



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:30 AM UTC

PDB ID : 4Z3S / pdb_00004z3s
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with antibiotic A201A, mRNA and three tRNAs in the A, P and E sites at 2.65Å resolution
Authors : Polikanov, Y.S.; Starosta, A.L.; Juetter, M.F.; Altman, R.B.; Terry, D.S.; Lu, W.; Burnett, B.J.; Dinos, G.; Reynolds, K.; Blanchard, S.C.; Steitz, T.A.; Wilson, D.N.
Deposited on : 2015-03-31
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	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

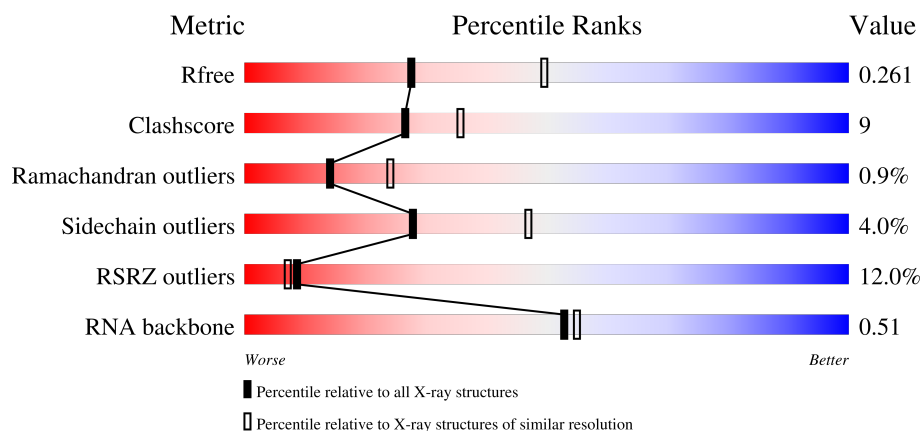
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	6% 64% 28% 7%
1	2A	2915	4% 52% 36% 8%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
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	
14	1S	112	

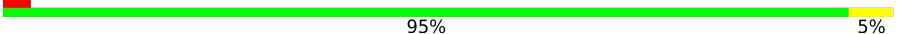
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Mol	Chain	Length	Quality of chain
14	2S	112	
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24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

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Mol	Chain	Length	Quality of chain
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	
39	1h	138	

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Mol	Chain	Length	Quality of chain
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	
51	2t	106	

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	3059	-	-	-	X
56	MG	1A	3216	-	-	-	X
56	MG	2B	3011	-	-	-	X
56	MG	2a	1691	-	-	-	X
56	MG	2a	1760	-	-	-	X

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 299169 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
			61852	27531	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60322	26848	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	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1429	916	256	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 mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1v	14	Total	C	N	O	P	0	0	0
			281	125	51	91	14			
53	2v	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			

- Molecule 54 is a RNA chain called A/E-site tRNAs.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1588	713	285	515	73	2			
54	1y	74	Total	C	N	O	P	S	0	0	0
			1581	707	285	515	73	1			
54	2w	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			
54	2y	73	Total	C	N	O	P	S	0	0	0
			1561	698	283	507	72	1			

- Molecule 55 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
55	1x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
55	2x	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	935	Total	Mg	0	0
			935	935		
56	1B	25	Total	Mg	0	0
			25	25		
56	1D	9	Total	Mg	0	0
			9	9		
56	1E	8	Total	Mg	0	0
			8	8		
56	1F	8	Total	Mg	0	0
			8	8		
56	1G	5	Total	Mg	0	0
			5	5		
56	1I	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1N	6	Total 6	Mg 6	0	0
56	1O	3	Total 3	Mg 3	0	0
56	1P	3	Total 3	Mg 3	0	0
56	1Q	5	Total 5	Mg 5	0	0
56	1R	2	Total 2	Mg 2	0	0
56	1S	1	Total 1	Mg 1	0	0
56	1T	2	Total 2	Mg 2	0	0
56	1U	4	Total 4	Mg 4	0	0
56	1V	3	Total 3	Mg 3	0	0
56	1W	4	Total 4	Mg 4	0	0
56	1X	3	Total 3	Mg 3	0	0
56	1Y	2	Total 2	Mg 2	0	0
56	1Z	3	Total 3	Mg 3	0	0
56	10	6	Total 6	Mg 6	0	0
56	11	2	Total 2	Mg 2	0	0
56	12	2	Total 2	Mg 2	0	0
56	13	1	Total 1	Mg 1	0	0
56	15	4	Total 4	Mg 4	0	0
56	16	2	Total 2	Mg 2	0	0
56	17	1	Total 1	Mg 1	0	0
56	18	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	19	2	Total 2	Mg 2	0	0
56	1a	234	Total 234	Mg 234	0	0
56	1b	2	Total 2	Mg 2	0	0
56	1c	1	Total 1	Mg 1	0	0
56	1d	1	Total 1	Mg 1	0	0
56	1e	1	Total 1	Mg 1	0	0
56	1f	1	Total 1	Mg 1	0	0
56	1g	1	Total 1	Mg 1	0	0
56	1l	3	Total 3	Mg 3	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1r	1	Total 1	Mg 1	0	0
56	1s	1	Total 1	Mg 1	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1v	1	Total 1	Mg 1	0	0
56	1w	5	Total 5	Mg 5	0	0
56	1x	14	Total 14	Mg 14	0	0
56	1y	7	Total 7	Mg 7	0	0
56	2A	679	Total 679	Mg 679	0	0
56	2B	21	Total 21	Mg 21	0	0
56	2D	4	Total 4	Mg 4	0	0
56	2E	7	Total 7	Mg 7	0	0

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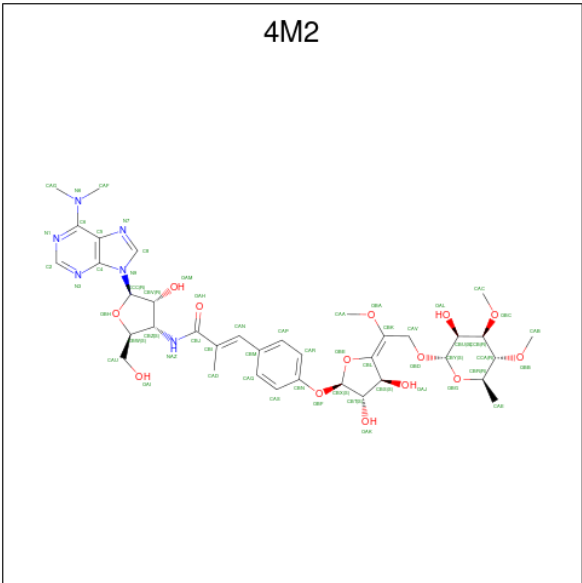
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2F	5	Total 5	Mg 5	0	0
56	2G	1	Total 1	Mg 1	0	0
56	2N	1	Total 1	Mg 1	0	0
56	2O	2	Total 2	Mg 2	0	0
56	2Q	3	Total 3	Mg 3	0	0
56	2R	1	Total 1	Mg 1	0	0
56	2T	1	Total 1	Mg 1	0	0
56	2U	2	Total 2	Mg 2	0	0
56	2V	3	Total 3	Mg 3	0	0
56	2X	2	Total 2	Mg 2	0	0
56	2Z	1	Total 1	Mg 1	0	0
56	20	3	Total 3	Mg 3	0	0
56	21	2	Total 2	Mg 2	0	0
56	23	1	Total 1	Mg 1	0	0
56	25	1	Total 1	Mg 1	0	0
56	28	1	Total 1	Mg 1	0	0
56	2a	200	Total 200	Mg 200	0	0
56	2d	1	Total 1	Mg 1	0	0
56	2e	2	Total 2	Mg 2	0	0
56	2f	2	Total 2	Mg 2	0	0
56	2g	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2j	2	Total	Mg	0	0
			2	2		
56	2l	2	Total	Mg	0	0
			2	2		
56	2p	1	Total	Mg	0	0
			1	1		
56	2q	3	Total	Mg	0	0
			3	3		
56	2r	1	Total	Mg	0	0
			1	1		
56	2t	1	Total	Mg	0	0
			1	1		
56	2v	2	Total	Mg	0	0
			2	2		
56	2w	3	Total	Mg	0	0
			3	3		
56	2x	2	Total	Mg	0	0
			2	2		

- Molecule 57 is 3'-deoxy-3'-{[(2E)-3-(4-{[(4Z)-6-O-(6-deoxy-3,4-di-O-methyl-alpha-D-manno pyranosyl)-5-O-methyl-alpha-D-threo-hex-4-enofuranosyl]oxy}phenyl)-2-methylprop-2-enoyl]amino}-N,N-dimethyladenosine (CCD ID: 4M2) (formula: C₃₇H₅₀N₆O₁₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	1A	1	Total	C	N	O	
			57	37	6	14	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	2A	1	Total	C	N	O	0	0
			57	37	6	14		

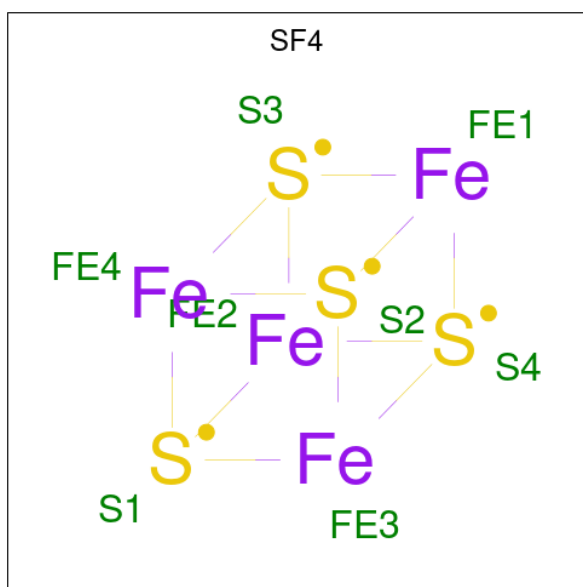
- Molecule 58 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1A	1	Total	K	0	0
			1	1		
58	2A	1	Total	K	0	0
			1	1		

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

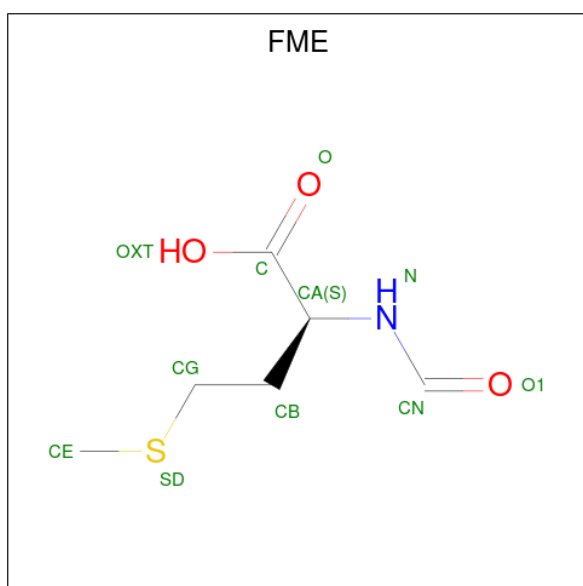
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1Y	1	Total	Zn	0	0
			1	1		
59	14	1	Total	Zn	0	0
			1	1		
59	15	1	Total	Zn	0	0
			1	1		
59	16	1	Total	Zn	0	0
			1	1		
59	19	1	Total	Zn	0	0
			1	1		
59	1n	1	Total	Zn	0	0
			1	1		
59	2Y	1	Total	Zn	0	0
			1	1		
59	24	1	Total	Zn	0	0
			1	1		
59	25	1	Total	Zn	0	0
			1	1		
59	26	1	Total	Zn	0	0
			1	1		
59	29	1	Total	Zn	0	0
			1	1		
59	2n	1	Total	Zn	0	0
			1	1		

- Molecule 60 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
60	1d	1	Total	Fe	S	0	0
			8	4	4		
60	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 61 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
61	1x	1	Total	C	N	O	S	0
			10	6	1	2	1	
61	2x	1	Total	C	N	O	S	0
			10	6	1	2	1	

- Molecule 62 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	1A	1741	Total 1741	O 1741	0	0
62	1B	49	Total 49	O 49	0	0
62	1D	21	Total 21	O 21	0	0
62	1E	27	Total 27	O 27	0	0
62	1F	22	Total 22	O 22	0	0
62	1G	3	Total 3	O 3	0	0
62	1I	1	Total 1	O 1	0	0
62	1N	6	Total 6	O 6	0	0
62	1O	4	Total 4	O 4	0	0
62	1P	21	Total 21	O 21	0	0
62	1Q	5	Total 5	O 5	0	0
62	1R	5	Total 5	O 5	0	0
62	1S	6	Total 6	O 6	0	0
62	1T	13	Total 13	O 13	0	0
62	1U	12	Total 12	O 12	0	0
62	1V	10	Total 10	O 10	0	0
62	1W	6	Total 6	O 6	0	0
62	1X	4	Total 4	O 4	0	0
62	1Y	4	Total 4	O 4	0	0
62	1Z	1	Total 1	O 1	0	0
62	10	6	Total 6	O 6	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	11	3	Total 3	O 3	0	0
62	12	4	Total 4	O 4	0	0
62	13	5	Total 5	O 5	0	0
62	15	1	Total 1	O 1	0	0
62	17	6	Total 6	O 6	0	0
62	18	10	Total 10	O 10	0	0
62	19	2	Total 2	O 2	0	0
62	1a	309	Total 309	O 309	0	0
62	1d	1	Total 1	O 1	0	0
62	1g	1	Total 1	O 1	0	0
62	1j	1	Total 1	O 1	0	0
62	1l	3	Total 3	O 3	0	0
62	1m	1	Total 1	O 1	0	0
62	1o	2	Total 2	O 2	0	0
62	1p	2	Total 2	O 2	0	0
62	1q	1	Total 1	O 1	0	0
62	1r	1	Total 1	O 1	0	0
62	1v	6	Total 6	O 6	0	0
62	1w	6	Total 6	O 6	0	0
62	1x	13	Total 13	O 13	0	0
62	1y	5	Total 5	O 5	0	0

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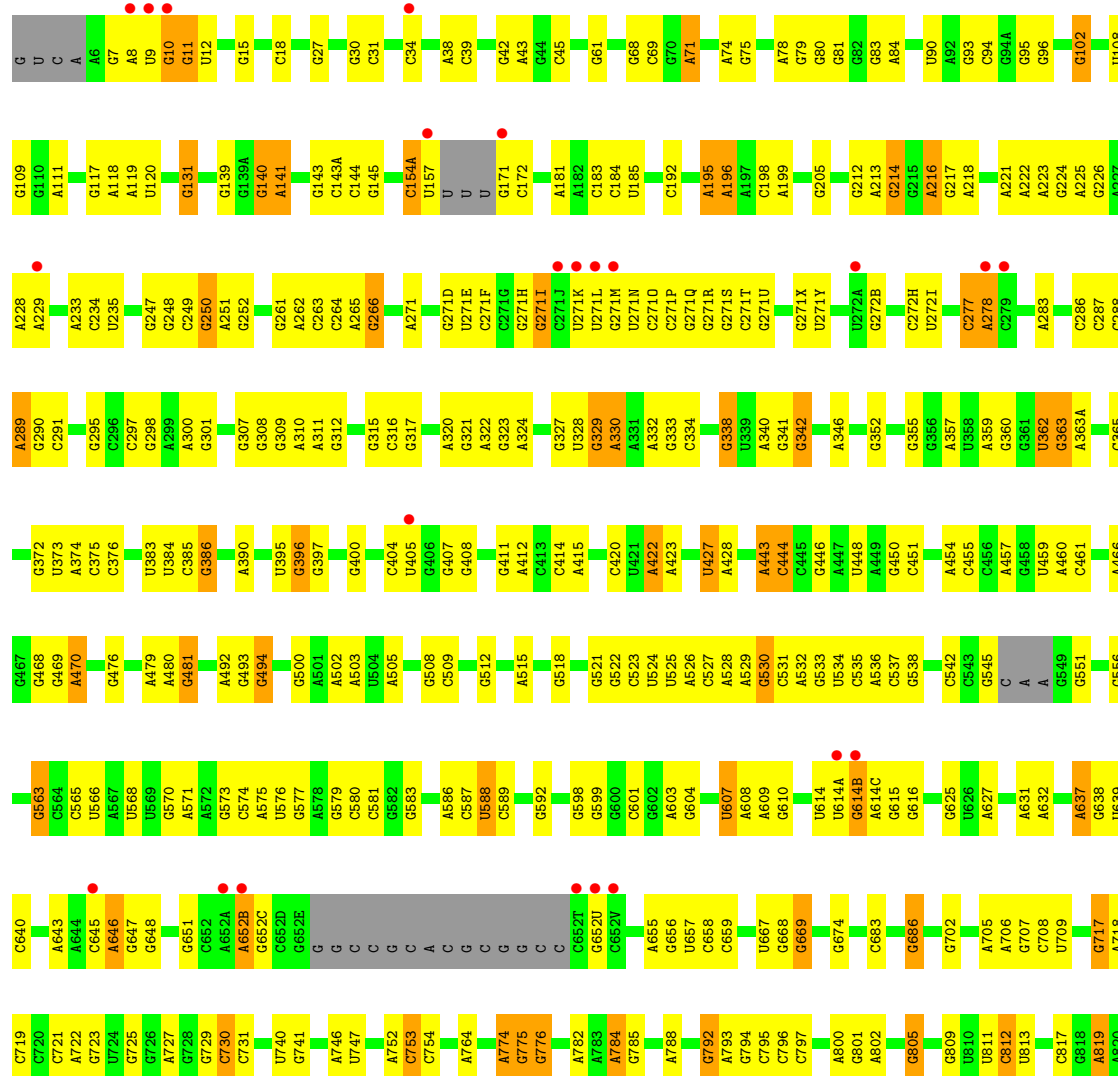
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	2A	1031	Total 1031	O 1031	0	0
62	2B	10	Total 10	O 10	0	0
62	2D	16	Total 16	O 16	0	0
62	2E	10	Total 10	O 10	0	0
62	2F	7	Total 7	O 7	0	0
62	2I	2	Total 2	O 2	0	0
62	2N	1	Total 1	O 1	0	0
62	2O	1	Total 1	O 1	0	0
62	2P	14	Total 14	O 14	0	0
62	2Q	1	Total 1	O 1	0	0
62	2R	2	Total 2	O 2	0	0
62	2T	3	Total 3	O 3	0	0
62	2U	1	Total 1	O 1	0	0
62	2V	2	Total 2	O 2	0	0
62	2W	1	Total 1	O 1	0	0
62	2X	3	Total 3	O 3	0	0
62	2Y	1	Total 1	O 1	0	0
62	2Z	2	Total 2	O 2	0	0
62	20	6	Total 6	O 6	0	0
62	21	5	Total 5	O 5	0	0
62	22	1	Total 1	O 1	0	0

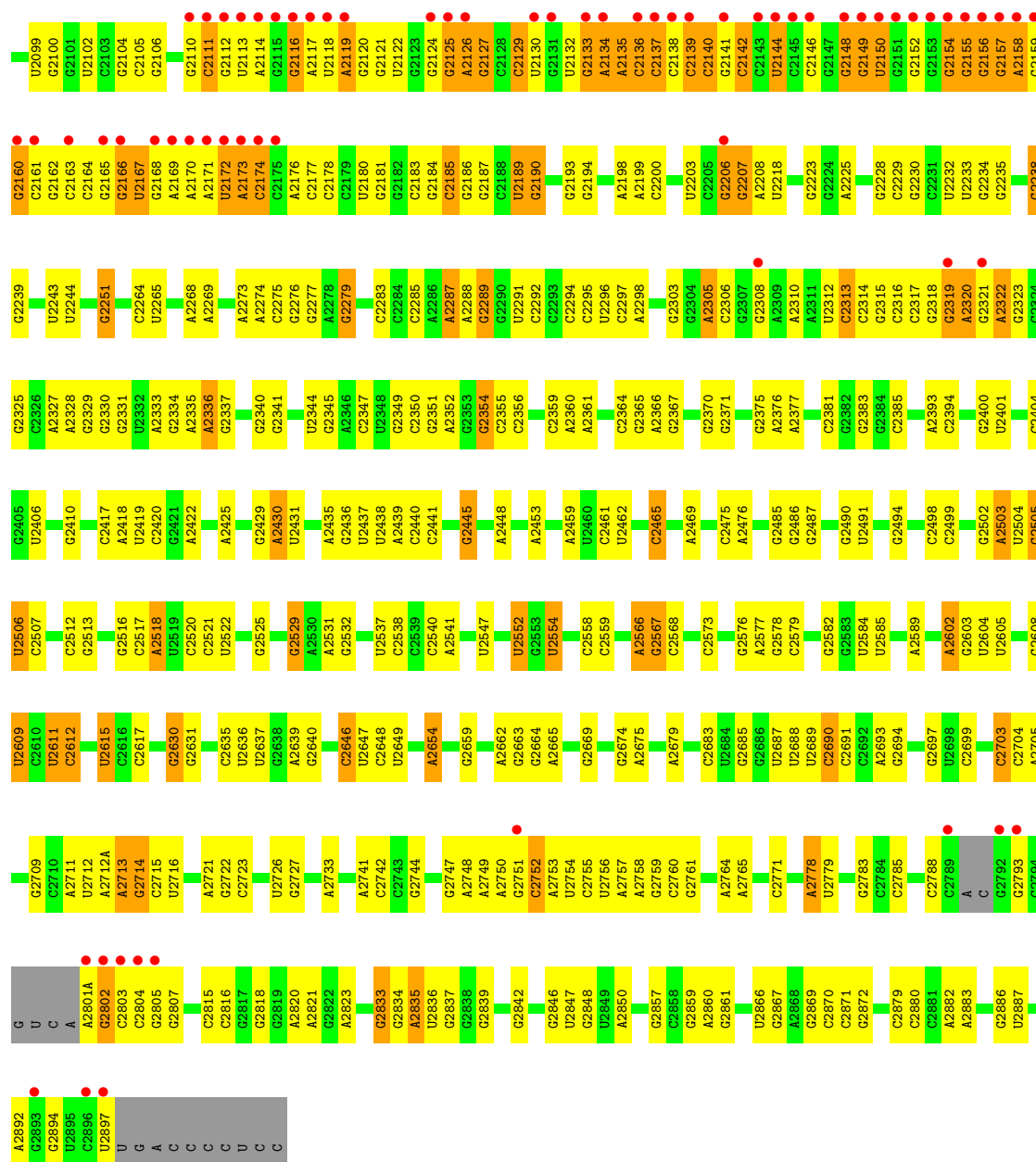
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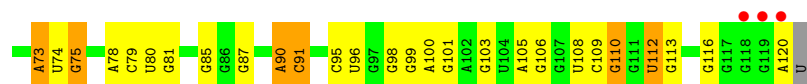
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	23	1	Total 1	O 1	0	0
62	25	3	Total 3	O 3	0	0
62	27	3	Total 3	O 3	0	0
62	28	4	Total 4	O 4	0	0
62	29	1	Total 1	O 1	0	0
62	2a	203	Total 203	O 203	0	0
62	2d	4	Total 4	O 4	0	0
62	2g	1	Total 1	O 1	0	0
62	2i	1	Total 1	O 1	0	0
62	2j	4	Total 4	O 4	0	0
62	2l	3	Total 3	O 3	0	0
62	2o	1	Total 1	O 1	0	0
62	2p	2	Total 2	O 2	0	0
62	2r	1	Total 1	O 1	0	0
62	2t	2	Total 2	O 2	0	0
62	2v	3	Total 3	O 3	0	0
62	2x	6	Total 6	O 6	0	0

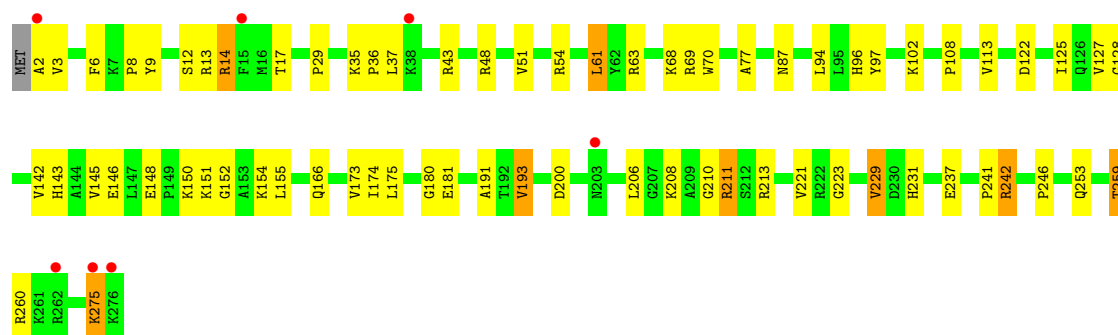
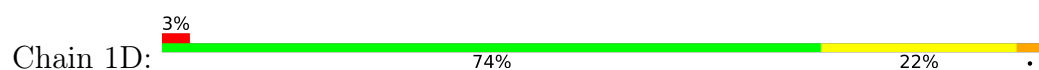


C1999	G1906	U1794	U1688	A1469	A1379	U1288	G1184	U	C1041	G975A	A900	A821
G2000	U1911	C1795	A1689	G1470	G1380	C1289	C1185	C	G1042	A980	A901	U826
A2001	A1912	U1796	U1693	A1471	A1384	G1289	G1186	C	C1043	A981	C902	U827
G2002	C1797	U1798	C1694	G1482	G1385	U1292	G1187	A	G	A982	C903	U828
C2006	U1578	A1569	G1695	G1482	C1386	C1293	U1188	U	A	A983	U905	G831
G2010	U1579	A1567	G1696	A1490	U1394	G1296	A1204	G	A	A984	G906	G832
U2011	A1580	A1568	G1697	C1493	U1395	C1297	U1205	U	A	A988	A909	U833
G2012	A1581	G1568	U1698	A1494	A1396	C1298	U1199	C	C	A989	A910	U834
C2013	C1582	A1569	C1699	A1495	U1396	G1299	C1201	A	G	A990	A911	U839
A2014	A1583	U1578	G1700	A1496	C1403	G1299	A1201	G	A	A991	C912	C840
U2017	C1584	A1586	G1702	U1497	C1404	A1301	A1204	C	C	C992	U913	
G2018	A1586	A1586	G1703	C1501	U1405	A1302	U1205	A	A	G993	C914	G848
A2019	C1589	C1589	G1704	C1502	U1406	G1303	U1206	G	G	C994	C915	A849
G2020	U1590	C1599	C1710	U1503	C1407	G1309	A1210	G	G	A996	C916	C850
C2021	G1591	U1591	C1711	C1504	C1408	G1309	U1211	A	A	A997	A917	U851
U2022	C1592	G1592	C1712	C1505	C1408	G1309	U1211	G	A	A998	A918	G852
G2023	G1593	G1593	C1712	C1506	C1408	G1309	U1211	G	G	A999	C919	G853
C2027	U1594	G1594	C1712	C1507	C1408	G1309	U1211	U	U	A1000	G920	G854
A2030	A1603	A1603	C1712	C1508	C1408	G1309	U1211	G	G	G1003	U922	C856
G2031	C1607	C1607	C1712	C1509	C1408	G1309	U1211	G	G	C1004	C923	C857
U2032	A1608	A1608	C1712	C1510	C1408	G1309	U1211	C	C	G1005	C924	U858
C2033	U1609	A1609	C1712	C1511	C1408	G1309	U1211	U	U	C1006	C925	G859
G2034	A1610	A1610	C1712	C1512	C1408	G1309	U1211	U	U	C1007	A926	U860
C2035	G1622	G1622	C1712	C1513	C1408	G1309	U1211	A	A	C1008	G932	G862
G2036	U1630	U1630	C1712	C1514	C1408	G1309	U1211	G	G	C1009	A933	A863
C2037	A1631	A1631	C1712	C1515	C1408	G1309	U1211	A	A	A1010	C936	G864
U2042	G1632	G1632	C1712	C1516	C1408	G1309	U1211	G	G	U1011	U937	C865
G2048	A1633	A1633	C1712	C1517	C1408	G1309	U1211	C	C	U1012	U938	A866
C2049	U1634	U1634	C1712	C1518	C1408	G1309	U1211	G	G	U1013	G936	C867
G2050	G1635	G1635	C1712	C1519	C1408	G1309	U1211	C	C	U1014	U1015	U868
A2051	A1636	A1636	C1712	C1520	C1408	G1309	U1211	A	A	U1016	G1016	G869
C2055	U1637	U1637	C1712	C1521	C1408	G1309	U1211	C	C	G1017	G944	G874
G2056	A1638	A1638	C1712	C1522	C1408	G1309	U1211	U	U	C1018	A945	G875
A2059	U1639	U1639	C1712	C1523	C1408	G1309	U1211	C	C	U1019	A946	A878
G2060	C1640	C1640	C1712	C1524	C1408	G1309	U1211	U	U	A1020	G947	G879
A2061	A1641	A1641	C1712	C1525	C1408	G1309	U1211	U	U	G1022	G948	G880
C2065	U1642	U1642	C1712	C1526	C1408	G1309	U1211	A	A	U1023	A953	G881
G2066	G1643	G1643	C1712	C1527	C1408	G1309	U1211	G	G	G1024	G954	G882
A2069	A1644	A1644	C1712	C1528	C1408	G1309	U1211	A	A	U1025	A957	G883
G2070	U1645	U1645	C1712	C1529	C1408	G1309	U1211	G	G	A1026	U958	C884
C2071	A1646	A1646	C1712	C1530	C1408	G1309	U1211	A	A	A1027	U959	C885
U2074	U1647	U1647	C1712	C1531	C1408	G1309	U1211	G	G	A1028	A960	A887
G2075	A1648	A1648	C1712	C1532	C1408	G1309	U1211	U	U	A1029	C961	C888
U2076	U1649	U1649	C1712	C1533	C1408	G1309	U1211	G	G	G1030	G962	C889
C2078	A1650	A1650	C1712	C1534	C1408	G1309	U1211	C	C	A1032	A890	A890
U2079	U1651	U1651	C1712	C1535	C1408	G1309	U1211	G	G	U1033	G967	G892
	G1652	G1652	C1712	C1536	C1408	G1309	U1211	U	U	G1034	C966	C893
	A1653	A1653	C1712	C1537	C1408	G1309	U1211	A	A	U1035	C971	U895
	U1654	U1654	C1712	C1538	C1408	G1309	U1211	G	G	G1036	G972	A886
	A1655	A1655	C1712	C1539	C1408	G1309	U1211	U	U	U1037	A973	C897
	G1656	G1656	C1712	C1540	C1408	G1309	U1211	A	A	C1038	G974	C898
	U1657	U1657	C1712	C1541	C1408	G1309	U1211	C	C	U1039	C975	A899
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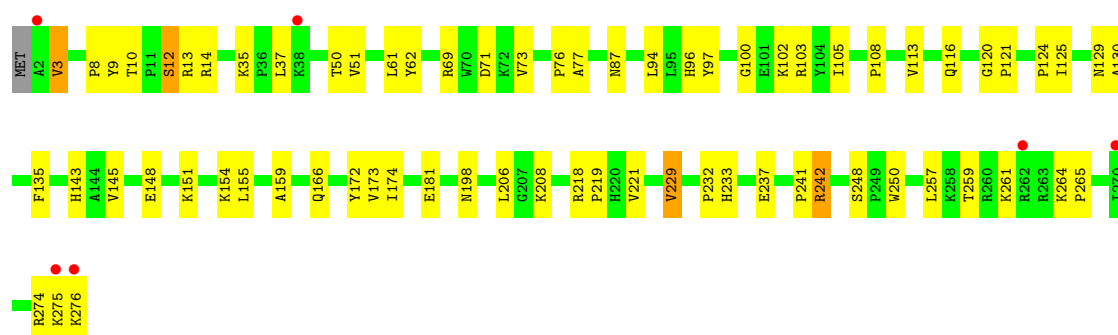
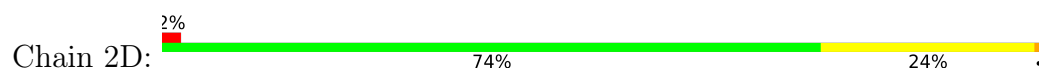




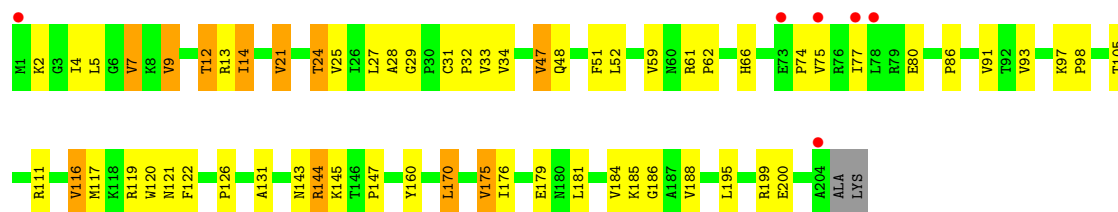
• Molecule 3: 50S ribosomal protein L2



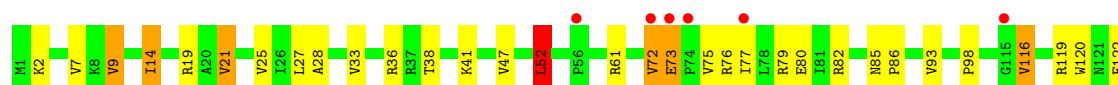
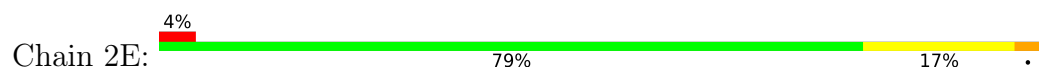
• Molecule 3: 50S ribosomal protein L2



• Molecule 4: 50S ribosomal protein L3



• Molecule 4: 50S ribosomal protein L3

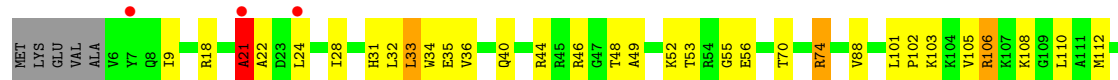




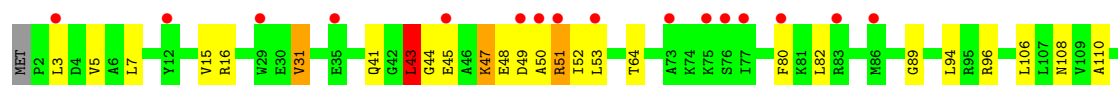
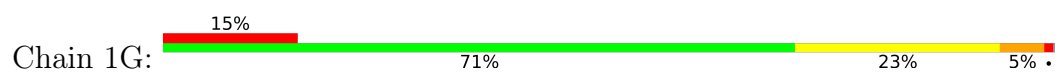
• Molecule 5: 50S ribosomal protein L4



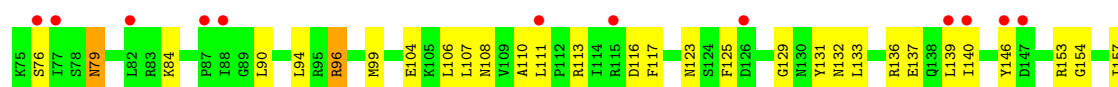
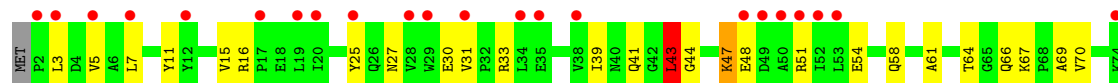
• Molecule 5: 50S ribosomal protein L4



• Molecule 6: 50S ribosomal protein L5

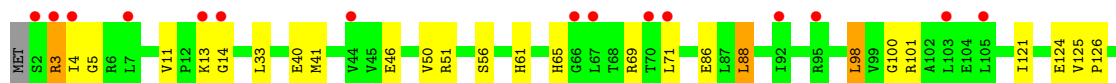
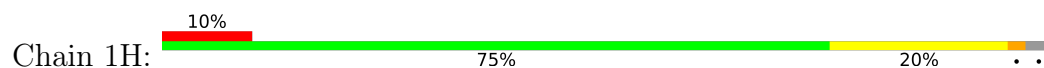


• Molecule 6: 50S ribosomal protein L5

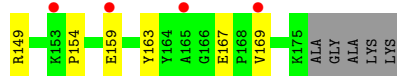
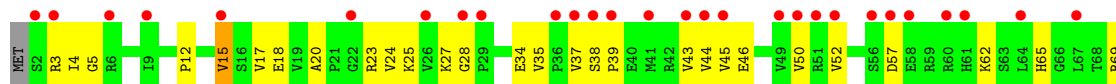




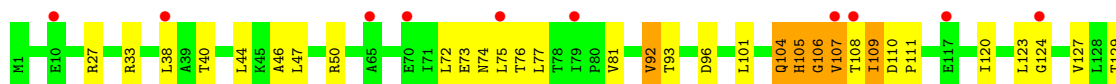
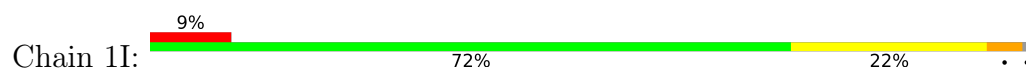
- Molecule 7: 50S ribosomal protein L6



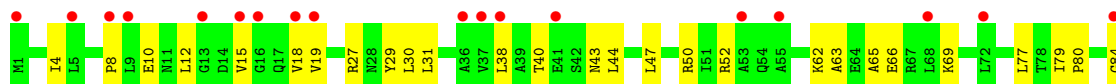
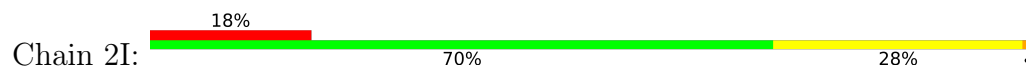
- Molecule 7: 50S ribosomal protein L6



