



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2026 – 07:36 AM EDT

PDB ID : 8G2C / pdb_00008g2c
Title : Crystal structure of the A2503-C2,C8-dimethylated *Thermus thermophilus* 70S ribosome in complex with tylosin, mRNA, aminoacylated A-site Phe-tRNA_{phe}, aminoacylated P-site fMet-tRNA_{met}, and deacylated E-site tRNA_{phe} at 2.65Å resolution
Authors : Aleksandrova, E.V.; Wu, K.J.Y.; Tresco, B.I.C.; Syroegin, E.A.; Killeavy, E.E.; Balasanyants, S.M.; Svetlov, M.S.; Gregory, S.T.; Atkinson, G.C.; Myers, A.G.; Polikanov, Y.S.
Deposited on : 2023-02-03
Resolution : 2.65 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12

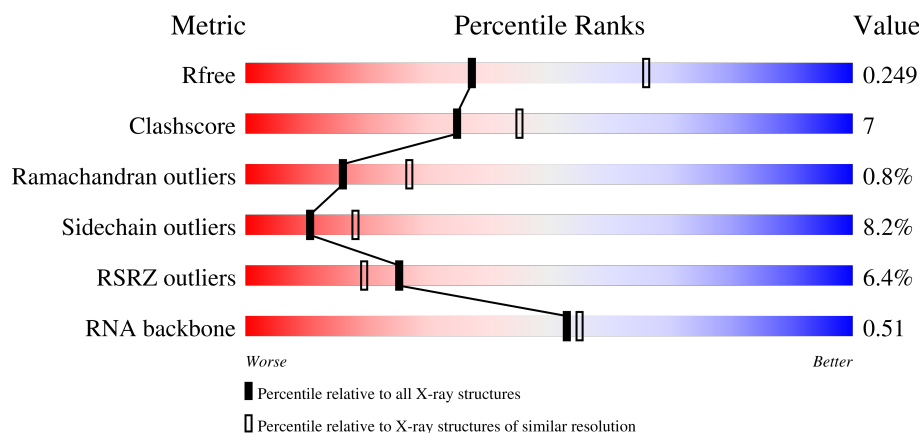
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)
RNA backbone	3983	1090 (2.90-2.42)

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

Mol	Chain	Length	Quality of chain
1	1A	2915	

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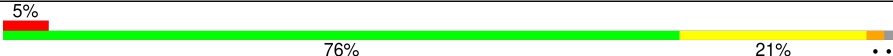
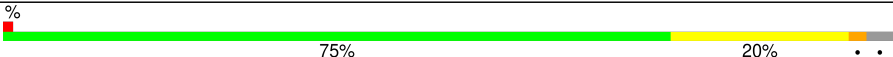
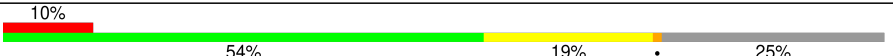
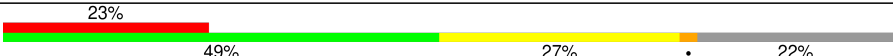
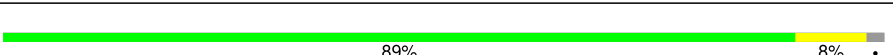
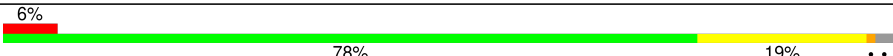
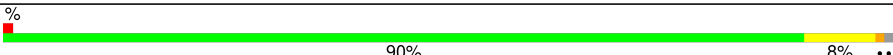
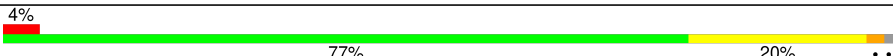
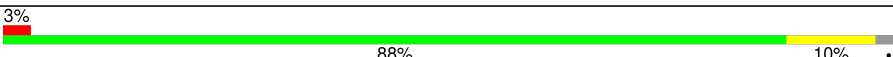
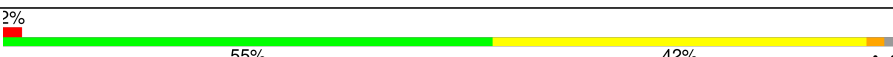
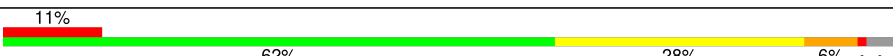
Ideal geometry (proteins) : Engh & Huber (2001)
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.50

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Mol	Chain	Length	Quality of chain
1	2A	2915	
2	1B	121	
2	2B	121	
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	

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Mol	Chain	Length	Quality of chain
14	1S	112	
14	2S	112	
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	

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Mol	Chain	Length	Quality of chain
26	24	71	
27	15	60	
27	25	60	
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	

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Mol	Chain	Length	Quality of chain
39	1h	138	
39	2h	138	
40	1i	128	
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	

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Mol	Chain	Length	Quality of chain
51	2t	106	
52	1u	27	
52	2u	27	
53	1v	24	
53	2v	24	
54	1w	76	
54	2w	76	
55	1x	77	
55	2x	77	
56	1y	76	
56	2y	76	

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	PSU	2y	55	-	-	X	-
57	MG	2A	3177	-	-	-	X
57	MG	2A	3252	-	-	-	X
57	MG	2A	3775	-	-	-	X
57	MG	2a	1610	-	-	-	X
57	MG	2a	1629	-	-	-	X
57	MG	2v	102	-	-	-	X

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 300115 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	2871	Total	C	N	O	P	0	0	0
			61853	27532	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60323	26849	11284	19390	2800			

- 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
			2577	1146	476	835	120			
2	2B	120	Total	C	N	O	P	0	0	0
			2575	1146	476	833	120			

- 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
			2136	1349	423	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	202	Total	C	N	O	S	0	0	0
			1583	1009	297	275	2			
5	2F	202	Total	C	N	O	S	0	0	0
			1579	1007	296	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
			1423	913	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	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
			1097	701	191	204	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	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	C	N	O	S	0	0	0
			933	588	171	170	4			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total	C	N	O	0	0	0
			873	550	174	149			
14	2S	110	Total	C	N	O	0	0	0
			870	549	173	148			

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

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

- 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	154	Total	C	N	O	S	0	0	0
			1240	795	222	220	3			
21	2Z	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
22	20	83	Total	C	N	O	S	0	0	0
			653	404	139	109	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
			552	349	99	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	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1503	Total	C	N	O	P	0	0	0
			32327	14396	5990	10438	1503			

- 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
			1846	1179	331	331	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	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
			1548	973	301	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	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
			1655	1038	326	284	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	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
			1133	716	214	199	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
			810	514	144	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	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
			1231	766	243	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	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
			1088	689	206	191	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
			983	623	193	167			
40	2i	127	Total	C	N	O	0	0	0
			978	619	190	169			

- 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
			709	440	138	131			
41	2j	96	Total	C	N	O	0	0	0
			714	445	138	131			

- 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
			829	516	155	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			833	519	156	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
			932	586	185	159	2			
43	2l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	123	Total	C	N	O	S	0	0	0
			958	592	198	166	2			
44	2m	122	Total	C	N	O	S	0	0	0
			950	586	197	165	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
			492	312	104	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	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
			728	456	144	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
			681	433	134	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
			823	528	151	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	83	Total	C	N	O	S	0	0	0
			652	417	120	113	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
			728	446	156	124	2			
51	2t	96	Total	C	N	O	S	0	0	0
			727	446	155	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
			199	122	48	29				
52	2u	23	Total	C	N	O		0	0	0
			199	122	48	29				

- Molecule 53 is a RNA chain called MF-mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
53	2v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			

- Molecule 54 is a RNA chain called A-site Aminoacylated Phe-tRNA^{phe}.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1603	722	287	518	74	2			
54	2w	72	Total	C	N	O	P	S	0	0	0
			1555	699	280	502	72	2			

- Molecule 55 is a RNA chain called P-site Aminoacylated fMet-tRNA^{met}.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	77	Total	C	N	O	P	S	0	0	0
			1656	740	299	538	77	2			
55	2x	77	Total	C	N	O	P	S	0	0	0
			1656	740	299	538	77	2			

- Molecule 56 is a RNA chain called E-site Deacylated tRNA^{phe}.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
56	1y	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
56	2y	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1099	Total	Mg	0	0
			1099	1099		
57	1B	34	Total	Mg	0	0
			34	34		
57	1D	12	Total	Mg	0	0
			12	12		
57	1E	10	Total	Mg	0	0
			10	10		
57	1F	15	Total	Mg	0	0
			15	15		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1G	5	Total 5	Mg 5	0	0
57	1H	1	Total 1	Mg 1	0	0
57	1I	1	Total 1	Mg 1	0	0
57	1N	5	Total 5	Mg 5	0	0
57	1O	6	Total 6	Mg 6	0	0
57	1P	5	Total 5	Mg 5	0	0
57	1Q	7	Total 7	Mg 7	0	0
57	1R	6	Total 6	Mg 6	0	0
57	1S	3	Total 3	Mg 3	0	0
57	1T	3	Total 3	Mg 3	0	0
57	1U	10	Total 10	Mg 10	0	0
57	1V	5	Total 5	Mg 5	0	0
57	1W	6	Total 6	Mg 6	0	0
57	1X	6	Total 6	Mg 6	0	0
57	1Y	2	Total 2	Mg 2	0	0
57	1Z	2	Total 2	Mg 2	0	0
57	10	10	Total 10	Mg 10	0	0
57	11	5	Total 5	Mg 5	0	0
57	12	3	Total 3	Mg 3	0	0
57	13	5	Total 5	Mg 5	0	0
57	14	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	15	6	Total 6	Mg 6	0	0
57	16	1	Total 1	Mg 1	0	0
57	17	5	Total 5	Mg 5	0	0
57	18	7	Total 7	Mg 7	0	0
57	19	1	Total 1	Mg 1	0	0
57	1a	214	Total 214	Mg 214	0	0
57	1b	1	Total 1	Mg 1	0	0
57	1e	2	Total 2	Mg 2	0	0
57	1f	1	Total 1	Mg 1	0	0
57	1h	1	Total 1	Mg 1	0	0
57	1l	2	Total 2	Mg 2	0	0
57	1m	1	Total 1	Mg 1	0	0
57	1n	1	Total 1	Mg 1	0	0
57	1p	1	Total 1	Mg 1	0	0
57	1r	1	Total 1	Mg 1	0	0
57	1t	1	Total 1	Mg 1	0	0
57	1v	1	Total 1	Mg 1	0	0
57	1w	5	Total 5	Mg 5	0	0
57	1x	13	Total 13	Mg 13	0	0
57	1y	1	Total 1	Mg 1	0	0
57	2A	797	Total 797	Mg 797	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	2B	19	Total 19	Mg 19	0	0
57	2D	8	Total 8	Mg 8	0	0
57	2E	9	Total 9	Mg 9	0	0
57	2F	8	Total 8	Mg 8	0	0
57	2G	1	Total 1	Mg 1	0	0
57	2N	1	Total 1	Mg 1	0	0
57	2O	1	Total 1	Mg 1	0	0
57	2P	2	Total 2	Mg 2	0	0
57	2Q	4	Total 4	Mg 4	0	0
57	2R	2	Total 2	Mg 2	0	0
57	2T	2	Total 2	Mg 2	0	0
57	2U	1	Total 1	Mg 1	0	0
57	2V	2	Total 2	Mg 2	0	0
57	2W	2	Total 2	Mg 2	0	0
57	2X	2	Total 2	Mg 2	0	0
57	2Y	1	Total 1	Mg 1	0	0
57	20	2	Total 2	Mg 2	0	0
57	21	2	Total 2	Mg 2	0	0
57	23	2	Total 2	Mg 2	0	0
57	25	4	Total 4	Mg 4	0	0
57	27	2	Total 2	Mg 2	0	0

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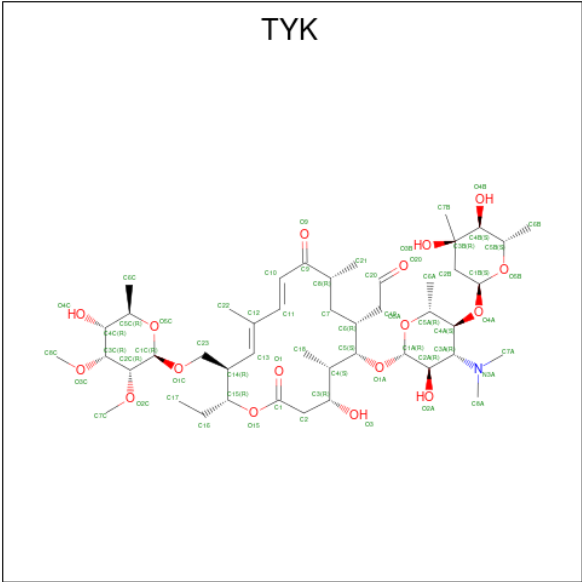
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	28	5	Total 5	Mg 5	0	0
57	29	1	Total 1	Mg 1	0	0
57	2a	221	Total 221	Mg 221	0	0
57	2d	2	Total 2	Mg 2	0	0
57	2e	1	Total 1	Mg 1	0	0
57	2f	3	Total 3	Mg 3	0	0
57	2j	1	Total 1	Mg 1	0	0
57	2k	1	Total 1	Mg 1	0	0
57	2l	1	Total 1	Mg 1	0	0
57	2q	2	Total 2	Mg 2	0	0
57	2t	1	Total 1	Mg 1	0	0
57	2v	4	Total 4	Mg 4	0	0
57	2w	7	Total 7	Mg 7	0	0
57	2x	9	Total 9	Mg 9	0	0
57	2y	2	Total 2	Mg 2	0	0

- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1A	1	Total 1	K 1	0	0

- Molecule 59 is TYLOSIN (CCD ID: TYK) (formula: C₄₆H₇₇NO₁₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
59	1A	1	Total	C	N	O	0	0
			64	46	1	17		
59	2A	1	Total	C	N	O	0	0
			64	46	1	17		

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

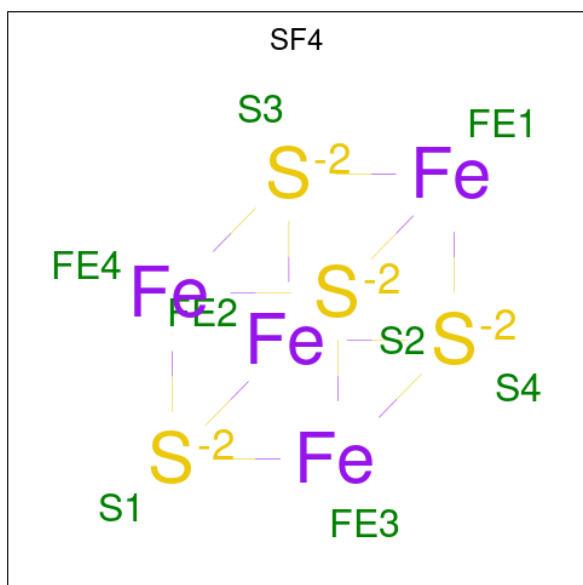
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1Y	1	Total	Zn	0	0
			1	1		
60	14	1	Total	Zn	0	0
			1	1		
60	15	1	Total	Zn	0	0
			1	1		
60	16	1	Total	Zn	0	0
			1	1		
60	19	1	Total	Zn	0	0
			1	1		
60	1n	1	Total	Zn	0	0
			1	1		
60	2Y	1	Total	Zn	0	0
			1	1		
60	24	1	Total	Zn	0	0
			1	1		
60	25	1	Total	Zn	0	0
			1	1		
60	26	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	29	1	Total	Zn	0	0
			1	1		
60	2n	1	Total	Zn	0	0
			1	1		

- Molecule 61 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
61	1d	1	Total	Fe	S	0	0
			8	4	4		
61	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 62 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	1A	1975	Total	O	0	0
			1975	1975		
62	1B	59	Total	O	0	0
			59	59		
62	1D	25	Total	O	0	0
			25	25		
62	1E	25	Total	O	0	0
			25	25		
62	1F	13	Total	O	0	0
			13	13		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	1G	2	Total	O	0	0
			2	2		
62	1H	2	Total	O	0	0
			2	2		
62	1N	5	Total	O	0	0
			5	5		
62	1O	4	Total	O	0	0
			4	4		
62	1P	23	Total	O	0	0
			23	23		
62	1Q	6	Total	O	0	0
			6	6		
62	1R	9	Total	O	0	0
			9	9		
62	1S	2	Total	O	0	0
			2	2		
62	1T	7	Total	O	0	0
			7	7		
62	1U	11	Total	O	0	0
			11	11		
62	1V	8	Total	O	0	0
			8	8		
62	1W	7	Total	O	0	0
			7	7		
62	1X	6	Total	O	0	0
			6	6		
62	1Y	3	Total	O	0	0
			3	3		
62	1Z	1	Total	O	0	0
			1	1		
62	10	10	Total	O	0	0
			10	10		
62	11	6	Total	O	0	0
			6	6		
62	12	3	Total	O	0	0
			3	3		
62	13	3	Total	O	0	0
			3	3		
62	14	1	Total	O	0	0
			1	1		
62	15	6	Total	O	0	0
			6	6		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	16	2	Total 2	O 2	0	0
62	17	10	Total 10	O 10	0	0
62	18	12	Total 12	O 12	0	0
62	1a	377	Total 377	O 377	0	0
62	1b	1	Total 1	O 1	0	0
62	1e	2	Total 2	O 2	0	0
62	1f	2	Total 2	O 2	0	0
62	1l	6	Total 6	O 6	0	0
62	1m	1	Total 1	O 1	0	0
62	1o	1	Total 1	O 1	0	0
62	1p	1	Total 1	O 1	0	0
62	1q	2	Total 2	O 2	0	0
62	1u	1	Total 1	O 1	0	0
62	1v	5	Total 5	O 5	0	0
62	1w	12	Total 12	O 12	0	0
62	1x	15	Total 15	O 15	0	0
62	1y	1	Total 1	O 1	0	0
62	2A	1136	Total 1136	O 1136	0	0
62	2B	22	Total 22	O 22	0	0
62	2D	21	Total 21	O 21	0	0
62	2E	16	Total 16	O 16	0	0

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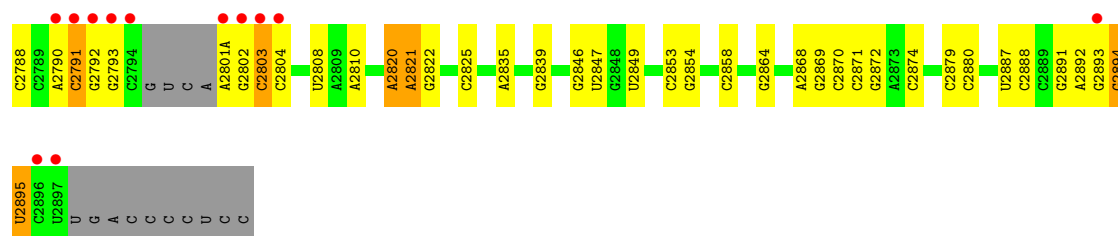
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	2F	13	Total 13	O 13	0	0
62	2O	2	Total 2	O 2	0	0
62	2P	5	Total 5	O 5	0	0
62	2Q	1	Total 1	O 1	0	0
62	2R	2	Total 2	O 2	0	0
62	2T	7	Total 7	O 7	0	0
62	2U	4	Total 4	O 4	0	0
62	2W	3	Total 3	O 3	0	0
62	2X	2	Total 2	O 2	0	0
62	2Z	1	Total 1	O 1	0	0
62	20	4	Total 4	O 4	0	0
62	21	7	Total 7	O 7	0	0
62	23	2	Total 2	O 2	0	0
62	25	1	Total 1	O 1	0	0
62	26	2	Total 2	O 2	0	0
62	27	4	Total 4	O 4	0	0
62	28	4	Total 4	O 4	0	0
62	29	1	Total 1	O 1	0	0
62	2a	254	Total 254	O 254	0	0
62	2c	1	Total 1	O 1	0	0
62	2d	1	Total 1	O 1	0	0

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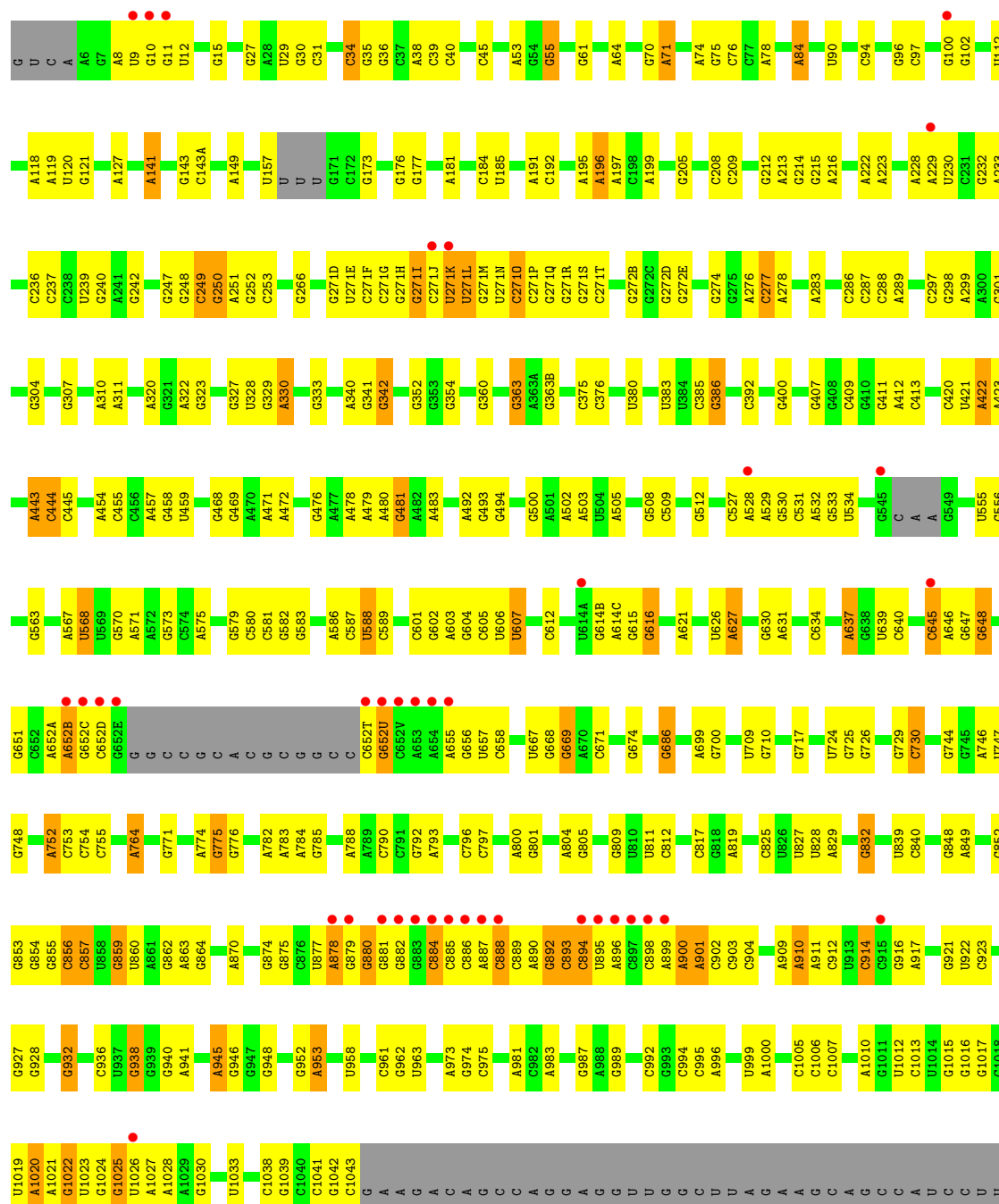
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	2e	1	Total	O	0	0
			1	1		
62	2j	4	Total	O	0	0
			4	4		
62	2l	4	Total	O	0	0
			4	4		
62	2n	1	Total	O	0	0
			1	1		
62	2o	1	Total	O	0	0
			1	1		
62	2p	1	Total	O	0	0
			1	1		
62	2q	2	Total	O	0	0
			2	2		
62	2t	2	Total	O	0	0
			2	2		
62	2v	2	Total	O	0	0
			2	2		
62	2w	3	Total	O	0	0
			3	3		
62	2x	10	Total	O	0	0
			10	10		
62	2y	1	Total	O	0	0
			1	1		

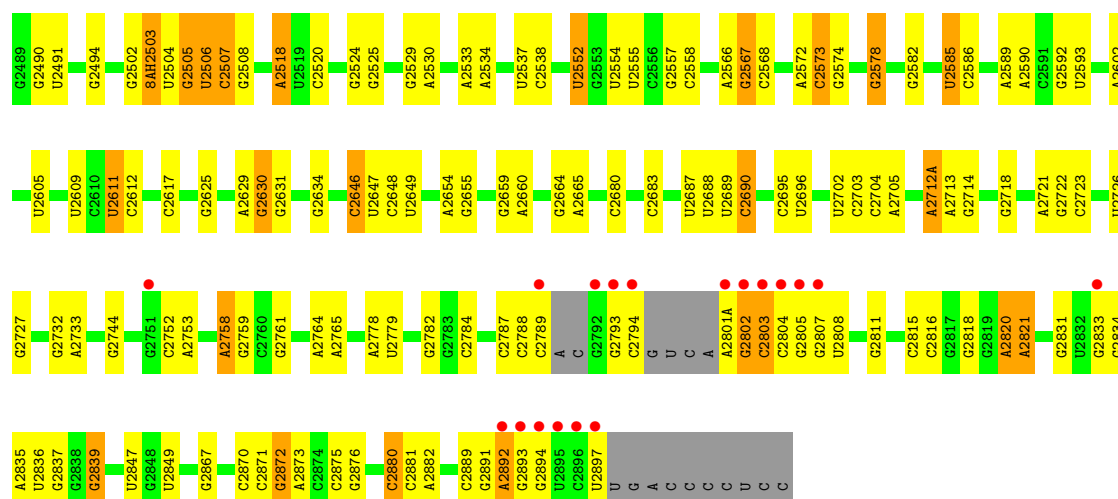
C2667	G2668	U2537	C2538	G2410	C2306	G2181	G2121	G2020	C1882	U1739	C1584	A1445	A1301	A1424A	A1070
G2669	C2670	C2539	C2540	A2422	G2307	G2182	U2122	C2021	G1883	G1740	A1586	G1448	A1302	A1143	G1071
C2683	U2541	G2542	G2543	U2423	G2308	G2183	G2123	C2022	A1587	A1741	C1587	G1449	G1303	G1144	A1072
G2685	U2542	G2543	G2544	U2424	U2312	G2184	G2124	G2023	C1588	G1745	C1589	G1450	U1313	C1163	G1074
U2689	C2690	U2552	U2553	A2425	C2316	G2185	A2126	G2029	G1899	G1756	G1593	U1453	G1314	G1164	G1075
C2691	U2554	U2555	U2556	A2426	G2319	G2186	G2127	A2030	A1900	A1762	G1594	G1456	C1315	A1165	G1076
U2693	C2694	U2563	U2564	A2427	A2320	G2187	G2128	A2031	G1763	G1764	G1595	G1461	A1317	U1166	A1077
G2695	U2565	U2566	U2567	A2428	G2325	G2188	G2129	A2032	U1602	A1603	U1602	G1461	G1324	C1166	C1080
C2699	C2700	U2572	U2573	A2429	A2327	G2189	G2130	A2033	A1607	C1607	C1607	C1467	G1332	G1171	U1081
G2701	U2702	G2574	G2575	A2430	A2328	U2190	G2131	A2034	A1609	A1608	A1608	G1480	G1338	G1173	U1082
C2703	U2704	G2576	G2577	A2431	G2329	G2191	G2132	A2035	A1610	A1609	A1610	U1481	U1352	A1174	A1085
U2712	A2713	G2578	G2579	A2435	G2330	G2192	G2133	G2038	U1603	A1603	A1603	G1482	U1352	U1175	A1086
A2714	G2715	U2585	U2586	G2445	G2331	G2193	G2134	C2043	U1604	A1604	A1604	G1483	U1352	G1176	G1087
U2721	A2722	G2588	G2589	G2446	G2332	G2194	G2135	G2039	U1605	A1605	A1605	G1484	U1352	A1177	A1088
U2726	G2727	U2590	U2591	G2447	G2333	G2195	G2136	C2040	U1606	A1606	A1606	G1485	U1352	C1178	U1089
G2732	A2733	G2592	G2593	G2448	G2334	G2196	G2137	G2041	U1607	A1607	A1607	G1486	U1352	C1179	G1091
U2741	G2742	U2602	U2603	G2449	G2335	G2197	G2138	G2042	U1608	A1608	A1608	G1487	U1352	U1188	G1092
G2747	A2748	G2604	G2605	G2450	G2336	G2198	G2139	G2043	U1609	A1609	A1609	G1488	U1352	G1191	G1093
U2751	G2752	U2606	U2607	G2451	G2337	G2199	G2140	G2044	U1610	A1610	A1610	G1489	U1352	G1192	U1094
G2755	U2756	G2608	G2609	G2452	G2338	G2200	G2141	G2045	U1611	A1611	A1611	G1490	U1352	A1095	A1095
A2757	C2617	U2610	U2611	G2453	G2339	G2201	G2142	G2046	U1612	A1612	A1612	G1491	U1352	A1096	A1096
G2762	G2763	U2612	U2613	G2454	G2340	G2202	G2143	G2047	U1613	A1613	A1613	G1492	U1352	A1097	A1097
A2764	A2765	G2614	G2615	G2455	G2341	G2203	G2144	G2048	U1614	A1614	A1614	G1493	U1352	A1098	A1098
G2766	U2767	U2616	U2617	G2456	G2342	G2204	G2145	G2049	U1615	A1615	A1615	G1494	U1352	A1099	A1099
U2775	A2776	G2618	G2619	G2457	G2343	G2205	G2146	G2050	U1616	A1616	A1616	G1495	U1352	A1100	U1101
A2778	U2779	U2620	U2621	G2458	G2344	G2206	G2147	G2051	U1617	A1617	A1617	G1496	U1352	A1102	A1103
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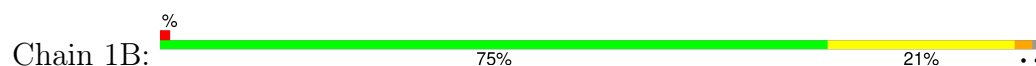
- Molecule 1: 23S Ribosomal RNA



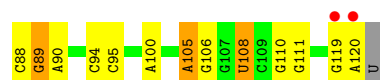




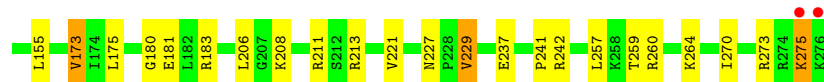
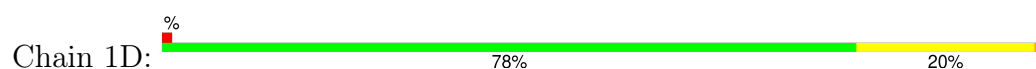
• Molecule 2: 5S Ribosomal RNA



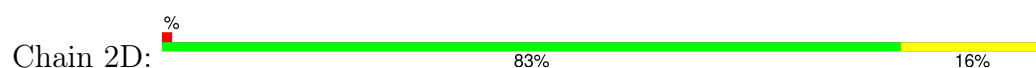
• Molecule 2: 5S Ribosomal RNA



• Molecule 3: 50S ribosomal protein L2



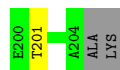
• Molecule 3: 50S ribosomal protein L2





• Molecule 4: 50S ribosomal protein L3

Chain 1E: 82% 16% ..



• Molecule 4: 50S ribosomal protein L3

Chain 2E: 75% 21% ..



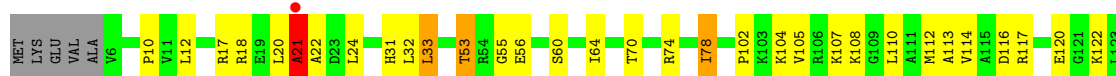
• Molecule 5: 50S ribosomal protein L4

Chain 1F: 69% 23% ..



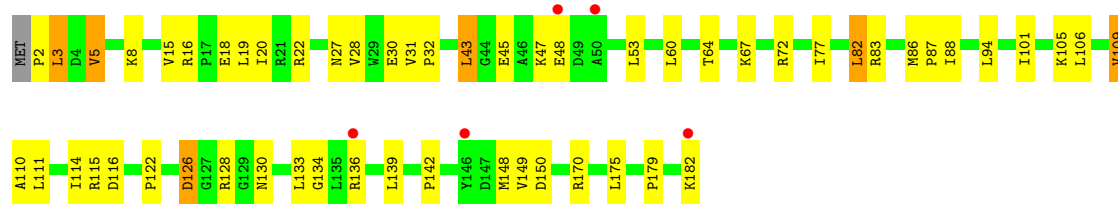
• Molecule 5: 50S ribosomal protein L4

Chain 2F: 68% 27% ..

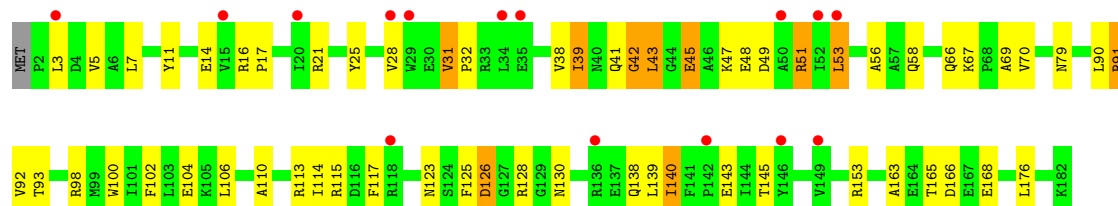


• Molecule 6: 50S ribosomal protein L5

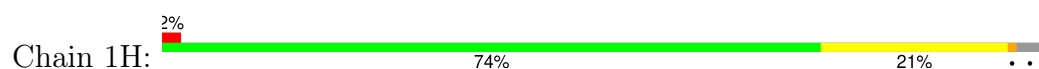
Chain 1G: 69% 27% ..



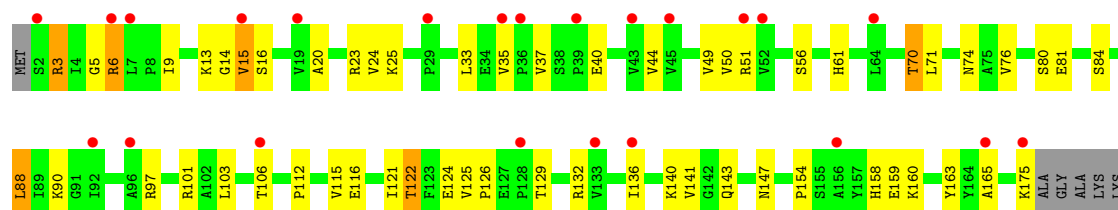
• Molecule 6: 50S ribosomal protein L5



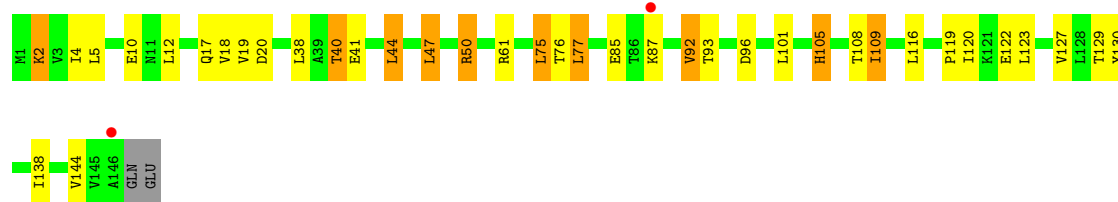
• Molecule 7: 50S ribosomal protein L6



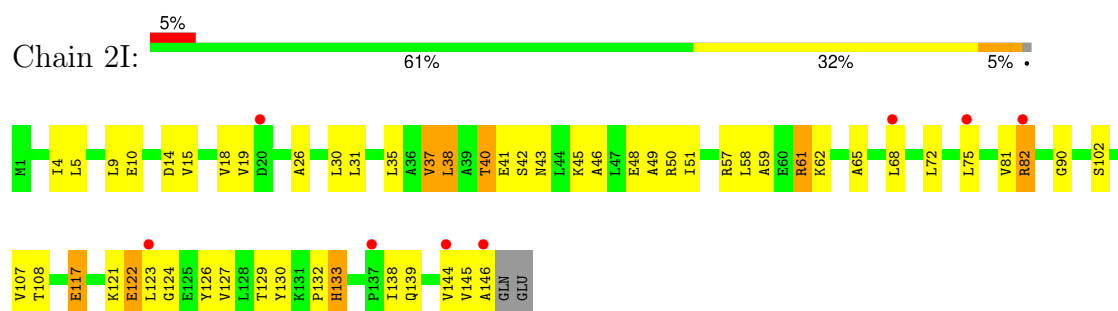
• Molecule 7: 50S ribosomal protein L6



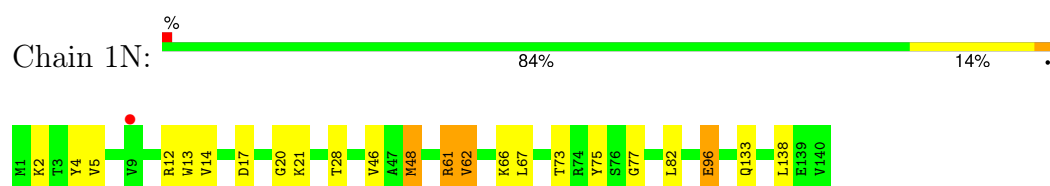
• Molecule 8: 50S ribosomal protein L9



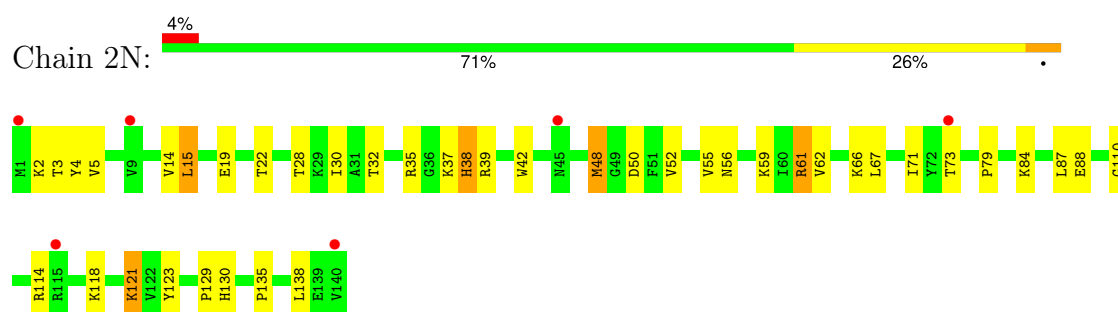
- Molecule 8: 50S ribosomal protein L9



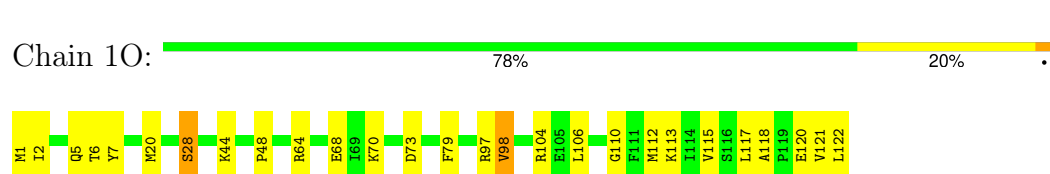
- Molecule 9: 50S ribosomal protein L13



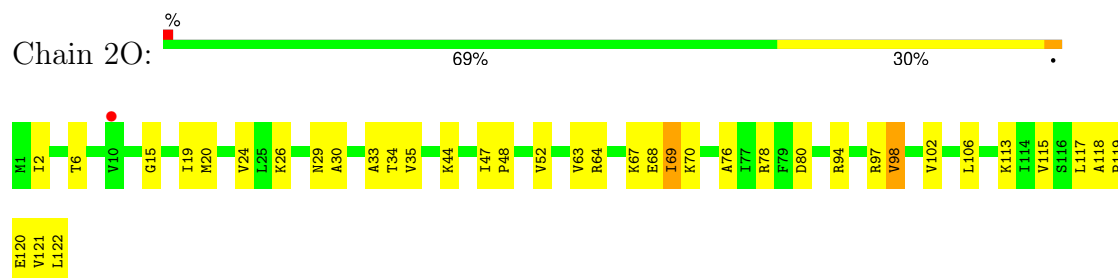
- Molecule 9: 50S ribosomal protein L13



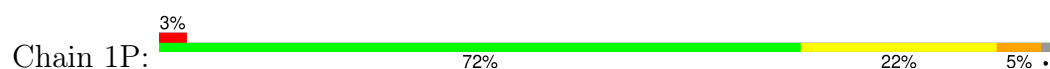
- Molecule 10: 50S ribosomal protein L14

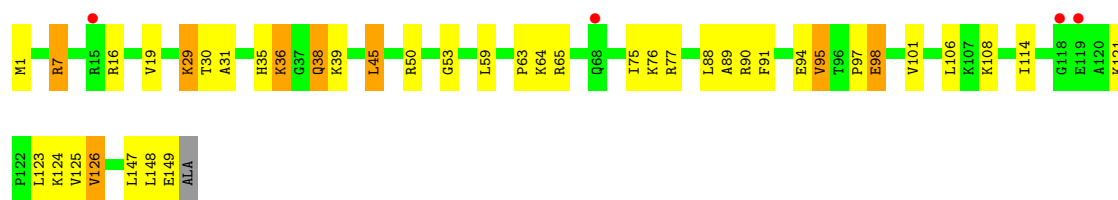


- Molecule 10: 50S ribosomal protein L14

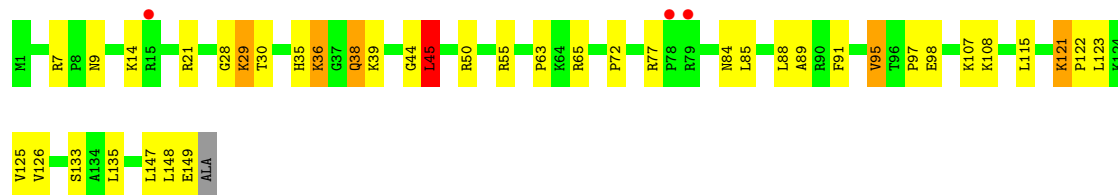
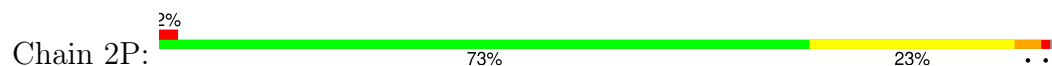


- Molecule 11: 50S ribosomal protein L15

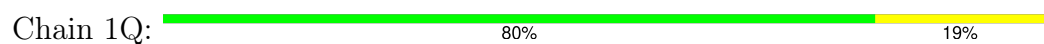




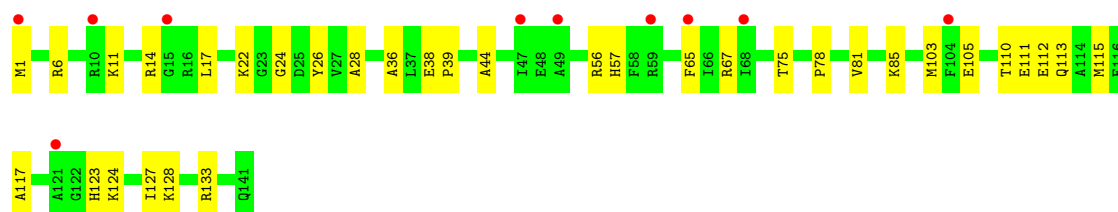
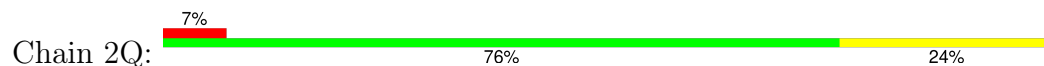
- Molecule 11: 50S ribosomal protein L15



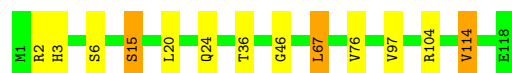
- Molecule 12: 50S ribosomal protein L16



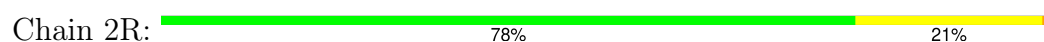
- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17

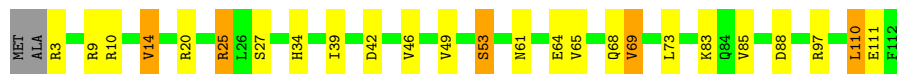


- Molecule 13: 50S ribosomal protein L17



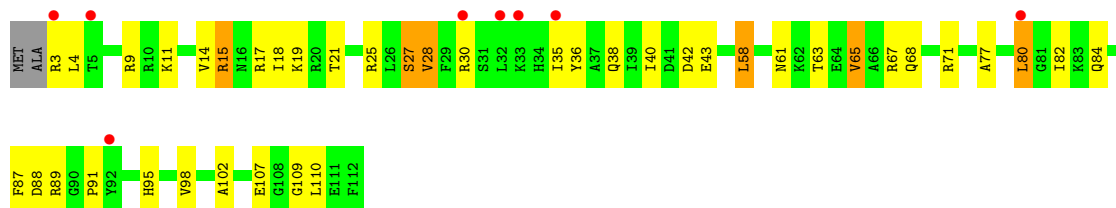
- Molecule 14: 50S ribosomal protein L18

Chain 1S:  76% 18% . .



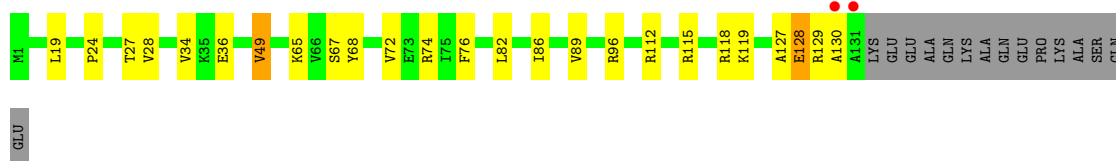
- Molecule 14: 50S ribosomal protein L18

Chain 2S:  7% 62% 31% 5% .



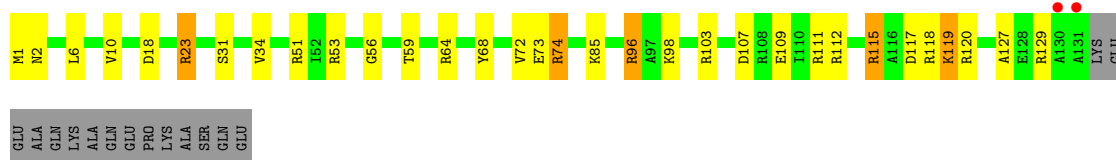
- Molecule 15: 50S ribosomal protein L19

Chain 1T:  73% 16% 10% .



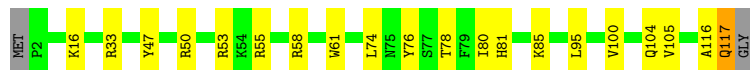
- Molecule 15: 50S ribosomal protein L19

Chain 2T:  68% 18% 10% .



- Molecule 16: 50S ribosomal protein L20

Chain 1U:  81% 16% . .

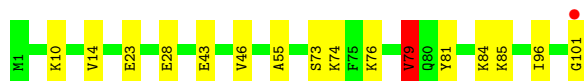
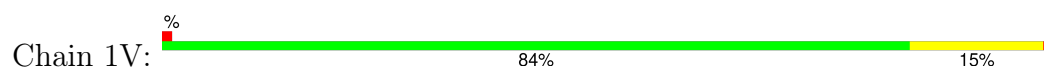


- Molecule 16: 50S ribosomal protein L20

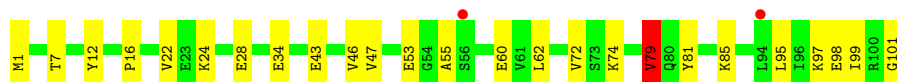
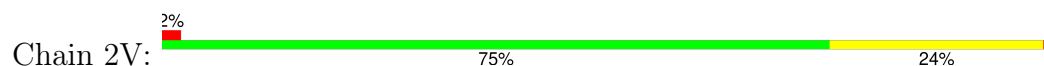
Chain 2U:  79% 18% . .



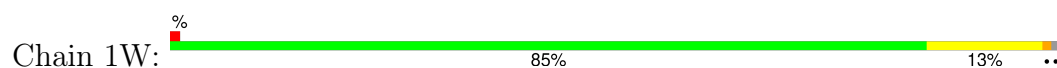
- Molecule 17: 50S ribosomal protein L21



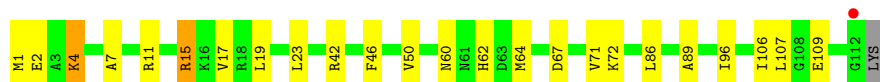
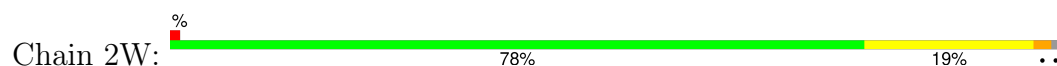
- Molecule 17: 50S ribosomal protein L21



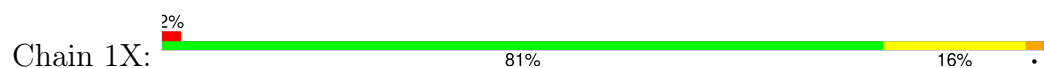
- Molecule 18: 50S ribosomal protein L22



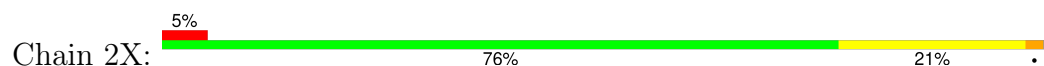
- Molecule 18: 50S ribosomal protein L22



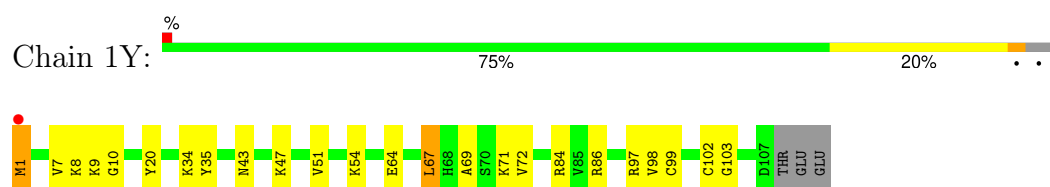
- Molecule 19: 50S ribosomal protein L23



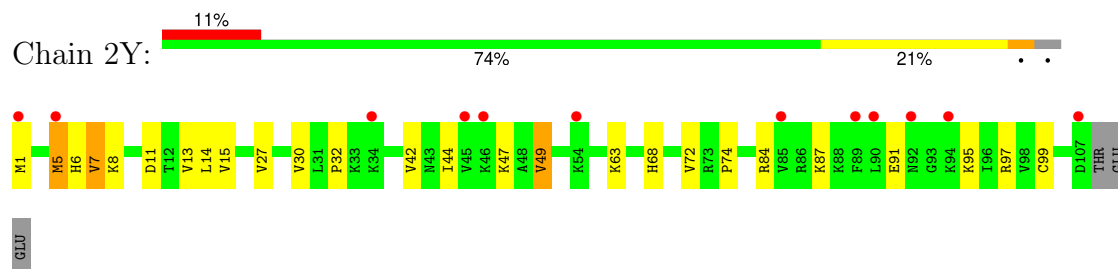
- Molecule 19: 50S ribosomal protein L23



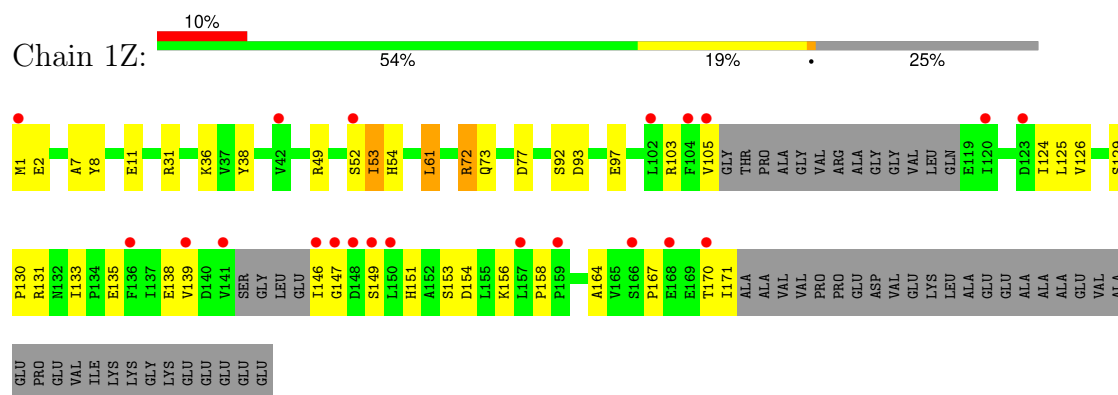
- Molecule 20: 50S ribosomal protein L24



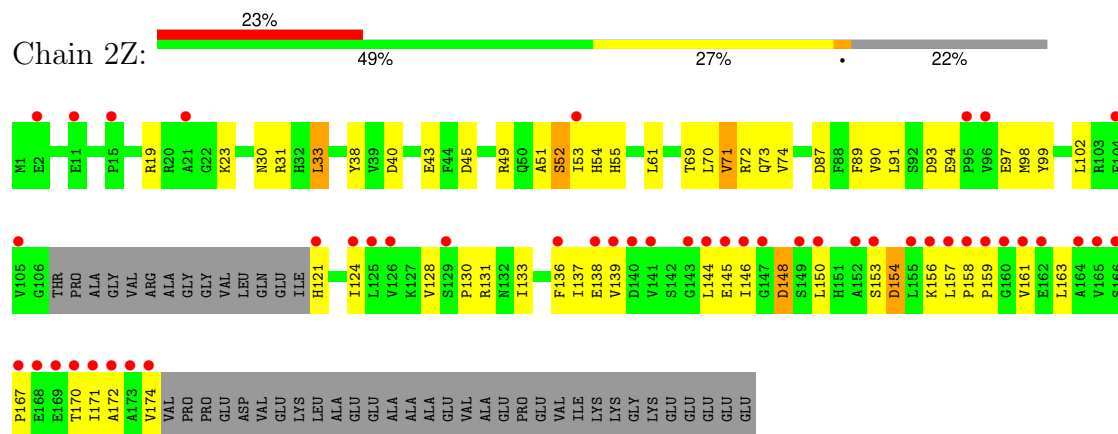
- Molecule 20: 50S ribosomal protein L24



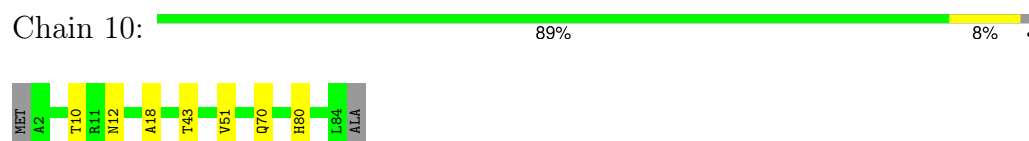
- Molecule 21: 50S ribosomal protein L25



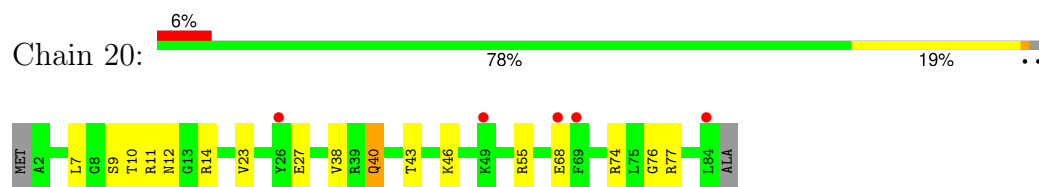
- Molecule 21: 50S ribosomal protein L25



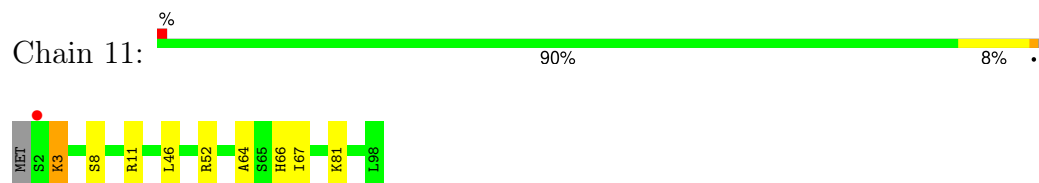
- Molecule 22: 50S ribosomal protein L27



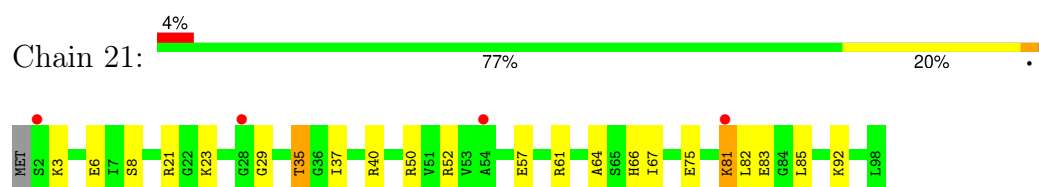
- Molecule 22: 50S ribosomal protein L27



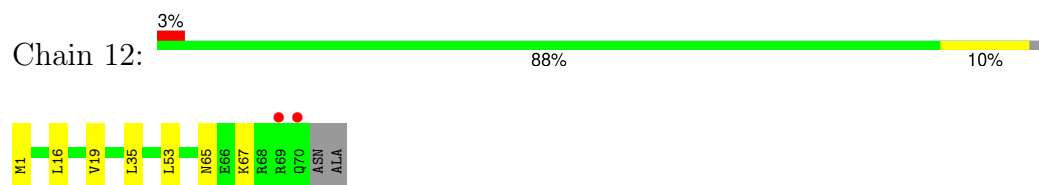
- Molecule 23: 50S ribosomal protein L28



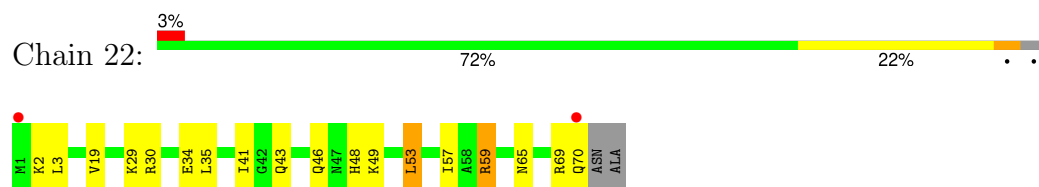
- Molecule 23: 50S ribosomal protein L28



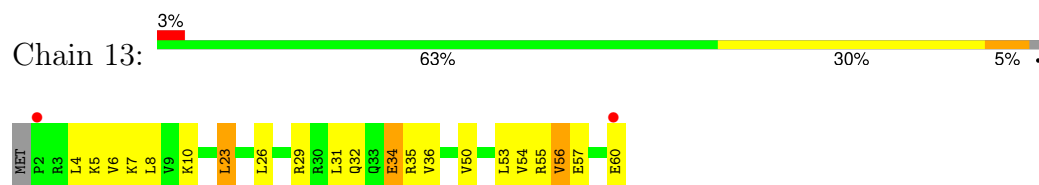
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

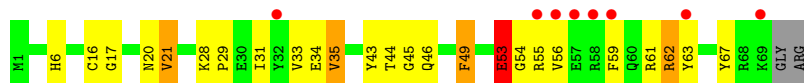


- Molecule 25: 50S ribosomal protein L30





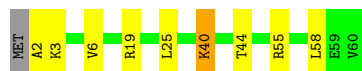
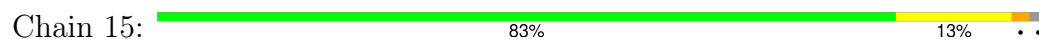
- Molecule 26: 50S ribosomal protein L31



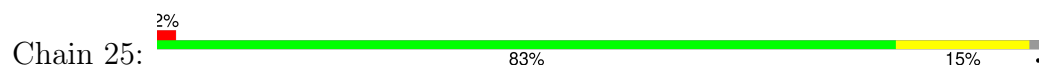
- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L32



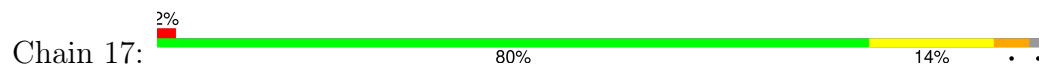
- Molecule 28: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L33

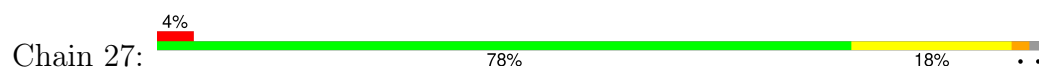


- Molecule 29: 50S ribosomal protein L34

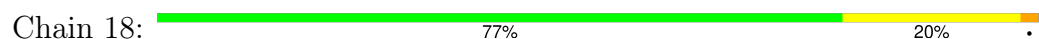




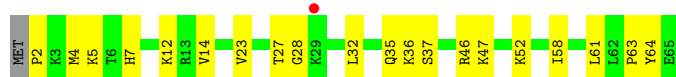
- Molecule 29: 50S ribosomal protein L34



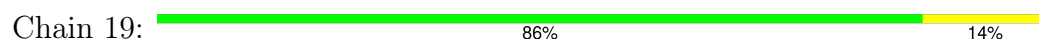
- Molecule 30: 50S ribosomal protein L35



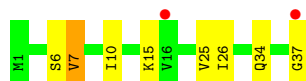
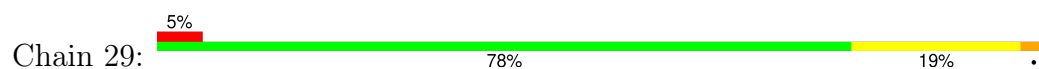
- Molecule 30: 50S ribosomal protein L35



- Molecule 31: 50S ribosomal protein L36

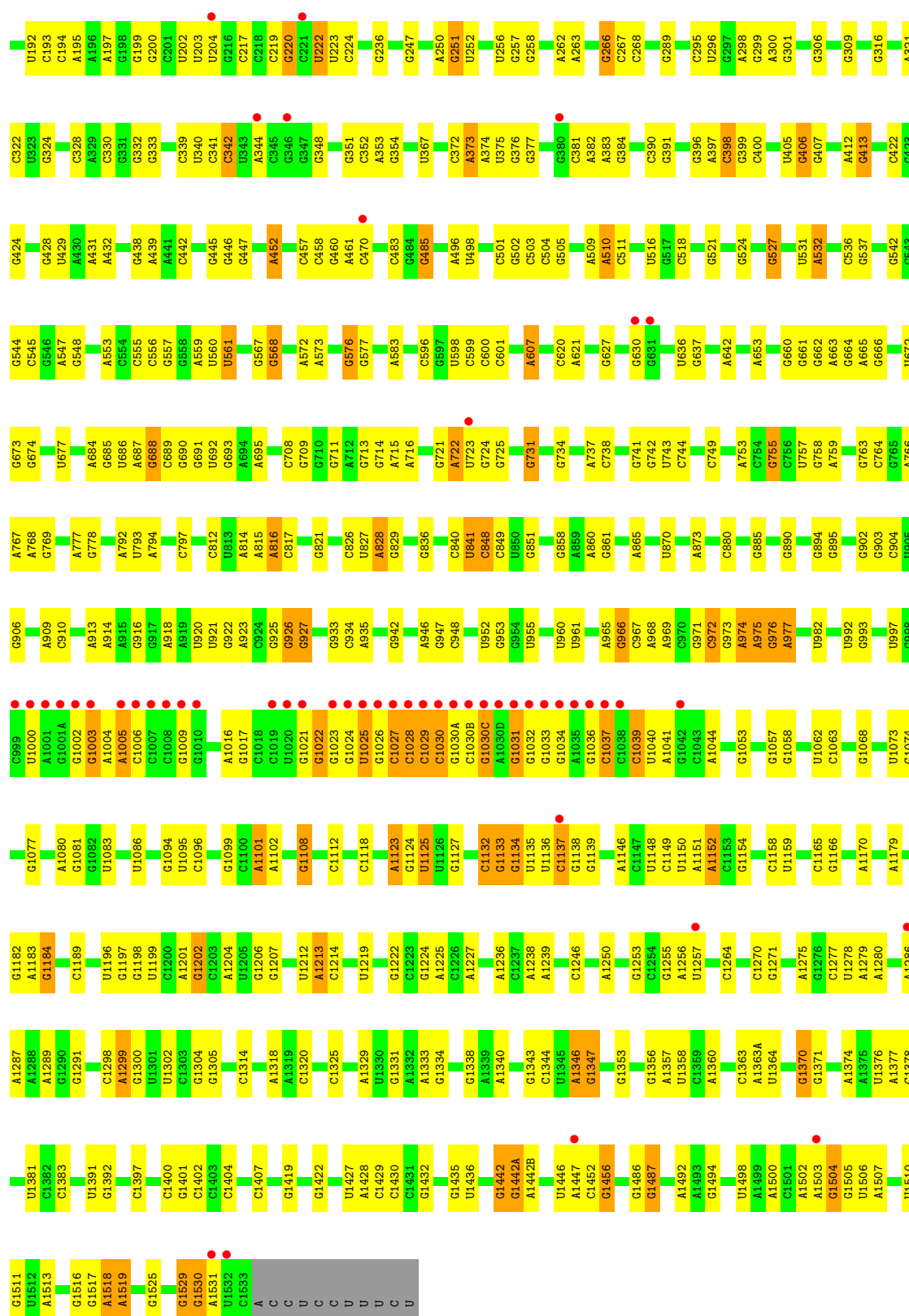


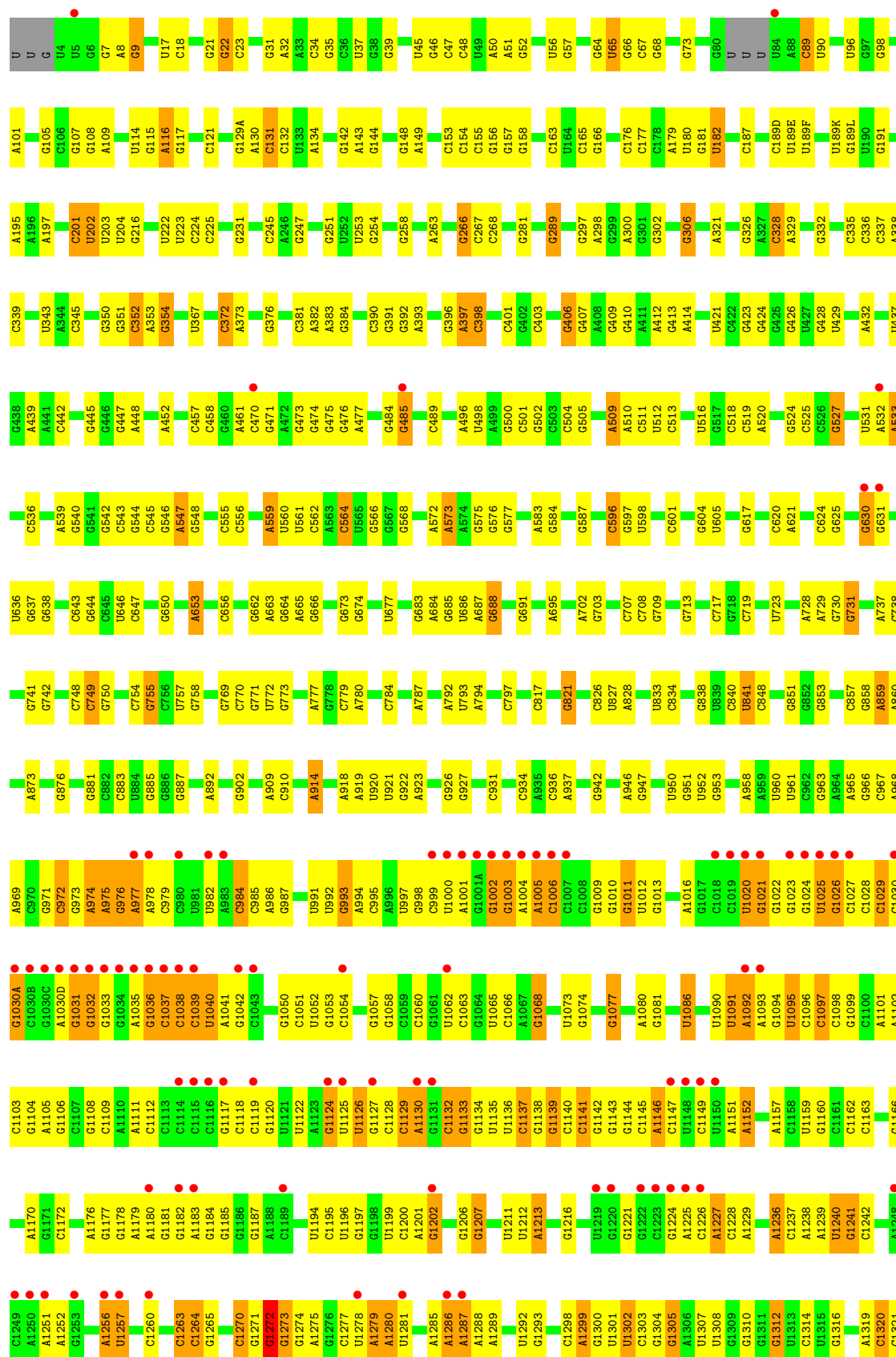
- Molecule 31: 50S ribosomal protein L36

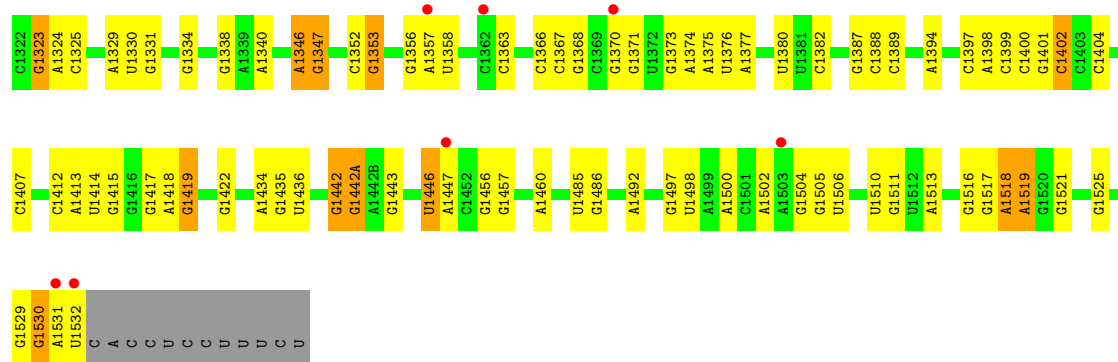


- Molecule 32: 16S Ribosomal RNA

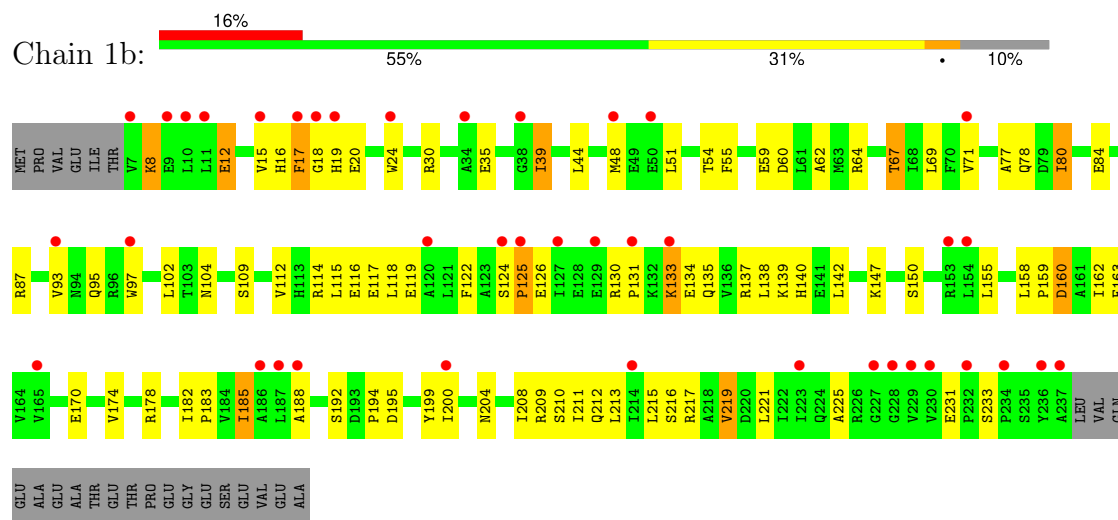




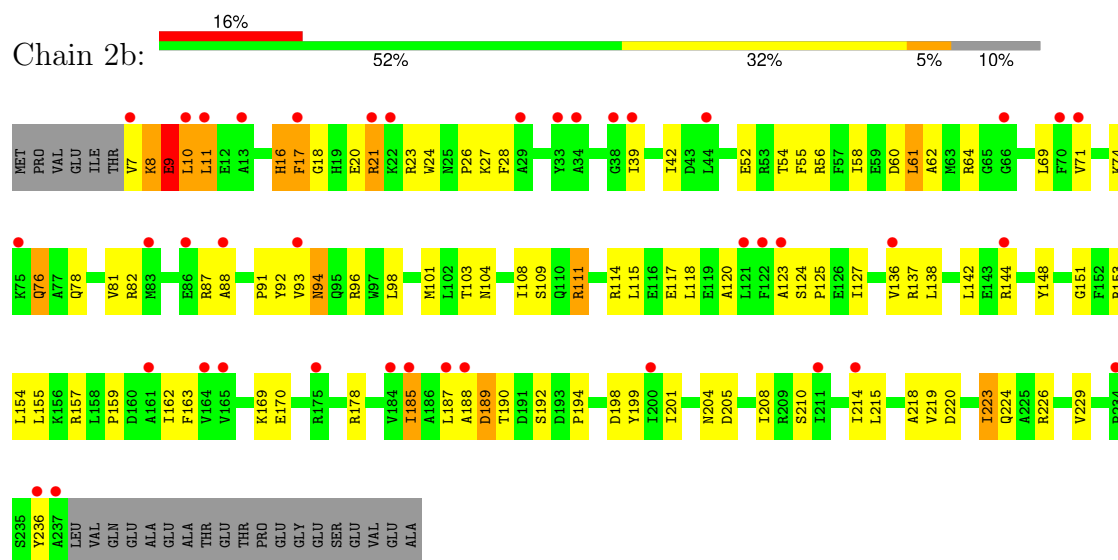


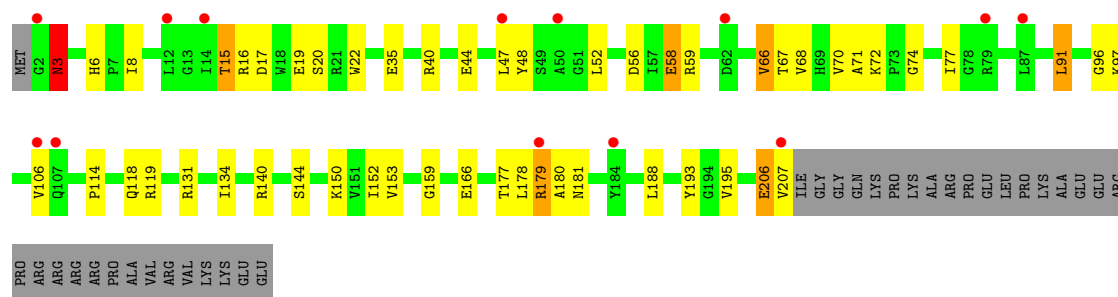


• Molecule 33: 30S ribosomal protein S2

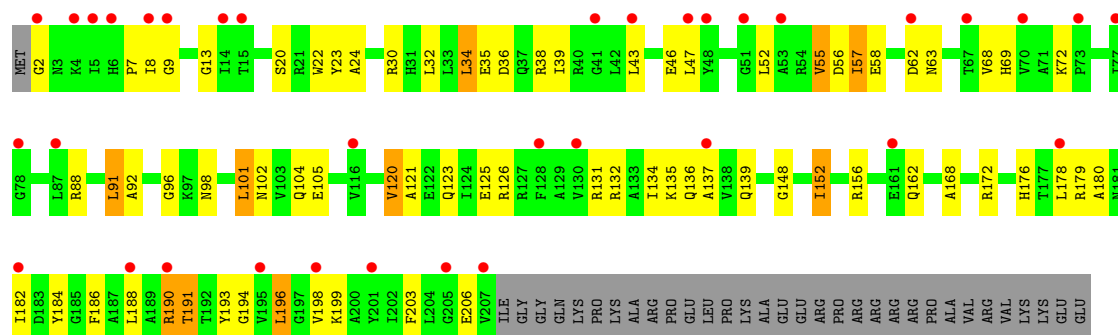


• Molecule 34: 30S ribosomal protein S3

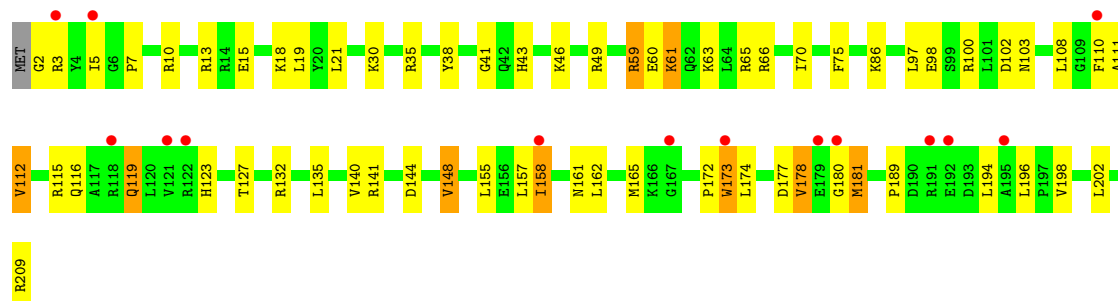




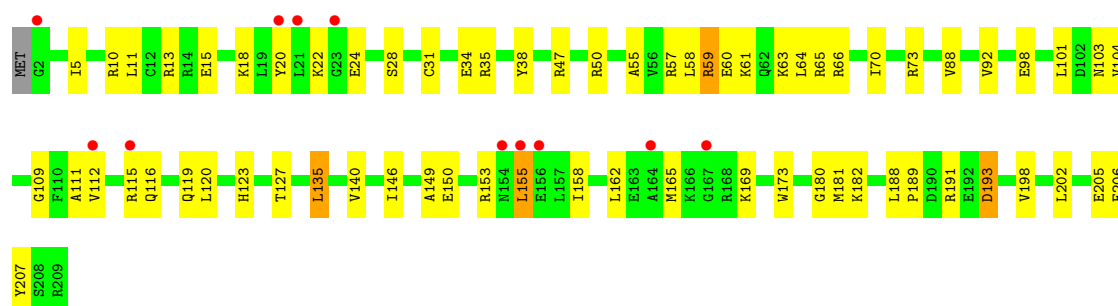
• Molecule 34: 30S ribosomal protein S3



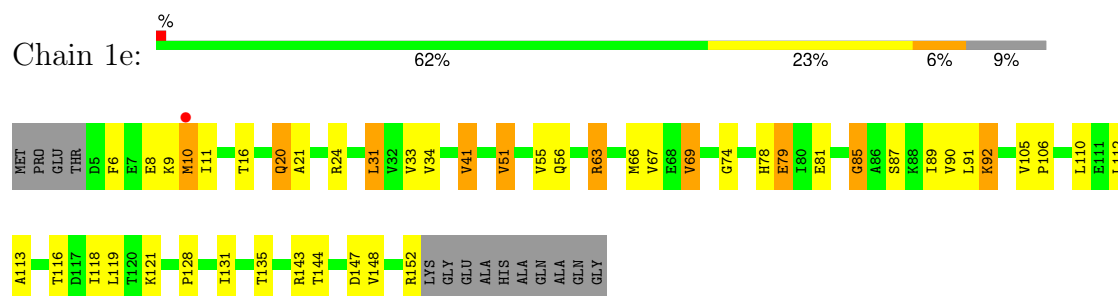
• Molecule 35: 30S ribosomal protein S4



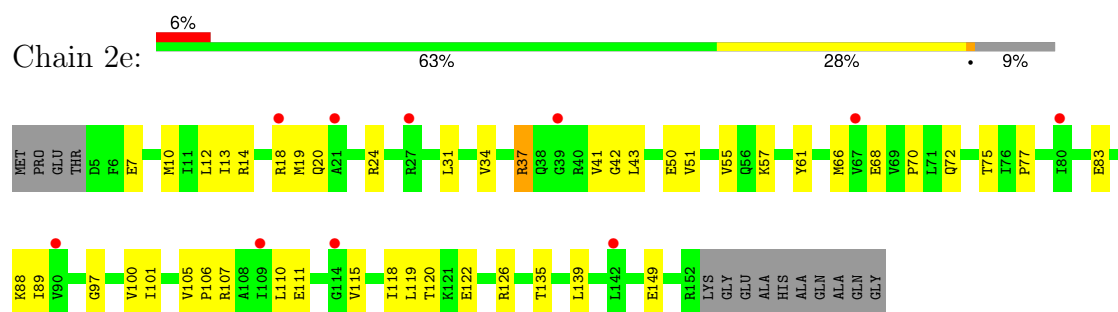
• Molecule 35: 30S ribosomal protein S4



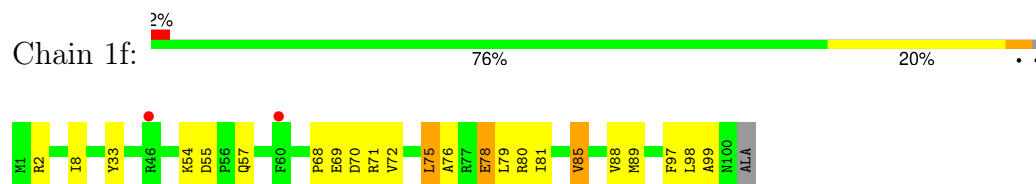
- Molecule 36: 30S ribosomal protein S5



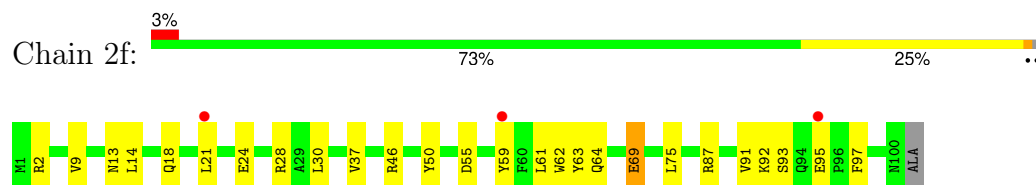
- Molecule 36: 30S ribosomal protein S5



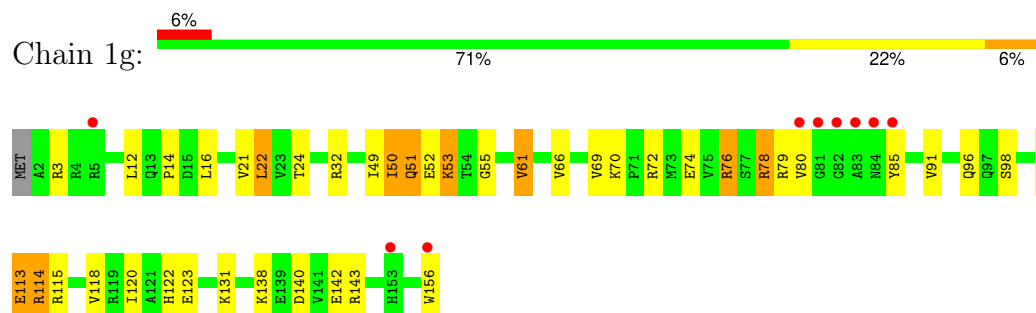
- Molecule 37: 30S ribosomal protein S6



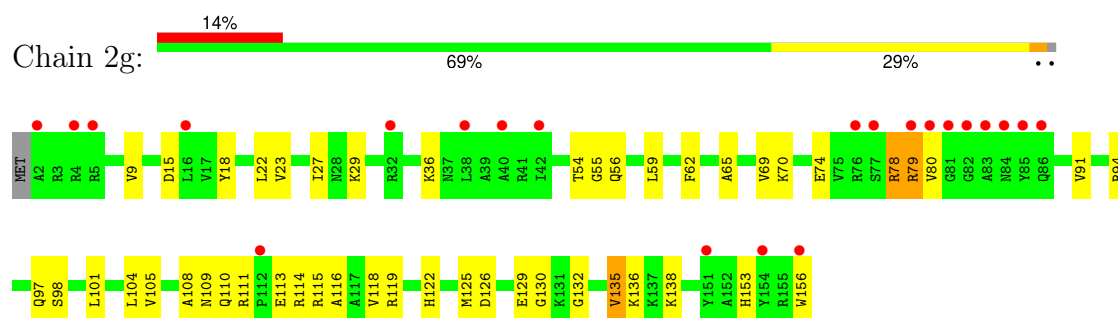
- Molecule 37: 30S ribosomal protein S6



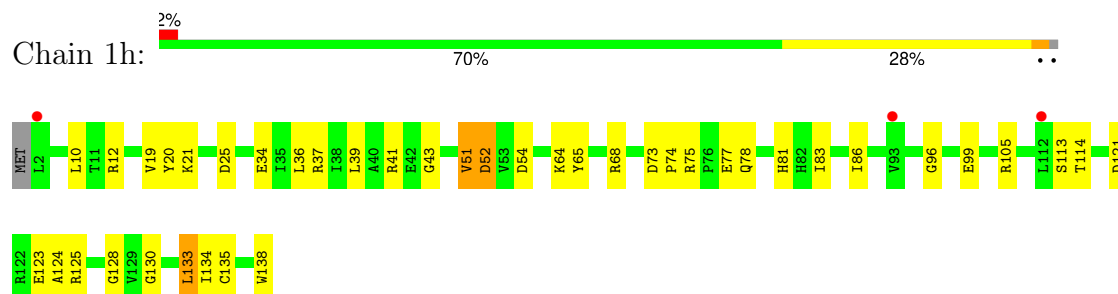
- Molecule 38: 30S ribosomal protein S7



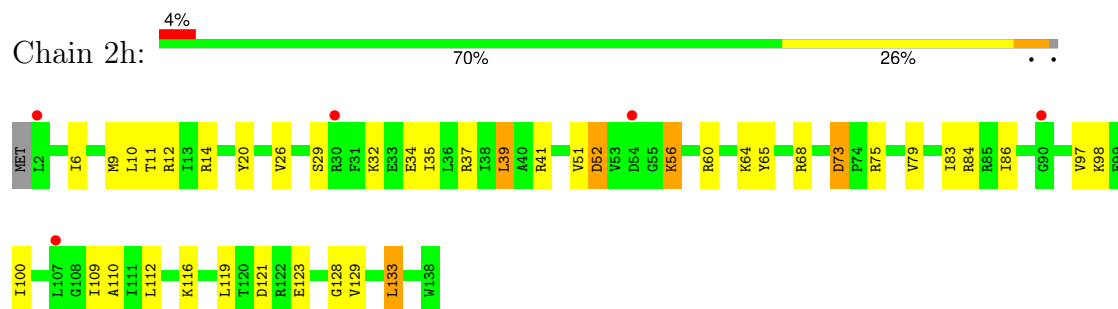
- Molecule 38: 30S ribosomal protein S7



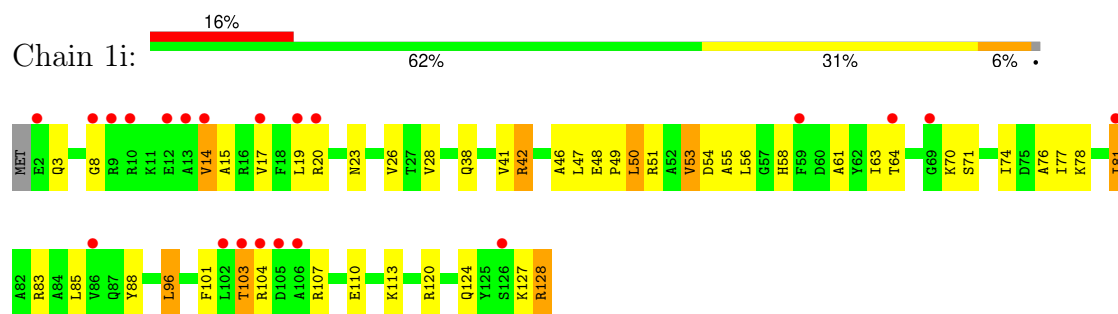
- Molecule 39: 30S ribosomal protein S8



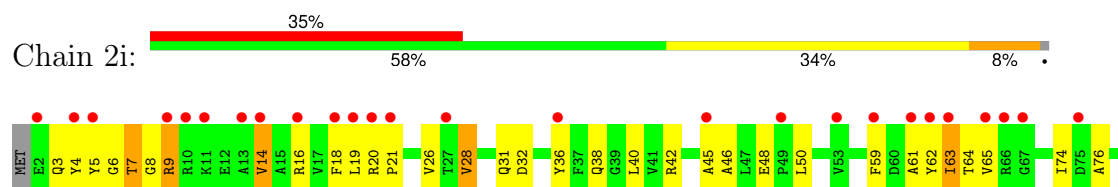
- Molecule 39: 30S ribosomal protein S8

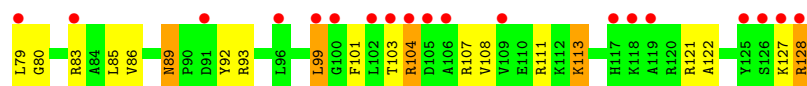


- Molecule 40: 30S ribosomal protein S9



- Molecule 40: 30S ribosomal protein S9

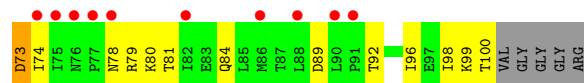
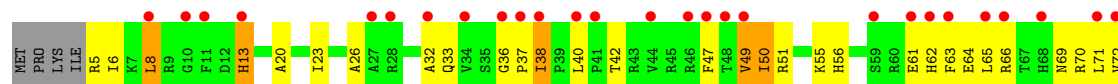




- Molecule 41: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S10



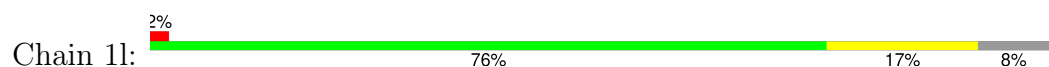
- Molecule 42: 30S ribosomal protein S11

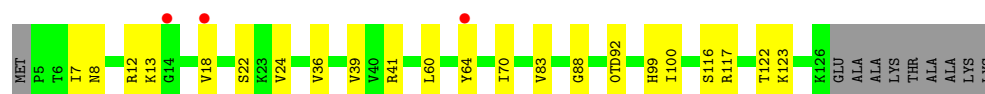


- Molecule 42: 30S ribosomal protein S11

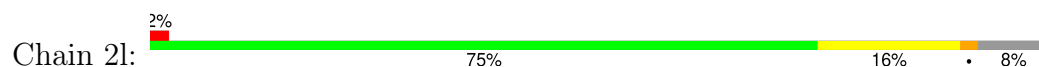


- Molecule 43: 30S ribosomal protein S12

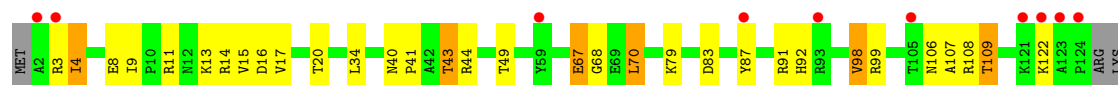




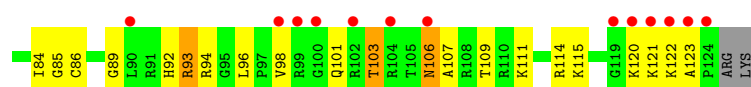
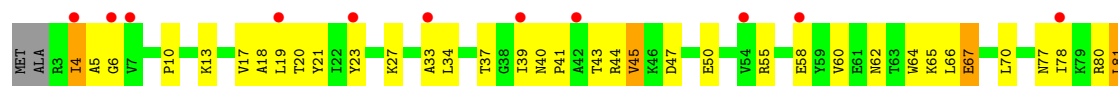
- Molecule 43: 30S ribosomal protein S12



- Molecule 44: 30S ribosomal protein S13



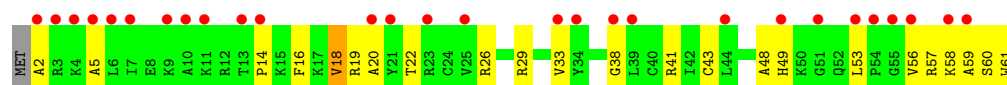
- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14 type Z



- Molecule 45: 30S ribosomal protein S14 type Z

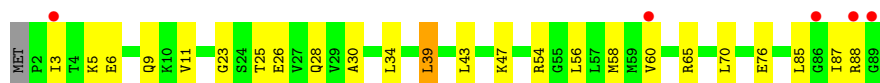
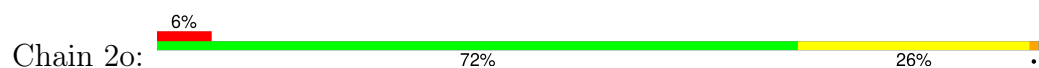


- Molecule 46: 30S ribosomal protein S15





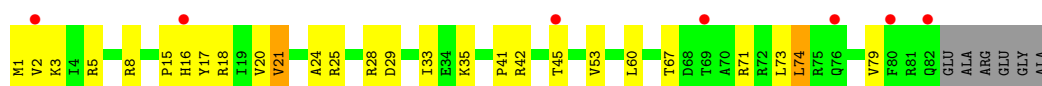
- Molecule 46: 30S ribosomal protein S15



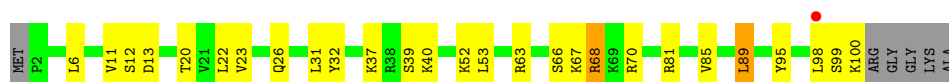
- Molecule 47: 30S ribosomal protein S16



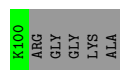
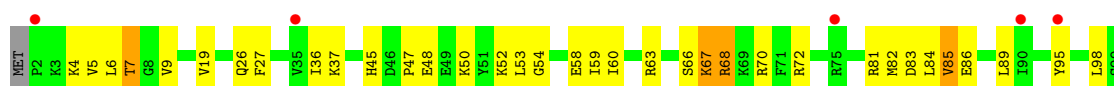
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17



- Molecule 48: 30S ribosomal protein S17

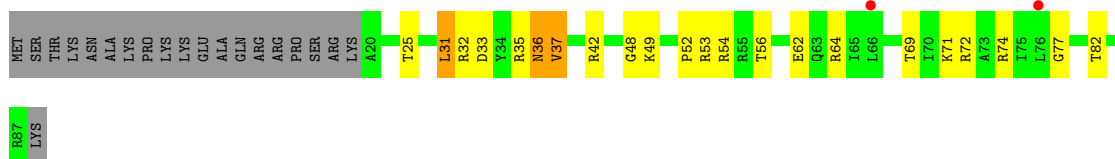


- Molecule 49: 30S ribosomal protein S18





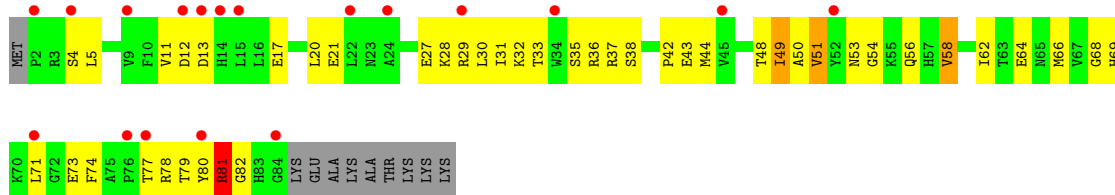
- Molecule 49: 30S ribosomal protein S18



