VAL
55	D8	26	LYS
55	D8	30	ARG
55	D8	32	LEU
55	D8	41	ILE
56	D9	7	VAL
56	D9	26	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (153) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	94	ASN
3	AC	6	HIS
3	AC	28	GLN
3	AC	69	HIS
3	AC	98	ASN
3	AC	104	GLN
3	AC	123	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	43	HIS
4	AD	45	GLN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
4	AD	161	ASN
5	AE	20	GLN
5	AE	38	GLN
6	AF	94	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	51	GLN
8	AH	82	HIS
9	AI	23	ASN
9	AI	34	ASN
9	AI	73	GLN
9	AI	124	GLN
10	AJ	56	HIS
11	AK	93	GLN
11	AK	104	GLN
12	AL	78	GLN
12	AL	99	HIS
13	AM	92	HIS
15	AO	9	GLN
15	AO	28	GLN
15	AO	46	HIS
15	AO	62	GLN
15	AO	71	GLN
19	AS	57	HIS
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS
20	AT	9	ASN

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Mol	Chain	Res	Type
20	AT	90	GLN
28	BD	164	GLN
28	BD	253	GLN
29	BE	143	ASN
30	BF	8	GLN
30	BF	69	HIS
30	BF	169	ASN
30	BF	203	GLN
30	BF	204	ASN
31	BG	26	GLN
33	BI	43	ASN
33	BI	54	GLN
34	BN	56	ASN
34	BN	94	HIS
35	BO	3	GLN
35	BO	5	GLN
36	BP	38	GLN
36	BP	70	GLN
38	BR	71	GLN
40	BT	43	GLN
40	BT	123	GLN
44	BX	31	HIS
44	BX	82	GLN
45	BY	6	HIS
45	BY	43	ASN
46	BZ	34	ASN
46	BZ	121	HIS
49	B2	70	GLN
51	B4	46	GLN
51	B4	47	GLN
56	B9	36	GLN
2	CB	40	HIS
2	CB	224	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	69	HIS
3	CC	118	GLN
3	CC	123	GLN
3	CC	136	GLN
4	CD	77	ASN
4	CD	119	GLN
4	CD	123	HIS

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Mol	Chain	Res	Type
4	CD	125	HIS
4	CD	160	GLN
5	CE	20	GLN
5	CE	56	GLN
6	CF	94	GLN
7	CG	28	ASN
7	CG	51	GLN
7	CG	56	GLN
7	CG	64	GLN
7	CG	97	GLN
7	CG	148	ASN
9	CI	23	ASN
9	CI	31	GLN
9	CI	58	HIS
9	CI	89	ASN
9	CI	124	GLN
10	CJ	62	HIS
11	CK	22	HIS
11	CK	93	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	92	HIS
15	CO	28	GLN
16	CP	16	HIS
19	CS	56	GLN
19	CS	57	HIS
19	CS	65	ASN
19	CS	69	HIS
19	CS	83	HIS
20	CT	73	HIS
28	DD	126	GLN
28	DD	164	GLN
28	DD	166	GLN
28	DD	253	GLN
29	DE	85	ASN
30	DF	69	HIS
30	DF	169	ASN
30	DF	203	GLN
31	DG	26	GLN
31	DG	40	ASN
31	DG	41	GLN
33	DI	43	ASN

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Mol	Chain	Res	Type
34	DN	69	GLN
34	DN	94	HIS
35	DO	3	GLN
35	DO	89	ASN
38	DR	50	HIS
38	DR	71	GLN
39	DS	68	GLN
40	DT	43	GLN
40	DT	58	ASN
40	DT	79	HIS
40	DT	123	GLN
41	DU	94	ASN
41	DU	117	GLN
42	DV	64	HIS
43	DW	34	ASN
44	DX	31	HIS
44	DX	82	GLN
45	DY	43	ASN
46	DZ	50	GLN
46	DZ	55	HIS
46	DZ	118	GLN
46	DZ	121	HIS
46	DZ	151	HIS
47	D0	35	ASN
49	D2	38	GLN
56	D9	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1495/1521 (98%)	307 (20%)	25 (1%)
1	CA	1501/1521 (98%)	317 (21%)	28 (1%)
22	AV	12/24 (50%)	3 (25%)	0
22	CV	11/24 (45%)	2 (18%)	0
23	AW	71/76 (93%)	30 (42%)	2 (2%)
23	CW	68/76 (89%)	32 (47%)	2 (2%)
24	AX	75/77 (97%)	16 (21%)	0
24	CX	75/77 (97%)	21 (28%)	0
25	AY	72/76 (94%)	37 (51%)	4 (5%)
25	CY	70/76 (92%)	33 (47%)	1 (1%)
26	BA	2811/2915 (96%)	450 (16%)	34 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	DA	2791/2915 (95%)	553 (19%)	30 (1%)
27	BB	119/121 (98%)	14 (11%)	0
27	DB	119/121 (98%)	17 (14%)	0
All	All	9290/9620 (96%)	1832 (19%)	126 (1%)

All (1832) 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	29	G
1	AA	32	A
1	AA	39	G
1	AA	47	C
1	AA	48	C
1	AA	51	A
1	AA	59	A
1	AA	61	G
1	AA	65	U
1	AA	73	G
1	AA	77	G
1	AA	78	G
1	AA	79	G
1	AA	91	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	146	G
1	AA	155	C
1	AA	163	C
1	AA	166	G
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(D)	C
1	AA	189(F)	U
1	AA	189(H)	G
1	AA	189(I)	G
1	AA	189(K)	U
1	AA	190	U
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	221	C
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C
1	AA	279	A
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	342	C
1	AA	346	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	382	A
1	AA	384	G
1	AA	397	A
1	AA	398	C

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Mol	Chain	Res	Type
1	AA	406	G
1	AA	412	A
1	AA	414	A
1	AA	421	U
1	AA	424	G
1	AA	429	U
1	AA	430	A
1	AA	439	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	461	A
1	AA	470	C
1	AA	471	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	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	560	U
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	592	G
1	AA	596	C
1	AA	629	G
1	AA	630	G
1	AA	632	A
1	AA	633	G

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Mol	Chain	Res	Type
1	AA	649	G
1	AA	653	A
1	AA	665	A
1	AA	673	G
1	AA	680	C
1	AA	687	A
1	AA	688	G
1	AA	695	A
1	AA	711	G
1	AA	712	A
1	AA	721	G
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	753	A
1	AA	755	G
1	AA	774	G
1	AA	777	A
1	AA	792	A
1	AA	793	U
1	AA	794	A
1	AA	815	A
1	AA	816	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	833	U
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	853	G
1	AA	859	A
1	AA	874	G
1	AA	902	G
1	AA	914	A
1	AA	922	G
1	AA	926	G
1	AA	927	G
1	AA	932	C
1	AA	934	C
1	AA	935	A

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Mol	Chain	Res	Type
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	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1002	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1008	C
1	AA	1009	G
1	AA	1019	C
1	AA	1021	G
1	AA	1022	G
1	AA	1023	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(B)	C
1	AA	1030(C)	G
1	AA	1030(D)	A
1	AA	1031	G
1	AA	1033	G
1	AA	1037	C
1	AA	1039	C
1	AA	1043	C
1	AA	1044	A

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Mol	Chain	Res	Type
1	AA	1045	C
1	AA	1052	U
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1066	C
1	AA	1068	G
1	AA	1076	C
1	AA	1081	G
1	AA	1088	G
1	AA	1094	G
1	AA	1095	U
1	AA	1096	C
1	AA	1097	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1110	A
1	AA	1113	C
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	1141	C
1	AA	1146	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1181	G
1	AA	1182	G
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G

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Mol	Chain	Res	Type
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1224	G
1	AA	1227	A
1	AA	1228	C
1	AA	1236	A
1	AA	1238	A
1	AA	1240	U
1	AA	1244	C
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1260	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	1286	A
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1314	C
1	AA	1317	C
1	AA	1322	C
1	AA	1338	G
1	AA	1340	A
1	AA	1346	A
1	AA	1347	G
1	AA	1353	G
1	AA	1355	G
1	AA	1360	A
1	AA	1363	C
1	AA	1364	U
1	AA	1370	G
1	AA	1397	C
1	AA	1402	C
1	AA	1419	G

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Mol	Chain	Res	Type
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1442(B)	A
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1487	G
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1519	A
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	14	A
22	AV	24	A
23	AW	2	C
23	AW	3	C
23	AW	4	C
23	AW	8	4SU
23	AW	12	U
23	AW	14	A
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G
23	AW	23	A
23	AW	24	G
23	AW	26	A
23	AW	27	G
23	AW	30	G
23	AW	42	C
23	AW	43	C
23	AW	45	U

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Mol	Chain	Res	Type
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	52	G
23	AW	53	G
23	AW	59	U
23	AW	61	C
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	3	C
24	AX	9	G
24	AX	13	C
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	42	G
24	AX	48	C
24	AX	56	C
24	AX	59	A
24	AX	63	G
24	AX	67	C
24	AX	68	C
24	AX	70	G
24	AX	76	A
25	AY	2	C
25	AY	5	G
25	AY	9	A
25	AY	11	C
25	AY	13	C
25	AY	15	G
25	AY	19	G
25	AY	20	U
25	AY	21	A
25	AY	22	G
25	AY	25	C
25	AY	26	A
25	AY	29	G
25	AY	30	G

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Mol	Chain	Res	Type
25	AY	33	U
25	AY	34	G
25	AY	35	A
25	AY	36	A
25	AY	37	MIA
25	AY	39	PSU
25	AY	41	C
25	AY	44	G
25	AY	45	U
25	AY	46	7MG
25	AY	47	U
25	AY	48	C
25	AY	49	C
25	AY	54	5MU
25	AY	57	G
25	AY	58	A
25	AY	59	U
25	AY	60	U
25	AY	62	C
25	AY	65	G
25	AY	67	C
25	AY	70	G
25	AY	73	A
26	BA	12	U
26	BA	34	C
26	BA	36	G
26	BA	45	C
26	BA	64	A
26	BA	71	A
26	BA	72	U
26	BA	74	A
26	BA	75	G
26	BA	84	A
26	BA	95	G
26	BA	99	U
26	BA	100	G
26	BA	102	G
26	BA	118	A
26	BA	119	A
26	BA	120	U
26	BA	151	C
26	BA	154(A)	C

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Mol	Chain	Res	Type
26	BA	172	C
26	BA	181	A
26	BA	182	A
26	BA	188	G
26	BA	196	A
26	BA	197	A
26	BA	199	A
26	BA	205	G
26	BA	215	G
26	BA	216	A
26	BA	221	A
26	BA	222	A
26	BA	223	A
26	BA	229	A
26	BA	233	A
26	BA	248	G
26	BA	271(E)	U
26	BA	271(I)	G
26	BA	271(K)	U
26	BA	271(L)	U
26	BA	271(M)	G
26	BA	271(N)	U
26	BA	271(S)	G
26	BA	272(A)	U
26	BA	272(B)	G
26	BA	272(G)	C
26	BA	272(I)	U
26	BA	279	C
26	BA	282	A
26	BA	283	A
26	BA	311	A
26	BA	329	G
26	BA	330	A
26	BA	352	G
26	BA	363	G
26	BA	363(B)	G
26	BA	372	G
26	BA	380	U
26	BA	386	G
26	BA	396	G
26	BA	405	U
26	BA	411	G

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Mol	Chain	Res	Type
26	BA	428	A
26	BA	443	A
26	BA	444	C
26	BA	448	U
26	BA	454	A
26	BA	456	C
26	BA	470	A
26	BA	479	A
26	BA	481	G
26	BA	504	U
26	BA	505	A
26	BA	509	C
26	BA	528	A
26	BA	529	A
26	BA	530	G
26	BA	531	C
26	BA	532	A
26	BA	533	G
26	BA	545	G
26	BA	549	G
26	BA	563	G
26	BA	573	G
26	BA	575	A
26	BA	592	G
26	BA	603	A
26	BA	604	G
26	BA	607	U
26	BA	614(A)	U
26	BA	614(B)	G
26	BA	615	G
26	BA	616	G
26	BA	627	A
26	BA	637	A
26	BA	645	C
26	BA	646	A
26	BA	652(F)	G
26	BA	652(T)	C
26	BA	652(U)	G
26	BA	669	G
26	BA	677	A
26	BA	686	G
26	BA	730	C

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Mol	Chain	Res	Type
26	BA	732	C
26	BA	764	A
26	BA	765	G
26	BA	775	G
26	BA	776	G
26	BA	782	A
26	BA	784	A
26	BA	785	G
26	BA	792	G
26	BA	805	G
26	BA	812	C
26	BA	819	A
26	BA	824	A
26	BA	827	U
26	BA	828	U
26	BA	830	G
26	BA	855	G
26	BA	859	G
26	BA	862	G
26	BA	866	A
26	BA	877	U
26	BA	879	G
26	BA	880	G
26	BA	882	G
26	BA	884	C
26	BA	885	C
26	BA	886	C
26	BA	887	A
26	BA	888	C
26	BA	889	C
26	BA	890	A
26	BA	892	G
26	BA	893	C
26	BA	894	C
26	BA	895	U
26	BA	896	A
26	BA	897	C
26	BA	898	C
26	BA	899	A
26	BA	900	A
26	BA	901	A
26	BA	907	U

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Mol	Chain	Res	Type
26	BA	910	A
26	BA	932	G
26	BA	941	A
26	BA	945	A
26	BA	946	G
26	BA	958	U
26	BA	959	A
26	BA	961	C
26	BA	974	G
26	BA	975	C
26	BA	983	A
26	BA	996	A
26	BA	1012	U
26	BA	1013	C
26	BA	1022	G
26	BA	1033	U
26	BA	1038	C
26	BA	1041	C
26	BA	1045	A
26	BA	1046	A
26	BA	1047	G
26	BA	1048	A
26	BA	1051	G
26	BA	1107	G
26	BA	1108	U
26	BA	1110	G
26	BA	1112	G
26	BA	1128	A
26	BA	1130	U
26	BA	1135	C
26	BA	1136	G
26	BA	1170	G
26	BA	1171	G
26	BA	1173	G
26	BA	1174	A
26	BA	1175	U
26	BA	1176	G
26	BA	1177	A
26	BA	1178	C
26	BA	1210	A
26	BA	1211	U
26	BA	1220	A

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Mol	Chain	Res	Type
26	BA	1244	G
26	BA	1248	G
26	BA	1253	A
26	BA	1256	G
26	BA	1271	G
26	BA	1272	A
26	BA	1273	U
26	BA	1289	C
26	BA	1300	U
26	BA	1301	A
26	BA	1303	G
26	BA	1314	C
26	BA	1319	G
26	BA	1352	U
26	BA	1359	A
26	BA	1360	A
26	BA	1365	A
26	BA	1370	C
26	BA	1380	G
26	BA	1384	A
26	BA	1385	G
26	BA	1416	G
26	BA	1417	C
26	BA	1420	U
26	BA	1421	G
26	BA	1428	C
26	BA	1445	A
26	BA	1449	A
26	BA	1450	G
26	BA	1459	G
26	BA	1467	C
26	BA	1471	A
26	BA	1478	G
26	BA	1482	G
26	BA	1484	G
26	BA	1493	C
26	BA	1507	A
26	BA	1508	A
26	BA	1509	C
26	BA	1509(A)	A
26	BA	1531	C
26	BA	1538	G

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Mol	Chain	Res	Type
26	BA	1543	C
26	BA	1558	A
26	BA	1566	A
26	BA	1569	A
26	BA	1578	U
26	BA	1580	A
26	BA	1581	G
26	BA	1584	C
26	BA	1586	A
26	BA	1608	A
26	BA	1610	A
26	BA	1648	C
26	BA	1654	A
26	BA	1664	A
26	BA	1674	G
26	BA	1694	C
26	BA	1700	A
26	BA	1701	A
26	BA	1703	G
26	BA	1722	A
26	BA	1739	U
26	BA	1746	G
26	BA	1748	G
26	BA	1756	G
26	BA	1759	A
26	BA	1762	A
26	BA	1763	G
26	BA	1764	G
26	BA	1773	A
26	BA	1780	A
26	BA	1782	C
26	BA	1786	A
26	BA	1791	A
26	BA	1800	C
26	BA	1816	G
26	BA	1839	G
26	BA	1847	A
26	BA	1848	A
26	BA	1861	G
26	BA	1877	A
26	BA	1878	G
26	BA	1886	C

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Mol	Chain	Res	Type
26	BA	1889	A
26	BA	1900	A
26	BA	1906	G
26	BA	1915	U
26	BA	1919	A
26	BA	1924	C
26	BA	1927	A
26	BA	1929	G
26	BA	1930	G
26	BA	1937	A
26	BA	1938	A
26	BA	1955	U
26	BA	1963	U
26	BA	1967	C
26	BA	1970	A
26	BA	1971	A
26	BA	1972	A
26	BA	1992	G
26	BA	1993	U
26	BA	1997	G
26	BA	2020	A
26	BA	2023	G
26	BA	2031	A
26	BA	2032	G
26	BA	2033	A
26	BA	2043	C
26	BA	2055	C
26	BA	2056	G
26	BA	2060	A
26	BA	2061	G
26	BA	2062	A
26	BA	2069	G
26	BA	2098	U
26	BA	2102	U
26	BA	2110	G
26	BA	2111	C
26	BA	2119	A
26	BA	2120	G
26	BA	2121	G
26	BA	2125	G
26	BA	2126	A
26	BA	2127	G

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Mol	Chain	Res	Type
26	BA	2128	C
26	BA	2129	C
26	BA	2132	U
26	BA	2133	G
26	BA	2134	A
26	BA	2135	A
26	BA	2136	C
26	BA	2138	C
26	BA	2140	C
26	BA	2141	G
26	BA	2142	C
26	BA	2143	C
26	BA	2145	C
26	BA	2146	C
26	BA	2147	G
26	BA	2149	G
26	BA	2157	G
26	BA	2158	A
26	BA	2159	G
26	BA	2160	G
26	BA	2165	G
26	BA	2167	U
26	BA	2168	G
26	BA	2169	A
26	BA	2171	A
26	BA	2172	U
26	BA	2173	A
26	BA	2174	C
26	BA	2178	C
26	BA	2181	G
26	BA	2182	G
26	BA	2184	G
26	BA	2188	C
26	BA	2189	U
26	BA	2192	G
26	BA	2198	A
26	BA	2199	A
26	BA	2206	G
26	BA	2207	G
26	BA	2208	A
26	BA	2218	U
26	BA	2225	A

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Mol	Chain	Res	Type
26	BA	2238	G
26	BA	2239	G
26	BA	2268	A
26	BA	2269	A
26	BA	2275	C
26	BA	2283	C
26	BA	2287	A
26	BA	2289	G
26	BA	2305	A
26	BA	2308	G
26	BA	2320	A
26	BA	2325	G
26	BA	2334	G
26	BA	2336	A
26	BA	2343	C
26	BA	2347	C
26	BA	2350	C
26	BA	2361	A
26	BA	2383	G
26	BA	2385	C
26	BA	2393	A
26	BA	2400	G
26	BA	2406	U
26	BA	2414	G
26	BA	2419	U
26	BA	2425	A
26	BA	2429	G
26	BA	2430	A
26	BA	2435	A
26	BA	2439	A
26	BA	2441	C
26	BA	2448	A
26	BA	2464	C
26	BA	2468	G
26	BA	2469	A
26	BA	2471	C
26	BA	2474	C
26	BA	2476	A
26	BA	2487	G
26	BA	2490	G
26	BA	2502	G
26	BA	2505	G

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Mol	Chain	Res	Type
26	BA	2518	A
26	BA	2529	G
26	BA	2535	G
26	BA	2549	G
26	BA	2554	U
26	BA	2566	A
26	BA	2567	G
26	BA	2573	C
26	BA	2574	G
26	BA	2602	A
26	BA	2609	U
26	BA	2611	U
26	BA	2612	C
26	BA	2629	A
26	BA	2630	G
26	BA	2654	A
26	BA	2669	G
26	BA	2689	U
26	BA	2690	C
26	BA	2691	C
26	BA	2702	U
26	BA	2712(A)	A
26	BA	2713	A
26	BA	2726	U
26	BA	2733	A
26	BA	2757	A
26	BA	2758	A
26	BA	2761	G
26	BA	2764	A
26	BA	2765	A
26	BA	2766	G
26	BA	2778	A
26	BA	2790	A
26	BA	2791	C
26	BA	2792	G
26	BA	2793	G
26	BA	2802	G
26	BA	2805	G
26	BA	2808	U
26	BA	2818	G
26	BA	2820	A
26	BA	2821	A

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Mol	Chain	Res	Type
26	BA	2833	G
26	BA	2834	G
26	BA	2835	A
26	BA	2872	G
26	BA	2873	A
26	BA	2876	G
26	BA	2880	C
26	BA	2882	A
26	BA	2883	A
26	BA	2892	A
26	BA	2894	G
27	BB	2	C
27	BB	7	G
27	BB	34	U
27	BB	42	C
27	BB	56	G
27	BB	73	A
27	BB	75	G
27	BB	85	G
27	BB	93	G
27	BB	106	G
27	BB	110	G
27	BB	111	G
27	BB	112	U
27	BB	120	A
1	CA	5	U
1	CA	6	G
1	CA	7	G
1	CA	9	G
1	CA	13	U
1	CA	22	G
1	CA	29	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	59	A
1	CA	61	G
1	CA	65	U
1	CA	66	G
1	CA	77	G

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Mol	Chain	Res	Type
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	91	C
1	CA	96	U
1	CA	97	G
1	CA	98	G
1	CA	100	C
1	CA	101	A
1	CA	111	G
1	CA	112	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	146	G
1	CA	155	C
1	CA	163	C
1	CA	166	G
1	CA	173	U
1	CA	174	C
1	CA	180	U
1	CA	182	U
1	CA	189(D)	C
1	CA	189(K)	U
1	CA	190	U
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	202	U
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	221	C
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	279	A
1	CA	289	G
1	CA	301	G

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Mol	Chain	Res	Type
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	342	C
1	CA	344	A
1	CA	346	G
1	CA	350	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	382	A
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	412	A
1	CA	413	G
1	CA	414	A
1	CA	421	U
1	CA	424	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	461	A
1	CA	471	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

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Mol	Chain	Res	Type
1	CA	521	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	545	C
1	CA	547	A
1	CA	559	A
1	CA	560	U
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	592	G
1	CA	596	C
1	CA	629	G
1	CA	630	G
1	CA	632	A
1	CA	633	G
1	CA	649	G
1	CA	650	G
1	CA	653	A
1	CA	664	G
1	CA	665	A
1	CA	673	G
1	CA	680	C
1	CA	687	A
1	CA	688	G
1	CA	693	G
1	CA	695	A
1	CA	711	G
1	CA	712	A
1	CA	721	G
1	CA	723	U
1	CA	724	G
1	CA	731	G
1	CA	749	C
1	CA	753	A
1	CA	755	G
1	CA	774	G
1	CA	777	A
1	CA	792	A

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Mol	Chain	Res	Type
1	CA	793	U
1	CA	794	A
1	CA	815	A
1	CA	817	C
1	CA	821	G
1	CA	828	A
1	CA	833	U
1	CA	840	C
1	CA	841	U
1	CA	851	G
1	CA	853	G
1	CA	859	A
1	CA	874	G
1	CA	902	G
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	932	C
1	CA	934	C
1	CA	935	A
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	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	997	U
1	CA	1000	U
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C

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Mol	Chain	Res	Type
1	CA	1009	G
1	CA	1019	C
1	CA	1021	G
1	CA	1022	G
1	CA	1023	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1030(C)	G
1	CA	1030(D)	A
1	CA	1031	G
1	CA	1032	G
1	CA	1037	C
1	CA	1039	C
1	CA	1041	A
1	CA	1043	C
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1065	U
1	CA	1066	C
1	CA	1068	G
1	CA	1076	C
1	CA	1081	G
1	CA	1088	G
1	CA	1094	G
1	CA	1095	U
1	CA	1096	C
1	CA	1097	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1109	C
1	CA	1110	A
1	CA	1113	C
1	CA	1117	G
1	CA	1124	G
1	CA	1125	U

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Mol	Chain	Res	Type
1	CA	1126	U
1	CA	1129	C
1	CA	1130	A
1	CA	1131	G
1	CA	1132	C
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1146	A
1	CA	1147	C
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1183	A
1	CA	1184	G
1	CA	1196	U
1	CA	1197	G
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A
1	CA	1224	G
1	CA	1227	A
1	CA	1228	C
1	CA	1236	A
1	CA	1238	A
1	CA	1240	U
1	CA	1244	C
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1260	C
1	CA	1262	C
1	CA	1270	C
1	CA	1273	G
1	CA	1278	U

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Mol	Chain	Res	Type
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1286	A
1	CA	1287	A
1	CA	1299	A
1	CA	1300	G
1	CA	1305	G
1	CA	1314	C
1	CA	1317	C
1	CA	1322	C
1	CA	1338	G
1	CA	1340	A
1	CA	1346	A
1	CA	1347	G
1	CA	1353	G
1	CA	1355	G
1	CA	1363	C
1	CA	1364	U
1	CA	1370	G
1	CA	1397	C
1	CA	1402	C
1	CA	1419	G
1	CA	1422	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1442(B)	A
1	CA	1446	U
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

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Mol	Chain	Res	Type
1	CA	1519	A
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	14	A
22	CV	24	A
23	CW	3	C
23	CW	4	C
23	CW	5	G
23	CW	6	G
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	14	A
23	CW	19	G
23	CW	22	G
23	CW	23	A
23	CW	25	C
23	CW	26	A
23	CW	27	G
23	CW	30	G
23	CW	42	C
23	CW	43	C
23	CW	45	U
23	CW	46	7MG
23	CW	47	U
23	CW	48	C
23	CW	49	C
23	CW	52	G
23	CW	53	G
23	CW	61	C
23	CW	62	C
23	CW	64	A
23	CW	66	U
23	CW	67	C
23	CW	68	C
23	CW	70	G
23	CW	74	C
24	CX	8	4SU
24	CX	9	G

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Mol	Chain	Res	Type
24	CX	13	C
24	CX	16	C
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	31	G
24	CX	42	G
24	CX	47	U
24	CX	48	C
24	CX	50	U
24	CX	52	G
24	CX	56	C
24	CX	59	A
24	CX	60	U
24	CX	61	C
24	CX	63	G
24	CX	67	C
24	CX	68	C
24	CX	76	A
25	CY	2	C
25	CY	8	4SU
25	CY	9	A
25	CY	11	C
25	CY	13	C
25	CY	15	G
25	CY	19	G
25	CY	23	A
25	CY	27	G
25	CY	29	G
25	CY	30	G
25	CY	33	U
25	CY	34	G
25	CY	35	A
25	CY	36	A
25	CY	37	MIA
25	CY	39	PSU
25	CY	41	C
25	CY	45	U
25	CY	46	7MG
25	CY	47	U
25	CY	49	C
25	CY	52	G

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Mol	Chain	Res	Type
25	CY	54	5MU
25	CY	56	C
25	CY	57	G
25	CY	58	A
25	CY	59	U
25	CY	62	C
25	CY	65	G
25	CY	67	C
25	CY	70	G
25	CY	73	A
26	DA	10	G
26	DA	12	U
26	DA	15	G
26	DA	16	G
26	DA	34	C
26	DA	35	G
26	DA	45	C
26	DA	51	G
26	DA	61	G
26	DA	71	A
26	DA	74	A
26	DA	75	G
26	DA	78	A
26	DA	83	G
26	DA	84	A
26	DA	90	U
26	DA	95	G
26	DA	100	G
26	DA	102	G
26	DA	118	A
26	DA	119	A
26	DA	120	U
26	DA	141	A
26	DA	154(A)	C
26	DA	157	U
26	DA	173	G
26	DA	181	A
26	DA	182	A
26	DA	196	A
26	DA	199	A
26	DA	205	G
26	DA	214	G

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Mol	Chain	Res	Type
26	DA	215	G
26	DA	216	A
26	DA	221	A
26	DA	222	A
26	DA	225	A
26	DA	228	A
26	DA	229	A
26	DA	233	A
26	DA	248	G
26	DA	266	G
26	DA	271(I)	G
26	DA	271(K)	U
26	DA	271(L)	U
26	DA	271(M)	G
26	DA	271(N)	U
26	DA	271(V)	G
26	DA	271(W)	G
26	DA	272(A)	U
26	DA	272(B)	G
26	DA	272(C)	G
26	DA	272(J)	C
26	DA	274	G
26	DA	277	C
26	DA	278	A
26	DA	285	C
26	DA	288	C
26	DA	292	C
26	DA	294	A
26	DA	311	A
26	DA	324	A
26	DA	327	G
26	DA	329	G
26	DA	330	A
26	DA	333	G
26	DA	352	G
26	DA	363	G
26	DA	372	G
26	DA	386	G
26	DA	389	G
26	DA	396	G
26	DA	399	G
26	DA	405	U

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Mol	Chain	Res	Type
26	DA	407	G
26	DA	411	G
26	DA	412	A
26	DA	415	A
26	DA	421	U
26	DA	428	A
26	DA	442	G
26	DA	443	A
26	DA	444	C
26	DA	447	A
26	DA	454	A
26	DA	455	C
26	DA	457	A
26	DA	470	A
26	DA	481	G
26	DA	485	C
26	DA	494	G
26	DA	498	G
26	DA	504	U
26	DA	505	A
26	DA	509	C
26	DA	521	G
26	DA	530	G
26	DA	531	C
26	DA	532	A
26	DA	533	G
26	DA	545	G
26	DA	563	G
26	DA	568	U
26	DA	573	G
26	DA	574	C
26	DA	575	A
26	DA	586	A
26	DA	587	C
26	DA	588	U
26	DA	592	G
26	DA	603	A
26	DA	604	G
26	DA	607	U
26	DA	614(B)	G
26	DA	614(C)	A
26	DA	615	G

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Mol	Chain	Res	Type
26	DA	616	G
26	DA	620	G
26	DA	627	A
26	DA	637	A
26	DA	645	C
26	DA	646	A
26	DA	652(B)	A
26	DA	652(C)	G
26	DA	652(D)	C
26	DA	652(U)	G
26	DA	656	G
26	DA	668	G
26	DA	669	G
26	DA	686	G
26	DA	698	C
26	DA	699	A
26	DA	715	G
26	DA	726	G
26	DA	730	C
26	DA	752	A
26	DA	753	C
26	DA	765	G
26	DA	775	G
26	DA	776	G
26	DA	782	A
26	DA	783	A
26	DA	784	A
26	DA	785	G
26	DA	790	C
26	DA	792	G
26	DA	794	G
26	DA	803	U
26	DA	805	G
26	DA	812	C
26	DA	819	A
26	DA	827	U
26	DA	828	U
26	DA	851	U
26	DA	852	G
26	DA	854	G
26	DA	857	C
26	DA	859	G

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Mol	Chain	Res	Type
26	DA	866	A
26	DA	868	U
26	DA	874	G
26	DA	879	G
26	DA	880	G
26	DA	882	G
26	DA	884	C
26	DA	886	C
26	DA	887	A
26	DA	888	C
26	DA	889	C
26	DA	890	A
26	DA	893	C
26	DA	896	A
26	DA	897	C
26	DA	898	C
26	DA	900	A
26	DA	901	A
26	DA	903	C
26	DA	910	A
26	DA	917	A
26	DA	932	G
26	DA	938	G
26	DA	941	A
26	DA	945	A
26	DA	946	G
26	DA	950	G
26	DA	952	G
26	DA	953	A
26	DA	958	U
26	DA	959	A
26	DA	961	C
26	DA	974	G
26	DA	975	C
26	DA	983	A
26	DA	996	A
26	DA	1005	C
26	DA	1006	C
26	DA	1012	U
26	DA	1013	C
26	DA	1017	G
26	DA	1022	G

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Mol	Chain	Res	Type
26	DA	1025	G
26	DA	1026	U
26	DA	1033	U
26	DA	1034	G
26	DA	1038	C
26	DA	1039	G
26	DA	1042	G
26	DA	1043	C
26	DA	1114	G
26	DA	1118	C
26	DA	1126	A
26	DA	1128	A
26	DA	1130	U
26	DA	1135	C
26	DA	1136	G
26	DA	1139	G
26	DA	1142(A)	A
26	DA	1144	G
26	DA	1171	G
26	DA	1180	C
26	DA	1196	C
26	DA	1205	U
26	DA	1210	A
26	DA	1211	U
26	DA	1220	A
26	DA	1221	C
26	DA	1229	G
26	DA	1242	A
26	DA	1247	A
26	DA	1253	A
26	DA	1256	G
26	DA	1271	G
26	DA	1272	A
26	DA	1273	U
26	DA	1287	A
26	DA	1300	U
26	DA	1301	A
26	DA	1303	G
26	DA	1305	C
26	DA	1314	C
26	DA	1332	G
26	DA	1352	U

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Mol	Chain	Res	Type
26	DA	1359	A
26	DA	1360	A
26	DA	1365	A
26	DA	1368	G
26	DA	1370	C
26	DA	1380	G
26	DA	1384	A
26	DA	1385	G
26	DA	1412	A
26	DA	1416	G
26	DA	1417	C
26	DA	1419	A
26	DA	1420	U
26	DA	1421	G
26	DA	1428	C
26	DA	1437	C
26	DA	1445	A
26	DA	1445(A)	C
26	DA	1449	A
26	DA	1450	G
26	DA	1459	G
26	DA	1467	C
26	DA	1471	A
26	DA	1482	G
26	DA	1490	A
26	DA	1493	C
26	DA	1494	A
26	DA	1495	A
26	DA	1496	A
26	DA	1497	U
26	DA	1508	A
26	DA	1509	C
26	DA	1509(A)	A
26	DA	1523	U
26	DA	1525	G
26	DA	1531	C
26	DA	1541	G
26	DA	1542	A
26	DA	1543	C
26	DA	1547	C
26	DA	1554	A
26	DA	1558	A

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Mol	Chain	Res	Type
26	DA	1559	G
26	DA	1566	A
26	DA	1569	A
26	DA	1578	U
26	DA	1580	A
26	DA	1583	A
26	DA	1584	C
26	DA	1586	A
26	DA	1595	G
26	DA	1598	C
26	DA	1608	A
26	DA	1609	A
26	DA	1610	A
26	DA	1612	C
26	DA	1639	U
26	DA	1640	C
26	DA	1647	G
26	DA	1648	C
26	DA	1654	A
26	DA	1674	G
26	DA	1696	G
26	DA	1700	A
26	DA	1703	G
26	DA	1721	G
26	DA	1722	A
26	DA	1740	G
26	DA	1756	G
26	DA	1758	G
26	DA	1763	G
26	DA	1764	G
26	DA	1773	A
26	DA	1780	A
26	DA	1782	C
26	DA	1791	A
26	DA	1800	C
26	DA	1801	G
26	DA	1812	A
26	DA	1816	G
26	DA	1835	G
26	DA	1836	C
26	DA	1847	A
26	DA	1848	A

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Mol	Chain	Res	Type
26	DA	1866	C
26	DA	1877	A
26	DA	1887	C
26	DA	1889	A
26	DA	1895	C
26	DA	1900	A
26	DA	1906	G
26	DA	1914	C
26	DA	1929	G
26	DA	1930	G
26	DA	1931	U
26	DA	1936	A
26	DA	1937	A
26	DA	1938	A
26	DA	1955	U
26	DA	1963	U
26	DA	1964	G
26	DA	1967	C
26	DA	1970	A
26	DA	1971	A
26	DA	1972	A
26	DA	1993	U
26	DA	1997	G
26	DA	2020	A
26	DA	2023	G
26	DA	2031	A
26	DA	2032	G
26	DA	2033	A
26	DA	2043	C
26	DA	2046	G
26	DA	2055	C
26	DA	2056	G
26	DA	2060	A
26	DA	2061	G
26	DA	2062	A
26	DA	2069	G
26	DA	2082	A
26	DA	2093	G
26	DA	2095	C
26	DA	2096	U
26	DA	2099	U
26	DA	2101	G

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Mol	Chain	Res	Type
26	DA	2102	U
26	DA	2103	C
26	DA	2104	G
26	DA	2105	C
26	DA	2108	C
26	DA	2111	C
26	DA	2112	G
26	DA	2113	U
26	DA	2115	G
26	DA	2116	G
26	DA	2117	A
26	DA	2119	A
26	DA	2122	U
26	DA	2124	G
26	DA	2125	G
26	DA	2126	A
26	DA	2127	G
26	DA	2129	C
26	DA	2130	U
26	DA	2131	G
26	DA	2132	U
26	DA	2133	G
26	DA	2134	A
26	DA	2135	A
26	DA	2136	C
26	DA	2137	C
26	DA	2138	C
26	DA	2139	C
26	DA	2143	C
26	DA	2145	C
26	DA	2146	C
26	DA	2148	G
26	DA	2150	U
26	DA	2151	G
26	DA	2153	G
26	DA	2154	G
26	DA	2155	G
26	DA	2157	G
26	DA	2158	A
26	DA	2159	G
26	DA	2160	G
26	DA	2163	C

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Mol	Chain	Res	Type
26	DA	2164	C
26	DA	2165	G
26	DA	2167	U
26	DA	2168	G
26	DA	2169	A
26	DA	2170	A
26	DA	2172	U
26	DA	2173	A
26	DA	2174	C
26	DA	2177	C
26	DA	2178	C
26	DA	2181	G
26	DA	2184	G
26	DA	2185	C
26	DA	2186	G
26	DA	2189	U
26	DA	2192	G
26	DA	2193	G
26	DA	2198	A
26	DA	2206	G
26	DA	2207	G
26	DA	2208	A
26	DA	2218	U
26	DA	2219	G
26	DA	2225	A
26	DA	2235	G
26	DA	2238	G
26	DA	2239	G
26	DA	2259	G
26	DA	2273	A
26	DA	2275	C
26	DA	2278	A
26	DA	2280	G
26	DA	2283	C
26	DA	2287	A
26	DA	2288	A
26	DA	2294	C
26	DA	2299	G
26	DA	2302	G
26	DA	2303	G
26	DA	2305	A
26	DA	2308	G

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Mol	Chain	Res	Type
26	DA	2312	U
26	DA	2318	G
26	DA	2319	G
26	DA	2320	A
26	DA	2321	G
26	DA	2325	G
26	DA	2327	A
26	DA	2328	A
26	DA	2334	G
26	DA	2336	A
26	DA	2339	G
26	DA	2343	C
26	DA	2347	C
26	DA	2350	C
26	DA	2354	G
26	DA	2366	A
26	DA	2376	A
26	DA	2383	G
26	DA	2385	C
26	DA	2388	A
26	DA	2400	G
26	DA	2406	U
26	DA	2410	G
26	DA	2422	A
26	DA	2425	A
26	DA	2429	G
26	DA	2430	A
26	DA	2435	A
26	DA	2439	A
26	DA	2441	C
26	DA	2445	G
26	DA	2448	A
26	DA	2465	C
26	DA	2468	G
26	DA	2469	A
26	DA	2474	C
26	DA	2476	A
26	DA	2478	A
26	DA	2490	G
26	DA	2494	G
26	DA	2497	A
26	DA	2502	G

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Mol	Chain	Res	Type
26	DA	2505	G
26	DA	2506	U
26	DA	2518	A
26	DA	2529	G
26	DA	2549	G
26	DA	2554	U
26	DA	2555	U
26	DA	2566	A
26	DA	2567	G
26	DA	2573	C
26	DA	2586	C
26	DA	2602	A
26	DA	2603	G
26	DA	2609	U
26	DA	2611	U
26	DA	2612	C
26	DA	2615	U
26	DA	2629	A
26	DA	2630	G
26	DA	2652	C
26	DA	2654	A
26	DA	2663	G
26	DA	2669	G
26	DA	2689	U
26	DA	2690	C
26	DA	2691	C
26	DA	2703	C
26	DA	2712(A)	A
26	DA	2713	A
26	DA	2714	G
26	DA	2726	U
26	DA	2733	A
26	DA	2734	A
26	DA	2751	G
26	DA	2757	A
26	DA	2758	A
26	DA	2760	C
26	DA	2764	A
26	DA	2765	A
26	DA	2766	G
26	DA	2778	A
26	DA	2784	C

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Mol	Chain	Res	Type
26	DA	2793	G
26	DA	2794	C
26	DA	2809	A
26	DA	2818	G
26	DA	2820	A
26	DA	2821	A
26	DA	2833	G
26	DA	2834	G
26	DA	2835	A
26	DA	2872	G
26	DA	2873	A
26	DA	2879	C
26	DA	2880	C
26	DA	2892	A
26	DA	2894	G
26	DA	2895	U
26	DA	2897	U
27	DB	2	C
27	DB	7	G
27	DB	8	U
27	DB	34	U
27	DB	42	C
27	DB	56	G
27	DB	73	A
27	DB	75	G
27	DB	85	G
27	DB	90	A
27	DB	93	G
27	DB	106	G
27	DB	108	U
27	DB	110	G
27	DB	111	G
27	DB	112	U
27	DB	120	A

All (126) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	96	U
1	AA	115	G
1	AA	266	G
1	AA	347	G

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Mol	Chain	Res	Type
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	839	U
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1181	G
1	AA	1201	A
1	AA	1256	A
1	AA	1285	A
1	AA	1442	G
1	AA	1492	A
23	AW	13	C
23	AW	22	G
25	AY	19	G
25	AY	21	A
25	AY	25	C
25	AY	58	A
26	BA	71	A
26	BA	196	A
26	BA	271(J)	C
26	BA	271(K)	U
26	BA	271(M)	G
26	BA	278	A
26	BA	746	A
26	BA	764	A
26	BA	774	A
26	BA	899	A
26	BA	974	G
26	BA	1047	G
26	BA	1142(A)	A
26	BA	1174	A
26	BA	1175	U

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Mol	Chain	Res	Type
26	BA	1176	G
26	BA	1210	A
26	BA	1300	U
26	BA	1301	A
26	BA	1379	A
26	BA	1420	U
26	BA	1530	C
26	BA	1653	G
26	BA	1992	G
26	BA	2110	G
26	BA	2126	A
26	BA	2181	G
26	BA	2183	C
26	BA	2187	G
26	BA	2406	U
26	BA	2430	A
26	BA	2689	U
26	BA	2756	U
26	BA	2893	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	840	C
1	CA	913	A
1	CA	991	U
1	CA	992	U
1	CA	1027	C
1	CA	1054	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1181	G
1	CA	1183	A
1	CA	1201	A

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Mol	Chain	Res	Type
1	CA	1212	U
1	CA	1256	A
1	CA	1299	A
1	CA	1442	G
1	CA	1492	A
23	CW	4	C
23	CW	13	C
25	CY	46	7MG
26	DA	271(K)	U
26	DA	271(M)	G
26	DA	277	C
26	DA	587	C
26	DA	752	A
26	DA	764	A
26	DA	774	A
26	DA	827	U
26	DA	856	C
26	DA	900	A
26	DA	1210	A
26	DA	1300	U
26	DA	1379	A
26	DA	1420	U
26	DA	1427	A
26	DA	1493	C
26	DA	1530	C
26	DA	1558	A
26	DA	1653	G
26	DA	1913	A
26	DA	1992	G
26	DA	2110	G
26	DA	2126	A
26	DA	2136	C
26	DA	2169	A
26	DA	2177	C
26	DA	2318	G
26	DA	2689	U
26	DA	2756	U
26	DA	2893	G