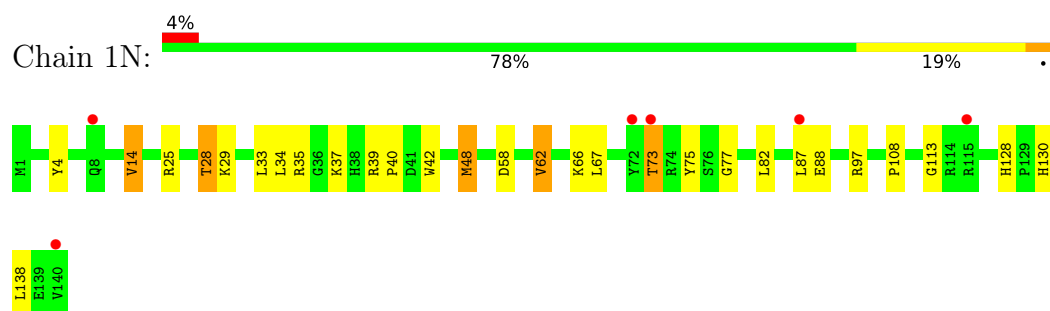
- Molecule 8: 50S ribosomal protein L9



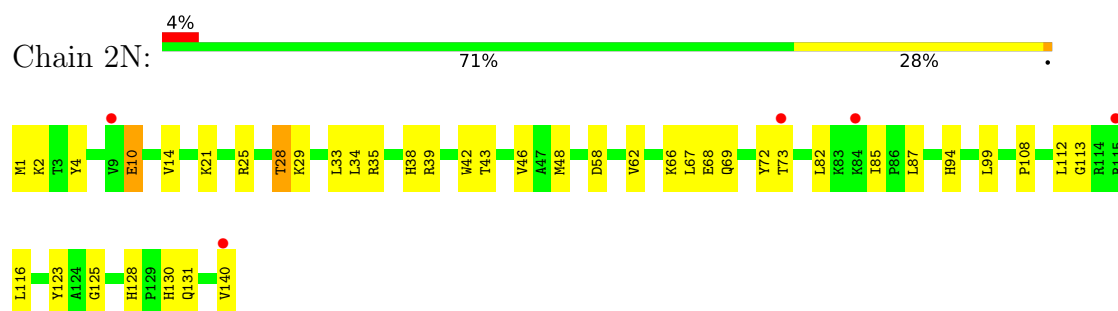
- Molecule 8: 50S ribosomal protein L9



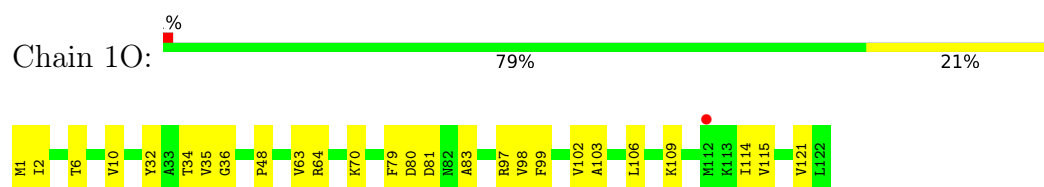
- Molecule 9: 50S ribosomal protein L13



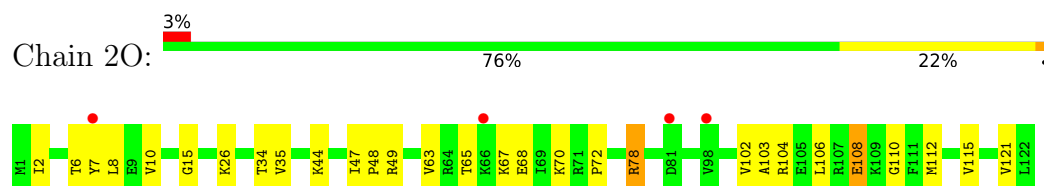
- Molecule 9: 50S ribosomal protein L13



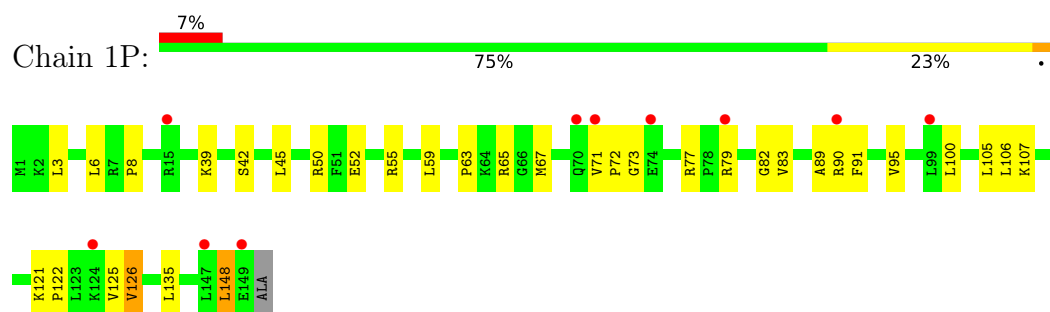
- Molecule 10: 50S ribosomal protein L14



- Molecule 10: 50S ribosomal protein L14

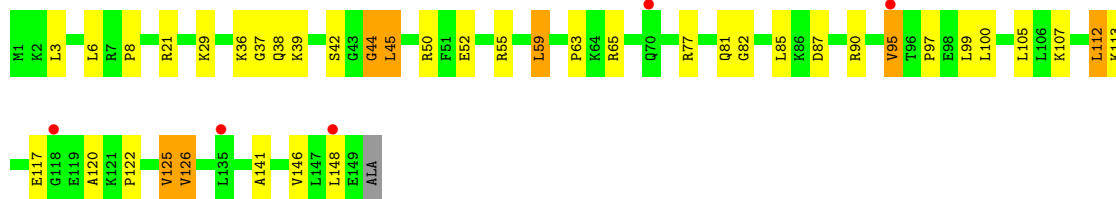


- Molecule 11: 50S ribosomal protein L15



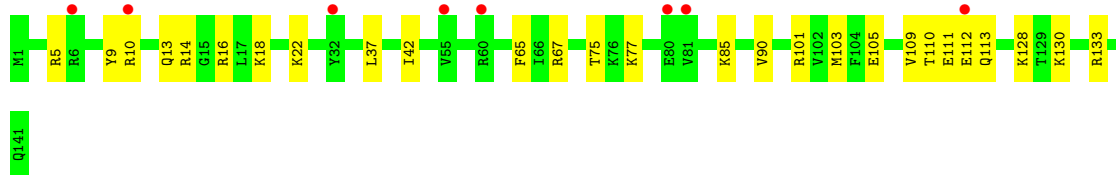
- Molecule 11: 50S ribosomal protein L15

Chain 2P: 



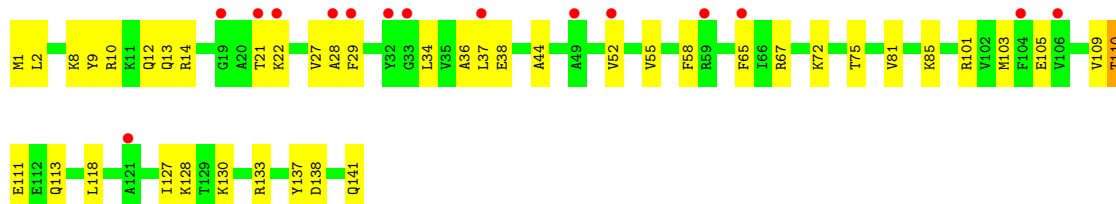
- Molecule 12: 50S ribosomal protein L16

Chain 1Q: 



- Molecule 12: 50S ribosomal protein L16

Chain 2Q: 



- Molecule 13: 50S ribosomal protein L17

Chain 1R: 



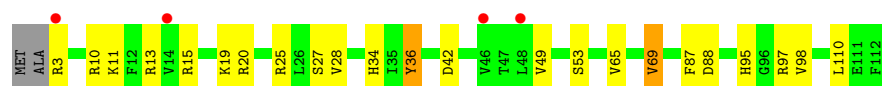
- Molecule 13: 50S ribosomal protein L17

Chain 2R: 

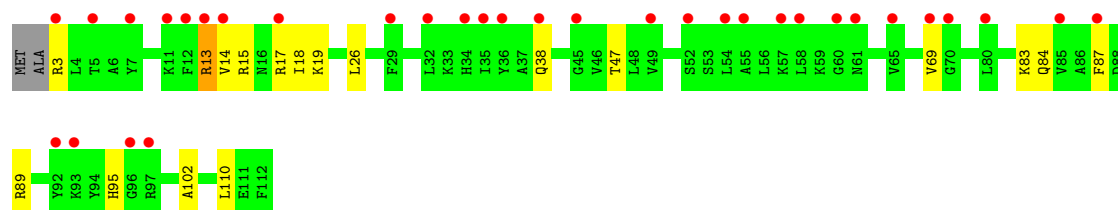
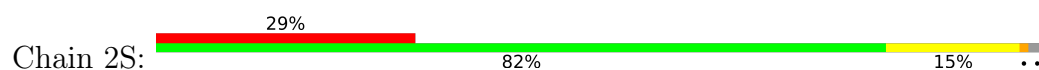


- Molecule 14: 50S ribosomal protein L18

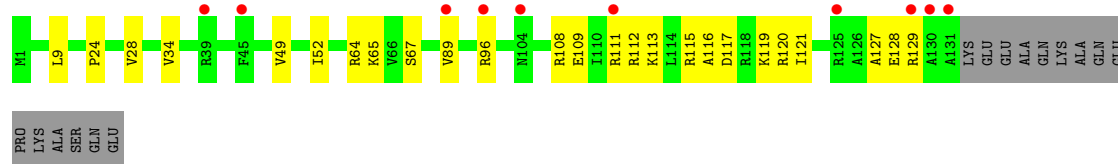
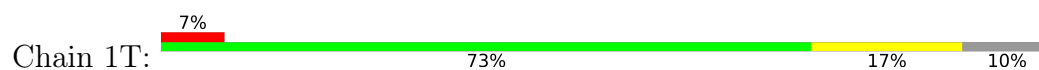
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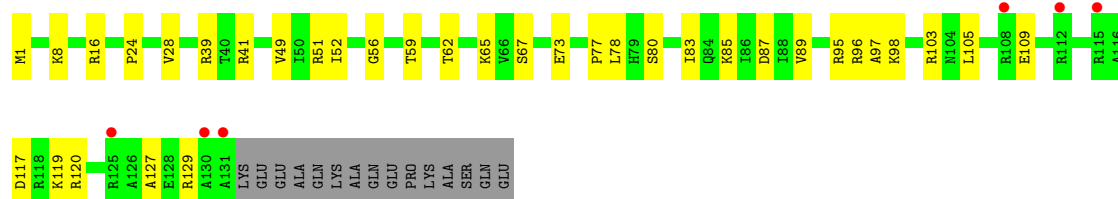
- Molecule 14: 50S ribosomal protein L18



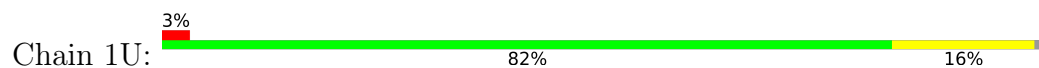
- Molecule 15: 50S ribosomal protein L19



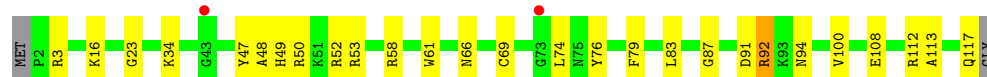
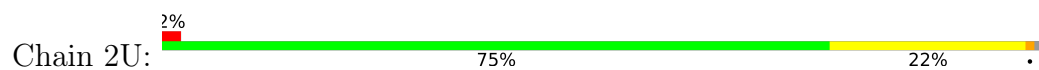
- Molecule 15: 50S ribosomal protein L19



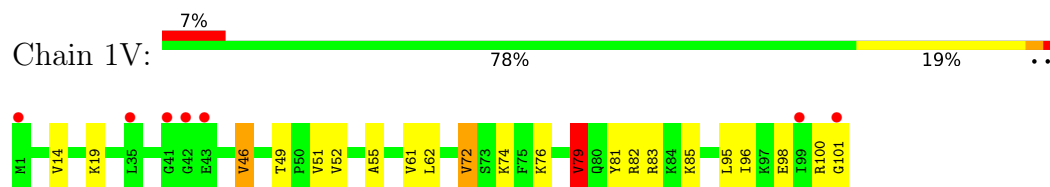
- Molecule 16: 50S ribosomal protein L20



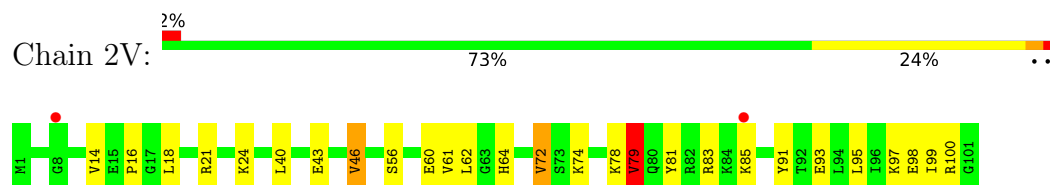
- Molecule 16: 50S ribosomal protein L20



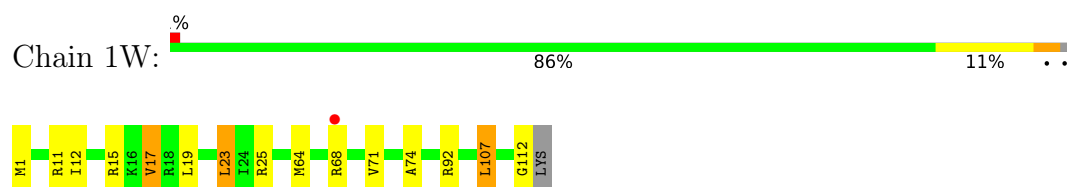
- Molecule 17: 50S ribosomal protein L21



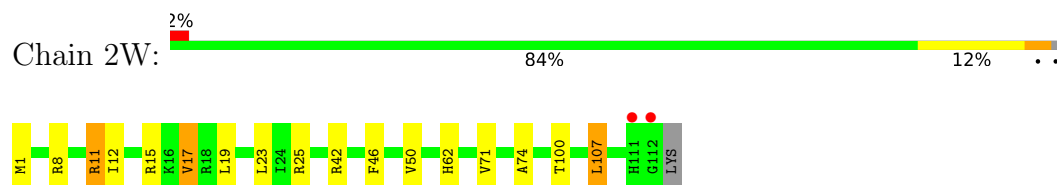
- Molecule 17: 50S ribosomal protein L21



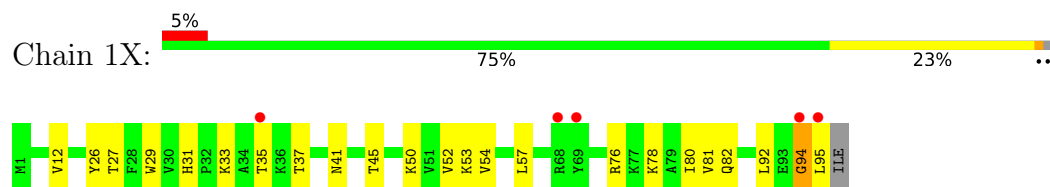
- Molecule 18: 50S ribosomal protein L22



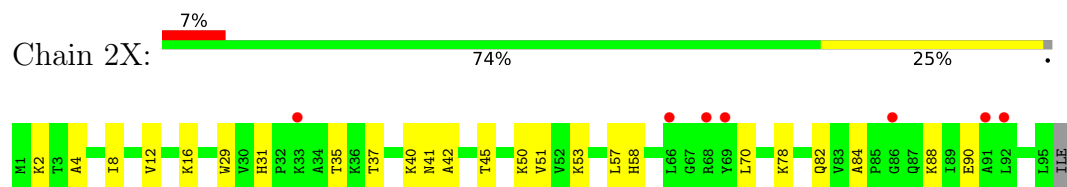
- Molecule 18: 50S ribosomal protein L22



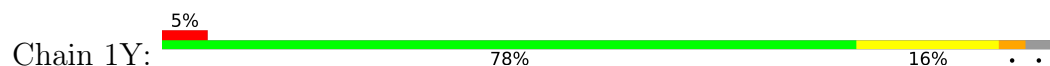
- Molecule 19: 50S ribosomal protein L23



- Molecule 19: 50S ribosomal protein L23

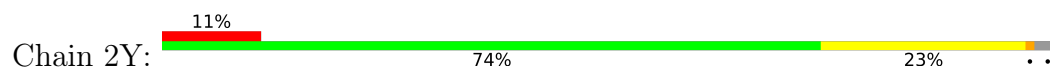


- Molecule 20: 50S ribosomal protein L24

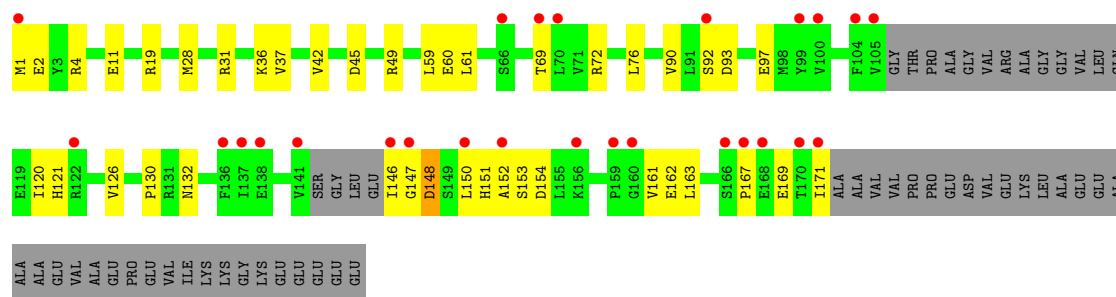




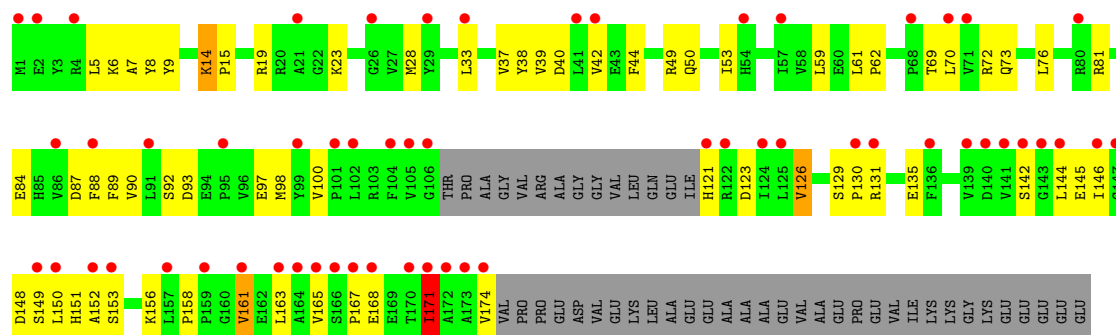
- Molecule 20: 50S ribosomal protein L24



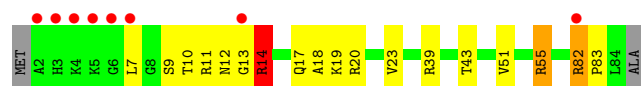
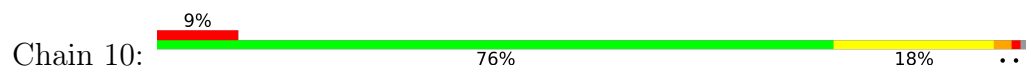
- Molecule 21: 50S ribosomal protein L25



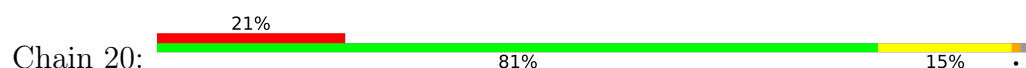
- Molecule 21: 50S ribosomal protein L25

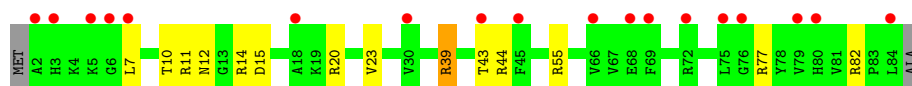


- Molecule 22: 50S ribosomal protein L27

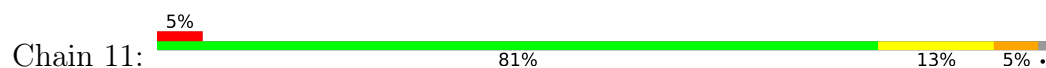


- Molecule 22: 50S ribosomal protein L27

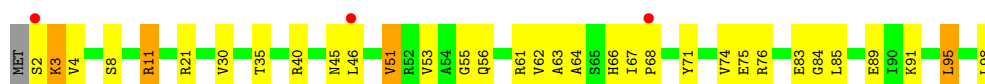




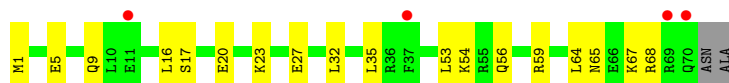
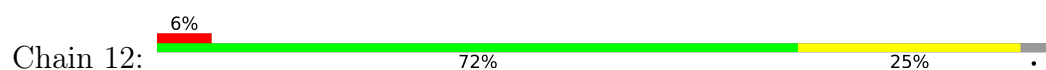
- Molecule 23: 50S ribosomal protein L28



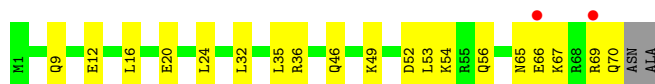
- Molecule 23: 50S ribosomal protein L28



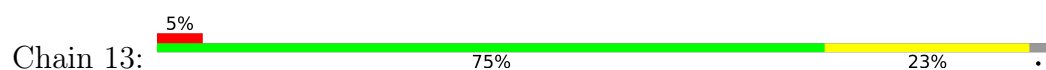
- Molecule 24: 50S ribosomal protein L29



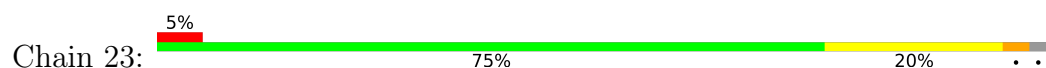
- Molecule 24: 50S ribosomal protein L29



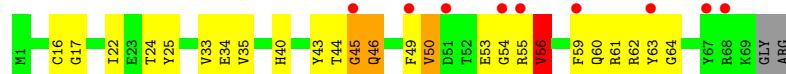
- Molecule 25: 50S ribosomal protein L30



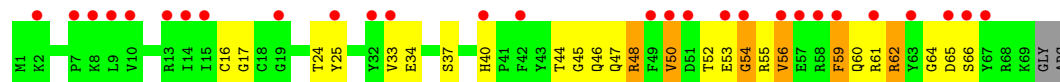
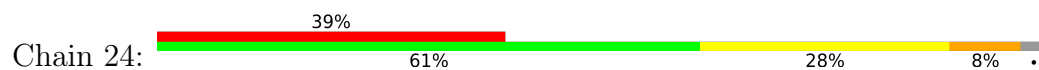
- Molecule 25: 50S ribosomal protein L30



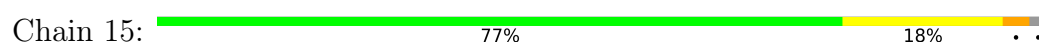
- Molecule 26: 50S ribosomal protein L31



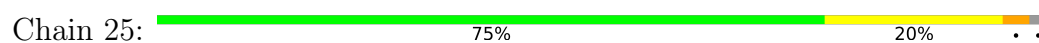
- Molecule 26: 50S ribosomal protein L31



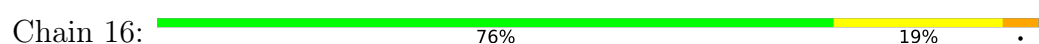
- Molecule 27: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L32



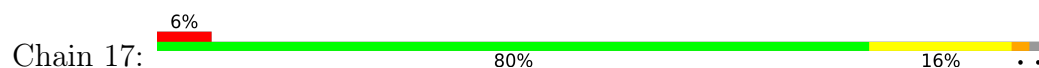
- Molecule 28: 50S ribosomal protein L33



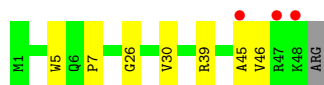
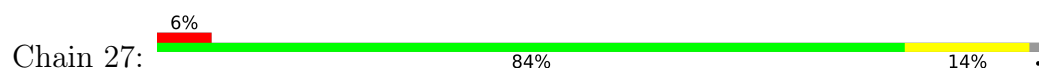
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



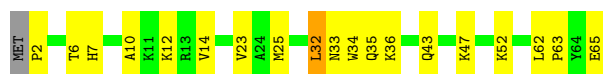
- Molecule 29: 50S ribosomal protein L34



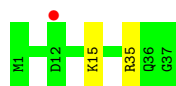
- Molecule 30: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L35



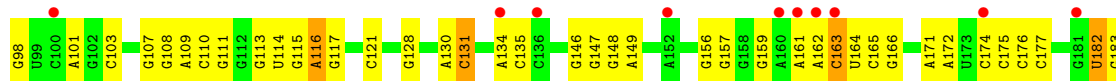
- Molecule 31: 50S ribosomal protein L36

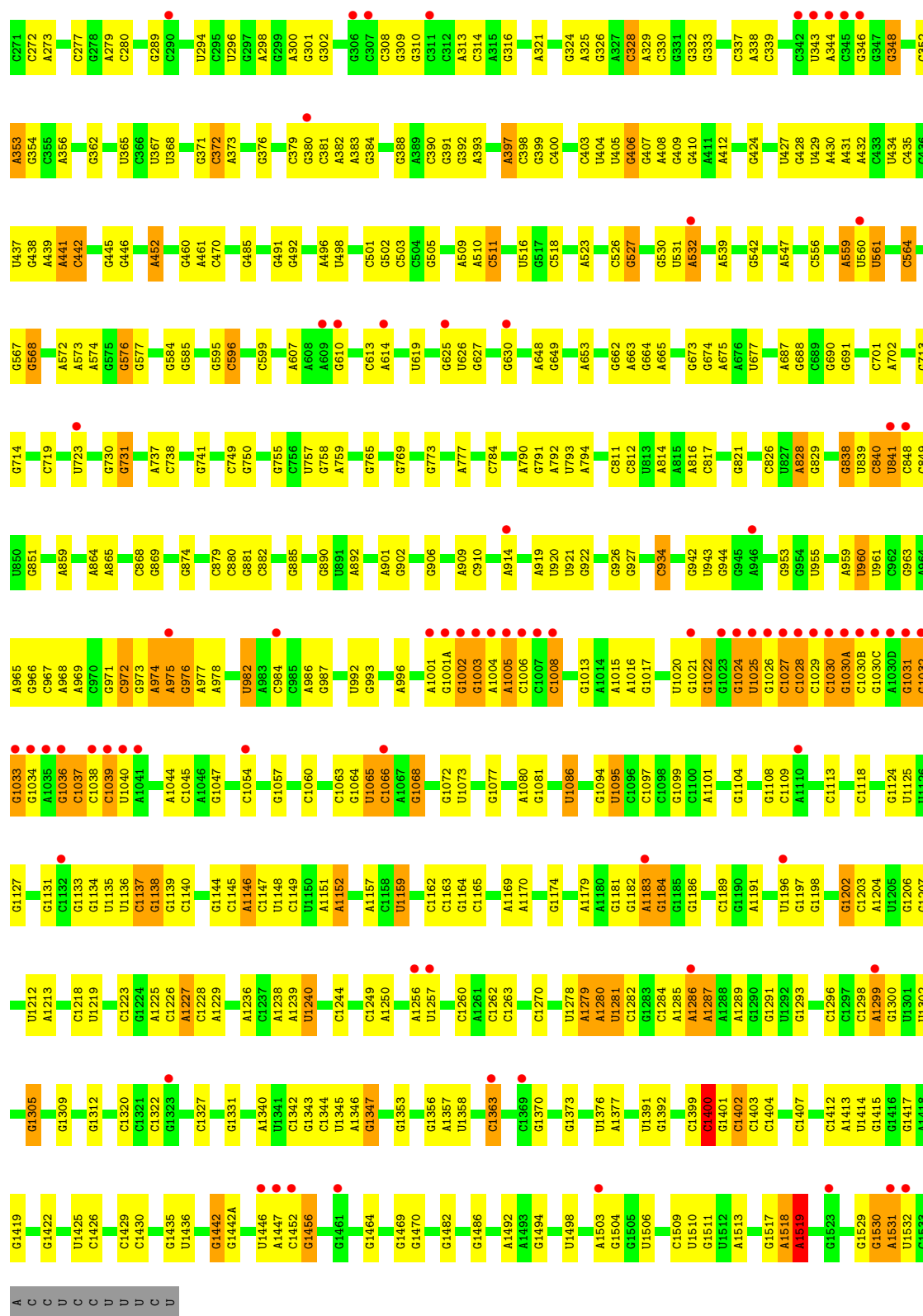


- Molecule 31: 50S ribosomal protein L36

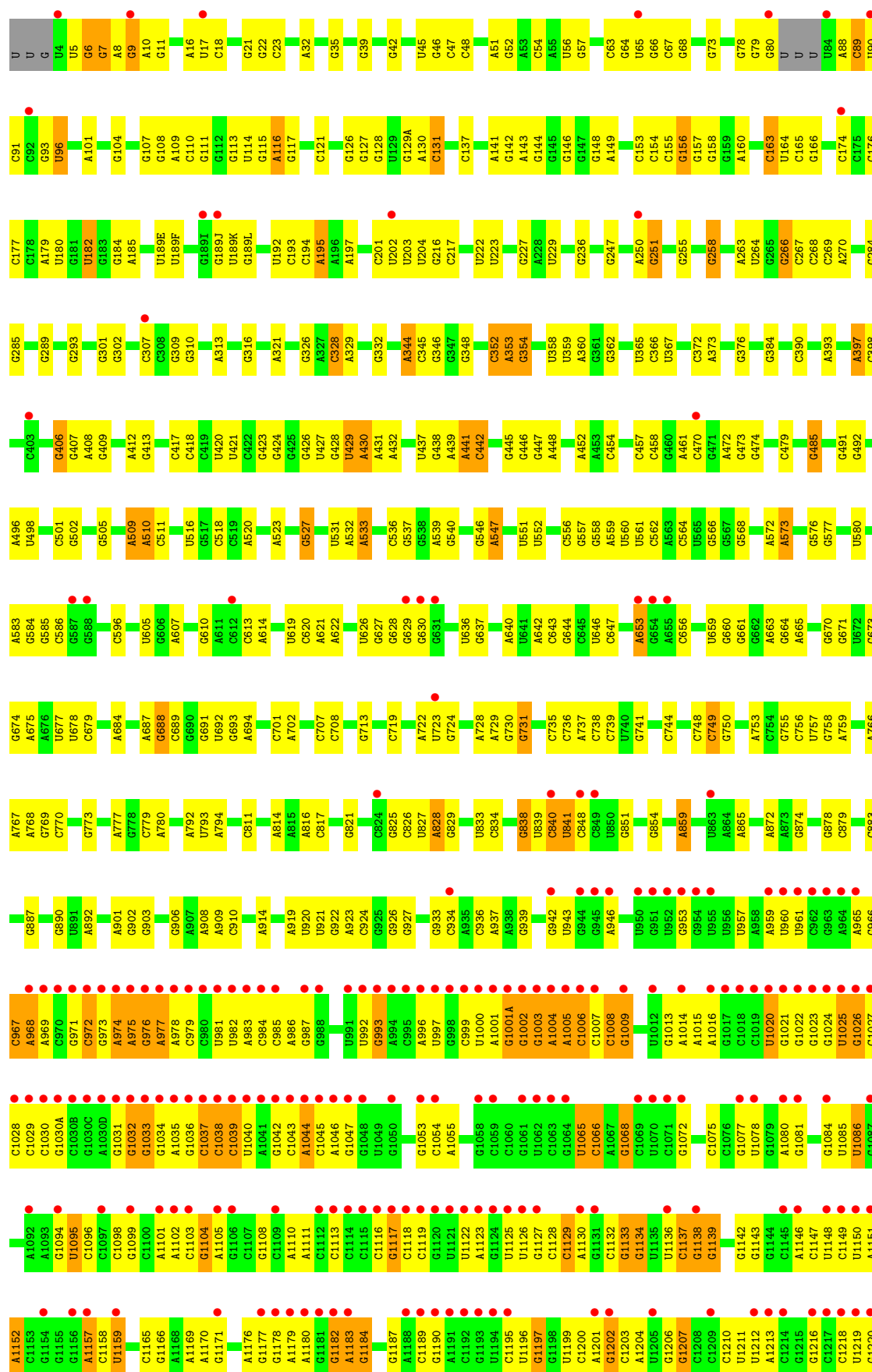


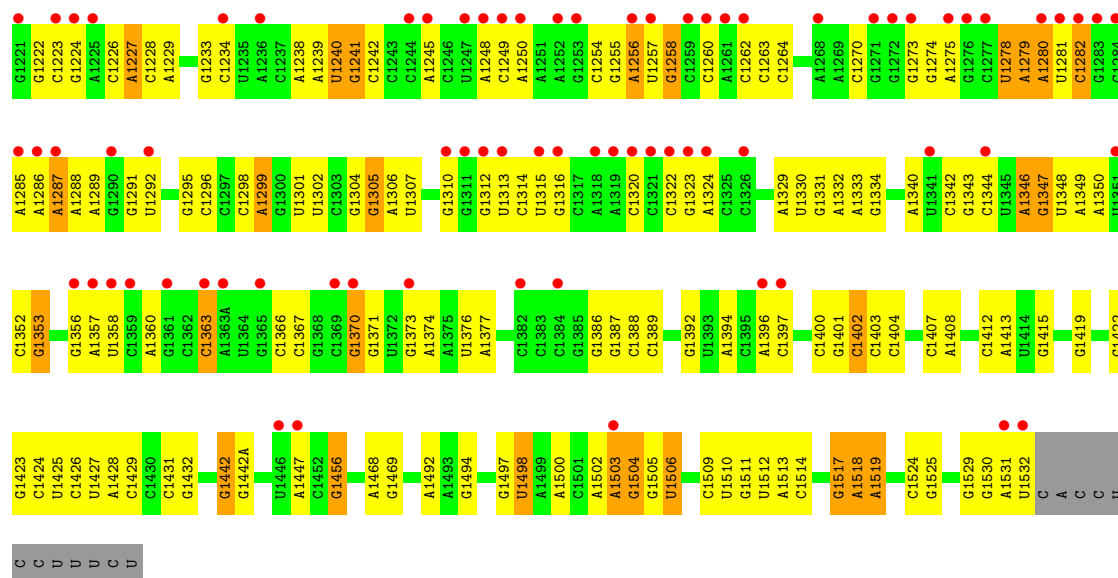
- Molecule 32: 16S Ribosomal RNA



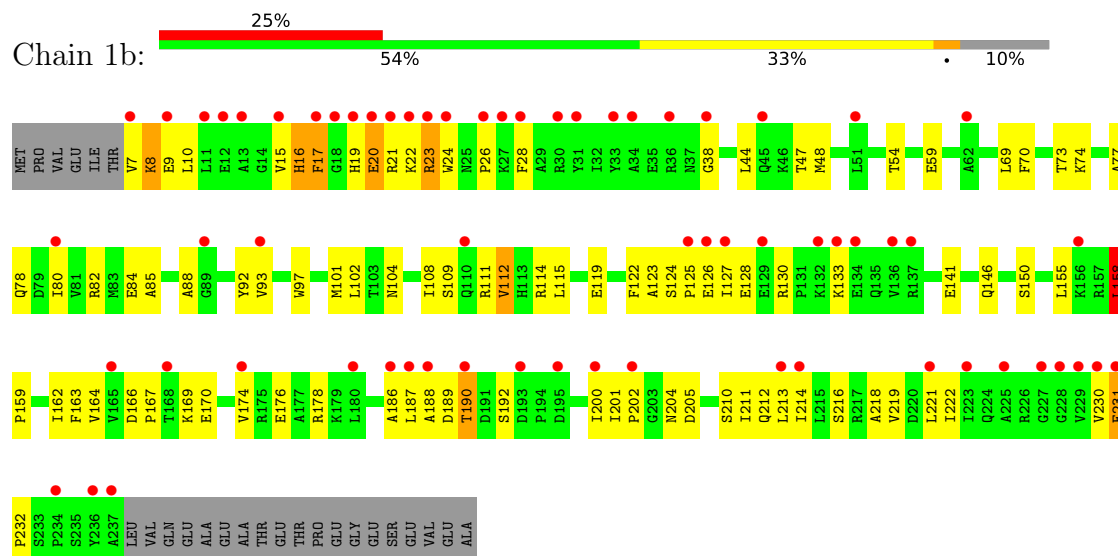


• Molecule 32: 16S Ribosomal RNA

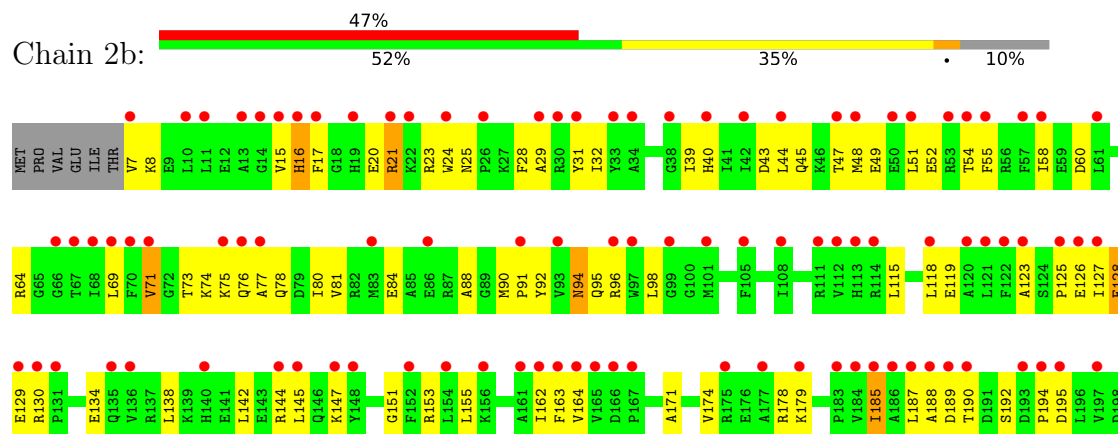




• Molecule 33: 30S ribosomal protein S2

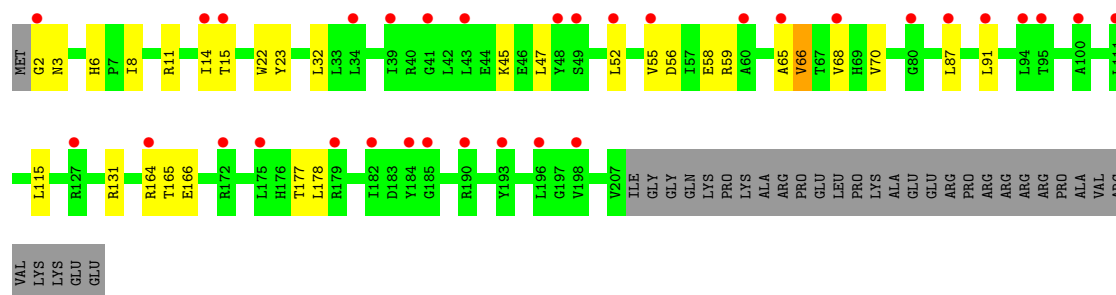
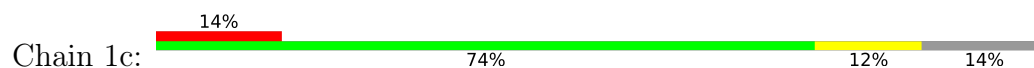