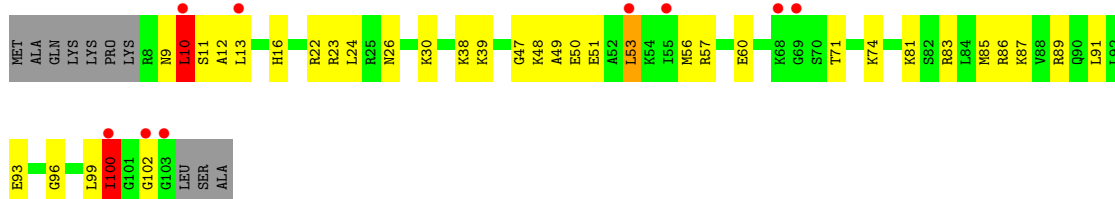
- Molecule 50: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S19

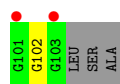


- Molecule 51: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S20

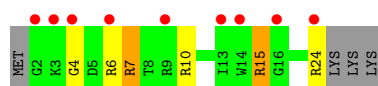




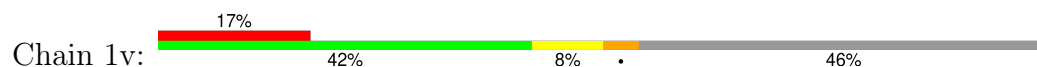
- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



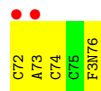
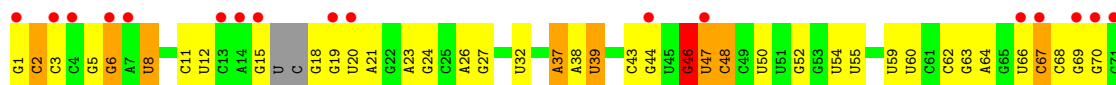
- Molecule 53: MF-mRNA



- Molecule 53: MF-mRNA



- Molecule 54: A-site Aminoacylated Phe-tRNAphe



- Molecule 54: A-site Aminoacylated Phe-tRNAphe



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.65Å 448.12Å 621.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	162.05 – 2.65 162.05 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.7 (162.05-2.65) 98.7 (162.05-2.65)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.207 , 0.249 0.209 , 0.249	Depositor DCC
R_{free} test set	82773 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	300115	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, MG, MIA, UR3, 2MG, 5MU, 31H, PSU, 0TD, ZN, M2G, 5MC, TYK, OMG, 2MU, MA6, 8AH, SF4, 4SU, 4OC, F3N, K, G7M

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	0.28	0/69010	0.46	3/107716 (0.0%)
1	2A	0.21	0/67294	0.39	1/105038 (0.0%)
2	1B	0.21	0/2882	0.40	0/4494
2	2B	0.18	0/2879	0.34	0/4487
3	1D	0.27	0/2186	0.51	0/2944
3	2D	0.23	0/2186	0.47	0/2944
4	1E	0.27	0/1592	0.50	0/2149
4	2E	0.20	0/1592	0.43	0/2149
5	1F	0.25	0/1618	0.47	0/2191
5	2F	0.21	0/1614	0.48	3/2186 (0.1%)
6	1G	0.24	0/1448	0.50	1/1957 (0.1%)
6	2G	0.19	0/1453	0.43	0/1963
7	1H	0.22	0/1356	0.42	0/1834
7	2H	0.19	0/1356	0.37	0/1834
8	1I	0.21	0/1112	0.50	1/1514 (0.1%)
8	2I	0.21	0/1079	0.45	0/1475
9	1N	0.25	0/1144	0.49	0/1543
9	2N	0.18	0/1144	0.39	0/1543
10	1O	0.25	0/943	0.46	0/1269
10	2O	0.21	0/943	0.45	0/1269
11	1P	0.25	0/1152	0.61	0/1533
11	2P	0.20	0/1152	0.49	0/1533
12	1Q	0.28	0/1143	0.47	0/1527
12	2Q	0.21	0/1143	0.44	0/1527
13	1R	0.28	0/982	0.47	0/1312
13	2R	0.21	0/982	0.50	0/1312
14	1S	0.23	0/883	0.46	0/1176
14	2S	0.20	0/880	0.41	0/1172
15	1T	0.24	0/1105	0.46	0/1477
15	2T	0.20	0/1097	0.41	0/1468
16	1U	0.28	0/977	0.45	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.19	0/977	0.39	0/1301
17	1V	0.25	0/782	0.47	0/1049
17	2V	0.19	0/782	0.42	0/1049
18	1W	0.28	0/897	0.46	0/1205
18	2W	0.20	0/897	0.39	0/1205
19	1X	0.27	0/764	0.55	2/1025 (0.2%)
19	2X	0.20	0/764	0.48	2/1025 (0.2%)
20	1Y	0.22	0/819	0.48	0/1095
20	2Y	0.19	0/819	0.43	0/1095
21	1Z	0.21	0/1267	0.44	0/1717
21	2Z	0.20	0/1299	0.44	0/1763
22	10	0.28	0/662	0.51	0/881
22	20	0.20	0/662	0.45	0/881
23	11	0.23	0/762	0.44	0/1014
23	21	0.22	0/762	0.39	0/1014
24	12	0.24	0/590	0.41	0/781
24	22	0.18	0/590	0.37	0/781
25	13	0.24	0/474	0.44	0/635
25	23	0.20	0/469	0.45	0/630
26	14	0.24	0/565	0.61	0/761
26	24	0.26	0/545	0.44	0/737
27	15	0.27	0/469	0.50	0/635
27	25	0.22	0/469	0.44	0/635
28	16	0.27	0/460	0.48	0/613
28	26	0.23	0/456	0.44	0/608
29	17	0.29	0/426	0.53	0/561
29	27	0.25	0/426	0.50	0/561
30	18	0.28	0/525	0.47	0/691
30	28	0.21	0/525	0.40	0/691
31	19	0.26	0/310	0.51	0/407
31	29	0.20	0/310	0.55	1/407 (0.2%)
32	1a	0.20	0/35795	0.38	0/55864
32	2a	0.19	0/35886	0.37	3/56005 (0.0%)
33	1b	0.22	0/1881	0.47	0/2542
33	2b	0.23	0/1860	0.46	0/2518
34	1c	0.20	0/1572	0.40	1/2126 (0.0%)
34	2c	0.25	0/1566	0.44	0/2119
35	1d	0.19	0/1685	0.42	0/2262
35	2d	0.19	0/1704	0.44	0/2284
36	1e	0.20	0/1145	0.44	0/1543
36	2e	0.22	0/1149	0.45	0/1548
37	1f	0.19	0/823	0.40	0/1115
37	2f	0.19	0/829	0.40	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.19	0/1250	0.39	0/1679
38	2g	0.22	0/1254	0.43	0/1683
39	1h	0.19	0/1108	0.41	0/1494
39	2h	0.23	0/1108	0.42	0/1494
40	1i	0.22	0/1002	0.47	0/1346
40	2i	0.21	0/997	0.44	0/1343
41	1j	0.22	0/722	0.45	0/982
41	2j	0.22	0/727	0.50	0/988
42	1k	0.25	0/844	0.38	0/1145
42	2k	0.20	0/848	0.41	0/1149
43	1l	0.25	0/937	0.45	0/1260
43	2l	0.18	0/937	0.40	0/1260
44	1m	0.19	0/969	0.50	0/1302
44	2m	0.23	0/961	0.58	2/1291 (0.2%)
45	1n	0.21	0/501	0.45	0/664
45	2n	0.20	0/501	0.46	0/664
46	1o	0.19	0/739	0.37	0/985
46	2o	0.18	0/739	0.39	0/985
47	1p	0.19	0/697	0.44	0/939
47	2p	0.19	0/693	0.44	0/935
48	1q	0.19	0/836	0.45	0/1117
48	2q	0.17	0/836	0.43	0/1117
49	1r	0.19	0/560	0.41	0/746
49	2r	0.19	0/560	0.41	0/746
50	1s	0.22	0/667	0.45	0/900
50	2s	0.30	0/661	0.58	0/893
51	1t	0.21	0/730	0.48	0/965
51	2t	0.20	0/729	0.42	0/965
52	1u	0.18	0/203	0.42	0/266
52	2u	0.23	0/203	0.45	0/266
53	1v	0.23	0/310	0.37	0/480
53	2v	0.20	0/310	0.33	0/480
54	1w	0.30	1/1581 (0.1%)	0.40	0/2458
54	2w	0.29	1/1531 (0.1%)	0.40	0/2379
55	1x	0.27	0/1723	0.40	0/2684
55	2x	0.25	0/1723	0.37	0/2684
56	1y	0.31	2/1606 (0.1%)	0.40	0/2497
56	2y	0.30	2/1583 (0.1%)	0.40	0/2459
All	All	0.23	6/316632 (0.0%)	0.42	20/474029 (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
33	1b	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	46	G7M	O3'-P	5.75	1.61	1.56
54	2w	46	G7M	O3'-P	5.52	1.61	1.56
56	2y	46	G7M	O3'-P	5.44	1.61	1.56
56	1y	46	G7M	O3'-P	5.43	1.61	1.56
56	1y	8	4SU	O3'-P	5.30	1.61	1.56
56	2y	8	4SU	O3'-P	5.05	1.61	1.56

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1G	150	ASP	N-CA-C	-9.76	103.50	114.62
8	1I	50	ARG	N-CA-C	-9.26	104.07	114.62
1	1A	1992	G	C2'-C3'-O3'	7.09	120.14	109.50
44	2m	107	ALA	N-CA-C	-7.07	104.59	112.57
19	1X	94	GLY	CA-C-N	5.73	132.02	121.70
19	1X	94	GLY	C-N-CA	5.73	132.02	121.70
32	2a	1272	G	N3-C2-N2	5.62	136.78	119.90
32	2a	1272	G	N1-C2-N2	-5.58	99.47	116.20
31	29	10	ILE	N-CA-C	-5.58	106.76	111.56
1	2A	1992	G	C2'-C3'-O3'	5.55	117.82	109.50
19	2X	94	GLY	CA-C-N	5.53	131.65	121.70
19	2X	94	GLY	C-N-CA	5.53	131.65	121.70
1	1A	2689	U	C4'-C3'-O3'	5.53	117.69	109.40
32	2a	1263	C	N1-C2-O2	5.46	135.27	118.90
5	2F	78	ILE	N-CA-C	-5.33	106.32	112.98
44	2m	84	ILE	N-CA-C	-5.16	107.44	112.29
1	1A	1992	G	P-O3'-C3'	5.09	127.84	120.20
5	2F	21	ALA	CA-C-N	5.08	130.84	121.70
5	2F	21	ALA	C-N-CA	5.08	130.84	121.70
34	1c	144	SER	N-CA-C	-5.04	107.63	112.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	125	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61853	0	31182	521	0
1	2A	60323	0	30412	600	0
2	1B	2577	0	1305	19	0
2	2B	2575	0	1303	34	0
3	1D	2136	0	2218	48	0
3	2D	2136	0	2218	32	0
4	1E	1559	0	1618	19	0
4	2E	1559	0	1618	31	0
5	1F	1583	0	1625	33	0
5	2F	1579	0	1619	37	0
6	1G	1423	0	1436	35	0
6	2G	1428	0	1438	42	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	28	0
8	1I	1097	0	1140	23	0
8	2I	1064	0	1082	36	0
9	1N	1117	0	1184	10	0
9	2N	1117	0	1184	26	0
10	1O	933	0	996	21	0
10	2O	933	0	996	25	0
11	1P	1135	0	1212	32	0
11	2P	1135	0	1212	32	0
12	1Q	1122	0	1179	18	0
12	2Q	1122	0	1179	22	0
13	1R	968	0	1033	7	0
13	2R	968	0	1033	18	0
14	1S	873	0	927	17	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	16	0
15	2T	1083	0	1136	26	0
16	1U	959	0	1019	17	0
16	2U	959	0	1019	17	0
17	1V	771	0	830	9	0
17	2V	771	0	830	13	0
18	1W	886	0	940	8	0
18	2W	886	0	940	12	0
19	1X	750	0	814	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	2X	750	0	814	15	0
20	1Y	806	0	881	14	0
20	2Y	806	0	881	13	0
21	1Z	1240	0	1240	24	0
21	2Z	1271	0	1273	34	0
22	10	653	0	674	8	0
22	20	653	0	674	16	0
23	11	755	0	826	5	0
23	21	755	0	826	15	0
24	12	588	0	643	4	0
24	22	588	0	643	9	0
25	13	469	0	518	12	0
25	23	464	0	514	14	0
26	14	552	0	533	19	0
26	24	532	0	503	26	0
27	15	455	0	465	5	0
27	25	455	0	465	6	0
28	16	453	0	473	9	0
28	26	449	0	469	10	0
29	17	418	0	467	5	0
29	27	418	0	467	7	0
30	18	517	0	582	12	0
30	28	517	0	582	15	0
31	19	307	0	335	3	0
31	29	307	0	335	4	0
32	1a	32246	0	16295	315	0
32	2a	32327	0	16338	443	0
33	1b	1846	0	1867	58	0
33	2b	1825	0	1828	62	0
34	1c	1548	0	1535	33	0
34	2c	1542	0	1517	48	0
35	1d	1655	0	1672	48	0
35	2d	1674	0	1714	53	0
36	1e	1129	0	1185	26	0
36	2e	1133	0	1191	31	0
37	1f	810	0	804	12	0
37	2f	816	0	808	17	0
38	1g	1231	0	1238	24	0
38	2g	1235	0	1249	33	0
39	1h	1088	0	1126	26	0
39	2h	1088	0	1126	26	0
40	1i	983	0	986	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	2i	978	0	966	38	0
41	1j	709	0	650	28	0
41	2j	714	0	672	35	0
42	1k	829	0	825	15	0
42	2k	833	0	836	18	0
43	1l	932	0	981	10	0
43	2l	932	0	981	13	0
44	1m	958	0	1002	19	0
44	2m	950	0	988	38	0
45	1n	492	0	529	11	0
45	2n	492	0	529	22	0
46	1o	728	0	760	16	0
46	2o	728	0	760	15	0
47	1p	681	0	697	15	0
47	2p	677	0	686	16	0
48	1q	823	0	891	15	0
48	2q	823	0	891	19	0
49	1r	555	0	618	10	0
49	2r	555	0	618	18	0
50	1s	652	0	662	17	0
50	2s	646	0	644	34	0
51	1t	728	0	798	22	0
51	2t	727	0	796	14	0
52	1u	199	0	208	4	0
52	2u	199	0	208	6	0
53	1v	277	0	140	2	0
53	2v	277	0	140	1	0
54	1w	1603	0	828	18	0
54	2w	1555	0	797	28	0
55	1x	1656	0	849	11	0
55	2x	1656	0	850	19	0
56	1y	1585	0	803	26	0
56	2y	1565	0	794	33	0
57	10	10	0	0	0	0
57	11	5	0	0	0	0
57	12	3	0	0	0	0
57	13	5	0	0	0	0
57	14	1	0	0	0	0
57	15	6	0	0	0	0
57	16	1	0	0	0	0
57	17	5	0	0	0	0
57	18	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	19	1	0	0	0	0
57	1A	1099	0	0	0	0
57	1B	34	0	0	0	0
57	1D	12	0	0	0	0
57	1E	10	0	0	0	0
57	1F	15	0	0	0	0
57	1G	5	0	0	0	0
57	1H	1	0	0	0	0
57	1I	1	0	0	0	0
57	1N	5	0	0	0	0
57	1O	6	0	0	0	0
57	1P	5	0	0	0	0
57	1Q	7	0	0	0	0
57	1R	6	0	0	0	0
57	1S	3	0	0	0	0
57	1T	3	0	0	0	0
57	1U	10	0	0	0	0
57	1V	5	0	0	0	0
57	1W	6	0	0	0	0
57	1X	6	0	0	0	0
57	1Y	2	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	214	0	0	0	0
57	1b	1	0	0	0	0
57	1e	2	0	0	0	0
57	1f	1	0	0	0	0
57	1h	1	0	0	0	0
57	1l	2	0	0	0	0
57	1m	1	0	0	0	0
57	1n	1	0	0	0	0
57	1p	1	0	0	0	0
57	1r	1	0	0	0	0
57	1t	1	0	0	0	0
57	1v	1	0	0	0	0
57	1w	5	0	0	0	0
57	1x	13	0	0	0	0
57	1y	1	0	0	0	0
57	20	2	0	0	0	0
57	21	2	0	0	0	0
57	23	2	0	0	0	0
57	25	4	0	0	0	0
57	27	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	28	5	0	0	0	0
57	29	1	0	0	0	0
57	2A	797	0	0	0	0
57	2B	19	0	0	0	0
57	2D	8	0	0	0	0
57	2E	9	0	0	0	0
57	2F	8	0	0	0	0
57	2G	1	0	0	0	0
57	2N	1	0	0	0	0
57	2O	1	0	0	0	0
57	2P	2	0	0	0	0
57	2Q	4	0	0	0	0
57	2R	2	0	0	0	0
57	2T	2	0	0	0	0
57	2U	1	0	0	0	0
57	2V	2	0	0	0	0
57	2W	2	0	0	0	0
57	2X	2	0	0	0	0
57	2Y	1	0	0	0	0
57	2a	221	0	0	0	0
57	2d	2	0	0	0	0
57	2e	1	0	0	0	0
57	2f	3	0	0	0	0
57	2j	1	0	0	0	0
57	2k	1	0	0	0	0
57	2l	1	0	0	0	0
57	2q	2	0	0	0	0
57	2t	1	0	0	0	0
57	2v	4	0	0	0	0
57	2w	7	0	0	0	0
57	2x	9	0	0	0	0
57	2y	2	0	0	0	0
58	1A	1	0	0	0	0
59	1A	64	0	76	1	0
59	2A	64	0	76	1	0
60	14	1	0	0	0	0
60	15	1	0	0	0	0
60	16	1	0	0	0	0
60	19	1	0	0	0	0
60	1Y	1	0	0	0	0
60	1n	1	0	0	0	0
60	24	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	29	1	0	0	0	0
60	2Y	1	0	0	0	0
60	2n	1	0	0	0	0
61	1d	8	0	0	1	0
61	2d	8	0	0	1	0
62	10	10	0	0	0	0
62	11	6	0	0	0	0
62	12	3	0	0	0	0
62	13	3	0	0	0	0
62	14	1	0	0	0	0
62	15	6	0	0	0	0
62	16	2	0	0	0	0
62	17	10	0	0	0	0
62	18	12	0	0	1	0
62	1A	1975	0	0	69	0
62	1B	59	0	0	0	0
62	1D	25	0	0	1	0
62	1E	25	0	0	1	0
62	1F	13	0	0	0	0
62	1G	2	0	0	0	0
62	1H	2	0	0	0	0
62	1N	5	0	0	0	0
62	1O	4	0	0	0	0
62	1P	23	0	0	1	0
62	1Q	6	0	0	0	0
62	1R	9	0	0	0	0
62	1S	2	0	0	0	0
62	1T	7	0	0	0	0
62	1U	11	0	0	0	0
62	1V	8	0	0	0	0
62	1W	7	0	0	1	0
62	1X	6	0	0	0	0
62	1Y	3	0	0	1	0
62	1Z	1	0	0	0	0
62	1a	377	0	0	24	0
62	1b	1	0	0	0	0
62	1e	2	0	0	0	0
62	1f	2	0	0	0	0
62	1l	6	0	0	0	0
62	1m	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	1o	1	0	0	0	0
62	1p	1	0	0	0	0
62	1q	2	0	0	0	0
62	1u	1	0	0	1	0
62	1v	5	0	0	0	0
62	1w	12	0	0	1	0
62	1x	15	0	0	0	0
62	1y	1	0	0	0	0
62	20	4	0	0	0	0
62	21	7	0	0	0	0
62	23	2	0	0	0	0
62	25	1	0	0	0	0
62	26	2	0	0	1	0
62	27	4	0	0	0	0
62	28	4	0	0	0	0
62	29	1	0	0	0	0
62	2A	1136	0	0	67	0
62	2B	22	0	0	0	0
62	2D	21	0	0	1	0
62	2E	16	0	0	0	0
62	2F	13	0	0	0	0
62	2O	2	0	0	0	0
62	2P	5	0	0	2	0
62	2Q	1	0	0	0	0
62	2R	2	0	0	0	0
62	2T	7	0	0	0	0
62	2U	4	0	0	0	0
62	2W	3	0	0	0	0
62	2X	2	0	0	1	0
62	2Z	1	0	0	0	0
62	2a	254	0	0	29	0
62	2c	1	0	0	0	0
62	2d	1	0	0	0	0
62	2e	1	0	0	0	0
62	2j	4	0	0	1	0
62	2l	4	0	0	1	0
62	2n	1	0	0	0	0
62	2o	1	0	0	0	0
62	2p	1	0	0	0	0
62	2q	2	0	0	0	0
62	2t	2	0	0	0	0
62	2v	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	2w	3	0	0	0	0
62	2x	10	0	0	1	0
62	2y	1	0	0	0	0
All	All	300115	0	196876	3588	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 7.