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

38 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$
25	MIA	CY	37	25	21,24,32	1.65	4 (19%)	30,35,47	2.01	9 (30%)
25	5MU	AY	54	25	19,22,23	1.49	5 (26%)	27,32,35	2.16	7 (25%)
23	PSU	CW	55	23	18,21,22	1.37	2 (11%)	21,30,33	2.11	3 (14%)
25	PSU	AY	39	25	18,21,22	1.57	4 (22%)	21,30,33	1.95	5 (23%)
23	5MU	CW	54	23	19,22,23	1.34	4 (21%)	27,32,35	2.00	7 (25%)
25	4SU	AY	8	25	18,21,22	1.87	5 (27%)	25,30,33	2.06	5 (20%)
23	PSU	CW	32	23	18,21,22	1.34	2 (11%)	21,30,33	1.99	3 (14%)
23	4SU	CW	8	23	18,21,22	1.67	4 (22%)	25,30,33	2.41	5 (20%)
23	7MG	CW	46	23	23,26,27	1.41	4 (17%)	27,39,42	2.51	6 (22%)
24	5MC	CX	32	24	19,22,23	1.64	3 (15%)	26,32,35	1.17	3 (11%)
24	5MU	AX	54	24,57	19,22,23	1.43	5 (26%)	27,32,35	1.96	5 (18%)
25	MIA	AY	37	25	21,24,32	1.63	4 (19%)	30,35,47	2.02	8 (26%)
24	4SU	AX	8	24	18,21,22	2.28	5 (27%)	25,30,33	1.72	6 (24%)
23	31M	AW	76	23	41,44,45	1.46	6 (14%)	50,61,64	1.72	11 (22%)
23	PSU	AW	39	23	18,21,22	1.40	2 (11%)	21,30,33	1.85	4 (19%)
25	7MG	CY	46	25	23,26,27	1.42	5 (21%)	27,39,42	2.67	9 (33%)
23	PSU	AW	32	23	18,21,22	1.36	2 (11%)	21,30,33	2.01	4 (19%)
24	5MC	AX	32	24	19,22,23	1.69	3 (15%)	26,32,35	1.28	3 (11%)
25	PSU	AY	55	25	18,21,22	1.37	3 (16%)	21,30,33	2.34	6 (28%)
23	5MU	AW	54	23	19,22,23	1.39	5 (26%)	27,32,35	1.93	6 (22%)
23	4SU	AW	8	23	18,21,22	1.80	4 (22%)	25,30,33	2.15	5 (20%)
25	PSU	CY	55	25	18,21,22	1.46	4 (22%)	21,30,33	2.45	6 (28%)
23	PSU	AW	55	23	18,21,22	1.39	2 (11%)	21,30,33	1.95	3 (14%)
25	PSU	AY	32	25	18,21,22	1.38	2 (11%)	21,30,33	2.01	4 (19%)
24	PSU	AX	55	24,57	18,21,22	1.33	2 (11%)	21,30,33	2.06	4 (19%)
25	7MG	AY	46	25	23,26,27	1.29	3 (13%)	27,39,42	2.94	7 (25%)
23	7MG	AW	46	23	23,26,27	1.36	3 (13%)	27,39,42	2.63	7 (25%)
24	PSU	CX	55	24	18,21,22	1.35	2 (11%)	21,30,33	2.00	4 (19%)
23	31M	CW	76	23	41,44,45	1.38	5 (12%)	50,61,64	1.66	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	5MU	CY	54	25	19,22,23	1.34	4 (21%)	27,32,35	2.19	6 (22%)
23	PSU	CW	39	23	18,21,22	1.35	2 (11%)	21,30,33	1.86	4 (19%)
24	5MU	CX	54	24	19,22,23	1.39	5 (26%)	27,32,35	2.30	6 (22%)
23	MIA	CW	37	23	21,24,32	1.60	4 (19%)	30,35,47	2.04	7 (23%)
24	4SU	CX	8	24	18,21,22	2.04	6 (33%)	25,30,33	1.37	4 (16%)
25	PSU	CY	39	25	18,21,22	1.44	3 (16%)	21,30,33	2.33	3 (14%)
25	4SU	CY	8	25	18,21,22	1.72	4 (22%)	25,30,33	3.08	6 (24%)
23	MIA	AW	37	23	28,31,32	2.30	7 (25%)	38,44,47	2.73	13 (34%)
25	PSU	CY	32	25	18,21,22	1.38	2 (11%)	21,30,33	1.99	4 (19%)

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
25	MIA	CY	37	25	-	3/7/25/34	0/3/3/3
25	5MU	AY	54	25	-	2/7/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
25	PSU	AY	39	25	-	2/7/25/26	0/2/2/2
23	5MU	CW	54	23	-	0/7/25/26	0/2/2/2
25	4SU	AY	8	25	-	1/7/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/7/25/26	0/2/2/2
23	4SU	CW	8	23	-	0/7/25/26	0/2/2/2
23	7MG	CW	46	23	-	3/7/37/38	0/3/3/3
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
24	5MU	AX	54	24,57	-	0/7/25/26	0/2/2/2
25	MIA	AY	37	25	-	2/7/25/34	0/3/3/3
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
23	31M	AW	76	23	-	8/31/49/50	0/4/4/4
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
25	7MG	CY	46	25	-	4/7/37/38	0/3/3/3
23	PSU	AW	32	23	-	0/7/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/7/25/26	0/2/2/2
25	PSU	AY	55	25	-	2/7/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	PSU	CY	55	25	-	4/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
25	PSU	AY	32	25	-	1/7/25/26	0/2/2/2
24	PSU	AX	55	24,57	-	0/7/25/26	0/2/2/2
25	7MG	AY	46	25	-	2/7/37/38	0/3/3/3
23	7MG	AW	46	23	-	3/7/37/38	0/3/3/3
24	PSU	CX	55	24	-	1/7/25/26	0/2/2/2
23	31M	CW	76	23	-	11/31/49/50	0/4/4/4
25	5MU	CY	54	25	-	2/7/25/26	0/2/2/2
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	0/7/25/34	0/3/3/3
24	4SU	CX	8	24	-	0/7/25/26	0/2/2/2
25	PSU	CY	39	25	-	2/7/25/26	0/2/2/2
25	4SU	CY	8	25	-	2/7/25/26	0/2/2/2
23	MIA	AW	37	23	-	1/15/33/34	0/3/3/3
25	PSU	CY	32	25	-	1/7/25/26	0/2/2/2

All (141) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C13-C14	6.94	1.53	1.32
23	AW	37	MIA	C2-S10	-6.49	1.70	1.75
24	AX	32	5MC	C5-C4	6.12	1.48	1.44
24	CX	32	5MC	C5-C4	5.90	1.48	1.44
24	AX	8	4SU	C4-N3	-5.37	1.32	1.37
25	CY	37	MIA	C5-C4	5.31	1.48	1.39
25	CY	8	4SU	C4-S4	-5.14	1.59	1.68
23	AW	76	31M	CB-CG	-5.14	1.39	1.51
25	AY	37	MIA	C5-C4	5.09	1.48	1.39
23	CW	37	MIA	C5-C4	5.02	1.48	1.39
23	CW	76	31M	CB-CG	-4.95	1.39	1.51
25	AY	8	4SU	C4-S4	-4.87	1.60	1.68
23	AW	8	4SU	C4-S4	-4.82	1.60	1.68
24	AX	8	4SU	C4-S4	-4.80	1.60	1.68
23	AW	37	MIA	C5-C4	4.75	1.47	1.39
23	CW	8	4SU	C4-S4	-4.72	1.60	1.68
24	CX	8	4SU	C4-S4	-4.71	1.60	1.68
24	CX	8	4SU	C4-N3	-4.52	1.32	1.37
25	AY	39	PSU	C6-C5	4.40	1.40	1.35
24	AX	8	4SU	C2-N3	-4.04	1.30	1.38
23	CW	55	PSU	C6-C5	4.01	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	76	31M	C5-N7	-3.91	1.32	1.39
25	CY	32	PSU	C6-C5	3.87	1.39	1.35
23	AW	55	PSU	C6-C5	3.82	1.39	1.35
25	AY	32	PSU	C6-C5	3.74	1.39	1.35
24	CX	55	PSU	C6-C5	3.63	1.39	1.35
24	AX	8	4SU	C5-C4	-3.60	1.38	1.42
23	CW	39	PSU	C6-C5	3.60	1.39	1.35
23	CW	32	PSU	C6-C5	3.59	1.39	1.35
23	AW	76	31M	C5-C4	-3.52	1.32	1.39
25	CY	46	7MG	C4-N9	-3.52	1.33	1.37
25	AY	8	4SU	C4-N3	-3.50	1.34	1.37
23	CW	76	31M	C5-C4	-3.47	1.32	1.39
23	AW	39	PSU	C6-C5	3.45	1.39	1.35
25	CY	39	PSU	C6-C5	3.42	1.39	1.35
23	AW	46	7MG	C5-C4	3.39	1.48	1.37
23	CW	46	7MG	C5-C4	3.35	1.48	1.37
23	AW	32	PSU	C6-C5	3.35	1.39	1.35
25	AY	46	7MG	C5-C4	3.33	1.47	1.37
25	CY	55	PSU	C6-C5	3.33	1.39	1.35
25	AY	55	PSU	C6-C5	3.30	1.38	1.35
25	CY	46	7MG	C5-C4	3.28	1.47	1.37
23	CW	46	7MG	C4-N9	-3.28	1.33	1.37
24	CX	8	4SU	C5-C4	-3.26	1.38	1.42
24	AX	55	PSU	C6-C5	3.05	1.38	1.35
25	AY	54	5MU	C2-N1	3.03	1.43	1.38
23	AW	8	4SU	C4-N3	-3.02	1.34	1.37
25	AY	37	MIA	C5-C6	3.01	1.49	1.41
24	CX	54	5MU	C6-C5	3.00	1.39	1.34
23	AW	76	31M	C5-N7	-2.99	1.33	1.39
23	AW	54	5MU	C6-C5	2.97	1.39	1.34
24	AX	54	5MU	C6-C5	2.89	1.39	1.34
23	AW	37	MIA	C5-C6	2.87	1.48	1.41
23	CW	37	MIA	C5-C6	2.87	1.49	1.41
25	CY	55	PSU	C4-N3	-2.85	1.33	1.38
23	AW	46	7MG	C4-N9	-2.84	1.34	1.37
25	CY	8	4SU	C5-C4	-2.84	1.39	1.42
23	AW	39	PSU	C4-N3	-2.82	1.33	1.38
23	AW	76	31M	C8-N9	-2.82	1.32	1.37
23	AW	76	31M	C5-C6	-2.81	1.33	1.41
24	AX	54	5MU	C4-N3	-2.76	1.33	1.38
25	CY	37	MIA	C5-C6	2.74	1.48	1.41
24	CX	32	5MC	C6-C5	2.74	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	AY	54	5MU	C4-C5	2.74	1.49	1.44
25	AY	54	5MU	C6-C5	2.72	1.39	1.34
25	AY	8	4SU	C5-C4	-2.71	1.39	1.42
24	AX	32	5MC	C6-N1	-2.70	1.33	1.38
25	CY	54	5MU	C4-N3	-2.69	1.33	1.38
23	AW	8	4SU	C5-C4	-2.69	1.39	1.42
23	CW	8	4SU	C4-N3	-2.69	1.34	1.37
24	CX	54	5MU	C4-N3	-2.67	1.33	1.38
25	CY	46	7MG	C8-N9	2.65	1.47	1.45
23	CW	54	5MU	C6-C5	2.65	1.38	1.34
23	AW	32	PSU	C4-N3	-2.60	1.34	1.38
25	AY	55	PSU	C4-N3	-2.57	1.34	1.38
23	CW	76	31M	C5-C6	-2.57	1.33	1.41
25	AY	32	PSU	C4-N3	-2.56	1.34	1.38
23	AW	55	PSU	C4-N3	-2.55	1.34	1.38
24	CX	8	4SU	O2-C2	2.53	1.27	1.23
23	CW	46	7MG	C8-N9	2.51	1.47	1.45
23	AW	54	5MU	C4-N3	-2.51	1.34	1.38
24	AX	55	PSU	C4-N3	-2.49	1.34	1.38
23	CW	54	5MU	C4-C5	2.47	1.48	1.44
25	CY	54	5MU	C2-N3	-2.47	1.33	1.38
23	AW	76	31M	C2-N1	2.45	1.38	1.33
23	AW	8	4SU	C2-N1	2.44	1.42	1.38
24	CX	54	5MU	C4-C5	2.43	1.48	1.44
23	CW	39	PSU	C4-N3	-2.41	1.34	1.38
25	CY	54	5MU	C6-C5	2.41	1.38	1.34
23	AW	37	MIA	C8-N7	2.40	1.36	1.31
25	AY	55	PSU	O4'-C1'	-2.39	1.40	1.43
25	AY	8	4SU	C2-N1	2.39	1.42	1.38
25	CY	55	PSU	C2-N3	-2.38	1.33	1.37
23	CW	54	5MU	C2-N1	2.38	1.42	1.38
24	AX	32	5MC	C6-C5	2.37	1.38	1.34
25	AY	37	MIA	C8-N7	2.37	1.36	1.31
25	AY	46	7MG	C8-N9	2.36	1.47	1.45
24	CX	55	PSU	C4-N3	-2.36	1.34	1.38
23	CW	55	PSU	C4-N3	-2.36	1.34	1.38
23	AW	46	7MG	C6-N1	-2.35	1.34	1.38
25	AY	46	7MG	C6-N1	-2.32	1.34	1.38
25	CY	46	7MG	C6-N1	-2.32	1.34	1.38
25	AY	39	PSU	C4-N3	-2.31	1.34	1.38
25	AY	39	PSU	O4'-C1'	-2.31	1.40	1.43
23	CW	37	MIA	C8-N7	2.30	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	32	PSU	C4-N3	-2.30	1.34	1.38
24	AX	54	5MU	C2-N1	2.30	1.42	1.38
25	CY	39	PSU	C4-N3	-2.30	1.34	1.38
23	CW	8	4SU	C2-N1	2.29	1.42	1.38
24	CX	32	5MC	C6-N1	-2.29	1.34	1.38
24	AX	54	5MU	C4-C5	2.28	1.48	1.44
25	AY	8	4SU	C2-N3	-2.27	1.34	1.38
24	AX	8	4SU	O2-C2	2.27	1.27	1.23
25	CY	8	4SU	C2-N1	2.26	1.42	1.38
25	CY	37	MIA	C8-N7	2.26	1.36	1.31
24	CX	8	4SU	C2-N3	-2.24	1.34	1.38
25	CY	54	5MU	C6-N1	-2.22	1.34	1.38
23	AW	54	5MU	C2-N1	2.22	1.41	1.38
25	CY	55	PSU	C4-C5	2.21	1.50	1.44
23	AW	37	MIA	C5-N7	-2.19	1.35	1.39
23	AW	54	5MU	C4-C5	2.17	1.48	1.44
25	AY	54	5MU	C6-N1	-2.16	1.34	1.38
25	AY	39	PSU	C2-N1	-2.16	1.33	1.36
23	CW	8	4SU	C5-C4	-2.15	1.39	1.42
25	CY	46	7MG	C5-C6	2.15	1.48	1.43
23	CW	46	7MG	C6-N1	-2.15	1.34	1.38
23	CW	37	MIA	C5-N7	-2.15	1.35	1.39
24	CX	8	4SU	C2-N1	2.14	1.41	1.38
25	CY	37	MIA	C5-N7	-2.13	1.35	1.39
24	AX	54	5MU	C2-N3	-2.13	1.34	1.38
25	AY	54	5MU	C4-N3	-2.12	1.34	1.38
24	CX	54	5MU	C6-N1	-2.11	1.34	1.38
25	CY	8	4SU	C4-N3	-2.11	1.35	1.37
23	CW	54	5MU	C4-N3	-2.11	1.34	1.38
25	CY	32	PSU	C4-N3	-2.10	1.34	1.38
23	AW	54	5MU	C2-N3	-2.06	1.34	1.38
23	AW	37	MIA	C4-N9	-2.04	1.33	1.37
23	CW	76	31M	C3'-N3'	2.04	1.49	1.45
25	AY	37	MIA	C5-N7	-2.03	1.35	1.39
24	CX	54	5MU	C2-N3	-2.02	1.34	1.38
25	CY	39	PSU	C2-N1	-2.02	1.34	1.36

All (218) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	46	7MG	N9-C4-N3	10.29	140.54	125.46
23	AW	37	MIA	C12-C13-C14	-9.12	110.65	127.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	46	7MG	N9-C4-N3	9.11	138.81	125.46
25	CY	8	4SU	C4-N3-C2	-8.94	118.75	127.31
23	CW	46	7MG	N9-C4-N3	8.27	137.58	125.46
25	CY	46	7MG	N9-C4-N3	8.09	137.32	125.46
23	AW	37	MIA	C5-C4-N3	-7.56	119.22	127.18
23	CW	8	4SU	C4-N3-C2	-7.44	120.18	127.31
25	CY	39	PSU	N1-C2-N3	7.21	122.77	115.17
25	AY	55	PSU	N1-C2-N3	7.04	122.59	115.17
25	CY	8	4SU	C5-C4-N3	6.97	121.24	114.75
25	CY	8	4SU	C5-C4-S4	-6.92	116.40	124.31
25	CY	55	PSU	N1-C2-N3	6.78	122.33	115.17
23	CW	55	PSU	N1-C2-N3	6.32	121.84	115.17
24	CX	55	PSU	N1-C2-N3	6.28	121.79	115.17
25	AY	46	7MG	C5-C4-N3	-6.25	116.40	128.13
23	CW	32	PSU	N1-C2-N3	6.18	121.69	115.17
24	AX	55	PSU	N1-C2-N3	6.15	121.65	115.17
24	CX	54	5MU	N3-C2-N1	6.15	122.89	114.89
23	AW	8	4SU	C4-N3-C2	-6.14	121.43	127.31
23	AW	32	PSU	N1-C2-N3	6.13	121.64	115.17
25	AY	32	PSU	N1-C2-N3	6.10	121.60	115.17
23	CW	37	MIA	C5-C4-N3	-6.06	118.37	126.72
23	AW	55	PSU	N1-C2-N3	6.05	121.55	115.17
25	CY	32	PSU	N1-C2-N3	6.03	121.53	115.17
25	CY	46	7MG	N9-C8-N7	-5.92	94.99	103.37
23	AW	39	PSU	N1-C2-N3	5.91	121.40	115.17
23	AW	8	4SU	C5-C4-N3	5.79	120.13	114.75
23	CW	39	PSU	N1-C2-N3	5.74	121.22	115.17
25	AY	37	MIA	C5-C4-N3	-5.74	118.81	126.72
23	AW	37	MIA	N3-C4-N9	5.70	134.22	126.99
25	AY	39	PSU	N1-C2-N3	5.65	121.13	115.17
25	AY	8	4SU	C4-N3-C2	-5.61	121.93	127.31
23	AW	76	31M	N1-C2-N3	-5.61	120.09	128.58
24	CX	54	5MU	C4-N3-C2	-5.60	120.00	127.34
23	CW	8	4SU	C5-C4-N3	5.59	119.95	114.75
25	CY	37	MIA	C5-C4-N3	-5.55	119.07	126.72
25	AY	8	4SU	C5-C4-N3	5.49	119.85	114.75
23	AW	46	7MG	N9-C8-N7	-5.47	95.63	103.37
23	CW	76	31M	N1-C2-N3	-5.42	120.38	128.58
25	CY	55	PSU	C4-N3-C2	-5.25	119.14	126.37
23	CW	46	7MG	C5-C4-N3	-5.25	118.28	128.13
25	CY	54	5MU	C5-C4-N3	5.23	119.87	115.32
25	CY	54	5MU	C4-N3-C2	-5.15	120.58	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	54	5MU	C4-N3-C2	-5.13	120.61	127.34
23	CW	46	7MG	N9-C8-N7	-5.12	96.12	103.37
25	CY	39	PSU	O2-C2-N1	-5.09	117.54	122.79
25	CY	54	5MU	O4-C4-C5	-5.09	119.10	124.92
23	AW	46	7MG	C5-C4-N3	-5.04	118.68	128.13
25	AY	46	7MG	C2-N3-C4	4.98	120.88	112.30
25	CY	37	MIA	N3-C4-N9	4.95	135.58	127.17
23	CW	37	MIA	N3-C4-N9	4.91	135.52	127.17
25	AY	46	7MG	N9-C8-N7	-4.91	96.42	103.37
25	CY	46	7MG	C5-C4-N3	-4.88	118.96	128.13
23	CW	76	31M	C5-C4-N3	-4.82	120.08	126.72
24	AX	54	5MU	N3-C2-N1	4.82	121.17	114.89
25	CY	39	PSU	C4-N3-C2	-4.71	119.89	126.37
25	AY	54	5MU	C5-C4-N3	4.70	119.41	115.32
23	CW	8	4SU	N3-C2-N1	4.68	120.99	114.89
25	AY	37	MIA	N3-C4-N9	4.67	135.10	127.17
24	AX	54	5MU	C4-N3-C2	-4.66	121.23	127.34
23	AW	54	5MU	N3-C2-N1	4.64	120.93	114.89
23	CW	54	5MU	C4-N3-C2	-4.63	121.27	127.34
25	AY	55	PSU	C4-N3-C2	-4.59	120.05	126.37
25	CY	8	4SU	N3-C2-N1	4.59	120.86	114.89
25	AY	54	5MU	N3-C2-N1	4.57	120.84	114.89
23	AW	54	5MU	C4-N3-C2	-4.50	121.44	127.34
23	CW	54	5MU	N3-C2-N1	4.50	120.74	114.89
25	CY	54	5MU	N3-C2-N1	4.47	120.71	114.89
25	CY	46	7MG	C2-N3-C4	4.46	119.98	112.30
24	AX	8	4SU	C6-C5-C4	-4.45	116.10	119.95
25	CY	8	4SU	O2-C2-N1	-4.44	117.02	122.80
24	AX	54	5MU	C5-C4-N3	4.39	119.14	115.32
23	CW	46	7MG	C2-N3-C4	4.35	119.79	112.30
25	AY	54	5MU	O4-C4-C5	-4.34	119.95	124.92
25	CY	55	PSU	O2-C2-N1	-4.34	118.31	122.79
25	AY	32	PSU	C4-N3-C2	-4.33	120.41	126.37
23	AW	46	7MG	C2-N3-C4	4.27	119.66	112.30
23	CW	54	5MU	O4-C4-C5	-4.24	120.07	124.92
24	AX	55	PSU	C4-N3-C2	-4.22	120.55	126.37
23	CW	55	PSU	C4-N3-C2	-4.18	120.61	126.37
24	CX	54	5MU	C5-C4-N3	4.18	118.96	115.32
23	AW	54	5MU	O4-C4-C5	-4.18	120.14	124.92
24	CX	55	PSU	C4-N3-C2	-4.17	120.62	126.37
25	AY	55	PSU	O2-C2-N1	-4.12	118.55	122.79
23	AW	32	PSU	C4-N3-C2	-4.11	120.71	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	76	31M	C5-C4-N3	-4.09	121.09	126.72
23	AW	54	5MU	C5-C4-N3	4.09	118.88	115.32
24	CX	54	5MU	O2-C2-N1	-4.07	117.50	122.80
23	CW	54	5MU	C5-C4-N3	4.06	118.86	115.32
23	CW	8	4SU	C5-C4-S4	-4.04	119.69	124.31
23	CW	32	PSU	C4-N3-C2	-4.04	120.81	126.37
24	AX	32	5MC	C5-C6-N1	-4.03	118.94	123.31
24	CX	54	5MU	O4-C4-C5	-3.98	120.36	124.92
25	AY	39	PSU	O2-C2-N1	-3.95	118.71	122.79
23	AW	8	4SU	C5-C4-S4	-3.90	119.86	124.31
23	CW	55	PSU	O2-C2-N1	-3.87	118.80	122.79
24	AX	8	4SU	O2-C2-N1	3.86	127.82	122.80
23	AW	37	MIA	C16-C14-C13	-3.85	111.09	122.66
25	CY	54	5MU	C5-C6-N1	-3.79	119.20	123.31
25	CY	32	PSU	O2-C2-N1	-3.79	118.88	122.79
23	AW	8	4SU	N3-C2-N1	3.78	119.81	114.89
24	AX	8	4SU	C5-C4-N3	3.75	118.24	114.75
24	CX	8	4SU	C5-C4-N3	3.73	118.22	114.75
25	CY	32	PSU	C4-N3-C2	-3.73	121.23	126.37
23	CW	39	PSU	C4-N3-C2	-3.72	121.24	126.37
23	AW	55	PSU	C4-N3-C2	-3.72	121.25	126.37
23	AW	37	MIA	C15-C14-C13	-3.69	111.57	122.66
24	AX	54	5MU	O4-C4-C5	-3.68	120.71	124.92
23	CW	37	MIA	C2-N3-C4	3.67	120.79	111.83
23	AW	37	MIA	C6-C5-N7	3.63	136.39	132.43
24	AX	55	PSU	O2-C2-N1	-3.61	119.07	122.79
25	AY	37	MIA	C2-N3-C4	3.59	120.61	111.83
23	CW	32	PSU	O2-C2-N1	-3.54	119.14	122.79
25	AY	8	4SU	N3-C2-N1	3.54	119.50	114.89
23	AW	76	31M	C5-N7-C8	3.53	109.00	103.45
23	AW	76	31M	N9-C8-N7	-3.53	108.92	113.94
25	CY	55	PSU	C6-C5-C4	-3.53	115.79	118.17
23	AW	37	MIA	C4-C5-N7	-3.52	106.56	110.58
25	AY	37	MIA	C4-C5-N7	-3.51	106.56	110.58
23	AW	32	PSU	O2-C2-N1	-3.48	119.20	122.79
23	AW	39	PSU	C4-N3-C2	-3.48	121.58	126.37
23	CW	37	MIA	C4-C5-N7	-3.48	106.61	110.58
23	AW	37	MIA	C2-N3-C4	3.44	121.29	112.29
24	CX	32	5MC	C5-C6-N1	-3.35	119.68	123.31
24	CX	54	5MU	C5-C6-N1	-3.33	119.69	123.31
25	CY	37	MIA	C2-N3-C4	3.33	119.96	111.83
25	AY	46	7MG	C5-C6-N1	3.26	116.69	110.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	AY	37	MIA	N3-C2-N1	-3.26	123.64	128.58
23	AW	55	PSU	O2-C2-N1	-3.24	119.45	122.79
23	CW	76	31M	N9-C8-N7	-3.20	109.40	113.94
23	CW	37	MIA	N3-C2-N1	-3.19	123.75	128.58
23	AW	76	31M	OTM-CTM-CAM	-3.19	113.55	120.28
23	CW	76	31M	C2-N3-C4	3.19	119.61	111.83
23	AW	76	31M	CAM-CTM-N	3.18	120.52	116.21
25	AY	54	5MU	C5-C6-N1	-3.16	119.88	123.31
25	CY	37	MIA	N3-C2-N1	-3.16	123.80	128.58
23	AW	54	5MU	C5-C6-N1	-3.13	119.91	123.31
24	CX	55	PSU	O2-C2-N1	-3.12	119.57	122.79
23	CW	76	31M	OTM-CTM-CAM	-3.08	113.79	120.28
23	CW	8	4SU	O2-C2-N1	-3.07	118.80	122.80
23	CW	76	31M	C5-C4-N9	3.07	109.16	105.81
24	AX	54	5MU	C5-C6-N1	-3.06	119.99	123.31
24	CX	8	4SU	C1'-N1-C2	3.05	123.08	117.59
25	AY	8	4SU	C5-C4-S4	-3.03	120.85	124.31
25	CY	37	MIA	C4-N9-C8	3.02	108.91	105.74
23	AW	76	31M	C2-N3-C4	2.99	119.14	111.83
23	AW	46	7MG	C5-C4-N9	-2.98	102.51	106.33
25	AY	39	PSU	C6-C5-C4	-2.95	116.18	118.17
25	AY	46	7MG	O6-C6-C5	-2.93	120.44	127.62
25	AY	8	4SU	C1'-N1-C2	2.90	122.79	117.59
25	CY	37	MIA	C4-C5-N7	-2.87	107.30	110.58
24	AX	32	5MC	C5-C4-N3	-2.85	118.83	121.75
23	CW	76	31M	C5-N7-C8	2.83	107.90	103.45
25	AY	37	MIA	C4-N9-C8	2.82	108.70	105.74
24	CX	8	4SU	C6-C5-C4	-2.82	117.51	119.95
23	CW	39	PSU	O2-C2-N1	-2.81	119.89	122.79
25	AY	39	PSU	C6-N1-C2	-2.81	120.08	122.69
25	AY	32	PSU	O2-C2-N1	-2.75	119.95	122.79
24	CX	32	5MC	C5-C4-N3	-2.73	118.95	121.75
25	CY	46	7MG	C5-C6-N1	2.73	115.75	110.94
23	AW	76	31M	C4-C5-N7	-2.72	107.47	110.58
25	CY	46	7MG	O4'-C1'-N9	-2.71	105.60	109.30
23	AW	39	PSU	O2-C2-N1	-2.68	120.03	122.79
23	CW	46	7MG	C5-C6-N1	2.68	115.65	110.94
25	AY	54	5MU	C5M-C5-C4	2.67	121.63	118.78
23	CW	54	5MU	C5-C6-N1	-2.65	120.43	123.31
23	CW	76	31M	CAM-CTM-N	2.63	119.77	116.21
25	AY	37	MIA	C5-N7-C8	2.60	107.54	103.45
23	AW	76	31M	O4'-C4'-C3'	2.60	107.90	104.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	37	MIA	N3-C2-N1	-2.60	122.26	127.00
23	CW	37	MIA	C5-N7-C8	2.58	107.51	103.45
25	AY	46	7MG	C5-C4-N9	-2.57	103.05	106.33
23	AW	37	MIA	C2-N1-C6	2.55	122.38	117.54
24	AX	8	4SU	S4-C4-N3	-2.52	117.56	120.20
23	CW	37	MIA	C4-N9-C8	2.52	108.39	105.74
23	CW	54	5MU	C5M-C5-C4	2.52	121.47	118.78
23	AW	37	MIA	C4-N9-C8	2.51	108.38	105.74
23	AW	46	7MG	C5-C6-N1	2.48	115.31	110.94
24	AX	8	4SU	C1'-N1-C2	2.45	122.00	117.59
25	AY	55	PSU	O4'-C1'-C2'	2.45	108.55	105.15
23	AW	37	MIA	C5-N7-C8	2.44	107.28	103.45
24	AX	55	PSU	C5-C6-N1	-2.36	118.87	122.14
25	AY	55	PSU	C5-C6-N1	-2.35	118.88	122.14
23	AW	37	MIA	C11-S10-C2	-2.35	100.49	102.25
23	CW	76	31M	C6-C5-C4	2.34	120.37	117.18
25	AY	32	PSU	C5-C6-N1	-2.30	118.95	122.14
23	CW	54	5MU	O2-C2-N1	-2.28	119.83	122.80
24	CX	55	PSU	C5-C6-N1	-2.26	119.00	122.14
25	CY	55	PSU	C5-C6-N1	-2.24	119.03	122.14
25	CY	37	MIA	C5-N7-C8	2.24	106.97	103.45
23	AW	76	31M	C5-C4-N9	2.24	108.25	105.81
25	AY	39	PSU	C4-N3-C2	-2.23	123.29	126.37
24	AX	32	5MC	CM5-C5-C6	-2.23	119.83	122.85
25	CY	54	5MU	O2-C2-N1	-2.23	119.90	122.80
24	AX	8	4SU	O2-C2-N3	-2.23	117.38	121.49
23	AW	8	4SU	C1'-N1-C2	2.21	121.56	117.59
23	AW	54	5MU	O2-C2-N1	-2.16	119.99	122.80
25	CY	46	7MG	C6-C5-C4	-2.15	118.62	122.40
24	CX	8	4SU	C6-N1-C2	-2.15	118.39	121.00
25	CY	32	PSU	O4'-C1'-C2'	2.12	108.09	105.15
23	CW	76	31M	N3-C4-N9	2.11	130.76	127.17
24	CX	32	5MC	O2-C2-N3	-2.10	119.01	122.33
23	AW	32	PSU	C5-C6-N1	-2.08	119.25	122.14
25	CY	46	7MG	C5-C4-N9	-2.07	103.69	106.33
25	CY	8	4SU	S4-C4-N3	2.06	122.36	120.20
25	CY	37	MIA	C2-N1-C6	2.06	122.11	118.73
23	CW	46	7MG	O6-C6-C5	-2.06	122.57	127.62
25	CY	46	7MG	C6-C5-N7	2.06	135.12	131.93
23	CW	39	PSU	C5-C6-N1	-2.06	119.29	122.14
25	CY	37	MIA	C1'-N9-C8	-2.06	122.53	127.09
23	AW	39	PSU	C5-C6-N1	-2.05	119.29	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	76	31M	N3-C4-N9	2.05	130.66	127.17
25	AY	54	5MU	C5M-C5-C6	-2.05	120.08	122.85
23	AW	46	7MG	O6-C6-C5	-2.02	122.67	127.62
25	AY	55	PSU	O4-C4-C5	-2.02	119.00	124.01
25	AY	37	MIA	C6-C5-N7	2.00	135.96	132.09
25	CY	55	PSU	O4-C4-N3	-2.00	116.35	120.11

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	37	MIA	C12-C13-C14-C16
23	AW	76	31M	NM-CAM-CTM-N
23	AW	76	31M	CBM-CAM-CTM-N
23	AW	76	31M	CBM-CAM-CTM-OTM
25	AY	46	7MG	C4'-C5'-O5'-P
25	AY	54	5MU	C3'-C4'-C5'-O5'
25	AY	54	5MU	O4'-C4'-C5'-O5'
23	CW	46	7MG	C2'-C1'-N9-C8
23	CW	76	31M	O4'-C4'-C5'-O5'
23	CW	76	31M	NM-CAM-CTM-N
25	CY	46	7MG	O4'-C4'-C5'-O5'
25	CY	54	5MU	C3'-C4'-C5'-O5'
25	CY	54	5MU	O4'-C4'-C5'-O5'
25	CY	55	PSU	C2'-C1'-C5-C4
23	CW	76	31M	C-CA-CB-CG
23	CW	76	31M	N-CA-CB-CG
23	CW	76	31M	C3'-C4'-C5'-O5'
25	AY	39	PSU	C3'-C4'-C5'-O5'
25	AY	39	PSU	O4'-C4'-C5'-O5'
25	CY	37	MIA	C3'-C4'-C5'-O5'
25	CY	8	4SU	C3'-C4'-C5'-O5'
25	CY	8	4SU	O4'-C4'-C5'-O5'
25	CY	37	MIA	O4'-C4'-C5'-O5'
25	CY	46	7MG	C3'-C4'-C5'-O5'
25	CY	39	PSU	C3'-C4'-C5'-O5'
23	CW	76	31M	CA-CB-CG-CD1
23	CW	76	31M	CA-CB-CG-CD2
25	CY	39	PSU	O4'-C4'-C5'-O5'
23	AW	76	31M	CTM-CAM-CBM-CGM
23	AW	76	31M	NM-CAM-CTM-OTM
23	CW	76	31M	NM-CAM-CTM-OTM

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Mol	Chain	Res	Type	Atoms
23	CW	76	31M	CBM-CAM-CTM-OTM
25	CY	46	7MG	C2'-C1'-N9-C8
23	AW	46	7MG	C3'-C4'-C5'-O5'
25	AY	37	MIA	C3'-C4'-C5'-O5'
23	AW	76	31M	NM-CAM-CBM-CGM
25	AY	46	7MG	C3'-C4'-C5'-O5'
25	AY	32	PSU	O4'-C4'-C5'-O5'
25	AY	37	MIA	C4'-C5'-O5'-P
23	AW	76	31M	CBM-CGM-SDM-CEM
23	AW	46	7MG	C4'-C5'-O5'-P
23	CW	76	31M	CBM-CGM-SDM-CEM
25	AY	55	PSU	O4'-C1'-C5-C4
23	AW	46	7MG	O4'-C4'-C5'-O5'
25	CY	37	MIA	C4'-C5'-O5'-P
23	CW	46	7MG	C4'-C5'-O5'-P
25	CY	32	PSU	O4'-C4'-C5'-O5'
25	CY	46	7MG	O4'-C1'-N9-C8
25	AY	55	PSU	O4'-C1'-C5-C6
25	CY	55	PSU	O4'-C1'-C5-C6
24	CX	55	PSU	O4'-C4'-C5'-O5'
23	CW	76	31M	CBM-CAM-CTM-N
25	AY	8	4SU	C2'-C1'-N1-C6
23	CW	46	7MG	C2'-C1'-N9-C4
25	CY	55	PSU	C3'-C4'-C5'-O5'
25	CY	55	PSU	C2'-C1'-C5-C6
23	AW	76	31M	C4'-C5'-O5'-P

There are no ring outliers.

28 monomers are involved in 63 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	CY	37	MIA	2	0
25	AY	54	5MU	1	0
23	CW	55	PSU	1	0
25	AY	39	PSU	4	0
23	CW	54	5MU	1	0
25	AY	8	4SU	1	0
23	CW	8	4SU	2	0
23	CW	46	7MG	1	0
24	CX	32	5MC	1	0
25	AY	37	MIA	3	0
24	AX	8	4SU	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	AW	76	31M	5	0
23	AW	39	PSU	1	0
25	CY	46	7MG	1	0
25	AY	55	PSU	4	0
23	AW	8	4SU	1	0
25	CY	55	PSU	4	0
25	AY	32	PSU	2	0
24	AX	55	PSU	1	0
25	AY	46	7MG	3	0
23	AW	46	7MG	1	0
23	CW	76	31M	7	0
23	CW	39	PSU	3	0
24	CX	54	5MU	1	0
24	CX	8	4SU	2	0
25	CY	39	PSU	4	0
25	CY	8	4SU	5	0
23	AW	37	MIA	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2093 ligands modelled in this entry, 2091 are monoatomic - leaving 2 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	$\# Z > 2$
58	SF4	CD	302	4	0,12,12	-	-	-		
58	SF4	AD	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
58	SF4	CD	302	4	-	-	0/6/5/5
58	SF4	AD	501	4	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	1498/1521 (98%)	0.70	82 (5%) 30 30	42, 72, 93, 108	0
1	CA	1503/1521 (98%)	0.91	191 (12%) 8 7	44, 74, 94, 109	0
2	AB	231/256 (90%)	1.68	69 (29%) 1 1	72, 82, 90, 94	0
2	CB	231/256 (90%)	2.11	109 (47%) 0 0	73, 84, 90, 95	0
3	AC	206/239 (86%)	1.55	50 (24%) 2 1	68, 79, 87, 94	0
3	CC	206/239 (86%)	2.37	129 (62%) 0 0	71, 81, 89, 94	0
4	AD	208/209 (99%)	1.50	50 (24%) 2 1	57, 72, 81, 90	0
4	CD	208/209 (99%)	1.31	28 (13%) 7 5	58, 71, 80, 91	0
5	AE	148/162 (91%)	1.27	18 (12%) 8 7	58, 71, 80, 85	0
5	CE	148/162 (91%)	1.72	45 (30%) 1 0	60, 73, 81, 86	0
6	AF	100/101 (99%)	1.17	8 (8%) 18 18	56, 69, 78, 82	0
6	CF	100/101 (99%)	1.04	5 (5%) 34 33	57, 70, 78, 82	0
7	AG	155/156 (99%)	1.33	23 (14%) 5 5	65, 75, 83, 91	0
7	CG	155/156 (99%)	1.36	27 (17%) 4 3	66, 76, 84, 92	0
8	AH	137/138 (99%)	1.24	17 (12%) 8 7	62, 72, 79, 87	0
8	CH	137/138 (99%)	1.57	31 (22%) 2 2	64, 74, 80, 87	0
9	AI	127/128 (99%)	1.79	50 (39%) 1 0	65, 80, 86, 89	0
9	CI	127/128 (99%)	2.59	82 (64%) 0 0	68, 82, 88, 91	0
10	AJ	97/105 (92%)	1.97	46 (47%) 0 0	64, 82, 90, 93	0
10	CJ	96/105 (91%)	2.43	57 (59%) 0 0	67, 84, 91, 93	0
11	AK	114/129 (88%)	1.11	14 (12%) 8 7	48, 70, 79, 84	0
11	CK	114/129 (88%)	1.27	17 (14%) 5 5	51, 71, 79, 84	0
12	AL	122/132 (92%)	0.94	9 (7%) 20 19	50, 65, 73, 78	0
12	CL	122/132 (92%)	1.27	22 (18%) 3 3	53, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	AM	123/126 (97%)	1.28	18 (14%)	6	5	55, 70, 81, 89	0
13	CM	122/126 (96%)	2.45	70 (57%)	0	0	70, 84, 91, 99	0
14	AN	60/61 (98%)	1.69	14 (23%)	2	1	67, 74, 83, 84	0
14	CN	60/61 (98%)	3.17	54 (90%)	0	0	69, 77, 84, 88	0
15	AO	88/89 (98%)	1.23	12 (13%)	7	5	56, 67, 80, 81	0
15	CO	88/89 (98%)	1.28	14 (15%)	5	4	59, 69, 80, 83	0
16	AP	82/88 (93%)	1.78	29 (35%)	1	0	57, 71, 80, 84	0
16	CP	82/88 (93%)	1.36	14 (17%)	4	3	58, 70, 80, 84	0
17	AQ	99/105 (94%)	1.28	14 (14%)	6	5	59, 71, 80, 84	0
17	CQ	99/105 (94%)	1.13	11 (11%)	10	9	61, 71, 81, 85	0
18	AR	68/88 (77%)	0.97	6 (8%)	15	15	59, 68, 81, 83	0
18	CR	68/88 (77%)	1.21	7 (10%)	12	11	61, 70, 80, 84	0
19	AS	83/93 (89%)	1.62	19 (22%)	2	2	71, 80, 86, 95	0
19	CS	83/93 (89%)	2.82	66 (79%)	0	0	74, 82, 89, 96	0
20	AT	96/106 (90%)	1.43	20 (20%)	2	2	57, 71, 81, 85	0
20	CT	96/106 (90%)	1.24	12 (12%)	8	7	58, 70, 82, 85	0
21	AU	23/27 (85%)	2.13	13 (56%)	0	0	67, 74, 77, 81	0
21	CU	23/27 (85%)	2.66	19 (82%)	0	0	70, 75, 80, 84	0
22	AV	13/24 (54%)	1.45	4 (30%)	1	0	58, 81, 96, 99	0
22	CV	12/24 (50%)	2.05	5 (41%)	0	0	63, 84, 93, 94	0
23	AW	66/76 (86%)	1.47	14 (21%)	2	2	68, 96, 103, 105	0
23	CW	64/76 (84%)	1.75	18 (28%)	1	1	73, 97, 103, 106	0
24	AX	72/77 (93%)	0.45	2 (2%)	55	56	39, 68, 87, 91	0
24	CX	72/77 (93%)	0.92	2 (2%)	55	56	53, 82, 93, 97	0
25	AY	67/76 (88%)	2.05	34 (50%)	0	0	44, 97, 102, 105	0
25	CY	66/76 (86%)	2.26	40 (60%)	0	0	47, 97, 102, 105	0
26	BA	2819/2915 (96%)	-0.04	116 (4%)	41	42	26, 45, 89, 104	0
26	DA	2800/2915 (96%)	0.05	100 (3%)	46	47	30, 49, 90, 108	0
27	BB	120/121 (99%)	0.46	1 (0%)	82	84	40, 64, 73, 86	0
27	DB	120/121 (99%)	1.16	16 (13%)	7	6	46, 69, 76, 90	0
28	BD	275/276 (99%)	0.43	5 (1%)	67	68	27, 43, 58, 82	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	DD	275/276 (99%)	0.32	7 (2%) 58 59	29, 45, 61, 81	0
29	BE	204/206 (99%)	0.45	5 (2%) 58 59	25, 48, 66, 80	0
29	DE	204/206 (99%)	0.55	4 (1%) 65 65	29, 52, 67, 81	0
30	BF	203/210 (96%)	0.55	4 (1%) 65 65	26, 53, 76, 87	0
30	DF	203/210 (96%)	0.64	4 (1%) 65 65	30, 58, 77, 87	0
31	BG	181/182 (99%)	1.34	29 (16%) 5 4	51, 69, 81, 88	0
31	DG	181/182 (99%)	1.83	67 (37%) 1 0	56, 73, 82, 90	0
32	BH	174/180 (96%)	1.10	13 (7%) 20 19	51, 65, 75, 88	0
32	DH	174/180 (96%)	1.38	31 (17%) 4 3	55, 70, 78, 88	0
33	BI	146/148 (98%)	1.13	13 (8%) 15 14	50, 74, 82, 87	0
33	DI	146/148 (98%)	1.55	33 (22%) 2 2	52, 75, 82, 86	0
34	BN	140/140 (100%)	0.68	5 (3%) 46 47	32, 50, 67, 76	0
34	DN	140/140 (100%)	0.77	3 (2%) 63 64	36, 55, 70, 77	0
35	BO	122/122 (100%)	0.13	1 (0%) 82 84	30, 43, 59, 70	0
35	DO	122/122 (100%)	0.81	5 (4%) 41 42	45, 59, 73, 78	0
36	BP	149/150 (99%)	0.79	6 (4%) 42 43	26, 55, 75, 83	0
36	DP	149/150 (99%)	0.91	10 (6%) 24 23	30, 59, 77, 85	0
37	BQ	141/141 (100%)	0.63	3 (2%) 63 64	36, 52, 67, 80	0
37	DQ	141/141 (100%)	1.05	11 (7%) 19 18	41, 57, 70, 82	0
38	BR	118/118 (100%)	-0.02	0 100 100	25, 36, 54, 59	0
38	DR	118/118 (100%)	0.45	0 100 100	40, 54, 65, 72	0
39	BS	110/112 (98%)	0.35	0 100 100	38, 51, 65, 72	0
39	DS	110/112 (98%)	1.75	36 (32%) 1 0	63, 77, 84, 92	0
40	BT	131/146 (89%)	0.32	7 (5%) 32 31	32, 47, 69, 82	0
40	DT	131/146 (89%)	0.95	13 (9%) 13 12	48, 63, 79, 85	0
41	BU	116/118 (98%)	-0.13	1 (0%) 81 83	18, 33, 49, 59	0
41	DU	116/118 (98%)	0.88	4 (3%) 48 49	42, 61, 78, 84	0
42	BV	101/101 (100%)	-0.04	0 100 100	21, 41, 58, 67	0
42	DV	101/101 (100%)	1.15	10 (9%) 13 12	41, 71, 83, 91	0
43	BW	112/113 (99%)	-0.05	2 (1%) 67 68	23, 34, 54, 79	0
43	DW	112/113 (99%)	0.35	1 (0%) 81 83	39, 50, 67, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	BX	95/96 (98%)	0.10	1 (1%) 78 79	23, 38, 61, 84	0
44	DX	95/96 (98%)	1.01	14 (14%) 6 5	43, 60, 76, 79	0
45	BY	107/110 (97%)	0.39	3 (2%) 55 56	32, 50, 69, 83	0
45	DY	107/110 (97%)	1.32	16 (14%) 5 5	57, 71, 81, 88	0
46	BZ	171/206 (83%)	1.21	42 (24%) 2 1	39, 64, 91, 95	0
46	DZ	174/206 (84%)	2.12	80 (45%) 0 0	66, 84, 94, 101	0
47	B0	83/85 (97%)	0.25	3 (3%) 46 47	27, 39, 61, 73	0
47	D0	83/85 (97%)	1.33	15 (18%) 3 3	46, 66, 75, 82	0
48	B1	97/98 (98%)	0.50	3 (3%) 51 52	30, 48, 70, 76	0
48	D1	97/98 (98%)	0.79	9 (9%) 14 13	38, 58, 74, 83	0
49	B2	70/72 (97%)	0.39	2 (2%) 53 55	34, 50, 64, 79	0
49	D2	70/72 (97%)	1.25	13 (18%) 3 2	56, 70, 80, 86	0
50	B3	59/60 (98%)	0.08	1 (1%) 69 69	24, 37, 63, 71	0
50	D3	59/60 (98%)	0.74	2 (3%) 48 49	49, 64, 79, 85	0
51	B4	69/71 (97%)	1.36	15 (21%) 2 2	54, 73, 87, 92	0
51	D4	69/71 (97%)	2.08	31 (44%) 0 0	74, 88, 94, 99	0
52	B5	59/60 (98%)	-0.20	0 100 100	20, 33, 54, 67	0
52	D5	59/60 (98%)	0.32	1 (1%) 69 69	36, 51, 67, 73	0
53	B6	53/54 (98%)	0.14	1 (1%) 66 66	31, 44, 61, 68	0
53	D6	53/54 (98%)	1.00	4 (7%) 20 19	52, 63, 76, 79	0
54	B7	48/49 (97%)	0.12	4 (8%) 17 17	21, 30, 62, 76	0
54	D7	48/49 (97%)	0.38	3 (6%) 26 25	33, 42, 61, 70	0
55	B8	64/65 (98%)	0.15	1 (1%) 70 71	25, 36, 45, 60	0
55	D8	64/65 (98%)	1.01	2 (3%) 51 52	46, 58, 66, 72	0
56	B9	37/37 (100%)	0.40	1 (2%) 56 57	31, 49, 73, 74	0
56	D9	37/37 (100%)	1.21	5 (13%) 7 5	46, 57, 73, 76	0
All	All	20897/21748 (96%)	0.77	2548 (12%) 8 7	18, 64, 89, 109	0

