Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 02:46 PM EDT

PDB ID	:	5HD1 / pdb_00005hd1
Title	:	Crystal structure of antimicrobial peptide Pyrrhocoricin bound to the Thermus thermophilus 70S ribosome
Authors	:	Gagnon, M.G.; Roy, R.N.; Lomakin, I.B.; Florin, T.; Mankin, A.S.; Steitz, T.A.
Deposited on	:	2016-01-04
Resolution	:	2.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

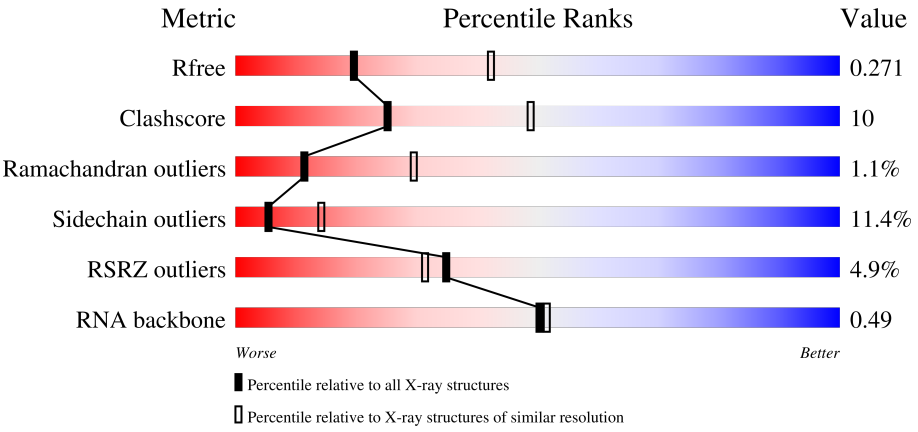
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)
RNA backbone	3983	1044 (2.90-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1A	2915	% 63% 26% 5% 6%
1	2A	2915	% 53% 36% 7% .
2	1B	121	% 74% 25% ..
2	2B	121	3% 38% 51% 10% .

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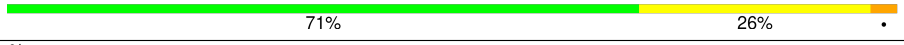
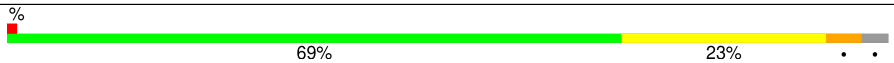
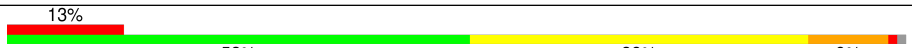
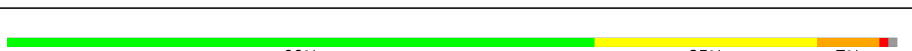
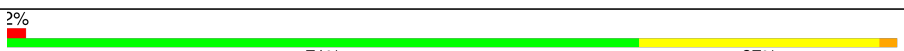
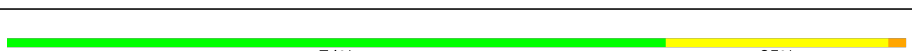
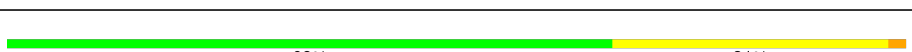
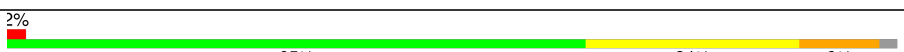
Mol	Chain	Length	Quality of chain
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	
15	1T	146	

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Mol	Chain	Length	Quality of chain
15	2T	146	2% 62% 25% 10%
16	1U	118	2% 81% 15%
16	2U	118	71% 24%
17	1V	101	% 79% 17%
17	2V	101	% 71% 25%
18	1W	113	82% 14%
18	2W	113	% 69% 26%
19	1X	96	3% 72% 25%
19	2X	96	4% 70% 27%
20	1Y	110	% 71% 24%
20	2Y	110	% 65% 28% 5%
21	1Z	206	% 65% 22% 10%
21	2Z	206	3% 58% 26% 5% 10%
22	10	85	% 65% 20% 12%
22	20	85	4% 66% 20% 12%
23	11	98	2% 81% 15%
23	21	98	2% 77% 19%
24	12	72	7% 68% 28%
24	22	72	72% 22%
25	13	60	82% 13%
25	23	60	3% 62% 35%
26	14	71	15% 46% 35% 15%
26	24	71	24% 51% 28% 15%
27	15	60	2% 83% 12%
27	25	60	72% 23%

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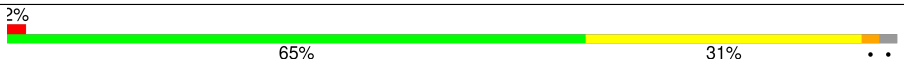
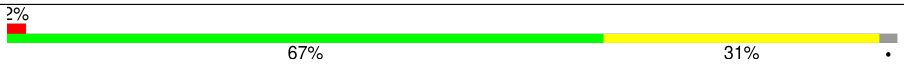
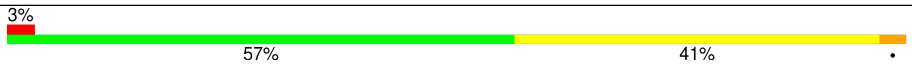
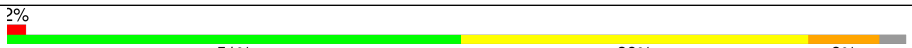
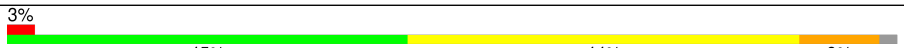
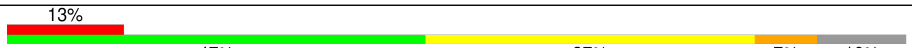
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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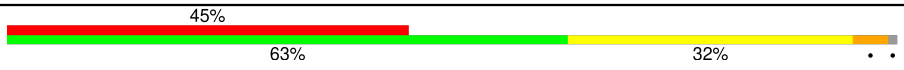
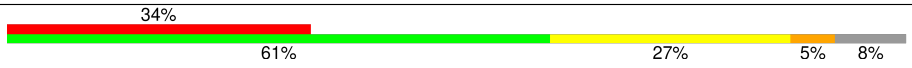
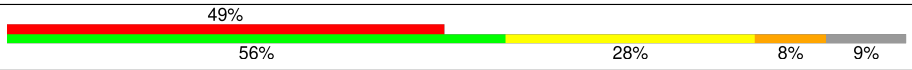
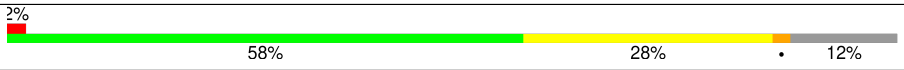
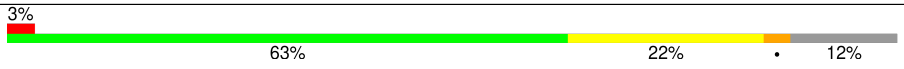
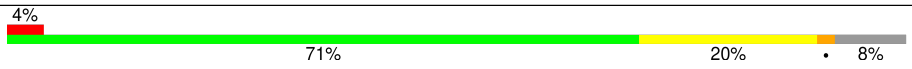
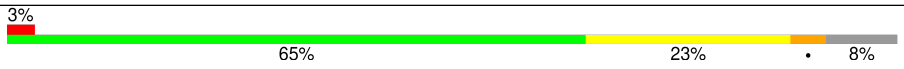
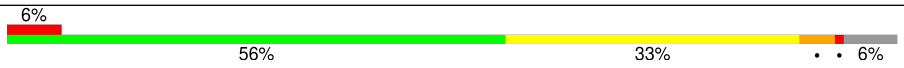
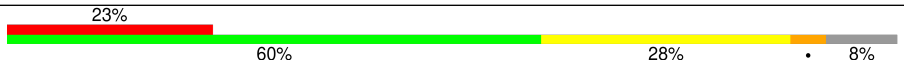
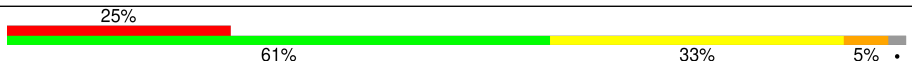
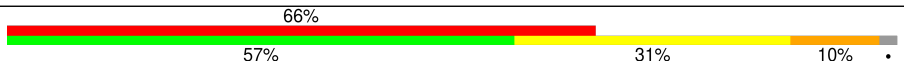
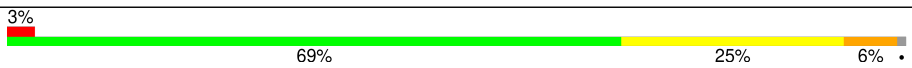
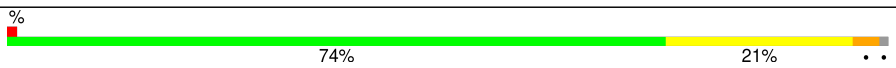
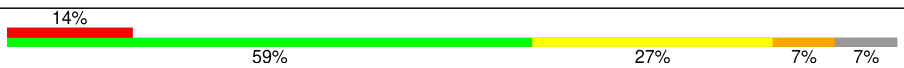
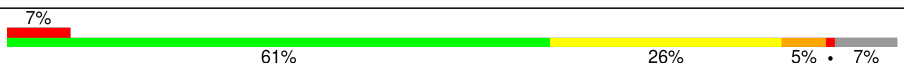
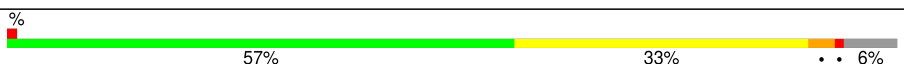
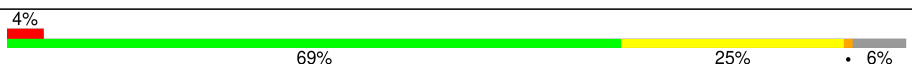
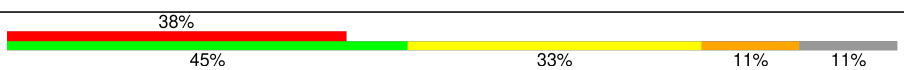
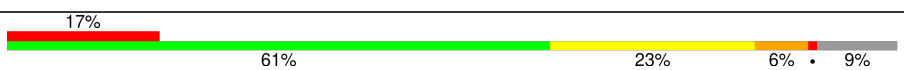
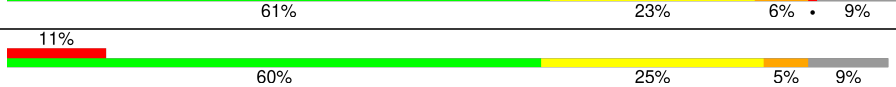
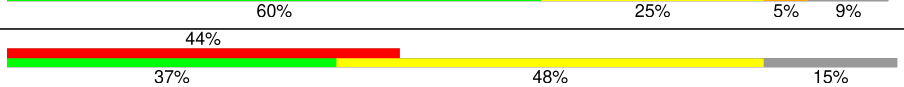
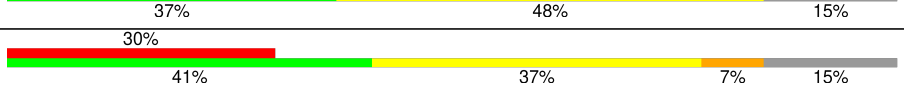
Mol	Chain	Length	Quality of chain
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	
52	2u	27	

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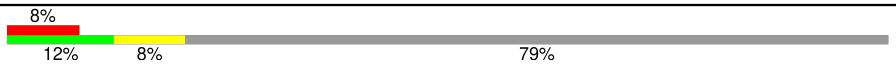
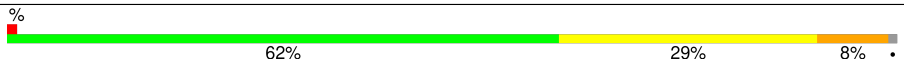
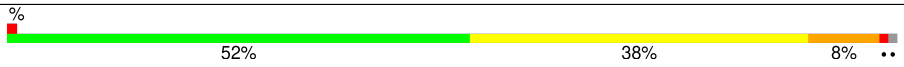
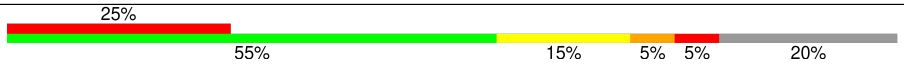
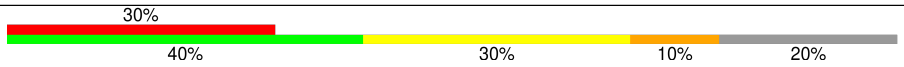
Mol	Chain	Length	Quality of chain
53	1v	24	
53	2v	24	
54	1x	77	
54	2x	77	
55	1z	20	
55	2z	20	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	4203	-	-	-	X
56	MG	2a	1673	-	-	-	X
58	SF4	1d	501	-	-	X	-
58	SF4	2d	501	-	-	X	-

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 288775 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 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2746	Total	C	N	O	P	0	0	0
			59154	26327	11077	19005	2745			
1	2A	2790	Total	C	N	O	P	0	0	0
			60091	26746	11243	19313	2789			

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1146	476	831	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2142	1352	426	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	1E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	2E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	1F	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1425	914	256	251	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	911	258	251	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1085	693	189	202	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1061	680	186	194	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	2O	122	Total 933	C 588	N 171	O 170	S 4	0	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total 1139	C 709	N 231	O 196	S 3	0	0	0
11	2P	149	Total 1135	C 706	N 230	O 196	S 3	0	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	1Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0
12	2Q	141	Total 1122	C 715	N 212	O 188	S 7	0	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	1R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0
13	2R	118	Total 968	C 604	N 203	O 160	S 1	0	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total 877	C 553	N 175	O 149	0	0	0
14	2S	110	Total 870	C 549	N 173	O 148	0	0	0

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	1T	131	Total 1091	C 680	N 225	O 185	S 1	0	0	0
15	2T	131	Total 1083	C 675	N 224	O 183	S 1	0	0	0

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	1U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	2U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	1W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	2W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	186	Total	C	N	O	S	0	0	0
			1470	937	262	269	2			
21	2Z	186	Total	C	N	O	S	0	0	0
			1454	929	256	267	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			
22	20	75	Total	C	N	O	S	0	0	0
			598	370	127	100	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			
23	21	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	13	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	23	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			558	352	102	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	16	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	26	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	17	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	27	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	19	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	29	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1477	Total	C	N	O	P	0	0	0
			31750	14131	5883	10259	1477			
32	2a	1483	Total	C	N	O	P	0	0	0
			31877	14188	5905	10301	1483			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1786	1136	321	325	4			
33	2b	231	Total	C	N	O	S	0	0	0
			1697	1079	292	321	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1480	932	281	266	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1412	883	269	259	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1618	1013	312	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1630	1022	321	280	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1095	695	203	193	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			806	511	143	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			817	516	146	152	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1183	732	232	213	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1167	728	220	213	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1074	681	202	189	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			976	620	189	167			
40	2i	127	Total	C	N	O	0	0	0
			932	589	177	166			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			682	424	130	128			
41	2j	96	Total	C	N	O	0	0	0
			678	424	126	128			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			826	513	156	154	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			829	516	155	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			920	579	181	159	1			
43	2l	122	Total	C	N	O	S	0	0	0
			918	576	182	159	1			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	118	Total	C	N	O	S	0	0	0
			923	569	191	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			903	555	187	159	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			482	306	100	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			459	291	93	71	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	1o	88	Total	C	N	O	S	0	0	0
			715	447	140	126	2			
46	2o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			671	424	133	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	1q	99	Total	C	N	O	S	0	0	0
			811	519	148	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O	0	0	0
			555	355	108	92			
49	2r	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	84	Total	C	N	O	S	0	0	0
			642	409	119	112	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			712	435	152	123	2			
51	2t	96	Total	C	N	O	S	0	0	0
			731	449	156	124	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O	0	0	0
			187	116	42	29			
52	2u	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			
53	2v	5	Total	C	N	O	P	0	0	0
			109	49	22	33	5			

- Molecule 54 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
54	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 55 is a protein called Pyrrhocoricin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
55	1z	16	Total	C	N	O	0	0	0
			126	82	23	21			
55	2z	16	Total	C	N	O	0	0	0
			126	82	23	21			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	1233	Total	Mg	0	0
			1233	1233		
56	1B	25	Total	Mg	0	0
			25	25		
56	1D	15	Total	Mg	0	0
			15	15		
56	1E	8	Total	Mg	0	0
			8	8		
56	1F	9	Total	Mg	0	0
			9	9		
56	1G	3	Total	Mg	0	0
			3	3		
56	1H	1	Total	Mg	0	0
			1	1		
56	1N	7	Total	Mg	0	0
			7	7		
56	1O	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1P	5	Total Mg 5 5	0	0
56	1Q	5	Total Mg 5 5	0	0
56	1R	8	Total Mg 8 8	0	0
56	1T	4	Total Mg 4 4	0	0
56	1U	6	Total Mg 6 6	0	0
56	1V	2	Total Mg 2 2	0	0
56	1W	6	Total Mg 6 6	0	0
56	1X	1	Total Mg 1 1	0	0
56	1Y	1	Total Mg 1 1	0	0
56	1Z	3	Total Mg 3 3	0	0
56	10	7	Total Mg 7 7	0	0
56	11	3	Total Mg 3 3	0	0
56	12	1	Total Mg 1 1	0	0
56	13	1	Total Mg 1 1	0	0
56	15	4	Total Mg 4 4	0	0
56	16	2	Total Mg 2 2	0	0
56	17	3	Total Mg 3 3	0	0
56	18	5	Total Mg 5 5	0	0
56	19	3	Total Mg 3 3	0	0
56	1a	295	Total Mg 295 295	0	0
56	1b	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1d	1	Total Mg 1 1	0	0
56	1e	3	Total Mg 3 3	0	0
56	1f	1	Total Mg 1 1	0	0
56	1h	2	Total Mg 2 2	0	0
56	1k	2	Total Mg 2 2	0	0
56	1l	1	Total Mg 1 1	0	0
56	1n	1	Total Mg 1 1	0	0
56	1o	1	Total Mg 1 1	0	0
56	1p	1	Total Mg 1 1	0	0
56	1q	2	Total Mg 2 2	0	0
56	1r	2	Total Mg 2 2	0	0
56	1t	1	Total Mg 1 1	0	0
56	1x	12	Total Mg 12 12	0	0
56	2A	592	Total Mg 592 592	0	0
56	2B	9	Total Mg 9 9	0	0
56	2D	6	Total Mg 6 6	0	0
56	2E	6	Total Mg 6 6	0	0
56	2F	2	Total Mg 2 2	0	0
56	2G	1	Total Mg 1 1	0	0
56	2N	1	Total Mg 1 1	0	0
56	2O	3	Total Mg 3 3	0	0

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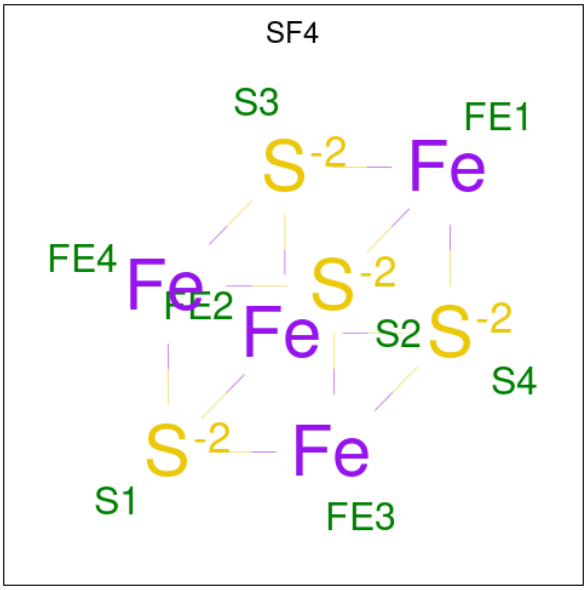
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	2Q	5	Total Mg 5 5	0	0
56	2X	1	Total Mg 1 1	0	0
56	2Y	1	Total Mg 1 1	0	0
56	2Z	1	Total Mg 1 1	0	0
56	20	1	Total Mg 1 1	0	0
56	23	1	Total Mg 1 1	0	0
56	25	1	Total Mg 1 1	0	0
56	28	2	Total Mg 2 2	0	0
56	2a	248	Total Mg 248 248	0	0
56	2d	1	Total Mg 1 1	0	0
56	2e	2	Total Mg 2 2	0	0
56	2f	1	Total Mg 1 1	0	0
56	2l	5	Total Mg 5 5	0	0
56	2n	1	Total Mg 1 1	0	0
56	2p	1	Total Mg 1 1	0	0
56	2q	2	Total Mg 2 2	0	0
56	2t	1	Total Mg 1 1	0	0
56	2u	1	Total Mg 1 1	0	0
56	2x	4	Total Mg 4 4	0	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1Y	1	Total Zn 1 1	0	0
57	14	1	Total Zn 1 1	0	0
57	15	1	Total Zn 1 1	0	0
57	16	1	Total Zn 1 1	0	0
57	19	1	Total Zn 1 1	0	0
57	1n	1	Total Zn 1 1	0	0
57	2Y	1	Total Zn 1 1	0	0
57	24	1	Total Zn 1 1	0	0
57	25	1	Total Zn 1 1	0	0
57	26	1	Total Zn 1 1	0	0
57	29	1	Total Zn 1 1	0	0
57	2n	1	Total Zn 1 1	0	0

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1d	1	Total Fe S 8 4 4	0	0
58	2d	1	Total Fe S 8 4 4	0	0

- Molecule 59 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1A	2217	Total O 2217 2217	0	0
59	1B	37	Total O 37 37	0	0
59	1D	23	Total O 23 23	0	0
59	1E	29	Total O 29 29	0	0
59	1F	19	Total O 19 19	0	0
59	1G	2	Total O 2 2	0	0
59	1H	4	Total O 4 4	0	0
59	1I	1	Total O 1 1	0	0
59	1N	6	Total O 6 6	0	0
59	1O	7	Total O 7 7	0	0
59	1P	27	Total O 27 27	0	0
59	1Q	14	Total O 14 14	0	0
59	1R	11	Total O 11 11	0	0
59	1S	2	Total O 2 2	0	0
59	1T	13	Total O 13 13	0	0
59	1U	14	Total O 14 14	0	0
59	1V	7	Total O 7 7	0	0
59	1W	8	Total O 8 8	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1X	5	Total O 5 5	0	0
59	1Y	1	Total O 1 1	0	0
59	1Z	7	Total O 7 7	0	0
59	10	12	Total O 12 12	0	0
59	11	5	Total O 5 5	0	0
59	12	3	Total O 3 3	0	0
59	13	4	Total O 4 4	0	0
59	15	9	Total O 9 9	0	0
59	16	9	Total O 9 9	0	0
59	17	10	Total O 10 10	0	0
59	18	12	Total O 12 12	0	0
59	19	2	Total O 2 2	0	0
59	1a	338	Total O 338 338	0	0
59	1b	2	Total O 2 2	0	0
59	1d	3	Total O 3 3	0	0
59	1e	7	Total O 7 7	0	0
59	1f	1	Total O 1 1	0	0
59	1h	3	Total O 3 3	0	0
59	1i	1	Total O 1 1	0	0
59	1j	1	Total O 1 1	0	0
59	1k	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	1l	3	Total O 3 3	0	0
59	1m	1	Total O 1 1	0	0
59	1o	1	Total O 1 1	0	0
59	1q	1	Total O 1 1	0	0
59	1r	1	Total O 1 1	0	0
59	1s	2	Total O 2 2	0	0
59	1t	1	Total O 1 1	0	0
59	1v	3	Total O 3 3	0	0
59	1x	9	Total O 9 9	0	0
59	2A	809	Total O 809 809	0	0
59	2B	12	Total O 12 12	0	0
59	2D	20	Total O 20 20	0	0
59	2E	11	Total O 11 11	0	0
59	2F	7	Total O 7 7	0	0
59	2N	1	Total O 1 1	0	0
59	2O	3	Total O 3 3	0	0
59	2P	3	Total O 3 3	0	0
59	2Q	2	Total O 2 2	0	0
59	2R	3	Total O 3 3	0	0
59	2T	3	Total O 3 3	0	0
59	2U	3	Total O 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	2W	1	Total O 1 1	0	0
59	2X	2	Total O 2 2	0	0
59	2Y	1	Total O 1 1	0	0
59	2Z	6	Total O 6 6	0	0
59	20	4	Total O 4 4	0	0
59	21	1	Total O 1 1	0	0
59	23	1	Total O 1 1	0	0
59	25	1	Total O 1 1	0	0
59	27	1	Total O 1 1	0	0
59	28	4	Total O 4 4	0	0
59	2a	274	Total O 274 274	0	0
59	2c	2	Total O 2 2	0	0
59	2d	1	Total O 1 1	0	0
59	2i	2	Total O 2 2	0	0
59	2j	2	Total O 2 2	0	0
59	2l	2	Total O 2 2	0	0
59	2p	1	Total O 1 1	0	0
59	2t	3	Total O 3 3	0	0
59	2v	1	Total O 1 1	0	0
59	2x	2	Total O 2 2	0	0

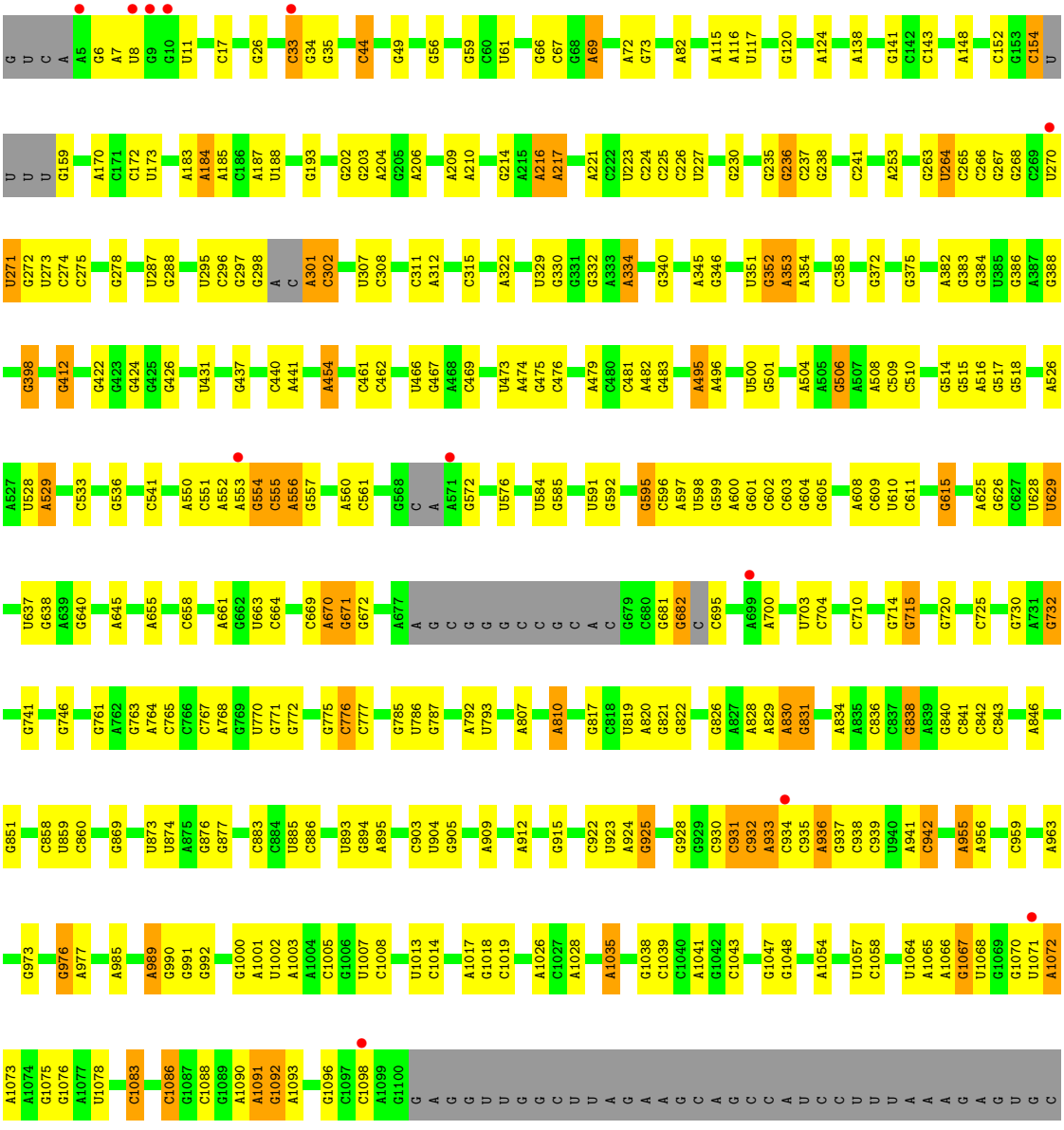
3 Residue-property plots (i)

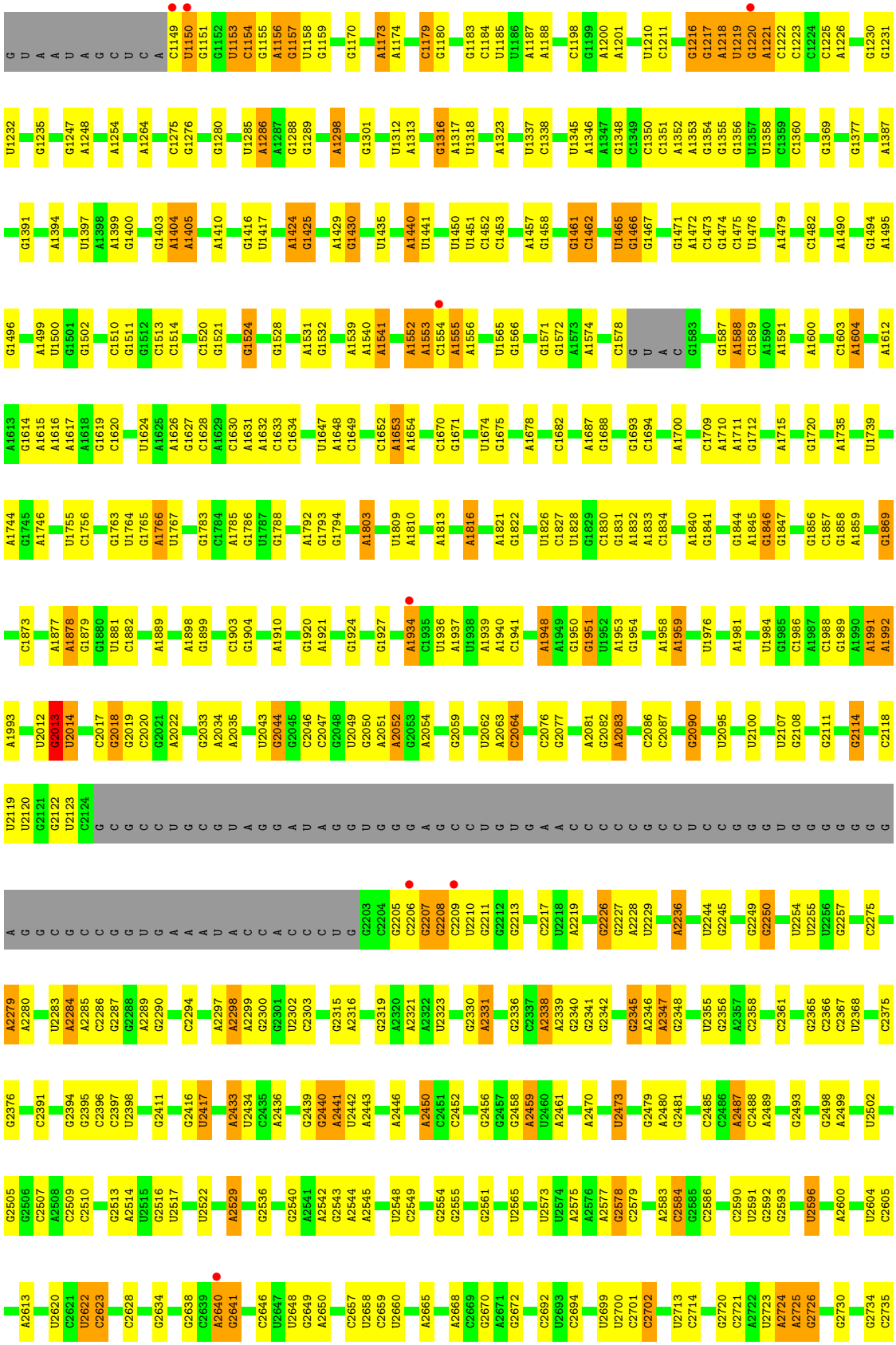
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

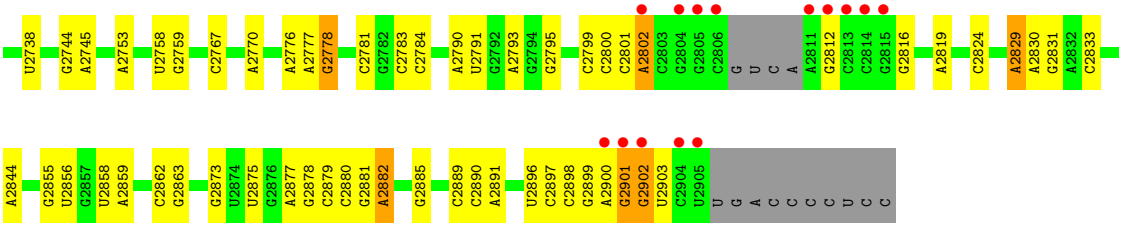
• Molecule 1: 23S Ribosomal RNA

Chain 1A:





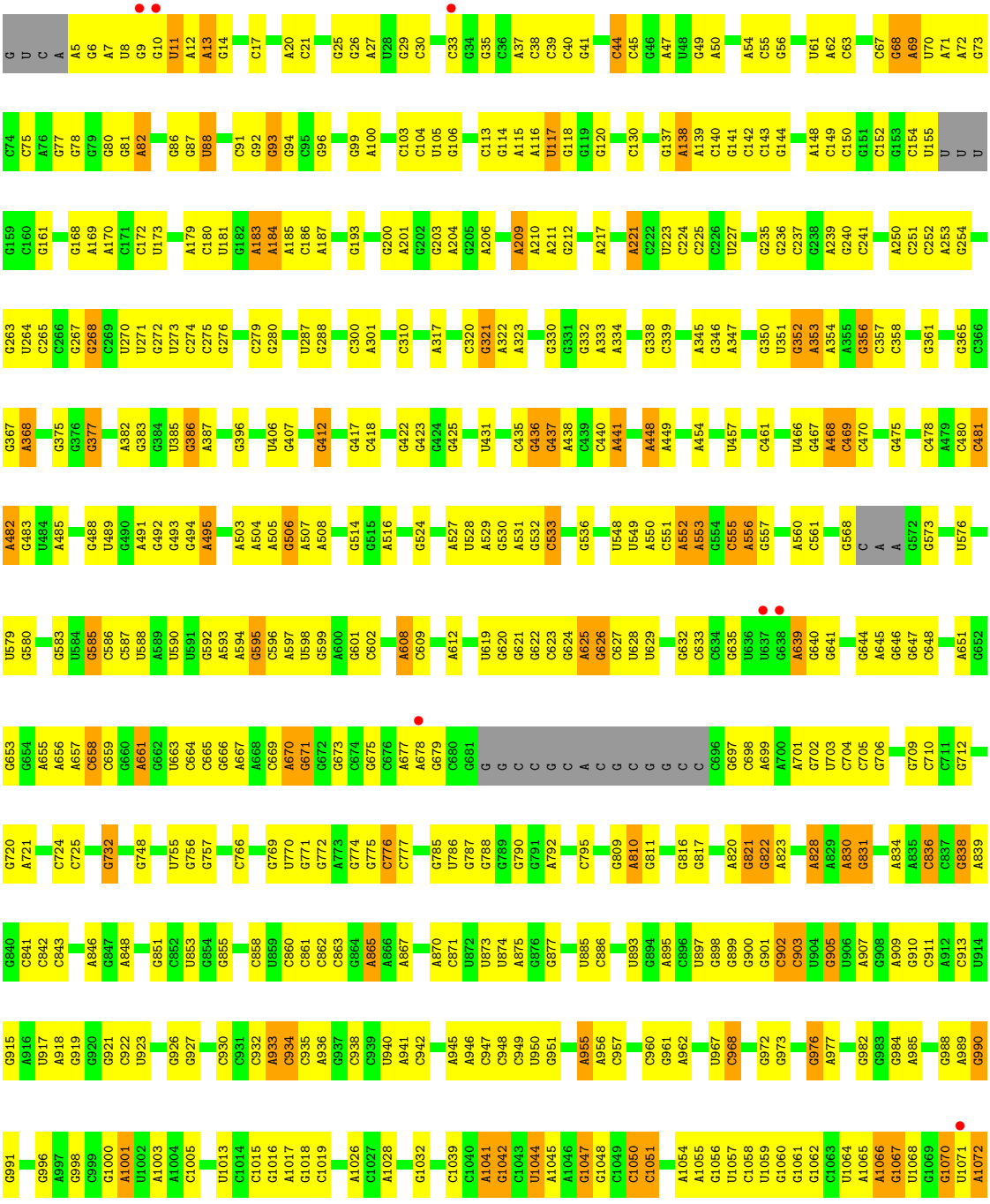

G U A A U A G C U C
C1149 U1150 G1151 G1152 U1153 C1154 G1155 A1156 G1157 U1158 G1159 G1170 A1173 A1174 C1179 G1180 G1183 C1184 U1185 U1186 A1187 A1188 C1198 G1199 A1200 A1201 U1210 C1211 G1216 G1217 A1218 U1219 G1220 A1221 C1222 C1223 C1224 C1225 A1226 G1230 G1231
U1232 G1235 G1247 A1248 A1254 A1264 C1275 G1276 G1280 U1285 A1286 A1287 G1288 G1289 A1298 G1301 U1312 A1313 G1316 A1317 U1318 A1323 U1337 C1338 U1345 A1346 A1347 G1348 C1349 C1350 C1351 A1352 A1353 G1354 G1355 G1356 U1357 U1358 C1359 C1360 G1369 G1377 A1387
G1391 A1394 U1397 A1398 A1399 C1400 G1403 A1404 A1405 A1410 G1416 U1417 A1424 G1425 A1429 G1430 U1435 A1440 U1441 U1450 U1451 C1452 C1453 A1457 G1458 G1461 C1462 U1465 G1466 G1467 G1471 A1472 C1473 G1474 C1475 U1476 A1479 C1482 A1490 G1494 A1495
G1496 A1499 U1500 G1501 G1502 C1510 G1511 G1512 C1513 C1514 C1520 G1521 G1524 G1528 A1531 G1532 A1539 A1540 A1541 A1552 A1553 C1554 A1555 A1556 U1565 G1566 G1571 G1572 A1573 A1574 C1578 G U A C G1583 G1587 A1588 C1589 A1590 A1591 A1600 C1603 A1604 A1612
A1613 G1614 A1615 A1616 A1617 A1618 G1619 C1620 U1624 A1625 A1626 G1627 C1628 A1629 C1630 A1631 A1632 C1633 C1634 U1647 A1648 C1649 C1652 A1653 A1654 C1670 G1671 U1674 G1675 A1678 C1682 A1687 G1688 G1693 C1694 A1700 C1709 A1710 A1711 G1712 A1715 G1720 A1735 U1739
A1744 G1745 A1746 U1755 C1756 G1763 U1764 G1765 A1766 U1767 G1783 C1784 A1785 G1786 U1787 G1788 A1792 G1793 G1794 A1803 U1809 A1810 A1813 A1816 A1821 G1822 U1826 C1827 U1828 G1829 C1830 G1831 A1832 A1833 C1834 A1840 G1841 G1844 A1845 G1846 G1847 G1856 C1857 G1858 A1859 G1869
C1873 A1877 A1878 G1879 G1880 U1881 C1882 A1889 A1898 G1899 C1903 G1904 A1910 G1920 A1921 G1924 G1927 A1934 C1935 U1936 A1937 U1938 A1939 A1940 C1941 A1948 A1949 G1950 G1951 U1952 A1953 G1954 A1958 A1959 U1976 A1981 U1984 G1985 C1986 A1987 C1988 G1989 A1990 A1991 A1992
A1993 U2012 G2013 U2014 C2017 G2018 G2019 C2020 G2021 A2022 G2033 A2034 A2035 U2043 G2044 G2045 C2046 C2047 G2048 U2049 G2050 A2051 A2052 G2053 A2054 G2059 U2062 A2063 C2064 C2076 G2077 A2081 G2082 A2083 C2086 C2087 G2090 U2095 U2100 U2107 G2108 G2111 G2114 C2118
U2119 U2120 G2121 G2122 U2123 C2124 G C C G C C U G C C C U G U A C G C C C

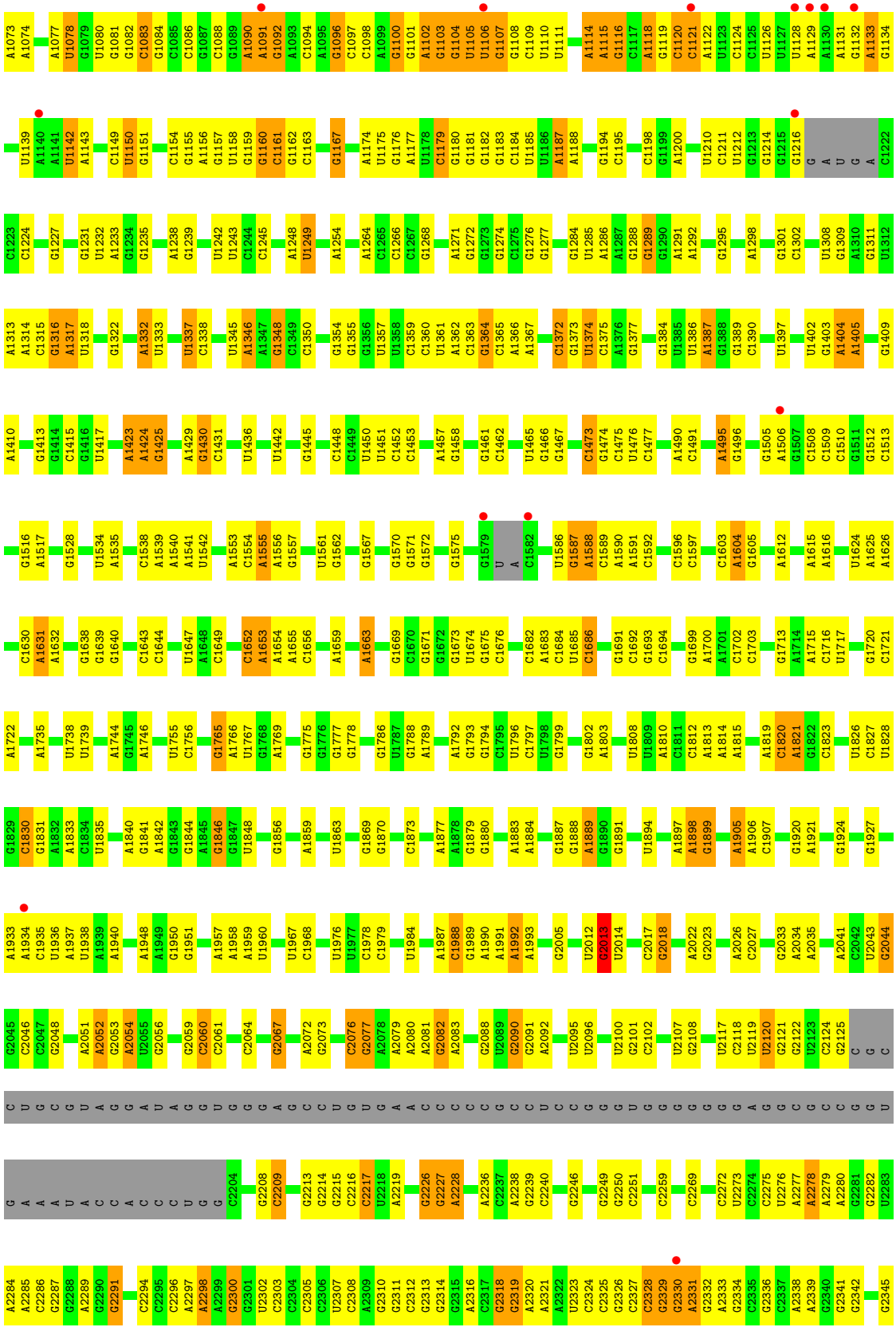


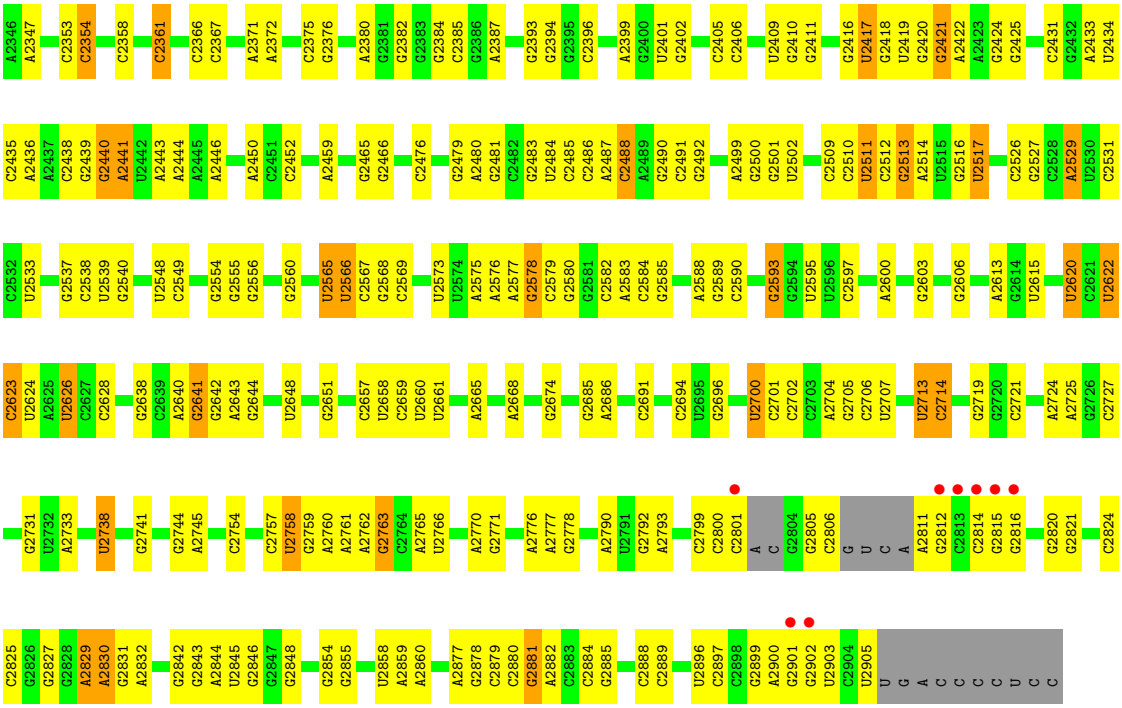
• Molecule 1: 23S Ribosomal RNA

Chain 2A:





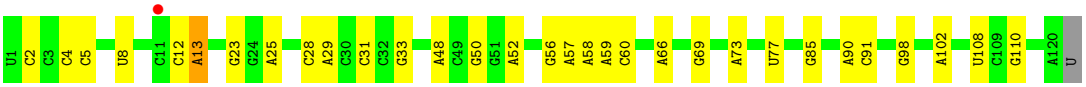




• Molecule 2: 5S Ribosomal RNA

Chain 1B:

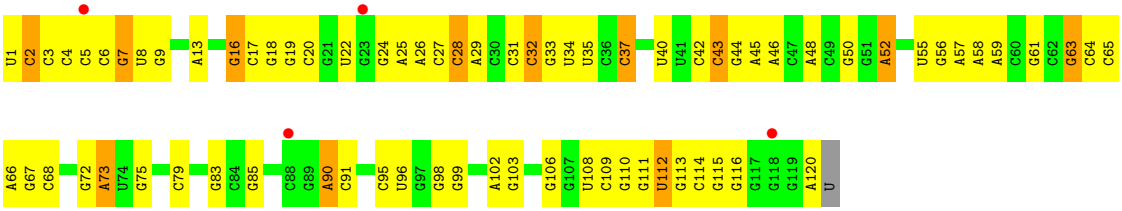




• Molecule 2: 5S Ribosomal RNA

Chain 2B:

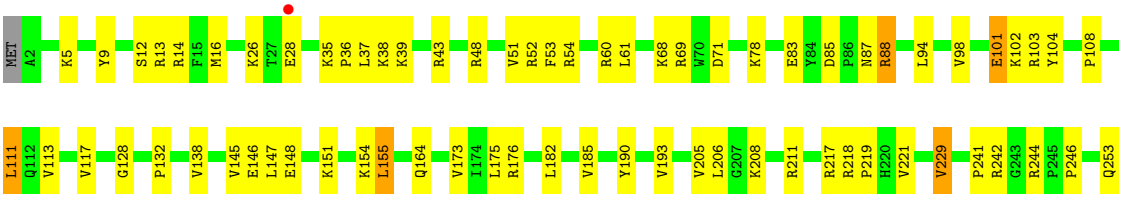




• Molecule 3: 50S ribosomal protein L2

Chain 1D:



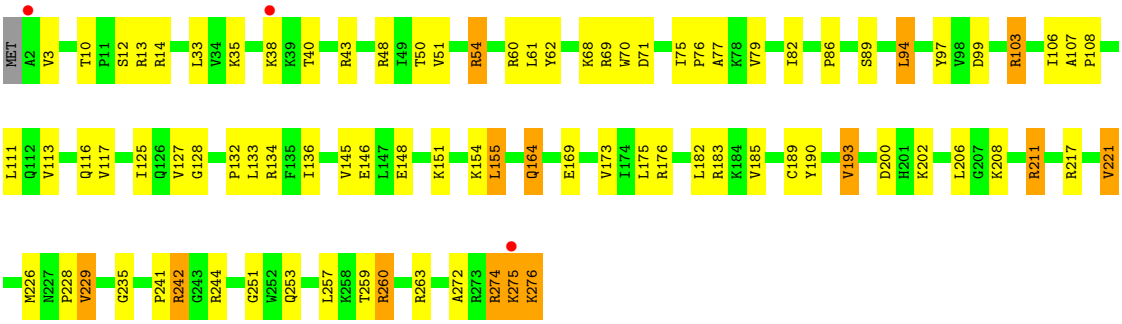




• Molecule 3: 50S ribosomal protein L2

Chain 2D:

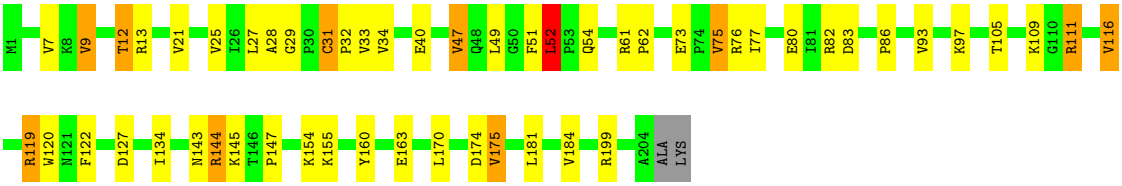




• Molecule 4: 50S ribosomal protein L3

Chain 1E:

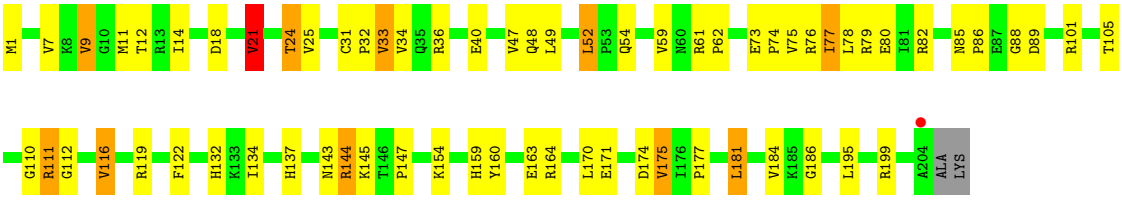




• Molecule 4: 50S ribosomal protein L3

Chain 2E:

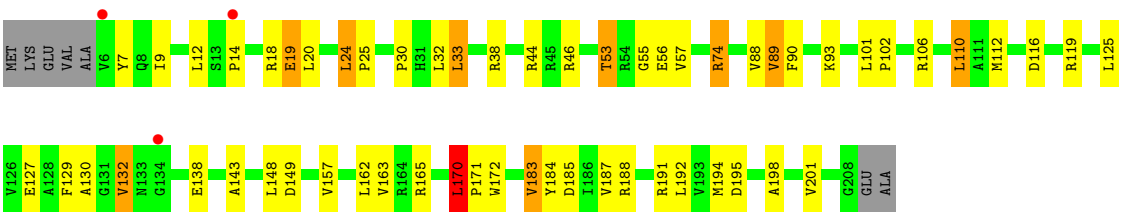




• Molecule 5: 50S ribosomal protein L4

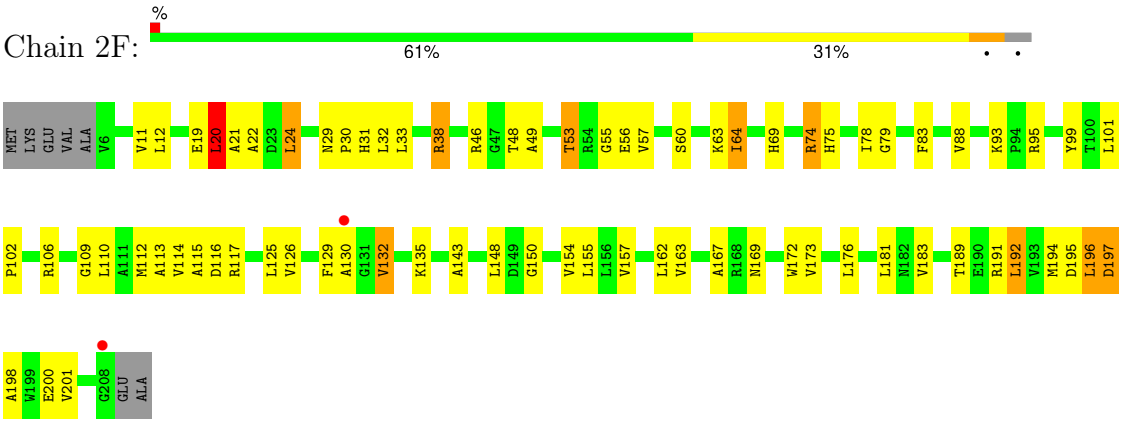
Chain 1F:





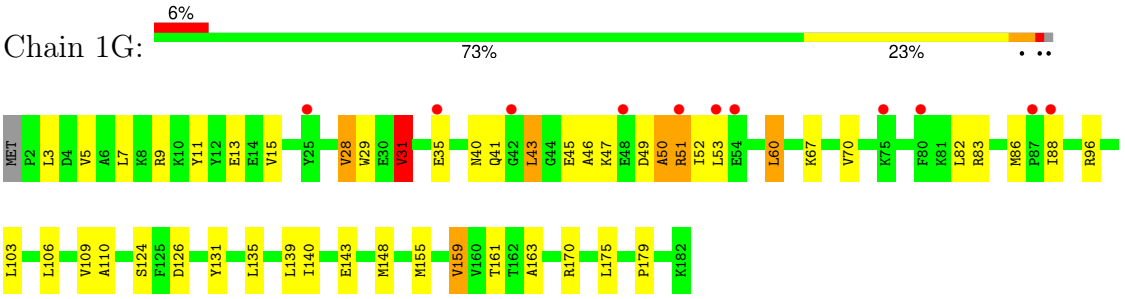
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



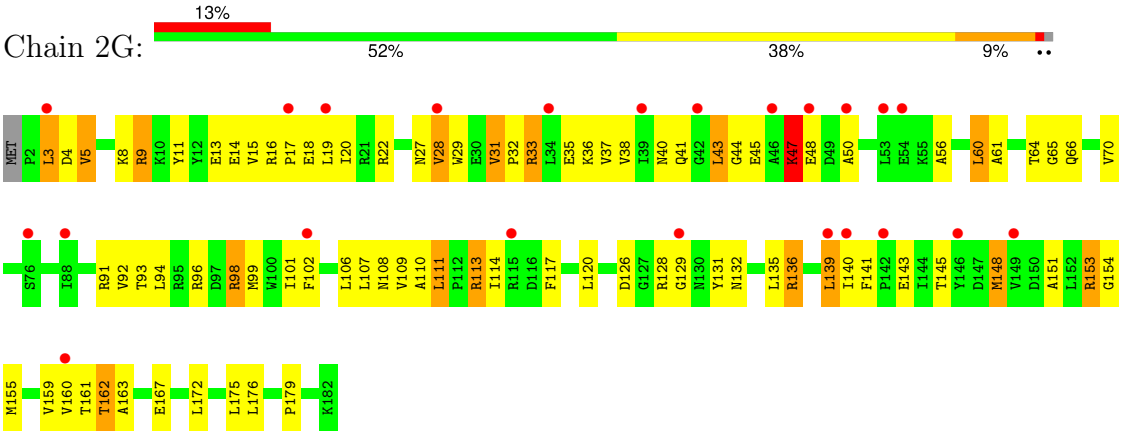
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



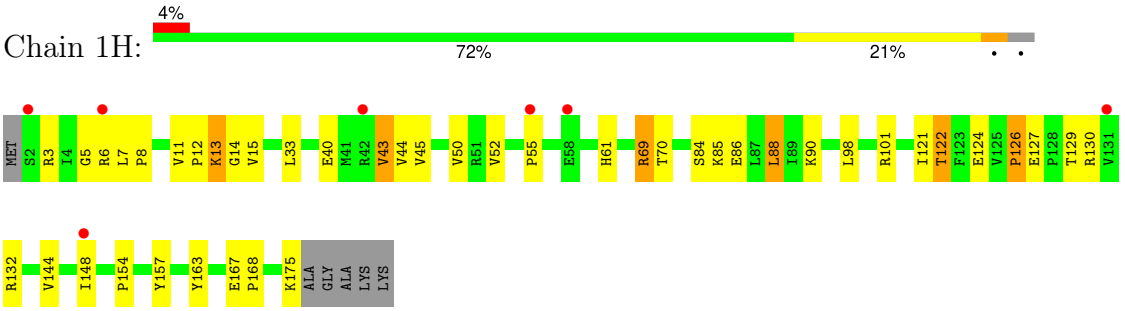
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



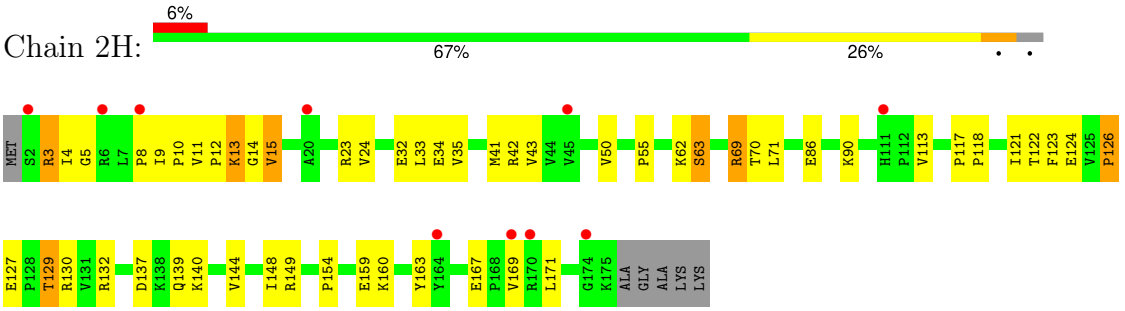
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



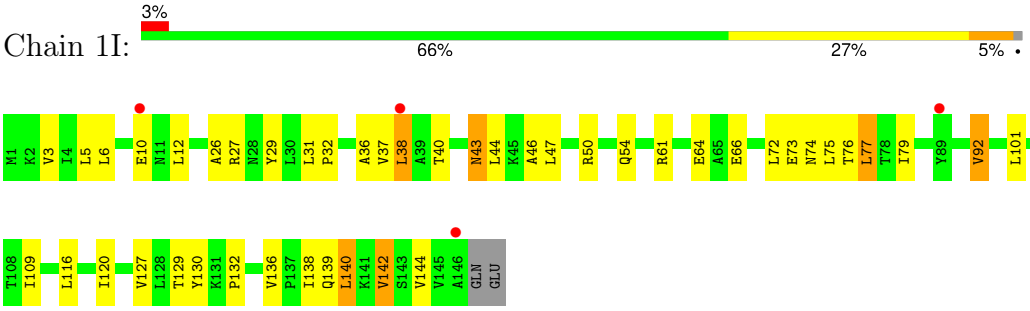
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



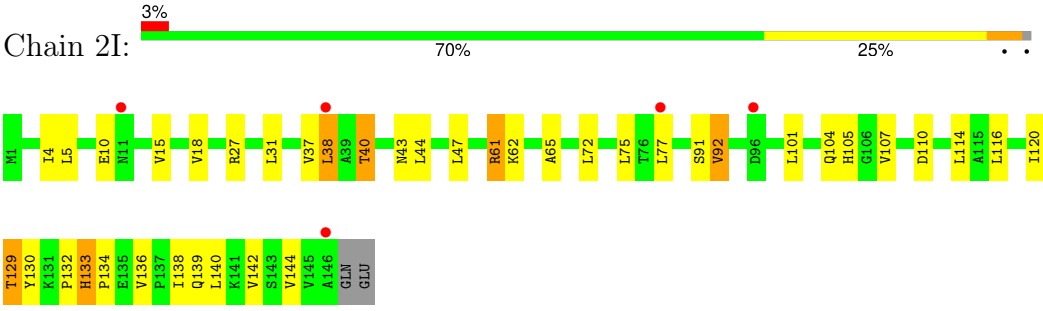
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



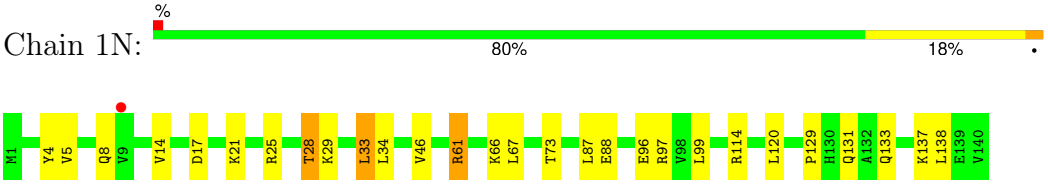
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



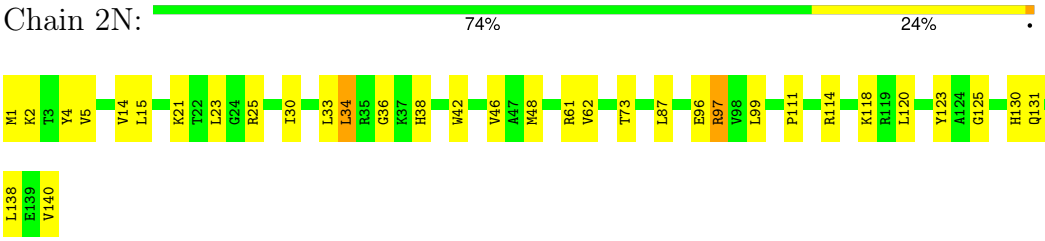
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



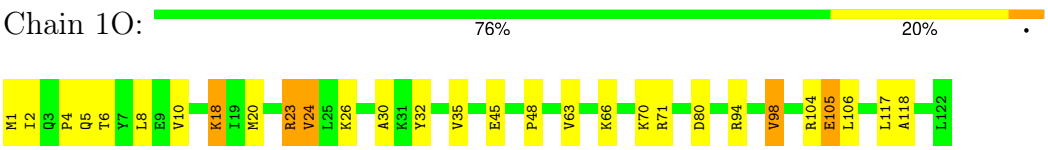
• Molecule 9: 50S ribosomal protein L13

Chain 2N:



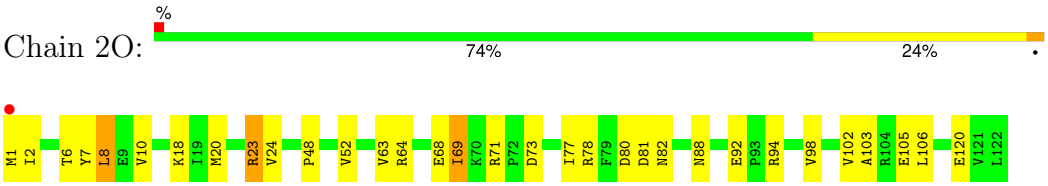
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



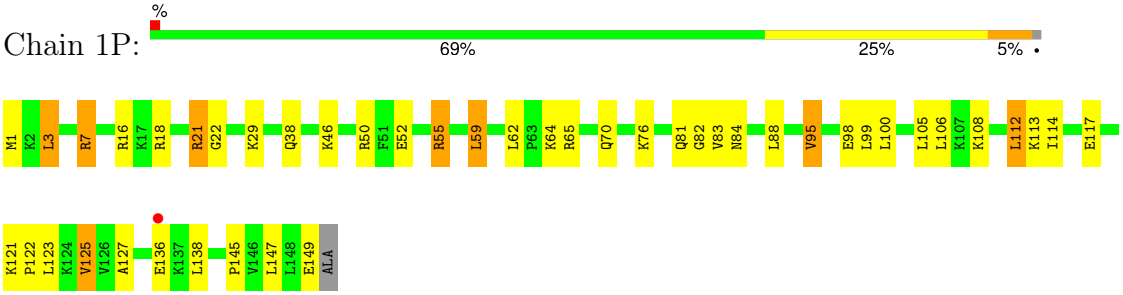
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



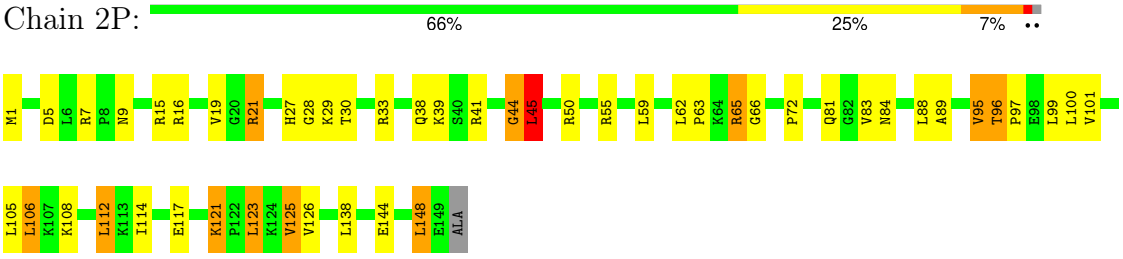
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



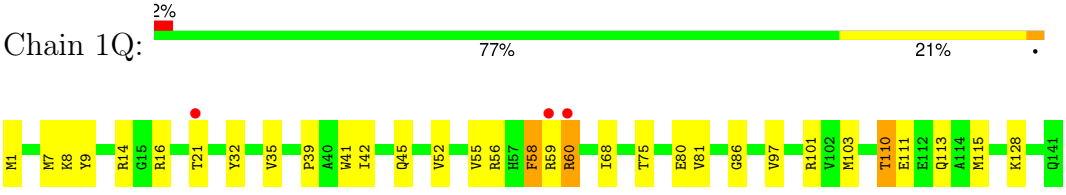
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



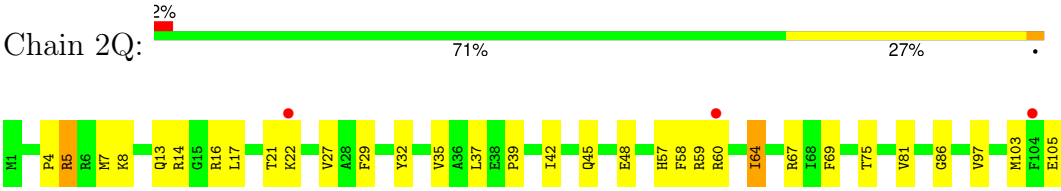
• Molecule 12: 50S ribosomal protein L16

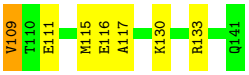
Chain 1Q:



• Molecule 12: 50S ribosomal protein L16

Chain 2Q:





• Molecule 13: 50S ribosomal protein L17

Chain 1R:

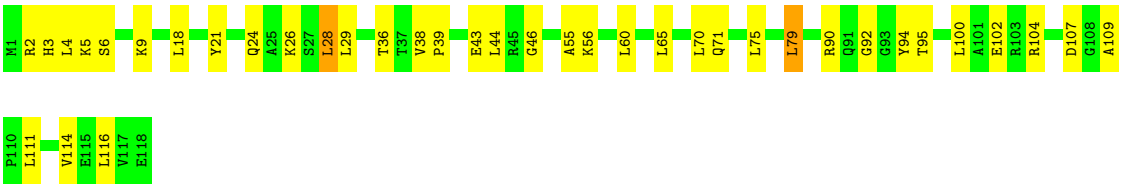




• Molecule 13: 50S ribosomal protein L17

Chain 2R:

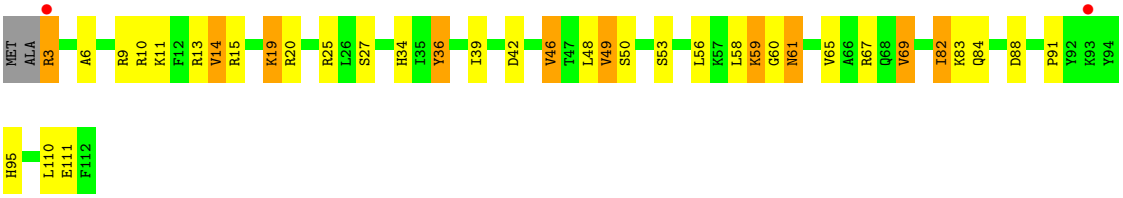




• Molecule 14: 50S ribosomal protein L18

Chain 1S:

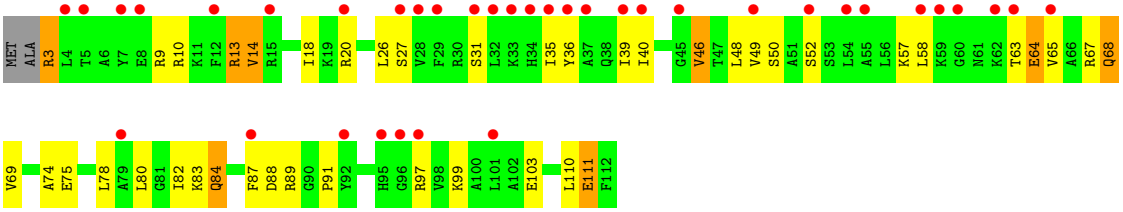




• Molecule 14: 50S ribosomal protein L18

Chain 2S:

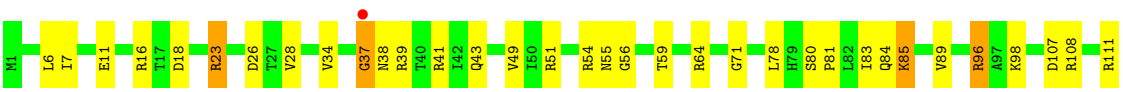


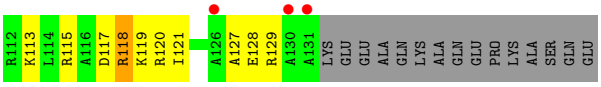


• Molecule 15: 50S ribosomal protein L19

Chain 1T:



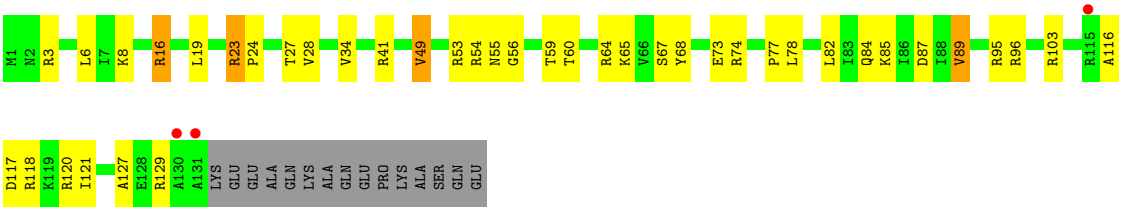




• Molecule 15: 50S ribosomal protein L19

Chain 2T:





• Molecule 16: 50S ribosomal protein L20

Chain 1U:





• Molecule 16: 50S ribosomal protein L20

Chain 2U:

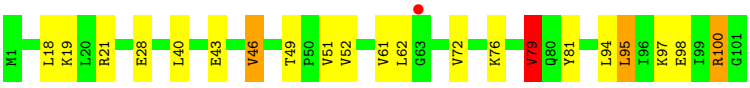




• Molecule 17: 50S ribosomal protein L21

Chain 1V:

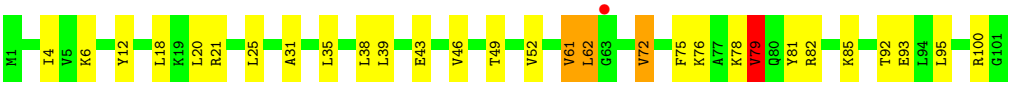




• Molecule 17: 50S ribosomal protein L21

Chain 2V:

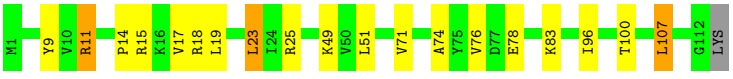




• Molecule 18: 50S ribosomal protein L22

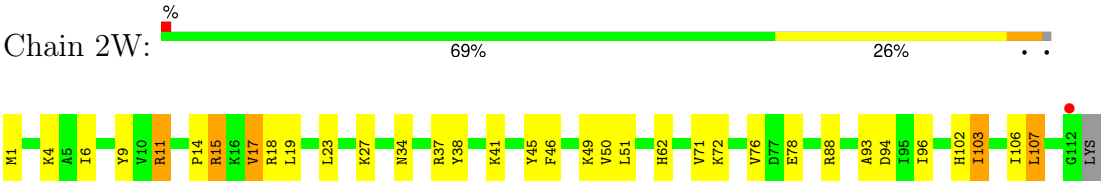
Chain 1W:





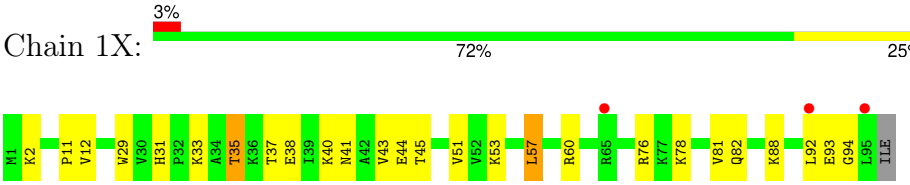
• Molecule 18: 50S ribosomal protein L22

Chain 2W:



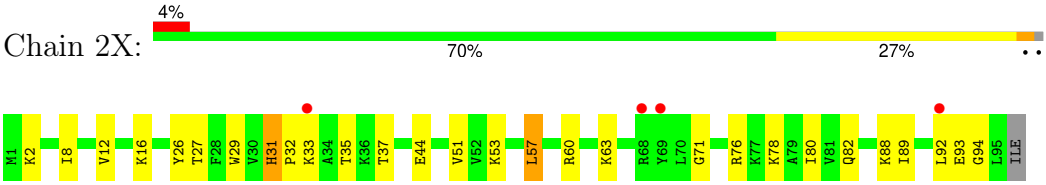
• Molecule 19: 50S ribosomal protein L23

Chain 1X:



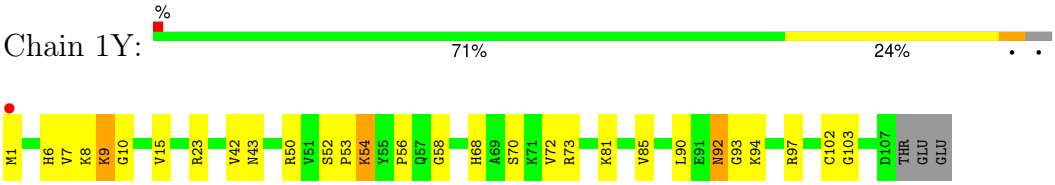
• Molecule 19: 50S ribosomal protein L23

Chain 2X:



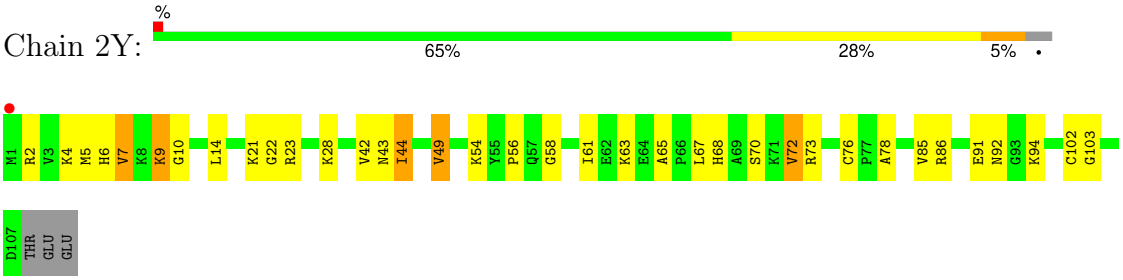
• Molecule 20: 50S ribosomal protein L24

Chain 1Y:



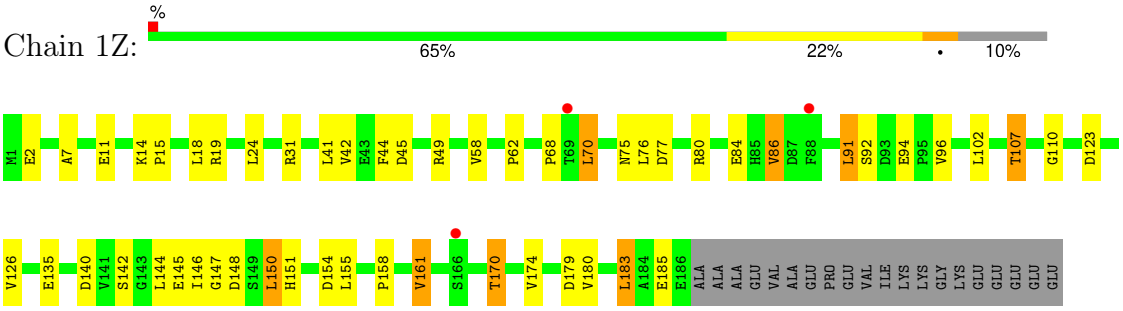
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



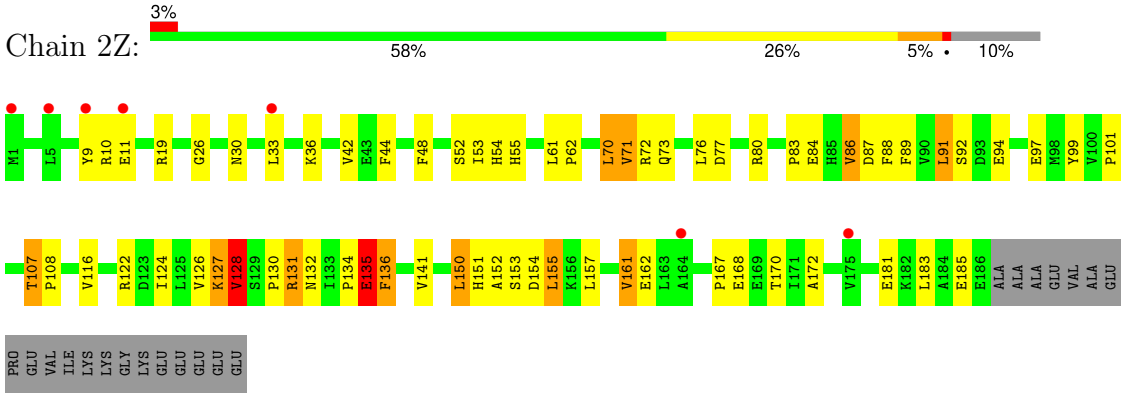
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



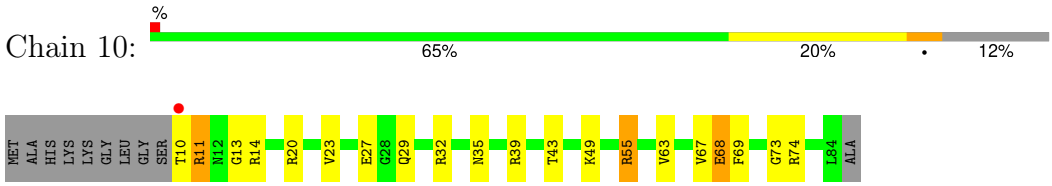
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



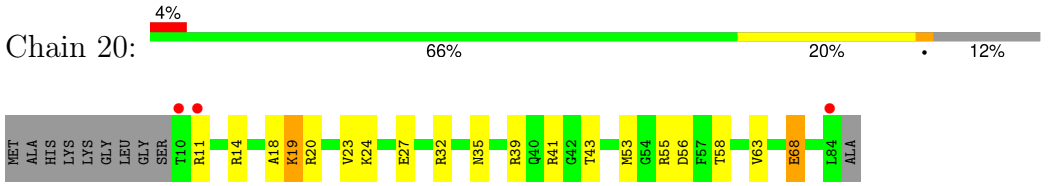
• Molecule 22: 50S ribosomal protein L27

Chain 10:



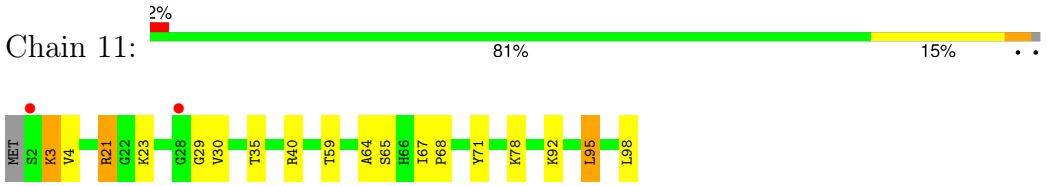
• Molecule 22: 50S ribosomal protein L27

Chain 20:



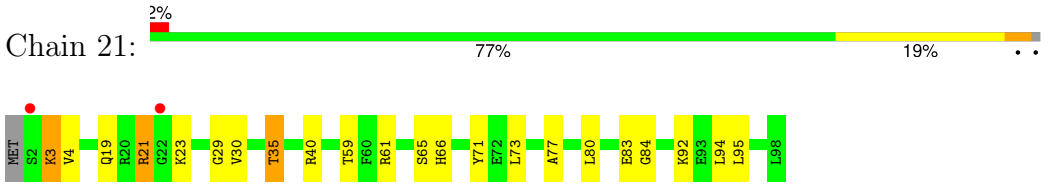
• Molecule 23: 50S ribosomal protein L28

Chain 11:



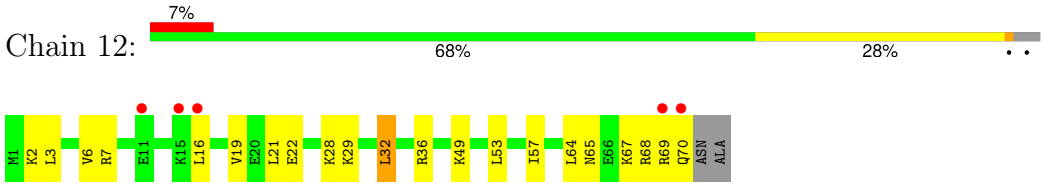
• Molecule 23: 50S ribosomal protein L28

Chain 21:



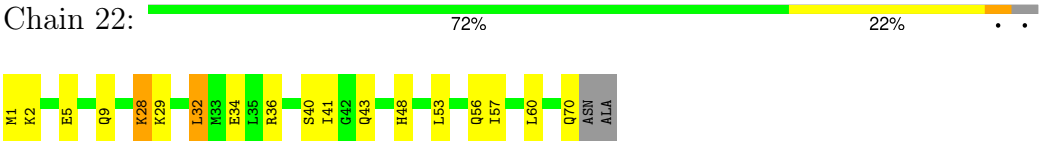
• Molecule 24: 50S ribosomal protein L29

Chain 12:



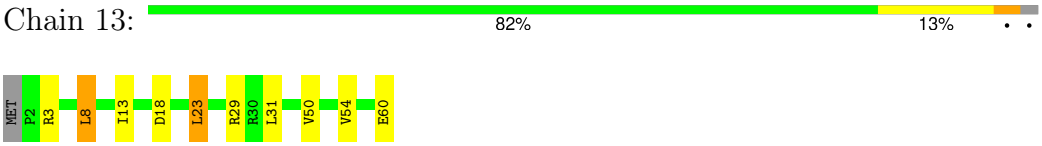
• Molecule 24: 50S ribosomal protein L29

Chain 22:



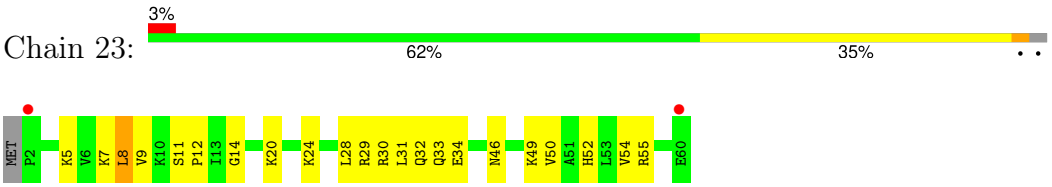
• Molecule 25: 50S ribosomal protein L30

Chain 13:



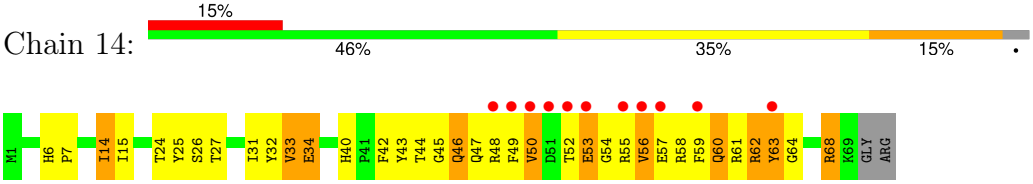
• Molecule 25: 50S ribosomal protein L30

Chain 23:



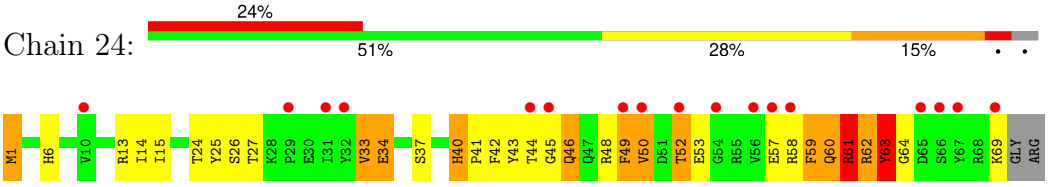
• Molecule 26: 50S ribosomal protein L31

Chain 14:



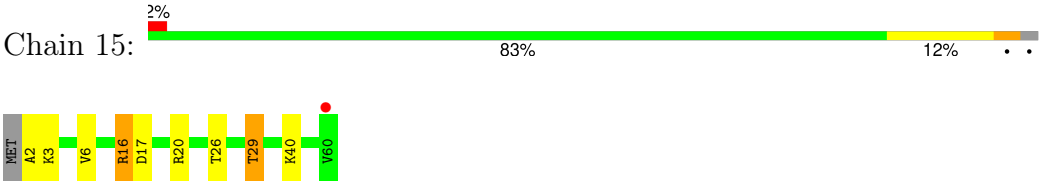
• Molecule 26: 50S ribosomal protein L31

Chain 24:



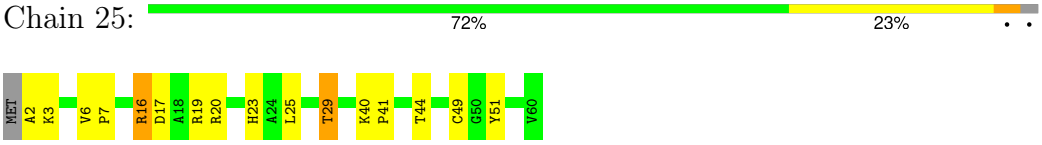
• Molecule 27: 50S ribosomal protein L32

Chain 15:



• Molecule 27: 50S ribosomal protein L32

Chain 25:



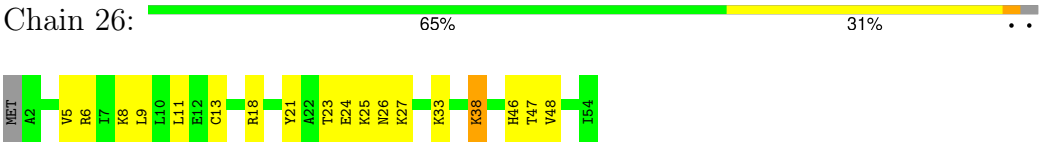
• Molecule 28: 50S ribosomal protein L33

Chain 16:



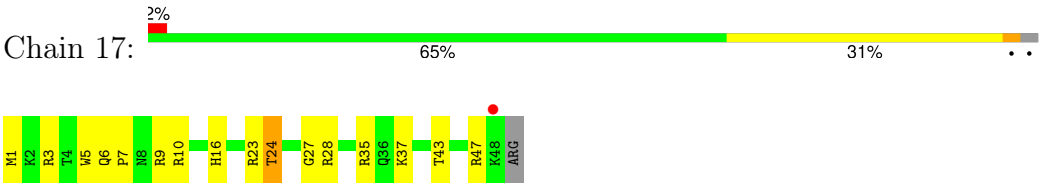
• Molecule 28: 50S ribosomal protein L33

Chain 26:



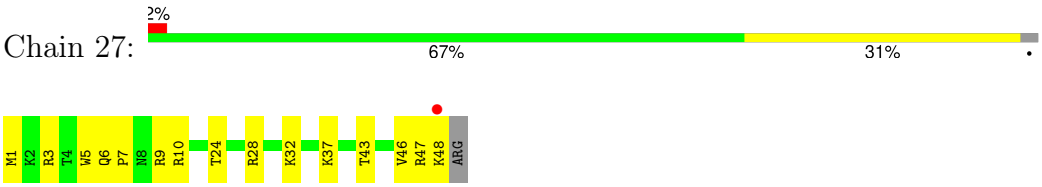
• Molecule 29: 50S ribosomal protein L34

Chain 17:



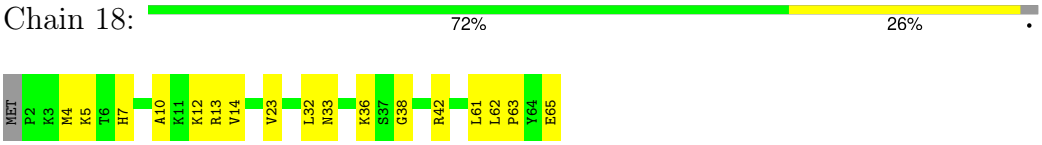
• Molecule 29: 50S ribosomal protein L34

Chain 27:



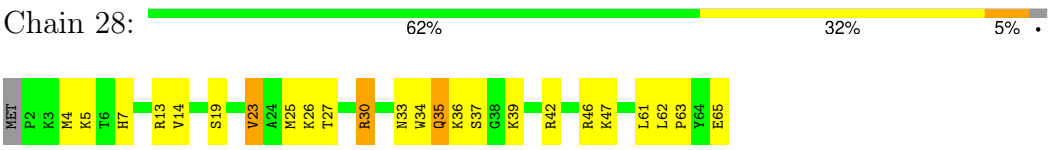
• Molecule 30: 50S ribosomal protein L35

Chain 18:



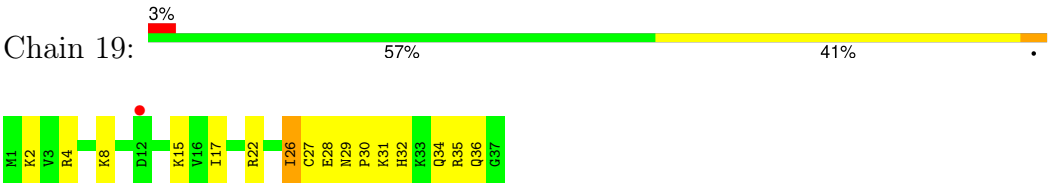
• Molecule 30: 50S ribosomal protein L35

Chain 28:



• Molecule 31: 50S ribosomal protein L36

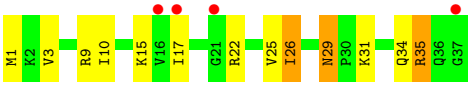
Chain 19:



• Molecule 31: 50S ribosomal protein L36

Chain 29:

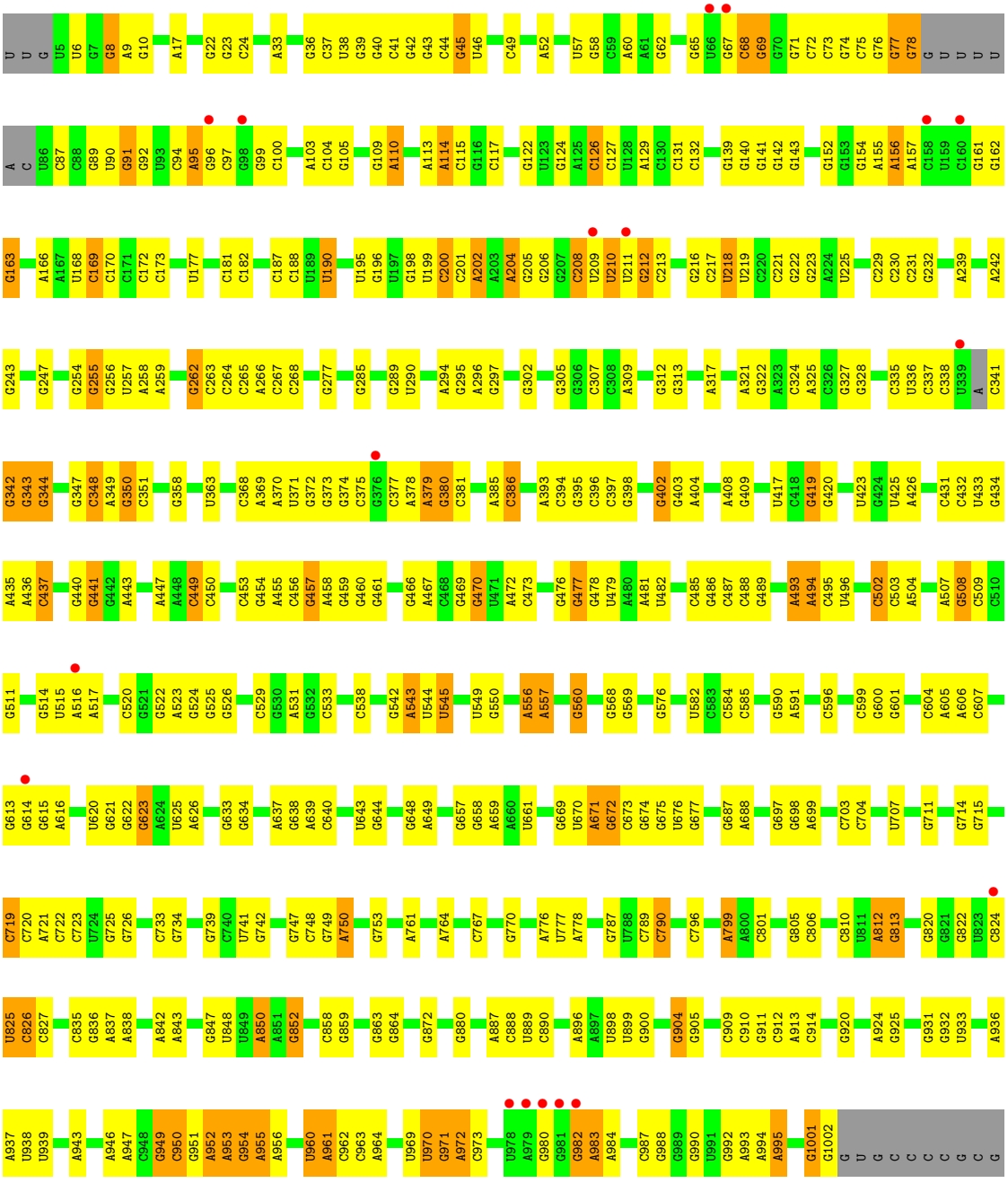


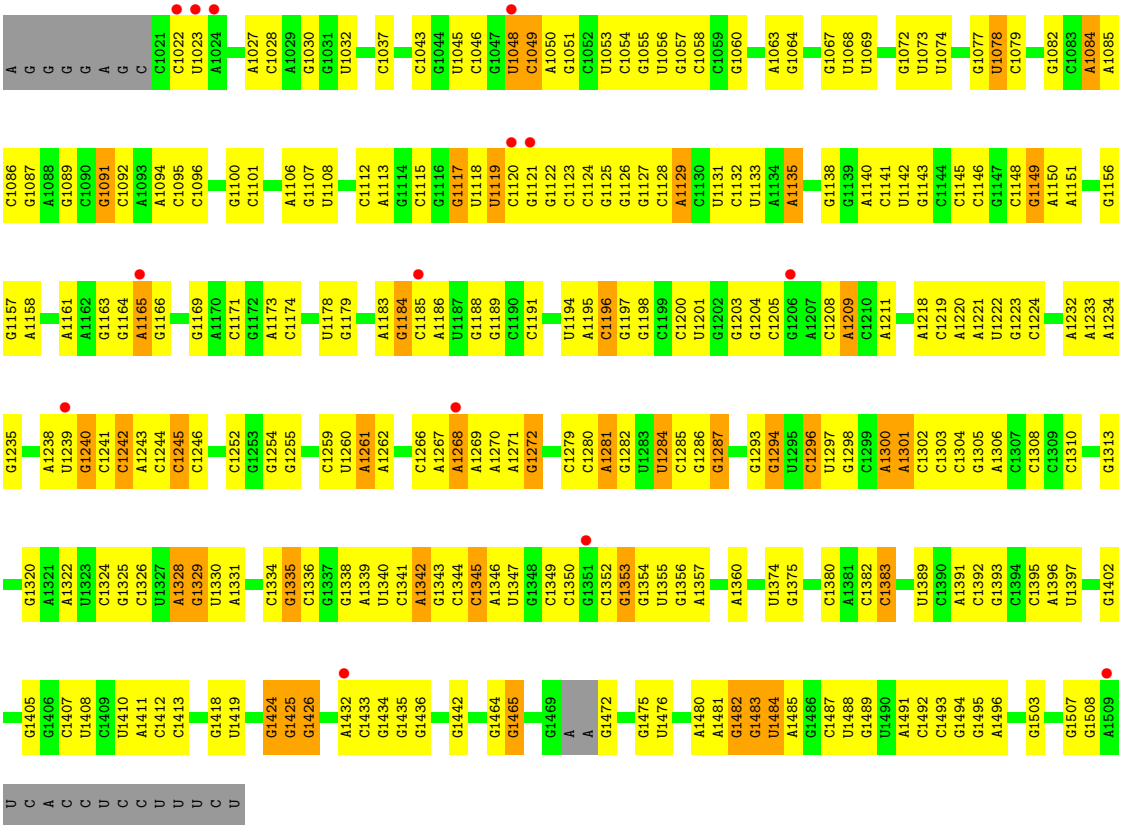


• Molecule 32: 16S Ribosomal RNA

Chain 1a:



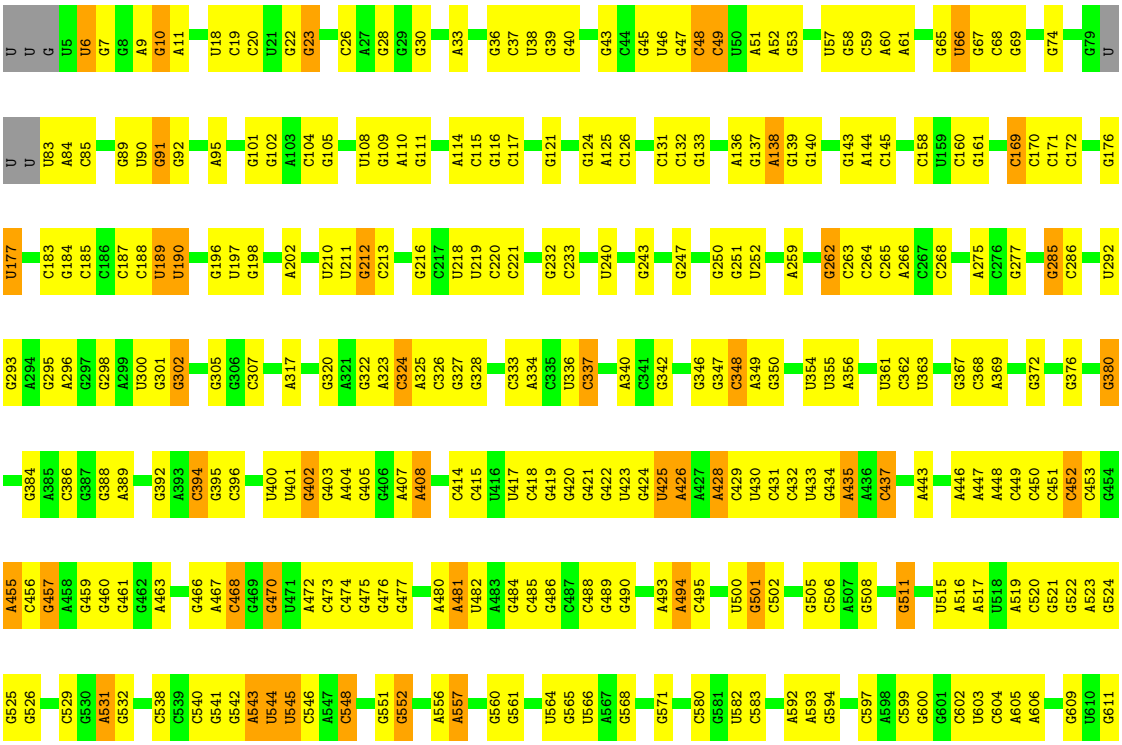


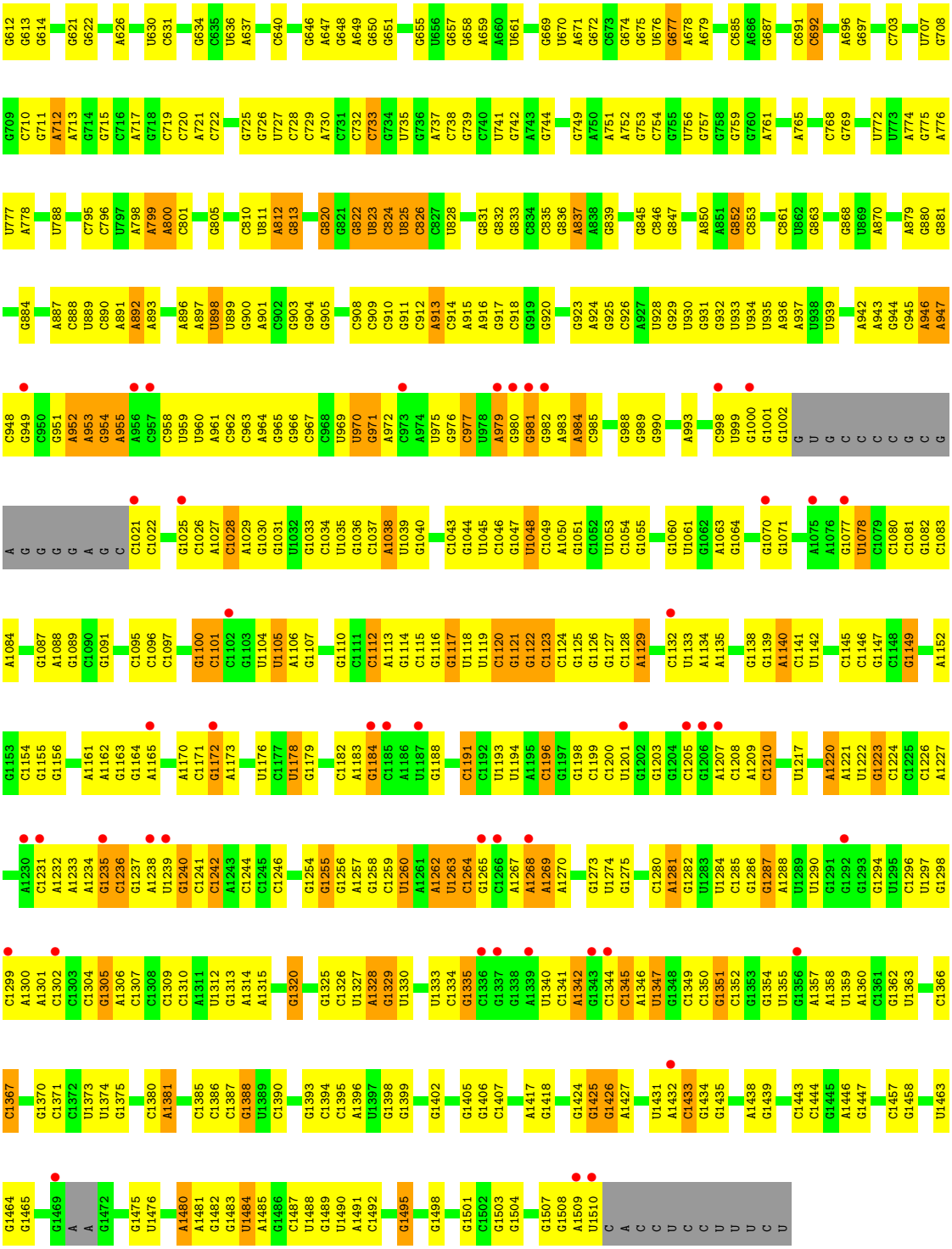


• Molecule 32: 16S Ribosomal RNA

Chain 2a:



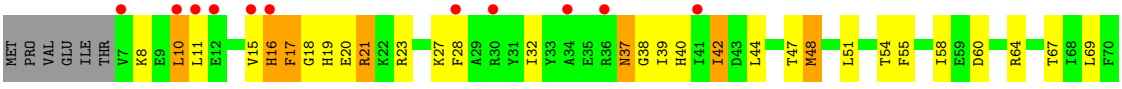


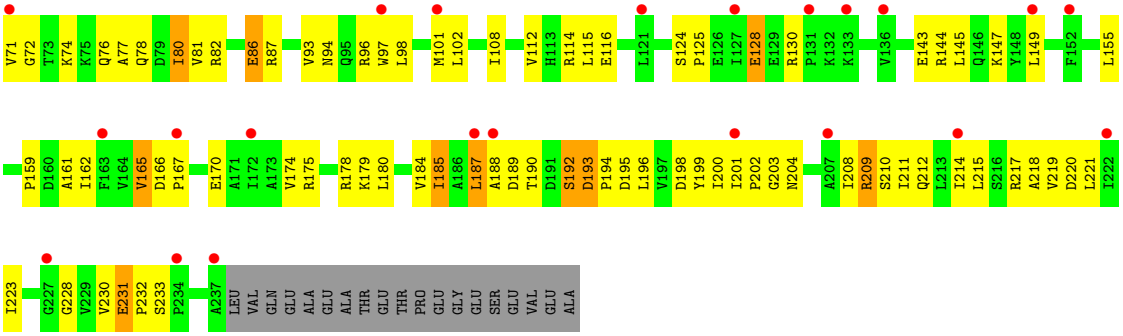


• Molecule 33: 30S ribosomal protein S2

Chain 1b:



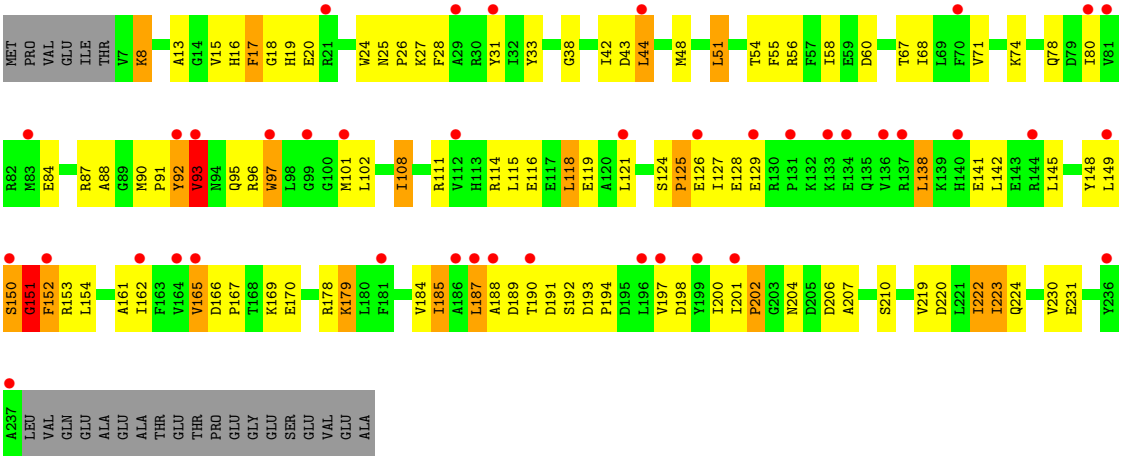




• Molecule 33: 30S ribosomal protein S2

Chain 2b:

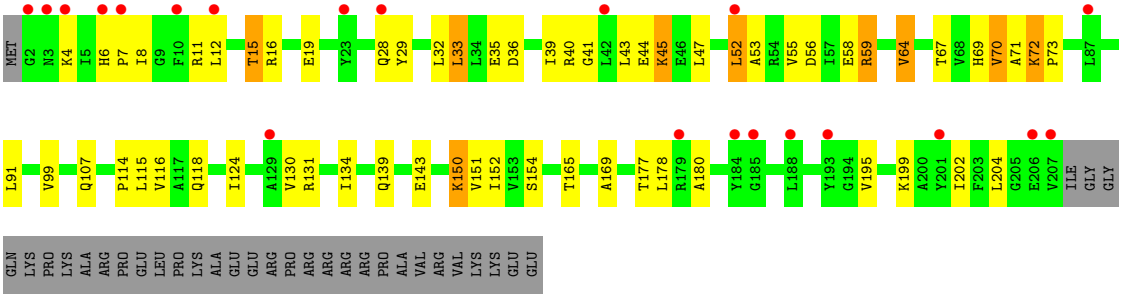




• Molecule 34: 30S ribosomal protein S3

Chain 1c:

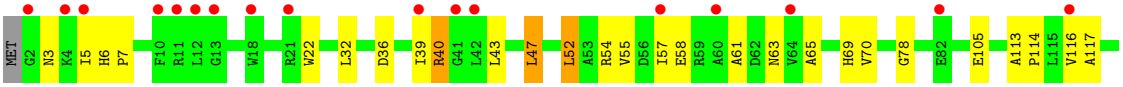


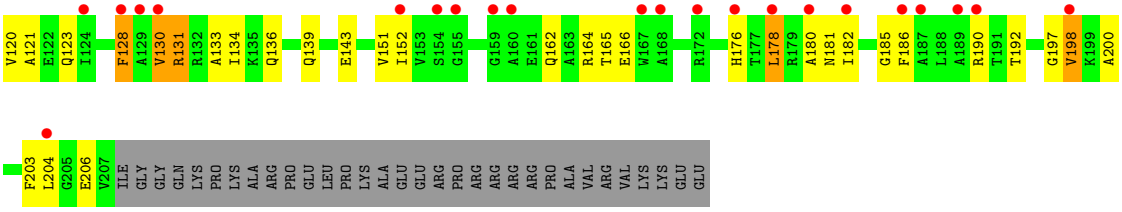


• Molecule 34: 30S ribosomal protein S3

Chain 2c:



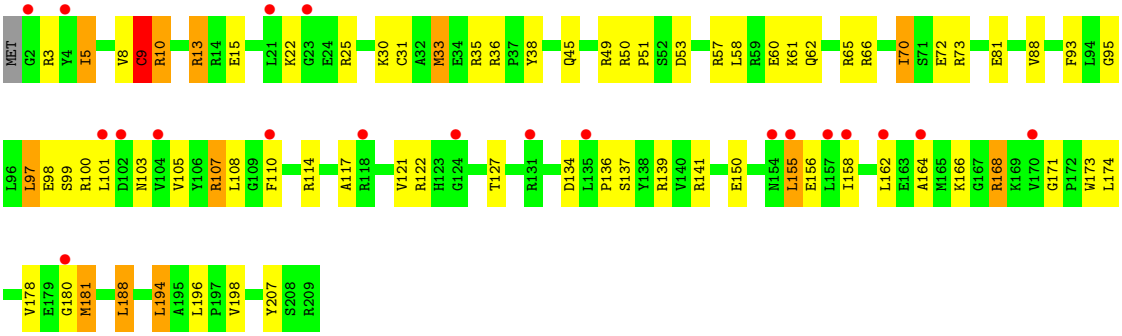




• Molecule 35: 30S ribosomal protein S4

Chain 1d:

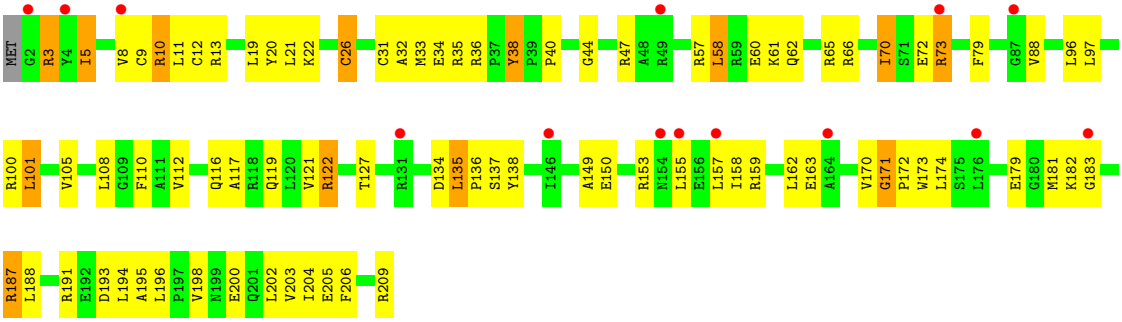




• Molecule 35: 30S ribosomal protein S4

Chain 2d:

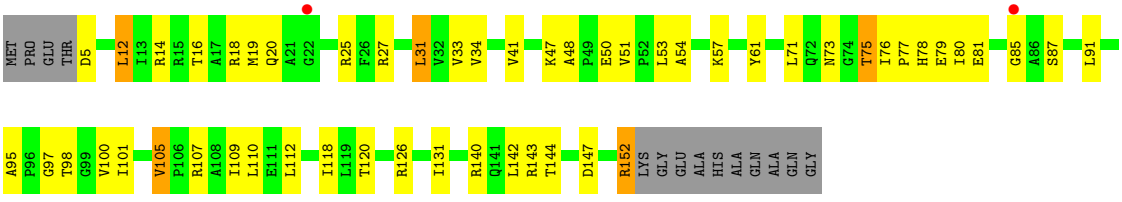




• Molecule 36: 30S ribosomal protein S5

Chain 1e:

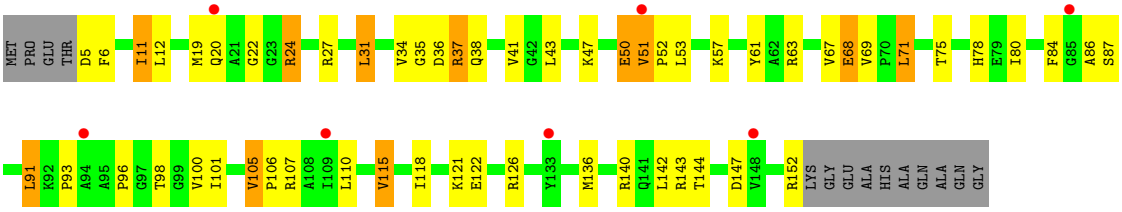




• Molecule 36: 30S ribosomal protein S5

Chain 2e:

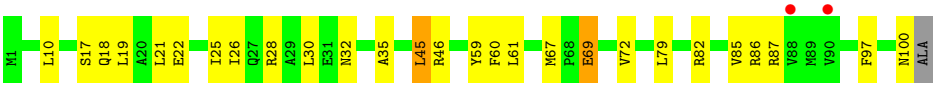




• Molecule 37: 30S ribosomal protein S6

Chain 1f:

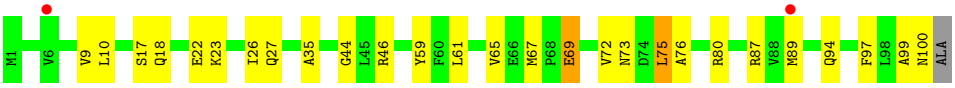




• Molecule 37: 30S ribosomal protein S6

Chain 2f:

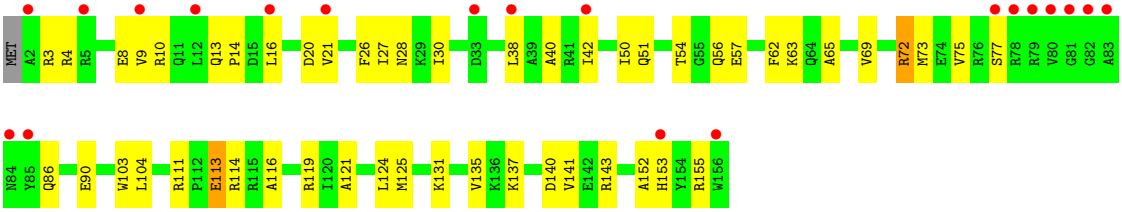




• Molecule 38: 30S ribosomal protein S7

Chain 1g:

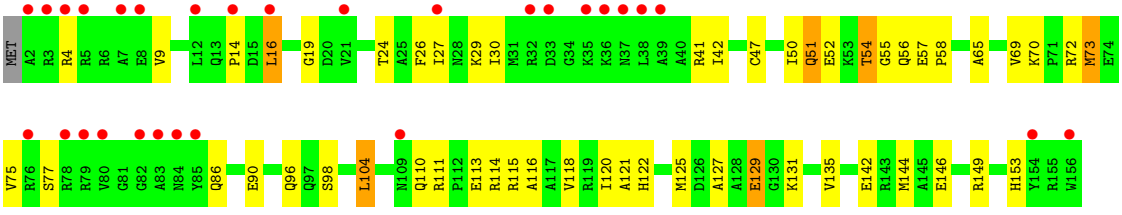




• Molecule 38: 30S ribosomal protein S7

Chain 2g:

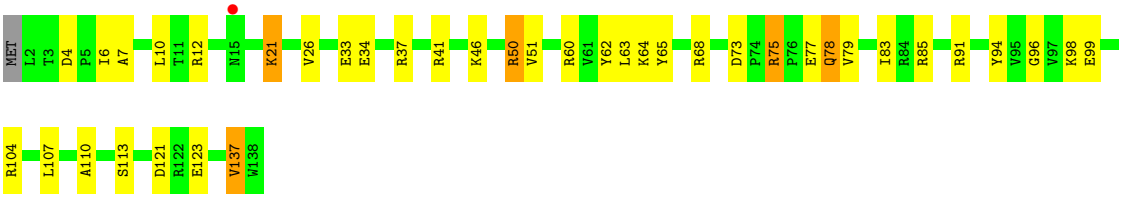




• Molecule 39: 30S ribosomal protein S8

Chain 1h:

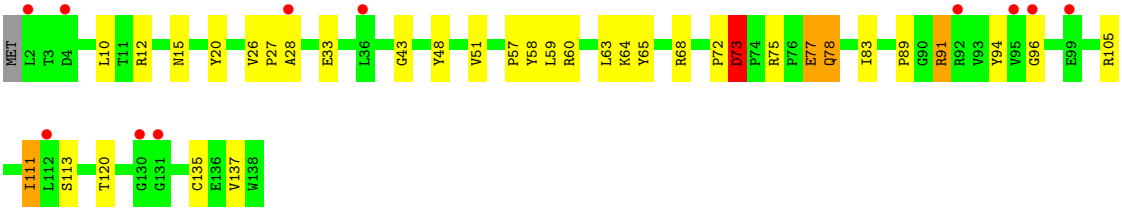




• Molecule 39: 30S ribosomal protein S8

Chain 2h:

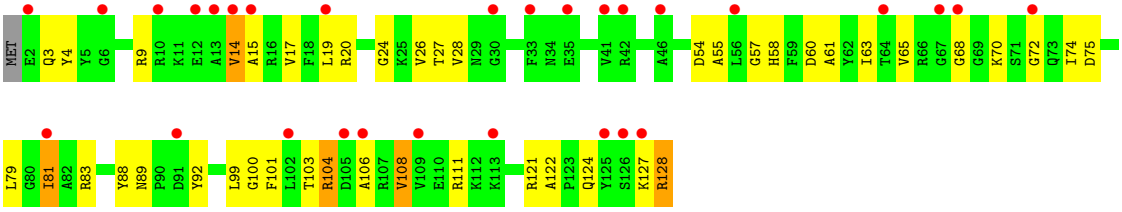




• Molecule 40: 30S ribosomal protein S9

Chain 1i:

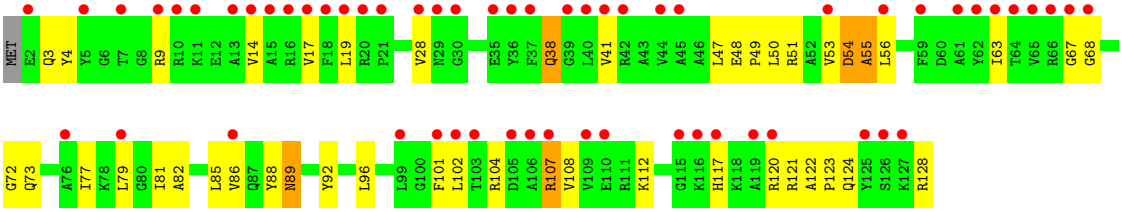




• Molecule 40: 30S ribosomal protein S9

Chain 2i:

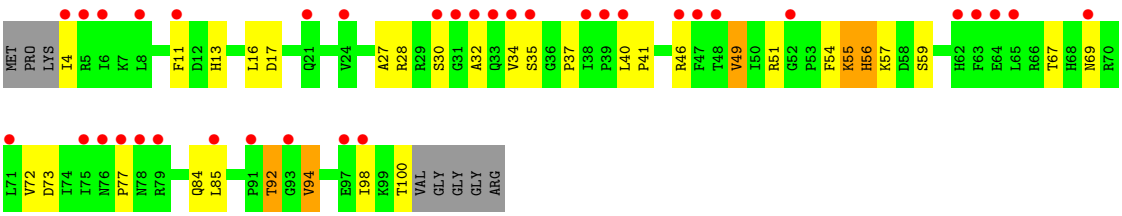




• Molecule 41: 30S ribosomal protein S10

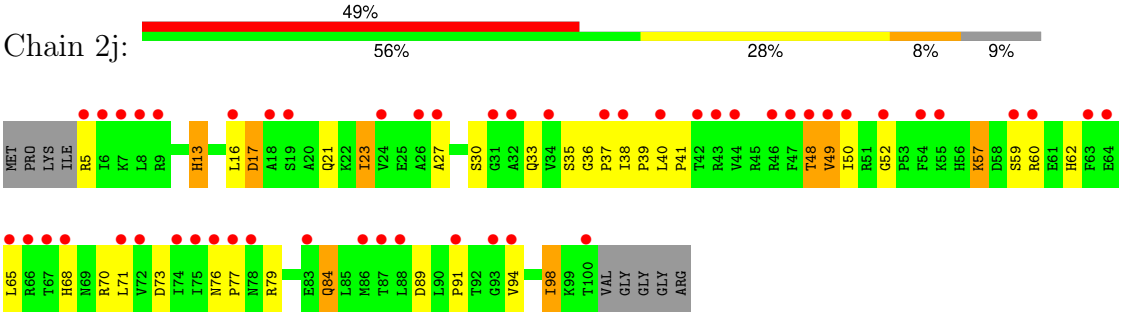
Chain 1j:





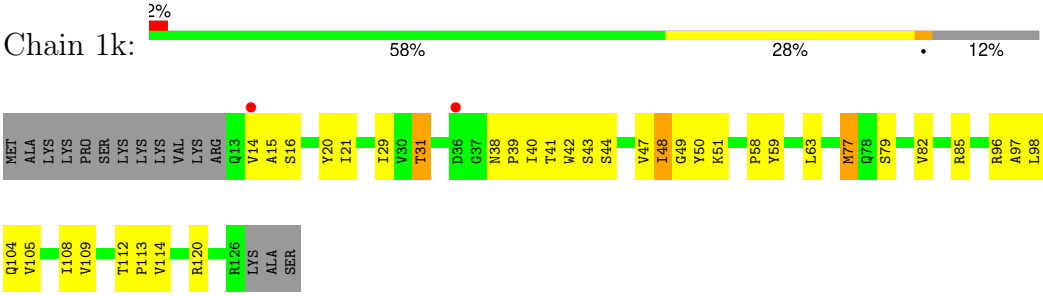
• Molecule 41: 30S ribosomal protein S10

Chain 2j:



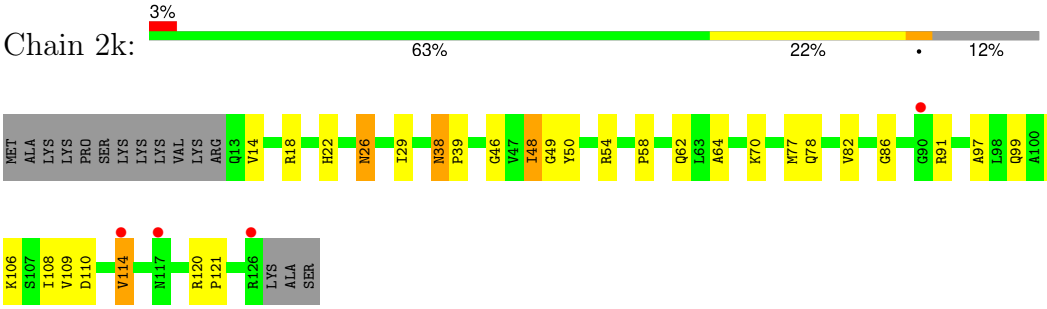
• Molecule 42: 30S ribosomal protein S11

Chain 1k:



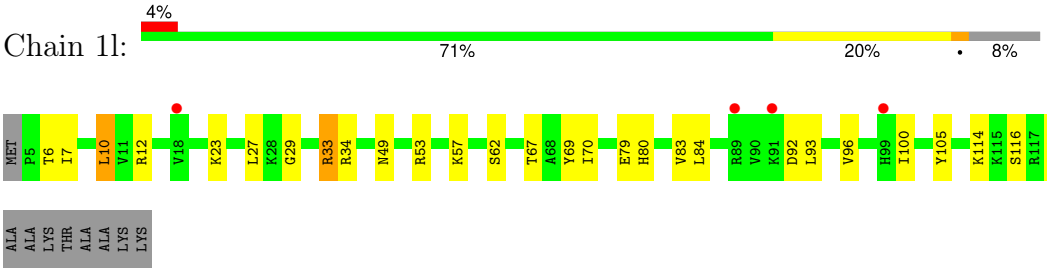
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



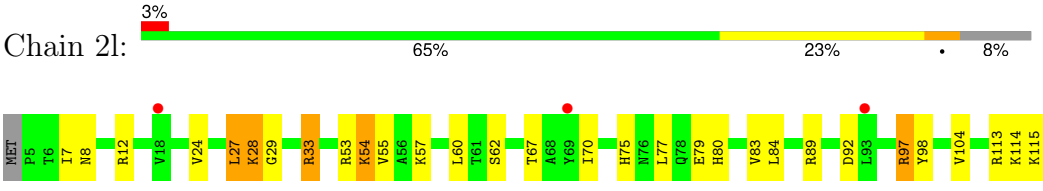
• Molecule 43: 30S ribosomal protein S12

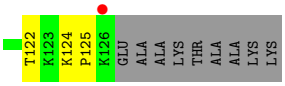
Chain 1l:



• Molecule 43: 30S ribosomal protein S12

Chain 2l:

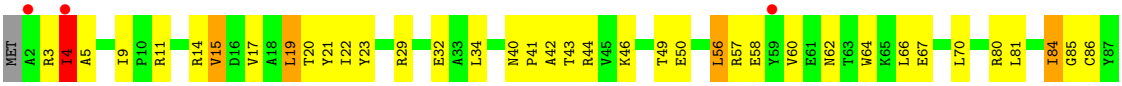


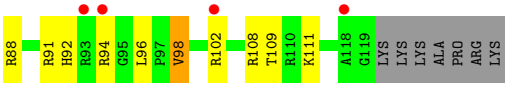


• Molecule 44: 30S ribosomal protein S13

Chain 1m:



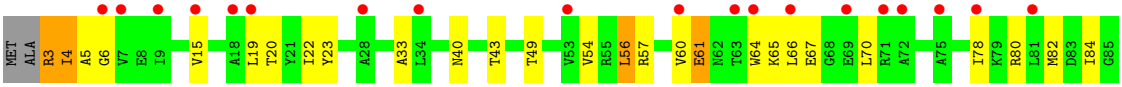


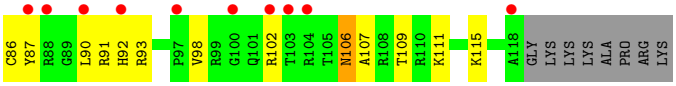


• Molecule 44: 30S ribosomal protein S13

Chain 2m:



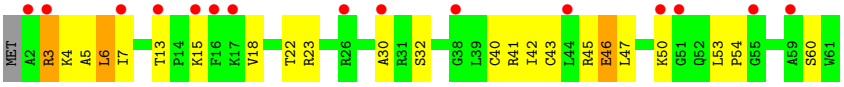




• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:

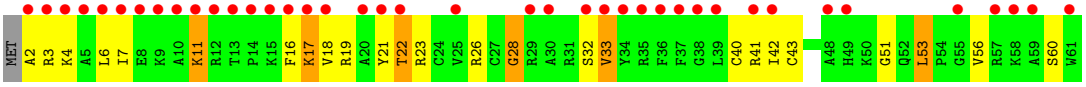




• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:

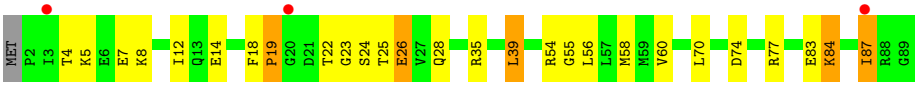




• Molecule 46: 30S ribosomal protein S15

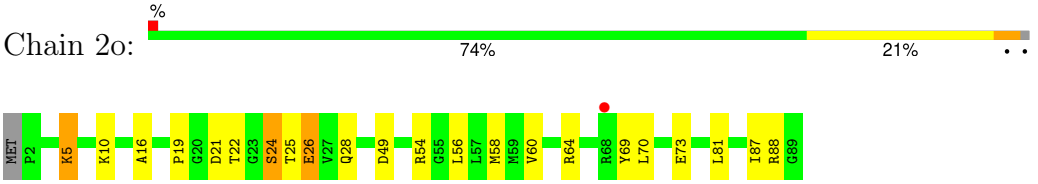
Chain 1o:





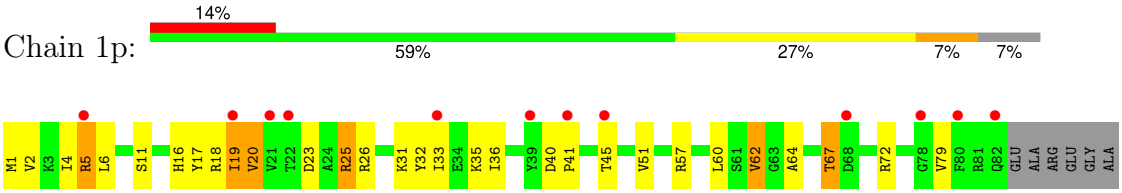
• Molecule 46: 30S ribosomal protein S15

Chain 2o:



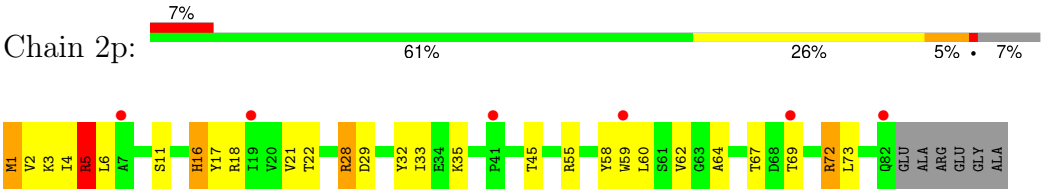
• Molecule 47: 30S ribosomal protein S16

Chain 1p:



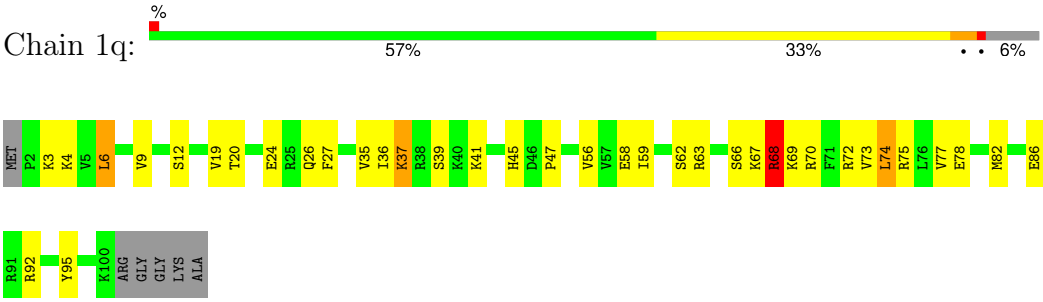
• Molecule 47: 30S ribosomal protein S16

Chain 2p:



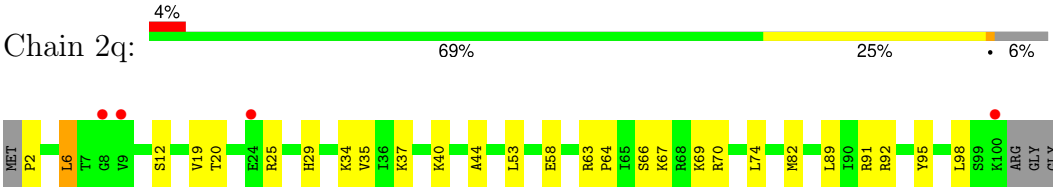
• Molecule 48: 30S ribosomal protein S17

Chain 1q:



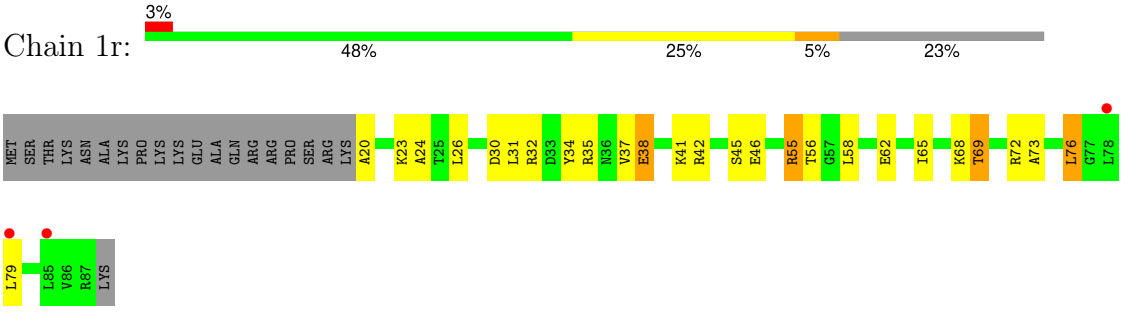
• Molecule 48: 30S ribosomal protein S17

Chain 2q:



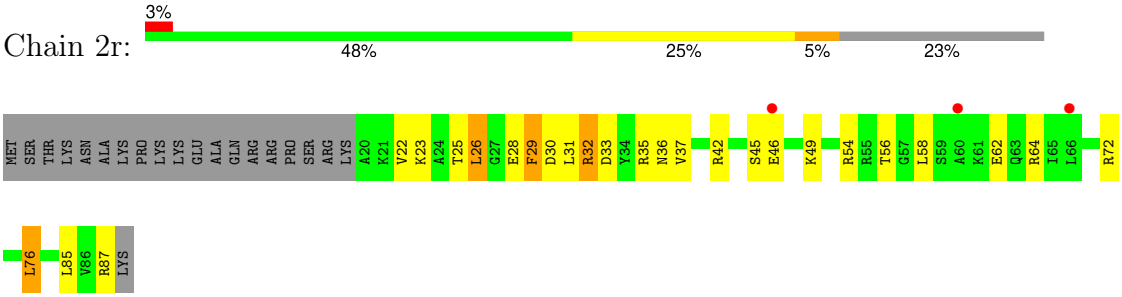
• Molecule 49: 30S ribosomal protein S18

Chain 1r:



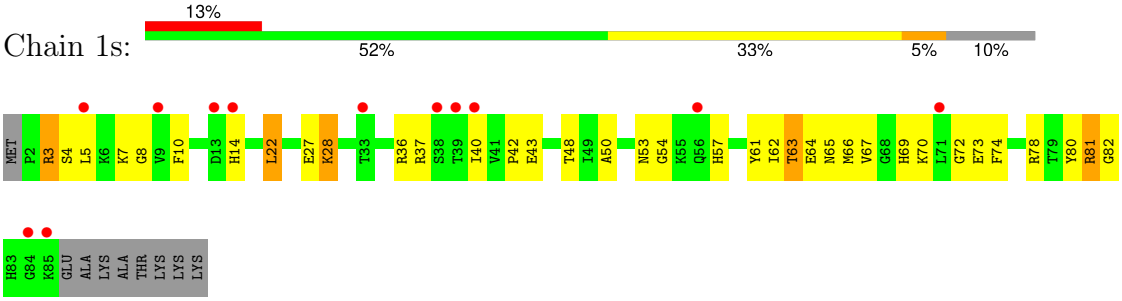
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



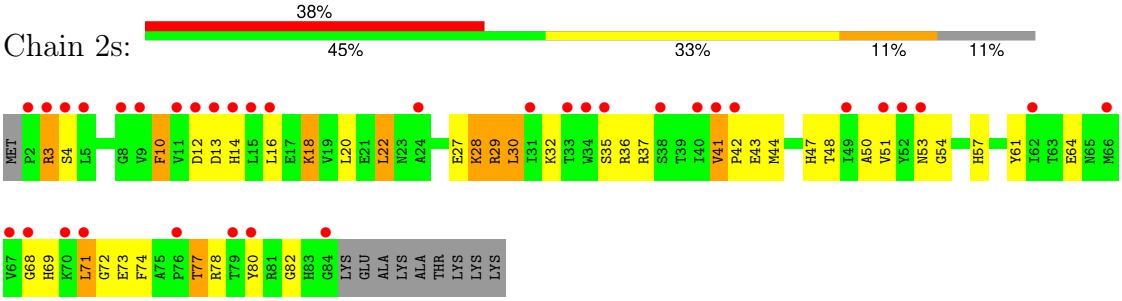
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



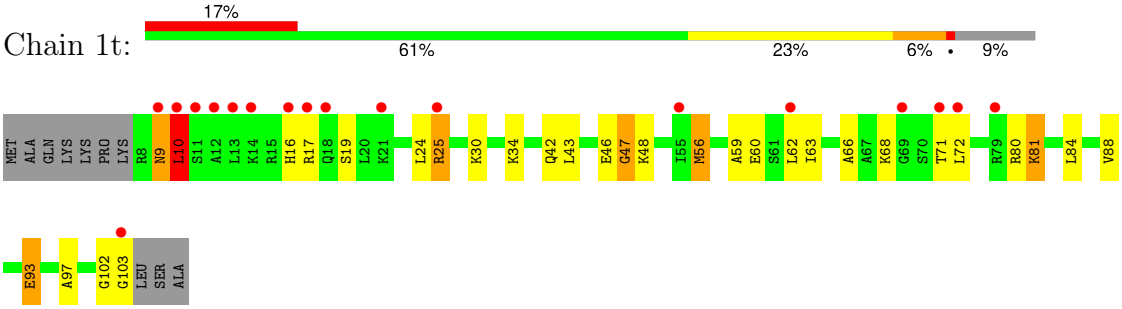
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



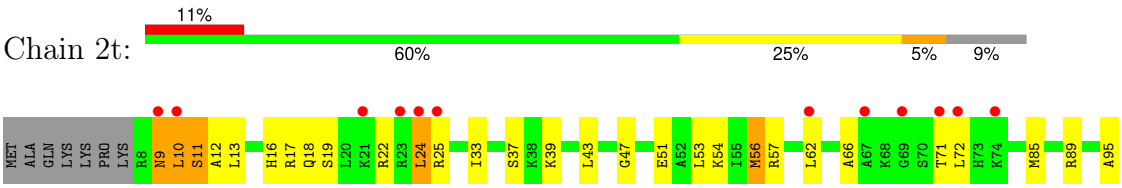
• Molecule 51: 30S ribosomal protein S20

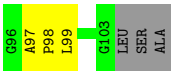
Chain 1t:



• Molecule 51: 30S ribosomal protein S20

Chain 2t:





• Molecule 52: 30S ribosomal protein Thx

Chain 1u:

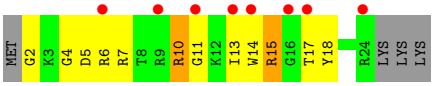




• Molecule 52: 30S ribosomal protein Thx

Chain 2u:

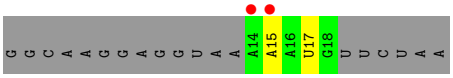




• Molecule 53: mRNA

Chain 1v:

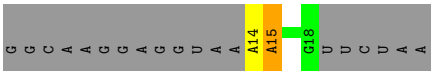




• Molecule 53: mRNA

Chain 2v:





• Molecule 54: P-site tRNA

Chain 1x:

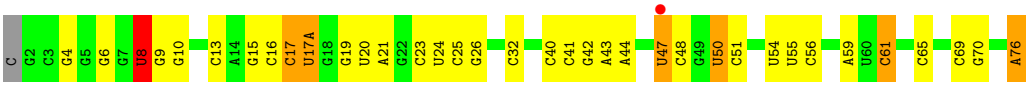




• Molecule 54: P-site tRNA

Chain 2x:

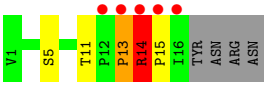




• Molecule 55: Pyrrhocoricin

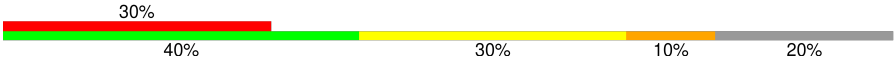
Chain 1z:





• Molecule 55: Pyrrhocoricin

Chain 2z:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	210.01Å 450.12Å 622.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.69 – 2.70 49.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.69-2.70) 99.4 (49.69-2.70)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.14 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.220 , 0.272 0.220 , 0.271	Depositor DCC
R_{free} test set	79488 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	54.9	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 55.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	288775	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SF4, 5MU, PSU, 4SU, 5MC, ZN, MG

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	1A	0.32	0/66249	0.47	1/103407 (0.0%)
1	2A	0.25	0/67298	0.44	1/105044 (0.0%)
2	1B	0.24	0/2877	0.39	0/4488
2	2B	0.27	0/2878	0.43	0/4490
3	1D	0.52	0/2186	0.89	1/2944 (0.0%)
3	2D	0.45	0/2192	0.88	3/2951 (0.1%)
4	1E	0.54	0/1592	0.92	4/2149 (0.2%)
4	2E	0.45	0/1592	0.90	2/2149 (0.1%)
5	1F	0.52	0/1619	0.91	5/2193 (0.2%)
5	2F	0.43	0/1615	0.93	3/2188 (0.1%)
6	1G	0.42	0/1450	0.89	4/1959 (0.2%)
6	2G	0.41	0/1449	0.98	5/1958 (0.3%)
7	1H	0.45	0/1356	0.89	0/1834
7	2H	0.45	0/1356	0.92	1/1834 (0.1%)
8	1I	0.42	0/1100	0.94	0/1501
8	2I	0.43	0/1076	0.95	4/1471 (0.3%)
9	1N	0.52	0/1144	0.84	0/1543
9	2N	0.41	0/1144	0.88	2/1543 (0.1%)
10	1O	0.54	0/943	0.84	0/1269
10	2O	0.44	0/943	0.88	0/1269
11	1P	0.49	0/1156	0.87	4/1537 (0.3%)
11	2P	0.42	0/1152	0.93	4/1533 (0.3%)
12	1Q	0.49	0/1143	0.82	0/1527
12	2Q	0.43	0/1143	0.89	0/1527
13	1R	0.55	0/982	0.86	0/1312
13	2R	0.42	0/982	0.79	0/1312
14	1S	0.47	0/887	0.83	0/1180
14	2S	0.41	0/880	0.89	1/1172 (0.1%)
15	1T	0.48	0/1105	0.84	0/1477
15	2T	0.39	0/1097	0.81	0/1468
16	1U	0.59	0/977	0.83	1/1301 (0.1%)
16	2U	0.44	0/977	0.81	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	1V	0.51	0/782	0.82	0/1049
17	2V	0.44	0/782	0.87	0/1049
18	1W	0.59	0/897	0.86	0/1205
18	2W	0.47	0/897	0.88	1/1205 (0.1%)
19	1X	0.48	0/764	0.85	0/1025
19	2X	0.41	0/764	0.90	2/1025 (0.2%)
20	1Y	0.46	0/819	0.89	1/1095 (0.1%)
20	2Y	0.40	0/819	0.90	1/1095 (0.1%)
21	1Z	0.43	0/1502	0.88	2/2041 (0.1%)
21	2Z	0.41	0/1486	0.90	4/2022 (0.2%)
22	10	0.47	0/606	0.86	0/808
22	20	0.40	0/606	0.81	0/808
23	11	0.47	0/762	0.78	0/1014
23	21	0.43	0/762	0.79	0/1014
24	12	0.50	0/590	0.80	0/781
24	22	0.37	0/590	0.75	0/781
25	13	0.52	0/474	0.88	0/635
25	23	0.40	0/469	0.95	0/630
26	14	0.42	0/571	0.98	3/768 (0.4%)
26	24	0.47	0/545	1.08	5/737 (0.7%)
27	15	0.57	0/469	0.91	2/635 (0.3%)
27	25	0.48	0/469	0.94	0/635
28	16	0.48	0/460	0.79	0/613
28	26	0.41	0/456	0.81	0/608
29	17	0.54	0/426	0.85	2/561 (0.4%)
29	27	0.48	0/426	0.82	2/561 (0.4%)
30	18	0.53	0/525	0.85	1/691 (0.1%)
30	28	0.45	0/525	0.87	0/691
31	19	0.52	0/310	0.81	0/407
31	29	0.37	0/310	0.91	0/407
32	1a	0.22	0/35537	0.40	0/55456
32	2a	0.20	0/35680	0.38	0/55681
33	1b	0.40	0/1820	0.97	5/2468 (0.2%)
33	2b	1.62	8/1728 (0.5%)	1.16	7/2352 (0.3%)
34	1c	0.39	0/1504	0.88	2/2047 (0.1%)
34	2c	0.43	0/1435	0.88	3/1960 (0.2%)
35	1d	0.39	0/1648	0.92	4/2222 (0.2%)
35	2d	0.40	0/1659	0.92	3/2230 (0.1%)
36	1e	0.41	0/1145	0.89	5/1543 (0.3%)
36	2e	0.41	0/1111	0.93	3/1504 (0.2%)
37	1f	0.38	0/819	0.75	0/1111
37	2f	0.40	0/830	0.80	0/1125
38	1g	0.37	0/1198	0.81	0/1613

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	2g	0.36	0/1185	0.82	0/1602
39	1h	0.39	0/1108	0.87	2/1494 (0.1%)
39	2h	0.37	0/1094	0.90	2/1478 (0.1%)
40	1i	0.38	0/995	0.87	0/1339
40	2i	0.42	0/949	0.84	0/1284
41	1j	0.43	0/695	0.97	2/950 (0.2%)
41	2j	0.44	0/690	1.01	5/943 (0.5%)
42	1k	0.41	0/840	0.89	1/1138 (0.1%)
42	2k	0.40	0/844	0.87	2/1145 (0.2%)
43	1l	0.41	0/936	0.86	0/1263
43	2l	0.43	0/934	0.89	2/1262 (0.2%)
44	1m	0.37	0/933	0.86	1/1254 (0.1%)
44	2m	0.43	0/913	0.85	0/1230
45	1n	0.38	0/491	0.99	2/653 (0.3%)
45	2n	0.38	0/467	0.91	1/624 (0.2%)
46	1o	0.42	0/726	0.98	2/970 (0.2%)
46	2o	0.37	0/739	0.85	0/985
47	1p	0.36	0/686	0.86	0/926
47	2p	0.39	0/693	0.84	1/935 (0.1%)
48	1q	0.38	0/824	0.84	0/1105
48	2q	0.36	0/836	0.88	2/1117 (0.2%)
49	1r	0.38	0/560	0.80	0/746
49	2r	0.35	0/560	0.81	0/746
50	1s	0.38	0/657	0.93	0/890
50	2s	0.44	0/661	0.97	2/893 (0.2%)
51	1t	0.39	0/714	0.98	1/948 (0.1%)
51	2t	0.38	0/733	0.88	1/969 (0.1%)
52	1u	0.32	0/191	0.71	0/252
52	2u	0.40	0/203	0.86	0/266
53	1v	0.35	0/122	0.65	0/188
53	2v	0.29	0/122	0.46	0/188
54	1x	0.28	0/1725	0.43	0/2689
54	2x	0.28	0/1725	0.43	0/2689
55	1z	0.61	0/131	1.18	2/180 (1.1%)
55	2z	0.69	0/131	1.24	0/180
All	All	0.35	8/306330 (0.0%)	0.59	135/458260 (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
5	2F	0	1
35	1d	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2b	92	TYR	CD1-CE1	29.49	2.27	1.38
33	2b	92	TYR	CD2-CE2	27.48	2.21	1.38
33	2b	151	GLY	N-CA	23.91	1.80	1.45
33	2b	92	TYR	CE1-CZ	22.53	1.92	1.38
33	2b	92	TYR	CE2-CZ	22.48	1.92	1.38
33	2b	92	TYR	CG-CD1	20.76	1.82	1.39
33	2b	92	TYR	CG-CD2	20.02	1.81	1.39
33	2b	150	SER	C-N	12.46	1.51	1.33

All (135) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	2b	150	SER	CA-C-N	17.98	156.66	121.41
33	2b	150	SER	C-N-CA	17.98	156.66	121.41
35	1d	10	ARG	N-CA-C	-13.64	96.51	113.97
33	2b	231	GLU	CA-C-N	12.39	133.22	119.83
33	2b	231	GLU	C-N-CA	12.39	133.22	119.83
35	2d	10	ARG	N-CA-C	-10.71	100.32	113.50
33	2b	151	GLY	N-CA-C	9.73	136.23	113.18
46	1o	23	GLY	N-CA-C	8.59	126.03	113.48
45	1n	13	THR	CA-C-N	7.95	127.90	120.03
45	1n	13	THR	C-N-CA	7.95	127.90	120.03
55	1z	14	ARG	CA-C-N	7.82	129.62	119.84
55	1z	14	ARG	C-N-CA	7.82	129.62	119.84
6	1G	31	VAL	CA-C-N	7.65	128.12	119.93
6	1G	31	VAL	C-N-CA	7.65	128.12	119.93
39	2h	73	ASP	CA-C-N	7.60	128.25	120.04
39	2h	73	ASP	C-N-CA	7.60	128.25	120.04
1	1A	2013	G	C2'-C3'-O3'	7.35	120.52	109.50
44	1m	84	ILE	N-CA-C	7.20	118.00	110.72
6	2G	141	PHE	CA-C-N	7.17	126.43	118.97
6	2G	141	PHE	C-N-CA	7.17	126.43	118.97
45	2n	28	GLY	N-CA-C	-6.95	106.12	115.36
33	1b	193	ASP	CA-C-N	6.78	126.02	118.97
33	1b	193	ASP	C-N-CA	6.78	126.02	118.97
46	1o	87	ILE	N-CA-C	6.77	116.97	111.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	2G	44	GLY	N-CA-C	-6.76	106.37	115.36
11	2P	44	GLY	CA-C-N	6.72	133.79	121.70
11	2P	44	GLY	C-N-CA	6.72	133.79	121.70
41	2j	79	ARG	N-CA-C	-6.69	105.15	113.38
34	1c	72	LYS	CA-C-N	6.63	126.33	119.56
34	1c	72	LYS	C-N-CA	6.63	126.33	119.56
48	2q	29	HIS	CA-C-N	6.49	127.95	119.84
48	2q	29	HIS	C-N-CA	6.49	127.95	119.84
36	1e	105	VAL	CA-C-N	-6.45	113.05	119.56
36	1e	105	VAL	C-N-CA	-6.45	113.05	119.56
5	2F	24	LEU	CA-C-N	6.42	126.37	119.76
5	2F	24	LEU	C-N-CA	6.42	126.37	119.76
36	2e	105	VAL	CA-C-N	-6.35	113.26	119.87
36	2e	105	VAL	C-N-CA	-6.35	113.26	119.87
50	2s	82	GLY	N-CA-C	6.34	119.38	110.38
21	2Z	107	THR	CA-C-N	6.22	126.25	119.90
21	2Z	107	THR	C-N-CA	6.22	126.25	119.90
35	2d	171	GLY	CA-C-N	6.20	126.67	119.47
35	2d	171	GLY	C-N-CA	6.20	126.67	119.47
51	2t	11	SER	N-CA-C	-6.14	105.36	112.92
16	1U	9	VAL	N-CA-C	6.11	116.28	110.42
1	2A	2013	G	C2'-C3'-O3'	6.11	118.66	109.50
33	2b	152	PHE	N-CA-C	-6.08	105.90	113.38
41	1j	27	ALA	N-CA-C	-6.08	107.09	114.75
33	2b	114	ARG	N-CA-C	-5.99	106.61	114.04
5	1F	89	VAL	N-CA-C	5.97	116.18	110.74
26	14	40	HIS	CA-C-N	5.93	127.25	119.84
26	14	40	HIS	C-N-CA	5.93	127.25	119.84
34	2c	190	ARG	N-CA-C	5.92	118.10	108.63
11	2P	144	GLU	CA-C-N	5.91	126.37	119.99
11	2P	144	GLU	C-N-CA	5.91	126.37	119.99
26	24	61	ARG	N-CA-C	-5.90	104.43	111.69
5	1F	9	ILE	CA-C-N	5.86	126.16	119.83
5	1F	9	ILE	C-N-CA	5.86	126.16	119.83
5	1F	170	LEU	CA-C-N	5.86	125.72	119.28
5	1F	170	LEU	C-N-CA	5.86	125.72	119.28
6	2G	43	LEU	CB-CA-C	-5.80	109.86	116.54
29	27	6	GLN	CA-C-N	5.79	125.80	119.90
29	27	6	GLN	C-N-CA	5.79	125.80	119.90
11	1P	22	GLY	CA-C-N	5.75	125.12	118.85
11	1P	22	GLY	C-N-CA	5.75	125.12	118.85
4	1E	31	CYS	CA-C-N	5.69	125.88	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	1E	31	CYS	C-N-CA	5.69	125.88	119.90
3	1D	244	ARG	N-CA-C	-5.68	103.02	108.07
26	24	59	PHE	N-CA-C	5.67	117.84	108.49
19	2X	31	HIS	CA-C-N	5.63	125.73	119.32
19	2X	31	HIS	C-N-CA	5.63	125.73	119.32
42	1k	40	ILE	N-CA-C	-5.61	107.35	111.90
20	1Y	92	ASN	N-CA-C	5.61	117.40	111.28
6	1G	43	LEU	CB-CA-C	-5.61	110.09	116.54
26	14	52	THR	N-CA-C	-5.61	106.11	113.17
33	1b	228	GLY	N-CA-C	5.60	118.47	110.46
41	2j	98	ILE	N-CA-C	5.60	115.75	108.35
4	1E	52	LEU	CA-C-N	5.59	125.35	119.76
4	1E	52	LEU	C-N-CA	5.59	125.35	119.76
4	2E	21	VAL	CA-C-N	5.57	125.85	119.83
4	2E	21	VAL	C-N-CA	5.57	125.85	119.83
43	2l	29	GLY	N-CA-C	-5.57	97.14	113.30
36	1e	95	ALA	CA-C-N	5.57	126.80	119.84
36	1e	95	ALA	C-N-CA	5.57	126.80	119.84
5	2F	79	GLY	N-CA-C	-5.53	108.07	115.32
20	2Y	91	GLU	N-CA-C	-5.52	106.04	112.89
35	1d	33	MET	N-CA-C	-5.50	105.37	111.36
34	2c	78	GLY	N-CA-C	5.49	117.44	110.20
34	2c	130	VAL	N-CA-C	5.48	115.68	110.42
41	1j	28	ARG	N-CA-C	-5.47	105.86	112.54
26	24	53	GLU	N-CA-C	-5.47	106.97	113.97
42	2k	38	ASN	CA-C-N	5.46	125.39	119.76
42	2k	38	ASN	C-N-CA	5.46	125.39	119.76
21	2Z	132	ASN	CA-C-N	-5.45	118.89	122.60
21	2Z	132	ASN	C-N-CA	-5.45	118.89	122.60
11	1P	7	ARG	CA-C-N	-5.42	115.00	120.31
11	1P	7	ARG	C-N-CA	-5.42	115.00	120.31
36	1e	71	LEU	N-CA-C	5.42	117.07	110.41
30	18	38	GLY	N-CA-C	-5.39	106.15	113.37
41	2j	52	GLY	CA-C-N	5.38	125.07	119.64
41	2j	52	GLY	C-N-CA	5.38	125.07	119.64
33	1b	42	ILE	N-CA-C	5.36	115.97	108.89
43	2l	119	LYS	N-CA-C	-5.32	103.00	110.50
8	2I	110	ASP	CA-C-N	5.25	124.70	119.24
8	2I	110	ASP	C-N-CA	5.25	124.70	119.24
51	1t	93	GLU	N-CA-C	-5.22	106.88	113.20
21	1Z	107	THR	CA-C-N	5.20	126.34	119.84
21	1Z	107	THR	C-N-CA	5.20	126.34	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	1h	4	ASP	CA-C-N	5.20	124.38	118.97
39	1h	4	ASP	C-N-CA	5.20	124.38	118.97
6	2G	48	GLU	N-CA-C	-5.20	107.11	113.50
3	2D	244	ARG	CA-C-N	-5.19	115.03	120.38
3	2D	244	ARG	C-N-CA	-5.19	115.03	120.38
18	2W	103	ILE	N-CA-C	5.17	115.54	107.99
26	24	40	HIS	CA-C-N	5.17	126.30	119.84
26	24	40	HIS	C-N-CA	5.17	126.30	119.84
27	15	26	THR	CA-C-N	5.16	123.42	119.66
27	15	26	THR	C-N-CA	5.16	123.42	119.66
33	1b	114	ARG	N-CA-C	-5.15	107.66	114.04
29	17	6	GLN	CA-C-N	5.14	125.14	119.90
29	17	6	GLN	C-N-CA	5.14	125.14	119.90
36	2e	35	GLY	N-CA-C	5.14	119.09	110.56
50	2s	10	PHE	N-CA-C	5.14	117.11	109.25
6	1G	96	ARG	CB-CA-C	-5.12	110.65	116.54
9	2N	125	GLY	CA-C-N	5.11	125.18	119.87
9	2N	125	GLY	C-N-CA	5.11	125.18	119.87
14	2S	40	ILE	N-CA-C	5.09	115.90	108.53
35	1d	171	GLY	CA-C-N	5.08	126.18	119.84
35	1d	171	GLY	C-N-CA	5.08	126.18	119.84
8	2I	133	HIS	CA-C-N	5.05	125.04	119.89
8	2I	133	HIS	C-N-CA	5.05	125.04	119.89
41	2j	27	ALA	N-CA-C	-5.03	108.88	114.62
47	2p	5	ARG	N-CA-C	5.02	114.78	108.45
3	2D	251	GLY	N-CA-C	5.02	119.66	113.79
7	2H	113	VAL	N-CA-C	5.01	115.12	108.11

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
35	1d	9	CYS	Peptide
5	2F	20	LEU	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	59154	0	29828	564	0
1	2A	60091	0	30297	814	0
2	1B	2572	0	1306	21	0
2	2B	2573	0	1306	53	0
3	1D	2136	0	2218	54	0
3	2D	2142	0	2229	67	0
4	1E	1559	0	1618	32	0
4	2E	1559	0	1618	44	0
5	1F	1584	0	1625	31	0
5	2F	1580	0	1619	50	0
6	1G	1425	0	1443	24	0
6	2G	1424	0	1434	66	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	28	0
8	1I	1085	0	1114	27	0
8	2I	1061	0	1080	20	0
9	1N	1117	0	1184	15	0
9	2N	1117	0	1184	17	0
10	1O	933	0	996	18	0
10	2O	933	0	996	22	0
11	1P	1139	0	1223	27	0
11	2P	1135	0	1212	47	0
12	1Q	1122	0	1178	26	0
12	2Q	1122	0	1179	27	0
13	1R	968	0	1033	12	0
13	2R	968	0	1033	18	0
14	1S	877	0	938	27	0
14	2S	870	0	923	25	0
15	1T	1091	0	1151	34	0
15	2T	1083	0	1136	28	0
16	1U	959	0	1019	12	0
16	2U	959	0	1018	23	0
17	1V	771	0	830	9	0
17	2V	771	0	830	16	0
18	1W	886	0	940	9	0
18	2W	886	0	940	20	0
19	1X	750	0	814	18	0
19	2X	750	0	814	21	0
20	1Y	806	0	881	19	0
20	2Y	806	0	881	22	0
21	1Z	1470	0	1478	27	0
21	2Z	1454	0	1452	44	0
22	10	598	0	614	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	20	598	0	614	13	0
23	11	755	0	826	11	0
23	21	755	0	826	18	0
24	12	588	0	643	11	0
24	22	588	0	643	9	0
25	13	469	0	518	6	0
25	23	464	0	514	15	0
26	14	558	0	544	26	0
26	24	532	0	503	25	0
27	15	455	0	465	6	0
27	25	455	0	465	13	0
28	16	453	0	473	8	0
28	26	449	0	469	10	0
29	17	418	0	467	13	0
29	27	418	0	467	10	0
30	18	517	0	582	13	0
30	28	517	0	582	19	0
31	19	307	0	335	10	0
31	29	307	0	335	14	0
32	1a	31750	0	16028	478	0
32	2a	31877	0	16089	577	0
33	1b	1786	0	1744	67	0
33	2b	1697	0	1574	115	0
34	1c	1480	0	1400	42	0
34	2c	1412	0	1246	41	0
35	1d	1618	0	1579	47	0
35	2d	1630	0	1633	63	0
36	1e	1129	0	1185	33	0
36	2e	1095	0	1124	38	0
37	1f	806	0	793	19	0
37	2f	817	0	808	18	0
38	1g	1183	0	1165	23	0
38	2g	1167	0	1119	30	0
39	1h	1088	0	1126	26	0
39	2h	1074	0	1100	23	0
40	1i	976	0	973	31	0
40	2i	932	0	891	37	0
41	1j	682	0	598	23	0
41	2j	678	0	612	29	0
42	1k	826	0	829	23	0
42	2k	829	0	825	16	0
43	1l	920	0	958	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	2l	918	0	947	27	0
44	1m	923	0	962	35	0
44	2m	903	0	923	32	0
45	1n	482	0	507	24	0
45	2n	459	0	467	30	0
46	1o	715	0	729	16	0
46	2o	728	0	760	13	0
47	1p	671	0	679	18	0
47	2p	677	0	686	17	0
48	1q	811	0	858	26	0
48	2q	823	0	891	19	0
49	1r	555	0	618	17	0
49	2r	555	0	618	22	0
50	1s	642	0	629	34	0
50	2s	646	0	644	37	0
51	1t	712	0	759	19	0
51	2t	731	0	807	18	0
52	1u	187	0	186	10	0
52	2u	199	0	208	9	0
53	1v	109	0	55	1	0
53	2v	109	0	55	1	0
54	1x	1625	0	829	14	0
54	2x	1625	0	829	17	0
55	1z	126	0	135	3	0
55	2z	126	0	135	3	0
56	10	7	0	0	0	0
56	11	3	0	0	0	0
56	12	1	0	0	0	0
56	13	1	0	0	0	0
56	15	4	0	0	0	0
56	16	2	0	0	0	0
56	17	3	0	0	0	0
56	18	5	0	0	0	0
56	19	3	0	0	0	0
56	1A	1233	0	0	0	0
56	1B	25	0	0	0	0
56	1D	15	0	0	0	0
56	1E	8	0	0	0	0
56	1F	9	0	0	0	0
56	1G	3	0	0	0	0
56	1H	1	0	0	0	0
56	1N	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1O	3	0	0	0	0
56	1P	5	0	0	0	0
56	1Q	5	0	0	0	0
56	1R	8	0	0	0	0
56	1T	4	0	0	0	0
56	1U	6	0	0	0	0
56	1V	2	0	0	0	0
56	1W	6	0	0	0	0
56	1X	1	0	0	0	0
56	1Y	1	0	0	0	0
56	1Z	3	0	0	0	0
56	1a	295	0	0	0	0
56	1b	2	0	0	0	0
56	1d	1	0	0	0	0
56	1e	3	0	0	0	0
56	1f	1	0	0	0	0
56	1h	2	0	0	0	0
56	1k	2	0	0	0	0
56	1l	1	0	0	0	0
56	1n	1	0	0	0	0
56	1o	1	0	0	0	0
56	1p	1	0	0	0	0
56	1q	2	0	0	0	0
56	1r	2	0	0	0	0
56	1t	1	0	0	0	0
56	1x	12	0	0	0	0
56	20	1	0	0	0	0
56	23	1	0	0	0	0
56	25	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	592	0	0	0	0
56	2B	9	0	0	0	0
56	2D	6	0	0	0	0
56	2E	6	0	0	0	0
56	2F	2	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	3	0	0	0	0
56	2Q	5	0	0	0	0
56	2X	1	0	0	0	0
56	2Y	1	0	0	0	0
56	2Z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2a	248	0	0	1	0
56	2d	1	0	0	0	0
56	2e	2	0	0	0	0
56	2f	1	0	0	0	0
56	2l	5	0	0	0	0
56	2n	1	0	0	0	0
56	2p	1	0	0	0	0
56	2q	2	0	0	0	0
56	2t	1	0	0	0	0
56	2u	1	0	0	0	0
56	2x	4	0	0	0	0
57	14	1	0	0	0	0
57	15	1	0	0	0	0
57	16	1	0	0	0	0
57	19	1	0	0	0	0
57	1Y	1	0	0	0	0
57	1n	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0
57	29	1	0	0	0	0
57	2Y	1	0	0	0	0
57	2n	1	0	0	0	0
58	1d	8	0	0	2	0
58	2d	8	0	0	6	0
59	10	12	0	0	0	0
59	11	5	0	0	0	0
59	12	3	0	0	0	0
59	13	4	0	0	1	0
59	15	9	0	0	0	0
59	16	9	0	0	3	0
59	17	10	0	0	1	0
59	18	12	0	0	1	0
59	19	2	0	0	0	0
59	1A	2217	0	0	121	0
59	1B	37	0	0	4	0
59	1D	23	0	0	1	0
59	1E	29	0	0	4	0
59	1F	19	0	0	1	0
59	1G	2	0	0	0	0
59	1H	4	0	0	0	0
59	1I	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	1N	6	0	0	2	0
59	1O	7	0	0	0	0
59	1P	27	0	0	0	0
59	1Q	14	0	0	0	0
59	1R	11	0	0	0	0
59	1S	2	0	0	0	0
59	1T	13	0	0	4	0
59	1U	14	0	0	0	0
59	1V	7	0	0	0	0
59	1W	8	0	0	0	0
59	1X	5	0	0	0	0
59	1Y	1	0	0	0	0
59	1Z	7	0	0	0	0
59	1a	338	0	0	28	0
59	1b	2	0	0	0	0
59	1d	3	0	0	0	0
59	1e	7	0	0	0	0
59	1f	1	0	0	0	0
59	1h	3	0	0	0	0
59	1i	1	0	0	0	0
59	1j	1	0	0	0	0
59	1k	1	0	0	0	0
59	1l	3	0	0	1	0
59	1m	1	0	0	0	0
59	1o	1	0	0	0	0
59	1q	1	0	0	0	0
59	1r	1	0	0	0	0
59	1s	2	0	0	2	0
59	1t	1	0	0	0	0
59	1v	3	0	0	0	0
59	1x	9	0	0	1	0
59	20	4	0	0	0	0
59	21	1	0	0	0	0
59	23	1	0	0	0	0
59	25	1	0	0	0	0
59	27	1	0	0	0	0
59	28	4	0	0	0	0
59	2A	809	0	0	86	0
59	2B	12	0	0	1	0
59	2D	20	0	0	1	0
59	2E	11	0	0	1	0
59	2F	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	2N	1	0	0	0	0
59	2O	3	0	0	0	0
59	2P	3	0	0	1	0
59	2Q	2	0	0	0	0
59	2R	3	0	0	0	0
59	2T	3	0	0	0	0
59	2U	3	0	0	1	0
59	2W	1	0	0	0	0
59	2X	2	0	0	1	0
59	2Y	1	0	0	1	0
59	2Z	6	0	0	2	0
59	2a	274	0	0	38	0
59	2c	2	0	0	4	0
59	2d	1	0	0	0	0
59	2i	2	0	0	0	0
59	2j	2	0	0	0	0
59	2l	2	0	0	0	0
59	2p	1	0	0	0	0
59	2t	3	0	0	0	0
59	2v	1	0	0	0	0
59	2x	2	0	0	1	0
All	All	288775	0	190012	4404	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 10.