All (3588) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:H3	1:1A:1086:A:N6	1.47	1.13
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.47	0.96
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.48	0.95
1:1A:1082:U:O4	1:1A:1086:A:N1	2.01	0.94
22:20:10:THR:HG22	22:20:12:ASN:H	1.33	0.94
56:2y:55:PSU:HN1	56:2y:57:G:H5''	1.34	0.91
29:17:24:THR:HG22	29:17:27:GLY:H	1.34	0.90
56:2y:18:G:N2	56:2y:55:PSU:N3	2.21	0.89
1:1A:2136:C:N3	1:1A:2155:G:C2	2.42	0.87
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.40	0.87
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.57	0.86
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.08	0.86
32:1a:1027:C:C2	32:1a:1034:G:N2	2.43	0.86
1:2A:2592:G:OP1	62:2A:3805:HOH:O	1.95	0.84
47:1p:53:VAL:HG12	47:1p:79:VAL:HG22	1.57	0.84
1:1A:2427:C:OP1	62:1A:4205:HOH:O	1.97	0.83
32:2a:953:G:H5'	32:2a:965:A:H61	1.42	0.83
1:2A:2319:G:H22	14:2S:3:ARG:HH11	1.22	0.83
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.61	0.82
1:2A:1204:A:H2	1:2A:1241:A:H62	1.27	0.82
22:10:10:THR:HG22	22:10:12:ASN:H	1.42	0.81
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.62	0.81
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.13	0.81
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.15	0.80
1:1A:1041:C:H42	1:1A:1114:G:H1	1.29	0.80
32:2a:972:C:OP1	62:2a:1902:HOH:O	1.99	0.80
42:1k:99:GLN:HG2	42:1k:105:VAL:HG11	1.63	0.80
47:2p:15:PRO:HD2	47:2p:42:ARG:HD2	1.62	0.80
50:2s:28:LYS:HB3	50:2s:29:ARG:HA	1.62	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:557:G:OP1	62:1a:1902:HOH:O	2.00	0.79
1:2A:2625:G:O6	62:2A:3806:HOH:O	2.00	0.79
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.14	0.79
1:2A:2138:C:H42	1:2A:2153:G:H1	1.29	0.79
1:2A:1689:A:H62	1:2A:1698:A:H2	1.28	0.79
1:1A:826:U:OP1	62:1A:4205:HOH:O	2.00	0.79
32:1a:1505:G:OP2	62:1a:1903:HOH:O	2.01	0.79
41:1j:27:ALA:HA	41:1j:81:THR:HG21	1.64	0.78
32:2a:1086:U:H3	32:2a:1099:G:H22	1.32	0.78
32:2a:1029:C:C4	32:2a:1032:G:N1	2.51	0.78
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.66	0.78
54:2w:4:C:H42	54:2w:69:G:H1	1.30	0.78
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.65	0.78
1:2A:1253:A:OP1	62:2A:3807:HOH:O	2.01	0.78
1:1A:869:G:O6	62:1A:4206:HOH:O	2.00	0.78
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.16	0.78
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.16	0.78
1:1A:1632:A:OP2	62:1A:4207:HOH:O	2.00	0.78
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.65	0.78
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.65	0.78
1:2A:568:U:O4	62:2A:3808:HOH:O	2.02	0.77
32:2a:975:A:H4'	32:2a:976:G:H5''	1.67	0.77
32:1a:1381:U:H1'	38:1g:79:ARG:HG2	1.66	0.77
32:1a:664:G:H22	32:1a:741:G:H1	1.31	0.77
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.15	0.77
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.18	0.77
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.30	0.77
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.18	0.77
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.18	0.77
1:1A:1648:C:OP1	62:1A:4208:HOH:O	2.02	0.76
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.01	0.76
1:1A:668:G:N7	62:1A:4238:HOH:O	2.18	0.76
1:1A:1058:G:N2	1:1A:1081:U:O2	2.18	0.76
32:1a:376:G:H5''	47:1p:5:ARG:HG2	1.65	0.76
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.66	0.76
40:1i:110:GLU:OE2	40:1i:113:LYS:NZ	2.19	0.76
1:1A:428:A:OP1	62:1A:4211:HOH:O	2.03	0.76
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.50	0.76
1:2A:1721:G:H8	1:2A:1741:A:H62	1.31	0.76
10:1O:110:GLY:HA2	10:1O:112:MET:HE2	1.68	0.76
33:2b:189:ASP:N	33:2b:189:ASP:OD1	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:77:THR:HG23	50:2s:78:ARG:HG3	1.67	0.76
1:1A:1602:U:O4	62:1A:4209:HOH:O	2.03	0.76
32:2a:598:U:O4	62:2a:1903:HOH:O	2.04	0.76
1:1A:1082:U:N3	1:1A:1086:A:N6	2.18	0.75
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.18	0.75
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.69	0.75
1:1A:2499:C:OP1	62:1A:4213:HOH:O	2.05	0.75
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.51	0.75
32:1a:505:G:N7	62:1a:1911:HOH:O	2.18	0.75
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.69	0.75
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.51	0.75
32:1a:405:U:O4	35:1d:2:GLY:N	2.21	0.74
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.20	0.74
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.69	0.74
1:1A:1007:C:OP2	62:1A:4214:HOH:O	2.05	0.74
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.69	0.74
21:2Z:53:ILE:HA	21:2Z:71:VAL:HG23	1.70	0.74
1:1A:2550:G:OP1	62:1A:4210:HOH:O	2.03	0.74
1:1A:2821:A:OP2	62:1A:4212:HOH:O	2.04	0.74
42:1k:48:ILE:HD12	42:1k:63:LEU:HB2	1.68	0.74
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.19	0.74
1:1A:642:G:OP1	62:1A:4215:HOH:O	2.05	0.74
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.21	0.74
56:1y:8:4SU:H4'	56:1y:48:C:H4'	1.67	0.74
1:1A:2136:C:N4	1:1A:2155:G:C6	2.56	0.74
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.61	0.74
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.70	0.74
37:2f:46:ARG:HH22	49:2r:37:VAL:HG11	1.52	0.74
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.70	0.74
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.69	0.74
32:1a:812:C:N3	62:1a:1913:HOH:O	2.19	0.73
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.70	0.73
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.17	0.73
26:24:53:GLU:HG2	26:24:55:ARG:H	1.52	0.73
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.21	0.73
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.53	0.73
1:2A:53:A:OP2	62:2A:3809:HOH:O	2.05	0.73
1:2A:948:G:OP1	62:2A:3810:HOH:O	2.05	0.73
1:1A:2306:C:O2	62:1A:4216:HOH:O	2.06	0.73
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.70	0.73
1:2A:1648:C:OP1	62:2A:3811:HOH:O	2.05	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:9:ARG:HG3	40:2i:14:VAL:HG13	1.71	0.73
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.21	0.73
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.32	0.73
46:2o:39:LEU:HB3	46:2o:56:LEU:HD12	1.71	0.73
1:1A:11:G:H2'	1:1A:12:U:H5''	1.71	0.73
35:2d:193:ASP:N	35:2d:193:ASP:OD1	2.17	0.73
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.22	0.72
48:2q:81:ARG:HH21	48:2q:84:LEU:HD21	1.53	0.72
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.70	0.72
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.70	0.72
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.23	0.72
1:2A:2782:G:OP2	62:2A:3812:HOH:O	2.07	0.72
56:2y:18:G:H22	56:2y:55:PSU:HN3	1.35	0.72
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.72	0.72
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.72	0.72
33:1b:30:ARG:HH21	33:1b:194:PRO:HB2	1.54	0.71
32:2a:1279:A:H4'	32:2a:1280:A:OP1	1.90	0.71
1:1A:947:G:OP2	62:1A:4217:HOH:O	2.08	0.71
11:1P:29:LYS:HG3	11:1P:30:THR:N	2.05	0.71
1:1A:1054:A:H61	1:1A:1105:U:H3	1.39	0.71
1:2A:481:G:N7	62:2A:3861:HOH:O	2.23	0.71
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.54	0.71
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.23	0.71
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.71	0.71
1:2A:2589:A:OP1	62:2A:3813:HOH:O	2.08	0.71
32:2a:673:G:H2'	32:2a:674:G:C8	2.25	0.71
32:2a:972:C:O2'	41:2j:55:LYS:O	2.09	0.71
62:1A:4216:HOH:O	6:1G:45:GLU:OE2	2.09	0.71
32:1a:504:C:OP1	62:1a:1904:HOH:O	2.09	0.71
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.70	0.71
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.37	0.71
1:1A:1779:U:OP2	62:1A:4218:HOH:O	2.09	0.71
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.24	0.71
1:1A:1439:A:OP1	62:1A:4219:HOH:O	2.09	0.71
32:2a:547:A:OP1	62:2a:1904:HOH:O	2.09	0.71
1:1A:2099:U:H3	1:1A:2190:G:H1	1.37	0.70
40:1i:48:GLU:HA	40:1i:51:ARG:HD3	1.71	0.70
32:2a:1239:A:H62	32:2a:1299:A:H62	1.39	0.70
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.24	0.70
1:2A:570:G:O6	62:2A:3814:HOH:O	2.08	0.70
1:2A:1021:A:H62	1:2A:1141:U:H3	1.40	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:1:MET:HE2	17:2V:43:GLU:HB2	1.74	0.70
32:2a:1029:C:N3	32:2a:1032:G:N2	2.40	0.70
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.57	0.70
1:2A:783:A:OP2	62:2A:3813:HOH:O	2.09	0.70
1:2A:981:A:OP1	62:2A:3815:HOH:O	2.09	0.70
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.39	0.70
38:2g:115:ARG:HB2	38:2g:118:VAL:HG12	1.73	0.70
1:1A:1669:A:OP2	62:1A:4210:HOH:O	2.09	0.70
1:2A:1568:G:N7	62:2A:3869:HOH:O	2.24	0.70
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.40	0.70
1:2A:1938:A:OP2	62:2A:3816:HOH:O	2.09	0.70
1:1A:762:U:OP1	62:1A:4221:HOH:O	2.10	0.70
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.73	0.70
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.27	0.70
50:1s:12:ASP:OD2	50:1s:35:SER:OG	2.10	0.70
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.25	0.70
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.25	0.70
17:2V:55:ALA:HA	17:2V:101:GLY:HA2	1.73	0.69
56:1y:7:A:O2'	56:1y:49:C:OP2	2.06	0.69
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	1.74	0.69
1:1A:641:C:O2'	1:1A:2350:C:OP1	2.08	0.69
32:1a:975:A:H4'	32:1a:976:G:H5''	1.73	0.69
1:2A:1007:C:OP2	62:2A:3817:HOH:O	2.10	0.69
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.74	0.69
32:2a:1272:G:N2	32:2a:1273:G:N7	2.39	0.69
32:2a:1334:G:OP2	62:2a:1905:HOH:O	2.09	0.69
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.25	0.69
1:1A:1506:C:H2'	1:1A:1507:A:H8	1.57	0.69
28:16:13:CYS:SG	28:16:47:THR:HG21	2.32	0.69
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH12	1.57	0.69
1:1A:868:U:O4	62:1A:4206:HOH:O	2.08	0.69
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.28	0.69
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.75	0.69
7:2H:88:LEU:HD11	7:2H:165:ALA:HA	1.74	0.69
32:2a:1152:A:H5'	41:2j:13:HIS:HD2	1.57	0.69
34:2c:34:LEU:HD11	34:2c:38:ARG:HH21	1.57	0.69
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.26	0.69
1:2A:412:A:OP1	62:2A:3818:HOH:O	2.10	0.69
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.26	0.69
40:1i:49:PRO:HG2	40:1i:81:ILE:HG23	1.75	0.69
18:1W:31:GLU:OE1	62:1W:301:HOH:O	2.12	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1086:U:H3	32:1a:1099:G:H22	1.42	0.68
33:1b:95:GLN:HE22	33:1b:147:LYS:HE2	1.58	0.68
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.29	0.68
1:1A:1332:G:OP1	62:1A:4222:HOH:O	2.11	0.68
1:1A:2316:C:O2'	6:1G:128:ARG:NH2	2.26	0.68
41:1j:64:GLU:HG2	45:1n:59:ALA:HB2	1.73	0.68
1:2A:963:U:OP2	62:2A:3810:HOH:O	2.11	0.68
41:2j:8:LEU:HB3	41:2j:96:ILE:HD13	1.75	0.68
32:1a:1224:G:OP1	62:1a:1906:HOH:O	2.11	0.68
1:2A:1125:G:H5'	31:29:37:GLY:HA2	1.76	0.68
34:2c:125:GLU:HB2	34:2c:190:ARG:HH21	1.59	0.68
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.76	0.68
55:2x:75:C:OP1	62:2x:201:HOH:O	2.11	0.68
9:1N:20:GLY:HA2	9:1N:61:ARG:HD2	1.75	0.68
32:1a:36:C:OP1	43:1l:123:LYS:NZ	2.26	0.68
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.11	0.68
1:2A:2518:A:OP2	62:2A:3819:HOH:O	2.10	0.68
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.76	0.68
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.76	0.68
12:1Q:10:ARG:HH11	12:1Q:11:LYS:HE2	1.59	0.68
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.27	0.68
32:2a:597:G:OP2	62:2a:1903:HOH:O	2.11	0.68
54:2w:18:G:O2'	54:2w:57:G:N2	2.19	0.68
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.10	0.68
32:1a:673:G:H2'	32:1a:674:G:C8	2.29	0.67
1:2A:1006:C:OP2	62:2A:3821:HOH:O	2.12	0.67
1:2A:2448:A:OP1	62:2A:3814:HOH:O	2.12	0.67
33:1b:12:GLU:HB2	33:1b:213:LEU:HD21	1.75	0.67
1:2A:297:C:OP2	62:2A:3820:HOH:O	2.11	0.67
8:2I:129:THR:HG22	8:2I:139:GLN:HE21	1.59	0.67
11:2P:35:HIS:O	62:2P:301:HOH:O	2.12	0.67
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.26	0.67
35:2d:153:ARG:HE	35:2d:181:MET:HG3	1.57	0.67
1:1A:1253:A:OP1	62:1A:4224:HOH:O	2.13	0.67
1:1A:2136:C:C2	1:1A:2155:G:N2	2.63	0.67
11:1P:35:HIS:O	62:1P:301:HOH:O	2.12	0.67
1:1A:1603:A:OP1	62:1A:4223:HOH:O	2.11	0.67
37:1f:2:ARG:HD2	37:1f:69:GLU:HB3	1.77	0.67
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.27	0.67
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.27	0.67
8:1I:75:LEU:HD22	8:1I:105:HIS:HD2	1.56	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	1.75	0.67
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.27	0.67
5:2F:18:ARG:NH1	5:2F:127:GLU:OE2	2.28	0.67
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.75	0.67
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.12	0.67
50:2s:49:ILE:HG22	50:2s:62:ILE:HD11	1.77	0.67
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.60	0.67
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.09	0.67
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.28	0.67
7:2H:9:ILE:N	7:2H:50:VAL:O	2.28	0.67
21:2Z:154:ASP:N	21:2Z:154:ASP:OD1	2.28	0.67
32:2a:979:C:N4	62:2a:1927:HOH:O	2.27	0.67
32:1a:903:G:OP1	62:1a:1905:HOH:O	2.11	0.67
1:2A:2166:G:H3'	1:2A:2167:U:H5''	1.77	0.67
1:2A:2712(A):A:OP2	62:2A:3825:HOH:O	2.13	0.67
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	1.76	0.67
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.26	0.67
1:2A:2759:G:OP2	62:2A:3824:HOH:O	2.13	0.67
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.28	0.67
32:2a:1271:G:N2	32:2a:1272:G:N7	2.42	0.67
35:2d:150:GLU:HA	35:2d:153:ARG:HD2	1.75	0.67
40:2i:7:THR:O	40:2i:83:ARG:NH1	2.28	0.67
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.20	0.66
1:2A:1237:A:OP1	62:2A:3823:HOH:O	2.13	0.66
1:2A:1742:G:N7	62:2A:3888:HOH:O	2.27	0.66
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.22	0.66
32:2a:1025:U:H3	32:2a:1036:G:H1	1.39	0.66
1:1A:847:U:OP2	62:1A:4225:HOH:O	2.13	0.66
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.28	0.66
3:1D:183:ARG:HG3	3:1D:270:ILE:HD13	1.76	0.66
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.77	0.66
1:2A:1352:U:OP2	62:2A:3822:HOH:O	2.12	0.66
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.27	0.66
32:2a:1417:G:O6	62:2a:1906:HOH:O	2.12	0.66
16:1U:81:HIS:CE1	16:1U:85:LYS:HD2	2.29	0.66
32:1a:972:C:O2'	41:1j:55:LYS:O	2.13	0.66
22:20:11:ARG:O	22:20:14:ARG:NH2	2.28	0.66
17:1V:55:ALA:HA	17:1V:101:GLY:HA2	1.77	0.66
11:2P:36:LYS:O	62:2P:301:HOH:O	2.13	0.66
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.29	0.66
32:1a:1083:U:OP1	62:1a:1907:HOH:O	2.14	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1670:C:OP1	62:2A:3829:HOH:O	2.14	0.66
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.27	0.66
26:24:16:CYS:SG	26:24:17:GLY:N	2.69	0.66
11:1P:39:LYS:HB2	11:1P:45:LEU:HD13	1.77	0.66
32:1a:890:G:O2'	32:1a:906:G:O6	2.12	0.66
1:2A:1434:A:H61	1:2A:1558:A:H62	1.43	0.66
2:2B:43:C:H5''	26:24:1:MET:HG2	1.77	0.66
32:2a:289:G:OP2	62:2a:1907:HOH:O	2.13	0.66
1:1A:1315:C:OP2	62:1A:4222:HOH:O	2.13	0.66
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.31	0.66
32:2a:617:G:N7	62:2a:1929:HOH:O	2.28	0.66
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.31	0.66
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.78	0.66
1:1A:602:G:O2'	1:1A:655:A:N6	2.29	0.66
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.61	0.66
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.61	0.66
1:2A:2268:A:OP1	62:2A:3830:HOH:O	2.14	0.66
33:2b:87:ARG:NH1	33:2b:220:ASP:OD1	2.29	0.66
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.31	0.65
32:2a:1239:A:H62	32:2a:1299:A:N6	1.94	0.65
32:2a:142:G:H2'	32:2a:143:A:C8	2.31	0.65
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.28	0.65
42:2k:54:ARG:HH22	56:2y:40:C:H5'	1.61	0.65
1:1A:1993:U:OP2	62:1A:4228:HOH:O	2.14	0.65
14:2S:67:ARG:NH1	14:2S:107:GLU:OE2	2.29	0.65
32:2a:1202:G:O4'	45:2n:29:ARG:NH1	2.30	0.65
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.77	0.65
1:2A:1973:G:OP1	62:2A:3827:HOH:O	2.14	0.65
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.11	0.65
41:2j:98:ILE:O	62:2j:301:HOH:O	2.13	0.65
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.29	0.65
32:2a:1334:G:OP2	62:2a:1908:HOH:O	2.14	0.65
11:1P:29:LYS:HG3	11:1P:30:THR:H	1.61	0.65
50:1s:28:LYS:HB3	50:1s:47:HIS:HD2	1.62	0.65
21:2Z:31:ARG:HH11	21:2Z:94:GLU:HG2	1.61	0.65
1:1A:338:G:OP2	62:1A:4227:HOH:O	2.14	0.65
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.76	0.65
34:2c:13:GLY:HA3	45:2n:57:ARG:HH12	1.62	0.65
54:2w:14:A:H61	54:2w:21:A:H2	1.45	0.65
26:14:55:ARG:N	26:14:56:VAL:HA	2.11	0.65
27:15:40:LYS:NZ	27:15:44:THR:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:17:GLU:O	50:2s:21:GLU:N	2.24	0.65
32:1a:953:G:H5'	32:1a:965:A:H61	1.62	0.64
19:2X:94:GLY:H	19:2X:95:LEU:HB2	1.62	0.64
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.77	0.64
1:2A:1010:A:OP2	62:2A:3828:HOH:O	2.14	0.64
1:1A:192:C:OP1	62:1A:4226:HOH:O	2.14	0.64
1:1A:968:G:O6	62:1A:4220:HOH:O	2.10	0.64
32:1a:78:G:O6	32:1a:92:C:N4	2.30	0.64
32:1a:1401:G:N7	62:1a:1930:HOH:O	2.30	0.64
1:2A:962:G:OP1	62:2A:3810:HOH:O	2.15	0.64
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.14	0.64
32:2a:504:C:OP1	62:2a:1911:HOH:O	2.15	0.64
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.31	0.64
32:1a:1500:A:OP2	62:1a:1908:HOH:O	2.15	0.64
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.78	0.64
32:1a:171:A:H2'	32:1a:172:A:C8	2.32	0.64
33:2b:9:GLU:O	33:2b:11:LEU:N	2.31	0.64
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.79	0.64
2:2B:48:A:OP1	14:2S:30:ARG:NH2	2.31	0.64
1:1A:2439:A:N1	62:1A:4291:HOH:O	2.30	0.64
32:1a:642:A:N3	39:1h:113:SER:OG	2.29	0.64
8:2I:37:VAL:HG12	8:2I:38:LEU:HD12	1.79	0.64
25:13:26:LEU:O	25:13:35:ARG:NE	2.30	0.64
56:1y:37:MIA:H8	56:1y:37:MIA:H5''	1.79	0.64
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.62	0.64
1:1A:1671:U:O4	62:1A:4210:HOH:O	2.14	0.64
41:1j:30:SER:HB3	41:1j:81:THR:HG23	1.79	0.64
13:2R:36:THR:HG22	13:2R:37:THR:H	1.62	0.64
56:2y:18:G:N2	56:2y:55:PSU:HN3	1.93	0.64
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.63	0.63
33:1b:178:ARG:HH22	39:1h:74:PRO:HB3	1.62	0.63
4:2E:7:VAL:HG13	4:2E:27:LEU:HB3	1.80	0.63
50:2s:38:SER:HB2	50:2s:71:LEU:HD22	1.78	0.63
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.80	0.63
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.31	0.63
1:1A:2727:G:O2'	10:1O:70:LYS:NZ	2.30	0.63
11:1P:89:ALA:HA	11:1P:121:LYS:HD3	1.81	0.63
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.79	0.63
32:2a:664:G:H22	32:2a:741:G:H1	1.45	0.63
39:2h:116:LYS:HD2	39:2h:129:VAL:HG11	1.81	0.63
1:1A:1271:G:OP2	62:1A:4208:HOH:O	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.80	0.63
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.47	0.63
18:2W:2:GLU:OE2	18:2W:72:LYS:NZ	2.27	0.63
30:28:28:GLY:O	30:28:36:LYS:NZ	2.30	0.63
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.80	0.63
32:2a:1134:G:C2	32:2a:1135:U:H1'	2.33	0.63
6:1G:115:ARG:HG2	6:1G:136:ARG:HH22	1.62	0.63
1:1A:884:C:H42	1:1A:892:G:H1	1.46	0.63
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.32	0.63
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.17	0.63
1:2A:1632:A:OP2	62:2A:3831:HOH:O	2.15	0.63
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.17	0.63
34:2c:120:VAL:HG11	34:2c:137:ALA:HB2	1.81	0.63
54:2w:4:C:N4	54:2w:69:G:H1	1.97	0.63
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.78	0.63
32:1a:92:C:H2'	32:1a:93:G:C8	2.33	0.63
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	1.80	0.63
1:2A:476:G:O6	62:2A:3826:HOH:O	2.13	0.63
22:20:38:VAL:HG12	22:20:40:GLN:HG2	1.80	0.63
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.99	0.63
32:2a:1029:C:N4	32:2a:1032:G:N1	2.47	0.63
33:2b:16:HIS:HB2	33:2b:204:ASN:HD22	1.63	0.63
1:2A:2138:C:N4	1:2A:2153:G:H1	1.97	0.63
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.31	0.62
1:2A:882:G:H22	1:2A:894:C:H42	1.46	0.62
32:2a:1152:A:OP1	41:2j:70:ARG:NH2	2.31	0.62
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.31	0.62
3:1D:237:GLU:OE2	62:1D:401:HOH:O	2.16	0.62
10:1O:7:TYR:HE2	10:1O:20:MET:HE3	1.63	0.62
25:13:55:ARG:HH22	25:13:57:GLU:HB2	1.64	0.62
49:1r:47:THR:O	49:1r:83:GLU:N	2.29	0.62
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.34	0.62
32:2a:1026:G:O6	32:2a:1036:G:N2	2.32	0.62
1:1A:2096:U:H3	1:1A:2193:G:H1	1.48	0.62
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.64	0.62
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.31	0.62
7:2H:90:LYS:HD2	7:2H:159:GLU:HG2	1.80	0.62
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.81	0.62
32:2a:1375:A:H4'	38:2g:29:LYS:HE3	1.81	0.62
38:2g:78:ARG:HE	38:2g:79:ARG:HG3	1.63	0.62
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.80	0.62
32:2a:1302:U:OP2	44:2m:21:TYR:OH	2.14	0.62
32:1a:920:U:H2'	32:1a:921:U:C6	2.34	0.62
1:2A:2306:C:N4	6:2G:42:GLY:O	2.30	0.62
1:2A:2847:U:OP1	15:2T:98:LYS:NZ	2.32	0.62
4:2E:48:GLN:HE21	4:2E:78:LEU:HD22	1.65	0.62
32:2a:1004:A:C6	32:2a:1037:C:H1'	2.34	0.62
32:1a:1025:U:O2	32:1a:1036:G:O6	2.17	0.62
33:1b:114:ARG:NH1	33:1b:117:GLU:OE1	2.32	0.62
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.81	0.62
32:2a:1521:G:N3	62:2a:1934:HOH:O	2.31	0.62
2:1B:66:A:H61	2:1B:109:C:H5'	1.65	0.62
38:1g:70:LYS:HG2	38:1g:96:GLN:HB3	1.81	0.62
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.82	0.62
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.29	0.62
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.80	0.62
33:2b:81:VAL:HB	33:2b:94:ASN:HD21	1.64	0.62
1:1A:1090:U:C2	1:1A:1102:C:H1'	2.34	0.62
32:1a:711:G:OP1	37:1f:54:LYS:NZ	2.32	0.62
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.32	0.62
1:1A:1062:G:H1	1:1A:1077:A:H61	1.47	0.62
32:1a:316:G:OP2	32:1a:351:G:O2'	2.18	0.62
1:2A:400:G:N7	62:2A:3907:HOH:O	2.31	0.62
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.65	0.62
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.80	0.62
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.32	0.62
32:1a:1198:G:OP1	62:1a:1909:HOH:O	2.16	0.62
51:1t:22:ARG:O	51:1t:26:ASN:ND2	2.27	0.62
1:2A:652(A):A:H3'	1:2A:652(B):A:H5''	1.81	0.62
24:22:41:ILE:HG13	24:22:43:GLN:HG2	1.80	0.62
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.82	0.62
12:1Q:78:PRO:HG2	12:1Q:81:VAL:HG11	1.82	0.61
32:1a:159:G:N2	32:1a:162:A:OP2	2.33	0.61
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.15	0.61
33:1b:60:ASP:OD1	33:1b:64:ARG:NH2	2.33	0.61
32:2a:673:G:O3'	37:2f:87:ARG:NH2	2.33	0.61
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.81	0.61
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.82	0.61
1:2A:468:G:N7	29:27:39:ARG:NH2	2.47	0.61
28:26:22:ALA:O	62:26:601:HOH:O	2.16	0.61
32:2a:165:C:H2'	32:2a:166:G:C8	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.82	0.61
41:2j:47:PHE:N	41:2j:63:PHE:O	2.28	0.61
1:2A:2154:G:N7	1:2A:2156:G:N2	2.49	0.61
1:2A:2394:C:N3	56:2y:76:A:O2'	2.30	0.61
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.35	0.61
32:2a:35:G:O2'	43:2l:118:SER:O	2.18	0.61
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.33	0.61
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.82	0.61
44:2m:13:LYS:O	44:2m:45:VAL:N	2.28	0.61
33:1b:59:GLU:HG2	33:1b:225:ALA:HB2	1.83	0.61
35:1d:148:VAL:HG21	35:1d:158:ILE:HG21	1.81	0.61
50:1s:22:LEU:HD12	50:1s:31:ILE:HD11	1.82	0.61
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.47	0.61
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.82	0.61
15:2T:31:SER:OG	15:2T:85:LYS:NZ	2.34	0.61
32:1a:396:G:O2'	32:1a:398:C:OP1	2.17	0.61
32:1a:1036:G:H5''	32:1a:1037:C:C5	2.36	0.61
40:1i:77:ILE:O	40:1i:81:ILE:HG22	2.00	0.61
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.34	0.61
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.34	0.61
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.83	0.61
1:1A:303:U:O4	62:1A:4229:HOH:O	2.15	0.61
3:1D:37:LEU:HD12	3:1D:62:TYR:HB2	1.83	0.61
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.82	0.61
25:13:7:LYS:HB2	25:13:34:GLU:HG3	1.83	0.61
1:2A:253:C:O2'	62:2A:3834:HOH:O	2.16	0.61
1:2A:2133:G:O2'	1:2A:2157:G:N2	2.34	0.61
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.82	0.61
32:2a:297:G:N2	32:2a:300:A:OP2	2.30	0.61
1:1A:668:G:H5'	1:1A:669:G:OP2	2.00	0.61
32:2a:620:C:C2	35:2d:135:LEU:HG	2.36	0.61
32:2a:953:G:H5'	32:2a:965:A:N6	2.14	0.61
32:2a:974:A:P	45:2n:29:ARG:HH21	2.23	0.61
56:2y:14:A:H61	56:2y:21:A:H2	1.48	0.61
1:2A:2183:C:H2'	1:2A:2184:G:C8	2.36	0.61
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.36	0.61
41:2j:78:ASN:O	41:2j:80:LYS:N	2.33	0.61
1:1A:71:A:N7	19:1X:31:HIS:HE1	1.99	0.61
32:2a:771:G:N7	62:2a:1933:HOH:O	2.31	0.61
32:2a:1272:G:N2	32:2a:1273:G:C5	2.69	0.61
1:1A:1094:U:N3	1:1A:1097:U:OP2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1968:G:OP1	62:2A:3805:HOH:O	2.15	0.61
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.28	0.61
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.66	0.61
32:1a:757:U:H2'	32:1a:758:G:O4'	2.01	0.60
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.01	0.60
35:2d:59:ARG:HH11	35:2d:59:ARG:HA	1.66	0.60
54:1w:68:C:H2'	54:1w:69:G:H8	1.66	0.60
1:2A:890:A:H2'	1:2A:892:G:H8	1.66	0.60
32:2a:187:C:O2'	51:2t:89:ARG:NH2	2.35	0.60
32:2a:770:C:OP1	62:2a:1912:HOH:O	2.15	0.60
11:1P:91:PHE:O	11:1P:121:LYS:NZ	2.29	0.60
1:2A:2099:U:H3	1:2A:2190:G:H1	1.50	0.60
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.83	0.60
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.33	0.60
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.37	0.60
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.85	0.60
44:2m:86:CYS:HB2	50:2s:73:GLU:HG2	1.84	0.60
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.82	0.60
19:1X:11:PRO:HB3	19:1X:92:LEU:HD11	1.83	0.60
26:14:16:CYS:SG	26:14:17:GLY:N	2.74	0.60
32:1a:130:A:O2'	32:1a:131:C:O5'	2.17	0.60
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.34	0.60
1:2A:1300:U:H4'	1:2A:1301:A:H5''	1.84	0.60
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.84	0.60
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.83	0.60
26:14:55:ARG:H	26:14:56:VAL:HA	1.66	0.60
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.84	0.60
1:2A:637:A:OP1	11:2P:133:SER:OG	2.16	0.60
1:2A:752:A:H3'	29:27:1:MET:HE1	1.82	0.60
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.37	0.60
1:2A:2660:A:N7	7:2H:175:LYS:NZ	2.49	0.60
32:2a:7:G:H5'	32:2a:298:A:O4'	2.01	0.60
1:1A:271(I):G:N7	1:1A:271(J):C:N4	2.49	0.60
32:1a:1525:G:OP1	42:1k:120:ARG:NH2	2.35	0.60
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.17	0.60
48:2q:26:GLN:HG2	48:2q:37:LYS:HG2	1.83	0.60
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.83	0.60
56:2y:62:C:H2'	56:2y:63:G:C8	2.36	0.60
39:1h:121:ASP:HB2	39:1h:125:ARG:HH21	1.67	0.60
40:1i:53:VAL:O	40:1i:55:ALA:N	2.35	0.60
1:2A:1812:A:OP2	62:2A:3832:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2218:U:O2	23:21:52:ARG:NH1	2.35	0.60
1:2A:2506:U:H1'	54:2w:76:F3N:HD2	1.83	0.60
1:2A:2721:A:OP1	62:2A:3835:HOH:O	2.17	0.60
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.33	0.60
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.16	0.60
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.67	0.60
1:2A:2060:A:N3	62:2A:3900:HOH:O	2.30	0.60
1:2A:2816:C:O3'	13:2R:99:LYS:NZ	2.35	0.60
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.17	0.60
32:2a:1053:G:O2'	62:2a:1913:HOH:O	2.16	0.60
34:2c:156:ARG:H	34:2c:196:LEU:HD22	1.67	0.60
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.84	0.60
9:2N:15:LEU:HB2	9:2N:135:PRO:HB2	1.83	0.60
28:16:35:GLU:OE2	28:16:50:ARG:NH1	2.33	0.59
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.37	0.59
32:2a:56:U:H2'	32:2a:57:G:C8	2.37	0.59
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.67	0.59
1:1A:1054:A:N6	1:1A:1105:U:H3	2.00	0.59
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.84	0.59
32:2a:1264:C:H42	32:2a:1271:G:H1	1.49	0.59
6:1G:122:PRO:HG3	6:1G:182:LYS:H	1.66	0.59
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.11	0.59
35:1d:162:LEU:HA	35:1d:165:MET:HB2	1.83	0.59
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.35	0.59
14:2S:28:VAL:HG11	14:2S:98:VAL:HG13	1.83	0.59
32:2a:1228:C:H2'	32:2a:1229:A:H8	1.67	0.59
32:1a:324:G:N7	62:1a:1934:HOH:O	2.31	0.59
1:2A:1713:U:H2'	1:2A:1714:G:H8	1.67	0.59
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.32	0.59
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.85	0.59
32:2a:596:C:OP2	62:2a:1903:HOH:O	2.15	0.59
35:2d:191:ARG:NH1	35:2d:191:ARG:O	2.35	0.59
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.66	0.59
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.84	0.59
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.33	0.59
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	1.83	0.59
32:2a:372:C:O2	62:2a:1910:HOH:O	2.15	0.59
49:2r:31:LEU:HD23	49:2r:31:LEU:H	1.67	0.59
1:1A:481:G:OP2	20:1Y:47:LYS:NZ	2.33	0.59
1:1A:1057:A:H61	1:1A:1081:U:H3	1.49	0.59
1:1A:1062:G:H22	1:1A:1077:A:H61	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.67	0.59
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.84	0.59
46:1o:15:PHE:CZ	46:1o:84:LYS:HD2	2.37	0.59
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.85	0.59
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.68	0.59
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.68	0.59
11:2P:29:LYS:HG3	11:2P:30:THR:H	1.68	0.59
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.38	0.59
19:2X:44:GLU:OE2	62:2X:201:HOH:O	2.17	0.59
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.85	0.59
41:2j:47:PHE:HB2	41:2j:63:PHE:HB2	1.83	0.59
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.38	0.59
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.20	0.59
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.84	0.59
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.68	0.59
1:1A:2136:C:C4	1:1A:2155:G:C2	2.91	0.59
56:1y:70:G:H3'	56:1y:71:G:H8	1.67	0.59
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.84	0.59
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.83	0.59
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.29	0.59
2:2B:83:G:N1	2:2B:94:C:N3	2.45	0.59
32:2a:64:G:H4'	32:2a:65:U:H3'	1.83	0.59
32:2a:428:G:OP2	35:2d:10:ARG:NH1	2.36	0.59
1:1A:530:G:N1	1:1A:2023:G:OP1	2.30	0.58
1:2A:2114:A:H1'	1:2A:2168:G:H1'	1.85	0.58
1:2A:2439:A:N6	55:2x:76:31H:OP1	2.36	0.58
14:2S:67:ARG:HG2	14:2S:71:ARG:HD2	1.84	0.58
32:2a:1126:U:H3	41:2j:40:LEU:HD11	1.67	0.58
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.03	0.58
32:1a:1239:A:H62	32:1a:1299:A:N6	2.01	0.58
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.84	0.58
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.18	0.58
1:1A:588:U:H2'	1:1A:589:C:C6	2.38	0.58
1:1A:2337:G:OP1	62:1A:4233:HOH:O	2.17	0.58
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	1.85	0.58
32:1a:341:C:H2'	32:1a:342:C:C6	2.37	0.58
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.18	0.58
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.84	0.58
32:2a:748:C:H4'	32:2a:749:C:O5'	2.04	0.58
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.84	0.58
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1173:G:O2'	1:1A:1174:A:O4'	2.20	0.58
6:1G:77:ILE:HD12	6:1G:82:LEU:HD12	1.84	0.58
38:1g:115:ARG:H	38:1g:115:ARG:HD2	1.69	0.58
48:1q:67:LYS:HA	48:1q:70:ARG:HH12	1.67	0.58
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.84	0.58
32:2a:1310:G:H5'	44:2m:77:ASN:HD21	1.68	0.58
34:2c:152:ILE:HG12	34:2c:199:LYS:HB2	1.85	0.58
21:1Z:1:MET:HE3	21:1Z:135:GLU:HG3	1.86	0.58
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.67	0.58
32:2a:148:G:H2'	32:2a:149:A:C8	2.37	0.58
28:16:12:GLU:OE1	28:16:19:ARG:NH1	2.37	0.58
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.35	0.58
32:2a:921:U:O2	36:2e:19:MET:HB2	2.04	0.58
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.85	0.58
48:2q:54:GLY:O	48:2q:81:ARG:N	2.33	0.58
1:1A:739:G:OP1	62:1A:4230:HOH:O	2.16	0.58
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.21	0.58
35:1d:155:LEU:HB3	35:1d:158:ILE:HD11	1.86	0.58
39:1h:86:ILE:HD12	39:1h:133:LEU:HD22	1.86	0.58
40:1i:28:VAL:HG22	40:1i:63:ILE:HB	1.85	0.58
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.51	0.58
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.86	0.58
32:2a:254:G:OP1	48:2q:66:SER:OG	2.22	0.58
1:1A:184:C:H2'	1:1A:185:U:C6	2.38	0.58
1:1A:867:C:OP2	62:1A:4231:HOH:O	2.16	0.58
38:1g:50:ILE:HD12	38:1g:61:VAL:HG11	1.85	0.58
1:2A:323:G:O2'	1:2A:1205:U:N3	2.31	0.58
1:2A:668:G:H5'	1:2A:669:G:OP2	2.04	0.58
13:2R:72:ASP:HB3	13:2R:75:LEU:HB3	1.86	0.58
32:2a:1274:G:N2	32:2a:1275:A:N7	2.52	0.58
32:2a:1446:U:O4	62:2a:1909:HOH:O	2.14	0.58
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.84	0.58
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	1.86	0.58
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.37	0.58
46:2o:43:LEU:HD12	46:2o:56:LEU:HD13	1.86	0.58
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.01	0.58
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.17	0.58
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.84	0.58
11:2P:39:LYS:HB2	11:2P:45:LEU:HD13	1.86	0.58
26:24:44:THR:O	26:24:46:GLN:N	2.37	0.58
32:2a:352:C:O2'	32:2a:354:G:OP1	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.37	0.58
1:1A:1055:G:H1	1:1A:1104:C:H42	1.52	0.58
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.39	0.58
12:1Q:110:THR:HG22	12:1Q:112:GLU:H	1.69	0.58
32:1a:1118:C:OP1	40:1i:104:ARG:NH1	2.33	0.58
32:2a:148:G:H2'	32:2a:149:A:H8	1.67	0.58
38:2g:54:THR:O	38:2g:56:GLN:N	2.36	0.58
1:1A:801:G:O6	5:1F:53:THR:OG1	2.21	0.57
1:1A:1013:C:OP2	62:1A:4232:HOH:O	2.17	0.57
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.37	0.57
1:1A:2319:G:H1	14:1S:3:ARG:HD3	1.67	0.57
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.86	0.57
46:1o:43:LEU:HD12	46:1o:56:LEU:HD13	1.86	0.57
26:24:13:ARG:NH2	26:24:23:GLU:OE2	2.36	0.57
34:2c:39:ILE:O	34:2c:43:LEU:HG	2.04	0.57
1:1A:2136:C:N4	1:1A:2155:G:N1	2.52	0.57
1:2A:709:U:H2'	1:2A:710:G:C8	2.40	0.57
1:2A:855:G:O2'	22:20:27:GLU:OE2	2.21	0.57
2:2B:105:A:OP1	21:2Z:72:ARG:NH2	2.37	0.57
12:2Q:85:LYS:HG2	22:20:7:LEU:HB3	1.85	0.57
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.85	0.57
1:1A:1014:U:OP2	62:1A:4232:HOH:O	2.17	0.57
1:1A:1721:G:H1'	1:1A:1741:A:H61	1.69	0.57
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.68	0.57
2:2B:83:G:N2	2:2B:94:C:O2	2.31	0.57
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.86	0.57
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.51	0.57
34:2c:63:ASN:HB3	34:2c:98:ASN:HD22	1.68	0.57
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.31	0.57
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.85	0.57
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.85	0.57
1:1A:2136:C:C4	1:1A:2155:G:N1	2.73	0.57
32:1a:17:U:H2'	32:1a:18:C:C6	2.39	0.57
32:1a:406:G:N3	35:1d:119:GLN:NE2	2.51	0.57
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.86	0.57
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.86	0.57
32:2a:448:A:P	32:2a:485:G:H22	2.27	0.57
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.85	0.57
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.39	0.57
1:1A:2123:G:H2'	1:1A:2124:G:C8	2.38	0.57
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1004:A:H5''	32:1a:1025:U:H5	1.69	0.57
1:2A:627:A:N7	11:2P:84:ASN:ND2	2.52	0.57
15:2T:127:ALA:C	15:2T:129:ARG:H	2.11	0.57
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.68	0.57
32:2a:1289:A:OP1	52:2u:10:ARG:NH2	2.37	0.57
33:2b:114:ARG:O	33:2b:118:LEU:N	2.36	0.57
38:2g:105:VAL:O	38:2g:109:ASN:ND2	2.37	0.57
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.87	0.57
42:2k:54:ARG:NH2	56:2y:39:PSU:O2'	2.37	0.57
54:2w:19:G:H1	54:2w:56:C:H42	1.52	0.57
1:1A:881:G:H3'	1:1A:882:G:H8	1.70	0.57
62:1A:4212:HOH:O	13:1R:3:HIS:NE2	2.32	0.57
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.40	0.57
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.39	0.57
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.40	0.57
32:2a:401:C:P	35:2d:73:ARG:HH21	2.28	0.57
44:2m:17:VAL:O	44:2m:20:THR:OG1	2.19	0.57
48:2q:4:LYS:HE2	48:2q:6:LEU:HD21	1.87	0.57
1:1A:602:G:N1	1:1A:655:A:OP2	2.32	0.57
1:1A:2439:A:N6	55:1x:76:31H:OP1	2.37	0.57
32:1a:78:G:N2	32:1a:91:C:N3	2.53	0.57
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.87	0.57
32:2a:838:G:H1	32:2a:848:C:H42	1.53	0.57
33:2b:120:ALA:O	33:2b:125:PRO:HD2	2.05	0.57
34:2c:52:LEU:HD13	34:2c:68:VAL:HG13	1.86	0.57
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.40	0.57
18:1W:11:ARG:HA	18:1W:100:THR:HG22	1.86	0.57
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.40	0.57
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.40	0.57
1:1A:992:C:OP1	17:1V:74:LYS:NZ	2.35	0.57
1:1A:1365:A:O2'	23:11:11:ARG:NH1	2.38	0.57
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.38	0.57
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.38	0.57
32:1a:1246:C:H42	32:1a:1291:G:H1	1.53	0.57
1:2A:2347:C:OP2	62:2A:3836:HOH:O	2.17	0.57
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.68	0.57
1:1A:1670:C:OP2	62:1A:4210:HOH:O	2.17	0.57
62:1A:4829:HOH:O	13:1R:15:SER:HB3	2.04	0.57
9:2N:32:THR:HG23	9:2N:37:LYS:HB2	1.87	0.57
12:2Q:78:PRO:HD3	55:2x:1:C:N3	2.20	0.57
32:2a:306:G:OP2	62:2a:1915:HOH:O	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.86	0.57
1:1A:1359:A:H2	1:1A:1372:U:O4	1.88	0.56
14:1S:34:HIS:ND1	14:1S:53:SER:HB2	2.19	0.56
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.40	0.56
36:1e:11:ILE:HB	36:1e:31:LEU:HD23	1.87	0.56
6:2G:138:GLN:OE1	6:2G:138:GLN:N	2.38	0.56
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.87	0.56
32:2a:17:U:H2'	32:2a:18:C:C6	2.40	0.56
32:2a:396:G:O2'	32:2a:398:C:OP1	2.21	0.56
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.40	0.56
54:2w:25:C:H2'	54:2w:26:A:H8	1.69	0.56
1:1A:528:A:O2'	1:1A:529:A:H5'	2.05	0.56
32:1a:165:C:H2'	32:1a:166:G:H8	1.70	0.56
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.88	0.56
1:2A:252:G:OP1	11:2P:50:ARG:NH1	2.32	0.56
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.38	0.56
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.86	0.56
42:2k:98:LEU:O	42:2k:101:SER:OG	2.19	0.56
1:1A:1176:G:H21	1:1A:1178:C:P	2.29	0.56
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.13	0.56
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.88	0.56
33:1b:118:LEU:HB3	33:1b:142:LEU:HD12	1.87	0.56
39:1h:96:GLY:N	39:1h:99:GLU:OE1	2.33	0.56
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.87	0.56
1:2A:2722:G:H5'	13:2R:4:LEU:HD12	1.85	0.56
6:2G:163:ALA:HB1	6:2G:168:GLU:HB2	1.87	0.56
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.03	0.56
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.88	0.56
21:2Z:72:ARG:HH22	21:2Z:97:GLU:HB2	1.69	0.56
34:2c:39:ILE:HG22	34:2c:43:LEU:HD11	1.85	0.56
1:1A:1300:U:H4'	1:1A:1301:A:H5''	1.88	0.56
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.40	0.56
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.53	0.56
8:1I:4:ILE:HD11	8:1I:44:LEU:HD12	1.87	0.56
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.87	0.56
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	1.87	0.56
1:2A:900:A:O2'	1:2A:901:A:OP1	2.22	0.56
2:2B:72:G:O2'	2:2B:105:A:N6	2.38	0.56
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.05	0.56
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.39	0.56
32:2a:1178:G:OP1	40:2i:93:ARG:NH1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1263:C:C4	32:2a:1272:G:O6	2.58	0.56
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.87	0.56
1:1A:1041:C:N4	1:1A:1114:G:H1	2.03	0.56
3:1D:71:ASP:HB2	3:1D:103:ARG:HH12	1.70	0.56
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.87	0.56
32:1a:78:G:C6	32:1a:91:C:N4	2.73	0.56
32:1a:828:A:H2'	32:1a:829:G:O4'	2.04	0.56
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.30	0.56
37:1f:33:TYR:OH	37:1f:78:GLU:HG3	2.05	0.56
1:2A:330:A:H2	1:2A:1210:A:HO2'	1.53	0.56
4:2E:52:LEU:O	4:2E:76:ARG:N	2.34	0.56
5:2F:104:LYS:HA	5:2F:107:LYS:HE3	1.87	0.56
32:2a:1133:G:H1	32:2a:1141:C:H42	1.54	0.56
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.14	0.56
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	1.88	0.56
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.41	0.56
7:1H:15:VAL:HG21	7:1H:76:VAL:HG23	1.87	0.56
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.05	0.56
1:2A:2131:G:OP2	1:2A:2131:G:N2	2.34	0.56
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.36	0.56
1:2A:2801(A):A:H3'	1:2A:2802:G:H5'	1.87	0.56
32:2a:1237:C:HO2'	32:2a:1300:G:H1	1.53	0.56
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.06	0.56
1:2A:307:G:H21	1:2A:330:A:H62	1.54	0.56
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.06	0.56
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.24	0.56
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.71	0.56
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.24	0.56
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.41	0.56
35:2d:119:GLN:HE21	35:2d:123:HIS:CD2	2.24	0.56
36:2e:89:ILE:HG12	36:2e:135:THR:HG22	1.87	0.56
1:1A:278:A:O2'	1:1A:279:C:OP1	2.21	0.56
1:1A:880:G:H2'	1:1A:881:G:H8	1.71	0.56
1:1A:897:C:N3	1:1A:898:C:N4	2.53	0.56
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.41	0.56
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	1.88	0.56
1:2A:38:A:H2'	1:2A:39:C:C6	2.40	0.56
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.41	0.56
5:2F:32:LEU:HD22	5:2F:112:MET:HE2	1.87	0.56
8:2I:43:ASN:ND2	23:2I:75:GLU:OE2	2.39	0.56
47:2p:5:ARG:HH21	47:2p:28:ARG:HA	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.40	0.56
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.86	0.56
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.06	0.56
12:1Q:78:PRO:HD3	55:1x:1:C:N3	2.20	0.56
32:1a:78:G:N1	32:1a:91:C:N4	2.54	0.56
32:1a:664:G:P	49:1r:64:ARG:HH21	2.28	0.56
33:1b:178:ARG:NH2	39:1h:74:PRO:HB3	2.20	0.56
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.88	0.56
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.04	0.56
32:1a:1027:C:C4	32:1a:1034:G:N1	2.74	0.56
1:2A:856:C:N4	62:2A:3838:HOH:O	2.38	0.56
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.41	0.56
1:1A:1171:G:OP2	1:1A:1174:A:N6	2.39	0.55
32:1a:1525:G:P	42:1k:120:ARG:HH22	2.29	0.55
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.39	0.55
3:2D:8:PRO:HB3	3:2D:14:ARG:HG2	1.89	0.55
32:2a:142:G:H2'	32:2a:143:A:H8	1.70	0.55
1:1A:2102:U:H3	1:1A:2187:G:H1	1.54	0.55
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.06	0.55
32:1a:567:G:N3	62:1a:1939:HOH:O	2.32	0.55
32:2a:45:U:H2'	32:2a:46:G:C8	2.42	0.55
38:2g:22:LEU:HG	38:2g:62:PHE:CE2	2.40	0.55
50:2s:32:LYS:HA	50:2s:50:ALA:HB3	1.88	0.55
56:2y:58:A:O2'	56:2y:60:U:OP2	2.23	0.55
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.39	0.55
32:1a:405:U:OP2	35:1d:3:ARG:NH1	2.38	0.55
32:1a:560:U:O2'	32:1a:561:U:OP2	2.23	0.55
33:1b:134:GLU:HA	33:1b:137:ARG:HE	1.70	0.55
1:2A:1324:G:N7	62:2A:3927:HOH:O	2.33	0.55
1:1A:271(W):G:O6	62:1A:4236:HOH:O	2.18	0.55
1:1A:1385:G:N7	62:1A:4307:HOH:O	2.33	0.55
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.21	0.55
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.71	0.55
33:2b:92:TYR:CE2	33:2b:151:GLY:HA3	2.42	0.55
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.88	0.55
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.87	0.55
32:1a:1166:G:N2	32:1a:1170:A:OP2	2.40	0.55
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.40	0.55
51:1t:83:ARG:HG2	51:1t:86:ARG:HH12	1.71	0.55
1:2A:304:G:O6	62:2A:3833:HOH:O	2.16	0.55
3:2D:71:ASP:HB2	3:2D:103:ARG:HH12	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.25	0.55
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.21	0.55
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	1.89	0.55
40:2i:18:PHE:HD2	40:2i:62:TYR:HD2	1.55	0.55
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.89	0.55
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.07	0.55
56:2y:65:G:H2'	56:2y:66:U:C6	2.42	0.55
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.88	0.55
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.89	0.55
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.89	0.55
1:2A:492:A:H2'	1:2A:493:G:O4'	2.06	0.55
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.42	0.55
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.06	0.55
38:2g:22:LEU:HD11	38:2g:101:LEU:HD11	1.89	0.55
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.22	0.55
1:1A:2803:C:H2'	1:1A:2804:C:C6	2.42	0.55
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.88	0.55
8:1I:17:GLN:HG2	8:1I:18:VAL:H	1.72	0.55
32:1a:1291:G:O2'	40:1i:38:GLN:OE1	2.24	0.55
1:2A:1452:A:OP2	62:2A:3839:HOH:O	2.18	0.55
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.42	0.55
32:2a:165:C:H2'	32:2a:166:G:H8	1.71	0.55
32:2a:650:G:N7	62:2a:1941:HOH:O	2.33	0.55
44:2m:92:HIS:CE1	44:2m:98:VAL:HG21	2.42	0.55
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.89	0.55
32:1a:169:C:H2'	32:1a:170:U:H6	1.71	0.55
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.07	0.55
1:2A:1193:G:OP1	11:2P:14:LYS:NZ	2.34	0.55
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.42	0.55
6:2G:43:LEU:HD11	6:2G:153:ARG:HG2	1.89	0.55
24:22:35:LEU:HD12	24:22:53:LEU:HD12	1.89	0.55
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.39	0.55
32:2a:560:U:H5'	32:2a:566:G:N2	2.21	0.55
47:2p:21:VAL:HG22	47:2p:33:ILE:HB	1.89	0.55
1:1A:639:U:H2'	1:1A:640:C:C6	2.42	0.55
1:1A:796:C:H2'	1:1A:797:C:C6	2.42	0.55
25:13:6:VAL:HG22	25:13:56:VAL:HG13	1.88	0.55
32:1a:948:C:OP1	44:1m:109:THR:OG1	2.25	0.55
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.07	0.55
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.42	0.55
39:2h:12:ARG:HD3	39:2h:26:VAL:HG12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.42	0.55
1:1A:2165:G:H1	1:1A:2171:A:H2'	1.72	0.54
18:1W:23:LEU:HD21	27:15:25:LEU:HB2	1.88	0.54
1:2A:639:U:H2'	1:2A:640:C:C6	2.42	0.54
1:2A:893:C:H5'	1:2A:894:C:C5	2.42	0.54
28:26:23:THR:OG1	28:26:24:GLU:N	2.40	0.54
32:2a:1316:G:H22	32:2a:1319:A:H5'	1.72	0.54
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.43	0.54
1:1A:800:A:H8	1:1A:800:A:OP1	1.90	0.54
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.71	0.54
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.40	0.54
1:2A:796:C:H2'	1:2A:797:C:C6	2.42	0.54
1:2A:878:A:H61	1:2A:899:A:H1'	1.71	0.54
1:2A:992:C:OP1	17:2V:74:LYS:NZ	2.34	0.54
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.42	0.54
6:2G:41:GLN:O	6:2G:43:LEU:N	2.39	0.54
34:2c:52:LEU:HD11	34:2c:55:VAL:HB	1.89	0.54
34:2c:191:THR:OG1	34:2c:194:GLY:O	2.25	0.54
1:1A:218:A:OP2	62:1A:4239:HOH:O	2.18	0.54
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.89	0.54
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.42	0.54
1:2A:212:G:H2'	1:2A:213:A:O4'	2.06	0.54
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.42	0.54
2:2B:3:C:H2'	2:2B:4:C:C6	2.43	0.54
6:2G:67:LYS:H	26:24:6:HIS:CE1	2.26	0.54
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.89	0.54
33:2b:55:PHE:HE1	33:2b:218:ALA:HA	1.72	0.54
50:2s:80:TYR:O	50:2s:82:GLY:N	2.39	0.54
1:1A:2123:G:H2'	1:1A:2124:G:H8	1.73	0.54
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.72	0.54
21:1Z:105:VAL:N	21:1Z:139:VAL:O	2.30	0.54
32:1a:22:G:H4'	32:1a:885:G:C8	2.42	0.54
32:1a:193:C:H2'	32:1a:194:C:C6	2.43	0.54
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.89	0.54
54:1w:18:G:H4'	54:1w:60:U:C5	2.42	0.54
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.72	0.54
35:2d:63:LYS:HD2	35:2d:198:VAL:HG22	1.89	0.54
54:2w:21:A:O2'	54:2w:22:G:OP1	2.25	0.54
6:1G:19:LEU:HD13	6:1G:32:PRO:HD2	1.89	0.54
10:1O:98:VAL:HG13	10:1O:117:LEU:HB2	1.87	0.54
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.25	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:14:LEU:HD22	37:2f:18:GLN:HB3	1.90	0.54
4:1E:29:GLY:HA3	62:1E:402:HOH:O	2.07	0.54
32:1a:26:A:O2'	35:1d:209:ARG:NH2	2.40	0.54
34:1c:44:GLU:HA	34:1c:52:LEU:HD23	1.89	0.54
1:2A:333:G:N7	62:2A:3928:HOH:O	2.33	0.54
1:2A:764:A:H5'	3:2D:210:GLY:HA2	1.88	0.54
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.43	0.54
32:2a:1004:A:N6	32:2a:1037:C:O2	2.21	0.54
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.89	0.54
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.43	0.54
1:1A:1506:C:H2'	1:1A:1507:A:C8	2.41	0.54
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.90	0.54
32:1a:677:U:H3	32:1a:713:G:H22	1.55	0.54
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.72	0.54
34:1c:177:THR:HG22	34:1c:180:ALA:H	1.72	0.54
1:1A:2136:C:N3	1:1A:2155:G:N2	2.55	0.54
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.41	0.54
32:1a:814:A:H2'	32:1a:816:A:H5''	1.90	0.54
42:1k:34:ASP:HB3	42:1k:40:ILE:HD11	1.89	0.54
1:2A:1603:A:OP1	62:2A:3841:HOH:O	2.18	0.54
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.88	0.54
32:2a:222:U:H2'	32:2a:223:U:C6	2.42	0.54
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.34	0.54
33:2b:58:ILE:HA	33:2b:61:LEU:HB3	1.89	0.54
1:1A:1899:G:O2'	1:1A:1900:A:OP2	2.26	0.54
32:1a:382:A:H2'	32:1a:383:A:C8	2.43	0.54
33:1b:80:ILE:HD12	33:1b:211:ILE:HG22	1.90	0.54
1:2A:568:U:H5'	1:2A:945:A:N1	2.23	0.54
32:2a:1119:C:OP2	40:2i:9:ARG:NH2	2.41	0.54
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.89	0.54
32:2a:1270:C:OP2	52:2u:24:ARG:NH2	2.41	0.54
35:2d:109:GLY:HA3	35:2d:165:MET:HG3	1.90	0.54
1:1A:615:G:OP1	5:1F:40:GLN:NE2	2.39	0.54
1:1A:2006:C:OP2	62:1A:4237:HOH:O	2.18	0.54
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.21	0.54
1:1A:2336:A:H61	22:10:43:THR:HG22	1.72	0.54
20:1Y:34:LYS:NZ	62:1Y:301:HOH:O	2.24	0.54
35:1d:112:VAL:HG23	35:1d:116:GLN:HE22	1.72	0.54
39:1h:36:LEU:HD23	39:1h:39:LEU:HD12	1.90	0.54
1:2A:247:G:H4'	1:2A:386:G:C5	2.43	0.54
1:2A:1713:U:H2'	1:2A:1714:G:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.39	0.54
32:2a:1060:C:HO2'	41:2j:56:HIS:HD1	1.56	0.54
56:2y:34:G:H2'	56:2y:35:A:C8	2.43	0.54
56:2y:43:C:H2'	56:2y:44:G:C8	2.42	0.54
1:1A:899:A:H2'	1:1A:899:A:N3	2.23	0.53
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.55	0.53
26:14:34:GLU:HG2	26:14:35:VAL:HG12	1.89	0.53
26:14:54:GLY:N	26:14:55:ARG:HA	2.22	0.53
32:1a:67:C:H2'	32:1a:68:G:C8	2.43	0.53
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.43	0.53
54:1w:43:C:H2'	54:1w:44:G:C8	2.43	0.53
1:2A:1299:G:OP1	62:2A:3840:HOH:O	2.18	0.53
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.89	0.53
1:2A:2131:G:H4'	1:2A:2132:U:H3'	1.88	0.53
2:2B:2:C:H2'	2:2B:3:C:C6	2.43	0.53
10:2O:98:VAL:HG22	10:2O:118:ALA:HA	1.89	0.53
33:2b:219:VAL:O	33:2b:223:ILE:HG12	2.07	0.53
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.92	0.53
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.42	0.53
32:1a:1030:C:H42	32:1a:1031:G:H1	1.55	0.53
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.43	0.53
1:2A:989:G:OP2	25:23:11:SER:OG	2.19	0.53
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.72	0.53
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.73	0.53
12:2Q:110:THR:HG22	12:2Q:112:GLU:H	1.73	0.53
27:25:35:GLU:HG2	27:25:51:TYR:CG	2.43	0.53
54:2w:39:PSU:H2'	54:2w:40:C:H6	1.72	0.53
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.44	0.53
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.06	0.53
32:1a:21:G:H2'	32:1a:22:G:C8	2.44	0.53
32:1a:224:C:OP1	51:1t:74:LYS:NZ	2.38	0.53
33:1b:115:LEU:O	33:1b:119:GLU:N	2.39	0.53
32:2a:117:G:OP2	62:2a:1907:HOH:O	2.18	0.53
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.44	0.53
33:2b:60:ASP:O	33:2b:64:ARG:HG2	2.08	0.53
38:2g:111:ARG:NH2	38:2g:126:ASP:OD2	2.41	0.53
41:2j:64:GLU:OE2	41:2j:66:ARG:NH2	2.23	0.53
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.44	0.53
1:1A:2147:G:H2'	1:1A:2148:G:H4'	1.91	0.53
1:1A:2344:U:OP1	28:16:37:ARG:NH1	2.39	0.53
8:1I:5:LEU:HD11	8:1I:19:VAL:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.40	0.53
21:1Z:7:ALA:HB3	21:1Z:61:LEU:HD12	1.90	0.53
32:1a:1150:U:H4'	41:1j:41:PRO:HG3	1.91	0.53
36:1e:105:VAL:HG21	36:1e:128:PRO:HB3	1.90	0.53
37:1f:79:LEU:O	37:1f:85:VAL:HG11	2.09	0.53
1:2A:30:G:H2'	1:2A:31:C:C6	2.43	0.53
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.22	0.53
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.41	0.53
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.08	0.53
6:2G:70:VAL:HA	6:2G:90:LEU:HD23	1.89	0.53
21:2Z:102:LEU:HD13	21:2Z:139:VAL:HG21	1.89	0.53
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.36	0.53
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.43	0.53
37:2f:97:PHE:HE2	49:2r:62:GLU:HG2	1.73	0.53
56:2y:7:A:H61	56:2y:66:U:H3	1.57	0.53
1:1A:1025:G:C4	1:1A:1135:C:HI1'	2.44	0.53
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.90	0.53
21:1Z:103:ARG:O	21:1Z:139:VAL:N	2.41	0.53
32:1a:116:A:OP1	62:1a:1912:HOH:O	2.19	0.53
38:1g:78:ARG:HG3	38:1g:156:TRP:HZ3	1.73	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.09	0.53
32:2a:1010:G:N2	32:2a:1020:U:O2'	2.42	0.53
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.89	0.53
1:1A:576:U:H2'	1:1A:577:G:C8	2.44	0.53
1:1A:1082:U:H3	1:1A:1086:A:H61	0.64	0.53
25:13:5:LYS:NZ	25:13:34:GLU:OE2	2.32	0.53
35:1d:60:GLU:OE2	35:1d:63:LYS:NZ	2.30	0.53
43:1l:39:VAL:HG11	43:1l:41:ARG:HH11	1.74	0.53
1:2A:323:G:H2'	5:2F:169:ASN:OD1	2.09	0.53
10:2O:97:ARG:NH1	32:2a:339:C:OP2	2.34	0.53
14:2S:77:ALA:HB1	14:2S:82:ILE:HB	1.90	0.53
32:2a:512:U:H2'	32:2a:513:C:C6	2.44	0.53
32:2a:1271:G:C2	32:2a:1272:G:N7	2.77	0.53
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.90	0.53
1:1A:7:G:H2'	1:1A:8:A:O4'	2.08	0.53
1:1A:1762:A:H2'	62:1A:5910:HOH:O	2.09	0.53
32:1a:731:G:H5'	32:1a:766:A:H4'	1.91	0.53
33:1b:109:SER:O	33:1b:112:VAL:HG12	2.09	0.53
1:2A:236:C:H2'	1:2A:237:C:C6	2.44	0.53
1:2A:2125:G:H1	1:2A:2172:U:P	2.31	0.53
3:2D:5:LYS:HG2	3:2D:17:THR:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:110:THR:HB	12:2Q:113:GLN:H	1.74	0.53
32:2a:709:G:O6	62:2a:1914:HOH:O	2.16	0.53
32:2a:1240:U:OP2	38:2g:116:ALA:N	2.41	0.53
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.44	0.53
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.90	0.53
26:14:61:ARG:NH1	50:1s:42:PRO:HD3	2.24	0.53
50:1s:12:ASP:OD1	50:1s:37:ARG:NH2	2.41	0.53
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.44	0.53
22:20:46:LYS:HE3	22:20:76:GLY:HA3	1.91	0.53
32:2a:7:G:O2'	36:2e:120:THR:O	2.26	0.53
32:2a:624:C:H2'	32:2a:625:G:H8	1.74	0.53
34:2c:134:ILE:HG22	34:2c:168:ALA:HB3	1.91	0.53
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.09	0.53
1:1A:2144:U:H3'	1:1A:2146:C:H41	1.73	0.53
1:1A:2428:G:OP1	62:1A:4205:HOH:O	2.19	0.53
8:1I:38:LEU:HG	8:1I:40:THR:HG22	1.90	0.53
32:1a:130:A:H5'	48:1q:63:ARG:HH11	1.74	0.53
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.29	0.53
32:1a:865:A:H2	32:1a:918:A:H4'	1.73	0.53
1:2A:8:A:H2'	1:2A:9:U:C6	2.44	0.53
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.91	0.53
1:2A:1364:G:P	23:21:3:LYS:HG3	2.49	0.53
32:2a:407:G:H5''	35:2d:115:ARG:HB3	1.90	0.53
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.09	0.53
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.90	0.53
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.24	0.53
37:2f:2:ARG:NE	37:2f:69:GLU:HG2	2.24	0.53
38:2g:113:GLU:OE2	38:2g:122:HIS:ND1	2.41	0.53
41:2j:38:ILE:HG13	41:2j:71:LEU:HB3	1.91	0.53
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.41	0.53
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.42	0.53
22:10:10:THR:HG22	22:10:12:ASN:N	2.17	0.53
32:1a:56:U:H2'	32:1a:57:G:C8	2.44	0.53
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	1.91	0.53
41:1j:55:LYS:HE3	41:1j:56:HIS:CE1	2.44	0.53
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.91	0.53
54:1w:5:G:H2'	54:1w:6:G:C8	2.44	0.53
1:2A:1183:G:H5''	25:23:30:ARG:NH2	2.24	0.53
32:2a:1102:A:O3'	33:2b:96:ARG:NH2	2.42	0.53
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.24	0.53
7:1H:86:GLU:OE2	7:1H:130:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:778:G:H1'	42:1k:119:CYS:HB3	1.91	0.52
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.44	0.52
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.40	0.52
34:1c:119:ARG:HE	34:1c:140:ARG:CZ	2.22	0.52
38:1g:78:ARG:HG3	38:1g:156:TRP:CZ3	2.44	0.52
1:2A:2390:U:P	30:28:35:GLN:HE22	2.33	0.52
2:2B:41:U:H5	6:2G:70:VAL:H	1.57	0.52
6:2G:115:ARG:NH1	44:2m:6:GLY:O	2.43	0.52
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.90	0.52
1:1A:2235:G:N7	62:1A:4315:HOH:O	2.34	0.52
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.43	0.52
12:1Q:18:LYS:O	12:1Q:98:LYS:NZ	2.30	0.52
17:1V:10:LYS:NZ	17:1V:23:GLU:OE2	2.41	0.52
26:14:28:LYS:HZ3	26:14:29:PRO:HD2	1.73	0.52
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.44	0.52
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.08	0.52
14:2S:15:ARG:HG2	14:2S:19:LYS:HE3	1.90	0.52
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.23	0.52
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	1.90	0.52
48:2q:6:LEU:HB2	48:2q:59:ILE:HG12	1.92	0.52
56:2y:14:A:O2'	56:2y:15:G:OP1	2.25	0.52
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.90	0.52
1:1A:2100:G:H1	1:1A:2189:U:H3	1.57	0.52
1:1A:2139:C:H2'	1:1A:2140:C:O4'	2.09	0.52
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.43	0.52
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.44	0.52
1:1A:2822:G:OP2	62:1A:4212:HOH:O	2.19	0.52
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.75	0.52
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.91	0.52
21:2Z:31:ARG:NH1	21:2Z:94:GLU:HG2	2.23	0.52
25:23:15:TYR:O	25:23:20:LYS:NZ	2.43	0.52
32:2a:1124:G:N7	32:2a:1145:C:O2'	2.42	0.52
33:2b:52:GLU:HG2	33:2b:56:ARG:HH12	1.74	0.52
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.09	0.52
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.10	0.52
1:1A:919:G:N2	1:1A:2269:A:OP2	2.40	0.52
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.24	0.52
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.74	0.52
32:1a:966:M2G:HM11	40:1i:127:LYS:HE2	1.90	0.52
32:1a:1432:G:N7	62:1a:1944:HOH:O	2.34	0.52
1:2A:800:A:H8	1:2A:800:A:OP1	1.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.09	0.52
2:2B:94:C:H2'	2:2B:95:C:C6	2.45	0.52
16:2U:49:HIS:HA	16:2U:52:ARG:HB2	1.90	0.52
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.24	0.52
41:2j:49:VAL:HG22	45:2n:41:ARG:HB2	1.91	0.52
56:2y:8:4SU:H2'	56:2y:46:G7M:H22	1.74	0.52
1:1A:1740:G:H2'	1:1A:1741:A:C8	2.44	0.52
8:1I:4:ILE:HD13	8:1I:47:LEU:HG	1.91	0.52
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.44	0.52
30:18:42:ARG:HD2	62:18:205:HOH:O	2.09	0.52
32:1a:130:A:N3	32:1a:263:A:O2'	2.34	0.52
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.09	0.52
32:1a:1040:U:H2'	32:1a:1041:A:H8	1.74	0.52
33:1b:93:VAL:HG11	33:1b:97:TRP:CD1	2.45	0.52
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.09	0.52
1:2A:700:G:O2'	1:2A:1632:A:N3	2.34	0.52
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.91	0.52
12:2Q:78:PRO:HG2	12:2Q:81:VAL:HG11	1.92	0.52
26:24:45:GLY:O	26:24:47:GLN:N	2.38	0.52
26:24:46:GLN:NE2	26:24:48:ARG:HD3	2.24	0.52
32:2a:1132:C:H42	32:2a:1142:G:H1	1.56	0.52
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.42	0.52
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.45	0.52
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.44	0.52
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.92	0.52
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.26	0.52
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.44	0.52
32:2a:157:G:H2'	32:2a:158:G:H8	1.74	0.52
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.09	0.52
1:1A:1062:G:H22	1:1A:1077:A:N6	2.08	0.52
1:1A:1062:G:H2'	1:1A:1063:G:C8	2.45	0.52
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.10	0.52
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.44	0.52
35:1d:7:PRO:HB2	35:1d:10:ARG:HD2	1.91	0.52
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.08	0.52
1:2A:2331:G:O2'	1:2A:2336:A:N1	2.42	0.52
1:2A:2365:G:OP1	22:20:55:ARG:N	2.43	0.52
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.35	0.52
51:2t:67:ALA:HA	51:2t:72:LEU:O	2.10	0.52
1:1A:1226:A:OP1	17:1V:84:LYS:HE2	2.10	0.52
1:1A:2149:G:C6	1:1A:2150:U:C2	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2181:G:O2'	1:1A:2182:G:OP1	2.28	0.52
32:1a:219:C:H2'	32:1a:220:G:O4'	2.10	0.52
1:2A:2114:A:H62	1:2A:2115:G:H21	1.57	0.52
28:26:13:CYS:SG	28:26:47:THR:HG21	2.49	0.52
32:2a:266:G:H5''	32:2a:268:C:H41	1.75	0.52
41:2j:50:ILE:O	45:2n:41:ARG:NH1	2.43	0.52
56:2y:5:G:H1	56:2y:68:C:H42	1.55	0.52
1:1A:932:G:OP2	25:13:29:ARG:NH2	2.43	0.52
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.26	0.52
26:14:33:VAL:HG12	26:14:35:VAL:H	1.75	0.52
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.09	0.52
1:2A:271(P):C:O3'	8:2I:42:SER:OG	2.27	0.52
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.45	0.52
1:2A:2504:U:OP2	62:2A:3842:HOH:O	2.18	0.52
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.09	0.52
8:2I:38:LEU:HD12	8:2I:38:LEU:H	1.75	0.52
54:2w:51:U:H2'	54:2w:52:G:C8	2.45	0.52
1:1A:657:U:H2'	1:1A:658:C:C6	2.45	0.52
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.45	0.52
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.44	0.52
32:1a:721:G:H4'	32:1a:722:A:O4'	2.10	0.52
36:1e:144:THR:H	36:1e:147:ASP:HB2	1.74	0.52
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.10	0.52
1:2A:307:G:N1	1:2A:310:A:OP2	2.42	0.52
1:2A:2278:A:OP2	22:20:12:ASN:ND2	2.42	0.52
1:2A:2507:C:H5''	1:2A:2573:C:N4	2.25	0.52
7:2H:15:VAL:HG21	7:2H:76:VAL:HG23	1.90	0.52
14:2S:25:ARG:HB3	14:2S:40:ILE:HB	1.91	0.52
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.91	0.52
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.07	0.52
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.45	0.51
1:1A:2629:A:H1'	1:1A:2630:G:C5'	2.40	0.51
3:1D:37:LEU:HD13	3:1D:87:ASN:ND2	2.24	0.51
32:1a:708:C:H2'	32:1a:709:G:C8	2.45	0.51
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.25	0.51
1:2A:880:G:N1	1:2A:898:C:O2	2.42	0.51
1:2A:882:G:H22	1:2A:894:C:N4	2.08	0.51
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.09	0.51
8:2I:45:LYS:O	8:2I:49:ALA:N	2.43	0.51
28:26:35:GLU:HG2	28:26:50:ARG:HD3	1.92	0.51
32:2a:921:U:O2'	36:2e:19:MET:O	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.24	0.51
39:2h:110:ALA:HB3	39:2h:121:ASP:HB3	1.92	0.51
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.45	0.51
32:1a:373:A:H2'	32:1a:374:A:H8	1.74	0.51
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.43	0.51
12:2Q:24:GLY:HA2	12:2Q:67:ARG:NH2	2.25	0.51
23:21:50:ARG:HD2	23:21:57:GLU:OE2	2.10	0.51
42:2k:81:ASP:OD1	42:2k:107:SER:OG	2.26	0.51
44:2m:94:ARG:HB3	44:2m:96:LEU:HD12	1.93	0.51
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.10	0.51
32:1a:1003:G:C4	32:1a:1004:A:H2	2.28	0.51
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.42	0.51
1:2A:900:A:HO2'	1:2A:901:A:P	2.33	0.51
1:2A:2892:A:H2'	1:2A:2893:G:H5'	1.92	0.51
7:2H:6:ARG:HB3	7:2H:6:ARG:HH11	1.75	0.51
14:2S:58:LEU:HD13	14:2S:65:VAL:HB	1.91	0.51
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.25	0.51
41:2j:8:LEU:HD11	41:2j:20:ALA:HB2	1.92	0.51
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	1.93	0.51
1:1A:247:G:H4'	1:1A:386:G:C5	2.44	0.51
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.92	0.51
1:2A:2319:G:H22	14:2S:3:ARG:NH1	2.02	0.51
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.26	0.51
11:2P:89:ALA:HA	11:2P:121:LYS:HD3	1.92	0.51
26:24:58:ARG:HD2	50:2s:68:GLY:H	1.74	0.51
32:2a:838:G:H1	32:2a:848:C:N4	2.08	0.51
32:2a:1051:C:H42	32:2a:1207:2MG:HN1	1.59	0.51
32:2a:1263:C:N3	32:2a:1272:G:O6	2.43	0.51
33:2b:16:HIS:CB	33:2b:210:SER:HB2	2.40	0.51
34:2c:178:LEU:C	34:2c:180:ALA:H	2.17	0.51
48:2q:45:HIS:NE2	48:2q:47:PRO:HG3	2.25	0.51
1:1A:1003:G:O2'	1:1A:1010:A:N1	2.38	0.51
1:1A:2810:A:N6	1:1A:2891:G:O2'	2.33	0.51
21:1Z:52:SER:O	21:1Z:54:HIS:N	2.43	0.51
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.45	0.51
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.20	0.51
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.37	0.51
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.92	0.51
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.75	0.51
32:2a:1485:U:H2'	32:2a:1486:G:C8	2.45	0.51
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.44	0.51
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.43	0.51
11:1P:38:GLN:O	11:1P:39:LYS:HB3	2.10	0.51
32:1a:691:G:H2'	32:1a:692:U:C6	2.46	0.51
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.92	0.51
38:1g:22:LEU:HD21	38:1g:66:VAL:HG21	1.91	0.51
44:1m:98:VAL:HG12	44:1m:99:ARG:HG3	1.92	0.51
1:2A:249:C:O2	30:28:12:LYS:NZ	2.33	0.51
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.11	0.51
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.10	0.51
1:2A:2524:G:N7	62:2A:3921:HOH:O	2.33	0.51
4:2E:49:LEU:HD22	4:2E:81:ILE:HD12	1.92	0.51
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.92	0.51
8:2I:48:GLU:HA	8:2I:51:ILE:HG22	1.93	0.51
26:24:14:ILE:HG12	26:24:31:ILE:HB	1.92	0.51
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.46	0.51
32:2a:1374:A:OP1	38:2g:36:LYS:NZ	2.32	0.51
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.92	0.51
38:2g:108:ALA:O	38:2g:119:ARG:HD2	2.10	0.51
43:2l:86:ARG:NH1	62:2l:302:HOH:O	2.43	0.51
44:2m:85:GLY:HA2	44:2m:93:ARG:HH21	1.76	0.51
54:2w:68:C:H2'	54:2w:69:G:H8	1.75	0.51
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.45	0.51
10:1O:104:ARG:CZ	15:1T:34:VAL:HG11	2.41	0.51
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.92	0.51
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.59	0.51
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.58	0.51
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.44	0.51
5:2F:33:LEU:HD22	5:2F:112:MET:HE3	1.93	0.51
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.11	0.51
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.93	0.51
31:29:15:LYS:HD3	31:29:26:ILE:HD11	1.93	0.51
32:2a:201:C:H5'	32:2a:202:U:OP2	2.10	0.51
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.92	0.51
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.46	0.51
21:1Z:93:ASP:HB2	21:1Z:131:ARG:HH12	1.76	0.51
32:1a:1004:A:H5''	32:1a:1025:U:C5	2.44	0.51
41:1j:38:ILE:CG1	41:1j:71:LEU:HB3	2.41	0.51
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.44	0.51
1:2A:892:G:H3'	1:2A:893:C:H5''	1.93	0.51
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:131:ARG:HE	34:2c:135:LYS:NZ	2.08	0.51
42:2k:48:ILE:O	42:2k:50:TYR:N	2.44	0.51
1:1A:536:A:H2'	1:1A:537:C:C6	2.46	0.51
1:1A:880:G:H2'	1:1A:881:G:C8	2.45	0.51
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.11	0.51
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.45	0.51
40:1i:19:LEU:HD21	40:1i:81:ILE:HG13	1.92	0.51
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.93	0.51
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.93	0.51
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.46	0.51
6:2G:53:LEU:HD12	6:2G:56:ALA:HB2	1.93	0.51
10:2O:120:GLU:HG2	10:2O:122:LEU:HG	1.93	0.51
23:21:83:GLU:OE2	23:21:83:GLU:N	2.44	0.51
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.38	0.51
32:2a:1216:G:H5''	45:2n:5:ALA:HB2	1.93	0.51
38:2g:78:ARG:HG3	38:2g:156:TRP:HZ3	1.76	0.51
6:1G:83:ARG:O	6:1G:86:MET:HG3	2.11	0.51
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.11	0.51
20:1Y:8:LYS:HD3	20:1Y:97:ARG:NH1	2.26	0.51
31:19:2:LYS:HE2	31:19:31:LYS:O	2.10	0.51
32:1a:600:C:H2'	32:1a:601:C:C6	2.46	0.51
33:1b:15:VAL:HB	33:1b:209:ARG:HG3	1.93	0.51
1:2A:236:C:H2'	1:2A:237:C:H6	1.76	0.51
1:2A:2134:A:O2'	1:2A:2159:G:N2	2.43	0.51
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.46	0.51
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.44	0.51
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.25	0.51
32:2a:1002:G:N3	32:2a:1003:G:H1'	2.26	0.51
56:2y:18:G:N2	56:2y:55:PSU:C4	2.75	0.51
1:1A:671:C:N4	62:1A:4404:HOH:O	2.44	0.50
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.26	0.50
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.27	0.50
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.25	0.50
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.26	0.50
33:1b:17:PHE:HB3	33:1b:44:LEU:HD11	1.92	0.50
36:1e:85:GLY:O	36:1e:87:SER:N	2.40	0.50
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.46	0.50
1:2A:443:A:H5''	1:2A:444:C:OP1	2.11	0.50
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.46	0.50
1:2A:995:C:O2	9:2N:3:THR:OG1	2.29	0.50
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2407:G:N7	62:2A:3844:HOH:O	2.34	0.50
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.45	0.50
3:2D:253:GLN:HG3	62:2D:410:HOH:O	2.11	0.50
7:2H:33:LEU:HD21	7:2H:136:ILE:HG13	1.93	0.50
12:2Q:38:GLU:HB2	12:2Q:127:ILE:HG22	1.93	0.50
30:28:58:ILE:HA	30:28:61:LEU:HD12	1.94	0.50
32:2a:376:G:H5''	47:2p:5:ARG:HD2	1.93	0.50
32:2a:1321:C:O2'	50:2s:77:THR:HG21	2.12	0.50
32:2a:1347:G:H22	32:2a:1374:A:P	2.34	0.50
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.45	0.50
32:1a:45:U:H2'	32:1a:46:G:C8	2.46	0.50
32:1a:222:U:H2'	32:1a:223:U:C6	2.46	0.50
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.94	0.50
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.76	0.50
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.10	0.50
5:2F:110:LEU:HD21	5:2F:181:LEU:HD23	1.93	0.50
7:2H:101:ARG:HH12	7:2H:122:THR:HG23	1.77	0.50
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.76	0.50
34:2c:20:SER:HB3	34:2c:22:TRP:HE1	1.76	0.50
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	1.93	0.50
42:2k:33:THR:HG22	42:2k:39:PRO:HA	1.93	0.50
50:2s:53:ASN:OD1	50:2s:54:GLY:N	2.45	0.50
1:1A:388:G:O2'	1:1A:389:G:N7	2.39	0.50
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.10	0.50
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.47	0.50
8:1I:116:LEU:HD21	8:1I:119:PRO:HA	1.93	0.50
18:1W:82:LEU:HD22	18:1W:84:ARG:HH22	1.76	0.50
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.94	0.50
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.36	0.50
1:2A:286:C:H2'	1:2A:287:C:C6	2.46	0.50
1:2A:2407:G:OP1	62:2A:3844:HOH:O	2.19	0.50
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.11	0.50
32:2a:524:G:H2'	32:2a:525:C:C6	2.47	0.50
32:2a:1124:G:H4'	41:2j:38:ILE:HD13	1.93	0.50
41:2j:36:GLY:O	41:2j:38:ILE:HG12	2.12	0.50
1:1A:326:G:N7	62:1A:4314:HOH:O	2.34	0.50
1:1A:1087:G:H2'	1:1A:1089:G:C8	2.46	0.50
32:1a:399:G:H2'	32:1a:400:C:C6	2.47	0.50
32:1a:458:C:H2'	32:1a:460:G:O4'	2.12	0.50
32:1a:953:G:H5'	32:1a:965:A:N6	2.24	0.50
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:176:ILE:HB	4:2E:181:LEU:HB2	1.94	0.50
6:2G:98:ARG:NH1	26:24:1:MET:SD	2.84	0.50
16:2U:65:ILE:HD11	16:2U:95:LEU:HB3	1.93	0.50
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.11	0.50
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.46	0.50
1:1A:2762:G:OP2	62:1A:4242:HOH:O	2.20	0.50
11:1P:64:LYS:HE3	30:18:12:LYS:HD3	1.94	0.50
32:1a:708:C:H2'	32:1a:709:G:H8	1.76	0.50
32:1a:858:G:OP2	62:1a:1914:HOH:O	2.19	0.50
32:1a:1108:G:O6	62:1a:1910:HOH:O	2.18	0.50
1:2A:1654:A:OP1	13:2R:1:MET:N	2.33	0.50
1:2A:2135:A:C8	1:2A:2136:C:H5	2.30	0.50
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.10	0.50
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.46	0.50
25:23:39:ASP:OD1	25:23:44:ARG:NH1	2.44	0.50
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.11	0.50
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.26	0.50
47:2p:1:MET:O	47:2p:24:ALA:N	2.43	0.50
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.12	0.50
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.12	0.50
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.93	0.50
44:1m:40:ASN:O	44:1m:43:THR:OG1	2.29	0.50
54:1w:5:G:H2'	54:1w:6:G:H8	1.75	0.50
1:2A:1359:A:H2	1:2A:1372:U:O4	1.93	0.50
7:2H:160:LYS:N	7:2H:163:TYR:OH	2.42	0.50
32:2a:664:G:N2	32:2a:741:G:H1	2.09	0.50
32:2a:973:G:H3'	32:2a:974:A:H5''	1.93	0.50
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.47	0.50
33:2b:163:PHE:CD1	33:2b:185:ILE:HG13	2.47	0.50
35:2d:10:ARG:HG3	35:2d:11:LEU:HD12	1.94	0.50
40:2i:3:GLN:HE21	40:2i:20:ARG:HE	1.60	0.50
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.45	0.50
54:2w:8:4SU:S4	54:2w:14:A:N7	2.85	0.50
55:2x:55:PSU:O2'	55:2x:57:A:N7	2.39	0.50
56:2y:55:PSU:N1	56:2y:57:G:H5''	2.15	0.50
1:1A:2182:G:H2'	1:1A:2183:C:C6	2.47	0.50
14:1S:39:ILE:HB	14:1S:49:VAL:HG12	1.94	0.50
25:13:4:LEU:O	25:13:36:VAL:HA	2.12	0.50
32:1a:60:A:N1	32:1a:107:G:O2'	2.40	0.50
55:1x:23:C:H2'	55:1x:24:U:C6	2.47	0.50
2:2B:48:A:P	14:2S:30:ARG:HH22	2.33	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.94	0.50
26:24:41:PRO:HG3	26:24:49:PHE:CE1	2.46	0.50
32:2a:923:A:O2'	32:2a:1399:C:OP2	2.29	0.50
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.45	0.50
33:2b:55:PHE:HD1	33:2b:58:ILE:HD11	1.74	0.50
39:2h:34:GLU:OE1	39:2h:37:ARG:NH1	2.45	0.50
45:2n:18:VAL:O	45:2n:20:ALA:N	2.36	0.50
56:2y:18:G:N1	56:2y:55:PSU:C4	2.80	0.50
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.77	0.50
15:1T:127:ALA:C	15:1T:129:ARG:H	2.20	0.50
42:1k:62:GLN:HB2	42:1k:93:GLN:HE21	1.76	0.50
1:2A:774:A:H2'	1:2A:774:A:N3	2.27	0.50
1:2A:859:G:O2'	1:2A:916:G:O6	2.28	0.50
1:2A:921:G:O6	62:2A:3838:HOH:O	2.18	0.50
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.28	0.50
1:2A:2336:A:H61	22:20:43:THR:HG22	1.77	0.50
1:2A:2482:G:HO2'	54:2w:64:A:HO2'	1.60	0.50
32:2a:920:U:H2'	32:2a:921:U:C6	2.47	0.50
32:2a:984:C:H2'	32:2a:985:C:C6	2.47	0.50
32:2a:1325:C:OP1	52:2u:15:ARG:NH1	2.45	0.50
40:2i:3:GLN:HG3	40:2i:20:ARG:HG2	1.92	0.50
1:1A:272(J):C:H2'	1:1A:274:G:C8	2.46	0.50
1:1A:637:A:H4'	1:1A:638:G:O5'	2.12	0.50
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.46	0.50
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.93	0.50
33:1b:8:LYS:O	33:1b:217:ARG:NH1	2.45	0.50
54:1w:63:G:H2'	54:1w:64:A:C8	2.47	0.50
1:2A:570:G:H2'	1:2A:2030:A:C5	2.47	0.50
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.11	0.50
1:2A:893:C:H2'	1:2A:894:C:C4	2.47	0.50
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.44	0.50
21:2Z:145:GLU:HB3	21:2Z:148:ASP:HB2	1.94	0.50
32:2a:300:A:O2'	32:2a:564:C:N3	2.42	0.50
32:2a:1397:C:OP2	36:2e:24:ARG:NH2	2.45	0.50
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.47	0.49
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.41	0.49
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	1.93	0.49
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	1.93	0.49
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.45	0.49
40:1i:49:PRO:HD3	40:1i:78:LYS:HG3	1.94	0.49
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:1y:51:U:H2'	56:1y:52:G:C8	2.47	0.49
1:2A:287:C:H2'	1:2A:288:C:H6	1.77	0.49
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.29	0.49
1:2A:2096:U:H2'	1:2A:2097:C:C6	2.47	0.49
4:2E:48:GLN:HA	4:2E:80:GLU:HA	1.94	0.49
7:2H:80:SER:OG	7:2H:81:GLU:OE2	2.17	0.49
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	1.94	0.49
16:2U:91:ASP:O	16:2U:95:LEU:HB2	2.12	0.49
19:2X:60:ARG:HH12	29:27:47:ARG:HH12	1.59	0.49
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.77	0.49
33:2b:91:PRO:HG3	33:2b:154:LEU:HB2	1.93	0.49
54:2w:34:G:H2'	54:2w:35:A:C8	2.46	0.49
1:1A:831:G:N2	11:1P:53:GLY:O	2.45	0.49
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.47	0.49
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.94	0.49
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.77	0.49
1:2A:2171:A:H1'	1:2A:2172:U:C6	2.46	0.49
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.93	0.49
14:2S:11:LYS:O	14:2S:15:ARG:HB2	2.13	0.49
25:23:40:THR:HG22	25:23:42:ALA:H	1.77	0.49
38:2g:29:LYS:HB3	38:2g:105:VAL:HG21	1.94	0.49
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.47	0.49
40:2i:28:VAL:HB	40:2i:63:ILE:HB	1.94	0.49
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.94	0.49
11:1P:98:GLU:O	11:1P:101:VAL:HG12	2.12	0.49
47:1p:19:ILE:N	47:1p:37:GLY:O	2.41	0.49
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.47	0.49
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.94	0.49
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	1.95	0.49
7:2H:20:ALA:HB3	7:2H:23:ARG:HG2	1.94	0.49
15:2T:118:ARG:HG2	32:2a:1442(A):G:C8	2.47	0.49
26:24:50:VAL:HG21	44:2m:64:TRP:C	2.37	0.49
32:2a:1224:G:OP1	62:2a:1916:HOH:O	2.20	0.49
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.47	0.49
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.77	0.49
1:1A:2629:A:H1'	1:1A:2630:G:H5''	1.95	0.49
34:1c:179:ARG:HG3	34:1c:206:GLU:HB3	1.93	0.49
35:1d:30:LYS:HA	35:1d:35:ARG:NH1	2.27	0.49
1:2A:804:A:OP1	62:2A:3843:HOH:O	2.19	0.49
1:2A:832:G:H5'	11:2P:45:LEU:HD11	1.93	0.49
1:2A:1496:A:N3	1:2A:1577:C:O2'	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1264:C:N4	32:2a:1265:G:O6	2.46	0.49
50:2s:80:TYR:C	50:2s:82:GLY:H	2.20	0.49
1:1A:251:A:C5	1:1A:252:G:H1'	2.47	0.49
1:1A:1364:G:P	23:11:3:LYS:HG3	2.52	0.49
6:1G:111:LEU:HA	6:1G:114:ILE:HD12	1.95	0.49
32:1a:1179:A:H4'	40:1i:103:THR:HA	1.93	0.49
42:1k:34:ASP:HB2	42:1k:35:PRO:HD2	1.94	0.49
42:1k:87:THR:O	42:1k:87:THR:OG1	2.29	0.49
1:2A:579:G:H2'	1:2A:580:C:C6	2.48	0.49
1:2A:2379:G:HO2'	14:2S:17:ARG:HH12	1.55	0.49
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.29	0.49
4:2E:101:ARG:HB2	4:2E:201:THR:HG21	1.94	0.49
32:2a:328:C:H4'	32:2a:329:A:H5'	1.95	0.49
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.13	0.49
1:1A:55:G:O2'	1:1A:127:A:N1	2.42	0.49
1:1A:839:U:H1'	1:1A:1191:G:H1'	1.95	0.49
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.45	0.49
44:1m:14:ARG:NH2	44:1m:16:ASP:OD2	2.32	0.49
14:2S:3:ARG:NH1	14:2S:4:LEU:H	2.10	0.49
32:2a:1376:U:P	38:2g:94:ARG:HH22	2.35	0.49
34:2c:88:ARG:HA	34:2c:91:LEU:HD13	1.95	0.49
35:2d:153:ARG:HA	35:2d:158:ILE:HD11	1.93	0.49
1:1A:86:C:H4'	1:1A:104:U:H1'	1.95	0.49
1:1A:1068:G:O2'	1:1A:1070:A:N7	2.44	0.49
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.11	0.49
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.30	0.49
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.47	0.49
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.43	0.49
32:1a:692:U:H5'	32:1a:797:C:H5'	1.94	0.49
1:2A:176:G:O2'	1:2A:177:G:H5'	2.13	0.49
6:2G:3:LEU:HD23	26:24:25:TYR:CZ	2.47	0.49
32:2a:130:A:H5'	48:2q:63:ARG:HH11	1.77	0.49
32:2a:1346:A:H61	32:2a:1374:A:H3'	1.78	0.49
33:2b:16:HIS:O	33:2b:18:GLY:N	2.46	0.49
36:2e:100:VAL:HG13	36:2e:118:ILE:HG22	1.93	0.49
1:1A:1243:G:O2'	11:1P:7:ARG:NH2	2.46	0.49
1:1A:2748:A:H5'	7:1H:4:ILE:HD12	1.95	0.49
32:1a:7:G:H5'	32:1a:298:A:O4'	2.12	0.49
33:1b:15:VAL:HG21	33:1b:213:LEU:HD23	1.94	0.49
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.42	0.49
36:1e:81:GLU:HG2	36:1e:90:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:50:GLU:HG2	51:1t:100:ILE:HD13	1.94	0.49
1:2A:55:G:O2'	1:2A:127:A:N1	2.41	0.49
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.48	0.49
1:2A:910:A:N1	1:2A:2277:G:H1'	2.27	0.49
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.48	0.49
12:2Q:1:MET:HG2	12:2Q:44:ALA:HB1	1.95	0.49
26:24:60:GLN:O	26:24:62:ARG:NH1	2.45	0.49
39:2h:51:VAL:HG21	39:2h:60:ARG:HB2	1.95	0.49
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.13	0.49
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.46	0.49
1:1A:1851:U:H2'	1:1A:1852:C:O4'	2.13	0.49
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.47	0.49
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	1.95	0.49
1:2A:884:C:H3'	1:2A:885:C:C6	2.48	0.49
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.13	0.49
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.46	0.49
4:2E:50:GLY:HA3	4:2E:75:VAL:HG21	1.94	0.49
7:2H:70:THR:O	7:2H:74:ASN:ND2	2.46	0.49
28:26:10:LEU:HB2	28:26:52:VAL:HG13	1.94	0.49
32:2a:573:A:N3	32:2a:883:C:O2'	2.46	0.49
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.46	0.49
32:2a:909:A:H2'	32:2a:910:C:O4'	2.12	0.49
32:2a:1256:A:O3'	32:2a:1257:U:H4'	2.12	0.49
44:2m:10:PRO:HD2	44:2m:18:ALA:HB1	1.95	0.49
1:1A:295:G:H4'	20:1Y:1:MET:HE3	1.95	0.49
1:1A:1252:G:N3	16:1U:33:ARG:HG2	2.28	0.49
4:1E:101:ARG:HB2	4:1E:201:THR:HG21	1.95	0.49
32:1a:1025:U:C2	32:1a:1036:G:O6	2.66	0.49
32:1a:1096:C:OP2	62:1a:1915:HOH:O	2.20	0.49
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.48	0.49
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.48	0.49
5:2F:20:LEU:HG	5:2F:21:ALA:H	1.77	0.49
6:2G:31:VAL:HG22	6:2G:32:PRO:HD2	1.94	0.49
9:2N:38:HIS:NE2	9:2N:50:ASP:OD2	2.44	0.49
32:2a:1146:A:H2'	32:2a:1147:C:O4'	2.13	0.49
37:2f:91:VAL:HG11	49:2r:72:ARG:NH1	2.28	0.49
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.95	0.49
54:2w:18:G:HO2'	54:2w:57:G:H22	1.53	0.49
1:1A:642:G:N2	1:1A:645:C:OP2	2.45	0.48
7:1H:77:LYS:HE3	7:1H:83:TYR:CE1	2.48	0.48
51:1t:99:LEU:HA	51:1t:100:ILE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:500:G:N1	1:2A:503:A:OP2	2.45	0.48
1:2A:892:G:H3'	1:2A:893:C:C5'	2.43	0.48
8:2I:26:ALA:HA	8:2I:30:LEU:HB2	1.94	0.48
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.13	0.48
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.94	0.48
26:24:24:THR:OG1	26:24:25:TYR:N	2.46	0.48
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.78	0.48
55:2x:61:C:H2'	55:2x:62:C:C6	2.47	0.48
1:1A:271(L):U:OP1	8:1I:50:ARG:NH1	2.46	0.48
1:1A:695:G:OP1	1:1A:1380:G:O2'	2.25	0.48
1:1A:1068:G:H1'	1:1A:1096:A:N3	2.28	0.48
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	1.95	0.48
16:1U:47:TYR:HA	16:1U:50:ARG:NH2	2.28	0.48
32:1a:973:G:H3'	32:1a:974:A:H5''	1.96	0.48
33:1b:174:VAL:O	33:1b:178:ARG:HG2	2.13	0.48
50:1s:27:GLU:HG3	50:1s:28:LYS:HE3	1.96	0.48
1:2A:2655:G:O2'	1:2A:2664:G:O6	2.27	0.48
8:2I:124:GLY:H	8:2I:144:VAL:HG23	1.77	0.48
14:2S:11:LYS:HG3	14:2S:91:PRO:HB3	1.94	0.48
21:2Z:73:GLN:O	21:2Z:87:ASP:N	2.46	0.48
21:2Z:138:GLU:HB2	21:2Z:156:LYS:HD3	1.95	0.48
26:24:15:ILE:HB	26:24:32:TYR:HD1	1.78	0.48
32:2a:674:G:N2	32:2a:717:C:O2	2.47	0.48
32:2a:922:G:O5'	36:2e:20:GLN:NE2	2.46	0.48
32:2a:1485:U:H2'	32:2a:1486:G:H8	1.77	0.48
34:2c:35:GLU:O	34:2c:39:ILE:HG12	2.13	0.48
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.95	0.48
1:1A:264:C:O2'	1:1A:265:A:H2'	2.13	0.48
1:1A:862:G:H2'	1:1A:863:A:O4'	2.14	0.48
1:1A:1903:G:OP1	3:1D:241:PRO:HB2	2.14	0.48
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.48	0.48
32:1a:841:U:C4	32:1a:848:C:H1'	2.48	0.48
33:1b:78:GLN:HE21	33:1b:95:GLN:HA	1.78	0.48
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.48	0.48
6:2G:25:TYR:CD2	6:2G:31:VAL:HG23	2.48	0.48
8:2I:82:ARG:NH2	8:2I:90:GLY:H	2.10	0.48
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.53	0.48
32:2a:662:G:H2'	32:2a:663:A:C8	2.48	0.48
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.80	0.48
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.48	0.48
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:15:G:H2'	55:2x:59:A:N1	2.28	0.48
4:1E:47:VAL:HG22	4:1E:84:PHE:O	2.12	0.48
8:1I:5:LEU:H	8:1I:5:LEU:HD12	1.79	0.48
32:1a:583:A:N6	32:1a:758:G:O2'	2.47	0.48
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.95	0.48
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.77	0.48
2:2B:66:A:N6	2:2B:108:U:H3'	2.29	0.48
39:2h:51:VAL:HG12	39:2h:52:ASP:H	1.78	0.48
54:2w:51:U:H2'	54:2w:52:G:H8	1.79	0.48
1:1A:2118:U:H4'	1:1A:2119:A:OP1	2.14	0.48
1:1A:2336:A:H61	22:10:43:THR:CG2	2.25	0.48
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.47	0.48
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.47	0.48
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.47	0.48
4:1E:119:ARG:HD2	4:1E:160:TYR:HB2	1.95	0.48
5:1F:31:HIS:NE2	5:1F:35:GLU:OE2	2.46	0.48
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.60	0.48
33:1b:158:LEU:HD22	33:1b:182:ILE:HD11	1.96	0.48
48:1q:12:SER:HB3	48:1q:20:THR:HB	1.95	0.48
1:2A:320:A:H4'	1:2A:322:A:N7	2.28	0.48
1:2A:413:C:OP2	62:2A:3845:HOH:O	2.20	0.48
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.39	0.48
2:2B:2:C:H2'	2:2B:3:C:H6	1.78	0.48
11:2P:29:LYS:HG3	11:2P:30:THR:N	2.27	0.48
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.25	0.48
32:2a:833:U:H2'	32:2a:834:C:C6	2.49	0.48
33:2b:21:ARG:HA	33:2b:39:ILE:HG23	1.94	0.48
37:2f:30:LEU:HD23	37:2f:75:LEU:HD11	1.94	0.48
44:2m:122:LYS:HG3	44:2m:123:ALA:H	1.78	0.48
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.93	0.48
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.38	0.48
9:1N:17:ASP:O	9:1N:21:LYS:HE2	2.14	0.48
32:1a:165:C:H2'	32:1a:166:G:C8	2.47	0.48
33:1b:55:PHE:CD1	33:1b:221:LEU:HD22	2.49	0.48
44:1m:16:ASP:OD1	44:1m:16:ASP:N	2.46	0.48
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.78	0.48
1:2A:360:G:OP1	62:2A:3848:HOH:O	2.20	0.48
1:2A:602:G:N1	1:2A:655:A:OP2	2.42	0.48
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.49	0.48
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.26	0.48
1:2A:2506:U:O2'	54:2w:76:F3N:H4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.48	0.48
8:2I:65:ALA:HB1	8:2I:132:PRO:HG2	1.95	0.48
10:2O:98:VAL:HG13	10:2O:117:LEU:HB3	1.95	0.48
32:2a:447:G:O6	32:2a:485:G:O2'	2.26	0.48
32:2a:757:U:H2'	32:2a:758:G:O4'	2.14	0.48
32:2a:1005:A:H5''	32:2a:1006:C:C5	2.49	0.48
35:2d:149:ALA:O	35:2d:153:ARG:HG3	2.14	0.48
35:2d:150:GLU:H	35:2d:150:GLU:CD	2.22	0.48
1:1A:910:A:N1	1:1A:2277:G:H1'	2.28	0.48
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.36	0.48
1:1A:2277:G:OP2	22:10:10:THR:HG21	2.14	0.48
32:1a:79:G:C6	32:1a:90:U:O2	2.66	0.48
32:1a:576:G:O6	32:1a:880:C:O2'	2.30	0.48
45:1n:6:LEU:HB3	45:1n:23:ARG:NH2	2.28	0.48
1:2A:992:C:OP1	16:2U:47:TYR:OH	2.22	0.48
1:2A:1024:G:OP2	62:2A:3849:HOH:O	2.20	0.48
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.49	0.48
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.49	0.48
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.30	0.48
32:2a:653:A:OP1	39:2h:56:LYS:NZ	2.42	0.48
50:2s:11:VAL:HG12	50:2s:13:ASP:H	1.78	0.48
1:1A:818:G:H5'	1:1A:839:U:OP1	2.13	0.48
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.78	0.48
1:1A:1077:A:H2'	1:1A:1078:U:H4'	1.96	0.48
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.14	0.48
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.49	0.48
1:2A:479:A:H4'	1:2A:480:A:OP1	2.14	0.48
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.13	0.48
32:2a:1002:G:C6	32:2a:1003:G:H8	2.31	0.48
1:1A:484:C:H2'	1:1A:485:C:C6	2.49	0.48
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.49	0.48
5:1F:9:ILE:HD12	5:1F:123:LEU:HD23	1.96	0.48
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.95	0.48
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	1.95	0.48
16:1U:85:LYS:HE3	16:1U:116:ALA:O	2.14	0.48
21:1Z:8:TYR:HB2	21:1Z:38:TYR:CE2	2.49	0.48
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.96	0.48
48:1q:26:GLN:HG2	48:1q:37:LYS:HG2	1.94	0.48
1:2A:121:G:H4'	1:2A:149:A:H5'	1.95	0.48
1:2A:271(K):U:C2	8:2I:50:ARG:HD3	2.49	0.48
1:2A:342:G:O6	62:2A:3847:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.27	0.48
8:2I:72:LEU:HD23	8:2I:75:LEU:HD22	1.96	0.48
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.96	0.48
32:2a:107:G:H2'	32:2a:108:G:O4'	2.13	0.48
32:2a:984:C:H2'	32:2a:985:C:H6	1.79	0.48
32:2a:1221:G:H4'	50:2s:53:ASN:O	2.13	0.48
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	1.95	0.48
36:2e:7:GLU:CD	36:2e:37:ARG:HH21	2.22	0.48
39:2h:35:ILE:O	39:2h:39:LEU:HD12	2.14	0.48
50:2s:27:GLU:HB3	50:2s:28:LYS:HD3	1.95	0.48
1:1A:684:G:OP1	29:17:16:HIS:ND1	2.47	0.48
21:1Z:72:ARG:HD3	21:1Z:72:ARG:HA	1.64	0.48
33:1b:131:PRO:O	33:1b:135:GLN:N	2.47	0.48
33:1b:163:PHE:CD1	33:1b:185:ILE:HG13	2.49	0.48
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.47	0.48
56:1y:40:C:H2'	56:1y:41:C:C6	2.48	0.48
56:1y:53:G:H1	56:1y:61:C:H42	1.61	0.48
1:2A:31:C:OP1	62:2A:3846:HOH:O	2.20	0.48
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.11	0.48
1:2A:242:G:C8	30:28:5:LYS:HG2	2.49	0.48
1:2A:602:G:O2'	1:2A:655:A:N6	2.47	0.48
8:2I:5:LEU:HD22	8:2I:9:LEU:HD13	1.95	0.48
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.79	0.48
32:2a:664:G:P	49:2r:64:ARG:HH21	2.37	0.48
56:2y:48:C:H5'	56:2y:49:C:OP1	2.13	0.48
1:1A:2864:G:OP1	15:1T:119:LYS:HD2	2.14	0.47
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.95	0.47
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.49	0.47
26:14:44:THR:O	26:14:46:GLN:N	2.47	0.47
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.13	0.47
32:1a:1182:G:H5'	32:1a:1184:G:H5'	1.96	0.47
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.14	0.47
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.29	0.47
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.46	0.47
1:2A:534:U:H5'	16:2U:42:ALA:HB1	1.94	0.47
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.96	0.47
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.49	0.47
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.14	0.47
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.40	0.47
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.49	0.47
9:2N:35:ARG:HD3	9:2N:37:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:39:PSU:H2'	54:2w:40:C:C6	2.49	0.47
1:1A:752:A:H3'	29:17:1:MET:HE1	1.95	0.47
32:1a:737:A:H2'	32:1a:738:C:C6	2.48	0.47
1:2A:76:C:O3'	24:22:59:ARG:HG3	2.13	0.47
1:2A:775:G:O3'	62:2A:3850:HOH:O	2.20	0.47
1:2A:1639:U:H2'	1:2A:1640:C:H5''	1.96	0.47
1:2A:1889:A:N1	1:2A:2234:G:HI'	2.30	0.47
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.49	0.47
1:2A:2831:G:OP1	1:2A:2834:G:H4'	2.15	0.47
8:2I:59:ALA:HA	8:2I:62:LYS:HE2	1.96	0.47
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.53	0.47
10:2O:68:GLU:HB3	10:2O:78:ARG:HD3	1.96	0.47
32:2a:1073:U:O2'	33:2b:104:ASN:OD1	2.32	0.47
32:2a:1256:A:H61	32:2a:1278:U:C2'	2.27	0.47
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	1.96	0.47
1:1A:279:C:H42	1:1A:361:G:H1	1.61	0.47
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.97	0.47
9:1N:73:THR:OG1	9:1N:82:LEU:HD11	2.14	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.58	0.47
32:1a:97:G:H2'	32:1a:98:G:O4'	2.14	0.47
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.31	0.47
38:1g:111:ARG:HD2	38:1g:123:GLU:HB2	1.96	0.47
40:1i:55:ALA:HB1	40:1i:58:HIS:HB2	1.96	0.47
56:1y:51:U:H2'	56:1y:52:G:H8	1.79	0.47
1:2A:375:C:H2'	1:2A:376:C:C6	2.50	0.47
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.49	0.47
32:2a:719:C:N4	49:2r:71:LYS:HE2	2.29	0.47
32:2a:1162:C:H2'	32:2a:1163:C:H6	1.78	0.47
1:1A:322:A:OP1	5:1F:168:ARG:HD3	2.14	0.47
1:1A:1005:C:H5''	62:1A:4999:HOH:O	2.14	0.47
19:1X:94:GLY:N	19:1X:95:LEU:HB2	2.26	0.47
32:1a:406:G:N2	35:1d:119:GLN:HE22	2.12	0.47
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.15	0.47
32:1a:975:A:H5'	32:1a:975:A:H8	1.79	0.47
34:1c:71:ALA:HA	34:1c:106:VAL:HG21	1.96	0.47
35:1d:172:PRO:C	35:1d:174:LEU:H	2.22	0.47
1:2A:340:A:H2'	1:2A:341:G:O4'	2.14	0.47
1:2A:884:C:H3'	1:2A:885:C:H6	1.80	0.47
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.12	0.47
1:2A:1815:A:H8	1:2A:1815:A:OP1	1.97	0.47
2:2B:88:C:H2'	2:2B:89:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:12:LEU:HD12	5:2F:124:LEU:HD11	1.95	0.47
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.25	0.47
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.47	0.47
32:2a:67:C:H2'	32:2a:68:G:C8	2.50	0.47
32:2a:1029:C:N4	32:2a:1032:G:C6	2.82	0.47
32:2a:1227:A:OP2	44:2m:111:LYS:HD3	2.14	0.47