All (2548) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	AG	82	GLY	8.4
14	AN	2	ALA	8.1

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Mol	Chain	Res	Type	RSRZ
13	CM	123	ALA	7.0
13	CM	124	PRO	7.0
28	BD	276	LYS	6.8
5	CE	22	GLY	6.5
14	CN	2	ALA	6.4
13	CM	122	LYS	6.4
2	AB	7	VAL	6.4
7	CG	83	ALA	6.2
9	CI	14	VAL	6.1
32	BH	2	SER	6.1
9	CI	9	ARG	5.9
22	CV	13	A	5.8
2	CB	165	VAL	5.8
19	CS	52	TYR	5.8
10	CJ	63	PHE	5.8
26	DA	2112	G	5.8
51	D4	49	PHE	5.7
14	CN	5	ALA	5.6
1	AA	1532	U	5.6
9	CI	106	ALA	5.5
13	AM	123	ALA	5.5
19	CS	79	THR	5.5
13	CM	78	ILE	5.5
9	CI	126	SER	5.5
3	AC	207	VAL	5.4
13	AM	2	ALA	5.4
9	CI	102	LEU	5.4
3	CC	155	GLY	5.3
26	DA	2125	G	5.2
13	CM	72	ALA	5.2
13	CM	4	ILE	5.2
9	CI	13	ALA	5.1
3	CC	189	ALA	5.1
13	CM	102	ARG	5.1
2	CB	21	ARG	5.0
9	CI	19	LEU	5.0
9	CI	67	GLY	5.0
26	BA	2793	G	5.0
51	D4	54	GLY	4.9
9	CI	66	ARG	4.9
9	CI	105	ASP	4.9
2	CB	123	ALA	4.9

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Mol	Chain	Res	Type	RSRZ
10	CJ	47	PHE	4.9
3	CC	128	PHE	4.8
10	CJ	54	PHE	4.8
3	CC	129	ALA	4.8
14	CN	21	TYR	4.8
25	CY	34	G	4.8
7	AG	83	ALA	4.8
14	CN	29	ARG	4.8
14	CN	39	LEU	4.8
4	AD	2	GLY	4.7
2	CB	185	ILE	4.7
46	DZ	171	ILE	4.7
31	DG	28	VAL	4.7
10	CJ	55	LYS	4.7
9	CI	2	GLU	4.7
10	CJ	26	ALA	4.7
26	BA	885	C	4.6
10	CJ	32	ALA	4.6
14	CN	49	HIS	4.6
25	CY	18	G	4.6
1	AA	1027	C	4.6
14	CN	53	LEU	4.6
19	CS	66	MET	4.6
2	CB	7	VAL	4.6
13	CM	121	LYS	4.6
14	CN	3	ARG	4.5
46	DZ	114	GLY	4.5
46	DZ	115	GLY	4.5
3	CC	124	ILE	4.5
14	CN	25	VAL	4.5
46	BZ	104	PHE	4.5
46	DZ	166	SER	4.5
16	AP	68	ASP	4.5
19	CS	5	LEU	4.5
51	B4	49	PHE	4.5
26	DA	2119	A	4.5
19	CS	80	TYR	4.4
7	CG	82	GLY	4.4
19	CS	9	VAL	4.4
19	CS	11	VAL	4.4
46	DZ	111	VAL	4.4
2	CB	237	ALA	4.4

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Mol	Chain	Res	Type	RSRZ
26	BA	2119	A	4.4
26	BA	2113	U	4.4
1	AA	1036	G	4.4
46	DZ	170	THR	4.4
14	CN	38	GLY	4.4
20	CT	9	ASN	4.4
39	DS	32	LEU	4.4
19	CS	2	PRO	4.4
31	DG	2	PRO	4.4
13	CM	60	VAL	4.4
10	CJ	85	LEU	4.4
46	BZ	114	GLY	4.3
13	CM	87	TYR	4.3
26	BA	2125	G	4.3
51	D4	65	ASP	4.3
3	CC	190	ARG	4.3
39	DS	3	ARG	4.3
26	DA	2132	U	4.3
13	CM	6	GLY	4.3
26	BA	2794	C	4.3
23	CW	73	A	4.3
46	DZ	172	ALA	4.3
1	AA	1023	G	4.2
3	CC	2	GLY	4.2
3	CC	185	GLY	4.2
8	AH	3	THR	4.2
46	BZ	116	VAL	4.2
46	DZ	150	LEU	4.2
14	CN	34	TYR	4.2
13	AM	124	PRO	4.2
16	AP	82	GLN	4.2
21	CU	14	TRP	4.2
19	CS	15	LEU	4.2
46	DZ	33	LEU	4.2
26	BA	2803	C	4.2
14	CN	40	CYS	4.2
3	CC	157	ILE	4.2
26	DA	2133	G	4.2
26	DA	2155	G	4.2
5	CE	94	ALA	4.2
1	AA	1447	A	4.2
7	AG	80	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
51	D4	50	VAL	4.2
51	B4	59	PHE	4.2
25	AY	18	G	4.2
3	CC	187	ALA	4.2
10	CJ	41	PRO	4.1
9	CI	4	TYR	4.1
3	AC	204	LEU	4.1
3	CC	94	LEU	4.1
19	CS	18	LYS	4.1
51	D4	56	VAL	4.1
7	CG	37	ASN	4.1
1	AA	1030(A)	G	4.1
1	CA	1220	G	4.1
31	DG	146	TYR	4.1
21	CU	24	ARG	4.1
3	CC	195	VAL	4.1
11	AK	14	VAL	4.1
14	CN	33	VAL	4.1
3	CC	171	GLY	4.1
12	AL	63	GLY	4.1
14	CN	10	ALA	4.0
2	CB	187	LEU	4.0
1	AA	630	G	4.0
2	CB	122	PHE	4.0
9	CI	61	ALA	4.0
20	AT	103	GLY	4.0
1	CA	1002	G	4.0
9	AI	59	PHE	4.0
20	AT	74	LYS	4.0
19	CS	84	GLY	4.0
2	CB	97	TRP	4.0
2	CB	201	ILE	4.0
3	CC	153	VAL	4.0
13	CM	118	ALA	4.0
46	DZ	147	GLY	4.0
1	CA	980	C	4.0
1	CA	1030(B)	C	4.0
1	CA	1149	C	4.0
3	CC	8	ILE	4.0
9	CI	36	TYR	4.0
21	CU	6	ARG	4.0
14	CN	30	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
3	CC	194	GLY	3.9
2	AB	97	TRP	3.9
2	CB	164	VAL	3.9
3	CC	198	VAL	3.9
46	DZ	113	ALA	3.9
1	CA	1216	G	3.9
8	CH	2	LEU	3.9
14	CN	18	VAL	3.9
46	DZ	164	ALA	3.9
4	AD	194	LEU	3.9
46	BZ	144	LEU	3.9
14	CN	22	THR	3.9
26	DA	2113	U	3.9
1	CA	1033	G	3.9
2	CB	71	VAL	3.9
3	CC	55	VAL	3.9
26	BA	2805	G	3.9
33	DI	92	VAL	3.9
14	CN	20	ALA	3.9
21	CU	11	GLY	3.9
16	AP	19	ILE	3.9
19	CS	71	LEU	3.9
54	B7	48	LYS	3.9
26	DA	2115	G	3.8
26	DA	2116	G	3.8
9	CI	18	PHE	3.8
26	BA	2804	C	3.8
19	CS	53	ASN	3.8
56	D9	37	GLY	3.8
10	AJ	77	PRO	3.8
5	CE	41	VAL	3.8
46	BZ	109	ALA	3.8
5	CE	13	ILE	3.8
31	DG	20	ILE	3.8
46	DZ	167	PRO	3.8
3	CC	192	THR	3.8
51	B4	50	VAL	3.8
1	AA	1025	U	3.8
2	AB	237	ALA	3.8
3	CC	167	TRP	3.8
9	AI	15	ALA	3.8
26	DA	2173	A	3.8

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Mol	Chain	Res	Type	RSRZ
31	DG	29	TRP	3.8
1	AA	1026	G	3.8
25	CY	15	G	3.8
26	BA	2162	G	3.8
2	CB	163	PHE	3.8
3	CC	53	ALA	3.8
26	DA	2170	A	3.8
1	CA	1030(A)	G	3.8
9	CI	7	THR	3.7
44	DX	91	ALA	3.7
2	CB	92	TYR	3.7
3	CC	22	TRP	3.7
3	CC	91	LEU	3.7
10	AJ	98	ILE	3.7
9	CI	21	PRO	3.7
3	CC	4	LYS	3.7
1	AA	1024	G	3.7
2	AB	163	PHE	3.7
16	AP	80	PHE	3.7
19	CS	82	GLY	3.7
42	DV	63	GLY	3.7
14	CN	7	ILE	3.7
44	BX	95	LEU	3.7
46	DZ	102	LEU	3.7
2	AB	133	LYS	3.7
9	CI	27	THR	3.7
14	CN	60	SER	3.7
1	CA	1202	G	3.7
25	CY	1	G	3.7
46	DZ	173	ALA	3.7
39	DS	12	PHE	3.7
20	CT	103	GLY	3.7
13	CM	90	LEU	3.7
31	DG	53	LEU	3.7
9	CI	91	ASP	3.7
9	CI	5	TYR	3.7
26	DA	229	A	3.7
25	CY	72	C	3.7
10	AJ	32	ALA	3.7
2	CB	99	GLY	3.7
37	DQ	104	PHE	3.7
26	DA	2159	G	3.7

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Mol	Chain	Res	Type	RSRZ
14	CN	42	ILE	3.7
44	DX	92	LEU	3.7
13	CM	94	ARG	3.7
31	BG	146	TYR	3.7
12	AL	18	VAL	3.6
34	DN	9	VAL	3.6
46	DZ	96	VAL	3.6
3	CC	71	ALA	3.6
28	BD	2	ALA	3.6
31	BG	50	ALA	3.6
3	CC	9	GLY	3.6
2	AB	214	ILE	3.6
31	BG	88	ILE	3.6
26	DA	2156	G	3.6
3	CC	191	THR	3.6
26	BA	2114	A	3.6
9	CI	11	LYS	3.6
39	DS	33	LYS	3.6
3	AC	81	GLY	3.6
1	CA	979	C	3.6
1	CA	1038	C	3.6
19	CS	22	LEU	3.6
31	BG	53	LEU	3.6
26	BA	271(K)	U	3.6
26	BA	2112	G	3.6
26	DA	1171	G	3.6
47	B0	3	HIS	3.6
31	DG	160	VAL	3.6
46	BZ	107	THR	3.6
11	CK	89	ALA	3.6
43	BW	112	GLY	3.6
19	CS	40	ILE	3.6
32	DH	21	PRO	3.6
51	D4	25	TYR	3.6
2	AB	15	VAL	3.6
9	CI	44	VAL	3.6
10	AJ	34	VAL	3.6
13	CM	105	THR	3.6
51	D4	57	GLU	3.6
13	CM	120	LYS	3.6
14	CN	61	TRP	3.6
21	AU	24	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
5	AE	85	GLY	3.6
10	CJ	8	LEU	3.6
10	CJ	93	GLY	3.6
14	CN	55	GLY	3.6
46	DZ	155	LEU	3.6
46	DZ	104	PHE	3.6
10	CJ	78	ASN	3.6
1	CA	1030	C	3.5
25	AY	72	C	3.5
1	CA	1219	U	3.5
31	DG	12	TYR	3.5
39	DS	28	VAL	3.5
26	BA	1176	G	3.5
13	CM	119	GLY	3.5
19	CS	8	GLY	3.5
33	DI	46	ALA	3.5
1	CA	983	A	3.5
10	AJ	4	ILE	3.5
19	CS	31	ILE	3.5
25	CY	56	C	3.5
9	AI	108	VAL	3.5
13	CM	74	VAL	3.5
31	DG	159	VAL	3.5
46	DZ	107	THR	3.5
2	CB	31	TYR	3.5
9	CI	92	TYR	3.5
7	CG	38	LEU	3.5
13	CM	64	TRP	3.5
13	CM	31	LYS	3.5
46	DZ	168	GLU	3.5
1	CA	1039	C	3.5
13	CM	117	VAL	3.5
19	CS	33	THR	3.5
45	DY	5	MET	3.5
46	DZ	116	VAL	3.5
26	DA	2172	U	3.5
2	CB	33	TYR	3.5
11	CK	75	TYR	3.5
13	CM	81	LEU	3.5
46	BZ	117	LEU	3.5
46	DZ	108	PRO	3.5
19	CS	10	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
47	D0	69	PHE	3.5
10	AJ	72	VAL	3.5
10	CJ	34	VAL	3.5
16	CP	82	GLN	3.5
19	CS	41	VAL	3.5
31	DG	31	VAL	3.5
1	CA	1116	C	3.5
9	AI	47	LEU	3.5
53	D6	11	LEU	3.5
11	CK	50	TYR	3.5
15	AO	69	TYR	3.5
46	DZ	21	ALA	3.5
3	AC	39	ILE	3.5
2	AB	126	GLU	3.4
4	AD	154	ASN	3.4
25	CY	71	G	3.4
26	BA	1106	G	3.4
26	BA	2115	G	3.4
26	DA	2154	G	3.4
3	CC	76	VAL	3.4
4	AD	140	VAL	3.4
9	CI	109	VAL	3.4
20	AT	10	LEU	3.4
9	CI	125	TYR	3.4
11	AK	75	TYR	3.4
37	DQ	22	LYS	3.4
13	CM	104	ARG	3.4
26	BA	2173	A	3.4
26	BA	2790	A	3.4
33	DI	15	VAL	3.4
10	CJ	90	LEU	3.4
45	DY	106	LEU	3.4
13	AM	122	LYS	3.4
46	BZ	108	PRO	3.4
2	AB	29	ALA	3.4
13	CM	33	ALA	3.4
10	CJ	74	ILE	3.4
26	BA	2145	C	3.4
26	DA	2136	C	3.4
47	D0	45	PHE	3.4
9	CI	10	ARG	3.4
7	AG	84	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	CA	1001	A	3.4
26	DA	896	A	3.4
32	DH	52	VAL	3.4
2	CB	196	LEU	3.4
2	CB	221	LEU	3.4
10	CJ	40	LEU	3.4
46	BZ	143	GLY	3.4
1	CA	1017	G	3.4
2	CB	200	ILE	3.4
19	AS	40	ILE	3.4
19	CS	75	ALA	3.4
40	DT	130	ALA	3.4
2	CB	236	TYR	3.4
49	D2	66	GLU	3.4
1	AA	163	C	3.4
26	BA	2161	C	3.4
28	BD	38	LYS	3.4
7	CG	16	LEU	3.4
10	CJ	42	THR	3.4
31	DG	19	LEU	3.4
37	DQ	61	GLY	3.4
41	DU	73	GLY	3.4
2	CB	222	ILE	3.4
9	CI	63	ILE	3.4
3	CC	142	MET	3.3
19	CS	13	ASP	3.3
1	CA	1054	C	3.3
10	CJ	76	ASN	3.3
31	DG	74	LYS	3.3
4	AD	155	LEU	3.3
9	CI	17	VAL	3.3
11	CK	114	VAL	3.3
3	CC	41	GLY	3.3
13	CM	95	GLY	3.3
32	BH	3	ARG	3.3
51	B4	64	GLY	3.3
2	CB	161	ALA	3.3
10	AJ	38	ILE	3.3
32	DH	2	SER	3.3
14	AN	16	PHE	3.3
1	CA	1281	U	3.3
1	AA	1031	G	3.3

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Mol	Chain	Res	Type	RSRZ
8	CH	32	LYS	3.3
13	CM	101	GLN	3.3
1	AA	1028	C	3.3
1	CA	1119	C	3.3
26	BA	888	C	3.3
26	DA	2804	C	3.3
2	CB	154	LEU	3.3
10	CJ	88	LEU	3.3
2	CB	197	VAL	3.3
51	D4	52	THR	3.3
3	AC	2	GLY	3.3
3	CC	13	GLY	3.3
5	CE	85	GLY	3.3
13	CM	92	HIS	3.3
46	DZ	121	HIS	3.3
46	BZ	120	ILE	3.3
1	CA	1035	A	3.3
22	AV	13	A	3.3
26	BA	2117	A	3.3
26	DA	2117	A	3.3
3	CC	193	TYR	3.3
51	D4	67	TYR	3.3
25	AY	19	G	3.3
26	BA	2168	G	3.3
23	AW	4	C	3.3
23	CW	2	C	3.3
3	CC	161	GLU	3.3
21	CU	17	THR	3.3
15	AO	87	ILE	3.3
40	BT	130	ALA	3.3
1	AA	1531	A	3.3
26	DA	2126	A	3.3
19	CS	4	SER	3.3
31	BG	80	PHE	3.3
2	CB	205	ASP	3.3
10	AJ	73	ASP	3.3
27	DB	1	U	3.3
2	AB	125	PRO	3.3
2	CB	234	PRO	3.3
19	CS	78	ARG	3.3
46	BZ	150	LEU	3.3
46	DZ	144	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1024	G	3.3
2	CB	126	GLU	3.3
16	AP	2	VAL	3.3
25	CY	53	G	3.3
26	BA	2131	G	3.3
26	BA	2893	G	3.3
19	AS	84	GLY	3.3
26	DA	2164	C	3.3
2	CB	39	ILE	3.3
2	CB	162	ILE	3.3
3	CC	5	ILE	3.3
46	DZ	137	ILE	3.3
9	CI	15	ALA	3.3
14	CN	4	LYS	3.3
9	CI	101	PHE	3.2
1	CA	981	U	3.2
4	CD	188	LEU	3.2
6	CF	45	LEU	3.2
3	CC	75	VAL	3.2
9	AI	41	VAL	3.2
46	BZ	141	VAL	3.2
3	CC	134	ILE	3.2
1	AA	1034	G	3.2
1	CA	1045	C	3.2
1	CA	1117	G	3.2
1	CA	1277	C	3.2
1	CA	1322	C	3.2
1	CA	1325	C	3.2
23	CW	72	C	3.2
26	DA	2131	G	3.2
1	CA	994	A	3.2
9	AI	10	ARG	3.2
2	CB	199	TYR	3.2
8	CH	94	TYR	3.2
13	CM	23	TYR	3.2
9	AI	2	GLU	3.2
19	CS	14	HIS	3.2
1	CA	1040	U	3.2
46	DZ	174	VAL	3.2
3	AC	67	THR	3.2
31	DG	24	GLY	3.2
31	DG	161	THR	3.2

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Mol	Chain	Res	Type	RSRZ
46	BZ	115	GLY	3.2
10	CJ	6	ILE	3.2
20	AT	55	ILE	3.2
46	DZ	120	ILE	3.2
9	AI	106	ALA	3.2
9	CI	76	ALA	3.2
26	DA	2803	C	3.2
23	AW	70	G	3.2
26	DA	2124	G	3.2
8	AH	29	SER	3.2
17	AQ	99	SER	3.2
7	AG	12	LEU	3.2
21	CU	23	PRO	3.2
22	CV	14	A	3.2
27	DB	120	A	3.2
2	CB	48	MET	3.2
4	CD	20	TYR	3.2
9	CI	64	THR	3.2
13	CM	112	GLY	3.2
16	AP	69	THR	3.2
21	AU	17	THR	3.2
46	DZ	106	GLY	3.2
46	BZ	113	ALA	3.2
1	CA	1362	C	3.2
19	CS	74	PHE	3.2
26	BA	2143	C	3.2
27	DB	119	G	3.2
2	AB	11	LEU	3.2
2	AB	12	GLU	3.2
2	CB	10	LEU	3.2
5	CE	12	LEU	3.2
39	DS	57	LYS	3.2
7	AG	154	TYR	3.2
9	CI	28	VAL	3.2
10	AJ	44	VAL	3.2
10	CJ	72	VAL	3.2
19	CS	19	VAL	3.2
19	CS	26	GLY	3.2
1	CA	1150	U	3.2
15	CO	4	THR	3.2
5	CE	30	ALA	3.1
10	CJ	79	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
15	AO	68	ARG	3.1
37	DQ	60	ARG	3.1
46	DZ	136	PHE	3.1
1	CA	1260	C	3.1
1	CA	1321	C	3.1
19	CS	73	GLU	3.1
9	AI	19	LEU	3.1
33	DI	77	LEU	3.1
48	B1	97	LEU	3.1
1	CA	1224	G	3.1
26	BA	2802	G	3.1
26	DA	2160	G	3.1
13	CM	100	GLY	3.1
21	AU	18	TYR	3.1
26	BA	1046	A	3.1
46	DZ	105	VAL	3.1
46	DZ	165	VAL	3.1
2	AB	200	ILE	3.1
2	CB	42	ILE	3.1
2	CB	127	ILE	3.1
26	BA	2132	U	3.1
10	AJ	79	ARG	3.1
19	CS	81	ARG	3.1
46	BZ	167	PRO	3.1
45	DY	90	LEU	3.1
1	CA	1066	C	3.1
1	CA	1214	C	3.1
25	AY	48	C	3.1
19	AS	26	GLY	3.1
25	CY	19	G	3.1
26	DA	2793	G	3.1
34	DN	140	VAL	3.1
1	CA	1213	A	3.1
7	AG	151	TYR	3.1
9	AI	81	ILE	3.1
10	AJ	74	ILE	3.1
10	CJ	46	ARG	3.1
26	DA	652(B)	A	3.1
26	DA	2114	A	3.1
51	B4	63	TYR	3.1
51	D4	32	TYR	3.1
20	AT	12	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
31	DG	41	GLN	3.1
20	CT	74	LYS	3.1
10	CJ	64	GLU	3.1
5	AE	6	PHE	3.1
9	CI	123	PRO	3.1
31	DG	17	PRO	3.1
3	CC	12	LEU	3.1
7	CG	12	LEU	3.1
14	CN	6	LEU	3.1
13	CM	68	GLY	3.1
26	DA	1536	C	3.1
2	AB	230	VAL	3.1
2	CB	230	VAL	3.1
9	AI	109	VAL	3.1
10	CJ	49	VAL	3.1
14	AN	3	ARG	3.1
51	D4	64	GLY	3.1
10	CJ	87	THR	3.1
51	B4	67	TYR	3.1
46	BZ	118	GLN	3.1
49	B2	70	GLN	3.1
1	CA	1048	G	3.1
1	CA	1286	A	3.1
23	AW	1	G	3.1
23	CW	70	G	3.1
26	DA	2802	G	3.1
27	DB	118	G	3.1
40	BT	131	ALA	3.1
25	AY	20	U	3.1
2	CB	70	PHE	3.1
2	CB	118	LEU	3.1
9	AI	126	SER	3.1
10	CJ	59	SER	3.1
19	CS	35	SER	3.1
51	D4	66	SER	3.1
16	AP	48	TRP	3.1
7	AG	81	GLY	3.1
9	CI	6	GLY	3.1
19	CS	72	GLY	3.1
46	DZ	143	GLY	3.1
13	AM	121	LYS	3.0
25	CY	4	C	3.1

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Mol	Chain	Res	Type	RSRZ
26	BA	2164	C	3.1
1	AA	1257	U	3.0
4	AD	33	MET	3.0
45	DY	1	MET	3.0
55	B8	65	GLU	3.0
15	AO	19	PRO	3.0
23	CW	71	G	3.0
26	DA	2168	G	3.0
26	DA	2318	G	3.0
2	AB	10	LEU	3.0
2	AB	152	PHE	3.0
2	CB	57	PHE	3.0
9	CI	50	LEU	3.0
14	CN	16	PHE	3.0
19	AS	13	ASP	3.0
46	BZ	154	ASP	3.0
32	BH	59	ARG	3.0
4	AD	6	GLY	3.0
40	BT	37	GLY	3.0
3	CC	152	ILE	3.0
10	CJ	82	ILE	3.0
19	CS	67	VAL	3.0
31	DG	15	VAL	3.0
19	CS	77	THR	3.0
1	CA	1115	C	3.0
4	AD	195	ALA	3.0
5	CE	17	ALA	3.0
3	AC	184	TYR	3.0
13	CM	59	TYR	3.0
21	AU	21	TYR	3.0
44	DX	69	TYR	3.0
10	CJ	13	HIS	3.0
3	CC	73	PRO	3.0
25	CY	35	A	3.0
26	BA	1045	A	3.0
14	CN	47	LEU	3.0
42	DV	38	LEU	3.0
46	DZ	117	LEU	3.0
9	CI	75	ASP	3.0
37	DQ	65	PHE	3.0
1	AA	1002	G	3.0
1	CA	973	G	3.0

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Mol	Chain	Res	Type	RSRZ
1	CA	1003	G	3.0
25	CY	5	G	3.0
25	CY	24	G	3.0
26	DA	2805	G	3.0
14	CN	58	LYS	3.0
7	AG	86	GLN	3.0
10	CJ	75	ILE	3.0
19	CS	34	TRP	3.0
51	D4	14	ILE	3.0
14	CN	13	THR	3.0
32	BH	145	ALA	3.0
3	CC	48	TYR	3.0
39	DS	34	HIS	3.0
25	CY	25	C	3.0
46	DZ	158	PRO	3.0
9	CI	40	LEU	3.0
22	AV	12	A	3.0
22	AV	14	A	3.0
25	CY	14	A	3.0
26	DA	2135	A	3.0
1	CA	1034	G	3.0
25	AY	15	G	3.0
9	CI	8	GLY	3.0
3	AC	14	ILE	3.0
17	AQ	36	ILE	3.0
33	DI	79	ILE	3.0
51	B4	56	VAL	3.0
2	AB	101	MET	3.0
10	AJ	100	THR	3.0
13	CM	67	GLU	3.0
5	CE	21	ALA	3.0
13	CM	75	ALA	3.0
13	CM	76	ALA	3.0
14	AN	59	ALA	3.0
46	DZ	159	PRO	3.0
31	DG	11	TYR	3.0
51	D4	63	TYR	3.0
3	CC	52	LEU	3.0
9	AI	56	LEU	3.0
39	DS	56	LEU	3.0
40	BT	125	ARG	3.0
26	DA	886	C	3.0

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Mol	Chain	Res	Type	RSRZ
16	AP	43	LYS	3.0
26	BA	2126	A	3.0
39	DS	60	GLY	3.0
2	AB	127	ILE	2.9
3	CC	86	VAL	2.9
10	CJ	44	VAL	2.9
23	AW	71	G	2.9
25	CY	57	G	2.9
26	DA	2123	G	2.9
2	AB	19	HIS	2.9
3	CC	121	ALA	2.9
9	AI	13	ALA	2.9
9	CI	45	ALA	2.9
16	AP	16	HIS	2.9
20	CT	97	ALA	2.9
31	DG	61	ALA	2.9
13	AM	102	ARG	2.9
13	CM	29	ARG	2.9
13	CM	88	ARG	2.9
4	CD	21	LEU	2.9
8	CH	39	LEU	2.9
39	DS	93	LYS	2.9
46	DZ	125	LEU	2.9
17	AQ	27	PHE	2.9
26	BA	1509	C	2.9
1	CA	992	U	2.9
1	CA	1126	U	2.9
1	AA	1001	A	2.9
25	AY	36	A	2.9
31	BG	76	SER	2.9
7	CG	81	GLY	2.9
9	AI	57	GLY	2.9
21	CU	16	GLY	2.9
43	DW	112	GLY	2.9
51	B4	4	GLY	2.9
51	B4	47	GLN	2.9
2	CB	41	ILE	2.9
2	AB	229	VAL	2.9
28	BD	28	GLU	2.9
31	DG	70	VAL	2.9
32	DH	76	VAL	2.9
46	DZ	74	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
10	CJ	68	HIS	2.9
2	AB	225	ALA	2.9
1	AA	1033	G	2.9
7	AG	79	ARG	2.9
14	CN	48	ALA	2.9
21	CU	15	ARG	2.9
28	DD	262	ARG	2.9
39	DS	72	ALA	2.9
8	CH	74	PRO	2.9
14	AN	14	PRO	2.9
25	CY	22	G	2.9
26	BA	2792	G	2.9
26	DA	2157	G	2.9
21	CU	3	LYS	2.9
4	AD	135	LEU	2.9
10	AJ	65	LEU	2.9
14	CN	44	LEU	2.9
19	CS	20	LEU	2.9
2	AB	33	TYR	2.9
16	CP	38	TYR	2.9
1	CA	962	C	2.9
26	BA	2167	U	2.9
2	CB	66	GLY	2.9
3	CC	25	GLY	2.9
5	CE	10	MET	2.9
9	CI	39	GLY	2.9
48	B1	2	SER	2.9
1	AA	161	A	2.9
3	AC	206	GLU	2.9
13	AM	84	ILE	2.9
14	CN	27	CYS	2.9
3	CC	64	VAL	2.9
30	DF	6	VAL	2.9
33	DI	81	VAL	2.9
16	CP	69	THR	2.9
19	AS	48	THR	2.9
46	BZ	170	THR	2.9
3	CC	149	ALA	2.9
19	CS	6	LYS	2.9
32	DH	102	ALA	2.9
33	DI	53	ALA	2.9
3	CC	111	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
10	AJ	71	LEU	2.9
10	AJ	88	LEU	2.9
39	DS	58	LEU	2.9
16	CP	48	TRP	2.9
1	AA	1001(A)	G	2.9
1	CA	1036	G	2.9
1	CA	1190	G	2.9
25	AY	24	G	2.9
7	AG	85	TYR	2.9
2	CB	152	PHE	2.9
3	CC	10	PHE	2.9
26	DA	2122	U	2.9
13	CM	84	ILE	2.9
26	DA	2794	C	2.9
1	AA	197	A	2.9
2	CB	184	VAL	2.9
3	AC	86	VAL	2.9
6	AF	88	VAL	2.9
13	CM	7	VAL	2.9
12	AL	126	LYS	2.9
13	CM	86	CYS	2.9
33	DI	127	VAL	2.9
46	DZ	71	VAL	2.9
46	DZ	86	VAL	2.9
14	CN	50	LYS	2.9
9	AI	7	THR	2.9
19	CS	63	THR	2.9
51	D4	44	THR	2.9
3	CC	92	ALA	2.9
3	CC	146	ALA	2.9
7	CG	39	ALA	2.9
3	CC	42	LEU	2.9
9	CI	85	LEU	2.9
10	AJ	40	LEU	2.9
46	DZ	76	LEU	2.9
46	DZ	157	LEU	2.9
1	CA	976	G	2.9
1	CA	1021	G	2.9
1	CA	1058	G	2.9
26	BA	2120	G	2.9
26	BA	2133	G	2.9
26	DA	2166	G	2.9

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Mol	Chain	Res	Type	RSRZ
14	CN	46	GLU	2.9
31	DG	119	GLY	2.9
3	CC	6	HIS	2.8
10	AJ	28	ARG	2.8
19	AS	4	SER	2.8
46	DZ	53	ILE	2.8
51	B4	69	LYS	2.8
2	AB	165	VAL	2.8
32	DH	45	VAL	2.8
46	BZ	111	VAL	2.8
46	DZ	139	VAL	2.8
23	CW	3	C	2.8
26	DA	2174	C	2.8
9	CI	49	PRO	2.8
13	AM	49	THR	2.8
14	CN	59	ALA	2.8
25	AY	21	A	2.8
41	DU	2	PRO	2.8
2	CB	173	ALA	2.8
3	CC	200	ALA	2.8
3	CC	47	LEU	2.8
9	CI	96	LEU	2.8
18	AR	79	LEU	2.8
51	D4	59	PHE	2.8
5	CE	133	TYR	2.8
9	CI	42	ARG	2.8
14	AN	51	GLY	2.8
32	DH	60	ARG	2.8
44	DX	33	LYS	2.8
46	BZ	160	GLY	2.8
1	CA	630	G	2.8
2	CB	32	ILE	2.8
8	CH	83	ILE	2.8
13	CM	9	ILE	2.8
26	BA	2166	G	2.8
26	DA	10	G	2.8
46	DZ	34	ASN	2.8
4	AD	105	VAL	2.8
10	CJ	77	PRO	2.8
17	AQ	28	PRO	2.8
8	CH	3	THR	2.8
12	CL	56	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
26	DA	2138	C	2.8
1	CA	1363(A)	A	2.8
10	CJ	71	LEU	2.8
26	BA	2892	A	2.8
7	CG	5	ARG	2.8
7	CG	32	ARG	2.8
10	CJ	5	ARG	2.8
14	CN	17	LYS	2.8
16	AP	75	ARG	2.8
9	CI	88	TYR	2.8
10	AJ	31	GLY	2.8
33	BI	89	TYR	2.8
9	CI	29	ASN	2.8
17	AQ	66	SER	2.8
46	DZ	149	SER	2.8
48	D1	2	SER	2.8
3	CC	173	VAL	2.8
1	AA	625	G	2.8
1	AA	1387	G	2.8
1	CA	1127	G	2.8
10	CJ	91	PRO	2.8
31	DG	142	PRO	2.8
32	DH	37	VAL	2.8
25	AY	1	G	2.8
32	DH	55	PRO	2.8
2	CB	44	LEU	2.8
2	CB	115	LEU	2.8
3	CC	65	ALA	2.8
39	DS	47	THR	2.8
3	CC	178	LEU	2.8
4	CD	155	LEU	2.8
19	CS	16	LEU	2.8
19	CS	30	LEU	2.8
1	CA	1029	C	2.8
26	BA	2128	C	2.8
26	DA	2139	C	2.8
26	DA	2140	C	2.8
1	CA	974	A	2.8
1	CA	1030(D)	A	2.8
46	DZ	138	GLU	2.8
2	AB	175	ARG	2.8
11	CK	126	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
40	BT	129	ARG	2.8
47	D0	74	ARG	2.8
51	B4	55	ARG	2.8
54	B7	47	ARG	2.8
4	AD	173	TRP	2.8
30	BF	208	GLY	2.8
3	AC	201	TYR	2.8
8	CH	111	ILE	2.8
18	CR	65	ILE	2.8
7	CG	77	SER	2.8
2	CB	15	VAL	2.8
1	CA	1532	U	2.8
3	CC	33	LEU	2.8
3	CC	196	LEU	2.8
7	AG	2	ALA	2.8
25	CY	6	G	2.8
25	CY	70	G	2.8
46	BZ	1	MET	2.8
2	AB	30	ARG	2.8
3	AC	107	GLN	2.8
10	CJ	83	GLU	2.8
14	CN	8	GLU	2.8
1	CA	1151	A	2.8
26	BA	2801(A)	A	2.8
26	DA	2175	C	2.8
3	CC	69	HIS	2.8
47	D0	3	HIS	2.8
2	CB	55	PHE	2.8
4	CD	206	PHE	2.8
21	CU	2	GLY	2.7
5	CE	109	ILE	2.7
45	DY	44	ILE	2.7
46	BZ	146	ILE	2.7
2	CB	131	PRO	2.7
10	CJ	37	PRO	2.7
13	CM	21	TYR	2.7
50	B3	2	PRO	2.7
5	AE	69	VAL	2.7
5	CE	115	VAL	2.7
41	DU	90	VAL	2.7
2	CB	142	LEU	2.7
10	CJ	65	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
46	DZ	5	LEU	2.7
47	D0	7	LEU	2.7
2	CB	13	ALA	2.7
9	CI	52	ALA	2.7
13	CM	51	ALA	2.7
31	DG	50	ALA	2.7
5	CE	81	GLU	2.7
32	BH	47	GLU	2.7
33	DI	54	GLN	2.7
46	DZ	119	GLU	2.7
25	CY	10	G	2.7
25	CY	69	G	2.7
26	DA	2319	G	2.7
25	AY	38	A	2.7
25	AY	56	C	2.7
26	BA	2108	C	2.7
11	CK	49	GLY	2.7
13	CM	89	GLY	2.7
16	AP	37	GLY	2.7
2	AB	222	ILE	2.7
11	AK	95	ILE	2.7
19	CS	49	ILE	2.7
31	DG	157	ILE	2.7
56	D9	17	ILE	2.7
10	AJ	91	PRO	2.7
2	CB	229	VAL	2.7
4	AD	170	VAL	2.7
5	CE	67	VAL	2.7
12	CL	55	VAL	2.7
32	DH	50	VAL	2.7
33	DI	144	VAL	2.7
39	DS	36	TYR	2.7
2	AB	221	LEU	2.7
3	CC	175	LEU	2.7
13	CM	34	LEU	2.7
2	CB	67	THR	2.7
3	CC	135	LYS	2.7
3	CC	160	ALA	2.7
10	CJ	86	MET	2.7
16	AP	44	THR	2.7
3	CC	126	ARG	2.7
44	DX	68	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
9	AI	91	ASP	2.7
19	CS	12	ASP	2.7
2	CB	228	GLY	2.7
1	AA	162	A	2.7
1	CA	949	A	2.7
1	CA	958	A	2.7
1	CA	1320	C	2.7
3	CC	186	PHE	2.7
12	AL	29	GLY	2.7
25	AY	71	G	2.7
26	BA	2141	G	2.7
26	BA	2157	G	2.7
25	CY	2	C	2.7
26	DA	2176	A	2.7
3	AC	124	ILE	2.7
13	AM	4	ILE	2.7
27	DB	88	C	2.7
46	DZ	146	ILE	2.7
8	CH	15	ASN	2.7
7	CG	80	VAL	2.7
9	CI	65	VAL	2.7
13	CM	98	VAL	2.7
19	CS	28	LYS	2.7
19	CS	32	LYS	2.7
51	D4	35	VAL	2.7
56	D9	16	VAL	2.7
2	CB	61	LEU	2.7
4	AD	21	LEU	2.7
12	CL	64	TYR	2.7
31	BG	152	LEU	2.7
31	DG	25	TYR	2.7
2	CB	53	ARG	2.7
5	AE	86	ALA	2.7
9	CI	107	ARG	2.7
14	AN	20	ALA	2.7
17	AQ	68	ARG	2.7
46	BZ	164	ALA	2.7
47	D0	2	ALA	2.7
13	CM	50	GLU	2.7
34	BN	68	GLU	2.7
19	CS	57	HIS	2.7
25	CY	33	U	2.7