All (4404) 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)
33:2b:92:TYR:CD1	33:2b:92:TYR:CG	1.83	1.62
33:2b:92:TYR:CG	33:2b:92:TYR:CD2	1.81	1.57
33:2b:92:TYR:CZ	33:2b:92:TYR:CE2	1.92	1.57
33:2b:92:TYR:CZ	33:2b:92:TYR:CE1	1.92	1.53
33:2b:151:GLY:N	33:2b:151:GLY:CA	1.80	1.44
33:2b:92:TYR:CZ	33:2b:151:GLY:N	1.89	1.37
33:2b:92:TYR:CE2	33:2b:151:GLY:N	1.90	1.36
33:2b:92:TYR:CE1	33:2b:151:GLY:N	1.96	1.34
33:2b:92:TYR:CD2	33:2b:92:TYR:CE2	2.21	1.29
33:2b:92:TYR:CD2	33:2b:151:GLY:N	2.03	1.26
33:2b:92:TYR:CD1	33:2b:92:TYR:CE1	2.27	1.21
33:2b:92:TYR:CD1	33:2b:151:GLY:N	2.11	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:981:G:H1	32:2a:1021:C:N4	1.43	1.17
33:2b:92:TYR:CG	33:2b:151:GLY:HA3	1.83	1.14
33:2b:92:TYR:CG	33:2b:151:GLY:N	2.19	1.09
33:2b:92:TYR:CD1	33:2b:151:GLY:CA	2.36	1.09
32:2a:1112:C:N4	32:2a:1126:G:H1	1.55	1.04
33:2b:92:TYR:CG	33:2b:151:GLY:CA	2.41	1.03
32:2a:1112:C:H42	32:2a:1126:G:H1	1.04	1.00
33:2b:92:TYR:CD2	33:2b:151:GLY:CA	2.48	0.96
15:2T:55:ASN:H	15:2T:59:THR:HG22	1.30	0.96
32:2a:975:U:H3	32:2a:1027:A:H61	1.06	0.96
1:1A:353:A:H2	1:1A:1254:A:HO2'	0.98	0.95
33:2b:13:ALA:HA	33:2b:15:VAL:H	1.31	0.94
32:2a:1116:G:H1	32:2a:1124:C:H42	1.12	0.93
33:2b:92:TYR:CE1	33:2b:151:GLY:CA	2.52	0.93
1:1A:1404:A:H61	1:1A:1417:U:H3	1.16	0.93
1:1A:786:U:OP2	59:1A:4301:HOH:O	1.88	0.92
32:2a:981:G:N2	32:2a:1021:C:N3	2.16	0.92
1:2A:183:A:N7	59:2A:3605:HOH:O	2.04	0.90
1:1A:2510:C:OP1	59:1A:4302:HOH:O	1.88	0.90
32:1a:77:G:H1	32:1a:87:C:N4	1.70	0.90
32:1a:1480:A:H2	32:1a:1483:G:H1	1.18	0.89
33:2b:92:TYR:CD1	33:2b:150:SER:C	2.50	0.89
1:1A:1735:A:H62	1:1A:1744:A:H2	1.20	0.89
32:2a:900:G:H4'	36:2e:20:GLN:HA	1.55	0.88
32:1a:1298:G:H22	32:1a:1301:A:H5"	1.35	0.88
32:2a:977:C:H42	32:2a:1025:G:H1	1.19	0.87
32:1a:143:G:H1	32:1a:169:C:H42	1.24	0.86
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.41	0.86
32:1a:402:G:H5'	35:1d:5:ILE:HD11	1.55	0.86
33:2b:92:TYR:CD1	33:2b:151:GLY:HA2	2.12	0.85
33:2b:92:TYR:CG	33:2b:150:SER:C	2.55	0.85
21:2Z:130:PRO:HB2	21:2Z:131:ARG:HH21	1.40	0.85
32:1a:77:G:H1	32:1a:87:C:H42	0.85	0.85
32:2a:648:G:H22	32:2a:725:G:H1	1.23	0.85
32:2a:976:G:H1	32:2a:1026:C:H42	1.24	0.85
1:1A:776:C:OP2	59:1A:4303:HOH:O	1.94	0.85
33:2b:92:TYR:CE1	33:2b:151:GLY:HA2	2.12	0.84
1:2A:2831:G:OP2	59:2A:3601:HOH:O	1.96	0.84
32:2a:1038:A:N7	32:2a:1182:C:N4	2.26	0.84
32:2a:543:A:H4'	32:2a:544:U:H3'	1.60	0.84
32:2a:1116:G:H1	32:2a:1124:C:N4	1.74	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:621:G:N7	59:2A:3616:HOH:O	2.11	0.83
1:2A:1828:U:H5'	3:2D:259:THR:HG22	1.60	0.83
35:1d:30:LYS:HA	35:1d:35:ARG:HE	1.44	0.83
32:1a:1397:U:H3	32:1a:1464:G:H1	1.27	0.82
1:1A:893:U:O4	1:1A:977:A:N6	2.12	0.82
35:1d:53:ASP:HB3	35:1d:57:ARG:HH12	1.43	0.82
32:1a:262:G:H5"	32:1a:264:C:H41	1.45	0.82
32:2a:1125:G:H3'	32:2a:1126:G:H8	1.45	0.82
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.60	0.82
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.61	0.81
1:1A:1647:U:O4	59:1A:4304:HOH:O	1.97	0.81
32:2a:1112:C:N3	32:2a:1126:G:N2	2.27	0.81
32:2a:1263:U:H5"	32:2a:1264:C:H5	1.46	0.81
54:1x:47:U:H4'	54:1x:48:C:H5'	1.60	0.81
33:2b:92:TYR:CE2	33:2b:151:GLY:CA	2.63	0.81
32:2a:917:G:HO2'	32:2a:1358:A:HO2'	1.28	0.81
50:2s:22:LEU:HB3	50:2s:27:GLU:HG3	1.62	0.81
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.63	0.81
1:1A:2298:A:H62	1:1A:2355:U:H3	1.29	0.80
36:2e:36:ASP:O	36:2e:38:GLN:N	2.13	0.80
6:2G:33:ARG:HH11	6:2G:33:ARG:HB2	1.45	0.80
33:2b:92:TYR:CZ	33:2b:151:GLY:CA	2.65	0.80
21:2Z:134:PRO:O	21:2Z:136:PHE:N	2.15	0.80
29:17:24:THR:HG22	29:17:27:GLY:H	1.46	0.80
1:2A:1098:C:H42	1:2A:1151:G:H1	1.28	0.79
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.64	0.79
32:2a:975:U:H3	32:2a:1027:A:N6	1.79	0.79
33:2b:92:TYR:CD2	33:2b:150:SER:C	2.59	0.79
1:1A:829:A:OP2	59:1A:4305:HOH:O	1.99	0.79
1:1A:2330:G:N7	59:1A:4339:HOH:O	2.14	0.79
1:1A:893:U:OP2	59:1A:4306:HOH:O	1.99	0.79
1:1A:1066:A:H62	1:1A:1185:U:H3	1.31	0.78
2:2B:20:C:H42	2:2B:63:G:H1	1.31	0.78
10:2O:48:PRO:HB3	32:2a:1405:G:H5"	1.65	0.78
1:1A:426:G:N7	59:1A:4346:HOH:O	2.15	0.78
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.49	0.78
32:1a:77:G:N2	32:1a:87:C:N3	2.32	0.78
32:1a:507:A:H61	43:1l:92:ASP:HB2	1.48	0.78
1:1A:807:A:OP1	59:1A:4303:HOH:O	2.02	0.77
32:1a:1171:C:OP1	41:1j:51:ARG:NH2	2.17	0.77
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.17	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:62:LEU:HD23	17:2V:93:GLU:HG2	1.66	0.77
32:2a:36:G:O2'	43:2l:118:SER:O	2.01	0.77
1:2A:2441:A:OP2	59:2A:3603:HOH:O	2.01	0.77
32:2a:932:G:H21	32:2a:1209:A:H62	1.32	0.77
4:2E:132:HIS:NE2	59:2E:401:HOH:O	2.17	0.76
32:2a:386:C:O3'	47:2p:28:ARG:NH2	2.18	0.76
1:1A:1355:G:OP2	29:17:9:ARG:NH1	2.18	0.76
22:10:11:ARG:O	22:10:14:ARG:NH2	2.19	0.76
36:1e:78:HIS:HD1	39:1h:104:ARG:HD3	1.50	0.76
1:1A:1828:U:H5'	3:1D:259:THR:HG22	1.66	0.76
1:2A:1355:G:OP2	29:27:9:ARG:NH1	2.19	0.76
1:2A:1735:A:H62	1:2A:1744:A:H2	1.32	0.76
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.68	0.76
32:2a:1238:A:N6	32:2a:1260:U:O2	2.19	0.76
32:1a:65:G:O6	32:1a:94:C:N4	2.17	0.76
1:1A:1000:G:O6	59:1A:4309:HOH:O	2.04	0.76
1:1A:1377:G:OP1	59:1A:4307:HOH:O	2.02	0.76
32:2a:929:G:N2	32:2a:948:C:O2	2.19	0.76
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.19	0.76
1:1A:1619:G:OP2	59:1A:4310:HOH:O	2.04	0.75
1:1A:2111:G:O6	59:1A:4308:HOH:O	2.03	0.75
1:2A:1404:A:N6	1:2A:1417:U:O4	2.16	0.75
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.18	0.75
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.19	0.75
1:1A:474:A:N7	59:1A:4361:HOH:O	2.18	0.75
1:1A:655:A:OP1	11:1P:65:ARG:NH1	2.20	0.75
1:2A:2816:G:N1	1:2A:2901:G:O6	2.18	0.75
1:1A:550:A:OP1	59:1A:4311:HOH:O	2.05	0.75
32:1a:543:A:OP1	36:1e:126:ARG:NH2	2.16	0.75
44:1m:84:ILE:HG13	44:1m:85:GLY:HA2	1.69	0.75
44:2m:60:VAL:HG23	44:2m:64:TRP:HE3	1.51	0.75
1:2A:1989:G:OP1	59:2A:3604:HOH:O	2.04	0.75
33:2b:92:TYR:CE1	33:2b:150:SER:C	2.64	0.75
1:2A:1214:G:H1	1:2A:1224:C:H42	1.32	0.74
32:2a:953:A:H4'	32:2a:954:G:H5"	1.68	0.74
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.20	0.74
1:2A:2626:U:OP1	59:2A:3606:HOH:O	2.05	0.74
1:1A:830:A:OP2	59:1A:4305:HOH:O	2.03	0.74
32:1a:423:U:OP1	35:1d:13:ARG:NH2	2.19	0.74
32:2a:488:C:OP1	59:2a:3303:HOH:O	2.06	0.74
32:2a:936:A:N6	50:2s:77:THR:O	2.19	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2x:47:U:H4'	54:2x:48:C:H5'	1.69	0.74
32:1a:953:A:H4'	32:1a:954:G:H5"	1.69	0.74
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.69	0.74
15:1T:51:ARG:NH1	59:1T:301:HOH:O	2.13	0.74
1:1A:1360:C:OP2	59:1A:4307:HOH:O	2.05	0.74
1:2A:900:G:H2'	1:2A:901:G:H8	1.52	0.74
1:2A:1056:G:OP2	16:2U:66:ASN:ND2	2.20	0.74
1:2A:1830:C:OP2	3:2D:183:ARG:NH2	2.21	0.74
32:2a:348:C:OP2	59:2a:3302:HOH:O	2.05	0.74
32:2a:1033:G:OP2	59:2a:3305:HOH:O	2.06	0.74
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.70	0.74
47:2p:4:ILE:HG12	47:2p:21:VAL:HG12	1.69	0.74
32:1a:796:C:O2	59:1a:1901:HOH:O	2.05	0.74
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.21	0.74
32:2a:571:G:OP2	59:2a:3301:HOH:O	2.05	0.74
1:1A:1354:G:H4'	29:17:7:PRO:HB2	1.68	0.73
3:2D:276:LYS:HD3	3:2D:276:LYS:H	1.50	0.73
1:1A:894:G:OP1	59:1A:4315:HOH:O	2.06	0.73
1:2A:1248:A:H2	1:2A:1286:A:H62	1.33	0.73
1:1A:1846:G:O6	3:1D:35:LYS:NZ	2.16	0.73
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.69	0.73
1:1A:1461:G:N2	1:1A:1628:C:O2	2.16	0.73
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.20	0.73
32:2a:640:C:O2'	46:2o:28:GLN:NE2	2.21	0.73
42:2k:48:ILE:O	42:2k:50:TYR:N	2.21	0.73
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.52	0.73
1:2A:1066:A:H62	1:2A:1185:U:H3	1.32	0.73
1:2A:2053:G:N7	59:2A:3665:HOH:O	2.22	0.73
32:2a:59:C:O2'	32:2a:384:G:N7	2.21	0.73
32:2a:307:C:OP1	59:2a:3306:HOH:O	2.07	0.73
32:1a:1242:C:O2'	59:1a:1903:HOH:O	2.07	0.73
1:2A:1649:C:OP2	59:2A:3609:HOH:O	2.06	0.73
32:2a:111:G:OP2	59:2a:3304:HOH:O	2.06	0.73
1:2A:655:A:OP1	11:2P:65:ARG:NH1	2.22	0.73
1:2A:2517:U:OP1	4:2E:144:ARG:NH2	2.21	0.73
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.71	0.72
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.21	0.72
32:1a:60:A:H3'	32:1a:327:G:H22	1.54	0.72
35:1d:9:CYS:HB3	58:1d:501:SF4:S2	2.28	0.72
1:2A:2858:U:OP2	15:2T:95:ARG:NH1	2.22	0.72
20:2Y:49:VAL:HG21	20:2Y:61:ILE:HG23	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.22	0.72
1:1A:1075:G:OP2	12:1Q:128:LYS:NZ	2.22	0.72
1:1A:2441:A:OP2	59:1A:4312:HOH:O	2.06	0.72
33:2b:92:TYR:CD2	33:2b:151:GLY:HA3	2.22	0.72
1:1A:909:A:OP2	59:1A:4313:HOH:O	2.06	0.72
1:1A:1035:A:OP2	59:1A:4320:HOH:O	2.08	0.72
32:1a:640:C:O2'	46:1o:28:GLN:NE2	2.21	0.72
1:2A:396:G:OP2	59:2A:3608:HOH:O	2.06	0.72
1:2A:2694:C:OP1	15:2T:53:ARG:NH2	2.21	0.72
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.70	0.72
1:2A:816:G:OP2	59:2A:3610:HOH:O	2.07	0.72
1:2A:1064:U:H3	1:2A:1187:A:H62	1.36	0.72
32:2a:717:A:OP2	59:2a:3308:HOH:O	2.07	0.72
1:1A:120:G:OP2	59:1A:4316:HOH:O	2.07	0.72
1:2A:2026:A:OP1	59:2A:3607:HOH:O	2.05	0.72
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	1.71	0.72
1:1A:1098:C:H42	1:1A:1151:G:H1	1.37	0.72
1:2A:117:U:OP1	59:2A:3613:HOH:O	2.08	0.72
33:2b:13:ALA:HA	33:2b:15:VAL:N	2.04	0.72
44:2m:91:ARG:HB2	44:2m:98:VAL:HG12	1.70	0.72
1:1A:2801:C:O2	1:1A:2902:G:N2	2.22	0.72
32:1a:348:C:OP2	59:1a:1902:HOH:O	2.07	0.72
33:2b:92:TYR:CG	33:2b:150:SER:O	2.43	0.72
1:1A:598:U:OP1	59:1A:4317:HOH:O	2.07	0.72
32:1a:1030:G:H5"	45:1n:4:LYS:HD3	1.72	0.72
32:1a:1069:U:H3	32:1a:1082:G:H22	1.37	0.72
32:1a:1096:C:H42	32:1a:1169:G:H1	1.35	0.72
1:2A:186:C:OP2	59:2A:3605:HOH:O	2.08	0.72
1:1A:1502:G:OP2	59:1A:4318:HOH:O	2.07	0.72
1:1A:2100:U:OP1	23:11:21:ARG:NH2	2.22	0.71
42:1k:48:ILE:O	42:1k:50:TYR:N	2.23	0.71
32:2a:646:G:H2'	32:2a:647:A:H8	1.55	0.71
32:2a:721:A:H1'	37:2f:73:ASN:HD21	1.54	0.71
32:2a:1236:C:H42	32:2a:1265:G:H1	1.37	0.71
1:1A:1248:A:H2	1:1A:1286:A:H62	1.38	0.71
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.24	0.71
32:1a:864:G:N7	59:1a:1924:HOH:O	2.22	0.71
33:1b:185:ILE:HG23	33:1b:199:TYR:HB2	1.73	0.71
1:2A:1377:G:OP1	59:2A:3611:HOH:O	2.07	0.71
1:1A:1649:C:OP2	59:1A:4322:HOH:O	2.08	0.71
35:1d:9:CYS:CB	58:1d:501:SF4:S2	2.78	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2338:A:H2'	1:2A:2339:A:C8	2.25	0.71
20:2Y:94:LYS:NZ	59:2Y:601:HOH:O	2.23	0.71
32:2a:657:G:H2'	32:2a:658:G:C8	2.25	0.71
43:2l:75:HIS:HD2	43:2l:77:LEU:H	1.38	0.71
1:1A:1435:U:O2	1:1A:1440:A:N6	2.19	0.71
1:1A:2459:A:OP1	59:1A:4302:HOH:O	2.08	0.71
32:2a:891:A:OP1	59:2a:3307:HOH:O	2.07	0.71
1:1A:1001:A:OP2	59:1A:4319:HOH:O	2.07	0.71
32:2a:423:U:OP1	35:2d:13:ARG:NH2	2.23	0.71
1:1A:2123:U:H3	1:1A:2208:G:H1	1.37	0.71
1:2A:1828:U:OP2	3:2D:274:ARG:NH2	2.23	0.71
1:2A:2513:G:N7	59:2A:3677:HOH:O	2.23	0.71
1:1A:1007:U:OP2	59:1A:4314:HOH:O	2.06	0.71
1:1A:1991:A:OP1	59:1A:4321:HOH:O	2.08	0.71
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.26	0.71
35:1d:166:LYS:HG2	35:1d:178:VAL:HG11	1.70	0.71
1:2A:2310:G:H2'	1:2A:2311:G:H8	1.55	0.71
1:2A:2696:G:O6	59:2A:3612:HOH:O	2.08	0.71
1:1A:2014:U:OP2	59:1A:4324:HOH:O	2.08	0.71
1:1A:2648:U:H5"	4:1E:82:ARG:HH21	1.55	0.71
1:2A:2405:C:OP2	30:28:30:ARG:NH1	2.24	0.71
15:2T:41:ARG:NH2	32:2a:342:G:OP1	2.21	0.71
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.71	0.71
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.73	0.71
1:2A:152:C:OP2	23:21:92:LYS:NZ	2.24	0.71
32:1a:208:C:H42	32:1a:212:G:H1	1.38	0.70
32:1a:358:G:N7	59:1a:1929:HOH:O	2.23	0.70
32:1a:872:G:N7	59:1a:1930:HOH:O	2.23	0.70
31:19:2:LYS:NZ	31:19:31:LYS:O	2.24	0.70
32:2a:506:C:H41	43:2l:53:ARG:HH22	1.37	0.70
32:2a:977:C:N4	32:2a:1025:G:H1	1.89	0.70
15:1T:84:GLN:HG2	15:1T:85:LYS:HD3	1.72	0.70
1:2A:1367:A:OP1	59:2A:3614:HOH:O	2.09	0.70
1:1A:2586:C:OP2	59:1A:4323:HOH:O	2.08	0.70
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.74	0.70
2:2B:58:A:OP2	59:2B:3101:HOH:O	2.08	0.70
4:1E:127:ASP:OD2	59:1E:401:HOH:O	2.10	0.70
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.74	0.70
41:1j:37:PRO:HA	41:1j:72:VAL:HG12	1.74	0.70
1:2A:1716:C:OP1	59:2A:3615:HOH:O	2.10	0.70
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.73	0.70
1:1A:2699:U:O4	59:1A:4326:HOH:O	2.10	0.70
15:1T:115:ARG:NH2	59:1T:303:HOH:O	2.25	0.69
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.57	0.69
32:2a:61:A:N6	32:2a:104:C:N3	2.39	0.69
32:2a:961:A:O2'	32:2a:1033:G:OP2	2.09	0.69
32:1a:932:G:H21	32:1a:1209:A:H62	1.39	0.69
34:2c:186:PHE:HD1	34:2c:198:VAL:HB	1.56	0.69
1:1A:1316:G:OP2	59:1A:4325:HOH:O	2.09	0.69
2:1B:58:A:OP2	59:1B:301:HOH:O	2.09	0.69
32:2a:937:A:O2'	32:2a:962:C:O2'	2.10	0.69
1:1A:2250:G:OP2	59:1A:4328:HOH:O	2.10	0.69
28:16:2:ALA:N	59:16:201:HOH:O	2.26	0.69
32:1a:568:G:O6	59:1a:1904:HOH:O	2.11	0.69
34:2c:181:ASN:HD22	34:2c:204:LEU:HB2	1.58	0.69
1:1A:777:C:OP2	59:1A:4303:HOH:O	2.11	0.69
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	1.75	0.69
41:1j:55:LYS:O	41:1j:57:LYS:N	2.25	0.69
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.24	0.69
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.74	0.69
32:1a:1072:G:H1	32:1a:1079:C:H42	1.39	0.69
19:2X:35:THR:HG22	19:2X:37:THR:H	1.57	0.69
32:2a:1125:G:H3'	32:2a:1126:G:C8	2.27	0.69
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	1.73	0.69
1:1A:1054:A:OP2	59:1A:4331:HOH:O	2.11	0.69
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.74	0.69
1:2A:706:G:H5'	5:2F:99:TYR:CE2	2.28	0.69
1:2A:1314:A:OP2	59:2A:3607:HOH:O	2.10	0.69
6:2G:5:VAL:HG13	6:2G:8:LYS:HB3	1.75	0.69
32:2a:83:U:OP1	59:2a:3309:HOH:O	2.09	0.69
1:1A:8:U:H3	1:1A:2640:A:H2	1.40	0.69
1:1A:1514:C:OP1	59:1A:4330:HOH:O	2.11	0.69
32:2a:1149:G:N2	32:2a:1152:A:OP2	2.26	0.69
32:1a:77:G:N1	32:1a:87:C:N4	2.35	0.69
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	1.74	0.69
14:2S:84:GLN:HA	14:2S:111:GLU:HB2	1.73	0.69
48:2q:66:SER:OG	48:2q:67:LYS:N	2.25	0.69
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.26	0.68
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.74	0.68
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.75	0.68
1:2A:1813:A:OP2	59:2A:3617:HOH:O	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:407:A:O2'	59:2a:3311:HOH:O	2.10	0.68
33:2b:92:TYR:CD1	33:2b:151:GLY:HA3	2.28	0.68
1:1A:1369:G:OP2	59:1A:4327:HOH:O	2.10	0.68
1:1A:2342:G:N7	59:1A:4428:HOH:O	2.26	0.68
32:1a:1058:C:OP1	33:1b:179:LYS:NZ	2.26	0.68
33:1b:87:ARG:HH21	33:1b:219:VAL:HG23	1.58	0.68
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	1.75	0.68
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.58	0.68
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.75	0.68
32:2a:143:G:H2'	32:2a:144:A:H8	1.59	0.68
38:2g:122:HIS:HA	38:2g:125:MET:HE2	1.75	0.68
1:1A:1352:A:N3	59:1A:4422:HOH:O	2.25	0.68
32:1a:343:G:C2	32:1a:344:G:H1'	2.28	0.68
2:2B:22:U:H3	2:2B:61:G:H1	1.40	0.68
2:2B:55:U:H1'	6:2G:29:TRP:HE1	1.58	0.68
32:2a:49:C:OP2	59:2a:3310:HOH:O	2.10	0.68
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.75	0.68
1:1A:138:A:H8	1:1A:1453:C:HO2'	1.42	0.68
1:1A:710:C:O2'	59:1A:4329:HOH:O	2.11	0.68
32:1a:1286:G:OP2	59:1a:1905:HOH:O	2.11	0.68
33:2b:138:LEU:HA	33:2b:141:GLU:HB3	1.75	0.68
54:2x:76:A:OP2	59:2x:3101:HOH:O	2.10	0.68
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	1.76	0.68
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.75	0.68
1:2A:661:A:H8	11:2P:117:GLU:HG3	1.58	0.68
59:2A:3601:HOH:O	13:2R:3:HIS:NE2	2.26	0.68
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.76	0.68
32:2a:976:G:H1	32:2a:1026:C:N4	1.92	0.68
1:1A:1000:G:OP2	12:1Q:14:ARG:NH2	2.27	0.68
5:1F:56:GLU:OE2	5:1F:93:LYS:NZ	2.27	0.68
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.74	0.68
5:2F:116:ASP:OD2	11:2P:1:MET:N	2.26	0.68
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.57	0.68
1:1A:869:G:OP1	59:1A:4333:HOH:O	2.12	0.68
1:2A:877:G:O2'	11:2P:38:GLN:NE2	2.26	0.68
1:2A:1361:U:H2'	1:2A:1362:A:H8	1.59	0.68
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.26	0.68
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.75	0.68
32:2a:485:C:H2'	32:2a:486:G:H8	1.59	0.68
32:2a:548:C:O2'	39:2h:91:ARG:NH2	2.27	0.68
1:1A:2433:A:N3	59:1A:4437:HOH:O	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:770:G:OP2	59:1a:1906:HOH:O	2.11	0.68
1:2A:777:C:OP1	59:2A:3622:HOH:O	2.12	0.68
2:2B:50:G:OP1	14:2S:63:THR:N	2.27	0.68
32:2a:1115:C:H2'	32:2a:1116:G:H8	1.59	0.68
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.76	0.67
32:1a:91:G:HO2'	32:1a:92:G:H8	1.42	0.67
35:1d:166:LYS:HA	35:1d:178:VAL:HG21	1.75	0.67
1:2A:514:G:N7	18:2W:49:LYS:NZ	2.41	0.67
1:2A:1083:C:H42	1:2A:1162:G:H1	1.42	0.67
32:2a:1128:C:H4'	32:2a:1129:A:H5'	1.76	0.67
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.27	0.67
48:2q:66:SER:HB3	48:2q:69:LYS:HB2	1.76	0.67
1:1A:1043:C:OP1	59:1A:4332:HOH:O	2.11	0.67
1:1A:1648:A:OP1	59:1A:4322:HOH:O	2.13	0.67
59:1E:403:HOH:O	13:1R:3:HIS:NE2	2.26	0.67
1:2A:2510:C:OP2	59:2A:3625:HOH:O	2.13	0.67
11:2P:126:VAL:HG12	11:2P:148:LEU:HD22	1.76	0.67
32:2a:1256:G:N2	32:2a:1257:A:N7	2.42	0.67
32:2a:1273:G:O2'	40:2i:38:GLN:NE2	2.27	0.67
1:1A:1387:A:OP2	59:1A:4304:HOH:O	2.12	0.67
1:2A:2043:U:OP1	59:2A:3623:HOH:O	2.12	0.67
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.27	0.67
32:2a:661:U:H3	32:2a:697:G:H22	1.40	0.67
1:2A:785:G:OP1	59:2A:3621:HOH:O	2.12	0.67
1:2A:839:A:O2'	59:2A:3602:HOH:O	1.97	0.67
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.28	0.67
32:2a:1268:A:H8	32:2a:1269:A:H4'	1.59	0.67
34:2c:43:LEU:HD22	34:2c:47:LEU:HD13	1.76	0.67
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.59	0.67
32:1a:1198:G:H5"	45:1n:5:ALA:HB2	1.77	0.67
32:1a:1484:U:OP1	59:1a:1908:HOH:O	2.13	0.67
32:2a:647:A:O3'	49:2r:64:ARG:NH2	2.25	0.67
32:2a:913:A:OP1	59:2a:3312:HOH:O	2.11	0.67
32:1a:1191:C:O2'	32:1a:1196:C:N4	2.21	0.67
1:2A:1233:A:OP2	59:2A:3628:HOH:O	2.13	0.67
33:2b:162:ILE:O	33:2b:185:ILE:HG13	1.95	0.67
1:1A:1813:A:OP1	59:1A:4301:HOH:O	2.12	0.67
32:1a:1072:G:H1	32:1a:1079:C:N4	1.93	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.75	0.66
18:2W:4:LYS:HE2	18:2W:6:ILE:HD11	1.77	0.66
32:1a:68:C:H2'	32:1a:69:G:H8	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:646:G:O2'	32:2a:820:G:OP1	2.12	0.66
35:2d:19:LEU:O	35:2d:21:LEU:N	2.28	0.66
35:2d:100:ARG:NH1	35:2d:137:SER:OG	2.28	0.66
37:2f:94:GLN:OE1	49:2r:32:ARG:NH1	2.28	0.66
3:1D:164:GLN:HE21	3:1D:176:ARG:HH12	1.42	0.66
32:1a:626:A:N3	39:1h:113:SER:OG	2.28	0.66
32:1a:648:G:H22	32:1a:725:G:H1	1.44	0.66
1:2A:795:C:OP2	59:2A:3627:HOH:O	2.13	0.66
1:2A:2022:A:H2'	1:2A:2023:G:C8	2.30	0.66
6:2G:33:ARG:HB2	6:2G:33:ARG:NH1	2.10	0.66
32:2a:958:C:OP2	59:2a:3314:HOH:O	2.13	0.66
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.76	0.66
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.11	0.66
32:2a:1286:G:O2'	32:2a:1315:A:N6	2.28	0.66
1:1A:785:G:OP1	59:1A:4335:HOH:O	2.13	0.66
1:2A:1077:A:H2	1:2A:1167:G:H22	1.43	0.66
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.78	0.66
20:2Y:9:LYS:NZ	20:2Y:28:LYS:O	2.21	0.66
32:2a:22:G:OP1	59:2a:3313:HOH:O	2.13	0.66
32:2a:566:U:OP1	46:2o:64:ARG:NH1	2.28	0.66
1:1A:932:C:H2'	1:1A:933:A:H5"	1.77	0.66
1:1A:1220:G:N2	1:1A:1222:C:OP2	2.28	0.66
1:1A:2090:G:OP2	59:1A:4334:HOH:O	2.13	0.66
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.78	0.66
32:1a:1112:C:H42	32:1a:1126:G:H1	1.43	0.66
32:1a:1287:G:N2	32:1a:1313:G:H1'	2.10	0.66
32:1a:764:A:N7	59:1a:1942:HOH:O	2.29	0.66
1:2A:1802:G:OP1	59:2A:3626:HOH:O	2.13	0.66
26:24:60:GLN:HA	26:24:62:ARG:HG2	1.78	0.66
32:2a:262:G:H5"	32:2a:264:C:H41	1.60	0.66
32:2a:735:U:OP2	59:2a:3315:HOH:O	2.13	0.66
32:2a:1116:G:N2	32:2a:1124:C:N3	2.44	0.66
1:1A:1499:A:OP2	59:1A:4337:HOH:O	2.13	0.66
32:1a:835:C:OP2	59:1a:1911:HOH:O	2.14	0.66
1:2A:609:C:OP2	11:2P:21:ARG:NH2	2.28	0.66
32:2a:1233:A:O2'	32:2a:1352:C:O2'	2.11	0.66
1:2A:2643:A:HO2'	1:2A:2820:G:HO2'	1.36	0.66
1:1A:152:C:OP2	23:11:92:LYS:NZ	2.28	0.65
1:1A:1394:A:OP1	59:1A:4341:HOH:O	2.14	0.65
1:1A:2059:G:O6	59:1A:4340:HOH:O	2.14	0.65
32:1a:638:G:OP2	59:1a:1912:HOH:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:608:A:N1	1:2A:855:G:O2'	2.27	0.65
32:2a:1220:A:OP2	59:2a:3316:HOH:O	2.14	0.65
48:2q:19:VAL:HG23	48:2q:44:ALA:HB3	1.78	0.65
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.79	0.65
34:2c:151:VAL:HG13	34:2c:200:ALA:HB2	1.78	0.65
38:2g:69:VAL:HG21	38:2g:104:LEU:HD11	1.79	0.65
32:1a:437:C:OP2	59:1a:1907:HOH:O	2.13	0.65
46:1o:84:LYS:O	46:1o:84:LYS:HD3	1.96	0.65
14:1S:59:LYS:H	14:1S:59:LYS:HE3	1.60	0.65
32:1a:90:U:H2'	32:1a:91:G:H5'	1.79	0.65
33:1b:93:VAL:HG21	33:1b:97:TRP:HD1	1.62	0.65
1:2A:1360:C:OP2	59:2A:3611:HOH:O	2.13	0.65
1:2A:2606:G:N7	59:2A:3705:HOH:O	2.29	0.65
32:2a:176:G:N2	32:2a:177:U:O4	2.26	0.65
32:2a:853:C:H1'	39:2h:15:ASN:HD21	1.61	0.65
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.30	0.65
1:1A:1298:A:OP1	59:1A:4336:HOH:O	2.13	0.65
1:1A:1358:U:OP1	59:1A:4344:HOH:O	2.15	0.65
1:1A:1715:A:OP2	59:1A:4342:HOH:O	2.14	0.65
1:1A:2584:C:OP1	59:1A:4323:HOH:O	2.13	0.65
15:1T:108:ARG:HG2	15:1T:111:ARG:HH12	1.62	0.65
25:13:3:ARG:NH1	25:13:60:GLU:OE1	2.29	0.65
1:1A:1039:C:OP1	16:1U:53:ARG:NH2	2.29	0.65
32:1a:94:C:H2'	32:1a:95:A:C8	2.32	0.65
32:1a:1078:U:OP2	59:1a:1909:HOH:O	2.13	0.65
1:1A:2095:U:OP1	59:1A:4343:HOH:O	2.15	0.65
1:1A:2210:U:H2'	1:1A:2211:G:H8	1.61	0.65
1:1A:2800:C:OP1	4:1E:61:ARG:NH2	2.29	0.65
32:1a:1338:G:H2'	32:1a:1339:A:C8	2.32	0.65
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.78	0.65
1:2A:1026:A:OP1	59:2A:3632:HOH:O	2.14	0.65
1:2A:1512:G:HO2'	1:2A:1592:C:HO2'	1.38	0.65
35:2d:57:ARG:HH22	36:2e:107:ARG:HD3	1.62	0.65
15:1T:108:ARG:NH2	32:1a:1442:G:OP1	2.29	0.65
1:2A:551:C:OP1	59:2A:3631:HOH:O	2.14	0.65
1:2A:1625:A:N7	59:2A:3704:HOH:O	2.29	0.65
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.77	0.65
9:1N:17:ASP:O	9:1N:21:LYS:NZ	2.25	0.65
32:1a:920:G:H21	40:1i:124:GLN:NE2	1.95	0.65
1:2A:1090:A:N1	1:2A:1155:G:O2'	2.28	0.65
1:2A:2046:C:N4	59:2A:3709:HOH:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2323:U:H5'	6:1G:88:ILE:HD11	1.78	0.65
1:2A:673:G:H4'	30:28:46:ARG:HH22	1.62	0.65
1:2A:1815:A:OP1	59:2A:3633:HOH:O	2.14	0.65
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.32	0.65
1:1A:1068:U:OP2	59:1A:4338:HOH:O	2.13	0.64
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.70	0.64
32:1a:962:C:H42	32:1a:1203:G:H1	1.43	0.64
48:1q:26:GLN:HE21	48:1q:37:LYS:HE3	1.61	0.64
1:2A:996:G:OP1	12:2Q:16:ARG:NH2	2.30	0.64
59:2A:3601:HOH:O	4:2E:110:GLY:O	2.15	0.64
32:2a:646:G:H2'	32:2a:647:A:C8	2.32	0.64
1:2A:1992:A:OP1	59:2A:3629:HOH:O	2.13	0.64
1:2A:2595:U:O4	59:2A:3618:HOH:O	2.11	0.64
2:2B:24:G:N2	2:2B:27:C:N3	2.35	0.64
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.77	0.64
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	1.97	0.64
32:2a:57:U:H2'	32:2a:58:G:H8	1.61	0.64
32:2a:630:U:H2'	32:2a:631:C:C6	2.31	0.64
32:2a:1095:C:C2	34:2c:178:LEU:HD22	2.32	0.64
1:1A:2657:C:OP2	1:1A:2744:G:O2'	2.13	0.64
15:1T:39:ARG:NH2	32:1a:341:C:OP1	2.31	0.64
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.23	0.64
1:2A:330:G:H21	1:2A:353:A:H62	1.44	0.64
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.45	0.64
32:2a:1480:A:H2	32:2a:1483:G:H1	1.46	0.64
1:2A:1516:G:N2	1:2A:1567:G:OP2	2.31	0.64
32:2a:1209:A:OP2	59:2a:3318:HOH:O	2.15	0.64
32:1a:131:C:OP1	59:1a:1913:HOH:O	2.15	0.64
32:1a:302:G:OP2	59:1a:1910:HOH:O	2.14	0.64
32:1a:544:U:O2'	32:1a:545:U:OP2	2.14	0.64
41:1j:4:ILE:N	41:1j:100:THR:HG1	1.96	0.64
1:1A:877:G:O2'	11:1P:38:GLN:NE2	2.31	0.64
1:1A:2634:G:OP1	59:1A:4345:HOH:O	2.15	0.64
19:2X:44:GLU:OE2	59:2X:8101:HOH:O	2.15	0.64
32:2a:1132:C:O2'	32:2a:1262:A:N1	2.29	0.64
1:1A:2882:A:OP2	59:1A:4347:HOH:O	2.15	0.64
32:1a:140:G:N2	32:1a:173:C:N3	2.46	0.64
1:2A:322:A:N7	59:2A:3708:HOH:O	2.30	0.64
1:2A:2509:C:OP2	59:2A:3625:HOH:O	2.15	0.64
32:2a:37:C:O2'	43:2l:117:ARG:NH2	2.31	0.64
45:2n:16:PHE:HB3	45:2n:17:LYS:HE2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2623:C:OP2	27:15:2:ALA:N	2.30	0.64
1:2A:2100:U:OP1	23:21:21:ARG:NH2	2.31	0.64
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.80	0.64
1:1A:1210:U:H2'	1:1A:1211:C:C6	2.32	0.64
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	1.79	0.64
42:1k:20:TYR:HB2	42:1k:31:THR:HG23	1.80	0.64
1:2A:1059:U:H2'	1:2A:1060:G:C8	2.32	0.64
1:2A:1102:A:N6	1:2A:1132:G:OP2	2.31	0.64
1:2A:1870:G:OP2	59:2A:3634:HOH:O	2.15	0.64
33:1b:15:VAL:HG21	33:1b:209:ARG:HB3	1.78	0.63
1:2A:1691:G:H5"	1:2A:1692:C:H5'	1.80	0.63
1:2A:1826:U:H2'	1:2A:1827:C:C6	2.33	0.63
1:2A:2079:A:N7	59:2A:3711:HOH:O	2.30	0.63
38:2g:115:ARG:HB2	38:2g:118:VAL:HG23	1.79	0.63
2:1B:102:A:N7	59:1B:304:HOH:O	2.30	0.63
6:2G:107:LEU:HA	6:2G:111:LEU:HD22	1.80	0.63
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.79	0.63
24:12:29:LYS:HG2	24:12:57:ILE:HD13	1.81	0.63
32:1a:741:U:H2'	32:1a:742:G:O4'	1.98	0.63
32:1a:1287:G:H22	32:1a:1313:G:H1'	1.62	0.63
32:2a:420:G:H2'	32:2a:421:G:H8	1.63	0.63
32:2a:676:U:H5	42:2k:26:ASN:HD21	1.43	0.63
32:2a:1306:A:H4'	32:2a:1344:C:H4'	1.80	0.63
33:2b:92:TYR:CE2	33:2b:150:SER:C	2.77	0.63
45:2n:26:ARG:HH11	45:2n:43:CYS:HB2	1.63	0.63
1:1A:807:A:H5'	59:1A:4393:HOH:O	1.97	0.63
1:1A:1430:G:O2'	1:1A:1441:U:O2	2.13	0.63
32:1a:971:G:H1	32:1a:1028:C:H42	1.45	0.63
39:1h:10:LEU:HD23	39:1h:83:ILE:HD11	1.81	0.63
1:2A:1060:G:H2'	1:2A:1061:G:H8	1.62	0.63
1:2A:2657:C:OP2	1:2A:2744:G:O2'	2.15	0.63
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.81	0.63
1:2A:2603:G:OP1	59:2A:3604:HOH:O	2.16	0.63
15:2T:56:GLY:O	15:2T:59:THR:HG23	1.98	0.63
32:2a:1349:C:O2'	41:2j:60:ARG:NH2	2.24	0.63
32:2a:1112:C:N4	32:2a:1126:G:N1	2.36	0.63
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.64	0.63
9:1N:67:LEU:HB3	9:1N:88:GLU:HG3	1.80	0.63
1:2A:842:C:H2'	1:2A:843:C:C6	2.34	0.63
21:2Z:70:LEU:HG	21:2Z:91:LEU:HD21	1.81	0.63
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:53:GLU:HB2	26:14:54:GLY:HA2	1.81	0.63
2:2B:5:C:OP1	2:2B:61:G:O2'	2.15	0.63
8:2I:65:ALA:HB1	8:2I:136:VAL:HG11	1.79	0.63
11:2P:62:LEU:O	30:28:13:ARG:NH1	2.32	0.63
32:2a:251:G:P	48:2q:69:LYS:HZ1	2.22	0.63
44:2m:57:ARG:O	44:2m:61:GLU:HB2	1.99	0.63
1:1A:1091:A:H3'	1:1A:1092:G:H5'	1.79	0.63
7:1H:86:GLU:OE2	7:1H:130:ARG:NH1	2.32	0.63
15:1T:54:ARG:HA	15:1T:59:THR:HG22	1.81	0.63
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.13	0.63
32:1a:1132:C:OP1	40:1i:9:ARG:NH2	2.30	0.63
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.79	0.63
1:2A:1100:G:H3'	1:2A:1101:G:H8	1.64	0.63
32:2a:57:U:H2'	32:2a:58:G:C8	2.33	0.63
32:2a:1101:C:OP1	40:2i:104:ARG:NH1	2.31	0.63
33:2b:118:LEU:HD11	33:2b:142:LEU:HB2	1.81	0.63
32:1a:258:A:H2'	32:1a:259:A:C8	2.34	0.62
32:1a:372:G:H4'	47:1p:5:ARG:HE	1.64	0.62
1:2A:1846:G:O6	3:2D:35:LYS:NZ	2.26	0.62
32:2a:68:C:H2'	32:2a:69:G:C8	2.34	0.62
32:1a:1334:C:OP1	52:1u:3:LYS:NZ	2.26	0.62
1:2A:624:G:O2'	1:2A:701:A:N6	2.33	0.62
1:2A:1039:C:OP1	16:2U:53:ARG:NH2	2.31	0.62
1:2A:2302:U:H2'	1:2A:2303:C:C6	2.34	0.62
21:2Z:70:LEU:O	21:2Z:89:PHE:N	2.26	0.62
32:2a:823:U:H5"	32:2a:824:C:H5	1.64	0.62
33:2b:71:VAL:HA	33:2b:93:VAL:HG23	1.82	0.62
1:1A:541:C:OP1	27:15:16:ARG:NH2	2.32	0.62
33:1b:16:HIS:O	33:1b:18:GLY:N	2.33	0.62
24:22:32:LEU:HD22	24:22:36:ARG:HD3	1.80	0.62
1:1A:682:G:H1	1:1A:695:C:H42	1.48	0.62
1:1A:1500:U:OP1	13:1R:77:ARG:NH1	2.32	0.62
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.80	0.62
49:1r:34:TYR:HB3	49:1r:69:THR:HG22	1.80	0.62
1:2A:2375:C:OP1	22:20:55:ARG:NH1	2.32	0.62
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.81	0.62
32:2a:1233:A:H2'	32:2a:1234:A:C8	2.34	0.62
1:1A:610:U:H2'	1:1A:611:C:C6	2.34	0.62
1:1A:1231:G:H5"	17:1V:81:TYR:CE1	2.34	0.62
14:1S:83:LYS:HG2	14:1S:111:GLU:HG3	1.82	0.62
32:1a:454:G:N2	32:1a:457:G:OP2	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.32	0.62
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.81	0.62
51:2t:56:MET:HE2	51:2t:85:MET:HG2	1.81	0.62
32:1a:312:G:OP2	32:1a:347:G:O2'	2.16	0.62
48:1q:9:VAL:HG22	48:1q:56:VAL:HG22	1.81	0.62
32:2a:9:A:H5'	36:2e:101:ILE:HG22	1.81	0.62
1:1A:2339:A:H2'	1:1A:2340:G:C8	2.35	0.62
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.47	0.62
21:1Z:70:LEU:HG	21:1Z:91:LEU:HD21	1.82	0.62
39:1h:7:ALA:HA	39:1h:10:LEU:HD12	1.81	0.62
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.80	0.62
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.33	0.62
32:2a:1043:C:H2'	32:2a:1044:G:H8	1.65	0.62
32:2a:964:A:H1'	50:2s:54:GLY:O	1.99	0.62
32:1a:156:A:H2	32:1a:343:G:H21	1.45	0.62
32:1a:1164:G:H4'	32:1a:1165:A:H5'	1.82	0.62
1:2A:332:G:N3	1:2A:352:G:O2'	2.33	0.62
6:2G:13:GLU:O	6:2G:15:VAL:N	2.33	0.62
16:2U:104:GLN:OE1	16:2U:105:VAL:N	2.29	0.62
38:2g:47:CYS:HB3	38:2g:58:PRO:HB3	1.80	0.62
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.80	0.62
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.15	0.62
1:2A:590:U:O4	59:2A:3636:HOH:O	2.15	0.62
1:2A:2641:G:H2'	1:2A:2642:G:C8	2.35	0.62
32:2a:460:G:H2'	32:2a:461:G:H8	1.65	0.62
1:1A:976:G:OP2	25:13:29:ARG:NH2	2.32	0.61
1:2A:483:G:O2'	1:2A:494:G:O6	2.10	0.61
1:2A:1361:U:H2'	1:2A:1362:A:C8	2.35	0.61
1:2A:1735:A:OP2	1:2A:1744:A:N6	2.32	0.61
1:2A:2100:U:O3'	23:21:35:THR:OG1	2.18	0.61
1:2A:2765:A:N3	31:29:15:LYS:NZ	2.48	0.61
15:2T:24:PRO:HA	15:2T:49:VAL:HG22	1.82	0.61
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.33	0.61
50:2s:53:ASN:HB2	50:2s:77:THR:HA	1.82	0.61
1:1A:2573:U:H1'	10:1O:23:ARG:HH11	1.65	0.61
1:1A:2816:G:N1	1:1A:2901:G:O6	2.19	0.61
4:1E:111:ARG:HG3	4:1E:160:TYR:CD2	2.35	0.61
51:1t:16:HIS:O	51:1t:19:SER:OG	2.17	0.61
1:2A:1276:G:H2'	1:2A:1277:G:H8	1.64	0.61
35:2d:65:ARG:NH1	35:2d:70:ILE:O	2.33	0.61
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.83	0.61
32:2a:1231:C:O2'	40:2i:73:GLN:NE2	2.32	0.61
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.82	0.61
15:2T:55:ASN:N	15:2T:59:THR:HG22	2.10	0.61
32:2a:466:G:O2'	32:2a:468:C:N4	2.32	0.61
34:2c:181:ASN:H	34:2c:203:PHE:HE1	1.49	0.61
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.82	0.61
1:2A:786:U:H2'	1:2A:787:G:C8	2.35	0.61
1:2A:2588:A:H5'	27:25:3:LYS:HD2	1.81	0.61
16:2U:78:THR:O	16:2U:117:GLN:NE2	2.33	0.61
17:2V:43:GLU:N	17:2V:43:GLU:OE2	2.34	0.61
14:1S:15:ARG:O	14:1S:19:LYS:HG2	1.99	0.61
32:1a:1328:A:N1	32:1a:1357:A:H5"	2.15	0.61
32:2a:1210:C:OP1	44:2m:115:LYS:N	2.30	0.61
33:2b:92:TYR:CD1	33:2b:150:SER:O	2.53	0.61
33:2b:92:TYR:CE2	33:2b:152:PHE:N	2.68	0.61
36:2e:36:ASP:C	36:2e:38:GLN:H	2.07	0.61
38:2g:111:ARG:NH1	38:2g:113:GLU:OE1	2.32	0.61
1:1A:236:G:OP1	59:1A:4348:HOH:O	2.16	0.61
1:1A:2799:C:H1'	4:1E:62:PRO:HG3	1.82	0.61
15:1T:51:ARG:NH2	59:1T:304:HOH:O	2.34	0.61
38:1g:20:ASP:OD2	38:1g:63:LYS:NZ	2.27	0.61
1:2A:2573:U:H1'	10:2O:23:ARG:HH11	1.65	0.61
32:2a:955:A:O3'	32:2a:958:C:N4	2.32	0.61
32:2a:1299:C:OP1	45:2n:17:LYS:HD2	2.01	0.61
33:2b:16:HIS:O	33:2b:18:GLY:N	2.33	0.61
40:2i:17:VAL:HG23	40:2i:63:ILE:HG12	1.82	0.61
26:14:57:GLU:HB3	26:14:58:ARG:HG2	1.80	0.61
32:1a:582:U:H4'	39:1h:94:TYR:CD2	2.36	0.61
54:1x:17:C:H2'	54:1x:17(A):U:H2'	1.82	0.61
1:2A:934:C:OP1	44:2m:93:ARG:NH1	2.25	0.61
1:2A:1121:C:H3'	1:2A:1122:A:H8	1.65	0.61
1:2A:1188:A:OP1	9:2N:25:ARG:NH2	2.34	0.61
1:2A:1906:A:H2'	1:2A:1907:C:O4'	2.00	0.61
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.82	0.61
32:2a:402:G:N2	35:2d:119:GLN:OE1	2.31	0.61
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.83	0.61
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.82	0.61
9:2N:21:LYS:NZ	9:2N:140:VAL:O	2.33	0.61
21:2Z:134:PRO:C	21:2Z:136:PHE:H	2.07	0.61
32:2a:183:C:O4'	51:2t:89:ARG:NH2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:271:U:OP1	8:1I:50:ARG:NH2	2.34	0.61
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.65	0.61
51:1t:42:GLN:NE2	51:1t:46:GLU:OE2	2.34	0.61
1:2A:2095:U:H2'	1:2A:2096:U:C6	2.36	0.61
3:2D:79:VAL:HG21	3:2D:111:LEU:HD11	1.83	0.61
33:2b:178:ARG:HH12	39:2h:68:ARG:HH22	1.49	0.61
1:1A:302:C:H42	1:1A:384:G:H1	1.49	0.60
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.25	0.60
32:1a:556:A:OP1	59:1a:1914:HOH:O	2.16	0.60
32:1a:1418:G:H2'	32:1a:1419:U:C6	2.35	0.60
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.84	0.60
32:2a:965:G:OP2	59:2a:3319:HOH:O	2.16	0.60
32:2a:1051:G:N2	32:2a:1173:A:N3	2.47	0.60
32:2a:1490:U:H2'	32:2a:1491:A:C8	2.36	0.60
1:1A:1323:A:OP1	13:1R:36:THR:HG23	2.01	0.60
1:1A:1540:A:H2'	1:1A:1541:A:C8	2.35	0.60
1:1A:2441:A:N3	1:1A:2441:A:H2'	2.15	0.60
28:16:6:ARG:NH2	59:16:202:HOH:O	2.33	0.60
32:1a:181:C:O4'	51:1t:81:LYS:NZ	2.34	0.60
34:1c:15:THR:HG22	34:1c:16:ARG:HG2	1.82	0.60
1:2A:1495:A:O2'	1:2A:1575:G:N2	2.27	0.60
36:2e:50:GLU:HB3	36:2e:53:LEU:HD13	1.83	0.60
1:1A:1934:A:N6	32:1a:1472:G:OP1	2.33	0.60
1:1A:2087:C:OP1	59:1A:4349:HOH:O	2.16	0.60
37:1f:18:GLN:HA	37:1f:21:LEU:HD12	1.83	0.60
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.83	0.60
1:2A:2226:G:H5"	1:2A:2227:G:N7	2.15	0.60
1:2A:2622:U:C4	27:25:3:LYS:HG2	2.36	0.60
1:1A:903:C:H4'	22:10:23:VAL:HG21	1.83	0.60
1:1A:2672:G:OP1	59:1A:4350:HOH:O	2.16	0.60
6:1G:49:ASP:O	6:1G:51:ARG:N	2.31	0.60
32:1a:1296:C:OP2	50:1s:4:SER:OG	2.20	0.60
1:2A:1647:U:O4	59:2A:3619:HOH:O	2.12	0.60
1:2A:1826:U:H2'	1:2A:1827:C:H6	1.66	0.60
32:2a:6:U:H5"	32:2a:7:G:C5	2.37	0.60
32:2a:1491:A:H2'	32:2a:1492:C:C6	2.35	0.60
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	1.84	0.60
1:1A:1693:G:OP1	59:1A:4325:HOH:O	2.17	0.60
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.27	0.60
1:2A:706:G:H5'	5:2F:99:TYR:CD2	2.36	0.60
1:2A:721:A:OP1	5:2F:63:LYS:NZ	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:27:ARG:HD2	23:21:71:TYR:CE2	2.36	0.60
32:2a:302:G:N7	59:2a:3347:HOH:O	2.31	0.60
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.83	0.60
8:1I:37:VAL:HG13	8:1I:38:LEU:HD12	1.84	0.60
8:1I:72:LEU:C	8:1I:74:ASN:H	2.07	0.60
1:2A:82:A:N1	1:2A:96:G:O2'	2.28	0.60
1:2A:867:A:H2'	1:2A:990:G:H5"	1.82	0.60
41:2j:57:LYS:HD2	41:2j:60:ARG:NH2	2.16	0.60
1:2A:1015:C:OP2	59:2A:3640:HOH:O	2.17	0.60
1:2A:2811:A:H1'	1:2A:2903:U:H1'	1.83	0.60
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.99	0.60
1:1A:154:C:H42	1:1A:159:G:H1	1.48	0.60
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.34	0.60
1:2A:1059:U:H2'	1:2A:1060:G:H8	1.66	0.60
1:2A:1738:U:OP2	59:2A:3635:HOH:O	2.15	0.60
32:2a:388:G:H2'	32:2a:389:A:C8	2.36	0.60
33:2b:92:TYR:CZ	33:2b:150:SER:C	2.79	0.60
38:2g:72:ARG:N	38:2g:142:GLU:OE2	2.22	0.60
1:1A:883:C:N4	59:1A:4499:HOH:O	2.33	0.60
2:1B:66:A:H61	2:1B:108:U:H2'	1.67	0.60
32:1a:596:C:O2	32:1a:613:G:N2	2.35	0.60
32:1a:1259:C:O2'	32:1a:1261:A:H1'	2.01	0.60
1:2A:552:A:O2'	1:2A:553:A:H5'	2.01	0.60
1:2A:2366:C:H1'	22:20:39:ARG:HH21	1.67	0.60
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.35	0.60
32:1a:460:G:H2'	32:1a:461:G:H8	1.67	0.60
32:1a:1208:C:O2'	44:1m:111:LYS:NZ	2.30	0.60
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.83	0.60
48:1q:24:GLU:HG2	48:1q:39:SER:HB3	1.84	0.60
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.37	0.60
3:2D:202:LYS:NZ	32:2a:757:G:O3'	2.34	0.60
8:2I:62:LYS:HE2	8:2I:133:HIS:HE1	1.67	0.60
14:2S:48:LEU:HD23	14:2S:82:ILE:HD11	1.84	0.60
18:2W:37:ARG:HD2	18:2W:38:TYR:CE2	2.37	0.60
1:1A:992:G:OP1	59:1A:4314:HOH:O	2.16	0.59
1:1A:2670:G:O2'	7:1H:175:LYS:NZ	2.34	0.59
38:1g:72:ARG:HB3	38:1g:72:ARG:HH11	1.67	0.59
2:2B:114:C:H4'	14:2S:46:VAL:HG22	1.83	0.59
5:2F:32:LEU:HB3	5:2F:112:MET:HE1	1.82	0.59
7:2H:9:ILE:HB	7:2H:50:VAL:HB	1.84	0.59
23:21:65:SER:OG	23:21:66:HIS:ND1	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:145:LEU:O	33:2b:149:LEU:HB2	2.02	0.59
34:2c:3:ASN:O	59:2c:301:HOH:O	2.17	0.59
41:2j:5:ARG:N	41:2j:73:ASP:OD1	2.35	0.59
32:2a:954:G:H5'	32:2a:1340:U:O2'	2.01	0.59
32:2a:981:G:H1	32:2a:1021:C:H42	0.69	0.59
1:1A:1090:A:H4'	1:1A:1091:A:H5"	1.84	0.59
1:2A:1198:C:OP2	59:2A:3639:HOH:O	2.17	0.59
1:2A:2815:G:H2'	1:2A:2816:G:C8	2.36	0.59
38:2g:16:LEU:HD23	40:2i:41:VAL:HG12	1.84	0.59
5:1F:18:ARG:HG2	5:1F:19:GLU:H	1.67	0.59
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.20	0.59
1:2A:951:G:O2'	12:2Q:67:ARG:NH2	2.33	0.59
2:2B:1:U:H2'	2:2B:2:C:C5	2.36	0.59
32:2a:753:G:H4'	32:2a:1491:A:H4'	1.84	0.59
32:2a:1287:G:N2	32:2a:1313:G:H1'	2.18	0.59
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.34	0.59
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.21	0.59
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.68	0.59
32:1a:36:G:O2'	43:1l:118:SER:O	2.20	0.59
32:1a:68:C:H2'	32:1a:69:G:C8	2.37	0.59
32:1a:1135:A:H5'	41:1j:13:HIS:ND1	2.18	0.59
48:1q:66:SER:HB3	48:1q:69:LYS:HB2	1.85	0.59
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.84	0.59
1:2A:80:G:N1	1:2A:100:A:OP2	2.28	0.59
1:2A:2305:C:OP1	14:2S:89:ARG:NH1	2.31	0.59
32:2a:910:C:H2'	32:2a:911:G:H8	1.67	0.59
32:2a:1294:G:H1	32:2a:1307:C:H42	1.48	0.59
1:1A:928:G:H1	1:1A:939:C:H42	1.51	0.59
1:1A:1064:U:H3	1:1A:1187:A:H62	1.49	0.59
1:1A:2044:G:H5'	1:1A:2628:C:H4'	1.84	0.59
32:1a:154:G:O2'	32:1a:156:A:N6	2.32	0.59
32:1a:372:G:H5"	47:1p:5:ARG:HB2	1.84	0.59
1:2A:555:C:OP1	1:2A:583:G:N1	2.33	0.59
6:2G:135:LEU:HB2	6:2G:155:MET:HG2	1.83	0.59
32:2a:971:G:O6	32:2a:1028:C:N4	2.34	0.59
43:2l:79:GLU:HG2	43:2l:80:HIS:CD2	2.38	0.59
44:2m:107:ALA:HB3	44:2m:111:LYS:HD2	1.84	0.59
1:1A:826:G:OP1	3:1D:218:ARG:NH2	2.36	0.59
32:1a:155:A:N6	32:1a:341:C:OP2	2.32	0.59
33:2b:27:LYS:NZ	33:2b:193:ASP:OD1	2.36	0.59
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.28	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.85	0.59
1:2A:885:U:H2'	1:2A:886:C:C6	2.38	0.59
1:2A:1120:C:O5'	12:2Q:59:ARG:NH1	2.36	0.59
1:2A:1295:G:OP2	11:2P:21:ARG:NH1	2.34	0.59
1:2A:2314:G:O2'	6:2G:132:ASN:HB2	2.02	0.59
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.35	0.59
32:2a:109:G:OP1	59:2a:3310:HOH:O	2.16	0.59
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.83	0.59
1:1A:1552:A:O2'	1:1A:1553:A:O5'	2.21	0.59
32:2a:1088:A:H2'	32:2a:1089:G:H8	1.67	0.59
1:1A:1826:U:H2'	1:1A:1827:C:C6	2.38	0.59
1:2A:2367:C:OP1	22:20:24:LYS:NZ	2.34	0.59
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.21	0.59
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.51	0.59
28:26:21:TYR:CE1	28:26:38:LYS:HG2	2.38	0.59
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE1	2.19	0.58
32:1a:950:C:O2'	41:1j:55:LYS:O	2.21	0.58
32:2a:1046:C:OP2	32:2a:1047:G:O2'	2.19	0.58
33:2b:119:GLU:HG3	33:2b:142:LEU:HD11	1.84	0.58
33:2b:127:ILE:HG12	33:2b:128:GLU:H	1.68	0.58
46:2o:5:LYS:HZ3	46:2o:5:LYS:HB2	1.67	0.58
33:1b:28:PHE:HD2	33:1b:194:PRO:HG3	1.67	0.58
51:1t:9:ASN:HD22	51:1t:10:LEU:H	1.51	0.58
32:2a:65:G:H4'	32:2a:66:U:H3'	1.85	0.58
35:2d:158:ILE:HG22	35:2d:162:LEU:HD12	1.84	0.58
38:2g:70:LYS:HD3	38:2g:96:GLN:HB3	1.85	0.58
1:1A:1070:G:C4	1:1A:1179:C:H1'	2.38	0.58
32:1a:698:G:H2'	32:1a:699:A:C8	2.38	0.58
1:2A:732:G:N2	1:2A:834:A:H61	2.01	0.58
1:2A:757:G:N2	1:2A:766:C:O2	2.34	0.58
1:2A:1154:C:H3'	1:2A:1155:G:C8	2.37	0.58
34:2c:58:GLU:HG3	34:2c:65:ALA:HB3	1.85	0.58
1:1A:514:G:N7	18:1W:49:LYS:NZ	2.51	0.58
1:1A:2206:C:O2'	1:1A:2207:G:H5'	2.04	0.58
35:1d:98:GLU:O	35:1d:103:ASN:ND2	2.37	0.58
1:2A:1124:C:H41	1:2A:1133:A:H5"	1.69	0.58
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.36	0.58
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.39	0.58
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.36	0.58
32:2a:1328:A:N1	32:2a:1357:A:H5"	2.19	0.58
34:2c:186:PHE:CZ	34:2c:200:ALA:HB3	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1201:A:OP2	59:1A:4353:HOH:O	2.17	0.58
1:1A:1844:G:H4'	3:1D:51:VAL:HG21	1.86	0.58
32:1a:954:G:OP2	32:1a:1340:U:O2'	2.17	0.58
32:1a:1480:A:H2	32:1a:1483:G:N1	1.96	0.58
39:1h:64:LYS:HB2	39:1h:79:VAL:HG21	1.84	0.58
32:2a:143:G:H2'	32:2a:144:A:C8	2.38	0.58
32:2a:953:A:H5"	32:2a:1346:A:H62	1.67	0.58
34:2c:186:PHE:CE2	34:2c:200:ALA:HB3	2.38	0.58
1:1A:1219:U:OP1	1:1A:1221:A:N6	2.34	0.58
1:1A:2210:U:H2'	1:1A:2211:G:C8	2.39	0.58
3:1D:164:GLN:NE2	3:1D:176:ARG:HH12	2.02	0.58
11:1P:121:LYS:O	11:1P:123:LEU:N	2.35	0.58
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.85	0.58
43:1l:79:GLU:HG2	43:1l:80:HIS:CD2	2.38	0.58
1:2A:533:C:OP1	59:2A:3642:HOH:O	2.17	0.58
32:2a:935:U:OP2	59:2a:3322:HOH:O	2.17	0.58
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.85	0.58
40:2i:53:VAL:O	40:2i:55:ALA:N	2.29	0.58
46:2o:5:LYS:H	46:2o:5:LYS:HD3	1.68	0.58
50:2s:3:ARG:NH2	50:2s:10:PHE:HB2	2.19	0.58
50:2s:30:LEU:HD21	50:2s:32:LYS:HG3	1.86	0.58
41:1j:16:LEU:HD12	41:1j:94:VAL:HG13	1.86	0.58
1:2A:120:G:O6	59:2A:3638:HOH:O	2.16	0.58
1:2A:2738:U:H4'	10:2O:1:MET:HE1	1.84	0.58
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.86	0.58
32:2a:298:G:N3	32:2a:540:C:H4'	2.18	0.58
1:1A:2734:G:OP2	59:1A:4354:HOH:O	2.17	0.58
32:1a:1266:C:OP2	32:1a:1267:A:O2'	2.21	0.58
32:2a:1030:G:OP1	45:2n:4:LYS:NZ	2.35	0.58
32:2a:1237:G:O2'	32:2a:1240:G:N3	2.28	0.58
1:1A:2819:A:N6	1:1A:2899:G:O2'	2.34	0.58
1:2A:1017:A:OP2	59:2A:3636:HOH:O	2.17	0.58
1:2A:2440:G:OP2	59:2A:3603:HOH:O	2.17	0.58
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.18	0.58
36:2e:51:VAL:HG23	36:2e:52:PRO:HD3	1.86	0.58
1:1A:172:C:H2'	1:1A:173:U:C6	2.38	0.58
1:1A:550:A:OP1	59:1A:4358:HOH:O	2.18	0.58
32:1a:1285:C:OP1	59:1a:1905:HOH:O	2.17	0.58
1:2A:1078:U:OP1	31:29:9:ARG:NH2	2.36	0.58
18:2W:17:VAL:HG11	18:2W:103:ILE:HD11	1.86	0.58
34:2c:54:ARG:H	34:2c:69:HIS:HB2	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1153:U:O2'	1:1A:1154:C:O5'	2.20	0.57
1:1A:1450:U:H2'	1:1A:1451:U:C6	2.39	0.57
1:1A:2366:C:H1'	22:10:39:ARG:HH21	1.69	0.57
32:1a:460:G:H2'	32:1a:461:G:C8	2.39	0.57
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.37	0.57
32:2a:754:C:OP1	59:2a:3320:HOH:O	2.17	0.57
1:1A:1391:G:OP2	59:1A:4352:HOH:O	2.17	0.57
50:1s:80:TYR:O	59:1s:3101:HOH:O	2.17	0.57
1:2A:524:G:N1	1:2A:527:A:OP2	2.37	0.57
1:2A:2800:C:OP1	4:2E:61:ARG:NH2	2.37	0.57
4:2E:111:ARG:HG3	4:2E:160:TYR:CD2	2.39	0.57
32:2a:46:U:H2'	32:2a:47:G:C8	2.39	0.57
32:2a:953:A:H5"	32:2a:1346:A:N6	2.19	0.57
1:1A:1833:A:H4'	3:1D:259:THR:HG23	1.85	0.57
1:1A:2033:G:OP1	18:1W:11:ARG:NH2	2.37	0.57
1:2A:1833:A:O2'	3:2D:259:THR:HG21	2.03	0.57
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.85	0.57
15:2T:127:ALA:C	15:2T:129:ARG:H	2.12	0.57
32:2a:443:A:OP2	32:2a:470:G:N2	2.29	0.57
32:2a:1133:U:O4	32:2a:1134:A:N6	2.37	0.57
45:2n:22:THR:HB	45:2n:33:VAL:HG21	1.86	0.57
51:2t:51:GLU:HA	51:2t:54:LYS:HE2	1.86	0.57
1:1A:1088:C:O2	1:1A:1157:G:N2	2.25	0.57
1:1A:1093:A:OP2	1:1A:1154:C:N4	2.37	0.57
15:1T:118:ARG:HG2	32:1a:1426:G:C8	2.40	0.57
32:1a:657:G:H2'	32:1a:658:G:C8	2.39	0.57
48:1q:66:SER:OG	48:1q:67:LYS:N	2.36	0.57
1:2A:437:G:OP1	59:2A:3643:HOH:O	2.17	0.57
1:2A:2548:U:H2'	1:2A:2549:C:C6	2.39	0.57
32:2a:1115:C:H2'	32:2a:1116:G:C8	2.40	0.57
10:1O:48:PRO:HB3	32:1a:1405:G:H5'	1.85	0.57
37:1f:35:ALA:HA	37:1f:67:MET:HB3	1.85	0.57
47:1p:18:ARG:HD3	47:1p:35:LYS:HE3	1.87	0.57
1:2A:2226:G:H3'	1:2A:2227:G:C8	2.40	0.57
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.20	0.57
32:2a:691:C:H2'	32:2a:692:C:C6	2.40	0.57
1:1A:1404:A:N6	1:1A:1417:U:H3	1.95	0.57
1:1A:2254:U:H2'	1:1A:2255:U:C6	2.38	0.57
12:1Q:52:VAL:O	12:1Q:56:ARG:HG3	2.05	0.57
32:1a:504:A:N1	32:1a:520:C:H1'	2.20	0.57
32:1a:726:G:OP2	46:1o:35:ARG:NH2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:67:LYS:O	48:1q:69:LYS:N	2.38	0.57
1:2A:1424:A:H4'	1:2A:1425:G:OP2	2.03	0.57
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.85	0.57
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.87	0.57
26:24:69:LYS:HG2	50:2s:20:LEU:HD11	1.86	0.57
32:2a:836:G:O6	32:2a:847:G:H3'	2.03	0.57
32:2a:1172:G:H3'	59:2c:301:HOH:O	2.04	0.57
33:2b:74:LYS:HG2	33:2b:169:LYS:HD2	1.86	0.57
35:2d:9:CYS:CB	58:2d:501:SF4:S2	2.92	0.57
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.85	0.57
1:1A:235:G:H4'	1:1A:412:G:C5	2.40	0.57
1:1A:629:U:OP1	5:1F:102:PRO:HA	2.04	0.57
1:1A:876:G:OP2	59:1A:4355:HOH:O	2.17	0.57
1:1A:2395:G:OP2	22:10:55:ARG:NH1	2.38	0.57
1:1A:2450:A:C8	1:1A:2450:A:H5'	2.40	0.57
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.20	0.57
35:1d:188:LEU:HD23	35:1d:188:LEU:H	1.68	0.57
40:1i:79:LEU:HG	40:1i:83:ARG:HD2	1.86	0.57
43:1l:33:ARG:HD3	43:1l:62:SER:HB3	1.87	0.57
1:2A:310:C:H42	1:2A:377:G:H1	1.53	0.57
1:2A:1082:G:H1	1:2A:1163:C:H42	1.49	0.57
1:2A:1309:G:H2'	1:2A:2035:A:N6	2.19	0.57
32:2a:1112:C:H2'	32:2a:1122:G:N7	2.19	0.57
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.85	0.57
1:1A:481:C:H4'	59:1A:5847:HOH:O	2.05	0.57
1:1A:1524:G:O2'	1:1A:1604:A:N1	2.37	0.57
15:1T:41:ARG:NH2	32:1a:342:G:OP1	2.37	0.57
32:1a:721:A:H2'	32:1a:722:C:C6	2.39	0.57
32:1a:1425:G:O2'	32:1a:1426:G:OP1	2.21	0.57
1:2A:821:G:O3'	59:2A:3644:HOH:O	2.18	0.57
1:2A:1184:C:O3'	9:2N:25:ARG:NH1	2.38	0.57
32:2a:285:G:OP2	59:2a:3304:HOH:O	2.17	0.57
1:1A:846:A:H8	1:1A:846:A:OP1	1.88	0.57
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.85	0.57
6:2G:16:ARG:HH22	6:2G:28:VAL:HG12	1.69	0.57
8:2I:37:VAL:HG13	8:2I:38:LEU:HD12	1.87	0.57
32:2a:424:G:OP2	35:2d:10:ARG:NH1	2.38	0.57
40:2i:17:VAL:HG21	40:2i:81:ILE:HG22	1.85	0.57
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.37	0.57
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.34	0.57
32:1a:1221:A:H62	32:1a:1281:A:N6	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:1l:33:ARG:HH11	43:1l:62:SER:HB3	1.70	0.57
47:1p:19:ILE:HG12	47:1p:36:ILE:HG13	1.87	0.57
1:2A:2328:C:H2'	1:2A:2329:G:H8	1.70	0.57
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.87	0.57
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HG2	1.87	0.57
15:2T:116:ALA:HB1	15:2T:121:ILE:HD11	1.87	0.57
12:1Q:59:ARG:HA	12:1Q:60:ARG:NH2	2.20	0.56
1:2A:1104:G:H3'	1:2A:1105:U:H6	1.67	0.56
1:2A:1588:A:OP2	59:2A:3641:HOH:O	2.17	0.56
1:2A:2297:A:H4'	1:2A:2298:A:O4'	2.05	0.56
5:2F:56:GLU:OE2	5:2F:93:LYS:NZ	2.36	0.56
32:2a:982:G:H2'	32:2a:983:A:H4'	1.87	0.56
32:2a:1241:C:N4	32:2a:1242:C:O2	2.38	0.56
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.85	0.56
1:1A:2107:U:H2'	1:1A:2108:G:C8	2.40	0.56
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.05	0.56
32:1a:487:C:H2'	32:1a:488:C:H6	1.70	0.56
32:1a:1435:G:H2'	32:1a:1436:G:C8	2.39	0.56
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.36	0.56
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.87	0.56
32:2a:925:G:O3'	44:2m:109:THR:OG1	2.23	0.56
41:2j:57:LYS:HD2	41:2j:60:ARG:HH21	1.70	0.56
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.70	0.56
1:1A:1280:G:OP1	59:1A:4351:HOH:O	2.17	0.56
1:1A:2522:U:OP2	59:1A:4357:HOH:O	2.17	0.56
1:1A:2702:C:OP2	59:1A:4356:HOH:O	2.17	0.56
6:1G:135:LEU:HB2	6:1G:155:MET:HG2	1.87	0.56
32:1a:141:G:N2	32:1a:172:C:N3	2.53	0.56
32:1a:734:G:OP2	59:1a:1915:HOH:O	2.18	0.56
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.87	0.56
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.87	0.56
1:2A:412:G:OP1	59:2A:3646:HOH:O	2.18	0.56
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.39	0.56
7:2H:159:GLU:HG3	7:2H:169:VAL:HG11	1.87	0.56
33:2b:16:HIS:HD2	33:2b:204:ASN:H	1.52	0.56
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.70	0.56
41:2j:17:ASP:OD1	41:2j:70:ARG:NH1	2.32	0.56
1:1A:2257:G:N2	59:1A:4460:HOH:O	2.29	0.56
19:1X:35:THR:HG23	19:1X:37:THR:H	1.71	0.56
32:1a:443:A:OP2	32:1a:470:G:N1	2.30	0.56
32:1a:449:C:H5"	32:1a:450:C:H5	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:74:LYS:HD2	33:1b:166:ASP:HB2	1.87	0.56
1:2A:903:C:H4'	22:20:23:VAL:HG21	1.88	0.56
1:2A:2858:U:O4	15:2T:23:ARG:NH2	2.38	0.56
32:2a:20:C:O2'	59:2a:3321:HOH:O	2.17	0.56
32:2a:993:A:OP2	50:2s:18:LYS:NZ	2.36	0.56
32:2a:1200:C:H2'	32:2a:1201:U:C6	2.40	0.56
32:2a:1346:A:H4'	32:2a:1347:U:H5"	1.88	0.56
33:2b:165:VAL:HG23	33:2b:166:ASP:H	1.69	0.56
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.41	0.56
19:1X:60:ARG:HH22	29:17:47:ARG:HH22	1.53	0.56
21:1Z:77:ASP:OD2	21:1Z:80:ARG:NH1	2.34	0.56
32:1a:1128:C:H4'	32:1a:1129:A:H8	1.71	0.56
33:1b:19:HIS:CE1	33:1b:204:ASN:HA	2.41	0.56
49:1r:58:LEU:HD12	49:1r:62:GLU:HB3	1.86	0.56
50:1s:7:LYS:NZ	59:1s:3102:HOH:O	2.39	0.56
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.87	0.56
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD22	1.86	0.56
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.35	0.56
32:2a:408:A:O4'	35:2d:35:ARG:NH2	2.39	0.56
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.87	0.56
32:1a:973:C:O2	45:1n:4:LYS:NZ	2.38	0.56
1:2A:647:G:H2'	1:2A:648:C:C6	2.41	0.56
1:2A:2651:G:OP1	9:2N:97:ARG:NH2	2.39	0.56
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.87	0.56
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.88	0.56
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.87	0.56
1:1A:330:G:H21	1:1A:353:A:H62	1.54	0.56
1:1A:2022:A:OP1	13:1R:9:LYS:NZ	2.34	0.56
2:1B:23:G:O6	59:1B:302:HOH:O	2.17	0.56
32:1a:77:G:C2	32:1a:87:C:N3	2.74	0.56
1:2A:1835:U:O2	3:2D:50:THR:HB	2.05	0.56
32:2a:835:C:H2'	32:2a:836:G:O4'	2.05	0.56
32:2a:1350:C:O2'	41:2j:48:THR:HG21	2.04	0.56
47:2p:2:VAL:HG23	47:2p:64:ALA:HA	1.87	0.56
2:1B:12:C:H2'	22:10:73:GLY:HA3	1.87	0.56
4:1E:29:GLY:HA3	59:1E:404:HOH:O	2.06	0.56
14:1S:56:LEU:HB2	14:1S:58:LEU:HG	1.88	0.56
19:1X:88:LYS:HE3	19:1X:93:GLU:HG3	1.86	0.56
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.88	0.56
26:14:14:ILE:HG23	26:14:31:ILE:HB	1.85	0.56
32:1a:485:C:H1'	32:1a:533:C:H1'	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1096:C:N4	32:1a:1169:G:H1	2.03	0.56
32:1a:1169:G:N3	45:1n:60:SER:OG	2.36	0.56
45:1n:4:LYS:HA	45:1n:7:ILE:HG12	1.87	0.56
1:2A:656:A:H2'	1:2A:657:A:C8	2.41	0.56
14:2S:84:GLN:H	14:2S:111:GLU:HG3	1.70	0.56
33:2b:187:LEU:HB3	33:2b:201:ILE:HB	1.87	0.56
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.69	0.56
35:2d:108:LEU:HD13	35:2d:174:LEU:HD13	1.87	0.56
35:2d:191:ARG:NE	35:2d:200:GLU:OE1	2.36	0.56
41:2j:65:LEU:HD13	45:2n:56:VAL:HG22	1.85	0.56
45:2n:17:LYS:HE2	45:2n:17:LYS:H	1.69	0.56
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.71	0.56
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.70	0.56
1:2A:320:C:H2'	1:2A:321:G:O4'	2.06	0.56
1:2A:1404:A:H2'	1:2A:1405:A:H5'	1.88	0.56
32:2a:557:A:N3	32:2a:861:C:O2'	2.38	0.56
32:2a:1270:A:N1	32:2a:1354:G:H1'	2.21	0.56
40:2i:4:TYR:O	40:2i:19:LEU:N	2.39	0.56
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.87	0.56
1:1A:1067:G:N2	1:1A:1068:U:O4	2.34	0.56
1:1A:2898:C:OP2	59:1A:4360:HOH:O	2.18	0.56
32:1a:1128:C:H4'	32:1a:1129:A:H5'	1.88	0.56
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.38	0.56
1:2A:666:G:H21	1:2A:670:A:H2	1.52	0.56
1:2A:1685:U:H2'	1:2A:1686:C:H5"	1.88	0.56
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.88	0.56
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.06	0.56
32:2a:240:U:O2	59:2a:3317:HOH:O	2.14	0.56
32:2a:392:G:O2'	32:2a:394:C:OP1	2.18	0.56
32:2a:868:G:O2'	32:2a:884:G:O6	2.22	0.56
32:2a:1100:G:N2	32:2a:1162:A:O2'	2.39	0.56
1:1A:552:A:C2	1:1A:2063:A:H2'	2.41	0.55
5:1F:18:ARG:NH2	5:1F:127:GLU:OE2	2.39	0.55
10:1O:80:ASP:OD1	15:1T:64:ARG:NH2	2.39	0.55
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	1.88	0.55
24:12:32:LEU:HD22	24:12:36:ARG:NH1	2.20	0.55
32:1a:1218:A:H4'	32:1a:1286:G:H4'	1.86	0.55
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.87	0.55
1:2A:957:C:OP1	12:2Q:8:LYS:NZ	2.29	0.55
1:2A:1924:G:OP1	3:2D:241:PRO:HB2	2.06	0.55
7:2H:23:ARG:NH1	7:2H:34:GLU:OE2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:23:9:VAL:HG12	25:23:32:GLN:HE22	1.71	0.55
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.87	0.55
38:2g:24:THR:HA	38:2g:27:ILE:HD12	1.87	0.55
1:1A:1222:C:H2'	1:1A:1223:C:C6	2.41	0.55
1:1A:1845:A:OP2	3:1D:54:ARG:NH2	2.33	0.55
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.07	0.55
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.88	0.55
32:1a:38:U:H2'	32:1a:39:G:H8	1.71	0.55
32:1a:295:G:O6	59:1a:1916:HOH:O	2.18	0.55
36:1e:100:VAL:O	36:1e:107:ARG:NH2	2.31	0.55
54:1x:8:4SU:O5'	54:1x:8:4SU:H6	2.06	0.55
1:2A:78:G:H1	1:2A:103:C:H42	1.53	0.55
1:2A:323:A:OP1	20:2Y:86:ARG:NH2	2.39	0.55
1:2A:667:A:N1	1:2A:2380:A:O2'	2.35	0.55
1:2A:1808:U:H2'	1:2A:1814:A:N6	2.21	0.55
1:2A:2226:G:H8	1:2A:2227:G:N7	2.03	0.55
1:2A:2278:A:H5"	1:2A:2279:A:H5'	1.88	0.55
2:2B:90:A:C5	2:2B:91:C:H1'	2.41	0.55
11:2P:15:ARG:N	11:2P:15:ARG:HD2	2.21	0.55
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.42	0.55
11:2P:95:VAL:HG12	11:2P:123:LEU:HD22	1.88	0.55
32:2a:121:G:HO2'	48:2q:2:PRO:N	2.05	0.55
44:2m:60:VAL:HG22	44:2m:66:LEU:HD11	1.87	0.55
1:1A:1067:G:H22	1:1A:1187:A:H2	1.53	0.55
34:1c:53:ALA:HB2	34:1c:115:LEU:HD21	1.88	0.55
1:2A:895:A:H2	25:23:24:LYS:HB3	1.71	0.55
1:2A:1354:G:H4'	29:27:7:PRO:HB2	1.88	0.55
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.41	0.55
54:2x:4:G:H1	54:2x:69:C:H42	1.55	0.55
1:1A:267:G:OP2	59:1A:4362:HOH:O	2.18	0.55
1:1A:1066:A:C8	1:1A:1066:A:H3'	2.42	0.55
32:1a:1001:G:C2	32:1a:1002:G:H1'	2.41	0.55
11:2P:16:ARG:NH2	59:2P:5001:HOH:O	2.27	0.55
32:2a:1307:C:H4'	52:2u:17:THR:HG21	1.88	0.55
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.38	0.55
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.87	0.55
44:2m:80:ARG:O	44:2m:84:ILE:HG12	2.06	0.55
1:1A:595:G:N1	1:1A:2052:A:OP2	2.30	0.55
32:1a:961:A:H1'	32:1a:1032:U:O2	2.06	0.55
33:1b:144:ARG:HA	33:1b:147:LYS:HG3	1.88	0.55
1:2A:1682:C:H2'	1:2A:1683:A:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:117:ARG:NH2	5:2F:189:THR:O	2.40	0.55
22:20:11:ARG:O	22:20:14:ARG:NH2	2.39	0.55
32:2a:10:G:H2'	32:2a:11:A:H8	1.71	0.55
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	1.89	0.55
18:1W:14:PRO:HG2	18:1W:78:GLU:HG2	1.88	0.55
19:1X:43:VAL:HG21	19:1X:81:VAL:HG11	1.88	0.55
32:1a:526:G:OP1	35:1d:10:ARG:NH2	2.32	0.55
44:1m:60:VAL:HG12	44:1m:66:LEU:HD11	1.87	0.55
48:1q:41:LYS:NZ	48:1q:92:ARG:HH21	2.04	0.55
1:2A:898:G:H2'	1:2A:899:G:C8	2.42	0.55
1:2A:900:G:H2'	1:2A:901:G:C8	2.36	0.55
2:2B:3:C:H2'	2:2B:4:C:C6	2.41	0.55
32:2a:795:C:O2'	32:2a:879:A:N1	2.40	0.55
1:1A:2648:U:H5"	4:1E:82:ARG:NH2	2.21	0.55
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.07	0.55
32:1a:110:A:H61	32:1a:309:A:H1'	1.72	0.55
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.87	0.55
1:2A:998:G:H5"	12:2Q:13:GLN:HB3	1.88	0.55
1:2A:2044:G:H5'	1:2A:2628:C:H4'	1.89	0.55
1:2A:2845:U:H2'	1:2A:2846:G:C8	2.41	0.55
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	1.88	0.55
6:2G:114:ILE:HB	6:2G:117:PHE:HB2	1.89	0.55
32:2a:449:C:OP2	32:2a:450:C:N4	2.38	0.55
32:2a:603:U:N3	35:2d:134:ASP:OD1	2.32	0.55
33:2b:28:PHE:CD1	33:2b:190:THR:HA	2.41	0.55
43:2l:75:HIS:CD2	43:2l:77:LEU:H	2.22	0.55
1:1A:2319:G:O2'	1:1A:2321:A:N7	2.40	0.55
1:1A:2858:U:O4	15:1T:23:ARG:NH2	2.33	0.55
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.40	0.55
32:1a:1060:G:N2	32:1a:1063:A:OP2	2.34	0.55
7:2H:8:PRO:O	7:2H:10:PRO:HD3	2.07	0.55
18:2W:14:PRO:HG2	18:2W:78:GLU:HG2	1.88	0.55
1:1A:2207:G:H2'	1:1A:2208:G:C8	2.42	0.55
1:1A:2302:U:H2'	1:1A:2303:C:C6	2.42	0.55
21:1Z:58:VAL:HG12	21:1Z:68:PRO:HA	1.88	0.55
32:1a:434:G:O2'	32:1a:479:U:O4	2.17	0.55
33:1b:162:ILE:HD11	33:1b:184:VAL:HG22	1.89	0.55
51:1t:71:THR:HG22	51:1t:72:LEU:HG	1.89	0.55
52:1u:5:ASP:C	52:1u:7:ARG:H	2.15	0.55
1:2A:1105:U:N3	1:2A:1133:A:N7	2.55	0.55
1:2A:1276:G:H2'	1:2A:1277:G:C8	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1337:U:H2'	1:2A:1338:C:C6	2.42	0.55
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	1.89	0.55
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.88	0.55
11:2P:89:ALA:O	11:2P:121:LYS:NZ	2.40	0.55
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.06	0.55
35:2d:173:TRP:HB3	35:2d:187:ARG:HE	1.72	0.55
38:2g:116:ALA:O	38:2g:120:ILE:HG12	2.07	0.55
1:1A:1217:G:O2'	1:1A:1218:A:O4'	2.24	0.55
32:1a:198:G:N2	51:1t:102:GLY:O	2.36	0.55
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.89	0.55
34:1c:35:GLU:OE2	34:1c:59:ARG:NH2	2.40	0.55
36:1e:57:LYS:HG2	36:1e:61:TYR:HE2	1.71	0.55
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.88	0.55
1:2A:1054:A:H5'	16:2U:59:ARG:HD3	1.89	0.55
1:2A:1070:G:C4	1:2A:1179:C:H1'	2.42	0.55
6:2G:66:GLN:HB3	6:2G:92:VAL:HG21	1.89	0.55
32:2a:571:G:N2	32:2a:738:C:OP2	2.35	0.55
32:1a:169:C:OP1	59:1a:1917:HOH:O	2.18	0.54
32:1a:911:G:O6	38:1g:3:ARG:NH2	2.39	0.54
34:1c:39:ILE:HG22	34:1c:43:LEU:HD12	1.89	0.54
34:1c:39:ILE:HG23	34:1c:91:LEU:HD11	1.88	0.54
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.07	0.54
23:21:3:LYS:HB2	23:21:61:ARG:HH11	1.73	0.54
32:2a:372:G:H5"	47:2p:5:ARG:HD3	1.89	0.54
32:2a:425:U:H1'	32:2a:426:A:H5"	1.89	0.54
32:2a:719:C:H2'	32:2a:720:C:H6	1.72	0.54
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.74	0.54
33:2b:44:LEU:HD22	33:2b:44:LEU:H	1.72	0.54
33:2b:92:TYR:H	33:2b:151:GLY:HA3	1.71	0.54
1:1A:682:G:N2	1:1A:695:C:N3	2.53	0.54
1:1A:1155:G:H21	1:1A:1156:A:H2	1.54	0.54
32:1a:199:U:H2'	32:1a:200:C:C6	2.42	0.54
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.07	0.54
49:1r:38:GLU:HA	49:1r:41:LYS:HD3	1.89	0.54
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.89	0.54
32:2a:388:G:H2'	32:2a:389:A:H8	1.69	0.54
1:1A:645:A:OP2	11:1P:108:LYS:NZ	2.38	0.54
1:1A:1992:A:OP2	3:1D:242:ARG:NH2	2.40	0.54
4:1E:54:GLN:HB2	4:1E:76:ARG:HG2	1.88	0.54
8:1I:6:LEU:HG	8:1I:36:ALA:HA	1.88	0.54
8:1I:77:LEU:HB3	8:1I:142:VAL:HG13	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:459:G:H2'	32:1a:460:G:C8	2.42	0.54
33:1b:145:LEU:HD11	33:1b:149:LEU:HD12	1.89	0.54
48:1q:86:GLU:O	48:1q:90:ILE:HG13	2.07	0.54
1:2A:622:G:N2	1:2A:627:C:O3'	2.40	0.54
21:2Z:92:SER:O	21:2Z:94:GLU:N	2.33	0.54
26:24:62:ARG:H	26:24:62:ARG:CZ	2.20	0.54
32:2a:1312:U:H4'	44:2m:23:TYR:CE1	2.42	0.54
33:2b:115:LEU:HD13	33:2b:145:LEU:HB3	1.90	0.54
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.43	0.54
36:2e:75:THR:HA	36:2e:115:VAL:HG23	1.88	0.54
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.40	0.54
1:1A:1813:A:N7	59:1A:4496:HOH:O	2.33	0.54
1:1A:2461:A:O2'	54:1x:76:A:N6	2.40	0.54
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.88	0.54
1:2A:2312:C:H2'	1:2A:2313:G:H8	1.73	0.54
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.88	0.54
11:2P:44:GLY:CA	11:2P:45:LEU:HB2	2.37	0.54
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.90	0.54
51:2t:33:ILE:O	51:2t:37:SER:OG	2.23	0.54
1:1A:885:U:H2'	1:1A:886:C:C6	2.42	0.54
1:1A:1026:A:OP1	59:1A:4365:HOH:O	2.19	0.54
32:1a:508:G:H2'	32:1a:509:C:C6	2.42	0.54
38:1g:28:ASN:H	38:1g:28:ASN:HD22	1.53	0.54
39:1h:110:ALA:HB3	39:1h:121:ASP:HB3	1.88	0.54
55:1z:14:ARG:O	55:1z:14:ARG:NE	2.38	0.54
1:2A:141:G:H4'	19:2X:35:THR:HG21	1.88	0.54
26:24:24:THR:OG1	26:24:25:TYR:N	2.30	0.54
26:24:48:ARG:HB2	26:24:52:THR:OG1	2.08	0.54
32:2a:433:U:H5'	35:2d:155:LEU:HD21	1.88	0.54
32:2a:1097:C:O2'	45:2n:60:SER:O	2.18	0.54
1:1A:2783:C:H2'	1:1A:2784:C:C6	2.42	0.54
45:1n:41:ARG:HG3	45:1n:42:ILE:N	2.23	0.54
1:2A:172:C:H2'	1:2A:173:U:C6	2.43	0.54
1:2A:1111:U:N3	1:2A:1114:A:OP2	2.23	0.54
1:2A:1450:U:H2'	1:2A:1451:U:C6	2.42	0.54
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.43	0.54
16:2U:44:ASN:ND2	17:2V:75:PHE:HB3	2.22	0.54
32:2a:511:G:O2'	32:2a:519:A:N1	2.37	0.54
1:1A:2052:A:C6	1:1A:2509:C:H1'	2.43	0.54
19:1X:60:ARG:NH2	29:17:47:ARG:HH22	2.05	0.54
26:14:68:ARG:HH21	26:14:68:ARG:HA	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:178:ARG:HH22	39:1h:68:ARG:HH12	1.56	0.54
54:1x:23:C:H2'	54:1x:24:U:C6	2.43	0.54
1:2A:1102:A:O2'	1:2A:1103:G:OP1	2.26	0.54
1:2A:2121:G:H2'	1:2A:2122:G:H8	1.72	0.54
15:2T:27:THR:HB	15:2T:89:VAL:HG22	1.90	0.54
32:2a:833:G:OP2	59:2a:3324:HOH:O	2.18	0.54
32:2a:989:G:H2'	32:2a:990:G:C8	2.43	0.54
32:2a:1329:G:C5	40:2i:107:ARG:HD2	2.42	0.54
35:2d:9:CYS:HB3	58:2d:501:SF4:S4	2.48	0.54
1:1A:238:G:OP2	30:18:13:ARG:NH2	2.40	0.54
1:1A:1479:A:H61	1:1A:1604:A:H62	1.56	0.54
1:1A:2859:A:OP2	1:1A:2875:U:H5	1.91	0.54
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.08	0.54
32:1a:522:G:H5"	43:1l:114:LYS:HB2	1.89	0.54
32:1a:1184:G:H21	45:1n:43:CYS:HB3	1.72	0.54
3:2D:68:LYS:HD2	3:2D:70:TRP:CZ2	2.42	0.54
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.89	0.54
6:2G:15:VAL:HA	6:2G:175:LEU:HD23	1.90	0.54
33:2b:25:ASN:OD1	33:2b:27:LYS:HG2	2.07	0.54
36:2e:52:PRO:HG2	36:2e:53:LEU:HD12	1.89	0.54
1:1A:601:G:H2'	1:1A:602:C:C6	2.43	0.54
12:1Q:60:ARG:H	12:1Q:60:ARG:NH1	2.06	0.54
14:1S:34:HIS:HD1	14:1S:53:SER:HG	1.51	0.54
15:1T:117:ASP:O	15:1T:121:ILE:HG13	2.08	0.54
32:1a:487:C:OP2	43:1l:116:SER:OG	2.10	0.54
32:1a:898:U:H2'	32:1a:899:U:C6	2.42	0.54
32:1a:1395:C:H2'	32:1a:1396:A:H8	1.73	0.54
37:1f:26:ILE:O	37:1f:30:LEU:HG	2.08	0.54
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.88	0.54
1:2A:665:C:O2'	1:2A:2361:C:OP1	2.18	0.54
1:2A:1039:C:O2'	1:2A:1041:A:OP1	2.24	0.54
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.07	0.54
32:2a:26:C:H5'	32:2a:508:G:H1'	1.89	0.54
32:2a:543:A:OP1	36:2e:126:ARG:NH2	2.41	0.54
1:1A:2529:A:OP2	59:1A:4359:HOH:O	2.18	0.54
4:1E:7:VAL:HG22	4:1E:27:LEU:HB3	1.88	0.54
32:1a:476:G:H2'	32:1a:477:G:O4'	2.08	0.54
34:1c:32:LEU:HD22	34:1c:59:ARG:HH12	1.73	0.54
1:2A:905:G:O2'	1:2A:961:G:O6	2.21	0.54
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.41	0.54
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:268:C:O2'	59:2a:3323:HOH:O	2.18	0.54
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.90	0.53
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.89	0.53
1:2A:586:C:O2'	59:2A:3620:HOH:O	2.12	0.53
1:2A:836:C:OP1	59:2A:3648:HOH:O	2.19	0.53
1:2A:2124:C:H1'	1:2A:2208:G:N2	2.23	0.53
1:2A:2318:G:N1	6:2G:43:LEU:O	2.34	0.53
1:2A:2760:A:H5'	7:2H:4:ILE:HD12	1.89	0.53
36:2e:24:ARG:HB2	36:2e:24:ARG:HH11	1.72	0.53
32:1a:57:U:H2'	32:1a:58:G:C8	2.43	0.53
32:1a:385:A:C6	32:1a:386:C:H1'	2.43	0.53
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.90	0.53
1:2A:70:U:OP2	24:22:29:LYS:NZ	2.41	0.53
1:2A:206:A:C2	1:2A:223:U:H4'	2.43	0.53
1:2A:1713:G:O2'	1:2A:2012:U:O4	2.19	0.53
26:24:61:ARG:O	26:24:63:TYR:N	2.42	0.53
33:2b:8:LYS:HD2	33:2b:51:LEU:HD23	1.90	0.53
33:2b:51:LEU:HD11	33:2b:201:ILE:HG23	1.90	0.53
34:2c:117:ALA:HA	34:2c:186:PHE:CE1	2.42	0.53
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.07	0.53
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.91	0.53
20:1Y:23:ARG:HG2	20:1Y:42:VAL:HG22	1.89	0.53
32:1a:254:G:H2'	32:1a:255:G:H8	1.73	0.53
32:1a:658:G:H2'	32:1a:659:A:H8	1.73	0.53
32:1a:1057:G:O2'	32:1a:1084:A:N1	2.28	0.53
1:2A:1050:C:H2'	1:2A:1051:C:C6	2.43	0.53
1:2A:2759:G:H1	1:2A:2766:U:H2'	1.73	0.53
6:2G:179:PRO:HB2	26:24:42:PHE:HE1	1.73	0.53
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.90	0.53
32:2a:336:U:H2'	32:2a:337:C:C6	2.43	0.53
44:2m:92:HIS:CE1	44:2m:98:VAL:HG11	2.44	0.53
1:1A:1614:G:H5'	3:1D:60:ARG:HA	1.91	0.53
10:1O:104:ARG:NH2	15:1T:43:GLN:OE1	2.41	0.53
36:1e:78:HIS:NE2	36:1e:142:LEU:HA	2.23	0.53
39:1h:46:LYS:HG3	39:1h:64:LYS:HG2	1.89	0.53
1:2A:1409:G:P	23:21:3:LYS:HG3	2.49	0.53
3:2D:127:VAL:HA	3:2D:193:VAL:HG22	1.91	0.53
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG21	1.73	0.53
32:2a:1114:G:H2'	32:2a:1115:C:C6	2.44	0.53
32:2a:1236:C:N4	32:2a:1265:G:H1	2.05	0.53
32:2a:1298:G:N2	32:2a:1300:A:H3'	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1309:C:H2'	32:2a:1310:C:C6	2.44	0.53
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.74	0.53
45:2n:41:ARG:HG3	45:2n:42:ILE:HG13	1.90	0.53
12:1Q:97:VAL:HG21	12:1Q:103:MET:HE3	1.90	0.53
32:1a:1482:G:OP1	32:1a:1485:A:H4'	2.08	0.53
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	1.90	0.53
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.89	0.53
41:1j:40:LEU:HB2	41:1j:69:ASN:CB	2.38	0.53
44:1m:20:THR:C	44:1m:22:ILE:H	2.17	0.53
1:2A:2052:A:N3	1:2A:2466:G:O2'	2.33	0.53
1:2A:2226:G:H5"	1:2A:2227:G:C8	2.43	0.53
1:2A:2284:A:H2'	1:2A:2285:A:C8	2.44	0.53
11:2P:121:LYS:O	11:2P:123:LEU:N	2.36	0.53
32:2a:45:G:N2	32:2a:394:C:O2	2.38	0.53
32:2a:293:G:N2	32:2a:296:A:OP2	2.41	0.53
32:2a:741:U:H2'	32:2a:742:G:O4'	2.09	0.53
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.90	0.53
39:2h:77:GLU:HG3	39:2h:78:GLN:N	2.23	0.53
1:1A:720:G:O2'	5:1F:74:ARG:HD3	2.08	0.53
1:1A:1465:U:O2'	1:1A:1466:G:OP1	2.25	0.53
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.91	0.53
31:19:27:CYS:SG	31:19:28:GLU:N	2.81	0.53
32:1a:584:C:H2'	32:1a:585:C:C6	2.44	0.53
32:1a:1156:G:H2'	32:1a:1157:G:H8	1.72	0.53
34:1c:41:GLY:O	34:1c:45:LYS:HG2	2.09	0.53
1:2A:330:G:N2	1:2A:333:A:O5'	2.32	0.53
1:2A:417:G:O2'	1:2A:436:G:OP1	2.19	0.53
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.91	0.53
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.09	0.53
13:2R:21:TYR:CZ	13:2R:43:GLU:HG2	2.43	0.53
32:2a:1417:A:H2'	32:2a:1418:G:O4'	2.09	0.53
32:2a:1480:A:H2	32:2a:1483:G:N1	2.06	0.53
34:2c:133:ALA:HA	34:2c:136:GLN:HG2	1.90	0.53
1:1A:69:A:N7	19:1X:31:HIS:HE1	2.06	0.53
1:1A:296:C:H2'	1:1A:297:G:H8	1.74	0.53
1:1A:1064:U:O2'	1:1A:1066:A:H2	1.92	0.53
1:1A:1404:A:N1	1:1A:1417:U:O4	2.42	0.53
7:1H:144:VAL:O	7:1H:148:ILE:HG12	2.09	0.53
32:1a:97:C:OP2	51:1t:17:ARG:NH2	2.40	0.53
32:1a:789:C:H2'	32:1a:790:C:H6	1.73	0.53
1:2A:423:G:N7	59:2A:3725:HOH:O	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2072:A:H5'	1:2A:2589:G:O4'	2.08	0.53
1:2A:2583:A:OP1	1:2A:2585:G:O2'	2.23	0.53
29:27:24:THR:O	29:27:28:ARG:HG3	2.08	0.53
35:2d:61:LYS:NZ	35:2d:72:GLU:OE2	2.38	0.53
40:2i:117:HIS:CD2	40:2i:123:PRO:HA	2.43	0.53
1:1A:1218:A:H4'	1:1A:1219:U:OP1	2.08	0.53
32:1a:720:C:H2'	32:1a:721:A:C8	2.43	0.53
32:1a:982:G:H2'	32:1a:983:A:H4'	1.90	0.53
37:1f:97:PHE:O	49:1r:31:LEU:HD23	2.08	0.53
3:2D:276:LYS:H	3:2D:276:LYS:CD	2.22	0.53
4:2E:78:LEU:O	4:2E:79:ARG:HG2	2.09	0.53
32:2a:719:C:H2'	32:2a:720:C:C6	2.44	0.53
32:2a:979:A:H2'	32:2a:980:G:C8	2.44	0.53
32:2a:1223:G:H2'	32:2a:1224:C:C6	2.44	0.53
52:2u:14:TRP:HZ3	52:2u:15:ARG:HH22	1.57	0.53
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.31	0.53
15:1T:127:ALA:C	15:1T:129:ARG:H	2.17	0.53
32:1a:378:A:H2'	32:1a:379:A:H8	1.72	0.53
32:1a:963:C:H2'	32:1a:964:A:C8	2.43	0.53
34:1c:114:PRO:O	34:1c:118:GLN:NE2	2.42	0.53
41:1j:54:PHE:O	41:1j:56:HIS:N	2.41	0.53
49:1r:56:THR:HB	49:1r:58:LEU:HD23	1.90	0.53
1:2A:2573:U:H1'	10:2O:23:ARG:HD3	1.90	0.53
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.90	0.53
32:2a:403:G:H2'	32:2a:404:A:C8	2.44	0.53
32:2a:937:A:HO2'	32:2a:962:C:HO2'	1.44	0.53
1:1A:17:C:O2'	1:1A:576:U:OP1	2.27	0.53
1:1A:184:A:H62	11:1P:38:GLN:HE22	1.57	0.53
1:1A:1920:G:N3	1:1A:1920:G:H2'	2.23	0.53
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.91	0.53
26:14:59:PHE:O	26:14:62:ARG:HD3	2.09	0.53
1:2A:704:C:H2'	1:2A:705:C:C6	2.44	0.53
1:2A:732:G:H21	1:2A:834:A:H61	1.55	0.53
1:2A:792:A:H2'	1:2A:2623:C:H5"	1.90	0.53
1:2A:2017:C:H4'	1:2A:2018:G:OP1	2.09	0.53
1:2A:2691:C:OP2	4:2E:111:ARG:NH2	2.42	0.53
2:2B:32:C:H2'	2:2B:33:G:O4'	2.09	0.53
32:2a:626:A:N3	39:2h:113:SER:OG	2.42	0.53
34:2c:40:ARG:NH2	34:2c:55:VAL:O	2.41	0.53
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.44	0.52
3:1D:52:ARG:NH2	59:1D:402:HOH:O	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:900:G:H4'	36:1e:20:GLN:HA	1.90	0.52
32:1a:1355:U:OP1	40:1i:72:GLY:N	2.42	0.52
44:1m:84:ILE:HG13	44:1m:86:CYS:H	1.74	0.52
1:2A:2529:A:OP2	59:2A:3652:HOH:O	2.19	0.52
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.39	0.52
5:2F:155:LEU:HD11	5:2F:176:LEU:HD12	1.91	0.52
32:2a:831:G:H2'	32:2a:832:G:H8	1.75	0.52
32:2a:1359:U:H2'	32:2a:1360:A:C8	2.44	0.52
1:1A:2120:U:H3	1:1A:2211:G:H1	1.56	0.52
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.90	0.52
48:1q:41:LYS:HZ1	48:1q:92:ARG:HH21	1.56	0.52
32:2a:712:A:H2'	32:2a:713:A:C8	2.44	0.52
5:1F:195:ASP:HB3	5:1F:198:ALA:H	1.75	0.52
6:1G:179:PRO:HB2	26:14:42:PHE:HE1	1.74	0.52
12:1Q:60:ARG:NH1	21:1Z:180:VAL:HG23	2.24	0.52
1:2A:885:U:H2'	1:2A:886:C:H6	1.73	0.52
1:2A:2879:C:H2'	1:2A:2880:C:O4'	2.10	0.52
11:2P:114:ILE:HG13	11:2P:125:VAL:HG21	1.92	0.52
25:23:30:ARG:H	25:23:33:GLN:NE2	2.06	0.52
32:2a:117:C:O2'	32:2a:286:C:O2	2.18	0.52
35:2d:62:GLN:O	35:2d:66:ARG:HB2	2.08	0.52
50:2s:69:HIS:HB2	50:2s:74:PHE:HE1	1.75	0.52
1:1A:703:U:H2'	1:1A:704:C:C6	2.44	0.52
1:1A:1158:U:H2'	1:1A:1159:G:C8	2.44	0.52
14:1S:11:LYS:O	14:1S:15:ARG:HG3	2.09	0.52
15:1T:96:ARG:HB3	15:1T:96:ARG:CZ	2.40	0.52
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.91	0.52
32:1a:266:A:H2'	32:1a:267:C:C6	2.44	0.52
35:1d:31:CYS:SG	35:1d:33:MET:HB2	2.49	0.52
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.26	0.52
45:1n:41:ARG:HG3	45:1n:42:ILE:HG13	1.91	0.52
49:1r:45:SER:OG	49:1r:46:GLU:N	2.40	0.52
1:2A:635:G:O2'	1:2A:639:A:N1	2.41	0.52
1:2A:675:G:OP1	30:28:19:SER:OG	2.25	0.52
1:2A:1032:G:O2'	1:2A:1045:A:N3	2.32	0.52
1:2A:1879:G:H2'	1:2A:1880:G:H8	1.74	0.52
2:2B:55:U:HO2'	6:2G:29:TRP:CD1	2.27	0.52
6:2G:16:ARG:NH2	6:2G:28:VAL:HG12	2.24	0.52
22:20:32:ARG:H	22:20:35:ASN:ND2	2.07	0.52
24:22:41:ILE:HG13	24:22:43:GLN:HB2	1.90	0.52
32:2a:1147:G:H1	32:2a:1154:C:H42	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1298:G:N2	32:2a:1301:A:OP2	2.35	0.52
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.10	0.52
45:2n:17:LYS:H	45:2n:17:LYS:CD	2.23	0.52
1:1A:2338:A:H2'	1:1A:2339:A:C8	2.43	0.52
6:1G:46:ALA:HB2	6:1G:53:LEU:HD12	1.90	0.52
10:1O:35:VAL:HG21	10:1O:105:GLU:HG3	1.90	0.52
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.91	0.52
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.73	0.52
32:1a:432:C:H2'	32:1a:433:U:H6	1.74	0.52
32:1a:826:C:H2'	32:1a:827:C:H6	1.75	0.52
1:2A:181:U:OP2	59:2A:3650:HOH:O	2.19	0.52
1:2A:1317:A:H3'	1:2A:1318:U:H5"	1.92	0.52
1:2A:2307:U:OP2	14:2S:9:ARG:NH2	2.42	0.52
6:2G:61:ALA:HA	6:2G:66:GLN:O	2.09	0.52
32:2a:1121:G:C6	32:2a:1123:C:H1'	2.45	0.52
33:2b:200:ILE:O	33:2b:202:PRO:HD3	2.10	0.52
35:2d:31:CYS:HB2	58:2d:501:SF4:S3	2.49	0.52
40:2i:77:ILE:O	40:2i:81:ILE:HG23	2.10	0.52
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.09	0.52
1:1A:296:C:H2'	1:1A:297:G:C8	2.44	0.52
1:1A:2226:G:OP2	1:1A:2226:G:H4'	2.07	0.52
1:1A:2583:A:N7	4:1E:144:ARG:HD2	2.23	0.52
32:1a:305:G:O2'	32:1a:591:A:N1	2.38	0.52
43:1l:34:ARG:NH2	59:1l:5001:HOH:O	2.35	0.52
47:1p:18:ARG:NH1	47:1p:32:TYR:OH	2.43	0.52
1:2A:44:C:H2'	1:2A:45:C:C6	2.45	0.52
1:2A:235:G:H4'	1:2A:412:G:C5	2.44	0.52