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.49	0.47
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.47	0.47
47:2p:71:ARG:HA	47:2p:74:LEU:HB2	1.96	0.47
1:1A:226:G:H21	1:1A:228:A:H62	1.62	0.47
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.80	0.47
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.78	0.47
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.15	0.47
32:1a:78:G:O2'	32:1a:79:G:O5'	2.31	0.47
32:1a:447:G:O6	32:1a:485:G:O2'	2.27	0.47
38:1g:140:ASP:OD1	56:1y:41:C:O2'	2.32	0.47
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.97	0.47
1:2A:657:U:H2'	1:2A:658:C:C6	2.49	0.47
1:2A:1607:C:H5''	1:2A:1608:A:H5'	1.96	0.47
32:2a:1130:A:H5''	40:2i:18:PHE:CE2	2.49	0.47
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.15	0.47
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.95	0.47
36:2e:68:GLU:HG2	36:2e:70:PRO:HD3	1.96	0.47
44:2m:23:TYR:HE2	44:2m:70:LEU:HD22	1.80	0.47
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.49	0.47
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.79	0.47
32:1a:381:C:H2'	32:1a:382:A:O4'	2.14	0.47
33:1b:95:GLN:NE2	33:1b:147:LYS:HE2	2.25	0.47
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.15	0.47
48:1q:31:LEU:HD23	48:1q:32:TYR:CZ	2.50	0.47
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.28	0.47
1:2A:2133:G:HO2'	1:2A:2157:G:N2	2.12	0.47
7:2H:84:SER:OG	7:2H:132:ARG:NH1	2.47	0.47
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.95	0.47
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.48	0.47
51:2t:16:HIS:O	51:2t:19:SER:OG	2.30	0.47
54:2w:11:C:H2'	54:2w:12:U:C6	2.49	0.47
1:1A:10:G:O2'	1:1A:2801(A):A:N7	2.41	0.47
1:1A:484:C:OP1	20:1Y:51:VAL:HG22	2.14	0.47
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.30	0.47
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:176:ILE:HB	4:1E:181:LEU:HB2	1.96	0.47
15:1T:27:THR:HG22	15:1T:89:VAL:HB	1.97	0.47
15:1T:118:ARG:HG2	32:1a:1442(A):G:C8	2.50	0.47
28:16:26:ASN:HD21	28:16:28:ARG:NH2	2.13	0.47
32:1a:78:G:N1	32:1a:91:C:C4	2.83	0.47
32:1a:826:C:H2'	32:1a:827:U:C6	2.50	0.47
32:1a:1039:C:H2'	32:1a:1040:U:H6	1.80	0.47
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.96	0.47
33:1b:60:ASP:O	33:1b:64:ARG:HG2	2.14	0.47
34:1c:66:VAL:HG11	34:1c:91:LEU:HD21	1.97	0.47
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.97	0.47
38:1g:78:ARG:HD3	38:1g:80:VAL:HG23	1.96	0.47
40:1i:8:GLY:O	40:1i:15:ALA:N	2.48	0.47
43:1l:60:LEU:HD12	43:1l:64:TYR:HB2	1.95	0.47
1:2A:686:G:N2	1:2A:788:A:H61	2.12	0.47
1:2A:1426:G:OP2	1:2A:1427:A:O2'	2.32	0.47
2:2B:60:C:H2'	2:2B:61:G:C8	2.50	0.47
9:2N:4:TYR:HB2	16:2U:101:ARG:NH1	2.29	0.47
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.80	0.47
13:2R:57:ARG:HH22	13:2R:61:HIS:HD2	1.63	0.47
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.14	0.47
19:2X:5:TYR:CE2	24:22:30:ARG:HB2	2.50	0.47
19:2X:94:GLY:N	19:2X:95:LEU:HB2	2.29	0.47
32:2a:520:A:N1	32:2a:536:C:H1'	2.29	0.47
32:2a:936:C:H2'	32:2a:937:A:O4'	2.15	0.47
32:2a:1005:A:H1'	32:2a:1025:U:H3	1.79	0.47
32:2a:1029:C:H1'	32:2a:1033:G:N2	2.30	0.47
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.47	0.47
34:2c:131:ARG:NH2	36:2e:50:GLU:HG3	2.30	0.47
35:2d:22:LYS:HG3	61:2d:303:SF4:S4	2.55	0.47
40:2i:31:GLN:HB2	40:2i:36:TYR:HB2	1.96	0.47
41:2j:6:ILE:HG12	41:2j:98:ILE:HG22	1.96	0.47
43:2l:117:ARG:NH1	43:2l:124:LYS:HG3	2.30	0.47
54:2w:43:C:H2'	54:2w:44:G:C8	2.49	0.47
1:1A:284:U:H2'	1:1A:285:C:C6	2.49	0.47
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.14	0.47
32:1a:96:U:H2'	32:1a:97:G:C8	2.50	0.47
32:1a:390:C:H2'	32:1a:391:G:C8	2.50	0.47
32:1a:555:C:H2'	32:1a:556:C:C6	2.50	0.47
32:1a:1036:G:H3'	32:1a:1037:C:C6	2.50	0.47
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:1y:55:PSU:C4	56:1y:57:G:H5'	2.50	0.47
10:2O:2:ILE:HB	10:2O:33:ALA:HB3	1.95	0.47
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.45	0.47
21:2Z:30:ASN:HA	21:2Z:89:PHE:CE1	2.50	0.47
32:2a:392:G:OP1	47:2p:8:ARG:NH2	2.42	0.47
33:2b:114:ARG:HA	33:2b:117:GLU:HB2	1.97	0.47
34:2c:47:LEU:HD12	34:2c:68:VAL:HG11	1.97	0.47
1:1A:1108:U:H2'	1:1A:1109:C:O4'	2.14	0.47
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.49	0.47
5:1F:135:LYS:HB2	5:1F:138:GLU:HG3	1.97	0.47
25:13:55:ARG:NH2	25:13:57:GLU:HB2	2.29	0.47
32:1a:250:A:H4'	32:1a:251:G:O5'	2.15	0.47
32:1a:413:G:N2	32:1a:428:G:H1'	2.30	0.47
1:2A:848:G:H2'	1:2A:849:A:C8	2.50	0.47
2:2B:42:C:O2'	6:2G:66:GLN:HG2	2.15	0.47
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.30	0.47
32:2a:1236:A:O2'	32:2a:1304:G:H4'	2.15	0.47
32:2a:1239:A:H4'	32:2a:1240:U:H5'	1.97	0.47
1:1A:881:G:C2	1:1A:882:G:H1'	2.50	0.47
1:1A:1078:U:H5'	1:1A:1079:C:OP1	2.15	0.47
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.15	0.47
1:1A:2319:G:H22	14:1S:3:ARG:CD	2.28	0.47
1:1A:2552:2MU:O5'	1:1A:2552:2MU:H6	2.14	0.47
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.13	0.47
3:1D:2:ALA:O	3:1D:20:ASP:HB3	2.15	0.47
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.96	0.47
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.60	0.47
21:1Z:124:ILE:HG23	21:1Z:126:VAL:HG23	1.95	0.47
32:1a:431:A:H2'	32:1a:432:A:O4'	2.15	0.47
32:1a:1152:A:H5'	41:1j:13:HIS:ND1	2.30	0.47
35:1d:178:VAL:C	35:1d:180:GLY:H	2.23	0.47
36:1e:24:ARG:H	36:1e:24:ARG:HG2	1.53	0.47
38:1g:76:ARG:HD3	38:1g:156:TRP:HZ2	1.80	0.47
1:2A:586:A:N1	1:2A:809:G:O2'	2.35	0.47
1:2A:1647:G:OP1	62:2A:3811:HOH:O	2.21	0.47
1:2A:2135:A:N1	1:2A:2156:G:O2'	2.47	0.47
1:2A:2164:C:H3'	1:2A:2165:G:O4'	2.15	0.47
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.27	0.47
11:2P:121:LYS:O	11:2P:123:LEU:N	2.47	0.47
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.97	0.47
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1518:MA6:H93	32:2a:1519:MA6:C9	2.45	0.47
41:2j:78:ASN:C	41:2j:80:LYS:H	2.23	0.47
56:2y:50:U:H2'	56:2y:51:U:O4'	2.15	0.47
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.49	0.46
6:1G:53:LEU:HD11	6:1G:87:PRO:HB2	1.97	0.46
18:1W:82:LEU:HD22	18:1W:84:ARG:NH2	2.30	0.46
32:1a:690:G:C6	32:1a:691:G:C6	3.03	0.46
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.98	0.46
49:1r:53:ARG:HA	49:1r:56:THR:OG1	2.15	0.46
1:2A:27:G:N2	1:2A:512:G:H1'	2.29	0.46
1:2A:39:C:H2'	1:2A:40:C:C6	2.50	0.46
1:2A:208:C:H2'	1:2A:209:C:C6	2.50	0.46
1:2A:655:A:H8	1:2A:656:G:O4'	1.98	0.46
1:2A:1662:C:O2'	1:2A:2687:U:OP1	2.31	0.46
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.45	0.46
5:2F:24:LEU:HD13	5:2F:114:VAL:HG23	1.97	0.46
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.48	0.46
32:2a:1206:G:H2'	32:2a:1207:2MG:H8	1.79	0.46
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.58	0.46
33:2b:118:LEU:HD11	33:2b:138:LEU:HD23	1.97	0.46
45:2n:57:ARG:HG2	45:2n:58:LYS:N	2.30	0.46
1:1A:428:A:H8	1:1A:428:A:OP2	1.98	0.46
1:1A:918:A:H5''	2:1B:98:G:O2'	2.16	0.46
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.15	0.46
32:1a:7:G:H2'	36:1e:119:LEU:HD22	1.97	0.46
32:1a:1179:A:O3'	40:1i:103:THR:HB	2.16	0.46
34:1c:16:ARG:HE	34:1c:16:ARG:HB3	1.61	0.46
35:1d:97:LEU:O	35:1d:100:ARG:HG2	2.15	0.46
38:1g:140:ASP:OD1	38:1g:143:ARG:NH2	2.48	0.46
1:2A:646:A:H2'	1:2A:647:G:O4'	2.15	0.46
1:2A:747:U:O2	1:2A:2014:A:H1'	2.14	0.46
1:2A:902:C:H2'	1:2A:903:C:C6	2.50	0.46
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.48	0.46
32:2a:157:G:H2'	32:2a:158:G:C8	2.50	0.46
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.81	0.46
1:1A:1263:U:H2'	1:1A:1264:G:C8	2.51	0.46
1:1A:1268:A:C2	1:1A:2013:A:C4	3.03	0.46
1:1A:1338:G:O2'	1:1A:1393:A:N1	2.46	0.46
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.24	0.46
9:1N:96:GLU:CD	9:1N:96:GLU:H	2.23	0.46
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.67	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:266:G:H2'	32:1a:266:G:N3	2.30	0.46
32:1a:510:A:OP2	35:1d:49:ARG:NH1	2.47	0.46
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.50	0.46
40:1i:56:LEU:H	40:1i:56:LEU:HD12	1.80	0.46
32:2a:473:G:H2'	32:2a:474:G:H8	1.80	0.46
34:2c:69:HIS:CD2	34:2c:104:GLN:HG2	2.50	0.46
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.50	0.46
38:2g:23:VAL:O	38:2g:27:ILE:HG13	2.16	0.46
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.97	0.46
51:2t:9:ASN:O	51:2t:10:LEU:HB2	2.14	0.46
56:2y:68:C:H2'	56:2y:69:G:O4'	2.15	0.46
1:1A:1055:G:H1	1:1A:1104:C:N4	2.13	0.46
1:1A:2171:A:O2'	1:1A:2172:U:H5''	2.16	0.46
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.16	0.46
11:1P:39:LYS:HB2	11:1P:45:LEU:CD1	2.45	0.46
19:1X:47:PHE:O	19:1X:49:VAL:HG13	2.16	0.46
32:1a:688:G:H2'	32:1a:689:C:H6	1.81	0.46
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.51	0.46
36:1e:79:GLU:HG2	36:1e:92:LYS:HD2	1.96	0.46
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.50	0.46
21:2Z:69:THR:HA	21:2Z:90:VAL:HA	1.97	0.46
32:2a:302:G:N3	32:2a:556:C:H4'	2.31	0.46
32:2a:403:C:N4	62:2a:1919:HOH:O	2.49	0.46
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.96	0.46
50:2s:28:LYS:HB3	50:2s:29:ARG:CA	2.41	0.46
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.96	0.46
1:1A:2144:U:H3'	1:1A:2146:C:N4	2.29	0.46
3:1D:145:VAL:HG11	3:1D:175:LEU:HD11	1.98	0.46
32:1a:767:A:H2'	32:1a:768:A:O4'	2.15	0.46
32:1a:1198:G:H2'	32:1a:1199:U:C6	2.50	0.46
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.31	0.46
34:1c:72:LYS:HZ2	34:1c:74:GLY:H	1.63	0.46
1:2A:479:A:N3	1:2A:481:G:H5''	2.29	0.46
1:2A:958:U:OP2	12:2Q:14:ARG:NE	2.45	0.46
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.51	0.46
1:2A:2126:A:N3	1:2A:2127:G:H1'	2.31	0.46
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.49	0.46
33:2b:71:VAL:HG12	33:2b:170:GLU:HG2	1.98	0.46
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.15	0.46
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.95	0.46
45:2n:59:ALA:HB1	45:2n:61:TRP:HZ3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:35:ARG:O	49:2r:37:VAL:N	2.48	0.46
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.49	0.46
2:1B:2:C:H2'	2:1B:3:C:C6	2.50	0.46
32:1a:119:A:H4'	32:1a:120:A:C8	2.50	0.46
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.31	0.46
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.51	0.46
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.51	0.46
1:2A:1923:U:OP1	55:2x:24:U:O2'	2.31	0.46
1:2A:2284:C:OP2	28:26:2:ALA:N	2.48	0.46
18:2W:64:MET:HE2	18:2W:109:GLU:HG3	1.98	0.46
32:2a:410:G:H21	32:2a:432:A:H62	1.64	0.46
32:2a:1024:G:H2'	32:2a:1025:U:H5''	1.96	0.46
56:2y:9:A:O2'	56:2y:11:C:N4	2.38	0.46
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.98	0.46
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.16	0.46
32:1a:262:A:H2'	32:1a:263:A:C8	2.51	0.46
32:1a:1032:G:H2'	32:1a:1033:G:O4'	2.15	0.46
33:1b:67:THR:N	33:1b:160:ASP:OD1	2.43	0.46
50:1s:22:LEU:HD22	50:1s:27:GLU:HA	1.97	0.46
1:2A:10:G:N2	1:2A:2629:A:N7	2.63	0.46
1:2A:922:U:H2'	1:2A:923:C:C6	2.51	0.46
1:2A:2207:G:H3'	1:2A:2208:A:H5''	1.97	0.46
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.15	0.46
3:2D:77:ALA:HA	3:2D:97:TYR:HA	1.97	0.46
30:28:23:VAL:HG22	30:28:47:LYS:HB3	1.97	0.46
32:2a:473:G:H2'	32:2a:474:G:C8	2.50	0.46
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.80	0.46
1:1A:709:U:H2'	1:1A:710:G:C8	2.50	0.46
3:1D:180:GLY:HA3	3:1D:275:LYS:HG2	1.97	0.46
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.50	0.46
32:1a:1505:G:O2'	53:1v:13:A:O2'	2.34	0.46
35:1d:111:ALA:HA	35:1d:161:ASN:HD22	1.81	0.46
45:1n:14:PRO:HG2	45:1n:16:PHE:O	2.15	0.46
49:1r:31:LEU:HD23	49:1r:31:LEU:H	1.80	0.46
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.16	0.46
1:2A:271(O):C:H4'	8:2I:49:ALA:HB1	1.96	0.46
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.15	0.46
6:2G:69:ALA:HB3	6:2G:91:ARG:NH2	2.31	0.46
21:2Z:146:ILE:HG12	21:2Z:174:VAL:HG23	1.97	0.46
32:2a:115:G:H4'	32:2a:116:A:O5'	2.15	0.46
32:2a:445:G:H1	32:2a:489:C:H42	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:509:A:H5''	35:2d:55:ALA:HB2	1.98	0.46
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.98	0.46
1:1A:224:G:H2'	1:1A:225:A:O4'	2.15	0.46
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.16	0.46
32:1a:660:G:OP1	46:1o:5:LYS:HE2	2.16	0.46
32:1a:1347:G:C8	40:1i:107:ARG:HB3	2.51	0.46
32:1a:1370:G:C2	32:1a:1371:G:C8	3.04	0.46
35:1d:108:LEU:HD21	35:1d:174:LEU:HD22	1.98	0.46
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.46	0.46
52:1u:5:ASP:OD2	62:1u:101:HOH:O	2.21	0.46
54:1w:68:C:H2'	54:1w:69:G:C8	2.49	0.46
1:2A:2125:G:N1	1:2A:2172:U:OP1	2.45	0.46
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.97	0.46
5:2F:137:LYS:HA	5:2F:140:LEU:HD12	1.98	0.46
17:2V:24:LYS:HB3	17:2V:24:LYS:HE2	1.71	0.46
21:2Z:40:ASP:OD2	21:2Z:43:GLU:N	2.36	0.46
32:2a:1053:G:N7	32:2a:1200:C:H5''	2.30	0.46
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.16	0.46
41:2j:32:ALA:HA	41:2j:33:GLN:HA	1.76	0.46
1:1A:747:U:O2	1:1A:2014:A:H1'	2.16	0.46
1:1A:1316:U:H2'	1:1A:1317:A:C8	2.50	0.46
1:1A:2389:G:H5''	1:1A:2390:U:O4'	2.16	0.46
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.51	0.46
26:14:63:TYR:N	26:14:63:TYR:CD1	2.83	0.46
32:1a:826:C:H4'	39:1h:12:ARG:HG2	1.98	0.46
37:1f:76:ALA:HA	37:1f:79:LEU:HD12	1.98	0.46
40:1i:3:GLN:HE21	40:1i:20:ARG:NE	2.13	0.46
42:1k:48:ILE:O	42:1k:50:TYR:N	2.43	0.46
1:2A:839:U:H2'	1:2A:840:C:C6	2.51	0.46
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.16	0.46
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.33	0.46
2:2B:24:G:N7	2:2B:56:G:H2'	2.31	0.46
21:2Z:45:ASP:OD1	21:2Z:49:ARG:NE	2.48	0.46
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.51	0.46
32:2a:643:C:H2'	32:2a:644:G:H8	1.81	0.46
36:2e:41:VAL:O	36:2e:66:MET:HA	2.16	0.46
44:2m:40:ASN:ND2	44:2m:43:THR:HG23	2.30	0.46
44:2m:86:CYS:O	44:2m:89:GLY:N	2.47	0.46
1:1A:1057:A:N6	1:1A:1081:U:H3	2.13	0.45
1:1A:1093:G:H3'	1:1A:1094:U:H5''	1.98	0.45
1:1A:2065:C:H4'	1:1A:2251:OMG:HM22	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2180:U:H2'	1:1A:2181:G:O4'	2.15	0.45
1:1A:2747:G:O6	1:1A:2755:C:H5''	2.16	0.45
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.51	0.45
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.98	0.45
32:1a:110:C:H2'	32:1a:111:G:O4'	2.15	0.45
32:1a:1376:U:H2'	32:1a:1377:A:H8	1.81	0.45
38:1g:113:GLU:OE1	38:1g:122:HIS:ND1	2.49	0.45
4:2E:89:ASP:OD1	4:2E:89:ASP:N	2.49	0.45
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.32	0.45
8:2I:117:GLU:OE1	8:2I:117:GLU:N	2.47	0.45
26:24:45:GLY:C	26:24:47:GLN:H	2.22	0.45
32:2a:1030(A):G:N1	32:2a:1030(D):A:OP2	2.45	0.45
40:2i:8:GLY:HA3	40:2i:76:ALA:O	2.16	0.45
44:2m:60:VAL:HG12	44:2m:66:LEU:HD11	1.97	0.45
44:2m:65:LYS:O	44:2m:70:LEU:HD12	2.16	0.45
45:2n:26:ARG:HH11	45:2n:43:CYS:HB3	1.82	0.45
48:2q:7:THR:HG23	48:2q:58:GLU:HG3	1.97	0.45
1:1A:1176:G:N2	1:1A:1178:C:OP2	2.41	0.45
1:1A:1405:U:H2'	1:1A:1406:U:H6	1.79	0.45
2:1B:24:G:N7	2:1B:56:G:H2'	2.31	0.45
6:1G:116:ASP:OD2	44:1m:68:GLY:HA3	2.17	0.45
31:19:27:CYS:SG	31:19:28:GLU:N	2.89	0.45
32:1a:904:C:OP2	62:1a:1916:HOH:O	2.21	0.45
33:1b:133:LYS:NZ	33:1b:137:ARG:HD3	2.32	0.45
33:1b:188:ALA:HB1	33:1b:192:SER:OG	2.15	0.45
36:1e:10:MET:H	36:1e:10:MET:HG2	1.64	0.45
1:2A:191:A:H2'	1:2A:192:C:C6	2.51	0.45
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.46	0.45
1:2A:1015:G:H2'	1:2A:1016:G:C8	2.50	0.45
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.79	0.45
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.81	0.45
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.99	0.45
8:2I:43:ASN:HA	8:2I:46:ALA:HB3	1.99	0.45
16:2U:83:LEU:HB3	16:2U:88:ILE:HB	1.97	0.45
32:2a:1010:G:N1	32:2a:1020:U:H1'	2.31	0.45
33:2b:144:ARG:NH2	33:2b:148:TYR:OH	2.49	0.45
40:2i:5:TYR:HE1	40:2i:16:ARG:HB3	1.81	0.45
45:2n:14:PRO:HG2	45:2n:16:PHE:O	2.16	0.45
51:2t:79:ARG:O	51:2t:83:ARG:HG3	2.16	0.45
1:1A:784:A:N6	3:1D:229:VAL:HG11	2.31	0.45
1:1A:1094:U:H1'	1:1A:1097:U:C4	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.50	0.45
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.50	0.45
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.16	0.45
11:1P:35:HIS:O	11:1P:36:LYS:O	2.34	0.45
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	1.97	0.45
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.31	0.45
32:1a:1429:C:H2'	32:1a:1430:C:H6	1.80	0.45
35:1d:19:LEU:O	35:1d:21:LEU:HG	2.15	0.45
36:1e:85:GLY:C	36:1e:87:SER:H	2.22	0.45
56:1y:2:C:H2'	56:1y:3:C:C6	2.51	0.45
1:2A:392:C:H5''	1:2A:409:C:H5''	1.98	0.45
1:2A:652(A):A:H3'	1:2A:652(B):A:C5'	2.46	0.45
1:2A:829:A:N7	1:2A:2248:C:H5'	2.31	0.45
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.15	0.45
1:2A:2129:C:H5'	1:2A:2130:U:OP2	2.17	0.45
8:2I:9:LEU:HD21	8:2I:35:LEU:HD13	1.98	0.45
25:23:46:ASN:O	25:23:50:VAL:HG22	2.16	0.45
32:2a:1040:U:H2'	32:2a:1041:A:H8	1.80	0.45
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.51	0.45
32:2a:1206:G:O2'	34:2c:193:TYR:HA	2.16	0.45
34:2c:9:GLY:HA3	45:2n:49:HIS:HA	1.99	0.45
39:2h:73:ASP:OD1	39:2h:75:ARG:NE	2.46	0.45
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.98	0.45
1:1A:518:G:H2'	1:1A:519:U:C6	2.51	0.45
1:1A:839:U:H2'	1:1A:840:C:C6	2.51	0.45
8:1I:2:LYS:HG2	8:1I:18:VAL:HG12	1.97	0.45
38:1g:49:ILE:O	38:1g:53:LYS:HG3	2.17	0.45
39:1h:43:GLY:O	39:1h:64:LYS:NZ	2.43	0.45
39:1h:81:HIS:N	39:1h:138:TRP:O	2.49	0.45
46:1o:47:LYS:HE2	46:1o:47:LYS:HB2	1.67	0.45
1:2A:555:U:O2'	1:2A:556:G:N7	2.49	0.45
1:2A:1837:C:O2'	1:2A:1927:A:N3	2.40	0.45
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.98	0.45
8:2I:62:LYS:HB3	8:2I:133:HIS:CE1	2.51	0.45
20:2Y:15:VAL:HG21	20:2Y:42:VAL:HG11	1.98	0.45
28:26:7:ILE:HD13	28:26:27:LYS:HD3	1.97	0.45
32:2a:191:G:O2'	51:2t:102:GLY:N	2.46	0.45
32:2a:224:C:H2'	32:2a:225:C:C6	2.52	0.45
32:2a:1414:U:H2'	32:2a:1415:G:H8	1.81	0.45
33:2b:76:GLN:HB2	33:2b:208:ILE:HD11	1.99	0.45
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:13:ASN:ND2	37:2f:55:ASP:OD2	2.50	0.45
39:2h:84:ARG:NH1	39:2h:86:ILE:HG12	2.32	0.45
41:2j:5:ARG:N	41:2j:99:LYS:O	2.49	0.45
1:1A:226:G:N2	1:1A:228:A:H62	2.14	0.45
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.42	0.45
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.52	0.45
2:1B:66:A:H61	2:1B:108:U:H2'	1.82	0.45
21:1Z:125:LEU:HG	21:1Z:164:ALA:HB3	1.99	0.45
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.52	0.45
32:1a:181:G:H4'	32:1a:182:U:H5'	1.99	0.45
32:1a:501:C:H2'	32:1a:502:G:C8	2.51	0.45
32:1a:1003:G:H2'	32:1a:1004:A:N3	2.32	0.45
32:1a:1040:U:H2'	32:1a:1041:A:C8	2.51	0.45
55:1x:8:4SU:O2	55:1x:21:A:H2	1.99	0.45
1:2A:567:A:OP2	11:2P:29:LYS:NZ	2.50	0.45
1:2A:927:G:H2'	1:2A:928:G:O4'	2.17	0.45
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.51	0.45
1:2A:2752:C:H2'	1:2A:2753:A:O4'	2.16	0.45
8:2I:40:THR:OG1	8:2I:41:GLU:N	2.49	0.45
17:2V:72:VAL:HB	17:2V:85:LYS:HB3	1.98	0.45
32:2a:109:A:C6	32:2a:326:G:C6	3.05	0.45
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.35	0.45
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.52	0.45
33:2b:169:LYS:O	33:2b:169:LYS:HD3	2.17	0.45
39:2h:51:VAL:HG11	39:2h:60:ARG:HH12	1.82	0.45
41:2j:5:ARG:HA	41:2j:73:ASP:OD1	2.17	0.45
1:1A:27:G:N2	1:1A:512:G:H1'	2.32	0.45
1:1A:652(C):G:H1	1:1A:652(V):C:H42	1.63	0.45
1:1A:662:G:H5''	11:1P:16:ARG:HG2	1.97	0.45
1:1A:884:C:C4	1:1A:885:C:H1'	2.51	0.45
1:1A:2633:G:H2'	1:1A:2634:G:O4'	2.16	0.45
1:1A:2721:A:O2'	1:1A:2874:C:H5'	2.16	0.45
6:1G:170:ARG:NH2	6:1G:182:LYS:O	2.49	0.45
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	1.98	0.45
34:1c:119:ARG:HE	34:1c:140:ARG:NH2	2.15	0.45
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.51	0.45
41:1j:49:VAL:HG21	45:1n:41:ARG:O	2.16	0.45
51:1t:10:LEU:HD12	51:1t:11:SER:H	1.82	0.45
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.52	0.45
9:2N:55:VAL:HG23	9:2N:56:ASN:HD22	1.82	0.45
32:2a:23:C:H5	32:2a:561:U:O4	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1053:G:H4'	32:2a:1054:C:H3'	1.97	0.45
32:2a:1074:G:O2'	33:2b:103:THR:OG1	2.34	0.45
1:1A:1494:A:OP1	62:1A:4247:HOH:O	2.21	0.45
1:1A:1878:G:H2'	1:1A:1879:C:C6	2.52	0.45
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.14	0.45
6:1G:82:LEU:HD21	6:1G:88:ILE:HG21	1.99	0.45
11:1P:121:LYS:O	11:1P:123:LEU:N	2.49	0.45
32:1a:4:U:O4	39:1h:105:ARG:HD3	2.17	0.45
32:1a:684:A:O2'	42:1k:39:PRO:O	2.30	0.45
1:2A:667:U:O2	30:28:2:PRO:HD2	2.16	0.45
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.81	0.45
1:2A:2061:G:H5''	1:2A:2503:8AH:C2	2.47	0.45
4:2E:151:TYR:HB3	9:2N:79:PRO:HG3	1.99	0.45
5:2F:102:PRO:HB2	5:2F:105:VAL:HG23	1.99	0.45
32:2a:130:A:O2'	32:2a:131:C:O5'	2.28	0.45
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.99	0.45
32:2a:1106:G:H5''	34:2c:172:ARG:HB3	1.99	0.45
34:2c:92:ALA:O	34:2c:96:GLY:N	2.49	0.45
35:2d:88:VAL:O	35:2d:92:VAL:HG12	2.15	0.45
56:2y:62:C:H2'	56:2y:63:G:H8	1.79	0.45
1:1A:118:A:C8	1:1A:119:A:C8	3.05	0.45
1:1A:414:C:H2'	1:1A:415:A:C8	2.51	0.45
1:1A:568:U:H5'	1:1A:945:A:N6	2.32	0.45
1:1A:652(U):G:C2	1:1A:652(V):C:C2	3.05	0.45
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.16	0.45
1:1A:1495:A:C6	1:1A:1496:A:C6	3.05	0.45
1:1A:1568:G:H4'	3:1D:59:LYS:HG2	1.99	0.45
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.52	0.45
10:1O:120:GLU:HB2	15:1T:68:TYR:CE2	2.52	0.45
19:1X:92:LEU:HD12	19:1X:92:LEU:HA	1.79	0.45
32:1a:636:U:H2'	32:1a:637:G:H8	1.81	0.45
1:2A:97:C:OP1	24:22:2:LYS:NZ	2.46	0.45
1:2A:881:G:H3'	1:2A:882:G:H8	1.81	0.45
1:2A:894:C:O2'	1:2A:895:U:H5''	2.16	0.45
1:2A:1359:A:C2	1:2A:1372:U:O4	2.69	0.45
21:2Z:23:LYS:HB3	21:2Z:38:TYR:CD1	2.52	0.45
32:2a:105:G:O6	62:2a:1917:HOH:O	2.20	0.45
32:2a:630:G:H2'	32:2a:631:G:C8	2.52	0.45
32:2a:1129:C:O2'	32:2a:1139:G:O6	2.28	0.45
43:2l:113:ARG:NE	43:2l:115:LYS:O	2.47	0.45
44:2m:33:ALA:HB2	44:2m:64:TRP:CH2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:40:C:H2'	55:2x:41:C:H6	1.82	0.45
1:1A:602:G:HO2'	1:1A:655:A:N6	2.14	0.45
1:1A:1075:C:H2'	1:1A:1076:C:H5'	1.99	0.45
1:1A:2846:G:H2'	1:1A:2847:U:O4'	2.17	0.45
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.52	0.45
32:1a:299:G:C6	32:1a:300:A:C6	3.05	0.45
32:1a:865:A:C2	32:1a:918:A:H4'	2.51	0.45
32:1a:925:G:H1'	32:1a:1502:A:C4	2.52	0.45
32:1a:1123:A:O2'	41:1j:37:PRO:O	2.29	0.45
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.17	0.45
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.99	0.45
2:2B:13:A:N1	2:2B:69:G:O2'	2.38	0.45
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.99	0.45
32:2a:181:G:H4'	32:2a:182:U:H5'	1.99	0.45
32:2a:512:U:H2'	32:2a:513:C:H6	1.82	0.45
32:2a:737:A:H2'	32:2a:738:C:C6	2.52	0.45
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.99	0.45
1:1A:2879:C:OP2	62:1A:4244:HOH:O	2.21	0.45
6:1G:105:LYS:O	6:1G:109:VAL:HG22	2.17	0.45
8:1I:77:LEU:HD23	8:1I:77:LEU:HA	1.83	0.45
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.99	0.45
32:1a:860:A:H2'	32:1a:861:G:O4'	2.17	0.45
38:1g:74:GLU:HG2	38:1g:91:VAL:HG22	1.99	0.45
41:1j:81:THR:C	41:1j:83:GLU:N	2.75	0.45
54:1w:52:G:C6	54:1w:63:G:C6	3.05	0.45
55:1x:17:C:OP2	55:1x:17(A):U:O2'	2.34	0.45
1:2A:10:G:H2'	1:2A:11:G:C8	2.51	0.45
2:2B:80:U:H2'	2:2B:81:G:C8	2.52	0.45
32:2a:542:G:P	35:2d:10:ARG:HH22	2.39	0.45
33:2b:162:ILE:O	33:2b:185:ILE:HG12	2.17	0.45
35:2d:65:ARG:NH1	35:2d:70:ILE:O	2.50	0.45
36:2e:57:LYS:CG	36:2e:61:TYR:HE2	2.30	0.45
36:2e:83:GLU:HA	36:2e:88:LYS:HA	1.98	0.45
56:2y:61:C:H2'	56:2y:62:C:C6	2.52	0.45
1:1A:1051:G:H2'	1:1A:1052:C:O4'	2.16	0.44
2:1B:88:C:H2'	2:1B:89:G:O4'	2.17	0.44
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.52	0.44
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.32	0.44
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.52	0.44
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.52	0.44
11:1P:101:VAL:HG23	11:1P:106:LEU:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:193:C:H2'	32:1a:194:C:H6	1.82	0.44
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.99	0.44
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.34	0.44
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.48	0.44
54:1w:3:C:H5	62:1w:208:HOH:O	1.99	0.44
1:2A:459:U:H5''	29:27:40:TRP:CD2	2.52	0.44
1:2A:932:G:OP1	25:23:29:ARG:NH1	2.50	0.44
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.53	0.44
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.52	0.44
7:2H:25:LYS:HE2	7:2H:25:LYS:HB2	1.85	0.44
7:2H:121:ILE:HD11	7:2H:140:LYS:HG2	1.98	0.44
9:2N:110:GLY:O	9:2N:114:ARG:HG3	2.17	0.44
18:2W:1:MET:HE3	18:2W:62:HIS:HB3	1.99	0.44
32:2a:1032:G:H2'	32:2a:1033:G:C8	2.53	0.44
32:2a:1077:G:N1	32:2a:1080:A:OP2	2.50	0.44
32:2a:1152:A:H5'	41:2j:13:HIS:CD2	2.44	0.44
32:2a:1194:U:H2'	32:2a:1195:C:C6	2.52	0.44
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.99	0.44
37:2f:24:GLU:O	37:2f:28:ARG:N	2.44	0.44
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.82	0.44
46:2o:87:ILE:HG22	46:2o:88:ARG:N	2.32	0.44
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.24	0.44
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.17	0.44
6:1G:179:PRO:HG3	26:14:43:TYR:CZ	2.52	0.44
32:1a:179:A:H2'	32:1a:180:U:C6	2.52	0.44
32:1a:266:G:H5''	32:1a:268:C:H41	1.81	0.44
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.52	0.44
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.49	0.44
1:2A:1937:A:H1'	1:2A:1939:5MU:H72	1.98	0.44
1:2A:2305:A:H2'	1:2A:2306:C:O4'	2.18	0.44
1:2A:2336:A:H61	22:20:43:THR:CG2	2.30	0.44
8:2I:90:GLY:O	8:2I:121:LYS:HE3	2.18	0.44
32:2a:1272:G:C2	32:2a:1273:G:C8	3.06	0.44
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.51	0.44
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.99	0.44
50:2s:35:SER:O	50:2s:71:LEU:HD23	2.18	0.44
1:1A:774:A:N3	1:1A:774:A:H2'	2.31	0.44
1:1A:1076:C:O2'	1:1A:1077:A:N7	2.46	0.44
16:1U:16:LYS:HB3	16:1U:16:LYS:HE2	1.79	0.44
28:16:12:GLU:OE1	28:16:52:VAL:HG11	2.18	0.44
32:1a:1112:C:H1'	34:1c:179:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1136:U:H5''	32:1a:1137:C:N3	2.32	0.44
35:1d:110:PHE:CD1	35:1d:148:VAL:HG23	2.52	0.44
56:1y:66:U:H2'	56:1y:67:C:C6	2.52	0.44
1:2A:458:G:O2'	1:2A:469:G:O6	2.34	0.44
1:2A:724:U:H2'	1:2A:725:G:O4'	2.18	0.44
1:2A:1645:G:H5''	1:2A:1646:C:H5'	2.00	0.44
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.53	0.44
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	2.00	0.44
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.50	0.44
26:24:61:ARG:HE	50:2s:42:PRO:HD3	1.82	0.44
32:2a:131:C:H2'	32:2a:132:C:C6	2.52	0.44
32:2a:677:U:H3	32:2a:713:G:H22	1.64	0.44
32:2a:728:A:H2'	32:2a:729:A:C8	2.51	0.44
32:2a:1111:A:H2'	32:2a:1112:C:H6	1.82	0.44
34:2c:62:ASP:O	34:2c:98:ASN:ND2	2.51	0.44
34:2c:136:GLN:O	34:2c:139:GLN:N	2.50	0.44
50:2s:32:LYS:HG2	50:2s:50:ALA:HB3	2.00	0.44
51:2t:53:LEU:O	51:2t:57:ARG:HG3	2.17	0.44
51:2t:87:LYS:O	51:2t:91:LEU:HG	2.16	0.44
1:1A:1075:C:C2'	1:1A:1076:C:H5'	2.47	0.44
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.16	0.44
6:1G:3:LEU:O	6:1G:8:LYS:NZ	2.44	0.44
11:1P:59:LEU:HD11	30:18:10:ALA:HA	2.00	0.44
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.98	0.44
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.98	0.44
32:1a:341:C:H2'	32:1a:342:C:H6	1.80	0.44
32:1a:1002:G:H3'	32:1a:1003:G:C4'	2.37	0.44
32:1a:1028:C:H2'	32:1a:1029:C:O4'	2.17	0.44
33:1b:12:GLU:O	33:1b:15:VAL:HG22	2.18	0.44
41:1j:81:THR:C	41:1j:83:GLU:H	2.25	0.44
51:1t:49:ALA:O	51:1t:53:LEU:HD12	2.18	0.44
56:1y:38:A:H2'	56:1y:39:PSU:O4'	2.16	0.44
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.18	0.44
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.33	0.44
1:2A:2106:G:H2'	1:2A:2107:C:O4'	2.17	0.44
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.98	0.44
32:2a:1264:C:N4	32:2a:1271:G:H1	2.14	0.44
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.99	0.44
38:2g:70:LYS:O	38:2g:138:LYS:HD2	2.16	0.44
1:1A:1952:A:C6	1:1A:1953:A:N1	2.86	0.44
1:1A:2271:G:OP1	22:10:18:ALA:HB1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.53	0.44
1:1A:2590:A:H2'	1:1A:2591:C:H6	1.83	0.44
1:1A:2615:U:H2'	1:1A:2616:C:H6	1.82	0.44
4:1E:48:GLN:HE21	4:1E:78:LEU:HD22	1.82	0.44
10:1O:1:MET:HE2	10:1O:1:MET:HB3	1.78	0.44
12:1Q:89:ASN:HB2	55:1x:1:C:C4	2.53	0.44
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.33	0.44
32:1a:848:C:H2'	32:1a:849:C:C6	2.53	0.44
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	2.00	0.44
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.18	0.44
1:2A:271(K):U:H4'	1:2A:271(L):U:OP1	2.18	0.44
1:2A:286:C:H2'	1:2A:287:C:H6	1.82	0.44
1:2A:1357:U:H2'	1:2A:1358:G:O4'	2.17	0.44
1:2A:2134:A:H2	1:2A:2159:G:H1'	1.83	0.44
2:2B:8:U:O3'	14:2S:25:ARG:NH2	2.47	0.44
9:2N:118:LYS:O	9:2N:121:LYS:HE2	2.18	0.44
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.18	0.44
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.36	0.44
15:2T:127:ALA:C	15:2T:129:ARG:N	2.76	0.44
20:2Y:5:MET:HB2	20:2Y:5:MET:HE2	1.64	0.44
32:2a:1280:A:OP2	41:2j:40:LEU:HD13	2.17	0.44
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.18	0.44
38:2g:125:MET:O	38:2g:129:GLU:HG3	2.17	0.44
38:2g:126:ASP:O	38:2g:130:GLY:N	2.42	0.44
1:1A:479:A:N3	1:1A:481:G:H5''	2.32	0.44
1:1A:878:A:N6	1:1A:899:A:O2'	2.50	0.44
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.17	0.44
2:1B:74:U:H2'	2:1B:75:G:O4'	2.17	0.44
7:1H:72:ILE:O	7:1H:76:VAL:HG12	2.18	0.44
10:1O:120:GLU:OE1	15:1T:67:SER:OG	2.28	0.44
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.18	0.44
32:1a:1304:G:C6	32:1a:1305:G:N1	2.86	0.44
33:1b:160:ASP:O	33:1b:183:PRO:HD2	2.17	0.44
35:1d:30:LYS:HA	35:1d:35:ARG:HH11	1.83	0.44
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.53	0.44
47:1p:14:ASN:HA	47:1p:42:ARG:NH2	2.33	0.44
47:1p:74:LEU:O	47:1p:79:VAL:HG23	2.18	0.44
1:2A:223:A:O2'	1:2A:420:C:O2	2.33	0.44
1:2A:630:G:OP1	30:28:47:LYS:NZ	2.45	0.44
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.17	0.44
1:2A:1711:C:H2'	1:2A:1712:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2134:A:H62	1:2A:2157:G:H4'	1.83	0.44
5:2F:114:VAL:HG21	5:2F:202:PHE:CZ	2.53	0.44
6:2G:16:ARG:HD2	6:2G:16:ARG:HA	1.74	0.44
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.99	0.44
21:2Z:54:HIS:O	21:2Z:55:HIS:ND1	2.51	0.44
23:21:82:LEU:HA	23:21:85:LEU:HD12	2.00	0.44
26:24:44:THR:OG1	26:24:45:GLY:N	2.51	0.44
32:2a:56:U:H2'	32:2a:57:G:H8	1.82	0.44
32:2a:548:G:OP1	62:2a:1919:HOH:O	2.21	0.44
32:2a:587:G:N2	32:2a:754:C:OP2	2.49	0.44
32:2a:683:G:H2'	32:2a:684:A:C8	2.53	0.44
32:2a:1004:A:N1	32:2a:1037:C:H1'	2.33	0.44
37:2f:9:VAL:HA	37:2f:59:TYR:O	2.17	0.44
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	2.00	0.44
1:1A:2352:A:N6	1:1A:2365:G:O2'	2.50	0.44
32:1a:548:G:OP1	62:1a:1918:HOH:O	2.21	0.44
32:1a:715:A:H2'	32:1a:716:A:C8	2.53	0.44
32:1a:1005:A:OP2	32:1a:1024:G:N2	2.50	0.44
32:1a:1225:A:N6	62:1a:1989:HOH:O	2.51	0.44
34:1c:72:LYS:NZ	34:1c:74:GLY:H	2.16	0.44
39:1h:124:ALA:O	39:1h:128:GLY:N	2.50	0.44
40:1i:85:LEU:O	40:1i:88:TYR:HB3	2.18	0.44
45:1n:23:ARG:NH1	45:1n:30:ALA:HB2	2.32	0.44
51:1t:56:MET:HE3	51:1t:85:MET:HG2	1.99	0.44
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.32	0.44
1:2A:1508:A:H4'	1:2A:1509(A):A:N7	2.33	0.44
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.17	0.44
1:2A:2507:C:H5''	1:2A:2573:C:C4	2.52	0.44
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	1.98	0.44
6:2G:14:GLU:O	6:2G:17:PRO:HD2	2.18	0.44
32:2a:397:A:H5'	32:2a:398:C:OP1	2.18	0.44
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.40	0.44
32:2a:1005:A:H3'	32:2a:1006:C:H6	1.82	0.44
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.18	0.44
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.17	0.44
32:2a:1264:C:C4	32:2a:1272:G:O6	2.71	0.44
47:2p:17:TYR:HE2	47:2p:41:PRO:HG3	1.83	0.44
56:2y:18:G:O3'	56:2y:60:U:H5	2.00	0.44
1:1A:570:G:H2'	1:1A:2030:A:N7	2.33	0.44
1:1A:784:A:O4'	3:1D:227:ASN:ND2	2.50	0.44
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	2.00	0.44
5:1F:141:ALA:HA	5:1F:144:LYS:HE3	1.99	0.44
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.17	0.44
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	2.00	0.44
8:1I:17:GLN:HG2	8:1I:18:VAL:N	2.32	0.44
9:1N:4:TYR:CE2	16:1U:100:VAL:HG11	2.53	0.44
12:1Q:1:MET:SD	12:1Q:45:GLN:HG3	2.58	0.44
14:1S:83:LYS:HB3	14:1S:111:GLU:HG3	1.99	0.44
32:1a:1148:U:O3'	40:1i:14:VAL:HG11	2.18	0.44
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.86	0.44
34:1c:52:LEU:HD13	34:1c:68:VAL:HG13	2.00	0.44
37:1f:8:ILE:HG12	37:1f:88:VAL:HG22	1.99	0.44
40:1i:96:LEU:HD22	40:1i:101:PHE:HD2	1.82	0.44
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.83	0.44
54:1w:26:A:H61	54:1w:44:G:H1	1.66	0.44
54:1w:38:A:H2'	54:1w:39:PSU:O4'	2.18	0.44
54:1w:48:C:C2	54:1w:59:U:H1'	2.52	0.44
1:2A:251:A:C5	1:2A:252:G:H1'	2.53	0.44
1:2A:878:A:N6	1:2A:899:A:O2'	2.51	0.44
1:2A:2592:G:H2'	1:2A:2593:U:O4'	2.18	0.44
1:2A:2807:G:C2	1:2A:2893:G:O6	2.71	0.44
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.30	0.44
32:2a:950:U:H2'	32:2a:951:G:C8	2.52	0.44
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.52	0.44
34:2c:186:PHE:HD1	34:2c:198:VAL:O	2.00	0.44
50:2s:12:ASP:CG	50:2s:37:ARG:HD2	2.43	0.44
54:2w:25:C:H2'	54:2w:26:A:C8	2.51	0.44
1:1A:34:C:H5''	1:1A:35:G:OP2	2.17	0.44
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.82	0.44
1:1A:1498:C:OP1	62:1A:4250:HOH:O	2.21	0.44
1:1A:1503:U:H2'	1:1A:1504:C:H6	1.83	0.44
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.33	0.44
5:1F:28:ILE:HA	5:1F:112:MET:HG2	1.99	0.44
32:1a:200:G:H1	32:1a:217:C:H42	1.65	0.44
32:1a:537:G:OP2	62:1a:1920:HOH:O	2.21	0.44
32:1a:662:G:H2'	32:1a:663:A:C8	2.52	0.44
32:1a:836:G:OP1	49:1r:61:LYS:NZ	2.33	0.44
32:1a:1212:U:H4'	32:1a:1213:A:C8	2.53	0.44
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.52	0.44
35:1d:65:ARG:HG3	35:1d:75:PHE:CD1	2.53	0.44
1:2A:197:A:N6	1:2A:2430:A:H2'	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:647:G:H2'	1:2A:648:G:O4'	2.18	0.44
1:2A:1473:G:C6	1:2A:1474:C:C4	3.06	0.44
11:2P:95:VAL:HG13	11:2P:125:VAL:HG12	1.98	0.44
32:2a:918:A:H2'	32:2a:919:A:C8	2.52	0.44
34:2c:23:TYR:CG	34:2c:24:ALA:N	2.85	0.44
38:2g:69:VAL:HG21	38:2g:104:LEU:HD21	2.00	0.44
48:2q:85:VAL:HG23	48:2q:89:LEU:HD12	2.00	0.44
1:1A:582:G:H2'	1:1A:583:G:C8	2.53	0.43
1:1A:783:A:O2'	1:1A:785:G:OP1	2.28	0.43
1:1A:884:C:C5	1:1A:885:C:H1'	2.53	0.43
1:1A:957:A:N1	1:1A:2458:G:H4'	2.33	0.43
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.18	0.43
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.17	0.43
1:1A:2464:C:H1'	62:1A:5370:HOH:O	2.17	0.43
1:1A:2590:A:H2'	1:1A:2591:C:C6	2.53	0.43
3:1D:130:ALA:C	3:1D:131:LEU:HD12	2.43	0.43
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.18	0.43
10:1O:64:ARG:HD2	10:1O:79:PHE:CD1	2.52	0.43
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.51	0.43
16:1U:78:THR:HG23	16:1U:117:GLN:HE22	1.83	0.43
20:1Y:86:ARG:HB3	20:1Y:98:VAL:HG23	2.00	0.43
34:1c:134:ILE:HD11	34:1c:153:VAL:HB	2.00	0.43
35:1d:18:LYS:HG2	61:1d:501:SF4:S1	2.58	0.43
35:1d:127:THR:HG22	35:1d:132:ARG:HA	2.00	0.43
41:1j:31:GLY:HA3	41:1j:32:ALA:HA	1.68	0.43
54:1w:46:G7M:H3'	54:1w:47:U:H5''	2.00	0.43
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.99	0.43
9:2N:123:TYR:CZ	9:2N:129:PRO:HD2	2.52	0.43
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.18	0.43
29:27:24:THR:HG22	29:27:26:GLY:N	2.33	0.43
30:28:4:MET:HE3	30:28:63:PRO:HG3	2.00	0.43
32:2a:179:A:H2'	32:2a:180:U:C6	2.53	0.43
32:2a:1097:C:H2'	32:2a:1098:C:H6	1.83	0.43
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.53	0.43
32:2a:1263:C:H3'	32:2a:1263:C:H6	1.82	0.43
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.36	0.43
34:2c:182:ILE:HG12	34:2c:203:PHE:HD1	1.83	0.43
50:2s:64:GLU:H	50:2s:64:GLU:CD	2.26	0.43
1:1A:81:G:H21	20:1Y:1:MET:HE1	1.83	0.43
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.53	0.43
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:7:TYR:CZ	10:1O:44:LYS:HG3	2.53	0.43
10:1O:113:LYS:HA	10:1O:113:LYS:HD2	1.84	0.43
32:1a:909:A:H2'	32:1a:910:C:O4'	2.17	0.43
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.16	0.43
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.01	0.43
32:1a:1325:C:OP1	52:1u:15:ARG:NH1	2.51	0.43
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.35	0.43
37:1f:97:PHE:O	49:1r:31:LEU:HD23	2.18	0.43
39:1h:73:ASP:OD1	39:1h:75:ARG:NE	2.50	0.43
56:1y:19:G:H5''	56:1y:57:G:H1	1.83	0.43
1:2A:1248:G:C2	16:2U:3:ARG:HD2	2.53	0.43
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.53	0.43
1:2A:2592:G:OP2	62:2A:3853:HOH:O	2.21	0.43
4:2E:73:GLU:H	4:2E:73:GLU:HG3	1.50	0.43
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.53	0.43
11:2P:85:LEU:HD23	11:2P:88:LEU:HD12	2.00	0.43
31:29:7:VAL:HG12	31:29:34:GLN:HB3	1.99	0.43
32:2a:833:U:H2'	32:2a:834:C:H6	1.83	0.43
32:2a:1265:G:C2	32:2a:1271:G:C2	3.06	0.43
38:2g:153:HIS:ND1	42:2k:58:PRO:HD2	2.33	0.43
1:1A:1173:G:OP2	1:1A:1173:G:H2'	2.19	0.43
1:1A:2774:C:H2'	1:1A:2775:A:O4'	2.18	0.43
32:1a:532:A:N6	32:1a:1206:G:O2'	2.50	0.43
32:1a:1486:G:H2'	32:1a:1487:G:O4'	2.18	0.43
36:1e:51:VAL:O	36:1e:55:VAL:HG23	2.18	0.43
44:1m:67:GLU:HB3	44:1m:68:GLY:H	1.67	0.43
1:2A:196:A:N3	1:2A:196:A:H2'	2.33	0.43
1:2A:587:C:C6	1:2A:671:C:H1'	2.54	0.43
1:2A:1462:C:H4'	1:2A:2703:C:H5'	2.00	0.43
1:2A:2484:G:C2	1:2A:2485:G:C8	3.06	0.43
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.53	0.43
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.19	0.43
4:2E:27:LEU:HD22	15:2T:1:MET:SD	2.58	0.43
8:2I:81:VAL:O	8:2I:146:ALA:HA	2.18	0.43
12:2Q:85:LYS:HE2	22:20:7:LEU:HD12	2.00	0.43
22:20:23:VAL:HG22	22:20:38:VAL:HG22	2.00	0.43
32:2a:34:C:H2'	32:2a:35:G:H8	1.83	0.43
32:2a:89:C:H2'	32:2a:90:U:O4'	2.17	0.43
33:2b:215:LEU:HD23	33:2b:215:LEU:HA	1.86	0.43
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.53	0.43
54:2w:76:F3N:N	55:2x:76:31H:O2'	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.34	0.43
1:1A:2584:U:H2'	1:1A:2585:U:C6	2.53	0.43
15:1T:128:GLU:C	15:1T:130:ALA:H	2.27	0.43
21:1Z:1:MET:HE1	21:1Z:133:ILE:O	2.19	0.43
26:14:20:ASN:OD1	26:14:21:VAL:N	2.51	0.43
32:1a:926:G:H5''	32:1a:927:G:O5'	2.19	0.43
32:1a:1025:U:O2	32:1a:1036:G:C6	2.71	0.43
32:1a:1033:G:H3'	32:1a:1034:G:H8	1.84	0.43
38:1g:14:PRO:HG3	38:1g:21:VAL:HG13	2.00	0.43
41:1j:78:ASN:O	41:1j:80:LYS:N	2.51	0.43
51:1t:100:ILE:H	51:1t:100:ILE:HG12	1.60	0.43
1:2A:271(L):U:H5'	8:2I:50:ARG:HH11	1.84	0.43
1:2A:801:G:O6	5:2F:53:THR:OG1	2.36	0.43
1:2A:958:U:O2	2:2B:90:A:O2'	2.32	0.43
1:2A:2002:G:OP2	13:2R:9:LYS:NZ	2.51	0.43
1:2A:2572:A:OP1	1:2A:2574:G:O2'	2.35	0.43
1:2A:2815:C:H2'	1:2A:2816:C:C6	2.53	0.43
7:2H:3:ARG:HA	7:2H:3:ARG:HD2	1.21	0.43
10:2O:26:LYS:O	10:2O:30:ALA:HB2	2.17	0.43
10:2O:76:ALA:O	15:2T:74:ARG:HG3	2.17	0.43
19:2X:60:ARG:NH1	29:27:47:ARG:HH12	2.17	0.43
32:2a:533:A:OP1	62:2a:1918:HOH:O	2.20	0.43
32:2a:637:G:H2'	32:2a:638:G:H8	1.83	0.43
32:2a:707:C:H2'	32:2a:708:C:C6	2.53	0.43
32:2a:1287:A:H61	32:2a:1371:G:C1'	2.31	0.43
40:2i:9:ARG:HB3	40:2i:104:ARG:CZ	2.48	0.43
40:2i:99:LEU:HB3	40:2i:101:PHE:CD2	2.54	0.43
44:2m:115:LYS:HE2	44:2m:115:LYS:HB2	1.92	0.43
49:2r:48:GLY:O	49:2r:74:ARG:NH2	2.51	0.43
1:1A:922:U:H2'	1:1A:923:C:C6	2.53	0.43
1:1A:1006:C:C2	1:1A:1138:G:N2	2.86	0.43
1:1A:1050:A:H2'	1:1A:1051:G:O4'	2.18	0.43
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.53	0.43
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.53	0.43
24:12:1:MET:HE3	24:12:1:MET:HB2	1.90	0.43
28:16:6:ARG:HD3	28:16:24:GLU:OE2	2.18	0.43
30:18:26:LYS:HG2	30:18:46:ARG:O	2.19	0.43
32:1a:322:C:HO2'	51:1t:23:ARG:HD2	1.83	0.43
32:1a:894:G:H2'	32:1a:895:G:O4'	2.18	0.43
32:1a:1204:A:OP2	62:1a:1919:HOH:O	2.21	0.43
38:1g:72:ARG:HD3	38:1g:142:GLU:OE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:85:VAL:O	48:1q:89:LEU:HD12	2.19	0.43
50:1s:28:LYS:HB3	50:1s:47:HIS:CD2	2.49	0.43
51:1t:60:GLU:HG3	51:1t:81:LYS:HD2	2.01	0.43
1:2A:239:U:H2'	1:2A:240:G:O4'	2.18	0.43
1:2A:854:G:H2'	1:2A:855:G:H8	1.84	0.43
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.54	0.43
1:2A:1372:U:H2'	1:2A:1373:A:O4'	2.17	0.43
1:2A:1645:G:H5''	1:2A:1646:C:O4'	2.19	0.43
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.35	0.43
6:2G:39:ILE:HD11	6:2G:102:PHE:CZ	2.53	0.43
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.53	0.43
32:2a:391:G:C6	32:2a:392:G:C5	3.07	0.43
32:2a:587:G:N1	32:2a:754:C:OP2	2.48	0.43
32:2a:859:A:H2'	32:2a:860:A:O4'	2.19	0.43
32:2a:1394:A:N1	32:2a:1500:A:O2'	2.50	0.43
33:2b:27:LYS:HB2	33:2b:194:PRO:HD2	2.00	0.43
46:2o:30:ALA:HA	46:2o:85:LEU:HD11	2.00	0.43
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.19	0.43
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	2.00	0.43
50:2s:42:PRO:C	50:2s:44:MET:H	2.26	0.43
1:1A:432:A:N6	62:1A:4455:HOH:O	2.49	0.43
1:1A:652(S):C:H2'	1:1A:652(T):C:C6	2.53	0.43
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.33	0.43
1:1A:1324:G:O6	62:1A:4245:HOH:O	2.21	0.43
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.18	0.43
1:1A:1991:U:H2'	1:1A:1992:G:H5''	1.99	0.43
8:1I:109:ILE:HD13	8:1I:109:ILE:HA	1.71	0.43
8:1I:109:ILE:HG23	8:1I:130:TYR:CZ	2.53	0.43
30:18:61:LEU:O	30:18:63:PRO:HD3	2.17	0.43
32:1a:880:C:OP1	43:1l:8:ASN:ND2	2.47	0.43
32:1a:946:A:H2'	32:1a:947:G:C8	2.53	0.43
33:1b:122:PHE:HE2	33:1b:139:LYS:HB2	1.83	0.43
35:1d:43:HIS:HA	35:1d:46:LYS:HE3	2.01	0.43
39:1h:114:THR:HG22	39:1h:130:GLY:O	2.17	0.43
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	2.00	0.43
1:2A:288:C:H2'	1:2A:289:A:C8	2.54	0.43
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.54	0.43
1:2A:588:U:H2'	1:2A:589:C:C6	2.53	0.43
1:2A:1163:G:OP1	17:2V:24:LYS:NZ	2.43	0.43
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.19	0.43
5:2F:31:HIS:HB2	11:2P:9:ASN:OD1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	1.99	0.43
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.18	0.43
27:25:51:TYR:CZ	27:25:56:LYS:HB2	2.54	0.43
32:2a:9:G:OP1	36:2e:122:GLU:N	2.47	0.43
32:2a:575:G:O2'	32:2a:821:G:H5'	2.19	0.43
32:2a:986:A:H2'	32:2a:987:G:O4'	2.19	0.43
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.34	0.43
33:2b:78:GLN:O	33:2b:94:ASN:ND2	2.51	0.43
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.19	0.43
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.46	0.43
6:1G:43:LEU:HD13	6:1G:43:LEU:HA	1.84	0.43
22:10:70:GLN:OE1	22:10:80:HIS:NE2	2.48	0.43
24:12:53:LEU:HD23	24:12:53:LEU:HA	1.81	0.43
32:1a:977:A:H1'	32:1a:982:U:O4	2.18	0.43
35:1d:116:GLN:HE22	35:1d:161:ASN:HD21	1.67	0.43
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.53	0.43
40:1i:70:LYS:O	40:1i:74:ILE:HG13	2.18	0.43
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.18	0.43
1:2A:298:G:H5''	1:2A:299:A:OP1	2.18	0.43
1:2A:881:G:H3'	1:2A:882:G:C8	2.54	0.43
1:2A:1926:U:O2'	1:2A:1928:A:N7	2.48	0.43
1:2A:2130:U:C2'	1:2A:2158:A:H61	2.32	0.43
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.54	0.43
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.01	0.43
8:2I:38:LEU:HB2	8:2I:40:THR:HG23	1.99	0.43
11:2P:28:GLY:O	11:2P:30:THR:N	2.51	0.43
32:2a:993:G:N3	32:2a:993:G:H2'	2.33	0.43
32:2a:1206:G:H2'	32:2a:1207:2MG:C8	2.53	0.43
38:2g:74:GLU:HG2	38:2g:91:VAL:HG22	2.01	0.43
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	2.00	0.43
44:2m:120:LYS:HG2	44:2m:121:LYS:H	1.83	0.43
1:1A:185:U:H4'	1:1A:218:A:H4'	2.00	0.43
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.19	0.43
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.19	0.43
1:1A:2126:A:N3	1:1A:2127:G:H1'	2.34	0.43
20:1Y:67:LEU:HD23	20:1Y:71:LYS:HD3	2.01	0.43
26:14:53:GLU:H	26:14:53:GLU:HG3	1.42	0.43
26:14:61:ARG:O	26:14:62:ARG:C	2.62	0.43
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.33	0.43
32:1a:922:G:C6	32:1a:923:A:C6	3.06	0.43
32:1a:974:A:H8	32:1a:974:A:OP1	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1030(B):C:H2'	32:1a:1030(C):G:H5'	1.99	0.43
35:1d:116:GLN:NE2	35:1d:161:ASN:HD21	2.17	0.43
36:1e:89:ILE:HG21	36:1e:135:THR:HA	2.00	0.43
41:1j:7:LYS:HE3	41:1j:9:ARG:NH1	2.33	0.43
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	2.01	0.43
42:1k:58:PRO:O	42:1k:93:GLN:HG2	2.19	0.43
1:2A:1181:C:H2'	1:2A:1182:A:C8	2.54	0.43
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.54	0.43
1:2A:2318:G:H21	14:2S:3:ARG:CD	2.31	0.43
1:2A:2585:U:OP1	62:2A:3854:HOH:O	2.21	0.43
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.18	0.43
3:2D:211:ARG:HG3	3:2D:214:TRP:CE3	2.54	0.43
6:2G:43:LEU:HD12	6:2G:43:LEU:HA	1.81	0.43
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.44	0.43
30:28:23:VAL:CG2	30:28:47:LYS:HB3	2.48	0.43
32:2a:685:G:C2	32:2a:686:U:C4	3.07	0.43
32:2a:1320:C:H42	50:2s:36:ARG:NE	2.17	0.43
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.53	0.43
35:2d:50:ARG:HH12	36:2e:10:MET:HG3	1.84	0.43
40:2i:42:ARG:HE	40:2i:42:ARG:HB3	1.67	0.43
1:1A:444:C:H4'	5:1F:49:ALA:HB2	2.00	0.43
1:1A:491:G:H2'	1:1A:492:A:C8	2.53	0.43
1:1A:620:G:H2'	1:1A:620:G:N3	2.34	0.43
1:1A:1668:A:O2'	1:1A:1674:G:N7	2.47	0.43
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.54	0.43
1:1A:2741:A:H2'	1:1A:2742:C:O4'	2.19	0.43
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.53	0.43
11:1P:1:MET:HE3	11:1P:1:MET:HB2	1.84	0.43
28:16:17:LYS:HE3	28:16:17:LYS:HB3	1.91	0.43
32:1a:148:G:H2'	32:1a:149:A:C8	2.54	0.43
32:1a:1136:U:H5''	32:1a:1137:C:C4	2.54	0.43
32:1a:1378:C:O2	38:1g:76:ARG:NH1	2.52	0.43
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.18	0.43
33:1b:71:VAL:HG12	33:1b:170:GLU:HG3	2.01	0.43
35:1d:112:VAL:H	35:1d:116:GLN:NE2	2.17	0.43
40:1i:128:ARG:NH1	55:1x:35:A:OP2	2.52	0.43
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.84	0.43
56:1y:35:A:OP2	56:1y:35:A:H8	2.02	0.43
1:2A:271(F):C:H2'	1:2A:271(G):C:H6	1.84	0.43
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.19	0.43
5:2F:10:PRO:HB3	5:2F:17:ARG:NH1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:79:ASN:N	6:2G:79:ASN:OD1	2.51	0.43
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	2.01	0.43
21:2Z:70:LEU:HD12	21:2Z:70:LEU:HA	1.77	0.43
32:2a:37:U:O2'	32:2a:500:G:H4'	2.19	0.43
32:2a:266:G:H2'	32:2a:266:G:N3	2.34	0.43
32:2a:457:C:H2'	32:2a:458:C:C6	2.54	0.43
32:2a:555:C:H2'	32:2a:556:C:C6	2.54	0.43
32:2a:625:G:H4'	47:2p:16:HIS:CD2	2.54	0.43
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.53	0.43
32:2a:1133:G:H1	32:2a:1141:C:N4	2.17	0.43
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.53	0.43
35:2d:61:LYS:HD3	35:2d:206:PHE:CE2	2.53	0.43
42:2k:74:ALA:C	42:2k:76:GLY:H	2.27	0.43
43:2l:84:LEU:HB2	43:2l:105:TYR:CE2	2.54	0.43
44:2m:10:PRO:HG2	44:2m:21:TYR:CE1	2.54	0.43
1:1A:1052:C:H2'	1:1A:1053:C:H6	1.83	0.43
1:1A:1783:A:H5'	1:1A:2608:G:H4'	2.00	0.43
1:1A:2038:G:O6	62:1A:4241:HOH:O	2.19	0.43
1:1A:2145:C:O2'	1:1A:2147:G:N7	2.50	0.43
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	2.00	0.43
5:1F:32:LEU:HB3	5:1F:112:MET:HE1	2.00	0.43
7:1H:97:ARG:NE	7:1H:104:GLU:OE1	2.51	0.43
12:1Q:10:ARG:HH12	12:1Q:90:VAL:H	1.67	0.43
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.53	0.43
32:1a:186:C:H2'	32:1a:187:C:C6	2.54	0.43
32:1a:1264:C:H42	32:1a:1271:G:H1	1.67	0.43
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.43	0.43
1:2A:764:A:O4'	3:2D:213:ARG:HG3	2.19	0.43
1:2A:940:G:N3	1:2A:1191:G:H4'	2.34	0.43
1:2A:973:A:H8	1:2A:973:A:OP1	2.02	0.43
1:2A:2032:G:OP2	1:2A:2454:G:O2'	2.30	0.43
1:2A:2100:G:H1	1:2A:2189:U:H3	1.66	0.43
1:2A:2135:A:C5	1:2A:2136:C:H5	2.37	0.43
1:2A:2135:A:OP1	1:2A:2160:G:O2'	2.34	0.43
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.54	0.43
6:2G:143:GLU:OE2	26:24:26:SER:HB2	2.19	0.43
7:2H:56:SER:HB3	7:2H:61:HIS:ND1	2.34	0.43
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.18	0.43
21:2Z:153:SER:HB2	21:2Z:167:PRO:HB3	2.00	0.43
25:23:4:LEU:O	25:23:36:VAL:HA	2.19	0.43
32:2a:637:G:H2'	32:2a:638:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1388:C:H2'	32:2a:1389:C:C6	2.54	0.43
34:2c:30:ARG:HH21	45:2n:38:GLY:HA2	1.83	0.43
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.84	0.43
1:1A:1044:G:H5'	1:1A:1045:A:OP2	2.19	0.42
1:1A:1142(A):A:C4	1:1A:1144:G:N7	2.87	0.42
1:1A:1359:A:C2	1:1A:1372:U:O4	2.69	0.42
1:1A:1622:G:C2	1:1A:1623:G:C8	3.07	0.42
1:1A:2405:G:OP1	11:1P:77:ARG:NH2	2.52	0.42
1:1A:2701:C:H2'	1:1A:2702:U:H2'	2.01	0.42
1:1A:2808:U:H5''	1:1A:2891:G:O6	2.17	0.42
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.54	0.42
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.54	0.42
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.45	0.42
32:1a:553:A:H5''	43:1l:24:VAL:HG21	2.01	0.42
39:1h:77:GLU:HG2	39:1h:78:GLN:N	2.34	0.42
48:1q:99:SER:OG	48:1q:100:LYS:N	2.52	0.42
53:1v:12:A:H2'	53:1v:13:A:C8	2.54	0.42
1:2A:1027:A:C6	1:2A:1126:A:C4	3.07	0.42
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.54	0.42
1:2A:2659:G:OP1	7:2H:158:HIS:NE2	2.42	0.42
7:2H:140:LYS:HB2	7:2H:140:LYS:HE3	1.74	0.42
14:2S:80:LEU:HD12	14:2S:80:LEU:HA	1.88	0.42
14:2S:87:PHE:CE1	14:2S:102:ALA:HB2	2.54	0.42
15:2T:107:ASP:O	15:2T:111:ARG:HG3	2.19	0.42
20:2Y:6:HIS:H	20:2Y:6:HIS:CD2	2.36	0.42
32:2a:985:C:H2'	32:2a:986:A:C8	2.54	0.42
32:2a:1002:G:H1	32:2a:1038:C:H42	1.67	0.42
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.19	0.42
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.54	0.42
33:2b:118:LEU:HD23	33:2b:142:LEU:HB2	2.01	0.42
39:2h:100:ILE:H	39:2h:100:ILE:HG13	1.64	0.42
1:1A:340:A:H2'	1:1A:341:G:O4'	2.19	0.42
1:1A:363:G:H2'	1:1A:363(A):A:H8	1.84	0.42
1:1A:603:A:O4'	1:1A:655:A:N6	2.51	0.42
1:1A:1693:U:H1'	3:1D:14:ARG:HH21	1.84	0.42
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.54	0.42
7:1H:149:ARG:HH12	7:1H:167:GLU:CD	2.27	0.42
23:11:64:ALA:HA	23:11:67:ILE:HG13	2.01	0.42
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.20	0.42
34:1c:131:ARG:NH1	34:1c:166:GLU:HG3	2.33	0.42
34:1c:159:GLY:HA2	34:1c:193:TYR:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:99:ALA:O	49:1r:28:GLU:HA	2.18	0.42
1:2A:1179:C:H2'	1:2A:1180:C:C6	2.54	0.42
59:2A:3798:TYK:H14	59:2A:3798:TYK:H221	1.83	0.42
10:2O:120:GLU:HB2	15:2T:68:TYR:HE2	1.84	0.42
22:20:43:THR:HG23	22:20:43:THR:O	2.19	0.42
23:21:81:LYS:HB3	23:21:81:LYS:HE2	1.77	0.42
32:2a:501:C:H2'	32:2a:502:G:C8	2.53	0.42
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.19	0.42
32:2a:1004:A:H2'	32:2a:1005:A:H5'	2.01	0.42
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.54	0.42
32:2a:1502:A:C8	32:2a:1505:G:N2	2.87	0.42
35:2d:112:VAL:H	35:2d:116:GLN:NE2	2.17	0.42
55:2x:21:A:N6	55:2x:46:G:H2'	2.34	0.42
1:1A:694:U:OP1	3:1D:59:LYS:NZ	2.51	0.42
1:1A:1023:U:OP2	62:1A:4246:HOH:O	2.21	0.42
1:1A:2128:C:O2'	1:1A:2174:C:H4'	2.19	0.42
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.20	0.42
6:1G:60:LEU:HD12	6:1G:60:LEU:HA	1.85	0.42
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.19	0.42
15:1T:19:LEU:HD22	15:1T:86:ILE:HG13	2.01	0.42
32:1a:567:G:H2'	32:1a:568:G:O4'	2.19	0.42
33:1b:16:HIS:CG	33:1b:17:PHE:H	2.37	0.42
56:1y:70:G:H3'	56:1y:71:G:C8	2.52	0.42
1:2A:383:U:H2'	1:2A:385:C:H5	1.84	0.42
1:2A:445:C:OP1	16:2U:2:PRO:HA	2.20	0.42
1:2A:645:C:H5''	1:2A:646:A:OP2	2.20	0.42
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.34	0.42
1:2A:1999:C:H5''	1:2A:2723:C:O2'	2.19	0.42
1:2A:2164:C:C5	1:2A:2165:G:H1'	2.54	0.42
1:2A:2802:G:C4	1:2A:2803:C:H1'	2.53	0.42
2:2B:83:G:H5''	25:23:52:HIS:CD2	2.54	0.42
8:2I:61:ARG:HD3	8:2I:61:ARG:HA	1.79	0.42
9:2N:19:GLU:HA	9:2N:59:LYS:HB3	2.01	0.42
32:2a:114:U:O2'	32:2a:115:G:H5'	2.19	0.42
32:2a:1288:A:H2'	32:2a:1289:A:O4'	2.20	0.42
32:2a:1330:U:H2'	32:2a:1331:G:H5'	2.01	0.42
33:2b:223:ILE:HA	33:2b:226:ARG:HG2	2.00	0.42
36:2e:7:GLU:OE1	36:2e:37:ARG:NH2	2.47	0.42
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.84	0.42
1:1A:249:C:O2	30:18:12:LYS:NZ	2.41	0.42
1:1A:1584:C:O2'	1:1A:1586:A:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.54	0.42
3:1D:8:PRO:HB3	3:1D:14:ARG:HG3	1.99	0.42
12:1Q:17:LEU:HD23	12:1Q:17:LEU:HA	1.94	0.42
32:1a:724:G:C2	32:1a:725:G:C8	3.07	0.42
34:1c:119:ARG:HH21	34:1c:140:ARG:NH1	2.17	0.42
38:1g:69:VAL:O	38:1g:138:LYS:HG3	2.19	0.42
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.99	0.42
4:2E:35:GLN:OE1	4:2E:66:HIS:HE1	2.03	0.42
7:2H:97:ARG:HA	7:2H:125:VAL:HG11	2.02	0.42
10:2O:119:PRO:HB2	15:2T:68:TYR:CZ	2.55	0.42
15:2T:51:ARG:HG3	15:2T:98:LYS:HD2	2.01	0.42
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	2.01	0.42
18:2W:71:VAL:HA	18:2W:107:LEU:HD23	2.00	0.42
32:2a:176:C:H2'	32:2a:177:C:C6	2.55	0.42
32:2a:343:U:H2'	32:2a:345:C:C5	2.54	0.42
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.84	0.42
32:2a:1273:G:C6	32:2a:1274:G:C4	3.08	0.42
32:2a:1320:C:N3	50:2s:36:ARG:NH2	2.67	0.42
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.19	0.42
38:2g:18:TYR:CG	38:2g:59:LEU:HD13	2.55	0.42
45:2n:18:VAL:C	45:2n:20:ALA:H	2.26	0.42
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.19	0.42
1:1A:113:G:H5'	62:1A:4295:HOH:O	2.18	0.42
1:1A:370:G:H8	1:1A:370:G:OP2	2.03	0.42
1:1A:1568:G:H5'	3:1D:60:ARG:HA	2.02	0.42
1:1A:2667:C:H2'	1:1A:2668:G:O4'	2.19	0.42
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.18	0.42
2:1B:32:C:C2	2:1B:51:G:N2	2.88	0.42
32:1a:1005:A:H1'	32:1a:1036:G:O6	2.19	0.42
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.19	0.42
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.37	0.42
34:1c:19:GLU:HB3	34:1c:40:ARG:NH2	2.35	0.42
43:1l:12:ARG:NH1	43:1l:13:LYS:HE3	2.35	0.42
54:1w:1:G:H2'	54:1w:2:C:C6	2.54	0.42
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.83	0.42
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.54	0.42
1:2A:2680:C:H5'	4:2E:189:PRO:HA	2.02	0.42
1:2A:2808:U:H5''	1:2A:2891:G:O6	2.19	0.42
2:2B:17:C:H2'	2:2B:18:G:O4'	2.20	0.42
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	2.02	0.42
18:2W:23:LEU:HD21	27:25:25:LEU:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.54	0.42
21:2Z:130:PRO:HA	21:2Z:133:ILE:HD11	2.02	0.42
26:24:40:HIS:O	26:24:44:THR:HG22	2.18	0.42
32:2a:977:A:H2'	32:2a:978:A:H5''	2.01	0.42
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.54	0.42
32:2a:1053:G:O6	32:2a:1199:U:H2'	2.19	0.42
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.54	0.42
35:2d:180:GLY:O	35:2d:182:LYS:HG3	2.19	0.42
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.55	0.42
56:2y:2:C:H2'	56:2y:3:C:C6	2.54	0.42
1:1A:210:C:OP2	29:17:29:LYS:HE3	2.20	0.42
1:1A:400:G:N7	62:1A:4332:HOH:O	2.37	0.42
1:1A:889:C:O2'	1:1A:890:A:O4'	2.36	0.42
1:1A:1065:U:H1'	1:1A:1074:G:C2	2.55	0.42
1:1A:1156:A:OP1	16:1U:55:ARG:NH1	2.53	0.42
1:1A:2612:C:OP2	27:15:2:ALA:N	2.52	0.42
8:1I:2:LYS:HB2	8:1I:2:LYS:NZ	2.34	0.42
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	2.01	0.42
14:1S:61:ASN:HB3	14:1S:64:GLU:HB2	2.01	0.42
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.89	0.42
32:1a:688:G:H5'	42:1k:46:GLY:C	2.45	0.42
32:1a:952:U:H2'	32:1a:953:G:C8	2.53	0.42
32:1a:1027:C:H5	32:1a:1028:C:C4	2.37	0.42
32:1a:1134:G:H5'	32:1a:1135:U:OP2	2.19	0.42
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.50	0.42
33:1b:16:HIS:C	33:1b:18:GLY:H	2.28	0.42
36:1e:148:VAL:O	36:1e:152:ARG:HG3	2.20	0.42
1:2A:70:G:H5''	1:2A:112:U:O2	2.20	0.42
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.54	0.42
1:2A:571:A:H5'	1:2A:2030:A:N7	2.34	0.42
1:2A:754:C:H2'	1:2A:755:C:C6	2.55	0.42
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.20	0.42
1:2A:2123:G:H2'	1:2A:2124:G:C8	2.54	0.42
4:2E:16:ARG:NH1	4:2E:171:GLU:OE2	2.53	0.42
5:2F:160:ASN:HD22	5:2F:160:ASN:C	2.27	0.42
9:2N:4:TYR:HB2	16:2U:101:ARG:HH12	1.84	0.42
9:2N:67:LEU:C	9:2N:88:GLU:HG3	2.43	0.42
21:2Z:159:PRO:HA	21:2Z:161:VAL:H	1.84	0.42
32:2a:772:U:H2'	32:2a:773:G:O4'	2.20	0.42
32:2a:881:G:P	43:2l:12:ARG:HH22	2.43	0.42
32:2a:1005:A:H5''	32:2a:1006:C:H5	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1376:U:OP1	38:2g:98:SER:OG	2.36	0.42
34:2c:47:LEU:CD1	34:2c:68:VAL:HG11	2.49	0.42
35:2d:57:ARG:NH1	35:2d:205:GLU:HB3	2.34	0.42
41:2j:8:LEU:HD23	41:2j:8:LEU:H	1.85	0.42
41:2j:23:ILE:HA	41:2j:26:ALA:HB3	2.00	0.42
54:2w:37:MIA:H8	54:2w:37:MIA:O5'	2.19	0.42
55:2x:8:4SU:H1'	55:2x:48:C:O2	2.20	0.42
1:1A:476:G:H4'	1:1A:502:A:N1	2.35	0.42
1:1A:818:G:H4'	1:1A:838:C:O3'	2.19	0.42
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.20	0.42
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.34	0.42
5:1F:107:LYS:HE3	5:1F:206:ILE:C	2.44	0.42
6:1G:101:ILE:HG22	6:1G:105:LYS:HE2	2.00	0.42
32:1a:382:A:H2'	32:1a:383:A:H8	1.82	0.42
32:1a:685:G:O2'	32:1a:686:U:H5'	2.19	0.42
32:1a:743:U:H2'	32:1a:744:C:C6	2.54	0.42
32:1a:952:U:H2'	32:1a:953:G:H8	1.84	0.42
32:1a:1289:A:N1	32:1a:1371:G:O2'	2.52	0.42
35:1d:196:LEU:C	35:1d:198:VAL:H	2.27	0.42
38:1g:113:GLU:HB2	38:1g:118:VAL:HG13	2.02	0.42
38:1g:114:ARG:HB2	38:1g:115:ARG:NH1	2.35	0.42
1:2A:271(F):C:H2'	1:2A:271(G):C:C6	2.54	0.42
1:2A:272(D):G:C2	1:2A:272(E):G:C8	3.08	0.42
1:2A:909:A:C6	1:2A:912:C:C2	3.08	0.42
1:2A:1830:C:OP2	62:2A:3851:HOH:O	2.21	0.42
1:2A:2818:G:OP1	1:2A:2837:G:O2'	2.29	0.42
2:2B:60:C:H2'	2:2B:61:G:H8	1.83	0.42
2:2B:78:A:C2	2:2B:100:A:C4	3.08	0.42
6:2G:7:LEU:HD22	6:2G:104:GLU:N	2.35	0.42
32:2a:620:C:H2'	32:2a:621:A:O4'	2.19	0.42
32:2a:841:U:H6	32:2a:841:U:P	2.42	0.42
32:2a:841:U:H6	32:2a:841:U:OP2	2.03	0.42
32:2a:1092:A:N3	32:2a:1183:A:N6	2.67	0.42
32:2a:1103:C:H2'	32:2a:1104:G:O4'	2.20	0.42
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.19	0.42
37:2f:62:TRP:CH2	37:2f:64:GLN:HB2	2.54	0.42
1:1A:614:U:H2'	1:1A:614(A):U:O4'	2.20	0.42
1:1A:1455:G:O2'	1:1A:2853:C:OP1	2.29	0.42
18:1W:62:HIS:O	18:1W:64:MET:HG3	2.20	0.42
32:1a:377:G:OP1	47:1p:5:ARG:HD2	2.19	0.42
34:1c:96:GLY:O	34:1c:97:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:150:LYS:HD3	34:1c:152:ILE:HD11	2.01	0.42
36:1e:69:VAL:HG11	36:1e:113:ALA:HB1	2.02	0.42
1:2A:299:A:N1	1:2A:322:A:O2'	2.42	0.42
1:2A:856:C:H2'	1:2A:857:C:C6	2.55	0.42
1:2A:1651:G:H2'	1:2A:1652:A:O4'	2.20	0.42
1:2A:2419:U:H2'	1:2A:2420:C:C6	2.55	0.42
12:2Q:85:LYS:HG2	22:20:7:LEU:CB	2.49	0.42
14:2S:25:ARG:NH1	14:2S:42:ASP:OD2	2.49	0.42
26:24:48:ARG:HD2	26:24:48:ARG:HA	1.85	0.42
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.19	0.42
43:2l:56:ALA:HB2	43:2l:70:ILE:HD11	2.02	0.42
43:2l:117:ARG:HB3	43:2l:122:THR:HB	2.01	0.42
48:2q:95:TYR:HA	48:2q:98:LEU:HG	2.02	0.42
50:2s:51:VAL:O	50:2s:58:VAL:N	2.53	0.42
1:1A:535:C:O3'	16:1U:53:ARG:NH1	2.51	0.42
1:1A:832:G:N3	11:1P:53:GLY:HA3	2.35	0.42
1:1A:1082:U:C4	1:1A:1086:A:N1	2.83	0.42
1:1A:1418:G:OP2	62:1A:4253:HOH:O	2.21	0.42
1:1A:1812:A:O2'	3:1D:45:ASN:N	2.49	0.42
1:1A:2375:G:O2'	1:1A:2377:A:N7	2.42	0.42
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.55	0.42
21:1Z:36:LYS:HB2	21:1Z:36:LYS:HE3	1.85	0.42
32:1a:763:G:H2'	32:1a:764:C:C6	2.55	0.42
32:1a:1329:A:N7	52:1u:7:ARG:NH2	2.67	0.42
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.54	0.42
32:1a:1516:G:H2'	32:1a:1518:MA6:OP2	2.19	0.42
42:1k:51:LYS:HD2	42:1k:51:LYS:HA	1.76	0.42
56:1y:6:G:C6	56:1y:7:A:C6	3.08	0.42
56:1y:65:G:C6	56:1y:66:U:C4	3.08	0.42
1:2A:478:A:N1	1:2A:500:G:H4'	2.34	0.42
1:2A:626:U:O4	11:2P:107:LYS:HE2	2.19	0.42
1:2A:1604:C:O2'	1:2A:1610:A:N1	2.50	0.42
1:2A:2156:G:H4'	1:2A:2157:G:OP1	2.19	0.42
3:2D:85:ASP:OD2	3:2D:88:ARG:HD2	2.20	0.42
9:2N:59:LYS:HA	9:2N:61:ARG:HH21	1.84	0.42
21:2Z:146:ILE:HG23	21:2Z:174:VAL:O	2.20	0.42
25:23:8:LEU:HB2	25:23:28:LEU:HD22	2.02	0.42
26:24:69:LYS:HB2	26:24:69:LYS:HE2	1.70	0.42
32:2a:109:A:H2'	32:2a:326:G:N2	2.35	0.42
32:2a:155:C:H2'	32:2a:156:G:O4'	2.20	0.42
32:2a:544:G:C6	32:2a:545:C:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:691:G:O2'	32:2a:797:C:H4'	2.20	0.42
32:2a:779:C:H2'	32:2a:780:A:O4'	2.20	0.42
32:2a:922:G:N3	32:2a:1398:A:H2	2.18	0.42
32:2a:1004:A:C8	32:2a:1005:A:H4'	2.54	0.42
32:2a:1212:U:H5'	32:2a:1213:A:C8	2.55	0.42
32:2a:1418:A:H5''	32:2a:1419:G:OP2	2.20	0.42
33:2b:82:ARG:HB3	33:2b:94:ASN:OD1	2.20	0.42
42:2k:54:ARG:O	42:2k:57:THR:OG1	2.37	0.42
1:1A:586:A:N1	1:1A:809:G:O2'	2.46	0.42
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.20	0.42
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.20	0.42
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.44	0.42
1:1A:2023:G:H5'	1:1A:2617:C:H4'	2.02	0.42
1:1A:2040:C:H2'	1:1A:2041:U:O4'	2.20	0.42
1:1A:2098:U:H3	1:1A:2191:G:H1	1.66	0.42
1:1A:2117:A:H1'	1:1A:2118:U:H3'	2.00	0.42
1:1A:2477:C:N4	31:19:10:ILE:HG23	2.35	0.42
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	2.02	0.42
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	2.02	0.42
11:1P:19:VAL:HB	11:1P:31:ALA:HB1	2.02	0.42
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.19	0.42
26:14:59:PHE:CE2	50:1s:64:GLU:HB3	2.54	0.42
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.85	0.42
44:1m:70:LEU:HD23	44:1m:70:LEU:HA	1.92	0.42
47:1p:9:PHE:HB3	47:1p:10:GLY:H	1.72	0.42
1:2A:582:G:H2'	1:2A:583:G:C8	2.55	0.42
1:2A:987:G:O2'	1:2A:1000:A:N3	2.44	0.42
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.55	0.42
1:2A:1158:C:H4'	25:23:32:GLN:HB2	2.01	0.42
1:2A:2804:C:H2'	1:2A:2805:G:H8	1.85	0.42
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.20	0.42
20:2Y:5:MET:HE1	20:2Y:32:PRO:HA	2.01	0.42
32:2a:646:U:H2'	32:2a:647:C:C6	2.55	0.42
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.20	0.42
32:2a:1145:C:H4'	32:2a:1146:A:H8	1.85	0.42
32:2a:1183:A:O2'	32:2a:1185:G:OP2	2.38	0.42
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.55	0.42
33:2b:58:ILE:O	33:2b:62:ALA:N	2.40	0.42
33:2b:192:SER:O	33:2b:194:PRO:HD3	2.20	0.42
35:2d:88:VAL:HA	36:2e:97:GLY:HA3	2.02	0.42
42:2k:48:ILE:C	42:2k:50:TYR:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:53:ARG:HA	49:2r:56:THR:OG1	2.20	0.42
55:2x:23:C:H2'	55:2x:24:U:C6	2.55	0.42
1:1A:858:U:O2	1:1A:2268:A:H2'	2.20	0.41
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.20	0.41
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.20	0.41
1:1A:2512:C:H2'	1:1A:2513:G:O4'	2.20	0.41
1:1A:2853:C:H2'	1:1A:2854:G:C8	2.55	0.41
7:1H:98:LEU:HD23	7:1H:102:ALA:O	2.19	0.41
11:1P:94:GLU:HG3	11:1P:124:LYS:HB3	2.02	0.41
24:12:16:LEU:O	24:12:67:LYS:NZ	2.52	0.41
25:13:23:LEU:HD13	25:13:50:VAL:HG11	2.01	0.41
26:14:53:GLU:HB2	26:14:55:ARG:C	2.45	0.41
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.26	0.41
32:1a:1518:MA6:H93	32:1a:1519:MA6:C9	2.49	0.41
44:1m:79:LYS:NZ	44:1m:83:ASP:OD2	2.48	0.41
47:1p:6:LEU:HB3	47:1p:17:TYR:CD1	2.55	0.41
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.55	0.41
1:2A:1265:A:OP2	62:2A:3855:HOH:O	2.22	0.41
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	2.02	0.41
1:2A:2802:G:N3	1:2A:2803:C:H1'	2.35	0.41
4:2E:56:PRO:C	4:2E:58:ARG:H	2.28	0.41
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.51	0.41
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	2.02	0.41
11:2P:85:LEU:HG	11:2P:115:LEU:O	2.20	0.41
20:2Y:7:VAL:CG1	20:2Y:27:VAL:HG21	2.50	0.41
21:2Z:121:HIS:N	21:2Z:172:ALA:HB2	2.35	0.41
25:23:7:LYS:HG3	25:23:34:GLU:HG3	2.02	0.41
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.60	0.41
30:28:32:LEU:O	30:28:36:LYS:HE3	2.19	0.41
32:2a:539:A:H2'	32:2a:540:G:C8	2.55	0.41
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.55	0.41
34:2c:101:LEU:HD22	34:2c:102:ASN:N	2.35	0.41
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.53	0.41
38:2g:97:GLN:O	38:2g:101:LEU:HD13	2.20	0.41
43:2l:37:CYS:SG	43:2l:81:SER:HB2	2.60	0.41
51:2t:79:ARG:HD2	51:2t:83:ARG:NH2	2.35	0.41
55:2x:40:C:H2'	55:2x:41:C:C6	2.54	0.41
55:2x:43:A:H2'	55:2x:44:A:C8	2.55	0.41
1:1A:784:A:OP1	1:1A:2588:G:H5''	2.20	0.41
1:1A:1065:U:H5''	1:1A:1066:U:OP2	2.20	0.41
1:1A:1359:A:H2'	1:1A:1360:A:H5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1683:C:H2'	1:1A:1684:C:C6	2.56	0.41
1:1A:1710:C:O2'	1:1A:2858:C:N3	2.52	0.41
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.34	0.41
7:1H:105:LEU:HD12	7:1H:151:ILE:HD12	2.02	0.41
19:1X:63:LYS:O	19:1X:64:LYS:HD3	2.19	0.41
32:1a:262:A:C6	32:1a:263:A:C6	3.08	0.41
32:1a:452:A:H4'	47:1p:72:ARG:CZ	2.50	0.41
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.34	0.41
33:1b:48:MET:HA	33:1b:51:LEU:HD12	2.01	0.41
36:1e:9:LYS:HB2	36:1e:112:LEU:HD11	2.02	0.41
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.84	0.41
1:2A:274:G:C2	1:2A:363:G:C6	3.08	0.41
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.55	0.41
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.84	0.41
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.19	0.41
2:2B:94:C:H2'	2:2B:95:C:H6	1.85	0.41
6:2G:53:LEU:HD22	6:2G:53:LEU:HA	1.87	0.41
15:2T:73:GLU:OE2	15:2T:103:ARG:NE	2.51	0.41
32:2a:519:C:H2'	32:2a:520:A:O4'	2.21	0.41
32:2a:583:A:H2'	32:2a:584:G:O4'	2.20	0.41
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.19	0.41
32:2a:1039:C:C2	32:2a:1040:U:H1'	2.54	0.41
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.55	0.41
35:2d:191:ARG:HA	35:2d:191:ARG:HD2	1.96	0.41
48:2q:53:LEU:HD12	48:2q:53:LEU:HA	1.90	0.41
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.56	0.41
1:1A:1062:G:O5'	1:1A:1070:A:O2'	2.37	0.41
1:1A:1155:A:OP1	16:1U:55:ARG:HD2	2.21	0.41
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.20	0.41
1:1A:2206:G:H3'	1:1A:2207:G:N7	2.34	0.41
1:1A:2563:U:H4'	10:1O:28:SER:HA	2.03	0.41
5:1F:170:LEU:HD13	5:1F:172:TRP:CZ2	2.55	0.41
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.36	0.41
21:1Z:156:LYS:HG3	21:1Z:158:PRO:HD3	2.02	0.41
32:1a:44:G:C2	32:1a:45:U:H1'	2.55	0.41
32:1a:339:C:H2'	32:1a:340:U:C6	2.56	0.41
32:1a:1021:G:HO2'	32:1a:1022:G:P	2.39	0.41
32:1a:1219:U:OP1	45:1n:19:ARG:NH1	2.40	0.41
33:1b:62:ALA:HB3	33:1b:225:ALA:HB3	2.03	0.41
34:1c:22:TRP:CD1	34:1c:59:ARG:HD2	2.55	0.41
34:1c:35:GLU:HB3	34:1c:59:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:1y:6:G:O6	56:1y:7:A:N6	2.53	0.41
1:2A:860:U:C2	1:2A:2268:A:C8	3.08	0.41
1:2A:862:G:H2'	1:2A:863:A:O4'	2.20	0.41
1:2A:1364:G:C8	23:21:3:LYS:HD2	2.55	0.41
1:2A:2166:G:O6	1:2A:2171:A:N6	2.53	0.41
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.20	0.41
8:2I:129:THR:HA	8:2I:138:ILE:O	2.21	0.41
32:2a:509:A:N3	32:2a:543:C:O2'	2.45	0.41
32:2a:826:C:H4'	39:2h:12:ARG:HG2	2.02	0.41
32:2a:1103:C:P	33:2b:96:ARG:HH22	2.43	0.41
32:2a:1144:G:N2	32:2a:1146:A:H62	2.17	0.41
33:2b:178:ARG:NH1	33:2b:198:ASP:OD1	2.53	0.41
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.90	0.41
41:2j:74:ILE:HD12	41:2j:74:ILE:HA	1.87	0.41
46:2o:6:GLU:OE1	46:2o:6:GLU:N	2.52	0.41
46:2o:85:LEU:HD23	46:2o:85:LEU:HA	1.76	0.41
54:2w:8:4SU:HN3	54:2w:14:A:H62	1.67	0.41
54:2w:24:G:C6	54:2w:25:C:C4	3.08	0.41
1:1A:208:C:H2'	1:1A:209:C:C6	2.56	0.41
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.31	0.41
1:1A:2178:C:H2'	1:1A:2179:C:C6	2.54	0.41
1:1A:2893:G:H5''	1:1A:2894:G:O4'	2.21	0.41
19:1X:66:LEU:HD12	19:1X:66:LEU:HA	1.87	0.41
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.39	0.41
51:1t:89:ARG:O	51:1t:93:GLU:HG2	2.20	0.41
1:2A:29:U:H2'	1:2A:30:G:C8	2.56	0.41
1:2A:699:A:H2'	1:2A:700:G:O4'	2.20	0.41
1:2A:910:A:N3	1:2A:2264:C:O2'	2.51	0.41
1:2A:2104:G:H1	1:2A:2185:C:H42	1.68	0.41
1:2A:2503:8AH:O2'	1:2A:2505:G:OP2	2.38	0.41
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.53	0.41
3:2D:5:LYS:HE3	3:2D:5:LYS:HB3	1.89	0.41
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.21	0.41
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.50	0.41
32:2a:382:A:H2'	32:2a:383:A:C8	2.54	0.41
32:2a:741:G:H2'	32:2a:742:G:O4'	2.21	0.41
32:2a:885:G:O2'	32:2a:914:A:N1	2.51	0.41
32:2a:1320:C:H42	50:2s:36:ARG:HE	1.68	0.41
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.53	0.41
32:2a:1530:G:OP1	32:2a:1530:G:H4'	2.20	0.41
34:2c:123:GLN:HA	34:2c:126:ARG:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.20	0.41
40:2i:45:ALA:O	40:2i:48:GLU:HB2	2.20	0.41
42:2k:77:MET:HE2	42:2k:77:MET:HB2	1.92	0.41
48:2q:48:GLU:OE1	48:2q:50:LYS:HD2	2.21	0.41
50:2s:28:LYS:CB	50:2s:29:ARG:HA	2.42	0.41
52:2u:6:ARG:HH21	52:2u:15:ARG:NH2	2.18	0.41
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.55	0.41
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.55	0.41
1:1A:1797:C:H4'	3:1D:257:LEU:O	2.21	0.41
1:1A:2153:G:H2'	1:1A:2154:G:C8	2.55	0.41
3:1D:9:TYR:CE1	3:1D:13:ARG:HG3	2.55	0.41
5:1F:126:VAL:HG21	5:1F:129:PHE:CZ	2.55	0.41
32:1a:167:G:H2'	32:1a:168:G:C8	2.55	0.41
34:1c:114:PRO:O	34:1c:118:GLN:NE2	2.53	0.41
40:1i:8:GLY:HA3	40:1i:76:ALA:O	2.20	0.41
45:1n:33:VAL:HA	45:1n:40:CYS:HA	2.01	0.41
47:1p:60:LEU:HD12	47:1p:60:LEU:HA	1.94	0.41
54:1w:37:MIA:H8	54:1w:37:MIA:O5'	2.20	0.41
1:2A:276:A:H5''	1:2A:277:C:H5'	2.02	0.41
1:2A:900:A:H2'	1:2A:901:A:H8	1.85	0.41
1:2A:921:G:H2'	1:2A:922:U:C6	2.55	0.41
1:2A:1283:G:N2	1:2A:1285:G:H3'	2.35	0.41
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.56	0.41
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.36	0.41
2:2B:51:G:OP2	14:2S:61:ASN:HA	2.21	0.41
10:2O:29:ASN:OD1	10:2O:29:ASN:N	2.50	0.41
10:2O:69:ILE:HD13	10:2O:69:ILE:HA	1.82	0.41
12:2Q:26:TYR:CE1	12:2Q:28:ALA:HB2	2.55	0.41
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.36	0.41
21:2Z:98:MET:HE3	21:2Z:98:MET:HB2	1.95	0.41
32:2a:688:G:H5'	42:2k:46:GLY:C	2.46	0.41
32:2a:826:C:H2'	32:2a:827:U:C6	2.55	0.41
32:2a:952:U:H2'	32:2a:953:G:C8	2.55	0.41
32:2a:1307:U:H2'	32:2a:1308:U:C6	2.55	0.41
34:2c:20:SER:HB3	34:2c:22:TRP:NE1	2.35	0.41
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.20	0.41
38:2g:69:VAL:HG22	38:2g:135:VAL:HG13	2.02	0.41
40:2i:3:GLN:NE2	40:2i:20:ARG:HE	2.19	0.41
41:2j:61:GLU:OE1	45:2n:49:HIS:HE1	2.03	0.41
48:2q:45:HIS:O	48:2q:47:PRO:HD3	2.20	0.41
50:2s:81:ARG:HE	50:2s:81:ARG:HB3	1.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:2y:23:A:C6	56:2y:24:G:C5	3.09	0.41
56:2y:43:C:H2'	56:2y:44:G:H8	1.86	0.41
1:1A:217:G:OP2	62:1A:4248:HOH:O	2.21	0.41
1:1A:1124:C:OP1	62:1A:4252:HOH:O	2.21	0.41
2:1B:14:U:O2	2:1B:108:U:H4'	2.21	0.41
6:1G:18:GLU:HG3	6:1G:22:ARG:HD3	2.03	0.41
7:1H:7:LEU:HD12	7:1H:7:LEU:HA	1.90	0.41
7:1H:126:PRO:HD2	7:1H:130:ARG:O	2.20	0.41
10:1O:98:VAL:HG22	10:1O:118:ALA:HA	2.02	0.41
32:1a:104:G:C2	32:1a:105:G:C8	3.08	0.41
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.55	0.41
32:1a:502:G:H2'	32:1a:503:C:O4'	2.21	0.41
32:1a:935:A:O2'	32:1a:1383:C:N3	2.49	0.41
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	2.01	0.41
48:1q:81:ARG:HA	48:1q:81:ARG:HD2	1.80	0.41
51:1t:38:LYS:HG3	51:1t:39:LYS:N	2.35	0.41
1:2A:27:G:C2	1:2A:512:G:N3	2.88	0.41
1:2A:34:C:N4	1:2A:454:A:O2'	2.54	0.41
1:2A:84:A:H5''	20:2Y:8:LYS:HE3	2.02	0.41
1:2A:208:C:H2'	1:2A:209:C:H6	1.84	0.41
1:2A:493:G:H2'	1:2A:494:G:O4'	2.21	0.41
1:2A:881:G:C2	1:2A:882:G:H1'	2.55	0.41
1:2A:1147:C:H2'	1:2A:1148:A:C8	2.55	0.41
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.21	0.41
1:2A:1589:C:H2'	1:2A:1590:U:C6	2.56	0.41
1:2A:2130:U:O2'	1:2A:2133:G:H4'	2.20	0.41
1:2A:2875:C:O2'	15:2T:2:ASN:OD1	2.33	0.41
9:2N:67:LEU:HA	9:2N:87:LEU:HD23	2.01	0.41
9:2N:71:ILE:CG2	9:2N:84:LYS:HB3	2.51	0.41
10:2O:52:VAL:HG22	10:2O:94:ARG:NH2	2.36	0.41
21:2Z:158:PRO:O	21:2Z:161:VAL:HG12	2.20	0.41
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.53	0.41
33:2b:187:LEU:HD12	33:2b:214:ILE:HG21	2.02	0.41
1:1A:459:U:H5''	29:17:40:TRP:CD2	2.56	0.41
1:1A:2218:U:O4'	23:11:52:ARG:NH2	2.54	0.41
2:1B:2:C:H2'	2:1B:3:C:H6	1.86	0.41
2:1B:78:A:C2	2:1B:100:A:C4	3.08	0.41
11:1P:95:VAL:HG22	11:1P:125:VAL:HG12	2.03	0.41
15:1T:127:ALA:C	15:1T:129:ARG:N	2.78	0.41
32:1a:92:C:H2'	32:1a:93:G:H8	1.82	0.41
32:1a:445:G:H2'	32:1a:446:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:44:GLU:O	34:1c:48:TYR:HB2	2.20	0.41
56:1y:41:C:H2'	56:1y:42:C:O4'	2.21	0.41
1:2A:184:C:H2'	1:2A:185:U:C6	2.56	0.41
1:2A:601:C:O2	1:2A:605:C:H4'	2.21	0.41
1:2A:870:A:P	12:2Q:6:ARG:HH21	2.44	0.41
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	2.02	0.41
3:2D:97:TYR:C	3:2D:99:ASP:H	2.29	0.41
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.56	0.41
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.56	0.41
32:2a:335:C:H2'	32:2a:336:C:C6	2.56	0.41
32:2a:946:A:H2'	32:2a:947:G:C8	2.56	0.41
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	2.02	0.41
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.56	0.41
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.56	0.41
34:2c:88:ARG:HA	34:2c:91:LEU:CD1	2.50	0.41
54:2w:21:A:N6	54:2w:46:G7M:C4	2.84	0.41
54:2w:51:U:H3	54:2w:63:G:H1	1.69	0.41
56:2y:40:C:H2'	56:2y:41:C:C6	2.55	0.41
1:1A:2763:G:OP2	62:1A:4254:HOH:O	2.22	0.41
6:1G:3:LEU:HD12	6:1G:5:VAL:HG12	2.02	0.41
12:1Q:78:PRO:HD3	55:1x:1:C:C4	2.56	0.41
32:1a:192:U:H4'	51:1t:57:ARG:HD3	2.02	0.41
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.21	0.41
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.56	0.41
33:1b:116:GLU:HA	33:1b:119:GLU:HB2	2.02	0.41
36:1e:41:VAL:O	36:1e:66:MET:HA	2.20	0.41
38:1g:51:GLN:O	38:1g:55:GLY:HA2	2.20	0.41
56:1y:4:C:H2'	56:1y:5:G:O4'	2.20	0.41
1:2A:422:A:H2'	1:2A:423:A:C8	2.56	0.41
1:2A:911:A:N6	12:2Q:11:LYS:O	2.52	0.41
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.36	0.41
1:2A:2238:G:H5''	62:2A:4075:HOH:O	2.20	0.41
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.69	0.41
6:2G:45:GLU:H	6:2G:45:GLU:HG2	1.54	0.41
13:2R:33:ARG:HA	13:2R:114:VAL:O	2.20	0.41
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	2.02	0.41
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.20	0.41
32:2a:409:G:OP1	35:2d:24:GLU:N	2.54	0.41
32:2a:719:C:H42	49:2r:71:LYS:HE2	1.86	0.41
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.56	0.41
35:2d:13:ARG:HB3	35:2d:38:TYR:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.56	0.41
40:2i:127:LYS:O	40:2i:128:ARG:HB3	2.19	0.41
49:2r:25:THR:OG1	49:2r:42:ARG:NH2	2.53	0.41
51:2t:50:GLU:HA	51:2t:100:ILE:HG12	2.03	0.41
51:2t:79:ARG:HD2	51:2t:83:ARG:HH21	1.86	0.41
1:1A:362:U:H6	1:1A:362:U:H2'	1.67	0.41
1:1A:524:U:H2'	1:1A:525:U:C6	2.56	0.41
1:1A:556:G:H2'	1:1A:557:U:C6	2.56	0.41
1:1A:797:C:OP1	5:1F:60:SER:OG	2.35	0.41
1:1A:828:U:H4'	1:1A:831:G:N1	2.36	0.41
1:1A:1639:U:O2'	1:1A:2699:C:H4'	2.20	0.41
1:1A:2156:G:OP2	1:1A:2156:G:H8	2.04	0.41
1:1A:2406:U:H2'	1:1A:2406:U:H6	1.70	0.41
1:1A:2422:A:O4'	56:1y:76:A:N6	2.53	0.41
59:1A:4101:TYK:H14	59:1A:4101:TYK:H221	1.91	0.41
5:1F:178:PRO:O	5:1F:205:ARG:NH2	2.52	0.41
7:1H:127:GLU:CD	7:1H:130:ARG:HE	2.29	0.41
8:1I:61:ARG:HD3	8:1I:61:ARG:HA	1.95	0.41
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	2.03	0.41
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	2.01	0.41
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.56	0.41
24:12:35:LEU:HD12	24:12:53:LEU:HD12	2.02	0.41
32:1a:713:G:H2'	32:1a:714:G:C8	2.55	0.41
32:1a:1027:C:N1	32:1a:1034:G:N2	2.69	0.41
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.21	0.41
33:1b:155:LEU:HD12	33:1b:155:LEU:HA	1.92	0.41
35:1d:13:ARG:HB3	35:1d:38:TYR:O	2.21	0.41
35:1d:86:LYS:HE2	35:1d:86:LYS:HB2	1.89	0.41
35:1d:102:ASP:OD1	35:1d:103:ASN:N	2.54	0.41
35:1d:111:ALA:HA	35:1d:161:ASN:ND2	2.36	0.41
54:1w:63:G:H2'	54:1w:64:A:H8	1.85	0.41
55:1x:50:U:H2'	55:1x:51:C:C6	2.56	0.41
56:1y:35:A:H2'	56:1y:36:A:C8	2.55	0.41
1:2A:287:C:H2'	1:2A:288:C:C6	2.55	0.41
1:2A:1777:U:O2'	1:2A:1778:U:H5'	2.20	0.41
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.21	0.41
1:2A:2252:G:H2'	1:2A:2253:G:O4'	2.21	0.41
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.56	0.41
1:2A:2820:A:C5	13:2R:4:LEU:HD11	2.56	0.41
4:2E:170:LEU:HB3	4:2E:184:VAL:HG22	2.03	0.41
5:2F:116:ASP:OD2	5:2F:117:ARG:NH1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:123:LEU:HD21	8:2I:145:VAL:HA	2.01	0.41
11:2P:45:LEU:HA	11:2P:45:LEU:HD12	1.86	0.41
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.20	0.41
18:2W:7:ALA:HB2	18:2W:50:VAL:HG22	2.02	0.41
23:21:35:THR:OG1	23:21:35:THR:O	2.39	0.41
28:26:40:CYS:O	28:26:44:ARG:N	2.50	0.41
32:2a:153:C:H2'	32:2a:154:C:C6	2.55	0.41
32:2a:406:G:H4'	35:2d:5:ILE:HD11	2.03	0.41
32:2a:604:G:H2'	32:2a:605:U:O4'	2.21	0.41
32:2a:1095:U:H5''	32:2a:1109:C:O2	2.21	0.41
32:2a:1256:A:H61	32:2a:1278:U:H2'	1.85	0.41
33:2b:71:VAL:HA	33:2b:93:VAL:HG23	2.03	0.41
34:2c:7:PRO:HG2	34:2c:184:TYR:HB2	2.03	0.41
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	2.01	0.41
41:2j:50:ILE:HB	45:2n:41:ARG:NH1	2.36	0.41
55:2x:50:U:H2'	55:2x:51:C:C6	2.55	0.41
55:2x:66:C:H2'	55:2x:67:C:O4'	2.21	0.41
1:1A:810:U:H6	1:1A:810:U:O5'	2.04	0.41
1:1A:1456:G:OP2	62:1A:4251:HOH:O	2.21	0.41
1:1A:1907:G:H2'	1:1A:1908:C:C6	2.57	0.41
1:1A:2108:C:H2'	1:1A:2109:U:H6	1.86	0.41
3:1D:206:LEU:HD23	3:1D:206:LEU:HA	1.71	0.41
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.21	0.41
32:1a:309:G:O2'	32:1a:607:A:N1	2.49	0.41
32:1a:1002:G:N7	32:1a:1003:G:H1'	2.36	0.41
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.89	0.41
33:1b:212:GLN:O	33:1b:216:SER:N	2.33	0.41
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.56	0.41
48:1q:6:LEU:HB3	48:1q:23:VAL:HG11	2.02	0.41
1:2A:471:A:H2'	1:2A:472:A:O4'	2.21	0.41
1:2A:856:C:O4'	22:20:27:GLU:HB3	2.20	0.41
1:2A:952:G:C6	1:2A:953:A:N7	2.89	0.41
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.56	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.74	0.41
1:2A:1394:U:C4	1:2A:1395:A:C5	3.09	0.41
1:2A:2480:C:N4	1:2A:2481:G:C6	2.88	0.41
1:2A:2811:G:N2	1:2A:2891:G:H1'	2.35	0.41
2:2B:7:G:H2'	2:2B:8:U:O4'	2.21	0.41
5:2F:113:ALA:HB1	5:2F:186:ILE:HG21	2.03	0.41
6:2G:3:LEU:HD12	6:2G:3:LEU:H	1.86	0.41
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:2N:138:LEU:HD12	9:2N:138:LEU:HA	1.82	0.41
32:2a:337:C:H2'	32:2a:338:A:C8	2.56	0.41
32:2a:381:C:H2'	32:2a:382:A:O4'	2.21	0.41
32:2a:730:G:C5	32:2a:731:G:H1'	2.56	0.41
32:2a:876:G:O5'	39:2h:14:ARG:NH1	2.54	0.41
32:2a:1080:A:H5'	36:2e:14:ARG:HH21	1.86	0.41
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.50	0.41
50:2s:30:LEU:HA	50:2s:48:THR:O	2.20	0.41
1:1A:57:C:H2'	1:1A:58:G:O4'	2.21	0.40
1:1A:184:C:H2'	1:1A:185:U:H6	1.85	0.40
1:1A:272(G):C:H42	1:1A:363(C):G:H1	1.69	0.40
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.54	0.40
1:1A:1480:G:C6	1:1A:1481:U:N3	2.89	0.40
1:1A:2691:C:O3'	1:1A:2871:C:H4'	2.21	0.40
2:1B:66:A:N6	2:1B:109:C:H5'	2.33	0.40
5:1F:133:ASN:N	5:1F:138:GLU:OE1	2.37	0.40
7:1H:17:VAL:HG11	7:1H:50:VAL:HG21	2.03	0.40
11:1P:63:PRO:HD3	30:18:27:THR:HG22	2.03	0.40
32:1a:250:A:H5'	32:1a:252:U:O4'	2.21	0.40
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.49	0.40
39:1h:86:ILE:HG13	39:1h:135:CYS:HA	2.03	0.40
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	2.02	0.40
46:1o:17:ARG:HH11	46:1o:17:ARG:HG3	1.86	0.40
48:1q:13:ASP:OD1	48:1q:13:ASP:N	2.54	0.40
50:1s:51:VAL:O	50:1s:58:VAL:N	2.41	0.40
1:2A:223:A:N1	1:2A:407:G:O2'	2.43	0.40
1:2A:864:G:H1'	1:2A:914:C:H42	1.86	0.40
1:2A:981:A:N1	1:2A:2027:G:O2'	2.49	0.40
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.20	0.40
1:2A:1461:G:H2'	1:2A:1462:C:C6	2.56	0.40
1:2A:2875:C:H2'	1:2A:2876:G:O4'	2.21	0.40
6:2G:126:ASP:HB2	6:2G:130:ASN:O	2.22	0.40
10:2O:63:VAL:HG23	10:2O:64:ARG:HG3	2.02	0.40
15:2T:115:ARG:H	15:2T:115:ARG:HG3	1.62	0.40
19:2X:50:LYS:HB3	19:2X:87:GLN:HE22	1.86	0.40
26:24:47:GLN:O	26:24:49:PHE:HD1	2.04	0.40
32:2a:21:G:H2'	32:2a:22:G:C8	2.55	0.40
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.21	0.40
32:2a:393:A:OP1	62:2a:1921:HOH:O	2.22	0.40
32:2a:542:G:OP1	35:2d:10:ARG:NH2	2.39	0.40
32:2a:1057:G:H2'	32:2a:1058:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1329:A:OP2	52:2u:7:ARG:NH1	2.48	0.40
32:2a:1443:G:N2	32:2a:1460:A:H1'	2.36	0.40
34:2c:56:ASP:O	34:2c:57:ILE:HD12	2.20	0.40
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.20	0.40
40:2i:86:VAL:HA	40:2i:89:ASN:O	2.22	0.40
54:2w:68:C:H2'	54:2w:69:G:C8	2.56	0.40
1:1A:657:U:H2'	1:1A:658:C:H6	1.85	0.40
1:1A:875:G:O2'	21:1Z:151:HIS:HE1	2.05	0.40
1:1A:1800:C:OP1	3:1D:264:LYS:NZ	2.49	0.40
1:1A:2126:A:N1	1:1A:2162:G:O2'	2.51	0.40
1:1A:2469:A:O3'	12:1Q:56:ARG:NH1	2.54	0.40
2:1B:33:G:H5'	6:1G:2:PRO:HD3	2.03	0.40
2:1B:80:U:H2'	2:1B:81:G:C8	2.57	0.40
13:1R:20:LEU:O	13:1R:24:GLN:HG3	2.21	0.40
32:1a:256:U:H2'	32:1a:257:G:O4'	2.21	0.40
32:1a:375:U:C2	32:1a:376:G:C8	3.09	0.40
32:1a:627:G:O6	62:1a:1917:HOH:O	2.21	0.40
44:1m:13:LYS:HA	44:1m:44:ARG:HH11	1.87	0.40
48:1q:95:TYR:HA	48:1q:98:LEU:HG	2.02	0.40
1:2A:250:G:H2'	1:2A:251:A:C8	2.56	0.40
1:2A:271(S):G:C6	1:2A:271(T):C:C4	3.09	0.40
1:2A:527:C:C5	1:2A:2779:U:H2'	2.56	0.40
1:2A:652(B):A:N6	1:2A:655:A:O2'	2.52	0.40
1:2A:730:C:H5'	62:2A:3905:HOH:O	2.20	0.40
1:2A:852:G:H2'	1:2A:853:G:H8	1.87	0.40
1:2A:2033:A:O2'	1:2A:2035:G:OP2	2.30	0.40
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.43	0.40
6:2G:91:ARG:CZ	6:2G:91:ARG:HB3	2.51	0.40
13:2R:52:ILE:HD11	13:2R:116:LEU:HD22	2.02	0.40
32:2a:253:U:H2'	32:2a:254:G:C8	2.57	0.40
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.56	0.40
32:2a:1060:C:H4'	41:2j:51:ARG:HB3	2.04	0.40
33:2b:187:LEU:HD23	33:2b:188:ALA:N	2.36	0.40
39:2h:11:THR:HG23	39:2h:14:ARG:NH1	2.36	0.40
45:2n:53:LEU:HD23	45:2n:53:LEU:HA	1.91	0.40
1:1A:59:U:O2'	1:1A:74:A:OP2	2.37	0.40
1:1A:84:A:C5'	20:1Y:8:LYS:HG2	2.52	0.40
1:1A:764:A:O4'	3:1D:213:ARG:HG3	2.22	0.40
1:1A:1401:G:H2'	1:1A:1402:C:O4'	2.21	0.40
1:1A:2053:G:OP1	4:1E:144:ARG:HG3	2.20	0.40
1:1A:2156:G:OP2	1:1A:2156:G:C8	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:60:C:C2	2:1B:61:G:C8	3.09	0.40
4:1E:11:MET:HE2	4:1E:11:MET:HB3	1.96	0.40
12:1Q:63:LYS:HE2	12:1Q:65:PHE:CE1	2.57	0.40
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.21	0.40
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	2.03	0.40
32:1a:598:U:H2'	32:1a:599:C:C6	2.56	0.40
32:1a:620:C:H2'	32:1a:621:A:O4'	2.22	0.40
32:1a:1318:A:H4'	50:1s:10:PHE:CZ	2.56	0.40
33:1b:19:HIS:HA	33:1b:39:ILE:HG23	2.03	0.40
33:1b:97:TRP:CZ2	33:1b:102:LEU:HD13	2.57	0.40
37:1f:33:TYR:CD2	37:1f:75:LEU:HD23	2.56	0.40
47:1p:29:ASP:OD1	47:1p:29:ASP:N	2.53	0.40
56:1y:35:A:C6	56:1y:36:A:N6	2.89	0.40
56:1y:37:MIA:H8	56:1y:37:MIA:C5'	2.51	0.40
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.56	0.40
1:2A:500:G:N2	1:2A:502:A:H3'	2.35	0.40
1:2A:580:C:H2'	1:2A:581:C:C6	2.57	0.40
1:2A:612:C:C2	1:2A:616:G:N2	2.89	0.40
1:2A:817:C:O2'	1:2A:839:U:H5''	2.21	0.40
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.54	0.40
1:2A:1502:C:H2'	1:2A:1503:U:C6	2.56	0.40
1:2A:1557:C:H5''	1:2A:1558:A:OP2	2.21	0.40
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.22	0.40
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.22	0.40
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.36	0.40
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.54	0.40
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.86	0.40
1:2A:2802:G:C2	1:2A:2803:C:H1'	2.56	0.40
1:2A:2815:C:H2'	1:2A:2816:C:H6	1.86	0.40
4:2E:181:LEU:HD23	4:2E:181:LEU:HA	1.86	0.40
6:2G:114:ILE:HD12	6:2G:117:PHE:CD1	2.56	0.40
8:2I:57:ARG:O	8:2I:61:ARG:HB2	2.22	0.40
16:2U:74:LEU:H	16:2U:74:LEU:HD12	1.86	0.40
32:2a:636:U:H2'	32:2a:637:G:C8	2.55	0.40
32:2a:1010:G:C2	32:2a:1020:U:H1'	2.56	0.40
32:2a:1118:C:P	40:2i:104:ARG:HH11	2.40	0.40
34:2c:162:GLN:NE2	53:2v:24:A:O3'	2.55	0.40
35:2d:18:LYS:HE2	35:2d:20:TYR:CE1	2.57	0.40
35:2d:101:LEU:O	35:2d:104:VAL:HG22	2.21	0.40
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	2.04	0.40
55:2x:15:G:H5''	55:2x:16:C:OP2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:784:A:C5	3:1D:229:VAL:HG21	2.57	0.40
1:1A:784:A:C8	1:1A:792:G:C5	3.09	0.40
1:1A:1062:G:N2	1:1A:1077:A:H61	2.19	0.40
1:1A:1104:C:H2'	1:1A:1105:U:C6	2.56	0.40
1:1A:1313:U:H2'	1:1A:1610:A:C2	2.57	0.40
1:1A:1540:U:H2'	1:1A:1541:G:O4'	2.22	0.40
1:1A:1628:G:H2'	1:1A:1629:U:C6	2.57	0.40
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.57	0.40
1:1A:2148:G:C6	1:1A:2149:G:C5	3.08	0.40
1:1A:2206:G:H5''	1:1A:2207:G:C5	2.57	0.40
12:1Q:59:ARG:O	12:1Q:60:ARG:HB2	2.21	0.40
32:1a:257:G:C6	32:1a:258:G:C5	3.09	0.40
32:1a:295:C:H2'	32:1a:296:U:O4'	2.22	0.40
32:1a:1298:C:C4	38:1g:114:ARG:HD2	2.57	0.40
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	2.04	0.40
46:1o:84:LYS:O	46:1o:84:LYS:HD3	2.21	0.40
52:1u:6:ARG:HH21	52:1u:15:ARG:NH1	2.20	0.40
54:1w:2:C:H2'	54:1w:3:C:C6	2.57	0.40
56:1y:5:G:H1'	56:1y:69:G:N2	2.36	0.40
1:2A:271(K):U:O2	8:2I:50:ARG:HD3	2.21	0.40
1:2A:854:G:H2'	1:2A:855:G:C8	2.56	0.40
1:2A:921:G:H4'	1:2A:2269:A:C5	2.57	0.40
1:2A:1127:A:N7	1:2A:2488:A:O2'	2.47	0.40
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.08	0.40
1:2A:2393:A:H5''	11:2P:63:PRO:HB3	2.02	0.40
1:2A:2405:G:O2'	1:2A:2411:A:N6	2.54	0.40
1:2A:2557:G:H2'	1:2A:2558:C:H6	1.84	0.40
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.56	0.40
9:2N:71:ILE:HG21	9:2N:84:LYS:HB3	2.04	0.40
17:2V:12:TYR:CZ	17:2V:22:VAL:HG12	2.55	0.40
18:2W:86:LEU:HB2	18:2W:96:ILE:HG13	2.03	0.40
24:22:46:GLN:O	24:22:49:LYS:HG3	2.22	0.40
32:2a:730:G:OP1	62:2a:1922:HOH:O	2.22	0.40
32:2a:857:C:H2'	32:2a:858:G:O4'	2.22	0.40
32:2a:1000:U:H2'	32:2a:1001:A:C8	2.56	0.40
32:2a:1292:U:C2	32:2a:1293:G:C8	3.10	0.40
35:2d:88:VAL:HG13	36:2e:97:GLY:HA2	2.03	0.40
38:2g:111:ARG:HB3	38:2g:113:GLU:OE1	2.22	0.40
41:2j:42:THR:HG22	41:2j:66:ARG:HB2	2.03	0.40
1:1A:1971:A:C4	3:1D:241:PRO:HD3	2.57	0.40
1:1A:2029:G:H2'	1:1A:2031:A:OP1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.22	0.40
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	2.04	0.40
3:1D:133:LEU:HB3	3:1D:173:VAL:HG11	2.02	0.40
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	2.03	0.40
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.57	0.40
25:13:10:LYS:HB3	25:13:53:LEU:HA	2.04	0.40
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.26	0.40
41:1j:38:ILE:HG12	41:1j:71:LEU:HB3	2.03	0.40
44:1m:11:ARG:C	44:1m:13:LYS:H	2.30	0.40
49:1r:84:LYS:HE2	49:1r:84:LYS:HB2	1.86	0.40
54:1w:67:C:H2'	54:1w:68:C:C6	2.56	0.40
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.37	0.40
1:2A:1494:A:C6	1:2A:1495:A:C6	3.10	0.40
1:2A:1803:A:H4'	3:2D:259:THR:HG23	2.02	0.40
6:2G:43:LEU:C	6:2G:45:GLU:H	2.29	0.40
7:2H:24:VAL:HG13	7:2H:37:VAL:HG21	2.04	0.40
23:21:64:ALA:HA	23:21:67:ILE:HG13	2.02	0.40
32:2a:34:C:H2'	32:2a:35:G:C8	2.57	0.40
32:2a:130:A:H1'	32:2a:263:A:O2'	2.20	0.40
32:2a:994:A:N7	32:2a:1216:G:H4'	2.37	0.40
32:2a:1096:C:C2'	32:2a:1097:C:H5'	2.51	0.40
32:2a:1202:G:C1'	45:2n:29:ARG:HH11	2.35	0.40
32:2a:1278:U:H5'	32:2a:1279:A:H5'	2.03	0.40
32:2a:1434:A:H2'	32:2a:1435:G:O4'	2.21	0.40
35:2d:169:LYS:HE3	35:2d:169:LYS:HB2	1.81	0.40
36:2e:24:ARG:H	36:2e:24:ARG:HG2	1.73	0.40
36:2e:34:VAL:O	36:2e:42:GLY:N	2.50	0.40
36:2e:110:LEU:HD21	36:2e:139:LEU:HD21	2.03	0.40
41:2j:81:THR:HA	41:2j:84:GLN:HG3	2.04	0.40
47:2p:1:MET:HE2	47:2p:1:MET:HB3	1.93	0.40
56:2y:8:4SU:H1'	56:2y:48:C:H1'	2.03	0.40
56:2y:11:C:H2'	56:2y:12:U:C6	2.57	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%)	258 (94%)	15 (6%)	0	100	100
3	2D	273/276 (99%)	255 (93%)	18 (7%)	0	100	100
4	1E	202/206 (98%)	189 (94%)	12 (6%)	1 (0%)	24	39
4	2E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	24	39
5	1F	200/210 (95%)	195 (98%)	4 (2%)	1 (0%)	24	39
5	2F	200/210 (95%)	194 (97%)	4 (2%)	2 (1%)	12	20
6	1G	179/182 (98%)	168 (94%)	11 (6%)	0	100	100
6	2G	179/182 (98%)	159 (89%)	17 (10%)	3 (2%)	7	12
7	1H	172/180 (96%)	165 (96%)	7 (4%)	0	100	100
7	2H	172/180 (96%)	156 (91%)	15 (9%)	1 (1%)	21	34
8	1I	144/148 (97%)	124 (86%)	20 (14%)	0	100	100
8	2I	144/148 (97%)	123 (85%)	19 (13%)	2 (1%)	9	14
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	18	30
10	1O	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	16	27
10	2O	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
11	1P	147/150 (98%)	133 (90%)	11 (8%)	3 (2%)	6	10
11	2P	147/150 (98%)	130 (88%)	11 (8%)	6 (4%)	2	3
12	1Q	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
12	2Q	139/141 (99%)	122 (88%)	17 (12%)	0	100	100
13	1R	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
13	2R	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
14	1S	108/112 (96%)	103 (95%)	5 (5%)	0	100	100
14	2S	108/112 (96%)	102 (94%)	4 (4%)	2 (2%)	6	10
15	1T	129/146 (88%)	120 (93%)	9 (7%)	0	100	100
15	2T	129/146 (88%)	124 (96%)	5 (4%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	112 (98%)	2 (2%)	0	100	100
17	1V	99/101 (98%)	93 (94%)	5 (5%)	1 (1%)	12	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	2V	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12	20
18	1W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
18	2W	110/113 (97%)	107 (97%)	2 (2%)	1 (1%)	14	24
19	1X	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
19	2X	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
20	1Y	105/110 (96%)	98 (93%)	6 (6%)	1 (1%)	12	20
20	2Y	105/110 (96%)	100 (95%)	5 (5%)	0	100	100
21	1Z	148/206 (72%)	135 (91%)	12 (8%)	1 (1%)	18	30
21	2Z	156/206 (76%)	130 (83%)	22 (14%)	4 (3%)	4	6
22	10	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
22	20	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
23	11	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11	19
23	21	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
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%)	53 (93%)	3 (5%)	1 (2%)	6	11
26	14	67/71 (94%)	54 (81%)	9 (13%)	4 (6%)	1	1
26	24	67/71 (94%)	52 (78%)	12 (18%)	3 (4%)	2	2
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	47 (92%)	4 (8%)	0	100	100
29	17	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
29	27	46/49 (94%)	46 (100%)	0	0	100	100
30	18	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
30	28	62/65 (95%)	62 (100%)	0	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	197 (86%)	27 (12%)	5 (2%)	5	9
33	2b	229/256 (90%)	194 (85%)	28 (12%)	7 (3%)	3	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	1c	204/239 (85%)	186 (91%)	17 (8%)	1 (0%)	24	39
34	2c	204/239 (85%)	180 (88%)	24 (12%)	0	100	100
35	1d	206/209 (99%)	191 (93%)	14 (7%)	1 (0%)	24	39
35	2d	206/209 (99%)	193 (94%)	13 (6%)	0	100	100
36	1e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	9	14
36	2e	146/162 (90%)	137 (94%)	7 (5%)	2 (1%)	9	14
37	1f	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
37	2f	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
38	1g	153/156 (98%)	143 (94%)	9 (6%)	1 (1%)	18	30
38	2g	153/156 (98%)	133 (87%)	18 (12%)	2 (1%)	9	16
39	1h	135/138 (98%)	128 (95%)	7 (5%)	0	100	100
39	2h	135/138 (98%)	121 (90%)	13 (10%)	1 (1%)	18	30
40	1i	125/128 (98%)	112 (90%)	12 (10%)	1 (1%)	16	27
40	2i	125/128 (98%)	104 (83%)	21 (17%)	0	100	100
41	1j	95/105 (90%)	84 (88%)	9 (10%)	2 (2%)	5	9
41	2j	94/105 (90%)	82 (87%)	10 (11%)	2 (2%)	5	9
42	1k	112/129 (87%)	101 (90%)	8 (7%)	3 (3%)	4	6
42	2k	112/129 (87%)	101 (90%)	10 (9%)	1 (1%)	14	24
43	1l	119/132 (90%)	113 (95%)	6 (5%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	7 (6%)	1 (1%)	16	27
44	1m	121/126 (96%)	107 (88%)	12 (10%)	2 (2%)	7	12
44	2m	120/126 (95%)	103 (86%)	15 (12%)	2 (2%)	7	12
45	1n	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
45	2n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	12
46	1o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
46	2o	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
47	1p	80/88 (91%)	73 (91%)	7 (9%)	0	100	100
47	2p	80/88 (91%)	71 (89%)	9 (11%)	0	100	100
48	1q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12	20
48	2q	97/105 (92%)	90 (93%)	5 (5%)	2 (2%)	5	9
49	1r	66/88 (75%)	61 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	2r	66/88 (75%)	62 (94%)	3 (4%)	1 (2%)	8	13
50	1s	81/93 (87%)	73 (90%)	8 (10%)	0	100	100
50	2s	81/93 (87%)	66 (82%)	14 (17%)	1 (1%)	10	17
51	1t	94/106 (89%)	86 (92%)	4 (4%)	4 (4%)	2	2
51	2t	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	5	9
52	1u	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
52	2u	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
All	All	11368/12128 (94%)	10509 (92%)	769 (7%)	90 (1%)	16	27