• Molecule 33: 30S ribosomal protein S2

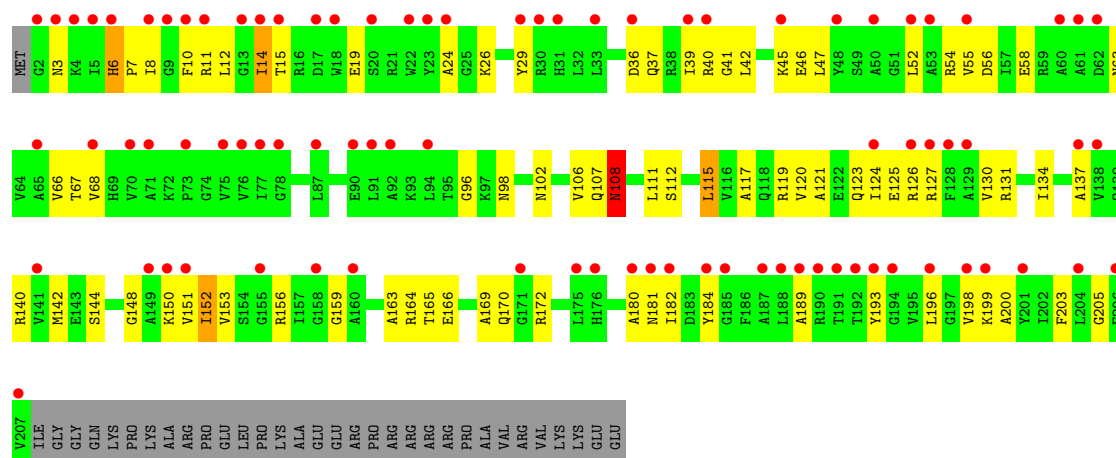




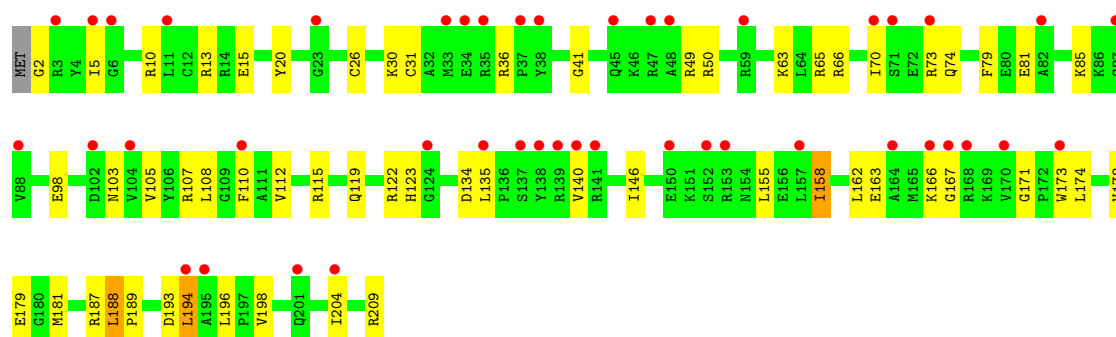
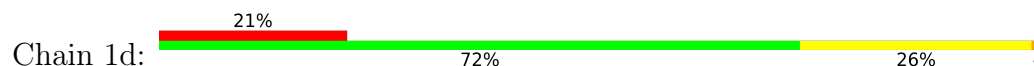
• Molecule 34: 30S ribosomal protein S3



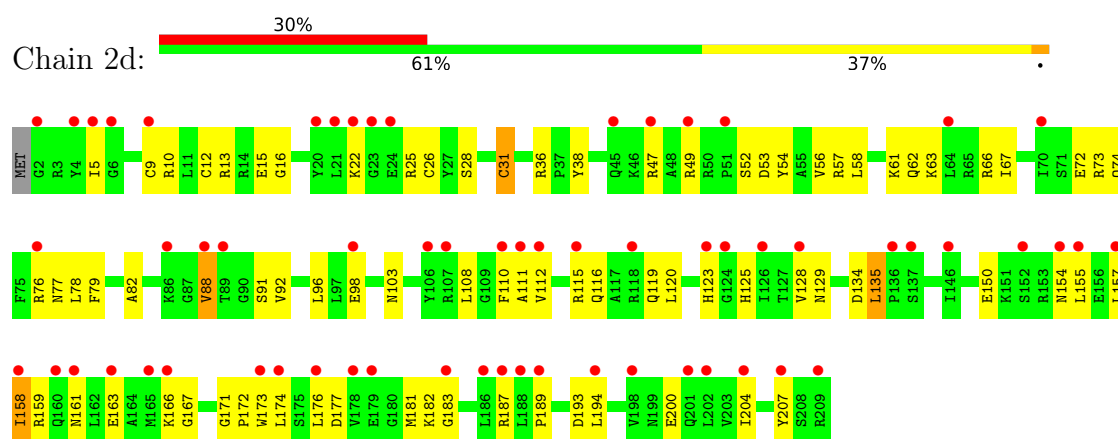
• Molecule 34: 30S ribosomal protein S3



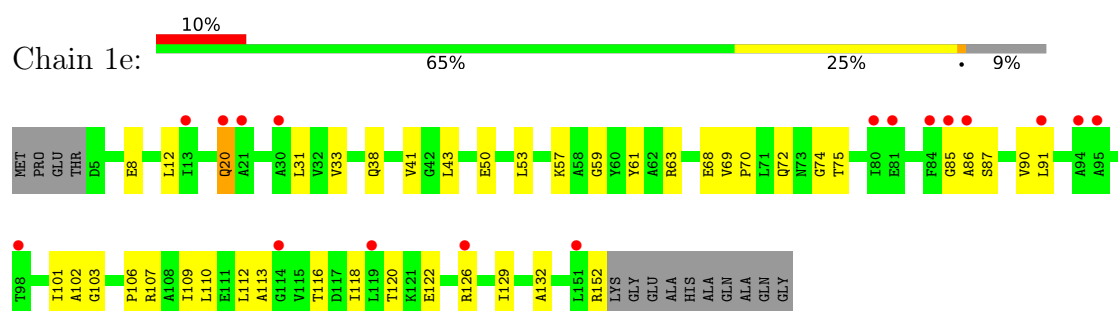
• Molecule 35: 30S ribosomal protein S4



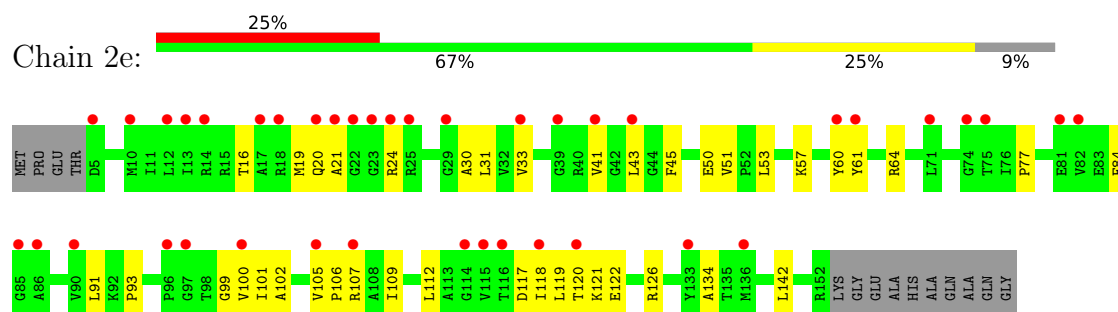
• Molecule 35: 30S ribosomal protein S4



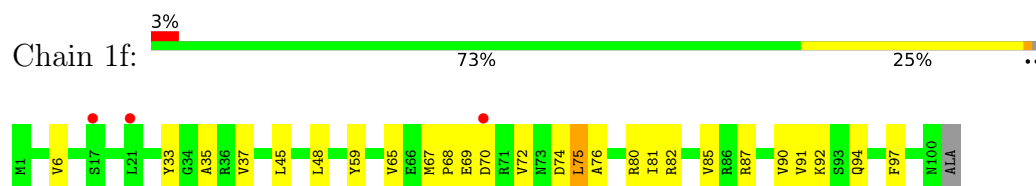
- Molecule 36: 30S ribosomal protein S5



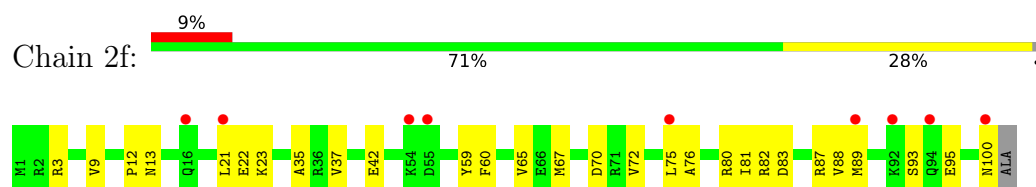
- Molecule 36: 30S ribosomal protein S5



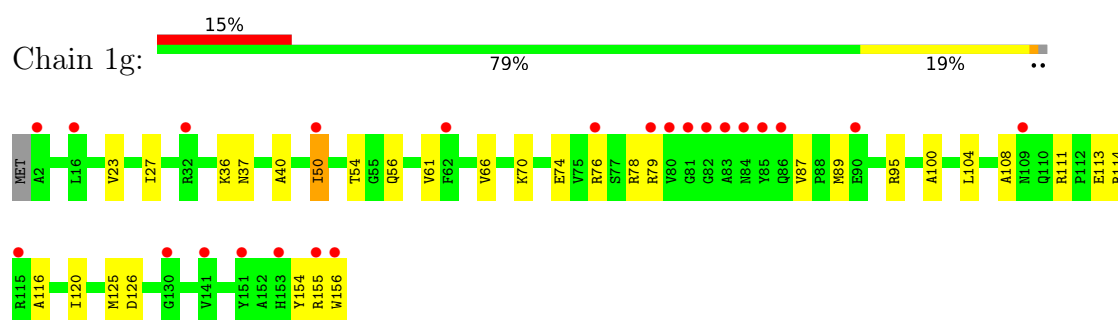
- Molecule 37: 30S ribosomal protein S6



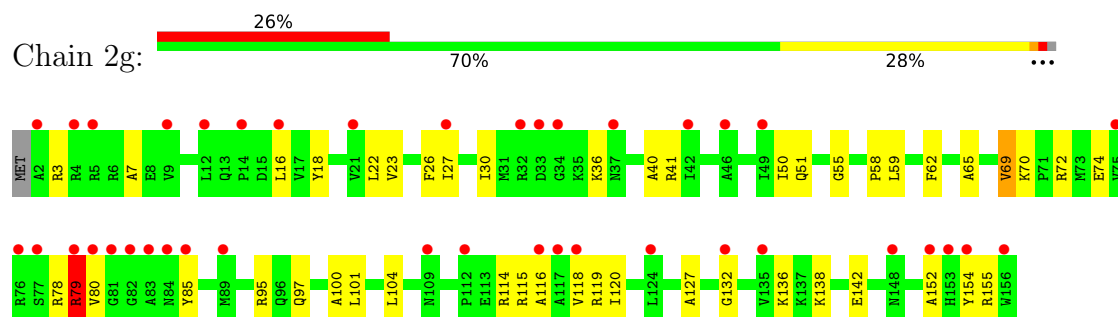
- Molecule 37: 30S ribosomal protein S6



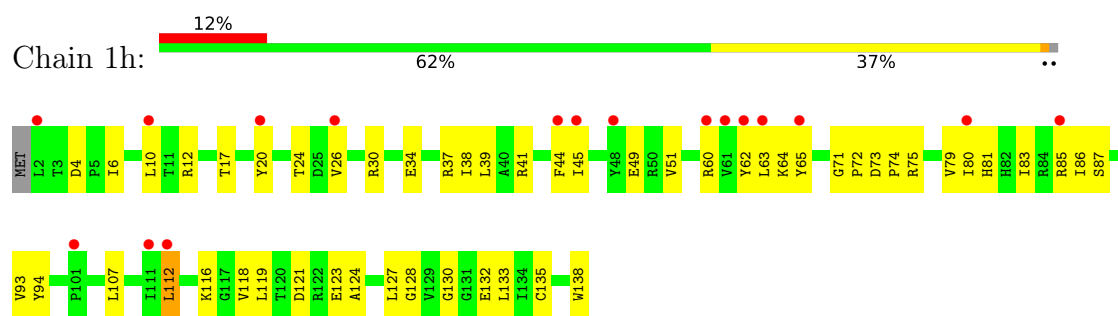
- Molecule 38: 30S ribosomal protein S7



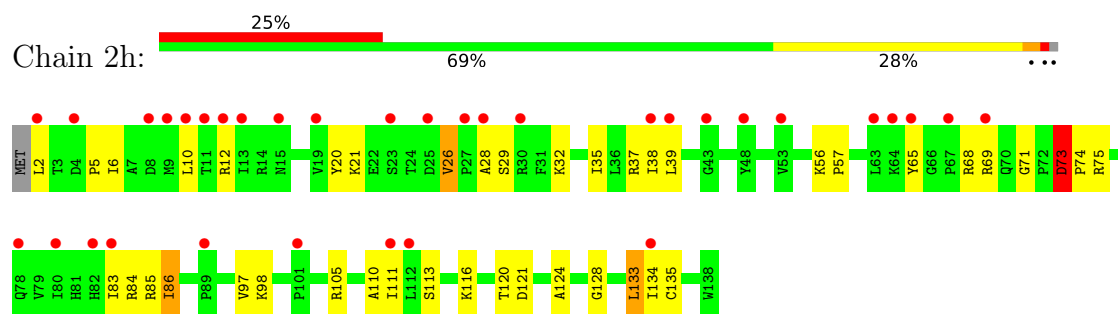
- Molecule 38: 30S ribosomal protein S7



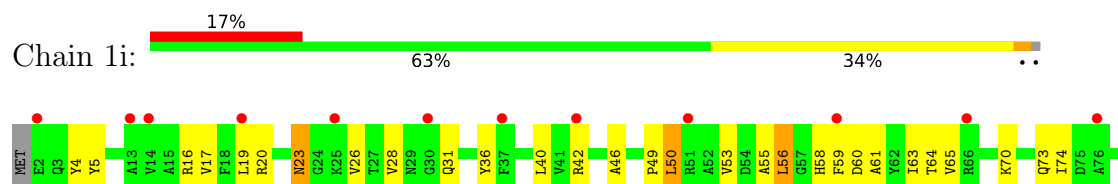
- Molecule 39: 30S ribosomal protein S8

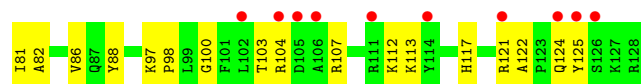


- Molecule 39: 30S ribosomal protein S8

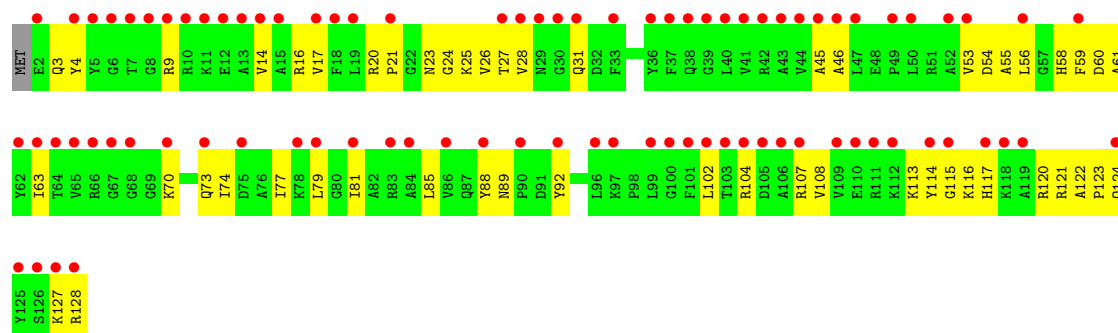


- Molecule 40: 30S ribosomal protein S9

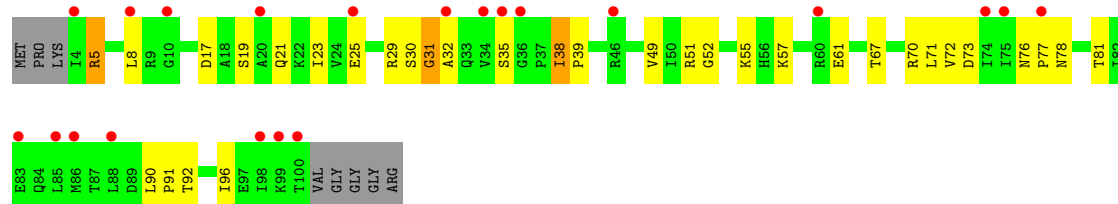




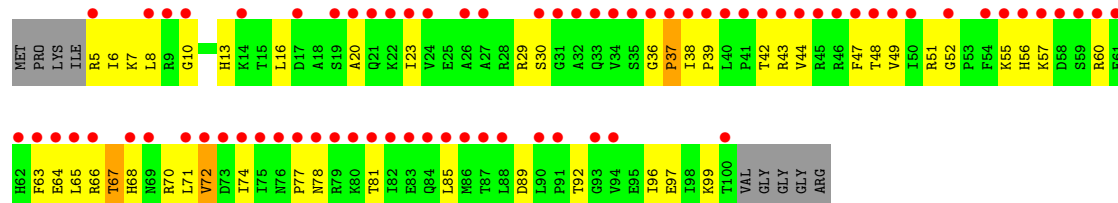
- Molecule 40: 30S ribosomal protein S9



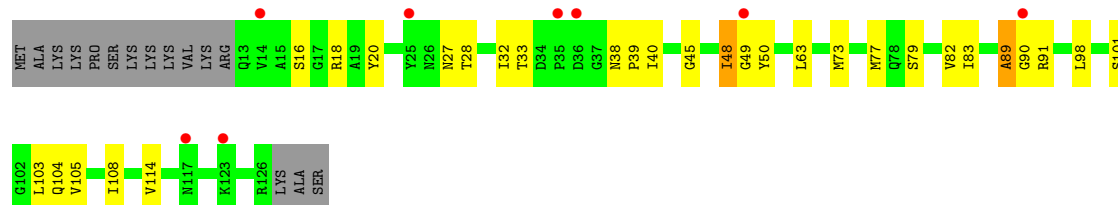
- Molecule 41: 30S ribosomal protein S10



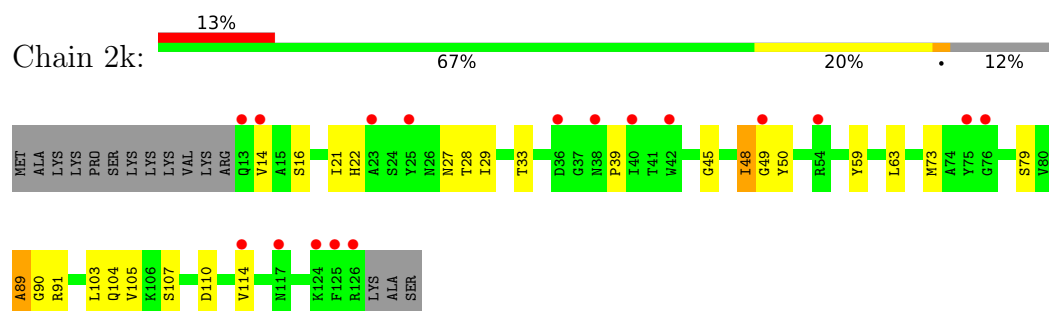
- Molecule 41: 30S ribosomal protein S10



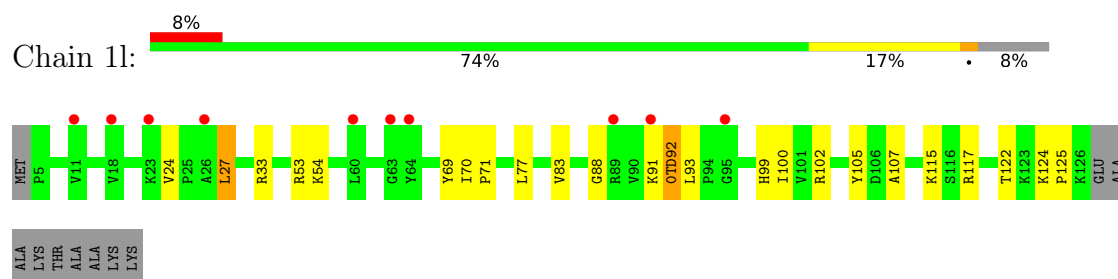
- Molecule 42: 30S ribosomal protein S11



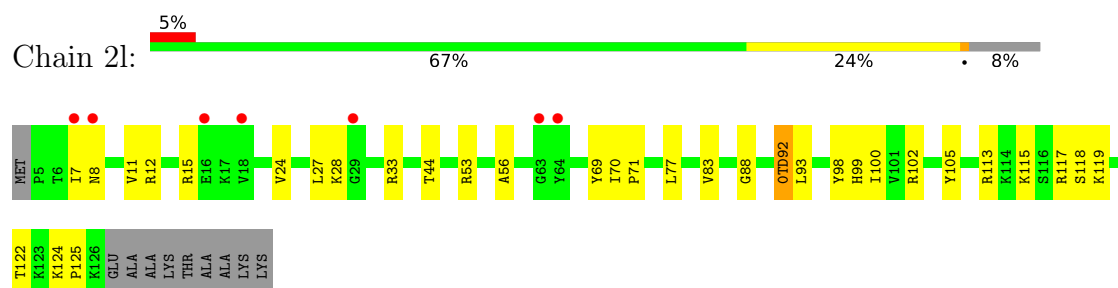
- Molecule 42: 30S ribosomal protein S11



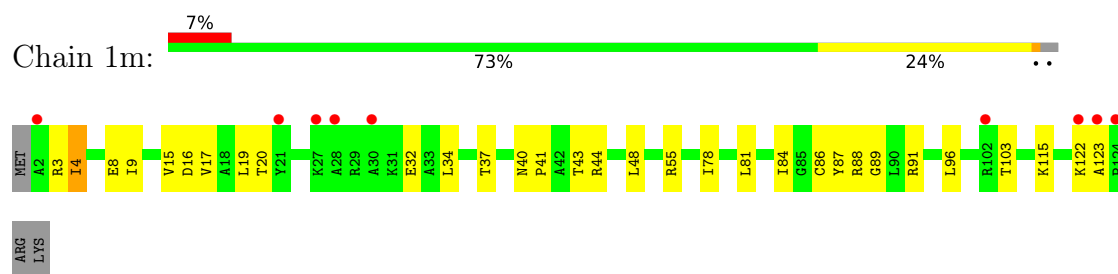
- Molecule 43: 30S ribosomal protein S12



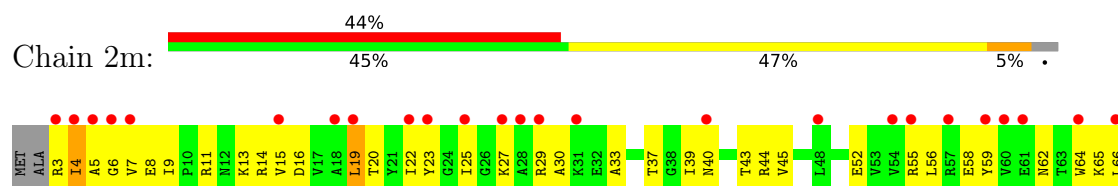
- Molecule 43: 30S ribosomal protein S12

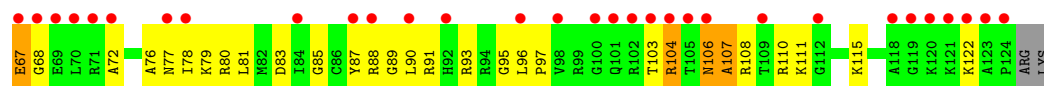


- Molecule 44: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S13

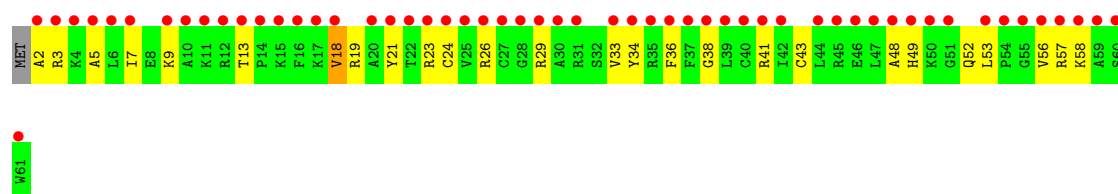




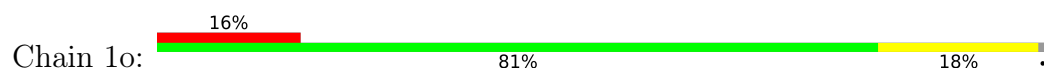
- Molecule 45: 30S ribosomal protein S14 type Z



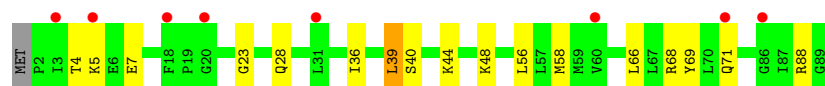
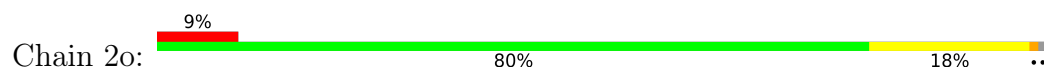
- Molecule 45: 30S ribosomal protein S14 type Z



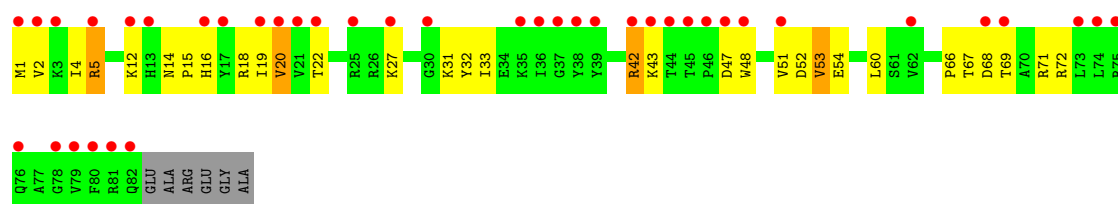
- Molecule 46: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S15

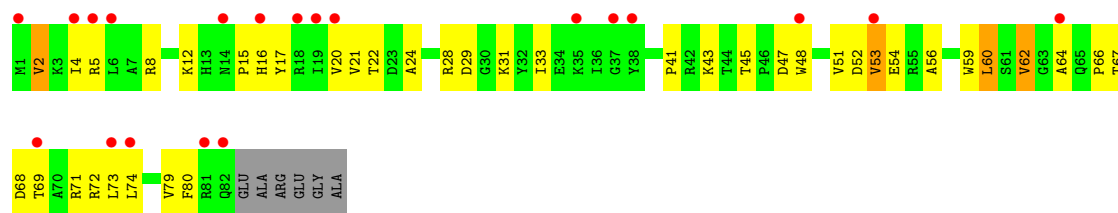


- Molecule 47: 30S ribosomal protein S16

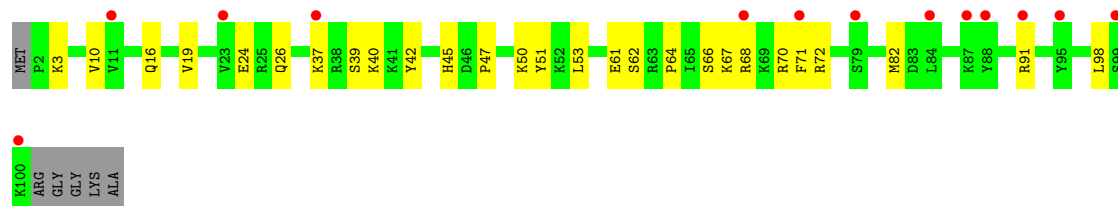


- Molecule 47: 30S ribosomal protein S16

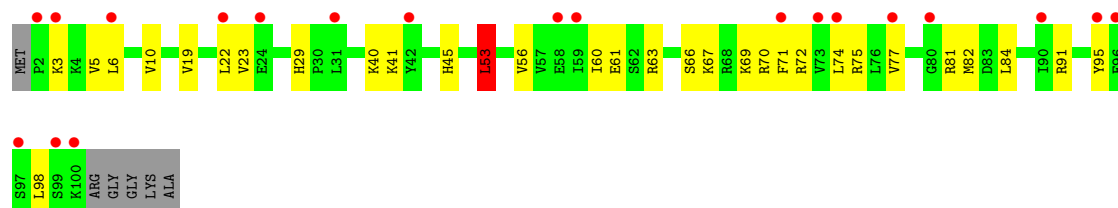




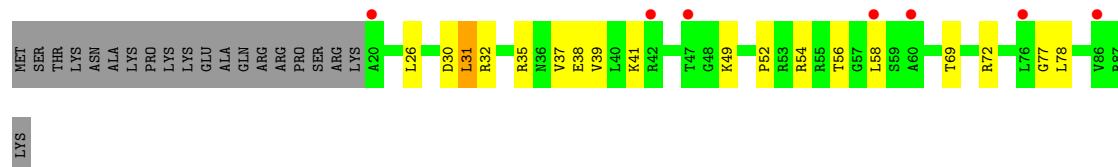
• Molecule 48: 30S ribosomal protein S17



• Molecule 48: 30S ribosomal protein S17



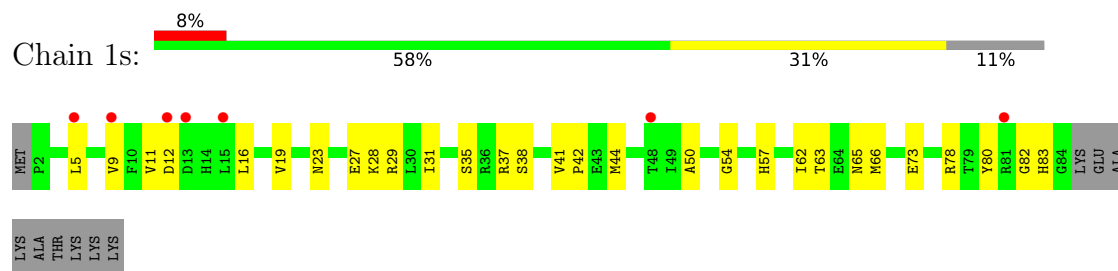
• Molecule 49: 30S ribosomal protein S18



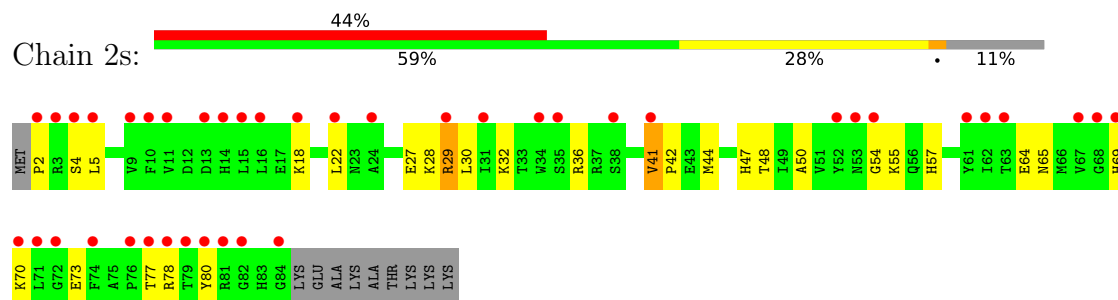
• Molecule 49: 30S ribosomal protein S18



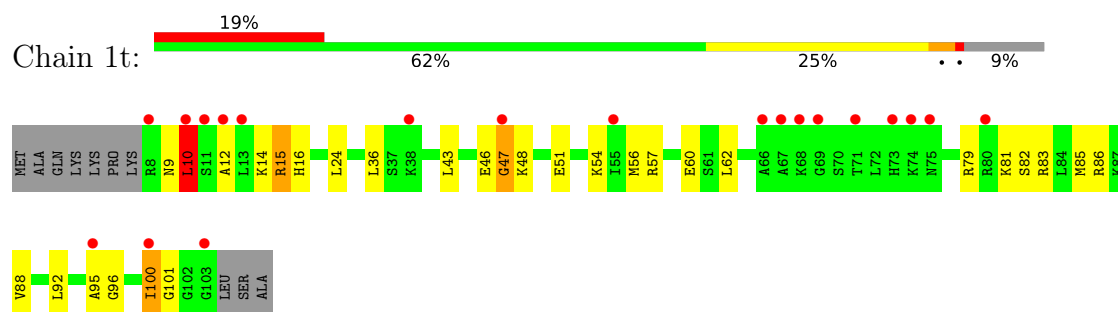
- Molecule 50: 30S ribosomal protein S19



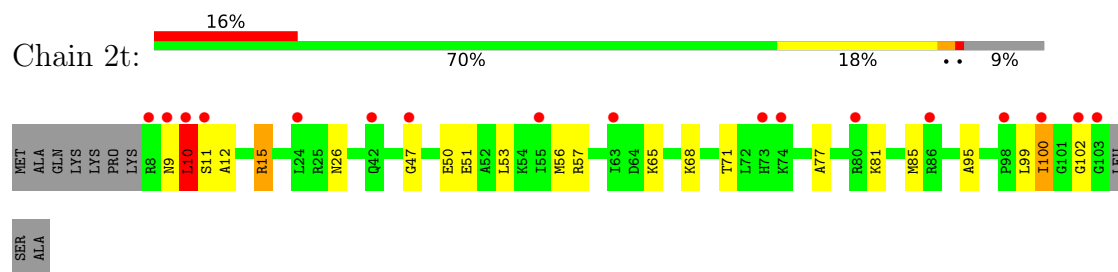
- Molecule 50: 30S ribosomal protein S19



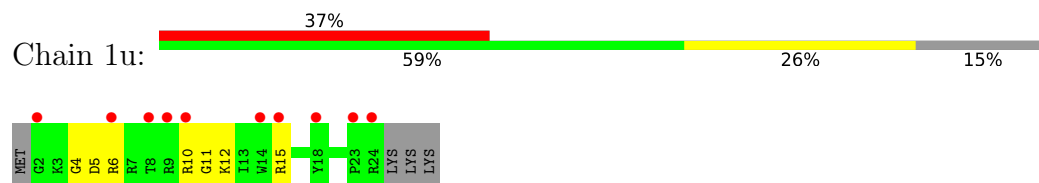
- Molecule 51: 30S ribosomal protein S20



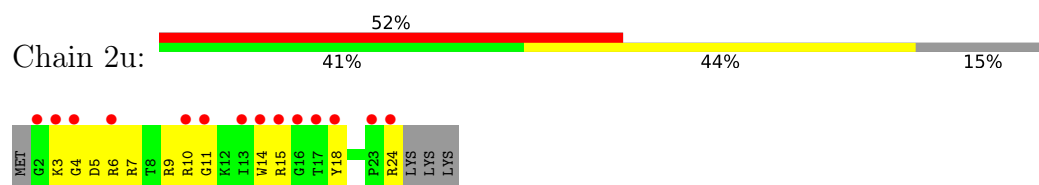
- Molecule 51: 30S ribosomal protein S20



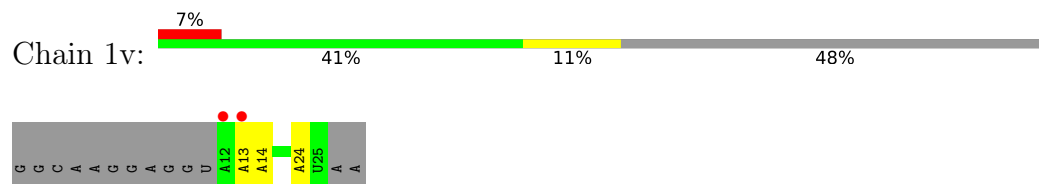
- Molecule 52: 30S ribosomal protein Thx



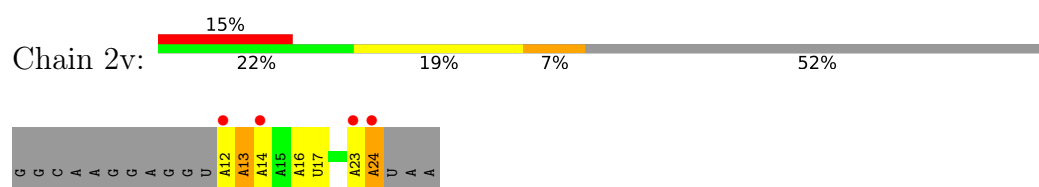
- Molecule 52: 30S ribosomal protein Thx



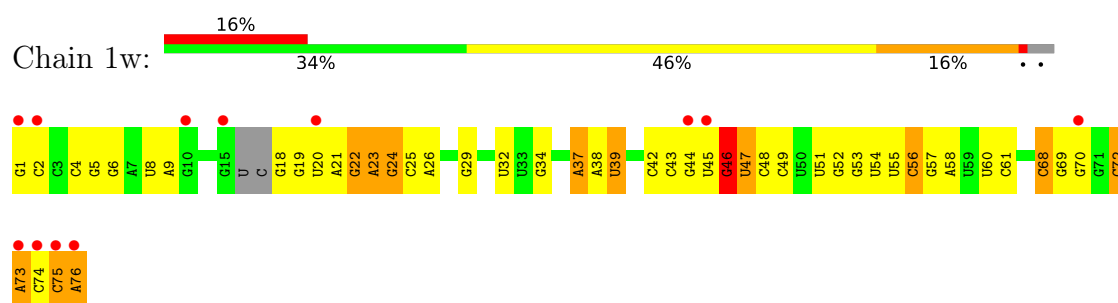
- Molecule 53: mRNA



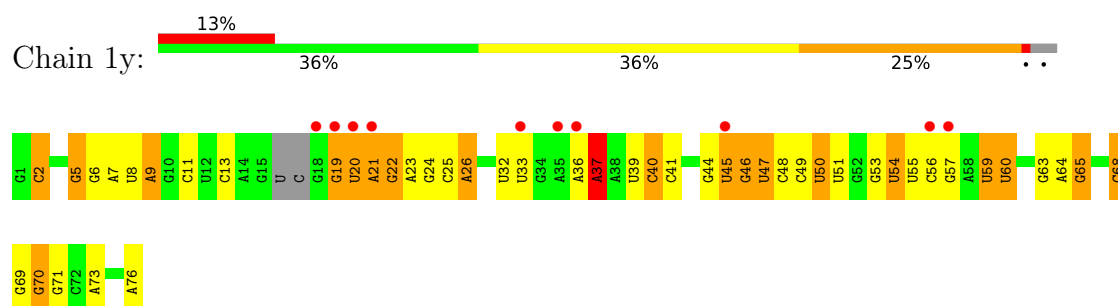
- Molecule 53: mRNA



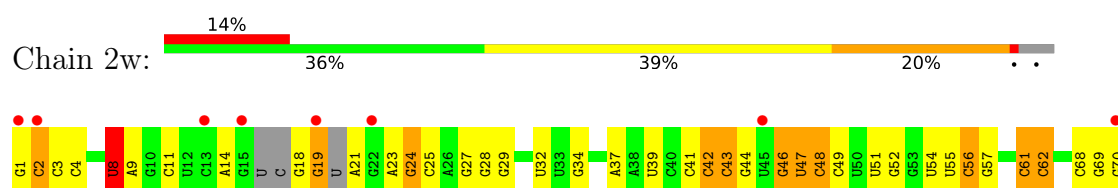
- Molecule 54: A/E-site tRNAs

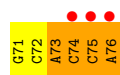


- Molecule 54: A/E-site tRNAs

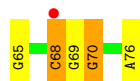
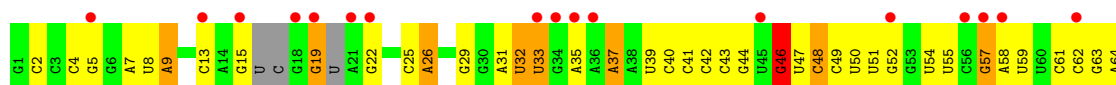