1:2A:351:U:H4'	20:2Y:68:HIS:CE1	2.45	0.52
1:2A:1174:A:N6	1:2A:2502:U:OP1	2.42	0.52
21:2Z:150:LEU:HD11	21:2Z:172:ALA:HB3	1.91	0.52
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.92	0.52
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.74	0.52
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.25	0.52
32:1a:924:A:H2'	32:1a:925:G:C8	2.45	0.52
32:1a:1374:U:H2'	32:1a:1375:G:C8	2.45	0.52
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.24	0.52
50:1s:63:THR:OG1	50:1s:64:GLU:N	2.42	0.52
1:2A:353:A:HO2'	1:2A:354:A:H8	1.56	0.52
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.10	0.52
38:2g:42:ILE:HG22	38:2g:120:ILE:HD11	1.92	0.52
42:2k:99:GLN:C	42:2k:101:SER:H	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:3:ARG:HH21	45:2n:4:LYS:HE3	1.75	0.52
49:2r:58:LEU:HD12	49:2r:62:GLU:HB3	1.92	0.52
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.91	0.52
1:1A:1086:C:H42	1:1A:1159:G:H1	1.56	0.52
4:1E:82:ARG:HG2	4:1E:83:ASP:N	2.24	0.52
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.91	0.52
22:10:32:ARG:H	22:10:35:ASN:ND2	2.07	0.52
32:1a:672:G:H2'	32:1a:673:C:C6	2.45	0.52
33:1b:78:GLN:NE2	33:1b:94:ASN:O	2.39	0.52
1:2A:947:C:H2'	1:2A:948:C:C6	2.45	0.52
1:2A:1812:C:H1'	1:2A:2620:U:H5"	1.92	0.52
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.45	0.52
32:2a:1116:G:H2'	32:2a:1117:G:H8	1.75	0.52
36:2e:93:PRO:HG2	39:2h:105:ARG:NH2	2.25	0.52
1:1A:440:C:H2'	1:1A:441:A:C8	2.44	0.52
1:1A:1076:G:H5"	31:19:8:LYS:HE3	1.90	0.52
32:1a:493:A:O2'	32:1a:494:A:OP1	2.23	0.52
32:1a:1395:C:H2'	32:1a:1396:A:C8	2.45	0.52
32:1a:1424:G:H5"	32:1a:1425:G:H5'	1.92	0.52
35:1d:155:LEU:HD23	35:1d:156:GLU:H	1.75	0.52
3:2D:71:ASP:CB	3:2D:103:ARG:HH22	2.23	0.52
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.90	0.52
12:2Q:60:ARG:NH2	21:2Z:181:GLU:OE2	2.40	0.52
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.42	0.52
32:2a:914:C:H2'	32:2a:915:A:O4'	2.09	0.52
32:2a:928:U:H3'	44:2m:102:ARG:NH2	2.24	0.52
32:2a:1154:C:H2'	32:2a:1155:G:C8	2.45	0.52
34:2c:186:PHE:HB3	34:2c:198:VAL:O	2.09	0.52
32:1a:1223:G:H2'	32:1a:1224:C:C6	2.44	0.52
1:2A:117:U:OP2	59:2A:3651:HOH:O	2.19	0.52
1:2A:703:U:H2'	1:2A:704:C:C6	2.45	0.52
1:2A:1291:A:OP1	5:2F:38:ARG:NH1	2.42	0.52
1:2A:1828:U:H5"	3:2D:260:ARG:HB3	1.91	0.52
1:2A:2858:U:H4'	1:2A:2877:A:C2	2.45	0.52
8:2I:104:GLN:HG3	8:2I:105:HIS:CD2	2.45	0.52
32:2a:30:G:N2	32:2a:538:C:O2	2.38	0.52
32:2a:810:C:H2'	32:2a:811:U:C6	2.44	0.52
33:2b:15:VAL:O	33:2b:16:HIS:ND1	2.42	0.52
33:2b:179:LYS:HA	39:2h:72:PRO:HG3	1.92	0.52
44:2m:20:THR:C	44:2m:22:ILE:H	2.18	0.52
45:2n:32:SER:O	45:2n:40:CYS:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2347:A:H61	22:10:43:THR:CG2	2.23	0.51
32:1a:1267:A:H4'	32:1a:1268:A:O5'	2.09	0.51
32:1a:1270:A:N3	32:1a:1334:C:O2'	2.35	0.51
35:1d:60:GLU:OE1	35:1d:198:VAL:HA	2.10	0.51
50:1s:63:THR:HG23	50:1s:66:MET:HG2	1.91	0.51
1:2A:1457:A:H2'	1:2A:1458:G:C8	2.45	0.51
32:2a:522:G:H5"	43:2l:114:LYS:HB2	1.91	0.51
32:2a:609:G:H4'	47:2p:16:HIS:CD2	2.44	0.51
32:2a:703:C:O2'	49:2r:49:LYS:HB3	2.09	0.51
32:2a:1208:C:O2'	44:2m:111:LYS:NZ	2.26	0.51
37:2f:44:GLY:HA2	37:2f:59:TYR:CZ	2.45	0.51
50:2s:27:GLU:O	50:2s:28:LYS:NZ	2.42	0.51
50:2s:48:THR:HG22	50:2s:61:TYR:HA	1.92	0.51
1:1A:346:G:C8	5:1F:171:PRO:HG3	2.45	0.51
1:1A:894:G:H2'	1:1A:895:A:C8	2.46	0.51
1:1A:1232:U:H4'	17:1V:79:VAL:HG22	1.93	0.51
34:1c:64:VAL:HG13	34:1c:99:VAL:HA	1.91	0.51
1:2A:846:A:H8	1:2A:846:A:OP1	1.93	0.51
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.92	0.51
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.34	0.51
32:2a:981:G:C2	32:2a:982:G:C8	2.98	0.51
32:2a:1328:A:H5"	40:2i:120:ARG:HH12	1.74	0.51
45:2n:4:LYS:O	45:2n:7:ILE:HG12	2.10	0.51
1:1A:904:U:O2	1:1A:2279:A:H2'	2.09	0.51
1:1A:1674:U:H2'	1:1A:1675:G:C8	2.44	0.51
38:1g:73:MET:HA	38:1g:90:GLU:HA	1.93	0.51
41:1j:49:VAL:HG23	45:1n:41:ARG:HD2	1.90	0.51
1:2A:2354:C:HO2'	1:2A:2384:G:HO2'	1.57	0.51
1:2A:2554:G:H2'	1:2A:2555:G:C8	2.45	0.51
1:1A:138:A:H8	1:1A:1453:C:O2'	1.94	0.51
1:1A:761:G:C2	46:1o:56:LEU:HD21	2.46	0.51
1:1A:1312:U:OP1	59:1A:4364:HOH:O	2.19	0.51
1:1A:1873:C:H5'	3:1D:253:GLN:NE2	2.25	0.51
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.93	0.51
32:1a:584:C:H2'	32:1a:585:C:H6	1.75	0.51
32:1a:1048:U:O2'	32:1a:1049:C:OP2	2.22	0.51
33:1b:15:VAL:HG22	33:1b:210:SER:HB2	1.92	0.51
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.91	0.51
1:2A:645:A:OP2	11:2P:108:LYS:NZ	2.43	0.51
1:2A:1476:U:H2'	1:2A:1477:C:C6	2.46	0.51
1:2A:1643:C:H2'	1:2A:1644:C:H6	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1887:G:O6	59:2A:3630:HOH:O	2.14	0.51
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.41	0.51
32:2a:768:C:H2'	32:2a:769:G:H8	1.74	0.51
32:2a:1054:C:H2'	32:2a:1055:G:H8	1.76	0.51
34:2c:139:GLN:O	34:2c:143:GLU:HG2	2.11	0.51
1:1A:2622:U:C4	27:15:3:LYS:HG2	2.46	0.51
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.75	0.51
26:14:63:TYR:N	26:14:64:GLY:HA2	2.25	0.51
32:1a:672:G:O2'	32:1a:688:A:N1	2.37	0.51
32:1a:1222:U:OP2	38:1g:116:ALA:N	2.36	0.51
1:2A:661:A:H2'	11:2P:117:GLU:OE2	2.10	0.51
32:2a:1263:U:H5"	32:2a:1264:C:C5	2.37	0.51
54:2x:17:C:H2'	54:2x:17(A):U:H2'	1.91	0.51
1:1A:1934:A:N7	32:1a:1472:G:H5"	2.26	0.51
1:1A:2795:G:N7	59:1A:4502:HOH:O	2.34	0.51
15:1T:55:ASN:N	15:1T:59:THR:HG22	2.19	0.51
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.44	0.51
32:1a:265:C:H2'	32:1a:266:A:C8	2.46	0.51
33:1b:15:VAL:O	33:1b:16:HIS:HB3	2.10	0.51
33:1b:77:ALA:HA	33:1b:80:ILE:HG22	1.93	0.51
45:1n:4:LYS:HG3	45:1n:7:ILE:HD11	1.92	0.51
1:2A:843:C:OP1	5:2F:60:SER:OG	2.27	0.51
1:2A:1227:G:O3'	25:23:29:ARG:NH1	2.37	0.51
1:2A:2595:U:O4	55:2z:9:ARG:NH2	2.41	0.51
1:2A:2824:C:C5'	27:25:29:THR:HG21	2.41	0.51
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.11	0.51
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.25	0.51
32:2a:931:G:H5'	32:2a:943:A:H61	1.74	0.51
32:2a:989:G:H2'	32:2a:990:G:H8	1.76	0.51
32:2a:1329:G:H2'	40:2i:107:ARG:HG3	1.93	0.51
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.45	0.51
43:2l:28:LYS:HE3	43:2l:62:SER:HB2	1.91	0.51
1:1A:6:G:H2'	1:1A:7:A:O4'	2.10	0.51
1:1A:33:C:H5"	1:1A:34:G:OP2	2.10	0.51
1:1A:2249:G:N3	1:1A:2249:G:H2'	2.25	0.51
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.39	0.51
26:14:58:ARG:HB3	26:14:58:ARG:HH11	1.75	0.51
28:16:4:GLU:O	28:16:27:LYS:HE2	2.11	0.51
32:1a:994:A:O3'	45:1n:15:LYS:NZ	2.44	0.51
44:1m:4:ILE:HG13	44:1m:57:ARG:HA	1.93	0.51
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:560:A:H2'	1:2A:561:C:C6	2.46	0.51
1:2A:625:A:H4'	1:2A:626:G:H5'	1.93	0.51
1:2A:1673:G:H2'	1:2A:1674:U:H6	1.76	0.51
9:2N:36:GLY:HA2	9:2N:38:HIS:CE1	2.45	0.51
32:2a:812:A:H2'	32:2a:813:G:O4'	2.11	0.51
46:2o:24:SER:OG	46:2o:25:THR:N	2.43	0.51
1:1A:1803:A:OP2	59:1A:4363:HOH:O	2.18	0.51
1:1A:1816:A:H1'	1:1A:1959:A:N6	2.25	0.51
32:1a:954:G:H5'	32:1a:1340:U:O2'	2.11	0.51
32:1a:1240:G:H2'	32:1a:1241:C:H6	1.75	0.51
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.93	0.51
41:1j:13:HIS:H	41:1j:13:HIS:CD2	2.27	0.51
1:2A:552:A:OP2	9:2N:114:ARG:NH1	2.43	0.51
1:2A:663:U:H2'	1:2A:664:C:C6	2.45	0.51
1:2A:1103:G:H2'	1:2A:1104:G:C8	2.45	0.51
1:2A:1739:U:O2'	3:2D:14:ARG:NH2	2.44	0.51
32:2a:811:U:H2'	32:2a:837:A:H61	1.76	0.51
32:2a:1043:C:H2'	32:2a:1044:G:C8	2.45	0.51
32:2a:1268:A:N1	52:2u:18:TYR:OH	2.43	0.51
1:1A:2244:U:H2'	1:1A:2245:G:C8	2.45	0.51
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.76	0.51
12:1Q:42:ILE:HG12	12:1Q:103:MET:HE1	1.92	0.51
32:1a:155:A:H61	32:1a:341:C:P	2.34	0.51
48:1q:74:LEU:HD13	48:1q:75:ARG:HG2	1.92	0.51
1:2A:990:G:N2	1:2A:1016:G:H1'	2.26	0.51
1:2A:2033:G:OP1	18:2W:11:ARG:NH2	2.43	0.51
5:2F:197:ASP:O	5:2F:200:GLU:HB2	2.10	0.51
19:2X:57:LEU:HD11	19:2X:78:LYS:HD2	1.92	0.51
39:2h:12:ARG:NH1	39:2h:27:PRO:HD3	2.25	0.51
42:2k:82:VAL:HB	42:2k:108:ILE:HG12	1.92	0.51
1:1A:2315:G:H22	1:1A:2323:U:H3	1.58	0.51
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.75	0.51
8:1I:132:PRO:O	59:1I:5001:HOH:O	2.19	0.51
12:1Q:21:THR:HG21	12:1Q:101:ARG:N	2.26	0.51
13:1R:36:THR:HG22	13:1R:37:THR:H	1.75	0.51
32:1a:71:G:H2'	32:1a:72:C:H6	1.76	0.51
32:1a:1331:A:H5"	40:1i:121:ARG:HB2	1.93	0.51
35:1d:88:VAL:HA	36:1e:97:GLY:HA2	1.94	0.51
36:1e:85:GLY:C	36:1e:87:SER:H	2.19	0.51
48:1q:4:LYS:HE2	48:1q:6:LEU:HD11	1.91	0.51
1:2A:1765:G:H8	1:2A:1769:A:H62	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2012:U:H2'	1:2A:2013:G:H5"	1.93	0.51
1:2A:2824:C:H2'	1:2A:2825:C:C6	2.45	0.51
6:2G:114:ILE:HG23	6:2G:136:ARG:NH2	2.26	0.51
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.92	0.51
32:2a:955:A:O2'	32:2a:959:U:N3	2.43	0.51
32:2a:1034:C:H2'	32:2a:1035:U:C6	2.46	0.51
33:2b:127:ILE:C	33:2b:129:GLU:H	2.18	0.51
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.92	0.51
49:2r:45:SER:OG	49:2r:46:GLU:N	2.44	0.51
1:1A:2488:C:O2	31:19:4:ARG:NH2	2.43	0.50
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.92	0.50
7:1H:55:PRO:HG2	7:1H:61:HIS:CE1	2.45	0.50
32:1a:1310:C:OP1	52:1u:21:TYR:OH	2.20	0.50
1:2A:239:A:C5	1:2A:240:G:H1'	2.46	0.50
1:2A:330:G:N1	1:2A:333:A:OP2	2.44	0.50
1:2A:902:C:O2'	1:2A:903:C:OP1	2.25	0.50
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.46	0.50
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.11	0.50
35:2d:150:GLU:HA	35:2d:153:ARG:HE	1.75	0.50
38:2g:47:CYS:O	38:2g:50:ILE:HG12	2.11	0.50
1:1A:2604:U:H2'	1:1A:2605:C:C6	2.46	0.50
1:1A:2831:G:O2'	1:1A:2833:C:OP2	2.23	0.50
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.93	0.50
15:1T:51:ARG:HD3	59:1T:302:HOH:O	2.12	0.50
33:1b:42:ILE:HG21	33:1b:202:PRO:O	2.11	0.50
1:2A:63:C:O2'	1:2A:481:C:N3	2.41	0.50
1:2A:2043:U:O2'	1:2A:2628:C:H5'	2.12	0.50
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.76	0.50
32:2a:630:U:H2'	32:2a:631:C:H6	1.73	0.50
32:2a:900:G:N3	32:2a:1381:A:H2	2.09	0.50
32:2a:910:C:H2'	32:2a:911:G:C8	2.46	0.50
32:2a:945:C:H3'	32:2a:946:A:H2'	1.93	0.50
32:2a:1070:G:N2	32:2a:1082:G:H1'	2.26	0.50
54:2x:15:G:H2'	54:2x:59:A:N1	2.26	0.50
1:1A:2017:C:H4'	1:1A:2018:G:OP1	2.12	0.50
1:1A:2622:U:H5'	1:1A:2622:U:H6	1.75	0.50
32:1a:719:C:H2'	32:1a:720:C:C6	2.47	0.50
32:1a:1101:C:H1'	32:1a:1161:A:C4	2.47	0.50
32:1a:1117:G:H2'	32:1a:1117:G:N3	2.27	0.50
38:1g:65:ALA:O	38:1g:69:VAL:HG23	2.11	0.50
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:75:C:H42	1:2A:106:G:H1	1.58	0.50
1:2A:200:G:H2'	1:2A:201:A:O4'	2.11	0.50
1:2A:1673:G:H2'	1:2A:1674:U:C6	2.47	0.50
1:2A:2565:U:H2'	1:2A:2566:U:C6	2.47	0.50
10:2O:64:ARG:NH1	10:2O:81:ASP:OD1	2.44	0.50
12:2Q:64:ILE:HG22	12:2Q:106:VAL:HG12	1.93	0.50
32:2a:171:C:H2'	32:2a:172:C:C6	2.46	0.50
32:2a:1288:A:N6	32:2a:1313:G:O4'	2.44	0.50
41:2j:16:LEU:HD13	41:2j:70:ARG:HG2	1.93	0.50
41:2j:50:ILE:HD11	41:2j:57:LYS:HZ2	1.75	0.50
47:2p:21:VAL:HG23	47:2p:33:ILE:HB	1.93	0.50
1:1A:714:G:H5'	1:1A:715:G:OP2	2.11	0.50
1:1A:725:C:OP1	59:1A:4369:HOH:O	2.19	0.50
1:1A:991:G:H2'	1:1A:992:G:C8	2.47	0.50
1:1A:1184:C:O3'	9:1N:25:ARG:NH1	2.43	0.50
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.92	0.50
33:1b:55:PHE:HA	33:1b:58:ILE:HG12	1.94	0.50
39:1h:96:GLY:H	39:1h:99:GLU:CD	2.18	0.50
1:2A:2593:G:OP2	59:2A:3649:HOH:O	2.19	0.50
3:2D:60:ARG:HD3	3:2D:86:PRO:HB2	1.93	0.50
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.94	0.50
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.12	0.50
11:2P:81:GLN:NE2	11:2P:105:LEU:O	2.44	0.50
32:2a:1435:G:OP1	51:2t:39:LYS:NZ	2.39	0.50
1:1A:124:A:OP1	59:1A:4370:HOH:O	2.19	0.50
1:1A:894:G:C4	1:1A:977:A:H8	2.30	0.50
1:1A:922:C:H2'	1:1A:923:U:O4'	2.11	0.50
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.94	0.50
26:14:46:GLN:HB2	26:14:48:ARG:CZ	2.42	0.50
32:1a:812:A:H2'	32:1a:813:G:O4'	2.11	0.50
32:1a:1112:C:N4	32:1a:1126:G:H1	2.09	0.50
32:1a:1330:U:OP2	32:1a:1356:G:N1	2.36	0.50
33:1b:167:PRO:HG3	33:1b:188:ALA:HB2	1.94	0.50
33:1b:174:VAL:HG11	33:1b:196:LEU:HD23	1.94	0.50
1:2A:466:U:H2'	1:2A:467:G:C8	2.47	0.50
1:2A:1050:C:H2'	1:2A:1051:C:H6	1.77	0.50
1:2A:1587:G:H2'	1:2A:1588:A:H8	1.77	0.50
6:2G:151:ALA:O	6:2G:153:ARG:HD3	2.12	0.50
32:2a:485:C:H2'	32:2a:486:G:C8	2.42	0.50
32:2a:942:A:N3	32:2a:947:A:O2'	2.40	0.50
32:2a:1268:A:C8	32:2a:1269:A:H4'	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:16:HIS:CD2	33:2b:204:ASN:H	2.29	0.50
40:2i:54:ASP:O	40:2i:56:LEU:N	2.44	0.50
41:2j:48:THR:HB	41:2j:62:HIS:CE1	2.47	0.50
43:2l:27:LEU:HD13	43:2l:98:TYR:CE1	2.47	0.50
1:1A:2638:G:O2'	1:1A:2793:A:N1	2.37	0.50
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.94	0.50
20:1Y:92:ASN:CB	20:1Y:94:LYS:H	2.23	0.50
42:1k:48:ILE:HG21	42:1k:63:LEU:HB3	1.93	0.50
1:2A:1302:C:O5'	1:2A:1302:C:H6	1.94	0.50
1:2A:1820:C:H2'	1:2A:1821:A:C5	2.46	0.50
1:2A:2700:U:P	1:2A:2731:G:H22	2.35	0.50
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.75	0.50
14:2S:10:ARG:HH21	14:2S:91:PRO:HB2	1.76	0.50
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.93	0.50
32:2a:407:A:H2'	32:2a:408:A:H4'	1.93	0.50
32:2a:982:G:H2'	32:2a:983:A:C4'	2.42	0.50
33:2b:19:HIS:CE1	33:2b:206:ASP:HB2	2.46	0.50
35:2d:3:ARG:HH12	35:2d:5:ILE:H	1.59	0.50
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.94	0.50
1:1A:1230:G:OP2	59:1A:4320:HOH:O	2.20	0.50
1:1A:1785:A:OP2	15:1T:113:LYS:NZ	2.43	0.50
1:1A:2458:G:OP2	59:1A:4374:HOH:O	2.19	0.50
8:1I:132:PRO:HD2	8:1I:136:VAL:O	2.12	0.50
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	1.93	0.50
26:14:26:SER:OG	26:14:27:THR:N	2.44	0.50
32:1a:372:G:H2'	32:1a:373:G:H8	1.77	0.50
1:2A:26:G:N2	1:2A:536:G:H1'	2.26	0.50
1:2A:720:G:H1'	5:2F:74:ARG:HD3	1.94	0.50
1:2A:998:G:O2'	1:2A:2285:A:N1	2.43	0.50
32:2a:74:G:H1	32:2a:90:U:H3	1.60	0.50
32:2a:582:U:O4	59:2a:3325:HOH:O	2.19	0.50
32:2a:651:G:O2'	46:2o:49:ASP:OD1	2.16	0.50
32:2a:799:A:N7	32:2a:1487:C:O2'	2.38	0.50
41:2j:89:ASP:O	41:2j:91:PRO:HD3	2.12	0.50
1:1A:2297:A:H4'	1:1A:2298:A:O4'	2.11	0.50
21:1Z:19:ARG:NH1	21:1Z:84:GLU:O	2.44	0.50
32:1a:1150:A:H2'	32:1a:1151:A:C8	2.47	0.50
1:2A:1026:A:N1	1:2A:2048:G:O2'	2.45	0.50
1:2A:1105:U:O4'	1:2A:1107:G:H5"	2.12	0.50
6:2G:18:GLU:HG2	6:2G:175:LEU:HD21	1.94	0.50
32:2a:915:A:H1'	32:2a:1362:G:N2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1296:C:OP2	50:2s:4:SER:OG	2.24	0.50
36:2e:43:LEU:HB2	36:2e:136:MET:SD	2.52	0.50
50:2s:51:VAL:HG22	50:2s:71:LEU:HG	1.94	0.50
1:1A:358:C:H4'	20:1Y:73:ARG:HD3	1.94	0.50
1:1A:600:A:H3'	59:1A:4647:HOH:O	2.11	0.50
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.94	0.50
12:1Q:60:ARG:HD2	21:1Z:179:ASP:OD1	2.12	0.50
34:1c:70:VAL:HG22	34:1c:72:LYS:H	1.76	0.50
34:1c:124:ILE:HG12	34:1c:130:VAL:HG22	1.94	0.50
44:1m:92:HIS:CE1	44:1m:98:VAL:HG11	2.47	0.50
10:2O:88:ASN:HD21	10:2O:92:GLU:HB2	1.77	0.50
26:24:41:PRO:HG3	26:24:49:PHE:CZ	2.47	0.50
32:2a:1406:G:H2'	32:2a:1407:C:C6	2.46	0.50
34:2c:47:LEU:HD21	34:2c:52:LEU:HG	1.94	0.50
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.12	0.50
1:1A:2019:G:OP1	59:1A:4375:HOH:O	2.20	0.49
1:1A:2544:A:H2'	1:1A:2545:A:O4'	2.12	0.49
1:1A:2855:G:H2'	1:1A:2856:U:O4'	2.12	0.49
19:1X:57:LEU:CD1	19:1X:78:LYS:HB2	2.41	0.49
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.77	0.49
32:1a:459:G:H2'	32:1a:460:G:H8	1.76	0.49
34:1c:44:GLU:HA	34:1c:52:LEU:HD12	1.93	0.49
1:2A:820:A:N3	1:2A:820:A:H2'	2.27	0.49
1:2A:885:U:H1'	1:2A:1235:G:H1'	1.93	0.49
1:2A:2375:C:H2'	1:2A:2376:G:O4'	2.11	0.49
2:2B:37:C:N3	2:2B:48:A:O2'	2.45	0.49
21:2Z:157:LEU:HD13	21:2Z:162:GLU:HA	1.94	0.49
32:2a:91:G:O2'	32:2a:92:G:H5"	2.12	0.49
32:2a:108:U:H2'	32:2a:109:G:C8	2.47	0.49
32:2a:488:C:H1'	32:2a:494:A:C4	2.47	0.49
32:2a:583:C:H5"	39:2h:96:GLY:HA2	1.94	0.49
32:2a:711:G:OP1	32:2a:726:G:N2	2.24	0.49
32:2a:749:G:N1	32:2a:796:C:O2'	2.39	0.49
32:2a:1246:C:O2	32:2a:1254:G:N2	2.45	0.49
1:1A:307:U:H2'	1:1A:308:C:H6	1.76	0.49
1:1A:1073:A:N6	1:1A:1170:G:H2'	2.26	0.49
1:1A:1096:G:H22	1:1A:1153:U:H5	1.60	0.49
1:1A:2341:G:H2'	1:1A:2342:G:O4'	2.12	0.49
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.12	0.49
14:1S:6:ALA:O	14:1S:10:ARG:HG3	2.13	0.49
32:1a:57:U:H2'	32:1a:58:G:H8	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:48:THR:HG22	50:1s:61:TYR:HA	1.94	0.49
1:2A:489:U:O4	59:2A:3645:HOH:O	2.18	0.49
1:2A:909:A:H2'	1:2A:910:G:C8	2.48	0.49
1:2A:1423:A:O2'	1:2A:1424:A:H3'	2.11	0.49
1:2A:1508:C:H4'	1:2A:2714:C:H5'	1.94	0.49
32:2a:250:G:O3'	48:2q:69:LYS:NZ	2.44	0.49
32:2a:1135:A:H5'	41:2j:13:HIS:HD2	1.77	0.49
33:2b:167:PRO:HG3	33:2b:188:ALA:HB2	1.94	0.49
33:2b:219:VAL:O	33:2b:223:ILE:HG12	2.12	0.49
32:1a:141:G:H2'	32:1a:142:G:H8	1.78	0.49
34:1c:33:LEU:HD21	45:1n:53:LEU:HD21	1.94	0.49
32:2a:60:A:H3'	32:2a:327:G:H22	1.77	0.49
32:2a:925:G:H2'	32:2a:926:C:O4'	2.12	0.49
32:2a:1385:C:H2'	32:2a:1386:C:O4'	2.13	0.49
32:2a:1490:U:H2'	32:2a:1491:A:H8	1.77	0.49
1:1A:550:A:O2'	1:1A:2064:C:O2	2.26	0.49
32:1a:77:G:H1'	32:1a:78:G:H8	1.77	0.49
32:1a:221:C:H2'	32:1a:222:G:H8	1.76	0.49
32:1a:1148:C:H2'	32:1a:1149:G:O4'	2.13	0.49
34:1c:40:ARG:HG2	34:1c:55:VAL:HG11	1.95	0.49
36:1e:75:THR:OG1	36:1e:76:ILE:N	2.43	0.49
1:2A:50:A:OP2	1:2A:114:G:N1	2.40	0.49
1:2A:168:G:OP2	29:27:32:LYS:HE3	2.13	0.49
1:2A:1051:C:C2	1:2A:1182:G:N2	2.80	0.49
1:2A:1473:C:N4	1:2A:1616:A:OP2	2.37	0.49
1:2A:1586:U:C2'	1:2A:1587:G:H5'	2.42	0.49
6:2G:28:VAL:O	6:2G:31:VAL:HG13	2.11	0.49
6:2G:33:ARG:HH12	6:2G:162:THR:HG21	1.77	0.49
24:22:1:MET:HE3	24:22:5:GLU:HB3	1.94	0.49
32:2a:727:U:H2'	32:2a:728:C:C6	2.48	0.49
32:2a:1287:G:H5'	52:2u:4:GLY:HA3	1.95	0.49
45:2n:17:LYS:H	45:2n:17:LYS:CE	2.24	0.49
1:1A:274:C:H2'	1:1A:275:C:C6	2.47	0.49
1:1A:817:G:OP2	59:1A:4372:HOH:O	2.19	0.49
1:1A:2284:A:H2'	1:1A:2285:A:C8	2.47	0.49
21:1Z:75:ASN:O	21:1Z:84:GLU:HG2	2.13	0.49
32:1a:267:C:H2'	32:1a:268:C:H6	1.77	0.49
32:1a:661:U:H3	32:1a:697:G:H22	1.61	0.49
32:1a:825:U:C4	32:1a:826:C:H1'	2.48	0.49
39:1h:7:ALA:HB2	39:1h:85:ARG:HD2	1.95	0.49
1:2A:184:A:H62	11:2P:38:GLN:HE22	1.59	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:755:U:H2'	1:2A:756:G:C8	2.47	0.49
1:2A:947:C:H2'	1:2A:948:C:H6	1.78	0.49
1:2A:1397:U:OP2	59:2A:3653:HOH:O	2.19	0.49
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.78	0.49
32:2a:212:G:O2'	32:2a:213:C:O5'	2.31	0.49
32:2a:823:U:O2'	32:2a:824:C:OP1	2.30	0.49
32:2a:969:U:H4'	32:2a:970:U:OP2	2.12	0.49
32:2a:1053:U:H2'	32:2a:1054:C:H6	1.77	0.49
32:1a:335:C:H2'	32:1a:336:U:C6	2.48	0.49
32:1a:887:A:H2'	32:1a:888:C:O4'	2.13	0.49
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.47	0.49
1:2A:67:C:H2'	1:2A:68:G:H8	1.78	0.49
1:2A:1284:G:H2'	1:2A:1285:U:O4'	2.13	0.49
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.78	0.49
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.47	0.49
11:2P:39:LYS:HA	11:2P:45:LEU:HG	1.94	0.49
34:2c:131:ARG:NH1	36:2e:50:GLU:HG2	2.28	0.49
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.20	0.49
1:1A:584:U:OP2	59:1A:4377:HOH:O	2.20	0.49
1:1A:1809:U:H2'	59:1A:4496:HOH:O	2.12	0.49
1:1A:2723:U:H1'	1:1A:2724:A:C8	2.48	0.49
1:1A:2824:C:H5'	27:15:29:THR:HG21	1.95	0.49
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.77	0.49
32:1a:71:G:H2'	32:1a:72:C:C6	2.48	0.49
32:1a:526:G:P	35:1d:10:ARG:HH22	2.34	0.49
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.60	0.49
1:2A:628:U:H4'	1:2A:704:C:H4'	1.95	0.49
1:2A:1121:C:H3'	1:2A:1122:A:C8	2.47	0.49
1:2A:1159:G:H2'	1:2A:1160:G:C8	2.48	0.49
1:2A:2121:G:H2'	1:2A:2122:G:C8	2.48	0.49
1:2A:2578:G:H2'	1:2A:2579:C:C6	2.47	0.49
3:2D:133:LEU:HD23	3:2D:136:ILE:HD12	1.95	0.49
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.47	0.49
32:2a:933:U:H2'	32:2a:934:U:O4'	2.13	0.49
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.95	0.49
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.13	0.49
50:2s:13:ASP:HA	50:2s:16:LEU:HB3	1.94	0.49
1:1A:663:U:H2'	1:1A:664:C:C6	2.48	0.49
1:1A:1616:A:H2'	1:1A:1617:A:C8	2.47	0.49
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.94	0.49
32:1a:1169:G:H4'	40:1i:111:ARG:HH11	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.13	0.49
48:1q:67:LYS:C	48:1q:69:LYS:H	2.19	0.49
49:1r:42:ARG:HA	49:1r:42:ARG:HH21	1.77	0.49
1:2A:466:U:O2	5:2F:46:ARG:NH2	2.40	0.49
1:2A:2435:C:O2	1:2A:2440:G:O2'	2.26	0.49
10:2O:77:ILE:HB	15:2T:74:ARG:HD3	1.93	0.49
14:2S:3:ARG:HG2	14:2S:3:ARG:HH11	1.77	0.49
16:2U:44:ASN:HD21	17:2V:75:PHE:HB3	1.77	0.49
17:2V:25:LEU:H	17:2V:92:THR:HG1	1.59	0.49
32:2a:1207:A:H2'	32:2a:1208:C:C5	2.48	0.49
50:2s:36:ARG:NH2	50:2s:72:GLY:O	2.45	0.49
1:1A:2416:G:O2'	1:1A:2417:U:OP1	2.23	0.49
1:1A:2650:A:OP2	59:1A:4373:HOH:O	2.19	0.49
15:1T:23:ARG:HG3	15:1T:120:ARG:NH1	2.26	0.49
15:1T:108:ARG:CZ	15:1T:108:ARG:HB3	2.42	0.49
32:1a:205:G:H2'	32:1a:206:G:H8	1.77	0.49
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.78	0.49
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	1.94	0.49
1:2A:322:A:N1	1:2A:345:A:O2'	2.38	0.49
1:2A:1643:C:H2'	1:2A:1644:C:C6	2.47	0.49
1:2A:1675:G:H2'	1:2A:1676:C:C6	2.47	0.49
1:2A:1685:U:C2'	1:2A:1686:C:H5"	2.42	0.49
1:2A:1777:G:H2'	1:2A:1778:G:H8	1.78	0.49
1:2A:2080:A:O2'	5:2F:69:HIS:HD2	1.96	0.49
6:2G:36:LYS:HG2	6:2G:160:VAL:HB	1.94	0.49
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.13	0.49
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.94	0.49
32:2a:417:U:O2'	32:2a:419:G:N7	2.43	0.49
32:2a:759:G:N2	32:2a:788:U:O4	2.46	0.49
32:2a:960:U:N3	32:2a:1205:C:N3	2.61	0.49
32:2a:1170:A:H2'	32:2a:1171:C:O4'	2.12	0.49
35:2d:196:LEU:O	35:2d:198:VAL:N	2.40	0.49
36:2e:19:MET:SD	36:2e:24:ARG:HG3	2.53	0.49
38:2g:121:ALA:O	38:2g:125:MET:HG3	2.12	0.49
51:2t:16:HIS:O	51:2t:19:SER:OG	2.21	0.49
1:1A:466:U:O2	5:1F:46:ARG:NH2	2.41	0.49
1:1A:1633:C:H2'	1:1A:1634:C:H6	1.77	0.49
7:1H:101:ARG:HH22	7:1H:122:THR:HA	1.78	0.49
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.13	0.49
10:1O:71:ARG:NH2	10:1O:105:GLU:OE1	2.40	0.49
32:1a:122:G:O2'	48:1q:3:LYS:HE2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1184:G:N2	45:1n:43:CYS:HB3	2.27	0.49
32:1a:1346:A:H4'	32:1a:1347:U:H2'	1.95	0.49
35:1d:181:MET:HE3	35:1d:181:MET:HB3	1.65	0.49
36:1e:140:ARG:O	36:1e:143:ARG:NH2	2.46	0.49
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.45	0.49
1:2A:1000:G:OP2	12:2Q:14:ARG:NH2	2.46	0.49
7:2H:3:ARG:HH22	7:2H:5:GLY:H	1.61	0.49
32:2a:262:G:O2'	48:2q:67:LYS:HB2	2.13	0.49
32:2a:265:C:H2'	32:2a:266:A:C8	2.48	0.49
32:2a:544:U:H4'	32:2a:545:U:O5'	2.12	0.49
32:2a:604:C:C2	35:2d:135:LEU:HG	2.48	0.49
32:2a:963:C:H2'	32:2a:964:A:C8	2.48	0.49
32:2a:1355:U:OP1	40:2i:72:GLY:N	2.46	0.49
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.13	0.49
1:1A:1924:G:OP1	3:1D:241:PRO:HB2	2.13	0.48
1:1A:1937:A:N1	32:1a:1391:A:O2'	2.43	0.48
8:1I:27:ARG:HD2	23:11:71:TYR:CE1	2.47	0.48
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.93	0.48
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.27	0.48
32:1a:1100:G:H5"	40:1i:104:ARG:NH2	2.28	0.48
33:1b:93:VAL:HG21	33:1b:97:TRP:CD1	2.45	0.48
40:1i:106:ALA:O	40:1i:108:VAL:HG22	2.13	0.48
1:2A:330:G:O2'	1:2A:332:G:N7	2.44	0.48
1:2A:775:G:C5	3:2D:208:LYS:HB2	2.48	0.48
1:2A:2122:G:O6	1:2A:2209:C:N4	2.45	0.48
1:2A:2660:U:H2'	1:2A:2661:U:C6	2.48	0.48
2:2B:55:U:C1'	6:2G:29:TRP:HE1	2.26	0.48
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.60	0.48
3:2D:200:ASP:HB2	59:2D:416:HOH:O	2.12	0.48
26:24:59:PHE:HA	26:24:61:ARG:N	2.28	0.48
32:2a:658:G:H2'	32:2a:659:A:H8	1.77	0.48
32:2a:898:U:H2'	32:2a:899:U:C6	2.47	0.48
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.95	0.48
45:2n:7:ILE:HG22	45:2n:23:ARG:HD3	1.95	0.48
52:2u:10:ARG:HH22	52:2u:13:ILE:HD12	1.78	0.48
1:1A:1091:A:H8	1:1A:1091:A:OP1	1.96	0.48
1:1A:1337:U:H2'	1:1A:1338:C:C6	2.48	0.48
1:1A:2083:A:C2	1:1A:2514:A:N6	2.81	0.48
1:1A:2579:C:OP1	59:1A:4371:HOH:O	2.19	0.48
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.30	0.48
32:1a:672:G:H2'	32:1a:673:C:H6	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:719:C:H2'	32:1a:720:C:H6	1.78	0.48
32:1a:720:C:H2'	32:1a:721:A:H8	1.78	0.48
32:1a:1125:G:H3'	32:1a:1126:G:H8	1.78	0.48
32:1a:1211:A:O2'	54:1x:30:G:OP1	2.31	0.48
33:1b:32:ILE:HD12	33:1b:40:HIS:HB3	1.95	0.48
1:2A:183:A:H5"	1:2A:184:A:O5'	2.12	0.48
1:2A:661:A:H5"	11:2P:117:GLU:HG2	1.95	0.48
1:2A:2120:U:H2'	1:2A:2121:G:H5'	1.93	0.48
1:2A:2762:A:H8	1:2A:2762:A:OP1	1.96	0.48
14:2S:35:ILE:HD11	14:2S:97:ARG:HE	1.77	0.48
32:2a:28:G:N7	59:2a:3354:HOH:O	2.35	0.48
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.95	0.48
47:2p:1:MET:SD	47:2p:3:LYS:NZ	2.86	0.48
1:1A:859:U:H2'	1:1A:860:C:C6	2.48	0.48
1:1A:2829:A:OP2	13:1R:2:ARG:NH2	2.46	0.48
3:1D:26:LYS:HB3	3:1D:83:GLU:HG2	1.95	0.48
4:1E:120:TRP:CE3	4:1E:155:LYS:HD3	2.48	0.48
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.21	0.48
1:2A:1389:G:O2'	1:2A:1430:G:H2'	2.13	0.48
1:2A:2214:G:H2'	1:2A:2215:G:C8	2.48	0.48
1:2A:2590:C:H4'	4:2E:134:ILE:HG12	1.95	0.48
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.48	0.48
15:2T:16:ARG:HD3	15:2T:19:LEU:HG	1.94	0.48
21:2Z:134:PRO:HG3	21:2Z:161:VAL:HG11	1.95	0.48
32:2a:125:A:N3	32:2a:259:A:O2'	2.43	0.48
33:2b:71:VAL:O	33:2b:165:VAL:HG22	2.13	0.48
35:2d:117:ALA:O	35:2d:121:VAL:HG23	2.12	0.48
36:2e:68:GLU:HG2	36:2e:69:VAL:N	2.28	0.48
1:1A:301:A:O2'	1:1A:302:C:OP1	2.29	0.48
3:1D:83:GLU:OE1	3:1D:104:TYR:OH	2.13	0.48
11:1P:59:LEU:HD21	30:18:10:ALA:HA	1.95	0.48
21:1Z:91:LEU:HD11	21:1Z:96:VAL:HG11	1.95	0.48
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.46	0.48
32:1a:658:G:H2'	32:1a:659:A:C8	2.48	0.48
32:1a:675:G:H2'	32:1a:676:U:C6	2.48	0.48
44:1m:80:ARG:NH2	50:1s:69:HIS:HE1	2.10	0.48
51:1t:34:LYS:HG2	51:1t:80:ARG:HH12	1.77	0.48
1:2A:475:G:OP2	59:2A:3655:HOH:O	2.20	0.48
1:2A:601:G:H2'	1:2A:602:C:C6	2.49	0.48
1:2A:972:G:H2'	1:2A:973:G:O4'	2.13	0.48
1:2A:1070:G:O2'	59:2A:3656:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1346:A:C8	1:2A:1348:G:C8	3.01	0.48
1:2A:1789:A:H4'	1:2A:2727:C:O4'	2.13	0.48
1:2A:1844:G:H5"	3:2D:54:ARG:HH21	1.77	0.48
2:2B:108:U:H2'	2:2B:109:C:H5"	1.95	0.48
32:2a:1287:G:H22	32:2a:1313:G:H1'	1.77	0.48
32:2a:1354:G:H5"	40:2i:68:GLY:HA2	1.95	0.48
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.95	0.48
50:2s:27:GLU:HG2	50:2s:47:HIS:NE2	2.29	0.48
1:1A:730:G:OP1	29:17:16:HIS:ND1	2.47	0.48
1:1A:1833:A:O2'	3:1D:259:THR:HG21	2.13	0.48
5:1F:44:ARG:NH1	59:1F:402:HOH:O	2.38	0.48
32:1a:1488:U:H2'	32:1a:1489:G:C8	2.48	0.48
1:2A:830:A:C8	1:2A:838:G:C5	3.02	0.48
1:2A:1176:G:O6	1:2A:2061:C:H1'	2.14	0.48
1:2A:1451:U:H2'	1:2A:1452:C:C6	2.49	0.48
6:2G:108:ASN:HA	26:24:37:SER:HB2	1.95	0.48
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.96	0.48
32:2a:18:U:H2'	32:2a:19:C:C6	2.48	0.48
32:2a:887:A:H2'	32:2a:888:C:O4'	2.14	0.48
32:2a:1045:U:H2'	32:2a:1046:C:C6	2.49	0.48
32:2a:1053:U:H2'	32:2a:1054:C:C6	2.49	0.48
32:2a:1294:G:H1	32:2a:1307:C:N4	2.12	0.48
32:2a:1395:C:H2'	32:2a:1396:A:C8	2.48	0.48
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.27	0.48
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.13	0.48
24:12:3:LEU:O	24:12:7:ARG:HG3	2.14	0.48
32:1a:395:G:H2'	32:1a:396:C:C6	2.48	0.48
32:1a:643:U:H2'	32:1a:644:G:C8	2.48	0.48
32:1a:1132:C:P	40:1i:9:ARG:HH21	2.35	0.48
35:1d:61:LYS:NZ	35:1d:72:GLU:OE2	2.37	0.48
37:1f:60:PHE:HE2	49:1r:76:LEU:HD12	1.77	0.48
45:1n:3:ARG:O	45:1n:7:ILE:HG23	2.13	0.48
45:1n:43:CYS:HA	45:1n:46:GLU:HB2	1.94	0.48
47:1p:57:ARG:NH1	47:1p:79:VAL:O	2.47	0.48
1:2A:435:C:O2'	1:2A:436:G:H5'	2.14	0.48
1:2A:585:G:OP2	59:2A:3654:HOH:O	2.20	0.48
1:2A:822:G:H4'	1:2A:823:A:O5'	2.13	0.48
1:2A:1017:A:C8	1:2A:1232:U:C2	3.01	0.48
1:2A:1042:G:OP1	16:2U:92:ARG:HG2	2.13	0.48
1:2A:2117:U:H2'	1:2A:2118:C:C6	2.48	0.48
3:2D:77:ALA:HB2	3:2D:97:TYR:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:13:GLU:O	6:2G:17:PRO:HD2	2.14	0.48
10:2O:71:ARG:NE	10:2O:105:GLU:OE2	2.42	0.48
12:2Q:58:PHE:CZ	12:2Q:109:VAL:HG21	2.49	0.48
25:23:46:ASN:O	25:23:50:VAL:HG22	2.12	0.48
32:2a:822:G:O6	32:2a:826:C:N4	2.47	0.48
33:2b:92:TYR:CE2	33:2b:150:SER:N	2.81	0.48
1:1A:353:A:HO2'	1:1A:354:A:H8	1.58	0.48
1:1A:1475:C:H2'	1:1A:1476:U:C6	2.49	0.48
4:1E:145:LYS:NZ	59:1E:402:HOH:O	2.22	0.48
11:1P:62:LEU:O	30:18:13:ARG:HD3	2.14	0.48
21:1Z:44:PHE:CZ	21:1Z:86:VAL:HG11	2.48	0.48
27:15:16:ARG:HD2	27:15:20:ARG:NH1	2.29	0.48
28:16:11:LEU:HB2	28:16:21:TYR:HB2	1.95	0.48
32:1a:1030:G:O2'	32:1a:1197:G:O2'	2.28	0.48
32:1a:1101:C:H1'	32:1a:1161:A:C5	2.49	0.48
1:2A:579:U:H2'	1:2A:580:G:H8	1.78	0.48
1:2A:830:A:N6	3:2D:229:VAL:HG11	2.28	0.48
2:2B:72:G:O2'	2:2B:73:A:O4'	2.30	0.48
7:2H:69:ARG:HG3	7:2H:70:THR:N	2.29	0.48
16:2U:86:ALA:O	17:2V:49:THR:HG23	2.13	0.48
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.59	0.48
21:2Z:44:PHE:CZ	21:2Z:86:VAL:HG11	2.48	0.48
29:27:46:VAL:HG13	29:27:48:LYS:HE2	1.96	0.48
30:28:34:TRP:CE2	30:28:35:GLN:HB2	2.49	0.48
32:2a:422:G:OP1	35:2d:38:TYR:OH	2.25	0.48
35:2d:8:VAL:O	35:2d:11:LEU:HB2	2.14	0.48
1:1A:1565:U:H2'	1:1A:1566:G:O4'	2.13	0.48
10:1O:98:VAL:HG13	10:1O:117:LEU:HB3	1.95	0.48
32:1a:936:A:C6	32:1a:937:A:N1	2.82	0.48
32:1a:1280:C:H4'	32:1a:1281:A:C4	2.48	0.48
33:1b:115:LEU:HD13	33:1b:145:LEU:HG	1.96	0.48
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.95	0.48
1:2A:1978:C:H2'	1:2A:1979:C:C6	2.49	0.48
1:2A:2511:U:H5"	1:2A:2512:C:OP2	2.14	0.48
1:2A:2641:G:H2'	1:2A:2642:G:H8	1.78	0.48
12:2Q:97:VAL:HG21	12:2Q:103:MET:HE3	1.95	0.48
15:2T:117:ASP:O	15:2T:121:ILE:HG13	2.13	0.48
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.65	0.48
32:2a:212:G:O2'	32:2a:213:C:O4'	2.32	0.48
32:2a:685:C:O2	32:2a:687:G:N1	2.47	0.48
32:2a:1286:G:N2	32:2a:1314:A:OP2	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1290:U:H5”	44:2m:98:VAL:HG22	1.95	0.48
1:1A:2596:U:H5	55:1z:5:SER:O	1.96	0.48
1:1A:2723:U:O2’	1:1A:2725:A:H5’	2.14	0.48
32:1a:487:C:H2’	32:1a:488:C:C6	2.49	0.48
32:1a:787:G:OP1	59:1a:1918:HOH:O	2.20	0.48
33:1b:192:SER:O	33:1b:194:PRO:HD3	2.14	0.48
1:2A:483:G:C8	29:27:37:LYS:HG2	2.49	0.48
1:2A:724:C:H2’	1:2A:725:C:C6	2.49	0.48
1:2A:2310:G:H2’	1:2A:2311:G:C8	2.41	0.48
1:2A:2312:C:H2’	1:2A:2313:G:C8	2.48	0.48
1:2A:2376:G:O6	30:28:39:LYS:HE3	2.14	0.48
2:2B:44:G:OP1	6:2G:98:ARG:NH2	2.47	0.48
4:2E:11:MET:HG2	4:2E:24:THR:HB	1.96	0.48
15:2T:65:LYS:HE2	15:2T:67:SER:HB2	1.94	0.48
32:2a:1106:A:H1’	41:2j:37:PRO:O	2.13	0.48
32:2a:1226:C:H2’	32:2a:1227:A:C8	2.49	0.48
32:2a:1351:G:H5’	40:2i:112:LYS:HB3	1.95	0.48
38:2g:90:GLU:N	38:2g:90:GLU:OE2	2.43	0.48
1:1A:810:A:H2	3:1D:219:PRO:HG3	1.79	0.48
1:1A:2692:C:OP2	4:1E:109:LYS:NZ	2.45	0.48
1:1A:2878:G:H2’	1:1A:2879:C:O4’	2.13	0.48
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.14	0.48
7:1H:88:LEU:HD22	7:1H:130:ARG:HG2	1.96	0.48
16:1U:76:TYR:CE1	16:1U:80:ILE:HG13	2.49	0.48
32:1a:117:C:OP1	32:1a:307:C:O2’	2.28	0.48
32:1a:835:C:H2’	32:1a:836:G:O4’	2.14	0.48
32:1a:963:C:H2’	32:1a:964:A:H8	1.78	0.48
32:1a:1156:G:H2’	32:1a:1157:G:C8	2.48	0.48
41:1j:55:LYS:HE3	41:1j:56:HIS:CE1	2.49	0.48
1:2A:790:G:OP1	4:2E:132:HIS:ND1	2.45	0.48
1:2A:1699:G:C4	13:2R:9:LYS:HD2	2.49	0.48
2:2B:20:C:N4	2:2B:63:G:H1	2.06	0.48
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.96	0.48
32:2a:361:U:H5’	32:2a:362:C:OP1	2.14	0.48
32:2a:1273:G:H2’	32:2a:1274:U:C6	2.49	0.48
32:2a:1344:C:H2’	32:2a:1345:C:H5”	1.96	0.48
33:2b:184:VAL:HG12	33:2b:197:VAL:HG13	1.95	0.48
40:2i:49:PRO:HB3	40:2i:101:PHE:HB3	1.96	0.48
54:2x:23:C:H2’	54:2x:24:U:C6	2.49	0.48
1:1A:1222:C:H2’	1:1A:1223:C:H6	1.78	0.47
1:1A:1555:A:H3’	1:1A:1556:A:H8	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2702:C:O3'	1:1A:2880:C:H4'	2.13	0.47
1:1A:2800:C:P	4:1E:61:ARG:HH21	2.37	0.47
9:1N:61:ARG:HA	9:1N:61:ARG:HE	1.78	0.47
14:1S:46:VAL:HG12	14:1S:48:LEU:HD12	1.96	0.47
32:1a:1174:C:OP2	34:1c:4:LYS:NZ	2.38	0.47
32:1a:1305:G:H2'	32:1a:1306:A:C8	2.49	0.47
32:1a:1494:G:H2'	32:1a:1496:A:OP2	2.14	0.47
37:1f:25:ILE:HD12	37:1f:82:ARG:HH11	1.78	0.47
1:2A:105:U:H2'	1:2A:106:G:H8	1.78	0.47
1:2A:330:G:H2'	1:2A:332:G:OP2	2.13	0.47
1:2A:345:A:OP2	5:2F:169:ASN:HB2	2.14	0.47
1:2A:917:U:OP1	12:2Q:5:ARG:HD3	2.13	0.47
1:2A:984:G:N3	1:2A:1235:G:H4'	2.30	0.47
1:2A:1066:A:H61	1:2A:1187:A:H61	1.62	0.47
1:2A:2854:G:H2'	1:2A:2855:G:C8	2.49	0.47
5:2F:30:PRO:HB3	11:2P:1:MET:HE1	1.96	0.47
32:2a:395:G:H2'	32:2a:396:C:C6	2.48	0.47
1:1A:206:A:C2	1:1A:223:U:H4'	2.49	0.47
1:1A:1073:A:H61	1:1A:1170:G:H2'	1.79	0.47
1:1A:1474:G:H2'	1:1A:1475:C:C6	2.48	0.47
1:1A:1783:G:N7	59:1A:4510:HOH:O	2.35	0.47
1:1A:1846:G:OP2	59:1A:4380:HOH:O	2.20	0.47
1:1A:2043:U:O2'	1:1A:2628:C:H5'	2.14	0.47
1:1A:2759:G:O6	1:1A:2767:C:H5"	2.14	0.47
32:1a:217:C:H2'	32:1a:218:U:H6	1.79	0.47
32:1a:904:G:C6	32:1a:1483:G:C6	3.02	0.47
38:1g:77:SER:OG	38:1g:86:GLN:NE2	2.33	0.47
40:1i:55:ALA:HA	40:1i:58:HIS:CG	2.49	0.47
1:2A:172:C:H2'	1:2A:173:U:H6	1.79	0.47
1:2A:2685:G:H2'	1:2A:2686:A:C8	2.48	0.47
1:2A:2824:C:H2'	1:2A:2825:C:H6	1.79	0.47
32:2a:524:G:H2'	32:2a:525:G:H8	1.79	0.47
32:2a:935:U:H2'	32:2a:937:A:OP2	2.15	0.47
32:2a:1234:A:H2'	32:2a:1235:G:O4'	2.15	0.47
32:2a:1359:U:H2'	32:2a:1360:A:H8	1.79	0.47
35:2d:61:LYS:HE3	35:2d:61:LYS:HB3	1.73	0.47
41:2j:33:GLN:H	41:2j:76:ASN:H	1.62	0.47
45:2n:11:LYS:NZ	45:2n:11:LYS:HB2	2.29	0.47
47:2p:18:ARG:NH1	47:2p:32:TYR:OH	2.47	0.47
1:1A:138:A:C8	1:1A:1453:C:O2'	2.66	0.47
1:1A:529:A:OP2	59:1A:4351:HOH:O	2.20	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:552:A:N1	1:1A:2063:A:H2'	2.29	0.47
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.14	0.47
36:1e:80:ILE:HG13	39:1h:104:ARG:HH22	1.80	0.47
54:1x:75:C:H2'	54:1x:76:A:C2	2.48	0.47
1:2A:632:G:H2'	1:2A:633:C:C6	2.49	0.47
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.49	0.47
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.14	0.47
21:2Z:108:PRO:HG3	21:2Z:141:VAL:HB	1.95	0.47
32:2a:405:G:N2	32:2a:429:C:O2	2.47	0.47
32:2a:521:G:H5"	43:2l:113:ARG:NH1	2.30	0.47
32:2a:582:U:H4'	39:2h:94:TYR:CG	2.49	0.47
1:1A:741:G:OP1	1:1A:1425:G:O2'	2.29	0.47
32:1a:8:G:H5'	32:1a:294:A:O4'	2.13	0.47
32:1a:348:C:O2'	32:1a:350:G:OP1	2.25	0.47
32:1a:403:G:H2'	32:1a:404:A:C8	2.50	0.47
32:1a:1343:G:H2'	32:1a:1344:C:O4'	2.15	0.47
32:1a:1375:G:N2	32:1a:1480:A:H8	2.12	0.47
44:1m:91:ARG:HB2	44:1m:98:VAL:HG13	1.96	0.47
1:2A:1160:G:H2'	1:2A:1161:C:O4'	2.15	0.47
1:2A:1457:A:H2'	1:2A:1458:G:H8	1.78	0.47
1:2A:2091:G:H2'	1:2A:2092:A:H8	1.80	0.47
1:2A:2313:G:C2	1:2A:2314:G:C8	3.03	0.47
1:2A:2582:C:H5"	1:2A:2583:A:H5"	1.97	0.47
2:2B:6:C:H42	2:2B:115:G:H1	1.60	0.47
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.87	0.47
32:2a:846:C:H2'	32:2a:847:G:O4'	2.14	0.47
33:2b:92:TYR:O	33:2b:93:VAL:HG13	2.14	0.47
42:2k:62:GLN:HG3	42:2k:97:ALA:HB2	1.96	0.47
50:2s:27:GLU:HB3	50:2s:28:LYS:HB3	1.95	0.47
54:2x:40:C:H2'	54:2x:41:C:H6	1.80	0.47
12:1Q:86:GLY:HA3	22:10:10:THR:HG21	1.96	0.47
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.66	0.47
32:1a:1022:C:H2'	32:1a:1023:U:C6	2.50	0.47
32:1a:1117:G:N2	32:1a:1119:U:O4	2.48	0.47
32:1a:1412:C:H2'	32:1a:1413:C:H6	1.80	0.47
32:1a:1503:G:OP1	42:1k:120:ARG:NH2	2.48	0.47
1:2A:44:C:H2'	1:2A:45:C:H6	1.80	0.47
1:2A:448:A:H2'	1:2A:449:A:C8	2.49	0.47
1:2A:1231:G:H5'	17:2V:81:TYR:CE1	2.49	0.47
1:2A:2216:C:C2'	1:2A:2217:C:H5'	2.45	0.47
6:2G:129:GLY:O	6:2G:161:THR:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:2:ILE:HG13	10:2O:8:LEU:HD11	1.97	0.47
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.47	0.47
20:2Y:44:ILE:H	20:2Y:44:ILE:HD13	1.79	0.47
32:2a:526:G:P	35:2d:10:ARG:HH22	2.38	0.47
32:2a:1325:G:H2'	32:2a:1326:C:C6	2.49	0.47
54:2x:17:C:H5"	54:2x:61:C:H5"	1.96	0.47
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.79	0.47
5:1F:170:LEU:HG	5:1F:172:TRP:NE1	2.30	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.49	0.47
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.65	0.47
32:1a:223:G:H21	47:1p:62:VAL:HG12	1.80	0.47
32:1a:899:U:O2	36:1e:19:MET:HB2	2.14	0.47
32:1a:955:A:H2'	32:1a:956:A:H5"	1.96	0.47
32:1a:1325:G:H2'	32:1a:1326:C:C6	2.49	0.47
35:1d:166:LYS:H	35:1d:168:ARG:NH1	2.12	0.47
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.13	0.47
38:1g:121:ALA:O	38:1g:125:MET:HG3	2.14	0.47
52:1u:12:LYS:HB3	52:1u:22:ARG:HD2	1.96	0.47
1:2A:275:C:H2'	1:2A:276:G:O4'	2.14	0.47
1:2A:406:U:H2'	1:2A:407:G:H8	1.80	0.47
1:2A:776:C:H3'	59:2A:3794:HOH:O	2.15	0.47
1:2A:948:C:H2'	1:2A:949:C:C6	2.49	0.47
1:2A:1992:A:OP2	3:2D:242:ARG:NH2	2.45	0.47
1:2A:2269:C:O2'	1:2A:2438:C:OP2	2.27	0.47
1:2A:2830:A:C2	1:2A:2831:G:C4	3.03	0.47
2:2B:16:G:H1	2:2B:68:C:H42	1.61	0.47
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.47	0.47
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.28	0.47
32:2a:9:A:N6	35:2d:209:ARG:HB2	2.30	0.47
32:2a:1105:U:C4	32:2a:1106:A:N7	2.82	0.47
35:2d:101:LEU:HD12	35:2d:138:TYR:HB3	1.96	0.47
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.79	0.47
43:2l:8:ASN:OD1	48:2q:34:LYS:HE2	2.14	0.47
44:2m:33:ALA:HB2	44:2m:64:TRP:CZ3	2.49	0.47
1:1A:26:G:N2	1:1A:536:G:H1'	2.29	0.47
1:1A:322:A:N1	1:1A:345:A:O2'	2.44	0.47
1:1A:551:C:C5	1:1A:2791:U:H2'	2.50	0.47
1:1A:1173:A:H5"	59:1A:4430:HOH:O	2.13	0.47
1:1A:1826:U:H2'	1:1A:1827:C:H6	1.78	0.47
1:1A:2783:C:H2'	1:1A:2784:C:H6	1.80	0.47
2:1B:66:A:N6	2:1B:108:U:H2'	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:91:C:OP1	12:1Q:16:ARG:HG2	2.15	0.47
7:1H:101:ARG:NH2	7:1H:122:THR:OG1	2.48	0.47
8:1I:72:LEU:O	8:1I:74:ASN:N	2.48	0.47
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.97	0.47
21:1Z:45:ASP:O	21:1Z:49:ARG:HG3	2.14	0.47
32:1a:156:A:H2	32:1a:343:G:N2	2.11	0.47
32:1a:199:U:H2'	32:1a:200:C:H6	1.79	0.47
32:1a:622:G:H2'	32:1a:623:G:O4'	2.15	0.47
32:1a:741:U:OP1	32:1a:806:C:O2'	2.32	0.47
32:1a:1045:U:H2'	32:1a:1046:C:C6	2.49	0.47
32:1a:1126:G:H2'	32:1a:1127:G:C8	2.50	0.47
34:1c:29:TYR:CE1	45:1n:54:PRO:HG2	2.50	0.47
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.48	0.47
49:1r:24:ALA:C	49:1r:26:LEU:H	2.23	0.47
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.49	0.47
1:2A:69:A:H5"	1:2A:71:A:C8	2.49	0.47
1:2A:592:G:H2'	1:2A:2051:A:C5	2.50	0.47
1:2A:712:G:H1'	30:28:4:MET:HE3	1.97	0.47
1:2A:1311:G:O5'	18:2W:15:ARG:NH2	2.47	0.47
1:2A:1777:G:H2'	1:2A:1778:G:C8	2.50	0.47
1:2A:1833:A:HO2'	3:2D:259:THR:HG21	1.79	0.47
1:2A:2537:G:H2'	1:2A:2538:C:C6	2.50	0.47
3:2D:10:THR:OG1	3:2D:13:ARG:HG2	2.14	0.47
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.47	0.47
21:2Z:54:HIS:CG	21:2Z:101:PRO:HG3	2.49	0.47
21:2Z:71:VAL:HG13	21:2Z:88:PHE:CE1	2.50	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.15	0.47
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.55	0.47
32:2a:160:C:H2'	32:2a:161:G:H8	1.79	0.47
32:2a:320:G:N7	59:2a:3353:HOH:O	2.35	0.47
32:2a:774:A:N6	32:2a:1476:U:OP1	2.45	0.47
32:2a:954:G:P	45:2n:32:SER:H	2.37	0.47
32:2a:961:A:O3'	59:2a:3305:HOH:O	2.20	0.47
32:2a:1031:G:OP1	45:2n:3:ARG:HB3	2.14	0.47
33:2b:16:HIS:CG	33:2b:17:PHE:H	2.33	0.47
35:2d:159:ARG:O	35:2d:163:GLU:N	2.47	0.47
35:2d:205:GLU:OE1	36:2e:100:VAL:HG12	2.14	0.47
40:2i:49:PRO:HG2	40:2i:81:ILE:HD11	1.97	0.47
45:2n:51:GLY:C	45:2n:53:LEU:H	2.23	0.47
47:2p:18:ARG:HD3	47:2p:35:LYS:HE2	1.96	0.47
51:2t:43:LEU:HD13	51:2t:51:GLU:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2u:5:ASP:C	52:2u:7:ARG:H	2.23	0.47
10:1O:1:MET:HE3	10:1O:32:TYR:CZ	2.50	0.47
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.97	0.47
32:1a:674:G:C6	32:1a:675:G:C6	3.03	0.47
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	1.96	0.47
1:2A:945:A:H2'	1:2A:946:A:O4'	2.15	0.47
1:2A:1894:U:OP1	1:2A:2421:G:O2'	2.32	0.47
1:2A:2566:U:H5"	1:2A:2567:C:OP2	2.13	0.47
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.13	0.47
3:2D:164:GLN:HE21	3:2D:176:ARG:HH12	1.63	0.47
4:2E:48:GLN:HA	4:2E:80:GLU:HA	1.97	0.47
6:2G:11:TYR:O	6:2G:16:ARG:HG3	2.14	0.47
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.96	0.47
32:2a:298:G:O2'	32:2a:540:C:H5"	2.14	0.47
38:2g:14:PRO:HB3	38:2g:19:GLY:C	2.40	0.47
44:2m:86:CYS:HA	50:2s:73:GLU:O	2.15	0.47
45:2n:3:ARG:NH2	45:2n:4:LYS:HE3	2.30	0.47
1:1A:615:G:H4'	30:18:4:MET:HE2	1.96	0.47
1:1A:793:U:O2	1:1A:2035:A:H1'	2.15	0.47
1:1A:820:A:H2'	1:1A:820:A:N3	2.30	0.47
1:1A:1462:C:OP2	59:1A:4384:HOH:O	2.21	0.47
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.48	0.47
32:1a:267:C:H2'	32:1a:268:C:C6	2.50	0.47
32:1a:485:C:O2	32:1a:533:C:O2'	2.27	0.47
32:1a:859:G:P	43:1l:12:ARG:HH22	2.38	0.47
32:1a:1078:U:OP1	32:1a:1091:G:N2	2.40	0.47
32:1a:1352:C:H2'	32:1a:1353:G:C8	2.50	0.47
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.97	0.47
37:1f:10:LEU:HB2	37:1f:59:TYR:HB3	1.97	0.47
54:1x:23:C:H2'	54:1x:24:U:H6	1.79	0.47
1:2A:1883:A:H2'	1:2A:1884:A:C8	2.50	0.47
1:2A:1887:G:C6	1:2A:1888:G:C6	3.03	0.47
1:2A:2416:G:O2'	1:2A:2417:U:OP1	2.21	0.47
1:2A:2509:C:H3'	59:2A:3625:HOH:O	2.15	0.47
14:2S:68:GLN:HA	14:2S:68:GLN:HE21	1.79	0.47
32:2a:775:G:O6	32:2a:776:A:N6	2.45	0.47
32:2a:1457:C:H2'	32:2a:1458:G:H8	1.80	0.47
45:2n:7:ILE:HA	45:2n:23:ARG:HD2	1.97	0.47
50:2s:28:LYS:HB2	50:2s:29:ARG:CB	2.45	0.47
1:1A:746:G:O2'	1:1A:1678:A:N3	2.45	0.47
1:1A:830:A:H5'	1:1A:831:G:OP1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:956:A:H2'	12:1Q:9:TYR:OH	2.14	0.47
7:1H:167:GLU:HA	7:1H:168:PRO:HD3	1.80	0.47
11:1P:46:LYS:HB3	11:1P:46:LYS:HE3	1.70	0.47
32:1a:994:A:H2'	32:1a:995:A:C8	2.50	0.47
32:1a:1069:U:H3	32:1a:1082:G:N2	2.11	0.47
32:1a:1284:U:OP2	44:1m:21:TYR:OH	2.25	0.47
33:1b:155:LEU:HD21	33:1b:159:PRO:HD3	1.97	0.47
52:1u:18:TYR:CG	52:1u:24:ARG:HG2	2.50	0.47
1:2A:104:C:H2'	1:2A:105:U:H6	1.80	0.47
1:2A:990:G:H2'	1:2A:991:G:H8	1.80	0.47
1:2A:1288:G:O2'	11:2P:7:ARG:NH2	2.47	0.47
1:2A:1337:U:H2'	1:2A:1338:C:H6	1.80	0.47
1:2A:1846:G:H3'	3:2D:62:TYR:CE1	2.50	0.47
3:2D:145:VAL:HG12	3:2D:146:GLU:O	2.15	0.47
1:1A:1188:A:OP1	9:1N:25:ARG:NH2	2.48	0.46
1:1A:1840:A:H2'	1:1A:1841:G:O4'	2.14	0.46
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.97	0.46
9:1N:114:ARG:NH1	59:1N:3101:HOH:O	2.27	0.46
26:14:50:VAL:HG11	44:1m:64:TRP:C	2.40	0.46
29:17:24:THR:O	29:17:28:ARG:HG3	2.16	0.46
31:19:32:HIS:O	31:19:34:GLN:HG3	2.15	0.46
32:1a:113:A:H4'	32:1a:114:A:C8	2.51	0.46
39:1h:6:ILE:HG22	39:1h:10:LEU:HD11	1.97	0.46
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.96	0.46
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	1.96	0.46
49:1r:20:ALA:O	49:1r:55:ARG:NH2	2.48	0.46
50:1s:3:ARG:NH1	50:1s:8:GLY:O	2.48	0.46
54:1x:17:C:H2'	54:1x:17(A):U:H6	1.79	0.46
1:2A:20:A:H2'	1:2A:21:C:C6	2.50	0.46
1:2A:143:C:H2'	1:2A:144:G:H8	1.80	0.46
1:2A:623:C:O2	1:2A:627:C:H4'	2.15	0.46
1:2A:1603:C:OP2	1:2A:1604:A:O2'	2.26	0.46
10:2O:103:ALA:HB1	10:2O:105:GLU:OE1	2.15	0.46
32:2a:604:C:H2'	32:2a:605:A:O4'	2.15	0.46
32:2a:621:G:H2'	32:2a:622:G:C8	2.50	0.46
32:2a:954:G:C8	32:2a:1344:C:N4	2.83	0.46
32:2a:972:A:N7	32:2a:1198:G:H4'	2.30	0.46
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.97	0.46
54:2x:40:C:H2'	54:2x:41:C:C6	2.50	0.46
1:1A:515:G:H2'	1:1A:516:A:C8	2.50	0.46
1:1A:842:C:H2'	1:1A:843:C:C6	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:894:G:O6	1:1A:973:G:H2'	2.15	0.46
1:1A:1356:G:O2'	29:17:47:ARG:NH2	2.48	0.46
1:1A:1652:C:H4'	1:1A:1653:A:O5'	2.15	0.46
1:1A:2659:C:H2'	1:1A:2660:U:C6	2.49	0.46
1:1A:2694:C:O2	10:1O:70:LYS:NZ	2.29	0.46
8:1I:29:TYR:O	8:1I:32:PRO:HD2	2.15	0.46
8:1I:61:ARG:HD2	8:1I:61:ARG:HA	1.66	0.46
21:1Z:24:LEU:HB2	21:1Z:41:LEU:HD23	1.96	0.46
32:1a:225:U:H5"	47:1p:33:ILE:HD13	1.95	0.46
32:1a:1329:G:N2	32:1a:1356:G:H2'	2.30	0.46
35:1d:65:ARG:NH1	35:1d:70:ILE:O	2.48	0.46
35:1d:164:ALA:C	35:1d:168:ARG:HH11	2.24	0.46
1:2A:862:C:H2'	1:2A:863:C:H6	1.79	0.46
1:2A:1586:U:O2'	1:2A:1587:G:H5'	2.15	0.46
1:2A:2567:C:H2'	1:2A:2568:G:O4'	2.16	0.46
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.98	0.46
6:2G:56:ALA:O	6:2G:60:LEU:HB2	2.15	0.46
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.30	0.46
13:2R:38:VAL:HB	13:2R:39:PRO:HD3	1.97	0.46
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.81	0.46
32:2a:522:G:H2'	32:2a:523:A:H8	1.80	0.46
32:2a:942:A:OP1	59:2a:3326:HOH:O	2.20	0.46
32:2a:1350:C:HO2'	41:2j:48:THR:HG21	1.80	0.46
34:2c:114:PRO:HG3	34:2c:185:GLY:HA3	1.97	0.46
37:2f:10:LEU:HB2	37:2f:59:TYR:HB3	1.97	0.46
1:1A:670:A:H2'	1:1A:671:G:O4'	2.15	0.46
1:1A:1216:G:H3'	1:1A:1217:G:H5'	1.96	0.46
1:1A:2290:G:N7	22:10:14:ARG:NH1	2.63	0.46
1:1A:2299:A:OP2	59:1A:4376:HOH:O	2.20	0.46
2:1B:102:A:OP2	59:1B:303:HOH:O	2.20	0.46
32:1a:170:C:H5'	51:1t:25:ARG:HH21	1.80	0.46
32:1a:231:C:H5'	48:1q:70:ARG:HG2	1.96	0.46
32:1a:560:G:O6	32:1a:858:C:O2'	2.30	0.46
32:1a:633:G:H2'	32:1a:634:G:H8	1.80	0.46
33:1b:55:PHE:CE1	33:1b:218:ALA:HA	2.50	0.46
48:1q:58:GLU:HG3	48:1q:77:VAL:HG21	1.97	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:HD3	1.96	0.46
1:2A:663:U:H2'	1:2A:664:C:H6	1.79	0.46
1:2A:1098:C:N4	1:2A:1151:G:H1	2.07	0.46
1:2A:1467:G:H1'	1:2A:1541:A:N1	2.30	0.46
1:2A:1596:C:H2'	1:2A:1597:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1656:C:OP1	59:2A:3659:HOH:O	2.21	0.46
1:2A:2330:G:C2	14:2S:3:ARG:HA	2.50	0.46
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.15	0.46
10:2O:6:THR:HG22	10:2O:8:LEU:HD22	1.98	0.46
32:2a:1394:C:H2'	32:2a:1395:C:C6	2.50	0.46
1:1A:1076:G:H21	31:19:36:GLN:HE22	1.62	0.46
1:1A:2505:G:O2'	12:1Q:80:GLU:HA	2.15	0.46
2:1B:33:G:C2	2:1B:50:G:C2	3.04	0.46
32:1a:949:G:O6	32:1a:1347:U:O2'	2.33	0.46
32:1a:1223:G:H2'	32:1a:1224:C:H6	1.80	0.46
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	1.97	0.46
42:1k:59:TYR:CZ	42:1k:63:LEU:HD11	2.50	0.46
1:2A:860:C:H2'	1:2A:861:C:H6	1.81	0.46
1:2A:1232:U:H4'	17:2V:79:VAL:HG22	1.96	0.46
1:2A:2067:G:H5'	27:25:19:ARG:HA	1.97	0.46
3:2D:33:LEU:HD11	3:2D:103:ARG:HA	1.97	0.46
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.96	0.46
27:25:41:PRO:HG2	27:25:44:THR:OG1	2.15	0.46
32:2a:104:C:H2'	32:2a:105:G:O4'	2.14	0.46
33:2b:125:PRO:HB2	33:2b:126:GLU:H	1.61	0.46
35:2d:26:CYS:HA	58:2d:501:SF4:S3	2.55	0.46
43:2l:54:LYS:HG3	43:2l:75:HIS:CE1	2.50	0.46
1:1A:230:G:C8	30:18:5:LYS:HG2	2.51	0.46
1:1A:266:C:H3'	59:1A:4362:HOH:O	2.16	0.46
1:1A:1451:U:H2'	1:1A:1452:C:C6	2.50	0.46
5:1F:129:PHE:CD1	5:1F:163:VAL:HG21	2.50	0.46
32:1a:200:C:H2'	32:1a:201:C:H6	1.81	0.46
32:1a:954:G:N2	32:1a:1345:C:OP2	2.49	0.46
32:1a:1068:U:OP2	59:1a:1919:HOH:O	2.21	0.46
32:1a:1140:A:H4'	32:1a:1141:C:O5'	2.16	0.46
40:1i:99:LEU:HB3	40:1i:101:PHE:CE1	2.50	0.46
44:1m:86:CYS:SG	44:1m:88:ARG:HB2	2.55	0.46
1:2A:437:G:C5	11:2P:72:PRO:HB3	2.50	0.46
1:2A:927:G:H1	1:2A:940:U:H3	1.62	0.46
1:2A:1042:G:H5'	16:2U:92:ARG:HH21	1.81	0.46
1:2A:1625:A:H2'	1:2A:1626:A:C8	2.50	0.46
1:2A:1879:G:H2'	1:2A:1880:G:C8	2.50	0.46
1:2A:2419:U:H2'	1:2A:2420:G:C8	2.51	0.46
6:2G:32:PRO:HB3	6:2G:172:LEU:HD22	1.97	0.46
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.97	0.46
7:2H:127:GLU:C	7:2H:129:THR:H	2.22	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.47	0.46
32:2a:36:G:H2'	32:2a:37:C:C6	2.51	0.46
32:2a:196:G:H2'	32:2a:197:U:H6	1.80	0.46
32:2a:959:U:H2'	32:2a:960:U:C5	2.51	0.46
32:2a:979:A:H61	32:2a:1022:C:N4	2.13	0.46
32:2a:1080:C:H2'	32:2a:1081:C:H6	1.81	0.46
32:2a:1306:A:C4'	32:2a:1344:C:H4'	2.43	0.46
33:2b:84:GLU:O	33:2b:219:VAL:HG21	2.14	0.46
36:2e:78:HIS:CD2	36:2e:142:LEU:HD23	2.50	0.46
44:2m:15:VAL:HG13	44:2m:43:THR:O	2.15	0.46
1:1A:307:U:H2'	1:1A:308:C:C6	2.50	0.46
1:1A:508:A:OP1	20:1Y:50:ARG:NH2	2.48	0.46
1:1A:1788:G:O2'	59:1A:4381:HOH:O	2.20	0.46
1:1A:2758:U:OP1	7:1H:85:LYS:NZ	2.33	0.46
26:14:46:GLN:O	26:14:48:ARG:HG2	2.15	0.46
32:1a:753:G:H4'	32:1a:1491:A:H4'	1.98	0.46
32:1a:1084:A:H4'	32:1a:1085:A:O5'	2.16	0.46
32:1a:1335:G:H2'	32:1a:1336:C:H6	1.81	0.46
32:1a:1392:C:H2'	32:1a:1393:G:H8	1.80	0.46
32:1a:1410:U:H2'	32:1a:1411:A:C8	2.50	0.46
35:1d:100:ARG:NH1	35:1d:137:SER:OG	2.48	0.46
37:1f:10:LEU:HD23	37:1f:61:LEU:HD23	1.97	0.46
40:1i:9:ARG:HG2	40:1i:14:VAL:HG23	1.96	0.46
44:1m:11:ARG:HB2	44:1m:46:LYS:HB3	1.96	0.46
48:1q:67:LYS:O	48:1q:68:ARG:HG2	2.16	0.46
1:2A:105:U:H2'	1:2A:106:G:C8	2.51	0.46
1:2A:810:A:N1	1:2A:1819:A:O2'	2.41	0.46
1:2A:990:G:H2'	1:2A:991:G:C8	2.50	0.46
1:2A:1090:A:O4'	1:2A:1092:G:H8	1.99	0.46
1:2A:1100:G:H3'	1:2A:1101:G:C8	2.45	0.46
1:2A:1104:G:H5"	1:2A:1105:U:H2'	1.97	0.46
1:2A:1402:U:H2'	1:2A:1403:G:O4'	2.16	0.46
1:2A:2227:G:H8	1:2A:2227:G:OP1	1.98	0.46
1:2A:2465:G:H1'	59:2A:3665:HOH:O	2.15	0.46
1:2A:2638:G:N3	1:2A:2793:A:H2	2.14	0.46
1:2A:2884:C:H2'	1:2A:2885:G:O4'	2.16	0.46
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.30	0.46
33:2b:92:TYR:CD2	33:2b:92:TYR:C	2.94	0.46
46:2o:69:TYR:O	46:2o:73:GLU:HG2	2.14	0.46
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.15	0.46
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.98	0.46
24:12:21:LEU:HD13	24:12:64:LEU:HA	1.98	0.46
32:1a:258:A:C6	32:1a:259:A:C6	3.04	0.46
32:1a:385:A:C5	32:1a:386:C:H1'	2.49	0.46
32:1a:969:U:H1'	32:1a:970:U:OP2	2.16	0.46
32:1a:1118:U:H4'	32:1a:1119:U:H5	1.80	0.46
32:1a:1131:U:H2'	32:1a:1132:C:O4'	2.15	0.46
50:1s:70:LYS:HB2	50:1s:73:GLU:HG2	1.98	0.46
1:2A:17:C:O2'	1:2A:576:U:OP1	2.31	0.46
1:2A:94:G:H4'	24:22:48:HIS:CD2	2.51	0.46
1:2A:863:C:O2'	1:2A:885:U:H5"	2.15	0.46
1:2A:1039:C:OP2	16:2U:54:LYS:NZ	2.37	0.46
1:2A:1404:A:H2'	1:2A:1405:A:C5'	2.46	0.46
1:2A:1652:C:H5"	1:2A:1653:A:H5'	1.96	0.46
1:2A:1828:U:H5'	3:2D:259:THR:CG2	2.40	0.46
1:2A:2328:C:O2'	1:2A:2329:G:OP1	2.33	0.46
1:2A:2854:G:H2'	1:2A:2855:G:H8	1.81	0.46
2:2B:40:U:N3	2:2B:43:C:OP2	2.49	0.46
5:2F:20:LEU:HD13	5:2F:21:ALA:H	1.81	0.46
17:2V:4:ILE:HD12	17:2V:39:LEU:HB3	1.98	0.46
32:2a:22:G:H2'	32:2a:23:G:C8	2.51	0.46
32:2a:1217:U:O2'	32:2a:1287:G:O5'	2.34	0.46
32:2a:1329:G:C8	40:2i:107:ARG:HG3	2.51	0.46
33:2b:119:GLU:CD	33:2b:153:ARG:HH12	2.23	0.46
35:2d:61:LYS:HA	35:2d:203:VAL:HG22	1.98	0.46
1:1A:241:C:OP2	30:18:5:LYS:NZ	2.33	0.46
1:1A:1833:A:H2'	1:1A:1834:C:O4'	2.16	0.46
1:1A:2440:G:OP2	59:1A:4312:HOH:O	2.21	0.46
1:1A:2862:C:H2'	1:1A:2863:G:C8	2.50	0.46
11:1P:84:ASN:OD1	11:1P:117:GLU:HB2	2.16	0.46
21:1Z:110:GLY:HA3	21:1Z:174:VAL:HG11	1.98	0.46
25:13:13:ILE:O	59:13:201:HOH:O	2.20	0.46
32:1a:181:C:H2'	32:1a:182:C:C6	2.51	0.46
32:1a:380:G:N2	32:1a:381:C:N3	2.63	0.46
32:1a:1298:G:N2	32:1a:1301:A:H5"	2.17	0.46
44:1m:40:ASN:C	44:1m:42:ALA:H	2.24	0.46
1:2A:67:C:H2'	1:2A:68:G:C8	2.50	0.46
1:2A:440:C:H2'	1:2A:441:A:C8	2.51	0.46
1:2A:1067:G:N2	1:2A:1068:U:O4	2.48	0.46
1:2A:1139:U:N3	1:2A:1142:U:OP2	2.47	0.46
1:2A:1210:U:H2'	1:2A:1211:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2251:C:OP2	59:2A:3660:HOH:O	2.21	0.46
1:2A:2820:G:N2	1:2A:2899:G:H1'	2.31	0.46
15:2T:23:ARG:HG3	15:2T:120:ARG:NH1	2.30	0.46
32:2a:675:G:H2'	32:2a:676:U:C6	2.49	0.46
32:2a:677:G:H2'	32:2a:678:A:C8	2.51	0.46
32:2a:774:A:C6	32:2a:775:G:C6	3.03	0.46
32:2a:1221:A:H62	32:2a:1281:A:N6	2.14	0.46
32:2a:1305:G:H2'	32:2a:1306:A:C8	2.51	0.46
50:2s:27:GLU:H	50:2s:27:GLU:CD	2.24	0.46
52:2u:5:ASP:O	52:2u:7:ARG:N	2.49	0.46
54:2x:17:C:H2'	54:2x:17(A):U:H6	1.81	0.46
1:1A:2397:C:H2'	1:1A:2398:U:C6	2.50	0.46
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.97	0.46
26:14:56:VAL:HA	26:14:60:GLN:CD	2.41	0.46
32:1a:205:G:H2'	32:1a:206:G:C8	2.50	0.46
33:1b:101:MET:HA	33:1b:108:ILE:HG13	1.97	0.46
50:1s:27:GLU:CD	50:1s:27:GLU:H	2.23	0.46
1:2A:25:G:C6	1:2A:26:G:N1	2.84	0.46
1:2A:267:G:O2'	1:2A:268:G:H8	1.99	0.46
13:2R:28:LEU:HD23	13:2R:28:LEU:HA	1.80	0.46
32:2a:751:A:H2'	32:2a:752:A:O4'	2.16	0.46
38:2g:129:GLU:H	38:2g:129:GLU:HG2	1.49	0.46
43:2l:89:ARG:HA	43:2l:97:ARG:HA	1.98	0.46
48:2q:89:LEU:HD23	48:2q:89:LEU:HA	1.82	0.46
54:2x:10:G:N2	54:2x:26:G:H1'	2.31	0.46
1:1A:628:U:H4'	1:1A:704:C:H4'	1.97	0.46
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.97	0.46
32:1a:436:A:N6	32:1a:478:G:O2'	2.49	0.46
32:1a:1392:C:H2'	32:1a:1393:G:C8	2.51	0.46
34:1c:154:SER:HB3	34:1c:165:THR:HG23	1.98	0.46
1:2A:774:G:O2'	1:2A:809:G:OP2	2.32	0.46
1:2A:1322:G:O2'	13:2R:24:GLN:HG2	2.15	0.46
1:2A:2484:U:O2	1:2A:2484:U:H2'	2.16	0.46
1:2A:2733:A:OP1	59:2A:3661:HOH:O	2.21	0.46
2:2B:98:G:H2'	2:2B:99:G:O4'	2.16	0.46
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.16	0.46
19:2X:27:THR:OG1	19:2X:80:ILE:HG12	2.16	0.46
26:24:33:VAL:HG12	26:24:34:GLU:H	1.81	0.46
32:2a:602:C:N4	32:2a:605:A:N7	2.64	0.46
32:2a:768:C:H2'	32:2a:769:G:C8	2.50	0.46
32:2a:1172:G:H8	59:2c:301:HOH:O	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1298:G:H2'	32:2a:1300:A:OP2	2.16	0.46
32:2a:1387:C:H2'	32:2a:1388:G:C8	2.51	0.46
34:2c:116:VAL:HB	34:2c:186:PHE:HZ	1.81	0.46
1:1A:1510:C:H2'	1:1A:1511:G:C8	2.51	0.45
1:1A:2122:G:H2'	1:1A:2123:U:O4'	2.16	0.45
1:1A:2543:G:O2'	1:1A:2668:A:N1	2.49	0.45
1:1A:2548:U:H2'	1:1A:2549:C:C6	2.52	0.45
11:1P:95:VAL:HG13	11:1P:125:VAL:HB	1.96	0.45
35:1d:8:VAL:HG22	35:1d:9:CYS:H	1.80	0.45
35:1d:81:GLU:CD	35:1d:139:ARG:HH12	2.24	0.45
36:1e:105:VAL:O	36:1e:109:ILE:HG13	2.16	0.45
42:1k:85:ARG:HA	42:1k:112:THR:OG1	2.16	0.45
50:1s:37:ARG:H	50:1s:37:ARG:HG3	1.54	0.45
1:2A:264:U:H2'	1:2A:265:C:C6	2.51	0.45
1:2A:1106:U:O2'	1:2A:1115:A:O4'	2.30	0.45
1:2A:1920:G:H2'	1:2A:1920:G:N3	2.31	0.45
1:2A:2417:U:OP1	1:2A:2422:A:N6	2.49	0.45
12:2Q:32:TYR:CE1	12:2Q:133:ARG:HG3	2.51	0.45
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.98	0.45
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.17	0.45
21:2Z:127:LYS:O	21:2Z:128:VAL:HG12	2.16	0.45
26:24:62:ARG:H	26:24:62:ARG:NE	2.13	0.45
26:24:62:ARG:O	26:24:64:GLY:N	2.43	0.45
32:2a:136:A:H1'	32:2a:177:U:O2	2.15	0.45
32:2a:500:U:C4	32:2a:501:G:C6	3.04	0.45
32:2a:621:G:H2'	32:2a:622:G:H8	1.81	0.45
32:2a:1296:C:H2'	32:2a:1297:U:C6	2.51	0.45
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.49	0.45
36:2e:152:ARG:HG3	39:2h:43:GLY:O	2.17	0.45
43:2l:8:ASN:O	43:2l:12:ARG:HG3	2.16	0.45
1:1A:2330:G:N2	14:1S:3:ARG:HA	2.32	0.45
1:1A:2339:A:H2'	1:1A:2340:G:H8	1.81	0.45
15:1T:7:ILE:O	15:1T:11:GLU:HG3	2.16	0.45
32:1a:96:G:H2'	32:1a:97:C:C6	2.52	0.45
32:1a:204:A:C6	32:1a:217:C:H4'	2.51	0.45
32:1a:231:C:OP2	59:1a:1920:HOH:O	2.21	0.45
32:1a:964:A:H1'	50:1s:54:GLY:O	2.16	0.45
39:1h:73:ASP:OD1	39:1h:75:ARG:HD3	2.16	0.45
47:1p:6:LEU:HD23	47:1p:17:TYR:CG	2.51	0.45
50:1s:43:GLU:OE1	50:1s:43:GLU:N	2.50	0.45
1:2A:1090:A:H4'	1:2A:1091:A:H5"	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2342:G:O2'	1:2A:2347:A:N1	2.45	0.45
7:2H:71:LEU:HD12	7:2H:71:LEU:HA	1.72	0.45
11:2P:96:THR:HG23	11:2P:99:LEU:HD23	1.97	0.45
14:2S:3:ARG:HG2	14:2S:3:ARG:NH1	2.31	0.45
32:2a:452:C:H2'	32:2a:453:C:H6	1.81	0.45
32:2a:522:G:H2'	32:2a:523:A:C8	2.51	0.45
33:2b:16:HIS:CD2	33:2b:17:PHE:N	2.84	0.45
41:2j:23:ILE:HD13	41:2j:23:ILE:HA	1.79	0.45
44:2m:6:GLY:HA3	44:2m:67:GLU:HG3	1.99	0.45
49:2r:56:THR:HB	49:2r:58:LEU:HD23	1.98	0.45
49:2r:85:LEU:HD12	49:2r:87:ARG:HH21	1.82	0.45
1:1A:329:U:H2'	1:1A:330:G:O4'	2.16	0.45
1:1A:963:A:H5"	2:1B:98:G:O2'	2.17	0.45
1:1A:1288:G:O2'	11:1P:7:ARG:NH2	2.50	0.45
1:1A:1399:A:H2'	1:1A:1400:G:O4'	2.16	0.45
1:1A:1520:C:H2'	1:1A:1521:G:C8	2.51	0.45
1:1A:2753:A:OP1	31:19:22:ARG:NH2	2.35	0.45
3:1D:37:LEU:HD22	3:1D:87:ASN:ND2	2.32	0.45
9:1N:28:THR:HG22	9:1N:29:LYS:HG3	1.98	0.45
13:1R:28:LEU:HD12	13:1R:48:VAL:HG21	1.98	0.45
32:1a:89:G:H2'	32:1a:90:U:C6	2.51	0.45
32:1a:472:A:H2'	32:1a:473:C:O4'	2.17	0.45
32:1a:722:C:H2'	32:1a:723:C:C6	2.51	0.45
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.46	0.45
34:1c:43:LEU:O	34:1c:47:LEU:HB2	2.16	0.45
36:1e:78:HIS:CD2	36:1e:78:HIS:H	2.35	0.45
1:2A:26:G:O2'	1:2A:27:A:OP2	2.30	0.45
1:2A:263:G:H2'	1:2A:264:U:C6	2.51	0.45
1:2A:1242:U:H2'	1:2A:1243:U:C6	2.51	0.45
1:2A:2488:C:H5"	1:2A:2490:G:O6	2.17	0.45
1:2A:2556:G:N3	1:2A:2576:A:H2	2.14	0.45
32:2a:1106:A:O3'	41:2j:36:GLY:HA3	2.17	0.45
32:2a:1232:A:O3'	40:2i:67:GLY:HA2	2.17	0.45
32:2a:1274:U:OP1	38:2g:41:ARG:NH2	2.49	0.45
35:2d:112:VAL:HG22	35:2d:116:GLN:OE1	2.17	0.45
1:1A:332:G:N3	1:1A:352:G:O2'	2.48	0.45
1:1A:1620:C:N4	59:1A:4310:HOH:O	2.48	0.45
1:1A:1633:C:H2'	1:1A:1634:C:C6	2.51	0.45
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.15	0.45
20:1Y:54:LYS:HA	20:1Y:56:PRO:CD	2.39	0.45
26:14:33:VAL:HG12	26:14:34:GLU:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:721:A:H2'	32:1a:722:C:H6	1.82	0.45
40:1i:70:LYS:O	40:1i:74:ILE:HG12	2.16	0.45
1:2A:555:C:H4'	1:2A:556:A:H5"	1.99	0.45
1:2A:1302:C:H4'	5:2F:83:PHE:CD1	2.52	0.45
2:2B:111:G:H2'	2:2B:112:U:O4'	2.17	0.45
4:2E:36:ARG:HD3	4:2E:85:ASN:HD21	1.81	0.45
5:2F:64:ILE:HD11	5:2F:75:HIS:HB2	1.97	0.45
14:2S:39:ILE:HB	14:2S:49:VAL:HG22	1.98	0.45
32:2a:881:G:OP1	59:2a:3327:HOH:O	2.21	0.45
32:2a:903:G:C2	32:2a:1375:G:C2	3.05	0.45
35:2d:12:CYS:SG	35:2d:19:LEU:HB2	2.56	0.45
1:1A:224:C:H2'	1:1A:225:C:C6	2.52	0.45
1:1A:1217:G:N2	1:1A:1221:A:OP2	2.45	0.45
1:1A:1649:C:H5'	59:1A:4723:HOH:O	2.16	0.45
32:1a:68:C:O2'	32:1a:166:A:N3	2.35	0.45
32:1a:961:A:H5"	32:1a:962:C:OP2	2.17	0.45
32:1a:971:G:H1	32:1a:1028:C:N4	2.14	0.45
33:1b:28:PHE:CD1	33:1b:190:THR:HA	2.51	0.45
44:1m:84:ILE:HD12	50:1s:74:PHE:CZ	2.51	0.45
46:1o:84:LYS:HD3	46:1o:84:LYS:C	2.42	0.45
1:2A:7:A:H2'	1:2A:8:U:H6	1.81	0.45
1:2A:508:A:O2'	20:2Y:49:VAL:O	2.26	0.45
1:2A:1129:A:N3	1:2A:1150:U:O2'	2.41	0.45
1:2A:1937:A:H2'	1:2A:1938:U:O4'	2.17	0.45
2:2B:57:A:C4	6:2G:29:TRP:HB2	2.52	0.45
3:2D:38:LYS:HE3	3:2D:40:THR:HG22	1.98	0.45
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.97	0.45
19:2X:35:THR:HG22	19:2X:37:THR:N	2.27	0.45
21:2Z:92:SER:O	21:2Z:92:SER:OG	2.35	0.45
32:2a:30:G:H5'	32:2a:292:U:OP1	2.16	0.45
32:2a:475:G:H2'	32:2a:476:G:H8	1.82	0.45
40:2i:85:LEU:HD12	40:2i:92:TYR:HD2	1.80	0.45
1:1A:1013:U:H2'	1:1A:1014:C:C6	2.52	0.45
1:1A:1200:A:OP1	16:1U:55:ARG:HD3	2.17	0.45
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.16	0.45
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.98	0.45
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.24	0.45
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.31	0.45
31:19:26:ILE:H	31:19:26:ILE:HD13	1.81	0.45
32:1a:1491:A:H2'	32:1a:1492:C:C6	2.52	0.45
39:1h:78:GLN:HE21	39:1h:78:GLN:HB2	1.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:1u:19:GLY:N	52:1u:22:ARG:O	2.39	0.45
1:2A:470:C:OP1	16:2U:2:PRO:HA	2.16	0.45
1:2A:786:U:H2'	1:2A:787:G:H8	1.79	0.45
1:2A:1699:G:C6	13:2R:9:LYS:HB2	2.52	0.45
3:2D:75:ILE:HG21	3:2D:99:ASP:HB2	1.99	0.45
15:2T:84:GLN:HG2	15:2T:85:LYS:HG2	1.98	0.45
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.50	0.45
32:2a:472:A:H2'	32:2a:473:C:O4'	2.15	0.45
32:2a:531:A:H4'	32:2a:532:G:O5'	2.16	0.45
32:2a:571:G:OP1	39:2h:89:PRO:HB3	2.17	0.45
32:2a:1191:C:O2'	32:2a:1196:C:N4	2.49	0.45
32:2a:1394:C:H2'	32:2a:1395:C:H6	1.82	0.45
33:2b:19:HIS:HE1	33:2b:206:ASP:HB2	1.80	0.45
34:2c:113:ALA:HB3	34:2c:114:PRO:HD3	1.99	0.45
1:1A:1687:A:H2'	1:1A:1688:G:O4'	2.17	0.45
1:1A:1869:G:C8	1:1A:1948:A:H1'	2.52	0.45
1:1A:2356:G:OP2	28:16:38:LYS:NZ	2.37	0.45
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.45	0.45
8:1I:72:LEU:C	8:1I:74:ASN:N	2.74	0.45
32:1a:239:A:C2	32:1a:242:A:C8	3.05	0.45
32:1a:954:G:OP1	45:1n:32:SER:N	2.43	0.45
32:1a:1053:U:H2'	32:1a:1054:C:C6	2.51	0.45
32:1a:1055:G:C5	32:1a:1056:U:C4	3.05	0.45
32:1a:1412:C:H2'	32:1a:1413:C:C6	2.52	0.45
40:1i:4:TYR:CZ	40:1i:88:TYR:HD1	2.35	0.45
43:1l:7:ILE:HD13	43:1l:7:ILE:HA	1.87	0.45
46:1o:4:THR:H	46:1o:7:GLU:CD	2.24	0.45
48:1q:27:PHE:CZ	48:1q:36:ILE:HD11	2.52	0.45
1:2A:386:G:H2'	1:2A:387:A:H8	1.81	0.45
1:2A:386:G:H2'	1:2A:387:A:C8	2.51	0.45
1:2A:1096:G:H5"	1:2A:1097:C:OP2	2.17	0.45
1:2A:2347:A:H61	22:20:43:THR:HG22	1.82	0.45
14:2S:10:ARG:HG2	14:2S:13:ARG:NH2	2.31	0.45
32:2a:20:C:H5"	36:2e:86:ALA:HB3	1.99	0.45
32:2a:414:C:H2'	32:2a:415:C:C6	2.51	0.45
41:2j:49:VAL:HG13	45:2n:41:ARG:HB2	1.98	0.45
44:2m:3:ARG:HG3	44:2m:4:ILE:N	2.32	0.45
50:2s:69:HIS:HB2	50:2s:74:PHE:CE1	2.52	0.45
1:1A:2542:A:H5'	7:1H:157:TYR:CZ	2.52	0.45
1:1A:2600:A:OP2	59:1A:4383:HOH:O	2.20	0.45
3:1D:242:ARG:HG2	3:1D:246:PRO:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:24:LEU:HD12	5:1F:25:PRO:HD2	1.98	0.45
8:1I:140:LEU:HD22	8:1I:140:LEU:HA	1.75	0.45
10:1O:80:ASP:OD2	15:1T:71:GLY:HA3	2.16	0.45
20:1Y:6:HIS:H	20:1Y:6:HIS:HD2	1.65	0.45
21:1Z:102:LEU:HD13	21:1Z:123:ASP:HA	1.99	0.45
26:14:44:THR:O	26:14:46:GLN:N	2.49	0.45
32:1a:187:C:H2'	32:1a:188:C:O4'	2.16	0.45
32:1a:524:G:H2'	32:1a:525:G:O4'	2.17	0.45
32:1a:843:A:C2	32:1a:896:A:H4'	2.51	0.45
32:1a:1051:G:N2	32:1a:1173:A:N3	2.62	0.45
35:1d:158:ILE:HG22	35:1d:162:LEU:HD22	1.98	0.45
1:2A:241:C:OP2	30:28:5:LYS:NZ	2.36	0.45
1:2A:679:G:O6	1:2A:698:C:N4	2.40	0.45
1:2A:1682:C:OP2	59:2A:3662:HOH:O	2.21	0.45
1:2A:2287:G:H5'	12:2Q:86:GLY:HA2	1.98	0.45
1:2A:2431:C:P	30:28:33:ASN:H	2.39	0.45
1:2A:2832:A:OP1	4:2E:159:HIS:NE2	2.48	0.45
2:2B:2:C:H2'	2:2B:3:C:C6	2.52	0.45
6:2G:61:ALA:O	6:2G:65:GLY:N	2.48	0.45
7:2H:3:ARG:HH12	7:2H:5:GLY:N	2.15	0.45
12:2Q:59:ARG:NH1	12:2Q:60:ARG:HE	2.15	0.45
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.52	0.45
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.99	0.45
32:2a:541:G:N1	32:2a:542:G:C2	2.85	0.45
33:2b:87:ARG:HB2	33:2b:219:VAL:HG11	1.99	0.45
35:2d:31:CYS:SG	35:2d:33:MET:HB2	2.56	0.45
36:2e:71:LEU:H	36:2e:71:LEU:HD22	1.81	0.45
37:2f:99:ALA:HB2	49:2r:31:LEU:HD21	1.98	0.45
1:1A:1520:C:H2'	1:1A:1521:G:H8	1.82	0.45
1:1A:1603:C:OP2	1:1A:1604:A:O2'	2.23	0.45
1:1A:2345:G:H5'	14:1S:9:ARG:HG2	1.99	0.45
1:1A:2481:G:O6	1:1A:2487:A:O2'	2.26	0.45
1:1A:2554:G:H2'	1:1A:2555:G:C8	2.51	0.45
1:1A:2873:G:OP1	15:1T:119:LYS:HD2	2.17	0.45
2:1B:28:C:H2'	2:1B:29:A:O4'	2.17	0.45
14:1S:36:TYR:N	14:1S:36:TYR:CD1	2.85	0.45
20:1Y:52:SER:O	20:1Y:54:LYS:N	2.50	0.45
32:1a:711:G:N2	32:1a:714:G:OP2	2.48	0.45
32:1a:932:G:H2'	32:1a:933:U:O4'	2.17	0.45
32:1a:1125:G:H5'	32:1a:1126:G:OP2	2.17	0.45
34:1c:139:GLN:O	34:1c:143:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:250:A:H2'	1:2A:251:C:O4'	2.17	0.45
1:2A:323:A:P	20:2Y:86:ARG:HH21	2.40	0.45
1:2A:609:C:O2	11:2P:33:ARG:NH2	2.35	0.45
1:2A:909:A:H2'	1:2A:910:G:H8	1.82	0.45
1:2A:1475:C:H2'	1:2A:1476:U:C6	2.52	0.45
1:2A:1495:A:OP2	1:2A:1495:A:H8	1.99	0.45
1:2A:1702:C:H2'	1:2A:1703:C:H6	1.81	0.45
1:2A:2272:C:O2'	1:2A:2273:U:H5'	2.17	0.45
1:2A:2296:C:OP2	28:26:6:ARG:NH1	2.50	0.45
1:2A:2623:C:OP2	27:25:2:ALA:N	2.50	0.45
2:2B:83:G:H4'	25:23:52:HIS:CG	2.52	0.45
8:2I:134:PRO:C	8:2I:136:VAL:H	2.25	0.45
10:2O:69:ILE:HD11	10:2O:77:ILE:HG23	1.99	0.45
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.97	0.45
21:2Z:91:LEU:HD13	21:2Z:91:LEU:HA	1.76	0.45
32:2a:333:C:H2'	32:2a:334:A:C8	2.52	0.45
32:2a:568:G:H5'	48:2q:91:ARG:HH22	1.82	0.45
32:2a:839:G:HO2'	32:2a:852:G:HO2'	1.56	0.45
32:2a:1127:G:N2	32:2a:1129:A:H62	2.13	0.45
32:2a:1199:C:H2'	32:2a:1200:C:O4'	2.16	0.45
41:2j:57:LYS:C	41:2j:59:SER:H	2.24	0.45
1:1A:214:G:H21	1:1A:216:A:H62	1.65	0.45
1:1A:603:C:H2'	1:1A:604:G:C8	2.52	0.45
1:1A:775:G:C6	3:1D:208:LYS:HB2	2.51	0.45
1:1A:1017:A:H5'	1:1A:1232:U:H1'	1.98	0.45
1:1A:1091:A:H3'	1:1A:1092:G:C5'	2.45	0.45
1:1A:1715:A:H5"	1:1A:2561:G:OP1	2.16	0.45
1:1A:1934:A:C5	32:1a:1472:G:H5"	2.52	0.45
1:1A:2578:G:H2'	1:1A:2579:C:C6	2.52	0.45
5:1F:32:LEU:HB3	5:1F:112:MET:HE1	1.99	0.45
7:1H:3:ARG:CG	7:1H:6:ARG:HG2	2.44	0.45
14:1S:48:LEU:HD23	14:1S:82:ILE:HD11	1.97	0.45
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.40	0.45
32:1a:154:G:H21	32:1a:156:A:H3'	1.81	0.45
32:1a:982:G:C2'	32:1a:983:A:H4'	2.47	0.45
32:1a:1407:C:H2'	32:1a:1408:U:O4'	2.17	0.45
33:1b:71:VAL:O	33:1b:165:VAL:HG23	2.16	0.45
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.99	0.45
50:1s:36:ARG:NH1	50:1s:53:ASN:HA	2.32	0.45
54:1x:17:C:H5"	54:1x:61:C:H5"	1.99	0.45
1:2A:180:C:O2'	1:2A:848:A:N3	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:358:C:H4'	20:2Y:73:ARG:HD2	1.98	0.45
1:2A:1587:G:H2'	1:2A:1588:A:C8	2.51	0.45
1:2A:1631:A:H2'	1:2A:1632:A:O4'	2.16	0.45
1:2A:1856:G:H4'	3:2D:242:ARG:CZ	2.47	0.45
4:2E:79:ARG:HD2	4:2E:195:LEU:HD21	1.99	0.45
6:2G:167:GLU:H	6:2G:167:GLU:CD	2.25	0.45
7:2H:126:PRO:HD2	7:2H:130:ARG:O	2.17	0.45
32:2a:144:A:H2'	32:2a:145:C:C6	2.52	0.45
32:2a:400:U:H2'	32:2a:401:U:C6	2.51	0.45
32:2a:1134:A:HO2'	32:2a:1135:A:H8	1.63	0.45
32:2a:1334:C:H2'	32:2a:1335:G:C8	2.51	0.45
33:2b:119:GLU:OE2	33:2b:153:ARG:NH1	2.46	0.45
33:2b:222:ILE:HG13	33:2b:223:ILE:N	2.31	0.45
49:2r:22:VAL:HA	49:2r:25:THR:HG22	1.98	0.45
54:2x:25:C:H2'	54:2x:26:G:O4'	2.17	0.45
2:1B:4:C:H2'	2:1B:5:C:O4'	2.17	0.44
8:1I:104:GLN:O	8:1I:106:GLY:N	2.44	0.44
32:1a:154:G:N2	32:1a:156:A:H3'	2.32	0.44
32:1a:502:C:O2'	32:1a:514:G:N2	2.50	0.44
32:1a:590:G:N2	32:1a:615:G:N7	2.65	0.44
32:1a:843:A:H2	32:1a:896:A:H4'	1.82	0.44
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.40	0.44
41:1j:67:THR:O	41:1j:67:THR:OG1	2.31	0.44
43:1l:6:THR:O	43:1l:10:LEU:HD22	2.17	0.44
1:2A:137:G:N3	1:2A:139:A:N6	2.60	0.44
1:2A:173:U:H4'	1:2A:206:A:H4'	1.99	0.44
1:2A:594:A:OP2	17:2V:78:LYS:HE2	2.17	0.44
1:2A:1898:A:H5'	1:2A:1899:G:OP2	2.17	0.44
1:2A:2371:A:H2'	1:2A:2372:A:O4'	2.16	0.44
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.51	0.44
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	1.99	0.44
32:2a:434:G:N1	32:2a:480:A:OP2	2.41	0.44
32:2a:1138:G:H3'	32:2a:1139:G:C8	2.52	0.44
32:2a:1208:C:OP2	44:2m:91:ARG:NH2	2.43	0.44
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.17	0.44
41:2j:50:ILE:HD11	41:2j:57:LYS:NZ	2.32	0.44
49:2r:29:PHE:HD1	49:2r:29:PHE:H	1.65	0.44
50:2s:27:GLU:HG2	50:2s:47:HIS:CE1	2.53	0.44
1:1A:235:G:H4'	1:1A:412:G:C6	2.52	0.44
1:1A:1844:G:OP1	59:1A:4388:HOH:O	2.21	0.44
1:1A:2649:G:P	4:1E:82:ARG:HH22	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2730:G:O2'	1:1A:2856:U:OP1	2.25	0.44
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.98	0.44
32:1a:620:U:H2'	32:1a:621:G:H8	1.82	0.44
32:1a:920:G:C2	32:1a:1324:C:C2	3.06	0.44
38:1g:103:TRP:CH2	38:1g:141:VAL:HG21	2.52	0.44
40:1i:15:ALA:HB2	40:1i:65:VAL:HG23	2.00	0.44
1:2A:2741:G:O2'	4:2E:186:GLY:HA3	2.18	0.44
1:2A:2878:G:H2'	1:2A:2879:C:O4'	2.17	0.44
6:2G:107:LEU:HD23	6:2G:111:LEU:HD21	1.99	0.44
15:2T:54:ARG:HA	15:2T:59:THR:HG22	1.99	0.44
21:2Z:76:LEU:HD12	21:2Z:83:PRO:HA	1.98	0.44
32:2a:429:C:H2'	32:2a:430:U:C6	2.53	0.44
32:2a:900:G:H2'	32:2a:901:A:C8	2.51	0.44
32:2a:930:U:H4'	32:2a:942:A:N1	2.32	0.44
32:2a:1054:C:H2'	32:2a:1055:G:C8	2.51	0.44
32:2a:1257:A:H2'	32:2a:1258:G:O4'	2.17	0.44
32:2a:1487:C:H2'	32:2a:1488:U:O4'	2.16	0.44
35:2d:36:ARG:HB3	35:2d:38:TYR:CE2	2.52	0.44
51:2t:97:ALA:HA	51:2t:98:PRO:HD2	1.89	0.44
1:1A:495:A:H2'	1:1A:496:A:O4'	2.18	0.44
1:1A:598:U:H2'	1:1A:599:G:C8	2.53	0.44
1:1A:1856:G:H2'	1:1A:1857:C:O4'	2.17	0.44
1:1A:2086:C:H2'	1:1A:2087:C:C6	2.52	0.44
32:1a:256:G:H2'	32:1a:257:U:C6	2.52	0.44
32:1a:826:C:H2'	32:1a:827:C:C6	2.53	0.44
32:1a:1300:A:H1'	50:1s:37:ARG:HH21	1.82	0.44
35:1d:107:ARG:HH22	35:1d:194:LEU:HD11	1.81	0.44
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.99	0.44
41:1j:40:LEU:HB3	41:1j:41:PRO:HD2	1.99	0.44
49:1r:73:ALA:HB3	49:1r:79:LEU:HD12	1.98	0.44
1:2A:2331:A:N3	1:2A:2331:A:H2'	2.32	0.44
1:2A:2848:G:H5'	13:2R:46:GLY:HA2	1.99	0.44
11:2P:28:GLY:O	11:2P:30:THR:N	2.51	0.44
31:29:29:ASN:C	31:29:29:ASN:HD22	2.25	0.44
32:2a:131:C:O4'	47:2p:1:MET:HG2	2.16	0.44
32:2a:756:U:H2'	32:2a:757:G:O4'	2.17	0.44
32:2a:1488:U:H2'	32:2a:1489:G:C8	2.51	0.44
33:2b:118:LEU:HG	33:2b:142:LEU:HD13	1.98	0.44
35:2d:121:VAL:O	35:2d:134:ASP:HA	2.17	0.44
43:2l:24:VAL:HG21	43:2l:27:LEU:HD22	1.98	0.44
47:2p:21:VAL:HG11	47:2p:59:TRP:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:424:G:O6	59:1A:4378:HOH:O	2.20	0.44
1:1A:552:A:O2'	1:1A:553:A:H5'	2.18	0.44
1:1A:885:U:H1'	1:1A:1235:G:H1'	2.00	0.44
1:1A:924:A:H2'	1:1A:925:G:H5'	1.99	0.44
1:1A:1494:G:O2'	1:1A:1574:A:N1	2.46	0.44
1:1A:2480:A:OP2	59:1A:4382:HOH:O	2.20	0.44
1:1A:2646:C:O2'	4:1E:80:GLU:OE1	2.33	0.44
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.75	0.44
32:1a:1382:C:C2	32:1a:1480:A:N6	2.85	0.44
37:1f:100:ASN:ND2	49:1r:23:LYS:HE2	2.32	0.44
42:1k:16:SER:HA	42:1k:79:SER:O	2.18	0.44
1:2A:38:C:H2'	1:2A:39:C:C6	2.52	0.44
1:2A:118:G:H4'	1:2A:148:A:H5'	1.99	0.44
1:2A:241:C:O2'	59:2A:3658:HOH:O	2.20	0.44
1:2A:1844:G:H4'	3:2D:51:VAL:HG21	1.98	0.44
1:2A:2054:A:O2'	1:2A:2056:G:OP2	2.29	0.44
1:2A:2333:A:H2'	1:2A:2334:G:O4'	2.17	0.44
1:2A:2409:U:H2'	1:2A:2410:G:H8	1.82	0.44
4:2E:144:ARG:HB3	4:2E:145:LYS:H	1.44	0.44
8:2I:61:ARG:HD3	8:2I:61:ARG:HA	1.71	0.44
32:2a:1088:A:H2'	32:2a:1089:G:C8	2.50	0.44
32:2a:1176:U:H4'	36:2e:22:GLY:O	2.17	0.44
32:2a:1299:C:H2'	32:2a:1300:A:O4'	2.18	0.44
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.18	0.44
1:1A:604:G:H2'	1:1A:605:G:C8	2.53	0.44
6:1G:50:ALA:C	6:1G:52:ILE:H	2.25	0.44
7:1H:43:VAL:HG13	7:1H:52:VAL:HG22	1.99	0.44
8:1I:43:ASN:HA	8:1I:46:ALA:HB3	1.99	0.44
15:1T:39:ARG:HH21	32:1a:341:C:H5	1.64	0.44
32:1a:1232:A:H4'	40:1i:68:GLY:N	2.33	0.44
32:1a:1235:G:OP1	41:1j:46:ARG:NH1	2.50	0.44
32:1a:1297:U:O2'	32:1a:1342:A:N3	2.47	0.44
35:1d:117:ALA:O	35:1d:121:VAL:HG23	2.18	0.44
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.50	0.44
42:1k:48:ILE:O	42:1k:48:ILE:HG12	2.16	0.44
1:2A:149:C:H2'	1:2A:150:C:C6	2.52	0.44
1:2A:593:A:O2'	17:2V:78:LYS:HE3	2.17	0.44
1:2A:1042:G:N3	1:2A:1042:G:H2'	2.32	0.44
1:2A:1227:G:H4'	25:23:29:ARG:HH22	1.83	0.44
1:2A:1659:A:P	1:2A:1659:A:H8	2.40	0.44
2:2B:2:C:H2'	2:2B:3:C:H6	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:11:VAL:HG13	7:2H:15:VAL:HG22	2.00	0.44
7:2H:154:PRO:HB3	7:2H:163:TYR:CE2	2.52	0.44
8:2I:91:SER:HB3	8:2I:121:LYS:HE3	1.99	0.44
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	2.00	0.44
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.26	0.44
32:2a:403:G:H2'	32:2a:404:A:H8	1.82	0.44
32:2a:523:A:OP2	43:2l:115:LYS:NZ	2.31	0.44
32:2a:896:A:H2'	32:2a:897:A:C8	2.52	0.44
32:2a:1134:A:N3	41:2j:39:PRO:HG3	2.33	0.44
39:2h:33:GLU:HG2	39:2h:48:TYR:CE1	2.53	0.44
1:1A:609:C:OP2	11:1P:21:ARG:NH2	2.50	0.44
1:1A:930:C:H2'	1:1A:931:C:O4'	2.18	0.44
1:1A:2375:C:H2'	1:1A:2376:G:O4'	2.18	0.44
1:1A:2896:U:H2'	1:1A:2897:C:C6	2.52	0.44
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.44
31:19:15:LYS:HD3	31:19:26:ILE:HD11	2.00	0.44
32:1a:542:G:OP1	59:1a:1921:HOH:O	2.21	0.44
32:1a:1145:C:H2'	32:1a:1146:C:C6	2.53	0.44
36:1e:80:ILE:HG13	39:1h:104:ARG:NH2	2.32	0.44
1:2A:267:G:HO2'	1:2A:268:G:H8	1.57	0.44
1:2A:677:A:N3	1:2A:677:A:H2'	2.33	0.44
1:2A:1268:G:C2	1:2A:1272:G:C5	3.06	0.44
4:2E:175:VAL:O	4:2E:177:PRO:HD3	2.18	0.44
5:2F:109:GLY:O	5:2F:113:ALA:N	2.46	0.44
10:2O:63:VAL:HG12	10:2O:106:LEU:HD11	2.00	0.44