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Mol	Chain	Res	Type	RSRZ
26	BA	1026	U	2.7
5	AE	5	ASP	2.7
3	CC	158	GLY	2.7
9	CI	57	GLY	2.7
41	DU	43	GLY	2.7
2	CB	172	ILE	2.7
31	DG	88	ILE	2.7
51	D4	22	ILE	2.7
1	CA	1001(A)	G	2.7
26	BA	2160	G	2.7
1	CA	995	C	2.7
1	CA	1217	C	2.7
20	CT	26	ASN	2.7
26	BA	2146	C	2.7
26	DA	2145	C	2.7
26	DA	2789	C	2.7
3	CC	130	VAL	2.7
4	AD	132	ARG	2.7
4	CD	170	VAL	2.7
8	AH	102	ARG	2.7
8	CH	9	MET	2.7
9	CI	56	LEU	2.7
13	CM	66	LEU	2.7
15	AO	60	VAL	2.7
15	CO	79	ARG	2.7
19	AS	71	LEU	2.7
20	AT	86	ARG	2.7
31	BG	139	LEU	2.7
33	DI	3	VAL	2.7
40	DT	111	ARG	2.7
44	DX	1	MET	2.7
39	DS	7	TYR	2.7
45	DY	55	TYR	2.7
46	DZ	99	TYR	2.7
2	AB	13	ALA	2.7
2	CB	88	ALA	2.7
3	CC	60	ALA	2.7
3	CC	67	THR	2.7
3	CC	137	ALA	2.7
31	DG	171	ALA	2.7
1	CA	1049	U	2.7
2	AB	228	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
2	CB	151	GLY	2.6
3	CC	197	GLY	2.6
5	CE	74	GLY	2.6
21	AU	2	GLY	2.6
32	BH	14	GLY	2.6
11	CK	125	PHE	2.6
15	CO	19	PRO	2.6
19	CS	76	PRO	2.6
31	BG	182	LYS	2.6
49	D2	8	LYS	2.6
5	CE	107	ARG	2.6
1	AA	1503	A	2.6
1	CA	978	A	2.6
1	CA	1285	A	2.6
10	AJ	78	ASN	2.6
2	CB	69	LEU	2.6
17	CQ	5	VAL	2.6
23	AW	73	A	2.6
26	DA	2134	A	2.6
26	DA	2171	A	2.6
27	DB	26	A	2.6
33	BI	44	LEU	2.6
1	CA	1262	C	2.6
23	CW	74	C	2.6
26	BA	34	C	2.6
26	BA	2142	C	2.6
26	DA	885	C	2.6
26	DA	2896	C	2.6
54	B7	46	VAL	2.6
10	AJ	25	GLU	2.6
27	DB	23	G	2.6
33	DI	99	GLU	2.6
3	CC	168	ALA	2.6
21	CU	18	TYR	2.6
29	DE	204	ALA	2.6
33	DI	146	ALA	2.6
37	DQ	28	ALA	2.6
46	BZ	152	ALA	2.6
3	CC	176	HIS	2.6
6	CF	55	ASP	2.6
8	AH	4	ASP	2.6
26	DA	2144	U	2.6

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Mol	Chain	Res	Type	RSRZ
6	AF	92	LYS	2.6
9	CI	72	GLY	2.6
54	D7	48	LYS	2.6
4	AD	110	PHE	2.6
14	CN	14	PRO	2.6
14	CN	36	PHE	2.6
15	CO	18	PHE	2.6
21	AU	23	PRO	2.6
33	DI	88	ILE	2.6
9	AI	66	ARG	2.6
10	CJ	43	ARG	2.6
2	AB	44	LEU	2.6
2	CB	145	LEU	2.6
2	CB	112	VAL	2.6
5	CE	51	VAL	2.6
5	CE	55	VAL	2.6
8	AH	129	VAL	2.6
9	CI	41	VAL	2.6
1	CA	996	A	2.6
9	CI	71	SER	2.6
25	CY	36	A	2.6
26	BA	896	A	2.6
39	DS	31	SER	2.6
1	CA	1028	C	2.6
4	CD	164	ALA	2.6
7	AG	7	ALA	2.6
9	CI	43	ALA	2.6
16	AP	45	THR	2.6
23	AW	72	C	2.6
26	DA	645	C	2.6
26	DA	888	C	2.6
26	DA	2137	C	2.6
36	BP	12	ALA	2.6
1	CA	1222	G	2.6
5	CE	60	TYR	2.6
25	AY	22	G	2.6
26	DA	883	G	2.6
6	AF	54	LYS	2.6
48	D1	78	LYS	2.6
3	CC	78	GLY	2.6
4	AD	23	GLY	2.6
19	CS	54	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
20	AT	69	GLY	2.6
21	CU	5	ASP	2.6
32	BH	100	GLY	2.6
1	CA	952	U	2.6
2	AB	234	PRO	2.6
2	AB	32	ILE	2.6
2	CB	80	ILE	2.6
3	CC	77	ILE	2.6
4	AD	204	ILE	2.6
6	CF	46	ARG	2.6
26	BA	2172	U	2.6
32	DH	39	PRO	2.6
50	D3	2	PRO	2.6
5	AE	10	MET	2.6
10	AJ	6	ILE	2.6
51	D4	55	ARG	2.6
8	CH	31	PHE	2.6
9	CI	59	PHE	2.6
9	AI	12	GLU	2.6
20	AT	62	LEU	2.6
39	DS	54	LEU	2.6
42	DV	25	LEU	2.6
48	B1	98	LEU	2.6
3	AC	66	VAL	2.6
3	CC	120	VAL	2.6
3	CC	138	VAL	2.6
8	CH	93	VAL	2.6
12	CL	18	VAL	2.6
32	DH	79	VAL	2.6
37	BQ	55	VAL	2.6
14	CN	32	SER	2.6
41	BU	117	GLN	2.6
5	CE	86	ALA	2.6
1	AA	1035	A	2.6
1	CA	1531	A	2.6
9	AI	103	THR	2.6
20	AT	67	ALA	2.6
33	DI	55	ALA	2.6
26	BA	548	A	2.6
39	DS	95	HIS	2.6
7	CG	154	TYR	2.6
14	CN	15	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
39	DS	19	LYS	2.6
1	CA	1032	G	2.6
25	AY	70	G	2.6
26	BA	2165	G	2.6
26	DA	2127	G	2.6
26	DA	2153	G	2.6
2	AB	14	GLY	2.6
3	CC	145	GLY	2.6
3	CC	205	GLY	2.6
4	AD	90	GLY	2.6
4	CD	134	ASP	2.6
12	CL	92	ASP	2.6
14	CN	19	ARG	2.6
14	CN	26	ARG	2.6
49	D2	18	PRO	2.6
39	DS	35	ILE	2.6
46	BZ	136	PHE	2.6
2	AB	231	GLU	2.6
10	AJ	90	LEU	2.6
47	D0	84	LEU	2.6
2	AB	136	VAL	2.6
3	CC	151	VAL	2.6
4	CD	45	GLN	2.6
11	CK	14	VAL	2.6
28	BD	203	ASN	2.6
42	DV	52	VAL	2.6
46	DZ	118	GLN	2.6
2	CB	107	THR	2.6
5	CE	104	ALA	2.6
28	DD	2	ALA	2.6
33	DI	100	ALA	2.6
47	D0	5	LYS	2.6
1	AA	1183	A	2.6
22	CV	24	A	2.6
8	AH	94	TYR	2.6
9	CI	62	TYR	2.6
1	CA	1118	C	2.5
2	AB	130	ARG	2.5
3	AC	79	ARG	2.5
4	AD	153	ARG	2.5
8	CH	92	ARG	2.5
25	AY	49	C	2.5

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Mol	Chain	Res	Type	RSRZ
26	DA	2108	C	2.5
9	AI	90	PRO	2.5
9	CI	100	GLY	2.5
10	AJ	36	GLY	2.5
10	CJ	10	GLY	2.5
15	AO	89	GLY	2.5
46	DZ	15	PRO	2.5
2	AB	41	ILE	2.5
15	CO	3	ILE	2.5
26	BA	11	G	2.5
26	DA	2110	G	2.5
26	DA	2120	G	2.5
46	DZ	124	ILE	2.5
2	AB	134	GLU	2.5
11	AK	92	GLU	2.5
39	DS	29	PHE	2.5
1	AA	204	U	2.5
1	CA	1358	U	2.5
2	CB	121	LEU	2.5
3	AC	188	LEU	2.5
3	CC	32	LEU	2.5
6	CF	48	LEU	2.5
13	CM	48	LEU	2.5
25	AY	47	U	2.5
25	AY	60	U	2.5
31	DG	175	LEU	2.5
2	CB	136	VAL	2.5
4	AD	148	VAL	2.5
7	CG	84	ASN	2.5
9	CI	86	VAL	2.5
10	AJ	76	ASN	2.5
16	CP	53	VAL	2.5
32	DH	17	VAL	2.5
20	AT	94	ALA	2.5
31	DG	57	ALA	2.5
40	DT	131	ALA	2.5
42	DV	85	LYS	2.5
14	CN	57	ARG	2.5
15	AO	88	ARG	2.5
16	AP	81	ARG	2.5
19	CS	3	ARG	2.5
21	AU	9	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	CA	1250	A	2.5
4	CD	165	MET	2.5
26	BA	2158	A	2.5
26	DA	1445	A	2.5
49	D2	1	MET	2.5
1	AA	1119	C	2.5
1	CA	1019	C	2.5
1	CA	1043	C	2.5
2	CB	14	GLY	2.5
2	CB	91	PRO	2.5
2	CB	232	PRO	2.5
4	AD	16	GLY	2.5
11	CK	90	GLY	2.5
12	AL	95	GLY	2.5
19	CS	68	GLY	2.5
20	CT	96	GLY	2.5
21	CU	4	GLY	2.5
21	AU	14	TRP	2.5
23	CW	4	C	2.5
26	BA	884	C	2.5
26	DA	2143	C	2.5
26	DA	2146	C	2.5
27	DB	6	C	2.5
37	DQ	33	GLY	2.5
51	D4	4	GLY	2.5
3	AC	18	TRP	2.5
4	AD	5	ILE	2.5
32	BH	4	ILE	2.5
46	BZ	171	ILE	2.5
31	DG	35	GLU	2.5
1	CA	993	G	2.5
1	CA	1283	G	2.5
1	CA	1310	G	2.5
3	CC	87	LEU	2.5
23	CW	19	G	2.5
26	BA	879	G	2.5
26	BA	1537	G	2.5
26	DA	2165	G	2.5
23	AW	20	U	2.5
13	CM	77	ASN	2.5
44	DX	49	VAL	2.5
2	AB	120	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
8	AH	7	ALA	2.5
19	CS	24	ALA	2.5
14	CN	24	CYS	2.5
53	D6	14	THR	2.5
4	CD	141	ARG	2.5
40	DT	108	ARG	2.5
37	DQ	1	MET	2.5
3	CC	23	TYR	2.5
9	AI	125	TYR	2.5
31	DG	32	PRO	2.5
51	D4	29	PRO	2.5
1	CA	969	A	2.5
1	CA	1357	A	2.5
3	CC	80	GLY	2.5
31	BG	42	GLY	2.5
45	BY	93	GLY	2.5
45	DY	103	GLY	2.5
46	BZ	106	GLY	2.5
3	CC	62	ASP	2.5
4	CD	102	ASP	2.5
16	CP	68	ASP	2.5
31	DG	147	ASP	2.5
9	CI	81	ILE	2.5
10	AJ	75	ILE	2.5
13	AM	39	ILE	2.5
1	CA	985	C	2.5
1	CA	990	C	2.5
1	CA	1063	C	2.5
2	AB	70	PHE	2.5
2	CB	213	LEU	2.5
5	CE	142	LEU	2.5
9	CI	37	PHE	2.5
9	CI	79	LEU	2.5
12	CL	32	PHE	2.5
31	BG	178	PHE	2.5
33	BI	75	LEU	2.5
33	DI	38	LEU	2.5
36	BP	99	LEU	2.5
2	AB	95	GLN	2.5
1	AA	223	U	2.5
1	CA	1020	U	2.5
3	AC	64	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
7	AG	75	VAL	2.5
9	AI	17	VAL	2.5
10	CJ	94	VAL	2.5
12	CL	43	VAL	2.5
42	DV	72	VAL	2.5
1	CA	1215	G	2.5
1	CA	1338	G	2.5
27	DB	117	G	2.5
2	CB	29	ALA	2.5
2	CB	62	ALA	2.5
2	CB	171	ALA	2.5
3	AC	61	ALA	2.5
3	CC	163	ALA	2.5
4	CD	209	ARG	2.5
6	AF	46	ARG	2.5
9	AI	119	ALA	2.5
10	AJ	27	ALA	2.5
13	CM	3	ARG	2.5
13	CM	71	ARG	2.5
21	AU	6	ARG	2.5
31	DG	118	ARG	2.5
45	BY	1	MET	2.5
4	AD	172	PRO	2.5
31	BG	2	PRO	2.5
2	CB	38	GLY	2.5
2	CB	134	GLU	2.5
29	BE	73	GLU	2.5
51	B4	45	GLY	2.5
11	AK	25	TYR	2.5
2	AB	42	ILE	2.5
12	CL	85	ILE	2.5
20	AT	100	ILE	2.5
33	DI	20	ASP	2.5
1	CA	1275	A	2.5
25	AY	73	A	2.5
25	CY	26	A	2.5
26	DA	2062	A	2.5
2	CB	11	LEU	2.5
3	AC	87	LEU	2.5
10	CJ	16	LEU	2.5
16	AP	27	LYS	2.5
32	BH	67	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
33	DI	47	LEU	2.5
5	AE	45	PHE	2.5
7	AG	26	PHE	2.5
14	CN	37	PHE	2.5
19	CS	56	GLN	2.5
31	DG	180	PHE	2.5
51	D4	42	PHE	2.5
1	CA	931	C	2.5
1	CA	1145	C	2.5
1	CA	1282	C	2.5
25	AY	11	C	2.5
26	BA	2111	C	2.5
2	AB	71	VAL	2.5
5	CE	33	VAL	2.5
5	CE	105	VAL	2.5
19	CS	51	VAL	2.5
33	BI	19	VAL	2.5
1	CA	950	U	2.5
1	CA	982	U	2.5
1	CA	997	U	2.5
4	AD	168	ARG	2.5
14	CN	12	ARG	2.5
15	CO	17	ARG	2.5
26	DA	271(K)	U	2.5
33	BI	67	ARG	2.5
2	AB	207	ALA	2.5
35	DO	33	ALA	2.5
5	AE	120	THR	2.5
9	CI	103	THR	2.5
10	CJ	48	THR	2.5
1	CA	1064	G	2.5
1	CA	1323	G	2.5
23	CW	15	G	2.5
23	CW	18	G	2.5
25	AY	5	G	2.5
25	CY	30	G	2.5
26	BA	2121	G	2.5
46	BZ	166	SER	2.5
36	DP	122	PRO	2.4
48	D1	68	PRO	2.4
3	AC	185	GLY	2.4
11	AK	37	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
3	CC	57	ILE	2.4
3	CC	93	LYS	2.4
4	CD	146	ILE	2.4
10	CJ	50	ILE	2.4
13	AM	21	TYR	2.4
16	AP	38	TYR	2.4
20	AT	68	LYS	2.4
21	AU	13	ILE	2.4
34	BN	71	ILE	2.4
55	D8	29	LYS	2.4
3	CC	34	LEU	2.4
20	CT	99	LEU	2.4
49	D2	35	LEU	2.4
1	CA	1183	A	2.4
1	CA	1251	A	2.4
1	CA	1280	A	2.4
1	CA	1287	A	2.4
1	CA	1333	A	2.4
2	AB	17	PHE	2.4
3	CC	31	HIS	2.4
5	CE	84	PHE	2.4
22	CV	15	A	2.4
2	CB	36	ARG	2.4
21	AU	15	ARG	2.4
1	CA	1114	C	2.4
7	CG	75	VAL	2.4
13	CM	54	VAL	2.4
26	BA	2174	C	2.4
13	AM	5	ALA	2.4
13	CM	28	ALA	2.4
19	CS	44	MET	2.4
25	CY	12	U	2.4
26	BA	2150	U	2.4
36	DP	1	MET	2.4
13	AM	105	THR	2.4
2	CB	150	SER	2.4
2	AB	131	PRO	2.4
16	AP	41	PRO	2.4
4	CD	179	GLU	2.4
46	BZ	119	GLU	2.4
1	AA	1003	G	2.4
1	AA	1030(C)	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	CA	1221	G	2.4
1	CA	1316	G	2.4
2	CB	133	LYS	2.4
3	AC	27	LYS	2.4
9	CI	69	GLY	2.4
10	AJ	93	GLY	2.4
12	AL	91	LYS	2.4
23	AW	15	G	2.4
23	CW	10	G	2.4
25	AY	53	G	2.4
26	BA	2127	G	2.4
26	DA	2149	G	2.4
51	D4	2	LYS	2.4
8	AH	134	ILE	2.4
19	AS	12	ASP	2.4
3	CC	123	GLN	2.4
4	AD	4	TYR	2.4
7	CG	86	GLN	2.4
9	AI	87	GLN	2.4
9	CI	99	LEU	2.4
10	AJ	8	LEU	2.4
19	AS	5	LEU	2.4
19	CS	61	TYR	2.4
40	DT	68	TYR	2.4
46	BZ	121	HIS	2.4
20	AT	8	ARG	2.4
37	DQ	59	ARG	2.4
46	DZ	88	PHE	2.4
22	CV	23	A	2.4
25	AY	58	A	2.4
26	BA	529	A	2.4
2	CB	174	VAL	2.4
9	AI	26	VAL	2.4
13	CM	106	ASN	2.4
14	AN	56	VAL	2.4
14	AN	61	TRP	2.4
31	BG	149	VAL	2.4
45	DY	3	VAL	2.4
46	BZ	161	VAL	2.4
1	AA	1008	C	2.4
10	CJ	27	ALA	2.4
15	CO	16	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
26	BA	886	C	2.4
26	BA	2163	C	2.4
26	DA	2111	C	2.4
1	CA	1364	U	2.4
16	CP	45	THR	2.4
26	BA	2897	U	2.4
47	D0	43	THR	2.4
2	CB	192	SER	2.4
9	CI	110	GLU	2.4
10	CJ	35	SER	2.4
14	CN	9	LYS	2.4
7	AG	132	GLY	2.4
36	DP	93	GLY	2.4
46	BZ	12	GLY	2.4
2	AB	208	ILE	2.4
2	CB	223	ILE	2.4
3	AC	84	ILE	2.4
20	CT	100	ILE	2.4
21	CU	13	ILE	2.4
1	AA	1032	G	2.4
1	CA	1124	G	2.4
17	CQ	98	LEU	2.4
25	AY	34	G	2.4
26	BA	880	G	2.4
26	BA	1047	G	2.4
45	DY	57	GLN	2.4
46	DZ	41	LEU	2.4
5	CE	25	ARG	2.4
9	CI	128	ARG	2.4
10	CJ	62	HIS	2.4
19	AS	14	HIS	2.4
19	AS	29	ARG	2.4
9	CI	33	PHE	2.4
3	CC	66	VAL	2.4
5	CE	82	VAL	2.4
31	DG	149	VAL	2.4
46	DZ	27	VAL	2.4
1	AA	160	A	2.4
1	AA	1286	A	2.4
1	CA	415	A	2.4
25	CY	64	A	2.4
39	DS	61	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
2	AB	34	ALA	2.4
11	AK	68	ALA	2.4
46	DZ	152	ALA	2.4
2	AB	22	LYS	2.4
2	CB	54	THR	2.4
8	CH	101	PRO	2.4
13	CM	10	PRO	2.4
30	BF	14	PRO	2.4
35	DO	31	LYS	2.4
36	DP	76	LYS	2.4
53	B6	4	GLU	2.4
56	D9	8	LYS	2.4
1	CA	1012	U	2.4
8	CH	29	SER	2.4
17	CQ	99	SER	2.4
23	AW	13	C	2.4
25	CY	59	U	2.4
26	BA	9	U	2.4
26	DA	34	C	2.4
46	BZ	92	SER	2.4
31	DG	42	GLY	2.4
39	DS	45	GLY	2.4
46	DZ	26	GLY	2.4
8	CH	100	ILE	2.4
2	AB	118	LEU	2.4
4	AD	101	LEU	2.4
4	AD	186	LEU	2.4
15	AO	62	GLN	2.4
46	BZ	103	ARG	2.4
46	DZ	103	ARG	2.4
47	B0	7	LEU	2.4
51	B4	62	ARG	2.4
51	D4	40	HIS	2.4
8	CH	135	CYS	2.4
45	DY	79	CYS	2.4
1	AA	183	G	2.4
1	CA	1022	G	2.4
1	CA	1156	G	2.4
3	CC	29	TYR	2.4
6	AF	63	TYR	2.4
10	AJ	47	PHE	2.4
23	AW	65	G	2.4

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Mol	Chain	Res	Type	RSRZ
23	CW	65	G	2.4
26	BA	2116	G	2.4
51	B4	43	TYR	2.4
7	CG	17	VAL	2.4
15	CO	60	VAL	2.4
33	DI	145	VAL	2.4
39	DS	14	VAL	2.4
39	DS	46	VAL	2.4
54	D7	46	VAL	2.4
2	CB	37	ASN	2.4
20	AT	9	ASN	2.4
40	DT	104	ASN	2.4
2	CB	75	LYS	2.4
3	CC	61	ALA	2.4
44	DX	2	LYS	2.4
3	CC	18	TRP	2.4
4	AD	179	GLU	2.4
25	AY	9	A	2.4
26	BA	2169	A	2.4
26	BA	2170	A	2.4
7	AG	156	TRP	2.4
8	CH	5	PRO	2.3
9	AI	27	THR	2.3
10	AJ	87	THR	2.3
10	CJ	100	THR	2.3
21	CU	8	THR	2.3
31	DG	145	THR	2.3
17	CQ	97	SER	2.3
1	AA	1446	U	2.3
1	CA	961	U	2.3
1	CA	1205	U	2.3
26	BA	12	U	2.3
27	DB	22	U	2.3
9	CI	115	GLY	2.3
23	CW	25	C	2.3
24	AX	67	C	2.3
25	AY	13	C	2.3
26	BA	898	C	2.3
26	BA	2137	C	2.3
2	AB	213	LEU	2.3
3	AC	32	LEU	2.3
3	AC	182	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
14	CN	31	ARG	2.3
14	CN	41	ARG	2.3
31	DG	33	ARG	2.3
6	AF	19	LEU	2.3
18	AR	85	LEU	2.3
30	DF	12	LEU	2.3
51	D4	15	ILE	2.3
31	DG	102	PHE	2.3
32	DH	123	PHE	2.3
3	CC	68	VAL	2.3
9	AI	127	LYS	2.3
13	CM	36	LYS	2.3
14	AN	4	LYS	2.3
14	AN	15	LYS	2.3
21	CU	20	LYS	2.3
34	BN	9	VAL	2.3
39	DS	69	VAL	2.3
42	DV	51	VAL	2.3
1	CA	953	G	2.3
1	CA	998	G	2.3
1	CA	1088	G	2.3
1	CA	1184	G	2.3
10	CJ	69	ASN	2.3
24	CX	46	G	2.3
26	BA	614(B)	G	2.3
26	BA	883	G	2.3
26	DA	271(M)	G	2.3
26	DA	2206	G	2.3
27	DB	54	G	2.3
45	DY	69	ALA	2.3
51	D4	30	GLU	2.3
9	CI	98	PRO	2.3
15	CO	75	PRO	2.3
2	AB	107	THR	2.3
8	CH	138	TRP	2.3
23	AW	14	A	2.3
23	CW	26	A	2.3
25	CY	73	A	2.3
26	BA	887	A	2.3
26	BA	899	A	2.3
26	DA	2158	A	2.3
26	DA	2801(A)	A	2.3

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Mol	Chain	Res	Type	RSRZ
3	CC	20	SER	2.3
9	AI	69	GLY	2.3
9	AI	104	ARG	2.3
35	DO	110	GLY	2.3
36	DP	118	GLY	2.3
42	DV	41	GLY	2.3
1	CA	1000	U	2.3
1	CA	1232	U	2.3
20	AT	18	GLN	2.3
25	AY	33	U	2.3
3	CC	39	ILE	2.3
4	AD	188	LEU	2.3
5	CE	71	LEU	2.3
10	CJ	23	ILE	2.3
12	CL	27	LEU	2.3
46	BZ	151	HIS	2.3
1	AA	154	C	2.3
1	AA	1029	C	2.3
1	CA	1008	C	2.3
1	CA	1109	C	2.3
1	CA	1223	C	2.3
26	BA	889	C	2.3
27	DB	5	C	2.3
29	BE	1	MET	2.3
2	CB	22	LYS	2.3
12	CL	13	LYS	2.3
12	CL	123	LYS	2.3
14	CN	11	LYS	2.3
9	AI	65	VAL	2.3
9	CI	108	VAL	2.3
16	AP	79	VAL	2.3
37	DQ	35	VAL	2.3
39	DS	98	VAL	2.3
9	CI	12	GLU	2.3
15	CO	14	GLU	2.3
2	AB	123	ALA	2.3
2	CB	177	ALA	2.3
2	CB	207	ALA	2.3
4	AD	48	ALA	2.3
5	AE	138	ALA	2.3
7	CG	25	ALA	2.3
9	AI	46	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
10	CJ	18	ALA	2.3
40	DT	126	ALA	2.3
54	D7	45	ALA	2.3
1	AA	220	G	2.3
1	AA	927	G	2.3
1	AA	1530	G	2.3
1	CA	1031	G	2.3
10	CJ	67	THR	2.3
21	CU	9	ARG	2.3
26	DA	2151	G	2.3
31	BG	93	THR	2.3
3	CC	79	ARG	2.3
5	AE	18	ARG	2.3
10	AJ	5	ARG	2.3
31	DG	128	ARG	2.3
51	D4	58	ARG	2.3
1	AA	1030(D)	A	2.3
2	AB	224	GLN	2.3
4	AD	167	GLY	2.3
4	CD	130	GLY	2.3
4	CD	152	SER	2.3
16	CP	78	GLY	2.3
25	CY	21	A	2.3
26	BA	229	A	2.3
26	BA	2062	A	2.3
10	CJ	33	GLN	2.3
46	DZ	142	SER	2.3
2	CB	155	LEU	2.3
3	CC	101	LEU	2.3
4	CD	78	LEU	2.3
8	AH	112	LEU	2.3
15	AO	66	LEU	2.3
19	AS	15	LEU	2.3
31	DG	3	LEU	2.3
31	DG	52	ILE	2.3
48	D1	94	LEU	2.3
49	D2	3	LEU	2.3
1	CA	1196	U	2.3
26	BA	272(A)	U	2.3
26	DA	1026	U	2.3
26	DA	2150	U	2.3
2	CB	83	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	AA	1054	C	2.3
2	CB	132	LYS	2.3
3	CC	45	LYS	2.3
23	AW	2	C	2.3
26	BA	2140	C	2.3
26	DA	2161	C	2.3
7	CG	26	PHE	2.3
15	AO	18	PHE	2.3
35	DO	99	PHE	2.3
2	AB	9	GLU	2.3
3	AC	23	TYR	2.3
12	CL	104	VAL	2.3
32	BH	15	VAL	2.3
39	DS	85	VAL	2.3
46	DZ	90	VAL	2.3
46	DZ	141	VAL	2.3
2	CB	202	PRO	2.3
3	AC	63	ASN	2.3
4	AD	77	ASN	2.3
7	CG	7	ALA	2.3
9	AI	52	ALA	2.3
9	CI	46	ALA	2.3
9	CI	122	ALA	2.3
11	AK	23	ALA	2.3
13	CM	30	ALA	2.3
13	CM	97	PRO	2.3
14	CN	54	PRO	2.3
18	AR	87	ARG	2.3
19	CS	29	ARG	2.3
19	CS	36	ARG	2.3
32	DH	59	ARG	2.3
53	D6	44	ARG	2.3
4	AD	69	GLY	2.3
13	AM	26	GLY	2.3
16	AP	78	GLY	2.3
20	AT	101	GLY	2.3
33	DI	16	GLY	2.3
43	BW	111	HIS	2.3
46	BZ	52	SER	2.3
46	DZ	32	HIS	2.3
48	D1	28	GLY	2.3
49	D2	9	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	AA	346	G	2.3
1	AA	631	G	2.3
1	AA	928	G	2.3
1	AA	1010	G	2.3
1	CA	1182	G	2.3
1	CA	1305	G	2.3
2	AB	187	LEU	2.3
5	AE	31	LEU	2.3
12	CL	52	LEU	2.3
15	CO	57	LEU	2.3
25	AY	27	G	2.3
26	BA	2207	G	2.3
1	CA	1044	A	2.3
22	AV	24	A	2.3
32	BH	92	ILE	2.3
45	DY	61	ILE	2.3
11	AK	36	ASP	2.3
45	DY	21	LYS	2.3
23	AW	47	U	2.3
1	AA	174	C	2.3
1	CA	1359	C	2.3
5	CE	6	PHE	2.3
10	AJ	97	GLU	2.3
17	AQ	24	GLU	2.3
25	AY	25	C	2.3
25	CY	13	C	2.3
26	BA	652(S)	C	2.3
26	BA	2138	C	2.3
27	BB	88	C	2.3
31	BG	13	GLU	2.3
4	AD	121	VAL	2.3
5	CE	100	VAL	2.3
16	CP	51	VAL	2.3
31	DG	109	VAL	2.3
32	DH	43	VAL	2.3
33	BI	127	VAL	2.3
2	CB	148	TYR	2.3
3	CC	172	ARG	2.3
7	AG	3	ARG	2.3
8	CH	27	PRO	2.3
3	AC	60	ALA	2.2
3	AC	117	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
8	CH	124	ALA	2.2
9	AI	45	ALA	2.2
9	AI	114	TYR	2.3
31	DG	16	ARG	2.3
33	DI	50	ARG	2.3
33	BI	146	ALA	2.2
39	DS	94	TYR	2.3
44	DX	60	ARG	2.3
33	DI	108	THR	2.2
37	BQ	21	THR	2.2
3	AC	28	GLN	2.2
9	AI	24	GLY	2.2
9	AI	67	GLY	2.2
10	CJ	84	GLN	2.2
20	AT	102	GLY	2.2
31	BG	119	GLY	2.2
3	AC	34	LEU	2.2
5	CE	139	LEU	2.2
12	AL	100	ILE	2.2
28	DD	276	LYS	2.2
31	BG	140	ILE	2.2
33	DI	1	MET	2.2
48	D1	8	SER	2.2
49	D2	16	LEU	2.2
53	D6	54	ILE	2.2
56	B9	17	ILE	2.2
1	AA	532	A	2.2
1	AA	1041	A	2.2
1	CA	986	A	2.2
11	AK	42	TRP	2.2
31	BG	29	TRP	2.2
1	CA	631	G	2.2
1	CA	1013	G	2.2
1	CA	1087	G	2.2
26	BA	271(M)	G	2.2
1	AA	343	U	2.2
1	CA	1308	U	2.2
26	BA	2118	U	2.2
2	CB	17	PHE	2.2
1	AA	1030	C	2.2
1	CA	984	C	2.2
1	CA	1007	C	2.2

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Mol	Chain	Res	Type	RSRZ
2	AB	167	PRO	2.2
3	AC	75	VAL	2.2
3	CC	88	ARG	2.2
4	AD	3	ARG	2.2
4	AD	50	ARG	2.2
4	AD	88	VAL	2.2
4	AD	209	ARG	2.2
9	AI	21	PRO	2.2
17	AQ	77	VAL	2.2
17	CQ	56	VAL	2.2
21	CU	7	ARG	2.2
31	DG	83	ARG	2.2
31	DG	122	PRO	2.2
31	DG	136	ARG	2.2
32	DH	6	ARG	2.2
27	DB	4	C	2.2
33	DI	18	VAL	2.2
33	DI	52	ARG	2.2
46	BZ	112	ARG	2.2
46	DZ	42	VAL	2.2
47	D0	44	ARG	2.2
47	D0	55	ARG	2.2
48	D1	76	ARG	2.2
24	AX	69	C	2.2
26	BA	645	C	2.2
26	DA	2128	C	2.2
51	D4	33	VAL	2.2
3	CC	181	ASN	2.2
11	AK	89	ALA	2.2
13	AM	18	ALA	2.2
11	CK	25	TYR	2.2
31	BG	25	TYR	2.2
51	D4	43	TYR	2.2
2	AB	110	GLN	2.2
13	CM	49	THR	2.2
9	CI	97	LYS	2.2
19	CS	46	GLY	2.2
31	DG	129	GLY	2.2
35	DO	113	LYS	2.2
4	AD	19	LEU	2.2
31	BG	82	LEU	2.2
31	DG	133	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
32	DH	64	LEU	2.2
33	BI	68	LEU	2.2
2	AB	124	SER	2.2
2	CB	214	ILE	2.2
8	CH	35	ILE	2.2
30	BF	13	SER	2.2
31	DG	76	SER	2.2
39	DS	40	ILE	2.2
31	DG	4	ASP	2.2
30	DF	172	TRP	2.2
2	CB	231	GLU	2.2
3	CC	122	GLU	2.2
26	DA	655	A	2.2
27	DB	58	A	2.2
1	AA	1126	U	2.2
25	AY	59	U	2.2
1	AA	148	G	2.2
1	AA	1529	G	2.2
1	CA	988	G	2.2
1	CA	1023	G	2.2
1	CA	1094	G	2.2
5	CE	27	ARG	2.2
10	AJ	43	ARG	2.2
12	AL	89	ARG	2.2
25	CY	63	G	2.2
26	BA	1107	G	2.2
26	BA	2206	G	2.2
26	DA	171	G	2.2
26	DA	614(B)	G	2.2
26	DA	1537	G	2.2
49	B2	69	ARG	2.2
2	AB	232	PRO	2.2
3	AC	109	PRO	2.2
3	CC	70	VAL	2.2
3	CC	207	VAL	2.2
17	CQ	23	VAL	2.2
19	CS	58	VAL	2.2
29	BE	21	VAL	2.2
32	DH	49	VAL	2.2
32	DH	173	PRO	2.2
46	DZ	161	VAL	2.2
1	AA	63	C	2.2

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Mol	Chain	Res	Type	RSRZ
9	AI	43	ALA	2.2
17	CQ	44	ALA	2.2
19	AS	65	ASN	2.2
25	AY	4	C	2.2
26	BA	2896	C	2.2
45	DY	78	ALA	2.2
3	CC	150	LYS	2.2
3	CC	199	LYS	2.2
5	CE	20	GLN	2.2
15	CO	5	LYS	2.2
10	AJ	86	MET	2.2
11	CK	119	CYS	2.2
17	AQ	95	TYR	2.2
19	CS	48	THR	2.2
20	AT	71	THR	2.2
4	CD	174	LEU	2.2
8	CH	59	LEU	2.2
14	CN	28	GLY	2.2
16	CP	6	LEU	2.2
30	DF	131	GLY	2.2
31	BG	106	LEU	2.2
33	BI	38	LEU	2.2
51	D4	9	LEU	2.2
4	AD	146	ILE	2.2
5	CE	118	ILE	2.2
31	DG	101	ILE	2.2
3	CC	154	SER	2.2
4	AD	71	SER	2.2
3	CC	183	ASP	2.2
9	AI	75	ASP	2.2
4	CD	122	ARG	2.2
9	AI	120	ARG	2.2
18	CR	64	ARG	2.2
55	D8	46	ARG	2.2
1	AA	1040	U	2.2
1	CA	414	A	2.2
1	CA	532	A	2.2
1	CA	1056	U	2.2
1	CA	1093	A	2.2
1	CA	1110	A	2.2
1	CA	1191	A	2.2
8	AH	89	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
26	BA	1963	U	2.2
26	DA	2130	U	2.2
31	DG	23	PHE	2.2
11	AK	30	VAL	2.2
11	CK	109	VAL	2.2
34	DN	5	VAL	2.2
44	DX	81	VAL	2.2
1	CA	966	G	2.2
1	CA	1030(C)	G	2.2
1	CA	1047	G	2.2
1	CA	1053	G	2.2
16	AP	35	LYS	2.2
17	CQ	100	LYS	2.2
23	AW	6	G	2.2
25	CY	52	G	2.2
26	BA	2123	G	2.2
3	AC	98	ASN	2.2
3	CC	117	ALA	2.2
5	CE	134	ALA	2.2
10	AJ	69	ASN	2.2
16	CP	14	ASN	2.2
7	CG	144	MET	2.2
46	DZ	28	MET	2.2
1	CA	1354	C	2.2
2	AB	18	GLY	2.2
2	AB	227	GLY	2.2
4	AD	180	GLY	2.2
8	AH	2	LEU	2.2
8	CH	112	LEU	2.2
13	CM	70	LEU	2.2
21	AU	19	GLY	2.2
26	BA	2175	C	2.2
26	BA	2791	C	2.2
36	BP	105	LEU	2.2
44	DX	94	GLY	2.2
46	DZ	59	LEU	2.2
49	D2	32	LEU	2.2
49	D2	60	LEU	2.2
5	CE	131	ILE	2.2
11	CK	40	ILE	2.2
46	BZ	142	SER	2.2
46	BZ	149	SER	2.2