- Molecule 54: A/E-site tRNAs

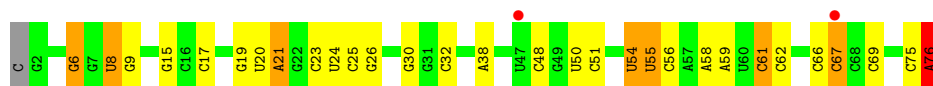




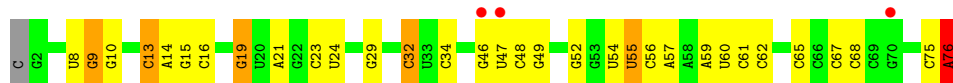
• Molecule 54: A/E-site tRNAs



• Molecule 55: P-site tRNA



• Molecule 55: P-site tRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.89Å 446.22Å 619.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	362.07 – 2.65 362.07 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.5 (362.07-2.65) 98.5 (362.07-2.65)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.65Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.226 , 0.271 (Not available) , 0.261	Depositor DCC
R_{free} test set	81734 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	50.7	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	299169	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 1.60% 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: 7MG, 2MU, 4SU, MG, UR3, K, FME, 4M2, M2G, 4OC, MIA, MA6, OMG, PSU, 5MU, 0TD, SF4, 5MC, 2MA, 2MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1A	0.28	0/69009	0.45	1/107712 (0.0%)
1	2A	0.23	0/67293	0.44	1/105034 (0.0%)
2	1B	0.22	0/2882	0.37	0/4494
2	2B	0.23	0/2879	0.42	0/4487
3	1D	0.48	0/2186	0.85	0/2944
3	2D	0.44	0/2186	0.85	0/2944
4	1E	0.48	0/1592	0.87	2/2149 (0.1%)
4	2E	0.41	0/1592	0.89	2/2149 (0.1%)
5	1F	0.47	0/1619	0.86	1/2193 (0.0%)
5	2F	0.39	0/1615	0.90	2/2188 (0.1%)
6	1G	0.40	0/1454	0.86	5/1964 (0.3%)
6	2G	0.37	0/1453	0.91	4/1963 (0.2%)
7	1H	0.42	0/1356	0.85	1/1834 (0.1%)
7	2H	0.41	0/1356	0.92	0/1834
8	1I	0.37	0/1112	0.91	1/1514 (0.1%)
8	2I	0.37	0/1079	0.85	0/1475
9	1N	0.47	0/1144	0.84	0/1543
9	2N	0.38	0/1144	0.91	6/1543 (0.4%)
10	1O	0.49	0/943	0.83	0/1269
10	2O	0.38	0/943	0.81	0/1269
11	1P	0.46	0/1152	0.83	0/1533
11	2P	0.39	0/1152	0.96	3/1533 (0.2%)
12	1Q	0.48	0/1143	0.83	0/1527
12	2Q	0.39	0/1143	0.83	0/1527
13	1R	0.47	0/982	0.79	0/1312
13	2R	0.41	0/982	0.78	0/1312
14	1S	0.41	0/883	0.83	0/1176
14	2S	0.37	0/880	0.88	0/1172
15	1T	0.41	0/1105	0.78	0/1477
15	2T	0.38	0/1097	0.81	0/1468
16	1U	0.52	0/977	0.85	1/1301 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.41	0/977	0.85	0/1301
17	1V	0.45	0/782	0.78	0/1049
17	2V	0.40	0/782	0.83	0/1049
18	1W	0.48	0/897	0.81	0/1205
18	2W	0.44	0/897	0.83	0/1205
19	1X	0.47	0/764	0.86	2/1025 (0.2%)
19	2X	0.39	0/764	0.80	0/1025
20	1Y	0.42	0/819	0.88	1/1095 (0.1%)
20	2Y	0.36	0/819	0.94	4/1095 (0.4%)
21	1Z	0.38	0/1267	0.86	0/1717
21	2Z	0.40	0/1299	0.96	7/1763 (0.4%)
22	10	0.45	0/662	0.95	5/881 (0.6%)
22	20	0.36	0/662	0.93	2/881 (0.2%)
23	11	0.46	0/762	0.79	0/1014
23	21	0.40	0/762	0.83	0/1014
24	12	0.44	0/590	0.78	0/781
24	22	0.36	0/590	0.78	0/781
25	13	0.47	0/474	0.86	0/635
25	23	0.37	0/469	0.86	0/630
26	14	0.41	0/565	1.03	3/761 (0.4%)
26	24	0.44	0/545	1.12	6/737 (0.8%)
27	15	0.49	0/469	0.87	0/635
27	25	0.41	0/469	0.74	0/635
28	16	0.44	0/460	0.75	0/613
28	26	0.35	0/456	0.70	0/608
29	17	0.46	0/426	0.91	0/561
29	27	0.51	0/426	0.89	1/561 (0.2%)
30	18	0.45	0/525	0.81	0/691
30	28	0.40	0/525	0.78	0/691
31	19	0.42	0/310	0.79	0/407
31	29	0.37	0/310	0.87	0/407
32	1a	0.21	0/35795	0.40	0/55864
32	2a	0.21	0/35886	0.41	0/56005
33	1b	0.39	0/1881	0.95	9/2542 (0.4%)
33	2b	0.41	0/1860	1.00	7/2518 (0.3%)
34	1c	0.37	0/1572	0.80	0/2126
34	2c	0.40	0/1566	0.94	5/2119 (0.2%)
35	1d	0.38	0/1685	0.88	6/2262 (0.3%)
35	2d	0.39	0/1704	0.86	3/2284 (0.1%)
36	1e	0.40	0/1145	0.87	0/1543
36	2e	0.41	0/1149	0.96	0/1548
37	1f	0.38	0/823	0.75	0/1115
37	2f	0.38	0/829	0.76	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.39	0/1250	0.85	1/1679 (0.1%)
38	2g	0.36	0/1254	0.87	2/1683 (0.1%)
39	1h	0.37	0/1108	0.89	2/1494 (0.1%)
39	2h	0.34	0/1108	0.94	3/1494 (0.2%)
40	1i	0.37	0/1002	0.84	0/1346
40	2i	0.36	0/997	0.83	0/1343
41	1j	0.38	0/722	1.02	6/982 (0.6%)
41	2j	0.44	0/727	0.90	2/988 (0.2%)
42	1k	0.39	0/844	0.82	1/1145 (0.1%)
42	2k	0.38	0/848	0.83	0/1149
43	1l	0.40	0/937	0.78	1/1260 (0.1%)
43	2l	0.36	0/937	0.91	5/1260 (0.4%)
44	1m	0.37	0/969	0.88	1/1302 (0.1%)
44	2m	0.40	0/961	0.90	2/1291 (0.2%)
45	1n	0.37	0/501	0.79	1/664 (0.2%)
45	2n	0.34	0/501	0.91	2/664 (0.3%)
46	1o	0.37	0/739	0.82	0/985
46	2o	0.35	0/739	0.81	0/985
47	1p	0.35	0/697	0.85	1/939 (0.1%)
47	2p	0.37	0/693	0.81	0/935
48	1q	0.35	0/836	0.84	0/1117
48	2q	0.35	0/836	0.85	3/1117 (0.3%)
49	1r	0.39	0/560	0.80	0/746
49	2r	0.35	0/560	0.78	0/746
50	1s	0.35	0/667	0.84	0/900
50	2s	0.44	0/661	1.00	2/893 (0.2%)
51	1t	0.36	0/730	0.87	0/965
51	2t	0.39	0/729	0.88	1/965 (0.1%)
52	1u	0.35	0/203	0.89	0/266
52	2u	0.34	0/203	0.81	0/266
53	1v	0.19	0/314	0.30	0/487
53	2v	0.21	0/310	0.36	0/480
54	1w	0.25	0/1602	0.46	0/2493
54	1y	0.27	1/1602 (0.1%)	0.51	0/2493
54	2w	0.27	1/1579 (0.1%)	0.45	0/2455
54	2y	0.27	1/1579 (0.1%)	0.45	0/2455
55	1x	0.32	0/1725	0.49	1/2689 (0.0%)
55	2x	0.30	0/1725	0.57	3/2689 (0.1%)
All	All	0.30	3/316707 (0.0%)	0.58	131/474152 (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
38	2g	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	8	4SU	O3'-P	5.37	1.61	1.56
54	1y	8	4SU	O3'-P	5.01	1.61	1.56
54	2y	8	4SU	O3'-P	5.01	1.61	1.56

All (131) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	76	A	O4'-C1'-N9	15.54	131.50	108.20
22	20	82	ARG	CA-C-N	9.90	129.99	119.89
22	20	82	ARG	C-N-CA	9.90	129.99	119.89
21	2Z	171	ILE	N-CA-C	8.13	119.12	111.48
33	2b	129	GLU	N-CA-C	-8.12	101.99	112.23
39	2h	73	ASP	CA-C-N	7.86	127.49	119.56
39	2h	73	ASP	C-N-CA	7.86	127.49	119.56
43	2l	119	LYS	N-CA-C	-7.82	100.44	110.53
55	1x	76	A	O4'-C1'-N9	7.62	119.64	108.20
26	24	40	HIS	CA-C-N	7.53	127.90	119.32
26	24	40	HIS	C-N-CA	7.53	127.90	119.32
11	2P	44	GLY	CA-C-N	7.48	135.17	121.70
11	2P	44	GLY	C-N-CA	7.48	135.17	121.70
38	1g	79	ARG	N-CA-C	7.47	119.07	111.07
4	2E	72	VAL	CA-C-N	7.30	134.84	121.70
4	2E	72	VAL	C-N-CA	7.30	134.84	121.70
55	2x	76	A	C1'-O4'-C4'	-7.28	102.42	109.70
22	10	13	GLY	N-CA-C	7.08	122.46	114.67
20	2Y	93	GLY	N-CA-C	-7.00	105.55	114.37
22	10	14	ARG	N-CA-C	6.82	120.71	110.14
33	1b	123	ALA	N-CA-C	-6.81	104.85	113.02
35	2d	171	GLY	CA-C-N	6.64	126.15	119.24
35	2d	171	GLY	C-N-CA	6.64	126.15	119.24
34	2c	108	ASN	CA-C-N	6.63	126.33	119.64
34	2c	108	ASN	C-N-CA	6.63	126.33	119.64
5	1F	89	VAL	N-CA-C	6.60	116.63	110.42
38	2g	79	ARG	N-CA-C	6.59	118.12	111.07
26	24	52	THR	N-CA-C	-6.59	104.87	113.17
33	2b	130	ARG	CA-C-N	6.58	126.62	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	2b	130	ARG	C-N-CA	6.58	126.62	119.90
1	1A	1992	G	C2'-C3'-O3'	6.57	119.36	109.50
9	2N	10	GLU	CA-C-N	6.56	126.52	119.76
9	2N	10	GLU	C-N-CA	6.56	126.52	119.76
33	1b	23	ARG	N-CA-C	-6.54	103.46	112.03
26	14	40	HIS	CA-C-N	6.50	126.73	119.32
26	14	40	HIS	C-N-CA	6.50	126.73	119.32
34	2c	96	GLY	N-CA-C	-6.48	106.37	115.32
33	2b	25	ASN	CA-C-N	6.46	126.15	119.82
33	2b	25	ASN	C-N-CA	6.46	126.15	119.82
26	24	54	GLY	N-CA-C	-6.42	103.82	114.48
35	1d	188	LEU	CA-C-N	6.34	126.35	119.89
35	1d	188	LEU	C-N-CA	6.34	126.35	119.89
6	1G	127	GLY	N-CA-C	-6.27	107.05	115.21
16	1U	9	VAL	N-CA-C	6.25	116.40	110.53
33	1b	38	GLY	N-CA-C	-6.22	107.12	115.21
6	2G	48	GLU	N-CA-C	-6.21	105.73	113.55
44	1m	84	ILE	N-CA-C	6.16	122.34	113.16
50	2s	41	VAL	CA-C-N	6.08	127.44	119.84
50	2s	41	VAL	C-N-CA	6.08	127.44	119.84
21	2Z	14	LYS	CA-C-N	6.06	126.50	119.47
21	2Z	14	LYS	C-N-CA	6.06	126.50	119.47
33	1b	128	GLU	N-CA-C	-6.01	105.90	113.72
39	1h	71	GLY	CA-C-N	6.01	125.72	119.05
39	1h	71	GLY	C-N-CA	6.01	125.72	119.05
4	1E	176	ILE	CA-C-N	6.00	126.17	119.32
4	1E	176	ILE	C-N-CA	6.00	126.17	119.32
1	2A	1992	G	C2'-C3'-O3'	5.99	118.49	109.50
41	1j	52	GLY	CA-C-N	5.95	125.57	119.56
41	1j	52	GLY	C-N-CA	5.95	125.57	119.56
9	2N	125	GLY	CA-C-N	5.91	125.53	119.56
9	2N	125	GLY	C-N-CA	5.91	125.53	119.56
6	2G	96	ARG	CB-CA-C	-5.84	109.82	116.54
43	2l	44	THR	CA-C-N	5.83	126.29	120.52
43	2l	44	THR	C-N-CA	5.83	126.29	120.52
21	2Z	129	SER	CA-C-N	5.77	125.63	119.28
21	2Z	129	SER	C-N-CA	5.77	125.63	119.28
45	2n	13	THR	CA-C-N	5.76	127.05	119.84
45	2n	13	THR	C-N-CA	5.76	127.05	119.84
20	1Y	92	ASN	N-CA-C	5.71	117.96	111.11
38	2g	69	VAL	N-CA-C	-5.66	107.47	112.90
6	1G	96	ARG	CB-CA-C	-5.65	110.05	116.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	27	45	ALA	N-CA-C	5.64	117.29	111.03
33	1b	158	LEU	CA-C-N	5.63	125.63	119.89
33	1b	158	LEU	C-N-CA	5.63	125.63	119.89
43	2l	28	LYS	N-CA-C	5.62	118.05	111.02
6	2G	31	VAL	CA-C-N	5.58	126.82	119.84
6	2G	31	VAL	C-N-CA	5.58	126.82	119.84
43	2l	105	TYR	CB-CA-C	-5.58	110.16	116.63
35	1d	50	ARG	CA-C-N	5.54	125.47	119.76
35	1d	50	ARG	C-N-CA	5.54	125.47	119.76
44	2m	106	ASN	N-CA-C	5.48	122.48	110.80
21	2Z	53	ILE	N-CA-C	-5.45	106.99	112.17
33	2b	71	VAL	N-CA-C	5.44	115.38	106.72
19	1X	94	GLY	CA-C-N	5.44	131.50	121.70
19	1X	94	GLY	C-N-CA	5.44	131.50	121.70
48	2q	53	LEU	N-CA-C	5.40	117.69	110.35
41	1j	38	ILE	CA-C-N	5.39	126.57	119.84
41	1j	38	ILE	C-N-CA	5.39	126.57	119.84
51	2t	11	SER	N-CA-C	-5.38	106.57	113.02
44	2m	67	GLU	CB-CA-C	-5.37	110.37	116.54
35	2d	88	VAL	N-CA-C	5.35	115.30	108.12
55	2x	76	A	C3'-C2'-O2'	-5.35	106.57	114.60
35	1d	171	GLY	CA-C-N	5.34	124.79	119.24
35	1d	171	GLY	C-N-CA	5.34	124.79	119.24
20	2Y	91	GLU	N-CA-C	-5.31	106.31	112.89
33	2b	23	ARG	N-CA-C	-5.31	104.60	111.71
33	1b	166	ASP	CA-C-N	5.28	124.91	119.05
33	1b	166	ASP	C-N-CA	5.28	124.91	119.05
43	1l	105	TYR	CB-CA-C	-5.26	110.52	116.63
9	2N	94	HIS	CA-C-N	5.25	124.91	119.56
9	2N	94	HIS	C-N-CA	5.25	124.91	119.56
22	10	9	SER	N-CA-C	5.23	116.24	108.60
42	1k	40	ILE	N-CA-C	-5.23	107.66	111.90
39	2h	86	ILE	N-CA-C	-5.22	106.57	111.48
11	2P	44	GLY	CA-C-O	-5.21	115.26	121.83
21	2Z	161	VAL	N-CA-C	5.21	115.00	106.72
6	1G	31	VAL	CA-C-N	5.21	126.35	119.84
6	1G	31	VAL	C-N-CA	5.21	126.35	119.84
6	1G	126	ASP	N-CA-C	5.19	117.68	111.71
47	1p	5	ARG	N-CA-C	5.17	117.04	109.24
45	1n	38	GLY	N-CA-C	-5.16	108.59	115.40
26	24	56	VAL	N-CA-C	-5.16	105.51	110.72
41	2j	52	GLY	CA-C-N	5.15	124.77	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	2j	52	GLY	C-N-CA	5.15	124.77	119.56
41	1j	76	ASN	CA-C-N	5.14	126.27	119.84
41	1j	76	ASN	C-N-CA	5.14	126.27	119.84
26	14	59	PHE	N-CA-C	-5.14	106.96	113.18
22	10	82	ARG	CA-C-N	5.13	125.13	119.90
22	10	82	ARG	C-N-CA	5.13	125.13	119.90
48	2q	29	HIS	CA-C-N	5.12	124.79	119.56
48	2q	29	HIS	C-N-CA	5.12	124.79	119.56
33	1b	190	THR	N-CA-C	5.12	117.60	111.71
20	2Y	73	ARG	CA-C-N	5.09	125.01	119.76
20	2Y	73	ARG	C-N-CA	5.09	125.01	119.76
5	2F	21	ALA	CA-C-N	5.08	130.85	121.70
5	2F	21	ALA	C-N-CA	5.08	130.85	121.70
8	1I	104	GLN	N-CA-C	-5.07	103.24	110.59
7	1H	3	ARG	N-CA-C	5.05	116.27	107.93
34	2c	6	HIS	CA-C-N	5.02	124.63	119.56
34	2c	6	HIS	C-N-CA	5.02	124.63	119.56
26	24	33	VAL	N-CA-C	5.01	115.93	108.46

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
38	2g	79	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31193	631	0
1	2A	60322	0	30423	856	0
2	1B	2577	0	1305	20	0
2	2B	2575	0	1303	49	0
3	1D	2136	0	2218	55	0
3	2D	2136	0	2218	56	0
4	1E	1559	0	1618	39	0
4	2E	1559	0	1618	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	1F	1584	0	1625	40	0
5	2F	1580	0	1619	54	0
6	1G	1429	0	1447	33	0
6	2G	1428	0	1438	49	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	40	0
8	1I	1097	0	1140	27	0
8	2I	1064	0	1082	24	0
9	1N	1117	0	1184	25	0
9	2N	1117	0	1184	23	0
10	1O	933	0	996	20	0
10	2O	933	0	996	21	0
11	1P	1135	0	1211	27	0
11	2P	1135	0	1212	38	0
12	1Q	1122	0	1179	21	0
12	2Q	1122	0	1179	34	0
13	1R	968	0	1033	18	0
13	2R	968	0	1033	26	0
14	1S	873	0	927	20	0
14	2S	870	0	923	15	0
15	1T	1091	0	1151	16	0
15	2T	1083	0	1136	21	0
16	1U	959	0	1019	12	0
16	2U	959	0	1019	25	0
17	1V	771	0	830	15	0
17	2V	771	0	830	20	0
18	1W	886	0	940	9	0
18	2W	886	0	940	10	0
19	1X	750	0	814	16	0
19	2X	750	0	814	15	0
20	1Y	806	0	881	13	0
20	2Y	806	0	881	17	0
21	1Z	1240	0	1240	25	0
21	2Z	1271	0	1273	50	0
22	10	653	0	674	16	0
22	20	653	0	674	17	0
23	11	755	0	826	13	0
23	21	755	0	826	23	0
24	12	588	0	643	13	0
24	22	588	0	643	16	0
25	13	469	0	518	9	0
25	23	464	0	514	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	14	552	0	533	19	0
26	24	532	0	503	14	0
27	15	455	0	465	11	0
27	25	455	0	465	12	0
28	16	453	0	473	8	0
28	26	449	0	469	13	0
29	17	418	0	467	7	0
29	27	418	0	467	5	0
30	18	517	0	582	17	0
30	28	517	0	582	15	0
31	19	307	0	335	2	0
31	29	307	0	335	8	0
32	1a	32246	0	16295	394	0
32	2a	32327	0	16340	523	0
33	1b	1846	0	1867	64	0
33	2b	1825	0	1828	73	0
34	1c	1548	0	1535	22	0
34	2c	1542	0	1517	57	0
35	1d	1655	0	1672	45	0
35	2d	1674	0	1714	60	0
36	1e	1129	0	1185	31	0
36	2e	1133	0	1191	32	0
37	1f	810	0	804	21	0
37	2f	816	0	808	20	0
38	1g	1231	0	1238	23	0
38	2g	1235	0	1249	34	0
39	1h	1088	0	1126	35	0
39	2h	1088	0	1126	35	0
40	1i	983	0	986	37	0
40	2i	978	0	966	40	0
41	1j	709	0	650	26	0
41	2j	714	0	672	34	0
42	1k	829	0	825	14	0
42	2k	833	0	836	14	0
43	1l	932	0	981	15	0
43	2l	932	0	981	16	0
44	1m	958	0	1002	22	0
44	2m	950	0	988	54	0
45	1n	492	0	529	14	0
45	2n	492	0	529	22	0
46	1o	728	0	760	9	0
46	2o	728	0	760	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	1p	681	0	697	22	0
47	2p	677	0	686	31	0
48	1q	823	0	891	27	0
48	2q	823	0	891	23	0
49	1r	555	0	618	14	0
49	2r	555	0	618	16	0
50	1s	652	0	662	21	0
50	2s	646	0	644	27	0
51	1t	728	0	798	20	0
51	2t	727	0	796	12	0
52	1u	199	0	208	6	0
52	2u	199	0	208	8	0
53	1v	281	0	139	0	0
53	2v	277	0	140	4	0
54	1w	1588	0	820	32	0
54	1y	1581	0	805	40	0
54	2w	1561	0	796	34	0
54	2y	1561	0	796	35	0
55	1x	1625	0	828	17	0
55	2x	1625	0	828	19	0
56	10	6	0	0	0	0
56	11	2	0	0	0	0
56	12	2	0	0	0	0
56	13	1	0	0	0	0
56	15	4	0	0	0	0
56	16	2	0	0	0	0
56	17	1	0	0	0	0
56	18	1	0	0	0	0
56	19	2	0	0	0	0
56	1A	935	0	0	0	0
56	1B	25	0	0	0	0
56	1D	9	0	0	0	0
56	1E	8	0	0	0	0
56	1F	8	0	0	0	0
56	1G	5	0	0	0	0
56	1I	1	0	0	0	0
56	1N	6	0	0	0	0
56	1O	3	0	0	0	0
56	1P	3	0	0	0	0
56	1Q	5	0	0	0	0
56	1R	2	0	0	0	0
56	1S	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1T	2	0	0	0	0
56	1U	4	0	0	0	0
56	1V	3	0	0	0	0
56	1W	4	0	0	0	0
56	1X	3	0	0	0	0
56	1Y	2	0	0	0	0
56	1Z	3	0	0	0	0
56	1a	234	0	0	0	0
56	1b	2	0	0	0	0
56	1c	1	0	0	0	0
56	1d	1	0	0	0	0
56	1e	1	0	0	0	0
56	1f	1	0	0	0	0
56	1g	1	0	0	0	0
56	1l	3	0	0	0	0
56	1n	1	0	0	0	0
56	1r	1	0	0	0	0
56	1s	1	0	0	0	0
56	1t	1	0	0	0	0
56	1v	1	0	0	0	0
56	1w	5	0	0	0	0
56	1x	14	0	0	0	0
56	1y	7	0	0	0	0
56	20	3	0	0	0	0
56	21	2	0	0	0	0
56	23	1	0	0	0	0
56	25	1	0	0	0	0
56	28	1	0	0	0	0
56	2A	679	0	0	0	0
56	2B	21	0	0	0	0
56	2D	4	0	0	0	0
56	2E	7	0	0	0	0
56	2F	5	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	2	0	0	0	0
56	2Q	3	0	0	0	0
56	2R	1	0	0	0	0
56	2T	1	0	0	0	0
56	2U	2	0	0	0	0
56	2V	3	0	0	0	0
56	2X	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2Z	1	0	0	0	0
56	2a	200	0	0	0	0
56	2d	1	0	0	0	0
56	2e	2	0	0	0	0
56	2f	2	0	0	0	0
56	2g	1	0	0	0	0
56	2j	2	0	0	0	0
56	2l	2	0	0	0	0
56	2p	1	0	0	0	0
56	2q	3	0	0	0	0
56	2r	1	0	0	0	0
56	2t	1	0	0	0	0
56	2v	2	0	0	0	0
56	2w	3	0	0	0	0
56	2x	2	0	0	0	0
57	1A	57	0	50	6	0
57	2A	57	0	50	6	0
58	1A	1	0	0	0	0
58	2A	1	0	0	0	0
59	14	1	0	0	0	0
59	15	1	0	0	0	0
59	16	1	0	0	0	0
59	19	1	0	0	0	0
59	1Y	1	0	0	0	0
59	1n	1	0	0	0	0
59	24	1	0	0	0	0
59	25	1	0	0	0	0
59	26	1	0	0	0	0
59	29	1	0	0	0	0
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	0	0
60	2d	8	0	0	0	0
61	1x	10	0	10	1	0
61	2x	10	0	10	0	0
62	10	6	0	0	0	0
62	11	3	0	0	0	0
62	12	4	0	0	1	0
62	13	5	0	0	0	0
62	15	1	0	0	0	0
62	17	6	0	0	0	0
62	18	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	19	2	0	0	0	0
62	1A	1741	0	0	69	0
62	1B	49	0	0	1	0
62	1D	21	0	0	1	0
62	1E	27	0	0	2	0
62	1F	22	0	0	1	0
62	1G	3	0	0	0	0
62	1I	1	0	0	0	0
62	1N	6	0	0	0	0
62	1O	4	0	0	0	0
62	1P	21	0	0	1	0
62	1Q	5	0	0	0	0
62	1R	5	0	0	0	0
62	1S	6	0	0	0	0
62	1T	13	0	0	0	0
62	1U	12	0	0	0	0
62	1V	10	0	0	0	0
62	1W	6	0	0	1	0
62	1X	4	0	0	1	0
62	1Y	4	0	0	1	0
62	1Z	1	0	0	0	0
62	1a	309	0	0	18	0
62	1d	1	0	0	0	0
62	1g	1	0	0	0	0
62	1j	1	0	0	0	0
62	1l	3	0	0	0	0
62	1m	1	0	0	0	0
62	1o	2	0	0	0	0
62	1p	2	0	0	0	0
62	1q	1	0	0	0	0
62	1r	1	0	0	0	0
62	1v	6	0	0	0	0
62	1w	6	0	0	0	0
62	1x	13	0	0	0	0
62	1y	5	0	0	0	0
62	20	6	0	0	0	0
62	21	5	0	0	0	0
62	22	1	0	0	0	0
62	23	1	0	0	0	0
62	25	3	0	0	0	0
62	27	3	0	0	0	0
62	28	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	29	1	0	0	0	0
62	2A	1031	0	0	89	0
62	2B	10	0	0	1	0
62	2D	16	0	0	4	0
62	2E	10	0	0	1	0
62	2F	7	0	0	0	0
62	2I	2	0	0	0	0
62	2N	1	0	0	0	0
62	2O	1	0	0	0	0
62	2P	14	0	0	2	0
62	2Q	1	0	0	0	0
62	2R	2	0	0	0	0
62	2T	3	0	0	0	0
62	2U	1	0	0	0	0
62	2V	2	0	0	0	0
62	2W	1	0	0	1	0
62	2X	3	0	0	0	0
62	2Y	1	0	0	1	0
62	2Z	2	0	0	0	0
62	2a	203	0	0	16	0
62	2d	4	0	0	0	0
62	2g	1	0	0	0	0
62	2i	1	0	0	0	0
62	2j	4	0	0	1	0
62	2l	3	0	0	0	0
62	2o	1	0	0	1	0
62	2p	2	0	0	0	0
62	2r	1	0	0	0	0
62	2t	2	0	0	0	0
62	2v	3	0	0	0	0
62	2x	6	0	0	2	0
All	All	299169	0	196829	4372	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 9.