32:2a:455:A:O2'	32:2a:457:G:N7	2.47	0.44
32:2a:917:G:H2'	32:2a:918:C:C6	2.53	0.44
32:2a:1140:A:C6	32:2a:1162:A:C5	3.06	0.44
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.53	0.44
34:2c:3:ASN:HB2	59:2c:301:HOH:O	2.18	0.44
34:2c:121:ALA:HB2	34:2c:198:VAL:HG21	1.99	0.44
35:2d:38:TYR:HB2	35:2d:44:GLY:O	2.18	0.44
37:2f:10:LEU:HD23	37:2f:61:LEU:HD13	2.00	0.44
41:2j:40:LEU:HB3	41:2j:41:PRO:HD2	2.00	0.44
49:2r:26:LEU:HD21	49:2r:42:ARG:HG3	2.00	0.44
1:1A:517:G:H2'	1:1A:518:G:O4'	2.17	0.44
14:1S:10:ARG:HG2	14:1S:13:ARG:NH2	2.33	0.44
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.51	0.44
32:1a:104:C:H2'	32:1a:105:G:O4'	2.17	0.44
32:1a:162:G:H2'	32:1a:163:G:H8	1.83	0.44
32:1a:1353:G:C2	32:1a:1354:G:C8	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:27:ARG:HE	36:1e:27:ARG:HB2	1.52	0.44
40:1i:128:ARG:NH2	54:1x:33:U:OP2	2.51	0.44
44:1m:94:ARG:CZ	50:1s:80:TYR:HD2	2.31	0.44
51:1t:66:ALA:HB3	51:1t:72:LEU:HD12	2.00	0.44
1:2A:976:G:H4'	1:2A:977:A:O5'	2.18	0.44
1:2A:1064:U:HO2'	1:2A:1066:A:H2	1.61	0.44
1:2A:1474:G:H2'	1:2A:1475:C:C6	2.53	0.44
1:2A:1571:G:H2'	1:2A:1572:G:O4'	2.18	0.44
4:2E:54:GLN:HB2	4:2E:76:ARG:HG2	2.00	0.44
5:2F:53:THR:CG2	5:2F:55:GLY:H	2.26	0.44
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.51	0.44
22:20:19:LYS:HG2	22:20:41:ARG:HH21	1.82	0.44
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.53	0.44
32:2a:132:C:H2'	32:2a:133:G:H8	1.83	0.44
32:2a:220:C:H2'	32:2a:221:C:C6	2.53	0.44
32:2a:729:C:H2'	32:2a:730:A:H8	1.83	0.44
32:2a:1101:C:H1'	32:2a:1161:A:C5	2.53	0.44
40:2i:85:LEU:HD12	40:2i:92:TYR:CD2	2.53	0.44
42:2k:104:GLN:NE2	42:2k:106:LYS:HG2	2.33	0.44
1:1A:1090:A:H4'	1:1A:1091:A:C5'	2.48	0.44
1:1A:1198:C:OP1	16:1U:92:ARG:NH1	2.50	0.44
1:1A:2249:G:H5"	59:1A:5557:HOH:O	2.18	0.44
2:1B:12:C:O2'	22:10:74:ARG:HG2	2.18	0.44
7:1H:11:VAL:HA	7:1H:12:PRO:HD3	1.79	0.44
12:1Q:7:MET:HE2	12:1Q:7:MET:HB2	1.80	0.44
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.18	0.44
32:1a:190:U:O2	48:1q:63:ARG:NH2	2.51	0.44
32:1a:198:G:H21	51:1t:103:GLY:HA2	1.82	0.44
32:1a:993:A:H4'	50:1s:14:HIS:CD2	2.53	0.44
32:1a:1221:A:H62	32:1a:1281:A:H61	1.64	0.44
32:1a:1375:G:H21	32:1a:1480:A:H8	1.63	0.44
47:1p:40:ASP:HA	47:1p:41:PRO:HD2	1.91	0.44
50:1s:80:TYR:CE2	50:1s:82:GLY:HA2	2.53	0.44
1:2A:330:G:H21	1:2A:353:A:N6	2.14	0.44
1:2A:1211:C:H2'	1:2A:1212:U:C6	2.53	0.44
1:2A:1315:C:H5"	1:2A:1316:G:O5'	2.18	0.44
1:2A:1693:G:H3'	1:2A:1693:G:OP2	2.17	0.44
1:2A:2302:U:O2'	1:2A:2385:C:O2	2.34	0.44
1:2A:2526:C:H2'	1:2A:2527:G:H8	1.83	0.44
1:2A:2706:C:H2'	1:2A:2707:U:C6	2.53	0.44
1:2A:2799:C:H1'	4:2E:62:PRO:HG3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.53	0.44
4:2E:163:GLU:HG2	4:2E:164:ARG:N	2.33	0.44
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.18	0.44
5:2F:117:ARG:HH12	11:2P:1:MET:H2	1.65	0.44
5:2F:196:LEU:HD13	5:2F:196:LEU:HA	1.82	0.44
16:2U:29:SER:C	16:2U:30:LYS:HD3	2.42	0.44
20:2Y:6:HIS:H	20:2Y:6:HIS:CD2	2.36	0.44
32:2a:74:G:C6	32:2a:91:G:C6	3.06	0.44
32:2a:295:G:H2'	32:2a:296:A:C8	2.52	0.44
32:2a:320:G:O2'	32:2a:322:G:N7	2.45	0.44
32:2a:897:A:H2'	32:2a:898:U:H5'	2.00	0.44
32:2a:917:G:O2'	32:2a:1358:A:O2'	2.07	0.44
32:2a:1034:C:H2'	32:2a:1035:U:H6	1.83	0.44
32:2a:1203:G:OP1	50:2s:36:ARG:HD3	2.17	0.44
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	2.00	0.44
35:2d:3:ARG:NH1	35:2d:5:ILE:H	2.15	0.44
35:2d:73:ARG:HH11	35:2d:73:ARG:HB2	1.83	0.44
43:2l:24:VAL:CG2	43:2l:27:LEU:HD22	2.47	0.44
50:2s:12:ASP:HB3	50:2s:14:HIS:CD2	2.53	0.44
1:1A:1092:G:H1'	1:1A:1155:G:N2	2.33	0.44
1:1A:1682:C:OP2	59:1A:4387:HOH:O	2.21	0.44
1:1A:2330:G:H22	14:1S:3:ARG:NE	2.16	0.44
1:1A:2480:A:H2'	1:1A:2481:G:O4'	2.18	0.44
9:1N:138:LEU:HD23	9:1N:138:LEU:HA	1.76	0.44
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.98	0.44
32:1a:45:G:C2	32:1a:46:U:H1'	2.53	0.44
32:1a:371:U:N3	32:1a:372:G:N7	2.66	0.44
1:2A:179:A:H2'	1:2A:180:C:C6	2.52	0.44
1:2A:1684:C:H5"	1:2A:2721:C:O2'	2.18	0.44
1:2A:2091:G:H2'	1:2A:2092:A:C8	2.53	0.44
1:2A:2291:G:O2'	1:2A:2399:A:N1	2.43	0.44
1:2A:2411:G:H4'	28:26:18:ARG:HG2	2.00	0.44
4:2E:33:VAL:HG13	4:2E:89:ASP:C	2.43	0.44
8:2I:132:PRO:HD2	8:2I:136:VAL:O	2.18	0.44
11:2P:21:ARG:HD3	11:2P:21:ARG:HA	1.74	0.44
11:2P:65:ARG:HG3	30:28:25:MET:HG3	2.00	0.44
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.99	0.44
14:2S:63:THR:HG23	14:2S:64:GLU:H	1.83	0.44
26:24:57:GLU:HA	26:24:58:ARG:HA	1.58	0.44
27:25:16:ARG:HG3	27:25:17:ASP:N	2.32	0.44
32:2a:89:G:H2'	32:2a:90:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:599:C:H2'	32:2a:600:G:O4'	2.17	0.44
32:2a:1241:C:C4	32:2a:1242:C:H1'	2.52	0.44
34:2c:39:ILE:HG22	34:2c:43:LEU:HD12	1.99	0.44
43:2l:33:ARG:HG2	43:2l:60:LEU:HD12	2.00	0.44
46:2o:26:GLU:HB3	46:2o:81:LEU:HD13	1.99	0.44
47:2p:72:ARG:HG3	47:2p:73:LEU:N	2.33	0.44
1:1A:1072:A:C2	1:1A:2499:A:H5'	2.52	0.43
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	2.00	0.43
9:1N:114:ARG:HD2	59:1N:3101:HOH:O	2.17	0.43
10:1O:1:MET:HE3	10:1O:32:TYR:CE2	2.53	0.43
12:1Q:39:PRO:HA	12:1Q:97:VAL:O	2.18	0.43
32:1a:720:C:H5"	49:1r:72:ARG:HE	1.82	0.43
40:1i:3:GLN:OE1	40:1i:20:ARG:NH2	2.50	0.43
51:1t:48:LYS:HA	51:1t:48:LYS:HD3	1.79	0.43
1:2A:671:G:H8	1:2A:671:G:O5'	2.01	0.43
1:2A:1214:G:H1	1:2A:1224:C:N4	2.07	0.43
1:2A:1333:U:C2	1:2A:1372:C:O2	2.71	0.43
1:2A:1844:G:O3'	3:2D:54:ARG:NH2	2.51	0.43
1:2A:2327:C:O2'	6:2G:128:ARG:NH2	2.51	0.43
1:2A:2626:U:OP1	59:2A:3657:HOH:O	2.20	0.43
2:2B:1:U:H2'	2:2B:2:C:H5	1.81	0.43
2:2B:28:C:H5"	14:2S:31:SER:OG	2.18	0.43
3:2D:71:ASP:HB3	3:2D:103:ARG:NH2	2.33	0.43
12:2Q:4:PRO:HG3	12:2Q:69:PHE:HE2	1.83	0.43
16:2U:52:ARG:HD3	59:2U:3101:HOH:O	2.18	0.43
21:2Z:11:GLU:O	21:2Z:36:LYS:NZ	2.51	0.43
28:26:13:CYS:SG	28:26:47:THR:HG21	2.58	0.43
32:2a:108:U:O2'	32:2a:109:G:H5'	2.18	0.43
32:2a:1320:G:N3	54:2x:41:C:O2'	2.46	0.43
43:2l:27:LEU:HD12	43:2l:27:LEU:HA	1.76	0.43
45:2n:17:LYS:HE2	45:2n:17:LYS:N	2.33	0.43
1:1A:767:C:H2'	1:1A:768:A:H8	1.84	0.43
1:1A:1951:G:O2'	1:1A:1989:G:O6	2.33	0.43
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	2.01	0.43
32:1a:202:A:OP1	51:1t:68:LYS:NZ	2.47	0.43
32:1a:295:G:H2'	32:1a:296:A:C8	2.52	0.43
32:1a:931:G:H5'	32:1a:943:A:H61	1.83	0.43
32:1a:972:A:N1	32:1a:1030:G:H4'	2.32	0.43
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.51	0.43
33:1b:231:GLU:H	33:1b:232:PRO:HD2	1.83	0.43
35:1d:168:ARG:H	35:1d:168:ARG:CD	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.37	0.43
38:1g:137:LYS:O	38:1g:141:VAL:HG23	2.18	0.43
40:1i:100:GLY:O	40:1i:103:THR:HG22	2.19	0.43
44:1m:81:LEU:HD21	44:1m:88:ARG:HH21	1.83	0.43
44:1m:84:ILE:HG13	44:1m:85:GLY:CA	2.43	0.43
1:2A:13:A:C6	1:2A:550:A:C2	3.06	0.43
1:2A:775:G:OP1	3:2D:12:SER:HB2	2.19	0.43
1:2A:1716:C:C5	1:2A:1717:U:C4	3.06	0.43
1:2A:1940:A:O3'	32:2a:1495:G:H1'	2.18	0.43
1:2A:1960:U:OP1	1:2A:2615:U:O2'	2.36	0.43
3:2D:164:GLN:HE21	3:2D:176:ARG:HH22	1.67	0.43
20:2Y:68:HIS:ND1	20:2Y:70:SER:HB3	2.33	0.43
23:21:19:GLN:HB3	23:21:35:THR:HG23	1.99	0.43
28:26:23:THR:OG1	28:26:24:GLU:N	2.51	0.43
32:2a:171:C:H2'	32:2a:172:C:H6	1.82	0.43
32:2a:691:C:H2'	32:2a:692:C:H6	1.81	0.43
32:2a:1117:G:N3	32:2a:1117:G:H2'	2.34	0.43
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.53	0.43
37:2f:18:GLN:O	37:2f:22:GLU:HG2	2.17	0.43
38:2g:146:GLU:O	38:2g:149:ARG:HB2	2.18	0.43
1:1A:552:A:C2	1:1A:2064:C:H4'	2.53	0.43
1:1A:767:C:H2'	1:1A:768:A:C8	2.53	0.43
1:1A:770:U:H2'	1:1A:771:G:O4'	2.18	0.43
1:1A:2829:A:P	13:1R:2:ARG:HH22	2.41	0.43
30:18:61:LEU:O	30:18:63:PRO:HD3	2.17	0.43
32:1a:1240:G:H2'	32:1a:1241:C:C6	2.53	0.43
1:2A:839:A:OP2	1:2A:2092:A:O2'	2.33	0.43
1:2A:2298:A:C5	1:2A:2300:G:C5	3.06	0.43
3:2D:117:VAL:HG11	3:2D:128:GLY:HA3	2.00	0.43
6:2G:106:LEU:O	6:2G:110:ALA:HB3	2.18	0.43
6:2G:109:VAL:HG21	26:24:14:ILE:HG21	1.99	0.43
7:2H:12:PRO:O	7:2H:15:VAL:HG13	2.18	0.43
20:2Y:23:ARG:HG2	20:2Y:42:VAL:HG22	2.00	0.43
22:20:53:MET:HA	22:20:58:THR:O	2.18	0.43
31:29:3:VAL:HA	31:29:35:ARG:O	2.19	0.43
32:2a:480:A:H1'	32:2a:481:A:H5"	1.98	0.43
32:2a:524:G:H2'	32:2a:525:G:C8	2.53	0.43
32:2a:979:A:H2'	32:2a:980:G:H8	1.80	0.43
32:2a:998:C:H2'	32:2a:999:U:O4'	2.18	0.43
32:2a:1188:G:H4'	34:2c:192:THR:O	2.17	0.43
32:2a:1342:A:H8	32:2a:1342:A:OP1	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:4:TYR:CE2	40:2i:88:TYR:HA	2.53	0.43
1:1A:1067:G:N7	9:1N:66:LYS:HE2	2.33	0.43
1:1A:1403:G:O2'	1:1A:1404:A:H5"	2.19	0.43
1:1A:1587:G:H5"	1:1A:1588:A:OP2	2.18	0.43
1:1A:2217:C:OP1	59:1A:4392:HOH:O	2.21	0.43
17:1V:95:LEU:HD13	17:1V:97:LYS:HD3	2.01	0.43
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.26	0.43
32:1a:370:A:O4'	32:1a:466:G:N2	2.50	0.43
32:1a:374:G:O6	32:1a:381:C:N4	2.51	0.43
32:1a:403:G:H1	32:1a:431:C:H42	1.67	0.43
32:1a:449:C:H5"	32:1a:450:C:C5	2.51	0.43
32:1a:599:C:H2'	32:1a:600:G:O4'	2.19	0.43
32:1a:952:A:H8	32:1a:952:A:OP1	2.00	0.43
32:1a:1073:U:H2'	32:1a:1074:U:C6	2.53	0.43
33:1b:72:GLY:HA3	33:1b:81:VAL:HG11	2.01	0.43
44:1m:40:ASN:HB3	44:1m:43:THR:OG1	2.18	0.43
51:1t:56:MET:HE3	51:1t:88:VAL:HG21	1.99	0.43
1:2A:54:A:H2'	1:2A:55:C:O4'	2.19	0.43
1:2A:1873:C:H5'	3:2D:253:GLN:NE2	2.33	0.43
1:2A:1933:A:N1	32:2a:1390:C:O2'	2.44	0.43
1:2A:2107:U:H2'	1:2A:2108:G:C8	2.54	0.43
1:2A:2272:C:H1'	1:2A:2399:A:N3	2.33	0.43
1:2A:2668:A:O3'	7:2H:160:LYS:NZ	2.52	0.43
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	2.00	0.43
32:2a:160:C:H2'	32:2a:161:G:C8	2.52	0.43
32:2a:232:G:OP1	48:2q:40:LYS:NZ	2.39	0.43
32:2a:233:C:H5"	48:2q:25:ARG:CZ	2.48	0.43
33:2b:178:ARG:NH1	39:2h:68:ARG:HH22	2.16	0.43
35:2d:31:CYS:CB	58:2d:501:SF4:S3	3.06	0.43
35:2d:127:THR:HG23	35:2d:149:ALA:HB2	2.00	0.43
1:1A:554:G:O4'	1:1A:554:G:N3	2.51	0.43
1:1A:671:G:H2'	1:1A:672:G:O4'	2.19	0.43
1:1A:785:G:O6	59:1A:4379:HOH:O	2.20	0.43
1:1A:1828:U:OP2	3:1D:274:ARG:NH2	2.52	0.43
1:1A:2342:G:O2'	22:10:43:THR:HG22	2.18	0.43
3:1D:16:MET:CG	3:1D:211:ARG:HH21	2.32	0.43
5:1F:170:LEU:HD12	5:1F:170:LEU:HA	1.90	0.43
6:1G:11:TYR:HA	6:1G:15:VAL:HB	2.00	0.43
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.53	0.43
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.01	0.43
21:1Z:151:HIS:HA	21:1Z:170:THR:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:9:A:H5'	36:1e:101:ILE:HG22	2.00	0.43
32:1a:218:U:H2'	32:1a:219:U:C6	2.53	0.43
32:1a:1293:G:H2'	32:1a:1294:G:O4'	2.19	0.43
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	1.99	0.43
37:1f:97:PHE:HD1	49:1r:31:LEU:HD21	1.82	0.43
40:1i:89:ASN:O	40:1i:92:TYR:HB2	2.19	0.43
49:1r:65:ILE:O	49:1r:69:THR:OG1	2.36	0.43
1:2A:279:C:H2'	1:2A:280:G:H8	1.83	0.43
1:2A:346:G:HO2'	1:2A:1249:U:H3	1.62	0.43
1:2A:468:A:H1'	1:2A:1245:C:O4'	2.18	0.43
1:2A:973:G:H8	1:2A:973:G:O5'	2.00	0.43
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.99	0.43
21:2Z:30:ASN:HB2	59:2Z:5002:HOH:O	2.19	0.43
23:21:23:LYS:HB2	23:21:23:LYS:HE3	1.86	0.43
26:24:46:GLN:OE1	26:24:48:ARG:NH2	2.52	0.43
32:2a:114:A:C6	32:2a:116:G:C2	3.06	0.43
32:2a:451:C:N4	32:2a:461:G:H1	2.16	0.43
32:2a:889:U:H2'	32:2a:890:C:C6	2.54	0.43
32:2a:1060:G:N2	32:2a:1063:A:OP2	2.42	0.43
32:2a:1183:A:H4'	32:2a:1184:G:O5'	2.19	0.43
32:2a:1370:G:H2'	32:2a:1371:C:C6	2.54	0.43
32:2a:1446:A:H2'	32:2a:1447:G:O4'	2.19	0.43
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.49	0.43
34:2c:130:VAL:O	34:2c:134:ILE:HG12	2.18	0.43
35:2d:58:LEU:HD22	35:2d:62:GLN:HG2	1.99	0.43
38:2g:54:THR:O	38:2g:56:GLN:N	2.45	0.43
46:2o:5:LYS:H	46:2o:5:LYS:CD	2.29	0.43
1:1A:66:G:H2'	1:1A:67:C:O4'	2.17	0.43
1:1A:894:G:N9	1:1A:977:A:H8	2.17	0.43
1:1A:936:A:H2'	1:1A:937:G:O4'	2.18	0.43
1:1A:1765:G:H2'	1:1A:1766:A:H2'	2.01	0.43
1:1A:1881:U:H2'	1:1A:1882:C:O4'	2.18	0.43
4:1E:51:PHE:CD2	4:1E:52:LEU:HG	2.54	0.43
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.18	0.43
26:14:58:ARG:HB3	26:14:58:ARG:NH1	2.32	0.43
33:1b:200:ILE:O	33:1b:202:PRO:HD3	2.19	0.43
44:1m:80:ARG:HH21	50:1s:69:HIS:HE1	1.67	0.43
1:2A:579:U:H2'	1:2A:580:G:C8	2.53	0.43
1:2A:907:A:N3	2:2B:79:C:O2'	2.43	0.43
1:2A:955:A:C6	1:2A:956:A:C6	3.07	0.43
1:2A:1357:U:OP2	19:2X:63:LYS:NZ	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1755:U:H2'	1:2A:1756:C:C6	2.53	0.43
3:2D:75:ILE:HA	3:2D:76:PRO:HD3	1.81	0.43
3:2D:146:GLU:OE1	3:2D:190:TYR:N	2.35	0.43
6:2G:145:THR:N	6:2G:148:MET:SD	2.70	0.43
11:2P:95:VAL:HG13	11:2P:125:VAL:HA	2.01	0.43
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.19	0.43
32:2a:187:C:H2'	32:2a:188:C:O4'	2.18	0.43
32:2a:981:G:N3	32:2a:982:G:C8	2.87	0.43
32:2a:1080:C:H2'	32:2a:1081:C:C6	2.54	0.43
32:2a:1155:G:H2'	32:2a:1156:G:C8	2.54	0.43
32:2a:1155:G:H2'	32:2a:1156:G:H8	1.83	0.43
35:2d:31:CYS:SG	35:2d:33:MET:N	2.84	0.43
39:2h:58:TYR:O	39:2h:59:LEU:HD23	2.19	0.43
49:2r:29:PHE:N	49:2r:29:PHE:CD1	2.87	0.43
1:1A:592:G:H2'	1:1A:2051:A:C5	2.54	0.43
3:1D:43:ARG:HA	3:1D:48:ARG:O	2.19	0.43
13:1R:21:TYR:OH	13:1R:43:GLU:HG2	2.19	0.43
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.19	0.43
16:1U:34:LYS:HE2	16:1U:34:LYS:HA	2.00	0.43
23:11:67:ILE:N	23:11:68:PRO:HD2	2.34	0.43
32:1a:103:A:C8	32:1a:322:G:H2'	2.54	0.43
32:1a:568:G:H2'	32:1a:569:G:C8	2.54	0.43
32:1a:1200:C:H2'	32:1a:1201:U:C6	2.54	0.43
33:1b:10:LEU:HB3	33:1b:48:MET:HE1	2.01	0.43
35:1d:107:ARG:HH12	35:1d:194:LEU:HG	1.83	0.43
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.53	0.43
42:1k:21:ILE:HD13	42:1k:82:VAL:HG13	2.01	0.43
44:1m:19:LEU:HD21	44:1m:56:LEU:HD11	2.00	0.43
1:2A:149:C:H2'	1:2A:150:C:H6	1.84	0.43
1:2A:338:G:H2'	1:2A:339:C:C6	2.54	0.43
1:2A:352:G:H8	1:2A:352:G:OP1	2.01	0.43
1:2A:504:A:C2	1:2A:505:A:C5	3.07	0.43
1:2A:901:G:C6	1:2A:902:C:N4	2.87	0.43
1:2A:1194:G:H2'	1:2A:1195:C:C6	2.53	0.43
1:2A:1373:G:H8	1:2A:1373:G:O5'	2.01	0.43
1:2A:1659:A:C2	18:2W:93:ALA:HB2	2.54	0.43
1:2A:2027:C:O5'	1:2A:2027:C:H6	2.01	0.43
1:2A:2227:G:H3'	1:2A:2228:A:H5"	2.00	0.43
1:2A:2418:G:OP1	59:2A:3643:HOH:O	2.21	0.43
1:2A:2761:A:H4'	7:2H:62:LYS:HB3	1.99	0.43
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:140:G:H1	32:2a:172:C:H42	1.65	0.43
32:2a:449:C:H3'	32:2a:450:C:H6	1.83	0.43
32:2a:981:G:N2	32:2a:1021:C:C2	2.85	0.43
32:2a:1087:G:H4'	33:2b:111:ARG:NH1	2.34	0.43
32:2a:1120:C:O2'	32:2a:1121:G:N3	2.51	0.43
33:2b:92:TYR:CZ	33:2b:150:SER:CA	3.01	0.43
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	2.01	0.43
37:2f:22:GLU:O	37:2f:26:ILE:HG13	2.19	0.43
1:1A:955:A:N3	1:1A:2275:C:O2'	2.46	0.43
1:1A:959:C:OP1	59:1A:4391:HOH:O	2.21	0.43
1:1A:2044:G:H4'	1:1A:2628:C:O3'	2.17	0.43
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.51	0.43
7:1H:69:ARG:HG3	7:1H:70:THR:N	2.34	0.43
18:1W:23:LEU:HD12	18:1W:23:LEU:HA	1.83	0.43
29:17:1:MET:HE3	29:17:3:ARG:NH2	2.33	0.43
32:1a:1349:C:H2'	32:1a:1350:C:H6	1.84	0.43
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	2.01	0.43
35:1d:196:LEU:O	35:1d:198:VAL:N	2.46	0.43
1:2A:6:G:H2'	1:2A:7:A:C8	2.52	0.43
1:2A:1048:G:O2'	1:2A:1055:A:N1	2.41	0.43
1:2A:1553:A:H4'	1:2A:1555:A:C5	2.53	0.43
1:2A:2480:A:H2'	1:2A:2481:G:O4'	2.19	0.43
1:2A:2575:A:C2	1:2A:2658:U:H4'	2.53	0.43
5:2F:29:ASN:HA	5:2F:30:PRO:HD2	1.86	0.43
6:2G:136:ARG:HA	6:2G:154:GLY:HA3	2.01	0.43
13:2R:92:GLY:HA2	13:2R:94:TYR:CZ	2.53	0.43
17:2V:81:TYR:C	17:2V:82:ARG:HD2	2.44	0.43
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	2.01	0.43
32:2a:367:G:H1'	32:2a:467:A:H1'	2.01	0.43
32:2a:1208:C:H4'	50:2s:80:TYR:OH	2.19	0.43
32:2a:1443:C:H2'	32:2a:1444:C:O4'	2.18	0.43
35:2d:9:CYS:HB3	58:2d:501:SF4:S2	2.58	0.43
37:2f:65:VAL:HG21	37:2f:67:MET:HE2	1.99	0.43
39:2h:51:VAL:HG21	39:2h:60:ARG:HH11	1.82	0.43
40:2i:88:TYR:CD2	40:2i:89:ASN:HB2	2.53	0.43
42:2k:46:GLY:HA2	42:2k:50:TYR:O	2.18	0.43
1:1A:26:G:C2	1:1A:536:G:N3	2.86	0.43
1:1A:2346:A:C8	1:1A:2348:G:C5	3.07	0.43
14:1S:15:ARG:HE	14:1S:88:ASP:CG	2.25	0.43
32:1a:231:C:H2'	32:1a:232:G:H8	1.84	0.43
32:1a:604:C:H2'	32:1a:605:A:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1084:A:OP2	33:1b:96:ARG:HD3	2.18	0.43
32:1a:1271:A:H2'	32:1a:1272:G:H5'	2.01	0.43
32:1a:1297:U:H2'	32:1a:1298:G:O4'	2.19	0.43
32:1a:1303:C:C4	32:1a:1304:C:C4	3.07	0.43
33:1b:71:VAL:HA	33:1b:93:VAL:CG2	2.49	0.43
33:1b:128:GLU:C	33:1b:130:ARG:H	2.27	0.43
34:1c:35:GLU:O	34:1c:39:ILE:HG13	2.18	0.43
38:1g:13:GLN:HA	38:1g:14:PRO:HD3	1.92	0.43
38:1g:140:ASP:O	38:1g:143:ARG:HB3	2.19	0.43
40:1i:24:GLY:HA2	40:1i:57:GLY:HA2	2.00	0.43
42:1k:31:THR:HA	42:1k:42:TRP:HA	2.00	0.43
47:1p:23:ASP:OD1	47:1p:25:ARG:HG2	2.18	0.43
1:2A:209:A:O4'	1:2A:221:A:H1'	2.18	0.43
1:2A:1118:A:H3'	1:2A:1119:G:C8	2.54	0.43
1:2A:1176:G:C8	1:2A:2046:C:H4'	2.54	0.43
6:2G:43:LEU:C	6:2G:45:GLU:H	2.27	0.43
11:2P:126:VAL:HG12	11:2P:148:LEU:CD2	2.47	0.43
19:2X:88:LYS:HG2	19:2X:93:GLU:HG3	2.00	0.43
32:2a:659:A:O2'	42:2k:114:VAL:O	2.34	0.43
32:2a:911:G:N2	32:2a:913:A:O4'	2.52	0.43
32:2a:1302:C:O2'	50:2s:73:GLU:HB3	2.19	0.43
32:2a:1330:U:H4'	40:2i:120:ARG:HD2	2.01	0.43
33:2b:55:PHE:HD1	33:2b:58:ILE:HD12	1.83	0.43
38:2g:144:MET:HE2	38:2g:144:MET:HB3	1.87	0.43
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	2.01	0.43
43:2l:124:LYS:HA	43:2l:125:PRO:HD3	1.82	0.43
44:2m:56:LEU:HD22	44:2m:56:LEU:HA	1.82	0.43
50:2s:35:SER:O	50:2s:71:LEU:HD23	2.19	0.43
51:2t:66:ALA:HB3	51:2t:72:LEU:HD12	2.01	0.43
1:1A:2575:A:C2	1:1A:2658:U:H4'	2.54	0.43
5:1F:149:ASP:OD1	5:1F:149:ASP:N	2.51	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.58	0.43
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	2.01	0.43
17:1V:49:THR:HG22	17:1V:49:THR:O	2.19	0.43
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.34	0.43
32:1a:810:C:H4'	39:1h:12:ARG:HD3	2.01	0.43
32:1a:962:C:N4	32:1a:1203:G:H1	2.10	0.43
32:1a:1050:A:N1	32:1a:1091:G:O2'	2.43	0.43
32:1a:1218:A:H2'	32:1a:1219:C:C6	2.53	0.43
32:1a:1233:A:H2'	32:1a:1234:A:C8	2.54	0.43
32:1a:1266:C:H3'	32:1a:1267:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:29:TYR:CZ	45:1n:54:PRO:HG2	2.54	0.43
34:1c:32:LEU:HD22	34:1c:59:ARG:NH1	2.33	0.43
44:1m:81:LEU:HD11	44:1m:88:ARG:NH2	2.34	0.43
1:2A:29:G:H2'	1:2A:30:C:C6	2.54	0.43
1:2A:37:A:H2'	1:2A:38:C:C6	2.54	0.43
1:2A:69:A:N7	19:2X:31:HIS:HE1	2.17	0.43
1:2A:1386:U:O4	19:2X:16:LYS:HE2	2.18	0.43
1:2A:1638:G:H2'	1:2A:1639:G:C8	2.54	0.43
1:2A:1765:G:H8	1:2A:1769:A:N6	2.17	0.43
1:2A:2239:G:C5	1:2A:2240:C:C4	3.07	0.43
1:2A:2406:C:O2'	23:21:30:VAL:HG22	2.18	0.43
1:2A:2700:U:OP2	1:2A:2731:G:N2	2.50	0.43
1:2A:2770:A:H2'	1:2A:2771:G:O4'	2.18	0.43
1:2A:2896:U:H2'	1:2A:2897:C:C6	2.54	0.43
2:2B:26:A:H8	2:2B:26:A:O5'	2.02	0.43
2:2B:66:A:H61	2:2B:108:U:H2'	1.83	0.43
3:2D:43:ARG:HA	3:2D:48:ARG:O	2.19	0.43
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	2.01	0.43
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	2.01	0.43
12:2Q:108:GLY:HA3	21:2Z:116:VAL:HG13	2.01	0.43
32:2a:218:U:H2'	32:2a:219:U:C6	2.54	0.43
32:2a:354:U:H2'	32:2a:355:U:C6	2.53	0.43
33:2b:95:GLN:HB2	33:2b:148:TYR:HA	2.01	0.43
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	2.01	0.43
43:2l:75:HIS:HD2	43:2l:77:LEU:N	2.11	0.43
51:2t:39:LYS:HE3	51:2t:39:LYS:HB2	1.81	0.43
1:1A:903:C:N4	1:1A:904:U:O4	2.52	0.42
1:1A:1739:U:O2'	3:1D:14:ARG:NH2	2.52	0.42
1:1A:1765:G:N7	59:1A:4519:HOH:O	2.36	0.42
5:1F:33:LEU:HD12	5:1F:33:LEU:HA	1.94	0.42
7:1H:124:GLU:OE1	7:1H:132:ARG:HD2	2.19	0.42
32:1a:458:A:H2'	32:1a:459:G:O4'	2.18	0.42
32:1a:615:G:H2'	32:1a:616:A:H8	1.84	0.42
32:1a:799:A:N7	32:1a:1487:C:O2'	2.48	0.42
32:1a:931:G:H2'	32:1a:932:G:O4'	2.19	0.42
37:1f:86:ARG:O	37:1f:87:ARG:HG2	2.19	0.42
1:2A:503:A:C6	1:2A:505:A:C6	3.07	0.42
1:2A:548:U:H2'	1:2A:549:U:C6	2.54	0.42
1:2A:655:A:H1'	11:2P:66:GLY:HA2	2.01	0.42
1:2A:862:C:O2'	1:2A:976:G:O6	2.35	0.42
1:2A:875:A:N7	1:2A:2259:C:H5'	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:988:G:O3'	59:2A:3666:HOH:O	2.22	0.42
1:2A:2282:G:OP1	22:20:18:ALA:HB1	2.19	0.42
1:2A:2325:C:H2'	1:2A:2326:G:C8	2.54	0.42
1:2A:2330:G:N1	14:2S:3:ARG:HA	2.33	0.42
1:2A:2589:G:H2'	1:2A:2590:C:C6	2.54	0.42
2:2B:19:G:H2'	2:2B:20:C:O4'	2.19	0.42
2:2B:64:C:H2'	2:2B:65:C:C6	2.54	0.42
6:2G:136:ARG:HD2	6:2G:136:ARG:C	2.44	0.42
8:2I:72:LEU:HD22	8:2I:101:LEU:HD11	2.00	0.42
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.27	0.42
15:2T:73:GLU:OE1	15:2T:103:ARG:NE	2.44	0.42
17:2V:12:TYR:CG	17:2V:20:LEU:HD21	2.53	0.42
32:2a:184:G:C6	32:2a:185:C:C4	3.06	0.42
32:2a:965:G:N2	32:2a:1201:U:C2	2.88	0.42
32:2a:1145:C:H2'	32:2a:1146:C:H6	1.84	0.42
32:2a:1287:G:OP1	52:2u:2:GLY:HA3	2.19	0.42
33:2b:127:ILE:HG12	33:2b:128:GLU:N	2.33	0.42
36:2e:6:PHE:HD2	36:2e:63:ARG:HD3	1.84	0.42
36:2e:31:LEU:HA	36:2e:31:LEU:HD23	1.75	0.42
49:2r:76:LEU:HD12	49:2r:76:LEU:HA	1.71	0.42
1:1A:1275:C:H2'	1:1A:1276:G:C8	2.53	0.42
1:1A:1424:A:H4'	1:1A:1425:G:OP2	2.19	0.42
1:1A:2802:A:H2'	1:1A:2802:A:N3	2.33	0.42
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	2.01	0.42
6:1G:9:ARG:O	6:1G:13:GLU:HG2	2.20	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CE2	2.54	0.42
9:1N:33:LEU:HD12	9:1N:33:LEU:HA	1.90	0.42
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.19	0.42
32:1a:23:G:H4'	32:1a:863:G:C8	2.54	0.42
32:1a:453:C:H2'	32:1a:454:G:O4'	2.19	0.42
32:1a:485:C:H2'	32:1a:486:G:C8	2.55	0.42
34:1c:52:LEU:HD23	34:1c:69:HIS:O	2.19	0.42
35:1d:188:LEU:H	35:1d:188:LEU:CD2	2.30	0.42
36:1e:12:LEU:HB3	36:1e:31:LEU:HB3	2.01	0.42
37:1f:22:GLU:O	37:1f:26:ILE:HG13	2.20	0.42
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.81	0.42
46:1o:26:GLU:H	46:1o:26:GLU:HG2	1.49	0.42
1:2A:1509:C:H2'	1:2A:1510:C:C6	2.54	0.42
1:2A:1823:C:OP1	59:2A:3664:HOH:O	2.21	0.42
1:2A:1833:A:H4'	3:2D:259:THR:HG23	2.00	0.42
1:2A:2059:G:H2'	1:2A:2060:C:O4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2101:G:H2'	1:2A:2102:C:C6	2.54	0.42
1:2A:2568:G:H2'	1:2A:2569:C:C6	2.54	0.42
1:2A:2754:C:OP1	31:29:35:ARG:HD3	2.19	0.42
1:2A:2757:C:C4	1:2A:2758:U:C4	3.07	0.42
22:20:56:ASP:CG	22:20:58:THR:HG1	2.27	0.42
31:29:29:ASN:HD22	31:29:31:LYS:H	1.66	0.42
32:2a:138:A:O3'	32:2a:139:G:H8	2.02	0.42
32:2a:196:G:H2'	32:2a:197:U:C6	2.54	0.42
32:2a:376:G:C2	32:2a:380:G:C6	3.07	0.42
32:2a:435:A:N1	32:2a:481:A:H1'	2.34	0.42
32:2a:870:A:O2'	32:2a:1398:G:H4'	2.19	0.42
32:2a:1433:C:H4'	32:2a:1435:G:C8	2.54	0.42
38:2g:26:PHE:CZ	38:2g:30:ILE:HD11	2.54	0.42
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.81	0.42
43:2l:84:LEU:HB3	43:2l:104:VAL:HG21	2.01	0.42
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.19	0.42
47:2p:28:ARG:HG3	47:2p:29:ASP:N	2.32	0.42
48:2q:63:ARG:HG2	48:2q:64:PRO:HD2	2.01	0.42
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.19	0.42
1:1A:141:G:H4'	19:1X:35:THR:HG21	2.01	0.42
1:1A:216:A:H8	1:1A:217:A:H5'	1.83	0.42
1:1A:398:G:H8	23:11:65:SER:O	2.02	0.42
1:1A:1822:G:H5'	3:1D:205:VAL:HG13	2.01	0.42
1:1A:2049:U:H2'	1:1A:2050:G:O4'	2.18	0.42
3:1D:69:ARG:C	3:1D:71:ASP:H	2.25	0.42
6:1G:83:ARG:N	6:1G:86:MET:SD	2.72	0.42
15:1T:108:ARG:HG2	15:1T:111:ARG:NH1	2.33	0.42
24:12:2:LYS:O	24:12:6:VAL:HG23	2.19	0.42
32:1a:469:G:H8	32:1a:469:G:OP1	2.03	0.42
32:1a:842:A:H2'	32:1a:843:A:C8	2.54	0.42
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.84	0.42
47:1p:51:VAL:HG11	47:1p:79:VAL:HG21	2.02	0.42
50:1s:40:ILE:HB	50:1s:67:VAL:O	2.20	0.42
1:2A:1561:U:H2'	1:2A:1562:G:H8	1.83	0.42
1:2A:1840:A:H2'	1:2A:1841:G:O4'	2.19	0.42
1:2A:1967:U:H2'	1:2A:1968:C:C6	2.54	0.42
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	2.02	0.42
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.84	0.42
11:2P:63:PRO:HD3	30:28:27:THR:HG22	2.01	0.42
32:2a:564:U:H2'	32:2a:565:G:O4'	2.19	0.42
32:2a:1116:G:H2'	32:2a:1117:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1374:U:H2'	32:2a:1375:G:C8	2.53	0.42
35:2d:60:GLU:HG2	35:2d:202:LEU:HB2	1.99	0.42
40:2i:28:VAL:HG22	40:2i:63:ILE:HD12	2.01	0.42
45:2n:2:ALA:O	45:2n:6:LEU:HD12	2.19	0.42
1:1A:603:C:H2'	1:1A:604:G:H8	1.85	0.42
1:1A:1217:G:H22	1:1A:1221:A:P	2.42	0.42
1:1A:1571:G:C6	1:1A:1572:G:C2	3.08	0.42
1:1A:1711:A:H2'	1:1A:1712:G:O4'	2.19	0.42
1:1A:2801:C:O2'	1:1A:2802:A:H4'	2.18	0.42
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.20	0.42
6:1G:60:LEU:HD22	6:1G:60:LEU:HA	1.79	0.42
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.90	0.42
11:1P:64:LYS:HE3	30:18:12:LYS:HD3	2.00	0.42
12:1Q:1:MET:HE2	12:1Q:1:MET:HB3	1.82	0.42
26:14:57:GLU:HA	26:14:58:ARG:HA	1.44	0.42
32:1a:44:C:H2'	32:1a:45:G:O4'	2.19	0.42
32:1a:221:C:H2'	32:1a:222:G:C8	2.54	0.42
32:1a:397:C:H2'	32:1a:398:G:C8	2.55	0.42
32:1a:1043:C:OP1	45:1n:45:ARG:NH2	2.44	0.42
32:1a:1302:C:O2'	50:1s:73:GLU:HB3	2.19	0.42
38:1g:153:HIS:CE1	42:1k:58:PRO:HD2	2.54	0.42
50:1s:40:ILE:HD12	50:1s:62:ILE:HD13	2.01	0.42
1:2A:624:G:N2	1:2A:701:A:OP2	2.42	0.42
1:2A:644:G:N3	1:2A:644:G:H5'	2.35	0.42
1:2A:658:C:H2'	1:2A:659:C:C6	2.55	0.42
1:2A:775:G:H5'	1:2A:776:C:H5"	2.02	0.42
1:2A:921:G:O2'	21:2Z:151:HIS:HE1	2.03	0.42
1:2A:1101:G:H5"	1:2A:1102:A:H5'	2.00	0.42
1:2A:2419:U:H2'	1:2A:2420:G:H8	1.83	0.42
1:2A:2590:C:C4'	4:2E:134:ILE:HG12	2.49	0.42
1:2A:2792:G:OP2	9:2N:118:LYS:HD3	2.19	0.42
3:2D:94:LEU:HD23	3:2D:94:LEU:HA	1.92	0.42
10:2O:73:ASP:HB2	15:2T:82:LEU:HD13	2.01	0.42
12:2Q:42:ILE:HG12	12:2Q:103:MET:HE1	2.00	0.42
13:2R:104:ARG:HD2	13:2R:109:ALA:HB3	2.00	0.42
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.44	0.42
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.19	0.42
26:24:50:VAL:HG11	44:2m:65:LYS:HB2	2.01	0.42
30:28:61:LEU:O	30:28:63:PRO:HD3	2.18	0.42
32:2a:262:G:H5"	32:2a:264:C:N4	2.31	0.42
32:2a:422:G:H2'	32:2a:423:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:448:A:C5	32:2a:449:C:C4	3.07	0.42
32:2a:721:A:H2'	32:2a:722:C:C6	2.54	0.42
32:2a:798:A:N7	32:2a:800:A:C4	2.87	0.42
32:2a:1040:G:O3'	34:2c:197:GLY:HA3	2.19	0.42
32:2a:1163:G:O2'	32:2a:1164:G:N7	2.52	0.42
32:2a:1333:U:OP2	59:2a:3328:HOH:O	2.21	0.42
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.83	0.42
40:2i:47:LEU:O	40:2i:51:ARG:HG3	2.20	0.42
51:2t:10:LEU:HD23	51:2t:11:SER:H	1.84	0.42
1:1A:173:U:H4'	1:1A:206:A:H4'	2.00	0.42
1:1A:214:G:N2	1:1A:216:A:H62	2.18	0.42
1:1A:1626:A:OP2	1:1A:1626:A:H8	2.03	0.42
1:1A:1755:U:H2'	1:1A:1756:C:C6	2.55	0.42
1:1A:2456:G:OP1	5:1F:74:ARG:NH2	2.52	0.42
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.20	0.42
3:1D:71:ASP:CB	3:1D:103:ARG:HH22	2.27	0.42
6:1G:50:ALA:O	6:1G:52:ILE:N	2.46	0.42
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.42
21:1Z:91:LEU:HD13	21:1Z:91:LEU:HA	1.80	0.42
32:1a:379:A:H2'	32:1a:380:G:H5'	2.01	0.42
32:1a:747:G:H2'	32:1a:748:C:H6	1.84	0.42
32:1a:955:A:H1'	32:1a:960:U:O4	2.20	0.42
32:1a:1173:A:OP1	34:1c:4:LYS:NZ	2.50	0.42
32:1a:1302:C:OP1	50:1s:70:LYS:NZ	2.48	0.42
32:1a:1476:U:O2'	53:1v:17:U:OP1	2.29	0.42
33:1b:28:PHE:CD2	33:1b:194:PRO:HG3	2.52	0.42
33:1b:155:LEU:HD11	33:1b:159:PRO:HD3	2.01	0.42
34:1c:71:ALA:C	34:1c:73:PRO:HD3	2.45	0.42
35:1d:62:GLN:O	35:1d:66:ARG:HD3	2.19	0.42
35:1d:180:GLY:O	35:1d:181:MET:HG2	2.19	0.42
40:1i:55:ALA:HA	40:1i:58:HIS:CD2	2.54	0.42
42:1k:21:ILE:HD11	42:1k:98:LEU:HD12	2.01	0.42
1:2A:142:C:H2'	1:2A:143:C:H6	1.84	0.42
1:2A:457:U:O5'	1:2A:457:U:H6	2.02	0.42
1:2A:619:U:H2'	1:2A:620:G:C8	2.54	0.42
1:2A:1080:U:H2'	1:2A:1081:G:C8	2.55	0.42
1:2A:1096:G:C5	1:2A:1097:C:C4	3.08	0.42
1:2A:1104:G:H3'	1:2A:1105:U:C6	2.51	0.42
1:2A:1988:C:H2'	1:2A:1989:G:O4'	2.20	0.42
1:2A:2088:G:O2'	1:2A:2090:G:H5"	2.19	0.42
1:2A:2118:C:H2'	1:2A:2119:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2713:U:H4'	1:2A:2714:C:OP1	2.20	0.42
1:2A:2824:C:H5'	27:25:29:THR:HG21	2.02	0.42
19:2X:26:TYR:CE2	19:2X:89:ILE:HG13	2.55	0.42
21:2Z:151:HIS:ND1	21:2Z:168:GLU:O	2.50	0.42
24:22:28:LYS:HD3	24:22:60:LEU:HD11	2.00	0.42
26:24:1:MET:HG2	26:24:6:HIS:CD2	2.55	0.42
32:2a:423:U:O2'	32:2a:525:G:OP1	2.25	0.42
32:2a:945:C:N3	59:2a:3356:HOH:O	2.36	0.42
32:2a:1030:G:H5"	45:2n:4:LYS:HD2	2.01	0.42
32:2a:1045:U:H2'	32:2a:1046:C:C5	2.55	0.42
33:2b:28:PHE:CE2	33:2b:31:TYR:HD2	2.37	0.42
34:2c:117:ALA:HB2	34:2c:186:PHE:CD2	2.54	0.42
36:2e:91:LEU:HG	36:2e:118:ILE:HD11	2.01	0.42
38:2g:16:LEU:H	38:2g:16:LEU:HD22	1.84	0.42
39:2h:73:ASP:OD1	39:2h:75:ARG:HG3	2.19	0.42
51:2t:56:MET:HE2	51:2t:85:MET:HA	2.01	0.42
53:2v:14:A:H2'	53:2v:15:A:O4'	2.20	0.42
1:1A:8:U:N3	1:1A:2640:A:H2	2.10	0.42
1:1A:817:G:OP1	29:17:10:ARG:NH1	2.51	0.42
1:1A:1471:G:C6	1:1A:1472:A:C6	3.07	0.42
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.55	0.42
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.33	0.42
21:1Z:14:LYS:HA	21:1Z:15:PRO:HD3	1.96	0.42
32:1a:200:C:H2'	32:1a:201:C:C6	2.55	0.42
32:1a:703:C:OP2	32:1a:704:C:N4	2.47	0.42
32:1a:951:G:OP1	41:1j:57:LYS:NZ	2.35	0.42
32:1a:1464:G:H2'	32:1a:1465:G:O4'	2.20	0.42
40:1i:4:TYR:CE2	40:1i:88:TYR:HA	2.53	0.42
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.34	0.42
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.50	0.42
1:2A:40:C:H2'	1:2A:41:G:H8	1.83	0.42
1:2A:80:G:N2	1:2A:100:A:OP2	2.51	0.42
1:2A:1047:G:H2'	1:2A:1048:G:O4'	2.20	0.42
1:2A:1364:G:C6	1:2A:1365:C:N4	2.87	0.42
1:2A:2276:U:C4	1:2A:2277:A:C5	3.07	0.42
1:2A:2488:C:N4	31:29:10:ILE:HG23	2.35	0.42
12:2Q:27:VAL:HG13	12:2Q:105:GLU:CD	2.45	0.42
19:2X:31:HIS:HA	19:2X:32:PRO:HD3	1.88	0.42
25:23:11:SER:HA	25:23:31:LEU:HD21	2.01	0.42
27:25:20:ARG:HG2	27:25:23:HIS:ND1	2.34	0.42
32:2a:1287:G:O2'	32:2a:1288:A:OP2	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:3:ARG:HB2	35:2d:3:ARG:HH11	1.84	0.42
39:2h:111:ILE:HG23	39:2h:135:CYS:SG	2.59	0.42
40:2i:96:LEU:HD23	40:2i:96:LEU:HA	1.91	0.42
44:2m:33:ALA:HB2	44:2m:64:TRP:HZ3	1.84	0.42
1:1A:263:G:H2'	1:1A:264:U:O4'	2.20	0.42
1:1A:615:G:C4'	30:18:4:MET:HE2	2.50	0.42
1:1A:1083:C:OP1	59:1A:4389:HOH:O	2.21	0.42
1:1A:1404:A:H2'	1:1A:1405:A:H5'	2.02	0.42
1:1A:2020:C:H4'	1:1A:2735:C:O2	2.20	0.42
1:1A:2591:U:C5	1:1A:2592:G:C6	3.08	0.42
2:1B:90:A:N7	2:1B:91:C:H1'	2.35	0.42
6:1G:131:TYR:HB3	6:1G:159:VAL:CG1	2.49	0.42
7:1H:5:GLY:HA2	7:1H:69:ARG:HB3	2.01	0.42
10:1O:26:LYS:O	10:1O:30:ALA:HB2	2.20	0.42
14:1S:15:ARG:NE	14:1S:88:ASP:OD2	2.37	0.42
18:1W:14:PRO:HG2	18:1W:78:GLU:CG	2.50	0.42
32:1a:1132:C:H2'	32:1a:1133:U:C6	2.55	0.42
32:1a:1185:C:H2'	32:1a:1186:A:H8	1.85	0.42
33:1b:162:ILE:HG13	33:1b:184:VAL:HA	2.02	0.42
34:1c:58:GLU:O	34:1c:59:ARG:HG3	2.20	0.42
36:1e:131:ILE:HD13	36:1e:131:ILE:HA	1.88	0.42
40:1i:20:ARG:O	40:1i:60:ASP:N	2.35	0.42
1:2A:251:C:H2'	1:2A:252:C:O4'	2.19	0.42
1:2A:321:G:H5"	1:2A:322:A:OP1	2.19	0.42
1:2A:367:G:N2	1:2A:368:A:H62	2.18	0.42
1:2A:531:A:H5"	1:2A:532:G:H3'	2.01	0.42
1:2A:901:G:H2'	1:2A:902:C:C6	2.55	0.42
1:2A:933:A:N3	1:2A:933:A:H2'	2.34	0.42
1:2A:1346:A:H2	1:2A:1671:G:N3	2.17	0.42
1:2A:1384:G:H5"	19:2X:16:LYS:HD2	2.02	0.42
1:2A:2815:G:H2'	1:2A:2816:G:H8	1.82	0.42
2:2B:17:C:H2'	2:2B:18:G:O4'	2.19	0.42
5:2F:46:ARG:HB3	5:2F:48:THR:HG23	2.02	0.42
5:2F:129:PHE:O	5:2F:132:VAL:HG13	2.20	0.42
6:2G:9:ARG:HD3	6:2G:13:GLU:OE1	2.19	0.42
6:2G:102:PHE:O	6:2G:106:LEU:HB2	2.20	0.42
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.20	0.42
11:2P:125:VAL:HG13	11:2P:138:LEU:HD21	2.01	0.42
31:29:15:LYS:HB3	31:29:26:ILE:HD12	2.02	0.42
32:2a:474:C:H2'	32:2a:475:G:C8	2.54	0.42
32:2a:952:A:P	45:2n:41:ARG:HH12	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1078:U:OP1	32:2a:1091:G:N1	2.48	0.42
32:2a:1258:G:H2'	32:2a:1259:C:H6	1.84	0.42
33:2b:118:LEU:HD13	33:2b:138:LEU:HB3	2.02	0.42
37:2f:100:ASN:HD21	49:2r:23:LYS:HE2	1.84	0.42
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	2.02	0.42
40:2i:53:VAL:C	40:2i:55:ALA:H	2.23	0.42
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.55	0.42
54:2x:43:A:H2'	54:2x:44:A:C8	2.54	0.42
1:1A:1065:A:N1	1:1A:1185:U:O2'	2.47	0.42
1:1A:1247:G:H5'	11:1P:3:LEU:HD23	2.01	0.42
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	2.01	0.42
8:1I:26:ALA:O	8:1I:31:LEU:HB2	2.20	0.42
12:1Q:68:ILE:HD13	12:1Q:103:MET:HE2	2.00	0.42
23:11:95:LEU:O	23:11:98:LEU:HB2	2.18	0.42
32:1a:23:G:H2'	32:1a:24:C:C6	2.55	0.42
32:1a:67:G:C6	32:1a:68:C:C4	3.08	0.42
32:1a:195:U:H2'	32:1a:196:G:C8	2.54	0.42
32:1a:417:U:O2'	32:1a:419:G:N7	2.52	0.42
32:1a:889:U:H2'	32:1a:890:C:C6	2.55	0.42
32:1a:925:G:O3'	44:1m:109:THR:OG1	2.37	0.42
32:1a:1330:U:H5	32:1a:1356:G:C2	2.38	0.42
37:1f:69:GLU:CD	37:1f:69:GLU:H	2.27	0.42
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	2.02	0.42
48:1q:87:LYS:HA	48:1q:87:LYS:HD3	1.84	0.42
1:2A:488:G:N1	1:2A:492:G:C6	2.87	0.42
1:2A:1101:G:C5'	1:2A:1102:A:H5'	2.50	0.42
1:2A:1109:C:H42	1:2A:1119:G:H1	1.67	0.42
1:2A:1292:A:OP1	5:2F:95:ARG:NH2	2.51	0.42
1:2A:1332:A:C5	1:2A:1333:U:C4	3.08	0.42
1:2A:2401:U:O2'	1:2A:2402:G:H5'	2.19	0.42
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.20	0.42
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.48	0.42
18:2W:41:LYS:HE3	27:25:25:LEU:HD11	2.02	0.42
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.52	0.42
25:23:28:LEU:HD23	25:23:28:LEU:HA	1.91	0.42
29:27:3:ARG:HD3	29:27:3:ARG:HA	1.80	0.42
32:2a:449:C:H3'	32:2a:450:C:C6	2.55	0.42
32:2a:775:G:C6	32:2a:776:A:N7	2.88	0.42
32:2a:951:G:P	41:2j:57:LYS:HZ3	2.42	0.42
32:2a:1362:G:C4	32:2a:1363:U:H5	2.37	0.42
35:2d:31:CYS:SG	35:2d:32:ALA:N	2.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:48:GLU:N	40:2i:49:PRO:HD2	2.35	0.42
1:1A:334:A:C6	1:1A:351:U:C4	3.08	0.42
1:1A:1313:A:C2	1:1A:2034:A:C4	3.08	0.42
1:1A:1856:G:H4'	3:1D:242:ARG:CZ	2.49	0.42
2:1B:13:A:N1	2:1B:69:G:O2'	2.45	0.42
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.02	0.42
20:1Y:81:LYS:HB3	20:1Y:81:LYS:HE2	1.74	0.42
32:1a:140:G:C2	32:1a:141:G:C4	3.07	0.42
32:1a:205:G:C6	32:1a:216:G:C2	3.08	0.42
32:1a:1183:A:H4'	32:1a:1184:G:O5'	2.19	0.42
32:1a:1329:G:O2'	32:1a:1356:G:O6	2.35	0.42
32:1a:1349:C:H2'	32:1a:1350:C:C6	2.55	0.42
32:1a:1435:G:H2'	32:1a:1436:G:H8	1.81	0.42
33:1b:98:LEU:HG	33:1b:101:MET:HE3	2.02	0.42
33:1b:161:ALA:HB1	33:1b:185:ILE:HD11	2.01	0.42
33:1b:198:ASP:OD2	33:1b:198:ASP:N	2.52	0.42
48:1q:12:SER:HB3	48:1q:20:THR:HB	2.00	0.42
1:2A:417:G:H1'	1:2A:437:G:O4'	2.20	0.42
1:2A:493:G:H5"	5:2F:60:SER:HB2	2.01	0.42
1:2A:598:U:H2'	1:2A:599:G:C8	2.55	0.42
1:2A:1114:A:H4'	1:2A:1115:A:H5"	2.02	0.42
1:2A:1332:A:H5"	1:2A:1333:U:OP2	2.20	0.42
1:2A:1409:G:OP2	23:21:3:LYS:HG3	2.20	0.42
1:2A:2249:G:H2'	1:2A:2249:G:N3	2.35	0.42
2:2B:95:C:H2'	2:2B:96:U:C6	2.55	0.42
3:2D:77:ALA:O	3:2D:116:GLN:HG3	2.19	0.42
3:2D:132:PRO:HG3	3:2D:190:TYR:CE1	2.55	0.42
3:2D:228:PRO:HD3	3:2D:235:GLY:HA3	2.02	0.42
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.20	0.42
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	2.02	0.42
6:2G:91:ARG:HE	6:2G:91:ARG:HB3	1.75	0.42
26:24:26:SER:OG	26:24:27:THR:N	2.53	0.42
32:2a:90:U:O2'	32:2a:91:G:H5'	2.20	0.42
32:2a:674:G:H8	32:2a:674:G:O5'	2.03	0.42
32:2a:900:G:C6	32:2a:901:A:C6	3.08	0.42
32:2a:1358:A:O3'	38:2g:29:LYS:NZ	2.53	0.42
32:2a:1424:G:H1'	32:2a:1439:G:N2	2.35	0.42
33:2b:187:LEU:HA	33:2b:201:ILE:HB	2.02	0.42
50:2s:27:GLU:HB2	50:2s:28:LYS:HD3	2.02	0.42
55:2z:12:PRO:HA	55:2z:13:PRO:HD3	1.80	0.42
1:1A:509:C:H2'	1:1A:510:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:989:A:C4	1:1A:2459:A:C2	3.08	0.42
1:1A:1149:C:H2'	1:1A:1150:U:C5	2.54	0.42
1:1A:1511:G:O2'	1:1A:1591:A:N1	2.52	0.42
1:1A:2046:C:H2'	1:1A:2047:C:C6	2.55	0.42
1:1A:2331:A:H2'	1:1A:2331:A:N3	2.35	0.42
1:1A:2640:A:O2'	1:1A:2641:G:OP2	2.29	0.42
3:1D:132:PRO:HG3	3:1D:190:TYR:CE1	2.54	0.42
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	2.02	0.42
17:1V:19:LYS:HA	17:1V:94:LEU:O	2.19	0.42
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.55	0.42
20:1Y:1:MET:HB2	20:1Y:1:MET:HE3	1.78	0.42
32:1a:443:A:P	32:1a:470:G:H22	2.42	0.42
32:1a:549:U:H3'	32:1a:550:G:H2'	2.02	0.42
32:1a:1325:G:H4'	40:1i:122:ALA:HB3	2.02	0.42
44:1m:84:ILE:HD12	50:1s:74:PHE:HZ	1.84	0.42
47:1p:26:ARG:HD3	47:1p:31:LYS:N	2.34	0.42
48:1q:45:HIS:O	48:1q:73:VAL:HG23	2.20	0.42
1:2A:224:C:H2'	1:2A:225:C:C6	2.55	0.42
1:2A:469:C:H4'	5:2F:49:ALA:HB2	2.01	0.42
1:2A:769:G:H2'	1:2A:770:U:O4'	2.20	0.42
1:2A:1072:A:C2	1:2A:2499:A:H5'	2.55	0.42
1:2A:1181:G:O2'	1:2A:2060:C:H5'	2.19	0.42
1:2A:1239:G:O2'	1:2A:1271:A:N1	2.45	0.42
1:2A:1374:U:H5"	1:2A:1375:C:H5	1.85	0.42
1:2A:1848:U:O4	3:2D:154:LYS:HD3	2.20	0.42
1:2A:2371:A:C2	1:2A:2372:A:H1'	2.54	0.42
1:2A:2533:U:O2'	1:2A:2658:U:OP1	2.25	0.42
3:2D:275:LYS:HA	3:2D:275:LYS:HD3	1.63	0.42
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.79	0.42
6:2G:37:VAL:O	6:2G:94:LEU:N	2.48	0.42
9:2N:111:PRO:HA	9:2N:114:ARG:NH1	2.35	0.42
31:29:17:ILE:HD12	31:29:17:ILE:HA	1.82	0.42
32:2a:197:U:C2	32:2a:198:G:C8	3.07	0.42
33:2b:97:TRP:HZ2	33:2b:102:LEU:HD13	1.85	0.42
33:2b:116:GLU:HG2	33:2b:153:ARG:HH21	1.83	0.42
48:2q:92:ARG:HD3	48:2q:92:ARG:HA	1.87	0.42
1:1A:315:C:C2	1:1A:372:G:C2	3.08	0.41
1:1A:483:G:C8	29:17:37:LYS:HG2	2.55	0.41
1:1A:1531:A:H2'	1:1A:1532:G:C8	2.55	0.41
1:1A:2302:U:OP1	1:1A:2391:C:O2'	2.37	0.41
3:1D:78:LYS:HE2	3:1D:78:LYS:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:182:LEU:HD23	3:1D:182:LEU:HA	1.90	0.41
4:1E:51:PHE:H	4:1E:75:VAL:HG11	1.85	0.41
18:1W:9:TYR:HA	18:1W:100:THR:CG2	2.50	0.41
30:18:33:ASN:HA	30:18:36:LYS:HD2	2.02	0.41
35:1d:36:ARG:HB2	35:1d:38:TYR:CZ	2.55	0.41
36:1e:48:ALA:HB3	36:1e:54:ALA:HB2	2.01	0.41
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.90	0.41
46:1o:70:LEU:HD11	46:1o:77:ARG:HB3	2.02	0.41
50:1s:22:LEU:HD11	50:1s:28:LYS:HA	2.01	0.41
52:1u:5:ASP:O	52:1u:7:ARG:N	2.51	0.41
1:2A:775:G:C6	3:2D:208:LYS:HB2	2.54	0.41
1:2A:910:G:H4'	2:2B:102:A:H4'	2.03	0.41
1:2A:2319:G:H5"	1:2A:2321:A:OP2	2.20	0.41
1:2A:2443:A:C6	1:2A:2444:A:C6	3.08	0.41
1:2A:2500:G:C6	1:2A:2501:G:C6	3.08	0.41
32:2a:101:G:H2'	32:2a:102:G:O4'	2.20	0.41
32:2a:251:G:H2'	32:2a:252:U:H6	1.84	0.41
32:2a:300:U:H2'	32:2a:301:G:C8	2.55	0.41
32:2a:437:C:H42	32:2a:477:G:H1	1.68	0.41
32:2a:984:A:OP2	32:2a:985:C:N4	2.53	0.41
32:2a:1120:C:O2'	32:2a:1121:G:H5"	2.20	0.41
32:2a:1312:U:H4'	44:2m:23:TYR:CZ	2.55	0.41
1:1A:143:C:H5'	19:1X:2:LYS:HD3	2.02	0.41
1:1A:840:G:C6	1:1A:841:C:C4	3.08	0.41
1:1A:2347:A:H61	22:10:43:THR:HG22	1.83	0.41
1:1A:2583:A:C8	4:1E:144:ARG:HD2	2.55	0.41
1:1A:2778:G:H2'	1:1A:2778:G:N3	2.35	0.41
3:1D:38:LYS:HA	3:1D:38:LYS:HD2	1.87	0.41
4:1E:119:ARG:HD2	4:1E:120:TRP:CE2	2.54	0.41
7:1H:121:ILE:HD13	7:1H:121:ILE:HA	1.92	0.41
11:1P:123:LEU:HD23	11:1P:123:LEU:HA	1.90	0.41
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.20	0.41
22:10:29:GLN:O	22:10:67:VAL:HG23	2.21	0.41
24:12:32:LEU:HD12	24:12:57:ILE:HD12	2.02	0.41
26:14:24:THR:OG1	26:14:25:TYR:N	2.36	0.41
32:1a:289:G:C6	32:1a:290:U:C4	3.08	0.41
32:1a:1053:U:OP1	36:1e:25:ARG:NH1	2.53	0.41
38:1g:10:ARG:HE	38:1g:10:ARG:HB2	1.78	0.41
38:1g:38:LEU:O	38:1g:42:ILE:HG13	2.20	0.41
40:1i:54:ASP:HB3	40:1i:55:ALA:H	1.61	0.41
44:1m:14:ARG:HG3	44:1m:44:ARG:NH1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:1r:31:LEU:HD23	49:1r:31:LEU:H	1.86	0.41
1:2A:10:G:H2'	1:2A:11:U:H5"	2.01	0.41
1:2A:113:C:H2'	1:2A:114:G:O4'	2.21	0.41
1:2A:485:A:C2	1:2A:495:A:C4	3.08	0.41
1:2A:853:U:OP2	11:2P:41:ARG:NH2	2.50	0.41
1:2A:1308:U:C4	1:2A:1309:G:C6	3.08	0.41
1:2A:1556:A:H2'	1:2A:1557:G:C8	2.54	0.41
1:2A:2324:C:O2'	1:2A:2325:C:H5'	2.19	0.41
1:2A:2888:C:OP2	59:2A:3670:HOH:O	2.22	0.41
4:2E:77:ILE:HD13	4:2E:195:LEU:HD22	2.01	0.41
6:2G:18:GLU:CG	6:2G:175:LEU:HD21	2.50	0.41
10:2O:64:ARG:O	10:2O:82:ASN:HA	2.20	0.41
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	2.02	0.41
11:2P:63:PRO:HG2	30:28:25:MET:HB2	2.02	0.41
32:2a:38:U:O2'	32:2a:484:G:H4'	2.20	0.41
32:2a:1438:A:H2'	32:2a:1439:G:O4'	2.19	0.41
34:2c:54:ARG:HB2	34:2c:69:HIS:CG	2.55	0.41
35:2d:171:GLY:HA2	35:2d:172:PRO:HD2	1.77	0.41
41:2j:30:SER:HB3	41:2j:84:GLN:CD	2.45	0.41
43:2l:53:ARG:NH1	43:2l:92:ASP:OD2	2.52	0.41
44:2m:78:ILE:HD13	44:2m:92:HIS:CD2	2.55	0.41
1:1A:1763:G:C6	1:1A:1764:U:C4	3.08	0.41
1:1A:2659:C:H2'	1:1A:2660:U:H6	1.86	0.41
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	2.01	0.41
11:1P:112:LEU:HD13	11:1P:127:ALA:HB2	2.01	0.41
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	2.01	0.41
23:11:3:LYS:HG2	23:11:4:VAL:HG23	2.02	0.41
24:12:29:LYS:HE2	24:12:57:ILE:HG21	2.01	0.41
26:14:6:HIS:HA	26:14:7:PRO:HD3	1.96	0.41
32:1a:380:G:H2'	32:1a:381:C:C6	2.55	0.41
32:1a:1245:C:H2'	32:1a:1246:C:C6	2.56	0.41
33:1b:8:LYS:H	33:1b:8:LYS:HG2	1.65	0.41
33:1b:60:ASP:O	33:1b:64:ARG:HB2	2.20	0.41
35:1d:141:ARG:H	35:1d:141:ARG:HG2	1.64	0.41
41:1j:57:LYS:C	41:1j:59:SER:H	2.28	0.41
51:1t:43:LEU:HD23	51:1t:43:LEU:HA	1.90	0.41
54:1x:75:C:OP1	59:1x:201:HOH:O	2.22	0.41
1:2A:29:G:H2'	1:2A:30:C:O4'	2.20	0.41
1:2A:828:A:C6	3:2D:226:MET:HE2	2.55	0.41
1:2A:909:A:P	12:2Q:22:LYS:HG3	2.60	0.41
1:2A:1362:A:H2'	1:2A:1363:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1863:U:O2'	1:2A:1990:A:N1	2.40	0.41
1:2A:2657:C:H2'	1:2A:2658:U:O4'	2.21	0.41
1:2A:2658:U:H2'	1:2A:2659:C:C6	2.56	0.41
4:2E:18:ASP:HB3	15:2T:82:LEU:HD21	2.02	0.41
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.95	0.41
6:2G:41:GLN:HB3	6:2G:43:LEU:HD13	2.01	0.41
11:2P:95:VAL:HG13	11:2P:125:VAL:HB	2.01	0.41
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.21	0.41
20:2Y:14:LEU:HD11	20:2Y:22:GLY:HA2	2.03	0.41
23:21:73:LEU:HA	23:21:73:LEU:HD23	1.81	0.41
32:2a:822:G:H1	32:2a:826:C:N4	2.17	0.41
32:2a:1134:A:O2'	32:2a:1135:A:H8	2.03	0.41
32:2a:1269:A:H2'	32:2a:1270:A:C8	2.55	0.41
32:2a:1373:U:H2'	32:2a:1374:U:C6	2.54	0.41
32:2a:1503:G:H2'	32:2a:1504:G:O4'	2.19	0.41
37:2f:67:MET:HE1	37:2f:75:LEU:HD12	2.03	0.41
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.20	0.41
1:1A:555:C:H4'	1:1A:556:A:H5"	2.02	0.41
1:1A:830:A:C8	1:1A:838:G:C5	3.08	0.41
1:1A:1038:G:OP1	16:1U:50:ARG:NH2	2.50	0.41
1:1A:2283:U:H5"	1:1A:2284:A:OP1	2.20	0.41
7:1H:7:LEU:HA	7:1H:8:PRO:HD3	1.88	0.41
8:1I:27:ARG:HD2	23:11:71:TYR:CZ	2.56	0.41
18:1W:18:ARG:HG3	18:1W:76:VAL:HB	2.02	0.41
32:1a:22:G:H2'	32:1a:23:G:C8	2.56	0.41
32:1a:523:A:H2'	32:1a:524:G:H8	1.85	0.41
32:1a:606:A:H3'	32:1a:607:C:C6	2.56	0.41
32:1a:1243:A:H3'	32:1a:1244:C:C6	2.56	0.41
33:1b:54:THR:O	33:1b:58:ILE:HG12	2.21	0.41
33:1b:201:ILE:O	33:1b:203:GLY:N	2.53	0.41
47:1p:4:ILE:HG13	47:1p:64:ALA:HB1	2.02	0.41
51:1t:9:ASN:ND2	51:1t:10:LEU:H	2.18	0.41
1:2A:78:G:H1	1:2A:103:C:N4	2.17	0.41
1:2A:478:C:O2	1:2A:482:A:O2'	2.38	0.41
1:2A:594:A:H5"	1:2A:595:G:OP2	2.20	0.41
1:2A:897:U:H5'	25:23:49:LYS:HD2	2.03	0.41
1:2A:948:C:H2'	1:2A:949:C:H6	1.85	0.41
1:2A:1000:G:H2'	1:2A:1001:A:H2'	2.02	0.41
1:2A:1013:U:H4'	25:23:14:GLY:O	2.20	0.41
1:2A:1266:C:C2	1:2A:1274:G:C2	3.07	0.41
1:2A:2393:G:H21	30:28:42:ARG:NH2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:47:LYS:HE2	6:2G:47:LYS:HB2	1.68	0.41
10:2O:88:ASN:ND2	10:2O:92:GLU:HB2	2.35	0.41
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	2.02	0.41
12:2Q:27:VAL:HG12	12:2Q:29:PHE:H	1.85	0.41
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.20	0.41
16:2U:110:VAL:O	16:2U:113:ALA:HB3	2.20	0.41
18:2W:1:MET:HE2	18:2W:62:HIS:HB3	2.02	0.41
20:2Y:5:MET:HE2	20:2Y:5:MET:HB2	1.83	0.41
21:2Z:53:ILE:HA	59:2Z:5006:HOH:O	2.20	0.41
32:2a:650:G:H5'	32:2a:710:C:H1'	2.02	0.41
32:2a:1047:G:H4'	32:2a:1048:U:O5'	2.20	0.41
32:2a:1104:U:H2'	32:2a:1105:U:C6	2.56	0.41
32:2a:1302:C:C2	50:2s:72:GLY:HA3	2.55	0.41
32:2a:1483:G:H4'	32:2a:1484:U:H5"	2.03	0.41
32:2a:1488:U:H1'	32:2a:1504:G:N2	2.35	0.41
45:2n:3:ARG:HD2	45:2n:4:LYS:HG3	2.03	0.41
48:2q:53:LEU:HB3	48:2q:82:MET:HE1	2.02	0.41
1:1A:504:A:N3	1:1A:506:G:H5"	2.35	0.41
1:1A:764:A:C5	1:1A:765:C:H1'	2.56	0.41
1:1A:885:U:H2'	1:1A:886:C:H6	1.86	0.41
1:1A:1457:A:H2'	1:1A:1458:G:C8	2.55	0.41
1:1A:1903:C:H2'	1:1A:1904:G:O4'	2.20	0.41
10:1O:18:LYS:HB2	10:1O:45:GLU:HB3	2.02	0.41
11:1P:18:ARG:NH2	11:1P:21:ARG:HD2	2.36	0.41
12:1Q:58:PHE:O	12:1Q:60:ARG:NH1	2.53	0.41
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.01	0.41
32:1a:36:G:H2'	32:1a:37:C:C6	2.55	0.41
32:1a:538:C:OP2	59:1a:1925:HOH:O	2.22	0.41
32:1a:557:A:OP2	59:1a:1922:HOH:O	2.21	0.41
32:1a:749:G:H5"	32:1a:750:A:OP1	2.20	0.41
32:1a:836:G:O6	32:1a:847:G:H3'	2.20	0.41
32:1a:1188:G:H2'	32:1a:1189:G:O4'	2.20	0.41
33:1b:21:ARG:HB3	33:1b:38:GLY:O	2.21	0.41
35:1d:95:GLY:O	35:1d:99:SER:N	2.52	0.41
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.37	0.41
38:1g:152:ALA:HB1	38:1g:155:ARG:NH2	2.35	0.41
40:1i:28:VAL:HA	40:1i:63:ILE:O	2.20	0.41
1:2A:587:C:H2'	1:2A:588:U:O4'	2.20	0.41
1:2A:865:A:C4	1:2A:1233:A:C2	3.08	0.41
1:2A:1042:G:C5'	16:2U:92:ARG:HH21	2.34	0.41
1:2A:1288:G:H2'	1:2A:1289:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2382:G:O2'	28:26:46:HIS:ND1	2.45	0.41
1:2A:2560:G:O6	59:2A:3663:HOH:O	2.21	0.41
2:2B:28:C:H2'	2:2B:29:A:H8	1.84	0.41
6:2G:153:ARG:HE	6:2G:153:ARG:HB2	1.72	0.41
32:2a:169:C:H2'	32:2a:170:C:H6	1.86	0.41
32:2a:1106:A:N3	41:2j:38:ILE:HG22	2.36	0.41
32:2a:1116:G:C4	32:2a:1117:G:C8	3.09	0.41
33:2b:16:HIS:C	33:2b:18:GLY:H	2.28	0.41
35:2d:204:ILE:H	35:2d:204:ILE:HG12	1.69	0.41
36:2e:11:ILE:HG13	36:2e:31:LEU:HB3	2.02	0.41
47:2p:55:ARG:O	47:2p:58:TYR:HB3	2.20	0.41
50:2s:36:ARG:HH11	50:2s:53:ASN:HA	1.85	0.41
1:1A:475:G:OP2	59:1A:4390:HOH:O	2.21	0.41
1:1A:786:U:H2'	1:1A:787:G:C8	2.55	0.41
1:1A:1465:U:HO2'	1:1A:1466:G:P	2.42	0.41
1:1A:2507:C:H4'	59:1A:5205:HOH:O	2.20	0.41
3:1D:5:LYS:HE3	3:1D:5:LYS:HB3	1.85	0.41
3:1D:16:MET:HG3	3:1D:211:ARG:HH21	1.85	0.41
7:1H:126:PRO:HB2	7:1H:127:GLU:H	1.65	0.41
9:1N:131:GLN:CD	9:1N:131:GLN:H	2.28	0.41
11:1P:76:LYS:HE2	11:1P:76:LYS:HB3	1.77	0.41
14:1S:67:ARG:HE	14:1S:67:ARG:HB2	1.72	0.41
21:1Z:92:SER:O	21:1Z:92:SER:OG	2.28	0.41
32:1a:100:C:O2'	32:1a:375:C:H5"	2.21	0.41
32:1a:140:G:C2	32:1a:173:C:N3	2.89	0.41
32:1a:328:G:OP2	51:1t:10:LEU:HD13	2.20	0.41
34:1c:28:GLN:O	34:1c:32:LEU:HG	2.21	0.41
39:1h:33:GLU:CD	39:1h:50:ARG:HH21	2.29	0.41
42:1k:15:ALA:HA	42:1k:77:MET:HA	2.02	0.41
42:1k:41:THR:OG1	42:1k:42:TRP:N	2.53	0.41
42:1k:79:SER:HB2	42:1k:104:GLN:HB3	2.02	0.41
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	2.02	0.41
54:1x:46:G:H3'	54:1x:47:U:C2	2.55	0.41
1:2A:87:G:C6	1:2A:88:U:C4	3.09	0.41
1:2A:1067:G:C5	1:2A:1184:C:C4	3.08	0.41
1:2A:1350:C:C2	1:2A:1669:G:C2	3.08	0.41
1:2A:1897:A:H2'	1:2A:1898:A:C8	2.55	0.41
1:2A:1958:A:C8	1:2A:1960:U:H2'	2.55	0.41
1:2A:2323:U:C5	1:2A:2324:C:H5	2.39	0.41
1:2A:2341:G:H2'	1:2A:2342:G:O4'	2.20	0.41
1:2A:2409:U:H2'	1:2A:2410:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:8:U:H3	2:2B:113:G:H1	1.67	0.41
2:2B:28:C:H2'	2:2B:29:A:C8	2.55	0.41
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	2.01	0.41
8:2I:129:THR:HG23	8:2I:139:GLN:HE22	1.85	0.41
10:2O:7:TYR:HE1	10:2O:20:MET:HE3	1.83	0.41
25:23:8:LEU:HD13	25:23:31:LEU:HD23	2.01	0.41
32:2a:262:G:H8	32:2a:262:G:H2'	1.76	0.41
32:2a:320:G:N2	32:2a:323:A:C8	2.89	0.41
32:2a:369:A:O2'	32:2a:446:A:N7	2.53	0.41
32:2a:459:G:H2'	32:2a:460:G:H8	1.85	0.41
32:2a:1132:C:OP2	40:2i:9:ARG:NH2	2.54	0.41
32:2a:1172:G:H4'	34:2c:176:HIS:CE1	2.55	0.41
32:2a:1393:G:H2'	32:2a:1394:C:C6	2.55	0.41
32:2a:1433:C:H5'	32:2a:1435:G:C4	2.56	0.41
36:2e:71:LEU:HD12	36:2e:115:VAL:HB	2.01	0.41
39:2h:64:LYS:HE3	39:2h:64:LYS:HB2	1.79	0.41
43:2l:24:VAL:HG23	43:2l:98:TYR:CE1	2.55	0.41
1:1A:553:A:H62	1:1A:2062:U:H3	1.68	0.41
1:1A:591:U:C4	1:1A:592:G:C6	3.09	0.41
1:1A:1067:G:C5	1:1A:1184:C:C4	3.08	0.41
1:1A:1312:U:OP2	1:1A:2033:G:N1	2.40	0.41
1:1A:1939:A:O2'	1:1A:1941:C:N4	2.54	0.41
1:1A:2114:G:C6	1:1A:2236:A:C8	3.09	0.41
1:1A:2118:C:H2'	1:1A:2119:U:C6	2.55	0.41
1:1A:2657:C:H2'	1:1A:2658:U:O4'	2.21	0.41
6:1G:103:LEU:HA	6:1G:103:LEU:HD23	1.81	0.41
11:1P:81:GLN:NE2	11:1P:105:LEU:O	2.54	0.41
13:1R:53:HIS:O	13:1R:56:LYS:HB2	2.20	0.41
14:1S:10:ARG:HH21	14:1S:91:PRO:HB2	1.84	0.41
15:1T:80:SER:HA	15:1T:81:PRO:HD3	1.90	0.41
26:14:53:GLU:HB2	26:14:54:GLY:CA	2.48	0.41
30:18:42:ARG:NH1	59:18:203:HOH:O	2.42	0.41
32:1a:229:C:H2'	32:1a:230:C:H6	1.85	0.41
32:1a:606:A:H3'	32:1a:607:C:H6	1.86	0.41
32:1a:1078:U:H5'	32:1a:1092:C:O2	2.21	0.41
34:1c:178:LEU:C	34:1c:180:ALA:H	2.28	0.41
37:1f:28:ARG:C	37:1f:32:ASN:HD22	2.28	0.41
39:1h:121:ASP:OD2	39:1h:121:ASP:N	2.54	0.41
42:1k:97:ALA:O	42:1k:101:SER:HB3	2.21	0.41
43:1l:84:LEU:HB2	43:1l:105:TYR:CE2	2.55	0.41
45:1n:6:LEU:HB3	45:1n:23:ARG:NH2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.56	0.41
1:2A:488:G:N2	1:2A:491:A:OP2	2.46	0.41
1:2A:612:A:OP1	5:2F:95:ARG:NH1	2.54	0.41
1:2A:703:U:H2'	1:2A:704:C:H6	1.82	0.41
1:2A:917:U:H2'	1:2A:918:A:C8	2.55	0.41
1:2A:1073:A:H2'	1:2A:1074:A:C8	2.55	0.41
1:2A:2600:A:OP1	59:2A:3668:HOH:O	2.22	0.41
1:2A:2643:A:C2	1:2A:2799:C:C2	3.09	0.41
1:2A:2648:U:H5"	4:2E:82:ARG:NH1	2.36	0.41
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	2.03	0.41
18:2W:9:TYR:H	18:2W:102:HIS:CE1	2.38	0.41
18:2W:45:TYR:CZ	18:2W:49:LYS:HE3	2.55	0.41
28:26:25:LYS:HE3	28:26:27:LYS:HA	2.02	0.41
32:2a:916:A:C6	32:2a:917:G:C5	3.09	0.41
32:2a:958:C:H1'	45:2n:19:ARG:HA	2.03	0.41
32:2a:1463:U:H2'	32:2a:1464:G:C8	2.56	0.41
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.51	0.41
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	2.02	0.41
55:2z:9:ARG:HA	55:2z:10:PRO:HD3	1.68	0.41
1:1A:732:G:N2	1:1A:834:A:H61	2.18	0.41
1:1A:841:C:H2'	1:1A:842:C:C6	2.56	0.41
1:1A:1007:U:H2'	1:1A:1008:C:C6	2.56	0.41
1:1A:1153:U:O2'	1:1A:1154:C:H6	2.04	0.41
1:1A:1225:C:H2'	1:1A:1226:A:O4'	2.21	0.41
1:1A:2890:C:H2'	1:1A:2891:A:O4'	2.21	0.41
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	2.02	0.41
4:1E:31:CYS:HA	4:1E:32:PRO:HD2	1.87	0.41
6:1G:109:VAL:HG13	26:14:33:VAL:HG11	2.03	0.41
32:1a:210:U:OP2	32:1a:210:U:H6	2.04	0.41
32:1a:378:A:H2'	32:1a:379:A:C8	2.54	0.41
32:1a:1141:C:H5	32:1a:1163:G:H1	1.67	0.41
32:1a:1325:G:O2'	40:1i:121:ARG:HD2	2.20	0.41
35:1d:114:ARG:HA	35:1d:117:ALA:HB3	2.03	0.41
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.53	0.41
39:1h:83:ILE:HB	39:1h:137:VAL:HG13	2.02	0.41
55:1z:13:PRO:HB2	55:1z:14:ARG:H	1.77	0.41
1:2A:5:A:H2	1:2A:6:G:N7	2.19	0.41
1:2A:29:G:C5	1:2A:30:C:C4	3.09	0.41
1:2A:1387:A:C4	1:2A:1442:U:O4'	2.73	0.41
1:2A:1404:A:C6	1:2A:1417:U:O4	2.74	0.41
1:2A:2539:U:O2'	1:2A:2540:G:H3'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:24:G:H4'	2:2B:25:A:C8	2.55	0.41
2:2B:32:C:H42	2:2B:50:G:H1	1.67	0.41
3:2D:68:LYS:O	3:2D:69:ARG:HB2	2.21	0.41
3:2D:107:ALA:HA	3:2D:108:PRO:HD3	1.80	0.41
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	2.03	0.41
15:2T:65:LYS:CE	15:2T:67:SER:HB2	2.50	0.41
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	2.02	0.41
28:26:8:LYS:HD3	30:28:34:TRP:CG	2.56	0.41
28:26:11:LEU:HB2	28:26:21:TYR:HB2	2.02	0.41
32:2a:48:C:H5"	32:2a:361:U:O2	2.20	0.41
32:2a:324:C:H4'	32:2a:325:A:H5'	2.03	0.41
32:2a:1183:A:H1'	32:2a:1184:G:OP2	2.21	0.41
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.52	0.41
34:2c:6:HIS:HA	34:2c:7:PRO:HD3	1.88	0.41
40:2i:112:LYS:HE2	40:2i:117:HIS:O	2.21	0.41
49:2r:26:LEU:HD13	49:2r:26:LEU:HA	1.95	0.41
54:2x:23:C:H2'	54:2x:24:U:H6	1.85	0.41
1:1A:209:A:N1	1:1A:253:A:O2'	2.46	0.41
1:1A:382:A:H2'	1:1A:383:G:O4'	2.20	0.41
1:1A:454:A:OP2	1:1A:454:A:H8	2.03	0.41
1:1A:830:A:C6	3:1D:229:VAL:HG11	2.56	0.41
1:1A:1451:U:H2'	1:1A:1452:C:H6	1.86	0.41
1:1A:1670:C:H2'	1:1A:1671:G:O4'	2.21	0.41
1:1A:2012:U:H2'	1:1A:2013:G:H5"	2.02	0.41
1:1A:2285:A:O2'	1:1A:2287:G:OP1	2.35	0.41
1:1A:2342:G:O2'	1:1A:2347:A:N1	2.45	0.41
1:1A:2720:G:H2'	1:1A:2721:C:C6	2.56	0.41
2:1B:31:C:H4'	6:1G:29:TRP:CH2	2.55	0.41
3:1D:53:PHE:C	3:1D:218:ARG:HB2	2.45	0.41
6:1G:28:VAL:HG23	6:1G:29:TRP:CD1	2.56	0.41
15:1T:16:ARG:HD2	15:1T:18:ASP:OD2	2.21	0.41
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.86	0.41
28:16:2:ALA:N	59:16:203:HOH:O	2.54	0.41
32:1a:99:G:H2'	32:1a:100:C:C6	2.56	0.41
32:1a:372:G:P	47:1p:67:THR:HG21	2.61	0.41
32:1a:440:G:H2'	32:1a:441:G:C8	2.56	0.41
32:1a:633:G:H2'	32:1a:634:G:C8	2.55	0.41
32:1a:638:G:C5	32:1a:639:A:C8	3.09	0.41
32:1a:1067:G:C5	32:1a:1068:U:C4	3.09	0.41
32:1a:1086:C:H2'	32:1a:1087:G:O4'	2.21	0.41
32:1a:1094:A:H2'	32:1a:1095:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1205:C:OP2	50:1s:78:ARG:NH2	2.54	0.41
32:1a:1281:A:H5"	32:1a:1281:A:N3	2.36	0.41
35:1d:61:LYS:HD2	35:1d:207:TYR:CZ	2.56	0.41
39:1h:60:ARG:HD3	39:1h:62:TYR:OH	2.21	0.41
42:1k:43:SER:HA	42:1k:47:VAL:HG21	2.02	0.41
43:1l:69:TYR:HB2	43:1l:96:VAL:HG11	2.03	0.41
44:1m:29:ARG:HD3	44:1m:64:TRP:CE2	2.56	0.41
45:1n:32:SER:O	45:1n:40:CYS:HA	2.21	0.41
45:1n:47:LEU:HD23	45:1n:50:LYS:HE2	2.03	0.41
48:1q:45:HIS:NE2	48:1q:47:PRO:HG3	2.35	0.41
1:2A:209:A:N1	1:2A:253:A:O2'	2.49	0.41
1:2A:418:C:H5"	1:2A:435:C:H5"	2.02	0.41
1:2A:468:A:H5"	1:2A:469:C:OP1	2.21	0.41
1:2A:530:G:O3'	1:2A:531:A:H8	2.03	0.41
1:2A:653:G:H1'	1:2A:663:U:O2'	2.21	0.41
1:2A:709:G:C6	1:2A:710:C:C4	3.09	0.41
1:2A:748:G:C2	1:2A:777:C:C2	3.09	0.41
1:2A:788:G:H4'	1:2A:1722:A:H5'	2.03	0.41
1:2A:842:C:H2'	1:2A:843:C:H6	1.85	0.41
1:2A:910:G:C6	1:2A:911:C:N4	2.89	0.41
1:2A:922:C:H2'	1:2A:923:U:O4'	2.21	0.41
1:2A:955:A:N3	1:2A:2275:C:O2'	2.40	0.41
1:2A:1044:U:O2'	1:2A:1045:A:H5'	2.21	0.41
1:2A:1313:A:C2	1:2A:2034:A:C4	3.09	0.41
1:2A:2076:C:OP1	1:2A:2077:G:H4'	2.21	0.41
1:2A:2082:G:H5"	1:2A:2514:A:C2	2.56	0.41
1:2A:2479:G:O2'	1:2A:2492:G:N2	2.53	0.41
1:2A:2626:U:C2	27:25:7:PRO:HA	2.55	0.41
1:2A:2644:G:H5"	1:2A:2821:G:H5'	2.03	0.41
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.85	0.41
6:2G:120:LEU:HB3	6:2G:131:TYR:OH	2.21	0.41
13:2R:107:ASP:OD2	13:2R:109:ALA:HB2	2.21	0.41
14:2S:65:VAL:O	14:2S:68:GLN:HB2	2.21	0.41
21:2Z:55:HIS:CE1	21:2Z:135:GLU:HB2	2.56	0.41
32:2a:189:U:O2'	32:2a:190:U:H5'	2.21	0.41
32:2a:459:G:H2'	32:2a:460:G:C8	2.56	0.41
32:2a:605:A:H2'	32:2a:606:A:O4'	2.20	0.41
32:2a:669:G:C2	32:2a:670:U:C4	3.08	0.41
32:2a:924:A:H2'	32:2a:925:G:C8	2.56	0.41
32:2a:1240:G:H8	32:2a:1240:G:OP2	2.03	0.41
32:2a:1457:C:H2'	32:2a:1458:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:33:TYR:HB2	33:2b:43:ASP:HA	2.03	0.41
33:2b:198:ASP:OD1	39:2h:68:ARG:NH1	2.54	0.41
38:2g:73:MET:HA	38:2g:90:GLU:HA	2.01	0.41
41:2j:57:LYS:O	41:2j:59:SER:N	2.54	0.41
42:2k:86:GLY:O	42:2k:91:ARG:HD3	2.21	0.41
43:2l:117:ARG:HB3	43:2l:122:THR:HB	2.02	0.41
44:2m:87:TYR:O	44:2m:91:ARG:HG2	2.21	0.41
54:2x:50:U:H2'	54:2x:51:C:C6	2.55	0.41
1:1A:311:C:H2'	1:1A:312:A:H8	1.86	0.41
1:1A:515:G:H2'	1:1A:516:A:H8	1.85	0.41
1:1A:819:U:O2'	3:1D:48:ARG:HD3	2.20	0.41
1:1A:2367:C:H2'	1:1A:2368:U:O4'	2.21	0.41
10:1O:23:ARG:HG3	10:1O:24:VAL:N	2.36	0.41
12:1Q:52:VAL:HG22	21:1Z:183:LEU:HD21	2.03	0.41
12:1Q:60:ARG:HD3	12:1Q:60:ARG:HA	1.70	0.41
32:1a:43:G:O2'	32:1a:606:A:N1	2.45	0.41
32:1a:126:C:H2'	32:1a:127:C:C6	2.56	0.41
32:1a:825:U:H6	32:1a:825:U:OP2	2.04	0.41
32:1a:1072:G:N2	32:1a:1079:C:N3	2.63	0.41
32:1a:1127:G:N2	32:1a:1129:A:H62	2.18	0.41
36:1e:85:GLY:O	36:1e:87:SER:N	2.53	0.41
37:1f:17:SER:O	37:1f:21:LEU:HG	2.21	0.41
1:2A:138:A:C8	1:2A:1453:C:O2'	2.73	0.41
1:2A:140:C:H2'	1:2A:141:G:O4'	2.21	0.41
1:2A:504:A:N3	1:2A:506:G:H5"	2.36	0.41
1:2A:2540:G:O6	31:29:31:LYS:NZ	2.54	0.41
1:2A:2829:A:C5	13:2R:4:LEU:HD11	2.56	0.41
2:2B:18:G:H2'	2:2B:19:G:C8	2.56	0.41
9:2N:42:TRP:HA	9:2N:48:MET:HE1	2.03	0.41
21:2Z:48:PHE:O	21:2Z:52:SER:N	2.46	0.41
23:21:3:LYS:HB2	23:21:61:ARG:NH1	2.34	0.41
32:2a:825:U:H6	32:2a:825:U:OP1	2.03	0.41
32:2a:1178:U:H4'	59:2a:3469:HOH:O	2.21	0.41
33:2b:207:ALA:O	33:2b:210:SER:OG	2.37	0.41
34:2c:22:TRP:HD1	34:2c:57:ILE:O	2.04	0.41
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	2.03	0.41
37:2f:97:PHE:HB2	49:2r:32:ARG:HE	1.86	0.41
40:2i:82:ALA:O	40:2i:86:VAL:HG23	2.21	0.41
1:1A:44:C:OP2	1:1A:203:G:H2'	2.20	0.40
1:1A:637:U:H5"	59:1A:5896:HOH:O	2.21	0.40
1:1A:671:G:H8	1:1A:671:G:O5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1047:G:H2'	1:1A:1048:G:O4'	2.21	0.40
1:1A:1222:C:O5'	1:1A:1222:C:H6	2.03	0.40
1:1A:1416:G:H2'	1:1A:1417:U:H5	1.85	0.40
1:1A:1889:A:N6	1:1A:1904:G:O2'	2.54	0.40
1:1A:1953:A:H2'	1:1A:1954:G:O4'	2.21	0.40
3:1D:101:GLU:HG3	3:1D:102:LYS:N	2.36	0.40
5:1F:110:LEU:HD23	5:1F:110:LEU:HA	1.94	0.40
8:1I:106:GLY:HA2	8:1I:107:VAL:O	2.22	0.40
32:1a:523:A:H2'	32:1a:524:G:C8	2.56	0.40
32:1a:850:A:C8	32:1a:852:G:C8	3.09	0.40
32:1a:1254:G:H2'	32:1a:1255:G:O4'	2.21	0.40
32:1a:1382:C:H4'	32:1a:1383:C:H5"	2.04	0.40
33:1b:60:ASP:OD1	33:1b:64:ARG:NH2	2.45	0.40
34:1c:130:VAL:O	34:1c:134:ILE:HG13	2.21	0.40
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.54	0.40
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.80	0.40
50:1s:80:TYR:O	50:1s:81:ARG:HB2	2.21	0.40
51:1t:59:ALA:O	51:1t:63:ILE:HG13	2.21	0.40
1:2A:830:A:H5'	1:2A:831:G:OP1	2.21	0.40
1:2A:841:C:H2'	1:2A:842:C:C6	2.56	0.40
1:2A:870:A:H2'	1:2A:871:C:O4'	2.21	0.40
1:2A:1094:C:H42	1:2A:2763:G:H1	1.68	0.40
1:2A:2347:A:H61	22:20:43:THR:CG2	2.34	0.40
1:2A:2537:G:O2'	31:29:1:MET:N	2.34	0.40
1:2A:2704:A:H2'	1:2A:2705:G:C8	2.57	0.40
1:2A:2719:G:H1'	13:2R:71:GLN:HE22	1.86	0.40
8:2I:62:LYS:HG2	8:2I:133:HIS:CE1	2.56	0.40
18:2W:72:LYS:N	18:2W:106:ILE:O	2.50	0.40
20:2Y:76:CYS:SG	20:2Y:78:ALA:HB3	2.61	0.40
23:21:21:ARG:HD2	23:21:35:THR:HG21	2.02	0.40
23:21:94:LEU:HD23	23:21:94:LEU:HA	1.84	0.40
25:23:7:LYS:HE2	25:23:34:GLU:OE2	2.22	0.40
26:24:58:ARG:HH11	50:2s:68:GLY:H	1.69	0.40
32:2a:923:G:N7	59:2a:3358:HOH:O	2.37	0.40
33:2b:165:VAL:O	33:2b:187:LEU:HD22	2.21	0.40
34:2c:61:ALA:C	34:2c:63:ASN:H	2.28	0.40
36:2e:140:ARG:O	36:2e:143:ARG:NH2	2.54	0.40
42:2k:120:ARG:HA	42:2k:121:PRO:HD3	1.87	0.40
54:2x:8:4SU:O5'	54:2x:8:4SU:H6	2.20	0.40
1:1A:264:U:H2'	1:1A:265:C:C6	2.57	0.40
1:1A:611:C:P	11:1P:16:ARG:HH12	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:942:C:O5'	1:1A:942:C:H6	2.03	0.40
1:1A:2858:U:H4'	1:1A:2877:A:C2	2.56	0.40
2:1B:50:G:H5"	14:1S:61:ASN:HD22	1.86	0.40
3:1D:145:VAL:HB	3:1D:155:LEU:HB2	2.03	0.40
3:1D:257:LEU:HD23	3:1D:257:LEU:HA	1.94	0.40
3:1D:264:LYS:HA	3:1D:265:PRO:HD3	1.94	0.40
25:13:23:LEU:HD13	25:13:50:VAL:HG11	2.03	0.40
26:14:15:ILE:HB	26:14:32:TYR:CD2	2.56	0.40
32:1a:129:A:H1'	32:1a:321:A:C5	2.56	0.40
32:1a:377:C:H2'	32:1a:378:A:O4'	2.21	0.40
32:1a:1308:C:OP1	52:1u:12:LYS:NZ	2.53	0.40
34:1c:6:HIS:HA	34:1c:7:PRO:HD3	1.97	0.40
34:1c:36:ASP:HA	34:1c:39:ILE:HD12	2.03	0.40
37:1f:19:LEU:HD11	37:1f:59:TYR:CZ	2.56	0.40
43:1l:49:ASN:HD22	43:1l:92:ASP:CG	2.29	0.40
1:2A:224:C:H2'	1:2A:225:C:H6	1.86	0.40
1:2A:1116:G:C8	1:2A:1134:G:C6	3.09	0.40
1:2A:1184:C:OP1	9:2N:23:LEU:HB3	2.22	0.40
1:2A:1539:A:H2'	1:2A:1540:A:C8	2.56	0.40
1:2A:1814:A:N1	59:2A:3745:HOH:O	2.37	0.40
1:2A:2881:G:C2	1:2A:2882:A:N6	2.89	0.40
2:2B:6:C:H2'	2:2B:7:G:H5"	2.04	0.40
4:2E:31:CYS:HA	4:2E:32:PRO:HD2	1.88	0.40
4:2E:105:THR:HG21	4:2E:164:ARG:NH1	2.36	0.40
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	2.02	0.40
6:2G:19:LEU:HA	6:2G:22:ARG:HB2	2.02	0.40
11:2P:5:ASP:HA	11:2P:7:ARG:HH22	1.87	0.40
26:24:13:ARG:NH1	26:24:15:ILE:HD11	2.36	0.40
30:28:23:VAL:HG11	30:28:47:LYS:HD3	2.04	0.40
31:29:35:ARG:HD3	31:29:35:ARG:HH11	1.78	0.40
32:2a:355:U:H2'	32:2a:356:A:C8	2.56	0.40
32:2a:524:G:H2'	32:2a:525:G:O4'	2.20	0.40
32:2a:551:G:H2'	32:2a:552:G:O4'	2.20	0.40
32:2a:732:C:H1'	32:2a:733:C:OP2	2.19	0.40
32:2a:845:G:H8	32:2a:845:G:OP2	2.05	0.40
32:2a:863:G:O2'	32:2a:892:A:N1	2.42	0.40
32:2a:945:C:H2'	32:2a:946:A:C8	2.56	0.40
32:2a:1425:G:H2'	32:2a:1426:G:C5'	2.51	0.40
59:2a:3498:HOH:O	47:2p:16:HIS:HD2	2.04	0.40
33:2b:193:ASP:HA	33:2b:194:PRO:HD2	1.92	0.40
35:2d:195:ALA:C	35:2d:196:LEU:HD12	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:84:PHE:N	36:2e:87:SER:O	2.50	0.40
44:2m:15:VAL:O	44:2m:19:LEU:HD23	2.21	0.40
45:2n:21:TYR:HE1	45:2n:23:ARG:HE	1.69	0.40
1:1A:226:C:H2'	1:1A:227:U:O4'	2.21	0.40
1:1A:501:G:H4'	1:1A:526:A:N1	2.37	0.40
1:1A:560:A:H2'	1:1A:561:C:C6	2.57	0.40
1:1A:682:G:H1	1:1A:695:C:N4	2.16	0.40
1:1A:1066:A:H3'	1:1A:1066:A:H8	1.86	0.40
1:1A:1878:A:H2'	1:1A:1879:G:H8	1.85	0.40
9:1N:129:PRO:HA	9:1N:131:GLN:HE22	1.87	0.40
12:1Q:58:PHE:O	12:1Q:60:ARG:N	2.52	0.40
24:12:16:LEU:O	24:12:67:LYS:NZ	2.54	0.40
32:1a:17:A:O2'	36:1e:16:THR:HB	2.21	0.40
32:1a:426:A:OP2	35:1d:8:VAL:HG12	2.20	0.40
32:1a:747:G:H2'	32:1a:748:C:C6	2.57	0.40
32:1a:767:C:OP1	32:1a:1493:C:O2'	2.33	0.40
32:1a:1063:A:H5'	36:1e:14:ARG:NH2	2.37	0.40
33:1b:27:LYS:O	33:1b:194:PRO:HG2	2.22	0.40
33:1b:193:ASP:OD2	33:1b:196:LEU:HD13	2.21	0.40
35:1d:50:ARG:HA	35:1d:51:PRO:HD3	1.86	0.40
41:1j:35:SER:N	41:1j:73:ASP:O	2.53	0.40
42:1k:77:MET:HE2	42:1k:77:MET:HB2	1.91	0.40
54:1x:8:4SU:O2	54:1x:21:A:H2	2.04	0.40
1:2A:356:G:N3	1:2A:356:G:H2'	2.36	0.40
1:2A:382:A:H2'	1:2A:383:G:O4'	2.21	0.40
1:2A:702:G:H2'	1:2A:703:U:O4'	2.22	0.40
1:2A:795:C:O2	1:2A:1663:A:H2'	2.22	0.40
1:2A:817:G:OP1	29:27:10:ARG:NH1	2.50	0.40
1:2A:919:G:N2	1:2A:950:U:C2	2.89	0.40
1:2A:955:A:H2	1:2A:2275:C:O2	2.05	0.40
1:2A:967:U:H2'	1:2A:968:C:C6	2.56	0.40
1:2A:2704:A:H2'	1:2A:2705:G:H8	1.86	0.40
3:2D:133:LEU:HD23	3:2D:133:LEU:HA	1.85	0.40
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	2.02	0.40
4:2E:11:MET:HE2	4:2E:24:THR:HB	2.04	0.40
7:2H:4:ILE:HG22	7:2H:69:ARG:HG2	2.04	0.40
12:2Q:29:PHE:HB2	12:2Q:105:GLU:OE2	2.21	0.40
14:2S:74:ALA:O	14:2S:78:LEU:HG	2.21	0.40
20:2Y:2:ARG:NH2	20:2Y:4:LYS:HD3	2.35	0.40
31:29:22:ARG:NH1	31:29:35:ARG:HD2	2.36	0.40
32:2a:593:A:C5	32:2a:594:G:C8	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:597:C:H42	32:2a:611:G:H1	1.69	0.40
32:2a:612:G:H2'	32:2a:613:G:C8	2.57	0.40
32:2a:765:A:OP1	32:2a:1501:G:H5'	2.22	0.40
32:2a:980:G:H3'	32:2a:981:G:H4'	2.03	0.40
32:2a:981:G:N3	32:2a:982:G:H8	2.20	0.40
32:2a:1022:C:O5'	32:2a:1022:C:H6	2.05	0.40
32:2a:1300:A:O2'	50:2s:37:ARG:HB3	2.21	0.40
33:2b:56:ARG:HD2	33:2b:56:ARG:HA	1.89	0.40
33:2b:91:PRO:HA	33:2b:154:LEU:HD23	2.03	0.40
43:2l:7:ILE:HD13	43:2l:7:ILE:HA	1.97	0.40
51:2t:24:LEU:HA	51:2t:24:LEU:HD13	1.78	0.40
1:1A:2473:U:H1'	1:1A:2502:U:O4	2.22	0.40
1:1A:2723:U:OP1	1:1A:2726:G:H4'	2.22	0.40
1:1A:2898:C:H2'	1:1A:2899:G:O4'	2.21	0.40
16:1U:102:GLU:HB3	16:1U:104:GLN:HE22	1.87	0.40
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.22	0.40
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	2.03	0.40
25:13:18:ASP:OD1	25:13:18:ASP:N	2.50	0.40
26:14:61:ARG:NH2	50:1s:42:PRO:HD3	2.36	0.40
29:17:35:ARG:NH1	59:17:202:HOH:O	2.54	0.40
32:1a:73:C:N3	32:1a:91:G:O6	2.55	0.40
32:1a:714:G:C5	32:1a:715:G:H1'	2.56	0.40
32:1a:1126:G:H2'	32:1a:1127:G:H8	1.85	0.40
33:1b:71:VAL:HG13	33:1b:93:VAL:HG21	2.04	0.40
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	2.04	0.40
35:1d:155:LEU:HD23	35:1d:156:GLU:N	2.36	0.40
38:1g:16:LEU:HD22	38:1g:16:LEU:H	1.86	0.40
44:1m:96:LEU:HD23	44:1m:96:LEU:HA	1.96	0.40
1:2A:62:A:O3'	19:2X:71:GLY:HA3	2.20	0.40
1:2A:92:G:H2'	1:2A:93:G:O4'	2.21	0.40
1:2A:580:G:OP1	9:2N:111:PRO:HD2	2.22	0.40
1:2A:770:U:H2'	1:2A:771:G:O4'	2.21	0.40
1:2A:902:C:H2'	1:2A:903:C:C6	2.57	0.40
1:2A:1176:G:C2	1:2A:1177:A:C4	3.10	0.40
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.21	0.40
1:2A:1869:G:C8	1:2A:1948:A:H1'	2.57	0.40
1:2A:2238:A:OP1	3:2D:263:ARG:HD2	2.22	0.40
1:2A:2483:G:H2'	1:2A:2486:C:H42	1.86	0.40
1:2A:2859:A:H2'	1:2A:2860:A:O4'	2.21	0.40
8:2I:44:LEU:HD12	8:2I:44:LEU:HA	1.83	0.40
21:2Z:61:LEU:HA	21:2Z:62:PRO:HD3	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:431:C:H2'	32:2a:432:C:H6	1.86	0.40
32:2a:929:G:OP2	44:2m:102:ARG:NH2	2.54	0.40
32:2a:1254:G:H2'	32:2a:1255:G:O4'	2.22	0.40
32:2a:1274:U:H2'	32:2a:1275:G:O4'	2.22	0.40
32:2a:1327:U:H5'	56:2a:1664:MG:MG	1.46	0.40
32:2a:1366:C:C2'	32:2a:1367:C:H5'	2.52	0.40
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	2.03	0.40
38:2g:77:SER:HG	38:2g:86:GLN:HE21	1.65	0.40
1:1A:461:C:H2'	1:1A:462:C:H5'	2.04	0.40
1:1A:554:G:C5	1:1A:2043:U:H5"	2.57	0.40
1:1A:1466:G:C2	1:1A:1467:G:C8	3.10	0.40
31:19:29:ASN:HA	31:19:30:PRO:HD3	1.94	0.40
32:1a:669:G:O2'	32:1a:670:U:H5'	2.21	0.40
32:1a:671:A:N3	32:1a:672:G:H1'	2.36	0.40
32:1a:1286:G:C6	32:1a:1287:G:N1	2.90	0.40
32:1a:1482:G:H4'	32:1a:1483:G:C4	2.57	0.40
33:1b:37:ASN:C	33:1b:39:ILE:H	2.30	0.40
34:1c:12:LEU:HA	34:1c:16:ARG:O	2.22	0.40
34:1c:124:ILE:HD11	34:1c:130:VAL:HG13	2.03	0.40
35:1d:93:PHE:O	35:1d:97:LEU:HB2	2.20	0.40
36:1e:78:HIS:H	36:1e:78:HIS:HD2	1.68	0.40
44:1m:15:VAL:O	44:1m:19:LEU:HD22	2.22	0.40
48:1q:92:ARG:O	48:1q:95:TYR:HB2	2.20	0.40
1:2A:644:G:H8	1:2A:646:G:O6	2.04	0.40
1:2A:1889:A:C2	1:2A:1905:A:H1'	2.57	0.40
1:2A:2760:A:C2	7:2H:63:SER:HB3	2.56	0.40
2:2B:52:A:H8	2:2B:52:A:OP2	2.04	0.40
4:2E:36:ARG:NH2	4:2E:88:GLY:O	2.53	0.40
6:2G:3:LEU:HD12	6:2G:4:ASP:O	2.22	0.40
6:2G:56:ALA:HA	6:2G:153:ARG:NH2	2.36	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:CE1	2.56	0.40
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	2.03	0.40
32:2a:305:G:H1'	32:2a:592:A:C2	2.57	0.40
32:2a:428:A:H3'	32:2a:429:C:H6	1.86	0.40
32:2a:655:G:H1	32:2a:719:C:H42	1.69	0.40
32:2a:1106:A:O2'	41:2j:38:ILE:HG23	2.21	0.40
32:2a:1354:G:C2	32:2a:1355:U:C2	3.09	0.40
32:2a:1354:G:C6	32:2a:1355:U:C4	3.09	0.40
33:2b:24:TRP:CZ2	33:2b:26:PRO:HB3	2.56	0.40
33:2b:42:ILE:HG21	33:2b:202:PRO:O	2.21	0.40
33:2b:54:THR:O	33:2b:58:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:13:ARG:HB2	35:2d:40:PRO:HD3	2.03	0.40
35:2d:150:GLU:HA	35:2d:153:ARG:NE	2.35	0.40
44:2m:54:VAL:HG12	44:2m:57:ARG:NH1	2.37	0.40
49:2r:25:THR:HG23	49:2r:26:LEU:HD22	2.03	0.40
49:2r:30:ASP:C	49:2r:32:ARG:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	260 (95%)	13 (5%)	0	100	100
3	2D	273/276 (99%)	252 (92%)	19 (7%)	2 (1%)	18	41
4	1E	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24	48
4	2E	202/206 (98%)	196 (97%)	5 (2%)	1 (0%)	24	48
5	1F	201/210 (96%)	192 (96%)	7 (4%)	2 (1%)	12	32
5	2F	201/210 (96%)	190 (94%)	10 (5%)	1 (0%)	24	48
6	1G	179/182 (98%)	164 (92%)	10 (6%)	5 (3%)	4	9
6	2G	179/182 (98%)	157 (88%)	18 (10%)	4 (2%)	5	14
7	1H	172/180 (96%)	159 (92%)	12 (7%)	1 (1%)	21	44
7	2H	172/180 (96%)	158 (92%)	12 (7%)	2 (1%)	10	27
8	1I	144/148 (97%)	124 (86%)	17 (12%)	3 (2%)	5	15
8	2I	144/148 (97%)	122 (85%)	20 (14%)	2 (1%)	9	23
9	1N	138/140 (99%)	138 (100%)	0	0	100	100
9	2N	138/140 (99%)	135 (98%)	2 (1%)	1 (1%)	18	41
10	1O	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
10	2O	120/122 (98%)	116 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
11	1P	147/150 (98%)	137 (93%)	8 (5%)	2 (1%)	9 23
11	2P	147/150 (98%)	136 (92%)	9 (6%)	2 (1%)	9 23
12	1Q	139/141 (99%)	132 (95%)	6 (4%)	1 (1%)	18 41
12	2Q	139/141 (99%)	131 (94%)	8 (6%)	0	100 100
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100 100
13	2R	116/118 (98%)	110 (95%)	6 (5%)	0	100 100
14	1S	108/112 (96%)	102 (94%)	5 (5%)	1 (1%)	14 35
14	2S	108/112 (96%)	99 (92%)	7 (6%)	2 (2%)	6 17
15	1T	129/146 (88%)	120 (93%)	8 (6%)	1 (1%)	16 37
15	2T	129/146 (88%)	123 (95%)	6 (5%)	0	100 100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
16	2U	114/118 (97%)	113 (99%)	1 (1%)	0	100 100
17	1V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12 32
17	2V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12 32
18	1W	110/113 (97%)	110 (100%)	0	0	100 100
18	2W	110/113 (97%)	110 (100%)	0	0	100 100
19	1X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11 29
19	2X	93/96 (97%)	88 (95%)	3 (3%)	2 (2%)	5 14
20	1Y	105/110 (96%)	97 (92%)	6 (6%)	2 (2%)	6 17
20	2Y	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	12 32
21	1Z	184/206 (89%)	170 (92%)	14 (8%)	0	100 100
21	2Z	184/206 (89%)	168 (91%)	13 (7%)	3 (2%)	7 20
22	10	73/85 (86%)	70 (96%)	2 (3%)	1 (1%)	9 23
22	20	73/85 (86%)	69 (94%)	4 (6%)	0	100 100
23	11	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 29
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11 29
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100 100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
25	23	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
26	14	67/71 (94%)	50 (75%)	10 (15%)	7 (10%)	0 0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
26	24	67/71 (94%)	49 (73%)	12 (18%)	6 (9%)	0 0
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
28	16	51/54 (94%)	51 (100%)	0	0	100 100
28	26	51/54 (94%)	51 (100%)	0	0	100 100
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100 100
30	18	62/65 (95%)	62 (100%)	0	0	100 100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100 100
31	19	35/37 (95%)	35 (100%)	0	0	100 100
31	29	35/37 (95%)	35 (100%)	0	0	100 100
33	1b	229/256 (90%)	187 (82%)	33 (14%)	9 (4%)	2 5
33	2b	229/256 (90%)	191 (83%)	25 (11%)	13 (6%)	1 2
34	1c	204/239 (85%)	176 (86%)	27 (13%)	1 (0%)	24 48
34	2c	204/239 (85%)	176 (86%)	28 (14%)	0	100 100
35	1d	206/209 (99%)	185 (90%)	19 (9%)	2 (1%)	12 32
35	2d	206/209 (99%)	186 (90%)	18 (9%)	2 (1%)	12 32
36	1e	146/162 (90%)	129 (88%)	15 (10%)	2 (1%)	9 23
36	2e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	9 23
37	1f	98/101 (97%)	91 (93%)	7 (7%)	0	100 100
37	2f	98/101 (97%)	91 (93%)	7 (7%)	0	100 100
38	1g	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	9 25
38	2g	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	9 25
39	1h	135/138 (98%)	129 (96%)	6 (4%)	0	100 100
39	2h	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	18 41
40	1i	125/128 (98%)	109 (87%)	16 (13%)	0	100 100
40	2i	125/128 (98%)	107 (86%)	16 (13%)	2 (2%)	7 20
41	1j	95/105 (90%)	81 (85%)	10 (10%)	4 (4%)	2 4
41	2j	94/105 (90%)	83 (88%)	10 (11%)	1 (1%)	11 29
42	1k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14 35
42	2k	112/129 (87%)	102 (91%)	9 (8%)	1 (1%)	14 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	1l	120/132 (91%)	114 (95%)	5 (4%)	1 (1%)	16 37
43	2l	120/132 (91%)	115 (96%)	5 (4%)	0	100 100
44	1m	116/126 (92%)	104 (90%)	11 (10%)	1 (1%)	14 35
44	2m	114/126 (90%)	100 (88%)	12 (10%)	2 (2%)	6 18
45	1n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	7 19
45	2n	58/61 (95%)	51 (88%)	7 (12%)	0	100 100
46	1o	86/89 (97%)	79 (92%)	6 (7%)	1 (1%)	10 27
46	2o	86/89 (97%)	77 (90%)	7 (8%)	2 (2%)	5 13
47	1p	80/88 (91%)	73 (91%)	7 (9%)	0	100 100
47	2p	80/88 (91%)	73 (91%)	7 (9%)	0	100 100
48	1q	97/105 (92%)	87 (90%)	9 (9%)	1 (1%)	12 32
48	2q	97/105 (92%)	87 (90%)	10 (10%)	0	100 100
49	1r	66/88 (75%)	61 (92%)	5 (8%)	0	100 100
49	2r	66/88 (75%)	61 (92%)	5 (8%)	0	100 100
50	1s	82/93 (88%)	69 (84%)	13 (16%)	0	100 100
50	2s	81/93 (87%)	66 (82%)	13 (16%)	2 (2%)	4 11
51	1t	94/106 (89%)	82 (87%)	9 (10%)	3 (3%)	3 7
51	2t	94/106 (89%)	81 (86%)	10 (11%)	3 (3%)	3 7
52	1u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2 3
52	2u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2 3
55	1z	14/20 (70%)	9 (64%)	3 (21%)	2 (14%)	0 0
55	2z	14/20 (70%)	7 (50%)	4 (29%)	3 (21%)	0 0
All	All	11438/12168 (94%)	10532 (92%)	776 (7%)	130 (1%)	11 29