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Mol	Chain	Res	Type	RSRZ
8	CH	99	GLU	2.2
31	DG	30	GLU	2.2
31	DG	116	ASP	2.2
36	BP	149	GLU	2.2
46	DZ	169	GLU	2.2
4	CD	47	ARG	2.2
7	CG	115	ARG	2.2
8	AH	30	ARG	2.2
8	CH	104	ARG	2.2
13	CM	99	ARG	2.2
20	CT	86	ARG	2.2
31	DG	95	ARG	2.2
39	DS	97	ARG	2.2
33	DI	137	PRO	2.2
1	AA	228	A	2.1
1	AA	1005	A	2.1
1	CA	991	U	2.2
5	AE	28	PHE	2.2
9	AI	37	PHE	2.2
15	CO	10	LYS	2.2
19	CS	7	LYS	2.2
31	DG	125	PHE	2.2
36	DP	91	PHE	2.2
1	CA	1014	A	2.1
1	CA	1252	A	2.1
1	CA	1324	A	2.1
1	CA	1447	A	2.1
3	AC	120	VAL	2.1
5	AE	67	VAL	2.1
8	AH	61	VAL	2.1
9	AI	14	VAL	2.1
12	CL	24	VAL	2.1
13	AM	45	VAL	2.1
17	CQ	77	VAL	2.1
26	BA	1508	A	2.1
29	DE	75	VAL	2.1
32	DH	44	VAL	2.1
33	BI	136	VAL	2.1
3	AC	31	HIS	2.1
3	AC	200	ALA	2.1
5	CE	66	MET	2.1
10	AJ	33	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
16	AP	76	GLN	2.1
18	CR	20	ALA	2.1
31	DG	169	ALA	2.1
39	DS	79	ALA	2.1
40	DT	55	ASN	2.1
54	B7	45	ALA	2.1
1	CA	1276	G	2.1
1	CA	1312	G	2.1
2	CB	203	GLY	2.1
4	AD	174	LEU	2.1
7	CG	34	GLY	2.1
7	CG	59	LEU	2.1
9	CI	30	GLY	2.1
13	CM	37	THR	2.1
15	AO	22	THR	2.1
18	AR	25	THR	2.1
21	CU	19	GLY	2.1
24	CX	70	G	2.1
26	BA	275	G	2.1
26	BA	882	G	2.1
26	BA	2151	G	2.1
26	BA	2152	G	2.1
32	DH	103	LEU	2.1
32	DH	166	GLY	2.1
36	DP	105	LEU	2.1
40	DT	69	GLY	2.1
42	DV	48	GLY	2.1
46	DZ	91	LEU	2.1
3	AC	77	ILE	2.1
3	CC	184	TYR	2.1
8	CH	58	TYR	2.1
15	AO	3	ILE	2.1
32	DH	148	ILE	2.1
39	DS	82	ILE	2.1
1	AA	1007	C	2.1
1	CA	1218	C	2.1
26	DA	2297	C	2.1
2	CB	49	GLU	2.1
2	CB	129	GLU	2.1
3	CC	16	ARG	2.1
3	CC	131	ARG	2.1
7	AG	155	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
10	AJ	64	GLU	2.1
28	DD	268	ARG	2.1
31	BG	16	ARG	2.1
47	D0	68	GLU	2.1
12	CL	50	SER	2.1
46	DZ	92	SER	2.1
49	D2	51	ARG	2.1
2	CB	167	PRO	2.1
5	CE	128	PRO	2.1
17	AQ	37	LYS	2.1
31	DG	87	PRO	2.1
1	AA	65	U	2.1
1	CA	1083	U	2.1
2	AB	16	HIS	2.1
15	CO	27	VAL	2.1
16	AP	53	VAL	2.1
46	BZ	165	VAL	2.1
1	CA	1041	A	2.1
3	CC	136	GLN	2.1
25	CY	60	U	2.1
26	DA	895	U	2.1
3	AC	169	ALA	2.1
6	AF	99	ALA	2.1
7	AG	39	ALA	2.1
26	BA	278	A	2.1
26	BA	890	A	2.1
40	DT	116	ALA	2.1
2	CB	204	ASN	2.1
3	AC	52	LEU	2.1
3	AC	155	GLY	2.1
5	CE	23	GLY	2.1
5	CE	114	GLY	2.1
5	CE	116	THR	2.1
8	CH	128	GLY	2.1
8	CH	131	GLY	2.1
12	AL	27	LEU	2.1
14	CN	51	GLY	2.1
16	AP	49	LEU	2.1
32	BH	103	LEU	2.1
36	DP	88	LEU	2.1
39	DS	90	GLY	2.1
3	AC	57	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
3	CC	14	ILE	2.1
4	AD	70	ILE	2.1
5	AE	11	ILE	2.1
8	AH	100	ILE	2.1
13	CM	22	ILE	2.1
39	DS	39	ILE	2.1
2	AB	21	ARG	2.1
1	AA	102	G	2.1
1	AA	159	G	2.1
1	AA	1009	G	2.1
1	AA	1022	G	2.1
1	CA	1373	G	2.1
2	AB	129	GLU	2.1
7	CG	151	TYR	2.1
9	AI	9	ARG	2.1
13	CM	110	ARG	2.1
16	AP	32	TYR	2.1
16	CP	75	ARG	2.1
20	CT	8	ARG	2.1
26	BA	100	G	2.1
26	DA	11	G	2.1
26	DA	2207	G	2.1
27	DB	87	G	2.1
48	D1	75	GLU	2.1
1	CA	989	C	2.1
1	CA	1129	C	2.1
1	CA	1203	C	2.1
10	AJ	17	ASP	2.1
20	AT	82	SER	2.1
25	CY	3	C	2.1
26	DA	902	C	2.1
51	B4	66	SER	2.1
4	AD	86	LYS	2.1
10	CJ	80	LYS	2.1
13	AM	120	LYS	2.1
18	CR	21	LYS	2.1
19	CS	70	LYS	2.1
28	DD	38	LYS	2.1
12	CL	94	PRO	2.1
19	CS	59	PRO	2.1
32	DH	8	PRO	2.1
7	AG	153	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
8	AH	31	PHE	2.1
18	CR	43	PHE	2.1
40	DT	22	PHE	2.1
4	CD	112	VAL	2.1
9	CI	3	GLN	2.1
16	AP	20	VAL	2.1
17	AQ	11	VAL	2.1
17	AQ	35	VAL	2.1
18	CR	86	VAL	2.1
29	BE	75	VAL	2.1
32	DH	35	VAL	2.1
1	AA	173	U	2.1
1	AA	1000	U	2.1
7	AG	116	ALA	2.1
11	AK	74	ALA	2.1
20	CT	95	ALA	2.1
26	DA	2189	U	2.1
39	DS	55	ALA	2.1
1	AA	143	A	2.1
1	AA	452	A	2.1
1	AA	1502	A	2.1
1	CA	1236	A	2.1
3	AC	94	LEU	2.1
13	CM	96	LEU	2.1
25	CY	58	A	2.1
26	DA	2169	A	2.1
26	DA	2310	A	2.1
31	DG	172	LEU	2.1
36	BP	138	LEU	2.1
52	D5	58	LEU	2.1
16	CP	67	THR	2.1
51	D4	24	THR	2.1
2	AB	56	ARG	2.1
31	DG	9	ARG	2.1
34	BN	12	ARG	2.1
3	CC	84	ILE	2.1
3	CC	90	GLU	2.1
10	AJ	50	ILE	2.1
37	BQ	139	GLU	2.1
3	CC	201	TYR	2.1
9	CI	114	TYR	2.1
12	CL	120	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
16	CP	39	TYR	2.1
47	D0	26	TYR	2.1
11	CK	51	LYS	2.1
17	AQ	13	ASP	2.1
31	BG	75	LYS	2.1
47	B0	5	LYS	2.1
33	BI	91	SER	2.1
46	DZ	52	SER	2.1
49	D2	45	SER	2.1
1	AA	66	G	2.1
1	AA	348	G	2.1
1	CA	1011	G	2.1
1	CA	1084	G	2.1
1	CA	1258	G	2.1
1	CA	1365	G	2.1
25	AY	57	G	2.1
26	DA	1533	G	2.1
1	AA	1030(B)	C	2.1
1	CA	1209	C	2.1
4	AD	197	PRO	2.1
25	CY	11	C	2.1
27	DB	62	C	2.1
46	DZ	134	PRO	2.1
9	CI	117	HIS	2.1
4	CD	201	GLN	2.1
10	AJ	63	PHE	2.1
11	CK	13	GLN	2.1
29	DE	51	PHE	2.1
31	BG	26	GLN	2.1
3	CC	99	VAL	2.1
31	BG	28	VAL	2.1
31	DG	178	PHE	2.1
33	BI	107	VAL	2.1
45	DY	45	VAL	2.1
2	CB	186	ALA	2.1
3	AC	168	ALA	2.1
4	CD	195	ALA	2.1
5	AE	134	ALA	2.1
9	AI	82	ALA	2.1
12	CL	30	ALA	2.1
33	BI	59	ALA	2.1
50	D3	25	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	CA	1235	U	2.1
2	AB	37	ASN	2.1
6	AF	13	ASN	2.1
6	CF	19	LEU	2.1
11	CK	42	TRP	2.1
16	AP	59	TRP	2.1
2	CB	30	ARG	2.1
3	AC	83	ARG	2.1
5	AE	22	GLY	2.1
8	CH	43	GLY	2.1
9	CI	93	ARG	2.1
10	AJ	29	ARG	2.1
14	AN	23	ARG	2.1
18	CR	40	LEU	2.1
19	AS	81	ARG	2.1
26	DA	271(L)	U	2.1
32	BH	98	LEU	2.1
33	DI	31	LEU	2.1
35	BO	49	ARG	2.1
37	DQ	6	ARG	2.1
46	DZ	18	LEU	2.1
48	D1	46	LEU	2.1
14	AN	55	GLY	2.1
47	D0	73	GLY	2.1
56	D9	4	ARG	2.1
3	CC	19	GLU	2.1
10	AJ	42	THR	2.1
13	CM	58	GLU	2.1
19	CS	64	GLU	2.1
33	DI	76	THR	2.1
33	DI	86	THR	2.1
1	AA	134	A	2.1
1	CA	250	A	2.1
1	CA	946	A	2.1
1	CA	1015	A	2.1
8	AH	86	ILE	2.1
13	CM	25	ILE	2.1
19	AS	49	ILE	2.1
25	AY	64	A	2.1
31	BG	63	ILE	2.1
19	CS	25	LYS	2.1
46	DZ	156	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	AB	236	TYR	2.1
4	AD	20	TYR	2.1
9	AI	5	TYR	2.1
12	CL	69	TYR	2.1
16	AP	39	TYR	2.1
19	AS	80	TYR	2.1
33	DI	29	TYR	2.1
32	DH	128	PRO	2.1
46	DZ	130	PRO	2.1
1	AA	70	G	2.0
1	AA	1038	C	2.1
1	CA	971	G	2.0
1	CA	972	C	2.1
1	CA	1057	G	2.0
1	CA	1060	C	2.1
1	CA	1253	G	2.0
23	CW	5	G	2.0
23	CW	56	C	2.1
25	CY	48	C	2.1
26	BA	10	G	2.0
26	BA	530	G	2.0
26	BA	2124	G	2.0
26	DA	545	G	2.0
3	AC	106	VAL	2.0
5	CE	26	PHE	2.0
9	AI	86	VAL	2.0
10	AJ	54	PHE	2.0
13	CM	15	VAL	2.0
18	AR	86	VAL	2.0
19	AS	10	PHE	2.0
19	CS	60	VAL	2.0
32	DH	26	VAL	2.0
44	DX	52	VAL	2.0
46	DZ	128	VAL	2.0
4	AD	49	ARG	2.0
7	CG	4	ARG	2.0
12	CL	19	ARG	2.0
16	AP	25	ARG	2.0
31	BG	51	ARG	2.0
40	BT	115	ARG	2.0
40	DT	115	ARG	2.0
4	CD	154	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
4	CD	194	LEU	2.0
7	CG	22	LEU	2.0
17	CQ	84	LEU	2.0
28	DD	37	LEU	2.0
31	DG	34	LEU	2.0
44	DX	95	LEU	2.0
45	BY	92	ASN	2.0
46	BZ	125	LEU	2.0
3	AC	148	GLY	2.0
19	AS	21	GLU	2.0
29	BE	88	GLY	2.0
31	BG	137	GLU	2.0
1	CA	955	U	2.0
2	CB	8	LYS	2.0
2	CB	190	THR	2.0
10	AJ	81	THR	2.0
10	CJ	7	LYS	2.0
26	BA	1175	U	2.0
29	DE	201	THR	2.0
31	DG	84	LYS	2.0
1	CA	975	A	2.0
1	CA	1289	A	2.0
26	BA	2176	A	2.0
2	AB	202	PRO	2.0
4	AD	37	PRO	2.0
4	AD	138	TYR	2.0
4	CD	7	PRO	2.0
5	CE	61	TYR	2.0
9	AI	4	TYR	2.0
17	CQ	32	TYR	2.0
31	BG	49	ASP	2.0
10	AJ	41	PRO	2.0
33	DI	143	SER	2.0
2	CB	140	HIS	2.0
36	DP	68	GLN	2.0
49	D2	46	GLN	2.0
1	CA	1363	C	2.0
3	CC	140	ARG	2.0
3	CC	156	ARG	2.0
8	CH	95	VAL	2.0
16	AP	5	ARG	2.0
19	AS	78	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
25	AY	61	C	2.0
26	BA	2136	C	2.0
28	DD	34	VAL	2.0
34	BN	140	VAL	2.0
36	BP	91	PHE	2.0
40	BT	112	ARG	2.0
46	DZ	39	VAL	2.0
46	DZ	72	ARG	2.0
1	CA	1042	G	2.0
2	CB	138	LEU	2.0
3	AC	47	LEU	2.0
3	CC	50	ALA	2.0
3	CC	133	ALA	2.0
3	CC	188	LEU	2.0
5	AE	17	ALA	2.0
5	AE	21	ALA	2.0
7	AG	101	LEU	2.0
9	CI	84	ALA	2.0
14	AN	48	ALA	2.0
23	CW	24	G	2.0
26	BA	171	G	2.0
18	AR	31	LEU	2.0
20	AT	13	LEU	2.0
20	CT	10	LEU	2.0
30	BF	19	GLU	2.0
31	DG	120	LEU	2.0
31	DG	139	LEU	2.0
32	DH	7	LEU	2.0
33	DI	83	ALA	2.0
12	CL	16	GLU	2.0
36	DP	85	LEU	2.0
40	DT	128	GLU	2.0
42	DV	20	LEU	2.0
2	CB	18	GLY	2.0
3	AC	181	ASN	2.0
3	CC	3	ASN	2.0
4	CD	87	GLY	2.0
9	AI	68	GLY	2.0
9	AI	113	LYS	2.0
11	AK	117	ASN	2.0
12	CL	49	ASN	2.0
13	CM	62	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
17	AQ	87	LYS	2.0
21	AU	16	GLY	2.0
31	DG	44	GLY	2.0
46	DZ	12	GLY	2.0
3	AC	15	THR	2.0
11	CK	29	ILE	2.0
13	AM	78	ILE	2.0
32	DH	72	ILE	2.0
1	AA	531	U	2.0
1	AA	723	U	2.0
1	CA	1025	U	2.0
1	CA	1085	U	2.0
26	BA	2189	U	2.0
1	AA	1004	A	2.0
1	CA	959	A	2.0
3	CC	109	PRO	2.0
5	CE	5	ASP	2.0
8	AH	5	PRO	2.0
25	CY	7	A	2.0
26	BA	655	A	2.0
26	BA	878	A	2.0
44	DX	85	PRO	2.0
45	DY	107	ASP	2.0
46	BZ	95	PRO	2.0
32	DH	84	SER	2.0
47	D0	78	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
23	7MG	AW	46	24/25	0.42	0.18	84,99,117,133	0
23	7MG	CW	46	24/25	0.44	0.16	79,96,109,133	0
25	7MG	CY	46	24/25	0.52	0.21	86,105,111,137	0
25	MIA	CY	37	22/30	0.54	0.18	72,95,113,138	0
23	4SU	CW	8	20/21	0.59	0.15	81,98,120,127	0
25	PSU	CY	55	20/21	0.59	0.26	94,102,110,124	0
25	4SU	CY	8	20/21	0.62	0.18	93,103,113,128	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	PSU	AY	55	20/21	0.64	0.17	93,101,108,122	0
25	5MU	CY	54	21/22	0.67	0.25	78,94,109,140	0
25	PSU	CY	39	20/21	0.68	0.17	79,90,116,130	0
23	4SU	AW	8	20/21	0.68	0.15	86,95,112,128	0
25	5MU	AY	54	21/22	0.69	0.15	80,96,105,131	0
25	7MG	AY	46	24/25	0.69	0.19	75,101,111,123	0
25	PSU	CY	32	20/21	0.71	0.15	80,92,101,107	0
25	4SU	AY	8	20/21	0.71	0.14	82,96,103,118	0
25	MIA	AY	37	22/30	0.75	0.15	77,90,111,119	0
23	PSU	CW	55	20/21	0.75	0.13	79,89,99,104	0
25	PSU	AY	39	20/21	0.75	0.16	78,90,117,123	0
23	5MU	CW	54	21/22	0.78	0.14	74,88,99,101	0
23	MIA	CW	37	22/30	0.80	0.13	75,85,92,100	0
23	PSU	AW	55	20/21	0.81	0.12	77,90,98,104	0
23	31M	CW	76	41/42	0.83	0.24	50,63,73,88	20
23	PSU	CW	39	20/21	0.83	0.14	78,84,97,98	0
23	PSU	CW	32	20/21	0.84	0.15	81,87,94,103	0
25	PSU	AY	32	20/21	0.84	0.15	78,93,100,106	0
24	4SU	CX	8	20/21	0.85	0.14	77,87,95,97	0
24	5MU	CX	54	21/22	0.86	0.12	70,81,89,99	0
24	PSU	CX	55	20/21	0.86	0.12	70,80,91,96	0
23	PSU	AW	32	20/21	0.86	0.15	77,83,92,98	0
23	5MU	AW	54	21/22	0.88	0.12	65,82,91,93	0
23	PSU	AW	39	20/21	0.89	0.12	73,82,95,97	0
24	5MU	AX	54	21/22	0.92	0.12	49,68,79,84	0
23	31M	AW	76	41/42	0.92	0.16	37,54,66,83	9
24	5MC	CX	32	21/22	0.92	0.14	63,76,86,88	0
24	4SU	AX	8	20/21	0.92	0.12	54,66,82,89	0
24	PSU	AX	55	20/21	0.93	0.10	50,63,73,83	0
23	MIA	AW	37	29/30	0.94	0.11	59,71,81,86	0
24	5MC	AX	32	21/22	0.95	0.11	43,53,62,78	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
57	MG	DA	3448	1/1	0.54	0.40	70,70,70,70	0
57	MG	BA	3670	1/1	0.60	0.27	61,61,61,61	0
57	MG	CA	3156	1/1	0.65	0.24	73,73,73,73	0
57	MG	BA	3730	1/1	0.65	0.19	71,71,71,71	0
57	MG	BA	3721	1/1	0.66	0.35	82,82,82,82	0
57	MG	DA	3530	1/1	0.68	0.27	74,74,74,74	0
57	MG	DA	3531	1/1	0.68	0.20	61,61,61,61	0
57	MG	DA	3544	1/1	0.68	0.22	65,65,65,65	0
57	MG	BA	3757	1/1	0.70	0.19	76,76,76,76	0
57	MG	BA	3616	1/1	0.70	0.22	65,65,65,65	0
57	MG	DB	3011	1/1	0.70	0.23	72,72,72,72	0
57	MG	BA	3745	1/1	0.71	0.26	75,75,75,75	0
57	MG	DR	5001	1/1	0.71	0.25	70,70,70,70	0
57	MG	DA	3259	1/1	0.72	0.22	43,43,43,43	0
57	MG	DA	3630	1/1	0.72	0.14	61,61,61,61	0
57	MG	AA	3059	1/1	0.74	0.39	78,78,78,78	0
57	MG	BA	3658	1/1	0.74	0.29	61,61,61,61	0
57	MG	DA	3469	1/1	0.74	0.21	44,44,44,44	0
57	MG	DA	3413	1/1	0.75	0.20	48,48,48,48	0
57	MG	BA	3362	1/1	0.75	0.22	41,41,41,41	0
57	MG	BA	3707	1/1	0.75	0.21	44,44,44,44	0
57	MG	DA	3518	1/1	0.75	0.24	54,54,54,54	0
57	MG	CA	3098	1/1	0.75	0.19	65,65,65,65	0
57	MG	AA	3105	1/1	0.75	0.34	69,69,69,69	0
57	MG	CV	101	1/1	0.75	0.28	72,72,72,72	0
57	MG	AA	3199	1/1	0.75	0.26	73,73,73,73	0
57	MG	DA	3673	1/1	0.75	0.25	69,69,69,69	0
57	MG	DA	3262	1/1	0.75	0.23	65,65,65,65	0
57	MG	DA	3320	1/1	0.75	0.15	55,55,55,55	0
57	MG	BA	3728	1/1	0.76	0.24	48,48,48,48	0
57	MG	BA	3724	1/1	0.76	0.15	62,62,62,62	0
57	MG	DA	3521	1/1	0.76	0.16	58,58,58,58	0
57	MG	DB	3001	1/1	0.76	0.25	64,64,64,64	0
57	MG	BB	218	1/1	0.76	0.21	77,77,77,77	0
57	MG	CA	3070	1/1	0.76	0.24	63,63,63,63	0
57	MG	DA	3215	1/1	0.77	0.22	59,59,59,59	0
57	MG	DA	3563	1/1	0.77	0.21	74,74,74,74	0
57	MG	BA	3427	1/1	0.77	0.17	61,61,61,61	0
57	MG	DA	3632	1/1	0.77	0.17	36,36,36,36	0
57	MG	DA	3646	1/1	0.77	0.23	59,59,59,59	0
57	MG	BA	3760	1/1	0.77	0.18	44,44,44,44	0
57	MG	BA	3779	1/1	0.77	0.28	66,66,66,66	0
57	MG	DA	3408	1/1	0.77	0.13	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AA	3166	1/1	0.77	0.23	69,69,69,69	0
57	MG	DA	3651	1/1	0.78	0.32	75,75,75,75	0
57	MG	DA	3575	1/1	0.78	0.24	64,64,64,64	0
57	MG	BA	3794	1/1	0.78	0.22	51,51,51,51	0
57	MG	CA	3140	1/1	0.78	0.16	67,67,67,67	0
57	MG	DA	3487	1/1	0.78	0.18	62,62,62,62	0
57	MG	BA	3703	1/1	0.79	0.21	64,64,64,64	0
57	MG	DA	3256	1/1	0.79	0.22	62,62,62,62	0
57	MG	BA	3769	1/1	0.79	0.21	52,52,52,52	0
57	MG	DA	3633	1/1	0.79	0.14	58,58,58,58	0
57	MG	BA	3641	1/1	0.79	0.19	68,68,68,68	0
57	MG	BA	3602	1/1	0.79	0.12	53,53,53,53	0
57	MG	DA	3355	1/1	0.79	0.12	58,58,58,58	0
57	MG	AA	3175	1/1	0.79	0.20	63,63,63,63	0
57	MG	DA	3185	1/1	0.79	0.20	68,68,68,68	0
57	MG	DD	303	1/1	0.79	0.20	87,87,87,87	0
57	MG	DA	3415	1/1	0.79	0.24	68,68,68,68	0
57	MG	DA	3313	1/1	0.80	0.12	47,47,47,47	0
57	MG	CA	3102	1/1	0.80	0.14	68,68,68,68	0
57	MG	CA	3128	1/1	0.80	0.23	65,65,65,65	0
57	MG	DA	3607	1/1	0.80	0.17	65,65,65,65	0
57	MG	DA	3626	1/1	0.80	0.13	67,67,67,67	0
57	MG	BA	3583	1/1	0.80	0.19	45,45,45,45	0
57	MG	BA	3771	1/1	0.80	0.23	50,50,50,50	0
57	MG	AA	3020	1/1	0.80	0.20	76,76,76,76	0
57	MG	DA	3140	1/1	0.80	0.20	58,58,58,58	0
57	MG	BA	3683	1/1	0.80	0.26	73,73,73,73	0
57	MG	BA	3434	1/1	0.80	0.14	55,55,55,55	0
57	MG	CA	3039	1/1	0.80	0.15	68,68,68,68	0
57	MG	BA	3638	1/1	0.80	0.23	63,63,63,63	0
57	MG	BA	3463	1/1	0.80	0.21	48,48,48,48	0
57	MG	DA	3279	1/1	0.80	0.12	56,56,56,56	0
57	MG	CA	3136	1/1	0.81	0.24	72,72,72,72	0
57	MG	BA	3642	1/1	0.81	0.10	48,48,48,48	0
57	MG	CA	3115	1/1	0.81	0.14	63,63,63,63	0
57	MG	BA	3754	1/1	0.81	0.13	48,48,48,48	0
57	MG	DA	3335	1/1	0.81	0.16	47,47,47,47	0
57	MG	DA	3125	1/1	0.81	0.35	70,70,70,70	0
57	MG	DB	3008	1/1	0.81	0.26	67,67,67,67	0
57	MG	DA	3623	1/1	0.81	0.19	66,66,66,66	0
57	MG	DA	3362	1/1	0.81	0.13	44,44,44,44	0
57	MG	DA	3402	1/1	0.81	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
57	MG	DV	3003	1/1	0.81	0.15	65,65,65,65	0
57	MG	DA	3308	1/1	0.82	0.15	61,61,61,61	0
57	MG	AA	3204	1/1	0.82	0.14	53,53,53,53	0
57	MG	BA	3512	1/1	0.82	0.15	52,52,52,52	0
57	MG	BA	3574	1/1	0.82	0.28	66,66,66,66	0
57	MG	AX	3014	1/1	0.82	0.18	72,72,72,72	0
57	MG	DA	3608	1/1	0.82	0.20	68,68,68,68	0
57	MG	BA	3257	1/1	0.82	0.18	53,53,53,53	0
57	MG	DA	3380	1/1	0.82	0.12	55,55,55,55	0
57	MG	DA	3118	1/1	0.82	0.14	77,77,77,77	0
57	MG	BA	3302	1/1	0.82	0.34	69,69,69,69	0
57	MG	CA	3018	1/1	0.82	0.25	69,69,69,69	0
57	MG	AA	3153	1/1	0.82	0.14	74,74,74,74	0
57	MG	BA	3396	1/1	0.82	0.14	50,50,50,50	0
57	MG	DA	3462	1/1	0.82	0.21	42,42,42,42	0
57	MG	CA	3083	1/1	0.82	0.19	79,79,79,79	0
57	MG	DA	3484	1/1	0.82	0.19	62,62,62,62	0
57	MG	AA	3193	1/1	0.82	0.14	72,72,72,72	0
57	MG	BA	3654	1/1	0.82	0.15	57,57,57,57	0
57	MG	DA	3274	1/1	0.82	0.17	58,58,58,58	0
57	MG	AA	3127	1/1	0.82	0.14	65,65,65,65	0
57	MG	BA	3550	1/1	0.83	0.16	36,36,36,36	0
57	MG	DA	3399	1/1	0.83	0.28	59,59,59,59	0
57	MG	AA	3196	1/1	0.83	0.13	74,74,74,74	0
57	MG	BB	215	1/1	0.83	0.18	73,73,73,73	0
57	MG	BA	3453	1/1	0.83	0.20	45,45,45,45	0
57	MG	B4	502	1/1	0.83	0.13	71,71,71,71	0
57	MG	DA	3421	1/1	0.83	0.12	50,50,50,50	0
57	MG	DA	3430	1/1	0.83	0.12	37,37,37,37	0
57	MG	AA	3002	1/1	0.83	0.26	71,71,71,71	0
57	MG	CA	3027	1/1	0.83	0.26	64,64,64,64	0
57	MG	CA	3152	1/1	0.83	0.28	76,76,76,76	0
57	MG	BA	3335	1/1	0.83	0.19	52,52,52,52	0
57	MG	CE	3001	1/1	0.83	0.11	79,79,79,79	0
57	MG	CJ	5001	1/1	0.83	0.13	73,73,73,73	0
57	MG	DA	3329	1/1	0.83	0.16	54,54,54,54	0
57	MG	CA	3066	1/1	0.83	0.28	66,66,66,66	0
57	MG	BA	3514	1/1	0.83	0.16	48,48,48,48	0
57	MG	CA	3082	1/1	0.83	0.24	79,79,79,79	0
57	MG	AA	3108	1/1	0.84	0.17	67,67,67,67	0
57	MG	BA	3631	1/1	0.84	0.13	42,42,42,42	0
57	MG	BA	3455	1/1	0.84	0.24	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3577	1/1	0.84	0.14	58,58,58,58	0
57	MG	BB	206	1/1	0.84	0.17	47,47,47,47	0
57	MG	AA	3117	1/1	0.84	0.14	79,79,79,79	0
57	MG	DA	3614	1/1	0.84	0.10	65,65,65,65	0
57	MG	AA	3057	1/1	0.84	0.27	64,64,64,64	0
57	MG	DA	3417	1/1	0.84	0.14	52,52,52,52	0
57	MG	BA	3741	1/1	0.84	0.18	64,64,64,64	0
57	MG	AA	3026	1/1	0.84	0.23	70,70,70,70	0
57	MG	AA	3054	1/1	0.84	0.12	53,53,53,53	0
57	MG	DA	3641	1/1	0.84	0.20	69,69,69,69	0
57	MG	DA	3301	1/1	0.84	0.15	52,52,52,52	0
57	MG	CA	3153	1/1	0.84	0.28	70,70,70,70	0
57	MG	AA	3172	1/1	0.84	0.15	72,72,72,72	0
57	MG	CA	3049	1/1	0.84	0.27	63,63,63,63	0
57	MG	CA	3059	1/1	0.84	0.18	72,72,72,72	0
57	MG	BA	3225	1/1	0.84	0.30	61,61,61,61	0
57	MG	DA	3524	1/1	0.84	0.13	61,61,61,61	0
57	MG	DA	3093	1/1	0.84	0.15	62,62,62,62	0
57	MG	BA	3443	1/1	0.84	0.17	37,37,37,37	0
57	MG	BA	3669	1/1	0.85	0.14	62,62,62,62	0
57	MG	DA	3470	1/1	0.85	0.15	45,45,45,45	0
57	MG	DA	3478	1/1	0.85	0.17	59,59,59,59	0
57	MG	BA	3070	1/1	0.85	0.32	59,59,59,59	0
57	MG	BA	3681	1/1	0.85	0.13	66,66,66,66	0
57	MG	BA	3128	1/1	0.85	0.15	69,69,69,69	0
57	MG	AA	3187	1/1	0.85	0.14	62,62,62,62	0
57	MG	AA	3028	1/1	0.85	0.39	76,76,76,76	0
57	MG	BA	3540	1/1	0.85	0.16	37,37,37,37	0
57	MG	AA	3170	1/1	0.85	0.13	75,75,75,75	0
57	MG	DA	3541	1/1	0.85	0.17	44,44,44,44	0
57	MG	BA	3316	1/1	0.85	0.14	66,66,66,66	0
57	MG	DA	3554	1/1	0.85	0.13	62,62,62,62	0
57	MG	AA	3197	1/1	0.85	0.16	70,70,70,70	0
57	MG	DA	3317	1/1	0.85	0.13	44,44,44,44	0
57	MG	BA	3590	1/1	0.85	0.17	50,50,50,50	0
57	MG	BA	3598	1/1	0.85	0.13	63,63,63,63	0
57	MG	AA	3004	1/1	0.85	0.11	67,67,67,67	0
57	MG	DA	3339	1/1	0.85	0.13	61,61,61,61	0
57	MG	DA	3618	1/1	0.85	0.18	53,53,53,53	0
57	MG	BA	3388	1/1	0.85	0.15	48,48,48,48	0
57	MG	CA	3146	1/1	0.85	0.27	66,66,66,66	0
57	MG	BA	3619	1/1	0.85	0.16	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3623	1/1	0.85	0.20	55,55,55,55	0
57	MG	AA	3111	1/1	0.85	0.17	79,79,79,79	0
57	MG	AA	3209	1/1	0.85	0.12	59,59,59,59	0
57	MG	AE	202	1/1	0.85	0.16	80,80,80,80	0
57	MG	CT	3001	1/1	0.85	0.14	56,56,56,56	0
57	MG	DA	3667	1/1	0.85	0.13	50,50,50,50	0
57	MG	BA	3438	1/1	0.85	0.10	60,60,60,60	0
57	MG	BA	3652	1/1	0.85	0.25	67,67,67,67	0
57	MG	DA	3425	1/1	0.85	0.15	61,61,61,61	0
57	MG	AA	3185	1/1	0.85	0.29	82,82,82,82	0
57	MG	BA	3656	1/1	0.85	0.28	53,53,53,53	0
57	MG	AX	3016	1/1	0.85	0.19	56,56,56,56	0
57	MG	DA	3467	1/1	0.85	0.14	40,40,40,40	0
57	MG	BA	3523	1/1	0.86	0.10	48,48,48,48	0
57	MG	BA	3399	1/1	0.86	0.16	45,45,45,45	0
57	MG	BA	3419	1/1	0.86	0.16	37,37,37,37	0
57	MG	BA	3755	1/1	0.86	0.13	55,55,55,55	0
57	MG	AA	3192	1/1	0.86	0.21	71,71,71,71	0
57	MG	DA	3523	1/1	0.86	0.14	59,59,59,59	0
57	MG	BA	3429	1/1	0.86	0.18	65,65,65,65	0
57	MG	AA	3031	1/1	0.86	0.27	70,70,70,70	0
57	MG	AA	3107	1/1	0.86	0.20	64,64,64,64	0
57	MG	DA	3532	1/1	0.86	0.16	69,69,69,69	0
57	MG	CA	3121	1/1	0.86	0.16	63,63,63,63	0
57	MG	BA	3680	1/1	0.86	0.18	68,68,68,68	0
57	MG	DA	3553	1/1	0.86	0.10	49,49,49,49	0
57	MG	BA	3783	1/1	0.86	0.20	56,56,56,56	0
57	MG	AA	3027	1/1	0.86	0.20	50,50,50,50	0
57	MG	BA	3811	1/1	0.86	0.15	65,65,65,65	0
57	MG	BB	202	1/1	0.86	0.27	59,59,59,59	0
57	MG	DA	3591	1/1	0.86	0.14	55,55,55,55	0
57	MG	BA	3353	1/1	0.86	0.12	50,50,50,50	0
57	MG	AA	3160	1/1	0.86	0.21	59,59,59,59	0
57	MG	CA	3159	1/1	0.86	0.25	70,70,70,70	0
57	MG	AA	3200	1/1	0.86	0.19	73,73,73,73	0
57	MG	DA	3403	1/1	0.86	0.10	57,57,57,57	0
57	MG	DA	3406	1/1	0.86	0.13	51,51,51,51	0
57	MG	BA	3470	1/1	0.86	0.10	62,62,62,62	0
57	MG	CA	3012	1/1	0.86	0.21	60,60,60,60	0
57	MG	DA	3414	1/1	0.86	0.13	43,43,43,43	0
57	MG	DA	3638	1/1	0.86	0.15	51,51,51,51	0
57	MG	BA	3636	1/1	0.86	0.12	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3062	1/1	0.86	0.12	63,63,63,63	0
57	MG	DA	3075	1/1	0.86	0.16	59,59,59,59	0
57	MG	DA	3652	1/1	0.86	0.20	67,67,67,67	0
57	MG	DA	3662	1/1	0.86	0.19	62,62,62,62	0
57	MG	CA	3021	1/1	0.86	0.24	61,61,61,61	0
57	MG	BA	3391	1/1	0.86	0.22	63,63,63,63	0
57	MG	DA	3447	1/1	0.86	0.20	58,58,58,58	0
57	MG	CA	3037	1/1	0.86	0.33	73,73,73,73	0
57	MG	AA	3069	1/1	0.86	0.14	68,68,68,68	0
57	MG	BA	3740	1/1	0.86	0.18	28,28,28,28	0
57	MG	CA	3055	1/1	0.86	0.21	69,69,69,69	0
57	MG	DA	3230	1/1	0.86	0.17	73,73,73,73	0
57	MG	DA	3433	1/1	0.87	0.15	46,46,46,46	0
57	MG	DA	3076	1/1	0.87	0.14	58,58,58,58	0
57	MG	DA	3079	1/1	0.87	0.15	55,55,55,55	0
57	MG	BA	3548	1/1	0.87	0.10	40,40,40,40	0
57	MG	BA	3750	1/1	0.87	0.12	27,27,27,27	0
57	MG	AA	3184	1/1	0.87	0.13	60,60,60,60	0
57	MG	BA	3066	1/1	0.87	0.10	49,49,49,49	0
57	MG	AA	3076	1/1	0.87	0.38	77,77,77,77	0
57	MG	DA	3194	1/1	0.87	0.13	56,56,56,56	0
57	MG	DA	3213	1/1	0.87	0.16	63,63,63,63	0
57	MG	DA	3502	1/1	0.87	0.15	55,55,55,55	0
57	MG	DA	3505	1/1	0.87	0.11	56,56,56,56	0
57	MG	AA	3091	1/1	0.87	0.20	60,60,60,60	0
57	MG	DA	3218	1/1	0.87	0.11	59,59,59,59	0
57	MG	BA	3673	1/1	0.87	0.14	55,55,55,55	0
57	MG	DA	3244	1/1	0.87	0.17	71,71,71,71	0
57	MG	BA	3212	1/1	0.87	0.19	54,54,54,54	0
57	MG	BA	3459	1/1	0.87	0.14	48,48,48,48	0
57	MG	DA	3261	1/1	0.87	0.09	49,49,49,49	0
57	MG	DA	3539	1/1	0.87	0.11	53,53,53,53	0
57	MG	CA	3090	1/1	0.87	0.16	67,67,67,67	0
57	MG	BA	3781	1/1	0.87	0.17	41,41,41,41	0
57	MG	DA	3546	1/1	0.87	0.09	71,71,71,71	0
57	MG	DA	3550	1/1	0.87	0.18	57,57,57,57	0
57	MG	DA	3276	1/1	0.87	0.15	49,49,49,49	0
57	MG	AA	3191	1/1	0.87	0.19	47,47,47,47	0
57	MG	DA	3291	1/1	0.87	0.13	44,44,44,44	0
57	MG	CA	3112	1/1	0.87	0.15	69,69,69,69	0
57	MG	BA	3686	1/1	0.87	0.23	60,60,60,60	0
57	MG	DA	3586	1/1	0.87	0.15	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3466	1/1	0.87	0.17	49,49,49,49	0
57	MG	CA	3124	1/1	0.87	0.19	59,59,59,59	0
57	MG	DA	3318	1/1	0.87	0.12	40,40,40,40	0
57	MG	CA	3126	1/1	0.87	0.18	67,67,67,67	0
57	MG	AA	3100	1/1	0.87	0.15	65,65,65,65	0
57	MG	DA	3620	1/1	0.87	0.15	68,68,68,68	0
57	MG	BA	3486	1/1	0.87	0.15	57,57,57,57	0
57	MG	BA	3411	1/1	0.87	0.10	33,33,33,33	0
57	MG	DA	3628	1/1	0.87	0.19	76,76,76,76	0
57	MG	AA	3047	1/1	0.87	0.28	63,63,63,63	0
57	MG	CA	3149	1/1	0.87	0.14	52,52,52,52	0
57	MG	BF	308	1/1	0.87	0.10	46,46,46,46	0
57	MG	DA	3634	1/1	0.87	0.13	60,60,60,60	0
57	MG	DA	3635	1/1	0.87	0.10	38,38,38,38	0
57	MG	DA	3382	1/1	0.87	0.11	48,48,48,48	0
57	MG	BA	3304	1/1	0.87	0.18	67,67,67,67	0
57	MG	DA	3642	1/1	0.87	0.13	54,54,54,54	0
57	MG	B6	102	1/1	0.87	0.15	68,68,68,68	0
57	MG	CA	3157	1/1	0.87	0.11	58,58,58,58	0
57	MG	CA	3006	1/1	0.87	0.26	64,64,64,64	0
57	MG	BA	3732	1/1	0.87	0.17	51,51,51,51	0
57	MG	DA	3409	1/1	0.87	0.12	57,57,57,57	0
57	MG	BA	3735	1/1	0.87	0.31	57,57,57,57	0
57	MG	BA	3530	1/1	0.87	0.23	49,49,49,49	0
57	MG	CA	3024	1/1	0.87	0.29	74,74,74,74	0
57	MG	CX	3003	1/1	0.87	0.17	54,54,54,54	0
57	MG	AA	3049	1/1	0.87	0.24	64,64,64,64	0
57	MG	DA	3073	1/1	0.87	0.10	42,42,42,42	0
57	MG	CA	3033	1/1	0.87	0.25	71,71,71,71	0
57	MG	BA	3418	1/1	0.88	0.10	30,30,30,30	0
57	MG	DA	3437	1/1	0.88	0.23	52,52,52,52	0
57	MG	BA	3738	1/1	0.88	0.16	43,43,43,43	0
57	MG	DA	3111	1/1	0.88	0.15	61,61,61,61	0
57	MG	CA	3051	1/1	0.88	0.18	81,81,81,81	0
57	MG	AX	3009	1/1	0.88	0.22	64,64,64,64	0
57	MG	CA	3057	1/1	0.88	0.18	76,76,76,76	0
57	MG	DA	3141	1/1	0.88	0.19	61,61,61,61	0
57	MG	DA	3181	1/1	0.88	0.12	50,50,50,50	0
57	MG	CA	3058	1/1	0.88	0.21	68,68,68,68	0
57	MG	BA	3615	1/1	0.88	0.29	68,68,68,68	0
57	MG	DA	3495	1/1	0.88	0.10	47,47,47,47	0
57	MG	BA	3424	1/1	0.88	0.17	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	CA	3069	1/1	0.88	0.14	60,60,60,60	0
57	MG	AX	3011	1/1	0.88	0.21	78,78,78,78	0
57	MG	BA	3231	1/1	0.88	0.31	63,63,63,63	0
57	MG	BA	3238	1/1	0.88	0.25	62,62,62,62	0
57	MG	CA	3088	1/1	0.88	0.10	74,74,74,74	0
57	MG	AA	3176	1/1	0.88	0.11	67,67,67,67	0
57	MG	BA	3267	1/1	0.88	0.12	65,65,65,65	0
57	MG	AA	3177	1/1	0.88	0.09	66,66,66,66	0
57	MG	DA	3273	1/1	0.88	0.11	47,47,47,47	0
57	MG	CA	3107	1/1	0.88	0.11	80,80,80,80	0
57	MG	BA	3023	1/1	0.88	0.12	36,36,36,36	0
57	MG	BA	3648	1/1	0.88	0.17	65,65,65,65	0
57	MG	BA	3306	1/1	0.88	0.12	37,37,37,37	0
57	MG	BA	3034	1/1	0.88	0.24	56,56,56,56	0
57	MG	BA	3318	1/1	0.88	0.12	41,41,41,41	0
57	MG	DA	3309	1/1	0.88	0.09	51,51,51,51	0
57	MG	DA	3564	1/1	0.88	0.10	61,61,61,61	0
57	MG	BA	3053	1/1	0.88	0.18	54,54,54,54	0
57	MG	DA	3314	1/1	0.88	0.11	43,43,43,43	0
57	MG	BA	3482	1/1	0.88	0.10	51,51,51,51	0
57	MG	DA	3588	1/1	0.88	0.12	65,65,65,65	0
57	MG	CA	3138	1/1	0.88	0.15	80,80,80,80	0
57	MG	DA	3598	1/1	0.88	0.15	61,61,61,61	0
57	MG	DA	3604	1/1	0.88	0.12	59,59,59,59	0
57	MG	BA	3342	1/1	0.88	0.09	46,46,46,46	0
57	MG	CA	3144	1/1	0.88	0.11	71,71,71,71	0
57	MG	BB	207	1/1	0.88	0.19	54,54,54,54	0
57	MG	AA	3037	1/1	0.88	0.21	55,55,55,55	0
57	MG	DA	3340	1/1	0.88	0.12	58,58,58,58	0
57	MG	AA	3036	1/1	0.88	0.17	61,61,61,61	0
57	MG	DA	3356	1/1	0.88	0.08	36,36,36,36	0
57	MG	DA	3627	1/1	0.88	0.16	63,63,63,63	0
57	MG	DA	3360	1/1	0.88	0.11	46,46,46,46	0
57	MG	BA	3387	1/1	0.88	0.09	54,54,54,54	0
57	MG	BA	3109	1/1	0.88	0.17	51,51,51,51	0
57	MG	BA	3117	1/1	0.88	0.12	59,59,59,59	0
57	MG	DA	3383	1/1	0.88	0.11	54,54,54,54	0
57	MG	DA	3388	1/1	0.88	0.16	53,53,53,53	0
57	MG	DA	3398	1/1	0.88	0.08	45,45,45,45	0
57	MG	CA	3004	1/1	0.88	0.14	66,66,66,66	0
57	MG	CA	3168	1/1	0.88	0.17	56,56,56,56	0
57	MG	BA	3545	1/1	0.88	0.15	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3649	1/1	0.88	0.15	58,58,58,58	0
57	MG	AA	3138	1/1	0.88	0.22	71,71,71,71	0
57	MG	BA	3709	1/1	0.88	0.15	62,62,62,62	0
57	MG	DA	3655	1/1	0.88	0.09	64,64,64,64	0
57	MG	DA	3661	1/1	0.88	0.13	62,62,62,62	0
57	MG	BA	3129	1/1	0.88	0.22	58,58,58,58	0
57	MG	BA	3401	1/1	0.88	0.09	35,35,35,35	0
57	MG	DA	3669	1/1	0.88	0.16	55,55,55,55	0
57	MG	DA	3025	1/1	0.88	0.14	54,54,54,54	0
57	MG	DA	3676	1/1	0.88	0.18	67,67,67,67	0
57	MG	DA	3035	1/1	0.88	0.11	52,52,52,52	0
57	MG	BA	3179	1/1	0.88	0.11	50,50,50,50	0
57	MG	CA	3031	1/1	0.88	0.15	68,68,68,68	0
57	MG	BA	3415	1/1	0.88	0.08	28,28,28,28	0
57	MG	DP	201	1/1	0.88	0.21	70,70,70,70	0