All (4372) 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)
54:2y:52:G:H1	54:2y:62:C:N4	1.54	1.06
1:1A:1082:U:H3	1:1A:1086:A:N6	1.56	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:N3	1:1A:1086:A:N6	2.09	1.01
1:1A:1082:U:O4	1:1A:1086:A:N1	1.95	0.99
54:1y:19:G:H1	54:1y:56:C:H42	1.09	0.99
32:1a:1008:C:H42	32:1a:1021:G:H1	1.05	0.98
54:1y:51:U:H3	54:1y:63:G:H1	1.08	0.97
32:2a:1029:C:C4	32:2a:1032:G:N1	2.33	0.97
32:2a:1002:G:H1	32:2a:1038:C:N4	1.62	0.97
54:1y:19:G:N2	54:1y:56:C:N3	2.14	0.94
54:1y:49:C:H42	54:1y:65:G:H1	1.04	0.94
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.50	0.94
32:2a:1002:G:H1	32:2a:1038:C:H42	1.02	0.94
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.10	0.92
44:2m:106:ASN:O	44:2m:108:ARG:N	2.01	0.92
1:2A:2129:C:H42	1:2A:2159:G:H1	1.01	0.92
54:2y:15:G:H22	54:2y:48:C:H42	1.17	0.92
32:1a:376:G:H5''	47:1p:5:ARG:HG2	1.50	0.91
32:1a:78:G:H1	32:1a:91:C:N4	1.67	0.91
1:1A:1359:A:N1	1:1A:1372:U:N3	2.18	0.91
1:1A:2099:U:H3	1:1A:2190:G:H1	1.18	0.91
22:20:10:THR:HG22	22:20:12:ASN:H	1.34	0.91
1:1A:2135:A:H61	1:1A:2157:G:H21	1.16	0.90
20:1Y:92:ASN:HB3	20:1Y:94:LYS:H	1.36	0.90
55:1x:6:G:H1	55:1x:67:C:H42	1.20	0.89
29:17:24:THR:HG22	29:17:27:GLY:H	1.37	0.89
3:2D:242:ARG:HH11	3:2D:242:ARG:HG3	1.33	0.88
54:2y:5:G:H1	54:2y:68:C:H42	1.20	0.88
1:2A:198:C:OP2	62:2A:9701:HOH:O	1.91	0.88
32:1a:1008:C:N4	32:1a:1021:G:H1	1.71	0.88
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.51	0.88
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.07	0.88
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.07	0.88
32:2a:1352:C:H42	32:2a:1370:G:H1	1.20	0.88
54:1y:19:G:H1	54:1y:56:C:N4	1.70	0.87
54:1y:49:C:N4	54:1y:65:G:H1	1.72	0.87
16:2U:76:TYR:OH	16:2U:92:ARG:NH1	2.06	0.87
1:2A:195:A:N7	62:2A:9701:HOH:O	2.08	0.87
54:2y:52:G:N2	54:2y:62:C:N3	2.23	0.86
32:2a:1009:G:H22	32:2a:1021:G:H1'	1.38	0.86
1:1A:1670:C:OP1	62:1A:4001:HOH:O	1.94	0.86
1:1A:1082:U:H3	1:1A:1086:A:H61	0.87	0.86
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.07	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.09	0.85
22:10:10:THR:HG22	22:10:12:ASN:H	1.40	0.85
1:2A:882:G:N2	1:2A:894:C:N3	2.23	0.85
1:2A:1204:A:H2	1:2A:1241:A:H62	1.21	0.85
1:2A:2129:C:N4	1:2A:2159:G:H1	1.72	0.85
32:1a:78:G:N2	32:1a:91:C:N3	2.24	0.85
1:1A:2508:G:H5'	54:1w:75:C:H42	1.41	0.85
32:1a:78:G:N1	32:1a:91:C:N4	2.25	0.85
32:2a:1262:C:H42	32:2a:1273:G:H1	1.26	0.84
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.09	0.84
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.39	0.84
32:1a:116:A:OP1	62:1a:1901:HOH:O	1.95	0.84
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.59	0.84
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.09	0.84
51:2t:10:LEU:HB3	51:2t:12:ALA:H	1.42	0.84
32:2a:1002:G:N2	32:2a:1038:C:N3	2.24	0.84
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.59	0.84
32:2a:987:G:H1	32:2a:1218:C:H42	1.26	0.83
47:2p:51:VAL:HG12	47:2p:53:VAL:H	1.44	0.83
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.61	0.83
54:1y:19:G:N1	54:1y:56:C:N4	2.26	0.83
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.61	0.83
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.43	0.83
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.59	0.83
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.12	0.83
42:1k:48:ILE:HD12	42:1k:63:LEU:HB2	1.61	0.82
54:2y:15:G:N2	54:2y:48:C:H42	1.77	0.82
1:1A:279:C:H42	1:1A:361:G:H1	1.27	0.82
1:1A:400:G:N7	62:1A:4018:HOH:O	2.11	0.82
32:2a:997:U:H3	32:2a:1044:A:H61	1.23	0.82
1:1A:998:C:OP1	62:1A:4002:HOH:O	1.98	0.82
1:2A:1315:C:OP2	62:2A:9702:HOH:O	1.97	0.82
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.59	0.82
4:1E:77:ILE:HD13	4:1E:195:LEU:HD11	1.59	0.82
32:1a:1004:A:H5'	32:1a:1024:G:H1	1.44	0.82
1:1A:958:U:OP2	12:1Q:14:ARG:NH1	2.13	0.82
1:1A:2140:C:H42	1:1A:2151:G:H1	1.27	0.81
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.14	0.81
32:1a:664:G:H22	32:1a:741:G:H1	1.27	0.81
1:2A:2124:G:H1	1:2A:2174:C:H42	1.27	0.81
32:1a:1030:C:N4	32:1a:1031:G:N1	2.29	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:574:A:OP2	62:1a:1902:HOH:O	1.97	0.81
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.13	0.81
32:1a:975:A:H4'	32:1a:976:G:H5''	1.63	0.81
36:2e:60:TYR:OH	36:2e:64:ARG:NH2	2.14	0.81
54:2y:52:G:H1	54:2y:62:C:H42	0.85	0.81
32:2a:1227:A:OP1	50:2s:80:TYR:OH	1.99	0.81
1:2A:397:G:N7	62:2A:9730:HOH:O	2.13	0.80
11:2P:39:LYS:HB2	11:2P:45:LEU:HD13	1.64	0.80
54:1w:18:G:O2'	54:1w:57:G:N2	2.13	0.80
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.14	0.80
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.15	0.80
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.14	0.80
32:2a:677:U:H3	32:2a:713:G:H22	1.30	0.80
32:2a:1113:C:H42	32:2a:1187:G:H1	1.29	0.80
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.63	0.80
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.63	0.80
9:2N:123:TYR:HH	9:2N:130:HIS:HE2	1.20	0.79
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.00	0.79
1:2A:2499:C:OP2	62:2A:9704:HOH:O	2.00	0.79
1:1A:847:U:OP2	62:1A:4003:HOH:O	2.00	0.79
32:1a:1030:C:N3	32:1a:1031:G:N2	2.29	0.79
32:2a:1029:C:N3	32:2a:1032:G:N2	2.30	0.79
32:1a:1001:A:H2'	32:1a:1001(A):G:C8	2.17	0.79
1:2A:1648:C:OP1	62:2A:9703:HOH:O	1.99	0.79
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.62	0.79
54:1y:49:C:N3	54:1y:65:G:N2	2.29	0.79
1:1A:1754:C:OP1	15:1T:96:ARG:NH1	2.16	0.79
1:1A:2507:C:O2'	54:1w:76:A:N6	2.16	0.79
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.64	0.79
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.15	0.78
1:1A:2723:C:OP1	13:1R:3:HIS:ND1	2.14	0.78
54:2y:15:G:H22	54:2y:48:C:N4	1.80	0.78
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.65	0.78
47:1p:51:VAL:HG12	47:1p:53:VAL:H	1.49	0.78
1:2A:2104:G:H1	1:2A:2185:C:H42	1.32	0.78
54:2w:18:G:O2'	54:2w:57:G:N2	2.16	0.78
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.49	0.78
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.66	0.78
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.17	0.77
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.65	0.77
32:2a:997:U:H3	32:2a:1044:A:N6	1.81	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1030:C:N4	32:1a:1031:G:H1	1.83	0.77
32:1a:1399:C:H4'	32:1a:1400:5MC:H5''	1.66	0.77
1:1A:1070:A:N7	1:1A:1096:A:O2'	2.17	0.77
1:2A:2507:C:O2'	54:2w:76:A:N6	2.17	0.77
32:2a:407:G:H5''	35:2d:115:ARG:HG2	1.67	0.77
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.66	0.76
54:2w:27:G:H1	54:2w:43:C:H42	1.30	0.76
32:1a:266:G:H5''	32:1a:268:C:H41	1.49	0.76
32:1a:953:G:H5'	32:1a:965:A:H61	1.49	0.76
1:2A:1171:G:H1	1:2A:1178:C:H42	1.33	0.76
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.66	0.76
1:2A:81:G:N7	62:2A:9748:HOH:O	2.19	0.76
1:2A:1689:A:H62	1:2A:1698:A:H2	1.34	0.76
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.68	0.76
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.17	0.76
54:2y:29:G:H1	54:2y:41:C:H42	1.29	0.76
32:1a:944:G:OP1	62:1a:1903:HOH:O	2.03	0.76
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.67	0.76
54:1w:46:7MG:H3'	54:1w:47:U:H5''	1.67	0.76
1:2A:2042:A:OP1	62:2A:9705:HOH:O	2.02	0.76
1:2A:83:G:H1	1:2A:102:G:HO2'	1.33	0.76
32:2a:1029:C:N4	32:2a:1032:G:N1	2.33	0.76
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.68	0.75
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.67	0.75
1:2A:1153:C:OP2	62:2A:9707:HOH:O	2.04	0.75
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD11	1.67	0.75
32:2a:975:A:H4'	32:2a:976:G:H5''	1.67	0.75
1:1A:1013:C:OP2	62:1A:4004:HOH:O	2.02	0.75
12:1Q:16:ARG:HG2	12:1Q:18:LYS:HG3	1.68	0.75
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.68	0.75
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.68	0.75
54:1y:59:U:H5'	54:1y:60:U:H5	1.51	0.75
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.69	0.75
1:2A:2297:C:O2	1:2A:2321:G:N2	2.18	0.75
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.69	0.75
1:2A:912:C:OP1	12:2Q:8:LYS:NZ	2.19	0.75
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.16	0.74
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.18	0.74
1:2A:833:U:O2	11:2P:55:ARG:NH2	2.19	0.74
1:2A:2268:A:OP1	62:2A:9706:HOH:O	2.03	0.74
1:1A:2822:G:N7	62:1A:4046:HOH:O	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:5:G:H1	54:1w:68:C:H42	1.32	0.74
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.19	0.74
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.20	0.74
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.53	0.74
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.20	0.74
1:2A:740:U:OP2	62:2A:9711:HOH:O	2.06	0.74
1:2A:1023:U:OP2	62:2A:9708:HOH:O	2.05	0.74
1:1A:2448:A:OP1	62:1A:4005:HOH:O	2.05	0.74
1:2A:2139:C:H42	1:2A:2152:G:H1	1.34	0.74
1:2A:2685:G:O6	62:2A:9713:HOH:O	2.06	0.74
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.68	0.74
1:1A:2629:A:O2'	1:1A:2630:G:OP2	2.05	0.74
55:2x:49:G:H1	55:2x:65:C:H42	1.34	0.74
21:1Z:151:HIS:O	21:1Z:153:SER:N	2.20	0.74
32:1a:812:C:N3	62:1a:1911:HOH:O	2.20	0.74
1:2A:2615:U:OP1	62:2A:9712:HOH:O	2.06	0.74
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.70	0.73
48:1q:26:GLN:HG2	48:1q:37:LYS:HG2	1.68	0.73
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.70	0.73
1:1A:2763:G:OP2	62:1A:4007:HOH:O	2.05	0.73
40:1i:55:ALA:HA	40:1i:58:HIS:HD2	1.52	0.73
32:2a:953:G:H5'	32:2a:965:A:H61	1.52	0.73
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.06	0.73
55:1x:6:G:H1	55:1x:67:C:N4	1.87	0.73
54:2w:1:G:H1	54:2w:72:C:H42	1.36	0.73
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.69	0.73
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.22	0.73
1:2A:990:A:OP2	62:2A:9710:HOH:O	2.05	0.73
1:1A:1602:U:O4	62:1A:4006:HOH:O	2.05	0.73
1:2A:249:C:O2	30:28:12:LYS:NZ	2.21	0.73
1:2A:921:G:O6	62:2A:9709:HOH:O	2.05	0.73
1:2A:2287:A:H62	1:2A:2344:U:H3	1.35	0.73
1:1A:1365:A:O2'	23:11:11:ARG:NH2	2.19	0.73
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.71	0.73
1:2A:2310:A:N1	6:2G:79:ASN:ND2	2.37	0.73
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.71	0.73
1:1A:1014:U:OP2	62:1A:4004:HOH:O	2.07	0.72
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.70	0.72
21:1Z:28:MET:HE3	21:1Z:37:VAL:HG11	1.68	0.72
1:2A:1042:G:H1	1:2A:1113:U:H3	1.37	0.72
1:2A:2126:A:N6	1:2A:2163:C:O4'	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.69	0.72
32:2a:1239:A:H62	32:2a:1299:A:H62	1.35	0.72
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.71	0.72
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.22	0.72
1:2A:1024:G:OP2	62:2A:9708:HOH:O	2.07	0.72
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.70	0.72
32:2a:1086:U:H3	32:2a:1099:G:H22	1.34	0.72
48:2q:6:LEU:HD23	48:2q:23:VAL:HG11	1.70	0.72
1:1A:882:G:H1	1:1A:894:C:H42	1.37	0.72
33:1b:93:VAL:HG21	33:1b:97:TRP:HD1	1.52	0.72
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.22	0.72
35:2d:172:PRO:HB2	35:2d:187:ARG:HH21	1.55	0.72
54:1y:2:C:H42	54:1y:71:G:H1	1.37	0.72
17:2V:72:VAL:HG13	17:2V:85:LYS:HB2	1.70	0.72
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.21	0.72
1:2A:11:G:N7	62:2A:9768:HOH:O	2.22	0.72
32:2a:376:G:H5''	47:2p:5:ARG:HB2	1.72	0.72
1:1A:2447:G:OP2	62:1A:4010:HOH:O	2.06	0.72
32:2a:826:C:H4'	39:2h:12:ARG:HG3	1.72	0.72
1:1A:1007:C:OP2	62:1A:4011:HOH:O	2.08	0.72
1:1A:2407:G:OP1	62:1A:4009:HOH:O	2.06	0.72
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.22	0.72
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.23	0.72
1:1A:880:G:N2	1:1A:898:C:N3	2.33	0.71
35:2d:157:LEU:O	35:2d:161:ASN:ND2	2.23	0.71
11:2P:95:VAL:HA	11:2P:99:LEU:HD21	1.71	0.71
32:2a:1013:G:N2	32:2a:1016:A:OP2	2.20	0.71
42:2k:89:ALA:O	42:2k:91:ARG:N	2.21	0.71
1:1A:1986:A:OP1	62:1A:4012:HOH:O	2.08	0.71
1:2A:1890:A:OP2	62:2A:9714:HOH:O	2.08	0.71
1:1A:1754:C:H5	15:1T:96:ARG:HH21	1.39	0.71
32:1a:1027:C:H2'	32:1a:1028:C:C6	2.25	0.71
32:1a:1136:U:H5''	32:1a:1137:C:C4	2.25	0.71
1:2A:988:A:N7	62:2A:9770:HOH:O	2.23	0.71
1:2A:1309:G:H4'	29:27:7:PRO:HB2	1.72	0.71
3:2D:237:GLU:OE2	62:2D:401:HOH:O	2.08	0.71
5:2F:18:ARG:NH1	5:2F:127:GLU:OE2	2.23	0.71
1:1A:880:G:H1	1:1A:898:C:H42	1.36	0.71
1:2A:271(R):G:OP1	23:21:76:ARG:NH1	2.23	0.71
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.73	0.71
1:2A:2049:G:N7	62:2A:9773:HOH:O	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2w:8:4SU:O2'	54:2w:21:A:N6	2.23	0.71
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.38	0.71
1:2A:775:G:O3'	62:2A:9717:HOH:O	2.09	0.71
1:1A:2228:G:O6	62:1A:4008:HOH:O	2.06	0.71
32:1a:407:G:H5''	35:1d:115:ARG:HG2	1.72	0.71
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.72	0.71
3:2D:232:PRO:O	62:2D:402:HOH:O	2.09	0.71
40:2i:55:ALA:HA	40:2i:58:HIS:HD2	1.56	0.71
32:1a:559:A:H4'	32:1a:560:U:H3'	1.72	0.71
1:2A:2228:G:OP1	3:2D:261:LYS:NZ	2.21	0.71
7:2H:98:LEU:HG	7:2H:125:VAL:HG22	1.71	0.71
32:1a:1027:C:N3	32:1a:1034:G:C2	2.59	0.71
1:2A:526:A:OP1	62:2A:9718:HOH:O	2.09	0.71
2:2B:66:A:H61	2:2B:109:C:H5''	1.55	0.71
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.73	0.71
32:2a:157:G:H1	32:2a:164:U:H3	1.35	0.71
1:1A:1237:A:OP1	62:1A:4013:HOH:O	2.09	0.70
51:1t:46:GLU:HG3	51:1t:48:LYS:HG3	1.73	0.70
5:2F:132:VAL:HA	5:2F:138:GLU:HB3	1.72	0.70
32:2a:117:G:OP2	62:2a:1901:HOH:O	2.08	0.70
1:1A:11:G:H2'	1:1A:12:U:H5''	1.73	0.70
13:1R:28:LEU:HD12	13:1R:44:LEU:HD13	1.72	0.70
21:1Z:120:ILE:O	21:1Z:121:HIS:ND1	2.24	0.70
32:2a:393:A:OP2	47:2p:12:LYS:NZ	2.16	0.70
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.25	0.70
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.73	0.70
54:2y:5:G:H1	54:2y:68:C:N4	1.90	0.70
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.74	0.70
7:1H:86:GLU:OE2	7:1H:130:ARG:NH1	2.24	0.70
11:1P:91:PHE:O	11:1P:121:LYS:NZ	2.22	0.70
1:2A:948:G:OP1	62:2A:9715:HOH:O	2.08	0.70
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.25	0.70
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.24	0.70
1:2A:542:C:H42	1:2A:551:G:H1	1.38	0.70
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH12	1.57	0.70
32:2a:407:G:OP1	35:2d:115:ARG:NH2	2.22	0.70
7:2H:18:GLU:HB3	7:2H:25:LYS:HB2	1.72	0.70
32:2a:107:G:N7	51:2t:15:ARG:NH2	2.40	0.70
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.24	0.70
54:1w:18:G:HO2'	54:1w:57:G:H22	1.38	0.70
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.73	0.70
1:2A:2375:G:O2'	1:2A:2377:A:N7	2.24	0.70
32:2a:1506:U:OP1	62:2a:1902:HOH:O	2.09	0.70
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.27	0.70
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.72	0.69
32:2a:1165:C:H42	32:2a:1171:G:H1	1.38	0.69
54:2w:2:C:H42	54:2w:71:G:H1	1.39	0.69
32:1a:67:C:H2'	32:1a:68:G:C8	2.27	0.69
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.26	0.69
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.24	0.69
32:1a:1027:C:N4	32:1a:1034:G:C6	2.60	0.69
1:2A:1783:A:N7	62:2A:9787:HOH:O	2.26	0.69
1:1A:592:G:O6	62:1A:4015:HOH:O	2.10	0.69
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.40	0.69
3:2D:76:PRO:HB2	3:2D:116:GLN:HE21	1.57	0.69
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.57	0.69
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.24	0.69
1:2A:962:G:OP1	62:2A:9715:HOH:O	2.08	0.69
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.74	0.69
32:1a:251:G:N7	62:1a:1919:HOH:O	2.26	0.69
1:2A:11:G:H2'	1:2A:12:U:H5'	1.74	0.69
1:2A:1973:G:OP1	62:2A:9719:HOH:O	2.09	0.69
6:2G:11:TYR:OH	6:2G:16:ARG:NH1	2.24	0.69
9:2N:68:GLU:HG3	9:2N:69:GLN:HG3	1.73	0.69
13:2R:28:LEU:HD12	13:2R:44:LEU:HD13	1.74	0.69
32:1a:530:G:N7	62:1a:1917:HOH:O	2.26	0.69
26:24:53:GLU:HG2	26:24:54:GLY:H	1.56	0.69
32:2a:35:G:O2'	43:2l:118:SER:O	2.11	0.69
38:2g:78:ARG:NH1	38:2g:154:TYR:O	2.24	0.69
1:1A:668:G:N7	62:1A:4065:HOH:O	2.25	0.69
1:1A:927:G:N7	62:1A:4067:HOH:O	2.25	0.69
1:1A:2154:G:C2	1:1A:2155:G:H1'	2.28	0.69
21:1Z:28:MET:HE1	21:1Z:61:LEU:HD11	1.75	0.69
1:2A:2251:OMG:OP1	62:2A:9723:HOH:O	2.11	0.69
1:1A:947:G:OP2	62:1A:4020:HOH:O	2.11	0.69
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.28	0.69
1:1A:2250:G:OP1	12:1Q:85:LYS:NZ	2.23	0.69
1:1A:2384:G:OP2	22:10:55:ARG:NH1	2.22	0.69
6:1G:50:ALA:O	6:1G:52:ILE:N	2.26	0.69
32:1a:103:C:OP2	51:1t:14:LYS:NZ	2.24	0.69
34:1c:52:LEU:HD21	34:1c:55:VAL:HG23	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.75	0.69
1:1A:674:G:OP2	62:1A:4019:HOH:O	2.11	0.69
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.75	0.69
39:1h:116:LYS:HD3	39:1h:127:LEU:HD23	1.74	0.69
1:2A:1022:G:N2	1:2A:1023:U:O4	2.25	0.69
32:2a:1029:C:N4	32:2a:1032:G:C6	2.61	0.69
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.08	0.69
46:2o:4:THR:OG1	46:2o:7:GLU:OE1	2.11	0.69
1:1A:1062:G:H8	1:1A:1070:A:H5''	1.58	0.68
11:1P:42:SER:O	62:1P:301:HOH:O	2.10	0.68
32:1a:1198:G:OP1	62:1a:1904:HOH:O	2.11	0.68
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.75	0.68
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.26	0.68
1:2A:1186:G:OP2	62:2A:9710:HOH:O	2.10	0.68
1:1A:248:G:OP1	62:1A:4014:HOH:O	2.10	0.68
32:1a:1125:U:H4'	41:1j:5:ARG:HH22	1.58	0.68
1:2A:476:G:O6	62:2A:9720:HOH:O	2.10	0.68
1:2A:1622:G:OP2	62:2A:9721:HOH:O	2.10	0.68
1:1A:2350:C:OP2	62:1A:4017:HOH:O	2.11	0.68
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.76	0.68
32:1a:677:U:H3	32:1a:713:G:H22	1.39	0.68
1:2A:792:G:O6	62:2A:9716:HOH:O	2.08	0.68
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.26	0.68
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.74	0.68
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.12	0.68
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.76	0.68
1:1A:2049:G:N7	62:1A:4072:HOH:O	2.26	0.68
32:2a:115:G:OP1	62:2a:1903:HOH:O	2.11	0.68
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.26	0.68
1:2A:878:A:N6	1:2A:899:A:O2'	2.27	0.68
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.29	0.68
32:2a:1352:C:N4	32:2a:1370:G:H1	1.90	0.68
54:2w:1:G:H1	54:2w:72:C:N4	1.91	0.68
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.27	0.68
32:2a:972:C:O2'	41:2j:55:LYS:O	2.12	0.68
32:1a:1008:C:N3	32:1a:1021:G:N2	2.39	0.68
32:1a:324:G:N7	62:1a:1920:HOH:O	2.27	0.68
1:2A:1647:G:OP1	62:2A:9703:HOH:O	2.12	0.68
1:2A:2518:A:OP2	62:2A:9722:HOH:O	2.11	0.68
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.76	0.68
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.59	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.08	0.68
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.75	0.68
30:18:6:THR:HG22	30:18:63:PRO:HD2	1.76	0.68
54:1y:47:U:O2'	54:1y:50:U:OP1	2.12	0.68
54:1y:50:U:O4	54:1y:64:A:N1	2.27	0.68
1:2A:1314:C:OP1	62:2A:9702:HOH:O	2.10	0.68
51:1t:57:ARG:NH1	51:1t:101:GLY:O	2.27	0.67
1:1A:1653:G:H3'	13:1R:2:ARG:HD3	1.76	0.67
35:1d:79:PHE:HE1	35:1d:204:ILE:HD13	1.56	0.67
36:2e:50:GLU:HB3	36:2e:53:LEU:HD13	1.76	0.67
12:2Q:67:ARG:O	12:2Q:101:ARG:NH2	2.27	0.67
1:2A:2141:G:O6	1:2A:2150:U:O2	2.13	0.67
1:1A:1062:G:C8	1:1A:1070:A:H5''	2.29	0.67
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.30	0.67
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.75	0.67
32:2a:1025:U:H3	32:2a:1036:G:H1	1.42	0.67
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.74	0.67
1:1A:72:U:OP1	62:1A:4016:HOH:O	2.11	0.67
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.27	0.67
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.60	0.67
32:2a:533:A:OP1	62:2a:1906:HOH:O	2.13	0.67
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.77	0.67
32:1a:92:C:H2'	32:1a:93:G:C8	2.29	0.67
1:2A:1418:G:OP2	62:2A:9725:HOH:O	2.12	0.67
1:2A:1840:G:OP2	62:2A:9727:HOH:O	2.13	0.67
1:2A:2121:G:H1	1:2A:2177:C:H42	1.42	0.67
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.77	0.67
18:1W:68:ARG:HH12	18:1W:112:GLY:H	1.41	0.67
32:1a:45:U:H2'	32:1a:46:G:C8	2.30	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.77	0.67
1:2A:1332:G:OP1	62:2A:9702:HOH:O	2.11	0.67
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.30	0.67
1:2A:2721:A:OP1	62:2A:9729:HOH:O	2.13	0.67
32:2a:1123:A:H4'	41:2j:37:PRO:HD2	1.77	0.67
1:1A:84:A:H5'	20:1Y:8:LYS:HG2	1.76	0.66
1:1A:1124:C:OP1	62:1A:4021:HOH:O	2.13	0.66
1:2A:1141:U:OP1	9:2N:25:ARG:NH1	2.26	0.66
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.60	0.66
1:1A:1059:G:H1	1:1A:1079:C:H42	1.41	0.66
43:1l:117:ARG:HG2	43:1l:122:THR:HB	1.78	0.66
49:1r:26:LEU:HD21	49:1r:39:VAL:HG13	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:5:ARG:N	41:2j:99:LYS:O	2.28	0.66
1:1A:1762:A:N1	62:1A:4078:HOH:O	2.28	0.66
24:12:16:LEU:HB3	24:12:20:GLU:HG3	1.77	0.66
1:2A:563:G:OP2	62:2A:9726:HOH:O	2.12	0.66
1:2A:1603:A:OP1	62:2A:9724:HOH:O	2.12	0.66
32:2a:640:A:O2'	39:2h:116:LYS:NZ	2.29	0.66
33:2b:163:PHE:HD1	33:2b:185:ILE:HG13	1.60	0.66
1:1A:2136:C:N3	1:1A:2155:G:N2	2.43	0.66
1:2A:1395:A:OP1	62:2A:9724:HOH:O	2.13	0.66
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.29	0.66
55:2x:15:G:N2	55:2x:21:A:N3	2.44	0.66
1:1A:2136:C:N4	1:1A:2155:G:N1	2.44	0.66
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.28	0.66
1:2A:2223:G:OP1	3:2D:172:TYR:OH	2.11	0.66
17:2V:56:SER:H	17:2V:100:ARG:HB2	1.60	0.66
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.28	0.66
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.25	0.66
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.76	0.66
14:2S:14:VAL:O	14:2S:18:ILE:HG12	1.96	0.66
22:10:11:ARG:O	22:10:14:ARG:NH2	2.28	0.66
4:2E:27:LEU:HD22	15:2T:1:MET:HE1	1.78	0.66
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.77	0.66
24:12:59:ARG:NH2	62:12:201:HOH:O	2.29	0.66
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.23	0.66
32:2a:1224:G:OP1	62:2a:1905:HOH:O	2.13	0.66
55:2x:29:G:N7	62:2x:3102:HOH:O	2.28	0.66
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.26	0.66
9:1N:73:THR:HG23	9:1N:82:LEU:HD11	1.78	0.66
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.78	0.66
47:2p:52:ASP:O	47:2p:54:GLU:N	2.28	0.66
49:2r:26:LEU:HD21	49:2r:39:VAL:HG13	1.78	0.66
1:1A:1676:A:N7	62:1A:4083:HOH:O	2.29	0.66
32:1a:972:C:O2'	41:1j:55:LYS:O	2.13	0.66
1:2A:1271:G:OP2	62:2A:9703:HOH:O	2.14	0.66
21:2Z:93:ASP:HB3	21:2Z:131:ARG:HH22	1.61	0.66
32:2a:158:G:N2	32:2a:163:C:O2	2.29	0.66
33:2b:118:LEU:HB3	33:2b:142:LEU:HD12	1.76	0.66
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.31	0.65
50:1s:27:GLU:HB3	50:1s:28:LYS:HA	1.78	0.65
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.15	0.65
1:2A:1300:U:H4'	1:2A:1301:A:H5'	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:49:G:H1	55:2x:65:C:N4	1.94	0.65
3:1D:237:GLU:OE2	62:1D:401:HOH:O	2.14	0.65
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.78	0.65
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.78	0.65
34:2c:7:PRO:O	34:2c:11:ARG:NH1	2.28	0.65
5:1F:44:ARG:NH1	62:1F:401:HOH:O	2.21	0.65
1:2A:2060:A:N3	62:2A:9810:HOH:O	2.30	0.65
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.77	0.65
26:24:64:GLY:C	26:24:66:SER:H	2.04	0.65
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.30	0.65
55:2x:76:A:OP1	62:2x:3101:HOH:O	2.13	0.65
3:1D:17:THR:O	3:1D:211:ARG:NH2	2.29	0.65
1:2A:1434:A:H61	1:2A:1558:A:H62	1.44	0.65
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.14	0.65
6:2G:79:ASN:OD1	6:2G:79:ASN:N	2.27	0.65
32:2a:1020:U:H2'	32:2a:1021:G:H8	1.61	0.65
39:2h:69:ARG:NH2	39:2h:75:ARG:O	2.30	0.65
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.29	0.65
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.31	0.65
32:2a:767:A:OP2	62:2a:1907:HOH:O	2.13	0.65
32:2a:1008:C:H42	32:2a:1021:G:H1	1.43	0.65
32:2a:1129:C:N4	32:2a:1143:G:H1	1.95	0.65
32:1a:511:C:OP2	35:1d:49:ARG:NH1	2.30	0.65
32:1a:826:C:H4'	39:1h:12:ARG:HG3	1.79	0.65
1:2A:2048:G:OP1	62:2A:9732:HOH:O	2.14	0.65
41:2j:64:GLU:OE2	41:2j:66:ARG:NH1	2.29	0.65
32:1a:78:G:N2	32:1a:91:C:C2	2.65	0.65
1:2A:1026:U:OP1	62:2A:9708:HOH:O	2.15	0.65
1:2A:1830:C:OP2	62:2A:9728:HOH:O	2.13	0.65
14:2S:83:LYS:HG2	14:2S:84:GLN:HG3	1.78	0.65
1:1A:1342:A:OP2	62:1A:4006:HOH:O	2.13	0.65
3:1D:180:GLY:HA3	3:1D:275:LYS:HB2	1.79	0.65
4:1E:119:ARG:HG3	4:1E:160:TYR:HB2	1.79	0.65
1:2A:223:A:O2'	1:2A:420:C:O2	2.15	0.65
1:2A:2171:A:H1'	1:2A:2172:U:C6	2.32	0.65
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.78	0.65
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.32	0.65
54:2y:15:G:N1	54:2y:48:C:N3	2.41	0.65
1:1A:1094:U:H1'	1:1A:1097:U:H5	1.62	0.64
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.78	0.64
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:28:MET:HE3	21:2Z:37:VAL:HG11	1.79	0.64
32:2a:113:G:OP1	62:2a:1908:HOH:O	2.14	0.64
32:2a:1129:C:H42	32:2a:1143:G:H1	1.45	0.64
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.32	0.64
1:1A:123:G:OP2	62:1A:4022:HOH:O	2.15	0.64
11:2P:126:VAL:HG13	11:2P:146:VAL:HB	1.79	0.64
1:2A:1973:G:OP2	62:2A:9734:HOH:O	2.14	0.64
1:2A:568:U:H5'	1:2A:945:A:N1	2.12	0.64
32:2a:67:C:H2'	32:2a:68:G:C8	2.33	0.64
32:1a:750:G:OP2	62:1a:1905:HOH:O	2.14	0.64
50:2s:32:LYS:HA	50:2s:50:ALA:HB3	1.79	0.64
1:1A:2127:G:H21	1:1A:2173:A:H1'	1.61	0.64
32:1a:1002:G:C5	32:1a:1003:G:H1'	2.32	0.64
33:1b:73:THR:OG1	33:1b:170:GLU:OE2	2.16	0.64
1:2A:1568:G:N7	62:2A:9808:HOH:O	2.29	0.64
1:2A:1721:G:H8	1:2A:1741:A:H62	1.45	0.64
1:2A:2349:G:OP1	62:2A:9733:HOH:O	2.14	0.64
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.79	0.64
35:2d:154:ASN:HA	35:2d:159:ARG:HH21	1.62	0.64
1:1A:1309:G:H4'	29:17:7:PRO:HB2	1.79	0.64
1:2A:574:C:N3	4:2E:145:LYS:NZ	2.44	0.64
1:1A:2748:A:H5'	7:1H:4:ILE:HD12	1.80	0.64
1:2A:1031:G:H5''	31:29:8:LYS:HE3	1.80	0.64
1:2A:2102:U:H3	1:2A:2187:G:H1	1.46	0.64
7:2H:3:ARG:NH1	7:2H:5:GLY:H	1.95	0.64
47:2p:17:TYR:HE2	47:2p:41:PRO:HG3	1.63	0.64
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.79	0.64
32:2a:673:G:H2'	32:2a:674:G:C8	2.32	0.64
32:2a:997:U:O2	32:2a:1044:A:N1	2.31	0.64
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.63	0.64
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.80	0.64
32:1a:130:A:N3	32:1a:263:A:O2'	2.31	0.64
32:2a:920:U:H2'	32:2a:921:U:C6	2.33	0.64
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.80	0.64
24:12:32:LEU:HD12	24:12:53:LEU:HB3	1.79	0.63
33:1b:114:ARG:NE	33:1b:141:GLU:OE2	2.27	0.63
1:2A:1379:A:H4'	1:2A:1380:G:OP2	1.98	0.63
32:2a:1009:G:N2	32:2a:1021:G:H1'	2.12	0.63
32:2a:1301:U:O2'	32:2a:1302:U:H5'	1.97	0.63
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.79	0.63
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:503:A:O2'	62:1A:4023:HOH:O	2.15	0.63
20:1Y:34:LYS:NZ	62:1Y:601:HOH:O	2.20	0.63
7:2H:80:SER:OG	7:2H:81:GLU:OE1	2.16	0.63
32:2a:11:G:O6	62:2a:1904:HOH:O	2.12	0.63
1:1A:882:G:N2	1:1A:894:C:N3	2.39	0.63
2:1B:13:A:N1	2:1B:69:G:O2'	2.31	0.63
32:1a:7:G:H5'	32:1a:298:A:O4'	1.98	0.63
32:2a:127:G:N2	48:2q:61:GLU:OE2	2.30	0.63
6:1G:115:ARG:HB3	6:1G:136:ARG:HH22	1.63	0.63
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.81	0.63
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.62	0.63
1:2A:2659:G:N2	1:2A:2662:A:OP2	2.32	0.63
4:2E:72:VAL:HG12	4:2E:73:GLU:O	1.98	0.63
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.46	0.63
1:2A:1278:A:OP1	13:2R:36:THR:HG23	1.99	0.63
1:2A:2124:G:H1	1:2A:2174:C:N4	1.95	0.63
2:2B:8:U:H3	2:2B:113:G:H1	1.47	0.63
7:2H:23:ARG:NH1	7:2H:34:GLU:OE1	2.32	0.63
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.34	0.63
1:1A:1967:C:OP1	62:1A:4024:HOH:O	2.16	0.63
23:11:3:LYS:HB2	23:11:61:ARG:HH11	1.64	0.63
6:2G:41:GLN:NE2	6:2G:153:ARG:O	2.31	0.63
28:26:14:THR:OG1	28:26:48:VAL:O	2.13	0.63
32:2a:437:U:H5''	35:2d:155:LEU:HD13	1.81	0.63
32:2a:458:C:H42	32:2a:473:G:H1	1.47	0.63
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.12	0.63
44:2m:22:ILE:HB	44:2m:25:ILE:HD13	1.80	0.63
54:2w:9:A:H4'	54:2w:46:7MG:H5'	1.80	0.63
1:1A:453:C:O2	1:1A:457:A:O2'	2.17	0.63
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.99	0.63
32:2a:1262:C:N4	32:2a:1273:G:H1	1.96	0.63
39:1h:39:LEU:HB3	39:1h:45:ILE:HG12	1.80	0.63
50:1s:27:GLU:HB3	50:1s:28:LYS:HD3	1.81	0.63
1:2A:2135:A:O4'	1:2A:2159:G:O2'	2.17	0.63
1:1A:2336:A:H61	22:10:43:THR:HG22	1.63	0.62
4:1E:119:ARG:HD3	4:1E:120:TRP:NE1	2.14	0.62
32:1a:1002:G:H3'	32:1a:1003:G:O4'	1.98	0.62
1:2A:2552:2MU:H2'	1:2A:2554:U:OP2	1.99	0.62
26:24:59:PHE:N	26:24:60:GLN:HB2	2.14	0.62
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.32	0.62
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1004:A:H5'	32:1a:1024:G:N1	2.12	0.62
15:2T:73:GLU:OE2	15:2T:103:ARG:NE	2.32	0.62
32:2a:1240:U:N3	38:2g:30:ILE:O	2.23	0.62
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.25	0.62
54:1w:58:A:O2'	54:1w:60:U:OP2	2.16	0.62
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.65	0.62
1:2A:2167:U:H2'	1:2A:2168:G:H21	1.64	0.62
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HG3	1.63	0.62
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.79	0.62
32:2a:222:U:H2'	32:2a:223:U:C6	2.34	0.62
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.33	0.62
17:1V:98:GLU:OE2	17:1V:100:ARG:NH1	2.32	0.62
51:1t:60:GLU:HG3	51:1t:81:LYS:HD2	1.81	0.62
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.81	0.62
33:1b:167:PRO:HG3	33:1b:188:ALA:HB2	1.82	0.62
43:2l:117:ARG:HG2	43:2l:122:THR:HB	1.81	0.62
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.32	0.62
12:2Q:109:VAL:HG22	12:2Q:113:GLN:HB3	1.81	0.62
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.80	0.62
5:1F:34:TRP:CZ2	11:1P:8:PRO:HG3	2.35	0.62
33:1b:230:VAL:HG22	33:1b:231:GLU:H	1.65	0.62
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.80	0.62
1:2A:1250:G:OP2	11:2P:21:ARG:NH1	2.33	0.62
8:2I:43:ASN:ND2	23:21:75:GLU:OE2	2.33	0.62
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.28	0.62
32:2a:473:G:H2'	32:2a:474:G:H8	1.64	0.62
32:2a:890:G:O2'	32:2a:906:G:O6	2.17	0.62
32:2a:985:C:H42	32:2a:1220:G:H1	1.46	0.62
1:1A:2196:C:OP2	62:1A:4027:HOH:O	2.16	0.62
1:2A:848:G:C4	1:2A:933:A:H8	2.17	0.62
1:2A:1916:A:N1	32:2a:1408:A:O2'	2.31	0.62
33:2b:48:MET:O	33:2b:52:GLU:N	2.31	0.62
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.81	0.62
13:1R:33:ARG:NH1	13:1R:115:GLU:OE1	2.32	0.62
1:2A:2137:C:H2'	1:2A:2138:C:C6	2.35	0.62
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	1.82	0.62
32:2a:1228:C:OP1	44:2m:115:LYS:NZ	2.29	0.62
1:1A:2691:C:OP2	62:1A:4026:HOH:O	2.16	0.62
1:2A:890:A:H2'	1:2A:892:G:H8	1.65	0.62
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.82	0.62
32:2a:987:G:H1	32:2a:1218:C:N4	1.95	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:72:LEU:C	8:1I:74:ASN:H	2.06	0.61
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.33	0.61
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.33	0.61
47:2p:56:ALA:HB1	47:2p:74:LEU:HD21	1.82	0.61
1:1A:278:A:H2'	1:1A:279:C:C6	2.34	0.61
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.36	0.61
40:1i:20:ARG:O	40:1i:60:ASP:N	2.27	0.61
1:2A:131:G:OP1	62:2A:9739:HOH:O	2.16	0.61
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.33	0.61
57:2A:3670:4M2:H31	57:2A:3670:4M2:H35	1.83	0.61