All (130) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	126	ASP
7	1H	126	PRO
26	14	49	PHE
26	14	53	GLU
26	14	68	ARG
33	1b	17	PHE

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Mol	Chain	Res	Type
33	1b	125	PRO
36	1e	98	THR
38	1g	4	ARG
41	1j	55	LYS
41	1j	56	HIS
42	1k	49	GLY
44	1m	4	ILE
45	1n	3	ARG
46	1o	19	PRO
48	1q	68	ARG
5	2F	130	ALA
6	2G	14	GLU
6	2G	47	LYS
7	2H	126	PRO
8	2I	10	GLU
21	2Z	127	LYS
21	2Z	128	VAL
21	2Z	135	GLU
26	24	45	GLY
26	24	49	PHE
26	24	62	ARG
33	2b	17	PHE
33	2b	97	TRP
33	2b	125	PRO
33	2b	165	VAL
33	2b	230	VAL
35	2d	20	TYR
36	2e	37	ARG
40	2i	54	ASP
42	2k	49	GLY
46	2o	19	PRO
50	2s	30	LEU
5	1F	7	TYR
8	1I	106	GLY
12	1Q	58	PHE
17	1V	79	VAL
19	1X	94	GLY
22	10	13	GLY
26	14	45	GLY
26	14	50	VAL
33	1b	16	HIS
34	1c	107	GLN

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Mol	Chain	Res	Type
35	1d	9	CYS
43	1l	29	GLY
51	1t	47	GLY
52	1u	6	ARG
7	2H	55	PRO
17	2V	79	VAL
19	2X	94	GLY
20	2Y	54	LYS
26	24	63	TYR
33	2b	93	VAL
33	2b	96	ARG
33	2b	121	LEU
36	2e	98	THR
41	2j	77	PRO
44	2m	106	ASN
51	2t	99	LEU
52	2u	6	ARG
55	2z	13	PRO
6	1G	47	LYS
6	1G	50	ALA
6	1G	51	ARG
8	1I	73	GLU
20	1Y	53	PRO
23	11	3	LYS
33	1b	20	GLU
38	1g	54	THR
55	1z	13	PRO
55	1z	15	PRO
6	2G	50	ALA
6	2G	126	ASP
8	2I	40	THR
9	2N	2	LYS
11	2P	29	LYS
14	2S	57	LYS
38	2g	4	ARG
40	2i	55	ALA
44	2m	4	ILE
51	2t	47	GLY
55	2z	2	ASP
4	1E	52	LEU
11	1P	29	LYS
20	1Y	54	LYS

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Mol	Chain	Res	Type
33	1b	37	ASN
33	1b	128	GLU
33	1b	231	GLU
4	2E	52	LEU
11	2P	45	LEU
14	2S	84	GLN
26	24	46	GLN
33	2b	124	SER
38	2g	54	THR
50	2s	29	ARG
55	2z	3	LYS
8	1I	107	VAL
26	14	47	GLN
33	1b	124	SER
33	1b	165	VAL
51	1t	10	LEU
51	1t	97	ALA
3	2D	3	VAL
19	2X	2	LYS
23	21	3	LYS
33	2b	20	GLU
35	2d	136	PRO
46	2o	88	ARG
6	1G	124	SER
26	14	46	GLN
41	1j	32	ALA
51	2t	95	ALA
33	2b	38	GLY
14	1S	60	GLY
41	1j	77	PRO
33	2b	151	GLY
3	2D	125	ILE
26	24	50	VAL
39	2h	73	ASP
11	1P	122	PRO
35	1d	136	PRO
15	1T	37	GLY
36	1e	77	PRO
33	2b	202	PRO

5.3.2 Protein sidechains (i)

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
3	1D	215/218 (99%)	193 (90%)	22 (10%)	7 18
3	2D	216/218 (99%)	192 (89%)	24 (11%)	6 15
4	1E	164/166 (99%)	143 (87%)	21 (13%)	4 11
4	2E	164/166 (99%)	144 (88%)	20 (12%)	5 12
5	1F	160/166 (96%)	139 (87%)	21 (13%)	4 10
5	2F	159/166 (96%)	139 (87%)	20 (13%)	4 11
6	1G	143/156 (92%)	125 (87%)	18 (13%)	4 11
6	2G	142/156 (91%)	120 (84%)	22 (16%)	2 7
7	1H	144/148 (97%)	131 (91%)	13 (9%)	9 23
7	2H	144/148 (97%)	129 (90%)	15 (10%)	7 17
8	1I	110/124 (89%)	92 (84%)	18 (16%)	2 6
8	2I	104/124 (84%)	89 (86%)	15 (14%)	3 8
9	1N	118/119 (99%)	103 (87%)	15 (13%)	4 11
9	2N	118/119 (99%)	103 (87%)	15 (13%)	4 11
10	1O	100/100 (100%)	90 (90%)	10 (10%)	7 19
10	2O	100/100 (100%)	91 (91%)	9 (9%)	9 23
11	1P	116/116 (100%)	101 (87%)	15 (13%)	4 10
11	2P	115/116 (99%)	101 (88%)	14 (12%)	5 12
12	1Q	111/111 (100%)	103 (93%)	8 (7%)	13 32
12	2Q	111/111 (100%)	101 (91%)	10 (9%)	9 23
13	1R	101/101 (100%)	84 (83%)	17 (17%)	2 6
13	2R	101/101 (100%)	87 (86%)	14 (14%)	3 9
14	1S	87/88 (99%)	73 (84%)	14 (16%)	2 6
14	2S	85/88 (97%)	67 (79%)	18 (21%)	1 3
15	1T	115/127 (91%)	103 (90%)	12 (10%)	7 17
15	2T	113/127 (89%)	102 (90%)	11 (10%)	8 20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
16	1U	93/94 (99%)	84 (90%)	9 (10%)	8 20
16	2U	93/94 (99%)	83 (89%)	10 (11%)	6 16
17	1V	80/82 (98%)	67 (84%)	13 (16%)	2 6
17	2V	80/82 (98%)	67 (84%)	13 (16%)	2 6
18	1W	90/92 (98%)	81 (90%)	9 (10%)	7 19
18	2W	90/92 (98%)	81 (90%)	9 (10%)	7 19
19	1X	77/78 (99%)	74 (96%)	3 (4%)	28 57
19	2X	77/78 (99%)	74 (96%)	3 (4%)	28 57
20	1Y	85/91 (93%)	79 (93%)	6 (7%)	13 33
20	2Y	85/91 (93%)	76 (89%)	9 (11%)	6 17
21	1Z	159/179 (89%)	140 (88%)	19 (12%)	5 13
21	2Z	156/179 (87%)	137 (88%)	19 (12%)	5 12
22	10	60/67 (90%)	54 (90%)	6 (10%)	7 19
22	20	60/67 (90%)	56 (93%)	4 (7%)	15 36
23	11	80/83 (96%)	74 (92%)	6 (8%)	12 31
23	21	80/83 (96%)	74 (92%)	6 (8%)	12 31
24	12	65/67 (97%)	59 (91%)	6 (9%)	8 22
24	22	65/67 (97%)	58 (89%)	7 (11%)	6 16
25	13	51/52 (98%)	48 (94%)	3 (6%)	18 42
25	23	50/52 (96%)	47 (94%)	3 (6%)	17 41
26	14	60/63 (95%)	52 (87%)	8 (13%)	4 10
26	24	53/63 (84%)	45 (85%)	8 (15%)	3 7
27	15	50/52 (96%)	46 (92%)	4 (8%)	11 28
27	25	50/52 (96%)	46 (92%)	4 (8%)	11 28
28	16	51/52 (98%)	46 (90%)	5 (10%)	7 19
28	26	50/52 (96%)	45 (90%)	5 (10%)	7 19
29	17	41/42 (98%)	38 (93%)	3 (7%)	13 32
29	27	41/42 (98%)	39 (95%)	2 (5%)	22 49
30	18	54/55 (98%)	51 (94%)	3 (6%)	19 44
30	28	54/55 (98%)	48 (89%)	6 (11%)	6 15
31	19	34/34 (100%)	31 (91%)	3 (9%)	9 23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
31	29	34/34 (100%)	31 (91%)	3 (9%)	9 23
33	1b	177/220 (80%)	149 (84%)	28 (16%)	2 7
33	2b	158/220 (72%)	138 (87%)	20 (13%)	4 11
34	1c	127/188 (68%)	116 (91%)	11 (9%)	9 24
34	2c	108/188 (57%)	95 (88%)	13 (12%)	5 12
35	1d	161/181 (89%)	138 (86%)	23 (14%)	3 8
35	2d	164/181 (91%)	141 (86%)	23 (14%)	3 9
36	1e	113/123 (92%)	99 (88%)	14 (12%)	4 11
36	2e	106/123 (86%)	89 (84%)	17 (16%)	2 6
37	1f	83/90 (92%)	78 (94%)	5 (6%)	17 41
37	2f	86/90 (96%)	79 (92%)	7 (8%)	11 27
38	1g	111/127 (87%)	97 (87%)	14 (13%)	4 11
38	2g	107/127 (84%)	93 (87%)	14 (13%)	4 10
39	1h	114/119 (96%)	103 (90%)	11 (10%)	8 20
39	2h	111/119 (93%)	103 (93%)	8 (7%)	13 32
40	1i	89/99 (90%)	81 (91%)	8 (9%)	9 23
40	2i	80/99 (81%)	71 (89%)	9 (11%)	5 14
41	1j	60/92 (65%)	51 (85%)	9 (15%)	3 7
41	2j	62/92 (67%)	51 (82%)	11 (18%)	2 5
42	1k	82/99 (83%)	74 (90%)	8 (10%)	7 19
42	2k	82/99 (83%)	72 (88%)	10 (12%)	5 12
43	1l	95/109 (87%)	88 (93%)	7 (7%)	13 32
43	2l	94/109 (86%)	85 (90%)	9 (10%)	8 20
44	1m	90/101 (89%)	80 (89%)	10 (11%)	6 15
44	2m	87/101 (86%)	78 (90%)	9 (10%)	7 18
45	1n	47/50 (94%)	43 (92%)	4 (8%)	10 25
45	2n	43/50 (86%)	37 (86%)	6 (14%)	3 9
46	1o	75/80 (94%)	66 (88%)	9 (12%)	5 12
46	2o	78/80 (98%)	72 (92%)	6 (8%)	12 30
47	1p	67/74 (90%)	54 (81%)	13 (19%)	1 4
47	2p	68/74 (92%)	57 (84%)	11 (16%)	2 6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
48	1q	91/97 (94%)	83 (91%)	8 (9%)	9 23
48	2q	94/97 (97%)	90 (96%)	4 (4%)	26 54
49	1r	59/77 (77%)	51 (86%)	8 (14%)	3 9
49	2r	59/77 (77%)	51 (86%)	8 (14%)	3 9
50	1s	65/80 (81%)	58 (89%)	7 (11%)	6 16
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4 9
51	1t	66/82 (80%)	55 (83%)	11 (17%)	2 6
51	2t	71/82 (87%)	64 (90%)	7 (10%)	7 19
52	1u	16/22 (73%)	15 (94%)	1 (6%)	16 39
52	2u	18/22 (82%)	16 (89%)	2 (11%)	6 15
55	1z	15/19 (79%)	13 (87%)	2 (13%)	4 10
55	2z	15/19 (79%)	12 (80%)	3 (20%)	1 4
All	All	9165/10104 (91%)	8120 (89%)	1045 (11%)	5 14

All (1045) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	39	LYS
3	1D	61	LEU
3	1D	68	LYS
3	1D	88	ARG
3	1D	94	LEU
3	1D	98	VAL
3	1D	101	GLU
3	1D	111	LEU
3	1D	113	VAL
3	1D	117	VAL
3	1D	138	VAL
3	1D	154	LYS
3	1D	155	LEU
3	1D	173	VAL
3	1D	193	VAL
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	257	LEU
3	1D	260	ARG
3	1D	274	ARG

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Mol	Chain	Res	Type
3	1D	275	LYS
4	1E	9	VAL
4	1E	12	THR
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	40	GLU
4	1E	47	VAL
4	1E	49	LEU
4	1E	73	GLU
4	1E	75	VAL
4	1E	77	ILE
4	1E	97	LYS
4	1E	111	ARG
4	1E	116	VAL
4	1E	119	ARG
4	1E	134	ILE
4	1E	144	ARG
4	1E	154	LYS
4	1E	163	GLU
4	1E	175	VAL
4	1E	181	LEU
5	1F	12	LEU
5	1F	19	GLU
5	1F	20	LEU
5	1F	24	LEU
5	1F	33	LEU
5	1F	38	ARG
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	110	LEU
5	1F	125	LEU
5	1F	132	VAL
5	1F	162	LEU
5	1F	165	ARG
5	1F	170	LEU
5	1F	183	VAL
5	1F	191	ARG
5	1F	192	LEU

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Mol	Chain	Res	Type
5	1F	201	VAL
6	1G	3	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	31	VAL
6	1G	35	GLU
6	1G	40	ASN
6	1G	45	GLU
6	1G	60	LEU
6	1G	70	VAL
6	1G	82	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	143	GLU
6	1G	148	MET
6	1G	159	VAL
6	1G	170	ARG
6	1G	175	LEU
7	1H	13	LYS
7	1H	15	VAL
7	1H	33	LEU
7	1H	43	VAL
7	1H	44	VAL
7	1H	45	VAL
7	1H	69	ARG
7	1H	84	SER
7	1H	88	LEU
7	1H	90	LYS
7	1H	98	LEU
7	1H	122	THR
7	1H	129	THR
8	1I	5	LEU
8	1I	10	GLU
8	1I	38	LEU
8	1I	43	ASN
8	1I	47	LEU
8	1I	54	GLN
8	1I	64	GLU
8	1I	66	GLU
8	1I	75	LEU
8	1I	76	THR

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Mol	Chain	Res	Type
8	1I	77	LEU
8	1I	92	VAL
8	1I	101	LEU
8	1I	109	ILE
8	1I	116	LEU
8	1I	127	VAL
8	1I	140	LEU
8	1I	142	VAL
9	1N	5	VAL
9	1N	8	GLN
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	46	VAL
9	1N	61	ARG
9	1N	73	THR
9	1N	87	LEU
9	1N	97	ARG
9	1N	99	LEU
9	1N	120	LEU
9	1N	133	GLN
9	1N	137	LYS
10	1O	8	LEU
10	1O	10	VAL
10	1O	18	LYS
10	1O	20	MET
10	1O	23	ARG
10	1O	24	VAL
10	1O	66	LYS
10	1O	94	ARG
10	1O	98	VAL
10	1O	105	GLU
11	1P	3	LEU
11	1P	21	ARG
11	1P	55	ARG
11	1P	59	LEU
11	1P	70	GLN
11	1P	83	VAL
11	1P	95	VAL
11	1P	98	GLU
11	1P	99	LEU

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Mol	Chain	Res	Type
11	1P	106	LEU
11	1P	112	LEU
11	1P	125	VAL
11	1P	136	GLU
11	1P	147	LEU
11	1P	149	GLU
12	1Q	8	LYS
12	1Q	35	VAL
12	1Q	45	GLN
12	1Q	55	VAL
12	1Q	60	ARG
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	18	LEU
13	1R	28	LEU
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	60	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	75	LEU
13	1R	79	LEU
13	1R	100	LEU
13	1R	102	GLU
13	1R	111	LEU
13	1R	114	VAL
14	1S	3	ARG
14	1S	14	VAL
14	1S	19	LYS
14	1S	20	ARG
14	1S	36	TYR
14	1S	42	ASP
14	1S	46	VAL
14	1S	49	VAL
14	1S	50	SER
14	1S	59	LYS
14	1S	61	ASN