All (90) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
11	1P	29	LYS
11	1P	36	LYS
21	1Z	53	ILE
26	14	45	GLY
26	14	62	ARG
33	1b	17	PHE
40	1i	54	ASP
44	1m	107	ALA
5	2F	130	ALA
8	2I	10	GLU
11	2P	29	LYS
11	2P	36	LYS
21	2Z	52	SER
33	2b	10	LEU
33	2b	17	PHE
33	2b	123	ALA
38	2g	80	VAL
41	2j	79	ARG
44	2m	67	GLU
48	2q	68	ARG
50	2s	81	ARG
17	1V	79	VAL
26	14	49	PHE
26	14	53	GLU
33	1b	124	SER
33	1b	126	GLU
35	1d	173	TRP

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Mol	Chain	Res	Type
41	1j	79	ARG
44	1m	67	GLU
48	1q	68	ARG
51	1t	100	ILE
8	2I	40	THR
11	2P	44	GLY
11	2P	45	LEU
17	2V	79	VAL
26	24	45	GLY
33	2b	21	ARG
38	2g	55	GLY
42	2k	49	GLY
51	2t	95	ALA
20	1Y	54	LYS
23	1l	3	LYS
36	1e	85	GLY
42	1k	77	MET
51	1t	10	LEU
6	2G	43	LEU
9	2N	2	LYS
11	2P	38	GLN
21	2Z	51	ALA
21	2Z	144	LEU
33	2b	8	LYS
36	2e	37	ARG
43	2l	105	TYR
45	2n	19	ARG
49	2r	36	ASN
4	1E	52	LEU
11	1P	38	GLN
33	1b	231	GLU
34	1c	3	ASN
41	1j	77	PRO
51	1t	96	GLY
51	1t	102	GLY
4	2E	52	LEU
26	24	48	ARG
44	2m	106	ASN
48	2q	67	LYS
38	1g	52	GLU
42	1k	105	VAL
5	2F	21	ALA

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Mol	Chain	Res	Type
6	2G	42	GLY
6	2G	51	ARG
7	2H	126	PRO
18	2W	60	ASN
33	2b	20	GLU
10	1O	5	GLN
14	2S	84	GLN
33	2b	9	GLU
36	2e	77	PRO
11	2P	122	PRO
25	23	59	VAL
42	1k	49	GLY
14	2S	109	GLY
26	24	29	PRO
39	2h	73	ASP
51	2t	47	GLY
36	1e	69	VAL
21	2Z	171	ILE
41	2j	37	PRO
33	1b	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	204 (95%)	11 (5%)	21	36
3	2D	215/218 (99%)	200 (93%)	15 (7%)	14	24
4	1E	164/166 (99%)	157 (96%)	7 (4%)	26	44
4	2E	164/166 (99%)	156 (95%)	8 (5%)	22	38
5	1F	160/166 (96%)	142 (89%)	18 (11%)	5	8
5	2F	159/166 (96%)	151 (95%)	8 (5%)	22	37
6	1G	143/156 (92%)	131 (92%)	12 (8%)	10	17
6	2G	143/156 (92%)	126 (88%)	17 (12%)	5	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	1H	144/148 (97%)	138 (96%)	6 (4%)	26	45
7	2H	144/148 (97%)	127 (88%)	17 (12%)	5	7
8	1I	113/124 (91%)	91 (80%)	22 (20%)	1	2
8	2I	105/124 (85%)	90 (86%)	15 (14%)	3	4
9	1N	118/119 (99%)	107 (91%)	11 (9%)	8	13
9	2N	118/119 (99%)	107 (91%)	11 (9%)	8	13
10	1O	100/100 (100%)	97 (97%)	3 (3%)	36	57
10	2O	100/100 (100%)	96 (96%)	4 (4%)	28	47
11	1P	115/116 (99%)	105 (91%)	10 (9%)	9	16
11	2P	115/116 (99%)	105 (91%)	10 (9%)	9	16
12	1Q	111/111 (100%)	107 (96%)	4 (4%)	31	51
12	2Q	111/111 (100%)	107 (96%)	4 (4%)	31	51
13	1R	101/101 (100%)	95 (94%)	6 (6%)	18	30
13	2R	101/101 (100%)	97 (96%)	4 (4%)	28	47
14	1S	86/88 (98%)	77 (90%)	9 (10%)	6	10
14	2S	85/88 (97%)	72 (85%)	13 (15%)	3	4
15	1T	115/127 (91%)	110 (96%)	5 (4%)	26	44
15	2T	113/127 (89%)	106 (94%)	7 (6%)	16	29
16	1U	93/94 (99%)	90 (97%)	3 (3%)	34	55
16	2U	93/94 (99%)	88 (95%)	5 (5%)	20	35
17	1V	80/82 (98%)	75 (94%)	5 (6%)	16	29
17	2V	80/82 (98%)	72 (90%)	8 (10%)	7	11
18	1W	90/92 (98%)	84 (93%)	6 (7%)	15	25
18	2W	90/92 (98%)	84 (93%)	6 (7%)	15	25
19	1X	77/78 (99%)	75 (97%)	2 (3%)	40	63
19	2X	77/78 (99%)	74 (96%)	3 (4%)	28	48
20	1Y	85/91 (93%)	79 (93%)	6 (7%)	13	23
20	2Y	85/91 (93%)	74 (87%)	11 (13%)	4	6
21	1Z	135/179 (75%)	124 (92%)	11 (8%)	11	18
21	2Z	137/179 (76%)	123 (90%)	14 (10%)	7	10
22	10	65/67 (97%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	20	65/67 (97%)	61 (94%)	4 (6%)	16	29
23	11	80/83 (96%)	78 (98%)	2 (2%)	42	64
23	21	80/83 (96%)	73 (91%)	7 (9%)	9	15
24	12	65/67 (97%)	63 (97%)	2 (3%)	35	56
24	22	65/67 (97%)	59 (91%)	6 (9%)	8	14
25	13	51/52 (98%)	46 (90%)	5 (10%)	7	11
25	23	50/52 (96%)	45 (90%)	5 (10%)	7	11
26	14	59/63 (94%)	54 (92%)	5 (8%)	10	17
26	24	53/63 (84%)	49 (92%)	4 (8%)	12	21
27	15	50/52 (96%)	46 (92%)	4 (8%)	11	19
27	25	50/52 (96%)	48 (96%)	2 (4%)	28	47
28	16	51/52 (98%)	45 (88%)	6 (12%)	5	7
28	26	50/52 (96%)	41 (82%)	9 (18%)	2	2
29	17	41/42 (98%)	36 (88%)	5 (12%)	5	7
29	27	41/42 (98%)	38 (93%)	3 (7%)	13	22
30	18	54/55 (98%)	51 (94%)	3 (6%)	19	32
30	28	54/55 (98%)	51 (94%)	3 (6%)	19	32
31	19	34/34 (100%)	34 (100%)	0	100	100
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	30
33	1b	192/220 (87%)	174 (91%)	18 (9%)	8	13
33	2b	187/220 (85%)	163 (87%)	24 (13%)	4	6
34	1c	142/188 (76%)	127 (89%)	15 (11%)	6	10
34	2c	140/188 (74%)	126 (90%)	14 (10%)	7	11
35	1d	169/181 (93%)	152 (90%)	17 (10%)	7	11
35	2d	173/181 (96%)	162 (94%)	11 (6%)	16	28
36	1e	113/123 (92%)	100 (88%)	13 (12%)	5	8
36	2e	114/123 (93%)	103 (90%)	11 (10%)	8	12
37	1f	84/90 (93%)	75 (89%)	9 (11%)	6	9
37	2f	85/90 (94%)	80 (94%)	5 (6%)	18	30
38	1g	119/127 (94%)	100 (84%)	19 (16%)	2	3
38	2g	120/127 (94%)	114 (95%)	6 (5%)	22	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	1h	114/119 (96%)	108 (95%)	6 (5%)	20	35
39	2h	114/119 (96%)	107 (94%)	7 (6%)	17	30
40	1i	90/99 (91%)	76 (84%)	14 (16%)	2	3
40	2i	89/99 (90%)	72 (81%)	17 (19%)	1	2
41	1j	66/92 (72%)	58 (88%)	8 (12%)	5	7
41	2j	69/92 (75%)	59 (86%)	10 (14%)	3	4
42	1k	82/99 (83%)	74 (90%)	8 (10%)	7	11
42	2k	83/99 (84%)	79 (95%)	4 (5%)	23	39
43	1l	96/108 (89%)	90 (94%)	6 (6%)	16	29
43	2l	96/108 (89%)	91 (95%)	5 (5%)	21	36
44	1m	93/101 (92%)	84 (90%)	9 (10%)	8	12
44	2m	92/101 (91%)	80 (87%)	12 (13%)	4	6
45	1n	49/50 (98%)	45 (92%)	4 (8%)	10	18
45	2n	49/50 (98%)	44 (90%)	5 (10%)	7	10
46	1o	78/80 (98%)	75 (96%)	3 (4%)	29	49
46	2o	78/80 (98%)	73 (94%)	5 (6%)	16	28
47	1p	69/74 (93%)	62 (90%)	7 (10%)	7	11
47	2p	68/74 (92%)	60 (88%)	8 (12%)	5	7
48	1q	94/97 (97%)	90 (96%)	4 (4%)	26	44
48	2q	94/97 (97%)	85 (90%)	9 (10%)	8	12
49	1r	59/77 (77%)	57 (97%)	2 (3%)	32	53
49	2r	59/77 (77%)	56 (95%)	3 (5%)	21	36
50	1s	69/80 (86%)	67 (97%)	2 (3%)	37	58
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4	5
51	1t	70/82 (85%)	63 (90%)	7 (10%)	7	11
51	2t	70/82 (85%)	64 (91%)	6 (9%)	10	16
52	1u	18/22 (82%)	17 (94%)	1 (6%)	19	32
52	2u	18/22 (82%)	16 (89%)	2 (11%)	6	9
All	All	9303/10064 (92%)	8544 (92%)	759 (8%)	10	18

All (759) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	12	SER
3	1D	37	LEU
3	1D	38	LYS
3	1D	99	ASP
3	1D	106	ILE
3	1D	173	VAL
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	273	ARG
3	1D	275	LYS
4	1E	12	THR
4	1E	47	VAL
4	1E	49	LEU
4	1E	73	GLU
4	1E	116	VAL
4	1E	184	VAL
4	1E	195	LEU
5	1F	12	LEU
5	1F	24	LEU
5	1F	28	ILE
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	112	MET
5	1F	127	GLU
5	1F	140	LEU
5	1F	144	LYS
5	1F	158	THR
5	1F	162	LEU
5	1F	168	ARG
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	3	LEU
6	1G	5	VAL
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	82	LEU
6	1G	109	VAL

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Mol	Chain	Res	Type
6	1G	126	ASP
6	1G	133	LEU
6	1G	139	LEU
6	1G	148	MET
6	1G	149	VAL
7	1H	15	VAL
7	1H	84	SER
7	1H	89	ILE
7	1H	116	GLU
7	1H	119	GLU
7	1H	129	THR
8	1I	2	LYS
8	1I	10	GLU
8	1I	12	LEU
8	1I	20	ASP
8	1I	40	THR
8	1I	41	GLU
8	1I	44	LEU
8	1I	47	LEU
8	1I	75	LEU
8	1I	76	THR
8	1I	77	LEU
8	1I	85	GLU
8	1I	87	LYS
8	1I	92	VAL
8	1I	101	LEU
8	1I	105	HIS
8	1I	108	THR
8	1I	109	ILE
8	1I	122	GLU
8	1I	123	LEU
8	1I	127	VAL
8	1I	129	THR
9	1N	2	LYS
9	1N	5	VAL
9	1N	12	ARG
9	1N	14	VAL
9	1N	28	THR
9	1N	48	MET
9	1N	61	ARG
9	1N	62	VAL
9	1N	67	LEU

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Mol	Chain	Res	Type
9	1N	96	GLU
9	1N	138	LEU
10	1O	28	SER
10	1O	98	VAL
10	1O	106	LEU
11	1P	7	ARG
11	1P	45	LEU
11	1P	75	ILE
11	1P	76	LYS
11	1P	90	ARG
11	1P	95	VAL
11	1P	98	GLU
11	1P	126	VAL
11	1P	147	LEU
11	1P	149	GLU
12	1Q	8	LYS
12	1Q	56	ARG
12	1Q	75	THR
12	1Q	109	VAL
13	1R	6	SER
13	1R	15	SER
13	1R	36	THR
13	1R	67	LEU
13	1R	104	ARG
13	1R	114	VAL
14	1S	14	VAL
14	1S	25	ARG
14	1S	46	VAL
14	1S	53	SER
14	1S	68	GLN
14	1S	69	VAL
14	1S	73	LEU
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	36	GLU
15	1T	49	VAL
15	1T	96	ARG
15	1T	128	GLU
16	1U	74	LEU
16	1U	95	LEU
16	1U	117	GLN

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Mol	Chain	Res	Type
17	1V	28	GLU
17	1V	46	VAL
17	1V	73	SER
17	1V	79	VAL
17	1V	85	LYS
18	1W	4	LYS
18	1W	11	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	60	ASN
18	1W	101	SER
19	1X	72	LYS
19	1X	92	LEU
20	1Y	1	MET
20	1Y	7	VAL
20	1Y	64	GLU
20	1Y	67	LEU
20	1Y	72	VAL
20	1Y	99	CYS
21	1Z	49	ARG
21	1Z	53	ILE
21	1Z	61	LEU
21	1Z	72	ARG
21	1Z	77	ASP
21	1Z	129	SER
21	1Z	138	GLU
21	1Z	149	SER
21	1Z	154	ASP
21	1Z	170	THR
21	1Z	171	ILE
23	11	46	LEU
23	11	81	LYS
24	12	19	VAL
24	12	65	ASN
25	13	23	LEU
25	13	34	GLU
25	13	54	VAL
25	13	56	VAL
25	13	60	GLU
26	14	21	VAL
26	14	35	VAL
26	14	49	PHE

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Mol	Chain	Res	Type
26	14	53	GLU
26	14	67	TYR
27	15	6	VAL
27	15	40	LYS
27	15	55	ARG
27	15	58	LEU
28	16	4	GLU
28	16	5	VAL
28	16	9	LEU
28	16	19	ARG
28	16	47	THR
28	16	48	VAL
29	17	24	THR
29	17	29	LYS
29	17	41	ARG
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	23	VAL
30	18	29	LYS
33	1b	8	LYS
33	1b	12	GLU
33	1b	35	GLU
33	1b	39	ILE
33	1b	54	THR
33	1b	67	THR
33	1b	80	ILE
33	1b	130	ARG
33	1b	133	LYS
33	1b	138	LEU
33	1b	140	HIS
33	1b	150	SER
33	1b	160	ASP
33	1b	185	ILE
33	1b	200	ILE
33	1b	208	ILE
33	1b	215	LEU
33	1b	219	VAL
34	1c	3	ASN
34	1c	15	THR
34	1c	17	ASP
34	1c	20	SER

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Mol	Chain	Res	Type
34	1c	58	GLU
34	1c	66	VAL
34	1c	70	VAL
34	1c	77	ILE
34	1c	91	LEU
34	1c	178	LEU
34	1c	179	ARG
34	1c	188	LEU
34	1c	195	VAL
34	1c	206	GLU
34	1c	207	VAL
35	1d	5	ILE
35	1d	59	ARG
35	1d	61	LYS
35	1d	70	ILE
35	1d	112	VAL
35	1d	119	GLN
35	1d	135	LEU
35	1d	140	VAL
35	1d	141	ARG
35	1d	144	ASP
35	1d	148	VAL
35	1d	157	LEU
35	1d	158	ILE
35	1d	177	ASP
35	1d	178	VAL
35	1d	181	MET
35	1d	194	LEU
36	1e	10	MET
36	1e	16	THR
36	1e	20	GLN
36	1e	31	LEU
36	1e	41	VAL
36	1e	51	VAL
36	1e	56	GLN
36	1e	63	ARG
36	1e	67	VAL
36	1e	79	GLU
36	1e	91	LEU
36	1e	92	LYS
36	1e	131	ILE
37	1f	55	ASP

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Mol	Chain	Res	Type
37	1f	57	GLN
37	1f	70	ASP
37	1f	72	VAL
37	1f	75	LEU
37	1f	78	GLU
37	1f	81	ILE
37	1f	85	VAL
37	1f	98	LEU
38	1g	12	LEU
38	1g	16	LEU
38	1g	22	LEU
38	1g	24	THR
38	1g	32	ARG
38	1g	50	ILE
38	1g	51	GLN
38	1g	53	LYS
38	1g	61	VAL
38	1g	76	ARG
38	1g	78	ARG
38	1g	85	TYR
38	1g	98	SER
38	1g	104	LEU
38	1g	110	GLN
38	1g	113	GLU
38	1g	114	ARG
38	1g	120	ILE
38	1g	131	LYS
39	1h	19	VAL
39	1h	25	ASP
39	1h	51	VAL
39	1h	52	ASP
39	1h	54	ASP
39	1h	133	LEU
40	1i	14	VAL
40	1i	17	VAL
40	1i	23	ASN
40	1i	41	VAL
40	1i	42	ARG
40	1i	47	LEU
40	1i	50	LEU
40	1i	53	VAL
40	1i	64	THR

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Mol	Chain	Res	Type
40	1i	81	ILE
40	1i	83	ARG
40	1i	96	LEU
40	1i	103	THR
40	1i	128	ARG
41	1j	8	LEU
41	1j	38	ILE
41	1j	46	ARG
41	1j	72	VAL
41	1j	81	THR
41	1j	92	THR
41	1j	98	ILE
41	1j	100	THR
42	1k	14	VAL
42	1k	33	THR
42	1k	48	ILE
42	1k	84	VAL
42	1k	87	THR
42	1k	105	VAL
42	1k	109	VAL
42	1k	114	VAL
43	1l	7	ILE
43	1l	18	VAL
43	1l	22	SER
43	1l	36	VAL
43	1l	83	VAL
43	1l	116	SER
44	1m	4	ILE
44	1m	15	VAL
44	1m	43	THR
44	1m	49	THR
44	1m	70	LEU
44	1m	98	VAL
44	1m	106	ASN
44	1m	109	THR
44	1m	122	LYS
45	1n	13	THR
45	1n	18	VAL
45	1n	33	VAL
45	1n	56	VAL
46	1o	39	LEU
46	1o	45	VAL

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Mol	Chain	Res	Type
46	1o	76	GLU
47	1p	20	VAL
47	1p	21	VAL
47	1p	27	LYS
47	1p	45	THR
47	1p	53	VAL
47	1p	67	THR
47	1p	76	GLN
48	1q	11	VAL
48	1q	52	LYS
48	1q	53	LEU
48	1q	89	LEU
49	1r	36	ASN
49	1r	42	ARG
50	1s	28	LYS
50	1s	37	ARG
51	1t	10	LEU
51	1t	13	LEU
51	1t	24	LEU
51	1t	30	LYS
51	1t	53	LEU
51	1t	71	THR
51	1t	100	ILE
52	1u	15	ARG
3	2D	3	VAL
3	2D	22	SER
3	2D	38	LYS
3	2D	88	ARG
3	2D	142	VAL
3	2D	173	VAL
3	2D	185	VAL
3	2D	200	ASP
3	2D	204	ILE
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	270	ILE
3	2D	275	LYS
4	2E	7	VAL
4	2E	38	THR
4	2E	73	GLU

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Mol	Chain	Res	Type
4	2E	90	THR
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	196	VAL
5	2F	33	LEU
5	2F	53	THR
5	2F	60	SER
5	2F	70	THR
5	2F	158	THR
5	2F	162	LEU
5	2F	183	VAL
5	2F	192	LEU
6	2G	5	VAL
6	2G	21	ARG
6	2G	28	VAL
6	2G	31	VAL
6	2G	39	ILE
6	2G	45	GLU
6	2G	49	ASP
6	2G	51	ARG
6	2G	53	LEU
6	2G	58	GLN
6	2G	91	ARG
6	2G	92	VAL
6	2G	123	ASN
6	2G	126	ASP
6	2G	140	ILE
6	2G	145	THR
6	2G	165	THR
7	2H	3	ARG
7	2H	6	ARG
7	2H	15	VAL
7	2H	16	SER
7	2H	40	GLU
7	2H	44	VAL
7	2H	49	VAL
7	2H	51	ARG
7	2H	70	THR
7	2H	71	LEU
7	2H	88	LEU
7	2H	103	LEU

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Mol	Chain	Res	Type
7	2H	115	VAL
7	2H	116	GLU
7	2H	122	THR
7	2H	129	THR
7	2H	141	VAL
8	2I	14	ASP
8	2I	15	VAL
8	2I	19	VAL
8	2I	37	VAL
8	2I	38	LEU
8	2I	58	LEU
8	2I	61	ARG
8	2I	68	LEU
8	2I	82	ARG
8	2I	102	SER
8	2I	108	THR
8	2I	117	GLU
8	2I	122	GLU
8	2I	127	VAL
8	2I	133	HIS
9	2N	5	VAL
9	2N	14	VAL
9	2N	15	LEU
9	2N	22	THR
9	2N	28	THR
9	2N	38	HIS
9	2N	48	MET
9	2N	61	ARG
9	2N	62	VAL
9	2N	73	THR
9	2N	121	LYS
10	2O	19	ILE
10	2O	69	ILE
10	2O	98	VAL
10	2O	113	LYS
11	2P	7	ARG
11	2P	45	LEU
11	2P	77	ARG
11	2P	95	VAL
11	2P	98	GLU
11	2P	121	LYS
11	2P	135	LEU

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Mol	Chain	Res	Type
11	2P	147	LEU
11	2P	148	LEU
11	2P	149	GLU
12	2Q	22	LYS
12	2Q	56	ARG
12	2Q	75	THR
12	2Q	133	ARG
13	2R	6	SER
13	2R	15	SER
13	2R	74	LYS
13	2R	114	VAL
14	2S	15	ARG
14	2S	21	THR
14	2S	27	SER
14	2S	28	VAL
14	2S	35	ILE
14	2S	36	TYR
14	2S	43	GLU
14	2S	58	LEU
14	2S	63	THR
14	2S	65	VAL
14	2S	68	GLN
14	2S	80	LEU
14	2S	110	LEU
15	2T	23	ARG
15	2T	34	VAL
15	2T	72	VAL
15	2T	74	ARG
15	2T	96	ARG
15	2T	115	ARG
15	2T	119	LYS
16	2U	5	LYS
16	2U	27	LEU
16	2U	74	LEU
16	2U	78	THR
16	2U	95	LEU
17	2V	7	THR
17	2V	28	GLU
17	2V	34	GLU
17	2V	46	VAL
17	2V	47	VAL
17	2V	53	GLU