14:2S:15:ARG:HB3	14:2S:19:LYS:NZ	2.15	0.61
32:2a:64:G:H4'	32:2a:65:U:H3'	1.82	0.61
32:2a:501:C:H2'	32:2a:502:G:C8	2.35	0.61
32:2a:1028:C:N3	32:2a:1033:G:C6	2.68	0.61
42:2k:33:THR:HG22	42:2k:39:PRO:HA	1.83	0.61
50:2s:64:GLU:OE2	50:2s:65:ASN:ND2	2.33	0.61
1:1A:2127:G:N2	1:1A:2173:A:H1'	2.15	0.61
1:1A:2168:G:O6	1:1A:2171:A:H5''	2.01	0.61
1:2A:2133:G:O2'	1:2A:2157:G:N2	2.32	0.61
32:2a:1047:G:H1	32:2a:1210:C:H42	1.49	0.61
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.35	0.61
17:1V:72:VAL:HG13	17:1V:85:LYS:HB3	1.80	0.61
18:1W:12:ILE:HD13	18:1W:17:VAL:HG13	1.82	0.61
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.82	0.61
32:1a:1227:A:OP1	50:1s:80:TYR:OH	2.14	0.61
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.30	0.61
32:2a:501:C:H2'	32:2a:502:G:H8	1.64	0.61
44:2m:80:ARG:NH1	50:2s:65:ASN:O	2.32	0.61
1:1A:1671:U:OP2	62:1A:4001:HOH:O	2.16	0.61
9:1N:42:TRP:HD1	9:1N:48:MET:HE1	1.63	0.61
54:1w:5:G:H2'	54:1w:6:G:C8	2.35	0.61
32:2a:1029:C:C2	32:2a:1032:G:N2	2.67	0.61
26:14:53:GLU:HG3	26:14:54:GLY:H	1.65	0.61
1:2A:1958:C:OP2	62:2A:9738:HOH:O	2.16	0.61
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.17	0.61
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.81	0.61
15:2T:16:ARG:NH2	15:2T:83:ILE:O	2.33	0.61
36:2e:93:PRO:HG2	39:2h:105:ARG:HE	1.66	0.61
46:2o:68:ARG:NH1	62:2o:101:HOH:O	2.33	0.61
32:1a:978:A:O2'	32:1a:1322:C:N3	2.33	0.61
55:1x:8:4SU:O2	55:1x:21:A:H2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.47	0.61
32:2a:1183:A:H3'	32:2a:1184:G:H5''	1.82	0.61
36:2e:93:PRO:HG2	39:2h:105:ARG:NE	2.15	0.61
1:1A:2140:C:N4	1:1A:2151:G:H1	1.97	0.61
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.32	0.61
32:1a:1057:G:OP2	62:1a:1906:HOH:O	2.16	0.61
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.14	0.61
2:2B:87:G:N2	2:2B:90:A:OP2	2.34	0.61
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.83	0.61
32:2a:684:A:O2'	42:2k:39:PRO:O	2.15	0.61
36:2e:84:PHE:HB2	36:2e:134:ALA:HB2	1.82	0.61
1:1A:1090:U:C2	1:1A:1102:C:H1'	2.36	0.61
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.64	0.61
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.82	0.61
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.83	0.61
49:1r:52:PRO:HB2	49:1r:54:ARG:HG2	1.81	0.61
1:2A:1022:G:N7	9:2N:66:LYS:HE2	2.16	0.61
1:2A:1639:U:OP1	62:2A:9741:HOH:O	2.16	0.61
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.65	0.61
32:1a:157:G:H1	32:1a:164:U:H3	1.49	0.61
33:1b:21:ARG:O	33:1b:23:ARG:N	2.34	0.61
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.34	0.61
39:1h:112:LEU:HD11	39:1h:124:ALA:HB2	1.82	0.61
41:2j:38:ILE:HG12	41:2j:71:LEU:O	2.01	0.61
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.82	0.61
26:14:24:THR:OG1	26:14:25:TYR:N	2.34	0.60
32:1a:428:G:OP2	35:1d:10:ARG:NH1	2.34	0.60
32:1a:1309:G:OP1	44:1m:88:ARG:NH2	2.34	0.60
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.35	0.60
10:2O:110:GLY:HA2	10:2O:112:MET:HE2	1.83	0.60
32:2a:1169:A:H2'	32:2a:1170:A:C8	2.36	0.60
33:1b:80:ILE:HD13	33:1b:211:ILE:HG22	1.83	0.60
1:2A:2169:A:H2'	1:2A:2170:A:C8	2.36	0.60
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.01	0.60
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.81	0.60
13:2R:36:THR:HG22	13:2R:37:THR:H	1.65	0.60
32:2a:1004:A:H8	32:2a:1005:A:H4'	1.66	0.60
35:2d:61:LYS:NZ	35:2d:72:GLU:OE2	2.32	0.60
54:2y:15:G:O6	54:2y:48:C:O2	2.19	0.60
1:1A:1769:G:O2'	1:1A:1958:C:OP1	2.17	0.60
7:1H:101:ARG:NH2	7:1H:121:ILE:O	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1228:C:OP1	44:1m:115:LYS:NZ	2.31	0.60
1:2A:1530:C:H42	1:2A:1539:G:H1	1.49	0.60
1:2A:2292:C:OP1	14:2S:17:ARG:NH2	2.34	0.60
32:2a:620:C:C2	35:2d:135:LEU:HG	2.37	0.60
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.32	0.60
32:1a:376:G:O3'	47:1p:5:ARG:HD2	2.02	0.60
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.36	0.60
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.36	0.60
33:2b:163:PHE:CD1	33:2b:185:ILE:HG13	2.36	0.60
1:1A:1652:A:C2'	1:1A:1653:G:H5'	2.31	0.60
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.82	0.60
32:1a:277:C:OP1	48:1q:68:ARG:NH2	2.32	0.60
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.83	0.60
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.18	0.60
33:2b:16:HIS:HB3	33:2b:210:SER:HB3	1.83	0.60
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.02	0.60
32:1a:1414:U:H3	32:1a:1486:G:H1	1.50	0.60
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.82	0.60
7:2H:28:GLY:HA3	7:2H:79:VAL:HB	1.82	0.60
32:2a:939:G:H1	32:2a:1344:C:H42	1.47	0.60
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.35	0.60
32:2a:976:G:OP2	32:2a:1358:U:O2'	2.17	0.60
1:1A:1094:U:H1'	1:1A:1097:U:C5	2.36	0.60
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.37	0.60
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.34	0.60
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.37	0.60
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.01	0.60
1:2A:2532:G:N2	1:2A:2663:G:O2'	2.34	0.60
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.34	0.60
9:1N:67:LEU:HA	9:1N:87:LEU:HD22	1.84	0.60
1:2A:10:G:O2'	1:2A:2801(A):A:N6	2.34	0.60
5:2F:40:GLN:HE22	5:2F:182:ASN:HB2	1.67	0.60
8:2I:38:LEU:H	8:2I:38:LEU:HD12	1.67	0.60
32:2a:17:U:H2'	32:2a:18:C:C6	2.37	0.60
32:2a:770:C:OP1	62:2a:1911:HOH:O	2.17	0.60
32:2a:943:U:H1'	40:2i:124:GLN:HE22	1.66	0.60
1:1A:1356:G:N7	62:1A:4100:HOH:O	2.32	0.60
13:1R:36:THR:HG22	13:1R:37:THR:H	1.67	0.60
32:2a:838:G:H2'	32:2a:839:U:H2'	1.84	0.60
1:1A:143:G:H4'	19:1X:35:THR:HG21	1.83	0.59
1:1A:548:A:H61	17:1V:19:LYS:H	1.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1823:G:OP1	3:1D:54:ARG:NH1	2.34	0.59
3:1D:125:ILE:HB	37:1f:81:ILE:HD11	1.83	0.59
32:1a:1029:C:N4	32:1a:1030:C:H41	2.00	0.59
36:1e:85:GLY:O	36:1e:87:SER:N	2.34	0.59
1:2A:2139:C:N4	1:2A:2152:G:H1	1.99	0.59
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.02	0.59
54:2y:29:G:H1	54:2y:41:C:N4	1.99	0.59
1:1A:2135:A:H2	1:1A:2155:G:H1	1.50	0.59
33:1b:73:THR:O	33:1b:78:GLN:NE2	2.35	0.59
1:2A:2104:G:H1	1:2A:2185:C:N4	2.00	0.59
32:2a:148:G:H2'	32:2a:149:A:H8	1.64	0.59
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.01	0.59
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.03	0.59
54:1w:5:G:H1	54:1w:68:C:N4	2.00	0.59
1:2A:451:C:H4'	5:2F:52:LYS:HE2	1.83	0.59
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.02	0.59
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.35	0.59
6:1G:131:TYR:HB3	6:1G:159:VAL:HG22	1.84	0.59
33:1b:19:HIS:CD2	33:1b:20:GLU:HG3	2.37	0.59
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.23	0.59
1:2A:2531:A:H61	1:2A:2662:A:H61	1.51	0.59
32:2a:753:A:OP1	46:2o:69:TYR:OH	2.15	0.59
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.68	0.59
33:1b:174:VAL:O	33:1b:178:ARG:HG2	2.02	0.59
1:2A:991:C:OP2	62:2A:9710:HOH:O	2.17	0.59
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.20	0.59
7:2H:129:THR:O	7:2H:129:THR:OG1	2.21	0.59
32:2a:63:C:H42	32:2a:104:G:H1	1.49	0.59
32:2a:1029:C:C4	32:2a:1032:G:C2	2.89	0.59
41:2j:55:LYS:HE3	41:2j:56:HIS:NE2	2.18	0.59
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.03	0.59
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.02	0.59
1:1A:2793:G:N2	1:1A:2804:C:H1'	2.18	0.59
6:2G:39:ILE:HG12	6:2G:157:ILE:HG12	1.85	0.59
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.84	0.59
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.66	0.59
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.84	0.59
40:2i:20:ARG:O	40:2i:60:ASP:N	2.27	0.59
42:2k:48:ILE:O	42:2k:50:TYR:N	2.33	0.59
54:2w:1:G:O2'	54:2w:2:C:OP1	2.19	0.59
54:2w:27:G:H1	54:2w:43:C:N4	1.97	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:50:ILE:HG13	38:1g:61:VAL:HG11	1.84	0.59
1:2A:527:C:N4	1:2A:2779:U:OP2	2.34	0.59
1:2A:2164:C:H3'	1:2A:2165:G:C8	2.38	0.59
1:2A:2365:G:O6	30:28:43:GLN:NE2	2.34	0.59
2:2B:24:G:H4'	2:2B:25:A:C8	2.37	0.59
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	1.83	0.59
1:2A:400:G:O6	62:2A:9735:HOH:O	2.16	0.59
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.83	0.59
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.17	0.59
36:2e:57:LYS:HG2	36:2e:61:TYR:HE2	1.68	0.59
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.37	0.59
30:18:28:GLY:O	30:18:36:LYS:NZ	2.31	0.59
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.37	0.59
1:2A:1021:A:H61	1:2A:1142(A):A:H61	1.51	0.59
2:2B:95:C:H2'	2:2B:96:U:C6	2.37	0.59
32:2a:946:A:OP2	62:2a:1910:HOH:O	2.16	0.59
51:2t:50:GLU:HB2	51:2t:99:LEU:HD22	1.85	0.59
28:16:11:LEU:HB2	28:16:21:TYR:HB2	1.84	0.59
1:2A:839:U:H2'	1:2A:840:C:C6	2.38	0.59
1:2A:2166:G:O6	1:2A:2171:A:N6	2.36	0.59
38:2g:72:ARG:NH2	38:2g:142:GLU:OE2	2.36	0.59
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.37	0.58
57:1A:3894:4M2:H35	57:1A:3894:4M2:H31	1.84	0.58
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.67	0.58
32:1a:406:G:N3	35:1d:119:GLN:NE2	2.49	0.58
32:1a:1347:G:H5''	40:1i:107:ARG:HB3	1.85	0.58
1:2A:450:G:OP2	62:2A:9736:HOH:O	2.16	0.58
34:2c:19:GLU:HG2	34:2c:54:ARG:NH1	2.18	0.58
6:1G:48:GLU:HA	6:1G:51:ARG:HE	1.68	0.58
9:1N:42:TRP:CD1	9:1N:48:MET:HE1	2.38	0.58
26:14:61:ARG:HG3	26:14:62:ARG:H	1.68	0.58
32:1a:163:C:H2'	32:1a:164:U:H6	1.67	0.58
1:2A:534:U:O2'	16:2U:49:HIS:ND1	2.26	0.58
1:2A:2453:A:N7	62:2A:9826:HOH:O	2.32	0.58
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.84	0.58
2:2B:40:U:H1'	2:2B:45:A:H61	1.68	0.58
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.84	0.58
23:21:2:SER:HB3	23:21:46:LEU:HD12	1.84	0.58
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.32	0.58
1:1A:1991:U:H2'	1:1A:1992:G:H5''	1.83	0.58
1:1A:2124:G:H1	1:1A:2174:C:H42	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:269:C:H2'	32:1a:270:A:C8	2.38	0.58
47:1p:4:ILE:HB	47:1p:66:PRO:HA	1.84	0.58
1:2A:900:A:O2'	1:2A:901:A:OP1	2.21	0.58
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.85	0.58
32:2a:1239:A:H62	32:2a:1299:A:N6	1.99	0.58
1:1A:2134:A:OP1	1:1A:2156:G:N2	2.36	0.58
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.00	0.58
37:1f:35:ALA:HB2	37:1f:67:MET:HE2	1.85	0.58
37:1f:67:MET:HE1	37:1f:75:LEU:HD22	1.83	0.58
40:1i:17:VAL:HG11	40:1i:81:ILE:HA	1.85	0.58
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.36	0.58
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.39	0.58
1:2A:2842:G:O6	62:2A:9731:HOH:O	2.14	0.58
4:2E:119:ARG:HG3	4:2E:160:TYR:HB2	1.85	0.58
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.50	0.58
34:2c:67:THR:HA	34:2c:102:ASN:HB2	1.85	0.58
44:2m:25:ILE:HD11	44:2m:66:LEU:HD13	1.85	0.58
1:1A:301:G:OP2	20:1Y:84:ARG:NH2	2.35	0.58
18:1W:92:ARG:NH1	62:1W:3103:HOH:O	2.36	0.58
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.37	0.58
41:1j:5:ARG:NH2	41:1j:73:ASP:OD2	2.36	0.58
1:2A:1857:G:O2'	1:2A:1885:A:N6	2.36	0.58
32:2a:1329:A:OP2	52:2u:7:ARG:NH2	2.26	0.58
1:1A:272:G:O2'	1:1A:421:U:OP2	2.18	0.58
1:1A:413:C:OP2	62:1A:4030:HOH:O	2.17	0.58
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.39	0.58
1:1A:2136:C:N4	1:1A:2155:G:C6	2.72	0.58
1:1A:2156:G:H2'	1:1A:2157:G:C2	2.39	0.58
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.37	0.58
21:1Z:148:ASP:OD1	21:1Z:148:ASP:N	2.36	0.58
28:16:13:CYS:SG	28:16:47:THR:HG21	2.44	0.58
21:2Z:39:VAL:HG21	21:2Z:44:PHE:HB2	1.85	0.58
32:2a:148:G:H2'	32:2a:149:A:C8	2.39	0.58
32:1a:135:C:O2	47:1p:1:MET:N	2.30	0.58
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.38	0.58
24:22:32:LEU:HD12	24:22:53:LEU:HB3	1.85	0.58
54:2w:1:G:H22	54:2w:72:C:H42	1.50	0.58
1:1A:1566:A:OP1	3:1D:211:ARG:NH1	2.37	0.58
32:1a:56:U:H2'	32:1a:57:G:C8	2.37	0.58
32:1a:406:G:H4'	35:1d:5:ILE:HD11	1.86	0.58
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:861:A:N3	2:2B:79:C:O2'	2.34	0.58
1:2A:1971:A:OP1	62:2A:9740:HOH:O	2.16	0.58
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.36	0.58
1:1A:2553:G:H22	54:1w:76:A:H62	1.51	0.58
32:1a:67:C:H2'	32:1a:68:G:H8	1.69	0.58
1:2A:1037:G:H1	1:2A:1118:C:H42	1.51	0.58
32:2a:766:A:OP2	62:2a:1912:HOH:O	2.17	0.58
33:2b:47:THR:HA	33:2b:202:PRO:HG2	1.86	0.58
52:2u:6:ARG:HH21	52:2u:15:ARG:HH22	1.49	0.58
1:1A:253:C:O2'	62:1A:4025:HOH:O	2.16	0.58
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.37	0.58
32:1a:17:U:H2'	32:1a:18:C:C6	2.39	0.58
32:1a:403:C:OP2	35:1d:74:GLN:NE2	2.37	0.58
52:1u:6:ARG:HH21	52:1u:15:ARG:HH22	1.50	0.58
54:1y:44:G:O2'	54:1y:45:U:OP1	2.14	0.58
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.69	0.58
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.36	0.58
7:2H:20:ALA:HB3	7:2H:23:ARG:HG3	1.84	0.58
19:2X:88:LYS:NZ	19:2X:90:GLU:OE1	2.37	0.58
21:2Z:92:SER:O	21:2Z:130:PRO:HG3	2.03	0.58
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.04	0.58
32:1a:1025:U:O2	32:1a:1036:G:O6	2.21	0.57
36:1e:102:ALA:O	36:1e:107:ARG:NH1	2.37	0.57
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.03	0.57
54:1w:5:G:H2'	54:1w:6:G:H8	1.67	0.57
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.04	0.57
1:2A:918:A:N6	1:2A:919:G:N3	2.52	0.57
1:2A:1288:U:O2'	1:2A:1647:G:N2	2.37	0.57
6:2G:7:LEU:HD11	6:2G:107:LEU:HD12	1.86	0.57
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.37	0.57
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.86	0.57
32:2a:128:G:O2'	48:2q:3:LYS:NZ	2.37	0.57
1:1A:762:U:OP1	62:1A:4031:HOH:O	2.17	0.57
1:1A:1632:A:N7	62:1A:4090:HOH:O	2.32	0.57
2:1B:11:C:H3'	2:1B:12:C:C6	2.40	0.57
9:1N:35:ARG:HH21	9:1N:42:TRP:HZ2	1.52	0.57
32:1a:790:A:OP1	55:1x:38:A:O2'	2.22	0.57
33:1b:127:ILE:HG13	33:1b:130:ARG:HG3	1.86	0.57
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.39	0.57
54:1y:50:U:H3	54:1y:64:A:H2	1.51	0.57
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:999:C:H2'	32:2a:1000:U:O4'	2.03	0.57
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.21	0.57
1:1A:817:C:OP1	62:1A:4034:HOH:O	2.18	0.57
2:1B:23:G:O6	62:1B:3101:HOH:O	2.13	0.57
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	1.85	0.57
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.37	0.57
32:1a:393:A:OP2	47:1p:12:LYS:NZ	2.36	0.57
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.38	0.57
35:1d:163:GLU:O	35:1d:166:LYS:HG2	2.05	0.57
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.87	0.57
1:2A:2206:G:H5''	1:2A:2207:G:C5	2.39	0.57
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.34	0.57
32:2a:1113:C:N4	32:2a:1187:G:H1	1.99	0.57
35:2d:119:GLN:HG2	35:2d:123:HIS:CD2	2.39	0.57
51:2t:57:ARG:HH12	51:2t:100:ILE:HD12	1.68	0.57
1:1A:1065:U:H2'	1:1A:1073:A:H61	1.69	0.57
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.37	0.57
15:2T:127:ALA:C	15:2T:129:ARG:H	2.12	0.57
32:2a:56:U:H2'	32:2a:57:G:C8	2.39	0.57
32:2a:441:A:H3'	32:2a:442:C:C6	2.40	0.57
32:2a:1262:C:H2'	32:2a:1263:C:C6	2.39	0.57
32:2a:1312:G:H5'	50:2s:5:LEU:HD11	1.87	0.57
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.19	0.57
23:11:91:LYS:HG2	23:11:95:LEU:HD22	1.87	0.57
32:1a:1118:C:OP1	40:1i:104:ARG:NH1	2.35	0.57
1:2A:271(H):G:O2'	1:2A:271(I):G:H8	1.87	0.57
1:2A:898:C:N4	1:2A:899:A:N1	2.52	0.57
1:2A:1805:U:O2	3:2D:50:THR:HB	2.04	0.57
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.39	0.57
9:2N:29:LYS:HD2	9:2N:140:VAL:HB	1.87	0.57
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.19	0.57
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.85	0.57
1:2A:312:G:O6	62:2A:9737:HOH:O	2.16	0.57
1:1A:1176:G:H1'	1:1A:1177:A:H5''	1.87	0.57
1:1A:1652:A:H2'	1:1A:1653:G:H5'	1.87	0.57
1:1A:2018:G:OP1	27:15:9:LYS:NZ	2.37	0.57
1:1A:2398:U:H2'	1:1A:2399:G:C8	2.40	0.57
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.85	0.57
5:1F:34:TRP:CE2	11:1P:8:PRO:HG3	2.40	0.57
32:1a:176:C:H2'	32:1a:177:C:H6	1.70	0.57
1:2A:83:G:O2'	1:2A:102:G:N2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:218:A:C2	1:2A:235:U:H4'	2.40	0.57
1:2A:1009:A:OP2	62:2A:9745:HOH:O	2.18	0.57
10:2O:49:ARG:NH2	32:2a:1423:G:OP1	2.36	0.57
12:2Q:137:TYR:HE2	21:2Z:49:ARG:HD3	1.70	0.57
32:2a:1108:G:O6	62:2a:1909:HOH:O	2.15	0.57
36:2e:101:ILE:O	36:2e:120:THR:OG1	2.23	0.57
44:2m:39:ILE:HD12	44:2m:52:GLU:HG2	1.86	0.57
1:1A:1069:A:H5'	1:1A:1070:A:OP1	2.05	0.57
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.20	0.57
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.38	0.57
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.87	0.57
54:1y:59:U:H5'	54:1y:60:U:C5	2.35	0.57
1:2A:1501:C:H2'	1:2A:1502:C:H6	1.70	0.57
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.44	0.57
32:2a:562:C:H1'	43:2l:15:ARG:HD2	1.85	0.57
32:2a:903:G:OP1	62:2a:1914:HOH:O	2.17	0.57
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.39	0.57
48:2q:61:GLU:HA	48:2q:71:PHE:CD1	2.39	0.57
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.86	0.57
1:1A:588:U:H2'	1:1A:589:C:C6	2.39	0.57
1:1A:635:C:O2'	1:1A:639:U:OP1	2.15	0.57
15:1T:112:ARG:HG3	15:1T:115:ARG:HH21	1.69	0.57
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.77	0.57
32:2a:613:C:H42	32:2a:627:G:H1	1.53	0.57
40:2i:117:HIS:CD2	40:2i:123:PRO:HA	2.40	0.57
1:1A:764:A:H5''	3:1D:210:GLY:HA2	1.87	0.56
1:1A:2747:G:O6	1:1A:2755:C:H5''	2.05	0.56
32:1a:1005:A:C2	32:1a:1025:U:H1'	2.40	0.56
39:1h:4:ASP:OD2	39:1h:85:ARG:NH1	2.38	0.56
2:2B:20:C:H42	2:2B:63:G:H1	1.51	0.56
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.21	0.56
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.05	0.56
23:21:83:GLU:OE1	23:21:83:GLU:N	2.38	0.56
51:2t:9:ASN:O	51:2t:10:LEU:HB2	2.05	0.56
1:1A:1141:U:OP1	9:1N:25:ARG:NH1	2.37	0.56
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.71	0.56
32:1a:162:A:H2	32:1a:348:G:H5'	1.69	0.56
32:1a:1030:C:N3	32:1a:1031:G:C2	2.73	0.56
1:2A:586:A:N1	1:2A:809:G:O2'	2.36	0.56
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.86	0.56
1:2A:2882:A:H5'	13:2R:96:ARG:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:14:U:OP2	2:2B:70:C:O2'	2.18	0.56
4:2E:119:ARG:HD2	4:2E:120:TRP:CE2	2.40	0.56
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.40	0.56
32:2a:1315:U:O2'	32:2a:1360:A:N3	2.36	0.56
40:2i:4:TYR:CZ	40:2i:88:TYR:HA	2.40	0.56
41:2j:10:GLY:HA3	41:2j:16:LEU:HD11	1.87	0.56
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.40	0.56
1:1A:1173:G:O2'	1:1A:1174:A:O4'	2.22	0.56
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.40	0.56
32:1a:976:G:H22	32:1a:1363:C:H5''	1.70	0.56
33:1b:178:ARG:HH22	39:1h:74:PRO:HB3	1.70	0.56
42:1k:79:SER:HA	42:1k:104:GLN:HB3	1.87	0.56
46:1o:37:ASN:O	46:1o:41:GLU:HG2	2.06	0.56
1:2A:992:C:OP1	16:2U:47:TYR:OH	2.19	0.56
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.40	0.56
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.38	0.56
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.04	0.56
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.40	0.56
1:2A:2136:C:H1'	1:2A:2137:C:H5'	1.87	0.56
7:2H:45:VAL:HG12	7:2H:50:VAL:HG22	1.87	0.56
32:2a:659:U:H2'	32:2a:660:G:H8	1.71	0.56
32:2a:1159:U:O4'	32:2a:1182:G:N2	2.38	0.56
32:2a:1373:G:H5''	38:2g:36:LYS:HE2	1.87	0.56
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.88	0.56
32:1a:279:A:C5	48:1q:98:LEU:HD23	2.40	0.56
32:1a:1305:G:H5''	52:1u:4:GLY:HA3	1.87	0.56
4:2E:2:LYS:HG2	4:2E:200:GLU:HB2	1.87	0.56
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.39	0.56
33:2b:187:LEU:HD12	33:2b:214:ILE:HG21	1.88	0.56
1:2A:2340:G:H2'	1:2A:2341:G:H8	1.70	0.56
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.21	0.56
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.70	0.56
23:21:4:VAL:HG12	23:21:11:ARG:HB3	1.88	0.56
32:2a:126:G:OP1	32:2a:605:U:O2'	2.20	0.56
32:2a:811:C:O2'	32:2a:901:A:N1	2.36	0.56
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.40	0.56
1:1A:956:G:H5''	12:1Q:77:LYS:HD2	1.87	0.56
1:1A:1059:G:H1	1:1A:1079:C:N4	2.04	0.56
7:1H:46:GLU:OE2	7:1H:51:ARG:NH2	2.32	0.56
15:1T:127:ALA:C	15:1T:129:ARG:H	2.13	0.56
26:14:34:GLU:HG3	26:14:35:VAL:HG12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:323:G:O2'	1:2A:1205:U:N3	2.33	0.56
1:2A:395:U:O2'	1:2A:396:G:N7	2.37	0.56
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.87	0.56
2:2B:101:G:OP2	62:2B:3101:HOH:O	2.18	0.56
32:2a:165:C:H2'	32:2a:166:G:H8	1.71	0.56
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.87	0.56
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.21	0.56
32:1a:1312:G:H5'	50:1s:5:LEU:HD11	1.86	0.56
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.87	0.56
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.87	0.56
12:2Q:29:PHE:HB3	12:2Q:65:PHE:CD2	2.41	0.56
14:2S:15:ARG:HB3	14:2S:19:LYS:HZ2	1.71	0.56
39:2h:124:ALA:O	39:2h:128:GLY:N	2.38	0.56
54:2w:23:A:H2'	54:2w:24:G:C8	2.41	0.56
1:1A:228:A:H8	1:1A:229:A:H5'	1.70	0.56
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.87	0.56
8:1I:46:ALA:HB1	8:1I:50:ARG:HH22	1.70	0.56
1:2A:7:G:H2'	1:2A:8:A:O4'	2.06	0.56
1:2A:852:G:H2'	1:2A:853:G:H8	1.70	0.56
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.88	0.56
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.20	0.56
1:2A:2576:G:O2'	1:2A:2579:C:OP2	2.16	0.56
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.87	0.56
21:2Z:121:HIS:N	21:2Z:171:ILE:O	2.39	0.56
37:2f:22:GLU:OE2	37:2f:82:ARG:HG2	2.06	0.56
1:1A:2639:A:O3'	9:1N:97:ARG:NH2	2.38	0.56
26:14:63:TYR:N	26:14:64:GLY:HA2	2.21	0.56
32:1a:148:G:H2'	32:1a:149:A:H8	1.71	0.56
32:1a:1358:U:OP1	45:1n:35:ARG:HG2	2.05	0.56
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.39	0.56
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.22	0.56
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.36	0.56
26:24:24:THR:OG1	26:24:25:TYR:N	2.31	0.56
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.87	0.56
51:2t:26:ASN:OD1	51:2t:71:THR:OG1	2.17	0.56
1:1A:295:G:H4'	20:1Y:1:MET:HE3	1.88	0.55
1:1A:671:C:N4	62:1A:4157:HOH:O	2.38	0.55
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.21	0.55
1:1A:2171:A:O2'	1:1A:2172:U:H6	1.89	0.55
32:1a:1047:G:H5''	45:1n:4:LYS:HD3	1.87	0.55
35:1d:81:GLU:O	35:1d:85:LYS:HG2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.88	0.55
1:2A:342:G:O6	62:2A:9744:HOH:O	2.18	0.55
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.41	0.55
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.06	0.55
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.40	0.55
23:21:85:LEU:HD23	23:21:89:GLU:HB3	1.87	0.55
34:2c:63:ASN:HA	34:2c:98:ASN:H	1.71	0.55
39:2h:73:ASP:OD1	39:2h:75:ARG:NE	2.39	0.55
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.88	0.55
15:1T:117:ASP:OD2	15:1T:120:ARG:NE	2.30	0.55
32:1a:539:A:OP2	43:1l:115:LYS:NZ	2.40	0.55
1:2A:1025:G:O2'	62:2A:9708:HOH:O	2.18	0.55
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.88	0.55
32:2a:921:U:H2'	32:2a:922:G:O4'	2.06	0.55
34:2c:120:VAL:HG11	34:2c:134:ILE:HD13	1.89	0.55
44:2m:40:ASN:O	44:2m:43:THR:OG1	2.24	0.55
12:1Q:67:ARG:O	12:1Q:101:ARG:NH2	2.39	0.55
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.87	0.55
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.21	0.55
54:1y:9:A:O3'	54:1y:45:U:O2'	2.21	0.55
1:2A:1783:A:OP1	62:2A:9711:HOH:O	2.17	0.55
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.89	0.55
32:2a:448:A:P	32:2a:485:G:H22	2.29	0.55
33:2b:195:ASP:O	39:2h:68:ARG:NH2	2.40	0.55
50:2s:28:LYS:HB3	50:2s:29:ARG:HA	1.88	0.55
1:1A:303:U:O4	62:1A:4032:HOH:O	2.17	0.55
1:1A:2100:G:H1	1:1A:2189:U:H3	1.53	0.55
8:1I:72:LEU:HD21	8:1I:107:VAL:HG11	1.87	0.55
11:1P:89:ALA:HA	11:1P:121:LYS:HD3	1.89	0.55
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.71	0.55
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.39	0.55
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.33	0.55
3:2D:9:TYR:CZ	3:2D:13:ARG:HG2	2.41	0.55
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.88	0.55
12:2Q:21:THR:HG21	12:2Q:101:ARG:HD3	1.88	0.55
35:2d:53:ASP:HB3	35:2d:57:ARG:HH12	1.72	0.55
47:2p:59:TRP:HA	47:2p:62:VAL:HG12	1.88	0.55
1:1A:999:U:OP2	62:1A:4035:HOH:O	2.18	0.55
1:1A:1055:G:C2	1:1A:1056:G:H1'	2.41	0.55
1:1A:2882:A:H5'	13:1R:96:ARG:HG3	1.87	0.55
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.42	0.55
1:2A:1693:U:O2'	3:2D:14:ARG:NH2	2.39	0.55
1:2A:2305:A:H2'	1:2A:2306:C:O4'	2.07	0.55
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.41	0.55
1:2A:2674:G:H5''	10:2O:26:LYS:HE3	1.88	0.55
7:2H:86:GLU:OE2	7:2H:130:ARG:NE	2.40	0.55
32:2a:441:A:H3'	32:2a:442:C:H6	1.71	0.55
32:2a:1347:G:H22	32:2a:1373:G:H2'	1.70	0.55
44:2m:89:GLY:O	44:2m:93:ARG:HG3	2.06	0.55
1:1A:1020:A:N1	1:1A:1141:U:O2'	2.31	0.55
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.24	0.55
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.88	0.55
1:2A:866:A:H2	1:2A:867:C:C4	2.24	0.55
1:2A:2295:C:H5	14:2S:13:ARG:HH12	1.55	0.55
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.89	0.55
32:2a:1118:C:OP1	40:2i:9:ARG:HD2	2.05	0.55
35:2d:163:GLU:O	35:2d:166:LYS:HG2	2.07	0.55
38:2g:27:ILE:HD12	38:2g:40:ALA:HA	1.88	0.55
1:1A:1762:A:H2'	62:1A:5424:HOH:O	2.06	0.55
32:1a:1181:G:O2'	32:1a:1182:G:N7	2.36	0.55
37:1f:37:VAL:HA	37:1f:65:VAL:HG12	1.89	0.55
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.23	0.55
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.88	0.55
20:2Y:94:LYS:NZ	62:2Y:601:HOH:O	2.38	0.55
1:1A:833:U:O2	11:1P:55:ARG:NH2	2.39	0.55
1:1A:2815:C:H5'	27:15:29:THR:HG21	1.88	0.55
13:1R:96:ARG:NH1	13:1R:115:GLU:OE2	2.40	0.55
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.41	0.55
1:2A:981:A:OP1	62:2A:9747:HOH:O	2.18	0.55
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.07	0.55
24:22:70:GLN:OE1	24:22:70:GLN:N	2.39	0.55
32:2a:1204:A:P	45:2n:3:ARG:HH12	2.29	0.55
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.69	0.55
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.21	0.55
33:2b:16:HIS:CB	33:2b:210:SER:HB3	2.36	0.55
34:2c:131:ARG:HH11	34:2c:166:GLU:HG3	1.72	0.55
41:2j:42:THR:HG23	41:2j:68:HIS:HA	1.88	0.55
1:1A:1693:U:O2	3:1D:14:ARG:NH1	2.40	0.55
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	1.89	0.55
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.42	0.55
34:1c:131:ARG:HH21	36:1e:50:GLU:HG3	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:332:A:O2'	1:2A:334:C:OP2	2.23	0.55
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.21	0.55
1:2A:2336:A:H61	22:20:43:THR:CG2	2.20	0.55
21:2Z:6:LYS:HE3	21:2Z:8:TYR:HE2	1.71	0.55
32:2a:194:C:H2'	32:2a:195:A:H5''	1.87	0.55
1:1A:458:G:O2'	1:1A:469:G:O6	2.19	0.55
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.42	0.55
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.88	0.55
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.71	0.55
32:1a:975:A:H5'	32:1a:975:A:H8	1.72	0.55
32:1a:987:G:H1	32:1a:1218:C:H42	1.55	0.55
1:2A:2833:G:H4'	1:2A:2834:G:OP2	2.07	0.55
6:2G:116:ASP:OD2	44:2m:68:GLY:HA3	2.06	0.55
8:2I:62:LYS:HE2	8:2I:133:HIS:CE1	2.42	0.55
17:2V:60:GLU:HB2	17:2V:97:LYS:HD3	1.88	0.55
32:2a:1289:A:N1	32:2a:1371:G:O2'	2.37	0.55
1:1A:530:G:H4'	1:1A:531:C:OP1	2.06	0.54
32:1a:1279:A:H4'	32:1a:1281:U:H5	1.71	0.54
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.25	0.54
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.89	0.54
33:1b:210:SER:O	33:1b:214:ILE:HG12	2.07	0.54
40:1i:31:GLN:HE21	40:1i:36:TYR:HD1	1.55	0.54
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	1.89	0.54
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.73	0.54
1:2A:2120:G:H2'	1:2A:2121:G:H8	1.71	0.54
32:2a:130:A:O2'	32:2a:131:C:O5'	2.22	0.54
32:2a:1013:G:N2	32:2a:1015:A:H3'	2.22	0.54
32:2a:1151:A:HO2'	32:2a:1152:A:H8	1.54	0.54
1:1A:2649:U:H2'	1:1A:2650:U:C6	2.42	0.54
12:1Q:10:ARG:HH12	12:1Q:90:VAL:H	1.55	0.54
30:18:26:LYS:HD3	30:18:48:PHE:HB3	1.89	0.54
32:1a:959:A:HO2'	32:1a:984:C:HO2'	1.54	0.54
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.39	0.54
54:1w:1:G:H1	54:1w:72:C:H42	1.54	0.54
55:1x:50:U:H2'	55:1x:51:C:C6	2.42	0.54
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.42	0.54
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.42	0.54
1:2A:2129:C:N3	1:2A:2159:G:N2	2.45	0.54
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	1.89	0.54
21:2Z:150:LEU:HB2	21:2Z:171:ILE:HD11	1.89	0.54
33:2b:96:ARG:HG2	33:2b:96:ARG:HH11	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:182:ILE:HG12	34:2c:203:PHE:CD1	2.43	0.54
35:2d:177:ASP:O	35:2d:181:MET:N	2.40	0.54
54:2y:61:C:H2'	54:2y:62:C:C6	2.42	0.54
1:1A:946:G:OP1	62:1A:4038:HOH:O	2.18	0.54
6:1G:41:GLN:HB3	6:1G:43:LEU:HD13	1.89	0.54
32:1a:330:C:O2	62:1a:1907:HOH:O	2.18	0.54
38:1g:89:MET:SD	38:1g:155:ARG:HB2	2.47	0.54
1:2A:524:U:H2'	1:2A:525:U:C6	2.43	0.54
1:2A:1300:U:H4'	1:2A:1301:A:C5'	2.37	0.54
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.42	0.54
2:2B:22:U:H2'	2:2B:23:G:C8	2.43	0.54
18:2W:15:ARG:NH1	62:2W:5001:HOH:O	2.40	0.54
32:2a:674:G:H2'	32:2a:675:A:H8	1.72	0.54
32:2a:1006:C:N3	32:2a:1023:G:O6	2.40	0.54
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.42	0.54
6:1G:16:ARG:HH21	6:1G:31:VAL:HG11	1.71	0.54
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	1.89	0.54
1:2A:878:A:H61	1:2A:899:A:H1'	1.73	0.54
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.42	0.54
1:2A:2760:C:H1'	7:2H:139:GLN:HE22	1.72	0.54
57:2A:3670:4M2:H33	55:2x:76:A:H2'	1.89	0.54
2:2B:105:A:OP1	21:2Z:72:ARG:NH1	2.41	0.54
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.22	0.54
33:2b:77:ALA:HA	33:2b:80:ILE:HG22	1.90	0.54
54:2w:74:C:O2'	54:2w:75:C:OP1	2.24	0.54
1:1A:1094:U:N3	1:1A:1097:U:OP2	2.41	0.54
4:1E:179:GLU:HG3	15:1T:9:LEU:HD21	1.90	0.54
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.39	0.54
1:2A:2180:U:H2'	1:2A:2181:G:O4'	2.08	0.54
2:2B:98:G:H3'	2:2B:99:G:H8	1.73	0.54
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.22	0.54
54:2y:26:A:N1	54:2y:44:G:C6	2.76	0.54
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.23	0.54
32:1a:117:G:OP2	62:1a:1901:HOH:O	2.18	0.54
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.40	0.54
54:1y:2:C:N4	54:1y:71:G:H1	2.05	0.54
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.54	0.54
1:2A:708:C:H42	1:2A:723:G:H1	1.54	0.54
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.28	0.54
16:2U:92:ARG:HD3	16:2U:92:ARG:N	2.22	0.54
32:2a:406:G:H5'	35:2d:5:ILE:HD11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:286:C:H2'	1:1A:287:C:C6	2.43	0.54
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.08	0.54
1:1A:2131:G:H5''	1:1A:2132:U:H3'	1.90	0.54
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.89	0.54
32:1a:310:G:OP2	47:1p:27:LYS:NZ	2.23	0.54
32:1a:1013:G:N2	32:1a:1016:A:OP2	2.41	0.54
32:1a:1373:G:H5''	38:1g:36:LYS:HE2	1.90	0.54
34:1c:14:ILE:HG22	34:1c:15:THR:HG23	1.88	0.54
36:1e:31:LEU:HD11	36:1e:129:ILE:HA	1.90	0.54
54:1y:20:U:H4'	54:1y:21:A:OP1	2.08	0.54
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.89	0.54
32:2a:1195:C:H2'	32:2a:1197:G:O4'	2.08	0.54
33:2b:115:LEU:HD12	33:2b:145:LEU:HB3	1.90	0.54
36:2e:91:LEU:HG	36:2e:118:ILE:HD11	1.90	0.54
49:2r:73:ALA:HB1	49:2r:78:LEU:HB2	1.88	0.54
54:2y:7:A:O2'	54:2y:49:C:O4'	2.25	0.54