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Mol	Chain	Res	Type
14	1S	69	VAL
14	1S	82	ILE
14	1S	110	LEU
15	1T	6	LEU
15	1T	23	ARG
15	1T	28	VAL
15	1T	34	VAL
15	1T	49	VAL
15	1T	78	LEU
15	1T	85	LYS
15	1T	89	VAL
15	1T	96	ARG
15	1T	107	ASP
15	1T	118	ARG
15	1T	128	GLU
16	1U	8	VAL
16	1U	36	ARG
16	1U	59	ARG
16	1U	60	LEU
16	1U	74	LEU
16	1U	92	ARG
16	1U	95	LEU
16	1U	104	GLN
16	1U	108	GLU
17	1V	18	LEU
17	1V	21	ARG
17	1V	28	GLU
17	1V	43	GLU
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
17	1V	95	LEU
17	1V	100	ARG
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU

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Mol	Chain	Res	Type
18	1W	51	LEU
18	1W	83	LYS
18	1W	96	ILE
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
19	1X	76	ARG
20	1Y	7	VAL
20	1Y	9	LYS
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
21	1Z	2	GLU
21	1Z	11	GLU
21	1Z	18	LEU
21	1Z	31	ARG
21	1Z	42	VAL
21	1Z	70	LEU
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	91	LEU
21	1Z	107	THR
21	1Z	126	VAL
21	1Z	135	GLU
21	1Z	150	LEU
21	1Z	154	ASP
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	170	THR
21	1Z	183	LEU
21	1Z	185	GLU
22	10	11	ARG
22	10	20	ARG
22	10	49	LYS
22	10	55	ARG
22	10	63	VAL
22	10	68	GLU
23	11	21	ARG
23	11	30	VAL
23	11	40	ARG
23	11	59	THR

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Mol	Chain	Res	Type
23	11	78	LYS
23	11	95	LEU
24	12	19	VAL
24	12	28	LYS
24	12	32	LEU
24	12	49	LYS
24	12	53	LEU
24	12	70	GLN
25	13	8	LEU
25	13	23	LEU
25	13	54	VAL
26	14	14	ILE
26	14	33	VAL
26	14	34	GLU
26	14	55	ARG
26	14	56	VAL
26	14	60	GLN
26	14	62	ARG
26	14	63	TYR
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	40	LYS
28	16	4	GLU
28	16	5	VAL
28	16	9	LEU
28	16	33	LYS
28	16	38	LYS
29	17	23	ARG
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	23	VAL
30	18	32	LEU
31	19	17	ILE
31	19	26	ILE
31	19	35	ARG
33	1b	10	LEU
33	1b	11	LEU
33	1b	17	PHE
33	1b	21	ARG
33	1b	23	ARG

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Mol	Chain	Res	Type
33	1b	44	LEU
33	1b	47	THR
33	1b	48	MET
33	1b	51	LEU
33	1b	67	THR
33	1b	76	GLN
33	1b	80	ILE
33	1b	86	GLU
33	1b	112	VAL
33	1b	116	GLU
33	1b	143	GLU
33	1b	170	GLU
33	1b	175	ARG
33	1b	185	ILE
33	1b	187	LEU
33	1b	192	SER
33	1b	208	ILE
33	1b	209	ARG
33	1b	215	LEU
33	1b	217	ARG
33	1b	221	LEU
33	1b	223	ILE
33	1b	230	VAL
34	1c	15	THR
34	1c	33	LEU
34	1c	45	LYS
34	1c	52	LEU
34	1c	59	ARG
34	1c	64	VAL
34	1c	70	VAL
34	1c	131	ARG
34	1c	150	LYS
34	1c	195	VAL
34	1c	204	LEU
35	1d	3	ARG
35	1d	5	ILE
35	1d	13	ARG
35	1d	15	GLU
35	1d	22	LYS
35	1d	25	ARG
35	1d	45	GLN
35	1d	49	ARG

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Mol	Chain	Res	Type
35	1d	58	LEU
35	1d	70	ILE
35	1d	73	ARG
35	1d	97	LEU
35	1d	101	LEU
35	1d	107	ARG
35	1d	108	LEU
35	1d	122	ARG
35	1d	127	THR
35	1d	150	GLU
35	1d	155	LEU
35	1d	168	ARG
35	1d	181	MET
35	1d	188	LEU
35	1d	194	LEU
36	1e	12	LEU
36	1e	18	ARG
36	1e	31	LEU
36	1e	34	VAL
36	1e	41	VAL
36	1e	47	LYS
36	1e	51	VAL
36	1e	73	ASN
36	1e	75	THR
36	1e	79	GLU
36	1e	81	GLU
36	1e	91	LEU
36	1e	120	THR
36	1e	152	ARG
37	1f	45	LEU
37	1f	46	ARG
37	1f	69	GLU
37	1f	72	VAL
37	1f	79	LEU
38	1g	8	GLU
38	1g	9	VAL
38	1g	21	VAL
38	1g	50	ILE
38	1g	51	GLN
38	1g	56	GLN
38	1g	57	GLU
38	1g	72	ARG

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Mol	Chain	Res	Type
38	1g	75	VAL
38	1g	104	LEU
38	1g	113	GLU
38	1g	114	ARG
38	1g	131	LYS
38	1g	135	VAL
39	1h	21	LYS
39	1h	26	VAL
39	1h	50	ARG
39	1h	51	VAL
39	1h	63	LEU
39	1h	75	ARG
39	1h	77	GLU
39	1h	78	GLN
39	1h	91	ARG
39	1h	98	LYS
39	1h	137	VAL
40	1i	14	VAL
40	1i	27	THR
40	1i	75	ASP
40	1i	81	ILE
40	1i	104	ARG
40	1i	108	VAL
40	1i	127	LYS
40	1i	128	ARG
41	1j	17	ASP
41	1j	30	SER
41	1j	34	VAL
41	1j	49	VAL
41	1j	84	GLN
41	1j	85	LEU
41	1j	92	THR
41	1j	94	VAL
41	1j	98	ILE
42	1k	14	VAL
42	1k	31	THR
42	1k	48	ILE
42	1k	51	LYS
42	1k	77	MET
42	1k	96	ARG
42	1k	109	VAL
42	1k	114	VAL

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Mol	Chain	Res	Type
43	1l	10	LEU
43	1l	23	LYS
43	1l	27	LEU
43	1l	33	ARG
43	1l	57	LYS
43	1l	67	THR
43	1l	83	VAL
44	1m	4	ILE
44	1m	15	VAL
44	1m	19	LEU
44	1m	32	GLU
44	1m	49	THR
44	1m	50	GLU
44	1m	56	LEU
44	1m	70	LEU
44	1m	98	VAL
44	1m	102	ARG
45	1n	6	LEU
45	1n	18	VAL
45	1n	22	THR
45	1n	46	GLU
46	1o	5	LYS
46	1o	14	GLU
46	1o	22	THR
46	1o	24	SER
46	1o	26	GLU
46	1o	39	LEU
46	1o	83	GLU
46	1o	84	LYS
46	1o	87	ILE
47	1p	1	MET
47	1p	2	VAL
47	1p	5	ARG
47	1p	11	SER
47	1p	16	HIS
47	1p	19	ILE
47	1p	20	VAL
47	1p	25	ARG
47	1p	45	THR
47	1p	60	LEU
47	1p	62	VAL
47	1p	67	THR

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Mol	Chain	Res	Type
47	1p	72	ARG
48	1q	6	LEU
48	1q	19	VAL
48	1q	35	VAL
48	1q	37	LYS
48	1q	68	ARG
48	1q	74	LEU
48	1q	78	GLU
48	1q	82	MET
49	1r	32	ARG
49	1r	35	ARG
49	1r	37	VAL
49	1r	38	GLU
49	1r	55	ARG
49	1r	68	LYS
49	1r	69	THR
49	1r	76	LEU
50	1s	3	ARG
50	1s	5	LEU
50	1s	22	LEU
50	1s	28	LYS
50	1s	63	THR
50	1s	65	ASN
50	1s	81	ARG
51	1t	9	ASN
51	1t	10	LEU
51	1t	24	LEU
51	1t	25	ARG
51	1t	30	LYS
51	1t	56	MET
51	1t	60	GLU
51	1t	62	LEU
51	1t	81	LYS
51	1t	84	LEU
51	1t	93	GLU
52	1u	15	ARG
55	1z	11	THR
55	1z	14	ARG
3	2D	54	ARG
3	2D	61	LEU
3	2D	82	ILE
3	2D	89	SER

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Mol	Chain	Res	Type
3	2D	94	LEU
3	2D	103	ARG
3	2D	106	ILE
3	2D	113	VAL
3	2D	134	ARG
3	2D	155	LEU
3	2D	164	GLN
3	2D	169	GLU
3	2D	173	VAL
3	2D	193	VAL
3	2D	211	ARG
3	2D	217	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	257	LEU
3	2D	260	ARG
3	2D	274	ARG
3	2D	275	LYS
3	2D	276	LYS
4	2E	7	VAL
4	2E	9	VAL
4	2E	12	THR
4	2E	21	VAL
4	2E	24	THR
4	2E	33	VAL
4	2E	34	VAL
4	2E	40	GLU
4	2E	49	LEU
4	2E	52	LEU
4	2E	73	GLU
4	2E	75	VAL
4	2E	77	ILE
4	2E	111	ARG
4	2E	116	VAL
4	2E	119	ARG
4	2E	144	ARG
4	2E	154	LYS
4	2E	175	VAL
4	2E	181	LEU
5	2F	12	LEU
5	2F	19	GLU

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Mol	Chain	Res	Type
5	2F	20	LEU
5	2F	33	LEU
5	2F	38	ARG
5	2F	53	THR
5	2F	57	VAL
5	2F	64	ILE
5	2F	74	ARG
5	2F	78	ILE
5	2F	88	VAL
5	2F	106	ARG
5	2F	132	VAL
5	2F	135	LYS
5	2F	162	LEU
5	2F	183	VAL
5	2F	192	LEU
5	2F	196	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	9	ARG
6	2G	28	VAL
6	2G	31	VAL
6	2G	33	ARG
6	2G	35	GLU
6	2G	40	ASN
6	2G	47	LYS
6	2G	60	LEU
6	2G	70	VAL
6	2G	98	ARG
6	2G	111	LEU
6	2G	113	ARG
6	2G	136	ARG
6	2G	139	LEU
6	2G	140	ILE
6	2G	143	GLU
6	2G	148	MET
6	2G	153	ARG
6	2G	159	VAL
6	2G	162	THR
7	2H	3	ARG
7	2H	13	LYS

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Mol	Chain	Res	Type
7	2H	15	VAL
7	2H	32	GLU
7	2H	33	LEU
7	2H	41	MET
7	2H	42	ARG
7	2H	43	VAL
7	2H	63	SER
7	2H	69	ARG
7	2H	90	LYS
7	2H	122	THR
7	2H	129	THR
7	2H	139	GLN
7	2H	171	LEU
8	2I	5	LEU
8	2I	15	VAL
8	2I	38	LEU
8	2I	43	ASN
8	2I	47	LEU
8	2I	61	ARG
8	2I	75	LEU
8	2I	77	LEU
8	2I	92	VAL
8	2I	116	LEU
8	2I	127	VAL
8	2I	129	THR
8	2I	140	LEU
8	2I	142	VAL
8	2I	144	VAL
9	2N	5	VAL
9	2N	14	VAL
9	2N	33	LEU
9	2N	34	LEU
9	2N	46	VAL
9	2N	61	ARG
9	2N	62	VAL
9	2N	73	THR
9	2N	87	LEU
9	2N	97	ARG
9	2N	99	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	137	LYS

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Mol	Chain	Res	Type
9	2N	138	LEU
10	2O	8	LEU
10	2O	10	VAL
10	2O	18	LYS
10	2O	23	ARG
10	2O	24	VAL
10	2O	52	VAL
10	2O	69	ILE
10	2O	94	ARG
10	2O	98	VAL
11	2P	21	ARG
11	2P	45	LEU
11	2P	55	ARG
11	2P	59	LEU
11	2P	65	ARG
11	2P	83	VAL
11	2P	95	VAL
11	2P	96	THR
11	2P	106	LEU
11	2P	112	LEU
11	2P	121	LYS
11	2P	123	LEU
11	2P	125	VAL
11	2P	148	LEU
12	2Q	5	ARG
12	2Q	7	MET
12	2Q	21	THR
12	2Q	35	VAL
12	2Q	45	GLN
12	2Q	48	GLU
12	2Q	64	ILE
12	2Q	75	THR
12	2Q	81	VAL
12	2Q	109	VAL
13	2R	6	SER
13	2R	18	LEU
13	2R	28	LEU
13	2R	29	LEU
13	2R	36	THR
13	2R	44	LEU
13	2R	60	LEU
13	2R	65	LEU

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Mol	Chain	Res	Type
13	2R	75	LEU
13	2R	79	LEU
13	2R	100	LEU
13	2R	102	GLU
13	2R	111	LEU
13	2R	114	VAL
14	2S	3	ARG
14	2S	13	ARG
14	2S	14	VAL
14	2S	20	ARG
14	2S	36	TYR
14	2S	46	VAL
14	2S	50	SER
14	2S	52	SER
14	2S	58	LEU
14	2S	64	GLU
14	2S	67	ARG
14	2S	68	GLN
14	2S	69	VAL
14	2S	75	GLU
14	2S	80	LEU
14	2S	83	LYS
14	2S	110	LEU
14	2S	111	GLU
15	2T	6	LEU
15	2T	8	LYS
15	2T	16	ARG
15	2T	23	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	49	VAL
15	2T	78	LEU
15	2T	89	VAL
15	2T	96	ARG
15	2T	118	ARG
16	2U	13	LYS
16	2U	36	ARG
16	2U	52	ARG
16	2U	60	LEU
16	2U	74	LEU
16	2U	83	LEU
16	2U	92	ARG

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Mol	Chain	Res	Type
16	2U	95	LEU
16	2U	104	GLN
16	2U	112	ARG
17	2V	6	LYS
17	2V	18	LEU
17	2V	21	ARG
17	2V	35	LEU
17	2V	38	LEU
17	2V	46	VAL
17	2V	52	VAL
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	79	VAL
17	2V	95	LEU
17	2V	100	ARG
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	27	LYS
18	2W	51	LEU
18	2W	96	ILE
18	2W	107	LEU
19	2X	57	LEU
19	2X	76	ARG
19	2X	92	LEU
20	2Y	7	VAL
20	2Y	9	LYS
20	2Y	21	LYS
20	2Y	44	ILE
20	2Y	49	VAL
20	2Y	67	LEU
20	2Y	72	VAL
20	2Y	85	VAL
20	2Y	92	ASN
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	70	LEU
21	2Z	71	VAL
21	2Z	86	VAL

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Mol	Chain	Res	Type
21	2Z	91	LEU
21	2Z	107	THR
21	2Z	126	VAL
21	2Z	128	VAL
21	2Z	131	ARG
21	2Z	135	GLU
21	2Z	136	PHE
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	170	THR
21	2Z	183	LEU
21	2Z	185	GLU
22	20	19	LYS
22	20	20	ARG
22	20	63	VAL
22	20	68	GLU
23	21	4	VAL
23	21	21	ARG
23	21	35	THR
23	21	40	ARG
23	21	59	THR
23	21	95	LEU
24	22	2	LYS
24	22	28	LYS
24	22	32	LEU
24	22	34	GLU
24	22	40	SER
24	22	53	LEU
24	22	70	GLN
25	23	8	LEU
25	23	54	VAL
25	23	55	ARG
26	24	1	MET
26	24	33	VAL
26	24	34	GLU
26	24	44	THR
26	24	52	THR
26	24	60	GLN
26	24	61	ARG
26	24	63	TYR

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Mol	Chain	Res	Type
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	40	LYS
28	26	5	VAL
28	26	9	LEU
28	26	33	LYS
28	26	38	LYS
28	26	48	VAL
29	27	1	MET
29	27	43	THR
30	28	14	VAL
30	28	23	VAL
30	28	26	LYS
30	28	30	ARG
30	28	35	GLN
30	28	37	SER
31	29	26	ILE
31	29	29	ASN
31	29	35	ARG
33	2b	8	LYS
33	2b	44	LEU
33	2b	48	MET
33	2b	51	LEU
33	2b	60	ASP
33	2b	67	THR
33	2b	80	ILE
33	2b	90	MET
33	2b	93	VAL
33	2b	108	ILE
33	2b	118	LEU
33	2b	138	LEU
33	2b	170	GLU
33	2b	179	LYS
33	2b	185	ILE
33	2b	187	LEU
33	2b	191	ASP
33	2b	222	ILE
33	2b	223	ILE
33	2b	224	GLN
34	2c	5	ILE
34	2c	40	ARG

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Mol	Chain	Res	Type
34	2c	47	LEU
34	2c	52	LEU
34	2c	70	VAL
34	2c	105	GLU
34	2c	128	PHE
34	2c	131	ARG
34	2c	152	ILE
34	2c	162	GLN
34	2c	178	LEU
34	2c	182	ILE
34	2c	198	VAL
35	2d	3	ARG
35	2d	5	ILE
35	2d	22	LYS
35	2d	26	CYS
35	2d	34	GLU
35	2d	38	TYR
35	2d	47	ARG
35	2d	58	LEU
35	2d	70	ILE
35	2d	73	ARG
35	2d	96	LEU
35	2d	97	LEU
35	2d	101	LEU
35	2d	122	ARG
35	2d	135	LEU
35	2d	157	LEU
35	2d	170	VAL
35	2d	179	GLU
35	2d	181	MET
35	2d	182	LYS
35	2d	187	ARG
35	2d	188	LEU
35	2d	194	LEU
36	2e	11	ILE
36	2e	12	LEU
36	2e	24	ARG
36	2e	27	ARG
36	2e	31	LEU
36	2e	34	VAL
36	2e	37	ARG
36	2e	41	VAL

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Mol	Chain	Res	Type
36	2e	47	LYS
36	2e	50	GLU
36	2e	51	VAL
36	2e	67	VAL
36	2e	68	GLU
36	2e	71	LEU
36	2e	91	LEU
36	2e	115	VAL
36	2e	121	LYS
37	2f	17	SER
37	2f	23	LYS
37	2f	27	GLN
37	2f	46	ARG
37	2f	69	GLU
37	2f	72	VAL
37	2f	75	LEU
38	2g	9	VAL
38	2g	16	LEU
38	2g	51	GLN
38	2g	52	GLU
38	2g	57	GLU
38	2g	73	MET
38	2g	75	VAL
38	2g	98	SER
38	2g	104	LEU
38	2g	110	GLN
38	2g	114	ARG
38	2g	129	GLU
38	2g	131	LYS
38	2g	135	VAL
39	2h	26	VAL
39	2h	63	LEU
39	2h	77	GLU
39	2h	78	GLN
39	2h	91	ARG
39	2h	111	ILE
39	2h	120	THR
39	2h	137	VAL
40	2i	3	GLN
40	2i	38	GLN
40	2i	50	LEU
40	2i	89	ASN

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Mol	Chain	Res	Type
40	2i	102	LEU
40	2i	107	ARG
40	2i	108	VAL
40	2i	124	GLN
40	2i	128	ARG
41	2j	13	HIS
41	2j	17	ASP
41	2j	21	GLN
41	2j	23	ILE
41	2j	48	THR
41	2j	49	VAL
41	2j	57	LYS
41	2j	68	HIS
41	2j	84	GLN
41	2j	94	VAL
41	2j	98	ILE
42	2k	14	VAL
42	2k	18	ARG
42	2k	26	ASN
42	2k	48	ILE
42	2k	54	ARG
42	2k	70	LYS
42	2k	77	MET
42	2k	78	GLN
42	2k	109	VAL
42	2k	114	VAL
43	2l	27	LEU
43	2l	28	LYS
43	2l	33	ARG
43	2l	54	LYS
43	2l	55	VAL
43	2l	57	LYS
43	2l	67	THR
43	2l	83	VAL
43	2l	97	ARG
44	2m	3	ARG
44	2m	40	ASN
44	2m	49	THR
44	2m	56	LEU
44	2m	61	GLU
44	2m	70	LEU
44	2m	82	MET

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Mol	Chain	Res	Type
44	2m	90	LEU
44	2m	106	ASN
45	2n	11	LYS
45	2n	17	LYS
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL
45	2n	53	LEU
46	2o	5	LYS
46	2o	10	LYS
46	2o	22	THR
46	2o	24	SER
46	2o	26	GLU
46	2o	87	ILE
47	2p	1	MET
47	2p	5	ARG
47	2p	11	SER
47	2p	16	HIS
47	2p	28	ARG
47	2p	45	THR
47	2p	60	LEU
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
47	2p	72	ARG
48	2q	6	LEU
48	2q	35	VAL
48	2q	37	LYS
48	2q	74	LEU
49	2r	26	LEU
49	2r	28	GLU
49	2r	29	PHE
49	2r	32	ARG
49	2r	35	ARG
49	2r	37	VAL
49	2r	54	ARG
49	2r	76	LEU
50	2s	3	ARG
50	2s	18	LYS
50	2s	22	LEU
50	2s	28	LYS
50	2s	41	VAL

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Mol	Chain	Res	Type
50	2s	64	GLU
50	2s	71	LEU
50	2s	77	THR
50	2s	78	ARG
51	2t	9	ASN
51	2t	10	LEU
51	2t	24	LEU
51	2t	25	ARG
51	2t	56	MET
51	2t	62	LEU
51	2t	71	THR
52	2u	10	ARG
52	2u	15	ARG
55	2z	9	ARG
55	2z	14	ARG
55	2z	16	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (169) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	126	GLN
3	1D	164	GLN
3	1D	166	GLN
3	1D	253	GLN
5	1F	8	GLN
5	1F	29	ASN
5	1F	69	HIS
5	1F	169	ASN
5	1F	203	GLN
8	1I	43	ASN
8	1I	139	GLN
9	1N	8	GLN
9	1N	131	GLN
10	1O	3	GLN
11	1P	38	GLN
13	1R	31	HIS
13	1R	50	HIS
13	1R	71	GLN
14	1S	95	HIS
15	1T	38	ASN
15	1T	123	GLN
16	1U	72	HIS

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Mol	Chain	Res	Type
16	1U	94	ASN
18	1W	111	HIS
19	1X	31	HIS
19	1X	55	ASN
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	121	HIS
21	1Z	151	HIS
24	12	38	GLN
24	12	70	GLN
26	14	60	GLN
27	15	4	HIS
31	19	36	GLN
33	1b	16	HIS
33	1b	19	HIS
33	1b	95	GLN
33	1b	110	GLN
34	1c	118	GLN
34	1c	136	GLN
34	1c	170	GLN
34	1c	181	ASN
35	1d	43	HIS
35	1d	45	GLN
35	1d	77	ASN
35	1d	123	HIS
35	1d	160	GLN
36	1e	38	GLN
36	1e	141	GLN
37	1f	94	GLN
38	1g	13	GLN
38	1g	56	GLN
38	1g	97	GLN
38	1g	148	ASN
40	1i	31	GLN
40	1i	38	GLN
40	1i	58	HIS
40	1i	73	GLN
40	1i	87	GLN
40	1i	89	ASN

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Mol	Chain	Res	Type
40	1i	117	HIS
40	1i	124	GLN
41	1j	56	HIS
41	1j	68	HIS
41	1j	84	GLN
42	1k	93	GLN
43	1l	78	GLN
43	1l	80	HIS
44	1m	77	ASN
45	1n	52	GLN
46	1o	9	GLN
46	1o	28	GLN
48	1q	16	GLN
48	1q	26	GLN
50	1s	23	ASN
50	1s	56	GLN
50	1s	65	ASN
50	1s	69	HIS
51	1t	9	ASN
51	1t	26	ASN
51	1t	45	GLN
3	2D	164	GLN
3	2D	253	GLN
4	2E	85	ASN
4	2E	180	ASN
5	2F	69	HIS
5	2F	169	ASN
5	2F	203	GLN
6	2G	108	ASN
8	2I	105	HIS
8	2I	133	HIS
8	2I	139	GLN
9	2N	8	GLN
11	2P	9	ASN
11	2P	38	GLN
12	2Q	12	GLN
12	2Q	45	GLN
14	2S	68	GLN
14	2S	95	HIS
15	2T	43	GLN
15	2T	123	GLN
16	2U	94	ASN

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Mol	Chain	Res	Type
17	2V	64	HIS
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	55	HIS
21	2Z	73	GLN
22	20	35	ASN
23	21	56	GLN
24	22	38	GLN
24	22	48	HIS
25	23	32	GLN
25	23	33	GLN
28	26	32	ASN
31	29	29	ASN
31	29	36	GLN
33	2b	16	HIS
33	2b	19	HIS
33	2b	45	GLN
33	2b	95	GLN
34	2c	37	GLN
34	2c	69	HIS
34	2c	176	HIS
34	2c	181	ASN
35	2d	74	GLN
35	2d	123	HIS
35	2d	160	GLN
35	2d	161	ASN
35	2d	201	GLN
36	2e	38	GLN
37	2f	73	ASN
38	2g	28	ASN
38	2g	86	GLN
38	2g	97	GLN
38	2g	109	ASN
38	2g	110	GLN
38	2g	148	ASN
38	2g	153	HIS
39	2h	78	GLN
40	2i	38	GLN
40	2i	58	HIS
40	2i	73	GLN

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Mol	Chain	Res	Type
40	2i	89	ASN
41	2j	13	HIS
41	2j	21	GLN
41	2j	56	HIS
42	2k	26	ASN
42	2k	93	GLN
42	2k	104	GLN
42	2k	116	HIS
43	2l	75	HIS
43	2l	78	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	40	ASN
46	2o	28	GLN
46	2o	62	GLN
47	2p	14	ASN
47	2p	16	HIS
48	2q	16	GLN
50	2s	56	GLN
50	2s	69	HIS
50	2s	83	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2737/2915 (93%)	377 (13%)	22 (0%)
1	2A	2781/2915 (95%)	477 (17%)	23 (0%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	119/121 (98%)	26 (21%)	2 (1%)
32	1a	1472/1521 (96%)	273 (18%)	0
32	2a	1479/1521 (97%)	278 (18%)	0
53	1v	4/24 (16%)	1 (25%)	0
53	2v	4/24 (16%)	1 (25%)	0
54	1x	75/77 (97%)	16 (21%)	0
54	2x	75/77 (97%)	18 (24%)	0
All	All	8865/9316 (95%)	1477 (16%)	47 (0%)

All (1477) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	11	U

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Mol	Chain	Res	Type
1	1A	33	C
1	1A	35	G
1	1A	44	C
1	1A	49	G
1	1A	56	G
1	1A	59	G
1	1A	61	U
1	1A	69	A
1	1A	72	A
1	1A	73	G
1	1A	82	A
1	1A	115	A
1	1A	116	A
1	1A	117	U
1	1A	148	A
1	1A	154	C
1	1A	170	A
1	1A	184	A
1	1A	185	A
1	1A	187	A
1	1A	188	U
1	1A	193	G
1	1A	202	G
1	1A	204	A
1	1A	210	A
1	1A	216	A
1	1A	217	A
1	1A	221	A
1	1A	236	G
1	1A	237	C
1	1A	264	U
1	1A	268	G
1	1A	271	U
1	1A	272	G
1	1A	273	U
1	1A	278	G
1	1A	287	U
1	1A	288	G
1	1A	295	U
1	1A	298	G
1	1A	302	C
1	1A	334	A

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Mol	Chain	Res	Type
1	1A	340	G
1	1A	352	G
1	1A	353	A
1	1A	375	G
1	1A	386	G
1	1A	388	G
1	1A	398	G
1	1A	412	G
1	1A	422	G
1	1A	431	U
1	1A	437	G
1	1A	454	A
1	1A	467	G
1	1A	469	C
1	1A	473	U
1	1A	476	C
1	1A	479	A
1	1A	482	A
1	1A	495	A
1	1A	500	U
1	1A	506	G
1	1A	528	U
1	1A	529	A
1	1A	533	C
1	1A	554	G
1	1A	555	C
1	1A	556	A
1	1A	557	G
1	1A	572	G
1	1A	585	G
1	1A	595	G
1	1A	596	C
1	1A	597	A
1	1A	608	A
1	1A	615	G
1	1A	625	A
1	1A	626	G
1	1A	629	U
1	1A	638	G
1	1A	640	G
1	1A	658	C
1	1A	661	A

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Mol	Chain	Res	Type
1	1A	669	C
1	1A	670	A
1	1A	671	G
1	1A	681	G
1	1A	682	G
1	1A	700	A
1	1A	715	G
1	1A	732	G
1	1A	763	G
1	1A	772	G
1	1A	776	C
1	1A	810	A
1	1A	821	G
1	1A	822	G
1	1A	828	A
1	1A	830	A
1	1A	831	G
1	1A	836	C
1	1A	838	G
1	1A	851	G
1	1A	858	C
1	1A	873	U
1	1A	874	U
1	1A	905	G
1	1A	912	A
1	1A	915	G
1	1A	925	G
1	1A	931	C
1	1A	932	C
1	1A	933	A
1	1A	934	C
1	1A	935	C
1	1A	936	A
1	1A	938	C
1	1A	941	A
1	1A	942	C
1	1A	955	A
1	1A	976	G
1	1A	985	A
1	1A	989	A
1	1A	990	G
1	1A	1002	U

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Mol	Chain	Res	Type
1	1A	1003	A
1	1A	1005	C
1	1A	1018	G
1	1A	1019	C
1	1A	1028	A
1	1A	1035	A
1	1A	1041	A
1	1A	1057	U
1	1A	1058	C
1	1A	1067	G
1	1A	1071	U
1	1A	1072	A
1	1A	1078	U
1	1A	1083	C
1	1A	1086	C
1	1A	1091	A
1	1A	1092	G
1	1A	1150	U
1	1A	1153	U
1	1A	1154	C
1	1A	1156	A
1	1A	1157	G
1	1A	1173	A
1	1A	1174	A
1	1A	1179	C
1	1A	1180	G
1	1A	1183	G
1	1A	1216	G
1	1A	1217	G
1	1A	1218	A
1	1A	1219	U
1	1A	1220	G
1	1A	1221	A
1	1A	1264	A
1	1A	1285	U
1	1A	1286	A
1	1A	1289	G
1	1A	1298	A
1	1A	1301	G
1	1A	1316	G
1	1A	1317	A
1	1A	1318	U

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Mol	Chain	Res	Type
1	1A	1345	U
1	1A	1346	A
1	1A	1348	G
1	1A	1350	C
1	1A	1351	C
1	1A	1353	A
1	1A	1397	U
1	1A	1404	A
1	1A	1405	A
1	1A	1410	A
1	1A	1424	A
1	1A	1429	A
1	1A	1430	G
1	1A	1440	A
1	1A	1461	G
1	1A	1462	C
1	1A	1465	U
1	1A	1466	G
1	1A	1473	C
1	1A	1482	C
1	1A	1490	A
1	1A	1495	A
1	1A	1496	G
1	1A	1513	C
1	1A	1524	G
1	1A	1528	G
1	1A	1539	A
1	1A	1541	A
1	1A	1552	A
1	1A	1553	A
1	1A	1554	C
1	1A	1555	A
1	1A	1578	C
1	1A	1588	A
1	1A	1589	C
1	1A	1600	A
1	1A	1604	A
1	1A	1612	A
1	1A	1615	A
1	1A	1624	U
1	1A	1627	G
1	1A	1630	C

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Mol	Chain	Res	Type
1	1A	1631	A
1	1A	1632	A
1	1A	1653	A
1	1A	1654	A
1	1A	1694	C
1	1A	1700	A
1	1A	1710	A
1	1A	1720	G
1	1A	1746	A
1	1A	1766	A
1	1A	1767	U
1	1A	1786	G
1	1A	1792	A
1	1A	1793	G
1	1A	1794	G
1	1A	1803	A
1	1A	1810	A
1	1A	1816	A
1	1A	1821	A
1	1A	1830	C
1	1A	1831	G
1	1A	1832	A
1	1A	1846	G
1	1A	1847	G
1	1A	1858	G
1	1A	1859	A
1	1A	1869	G
1	1A	1877	A
1	1A	1878	A
1	1A	1898	A
1	1A	1899	G
1	1A	1910	A
1	1A	1921	A
1	1A	1927	G
1	1A	1934	A
1	1A	1936	U
1	1A	1940	A
1	1A	1948	A
1	1A	1950	G
1	1A	1951	G
1	1A	1958	A
1	1A	1959	A

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Mol	Chain	Res	Type
1	1A	1976	U
1	1A	1981	A
1	1A	1984	U
1	1A	1986	C
1	1A	1988	C
1	1A	1991	A
1	1A	1992	A
1	1A	1993	A
1	1A	2013	G
1	1A	2014	U
1	1A	2018	G
1	1A	2044	G
1	1A	2052	A
1	1A	2054	A
1	1A	2064	C
1	1A	2076	C
1	1A	2077	G
1	1A	2081	A
1	1A	2082	G
1	1A	2083	A
1	1A	2090	G
1	1A	2114	G
1	1A	2205	G
1	1A	2207	G
1	1A	2208	G
1	1A	2209	C
1	1A	2213	G
1	1A	2219	A
1	1A	2226	G
1	1A	2227	G
1	1A	2228	A
1	1A	2229	U
1	1A	2236	A
1	1A	2250	G
1	1A	2279	A
1	1A	2280	A
1	1A	2284	A
1	1A	2286	C
1	1A	2289	A
1	1A	2294	C
1	1A	2298	A
1	1A	2300	G

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Mol	Chain	Res	Type
1	1A	2316	A
1	1A	2331	A
1	1A	2336	G
1	1A	2338	A
1	1A	2345	G
1	1A	2347	A
1	1A	2358	C
1	1A	2361	C
1	1A	2365	G
1	1A	2394	G
1	1A	2396	C
1	1A	2411	G
1	1A	2417	U
1	1A	2433	A
1	1A	2434	U
1	1A	2436	A
1	1A	2439	G
1	1A	2440	G
1	1A	2441	A
1	1A	2442	U
1	1A	2443	A
1	1A	2446	A
1	1A	2450	A
1	1A	2452	C
1	1A	2459	A
1	1A	2470	A
1	1A	2473	U
1	1A	2479	G
1	1A	2485	C
1	1A	2487	A
1	1A	2489	A
1	1A	2493	G
1	1A	2498	G
1	1A	2513	G
1	1A	2516	G
1	1A	2517	U
1	1A	2529	A
1	1A	2536	G
1	1A	2540	G
1	1A	2565	U
1	1A	2577	A
1	1A	2578	G

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Mol	Chain	Res	Type
1	1A	2584	C
1	1A	2590	C
1	1A	2593	G
1	1A	2596	U
1	1A	2613	A
1	1A	2620	U
1	1A	2622	U
1	1A	2623	C
1	1A	2640	A
1	1A	2641	G
1	1A	2665	A
1	1A	2700	U
1	1A	2701	C
1	1A	2702	C
1	1A	2713	U
1	1A	2714	C
1	1A	2724	A
1	1A	2725	A
1	1A	2726	G
1	1A	2738	U
1	1A	2745	A
1	1A	2770	A
1	1A	2776	A
1	1A	2777	A
1	1A	2778	G
1	1A	2781	C
1	1A	2790	A
1	1A	2802	A
1	1A	2812	G
1	1A	2829	A
1	1A	2830	A
1	1A	2844	A
1	1A	2881	G
1	1A	2882	A
1	1A	2885	G
1	1A	2889	C
1	1A	2900	A
1	1A	2901	G
1	1A	2902	G
1	1A	2903	U
2	1B	2	C
2	1B	13	A

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Mol	Chain	Res	Type
2	1B	25	A
2	1B	52	A
2	1B	56	G
2	1B	59	A
2	1B	60	C
2	1B	73	A
2	1B	85	G
2	1B	110	G
32	1a	6	U
32	1a	8	G
32	1a	10	G
32	1a	33	A
32	1a	40	G
32	1a	41	C
32	1a	42	G
32	1a	45	G
32	1a	49	C
32	1a	52	A
32	1a	62	G
32	1a	68	C
32	1a	69	G
32	1a	74	G
32	1a	75	C
32	1a	76	G
32	1a	77	G
32	1a	78	G
32	1a	91	G
32	1a	95	A
32	1a	109	G
32	1a	110	A
32	1a	114	A
32	1a	115	C
32	1a	124	G
32	1a	126	C
32	1a	132	C
32	1a	139	G
32	1a	152	G
32	1a	156	A
32	1a	157	A
32	1a	161	G
32	1a	163	G
32	1a	168	U

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Mol	Chain	Res	Type
32	1a	169	C
32	1a	177	U
32	1a	190	U
32	1a	200	C
32	1a	202	A
32	1a	204	A
32	1a	208	C
32	1a	209	U
32	1a	210	U
32	1a	211	U
32	1a	212	G
32	1a	213	C
32	1a	218	U
32	1a	243	G
32	1a	247	G
32	1a	255	G
32	1a	262	G
32	1a	263	C
32	1a	277	G
32	1a	285	G
32	1a	297	G
32	1a	313	G
32	1a	317	A
32	1a	324	C
32	1a	325	A
32	1a	337	C
32	1a	338	C
32	1a	342	G
32	1a	343	G
32	1a	344	G
32	1a	348	C
32	1a	349	A
32	1a	350	G
32	1a	351	C
32	1a	363	U
32	1a	368	C
32	1a	369	A
32	1a	379	A
32	1a	380	G
32	1a	386	C
32	1a	393	A
32	1a	394	C

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Mol	Chain	Res	Type
32	1a	402	G
32	1a	408	A
32	1a	409	G
32	1a	419	G
32	1a	420	G
32	1a	425	U
32	1a	435	A
32	1a	437	C
32	1a	441	G
32	1a	447	A
32	1a	449	C
32	1a	455	A
32	1a	456	C
32	1a	457	G
32	1a	467	A
32	1a	470	G
32	1a	477	G
32	1a	481	A
32	1a	482	U
32	1a	489	G
32	1a	493	A
32	1a	494	A
32	1a	495	C
32	1a	496	U
32	1a	502	C
32	1a	503	C
32	1a	508	G
32	1a	511	G
32	1a	515	U
32	1a	516	A
32	1a	517	A
32	1a	529	C
32	1a	531	A
32	1a	543	A
32	1a	545	U
32	1a	556	A
32	1a	557	A
32	1a	560	G
32	1a	576	G
32	1a	601	G
32	1a	614	G
32	1a	623	G

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Mol	Chain	Res	Type
32	1a	625	U
32	1a	637	A
32	1a	649	A
32	1a	671	A
32	1a	672	G
32	1a	677	G
32	1a	687	G
32	1a	707	U
32	1a	719	C
32	1a	733	C
32	1a	739	G
32	1a	750	A
32	1a	761	A
32	1a	776	A
32	1a	777	U
32	1a	778	A
32	1a	790	C
32	1a	799	A
32	1a	801	C
32	1a	805	G
32	1a	812	A
32	1a	813	G
32	1a	820	G
32	1a	822	G
32	1a	824	C
32	1a	825	U
32	1a	826	C
32	1a	837	A
32	1a	838	A
32	1a	848	U
32	1a	850	A
32	1a	852	G
32	1a	880	G
32	1a	904	G
32	1a	905	G
32	1a	909	C
32	1a	910	C
32	1a	912	C
32	1a	913	A
32	1a	914	C
32	1a	938	U
32	1a	939	U

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Mol	Chain	Res	Type
32	1a	946	A
32	1a	947	A
32	1a	949	G
32	1a	950	C
32	1a	952	A
32	1a	953	A
32	1a	954	G
32	1a	955	A
32	1a	960	U
32	1a	961	A
32	1a	970	U
32	1a	971	G
32	1a	972	A
32	1a	980	G
32	1a	982	G
32	1a	983	A
32	1a	984	A
32	1a	987	C
32	1a	988	G
32	1a	990	G
32	1a	992	G
32	1a	995	A
32	1a	1001	G
32	1a	1027	A
32	1a	1037	C
32	1a	1048	U
32	1a	1049	C
32	1a	1064	G
32	1a	1077	G
32	1a	1078	U
32	1a	1084	A
32	1a	1089	G
32	1a	1091	G
32	1a	1106	A
32	1a	1107	G
32	1a	1108	U
32	1a	1113	A
32	1a	1115	C
32	1a	1117	G
32	1a	1119	U
32	1a	1120	C
32	1a	1121	G

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Mol	Chain	Res	Type
32	1a	1122	G
32	1a	1123	C
32	1a	1124	C
32	1a	1129	A
32	1a	1135	A
32	1a	1138	G
32	1a	1142	U
32	1a	1143	G
32	1a	1149	G
32	1a	1158	A
32	1a	1165	A
32	1a	1166	G
32	1a	1178	U
32	1a	1179	G
32	1a	1184	G
32	1a	1194	U
32	1a	1195	A
32	1a	1196	C
32	1a	1204	G
32	1a	1209	A
32	1a	1220	A
32	1a	1238	A
32	1a	1239	U
32	1a	1240	G
32	1a	1242	C
32	1a	1245	C
32	1a	1252	C
32	1a	1260	U
32	1a	1261	A
32	1a	1262	A
32	1a	1268	A
32	1a	1269	A
32	1a	1272	G
32	1a	1279	C
32	1a	1281	A
32	1a	1282	G
32	1a	1284	U
32	1a	1287	G
32	1a	1294	G
32	1a	1296	C
32	1a	1300	A
32	1a	1301	A

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Mol	Chain	Res	Type
32	1a	1320	G
32	1a	1322	A
32	1a	1328	A
32	1a	1329	G
32	1a	1335	G
32	1a	1341	C
32	1a	1342	A
32	1a	1345	C
32	1a	1353	G
32	1a	1360	A
32	1a	1380	C
32	1a	1383	C
32	1a	1389	U
32	1a	1402	G
32	1a	1424	G
32	1a	1425	G
32	1a	1426	G
32	1a	1432	A
32	1a	1433	C
32	1a	1434	G
32	1a	1465	G
32	1a	1475	G
32	1a	1481	A
32	1a	1482	G
32	1a	1483	G
32	1a	1484	U
32	1a	1495	G
32	1a	1507	G
32	1a	1508	G
53	1v	15	A
54	1x	6	G
54	1x	9	G
54	1x	13	C
54	1x	16	C
54	1x	17	C
54	1x	17(A)	U
54	1x	19	G
54	1x	20	U
54	1x	21	A
54	1x	42	G
54	1x	47	U
54	1x	50	U

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Mol	Chain	Res	Type
54	1x	56	C
54	1x	65	C
54	1x	70	G
54	1x	76	A
1	2A	9	G
1	2A	11	U
1	2A	12	A
1	2A	13	A
1	2A	14	G
1	2A	33	C
1	2A	35	G
1	2A	44	C
1	2A	47	A
1	2A	49	G
1	2A	56	G
1	2A	61	U
1	2A	68	G
1	2A	69	A
1	2A	72	A
1	2A	73	G
1	2A	77	G
1	2A	81	G
1	2A	82	A
1	2A	86	G
1	2A	88	U
1	2A	91	C
1	2A	93	G
1	2A	99	G
1	2A	115	A
1	2A	116	A
1	2A	117	U
1	2A	130	C
1	2A	138	A
1	2A	154	C
1	2A	155	U
1	2A	161	G
1	2A	169	A
1	2A	170	A
1	2A	184	A
1	2A	185	A
1	2A	187	A
1	2A	193	G

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Mol	Chain	Res	Type
1	2A	203	G
1	2A	204	A
1	2A	209	A
1	2A	210	A
1	2A	211	A
1	2A	212	G
1	2A	217	A
1	2A	221	A
1	2A	227	U
1	2A	236	G
1	2A	237	C
1	2A	254	G
1	2A	268	G
1	2A	270	U
1	2A	271	U
1	2A	272	G
1	2A	273	U
1	2A	274	C
1	2A	287	U
1	2A	288	G
1	2A	300	C
1	2A	301	A
1	2A	317	A
1	2A	321	G
1	2A	334	A
1	2A	347	A
1	2A	350	G
1	2A	352	G
1	2A	353	A
1	2A	356	G
1	2A	357	C
1	2A	361	G
1	2A	365	G
1	2A	368	A
1	2A	375	G
1	2A	377	G
1	2A	385	U
1	2A	386	G
1	2A	412	G
1	2A	422	G
1	2A	425	G
1	2A	431	U

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Mol	Chain	Res	Type
1	2A	436	G
1	2A	437	G
1	2A	438	A
1	2A	441	A
1	2A	448	A
1	2A	454	A
1	2A	461	C
1	2A	468	A
1	2A	469	C
1	2A	480	C
1	2A	481	C
1	2A	482	A
1	2A	495	A
1	2A	506	G
1	2A	507	A
1	2A	516	A
1	2A	528	U
1	2A	529	A
1	2A	533	C
1	2A	552	A
1	2A	553	A
1	2A	555	C
1	2A	556	A
1	2A	557	G
1	2A	568	G
1	2A	573	G
1	2A	585	G
1	2A	595	G
1	2A	596	C
1	2A	597	A
1	2A	608	A
1	2A	625	A
1	2A	626	G
1	2A	629	U
1	2A	639	A
1	2A	640	G
1	2A	641	G
1	2A	651	A
1	2A	658	C
1	2A	661	A
1	2A	669	C
1	2A	670	A

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Mol	Chain	Res	Type
1	2A	671	G
1	2A	678	A
1	2A	697	G
1	2A	699	A
1	2A	732	G
1	2A	772	G
1	2A	776	C
1	2A	811	G
1	2A	821	G
1	2A	822	G
1	2A	828	A
1	2A	830	A
1	2A	831	G
1	2A	836	C
1	2A	838	G
1	2A	851	G
1	2A	858	C
1	2A	865	A
1	2A	873	U
1	2A	874	U
1	2A	893	U
1	2A	903	C
1	2A	905	G
1	2A	913	C
1	2A	915	G
1	2A	926	G
1	2A	930	C
1	2A	932	C
1	2A	933	A
1	2A	934	C
1	2A	935	C
1	2A	936	A
1	2A	938	C
1	2A	941	A
1	2A	942	C
1	2A	955	A
1	2A	960	C
1	2A	962	A
1	2A	968	C
1	2A	976	G
1	2A	982	G
1	2A	985	A

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Mol	Chain	Res	Type
1	2A	989	A
1	2A	990	G
1	2A	1001	A
1	2A	1003	A
1	2A	1005	C
1	2A	1018	G
1	2A	1019	C
1	2A	1028	A
1	2A	1041	A
1	2A	1042	G
1	2A	1044	U
1	2A	1050	C
1	2A	1051	C
1	2A	1057	U
1	2A	1058	C
1	2A	1062	G
1	2A	1065	A
1	2A	1066	A
1	2A	1067	G
1	2A	1070	G
1	2A	1071	U
1	2A	1072	A
1	2A	1078	U
1	2A	1083	C
1	2A	1084	G
1	2A	1086	C
1	2A	1088	C
1	2A	1090	A
1	2A	1091	A
1	2A	1092	G
1	2A	1096	G
1	2A	1100	G
1	2A	1103	G
1	2A	1104	G
1	2A	1105	U
1	2A	1106	U
1	2A	1107	G
1	2A	1108	G
1	2A	1110	U
1	2A	1115	A
1	2A	1116	G
1	2A	1118	A

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Mol	Chain	Res	Type
1	2A	1120	C
1	2A	1121	C
1	2A	1126	U
1	2A	1128	U
1	2A	1131	A
1	2A	1133	A
1	2A	1142	U
1	2A	1143	A
1	2A	1149	C
1	2A	1150	U
1	2A	1156	A
1	2A	1157	G
1	2A	1158	U
1	2A	1160	G
1	2A	1161	C
1	2A	1167	G
1	2A	1175	U
1	2A	1179	C
1	2A	1180	G
1	2A	1183	G
1	2A	1187	A
1	2A	1200	A
1	2A	1216	G
1	2A	1249	U
1	2A	1254	A
1	2A	1264	A
1	2A	1289	G
1	2A	1298	A
1	2A	1301	G
1	2A	1316	G
1	2A	1317	A
1	2A	1332	A
1	2A	1337	U
1	2A	1345	U
1	2A	1346	A
1	2A	1348	G
1	2A	1359	C
1	2A	1364	G
1	2A	1372	C
1	2A	1374	U
1	2A	1387	A
1	2A	1390	C

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Mol	Chain	Res	Type
1	2A	1404	A
1	2A	1405	A
1	2A	1410	A
1	2A	1413	G
1	2A	1415	C
1	2A	1423	A
1	2A	1425	G
1	2A	1429	A
1	2A	1430	G
1	2A	1431	C
1	2A	1436	U
1	2A	1445	G
1	2A	1448	C
1	2A	1461	G
1	2A	1462	C
1	2A	1465	U
1	2A	1466	G
1	2A	1473	C
1	2A	1490	A
1	2A	1491	C
1	2A	1495	A
1	2A	1496	G
1	2A	1505	G
1	2A	1506	A
1	2A	1513	C
1	2A	1517	A
1	2A	1528	G
1	2A	1534	U
1	2A	1535	A
1	2A	1538	C
1	2A	1542	U
1	2A	1554	C
1	2A	1555	A
1	2A	1570	G
1	2A	1587	G
1	2A	1588	A
1	2A	1589	C
1	2A	1590	A
1	2A	1591	A
1	2A	1604	A
1	2A	1605	G
1	2A	1612	A

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Mol	Chain	Res	Type
1	2A	1615	A
1	2A	1624	U
1	2A	1630	C
1	2A	1631	A
1	2A	1640	G
1	2A	1652	C
1	2A	1653	A
1	2A	1654	A
1	2A	1655	A
1	2A	1663	A
1	2A	1686	C
1	2A	1694	C
1	2A	1700	A
1	2A	1715	A
1	2A	1720	G
1	2A	1721	C
1	2A	1746	A
1	2A	1765	G
1	2A	1766	A
1	2A	1767	U
1	2A	1775	G
1	2A	1786	G
1	2A	1788	G
1	2A	1792	A
1	2A	1793	G
1	2A	1794	G
1	2A	1799	G
1	2A	1803	A
1	2A	1810	A
1	2A	1820	C
1	2A	1821	A
1	2A	1830	C
1	2A	1831	G
1	2A	1842	A
1	2A	1846	G
1	2A	1859	A
1	2A	1877	A
1	2A	1889	A
1	2A	1891	G
1	2A	1898	A
1	2A	1899	G
1	2A	1905	A

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Mol	Chain	Res	Type
1	2A	1921	A
1	2A	1927	G
1	2A	1934	A
1	2A	1935	C
1	2A	1936	U
1	2A	1950	G
1	2A	1951	G
1	2A	1957	A
1	2A	1959	A
1	2A	1976	U
1	2A	1984	U
1	2A	1987	A
1	2A	1988	C
1	2A	1991	A
1	2A	1992	A
1	2A	1993	A
1	2A	2005	G
1	2A	2014	U
1	2A	2018	G
1	2A	2041	A
1	2A	2044	G
1	2A	2052	A
1	2A	2054	A
1	2A	2060	C
1	2A	2064	C
1	2A	2067	G
1	2A	2073	G
1	2A	2076	C
1	2A	2077	G
1	2A	2081	A
1	2A	2082	G
1	2A	2083	A
1	2A	2090	G
1	2A	2120	U
1	2A	2125	G
1	2A	2209	C
1	2A	2213	G
1	2A	2217	C
1	2A	2219	A
1	2A	2226	G
1	2A	2227	G
1	2A	2228	A

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Mol	Chain	Res	Type
1	2A	2236	A
1	2A	2246	G
1	2A	2250	G
1	2A	2278	A
1	2A	2280	A
1	2A	2286	C
1	2A	2289	A
1	2A	2291	G
1	2A	2294	C
1	2A	2298	A
1	2A	2300	G
1	2A	2308	C
1	2A	2316	A
1	2A	2318	G
1	2A	2319	G
1	2A	2320	A
1	2A	2328	C
1	2A	2329	G
1	2A	2330	G
1	2A	2331	A
1	2A	2332	G
1	2A	2336	G
1	2A	2345	G
1	2A	2354	C
1	2A	2358	C
1	2A	2361	C
1	2A	2387	A
1	2A	2394	G
1	2A	2396	C
1	2A	2417	U
1	2A	2421	G
1	2A	2424	G
1	2A	2425	G
1	2A	2433	A
1	2A	2434	U
1	2A	2436	A
1	2A	2439	G
1	2A	2440	G
1	2A	2441	A
1	2A	2446	A
1	2A	2450	A
1	2A	2452	C

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Mol	Chain	Res	Type
1	2A	2459	A
1	2A	2476	C
1	2A	2485	C
1	2A	2487	A
1	2A	2488	C
1	2A	2491	C
1	2A	2511	U
1	2A	2513	G
1	2A	2516	G
1	2A	2517	U
1	2A	2529	A
1	2A	2531	C
1	2A	2565	U
1	2A	2566	U
1	2A	2577	A
1	2A	2578	G
1	2A	2580	G
1	2A	2584	C
1	2A	2593	G
1	2A	2597	C
1	2A	2613	A
1	2A	2620	U
1	2A	2622	U
1	2A	2623	C
1	2A	2624	U
1	2A	2626	U
1	2A	2640	A
1	2A	2641	G
1	2A	2665	A
1	2A	2674	G
1	2A	2700	U
1	2A	2701	C
1	2A	2702	C
1	2A	2713	U
1	2A	2714	C
1	2A	2724	A
1	2A	2725	A
1	2A	2738	U
1	2A	2745	A
1	2A	2758	U
1	2A	2763	G
1	2A	2776	A

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Mol	Chain	Res	Type
1	2A	2777	A
1	2A	2778	G
1	2A	2790	A
1	2A	2801	C
1	2A	2805	G
1	2A	2806	C
1	2A	2812	G
1	2A	2814	C
1	2A	2827	G
1	2A	2829	A
1	2A	2830	A
1	2A	2842	G
1	2A	2843	G
1	2A	2844	A
1	2A	2881	G
1	2A	2889	C
1	2A	2900	A
1	2A	2902	G
1	2A	2905	U
2	2B	2	C
2	2B	7	G
2	2B	9	G
2	2B	13	A
2	2B	16	G
2	2B	28	C
2	2B	32	C
2	2B	34	U
2	2B	35	U
2	2B	37	C
2	2B	43	C
2	2B	45	A
2	2B	46	A
2	2B	52	A
2	2B	56	G
2	2B	59	A
2	2B	63	G
2	2B	67	G
2	2B	73	A
2	2B	85	G
2	2B	90	A
2	2B	106	G
2	2B	110	G

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Mol	Chain	Res	Type
2	2B	112	U
2	2B	116	G
2	2B	120	A
32	2a	6	U
32	2a	10	G
32	2a	23	G
32	2a	33	A
32	2a	39	G
32	2a	40	G
32	2a	43	G
32	2a	48	C
32	2a	49	C
32	2a	51	A
32	2a	52	A
32	2a	53	G
32	2a	66	U
32	2a	67	G
32	2a	84	A
32	2a	85	C
32	2a	91	G
32	2a	95	A
32	2a	110	A
32	2a	115	C
32	2a	124	G
32	2a	126	C
32	2a	137	G
32	2a	138	A
32	2a	158	C
32	2a	169	C
32	2a	177	U
32	2a	189	U
32	2a	190	U
32	2a	202	A
32	2a	210	U
32	2a	211	U
32	2a	212	G
32	2a	216	G
32	2a	243	G
32	2a	247	G
32	2a	262	G
32	2a	263	C
32	2a	275	A

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Mol	Chain	Res	Type
32	2a	277	G
32	2a	285	G
32	2a	302	G
32	2a	317	A
32	2a	324	C
32	2a	326	C
32	2a	328	G
32	2a	337	C
32	2a	340	A
32	2a	346	G
32	2a	347	G
32	2a	348	C
32	2a	349	A
32	2a	350	G
32	2a	363	U
32	2a	368	C
32	2a	380	G
32	2a	394	C
32	2a	402	G
32	2a	408	A
32	2a	418	C
32	2a	425	U
32	2a	426	A
32	2a	428	A
32	2a	435	A
32	2a	437	C
32	2a	447	A
32	2a	452	C
32	2a	455	A
32	2a	456	C
32	2a	457	G
32	2a	463	A
32	2a	468	C
32	2a	470	G
32	2a	481	A
32	2a	482	U
32	2a	489	G
32	2a	490	G
32	2a	493	A
32	2a	494	A
32	2a	495	C
32	2a	501	G

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Mol	Chain	Res	Type
32	2a	502	C
32	2a	505	G
32	2a	511	G
32	2a	515	U
32	2a	516	A
32	2a	517	A
32	2a	520	C
32	2a	529	C
32	2a	531	A
32	2a	543	A
32	2a	544	U
32	2a	545	U
32	2a	546	C
32	2a	548	C
32	2a	552	G
32	2a	556	A
32	2a	557	A
32	2a	560	G
32	2a	561	G
32	2a	580	C
32	2a	614	G
32	2a	634	G
32	2a	636	U
32	2a	637	A
32	2a	649	A
32	2a	671	A
32	2a	672	G
32	2a	677	G
32	2a	679	A
32	2a	692	C
32	2a	696	A
32	2a	707	U
32	2a	708	G
32	2a	712	A
32	2a	715	G
32	2a	733	C
32	2a	737	A
32	2a	739	G
32	2a	744	G
32	2a	761	A
32	2a	772	U
32	2a	777	U

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Mol	Chain	Res	Type
32	2a	778	A
32	2a	799	A
32	2a	800	A
32	2a	801	C
32	2a	805	G
32	2a	812	A
32	2a	813	G
32	2a	820	G
32	2a	822	G
32	2a	823	U
32	2a	824	C
32	2a	825	U
32	2a	826	C
32	2a	828	U
32	2a	837	A
32	2a	850	A
32	2a	852	G
32	2a	880	G
32	2a	892	A
32	2a	893	A
32	2a	898	U
32	2a	904	G
32	2a	905	G
32	2a	908	C
32	2a	909	C
32	2a	912	C
32	2a	913	A
32	2a	920	G
32	2a	939	U
32	2a	944	G
32	2a	946	A
32	2a	947	A
32	2a	949	G
32	2a	952	A
32	2a	953	A
32	2a	954	G
32	2a	955	A
32	2a	966	G
32	2a	967	C
32	2a	970	U
32	2a	971	G
32	2a	977	C

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Mol	Chain	Res	Type
32	2a	979	A
32	2a	981	G
32	2a	984	A
32	2a	988	G
32	2a	1000	G
32	2a	1001	G
32	2a	1002	G
32	2a	1028	C
32	2a	1029	A
32	2a	1036	G
32	2a	1037	C
32	2a	1038	A
32	2a	1039	U
32	2a	1048	U
32	2a	1049	C
32	2a	1050	A
32	2a	1061	U
32	2a	1064	G
32	2a	1071	G
32	2a	1077	G
32	2a	1078	U
32	2a	1083	C
32	2a	1084	A
32	2a	1096	C
32	2a	1100	G
32	2a	1101	C
32	2a	1105	U
32	2a	1107	G
32	2a	1110	G
32	2a	1112	C
32	2a	1113	A
32	2a	1117	G
32	2a	1118	U
32	2a	1119	U
32	2a	1120	C
32	2a	1121	G
32	2a	1122	G
32	2a	1123	C
32	2a	1129	A
32	2a	1140	A
32	2a	1141	C
32	2a	1142	U

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Mol	Chain	Res	Type
32	2a	1149	G
32	2a	1165	A
32	2a	1172	G
32	2a	1178	U
32	2a	1179	G
32	2a	1184	G
32	2a	1191	C
32	2a	1193	U
32	2a	1194	U
32	2a	1196	C
32	2a	1210	C
32	2a	1220	A
32	2a	1222	U
32	2a	1223	G
32	2a	1235	G
32	2a	1236	C
32	2a	1239	U
32	2a	1240	G
32	2a	1242	C
32	2a	1244	C
32	2a	1255	G
32	2a	1260	U
32	2a	1262	A
32	2a	1263	U
32	2a	1264	C
32	2a	1267	A
32	2a	1268	A
32	2a	1269	A
32	2a	1280	C
32	2a	1281	A
32	2a	1282	G
32	2a	1284	U
32	2a	1285	C
32	2a	1287	G
32	2a	1304	C
32	2a	1305	G
32	2a	1320	G
32	2a	1328	A
32	2a	1329	G
32	2a	1335	G
32	2a	1341	C
32	2a	1342	A

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Mol	Chain	Res	Type
32	2a	1345	C
32	2a	1347	U
32	2a	1351	G
32	2a	1367	C
32	2a	1380	C
32	2a	1381	A
32	2a	1388	G
32	2a	1399	G
32	2a	1402	G
32	2a	1425	G
32	2a	1426	G
32	2a	1427	A
32	2a	1431	U
32	2a	1432	A
32	2a	1433	C
32	2a	1434	G
32	2a	1465	G
32	2a	1475	G
32	2a	1480	A
32	2a	1481	A
32	2a	1482	G
32	2a	1484	U
32	2a	1485	A
32	2a	1495	G
32	2a	1498	G
32	2a	1507	G
32	2a	1508	G
32	2a	1509	A
32	2a	1510	U
53	2v	15	A
54	2x	6	G
54	2x	8	4SU
54	2x	9	G
54	2x	13	C
54	2x	16	C
54	2x	17	C
54	2x	17(A)	U
54	2x	19	G
54	2x	20	U
54	2x	21	A
54	2x	42	G
54	2x	47	U

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Mol	Chain	Res	Type
54	2x	50	U
54	2x	56	C
54	2x	61	C
54	2x	65	C
54	2x	70	G
54	2x	76	A

All (47) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	183	A
1	1A	184	A
1	1A	187	A
1	1A	270	U
1	1A	301	A
1	1A	715	G
1	1A	792	A
1	1A	810	A
1	1A	1002	U
1	1A	1018	G
1	1A	1153	U
1	1A	1220	G
1	1A	1285	U
1	1A	1425	G
1	1A	1465	U
1	1A	1653	A
1	1A	1709	C
1	1A	2013	G
1	1A	2417	U
1	1A	2433	A
1	1A	2441	A
1	1A	2700	U
1	2A	11	U
1	2A	183	A
1	2A	184	A
1	2A	300	C
1	2A	516	A
1	2A	670	A
1	2A	810	A
1	2A	902	C
1	2A	1047	G
1	2A	1071	U

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Mol	Chain	Res	Type
1	2A	1102	A
1	2A	1114	A
1	2A	1238	A
1	2A	1424	A
1	2A	1465	U
1	2A	1604	A
1	2A	1820	C
1	2A	1934	A
1	2A	2013	G
1	2A	2328	C
1	2A	2353	C
1	2A	2450	A
1	2A	2700	U
2	2B	42	C
2	2B	45	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
54	4SU	2x	8	54	18,21,22	1.93	5 (27%)	25,30,33	1.23	3 (12%)
54	5MC	1x	32	54	19,22,23	1.73	3 (15%)	26,32,35	1.22	3 (11%)
54	PSU	1x	55	56,54	18,21,22	1.35	2 (11%)	21,30,33	2.01	3 (14%)
54	5MU	2x	54	54	19,22,23	1.41	5 (26%)	27,32,35	2.07	7 (25%)
54	5MU	1x	54	54	19,22,23	1.54	5 (26%)	27,32,35	1.84	6 (22%)
54	5MC	2x	32	54	19,22,23	1.60	2 (10%)	26,32,35	1.13	3 (11%)
54	PSU	2x	55	54	18,21,22	1.37	2 (11%)	21,30,33	1.97	4 (19%)
54	4SU	1x	8	54	18,21,22	2.14	4 (22%)	25,30,33	1.36	4 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	4SU	2x	8	54	-	0/7/25/26	0/2/2/2
54	5MC	1x	32	54	-	0/7/25/26	0/2/2/2
54	PSU	1x	55	56,54	-	2/7/25/26	0/2/2/2
54	5MU	2x	54	54	-	0/7/25/26	0/2/2/2
54	5MU	1x	54	54	-	0/7/25/26	0/2/2/2
54	5MC	2x	32	54	-	0/7/25/26	0/2/2/2
54	PSU	2x	55	54	-	2/7/25/26	0/2/2/2
54	4SU	1x	8	54	-	1/7/25/26	0/2/2/2

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1x	32	5MC	C5-C4	6.27	1.48	1.44
54	2x	32	5MC	C5-C4	5.63	1.48	1.44
54	1x	8	4SU	C4-N3	-4.94	1.32	1.37
54	1x	8	4SU	C4-S4	-4.59	1.60	1.68
54	2x	8	4SU	C4-N3	-4.27	1.33	1.37
54	2x	8	4SU	C4-S4	-4.25	1.61	1.68
54	2x	55	PSU	C6-C5	3.88	1.39	1.35
54	1x	8	4SU	C2-N3	-3.83	1.31	1.38
54	1x	55	PSU	C6-C5	3.59	1.39	1.35
54	1x	54	5MU	C6-C5	3.23	1.39	1.34
54	1x	8	4SU	C5-C4	-3.21	1.38	1.42
54	1x	54	5MU	C4-N3	-3.12	1.33	1.38
54	2x	8	4SU	C5-C4	-3.12	1.38	1.42
54	2x	32	5MC	C6-C5	3.00	1.39	1.34
54	1x	32	5MC	C6-C5	2.91	1.39	1.34
54	2x	54	5MU	C6-C5	2.81	1.39	1.34
54	1x	54	5MU	C2-N1	2.51	1.42	1.38
54	2x	54	5MU	C4-C5	2.49	1.48	1.44
54	2x	54	5MU	C4-N3	-2.46	1.34	1.38
54	2x	54	5MU	C2-N1	2.44	1.42	1.38
54	1x	54	5MU	C4-C5	2.41	1.48	1.44
54	1x	32	5MC	C6-N1	-2.35	1.34	1.38
54	1x	55	PSU	C4-N3	-2.33	1.34	1.38
54	2x	8	4SU	C2-N3	-2.32	1.33	1.38
54	2x	8	4SU	O2-C2	2.32	1.27	1.23
54	2x	55	PSU	C4-N3	-2.29	1.34	1.38
54	1x	54	5MU	C2-N3	-2.13	1.34	1.38
54	2x	54	5MU	C6-N1	-2.05	1.34	1.38

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1x	55	PSU	N1-C2-N3	6.13	121.64	115.17
54	2x	55	PSU	N1-C2-N3	6.03	121.53	115.17
54	2x	54	5MU	N3-C2-N1	5.19	121.64	114.89
54	2x	54	5MU	C4-N3-C2	-4.96	120.83	127.34
54	1x	54	5MU	N3-C2-N1	4.93	121.30	114.89
54	1x	54	5MU	C4-N3-C2	-4.31	121.69	127.34
54	1x	55	PSU	O2-C2-N1	-4.12	118.54	122.79
54	2x	54	5MU	C5-C4-N3	4.11	118.89	115.32
54	2x	55	PSU	C4-N3-C2	-4.05	120.79	126.37
54	1x	32	5MC	C5-C6-N1	-3.96	119.01	123.31
54	1x	55	PSU	C4-N3-C2	-3.83	121.09	126.37
54	2x	54	5MU	O4-C4-C5	-3.82	120.55	124.92
54	1x	54	5MU	C5-C4-N3	3.78	118.61	115.32
54	1x	8	4SU	C6-C5-C4	-3.65	116.79	119.95
54	1x	54	5MU	C5-C6-N1	-3.42	119.60	123.31
54	1x	8	4SU	C5-C4-N3	3.29	117.81	114.75
54	2x	8	4SU	C1'-N1-C2	3.27	123.47	117.59
54	2x	55	PSU	O2-C2-N1	-3.21	119.48	122.79
54	2x	32	5MC	C5-C6-N1	-2.97	120.08	123.31
54	2x	8	4SU	C5-C4-N3	2.90	117.45	114.75
54	2x	32	5MC	C5-C4-N3	-2.87	118.81	121.75
54	1x	32	5MC	C5-C4-N3	-2.77	118.92	121.75
54	2x	54	5MU	O2-C2-N1	-2.76	119.20	122.80
54	2x	54	5MU	C5-C6-N1	-2.75	120.33	123.31
54	1x	54	5MU	O4-C4-C5	-2.70	121.83	124.92
54	1x	8	4SU	O2-C2-N1	2.60	126.18	122.80
54	2x	32	5MC	O2-C2-N3	-2.55	118.32	122.33
54	2x	8	4SU	C6-C5-C4	-2.43	117.84	119.95
54	2x	55	PSU	C5-C6-N1	-2.39	118.82	122.14
54	2x	54	5MU	C5M-C5-C4	2.20	121.13	118.78
54	1x	32	5MC	O2-C2-N3	-2.14	118.96	122.33
54	1x	8	4SU	S4-C4-N3	-2.08	118.03	120.20
54	1x	54	5MU	O2-C2-N1	-2.06	120.11	122.80

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	1x	55	PSU	O4'-C4'-C5'-O5'
54	2x	55	PSU	O4'-C4'-C5'-O5'
54	1x	55	PSU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
54	2x	55	PSU	C3'-C4'-C5'-O5'
54	1x	8	4SU	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	2x	8	4SU	1	0
54	1x	8	4SU	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2615 ligands modelled in this entry, 2613 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	2d	501	35	0,12,12	-	-	-		
58	SF4	1d	501	35	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	2d	501	35	-	-	0/6/5/5
58	SF4	1d	501	35	-	-	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.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	2d	501	SF4	6	0
58	1d	501	SF4	2	0

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	1A	2746/2915 (94%)	-0.43	34 (1%) 76 75	20, 40, 84, 109	0
1	2A	2790/2915 (95%)	-0.35	29 (1%) 79 78	24, 44, 91, 107	0
2	1B	120/121 (99%)	0.19	1 (0%) 82 81	34, 63, 78, 92	0
2	2B	120/121 (99%)	0.63	4 (3%) 49 45	40, 69, 80, 94	0
3	1D	275/276 (99%)	-0.13	1 (0%) 88 87	19, 39, 57, 76	0
3	2D	275/276 (99%)	-0.11	3 (1%) 78 76	20, 41, 59, 76	0
4	1E	204/206 (99%)	-0.09	0 100 100	19, 42, 63, 80	0
4	2E	204/206 (99%)	-0.02	1 (0%) 87 86	22, 45, 65, 81	0
5	1F	203/210 (96%)	0.18	3 (1%) 72 70	19, 48, 74, 86	0
5	2F	203/210 (96%)	0.23	2 (0%) 79 78	22, 52, 76, 88	0
6	1G	181/182 (99%)	0.79	11 (6%) 27 24	53, 69, 81, 95	0
6	2G	181/182 (99%)	1.24	23 (12%) 8 7	58, 72, 83, 96	0
7	1H	174/180 (96%)	0.82	7 (4%) 42 38	45, 63, 75, 85	0
7	2H	174/180 (96%)	1.01	10 (5%) 29 26	53, 68, 78, 86	0
8	1I	146/148 (98%)	0.66	4 (2%) 56 53	48, 74, 83, 89	0
8	2I	146/148 (98%)	0.74	5 (3%) 48 44	50, 75, 83, 87	0
9	1N	140/140 (100%)	0.20	1 (0%) 84 83	28, 44, 65, 78	0
9	2N	140/140 (100%)	0.20	0 100 100	31, 49, 68, 79	0
10	1O	122/122 (100%)	-0.03	0 100 100	30, 42, 61, 66	0
10	2O	122/122 (100%)	-0.03	1 (0%) 82 81	33, 46, 62, 67	0
11	1P	149/150 (99%)	0.25	1 (0%) 84 83	21, 53, 74, 86	0
11	2P	149/150 (99%)	0.27	0 100 100	24, 56, 75, 84	0
12	1Q	141/141 (100%)	0.34	3 (2%) 63 61	33, 47, 63, 80	0
12	2Q	141/141 (100%)	0.36	3 (2%) 63 61	36, 51, 66, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	0.05	0 100 100	27, 38, 54, 60	0
13	2R	118/118 (100%)	-0.03	0 100 100	29, 40, 56, 61	0
14	1S	110/112 (98%)	0.06	2 (1%) 67 65	33, 50, 63, 71	0
14	2S	110/112 (98%)	1.60	37 (33%) 1 1	44, 77, 85, 92	0
15	1T	131/146 (89%)	-0.11	4 (3%) 51 48	27, 40, 70, 83	0
15	2T	131/146 (89%)	0.32	3 (2%) 61 58	43, 56, 77, 87	0
16	1U	116/118 (98%)	0.12	2 (1%) 69 67	21, 35, 54, 71	0
16	2U	116/118 (98%)	0.17	0 100 100	28, 41, 59, 72	0
17	1V	101/101 (100%)	0.14	1 (0%) 79 78	25, 47, 65, 79	0
17	2V	101/101 (100%)	0.24	1 (0%) 79 78	29, 52, 70, 79	0
18	1W	112/113 (99%)	-0.19	0 100 100	25, 33, 56, 86	0
18	2W	112/113 (99%)	-0.14	1 (0%) 81 80	27, 37, 57, 88	0
19	1X	95/96 (98%)	0.26	3 (3%) 50 46	30, 45, 65, 77	0
19	2X	95/96 (98%)	0.37	4 (4%) 40 37	34, 49, 67, 78	0
20	1Y	107/110 (97%)	0.53	1 (0%) 81 80	39, 57, 74, 84	0
20	2Y	107/110 (97%)	0.65	1 (0%) 81 80	44, 60, 76, 86	0
21	1Z	186/206 (90%)	0.61	3 (1%) 70 68	48, 67, 80, 87	0
21	2Z	186/206 (90%)	0.92	7 (3%) 44 40	53, 70, 81, 89	0
22	10	75/85 (88%)	0.30	1 (1%) 75 73	28, 45, 60, 67	0
22	20	75/85 (88%)	0.44	3 (4%) 42 38	31, 50, 63, 70	0
23	11	97/98 (98%)	0.24	2 (2%) 63 61	28, 47, 73, 80	0
23	21	97/98 (98%)	0.23	2 (2%) 63 61	31, 49, 73, 79	0
24	12	70/72 (97%)	0.61	5 (7%) 22 19	43, 55, 69, 78	0
24	22	70/72 (97%)	0.50	0 100 100	46, 59, 71, 77	0
25	13	59/60 (98%)	0.26	0 100 100	29, 42, 62, 73	0
25	23	59/60 (98%)	0.29	2 (3%) 48 44	34, 47, 66, 79	0
26	14	69/71 (97%)	1.10	11 (15%) 5 4	60, 81, 93, 96	0
26	24	69/71 (97%)	1.55	17 (24%) 2 1	68, 83, 95, 101	0
27	15	59/60 (98%)	-0.31	1 (1%) 69 67	19, 36, 52, 71	0
27	25	59/60 (98%)	-0.19	0 100 100	23, 38, 56, 72	0
28	16	53/54 (98%)	-0.01	0 100 100	37, 48, 65, 69	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.19	0 100 100	38, 51, 61, 69	0
29	17	48/49 (97%)	-0.12	1 (2%) 63 61	24, 30, 63, 75	0
29	27	48/49 (97%)	-0.15	1 (2%) 63 61	26, 32, 66, 75	0
30	18	64/65 (98%)	0.11	0 100 100	30, 39, 50, 58	0
30	28	64/65 (98%)	0.33	0 100 100	33, 42, 54, 59	0
31	19	37/37 (100%)	0.58	1 (2%) 56 53	38, 48, 65, 67	0
31	29	37/37 (100%)	0.94	4 (10%) 11 9	42, 52, 66, 71	0
32	1a	1477/1521 (97%)	0.25	32 (2%) 62 59	29, 71, 95, 112	0
32	2a	1483/1521 (97%)	0.47	47 (3%) 50 46	43, 77, 98, 110	0
33	1b	231/256 (90%)	1.14	33 (14%) 6 5	65, 81, 91, 101	0
33	2b	231/256 (90%)	1.34	41 (17%) 4 3	67, 86, 94, 102	0
34	1c	206/239 (86%)	1.13	21 (10%) 12 10	66, 82, 89, 95	0
34	2c	206/239 (86%)	1.35	39 (18%) 3 3	66, 83, 90, 96	0
35	1d	208/209 (99%)	1.06	20 (9%) 13 11	56, 76, 87, 95	0
35	2d	208/209 (99%)	0.92	14 (6%) 24 21	58, 73, 84, 89	0
36	1e	148/162 (91%)	0.56	2 (1%) 73 72	43, 66, 77, 86	0
36	2e	148/162 (91%)	0.85	7 (4%) 36 33	60, 74, 84, 91	0
37	1f	100/101 (99%)	0.66	2 (2%) 65 62	57, 72, 81, 84	0
37	2f	100/101 (99%)	0.67	2 (2%) 65 62	61, 74, 82, 87	0
38	1g	155/156 (99%)	0.88	20 (12%) 7 6	60, 74, 89, 97	0
38	2g	155/156 (99%)	1.20	29 (18%) 3 3	70, 83, 91, 96	0
39	1h	137/138 (99%)	0.58	1 (0%) 84 83	49, 66, 76, 78	0
39	2h	137/138 (99%)	0.98	11 (8%) 18 15	62, 75, 82, 88	0
40	1i	127/128 (99%)	1.44	29 (22%) 2 2	60, 80, 90, 94	0
40	2i	127/128 (99%)	2.04	58 (45%) 0 0	69, 89, 96, 102	0
41	1j	97/105 (92%)	1.80	36 (37%) 1 0	61, 85, 93, 97	0
41	2j	96/105 (91%)	2.08	51 (53%) 0 0	76, 89, 97, 102	0
42	1k	114/129 (88%)	0.44	2 (1%) 67 65	40, 67, 79, 92	0
42	2k	114/129 (88%)	0.76	4 (3%) 47 43	52, 76, 85, 90	0
43	1l	122/132 (92%)	0.57	5 (4%) 41 37	42, 62, 72, 81	0
43	2l	122/132 (92%)	0.80	4 (3%) 49 45	55, 67, 77, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	118/126 (93%)	1.01	7 (5%) 28 25	66, 79, 85, 91	0
44	2m	116/126 (92%)	1.58	29 (25%) 2 1	69, 81, 87, 92	0
45	1n	60/61 (98%)	1.67	15 (25%) 2 1	69, 81, 86, 92	0
45	2n	60/61 (98%)	2.55	40 (66%) 0 0	71, 82, 87, 92	0
46	1o	88/89 (98%)	0.62	3 (3%) 48 44	47, 64, 78, 85	0
46	2o	88/89 (98%)	0.67	1 (1%) 78 76	59, 71, 82, 89	0
47	1p	82/88 (93%)	1.36	12 (14%) 6 5	61, 77, 87, 92	0
47	2p	82/88 (93%)	0.99	6 (7%) 21 18	60, 70, 82, 89	0
48	1q	99/105 (94%)	0.73	1 (1%) 79 78	45, 65, 76, 78	0
48	2q	99/105 (94%)	0.75	4 (4%) 42 38	53, 71, 80, 86	0
49	1r	68/88 (77%)	0.57	3 (4%) 39 35	53, 68, 81, 87	0
49	2r	68/88 (77%)	0.79	3 (4%) 39 35	62, 74, 82, 90	0
50	1s	84/93 (90%)	1.33	12 (14%) 6 5	66, 80, 91, 94	0
50	2s	83/93 (89%)	2.01	35 (42%) 0 0	77, 90, 98, 104	0
51	1t	96/106 (90%)	1.19	18 (18%) 3 3	56, 73, 82, 88	0
51	2t	96/106 (90%)	0.97	12 (12%) 8 7	55, 72, 82, 86	0
52	1u	23/27 (85%)	1.77	12 (52%) 0 0	69, 75, 80, 81	0
52	2u	23/27 (85%)	1.98	8 (34%) 1 1	68, 78, 82, 82	0
53	1v	5/24 (20%)	1.22	2 (40%) 1 0	61, 64, 86, 94	0
53	2v	5/24 (20%)	0.94	0 100 100	65, 67, 86, 94	0
54	1x	72/77 (93%)	0.14	1 (1%) 73 72	37, 67, 85, 95	0
54	2x	72/77 (93%)	0.22	1 (1%) 73 72	39, 71, 87, 97	0
55	1z	16/20 (80%)	1.66	5 (31%) 1 1	30, 49, 74, 79	0
55	2z	16/20 (80%)	1.63	6 (37%) 1 0	32, 52, 76, 77	0
All	All	20528/21484 (95%)	0.32	1014 (4%) 35 31	19, 61, 90, 112	0

All (1014) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	6.6
32	1a	980	G	6.5
32	1a	981	G	5.9
38	1g	79	ARG	5.7
7	1H	2	SER	5.7

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Mol	Chain	Res	Type	RSRZ
40	2i	126	SER	5.6
40	2i	66	ARG	5.6
34	1c	2	GLY	5.5
55	2z	16	ILE	5.5
26	24	56	VAL	5.4
40	2i	15	ALA	5.4
1	1A	2815	G	5.3
20	1Y	1	MET	5.3
32	2a	981	G	5.1
50	2s	71	LEU	5.0
26	24	57	GLU	5.0
55	1z	16	ILE	5.0
1	1A	2813	C	4.9
45	1n	2	ALA	4.9
38	1g	80	VAL	4.8
41	1j	76	ASN	4.8
55	1z	13	PRO	4.8
38	1g	78	ARG	4.7
34	1c	207	VAL	4.7
45	2n	34	TYR	4.7
29	17	48	LYS	4.5
40	2i	29	ASN	4.4
50	2s	13	ASP	4.4
23	11	2	SER	4.4
45	2n	17	LYS	4.3
40	1i	15	ALA	4.3
38	2g	78	ARG	4.2
52	2u	6	ARG	4.2
40	1i	2	GLU	4.2
50	2s	12	ASP	4.2
33	2b	97	TRP	4.2
1	1A	8	U	4.2
14	2S	34	HIS	4.2
45	2n	33	VAL	4.1
33	2b	134	GLU	4.1
44	1m	4	ILE	4.1
50	2s	33	THR	4.1
26	14	59	PHE	4.1
32	2a	980	G	4.0
38	1g	83	ALA	4.0
51	1t	10	LEU	4.0
34	2c	186	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1268	A	4.0
50	2s	9	VAL	4.0
50	2s	38	SER	4.0
55	1z	15	PRO	4.0
44	2m	78	ILE	4.0
40	1i	106	ALA	4.0
33	2b	187	LEU	4.0
36	1e	22	GLY	4.0
55	2z	11	THR	3.9
45	2n	38	GLY	3.9
40	2i	5	TYR	3.9
35	1d	155	LEU	3.9
38	2g	83	ALA	3.9
45	2n	25	VAL	3.9
40	2i	36	TYR	3.8
40	2i	67	GLY	3.8
40	2i	65	VAL	3.8
45	2n	18	VAL	3.8
33	2b	237	ALA	3.8
51	1t	69	GLY	3.8
55	1z	12	PRO	3.8
26	14	57	GLU	3.8
41	2j	87	THR	3.8
45	2n	21	TYR	3.8
38	2g	16	LEU	3.8
41	1j	62	HIS	3.8
15	2T	131	ALA	3.8
26	24	49	PHE	3.8
26	24	50	VAL	3.8
22	20	10	THR	3.8
1	1A	2814	C	3.8
1	1A	2904	C	3.8
45	2n	5	ALA	3.8
32	1a	979	A	3.7
44	2m	102	ARG	3.7
38	1g	156	TRP	3.7
40	2i	62	TYR	3.7
38	2g	2	ALA	3.7
40	1i	72	GLY	3.7
1	1A	2811	A	3.7
55	2z	13	PRO	3.7
20	2Y	1	MET	3.7

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Mol	Chain	Res	Type	RSRZ
41	1j	98	ILE	3.7
52	2u	14	TRP	3.7
31	29	37	GLY	3.7
38	2g	7	ALA	3.7
24	12	69	ARG	3.6
1	1A	1149	C	3.6
33	1b	188	ALA	3.6
40	2i	14	VAL	3.6
29	27	48	LYS	3.6
45	2n	30	ALA	3.6
40	2i	21	PRO	3.6
33	1b	12	GLU	3.6
38	2g	38	LEU	3.6
40	2i	102	LEU	3.6
39	2h	131	GLY	3.6
50	1s	9	VAL	3.6
44	2m	118	ALA	3.6
40	2i	79	LEU	3.6
45	2n	15	LYS	3.6
45	1n	15	LYS	3.5
45	2n	37	PHE	3.5
48	2q	9	VAL	3.5
41	2j	40	LEU	3.5
41	2j	59	SER	3.5
41	1j	75	ILE	3.5
45	2n	3	ARG	3.5
51	1t	12	ALA	3.5
45	1n	16	PHE	3.5
47	2p	82	GLN	3.5
41	2j	8	LEU	3.5
43	1l	89	ARG	3.5
26	24	45	GLY	3.5
44	2m	75	ALA	3.5
41	1j	33	GLN	3.5
26	14	50	VAL	3.5
41	2j	65	LEU	3.5
50	2s	11	VAL	3.5
7	1H	58	GLU	3.5
41	2j	72	VAL	3.5
33	2b	31	TYR	3.4
51	1t	55	ILE	3.4
38	1g	84	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
41	1j	32	ALA	3.4
45	2n	8	GLU	3.4
47	1p	82	GLN	3.4
45	2n	16	PHE	3.4
33	2b	197	VAL	3.4
44	2m	60	VAL	3.4
33	1b	201	ILE	3.4
33	2b	101	MET	3.4
41	2j	100	THR	3.4
45	2n	22	THR	3.4
15	1T	130	ALA	3.4
38	2g	109	ASN	3.4
44	2m	97	PRO	3.4
45	2n	20	ALA	3.4
51	1t	9	ASN	3.4
26	14	49	PHE	3.4
40	2i	9	ARG	3.4
32	2a	1184	G	3.4
44	1m	2	ALA	3.4
44	1m	94	ARG	3.4
52	1u	15	ARG	3.4
41	2j	63	PHE	3.4
12	1Q	60	ARG	3.4
40	2i	42	ARG	3.4
50	2s	84	GLY	3.4
33	2b	133	LYS	3.3
40	2i	2	GLU	3.3
44	1m	102	ARG	3.3
50	1s	71	LEU	3.3
1	1A	2804	G	3.3
1	1A	2812	G	3.3
38	1g	16	LEU	3.3
34	2c	13	GLY	3.3
40	1i	13	ALA	3.3
41	2j	34	VAL	3.3
50	1s	13	ASP	3.3
12	1Q	59	ARG	3.3
1	1A	9	G	3.3
6	2G	53	LEU	3.3
44	2m	6	GLY	3.3
6	2G	50	ALA	3.3
41	2j	18	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
38	2g	84	ASN	3.3
40	2i	105	ASP	3.3
38	2g	156	TRP	3.2
40	2i	64	THR	3.2
41	1j	77	PRO	3.2
1	1A	2805	G	3.2
51	2t	25	ARG	3.2
40	1i	19	LEU	3.2
45	2n	49	HIS	3.2
41	1j	31	GLY	3.2
34	2c	180	ALA	3.2
53	1v	14	A	3.2
50	2s	40	ILE	3.2
1	1A	1220	G	3.2
32	2a	1077	G	3.2
32	2a	1265	G	3.2
40	2i	16	ARG	3.2
41	1j	52	GLY	3.2
14	2S	49	VAL	3.2
45	2n	7	ILE	3.2
47	1p	21	VAL	3.2
14	2S	58	LEU	3.2
33	1b	187	LEU	3.2
41	2j	16	LEU	3.2
41	2j	68	HIS	3.2
16	1U	117	GLN	3.2
14	2S	96	GLY	3.2
33	1b	127	ILE	3.2
41	1j	6	ILE	3.2
46	1o	87	ILE	3.2
14	2S	28	VAL	3.2
33	1b	7	VAL	3.2
40	2i	10	ARG	3.1
45	2n	35	ARG	3.1
44	2m	69	GLU	3.1
15	2T	130	ALA	3.1
6	2G	28	VAL	3.1
41	2j	44	VAL	3.1
32	2a	1206	G	3.1
34	1c	201	TYR	3.1
43	1l	91	LYS	3.1
50	2s	70	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
14	2S	54	LEU	3.1
35	1d	157	LEU	3.1
41	1j	71	LEU	3.1
50	2s	16	LEU	3.1
50	2s	2	PRO	3.1
36	2e	20	GLN	3.1
52	2u	13	ILE	3.1
33	1b	136	VAL	3.1
50	1s	85	LYS	3.1
14	2S	7	TYR	3.1
35	1d	162	LEU	3.1
1	1A	2901	G	3.1
55	2z	12	PRO	3.1
47	1p	22	THR	3.1
40	2i	76	ALA	3.1
41	1j	4	ILE	3.1
14	2S	31	SER	3.1
40	2i	17	VAL	3.1
32	2a	1172	G	3.1
33	2b	162	ILE	3.1
34	2c	129	ALA	3.1
40	2i	63	ILE	3.1
41	2j	27	ALA	3.1
47	1p	19	ILE	3.1
6	1G	51	ARG	3.1
38	2g	5	ARG	3.1
52	1u	10	ARG	3.1
52	2u	9	ARG	3.1
33	2b	70	PHE	3.1
44	2m	15	VAL	3.1
35	1d	4	TYR	3.0
50	2s	52	TYR	3.0
41	2j	37	PRO	3.0
5	2F	208	GLY	3.0
41	1j	38	ILE	3.0
41	1j	5	ARG	3.0
50	2s	34	TRP	3.0
1	1A	2806	C	3.0
50	2s	80	TYR	3.0
1	1A	1934	A	3.0
32	2a	1510	U	3.0
41	2j	31	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
14	2S	29	PHE	3.0
33	2b	152	PHE	3.0
14	2S	32	LEU	3.0
32	1a	982	G	3.0
1	1A	33	C	3.0
32	2a	1231	C	3.0
41	1j	46	ARG	3.0
15	1T	37	GLY	3.0
36	1e	85	GLY	3.0
51	1t	103	GLY	3.0
32	1a	1023	U	3.0
40	1i	41	VAL	3.0
8	1I	10	GLU	3.0
5	1F	14	PRO	3.0
40	1i	10	ARG	3.0
35	2d	146	ILE	3.0
50	2s	49	ILE	3.0
1	1A	2900	A	3.0
33	1b	28	PHE	3.0
41	2j	47	PHE	3.0
38	2g	12	LEU	2.9
41	2j	55	LYS	2.9
50	2s	66	MET	2.9
34	2c	182	ILE	2.9
41	2j	93	GLY	2.9
40	2i	109	VAL	2.9
32	1a	516	A	2.9
33	2b	21	ARG	2.9
38	2g	76	ARG	2.9
41	2j	76	ASN	2.9
55	1z	14	ARG	2.9
34	1c	184	TYR	2.9
38	1g	85	TYR	2.9
45	2n	42	ILE	2.9
50	1s	40	ILE	2.9
34	2c	155	GLY	2.9
35	1d	2	GLY	2.9
50	2s	8	GLY	2.9
50	2s	68	GLY	2.9
41	2j	94	VAL	2.9
43	1l	126	LYS	2.9
1	1A	1554	C	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2905	U	2.9
34	2c	124	ILE	2.9
41	2j	6	ILE	2.9
18	2W	112	GLY	2.9
40	1i	68	GLY	2.9
45	2n	13	THR	2.9
36	2e	94	ALA	2.9
40	2i	61	ALA	2.9
34	1c	10	PHE	2.9
44	2m	7	VAL	2.9
26	24	58	ARG	2.9
31	19	12	ASP	2.9
1	2A	33	C	2.9
32	2a	1239	U	2.9
52	2u	11	GLY	2.9
40	2i	28	VAL	2.9
41	1j	40	LEU	2.9
50	2s	15	LEU	2.9
6	2G	142	PRO	2.8
47	1p	41	PRO	2.8
35	1d	154	ASN	2.8
50	2s	31	ILE	2.8
42	2k	90	GLY	2.8
6	2G	19	LEU	2.8
15	1T	131	ALA	2.8
32	1a	978	U	2.8
33	1b	15	VAL	2.8
37	2f	6	VAL	2.8
32	1a	1268	A	2.8
1	1A	934	C	2.8
1	2A	2813	C	2.8
40	2i	20	ARG	2.8
33	2b	150	SER	2.8
36	2e	109	ILE	2.8
51	1t	11	SER	2.8
35	2d	154	ASN	2.8
3	2D	38	LYS	2.8
14	2S	60	GLY	2.8
34	2c	159	GLY	2.8
35	2d	87	GLY	2.8
41	1j	65	LEU	2.8
38	2g	21	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
40	2i	41	VAL	2.8
42	1k	14	VAL	2.8
1	2A	1934	A	2.8
32	1a	1432	A	2.8
32	2a	979	A	2.8
32	2a	957	C	2.8
33	1b	222	ILE	2.8
1	2A	2815	G	2.8
45	2n	39	LEU	2.8
49	1r	78	LEU	2.8
7	1H	131	VAL	2.8
8	2I	146	ALA	2.8
35	2d	8	VAL	2.8
38	2g	85	TYR	2.8
40	1i	14	VAL	2.8
41	1j	47	PHE	2.8
33	1b	131	PRO	2.8
33	2b	137	ARG	2.8
55	2z	15	PRO	2.8
51	2t	21	LYS	2.8
1	1A	1098	C	2.8
32	1a	158	C	2.8
34	2c	154	SER	2.8
44	2m	34	LEU	2.8
45	2n	6	LEU	2.8
34	1c	6	HIS	2.8
44	2m	92	HIS	2.8
43	1l	18	VAL	2.8
2	2B	23	G	2.8
38	2g	4	ARG	2.8
38	2g	154	TYR	2.8
44	2m	87	TYR	2.8
24	12	70	GLN	2.7
14	2S	35	ILE	2.7
41	2j	75	ILE	2.7
1	2A	1071	U	2.7
44	2m	90	LEU	2.7
50	2s	35	SER	2.7
14	2S	45	GLY	2.7
34	2c	2	GLY	2.7
50	2s	53	ASN	2.7
26	24	65	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
38	2g	33	ASP	2.7
40	2i	119	ALA	2.7
22	20	11	ARG	2.7
43	2l	18	VAL	2.7
45	1n	3	ARG	2.7
40	2i	125	TYR	2.7
52	1u	23	PRO	2.7
12	2Q	22	LYS	2.7
1	1A	2902	G	2.7
1	2A	1132	G	2.7
40	2i	40	LEU	2.7
44	2m	66	LEU	2.7
45	1n	44	LEU	2.7
33	1b	97	TRP	2.7
40	1i	126	SER	2.7
41	2j	52	GLY	2.7
50	2s	14	HIS	2.7
25	23	60	GLU	2.7
45	1n	13	THR	2.7
34	1c	28	GLN	2.7
32	2a	1205	C	2.7
26	24	31	ILE	2.7
40	1i	102	LEU	2.7
32	1a	1121	G	2.7
50	1s	38	SER	2.7
51	2t	9	ASN	2.7
31	29	16	VAL	2.7
40	1i	64	THR	2.7
41	2j	32	ALA	2.7
45	1n	59	ALA	2.7
47	2p	69	THR	2.7
41	2j	91	PRO	2.7
51	1t	21	LYS	2.7
6	1G	25	TYR	2.7
6	2G	140	ILE	2.7
2	2B	88	C	2.7
41	1j	85	LEU	2.7
45	2n	29	ARG	2.7
50	1s	84	GLY	2.7
41	1j	69	ASN	2.7
33	2b	165	VAL	2.7
14	2S	5	THR	2.7

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Mol	Chain	Res	Type	RSRZ
33	2b	186	ALA	2.7
34	2c	189	ALA	2.7
45	2n	4	LYS	2.7
47	2p	7	ALA	2.7
1	2A	1579	G	2.6
32	2a	1235	G	2.6
34	2c	5	ILE	2.6
45	1n	7	ILE	2.6
6	2G	3	LEU	2.6
7	2H	111	HIS	2.6
41	2j	66	ARG	2.6
40	2i	115	GLY	2.6
1	2A	1582	C	2.6
32	2a	1132	C	2.6
7	2H	45	VAL	2.6
41	2j	77	PRO	2.6
34	2c	152	ILE	2.6
1	1A	1071	U	2.6
2	2B	118	G	2.6
32	1a	211	U	2.6
32	1a	339	U	2.6
39	2h	2	LEU	2.6
41	2j	71	LEU	2.6
41	2j	43	ARG	2.6
6	2G	42	GLY	2.6
14	1S	93	LYS	2.6
52	1u	2	GLY	2.6
6	2G	46	ALA	2.6
23	21	2	SER	2.6
33	1b	237	ALA	2.6
40	2i	18	PHE	2.6
41	1j	39	PRO	2.6
50	1s	56	GLN	2.6
32	2a	1021	C	2.6
34	2c	39	ILE	2.6
38	1g	12	LEU	2.6
50	1s	14	HIS	2.6
51	1t	79	ARG	2.6
6	1G	48	GLU	2.6
1	2A	2812	G	2.6
32	1a	96	G	2.6
14	2S	65	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
50	2s	67	VAL	2.6
6	1G	80	PHE	2.6
42	1k	36	ASP	2.6
14	2S	101	LEU	2.6
51	2t	24	LEU	2.6
14	2S	20	ARG	2.6
33	2b	92	TYR	2.6
33	2b	199	TYR	2.6
34	2c	4	LYS	2.6
41	2j	64	GLU	2.6
48	2q	24	GLU	2.6
1	1A	270	U	2.6
25	23	2	PRO	2.6
33	1b	207	ALA	2.6
33	2b	136	VAL	2.6
40	2i	106	ALA	2.6
50	2s	41	VAL	2.6
7	2H	2	SER	2.5
47	1p	33	ILE	2.5
1	2A	678	A	2.5
32	2a	1165	A	2.5
35	1d	135	LEU	2.5
35	2d	155	LEU	2.5
34	1c	179	ARG	2.5
38	2g	3	ARG	2.5
26	24	67	TYR	2.5
1	2A	2801	C	2.5
7	2H	169	VAL	2.5
38	2g	80	VAL	2.5
50	2s	51	VAL	2.5
14	2S	55	ALA	2.5
21	1Z	88	PHE	2.5
34	2c	160	ALA	2.5
35	1d	110	PHE	2.5
45	2n	36	PHE	2.5
40	2i	103	THR	2.5
41	1j	78	ASN	2.5
44	2m	64	TRP	2.5
45	2n	61	TRP	2.5
7	1H	42	ARG	2.5
7	2H	6	ARG	2.5
43	2l	126	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
45	1n	17	LYS	2.5
46	2o	68	ARG	2.5
51	1t	16	HIS	2.5
32	2a	1025	G	2.5
26	14	53	GLU	2.5
38	1g	82	GLY	2.5
52	2u	16	GLY	2.5
50	2s	76	PRO	2.5
26	14	56	VAL	2.5
34	2c	198	VAL	2.5
35	1d	104	VAL	2.5
33	2b	181	PHE	2.5
26	24	66	SER	2.5
41	2j	19	SER	2.5
45	2n	58	LYS	2.5
1	2A	1128	U	2.5
6	1G	35	GLU	2.5
49	2r	46	GLU	2.5
33	2b	236	TYR	2.5
34	1c	193	TYR	2.5
7	2H	174	GLY	2.5
33	2b	99	GLY	2.5
40	2i	68	GLY	2.5
33	2b	131	PRO	2.5
1	2A	1216	G	2.5
34	2c	187	ALA	2.5
50	2s	24	ALA	2.5
41	2j	67	THR	2.5
41	2j	7	LYS	2.5
51	2t	74	LYS	2.5
14	2S	39	ILE	2.5
21	2Z	33	LEU	2.5
33	1b	30	ARG	2.5
49	1r	79	LEU	2.5
50	2s	5	LEU	2.5
51	1t	62	LEU	2.5
5	1F	134	GLY	2.5
40	2i	39	GLY	2.5
34	2c	130	VAL	2.5
34	2c	128	PHE	2.5
35	2d	164	ALA	2.5
40	1i	33	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
40	1i	127	LYS	2.4
45	2n	9	LYS	2.4
1	1A	571	A	2.4
7	2H	170	ARG	2.4
14	2S	97	ARG	2.4
19	1X	65	ARG	2.4
50	2s	3	ARG	2.4
51	1t	25	ARG	2.4
6	1G	53	LEU	2.4
6	2G	139	LEU	2.4
34	1c	188	LEU	2.4
34	2c	204	LEU	2.4
51	1t	13	LEU	2.4
14	2S	52	SER	2.4
41	1j	30	SER	2.4
38	1g	153	HIS	2.4
41	1j	97	GLU	2.4
32	2a	1187	U	2.4
34	1c	7	PRO	2.4
34	1c	185	GLY	2.4
41	1j	91	PRO	2.4
50	2s	42	PRO	2.4
26	14	63	TYR	2.4
40	1i	125	TYR	2.4
6	2G	149	VAL	2.4
21	2Z	175	VAL	2.4
36	2e	148	VAL	2.4
41	1j	34	VAL	2.4
51	1t	14	LYS	2.4
7	2H	20	ALA	2.4
33	2b	29	ALA	2.4
26	14	52	THR	2.4
26	24	52	THR	2.4
52	1u	6	ARG	2.4
7	1H	148	ILE	2.4
49	2r	66	LEU	2.4
6	2G	76	SER	2.4
14	2S	27	SER	2.4
41	1j	35	SER	2.4
55	2z	5	SER	2.4
39	2h	99	GLU	2.4
1	2A	9	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	10	G	2.4
1	2A	2902	G	2.4
32	2a	982	G	2.4
6	2G	129	GLY	2.4
35	1d	180	GLY	2.4
39	2h	96	GLY	2.4
1	1A	2206	C	2.4
9	1N	9	VAL	2.4
37	1f	88	VAL	2.4
41	2j	24	VAL	2.4
1	1A	1150	U	2.4
43	2l	69	TYR	2.4
33	2b	188	ALA	2.4
34	2c	10	PHE	2.4
45	2n	10	ALA	2.4
8	1I	38	LEU	2.4
14	2S	63	THR	2.4
19	1X	95	LEU	2.4
40	1i	56	LEU	2.4
40	2i	7	THR	2.4
41	2j	48	THR	2.4
50	2s	4	SER	2.4
8	2I	96	ASP	2.4
26	14	51	ASP	2.4
34	2c	167	TRP	2.4
32	1a	1509	A	2.4
38	2g	36	LYS	2.4
45	1n	55	GLY	2.4
45	2n	14	PRO	2.4
33	2b	81	VAL	2.4
41	2j	49	VAL	2.4
42	2k	114	VAL	2.4
1	2A	2330	G	2.4
1	2A	2901	G	2.4
7	2H	164	TYR	2.4
14	2S	36	TYR	2.4
32	1a	614	G	2.4
34	2c	21	ARG	2.4
40	2i	101	PHE	2.4
44	2m	18	ALA	2.4
45	1n	30	ALA	2.4
51	2t	23	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
6	2G	39	ILE	2.4
38	2g	27	ILE	2.4
46	1o	3	ILE	2.4
49	1r	85	LEU	2.4
32	1a	160	C	2.4
32	2a	1201	U	2.4
24	12	15	LYS	2.4
48	2q	100	LYS	2.4
38	1g	81	GLY	2.4
40	2i	30	GLY	2.4
38	2g	32	ARG	2.4
45	2n	12	ARG	2.4
45	2n	57	ARG	2.4
1	1A	699	A	2.4
41	2j	26	ALA	2.4
45	2n	48	ALA	2.4
21	2Z	5	LEU	2.3
33	1b	11	LEU	2.3
47	1p	39	TYR	2.3
52	1u	21	TYR	2.3
33	2b	140	HIS	2.3
34	1c	3	ASN	2.3
32	2a	1337	G	2.3
14	2S	8	GLU	2.3
1	1A	2209	C	2.3
32	2a	1266	C	2.3
32	2a	1336	C	2.3
39	2h	4	ASP	2.3
40	2i	11	LYS	2.3
45	1n	50	LYS	2.3
47	1p	78	GLY	2.3
26	14	55	ARG	2.3
41	2j	46	ARG	2.3
51	1t	18	GLN	2.3
52	1u	24	ARG	2.3
41	1j	63	PHE	2.3
47	1p	80	PHE	2.3
8	2I	77	LEU	2.3
33	2b	149	LEU	2.3
43	2l	93	LEU	2.3
33	1b	41	ILE	2.3
32	2a	1509	A	2.3