57	MG	DA	3426	1/1	0.88	0.16	49,49,49,49	0
57	MG	BA	3594	1/1	0.88	0.10	40,40,40,40	0
57	MG	DW	3003	1/1	0.88	0.13	72,72,72,72	0
57	MG	DA	3440	1/1	0.89	0.11	61,61,61,61	0
57	MG	CA	3046	1/1	0.89	0.17	69,69,69,69	0
57	MG	DA	3103	1/1	0.89	0.24	58,58,58,58	0
57	MG	DA	3451	1/1	0.89	0.12	55,55,55,55	0
57	MG	BA	3593	1/1	0.89	0.13	38,38,38,38	0
57	MG	DA	3117	1/1	0.89	0.12	52,52,52,52	0
57	MG	BA	3300	1/1	0.89	0.16	57,57,57,57	0
57	MG	BA	3596	1/1	0.89	0.10	64,64,64,64	0
57	MG	BA	3397	1/1	0.89	0.09	30,30,30,30	0
57	MG	DA	3482	1/1	0.89	0.13	50,50,50,50	0
57	MG	AA	3206	1/1	0.89	0.20	64,64,64,64	0
57	MG	BA	3608	1/1	0.89	0.14	62,62,62,62	0
57	MG	CA	3062	1/1	0.89	0.16	64,64,64,64	0
57	MG	DA	3499	1/1	0.89	0.10	53,53,53,53	0
57	MG	BA	3468	1/1	0.89	0.16	62,62,62,62	0
57	MG	CA	3067	1/1	0.89	0.28	61,61,61,61	0
57	MG	BA	3160	1/1	0.89	0.25	55,55,55,55	0
57	MG	BA	3473	1/1	0.89	0.14	56,56,56,56	0
57	MG	CA	3077	1/1	0.89	0.17	66,66,66,66	0
57	MG	DA	3231	1/1	0.89	0.12	62,62,62,62	0
57	MG	BA	3749	1/1	0.89	0.11	56,56,56,56	0
57	MG	DA	3248	1/1	0.89	0.14	56,56,56,56	0
57	MG	AA	3051	1/1	0.89	0.27	73,73,73,73	0
57	MG	BA	3624	1/1	0.89	0.17	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3185	1/1	0.89	0.14	57,57,57,57	0
57	MG	BA	3633	1/1	0.89	0.11	49,49,49,49	0
57	MG	BA	3487	1/1	0.89	0.13	50,50,50,50	0
57	MG	CA	3104	1/1	0.89	0.15	68,68,68,68	0
57	MG	BA	3488	1/1	0.89	0.18	60,60,60,60	0
57	MG	BA	3492	1/1	0.89	0.10	46,46,46,46	0
57	MG	DA	3287	1/1	0.89	0.09	41,41,41,41	0
57	MG	DA	3290	1/1	0.89	0.18	59,59,59,59	0
57	MG	DA	3567	1/1	0.89	0.17	62,62,62,62	0
57	MG	DA	3571	1/1	0.89	0.12	56,56,56,56	0
57	MG	BA	3503	1/1	0.89	0.15	49,49,49,49	0
57	MG	DA	3295	1/1	0.89	0.18	44,44,44,44	0
57	MG	AA	3145	1/1	0.89	0.19	66,66,66,66	0
57	MG	BA	3319	1/1	0.89	0.10	46,46,46,46	0
57	MG	BA	3515	1/1	0.89	0.10	53,53,53,53	0
57	MG	BA	3796	1/1	0.89	0.12	45,45,45,45	0
57	MG	BA	3799	1/1	0.89	0.10	49,49,49,49	0
57	MG	BA	3520	1/1	0.89	0.19	61,61,61,61	0
57	MG	BA	3423	1/1	0.89	0.13	44,44,44,44	0
57	MG	BA	3668	1/1	0.89	0.12	53,53,53,53	0
57	MG	DA	3615	1/1	0.89	0.16	65,65,65,65	0
57	MG	BA	3072	1/1	0.89	0.09	47,47,47,47	0
57	MG	DA	3331	1/1	0.89	0.15	37,37,37,37	0
57	MG	BA	3535	1/1	0.89	0.12	31,31,31,31	0
57	MG	DA	3625	1/1	0.89	0.09	69,69,69,69	0
57	MG	CA	3150	1/1	0.89	0.16	56,56,56,56	0
57	MG	BA	3671	1/1	0.89	0.13	63,63,63,63	0
57	MG	BA	3095	1/1	0.89	0.19	51,51,51,51	0
57	MG	BA	3679	1/1	0.89	0.16	62,62,62,62	0
57	MG	DA	3631	1/1	0.89	0.13	57,57,57,57	0
57	MG	BA	3022	1/1	0.89	0.13	60,60,60,60	0
57	MG	CA	3158	1/1	0.89	0.17	67,67,67,67	0
57	MG	BA	3243	1/1	0.89	0.17	53,53,53,53	0
57	MG	CA	3167	1/1	0.89	0.18	60,60,60,60	0
57	MG	BA	3385	1/1	0.89	0.23	59,59,59,59	0
57	MG	BA	3554	1/1	0.89	0.12	51,51,51,51	0
57	MG	BA	3700	1/1	0.89	0.10	61,61,61,61	0
57	MG	BA	3572	1/1	0.89	0.10	61,61,61,61	0
57	MG	CA	3022	1/1	0.89	0.18	78,78,78,78	0
57	MG	AX	3002	1/1	0.89	0.11	58,58,58,58	0
57	MG	DA	3001	1/1	0.89	0.09	60,60,60,60	0
57	MG	BA	3261	1/1	0.89	0.13	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3657	1/1	0.89	0.19	63,63,63,63	0
57	MG	BA	3711	1/1	0.89	0.22	54,54,54,54	0
57	MG	DA	3410	1/1	0.89	0.10	53,53,53,53	0
57	MG	DA	3044	1/1	0.89	0.18	62,62,62,62	0
57	MG	DA	3051	1/1	0.89	0.09	48,48,48,48	0
57	MG	DA	3060	1/1	0.89	0.19	64,64,64,64	0
57	MG	BA	3712	1/1	0.89	0.25	53,53,53,53	0
57	MG	DA	3420	1/1	0.89	0.12	60,60,60,60	0
57	MG	DA	3069	1/1	0.89	0.23	57,57,57,57	0
57	MG	CA	3036	1/1	0.89	0.21	66,66,66,66	0
57	MG	DB	3013	1/1	0.89	0.21	64,64,64,64	0
57	MG	BA	3718	1/1	0.89	0.12	71,71,71,71	0
57	MG	DE	303	1/1	0.89	0.15	54,54,54,54	0
57	MG	CA	3038	1/1	0.89	0.13	58,58,58,58	0
57	MG	DA	3432	1/1	0.89	0.10	37,37,37,37	0
57	MG	AA	3134	1/1	0.89	0.12	66,66,66,66	0
57	MG	DA	3090	1/1	0.89	0.13	52,52,52,52	0
57	MG	D3	3001	1/1	0.89	0.16	57,57,57,57	0
57	MG	D8	5001	1/1	0.89	0.28	66,66,66,66	0
57	MG	AA	3156	1/1	0.90	0.27	63,63,63,63	0
57	MG	BA	3471	1/1	0.90	0.15	53,53,53,53	0
57	MG	DA	3077	1/1	0.90	0.27	61,61,61,61	0
57	MG	BA	3622	1/1	0.90	0.12	48,48,48,48	0
57	MG	DA	3081	1/1	0.90	0.10	55,55,55,55	0
57	MG	BA	3375	1/1	0.90	0.14	68,68,68,68	0
57	MG	AA	3046	1/1	0.90	0.20	55,55,55,55	0
57	MG	AA	3161	1/1	0.90	0.26	65,65,65,65	0
57	MG	CA	3060	1/1	0.90	0.17	65,65,65,65	0
57	MG	AA	3017	1/1	0.90	0.26	71,71,71,71	0
57	MG	DA	3452	1/1	0.90	0.17	51,51,51,51	0
57	MG	BA	3634	1/1	0.90	0.13	62,62,62,62	0
57	MG	BA	3213	1/1	0.90	0.10	40,40,40,40	0
57	MG	BA	3005	1/1	0.90	0.09	30,30,30,30	0
57	MG	BA	3759	1/1	0.90	0.13	33,33,33,33	0
57	MG	DA	3147	1/1	0.90	0.18	56,56,56,56	0
57	MG	DA	3481	1/1	0.90	0.24	55,55,55,55	0
57	MG	DA	3149	1/1	0.90	0.07	56,56,56,56	0
57	MG	BA	3640	1/1	0.90	0.15	53,53,53,53	0
57	MG	BA	3761	1/1	0.90	0.14	59,59,59,59	0
57	MG	DA	3492	1/1	0.90	0.11	55,55,55,55	0
57	MG	BA	3764	1/1	0.90	0.12	51,51,51,51	0
57	MG	DA	3498	1/1	0.90	0.12	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3205	1/1	0.90	0.09	56,56,56,56	0
57	MG	DA	3206	1/1	0.90	0.09	50,50,50,50	0
57	MG	DA	3207	1/1	0.90	0.17	63,63,63,63	0
57	MG	DA	3516	1/1	0.90	0.10	67,67,67,67	0
57	MG	CA	3087	1/1	0.90	0.19	67,67,67,67	0
57	MG	BA	3501	1/1	0.90	0.11	71,71,71,71	0
57	MG	AA	3136	1/1	0.90	0.17	70,70,70,70	0
57	MG	DA	3219	1/1	0.90	0.14	53,53,53,53	0
57	MG	DA	3222	1/1	0.90	0.11	57,57,57,57	0
57	MG	CA	3097	1/1	0.90	0.20	69,69,69,69	0
57	MG	BA	3647	1/1	0.90	0.11	56,56,56,56	0
57	MG	DA	3536	1/1	0.90	0.10	48,48,48,48	0
57	MG	DA	3234	1/1	0.90	0.22	63,63,63,63	0
57	MG	DA	3242	1/1	0.90	0.10	52,52,52,52	0
57	MG	BA	3504	1/1	0.90	0.10	56,56,56,56	0
57	MG	AA	3104	1/1	0.90	0.26	59,59,59,59	0
57	MG	DA	3255	1/1	0.90	0.10	51,51,51,51	0
57	MG	AA	3139	1/1	0.90	0.10	59,59,59,59	0
57	MG	CA	3109	1/1	0.90	0.14	67,67,67,67	0
57	MG	DA	3556	1/1	0.90	0.17	67,67,67,67	0
57	MG	DA	3557	1/1	0.90	0.10	51,51,51,51	0
57	MG	DA	3558	1/1	0.90	0.14	61,61,61,61	0
57	MG	BA	3405	1/1	0.90	0.12	63,63,63,63	0
57	MG	BA	3409	1/1	0.90	0.09	30,30,30,30	0
57	MG	DA	3268	1/1	0.90	0.13	51,51,51,51	0
57	MG	DA	3569	1/1	0.90	0.18	49,49,49,49	0
57	MG	CA	3117	1/1	0.90	0.25	71,71,71,71	0
57	MG	CA	3118	1/1	0.90	0.31	68,68,68,68	0
57	MG	CA	3120	1/1	0.90	0.26	64,64,64,64	0
57	MG	BA	3052	1/1	0.90	0.12	56,56,56,56	0
57	MG	BA	3812	1/1	0.90	0.22	47,47,47,47	0
57	MG	AA	3202	1/1	0.90	0.14	57,57,57,57	0
57	MG	DA	3593	1/1	0.90	0.08	40,40,40,40	0
57	MG	DA	3594	1/1	0.90	0.11	54,54,54,54	0
57	MG	AA	3008	1/1	0.90	0.32	73,73,73,73	0
57	MG	CA	3133	1/1	0.90	0.28	59,59,59,59	0
57	MG	DA	3300	1/1	0.90	0.11	45,45,45,45	0
57	MG	BA	3294	1/1	0.90	0.21	61,61,61,61	0
57	MG	DA	3609	1/1	0.90	0.09	46,46,46,46	0
57	MG	BA	3541	1/1	0.90	0.14	38,38,38,38	0
57	MG	AA	3205	1/1	0.90	0.17	51,51,51,51	0
57	MG	DA	3311	1/1	0.90	0.13	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AA	3146	1/1	0.90	0.10	66,66,66,66	0
57	MG	BV	202	1/1	0.90	0.14	50,50,50,50	0
57	MG	DA	3624	1/1	0.90	0.14	56,56,56,56	0
57	MG	BX	3001	1/1	0.90	0.44	48,48,48,48	0
57	MG	BA	3426	1/1	0.90	0.11	37,37,37,37	0
57	MG	B5	101	1/1	0.90	0.18	51,51,51,51	0
57	MG	DA	3321	1/1	0.90	0.08	48,48,48,48	0
57	MG	AA	3147	1/1	0.90	0.16	70,70,70,70	0
57	MG	BA	3684	1/1	0.90	0.13	68,68,68,68	0
57	MG	BA	3555	1/1	0.90	0.11	29,29,29,29	0
57	MG	DA	3338	1/1	0.90	0.23	61,61,61,61	0
57	MG	CA	3008	1/1	0.90	0.26	51,51,51,51	0
57	MG	CA	3011	1/1	0.90	0.27	61,61,61,61	0
57	MG	DA	3636	1/1	0.90	0.14	63,63,63,63	0
57	MG	DA	3637	1/1	0.90	0.29	58,58,58,58	0
57	MG	DA	3348	1/1	0.90	0.10	34,34,34,34	0
57	MG	DA	3354	1/1	0.90	0.13	44,44,44,44	0
57	MG	BA	3693	1/1	0.90	0.12	56,56,56,56	0
57	MG	DA	3643	1/1	0.90	0.12	61,61,61,61	0
57	MG	BA	3102	1/1	0.90	0.15	44,44,44,44	0
57	MG	CA	3170	1/1	0.90	0.20	58,58,58,58	0
57	MG	BA	3431	1/1	0.90	0.11	59,59,59,59	0
57	MG	DA	3371	1/1	0.90	0.14	58,58,58,58	0
57	MG	BA	3314	1/1	0.90	0.19	58,58,58,58	0
57	MG	AA	3214	1/1	0.90	0.24	73,73,73,73	0
57	MG	CA	3026	1/1	0.90	0.22	63,63,63,63	0
57	MG	CX	3002	1/1	0.90	0.12	70,70,70,70	0
57	MG	DA	3663	1/1	0.90	0.11	60,60,60,60	0
57	MG	DA	3394	1/1	0.90	0.17	65,65,65,65	0
57	MG	BA	3114	1/1	0.90	0.13	53,53,53,53	0
57	MG	CA	3029	1/1	0.90	0.21	63,63,63,63	0
57	MG	DA	3002	1/1	0.90	0.10	48,48,48,48	0
57	MG	DA	3007	1/1	0.90	0.12	50,50,50,50	0
57	MG	DB	3005	1/1	0.90	0.10	59,59,59,59	0
57	MG	DA	3010	1/1	0.90	0.08	47,47,47,47	0
57	MG	AA	3121	1/1	0.90	0.14	70,70,70,70	0
57	MG	BA	3121	1/1	0.90	0.33	64,64,64,64	0
57	MG	AA	3155	1/1	0.90	0.23	48,48,48,48	0
57	MG	BA	3601	1/1	0.90	0.07	55,55,55,55	0
57	MG	BA	3351	1/1	0.90	0.12	30,30,30,30	0
57	MG	AX	3008	1/1	0.90	0.18	70,70,70,70	0
57	MG	CA	3041	1/1	0.90	0.14	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3071	1/1	0.90	0.14	59,59,59,59	0
57	MG	BA	3359	1/1	0.90	0.19	62,62,62,62	0
57	MG	DA	3422	1/1	0.90	0.11	46,46,46,46	0
57	MG	BA	3717	1/1	0.91	0.10	50,50,50,50	0
57	MG	DA	3431	1/1	0.91	0.15	50,50,50,50	0
57	MG	AA	3013	1/1	0.91	0.15	69,69,69,69	0
57	MG	BA	3591	1/1	0.91	0.14	35,35,35,35	0
57	MG	AA	3092	1/1	0.91	0.19	63,63,63,63	0
57	MG	BA	3725	1/1	0.91	0.10	44,44,44,44	0
57	MG	BA	3432	1/1	0.91	0.10	58,58,58,58	0
57	MG	BA	3078	1/1	0.91	0.23	51,51,51,51	0
57	MG	DA	3450	1/1	0.91	0.08	40,40,40,40	0
57	MG	CA	3052	1/1	0.91	0.14	72,72,72,72	0
57	MG	BA	3731	1/1	0.91	0.27	37,37,37,37	0
57	MG	DA	3454	1/1	0.91	0.17	56,56,56,56	0
57	MG	BA	3083	1/1	0.91	0.19	56,56,56,56	0
57	MG	DA	3465	1/1	0.91	0.12	46,46,46,46	0
57	MG	DA	3123	1/1	0.91	0.14	56,56,56,56	0
57	MG	DA	3468	1/1	0.91	0.15	66,66,66,66	0
57	MG	AA	3095	1/1	0.91	0.24	60,60,60,60	0
57	MG	BA	3315	1/1	0.91	0.11	31,31,31,31	0
57	MG	DA	3473	1/1	0.91	0.10	50,50,50,50	0
57	MG	BA	3604	1/1	0.91	0.09	36,36,36,36	0
57	MG	CA	3061	1/1	0.91	0.14	66,66,66,66	0
57	MG	AA	3183	1/1	0.91	0.16	65,65,65,65	0
57	MG	DA	3155	1/1	0.91	0.26	48,48,48,48	0
57	MG	DA	3160	1/1	0.91	0.14	56,56,56,56	0
57	MG	DA	3178	1/1	0.91	0.22	50,50,50,50	0
57	MG	CA	3063	1/1	0.91	0.27	58,58,58,58	0
57	MG	CA	3064	1/1	0.91	0.16	60,60,60,60	0
57	MG	DA	3188	1/1	0.91	0.19	48,48,48,48	0
57	MG	DA	3501	1/1	0.91	0.09	37,37,37,37	0
57	MG	BA	3742	1/1	0.91	0.15	65,65,65,65	0
57	MG	BA	3613	1/1	0.91	0.35	42,42,42,42	0
57	MG	BA	3747	1/1	0.91	0.17	52,52,52,52	0
57	MG	BA	3748	1/1	0.91	0.07	29,29,29,29	0
57	MG	DA	3520	1/1	0.91	0.13	57,57,57,57	0
57	MG	DA	3208	1/1	0.91	0.17	58,58,58,58	0
57	MG	CA	3071	1/1	0.91	0.21	68,68,68,68	0
57	MG	AN	503	1/1	0.91	0.14	54,54,54,54	0
57	MG	AW	3001	1/1	0.91	0.13	60,60,60,60	0
57	MG	BA	3465	1/1	0.91	0.13	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AW	3003	1/1	0.91	0.17	72,72,72,72	0
57	MG	DA	3534	1/1	0.91	0.21	55,55,55,55	0
57	MG	DA	3223	1/1	0.91	0.17	50,50,50,50	0
57	MG	BA	3120	1/1	0.91	0.22	55,55,55,55	0
57	MG	AA	3097	1/1	0.91	0.38	56,56,56,56	0
57	MG	BA	3626	1/1	0.91	0.16	44,44,44,44	0
57	MG	DA	3239	1/1	0.91	0.33	56,56,56,56	0
57	MG	BA	3126	1/1	0.91	0.17	54,54,54,54	0
57	MG	DA	3552	1/1	0.91	0.12	54,54,54,54	0
57	MG	BA	3355	1/1	0.91	0.16	61,61,61,61	0
57	MG	BA	3127	1/1	0.91	0.25	57,57,57,57	0
57	MG	DA	3251	1/1	0.91	0.12	62,62,62,62	0
57	MG	AA	3023	1/1	0.91	0.10	74,74,74,74	0
57	MG	CA	3108	1/1	0.91	0.14	68,68,68,68	0
57	MG	BA	3365	1/1	0.91	0.15	62,62,62,62	0
57	MG	BA	3639	1/1	0.91	0.28	48,48,48,48	0
57	MG	DA	3566	1/1	0.91	0.09	69,69,69,69	0
57	MG	CA	3113	1/1	0.91	0.11	67,67,67,67	0
57	MG	BA	3782	1/1	0.91	0.15	65,65,65,65	0
57	MG	DA	3271	1/1	0.91	0.11	48,48,48,48	0
57	MG	DA	3574	1/1	0.91	0.14	53,53,53,53	0
57	MG	CA	3116	1/1	0.91	0.11	68,68,68,68	0
57	MG	AA	3052	1/1	0.91	0.30	65,65,65,65	0
57	MG	DA	3583	1/1	0.91	0.18	51,51,51,51	0
57	MG	DA	3584	1/1	0.91	0.20	53,53,53,53	0
57	MG	BA	3788	1/1	0.91	0.12	51,51,51,51	0
57	MG	BA	3159	1/1	0.91	0.27	50,50,50,50	0
57	MG	BA	3499	1/1	0.91	0.10	58,58,58,58	0
57	MG	BA	3386	1/1	0.91	0.09	53,53,53,53	0
57	MG	AA	3040	1/1	0.91	0.10	60,60,60,60	0
57	MG	BA	3651	1/1	0.91	0.09	45,45,45,45	0
57	MG	DA	3298	1/1	0.91	0.14	59,59,59,59	0
57	MG	DA	3299	1/1	0.91	0.19	55,55,55,55	0
57	MG	AA	3041	1/1	0.91	0.17	46,46,46,46	0
57	MG	BA	3508	1/1	0.91	0.17	51,51,51,51	0
57	MG	DA	3610	1/1	0.91	0.21	64,64,64,64	0
57	MG	DA	3613	1/1	0.91	0.10	54,54,54,54	0
57	MG	AA	3003	1/1	0.91	0.12	72,72,72,72	0
57	MG	BA	3205	1/1	0.91	0.13	50,50,50,50	0
57	MG	CA	3142	1/1	0.91	0.24	69,69,69,69	0
57	MG	BA	3663	1/1	0.91	0.09	41,41,41,41	0
57	MG	DA	3621	1/1	0.91	0.08	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BD	302	1/1	0.91	0.11	50,50,50,50	0
57	MG	BE	301	1/1	0.91	0.08	35,35,35,35	0
57	MG	BE	308	1/1	0.91	0.12	40,40,40,40	0
57	MG	BA	3001	1/1	0.91	0.10	53,53,53,53	0
57	MG	AA	3064	1/1	0.91	0.19	60,60,60,60	0
57	MG	DA	3327	1/1	0.91	0.12	57,57,57,57	0
57	MG	BA	3218	1/1	0.91	0.17	47,47,47,47	0
57	MG	BA	3527	1/1	0.91	0.11	54,54,54,54	0
57	MG	BA	3672	1/1	0.91	0.18	43,43,43,43	0
57	MG	BA	3404	1/1	0.91	0.13	59,59,59,59	0
57	MG	CA	3161	1/1	0.91	0.11	56,56,56,56	0
57	MG	CA	3166	1/1	0.91	0.12	66,66,66,66	0
57	MG	B7	101	1/1	0.91	0.12	39,39,39,39	0
57	MG	B7	102	1/1	0.91	0.10	47,47,47,47	0
57	MG	BA	3018	1/1	0.91	0.14	56,56,56,56	0
57	MG	BA	3406	1/1	0.91	0.09	50,50,50,50	0
57	MG	AA	3065	1/1	0.91	0.24	63,63,63,63	0
57	MG	CA	3009	1/1	0.91	0.14	64,64,64,64	0
57	MG	DA	3644	1/1	0.91	0.08	55,55,55,55	0
57	MG	CA	3010	1/1	0.91	0.09	56,56,56,56	0
57	MG	DA	3374	1/1	0.91	0.16	56,56,56,56	0
57	MG	AA	3033	1/1	0.91	0.09	59,59,59,59	0
57	MG	AA	3048	1/1	0.91	0.26	57,57,57,57	0
57	MG	DA	3653	1/1	0.91	0.09	52,52,52,52	0
57	MG	CX	3004	1/1	0.91	0.14	63,63,63,63	0
57	MG	CA	3014	1/1	0.91	0.21	58,58,58,58	0
57	MG	DA	3659	1/1	0.91	0.12	48,48,48,48	0
57	MG	CA	3016	1/1	0.91	0.09	57,57,57,57	0
57	MG	CA	3017	1/1	0.91	0.18	53,53,53,53	0
57	MG	BA	3244	1/1	0.91	0.14	53,53,53,53	0
57	MG	DA	3017	1/1	0.91	0.14	55,55,55,55	0
57	MG	DA	3024	1/1	0.91	0.28	59,59,59,59	0
57	MG	AA	3078	1/1	0.91	0.31	66,66,66,66	0
57	MG	BA	3695	1/1	0.91	0.13	67,67,67,67	0
57	MG	AA	3173	1/1	0.91	0.19	54,54,54,54	0
57	MG	DB	3004	1/1	0.91	0.14	55,55,55,55	0
57	MG	DA	3048	1/1	0.91	0.08	53,53,53,53	0
57	MG	DA	3411	1/1	0.91	0.15	53,53,53,53	0
57	MG	BA	3264	1/1	0.91	0.16	58,58,58,58	0
57	MG	DB	3012	1/1	0.91	0.26	61,61,61,61	0
57	MG	BA	3057	1/1	0.91	0.10	34,34,34,34	0
57	MG	DA	3061	1/1	0.91	0.10	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3580	1/1	0.91	0.10	55,55,55,55	0
57	MG	DF	3001	1/1	0.91	0.08	44,44,44,44	0
57	MG	DA	3418	1/1	0.91	0.12	52,52,52,52	0
57	MG	DA	3067	1/1	0.91	0.23	57,57,57,57	0
57	MG	CA	3030	1/1	0.91	0.23	57,57,57,57	0
57	MG	AA	3174	1/1	0.91	0.08	50,50,50,50	0
57	MG	D0	101	1/1	0.91	0.16	71,71,71,71	0
57	MG	BA	3584	1/1	0.91	0.19	63,63,63,63	0
57	MG	BA	3714	1/1	0.91	0.10	57,57,57,57	0
59	ZN	D4	501	1/1	0.91	0.08	144,144,144,144	0
57	MG	DA	3429	1/1	0.92	0.11	41,41,41,41	0
57	MG	BA	3526	1/1	0.92	0.09	44,44,44,44	0
57	MG	DA	3087	1/1	0.92	0.24	58,58,58,58	0
57	MG	BA	3364	1/1	0.92	0.16	60,60,60,60	0
57	MG	BA	3145	1/1	0.92	0.09	44,44,44,44	0
57	MG	DA	3436	1/1	0.92	0.14	54,54,54,54	0
57	MG	DA	3095	1/1	0.92	0.28	58,58,58,58	0
57	MG	BA	3532	1/1	0.92	0.14	52,52,52,52	0
57	MG	DA	3110	1/1	0.92	0.14	58,58,58,58	0
57	MG	BA	3372	1/1	0.92	0.08	28,28,28,28	0
57	MG	DA	3112	1/1	0.92	0.17	59,59,59,59	0
57	MG	DA	3114	1/1	0.92	0.13	55,55,55,55	0
57	MG	BA	3715	1/1	0.92	0.12	63,63,63,63	0
57	MG	DA	3453	1/1	0.92	0.20	60,60,60,60	0
57	MG	BA	3154	1/1	0.92	0.11	47,47,47,47	0
57	MG	DA	3457	1/1	0.92	0.10	54,54,54,54	0
57	MG	BA	3003	1/1	0.92	0.11	60,60,60,60	0
57	MG	DA	3463	1/1	0.92	0.10	55,55,55,55	0
57	MG	BA	3720	1/1	0.92	0.16	65,65,65,65	0
57	MG	DA	3132	1/1	0.92	0.14	52,52,52,52	0
57	MG	DA	3133	1/1	0.92	0.24	50,50,50,50	0
57	MG	DA	3139	1/1	0.92	0.13	53,53,53,53	0
57	MG	AA	3198	1/1	0.92	0.15	61,61,61,61	0
57	MG	BA	3723	1/1	0.92	0.07	47,47,47,47	0
57	MG	DA	3474	1/1	0.92	0.12	51,51,51,51	0
57	MG	DA	3476	1/1	0.92	0.13	62,62,62,62	0
57	MG	BA	3177	1/1	0.92	0.12	46,46,46,46	0
57	MG	BA	3012	1/1	0.92	0.13	39,39,39,39	0
57	MG	BA	3389	1/1	0.92	0.12	55,55,55,55	0
57	MG	BA	3180	1/1	0.92	0.11	47,47,47,47	0
57	MG	DA	3485	1/1	0.92	0.15	52,52,52,52	0
57	MG	DA	3165	1/1	0.92	0.24	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3566	1/1	0.92	0.17	67,67,67,67	0
57	MG	DA	3180	1/1	0.92	0.18	42,42,42,42	0
57	MG	DA	3497	1/1	0.92	0.09	55,55,55,55	0
57	MG	BA	3570	1/1	0.92	0.11	42,42,42,42	0
57	MG	DA	3184	1/1	0.92	0.12	47,47,47,47	0
57	MG	AA	3038	1/1	0.92	0.32	68,68,68,68	0
57	MG	BA	3186	1/1	0.92	0.20	45,45,45,45	0
57	MG	DA	3503	1/1	0.92	0.18	52,52,52,52	0
57	MG	BA	3576	1/1	0.92	0.07	57,57,57,57	0
57	MG	DA	3513	1/1	0.92	0.12	52,52,52,52	0
57	MG	DA	3197	1/1	0.92	0.11	55,55,55,55	0
57	MG	BA	3202	1/1	0.92	0.21	60,60,60,60	0
57	MG	CA	3074	1/1	0.92	0.24	64,64,64,64	0
57	MG	BA	3021	1/1	0.92	0.10	49,49,49,49	0
57	MG	CA	3078	1/1	0.92	0.12	44,44,44,44	0
57	MG	DA	3212	1/1	0.92	0.12	45,45,45,45	0
57	MG	DA	3527	1/1	0.92	0.17	60,60,60,60	0
57	MG	AA	3068	1/1	0.92	0.17	69,69,69,69	0
57	MG	BA	3587	1/1	0.92	0.11	36,36,36,36	0
57	MG	DA	3216	1/1	0.92	0.27	56,56,56,56	0
57	MG	CA	3085	1/1	0.92	0.22	54,54,54,54	0
57	MG	BA	3589	1/1	0.92	0.14	27,27,27,27	0
57	MG	AA	3094	1/1	0.92	0.14	59,59,59,59	0
57	MG	DA	3540	1/1	0.92	0.08	42,42,42,42	0
57	MG	AA	3115	1/1	0.92	0.22	79,79,79,79	0
57	MG	DA	3225	1/1	0.92	0.10	49,49,49,49	0
57	MG	DA	3229	1/1	0.92	0.09	50,50,50,50	0
57	MG	BA	3592	1/1	0.92	0.14	28,28,28,28	0
57	MG	BA	3408	1/1	0.92	0.13	36,36,36,36	0
57	MG	BA	3224	1/1	0.92	0.28	65,65,65,65	0
57	MG	AA	3154	1/1	0.92	0.16	69,69,69,69	0
57	MG	BA	3229	1/1	0.92	0.16	54,54,54,54	0
57	MG	DA	3243	1/1	0.92	0.16	55,55,55,55	0
57	MG	BA	3599	1/1	0.92	0.16	43,43,43,43	0
57	MG	BA	3417	1/1	0.92	0.13	38,38,38,38	0
57	MG	CA	3110	1/1	0.92	0.10	65,65,65,65	0
57	MG	AA	3178	1/1	0.92	0.21	59,59,59,59	0
57	MG	AA	3180	1/1	0.92	0.13	73,73,73,73	0
57	MG	BA	3421	1/1	0.92	0.08	32,32,32,32	0
57	MG	BA	3064	1/1	0.92	0.09	43,43,43,43	0
57	MG	DA	3573	1/1	0.92	0.10	43,43,43,43	0
57	MG	AA	3058	1/1	0.92	0.19	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AA	3044	1/1	0.92	0.25	60,60,60,60	0
57	MG	BA	3258	1/1	0.92	0.07	44,44,44,44	0
57	MG	DA	3578	1/1	0.92	0.12	59,59,59,59	0
57	MG	BA	3793	1/1	0.92	0.16	40,40,40,40	0
57	MG	BA	3260	1/1	0.92	0.17	39,39,39,39	0
57	MG	CA	3125	1/1	0.92	0.12	63,63,63,63	0
57	MG	AA	3157	1/1	0.92	0.13	45,45,45,45	0
57	MG	DA	3283	1/1	0.92	0.12	51,51,51,51	0
57	MG	DA	3592	1/1	0.92	0.07	51,51,51,51	0
57	MG	BA	3073	1/1	0.92	0.16	61,61,61,61	0
57	MG	DA	3288	1/1	0.92	0.14	52,52,52,52	0
57	MG	DA	3289	1/1	0.92	0.15	53,53,53,53	0
57	MG	DA	3602	1/1	0.92	0.13	65,65,65,65	0
57	MG	BA	3800	1/1	0.92	0.08	38,38,38,38	0
57	MG	DA	3605	1/1	0.92	0.14	58,58,58,58	0
57	MG	BA	3075	1/1	0.92	0.17	45,45,45,45	0
57	MG	BA	3629	1/1	0.92	0.09	43,43,43,43	0
57	MG	BA	3630	1/1	0.92	0.13	58,58,58,58	0
57	MG	BA	3275	1/1	0.92	0.12	58,58,58,58	0
57	MG	DA	3612	1/1	0.92	0.10	62,62,62,62	0
57	MG	BA	3278	1/1	0.92	0.12	34,34,34,34	0
57	MG	BB	213	1/1	0.92	0.21	60,60,60,60	0
57	MG	DA	3302	1/1	0.92	0.14	70,70,70,70	0
57	MG	BA	3444	1/1	0.92	0.11	29,29,29,29	0
57	MG	BA	3445	1/1	0.92	0.20	63,63,63,63	0
57	MG	BB	219	1/1	0.92	0.17	67,67,67,67	0
57	MG	BA	3446	1/1	0.92	0.12	40,40,40,40	0
57	MG	BA	3285	1/1	0.92	0.13	50,50,50,50	0
57	MG	BA	3293	1/1	0.92	0.18	50,50,50,50	0
57	MG	BA	3076	1/1	0.92	0.13	43,43,43,43	0
57	MG	BG	202	1/1	0.92	0.12	41,41,41,41	0
57	MG	BN	3004	1/1	0.92	0.14	60,60,60,60	0
57	MG	BO	202	1/1	0.92	0.09	65,65,65,65	0
57	MG	BA	3460	1/1	0.92	0.21	62,62,62,62	0
57	MG	AA	3159	1/1	0.92	0.10	66,66,66,66	0
57	MG	DA	3334	1/1	0.92	0.15	52,52,52,52	0
57	MG	B2	3001	1/1	0.92	0.11	56,56,56,56	0
57	MG	DA	3337	1/1	0.92	0.09	41,41,41,41	0
57	MG	CD	301	1/1	0.92	0.17	56,56,56,56	0
57	MG	BA	3301	1/1	0.92	0.13	60,60,60,60	0
57	MG	BA	3650	1/1	0.92	0.10	52,52,52,52	0
57	MG	AA	3189	1/1	0.92	0.11	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3351	1/1	0.92	0.10	48,48,48,48	0
57	MG	BA	3091	1/1	0.92	0.26	56,56,56,56	0
57	MG	AW	3004	1/1	0.92	0.10	49,49,49,49	0
57	MG	B7	104	1/1	0.92	0.12	48,48,48,48	0
57	MG	DA	3358	1/1	0.92	0.09	45,45,45,45	0
57	MG	B7	105	1/1	0.92	0.14	56,56,56,56	0
57	MG	BA	3310	1/1	0.92	0.17	58,58,58,58	0
57	MG	BA	3313	1/1	0.92	0.07	53,53,53,53	0
57	MG	BA	3478	1/1	0.92	0.12	58,58,58,58	0
57	MG	DA	3656	1/1	0.92	0.09	58,58,58,58	0
57	MG	BA	3667	1/1	0.92	0.17	61,61,61,61	0
57	MG	AA	3190	1/1	0.92	0.10	58,58,58,58	0
57	MG	BA	3484	1/1	0.92	0.08	54,54,54,54	0
57	MG	AA	3012	1/1	0.92	0.11	46,46,46,46	0
57	MG	BA	3113	1/1	0.92	0.19	53,53,53,53	0
57	MG	DA	3037	1/1	0.92	0.13	43,43,43,43	0
57	MG	DA	3668	1/1	0.92	0.20	60,60,60,60	0
57	MG	AA	3101	1/1	0.92	0.11	43,43,43,43	0
57	MG	DA	3672	1/1	0.92	0.29	71,71,71,71	0
57	MG	DA	3400	1/1	0.92	0.08	54,54,54,54	0
57	MG	DA	3046	1/1	0.92	0.13	47,47,47,47	0
57	MG	AA	3103	1/1	0.92	0.35	73,73,73,73	0
57	MG	DB	3002	1/1	0.92	0.22	65,65,65,65	0
57	MG	DB	3003	1/1	0.92	0.09	57,57,57,57	0
57	MG	DA	3405	1/1	0.92	0.12	46,46,46,46	0
57	MG	BA	3322	1/1	0.92	0.18	52,52,52,52	0
57	MG	DA	3052	1/1	0.92	0.21	61,61,61,61	0
57	MG	DA	3054	1/1	0.92	0.27	48,48,48,48	0
57	MG	AX	3012	1/1	0.92	0.13	59,59,59,59	0
57	MG	AA	3195	1/1	0.92	0.12	57,57,57,57	0
57	MG	BA	3682	1/1	0.92	0.15	53,53,53,53	0
57	MG	DA	3066	1/1	0.92	0.10	42,42,42,42	0
57	MG	BA	3344	1/1	0.92	0.15	66,66,66,66	0
57	MG	AA	3083	1/1	0.92	0.26	57,57,57,57	0
57	MG	DQ	3004	1/1	0.92	0.13	54,54,54,54	0
57	MG	BA	3685	1/1	0.92	0.10	53,53,53,53	0
57	MG	AY	3002	1/1	0.92	0.15	56,56,56,56	0
57	MG	AA	3089	1/1	0.92	0.14	60,60,60,60	0
57	MG	BA	3002	1/1	0.92	0.10	50,50,50,50	0
57	MG	BA	3361	1/1	0.92	0.09	49,49,49,49	0
57	MG	BA	3143	1/1	0.92	0.11	45,45,45,45	0
57	MG	DA	3427	1/1	0.92	0.10	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	K	CX	3001	1/1	0.92	0.14	82,82,82,82	0
57	MG	BA	3767	1/1	0.93	0.12	73,73,73,73	0
57	MG	BA	3628	1/1	0.93	0.14	49,49,49,49	0
57	MG	DA	3158	1/1	0.93	0.15	60,60,60,60	0
57	MG	DA	3159	1/1	0.93	0.14	58,58,58,58	0
57	MG	AA	3088	1/1	0.93	0.27	65,65,65,65	0
57	MG	DA	3163	1/1	0.93	0.07	49,49,49,49	0
57	MG	AA	3016	1/1	0.93	0.08	63,63,63,63	0
57	MG	CA	3086	1/1	0.93	0.12	64,64,64,64	0
57	MG	BA	3780	1/1	0.93	0.09	62,62,62,62	0
57	MG	BA	3358	1/1	0.93	0.15	49,49,49,49	0
57	MG	BA	3087	1/1	0.93	0.12	42,42,42,42	0
57	MG	AY	3001	1/1	0.93	0.31	65,65,65,65	0
57	MG	BA	3228	1/1	0.93	0.24	59,59,59,59	0
57	MG	BA	3092	1/1	0.93	0.08	37,37,37,37	0
57	MG	AA	3067	1/1	0.93	0.23	57,57,57,57	0
57	MG	DA	3202	1/1	0.93	0.18	57,57,57,57	0
57	MG	BA	3366	1/1	0.93	0.08	57,57,57,57	0
57	MG	BA	3797	1/1	0.93	0.08	53,53,53,53	0
57	MG	BA	3371	1/1	0.93	0.09	35,35,35,35	0
57	MG	BA	3232	1/1	0.93	0.19	52,52,52,52	0
57	MG	BA	3802	1/1	0.93	0.29	54,54,54,54	0
57	MG	BA	3808	1/1	0.93	0.16	42,42,42,42	0
57	MG	BA	3809	1/1	0.93	0.08	63,63,63,63	0
57	MG	DA	3489	1/1	0.93	0.07	51,51,51,51	0
57	MG	DA	3490	1/1	0.93	0.12	47,47,47,47	0
57	MG	BA	3643	1/1	0.93	0.08	46,46,46,46	0
57	MG	DA	3493	1/1	0.93	0.10	66,66,66,66	0
57	MG	BA	3500	1/1	0.93	0.15	56,56,56,56	0
57	MG	AY	3003	1/1	0.93	0.12	53,53,53,53	0
57	MG	DA	3221	1/1	0.93	0.12	52,52,52,52	0
57	MG	BA	3376	1/1	0.93	0.11	48,48,48,48	0
57	MG	BA	3380	1/1	0.93	0.09	48,48,48,48	0
57	MG	BB	209	1/1	0.93	0.33	65,65,65,65	0
57	MG	BA	3506	1/1	0.93	0.10	58,58,58,58	0
57	MG	AA	3032	1/1	0.93	0.10	67,67,67,67	0
57	MG	CA	3127	1/1	0.93	0.16	62,62,62,62	0
57	MG	BA	3511	1/1	0.93	0.07	30,30,30,30	0
57	MG	DA	3236	1/1	0.93	0.24	47,47,47,47	0
57	MG	DA	3519	1/1	0.93	0.11	63,63,63,63	0
57	MG	AA	3150	1/1	0.93	0.15	57,57,57,57	0
57	MG	CA	3135	1/1	0.93	0.12	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3522	1/1	0.93	0.15	71,71,71,71	0
57	MG	BB	220	1/1	0.93	0.10	57,57,57,57	0
57	MG	BA	3662	1/1	0.93	0.10	61,61,61,61	0
57	MG	DA	3247	1/1	0.93	0.07	45,45,45,45	0
57	MG	BA	3248	1/1	0.93	0.21	42,42,42,42	0
57	MG	DA	3249	1/1	0.93	0.15	45,45,45,45	0
57	MG	BE	305	1/1	0.93	0.15	43,43,43,43	0
57	MG	DA	3254	1/1	0.93	0.06	52,52,52,52	0
57	MG	AA	3179	1/1	0.93	0.14	69,69,69,69	0
57	MG	DA	3538	1/1	0.93	0.15	58,58,58,58	0
57	MG	BF	306	1/1	0.93	0.22	31,31,31,31	0
57	MG	BA	3517	1/1	0.93	0.11	45,45,45,45	0
57	MG	DA	3260	1/1	0.93	0.16	55,55,55,55	0
57	MG	DA	3543	1/1	0.93	0.09	53,53,53,53	0
57	MG	BG	201	1/1	0.93	0.11	58,58,58,58	0
57	MG	AA	3152	1/1	0.93	0.12	62,62,62,62	0
57	MG	DA	3547	1/1	0.93	0.17	54,54,54,54	0
57	MG	DA	3263	1/1	0.93	0.09	41,41,41,41	0
57	MG	DA	3267	1/1	0.93	0.12	49,49,49,49	0
57	MG	AA	3109	1/1	0.93	0.13	62,62,62,62	0
57	MG	BA	3394	1/1	0.93	0.12	40,40,40,40	0
57	MG	BQ	3005	1/1	0.93	0.07	49,49,49,49	0
57	MG	AA	3210	1/1	0.93	0.25	59,59,59,59	0
57	MG	BV	204	1/1	0.93	0.12	49,49,49,49	0
57	MG	CA	3160	1/1	0.93	0.10	62,62,62,62	0
57	MG	BA	3263	1/1	0.93	0.17	49,49,49,49	0
57	MG	CA	3163	1/1	0.93	0.09	63,63,63,63	0
57	MG	B0	103	1/1	0.93	0.07	53,53,53,53	0
57	MG	BA	3398	1/1	0.93	0.09	32,32,32,32	0
57	MG	BA	3125	1/1	0.93	0.07	47,47,47,47	0
57	MG	BA	3537	1/1	0.93	0.10	45,45,45,45	0
57	MG	DA	3293	1/1	0.93	0.16	54,54,54,54	0
57	MG	BA	3538	1/1	0.93	0.09	40,40,40,40	0
57	MG	DA	3296	1/1	0.93	0.07	28,28,28,28	0
57	MG	AA	3093	1/1	0.93	0.10	66,66,66,66	0
57	MG	BA	3271	1/1	0.93	0.12	58,58,58,58	0
57	MG	BA	3543	1/1	0.93	0.11	37,37,37,37	0
57	MG	AA	3006	1/1	0.93	0.08	52,52,52,52	0
57	MG	CW	3001	1/1	0.93	0.16	67,67,67,67	0
57	MG	DA	3590	1/1	0.93	0.10	51,51,51,51	0
57	MG	DA	3305	1/1	0.93	0.15	50,50,50,50	0
57	MG	CA	3003	1/1	0.93	0.12	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AA	3070	1/1	0.93	0.11	52,52,52,52	0
57	MG	BA	3694	1/1	0.93	0.09	51,51,51,51	0
57	MG	BA	3279	1/1	0.93	0.21	43,43,43,43	0
57	MG	BA	3696	1/1	0.93	0.09	33,33,33,33	0
57	MG	DA	3316	1/1	0.93	0.09	45,45,45,45	0
57	MG	BA	3552	1/1	0.93	0.14	29,29,29,29	0
57	MG	DA	3009	1/1	0.93	0.11	48,48,48,48	0