1:1A:111:A:O2'	24:12:65:ASN:ND2	2.41	0.54
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.42	0.54
32:1a:890:G:O2'	32:1a:906:G:O6	2.20	0.54
32:1a:1054:C:C4	54:1w:34:G:H1'	2.43	0.54
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.31	0.54
1:2A:601:C:H5'	5:2F:108:LYS:HE3	1.89	0.54
1:2A:975(A):G:H1'	1:2A:990:A:C2	2.43	0.54
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.41	0.54
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.40	0.54
9:2N:72:TYR:N	9:2N:85:ILE:O	2.40	0.54
20:2Y:87:LYS:HG2	20:2Y:95:LYS:HD2	1.90	0.54
26:24:50:VAL:HG11	44:2m:65:LYS:N	2.23	0.54
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.88	0.54
32:2a:108:G:OP1	32:2a:326:G:N2	2.36	0.54
32:2a:184:G:H2'	32:2a:185:A:H8	1.72	0.54
54:2w:75:C:OP2	54:2w:76:A:H3'	2.07	0.54
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.42	0.54
1:1A:2324:C:H5''	1:1A:2325:G:H5'	1.90	0.54
6:1G:44:GLY:O	6:1G:47:LYS:HB2	2.08	0.54
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.43	0.54
32:1a:972:C:OP2	41:1j:57:LYS:NZ	2.29	0.54
1:2A:68:G:H2'	1:2A:69:C:O4'	2.08	0.54
12:2Q:21:THR:HG21	12:2Q:101:ARG:HG2	1.89	0.54
32:2a:1223:C:OP2	50:2s:78:ARG:NH2	2.40	0.54
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1038:C:H42	1:1A:1117:G:H1	1.53	0.54
32:1a:960:U:H2'	32:1a:1225:A:H62	1.72	0.54
32:1a:1147:C:HO2'	40:1i:5:TYR:HH	1.55	0.54
1:2A:851:U:O2'	25:23:42:ALA:O	2.20	0.54
1:2A:910:A:N1	1:2A:2277:G:H1'	2.23	0.54
1:2A:1637:A:OP2	62:2A:9749:HOH:O	2.19	0.54
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.27	0.54
2:2B:3:C:H2'	2:2B:4:C:C6	2.42	0.54
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.06	0.54
32:2a:584:G:H5'	48:2q:91:ARG:HH22	1.72	0.54
9:1N:67:LEU:HB3	9:1N:88:GLU:HG3	1.90	0.53
26:14:44:THR:O	26:14:46:GLN:N	2.41	0.53
32:1a:159:G:N2	32:1a:162:A:OP2	2.38	0.53
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.43	0.53
35:1d:187:ARG:NH2	35:1d:193:ASP:OD2	2.39	0.53
1:2A:93:G:H2'	1:2A:94:C:C6	2.44	0.53
1:2A:1043:C:N4	1:2A:1112:G:O6	2.41	0.53
32:2a:1254:C:H41	41:2j:43:ARG:HH12	1.54	0.53
33:2b:90:MET:HE3	33:2b:226:ARG:HH12	1.73	0.53
54:2w:19:G:H1	54:2w:56:C:H42	1.56	0.53
2:1B:84:C:OP1	25:13:15:TYR:OH	2.16	0.53
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.44	0.53
7:2H:25:LYS:HE3	7:2H:27:LYS:HZ3	1.73	0.53
33:2b:73:THR:HA	33:2b:94:ASN:O	2.08	0.53
1:1A:271(A):A:N7	1:1A:271(W):G:N2	2.55	0.53
1:1A:1085:A:H2'	1:1A:1086:A:N3	2.23	0.53
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.90	0.53
2:1B:14:U:OP2	2:1B:70:C:O2'	2.27	0.53
32:1a:309:G:O2'	32:1a:607:A:N1	2.42	0.53
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.92	0.53
32:1a:1086:U:H3	32:1a:1099:G:H22	1.56	0.53
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.42	0.53
1:2A:648:G:O2'	1:2A:2351:G:OP1	2.19	0.53
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.72	0.53
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.08	0.53
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.09	0.53
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.54	0.53
15:2T:77:PRO:HB2	15:2T:80:SER:HB2	1.91	0.53
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.39	0.53
32:2a:643:C:H2'	32:2a:644:G:H8	1.72	0.53
39:2h:113:SER:HB2	39:2h:134:ILE:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:184:C:H2'	1:1A:185:U:C6	2.44	0.53
1:1A:1406:U:H2'	1:1A:1407:C:H6	1.73	0.53
17:1V:52:VAL:HG23	17:1V:55:ALA:HB3	1.89	0.53
32:1a:1289:A:OP1	52:1u:10:ARG:NH2	2.41	0.53
1:2A:2320:A:N6	1:2A:2333:A:H2'	2.23	0.53
5:2F:137:LYS:HA	5:2F:140:LEU:HB2	1.91	0.53
35:2d:108:LEU:HD11	35:2d:174:LEU:HD22	1.91	0.53
41:2j:65:LEU:HD13	45:2n:56:VAL:HG22	1.90	0.53
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.40	0.53
1:1A:639:U:H2'	1:1A:640:C:C6	2.44	0.53
1:1A:2121:G:H1	1:1A:2177:C:H42	1.54	0.53
2:1B:88:C:H2'	2:1B:89:G:O4'	2.08	0.53
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.91	0.53
15:1T:108:ARG:HD3	62:1a:2078:HOH:O	2.08	0.53
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.90	0.53
32:1a:1151:A:HO2'	32:1a:1152:A:H8	1.55	0.53
32:1a:1179:A:O3'	40:1i:103:THR:OG1	2.27	0.53
32:1a:1298:C:C5	38:1g:114:ARG:HD3	2.44	0.53
1:2A:821:A:H2'	1:2A:946:G:H5''	1.90	0.53
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.07	0.53
1:2A:2355:C:H1'	22:20:39:ARG:HH21	1.73	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.09	0.53
33:2b:24:TRP:H	33:2b:24:TRP:HD1	1.55	0.53
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.91	0.53
1:1A:84:A:H5''	20:1Y:8:LYS:HE3	1.89	0.53
1:1A:2130:U:H2'	1:1A:2131:G:N2	2.23	0.53
1:1A:2206:G:H3'	1:1A:2207:G:N7	2.24	0.53
27:15:16:ARG:HG3	27:15:17:ASP:N	2.22	0.53
32:1a:576:G:O6	32:1a:880:C:O2'	2.23	0.53
32:1a:613:C:H2'	32:1a:614:A:H8	1.72	0.53
41:1j:21:GLN:NE2	41:1j:25:GLU:OE2	2.36	0.53
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.43	0.53
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.09	0.53
1:2A:2135:A:N1	1:2A:2156:G:O2'	2.37	0.53
6:2G:11:TYR:HA	6:2G:15:VAL:HB	1.90	0.53
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.90	0.53
13:2R:24:GLN:HB3	13:2R:44:LEU:HD11	1.90	0.53
32:2a:976:G:N2	32:2a:1363:C:OP2	2.36	0.53
32:2a:1503:A:O2'	53:2v:13:A:N1	2.42	0.53
33:2b:71:VAL:HG21	33:2b:164:VAL:HG22	1.90	0.53
35:2d:173:TRP:HZ3	35:2d:193:ASP:HB3	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.44	0.53
32:1a:232:G:H1'	32:1a:262:A:N1	2.23	0.53
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.22	0.53
1:2A:111:A:O2'	24:22:65:ASN:ND2	2.40	0.53
1:2A:448:U:O4	1:2A:583:G:H1'	2.09	0.53
1:2A:903:C:H2'	1:2A:904:C:C6	2.43	0.53
1:2A:2340:G:H2'	1:2A:2341:G:C8	2.44	0.53
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.89	0.53
32:2a:113:G:H2'	32:2a:114:U:H6	1.74	0.53
32:2a:269:C:H2'	32:2a:270:A:C8	2.44	0.53
34:2c:182:ILE:HG12	34:2c:203:PHE:HD1	1.74	0.53
1:1A:517:C:OP1	27:15:16:ARG:NH2	2.41	0.53
1:1A:900:A:H2'	1:1A:901:A:O4'	2.08	0.53
1:1A:1508:A:O2'	1:1A:1509:C:OP1	2.24	0.53
1:1A:2408:U:H2'	1:1A:2409:G:C8	2.44	0.53
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.90	0.53
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.43	0.53
42:1k:98:LEU:O	42:1k:101:SER:OG	2.18	0.53
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.06	0.53
32:2a:957:U:O2'	32:2a:959:A:N7	2.39	0.53
40:2i:24:GLY:HA2	40:2i:59:PHE:O	2.09	0.53
1:1A:548:A:N6	17:1V:19:LYS:H	2.07	0.53
1:1A:1647:G:OP1	62:1A:4041:HOH:O	2.19	0.53
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.73	0.53
1:1A:2879:C:OP2	62:1A:4039:HOH:O	2.19	0.53
2:1B:28:C:OP1	14:1S:36:TYR:OH	2.24	0.53
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.09	0.53
26:14:61:ARG:HH21	50:1s:9:VAL:HG21	1.74	0.53
32:1a:90:U:O2'	32:1a:91:C:OP1	2.23	0.53
32:1a:532:A:N6	32:1a:1206:G:O2'	2.42	0.53
32:1a:648:A:H2'	32:1a:649:G:H8	1.74	0.53
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.91	0.53
48:1q:10:VAL:HG13	48:1q:19:VAL:HB	1.89	0.53
3:2D:242:ARG:HG3	3:2D:242:ARG:NH1	2.12	0.53
7:2H:159:GLU:HG2	7:2H:169:VAL:HG11	1.89	0.53
16:2U:58:ARG:HA	16:2U:61:TRP:CE3	2.44	0.53
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.24	0.53
32:2a:79:G:H1	32:2a:90:U:H3	1.56	0.53
32:2a:757:U:O2'	32:2a:879:C:O2	2.25	0.53
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.44	0.53
35:2d:88:VAL:HG12	35:2d:91:SER:H	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2v:23:A:H4'	53:2v:24:A:O4'	2.08	0.53
1:1A:764:A:H5''	3:1D:210:GLY:CA	2.39	0.53
1:1A:2384:G:P	22:10:55:ARG:HH12	2.32	0.53
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	1.91	0.53
21:1Z:45:ASP:O	21:1Z:49:ARG:HG2	2.08	0.53
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.44	0.53
9:2N:67:LEU:HA	9:2N:87:LEU:HD22	1.90	0.53
25:23:8:LEU:HG	25:23:31:LEU:HD23	1.90	0.53
32:2a:664:G:H22	32:2a:741:G:H1	1.58	0.53
54:2w:51:U:H2'	54:2w:52:G:C8	2.44	0.53
1:1A:747:U:O2	1:1A:2014:A:H1'	2.09	0.52
1:1A:1538:G:H2'	1:1A:1539:G:C8	2.44	0.52
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.24	0.52
26:14:53:GLU:HB2	26:14:55:ARG:C	2.34	0.52
32:1a:1239:A:H62	32:1a:1299:A:N6	2.06	0.52
37:1f:70:ASP:OD1	37:1f:70:ASP:N	2.39	0.52
54:1y:59:U:H2'	54:1y:60:U:H5'	1.90	0.52
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.90	0.52
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD21	1.91	0.52
32:2a:22:G:O6	62:2a:1904:HOH:O	2.17	0.52
32:2a:264:U:H4'	48:2q:63:ARG:HD2	1.90	0.52
32:2a:1039:C:H2'	32:2a:1040:U:O4'	2.09	0.52
34:2c:36:ASP:O	34:2c:40:ARG:HG2	2.09	0.52
37:2f:82:ARG:HD3	37:2f:83:ASP:H	1.73	0.52
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.09	0.52
44:2m:3:ARG:NH1	44:2m:9:ILE:O	2.42	0.52
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.40	0.52
1:1A:131:G:OP1	62:1A:4037:HOH:O	2.18	0.52
1:1A:2198:A:O5'	8:1I:33:ARG:NH2	2.42	0.52
51:1t:36:LEU:HD12	51:1t:62:LEU:HD12	1.91	0.52
1:2A:286:C:H42	1:2A:355:G:H1	1.56	0.52
1:2A:588:U:H2'	1:2A:589:C:C6	2.44	0.52
1:2A:1509(B):A:H2'	1:2A:1510:G:H8	1.74	0.52
25:23:46:ASN:O	25:23:50:VAL:HG22	2.09	0.52
32:2a:736:C:H4'	37:2f:89:MET:HE3	1.91	0.52
32:2a:854:G:O6	62:2a:1913:HOH:O	2.17	0.52
33:2b:76:GLN:HE21	33:2b:206:ASP:HA	1.74	0.52
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.41	0.52
34:2c:41:GLY:O	34:2c:45:LYS:NZ	2.42	0.52
1:1A:1069:A:H1'	1:1A:1096:A:H4'	1.92	0.52
1:1A:1256:G:O6	62:1A:4028:HOH:O	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1531:C:H42	1:1A:1538:G:H1	1.58	0.52
32:1a:222:U:H2'	32:1a:223:U:C6	2.44	0.52
36:1e:69:VAL:HG11	36:1e:113:ALA:HB1	1.91	0.52
47:1p:18:ARG:NH1	47:1p:32:TYR:OH	2.42	0.52
54:1y:26:A:H61	54:1y:44:G:H1	1.58	0.52
1:2A:307:G:H21	1:2A:330:A:H62	1.57	0.52
4:2E:98:PRO:HD3	4:2E:175:VAL:HG13	1.91	0.52
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.49	0.52
11:2P:42:SER:O	62:2P:301:HOH:O	2.19	0.52
13:2R:2:ARG:NH1	13:2R:5:LYS:O	2.43	0.52
15:2T:105:LEU:HD22	15:2T:109:GLU:HB3	1.91	0.52
23:21:91:LYS:HG2	23:21:95:LEU:HD22	1.90	0.52
32:2a:418:C:H1'	32:2a:540:G:O2'	2.09	0.52
32:2a:735:C:H2'	32:2a:736:C:H6	1.72	0.52
32:2a:1279:A:O2'	32:2a:1282:C:N4	2.42	0.52
43:2l:88:GLY:O	43:2l:99:HIS:HD2	1.93	0.52
44:2m:78:ILE:HA	44:2m:81:LEU:HD12	1.91	0.52
1:1A:686:G:OP2	62:1A:4040:HOH:O	2.19	0.52
1:1A:883:G:H22	1:1A:892:G:H1	1.58	0.52
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.23	0.52
28:16:6:ARG:HH12	28:16:26:ASN:HB2	1.74	0.52
32:1a:362:G:OP2	62:1a:1909:HOH:O	2.19	0.52
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.10	0.52
41:1j:17:ASP:OD1	41:1j:70:ARG:NE	2.41	0.52
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.45	0.52
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.91	0.52
35:2d:172:PRO:CB	35:2d:187:ARG:HH21	2.23	0.52
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.92	0.52
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.44	0.52
32:1a:892:A:O2'	32:1a:1415:G:H4'	2.09	0.52
33:1b:44:LEU:H	33:1b:44:LEU:HD12	1.74	0.52
40:1i:100:GLY:O	40:1i:103:THR:HG22	2.09	0.52
55:1x:15:G:H2'	55:1x:59:A:N1	2.25	0.52
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.08	0.52
1:2A:614(B):G:N2	5:2F:44:ARG:O	2.39	0.52
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.42	0.52
1:2A:2206:G:H3'	1:2A:2207:G:N7	2.24	0.52
1:2A:2298:A:H1'	1:2A:2321:G:H21	1.74	0.52
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.24	0.52
6:2G:41:GLN:HB3	6:2G:43:LEU:HD13	1.90	0.52
32:2a:1305:G:H5'	52:2u:4:GLY:C	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:16:LEU:HD21	40:2i:45:ALA:HB2	1.90	0.52
44:2m:80:ARG:HH22	50:2s:69:HIS:HE1	1.58	0.52
1:1A:2574:G:OP1	62:1A:4036:HOH:O	2.18	0.52
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.43	0.52
33:1b:97:TRP:HH2	33:1b:176:GLU:CD	2.17	0.52
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.91	0.52
1:2A:796:C:H2'	1:2A:797:C:C6	2.44	0.52
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.57	0.52
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.45	0.52
3:2D:159:ALA:HB1	3:2D:198:ASN:O	2.09	0.52
26:24:59:PHE:HA	26:24:61:ARG:N	2.24	0.52
32:2a:811:C:N3	62:2a:1928:HOH:O	2.34	0.52
32:2a:1065:U:H5''	32:2a:1190:G:N2	2.24	0.52
32:2a:1152:A:H5'	41:2j:13:HIS:CG	2.44	0.52
33:2b:71:VAL:HB	33:2b:164:VAL:HA	1.92	0.52
33:2b:96:ARG:NH1	33:2b:98:LEU:HD23	2.25	0.52
1:1A:272(H):C:N4	1:1A:363(B):G:O6	2.19	0.52
1:1A:1044:G:H5'	1:1A:1045:A:OP2	2.09	0.52
21:1Z:150:LEU:HD21	21:1Z:154:ASP:HB2	1.92	0.52
32:1a:147:G:H1	32:1a:175:C:H42	1.58	0.52
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.44	0.52
1:2A:880:G:H22	1:2A:898:C:H1'	1.75	0.52
32:2a:560:U:H5'	32:2a:566:G:N2	2.25	0.52
32:2a:1053:G:N7	32:2a:1199:U:H3'	2.24	0.52
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.45	0.52
7:1H:4:ILE:O	7:1H:69:ARG:HD2	2.09	0.52
32:1a:26:A:O2'	35:1d:209:ARG:NH1	2.39	0.52
32:1a:163:C:H2'	32:1a:164:U:C6	2.44	0.52
36:1e:122:GLU:O	36:1e:126:ARG:NH1	2.42	0.52
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.22	0.52
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.45	0.52
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.44	0.52
5:2F:28:ILE:HG23	5:2F:112:MET:HE3	1.92	0.52
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.91	0.52
17:2V:60:GLU:OE1	17:2V:97:LYS:NZ	2.33	0.52
32:2a:825:G:O2'	39:2h:12:ARG:NH2	2.43	0.52
32:2a:1001:A:H2'	32:2a:1001(A):G:H5''	1.91	0.52
32:2a:1396:A:H2	36:2e:19:MET:HG3	1.74	0.52
1:1A:1045:A:H5'	1:1A:1046:A:H5''	1.91	0.52
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.09	0.52
32:1a:1183:A:H3'	32:1a:1184:G:H5''	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1244:C:H42	32:1a:1293:G:H1	1.57	0.52
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.24	0.52
39:1h:49:GLU:HG2	39:1h:62:TYR:HE2	1.73	0.52
42:1k:89:ALA:O	42:1k:91:ARG:N	2.41	0.52
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.92	0.52
1:2A:1226:A:OP1	16:2U:16:LYS:NZ	2.39	0.52
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.10	0.52
1:2A:1837:C:O2'	1:2A:1927:A:N3	2.36	0.52
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.74	0.52
8:2I:8:PRO:HD3	8:2I:15:VAL:HB	1.91	0.52
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.45	0.52
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.83	0.52
32:2a:923:A:OP1	36:2e:21:ALA:HB2	2.09	0.52
32:2a:1042:G:H2'	32:2a:1043:C:O4'	2.10	0.52
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.10	0.52
32:2a:1310:G:H5'	44:2m:77:ASN:ND2	2.25	0.52
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.09	0.52
39:2h:110:ALA:HB3	39:2h:121:ASP:HB3	1.92	0.52
44:2m:89:GLY:O	44:2m:93:ARG:N	2.42	0.52
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.45	0.52
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.38	0.52
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.43	0.52
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.92	0.52
49:1r:56:THR:HB	49:1r:58:LEU:HD13	1.92	0.52
1:2A:774:A:H2'	1:2A:774:A:N3	2.25	0.52
12:2Q:138:ASP:OD2	21:2Z:81:ARG:NH1	2.34	0.52
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.09	0.52
33:2b:44:LEU:H	33:2b:44:LEU:HD12	1.74	0.52
1:1A:2137:C:H2'	1:1A:2138:C:C6	2.45	0.51
1:1A:2271:G:H5''	22:10:20:ARG:NH1	2.25	0.51
18:1W:23:LEU:HD11	27:15:25:LEU:HB2	1.92	0.51
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.74	0.51
33:1b:101:MET:HA	33:1b:108:ILE:HG13	1.92	0.51
47:1p:52:ASP:O	47:1p:54:GLU:N	2.43	0.51
1:2A:890:A:H2'	1:2A:892:G:C8	2.44	0.51
21:2Z:144:LEU:HD22	21:2Z:174:VAL:HB	1.92	0.51
22:20:11:ARG:O	22:20:14:ARG:NH2	2.35	0.51
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.10	0.51
38:2g:23:VAL:O	38:2g:27:ILE:HG12	2.08	0.51
54:2w:2:C:N4	54:2w:71:G:H1	2.07	0.51
1:1A:226:G:H21	1:1A:228:A:H62	1.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1799:G:OP1	3:1D:260:ARG:NH1	2.41	0.51
1:1A:2106:G:H1	1:1A:2183:C:H42	1.56	0.51
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.92	0.51
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.43	0.51
32:1a:343:U:O2'	32:1a:346:G:O6	2.22	0.51
35:1d:65:ARG:HG3	35:1d:70:ILE:HG22	1.93	0.51
54:1w:26:A:H61	54:1w:44:G:H1	1.56	0.51
1:2A:468:G:N7	29:27:39:ARG:NH2	2.56	0.51
1:2A:974:G:OP1	1:2A:1187:G:O2'	2.21	0.51
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.37	0.51
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.45	0.51
1:2A:2356:C:H4'	22:20:20:ARG:HG3	1.92	0.51
30:28:10:ALA:HB3	30:28:62:LEU:HD21	1.92	0.51
32:2a:887:G:H1	32:2a:910:C:H42	1.56	0.51
32:2a:1004:A:N6	32:2a:1037:C:C2	2.79	0.51
35:2d:108:LEU:HD23	35:2d:110:PHE:CZ	2.44	0.51
36:2e:102:ALA:HB3	36:2e:107:ARG:HB2	1.92	0.51
38:2g:100:ALA:O	38:2g:104:LEU:HB2	2.10	0.51
50:2s:64:GLU:CD	50:2s:64:GLU:H	2.18	0.51
55:2x:14:A:C2	55:2x:15:G:H1'	2.45	0.51
54:2y:33:U:H2'	54:2y:35:A:OP2	2.11	0.51
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.10	0.51
1:1A:2804:C:H2'	1:1A:2805:G:C8	2.45	0.51
3:1D:145:VAL:HG11	3:1D:175:LEU:HD11	1.92	0.51
25:13:37:LEU:HB3	25:13:43:ILE:HD13	1.92	0.51
32:1a:1137:C:H5''	32:1a:1138:G:OP1	2.10	0.51
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.45	0.51
1:2A:801:G:OP2	5:2F:55:GLY:HA2	2.11	0.51
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.45	0.51
19:2X:41:ASN:O	19:2X:45:THR:HG23	2.10	0.51
32:2a:89:C:H2'	32:2a:90:U:O4'	2.10	0.51
32:2a:189(F):U:H3	48:2q:72:ARG:HH12	1.55	0.51
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.45	0.51
32:2a:1388:C:H2'	32:2a:1389:C:C6	2.45	0.51
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.46	0.51
42:2k:45:GLY:O	42:2k:50:TYR:HB2	2.11	0.51
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.92	0.51
1:1A:1364:G:P	23:11:3:LYS:HG3	2.50	0.51
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.10	0.51
1:1A:1701:A:OP2	62:1A:4042:HOH:O	2.19	0.51
1:1A:2135:A:N6	1:1A:2157:G:H21	1.96	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.75	0.51
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.46	0.51
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.92	0.51
10:1O:36:GLY:HA3	10:1O:109:LYS:HD2	1.91	0.51
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.37	0.51
51:1t:56:MET:HE3	51:1t:85:MET:HG2	1.92	0.51
2:2B:24:G:H4'	2:2B:25:A:H8	1.73	0.51
15:2T:51:ARG:HG3	15:2T:98:LYS:HD2	1.93	0.51
32:2a:420:U:O2'	32:2a:423:G:O6	2.20	0.51
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.93	0.51
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.45	0.51
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.92	0.51
1:1A:1062:G:H1'	1:1A:1088:A:C8	2.45	0.51
1:1A:1359:A:H2	1:1A:1372:U:O4	1.92	0.51
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.10	0.51
1:1A:2155:G:H5'	1:1A:2156:G:OP2	2.11	0.51
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.92	0.51
26:14:61:ARG:HG3	26:14:62:ARG:N	2.26	0.51
32:1a:78:G:C2	32:1a:91:C:N3	2.79	0.51
32:1a:182:U:C4	32:1a:183:G:H1'	2.46	0.51
44:1m:86:CYS:HB2	50:1s:73:GLU:HB3	1.93	0.51
54:1y:9:A:H1'	54:1y:45:U:H2'	1.91	0.51
1:2A:320:A:H4'	1:2A:322:A:N7	2.26	0.51
1:2A:324:A:N6	1:2A:338:G:O2'	2.43	0.51
1:2A:479:A:N3	1:2A:481:G:H5''	2.25	0.51
21:2Z:156:LYS:HE3	21:2Z:158:PRO:HD3	1.91	0.51
32:2a:1397:C:OP2	36:2e:24:ARG:NH2	2.44	0.51
1:1A:582:G:H2'	1:1A:583:G:C8	2.46	0.51
1:1A:1056:G:H5''	1:1A:1057:A:O4'	2.10	0.51
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.46	0.51
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.43	0.51
32:1a:69:G:H2'	32:1a:70:G:H8	1.76	0.51
32:1a:184:G:H2'	32:1a:185:A:H8	1.76	0.51
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.31	0.51
32:1a:445:G:H2'	32:1a:446:G:C8	2.46	0.51
44:1m:40:ASN:O	44:1m:43:THR:OG1	2.25	0.51
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.76	0.51
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.45	0.51
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.40	0.51
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.91	0.51
1:2A:2167:U:O2'	1:2A:2168:G:O4'	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.11	0.51
21:2Z:6:LYS:HE3	21:2Z:8:TYR:CE2	2.45	0.51
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.10	0.51
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.43	0.51
1:1A:2080:G:OP1	23:11:35:THR:HG21	2.10	0.51
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.45	0.51
8:1I:104:GLN:O	8:1I:106:GLY:N	2.43	0.51
24:12:64:LEU:HD21	24:12:68:ARG:HE	1.75	0.51
32:1a:431:A:H2'	32:1a:432:A:O4'	2.10	0.51
51:1t:79:ARG:HD2	51:1t:83:ARG:NH2	2.25	0.51
5:2F:53:THR:HG22	5:2F:56:GLU:CD	2.36	0.51
8:2I:92:VAL:HG11	8:2I:144:VAL:HG11	1.93	0.51
17:2V:98:GLU:CD	17:2V:100:ARG:HH12	2.19	0.51
21:2Z:146:ILE:HG12	21:2Z:174:VAL:HG12	1.92	0.51
32:2a:236:G:OP1	48:2q:40:LYS:NZ	2.39	0.51
32:2a:407:G:OP1	35:2d:115:ARG:HD3	2.10	0.51
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.93	0.51
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	1.91	0.51
38:2g:78:ARG:HH21	38:2g:79:ARG:HH22	1.57	0.51
50:2s:28:LYS:HB3	50:2s:29:ARG:CA	2.40	0.51
1:1A:2336:A:H61	22:10:43:THR:CG2	2.23	0.51
10:1O:80:ASP:OD2	15:1T:64:ARG:NH2	2.44	0.51
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.10	0.51
24:12:32:LEU:HD11	24:12:54:LYS:HG3	1.92	0.51
32:1a:673:G:O3'	37:1f:87:ARG:NH2	2.44	0.51
36:1e:91:LEU:HG	36:1e:118:ILE:HD11	1.92	0.51
54:1w:51:U:H2'	54:1w:52:G:C8	2.46	0.51
1:2A:571:A:O2'	17:2V:78:LYS:HE2	2.11	0.51
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.26	0.51
1:2A:1782:C:H1'	1:2A:2609:U:H5''	1.93	0.51
11:2P:59:LEU:HD21	30:28:10:ALA:HA	1.93	0.51
24:22:66:GLU:HG2	24:22:69:ARG:HH22	1.76	0.51
32:2a:661:G:H1	32:2a:744:C:H42	1.57	0.51
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.93	0.51
32:2a:977:A:O2'	32:2a:981:U:N3	2.42	0.51
32:2a:1053:G:N7	32:2a:1200:C:H5''	2.26	0.51
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.46	0.51
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.46	0.51
33:2b:60:ASP:O	33:2b:64:ARG:HG2	2.10	0.51
37:2f:80:ARG:NH1	37:2f:88:VAL:O	2.42	0.51
1:1A:897:C:N3	1:1A:898:C:N4	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:56:SER:HB3	7:1H:61:HIS:ND1	2.25	0.51
32:1a:78:G:N1	32:1a:91:C:C4	2.76	0.51
32:1a:193:C:H2'	32:1a:194:C:H6	1.76	0.51
32:1a:1032:G:H2'	32:1a:1033:G:C8	2.46	0.51
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.93	0.51
37:1f:97:PHE:N	49:1r:30:ASP:OD1	2.42	0.51
38:1g:108:ALA:O	38:1g:111:ARG:HB3	2.11	0.51
1:2A:1779:U:H2'	62:2A:9787:HOH:O	2.11	0.51
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.46	0.51
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.74	0.51
32:2a:108:G:P	32:2a:326:G:H22	2.33	0.51
32:2a:539:A:H2'	32:2a:540:G:C8	2.46	0.51
32:2a:1055:A:N3	34:2c:156:ARG:NH1	2.57	0.51
32:2a:1497:G:H1'	32:2a:1518:MA6:H2	1.93	0.51
1:1A:548:A:O2'	1:1A:549:G:O5'	2.28	0.51
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.46	0.51
1:1A:1801:G:OP2	3:1D:154:LYS:NZ	2.43	0.51
4:1E:7:VAL:HG13	4:1E:27:LEU:HB3	1.93	0.51
4:1E:34:VAL:CG2	4:1E:48:GLN:HE21	2.24	0.51
5:1F:31:HIS:NE2	5:1F:35:GLU:OE2	2.43	0.51
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.44	0.51
1:2A:1783:A:H5'	1:2A:2608:G:H4'	1.93	0.51
9:2N:43:THR:HB	9:2N:46:VAL:HG22	1.93	0.51
24:22:32:LEU:HD11	24:22:54:LYS:HG3	1.93	0.51
32:2a:5:U:H5'	32:2a:6:G:C5	2.46	0.51
32:2a:1132:C:H42	32:2a:1142:G:H1	1.59	0.51
32:2a:1176:A:H2'	32:2a:1177:G:O4'	2.11	0.51
34:2c:26:LYS:HA	45:2n:36:PHE:HE1	1.74	0.51
34:2c:106:VAL:O	34:2c:108:ASN:N	2.35	0.51
35:2d:187:ARG:HH22	35:2d:193:ASP:CG	2.18	0.51
36:2e:77:PRO:HD2	36:2e:142:LEU:HD13	1.92	0.51
36:2e:122:GLU:HB2	36:2e:126:ARG:HH11	1.76	0.51
39:2h:86:ILE:HB	39:2h:133:LEU:O	2.10	0.51
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.46	0.50
1:1A:1538:G:H2'	1:1A:1539:G:H8	1.76	0.50
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.23	0.50
5:1F:148:LEU:HD21	5:1F:191:ARG:HH21	1.75	0.50
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.93	0.50
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.09	0.50
23:11:83:GLU:OE1	23:11:83:GLU:N	2.44	0.50
32:1a:920:U:H2'	32:1a:921:U:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1144:G:N2	32:1a:1146:A:H62	2.10	0.50
32:1a:1202:G:H1'	45:1n:29:ARG:HD2	1.93	0.50
39:1h:24:THR:HG22	39:1h:63:LEU:HD11	1.93	0.50
32:2a:310:G:H4'	47:2p:31:LYS:HD2	1.93	0.50
32:2a:573:A:N3	32:2a:883:C:O2'	2.43	0.50
32:2a:973:G:O3'	45:2n:41:ARG:NH1	2.41	0.50
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.94	0.50
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.76	0.50
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.44	0.50
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.45	0.50
38:1g:111:ARG:NH2	38:1g:126:ASP:OD2	2.44	0.50
39:1h:73:ASP:OD2	39:1h:75:ARG:NH2	2.43	0.50
47:1p:22:THR:HA	47:1p:33:ILE:HG12	1.94	0.50
54:1y:21:A:O2'	54:1y:22:G:OP1	2.23	0.50
1:2A:821:A:N1	62:2A:9837:HOH:O	2.34	0.50
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.74	0.50
31:29:22:ARG:HB2	31:29:24:TYR:HE2	1.76	0.50
32:2a:189(F):U:O2	48:2q:63:ARG:NH2	2.40	0.50
32:2a:828:A:H2'	32:2a:829:G:O4'	2.11	0.50
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.11	0.50
32:2a:1009:G:OP2	32:2a:1009:G:H8	1.94	0.50
32:2a:1075:C:H5''	33:2b:179:LYS:NZ	2.26	0.50
32:2a:1165:C:N4	32:2a:1171:G:H1	2.06	0.50
40:2i:17:VAL:HG11	40:2i:81:ILE:HA	1.94	0.50
43:2l:56:ALA:HB3	43:2l:100:ILE:HD11	1.93	0.50
1:1A:2141:G:C6	1:1A:2151:G:C2	2.99	0.50
32:1a:757:U:H2'	32:1a:758:G:O4'	2.11	0.50
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.93	0.50
1:2A:646:A:H2'	1:2A:647:G:O4'	2.12	0.50
1:2A:2165:G:H2'	1:2A:2166:G:H4'	1.93	0.50
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	1.92	0.50
7:2H:125:VAL:HG12	7:2H:131:VAL:HG22	1.92	0.50
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	1.93	0.50
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.52	0.50
32:2a:309:G:O2'	32:2a:607:A:N1	2.43	0.50
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.46	0.50
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.46	0.50
1:1A:1106:G:H2'	1:1A:1107:G:O4'	2.11	0.50
1:1A:2151:G:N1	1:1A:2152:G:O6	2.45	0.50
32:1a:1345:U:OP1	62:1a:1910:HOH:O	2.19	0.50
1:2A:1501:C:O4'	3:2D:100:GLY:HA2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.26	0.50
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.76	0.50
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.11	0.50
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.93	0.50
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.44	0.50
32:2a:691:G:H2'	32:2a:692:U:C6	2.47	0.50
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.12	0.50
33:2b:78:GLN:NE2	33:2b:95:GLN:HE22	2.08	0.50
36:2e:99:GLY:N	36:2e:117:ASP:OD1	2.43	0.50
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.47	0.50
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.46	0.50
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.36	0.50
32:2a:701:C:OP1	32:2a:702:A:O2'	2.21	0.50
32:2a:1116:C:H2'	32:2a:1117:G:H5''	1.94	0.50
35:2d:76:ARG:HA	35:2d:79:PHE:HB3	1.94	0.50
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.92	0.50
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.40	0.50
1:2A:271(O):C:H2'	1:2A:271(P):C:C6	2.46	0.50
1:2A:2099:U:H2'	1:2A:2100:G:H8	1.77	0.50
3:2D:233:HIS:HA	62:2D:408:HOH:O	2.11	0.50
5:2F:34:TRP:CZ2	11:2P:8:PRO:HG3	2.47	0.50
33:2b:75:LYS:HA	33:2b:78:GLN:HG2	1.94	0.50
34:2c:47:LEU:HD12	34:2c:68:VAL:HG11	1.94	0.50
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.76	0.50
41:2j:74:ILE:HG22	62:2j:8102:HOH:O	2.11	0.50
43:2l:71:PRO:O	43:2l:102:ARG:HD2	2.10	0.50
1:1A:90:U:H4'	1:1A:92:A:H5'	1.94	0.50
1:1A:1063:G:H1	1:1A:1075:C:H42	1.58	0.50
1:1A:1065:U:C2'	1:1A:1073:A:H61	2.25	0.50
1:1A:2572:A:N7	4:1E:144:ARG:HD2	2.26	0.50
8:1I:130:TYR:CE2	8:1I:132:PRO:HB3	2.47	0.50
32:1a:442:C:H42	32:1a:492:G:H1	1.59	0.50
32:1a:1095:U:H5''	32:1a:1109:C:O2	2.12	0.50
40:1i:55:ALA:HB1	40:1i:59:PHE:HE2	1.77	0.50
1:2A:444:C:H4'	5:2F:49:ALA:HB2	1.93	0.50
1:2A:530:G:O4'	1:2A:530:G:N3	2.45	0.50
1:2A:958:U:O2	2:2B:90:A:H4'	2.11	0.50
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.46	0.50
1:2A:2422:A:O4'	54:2y:76:A:N6	2.45	0.50
21:2Z:28:MET:HE2	21:2Z:59:LEU:HD13	1.94	0.50
32:2a:407:G:H2'	32:2a:408:A:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:438:G:H4'	35:2d:123:HIS:ND1	2.26	0.50
32:2a:445:G:H2'	32:2a:446:G:C8	2.47	0.50
32:2a:1014:A:OP1	50:2s:18:LYS:NZ	2.44	0.50
32:2a:1136:U:H5''	32:2a:1137:C:C4	2.47	0.50
34:2c:137:ALA:HA	34:2c:140:ARG:NH2	2.26	0.50
47:2p:17:TYR:CE2	47:2p:41:PRO:HG3	2.46	0.50
1:1A:576:U:H2'	1:1A:577:G:C8	2.47	0.50
1:1A:1188:U:C2'	1:1A:1189:A:H5'	2.41	0.50
18:1W:68:ARG:NH1	18:1W:112:GLY:H	2.09	0.50
32:1a:300:A:O2'	32:1a:564:C:N3	2.41	0.50
1:2A:924:C:H2'	1:2A:925:C:C6	2.47	0.50
1:2A:2006:C:H6	1:2A:2006:C:O5'	1.95	0.50
17:2V:62:LEU:CD1	17:2V:95:LEU:HB2	2.42	0.50
26:24:62:ARG:HH11	26:24:62:ARG:H	1.59	0.50
32:2a:1054:C:C4	54:2w:34:G:H1'	2.47	0.50
32:2a:1249:C:O2'	40:2i:73:GLN:NE2	2.45	0.50
34:2c:24:ALA:HB3	34:2c:29:TYR:HD1	1.76	0.50
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.47	0.50
4:1E:5:LEU:HD13	4:1E:77:ILE:HD12	1.94	0.50
28:16:10:LEU:HG	28:16:54:ILE:HG13	1.94	0.50
1:2A:362:U:O2'	1:2A:363:G:H5''	2.11	0.50
1:2A:2697:G:OP1	62:2A:9751:HOH:O	2.19	0.50
32:2a:584:G:H2'	32:2a:585:G:C8	2.47	0.50
32:2a:1218:C:OP2	45:2n:9:LYS:NZ	2.44	0.50
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.47	0.50
33:2b:189:ASP:O	33:2b:192:SER:OG	2.29	0.50
47:2p:2:VAL:HG13	47:2p:64:ALA:HA	1.93	0.50
1:1A:1666:G:C2'	1:1A:1667:G:H5'	2.41	0.49
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.12	0.49
10:1O:98:VAL:HG11	10:1O:114:ILE:HG23	1.94	0.49
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.93	0.49
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.94	0.49
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.93	0.49
32:1a:996:A:N1	32:1a:1045:C:O2'	2.40	0.49
34:1c:87:LEU:O	34:1c:91:LEU:HB2	2.11	0.49
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.28	0.49
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.12	0.49
55:1x:66:C:H2'	55:1x:67:C:O4'	2.11	0.49
1:2A:1591:G:H2'	1:2A:1592:C:C6	2.47	0.49
6:2G:70:VAL:HA	6:2G:90:LEU:HD23	1.94	0.49
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.93	0.49
1:1A:2864:G:OP1	15:1T:119:LYS:HD2	2.12	0.49
6:1G:170:ARG:HE	6:1G:174:GLU:CD	2.20	0.49
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.11	0.49
33:1b:70:PHE:CD1	33:1b:163:PHE:HB3	2.47	0.49
52:1u:6:ARG:HH21	52:1u:15:ARG:NH2	2.08	0.49
1:2A:214:G:N3	1:2A:216:A:O2'	2.39	0.49
1:2A:321:G:OP2	5:2F:135:LYS:HD3	2.13	0.49
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.21	0.49
1:2A:1494:A:H2'	1:2A:1495:A:C8	2.47	0.49
1:2A:1882:C:H2'	1:2A:1883:G:O4'	2.11	0.49
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.12	0.49
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.27	0.49
32:2a:1182:G:H4'	32:2a:1183:A:H5'	1.93	0.49
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.12	0.49
1:1A:879:G:H8	1:1A:879:G:O5'	1.94	0.49
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.13	0.49
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.45	0.49
32:1a:1279:A:O2'	32:1a:1281:U:OP2	2.22	0.49
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.27	0.49
48:1q:24:GLU:OE2	48:1q:37:LYS:HD2	2.12	0.49
1:2A:30:G:H2'	1:2A:31:C:C6	2.48	0.49
1:2A:746:A:HO2'	1:2A:2611:U:HO2'	1.60	0.49
1:2A:1530:C:N4	1:2A:1539:G:H1	2.10	0.49
1:2A:2012:G:OP1	18:2W:11:ARG:NH2	2.45	0.49