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Mol	Chain	Res	Type
17	2V	79	VAL
17	2V	98	GLU
18	2W	4	LYS
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	67	ASP
19	2X	60	ARG
19	2X	66	LEU
19	2X	81	VAL
20	2Y	1	MET
20	2Y	5	MET
20	2Y	7	VAL
20	2Y	11	ASP
20	2Y	14	LEU
20	2Y	30	VAL
20	2Y	47	LYS
20	2Y	49	VAL
20	2Y	72	VAL
20	2Y	91	GLU
20	2Y	99	CYS
21	2Z	33	LEU
21	2Z	61	LEU
21	2Z	71	VAL
21	2Z	74	VAL
21	2Z	91	LEU
21	2Z	128	VAL
21	2Z	136	PHE
21	2Z	137	ILE
21	2Z	148	ASP
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	157	LEU
21	2Z	163	LEU
21	2Z	170	THR
22	20	9	SER
22	20	40	GLN
22	20	68	GLU
22	20	74	ARG
23	21	6	GLU
23	21	21	ARG

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Mol	Chain	Res	Type
23	21	35	THR
23	21	37	ILE
23	21	40	ARG
23	21	81	LYS
23	21	92	LYS
24	22	3	LEU
24	22	19	VAL
24	22	34	GLU
24	22	53	LEU
24	22	59	ARG
24	22	70	GLN
25	23	31	LEU
25	23	54	VAL
25	23	56	VAL
25	23	58	VAL
25	23	59	VAL
26	24	27	THR
26	24	34	GLU
26	24	56	VAL
26	24	59	PHE
27	25	6	VAL
27	25	40	LYS
28	26	7	ILE
28	26	9	LEU
28	26	19	ARG
28	26	20	ASN
28	26	23	THR
28	26	29	ASN
28	26	47	THR
28	26	48	VAL
28	26	52	VAL
29	27	1	MET
29	27	43	THR
29	27	46	VAL
30	28	14	VAL
30	28	37	SER
30	28	46	ARG
31	29	6	SER
31	29	7	VAL
33	2b	7	VAL
33	2b	8	LYS
33	2b	9	GLU

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Mol	Chain	Res	Type
33	2b	10	LEU
33	2b	11	LEU
33	2b	16	HIS
33	2b	23	ARG
33	2b	61	LEU
33	2b	76	GLN
33	2b	94	ASN
33	2b	109	SER
33	2b	111	ARG
33	2b	115	LEU
33	2b	127	ILE
33	2b	136	VAL
33	2b	137	ARG
33	2b	153	ARG
33	2b	157	ARG
33	2b	185	ILE
33	2b	189	ASP
33	2b	223	ILE
33	2b	224	GLN
33	2b	229	VAL
33	2b	236	TYR
34	2c	34	LEU
34	2c	46	GLU
34	2c	55	VAL
34	2c	57	ILE
34	2c	72	LYS
34	2c	91	LEU
34	2c	101	LEU
34	2c	105	GLU
34	2c	120	VAL
34	2c	132	ARG
34	2c	152	ILE
34	2c	190	ARG
34	2c	191	THR
34	2c	196	LEU
35	2d	28	SER
35	2d	34	GLU
35	2d	47	ARG
35	2d	58	LEU
35	2d	59	ARG
35	2d	127	THR
35	2d	135	LEU

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Mol	Chain	Res	Type
35	2d	155	LEU
35	2d	162	LEU
35	2d	188	LEU
35	2d	193	ASP
36	2e	12	LEU
36	2e	13	ILE
36	2e	18	ARG
36	2e	51	VAL
36	2e	55	VAL
36	2e	72	GLN
36	2e	75	THR
36	2e	111	GLU
36	2e	115	VAL
36	2e	119	LEU
36	2e	149	GLU
37	2f	21	LEU
37	2f	37	VAL
37	2f	69	GLU
37	2f	92	LYS
37	2f	93	SER
38	2g	9	VAL
38	2g	15	ASP
38	2g	78	ARG
38	2g	79	ARG
38	2g	110	GLN
38	2g	135	VAL
39	2h	39	LEU
39	2h	52	ASP
39	2h	56	LYS
39	2h	98	LYS
39	2h	109	ILE
39	2h	112	LEU
39	2h	133	LEU
40	2i	7	THR
40	2i	9	ARG
40	2i	14	VAL
40	2i	28	VAL
40	2i	32	ASP
40	2i	38	GLN
40	2i	40	LEU
40	2i	50	LEU
40	2i	63	ILE

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Mol	Chain	Res	Type
40	2i	65	VAL
40	2i	89	ASN
40	2i	99	LEU
40	2i	103	THR
40	2i	104	ARG
40	2i	108	VAL
40	2i	113	LYS
40	2i	128	ARG
41	2j	8	LEU
41	2j	13	HIS
41	2j	38	ILE
41	2j	49	VAL
41	2j	50	ILE
41	2j	65	LEU
41	2j	72	VAL
41	2j	73	ASP
41	2j	89	ASP
41	2j	100	THR
42	2k	14	VAL
42	2k	79	SER
42	2k	105	VAL
42	2k	109	VAL
43	2l	18	VAL
43	2l	40	VAL
43	2l	83	VAL
43	2l	104	VAL
43	2l	118	SER
44	2m	4	ILE
44	2m	19	LEU
44	2m	27	LYS
44	2m	39	ILE
44	2m	45	VAL
44	2m	47	ASP
44	2m	50	GLU
44	2m	81	LEU
44	2m	93	ARG
44	2m	103	THR
44	2m	106	ASN
44	2m	114	ARG
45	2n	18	VAL
45	2n	22	THR
45	2n	33	VAL

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Mol	Chain	Res	Type
45	2n	56	VAL
45	2n	60	SER
46	2o	3	ILE
46	2o	26	GLU
46	2o	39	LEU
46	2o	47	LYS
46	2o	76	GLU
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	45	THR
47	2p	60	LEU
47	2p	67	THR
47	2p	73	LEU
47	2p	74	LEU
48	2q	5	VAL
48	2q	7	THR
48	2q	9	VAL
48	2q	19	VAL
48	2q	52	LYS
48	2q	60	ILE
48	2q	83	ASP
48	2q	85	VAL
48	2q	86	GLU
49	2r	31	LEU
49	2r	37	VAL
49	2r	82	THR
50	2s	20	LEU
50	2s	31	ILE
50	2s	43	GLU
50	2s	49	ILE
50	2s	51	VAL
50	2s	56	GLN
50	2s	58	VAL
50	2s	79	THR
50	2s	81	ARG
51	2t	15	ARG
51	2t	45	GLN
51	2t	50	GLU
51	2t	51	GLU
51	2t	70	SER
51	2t	93	GLU

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Mol	Chain	Res	Type
52	2u	7	ARG
52	2u	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (148) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
4	1E	48	GLN
4	1E	143	ASN
5	1F	69	HIS
5	1F	133	ASN
5	1F	160	ASN
5	1F	203	GLN
6	1G	26	GLN
8	1I	11	ASN
8	1I	105	HIS
9	1N	8	GLN
9	1N	131	GLN
12	1Q	13	GLN
12	1Q	89	ASN
12	1Q	141	GLN
13	1R	61	HIS
13	1R	71	GLN
14	1S	61	ASN
14	1S	68	GLN
15	1T	84	GLN
18	1W	60	ASN
18	1W	111	HIS
19	1X	31	HIS
19	1X	82	GLN
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	75	ASN
21	1Z	151	HIS
22	10	3	HIS
22	10	50	ASN
25	13	32	GLN
30	18	35	GLN
31	19	20	HIS
33	1b	37	ASN
33	1b	40	HIS
33	1b	78	GLN

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Mol	Chain	Res	Type
34	1c	6	HIS
34	1c	98	ASN
34	1c	118	GLN
34	1c	162	GLN
34	1c	170	GLN
35	1d	77	ASN
35	1d	116	GLN
35	1d	123	HIS
35	1d	161	ASN
35	1d	199	ASN
36	1e	20	GLN
36	1e	73	ASN
36	1e	78	HIS
37	1f	57	GLN
38	1g	28	ASN
38	1g	51	GLN
40	1i	3	GLN
40	1i	31	GLN
40	1i	34	ASN
40	1i	124	GLN
41	1j	56	HIS
43	1l	99	HIS
44	1m	77	ASN
44	1m	92	HIS
46	1o	50	HIS
46	1o	62	GLN
47	1p	13	HIS
47	1p	76	GLN
49	1r	63	GLN
50	1s	47	HIS
50	1s	83	HIS
51	1t	42	GLN
51	1t	45	GLN
51	1t	73	HIS
3	2D	87	ASN
4	2E	48	GLN
5	2F	69	HIS
5	2F	160	ASN
5	2F	203	GLN
6	2G	58	GLN
6	2G	121	ASN
6	2G	132	ASN

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Mol	Chain	Res	Type
7	2H	74	ASN
8	2I	133	HIS
8	2I	139	GLN
9	2N	8	GLN
9	2N	128	HIS
10	2O	3	GLN
10	2O	89	ASN
11	2P	128	HIS
12	2Q	12	GLN
12	2Q	13	GLN
12	2Q	89	ASN
12	2Q	123	HIS
13	2R	50	HIS
13	2R	61	HIS
13	2R	71	GLN
14	2S	38	GLN
14	2S	84	GLN
14	2S	95	HIS
15	2T	58	ASN
16	2U	72	HIS
16	2U	94	ASN
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
21	2Z	34	ASN
21	2Z	73	GLN
21	2Z	75	ASN
24	22	70	GLN
25	23	32	GLN
26	24	46	GLN
28	26	20	ASN
30	28	35	GLN
30	28	43	GLN
33	2b	76	GLN
33	2b	94	ASN
33	2b	95	GLN
33	2b	135	GLN
34	2c	98	ASN
34	2c	162	GLN
34	2c	170	GLN
35	2d	45	GLN
35	2d	77	ASN

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Mol	Chain	Res	Type
35	2d	116	GLN
35	2d	119	GLN
35	2d	123	HIS
36	2e	72	GLN
36	2e	141	GLN
37	2f	73	ASN
37	2f	100	ASN
38	2g	28	ASN
40	2i	3	GLN
40	2i	38	GLN
40	2i	58	HIS
41	2j	62	HIS
41	2j	69	ASN
42	2k	104	GLN
42	2k	117	ASN
43	2l	78	GLN
43	2l	80	HIS
43	2l	99	HIS
44	2m	62	ASN
45	2n	49	HIS
46	2o	50	HIS
46	2o	62	GLN
47	2p	16	HIS
49	2r	63	GLN
50	2s	69	HIS
50	2s	83	HIS
51	2t	75	ASN
51	2t	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	435 (15%)	30 (1%)
1	2A	2791/2915 (95%)	463 (16%)	26 (0%)
2	1B	119/121 (98%)	7 (5%)	0
2	2B	118/121 (97%)	31 (26%)	0
32	1a	1497/1521 (98%)	242 (16%)	0
32	2a	1501/1521 (98%)	272 (18%)	0
53	1v	12/24 (50%)	2 (16%)	0
53	2v	12/24 (50%)	1 (8%)	0
54	1w	71/76 (93%)	23 (32%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
54	2w	68/76 (89%)	20 (29%)	0
55	1x	75/77 (97%)	5 (6%)	0
55	2x	75/77 (97%)	8 (10%)	0
56	1y	72/76 (94%)	35 (48%)	0
56	2y	70/76 (92%)	25 (35%)	0
All	All	9345/9620 (97%)	1569 (16%)	56 (0%)

All (1569) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	10	G
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	58	G
1	1A	63	U
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	84	A
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	181	A
1	1A	188	G
1	1A	196	A
1	1A	197	A
1	1A	200	U
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	269	U
1	1A	271(A)	A
1	1A	271(K)	U
1	1A	271(L)	U

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Mol	Chain	Res	Type
1	1A	271(M)	G
1	1A	271(O)	C
1	1A	271(S)	G
1	1A	272(B)	G
1	1A	272(I)	U
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	342	G
1	1A	352	G
1	1A	357	A
1	1A	363	G
1	1A	363(B)	G
1	1A	370	G
1	1A	380	U
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	428	A
1	1A	444	C
1	1A	448	U
1	1A	455	C
1	1A	467	G
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	508	G
1	1A	509	C
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	568	U
1	1A	573	G
1	1A	575	A
1	1A	593	G

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Mol	Chain	Res	Type
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	634	C
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(A)	A
1	1A	652(F)	G
1	1A	652(T)	C
1	1A	654	A
1	1A	669	G
1	1A	686	G
1	1A	717	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	762	U
1	1A	764	A
1	1A	765	G
1	1A	774	A
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	789	A
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	866	A
1	1A	877	U
1	1A	879	G
1	1A	880	G
1	1A	881	G

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Mol	Chain	Res	Type
1	1A	882	G
1	1A	883	G
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	892	G
1	1A	894	C
1	1A	896	A
1	1A	897	C
1	1A	898	C
1	1A	899	A
1	1A	907	U
1	1A	910	A
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	990	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1027	A
1	1A	1033	U
1	1A	1041	C
1	1A	1044	G
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1055	G
1	1A	1058	G
1	1A	1059	G

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Mol	Chain	Res	Type
1	1A	1063	G
1	1A	1064	C
1	1A	1067	A
1	1A	1068	G
1	1A	1069	A
1	1A	1071	G
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1076	C
1	1A	1078	U
1	1A	1079	C
1	1A	1081	U
1	1A	1083	U
1	1A	1085	A
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1093	G
1	1A	1094	U
1	1A	1099	G
1	1A	1101	U
1	1A	1111	A
1	1A	1112	G
1	1A	1116	C
1	1A	1128	A
1	1A	1132	A
1	1A	1135	C
1	1A	1136	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1220	A
1	1A	1236	G
1	1A	1244	G
1	1A	1248	G

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Mol	Chain	Res	Type
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1384	A
1	1A	1385	G
1	1A	1396	U
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G
1	1A	1461	G
1	1A	1467	C
1	1A	1482	G
1	1A	1493	C
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1539	G
1	1A	1540	U
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1610	A
1	1A	1648	C
1	1A	1664	A

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Mol	Chain	Res	Type
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1745	C
1	1A	1756	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1816	G
1	1A	1829	A
1	1A	1847	A
1	1A	1861	G
1	1A	1877	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1929	G
1	1A	1930	G
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A

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Mol	Chain	Res	Type
1	1A	2039	C
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2069	G
1	1A	2098	U
1	1A	2102	U
1	1A	2108	C
1	1A	2110	G
1	1A	2113	U
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2120	G
1	1A	2121	G
1	1A	2126	A
1	1A	2127	G
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2136	C
1	1A	2138	C
1	1A	2142	C
1	1A	2144	U
1	1A	2146	C
1	1A	2148	G
1	1A	2150	U
1	1A	2151	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2161	C
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2171	A

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Mol	Chain	Res	Type
1	1A	2172	U
1	1A	2173	A
1	1A	2174	C
1	1A	2181	G
1	1A	2182	G
1	1A	2183	C
1	1A	2184	G
1	1A	2189	U
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2219	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2279	G
1	1A	2280	G
1	1A	2283	C
1	1A	2286	A
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2308	G
1	1A	2312	U
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2354	G
1	1A	2358	G
1	1A	2361	A
1	1A	2383	G
1	1A	2385	C
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A
1	1A	2423	U

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Mol	Chain	Res	Type
1	1A	2424	C
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2449	U
1	1A	2474	C
1	1A	2476	A
1	1A	2478	A
1	1A	2491	U
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2520	C
1	1A	2529	G
1	1A	2535	G
1	1A	2549	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2582	G
1	1A	2585	U
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A

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Mol	Chain	Res	Type
1	1A	2714	G
1	1A	2726	U
1	1A	2727	G
1	1A	2733	A
1	1A	2757	A
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2778	A
1	1A	2780	G
1	1A	2790	A
1	1A	2791	C
1	1A	2793	G
1	1A	2802	G
1	1A	2803	C
1	1A	2820	A
1	1A	2821	A
1	1A	2825	C
1	1A	2835	A
1	1A	2872	G
1	1A	2880	C
1	1A	2892	A
1	1A	2894	G
1	1A	2895	U
2	1B	2	C
2	1B	13	A
2	1B	50	G
2	1B	56	G
2	1B	73	A
2	1B	106	G
2	1B	110	G
32	1a	6	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	77	G

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Mol	Chain	Res	Type
32	1a	79	G
32	1a	91	C
32	1a	98	G
32	1a	101	A
32	1a	105	G
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	145	G
32	1a	162	A
32	1a	163	C
32	1a	174	C
32	1a	180	U
32	1a	182	U
32	1a	189(D)	C
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A
32	1a	199	G
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	220	G
32	1a	222	U
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	306	G
32	1a	321	A
32	1a	328	C
32	1a	330	C
32	1a	332	G
32	1a	342	C
32	1a	344	A
32	1a	348	G
32	1a	352	C
32	1a	353	A

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Mol	Chain	Res	Type
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	457	C
32	1a	461	A
32	1a	470	C
32	1a	483	C
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	524	G
32	1a	527	G7M
32	1a	531	U
32	1a	532	A
32	1a	536	C
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C

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Mol	Chain	Res	Type
32	1a	607	A
32	1a	630	G
32	1a	653	A
32	1a	661	G
32	1a	665	A
32	1a	666	G
32	1a	672	U
32	1a	687	A
32	1a	688	G
32	1a	693	G
32	1a	695	A
32	1a	722	A
32	1a	723	U
32	1a	731	G
32	1a	734	G
32	1a	749	C
32	1a	753	A
32	1a	755	G
32	1a	759	A
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	851	G
32	1a	870	U
32	1a	873	A
32	1a	902	G
32	1a	913	A
32	1a	914	A
32	1a	916	G
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	960	U

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Mol	Chain	Res	Type
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1022	G
32	1a	1023	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1037	C
32	1a	1039	C
32	1a	1044	A
32	1a	1053	G
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G
32	1a	1123	A
32	1a	1124	G
32	1a	1125	U
32	1a	1127	G

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Mol	Chain	Res	Type
32	1a	1132	C
32	1a	1133	G
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1146	A
32	1a	1152	A
32	1a	1154	G
32	1a	1158	C
32	1a	1159	U
32	1a	1165	C
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1213	A
32	1a	1214	C
32	1a	1222	G
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1250	A
32	1a	1253	G
32	1a	1256	A
32	1a	1257	U
32	1a	1270	C
32	1a	1275	A
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G

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Mol	Chain	Res	Type
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1364	U
32	1a	1370	G
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1487	G
32	1a	1492	A
32	1a	1494	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1529	G
32	1a	1530	G
53	1v	13	A
53	1v	24	A
54	1w	2	C
54	1w	6	G
54	1w	8	4SU
54	1w	11	C
54	1w	12	U
54	1w	15	G
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	23	A
54	1w	24	G
54	1w	27	G
54	1w	46	G7M
54	1w	47	U
54	1w	48	C
54	1w	50	U
54	1w	62	C
54	1w	66	U

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Mol	Chain	Res	Type
54	1w	67	C
54	1w	70	G
54	1w	72	C
54	1w	73	A
54	1w	74	C
55	1x	9	G
55	1x	19	G
55	1x	20	U
55	1x	47	U
55	1x	61	C
56	1y	2	C
56	1y	5	G
56	1y	6	G
56	1y	7	A
56	1y	8	4SU
56	1y	11	C
56	1y	13	C
56	1y	14	A
56	1y	19	G
56	1y	20	U
56	1y	21	A
56	1y	28	G
56	1y	34	G
56	1y	35	A
56	1y	37	MIA
56	1y	40	C
56	1y	44	G
56	1y	45	U
56	1y	46	G7M
56	1y	47	U
56	1y	48	C
56	1y	49	C
56	1y	51	U
56	1y	57	G
56	1y	58	A
56	1y	59	U
56	1y	60	U
56	1y	61	C
56	1y	65	G
56	1y	66	U
56	1y	67	C
56	1y	69	G

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Mol	Chain	Res	Type
56	1y	70	G
56	1y	72	C
56	1y	76	A
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	36	G
1	2A	45	C
1	2A	55	G
1	2A	61	G
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	78	A
1	2A	84	A
1	2A	90	U
1	2A	94	C
1	2A	100	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	141	A
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	222	A
1	2A	228	A
1	2A	229	A
1	2A	230	U
1	2A	232	G
1	2A	233	A
1	2A	248	G
1	2A	250	G
1	2A	271(I)	G

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Mol	Chain	Res	Type
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	311	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	342	G
1	2A	352	G
1	2A	354	G
1	2A	363	G
1	2A	363(B)	G
1	2A	380	U
1	2A	386	G
1	2A	411	G
1	2A	421	U
1	2A	422	A
1	2A	443	A
1	2A	444	C
1	2A	455	C
1	2A	457	A
1	2A	481	G
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	588	U

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Mol	Chain	Res	Type
1	2A	603	A
1	2A	604	G
1	2A	606	U
1	2A	607	U
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	634	C
1	2A	637	A
1	2A	645	C
1	2A	648	G
1	2A	651	G
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(D)	C
1	2A	652(U)	G
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	771	G
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	790	C
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	832	G
1	2A	857	C
1	2A	859	G

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Mol	Chain	Res	Type
1	2A	874	G
1	2A	875	G
1	2A	877	U
1	2A	878	A
1	2A	879	G
1	2A	880	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	892	G
1	2A	893	C
1	2A	894	C
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	904	C
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	936	C
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	999	U
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A
1	2A	1022	G
1	2A	1023	U
1	2A	1025	G
1	2A	1026	U

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Mol	Chain	Res	Type
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1042	G
1	2A	1043	C
1	2A	1116	C
1	2A	1126	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142	U
1	2A	1148	A
1	2A	1170	G
1	2A	1171	G
1	2A	1195	G
1	2A	1210	A
1	2A	1211	U
1	2A	1220	A
1	2A	1236	G
1	2A	1244	G
1	2A	1252	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1373	A
1	2A	1379	A
1	2A	1384	A

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Mol	Chain	Res	Type
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1435	G
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1461	G
1	2A	1463	C
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1532	C
1	2A	1543	C
1	2A	1547	C
1	2A	1554	A
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1640	C

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Mol	Chain	Res	Type
1	2A	1648	C
1	2A	1654	A
1	2A	1664	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1717	G
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1746	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1812	A
1	2A	1816	G
1	2A	1828	G
1	2A	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1938	A
1	2A	1955	U

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Mol	Chain	Res	Type
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2036	C
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2080	G
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2117	A
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2139	C

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Mol	Chain	Res	Type
1	2A	2141	G
1	2A	2145	C
1	2A	2146	C
1	2A	2148	G
1	2A	2149	G
1	2A	2150	U
1	2A	2151	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2171	A
1	2A	2172	U
1	2A	2178	C
1	2A	2181	G
1	2A	2182	G
1	2A	2185	C
1	2A	2188	C
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2267	A
1	2A	2275	C
1	2A	2278	A
1	2A	2280	G
1	2A	2282	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2305	A
1	2A	2307	G

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Mol	Chain	Res	Type
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2372	G
1	2A	2376	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2400	G
1	2A	2402	C
1	2A	2406	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2465	C
1	2A	2469	A
1	2A	2476	A
1	2A	2480	C
1	2A	2487	G
1	2A	2490	G
1	2A	2491	U
1	2A	2494	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2507	C
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2530	A
1	2A	2534	A

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Mol	Chain	Res	Type
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2582	G
1	2A	2585	U
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2630	G
1	2A	2634	G
1	2A	2646	C
1	2A	2654	A
1	2A	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2718	G
1	2A	2726	U
1	2A	2733	A
1	2A	2744	G
1	2A	2758	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2789	C
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2803	C
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2839	G
1	2A	2872	G

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Mol	Chain	Res	Type
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	3	C
2	2B	5	C
2	2B	8	U
2	2B	12	C
2	2B	13	A
2	2B	17	C
2	2B	23	G
2	2B	25	A
2	2B	30	C
2	2B	33	G
2	2B	34	U
2	2B	40	U
2	2B	41	U
2	2B	42	C
2	2B	53	A
2	2B	56	G
2	2B	67	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	84	C
2	2B	85	G
2	2B	89	G
2	2B	105	A
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	111	G
2	2B	119	G
2	2B	120	A
32	2a	9	G
32	2a	22	G
32	2a	31	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C

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Mol	Chain	Res	Type
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	65	U
32	2a	66	G
32	2a	73	G
32	2a	89	C
32	2a	96	U
32	2a	98	G
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	129(A)	G
32	2a	131	C
32	2a	144	G
32	2a	163	C
32	2a	182	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	231	G
32	2a	245	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	281	G
32	2a	289	G
32	2a	306	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	350	G
32	2a	351	G
32	2a	352	C
32	2a	353	A

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Mol	Chain	Res	Type
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	373	A
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	414	A
32	2a	421	U
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	475	G
32	2a	476	G
32	2a	477	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	527	G7M
32	2a	531	U
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	564	C
32	2a	568	G
32	2a	572	A

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Mol	Chain	Res	Type
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	601	C
32	2a	630	G
32	2a	653	A
32	2a	665	A
32	2a	666	G
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	702	A
32	2a	703	G
32	2a	723	U
32	2a	731	G
32	2a	749	C
32	2a	755	G
32	2a	777	A
32	2a	787	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	853	G
32	2a	859	A
32	2a	873	A
32	2a	887	G
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	942	G
32	2a	958	A
32	2a	960	U

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Mol	Chain	Res	Type
32	2a	961	U
32	2a	963	G
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	984	C
32	2a	991	U
32	2a	992	U
32	2a	993	G
32	2a	995	C
32	2a	997	U
32	2a	998	G
32	2a	999	C
32	2a	1002	G
32	2a	1003	G
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1011	G
32	2a	1016	A
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1035	A
32	2a	1036	G
32	2a	1037	C

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Mol	Chain	Res	Type
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1042	G
32	2a	1050	G
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1081	G
32	2a	1086	U
32	2a	1091	U
32	2a	1092	A
32	2a	1093	A
32	2a	1094	G
32	2a	1095	U
32	2a	1097	C
32	2a	1101	A
32	2a	1117	G
32	2a	1122	U
32	2a	1124	G
32	2a	1125	U
32	2a	1126	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1133	G
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1141	C
32	2a	1146	A
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1160	G
32	2a	1172	C
32	2a	1181	G
32	2a	1182	G
32	2a	1184	G

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Mol	Chain	Res	Type
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1213	A
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1264	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1277	C
32	2a	1279	A
32	2a	1280	A
32	2a	1285	A
32	2a	1286	A
32	2a	1287	A
32	2a	1299	A
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1312	G
32	2a	1320	C
32	2a	1323	G
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1370	G
32	2a	1380	U
32	2a	1382	C
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G

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Mol	Chain	Res	Type
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1457	G
32	2a	1492	A
32	2a	1497	G
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	24	A
54	2w	4	C
54	2w	13	C
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	45	U
54	2w	46	G7M
54	2w	47	U
54	2w	48	C
54	2w	62	C
54	2w	64	A
54	2w	65	G
54	2w	66	U
54	2w	68	C
54	2w	69	G
54	2w	70	G
54	2w	71	G
54	2w	72	C
54	2w	73	A
54	2w	74	C
55	2x	9	G
55	2x	13	C
55	2x	18	G
55	2x	19	G
55	2x	20	U
55	2x	47	U
55	2x	48	C
55	2x	61	C

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Mol	Chain	Res	Type
56	2y	2	C
56	2y	15	G
56	2y	19	G
56	2y	23	A
56	2y	27	G
56	2y	37	MIA
56	2y	40	C
56	2y	41	C
56	2y	43	C
56	2y	45	U
56	2y	46	G7M
56	2y	47	U
56	2y	48	C
56	2y	49	C
56	2y	52	G
56	2y	53	G
56	2y	54	5MU
56	2y	55	PSU
56	2y	56	C
56	2y	58	A
56	2y	59	U
56	2y	63	G
56	2y	65	G
56	2y	69	G
56	2y	70	G

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	195	A
1	1A	196	A
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	548	A
1	1A	685	A
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	895	U
1	1A	974	G
1	1A	1047	G

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Mol	Chain	Res	Type
1	1A	1067	A
1	1A	1142(A)	A
1	1A	1174	A
1	1A	1176	G
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1992	G
1	1A	2134	A
1	1A	2181	G
1	1A	2183	C
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2629	A
1	1A	2689	U
1	1A	2756	U
1	2A	195	A
1	2A	196	A
1	2A	228	A
1	2A	249	C
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	746	A
1	2A	752	A
1	2A	827	U
1	2A	856	C
1	2A	900	A
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1608	A
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2156	G
1	2A	2439	A

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Mol	Chain	Res	Type
1	2A	2689	U

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

88 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
1	5MC	1A	1962	57,1	19,22,23	1.69	3 (15%)	26,32,35	1.17	2 (7%)
1	2MU	2A	2552	57,1	19,22,24	1.31	3 (15%)	25,31,36	1.86	6 (24%)
56	G7M	2y	46	56	23,26,27	1.66	4 (17%)	34,39,42	1.96	4 (11%)
56	MIA	2y	37	56	21,24,32	1.66	4 (19%)	30,35,47	1.99	7 (23%)
56	PSU	2y	39	56	18,21,22	1.41	2 (11%)	21,30,33	1.76	3 (14%)
32	5MC	1a	1407	32	19,22,23	1.63	3 (15%)	26,32,35	1.07	3 (11%)
56	4SU	1y	8	56	18,21,22	1.77	4 (22%)	25,30,33	2.10	5 (20%)
55	5MC	1x	32	55,57	19,22,23	1.68	3 (15%)	26,32,35	1.25	3 (11%)
1	5MC	2A	1942	1	19,22,23	1.70	3 (15%)	26,32,35	1.11	3 (11%)
54	MIA	1w	37	54	28,31,32	2.35	6 (21%)	38,44,47	2.59	12 (31%)
32	5MC	2a	1404	32	19,22,23	1.75	3 (15%)	26,32,35	1.16	3 (11%)
32	5MC	2a	1407	32	19,22,23	1.49	3 (15%)	26,32,35	1.11	2 (7%)
1	OMC	2A	1920	1	19,22,23	0.79	0	25,31,34	0.93	1 (4%)
54	PSU	1w	39	54	18,21,22	1.40	3 (16%)	21,30,33	1.82	3 (14%)
1	5MU	1A	1939	57,1	19,22,23	1.35	5 (26%)	27,32,35	2.19	6 (22%)
32	5MC	1a	967	32	19,22,23	1.60	3 (15%)	26,32,35	1.14	2 (7%)
54	PSU	2w	32	54	18,21,22	1.37	2 (11%)	21,30,33	1.96	4 (19%)
55	4SU	2x	8	55	18,21,22	2.15	5 (27%)	25,30,33	1.44	5 (20%)
56	PSU	1y	39	56	18,21,22	1.44	2 (11%)	21,30,33	1.81	4 (19%)
1	8AH	1A	2503	57,1	22,26,27	1.61	5 (22%)	29,39,42	2.24	5 (17%)
1	PSU	1A	1917	1	18,21,22	1.34	2 (11%)	21,30,33	2.04	3 (14%)
55	PSU	1x	55	55	18,21,22	1.33	2 (11%)	21,30,33	2.03	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	PSU	1w	55	54	18,21,22	1.38	2 (11%)	21,30,33	2.01	3 (14%)
54	PSU	2w	39	54	18,21,22	1.40	2 (11%)	21,30,33	1.70	4 (19%)
1	PSU	1A	2605	57,1	18,21,22	1.32	3 (16%)	21,30,33	2.03	4 (19%)
1	OMG	2A	2251	55,1	23,26,27	1.23	3 (13%)	32,38,41	1.96	6 (18%)
54	G7M	2w	46	54	23,26,27	1.51	3 (13%)	34,39,42	1.74	4 (11%)
54	4SU	1w	8	54	18,21,22	1.75	4 (22%)	25,30,33	1.89	4 (16%)
55	5MU	1x	54	55,57	19,22,23	1.39	5 (26%)	27,32,35	2.02	6 (22%)
54	G7M	1w	46	54	23,26,27	1.56	3 (13%)	34,39,42	1.68	4 (11%)
54	F3N	1w	76	54,1	33,36,37	1.56	5 (15%)	41,51,54	1.82	10 (24%)
54	5MU	1w	54	54	19,22,23	1.36	4 (21%)	27,32,35	1.94	6 (22%)
54	MIA	2w	37	54	24,27,32	2.15	5 (20%)	32,39,47	2.62	11 (34%)
1	5MU	2A	1915	1	19,22,23	1.46	6 (31%)	27,32,35	2.18	6 (22%)
1	PSU	2A	1911	1	18,21,22	1.37	2 (11%)	21,30,33	2.04	5 (23%)
43	0TD	2l	92	43	8,9,10	4.52	1 (12%)	6,11,13	1.91	2 (33%)
32	4OC	1a	1402	32	20,23,24	0.72	0	25,32,35	0.97	1 (4%)
32	2MG	2a	1207	32	23,26,27	1.24	2 (8%)	33,38,41	2.15	7 (21%)
1	5MU	2A	1939	57,1	19,22,23	1.40	5 (26%)	27,32,35	2.29	6 (22%)
55	31H	2x	76	55,57	31,34,35	1.20	3 (9%)	35,47,50	2.16	13 (37%)
56	5MU	1y	54	56	19,22,23	1.40	5 (26%)	27,32,35	2.16	7 (25%)
32	UR3	2a	1498	32	19,22,23	1.07	1 (5%)	26,32,35	1.75	2 (7%)
32	4OC	2a	1402	32	20,23,24	0.78	0	25,32,35	1.07	3 (12%)
32	PSU	1a	516	32	18,21,22	1.36	2 (11%)	21,30,33	1.96	6 (28%)
1	5MC	1A	1942	1	19,22,23	1.62	3 (15%)	26,32,35	1.19	4 (15%)
54	4SU	2w	8	54	18,21,22	1.72	4 (22%)	25,30,33	2.81	5 (20%)
1	OMG	1A	2251	55,57,1	23,26,27	1.27	3 (13%)	32,38,41	1.94	6 (18%)
1	OMC	1A	1920	1	19,22,23	0.81	0	25,31,34	0.86	0
1	8AH	2A	2503	57,1	22,26,27	1.66	5 (22%)	29,39,42	2.09	5 (17%)
55	PSU	2x	55	55	18,21,22	1.39	2 (11%)	21,30,33	2.07	4 (19%)
54	PSU	2w	55	54	18,21,22	1.37	2 (11%)	21,30,33	1.97	3 (14%)
1	PSU	1A	1911	1	18,21,22	1.43	2 (11%)	21,30,33	2.06	3 (14%)
56	PSU	1y	32	56	18,21,22	1.35	2 (11%)	21,30,33	1.95	3 (14%)
56	MIA	1y	37	56	21,24,32	1.65	4 (19%)	30,35,47	1.98	6 (20%)
32	PSU	2a	516	32	18,21,22	1.33	2 (11%)	21,30,33	1.98	4 (19%)
32	2MG	1a	1207	32	23,26,27	1.23	3 (13%)	33,38,41	2.27	8 (24%)
54	F3N	2w	76	54,1	33,36,37	1.49	4 (12%)	41,51,54	1.76	8 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	5MU	2x	54	55	19,22,23	1.41	6 (31%)	27,32,35	2.15	6 (22%)
32	MA6	1a	1519	32	23,26,27	0.46	0	33,38,41	2.13	8 (24%)
54	5MU	2w	54	54	19,22,23	1.36	4 (21%)	27,32,35	1.92	6 (22%)
1	PSU	2A	1917	1	18,21,22	1.38	2 (11%)	21,30,33	1.96	3 (14%)
1	5MU	1A	1915	1	19,22,23	1.38	5 (26%)	27,32,35	2.21	7 (25%)
32	M2G	1a	966	32	24,27,28	1.29	3 (12%)	33,40,43	1.81	6 (18%)
32	5MC	1a	1404	32	19,22,23	1.76	3 (15%)	26,32,35	1.19	4 (15%)
1	PSU	2A	2605	1	18,21,22	1.42	3 (16%)	21,30,33	2.08	4 (19%)
1	5MC	2A	1962	57,1	19,22,23	1.67	3 (15%)	26,32,35	1.17	2 (7%)
43	0TD	1l	92	43	8,9,10	4.54	2 (25%)	6,11,13	7.49	2 (33%)
55	4SU	1x	8	55	18,21,22	2.32	5 (27%)	25,30,33	1.74	6 (24%)
32	5MC	2a	967	32	19,22,23	1.69	3 (15%)	26,32,35	1.18	3 (11%)
32	5MC	2a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.23	4 (15%)
56	5MU	2y	54	56	19,22,23	1.48	4 (21%)	27,32,35	2.00	6 (22%)
56	PSU	2y	55	56	18,21,22	1.32	3 (16%)	21,30,33	1.99	4 (19%)
32	G7M	2a	527	57,32	23,26,27	1.53	3 (13%)	34,39,42	1.67	5 (14%)
32	UR3	1a	1498	32	19,22,23	1.06	2 (10%)	26,32,35	1.78	4 (15%)
56	4SU	2y	8	56	18,21,22	1.72	4 (22%)	25,30,33	2.41	6 (24%)
56	PSU	2y	32	56	18,21,22	1.32	2 (11%)	21,30,33	1.95	3 (14%)
56	G7M	1y	46	56	23,26,27	1.63	3 (13%)	34,39,42	1.87	4 (11%)
32	G7M	1a	527	57,32	23,26,27	1.51	3 (13%)	34,39,42	1.73	5 (14%)
32	MA6	2a	1519	32	23,26,27	0.46	0	33,38,41	2.16	8 (24%)
32	M2G	2a	966	32	24,27,28	1.28	4 (16%)	33,40,43	1.84	6 (18%)
1	2MU	1A	2552	57,1	19,22,24	1.19	2 (10%)	25,31,36	1.99	6 (24%)
55	5MC	2x	32	55	19,22,23	1.77	3 (15%)	26,32,35	1.23	3 (11%)
32	5MC	1a	1400	32	19,22,23	1.58	3 (15%)	26,32,35	1.14	3 (11%)
54	PSU	1w	32	57,54	18,21,22	1.31	2 (11%)	21,30,33	1.95	3 (14%)
56	PSU	1y	55	56	18,21,22	1.41	2 (11%)	21,30,33	2.09	4 (19%)
32	MA6	1a	1518	32	23,26,27	0.43	0	33,38,41	2.06	9 (27%)
55	31H	1x	76	55,57	31,34,35	1.23	3 (9%)	35,47,50	2.08	11 (31%)
32	MA6	2a	1518	32	23,26,27	0.43	0	33,38,41	2.07	9 (27%)

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
1	5MC	1A	1962	57,1	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	57,1	-	0/9/27/28	0/2/2/2
56	G7M	2y	46	56	-	2/7/25/26	0/3/3/3
56	MIA	2y	37	56	-	3/7/25/34	0/3/3/3
56	PSU	2y	39	56	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
56	4SU	1y	8	56	-	2/7/25/26	0/2/2/2
55	5MC	1x	32	55,57	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
54	MIA	1w	37	54	-	4/15/33/34	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	57,1	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
56	PSU	1y	39	56	-	0/7/25/26	0/2/2/2
1	8AH	1A	2503	57,1	-	1/7/25/26	0/3/3/3
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	57,1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	55,1	-	0/9/27/28	0/3/3/3
54	G7M	2w	46	54	-	1/7/25/26	0/3/3/3
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	55,57	-	0/7/25/26	0/2/2/2
54	G7M	1w	46	54	-	1/7/25/26	0/3/3/3
54	F3N	1w	76	54,1	-	2/19/37/38	0/4/4/4
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
54	MIA	2w	37	54	-	2/11/29/34	0/3/3/3
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	3/7/12/14	-
32	4OC	1a	1402	32	-	0/9/29/30	0/2/2/2
32	2MG	2a	1207	32	-	1/9/27/28	0/3/3/3
1	5MU	2A	1939	57,1	-	0/7/25/26	0/2/2/2
55	31H	2x	76	55,57	-	3/22/40/41	0/3/3/3
56	5MU	1y	54	56	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	1/9/29/30	0/2/2/2
32	PSU	1a	516	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	55,57,1	-	0/9/27/28	0/3/3/3
1	OMC	1A	1920	1	-	0/9/27/28	0/2/2/2
1	8AH	2A	2503	57,1	-	0/7/25/26	0/3/3/3
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
54	PSU	2w	55	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
56	PSU	1y	32	56	-	0/7/25/26	0/2/2/2
56	MIA	1y	37	56	-	2/7/25/34	0/3/3/3
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
54	F3N	2w	76	54,1	-	1/19/37/38	0/4/4/4
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	1/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	1/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	57,1	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	1/7/12/14	-
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
56	5MU	2y	54	56	-	2/7/25/26	0/2/2/2
56	PSU	2y	55	56	-	6/7/25/26	0/2/2/2
32	G7M	2a	527	57,32	-	3/7/25/26	0/3/3/3
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
56	4SU	2y	8	56	-	1/7/25/26	0/2/2/2
56	PSU	2y	32	56	-	0/7/25/26	0/2/2/2
56	G7M	1y	46	56	-	2/7/25/26	0/3/3/3
32	G7M	1a	527	57,32	-	3/7/25/26	0/3/3/3
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	2MU	1A	2552	57,1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	57,54	-	0/7/25/26	0/2/2/2
56	PSU	1y	55	56	-	1/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
55	31H	1x	76	55,57	-	3/22/40/41	0/3/3/3
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3

All (257) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.45	1.69	1.82
43	1l	92	0TD	CB-SB	-12.32	1.69	1.82
54	1w	37	MIA	C13-C14	7.03	1.53	1.32
54	2w	37	MIA	C2-S10	-6.98	1.70	1.75
54	1w	37	MIA	C2-S10	-6.77	1.70	1.75
55	2x	32	5MC	C5-C4	6.55	1.49	1.44
32	2a	1404	5MC	C5-C4	6.42	1.49	1.44
32	1a	1404	5MC	C5-C4	6.34	1.48	1.44
32	2a	967	5MC	C5-C4	6.28	1.48	1.44
1	2A	1942	5MC	C5-C4	6.22	1.48	1.44
1	1A	1962	5MC	C5-C4	6.16	1.48	1.44
32	2a	1400	5MC	C5-C4	6.15	1.48	1.44
1	2A	1962	5MC	C5-C4	6.09	1.48	1.44
55	1x	32	5MC	C5-C4	6.08	1.48	1.44
32	1a	1407	5MC	C5-C4	6.03	1.48	1.44
1	1A	1942	5MC	C5-C4	5.93	1.48	1.44
32	1a	967	5MC	C5-C4	5.68	1.48	1.44
32	1a	1400	5MC	C5-C4	5.64	1.48	1.44
55	1x	8	4SU	C4-N3	-5.60	1.31	1.37
56	1y	37	MIA	C5-C4	5.36	1.48	1.39
54	2w	37	MIA	C5-C4	5.28	1.48	1.39
56	2y	37	MIA	C5-C4	5.26	1.48	1.39
55	2x	8	4SU	C4-N3	-5.22	1.32	1.37
54	1w	76	F3N	CB-CG	-5.18	1.39	1.51
32	2a	1407	5MC	C5-C4	5.12	1.48	1.44
54	2w	8	4SU	C4-S4	-5.07	1.59	1.68
54	1w	37	MIA	C5-C4	4.95	1.47	1.39
54	2w	76	F3N	CB-CG	-4.87	1.39	1.51
54	1w	46	G7M	C5-N7	-4.86	1.33	1.39
55	1x	8	4SU	C4-S4	-4.82	1.60	1.68
56	2y	46	G7M	C5-N7	-4.80	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	527	G7M	C5-N7	-4.73	1.33	1.39
56	2y	8	4SU	C4-S4	-4.71	1.60	1.68
56	1y	8	4SU	C4-S4	-4.66	1.60	1.68
1	2A	2503	8AH	C5-C4	4.61	1.47	1.39
54	1w	8	4SU	C4-S4	-4.57	1.60	1.68
56	1y	46	G7M	C5-N7	-4.52	1.34	1.39
32	2a	527	G7M	C5-N7	-4.51	1.34	1.39
55	2x	8	4SU	C4-S4	-4.49	1.60	1.68
54	2w	46	G7M	C5-N7	-4.44	1.34	1.39
56	1y	39	PSU	C6-C5	4.30	1.40	1.35
1	1A	2503	8AH	C5-C4	4.14	1.46	1.39
55	1x	76	31H	C5-N7	-4.13	1.31	1.39
56	2y	39	PSU	C6-C5	4.04	1.39	1.35
56	1y	55	PSU	C6-C5	4.03	1.39	1.35
54	2w	76	F3N	C5-N7	-3.98	1.31	1.39
55	1x	8	4SU	C2-N3	-3.96	1.31	1.38
54	2w	55	PSU	C6-C5	3.95	1.39	1.35
54	2w	39	PSU	C6-C5	3.92	1.39	1.35
1	1A	1911	PSU	C6-C5	3.89	1.39	1.35
54	1w	55	PSU	C6-C5	3.87	1.39	1.35
55	2x	76	31H	C5-N7	-3.86	1.32	1.39
56	1y	32	PSU	C6-C5	3.78	1.39	1.35
54	1w	76	F3N	C5-N7	-3.75	1.32	1.39
56	2y	46	G7M	C5-C4	3.75	1.47	1.38
56	1y	46	G7M	C5-C4	3.70	1.47	1.38
54	2w	32	PSU	C6-C5	3.66	1.39	1.35
55	1x	8	4SU	C5-C4	-3.65	1.38	1.42
1	2A	2605	PSU	C6-C5	3.65	1.39	1.35
56	2y	32	PSU	C6-C5	3.64	1.39	1.35
1	2A	1911	PSU	C6-C5	3.61	1.39	1.35
32	2a	516	PSU	C6-C5	3.58	1.39	1.35
55	2x	55	PSU	C6-C5	3.57	1.39	1.35
32	1a	516	PSU	C6-C5	3.55	1.39	1.35
54	1w	32	PSU	C6-C5	3.51	1.39	1.35
54	2w	46	G7M	C5-C4	3.50	1.47	1.38
1	2A	1917	PSU	C6-C5	3.48	1.39	1.35
1	1A	1917	PSU	C6-C5	3.43	1.39	1.35
54	1w	39	PSU	C6-C5	3.38	1.39	1.35
32	2a	527	G7M	C5-C4	3.36	1.46	1.38
55	2x	8	4SU	C2-N3	-3.35	1.32	1.38
54	1w	46	G7M	C5-C4	3.34	1.46	1.38
32	1a	527	G7M	C5-C4	3.33	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	8	4SU	C4-N3	-3.32	1.34	1.37
54	1w	76	F3N	C5-C4	-3.31	1.33	1.39
1	1A	2503	8AH	C4-N9	-3.27	1.33	1.38
1	1A	2251	OMG	C5-C4	3.18	1.47	1.38
32	2a	1207	2MG	C5-C4	3.18	1.47	1.38
1	2A	2503	8AH	C4-N9	-3.17	1.34	1.38
56	2y	54	5MU	C6-C5	3.17	1.39	1.34
32	1a	966	M2G	C5-C4	3.15	1.47	1.38
1	1A	2503	8AH	C8-N7	3.15	1.35	1.31
32	2a	966	M2G	C5-C4	3.15	1.47	1.38
54	2w	76	F3N	C5-C4	-3.15	1.33	1.39
55	1x	55	PSU	C6-C5	3.14	1.38	1.35
55	2x	8	4SU	C5-C4	-3.13	1.38	1.42
55	2x	76	31H	C5-C4	-3.08	1.33	1.39
1	2A	2503	8AH	C8-N7	3.07	1.35	1.31
1	2A	2251	OMG	C5-C4	3.03	1.47	1.38
56	2y	37	MIA	C5-C6	3.01	1.49	1.41
1	2A	1915	5MU	C6-C5	3.00	1.39	1.34
32	2a	1404	5MC	C6-C5	2.97	1.39	1.34
56	1y	8	4SU	C4-N3	-2.96	1.34	1.37
1	2A	1939	5MU	C6-C5	2.95	1.39	1.34
55	1x	76	31H	C5-C4	-2.93	1.33	1.39
32	1a	1207	2MG	C5-C4	2.93	1.46	1.38
1	1A	1939	5MU	C6-C5	2.92	1.39	1.34
56	2y	8	4SU	C4-N3	-2.91	1.34	1.37
54	2w	8	4SU	C4-N3	-2.91	1.34	1.37
32	1a	966	M2G	C2-N2	2.90	1.40	1.35
1	2A	1939	5MU	C4-N3	-2.84	1.33	1.38
55	1x	54	5MU	C4-N3	-2.83	1.33	1.38
54	2w	37	MIA	C5-C6	2.83	1.48	1.41
32	1a	967	5MC	C6-C5	2.82	1.39	1.34
1	2A	2552	2MU	C4-N3	-2.82	1.33	1.38
1	1A	2552	2MU	C4-N3	-2.81	1.33	1.38
55	1x	32	5MC	C6-C5	2.81	1.39	1.34
1	1A	1915	5MU	C2-N1	2.80	1.42	1.38
54	1w	54	5MU	C6-C5	2.80	1.39	1.34
56	1y	37	MIA	C5-C6	2.79	1.48	1.41
55	2x	32	5MC	C6-C5	2.78	1.39	1.34
55	1x	54	5MU	C6-C5	2.78	1.39	1.34
55	2x	54	5MU	C6-C5	2.77	1.39	1.34
54	1w	39	PSU	C4-N3	-2.76	1.33	1.38
1	1A	2503	8AH	C5-C6	2.76	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1400	5MC	C6-C5	2.75	1.39	1.34
1	1A	2605	PSU	C4-N3	-2.75	1.33	1.38
54	2w	39	PSU	C4-N3	-2.73	1.33	1.38
56	1y	54	5MU	C6-C5	2.73	1.39	1.34
56	1y	8	4SU	C5-C4	-2.72	1.39	1.42
1	2A	1942	5MC	C6-C5	2.71	1.39	1.34
1	1A	1962	5MC	C6-C5	2.70	1.39	1.34
55	2x	55	PSU	C4-N3	-2.69	1.33	1.38
32	1a	1404	5MC	C6-C5	2.69	1.39	1.34
54	2w	54	5MU	C6-C5	2.68	1.39	1.34
32	2a	966	M2G	C2-N2	2.68	1.40	1.35
56	2y	54	5MU	C2-N1	2.67	1.42	1.38
54	1w	37	MIA	C5-C6	2.67	1.48	1.41
56	1y	54	5MU	C4-C5	2.67	1.49	1.44
32	2a	1407	5MC	C6-C5	2.67	1.39	1.34
54	1w	76	F3N	C5-C6	-2.65	1.33	1.41
1	2A	2503	8AH	C5-N7	-2.65	1.34	1.39
56	1y	46	G7M	C6-N1	-2.65	1.33	1.38
56	2y	46	G7M	C6-N1	-2.65	1.33	1.38
1	2A	1962	5MC	C6-C5	2.64	1.38	1.34
1	2A	2605	PSU	C4-N3	-2.64	1.33	1.38
55	2x	76	31H	C5-C6	-2.62	1.33	1.41
55	2x	54	5MU	C4-N3	-2.61	1.34	1.38
56	2y	54	5MU	C4-C5	2.61	1.49	1.44
54	2w	54	5MU	C4-N3	-2.60	1.34	1.38
56	2y	55	PSU	C4-N3	-2.60	1.34	1.38
32	1a	516	PSU	C4-N3	-2.60	1.34	1.38
1	1A	1939	5MU	C4-N3	-2.59	1.34	1.38
32	2a	527	G7M	C6-N1	-2.59	1.34	1.38
32	2a	1400	5MC	C6-C5	2.58	1.38	1.34
54	1w	37	MIA	C5-N7	-2.58	1.34	1.39
1	2A	1915	5MU	C4-N3	-2.57	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.57	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.56	1.34	1.38
1	1A	1911	PSU	C4-N3	-2.56	1.34	1.38
1	1A	2503	8AH	C5-N7	-2.56	1.34	1.39
1	2A	1917	PSU	C4-N3	-2.55	1.34	1.38
55	1x	55	PSU	C4-N3	-2.55	1.34	1.38
56	1y	39	PSU	C4-N3	-2.54	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.51	1.34	1.38
1	2A	2251	OMG	C6-N1	-2.51	1.34	1.38
56	2y	37	MIA	C8-N7	2.51	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1498	UR3	C2-N1	2.50	1.42	1.38
1	1A	1942	5MC	C6-C5	2.50	1.38	1.34
54	1w	55	PSU	C4-N3	-2.50	1.34	1.38
1	2A	1915	5MU	C4-C5	2.50	1.48	1.44
1	1A	2251	OMG	C5-N7	-2.50	1.34	1.39
56	2y	55	PSU	C6-C5	2.50	1.38	1.35
1	2A	1915	5MU	C2-N1	2.49	1.42	1.38
56	2y	39	PSU	C4-N3	-2.48	1.34	1.38
56	2y	8	4SU	C2-N1	2.48	1.42	1.38
32	1a	1407	5MC	C6-C5	2.48	1.38	1.34
32	1a	1404	5MC	C6-N1	-2.47	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.46	1.34	1.38
32	2a	967	5MC	C6-C5	2.46	1.38	1.34
56	2y	54	5MU	C4-N3	-2.45	1.34	1.38
1	1A	1915	5MU	C6-C5	2.44	1.38	1.34
54	1w	8	4SU	C5-C4	-2.44	1.39	1.42
54	1w	46	G7M	C6-N1	-2.44	1.34	1.38
55	2x	54	5MU	C4-C5	2.44	1.48	1.44
56	1y	54	5MU	C2-N1	2.43	1.42	1.38
1	2A	2251	OMG	C5-N7	-2.43	1.34	1.39
55	1x	32	5MC	C6-N1	-2.42	1.33	1.38
32	1a	966	M2G	C6-N1	-2.41	1.34	1.38
54	2w	55	PSU	C4-N3	-2.41	1.34	1.38
32	2a	1498	UR3	C2-N1	2.41	1.41	1.38
1	2A	1962	5MC	C6-N1	-2.41	1.33	1.38
54	2w	76	F3N	C5-C6	-2.39	1.34	1.41
1	1A	1915	5MU	C4-N3	-2.39	1.34	1.38
56	1y	32	PSU	C4-N3	-2.39	1.34	1.38
54	2w	37	MIA	C5-N7	-2.38	1.34	1.39
56	2y	8	4SU	C5-C4	-2.38	1.39	1.42
1	1A	1962	5MC	C6-N1	-2.38	1.34	1.38
56	1y	55	PSU	C4-N3	-2.38	1.34	1.38
1	1A	1942	5MC	C6-N1	-2.37	1.34	1.38
1	1A	1917	PSU	C4-N3	-2.36	1.34	1.38
54	1w	8	4SU	C2-N3	-2.35	1.33	1.38
54	1w	54	5MU	C4-N3	-2.35	1.34	1.38
56	1y	8	4SU	C2-N1	2.34	1.42	1.38
55	1x	76	31H	C5-C6	-2.34	1.34	1.41
32	2a	1407	5MC	C6-N1	-2.34	1.34	1.38
54	2w	32	PSU	C4-N3	-2.34	1.34	1.38
54	1w	54	5MU	C4-C5	2.32	1.48	1.44
1	2A	2503	8AH	C5-C6	2.32	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	32	PSU	C4-N3	-2.30	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.30	1.34	1.38
56	1y	37	MIA	C5-N7	-2.30	1.34	1.39
32	2a	1400	5MC	C6-N1	-2.29	1.34	1.38
56	1y	54	5MU	C4-N3	-2.29	1.34	1.38
54	2w	37	MIA	C2-N3	2.28	1.37	1.34
32	2a	516	PSU	C4-N3	-2.28	1.34	1.38
54	1w	37	MIA	C8-N7	2.28	1.36	1.31
1	2A	1939	5MU	C4-C5	2.27	1.48	1.44
1	2A	1942	5MC	C6-N1	-2.27	1.34	1.38
55	1x	8	4SU	O2-C2	2.27	1.27	1.23
32	2a	967	5MC	C6-N1	-2.27	1.34	1.38
55	1x	54	5MU	C4-C5	2.26	1.48	1.44
1	1A	1939	5MU	C4-C5	2.25	1.48	1.44
1	2A	2552	2MU	C5-C4	2.24	1.48	1.43
54	2w	54	5MU	C4-C5	2.24	1.48	1.44
55	2x	32	5MC	C6-N1	-2.23	1.34	1.38
54	1w	76	F3N	C2'-C3'	-2.22	1.49	1.53
1	2A	2605	PSU	C2-N3	-2.22	1.33	1.37
1	1A	2552	2MU	C2-N3	-2.22	1.34	1.38
55	2x	54	5MU	C2-N1	2.21	1.41	1.38
32	2a	966	M2G	C6-N1	-2.21	1.34	1.38
56	2y	32	PSU	C4-N3	-2.21	1.34	1.38
54	1w	54	5MU	C2-N1	2.21	1.41	1.38
56	2y	55	PSU	C2-N1	-2.20	1.33	1.36
1	2A	2552	2MU	C2-N3	-2.20	1.34	1.38
43	1l	92	0TD	CB-CG	2.18	1.55	1.52
32	1a	527	G7M	C6-N1	-2.18	1.34	1.38
32	1a	1407	5MC	C6-N1	-2.17	1.34	1.38
32	1a	967	5MC	C6-N1	-2.17	1.34	1.38
1	2A	1915	5MU	C6-N1	-2.17	1.34	1.38
55	2x	8	4SU	O2-C2	2.17	1.26	1.23
1	1A	1915	5MU	C4-C5	2.16	1.48	1.44
32	1a	1400	5MC	C6-N1	-2.16	1.34	1.38
55	1x	54	5MU	C2-N3	-2.16	1.34	1.38
1	1A	1939	5MU	C2-N3	-2.15	1.34	1.38
54	2w	8	4SU	C5-C4	-2.15	1.39	1.42
32	2a	1404	5MC	C6-N1	-2.14	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.13	1.34	1.38
32	1a	1498	UR3	C6-C5	2.13	1.40	1.35
55	2x	54	5MU	C6-N1	-2.12	1.34	1.38
56	1y	54	5MU	C6-N1	-2.11	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2y	46	G7M	C2-N3	2.10	1.38	1.33
1	1A	2605	PSU	C2-N1	-2.10	1.33	1.36
32	1a	1207	2MG	C4-N9	-2.10	1.32	1.38
55	2x	54	5MU	C2-N3	-2.09	1.34	1.38
32	2a	966	M2G	C5-N7	-2.09	1.34	1.39
1	2A	1915	5MU	C2-N3	-2.08	1.34	1.38
1	1A	2605	PSU	C6-C5	2.06	1.37	1.35
54	2w	54	5MU	C2-N3	-2.06	1.34	1.38
56	1y	37	MIA	C8-N7	2.05	1.35	1.31
1	1A	1939	5MU	C6-N1	-2.05	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.04	1.34	1.38
56	2y	37	MIA	C5-N7	-2.03	1.35	1.39
54	2w	46	G7M	C6-N1	-2.03	1.35	1.38
54	2w	8	4SU	C2-N1	2.01	1.41	1.38
55	1x	54	5MU	C6-N1	-2.01	1.34	1.38
54	1w	39	PSU	C2-N3	-2.00	1.34	1.37

All (429) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	1l	92	0TD	CSB-SB-CB	-17.81	70.35	102.36
54	2w	37	MIA	C5-C4-N3	-9.04	117.66	127.18
54	2w	8	4SU	C4-N3-C2	-8.98	118.71	127.31
1	1A	2503	8AH	C5-C4-N3	-8.24	118.50	127.18
1	2A	2503	8AH	C5-C4-N3	-8.22	118.52	127.18
54	1w	37	MIA	C5-C4-N3	-8.12	118.63	127.18
54	2w	37	MIA	N3-C4-N9	7.80	136.89	126.99
54	1w	37	MIA	C12-C13-C14	-7.49	113.57	127.01
56	2y	8	4SU	C4-N3-C2	-7.35	120.27	127.31
32	1a	1207	2MG	C2-N3-C4	7.08	120.86	112.00
32	2a	1498	UR3	C4-N3-C2	-6.97	118.97	124.58
32	1a	1498	UR3	C4-N3-C2	-6.90	119.02	124.58
32	2a	1207	2MG	C2-N3-C4	6.79	120.50	112.00
54	2w	8	4SU	C5-C4-N3	6.74	121.02	114.75
56	2y	46	G7M	N9-C4-N3	6.64	139.23	125.95
56	1y	55	PSU	N1-C2-N3	6.56	122.09	115.17
1	1A	1911	PSU	N1-C2-N3	6.48	122.01	115.17
1	2A	1911	PSU	N1-C2-N3	6.41	121.93	115.17
55	2x	55	PSU	N1-C2-N3	6.39	121.91	115.17
56	1y	46	G7M	N9-C4-N3	6.35	138.65	125.95
55	1x	55	PSU	N1-C2-N3	6.34	121.86	115.17
1	2A	2605	PSU	N1-C2-N3	6.30	121.81	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	1w	55	PSU	N1-C2-N3	6.27	121.78	115.17
54	1w	37	MIA	N3-C4-N9	6.20	134.86	126.99
1	2A	1917	PSU	N1-C2-N3	6.17	121.68	115.17
32	1a	516	PSU	N1-C2-N3	6.14	121.64	115.17
54	2w	32	PSU	N1-C2-N3	6.13	121.64	115.17
1	1A	2251	OMG	C5-C4-N3	-6.12	118.66	128.39
54	2w	55	PSU	N1-C2-N3	6.11	121.61	115.17
1	1A	1917	PSU	N1-C2-N3	6.09	121.59	115.17
1	2A	2251	OMG	C5-C4-N3	-6.03	118.80	128.39
56	1y	37	MIA	C5-C4-N3	-6.01	118.45	126.72
32	2a	516	PSU	N1-C2-N3	6.00	121.50	115.17
56	1y	32	PSU	N1-C2-N3	6.00	121.50	115.17
1	1A	2605	PSU	N1-C2-N3	5.99	121.48	115.17
55	1x	76	31H	N1-C2-N3	-5.95	119.58	128.58
54	1w	32	PSU	N1-C2-N3	5.94	121.44	115.17
56	2y	32	PSU	N1-C2-N3	5.94	121.43	115.17
32	2a	1207	2MG	C5-C4-N3	-5.87	119.05	128.39
54	2w	76	F3N	N1-C2-N3	-5.86	119.71	128.58
32	2a	966	M2G	C5-C4-N3	-5.86	119.07	128.39
56	2y	37	MIA	C5-C4-N3	-5.85	118.66	126.72
56	1y	8	4SU	C4-N3-C2	-5.84	121.71	127.31
56	1y	39	PSU	N1-C2-N3	5.80	121.29	115.17
54	1w	39	PSU	N1-C2-N3	5.79	121.27	115.17
55	2x	76	31H	N1-C2-N3	-5.75	119.89	128.58
32	1a	966	M2G	C5-C4-N3	-5.73	119.27	128.39
56	2y	55	PSU	N1-C2-N3	5.68	121.16	115.17
56	2y	46	G7M	C5-C4-N3	-5.67	117.43	128.15
1	2A	1939	5MU	C4-N3-C2	-5.67	119.91	127.34
54	2w	46	G7M	N9-C4-N3	5.64	137.22	125.95
32	1a	1207	2MG	C5-C4-N3	-5.60	119.48	128.39
56	2y	8	4SU	C5-C4-N3	5.59	119.95	114.75
54	1w	76	F3N	N1-C2-N3	-5.58	120.14	128.58
1	1A	2552	2MU	N3-C2-N1	5.57	122.14	114.89
54	1w	8	4SU	C4-N3-C2	-5.55	122.00	127.31
56	2y	39	PSU	N1-C2-N3	5.55	121.02	115.17
54	1w	46	G7M	N9-C4-N3	5.49	136.92	125.95
56	1y	46	G7M	C5-C4-N3	-5.46	117.83	128.15
32	2a	527	G7M	N9-C4-N3	5.42	136.80	125.95
1	1A	1915	5MU	C4-N3-C2	-5.40	120.26	127.34
1	1A	1939	5MU	C5-C4-N3	5.40	120.02	115.32
1	2A	1915	5MU	C4-N3-C2	-5.40	120.26	127.34
1	2A	1915	5MU	N3-C2-N1	5.34	121.84	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	1y	8	4SU	C5-C4-N3	5.33	119.71	114.75
32	2a	527	G7M	C5-C4-N3	-5.29	118.16	128.15
1	2A	1939	5MU	N3-C2-N1	5.27	121.75	114.89
54	2w	46	G7M	C5-C4-N3	-5.27	118.20	128.15
55	2x	54	5MU	C4-N3-C2	-5.26	120.44	127.34
56	1y	54	5MU	C4-N3-C2	-5.26	120.45	127.34
55	2x	54	5MU	N3-C2-N1	5.24	121.71	114.89
1	1A	1939	5MU	C4-N3-C2	-5.24	120.47	127.34
32	1a	527	G7M	N9-C4-N3	5.21	136.38	125.95
32	1a	527	G7M	C5-C4-N3	-5.20	118.33	128.15
32	2a	1519	MA6	N1-C2-N3	-5.17	120.76	128.58
1	1A	1915	5MU	N3-C2-N1	5.12	121.56	114.89
54	2w	8	4SU	N3-C2-N1	5.09	121.52	114.89
56	1y	37	MIA	N3-C4-N9	5.09	135.82	127.17
1	2A	2552	2MU	N3-C2-N1	5.09	121.51	114.89
32	2a	1518	MA6	N1-C2-N3	-5.08	120.89	128.58
56	2y	54	5MU	N3-C2-N1	5.07	121.49	114.89
54	2w	39	PSU	N1-C2-N3	5.06	120.51	115.17
1	1A	2552	2MU	C4-N3-C2	-5.06	120.33	126.61
54	1w	76	F3N	C5-C4-N3	-5.05	119.77	126.72
55	2x	76	31H	C5-C4-N3	-5.03	119.79	126.72
55	1x	54	5MU	N3-C2-N1	5.02	121.43	114.89
54	2w	76	F3N	C5-C4-N3	-5.02	119.81	126.72
1	1A	2251	OMG	C2-N3-C4	5.02	120.94	112.30
32	1a	1519	MA6	N1-C2-N3	-5.02	120.99	128.58
1	2A	1939	5MU	C5-C4-N3	5.01	119.68	115.32
54	1w	46	G7M	C5-C4-N3	-4.89	118.90	128.15
56	1y	54	5MU	N3-C2-N1	4.89	121.26	114.89
56	1y	46	G7M	C2-N3-C4	4.87	120.69	112.30
32	1a	1518	MA6	N1-C2-N3	-4.87	121.21	128.58
56	2y	54	5MU	C4-N3-C2	-4.84	121.00	127.34
55	1x	54	5MU	C4-N3-C2	-4.83	121.01	127.34
54	1w	8	4SU	C5-C4-N3	4.83	119.24	114.75
1	2A	2251	OMG	C2-N3-C4	4.81	120.59	112.30
56	2y	46	G7M	C2-N3-C4	4.77	120.51	112.30
55	1x	76	31H	C5-C4-N3	-4.77	120.16	126.72
32	2a	1518	MA6	C5-C4-N3	-4.76	120.17	126.72
1	2A	2552	2MU	C4-N3-C2	-4.73	120.74	126.61
56	2y	8	4SU	N3-C2-N1	4.73	121.05	114.89
1	1A	1915	5MU	C5-C4-N3	4.73	119.43	115.32
1	2A	1915	5MU	C5-C4-N3	4.68	119.39	115.32
56	1y	54	5MU	C5-C4-N3	4.67	119.38	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2251	OMG	N9-C4-N3	4.64	135.23	125.95
54	1w	54	5MU	N3-C2-N1	4.64	120.93	114.89
1	1A	2251	OMG	N9-C4-N3	4.61	135.17	125.95
1	1A	2503	8AH	C6-C5-N7	4.60	136.28	131.72
54	2w	46	G7M	C2-N3-C4	4.58	120.19	112.30
32	1a	527	G7M	C2-N3-C4	4.58	120.19	112.30
56	2y	37	MIA	N3-C4-N9	4.57	134.93	127.17
1	1A	1915	5MU	O4-C4-C5	-4.57	119.69	124.92
54	1w	54	5MU	C4-N3-C2	-4.53	121.40	127.34
32	1a	1519	MA6	C5-C4-N3	-4.53	120.48	126.72
32	2a	527	G7M	C2-N3-C4	4.52	120.09	112.30
1	1A	1939	5MU	N3-C2-N1	4.51	120.77	114.89
1	2A	1939	5MU	O4-C4-C5	-4.51	119.76	124.92
32	2a	1519	MA6	C5-C4-N3	-4.48	120.55	126.72
54	2w	8	4SU	C5-C4-S4	-4.48	119.19	124.31
1	1A	2503	8AH	C4-C5-N7	-4.47	106.34	110.91
32	2a	966	M2G	N9-C4-N3	4.45	134.84	125.95
54	2w	54	5MU	C4-N3-C2	-4.42	121.54	127.34
32	1a	1518	MA6	C5-C4-N3	-4.41	120.64	126.72
1	2A	2605	PSU	C4-N3-C2	-4.41	120.30	126.37
55	2x	55	PSU	C4-N3-C2	-4.40	120.31	126.37
55	2x	54	5MU	C5-C4-N3	4.39	119.14	115.32
1	1A	1939	5MU	O4-C4-C5	-4.35	119.94	124.92
32	1a	966	M2G	C2-N3-C4	4.32	120.50	112.51
54	1w	54	5MU	O4-C4-C5	-4.28	120.02	124.92
1	1A	2605	PSU	C4-N3-C2	-4.28	120.48	126.37
1	2A	1939	5MU	C5-C6-N1	-4.27	118.67	123.31
54	2w	54	5MU	N3-C2-N1	4.27	120.45	114.89
54	2w	54	5MU	C5-C4-N3	4.24	119.00	115.32
32	2a	966	M2G	C2-N3-C4	4.21	120.30	112.51
1	2A	1915	5MU	O4-C4-C5	-4.21	120.11	124.92
55	1x	8	4SU	C6-C5-C4	-4.19	116.32	119.95
54	1w	46	G7M	C2-N3-C4	4.18	119.50	112.30
55	1x	55	PSU	C4-N3-C2	-4.16	120.64	126.37
56	1y	8	4SU	C5-C4-S4	-4.14	119.58	124.31
1	2A	1911	PSU	C4-N3-C2	-4.14	120.67	126.37
55	1x	54	5MU	C5-C4-N3	4.13	118.91	115.32
56	1y	55	PSU	O2-C2-N1	-4.12	118.54	122.79
56	1y	54	5MU	O4-C4-C5	-4.11	120.22	124.92
56	2y	54	5MU	C5-C4-N3	4.10	118.89	115.32
32	1a	1207	2MG	C6-C5-N7	4.10	137.76	130.29
1	1A	1911	PSU	C4-N3-C2	-4.10	120.73	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	54	5MU	O4-C4-C5	-4.09	120.24	124.92
32	1a	516	PSU	C4-N3-C2	-4.07	120.77	126.37
54	2w	54	5MU	O4-C4-C5	-4.07	120.27	124.92
32	1a	966	M2G	N9-C4-N3	4.06	134.07	125.95
1	1A	1917	PSU	C4-N3-C2	-4.06	120.78	126.37
32	2a	1519	MA6	C5-N7-C8	4.06	109.83	103.45
32	1a	1519	MA6	C4-C5-N7	-4.06	105.94	110.58
32	2a	516	PSU	C4-N3-C2	-4.05	120.79	126.37
32	1a	1518	MA6	C4-C5-N7	-4.04	105.96	110.58
54	1w	54	5MU	C5-C4-N3	4.04	118.84	115.32
32	2a	1519	MA6	C4-C5-N7	-4.03	105.97	110.58
32	2a	1518	MA6	C2-N1-C6	4.02	121.64	111.83
1	1A	1917	PSU	O2-C2-N1	-4.00	118.67	122.79
32	1a	1518	MA6	C5-N7-C8	3.99	109.72	103.45
32	1a	1519	MA6	C5-N7-C8	3.98	109.71	103.45
32	2a	1519	MA6	C2-N1-C6	3.98	121.54	111.83
54	2w	8	4SU	O2-C2-N1	-3.97	117.62	122.80
54	2w	32	PSU	C4-N3-C2	-3.96	120.91	126.37
32	1a	1518	MA6	C2-N1-C6	3.95	121.49	111.83
55	1x	8	4SU	O2-C2-N1	3.94	127.93	122.80
1	1A	1939	5MU	C5-C6-N1	-3.94	119.04	123.31
56	2y	32	PSU	O2-C2-N1	-3.92	118.75	122.79
54	1w	32	PSU	C4-N3-C2	-3.92	120.97	126.37
56	2y	8	4SU	C5-C4-S4	-3.91	119.83	124.31
54	1w	55	PSU	C4-N3-C2	-3.91	120.99	126.37
54	2w	55	PSU	C4-N3-C2	-3.90	121.00	126.37
56	1y	32	PSU	C4-N3-C2	-3.89	121.01	126.37
55	1x	32	5MC	C5-C6-N1	-3.87	119.11	123.31
55	2x	76	31H	O4'-C1'-N9	3.86	115.51	108.09
32	1a	1519	MA6	C2-N1-C6	3.84	121.21	111.83
56	2y	55	PSU	O2-C2-N1	-3.84	118.83	122.79
54	1w	37	MIA	C15-C14-C13	-3.84	111.13	122.66
1	2A	1917	PSU	C4-N3-C2	-3.83	121.10	126.37
56	2y	54	5MU	O4-C4-C5	-3.83	120.54	124.92
56	2y	55	PSU	C4-N3-C2	-3.81	121.13	126.37
55	2x	32	5MC	C5-C6-N1	-3.80	119.18	123.31
56	1y	55	PSU	C4-N3-C2	-3.80	121.14	126.37
32	2a	1207	2MG	N9-C4-N3	3.76	133.48	125.95
1	1A	2552	2MU	O2-C2-N1	-3.75	117.92	122.80
54	1w	8	4SU	N3-C2-N1	3.74	119.76	114.89
55	1x	54	5MU	O4-C4-C5	-3.72	120.67	124.92
54	1w	32	PSU	O2-C2-N1	-3.71	118.97	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	54	5MU	C5-C6-N1	-3.70	119.30	123.31
56	2y	32	PSU	C4-N3-C2	-3.68	121.30	126.37
32	1a	1207	2MG	N9-C4-N3	3.68	133.31	125.95
1	1A	1962	5MC	C5-C6-N1	-3.67	119.33	123.31
56	2y	37	MIA	C2-N3-C4	3.66	120.78	111.83
32	2a	1519	MA6	C2-N3-C4	3.64	120.72	111.83
32	2a	1207	2MG	C6-C5-N7	3.64	136.91	130.29
32	2a	1518	MA6	C2-N3-C4	3.63	120.69	111.83
32	1a	1519	MA6	C2-N3-C4	3.63	120.69	111.83
1	2A	1917	PSU	O2-C2-N1	-3.62	119.06	122.79
32	2a	1518	MA6	C5-N7-C8	3.61	109.13	103.45
32	2a	1519	MA6	N9-C8-N7	-3.61	108.81	113.94
1	2A	1915	5MU	C5-C6-N1	-3.59	119.41	123.31
56	1y	8	4SU	N3-C2-N1	3.57	119.54	114.89
56	1y	37	MIA	C2-N3-C4	3.57	120.55	111.83
1	2A	2503	8AH	C6-C5-N7	3.57	135.26	131.72
55	1x	54	5MU	C5-C6-N1	-3.57	119.44	123.31
1	1A	2605	PSU	O2-C2-N1	-3.56	119.12	122.79
32	2a	1518	MA6	C4-C5-N7	-3.54	106.53	110.58
1	2A	2503	8AH	C4-C5-N7	-3.54	107.29	110.91
55	1x	76	31H	C4'-O4'-C1'	-3.53	101.67	109.47
32	1a	1207	2MG	N1-C2-N2	3.52	120.15	116.56
55	1x	76	31H	C2-N3-C4	3.50	120.38	111.83
56	2y	37	MIA	C4-C5-N7	-3.50	106.58	110.58
1	2A	1962	5MC	C5-C6-N1	-3.50	119.52	123.31
55	1x	76	31H	N9-C8-N7	-3.48	109.00	113.94
54	2w	76	F3N	C2-N3-C4	3.48	120.32	111.83
54	2w	76	F3N	N9-C8-N7	-3.47	109.02	113.94
32	1a	1518	MA6	N9-C8-N7	-3.46	109.02	113.94
55	2x	76	31H	N9-C8-N7	-3.45	109.03	113.94
32	2a	967	5MC	C5-C6-N1	-3.45	119.56	123.31
56	1y	39	PSU	C4-N3-C2	-3.45	121.62	126.37
32	1a	1518	MA6	C2-N3-C4	3.45	120.25	111.83
32	1a	1519	MA6	N9-C8-N7	-3.45	109.05	113.94
54	1w	39	PSU	C4-N3-C2	-3.44	121.63	126.37
32	1a	966	M2G	C6-C5-N7	3.43	136.54	130.29
32	2a	1404	5MC	C5-C6-N1	-3.43	119.58	123.31
43	1l	92	0TD	OD2-CG-CB	3.43	120.57	113.15
1	2A	1911	PSU	O2-C2-N1	-3.43	119.26	122.79
56	2y	54	5MU	C5-C6-N1	-3.42	119.60	123.31
1	1A	1911	PSU	O2-C2-N1	-3.41	119.27	122.79
32	2a	516	PSU	O2-C2-N1	-3.40	119.28	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	76	31H	C2-N3-C4	3.39	120.12	111.83
32	2a	1498	UR3	C5-C4-N3	3.39	119.51	115.04
32	1a	967	5MC	C5-C6-N1	-3.38	119.64	123.31
56	2y	37	MIA	N3-C2-N1	-3.38	123.47	128.58
1	1A	2503	8AH	N6-C6-N1	3.37	121.57	117.03
54	2w	32	PSU	O2-C2-N1	-3.36	119.33	122.79
54	1w	55	PSU	O2-C2-N1	-3.35	119.33	122.79
56	1y	32	PSU	O2-C2-N1	-3.35	119.33	122.79
54	1w	76	F3N	N9-C8-N7	-3.35	109.19	113.94
43	2l	92	0TD	OD2-CG-CB	3.33	120.35	113.15
55	1x	8	4SU	C5-C4-N3	3.33	117.85	114.75
55	2x	76	31H	C4'-O4'-C1'	-3.32	102.13	109.47
54	1w	37	MIA	C4-C5-N7	-3.31	106.79	110.58
54	2w	39	PSU	C4-N3-C2	-3.31	121.81	126.37
1	2A	2503	8AH	N6-C6-N1	3.31	121.50	117.03
32	2a	1400	5MC	C5-C6-N1	-3.31	119.72	123.31
54	2w	54	5MU	C5-C6-N1	-3.29	119.74	123.31
56	2y	39	PSU	C4-N3-C2	-3.29	121.84	126.37
54	1w	76	F3N	C2-N3-C4	3.28	119.83	111.83
56	1y	54	5MU	C5-C6-N1	-3.27	119.76	123.31
55	1x	55	PSU	O2-C2-N1	-3.26	119.42	122.79
56	1y	37	MIA	N3-C2-N1	-3.24	123.68	128.58
32	2a	1407	5MC	C5-C6-N1	-3.23	119.80	123.31
54	1w	37	MIA	C2-N3-C4	3.22	120.72	112.29
56	2y	55	PSU	C6-C5-C4	-3.21	116.01	118.17
54	1w	37	MIA	C16-C14-C13	-3.20	113.04	122.66
54	2w	37	MIA	C2-N3-C4	3.19	120.64	112.29
32	1a	1407	5MC	C5-C6-N1	-3.17	119.87	123.31
54	2w	55	PSU	O2-C2-N1	-3.16	119.53	122.79
32	2a	1518	MA6	N9-C8-N7	-3.16	109.45	113.94
32	2a	966	M2G	C6-C5-N7	3.15	136.02	130.29
32	1a	1498	UR3	C5-C4-N3	3.14	119.17	115.04
1	1A	1942	5MC	C5-C4-N3	-3.14	118.54	121.75
55	2x	55	PSU	O2-C2-N1	-3.12	119.57	122.79
32	2a	1407	5MC	C5-C4-N3	-3.12	118.56	121.75
54	1w	76	F3N	C5-N7-C8	3.12	108.35	103.45
54	1w	8	4SU	C5-C4-S4	-3.11	120.75	124.31
1	2A	1939	5MU	O2-C2-N1	-3.11	118.75	122.80
54	1w	76	F3N	C5-C4-N9	3.11	109.20	105.81
55	1x	32	5MC	C5-C4-N3	-3.09	118.58	121.75
1	1A	2552	2MU	C5-C4-N3	3.09	119.13	114.80
32	1a	1207	2MG	C4-C5-N7	-3.08	105.78	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1518	MA6	N3-C4-N9	3.06	132.37	127.17
55	2x	76	31H	C5-N7-C8	3.05	108.25	103.45
55	1x	8	4SU	S4-C4-N3	-3.04	117.02	120.20
55	2x	8	4SU	C5-C4-N3	3.03	117.57	114.75
54	2w	37	MIA	C12-N6-C6	-3.03	120.04	122.85
32	1a	1400	5MC	C5-C6-N1	-3.03	120.03	123.31
55	2x	8	4SU	C1'-N1-C2	3.03	123.03	117.59
55	2x	8	4SU	C6-C5-C4	-3.00	117.35	119.95
1	1A	1915	5MU	C5-C6-N1	-2.99	120.06	123.31
55	1x	54	5MU	O2-C2-N1	-2.99	118.90	122.80
1	1A	1942	5MC	C5-C6-N1	-2.98	120.08	123.31
32	1a	1404	5MC	C5-C4-N3	-2.97	118.71	121.75
1	2A	2552	2MU	C5-C4-N3	2.97	118.96	114.80
54	2w	37	MIA	C4-C5-N7	-2.96	107.19	110.58
1	2A	2552	2MU	O2-C2-N1	-2.96	118.94	122.80
54	2w	76	F3N	C5-N7-C8	2.96	108.11	103.45
1	2A	2251	OMG	C6-C5-N7	2.96	135.68	130.29
32	2a	1207	2MG	C4-C5-N7	-2.94	106.02	110.67
32	1a	1400	5MC	C5-C4-N3	-2.92	118.77	121.75
1	2A	1942	5MC	C5-C6-N1	-2.90	120.16	123.31
1	2A	1942	5MC	C5-C4-N3	-2.90	118.78	121.75
1	1A	2251	OMG	C6-C5-N7	2.88	135.52	130.29
54	1w	54	5MU	C5-C6-N1	-2.86	120.20	123.31
56	1y	37	MIA	C4-C5-N7	-2.86	107.31	110.58
55	2x	54	5MU	O2-C2-N1	-2.86	119.08	122.80
1	2A	2605	PSU	O2-C2-N1	-2.86	119.84	122.79
56	1y	8	4SU	C1'-N1-C2	2.85	122.72	117.59
1	2A	1962	5MC	C5-C4-N3	-2.83	118.85	121.75
1	1A	1939	5MU	O2-C2-N1	-2.83	119.12	122.80
54	1w	39	PSU	O2-C2-N1	-2.82	119.88	122.79
1	1A	2552	2MU	O4-C4-C5	-2.81	120.32	125.16
55	1x	76	31H	C5-N7-C8	2.80	107.85	103.45
55	2x	32	5MC	C5-C4-N3	-2.79	118.89	121.75
55	1x	76	31H	N3-C4-N9	2.79	131.92	127.17
32	1a	1404	5MC	C5-C6-N1	-2.75	120.33	123.31
54	2w	37	MIA	C11-S10-C2	-2.75	100.19	102.25
1	2A	2503	8AH	C2-N1-C6	2.75	122.33	118.10
55	2x	76	31H	C5-C4-N9	2.74	108.79	105.81
55	1x	8	4SU	C1'-N1-C2	2.70	122.45	117.59
32	2a	1404	5MC	C5-C4-N3	-2.69	118.99	121.75
54	1w	37	MIA	C6-C5-N7	2.69	135.36	132.43
54	2w	76	F3N	N3-C4-N9	2.69	131.73	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	527	G7M	O6-C6-C5	-2.68	122.02	128.01
55	2x	8	4SU	O2-C2-N1	2.68	126.28	122.80
32	1a	1207	2MG	N2-C2-N3	-2.68	117.10	120.51
54	2w	37	MIA	C1'-N9-C8	-2.67	121.17	127.09
1	1A	2503	8AH	C2-N1-C6	2.65	122.17	118.10
32	1a	516	PSU	O2-C2-N1	-2.64	120.07	122.79
1	1A	1962	5MC	C5-C4-N3	-2.64	119.05	121.75
32	2a	1519	MA6	N3-C4-N9	2.63	131.64	127.17
1	1A	2605	PSU	C5-C6-N1	-2.62	118.50	122.14
32	2a	1207	2MG	N2-C2-N3	-2.62	117.18	120.51
54	2w	46	G7M	O6-C6-C5	-2.61	122.20	128.01
32	1a	966	M2G	C4-C5-N7	-2.60	106.55	110.67
32	1a	1519	MA6	N3-C4-N9	2.60	131.58	127.17
56	2y	8	4SU	C1'-N1-C2	2.59	122.24	117.59
32	2a	966	M2G	C4-C5-N7	-2.58	106.58	110.67
54	1w	37	MIA	C11-S10-C2	-2.58	100.31	102.25
32	1a	967	5MC	C5-C4-N3	-2.58	119.11	121.75
32	2a	1207	2MG	N1-C2-N2	2.56	119.17	116.56
32	1a	1407	5MC	C5-C4-N3	-2.55	119.14	121.75
32	1a	1518	MA6	N3-C4-N9	2.54	131.49	127.17
43	2l	92	0TD	OD1-CG-CB	-2.54	117.13	122.44
32	2a	1518	MA6	C4-C5-C6	2.53	118.53	115.91
32	2a	967	5MC	C5-C4-N3	-2.52	119.17	121.75
32	1a	1402	4OC	C6-C5-C4	2.51	120.02	117.00
54	1w	37	MIA	C2-N1-C6	2.51	122.30	117.54
55	2x	76	31H	N3-C4-N9	2.50	131.42	127.17
32	1a	1404	5MC	CM5-C5-C6	-2.49	119.48	122.85
56	2y	37	MIA	C5-N7-C8	2.48	107.35	103.45
1	2A	2552	2MU	O4-C4-C5	-2.47	120.89	125.16
1	2A	2605	PSU	C5-C6-N1	-2.47	118.72	122.14
56	1y	54	5MU	O2-C2-N1	-2.46	119.59	122.80
56	1y	54	5MU	C5M-C5-C4	2.45	121.40	118.78
56	2y	8	4SU	O2-C2-N1	-2.45	119.61	122.80
1	2A	2251	OMG	O6-C6-C5	-2.44	120.10	126.53
54	1w	46	G7M	O6-C6-C5	-2.43	122.58	128.01
1	2A	1915	5MU	O2-C2-N1	-2.43	119.64	122.80
54	2w	76	F3N	C5-C4-N9	2.43	108.46	105.81
1	1A	1915	5MU	O2-C2-N1	-2.43	119.64	122.80
32	2a	1400	5MC	C5-C4-N3	-2.42	119.27	121.75
1	2A	2552	2MU	C2'-C1'-N1	-2.41	109.66	114.24
54	1w	76	F3N	C4-C5-N7	-2.41	107.82	110.58
55	2x	55	PSU	C5-C6-N1	-2.40	118.80	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2251	OMG	C4-C5-N7	-2.38	106.90	110.67
54	1w	54	5MU	O2-C2-N1	-2.36	119.72	122.80
54	2w	39	PSU	C6-C5-C4	-2.36	116.58	118.17
32	2a	1404	5MC	O2-C2-N3	-2.35	118.63	122.33
54	1w	37	MIA	C5-N7-C8	2.34	107.12	103.45
54	1w	76	F3N	C6-C5-C4	2.34	120.37	117.18
32	2a	1402	4OC	C6-C5-C4	2.33	119.81	117.00
55	2x	8	4SU	S4-C4-N3	-2.33	117.77	120.20
1	2A	2251	OMG	C4-C5-N7	-2.33	106.98	110.67
32	2a	1400	5MC	O2-C2-N3	-2.32	118.67	122.33
1	1A	2251	OMG	O6-C6-C5	-2.32	120.41	126.53
54	2w	54	5MU	O2-C2-N1	-2.32	119.78	122.80
1	2A	1920	OMC	O2-C2-N3	-2.31	118.68	122.33
1	1A	1942	5MC	CM5-C5-C6	-2.30	119.74	122.85
55	1x	76	31H	O2'-C2'-C3'	2.29	116.78	111.16
54	1w	76	F3N	N3-C4-N9	2.28	131.04	127.17
32	1a	1498	UR3	C1'-N1-C2	2.26	120.74	117.04
32	2a	1402	4OC	CM4-N4-C4	-2.26	118.04	122.45
55	1x	76	31H	O4'-C1'-N9	2.26	112.42	108.09
55	2x	76	31H	C4-C5-N7	-2.25	108.01	110.58
55	1x	55	PSU	C5-C6-N1	-2.25	119.02	122.14
54	1w	76	F3N	O2'-C2'-C3'	-2.24	105.67	111.16
32	1a	1400	5MC	O2-C2-N3	-2.24	118.80	122.33
32	1a	1518	MA6	C4-C5-C6	2.23	118.22	115.91
54	2w	37	MIA	C4-N9-C8	2.23	108.08	105.74
32	2a	1400	5MC	C1'-N1-C6	-2.23	117.48	121.15
32	1a	516	PSU	C5-C6-N1	-2.23	119.05	122.14
54	2w	37	MIA	C5-N7-C8	2.23	106.95	103.45
54	2w	76	F3N	C6-C5-C4	2.23	120.22	117.18
32	2a	966	M2G	O6-C6-C5	-2.22	120.66	126.53
55	2x	32	5MC	O2-C2-N3	-2.22	118.83	122.33
32	1a	1404	5MC	O2-C2-N3	-2.21	118.84	122.33
56	2y	39	PSU	O2-C2-N1	-2.21	120.51	122.79
55	1x	8	4SU	O2-C2-N3	-2.21	117.42	121.49
54	2w	37	MIA	C4-C5-C6	2.20	118.61	116.78
54	2w	37	MIA	C2-N1-C6	2.20	121.72	117.54
55	2x	76	31H	OCN-CN-N	-2.19	119.65	125.32
55	2x	76	31H	C6-C5-C4	2.19	120.17	117.18
32	1a	1498	UR3	C6-N1-C2	-2.17	120.02	121.80
54	1w	37	MIA	N3-C2-N1	-2.17	123.03	127.00
55	2x	76	31H	CA-N-CN	-2.17	119.49	122.82
56	1y	55	PSU	O4'-C1'-C2'	2.17	108.15	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	527	G7M	C5-C6-N1	2.16	116.30	111.84
56	1y	39	PSU	O2-C2-N1	-2.16	120.56	122.79
56	2y	37	MIA	C4-N9-C8	2.15	107.99	105.74
56	2y	54	5MU	O2-C2-N1	-2.14	120.00	122.80
32	2a	967	5MC	CM5-C5-C6	-2.14	119.95	122.85
32	1a	516	PSU	O4'-C1'-C2'	2.13	108.11	105.15
55	1x	32	5MC	O2-C2-N3	-2.13	118.97	122.33
56	2y	46	G7M	O6-C6-C5	-2.13	123.25	128.01
1	1A	1942	5MC	O2-C2-N3	-2.12	118.98	122.33
32	2a	527	G7M	O6-C6-C5	-2.12	123.27	128.01
32	2a	527	G7M	C5-C6-N1	2.10	116.18	111.84
56	1y	37	MIA	C5-N7-C8	2.10	106.75	103.45
32	1a	966	M2G	O6-C6-C5	-2.10	121.00	126.53
1	1A	2552	2MU	C2'-C1'-N1	-2.10	110.26	114.24
56	1y	39	PSU	O2-C2-N3	-2.09	118.15	121.86
1	1A	1915	5MU	C5M-C5-C4	2.07	121.00	118.78
54	2w	32	PSU	C5-C6-N1	-2.06	119.28	122.14
1	2A	1942	5MC	O2-C2-N3	-2.06	119.09	122.33
56	1y	46	G7M	O6-C6-C5	-2.05	123.43	128.01
1	2A	1911	PSU	O4'-C1'-C2'	2.05	107.99	105.15
32	1a	1407	5MC	CM5-C5-C6	-2.05	120.08	122.85
55	1x	76	31H	CA-N-CN	-2.05	119.68	122.82
32	2a	1402	4OC	O2-C2-N3	-2.04	119.11	122.33
1	2A	1911	PSU	C5-C6-N1	-2.04	119.31	122.14
32	2a	516	PSU	O4'-C1'-C2'	2.03	107.96	105.15
32	1a	1207	2MG	C8-N7-C5	2.03	107.87	104.26
32	1a	516	PSU	O2-C2-N3	-2.01	118.29	121.86
55	1x	76	31H	OCN-CN-N	-2.01	120.13	125.32
54	2w	39	PSU	O2-C2-N3	-2.01	118.30	121.86

There are no chirality outliers.

All (60) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	1w	37	MIA	C12-C13-C14-C15
55	1x	76	31H	C3'-C4'-C5'-O5'
56	1y	8	4SU	O4'-C4'-C5'-O5'
56	1y	46	G7M	C4'-C5'-O5'-P
32	2a	1207	2MG	N3-C2-N2-CM2
43	2l	92	0TD	O-C-CA-CB
43	2l	92	0TD	CG-CB-SB-CSB
54	2w	37	MIA	C5-C6-N6-C12

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Mol	Chain	Res	Type	Atoms
54	2w	37	MIA	N1-C6-N6-C12
55	2x	76	31H	C3'-C4'-C5'-O5'
55	2x	76	31H	O4'-C4'-C5'-O5'
56	2y	54	5MU	C3'-C4'-C5'-O5'
56	2y	54	5MU	O4'-C4'-C5'-O5'
56	2y	55	PSU	C2'-C1'-C5-C4
56	2y	55	PSU	C2'-C1'-C5-C6
56	2y	55	PSU	O4'-C1'-C5-C6
54	1w	76	F3N	C3'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
54	1w	76	F3N	O4'-C4'-C5'-O5'
56	1y	37	MIA	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
56	2y	37	MIA	C3'-C4'-C5'-O5'
56	2y	55	PSU	C3'-C4'-C5'-O5'
55	1x	76	31H	O4'-C4'-C5'-O5'
56	1y	8	4SU	C3'-C4'-C5'-O5'
56	1y	37	MIA	O4'-C4'-C5'-O5'
56	2y	37	MIA	O4'-C4'-C5'-O5'
56	2y	55	PSU	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
56	2y	46	G7M	O4'-C4'-C5'-O5'
56	2y	46	G7M	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
32	2a	527	G7M	O4'-C4'-C5'-O5'
54	2w	76	F3N	N-CA-CB-CG
54	1w	46	G7M	C4'-C5'-O5'-P
1	1A	1915	5MU	O4'-C4'-C5'-O5'
54	2w	46	G7M	C4'-C5'-O5'-P
55	1x	76	31H	C4'-C5'-O5'-P
55	2x	76	31H	C4'-C5'-O5'-P
56	2y	37	MIA	C4'-C5'-O5'-P
56	1y	55	PSU	O4'-C1'-C5-C4
56	2y	55	PSU	O4'-C1'-C5-C4
1	2A	1917	PSU	O4'-C4'-C5'-O5'
32	2a	527	G7M	C4'-C5'-O5'-P
56	1y	46	G7M	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	1w	37	MIA	N1-C2-S10-C11
54	1w	37	MIA	N3-C2-S10-C11

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Mol	Chain	Res	Type	Atoms
1	1A	2503	8AH	C4'-C5'-O5'-P
43	2l	92	0TD	CA-CB-SB-CSB
32	1a	527	G7M	C4'-C5'-O5'-P
32	2a	1402	4OC	O4'-C4'-C5'-O5'
54	1w	37	MIA	C12-C13-C14-C16
43	1l	92	0TD	CG-CB-SB-CSB
32	1a	1519	MA6	C4'-C5'-O5'-P
56	2y	8	4SU	C2'-C1'-N1-C2
32	2a	1519	MA6	C4'-C5'-O5'-P
32	1a	967	5MC	O4'-C4'-C5'-O5'

There are no ring outliers.