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Mol	Chain	Res	Type	RSRZ
52	2u	17	THR	2.3
53	1v	15	A	2.3
34	2c	82	GLU	2.3
40	1i	12	GLU	2.3
41	2j	83	GLU	2.3
47	1p	68	ASP	2.3
54	2x	47	U	2.3
1	2A	638	G	2.3
32	2a	949	G	2.3
32	2a	1070	G	2.3
35	2d	183	GLY	2.3
44	2m	88	ARG	2.3
46	1o	20	GLY	2.3
6	2G	160	VAL	2.3
27	15	60	VAL	2.3
6	2G	102	PHE	2.3
33	1b	214	ILE	2.3
34	2c	57	ILE	2.3
44	2m	9	ILE	2.3
14	2S	59	LYS	2.3
21	2Z	11	GLU	2.3
41	2j	78	ASN	2.3
1	2A	1129	A	2.3
32	2a	1207	A	2.3
34	2c	18	TRP	2.3
35	2d	73	ARG	2.3
34	2c	41	GLY	2.3
38	2g	82	GLY	2.3
33	2b	93	VAL	2.3
37	1f	90	VAL	2.3
40	2i	59	PHE	2.3
44	2m	19	LEU	2.3
3	2D	2	ALA	2.3
34	2c	168	ALA	2.3
40	2i	45	ALA	2.3
1	1A	10	G	2.3
32	2a	1292	G	2.3
32	2a	1299	C	2.3
22	10	10	THR	2.3
33	1b	133	LYS	2.3
38	2g	35	LYS	2.3
39	1h	15	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
7	2H	8	PRO	2.3
19	2X	68	ARG	2.3
21	1Z	166	SER	2.3
44	2m	104	ARG	2.3
1	1A	553	A	2.3
1	1A	2802	A	2.3
48	2q	8	GLY	2.3
22	20	84	LEU	2.3
34	2c	42	LEU	2.3
34	2c	178	LEU	2.3
40	2i	19	LEU	2.3
40	2i	86	VAL	2.3
41	2j	74	ILE	2.2
43	1l	99	HIS	2.2
52	1u	3	LYS	2.2
47	1p	45	THR	2.2
40	2i	110	GLU	2.2
35	2d	4	TYR	2.2
32	2a	1356	G	2.2
42	2k	117	ASN	2.2
41	1j	21	GLN	2.2
35	1d	124	GLY	2.2
45	1n	51	GLY	2.2
34	1c	12	LEU	2.2
34	1c	52	LEU	2.2
34	2c	12	LEU	2.2
32	2a	1339	A	2.2
33	1b	152	PHE	2.2
33	1b	163	PHE	2.2
37	2f	89	MET	2.2
32	1a	209	U	2.2
32	1a	1239	U	2.2
44	2m	63	THR	2.2
34	1c	23	TYR	2.2
15	2T	115	ARG	2.2
34	2c	11	ARG	2.2
51	1t	17	ARG	2.2
6	2G	17	PRO	2.2
47	2p	41	PRO	2.2
32	2a	1344	C	2.2
1	2A	2816	G	2.2
6	1G	42	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
23	21	22	GLY	2.2
36	2e	85	GLY	2.2
40	1i	105	ASP	2.2
40	2i	99	LEU	2.2
6	1G	75	LYS	2.2
33	2b	164	VAL	2.2
38	1g	21	VAL	2.2
40	1i	109	VAL	2.2
33	1b	101	MET	2.2
4	2E	204	ALA	2.2
5	2F	130	ALA	2.2
8	1I	146	ALA	2.2
40	2i	13	ALA	2.2
6	2G	48	GLU	2.2
33	2b	190	THR	2.2
40	2i	35	GLU	2.2
1	2A	1106	U	2.2
32	1a	1048	U	2.2
35	2d	49	ARG	2.2
52	2u	24	ARG	2.2
19	2X	69	TYR	2.2
21	2Z	9	TYR	2.2
3	2D	275	LYS	2.2
6	2G	34	LEU	2.2
14	2S	4	LEU	2.2
14	2S	62	LYS	2.2
19	2X	92	LEU	2.2
23	11	28	GLY	2.2
33	1b	121	LEU	2.2
33	1b	227	GLY	2.2
33	2b	196	LEU	2.2
35	1d	23	GLY	2.2
35	1d	102	ASP	2.2
38	1g	77	SER	2.2
39	2h	36	LEU	2.2
40	1i	67	GLY	2.2
44	2m	81	LEU	2.2
21	2Z	1	MET	2.2
12	2Q	104	PHE	2.2
14	2S	12	PHE	2.2
32	1a	824	C	2.2
32	2a	973	C	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	176	HIS	2.2
34	2c	60	ALA	2.2
35	1d	164	ALA	2.2
39	2h	28	ALA	2.2
44	2m	28	ALA	2.2
44	2m	72	ALA	2.2
32	2a	1469	G	2.2
48	1q	88	TYR	2.2
17	1V	63	GLY	2.2
35	2d	176	LEU	2.2
38	1g	38	LEU	2.2
40	2i	56	LEU	2.2
50	1s	5	LEU	2.2
38	1g	33	ASP	2.2
14	2S	95	HIS	2.2
33	2b	201	ILE	2.2
35	1d	158	ILE	2.2
38	1g	9	VAL	2.2
14	2S	37	ALA	2.1
34	1c	129	ALA	2.1
24	12	11	GLU	2.1
41	1j	64	GLU	2.1
33	2b	144	ARG	2.1
38	1g	5	ARG	2.1
32	1a	376	G	2.1
32	1a	1206	G	2.1
32	1a	1351	G	2.1
8	1I	89	TYR	2.1
14	2S	33	LYS	2.1
19	1X	92	LEU	2.1
41	1j	8	LEU	2.1
26	24	54	GLY	2.1
32	2a	1075	A	2.1
41	1j	93	GLY	2.1
14	2S	40	ILE	2.1
32	1a	66	U	2.1
40	2i	117	HIS	2.1
45	2n	32	SER	2.1
14	2S	87	PHE	2.1
40	1i	46	ALA	2.1
49	2r	60	ALA	2.1
51	2t	67	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
40	2i	107	ARG	2.1
41	1j	48	THR	2.1
45	2n	11	LYS	2.1
1	2A	1121	C	2.1
2	2B	5	C	2.1
32	2a	1102	C	2.1
32	2a	1302	C	2.1
35	1d	101	LEU	2.1
44	1m	59	TYR	2.1
51	1t	72	LEU	2.1
51	2t	10	LEU	2.1
31	29	21	GLY	2.1
40	1i	30	GLY	2.1
32	1a	98	G	2.1
33	2b	80	ILE	2.1
36	2e	51	VAL	2.1
40	1i	81	ILE	2.1
41	1j	24	VAL	2.1
44	2m	53	VAL	2.1
41	2j	54	PHE	2.1
1	2A	1091	A	2.1
14	2S	79	ALA	2.1
21	2Z	164	ALA	2.1
32	2a	956	A	2.1
45	2n	59	ALA	2.1
33	2b	126	GLU	2.1
54	1x	47	U	2.1
33	1b	36	ARG	2.1
39	2h	92	ARG	2.1
47	1p	5	ARG	2.1
52	1u	14	TRP	2.1
44	2m	103	THR	2.1
50	2s	79	THR	2.1
51	1t	71	THR	2.1
34	1c	4	LYS	2.1
40	2i	116	LYS	2.1
26	24	29	PRO	2.1
33	1b	234	PRO	2.1
33	2b	83	MET	2.1
41	2j	86	MET	2.1
33	2b	44	LEU	2.1
51	2t	62	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
8	2I	11	ASN	2.1
35	2d	2	GLY	2.1
39	2h	130	GLY	2.1
44	2m	100	GLY	2.1
45	2n	55	GLY	2.1
52	1u	18	TYR	2.1
26	24	10	VAL	2.1
32	1a	1120	C	2.1
34	2c	64	VAL	2.1
39	2h	95	VAL	2.1
40	2i	53	VAL	2.1
47	2p	19	ILE	2.1
40	1i	91	ASP	2.1
40	2i	37	PHE	2.1
41	1j	11	PHE	2.1
7	1H	6	ARG	2.1
15	1T	126	ALA	2.1
33	2b	129	GLU	2.1
35	1d	118	ARG	2.1
35	1d	131	ARG	2.1
40	1i	35	GLU	2.1
41	2j	9	ARG	2.1
45	1n	26	ARG	2.1
47	2p	59	TRP	2.1
1	1A	2640	A	2.1
1	2A	1506	A	2.1
21	1Z	69	THR	2.1
26	24	44	THR	2.1
32	1a	1165	A	2.1
51	2t	71	THR	2.1
7	1H	55	PRO	2.1
33	1b	167	PRO	2.1
10	2O	1	MET	2.1
33	1b	10	LEU	2.1
33	2b	121	LEU	2.1
35	2d	157	LEU	2.1
41	2j	88	LEU	2.1
51	2t	72	LEU	2.1
17	2V	63	GLY	2.1
40	1i	6	GLY	2.1
51	2t	69	GLY	2.1
6	2G	146	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
14	2S	92	TYR	2.1
36	2e	133	TYR	2.1
41	2j	50	ILE	2.1
34	2c	116	VAL	2.1
3	1D	28	GLU	2.0
6	2G	54	GLU	2.0
6	2G	115	ARG	2.0
11	1P	136	GLU	2.0
12	2Q	60	ARG	2.0
14	1S	3	ARG	2.0
34	1c	206	GLU	2.0
38	2g	79	ARG	2.0
40	1i	42	ARG	2.0
41	1j	79	ARG	2.0
41	2j	5	ARG	2.0
44	2m	71	ARG	2.0
38	2g	39	ALA	2.0
2	1B	11	C	2.0
19	2X	33	LYS	2.0
32	1a	1185	C	2.0
40	1i	113	LYS	2.0
12	1Q	21	THR	2.0
50	1s	39	THR	2.0
6	1G	87	PRO	2.0
33	1b	149	LEU	2.0
34	1c	42	LEU	2.0
34	1c	87	LEU	2.0
1	1A	5	A	2.0
32	1a	67	G	2.0
32	2a	1000	G	2.0
32	2a	1230	A	2.0
32	2a	1238	A	2.0
32	2a	1343	G	2.0
38	2g	37	ASN	2.0
6	2G	88	ILE	2.0
33	1b	172	ILE	2.0
38	1g	42	ILE	2.0
45	1n	38	GLY	2.0
26	24	32	TYR	2.0
33	1b	71	VAL	2.0
35	1d	170	VAL	2.0
40	2i	44	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
14	2S	15	ARG	2.0
45	2n	41	ARG	2.0
6	1G	54	GLU	2.0
38	2g	8	GLU	2.0
16	1U	116	ALA	2.0
26	24	69	LYS	2.0
33	1b	34	ALA	2.0
38	1g	2	ALA	2.0
40	2i	127	LYS	2.0
44	1m	118	ALA	2.0
38	2g	14	PRO	2.0
41	2j	42	THR	2.0
50	1s	33	THR	2.0
1	2A	2814	C	2.0
8	2I	38	LEU	2.0
24	12	16	LEU	2.0
32	1a	1022	C	2.0
32	2a	998	C	2.0
32	2a	1185	C	2.0
35	1d	21	LEU	2.0
39	2h	112	LEU	2.0
33	1b	16	HIS	2.0
1	2A	637	U	2.0
6	1G	88	ILE	2.0
31	29	17	ILE	2.0
41	2j	38	ILE	2.0
50	2s	62	ILE	2.0
1	2A	1130	A	2.0
1	2A	1140	A	2.0
5	1F	6	VAL	2.0
26	14	48	ARG	2.0
32	1a	1024	A	2.0
32	2a	1432	A	2.0
33	2b	112	VAL	2.0
34	2c	172	ARG	2.0
34	2c	190	ARG	2.0
35	2d	131	ARG	2.0
40	2i	120	ARG	2.0
41	2j	60	ARG	2.0
42	2k	126	ARG	2.0
44	1m	93	ARG	2.0
52	1u	9	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
52	1u	22	ARG	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
54	PSU	2x	55	20/21	0.82	0.12	68,72,83,84	0
54	5MC	2x	32	21/22	0.86	0.14	65,77,87,92	0
54	4SU	2x	8	20/21	0.88	0.10	69,79,87,88	0
54	5MU	2x	54	21/22	0.89	0.10	68,77,85,100	0
54	5MC	1x	32	21/22	0.92	0.12	47,63,73,74	0
54	5MU	1x	54	21/22	0.92	0.11	57,69,77,82	0
54	PSU	1x	55	20/21	0.93	0.10	63,69,80,81	0
54	4SU	1x	8	20/21	0.95	0.08	47,59,71,71	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(Å^2)	Q<0.9
56	MG	2a	1833	1/1	0.51	0.25	94,94,94,94	0
56	MG	2a	1767	1/1	0.54	0.22	88,88,88,88	0
56	MG	1A	4047	1/1	0.54	0.23	79,79,79,79	0
56	MG	1A	3732	1/1	0.58	0.12	59,59,59,59	0
56	MG	1A	4203	1/1	0.58	0.42	71,71,71,71	0
56	MG	2a	1784	1/1	0.59	0.23	80,80,80,80	0
56	MG	1A	3352	1/1	0.59	0.33	82,82,82,82	0
56	MG	2A	3003	1/1	0.63	0.21	67,67,67,67	0
56	MG	2a	1789	1/1	0.63	0.21	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1716	1/1	0.63	0.35	79,79,79,79	0
56	MG	2a	1837	1/1	0.63	0.23	75,75,75,75	0
56	MG	2A	3346	1/1	0.64	0.25	76,76,76,76	0
56	MG	1A	3907	1/1	0.64	0.13	53,53,53,53	0
56	MG	1a	1754	1/1	0.65	0.20	89,89,89,89	0
56	MG	1A	3517	1/1	0.65	0.18	58,58,58,58	0
56	MG	2a	1754	1/1	0.66	0.21	74,74,74,74	0
56	MG	1A	3943	1/1	0.66	0.14	74,74,74,74	0
56	MG	2Z	3001	1/1	0.66	0.16	62,62,62,62	0
56	MG	2B	3005	1/1	0.67	0.24	79,79,79,79	0
56	MG	1a	1766	1/1	0.67	0.26	73,73,73,73	0
56	MG	2a	1632	1/1	0.67	0.17	86,86,86,86	0
56	MG	2a	1655	1/1	0.67	0.18	92,92,92,92	0
56	MG	1a	1836	1/1	0.67	0.16	78,78,78,78	0
56	MG	1A	3426	1/1	0.68	0.12	65,65,65,65	0
56	MG	2a	1813	1/1	0.68	0.24	74,74,74,74	0
56	MG	1A	3913	1/1	0.68	0.23	58,58,58,58	0
56	MG	2B	3008	1/1	0.68	0.15	63,63,63,63	0
56	MG	2A	3436	1/1	0.69	0.16	55,55,55,55	0
56	MG	1a	1765	1/1	0.69	0.20	71,71,71,71	0
56	MG	1A	4035	1/1	0.69	0.20	78,78,78,78	0
56	MG	1a	1778	1/1	0.69	0.38	83,83,83,83	0
56	MG	2a	1768	1/1	0.69	0.30	86,86,86,86	0
56	MG	1a	1881	1/1	0.70	0.22	69,69,69,69	0
56	MG	2a	1608	1/1	0.70	0.27	75,75,75,75	0
56	MG	1A	4072	1/1	0.70	0.14	52,52,52,52	0
56	MG	1A	3465	1/1	0.70	0.17	71,71,71,71	0
56	MG	2A	3524	1/1	0.71	0.21	75,75,75,75	0
56	MG	1A	4104	1/1	0.71	0.20	63,63,63,63	0
56	MG	1A	3441	1/1	0.71	0.14	62,62,62,62	0
56	MG	1A	3418	1/1	0.72	0.30	52,52,52,52	0
56	MG	1A	3533	1/1	0.72	0.26	75,75,75,75	0
56	MG	2a	1668	1/1	0.72	0.25	69,69,69,69	0
56	MG	2a	1701	1/1	0.72	0.16	66,66,66,66	0
56	MG	1A	3376	1/1	0.72	0.23	69,69,69,69	0
56	MG	1A	4003	1/1	0.72	0.20	92,92,92,92	0
56	MG	2A	3515	1/1	0.73	0.20	55,55,55,55	0
56	MG	1x	112	1/1	0.73	0.21	78,78,78,78	0
56	MG	1A	4056	1/1	0.73	0.28	74,74,74,74	0
56	MG	2a	1633	1/1	0.73	0.16	70,70,70,70	0
56	MG	2A	3479	1/1	0.73	0.13	51,51,51,51	0
56	MG	1A	3127	1/1	0.74	0.19	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3562	1/1	0.74	0.25	41,41,41,41	0
56	MG	1Q	203	1/1	0.74	0.17	64,64,64,64	0
56	MG	1a	1822	1/1	0.74	0.39	76,76,76,76	0
56	MG	1A	4064	1/1	0.74	0.24	78,78,78,78	0
56	MG	1A	3716	1/1	0.74	0.17	37,37,37,37	0
56	MG	1A	4010	1/1	0.75	0.14	76,76,76,76	0
56	MG	1A	4189	1/1	0.75	0.13	43,43,43,43	0
56	MG	2A	3233	1/1	0.75	0.20	68,68,68,68	0
56	MG	1A	3139	1/1	0.75	0.18	52,52,52,52	0
56	MG	2a	1685	1/1	0.75	0.20	83,83,83,83	0
56	MG	1a	1846	1/1	0.75	0.30	75,75,75,75	0
56	MG	1A	3918	1/1	0.75	0.15	27,27,27,27	0
56	MG	2a	1846	1/1	0.75	0.19	78,78,78,78	0
56	MG	1a	1723	1/1	0.76	0.21	69,69,69,69	0
56	MG	1a	1727	1/1	0.76	0.20	80,80,80,80	0
56	MG	1A	3876	1/1	0.76	0.17	64,64,64,64	0
56	MG	1A	3445	1/1	0.76	0.13	57,57,57,57	0
56	MG	2a	1716	1/1	0.76	0.15	70,70,70,70	0
56	MG	1a	1629	1/1	0.76	0.20	85,85,85,85	0
56	MG	1A	4191	1/1	0.76	0.14	39,39,39,39	0
56	MG	1a	1767	1/1	0.77	0.18	72,72,72,72	0
56	MG	1A	4082	1/1	0.77	0.16	85,85,85,85	0
56	MG	1A	3004	1/1	0.77	0.30	47,47,47,47	0
56	MG	1A	3658	1/1	0.77	0.19	60,60,60,60	0
56	MG	2a	1642	1/1	0.77	0.24	85,85,85,85	0
56	MG	2a	1650	1/1	0.77	0.23	82,82,82,82	0
56	MG	1A	4061	1/1	0.77	0.12	89,89,89,89	0
56	MG	1A	3842	1/1	0.77	0.22	79,79,79,79	0
56	MG	1A	3860	1/1	0.77	0.27	62,62,62,62	0
56	MG	18	104	1/1	0.77	0.19	63,63,63,63	0
56	MG	2a	1733	1/1	0.78	0.32	80,80,80,80	0
56	MG	2A	3447	1/1	0.78	0.27	61,61,61,61	0
56	MG	1A	3506	1/1	0.78	0.18	37,37,37,37	0
56	MG	1A	3536	1/1	0.78	0.11	67,67,67,67	0
56	MG	2A	3518	1/1	0.78	0.15	58,58,58,58	0
56	MG	1A	4228	1/1	0.78	0.19	58,58,58,58	0
56	MG	2a	1793	1/1	0.78	0.14	67,67,67,67	0
56	MG	2a	1796	1/1	0.78	0.23	80,80,80,80	0
56	MG	2a	1800	1/1	0.78	0.29	65,65,65,65	0
56	MG	2a	1812	1/1	0.78	0.19	75,75,75,75	0
56	MG	2A	3266	1/1	0.78	0.15	60,60,60,60	0
56	MG	2A	3279	1/1	0.78	0.15	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	1836	1/1	0.78	0.18	72,72,72,72	0
56	MG	1a	1860	1/1	0.78	0.11	68,68,68,68	0
56	MG	1a	1691	1/1	0.78	0.15	59,59,59,59	0
56	MG	2l	3003	1/1	0.78	0.26	71,71,71,71	0
56	MG	1A	3368	1/1	0.79	0.12	65,65,65,65	0
56	MG	1A	3125	1/1	0.79	0.14	58,58,58,58	0
56	MG	1A	3446	1/1	0.79	0.21	45,45,45,45	0
56	MG	1A	3574	1/1	0.79	0.15	62,62,62,62	0
56	MG	1A	3912	1/1	0.79	0.19	54,54,54,54	0
56	MG	1a	1632	1/1	0.79	0.28	72,72,72,72	0
56	MG	1e	202	1/1	0.79	0.19	62,62,62,62	0
56	MG	1A	3045	1/1	0.79	0.09	60,60,60,60	0
56	MG	1A	4075	1/1	0.79	0.14	59,59,59,59	0
56	MG	1A	3365	1/1	0.79	0.27	74,74,74,74	0
56	MG	1A	3427	1/1	0.79	0.21	67,67,67,67	0
56	MG	2A	3267	1/1	0.79	0.20	62,62,62,62	0
56	MG	1A	4169	1/1	0.79	0.22	57,57,57,57	0
56	MG	1A	4173	1/1	0.79	0.17	21,21,21,21	0
56	MG	2a	1673	1/1	0.79	0.42	76,76,76,76	0
56	MG	1A	3750	1/1	0.79	0.17	43,43,43,43	0
56	MG	1A	3810	1/1	0.79	0.13	35,35,35,35	0
56	MG	1A	3537	1/1	0.80	0.20	55,55,55,55	0
56	MG	1a	1635	1/1	0.80	0.10	87,87,87,87	0
56	MG	2a	1709	1/1	0.80	0.21	78,78,78,78	0
56	MG	1q	201	1/1	0.80	0.20	65,65,65,65	0
56	MG	2A	3534	1/1	0.80	0.20	57,57,57,57	0
56	MG	2a	1734	1/1	0.80	0.20	80,80,80,80	0
56	MG	2A	3550	1/1	0.80	0.17	49,49,49,49	0
56	MG	2A	3552	1/1	0.80	0.16	59,59,59,59	0
56	MG	1A	3424	1/1	0.80	0.17	53,53,53,53	0
56	MG	2a	1769	1/1	0.80	0.19	76,76,76,76	0
56	MG	10	102	1/1	0.80	0.17	54,54,54,54	0
56	MG	1a	1721	1/1	0.80	0.17	78,78,78,78	0
56	MG	1a	1779	1/1	0.80	0.10	80,80,80,80	0
56	MG	1a	1786	1/1	0.80	0.20	64,64,64,64	0
56	MG	1A	4067	1/1	0.80	0.12	71,71,71,71	0
56	MG	2a	1805	1/1	0.80	0.21	73,73,73,73	0
56	MG	2A	3339	1/1	0.80	0.20	76,76,76,76	0
56	MG	2a	1648	1/1	0.80	0.18	79,79,79,79	0
56	MG	2a	1820	1/1	0.80	0.27	68,68,68,68	0
56	MG	2a	1823	1/1	0.80	0.22	76,76,76,76	0
56	MG	1A	3746	1/1	0.80	0.21	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	1653	1/1	0.80	0.10	85,85,85,85	0
56	MG	1a	1740	1/1	0.80	0.26	72,72,72,72	0
56	MG	1a	1847	1/1	0.80	0.20	72,72,72,72	0
56	MG	1a	1752	1/1	0.80	0.22	73,73,73,73	0
56	MG	1A	4017	1/1	0.81	0.31	70,70,70,70	0
56	MG	2A	3239	1/1	0.81	0.23	64,64,64,64	0
56	MG	1A	4081	1/1	0.81	0.17	73,73,73,73	0
56	MG	1A	4028	1/1	0.81	0.12	74,74,74,74	0
56	MG	1a	1609	1/1	0.81	0.16	64,64,64,64	0
56	MG	2A	3288	1/1	0.81	0.12	46,46,46,46	0
56	MG	1a	1618	1/1	0.81	0.11	42,42,42,42	0
56	MG	1A	4086	1/1	0.81	0.24	61,61,61,61	0
56	MG	2A	3368	1/1	0.81	0.15	49,49,49,49	0
56	MG	1A	3597	1/1	0.81	0.21	49,49,49,49	0
56	MG	2a	1764	1/1	0.81	0.28	69,69,69,69	0
56	MG	1a	1812	1/1	0.81	0.17	62,62,62,62	0
56	MG	1A	4140	1/1	0.81	0.22	77,77,77,77	0
56	MG	1a	1649	1/1	0.81	0.18	83,83,83,83	0
56	MG	1a	1844	1/1	0.81	0.13	56,56,56,56	0
56	MG	2a	1786	1/1	0.81	0.23	58,58,58,58	0
56	MG	1A	3644	1/1	0.81	0.24	66,66,66,66	0
56	MG	1a	1703	1/1	0.81	0.31	61,61,61,61	0
56	MG	1A	3528	1/1	0.81	0.11	60,60,60,60	0
56	MG	1a	1870	1/1	0.81	0.12	67,67,67,67	0
56	MG	1a	1879	1/1	0.81	0.19	78,78,78,78	0
56	MG	1A	3935	1/1	0.81	0.10	29,29,29,29	0
56	MG	1A	3514	1/1	0.81	0.19	59,59,59,59	0
56	MG	1A	3461	1/1	0.81	0.22	62,62,62,62	0
56	MG	1r	3001	1/1	0.81	0.24	80,80,80,80	0
56	MG	1x	102	1/1	0.81	0.28	69,69,69,69	0
56	MG	1A	3591	1/1	0.81	0.11	55,55,55,55	0
56	MG	1B	204	1/1	0.81	0.14	49,49,49,49	0
56	MG	2a	1845	1/1	0.81	0.18	63,63,63,63	0
56	MG	2A	3043	1/1	0.81	0.18	61,61,61,61	0
56	MG	2A	3190	1/1	0.81	0.21	46,46,46,46	0
56	MG	2A	3525	1/1	0.82	0.13	49,49,49,49	0
56	MG	2A	3170	1/1	0.82	0.10	46,46,46,46	0
56	MG	1A	3594	1/1	0.82	0.11	61,61,61,61	0
56	MG	2a	1755	1/1	0.82	0.22	68,68,68,68	0
56	MG	2A	3231	1/1	0.82	0.20	81,81,81,81	0
56	MG	1a	1697	1/1	0.82	0.18	73,73,73,73	0
56	MG	1A	3466	1/1	0.82	0.23	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4019	1/1	0.82	0.22	75,75,75,75	0
56	MG	2a	1778	1/1	0.82	0.14	61,61,61,61	0
56	MG	2a	1602	1/1	0.82	0.26	54,54,54,54	0
56	MG	1A	3634	1/1	0.82	0.09	29,29,29,29	0
56	MG	1a	1782	1/1	0.82	0.23	63,63,63,63	0
56	MG	1A	3476	1/1	0.82	0.23	61,61,61,61	0
56	MG	2a	1638	1/1	0.82	0.28	73,73,73,73	0
56	MG	1A	3438	1/1	0.82	0.14	60,60,60,60	0
56	MG	1A	3145	1/1	0.82	0.08	59,59,59,59	0
56	MG	2a	1808	1/1	0.82	0.20	65,65,65,65	0
56	MG	1A	4233	1/1	0.82	0.18	88,88,88,88	0
56	MG	2A	3405	1/1	0.82	0.17	64,64,64,64	0
56	MG	1A	3731	1/1	0.82	0.20	53,53,53,53	0
56	MG	1a	1764	1/1	0.82	0.11	73,73,73,73	0
56	MG	2A	3049	1/1	0.82	0.30	64,64,64,64	0
56	MG	2A	3480	1/1	0.82	0.17	39,39,39,39	0
56	MG	2A	3058	1/1	0.82	0.21	58,58,58,58	0
56	MG	2A	3060	1/1	0.82	0.12	46,46,46,46	0
56	MG	2A	3152	1/1	0.82	0.21	52,52,52,52	0
56	MG	2a	1731	1/1	0.82	0.20	70,70,70,70	0
56	MG	1a	1811	1/1	0.83	0.10	72,72,72,72	0
56	MG	2A	3243	1/1	0.83	0.12	59,59,59,59	0
56	MG	2A	3257	1/1	0.83	0.14	57,57,57,57	0
56	MG	1A	3050	1/1	0.83	0.10	48,48,48,48	0
56	MG	1A	3893	1/1	0.83	0.15	61,61,61,61	0
56	MG	1A	3389	1/1	0.83	0.25	72,72,72,72	0
56	MG	1a	1706	1/1	0.83	0.14	51,51,51,51	0
56	MG	2a	1690	1/1	0.83	0.25	58,58,58,58	0
56	MG	2a	1697	1/1	0.83	0.13	53,53,53,53	0
56	MG	2A	3310	1/1	0.83	0.14	38,38,38,38	0
56	MG	1a	1710	1/1	0.83	0.24	58,58,58,58	0
56	MG	1A	3590	1/1	0.83	0.20	54,54,54,54	0
56	MG	2A	3367	1/1	0.83	0.19	63,63,63,63	0
56	MG	1A	3524	1/1	0.83	0.14	51,51,51,51	0
56	MG	2A	3383	1/1	0.83	0.21	44,44,44,44	0
56	MG	1A	3436	1/1	0.83	0.12	52,52,52,52	0
56	MG	1A	4071	1/1	0.83	0.17	79,79,79,79	0
56	MG	1B	210	1/1	0.83	0.15	50,50,50,50	0
56	MG	2A	3455	1/1	0.83	0.10	47,47,47,47	0
56	MG	2A	3460	1/1	0.83	0.14	74,74,74,74	0
56	MG	1a	1750	1/1	0.83	0.15	70,70,70,70	0
56	MG	1E	307	1/1	0.83	0.16	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3498	1/1	0.83	0.14	48,48,48,48	0
56	MG	1A	3102	1/1	0.83	0.13	51,51,51,51	0
56	MG	2a	1787	1/1	0.83	0.25	65,65,65,65	0
56	MG	1a	1755	1/1	0.83	0.20	65,65,65,65	0
56	MG	1a	1756	1/1	0.83	0.17	80,80,80,80	0
56	MG	1A	3609	1/1	0.83	0.14	31,31,31,31	0
56	MG	2A	3007	1/1	0.83	0.22	72,72,72,72	0
56	MG	1A	4078	1/1	0.83	0.20	62,62,62,62	0
56	MG	1A	3997	1/1	0.83	0.11	25,25,25,25	0
56	MG	2A	3571	1/1	0.83	0.28	43,43,43,43	0
56	MG	1A	3825	1/1	0.83	0.15	62,62,62,62	0
56	MG	1a	1769	1/1	0.83	0.14	66,66,66,66	0
56	MG	2A	3077	1/1	0.83	0.17	61,61,61,61	0
56	MG	2a	1827	1/1	0.83	0.38	83,83,83,83	0
56	MG	2A	3082	1/1	0.83	0.08	44,44,44,44	0
56	MG	1A	3840	1/1	0.83	0.12	69,69,69,69	0
56	MG	1A	3023	1/1	0.83	0.18	49,49,49,49	0
56	MG	1A	3425	1/1	0.83	0.22	62,62,62,62	0
56	MG	1A	3869	1/1	0.83	0.23	64,64,64,64	0
56	MG	1a	1803	1/1	0.83	0.16	60,60,60,60	0
56	MG	2q	3002	1/1	0.83	0.14	48,48,48,48	0
56	MG	2A	3399	1/1	0.84	0.19	60,60,60,60	0
56	MG	2A	3025	1/1	0.84	0.18	59,59,59,59	0
56	MG	2a	1676	1/1	0.84	0.16	64,64,64,64	0
56	MG	2a	1679	1/1	0.84	0.20	61,61,61,61	0
56	MG	2A	3435	1/1	0.84	0.10	54,54,54,54	0
56	MG	1B	201	1/1	0.84	0.18	64,64,64,64	0
56	MG	1A	3298	1/1	0.84	0.20	57,57,57,57	0
56	MG	1a	1711	1/1	0.84	0.21	75,75,75,75	0
56	MG	2a	1706	1/1	0.84	0.27	63,63,63,63	0
56	MG	1A	3432	1/1	0.84	0.14	52,52,52,52	0
56	MG	1A	3541	1/1	0.84	0.18	56,56,56,56	0
56	MG	2a	1717	1/1	0.84	0.31	71,71,71,71	0
56	MG	1Q	201	1/1	0.84	0.20	60,60,60,60	0
56	MG	2a	1732	1/1	0.84	0.20	57,57,57,57	0
56	MG	2A	3497	1/1	0.84	0.09	52,52,52,52	0
56	MG	2A	3109	1/1	0.84	0.16	55,55,55,55	0
56	MG	2a	1743	1/1	0.84	0.29	64,64,64,64	0
56	MG	2A	3130	1/1	0.84	0.11	52,52,52,52	0
56	MG	2A	3148	1/1	0.84	0.22	65,65,65,65	0
56	MG	1a	1825	1/1	0.84	0.14	59,59,59,59	0
56	MG	1A	4038	1/1	0.84	0.16	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1R	208	1/1	0.84	0.13	45,45,45,45	0
56	MG	2A	3535	1/1	0.84	0.20	39,39,39,39	0
56	MG	2A	3196	1/1	0.84	0.12	50,50,50,50	0
56	MG	1a	1749	1/1	0.84	0.23	78,78,78,78	0
56	MG	1A	4090	1/1	0.84	0.18	76,76,76,76	0
56	MG	1a	1855	1/1	0.84	0.22	57,57,57,57	0
56	MG	1A	3434	1/1	0.84	0.12	53,53,53,53	0
56	MG	2D	306	1/1	0.84	0.14	65,65,65,65	0
56	MG	1A	3569	1/1	0.84	0.15	56,56,56,56	0
56	MG	1a	1616	1/1	0.84	0.24	74,74,74,74	0
56	MG	1A	3036	1/1	0.84	0.18	66,66,66,66	0
56	MG	2a	1619	1/1	0.84	0.11	91,91,91,91	0
56	MG	2a	1623	1/1	0.84	0.24	92,92,92,92	0
56	MG	1A	3962	1/1	0.84	0.12	55,55,55,55	0
56	MG	1A	3034	1/1	0.84	0.14	71,71,71,71	0
56	MG	1A	3529	1/1	0.84	0.11	61,61,61,61	0
56	MG	2a	1639	1/1	0.84	0.25	71,71,71,71	0
56	MG	2a	1640	1/1	0.84	0.39	72,72,72,72	0
56	MG	1A	3888	1/1	0.84	0.14	29,29,29,29	0
56	MG	1A	4213	1/1	0.84	0.11	49,49,49,49	0
56	MG	1A	3400	1/1	0.84	0.10	44,44,44,44	0
56	MG	1A	4076	1/1	0.84	0.12	71,71,71,71	0
56	MG	2A	3018	1/1	0.84	0.15	58,58,58,58	0
56	MG	2a	1656	1/1	0.84	0.08	94,94,94,94	0
56	MG	1T	201	1/1	0.85	0.20	56,56,56,56	0
56	MG	1A	3958	1/1	0.85	0.12	58,58,58,58	0
56	MG	1A	3818	1/1	0.85	0.08	32,32,32,32	0
56	MG	1A	3972	1/1	0.85	0.14	59,59,59,59	0
56	MG	2A	3441	1/1	0.85	0.15	58,58,58,58	0
56	MG	1A	3992	1/1	0.85	0.14	54,54,54,54	0
56	MG	2A	3453	1/1	0.85	0.15	49,49,49,49	0
56	MG	1A	3393	1/1	0.85	0.23	59,59,59,59	0
56	MG	1a	1777	1/1	0.85	0.31	72,72,72,72	0
56	MG	1a	1626	1/1	0.85	0.17	61,61,61,61	0
56	MG	1A	4002	1/1	0.85	0.23	82,82,82,82	0
56	MG	1A	4112	1/1	0.85	0.14	29,29,29,29	0
56	MG	2A	3089	1/1	0.85	0.14	51,51,51,51	0
56	MG	2A	3105	1/1	0.85	0.18	45,45,45,45	0
56	MG	1A	3456	1/1	0.85	0.09	41,41,41,41	0
56	MG	1a	1791	1/1	0.85	0.12	64,64,64,64	0
56	MG	1a	1639	1/1	0.85	0.20	77,77,77,77	0
56	MG	1A	3360	1/1	0.85	0.15	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3416	1/1	0.85	0.17	60,60,60,60	0
56	MG	2a	1760	1/1	0.85	0.11	67,67,67,67	0
56	MG	2A	3173	1/1	0.85	0.18	53,53,53,53	0
56	MG	1A	3024	1/1	0.85	0.12	48,48,48,48	0
56	MG	2A	3555	1/1	0.85	0.09	47,47,47,47	0
56	MG	2A	3564	1/1	0.85	0.10	35,35,35,35	0
56	MG	1A	3046	1/1	0.85	0.09	51,51,51,51	0
56	MG	2A	3579	1/1	0.85	0.17	69,69,69,69	0
56	MG	1A	3485	1/1	0.85	0.35	51,51,51,51	0
56	MG	1A	3493	1/1	0.85	0.17	58,58,58,58	0
56	MG	2a	1788	1/1	0.85	0.11	59,59,59,59	0
56	MG	1A	3899	1/1	0.85	0.12	36,36,36,36	0
56	MG	1A	4232	1/1	0.85	0.09	68,68,68,68	0
56	MG	2A	3244	1/1	0.85	0.14	49,49,49,49	0
56	MG	1A	3548	1/1	0.85	0.08	62,62,62,62	0
56	MG	1A	3500	1/1	0.85	0.15	55,55,55,55	0
56	MG	1A	3504	1/1	0.85	0.17	61,61,61,61	0
56	MG	1A	3323	1/1	0.85	0.11	58,58,58,58	0
56	MG	2A	3281	1/1	0.85	0.18	58,58,58,58	0
56	MG	1a	1747	1/1	0.85	0.25	68,68,68,68	0
56	MG	2A	3305	1/1	0.85	0.12	53,53,53,53	0
56	MG	1b	3002	1/1	0.85	0.19	88,88,88,88	0
56	MG	1B	213	1/1	0.85	0.27	59,59,59,59	0
56	MG	2A	3342	1/1	0.85	0.23	59,59,59,59	0
56	MG	1A	3780	1/1	0.85	0.11	24,24,24,24	0
56	MG	1A	3940	1/1	0.85	0.18	70,70,70,70	0
56	MG	1A	3111	1/1	0.85	0.11	59,59,59,59	0
56	MG	2e	3001	1/1	0.85	0.23	67,67,67,67	0
56	MG	1A	3944	1/1	0.85	0.19	77,77,77,77	0
56	MG	2a	1659	1/1	0.85	0.25	78,78,78,78	0
56	MG	2A	3034	1/1	0.86	0.11	58,58,58,58	0
56	MG	2a	1665	1/1	0.86	0.21	65,65,65,65	0
56	MG	1A	3675	1/1	0.86	0.15	55,55,55,55	0
56	MG	2A	3409	1/1	0.86	0.23	59,59,59,59	0
56	MG	1A	3069	1/1	0.86	0.16	50,50,50,50	0
56	MG	1a	1675	1/1	0.86	0.25	63,63,63,63	0
56	MG	2a	1680	1/1	0.86	0.23	70,70,70,70	0
56	MG	1A	3408	1/1	0.86	0.21	53,53,53,53	0
56	MG	1A	3545	1/1	0.86	0.18	56,56,56,56	0
56	MG	1a	1797	1/1	0.86	0.28	49,49,49,49	0
56	MG	1B	203	1/1	0.86	0.15	66,66,66,66	0
56	MG	1a	1810	1/1	0.86	0.16	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3076	1/1	0.86	0.10	60,60,60,60	0
56	MG	1A	3599	1/1	0.86	0.12	60,60,60,60	0
56	MG	2A	3136	1/1	0.86	0.14	56,56,56,56	0
56	MG	1A	4110	1/1	0.86	0.34	75,75,75,75	0
56	MG	2A	3509	1/1	0.86	0.09	35,35,35,35	0
56	MG	1A	3897	1/1	0.86	0.10	32,32,32,32	0
56	MG	1A	4115	1/1	0.86	0.09	36,36,36,36	0
56	MG	1A	3989	1/1	0.86	0.11	20,20,20,20	0
56	MG	1A	4161	1/1	0.86	0.14	45,45,45,45	0
56	MG	1a	1728	1/1	0.86	0.14	48,48,48,48	0
56	MG	2A	3197	1/1	0.86	0.06	49,49,49,49	0
56	MG	2A	3204	1/1	0.86	0.14	59,59,59,59	0
56	MG	2A	3209	1/1	0.86	0.09	56,56,56,56	0
56	MG	2A	3553	1/1	0.86	0.16	44,44,44,44	0
56	MG	1A	4163	1/1	0.86	0.17	61,61,61,61	0
56	MG	2A	3232	1/1	0.86	0.10	72,72,72,72	0
56	MG	1A	4164	1/1	0.86	0.26	66,66,66,66	0
56	MG	1A	4166	1/1	0.86	0.15	36,36,36,36	0
56	MG	1a	1871	1/1	0.86	0.18	55,55,55,55	0
56	MG	1a	1601	1/1	0.86	0.12	68,68,68,68	0
56	MG	1a	1751	1/1	0.86	0.13	70,70,70,70	0
56	MG	1a	1602	1/1	0.86	0.09	58,58,58,58	0
56	MG	1A	3990	1/1	0.86	0.13	53,53,53,53	0
56	MG	2A	3275	1/1	0.86	0.17	65,65,65,65	0
56	MG	1o	3001	1/1	0.86	0.13	47,47,47,47	0
56	MG	1a	1611	1/1	0.86	0.39	72,72,72,72	0
56	MG	1A	4172	1/1	0.86	0.19	22,22,22,22	0
56	MG	1A	3607	1/1	0.86	0.16	53,53,53,53	0
56	MG	1A	3558	1/1	0.86	0.12	49,49,49,49	0
56	MG	2A	3337	1/1	0.86	0.18	56,56,56,56	0
56	MG	1A	3006	1/1	0.86	0.14	64,64,64,64	0
56	MG	2A	3005	1/1	0.86	0.15	52,52,52,52	0
56	MG	2a	1646	1/1	0.86	0.19	63,63,63,63	0
56	MG	1a	1631	1/1	0.86	0.31	58,58,58,58	0
56	MG	2A	3014	1/1	0.86	0.17	54,54,54,54	0
56	MG	1A	3469	1/1	0.86	0.10	57,57,57,57	0
56	MG	2a	1654	1/1	0.86	0.14	80,80,80,80	0
56	MG	1A	3309	1/1	0.86	0.38	65,65,65,65	0
56	MG	2A	3388	1/1	0.86	0.19	56,56,56,56	0
56	MG	1A	3142	1/1	0.87	0.08	61,61,61,61	0
56	MG	1A	4157	1/1	0.87	0.18	53,53,53,53	0
56	MG	1A	3515	1/1	0.87	0.17	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3370	1/1	0.87	0.12	60,60,60,60	0
56	MG	2a	1658	1/1	0.87	0.20	79,79,79,79	0
56	MG	1A	3464	1/1	0.87	0.23	50,50,50,50	0
56	MG	2a	1660	1/1	0.87	0.10	86,86,86,86	0
56	MG	1A	3518	1/1	0.87	0.13	53,53,53,53	0
56	MG	2A	3037	1/1	0.87	0.14	51,51,51,51	0
56	MG	1a	1621	1/1	0.87	0.13	64,64,64,64	0
56	MG	1A	4037	1/1	0.87	0.10	77,77,77,77	0
56	MG	2A	3414	1/1	0.87	0.20	56,56,56,56	0
56	MG	2A	3419	1/1	0.87	0.12	66,66,66,66	0
56	MG	2A	3434	1/1	0.87	0.17	58,58,58,58	0
56	MG	1A	3522	1/1	0.87	0.11	52,52,52,52	0
56	MG	1A	4039	1/1	0.87	0.12	67,67,67,67	0
56	MG	1A	3922	1/1	0.87	0.16	47,47,47,47	0
56	MG	1A	3755	1/1	0.87	0.15	52,52,52,52	0
56	MG	1A	3396	1/1	0.87	0.18	49,49,49,49	0
56	MG	2A	3096	1/1	0.87	0.15	50,50,50,50	0
56	MG	1A	4062	1/1	0.87	0.19	63,63,63,63	0
56	MG	2a	1722	1/1	0.87	0.21	71,71,71,71	0
56	MG	2a	1727	1/1	0.87	0.28	70,70,70,70	0
56	MG	2A	3107	1/1	0.87	0.12	65,65,65,65	0
56	MG	1a	1652	1/1	0.87	0.10	54,54,54,54	0
56	MG	2A	3110	1/1	0.87	0.38	64,64,64,64	0
56	MG	1a	1653	1/1	0.87	0.11	52,52,52,52	0
56	MG	1A	3353	1/1	0.87	0.11	51,51,51,51	0
56	MG	1a	1688	1/1	0.87	0.09	74,74,74,74	0
56	MG	1A	3025	1/1	0.87	0.13	52,52,52,52	0
56	MG	1a	1696	1/1	0.87	0.24	61,61,61,61	0
56	MG	1A	3955	1/1	0.87	0.18	54,54,54,54	0
56	MG	1A	3956	1/1	0.87	0.12	53,53,53,53	0
56	MG	1A	3532	1/1	0.87	0.20	55,55,55,55	0
56	MG	1A	3363	1/1	0.87	0.21	71,71,71,71	0
56	MG	2a	1773	1/1	0.87	0.20	65,65,65,65	0
56	MG	1A	3104	1/1	0.87	0.19	60,60,60,60	0
56	MG	2a	1781	1/1	0.87	0.10	56,56,56,56	0
56	MG	1a	1712	1/1	0.87	0.26	75,75,75,75	0
56	MG	2a	1785	1/1	0.87	0.20	71,71,71,71	0
56	MG	1A	3975	1/1	0.87	0.11	57,57,57,57	0
56	MG	1A	3620	1/1	0.87	0.11	37,37,37,37	0
56	MG	1A	3627	1/1	0.87	0.13	59,59,59,59	0
56	MG	1F	309	1/1	0.87	0.11	57,57,57,57	0
56	MG	1A	4089	1/1	0.87	0.13	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1884	1/1	0.87	0.18	58,58,58,58	0
56	MG	2A	3253	1/1	0.87	0.18	58,58,58,58	0
56	MG	1a	1888	1/1	0.87	0.20	73,73,73,73	0
56	MG	1a	1731	1/1	0.87	0.26	62,62,62,62	0
56	MG	1a	1734	1/1	0.87	0.19	67,67,67,67	0
56	MG	2a	1610	1/1	0.87	0.13	74,74,74,74	0
56	MG	1k	3002	1/1	0.87	0.12	68,68,68,68	0
56	MG	1A	3132	1/1	0.87	0.09	52,52,52,52	0
56	MG	1R	202	1/1	0.87	0.25	56,56,56,56	0
56	MG	1A	3314	1/1	0.87	0.12	38,38,38,38	0
56	MG	1A	3891	1/1	0.87	0.24	61,61,61,61	0
56	MG	1A	3453	1/1	0.87	0.14	51,51,51,51	0
56	MG	2a	1840	1/1	0.87	0.15	58,58,58,58	0
56	MG	2A	3320	1/1	0.87	0.11	45,45,45,45	0
56	MG	2A	3331	1/1	0.87	0.10	55,55,55,55	0
56	MG	2A	3002	1/1	0.87	0.21	58,58,58,58	0
56	MG	1A	3007	1/1	0.87	0.25	69,69,69,69	0
56	MG	2n	101	1/1	0.87	0.30	65,65,65,65	0
56	MG	1A	4117	1/1	0.87	0.18	51,51,51,51	0
56	MG	1A	3471	1/1	0.88	0.15	47,47,47,47	0
56	MG	1A	4126	1/1	0.88	0.12	56,56,56,56	0
56	MG	1A	3831	1/1	0.88	0.14	53,53,53,53	0
56	MG	1A	3059	1/1	0.88	0.08	38,38,38,38	0
56	MG	2a	1601	1/1	0.88	0.30	67,67,67,67	0
56	MG	2A	3180	1/1	0.88	0.09	43,43,43,43	0
56	MG	2a	1603	1/1	0.88	0.15	59,59,59,59	0
56	MG	1A	3065	1/1	0.88	0.09	48,48,48,48	0
56	MG	1A	4004	1/1	0.88	0.11	68,68,68,68	0
56	MG	2a	1613	1/1	0.88	0.19	65,65,65,65	0
56	MG	2a	1614	1/1	0.88	0.15	68,68,68,68	0
56	MG	1a	1636	1/1	0.88	0.13	58,58,58,58	0
56	MG	1a	1813	1/1	0.88	0.24	59,59,59,59	0
56	MG	2a	1627	1/1	0.88	0.14	63,63,63,63	0
56	MG	2A	3208	1/1	0.88	0.11	49,49,49,49	0
56	MG	1A	3852	1/1	0.88	0.12	58,58,58,58	0
56	MG	2A	3212	1/1	0.88	0.17	50,50,50,50	0
56	MG	2A	3221	1/1	0.88	0.14	48,48,48,48	0
56	MG	1a	1823	1/1	0.88	0.12	46,46,46,46	0
56	MG	1A	3163	1/1	0.88	0.17	52,52,52,52	0
56	MG	1A	3867	1/1	0.88	0.17	52,52,52,52	0
56	MG	2a	1647	1/1	0.88	0.18	82,82,82,82	0
56	MG	1A	3241	1/1	0.88	0.27	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1665	1/1	0.88	0.20	74,74,74,74	0
56	MG	1A	3005	1/1	0.88	0.18	49,49,49,49	0
56	MG	1A	3307	1/1	0.88	0.12	37,37,37,37	0
56	MG	1A	3646	1/1	0.88	0.14	53,53,53,53	0
56	MG	1A	3549	1/1	0.88	0.08	45,45,45,45	0
56	MG	1A	4040	1/1	0.88	0.11	67,67,67,67	0
56	MG	1A	4043	1/1	0.88	0.11	62,62,62,62	0
56	MG	1A	3121	1/1	0.88	0.12	54,54,54,54	0
56	MG	2a	1664	1/1	0.88	0.18	84,84,84,84	0
56	MG	1A	3704	1/1	0.88	0.16	24,24,24,24	0
56	MG	1A	4059	1/1	0.88	0.14	60,60,60,60	0
56	MG	2a	1671	1/1	0.88	0.25	58,58,58,58	0
56	MG	1a	1895	1/1	0.88	0.12	78,78,78,78	0
56	MG	1A	3901	1/1	0.88	0.09	35,35,35,35	0
56	MG	2A	3314	1/1	0.88	0.24	63,63,63,63	0
56	MG	1A	3707	1/1	0.88	0.09	68,68,68,68	0
56	MG	1h	202	1/1	0.88	0.16	65,65,65,65	0
56	MG	1a	1717	1/1	0.88	0.38	62,62,62,62	0
56	MG	1A	3711	1/1	0.88	0.10	31,31,31,31	0
56	MG	1A	3073	1/1	0.88	0.10	69,69,69,69	0
56	MG	1a	1724	1/1	0.88	0.17	70,70,70,70	0
56	MG	1x	101	1/1	0.88	0.15	67,67,67,67	0
56	MG	1E	304	1/1	0.88	0.24	53,53,53,53	0
56	MG	1x	103	1/1	0.88	0.12	64,64,64,64	0
56	MG	1A	3564	1/1	0.88	0.16	41,41,41,41	0
56	MG	2A	3386	1/1	0.88	0.19	52,52,52,52	0
56	MG	1A	3317	1/1	0.88	0.12	73,73,73,73	0
56	MG	1A	3075	1/1	0.88	0.10	46,46,46,46	0
56	MG	2A	3401	1/1	0.88	0.14	60,60,60,60	0
56	MG	2A	3403	1/1	0.88	0.10	62,62,62,62	0
56	MG	2a	1737	1/1	0.88	0.14	64,64,64,64	0
56	MG	2a	1741	1/1	0.88	0.20	80,80,80,80	0
56	MG	1A	3575	1/1	0.88	0.16	65,65,65,65	0
56	MG	1a	1743	1/1	0.88	0.16	47,47,47,47	0
56	MG	2A	3412	1/1	0.88	0.10	44,44,44,44	0
56	MG	2A	3008	1/1	0.88	0.10	59,59,59,59	0
56	MG	2a	1762	1/1	0.88	0.13	64,64,64,64	0
56	MG	1a	1746	1/1	0.88	0.09	81,81,81,81	0
56	MG	2a	1765	1/1	0.88	0.21	65,65,65,65	0
56	MG	2A	3426	1/1	0.88	0.12	51,51,51,51	0
56	MG	1Q	204	1/1	0.88	0.19	42,42,42,42	0
56	MG	1A	3010	1/1	0.88	0.11	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	1771	1/1	0.88	0.20	50,50,50,50	0
56	MG	1A	3756	1/1	0.88	0.09	52,52,52,52	0
56	MG	1A	3759	1/1	0.88	0.13	56,56,56,56	0
56	MG	1U	201	1/1	0.88	0.11	32,32,32,32	0
56	MG	1a	1753	1/1	0.88	0.23	76,76,76,76	0
56	MG	2A	3454	1/1	0.88	0.09	30,30,30,30	0
56	MG	2A	3055	1/1	0.88	0.19	60,60,60,60	0
56	MG	1U	204	1/1	0.88	0.20	55,55,55,55	0
56	MG	2A	3477	1/1	0.88	0.11	39,39,39,39	0
56	MG	1U	205	1/1	0.88	0.28	35,35,35,35	0
56	MG	2a	1790	1/1	0.88	0.17	53,53,53,53	0
56	MG	2a	1791	1/1	0.88	0.23	64,64,64,64	0
56	MG	2A	3064	1/1	0.88	0.17	34,34,34,34	0
56	MG	2A	3491	1/1	0.88	0.14	56,56,56,56	0
56	MG	2A	3076	1/1	0.88	0.13	44,44,44,44	0
56	MG	2a	1803	1/1	0.88	0.21	72,72,72,72	0
56	MG	1Z	303	1/1	0.88	0.11	64,64,64,64	0
56	MG	1A	3772	1/1	0.88	0.13	35,35,35,35	0
56	MG	1A	3138	1/1	0.88	0.09	49,49,49,49	0
56	MG	1A	3800	1/1	0.88	0.11	50,50,50,50	0
56	MG	2A	3099	1/1	0.88	0.12	54,54,54,54	0
56	MG	1A	3809	1/1	0.88	0.09	16,16,16,16	0
56	MG	1a	1608	1/1	0.88	0.16	66,66,66,66	0
56	MG	1A	3100	1/1	0.88	0.12	47,47,47,47	0
56	MG	2A	3542	1/1	0.88	0.21	33,33,33,33	0
56	MG	1A	3141	1/1	0.88	0.13	46,46,46,46	0
56	MG	2a	1839	1/1	0.88	0.13	48,48,48,48	0
56	MG	2A	3115	1/1	0.88	0.11	51,51,51,51	0
56	MG	2A	3116	1/1	0.88	0.20	48,48,48,48	0
56	MG	2A	3117	1/1	0.88	0.17	52,52,52,52	0
56	MG	2A	3563	1/1	0.88	0.14	42,42,42,42	0
56	MG	1A	4113	1/1	0.88	0.11	39,39,39,39	0
56	MG	1A	3824	1/1	0.88	0.09	56,56,56,56	0
56	MG	2A	3141	1/1	0.88	0.26	53,53,53,53	0
56	MG	2x	3003	1/1	0.88	0.19	65,65,65,65	0
56	MG	1A	3770	1/1	0.89	0.14	25,25,25,25	0
56	MG	2a	1616	1/1	0.89	0.25	60,60,60,60	0
56	MG	2a	1618	1/1	0.89	0.23	63,63,63,63	0
56	MG	1E	301	1/1	0.89	0.10	23,23,23,23	0
56	MG	1k	3001	1/1	0.89	0.21	66,66,66,66	0
56	MG	2a	1624	1/1	0.89	0.17	61,61,61,61	0
56	MG	2A	3274	1/1	0.89	0.20	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	1631	1/1	0.89	0.13	49,49,49,49	0
56	MG	1A	3031	1/1	0.89	0.08	50,50,50,50	0
56	MG	2A	3276	1/1	0.89	0.26	48,48,48,48	0
56	MG	1A	4066	1/1	0.89	0.09	71,71,71,71	0
56	MG	1A	3209	1/1	0.89	0.20	46,46,46,46	0
56	MG	1G	203	1/1	0.89	0.20	61,61,61,61	0
56	MG	1A	3785	1/1	0.89	0.17	45,45,45,45	0
56	MG	2a	1644	1/1	0.89	0.17	60,60,60,60	0
56	MG	1a	1738	1/1	0.89	0.21	58,58,58,58	0
56	MG	1A	3487	1/1	0.89	0.15	46,46,46,46	0
56	MG	1x	111	1/1	0.89	0.18	61,61,61,61	0
56	MG	1A	4074	1/1	0.89	0.13	66,66,66,66	0
56	MG	1A	3803	1/1	0.89	0.17	62,62,62,62	0
56	MG	1A	3601	1/1	0.89	0.25	54,54,54,54	0
56	MG	1A	3489	1/1	0.89	0.15	42,42,42,42	0
56	MG	2A	3006	1/1	0.89	0.11	66,66,66,66	0
56	MG	2A	3359	1/1	0.89	0.15	39,39,39,39	0
56	MG	1A	3331	1/1	0.89	0.14	43,43,43,43	0
56	MG	1A	3351	1/1	0.89	0.19	59,59,59,59	0
56	MG	1A	3047	1/1	0.89	0.10	69,69,69,69	0
56	MG	1A	3827	1/1	0.89	0.11	70,70,70,70	0
56	MG	2A	3021	1/1	0.89	0.19	50,50,50,50	0
56	MG	1A	3978	1/1	0.89	0.31	38,38,38,38	0
56	MG	2A	3396	1/1	0.89	0.24	55,55,55,55	0
56	MG	2A	3032	1/1	0.89	0.14	45,45,45,45	0
56	MG	2A	3033	1/1	0.89	0.24	64,64,64,64	0
56	MG	18	102	1/1	0.89	0.10	40,40,40,40	0
56	MG	1A	3414	1/1	0.89	0.13	55,55,55,55	0
56	MG	1A	4106	1/1	0.89	0.17	45,45,45,45	0
56	MG	1A	3550	1/1	0.89	0.26	40,40,40,40	0
56	MG	1A	3293	1/1	0.89	0.05	42,42,42,42	0
56	MG	1A	3129	1/1	0.89	0.15	40,40,40,40	0
56	MG	2a	1707	1/1	0.89	0.16	52,52,52,52	0
56	MG	1A	4001	1/1	0.89	0.07	46,46,46,46	0
56	MG	2a	1712	1/1	0.89	0.27	62,62,62,62	0
56	MG	2A	3428	1/1	0.89	0.08	62,62,62,62	0
56	MG	1a	1771	1/1	0.89	0.10	56,56,56,56	0
56	MG	2a	1720	1/1	0.89	0.21	65,65,65,65	0
56	MG	1A	3855	1/1	0.89	0.20	62,62,62,62	0
56	MG	1A	3423	1/1	0.89	0.14	48,48,48,48	0
56	MG	1A	4134	1/1	0.89	0.09	38,38,38,38	0
56	MG	2A	3445	1/1	0.89	0.10	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1625	1/1	0.89	0.22	74,74,74,74	0
56	MG	1a	1785	1/1	0.89	0.15	43,43,43,43	0
56	MG	2a	1736	1/1	0.89	0.17	66,66,66,66	0
56	MG	1A	3697	1/1	0.89	0.10	47,47,47,47	0
56	MG	2A	3102	1/1	0.89	0.12	68,68,68,68	0
56	MG	2A	3457	1/1	0.89	0.18	54,54,54,54	0
56	MG	2a	1753	1/1	0.89	0.23	76,76,76,76	0
56	MG	1a	1628	1/1	0.89	0.17	55,55,55,55	0
56	MG	2A	3462	1/1	0.89	0.11	60,60,60,60	0
56	MG	2A	3464	1/1	0.89	0.19	57,57,57,57	0
56	MG	2A	3470	1/1	0.89	0.08	40,40,40,40	0
56	MG	2a	1763	1/1	0.89	0.12	69,69,69,69	0
56	MG	1A	4150	1/1	0.89	0.12	47,47,47,47	0
56	MG	1A	4007	1/1	0.89	0.09	49,49,49,49	0
56	MG	2a	1766	1/1	0.89	0.13	60,60,60,60	0
56	MG	1A	3567	1/1	0.89	0.14	49,49,49,49	0
56	MG	2A	3481	1/1	0.89	0.12	48,48,48,48	0
56	MG	2A	3486	1/1	0.89	0.11	47,47,47,47	0
56	MG	2a	1770	1/1	0.89	0.20	71,71,71,71	0
56	MG	1A	4012	1/1	0.89	0.12	40,40,40,40	0
56	MG	1A	3568	1/1	0.89	0.10	52,52,52,52	0
56	MG	1A	3878	1/1	0.89	0.20	68,68,68,68	0
56	MG	1a	1818	1/1	0.89	0.22	58,58,58,58	0
56	MG	2A	3133	1/1	0.89	0.13	55,55,55,55	0
56	MG	1A	4020	1/1	0.89	0.13	69,69,69,69	0
56	MG	1A	3884	1/1	0.89	0.28	37,37,37,37	0
56	MG	1A	3304	1/1	0.89	0.16	51,51,51,51	0
56	MG	1A	3571	1/1	0.89	0.18	52,52,52,52	0
56	MG	2A	3168	1/1	0.89	0.10	48,48,48,48	0
56	MG	2A	3536	1/1	0.89	0.14	66,66,66,66	0
56	MG	1A	3149	1/1	0.89	0.15	58,58,58,58	0
56	MG	1A	4197	1/1	0.89	0.16	72,72,72,72	0
56	MG	2a	1795	1/1	0.89	0.17	54,54,54,54	0
56	MG	1A	3153	1/1	0.89	0.17	49,49,49,49	0
56	MG	2A	3183	1/1	0.89	0.07	50,50,50,50	0
56	MG	1a	1851	1/1	0.89	0.23	60,60,60,60	0
56	MG	1A	3585	1/1	0.89	0.09	56,56,56,56	0
56	MG	1a	1859	1/1	0.89	0.15	67,67,67,67	0
56	MG	2a	1809	1/1	0.89	0.16	69,69,69,69	0
56	MG	2a	1810	1/1	0.89	0.22	59,59,59,59	0
56	MG	2a	1811	1/1	0.89	0.17	60,60,60,60	0
56	MG	1A	4041	1/1	0.89	0.12	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1863	1/1	0.89	0.12	73,73,73,73	0
56	MG	2a	1815	1/1	0.89	0.21	63,63,63,63	0
56	MG	2A	3584	1/1	0.89	0.09	55,55,55,55	0
56	MG	2B	3001	1/1	0.89	0.14	62,62,62,62	0
56	MG	1a	1865	1/1	0.89	0.12	55,55,55,55	0
56	MG	1A	3372	1/1	0.89	0.17	56,56,56,56	0
56	MG	2B	3009	1/1	0.89	0.12	65,65,65,65	0
56	MG	1A	3162	1/1	0.89	0.14	50,50,50,50	0
56	MG	2G	3001	1/1	0.89	0.14	61,61,61,61	0
56	MG	1A	4050	1/1	0.89	0.11	53,53,53,53	0
56	MG	1A	3909	1/1	0.89	0.24	34,34,34,34	0
56	MG	1A	3592	1/1	0.89	0.11	54,54,54,54	0
56	MG	2d	502	1/1	0.89	0.21	48,48,48,48	0
56	MG	1a	1714	1/1	0.89	0.21	53,53,53,53	0
56	MG	2a	1606	1/1	0.89	0.27	69,69,69,69	0
56	MG	1B	209	1/1	0.89	0.28	68,68,68,68	0
56	MG	1A	3593	1/1	0.89	0.13	49,49,49,49	0
56	MG	1d	502	1/1	0.89	0.24	68,68,68,68	0
56	MG	2Q	3001	1/1	0.90	0.11	46,46,46,46	0
56	MG	1A	3673	1/1	0.90	0.14	38,38,38,38	0
56	MG	28	102	1/1	0.90	0.26	60,60,60,60	0
56	MG	1A	3502	1/1	0.90	0.15	67,67,67,67	0
56	MG	2A	3203	1/1	0.90	0.14	51,51,51,51	0
56	MG	1A	3677	1/1	0.90	0.12	30,30,30,30	0
56	MG	1A	4128	1/1	0.90	0.21	53,53,53,53	0
56	MG	1A	3373	1/1	0.90	0.13	43,43,43,43	0
56	MG	1A	4138	1/1	0.90	0.17	57,57,57,57	0
56	MG	1a	1627	1/1	0.90	0.08	70,70,70,70	0
56	MG	1A	4009	1/1	0.90	0.11	65,65,65,65	0
56	MG	1A	4141	1/1	0.90	0.19	68,68,68,68	0
56	MG	2a	1617	1/1	0.90	0.09	69,69,69,69	0
56	MG	1A	4145	1/1	0.90	0.18	63,63,63,63	0
56	MG	1A	4149	1/1	0.90	0.16	52,52,52,52	0
56	MG	2a	1620	1/1	0.90	0.19	51,51,51,51	0
56	MG	1A	3374	1/1	0.90	0.18	53,53,53,53	0
56	MG	1A	4153	1/1	0.90	0.20	68,68,68,68	0
56	MG	1A	3315	1/1	0.90	0.16	55,55,55,55	0
56	MG	2a	1630	1/1	0.90	0.11	60,60,60,60	0
56	MG	1a	1646	1/1	0.90	0.10	53,53,53,53	0
56	MG	2A	3259	1/1	0.90	0.16	34,34,34,34	0
56	MG	1A	4159	1/1	0.90	0.19	50,50,50,50	0
56	MG	2a	1634	1/1	0.90	0.28	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2a	1636	1/1	0.90	0.09	50,50,50,50	0
56	MG	1A	3240	1/1	0.90	0.14	66,66,66,66	0
56	MG	1A	3318	1/1	0.90	0.17	63,63,63,63	0
56	MG	1A	3724	1/1	0.90	0.18	61,61,61,61	0
56	MG	2a	1641	1/1	0.90	0.08	60,60,60,60	0
56	MG	1A	4165	1/1	0.90	0.11	26,26,26,26	0
56	MG	1a	1680	1/1	0.90	0.15	70,70,70,70	0
56	MG	2a	1645	1/1	0.90	0.11	73,73,73,73	0
56	MG	1a	1682	1/1	0.90	0.10	57,57,57,57	0
56	MG	1A	4022	1/1	0.90	0.20	45,45,45,45	0
56	MG	2A	3304	1/1	0.90	0.21	51,51,51,51	0
56	MG	1A	4023	1/1	0.90	0.20	73,73,73,73	0
56	MG	2A	3308	1/1	0.90	0.09	56,56,56,56	0
56	MG	1a	1692	1/1	0.90	0.15	64,64,64,64	0
56	MG	2A	3312	1/1	0.90	0.13	35,35,35,35	0
56	MG	1A	4025	1/1	0.90	0.11	69,69,69,69	0
56	MG	2a	1657	1/1	0.90	0.16	58,58,58,58	0
56	MG	1A	3576	1/1	0.90	0.09	50,50,50,50	0
56	MG	1A	3581	1/1	0.90	0.09	62,62,62,62	0
56	MG	1A	3395	1/1	0.90	0.15	51,51,51,51	0
56	MG	2a	1663	1/1	0.90	0.10	74,74,74,74	0
56	MG	1A	3022	1/1	0.90	0.09	54,54,54,54	0
56	MG	1A	4198	1/1	0.90	0.07	42,42,42,42	0
56	MG	1A	4199	1/1	0.90	0.16	53,53,53,53	0
56	MG	1A	3262	1/1	0.90	0.10	52,52,52,52	0
56	MG	2A	3361	1/1	0.90	0.16	53,53,53,53	0
56	MG	1x	108	1/1	0.90	0.30	56,56,56,56	0
56	MG	1A	3906	1/1	0.90	0.10	34,34,34,34	0
56	MG	1A	3402	1/1	0.90	0.11	48,48,48,48	0
56	MG	2A	3375	1/1	0.90	0.10	32,32,32,32	0
56	MG	2a	1689	1/1	0.90	0.23	60,60,60,60	0
56	MG	1a	1718	1/1	0.90	0.41	72,72,72,72	0
56	MG	2a	1695	1/1	0.90	0.25	62,62,62,62	0
56	MG	1A	3282	1/1	0.90	0.14	73,73,73,73	0
56	MG	1A	3040	1/1	0.90	0.10	46,46,46,46	0
56	MG	1A	3771	1/1	0.90	0.09	21,21,21,21	0
56	MG	1A	3012	1/1	0.90	0.14	49,49,49,49	0
56	MG	1A	3356	1/1	0.90	0.15	61,61,61,61	0
56	MG	2A	3009	1/1	0.90	0.20	35,35,35,35	0
56	MG	1B	206	1/1	0.90	0.13	54,54,54,54	0
56	MG	2A	3408	1/1	0.90	0.18	57,57,57,57	0
56	MG	1a	1732	1/1	0.90	0.07	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3020	1/1	0.90	0.08	44,44,44,44	0
56	MG	1A	3928	1/1	0.90	0.14	51,51,51,51	0
56	MG	1A	3421	1/1	0.90	0.11	64,64,64,64	0
56	MG	2A	3423	1/1	0.90	0.12	60,60,60,60	0
56	MG	2A	3424	1/1	0.90	0.14	42,42,42,42	0
56	MG	1A	3301	1/1	0.90	0.20	77,77,77,77	0
56	MG	1B	223	1/1	0.90	0.14	66,66,66,66	0
56	MG	2A	3429	1/1	0.90	0.13	43,43,43,43	0
56	MG	2A	3430	1/1	0.90	0.08	54,54,54,54	0
56	MG	1D	302	1/1	0.90	0.17	71,71,71,71	0
56	MG	2a	1744	1/1	0.90	0.18	69,69,69,69	0
56	MG	2a	1751	1/1	0.90	0.17	57,57,57,57	0
56	MG	1D	308	1/1	0.90	0.20	29,29,29,29	0
56	MG	1D	314	1/1	0.90	0.19	43,43,43,43	0
56	MG	2A	3044	1/1	0.90	0.15	39,39,39,39	0
56	MG	2a	1756	1/1	0.90	0.08	62,62,62,62	0
56	MG	1A	3105	1/1	0.90	0.11	43,43,43,43	0
56	MG	1A	3479	1/1	0.90	0.23	44,44,44,44	0
56	MG	1E	306	1/1	0.90	0.09	47,47,47,47	0
56	MG	1A	3946	1/1	0.90	0.17	28,28,28,28	0
56	MG	1F	307	1/1	0.90	0.36	51,51,51,51	0
56	MG	2A	3071	1/1	0.90	0.26	66,66,66,66	0
56	MG	1A	3948	1/1	0.90	0.29	39,39,39,39	0
56	MG	1A	3018	1/1	0.90	0.16	56,56,56,56	0
56	MG	2A	3079	1/1	0.90	0.27	47,47,47,47	0
56	MG	2A	3080	1/1	0.90	0.10	51,51,51,51	0
56	MG	2A	3473	1/1	0.90	0.11	53,53,53,53	0
56	MG	1a	1763	1/1	0.90	0.16	88,88,88,88	0
56	MG	1A	3814	1/1	0.90	0.08	24,24,24,24	0
56	MG	2A	3095	1/1	0.90	0.17	48,48,48,48	0
56	MG	1A	3817	1/1	0.90	0.08	45,45,45,45	0
56	MG	2A	3484	1/1	0.90	0.13	43,43,43,43	0
56	MG	1A	3088	1/1	0.90	0.11	57,57,57,57	0
56	MG	2A	3487	1/1	0.90	0.12	42,42,42,42	0
56	MG	2A	3490	1/1	0.90	0.16	45,45,45,45	0
56	MG	1A	3964	1/1	0.90	0.15	41,41,41,41	0
56	MG	1A	3122	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3428	1/1	0.90	0.08	52,52,52,52	0
56	MG	1a	1775	1/1	0.90	0.10	55,55,55,55	0
56	MG	1A	3656	1/1	0.90	0.13	43,43,43,43	0
56	MG	1A	3985	1/1	0.90	0.24	60,60,60,60	0
56	MG	2a	1797	1/1	0.90	0.16	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3521	1/1	0.90	0.07	42,42,42,42	0
56	MG	1A	4094	1/1	0.90	0.12	34,34,34,34	0
56	MG	1a	1780	1/1	0.90	0.19	57,57,57,57	0
56	MG	2a	1806	1/1	0.90	0.13	67,67,67,67	0
56	MG	2A	3122	1/1	0.90	0.08	57,57,57,57	0
56	MG	2A	3124	1/1	0.90	0.28	58,58,58,58	0
56	MG	1A	4096	1/1	0.90	0.17	22,22,22,22	0
56	MG	2A	3540	1/1	0.90	0.12	36,36,36,36	0
56	MG	1A	4102	1/1	0.90	0.10	63,63,63,63	0
56	MG	2A	3135	1/1	0.90	0.14	48,48,48,48	0
56	MG	10	103	1/1	0.90	0.13	44,44,44,44	0
56	MG	2A	3138	1/1	0.90	0.17	55,55,55,55	0
56	MG	10	106	1/1	0.90	0.18	73,73,73,73	0
56	MG	1A	3431	1/1	0.90	0.15	56,56,56,56	0
56	MG	1a	1799	1/1	0.90	0.14	60,60,60,60	0
56	MG	2a	1834	1/1	0.90	0.23	52,52,52,52	0
56	MG	2A	3162	1/1	0.90	0.23	60,60,60,60	0
56	MG	1A	3836	1/1	0.90	0.13	33,33,33,33	0
56	MG	2A	3581	1/1	0.90	0.11	46,46,46,46	0
56	MG	1A	4107	1/1	0.90	0.22	35,35,35,35	0
56	MG	1A	3659	1/1	0.90	0.16	58,58,58,58	0
56	MG	2B	3002	1/1	0.90	0.21	54,54,54,54	0
56	MG	1A	3660	1/1	0.90	0.12	46,46,46,46	0
56	MG	2A	3182	1/1	0.90	0.20	49,49,49,49	0
56	MG	1A	3849	1/1	0.90	0.11	29,29,29,29	0
56	MG	2A	3187	1/1	0.90	0.18	44,44,44,44	0
56	MG	1a	1817	1/1	0.90	0.21	59,59,59,59	0
56	MG	2u	101	1/1	0.90	0.18	60,60,60,60	0
56	MG	2O	201	1/1	0.90	0.13	57,57,57,57	0
56	MG	1A	3747	1/1	0.91	0.09	22,22,22,22	0
56	MG	2A	3265	1/1	0.91	0.11	44,44,44,44	0
56	MG	1A	4052	1/1	0.91	0.10	24,24,24,24	0
56	MG	2a	1615	1/1	0.91	0.38	63,63,63,63	0
56	MG	1A	3231	1/1	0.91	0.25	53,53,53,53	0
56	MG	1a	1699	1/1	0.91	0.28	61,61,61,61	0
56	MG	1a	1700	1/1	0.91	0.21	48,48,48,48	0
56	MG	1A	3239	1/1	0.91	0.14	33,33,33,33	0
56	MG	2A	3277	1/1	0.91	0.09	38,38,38,38	0
56	MG	1A	3044	1/1	0.91	0.08	53,53,53,53	0
56	MG	1A	3332	1/1	0.91	0.08	45,45,45,45	0
56	MG	2A	3282	1/1	0.91	0.12	43,43,43,43	0
56	MG	1A	3914	1/1	0.91	0.12	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3299	1/1	0.91	0.09	25,25,25,25	0
56	MG	1A	3761	1/1	0.91	0.18	50,50,50,50	0
56	MG	1a	1713	1/1	0.91	0.28	67,67,67,67	0
56	MG	1A	3596	1/1	0.91	0.21	32,32,32,32	0
56	MG	1a	1715	1/1	0.91	0.17	51,51,51,51	0
56	MG	1A	3112	1/1	0.91	0.09	63,63,63,63	0
56	MG	1A	3598	1/1	0.91	0.12	57,57,57,57	0
56	MG	1A	3403	1/1	0.91	0.14	72,72,72,72	0
56	MG	2A	3322	1/1	0.91	0.09	39,39,39,39	0
56	MG	1a	1719	1/1	0.91	0.24	58,58,58,58	0
56	MG	2a	1643	1/1	0.91	0.13	65,65,65,65	0
56	MG	2A	3334	1/1	0.91	0.14	48,48,48,48	0
56	MG	1A	3942	1/1	0.91	0.14	44,44,44,44	0
56	MG	1A	3244	1/1	0.91	0.17	45,45,45,45	0
56	MG	1A	3790	1/1	0.91	0.09	29,29,29,29	0
56	MG	2A	3004	1/1	0.91	0.07	51,51,51,51	0
56	MG	1A	3794	1/1	0.91	0.10	43,43,43,43	0
56	MG	1A	3795	1/1	0.91	0.11	58,58,58,58	0
56	MG	1F	302	1/1	0.91	0.18	39,39,39,39	0
56	MG	1A	4085	1/1	0.91	0.16	53,53,53,53	0
56	MG	1A	3114	1/1	0.91	0.20	39,39,39,39	0
56	MG	2A	3012	1/1	0.91	0.16	53,53,53,53	0
56	MG	2A	3013	1/1	0.91	0.15	66,66,66,66	0
56	MG	1A	3096	1/1	0.91	0.12	50,50,50,50	0
56	MG	2A	3015	1/1	0.91	0.10	55,55,55,55	0
56	MG	2A	3017	1/1	0.91	0.09	50,50,50,50	0
56	MG	1P	201	1/1	0.91	0.14	52,52,52,52	0
56	MG	1P	202	1/1	0.91	0.11	49,49,49,49	0
56	MG	1A	3534	1/1	0.91	0.14	43,43,43,43	0
56	MG	2a	1670	1/1	0.91	0.13	62,62,62,62	0
56	MG	2A	3023	1/1	0.91	0.17	48,48,48,48	0
56	MG	1A	3359	1/1	0.91	0.17	43,43,43,43	0
56	MG	1A	3632	1/1	0.91	0.11	63,63,63,63	0
56	MG	1A	3419	1/1	0.91	0.11	75,75,75,75	0
56	MG	1R	203	1/1	0.91	0.13	59,59,59,59	0
56	MG	1A	3639	1/1	0.91	0.13	38,38,38,38	0
56	MG	1A	3977	1/1	0.91	0.09	58,58,58,58	0
56	MG	1A	3420	1/1	0.91	0.23	57,57,57,57	0
56	MG	2a	1691	1/1	0.91	0.07	45,45,45,45	0
56	MG	2A	3045	1/1	0.91	0.11	53,53,53,53	0
56	MG	2A	3427	1/1	0.91	0.08	41,41,41,41	0
56	MG	1A	4108	1/1	0.91	0.14	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3037	1/1	0.91	0.20	43,43,43,43	0
56	MG	1a	1758	1/1	0.91	0.10	53,53,53,53	0
56	MG	2a	1708	1/1	0.91	0.40	63,63,63,63	0
56	MG	1A	3988	1/1	0.91	0.16	53,53,53,53	0
56	MG	10	101	1/1	0.91	0.09	48,48,48,48	0
56	MG	2a	1713	1/1	0.91	0.23	56,56,56,56	0
56	MG	2A	3065	1/1	0.91	0.09	38,38,38,38	0
56	MG	2A	3067	1/1	0.91	0.32	54,54,54,54	0
56	MG	2A	3070	1/1	0.91	0.09	45,45,45,45	0
56	MG	1A	3478	1/1	0.91	0.24	41,41,41,41	0
56	MG	1A	3124	1/1	0.91	0.10	55,55,55,55	0
56	MG	2a	1729	1/1	0.91	0.09	70,70,70,70	0
56	MG	1A	3480	1/1	0.91	0.19	35,35,35,35	0
56	MG	1A	3838	1/1	0.91	0.19	54,54,54,54	0
56	MG	18	103	1/1	0.91	0.14	46,46,46,46	0
56	MG	1A	3026	1/1	0.91	0.14	56,56,56,56	0
56	MG	2a	1735	1/1	0.91	0.21	73,73,73,73	0
56	MG	2A	3461	1/1	0.91	0.18	52,52,52,52	0
56	MG	1A	3662	1/1	0.91	0.11	36,36,36,36	0
56	MG	1A	3367	1/1	0.91	0.14	56,56,56,56	0
56	MG	2A	3466	1/1	0.91	0.18	50,50,50,50	0
56	MG	2A	3468	1/1	0.91	0.12	60,60,60,60	0
56	MG	1A	3674	1/1	0.91	0.16	43,43,43,43	0
56	MG	1A	3103	1/1	0.91	0.08	54,54,54,54	0
56	MG	2A	3474	1/1	0.91	0.07	62,62,62,62	0
56	MG	2A	3475	1/1	0.91	0.16	57,57,57,57	0
56	MG	1a	1610	1/1	0.91	0.08	57,57,57,57	0
56	MG	2a	1757	1/1	0.91	0.15	61,61,61,61	0
56	MG	1A	3856	1/1	0.91	0.18	56,56,56,56	0
56	MG	1a	1612	1/1	0.91	0.09	82,82,82,82	0
56	MG	1a	1787	1/1	0.91	0.13	51,51,51,51	0
56	MG	1a	1789	1/1	0.91	0.17	62,62,62,62	0
56	MG	2A	3485	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	3858	1/1	0.91	0.13	48,48,48,48	0
56	MG	1a	1793	1/1	0.91	0.16	58,58,58,58	0
56	MG	1A	3490	1/1	0.91	0.06	59,59,59,59	0
56	MG	1A	4013	1/1	0.91	0.18	56,56,56,56	0
56	MG	1A	4156	1/1	0.91	0.12	59,59,59,59	0
56	MG	1a	1806	1/1	0.91	0.09	69,69,69,69	0
56	MG	2A	3499	1/1	0.91	0.13	60,60,60,60	0
56	MG	2A	3501	1/1	0.91	0.12	48,48,48,48	0
56	MG	2a	1779	1/1	0.91	0.15	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3507	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	3061	1/1	0.91	0.08	58,58,58,58	0
56	MG	1A	3496	1/1	0.91	0.14	46,46,46,46	0
56	MG	1A	3870	1/1	0.91	0.16	41,41,41,41	0
56	MG	2A	3520	1/1	0.91	0.10	50,50,50,50	0
56	MG	1A	3871	1/1	0.91	0.17	55,55,55,55	0
56	MG	1a	1816	1/1	0.91	0.17	60,60,60,60	0
56	MG	2A	3147	1/1	0.91	0.18	47,47,47,47	0
56	MG	1A	3174	1/1	0.91	0.12	40,40,40,40	0
56	MG	1A	3063	1/1	0.91	0.16	49,49,49,49	0
56	MG	1a	1820	1/1	0.91	0.16	69,69,69,69	0
56	MG	2A	3165	1/1	0.91	0.07	33,33,33,33	0
56	MG	1A	3879	1/1	0.91	0.12	25,25,25,25	0
56	MG	2A	3547	1/1	0.91	0.11	54,54,54,54	0
56	MG	1A	4030	1/1	0.91	0.16	59,59,59,59	0
56	MG	1A	4032	1/1	0.91	0.06	77,77,77,77	0
56	MG	1a	1832	1/1	0.91	0.17	52,52,52,52	0
56	MG	2a	1807	1/1	0.91	0.15	50,50,50,50	0
56	MG	1A	4033	1/1	0.91	0.12	56,56,56,56	0
56	MG	1a	1840	1/1	0.91	0.09	51,51,51,51	0
56	MG	1a	1842	1/1	0.91	0.17	49,49,49,49	0
56	MG	1A	3215	1/1	0.91	0.13	51,51,51,51	0
56	MG	1A	3886	1/1	0.91	0.15	60,60,60,60	0
56	MG	1A	3719	1/1	0.91	0.16	64,64,64,64	0
56	MG	2A	3582	1/1	0.91	0.15	38,38,38,38	0
56	MG	2a	1816	1/1	0.91	0.13	74,74,74,74	0
56	MG	1a	1848	1/1	0.91	0.09	53,53,53,53	0
56	MG	1a	1664	1/1	0.91	0.12	56,56,56,56	0
56	MG	1A	3505	1/1	0.91	0.09	47,47,47,47	0
56	MG	1a	1858	1/1	0.91	0.08	78,78,78,78	0
56	MG	1a	1670	1/1	0.91	0.14	68,68,68,68	0
56	MG	2A	3214	1/1	0.91	0.06	37,37,37,37	0
56	MG	1A	3726	1/1	0.91	0.19	57,57,57,57	0
56	MG	1A	3382	1/1	0.91	0.10	49,49,49,49	0
56	MG	1A	3510	1/1	0.91	0.13	42,42,42,42	0
56	MG	1a	1867	1/1	0.91	0.16	54,54,54,54	0
56	MG	2X	8001	1/1	0.91	0.15	37,37,37,37	0
56	MG	2a	1848	1/1	0.91	0.09	57,57,57,57	0
56	MG	1a	1684	1/1	0.91	0.08	52,52,52,52	0
56	MG	1a	1687	1/1	0.91	0.12	51,51,51,51	0
56	MG	1a	1872	1/1	0.91	0.15	47,47,47,47	0
56	MG	2l	3004	1/1	0.91	0.14	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3246	1/1	0.91	0.09	45,45,45,45	0
56	MG	2A	3250	1/1	0.91	0.16	58,58,58,58	0
56	MG	1A	4217	1/1	0.91	0.17	72,72,72,72	0
56	MG	1A	3217	1/1	0.91	0.11	43,43,43,43	0
56	MG	1e	201	1/1	0.92	0.15	63,63,63,63	0
56	MG	1A	3713	1/1	0.92	0.06	26,26,26,26	0
56	MG	2A	3264	1/1	0.92	0.13	47,47,47,47	0
56	MG	1e	203	1/1	0.92	0.08	54,54,54,54	0
56	MG	1F	304	1/1	0.92	0.23	21,21,21,21	0
56	MG	2a	1605	1/1	0.92	0.12	74,74,74,74	0
56	MG	1A	4088	1/1	0.92	0.09	76,76,76,76	0
56	MG	2A	3269	1/1	0.92	0.14	34,34,34,34	0
56	MG	1A	3525	1/1	0.92	0.22	56,56,56,56	0
56	MG	2a	1611	1/1	0.92	0.20	48,48,48,48	0
56	MG	1G	202	1/1	0.92	0.12	51,51,51,51	0
56	MG	1A	3070	1/1	0.92	0.08	48,48,48,48	0
56	MG	1N	203	1/1	0.92	0.15	44,44,44,44	0
56	MG	1r	3002	1/1	0.92	0.12	48,48,48,48	0
56	MG	1a	1725	1/1	0.92	0.19	75,75,75,75	0
56	MG	1A	4091	1/1	0.92	0.18	71,71,71,71	0
56	MG	2A	3283	1/1	0.92	0.11	51,51,51,51	0
56	MG	1A	3980	1/1	0.92	0.06	42,42,42,42	0
56	MG	2A	3289	1/1	0.92	0.08	49,49,49,49	0
56	MG	2A	3298	1/1	0.92	0.10	47,47,47,47	0
56	MG	2a	1625	1/1	0.92	0.10	61,61,61,61	0
56	MG	1x	107	1/1	0.92	0.23	55,55,55,55	0
56	MG	2a	1629	1/1	0.92	0.19	60,60,60,60	0
56	MG	2A	3301	1/1	0.92	0.20	40,40,40,40	0
56	MG	1A	3981	1/1	0.92	0.09	59,59,59,59	0
56	MG	1x	109	1/1	0.92	0.14	47,47,47,47	0
56	MG	1A	3013	1/1	0.92	0.12	62,62,62,62	0
56	MG	1A	4103	1/1	0.92	0.11	35,35,35,35	0
56	MG	2a	1635	1/1	0.92	0.21	66,66,66,66	0
56	MG	2A	3311	1/1	0.92	0.11	57,57,57,57	0
56	MG	1a	1736	1/1	0.92	0.36	76,76,76,76	0
56	MG	1a	1737	1/1	0.92	0.09	67,67,67,67	0
56	MG	2A	3315	1/1	0.92	0.11	41,41,41,41	0
56	MG	2A	3317	1/1	0.92	0.14	35,35,35,35	0
56	MG	1A	3859	1/1	0.92	0.06	44,44,44,44	0
56	MG	1A	3175	1/1	0.92	0.06	40,40,40,40	0
56	MG	1A	3863	1/1	0.92	0.11	58,58,58,58	0
56	MG	1A	3866	1/1	0.92	0.06	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1T	203	1/1	0.92	0.11	44,44,44,44	0
56	MG	1A	3595	1/1	0.92	0.07	65,65,65,65	0
56	MG	1A	3186	1/1	0.92	0.23	39,39,39,39	0
56	MG	1A	3131	1/1	0.92	0.14	43,43,43,43	0
56	MG	2A	3348	1/1	0.92	0.06	35,35,35,35	0
56	MG	1Z	302	1/1	0.92	0.12	50,50,50,50	0
56	MG	1A	3106	1/1	0.92	0.13	47,47,47,47	0
56	MG	1A	3375	1/1	0.92	0.22	57,57,57,57	0
56	MG	1A	3877	1/1	0.92	0.08	56,56,56,56	0
56	MG	1A	3600	1/1	0.92	0.21	54,54,54,54	0
56	MG	1A	3039	1/1	0.92	0.10	48,48,48,48	0
56	MG	1a	1761	1/1	0.92	0.09	57,57,57,57	0
56	MG	2A	3024	1/1	0.92	0.12	51,51,51,51	0
56	MG	12	3001	1/1	0.92	0.10	52,52,52,52	0
56	MG	2A	3390	1/1	0.92	0.21	56,56,56,56	0
56	MG	2a	1666	1/1	0.92	0.21	62,62,62,62	0
56	MG	2a	1667	1/1	0.92	0.20	60,60,60,60	0
56	MG	2A	3394	1/1	0.92	0.25	61,61,61,61	0
56	MG	2A	3027	1/1	0.92	0.15	47,47,47,47	0
56	MG	2A	3397	1/1	0.92	0.20	45,45,45,45	0
56	MG	16	101	1/1	0.92	0.17	47,47,47,47	0
56	MG	2a	1675	1/1	0.92	0.24	57,57,57,57	0
56	MG	1A	3880	1/1	0.92	0.14	52,52,52,52	0
56	MG	1A	3377	1/1	0.92	0.10	48,48,48,48	0
56	MG	2A	3404	1/1	0.92	0.12	58,58,58,58	0
56	MG	2A	3035	1/1	0.92	0.13	57,57,57,57	0
56	MG	2A	3036	1/1	0.92	0.10	48,48,48,48	0
56	MG	1A	3546	1/1	0.92	0.11	46,46,46,46	0
56	MG	2A	3040	1/1	0.92	0.25	52,52,52,52	0
56	MG	2a	1694	1/1	0.92	0.25	60,60,60,60	0
56	MG	1A	3618	1/1	0.92	0.17	40,40,40,40	0
56	MG	2A	3416	1/1	0.92	0.09	58,58,58,58	0
56	MG	1a	1770	1/1	0.92	0.11	56,56,56,56	0
56	MG	1A	3890	1/1	0.92	0.07	45,45,45,45	0
56	MG	1a	1604	1/1	0.92	0.13	79,79,79,79	0
56	MG	1a	1776	1/1	0.92	0.15	64,64,64,64	0
56	MG	2A	3056	1/1	0.92	0.20	45,45,45,45	0
56	MG	1A	3016	1/1	0.92	0.10	55,55,55,55	0
56	MG	1A	4152	1/1	0.92	0.19	54,54,54,54	0
56	MG	1A	3388	1/1	0.92	0.25	65,65,65,65	0
56	MG	1A	3894	1/1	0.92	0.09	27,27,27,27	0
56	MG	2a	1718	1/1	0.92	0.12	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3140	1/1	0.92	0.06	43,43,43,43	0
56	MG	1A	4029	1/1	0.92	0.22	64,64,64,64	0
56	MG	1A	3898	1/1	0.92	0.09	52,52,52,52	0
56	MG	2A	3442	1/1	0.92	0.08	59,59,59,59	0
56	MG	1A	3553	1/1	0.92	0.09	43,43,43,43	0
56	MG	1A	3113	1/1	0.92	0.13	49,49,49,49	0
56	MG	1A	3042	1/1	0.92	0.09	47,47,47,47	0
56	MG	1A	3645	1/1	0.92	0.11	59,59,59,59	0
56	MG	1a	1795	1/1	0.92	0.17	60,60,60,60	0
56	MG	1A	3440	1/1	0.92	0.12	52,52,52,52	0
56	MG	1A	3801	1/1	0.92	0.08	40,40,40,40	0
56	MG	1A	3566	1/1	0.92	0.13	44,44,44,44	0
56	MG	2A	3097	1/1	0.92	0.08	42,42,42,42	0
56	MG	1A	3805	1/1	0.92	0.09	54,54,54,54	0
56	MG	2a	1745	1/1	0.92	0.25	52,52,52,52	0
56	MG	2a	1748	1/1	0.92	0.20	51,51,51,51	0
56	MG	1a	1634	1/1	0.92	0.25	61,61,61,61	0
56	MG	1A	3333	1/1	0.92	0.17	63,63,63,63	0
56	MG	1A	4044	1/1	0.92	0.14	72,72,72,72	0
56	MG	1a	1637	1/1	0.92	0.10	60,60,60,60	0
56	MG	1A	3920	1/1	0.92	0.12	48,48,48,48	0
56	MG	1A	3398	1/1	0.92	0.20	46,46,46,46	0
56	MG	2a	1758	1/1	0.92	0.10	89,89,89,89	0
56	MG	1A	3032	1/1	0.92	0.12	50,50,50,50	0
56	MG	2a	1761	1/1	0.92	0.10	69,69,69,69	0
56	MG	1A	4204	1/1	0.92	0.18	56,56,56,56	0
56	MG	1A	4054	1/1	0.92	0.11	56,56,56,56	0
56	MG	1a	1657	1/1	0.92	0.13	54,54,54,54	0
56	MG	1A	3250	1/1	0.92	0.21	45,45,45,45	0
56	MG	1a	1829	1/1	0.92	0.16	60,60,60,60	0
56	MG	1A	4223	1/1	0.92	0.12	47,47,47,47	0
56	MG	1A	4227	1/1	0.92	0.08	34,34,34,34	0
56	MG	1a	1838	1/1	0.92	0.08	41,41,41,41	0
56	MG	1a	1839	1/1	0.92	0.18	54,54,54,54	0
56	MG	2A	3142	1/1	0.92	0.23	56,56,56,56	0
56	MG	2a	1772	1/1	0.92	0.14	57,57,57,57	0
56	MG	1a	1672	1/1	0.92	0.13	68,68,68,68	0
56	MG	1A	4057	1/1	0.92	0.18	71,71,71,71	0
56	MG	2A	3151	1/1	0.92	0.20	38,38,38,38	0
56	MG	2A	3506	1/1	0.92	0.08	52,52,52,52	0
56	MG	1a	1843	1/1	0.92	0.13	63,63,63,63	0
56	MG	2A	3508	1/1	0.92	0.11	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1679	1/1	0.92	0.23	52,52,52,52	0
56	MG	2A	3511	1/1	0.92	0.10	40,40,40,40	0
56	MG	1A	3939	1/1	0.92	0.10	34,34,34,34	0
56	MG	1A	3572	1/1	0.92	0.39	35,35,35,35	0
56	MG	2A	3519	1/1	0.92	0.09	45,45,45,45	0
56	MG	1a	1683	1/1	0.92	0.16	52,52,52,52	0
56	MG	2a	1792	1/1	0.92	0.12	62,62,62,62	0
56	MG	1A	3017	1/1	0.92	0.16	50,50,50,50	0
56	MG	1a	1852	1/1	0.92	0.15	62,62,62,62	0
56	MG	1A	4063	1/1	0.92	0.14	64,64,64,64	0
56	MG	2A	3531	1/1	0.92	0.15	52,52,52,52	0
56	MG	1A	3068	1/1	0.92	0.21	54,54,54,54	0
56	MG	2a	1801	1/1	0.92	0.20	64,64,64,64	0
56	MG	1a	1690	1/1	0.92	0.13	57,57,57,57	0
56	MG	1A	3291	1/1	0.92	0.21	57,57,57,57	0
56	MG	2A	3537	1/1	0.92	0.14	49,49,49,49	0
56	MG	1a	1861	1/1	0.92	0.15	50,50,50,50	0
56	MG	1a	1862	1/1	0.92	0.20	50,50,50,50	0
56	MG	2A	3546	1/1	0.92	0.12	51,51,51,51	0
56	MG	1A	3682	1/1	0.92	0.08	43,43,43,43	0
56	MG	2A	3548	1/1	0.92	0.18	53,53,53,53	0
56	MG	1a	1864	1/1	0.92	0.15	74,74,74,74	0
56	MG	1A	3692	1/1	0.92	0.21	37,37,37,37	0
56	MG	1A	3519	1/1	0.92	0.26	51,51,51,51	0
56	MG	2A	3210	1/1	0.92	0.13	50,50,50,50	0
56	MG	2a	1819	1/1	0.92	0.27	56,56,56,56	0
56	MG	2A	3558	1/1	0.92	0.14	42,42,42,42	0
56	MG	1A	3161	1/1	0.92	0.17	47,47,47,47	0
56	MG	1B	224	1/1	0.92	0.17	59,59,59,59	0
56	MG	2a	1832	1/1	0.92	0.08	59,59,59,59	0
56	MG	2A	3568	1/1	0.92	0.10	51,51,51,51	0
56	MG	1A	3957	1/1	0.92	0.16	46,46,46,46	0
56	MG	1D	305	1/1	0.92	0.12	35,35,35,35	0
56	MG	1A	3589	1/1	0.92	0.31	56,56,56,56	0
56	MG	1a	1883	1/1	0.92	0.12	62,62,62,62	0
56	MG	2A	3235	1/1	0.92	0.12	44,44,44,44	0
56	MG	2A	3237	1/1	0.92	0.22	67,67,67,67	0
56	MG	1A	3844	1/1	0.92	0.09	33,33,33,33	0
56	MG	1A	4080	1/1	0.92	0.10	56,56,56,56	0
56	MG	2B	3006	1/1	0.92	0.26	57,57,57,57	0
56	MG	1A	3845	1/1	0.92	0.06	22,22,22,22	0
56	MG	2e	3002	1/1	0.92	0.14	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2l	3002	1/1	0.92	0.09	74,74,74,74	0
56	MG	2A	3245	1/1	0.92	0.08	58,58,58,58	0
56	MG	1b	3001	1/1	0.92	0.13	78,78,78,78	0
56	MG	2A	3247	1/1	0.92	0.12	34,34,34,34	0
56	MG	2p	101	1/1	0.92	0.14	59,59,59,59	0
56	MG	1A	3971	1/1	0.92	0.08	47,47,47,47	0
56	MG	1A	3003	1/1	0.92	0.25	60,60,60,60	0
56	MG	2x	3002	1/1	0.92	0.20	57,57,57,57	0
56	MG	2A	3256	1/1	0.92	0.14	53,53,53,53	0
56	MG	2F	301	1/1	0.93	0.09	38,38,38,38	0
56	MG	1B	212	1/1	0.93	0.22	53,53,53,53	0
56	MG	1a	1704	1/1	0.93	0.32	55,55,55,55	0
56	MG	1A	3588	1/1	0.93	0.06	51,51,51,51	0
56	MG	1a	1707	1/1	0.93	0.23	45,45,45,45	0
56	MG	1a	1708	1/1	0.93	0.22	61,61,61,61	0
56	MG	25	502	1/1	0.93	0.21	54,54,54,54	0
56	MG	1a	1709	1/1	0.93	0.15	75,75,75,75	0
56	MG	1B	219	1/1	0.93	0.07	60,60,60,60	0
56	MG	1B	220	1/1	0.93	0.07	44,44,44,44	0
56	MG	1A	3495	1/1	0.93	0.07	41,41,41,41	0
56	MG	1A	3176	1/1	0.93	0.08	29,29,29,29	0
56	MG	1A	3763	1/1	0.93	0.21	53,53,53,53	0
56	MG	1A	3765	1/1	0.93	0.08	19,19,19,19	0
56	MG	1A	3499	1/1	0.93	0.10	58,58,58,58	0
56	MG	2A	3285	1/1	0.93	0.10	38,38,38,38	0
56	MG	2A	3286	1/1	0.93	0.07	41,41,41,41	0
56	MG	2A	3287	1/1	0.93	0.14	55,55,55,55	0
56	MG	1A	3300	1/1	0.93	0.12	44,44,44,44	0
56	MG	1D	315	1/1	0.93	0.07	39,39,39,39	0
56	MG	2A	3295	1/1	0.93	0.07	47,47,47,47	0
56	MG	1x	105	1/1	0.93	0.20	61,61,61,61	0
56	MG	1A	3097	1/1	0.93	0.16	48,48,48,48	0
56	MG	1A	4069	1/1	0.93	0.06	37,37,37,37	0
56	MG	1E	305	1/1	0.93	0.28	35,35,35,35	0
56	MG	1x	110	1/1	0.93	0.16	68,68,68,68	0
56	MG	1A	3773	1/1	0.93	0.09	31,31,31,31	0
56	MG	1A	3110	1/1	0.93	0.07	43,43,43,43	0
56	MG	1a	1726	1/1	0.93	0.07	56,56,56,56	0
56	MG	1F	301	1/1	0.93	0.15	56,56,56,56	0
56	MG	2A	3313	1/1	0.93	0.11	39,39,39,39	0
56	MG	1A	3929	1/1	0.93	0.18	55,55,55,55	0
56	MG	1A	3933	1/1	0.93	0.07	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3782	1/1	0.93	0.12	28,28,28,28	0
56	MG	1F	308	1/1	0.93	0.12	61,61,61,61	0
56	MG	1A	3371	1/1	0.93	0.08	41,41,41,41	0
56	MG	2A	3326	1/1	0.93	0.10	53,53,53,53	0
56	MG	2A	3328	1/1	0.93	0.07	59,59,59,59	0
56	MG	1A	3305	1/1	0.93	0.07	44,44,44,44	0
56	MG	1A	3941	1/1	0.93	0.16	32,32,32,32	0
56	MG	1N	201	1/1	0.93	0.12	54,54,54,54	0
56	MG	1a	1742	1/1	0.93	0.17	52,52,52,52	0
56	MG	1N	202	1/1	0.93	0.21	54,54,54,54	0
56	MG	2A	3345	1/1	0.93	0.13	55,55,55,55	0
56	MG	1A	3027	1/1	0.93	0.17	36,36,36,36	0
56	MG	1A	4084	1/1	0.93	0.15	73,73,73,73	0
56	MG	2A	3350	1/1	0.93	0.09	54,54,54,54	0
56	MG	2a	1649	1/1	0.93	0.18	77,77,77,77	0
56	MG	2A	3353	1/1	0.93	0.11	29,29,29,29	0
56	MG	2a	1652	1/1	0.93	0.08	86,86,86,86	0
56	MG	2A	3358	1/1	0.93	0.12	58,58,58,58	0
56	MG	1A	3430	1/1	0.93	0.13	44,44,44,44	0
56	MG	1A	3308	1/1	0.93	0.12	43,43,43,43	0
56	MG	1Q	202	1/1	0.93	0.17	35,35,35,35	0
56	MG	1A	3126	1/1	0.93	0.14	31,31,31,31	0
56	MG	2A	3369	1/1	0.93	0.16	42,42,42,42	0
56	MG	1A	3312	1/1	0.93	0.12	42,42,42,42	0
56	MG	1A	3951	1/1	0.93	0.08	36,36,36,36	0
56	MG	2A	3376	1/1	0.93	0.11	48,48,48,48	0
56	MG	2A	3028	1/1	0.93	0.14	63,63,63,63	0
56	MG	1A	3143	1/1	0.93	0.15	52,52,52,52	0
56	MG	2A	3387	1/1	0.93	0.12	52,52,52,52	0
56	MG	1A	4093	1/1	0.93	0.13	29,29,29,29	0
56	MG	2A	3389	1/1	0.93	0.10	46,46,46,46	0
56	MG	1a	1757	1/1	0.93	0.15	70,70,70,70	0
56	MG	1A	3084	1/1	0.93	0.30	53,53,53,53	0
56	MG	1a	1760	1/1	0.93	0.10	49,49,49,49	0
56	MG	1A	3383	1/1	0.93	0.14	42,42,42,42	0
56	MG	1A	3813	1/1	0.93	0.06	39,39,39,39	0
56	MG	2A	3041	1/1	0.93	0.27	49,49,49,49	0
56	MG	2A	3402	1/1	0.93	0.09	47,47,47,47	0
56	MG	2a	1683	1/1	0.93	0.16	67,67,67,67	0
56	MG	1U	203	1/1	0.93	0.18	42,42,42,42	0
56	MG	2a	1687	1/1	0.93	0.23	54,54,54,54	0
56	MG	1A	3385	1/1	0.93	0.22	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3963	1/1	0.93	0.11	45,45,45,45	0
56	MG	1W	3005	1/1	0.93	0.13	24,24,24,24	0
56	MG	2a	1693	1/1	0.93	0.19	50,50,50,50	0
56	MG	1A	3815	1/1	0.93	0.07	32,32,32,32	0
56	MG	1A	3816	1/1	0.93	0.09	48,48,48,48	0
56	MG	2A	3413	1/1	0.93	0.20	54,54,54,54	0
56	MG	2a	1698	1/1	0.93	0.08	62,62,62,62	0
56	MG	2A	3057	1/1	0.93	0.07	34,34,34,34	0
56	MG	2a	1705	1/1	0.93	0.13	60,60,60,60	0
56	MG	1A	3625	1/1	0.93	0.07	47,47,47,47	0
56	MG	2A	3059	1/1	0.93	0.19	59,59,59,59	0
56	MG	1A	3527	1/1	0.93	0.10	48,48,48,48	0
56	MG	1A	3443	1/1	0.93	0.08	59,59,59,59	0
56	MG	1A	3387	1/1	0.93	0.09	54,54,54,54	0
56	MG	2A	3066	1/1	0.93	0.29	60,60,60,60	0
56	MG	2a	1714	1/1	0.93	0.14	61,61,61,61	0
56	MG	1A	4114	1/1	0.93	0.08	47,47,47,47	0
56	MG	15	105	1/1	0.93	0.12	35,35,35,35	0
56	MG	1A	3530	1/1	0.93	0.14	61,61,61,61	0
56	MG	1a	1781	1/1	0.93	0.12	58,58,58,58	0
56	MG	1A	3128	1/1	0.93	0.27	46,46,46,46	0
56	MG	2a	1723	1/1	0.93	0.15	61,61,61,61	0
56	MG	2a	1724	1/1	0.93	0.31	58,58,58,58	0
56	MG	2a	1725	1/1	0.93	0.18	63,63,63,63	0
56	MG	1A	4120	1/1	0.93	0.19	50,50,50,50	0
56	MG	2A	3439	1/1	0.93	0.07	48,48,48,48	0
56	MG	1A	4125	1/1	0.93	0.14	48,48,48,48	0
56	MG	1A	3832	1/1	0.93	0.15	47,47,47,47	0
56	MG	2A	3444	1/1	0.93	0.06	30,30,30,30	0
56	MG	1A	3449	1/1	0.93	0.09	55,55,55,55	0
56	MG	2A	3090	1/1	0.93	0.05	38,38,38,38	0
56	MG	1a	1790	1/1	0.93	0.08	48,48,48,48	0
56	MG	1A	4132	1/1	0.93	0.18	52,52,52,52	0
56	MG	2a	1738	1/1	0.93	0.24	36,36,36,36	0
56	MG	1a	1792	1/1	0.93	0.08	34,34,34,34	0
56	MG	1A	4133	1/1	0.93	0.20	47,47,47,47	0
56	MG	1A	3052	1/1	0.93	0.08	54,54,54,54	0
56	MG	1A	3648	1/1	0.93	0.11	46,46,46,46	0
56	MG	2a	1746	1/1	0.93	0.14	43,43,43,43	0
56	MG	2a	1747	1/1	0.93	0.26	67,67,67,67	0
56	MG	1a	1798	1/1	0.93	0.10	59,59,59,59	0
56	MG	2a	1749	1/1	0.93	0.23	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3649	1/1	0.93	0.08	26,26,26,26	0
56	MG	1A	3392	1/1	0.93	0.17	46,46,46,46	0
56	MG	1A	3998	1/1	0.93	0.12	51,51,51,51	0
56	MG	1a	1617	1/1	0.93	0.17	61,61,61,61	0
56	MG	1A	4146	1/1	0.93	0.14	40,40,40,40	0
56	MG	1A	3458	1/1	0.93	0.16	28,28,28,28	0
56	MG	1a	1623	1/1	0.93	0.12	51,51,51,51	0
56	MG	2A	3127	1/1	0.93	0.18	49,49,49,49	0
56	MG	1a	1624	1/1	0.93	0.14	44,44,44,44	0
56	MG	1A	3160	1/1	0.93	0.09	42,42,42,42	0
56	MG	1A	4151	1/1	0.93	0.23	57,57,57,57	0
56	MG	1A	3463	1/1	0.93	0.23	39,39,39,39	0
56	MG	1a	1821	1/1	0.93	0.14	51,51,51,51	0
56	MG	1A	3329	1/1	0.93	0.05	62,62,62,62	0
56	MG	1A	4006	1/1	0.93	0.10	36,36,36,36	0
56	MG	2A	3489	1/1	0.93	0.09	46,46,46,46	0
56	MG	1A	3669	1/1	0.93	0.10	27,27,27,27	0
56	MG	1A	3670	1/1	0.93	0.14	37,37,37,37	0
56	MG	1A	3330	1/1	0.93	0.11	50,50,50,50	0
56	MG	1A	3130	1/1	0.93	0.22	49,49,49,49	0
56	MG	1A	3862	1/1	0.93	0.07	34,34,34,34	0
56	MG	1A	3468	1/1	0.93	0.14	57,57,57,57	0
56	MG	1A	3552	1/1	0.93	0.07	42,42,42,42	0
56	MG	2a	1780	1/1	0.93	0.17	56,56,56,56	0
56	MG	1a	1643	1/1	0.93	0.09	64,64,64,64	0
56	MG	1A	3260	1/1	0.93	0.14	50,50,50,50	0
56	MG	1A	3686	1/1	0.93	0.15	27,27,27,27	0
56	MG	1A	3470	1/1	0.93	0.12	47,47,47,47	0
56	MG	2A	3513	1/1	0.93	0.10	53,53,53,53	0
56	MG	2A	3514	1/1	0.93	0.13	54,54,54,54	0
56	MG	1A	3696	1/1	0.93	0.15	45,45,45,45	0
56	MG	1a	1656	1/1	0.93	0.17	53,53,53,53	0
56	MG	1a	1849	1/1	0.93	0.11	55,55,55,55	0
56	MG	2A	3193	1/1	0.93	0.12	48,48,48,48	0
56	MG	2A	3194	1/1	0.93	0.08	50,50,50,50	0
56	MG	2a	1794	1/1	0.93	0.19	46,46,46,46	0
56	MG	1a	1850	1/1	0.93	0.08	54,54,54,54	0
56	MG	1A	3091	1/1	0.93	0.15	50,50,50,50	0
56	MG	2A	3527	1/1	0.93	0.15	44,44,44,44	0
56	MG	2a	1799	1/1	0.93	0.22	65,65,65,65	0
56	MG	2A	3199	1/1	0.93	0.08	34,34,34,34	0
56	MG	1a	1659	1/1	0.93	0.13	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3472	1/1	0.93	0.09	47,47,47,47	0
56	MG	2a	1804	1/1	0.93	0.24	63,63,63,63	0
56	MG	1a	1856	1/1	0.93	0.20	64,64,64,64	0
56	MG	1A	3339	1/1	0.93	0.47	48,48,48,48	0
56	MG	1A	3405	1/1	0.93	0.22	45,45,45,45	0
56	MG	1A	3272	1/1	0.93	0.12	46,46,46,46	0
56	MG	2A	3545	1/1	0.93	0.07	54,54,54,54	0
56	MG	2A	3213	1/1	0.93	0.08	40,40,40,40	0
56	MG	1A	3883	1/1	0.93	0.16	49,49,49,49	0
56	MG	1A	3116	1/1	0.93	0.09	39,39,39,39	0
56	MG	2A	3228	1/1	0.93	0.05	63,63,63,63	0
56	MG	1A	3481	1/1	0.93	0.19	33,33,33,33	0
56	MG	1A	3720	1/1	0.93	0.07	47,47,47,47	0
56	MG	2a	1817	1/1	0.93	0.14	61,61,61,61	0
56	MG	1A	3484	1/1	0.93	0.16	34,34,34,34	0
56	MG	2A	3556	1/1	0.93	0.10	33,33,33,33	0
56	MG	1a	1866	1/1	0.93	0.20	72,72,72,72	0
56	MG	2a	1825	1/1	0.93	0.15	63,63,63,63	0
56	MG	2A	3562	1/1	0.93	0.17	44,44,44,44	0
56	MG	1A	3133	1/1	0.93	0.05	55,55,55,55	0
56	MG	1A	3892	1/1	0.93	0.14	50,50,50,50	0
56	MG	2A	3567	1/1	0.93	0.14	49,49,49,49	0
56	MG	2A	3241	1/1	0.93	0.07	41,41,41,41	0
56	MG	1A	3417	1/1	0.93	0.11	30,30,30,30	0
56	MG	2A	3577	1/1	0.93	0.07	40,40,40,40	0
56	MG	1a	1689	1/1	0.93	0.14	62,62,62,62	0
56	MG	1a	1877	1/1	0.93	0.17	59,59,59,59	0
56	MG	1A	3056	1/1	0.93	0.07	38,38,38,38	0
56	MG	1A	4048	1/1	0.93	0.10	50,50,50,50	0
56	MG	2A	3248	1/1	0.93	0.19	55,55,55,55	0
56	MG	1A	3295	1/1	0.93	0.20	45,45,45,45	0
56	MG	2A	3251	1/1	0.93	0.11	22,22,22,22	0
56	MG	2l	3001	1/1	0.93	0.12	66,66,66,66	0
56	MG	1A	3582	1/1	0.93	0.08	46,46,46,46	0
56	MG	1B	208	1/1	0.93	0.08	38,38,38,38	0
56	MG	1A	3584	1/1	0.93	0.07	50,50,50,50	0
56	MG	2l	3005	1/1	0.93	0.08	48,48,48,48	0
56	MG	2D	301	1/1	0.93	0.14	51,51,51,51	0
56	MG	2D	302	1/1	0.93	0.08	52,52,52,52	0
56	MG	2D	304	1/1	0.93	0.07	39,39,39,39	0
56	MG	1A	3296	1/1	0.93	0.24	56,56,56,56	0
56	MG	2E	301	1/1	0.93	0.10	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2E	304	1/1	0.93	0.09	40,40,40,40	0
56	MG	1A	3613	1/1	0.94	0.21	51,51,51,51	0
56	MG	1A	3616	1/1	0.94	0.08	42,42,42,42	0
56	MG	1A	3617	1/1	0.94	0.09	11,11,11,11	0
56	MG	1A	3357	1/1	0.94	0.14	49,49,49,49	0
56	MG	2A	3541	1/1	0.94	0.19	51,51,51,51	0
56	MG	1A	3819	1/1	0.94	0.12	38,38,38,38	0
56	MG	2A	3123	1/1	0.94	0.15	58,58,58,58	0
56	MG	1A	3822	1/1	0.94	0.17	56,56,56,56	0
56	MG	1A	4016	1/1	0.94	0.11	65,65,65,65	0
56	MG	2A	3129	1/1	0.94	0.20	56,56,56,56	0
56	MG	1B	221	1/1	0.94	0.09	44,44,44,44	0
56	MG	1B	222	1/1	0.94	0.12	64,64,64,64	0
56	MG	2A	3134	1/1	0.94	0.19	49,49,49,49	0
56	MG	2A	3554	1/1	0.94	0.06	35,35,35,35	0
56	MG	1A	3513	1/1	0.94	0.09	44,44,44,44	0
56	MG	1A	4018	1/1	0.94	0.23	27,27,27,27	0
56	MG	1B	225	1/1	0.94	0.07	33,33,33,33	0
56	MG	2A	3560	1/1	0.94	0.17	41,41,41,41	0
56	MG	1D	301	1/1	0.94	0.21	37,37,37,37	0
56	MG	1a	1759	1/1	0.94	0.10	58,58,58,58	0
56	MG	1A	3624	1/1	0.94	0.17	43,43,43,43	0
56	MG	1A	3277	1/1	0.94	0.14	39,39,39,39	0
56	MG	2A	3150	1/1	0.94	0.09	46,46,46,46	0
56	MG	1a	1762	1/1	0.94	0.17	67,67,67,67	0
56	MG	1A	3030	1/1	0.94	0.14	53,53,53,53	0
56	MG	2A	3578	1/1	0.94	0.23	45,45,45,45	0
56	MG	1D	309	1/1	0.94	0.16	56,56,56,56	0
56	MG	2A	3164	1/1	0.94	0.08	43,43,43,43	0
56	MG	1D	313	1/1	0.94	0.12	43,43,43,43	0
56	MG	2A	3583	1/1	0.94	0.24	39,39,39,39	0
56	MG	2A	3166	1/1	0.94	0.17	50,50,50,50	0
56	MG	1A	3631	1/1	0.94	0.10	47,47,47,47	0
56	MG	1A	3095	1/1	0.94	0.06	47,47,47,47	0
56	MG	1A	3292	1/1	0.94	0.07	35,35,35,35	0
56	MG	2A	3177	1/1	0.94	0.15	42,42,42,42	0
56	MG	2B	3007	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3839	1/1	0.94	0.11	56,56,56,56	0
56	MG	1A	3637	1/1	0.94	0.11	48,48,48,48	0
56	MG	1a	1774	1/1	0.94	0.08	63,63,63,63	0
56	MG	2A	3185	1/1	0.94	0.09	52,52,52,52	0
56	MG	1A	3060	1/1	0.94	0.13	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3843	1/1	0.94	0.10	46,46,46,46	0
56	MG	1E	308	1/1	0.94	0.09	29,29,29,29	0
56	MG	2E	302	1/1	0.94	0.13	27,27,27,27	0
56	MG	1A	3642	1/1	0.94	0.11	26,26,26,26	0
56	MG	2E	305	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3294	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3847	1/1	0.94	0.09	33,33,33,33	0
56	MG	1F	305	1/1	0.94	0.17	69,69,69,69	0
56	MG	2O	202	1/1	0.94	0.09	44,44,44,44	0
56	MG	1A	3071	1/1	0.94	0.14	60,60,60,60	0
56	MG	2Q	3002	1/1	0.94	0.14	53,53,53,53	0
56	MG	1a	1783	1/1	0.94	0.09	57,57,57,57	0
56	MG	2A	3207	1/1	0.94	0.26	60,60,60,60	0
56	MG	23	101	1/1	0.94	0.11	56,56,56,56	0
56	MG	1A	3192	1/1	0.94	0.12	46,46,46,46	0
56	MG	1A	3854	1/1	0.94	0.09	36,36,36,36	0
56	MG	1A	3647	1/1	0.94	0.08	47,47,47,47	0
56	MG	1A	3195	1/1	0.94	0.11	37,37,37,37	0
56	MG	1H	8001	1/1	0.94	0.12	72,72,72,72	0
56	MG	1A	3442	1/1	0.94	0.07	50,50,50,50	0
56	MG	2A	3216	1/1	0.94	0.13	33,33,33,33	0
56	MG	1A	3299	1/1	0.94	0.09	34,34,34,34	0
56	MG	1A	3444	1/1	0.94	0.11	54,54,54,54	0
56	MG	1A	3196	1/1	0.94	0.09	48,48,48,48	0
56	MG	2a	1612	1/1	0.94	0.25	59,59,59,59	0
56	MG	1A	3197	1/1	0.94	0.18	50,50,50,50	0
56	MG	1A	4055	1/1	0.94	0.08	42,42,42,42	0
56	MG	1A	3200	1/1	0.94	0.12	35,35,35,35	0
56	MG	1A	3668	1/1	0.94	0.10	38,38,38,38	0
56	MG	2A	3238	1/1	0.94	0.15	59,59,59,59	0
56	MG	1A	3208	1/1	0.94	0.12	17,17,17,17	0
56	MG	2A	3240	1/1	0.94	0.14	59,59,59,59	0
56	MG	1A	4060	1/1	0.94	0.08	52,52,52,52	0
56	MG	1A	3455	1/1	0.94	0.15	58,58,58,58	0
56	MG	1R	204	1/1	0.94	0.13	56,56,56,56	0
56	MG	1R	205	1/1	0.94	0.10	49,49,49,49	0
56	MG	2a	1626	1/1	0.94	0.23	74,74,74,74	0
56	MG	1a	1815	1/1	0.94	0.10	43,43,43,43	0
56	MG	1R	207	1/1	0.94	0.10	49,49,49,49	0
56	MG	1A	3540	1/1	0.94	0.25	45,45,45,45	0
56	MG	1A	3873	1/1	0.94	0.15	49,49,49,49	0
56	MG	1A	3306	1/1	0.94	0.25	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1T	204	1/1	0.94	0.07	49,49,49,49	0
56	MG	2A	3255	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3384	1/1	0.94	0.09	55,55,55,55	0
56	MG	1A	3051	1/1	0.94	0.12	57,57,57,57	0
56	MG	1A	4068	1/1	0.94	0.08	37,37,37,37	0
56	MG	2A	3261	1/1	0.94	0.10	41,41,41,41	0
56	MG	2A	3262	1/1	0.94	0.09	36,36,36,36	0
56	MG	1a	1828	1/1	0.94	0.11	57,57,57,57	0
56	MG	1A	3678	1/1	0.94	0.06	27,27,27,27	0
56	MG	1V	201	1/1	0.94	0.11	44,44,44,44	0
56	MG	1a	1835	1/1	0.94	0.07	36,36,36,36	0
56	MG	2A	3268	1/1	0.94	0.05	33,33,33,33	0
56	MG	1W	3001	1/1	0.94	0.18	45,45,45,45	0
56	MG	2A	3271	1/1	0.94	0.08	41,41,41,41	0
56	MG	2A	3272	1/1	0.94	0.11	50,50,50,50	0
56	MG	2A	3273	1/1	0.94	0.12	56,56,56,56	0
56	MG	1W	3004	1/1	0.94	0.14	31,31,31,31	0
56	MG	1A	3462	1/1	0.94	0.19	64,64,64,64	0
56	MG	1A	3043	1/1	0.94	0.16	44,44,44,44	0
56	MG	1A	3216	1/1	0.94	0.07	35,35,35,35	0
56	MG	1A	3064	1/1	0.94	0.09	41,41,41,41	0
56	MG	1A	3390	1/1	0.94	0.06	46,46,46,46	0
56	MG	1A	4077	1/1	0.94	0.17	62,62,62,62	0
56	MG	1A	3700	1/1	0.94	0.14	28,28,28,28	0
56	MG	11	101	1/1	0.94	0.07	42,42,42,42	0
56	MG	1A	3555	1/1	0.94	0.08	51,51,51,51	0
56	MG	2a	1661	1/1	0.94	0.11	64,64,64,64	0
56	MG	13	101	1/1	0.94	0.14	50,50,50,50	0
56	MG	1A	3556	1/1	0.94	0.17	49,49,49,49	0
56	MG	1A	3709	1/1	0.94	0.12	29,29,29,29	0
56	MG	1A	3467	1/1	0.94	0.18	55,55,55,55	0
56	MG	1A	3896	1/1	0.94	0.08	55,55,55,55	0
56	MG	1A	3712	1/1	0.94	0.11	28,28,28,28	0
56	MG	18	105	1/1	0.94	0.11	37,37,37,37	0
56	MG	19	103	1/1	0.94	0.16	51,51,51,51	0
56	MG	1A	3218	1/1	0.94	0.17	35,35,35,35	0
56	MG	1A	3715	1/1	0.94	0.12	22,22,22,22	0
56	MG	1A	3223	1/1	0.94	0.15	40,40,40,40	0
56	MG	1A	3905	1/1	0.94	0.12	32,32,32,32	0
56	MG	1A	3718	1/1	0.94	0.15	39,39,39,39	0
56	MG	1A	3394	1/1	0.94	0.15	45,45,45,45	0
56	MG	1A	3908	1/1	0.94	0.25	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4098	1/1	0.94	0.08	24,24,24,24	0
56	MG	1a	1613	1/1	0.94	0.30	61,61,61,61	0
56	MG	2A	3319	1/1	0.94	0.10	38,38,38,38	0
56	MG	1A	4101	1/1	0.94	0.11	39,39,39,39	0
56	MG	1A	3077	1/1	0.94	0.06	43,43,43,43	0
56	MG	2A	3323	1/1	0.94	0.13	35,35,35,35	0
56	MG	2A	3324	1/1	0.94	0.15	47,47,47,47	0
56	MG	1A	3146	1/1	0.94	0.06	46,46,46,46	0
56	MG	1a	1880	1/1	0.94	0.16	46,46,46,46	0
56	MG	1A	3474	1/1	0.94	0.17	61,61,61,61	0
56	MG	2a	1702	1/1	0.94	0.18	51,51,51,51	0
56	MG	1a	1882	1/1	0.94	0.12	59,59,59,59	0
56	MG	1a	1622	1/1	0.94	0.14	43,43,43,43	0
56	MG	1A	3727	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3917	1/1	0.94	0.09	37,37,37,37	0
56	MG	2A	3344	1/1	0.94	0.17	47,47,47,47	0
56	MG	1a	1893	1/1	0.94	0.08	59,59,59,59	0
56	MG	1a	1894	1/1	0.94	0.17	65,65,65,65	0
56	MG	1A	3729	1/1	0.94	0.20	44,44,44,44	0
56	MG	1A	3570	1/1	0.94	0.17	49,49,49,49	0
56	MG	2A	3351	1/1	0.94	0.15	50,50,50,50	0
56	MG	2A	3352	1/1	0.94	0.07	31,31,31,31	0
56	MG	1A	3147	1/1	0.94	0.16	50,50,50,50	0
56	MG	2A	3354	1/1	0.94	0.14	54,54,54,54	0
56	MG	2A	3356	1/1	0.94	0.12	49,49,49,49	0
56	MG	2A	3357	1/1	0.94	0.08	29,29,29,29	0
56	MG	1A	3743	1/1	0.94	0.08	45,45,45,45	0
56	MG	2a	1726	1/1	0.94	0.15	61,61,61,61	0
56	MG	1A	3326	1/1	0.94	0.14	46,46,46,46	0
56	MG	1A	3932	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3079	1/1	0.94	0.06	63,63,63,63	0
56	MG	1f	3001	1/1	0.94	0.14	47,47,47,47	0
56	MG	1A	4119	1/1	0.94	0.11	35,35,35,35	0
56	MG	1A	3934	1/1	0.94	0.06	27,27,27,27	0
56	MG	1A	4121	1/1	0.94	0.20	55,55,55,55	0
56	MG	1A	3748	1/1	0.94	0.08	30,30,30,30	0
56	MG	1A	3083	1/1	0.94	0.11	44,44,44,44	0
56	MG	1q	202	1/1	0.94	0.19	55,55,55,55	0
56	MG	1A	4127	1/1	0.94	0.14	29,29,29,29	0
56	MG	2a	1742	1/1	0.94	0.09	56,56,56,56	0
56	MG	1a	1645	1/1	0.94	0.10	53,53,53,53	0
56	MG	1A	3751	1/1	0.94	0.23	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3246	1/1	0.94	0.04	13,13,13,13	0
56	MG	1A	3406	1/1	0.94	0.15	42,42,42,42	0
56	MG	1A	3109	1/1	0.94	0.21	62,62,62,62	0
56	MG	1x	106	1/1	0.94	0.13	52,52,52,52	0
56	MG	1A	3760	1/1	0.94	0.10	58,58,58,58	0
56	MG	2a	1750	1/1	0.94	0.19	54,54,54,54	0
56	MG	1A	3411	1/1	0.94	0.17	43,43,43,43	0
56	MG	1a	1658	1/1	0.94	0.13	44,44,44,44	0
56	MG	1A	3488	1/1	0.94	0.07	44,44,44,44	0
56	MG	1a	1663	1/1	0.94	0.11	61,61,61,61	0
56	MG	1A	4142	1/1	0.94	0.10	39,39,39,39	0
56	MG	2A	3406	1/1	0.94	0.11	48,48,48,48	0
56	MG	1A	4144	1/1	0.94	0.20	67,67,67,67	0
56	MG	1a	1666	1/1	0.94	0.05	51,51,51,51	0
56	MG	1a	1667	1/1	0.94	0.13	47,47,47,47	0
56	MG	1A	3252	1/1	0.94	0.08	48,48,48,48	0
56	MG	1a	1671	1/1	0.94	0.21	55,55,55,55	0
56	MG	1A	3953	1/1	0.94	0.14	65,65,65,65	0
56	MG	2A	3418	1/1	0.94	0.18	58,58,58,58	0
56	MG	1a	1674	1/1	0.94	0.24	63,63,63,63	0
56	MG	1A	4147	1/1	0.94	0.10	40,40,40,40	0
56	MG	1a	1677	1/1	0.94	0.11	48,48,48,48	0
56	MG	1A	3766	1/1	0.94	0.10	45,45,45,45	0
56	MG	1A	3769	1/1	0.94	0.12	45,45,45,45	0
56	MG	1a	1681	1/1	0.94	0.14	39,39,39,39	0
56	MG	1A	3334	1/1	0.94	0.09	51,51,51,51	0
56	MG	1A	3491	1/1	0.94	0.06	63,63,63,63	0
56	MG	1A	3960	1/1	0.94	0.20	48,48,48,48	0
56	MG	1A	4154	1/1	0.94	0.13	33,33,33,33	0
56	MG	1A	3337	1/1	0.94	0.10	46,46,46,46	0
56	MG	2A	3437	1/1	0.94	0.05	41,41,41,41	0
56	MG	1A	3254	1/1	0.94	0.12	51,51,51,51	0
56	MG	1A	3340	1/1	0.94	0.12	38,38,38,38	0
56	MG	1A	3965	1/1	0.94	0.07	63,63,63,63	0
56	MG	2A	3443	1/1	0.94	0.07	39,39,39,39	0
56	MG	1A	3966	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3970	1/1	0.94	0.12	54,54,54,54	0
56	MG	1A	3497	1/1	0.94	0.07	55,55,55,55	0
56	MG	2A	3451	1/1	0.94	0.06	41,41,41,41	0
56	MG	1A	3783	1/1	0.94	0.25	58,58,58,58	0
56	MG	1A	3498	1/1	0.94	0.06	46,46,46,46	0
56	MG	1A	3789	1/1	0.94	0.08	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3347	1/1	0.94	0.18	61,61,61,61	0
56	MG	2A	3039	1/1	0.94	0.20	43,43,43,43	0
56	MG	1A	4174	1/1	0.94	0.17	62,62,62,62	0
56	MG	2a	1798	1/1	0.94	0.12	47,47,47,47	0
56	MG	1A	4176	1/1	0.94	0.18	41,41,41,41	0
56	MG	2A	3042	1/1	0.94	0.15	50,50,50,50	0
56	MG	1A	4178	1/1	0.94	0.06	54,54,54,54	0
56	MG	1A	4185	1/1	0.94	0.20	41,41,41,41	0
56	MG	1A	3792	1/1	0.94	0.08	21,21,21,21	0
56	MG	2A	3471	1/1	0.94	0.07	38,38,38,38	0
56	MG	1A	3348	1/1	0.94	0.08	57,57,57,57	0
56	MG	1A	4193	1/1	0.94	0.13	51,51,51,51	0
56	MG	1A	3983	1/1	0.94	0.09	51,51,51,51	0
56	MG	2A	3476	1/1	0.94	0.12	56,56,56,56	0
56	MG	1A	3984	1/1	0.94	0.14	52,52,52,52	0
56	MG	1A	3501	1/1	0.94	0.16	36,36,36,36	0
56	MG	1A	4202	1/1	0.94	0.29	67,67,67,67	0
56	MG	1A	3053	1/1	0.94	0.18	54,54,54,54	0
56	MG	2a	1814	1/1	0.94	0.11	44,44,44,44	0
56	MG	2A	3482	1/1	0.94	0.07	34,34,34,34	0
56	MG	1A	3087	1/1	0.94	0.12	51,51,51,51	0
56	MG	1A	4211	1/1	0.94	0.16	31,31,31,31	0
56	MG	2a	1818	1/1	0.94	0.16	63,63,63,63	0
56	MG	1a	1720	1/1	0.94	0.13	58,58,58,58	0
56	MG	1A	4212	1/1	0.94	0.09	40,40,40,40	0
56	MG	2a	1821	1/1	0.94	0.17	66,66,66,66	0
56	MG	2A	3488	1/1	0.94	0.09	40,40,40,40	0
56	MG	2A	3069	1/1	0.94	0.26	58,58,58,58	0
56	MG	1A	3268	1/1	0.94	0.07	34,34,34,34	0
56	MG	2a	1829	1/1	0.94	0.09	53,53,53,53	0
56	MG	1A	4216	1/1	0.94	0.10	46,46,46,46	0
56	MG	1A	3991	1/1	0.94	0.15	64,64,64,64	0
56	MG	1A	3602	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3994	1/1	0.94	0.06	62,62,62,62	0
56	MG	1A	3806	1/1	0.94	0.14	66,66,66,66	0
56	MG	2a	1838	1/1	0.94	0.14	54,54,54,54	0
56	MG	1a	1729	1/1	0.94	0.25	49,49,49,49	0
56	MG	1a	1730	1/1	0.94	0.09	56,56,56,56	0
56	MG	2a	1842	1/1	0.94	0.29	54,54,54,54	0
56	MG	2a	1844	1/1	0.94	0.17	64,64,64,64	0
56	MG	1A	3808	1/1	0.94	0.11	14,14,14,14	0
56	MG	2A	3092	1/1	0.94	0.19	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3510	1/1	0.94	0.11	61,61,61,61	0
56	MG	1A	4000	1/1	0.94	0.11	53,53,53,53	0
56	MG	1A	3605	1/1	0.94	0.10	40,40,40,40	0
56	MG	1B	202	1/1	0.94	0.13	41,41,41,41	0
56	MG	2A	3098	1/1	0.94	0.11	48,48,48,48	0
56	MG	2A	3516	1/1	0.94	0.06	32,32,32,32	0
56	MG	1A	3020	1/1	0.94	0.14	38,38,38,38	0
56	MG	2A	3101	1/1	0.94	0.17	48,48,48,48	0
56	MG	1A	3508	1/1	0.94	0.10	48,48,48,48	0
56	MG	2A	3104	1/1	0.94	0.06	49,49,49,49	0
56	MG	1a	1739	1/1	0.94	0.10	64,64,64,64	0
56	MG	2A	3106	1/1	0.94	0.18	48,48,48,48	0
56	MG	1A	3610	1/1	0.94	0.11	36,36,36,36	0
56	MG	2x	3001	1/1	0.94	0.07	68,68,68,68	0
56	MG	2A	3108	1/1	0.94	0.15	30,30,30,30	0
56	MG	1B	207	1/1	0.94	0.15	52,52,52,52	0
57	ZN	2n	102	1/1	0.94	0.08	100,100,100,100	0
56	MG	1A	4177	1/1	0.95	0.09	34,34,34,34	0
56	MG	2A	3566	1/1	0.95	0.05	32,32,32,32	0
56	MG	1A	3123	1/1	0.95	0.14	55,55,55,55	0
56	MG	1A	3857	1/1	0.95	0.06	36,36,36,36	0
56	MG	2A	3569	1/1	0.95	0.11	32,32,32,32	0
56	MG	1A	3319	1/1	0.95	0.12	58,58,58,58	0
56	MG	2A	3572	1/1	0.95	0.06	43,43,43,43	0
56	MG	2A	3575	1/1	0.95	0.15	46,46,46,46	0
56	MG	1A	4190	1/1	0.95	0.22	51,51,51,51	0
56	MG	2A	3224	1/1	0.95	0.05	38,38,38,38	0
56	MG	2A	3225	1/1	0.95	0.12	43,43,43,43	0
56	MG	2A	3580	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3227	1/1	0.95	0.06	51,51,51,51	0
56	MG	1a	1641	1/1	0.95	0.22	58,58,58,58	0
56	MG	2A	3230	1/1	0.95	0.07	57,57,57,57	0
56	MG	1a	1857	1/1	0.95	0.08	70,70,70,70	0
56	MG	2A	3585	1/1	0.95	0.06	35,35,35,35	0
56	MG	1A	3698	1/1	0.95	0.20	51,51,51,51	0
56	MG	1a	1644	1/1	0.95	0.08	54,54,54,54	0
56	MG	1A	3320	1/1	0.95	0.07	57,57,57,57	0
56	MG	1A	4195	1/1	0.95	0.07	32,32,32,32	0
56	MG	1a	1648	1/1	0.95	0.09	52,52,52,52	0
56	MG	1A	3861	1/1	0.95	0.14	43,43,43,43	0
56	MG	1a	1651	1/1	0.95	0.12	48,48,48,48	0
56	MG	1A	3701	1/1	0.95	0.06	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4021	1/1	0.95	0.11	33,33,33,33	0
56	MG	2D	303	1/1	0.95	0.11	44,44,44,44	0
56	MG	1A	4200	1/1	0.95	0.14	47,47,47,47	0
56	MG	1a	1868	1/1	0.95	0.18	63,63,63,63	0
56	MG	1A	3702	1/1	0.95	0.08	25,25,25,25	0
56	MG	1A	3864	1/1	0.95	0.14	38,38,38,38	0
56	MG	1A	4024	1/1	0.95	0.07	46,46,46,46	0
56	MG	1a	1875	1/1	0.95	0.07	57,57,57,57	0
56	MG	1A	3865	1/1	0.95	0.12	50,50,50,50	0
56	MG	1A	4027	1/1	0.95	0.13	72,72,72,72	0
56	MG	1A	3703	1/1	0.95	0.20	38,38,38,38	0
56	MG	1A	4215	1/1	0.95	0.07	44,44,44,44	0
56	MG	1A	3152	1/1	0.95	0.10	45,45,45,45	0
56	MG	1A	3706	1/1	0.95	0.06	25,25,25,25	0
56	MG	2Q	3003	1/1	0.95	0.16	50,50,50,50	0
56	MG	2Q	3004	1/1	0.95	0.16	45,45,45,45	0
56	MG	1A	4218	1/1	0.95	0.10	36,36,36,36	0
56	MG	1A	4031	1/1	0.95	0.11	39,39,39,39	0
56	MG	20	101	1/1	0.95	0.11	56,56,56,56	0
56	MG	1a	1890	1/1	0.95	0.12	49,49,49,49	0
56	MG	1a	1891	1/1	0.95	0.19	68,68,68,68	0
56	MG	1a	1673	1/1	0.95	0.18	54,54,54,54	0
56	MG	1A	4226	1/1	0.95	0.21	45,45,45,45	0
56	MG	1A	3324	1/1	0.95	0.15	38,38,38,38	0
56	MG	1a	1676	1/1	0.95	0.16	69,69,69,69	0
56	MG	1A	3099	1/1	0.95	0.09	46,46,46,46	0
56	MG	1A	4034	1/1	0.95	0.13	54,54,54,54	0
56	MG	1A	3482	1/1	0.95	0.16	49,49,49,49	0
56	MG	1A	3327	1/1	0.95	0.17	29,29,29,29	0
56	MG	1A	3328	1/1	0.95	0.09	44,44,44,44	0
56	MG	1A	3714	1/1	0.95	0.08	53,53,53,53	0
56	MG	1A	3577	1/1	0.95	0.12	56,56,56,56	0
56	MG	1a	1685	1/1	0.95	0.13	61,61,61,61	0
56	MG	2A	3280	1/1	0.95	0.08	55,55,55,55	0
56	MG	1A	3580	1/1	0.95	0.08	46,46,46,46	0
56	MG	1A	4042	1/1	0.95	0.07	50,50,50,50	0
56	MG	1p	101	1/1	0.95	0.20	63,63,63,63	0
56	MG	2A	3284	1/1	0.95	0.10	42,42,42,42	0
56	MG	1A	3882	1/1	0.95	0.15	29,29,29,29	0
56	MG	1A	3062	1/1	0.95	0.21	49,49,49,49	0
56	MG	1A	3248	1/1	0.95	0.07	31,31,31,31	0
56	MG	1A	3412	1/1	0.95	0.19	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1t	3001	1/1	0.95	0.19	47,47,47,47	0
56	MG	1A	4049	1/1	0.95	0.08	37,37,37,37	0
56	MG	2a	1628	1/1	0.95	0.13	66,66,66,66	0
56	MG	2A	3296	1/1	0.95	0.08	32,32,32,32	0
56	MG	1A	3721	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	3249	1/1	0.95	0.10	44,44,44,44	0
56	MG	1A	3586	1/1	0.95	0.14	54,54,54,54	0
56	MG	2A	3302	1/1	0.95	0.07	30,30,30,30	0
56	MG	1a	1702	1/1	0.95	0.22	41,41,41,41	0
56	MG	1A	3101	1/1	0.95	0.12	54,54,54,54	0
56	MG	2A	3307	1/1	0.95	0.06	35,35,35,35	0
56	MG	2a	1637	1/1	0.95	0.09	60,60,60,60	0
56	MG	1A	3009	1/1	0.95	0.20	31,31,31,31	0
56	MG	1A	3078	1/1	0.95	0.06	54,54,54,54	0
56	MG	1A	3256	1/1	0.95	0.12	63,63,63,63	0
56	MG	1A	3258	1/1	0.95	0.15	46,46,46,46	0
56	MG	1A	3259	1/1	0.95	0.15	46,46,46,46	0
56	MG	1D	303	1/1	0.95	0.10	45,45,45,45	0
56	MG	1A	3021	1/1	0.95	0.09	46,46,46,46	0
56	MG	2A	3316	1/1	0.95	0.12	60,60,60,60	0
56	MG	1A	3261	1/1	0.95	0.13	22,22,22,22	0
56	MG	1A	3903	1/1	0.95	0.07	41,41,41,41	0
56	MG	1D	311	1/1	0.95	0.09	41,41,41,41	0
56	MG	2A	3321	1/1	0.95	0.16	43,43,43,43	0
56	MG	1A	3749	1/1	0.95	0.07	15,15,15,15	0
56	MG	1A	3080	1/1	0.95	0.13	51,51,51,51	0
56	MG	1A	3035	1/1	0.95	0.10	53,53,53,53	0
56	MG	1A	3503	1/1	0.95	0.06	48,48,48,48	0
56	MG	1A	4070	1/1	0.95	0.13	55,55,55,55	0
56	MG	1A	3269	1/1	0.95	0.09	20,20,20,20	0
56	MG	1A	3271	1/1	0.95	0.17	38,38,38,38	0
56	MG	2A	3016	1/1	0.95	0.05	56,56,56,56	0
56	MG	2A	3338	1/1	0.95	0.08	61,61,61,61	0
56	MG	1A	4073	1/1	0.95	0.11	58,58,58,58	0
56	MG	2A	3341	1/1	0.95	0.15	54,54,54,54	0
56	MG	1A	3429	1/1	0.95	0.06	43,43,43,43	0
56	MG	2A	3343	1/1	0.95	0.13	55,55,55,55	0
56	MG	2A	3019	1/1	0.95	0.05	59,59,59,59	0
56	MG	1A	3180	1/1	0.95	0.11	45,45,45,45	0
56	MG	1A	3915	1/1	0.95	0.08	44,44,44,44	0
56	MG	2A	3347	1/1	0.95	0.06	46,46,46,46	0
56	MG	1A	3762	1/1	0.95	0.08	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3604	1/1	0.95	0.09	66,66,66,66	0
56	MG	2a	1672	1/1	0.95	0.08	59,59,59,59	0
56	MG	1A	4079	1/1	0.95	0.14	28,28,28,28	0
56	MG	2A	3026	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	3764	1/1	0.95	0.18	46,46,46,46	0
56	MG	2a	1677	1/1	0.95	0.09	54,54,54,54	0
56	MG	1A	3509	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3031	1/1	0.95	0.17	46,46,46,46	0
56	MG	1G	201	1/1	0.95	0.09	40,40,40,40	0
56	MG	1A	3923	1/1	0.95	0.07	53,53,53,53	0
56	MG	1a	1735	1/1	0.95	0.13	47,47,47,47	0
56	MG	1A	3181	1/1	0.95	0.08	37,37,37,37	0
56	MG	2A	3365	1/1	0.95	0.10	46,46,46,46	0
56	MG	1A	3107	1/1	0.95	0.14	52,52,52,52	0
56	MG	1A	3931	1/1	0.95	0.07	36,36,36,36	0
56	MG	1A	3433	1/1	0.95	0.10	66,66,66,66	0
56	MG	1A	3611	1/1	0.95	0.15	40,40,40,40	0
56	MG	2a	1696	1/1	0.95	0.10	53,53,53,53	0
56	MG	2A	3371	1/1	0.95	0.09	50,50,50,50	0
56	MG	2A	3372	1/1	0.95	0.06	34,34,34,34	0
56	MG	2a	1699	1/1	0.95	0.17	46,46,46,46	0
56	MG	1N	206	1/1	0.95	0.06	29,29,29,29	0
56	MG	1O	3002	1/1	0.95	0.13	51,51,51,51	0
56	MG	1a	1745	1/1	0.95	0.13	55,55,55,55	0
56	MG	2A	3384	1/1	0.95	0.09	48,48,48,48	0
56	MG	2A	3385	1/1	0.95	0.16	36,36,36,36	0
56	MG	1O	3003	1/1	0.95	0.09	56,56,56,56	0
56	MG	1A	3362	1/1	0.95	0.10	45,45,45,45	0
56	MG	2A	3047	1/1	0.95	0.15	41,41,41,41	0
56	MG	1A	3284	1/1	0.95	0.06	37,37,37,37	0
56	MG	2A	3050	1/1	0.95	0.10	44,44,44,44	0
56	MG	2A	3052	1/1	0.95	0.12	31,31,31,31	0
56	MG	2A	3054	1/1	0.95	0.13	41,41,41,41	0
56	MG	1A	3936	1/1	0.95	0.11	55,55,55,55	0
56	MG	1A	3286	1/1	0.95	0.12	40,40,40,40	0
56	MG	2a	1721	1/1	0.95	0.16	52,52,52,52	0
56	MG	2A	3400	1/1	0.95	0.15	52,52,52,52	0
56	MG	1A	4095	1/1	0.95	0.14	34,34,34,34	0
56	MG	1A	3001	1/1	0.95	0.18	37,37,37,37	0
56	MG	1R	201	1/1	0.95	0.09	26,26,26,26	0
56	MG	1A	3520	1/1	0.95	0.07	47,47,47,47	0
56	MG	2A	3061	1/1	0.95	0.11	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3063	1/1	0.95	0.11	46,46,46,46	0
56	MG	1A	3784	1/1	0.95	0.11	65,65,65,65	0
56	MG	1A	3622	1/1	0.95	0.10	32,32,32,32	0
56	MG	1A	3521	1/1	0.95	0.16	54,54,54,54	0
56	MG	1A	3134	1/1	0.95	0.09	52,52,52,52	0
56	MG	1A	3626	1/1	0.95	0.14	55,55,55,55	0
56	MG	1A	3369	1/1	0.95	0.20	32,32,32,32	0
56	MG	1A	3630	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3073	1/1	0.95	0.15	48,48,48,48	0
56	MG	2A	3420	1/1	0.95	0.08	46,46,46,46	0
56	MG	2A	3422	1/1	0.95	0.20	51,51,51,51	0
56	MG	2A	3075	1/1	0.95	0.11	24,24,24,24	0
56	MG	1A	4109	1/1	0.95	0.07	37,37,37,37	0
56	MG	1A	3796	1/1	0.95	0.04	46,46,46,46	0
56	MG	2A	3078	1/1	0.95	0.20	51,51,51,51	0
56	MG	1A	3370	1/1	0.95	0.13	47,47,47,47	0
56	MG	1A	3137	1/1	0.95	0.11	44,44,44,44	0
56	MG	1A	3086	1/1	0.95	0.22	43,43,43,43	0
56	MG	2A	3084	1/1	0.95	0.19	49,49,49,49	0
56	MG	2A	3085	1/1	0.95	0.17	55,55,55,55	0
56	MG	1A	3057	1/1	0.95	0.08	57,57,57,57	0
56	MG	1A	3961	1/1	0.95	0.11	34,34,34,34	0
56	MG	1A	3206	1/1	0.95	0.19	46,46,46,46	0
56	MG	1a	1772	1/1	0.95	0.07	39,39,39,39	0
56	MG	1A	3531	1/1	0.95	0.33	51,51,51,51	0
56	MG	1X	3001	1/1	0.95	0.07	44,44,44,44	0
56	MG	2a	1759	1/1	0.95	0.08	58,58,58,58	0
56	MG	1A	3058	1/1	0.95	0.06	49,49,49,49	0
56	MG	1A	4124	1/1	0.95	0.17	33,33,33,33	0
56	MG	2A	3100	1/1	0.95	0.08	38,38,38,38	0
56	MG	2A	3448	1/1	0.95	0.07	44,44,44,44	0
56	MG	2A	3449	1/1	0.95	0.06	37,37,37,37	0
56	MG	1A	3454	1/1	0.95	0.09	56,56,56,56	0
56	MG	1A	3090	1/1	0.95	0.17	30,30,30,30	0
56	MG	1A	3028	1/1	0.95	0.18	39,39,39,39	0
56	MG	10	104	1/1	0.95	0.09	61,61,61,61	0
56	MG	2A	3456	1/1	0.95	0.14	65,65,65,65	0
56	MG	1A	3380	1/1	0.95	0.09	43,43,43,43	0
56	MG	1A	3459	1/1	0.95	0.17	43,43,43,43	0
56	MG	1a	1784	1/1	0.95	0.16	64,64,64,64	0
56	MG	11	102	1/1	0.95	0.07	34,34,34,34	0
56	MG	2a	1777	1/1	0.95	0.10	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3973	1/1	0.95	0.09	55,55,55,55	0
56	MG	2A	3465	1/1	0.95	0.05	39,39,39,39	0
56	MG	2A	3111	1/1	0.95	0.13	48,48,48,48	0
56	MG	2A	3467	1/1	0.95	0.12	60,60,60,60	0
56	MG	2a	1783	1/1	0.95	0.13	47,47,47,47	0
56	MG	2A	3114	1/1	0.95	0.13	46,46,46,46	0
56	MG	1A	3460	1/1	0.95	0.15	58,58,58,58	0
56	MG	15	104	1/1	0.95	0.12	53,53,53,53	0
56	MG	1A	4137	1/1	0.95	0.07	64,64,64,64	0
56	MG	1A	3543	1/1	0.95	0.24	46,46,46,46	0
56	MG	17	101	1/1	0.95	0.30	35,35,35,35	0
56	MG	17	103	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3125	1/1	0.95	0.07	41,41,41,41	0
56	MG	2A	3478	1/1	0.95	0.14	49,49,49,49	0
56	MG	18	101	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3128	1/1	0.95	0.09	47,47,47,47	0
56	MG	1A	3115	1/1	0.95	0.15	46,46,46,46	0
56	MG	1A	3979	1/1	0.95	0.17	39,39,39,39	0
56	MG	2A	3483	1/1	0.95	0.07	40,40,40,40	0
56	MG	1A	3820	1/1	0.95	0.09	17,17,17,17	0
56	MG	1a	1802	1/1	0.95	0.07	59,59,59,59	0
56	MG	1A	4143	1/1	0.95	0.11	34,34,34,34	0
56	MG	1a	1805	1/1	0.95	0.14	66,66,66,66	0
56	MG	2A	3137	1/1	0.95	0.17	42,42,42,42	0
56	MG	1A	3144	1/1	0.95	0.07	49,49,49,49	0
56	MG	1a	1807	1/1	0.95	0.14	60,60,60,60	0
56	MG	1A	3661	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3146	1/1	0.95	0.15	50,50,50,50	0
56	MG	1A	3014	1/1	0.95	0.16	51,51,51,51	0
56	MG	1A	3666	1/1	0.95	0.07	30,30,30,30	0
56	MG	1a	1605	1/1	0.95	0.09	66,66,66,66	0
56	MG	1a	1606	1/1	0.95	0.08	65,65,65,65	0
56	MG	1a	1607	1/1	0.95	0.09	73,73,73,73	0
56	MG	2A	3156	1/1	0.95	0.16	49,49,49,49	0
56	MG	2A	3160	1/1	0.95	0.07	46,46,46,46	0
56	MG	2A	3161	1/1	0.95	0.20	48,48,48,48	0
56	MG	1A	3074	1/1	0.95	0.16	41,41,41,41	0
56	MG	1A	3386	1/1	0.95	0.27	43,43,43,43	0
56	MG	1A	3834	1/1	0.95	0.11	36,36,36,36	0
56	MG	1A	3224	1/1	0.95	0.07	41,41,41,41	0
56	MG	1A	3228	1/1	0.95	0.12	25,25,25,25	0
56	MG	2A	3169	1/1	0.95	0.06	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3993	1/1	0.95	0.12	32,32,32,32	0
56	MG	2a	1824	1/1	0.95	0.06	41,41,41,41	0
56	MG	2A	3172	1/1	0.95	0.18	49,49,49,49	0
56	MG	1A	3229	1/1	0.95	0.10	23,23,23,23	0
56	MG	2a	1828	1/1	0.95	0.11	48,48,48,48	0
56	MG	2A	3523	1/1	0.95	0.09	27,27,27,27	0
56	MG	1a	1826	1/1	0.95	0.06	53,53,53,53	0
56	MG	2A	3179	1/1	0.95	0.15	31,31,31,31	0
56	MG	1a	1827	1/1	0.95	0.11	44,44,44,44	0
56	MG	2a	1835	1/1	0.95	0.15	58,58,58,58	0
56	MG	2A	3181	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3533	1/1	0.95	0.13	49,49,49,49	0
56	MG	1A	3019	1/1	0.95	0.30	49,49,49,49	0
56	MG	1A	3676	1/1	0.95	0.10	38,38,38,38	0
56	MG	1A	3999	1/1	0.95	0.09	55,55,55,55	0
56	MG	2A	3186	1/1	0.95	0.14	46,46,46,46	0
56	MG	2A	3539	1/1	0.95	0.08	43,43,43,43	0
56	MG	1a	1834	1/1	0.95	0.12	59,59,59,59	0
56	MG	1A	3557	1/1	0.95	0.09	53,53,53,53	0
56	MG	2a	1847	1/1	0.95	0.22	46,46,46,46	0
56	MG	2A	3192	1/1	0.95	0.15	36,36,36,36	0
56	MG	1A	3234	1/1	0.95	0.31	31,31,31,31	0
56	MG	1A	3679	1/1	0.95	0.06	24,24,24,24	0
56	MG	1A	3236	1/1	0.95	0.10	63,63,63,63	0
56	MG	1A	3148	1/1	0.95	0.18	40,40,40,40	0
56	MG	1a	1841	1/1	0.95	0.16	49,49,49,49	0
56	MG	2A	3551	1/1	0.95	0.08	40,40,40,40	0
56	MG	2A	3200	1/1	0.95	0.30	40,40,40,40	0
56	MG	1A	3850	1/1	0.95	0.06	40,40,40,40	0
56	MG	1A	3691	1/1	0.95	0.12	43,43,43,43	0
56	MG	2A	3206	1/1	0.95	0.09	39,39,39,39	0
56	MG	1A	3473	1/1	0.95	0.10	45,45,45,45	0
56	MG	2A	3557	1/1	0.95	0.07	32,32,32,32	0
56	MG	1A	4175	1/1	0.95	0.17	53,53,53,53	0
56	MG	1A	3694	1/1	0.95	0.10	29,29,29,29	0
56	MG	1a	1633	1/1	0.95	0.06	64,64,64,64	0
56	MG	2x	3004	1/1	0.95	0.19	62,62,62,62	0
57	ZN	24	501	1/1	0.95	0.07	122,122,122,122	0
56	MG	2A	3211	1/1	0.95	0.07	40,40,40,40	0
56	MG	1A	3996	1/1	0.96	0.05	43,43,43,43	0
56	MG	10	105	1/1	0.96	0.06	43,43,43,43	0
56	MG	1A	3603	1/1	0.96	0.08	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	10	107	1/1	0.96	0.06	52,52,52,52	0
56	MG	1A	3409	1/1	0.96	0.20	33,33,33,33	0
56	MG	1A	3410	1/1	0.96	0.15	22,22,22,22	0
56	MG	2O	203	1/1	0.96	0.08	47,47,47,47	0
56	MG	11	103	1/1	0.96	0.04	36,36,36,36	0
56	MG	1A	3606	1/1	0.96	0.09	28,28,28,28	0
56	MG	1A	3167	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3608	1/1	0.96	0.08	62,62,62,62	0
56	MG	2Q	3005	1/1	0.96	0.05	43,43,43,43	0
56	MG	2A	3325	1/1	0.96	0.12	28,28,28,28	0
56	MG	2Y	502	1/1	0.96	0.14	47,47,47,47	0
56	MG	1A	3717	1/1	0.96	0.13	59,59,59,59	0
56	MG	2A	3327	1/1	0.96	0.23	50,50,50,50	0
56	MG	1A	3169	1/1	0.96	0.09	40,40,40,40	0
56	MG	2A	3329	1/1	0.96	0.10	55,55,55,55	0
56	MG	28	101	1/1	0.96	0.17	40,40,40,40	0
56	MG	16	103	1/1	0.96	0.07	50,50,50,50	0
56	MG	1A	4005	1/1	0.96	0.12	47,47,47,47	0
56	MG	1A	3413	1/1	0.96	0.15	40,40,40,40	0
56	MG	1A	3170	1/1	0.96	0.07	31,31,31,31	0
56	MG	2a	1604	1/1	0.96	0.13	47,47,47,47	0
56	MG	1A	4008	1/1	0.96	0.06	47,47,47,47	0
56	MG	2A	3340	1/1	0.96	0.09	57,57,57,57	0
56	MG	2a	1607	1/1	0.96	0.22	45,45,45,45	0
56	MG	1A	3361	1/1	0.96	0.11	35,35,35,35	0
56	MG	2a	1609	1/1	0.96	0.12	55,55,55,55	0
56	MG	1A	3722	1/1	0.96	0.15	38,38,38,38	0
56	MG	1A	4160	1/1	0.96	0.16	45,45,45,45	0
56	MG	19	101	1/1	0.96	0.07	38,38,38,38	0
56	MG	1A	4011	1/1	0.96	0.06	41,41,41,41	0
56	MG	1A	3723	1/1	0.96	0.05	11,11,11,11	0
56	MG	1A	3257	1/1	0.96	0.08	35,35,35,35	0
56	MG	1A	4014	1/1	0.96	0.05	39,39,39,39	0
56	MG	2A	3349	1/1	0.96	0.10	64,64,64,64	0
56	MG	1A	4015	1/1	0.96	0.09	15,15,15,15	0
56	MG	1A	4167	1/1	0.96	0.16	44,44,44,44	0
56	MG	1A	3210	1/1	0.96	0.16	48,48,48,48	0
56	MG	2a	1622	1/1	0.96	0.13	70,70,70,70	0
56	MG	1A	3538	1/1	0.96	0.07	57,57,57,57	0
56	MG	1a	1800	1/1	0.96	0.09	37,37,37,37	0
56	MG	2A	3355	1/1	0.96	0.09	34,34,34,34	0
56	MG	1A	3728	1/1	0.96	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3874	1/1	0.96	0.12	53,53,53,53	0
56	MG	1A	3619	1/1	0.96	0.07	50,50,50,50	0
56	MG	1A	3475	1/1	0.96	0.14	50,50,50,50	0
56	MG	2A	3360	1/1	0.96	0.11	32,32,32,32	0
56	MG	1A	3621	1/1	0.96	0.14	42,42,42,42	0
56	MG	2A	3363	1/1	0.96	0.08	30,30,30,30	0
56	MG	2A	3364	1/1	0.96	0.07	44,44,44,44	0
56	MG	1A	3734	1/1	0.96	0.04	42,42,42,42	0
56	MG	1A	4183	1/1	0.96	0.06	35,35,35,35	0
56	MG	1A	3735	1/1	0.96	0.10	57,57,57,57	0
56	MG	1A	3742	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	4026	1/1	0.96	0.11	44,44,44,44	0
56	MG	1A	3033	1/1	0.96	0.14	53,53,53,53	0
56	MG	1A	4192	1/1	0.96	0.14	40,40,40,40	0
56	MG	2A	3374	1/1	0.96	0.10	43,43,43,43	0
56	MG	1A	3092	1/1	0.96	0.12	39,39,39,39	0
56	MG	1A	4194	1/1	0.96	0.06	41,41,41,41	0
56	MG	2A	3377	1/1	0.96	0.15	38,38,38,38	0
56	MG	2A	3382	1/1	0.96	0.11	43,43,43,43	0
56	MG	1A	3094	1/1	0.96	0.13	45,45,45,45	0
56	MG	1A	3422	1/1	0.96	0.09	50,50,50,50	0
56	MG	1A	3041	1/1	0.96	0.22	44,44,44,44	0
56	MG	2A	3113	1/1	0.96	0.15	40,40,40,40	0
56	MG	1A	3629	1/1	0.96	0.10	33,33,33,33	0
56	MG	1A	3264	1/1	0.96	0.07	48,48,48,48	0
56	MG	1A	4201	1/1	0.96	0.10	41,41,41,41	0
56	MG	1A	3483	1/1	0.96	0.08	38,38,38,38	0
56	MG	2A	3391	1/1	0.96	0.13	55,55,55,55	0
56	MG	2A	3393	1/1	0.96	0.13	35,35,35,35	0
56	MG	2A	3119	1/1	0.96	0.12	53,53,53,53	0
56	MG	2A	3120	1/1	0.96	0.12	40,40,40,40	0
56	MG	2A	3121	1/1	0.96	0.18	49,49,49,49	0
56	MG	2A	3398	1/1	0.96	0.10	54,54,54,54	0
56	MG	1A	3219	1/1	0.96	0.08	24,24,24,24	0
56	MG	1A	4036	1/1	0.96	0.09	30,30,30,30	0
56	MG	1A	3895	1/1	0.96	0.06	33,33,33,33	0
56	MG	1A	3758	1/1	0.96	0.04	46,46,46,46	0
56	MG	2A	3126	1/1	0.96	0.29	47,47,47,47	0
56	MG	1a	1640	1/1	0.96	0.14	62,62,62,62	0
56	MG	1a	1837	1/1	0.96	0.05	43,43,43,43	0
56	MG	2a	1669	1/1	0.96	0.07	69,69,69,69	0
56	MG	1A	3633	1/1	0.96	0.10	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3048	1/1	0.96	0.07	42,42,42,42	0
56	MG	2A	3131	1/1	0.96	0.08	43,43,43,43	0
56	MG	2A	3410	1/1	0.96	0.05	36,36,36,36	0
56	MG	2A	3132	1/1	0.96	0.12	45,45,45,45	0
56	MG	1A	3635	1/1	0.96	0.07	18,18,18,18	0
56	MG	1A	3900	1/1	0.96	0.05	45,45,45,45	0
56	MG	2a	1678	1/1	0.96	0.28	60,60,60,60	0
56	MG	2A	3415	1/1	0.96	0.07	61,61,61,61	0
56	MG	1A	3636	1/1	0.96	0.13	29,29,29,29	0
56	MG	2a	1681	1/1	0.96	0.14	47,47,47,47	0
56	MG	2A	3417	1/1	0.96	0.11	51,51,51,51	0
56	MG	2a	1684	1/1	0.96	0.09	44,44,44,44	0
56	MG	1a	1647	1/1	0.96	0.11	45,45,45,45	0
56	MG	1A	3554	1/1	0.96	0.11	61,61,61,61	0
56	MG	2a	1688	1/1	0.96	0.16	49,49,49,49	0
56	MG	1a	1845	1/1	0.96	0.14	48,48,48,48	0
56	MG	2A	3421	1/1	0.96	0.04	40,40,40,40	0
56	MG	1A	4224	1/1	0.96	0.25	23,23,23,23	0
56	MG	2a	1692	1/1	0.96	0.16	59,59,59,59	0
56	MG	1A	4045	1/1	0.96	0.10	49,49,49,49	0
56	MG	2A	3145	1/1	0.96	0.14	32,32,32,32	0
56	MG	1A	4046	1/1	0.96	0.07	61,61,61,61	0
56	MG	1A	3486	1/1	0.96	0.09	32,32,32,32	0
56	MG	1a	1654	1/1	0.96	0.20	51,51,51,51	0
56	MG	1a	1655	1/1	0.96	0.22	47,47,47,47	0
56	MG	1A	4230	1/1	0.96	0.19	47,47,47,47	0
56	MG	1a	1853	1/1	0.96	0.19	53,53,53,53	0
56	MG	2A	3154	1/1	0.96	0.06	41,41,41,41	0
56	MG	2a	1704	1/1	0.96	0.08	67,67,67,67	0
56	MG	1A	3640	1/1	0.96	0.19	53,53,53,53	0
56	MG	2A	3158	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3641	1/1	0.96	0.10	51,51,51,51	0
56	MG	1A	3767	1/1	0.96	0.07	36,36,36,36	0
56	MG	1A	3183	1/1	0.96	0.12	35,35,35,35	0
56	MG	2a	1710	1/1	0.96	0.11	47,47,47,47	0
56	MG	1A	3910	1/1	0.96	0.14	24,24,24,24	0
56	MG	1A	3322	1/1	0.96	0.08	45,45,45,45	0
56	MG	1A	3227	1/1	0.96	0.20	27,27,27,27	0
56	MG	2A	3167	1/1	0.96	0.05	31,31,31,31	0
56	MG	1A	3560	1/1	0.96	0.06	44,44,44,44	0
56	MG	1a	1668	1/1	0.96	0.14	44,44,44,44	0
56	MG	2a	1719	1/1	0.96	0.23	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1669	1/1	0.96	0.11	54,54,54,54	0
56	MG	2A	3171	1/1	0.96	0.07	39,39,39,39	0
56	MG	1A	4058	1/1	0.96	0.08	50,50,50,50	0
56	MG	1A	3184	1/1	0.96	0.06	44,44,44,44	0
56	MG	1A	3916	1/1	0.96	0.12	35,35,35,35	0
56	MG	1B	211	1/1	0.96	0.05	34,34,34,34	0
56	MG	2A	3459	1/1	0.96	0.05	33,33,33,33	0
56	MG	1A	3775	1/1	0.96	0.08	33,33,33,33	0
56	MG	1A	3777	1/1	0.96	0.12	31,31,31,31	0
56	MG	2a	1730	1/1	0.96	0.09	66,66,66,66	0
56	MG	1A	3278	1/1	0.96	0.06	44,44,44,44	0
56	MG	1A	3492	1/1	0.96	0.19	52,52,52,52	0
56	MG	1a	1678	1/1	0.96	0.11	41,41,41,41	0
56	MG	1a	1878	1/1	0.96	0.12	50,50,50,50	0
56	MG	1A	4065	1/1	0.96	0.09	43,43,43,43	0
56	MG	2A	3188	1/1	0.96	0.08	34,34,34,34	0
56	MG	2A	3189	1/1	0.96	0.09	33,33,33,33	0
56	MG	1A	3650	1/1	0.96	0.12	50,50,50,50	0
56	MG	2a	1739	1/1	0.96	0.22	39,39,39,39	0
56	MG	2a	1740	1/1	0.96	0.13	31,31,31,31	0
56	MG	2A	3191	1/1	0.96	0.19	48,48,48,48	0
56	MG	1A	3924	1/1	0.96	0.05	19,19,19,19	0
56	MG	1A	3652	1/1	0.96	0.14	48,48,48,48	0
56	MG	1A	3653	1/1	0.96	0.06	30,30,30,30	0
56	MG	1A	3930	1/1	0.96	0.12	47,47,47,47	0
56	MG	1a	1885	1/1	0.96	0.06	66,66,66,66	0
56	MG	1a	1887	1/1	0.96	0.12	49,49,49,49	0
56	MG	1A	3788	1/1	0.96	0.07	34,34,34,34	0
56	MG	1a	1889	1/1	0.96	0.09	39,39,39,39	0
56	MG	1A	3378	1/1	0.96	0.08	50,50,50,50	0
56	MG	1A	3379	1/1	0.96	0.14	26,26,26,26	0
56	MG	1D	306	1/1	0.96	0.08	13,13,13,13	0
56	MG	1A	3280	1/1	0.96	0.13	40,40,40,40	0
56	MG	1A	3381	1/1	0.96	0.06	44,44,44,44	0
56	MG	1D	310	1/1	0.96	0.07	46,46,46,46	0
56	MG	1a	1693	1/1	0.96	0.20	49,49,49,49	0
56	MG	1A	3049	1/1	0.96	0.06	39,39,39,39	0
56	MG	1A	3938	1/1	0.96	0.07	16,16,16,16	0
56	MG	1a	1698	1/1	0.96	0.07	57,57,57,57	0
56	MG	2A	3492	1/1	0.96	0.06	40,40,40,40	0
56	MG	2A	3493	1/1	0.96	0.10	40,40,40,40	0
56	MG	2A	3496	1/1	0.96	0.12	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3188	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3663	1/1	0.96	0.08	51,51,51,51	0
56	MG	1A	3664	1/1	0.96	0.12	42,42,42,42	0
56	MG	2A	3500	1/1	0.96	0.05	47,47,47,47	0
56	MG	1A	3665	1/1	0.96	0.09	40,40,40,40	0
56	MG	2A	3503	1/1	0.96	0.18	32,32,32,32	0
56	MG	2A	3504	1/1	0.96	0.12	39,39,39,39	0
56	MG	2A	3226	1/1	0.96	0.20	64,64,64,64	0
56	MG	1A	3573	1/1	0.96	0.07	44,44,44,44	0
56	MG	1l	201	1/1	0.96	0.06	50,50,50,50	0
56	MG	2a	1776	1/1	0.96	0.18	55,55,55,55	0
56	MG	2A	3229	1/1	0.96	0.07	38,38,38,38	0
56	MG	1n	502	1/1	0.96	0.13	59,59,59,59	0
56	MG	1A	3667	1/1	0.96	0.06	23,23,23,23	0
56	MG	1A	3945	1/1	0.96	0.21	33,33,33,33	0
56	MG	1A	3232	1/1	0.96	0.09	40,40,40,40	0
56	MG	1A	4087	1/1	0.96	0.09	66,66,66,66	0
56	MG	1A	3290	1/1	0.96	0.07	15,15,15,15	0
56	MG	1A	3949	1/1	0.96	0.06	37,37,37,37	0
56	MG	1A	3190	1/1	0.96	0.18	25,25,25,25	0
56	MG	1A	3811	1/1	0.96	0.13	37,37,37,37	0
56	MG	1A	4092	1/1	0.96	0.08	69,69,69,69	0
56	MG	1A	3671	1/1	0.96	0.11	30,30,30,30	0
56	MG	1A	3672	1/1	0.96	0.07	28,28,28,28	0
56	MG	1A	3191	1/1	0.96	0.11	35,35,35,35	0
56	MG	2A	3526	1/1	0.96	0.07	37,37,37,37	0
56	MG	1A	3119	1/1	0.96	0.10	54,54,54,54	0
56	MG	1A	3959	1/1	0.96	0.12	47,47,47,47	0
56	MG	1A	4099	1/1	0.96	0.07	33,33,33,33	0
56	MG	1A	3336	1/1	0.96	0.08	56,56,56,56	0
56	MG	1a	1722	1/1	0.96	0.08	48,48,48,48	0
56	MG	1A	3447	1/1	0.96	0.06	43,43,43,43	0
56	MG	1A	3193	1/1	0.96	0.15	23,23,23,23	0
56	MG	1A	3450	1/1	0.96	0.06	53,53,53,53	0
56	MG	1A	4105	1/1	0.96	0.15	45,45,45,45	0
56	MG	1A	3821	1/1	0.96	0.08	49,49,49,49	0
56	MG	2A	3260	1/1	0.96	0.06	41,41,41,41	0
56	MG	2A	3544	1/1	0.96	0.15	48,48,48,48	0
56	MG	1A	3451	1/1	0.96	0.09	38,38,38,38	0
56	MG	1P	204	1/1	0.96	0.07	46,46,46,46	0
56	MG	1A	3681	1/1	0.96	0.10	37,37,37,37	0
56	MG	1A	3587	1/1	0.96	0.07	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3010	1/1	0.96	0.11	53,53,53,53	0
56	MG	1A	3684	1/1	0.96	0.06	29,29,29,29	0
56	MG	1A	3338	1/1	0.96	0.05	32,32,32,32	0
56	MG	1A	3194	1/1	0.96	0.07	35,35,35,35	0
56	MG	1A	3833	1/1	0.96	0.08	54,54,54,54	0
56	MG	1A	3976	1/1	0.96	0.10	41,41,41,41	0
56	MG	1A	3098	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	4118	1/1	0.96	0.06	37,37,37,37	0
56	MG	1R	206	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3516	1/1	0.96	0.12	59,59,59,59	0
56	MG	1A	3837	1/1	0.96	0.07	50,50,50,50	0
56	MG	1a	1744	1/1	0.96	0.12	44,44,44,44	0
56	MG	2a	1822	1/1	0.96	0.10	71,71,71,71	0
56	MG	1A	3346	1/1	0.96	0.07	38,38,38,38	0
56	MG	2A	3565	1/1	0.96	0.06	33,33,33,33	0
56	MG	1A	4122	1/1	0.96	0.17	26,26,26,26	0
56	MG	1A	3297	1/1	0.96	0.11	37,37,37,37	0
56	MG	1a	1748	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	3011	1/1	0.96	0.06	49,49,49,49	0
56	MG	2a	1830	1/1	0.96	0.12	56,56,56,56	0
56	MG	2A	3570	1/1	0.96	0.10	53,53,53,53	0
56	MG	2A	3030	1/1	0.96	0.12	44,44,44,44	0
56	MG	1A	3350	1/1	0.96	0.08	45,45,45,45	0
56	MG	1A	3082	1/1	0.96	0.09	45,45,45,45	0
56	MG	2A	3576	1/1	0.96	0.19	39,39,39,39	0
56	MG	1A	3986	1/1	0.96	0.10	70,70,70,70	0
56	MG	1A	4130	1/1	0.96	0.12	38,38,38,38	0
56	MG	2A	3290	1/1	0.96	0.05	26,26,26,26	0
56	MG	2A	3291	1/1	0.96	0.08	30,30,30,30	0
56	MG	2A	3294	1/1	0.96	0.13	34,34,34,34	0
56	MG	2a	1843	1/1	0.96	0.10	43,43,43,43	0
56	MG	1V	202	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	4131	1/1	0.96	0.15	32,32,32,32	0
56	MG	2A	3297	1/1	0.96	0.09	33,33,33,33	0
56	MG	1A	3199	1/1	0.96	0.10	35,35,35,35	0
56	MG	2A	3587	1/1	0.96	0.19	44,44,44,44	0
56	MG	2A	3588	1/1	0.96	0.23	42,42,42,42	0
56	MG	2A	3589	1/1	0.96	0.09	43,43,43,43	0
56	MG	2A	3590	1/1	0.96	0.15	55,55,55,55	0
56	MG	2A	3592	1/1	0.96	0.09	51,51,51,51	0
56	MG	2A	3038	1/1	0.96	0.17	45,45,45,45	0
56	MG	2A	3300	1/1	0.96	0.14	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3523	1/1	0.96	0.08	50,50,50,50	0
56	MG	1W	3006	1/1	0.96	0.04	35,35,35,35	0
56	MG	2A	3303	1/1	0.96	0.20	56,56,56,56	0
56	MG	1A	3165	1/1	0.96	0.12	42,42,42,42	0
56	MG	2q	3001	1/1	0.96	0.29	65,65,65,65	0
56	MG	1Z	301	1/1	0.96	0.08	63,63,63,63	0
56	MG	2A	3306	1/1	0.96	0.10	55,55,55,55	0
56	MG	1A	4135	1/1	0.96	0.11	28,28,28,28	0
56	MG	1A	3705	1/1	0.96	0.10	21,21,21,21	0
56	MG	1A	3354	1/1	0.96	0.10	34,34,34,34	0
56	MG	2A	3046	1/1	0.96	0.07	33,33,33,33	0
56	MG	1A	3526	1/1	0.96	0.12	70,70,70,70	0
56	MG	1A	3303	1/1	0.96	0.07	44,44,44,44	0
56	MG	1A	3868	1/1	0.97	0.12	59,59,59,59	0
56	MG	1A	3657	1/1	0.97	0.16	39,39,39,39	0
56	MG	2A	3362	1/1	0.97	0.07	42,42,42,42	0
56	MG	1E	302	1/1	0.97	0.07	50,50,50,50	0
56	MG	1E	303	1/1	0.97	0.12	26,26,26,26	0
56	MG	1A	3578	1/1	0.97	0.18	53,53,53,53	0
56	MG	1a	1854	1/1	0.97	0.12	49,49,49,49	0
56	MG	1A	3995	1/1	0.97	0.22	32,32,32,32	0
56	MG	1A	3008	1/1	0.97	0.11	57,57,57,57	0
56	MG	1A	3872	1/1	0.97	0.07	16,16,16,16	0
56	MG	1A	3281	1/1	0.97	0.07	31,31,31,31	0
56	MG	1A	3118	1/1	0.97	0.13	44,44,44,44	0
56	MG	2A	3373	1/1	0.97	0.05	35,35,35,35	0
56	MG	1A	3448	1/1	0.97	0.08	35,35,35,35	0
56	MG	1F	303	1/1	0.97	0.06	37,37,37,37	0
56	MG	1A	3233	1/1	0.97	0.07	28,28,28,28	0
56	MG	1A	3285	1/1	0.97	0.23	30,30,30,30	0
56	MG	2A	3378	1/1	0.97	0.12	55,55,55,55	0
56	MG	2A	3379	1/1	0.97	0.09	31,31,31,31	0
56	MG	2A	3381	1/1	0.97	0.09	51,51,51,51	0
56	MG	1A	3335	1/1	0.97	0.16	36,36,36,36	0
56	MG	2A	3139	1/1	0.97	0.17	37,37,37,37	0
56	MG	2A	3140	1/1	0.97	0.18	41,41,41,41	0
56	MG	1A	3391	1/1	0.97	0.05	29,29,29,29	0
56	MG	1a	1686	1/1	0.97	0.12	45,45,45,45	0
56	MG	2A	3143	1/1	0.97	0.09	47,47,47,47	0
56	MG	2A	3144	1/1	0.97	0.20	45,45,45,45	0
56	MG	1A	3881	1/1	0.97	0.05	16,16,16,16	0
56	MG	1A	3002	1/1	0.97	0.05	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1869	1/1	0.97	0.11	62,62,62,62	0
56	MG	1A	3287	1/1	0.97	0.13	40,40,40,40	0
56	MG	2A	3149	1/1	0.97	0.09	35,35,35,35	0
56	MG	2A	3395	1/1	0.97	0.12	48,48,48,48	0
56	MG	1A	3172	1/1	0.97	0.14	28,28,28,28	0
56	MG	1A	3457	1/1	0.97	0.04	22,22,22,22	0
56	MG	1a	1873	1/1	0.97	0.10	42,42,42,42	0
56	MG	1a	1874	1/1	0.97	0.09	31,31,31,31	0
56	MG	1A	3887	1/1	0.97	0.05	40,40,40,40	0
56	MG	2A	3157	1/1	0.97	0.10	23,23,23,23	0
56	MG	1A	3237	1/1	0.97	0.12	24,24,24,24	0
56	MG	2A	3159	1/1	0.97	0.11	37,37,37,37	0
56	MG	1a	1694	1/1	0.97	0.11	48,48,48,48	0
56	MG	1a	1695	1/1	0.97	0.05	56,56,56,56	0
56	MG	1A	3238	1/1	0.97	0.07	35,35,35,35	0
56	MG	2A	3163	1/1	0.97	0.12	36,36,36,36	0
56	MG	1N	204	1/1	0.97	0.07	44,44,44,44	0
56	MG	1N	205	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3411	1/1	0.97	0.07	55,55,55,55	0
56	MG	1A	4136	1/1	0.97	0.08	38,38,38,38	0
56	MG	1N	207	1/1	0.97	0.04	41,41,41,41	0
56	MG	1a	1701	1/1	0.97	0.20	47,47,47,47	0
56	MG	1a	1886	1/1	0.97	0.09	40,40,40,40	0
56	MG	1O	3001	1/1	0.97	0.08	40,40,40,40	0
56	MG	1A	3397	1/1	0.97	0.07	57,57,57,57	0
56	MG	2a	1651	1/1	0.97	0.08	54,54,54,54	0
56	MG	1A	3341	1/1	0.97	0.07	25,25,25,25	0
56	MG	1a	1705	1/1	0.97	0.05	46,46,46,46	0
56	MG	2A	3174	1/1	0.97	0.15	38,38,38,38	0
56	MG	2A	3175	1/1	0.97	0.10	37,37,37,37	0
56	MG	2A	3176	1/1	0.97	0.04	23,23,23,23	0
56	MG	1A	3343	1/1	0.97	0.09	41,41,41,41	0
56	MG	1A	3778	1/1	0.97	0.07	30,30,30,30	0
56	MG	2A	3425	1/1	0.97	0.06	27,27,27,27	0
56	MG	1A	3779	1/1	0.97	0.07	26,26,26,26	0
56	MG	1A	3401	1/1	0.97	0.09	30,30,30,30	0
56	MG	2a	1662	1/1	0.97	0.06	71,71,71,71	0
56	MG	1A	3781	1/1	0.97	0.11	25,25,25,25	0
56	MG	1A	3173	1/1	0.97	0.13	40,40,40,40	0
56	MG	2A	3184	1/1	0.97	0.12	29,29,29,29	0
56	MG	2A	3431	1/1	0.97	0.07	48,48,48,48	0
56	MG	2A	3432	1/1	0.97	0.06	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3433	1/1	0.97	0.06	48,48,48,48	0
56	MG	1A	3151	1/1	0.97	0.08	31,31,31,31	0
56	MG	1Q	205	1/1	0.97	0.07	42,42,42,42	0
56	MG	1A	3120	1/1	0.97	0.16	37,37,37,37	0
56	MG	1A	4148	1/1	0.97	0.11	47,47,47,47	0
56	MG	1A	3349	1/1	0.97	0.10	32,32,32,32	0
56	MG	2A	3440	1/1	0.97	0.11	37,37,37,37	0
56	MG	1h	201	1/1	0.97	0.12	60,60,60,60	0
56	MG	1A	3902	1/1	0.97	0.09	38,38,38,38	0
56	MG	1A	3786	1/1	0.97	0.11	18,18,18,18	0
56	MG	1A	3904	1/1	0.97	0.07	52,52,52,52	0
56	MG	1A	3407	1/1	0.97	0.16	48,48,48,48	0
56	MG	2A	3446	1/1	0.97	0.12	53,53,53,53	0
56	MG	2a	1682	1/1	0.97	0.13	54,54,54,54	0
56	MG	2A	3195	1/1	0.97	0.09	46,46,46,46	0
56	MG	1A	3202	1/1	0.97	0.08	26,26,26,26	0
56	MG	1A	3203	1/1	0.97	0.14	30,30,30,30	0
56	MG	2a	1686	1/1	0.97	0.07	44,44,44,44	0
56	MG	2A	3198	1/1	0.97	0.14	44,44,44,44	0
56	MG	2A	3452	1/1	0.97	0.08	50,50,50,50	0
56	MG	1A	3687	1/1	0.97	0.10	21,21,21,21	0
56	MG	1A	3793	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3688	1/1	0.97	0.13	19,19,19,19	0
56	MG	1A	3911	1/1	0.97	0.12	25,25,25,25	0
56	MG	1A	4162	1/1	0.97	0.09	37,37,37,37	0
56	MG	2A	3458	1/1	0.97	0.04	43,43,43,43	0
56	MG	1A	3689	1/1	0.97	0.07	26,26,26,26	0
56	MG	1A	3054	1/1	0.97	0.07	45,45,45,45	0
56	MG	1A	3535	1/1	0.97	0.12	26,26,26,26	0
56	MG	1A	3178	1/1	0.97	0.23	39,39,39,39	0
56	MG	2A	3463	1/1	0.97	0.13	40,40,40,40	0
56	MG	1x	104	1/1	0.97	0.11	42,42,42,42	0
56	MG	1W	3002	1/1	0.97	0.18	41,41,41,41	0
56	MG	1a	1733	1/1	0.97	0.11	49,49,49,49	0
56	MG	1W	3003	1/1	0.97	0.13	32,32,32,32	0
56	MG	2A	3215	1/1	0.97	0.06	38,38,38,38	0
56	MG	2A	3469	1/1	0.97	0.04	45,45,45,45	0
56	MG	1A	3695	1/1	0.97	0.11	40,40,40,40	0
56	MG	2A	3220	1/1	0.97	0.06	38,38,38,38	0
56	MG	1A	4168	1/1	0.97	0.13	26,26,26,26	0
56	MG	2A	3223	1/1	0.97	0.08	31,31,31,31	0
56	MG	1A	3804	1/1	0.97	0.10	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	4170	1/1	0.97	0.10	10,10,10,10	0
56	MG	1Y	502	1/1	0.97	0.12	45,45,45,45	0
56	MG	2A	3001	1/1	0.97	0.04	38,38,38,38	0
56	MG	1A	4171	1/1	0.97	0.06	41,41,41,41	0
56	MG	1A	3179	1/1	0.97	0.16	36,36,36,36	0
56	MG	1A	3919	1/1	0.97	0.06	16,16,16,16	0
56	MG	1A	3355	1/1	0.97	0.24	47,47,47,47	0
56	MG	1A	3921	1/1	0.97	0.09	23,23,23,23	0
56	MG	1A	3539	1/1	0.97	0.05	41,41,41,41	0
56	MG	2A	3234	1/1	0.97	0.12	50,50,50,50	0
56	MG	1A	3612	1/1	0.97	0.11	41,41,41,41	0
56	MG	1A	3155	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	4179	1/1	0.97	0.15	34,34,34,34	0
56	MG	2a	1728	1/1	0.97	0.14	52,52,52,52	0
56	MG	2A	3011	1/1	0.97	0.10	49,49,49,49	0
56	MG	1A	4180	1/1	0.97	0.24	33,33,33,33	0
56	MG	1A	4182	1/1	0.97	0.10	42,42,42,42	0
56	MG	2A	3242	1/1	0.97	0.07	46,46,46,46	0
56	MG	1A	3925	1/1	0.97	0.05	39,39,39,39	0
56	MG	2A	3494	1/1	0.97	0.10	39,39,39,39	0
56	MG	2A	3495	1/1	0.97	0.06	38,38,38,38	0
56	MG	1A	3926	1/1	0.97	0.05	15,15,15,15	0
56	MG	1A	4186	1/1	0.97	0.14	17,17,17,17	0
56	MG	1A	3927	1/1	0.97	0.05	30,30,30,30	0
56	MG	15	102	1/1	0.97	0.19	45,45,45,45	0
56	MG	1A	3415	1/1	0.97	0.11	46,46,46,46	0
56	MG	2A	3249	1/1	0.97	0.08	29,29,29,29	0
56	MG	2A	3502	1/1	0.97	0.05	30,30,30,30	0
56	MG	1A	4051	1/1	0.97	0.10	49,49,49,49	0
56	MG	1A	3812	1/1	0.97	0.10	34,34,34,34	0
56	MG	2A	3505	1/1	0.97	0.08	45,45,45,45	0
56	MG	1A	4053	1/1	0.97	0.06	43,43,43,43	0
56	MG	2A	3254	1/1	0.97	0.11	43,43,43,43	0
56	MG	1A	3302	1/1	0.97	0.04	15,15,15,15	0
56	MG	1A	3212	1/1	0.97	0.16	63,63,63,63	0
56	MG	1A	4196	1/1	0.97	0.08	50,50,50,50	0
56	MG	1A	3255	1/1	0.97	0.05	68,68,68,68	0
56	MG	1A	3157	1/1	0.97	0.10	42,42,42,42	0
56	MG	2A	3029	1/1	0.97	0.08	54,54,54,54	0
56	MG	1A	3158	1/1	0.97	0.07	18,18,18,18	0
56	MG	2A	3263	1/1	0.97	0.08	30,30,30,30	0
56	MG	1A	3067	1/1	0.97	0.14	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1a	1768	1/1	0.97	0.11	32,32,32,32	0
56	MG	1A	3551	1/1	0.97	0.13	53,53,53,53	0
56	MG	1A	3185	1/1	0.97	0.05	24,24,24,24	0
56	MG	2A	3522	1/1	0.97	0.04	32,32,32,32	0
56	MG	1A	3366	1/1	0.97	0.09	37,37,37,37	0
56	MG	1A	3081	1/1	0.97	0.10	47,47,47,47	0
56	MG	1a	1773	1/1	0.97	0.06	25,25,25,25	0
56	MG	1a	1603	1/1	0.97	0.05	59,59,59,59	0
56	MG	1A	4205	1/1	0.97	0.05	36,36,36,36	0
56	MG	2A	3529	1/1	0.97	0.10	43,43,43,43	0
56	MG	2A	3530	1/1	0.97	0.07	31,31,31,31	0
56	MG	1A	4206	1/1	0.97	0.06	29,29,29,29	0
56	MG	2A	3532	1/1	0.97	0.08	36,36,36,36	0
56	MG	1A	4209	1/1	0.97	0.23	27,27,27,27	0
56	MG	1A	4210	1/1	0.97	0.12	43,43,43,43	0
56	MG	1A	3310	1/1	0.97	0.12	37,37,37,37	0
56	MG	2a	1774	1/1	0.97	0.27	57,57,57,57	0
56	MG	2a	1775	1/1	0.97	0.07	62,62,62,62	0
56	MG	2A	3278	1/1	0.97	0.14	44,44,44,44	0
56	MG	1A	3221	1/1	0.97	0.08	36,36,36,36	0
56	MG	2A	3538	1/1	0.97	0.05	42,42,42,42	0
56	MG	1A	3826	1/1	0.97	0.10	37,37,37,37	0
56	MG	1A	3313	1/1	0.97	0.07	56,56,56,56	0
56	MG	1A	3828	1/1	0.97	0.10	44,44,44,44	0
56	MG	2A	3048	1/1	0.97	0.12	43,43,43,43	0
56	MG	2A	3543	1/1	0.97	0.19	47,47,47,47	0
56	MG	1A	3830	1/1	0.97	0.05	36,36,36,36	0
56	MG	1A	3222	1/1	0.97	0.09	30,30,30,30	0
56	MG	2A	3051	1/1	0.97	0.13	51,51,51,51	0
56	MG	1A	4220	1/1	0.97	0.09	27,27,27,27	0
56	MG	1A	4221	1/1	0.97	0.07	32,32,32,32	0
56	MG	2A	3549	1/1	0.97	0.20	47,47,47,47	0
56	MG	1a	1788	1/1	0.97	0.10	46,46,46,46	0
56	MG	1a	1620	1/1	0.97	0.15	38,38,38,38	0
56	MG	1A	3559	1/1	0.97	0.13	41,41,41,41	0
56	MG	2A	3292	1/1	0.97	0.07	32,32,32,32	0
56	MG	2A	3293	1/1	0.97	0.12	37,37,37,37	0
56	MG	1A	3187	1/1	0.97	0.12	38,38,38,38	0
56	MG	1A	4225	1/1	0.97	0.09	23,23,23,23	0
56	MG	1A	3952	1/1	0.97	0.10	41,41,41,41	0
56	MG	1A	3561	1/1	0.97	0.08	51,51,51,51	0
56	MG	2A	3559	1/1	0.97	0.25	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3062	1/1	0.97	0.10	35,35,35,35	0
56	MG	1a	1796	1/1	0.97	0.05	55,55,55,55	0
56	MG	1A	3835	1/1	0.97	0.14	33,33,33,33	0
56	MG	1A	3266	1/1	0.97	0.09	31,31,31,31	0
56	MG	1A	3563	1/1	0.97	0.16	46,46,46,46	0
56	MG	1A	3267	1/1	0.97	0.04	23,23,23,23	0
56	MG	2A	3068	1/1	0.97	0.14	46,46,46,46	0
56	MG	1a	1630	1/1	0.97	0.11	42,42,42,42	0
56	MG	1A	3725	1/1	0.97	0.12	34,34,34,34	0
56	MG	1A	3565	1/1	0.97	0.10	53,53,53,53	0
56	MG	1A	3841	1/1	0.97	0.17	46,46,46,46	0
56	MG	2A	3074	1/1	0.97	0.14	47,47,47,47	0
56	MG	1A	3494	1/1	0.97	0.19	59,59,59,59	0
56	MG	1B	205	1/1	0.97	0.20	57,57,57,57	0
56	MG	1A	3038	1/1	0.97	0.08	48,48,48,48	0
56	MG	1A	3225	1/1	0.97	0.22	35,35,35,35	0
56	MG	1A	3321	1/1	0.97	0.09	47,47,47,47	0
56	MG	1a	1814	1/1	0.97	0.12	56,56,56,56	0
56	MG	2A	3081	1/1	0.97	0.12	45,45,45,45	0
56	MG	2A	3318	1/1	0.97	0.06	37,37,37,37	0
56	MG	1A	3846	1/1	0.97	0.05	23,23,23,23	0
56	MG	2A	3083	1/1	0.97	0.08	38,38,38,38	0
56	MG	1A	3967	1/1	0.97	0.04	20,20,20,20	0
56	MG	2A	3586	1/1	0.97	0.08	33,33,33,33	0
56	MG	2a	1826	1/1	0.97	0.14	53,53,53,53	0
56	MG	1A	3226	1/1	0.97	0.14	38,38,38,38	0
56	MG	2A	3087	1/1	0.97	0.14	41,41,41,41	0
56	MG	2A	3088	1/1	0.97	0.04	27,27,27,27	0
56	MG	1A	3733	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3437	1/1	0.97	0.09	33,33,33,33	0
56	MG	2A	3091	1/1	0.97	0.04	39,39,39,39	0
56	MG	1B	217	1/1	0.97	0.06	36,36,36,36	0
56	MG	2B	3003	1/1	0.97	0.19	51,51,51,51	0
56	MG	2A	3094	1/1	0.97	0.18	49,49,49,49	0
56	MG	1A	3851	1/1	0.97	0.11	33,33,33,33	0
56	MG	2A	3332	1/1	0.97	0.09	51,51,51,51	0
56	MG	1A	3029	1/1	0.97	0.25	55,55,55,55	0
56	MG	1a	1824	1/1	0.97	0.14	59,59,59,59	0
56	MG	2a	1841	1/1	0.97	0.16	42,42,42,42	0
56	MG	1A	3736	1/1	0.97	0.04	42,42,42,42	0
56	MG	1a	1650	1/1	0.97	0.25	52,52,52,52	0
56	MG	1A	3740	1/1	0.97	0.13	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3741	1/1	0.97	0.06	44,44,44,44	0
56	MG	2D	305	1/1	0.97	0.14	29,29,29,29	0
56	MG	1A	4097	1/1	0.97	0.17	27,27,27,27	0
56	MG	1a	1830	1/1	0.97	0.07	36,36,36,36	0
56	MG	1A	3275	1/1	0.97	0.09	48,48,48,48	0
56	MG	2E	303	1/1	0.97	0.16	44,44,44,44	0
56	MG	1A	3276	1/1	0.97	0.36	34,34,34,34	0
56	MG	2f	3001	1/1	0.97	0.10	49,49,49,49	0
56	MG	1A	3744	1/1	0.97	0.07	49,49,49,49	0
56	MG	2E	306	1/1	0.97	0.08	42,42,42,42	0
56	MG	1A	3651	1/1	0.97	0.14	52,52,52,52	0
56	MG	2F	302	1/1	0.97	0.10	41,41,41,41	0
56	MG	1A	3164	1/1	0.97	0.05	35,35,35,35	0
56	MG	1A	3136	1/1	0.97	0.15	37,37,37,37	0
56	MG	1a	1660	1/1	0.97	0.22	47,47,47,47	0
56	MG	1a	1661	1/1	0.97	0.08	34,34,34,34	0
56	MG	1a	1662	1/1	0.97	0.10	42,42,42,42	0
56	MG	2t	3001	1/1	0.97	0.17	50,50,50,50	0
56	MG	1A	3654	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	3987	1/1	0.97	0.06	12,12,12,12	0
56	MG	1A	3655	1/1	0.97	0.05	30,30,30,30	0
56	MG	1A	3279	1/1	0.97	0.11	41,41,41,41	0
56	MG	1D	312	1/1	0.97	0.14	41,41,41,41	0
57	ZN	1n	501	1/1	0.97	0.06	93,93,93,93	0
56	MG	1A	3752	1/1	0.97	0.07	34,34,34,34	0
56	MG	1A	3754	1/1	0.97	0.07	32,32,32,32	0
56	MG	2A	3178	1/1	0.98	0.07	43,43,43,43	0
56	MG	1A	4187	1/1	0.98	0.08	27,27,27,27	0
56	MG	1A	4188	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	3166	1/1	0.98	0.04	21,21,21,21	0
56	MG	2A	3053	1/1	0.98	0.10	56,56,56,56	0
56	MG	1A	3182	1/1	0.98	0.10	33,33,33,33	0
56	MG	1A	3547	1/1	0.98	0.05	38,38,38,38	0
56	MG	1A	3220	1/1	0.98	0.06	30,30,30,30	0
56	MG	1A	3937	1/1	0.98	0.07	47,47,47,47	0
56	MG	1A	3404	1/1	0.98	0.04	32,32,32,32	0
56	MG	1A	3791	1/1	0.98	0.06	53,53,53,53	0
56	MG	1A	3198	1/1	0.98	0.16	33,33,33,33	0
56	MG	1A	3251	1/1	0.98	0.07	36,36,36,36	0
56	MG	1a	1638	1/1	0.98	0.07	18,18,18,18	0
56	MG	1A	3452	1/1	0.98	0.07	48,48,48,48	0
56	MG	2A	3472	1/1	0.98	0.04	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2N	8001	1/1	0.98	0.04	55,55,55,55	0
56	MG	1A	3364	1/1	0.98	0.11	43,43,43,43	0
56	MG	2A	3336	1/1	0.98	0.10	36,36,36,36	0
56	MG	1A	3066	1/1	0.98	0.11	41,41,41,41	0
56	MG	1a	1642	1/1	0.98	0.06	47,47,47,47	0
56	MG	1A	3797	1/1	0.98	0.06	41,41,41,41	0
56	MG	1A	3288	1/1	0.98	0.09	13,13,13,13	0
56	MG	1A	4111	1/1	0.98	0.16	32,32,32,32	0
56	MG	1P	203	1/1	0.98	0.12	26,26,26,26	0
56	MG	1a	1876	1/1	0.98	0.07	37,37,37,37	0
56	MG	2A	3202	1/1	0.98	0.05	40,40,40,40	0
56	MG	2A	3072	1/1	0.98	0.07	39,39,39,39	0
56	MG	1A	3947	1/1	0.98	0.09	13,13,13,13	0
56	MG	1P	205	1/1	0.98	0.12	41,41,41,41	0
56	MG	1A	3289	1/1	0.98	0.11	24,24,24,24	0
56	MG	1A	3168	1/1	0.98	0.08	29,29,29,29	0
56	MG	1A	4207	1/1	0.98	0.19	30,30,30,30	0
56	MG	2a	1752	1/1	0.98	0.14	51,51,51,51	0
56	MG	1A	3950	1/1	0.98	0.03	16,16,16,16	0
56	MG	1A	3875	1/1	0.98	0.06	28,28,28,28	0
56	MG	1A	3201	1/1	0.98	0.14	17,17,17,17	0
56	MG	1A	3730	1/1	0.98	0.07	44,44,44,44	0
56	MG	1A	3954	1/1	0.98	0.08	53,53,53,53	0
56	MG	1A	4214	1/1	0.98	0.05	19,19,19,19	0
56	MG	1A	3135	1/1	0.98	0.06	49,49,49,49	0
56	MG	2A	3219	1/1	0.98	0.07	42,42,42,42	0
56	MG	1A	3807	1/1	0.98	0.03	18,18,18,18	0
56	MG	2A	3086	1/1	0.98	0.11	48,48,48,48	0
56	MG	1A	3015	1/1	0.98	0.14	42,42,42,42	0
56	MG	1A	3615	1/1	0.98	0.15	50,50,50,50	0
56	MG	1A	4219	1/1	0.98	0.14	25,25,25,25	0
56	MG	1T	202	1/1	0.98	0.06	39,39,39,39	0
56	MG	1A	3204	1/1	0.98	0.18	27,27,27,27	0
56	MG	2A	3366	1/1	0.98	0.07	45,45,45,45	0
56	MG	1A	3205	1/1	0.98	0.07	35,35,35,35	0
56	MG	1A	4222	1/1	0.98	0.08	68,68,68,68	0
56	MG	1A	3511	1/1	0.98	0.05	35,35,35,35	0
56	MG	1A	4129	1/1	0.98	0.06	56,56,56,56	0
56	MG	1A	3885	1/1	0.98	0.12	46,46,46,46	0
56	MG	1A	3739	1/1	0.98	0.10	22,22,22,22	0
56	MG	1A	3512	1/1	0.98	0.05	41,41,41,41	0
56	MG	2A	3512	1/1	0.98	0.08	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3093	1/1	0.98	0.07	35,35,35,35	0
56	MG	1A	4229	1/1	0.98	0.26	33,33,33,33	0
56	MG	1A	3889	1/1	0.98	0.03	29,29,29,29	0
56	MG	2A	3103	1/1	0.98	0.10	39,39,39,39	0
56	MG	2A	3517	1/1	0.98	0.03	43,43,43,43	0
56	MG	2a	1782	1/1	0.98	0.13	51,51,51,51	0
56	MG	1A	4231	1/1	0.98	0.13	17,17,17,17	0
56	MG	1A	3230	1/1	0.98	0.07	40,40,40,40	0
56	MG	1A	3968	1/1	0.98	0.03	34,34,34,34	0
56	MG	1A	3969	1/1	0.98	0.05	58,58,58,58	0
56	MG	1A	3207	1/1	0.98	0.15	50,50,50,50	0
56	MG	1A	3263	1/1	0.98	0.04	31,31,31,31	0
56	MG	1A	3680	1/1	0.98	0.10	20,20,20,20	0
56	MG	1A	3159	1/1	0.98	0.09	26,26,26,26	0
56	MG	1a	1794	1/1	0.98	0.10	24,24,24,24	0
56	MG	1A	3974	1/1	0.98	0.08	54,54,54,54	0
56	MG	2A	3528	1/1	0.98	0.07	38,38,38,38	0
56	MG	1A	3265	1/1	0.98	0.07	12,12,12,12	0
56	MG	1A	3072	1/1	0.98	0.11	32,32,32,32	0
56	MG	2A	3252	1/1	0.98	0.07	56,56,56,56	0
56	MG	2A	3392	1/1	0.98	0.05	41,41,41,41	0
56	MG	1A	3628	1/1	0.98	0.04	25,25,25,25	0
56	MG	2A	3118	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3089	1/1	0.98	0.08	53,53,53,53	0
56	MG	1A	3235	1/1	0.98	0.25	36,36,36,36	0
56	MG	2a	1802	1/1	0.98	0.10	53,53,53,53	0
56	MG	1a	1801	1/1	0.98	0.10	36,36,36,36	0
56	MG	1A	3753	1/1	0.98	0.09	44,44,44,44	0
56	MG	1A	3342	1/1	0.98	0.07	30,30,30,30	0
56	MG	1a	1804	1/1	0.98	0.10	42,42,42,42	0
56	MG	1B	215	1/1	0.98	0.07	31,31,31,31	0
56	MG	1B	216	1/1	0.98	0.08	54,54,54,54	0
56	MG	1A	3982	1/1	0.98	0.06	42,42,42,42	0
56	MG	1a	1808	1/1	0.98	0.12	33,33,33,33	0
56	MG	1a	1809	1/1	0.98	0.09	41,41,41,41	0
56	MG	1B	218	1/1	0.98	0.07	27,27,27,27	0
56	MG	2A	3407	1/1	0.98	0.07	46,46,46,46	0
56	MG	1A	3829	1/1	0.98	0.07	54,54,54,54	0
56	MG	15	103	1/1	0.98	0.07	34,34,34,34	0
56	MG	1A	3690	1/1	0.98	0.09	28,28,28,28	0
56	MG	1A	3211	1/1	0.98	0.13	39,39,39,39	0
56	MG	1A	4155	1/1	0.98	0.05	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3757	1/1	0.98	0.04	30,30,30,30	0
56	MG	1A	3344	1/1	0.98	0.10	41,41,41,41	0
56	MG	1A	4158	1/1	0.98	0.16	23,23,23,23	0
56	MG	1a	1819	1/1	0.98	0.09	32,32,32,32	0
56	MG	1A	3693	1/1	0.98	0.08	26,26,26,26	0
56	MG	1A	3345	1/1	0.98	0.12	25,25,25,25	0
56	MG	1A	3270	1/1	0.98	0.06	26,26,26,26	0
56	MG	1D	304	1/1	0.98	0.08	42,42,42,42	0
56	MG	2A	3561	1/1	0.98	0.10	46,46,46,46	0
56	MG	1A	3477	1/1	0.98	0.06	26,26,26,26	0
56	MG	1A	3108	1/1	0.98	0.17	46,46,46,46	0
56	MG	1D	307	1/1	0.98	0.04	27,27,27,27	0
56	MG	2a	1831	1/1	0.98	0.11	60,60,60,60	0
56	MG	19	104	1/1	0.98	0.12	59,59,59,59	0
56	MG	1A	3213	1/1	0.98	0.16	23,23,23,23	0
56	MG	1A	3699	1/1	0.98	0.09	20,20,20,20	0
56	MG	1A	3274	1/1	0.98	0.04	29,29,29,29	0
56	MG	1a	1831	1/1	0.98	0.12	51,51,51,51	0
56	MG	1A	3214	1/1	0.98	0.07	38,38,38,38	0
56	MG	2A	3153	1/1	0.98	0.12	29,29,29,29	0
56	MG	1a	1833	1/1	0.98	0.12	43,43,43,43	0
56	MG	2A	3573	1/1	0.98	0.09	42,42,42,42	0
56	MG	2A	3574	1/1	0.98	0.10	30,30,30,30	0
56	MG	2A	3155	1/1	0.98	0.11	37,37,37,37	0
56	MG	1A	3768	1/1	0.98	0.06	17,17,17,17	0
56	MG	1A	3435	1/1	0.98	0.04	44,44,44,44	0
56	MG	1A	3311	1/1	0.98	0.09	35,35,35,35	0
56	MG	1A	3150	1/1	0.98	0.07	22,22,22,22	0
56	MG	1A	3085	1/1	0.98	0.13	43,43,43,43	0
56	MG	1A	3848	1/1	0.98	0.04	23,23,23,23	0
56	MG	1A	3439	1/1	0.98	0.04	38,38,38,38	0
56	MG	1A	3242	1/1	0.98	0.15	22,22,22,22	0
56	MG	1A	3708	1/1	0.98	0.12	30,30,30,30	0
56	MG	1a	1614	1/1	0.98	0.05	59,59,59,59	0
56	MG	2a	1700	1/1	0.98	0.08	55,55,55,55	0
56	MG	1a	1615	1/1	0.98	0.04	52,52,52,52	0
56	MG	1A	3243	1/1	0.98	0.06	24,24,24,24	0
56	MG	1A	3853	1/1	0.98	0.08	35,35,35,35	0
56	MG	1A	3710	1/1	0.98	0.11	37,37,37,37	0
56	MG	1a	1619	1/1	0.98	0.06	31,31,31,31	0
56	MG	2A	3591	1/1	0.98	0.06	44,44,44,44	0
56	MG	1A	3316	1/1	0.98	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	2A	3450	1/1	0.98	0.04	30,30,30,30	0
56	MG	1A	4181	1/1	0.98	0.06	27,27,27,27	0
56	MG	2a	1711	1/1	0.98	0.06	38,38,38,38	0
56	MG	1A	3117	1/1	0.98	0.18	43,43,43,43	0
56	MG	2B	3004	1/1	0.98	0.08	41,41,41,41	0
56	MG	1A	3399	1/1	0.98	0.08	5,5,5,5	0
56	MG	2a	1715	1/1	0.98	0.13	65,65,65,65	0
57	ZN	14	501	1/1	0.98	0.04	104,104,104,104	0
56	MG	1A	4184	1/1	0.98	0.10	58,58,58,58	0
57	ZN	2Y	501	1/1	0.98	0.03	83,83,83,83	0
56	MG	1A	3542	1/1	0.98	0.06	37,37,37,37	0
57	ZN	29	501	1/1	0.98	0.04	61,61,61,61	0
56	MG	1A	3358	1/1	0.98	0.05	46,46,46,46	0
58	SF4	1d	501	8/8	0.98	0.05	62,69,78,87	0
58	SF4	2d	501	8/8	0.98	0.04	62,78,83,91	0
56	MG	2A	3205	1/1	0.99	0.03	23,23,23,23	0
56	MG	1A	3737	1/1	0.99	0.07	18,18,18,18	0
56	MG	2A	3258	1/1	0.99	0.09	34,34,34,34	0
56	MG	1B	214	1/1	0.99	0.03	37,37,37,37	0
56	MG	1A	3787	1/1	0.99	0.07	33,33,33,33	0
56	MG	1A	3738	1/1	0.99	0.08	32,32,32,32	0
56	MG	1A	3273	1/1	0.99	0.03	18,18,18,18	0
56	MG	1F	306	1/1	0.99	0.04	35,35,35,35	0
56	MG	1A	3283	1/1	0.99	0.12	25,25,25,25	0
56	MG	17	102	1/1	0.99	0.03	42,42,42,42	0
56	MG	1A	3638	1/1	0.99	0.03	17,17,17,17	0
56	MG	1A	4083	1/1	0.99	0.04	45,45,45,45	0
56	MG	1U	202	1/1	0.99	0.07	25,25,25,25	0
56	MG	2a	1703	1/1	0.99	0.03	60,60,60,60	0
56	MG	2A	3438	1/1	0.99	0.03	26,26,26,26	0
56	MG	2A	3380	1/1	0.99	0.04	47,47,47,47	0
56	MG	2A	3217	1/1	0.99	0.18	36,36,36,36	0
56	MG	2A	3270	1/1	0.99	0.03	23,23,23,23	0
56	MG	2A	3218	1/1	0.99	0.07	36,36,36,36	0
56	MG	1A	3154	1/1	0.99	0.08	21,21,21,21	0
56	MG	1A	4116	1/1	0.99	0.07	17,17,17,17	0
56	MG	1A	3325	1/1	0.99	0.07	37,37,37,37	0
56	MG	2A	3222	1/1	0.99	0.08	29,29,29,29	0
56	MG	2A	3330	1/1	0.99	0.07	41,41,41,41	0
56	MG	1U	206	1/1	0.99	0.12	32,32,32,32	0
56	MG	1A	3623	1/1	0.99	0.07	21,21,21,21	0
56	MG	2A	3333	1/1	0.99	0.04	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3055	1/1	0.99	0.05	54,54,54,54	0
56	MG	2A	3335	1/1	0.99	0.05	39,39,39,39	0
56	MG	1A	3643	1/1	0.99	0.12	12,12,12,12	0
56	MG	1A	3189	1/1	0.99	0.06	26,26,26,26	0
56	MG	1A	3798	1/1	0.99	0.08	31,31,31,31	0
56	MG	1A	4123	1/1	0.99	0.17	31,31,31,31	0
56	MG	1A	3799	1/1	0.99	0.03	38,38,38,38	0
56	MG	1A	3683	1/1	0.99	0.06	44,44,44,44	0
56	MG	1A	3579	1/1	0.99	0.15	38,38,38,38	0
56	MG	2A	3093	1/1	0.99	0.07	51,51,51,51	0
56	MG	1a	1892	1/1	0.99	0.15	54,54,54,54	0
56	MG	1A	3802	1/1	0.99	0.06	20,20,20,20	0
56	MG	2A	3236	1/1	0.99	0.05	45,45,45,45	0
56	MG	1A	3774	1/1	0.99	0.03	23,23,23,23	0
56	MG	1A	3685	1/1	0.99	0.08	17,17,17,17	0
56	MG	1A	3776	1/1	0.99	0.07	25,25,25,25	0
56	MG	1A	3245	1/1	0.99	0.14	30,30,30,30	0
56	MG	1A	3253	1/1	0.99	0.04	29,29,29,29	0
56	MG	1A	4100	1/1	0.99	0.14	22,22,22,22	0
56	MG	2a	1674	1/1	0.99	0.13	46,46,46,46	0
56	MG	1A	3177	1/1	0.99	0.10	14,14,14,14	0
56	MG	1A	3583	1/1	0.99	0.05	46,46,46,46	0
56	MG	1A	3614	1/1	0.99	0.08	27,27,27,27	0
56	MG	1A	3507	1/1	0.99	0.04	34,34,34,34	0
56	MG	1A	3544	1/1	0.99	0.04	10,10,10,10	0
56	MG	1A	4139	1/1	0.99	0.17	38,38,38,38	0
56	MG	1a	1741	1/1	0.99	0.20	47,47,47,47	0
57	ZN	1Y	501	1/1	0.99	0.03	66,66,66,66	0
56	MG	2a	1621	1/1	0.99	0.03	47,47,47,47	0
57	ZN	15	101	1/1	0.99	0.09	60,60,60,60	0
57	ZN	16	102	1/1	0.99	0.02	32,32,32,32	0
56	MG	2A	3022	1/1	0.99	0.05	44,44,44,44	0
56	MG	1A	4208	1/1	0.99	0.07	29,29,29,29	0
56	MG	2A	3201	1/1	0.99	0.04	25,25,25,25	0
57	ZN	26	501	1/1	0.99	0.03	55,55,55,55	0
56	MG	1A	3247	1/1	0.99	0.07	27,27,27,27	0
56	MG	2A	3112	1/1	0.99	0.13	34,34,34,34	0
56	MG	1A	3171	1/1	0.99	0.07	30,30,30,30	0
56	MG	2A	3309	1/1	0.99	0.12	35,35,35,35	0
57	ZN	19	102	1/1	1.00	0.01	36,36,36,36	0
56	MG	1A	3745	1/1	1.00	0.03	43,43,43,43	0
56	MG	1A	3156	1/1	1.00	0.06	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	1A	3823	1/1	1.00	0.03	11,11,11,11	0
57	ZN	25	501	1/1	1.00	0.06	55,55,55,55	0

6.5 Other polymers (i)

There are no such residues in this entry.