57	MG	BA	3033	1/1	0.93	0.11	53,53,53,53	0
57	MG	DA	3015	1/1	0.93	0.20	52,52,52,52	0
57	MG	BA	3288	1/1	0.93	0.11	56,56,56,56	0
57	MG	DA	3611	1/1	0.93	0.11	48,48,48,48	0
57	MG	DA	3019	1/1	0.93	0.10	37,37,37,37	0
57	MG	BA	3560	1/1	0.93	0.07	56,56,56,56	0
57	MG	BA	3562	1/1	0.93	0.08	37,37,37,37	0
57	MG	DA	3032	1/1	0.93	0.10	48,48,48,48	0
57	MG	DA	3616	1/1	0.93	0.09	71,71,71,71	0
57	MG	BA	3413	1/1	0.93	0.09	47,47,47,47	0
57	MG	BA	3568	1/1	0.93	0.07	59,59,59,59	0
57	MG	DA	3038	1/1	0.93	0.15	47,47,47,47	0
57	MG	BA	3131	1/1	0.93	0.15	58,58,58,58	0
57	MG	DA	3342	1/1	0.93	0.10	42,42,42,42	0
57	MG	AA	3118	1/1	0.93	0.11	47,47,47,47	0
57	MG	BA	3298	1/1	0.93	0.20	51,51,51,51	0
57	MG	DA	3352	1/1	0.93	0.13	63,63,63,63	0
57	MG	AA	3119	1/1	0.93	0.07	51,51,51,51	0
57	MG	BA	3153	1/1	0.93	0.15	47,47,47,47	0
57	MG	BA	3722	1/1	0.93	0.15	47,47,47,47	0
57	MG	DA	3056	1/1	0.93	0.11	51,51,51,51	0
57	MG	AA	3072	1/1	0.93	0.13	66,66,66,66	0
57	MG	BA	3303	1/1	0.93	0.18	36,36,36,36	0
57	MG	DA	3364	1/1	0.93	0.07	40,40,40,40	0
57	MG	DA	3366	1/1	0.93	0.15	42,42,42,42	0
57	MG	DA	3367	1/1	0.93	0.12	61,61,61,61	0
57	MG	DA	3368	1/1	0.93	0.16	50,50,50,50	0
57	MG	AA	3001	1/1	0.93	0.16	61,61,61,61	0
57	MG	CA	3034	1/1	0.93	0.12	59,59,59,59	0
57	MG	DA	3376	1/1	0.93	0.19	61,61,61,61	0
57	MG	BA	3061	1/1	0.93	0.11	29,29,29,29	0
57	MG	BA	3165	1/1	0.93	0.12	45,45,45,45	0
57	MG	DA	3070	1/1	0.93	0.14	58,58,58,58	0
57	MG	DA	3384	1/1	0.93	0.14	49,49,49,49	0
57	MG	BA	3311	1/1	0.93	0.16	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3168	1/1	0.93	0.14	47,47,47,47	0
57	MG	DA	3654	1/1	0.93	0.14	56,56,56,56	0
57	MG	BA	3734	1/1	0.93	0.10	52,52,52,52	0
57	MG	BA	3172	1/1	0.93	0.08	46,46,46,46	0
57	MG	CA	3048	1/1	0.93	0.15	67,67,67,67	0
57	MG	DA	3658	1/1	0.93	0.19	62,62,62,62	0
57	MG	DA	3078	1/1	0.93	0.14	57,57,57,57	0
57	MG	AX	3004	1/1	0.93	0.16	64,64,64,64	0
57	MG	BA	3065	1/1	0.93	0.16	60,60,60,60	0
57	MG	DA	3082	1/1	0.93	0.10	47,47,47,47	0
57	MG	DA	3083	1/1	0.93	0.07	40,40,40,40	0
57	MG	AX	3007	1/1	0.93	0.10	67,67,67,67	0
57	MG	CA	3054	1/1	0.93	0.31	69,69,69,69	0
57	MG	AA	3131	1/1	0.93	0.16	71,71,71,71	0
57	MG	AA	3061	1/1	0.93	0.30	55,55,55,55	0
57	MG	DA	3098	1/1	0.93	0.10	53,53,53,53	0
57	MG	BA	3325	1/1	0.93	0.09	48,48,48,48	0
57	MG	DA	3416	1/1	0.93	0.08	50,50,50,50	0
57	MG	BA	3200	1/1	0.93	0.31	67,67,67,67	0
57	MG	BA	3456	1/1	0.93	0.13	49,49,49,49	0
57	MG	BA	3337	1/1	0.93	0.11	58,58,58,58	0
57	MG	DB	3007	1/1	0.93	0.19	58,58,58,58	0
57	MG	BA	3751	1/1	0.93	0.09	26,26,26,26	0
57	MG	BA	3753	1/1	0.93	0.09	33,33,33,33	0
57	MG	DA	3424	1/1	0.93	0.08	61,61,61,61	0
57	MG	AX	3010	1/1	0.93	0.16	59,59,59,59	0
57	MG	BA	3461	1/1	0.93	0.14	62,62,62,62	0
57	MG	DA	3124	1/1	0.93	0.12	57,57,57,57	0
57	MG	BA	3462	1/1	0.93	0.12	36,36,36,36	0
57	MG	DA	3126	1/1	0.93	0.11	55,55,55,55	0
57	MG	DQ	3002	1/1	0.93	0.11	51,51,51,51	0
57	MG	DA	3130	1/1	0.93	0.17	52,52,52,52	0
57	MG	BA	3343	1/1	0.93	0.10	53,53,53,53	0
57	MG	AA	3102	1/1	0.93	0.28	59,59,59,59	0
57	MG	BA	3349	1/1	0.93	0.11	56,56,56,56	0
57	MG	DW	3004	1/1	0.93	0.09	52,52,52,52	0
57	MG	DY	502	1/1	0.93	0.07	50,50,50,50	0
57	MG	AA	3021	1/1	0.93	0.20	63,63,63,63	0
57	MG	DA	3439	1/1	0.93	0.11	42,42,42,42	0
57	MG	CA	3075	1/1	0.93	0.18	59,59,59,59	0
57	MG	DA	3443	1/1	0.93	0.12	54,54,54,54	0
57	MG	BA	3766	1/1	0.93	0.09	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3096	1/1	0.94	0.20	42,42,42,42	0
57	MG	BA	3317	1/1	0.94	0.07	53,53,53,53	0
57	MG	AX	3015	1/1	0.94	0.11	42,42,42,42	0
57	MG	DA	3106	1/1	0.94	0.12	52,52,52,52	0
57	MG	DA	3108	1/1	0.94	0.12	52,52,52,52	0
57	MG	DA	3423	1/1	0.94	0.12	49,49,49,49	0
57	MG	CA	3053	1/1	0.94	0.07	41,41,41,41	0
57	MG	BA	3448	1/1	0.94	0.11	32,32,32,32	0
57	MG	BA	3182	1/1	0.94	0.09	55,55,55,55	0
57	MG	BA	3320	1/1	0.94	0.10	48,48,48,48	0
57	MG	BA	3321	1/1	0.94	0.18	55,55,55,55	0
57	MG	BA	3457	1/1	0.94	0.12	32,32,32,32	0
57	MG	DA	3122	1/1	0.94	0.09	49,49,49,49	0
57	MG	BA	3183	1/1	0.94	0.07	42,42,42,42	0
57	MG	BA	3603	1/1	0.94	0.08	53,53,53,53	0
57	MG	DA	3435	1/1	0.94	0.17	50,50,50,50	0
57	MG	AA	3024	1/1	0.94	0.09	54,54,54,54	0
57	MG	BA	3607	1/1	0.94	0.09	38,38,38,38	0
57	MG	DA	3128	1/1	0.94	0.20	58,58,58,58	0
57	MG	AA	3025	1/1	0.94	0.10	62,62,62,62	0
57	MG	AA	3018	1/1	0.94	0.23	56,56,56,56	0
57	MG	BA	3080	1/1	0.94	0.23	60,60,60,60	0
57	MG	DA	3136	1/1	0.94	0.09	52,52,52,52	0
57	MG	DA	3138	1/1	0.94	0.17	55,55,55,55	0
57	MG	BA	3765	1/1	0.94	0.11	48,48,48,48	0
57	MG	AA	3079	1/1	0.94	0.17	68,68,68,68	0
57	MG	BA	3207	1/1	0.94	0.23	54,54,54,54	0
57	MG	CA	3073	1/1	0.94	0.17	57,57,57,57	0
57	MG	DA	3148	1/1	0.94	0.14	54,54,54,54	0
57	MG	BA	3768	1/1	0.94	0.10	47,47,47,47	0
57	MG	DA	3151	1/1	0.94	0.14	55,55,55,55	0
57	MG	DA	3153	1/1	0.94	0.18	47,47,47,47	0
57	MG	BA	3621	1/1	0.94	0.10	53,53,53,53	0
57	MG	DA	3157	1/1	0.94	0.10	47,47,47,47	0
57	MG	CA	3076	1/1	0.94	0.11	57,57,57,57	0
57	MG	BA	3770	1/1	0.94	0.10	45,45,45,45	0
57	MG	DA	3472	1/1	0.94	0.09	44,44,44,44	0
57	MG	BA	3347	1/1	0.94	0.10	44,44,44,44	0
57	MG	CA	3079	1/1	0.94	0.15	66,66,66,66	0
57	MG	DA	3164	1/1	0.94	0.12	51,51,51,51	0
57	MG	BA	3776	1/1	0.94	0.14	43,43,43,43	0
57	MG	DA	3169	1/1	0.94	0.12	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3170	1/1	0.94	0.09	53,53,53,53	0
57	MG	BA	3778	1/1	0.94	0.08	48,48,48,48	0
57	MG	BA	3469	1/1	0.94	0.12	49,49,49,49	0
57	MG	DA	3486	1/1	0.94	0.08	47,47,47,47	0
57	MG	BA	3348	1/1	0.94	0.10	36,36,36,36	0
57	MG	AA	3213	1/1	0.94	0.18	54,54,54,54	0
57	MG	AA	3188	1/1	0.94	0.15	69,69,69,69	0
57	MG	BA	3475	1/1	0.94	0.12	42,42,42,42	0
57	MG	DA	3192	1/1	0.94	0.12	60,60,60,60	0
57	MG	DA	3494	1/1	0.94	0.10	47,47,47,47	0
57	MG	CA	3095	1/1	0.94	0.23	64,64,64,64	0
57	MG	DA	3496	1/1	0.94	0.07	53,53,53,53	0
57	MG	BA	3787	1/1	0.94	0.20	45,45,45,45	0
57	MG	DA	3198	1/1	0.94	0.14	40,40,40,40	0
57	MG	DA	3200	1/1	0.94	0.11	66,66,66,66	0
57	MG	BA	3477	1/1	0.94	0.18	61,61,61,61	0
57	MG	DA	3203	1/1	0.94	0.20	50,50,50,50	0
57	MG	AA	3062	1/1	0.94	0.27	51,51,51,51	0
57	MG	BA	3093	1/1	0.94	0.22	56,56,56,56	0
57	MG	CA	3106	1/1	0.94	0.07	56,56,56,56	0
57	MG	AF	3001	1/1	0.94	0.17	44,44,44,44	0
57	MG	DA	3209	1/1	0.94	0.20	53,53,53,53	0
57	MG	DA	3210	1/1	0.94	0.14	53,53,53,53	0
57	MG	DA	3211	1/1	0.94	0.07	48,48,48,48	0
57	MG	BA	3635	1/1	0.94	0.13	58,58,58,58	0
57	MG	BA	3101	1/1	0.94	0.12	53,53,53,53	0
57	MG	DA	3214	1/1	0.94	0.28	59,59,59,59	0
57	MG	BA	3007	1/1	0.94	0.16	55,55,55,55	0
57	MG	CA	3111	1/1	0.94	0.08	64,64,64,64	0
57	MG	BA	3801	1/1	0.94	0.18	50,50,50,50	0
57	MG	BA	3106	1/1	0.94	0.10	42,42,42,42	0
57	MG	BA	3803	1/1	0.94	0.14	44,44,44,44	0
57	MG	AM	201	1/1	0.94	0.07	51,51,51,51	0
57	MG	BA	3493	1/1	0.94	0.16	58,58,58,58	0
57	MG	BA	3494	1/1	0.94	0.09	49,49,49,49	0
57	MG	DA	3228	1/1	0.94	0.22	38,38,38,38	0
57	MG	CA	3119	1/1	0.94	0.08	64,64,64,64	0
57	MG	BA	3237	1/1	0.94	0.07	45,45,45,45	0
57	MG	BA	3644	1/1	0.94	0.07	35,35,35,35	0
57	MG	CA	3122	1/1	0.94	0.21	64,64,64,64	0
57	MG	BB	205	1/1	0.94	0.22	60,60,60,60	0
57	MG	BA	3017	1/1	0.94	0.19	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3548	1/1	0.94	0.07	60,60,60,60	0
57	MG	DA	3549	1/1	0.94	0.13	57,57,57,57	0
57	MG	BA	3239	1/1	0.94	0.12	48,48,48,48	0
57	MG	BA	3649	1/1	0.94	0.09	40,40,40,40	0
57	MG	BB	210	1/1	0.94	0.07	61,61,61,61	0
57	MG	DA	3245	1/1	0.94	0.12	54,54,54,54	0
57	MG	CA	3129	1/1	0.94	0.09	43,43,43,43	0
57	MG	CA	3132	1/1	0.94	0.15	66,66,66,66	0
57	MG	BA	3502	1/1	0.94	0.09	56,56,56,56	0
57	MG	DA	3561	1/1	0.94	0.09	57,57,57,57	0
57	MG	DA	3250	1/1	0.94	0.13	69,69,69,69	0
57	MG	CA	3134	1/1	0.94	0.17	69,69,69,69	0
57	MG	DA	3565	1/1	0.94	0.09	59,59,59,59	0
57	MG	BB	214	1/1	0.94	0.08	49,49,49,49	0
57	MG	AA	3135	1/1	0.94	0.24	65,65,65,65	0
57	MG	BA	3116	1/1	0.94	0.18	50,50,50,50	0
57	MG	CA	3139	1/1	0.94	0.24	62,62,62,62	0
57	MG	BA	3505	1/1	0.94	0.09	55,55,55,55	0
57	MG	AA	3084	1/1	0.94	0.26	51,51,51,51	0
57	MG	CA	3143	1/1	0.94	0.10	64,64,64,64	0
57	MG	BA	3118	1/1	0.94	0.12	48,48,48,48	0
57	MG	DA	3265	1/1	0.94	0.10	30,30,30,30	0
57	MG	DA	3582	1/1	0.94	0.07	56,56,56,56	0
57	MG	BD	304	1/1	0.94	0.12	32,32,32,32	0
57	MG	CA	3147	1/1	0.94	0.20	64,64,64,64	0
57	MG	DA	3585	1/1	0.94	0.08	43,43,43,43	0
57	MG	CA	3148	1/1	0.94	0.16	70,70,70,70	0
57	MG	DA	3272	1/1	0.94	0.08	41,41,41,41	0
57	MG	BA	3659	1/1	0.94	0.13	61,61,61,61	0
57	MG	BE	303	1/1	0.94	0.14	51,51,51,51	0
57	MG	AA	3137	1/1	0.94	0.10	51,51,51,51	0
57	MG	BE	307	1/1	0.94	0.10	62,62,62,62	0
57	MG	AA	3005	1/1	0.94	0.18	62,62,62,62	0
57	MG	DA	3284	1/1	0.94	0.07	47,47,47,47	0
57	MG	BF	304	1/1	0.94	0.11	45,45,45,45	0
57	MG	BA	3665	1/1	0.94	0.14	49,49,49,49	0
57	MG	BA	3122	1/1	0.94	0.07	41,41,41,41	0
57	MG	BA	3024	1/1	0.94	0.18	49,49,49,49	0
57	MG	BA	3516	1/1	0.94	0.15	52,52,52,52	0
57	MG	AA	3009	1/1	0.94	0.11	57,57,57,57	0
57	MG	BN	3006	1/1	0.94	0.12	49,49,49,49	0
57	MG	AX	3003	1/1	0.94	0.10	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BQ	3004	1/1	0.94	0.14	42,42,42,42	0
57	MG	BA	3393	1/1	0.94	0.13	51,51,51,51	0
57	MG	BR	201	1/1	0.94	0.22	57,57,57,57	0
57	MG	BA	3268	1/1	0.94	0.10	55,55,55,55	0
57	MG	BA	3674	1/1	0.94	0.17	63,63,63,63	0
57	MG	BA	3269	1/1	0.94	0.10	53,53,53,53	0
57	MG	DA	3307	1/1	0.94	0.08	42,42,42,42	0
57	MG	BZ	3001	1/1	0.94	0.11	55,55,55,55	0
57	MG	B0	102	1/1	0.94	0.15	48,48,48,48	0
57	MG	BA	3035	1/1	0.94	0.12	39,39,39,39	0
57	MG	BA	3531	1/1	0.94	0.10	26,26,26,26	0
57	MG	BA	3273	1/1	0.94	0.14	54,54,54,54	0
57	MG	BA	3039	1/1	0.94	0.08	32,32,32,32	0
57	MG	BA	3047	1/1	0.94	0.19	60,60,60,60	0
57	MG	DA	3005	1/1	0.94	0.28	57,57,57,57	0
57	MG	DA	3006	1/1	0.94	0.07	38,38,38,38	0
57	MG	BA	3403	1/1	0.94	0.08	54,54,54,54	0
57	MG	BA	3134	1/1	0.94	0.18	48,48,48,48	0
57	MG	DA	3328	1/1	0.94	0.09	47,47,47,47	0
57	MG	BA	3138	1/1	0.94	0.18	42,42,42,42	0
57	MG	BA	3139	1/1	0.94	0.26	40,40,40,40	0
57	MG	DA	3332	1/1	0.94	0.10	53,53,53,53	0
57	MG	BA	3289	1/1	0.94	0.14	56,56,56,56	0
57	MG	DA	3018	1/1	0.94	0.13	62,62,62,62	0
57	MG	BA	3290	1/1	0.94	0.21	40,40,40,40	0
57	MG	AA	3066	1/1	0.94	0.29	60,60,60,60	0
57	MG	BA	3551	1/1	0.94	0.11	36,36,36,36	0
57	MG	DA	3645	1/1	0.94	0.07	45,45,45,45	0
57	MG	DA	3030	1/1	0.94	0.06	39,39,39,39	0
57	MG	BA	3704	1/1	0.94	0.09	77,77,77,77	0
57	MG	DA	3650	1/1	0.94	0.09	67,67,67,67	0
57	MG	AX	3006	1/1	0.94	0.08	65,65,65,65	0
57	MG	BA	3296	1/1	0.94	0.18	53,53,53,53	0
57	MG	AA	3022	1/1	0.94	0.17	71,71,71,71	0
57	MG	CA	3013	1/1	0.94	0.20	69,69,69,69	0
57	MG	BA	3058	1/1	0.94	0.09	49,49,49,49	0
57	MG	BA	3156	1/1	0.94	0.24	41,41,41,41	0
57	MG	BA	3564	1/1	0.94	0.10	44,44,44,44	0
57	MG	DA	3359	1/1	0.94	0.11	47,47,47,47	0
57	MG	AA	3007	1/1	0.94	0.10	57,57,57,57	0
57	MG	DA	3660	1/1	0.94	0.20	61,61,61,61	0
57	MG	DA	3361	1/1	0.94	0.08	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	CA	3019	1/1	0.94	0.17	65,65,65,65	0
57	MG	CA	3020	1/1	0.94	0.17	56,56,56,56	0
57	MG	AA	3112	1/1	0.94	0.22	63,63,63,63	0
57	MG	BA	3161	1/1	0.94	0.10	52,52,52,52	0
57	MG	BA	3162	1/1	0.94	0.08	38,38,38,38	0
57	MG	CA	3025	1/1	0.94	0.15	51,51,51,51	0
57	MG	DA	3372	1/1	0.94	0.12	56,56,56,56	0
57	MG	DA	3675	1/1	0.94	0.08	52,52,52,52	0
57	MG	BA	3573	1/1	0.94	0.11	51,51,51,51	0
57	MG	DA	3068	1/1	0.94	0.14	58,58,58,58	0
57	MG	DA	3378	1/1	0.94	0.21	57,57,57,57	0
57	MG	DA	3379	1/1	0.94	0.14	63,63,63,63	0
57	MG	BA	3307	1/1	0.94	0.09	29,29,29,29	0
57	MG	BA	3308	1/1	0.94	0.10	43,43,43,43	0
57	MG	BA	3579	1/1	0.94	0.10	49,49,49,49	0
57	MG	DA	3072	1/1	0.94	0.12	47,47,47,47	0
57	MG	BA	3163	1/1	0.94	0.06	55,55,55,55	0
57	MG	DA	3391	1/1	0.94	0.11	45,45,45,45	0
57	MG	BA	3729	1/1	0.94	0.10	47,47,47,47	0
57	MG	DA	3396	1/1	0.94	0.07	40,40,40,40	0
57	MG	DD	307	1/1	0.94	0.26	43,43,43,43	0
57	MG	BA	3581	1/1	0.94	0.09	30,30,30,30	0
57	MG	BA	3582	1/1	0.94	0.17	74,74,74,74	0
57	MG	DF	3002	1/1	0.94	0.09	48,48,48,48	0
57	MG	DN	5001	1/1	0.94	0.10	66,66,66,66	0
57	MG	AA	3056	1/1	0.94	0.15	61,61,61,61	0
57	MG	AA	3201	1/1	0.94	0.09	52,52,52,52	0
57	MG	DQ	3003	1/1	0.94	0.09	51,51,51,51	0
57	MG	BA	3585	1/1	0.94	0.07	46,46,46,46	0
57	MG	AA	3045	1/1	0.94	0.12	58,58,58,58	0
57	MG	DU	3001	1/1	0.94	0.13	55,55,55,55	0
57	MG	DU	3002	1/1	0.94	0.13	55,55,55,55	0
57	MG	BA	3442	1/1	0.94	0.10	44,44,44,44	0
57	MG	DW	3001	1/1	0.94	0.17	54,54,54,54	0
57	MG	DA	3085	1/1	0.94	0.08	53,53,53,53	0
57	MG	CA	3047	1/1	0.94	0.13	53,53,53,53	0
57	MG	DA	3088	1/1	0.94	0.12	47,47,47,47	0
57	MG	BA	3071	1/1	0.94	0.23	59,59,59,59	0
57	MG	DA	3091	1/1	0.94	0.10	48,48,48,48	0
57	MG	DA	3092	1/1	0.94	0.08	45,45,45,45	0
57	MG	AA	3096	1/1	0.94	0.34	63,63,63,63	0
57	MG	CA	3050	1/1	0.94	0.32	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3173	1/1	0.95	0.08	53,53,53,53	0
57	MG	DA	3175	1/1	0.95	0.07	41,41,41,41	0
57	MG	BA	3369	1/1	0.95	0.07	44,44,44,44	0
57	MG	BA	3370	1/1	0.95	0.10	39,39,39,39	0
57	MG	BA	3657	1/1	0.95	0.18	47,47,47,47	0
57	MG	BA	3509	1/1	0.95	0.09	31,31,31,31	0
57	MG	AX	3005	1/1	0.95	0.05	47,47,47,47	0
57	MG	BA	3041	1/1	0.95	0.14	40,40,40,40	0
57	MG	DA	3189	1/1	0.95	0.17	41,41,41,41	0
57	MG	BA	3513	1/1	0.95	0.09	59,59,59,59	0
57	MG	BA	3664	1/1	0.95	0.17	55,55,55,55	0
57	MG	DA	3196	1/1	0.95	0.21	49,49,49,49	0
57	MG	CA	3130	1/1	0.95	0.12	57,57,57,57	0
57	MG	BA	3242	1/1	0.95	0.12	55,55,55,55	0
57	MG	BA	3666	1/1	0.95	0.14	50,50,50,50	0
57	MG	DA	3466	1/1	0.95	0.14	41,41,41,41	0
57	MG	DA	3201	1/1	0.95	0.13	61,61,61,61	0
57	MG	AA	3011	1/1	0.95	0.26	57,57,57,57	0
57	MG	AA	3039	1/1	0.95	0.12	56,56,56,56	0
57	MG	BA	3382	1/1	0.95	0.09	63,63,63,63	0
57	MG	BA	3518	1/1	0.95	0.09	44,44,44,44	0
57	MG	BA	3383	1/1	0.95	0.09	53,53,53,53	0
57	MG	AA	3163	1/1	0.95	0.16	56,56,56,56	0
57	MG	BA	3251	1/1	0.95	0.07	44,44,44,44	0
57	MG	BG	203	1/1	0.95	0.06	42,42,42,42	0
57	MG	DA	3479	1/1	0.95	0.10	43,43,43,43	0
57	MG	BA	3252	1/1	0.95	0.19	60,60,60,60	0
57	MG	CA	3145	1/1	0.95	0.09	66,66,66,66	0
57	MG	BN	3005	1/1	0.95	0.04	36,36,36,36	0
57	MG	BA	3675	1/1	0.95	0.08	67,67,67,67	0
57	MG	BA	3676	1/1	0.95	0.11	33,33,33,33	0
57	MG	BA	3529	1/1	0.95	0.12	56,56,56,56	0
57	MG	DA	3488	1/1	0.95	0.07	41,41,41,41	0
57	MG	DA	3217	1/1	0.95	0.07	38,38,38,38	0
57	MG	BA	3055	1/1	0.95	0.13	45,45,45,45	0
57	MG	AA	3132	1/1	0.95	0.08	55,55,55,55	0
57	MG	DA	3220	1/1	0.95	0.17	46,46,46,46	0
57	MG	BU	204	1/1	0.95	0.17	35,35,35,35	0
57	MG	CA	3154	1/1	0.95	0.16	56,56,56,56	0
57	MG	BA	3130	1/1	0.95	0.07	44,44,44,44	0
57	MG	DA	3224	1/1	0.95	0.17	49,49,49,49	0
57	MG	AA	3087	1/1	0.95	0.07	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	AA	3029	1/1	0.95	0.25	53,53,53,53	0
57	MG	BA	3062	1/1	0.95	0.16	42,42,42,42	0
57	MG	BA	3266	1/1	0.95	0.14	39,39,39,39	0
57	MG	AA	3034	1/1	0.95	0.07	47,47,47,47	0
57	MG	DA	3233	1/1	0.95	0.09	53,53,53,53	0
57	MG	DA	3508	1/1	0.95	0.09	44,44,44,44	0
57	MG	DA	3510	1/1	0.95	0.18	49,49,49,49	0
57	MG	DA	3511	1/1	0.95	0.07	49,49,49,49	0
57	MG	CA	3162	1/1	0.95	0.09	66,66,66,66	0
57	MG	DA	3514	1/1	0.95	0.10	42,42,42,42	0
57	MG	AA	3071	1/1	0.95	0.08	53,53,53,53	0
57	MG	DA	3238	1/1	0.95	0.28	44,44,44,44	0
57	MG	CA	3164	1/1	0.95	0.14	60,60,60,60	0
57	MG	CA	3165	1/1	0.95	0.07	45,45,45,45	0
57	MG	AA	3035	1/1	0.95	0.23	56,56,56,56	0
57	MG	BA	3546	1/1	0.95	0.12	40,40,40,40	0
57	MG	BA	3697	1/1	0.95	0.11	61,61,61,61	0
57	MG	DA	3246	1/1	0.95	0.06	43,43,43,43	0
57	MG	BA	3147	1/1	0.95	0.09	45,45,45,45	0
57	MG	DA	3528	1/1	0.95	0.10	62,62,62,62	0
57	MG	DA	3529	1/1	0.95	0.06	38,38,38,38	0
57	MG	BA	3701	1/1	0.95	0.14	43,43,43,43	0
57	MG	BA	3549	1/1	0.95	0.19	39,39,39,39	0
57	MG	BA	3272	1/1	0.95	0.36	48,48,48,48	0
57	MG	CK	3001	1/1	0.95	0.08	45,45,45,45	0
57	MG	DA	3252	1/1	0.95	0.06	37,37,37,37	0
57	MG	B9	502	1/1	0.95	0.08	48,48,48,48	0
57	MG	CA	3001	1/1	0.95	0.14	75,75,75,75	0
57	MG	BA	3149	1/1	0.95	0.09	40,40,40,40	0
57	MG	BA	3708	1/1	0.95	0.08	50,50,50,50	0
57	MG	BA	3274	1/1	0.95	0.11	49,49,49,49	0
57	MG	CA	3007	1/1	0.95	0.09	57,57,57,57	0
57	MG	DA	3545	1/1	0.95	0.06	35,35,35,35	0
57	MG	BA	3151	1/1	0.95	0.10	52,52,52,52	0
57	MG	BA	3068	1/1	0.95	0.15	43,43,43,43	0
57	MG	AA	3073	1/1	0.95	0.10	56,56,56,56	0
57	MG	BA	3412	1/1	0.95	0.14	40,40,40,40	0
57	MG	BA	3716	1/1	0.95	0.09	65,65,65,65	0
57	MG	DA	3551	1/1	0.95	0.09	55,55,55,55	0
57	MG	DA	3269	1/1	0.95	0.10	49,49,49,49	0
57	MG	BA	3282	1/1	0.95	0.09	39,39,39,39	0
57	MG	AA	3141	1/1	0.95	0.18	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3555	1/1	0.95	0.08	53,53,53,53	0
57	MG	CA	3015	1/1	0.95	0.17	56,56,56,56	0
57	MG	BA	3567	1/1	0.95	0.11	34,34,34,34	0
57	MG	AA	3208	1/1	0.95	0.19	60,60,60,60	0
57	MG	DA	3559	1/1	0.95	0.10	43,43,43,43	0
57	MG	DA	3277	1/1	0.95	0.09	55,55,55,55	0
57	MG	DA	3562	1/1	0.95	0.12	64,64,64,64	0
57	MG	AA	3143	1/1	0.95	0.08	60,60,60,60	0
57	MG	DA	3281	1/1	0.95	0.10	53,53,53,53	0
57	MG	DA	3021	1/1	0.95	0.06	31,31,31,31	0
57	MG	DA	3022	1/1	0.95	0.13	51,51,51,51	0
57	MG	AA	3030	1/1	0.95	0.07	60,60,60,60	0
57	MG	BA	3292	1/1	0.95	0.09	48,48,48,48	0
57	MG	DA	3570	1/1	0.95	0.10	31,31,31,31	0
57	MG	DA	3026	1/1	0.95	0.19	59,59,59,59	0
57	MG	AA	3211	1/1	0.95	0.09	47,47,47,47	0
57	MG	AA	3077	1/1	0.95	0.25	56,56,56,56	0
57	MG	DA	3292	1/1	0.95	0.10	30,30,30,30	0
57	MG	DA	3033	1/1	0.95	0.08	42,42,42,42	0
57	MG	DA	3294	1/1	0.95	0.12	43,43,43,43	0
57	MG	DA	3579	1/1	0.95	0.08	48,48,48,48	0
57	MG	BA	3164	1/1	0.95	0.09	48,48,48,48	0
57	MG	AA	3181	1/1	0.95	0.16	51,51,51,51	0
57	MG	DA	3297	1/1	0.95	0.05	39,39,39,39	0
57	MG	BA	3428	1/1	0.95	0.06	46,46,46,46	0
57	MG	BA	3081	1/1	0.95	0.15	46,46,46,46	0
57	MG	DA	3587	1/1	0.95	0.09	56,56,56,56	0
57	MG	BA	3430	1/1	0.95	0.07	37,37,37,37	0
57	MG	DA	3047	1/1	0.95	0.19	49,49,49,49	0
57	MG	BA	3169	1/1	0.95	0.11	45,45,45,45	0
57	MG	DA	3303	1/1	0.95	0.07	48,48,48,48	0
57	MG	DA	3049	1/1	0.95	0.19	52,52,52,52	0
57	MG	BA	3170	1/1	0.95	0.10	38,38,38,38	0
57	MG	DA	3595	1/1	0.95	0.08	59,59,59,59	0
57	MG	CA	3032	1/1	0.95	0.29	62,62,62,62	0
57	MG	DA	3600	1/1	0.95	0.12	70,70,70,70	0
57	MG	BA	3006	1/1	0.95	0.10	48,48,48,48	0
57	MG	DA	3310	1/1	0.95	0.10	38,38,38,38	0
57	MG	BA	3173	1/1	0.95	0.10	48,48,48,48	0
57	MG	DA	3606	1/1	0.95	0.14	71,71,71,71	0
57	MG	DA	3059	1/1	0.95	0.08	43,43,43,43	0
57	MG	CA	3035	1/1	0.95	0.10	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3439	1/1	0.95	0.06	33,33,33,33	0
57	MG	BA	3743	1/1	0.95	0.09	44,44,44,44	0
57	MG	DA	3063	1/1	0.95	0.08	54,54,54,54	0
57	MG	BA	3305	1/1	0.95	0.10	62,62,62,62	0
57	MG	BA	3746	1/1	0.95	0.12	51,51,51,51	0
57	MG	DA	3326	1/1	0.95	0.09	43,43,43,43	0
57	MG	BA	3175	1/1	0.95	0.08	20,20,20,20	0
57	MG	CA	3042	1/1	0.95	0.20	59,59,59,59	0
57	MG	AA	3113	1/1	0.95	0.09	58,58,58,58	0
57	MG	DA	3619	1/1	0.95	0.08	69,69,69,69	0
57	MG	BA	3089	1/1	0.95	0.05	19,19,19,19	0
57	MG	BA	3595	1/1	0.95	0.07	51,51,51,51	0
57	MG	DA	3622	1/1	0.95	0.08	61,61,61,61	0
57	MG	AA	3149	1/1	0.95	0.07	46,46,46,46	0
57	MG	BA	3016	1/1	0.95	0.08	38,38,38,38	0
57	MG	BA	3450	1/1	0.95	0.07	48,48,48,48	0
57	MG	AA	3055	1/1	0.95	0.11	57,57,57,57	0
57	MG	AN	502	1/1	0.95	0.34	63,63,63,63	0
57	MG	BA	3098	1/1	0.95	0.13	40,40,40,40	0
57	MG	DA	3341	1/1	0.95	0.09	51,51,51,51	0
57	MG	DA	3080	1/1	0.95	0.16	55,55,55,55	0
57	MG	DA	3346	1/1	0.95	0.06	48,48,48,48	0
57	MG	BA	3191	1/1	0.95	0.11	43,43,43,43	0
57	MG	BA	3606	1/1	0.95	0.11	61,61,61,61	0
57	MG	BA	3763	1/1	0.95	0.09	24,24,24,24	0
57	MG	DA	3353	1/1	0.95	0.14	42,42,42,42	0
57	MG	BA	3193	1/1	0.95	0.15	48,48,48,48	0
57	MG	BA	3196	1/1	0.95	0.12	38,38,38,38	0
57	MG	DA	3640	1/1	0.95	0.11	43,43,43,43	0
57	MG	BA	3610	1/1	0.95	0.12	61,61,61,61	0
57	MG	BA	3100	1/1	0.95	0.11	39,39,39,39	0
57	MG	BA	3614	1/1	0.95	0.13	63,63,63,63	0
57	MG	BA	3201	1/1	0.95	0.30	62,62,62,62	0
57	MG	BA	3019	1/1	0.95	0.12	42,42,42,42	0
57	MG	BA	3618	1/1	0.95	0.11	65,65,65,65	0
57	MG	CA	3068	1/1	0.95	0.19	48,48,48,48	0
57	MG	BA	3773	1/1	0.95	0.12	52,52,52,52	0
57	MG	DA	3100	1/1	0.95	0.13	43,43,43,43	0
57	MG	BA	3775	1/1	0.95	0.14	33,33,33,33	0
57	MG	DA	3370	1/1	0.95	0.11	51,51,51,51	0
57	MG	BA	3203	1/1	0.95	0.14	40,40,40,40	0
57	MG	CA	3072	1/1	0.95	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3204	1/1	0.95	0.08	36,36,36,36	0
57	MG	BA	3326	1/1	0.95	0.10	20,20,20,20	0
57	MG	BA	3329	1/1	0.95	0.12	60,60,60,60	0
57	MG	AA	3019	1/1	0.95	0.10	66,66,66,66	0
57	MG	DA	3116	1/1	0.95	0.25	52,52,52,52	0
57	MG	BA	3206	1/1	0.95	0.20	49,49,49,49	0
57	MG	BA	3627	1/1	0.95	0.12	56,56,56,56	0
57	MG	DA	3119	1/1	0.95	0.08	39,39,39,39	0
57	MG	DA	3385	1/1	0.95	0.10	52,52,52,52	0
57	MG	DA	3120	1/1	0.95	0.13	49,49,49,49	0
57	MG	AA	3098	1/1	0.95	0.16	55,55,55,55	0
57	MG	DA	3392	1/1	0.95	0.12	70,70,70,70	0
57	MG	CA	3081	1/1	0.95	0.05	46,46,46,46	0
57	MG	DA	3395	1/1	0.95	0.07	47,47,47,47	0
57	MG	BA	3208	1/1	0.95	0.07	44,44,44,44	0
57	MG	BA	3789	1/1	0.95	0.07	12,12,12,12	0
57	MG	BA	3790	1/1	0.95	0.11	34,34,34,34	0
57	MG	BA	3792	1/1	0.95	0.14	54,54,54,54	0
57	MG	DA	3129	1/1	0.95	0.09	46,46,46,46	0
57	MG	BA	3209	1/1	0.95	0.14	54,54,54,54	0
57	MG	DA	3131	1/1	0.95	0.18	46,46,46,46	0
57	MG	BA	3345	1/1	0.95	0.08	38,38,38,38	0
57	MG	DB	3009	1/1	0.95	0.19	59,59,59,59	0
57	MG	BA	3480	1/1	0.95	0.09	35,35,35,35	0
57	MG	DA	3134	1/1	0.95	0.08	41,41,41,41	0
57	MG	CA	3093	1/1	0.95	0.08	55,55,55,55	0
57	MG	DD	301	1/1	0.95	0.10	47,47,47,47	0
57	MG	DA	3137	1/1	0.95	0.16	54,54,54,54	0
57	MG	DD	304	1/1	0.95	0.14	52,52,52,52	0
57	MG	DD	306	1/1	0.95	0.15	39,39,39,39	0
57	MG	BA	3211	1/1	0.95	0.17	55,55,55,55	0
57	MG	DD	309	1/1	0.95	0.11	59,59,59,59	0
57	MG	BA	3107	1/1	0.95	0.10	53,53,53,53	0
57	MG	DE	304	1/1	0.95	0.12	43,43,43,43	0
57	MG	BA	3485	1/1	0.95	0.09	42,42,42,42	0
57	MG	AA	3099	1/1	0.95	0.24	51,51,51,51	0
57	MG	DA	3145	1/1	0.95	0.12	43,43,43,43	0
57	MG	BA	3215	1/1	0.95	0.21	36,36,36,36	0
57	MG	AA	3120	1/1	0.95	0.09	45,45,45,45	0
57	MG	BA	3805	1/1	0.95	0.06	44,44,44,44	0
57	MG	BA	3354	1/1	0.95	0.09	48,48,48,48	0
57	MG	DA	3152	1/1	0.95	0.12	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3027	1/1	0.95	0.06	26,26,26,26	0
57	MG	BA	3115	1/1	0.95	0.14	59,59,59,59	0
57	MG	BA	3227	1/1	0.95	0.25	57,57,57,57	0
57	MG	BA	3645	1/1	0.95	0.05	33,33,33,33	0
57	MG	DA	3428	1/1	0.95	0.14	37,37,37,37	0
57	MG	BB	204	1/1	0.95	0.09	41,41,41,41	0
57	MG	BA	3030	1/1	0.95	0.13	46,46,46,46	0
57	MG	AA	3080	1/1	0.95	0.18	58,58,58,58	0
57	MG	AA	3122	1/1	0.95	0.08	56,56,56,56	0
57	MG	BA	3119	1/1	0.95	0.11	45,45,45,45	0
57	MG	AA	3123	1/1	0.95	0.12	51,51,51,51	0
57	MG	BA	3368	1/1	0.95	0.09	40,40,40,40	0
57	MG	DA	3464	1/1	0.96	0.06	46,46,46,46	0
57	MG	BA	3050	1/1	0.96	0.06	38,38,38,38	0
57	MG	BA	3762	1/1	0.96	0.10	46,46,46,46	0
57	MG	BA	3233	1/1	0.96	0.25	56,56,56,56	0
57	MG	DA	3004	1/1	0.96	0.15	40,40,40,40	0
57	MG	BA	3236	1/1	0.96	0.11	49,49,49,49	0
57	MG	DA	3226	1/1	0.96	0.26	45,45,45,45	0
57	MG	BA	3051	1/1	0.96	0.08	43,43,43,43	0
57	MG	BA	3528	1/1	0.96	0.15	56,56,56,56	0
57	MG	DA	3008	1/1	0.96	0.06	36,36,36,36	0
57	MG	AA	3130	1/1	0.96	0.09	56,56,56,56	0
57	MG	DA	3232	1/1	0.96	0.10	62,62,62,62	0
57	MG	BA	3646	1/1	0.96	0.11	42,42,42,42	0
57	MG	DA	3013	1/1	0.96	0.04	40,40,40,40	0
57	MG	AA	3010	1/1	0.96	0.15	52,52,52,52	0
57	MG	DA	3483	1/1	0.96	0.15	55,55,55,55	0
57	MG	DA	3237	1/1	0.96	0.19	56,56,56,56	0
57	MG	BA	3240	1/1	0.96	0.18	47,47,47,47	0
57	MG	AA	3060	1/1	0.96	0.13	46,46,46,46	0
57	MG	DA	3240	1/1	0.96	0.09	48,48,48,48	0
57	MG	DA	3241	1/1	0.96	0.08	45,45,45,45	0
57	MG	BA	3772	1/1	0.96	0.15	33,33,33,33	0
57	MG	BA	3324	1/1	0.96	0.12	45,45,45,45	0
57	MG	BA	3774	1/1	0.96	0.06	46,46,46,46	0
57	MG	BA	3536	1/1	0.96	0.22	49,49,49,49	0
57	MG	BA	3108	1/1	0.96	0.16	44,44,44,44	0
57	MG	AA	3133	1/1	0.96	0.16	56,56,56,56	0
57	MG	DA	3027	1/1	0.96	0.16	51,51,51,51	0
57	MG	DA	3028	1/1	0.96	0.13	52,52,52,52	0
57	MG	DA	3029	1/1	0.96	0.14	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3328	1/1	0.96	0.14	40,40,40,40	0
57	MG	DA	3031	1/1	0.96	0.25	43,43,43,43	0
57	MG	AA	3081	1/1	0.96	0.06	48,48,48,48	0
57	MG	BA	3330	1/1	0.96	0.11	37,37,37,37	0
57	MG	BA	3331	1/1	0.96	0.11	49,49,49,49	0
57	MG	DA	3507	1/1	0.96	0.09	43,43,43,43	0
57	MG	DA	3257	1/1	0.96	0.16	50,50,50,50	0
57	MG	DA	3509	1/1	0.96	0.08	59,59,59,59	0
57	MG	DA	3036	1/1	0.96	0.07	48,48,48,48	0
57	MG	CA	3044	1/1	0.96	0.23	62,62,62,62	0
57	MG	CA	3045	1/1	0.96	0.18	54,54,54,54	0
57	MG	DA	3043	1/1	0.96	0.14	38,38,38,38	0
57	MG	DA	3515	1/1	0.96	0.15	45,45,45,45	0
57	MG	BA	3332	1/1	0.96	0.11	38,38,38,38	0
57	MG	BA	3785	1/1	0.96	0.11	59,59,59,59	0
57	MG	BA	3786	1/1	0.96	0.06	35,35,35,35	0
57	MG	BA	3249	1/1	0.96	0.06	49,49,49,49	0
57	MG	BA	3336	1/1	0.96	0.10	64,64,64,64	0
57	MG	BA	3437	1/1	0.96	0.10	36,36,36,36	0
57	MG	BA	3250	1/1	0.96	0.38	42,42,42,42	0
57	MG	BA	3171	1/1	0.96	0.21	31,31,31,31	0
57	MG	DA	3526	1/1	0.96	0.06	48,48,48,48	0
57	MG	BA	3008	1/1	0.96	0.10	47,47,47,47	0
57	MG	DA	3275	1/1	0.96	0.08	42,42,42,42	0
57	MG	BA	3256	1/1	0.96	0.07	40,40,40,40	0
57	MG	BA	3556	1/1	0.96	0.12	36,36,36,36	0
57	MG	DA	3278	1/1	0.96	0.07	43,43,43,43	0
57	MG	BA	3557	1/1	0.96	0.09	33,33,33,33	0
57	MG	DA	3533	1/1	0.96	0.07	43,43,43,43	0
57	MG	DA	3280	1/1	0.96	0.09	33,33,33,33	0
57	MG	BA	3798	1/1	0.96	0.11	28,28,28,28	0
57	MG	DA	3282	1/1	0.96	0.06	52,52,52,52	0
57	MG	AA	3015	1/1	0.96	0.11	65,65,65,65	0
57	MG	DA	3064	1/1	0.96	0.06	49,49,49,49	0
57	MG	DA	3065	1/1	0.96	0.09	43,43,43,43	0
57	MG	BA	3346	1/1	0.96	0.05	27,27,27,27	0
57	MG	BA	3174	1/1	0.96	0.07	37,37,37,37	0
57	MG	BA	3063	1/1	0.96	0.25	59,59,59,59	0
57	MG	AA	3203	1/1	0.96	0.06	59,59,59,59	0
57	MG	BA	3804	1/1	0.96	0.32	53,53,53,53	0
57	MG	BA	3451	1/1	0.96	0.07	31,31,31,31	0