36 monomers are involved in 55 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	2552	2MU	1	0
56	2y	46	G7M	1	0
56	2y	39	PSU	1	0
56	1y	8	4SU	1	0
54	1w	37	MIA	1	0
54	1w	39	PSU	1	0
1	1A	1939	5MU	2	0
55	2x	8	4SU	1	0
56	1y	39	PSU	1	0
1	1A	1917	PSU	1	0
54	2w	39	PSU	2	0
54	2w	46	G7M	1	0
54	1w	46	G7M	1	0
54	2w	37	MIA	1	0
1	2A	1915	5MU	1	0
32	2a	1207	2MG	3	0
1	2A	1939	5MU	1	0
55	2x	76	31H	2	0
32	2a	1402	4OC	1	0
54	2w	8	4SU	2	0
1	1A	2251	OMG	1	0
1	2A	2503	8AH	2	0
55	2x	55	PSU	1	0
56	1y	37	MIA	2	0
54	2w	76	F3N	3	0
32	1a	1519	MA6	2	0
32	1a	966	M2G	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	1x	8	4SU	2	0
56	2y	55	PSU	7	0
56	2y	8	4SU	2	0
32	2a	1519	MA6	3	0
1	1A	2552	2MU	1	0
56	1y	55	PSU	1	0
32	1a	1518	MA6	3	0
55	1x	76	31H	1	0
32	2a	1518	MA6	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2685 ligands modelled in this entry, 2681 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	TYK	2A	3798	1	67,67,67	1.82	8 (11%)	87,97,97	1.52	16 (18%)
61	SF4	1d	501	35	0,12,12	-	-	-		
61	SF4	2d	303	35	0,12,12	-	-	-		
59	TYK	1A	4101	1	67,67,67	1.77	7 (10%)	87,97,97	1.35	15 (17%)

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
59	TYK	2A	3798	1	-	4/67/126/126	1/3/4/4
61	SF4	1d	501	35	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	SF4	2d	303	35	-	-	0/6/5/5
59	TYK	1A	4101	1	-	3/67/126/126	1/3/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	1A	4101	TYK	C8-C9	-8.59	1.38	1.51
59	2A	3798	TYK	C8-C9	-8.57	1.38	1.51
59	2A	3798	TYK	C14-C13	-7.21	1.37	1.50
59	1A	4101	TYK	C14-C13	-6.61	1.39	1.50
59	2A	3798	TYK	C2-C1	-4.91	1.41	1.50
59	1A	4101	TYK	C2-C1	-4.50	1.42	1.50
59	2A	3798	TYK	C11-C12	-3.23	1.39	1.46
59	1A	4101	TYK	C11-C12	-2.88	1.39	1.46
59	2A	3798	TYK	O5B-C1B	2.36	1.48	1.42
59	2A	3798	TYK	C2A-C3A	-2.30	1.49	1.53
59	2A	3798	TYK	O1C-C1C	2.28	1.44	1.40
59	2A	3798	TYK	C2B-C1B	2.07	1.56	1.51
59	1A	4101	TYK	C13-C12	2.06	1.39	1.34
59	1A	4101	TYK	C2B-C1B	2.05	1.56	1.51
59	1A	4101	TYK	C11-C10	2.04	1.39	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	2A	3798	TYK	C10-C11-C12	-4.40	119.72	126.23
59	1A	4101	TYK	C3B-C2B-C1B	-4.35	106.69	114.77
59	2A	3798	TYK	C1B-O4A-C4A	3.84	122.36	114.72
59	2A	3798	TYK	O4B-C4B-C5B	-3.73	103.04	109.46
59	2A	3798	TYK	C3B-C2B-C1B	-3.72	107.85	114.77
59	2A	3798	TYK	O5B-C5B-C6B	2.96	113.31	106.74
59	1A	4101	TYK	O5B-C5B-C6B	2.78	112.91	106.74
59	2A	3798	TYK	O15-C15-C16	-2.77	102.48	106.90
59	2A	3798	TYK	C1A-O1A-C5	-2.76	111.45	117.98
59	1A	4101	TYK	O4B-C4B-C5B	-2.75	104.73	109.46
59	1A	4101	TYK	O20-C20-C19	-2.68	117.58	125.38
59	1A	4101	TYK	C7C-O2C-C2C	-2.65	107.67	114.47
59	2A	3798	TYK	C1A-O5A-C5A	-2.62	109.16	113.63
59	2A	3798	TYK	C18-C4-C3	-2.62	106.91	111.09
59	2A	3798	TYK	C7C-O2C-C2C	-2.57	107.87	114.47
59	1A	4101	TYK	C23-O1C-C1C	-2.56	108.31	113.80
59	2A	3798	TYK	C14-C13-C12	-2.47	121.04	128.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	1A	4101	TYK	C10-C11-C12	-2.45	122.62	126.23
59	2A	3798	TYK	O20-C20-C19	-2.42	118.32	125.38
59	1A	4101	TYK	C1A-O5A-C5A	-2.31	109.69	113.63
59	2A	3798	TYK	C6C-C5C-C4C	-2.31	108.85	113.08
59	1A	4101	TYK	C22-C12-C11	2.31	121.62	118.09
59	1A	4101	TYK	C18-C4-C3	-2.31	107.41	111.09
59	1A	4101	TYK	O3B-C3B-C4B	2.24	111.47	107.52
59	1A	4101	TYK	C7-C8-C9	-2.23	105.32	110.64
59	1A	4101	TYK	C17-C16-C15	-2.16	107.51	113.23
59	2A	3798	TYK	C17-C16-C15	-2.12	107.61	113.23
59	2A	3798	TYK	O15-C15-C14	2.12	112.19	107.60
59	1A	4101	TYK	C1B-O4A-C4A	2.11	118.91	114.72
59	2A	3798	TYK	C7-C8-C9	-2.06	105.74	110.64
59	1A	4101	TYK	O4A-C4A-C3A	-2.01	103.94	109.02

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	1A	4101	TYK	C15-C14-C23-O1C
59	2A	3798	TYK	C15-C14-C23-O1C
59	1A	4101	TYK	C18-C4-C5-C6
59	2A	3798	TYK	C18-C4-C5-C6
59	2A	3798	TYK	C3-C4-C5-O1A
59	2A	3798	TYK	C3-C4-C5-C6
59	1A	4101	TYK	C2A-C1A-O1A-C5

All (2) ring outliers are listed below:

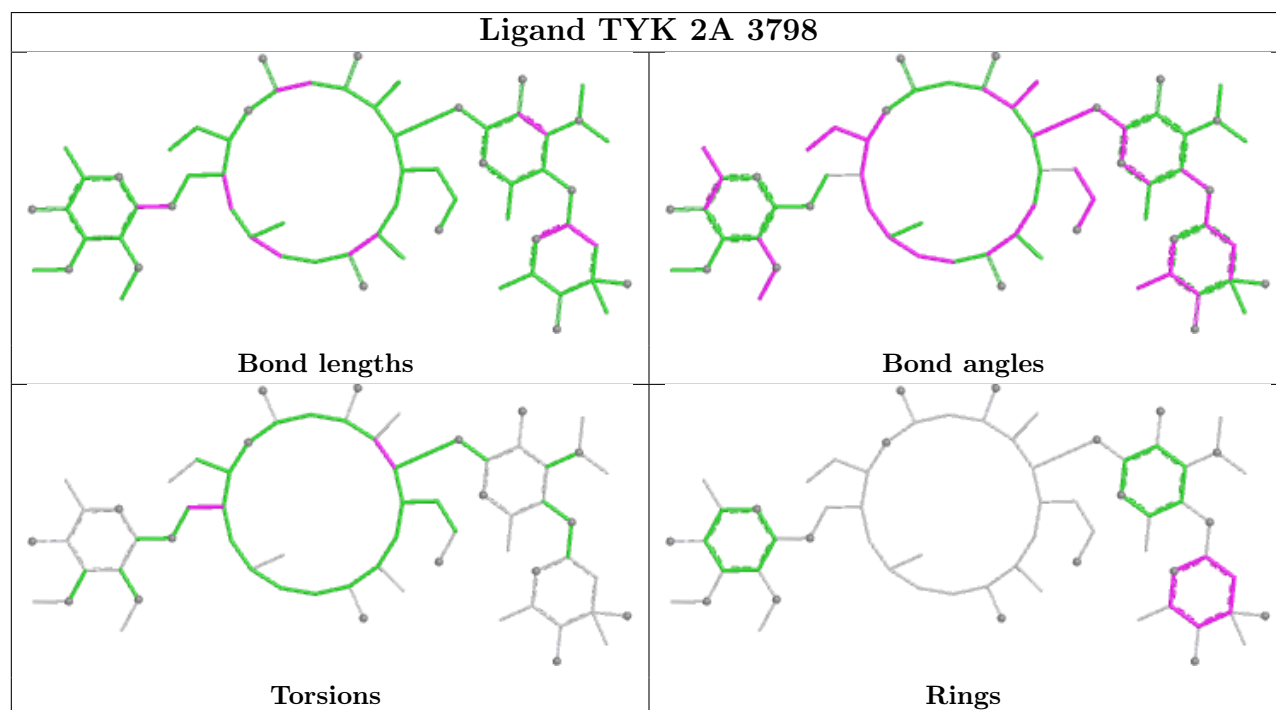
Mol	Chain	Res	Type	Atoms
59	2A	3798	TYK	C1B-C2B-C3B-C4B-C5B-O5B
59	1A	4101	TYK	C1B-C2B-C3B-C4B-C5B-O5B

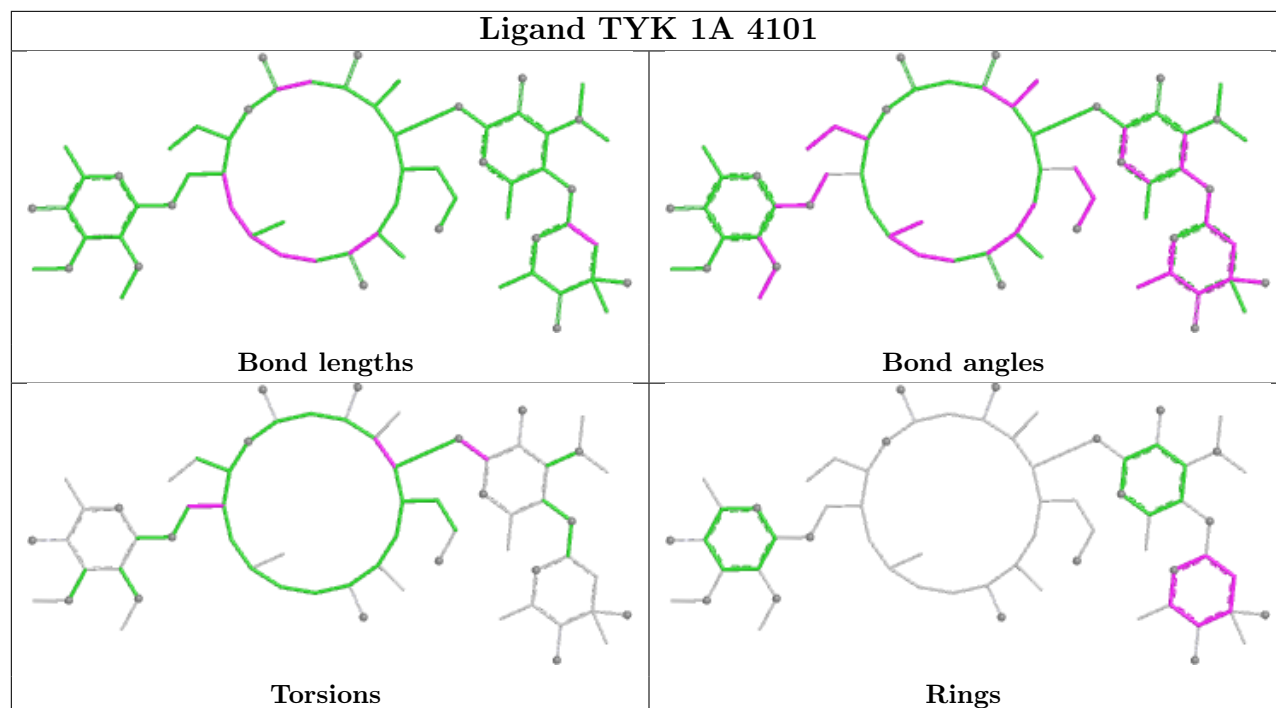
4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	2A	3798	TYK	1	0
61	1d	501	SF4	1	0
61	2d	303	SF4	1	0
59	1A	4101	TYK	1	0

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

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





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	2860/2915 (98%)	-0.42	186 (6%) 25 19	20, 36, 98, 108	0
1	2A	2789/2915 (95%)	0.07	147 (5%) 32 25	33, 57, 95, 107	0
2	1B	120/121 (99%)	-0.34	1 (0%) 82 79	29, 48, 63, 89	0
2	2B	120/121 (99%)	0.78	2 (1%) 69 64	61, 75, 84, 91	0
3	1D	275/276 (99%)	-0.26	3 (1%) 78 75	21, 37, 52, 77	0
3	2D	275/276 (99%)	0.13	2 (0%) 84 82	33, 50, 62, 82	0
4	1E	204/206 (99%)	-0.20	1 (0%) 87 85	20, 39, 59, 76	0
4	2E	204/206 (99%)	0.41	4 (1%) 65 59	38, 59, 72, 81	0
5	1F	202/210 (96%)	-0.15	1 (0%) 87 85	19, 41, 66, 84	0
5	2F	202/210 (96%)	0.45	1 (0%) 87 85	37, 66, 79, 87	0
6	1G	181/182 (99%)	0.39	5 (2%) 55 48	39, 56, 71, 81	0
6	2G	181/182 (99%)	1.03	15 (8%) 17 12	67, 77, 85, 94	0
7	1H	174/180 (96%)	0.27	4 (2%) 61 54	36, 53, 67, 73	0
7	2H	174/180 (96%)	1.25	23 (13%) 7 6	69, 83, 90, 95	0
8	1I	146/148 (98%)	0.71	2 (1%) 73 69	46, 72, 80, 83	0
8	2I	146/148 (98%)	0.87	8 (5%) 30 24	53, 73, 80, 85	0
9	1N	140/140 (100%)	-0.21	1 (0%) 84 82	25, 38, 61, 67	0
9	2N	140/140 (100%)	0.62	6 (4%) 40 32	48, 66, 79, 85	0
10	1O	122/122 (100%)	-0.28	0 100 100	28, 39, 57, 61	0
10	2O	122/122 (100%)	0.28	1 (0%) 82 79	47, 58, 70, 76	0
11	1P	149/150 (99%)	0.03	4 (2%) 56 49	23, 45, 68, 73	0
11	2P	149/150 (99%)	0.53	3 (2%) 65 59	40, 65, 80, 89	0
12	1Q	141/141 (100%)	-0.11	0 100 100	25, 39, 55, 72	0
12	2Q	141/141 (100%)	0.99	10 (7%) 22 16	48, 66, 77, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.40	0 100 100	25, 34, 46, 56	0
13	2R	118/118 (100%)	0.23	0 100 100	44, 53, 63, 70	0
14	1S	110/112 (98%)	0.17	0 100 100	38, 49, 60, 66	0
14	2S	110/112 (98%)	1.02	8 (7%) 21 15	61, 70, 78, 84	0
15	1T	131/146 (89%)	0.01	2 (1%) 72 67	33, 44, 68, 78	0
15	2T	131/146 (89%)	0.53	2 (1%) 72 67	52, 62, 75, 82	0
16	1U	116/118 (98%)	-0.43	0 100 100	22, 30, 44, 64	0
16	2U	116/118 (98%)	0.49	1 (0%) 81 78	44, 62, 72, 77	0
17	1V	101/101 (100%)	-0.43	1 (0%) 79 76	23, 38, 55, 65	0
17	2V	101/101 (100%)	0.79	2 (1%) 65 59	43, 71, 77, 83	0
18	1W	112/113 (99%)	-0.35	1 (0%) 81 78	25, 32, 49, 85	0
18	2W	112/113 (99%)	0.29	1 (0%) 81 78	40, 51, 69, 86	0
19	1X	95/96 (98%)	-0.17	2 (2%) 63 57	26, 38, 62, 77	0
19	2X	95/96 (98%)	0.51	5 (5%) 32 25	45, 58, 75, 82	0
20	1Y	107/110 (97%)	0.22	1 (0%) 81 78	36, 50, 67, 80	0
20	2Y	107/110 (97%)	1.07	12 (11%) 10 8	58, 71, 80, 86	0
21	1Z	154/206 (74%)	0.84	21 (13%) 7 5	38, 64, 83, 91	0
21	2Z	160/206 (77%)	1.65	47 (29%) 1 1	64, 81, 88, 92	0
22	10	83/85 (97%)	-0.14	0 100 100	29, 37, 50, 67	0
22	20	83/85 (97%)	0.88	5 (6%) 27 21	47, 61, 73, 78	0
23	11	97/98 (98%)	0.12	1 (1%) 79 76	29, 47, 71, 75	0
23	21	97/98 (98%)	0.35	4 (4%) 41 33	39, 55, 75, 84	0
24	12	70/72 (97%)	0.25	2 (2%) 53 46	35, 48, 59, 76	0
24	22	70/72 (97%)	0.78	2 (2%) 53 46	58, 69, 76, 80	0
25	13	59/60 (98%)	-0.22	2 (3%) 48 40	26, 36, 62, 79	0
25	23	59/60 (98%)	0.50	1 (1%) 69 64	57, 66, 79, 87	0
26	14	69/71 (97%)	0.92	8 (11%) 9 8	52, 73, 88, 89	0
26	24	69/71 (97%)	1.47	18 (26%) 1 1	75, 84, 92, 94	0
27	15	59/60 (98%)	-0.45	0 100 100	20, 32, 51, 54	0
27	25	59/60 (98%)	0.33	1 (1%) 69 64	39, 54, 66, 78	0
28	16	53/54 (98%)	-0.16	0 100 100	33, 43, 57, 60	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.57	0 100 100	51, 60, 68, 72	0
29	17	48/49 (97%)	-0.27	1 (2%) 63 57	24, 29, 54, 63	0
29	27	48/49 (97%)	0.14	2 (4%) 40 32	35, 42, 64, 74	0
30	18	64/65 (98%)	-0.28	0 100 100	29, 34, 42, 56	0
30	28	64/65 (98%)	0.38	1 (1%) 70 66	44, 55, 62, 65	0
31	19	37/37 (100%)	-0.25	0 100 100	30, 38, 54, 61	0
31	29	37/37 (100%)	1.01	2 (5%) 31 25	60, 68, 77, 83	0
32	1a	1488/1521 (97%)	0.26	62 (4%) 40 32	34, 64, 92, 105	0
32	2a	1491/1521 (98%)	0.62	96 (6%) 25 19	49, 75, 95, 106	0
33	1b	231/256 (90%)	1.22	40 (17%) 4 3	62, 77, 87, 92	0
33	2b	231/256 (90%)	1.34	40 (17%) 4 3	73, 83, 89, 92	0
34	1c	206/239 (86%)	0.75	13 (6%) 26 19	56, 68, 79, 86	0
34	2c	206/239 (86%)	1.27	35 (16%) 4 3	73, 82, 88, 92	0
35	1d	208/209 (99%)	0.74	14 (6%) 24 18	52, 67, 76, 82	0
35	2d	208/209 (99%)	0.84	11 (5%) 32 25	59, 71, 79, 82	0
36	1e	148/162 (91%)	0.34	1 (0%) 84 82	48, 62, 72, 80	0
36	2e	148/162 (91%)	1.04	10 (6%) 23 17	65, 75, 81, 86	0
37	1f	100/101 (99%)	0.46	2 (2%) 65 59	52, 65, 72, 77	0
37	2f	100/101 (99%)	0.52	3 (3%) 52 45	49, 67, 75, 82	0
38	1g	155/156 (99%)	0.73	9 (5%) 29 22	59, 70, 84, 88	0
38	2g	155/156 (99%)	1.17	22 (14%) 6 5	68, 78, 87, 92	0
39	1h	137/138 (99%)	0.50	3 (2%) 62 56	52, 65, 72, 76	0
39	2h	137/138 (99%)	0.85	5 (3%) 46 38	65, 74, 80, 83	0
40	1i	127/128 (99%)	1.20	21 (16%) 4 3	50, 74, 83, 87	0
40	2i	127/128 (99%)	1.78	45 (35%) 1 0	71, 83, 88, 92	0
41	1j	97/105 (92%)	1.16	13 (13%) 7 6	53, 76, 84, 91	0
41	2j	96/105 (91%)	1.82	37 (38%) 1 0	74, 84, 90, 92	0
42	1k	114/129 (88%)	0.61	5 (4%) 39 31	41, 66, 76, 80	0
42	2k	114/129 (88%)	0.88	9 (7%) 18 14	52, 72, 79, 82	0
43	1l	121/132 (91%)	0.26	3 (2%) 58 52	41, 50, 63, 71	0
43	2l	121/132 (91%)	0.63	3 (2%) 58 52	50, 66, 75, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	123/126 (97%)	0.83	10 (8%) 18 13	53, 67, 76, 88	0
44	2m	122/126 (96%)	1.52	24 (19%) 3 2	67, 80, 85, 88	0
45	1n	60/61 (98%)	0.96	5 (8%) 17 12	54, 64, 71, 76	0
45	2n	60/61 (98%)	2.21	28 (46%) 0 0	73, 82, 87, 90	0
46	1o	88/89 (98%)	0.60	4 (4%) 38 31	47, 63, 72, 79	0
46	2o	88/89 (98%)	0.69	5 (5%) 29 23	59, 70, 80, 85	0
47	1p	82/88 (93%)	1.27	10 (12%) 8 7	58, 69, 77, 86	0
47	2p	82/88 (93%)	0.98	7 (8%) 16 12	59, 69, 77, 81	0
48	1q	99/105 (94%)	0.64	1 (1%) 79 76	48, 66, 75, 76	0
48	2q	99/105 (94%)	0.68	5 (5%) 33 26	62, 72, 80, 81	0
49	1r	68/88 (77%)	0.47	1 (1%) 72 67	53, 64, 76, 77	0
49	2r	68/88 (77%)	0.66	2 (2%) 53 46	59, 69, 78, 83	0
50	1s	83/93 (89%)	0.78	4 (4%) 35 28	59, 69, 79, 84	0
50	2s	83/93 (89%)	1.56	18 (21%) 2 1	78, 83, 89, 95	0
51	1t	96/106 (90%)	0.97	9 (9%) 14 11	61, 68, 78, 82	0
51	2t	96/106 (90%)	0.84	8 (8%) 17 12	60, 70, 81, 87	0
52	1u	23/27 (85%)	0.88	2 (8%) 16 12	59, 64, 70, 74	0
52	2u	23/27 (85%)	1.74	9 (39%) 1 0	74, 78, 83, 89	0
53	1v	13/24 (54%)	0.92	4 (30%) 1 0	47, 51, 92, 98	0
53	2v	13/24 (54%)	1.30	4 (30%) 1 0	63, 73, 96, 102	0
54	1w	66/76 (86%)	1.32	19 (28%) 1 1	29, 86, 98, 103	0
54	2w	64/76 (84%)	1.53	16 (25%) 2 1	48, 91, 100, 102	0
55	1x	72/77 (93%)	0.12	2 (2%) 55 48	25, 58, 78, 91	0
55	2x	72/77 (93%)	0.53	1 (1%) 73 69	42, 73, 87, 97	0
56	1y	67/76 (88%)	2.02	29 (43%) 0 0	58, 99, 103, 105	0
56	2y	66/76 (86%)	2.00	28 (42%) 0 0	69, 101, 103, 105	0
All	All	20871/21748 (95%)	0.37	1343 (6%) 25 19	19, 63, 89, 108	0

All (1343) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	123	ALA	10.0
1	2A	652(U)	G	8.7

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Mol	Chain	Res	Type	RSRZ
1	2A	653	A	8.2
1	2A	652(V)	C	8.1
1	1A	653	A	7.7
44	2m	124	PRO	7.5
1	1A	654	A	7.3
1	2A	654	A	7.2
1	2A	652(C)	G	7.2
45	2n	2	ALA	7.2
44	2m	122	LYS	7.0
1	1A	652(V)	C	6.9
45	1n	2	ALA	6.8
44	1m	124	PRO	6.6
1	2A	652(T)	C	6.0
1	1A	1094	U	5.9
1	1A	652(C)	G	5.8
1	1A	1057	A	5.7
41	2j	65	LEU	5.6
44	2m	102	ARG	5.6
40	2i	102	LEU	5.6
54	2w	71	G	5.5
40	2i	11	LYS	5.4
1	1A	2114	A	5.4
1	1A	2174	C	5.4
1	2A	2802	G	5.3
1	2A	2112	G	5.3
21	1Z	146	ILE	5.3
1	1A	2115	G	5.2
21	1Z	141	VAL	5.2
32	1a	1025	U	5.1
1	1A	2112	G	5.1
1	1A	1087	G	5.0
38	2g	154	TYR	5.0
15	1T	130	ALA	4.9
1	1A	2119	A	4.9
51	1t	103	GLY	4.9
50	2s	2	PRO	4.9
1	2A	2111	C	4.9
7	1H	2	SER	4.9
32	2a	1149	C	4.9
1	1A	1058	G	4.8
44	1m	123	ALA	4.8
1	1A	1078	U	4.8

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Mol	Chain	Res	Type	RSRZ
1	1A	2130	U	4.8
1	2A	2803	C	4.8
1	1A	2173	A	4.7
1	2A	652(B)	A	4.7
1	1A	2159	G	4.7
1	1A	884	C	4.7
54	2w	72	C	4.7
32	1a	1035	A	4.7
1	2A	884	C	4.6
38	2g	80	VAL	4.6
1	1A	652(U)	G	4.6
1	2A	2147	G	4.6
40	2i	14	VAL	4.5
38	2g	85	TYR	4.5
33	1b	7	VAL	4.5
33	2b	21	ARG	4.5
56	1y	15	G	4.5
45	2n	7	ILE	4.5
38	2g	83	ALA	4.5
1	2A	883	G	4.5
32	2a	1033	G	4.5
23	1l	2	SER	4.4
40	2i	126	SER	4.4
53	1v	13	A	4.4
32	2a	1032	G	4.4
1	2A	2896	C	4.4
32	1a	1027	C	4.4
1	1A	2110	G	4.4
25	23	2	PRO	4.3
1	2A	2149	G	4.3
1	1A	2129	C	4.3
1	1A	1096	A	4.3
1	2A	2119	A	4.3
51	2t	103	GLY	4.3
45	2n	3	ARG	4.3
38	2g	82	GLY	4.3
1	1A	1086	A	4.3
33	1b	237	ALA	4.3
1	2A	2143	C	4.3
1	2A	2145	C	4.3
1	2A	2893	G	4.3
40	2i	9	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
33	2b	237	ALA	4.2
1	1A	2109	U	4.2
1	1A	652(S)	C	4.2
1	1A	2108	C	4.2
1	2A	2126	A	4.2
1	1A	2133	G	4.2
23	2l	2	SER	4.2
32	1a	630	G	4.2
32	1a	1030(A)	G	4.2
32	1a	1532	U	4.2
41	2j	32	ALA	4.1
40	2i	10	ARG	4.1
32	1a	1447	A	4.1
1	2A	2125	G	4.1
15	1T	131	ALA	4.1
1	1A	1081	U	4.1
1	1A	2143	C	4.1
21	2Z	146	ILE	4.1
1	1A	2125	G	4.1
45	2n	38	GLY	4.1
1	2A	2804	C	4.1
1	2A	2115	G	4.0
1	2A	2146	C	4.0
21	2Z	153	SER	4.0
32	2a	1030	C	4.0
1	2A	2133	G	4.0
32	1a	1034	G	4.0
1	1A	1060	U	4.0
1	1A	2170	A	4.0
1	1A	2111	C	4.0
1	1A	2136	C	4.0
1	1A	2145	C	4.0
1	1A	2113	U	4.0
1	1A	2166	G	4.0
32	1a	1024	G	4.0
32	1a	1531	A	4.0
21	2Z	164	ALA	4.0
21	2Z	173	ALA	4.0
1	1A	2803	C	4.0
21	2Z	174	VAL	4.0
21	2Z	170	THR	3.9
32	1a	1036	G	3.9

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Mol	Chain	Res	Type	RSRZ
47	1p	82	GLN	3.9
26	14	57	GLU	3.9
47	1p	81	ARG	3.9
1	1A	2117	A	3.9
1	2A	885	C	3.9
38	1g	80	VAL	3.9
24	12	70	GLN	3.9
1	1A	1068	G	3.9
1	1A	1089	G	3.9
21	2Z	150	LEU	3.9
56	2y	19	G	3.9
40	2i	62	TYR	3.9
54	2w	73	A	3.9
1	1A	1064	C	3.9
33	1b	188	ALA	3.9
23	21	28	GLY	3.9
21	2Z	139	VAL	3.9
1	1A	1098	A	3.9
35	1d	179	GLU	3.9
38	2g	84	ASN	3.8
26	14	58	ARG	3.8
45	2n	13	THR	3.8
1	2A	2127	G	3.8
1	2A	2117	A	3.8
45	2n	6	LEU	3.8
1	1A	888	C	3.8
41	2j	47	PHE	3.8
27	25	29	THR	3.8
34	1c	2	GLY	3.8
56	1y	36	A	3.8
26	14	59	PHE	3.8
1	1A	1082	U	3.8
1	2A	1509	C	3.8
1	2A	2113	U	3.8
32	2a	1030(B)	C	3.8
50	2s	13	ASP	3.8
45	2n	34	TYR	3.8
12	2Q	15	GLY	3.8
33	2b	165	VAL	3.8
1	1A	1059	G	3.8
1	1A	2165	G	3.8
1	2A	896	A	3.8

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Mol	Chain	Res	Type	RSRZ
1	2A	2154	G	3.8
32	2a	1117	G	3.8
54	1w	70	G	3.8
54	2w	70	G	3.8
38	2g	156	TRP	3.8
1	1A	2167	U	3.8
21	2Z	166	SER	3.8
45	2n	10	ALA	3.8
1	1A	2135	A	3.7
1	2A	2169	A	3.7
1	1A	2160	G	3.7
1	2A	2167	U	3.7
1	1A	1095	A	3.7
1	2A	2170	A	3.7
42	2k	89	ALA	3.7
1	1A	2128	C	3.7
56	2y	33	U	3.7
22	20	68	GLU	3.7
1	1A	2121	G	3.7
1	1A	2181	G	3.7
32	1a	1003	G	3.7
20	2Y	90	LEU	3.7
1	1A	2175	C	3.7
1	2A	2114	A	3.6
1	2A	2144	U	3.6
1	1A	2116	G	3.6
1	2A	2128	C	3.6
52	2u	16	GLY	3.6
26	24	50	VAL	3.6
1	1A	1073	A	3.6
53	2v	13	A	3.6
1	1A	883	G	3.6
1	1A	2104	G	3.6
32	1a	1030(B)	C	3.6
32	2a	1031	G	3.6
54	1w	71	G	3.6
21	2Z	126	VAL	3.6
33	1b	9	GLU	3.6
26	24	51	ASP	3.6
1	2A	2134	A	3.6
7	2H	2	SER	3.6
33	1b	229	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	2A	2138	C	3.6
1	2A	2116	G	3.6
1	1A	2172	U	3.6
12	2Q	10	ARG	3.5
1	2A	1536	C	3.5
1	1A	879	G	3.5
1	2A	2793	G	3.5
32	2a	1002	G	3.5
32	2a	1030(A)	G	3.5
56	2y	57	G	3.5
40	2i	67	GLY	3.5
51	1t	69	GLY	3.5
33	2b	17	PHE	3.5
42	2k	25	TYR	3.5
1	2A	2109	U	3.5
33	2b	185	ILE	3.5
4	2E	204	ALA	3.5
21	2Z	159	PRO	3.5
26	14	63	TYR	3.5
32	2a	1001(A)	G	3.5
45	2n	25	VAL	3.5
38	1g	85	TYR	3.5
56	1y	19	G	3.5
56	1y	20	U	3.5
1	1A	655	A	3.5
21	1Z	170	THR	3.5
32	2a	1005	A	3.5
56	1y	35	A	3.5
1	1A	885	C	3.5
1	2A	2107	C	3.5
1	1A	2131	G	3.5
1	2A	887	A	3.5
44	2m	58	GLU	3.5
21	2Z	157	LEU	3.5
39	1h	112	LEU	3.5
1	2A	2174	C	3.4
32	2a	1223	C	3.4
1	1A	1056	G	3.4
1	2A	2110	G	3.4
19	2X	91	ALA	3.4
21	2Z	172	ALA	3.4
34	2c	2	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
33	1b	10	LEU	3.4
1	1A	1103	A	3.4
54	1w	7	A	3.4
21	2Z	171	ILE	3.4
21	1Z	166	SER	3.4
44	2m	121	LYS	3.4
1	1A	897	C	3.4
1	1A	2896	C	3.4
33	1b	230	VAL	3.4
1	2A	2100	G	3.4
1	1A	1088	A	3.4
3	2D	276	LYS	3.4
26	24	32	TYR	3.4
33	2b	236	TYR	3.4
42	2k	117	ASN	3.4
1	2A	888	C	3.4
32	2a	1116	C	3.4
38	2g	77	SER	3.4
1	1A	1063	G	3.4
32	1a	1001(A)	G	3.4
32	1a	1026	G	3.4
54	1w	1	G	3.4
56	2y	18	G	3.4
40	1i	102	LEU	3.4
38	2g	86	GLN	3.4
40	2i	13	ALA	3.4
44	2m	6	GLY	3.4
33	1b	17	PHE	3.4
33	2b	22	LYS	3.3
1	1A	652(T)	C	3.3
1	1A	2107	C	3.3
1	1A	2142	C	3.3
1	2A	2164	C	3.3
32	2a	470	C	3.3
38	2g	16	LEU	3.3
41	2j	40	LEU	3.3
50	2s	22	LEU	3.3
8	2I	146	ALA	3.3
1	1A	1071	G	3.3
1	1A	1176	G	3.3
20	2Y	1	MET	3.3
1	2A	2897	U	3.3

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Mol	Chain	Res	Type	RSRZ
21	2Z	149	SER	3.3
26	14	55	ARG	3.3
32	1a	1019	C	3.3
45	2n	39	LEU	3.3
5	1F	207	GLY	3.3
44	1m	2	ALA	3.3
1	1A	652(E)	G	3.3
1	1A	1093	G	3.3
1	1A	2123	G	3.3
1	1A	2141	G	3.3
1	1A	2162	G	3.3
32	1a	1021	G	3.3
54	1w	15	G	3.3
36	2e	27	ARG	3.3
43	2l	64	TYR	3.3
50	2s	76	PRO	3.3
1	1A	2122	U	3.3
32	1a	1030	C	3.3
47	2p	2	VAL	3.3
1	1A	2171	A	3.3
38	2g	5	ARG	3.3
1	1A	2120	G	3.3
1	2A	2148	G	3.3
1	2A	2168	G	3.3
8	2I	68	LEU	3.3
32	2a	1003	G	3.3
32	2a	1034	G	3.3
6	1G	146	TYR	3.3
32	1a	204	U	3.3
40	1i	59	PHE	3.3
1	1A	652(D)	C	3.2
41	2j	66	ARG	3.2
1	1A	2158	A	3.2
19	1X	95	LEU	3.2
33	2b	121	LEU	3.2
34	2c	188	LEU	3.2
46	1o	19	PRO	3.2
47	2p	82	GLN	3.2
1	2A	2166	G	3.2
11	2P	15	ARG	3.2
52	2u	24	ARG	3.2
1	2A	2137	C	3.2

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Mol	Chain	Res	Type	RSRZ
21	1Z	1	MET	3.2
33	2b	187	LEU	3.2
54	2w	2	C	3.2
40	1i	103	THR	3.2
1	1A	1070	A	3.2
1	1A	2169	A	3.2
6	2G	52	ILE	3.2
7	2H	52	VAL	3.2
26	14	56	VAL	3.2
38	1g	84	ASN	3.2
1	2A	11	G	3.2
35	1d	191	ARG	3.2
12	2Q	1	MET	3.2
21	2Z	168	GLU	3.2
41	2j	71	LEU	3.2
50	2s	15	LEU	3.2
1	1A	1509	C	3.2
1	2A	652(D)	C	3.2
1	2A	886	C	3.2
56	1y	13	C	3.2
33	2b	70	PHE	3.2
32	2a	1030(D)	A	3.2
20	2Y	54	LYS	3.2
1	1A	2792	G	3.2
1	2A	882	G	3.2
1	2A	2131	G	3.2
1	2A	2151	G	3.2
56	1y	57	G	3.2
12	2Q	104	PHE	3.2
1	1A	1072	C	3.1
32	1a	1008	C	3.1
41	2j	76	ASN	3.1
25	13	60	GLU	3.1
41	2j	62	HIS	3.1
44	2m	100	GLY	3.1
32	2a	1219	U	3.1
1	1A	2124	G	3.1
44	1m	121	LYS	3.1
21	2Z	144	LEU	3.1
32	2a	1038	C	3.1
33	2b	11	LEU	3.1
33	1b	186	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
29	27	48	LYS	3.1
54	1w	20	U	3.1
32	1a	1032	G	3.1
56	1y	75	C	3.1
41	2j	27	ALA	3.1
1	2A	2171	A	3.1
32	1a	1030(D)	A	3.1
46	2o	88	ARG	3.1
45	2n	53	LEU	3.1
1	2A	2159	G	3.1
7	1H	174	GLY	3.1
32	1a	1030(C)	G	3.1
33	1b	227	GLY	3.1
40	1i	8	GLY	3.1
21	1Z	120	ILE	3.1
41	1j	32	ALA	3.1
26	24	61	ARG	3.1
52	1u	24	ARG	3.1
32	2a	1357	A	3.0
32	2a	1447	A	3.0
56	1y	21	A	3.0
26	14	32	TYR	3.0
40	2i	19	LEU	3.0
33	1b	131	PRO	3.0
26	24	55	ARG	3.0
1	1A	2151	G	3.0
32	2a	1024	G	3.0
32	2a	1224	G	3.0
41	2j	61	GLU	3.0
1	1A	1054	A	3.0
1	1A	2790	A	3.0
41	1j	4	ILE	3.0
33	1b	97	TRP	3.0
50	1s	71	LEU	3.0
21	2Z	121	HIS	3.0
50	2s	80	TYR	3.0
1	1A	882	G	3.0
1	2A	2165	G	3.0
3	1D	276	LYS	3.0
32	2a	1030(C)	G	3.0
1	1A	548	A	3.0
1	2A	2158	A	3.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1001	A	3.0
56	2y	7	A	3.0
1	1A	1066	U	3.0
1	1A	2189	U	3.0
32	2a	1257	U	3.0
6	2G	28	VAL	3.0
26	24	49	PHE	3.0
26	24	56	VAL	3.0
34	2c	195	VAL	3.0
41	2j	44	VAL	3.0
7	2H	128	PRO	3.0
34	2c	73	PRO	3.0
45	2n	14	PRO	3.0
14	2S	3	ARG	3.0
1	1A	880	G	3.0
1	2A	2155	G	3.0
32	1a	1023	G	3.0
32	1a	1033	G	3.0
32	2a	485	G	3.0
1	2A	2136	C	3.0
32	2a	1249	C	3.0
1	1A	2134	A	3.0
1	2A	1509(A)	A	3.0
47	1p	80	PHE	3.0
33	1b	129	GLU	2.9
21	2Z	167	PRO	2.9
41	2j	91	PRO	2.9
6	2G	146	TYR	2.9
37	1f	46	ARG	2.9
46	1o	88	ARG	2.9
21	2Z	147	GLY	2.9
38	2g	81	GLY	2.9
50	2s	84	GLY	2.9
38	1g	83	ALA	2.9
40	1i	106	ALA	2.9
1	1A	881	G	2.9
1	1A	1080	C	2.9
1	1A	2138	C	2.9
1	1A	2157	G	2.9
1	1A	2177	C	2.9
1	1A	2178	C	2.9
32	1a	1007	C	2.9

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Mol	Chain	Res	Type	RSRZ
32	1a	1029	C	2.9
1	2A	2801(A)	A	2.9
32	1a	1005	A	2.9
56	2y	5	G	2.9
21	2Z	141	VAL	2.9
44	2m	98	VAL	2.9
49	2r	66	LEU	2.9
51	1t	10	LEU	2.9
44	1m	122	LYS	2.9
1	2A	878	A	2.9
53	1v	12	A	2.9
56	1y	49	C	2.9
1	1A	2182	G	2.9
54	2w	15	G	2.9
55	2x	47	U	2.9
56	1y	59	U	2.9
51	1t	55	ILE	2.9
40	2i	103	THR	2.9
5	2F	21	ALA	2.9
26	24	59	PHE	2.9
41	2j	63	PHE	2.9
7	2H	6	ARG	2.9
24	12	69	ARG	2.9
50	2s	29	ARG	2.9
7	2H	136	ILE	2.9
1	1A	652(A)	A	2.9
1	1A	2140	C	2.9
1	1A	2897	U	2.9
1	2A	894	C	2.9
32	1a	1257	U	2.9
32	2a	1150	U	2.9
32	2a	1248	A	2.9
40	2i	36	TYR	2.9
54	2w	14	A	2.9
56	2y	56	C	2.9
1	1A	2156	G	2.9
20	2Y	94	LYS	2.9
32	1a	1031	G	2.9
32	2a	1131	G	2.9
33	1b	11	LEU	2.9
54	2w	5	G	2.9
56	2y	34	G	2.9

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Mol	Chain	Res	Type	RSRZ
8	2I	82	ARG	2.8
38	2g	32	ARG	2.8
31	29	37	GLY	2.8
35	2d	2	GLY	2.8
33	1b	187	LEU	2.8
40	1i	19	LEU	2.8
1	1A	896	A	2.8
53	2v	12	A	2.8
53	2v	15	A	2.8
56	1y	12	U	2.8
1	1A	34	C	2.8
1	1A	2105	C	2.8
54	1w	67	C	2.8
54	2w	4	C	2.8
41	2j	41	PRO	2.8
1	1A	2190	G	2.8
1	2A	1171	G	2.8
44	2m	4	ILE	2.8
35	2d	154	ASN	2.8
40	2i	118	LYS	2.8
33	1b	228	GLY	2.8
46	2o	89	GLY	2.8
50	1s	13	ASP	2.8
3	1D	2	ALA	2.8
50	2s	24	ALA	2.8
33	2b	71	VAL	2.8
45	1n	3	ARG	2.8
55	1x	47	U	2.8
1	1A	889	C	2.8
3	2D	38	LYS	2.8
34	2c	4	LYS	2.8
34	2c	77	ILE	2.8
41	2j	59	SER	2.8
1	1A	2207	G	2.8
1	2A	2157	G	2.8
1	2A	2751	G	2.8
33	1b	18	GLY	2.8
7	2H	19	VAL	2.8
33	2b	164	VAL	2.8
37	2f	59	TYR	2.8
38	1g	5	ARG	2.8
1	1A	1097	U	2.8

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Mol	Chain	Res	Type	RSRZ
32	1a	344	A	2.8
32	2a	1035	A	2.8
1	1A	2137	C	2.8
22	20	84	LEU	2.8
20	2Y	85	VAL	2.8
21	1Z	105	VAL	2.8
21	1Z	136	PHE	2.8
22	20	69	PHE	2.8
1	1A	652(F)	G	2.8
1	1A	2802	G	2.8
1	2A	2123	G	2.8
1	2A	2319	G	2.8
32	2a	1124	G	2.8
41	2j	77	PRO	2.7
51	2t	98	PRO	2.7
45	2n	4	LYS	2.7
34	1c	14	ILE	2.7
34	2c	5	ILE	2.7
34	2c	182	ILE	2.7
41	1j	74	ILE	2.7
46	2o	3	ILE	2.7
1	2A	2150	U	2.7
54	1w	47	U	2.7
50	2s	71	LEU	2.7
1	1A	887	A	2.7
32	2a	1092	A	2.7
32	2a	1183	A	2.7
1	1A	2804	C	2.7
32	1a	1028	C	2.7
45	2n	5	ALA	2.7
50	2s	45	VAL	2.7
56	1y	56	C	2.7
46	1o	69	TYR	2.7
8	1I	87	LYS	2.7
23	2I	81	LYS	2.7
1	1A	2793	G	2.7
1	2A	2153	G	2.7
1	2A	2792	G	2.7
1	2A	2805	G	2.7
32	2a	630	G	2.7
56	1y	18	G	2.7
7	2H	7	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
17	2V	94	LEU	2.7
33	2b	10	LEU	2.7
33	2b	44	LEU	2.7
37	2f	21	LEU	2.7
18	1W	112	GLY	2.7
45	2n	51	GLY	2.7
1	1A	2150	U	2.7
6	1G	48	GLU	2.7
8	1I	146	ALA	2.7
38	2g	76	ARG	2.7
40	2i	66	ARG	2.7
50	2s	12	ASP	2.7
1	1A	1069	A	2.7
6	2G	142	PRO	2.7
33	1b	125	PRO	2.7
1	1A	1079	C	2.7
1	1A	2163	C	2.7
1	2A	2142	C	2.7
32	1a	92	C	2.7
32	2a	1114	C	2.7
21	2Z	125	LEU	2.7
39	1h	2	LEU	2.7
1	2A	652(E)	G	2.7
1	2A	2160	G	2.7
1	2A	2318	G	2.7
11	1P	118	GLY	2.7
32	2a	1021	G	2.7
33	2b	38	GLY	2.7
41	1j	36	GLY	2.7
54	1w	69	G	2.7
36	2e	18	ARG	2.7
40	1i	2	GLU	2.7
40	1i	14	VAL	2.7
45	2n	33	VAL	2.7
46	2o	60	VAL	2.7
1	1A	1065	U	2.7
1	2A	2132	U	2.7
33	1b	232	PRO	2.7
40	2i	21	PRO	2.7
42	1k	25	TYR	2.7
42	2k	75	TYR	2.7
1	1A	1084	A	2.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2173	A	2.7
56	2y	38	A	2.7
40	2i	63	ILE	2.7
32	2a	1019	C	2.7
32	2a	1027	C	2.7
56	1y	48	C	2.7
41	2j	88	LEU	2.7
34	2c	51	GLY	2.7
51	1t	102	GLY	2.7
21	2Z	21	ALA	2.7
35	2d	112	VAL	2.7
11	2P	78	PRO	2.7
32	2a	1182	G	2.6
33	2b	33	TYR	2.6
34	2c	201	TYR	2.6
21	1Z	157	LEU	2.6
32	1a	1286	A	2.6
34	2c	87	LEU	2.6
53	2v	14	A	2.6
41	2j	46	ARG	2.6
40	2i	2	GLU	2.6
46	2o	86	GLY	2.6
1	1A	1075	C	2.6
3	1D	275	LYS	2.6
7	1H	175	LYS	2.6
29	17	48	LYS	2.6
44	2m	120	LYS	2.6
33	1b	120	ALA	2.6
36	2e	90	VAL	2.6
52	2u	14	TRP	2.6
35	2d	20	TYR	2.6
24	22	1	MET	2.6
1	1A	2118	U	2.6
1	1A	2132	U	2.6
6	2G	3	LEU	2.6
40	2i	96	LEU	2.6
21	2Z	162	GLU	2.6
42	1k	92	GLU	2.6
42	2k	49	GLY	2.6
51	2t	101	GLY	2.6
52	2u	4	GLY	2.6
21	1Z	149	SER	2.6

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Mol	Chain	Res	Type	RSRZ
21	2Z	95	PRO	2.6
21	2Z	104	PHE	2.6
40	2i	49	PRO	2.6
41	2j	37	PRO	2.6
1	1A	886	C	2.6
32	1a	999	C	2.6
54	1w	3	C	2.6
54	1w	72	C	2.6
56	2y	13	C	2.6
8	2I	123	LEU	2.6
1	2A	2130	U	2.6
32	1a	1000	U	2.6
33	2b	66	GLY	2.6
39	2h	90	GLY	2.6
1	2A	1533	G	2.6
56	2y	1	G	2.6
7	2H	45	VAL	2.6
7	2H	156	ALA	2.6
16	2U	44	ASN	2.6
34	1c	207	VAL	2.6
49	1r	86	VAL	2.6
33	1b	124	SER	2.6
1	1A	1067	A	2.6
1	1A	1077	A	2.6
32	1a	143	A	2.6
32	1a	1001	A	2.6
36	1e	10	MET	2.6
33	2b	39	ILE	2.6
38	2g	42	ILE	2.6
41	2j	75	ILE	2.6
1	1A	2185	C	2.6
8	2I	75	LEU	2.6
21	2Z	155	LEU	2.6
49	2r	76	LEU	2.6
54	2w	3	C	2.6
56	2y	4	C	2.6
41	2j	28	ARG	2.6
6	1G	182	LYS	2.6
47	2p	16	HIS	2.6
19	1X	94	GLY	2.6
41	2j	10	GLY	2.6
41	2j	36	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	2A	2895	U	2.6
7	2H	39	PRO	2.6
33	2b	13	ALA	2.6
38	2g	2	ALA	2.6
40	2i	61	ALA	2.6
50	1s	9	VAL	2.6
21	2Z	136	PHE	2.6
50	2s	4	SER	2.5
1	1A	2155	G	2.5
1	2A	2120	G	2.5
21	1Z	148	ASP	2.5
21	2Z	140	ASP	2.5
32	1a	1002	G	2.5
40	2i	99	LEU	2.5
54	1w	73	A	2.5
26	24	63	TYR	2.5
34	2c	48	TYR	2.5
44	1m	87	TYR	2.5
26	24	57	GLU	2.5
1	1A	898	C	2.5
1	1A	2146	C	2.5
1	1A	2161	C	2.5
1	2A	2105	C	2.5
1	2A	2140	C	2.5
1	2A	2183	C	2.5
33	1b	71	VAL	2.5
34	2c	53	ALA	2.5
44	2m	33	ALA	2.5
1	1A	895	U	2.5
38	1g	156	TRP	2.5
40	2i	105	ASP	2.5
47	1p	68	ASP	2.5
40	1i	10	ARG	2.5
54	2w	69	G	2.5
21	2Z	169	GLU	2.5
56	1y	38	A	2.5
33	2b	234	PRO	2.5
47	1p	2	VAL	2.5
40	2i	119	ALA	2.5
47	2p	80	PHE	2.5
1	2A	915	C	2.5
1	2A	2175	C	2.5

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Mol	Chain	Res	Type	RSRZ
20	1Y	1	MET	2.5
32	2a	1226	C	2.5
7	2H	92	ILE	2.5
22	20	49	LYS	2.5
44	2m	78	ILE	2.5
1	2A	1026	U	2.5
32	1a	1020	U	2.5
32	2a	1020	U	2.5
41	2j	8	LEU	2.5
33	1b	236	TYR	2.5
25	13	2	PRO	2.5
1	1A	1055	G	2.5
1	1A	2149	G	2.5
32	1a	346	G	2.5
32	2a	1251	A	2.5
32	2a	1503	A	2.5
32	2a	1531	A	2.5
41	2j	49	VAL	2.5
56	1y	10	G	2.5
56	2y	35	A	2.5
21	2Z	156	LYS	2.5
6	2G	136	ARG	2.5
11	1P	15	ARG	2.5
33	1b	214	ILE	2.5
34	1c	47	LEU	2.5
41	2j	74	ILE	2.5
56	2y	49	C	2.5
1	2A	2172	U	2.5
35	1d	180	GLY	2.5
40	1i	69	GLY	2.5
50	2s	52	TYR	2.5
47	1p	1	MET	2.5
7	2H	43	VAL	2.5
41	1j	34	VAL	2.5
38	2g	40	ALA	2.5
40	1i	13	ALA	2.5
45	2n	9	LYS	2.4
45	2n	58	LYS	2.4
1	1A	229	A	2.4
1	1A	1174	A	2.4
1	2A	2135	A	2.4
38	2g	4	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
33	2b	211	ILE	2.4
34	2c	47	LEU	2.4
1	1A	1062	G	2.4
1	2A	2104	G	2.4
1	2A	2182	G	2.4
32	1a	78	G	2.4
32	2a	1023	G	2.4
26	24	65	ASP	2.4
6	2G	35	GLU	2.4
37	2f	95	GLU	2.4
1	1A	2794	C	2.4
1	2A	2108	C	2.4
32	1a	1006	C	2.4
1	2A	2118	U	2.4
1	2A	2122	U	2.4
32	2a	1532	U	2.4
7	2H	29	PRO	2.4
45	2n	55	GLY	2.4
20	2Y	46	LYS	2.4
40	2i	59	PHE	2.4
40	2i	127	LYS	2.4
6	1G	50	ALA	2.4
42	2k	54	ARG	2.4
44	2m	90	LEU	2.4
1	1A	1508	A	2.4
1	2A	1847	A	2.4
32	2a	1093	A	2.4
54	1w	14	A	2.4
1	1A	2168	G	2.4
1	2A	1170	G	2.4
32	1a	1010	G	2.4
32	1a	1042	G	2.4
32	2a	1220	G	2.4
56	1y	24	G	2.4
56	2y	6	G	2.4
56	2y	52	G	2.4
4	2E	56	PRO	2.4
35	2d	23	GLY	2.4
21	2Z	105	VAL	2.4
32	1a	1137	C	2.4
32	2a	1115	C	2.4
40	2i	5	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
40	2i	109	VAL	2.4
32	1a	173	U	2.4
33	2b	34	ALA	2.4
35	1d	3	ARG	2.4
40	2i	104	ARG	2.4
12	2Q	68	ILE	2.4
40	2i	79	LEU	2.4
41	2j	90	LEU	2.4
52	2u	13	ILE	2.4
34	2c	161	GLU	2.4
41	1j	64	GLU	2.4
1	1A	2801(A)	A	2.4
1	2A	2176	A	2.4
32	2a	983	A	2.4
32	2a	1225	A	2.4
43	1l	14	GLY	2.4
21	2Z	96	VAL	2.4
34	2c	207	VAL	2.4
1	1A	2147	G	2.4
1	1A	2152	G	2.4
1	2A	2206	G	2.4
1	2A	2833	G	2.4
6	1G	136	ARG	2.4
32	1a	66	G	2.4
32	2a	1202	G	2.4
33	2b	188	ALA	2.4
35	1d	110	PHE	2.4
40	2i	20	ARG	2.4
4	2E	195	LEU	2.4
1	1A	1175	U	2.4
21	2Z	53	ILE	2.4
32	1a	182	U	2.4
32	2a	1018	C	2.4
32	2a	1119	C	2.4
47	1p	48	TRP	2.4
52	1u	23	PRO	2.4
19	2X	94	GLY	2.4
21	2Z	160	GLY	2.4
38	1g	81	GLY	2.4
33	2b	7	VAL	2.4
35	2d	115	ARG	2.4
2	2B	120	A	2.4

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Mol	Chain	Res	Type	RSRZ
56	1y	9	A	2.4
35	2d	164	ALA	2.4
19	2X	92	LEU	2.3
26	24	31	ILE	2.3
36	2e	80	ILE	2.3
1	1A	1091	G	2.3
1	1A	2180	U	2.3
1	2A	881	G	2.3
1	2A	2894	G	2.3
32	1a	723	U	2.3
32	2a	1026	G	2.3
32	2a	1127	G	2.3
32	2a	1148	U	2.3
32	2a	1278	U	2.3
32	2a	1281	U	2.3
1	2A	2188	C	2.3
32	1a	1037	C	2.3
56	1y	62	C	2.3
4	2E	115	GLY	2.3
7	2H	51	ARG	2.3
45	1n	57	ARG	2.3
51	2t	8	ARG	2.3
44	2m	7	VAL	2.3
45	1n	56	VAL	2.3
33	2b	88	ALA	2.3
40	2i	106	ALA	2.3
45	2n	20	ALA	2.3
33	1b	200	ILE	2.3
1	2A	528	A	2.3
32	2a	1004	A	2.3
56	2y	36	A	2.3
9	2N	1	MET	2.3
21	2Z	11	GLU	2.3
1	2A	271(K)	U	2.3
1	1A	2101	G	2.3
1	2A	2156	G	2.3
1	2A	2807	G	2.3
54	2w	19	G	2.3
56	1y	63	G	2.3
56	2y	15	G	2.3
1	2A	2794	C	2.3
32	2a	980	C	2.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1007	C	2.3
32	2a	1054	C	2.3
34	2c	41	GLY	2.3
38	2g	79	ARG	2.3
42	1k	91	ARG	2.3
44	1m	93	ARG	2.3
47	2p	76	GLN	2.3
51	2t	25	ARG	2.3
52	2u	2	GLY	2.3
54	2w	67	C	2.3
33	1b	93	VAL	2.3
34	1c	106	VAL	2.3
14	2S	80	LEU	2.3
21	1Z	104	PHE	2.3
36	2e	142	LEU	2.3
1	1A	890	A	2.3
1	1A	1085	A	2.3
1	1A	2176	A	2.3
1	2A	655	A	2.3
32	2a	1287	A	2.3
56	2y	21	A	2.3
21	1Z	159	PRO	2.3
21	2Z	158	PRO	2.3
38	1g	82	GLY	2.3
32	2a	1025	U	2.3
32	2a	1125	U	2.3
6	2G	34	LEU	2.3
35	1d	158	ILE	2.3
45	1n	5	ALA	2.3
1	1A	2893	G	2.3
1	2A	10	G	2.3
1	2A	645	C	2.3
1	2A	2139	C	2.3
1	2A	2163	C	2.3
2	2B	119	G	2.3
32	1a	1009	G	2.3
32	1a	1038	C	2.3
32	2a	1043	C	2.3
32	2a	1222	G	2.3
55	1x	46	G	2.3
56	1y	27	G	2.3
42	1k	51	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
44	1m	105	THR	2.3
47	2p	69	THR	2.3
41	2j	78	ASN	2.3
26	24	58	ARG	2.3
1	1A	1045	A	2.3
1	2A	1445	A	2.3
50	1s	68	GLY	2.3
33	1b	154	LEU	2.3
39	1h	93	VAL	2.3
44	2m	19	LEU	2.3
12	2Q	65	PHE	2.3
34	2c	128	PHE	2.3
40	2i	18	PHE	2.3
56	2y	59	U	2.2
50	2s	14	HIS	2.2
33	1b	48	MET	2.2
41	2j	86	MET	2.2
50	2s	77	THR	2.2
1	1A	2164	C	2.2
1	2A	898	C	2.2
1	1A	2106	G	2.2
1	1A	2154	G	2.2
1	2A	2101	G	2.2
34	2c	190	ARG	2.2
40	1i	104	ARG	2.2
40	2i	83	ARG	2.2
8	2I	137	PRO	2.2
41	1j	77	PRO	2.2
48	2q	2	PRO	2.2
35	2d	167	GLY	2.2
50	2s	34	TRP	2.2
10	2O	10	VAL	2.2
33	2b	136	VAL	2.2
40	2i	65	VAL	2.2
50	2s	9	VAL	2.2
1	1A	1046	A	2.2
32	2a	1130	A	2.2
34	2c	8	ILE	2.2
40	2i	117	HIS	2.2
41	2j	68	HIS	2.2
43	2l	68	ALA	2.2
51	1t	68	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	83	MET	2.2
21	2Z	145	GLU	2.2
32	1a	65	U	2.2
32	2a	1000	U	2.2
56	1y	47	U	2.2
9	2N	45	ASN	2.2
40	1i	20	ARG	2.2
44	2m	106	ASN	2.2
45	2n	54	PRO	2.2
1	2A	897	C	2.2
32	1a	91	C	2.2
56	2y	11	C	2.2
21	2Z	129	SER	2.2
1	2A	1112	G	2.2
32	2a	1036	G	2.2
34	2c	78	GLY	2.2
34	1c	87	LEU	2.2
45	2n	44	LEU	2.2
56	1y	5	G	2.2
8	2I	144	VAL	2.2
33	1b	133	LYS	2.2
33	2b	184	VAL	2.2
42	1k	14	VAL	2.2
45	2n	11	LYS	2.2
26	24	14	ILE	2.2
33	2b	214	ILE	2.2
41	2j	11	PHE	2.2
33	2b	161	ALA	2.2
51	2t	97	ALA	2.2
1	2A	899	A	2.2
32	2a	1180	A	2.2
34	2c	15	THR	2.2
40	2i	27	THR	2.2
41	1j	100	THR	2.2
47	2p	45	THR	2.2
56	1y	58	A	2.2
1	2A	895	U	2.2
32	2a	84	U	2.2
44	2m	23	TYR	2.2
54	2w	45	U	2.2
56	1y	33	U	2.2
33	1b	234	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
7	2H	175	LYS	2.2
8	2I	20	ASP	2.2
34	1c	62	ASP	2.2
34	2c	62	ASP	2.2
35	2d	155	LEU	2.2
36	2e	114	GLY	2.2
21	1Z	52	SER	2.2
39	2h	54	ASP	2.2
40	1i	105	ASP	2.2
41	1j	30	SER	2.2
51	1t	13	LEU	2.2
51	2t	74	LYS	2.2
21	2Z	165	VAL	2.2
34	2c	70	VAL	2.2
35	1d	121	VAL	2.2
40	2i	53	VAL	2.2
1	1A	154(A)	C	2.2
1	2A	2129	C	2.2
32	2a	1039	C	2.2
32	2a	1260	C	2.2
33	2b	122	PHE	2.2
15	2T	130	ALA	2.2
15	2T	131	ALA	2.2
23	2I	54	ALA	2.2
1	1A	545	G	2.2
1	2A	2124	G	2.2
35	1d	192	GLU	2.2
54	1w	6	G	2.2
54	1w	19	G	2.2
54	1w	44	G	2.2
56	2y	63	G	2.2
35	1d	118	ARG	2.2
39	2h	30	ARG	2.2
46	1o	68	ARG	2.2
1	1A	878	A	2.2
20	2Y	92	ASN	2.2
21	2Z	15	PRO	2.2
41	1j	76	ASN	2.2
53	1v	14	A	2.2
53	1v	15	A	2.2
21	2Z	143	GLY	2.2
41	1j	31	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
21	1Z	123	ASP	2.2
40	2i	75	ASP	2.2
40	2i	91	ASP	2.2
4	1E	77	ILE	2.2
7	2H	15	VAL	2.2
17	2V	56	SER	2.2
20	2Y	45	VAL	2.2
33	1b	223	ILE	2.2
35	1d	5	ILE	2.2
36	2e	67	VAL	2.2
38	1g	153	HIS	2.2
41	2j	13	HIS	2.2
41	2j	34	VAL	2.2
41	2j	82	ILE	2.2
42	2k	14	VAL	2.2
44	2m	54	VAL	2.2
7	2H	96	ALA	2.1
7	2H	165	ALA	2.1
33	1b	24	TRP	2.1
33	2b	123	ALA	2.1
35	2d	156	GLU	2.1
1	1A	2791	C	2.1
9	2N	115	ARG	2.1
14	2S	30	ARG	2.1
19	2X	68	ARG	2.1
40	2i	128	ARG	2.1
41	2j	48	THR	2.1
48	2q	75	ARG	2.1
54	2w	61	C	2.1
1	1A	275	G	2.1
1	1A	1099	G	2.1
38	2g	112	PRO	2.1
56	1y	22	G	2.1
56	2y	65	G	2.1
40	2i	4	TYR	2.1
38	2g	38	LEU	2.1
1	1A	1509(A)	A	2.1
1	2A	1508	A	2.1
21	1Z	147	GLY	2.1
32	2a	1286	A	2.1
47	1p	78	GLY	2.1
1	1A	1026	U	2.1

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Mol	Chain	Res	Type	RSRZ
1	2A	9	U	2.1
1	2A	614(A)	U	2.1
6	2G	149	VAL	2.1
34	2c	130	VAL	2.1
36	2e	109	ILE	2.1
41	2j	38	ILE	2.1
56	2y	51	U	2.1
37	1f	60	PHE	2.1
21	2Z	152	ALA	2.1
33	1b	34	ALA	2.1
33	2b	29	ALA	2.1
44	2m	42	ALA	2.1
45	2n	59	ALA	2.1
33	1b	50	GLU	2.1
33	2b	86	GLU	2.1
35	1d	173	TRP	2.1
40	1i	12	GLU	2.1
12	2Q	59	ARG	2.1
33	1b	153	ARG	2.1
33	2b	175	ARG	2.1
34	1c	79	ARG	2.1
40	1i	9	ARG	2.1
42	2k	126	ARG	2.1
44	1m	3	ARG	2.1
1	1A	1092	C	2.1
1	2A	271(J)	C	2.1
1	2A	2177	C	2.1
11	1P	68	GLN	2.1
24	22	70	GLN	2.1
32	2a	1006	C	2.1
54	1w	4	C	2.1
56	1y	25	C	2.1
19	2X	95	LEU	2.1
21	1Z	102	LEU	2.1
26	24	54	GLY	2.1
34	2c	205	GLY	2.1
35	1d	167	GLY	2.1
40	2i	100	GLY	2.1
1	1A	271(I)	G	2.1
1	1A	271(M)	G	2.1
1	2A	879	G	2.1
1	2A	2162	G	2.1

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Mol	Chain	Res	Type	RSRZ
7	2H	35	VAL	2.1
12	2Q	47	ILE	2.1
20	2Y	107	ASP	2.1
32	1a	631	G	2.1
32	2a	1253	G	2.1
33	1b	15	VAL	2.1
40	1i	81	ILE	2.1
44	2m	39	ILE	2.1
45	2n	56	VAL	2.1
54	2w	44	G	2.1
56	1y	34	G	2.1
56	2y	10	G	2.1
20	2Y	89	PHE	2.1
40	1i	126	SER	2.1
1	1A	1105	U	2.1
1	2A	229	A	2.1
1	2A	2892	A	2.1
12	2Q	49	ALA	2.1
21	1Z	168	GLU	2.1
32	2a	5	U	2.1
32	2a	978	A	2.1
32	2a	982	U	2.1
34	1c	50	ALA	2.1
36	2e	21	ALA	2.1
40	2i	45	ALA	2.1
41	1j	66	ARG	2.1
7	2H	106	THR	2.1
40	1i	64	THR	2.1
26	14	69	LYS	2.1
34	1c	107	GLN	2.1
21	1Z	150	LEU	2.1
34	1c	12	LEU	2.1
48	1q	98	LEU	2.1
33	1b	19	HIS	2.1
34	2c	9	GLY	2.1
44	1m	59	TYR	2.1
1	1A	1053	C	2.1
1	1A	1104	C	2.1
9	1N	9	VAL	2.1
21	2Z	161	VAL	2.1
32	2a	1037	C	2.1
32	2a	1189	C	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	127	ILE	2.1
33	2b	93	VAL	2.1
34	2c	14	ILE	2.1
34	2c	116	VAL	2.1
34	2c	198	VAL	2.1
40	1i	86	VAL	2.1
56	2y	48	C	2.1
12	2Q	121	ALA	2.1
21	2Z	2	GLU	2.1
21	2Z	138	GLU	2.1
34	1c	179	ARG	2.1
44	2m	104	ARG	2.1
45	2n	23	ARG	2.1
47	1p	72	ARG	2.1
52	2u	9	ARG	2.1
1	2A	100	G	2.1
1	2A	545	G	2.1
1	2A	2141	G	2.1
1	2A	2152	G	2.1
1	2A	2308	G	2.1
20	2Y	34	LYS	2.1
32	1a	380	G	2.1
32	2a	631	G	2.1
32	2a	1370	G	2.1
32	1a	90	U	2.1
32	1a	1503	A	2.1
33	2b	75	LYS	2.1
34	2c	67	THR	2.1
54	1w	66	U	2.1
56	2y	66	U	2.1
6	2G	53	LEU	2.1
7	2H	64	LEU	2.1
14	2S	32	LEU	2.1
34	2c	6	HIS	2.1
36	2e	39	GLY	2.1
44	2m	119	GLY	2.1
22	20	26	TYR	2.1
33	2b	200	ILE	2.1
38	2g	151	TYR	2.1
48	2q	90	ILE	2.1
9	2N	9	VAL	2.1
52	2u	6	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
35	1d	195	ALA	2.0
1	1A	2188	C	2.0
2	1B	88	C	2.0
14	2S	33	LYS	2.0
30	28	29	LYS	2.0
32	1a	470	C	2.0
32	2a	999	C	2.0
32	2a	1362	C	2.0
54	1w	13	C	2.0
6	2G	29	TRP	2.0
14	2S	5	THR	2.0
34	2c	178	LEU	2.0
35	2d	21	LEU	2.0
39	2h	107	LEU	2.0
51	1t	53	LEU	2.0
51	2t	99	LEU	2.0
56	2y	50	U	2.0
1	1A	529	A	2.0
1	1A	1074	G	2.0
1	1A	2148	G	2.0
1	1A	2206	G	2.0
32	2a	1042	G	2.0
32	2a	1256	A	2.0
6	2G	20	ILE	2.0
17	1V	101	GLY	2.0
21	2Z	124	ILE	2.0
33	1b	38	GLY	2.0
42	2k	48	ILE	2.0
7	2H	133	VAL	2.0
9	2N	140	VAL	2.0
21	1Z	42	VAL	2.0
26	24	18	CYS	2.0
29	27	46	VAL	2.0
31	29	16	VAL	2.0
33	1b	165	VAL	2.0
34	1c	184	TYR	2.0
40	1i	17	VAL	2.0
43	1l	18	VAL	2.0
43	1l	64	TYR	2.0
45	2n	21	TYR	2.0
48	2q	35	VAL	2.0
7	1H	3	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
11	2P	79	ARG	2.0
35	1d	122	ARG	2.0
40	2i	16	ARG	2.0
11	1P	119	GLU	2.0
6	2G	50	ALA	2.0
34	2c	137	ALA	2.0
52	2u	3	LYS	2.0
7	2H	36	PRO	2.0
9	2N	73	THR	2.0
20	2Y	5	MET	2.0
26	24	52	THR	2.0
1	1A	1076	C	2.0
1	2A	2789	C	2.0
32	1a	221	C	2.0
32	2a	1147	C	2.0
34	2c	43	LEU	2.0
39	2h	2	LEU	2.0
41	1j	33	GLN	2.0
47	1p	49	LEU	2.0
45	2n	49	HIS	2.0
32	2a	1062	U	2.0
14	2S	35	ILE	2.0
18	2W	112	GLY	2.0
26	24	15	ILE	2.0
51	1t	100	ILE	2.0
6	2G	15	VAL	2.0
6	2G	118	ARG	2.0
21	1Z	139	VAL	2.0
32	1a	172	A	2.0
32	2a	532	A	2.0
32	2a	977	A	2.0
32	2a	1250	A	2.0
33	2b	144	ARG	2.0
41	2j	72	VAL	2.0
43	2l	18	VAL	2.0
44	2m	99	ARG	2.0
14	2S	92	TYR	2.0
40	2i	125	TYR	2.0
48	2q	95	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
56	4SU	2y	8	20/21	0.43	0.19	95,104,112,126	0
56	G7M	2y	46	24/25	0.46	0.16	86,99,105,120	0
56	MIA	2y	37	22/30	0.52	0.16	83,97,109,123	0
56	PSU	1y	55	20/21	0.52	0.17	96,101,106,114	0
56	5MU	2y	54	21/22	0.54	0.18	91,96,106,126	0
56	G7M	1y	46	24/25	0.55	0.18	91,99,104,117	0
56	5MU	1y	54	21/22	0.59	0.15	89,99,104,118	0
56	PSU	2y	55	20/21	0.59	0.15	89,97,106,108	0
56	PSU	2y	39	20/21	0.61	0.16	90,95,104,111	0
56	MIA	1y	37	22/30	0.61	0.16	86,93,100,113	0
56	4SU	1y	8	20/21	0.63	0.14	93,97,105,116	0
56	PSU	2y	32	20/21	0.64	0.16	86,98,107,115	0
54	G7M	2w	46	24/25	0.66	0.17	84,94,109,123	0
56	PSU	1y	39	20/21	0.70	0.16	83,94,107,109	0
56	PSU	1y	32	20/21	0.70	0.14	88,96,106,112	0
54	G7M	1w	46	24/25	0.71	0.18	78,88,100,121	0
54	PSU	2w	55	20/21	0.82	0.12	77,83,94,96	0
54	4SU	2w	8	20/21	0.85	0.13	90,94,105,108	0
54	4SU	1w	8	20/21	0.85	0.14	71,85,92,94	0
54	5MU	2w	54	21/22	0.87	0.12	74,80,84,89	0
55	PSU	2x	55	20/21	0.88	0.10	69,75,84,86	0
55	5MU	2x	54	21/22	0.89	0.12	72,79,84,96	0
54	PSU	1w	55	20/21	0.89	0.10	61,73,81,81	0
32	2MG	2a	1207	24/25	0.89	0.12	76,83,86,90	0
54	PSU	2w	32	20/21	0.90	0.13	76,84,91,92	0
54	MIA	2w	37	25/30	0.90	0.12	68,76,85,103	0
55	4SU	2x	8	20/21	0.90	0.11	64,75,83,83	0
32	G7M	2a	527	24/25	0.90	0.13	61,67,71,76	0
32	M2G	2a	966	25/26	0.91	0.15	55,65,76,81	0
43	0TD	1l	92	10/11	0.91	0.11	41,49,50,61	0
32	5MC	2a	967	21/22	0.92	0.12	62,66,76,82	0
54	PSU	1w	32	20/21	0.92	0.12	60,65,74,77	0
1	5MU	2A	1915	21/22	0.92	0.10	57,64,73,75	0
32	5MC	2a	1400	21/22	0.93	0.17	63,71,76,80	0
32	4OC	2a	1402	22/23	0.93	0.11	55,60,66,71	0
54	MIA	1w	37	29/30	0.93	0.14	43,53,70,87	0
55	5MC	2x	32	21/22	0.93	0.12	63,69,78,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
55	PSU	1x	55	20/21	0.93	0.10	49,56,67,70	0
32	2MG	1a	1207	24/25	0.93	0.11	61,67,71,71	0
32	PSU	2a	516	20/21	0.93	0.11	61,71,78,79	0
54	PSU	2w	39	20/21	0.94	0.10	62,78,85,85	0
55	4SU	1x	8	20/21	0.94	0.10	52,60,67,77	0
32	5MC	2a	1407	21/22	0.94	0.10	50,57,61,65	0
43	0TD	2l	92	10/11	0.94	0.09	61,65,67,78	0
1	PSU	2A	1917	20/21	0.94	0.09	54,61,69,72	0
1	OMC	2A	1920	21/22	0.94	0.09	53,61,63,65	0
55	5MU	1x	54	21/22	0.95	0.08	55,61,65,70	0
1	PSU	2A	1911	20/21	0.95	0.09	52,62,67,71	0
32	UR3	2a	1498	21/22	0.95	0.11	52,58,61,65	0
55	5MC	1x	32	21/22	0.95	0.11	51,53,59,70	0
32	5MC	2a	1404	21/22	0.95	0.09	53,57,62,66	0
1	5MC	2A	1962	21/22	0.95	0.10	39,51,58,67	0
55	31H	2x	76	32/33	0.96	0.10	36,46,54,63	0
32	PSU	1a	516	20/21	0.96	0.08	51,55,58,59	0
32	5MC	1a	1400	21/22	0.96	0.09	39,47,49,50	0
54	5MU	1w	54	21/22	0.96	0.07	46,62,67,69	0
32	5MC	1a	1404	21/22	0.96	0.08	33,39,42,45	0
32	5MC	1a	1407	21/22	0.96	0.10	30,39,42,43	0
32	G7M	1a	527	24/25	0.96	0.09	36,42,50,50	0
32	M2G	1a	966	25/26	0.96	0.10	46,50,57,61	0
54	F3N	2w	76	33/34	0.96	0.10	38,43,48,51	0
1	5MU	1A	1915	21/22	0.96	0.09	42,51,55,55	0
32	5MC	1a	967	21/22	0.96	0.09	45,51,59,61	0
32	MA6	2a	1518	24/25	0.96	0.10	49,60,69,69	0
32	MA6	2a	1519	24/25	0.96	0.11	55,61,67,71	0
1	5MC	1A	1942	21/22	0.96	0.08	34,39,43,51	0
55	31H	1x	76	32/33	0.96	0.09	22,26,37,41	10
54	F3N	1w	76	33/34	0.97	0.07	22,25,30,32	0
1	PSU	1A	1917	20/21	0.97	0.07	39,45,50,52	0
32	4OC	1a	1402	22/23	0.97	0.08	38,45,48,49	0
1	OMC	1A	1920	21/22	0.97	0.08	35,43,45,52	0
1	PSU	1A	1911	20/21	0.97	0.07	42,46,49,50	0
1	5MU	2A	1939	21/22	0.97	0.08	32,38,42,45	0
32	MA6	1a	1519	24/25	0.97	0.09	35,42,45,47	0
1	5MC	2A	1942	21/22	0.97	0.08	43,53,57,62	0
1	5MC	1A	1962	21/22	0.97	0.06	24,32,37,42	0
54	PSU	1w	39	20/21	0.97	0.08	53,61,67,76	0
1	OMG	2A	2251	24/25	0.97	0.08	35,43,45,51	0
1	8AH	2A	2503	24/25	0.97	0.09	32,38,44,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	2MU	2A	2552	21/23	0.97	0.08	35,41,45,55	0
1	PSU	2A	2605	20/21	0.97	0.07	30,38,42,44	0
1	5MU	1A	1939	21/22	0.98	0.06	21,28,30,32	0
1	8AH	1A	2503	24/25	0.98	0.06	15,21,26,27	0
32	MA6	1a	1518	24/25	0.98	0.08	31,39,45,46	0
1	2MU	1A	2552	21/23	0.98	0.07	23,27,34,36	0
32	UR3	1a	1498	21/22	0.98	0.07	36,41,45,46	0
1	PSU	1A	2605	20/21	0.98	0.07	23,26,31,32	0
1	OMG	1A	2251	24/25	0.98	0.06	22,25,28,30	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1808	1/1	0.33	0.20	91,91,91,91	0
57	MG	1a	1792	1/1	0.42	0.40	74,74,74,74	0
57	MG	2v	102	1/1	0.53	0.42	80,80,80,80	0
57	MG	1A	4078	1/1	0.57	0.25	62,62,62,62	0
57	MG	2A	3557	1/1	0.64	0.20	83,83,83,83	0
57	MG	1A	4042	1/1	0.65	0.26	70,70,70,70	0
57	MG	2A	3762	1/1	0.66	0.14	53,53,53,53	0
57	MG	1A	3909	1/1	0.67	0.24	85,85,85,85	0
57	MG	2A	3547	1/1	0.67	0.20	72,72,72,72	0
57	MG	2l	201	1/1	0.67	0.20	78,78,78,78	0
57	MG	1A	3979	1/1	0.67	0.14	70,70,70,70	0
57	MG	1B	213	1/1	0.68	0.26	73,73,73,73	0
57	MG	1B	228	1/1	0.68	0.27	77,77,77,77	0
57	MG	1A	3178	1/1	0.68	0.18	74,74,74,74	0
57	MG	1a	1673	1/1	0.69	0.26	77,77,77,77	0
57	MG	1w	104	1/1	0.69	0.28	81,81,81,81	0
57	MG	2A	3482	1/1	0.69	0.19	69,69,69,69	0
57	MG	1a	1743	1/1	0.70	0.36	81,81,81,81	0
57	MG	2A	3603	1/1	0.70	0.18	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3690	1/1	0.70	0.19	58,58,58,58	0
57	MG	2A	3074	1/1	0.70	0.19	63,63,63,63	0
57	MG	2a	1781	1/1	0.70	0.23	81,81,81,81	0
57	MG	2A	3215	1/1	0.70	0.32	77,77,77,77	0
57	MG	1A	3841	1/1	0.70	0.18	24,24,24,24	0
57	MG	1a	1796	1/1	0.70	0.31	67,67,67,67	0
57	MG	2a	1643	1/1	0.71	0.25	73,73,73,73	0
57	MG	2a	1700	1/1	0.71	0.33	82,82,82,82	0
57	MG	2a	1770	1/1	0.71	0.21	70,70,70,70	0
57	MG	1a	1801	1/1	0.71	0.19	56,56,56,56	0
57	MG	2A	3645	1/1	0.71	0.23	48,48,48,48	0
57	MG	2a	1628	1/1	0.71	0.32	79,79,79,79	0
57	MG	2a	1632	1/1	0.71	0.37	74,74,74,74	0
57	MG	2A	3483	1/1	0.72	0.35	84,84,84,84	0
57	MG	2A	3573	1/1	0.72	0.30	68,68,68,68	0
57	MG	1A	4064	1/1	0.72	0.18	64,64,64,64	0
57	MG	1V	205	1/1	0.73	0.15	63,63,63,63	0
57	MG	2A	3516	1/1	0.73	0.14	40,40,40,40	0
57	MG	2A	3019	1/1	0.73	0.34	79,79,79,79	0
57	MG	1A	4023	1/1	0.73	0.18	50,50,50,50	0
57	MG	1A	3375	1/1	0.73	0.33	74,74,74,74	0
57	MG	1a	1812	1/1	0.73	0.19	67,67,67,67	0
57	MG	2Q	204	1/1	0.74	0.17	77,77,77,77	0
57	MG	1A	3766	1/1	0.74	0.30	51,51,51,51	0
57	MG	2A	3590	1/1	0.74	0.23	50,50,50,50	0
57	MG	1A	3394	1/1	0.74	0.34	69,69,69,69	0
57	MG	2A	3604	1/1	0.74	0.22	76,76,76,76	0
57	MG	1A	3747	1/1	0.74	0.25	82,82,82,82	0
57	MG	2A	3293	1/1	0.74	0.26	67,67,67,67	0
57	MG	2A	3436	1/1	0.74	0.20	66,66,66,66	0
57	MG	2A	3784	1/1	0.74	0.21	70,70,70,70	0
57	MG	2v	101	1/1	0.74	0.24	78,78,78,78	0
57	MG	2B	211	1/1	0.74	0.34	76,76,76,76	0
57	MG	2y	101	1/1	0.74	0.20	81,81,81,81	0
57	MG	2A	3580	1/1	0.75	0.17	55,55,55,55	0
57	MG	2a	1756	1/1	0.75	0.29	59,59,59,59	0
57	MG	1B	227	1/1	0.75	0.12	81,81,81,81	0
57	MG	2A	3057	1/1	0.75	0.15	65,65,65,65	0
57	MG	2a	1790	1/1	0.75	0.26	75,75,75,75	0
57	MG	11	104	1/1	0.75	0.24	78,78,78,78	0
57	MG	20	102	1/1	0.75	0.31	73,73,73,73	0
57	MG	2A	3606	1/1	0.75	0.19	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3564	1/1	0.75	0.15	75,75,75,75	0
57	MG	1A	3898	1/1	0.75	0.16	35,35,35,35	0
57	MG	1a	1738	1/1	0.76	0.36	76,76,76,76	0
57	MG	2A	3775	1/1	0.76	0.48	73,73,73,73	0
57	MG	2A	3779	1/1	0.76	0.29	82,82,82,82	0
57	MG	1v	101	1/1	0.76	0.35	82,82,82,82	0
57	MG	2a	1698	1/1	0.76	0.35	74,74,74,74	0
57	MG	2A	3662	1/1	0.76	0.29	60,60,60,60	0
57	MG	2a	1730	1/1	0.76	0.18	87,87,87,87	0
57	MG	2A	3419	1/1	0.76	0.32	61,61,61,61	0
57	MG	2y	102	1/1	0.76	0.33	75,75,75,75	0
57	MG	2A	3584	1/1	0.77	0.18	69,69,69,69	0
57	MG	2W	201	1/1	0.77	0.13	67,67,67,67	0
57	MG	1A	3863	1/1	0.77	0.13	44,44,44,44	0
57	MG	2A	3415	1/1	0.77	0.27	71,71,71,71	0
57	MG	2a	1629	1/1	0.77	0.44	73,73,73,73	0
57	MG	1A	3732	1/1	0.77	0.13	70,70,70,70	0
57	MG	1a	1662	1/1	0.77	0.32	71,71,71,71	0
57	MG	2a	1665	1/1	0.77	0.28	64,64,64,64	0
57	MG	2a	1670	1/1	0.77	0.33	74,74,74,74	0
57	MG	1A	3785	1/1	0.77	0.20	55,55,55,55	0
57	MG	2A	3658	1/1	0.77	0.22	67,67,67,67	0
57	MG	1A	3804	1/1	0.77	0.17	69,69,69,69	0
57	MG	2A	3675	1/1	0.77	0.29	69,69,69,69	0
57	MG	2a	1759	1/1	0.77	0.25	81,81,81,81	0
57	MG	1B	217	1/1	0.77	0.17	52,52,52,52	0
57	MG	2a	1777	1/1	0.77	0.17	75,75,75,75	0
57	MG	2A	3711	1/1	0.77	0.14	47,47,47,47	0
57	MG	1A	3491	1/1	0.77	0.23	64,64,64,64	0
57	MG	2A	3213	1/1	0.77	0.33	72,72,72,72	0
57	MG	1A	4039	1/1	0.77	0.14	48,48,48,48	0
57	MG	2A	3274	1/1	0.77	0.15	74,74,74,74	0
57	MG	2A	3289	1/1	0.77	0.17	62,62,62,62	0
57	MG	2B	214	1/1	0.77	0.29	66,66,66,66	0
57	MG	2N	201	1/1	0.77	0.25	85,85,85,85	0
57	MG	2A	3176	1/1	0.78	0.14	63,63,63,63	0
57	MG	1a	1719	1/1	0.78	0.20	82,82,82,82	0
57	MG	2A	3749	1/1	0.78	0.14	58,58,58,58	0
57	MG	2a	1686	1/1	0.78	0.30	72,72,72,72	0
57	MG	1O	204	1/1	0.78	0.18	71,71,71,71	0
57	MG	2A	3227	1/1	0.78	0.28	71,71,71,71	0
57	MG	2A	3248	1/1	0.78	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1732	1/1	0.78	0.35	83,83,83,83	0
57	MG	1A	3970	1/1	0.78	0.17	47,47,47,47	0
57	MG	1A	3600	1/1	0.78	0.18	66,66,66,66	0
57	MG	2A	3023	1/1	0.78	0.22	71,71,71,71	0
57	MG	1A	3810	1/1	0.78	0.20	69,69,69,69	0
57	MG	1A	4029	1/1	0.78	0.16	27,27,27,27	0
57	MG	2a	1783	1/1	0.78	0.34	66,66,66,66	0
57	MG	2V	202	1/1	0.78	0.24	67,67,67,67	0
57	MG	2A	3080	1/1	0.78	0.21	66,66,66,66	0
57	MG	2A	3450	1/1	0.78	0.18	49,49,49,49	0
57	MG	2q	202	1/1	0.78	0.18	82,82,82,82	0
57	MG	2A	3460	1/1	0.78	0.19	51,51,51,51	0
57	MG	2A	3102	1/1	0.78	0.24	66,66,66,66	0
57	MG	2A	3112	1/1	0.78	0.27	75,75,75,75	0
57	MG	2a	1633	1/1	0.78	0.36	73,73,73,73	0
57	MG	1a	1684	1/1	0.79	0.15	68,68,68,68	0
57	MG	1A	3690	1/1	0.79	0.19	62,62,62,62	0
57	MG	2A	3225	1/1	0.79	0.34	75,75,75,75	0
57	MG	2a	1696	1/1	0.79	0.39	74,74,74,74	0
57	MG	2a	1697	1/1	0.79	0.27	81,81,81,81	0
57	MG	1A	4040	1/1	0.79	0.19	67,67,67,67	0
57	MG	2A	3233	1/1	0.79	0.14	69,69,69,69	0
57	MG	2a	1711	1/1	0.79	0.26	83,83,83,83	0
57	MG	2A	3236	1/1	0.79	0.19	63,63,63,63	0
57	MG	2A	3055	1/1	0.79	0.18	57,57,57,57	0
57	MG	2A	3252	1/1	0.79	0.50	62,62,62,62	0
57	MG	2D	306	1/1	0.79	0.39	54,54,54,54	0
57	MG	2F	302	1/1	0.79	0.30	74,74,74,74	0
57	MG	1A	3446	1/1	0.79	0.16	65,65,65,65	0
57	MG	1A	3528	1/1	0.79	0.17	57,57,57,57	0
57	MG	1A	3989	1/1	0.79	0.14	58,58,58,58	0
57	MG	2A	3399	1/1	0.79	0.24	83,83,83,83	0
57	MG	1a	1657	1/1	0.79	0.16	65,65,65,65	0
57	MG	1A	3467	1/1	0.79	0.21	60,60,60,60	0
57	MG	2A	3156	1/1	0.79	0.18	76,76,76,76	0
57	MG	1A	3643	1/1	0.79	0.23	72,72,72,72	0
57	MG	2A	3177	1/1	0.79	0.51	80,80,80,80	0
57	MG	2a	1642	1/1	0.79	0.33	73,73,73,73	0
57	MG	2A	3474	1/1	0.79	0.30	78,78,78,78	0
57	MG	2A	3001	1/1	0.80	0.26	59,59,59,59	0
57	MG	14	101	1/1	0.80	0.20	80,80,80,80	0
57	MG	1A	3488	1/1	0.80	0.36	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3044	1/1	0.80	0.22	58,58,58,58	0
57	MG	1A	3704	1/1	0.80	0.20	61,61,61,61	0
57	MG	2A	3294	1/1	0.80	0.26	69,69,69,69	0
57	MG	2A	3639	1/1	0.80	0.15	72,72,72,72	0
57	MG	2a	1666	1/1	0.80	0.35	68,68,68,68	0
57	MG	2A	3320	1/1	0.80	0.10	69,69,69,69	0
57	MG	2A	3354	1/1	0.80	0.29	65,65,65,65	0
57	MG	1A	3854	1/1	0.80	0.16	58,58,58,58	0
57	MG	1A	3727	1/1	0.80	0.12	26,26,26,26	0
57	MG	1A	3039	1/1	0.80	0.29	63,63,63,63	0
57	MG	2A	3427	1/1	0.80	0.23	74,74,74,74	0
57	MG	2a	1710	1/1	0.80	0.29	79,79,79,79	0
57	MG	1a	1728	1/1	0.80	0.25	67,67,67,67	0
57	MG	2A	3760	1/1	0.80	0.17	73,73,73,73	0
57	MG	2A	3448	1/1	0.80	0.14	47,47,47,47	0
57	MG	1A	3314	1/1	0.80	0.18	54,54,54,54	0
57	MG	1A	3954	1/1	0.80	0.16	31,31,31,31	0
57	MG	2a	1768	1/1	0.80	0.14	69,69,69,69	0
57	MG	1A	3356	1/1	0.80	0.33	34,34,34,34	0
57	MG	1A	3607	1/1	0.80	0.18	68,68,68,68	0
57	MG	1O	201	1/1	0.80	0.13	72,72,72,72	0
57	MG	1a	1802	1/1	0.80	0.15	84,84,84,84	0
57	MG	2E	301	1/1	0.80	0.19	68,68,68,68	0
57	MG	2a	1793	1/1	0.80	0.23	64,64,64,64	0
57	MG	1a	1809	1/1	0.80	0.27	69,69,69,69	0
57	MG	2A	3548	1/1	0.80	0.20	65,65,65,65	0
57	MG	1A	3795	1/1	0.80	0.19	60,60,60,60	0
57	MG	2A	3560	1/1	0.80	0.16	74,74,74,74	0
57	MG	1A	3796	1/1	0.80	0.17	49,49,49,49	0
57	MG	1A	3374	1/1	0.80	0.22	61,61,61,61	0
57	MG	2a	1610	1/1	0.80	0.48	78,78,78,78	0
57	MG	2B	206	1/1	0.81	0.33	73,73,73,73	0
57	MG	2A	3582	1/1	0.81	0.15	70,70,70,70	0
57	MG	1A	3907	1/1	0.81	0.11	70,70,70,70	0
57	MG	2A	3223	1/1	0.81	0.19	63,63,63,63	0
57	MG	2a	1708	1/1	0.81	0.15	62,62,62,62	0
57	MG	1A	3514	1/1	0.81	0.26	48,48,48,48	0
57	MG	1A	3915	1/1	0.81	0.15	62,62,62,62	0
57	MG	2a	1714	1/1	0.81	0.23	74,74,74,74	0
57	MG	2a	1723	1/1	0.81	0.33	80,80,80,80	0
57	MG	2G	201	1/1	0.81	0.14	77,77,77,77	0
57	MG	1A	3620	1/1	0.81	0.14	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1l	103	1/1	0.81	0.10	42,42,42,42	0
57	MG	1A	4060	1/1	0.81	0.15	53,53,53,53	0
57	MG	1A	3962	1/1	0.81	0.15	58,58,58,58	0
57	MG	1A	3526	1/1	0.81	0.39	56,56,56,56	0
57	MG	2A	3281	1/1	0.81	0.26	67,67,67,67	0
57	MG	2a	1626	1/1	0.81	0.40	77,77,77,77	0
57	MG	1A	3395	1/1	0.81	0.23	69,69,69,69	0
57	MG	2a	1788	1/1	0.81	0.42	83,83,83,83	0
57	MG	1a	1670	1/1	0.81	0.32	75,75,75,75	0
57	MG	1A	3533	1/1	0.81	0.12	38,38,38,38	0
57	MG	2a	1798	1/1	0.81	0.26	73,73,73,73	0
57	MG	2A	3754	1/1	0.81	0.24	77,77,77,77	0
57	MG	2A	3559	1/1	0.81	0.17	67,67,67,67	0
57	MG	2A	3171	1/1	0.81	0.32	70,70,70,70	0
57	MG	1A	3432	1/1	0.81	0.16	64,64,64,64	0
57	MG	2A	3776	1/1	0.81	0.25	67,67,67,67	0
57	MG	1x	107	1/1	0.81	0.23	72,72,72,72	0
57	MG	1x	111	1/1	0.81	0.23	70,70,70,70	0
57	MG	2A	3441	1/1	0.82	0.23	59,59,59,59	0
57	MG	2a	1638	1/1	0.82	0.22	82,82,82,82	0
57	MG	2A	3680	1/1	0.82	0.11	63,63,63,63	0
57	MG	1A	3680	1/1	0.82	0.21	56,56,56,56	0
57	MG	2A	3695	1/1	0.82	0.13	70,70,70,70	0
57	MG	1A	3222	1/1	0.82	0.16	63,63,63,63	0
57	MG	1A	3802	1/1	0.82	0.17	50,50,50,50	0
57	MG	2a	1671	1/1	0.82	0.24	65,65,65,65	0
57	MG	1a	1704	1/1	0.82	0.36	72,72,72,72	0
57	MG	2A	3235	1/1	0.82	0.27	68,68,68,68	0
57	MG	2A	3035	1/1	0.82	0.34	69,69,69,69	0
57	MG	2A	3774	1/1	0.82	0.18	68,68,68,68	0
57	MG	1A	3558	1/1	0.82	0.15	55,55,55,55	0
57	MG	1A	3500	1/1	0.82	0.18	59,59,59,59	0
57	MG	2A	3255	1/1	0.82	0.14	65,65,65,65	0
57	MG	1A	3239	1/1	0.82	0.12	64,64,64,64	0
57	MG	2B	202	1/1	0.82	0.11	70,70,70,70	0
57	MG	2A	3277	1/1	0.82	0.12	72,72,72,72	0
57	MG	2B	210	1/1	0.82	0.16	78,78,78,78	0
57	MG	1A	3844	1/1	0.82	0.15	30,30,30,30	0
57	MG	1A	3485	1/1	0.82	0.18	65,65,65,65	0
57	MG	10	108	1/1	0.82	0.23	70,70,70,70	0
57	MG	1A	3855	1/1	0.82	0.15	34,34,34,34	0
57	MG	2A	3305	1/1	0.82	0.26	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2F	308	1/1	0.82	0.16	69,69,69,69	0
57	MG	2A	3309	1/1	0.82	0.19	66,66,66,66	0
57	MG	1A	3057	1/1	0.82	0.15	63,63,63,63	0
57	MG	2A	3353	1/1	0.82	0.17	81,81,81,81	0
57	MG	2A	3158	1/1	0.82	0.14	70,70,70,70	0
57	MG	2a	1792	1/1	0.82	0.28	76,76,76,76	0
57	MG	1A	3783	1/1	0.82	0.14	49,49,49,49	0
57	MG	2A	3615	1/1	0.82	0.37	68,68,68,68	0
57	MG	2I	101	1/1	0.82	0.17	54,54,54,54	0
57	MG	2a	1811	1/1	0.82	0.17	70,70,70,70	0
57	MG	2A	3633	1/1	0.82	0.12	64,64,64,64	0
57	MG	1a	1622	1/1	0.82	0.27	65,65,65,65	0
57	MG	1a	1639	1/1	0.82	0.35	67,67,67,67	0
57	MG	1A	3670	1/1	0.82	0.24	62,62,62,62	0
57	MG	2a	1631	1/1	0.82	0.25	66,66,66,66	0
57	MG	1A	3794	1/1	0.82	0.16	59,59,59,59	0
57	MG	2a	1608	1/1	0.83	0.22	67,67,67,67	0
57	MG	2A	3613	1/1	0.83	0.28	56,56,56,56	0
57	MG	1A	3765	1/1	0.83	0.19	54,54,54,54	0
57	MG	2A	3617	1/1	0.83	0.14	58,58,58,58	0
57	MG	2A	3631	1/1	0.83	0.22	86,86,86,86	0
57	MG	2A	3181	1/1	0.83	0.28	65,65,65,65	0
57	MG	2A	3634	1/1	0.83	0.15	45,45,45,45	0
57	MG	2A	3636	1/1	0.83	0.17	67,67,67,67	0
57	MG	2A	3367	1/1	0.83	0.28	74,74,74,74	0
57	MG	2A	3199	1/1	0.83	0.18	55,55,55,55	0
57	MG	2A	3405	1/1	0.83	0.26	61,61,61,61	0
57	MG	1B	220	1/1	0.83	0.18	57,57,57,57	0
57	MG	1a	1661	1/1	0.83	0.27	65,65,65,65	0
57	MG	2A	3678	1/1	0.83	0.17	68,68,68,68	0
57	MG	1B	221	1/1	0.83	0.24	56,56,56,56	0
57	MG	1A	3536	1/1	0.83	0.21	63,63,63,63	0
57	MG	1A	4028	1/1	0.83	0.11	62,62,62,62	0
57	MG	2A	3230	1/1	0.83	0.12	81,81,81,81	0
57	MG	1A	3372	1/1	0.83	0.33	53,53,53,53	0
57	MG	1A	3822	1/1	0.83	0.18	61,61,61,61	0
57	MG	1R	206	1/1	0.83	0.14	71,71,71,71	0
57	MG	1A	3583	1/1	0.83	0.18	58,58,58,58	0
57	MG	10	102	1/1	0.83	0.23	66,66,66,66	0
57	MG	2A	3509	1/1	0.83	0.17	68,68,68,68	0
57	MG	1A	3949	1/1	0.83	0.12	57,57,57,57	0
57	MG	2A	3777	1/1	0.83	0.20	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3523	1/1	0.83	0.15	59,59,59,59	0
57	MG	2A	3256	1/1	0.83	0.16	73,73,73,73	0
57	MG	10	109	1/1	0.83	0.21	69,69,69,69	0
57	MG	2a	1763	1/1	0.83	0.27	67,67,67,67	0
57	MG	2A	3275	1/1	0.83	0.45	78,78,78,78	0
57	MG	2A	3083	1/1	0.83	0.21	75,75,75,75	0
57	MG	1A	3445	1/1	0.83	0.17	58,58,58,58	0
57	MG	2B	213	1/1	0.83	0.11	65,65,65,65	0
57	MG	2A	3562	1/1	0.83	0.19	68,68,68,68	0
57	MG	1a	1800	1/1	0.83	0.30	76,76,76,76	0
57	MG	1A	3674	1/1	0.83	0.14	58,58,58,58	0
57	MG	2A	3574	1/1	0.83	0.15	71,71,71,71	0
57	MG	1A	3677	1/1	0.83	0.13	42,42,42,42	0
57	MG	2A	3159	1/1	0.83	0.26	82,82,82,82	0
57	MG	1A	3858	1/1	0.83	0.12	56,56,56,56	0
57	MG	2a	1810	1/1	0.83	0.09	77,77,77,77	0
57	MG	1a	1637	1/1	0.83	0.34	57,57,57,57	0
57	MG	2a	1816	1/1	0.83	0.19	81,81,81,81	0
57	MG	2A	3325	1/1	0.83	0.19	67,67,67,67	0
57	MG	2A	3333	1/1	0.83	0.22	61,61,61,61	0
57	MG	2A	3350	1/1	0.83	0.22	59,59,59,59	0
57	MG	2A	3612	1/1	0.83	0.27	68,68,68,68	0
57	MG	28	102	1/1	0.83	0.34	69,69,69,69	0
57	MG	2a	1602	1/1	0.83	0.21	81,81,81,81	0
57	MG	1A	3936	1/1	0.84	0.10	68,68,68,68	0
57	MG	2A	3278	1/1	0.84	0.22	59,59,59,59	0
57	MG	1A	3701	1/1	0.84	0.09	19,19,19,19	0
57	MG	2A	3283	1/1	0.84	0.34	83,83,83,83	0
57	MG	1A	3636	1/1	0.84	0.16	56,56,56,56	0
57	MG	1A	3722	1/1	0.84	0.14	30,30,30,30	0
57	MG	2A	3586	1/1	0.84	0.15	67,67,67,67	0
57	MG	1F	304	1/1	0.84	0.26	69,69,69,69	0
57	MG	2A	3298	1/1	0.84	0.38	76,76,76,76	0
57	MG	1A	3641	1/1	0.84	0.12	43,43,43,43	0
57	MG	1A	3821	1/1	0.84	0.15	56,56,56,56	0
57	MG	2A	3119	1/1	0.84	0.18	69,69,69,69	0
57	MG	2a	1619	1/1	0.84	0.13	71,71,71,71	0
57	MG	1A	3556	1/1	0.84	0.31	72,72,72,72	0
57	MG	1a	1755	1/1	0.84	0.14	64,64,64,64	0
57	MG	1a	1779	1/1	0.84	0.13	75,75,75,75	0
57	MG	2A	3628	1/1	0.84	0.19	76,76,76,76	0
57	MG	2A	3165	1/1	0.84	0.13	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3477	1/1	0.84	0.14	74,74,74,74	0
57	MG	2A	3359	1/1	0.84	0.41	73,73,73,73	0
57	MG	2A	3360	1/1	0.84	0.33	67,67,67,67	0
57	MG	2A	3363	1/1	0.84	0.26	65,65,65,65	0
57	MG	2a	1652	1/1	0.84	0.24	73,73,73,73	0
57	MG	1a	1795	1/1	0.84	0.14	68,68,68,68	0
57	MG	2A	3655	1/1	0.84	0.23	70,70,70,70	0
57	MG	1A	3757	1/1	0.84	0.13	61,61,61,61	0
57	MG	2A	3400	1/1	0.84	0.14	73,73,73,73	0
57	MG	2a	1673	1/1	0.84	0.15	64,64,64,64	0
57	MG	1A	3307	1/1	0.84	0.35	60,60,60,60	0
57	MG	2a	1688	1/1	0.84	0.22	71,71,71,71	0
57	MG	2A	3185	1/1	0.84	0.14	63,63,63,63	0
57	MG	1A	3139	1/1	0.84	0.13	47,47,47,47	0
57	MG	2A	3425	1/1	0.84	0.25	73,73,73,73	0
57	MG	2A	3692	1/1	0.84	0.13	71,71,71,71	0
57	MG	2a	1707	1/1	0.84	0.19	76,76,76,76	0
57	MG	1A	3773	1/1	0.84	0.15	58,58,58,58	0
57	MG	1a	1806	1/1	0.84	0.13	60,60,60,60	0
57	MG	2A	3733	1/1	0.84	0.13	68,68,68,68	0
57	MG	2A	3738	1/1	0.84	0.15	58,58,58,58	0
57	MG	2a	1722	1/1	0.84	0.12	62,62,62,62	0
57	MG	2A	3216	1/1	0.84	0.22	73,73,73,73	0
57	MG	1A	3237	1/1	0.84	0.14	56,56,56,56	0
57	MG	1A	4044	1/1	0.84	0.16	59,59,59,59	0
57	MG	1a	1814	1/1	0.84	0.28	65,65,65,65	0
57	MG	2A	3767	1/1	0.84	0.32	66,66,66,66	0
57	MG	1t	201	1/1	0.84	0.22	57,57,57,57	0
57	MG	2A	3478	1/1	0.84	0.15	50,50,50,50	0
57	MG	18	107	1/1	0.84	0.25	70,70,70,70	0
57	MG	2a	1776	1/1	0.84	0.33	75,75,75,75	0
57	MG	1A	3683	1/1	0.84	0.13	62,62,62,62	0
57	MG	2A	3485	1/1	0.84	0.11	67,67,67,67	0
57	MG	1A	3793	1/1	0.84	0.14	57,57,57,57	0
57	MG	2A	3795	1/1	0.84	0.15	71,71,71,71	0
57	MG	2A	3796	1/1	0.84	0.35	77,77,77,77	0
57	MG	2A	3797	1/1	0.84	0.15	69,69,69,69	0
57	MG	2A	3244	1/1	0.84	0.09	63,63,63,63	0
57	MG	2A	3246	1/1	0.84	0.09	68,68,68,68	0
57	MG	2B	209	1/1	0.84	0.32	69,69,69,69	0
57	MG	1A	3185	1/1	0.84	0.15	57,57,57,57	0
57	MG	1A	4085	1/1	0.84	0.14	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1659	1/1	0.84	0.18	61,61,61,61	0
57	MG	1A	3694	1/1	0.84	0.10	57,57,57,57	0
57	MG	2B	216	1/1	0.84	0.14	68,68,68,68	0
57	MG	1A	3930	1/1	0.84	0.12	62,62,62,62	0
57	MG	2A	3561	1/1	0.84	0.26	67,67,67,67	0
57	MG	2x	105	1/1	0.84	0.18	65,65,65,65	0
57	MG	2x	108	1/1	0.84	0.10	56,56,56,56	0
57	MG	2E	309	1/1	0.84	0.21	67,67,67,67	0
57	MG	1a	1666	1/1	0.84	0.27	72,72,72,72	0
57	MG	2A	3498	1/1	0.85	0.12	79,79,79,79	0
57	MG	2A	3702	1/1	0.85	0.13	69,69,69,69	0
57	MG	1A	3696	1/1	0.85	0.11	66,66,66,66	0
57	MG	1A	3997	1/1	0.85	0.11	53,53,53,53	0
57	MG	1A	4018	1/1	0.85	0.19	72,72,72,72	0
57	MG	2A	3741	1/1	0.85	0.12	48,48,48,48	0
57	MG	2A	3529	1/1	0.85	0.21	62,62,62,62	0
57	MG	2A	3196	1/1	0.85	0.38	74,74,74,74	0
57	MG	2A	3757	1/1	0.85	0.11	64,64,64,64	0
57	MG	2A	3310	1/1	0.85	0.16	64,64,64,64	0
57	MG	2a	1669	1/1	0.85	0.27	72,72,72,72	0
57	MG	2A	3552	1/1	0.85	0.11	39,39,39,39	0
57	MG	1A	3789	1/1	0.85	0.14	60,60,60,60	0
57	MG	1A	3623	1/1	0.85	0.15	30,30,30,30	0
57	MG	1a	1711	1/1	0.85	0.13	55,55,55,55	0
57	MG	2A	3347	1/1	0.85	0.23	70,70,70,70	0
57	MG	2a	1695	1/1	0.85	0.09	67,67,67,67	0
57	MG	1A	3144	1/1	0.85	0.23	32,32,32,32	0
57	MG	1A	3034	1/1	0.85	0.12	46,46,46,46	0
57	MG	1A	3541	1/1	0.85	0.17	65,65,65,65	0
57	MG	2A	3356	1/1	0.85	0.25	53,53,53,53	0
57	MG	2a	1704	1/1	0.85	0.20	69,69,69,69	0
57	MG	2A	3576	1/1	0.85	0.20	42,42,42,42	0
57	MG	1a	1740	1/1	0.85	0.17	43,43,43,43	0
57	MG	2A	3047	1/1	0.85	0.20	69,69,69,69	0
57	MG	1A	3546	1/1	0.85	0.15	44,44,44,44	0
57	MG	2B	208	1/1	0.85	0.17	56,56,56,56	0
57	MG	2a	1720	1/1	0.85	0.23	68,68,68,68	0
57	MG	1A	3419	1/1	0.85	0.20	66,66,66,66	0
57	MG	2A	3390	1/1	0.85	0.22	64,64,64,64	0
57	MG	1A	3807	1/1	0.85	0.23	43,43,43,43	0
57	MG	2A	3078	1/1	0.85	0.14	58,58,58,58	0
57	MG	1A	3428	1/1	0.85	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3407	1/1	0.85	0.17	66,66,66,66	0
57	MG	2a	1762	1/1	0.85	0.15	63,63,63,63	0
57	MG	2D	303	1/1	0.85	0.12	61,61,61,61	0
57	MG	1A	4067	1/1	0.85	0.17	59,59,59,59	0
57	MG	1a	1615	1/1	0.85	0.11	56,56,56,56	0
57	MG	2a	1771	1/1	0.85	0.20	76,76,76,76	0
57	MG	2A	3423	1/1	0.85	0.14	64,64,64,64	0
57	MG	2A	3254	1/1	0.85	0.15	67,67,67,67	0
57	MG	1A	3939	1/1	0.85	0.13	65,65,65,65	0
57	MG	1A	3258	1/1	0.85	0.20	55,55,55,55	0
57	MG	2A	3260	1/1	0.85	0.26	67,67,67,67	0
57	MG	2P	202	1/1	0.85	0.22	66,66,66,66	0
57	MG	2A	3143	1/1	0.85	0.34	72,72,72,72	0
57	MG	2R	202	1/1	0.85	0.14	50,50,50,50	0
57	MG	2U	201	1/1	0.85	0.19	54,54,54,54	0
57	MG	2A	3151	1/1	0.85	0.13	45,45,45,45	0
57	MG	1A	3262	1/1	0.85	0.14	51,51,51,51	0
57	MG	1A	3837	1/1	0.85	0.20	63,63,63,63	0
57	MG	2A	3477	1/1	0.85	0.17	50,50,50,50	0
57	MG	2f	202	1/1	0.85	0.23	76,76,76,76	0
57	MG	1A	3287	1/1	0.85	0.09	30,30,30,30	0
57	MG	1A	3299	1/1	0.85	0.24	37,37,37,37	0
57	MG	1A	3981	1/1	0.85	0.11	69,69,69,69	0
57	MG	1b	301	1/1	0.85	0.17	68,68,68,68	0
57	MG	2a	1614	1/1	0.85	0.26	63,63,63,63	0
57	MG	2A	3687	1/1	0.85	0.25	70,70,70,70	0
57	MG	2A	3491	1/1	0.85	0.17	73,73,73,73	0
57	MG	2A	3494	1/1	0.85	0.17	76,76,76,76	0
57	MG	1A	3320	1/1	0.86	0.22	56,56,56,56	0
57	MG	2A	3382	1/1	0.86	0.10	72,72,72,72	0
57	MG	1A	3993	1/1	0.86	0.14	50,50,50,50	0
57	MG	2A	3392	1/1	0.86	0.17	47,47,47,47	0
57	MG	1A	3709	1/1	0.86	0.09	44,44,44,44	0
57	MG	2a	1611	1/1	0.86	0.39	75,75,75,75	0
57	MG	2A	3229	1/1	0.86	0.34	72,72,72,72	0
57	MG	1A	3538	1/1	0.86	0.28	68,68,68,68	0
57	MG	2a	1620	1/1	0.86	0.25	76,76,76,76	0
57	MG	2A	3644	1/1	0.86	0.31	68,68,68,68	0
57	MG	1a	1717	1/1	0.86	0.18	67,67,67,67	0
57	MG	2A	3046	1/1	0.86	0.21	70,70,70,70	0
57	MG	1A	3881	1/1	0.86	0.10	26,26,26,26	0
57	MG	1A	3887	1/1	0.86	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3479	1/1	0.86	0.26	67,67,67,67	0
57	MG	2A	3247	1/1	0.86	0.28	65,65,65,65	0
57	MG	2a	1640	1/1	0.86	0.13	67,67,67,67	0
57	MG	1A	3800	1/1	0.86	0.12	69,69,69,69	0
57	MG	2A	3077	1/1	0.86	0.15	60,60,60,60	0
57	MG	1a	1742	1/1	0.86	0.15	65,65,65,65	0
57	MG	1A	3328	1/1	0.86	0.10	57,57,57,57	0
57	MG	2A	3457	1/1	0.86	0.12	71,71,71,71	0
57	MG	1A	3335	1/1	0.86	0.16	56,56,56,56	0
57	MG	2A	3085	1/1	0.86	0.16	47,47,47,47	0
57	MG	2A	3723	1/1	0.86	0.18	43,43,43,43	0
57	MG	2A	3730	1/1	0.86	0.12	63,63,63,63	0
57	MG	2a	1677	1/1	0.86	0.20	68,68,68,68	0
57	MG	2A	3262	1/1	0.86	0.19	71,71,71,71	0
57	MG	2A	3263	1/1	0.86	0.14	73,73,73,73	0
57	MG	2A	3270	1/1	0.86	0.12	51,51,51,51	0
57	MG	2A	3271	1/1	0.86	0.18	73,73,73,73	0
57	MG	2A	3753	1/1	0.86	0.15	66,66,66,66	0
57	MG	2A	3095	1/1	0.86	0.21	75,75,75,75	0
57	MG	1A	3928	1/1	0.86	0.14	59,59,59,59	0
57	MG	1A	3755	1/1	0.86	0.12	42,42,42,42	0
57	MG	1A	3423	1/1	0.86	0.28	65,65,65,65	0
57	MG	2A	3279	1/1	0.86	0.18	60,60,60,60	0
57	MG	2A	3768	1/1	0.86	0.17	72,72,72,72	0
57	MG	2A	3123	1/1	0.86	0.14	57,57,57,57	0
57	MG	2A	3518	1/1	0.86	0.10	51,51,51,51	0
57	MG	2a	1718	1/1	0.86	0.11	82,82,82,82	0
57	MG	1a	1610	1/1	0.86	0.24	65,65,65,65	0
57	MG	2a	1721	1/1	0.86	0.23	76,76,76,76	0
57	MG	2A	3149	1/1	0.86	0.38	72,72,72,72	0
57	MG	2A	3542	1/1	0.86	0.19	72,72,72,72	0
57	MG	2a	1724	1/1	0.86	0.14	69,69,69,69	0
57	MG	2A	3783	1/1	0.86	0.29	75,75,75,75	0
57	MG	2A	3543	1/1	0.86	0.14	35,35,35,35	0
57	MG	2a	1751	1/1	0.86	0.15	60,60,60,60	0
57	MG	2a	1754	1/1	0.86	0.13	49,49,49,49	0
57	MG	2A	3291	1/1	0.86	0.13	67,67,67,67	0
57	MG	1a	1798	1/1	0.86	0.17	70,70,70,70	0
57	MG	2a	1761	1/1	0.86	0.20	73,73,73,73	0
57	MG	1A	3068	1/1	0.86	0.25	58,58,58,58	0
57	MG	1A	3597	1/1	0.86	0.23	63,63,63,63	0
57	MG	2B	204	1/1	0.86	0.20	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3299	1/1	0.86	0.28	75,75,75,75	0
57	MG	2A	3301	1/1	0.86	0.17	67,67,67,67	0
57	MG	2A	3303	1/1	0.86	0.13	72,72,72,72	0
57	MG	1a	1629	1/1	0.86	0.40	69,69,69,69	0
57	MG	1A	3823	1/1	0.86	0.12	29,29,29,29	0
57	MG	2A	3568	1/1	0.86	0.14	60,60,60,60	0
57	MG	1a	1638	1/1	0.86	0.20	60,60,60,60	0
57	MG	2B	215	1/1	0.86	0.17	66,66,66,66	0
57	MG	2A	3315	1/1	0.86	0.09	65,65,65,65	0
57	MG	1A	4095	1/1	0.86	0.15	47,47,47,47	0
57	MG	1A	3961	1/1	0.86	0.18	64,64,64,64	0
57	MG	2A	3330	1/1	0.86	0.31	56,56,56,56	0
57	MG	1B	214	1/1	0.86	0.12	59,59,59,59	0
57	MG	1A	3096	1/1	0.86	0.24	65,65,65,65	0
57	MG	2a	1812	1/1	0.86	0.10	65,65,65,65	0
57	MG	2A	3195	1/1	0.86	0.14	56,56,56,56	0
57	MG	2A	3593	1/1	0.86	0.17	63,63,63,63	0
57	MG	2k	201	1/1	0.86	0.24	66,66,66,66	0
57	MG	2A	3597	1/1	0.86	0.21	74,74,74,74	0
57	MG	1A	3099	1/1	0.86	0.17	54,54,54,54	0
57	MG	1A	3277	1/1	0.86	0.23	64,64,64,64	0
57	MG	2A	3605	1/1	0.86	0.34	67,67,67,67	0
57	MG	2w	106	1/1	0.86	0.17	75,75,75,75	0
57	MG	2x	104	1/1	0.86	0.36	72,72,72,72	0
57	MG	1x	101	1/1	0.86	0.17	60,60,60,60	0
57	MG	1A	3378	1/1	0.86	0.26	62,62,62,62	0
57	MG	1a	1671	1/1	0.86	0.34	65,65,65,65	0
57	MG	2A	3217	1/1	0.86	0.15	70,70,70,70	0
57	MG	25	101	1/1	0.87	0.31	67,67,67,67	0
57	MG	1a	1761	1/1	0.87	0.13	58,58,58,58	0
57	MG	2a	1601	1/1	0.87	0.10	81,81,81,81	0
57	MG	1a	1764	1/1	0.87	0.15	48,48,48,48	0
57	MG	1a	1765	1/1	0.87	0.15	57,57,57,57	0
57	MG	2A	3339	1/1	0.87	0.16	58,58,58,58	0
57	MG	2A	3341	1/1	0.87	0.40	71,71,71,71	0
57	MG	2A	3343	1/1	0.87	0.36	64,64,64,64	0
57	MG	2a	1617	1/1	0.87	0.18	57,57,57,57	0
57	MG	2A	3346	1/1	0.87	0.34	68,68,68,68	0
57	MG	1A	3559	1/1	0.87	0.20	44,44,44,44	0
57	MG	2A	3164	1/1	0.87	0.21	66,66,66,66	0
57	MG	1a	1791	1/1	0.87	0.12	69,69,69,69	0
57	MG	2A	3166	1/1	0.87	0.16	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3167	1/1	0.87	0.21	57,57,57,57	0
57	MG	1A	3427	1/1	0.87	0.20	55,55,55,55	0
57	MG	1A	3045	1/1	0.87	0.12	39,39,39,39	0
57	MG	2A	3653	1/1	0.87	0.12	64,64,64,64	0
57	MG	2a	1639	1/1	0.87	0.27	71,71,71,71	0
57	MG	1A	3308	1/1	0.87	0.14	50,50,50,50	0
57	MG	1A	4030	1/1	0.87	0.13	43,43,43,43	0
57	MG	2A	3182	1/1	0.87	0.18	64,64,64,64	0
57	MG	2A	3664	1/1	0.87	0.13	71,71,71,71	0
57	MG	2a	1659	1/1	0.87	0.13	64,64,64,64	0
57	MG	12	101	1/1	0.87	0.13	38,38,38,38	0
57	MG	12	102	1/1	0.87	0.11	50,50,50,50	0
57	MG	13	104	1/1	0.87	0.10	55,55,55,55	0
57	MG	1A	3434	1/1	0.87	0.22	60,60,60,60	0
57	MG	1a	1807	1/1	0.87	0.23	70,70,70,70	0
57	MG	1A	3618	1/1	0.87	0.09	21,21,21,21	0
57	MG	2A	3412	1/1	0.87	0.14	57,57,57,57	0
57	MG	2a	1684	1/1	0.87	0.21	67,67,67,67	0
57	MG	2a	1685	1/1	0.87	0.18	65,65,65,65	0
57	MG	1a	1810	1/1	0.87	0.13	56,56,56,56	0
57	MG	1A	3922	1/1	0.87	0.13	49,49,49,49	0
57	MG	2a	1689	1/1	0.87	0.23	67,67,67,67	0
57	MG	2A	3221	1/1	0.87	0.22	65,65,65,65	0
57	MG	2A	3729	1/1	0.87	0.19	74,74,74,74	0
57	MG	1A	3924	1/1	0.87	0.20	55,55,55,55	0
57	MG	1A	3927	1/1	0.87	0.18	65,65,65,65	0
57	MG	1A	3803	1/1	0.87	0.10	57,57,57,57	0
57	MG	1A	3313	1/1	0.87	0.19	53,53,53,53	0
57	MG	1w	103	1/1	0.87	0.21	73,73,73,73	0
57	MG	1A	3214	1/1	0.87	0.20	49,49,49,49	0
57	MG	2a	1709	1/1	0.87	0.31	72,72,72,72	0
57	MG	1w	105	1/1	0.87	0.10	68,68,68,68	0
57	MG	1A	3449	1/1	0.87	0.15	48,48,48,48	0
57	MG	2A	3467	1/1	0.87	0.13	63,63,63,63	0
57	MG	2A	3238	1/1	0.87	0.24	60,60,60,60	0
57	MG	1x	104	1/1	0.87	0.18	66,66,66,66	0
57	MG	1a	1647	1/1	0.87	0.13	67,67,67,67	0
57	MG	2A	3769	1/1	0.87	0.20	71,71,71,71	0
57	MG	1a	1648	1/1	0.87	0.33	66,66,66,66	0
57	MG	1A	3944	1/1	0.87	0.11	27,27,27,27	0
57	MG	1A	3456	1/1	0.87	0.12	58,58,58,58	0
57	MG	1A	3466	1/1	0.87	0.19	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1749	1/1	0.87	0.14	78,78,78,78	0
57	MG	2A	3030	1/1	0.87	0.19	63,63,63,63	0
57	MG	1A	3758	1/1	0.87	0.08	49,49,49,49	0
57	MG	1A	3540	1/1	0.87	0.29	59,59,59,59	0
57	MG	2A	3785	1/1	0.87	0.13	57,57,57,57	0
57	MG	2A	3794	1/1	0.87	0.10	47,47,47,47	0
57	MG	1a	1668	1/1	0.87	0.16	56,56,56,56	0
57	MG	1A	3281	1/1	0.87	0.12	58,58,58,58	0
57	MG	2A	3519	1/1	0.87	0.22	50,50,50,50	0
57	MG	2A	3264	1/1	0.87	0.30	69,69,69,69	0
57	MG	2B	203	1/1	0.87	0.23	73,73,73,73	0
57	MG	1B	224	1/1	0.87	0.19	57,57,57,57	0
57	MG	1A	3975	1/1	0.87	0.08	61,61,61,61	0
57	MG	2a	1779	1/1	0.87	0.40	71,71,71,71	0
57	MG	2A	3069	1/1	0.87	0.09	52,52,52,52	0
57	MG	1A	3252	1/1	0.87	0.09	46,46,46,46	0
57	MG	1a	1696	1/1	0.87	0.16	57,57,57,57	0
57	MG	1D	311	1/1	0.87	0.13	55,55,55,55	0
57	MG	2a	1791	1/1	0.87	0.26	79,79,79,79	0
57	MG	1E	310	1/1	0.87	0.08	39,39,39,39	0
57	MG	1A	3033	1/1	0.87	0.39	39,39,39,39	0
57	MG	2A	3282	1/1	0.87	0.25	76,76,76,76	0
57	MG	2a	1805	1/1	0.87	0.22	58,58,58,58	0
57	MG	1A	3784	1/1	0.87	0.18	54,54,54,54	0
57	MG	2A	3088	1/1	0.87	0.12	75,75,75,75	0
57	MG	2A	3092	1/1	0.87	0.27	65,65,65,65	0
57	MG	2A	3094	1/1	0.87	0.12	67,67,67,67	0
57	MG	1a	1727	1/1	0.87	0.11	64,64,64,64	0
57	MG	2a	1820	1/1	0.87	0.16	69,69,69,69	0
57	MG	2A	3099	1/1	0.87	0.23	77,77,77,77	0
57	MG	2f	203	1/1	0.87	0.18	75,75,75,75	0
57	MG	1A	3557	1/1	0.87	0.38	66,66,66,66	0
57	MG	2A	3106	1/1	0.87	0.24	59,59,59,59	0
57	MG	1O	206	1/1	0.87	0.24	65,65,65,65	0
57	MG	1R	205	1/1	0.87	0.13	36,36,36,36	0
57	MG	2A	3307	1/1	0.87	0.34	71,71,71,71	0
57	MG	2A	3121	1/1	0.87	0.25	42,42,42,42	0
57	MG	2x	102	1/1	0.87	0.39	82,82,82,82	0
57	MG	1A	3305	1/1	0.87	0.19	63,63,63,63	0
57	MG	1U	209	1/1	0.87	0.39	37,37,37,37	0
57	MG	2A	3599	1/1	0.87	0.22	67,67,67,67	0
57	MG	1A	4012	1/1	0.87	0.16	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3321	1/1	0.87	0.16	64,64,64,64	0
57	MG	1a	1804	1/1	0.88	0.22	64,64,64,64	0
57	MG	1A	3770	1/1	0.88	0.20	68,68,68,68	0
57	MG	1A	3654	1/1	0.88	0.09	27,27,27,27	0
57	MG	1A	3906	1/1	0.88	0.18	48,48,48,48	0
57	MG	1A	3657	1/1	0.88	0.20	55,55,55,55	0
57	MG	15	106	1/1	0.88	0.13	61,61,61,61	0
57	MG	1A	3410	1/1	0.88	0.14	31,31,31,31	0
57	MG	1a	1605	1/1	0.88	0.12	62,62,62,62	0
57	MG	2a	1637	1/1	0.88	0.12	64,64,64,64	0
57	MG	2A	3205	1/1	0.88	0.38	47,47,47,47	0
57	MG	1l	3200	1/1	0.88	0.10	71,71,71,71	0
57	MG	2A	3214	1/1	0.88	0.17	77,77,77,77	0
57	MG	1A	3412	1/1	0.88	0.12	48,48,48,48	0
57	MG	1A	3413	1/1	0.88	0.13	67,67,67,67	0
57	MG	2a	1647	1/1	0.88	0.23	78,78,78,78	0
57	MG	2a	1650	1/1	0.88	0.28	66,66,66,66	0
57	MG	1A	3923	1/1	0.88	0.12	50,50,50,50	0
57	MG	2a	1654	1/1	0.88	0.19	64,64,64,64	0
57	MG	1A	4075	1/1	0.88	0.15	62,62,62,62	0
57	MG	2a	1661	1/1	0.88	0.19	59,59,59,59	0
57	MG	1A	4076	1/1	0.88	0.11	70,70,70,70	0
57	MG	1A	3547	1/1	0.88	0.09	42,42,42,42	0
57	MG	2A	3699	1/1	0.88	0.11	59,59,59,59	0
57	MG	1A	3475	1/1	0.88	0.12	60,60,60,60	0
57	MG	1A	4086	1/1	0.88	0.09	40,40,40,40	0
57	MG	2A	3720	1/1	0.88	0.10	58,58,58,58	0
57	MG	1x	108	1/1	0.88	0.21	67,67,67,67	0
57	MG	2a	1679	1/1	0.88	0.34	69,69,69,69	0
57	MG	2A	3231	1/1	0.88	0.13	71,71,71,71	0
57	MG	1A	4093	1/1	0.88	0.25	49,49,49,49	0
57	MG	1A	3414	1/1	0.88	0.10	51,51,51,51	0
57	MG	2A	3735	1/1	0.88	0.10	79,79,79,79	0
57	MG	1B	208	1/1	0.88	0.10	65,65,65,65	0
57	MG	2a	1691	1/1	0.88	0.38	76,76,76,76	0
57	MG	1A	3418	1/1	0.88	0.22	54,54,54,54	0
57	MG	2A	3025	1/1	0.88	0.15	63,63,63,63	0
57	MG	2A	3245	1/1	0.88	0.29	73,73,73,73	0
57	MG	1A	3363	1/1	0.88	0.29	41,41,41,41	0
57	MG	1a	1665	1/1	0.88	0.17	65,65,65,65	0
57	MG	2A	3043	1/1	0.88	0.28	70,70,70,70	0
57	MG	1A	3199	1/1	0.88	0.15	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3253	1/1	0.88	0.13	72,72,72,72	0
57	MG	1A	3702	1/1	0.88	0.32	67,67,67,67	0
57	MG	1A	3373	1/1	0.88	0.28	69,69,69,69	0
57	MG	2A	3487	1/1	0.88	0.19	63,63,63,63	0
57	MG	1A	3950	1/1	0.88	0.10	58,58,58,58	0
57	MG	1A	3707	1/1	0.88	0.11	67,67,67,67	0
57	MG	2A	3065	1/1	0.88	0.10	64,64,64,64	0
57	MG	2A	3508	1/1	0.88	0.19	76,76,76,76	0
57	MG	1A	3498	1/1	0.88	0.12	63,63,63,63	0
57	MG	2A	3071	1/1	0.88	0.22	60,60,60,60	0
57	MG	2A	3073	1/1	0.88	0.19	49,49,49,49	0
57	MG	2a	1726	1/1	0.88	0.12	66,66,66,66	0
57	MG	2A	3787	1/1	0.88	0.12	58,58,58,58	0
57	MG	2A	3791	1/1	0.88	0.27	71,71,71,71	0
57	MG	2a	1734	1/1	0.88	0.12	70,70,70,70	0
57	MG	1a	1692	1/1	0.88	0.23	69,69,69,69	0
57	MG	2A	3521	1/1	0.88	0.13	45,45,45,45	0
57	MG	2A	3522	1/1	0.88	0.21	69,69,69,69	0
57	MG	1B	231	1/1	0.88	0.22	63,63,63,63	0
57	MG	2A	3526	1/1	0.88	0.21	65,65,65,65	0
57	MG	1a	1697	1/1	0.88	0.11	49,49,49,49	0
57	MG	2A	3536	1/1	0.88	0.19	46,46,46,46	0
57	MG	1A	3259	1/1	0.88	0.09	40,40,40,40	0
57	MG	1E	305	1/1	0.88	0.11	28,28,28,28	0
57	MG	1E	307	1/1	0.88	0.14	67,67,67,67	0
57	MG	1A	3724	1/1	0.88	0.15	45,45,45,45	0
57	MG	1a	1720	1/1	0.88	0.15	44,44,44,44	0
57	MG	1a	1724	1/1	0.88	0.21	59,59,59,59	0
57	MG	2A	3286	1/1	0.88	0.17	61,61,61,61	0
57	MG	2A	3288	1/1	0.88	0.13	57,57,57,57	0
57	MG	2a	1782	1/1	0.88	0.22	70,70,70,70	0
57	MG	1A	3431	1/1	0.88	0.16	66,66,66,66	0
57	MG	1F	315	1/1	0.88	0.17	58,58,58,58	0
57	MG	2A	3101	1/1	0.88	0.18	50,50,50,50	0
57	MG	1A	3827	1/1	0.88	0.12	37,37,37,37	0
57	MG	2A	3297	1/1	0.88	0.18	69,69,69,69	0
57	MG	1A	3282	1/1	0.88	0.17	46,46,46,46	0
57	MG	2A	3110	1/1	0.88	0.13	76,76,76,76	0
57	MG	1A	3742	1/1	0.88	0.09	35,35,35,35	0
57	MG	1A	3990	1/1	0.88	0.12	54,54,54,54	0
57	MG	2A	3304	1/1	0.88	0.27	62,62,62,62	0
57	MG	1A	3061	1/1	0.88	0.27	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1T	201	1/1	0.88	0.28	65,65,65,65	0
57	MG	2A	3140	1/1	0.88	0.17	73,73,73,73	0
57	MG	1T	202	1/1	0.88	0.17	54,54,54,54	0
57	MG	1A	3849	1/1	0.88	0.08	35,35,35,35	0
57	MG	2A	3317	1/1	0.88	0.07	58,58,58,58	0
57	MG	1U	210	1/1	0.88	0.12	55,55,55,55	0
57	MG	1A	3999	1/1	0.88	0.14	34,34,34,34	0
57	MG	25	103	1/1	0.88	0.18	63,63,63,63	0
57	MG	1A	3348	1/1	0.88	0.24	61,61,61,61	0
57	MG	28	104	1/1	0.88	0.31	58,58,58,58	0
57	MG	2w	103	1/1	0.88	0.15	70,70,70,70	0
57	MG	10	103	1/1	0.88	0.14	52,52,52,52	0
57	MG	2A	3161	1/1	0.88	0.10	57,57,57,57	0
57	MG	10	105	1/1	0.88	0.27	43,43,43,43	0
57	MG	1A	3294	1/1	0.88	0.13	63,63,63,63	0
57	MG	1A	3401	1/1	0.88	0.23	56,56,56,56	0
57	MG	1A	3647	1/1	0.88	0.14	24,24,24,24	0
57	MG	1A	3653	1/1	0.88	0.10	37,37,37,37	0
57	MG	2A	3058	1/1	0.89	0.34	68,68,68,68	0
57	MG	1B	201	1/1	0.89	0.15	51,51,51,51	0
57	MG	2A	3267	1/1	0.89	0.20	64,64,64,64	0
57	MG	2A	3067	1/1	0.89	0.14	51,51,51,51	0
57	MG	1B	204	1/1	0.89	0.09	44,44,44,44	0
57	MG	1A	3203	1/1	0.89	0.06	40,40,40,40	0
57	MG	2V	201	1/1	0.89	0.34	51,51,51,51	0
57	MG	1A	3082	1/1	0.89	0.09	52,52,52,52	0
57	MG	1a	1679	1/1	0.89	0.32	47,47,47,47	0
57	MG	2A	3553	1/1	0.89	0.17	61,61,61,61	0
57	MG	1a	1682	1/1	0.89	0.27	62,62,62,62	0
57	MG	1A	3219	1/1	0.89	0.28	33,33,33,33	0
57	MG	1a	1688	1/1	0.89	0.11	51,51,51,51	0
57	MG	2A	3082	1/1	0.89	0.14	78,78,78,78	0
57	MG	1A	3679	1/1	0.89	0.15	66,66,66,66	0
57	MG	1a	1694	1/1	0.89	0.36	63,63,63,63	0
57	MG	2A	3565	1/1	0.89	0.15	66,66,66,66	0
57	MG	2a	1606	1/1	0.89	0.23	74,74,74,74	0
57	MG	1A	3023	1/1	0.89	0.26	55,55,55,55	0
57	MG	2A	3570	1/1	0.89	0.22	73,73,73,73	0
57	MG	1A	3934	1/1	0.89	0.09	61,61,61,61	0
57	MG	1A	3296	1/1	0.89	0.23	56,56,56,56	0
57	MG	1A	3223	1/1	0.89	0.11	57,57,57,57	0
57	MG	2A	3578	1/1	0.89	0.12	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3579	1/1	0.89	0.16	58,58,58,58	0
57	MG	2a	1624	1/1	0.89	0.38	64,64,64,64	0
57	MG	1A	3388	1/1	0.89	0.48	70,70,70,70	0
57	MG	1A	3947	1/1	0.89	0.13	50,50,50,50	0
57	MG	1A	3151	1/1	0.89	0.23	39,39,39,39	0
57	MG	1A	3159	1/1	0.89	0.10	40,40,40,40	0
57	MG	1A	3805	1/1	0.89	0.10	51,51,51,51	0
57	MG	2A	3302	1/1	0.89	0.26	57,57,57,57	0
57	MG	2a	1634	1/1	0.89	0.19	62,62,62,62	0
57	MG	2a	1636	1/1	0.89	0.32	69,69,69,69	0
57	MG	1A	3960	1/1	0.89	0.11	65,65,65,65	0
57	MG	1a	1734	1/1	0.89	0.14	76,76,76,76	0
57	MG	1A	3468	1/1	0.89	0.17	54,54,54,54	0
57	MG	1A	3576	1/1	0.89	0.11	41,41,41,41	0
57	MG	2A	3134	1/1	0.89	0.35	63,63,63,63	0
57	MG	2A	3135	1/1	0.89	0.23	44,44,44,44	0
57	MG	2a	1644	1/1	0.89	0.27	83,83,83,83	0
57	MG	2A	3609	1/1	0.89	0.16	40,40,40,40	0
57	MG	1A	3247	1/1	0.89	0.11	42,42,42,42	0
57	MG	2A	3316	1/1	0.89	0.24	75,75,75,75	0
57	MG	1A	3584	1/1	0.89	0.18	30,30,30,30	0
57	MG	2A	3144	1/1	0.89	0.30	44,44,44,44	0
57	MG	1A	3405	1/1	0.89	0.15	62,62,62,62	0
57	MG	2A	3630	1/1	0.89	0.13	65,65,65,65	0
57	MG	1a	1760	1/1	0.89	0.13	49,49,49,49	0
57	MG	2A	3329	1/1	0.89	0.19	43,43,43,43	0
57	MG	2A	3153	1/1	0.89	0.14	48,48,48,48	0
57	MG	2A	3635	1/1	0.89	0.15	68,68,68,68	0
57	MG	1A	3723	1/1	0.89	0.13	26,26,26,26	0
57	MG	2a	1675	1/1	0.89	0.22	53,53,53,53	0
57	MG	1A	3982	1/1	0.89	0.10	55,55,55,55	0
57	MG	1S	201	1/1	0.89	0.18	44,44,44,44	0
57	MG	2a	1683	1/1	0.89	0.14	75,75,75,75	0
57	MG	1A	3985	1/1	0.89	0.17	57,57,57,57	0
57	MG	2A	3648	1/1	0.89	0.10	46,46,46,46	0
57	MG	2A	3652	1/1	0.89	0.18	54,54,54,54	0
57	MG	2A	3345	1/1	0.89	0.26	56,56,56,56	0
57	MG	1A	3829	1/1	0.89	0.08	37,37,37,37	0
57	MG	1A	3478	1/1	0.89	0.20	74,74,74,74	0
57	MG	1A	3601	1/1	0.89	0.14	70,70,70,70	0
57	MG	2A	3352	1/1	0.89	0.25	63,63,63,63	0
57	MG	1A	3996	1/1	0.89	0.09	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3248	1/1	0.89	0.08	32,32,32,32	0
57	MG	2A	3173	1/1	0.89	0.10	70,70,70,70	0
57	MG	1A	3484	1/1	0.89	0.30	44,44,44,44	0
57	MG	1A	4011	1/1	0.89	0.12	51,51,51,51	0
57	MG	10	107	1/1	0.89	0.12	54,54,54,54	0
57	MG	2A	3364	1/1	0.89	0.15	54,54,54,54	0
57	MG	1A	3852	1/1	0.89	0.11	23,23,23,23	0
57	MG	2A	3380	1/1	0.89	0.20	58,58,58,58	0
57	MG	1A	3853	1/1	0.89	0.12	77,77,77,77	0
57	MG	2a	1716	1/1	0.89	0.27	63,63,63,63	0
57	MG	2A	3713	1/1	0.89	0.11	50,50,50,50	0
57	MG	2A	3385	1/1	0.89	0.30	73,73,73,73	0
57	MG	2A	3193	1/1	0.89	0.23	55,55,55,55	0
57	MG	11	102	1/1	0.89	0.17	60,60,60,60	0
57	MG	1A	3097	1/1	0.89	0.10	37,37,37,37	0
57	MG	2A	3198	1/1	0.89	0.14	69,69,69,69	0
57	MG	2A	3403	1/1	0.89	0.24	56,56,56,56	0
57	MG	1A	3257	1/1	0.89	0.26	58,58,58,58	0
57	MG	1A	3058	1/1	0.89	0.26	54,54,54,54	0
57	MG	2A	3209	1/1	0.89	0.16	47,47,47,47	0
57	MG	2a	1739	1/1	0.89	0.11	69,69,69,69	0
57	MG	2a	1748	1/1	0.89	0.14	78,78,78,78	0
57	MG	2A	3414	1/1	0.89	0.22	62,62,62,62	0
57	MG	1A	3861	1/1	0.89	0.21	37,37,37,37	0
57	MG	2A	3418	1/1	0.89	0.13	28,28,28,28	0
57	MG	2A	3759	1/1	0.89	0.16	64,64,64,64	0
57	MG	1A	4037	1/1	0.89	0.14	58,58,58,58	0
57	MG	1A	4038	1/1	0.89	0.12	62,62,62,62	0
57	MG	1A	3196	1/1	0.89	0.19	53,53,53,53	0
57	MG	1A	3872	1/1	0.89	0.11	41,41,41,41	0
57	MG	2a	1764	1/1	0.89	0.21	66,66,66,66	0
57	MG	2a	1765	1/1	0.89	0.13	67,67,67,67	0
57	MG	2A	3428	1/1	0.89	0.10	45,45,45,45	0
57	MG	2A	3430	1/1	0.89	0.09	39,39,39,39	0
57	MG	1a	1604	1/1	0.89	0.15	58,58,58,58	0
57	MG	2a	1775	1/1	0.89	0.26	78,78,78,78	0
57	MG	1A	3879	1/1	0.89	0.10	68,68,68,68	0
57	MG	1A	3759	1/1	0.89	0.10	55,55,55,55	0
57	MG	2A	3449	1/1	0.89	0.10	49,49,49,49	0
57	MG	1A	4047	1/1	0.89	0.18	55,55,55,55	0
57	MG	1A	4051	1/1	0.89	0.23	57,57,57,57	0
57	MG	1a	1626	1/1	0.89	0.31	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3885	1/1	0.89	0.09	43,43,43,43	0
57	MG	2A	3470	1/1	0.89	0.10	39,39,39,39	0
57	MG	1a	1634	1/1	0.89	0.25	74,74,74,74	0
57	MG	1x	113	1/1	0.89	0.24	62,62,62,62	0
57	MG	1A	3338	1/1	0.89	0.32	48,48,48,48	0
57	MG	1A	3897	1/1	0.89	0.09	18,18,18,18	0
57	MG	1A	3347	1/1	0.89	0.10	47,47,47,47	0
57	MG	1A	3424	1/1	0.89	0.23	60,60,60,60	0
57	MG	2A	3026	1/1	0.89	0.14	43,43,43,43	0
57	MG	1A	3198	1/1	0.89	0.19	59,59,59,59	0
57	MG	1a	1651	1/1	0.89	0.16	54,54,54,54	0
57	MG	2A	3495	1/1	0.89	0.23	63,63,63,63	0
57	MG	1A	4084	1/1	0.89	0.18	73,73,73,73	0
57	MG	2A	3502	1/1	0.89	0.13	67,67,67,67	0
57	MG	2A	3503	1/1	0.89	0.08	40,40,40,40	0
57	MG	2j	201	1/1	0.89	0.14	74,74,74,74	0
57	MG	1A	3774	1/1	0.89	0.23	32,32,32,32	0
57	MG	1A	3124	1/1	0.89	0.14	37,37,37,37	0
57	MG	2A	3514	1/1	0.89	0.12	65,65,65,65	0
57	MG	2B	218	1/1	0.89	0.33	78,78,78,78	0
57	MG	1A	4088	1/1	0.89	0.22	75,75,75,75	0
57	MG	2w	102	1/1	0.89	0.15	84,84,84,84	0
57	MG	2A	3050	1/1	0.89	0.28	65,65,65,65	0
57	MG	2w	104	1/1	0.89	0.11	87,87,87,87	0
57	MG	2D	308	1/1	0.89	0.16	59,59,59,59	0
57	MG	2A	3257	1/1	0.89	0.10	68,68,68,68	0
57	MG	2E	304	1/1	0.89	0.13	34,34,34,34	0
57	MG	2E	306	1/1	0.89	0.14	54,54,54,54	0
57	MG	2x	107	1/1	0.89	0.18	64,64,64,64	0
57	MG	2A	3259	1/1	0.89	0.17	65,65,65,65	0
57	MG	1A	3916	1/1	0.89	0.07	23,23,23,23	0
57	MG	1A	3666	1/1	0.89	0.12	43,43,43,43	0
57	MG	1A	3179	1/1	0.90	0.15	38,38,38,38	0
57	MG	1A	3656	1/1	0.90	0.08	31,31,31,31	0
57	MG	29	101	1/1	0.90	0.13	69,69,69,69	0
57	MG	1A	3523	1/1	0.90	0.34	42,42,42,42	0
57	MG	1Q	207	1/1	0.90	0.11	49,49,49,49	0
57	MG	2a	1605	1/1	0.90	0.23	69,69,69,69	0
57	MG	2A	3358	1/1	0.90	0.22	52,52,52,52	0
57	MG	1A	3786	1/1	0.90	0.21	47,47,47,47	0
57	MG	1a	1690	1/1	0.90	0.23	69,69,69,69	0
57	MG	2A	3222	1/1	0.90	0.12	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1612	1/1	0.90	0.17	60,60,60,60	0
57	MG	1A	4033	1/1	0.90	0.22	60,60,60,60	0
57	MG	1A	3293	1/1	0.90	0.19	57,57,57,57	0
57	MG	2a	1618	1/1	0.90	0.29	71,71,71,71	0
57	MG	2A	3368	1/1	0.90	0.33	57,57,57,57	0
57	MG	2A	3374	1/1	0.90	0.10	40,40,40,40	0
57	MG	2A	3379	1/1	0.90	0.29	58,58,58,58	0
57	MG	2A	3226	1/1	0.90	0.19	59,59,59,59	0
57	MG	1S	203	1/1	0.90	0.22	67,67,67,67	0
57	MG	1A	3668	1/1	0.90	0.15	61,61,61,61	0
57	MG	2a	1630	1/1	0.90	0.19	68,68,68,68	0
57	MG	1A	3914	1/1	0.90	0.10	32,32,32,32	0
57	MG	1A	3368	1/1	0.90	0.10	43,43,43,43	0
57	MG	2A	3398	1/1	0.90	0.39	62,62,62,62	0
57	MG	1A	3430	1/1	0.90	0.14	69,69,69,69	0
57	MG	2A	3059	1/1	0.90	0.22	55,55,55,55	0
57	MG	2A	3640	1/1	0.90	0.16	68,68,68,68	0
57	MG	2A	3642	1/1	0.90	0.09	69,69,69,69	0
57	MG	1A	3018	1/1	0.90	0.31	50,50,50,50	0
57	MG	1A	3295	1/1	0.90	0.33	63,63,63,63	0
57	MG	2A	3647	1/1	0.90	0.12	54,54,54,54	0
57	MG	2A	3239	1/1	0.90	0.16	55,55,55,55	0
57	MG	2A	3408	1/1	0.90	0.12	65,65,65,65	0
57	MG	2A	3410	1/1	0.90	0.10	76,76,76,76	0
57	MG	2a	1648	1/1	0.90	0.09	66,66,66,66	0
57	MG	2a	1649	1/1	0.90	0.32	67,67,67,67	0
57	MG	2A	3242	1/1	0.90	0.16	66,66,66,66	0
57	MG	2A	3413	1/1	0.90	0.12	38,38,38,38	0
57	MG	2A	3659	1/1	0.90	0.16	69,69,69,69	0
57	MG	1A	4050	1/1	0.90	0.12	61,61,61,61	0
57	MG	1A	3433	1/1	0.90	0.16	47,47,47,47	0
57	MG	1A	4059	1/1	0.90	0.18	61,61,61,61	0
57	MG	1a	1732	1/1	0.90	0.08	53,53,53,53	0
57	MG	1A	3242	1/1	0.90	0.22	57,57,57,57	0
57	MG	2A	3424	1/1	0.90	0.14	65,65,65,65	0
57	MG	1a	1737	1/1	0.90	0.11	56,56,56,56	0
57	MG	1A	3243	1/1	0.90	0.17	41,41,41,41	0
57	MG	1A	3193	1/1	0.90	0.09	47,47,47,47	0
57	MG	1A	3550	1/1	0.90	0.12	52,52,52,52	0
57	MG	1A	3381	1/1	0.90	0.12	57,57,57,57	0
57	MG	2a	1680	1/1	0.90	0.21	66,66,66,66	0
57	MG	2A	3709	1/1	0.90	0.10	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3439	1/1	0.90	0.27	68,68,68,68	0
57	MG	2A	3086	1/1	0.90	0.12	44,44,44,44	0
57	MG	2A	3717	1/1	0.90	0.12	64,64,64,64	0
57	MG	1a	1745	1/1	0.90	0.20	74,74,74,74	0
57	MG	2A	3091	1/1	0.90	0.30	70,70,70,70	0
57	MG	2A	3261	1/1	0.90	0.13	56,56,56,56	0
57	MG	1a	1748	1/1	0.90	0.14	71,71,71,71	0
57	MG	2A	3731	1/1	0.90	0.10	59,59,59,59	0
57	MG	1a	1752	1/1	0.90	0.09	63,63,63,63	0
57	MG	2A	3463	1/1	0.90	0.20	53,53,53,53	0
57	MG	2A	3737	1/1	0.90	0.14	48,48,48,48	0
57	MG	1A	3815	1/1	0.90	0.13	57,57,57,57	0
57	MG	2A	3739	1/1	0.90	0.10	52,52,52,52	0
57	MG	2A	3266	1/1	0.90	0.14	69,69,69,69	0
57	MG	2A	3743	1/1	0.90	0.21	70,70,70,70	0
57	MG	2A	3748	1/1	0.90	0.19	68,68,68,68	0
57	MG	2A	3473	1/1	0.90	0.22	54,54,54,54	0
57	MG	1A	3088	1/1	0.90	0.22	53,53,53,53	0
57	MG	2A	3100	1/1	0.90	0.23	70,70,70,70	0
57	MG	1A	3459	1/1	0.90	0.08	52,52,52,52	0
57	MG	1A	3461	1/1	0.90	0.12	62,62,62,62	0
57	MG	15	104	1/1	0.90	0.25	40,40,40,40	0
57	MG	1A	3089	1/1	0.90	0.08	76,76,76,76	0
57	MG	2A	3764	1/1	0.90	0.11	73,73,73,73	0
57	MG	2A	3765	1/1	0.90	0.09	63,63,63,63	0
57	MG	17	104	1/1	0.90	0.10	51,51,51,51	0
57	MG	1A	4089	1/1	0.90	0.13	58,58,58,58	0
57	MG	1a	1603	1/1	0.90	0.20	59,59,59,59	0
57	MG	2A	3771	1/1	0.90	0.28	61,61,61,61	0
57	MG	1A	4092	1/1	0.90	0.10	72,72,72,72	0
57	MG	1A	3309	1/1	0.90	0.18	58,58,58,58	0
57	MG	2A	3501	1/1	0.90	0.20	63,63,63,63	0
57	MG	1A	3830	1/1	0.90	0.18	45,45,45,45	0
57	MG	1A	3400	1/1	0.90	0.14	46,46,46,46	0
57	MG	2A	3506	1/1	0.90	0.19	62,62,62,62	0
57	MG	1A	3840	1/1	0.90	0.09	48,48,48,48	0
57	MG	1a	1623	1/1	0.90	0.28	58,58,58,58	0
57	MG	2A	3513	1/1	0.90	0.19	76,76,76,76	0
57	MG	2A	3292	1/1	0.90	0.12	58,58,58,58	0
57	MG	2A	3792	1/1	0.90	0.09	77,77,77,77	0
57	MG	2A	3515	1/1	0.90	0.09	34,34,34,34	0
57	MG	1a	1625	1/1	0.90	0.27	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1769	1/1	0.90	0.21	64,64,64,64	0
57	MG	1A	3966	1/1	0.90	0.13	40,40,40,40	0
57	MG	2A	3296	1/1	0.90	0.25	75,75,75,75	0
57	MG	2a	1772	1/1	0.90	0.20	62,62,62,62	0
57	MG	1A	3591	1/1	0.90	0.17	54,54,54,54	0
57	MG	1A	3025	1/1	0.90	0.15	55,55,55,55	0
57	MG	1A	3152	1/1	0.90	0.12	42,42,42,42	0
57	MG	1A	3319	1/1	0.90	0.23	67,67,67,67	0
57	MG	1A	3213	1/1	0.90	0.29	45,45,45,45	0
57	MG	2A	3530	1/1	0.90	0.16	39,39,39,39	0
57	MG	2A	3531	1/1	0.90	0.12	64,64,64,64	0
57	MG	1a	1642	1/1	0.90	0.31	64,64,64,64	0
57	MG	2A	3538	1/1	0.90	0.08	41,41,41,41	0
57	MG	1p	101	1/1	0.90	0.13	63,63,63,63	0
57	MG	1A	3158	1/1	0.90	0.23	62,62,62,62	0
57	MG	1A	3049	1/1	0.90	0.17	32,32,32,32	0
57	MG	1A	3278	1/1	0.90	0.09	53,53,53,53	0
57	MG	2a	1804	1/1	0.90	0.25	65,65,65,65	0
57	MG	2D	302	1/1	0.90	0.23	66,66,66,66	0
57	MG	2a	1807	1/1	0.90	0.17	69,69,69,69	0
57	MG	2A	3549	1/1	0.90	0.11	53,53,53,53	0
57	MG	1B	229	1/1	0.90	0.10	75,75,75,75	0
57	MG	2A	3174	1/1	0.90	0.21	60,60,60,60	0
57	MG	2A	3554	1/1	0.90	0.21	63,63,63,63	0
57	MG	1a	1658	1/1	0.90	0.23	65,65,65,65	0
57	MG	2a	1818	1/1	0.90	0.11	72,72,72,72	0
57	MG	1A	3859	1/1	0.90	0.14	50,50,50,50	0
57	MG	2A	3319	1/1	0.90	0.10	73,73,73,73	0
57	MG	2A	3180	1/1	0.90	0.15	60,60,60,60	0
57	MG	2F	305	1/1	0.90	0.10	63,63,63,63	0
57	MG	1A	3165	1/1	0.90	0.29	45,45,45,45	0
57	MG	2A	3322	1/1	0.90	0.09	57,57,57,57	0
57	MG	1A	3494	1/1	0.90	0.32	69,69,69,69	0
57	MG	1A	3422	1/1	0.90	0.17	48,48,48,48	0
57	MG	2A	3190	1/1	0.90	0.16	60,60,60,60	0
57	MG	1E	309	1/1	0.90	0.10	51,51,51,51	0
57	MG	1x	112	1/1	0.90	0.14	72,72,72,72	0
57	MG	1A	3646	1/1	0.90	0.14	34,34,34,34	0
57	MG	1A	3056	1/1	0.90	0.11	37,37,37,37	0
57	MG	2A	3013	1/1	0.90	0.43	78,78,78,78	0
57	MG	2A	3200	1/1	0.90	0.26	60,60,60,60	0
57	MG	2A	3017	1/1	0.90	0.16	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2I	102	1/1	0.90	0.21	68,68,68,68	0
57	MG	2A	3349	1/1	0.90	0.21	54,54,54,54	0
57	MG	1A	3511	1/1	0.90	0.36	58,58,58,58	0
57	MG	25	104	1/1	0.90	0.13	57,57,57,57	0
57	MG	1A	3825	1/1	0.91	0.09	38,38,38,38	0
57	MG	1A	4008	1/1	0.91	0.07	18,18,18,18	0
57	MG	2D	305	1/1	0.91	0.30	52,52,52,52	0
57	MG	1A	4009	1/1	0.91	0.19	56,56,56,56	0
57	MG	2A	3240	1/1	0.91	0.13	63,63,63,63	0
57	MG	2A	3504	1/1	0.91	0.29	72,72,72,72	0
57	MG	1A	4010	1/1	0.91	0.10	58,58,58,58	0
57	MG	2A	3507	1/1	0.91	0.09	61,61,61,61	0
57	MG	2E	307	1/1	0.91	0.12	45,45,45,45	0
57	MG	2A	3243	1/1	0.91	0.15	77,77,77,77	0
57	MG	1A	3283	1/1	0.91	0.08	50,50,50,50	0
57	MG	1A	3675	1/1	0.91	0.23	49,49,49,49	0
57	MG	1A	3364	1/1	0.91	0.19	34,34,34,34	0
57	MG	1A	3529	1/1	0.91	0.17	56,56,56,56	0
57	MG	1A	4024	1/1	0.91	0.10	22,22,22,22	0
57	MG	2A	3517	1/1	0.91	0.15	51,51,51,51	0
57	MG	1A	3367	1/1	0.91	0.08	47,47,47,47	0
57	MG	1A	3238	1/1	0.91	0.17	41,41,41,41	0
57	MG	2T	201	1/1	0.91	0.14	70,70,70,70	0
57	MG	2T	202	1/1	0.91	0.26	64,64,64,64	0
57	MG	1x	103	1/1	0.91	0.19	55,55,55,55	0
57	MG	15	101	1/1	0.91	0.18	39,39,39,39	0
57	MG	1x	106	1/1	0.91	0.27	61,61,61,61	0
57	MG	1A	3371	1/1	0.91	0.11	54,54,54,54	0
57	MG	2A	3258	1/1	0.91	0.10	51,51,51,51	0
57	MG	1A	3848	1/1	0.91	0.07	22,22,22,22	0
57	MG	1A	4035	1/1	0.91	0.27	58,58,58,58	0
57	MG	1A	3439	1/1	0.91	0.14	46,46,46,46	0
57	MG	1a	1601	1/1	0.91	0.24	55,55,55,55	0
57	MG	2A	3539	1/1	0.91	0.15	47,47,47,47	0
57	MG	28	101	1/1	0.91	0.23	70,70,70,70	0
57	MG	1a	1602	1/1	0.91	0.25	71,71,71,71	0
57	MG	2A	3007	1/1	0.91	0.13	59,59,59,59	0
57	MG	1A	3442	1/1	0.91	0.10	57,57,57,57	0
57	MG	1A	3545	1/1	0.91	0.41	61,61,61,61	0
57	MG	2A	3268	1/1	0.91	0.08	44,44,44,44	0
57	MG	1A	3444	1/1	0.91	0.10	57,57,57,57	0
57	MG	1A	3019	1/1	0.91	0.22	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1614	1/1	0.91	0.30	56,56,56,56	0
57	MG	2a	1609	1/1	0.91	0.22	71,71,71,71	0
57	MG	1A	3084	1/1	0.91	0.25	45,45,45,45	0
57	MG	1A	3552	1/1	0.91	0.14	42,42,42,42	0
57	MG	1A	3711	1/1	0.91	0.07	27,27,27,27	0
57	MG	2A	3039	1/1	0.91	0.13	56,56,56,56	0
57	MG	1a	1624	1/1	0.91	0.07	46,46,46,46	0
57	MG	1A	3718	1/1	0.91	0.09	20,20,20,20	0
57	MG	1A	3868	1/1	0.91	0.28	33,33,33,33	0
57	MG	2A	3567	1/1	0.91	0.10	59,59,59,59	0
57	MG	1A	3106	1/1	0.91	0.21	40,40,40,40	0
57	MG	1A	3876	1/1	0.91	0.10	61,61,61,61	0
57	MG	1a	1636	1/1	0.91	0.29	57,57,57,57	0
57	MG	1A	4066	1/1	0.91	0.11	52,52,52,52	0
57	MG	1A	3454	1/1	0.91	0.16	36,36,36,36	0
57	MG	1A	4072	1/1	0.91	0.15	57,57,57,57	0
57	MG	2A	3062	1/1	0.91	0.13	55,55,55,55	0
57	MG	2A	3295	1/1	0.91	0.23	70,70,70,70	0
57	MG	1A	4073	1/1	0.91	0.12	66,66,66,66	0
57	MG	2A	3066	1/1	0.91	0.19	68,68,68,68	0
57	MG	1a	1646	1/1	0.91	0.09	54,54,54,54	0
57	MG	1A	3245	1/1	0.91	0.17	77,77,77,77	0
57	MG	1A	3246	1/1	0.91	0.20	28,28,28,28	0
57	MG	1A	3561	1/1	0.91	0.12	39,39,39,39	0
57	MG	1a	1652	1/1	0.91	0.08	45,45,45,45	0
57	MG	1A	3565	1/1	0.91	0.08	23,23,23,23	0
57	MG	1A	3568	1/1	0.91	0.11	50,50,50,50	0
57	MG	1A	3899	1/1	0.91	0.12	66,66,66,66	0
57	MG	1a	1660	1/1	0.91	0.15	60,60,60,60	0
57	MG	1A	3900	1/1	0.91	0.14	65,65,65,65	0
57	MG	1A	3748	1/1	0.91	0.14	51,51,51,51	0
57	MG	1a	1663	1/1	0.91	0.22	68,68,68,68	0
57	MG	2A	3614	1/1	0.91	0.13	63,63,63,63	0
57	MG	1A	3570	1/1	0.91	0.18	50,50,50,50	0
57	MG	1A	3908	1/1	0.91	0.10	53,53,53,53	0
57	MG	2a	1663	1/1	0.91	0.19	67,67,67,67	0
57	MG	2A	3620	1/1	0.91	0.24	71,71,71,71	0
57	MG	2A	3626	1/1	0.91	0.15	62,62,62,62	0
57	MG	1A	3162	1/1	0.91	0.17	42,42,42,42	0
57	MG	1A	4099	1/1	0.91	0.26	53,53,53,53	0
57	MG	1A	3463	1/1	0.91	0.14	55,55,55,55	0
57	MG	1B	203	1/1	0.91	0.34	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3326	1/1	0.91	0.18	63,63,63,63	0
57	MG	2A	3328	1/1	0.91	0.20	61,61,61,61	0
57	MG	1a	1678	1/1	0.91	0.32	54,54,54,54	0
57	MG	1A	3204	1/1	0.91	0.14	53,53,53,53	0
57	MG	1A	3589	1/1	0.91	0.10	32,32,32,32	0
57	MG	1A	3251	1/1	0.91	0.20	64,64,64,64	0
57	MG	2A	3643	1/1	0.91	0.10	71,71,71,71	0
57	MG	1a	1686	1/1	0.91	0.29	62,62,62,62	0
57	MG	1A	3769	1/1	0.91	0.08	57,57,57,57	0
57	MG	2A	3114	1/1	0.91	0.07	62,62,62,62	0
57	MG	1A	3210	1/1	0.91	0.11	49,49,49,49	0
57	MG	2a	1692	1/1	0.91	0.13	73,73,73,73	0
57	MG	1B	218	1/1	0.91	0.16	46,46,46,46	0
57	MG	1A	3472	1/1	0.91	0.31	35,35,35,35	0
57	MG	2A	3128	1/1	0.91	0.20	56,56,56,56	0
57	MG	2A	3131	1/1	0.91	0.18	53,53,53,53	0
57	MG	2a	1699	1/1	0.91	0.16	57,57,57,57	0
57	MG	1A	3474	1/1	0.91	0.12	54,54,54,54	0
57	MG	1A	3776	1/1	0.91	0.08	46,46,46,46	0
57	MG	1a	1698	1/1	0.91	0.29	63,63,63,63	0
57	MG	2A	3671	1/1	0.91	0.09	73,73,73,73	0
57	MG	2A	3357	1/1	0.91	0.15	58,58,58,58	0
57	MG	2A	3676	1/1	0.91	0.09	61,61,61,61	0
57	MG	1A	3933	1/1	0.91	0.09	66,66,66,66	0
57	MG	2a	1713	1/1	0.91	0.33	68,68,68,68	0
57	MG	2A	3679	1/1	0.91	0.09	71,71,71,71	0
57	MG	1A	3163	1/1	0.91	0.25	59,59,59,59	0
57	MG	2a	1717	1/1	0.91	0.30	75,75,75,75	0
57	MG	2A	3146	1/1	0.91	0.16	66,66,66,66	0
57	MG	2a	1719	1/1	0.91	0.15	69,69,69,69	0
57	MG	1A	3617	1/1	0.91	0.09	25,25,25,25	0
57	MG	1a	1718	1/1	0.91	0.08	55,55,55,55	0
57	MG	2A	3365	1/1	0.91	0.12	69,69,69,69	0
57	MG	2A	3697	1/1	0.91	0.08	72,72,72,72	0
57	MG	1A	3085	1/1	0.91	0.17	54,54,54,54	0
57	MG	2A	3155	1/1	0.91	0.10	67,67,67,67	0
57	MG	2a	1728	1/1	0.91	0.12	64,64,64,64	0
57	MG	2A	3707	1/1	0.91	0.11	51,51,51,51	0
57	MG	2A	3369	1/1	0.91	0.15	70,70,70,70	0
57	MG	1B	232	1/1	0.91	0.18	68,68,68,68	0
57	MG	2A	3157	1/1	0.91	0.15	76,76,76,76	0
57	MG	2a	1740	1/1	0.91	0.11	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1747	1/1	0.91	0.12	72,72,72,72	0
57	MG	1B	233	1/1	0.91	0.15	61,61,61,61	0
57	MG	1A	3125	1/1	0.91	0.09	64,64,64,64	0
57	MG	2A	3722	1/1	0.91	0.20	61,61,61,61	0
57	MG	2A	3160	1/1	0.91	0.14	63,63,63,63	0
57	MG	2A	3386	1/1	0.91	0.16	56,56,56,56	0
57	MG	2a	1757	1/1	0.91	0.27	69,69,69,69	0
57	MG	2a	1758	1/1	0.91	0.12	67,67,67,67	0
57	MG	1E	302	1/1	0.91	0.19	36,36,36,36	0
57	MG	2A	3163	1/1	0.91	0.09	47,47,47,47	0
57	MG	2A	3394	1/1	0.91	0.19	57,57,57,57	0
57	MG	1A	3621	1/1	0.91	0.09	38,38,38,38	0
57	MG	1A	3220	1/1	0.91	0.12	51,51,51,51	0
57	MG	1A	3481	1/1	0.91	0.21	56,56,56,56	0
57	MG	1A	3326	1/1	0.91	0.29	62,62,62,62	0
57	MG	2A	3168	1/1	0.91	0.11	49,49,49,49	0
57	MG	1a	1739	1/1	0.91	0.15	67,67,67,67	0
57	MG	1A	3271	1/1	0.91	0.41	40,40,40,40	0
57	MG	1F	314	1/1	0.91	0.13	55,55,55,55	0
57	MG	2a	1773	1/1	0.91	0.14	68,68,68,68	0
57	MG	1A	3798	1/1	0.91	0.20	51,51,51,51	0
57	MG	1G	203	1/1	0.91	0.16	68,68,68,68	0
57	MG	2A	3756	1/1	0.91	0.19	48,48,48,48	0
57	MG	1a	1747	1/1	0.91	0.10	59,59,59,59	0
57	MG	1I	201	1/1	0.91	0.10	65,65,65,65	0
57	MG	2A	3417	1/1	0.91	0.17	63,63,63,63	0
57	MG	1A	3331	1/1	0.91	0.12	56,56,56,56	0
57	MG	2a	1785	1/1	0.91	0.28	66,66,66,66	0
57	MG	2a	1787	1/1	0.91	0.12	67,67,67,67	0
57	MG	2A	3184	1/1	0.91	0.27	66,66,66,66	0
57	MG	1A	3276	1/1	0.91	0.15	45,45,45,45	0
57	MG	1A	3026	1/1	0.91	0.34	65,65,65,65	0
57	MG	1P	205	1/1	0.91	0.14	41,41,41,41	0
57	MG	2A	3194	1/1	0.91	0.13	59,59,59,59	0
57	MG	2a	1794	1/1	0.91	0.19	67,67,67,67	0
57	MG	2a	1795	1/1	0.91	0.31	72,72,72,72	0
57	MG	1a	1763	1/1	0.91	0.16	64,64,64,64	0
57	MG	2a	1800	1/1	0.91	0.17	56,56,56,56	0
57	MG	2a	1801	1/1	0.91	0.13	83,83,83,83	0
57	MG	1A	3495	1/1	0.91	0.10	59,59,59,59	0
57	MG	1A	3977	1/1	0.91	0.14	56,56,56,56	0
57	MG	1a	1772	1/1	0.91	0.09	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1778	1/1	0.91	0.09	78,78,78,78	0
57	MG	2A	3444	1/1	0.91	0.25	70,70,70,70	0
57	MG	1A	3340	1/1	0.91	0.13	49,49,49,49	0
57	MG	2A	3207	1/1	0.91	0.32	56,56,56,56	0
57	MG	2a	1814	1/1	0.91	0.11	60,60,60,60	0
57	MG	1a	1780	1/1	0.91	0.09	64,64,64,64	0
57	MG	1a	1789	1/1	0.91	0.30	60,60,60,60	0
57	MG	2A	3788	1/1	0.91	0.12	64,64,64,64	0
57	MG	2e	201	1/1	0.91	0.07	73,73,73,73	0
57	MG	2f	201	1/1	0.91	0.14	49,49,49,49	0
57	MG	1A	3345	1/1	0.91	0.10	43,43,43,43	0
57	MG	1A	3808	1/1	0.91	0.09	22,22,22,22	0
57	MG	2A	3464	1/1	0.91	0.16	59,59,59,59	0
57	MG	1A	3663	1/1	0.91	0.11	28,28,28,28	0
57	MG	1A	3814	1/1	0.91	0.09	41,41,41,41	0
57	MG	1T	203	1/1	0.91	0.14	62,62,62,62	0
57	MG	1a	1799	1/1	0.91	0.13	73,73,73,73	0
57	MG	1U	202	1/1	0.91	0.12	36,36,36,36	0
57	MG	2v	103	1/1	0.91	0.20	60,60,60,60	0
57	MG	2v	104	1/1	0.91	0.20	62,62,62,62	0
57	MG	1U	205	1/1	0.91	0.14	36,36,36,36	0
57	MG	2A	3481	1/1	0.91	0.14	52,52,52,52	0
57	MG	1A	3064	1/1	0.91	0.15	48,48,48,48	0
57	MG	1A	3992	1/1	0.91	0.13	53,53,53,53	0
57	MG	2x	101	1/1	0.91	0.18	68,68,68,68	0
57	MG	2A	3484	1/1	0.91	0.10	32,32,32,32	0
57	MG	2x	103	1/1	0.91	0.13	65,65,65,65	0
57	MG	1A	3667	1/1	0.91	0.14	57,57,57,57	0
57	MG	2A	3486	1/1	0.91	0.18	60,60,60,60	0
57	MG	1W	201	1/1	0.91	0.24	49,49,49,49	0
57	MG	1A	3235	1/1	0.91	0.24	71,71,71,71	0
57	MG	1A	3001	1/1	0.91	0.07	43,43,43,43	0
57	MG	1a	1811	1/1	0.91	0.18	61,61,61,61	0
57	MG	2A	3064	1/1	0.92	0.09	49,49,49,49	0
57	MG	2A	3276	1/1	0.92	0.09	52,52,52,52	0
57	MG	1A	3118	1/1	0.92	0.23	52,52,52,52	0
57	MG	1A	3184	1/1	0.92	0.13	30,30,30,30	0
57	MG	1A	3493	1/1	0.92	0.25	49,49,49,49	0
57	MG	2P	201	1/1	0.92	0.08	63,63,63,63	0
57	MG	1A	3832	1/1	0.92	0.12	37,37,37,37	0
57	MG	1A	3321	1/1	0.92	0.12	41,41,41,41	0
57	MG	1A	3218	1/1	0.92	0.20	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3537	1/1	0.92	0.20	52,52,52,52	0
57	MG	2A	3284	1/1	0.92	0.11	66,66,66,66	0
57	MG	1F	305	1/1	0.92	0.10	60,60,60,60	0
57	MG	2A	3541	1/1	0.92	0.22	63,63,63,63	0
57	MG	1a	1691	1/1	0.92	0.18	56,56,56,56	0
57	MG	1A	3991	1/1	0.92	0.07	56,56,56,56	0
57	MG	2A	3290	1/1	0.92	0.07	64,64,64,64	0
57	MG	1A	3598	1/1	0.92	0.07	19,19,19,19	0
57	MG	1G	202	1/1	0.92	0.32	67,67,67,67	0
57	MG	2A	3550	1/1	0.92	0.15	68,68,68,68	0
57	MG	25	102	1/1	0.92	0.20	45,45,45,45	0
57	MG	2A	3551	1/1	0.92	0.13	40,40,40,40	0
57	MG	1A	3123	1/1	0.92	0.22	52,52,52,52	0
57	MG	1H	201	1/1	0.92	0.18	48,48,48,48	0
57	MG	1a	1700	1/1	0.92	0.19	50,50,50,50	0
57	MG	28	103	1/1	0.92	0.10	57,57,57,57	0
57	MG	2A	3087	1/1	0.92	0.24	69,69,69,69	0
57	MG	2A	3558	1/1	0.92	0.12	46,46,46,46	0
57	MG	1a	1703	1/1	0.92	0.32	53,53,53,53	0
57	MG	1A	3380	1/1	0.92	0.14	68,68,68,68	0
57	MG	2a	1603	1/1	0.92	0.21	58,58,58,58	0
57	MG	1a	1710	1/1	0.92	0.10	57,57,57,57	0
57	MG	1N	204	1/1	0.92	0.19	44,44,44,44	0
57	MG	1A	3736	1/1	0.92	0.11	33,33,33,33	0
57	MG	2A	3097	1/1	0.92	0.31	50,50,50,50	0
57	MG	2A	3566	1/1	0.92	0.08	33,33,33,33	0
57	MG	1A	3739	1/1	0.92	0.09	27,27,27,27	0
57	MG	1O	205	1/1	0.92	0.09	48,48,48,48	0
57	MG	2a	1613	1/1	0.92	0.20	53,53,53,53	0
57	MG	1A	4007	1/1	0.92	0.17	77,77,77,77	0
57	MG	2a	1616	1/1	0.92	0.19	79,79,79,79	0
57	MG	1a	1723	1/1	0.92	0.14	58,58,58,58	0
57	MG	1A	3740	1/1	0.92	0.06	71,71,71,71	0
57	MG	2A	3313	1/1	0.92	0.10	63,63,63,63	0
57	MG	2A	3314	1/1	0.92	0.43	74,74,74,74	0
57	MG	2a	1623	1/1	0.92	0.09	63,63,63,63	0
57	MG	1Q	204	1/1	0.92	0.13	54,54,54,54	0
57	MG	1A	3507	1/1	0.92	0.32	53,53,53,53	0
57	MG	1a	1731	1/1	0.92	0.15	57,57,57,57	0
57	MG	2A	3318	1/1	0.92	0.12	61,61,61,61	0
57	MG	2A	3116	1/1	0.92	0.17	65,65,65,65	0
57	MG	1A	3746	1/1	0.92	0.08	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3591	1/1	0.92	0.08	66,66,66,66	0
57	MG	1A	3608	1/1	0.92	0.10	44,44,44,44	0
57	MG	2A	3596	1/1	0.92	0.13	56,56,56,56	0
57	MG	2a	1635	1/1	0.92	0.21	69,69,69,69	0
57	MG	1A	3509	1/1	0.92	0.17	35,35,35,35	0
57	MG	2A	3598	1/1	0.92	0.12	61,61,61,61	0
57	MG	2A	3323	1/1	0.92	0.11	67,67,67,67	0
57	MG	2A	3324	1/1	0.92	0.28	55,55,55,55	0
57	MG	1A	4013	1/1	0.92	0.18	41,41,41,41	0
57	MG	1A	3754	1/1	0.92	0.08	19,19,19,19	0
57	MG	1A	4020	1/1	0.92	0.10	47,47,47,47	0
57	MG	1A	3510	1/1	0.92	0.20	54,54,54,54	0
57	MG	2A	3137	1/1	0.92	0.18	58,58,58,58	0
57	MG	2A	3138	1/1	0.92	0.13	45,45,45,45	0
57	MG	2A	3334	1/1	0.92	0.36	54,54,54,54	0
57	MG	2A	3139	1/1	0.92	0.24	61,61,61,61	0
57	MG	2A	3340	1/1	0.92	0.36	56,56,56,56	0
57	MG	1A	3865	1/1	0.92	0.10	47,47,47,47	0
57	MG	2a	1655	1/1	0.92	0.09	68,68,68,68	0
57	MG	2a	1657	1/1	0.92	0.15	62,62,62,62	0
57	MG	1A	3866	1/1	0.92	0.12	44,44,44,44	0
57	MG	2A	3627	1/1	0.92	0.16	61,61,61,61	0
57	MG	2A	3344	1/1	0.92	0.21	63,63,63,63	0
57	MG	1A	3867	1/1	0.92	0.11	33,33,33,33	0
57	MG	1A	3190	1/1	0.92	0.12	46,46,46,46	0
57	MG	2a	1668	1/1	0.92	0.14	58,58,58,58	0
57	MG	1A	3382	1/1	0.92	0.20	59,59,59,59	0
57	MG	2A	3348	1/1	0.92	0.28	58,58,58,58	0
57	MG	1A	3874	1/1	0.92	0.14	52,52,52,52	0
57	MG	1a	1758	1/1	0.92	0.08	63,63,63,63	0
57	MG	2A	3638	1/1	0.92	0.07	68,68,68,68	0
57	MG	2a	1676	1/1	0.92	0.29	61,61,61,61	0
57	MG	2A	3351	1/1	0.92	0.24	57,57,57,57	0
57	MG	1Y	201	1/1	0.92	0.26	69,69,69,69	0
57	MG	1Y	202	1/1	0.92	0.35	46,46,46,46	0
57	MG	1Z	301	1/1	0.92	0.15	67,67,67,67	0
57	MG	2A	3355	1/1	0.92	0.12	42,42,42,42	0
57	MG	1A	3384	1/1	0.92	0.09	51,51,51,51	0
57	MG	1A	3632	1/1	0.92	0.10	29,29,29,29	0
57	MG	2a	1687	1/1	0.92	0.14	57,57,57,57	0
57	MG	1A	3385	1/1	0.92	0.11	63,63,63,63	0
57	MG	2A	3650	1/1	0.92	0.27	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1690	1/1	0.92	0.12	66,66,66,66	0
57	MG	1a	1777	1/1	0.92	0.07	85,85,85,85	0
57	MG	1A	3639	1/1	0.92	0.18	61,61,61,61	0
57	MG	1A	4041	1/1	0.92	0.07	53,53,53,53	0
57	MG	2A	3656	1/1	0.92	0.13	56,56,56,56	0
57	MG	1A	3333	1/1	0.92	0.15	60,60,60,60	0
57	MG	1A	3157	1/1	0.92	0.15	52,52,52,52	0
57	MG	1A	3532	1/1	0.92	0.20	46,46,46,46	0
57	MG	2A	3663	1/1	0.92	0.12	66,66,66,66	0
57	MG	2a	1702	1/1	0.92	0.13	64,64,64,64	0
57	MG	1A	3016	1/1	0.92	0.20	66,66,66,66	0
57	MG	2A	3665	1/1	0.92	0.13	70,70,70,70	0
57	MG	2A	3666	1/1	0.92	0.15	72,72,72,72	0
57	MG	2A	3668	1/1	0.92	0.16	56,56,56,56	0
57	MG	1a	1794	1/1	0.92	0.14	57,57,57,57	0
57	MG	1A	3396	1/1	0.92	0.13	53,53,53,53	0
57	MG	2A	3376	1/1	0.92	0.21	62,62,62,62	0
57	MG	1A	3537	1/1	0.92	0.12	45,45,45,45	0
57	MG	2A	3175	1/1	0.92	0.23	65,65,65,65	0
57	MG	1A	3398	1/1	0.92	0.12	45,45,45,45	0
57	MG	2A	3685	1/1	0.92	0.13	88,88,88,88	0
57	MG	1A	4063	1/1	0.92	0.10	71,71,71,71	0
57	MG	2A	3689	1/1	0.92	0.16	54,54,54,54	0
57	MG	1A	3233	1/1	0.92	0.12	47,47,47,47	0
57	MG	2A	3388	1/1	0.92	0.25	66,66,66,66	0
57	MG	1A	3787	1/1	0.92	0.33	62,62,62,62	0
57	MG	2A	3696	1/1	0.92	0.13	73,73,73,73	0
57	MG	1A	3788	1/1	0.92	0.20	59,59,59,59	0
57	MG	1A	3341	1/1	0.92	0.15	35,35,35,35	0
57	MG	2a	1729	1/1	0.92	0.16	74,74,74,74	0
57	MG	2A	3395	1/1	0.92	0.20	58,58,58,58	0
57	MG	2A	3396	1/1	0.92	0.18	48,48,48,48	0
57	MG	2A	3397	1/1	0.92	0.28	62,62,62,62	0
57	MG	1a	1805	1/1	0.92	0.25	53,53,53,53	0
57	MG	2A	3187	1/1	0.92	0.09	63,63,63,63	0
57	MG	2a	1745	1/1	0.92	0.11	75,75,75,75	0
57	MG	2A	3714	1/1	0.92	0.09	52,52,52,52	0
57	MG	2A	3188	1/1	0.92	0.18	51,51,51,51	0
57	MG	1A	3790	1/1	0.92	0.11	70,70,70,70	0
57	MG	2A	3192	1/1	0.92	0.14	45,45,45,45	0
57	MG	2a	1753	1/1	0.92	0.16	52,52,52,52	0
57	MG	1A	4074	1/1	0.92	0.12	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3918	1/1	0.92	0.14	65,65,65,65	0
57	MG	1A	3920	1/1	0.92	0.16	52,52,52,52	0
57	MG	1A	4077	1/1	0.92	0.07	61,61,61,61	0
57	MG	1A	3791	1/1	0.92	0.12	40,40,40,40	0
57	MG	1a	1606	1/1	0.92	0.15	60,60,60,60	0
57	MG	1A	4083	1/1	0.92	0.17	31,31,31,31	0
57	MG	1e	201	1/1	0.92	0.16	72,72,72,72	0
57	MG	1h	201	1/1	0.92	0.07	66,66,66,66	0
57	MG	2A	3740	1/1	0.92	0.10	62,62,62,62	0
57	MG	2a	1766	1/1	0.92	0.26	61,61,61,61	0
57	MG	1A	3197	1/1	0.92	0.14	39,39,39,39	0
57	MG	2A	3210	1/1	0.92	0.19	63,63,63,63	0
57	MG	2A	3746	1/1	0.92	0.11	55,55,55,55	0
57	MG	1l	3201	1/1	0.92	0.18	60,60,60,60	0
57	MG	1A	3406	1/1	0.92	0.29	41,41,41,41	0
57	MG	2A	3752	1/1	0.92	0.19	71,71,71,71	0
57	MG	2a	1774	1/1	0.92	0.18	68,68,68,68	0
57	MG	1A	3302	1/1	0.92	0.12	54,54,54,54	0
57	MG	1A	3093	1/1	0.92	0.11	47,47,47,47	0
57	MG	1A	3126	1/1	0.92	0.17	48,48,48,48	0
57	MG	2a	1778	1/1	0.92	0.21	56,56,56,56	0
57	MG	2A	3218	1/1	0.92	0.10	58,58,58,58	0
57	MG	2A	3220	1/1	0.92	0.10	63,63,63,63	0
57	MG	1A	4091	1/1	0.92	0.17	40,40,40,40	0
57	MG	1A	3275	1/1	0.92	0.07	53,53,53,53	0
57	MG	2a	1784	1/1	0.92	0.25	65,65,65,65	0
57	MG	1A	3416	1/1	0.92	0.23	67,67,67,67	0
57	MG	1A	4094	1/1	0.92	0.21	42,42,42,42	0
57	MG	1a	1635	1/1	0.92	0.12	49,49,49,49	0
57	MG	1A	3417	1/1	0.92	0.15	45,45,45,45	0
57	MG	2A	3458	1/1	0.92	0.11	46,46,46,46	0
57	MG	1A	3938	1/1	0.92	0.11	66,66,66,66	0
57	MG	1A	3133	1/1	0.92	0.11	48,48,48,48	0
57	MG	1A	3942	1/1	0.92	0.09	31,31,31,31	0
57	MG	1a	1641	1/1	0.92	0.16	61,61,61,61	0
57	MG	1A	3943	1/1	0.92	0.09	33,33,33,33	0
57	MG	2a	1799	1/1	0.92	0.25	60,60,60,60	0
57	MG	1a	1645	1/1	0.92	0.21	54,54,54,54	0
57	MG	2A	3780	1/1	0.92	0.18	67,67,67,67	0
57	MG	2A	3004	1/1	0.92	0.18	50,50,50,50	0
57	MG	2A	3475	1/1	0.92	0.07	46,46,46,46	0
57	MG	2a	1806	1/1	0.92	0.17	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3476	1/1	0.92	0.12	71,71,71,71	0
57	MG	2A	3005	1/1	0.92	0.20	56,56,56,56	0
57	MG	1B	206	1/1	0.92	0.10	47,47,47,47	0
57	MG	1A	3681	1/1	0.92	0.16	62,62,62,62	0
57	MG	1B	209	1/1	0.92	0.25	57,57,57,57	0
57	MG	1A	3946	1/1	0.92	0.10	28,28,28,28	0
57	MG	1A	3104	1/1	0.92	0.26	29,29,29,29	0
57	MG	1A	3563	1/1	0.92	0.10	25,25,25,25	0
57	MG	1A	3480	1/1	0.92	0.11	52,52,52,52	0
57	MG	2d	301	1/1	0.92	0.10	69,69,69,69	0
57	MG	2A	3027	1/1	0.92	0.12	45,45,45,45	0
57	MG	2A	3489	1/1	0.92	0.16	60,60,60,60	0
57	MG	1A	3042	1/1	0.92	0.23	35,35,35,35	0
57	MG	2B	205	1/1	0.92	0.25	57,57,57,57	0
57	MG	2A	3033	1/1	0.92	0.17	55,55,55,55	0
57	MG	1A	3957	1/1	0.92	0.06	26,26,26,26	0
57	MG	2A	3036	1/1	0.92	0.18	66,66,66,66	0
57	MG	2A	3038	1/1	0.92	0.18	70,70,70,70	0
57	MG	1A	3698	1/1	0.92	0.08	25,25,25,25	0
57	MG	2B	212	1/1	0.92	0.23	65,65,65,65	0
57	MG	2A	3040	1/1	0.92	0.14	60,60,60,60	0
57	MG	2A	3041	1/1	0.92	0.16	62,62,62,62	0
57	MG	2A	3505	1/1	0.92	0.19	59,59,59,59	0
57	MG	1A	3816	1/1	0.92	0.32	41,41,41,41	0
57	MG	1A	3817	1/1	0.92	0.15	61,61,61,61	0
57	MG	1A	3369	1/1	0.92	0.14	55,55,55,55	0
57	MG	1A	3315	1/1	0.92	0.17	61,61,61,61	0
57	MG	1A	3974	1/1	0.92	0.09	62,62,62,62	0
57	MG	2A	3051	1/1	0.92	0.20	56,56,56,56	0
57	MG	1a	1669	1/1	0.92	0.21	64,64,64,64	0
57	MG	1A	3579	1/1	0.92	0.08	34,34,34,34	0
57	MG	1A	3582	1/1	0.92	0.11	51,51,51,51	0
57	MG	1D	312	1/1	0.92	0.14	39,39,39,39	0
57	MG	2x	109	1/1	0.92	0.13	70,70,70,70	0
57	MG	1a	1674	1/1	0.92	0.24	67,67,67,67	0
57	MG	2A	3520	1/1	0.92	0.12	41,41,41,41	0
57	MG	2E	308	1/1	0.93	0.11	61,61,61,61	0
57	MG	2A	3016	1/1	0.93	0.20	39,39,39,39	0
57	MG	1A	3361	1/1	0.93	0.29	33,33,33,33	0
57	MG	1A	3813	1/1	0.93	0.12	32,32,32,32	0
57	MG	2F	307	1/1	0.93	0.25	51,51,51,51	0
57	MG	1B	205	1/1	0.93	0.25	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3691	1/1	0.93	0.09	45,45,45,45	0
57	MG	1A	3948	1/1	0.93	0.13	40,40,40,40	0
57	MG	1a	1643	1/1	0.93	0.23	67,67,67,67	0
57	MG	2A	3029	1/1	0.93	0.22	48,48,48,48	0
57	MG	2Q	201	1/1	0.93	0.08	65,65,65,65	0
57	MG	1a	1644	1/1	0.93	0.12	49,49,49,49	0
57	MG	2R	201	1/1	0.93	0.33	50,50,50,50	0
57	MG	1A	3567	1/1	0.93	0.09	30,30,30,30	0
57	MG	1B	210	1/1	0.93	0.17	51,51,51,51	0
57	MG	1B	211	1/1	0.93	0.27	64,64,64,64	0
57	MG	1B	212	1/1	0.93	0.18	60,60,60,60	0
57	MG	1A	3002	1/1	0.93	0.12	60,60,60,60	0
57	MG	1A	3951	1/1	0.93	0.15	52,52,52,52	0
57	MG	1a	1653	1/1	0.93	0.23	50,50,50,50	0
57	MG	1a	1656	1/1	0.93	0.14	49,49,49,49	0
57	MG	2A	3272	1/1	0.93	0.14	52,52,52,52	0
57	MG	2A	3273	1/1	0.93	0.18	70,70,70,70	0
57	MG	1A	3569	1/1	0.93	0.11	39,39,39,39	0
57	MG	1A	3820	1/1	0.93	0.14	56,56,56,56	0
57	MG	1A	3059	1/1	0.93	0.19	44,44,44,44	0
57	MG	2A	3049	1/1	0.93	0.15	67,67,67,67	0
57	MG	27	102	1/1	0.93	0.10	57,57,57,57	0
57	MG	1A	3182	1/1	0.93	0.12	51,51,51,51	0
57	MG	1A	3578	1/1	0.93	0.17	35,35,35,35	0
57	MG	2A	3052	1/1	0.93	0.16	59,59,59,59	0
57	MG	1A	3487	1/1	0.93	0.18	41,41,41,41	0
57	MG	1A	3581	1/1	0.93	0.10	39,39,39,39	0
57	MG	2A	3555	1/1	0.93	0.18	50,50,50,50	0
57	MG	2A	3556	1/1	0.93	0.13	62,62,62,62	0
57	MG	1A	3421	1/1	0.93	0.18	52,52,52,52	0
57	MG	2a	1604	1/1	0.93	0.28	73,73,73,73	0
57	MG	1B	230	1/1	0.93	0.09	49,49,49,49	0
57	MG	2A	3287	1/1	0.93	0.28	58,58,58,58	0
57	MG	2a	1607	1/1	0.93	0.43	69,69,69,69	0
57	MG	1a	1667	1/1	0.93	0.08	50,50,50,50	0
57	MG	2A	3063	1/1	0.93	0.12	53,53,53,53	0
57	MG	1A	3712	1/1	0.93	0.14	61,61,61,61	0
57	MG	1A	3831	1/1	0.93	0.13	41,41,41,41	0
57	MG	1A	3978	1/1	0.93	0.09	66,66,66,66	0
57	MG	1A	3715	1/1	0.93	0.06	20,20,20,20	0
57	MG	1a	1672	1/1	0.93	0.27	70,70,70,70	0
57	MG	1A	3834	1/1	0.93	0.14	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3836	1/1	0.93	0.21	40,40,40,40	0
57	MG	1A	3716	1/1	0.93	0.11	44,44,44,44	0
57	MG	2A	3075	1/1	0.93	0.15	57,57,57,57	0
57	MG	2A	3076	1/1	0.93	0.09	52,52,52,52	0
57	MG	2A	3577	1/1	0.93	0.12	53,53,53,53	0
57	MG	1A	3986	1/1	0.93	0.09	41,41,41,41	0
57	MG	1E	308	1/1	0.93	0.18	40,40,40,40	0
57	MG	1A	3094	1/1	0.93	0.21	66,66,66,66	0
57	MG	2A	3081	1/1	0.93	0.07	52,52,52,52	0
57	MG	2A	3583	1/1	0.93	0.09	43,43,43,43	0
57	MG	1a	1685	1/1	0.93	0.23	61,61,61,61	0
57	MG	2A	3585	1/1	0.93	0.27	57,57,57,57	0
57	MG	1A	3006	1/1	0.93	0.17	55,55,55,55	0
57	MG	2A	3589	1/1	0.93	0.12	54,54,54,54	0
57	MG	2A	3308	1/1	0.93	0.25	70,70,70,70	0
57	MG	2A	3084	1/1	0.93	0.09	41,41,41,41	0
57	MG	1a	1687	1/1	0.93	0.32	55,55,55,55	0
57	MG	2A	3595	1/1	0.93	0.20	56,56,56,56	0
57	MG	2A	3311	1/1	0.93	0.11	65,65,65,65	0
57	MG	1F	303	1/1	0.93	0.12	31,31,31,31	0
57	MG	1A	3843	1/1	0.93	0.09	31,31,31,31	0
57	MG	1A	3586	1/1	0.93	0.06	33,33,33,33	0
57	MG	2A	3602	1/1	0.93	0.08	31,31,31,31	0
57	MG	1F	307	1/1	0.93	0.09	38,38,38,38	0
57	MG	1a	1693	1/1	0.93	0.13	61,61,61,61	0
57	MG	1F	309	1/1	0.93	0.22	29,29,29,29	0
57	MG	1F	311	1/1	0.93	0.09	46,46,46,46	0
57	MG	2a	1651	1/1	0.93	0.15	67,67,67,67	0
57	MG	2A	3096	1/1	0.93	0.12	62,62,62,62	0
57	MG	1F	312	1/1	0.93	0.16	54,54,54,54	0
57	MG	1A	3253	1/1	0.93	0.09	60,60,60,60	0
57	MG	1A	3590	1/1	0.93	0.08	24,24,24,24	0
57	MG	1A	3316	1/1	0.93	0.08	55,55,55,55	0
57	MG	1A	3595	1/1	0.93	0.10	36,36,36,36	0
57	MG	2A	3104	1/1	0.93	0.23	55,55,55,55	0
57	MG	2a	1664	1/1	0.93	0.15	64,64,64,64	0
57	MG	1a	1708	1/1	0.93	0.17	60,60,60,60	0
57	MG	2A	3109	1/1	0.93	0.16	45,45,45,45	0
57	MG	1G	204	1/1	0.93	0.14	62,62,62,62	0
57	MG	2A	3629	1/1	0.93	0.12	61,61,61,61	0
57	MG	2A	3332	1/1	0.93	0.21	39,39,39,39	0
57	MG	1A	4000	1/1	0.93	0.09	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3113	1/1	0.93	0.11	52,52,52,52	0
57	MG	2a	1674	1/1	0.93	0.27	59,59,59,59	0
57	MG	2A	3335	1/1	0.93	0.30	62,62,62,62	0
57	MG	2A	3336	1/1	0.93	0.23	47,47,47,47	0
57	MG	1A	4006	1/1	0.93	0.08	59,59,59,59	0
57	MG	2A	3637	1/1	0.93	0.11	54,54,54,54	0
57	MG	2A	3115	1/1	0.93	0.11	61,61,61,61	0
57	MG	1N	201	1/1	0.93	0.17	45,45,45,45	0
57	MG	2A	3342	1/1	0.93	0.31	54,54,54,54	0
57	MG	1A	3285	1/1	0.93	0.28	52,52,52,52	0
57	MG	2A	3120	1/1	0.93	0.09	53,53,53,53	0
57	MG	1N	205	1/1	0.93	0.11	44,44,44,44	0
57	MG	1A	3256	1/1	0.93	0.07	56,56,56,56	0
57	MG	2A	3646	1/1	0.93	0.10	56,56,56,56	0
57	MG	2A	3124	1/1	0.93	0.25	46,46,46,46	0
57	MG	1A	3505	1/1	0.93	0.15	33,33,33,33	0
57	MG	2A	3129	1/1	0.93	0.16	41,41,41,41	0
57	MG	2a	1693	1/1	0.93	0.22	65,65,65,65	0
57	MG	1A	3288	1/1	0.93	0.18	42,42,42,42	0
57	MG	2A	3132	1/1	0.93	0.21	64,64,64,64	0
57	MG	1A	3603	1/1	0.93	0.10	32,32,32,32	0
57	MG	1P	203	1/1	0.93	0.27	32,32,32,32	0
57	MG	2A	3657	1/1	0.93	0.10	49,49,49,49	0
57	MG	1A	3377	1/1	0.93	0.12	37,37,37,37	0
57	MG	1a	1733	1/1	0.93	0.21	71,71,71,71	0
57	MG	2A	3660	1/1	0.93	0.10	42,42,42,42	0
57	MG	1A	3325	1/1	0.93	0.12	39,39,39,39	0
57	MG	1Q	206	1/1	0.93	0.13	43,43,43,43	0
57	MG	2A	3142	1/1	0.93	0.11	62,62,62,62	0
57	MG	1A	4014	1/1	0.93	0.18	29,29,29,29	0
57	MG	1R	204	1/1	0.93	0.11	30,30,30,30	0
57	MG	2a	1712	1/1	0.93	0.17	51,51,51,51	0
57	MG	1A	3612	1/1	0.93	0.10	46,46,46,46	0
57	MG	2A	3147	1/1	0.93	0.08	56,56,56,56	0
57	MG	2A	3674	1/1	0.93	0.09	52,52,52,52	0
57	MG	1a	1741	1/1	0.93	0.09	58,58,58,58	0
57	MG	1A	3292	1/1	0.93	0.28	47,47,47,47	0
57	MG	1A	3513	1/1	0.93	0.17	50,50,50,50	0
57	MG	1S	202	1/1	0.93	0.10	54,54,54,54	0
57	MG	1a	1746	1/1	0.93	0.12	58,58,58,58	0
57	MG	2A	3681	1/1	0.93	0.06	40,40,40,40	0
57	MG	1A	3211	1/1	0.93	0.10	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3378	1/1	0.93	0.16	59,59,59,59	0
57	MG	2a	1725	1/1	0.93	0.06	84,84,84,84	0
57	MG	1A	3873	1/1	0.93	0.19	42,42,42,42	0
57	MG	1a	1751	1/1	0.93	0.12	64,64,64,64	0
57	MG	1A	3518	1/1	0.93	0.12	54,54,54,54	0
57	MG	2A	3383	1/1	0.93	0.11	42,42,42,42	0
57	MG	1A	3875	1/1	0.93	0.07	31,31,31,31	0
57	MG	1A	3440	1/1	0.93	0.15	46,46,46,46	0
57	MG	1A	3878	1/1	0.93	0.07	48,48,48,48	0
57	MG	2A	3389	1/1	0.93	0.28	54,54,54,54	0
57	MG	2a	1742	1/1	0.93	0.13	47,47,47,47	0
57	MG	2A	3703	1/1	0.93	0.09	63,63,63,63	0
57	MG	1A	4036	1/1	0.93	0.15	50,50,50,50	0
57	MG	1A	3767	1/1	0.93	0.08	38,38,38,38	0
57	MG	2A	3710	1/1	0.93	0.14	58,58,58,58	0
57	MG	2a	1750	1/1	0.93	0.23	63,63,63,63	0
57	MG	2A	3393	1/1	0.93	0.17	43,43,43,43	0
57	MG	1A	3880	1/1	0.93	0.09	51,51,51,51	0
57	MG	1A	3330	1/1	0.93	0.17	39,39,39,39	0
57	MG	2A	3170	1/1	0.93	0.18	62,62,62,62	0
57	MG	1a	1770	1/1	0.93	0.09	53,53,53,53	0
57	MG	1X	104	1/1	0.93	0.10	40,40,40,40	0
57	MG	1A	3116	1/1	0.93	0.26	45,45,45,45	0
57	MG	2A	3727	1/1	0.93	0.14	50,50,50,50	0
57	MG	1A	3156	1/1	0.93	0.31	35,35,35,35	0
57	MG	1A	3895	1/1	0.93	0.08	53,53,53,53	0
57	MG	10	101	1/1	0.93	0.20	43,43,43,43	0
57	MG	1A	3334	1/1	0.93	0.10	53,53,53,53	0
57	MG	1A	4046	1/1	0.93	0.11	43,43,43,43	0
57	MG	2A	3409	1/1	0.93	0.11	54,54,54,54	0
57	MG	1A	3389	1/1	0.93	0.20	38,38,38,38	0
57	MG	1A	4049	1/1	0.93	0.10	44,44,44,44	0
57	MG	1A	3780	1/1	0.93	0.08	37,37,37,37	0
57	MG	1A	3782	1/1	0.93	0.08	34,34,34,34	0
57	MG	2A	3742	1/1	0.93	0.17	48,48,48,48	0
57	MG	10	110	1/1	0.93	0.06	42,42,42,42	0
57	MG	1A	3904	1/1	0.93	0.08	74,74,74,74	0
57	MG	2A	3191	1/1	0.93	0.20	56,56,56,56	0
57	MG	1A	3534	1/1	0.93	0.07	40,40,40,40	0
57	MG	1A	3391	1/1	0.93	0.12	36,36,36,36	0
57	MG	1A	3648	1/1	0.93	0.09	20,20,20,20	0
57	MG	2a	1780	1/1	0.93	0.23	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3215	1/1	0.93	0.12	48,48,48,48	0
57	MG	1A	3910	1/1	0.93	0.19	67,67,67,67	0
57	MG	2A	3197	1/1	0.93	0.25	58,58,58,58	0
57	MG	1A	4069	1/1	0.93	0.08	63,63,63,63	0
57	MG	2A	3434	1/1	0.93	0.09	38,38,38,38	0
57	MG	1A	4071	1/1	0.93	0.13	59,59,59,59	0
57	MG	2A	3763	1/1	0.93	0.11	60,60,60,60	0
57	MG	2A	3438	1/1	0.93	0.11	69,69,69,69	0
57	MG	15	102	1/1	0.93	0.15	36,36,36,36	0
57	MG	2A	3440	1/1	0.93	0.14	55,55,55,55	0
57	MG	2A	3201	1/1	0.93	0.12	59,59,59,59	0
57	MG	2A	3203	1/1	0.93	0.23	54,54,54,54	0
57	MG	2A	3445	1/1	0.93	0.11	36,36,36,36	0
57	MG	2A	3204	1/1	0.93	0.21	48,48,48,48	0
57	MG	1A	3337	1/1	0.93	0.28	36,36,36,36	0
57	MG	2A	3206	1/1	0.93	0.26	45,45,45,45	0
57	MG	1A	3297	1/1	0.93	0.21	58,58,58,58	0
57	MG	2A	3778	1/1	0.93	0.07	60,60,60,60	0
57	MG	16	101	1/1	0.93	0.11	52,52,52,52	0
57	MG	1A	3166	1/1	0.93	0.18	60,60,60,60	0
57	MG	18	105	1/1	0.93	0.16	50,50,50,50	0
57	MG	18	106	1/1	0.93	0.17	53,53,53,53	0
57	MG	2A	3466	1/1	0.93	0.10	40,40,40,40	0
57	MG	1A	3544	1/1	0.93	0.13	27,27,27,27	0
57	MG	1A	3919	1/1	0.93	0.09	51,51,51,51	0
57	MG	2A	3472	1/1	0.93	0.09	47,47,47,47	0
57	MG	1A	3665	1/1	0.93	0.13	43,43,43,43	0
57	MG	1A	3792	1/1	0.93	0.07	28,28,28,28	0
57	MG	1A	3465	1/1	0.93	0.07	52,52,52,52	0
57	MG	1A	3300	1/1	0.93	0.12	56,56,56,56	0
57	MG	1A	3925	1/1	0.93	0.14	56,56,56,56	0
57	MG	2B	201	1/1	0.93	0.18	69,69,69,69	0
57	MG	1a	1608	1/1	0.93	0.10	52,52,52,52	0
57	MG	2A	3224	1/1	0.93	0.34	65,65,65,65	0
57	MG	1A	3342	1/1	0.93	0.16	60,60,60,60	0
57	MG	1A	3343	1/1	0.93	0.11	45,45,45,45	0
57	MG	1x	102	1/1	0.93	0.17	70,70,70,70	0
57	MG	1A	3469	1/1	0.93	0.24	29,29,29,29	0
57	MG	1A	3273	1/1	0.93	0.17	51,51,51,51	0
57	MG	1A	3407	1/1	0.93	0.17	43,43,43,43	0
57	MG	2A	3232	1/1	0.93	0.12	66,66,66,66	0
57	MG	1A	3303	1/1	0.93	0.19	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3304	1/1	0.93	0.21	45,45,45,45	0
57	MG	1x	109	1/1	0.93	0.29	71,71,71,71	0
57	MG	1A	3176	1/1	0.93	0.17	48,48,48,48	0
57	MG	1a	1627	1/1	0.93	0.27	63,63,63,63	0
57	MG	1A	4097	1/1	0.93	0.08	46,46,46,46	0
57	MG	1y	101	1/1	0.93	0.13	55,55,55,55	0
57	MG	1a	1630	1/1	0.93	0.48	71,71,71,71	0
57	MG	1a	1633	1/1	0.93	0.17	58,58,58,58	0
57	MG	1A	3359	1/1	0.93	0.27	36,36,36,36	0
57	MG	2x	106	1/1	0.93	0.11	67,67,67,67	0
57	MG	1A	4100	1/1	0.93	0.26	53,53,53,53	0
57	MG	2A	3008	1/1	0.93	0.21	49,49,49,49	0
57	MG	1A	3686	1/1	0.93	0.09	48,48,48,48	0
57	MG	2A	3251	1/1	0.93	0.15	62,62,62,62	0
57	MG	2A	3015	1/1	0.93	0.21	58,58,58,58	0
59	TYK	2A	3798	64/64	0.93	0.11	32,46,61,66	0
57	MG	1A	3554	1/1	0.94	0.19	63,63,63,63	0
57	MG	2A	3172	1/1	0.94	0.10	56,56,56,56	0
57	MG	27	101	1/1	0.94	0.24	59,59,59,59	0
57	MG	1e	202	1/1	0.94	0.16	58,58,58,58	0
57	MG	1A	3682	1/1	0.94	0.10	57,57,57,57	0
57	MG	1B	219	1/1	0.94	0.09	34,34,34,34	0
57	MG	1a	1631	1/1	0.94	0.19	59,59,59,59	0
57	MG	2A	3601	1/1	0.94	0.11	68,68,68,68	0
57	MG	1A	3241	1/1	0.94	0.10	49,49,49,49	0
57	MG	2A	3178	1/1	0.94	0.08	67,67,67,67	0
57	MG	1A	3195	1/1	0.94	0.08	34,34,34,34	0
57	MG	2A	3362	1/1	0.94	0.08	50,50,50,50	0
57	MG	1B	222	1/1	0.94	0.12	56,56,56,56	0
57	MG	1B	223	1/1	0.94	0.11	58,58,58,58	0
57	MG	2A	3611	1/1	0.94	0.09	55,55,55,55	0
57	MG	1A	3070	1/1	0.94	0.06	33,33,33,33	0
57	MG	1B	226	1/1	0.94	0.08	45,45,45,45	0
57	MG	1A	3471	1/1	0.94	0.32	40,40,40,40	0
57	MG	1A	3826	1/1	0.94	0.11	41,41,41,41	0
57	MG	2A	3372	1/1	0.94	0.12	59,59,59,59	0
57	MG	2A	3189	1/1	0.94	0.16	64,64,64,64	0
57	MG	2A	3622	1/1	0.94	0.13	48,48,48,48	0
57	MG	2A	3625	1/1	0.94	0.10	50,50,50,50	0
57	MG	2A	3375	1/1	0.94	0.09	69,69,69,69	0
57	MG	1A	3403	1/1	0.94	0.17	42,42,42,42	0
57	MG	1A	3828	1/1	0.94	0.22	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3695	1/1	0.94	0.08	44,44,44,44	0
57	MG	1A	3244	1/1	0.94	0.10	59,59,59,59	0
57	MG	1A	3344	1/1	0.94	0.21	45,45,45,45	0
57	MG	1D	309	1/1	0.94	0.16	52,52,52,52	0
57	MG	1A	3566	1/1	0.94	0.07	52,52,52,52	0
57	MG	2a	1627	1/1	0.94	0.23	45,45,45,45	0
57	MG	1a	1649	1/1	0.94	0.15	46,46,46,46	0
57	MG	1A	3476	1/1	0.94	0.10	49,49,49,49	0
57	MG	1A	3077	1/1	0.94	0.15	36,36,36,36	0
57	MG	1A	3408	1/1	0.94	0.21	46,46,46,46	0
57	MG	2A	3391	1/1	0.94	0.19	61,61,61,61	0
57	MG	2A	3003	1/1	0.94	0.23	57,57,57,57	0
57	MG	1a	1655	1/1	0.94	0.12	51,51,51,51	0
57	MG	1A	3838	1/1	0.94	0.08	36,36,36,36	0
57	MG	1A	3022	1/1	0.94	0.04	17,17,17,17	0
57	MG	1A	3571	1/1	0.94	0.09	43,43,43,43	0
57	MG	2A	3011	1/1	0.94	0.12	46,46,46,46	0
57	MG	1A	3411	1/1	0.94	0.10	58,58,58,58	0
57	MG	2A	3014	1/1	0.94	0.11	50,50,50,50	0
57	MG	2A	3212	1/1	0.94	0.10	58,58,58,58	0
57	MG	2A	3401	1/1	0.94	0.06	42,42,42,42	0
57	MG	2A	3402	1/1	0.94	0.24	71,71,71,71	0
57	MG	2a	1646	1/1	0.94	0.26	61,61,61,61	0
57	MG	1A	3994	1/1	0.94	0.08	29,29,29,29	0
57	MG	1A	3050	1/1	0.94	0.07	45,45,45,45	0
57	MG	1A	3845	1/1	0.94	0.08	29,29,29,29	0
57	MG	1A	3353	1/1	0.94	0.17	55,55,55,55	0
57	MG	1A	3202	1/1	0.94	0.15	36,36,36,36	0
57	MG	1A	3719	1/1	0.94	0.08	38,38,38,38	0
57	MG	2a	1653	1/1	0.94	0.12	47,47,47,47	0
57	MG	2A	3661	1/1	0.94	0.10	41,41,41,41	0
57	MG	2A	3219	1/1	0.94	0.14	49,49,49,49	0
57	MG	2a	1656	1/1	0.94	0.26	63,63,63,63	0
57	MG	1A	3486	1/1	0.94	0.25	43,43,43,43	0
57	MG	2a	1658	1/1	0.94	0.21	57,57,57,57	0
57	MG	1F	313	1/1	0.94	0.16	32,32,32,32	0
57	MG	2A	3028	1/1	0.94	0.13	50,50,50,50	0
57	MG	1A	3052	1/1	0.94	0.08	51,51,51,51	0
57	MG	1A	3360	1/1	0.94	0.09	57,57,57,57	0
57	MG	1A	3856	1/1	0.94	0.11	49,49,49,49	0
57	MG	1A	3725	1/1	0.94	0.12	27,27,27,27	0
57	MG	2a	1667	1/1	0.94	0.11	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3490	1/1	0.94	0.23	49,49,49,49	0
57	MG	1A	3103	1/1	0.94	0.29	34,34,34,34	0
57	MG	1a	1675	1/1	0.94	0.36	58,58,58,58	0
57	MG	1a	1676	1/1	0.94	0.07	73,73,73,73	0
57	MG	1a	1677	1/1	0.94	0.22	41,41,41,41	0
57	MG	2A	3432	1/1	0.94	0.07	30,30,30,30	0
57	MG	2A	3683	1/1	0.94	0.13	72,72,72,72	0
57	MG	2A	3684	1/1	0.94	0.19	50,50,50,50	0
57	MG	2A	3433	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3042	1/1	0.94	0.21	36,36,36,36	0
57	MG	2A	3435	1/1	0.94	0.17	69,69,69,69	0
57	MG	2a	1681	1/1	0.94	0.19	35,35,35,35	0
57	MG	2a	1682	1/1	0.94	0.35	60,60,60,60	0
57	MG	1A	3492	1/1	0.94	0.10	24,24,24,24	0
57	MG	1A	3208	1/1	0.94	0.08	50,50,50,50	0
57	MG	2A	3694	1/1	0.94	0.12	64,64,64,64	0
57	MG	1a	1680	1/1	0.94	0.24	40,40,40,40	0
57	MG	1a	1681	1/1	0.94	0.14	57,57,57,57	0
57	MG	1A	3254	1/1	0.94	0.13	34,34,34,34	0
57	MG	2A	3442	1/1	0.94	0.11	41,41,41,41	0
57	MG	2A	3443	1/1	0.94	0.08	44,44,44,44	0
57	MG	1A	3255	1/1	0.94	0.13	46,46,46,46	0
57	MG	2A	3704	1/1	0.94	0.07	72,72,72,72	0
57	MG	1A	3127	1/1	0.94	0.24	41,41,41,41	0
57	MG	1A	4025	1/1	0.94	0.07	53,53,53,53	0
57	MG	2A	3053	1/1	0.94	0.17	58,58,58,58	0
57	MG	1A	4027	1/1	0.94	0.14	49,49,49,49	0
57	MG	2A	3712	1/1	0.94	0.11	40,40,40,40	0
57	MG	2A	3452	1/1	0.94	0.08	39,39,39,39	0
57	MG	2A	3056	1/1	0.94	0.16	73,73,73,73	0
57	MG	1A	3499	1/1	0.94	0.07	58,58,58,58	0
57	MG	2a	1703	1/1	0.94	0.18	64,64,64,64	0
57	MG	2A	3719	1/1	0.94	0.07	56,56,56,56	0
57	MG	2a	1706	1/1	0.94	0.17	61,61,61,61	0
57	MG	2A	3249	1/1	0.94	0.16	55,55,55,55	0
57	MG	1P	201	1/1	0.94	0.27	32,32,32,32	0
57	MG	1A	3167	1/1	0.94	0.08	45,45,45,45	0
57	MG	2A	3060	1/1	0.94	0.10	50,50,50,50	0
57	MG	2A	3061	1/1	0.94	0.09	37,37,37,37	0
57	MG	1P	204	1/1	0.94	0.35	28,28,28,28	0
57	MG	1A	3750	1/1	0.94	0.09	53,53,53,53	0
57	MG	1A	3501	1/1	0.94	0.24	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1715	1/1	0.94	0.45	60,60,60,60	0
57	MG	1Q	205	1/1	0.94	0.12	46,46,46,46	0
57	MG	1A	3174	1/1	0.94	0.10	32,32,32,32	0
57	MG	1A	3129	1/1	0.94	0.11	39,39,39,39	0
57	MG	2A	3068	1/1	0.94	0.25	44,44,44,44	0
57	MG	1A	3610	1/1	0.94	0.07	41,41,41,41	0
57	MG	1A	3611	1/1	0.94	0.10	42,42,42,42	0
57	MG	2A	3072	1/1	0.94	0.07	57,57,57,57	0
57	MG	1A	3763	1/1	0.94	0.06	32,32,32,32	0
57	MG	1A	3882	1/1	0.94	0.08	43,43,43,43	0
57	MG	1A	3429	1/1	0.94	0.10	50,50,50,50	0
57	MG	1A	3613	1/1	0.94	0.10	43,43,43,43	0
57	MG	1A	3177	1/1	0.94	0.14	54,54,54,54	0
57	MG	1A	3216	1/1	0.94	0.08	53,53,53,53	0
57	MG	1A	3004	1/1	0.94	0.10	25,25,25,25	0
57	MG	2A	3755	1/1	0.94	0.17	62,62,62,62	0
57	MG	2a	1733	1/1	0.94	0.13	72,72,72,72	0
57	MG	1A	4048	1/1	0.94	0.13	61,61,61,61	0
57	MG	2a	1735	1/1	0.94	0.08	52,52,52,52	0
57	MG	1A	3771	1/1	0.94	0.18	73,73,73,73	0
57	MG	2A	3758	1/1	0.94	0.19	50,50,50,50	0
57	MG	2a	1741	1/1	0.94	0.10	77,77,77,77	0
57	MG	1A	3038	1/1	0.94	0.20	36,36,36,36	0
57	MG	2A	3499	1/1	0.94	0.11	54,54,54,54	0
57	MG	1A	3903	1/1	0.94	0.10	61,61,61,61	0
57	MG	1V	201	1/1	0.94	0.13	28,28,28,28	0
57	MG	1a	1729	1/1	0.94	0.26	45,45,45,45	0
57	MG	1V	204	1/1	0.94	0.14	49,49,49,49	0
57	MG	1A	3516	1/1	0.94	0.14	33,33,33,33	0
57	MG	1A	3627	1/1	0.94	0.07	43,43,43,43	0
57	MG	1A	3779	1/1	0.94	0.08	30,30,30,30	0
57	MG	1a	1736	1/1	0.94	0.08	54,54,54,54	0
57	MG	1A	3180	1/1	0.94	0.13	50,50,50,50	0
57	MG	2A	3510	1/1	0.94	0.12	51,51,51,51	0
57	MG	2A	3511	1/1	0.94	0.12	41,41,41,41	0
57	MG	1A	3435	1/1	0.94	0.13	56,56,56,56	0
57	MG	1A	3524	1/1	0.94	0.06	37,37,37,37	0
57	MG	1A	3912	1/1	0.94	0.12	64,64,64,64	0
57	MG	1A	3525	1/1	0.94	0.08	39,39,39,39	0
57	MG	2A	3782	1/1	0.94	0.08	54,54,54,54	0
57	MG	1A	3379	1/1	0.94	0.25	47,47,47,47	0
57	MG	1A	3645	1/1	0.94	0.08	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3917	1/1	0.94	0.07	52,52,52,52	0
57	MG	1A	3110	1/1	0.94	0.17	35,35,35,35	0
57	MG	2A	3107	1/1	0.94	0.10	70,70,70,70	0
57	MG	2A	3790	1/1	0.94	0.12	60,60,60,60	0
57	MG	1A	3327	1/1	0.94	0.11	59,59,59,59	0
57	MG	1A	3531	1/1	0.94	0.07	42,42,42,42	0
57	MG	2A	3793	1/1	0.94	0.07	64,64,64,64	0
57	MG	2A	3524	1/1	0.94	0.10	37,37,37,37	0
57	MG	2A	3111	1/1	0.94	0.23	57,57,57,57	0
57	MG	2A	3300	1/1	0.94	0.11	64,64,64,64	0
57	MG	1a	1749	1/1	0.94	0.08	73,73,73,73	0
57	MG	1A	3649	1/1	0.94	0.05	28,28,28,28	0
57	MG	2A	3532	1/1	0.94	0.09	38,38,38,38	0
57	MG	1A	4079	1/1	0.94	0.08	48,48,48,48	0
57	MG	1a	1754	1/1	0.94	0.08	64,64,64,64	0
57	MG	1A	4082	1/1	0.94	0.29	33,33,33,33	0
57	MG	2A	3118	1/1	0.94	0.11	49,49,49,49	0
57	MG	2a	1786	1/1	0.94	0.18	68,68,68,68	0
57	MG	2B	207	1/1	0.94	0.09	65,65,65,65	0
57	MG	1l	105	1/1	0.94	0.10	53,53,53,53	0
57	MG	1A	3147	1/1	0.94	0.26	38,38,38,38	0
57	MG	1A	3224	1/1	0.94	0.20	50,50,50,50	0
57	MG	2A	3545	1/1	0.94	0.11	50,50,50,50	0
57	MG	1A	3111	1/1	0.94	0.16	39,39,39,39	0
57	MG	1A	3447	1/1	0.94	0.23	50,50,50,50	0
57	MG	1A	4087	1/1	0.94	0.13	51,51,51,51	0
57	MG	1A	3660	1/1	0.94	0.06	16,16,16,16	0
57	MG	1A	3929	1/1	0.94	0.08	65,65,65,65	0
57	MG	2B	217	1/1	0.94	0.32	71,71,71,71	0
57	MG	1A	3661	1/1	0.94	0.13	46,46,46,46	0
57	MG	2a	1802	1/1	0.94	0.19	55,55,55,55	0
57	MG	2B	219	1/1	0.94	0.13	62,62,62,62	0
57	MG	2D	301	1/1	0.94	0.08	42,42,42,42	0
57	MG	1A	3797	1/1	0.94	0.06	36,36,36,36	0
57	MG	1A	3332	1/1	0.94	0.32	66,66,66,66	0
57	MG	2A	3136	1/1	0.94	0.11	32,32,32,32	0
57	MG	2a	1809	1/1	0.94	0.13	78,78,78,78	0
57	MG	1A	3234	1/1	0.94	0.09	52,52,52,52	0
57	MG	1a	1783	1/1	0.94	0.17	64,64,64,64	0
57	MG	1A	3390	1/1	0.94	0.22	37,37,37,37	0
57	MG	2E	302	1/1	0.94	0.11	55,55,55,55	0
57	MG	1a	1790	1/1	0.94	0.25	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2a	1817	1/1	0.94	0.14	54,54,54,54	0
57	MG	2E	305	1/1	0.94	0.10	63,63,63,63	0
57	MG	2A	3141	1/1	0.94	0.10	50,50,50,50	0
57	MG	1A	4096	1/1	0.94	0.09	50,50,50,50	0
57	MG	2d	302	1/1	0.94	0.22	56,56,56,56	0
57	MG	2A	3327	1/1	0.94	0.17	39,39,39,39	0
57	MG	19	101	1/1	0.94	0.20	52,52,52,52	0
57	MG	2F	301	1/1	0.94	0.09	47,47,47,47	0
57	MG	1A	3458	1/1	0.94	0.07	55,55,55,55	0
57	MG	2F	303	1/1	0.94	0.20	54,54,54,54	0
57	MG	1A	3940	1/1	0.94	0.17	51,51,51,51	0
57	MG	2F	306	1/1	0.94	0.16	48,48,48,48	0
57	MG	2q	201	1/1	0.94	0.09	77,77,77,77	0
57	MG	1A	3941	1/1	0.94	0.13	18,18,18,18	0
57	MG	2t	201	1/1	0.94	0.12	58,58,58,58	0
57	MG	1a	1797	1/1	0.94	0.12	66,66,66,66	0
57	MG	1A	3187	1/1	0.94	0.35	37,37,37,37	0
57	MG	1A	3460	1/1	0.94	0.06	51,51,51,51	0
57	MG	1A	3672	1/1	0.94	0.18	63,63,63,63	0
57	MG	2A	3575	1/1	0.94	0.13	60,60,60,60	0
57	MG	1A	3673	1/1	0.94	0.09	37,37,37,37	0
57	MG	1A	3809	1/1	0.94	0.19	45,45,45,45	0
57	MG	2w	105	1/1	0.94	0.20	51,51,51,51	0
57	MG	1a	1612	1/1	0.94	0.16	66,66,66,66	0
57	MG	1a	1613	1/1	0.94	0.11	62,62,62,62	0
57	MG	1A	3392	1/1	0.94	0.11	49,49,49,49	0
57	MG	1A	3189	1/1	0.94	0.35	38,38,38,38	0
57	MG	1a	1808	1/1	0.94	0.13	67,67,67,67	0
57	MG	1a	1616	1/1	0.94	0.12	61,61,61,61	0
57	MG	1A	3549	1/1	0.94	0.38	59,59,59,59	0
57	MG	1A	3112	1/1	0.94	0.18	30,30,30,30	0
57	MG	2A	3588	1/1	0.94	0.12	60,60,60,60	0
57	MG	1A	3953	1/1	0.94	0.12	60,60,60,60	0
57	MG	1A	3115	1/1	0.94	0.12	38,38,38,38	0
57	MG	1A	3956	1/1	0.94	0.18	38,38,38,38	0
58	K	1A	3512	1/1	0.94	0.10	54,54,54,54	0
57	MG	2A	3592	1/1	0.94	0.12	36,36,36,36	0
60	ZN	24	501	1/1	0.94	0.14	126,126,126,126	0
57	MG	1A	3024	1/1	0.95	0.16	35,35,35,35	0
57	MG	1A	3075	1/1	0.95	0.13	33,33,33,33	0
57	MG	2A	3669	1/1	0.95	0.13	73,73,73,73	0
57	MG	2A	3670	1/1	0.95	0.10	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1750	1/1	0.95	0.07	64,64,64,64	0
57	MG	2A	3672	1/1	0.95	0.08	65,65,65,65	0
57	MG	1A	3226	1/1	0.95	0.19	31,31,31,31	0
57	MG	2A	3456	1/1	0.95	0.16	51,51,51,51	0
57	MG	2A	3265	1/1	0.95	0.11	60,60,60,60	0
57	MG	2A	3677	1/1	0.95	0.06	60,60,60,60	0
57	MG	17	105	1/1	0.95	0.09	50,50,50,50	0
57	MG	18	103	1/1	0.95	0.16	33,33,33,33	0
57	MG	1A	3231	1/1	0.95	0.22	42,42,42,42	0
57	MG	2a	1641	1/1	0.95	0.16	67,67,67,67	0
57	MG	2A	3269	1/1	0.95	0.16	66,66,66,66	0
57	MG	1a	1756	1/1	0.95	0.09	64,64,64,64	0
57	MG	1A	3833	1/1	0.95	0.15	32,32,32,32	0
57	MG	2a	1645	1/1	0.95	0.13	70,70,70,70	0
57	MG	1A	3968	1/1	0.95	0.05	37,37,37,37	0
57	MG	2A	3686	1/1	0.95	0.06	55,55,55,55	0
57	MG	2A	3471	1/1	0.95	0.09	45,45,45,45	0
57	MG	2A	3688	1/1	0.95	0.09	50,50,50,50	0
57	MG	2A	3098	1/1	0.95	0.15	49,49,49,49	0
57	MG	1A	3415	1/1	0.95	0.10	55,55,55,55	0
57	MG	1A	3972	1/1	0.95	0.07	46,46,46,46	0
57	MG	1A	3835	1/1	0.95	0.10	25,25,25,25	0
57	MG	1A	3076	1/1	0.95	0.19	42,42,42,42	0
57	MG	2A	3103	1/1	0.95	0.38	68,68,68,68	0
57	MG	1A	3289	1/1	0.95	0.38	56,56,56,56	0
57	MG	2A	3698	1/1	0.95	0.17	54,54,54,54	0
57	MG	1A	3291	1/1	0.95	0.09	61,61,61,61	0
57	MG	1A	3130	1/1	0.95	0.08	42,42,42,42	0
57	MG	1A	3503	1/1	0.95	0.10	44,44,44,44	0
57	MG	1a	1609	1/1	0.95	0.32	56,56,56,56	0
57	MG	2A	3705	1/1	0.95	0.13	51,51,51,51	0
57	MG	2A	3706	1/1	0.95	0.07	39,39,39,39	0
57	MG	1A	3734	1/1	0.95	0.06	27,27,27,27	0
57	MG	1a	1782	1/1	0.95	0.10	54,54,54,54	0
57	MG	1A	3983	1/1	0.95	0.06	39,39,39,39	0
57	MG	1A	3606	1/1	0.95	0.06	31,31,31,31	0
57	MG	1A	3737	1/1	0.95	0.07	50,50,50,50	0
57	MG	2A	3493	1/1	0.95	0.07	64,64,64,64	0
57	MG	1A	3351	1/1	0.95	0.23	47,47,47,47	0
57	MG	2A	3117	1/1	0.95	0.08	54,54,54,54	0
57	MG	1A	3352	1/1	0.95	0.07	47,47,47,47	0
57	MG	1a	1793	1/1	0.95	0.17	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1620	1/1	0.95	0.07	50,50,50,50	0
57	MG	2a	1678	1/1	0.95	0.14	55,55,55,55	0
57	MG	1A	3851	1/1	0.95	0.06	24,24,24,24	0
57	MG	1A	3508	1/1	0.95	0.18	36,36,36,36	0
57	MG	1A	3745	1/1	0.95	0.06	39,39,39,39	0
57	MG	2A	3126	1/1	0.95	0.15	61,61,61,61	0
57	MG	1A	3101	1/1	0.95	0.06	31,31,31,31	0
57	MG	1A	3186	1/1	0.95	0.27	33,33,33,33	0
57	MG	2A	3734	1/1	0.95	0.07	24,24,24,24	0
57	MG	1D	302	1/1	0.95	0.23	40,40,40,40	0
57	MG	1a	1628	1/1	0.95	0.11	43,43,43,43	0
57	MG	1D	303	1/1	0.95	0.17	39,39,39,39	0
57	MG	1D	305	1/1	0.95	0.07	41,41,41,41	0
57	MG	2A	3512	1/1	0.95	0.08	53,53,53,53	0
57	MG	1A	3102	1/1	0.95	0.20	40,40,40,40	0
57	MG	1A	3998	1/1	0.95	0.12	34,34,34,34	0
57	MG	1A	3143	1/1	0.95	0.24	39,39,39,39	0
57	MG	1A	3753	1/1	0.95	0.10	22,22,22,22	0
57	MG	1E	303	1/1	0.95	0.17	36,36,36,36	0
57	MG	2A	3312	1/1	0.95	0.25	69,69,69,69	0
57	MG	2A	3751	1/1	0.95	0.07	65,65,65,65	0
57	MG	1A	4005	1/1	0.95	0.08	26,26,26,26	0
57	MG	1A	3035	1/1	0.95	0.07	29,29,29,29	0
57	MG	2a	1701	1/1	0.95	0.12	51,51,51,51	0
57	MG	1A	3862	1/1	0.95	0.13	47,47,47,47	0
57	MG	1a	1813	1/1	0.95	0.06	47,47,47,47	0
57	MG	1A	3145	1/1	0.95	0.38	39,39,39,39	0
57	MG	1A	3146	1/1	0.95	0.16	34,34,34,34	0
57	MG	1F	301	1/1	0.95	0.11	34,34,34,34	0
57	MG	2A	3527	1/1	0.95	0.12	59,59,59,59	0
57	MG	1F	302	1/1	0.95	0.11	33,33,33,33	0
57	MG	1A	3366	1/1	0.95	0.08	44,44,44,44	0
57	MG	1A	3626	1/1	0.95	0.07	32,32,32,32	0
57	MG	1A	3760	1/1	0.95	0.07	24,24,24,24	0
57	MG	2A	3533	1/1	0.95	0.06	60,60,60,60	0
57	MG	2A	3534	1/1	0.95	0.17	63,63,63,63	0
57	MG	1A	3871	1/1	0.95	0.10	24,24,24,24	0
57	MG	1r	101	1/1	0.95	0.11	69,69,69,69	0
57	MG	1F	308	1/1	0.95	0.09	50,50,50,50	0
57	MG	2A	3773	1/1	0.95	0.14	70,70,70,70	0
57	MG	1A	3081	1/1	0.95	0.18	37,37,37,37	0
57	MG	2A	3540	1/1	0.95	0.08	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1w	102	1/1	0.95	0.10	49,49,49,49	0
57	MG	1A	4017	1/1	0.95	0.07	43,43,43,43	0
57	MG	1A	3764	1/1	0.95	0.36	30,30,30,30	0
57	MG	2A	3331	1/1	0.95	0.32	48,48,48,48	0
57	MG	2A	3546	1/1	0.95	0.11	46,46,46,46	0
57	MG	1A	3048	1/1	0.95	0.10	27,27,27,27	0
57	MG	2a	1727	1/1	0.95	0.09	71,71,71,71	0
57	MG	1A	3108	1/1	0.95	0.10	37,37,37,37	0
57	MG	1A	3370	1/1	0.95	0.15	52,52,52,52	0
57	MG	1A	3768	1/1	0.95	0.09	45,45,45,45	0
57	MG	1A	3036	1/1	0.95	0.15	28,28,28,28	0
57	MG	1x	105	1/1	0.95	0.16	63,63,63,63	0
57	MG	2A	3789	1/1	0.95	0.13	55,55,55,55	0
57	MG	1A	3306	1/1	0.95	0.29	58,58,58,58	0
57	MG	2a	1738	1/1	0.95	0.06	75,75,75,75	0
57	MG	1G	205	1/1	0.95	0.10	49,49,49,49	0
57	MG	1A	3443	1/1	0.95	0.17	43,43,43,43	0
57	MG	1A	3200	1/1	0.95	0.10	36,36,36,36	0
57	MG	1x	110	1/1	0.95	0.07	22,22,22,22	0
57	MG	1a	1664	1/1	0.95	0.13	64,64,64,64	0
57	MG	1A	4031	1/1	0.95	0.11	40,40,40,40	0
57	MG	2A	3179	1/1	0.95	0.37	65,65,65,65	0
57	MG	1A	3249	1/1	0.95	0.13	40,40,40,40	0
57	MG	1A	3775	1/1	0.95	0.08	45,45,45,45	0
57	MG	1A	3892	1/1	0.95	0.12	62,62,62,62	0
57	MG	1O	203	1/1	0.95	0.18	55,55,55,55	0
57	MG	1A	3201	1/1	0.95	0.14	49,49,49,49	0
57	MG	2a	1755	1/1	0.95	0.11	46,46,46,46	0
57	MG	2A	3186	1/1	0.95	0.10	57,57,57,57	0
57	MG	1A	3777	1/1	0.95	0.06	26,26,26,26	0
57	MG	2A	3569	1/1	0.95	0.09	61,61,61,61	0
57	MG	1A	3310	1/1	0.95	0.12	51,51,51,51	0
57	MG	2a	1760	1/1	0.95	0.19	54,54,54,54	0
57	MG	1A	3312	1/1	0.95	0.16	49,49,49,49	0
57	MG	2A	3010	1/1	0.95	0.07	47,47,47,47	0
57	MG	1A	3781	1/1	0.95	0.08	31,31,31,31	0
57	MG	1A	3452	1/1	0.95	0.08	65,65,65,65	0
57	MG	1A	3060	1/1	0.95	0.18	39,39,39,39	0
57	MG	1A	3029	1/1	0.95	0.28	31,31,31,31	0
57	MG	1A	3457	1/1	0.95	0.17	39,39,39,39	0
57	MG	1A	3113	1/1	0.95	0.11	34,34,34,34	0
57	MG	2A	3581	1/1	0.95	0.09	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3160	1/1	0.95	0.14	35,35,35,35	0
57	MG	2A	3020	1/1	0.95	0.14	49,49,49,49	0
57	MG	2A	3022	1/1	0.95	0.28	47,47,47,47	0
57	MG	1R	202	1/1	0.95	0.19	37,37,37,37	0
57	MG	1A	3548	1/1	0.95	0.09	36,36,36,36	0
57	MG	2A	3202	1/1	0.95	0.18	50,50,50,50	0
57	MG	2D	307	1/1	0.95	0.15	68,68,68,68	0
57	MG	1a	1683	1/1	0.95	0.17	55,55,55,55	0
57	MG	1A	3911	1/1	0.95	0.06	43,43,43,43	0
57	MG	1A	3383	1/1	0.95	0.24	54,54,54,54	0
57	MG	1A	3318	1/1	0.95	0.25	54,54,54,54	0
57	MG	1A	3209	1/1	0.95	0.30	44,44,44,44	0
57	MG	2A	3381	1/1	0.95	0.18	50,50,50,50	0
57	MG	2A	3208	1/1	0.95	0.07	54,54,54,54	0
57	MG	2A	3031	1/1	0.95	0.12	47,47,47,47	0
57	MG	2A	3384	1/1	0.95	0.08	63,63,63,63	0
57	MG	1A	3669	1/1	0.95	0.07	61,61,61,61	0
57	MG	2A	3211	1/1	0.95	0.11	49,49,49,49	0
57	MG	2a	1789	1/1	0.95	0.10	60,60,60,60	0
57	MG	2A	3387	1/1	0.95	0.14	53,53,53,53	0
57	MG	2F	304	1/1	0.95	0.09	49,49,49,49	0
57	MG	1A	3386	1/1	0.95	0.06	48,48,48,48	0
57	MG	1A	3555	1/1	0.95	0.21	54,54,54,54	0
57	MG	1A	3114	1/1	0.95	0.13	43,43,43,43	0
57	MG	1A	4070	1/1	0.95	0.10	45,45,45,45	0
57	MG	2a	1796	1/1	0.95	0.22	63,63,63,63	0
57	MG	1A	3051	1/1	0.95	0.08	54,54,54,54	0
57	MG	1a	1695	1/1	0.95	0.20	43,43,43,43	0
57	MG	2O	201	1/1	0.95	0.14	51,51,51,51	0
57	MG	1A	3322	1/1	0.95	0.32	39,39,39,39	0
57	MG	1A	3676	1/1	0.95	0.08	45,45,45,45	0
57	MG	1A	3091	1/1	0.95	0.09	32,32,32,32	0
57	MG	2Q	202	1/1	0.95	0.22	47,47,47,47	0
57	MG	1V	203	1/1	0.95	0.12	27,27,27,27	0
57	MG	1A	3092	1/1	0.95	0.15	24,24,24,24	0
57	MG	2A	3618	1/1	0.95	0.08	47,47,47,47	0
57	MG	2A	3619	1/1	0.95	0.09	40,40,40,40	0
57	MG	1A	3562	1/1	0.95	0.07	46,46,46,46	0
57	MG	1a	1707	1/1	0.95	0.14	65,65,65,65	0
57	MG	1A	3393	1/1	0.95	0.17	47,47,47,47	0
57	MG	1W	204	1/1	0.95	0.09	38,38,38,38	0
57	MG	1A	3267	1/1	0.95	0.16	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	20	101	1/1	0.95	0.07	63,63,63,63	0
57	MG	1a	1712	1/1	0.95	0.06	31,31,31,31	0
57	MG	1a	1716	1/1	0.95	0.07	69,69,69,69	0
57	MG	1A	3806	1/1	0.95	0.10	58,58,58,58	0
57	MG	1A	4080	1/1	0.95	0.17	43,43,43,43	0
57	MG	2A	3632	1/1	0.95	0.06	61,61,61,61	0
57	MG	1A	3931	1/1	0.95	0.07	72,72,72,72	0
57	MG	2A	3234	1/1	0.95	0.15	62,62,62,62	0
57	MG	1A	3119	1/1	0.95	0.20	32,32,32,32	0
57	MG	1a	1721	1/1	0.95	0.06	39,39,39,39	0
57	MG	2A	3237	1/1	0.95	0.30	53,53,53,53	0
57	MG	1A	3329	1/1	0.95	0.17	54,54,54,54	0
57	MG	1A	3397	1/1	0.95	0.16	42,42,42,42	0
57	MG	1a	1726	1/1	0.95	0.08	52,52,52,52	0
57	MG	2A	3241	1/1	0.95	0.23	63,63,63,63	0
57	MG	1A	3272	1/1	0.95	0.20	46,46,46,46	0
57	MG	1A	3812	1/1	0.95	0.12	18,18,18,18	0
57	MG	1A	3173	1/1	0.95	0.08	20,20,20,20	0
57	MG	1A	3217	1/1	0.95	0.10	22,22,22,22	0
57	MG	2A	3429	1/1	0.95	0.07	67,67,67,67	0
57	MG	1A	3574	1/1	0.95	0.13	13,13,13,13	0
57	MG	2A	3649	1/1	0.95	0.07	51,51,51,51	0
57	MG	1l	101	1/1	0.95	0.41	39,39,39,39	0
57	MG	2A	3651	1/1	0.95	0.12	51,51,51,51	0
57	MG	2w	107	1/1	0.95	0.21	70,70,70,70	0
57	MG	1A	3402	1/1	0.95	0.07	61,61,61,61	0
57	MG	1A	3577	1/1	0.95	0.10	56,56,56,56	0
57	MG	2A	3654	1/1	0.95	0.08	58,58,58,58	0
57	MG	1A	3120	1/1	0.95	0.25	35,35,35,35	0
57	MG	1A	3066	1/1	0.95	0.18	31,31,31,31	0
57	MG	1A	3705	1/1	0.95	0.11	36,36,36,36	0
57	MG	1A	3005	1/1	0.95	0.09	45,45,45,45	0
57	MG	13	103	1/1	0.95	0.09	59,59,59,59	0
57	MG	1A	3824	1/1	0.95	0.09	42,42,42,42	0
57	MG	1A	3336	1/1	0.95	0.08	51,51,51,51	0
57	MG	1A	3280	1/1	0.95	0.07	39,39,39,39	0
57	MG	1A	3095	1/1	0.95	0.06	42,42,42,42	0
59	TYK	1A	4101	64/64	0.95	0.09	16,30,46,51	0
57	MG	1A	3713	1/1	0.95	0.13	51,51,51,51	0
57	MG	2A	3447	1/1	0.95	0.10	41,41,41,41	0
57	MG	1U	206	1/1	0.96	0.18	33,33,33,33	0
57	MG	1a	1699	1/1	0.96	0.20	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3048	1/1	0.96	0.09	48,48,48,48	0
57	MG	1U	207	1/1	0.96	0.24	38,38,38,38	0
57	MG	2a	1625	1/1	0.96	0.07	86,86,86,86	0
57	MG	2A	3437	1/1	0.96	0.05	33,33,33,33	0
57	MG	1a	1701	1/1	0.96	0.17	38,38,38,38	0
57	MG	1A	3453	1/1	0.96	0.27	48,48,48,48	0
57	MG	1A	3175	1/1	0.96	0.06	38,38,38,38	0
57	MG	1a	1705	1/1	0.96	0.11	55,55,55,55	0
57	MG	2A	3054	1/1	0.96	0.11	45,45,45,45	0
57	MG	1a	1706	1/1	0.96	0.31	63,63,63,63	0
57	MG	1A	3932	1/1	0.96	0.11	43,43,43,43	0
57	MG	1A	3818	1/1	0.96	0.12	41,41,41,41	0
57	MG	1A	3078	1/1	0.96	0.21	34,34,34,34	0
57	MG	1A	3298	1/1	0.96	0.21	39,39,39,39	0
57	MG	1A	3937	1/1	0.96	0.10	53,53,53,53	0
57	MG	1a	1713	1/1	0.96	0.12	37,37,37,37	0
57	MG	2A	3451	1/1	0.96	0.09	42,42,42,42	0
57	MG	1a	1715	1/1	0.96	0.14	57,57,57,57	0
57	MG	2A	3250	1/1	0.96	0.21	57,57,57,57	0
57	MG	1A	3720	1/1	0.96	0.07	29,29,29,29	0
57	MG	1W	205	1/1	0.96	0.06	35,35,35,35	0
57	MG	2A	3682	1/1	0.96	0.07	67,67,67,67	0
57	MG	2A	3459	1/1	0.96	0.13	38,38,38,38	0
57	MG	1W	206	1/1	0.96	0.13	28,28,28,28	0
57	MG	2A	3461	1/1	0.96	0.10	57,57,57,57	0
57	MG	2A	3462	1/1	0.96	0.07	31,31,31,31	0
57	MG	1X	102	1/1	0.96	0.12	37,37,37,37	0
57	MG	1A	3721	1/1	0.96	0.09	42,42,42,42	0
57	MG	2A	3465	1/1	0.96	0.06	60,60,60,60	0
57	MG	1X	105	1/1	0.96	0.07	51,51,51,51	0
57	MG	1A	3530	1/1	0.96	0.09	41,41,41,41	0
57	MG	2A	3693	1/1	0.96	0.13	71,71,71,71	0
57	MG	2A	3468	1/1	0.96	0.07	39,39,39,39	0
57	MG	1A	3117	1/1	0.96	0.22	37,37,37,37	0
57	MG	1a	1725	1/1	0.96	0.07	49,49,49,49	0
57	MG	1A	3614	1/1	0.96	0.16	50,50,50,50	0
57	MG	1Z	302	1/1	0.96	0.25	47,47,47,47	0
57	MG	1A	3615	1/1	0.96	0.11	36,36,36,36	0
57	MG	2A	3701	1/1	0.96	0.04	46,46,46,46	0
57	MG	1A	3726	1/1	0.96	0.06	31,31,31,31	0
57	MG	1A	3616	1/1	0.96	0.05	25,25,25,25	0
57	MG	1A	3080	1/1	0.96	0.11	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	10	106	1/1	0.96	0.27	64,64,64,64	0
57	MG	1A	3733	1/1	0.96	0.05	36,36,36,36	0
57	MG	1A	3399	1/1	0.96	0.25	34,34,34,34	0
57	MG	1A	3619	1/1	0.96	0.08	19,19,19,19	0
57	MG	1A	4090	1/1	0.96	0.31	31,31,31,31	0
57	MG	2a	1672	1/1	0.96	0.14	56,56,56,56	0
57	MG	1A	3346	1/1	0.96	0.14	38,38,38,38	0
57	MG	1A	3301	1/1	0.96	0.19	39,39,39,39	0
57	MG	1A	3148	1/1	0.96	0.06	32,32,32,32	0
57	MG	2A	3488	1/1	0.96	0.10	52,52,52,52	0
57	MG	2A	3715	1/1	0.96	0.07	38,38,38,38	0
57	MG	1A	3955	1/1	0.96	0.08	16,16,16,16	0
57	MG	2A	3089	1/1	0.96	0.10	46,46,46,46	0
57	MG	2A	3090	1/1	0.96	0.09	51,51,51,51	0
57	MG	1A	3625	1/1	0.96	0.05	21,21,21,21	0
57	MG	1A	3021	1/1	0.96	0.07	47,47,47,47	0
57	MG	2A	3726	1/1	0.96	0.06	61,61,61,61	0
57	MG	1A	3181	1/1	0.96	0.15	39,39,39,39	0
57	MG	2A	3280	1/1	0.96	0.14	47,47,47,47	0
57	MG	1A	4098	1/1	0.96	0.10	51,51,51,51	0
57	MG	1A	3631	1/1	0.96	0.05	17,17,17,17	0
57	MG	1A	3009	1/1	0.96	0.04	22,22,22,22	0
57	MG	1A	3963	1/1	0.96	0.06	34,34,34,34	0
57	MG	1A	3964	1/1	0.96	0.10	24,24,24,24	0
57	MG	2A	3736	1/1	0.96	0.05	56,56,56,56	0
57	MG	1A	3965	1/1	0.96	0.05	32,32,32,32	0
57	MG	15	105	1/1	0.96	0.13	43,43,43,43	0
57	MG	2a	1694	1/1	0.96	0.16	63,63,63,63	0
57	MG	1A	3749	1/1	0.96	0.10	47,47,47,47	0
57	MG	1A	3543	1/1	0.96	0.18	55,55,55,55	0
57	MG	17	101	1/1	0.96	0.05	32,32,32,32	0
57	MG	2A	3105	1/1	0.96	0.23	55,55,55,55	0
57	MG	1A	3847	1/1	0.96	0.07	42,42,42,42	0
57	MG	2A	3744	1/1	0.96	0.14	43,43,43,43	0
57	MG	1A	3354	1/1	0.96	0.20	43,43,43,43	0
57	MG	2A	3747	1/1	0.96	0.08	58,58,58,58	0
57	MG	2A	3108	1/1	0.96	0.12	40,40,40,40	0
57	MG	18	101	1/1	0.96	0.18	53,53,53,53	0
57	MG	2a	1705	1/1	0.96	0.16	44,44,44,44	0
57	MG	2A	3750	1/1	0.96	0.07	59,59,59,59	0
57	MG	18	102	1/1	0.96	0.12	39,39,39,39	0
57	MG	1A	3973	1/1	0.96	0.04	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	18	104	1/1	0.96	0.18	41,41,41,41	0
57	MG	1a	1771	1/1	0.96	0.09	45,45,45,45	0
57	MG	1A	3183	1/1	0.96	0.19	45,45,45,45	0
57	MG	1a	1775	1/1	0.96	0.06	62,62,62,62	0
57	MG	1A	3154	1/1	0.96	0.13	30,30,30,30	0
57	MG	1A	3473	1/1	0.96	0.30	38,38,38,38	0
57	MG	1A	3155	1/1	0.96	0.14	27,27,27,27	0
57	MG	2A	3525	1/1	0.96	0.08	35,35,35,35	0
57	MG	1A	3260	1/1	0.96	0.29	47,47,47,47	0
57	MG	1A	3980	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3063	1/1	0.96	0.04	31,31,31,31	0
57	MG	2A	3122	1/1	0.96	0.09	44,44,44,44	0
57	MG	1a	1784	1/1	0.96	0.07	46,46,46,46	0
57	MG	1a	1785	1/1	0.96	0.10	59,59,59,59	0
57	MG	1a	1788	1/1	0.96	0.20	50,50,50,50	0
57	MG	2A	3770	1/1	0.96	0.10	58,58,58,58	0
57	MG	1A	3761	1/1	0.96	0.10	20,20,20,20	0
57	MG	1A	3762	1/1	0.96	0.05	37,37,37,37	0
57	MG	2A	3130	1/1	0.96	0.15	43,43,43,43	0
57	MG	1A	3984	1/1	0.96	0.08	43,43,43,43	0
57	MG	1A	3311	1/1	0.96	0.13	54,54,54,54	0
57	MG	2A	3133	1/1	0.96	0.15	60,60,60,60	0
57	MG	1A	3650	1/1	0.96	0.07	61,61,61,61	0
57	MG	1B	225	1/1	0.96	0.08	37,37,37,37	0
57	MG	1A	3988	1/1	0.96	0.06	51,51,51,51	0
57	MG	2A	3781	1/1	0.96	0.06	52,52,52,52	0
57	MG	1A	3263	1/1	0.96	0.20	39,39,39,39	0
57	MG	1A	3266	1/1	0.96	0.23	28,28,28,28	0
57	MG	1A	3041	1/1	0.96	0.16	30,30,30,30	0
57	MG	1A	3017	1/1	0.96	0.15	28,28,28,28	0
57	MG	1A	3658	1/1	0.96	0.12	31,31,31,31	0
57	MG	2a	1744	1/1	0.96	0.17	64,64,64,64	0
57	MG	1a	1621	1/1	0.96	0.05	43,43,43,43	0
57	MG	1A	3659	1/1	0.96	0.04	23,23,23,23	0
57	MG	1a	1803	1/1	0.96	0.07	50,50,50,50	0
57	MG	2A	3145	1/1	0.96	0.06	55,55,55,55	0
57	MG	1A	3483	1/1	0.96	0.14	35,35,35,35	0
57	MG	1B	234	1/1	0.96	0.06	37,37,37,37	0
57	MG	2a	1752	1/1	0.96	0.09	53,53,53,53	0
57	MG	2A	3148	1/1	0.96	0.25	46,46,46,46	0
57	MG	1D	301	1/1	0.96	0.16	36,36,36,36	0
57	MG	2A	3150	1/1	0.96	0.13	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3338	1/1	0.96	0.08	39,39,39,39	0
57	MG	1A	3772	1/1	0.96	0.08	30,30,30,30	0
57	MG	1A	3054	1/1	0.96	0.06	28,28,28,28	0
57	MG	1A	3662	1/1	0.96	0.06	27,27,27,27	0
57	MG	1D	308	1/1	0.96	0.11	47,47,47,47	0
57	MG	1A	3420	1/1	0.96	0.17	43,43,43,43	0
57	MG	1D	310	1/1	0.96	0.15	26,26,26,26	0
57	MG	1A	4001	1/1	0.96	0.07	29,29,29,29	0
57	MG	1A	4003	1/1	0.96	0.07	45,45,45,45	0
57	MG	1A	3191	1/1	0.96	0.06	40,40,40,40	0
57	MG	1A	3877	1/1	0.96	0.14	33,33,33,33	0
57	MG	2a	1767	1/1	0.96	0.39	69,69,69,69	0
57	MG	2A	3571	1/1	0.96	0.07	46,46,46,46	0
57	MG	1A	3274	1/1	0.96	0.07	37,37,37,37	0
57	MG	1E	306	1/1	0.96	0.11	23,23,23,23	0
57	MG	1A	3778	1/1	0.96	0.09	28,28,28,28	0
57	MG	1a	1640	1/1	0.96	0.34	61,61,61,61	0
57	MG	1m	3001	1/1	0.96	0.13	58,58,58,58	0
57	MG	2A	3169	1/1	0.96	0.12	40,40,40,40	0
57	MG	1A	3228	1/1	0.96	0.16	24,24,24,24	0
57	MG	1A	3230	1/1	0.96	0.23	28,28,28,28	0
57	MG	1A	3192	1/1	0.96	0.13	29,29,29,29	0
57	MG	1A	3883	1/1	0.96	0.09	45,45,45,45	0
57	MG	1w	101	1/1	0.96	0.13	43,43,43,43	0
57	MG	1A	3376	1/1	0.96	0.06	42,42,42,42	0
57	MG	1A	3323	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3888	1/1	0.96	0.06	70,70,70,70	0
57	MG	2A	3587	1/1	0.96	0.15	68,68,68,68	0
57	MG	1A	3891	1/1	0.96	0.07	33,33,33,33	0
57	MG	1A	3232	1/1	0.96	0.05	46,46,46,46	0
57	MG	2A	3366	1/1	0.96	0.17	46,46,46,46	0
57	MG	1A	3893	1/1	0.96	0.10	43,43,43,43	0
57	MG	1A	3109	1/1	0.96	0.05	33,33,33,33	0
57	MG	1A	3573	1/1	0.96	0.07	35,35,35,35	0
57	MG	2A	3370	1/1	0.96	0.16	51,51,51,51	0
57	MG	2A	3183	1/1	0.96	0.19	56,56,56,56	0
57	MG	1a	1654	1/1	0.96	0.14	61,61,61,61	0
57	MG	1A	3194	1/1	0.96	0.07	22,22,22,22	0
57	MG	1A	3161	1/1	0.96	0.06	38,38,38,38	0
57	MG	2A	3600	1/1	0.96	0.08	58,58,58,58	0
57	MG	1A	3027	1/1	0.96	0.32	32,32,32,32	0
57	MG	1A	3902	1/1	0.96	0.06	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1G	201	1/1	0.96	0.14	39,39,39,39	0
57	MG	1A	3071	1/1	0.96	0.33	47,47,47,47	0
57	MG	1A	4032	1/1	0.96	0.13	40,40,40,40	0
57	MG	1A	3436	1/1	0.96	0.14	46,46,46,46	0
57	MG	2A	3607	1/1	0.96	0.09	50,50,50,50	0
57	MG	1A	4034	1/1	0.96	0.15	48,48,48,48	0
57	MG	2A	3610	1/1	0.96	0.08	39,39,39,39	0
57	MG	1A	3504	1/1	0.96	0.22	37,37,37,37	0
57	MG	1A	3132	1/1	0.96	0.15	29,29,29,29	0
57	MG	2Q	203	1/1	0.96	0.05	48,48,48,48	0
57	MG	1A	3506	1/1	0.96	0.17	34,34,34,34	0
57	MG	1A	3689	1/1	0.96	0.08	56,56,56,56	0
57	MG	2A	3006	1/1	0.96	0.06	40,40,40,40	0
57	MG	2a	1813	1/1	0.96	0.13	45,45,45,45	0
57	MG	1A	3073	1/1	0.96	0.10	31,31,31,31	0
57	MG	1A	3046	1/1	0.96	0.06	35,35,35,35	0
57	MG	1O	202	1/1	0.96	0.12	50,50,50,50	0
57	MG	1A	3387	1/1	0.96	0.08	51,51,51,51	0
57	MG	2a	1819	1/1	0.96	0.07	69,69,69,69	0
57	MG	1A	3290	1/1	0.96	0.06	35,35,35,35	0
57	MG	2A	3623	1/1	0.96	0.12	69,69,69,69	0
57	MG	2X	101	1/1	0.96	0.06	65,65,65,65	0
57	MG	1A	3169	1/1	0.96	0.26	29,29,29,29	0
57	MG	1A	4045	1/1	0.96	0.10	44,44,44,44	0
57	MG	1A	3593	1/1	0.96	0.07	22,22,22,22	0
57	MG	1P	202	1/1	0.96	0.22	26,26,26,26	0
57	MG	23	102	1/1	0.96	0.06	54,54,54,54	0
57	MG	1A	3172	1/1	0.96	0.10	35,35,35,35	0
57	MG	1A	3596	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3047	1/1	0.96	0.17	34,34,34,34	0
57	MG	1Q	201	1/1	0.96	0.09	35,35,35,35	0
57	MG	1A	3028	1/1	0.96	0.07	41,41,41,41	0
57	MG	1A	3706	1/1	0.96	0.09	40,40,40,40	0
57	MG	1A	4052	1/1	0.96	0.05	50,50,50,50	0
57	MG	1A	4054	1/1	0.96	0.12	64,64,64,64	0
57	MG	1A	4056	1/1	0.96	0.07	50,50,50,50	0
57	MG	2w	101	1/1	0.96	0.22	66,66,66,66	0
57	MG	1A	4057	1/1	0.96	0.07	51,51,51,51	0
57	MG	28	105	1/1	0.96	0.08	63,63,63,63	0
57	MG	2A	3411	1/1	0.96	0.08	52,52,52,52	0
57	MG	1A	4058	1/1	0.96	0.06	35,35,35,35	0
57	MG	2A	3032	1/1	0.96	0.07	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3450	1/1	0.96	0.05	43,43,43,43	0
57	MG	2A	3034	1/1	0.96	0.21	60,60,60,60	0
57	MG	2A	3416	1/1	0.96	0.09	35,35,35,35	0
57	MG	1a	1689	1/1	0.96	0.07	53,53,53,53	0
57	MG	1A	3522	1/1	0.96	0.28	38,38,38,38	0
57	MG	1A	4061	1/1	0.96	0.06	40,40,40,40	0
57	MG	2A	3420	1/1	0.96	0.15	48,48,48,48	0
57	MG	1A	4062	1/1	0.96	0.14	48,48,48,48	0
57	MG	1A	3451	1/1	0.96	0.17	46,46,46,46	0
57	MG	1A	3926	1/1	0.96	0.14	61,61,61,61	0
57	MG	2A	3228	1/1	0.96	0.09	54,54,54,54	0
57	MG	1A	3604	1/1	0.96	0.07	29,29,29,29	0
57	MG	2a	1615	1/1	0.96	0.32	62,62,62,62	0
57	MG	1A	3207	1/1	0.96	0.11	36,36,36,36	0
57	MG	1A	3714	1/1	0.96	0.08	51,51,51,51	0
60	ZN	2Y	202	1/1	0.96	0.05	105,105,105,105	0
57	MG	2A	3045	1/1	0.96	0.12	55,55,55,55	0
57	MG	1U	201	1/1	0.97	0.13	30,30,30,30	0
57	MG	2A	3422	1/1	0.97	0.11	59,59,59,59	0
57	MG	1A	3521	1/1	0.97	0.14	40,40,40,40	0
57	MG	1U	203	1/1	0.97	0.16	53,53,53,53	0
57	MG	1U	204	1/1	0.97	0.13	35,35,35,35	0
57	MG	2A	3426	1/1	0.97	0.06	44,44,44,44	0
57	MG	1A	3137	1/1	0.97	0.13	51,51,51,51	0
57	MG	1A	3339	1/1	0.97	0.16	48,48,48,48	0
57	MG	1A	3592	1/1	0.97	0.07	27,27,27,27	0
57	MG	2A	3125	1/1	0.97	0.17	44,44,44,44	0
57	MG	2A	3431	1/1	0.97	0.07	53,53,53,53	0
57	MG	1n	101	1/1	0.97	0.15	46,46,46,46	0
57	MG	2A	3127	1/1	0.97	0.18	44,44,44,44	0
57	MG	1A	3138	1/1	0.97	0.12	57,57,57,57	0
57	MG	1A	3594	1/1	0.97	0.11	58,58,58,58	0
57	MG	1A	3087	1/1	0.97	0.10	27,27,27,27	0
57	MG	1V	202	1/1	0.97	0.16	36,36,36,36	0
57	MG	1A	3470	1/1	0.97	0.20	35,35,35,35	0
57	MG	1A	3212	1/1	0.97	0.07	45,45,45,45	0
57	MG	1A	3684	1/1	0.97	0.15	50,50,50,50	0
57	MG	1A	3685	1/1	0.97	0.08	44,44,44,44	0
57	MG	1W	202	1/1	0.97	0.09	57,57,57,57	0
57	MG	1W	203	1/1	0.97	0.19	33,33,33,33	0
57	MG	2A	3285	1/1	0.97	0.07	58,58,58,58	0
57	MG	1B	202	1/1	0.97	0.17	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3188	1/1	0.97	0.28	31,31,31,31	0
57	MG	1A	3599	1/1	0.97	0.04	16,16,16,16	0
57	MG	2A	3621	1/1	0.97	0.07	34,34,34,34	0
57	MG	1A	3020	1/1	0.97	0.13	26,26,26,26	0
57	MG	1A	3425	1/1	0.97	0.20	37,37,37,37	0
57	MG	1B	207	1/1	0.97	0.07	42,42,42,42	0
57	MG	1A	3693	1/1	0.97	0.07	52,52,52,52	0
57	MG	2A	3453	1/1	0.97	0.10	38,38,38,38	0
57	MG	1A	3884	1/1	0.97	0.06	45,45,45,45	0
57	MG	1A	3065	1/1	0.97	0.06	14,14,14,14	0
57	MG	1A	3168	1/1	0.97	0.09	37,37,37,37	0
57	MG	1A	3605	1/1	0.97	0.04	27,27,27,27	0
57	MG	1A	3697	1/1	0.97	0.07	53,53,53,53	0
57	MG	1A	3090	1/1	0.97	0.19	37,37,37,37	0
57	MG	10	104	1/1	0.97	0.11	44,44,44,44	0
57	MG	1B	215	1/1	0.97	0.05	55,55,55,55	0
57	MG	2A	3154	1/1	0.97	0.09	60,60,60,60	0
57	MG	1A	3699	1/1	0.97	0.11	29,29,29,29	0
57	MG	1A	4002	1/1	0.97	0.05	34,34,34,34	0
57	MG	1A	3700	1/1	0.97	0.07	24,24,24,24	0
57	MG	2D	304	1/1	0.97	0.05	27,27,27,27	0
57	MG	1A	3535	1/1	0.97	0.15	28,28,28,28	0
57	MG	2A	3469	1/1	0.97	0.06	39,39,39,39	0
57	MG	1A	3171	1/1	0.97	0.07	34,34,34,34	0
57	MG	1a	1702	1/1	0.97	0.11	38,38,38,38	0
57	MG	1A	3349	1/1	0.97	0.09	40,40,40,40	0
57	MG	2A	3162	1/1	0.97	0.06	34,34,34,34	0
57	MG	2E	303	1/1	0.97	0.10	43,43,43,43	0
57	MG	1A	3350	1/1	0.97	0.17	24,24,24,24	0
57	MG	1A	3032	1/1	0.97	0.38	27,27,27,27	0
57	MG	1A	3801	1/1	0.97	0.05	53,53,53,53	0
57	MG	1A	3482	1/1	0.97	0.19	37,37,37,37	0
57	MG	1A	3905	1/1	0.97	0.07	62,62,62,62	0
57	MG	2A	3479	1/1	0.97	0.06	39,39,39,39	0
57	MG	2A	3480	1/1	0.97	0.07	31,31,31,31	0
57	MG	2a	1736	1/1	0.97	0.21	56,56,56,56	0
57	MG	1A	3542	1/1	0.97	0.08	37,37,37,37	0
57	MG	12	103	1/1	0.97	0.10	43,43,43,43	0
57	MG	2A	3021	1/1	0.97	0.08	44,44,44,44	0
57	MG	13	101	1/1	0.97	0.05	36,36,36,36	0
57	MG	13	102	1/1	0.97	0.10	39,39,39,39	0
57	MG	2A	3024	1/1	0.97	0.11	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3250	1/1	0.97	0.15	51,51,51,51	0
57	MG	2a	1746	1/1	0.97	0.09	64,64,64,64	0
57	MG	1A	4016	1/1	0.97	0.04	25,25,25,25	0
57	MG	13	105	1/1	0.97	0.06	52,52,52,52	0
57	MG	1A	3317	1/1	0.97	0.26	41,41,41,41	0
57	MG	1A	3286	1/1	0.97	0.10	31,31,31,31	0
57	MG	1A	3107	1/1	0.97	0.10	33,33,33,33	0
57	MG	1A	3043	1/1	0.97	0.08	42,42,42,42	0
57	MG	2A	3667	1/1	0.97	0.06	50,50,50,50	0
57	MG	1A	3441	1/1	0.97	0.12	64,64,64,64	0
57	MG	1A	3913	1/1	0.97	0.05	43,43,43,43	0
57	MG	1A	3489	1/1	0.97	0.18	38,38,38,38	0
57	MG	1A	3811	1/1	0.97	0.06	64,64,64,64	0
57	MG	17	102	1/1	0.97	0.11	33,33,33,33	0
57	MG	2A	3673	1/1	0.97	0.06	49,49,49,49	0
57	MG	1D	306	1/1	0.97	0.06	29,29,29,29	0
57	MG	1A	3037	1/1	0.97	0.16	32,32,32,32	0
57	MG	1a	1730	1/1	0.97	0.08	54,54,54,54	0
57	MG	1A	3624	1/1	0.97	0.05	29,29,29,29	0
57	MG	2W	202	1/1	0.97	0.06	47,47,47,47	0
57	MG	1A	3551	1/1	0.97	0.07	33,33,33,33	0
57	MG	1A	3010	1/1	0.97	0.08	31,31,31,31	0
57	MG	1A	3225	1/1	0.97	0.10	61,61,61,61	0
57	MG	1A	3324	1/1	0.97	0.20	30,30,30,30	0
57	MG	1A	3365	1/1	0.97	0.18	42,42,42,42	0
57	MG	1A	3819	1/1	0.97	0.05	43,43,43,43	0
57	MG	1A	3083	1/1	0.97	0.12	39,39,39,39	0
57	MG	1A	3637	1/1	0.97	0.08	45,45,45,45	0
57	MG	1A	3730	1/1	0.97	0.05	22,22,22,22	0
57	MG	1A	3638	1/1	0.97	0.05	31,31,31,31	0
57	MG	1A	3496	1/1	0.97	0.26	54,54,54,54	0
57	MG	1A	3640	1/1	0.97	0.07	22,22,22,22	0
57	MG	1A	4043	1/1	0.97	0.15	55,55,55,55	0
57	MG	2A	3691	1/1	0.97	0.08	57,57,57,57	0
57	MG	1a	1607	1/1	0.97	0.27	60,60,60,60	0
57	MG	1A	3735	1/1	0.97	0.09	25,25,25,25	0
57	MG	1A	3497	1/1	0.97	0.11	47,47,47,47	0
57	MG	1A	3560	1/1	0.97	0.07	21,21,21,21	0
57	MG	1A	3644	1/1	0.97	0.06	26,26,26,26	0
57	MG	1A	3448	1/1	0.97	0.11	37,37,37,37	0
57	MG	1A	3404	1/1	0.97	0.16	37,37,37,37	0
57	MG	2A	3528	1/1	0.97	0.04	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1F	310	1/1	0.97	0.09	29,29,29,29	0
57	MG	1A	3743	1/1	0.97	0.04	38,38,38,38	0
57	MG	2A	3361	1/1	0.97	0.20	54,54,54,54	0
57	MG	1a	1617	1/1	0.97	0.13	45,45,45,45	0
57	MG	1a	1759	1/1	0.97	0.05	67,67,67,67	0
57	MG	1a	1619	1/1	0.97	0.05	51,51,51,51	0
57	MG	1A	3128	1/1	0.97	0.04	36,36,36,36	0
57	MG	1A	3564	1/1	0.97	0.12	53,53,53,53	0
57	MG	1A	4053	1/1	0.97	0.13	24,24,24,24	0
57	MG	2A	3070	1/1	0.97	0.11	28,28,28,28	0
57	MG	1A	3229	1/1	0.97	0.09	45,45,45,45	0
57	MG	1a	1766	1/1	0.97	0.11	64,64,64,64	0
57	MG	2A	3371	1/1	0.97	0.07	24,24,24,24	0
57	MG	1a	1768	1/1	0.97	0.06	53,53,53,53	0
57	MG	2A	3544	1/1	0.97	0.13	50,50,50,50	0
57	MG	2a	1803	1/1	0.97	0.12	61,61,61,61	0
57	MG	2A	3373	1/1	0.97	0.40	42,42,42,42	0
57	MG	2a	1621	1/1	0.97	0.19	61,61,61,61	0
57	MG	2a	1622	1/1	0.97	0.08	59,59,59,59	0
57	MG	1A	4055	1/1	0.97	0.08	58,58,58,58	0
57	MG	2A	3721	1/1	0.97	0.13	64,64,64,64	0
57	MG	1A	3502	1/1	0.97	0.06	28,28,28,28	0
57	MG	1A	3015	1/1	0.97	0.16	37,37,37,37	0
57	MG	2A	3724	1/1	0.97	0.10	56,56,56,56	0
57	MG	1A	3055	1/1	0.97	0.22	49,49,49,49	0
57	MG	1A	3839	1/1	0.97	0.06	30,30,30,30	0
57	MG	2A	3079	1/1	0.97	0.09	58,58,58,58	0
57	MG	1A	3751	1/1	0.97	0.06	23,23,23,23	0
57	MG	1A	3655	1/1	0.97	0.06	28,28,28,28	0
57	MG	2A	3732	1/1	0.97	0.07	64,64,64,64	0
57	MG	1A	3842	1/1	0.97	0.05	23,23,23,23	0
57	MG	1a	1781	1/1	0.97	0.09	53,53,53,53	0
57	MG	2a	1821	1/1	0.97	0.06	66,66,66,66	0
57	MG	1A	3409	1/1	0.97	0.26	39,39,39,39	0
57	MG	1A	3455	1/1	0.97	0.17	28,28,28,28	0
57	MG	1A	4065	1/1	0.97	0.11	51,51,51,51	0
57	MG	1A	3952	1/1	0.97	0.04	48,48,48,48	0
57	MG	1a	1786	1/1	0.97	0.05	53,53,53,53	0
57	MG	1a	1787	1/1	0.97	0.05	52,52,52,52	0
57	MG	1A	3756	1/1	0.97	0.05	39,39,39,39	0
57	MG	2A	3563	1/1	0.97	0.09	71,71,71,71	0
57	MG	1A	4068	1/1	0.97	0.15	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3261	1/1	0.97	0.17	33,33,33,33	0
57	MG	2A	3745	1/1	0.97	0.09	57,57,57,57	0
57	MG	1A	3131	1/1	0.97	0.08	28,28,28,28	0
57	MG	1A	3086	1/1	0.97	0.09	59,59,59,59	0
57	MG	1A	3850	1/1	0.97	0.09	21,21,21,21	0
57	MG	1A	3959	1/1	0.97	0.06	53,53,53,53	0
57	MG	1A	3264	1/1	0.97	0.05	49,49,49,49	0
57	MG	1A	3265	1/1	0.97	0.18	40,40,40,40	0
57	MG	2A	3572	1/1	0.97	0.10	56,56,56,56	0
57	MG	1A	3205	1/1	0.97	0.06	48,48,48,48	0
57	MG	1Q	203	1/1	0.97	0.14	52,52,52,52	0
57	MG	1A	3664	1/1	0.97	0.07	38,38,38,38	0
57	MG	1A	3100	1/1	0.97	0.08	41,41,41,41	0
57	MG	1A	3515	1/1	0.97	0.11	31,31,31,31	0
57	MG	1A	3857	1/1	0.97	0.06	34,34,34,34	0
57	MG	2a	1660	1/1	0.97	0.17	42,42,42,42	0
57	MG	1R	201	1/1	0.97	0.18	43,43,43,43	0
57	MG	2a	1662	1/1	0.97	0.09	51,51,51,51	0
57	MG	1A	4081	1/1	0.97	0.07	57,57,57,57	0
57	MG	1R	203	1/1	0.97	0.36	38,38,38,38	0
57	MG	1A	3967	1/1	0.97	0.07	28,28,28,28	0
57	MG	1A	3464	1/1	0.97	0.19	29,29,29,29	0
57	MG	1A	3969	1/1	0.97	0.08	37,37,37,37	0
57	MG	1A	3517	1/1	0.97	0.14	23,23,23,23	0
57	MG	1A	3134	1/1	0.97	0.10	41,41,41,41	0
57	MG	1A	3520	1/1	0.97	0.22	40,40,40,40	0
57	MG	1A	3587	1/1	0.97	0.04	41,41,41,41	0
57	MG	1A	3588	1/1	0.97	0.04	18,18,18,18	0
60	ZN	14	102	1/1	0.97	0.07	100,100,100,100	0
57	MG	2A	3772	1/1	0.97	0.04	49,49,49,49	0
57	MG	1A	3976	1/1	0.97	0.06	57,57,57,57	0
57	MG	1D	307	1/1	0.98	0.16	36,36,36,36	0
57	MG	1A	3692	1/1	0.98	0.05	46,46,46,46	0
57	MG	1U	208	1/1	0.98	0.29	37,37,37,37	0
57	MG	2A	3446	1/1	0.98	0.07	45,45,45,45	0
57	MG	1a	1618	1/1	0.98	0.04	36,36,36,36	0
57	MG	1A	3074	1/1	0.98	0.11	42,42,42,42	0
57	MG	1A	3752	1/1	0.98	0.05	20,20,20,20	0
57	MG	1A	3642	1/1	0.98	0.07	29,29,29,29	0
57	MG	1A	3008	1/1	0.98	0.04	26,26,26,26	0
57	MG	1E	301	1/1	0.98	0.24	36,36,36,36	0
57	MG	1A	3236	1/1	0.98	0.18	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3454	1/1	0.98	0.09	35,35,35,35	0
57	MG	2A	3455	1/1	0.98	0.10	35,35,35,35	0
57	MG	2A	3152	1/1	0.98	0.10	58,58,58,58	0
57	MG	1a	1709	1/1	0.98	0.06	41,41,41,41	0
57	MG	1A	3003	1/1	0.98	0.04	22,22,22,22	0
57	MG	1E	304	1/1	0.98	0.14	29,29,29,29	0
57	MG	1A	3149	1/1	0.98	0.11	37,37,37,37	0
57	MG	1A	3519	1/1	0.98	0.17	35,35,35,35	0
57	MG	1A	3150	1/1	0.98	0.16	48,48,48,48	0
57	MG	1A	3240	1/1	0.98	0.06	48,48,48,48	0
57	MG	1A	3007	1/1	0.98	0.05	35,35,35,35	0
57	MG	1X	101	1/1	0.98	0.22	40,40,40,40	0
57	MG	1A	3945	1/1	0.98	0.07	26,26,26,26	0
57	MG	1X	103	1/1	0.98	0.05	44,44,44,44	0
57	MG	1A	3651	1/1	0.98	0.09	28,28,28,28	0
57	MG	1A	3602	1/1	0.98	0.14	24,24,24,24	0
57	MG	1f	201	1/1	0.98	0.10	41,41,41,41	0
57	MG	1A	4015	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3011	1/1	0.98	0.12	48,48,48,48	0
57	MG	1A	3269	1/1	0.98	0.08	30,30,30,30	0
57	MG	1F	306	1/1	0.98	0.20	36,36,36,36	0
57	MG	1A	3355	1/1	0.98	0.31	27,27,27,27	0
57	MG	1A	4019	1/1	0.98	0.05	41,41,41,41	0
57	MG	1A	3710	1/1	0.98	0.07	19,19,19,19	0
57	MG	1A	4021	1/1	0.98	0.09	19,19,19,19	0
57	MG	1A	3270	1/1	0.98	0.17	33,33,33,33	0
57	MG	1A	3527	1/1	0.98	0.23	34,34,34,34	0
57	MG	1A	3890	1/1	0.98	0.03	31,31,31,31	0
57	MG	1A	4026	1/1	0.98	0.05	46,46,46,46	0
57	MG	2A	3594	1/1	0.98	0.05	65,65,65,65	0
57	MG	2A	3708	1/1	0.98	0.11	39,39,39,39	0
57	MG	2A	3377	1/1	0.98	0.04	37,37,37,37	0
57	MG	1a	1650	1/1	0.98	0.08	44,44,44,44	0
57	MG	1A	3357	1/1	0.98	0.23	27,27,27,27	0
57	MG	1A	3609	1/1	0.98	0.06	39,39,39,39	0
57	MG	1A	3358	1/1	0.98	0.05	38,38,38,38	0
57	MG	1A	3958	1/1	0.98	0.04	37,37,37,37	0
57	MG	1A	3894	1/1	0.98	0.03	54,54,54,54	0
57	MG	1A	3153	1/1	0.98	0.11	32,32,32,32	0
57	MG	1a	1744	1/1	0.98	0.06	43,43,43,43	0
57	MG	1A	3896	1/1	0.98	0.03	36,36,36,36	0
57	MG	1A	3079	1/1	0.98	0.30	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	2A	3497	1/1	0.98	0.04	40,40,40,40	0
57	MG	1A	3105	1/1	0.98	0.06	40,40,40,40	0
57	MG	2a	1797	1/1	0.98	0.17	54,54,54,54	0
57	MG	1N	202	1/1	0.98	0.04	45,45,45,45	0
57	MG	2A	3725	1/1	0.98	0.06	42,42,42,42	0
57	MG	2A	3500	1/1	0.98	0.08	59,59,59,59	0
57	MG	2A	3093	1/1	0.98	0.05	28,28,28,28	0
57	MG	2A	3728	1/1	0.98	0.07	36,36,36,36	0
57	MG	1N	203	1/1	0.98	0.04	44,44,44,44	0
57	MG	1A	3362	1/1	0.98	0.04	29,29,29,29	0
57	MG	1A	3221	1/1	0.98	0.13	42,42,42,42	0
57	MG	1A	3901	1/1	0.98	0.04	53,53,53,53	0
57	MG	1a	1753	1/1	0.98	0.05	66,66,66,66	0
57	MG	2A	3002	1/1	0.98	0.27	49,49,49,49	0
57	MG	1A	3013	1/1	0.98	0.12	29,29,29,29	0
57	MG	1A	3135	1/1	0.98	0.10	33,33,33,33	0
57	MG	1A	3069	1/1	0.98	0.06	27,27,27,27	0
57	MG	1a	1757	1/1	0.98	0.06	45,45,45,45	0
57	MG	1A	3121	1/1	0.98	0.16	33,33,33,33	0
57	MG	2A	3624	1/1	0.98	0.06	33,33,33,33	0
57	MG	2a	1815	1/1	0.98	0.05	67,67,67,67	0
57	MG	1A	3971	1/1	0.98	0.07	38,38,38,38	0
57	MG	2A	3009	1/1	0.98	0.04	40,40,40,40	0
57	MG	2A	3404	1/1	0.98	0.07	63,63,63,63	0
57	MG	1A	3671	1/1	0.98	0.06	21,21,21,21	0
57	MG	2X	102	1/1	0.98	0.12	48,48,48,48	0
57	MG	2Y	201	1/1	0.98	0.16	60,60,60,60	0
57	MG	1A	3539	1/1	0.98	0.19	49,49,49,49	0
57	MG	2A	3012	1/1	0.98	0.06	48,48,48,48	0
57	MG	2A	3306	1/1	0.98	0.06	43,43,43,43	0
57	MG	1a	1762	1/1	0.98	0.06	64,64,64,64	0
57	MG	23	101	1/1	0.98	0.06	58,58,58,58	0
57	MG	1A	3728	1/1	0.98	0.05	54,54,54,54	0
57	MG	1B	216	1/1	0.98	0.15	38,38,38,38	0
57	MG	1A	3729	1/1	0.98	0.09	18,18,18,18	0
57	MG	1A	3580	1/1	0.98	0.07	27,27,27,27	0
57	MG	2A	3018	1/1	0.98	0.11	33,33,33,33	0
57	MG	1A	3731	1/1	0.98	0.05	40,40,40,40	0
57	MG	1a	1769	1/1	0.98	0.09	58,58,58,58	0
57	MG	1A	3622	1/1	0.98	0.05	39,39,39,39	0
57	MG	2A	3641	1/1	0.98	0.20	41,41,41,41	0
57	MG	1A	3846	1/1	0.98	0.07	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3044	1/1	0.98	0.05	35,35,35,35	0
57	MG	2A	3421	1/1	0.98	0.07	39,39,39,39	0
57	MG	2A	3761	1/1	0.98	0.06	57,57,57,57	0
57	MG	1a	1773	1/1	0.98	0.04	63,63,63,63	0
57	MG	1A	3227	1/1	0.98	0.13	29,29,29,29	0
57	MG	1A	3141	1/1	0.98	0.15	32,32,32,32	0
57	MG	1A	3142	1/1	0.98	0.06	32,32,32,32	0
57	MG	1A	3585	1/1	0.98	0.07	56,56,56,56	0
57	MG	1A	3738	1/1	0.98	0.09	48,48,48,48	0
57	MG	1A	3628	1/1	0.98	0.06	36,36,36,36	0
57	MG	1A	3629	1/1	0.98	0.04	21,21,21,21	0
57	MG	1A	3741	1/1	0.98	0.09	47,47,47,47	0
57	MG	1A	3437	1/1	0.98	0.07	45,45,45,45	0
57	MG	1A	3438	1/1	0.98	0.06	45,45,45,45	0
57	MG	1A	3744	1/1	0.98	0.05	42,42,42,42	0
57	MG	1A	3284	1/1	0.98	0.14	41,41,41,41	0
57	MG	2a	1731	1/1	0.98	0.04	70,70,70,70	0
57	MG	2A	3037	1/1	0.98	0.06	52,52,52,52	0
57	MG	1A	3030	1/1	0.98	0.09	22,22,22,22	0
57	MG	1A	3995	1/1	0.98	0.07	37,37,37,37	0
57	MG	1A	3164	1/1	0.98	0.10	17,17,17,17	0
57	MG	1a	1611	1/1	0.98	0.05	29,29,29,29	0
57	MG	1D	304	1/1	0.98	0.08	22,22,22,22	0
57	MG	1A	3072	1/1	0.98	0.12	39,39,39,39	0
57	MG	1A	3053	1/1	0.98	0.07	33,33,33,33	0
60	ZN	29	102	1/1	0.98	0.04	78,78,78,78	0
60	ZN	2n	501	1/1	0.98	0.04	86,86,86,86	0
61	SF4	2d	303	8/8	0.98	0.04	67,73,84,84	0
57	MG	1A	3268	1/1	0.99	0.14	33,33,33,33	0
57	MG	2A	3490	1/1	0.99	0.06	35,35,35,35	0
57	MG	2A	3716	1/1	0.99	0.07	37,37,37,37	0
57	MG	1Q	202	1/1	0.99	0.03	35,35,35,35	0
57	MG	2a	1743	1/1	0.99	0.09	69,69,69,69	0
57	MG	2A	3718	1/1	0.99	0.04	51,51,51,51	0
57	MG	2A	3492	1/1	0.99	0.04	59,59,59,59	0
57	MG	1A	3921	1/1	0.99	0.03	27,27,27,27	0
57	MG	2A	3337	1/1	0.99	0.05	32,32,32,32	0
57	MG	1A	3031	1/1	0.99	0.11	23,23,23,23	0
57	MG	1X	106	1/1	0.99	0.05	34,34,34,34	0
57	MG	1A	3886	1/1	0.99	0.03	12,12,12,12	0
57	MG	1a	1735	1/1	0.99	0.10	58,58,58,58	0
57	MG	2A	3786	1/1	0.99	0.03	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1A	3067	1/1	0.99	0.04	16,16,16,16	0
57	MG	1A	3098	1/1	0.99	0.21	35,35,35,35	0
57	MG	1A	3553	1/1	0.99	0.29	31,31,31,31	0
57	MG	1A	3426	1/1	0.99	0.07	43,43,43,43	0
57	MG	1A	3703	1/1	0.99	0.07	46,46,46,46	0
57	MG	2A	3616	1/1	0.99	0.04	49,49,49,49	0
57	MG	1A	4004	1/1	0.99	0.03	41,41,41,41	0
57	MG	1A	3652	1/1	0.99	0.05	40,40,40,40	0
57	MG	1A	3572	1/1	0.99	0.04	21,21,21,21	0
57	MG	1A	3678	1/1	0.99	0.04	16,16,16,16	0
57	MG	1A	3630	1/1	0.99	0.07	26,26,26,26	0
57	MG	1A	3860	1/1	0.99	0.04	36,36,36,36	0
57	MG	1A	3708	1/1	0.99	0.04	42,42,42,42	0
57	MG	1A	3935	1/1	0.99	0.04	39,39,39,39	0
57	MG	2A	3406	1/1	0.99	0.06	65,65,65,65	0
57	MG	1A	3799	1/1	0.99	0.06	32,32,32,32	0
57	MG	1A	3136	1/1	0.99	0.06	16,16,16,16	0
57	MG	1A	3062	1/1	0.99	0.11	30,30,30,30	0
57	MG	1A	3633	1/1	0.99	0.04	27,27,27,27	0
57	MG	1A	3634	1/1	0.99	0.05	20,20,20,20	0
57	MG	1A	3635	1/1	0.99	0.02	26,26,26,26	0
57	MG	1A	3869	1/1	0.99	0.03	25,25,25,25	0
57	MG	1A	3870	1/1	0.99	0.03	26,26,26,26	0
57	MG	1A	3575	1/1	0.99	0.06	29,29,29,29	0
57	MG	1A	3012	1/1	0.99	0.03	23,23,23,23	0
57	MG	1A	4022	1/1	0.99	0.05	22,22,22,22	0
57	MG	1A	3687	1/1	0.99	0.06	21,21,21,21	0
57	MG	1A	3717	1/1	0.99	0.07	41,41,41,41	0
57	MG	1a	1714	1/1	0.99	0.08	45,45,45,45	0
57	MG	1A	3688	1/1	0.99	0.05	21,21,21,21	0
57	MG	1A	3122	1/1	0.99	0.18	32,32,32,32	0
57	MG	1A	3987	1/1	0.99	0.03	21,21,21,21	0
57	MG	15	103	1/1	0.99	0.32	28,28,28,28	0
57	MG	2A	3700	1/1	0.99	0.03	47,47,47,47	0
57	MG	1a	1767	1/1	0.99	0.04	59,59,59,59	0
57	MG	1A	3170	1/1	0.99	0.14	27,27,27,27	0
57	MG	1A	3462	1/1	0.99	0.19	39,39,39,39	0
57	MG	2A	3535	1/1	0.99	0.08	38,38,38,38	0
57	MG	1A	3140	1/1	0.99	0.12	32,32,32,32	0
57	MG	1a	1722	1/1	0.99	0.05	35,35,35,35	0
57	MG	2A	3766	1/1	0.99	0.05	54,54,54,54	0
57	MG	1A	3014	1/1	0.99	0.04	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MG	1a	1632	1/1	0.99	0.09	23,23,23,23	0
60	ZN	1Y	203	1/1	0.99	0.03	68,68,68,68	0
57	MG	1a	1774	1/1	0.99	0.03	44,44,44,44	0
60	ZN	15	107	1/1	0.99	0.03	43,43,43,43	0
60	ZN	16	102	1/1	0.99	0.03	44,44,44,44	0
60	ZN	19	102	1/1	0.99	0.04	42,42,42,42	0
60	ZN	1n	102	1/1	0.99	0.03	57,57,57,57	0
57	MG	1A	3279	1/1	0.99	0.20	30,30,30,30	0
57	MG	1A	3206	1/1	0.99	0.11	39,39,39,39	0
60	ZN	25	105	1/1	0.99	0.04	57,57,57,57	0
60	ZN	26	501	1/1	0.99	0.03	61,61,61,61	0
57	MG	17	103	1/1	0.99	0.05	29,29,29,29	0
57	MG	2a	1737	1/1	0.99	0.03	52,52,52,52	0
61	SF4	1d	501	8/8	0.99	0.06	56,62,68,68	0
57	MG	1A	3040	1/1	0.99	0.06	35,35,35,35	0
57	MG	2A	3608	1/1	1.00	0.02	32,32,32,32	0
57	MG	2A	3496	1/1	1.00	0.05	33,33,33,33	0
57	MG	1A	3889	1/1	1.00	0.04	23,23,23,23	0
57	MG	1a	1776	1/1	1.00	0.05	49,49,49,49	0
57	MG	1A	3864	1/1	1.00	0.06	38,38,38,38	0

6.5 Other polymers

There are no such residues in this entry.