57	MG	BA	3350	1/1	0.96	0.10	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3262	1/1	0.96	0.09	41,41,41,41	0
57	MG	BA	3352	1/1	0.96	0.15	53,53,53,53	0
57	MG	BA	3178	1/1	0.96	0.07	46,46,46,46	0
57	MG	AA	3075	1/1	0.96	0.09	49,49,49,49	0
57	MG	BA	3578	1/1	0.96	0.06	46,46,46,46	0
57	MG	AA	3085	1/1	0.96	0.13	48,48,48,48	0
57	MG	BA	3687	1/1	0.96	0.09	22,22,22,22	0
57	MG	BA	3690	1/1	0.96	0.22	58,58,58,58	0
57	MG	BA	3691	1/1	0.96	0.11	55,55,55,55	0
57	MG	AA	3053	1/1	0.96	0.15	61,61,61,61	0
57	MG	DA	3306	1/1	0.96	0.15	55,55,55,55	0
57	MG	AA	3207	1/1	0.96	0.11	65,65,65,65	0
57	MG	CA	3080	1/1	0.96	0.07	49,49,49,49	0
57	MG	AA	3063	1/1	0.96	0.04	35,35,35,35	0
57	MG	DA	3089	1/1	0.96	0.21	52,52,52,52	0
57	MG	BA	3464	1/1	0.96	0.07	45,45,45,45	0
57	MG	DA	3312	1/1	0.96	0.06	54,54,54,54	0
57	MG	BB	216	1/1	0.96	0.17	51,51,51,51	0
57	MG	CA	3084	1/1	0.96	0.12	60,60,60,60	0
57	MG	AA	3140	1/1	0.96	0.09	53,53,53,53	0
57	MG	BA	3190	1/1	0.96	0.10	52,52,52,52	0
57	MG	AA	3043	1/1	0.96	0.14	51,51,51,51	0
57	MG	BA	3702	1/1	0.96	0.18	51,51,51,51	0
57	MG	DA	3576	1/1	0.96	0.06	53,53,53,53	0
57	MG	BD	303	1/1	0.96	0.11	39,39,39,39	0
57	MG	DA	3322	1/1	0.96	0.17	51,51,51,51	0
57	MG	DA	3323	1/1	0.96	0.06	50,50,50,50	0
57	MG	DA	3101	1/1	0.96	0.10	49,49,49,49	0
57	MG	CA	3091	1/1	0.96	0.11	55,55,55,55	0
57	MG	CA	3092	1/1	0.96	0.05	50,50,50,50	0
57	MG	DA	3107	1/1	0.96	0.10	51,51,51,51	0
57	MG	DA	3330	1/1	0.96	0.11	45,45,45,45	0
57	MG	BA	3074	1/1	0.96	0.06	46,46,46,46	0
57	MG	DA	3109	1/1	0.96	0.05	40,40,40,40	0
57	MG	DA	3333	1/1	0.96	0.09	41,41,41,41	0
57	MG	BD	305	1/1	0.96	0.09	35,35,35,35	0
57	MG	BD	309	1/1	0.96	0.12	57,57,57,57	0
57	MG	BA	3026	1/1	0.96	0.06	41,41,41,41	0
57	MG	DA	3113	1/1	0.96	0.24	60,60,60,60	0
57	MG	CA	3101	1/1	0.96	0.13	49,49,49,49	0
57	MG	DA	3596	1/1	0.96	0.10	56,56,56,56	0
57	MG	BA	3276	1/1	0.96	0.19	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BE	304	1/1	0.96	0.12	42,42,42,42	0
57	MG	DA	3601	1/1	0.96	0.06	44,44,44,44	0
57	MG	CA	3105	1/1	0.96	0.15	52,52,52,52	0
57	MG	DA	3343	1/1	0.96	0.13	50,50,50,50	0
57	MG	DA	3345	1/1	0.96	0.09	44,44,44,44	0
57	MG	BA	3472	1/1	0.96	0.04	20,20,20,20	0
57	MG	BA	3199	1/1	0.96	0.14	46,46,46,46	0
57	MG	DA	3350	1/1	0.96	0.09	51,51,51,51	0
57	MG	BA	3710	1/1	0.96	0.09	57,57,57,57	0
57	MG	BF	301	1/1	0.96	0.09	35,35,35,35	0
57	MG	BF	302	1/1	0.96	0.11	46,46,46,46	0
57	MG	BF	303	1/1	0.96	0.33	49,49,49,49	0
57	MG	AA	3142	1/1	0.96	0.05	41,41,41,41	0
57	MG	BA	3476	1/1	0.96	0.12	55,55,55,55	0
57	MG	CA	3114	1/1	0.96	0.06	57,57,57,57	0
57	MG	BA	3713	1/1	0.96	0.07	33,33,33,33	0
57	MG	BF	309	1/1	0.96	0.10	53,53,53,53	0
57	MG	BA	3077	1/1	0.96	0.16	49,49,49,49	0
57	MG	BA	3374	1/1	0.96	0.12	40,40,40,40	0
57	MG	DA	3363	1/1	0.96	0.06	29,29,29,29	0
57	MG	BA	3479	1/1	0.96	0.06	50,50,50,50	0
57	MG	DA	3135	1/1	0.96	0.07	38,38,38,38	0
57	MG	BN	3001	1/1	0.96	0.22	53,53,53,53	0
57	MG	BN	3002	1/1	0.96	0.06	39,39,39,39	0
57	MG	BN	3003	1/1	0.96	0.08	48,48,48,48	0
57	MG	CA	3123	1/1	0.96	0.07	58,58,58,58	0
57	MG	BA	3600	1/1	0.96	0.20	44,44,44,44	0
57	MG	BA	3284	1/1	0.96	0.19	43,43,43,43	0
57	MG	DA	3375	1/1	0.96	0.11	39,39,39,39	0
57	MG	DA	3142	1/1	0.96	0.07	47,47,47,47	0
57	MG	BA	3029	1/1	0.96	0.43	37,37,37,37	0
57	MG	DA	3146	1/1	0.96	0.13	55,55,55,55	0
57	MG	BA	3132	1/1	0.96	0.05	40,40,40,40	0
57	MG	BP	201	1/1	0.96	0.13	41,41,41,41	0
57	MG	BA	3381	1/1	0.96	0.10	46,46,46,46	0
57	MG	DA	3150	1/1	0.96	0.06	56,56,56,56	0
57	MG	BA	3133	1/1	0.96	0.11	45,45,45,45	0
57	MG	AA	3169	1/1	0.96	0.07	62,62,62,62	0
57	MG	DA	3389	1/1	0.96	0.08	46,46,46,46	0
57	MG	BU	201	1/1	0.96	0.10	43,43,43,43	0
57	MG	BU	202	1/1	0.96	0.16	40,40,40,40	0
57	MG	BA	3135	1/1	0.96	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
57	MG	BU	207	1/1	0.96	0.16	38,38,38,38	0
57	MG	DA	3647	1/1	0.96	0.08	54,54,54,54	0
57	MG	DA	3648	1/1	0.96	0.14	57,57,57,57	0
57	MG	CA	3137	1/1	0.96	0.09	56,56,56,56	0
57	MG	DA	3397	1/1	0.96	0.07	57,57,57,57	0
57	MG	BV	201	1/1	0.96	0.13	33,33,33,33	0
57	MG	DA	3162	1/1	0.96	0.21	50,50,50,50	0
57	MG	BA	3727	1/1	0.96	0.07	51,51,51,51	0
57	MG	DA	3401	1/1	0.96	0.05	38,38,38,38	0
57	MG	BA	3031	1/1	0.96	0.18	52,52,52,52	0
57	MG	BW	202	1/1	0.96	0.19	54,54,54,54	0
57	MG	DA	3404	1/1	0.96	0.06	48,48,48,48	0
57	MG	AA	3124	1/1	0.96	0.05	47,47,47,47	0
57	MG	BX	3002	1/1	0.96	0.10	46,46,46,46	0
57	MG	DA	3171	1/1	0.96	0.08	31,31,31,31	0
57	MG	DA	3172	1/1	0.96	0.10	62,62,62,62	0
57	MG	BA	3142	1/1	0.96	0.10	49,49,49,49	0
57	MG	AE	201	1/1	0.96	0.23	59,59,59,59	0
57	MG	DA	3664	1/1	0.96	0.13	48,48,48,48	0
57	MG	DA	3666	1/1	0.96	0.06	35,35,35,35	0
57	MG	DA	3412	1/1	0.96	0.21	50,50,50,50	0
57	MG	DA	3176	1/1	0.96	0.13	41,41,41,41	0
57	MG	BA	3088	1/1	0.96	0.14	48,48,48,48	0
57	MG	DA	3671	1/1	0.96	0.21	74,74,74,74	0
57	MG	DA	3179	1/1	0.96	0.18	52,52,52,52	0
57	MG	B1	101	1/1	0.96	0.19	51,51,51,51	0
57	MG	DA	3674	1/1	0.96	0.07	37,37,37,37	0
57	MG	BA	3733	1/1	0.96	0.08	58,58,58,58	0
57	MG	BA	3392	1/1	0.96	0.13	53,53,53,53	0
57	MG	DA	3677	1/1	0.96	0.19	52,52,52,52	0
57	MG	CA	3151	1/1	0.96	0.19	59,59,59,59	0
57	MG	DA	3186	1/1	0.96	0.13	54,54,54,54	0
57	MG	AA	3171	1/1	0.96	0.07	51,51,51,51	0
57	MG	B6	101	1/1	0.96	0.10	48,48,48,48	0
57	MG	BA	3736	1/1	0.96	0.18	42,42,42,42	0
57	MG	DA	3193	1/1	0.96	0.18	57,57,57,57	0
57	MG	BA	3620	1/1	0.96	0.08	40,40,40,40	0
57	MG	BA	3739	1/1	0.96	0.16	40,40,40,40	0
57	MG	DB	3010	1/1	0.96	0.10	57,57,57,57	0
57	MG	B7	103	1/1	0.96	0.07	42,42,42,42	0
57	MG	BA	3090	1/1	0.96	0.21	53,53,53,53	0
57	MG	BA	3395	1/1	0.96	0.05	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3217	1/1	0.96	0.07	37,37,37,37	0
57	MG	BA	3036	1/1	0.96	0.09	40,40,40,40	0
57	MG	BA	3222	1/1	0.96	0.10	37,37,37,37	0
57	MG	DA	3434	1/1	0.96	0.07	39,39,39,39	0
57	MG	AA	3126	1/1	0.96	0.07	49,49,49,49	0
57	MG	CA	3005	1/1	0.96	0.05	62,62,62,62	0
57	MG	BA	3510	1/1	0.96	0.07	46,46,46,46	0
57	MG	DA	3438	1/1	0.96	0.13	47,47,47,47	0
57	MG	AA	3090	1/1	0.96	0.24	66,66,66,66	0
57	MG	BA	3402	1/1	0.96	0.07	40,40,40,40	0
57	MG	DF	3003	1/1	0.96	0.15	43,43,43,43	0
57	MG	DA	3441	1/1	0.96	0.10	45,45,45,45	0
57	MG	CA	3169	1/1	0.96	0.07	51,51,51,51	0
57	MG	DA	3445	1/1	0.96	0.06	32,32,32,32	0
57	MG	DA	3446	1/1	0.96	0.07	45,45,45,45	0
57	MG	BA	3226	1/1	0.96	0.11	47,47,47,47	0
57	MG	BA	3155	1/1	0.96	0.22	44,44,44,44	0
57	MG	BA	3094	1/1	0.96	0.08	36,36,36,36	0
57	MG	BA	3312	1/1	0.96	0.12	32,32,32,32	0
57	MG	DV	3001	1/1	0.96	0.09	70,70,70,70	0
57	MG	DV	3002	1/1	0.96	0.12	49,49,49,49	0
57	MG	BA	3043	1/1	0.96	0.07	48,48,48,48	0
57	MG	BA	3756	1/1	0.96	0.08	48,48,48,48	0
57	MG	BA	3637	1/1	0.96	0.07	39,39,39,39	0
57	MG	DA	3455	1/1	0.96	0.07	47,47,47,47	0
57	MG	DX	101	1/1	0.96	0.09	51,51,51,51	0
57	MG	DA	3456	1/1	0.96	0.07	50,50,50,50	0
57	MG	BA	3758	1/1	0.96	0.07	45,45,45,45	0
57	MG	DA	3458	1/1	0.96	0.06	52,52,52,52	0
57	MG	DA	3461	1/1	0.96	0.14	62,62,62,62	0
57	MG	AA	3128	1/1	0.96	0.07	57,57,57,57	0
60	K	AX	3001	1/1	0.96	0.08	65,65,65,65	0
57	MG	BA	3519	1/1	0.96	0.06	55,55,55,55	0
57	MG	CA	3096	1/1	0.97	0.06	44,44,44,44	0
57	MG	BA	3390	1/1	0.97	0.11	38,38,38,38	0
57	MG	BA	3123	1/1	0.97	0.14	32,32,32,32	0
57	MG	CA	3099	1/1	0.97	0.09	44,44,44,44	0
57	MG	BA	3230	1/1	0.97	0.13	53,53,53,53	0
57	MG	DA	3512	1/1	0.97	0.05	47,47,47,47	0
57	MG	BA	3617	1/1	0.97	0.13	51,51,51,51	0
57	MG	CA	3103	1/1	0.97	0.12	46,46,46,46	0
57	MG	BA	3056	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
57	MG	BO	201	1/1	0.97	0.11	50,50,50,50	0
57	MG	AA	3158	1/1	0.97	0.06	45,45,45,45	0
57	MG	DA	3104	1/1	0.97	0.08	53,53,53,53	0
57	MG	DA	3105	1/1	0.97	0.10	48,48,48,48	0
57	MG	BA	3004	1/1	0.97	0.06	33,33,33,33	0
57	MG	DA	3304	1/1	0.97	0.08	48,48,48,48	0
57	MG	BP	204	1/1	0.97	0.07	46,46,46,46	0
57	MG	BP	205	1/1	0.97	0.10	65,65,65,65	0
57	MG	DA	3525	1/1	0.97	0.09	59,59,59,59	0
57	MG	BQ	3001	1/1	0.97	0.15	45,45,45,45	0
57	MG	BQ	3002	1/1	0.97	0.12	43,43,43,43	0
57	MG	BQ	3003	1/1	0.97	0.06	49,49,49,49	0
57	MG	BA	3309	1/1	0.97	0.11	41,41,41,41	0
57	MG	AA	3116	1/1	0.97	0.07	55,55,55,55	0
57	MG	AA	3186	1/1	0.97	0.06	42,42,42,42	0
57	MG	DA	3115	1/1	0.97	0.08	40,40,40,40	0
57	MG	BA	3176	1/1	0.97	0.07	45,45,45,45	0
57	MG	BA	3625	1/1	0.97	0.10	39,39,39,39	0
57	MG	DA	3535	1/1	0.97	0.06	56,56,56,56	0
57	MG	BU	203	1/1	0.97	0.09	47,47,47,47	0
57	MG	DA	3537	1/1	0.97	0.07	44,44,44,44	0
57	MG	AA	3125	1/1	0.97	0.11	37,37,37,37	0
57	MG	DA	3319	1/1	0.97	0.07	41,41,41,41	0
57	MG	AA	3014	1/1	0.97	0.07	32,32,32,32	0
57	MG	DA	3121	1/1	0.97	0.04	44,44,44,44	0
57	MG	DA	3542	1/1	0.97	0.06	24,24,24,24	0
57	MG	BA	3241	1/1	0.97	0.13	36,36,36,36	0
57	MG	AA	3162	1/1	0.97	0.06	66,66,66,66	0
57	MG	DA	3324	1/1	0.97	0.07	33,33,33,33	0
57	MG	DA	3325	1/1	0.97	0.06	35,35,35,35	0
57	MG	BV	203	1/1	0.97	0.14	38,38,38,38	0
57	MG	BA	3097	1/1	0.97	0.09	44,44,44,44	0
57	MG	BV	205	1/1	0.97	0.10	38,38,38,38	0
57	MG	BW	201	1/1	0.97	0.15	44,44,44,44	0
57	MG	BA	3181	1/1	0.97	0.15	43,43,43,43	0
57	MG	BW	204	1/1	0.97	0.09	42,42,42,42	0
57	MG	BA	3632	1/1	0.97	0.05	50,50,50,50	0
57	MG	BA	3407	1/1	0.97	0.07	47,47,47,47	0
57	MG	CA	3131	1/1	0.97	0.07	55,55,55,55	0
57	MG	BX	3003	1/1	0.97	0.07	35,35,35,35	0
57	MG	DA	3336	1/1	0.97	0.08	40,40,40,40	0
57	MG	BY	502	1/1	0.97	0.11	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3246	1/1	0.97	0.21	39,39,39,39	0
57	MG	B0	101	1/1	0.97	0.10	36,36,36,36	0
57	MG	AA	3110	1/1	0.97	0.07	48,48,48,48	0
57	MG	BA	3410	1/1	0.97	0.07	27,27,27,27	0
57	MG	BA	3038	1/1	0.97	0.09	35,35,35,35	0
57	MG	BA	3136	1/1	0.97	0.05	30,30,30,30	0
57	MG	DA	3344	1/1	0.97	0.07	31,31,31,31	0
57	MG	B3	3002	1/1	0.97	0.10	66,66,66,66	0
57	MG	DA	3568	1/1	0.97	0.09	52,52,52,52	0
57	MG	CA	3141	1/1	0.97	0.09	92,92,92,92	0
57	MG	BA	3323	1/1	0.97	0.11	30,30,30,30	0
57	MG	AA	3164	1/1	0.97	0.08	61,61,61,61	0
57	MG	BA	3187	1/1	0.97	0.14	29,29,29,29	0
57	MG	BA	3253	1/1	0.97	0.07	55,55,55,55	0
57	MG	BA	3254	1/1	0.97	0.13	25,25,25,25	0
57	MG	BA	3420	1/1	0.97	0.08	40,40,40,40	0
57	MG	BA	3255	1/1	0.97	0.08	47,47,47,47	0
57	MG	BA	3422	1/1	0.97	0.10	33,33,33,33	0
57	MG	BA	3189	1/1	0.97	0.07	39,39,39,39	0
57	MG	DA	3581	1/1	0.97	0.08	57,57,57,57	0
57	MG	B8	101	1/1	0.97	0.06	44,44,44,44	0
57	MG	BA	3534	1/1	0.97	0.09	44,44,44,44	0
57	MG	AA	3165	1/1	0.97	0.08	54,54,54,54	0
57	MG	CA	3002	1/1	0.97	0.08	63,63,63,63	0
57	MG	DA	3161	1/1	0.97	0.06	38,38,38,38	0
57	MG	BA	3140	1/1	0.97	0.05	47,47,47,47	0
57	MG	DA	3365	1/1	0.97	0.05	36,36,36,36	0
57	MG	BA	3333	1/1	0.97	0.12	38,38,38,38	0
57	MG	BA	3334	1/1	0.97	0.07	37,37,37,37	0
57	MG	BA	3653	1/1	0.97	0.12	39,39,39,39	0
57	MG	DA	3369	1/1	0.97	0.05	28,28,28,28	0
57	MG	DA	3166	1/1	0.97	0.16	55,55,55,55	0
57	MG	DA	3167	1/1	0.97	0.11	41,41,41,41	0
57	MG	DA	3168	1/1	0.97	0.10	45,45,45,45	0
57	MG	BA	3539	1/1	0.97	0.13	52,52,52,52	0
57	MG	BA	3655	1/1	0.97	0.14	50,50,50,50	0
57	MG	BA	3192	1/1	0.97	0.15	46,46,46,46	0
57	MG	BA	3141	1/1	0.97	0.20	42,42,42,42	0
57	MG	BA	3777	1/1	0.97	0.13	40,40,40,40	0
57	MG	BA	3194	1/1	0.97	0.08	47,47,47,47	0
57	MG	BA	3340	1/1	0.97	0.07	39,39,39,39	0
57	MG	DA	3177	1/1	0.97	0.16	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3661	1/1	0.97	0.11	44,44,44,44	0
57	MG	BA	3433	1/1	0.97	0.11	32,32,32,32	0
57	MG	BA	3547	1/1	0.97	0.17	39,39,39,39	0
57	MG	BA	3341	1/1	0.97	0.08	51,51,51,51	0
57	MG	DA	3182	1/1	0.97	0.23	51,51,51,51	0
57	MG	BA	3435	1/1	0.97	0.15	45,45,45,45	0
57	MG	DA	3393	1/1	0.97	0.07	50,50,50,50	0
57	MG	BA	3436	1/1	0.97	0.06	40,40,40,40	0
57	MG	BA	3104	1/1	0.97	0.11	42,42,42,42	0
57	MG	DA	3617	1/1	0.97	0.06	56,56,56,56	0
57	MG	DA	3187	1/1	0.97	0.11	42,42,42,42	0
57	MG	BA	3105	1/1	0.97	0.07	37,37,37,37	0
57	MG	BA	3265	1/1	0.97	0.10	54,54,54,54	0
57	MG	DA	3190	1/1	0.97	0.27	54,54,54,54	0
57	MG	CA	3023	1/1	0.97	0.07	44,44,44,44	0
57	MG	BA	3144	1/1	0.97	0.08	41,41,41,41	0
57	MG	AA	3082	1/1	0.97	0.10	46,46,46,46	0
57	MG	BA	3044	1/1	0.97	0.12	20,20,20,20	0
57	MG	BA	3558	1/1	0.97	0.05	32,32,32,32	0
57	MG	CA	3028	1/1	0.97	0.05	41,41,41,41	0
57	MG	DA	3199	1/1	0.97	0.07	47,47,47,47	0
57	MG	DA	3629	1/1	0.97	0.09	62,62,62,62	0
57	MG	BA	3148	1/1	0.97	0.18	44,44,44,44	0
57	MG	BA	3561	1/1	0.97	0.05	45,45,45,45	0
57	MG	BA	3046	1/1	0.97	0.17	41,41,41,41	0
57	MG	BA	3677	1/1	0.97	0.11	60,60,60,60	0
57	MG	BA	3678	1/1	0.97	0.05	65,65,65,65	0
57	MG	BA	3563	1/1	0.97	0.09	36,36,36,36	0
57	MG	BA	3150	1/1	0.97	0.07	55,55,55,55	0
57	MG	BA	3020	1/1	0.97	0.26	53,53,53,53	0
57	MG	DA	3011	1/1	0.97	0.05	48,48,48,48	0
57	MG	DA	3639	1/1	0.97	0.22	59,59,59,59	0
57	MG	DA	3012	1/1	0.97	0.07	33,33,33,33	0
57	MG	BA	3110	1/1	0.97	0.10	41,41,41,41	0
57	MG	DA	3419	1/1	0.97	0.07	32,32,32,32	0
57	MG	DA	3014	1/1	0.97	0.07	46,46,46,46	0
57	MG	BA	3452	1/1	0.97	0.11	55,55,55,55	0
57	MG	BA	3111	1/1	0.97	0.15	54,54,54,54	0
57	MG	CA	3040	1/1	0.97	0.05	51,51,51,51	0
57	MG	BA	3571	1/1	0.97	0.08	58,58,58,58	0
57	MG	DA	3020	1/1	0.97	0.13	55,55,55,55	0
57	MG	BA	3810	1/1	0.97	0.09	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	CA	3043	1/1	0.97	0.08	47,47,47,47	0
57	MG	BA	3454	1/1	0.97	0.09	27,27,27,27	0
57	MG	BA	3112	1/1	0.97	0.13	30,30,30,30	0
57	MG	BB	201	1/1	0.97	0.14	55,55,55,55	0
57	MG	BA	3689	1/1	0.97	0.07	42,42,42,42	0
57	MG	BB	203	1/1	0.97	0.13	43,43,43,43	0
57	MG	BA	3277	1/1	0.97	0.35	47,47,47,47	0
57	MG	BA	3575	1/1	0.97	0.10	48,48,48,48	0
57	MG	BA	3356	1/1	0.97	0.06	37,37,37,37	0
57	MG	BA	3210	1/1	0.97	0.14	49,49,49,49	0
57	MG	BB	208	1/1	0.97	0.09	45,45,45,45	0
57	MG	BA	3048	1/1	0.97	0.10	47,47,47,47	0
57	MG	BA	3360	1/1	0.97	0.06	41,41,41,41	0
57	MG	CA	3056	1/1	0.97	0.15	64,64,64,64	0
57	MG	BB	211	1/1	0.97	0.04	51,51,51,51	0
57	MG	DA	3665	1/1	0.97	0.10	42,42,42,42	0
57	MG	DA	3235	1/1	0.97	0.12	45,45,45,45	0
57	MG	DA	3444	1/1	0.97	0.05	44,44,44,44	0
57	MG	DA	3039	1/1	0.97	0.05	43,43,43,43	0
57	MG	DA	3041	1/1	0.97	0.05	38,38,38,38	0
57	MG	DA	3670	1/1	0.97	0.16	60,60,60,60	0
57	MG	BB	212	1/1	0.97	0.08	55,55,55,55	0
57	MG	BA	3281	1/1	0.97	0.29	60,60,60,60	0
57	MG	DA	3045	1/1	0.97	0.09	51,51,51,51	0
57	MG	BA	3698	1/1	0.97	0.12	31,31,31,31	0
57	MG	BA	3157	1/1	0.97	0.11	45,45,45,45	0
57	MG	BA	3283	1/1	0.97	0.09	35,35,35,35	0
57	MG	BB	217	1/1	0.97	0.05	29,29,29,29	0
57	MG	AA	3194	1/1	0.97	0.10	56,56,56,56	0
57	MG	CA	3065	1/1	0.97	0.25	49,49,49,49	0
57	MG	DA	3053	1/1	0.97	0.06	47,47,47,47	0
57	MG	AA	3168	1/1	0.97	0.06	59,59,59,59	0
57	MG	DA	3055	1/1	0.97	0.13	49,49,49,49	0
57	MG	DB	3006	1/1	0.97	0.11	57,57,57,57	0
57	MG	BA	3367	1/1	0.97	0.13	29,29,29,29	0
57	MG	DA	3057	1/1	0.97	0.07	42,42,42,42	0
57	MG	DA	3058	1/1	0.97	0.09	29,29,29,29	0
57	MG	BD	301	1/1	0.97	0.07	40,40,40,40	0
57	MG	BA	3706	1/1	0.97	0.05	53,53,53,53	0
57	MG	BA	3286	1/1	0.97	0.08	34,34,34,34	0
57	MG	BA	3287	1/1	0.97	0.06	42,42,42,42	0
57	MG	DA	3258	1/1	0.97	0.09	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3216	1/1	0.97	0.14	37,37,37,37	0
57	MG	BD	306	1/1	0.97	0.09	38,38,38,38	0
57	MG	BD	308	1/1	0.97	0.11	46,46,46,46	0
57	MG	BA	3079	1/1	0.97	0.09	39,39,39,39	0
57	MG	DA	3475	1/1	0.97	0.10	51,51,51,51	0
57	MG	DE	301	1/1	0.97	0.15	46,46,46,46	0
57	MG	DE	302	1/1	0.97	0.12	33,33,33,33	0
57	MG	AA	3148	1/1	0.97	0.14	57,57,57,57	0
57	MG	DA	3264	1/1	0.97	0.07	40,40,40,40	0
57	MG	BE	302	1/1	0.97	0.11	39,39,39,39	0
57	MG	BA	3219	1/1	0.97	0.12	36,36,36,36	0
57	MG	BA	3220	1/1	0.97	0.09	29,29,29,29	0
57	MG	DG	3001	1/1	0.97	0.04	55,55,55,55	0
57	MG	AA	3129	1/1	0.97	0.06	47,47,47,47	0
57	MG	DO	5001	1/1	0.97	0.11	59,59,59,59	0
57	MG	BA	3378	1/1	0.97	0.04	28,28,28,28	0
57	MG	DP	202	1/1	0.97	0.06	53,53,53,53	0
57	MG	BA	3295	1/1	0.97	0.06	38,38,38,38	0
57	MG	DA	3074	1/1	0.97	0.08	37,37,37,37	0
57	MG	BA	3223	1/1	0.97	0.06	41,41,41,41	0
57	MG	BA	3481	1/1	0.97	0.08	41,41,41,41	0
57	MG	BA	3297	1/1	0.97	0.08	43,43,43,43	0
57	MG	BA	3082	1/1	0.97	0.07	39,39,39,39	0
57	MG	DA	3491	1/1	0.97	0.06	51,51,51,51	0
57	MG	BA	3299	1/1	0.97	0.04	25,25,25,25	0
57	MG	BA	3054	1/1	0.97	0.14	36,36,36,36	0
57	MG	CA	3089	1/1	0.97	0.11	47,47,47,47	0
57	MG	BA	3167	1/1	0.97	0.07	41,41,41,41	0
57	MG	BA	3084	1/1	0.97	0.17	38,38,38,38	0
57	MG	DA	3084	1/1	0.97	0.09	39,39,39,39	0
57	MG	BA	3490	1/1	0.97	0.06	54,54,54,54	0
57	MG	DA	3286	1/1	0.97	0.06	42,42,42,42	0
57	MG	DA	3500	1/1	0.97	0.08	49,49,49,49	0
57	MG	DA	3086	1/1	0.97	0.04	43,43,43,43	0
59	ZN	CN	501	1/1	0.97	0.07	93,93,93,93	0
59	ZN	DY	501	1/1	0.97	0.06	96,96,96,96	0
57	MG	BA	3612	1/1	0.97	0.05	21,21,21,21	0
57	MG	CA	3094	1/1	0.97	0.19	70,70,70,70	0
57	MG	AA	3212	1/1	0.97	0.09	42,42,42,42	0
57	MG	BA	3569	1/1	0.98	0.07	49,49,49,49	0
57	MG	BA	3025	1/1	0.98	0.05	27,27,27,27	0
57	MG	BA	3137	1/1	0.98	0.18	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3442	1/1	0.98	0.05	39,39,39,39	0
57	MG	DA	3589	1/1	0.98	0.06	68,68,68,68	0
57	MG	BA	3049	1/1	0.98	0.12	36,36,36,36	0
57	MG	BA	3744	1/1	0.98	0.10	39,39,39,39	0
57	MG	BD	307	1/1	0.98	0.11	40,40,40,40	0
57	MG	BA	3489	1/1	0.98	0.04	59,59,59,59	0
57	MG	BA	3259	1/1	0.98	0.10	25,25,25,25	0
57	MG	DA	3183	1/1	0.98	0.10	38,38,38,38	0
57	MG	DA	3449	1/1	0.98	0.10	54,54,54,54	0
57	MG	BA	3491	1/1	0.98	0.06	45,45,45,45	0
57	MG	DA	3599	1/1	0.98	0.04	36,36,36,36	0
57	MG	BA	3214	1/1	0.98	0.08	41,41,41,41	0
57	MG	BA	3660	1/1	0.98	0.06	61,61,61,61	0
57	MG	BA	3577	1/1	0.98	0.13	51,51,51,51	0
57	MG	AA	3151	1/1	0.98	0.06	45,45,45,45	0
57	MG	BE	306	1/1	0.98	0.10	26,26,26,26	0
57	MG	BA	3752	1/1	0.98	0.07	32,32,32,32	0
57	MG	DA	3191	1/1	0.98	0.08	37,37,37,37	0
57	MG	BA	3009	1/1	0.98	0.06	28,28,28,28	0
57	MG	DA	3460	1/1	0.98	0.09	41,41,41,41	0
57	MG	BA	3425	1/1	0.98	0.04	40,40,40,40	0
57	MG	BA	3028	1/1	0.98	0.10	51,51,51,51	0
57	MG	DA	3195	1/1	0.98	0.05	43,43,43,43	0
57	MG	BA	3010	1/1	0.98	0.09	39,39,39,39	0
57	MG	BA	3011	1/1	0.98	0.05	35,35,35,35	0
57	MG	AA	3050	1/1	0.98	0.07	33,33,33,33	0
57	MG	BF	307	1/1	0.98	0.15	37,37,37,37	0
57	MG	BA	3221	1/1	0.98	0.05	37,37,37,37	0
57	MG	BA	3586	1/1	0.98	0.04	53,53,53,53	0
57	MG	BA	3032	1/1	0.98	0.06	47,47,47,47	0
57	MG	DA	3471	1/1	0.98	0.13	50,50,50,50	0
57	MG	BA	3146	1/1	0.98	0.07	40,40,40,40	0
57	MG	DA	3204	1/1	0.98	0.15	46,46,46,46	0
57	MG	BA	3373	1/1	0.98	0.10	48,48,48,48	0
57	MG	BA	3270	1/1	0.98	0.05	48,48,48,48	0
57	MG	BA	3013	1/1	0.98	0.07	32,32,32,32	0
57	MG	BA	3085	1/1	0.98	0.13	35,35,35,35	0
57	MG	BA	3377	1/1	0.98	0.06	44,44,44,44	0
57	MG	DA	3480	1/1	0.98	0.07	40,40,40,40	0
57	MG	BA	3184	1/1	0.98	0.22	43,43,43,43	0
57	MG	BA	3379	1/1	0.98	0.05	31,31,31,31	0
57	MG	BA	3440	1/1	0.98	0.05	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	CA	3155	1/1	0.98	0.12	53,53,53,53	0
57	MG	BA	3441	1/1	0.98	0.05	35,35,35,35	0
57	MG	BA	3086	1/1	0.98	0.07	22,22,22,22	0
57	MG	BP	202	1/1	0.98	0.18	36,36,36,36	0
57	MG	BP	203	1/1	0.98	0.07	33,33,33,33	0
57	MG	BA	3014	1/1	0.98	0.23	42,42,42,42	0
57	MG	DA	3347	1/1	0.98	0.09	27,27,27,27	0
57	MG	BA	3059	1/1	0.98	0.12	26,26,26,26	0
57	MG	DA	3349	1/1	0.98	0.06	52,52,52,52	0
57	MG	DA	3094	1/1	0.98	0.09	50,50,50,50	0
57	MG	BA	3188	1/1	0.98	0.16	49,49,49,49	0
57	MG	BA	3521	1/1	0.98	0.07	39,39,39,39	0
57	MG	DA	3097	1/1	0.98	0.04	33,33,33,33	0
57	MG	BA	3605	1/1	0.98	0.05	43,43,43,43	0
57	MG	DA	3099	1/1	0.98	0.13	32,32,32,32	0
57	MG	BA	3522	1/1	0.98	0.06	52,52,52,52	0
57	MG	DA	3357	1/1	0.98	0.05	50,50,50,50	0
57	MG	DA	3227	1/1	0.98	0.12	41,41,41,41	0
57	MG	BA	3384	1/1	0.98	0.06	41,41,41,41	0
57	MG	BA	3525	1/1	0.98	0.08	34,34,34,34	0
57	MG	DA	3504	1/1	0.98	0.04	47,47,47,47	0
57	MG	BR	202	1/1	0.98	0.07	31,31,31,31	0
57	MG	DA	3506	1/1	0.98	0.05	42,42,42,42	0
57	MG	BA	3692	1/1	0.98	0.05	40,40,40,40	0
57	MG	BA	3447	1/1	0.98	0.07	72,72,72,72	0
57	MG	BA	3611	1/1	0.98	0.09	46,46,46,46	0
57	MG	BA	3784	1/1	0.98	0.09	33,33,33,33	0
57	MG	CF	3001	1/1	0.98	0.05	46,46,46,46	0
57	MG	BU	205	1/1	0.98	0.18	47,47,47,47	0
57	MG	BU	206	1/1	0.98	0.14	35,35,35,35	0
57	MG	BA	3152	1/1	0.98	0.07	43,43,43,43	0
57	MG	BU	208	1/1	0.98	0.18	40,40,40,40	0
57	MG	BA	3449	1/1	0.98	0.08	35,35,35,35	0
57	MG	AA	3114	1/1	0.98	0.12	59,59,59,59	0
57	MG	BA	3280	1/1	0.98	0.04	37,37,37,37	0
57	MG	BA	3699	1/1	0.98	0.07	35,35,35,35	0
57	MG	AA	3042	1/1	0.98	0.11	57,57,57,57	0
57	MG	DA	3377	1/1	0.98	0.06	38,38,38,38	0
57	MG	BA	3791	1/1	0.98	0.07	28,28,28,28	0
57	MG	DA	3003	1/1	0.98	0.09	27,27,27,27	0
57	MG	BA	3234	1/1	0.98	0.03	38,38,38,38	0
57	MG	DA	3381	1/1	0.98	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BW	203	1/1	0.98	0.05	44,44,44,44	0
57	MG	BA	3235	1/1	0.98	0.05	42,42,42,42	0
57	MG	AW	3002	1/1	0.98	0.11	53,53,53,53	0
57	MG	AA	3144	1/1	0.98	0.07	46,46,46,46	0
57	MG	BA	3705	1/1	0.98	0.08	62,62,62,62	0
57	MG	DA	3253	1/1	0.98	0.05	45,45,45,45	0
57	MG	DA	3390	1/1	0.98	0.08	43,43,43,43	0
57	MG	DA	3127	1/1	0.98	0.12	35,35,35,35	0
57	MG	BA	3124	1/1	0.98	0.07	19,19,19,19	0
57	MG	BA	3195	1/1	0.98	0.06	46,46,46,46	0
57	MG	BA	3338	1/1	0.98	0.05	40,40,40,40	0
57	MG	BA	3339	1/1	0.98	0.05	23,23,23,23	0
57	MG	BA	3158	1/1	0.98	0.12	41,41,41,41	0
57	MG	BA	3542	1/1	0.98	0.07	45,45,45,45	0
57	MG	BA	3197	1/1	0.98	0.09	41,41,41,41	0
57	MG	B3	3001	1/1	0.98	0.08	34,34,34,34	0
57	MG	BA	3544	1/1	0.98	0.09	44,44,44,44	0
57	MG	BA	3807	1/1	0.98	0.08	47,47,47,47	0
57	MG	DD	302	1/1	0.98	0.04	42,42,42,42	0
57	MG	BA	3040	1/1	0.98	0.24	35,35,35,35	0
57	MG	BA	3400	1/1	0.98	0.05	33,33,33,33	0
57	MG	DD	305	1/1	0.98	0.04	36,36,36,36	0
57	MG	DA	3023	1/1	0.98	0.29	40,40,40,40	0
57	MG	BA	3291	1/1	0.98	0.17	33,33,33,33	0
57	MG	DD	308	1/1	0.98	0.19	48,48,48,48	0
57	MG	DA	3270	1/1	0.98	0.08	46,46,46,46	0
57	MG	DA	3407	1/1	0.98	0.03	66,66,66,66	0
57	MG	BA	3467	1/1	0.98	0.08	50,50,50,50	0
57	MG	AA	3106	1/1	0.98	0.14	57,57,57,57	0
57	MG	BA	3719	1/1	0.98	0.09	53,53,53,53	0
57	MG	CA	3100	1/1	0.98	0.06	52,52,52,52	0
57	MG	BA	3067	1/1	0.98	0.09	41,41,41,41	0
57	MG	BA	3245	1/1	0.98	0.16	34,34,34,34	0
57	MG	DF	3004	1/1	0.98	0.19	44,44,44,44	0
57	MG	BA	3096	1/1	0.98	0.23	54,54,54,54	0
57	MG	BA	3553	1/1	0.98	0.04	59,59,59,59	0
57	MG	BA	3247	1/1	0.98	0.16	25,25,25,25	0
57	MG	DA	3560	1/1	0.98	0.05	40,40,40,40	0
57	MG	DA	3034	1/1	0.98	0.08	38,38,38,38	0
57	MG	DQ	3001	1/1	0.98	0.04	47,47,47,47	0
57	MG	DA	3154	1/1	0.98	0.26	48,48,48,48	0
57	MG	BA	3042	1/1	0.98	0.10	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	BA	3726	1/1	0.98	0.14	63,63,63,63	0
57	MG	BA	3474	1/1	0.98	0.09	55,55,55,55	0
57	MG	DA	3285	1/1	0.98	0.06	32,32,32,32	0
57	MG	BA	3069	1/1	0.98	0.11	22,22,22,22	0
57	MG	AE	203	1/1	0.98	0.13	63,63,63,63	0
57	MG	DA	3040	1/1	0.98	0.05	31,31,31,31	0
57	MG	BA	3559	1/1	0.98	0.05	47,47,47,47	0
57	MG	DA	3042	1/1	0.98	0.08	38,38,38,38	0
57	MG	DW	3002	1/1	0.98	0.07	45,45,45,45	0
57	MG	DA	3572	1/1	0.98	0.05	62,62,62,62	0
57	MG	BA	3166	1/1	0.98	0.04	38,38,38,38	0
57	MG	AX	3013	1/1	0.98	0.06	58,58,58,58	0
57	MG	BA	3045	1/1	0.98	0.15	36,36,36,36	0
57	MG	AA	3182	1/1	0.98	0.09	49,49,49,49	0
57	MG	BA	3414	1/1	0.98	0.09	41,41,41,41	0
57	MG	AK	3001	1/1	0.98	0.13	44,44,44,44	0
58	SF4	AD	501	8/8	0.98	0.06	62,68,73,86	0
58	SF4	CD	302	8/8	0.98	0.06	60,68,83,86	0
59	ZN	B4	501	1/1	0.98	0.04	89,89,89,89	0
57	MG	BA	3737	1/1	0.98	0.16	43,43,43,43	0
57	MG	DA	3050	1/1	0.98	0.17	59,59,59,59	0
57	MG	BA	3416	1/1	0.98	0.07	21,21,21,21	0
59	ZN	D9	501	1/1	0.98	0.05	68,68,68,68	0
57	MG	BA	3357	1/1	0.98	0.09	25,25,25,25	0
57	MG	DA	3174	1/1	0.98	0.10	44,44,44,44	0
57	MG	BA	3037	1/1	0.99	0.14	34,34,34,34	0
57	MG	DA	3386	1/1	0.99	0.04	35,35,35,35	0
57	MG	DA	3459	1/1	0.99	0.05	47,47,47,47	0
57	MG	DA	3387	1/1	0.99	0.04	42,42,42,42	0
57	MG	DA	3102	1/1	0.99	0.09	40,40,40,40	0
57	MG	BA	3565	1/1	0.99	0.08	40,40,40,40	0
57	MG	BA	3495	1/1	0.99	0.06	37,37,37,37	0
57	MG	DA	3580	1/1	0.99	0.07	36,36,36,36	0
57	MG	BA	3496	1/1	0.99	0.08	41,41,41,41	0
57	MG	BA	3498	1/1	0.99	0.06	36,36,36,36	0
57	MG	BA	3609	1/1	0.99	0.04	39,39,39,39	0
57	MG	BA	3588	1/1	0.99	0.10	31,31,31,31	0
57	MG	BA	3483	1/1	0.99	0.06	28,28,28,28	0
57	MG	BA	3533	1/1	0.99	0.04	59,59,59,59	0
57	MG	AA	3167	1/1	0.99	0.05	57,57,57,57	0
57	MG	BA	3795	1/1	0.99	0.09	35,35,35,35	0
57	MG	BA	3198	1/1	0.99	0.19	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	DA	3266	1/1	0.99	0.04	57,57,57,57	0
57	MG	AA	3074	1/1	0.99	0.08	50,50,50,50	0
57	MG	DA	3143	1/1	0.99	0.10	38,38,38,38	0
57	MG	DA	3144	1/1	0.99	0.05	38,38,38,38	0
57	MG	DA	3477	1/1	0.99	0.03	43,43,43,43	0
57	MG	BA	3363	1/1	0.99	0.04	22,22,22,22	0
57	MG	DA	3517	1/1	0.99	0.04	51,51,51,51	0
57	MG	DA	3597	1/1	0.99	0.03	51,51,51,51	0
57	MG	BA	3103	1/1	0.99	0.07	38,38,38,38	0
57	MG	BA	3060	1/1	0.99	0.09	30,30,30,30	0
57	MG	BA	3597	1/1	0.99	0.13	25,25,25,25	0
57	MG	BA	3015	1/1	0.99	0.05	32,32,32,32	0
57	MG	DA	3373	1/1	0.99	0.07	44,44,44,44	0
57	MG	DA	3603	1/1	0.99	0.05	41,41,41,41	0
57	MG	BA	3507	1/1	0.99	0.08	49,49,49,49	0
57	MG	BF	305	1/1	0.99	0.03	49,49,49,49	0
57	MG	BA	3688	1/1	0.99	0.07	46,46,46,46	0
57	MG	BA	3524	1/1	0.99	0.03	42,42,42,42	0
59	ZN	AN	501	1/1	0.99	0.05	69,69,69,69	0
59	ZN	BY	501	1/1	0.99	0.03	58,58,58,58	0
57	MG	BA	3806	1/1	0.99	0.08	30,30,30,30	0
59	ZN	B5	102	1/1	0.99	0.05	48,48,48,48	0
59	ZN	B6	103	1/1	0.99	0.05	49,49,49,49	0
59	ZN	B9	501	1/1	0.99	0.03	38,38,38,38	0
57	MG	DA	3016	1/1	0.99	0.09	50,50,50,50	0
57	MG	DA	3156	1/1	0.99	0.04	51,51,51,51	0
57	MG	AA	3086	1/1	0.99	0.08	57,57,57,57	0
59	ZN	D5	501	1/1	0.99	0.04	58,58,58,58	0
59	ZN	D6	501	1/1	0.99	0.04	71,71,71,71	0
57	MG	DA	3315	1/1	0.99	0.03	42,42,42,42	0
57	MG	BA	3458	1/1	0.99	0.05	18,18,18,18	0
57	MG	BA	3099	1/1	0.99	0.04	41,41,41,41	0
57	MG	BA	3327	1/1	1.00	0.07	38,38,38,38	0
57	MG	BA	3497	1/1	1.00	0.06	28,28,28,28	0

6.5 Other polymers ⓘ

There are no such residues in this entry.