1:2A:2674:G:H2'	1:2A:2675:A:C8	2.48	0.49
5:2F:31:HIS:NE2	5:2F:35:GLU:OE2	2.45	0.49
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.11	0.49
21:2Z:7:ALA:HB2	21:2Z:59:LEU:HD22	1.93	0.49
40:2i:79:LEU:HD22	40:2i:104:ARG:HB3	1.93	0.49
1:1A:2279:G:O6	22:10:14:ARG:HG3	2.13	0.49
2:1B:24:G:N7	2:1B:56:G:H2'	2.27	0.49
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	1.93	0.49
21:1Z:28:MET:HE2	21:1Z:59:LEU:HD13	1.94	0.49
38:1g:76:ARG:HD2	38:1g:156:TRP:HZ2	1.76	0.49
54:1y:69:G:H2'	54:1y:70:G:O4'	2.13	0.49
1:2A:111:A:O3'	24:22:65:ASN:ND2	2.40	0.49
2:2B:2:C:H2'	2:2B:3:C:H6	1.77	0.49
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.48	0.49
12:2Q:138:ASP:CG	21:2Z:81:ARG:HH12	2.21	0.49
32:2a:1233:G:H2'	32:2a:1234:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.42	0.49
37:2f:42:GLU:OE2	37:2f:59:TYR:OH	2.24	0.49
46:2o:40:SER:O	46:2o:44:LYS:HG3	2.11	0.49
1:1A:2134:A:O2'	1:1A:2135:A:OP1	2.29	0.49
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.76	0.49
5:1F:33:LEU:HB3	11:1P:6:LEU:HD21	1.95	0.49
5:1F:161:GLU:HG2	5:1F:164:ARG:NH2	2.27	0.49
32:1a:613:C:H2'	32:1a:614:A:C8	2.47	0.49
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.48	0.49
40:1i:28:VAL:HG22	40:1i:63:ILE:HB	1.93	0.49
54:1w:22:G:O2'	54:1w:23:A:OP1	2.27	0.49
1:2A:1951:U:O2'	1:2A:1953:A:N7	2.43	0.49
1:2A:2006:C:O2'	1:2A:2823:A:N3	2.45	0.49
1:2A:2748:A:H2'	1:2A:2749:A:C8	2.47	0.49
21:2Z:145:GLU:HB3	21:2Z:148:ASP:HB2	1.94	0.49
26:24:64:GLY:O	26:24:66:SER:N	2.39	0.49
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.48	0.49
34:2c:120:VAL:HA	34:2c:123:GLN:HB2	1.95	0.49
35:2d:12:CYS:O	35:2d:16:GLY:N	2.41	0.49
45:2n:24:CYS:HA	45:2n:38:GLY:O	2.13	0.49
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.94	0.49
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.76	0.49
32:1a:171:A:H2'	32:1a:172:A:C8	2.48	0.49
32:1a:194:C:H2'	32:1a:195:A:H5''	1.95	0.49
32:1a:1030(A):G:H2'	32:1a:1030(C):G:OP2	2.13	0.49
32:1a:1135:U:O2'	32:1a:1138:G:O6	2.29	0.49
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.13	0.49
48:1q:67:LYS:HA	48:1q:70:ARG:HH12	1.76	0.49
50:1s:27:GLU:CD	50:1s:27:GLU:H	2.20	0.49
1:2A:309:G:N3	1:2A:329:G:O2'	2.43	0.49
1:2A:1019:U:OP1	1:2A:1035:U:O2'	2.24	0.49
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.48	0.49
1:2A:2506:U:H1'	57:2A:3670:4M2:H29	1.92	0.49
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.13	0.49
21:2Z:28:MET:HA	21:2Z:88:PHE:O	2.12	0.49
32:2a:165:C:H2'	32:2a:166:G:C8	2.47	0.49
32:2a:429:U:H3'	35:2d:9:CYS:SG	2.52	0.49
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.27	0.49
32:2a:1296:C:H5''	44:2m:44:ARG:HH22	1.77	0.49
33:2b:74:LYS:HG3	33:2b:77:ALA:HB3	1.94	0.49
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.34	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:674:G:H1'	5:1F:74:ARG:HD2	1.94	0.49
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.12	0.49
24:12:17:SER:N	24:12:20:GLU:OE2	2.39	0.49
32:1a:148:G:H2'	32:1a:149:A:C8	2.46	0.49
32:1a:280:C:N3	48:1q:39:SER:N	2.57	0.49
1:2A:288:C:H2'	1:2A:289:A:C8	2.48	0.49
1:2A:373:U:H2'	1:2A:374:A:C8	2.47	0.49
1:2A:1448:G:H5''	1:2A:1542:A:OP1	2.12	0.49
1:2A:1688:U:H1'	1:2A:1701:A:C6	2.48	0.49
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.24	0.49
1:2A:2112:G:H2'	1:2A:2113:U:O4'	2.13	0.49
2:2B:11:C:H3'	2:2B:12:C:H6	1.77	0.49
5:2F:110:LEU:HD21	5:2F:181:LEU:HD23	1.95	0.49
23:21:3:LYS:HB2	23:21:61:ARG:HH11	1.78	0.49
32:2a:523:A:N1	43:2l:92:0TD:H6	2.28	0.49
32:2a:678:U:H2'	32:2a:679:C:C6	2.47	0.49
33:2b:48:MET:HG3	33:2b:49:GLU:N	2.27	0.49
33:2b:76:GLN:HG3	33:2b:206:ASP:O	2.13	0.49
35:2d:172:PRO:C	35:2d:174:LEU:H	2.20	0.49
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.78	0.49
1:1A:1093:G:H3'	1:1A:1094:U:H5''	1.94	0.49
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.78	0.49
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.94	0.49
32:1a:110:C:H2'	32:1a:111:G:O4'	2.13	0.49
32:1a:526:C:OP2	43:1l:91:LYS:HE3	2.13	0.49
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.48	0.49
33:1b:212:GLN:OE1	33:1b:216:SER:HB3	2.13	0.49
36:1e:101:ILE:O	36:1e:120:THR:OG1	2.31	0.49
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.36	0.49
1:2A:373:U:H2'	1:2A:374:A:H8	1.77	0.49
1:2A:863:A:H2'	1:2A:864:G:C8	2.48	0.49
1:2A:1470:G:H5''	1:2A:1471:A:OP1	2.13	0.49
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.48	0.49
1:2A:2243:U:O4	62:2A:9743:HOH:O	2.18	0.49
1:2A:2320:A:H61	1:2A:2333:A:H2'	1.77	0.49
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.77	0.49
5:2F:187:VAL:HG12	11:2P:3:LEU:HD12	1.95	0.49
32:2a:693:G:H2'	32:2a:694:A:C8	2.48	0.49
40:2i:77:ILE:O	40:2i:81:ILE:HG12	2.13	0.49
41:2j:44:VAL:HG13	41:2j:66:ARG:HG2	1.94	0.49
1:1A:918:A:H5''	2:1B:98:G:O2'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2857:G:N2	1:1A:2860:A:OP2	2.37	0.49
40:1i:23:ASN:ND2	40:1i:23:ASN:H	2.10	0.49
41:1j:55:LYS:O	41:1j:57:LYS:N	2.46	0.49
1:2A:883:G:O2'	1:2A:884:C:OP1	2.30	0.49
1:2A:1430:C:H2'	1:2A:1431:U:H6	1.78	0.49
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.42	0.49
1:2A:2218:U:N3	23:21:55:GLY:O	2.46	0.49
11:2P:81:GLN:NE2	11:2P:105:LEU:O	2.46	0.49
20:2Y:37:VAL:HG21	20:2Y:72:VAL:HG21	1.94	0.49
32:2a:757:U:H2'	32:2a:758:G:O4'	2.12	0.49
32:2a:1220:G:O3'	50:2s:36:ARG:HD3	2.13	0.49
32:2a:1274:G:N2	32:2a:1275:A:N7	2.61	0.49
40:2i:53:VAL:O	40:2i:55:ALA:N	2.41	0.49
44:2m:79:LYS:NZ	44:2m:83:ASP:OD2	2.45	0.49
1:1A:1590:U:H2'	1:1A:1591:G:C8	2.48	0.49
4:1E:29:GLY:HA3	62:1E:401:HOH:O	2.13	0.49
32:1a:60:A:H4'	32:1a:61:G:H5'	1.95	0.49
32:1a:390:C:H2'	32:1a:391:G:C8	2.48	0.49
32:1a:812:C:O2	62:1a:1908:HOH:O	2.19	0.49
32:1a:982:U:H5''	45:1n:6:LEU:HD21	1.95	0.49
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.61	0.49
1:2A:141:A:H8	1:2A:1408:C:O2'	1.96	0.49
1:2A:372:G:O2'	1:2A:400:G:O6	2.29	0.49
1:2A:848:G:C4	1:2A:933:A:C8	2.99	0.49
1:2A:1235:G:C6	1:2A:1236:G:N1	2.80	0.49
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.13	0.49
1:2A:2149:G:H3'	1:2A:2150:U:O4'	2.13	0.49
1:2A:2771:C:H5''	4:2E:202:LYS:HD3	1.95	0.49
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.45	0.49
21:2Z:149:SER:OG	21:2Z:150:LEU:N	2.40	0.49
32:2a:1137:C:H5''	32:2a:1138:G:OP1	2.13	0.49
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.48	0.49
34:2c:56:ASP:HB2	34:2c:67:THR:HB	1.95	0.49
39:2h:86:ILE:HG13	39:2h:133:LEU:HD22	1.95	0.49
44:2m:3:ARG:NH2	44:2m:11:ARG:HE	2.11	0.49
1:1A:910:A:N1	1:1A:2277:G:H1'	2.28	0.48
1:1A:1094:U:H3	1:1A:1096:A:H3'	1.78	0.48
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.13	0.48
1:1A:1686:C:H2'	1:1A:1687:G:O4'	2.13	0.48
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.48	0.48
32:1a:730:G:C5	32:1a:731:G:H1'	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1038:C:C2'	32:1a:1039:C:H5'	2.43	0.48
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.48	0.48
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.95	0.48
54:1y:40:C:H2'	54:1y:41:C:H6	1.78	0.48
54:1y:63:G:H2'	54:1y:64:A:O4'	2.12	0.48
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.48	0.48
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.13	0.48
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.78	0.48
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.12	0.48
1:2A:2140:C:H2'	1:2A:2141:G:H5'	1.93	0.48
1:2A:2584:U:H2'	1:2A:2585:U:C6	2.48	0.48
1:2A:2742:C:OP1	31:29:35:ARG:HD3	2.13	0.48
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.95	0.48
3:2D:166:GLN:HB2	3:2D:174:ILE:HG22	1.94	0.48
9:2N:21:LYS:NZ	9:2N:140:VAL:OXT	2.43	0.48
28:26:19:ARG:NH2	28:26:52:VAL:HG11	2.27	0.48
32:2a:979:C:O2	45:2n:19:ARG:HG2	2.13	0.48
32:2a:1136:U:H5''	32:2a:1137:C:C5	2.47	0.48
33:2b:188:ALA:HB1	33:2b:192:SER:OG	2.13	0.48
35:2d:25:ARG:O	35:2d:28:SER:HB3	2.13	0.48
54:2w:24:G:H2'	54:2w:25:C:O4'	2.13	0.48
4:1E:24:THR:HG22	4:1E:186:GLY:O	2.12	0.48
5:1F:110:LEU:HA	5:1F:183:VAL:HG12	1.96	0.48
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.48	0.48
37:1f:91:VAL:HG11	49:1r:72:ARG:HH12	1.78	0.48
1:2A:184:C:H2'	1:2A:185:U:C6	2.48	0.48
1:2A:882:G:H1	1:2A:894:C:H42	1.60	0.48
1:2A:1013:C:H2'	1:2A:1014:U:H6	1.78	0.48
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.48	0.48
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.13	0.48
1:2A:2870:C:H5''	13:2R:65:LEU:HD21	1.95	0.48
4:2E:19:ARG:NH1	10:2O:72:PRO:HB3	2.28	0.48
54:2w:75:C:H4'	54:2w:76:A:OP2	2.13	0.48
1:1A:1213:A:N3	1:1A:1238:G:O2'	2.34	0.48
1:1A:1636:C:H2'	1:1A:1637:A:C8	2.48	0.48
1:1A:1913:A:N1	54:1w:37:MIA:O2'	2.45	0.48
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.49	0.48
1:1A:2742:C:OP1	31:19:35:ARG:HD3	2.13	0.48
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.93	0.48
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.95	0.48
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:62:LEU:HD11	17:1V:95:LEU:HB2	1.95	0.48
18:1W:25:ARG:NH2	18:1W:74:ALA:O	2.43	0.48
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.47	0.48
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.45	0.48
35:1d:63:LYS:HD2	35:1d:198:VAL:HG22	1.96	0.48
41:1j:38:ILE:HD11	41:1j:71:LEU:HD23	1.96	0.48
44:1m:15:VAL:HG23	44:1m:43:THR:O	2.12	0.48
2:2B:1:U:H2'	2:2B:2:C:C6	2.48	0.48
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.25	0.48
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.95	0.48
8:2I:116:LEU:HD11	8:2I:120:ILE:HG13	1.95	0.48
9:2N:58:ASP:N	9:2N:58:ASP:OD1	2.44	0.48
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.41	0.48
32:2a:266:G:H2'	32:2a:266:G:N3	2.28	0.48
32:2a:642:A:N3	39:2h:113:SER:OG	2.45	0.48
32:2a:1178:G:N2	32:2a:1180:A:H3'	2.28	0.48
38:2g:69:VAL:HG21	38:2g:104:LEU:HD13	1.95	0.48
39:2h:110:ALA:O	39:2h:120:THR:HA	2.13	0.48
1:1A:289:A:H2'	1:1A:290:G:O4'	2.13	0.48
1:1A:796:C:H2'	1:1A:797:C:C6	2.48	0.48
1:1A:1065:U:H1'	1:1A:1074:G:N1	2.28	0.48
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.94	0.48
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.14	0.48
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.13	0.48
32:1a:491:G:H2'	32:1a:492:G:O4'	2.12	0.48
32:1a:738:C:H5''	37:1f:69:GLU:HB2	1.94	0.48
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.48	0.48
36:1e:85:GLY:C	36:1e:87:SER:H	2.19	0.48
51:1t:9:ASN:OD1	51:1t:10:LEU:N	2.42	0.48
1:2A:224:G:H2'	1:2A:225:A:O4'	2.13	0.48
1:2A:832:G:OP1	62:2A:9756:HOH:O	2.20	0.48
2:2B:1:U:O2'	2:2B:2:C:O5'	2.24	0.48
7:2H:98:LEU:HD11	7:2H:124:GLU:HA	1.96	0.48
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.96	0.48
16:2U:50:ARG:HH12	17:2V:72:VAL:HA	1.79	0.48
32:2a:107:G:H2'	32:2a:108:G:O4'	2.14	0.48
32:2a:428:G:OP2	35:2d:10:ARG:NH1	2.46	0.48
34:2c:52:LEU:HD21	34:2c:55:VAL:HG23	1.95	0.48
37:2f:12:PRO:HG2	37:2f:13:ASN:HD22	1.77	0.48
48:2q:60:ILE:HB	48:2q:74:LEU:HD12	1.95	0.48
1:1A:331:A:N1	62:1A:4122:HOH:O	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:954:G:H5''	12:1Q:13:GLN:HB3	1.95	0.48
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.49	0.48
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.31	0.48
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.48	0.48
25:13:3:ARG:HD3	25:13:60:GLU:CD	2.38	0.48
32:1a:159:G:N2	32:1a:161:A:H3'	2.29	0.48
32:1a:262:A:H2'	32:1a:263:A:C8	2.48	0.48
35:1d:166:LYS:NZ	35:1d:179:GLU:OE2	2.47	0.48
55:1x:23:C:H2'	55:1x:24:U:C6	2.49	0.48
1:2A:921:G:H4'	1:2A:2269:A:C5	2.48	0.48
1:2A:1376:C:OP1	62:2A:9755:HOH:O	2.20	0.48
1:2A:1501:C:H2'	1:2A:1502:C:C6	2.47	0.48
1:2A:2121:G:H1	1:2A:2177:C:N4	2.09	0.48
1:2A:2154:G:H2'	1:2A:2155:G:H5''	1.94	0.48
6:2G:25:TYR:HB3	6:2G:30:GLU:HB2	1.95	0.48
6:2G:106:LEU:O	6:2G:110:ALA:HB3	2.14	0.48
32:2a:431:A:H2'	32:2a:432:A:O4'	2.13	0.48
32:2a:659:U:H2'	32:2a:660:G:C8	2.48	0.48
1:1A:579:G:H2'	1:1A:580:C:C6	2.49	0.48
1:1A:1231:G:H2'	1:1A:1232:G:C8	2.49	0.48
1:1A:1993:U:OP2	62:1A:4045:HOH:O	2.20	0.48
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.48	0.48
8:1I:77:LEU:HD11	8:1I:101:LEU:HB2	1.95	0.48
32:1a:1127:G:H5'	32:1a:1280:A:O2'	2.14	0.48
32:1a:1239:A:H62	32:1a:1299:A:H62	1.60	0.48
36:1e:102:ALA:HB1	36:1e:106:PRO:HB2	1.95	0.48
39:1h:81:HIS:HB2	39:1h:138:TRP:CD1	2.48	0.48
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.46	0.48
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.13	0.48
14:2S:15:ARG:O	14:2S:19:LYS:HD2	2.14	0.48
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.96	0.48
32:2a:67:C:H2'	32:2a:68:G:H8	1.77	0.48
32:2a:1029:C:N3	32:2a:1032:G:C2	2.81	0.48
34:2c:121:ALA:HB2	34:2c:198:VAL:HG21	1.96	0.48
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.13	0.48
54:2w:61:C:HO2'	54:2w:62:C:H6	1.62	0.48
1:1A:1740:G:H2'	1:1A:1741:A:C8	2.49	0.48
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.24	0.48
6:1G:47:LYS:O	6:1G:51:ARG:HG2	2.14	0.48
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.96	0.48
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:407:G:H2'	1:2A:408:G:C8	2.49	0.48
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.13	0.48
2:2B:42:C:O2'	6:2G:67:LYS:O	2.21	0.48
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.96	0.48
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.47	0.48
32:2a:229:U:H5''	47:2p:33:ILE:HD13	1.96	0.48
32:2a:978:A:O2'	32:2a:1322:C:N3	2.46	0.48
32:2a:1119:C:OP2	40:2i:9:ARG:NH1	2.37	0.48
35:2d:26:CYS:HA	35:2d:31:CYS:SG	2.53	0.48
1:1A:1359:A:C2	1:1A:1372:U:O4	2.66	0.48
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.78	0.48
1:1A:2794:C:N4	1:1A:2802:G:H22	2.11	0.48
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.96	0.48
9:1N:48:MET:HG2	9:1N:48:MET:O	2.14	0.48
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.96	0.48
1:2A:897:C:H3'	1:2A:898:C:C6	2.48	0.48
1:2A:2033:A:O2'	1:2A:2035:G:OP2	2.26	0.48
1:2A:2144:U:H1'	1:2A:2148:G:H22	1.78	0.48
1:2A:2336:A:H61	22:20:43:THR:HG21	1.77	0.48
2:2B:24:G:N7	2:2B:56:G:H2'	2.29	0.48
2:2B:95:C:H2'	2:2B:96:U:H6	1.79	0.48
24:22:46:GLN:HB3	24:22:49:LYS:HD3	1.96	0.48
25:23:4:LEU:O	25:23:36:VAL:HA	2.14	0.48
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.02	0.48
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.13	0.48
1:1A:897:C:H5'	54:1w:56:C:OP1	2.14	0.48
7:1H:133:VAL:HG12	7:1H:141:VAL:HG13	1.95	0.48
8:1I:76:THR:HG22	8:1I:141:LYS:HB2	1.95	0.48
33:1b:8:LYS:HB2	33:1b:48:MET:HE1	1.96	0.48
33:1b:44:LEU:HA	33:1b:47:THR:OG1	2.14	0.48
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.14	0.48
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.96	0.48
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	1.95	0.48
41:1j:5:ARG:HH21	41:1j:73:ASP:CG	2.20	0.48
1:2A:812:C:H2'	1:2A:813:U:H6	1.77	0.48
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.95	0.48
1:2A:2835:A:N3	62:2A:9845:HOH:O	2.35	0.48
3:2D:69:ARG:NH1	3:2D:105:ILE:HD13	2.29	0.48
21:2Z:5:LEU:HD11	21:2Z:44:PHE:HA	1.96	0.48
21:2Z:50:GLN:OE1	21:2Z:50:GLN:N	2.47	0.48
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.49	0.48
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.95	0.48
35:2d:61:LYS:HD2	35:2d:207:TYR:OH	2.13	0.48
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.96	0.48
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.78	0.48
54:2y:42:C:H2'	54:2y:43:C:C6	2.48	0.48
1:1A:2451:A:C6	57:1A:3894:4M2:H30	2.49	0.48
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.49	0.48
1:1A:2732:G:H3'	1:1A:2733:A:O4'	2.14	0.48
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.94	0.48
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.79	0.48
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.96	0.48
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.94	0.48
32:1a:380:G:N2	32:1a:383:A:OP2	2.46	0.48
32:1a:501:C:H2'	32:1a:502:G:C8	2.49	0.48
32:1a:1030(A):G:O2'	32:1a:1031:G:N2	2.47	0.48
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.79	0.48
39:1h:86:ILE:HG12	39:1h:135:CYS:HA	1.96	0.48
1:2A:359:A:H2'	1:2A:360:G:O4'	2.14	0.48
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.29	0.48
3:2D:71:ASP:CB	3:2D:103:ARG:HH12	2.27	0.48
3:2D:275:LYS:HA	3:2D:276:LYS:C	2.38	0.48
7:2H:73:ALA:O	7:2H:76:VAL:HG22	2.13	0.48
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.96	0.48
34:2c:10:PHE:HD1	45:2n:58:LYS:HE2	1.77	0.48
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.44	0.48
55:2x:49:G:N2	55:2x:65:C:N3	2.55	0.48
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.49	0.47
1:1A:2182:G:H2'	1:1A:2183:C:C6	2.49	0.47
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.29	0.47
7:1H:125:VAL:HG22	7:1H:131:VAL:HG22	1.95	0.47
8:1I:72:LEU:C	8:1I:74:ASN:N	2.72	0.47
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.96	0.47
14:1S:25:ARG:HD3	14:1S:42:ASP:OD2	2.12	0.47
32:1a:648:A:H2'	32:1a:649:G:C8	2.49	0.47
32:1a:701:C:OP1	32:1a:702:A:O2'	2.26	0.47
32:1a:1429:C:H2'	32:1a:1430:C:H6	1.78	0.47
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.47	0.47
1:2A:981:A:N1	1:2A:2027:G:O2'	2.42	0.47
1:2A:1364:G:P	23:21:3:LYS:HG3	2.53	0.47
1:2A:2099:U:H2'	1:2A:2100:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2322:A:H2'	1:2A:2323:G:O4'	2.14	0.47
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.95	0.47
7:2H:149:ARG:NH2	7:2H:167:GLU:OE2	2.47	0.47
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.78	0.47
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.47	0.47
12:2Q:1:MET:HG3	12:2Q:44:ALA:HB1	1.95	0.47
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.15	0.47
1:1A:39:C:O2	5:1F:46:ARG:NH2	2.39	0.47
1:1A:247:G:H4'	1:1A:386:G:C5	2.49	0.47
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.49	0.47
1:1A:1540:U:H2'	1:1A:1541:G:O4'	2.14	0.47
1:1A:2404:C:O3'	11:1P:77:ARG:NH2	2.47	0.47
5:1F:140:LEU:HD11	5:1F:170:LEU:HD11	1.96	0.47
24:12:16:LEU:O	24:12:67:LYS:NZ	2.48	0.47
32:1a:881:G:H2'	32:1a:882:C:O4'	2.14	0.47
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.95	0.47
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.14	0.47
40:1i:65:VAL:HG11	40:1i:73:GLN:HB3	1.97	0.47
44:1m:123:ALA:HB2	54:1w:39:PSU:H1'	1.96	0.47
1:2A:1204:A:H2	1:2A:1241:A:N6	2.01	0.47
1:2A:1772:G:OP1	62:2A:9757:HOH:O	2.20	0.47
1:2A:2748:A:H2'	1:2A:2749:A:H8	1.79	0.47
21:2Z:163:LEU:HG	21:2Z:165:VAL:HG22	1.96	0.47
32:2a:636:U:H2'	32:2a:637:G:H8	1.79	0.47
1:1A:36:G:N3	1:1A:450:G:O2'	2.48	0.47
1:1A:303:U:H2'	1:1A:304:G:H8	1.79	0.47
1:1A:721:C:H2'	1:1A:722:A:C8	2.49	0.47
1:1A:1064:C:N3	1:1A:1074:G:O6	2.47	0.47
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.49	0.47
1:1A:2573:C:H3'	62:1A:4036:HOH:O	2.14	0.47
32:1a:626:U:H2'	32:1a:627:G:H8	1.80	0.47
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.48	0.47
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.30	0.47
1:2A:340:A:H2'	1:2A:341:G:O4'	2.14	0.47
1:2A:994:C:O2'	1:2A:996:A:OP1	2.30	0.47
1:2A:1171:G:N2	1:2A:1178:C:N3	2.45	0.47
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.31	0.47
11:2P:95:VAL:HG13	11:2P:125:VAL:HB	1.97	0.47
32:2a:919:A:O2'	32:2a:1080:A:N1	2.42	0.47
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.95	0.47
1:1A:949:C:N4	62:1A:4092:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1039:G:H1	1:1A:1116:C:H42	1.62	0.47
4:1E:2:LYS:HG2	4:1E:200:GLU:HB2	1.96	0.47
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.45	0.47
19:1X:35:THR:HG22	19:1X:37:THR:H	1.79	0.47
32:1a:69:G:H2'	32:1a:70:G:C8	2.48	0.47
32:1a:1284:C:OP2	32:1a:1285:A:O2'	2.32	0.47
36:1e:91:LEU:HD12	36:1e:120:THR:HG22	1.95	0.47
54:1w:72:C:H5'	54:1w:73:A:OP2	2.13	0.47
1:2A:725:G:H8	1:2A:725:G:O5'	1.97	0.47
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.14	0.47
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.15	0.47
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.49	0.47
1:2A:2161:C:H2'	1:2A:2162:G:C8	2.50	0.47
3:2D:37:LEU:HD13	3:2D:87:ASN:ND2	2.28	0.47
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.49	0.47
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.96	0.47
1:1A:222:A:H5''	1:1A:421:U:OP1	2.14	0.47
54:1w:1:G:H1	54:1w:72:C:N4	2.12	0.47
54:1y:19:G:H4'	54:1y:20:U:OP2	2.13	0.47
1:2A:493:G:OP1	62:2A:9754:HOH:O	2.20	0.47
1:2A:521:G:H2'	1:2A:522:G:C8	2.49	0.47
1:2A:2155:G:H5'	1:2A:2155:G:H8	1.79	0.47
1:2A:2635:C:OP1	4:2E:79:ARG:NH1	2.38	0.47
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.44	0.47
32:2a:814:A:H2'	32:2a:816:A:H5''	1.96	0.47
32:2a:840:C:H4'	32:2a:841:U:OP1	2.13	0.47
34:2c:123:GLN:HA	34:2c:126:ARG:HH11	1.80	0.47
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	1.95	0.47
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.79	0.47
47:2p:56:ALA:O	47:2p:60:LEU:HB2	2.15	0.47
48:2q:10:VAL:HG13	48:2q:19:VAL:HB	1.96	0.47
54:2y:62:C:H2'	54:2y:63:G:H8	1.79	0.47
1:1A:464:U:H2'	1:1A:465:G:O4'	2.14	0.47
1:1A:744:G:OP1	62:1A:4044:HOH:O	2.20	0.47
1:1A:1913:A:C6	54:1w:38:A:H5'	2.49	0.47
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.12	0.47
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.14	0.47
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.95	0.47
25:13:39:ASP:OD1	25:13:44:ARG:NH1	2.48	0.47
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.24	0.47
32:1a:1131:G:P	40:1i:20:ARG:HH22	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:16:ARG:HH11	40:1i:64:THR:HB	1.80	0.47
43:1l:33:ARG:HD2	43:1l:33:ARG:HA	1.65	0.47
54:1y:6:G:O6	54:1y:7:A:N6	2.48	0.47
1:2A:1171:G:H1	1:2A:1178:C:N4	2.05	0.47
1:2A:2722:G:H5'	13:2R:4:LEU:HD12	1.96	0.47
1:2A:2869:G:H2'	1:2A:2870:C:O4'	2.15	0.47
4:2E:52:LEU:O	4:2E:76:ARG:N	2.41	0.47
8:2I:124:GLY:H	8:2I:144:VAL:HG23	1.80	0.47
13:2R:36:THR:HG22	13:2R:37:THR:N	2.28	0.47
32:2a:179:A:H2'	32:2a:180:U:C6	2.49	0.47
32:2a:454:C:N4	32:2a:479:C:N3	2.62	0.47
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.30	0.47
32:2a:1187:G:H5'	40:2i:113:LYS:HE2	1.95	0.47
33:2b:195:ASP:O	39:2h:74:PRO:HG3	2.14	0.47
41:2j:67:THR:O	41:2j:67:THR:OG1	2.30	0.47
51:2t:65:LYS:HA	51:2t:68:LYS:HD3	1.96	0.47
1:1A:210:C:OP1	29:17:29:LYS:HD2	2.15	0.47
1:1A:614(C):A:C4	5:1F:180:GLY:HA2	2.50	0.47
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.15	0.47
1:1A:1889:A:H2'	1:1A:1890:A:C8	2.49	0.47
1:1A:2111:C:OP2	1:1A:2145:C:N4	2.44	0.47
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.49	0.47
1:1A:2572:A:C8	4:1E:144:ARG:HD2	2.49	0.47
2:1B:66:A:H61	2:1B:109:C:H5'	1.79	0.47
32:1a:45:U:H2'	32:1a:46:G:H8	1.78	0.47
32:1a:130:A:O2'	32:1a:131:C:O5'	2.31	0.47
32:1a:1327:C:OP2	52:1u:12:LYS:NZ	2.48	0.47
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.49	0.47
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.96	0.47
36:1e:103:GLY:O	36:1e:106:PRO:HD2	2.14	0.47
44:1m:3:ARG:HG2	44:1m:8:GLU:HA	1.97	0.47
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.79	0.47
54:1y:5:G:H1	54:1y:68:C:H42	1.62	0.47
1:2A:856:C:H2'	1:2A:857:C:C6	2.50	0.47
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.48	0.47
1:2A:1376:C:OP2	62:2A:9758:HOH:O	2.20	0.47
1:2A:1493:C:H5	1:2A:2206:G:H2'	1.79	0.47
1:2A:1762:A:N1	62:2A:9848:HOH:O	2.36	0.47
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.40	0.47
1:2A:1903:G:OP1	3:2D:241:PRO:HB2	2.14	0.47
1:2A:2117:A:O2'	1:2A:2118:U:H5''	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2142:C:H42	1:2A:2150:U:H3	1.61	0.47
1:2A:2199:A:H3'	1:2A:2200:C:C6	2.50	0.47
2:2B:9:G:H1	2:2B:112:U:H3	1.62	0.47
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.14	0.47
5:2F:34:TRP:CE2	11:2P:8:PRO:HG3	2.50	0.47
6:2G:27:ASN:HB3	6:2G:30:GLU:HG3	1.96	0.47
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.28	0.47
21:2Z:126:VAL:HG13	21:2Z:161:VAL:HG23	1.95	0.47
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.95	0.47
32:2a:45:U:H2'	32:2a:46:G:C8	2.50	0.47
32:2a:109:A:H2'	32:2a:326:G:N2	2.29	0.47
32:2a:1028:C:C2	32:2a:1033:G:N1	2.83	0.47
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.96	0.47
33:2b:126:GLU:N	33:2b:126:GLU:OE1	2.47	0.47
40:2i:128:ARG:HH21	55:2x:32:5MC:P	2.37	0.47
41:2j:16:LEU:HD23	41:2j:70:ARG:HG2	1.97	0.47
41:2j:55:LYS:O	41:2j:57:LYS:N	2.48	0.47
46:2o:68:ARG:O	46:2o:71:GLN:HB3	2.14	0.47
54:2w:9:A:H8	54:2w:11:C:H41	1.62	0.47
54:2y:42:C:H2'	54:2y:43:C:H6	1.79	0.47
1:1A:243:U:OP1	30:18:6:THR:OG1	2.25	0.47
1:1A:893:C:H2'	1:1A:894:C:C6	2.50	0.47
1:1A:1030:G:OP2	12:1Q:128:LYS:NZ	2.47	0.47
1:1A:2207:G:H2'	1:1A:2208:A:C2	2.49	0.47
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.50	0.47
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.14	0.47
5:1F:106:ARG:H	5:1F:106:ARG:HG2	1.44	0.47
21:1Z:163:LEU:HD23	21:1Z:167:PRO:HG3	1.96	0.47
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.96	0.47
1:2A:800:A:H8	1:2A:800:A:OP1	1.98	0.47
1:2A:839:U:H2'	1:2A:840:C:H6	1.79	0.47
1:2A:998:C:P	16:2U:92:ARG:HH21	2.37	0.47
1:2A:2129:C:H5'	1:2A:2130:U:OP2	2.15	0.47
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.66	0.47
6:2G:146:TYR:CG	44:2m:8:GLU:HG2	2.50	0.47
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.50	0.47
32:2a:626:U:H2'	32:2a:627:G:H8	1.80	0.47
32:2a:841:U:C5	32:2a:848:C:H1'	2.50	0.47
1:1A:1007:C:OP1	9:1N:37:LYS:NZ	2.47	0.47
32:1a:1262:C:H2'	32:1a:1263:C:C6	2.50	0.47
1:2A:42:G:H2'	1:2A:43:A:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:323:G:H8	5:2F:171:PRO:HG3	1.78	0.47
1:2A:1927:A:C6	1:2A:1928:A:C6	3.02	0.47
1:2A:2141:G:O6	1:2A:2150:U:C2	2.67	0.47
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.50	0.47
1:2A:2512:C:H2'	1:2A:2513:G:O4'	2.14	0.47
10:2O:63:VAL:HB	10:2O:102:VAL:HG12	1.97	0.47
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.49	0.47
26:24:44:THR:O	26:24:46:GLN:N	2.48	0.47
32:2a:730:G:C5	32:2a:731:G:H1'	2.49	0.47
32:2a:1149:C:OP1	40:2i:14:VAL:HG11	2.15	0.47
32:2a:1239:A:H4'	32:2a:1240:U:H5'	1.95	0.47
32:2a:1245:A:N6	32:2a:1291:G:O6	2.48	0.47
34:2c:156:ARG:H	34:2c:196:LEU:HD22	1.80	0.47
38:2g:79:ARG:HG3	38:2g:80:VAL:N	2.29	0.47
47:2p:4:ILE:HB	47:2p:66:PRO:HA	1.97	0.47
54:2y:19:G:C2	54:2y:57:G:C6	3.03	0.47
1:1A:324:A:N6	1:1A:338:G:O2'	2.48	0.47
1:1A:839:U:H2'	1:1A:840:C:C6	2.49	0.47
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.80	0.47
1:1A:1268:A:C2	1:1A:2013:A:C4	3.03	0.47
26:14:16:CYS:HA	26:14:33:VAL:O	2.15	0.47
32:1a:189(F):U:N3	48:1q:72:ARG:NH1	2.63	0.47
32:1a:193:C:H2'	32:1a:194:C:C6	2.50	0.47
32:1a:262:A:C6	32:1a:263:A:C6	3.03	0.47
1:2A:83:G:C2	1:2A:102:G:H1'	2.50	0.47
1:2A:154(A):C:H42	1:2A:171:G:H1	1.62	0.47
1:2A:1421:G:C2	1:2A:1422:G:C8	3.03	0.47
1:2A:1530:C:H1'	1:2A:1531:C:OP1	2.15	0.47
1:2A:1639:U:H4'	1:2A:2699:C:H4'	1.96	0.47
1:2A:2371:G:O2'	28:26:46:HIS:ND1	2.41	0.47
12:2Q:21:THR:HG21	12:2Q:101:ARG:CD	2.45	0.47
31:29:10:ILE:HD12	31:29:32:HIS:HA	1.96	0.47
32:2a:142:G:H2'	32:2a:143:A:H8	1.80	0.47
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.14	0.47
32:2a:1126:U:O4	41:2j:71:LEU:HD22	2.14	0.47
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.15	0.47
38:2g:78:ARG:NH2	38:2g:79:ARG:HH12	2.13	0.47
1:1A:256:A:N3	62:1A:4124:HOH:O	2.36	0.46
1:1A:385:C:O2	11:1P:71:VAL:HG21	2.15	0.46
1:1A:1071:G:OP1	1:1A:1071:G:H3'	2.15	0.46
1:1A:1779:U:H2'	62:1A:4549:HOH:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:1A:3894:4M2:H49	54:1w:76:A:C8	2.50	0.46
2:1B:1:U:H2'	2:1B:2:C:C6	2.50	0.46
2:1B:66:A:H61	2:1B:108:U:H2'	1.80	0.46
32:1a:189(F):U:H3	48:1q:72:ARG:HH12	1.63	0.46
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.49	0.46
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.83	0.46
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.96	0.46
1:2A:247:G:H4'	1:2A:386:G:C5	2.50	0.46
1:2A:859:G:O2'	1:2A:916:G:O6	2.33	0.46
1:2A:863:A:H2'	1:2A:864:G:H8	1.80	0.46
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.30	0.46
1:2A:1545:A:H2'	1:2A:1546:C:O4'	2.15	0.46
1:2A:1637:A:H4'	1:2A:2711:A:O2'	2.14	0.46
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.15	0.46
1:2A:2061:G:H5''	1:2A:2503:2MA:C2	2.45	0.46
1:2A:2274:A:O2'	1:2A:2276:G:OP1	2.30	0.46
32:2a:1147:C:O2	40:2i:16:ARG:NH2	2.48	0.46
32:2a:1292:U:P	38:2g:41:ARG:HH22	2.38	0.46
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.31	0.46
37:2f:100:ASN:HD21	49:2r:23:LYS:HG2	1.80	0.46
40:2i:114:TYR:HB2	41:2j:60:ARG:HD2	1.97	0.46
41:2j:47:PHE:N	41:2j:63:PHE:O	2.44	0.46
42:2k:21:ILE:HD12	42:2k:84:VAL:HG22	1.97	0.46
44:2m:20:THR:HG21	44:2m:27:LYS:HD2	1.95	0.46
54:2w:73:A:H3'	54:2w:74:C:H5''	1.97	0.46
1:1A:871:U:OP1	12:1Q:5:ARG:HG3	2.14	0.46
1:1A:1271:G:OP2	62:1A:4041:HOH:O	2.20	0.46
1:1A:1512:U:H2'	1:1A:1513:C:H6	1.80	0.46
32:1a:93:G:H2'	32:1a:96:U:O4'	2.15	0.46
32:1a:585:G:OP1	48:1q:37:LYS:NZ	2.46	0.46
34:1c:56:ASP:O	34:1c:66:VAL:HA	2.15	0.46
37:1f:33:TYR:HB2	37:1f:75:LEU:HD12	1.97	0.46
42:1k:20:TYR:CZ	42:1k:83:ILE:HD12	2.51	0.46
1:2A:521:G:H2'	1:2A:522:G:H8	1.79	0.46
2:2B:20:C:N4	2:2B:63:G:H1	2.12	0.46
18:2W:1:MET:HE2	18:2W:62:HIS:HB3	1.97	0.46
32:2a:9:G:H2'	32:2a:10:A:H8	1.79	0.46
32:2a:109:A:C6	32:2a:326:G:C6	3.03	0.46
32:2a:266:G:O3'	48:2q:67:LYS:HB2	2.15	0.46
32:2a:1008:C:N4	32:2a:1021:G:H1	2.11	0.46
32:2a:1304:G:C6	32:2a:1305:G:N1	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:134:GLU:O	33:2b:138:LEU:HG	2.15	0.46
34:2c:36:ASP:HA	34:2c:39:ILE:HD12	1.97	0.46
42:2k:59:TYR:CZ	42:2k:63:LEU:HD11	2.51	0.46
43:2l:7:ILE:O	43:2l:11:VAL:HG23	2.15	0.46
54:2w:14:A:H61	54:2w:21:A:H2	1.63	0.46
1:1A:910:A:N3	1:1A:2264:C:O2'	2.44	0.46
1:1A:1371:G:H2'	1:1A:1372:U:C5	2.48	0.46
1:1A:1531:C:N4	1:1A:1538:G:H1	2.12	0.46
1:1A:1740:G:H2'	1:1A:1741:A:H8	1.80	0.46
13:1R:1:MET:HE3	13:1R:1:MET:HB2	1.79	0.46
35:1d:20:TYR:CD1	35:1d:26:CYS:HB3	2.50	0.46
50:1s:19:VAL:HG12	50:1s:23:ASN:HD21	1.81	0.46
54:1w:23:A:H2'	54:1w:24:G:C8	2.51	0.46
1:2A:819:A:C4	1:2A:1189:A:C2	3.04	0.46
1:2A:1805:U:H5''	3:2D:250:TRP:CD2	2.50	0.46
1:2A:2335:A:C8	1:2A:2337:G:C5	3.03	0.46
1:2A:2722:G:H2'	1:2A:2723:C:C6	2.50	0.46
11:2P:45:LEU:HA	11:2P:45:LEU:HD12	1.72	0.46
13:2R:33:ARG:HD2	13:2R:115:GLU:OE1	2.15	0.46
14:2S:26:LEU:HB3	14:2S:87:PHE:HA	1.98	0.46
32:2a:1001:A:C2'	32:2a:1001(A):G:H5''	2.45	0.46
33:2b:16:HIS:CG	33:2b:210:SER:HB3	2.51	0.46
42:2k:81:ASP:OD1	42:2k:107:SER:OG	2.27	0.46
44:2m:85:GLY:HA2	44:2m:93:ARG:HH21	1.80	0.46
1:1A:466:A:N3	1:1A:683:C:H1'	2.30	0.46
1:1A:2136:C:N3	1:1A:2155:G:C2	2.83	0.46
5:1F:28:ILE:O	5:1F:30:PRO:HD3	2.15	0.46
8:1I:109:ILE:HA	8:1I:109:ILE:HD13	1.71	0.46
30:18:42:ARG:HD2	62:18:206:HOH:O	2.15	0.46
32:1a:523:A:N1	43:1l:92:OTD:H6	2.31	0.46
32:1a:1376:U:H2'	32:1a:1377:A:H8	1.81	0.46
47:1p:20:VAL:HG21	47:1p:32:TYR:CG	2.50	0.46
55:1x:61:C:H2'	55:1x:62:C:H6	1.80	0.46
1:2A:265:A:H1'	1:2A:266:G:O4'	2.15	0.46
1:2A:383:U:H2'	1:2A:385:C:H5	1.80	0.46
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.29	0.46
38:2g:115:ARG:HB2	38:2g:118:VAL:HG23	1.97	0.46
38:2g:115:ARG:O	38:2g:119:ARG:HG3	2.15	0.46
54:2y:62:C:H2'	54:2y:63:G:C8	2.51	0.46
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.14	0.46
1:1A:1432:C:H2'	1:1A:1433:U:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2405:G:O2'	1:1A:2406:U:OP1	2.29	0.46
1:1A:2801(A):A:N3	1:1A:2895:U:H1'	2.30	0.46
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.50	0.46
19:1X:94:GLY:HA3	19:1X:95:LEU:HB2	1.97	0.46
32:1a:828:A:H2'	32:1a:829:G:O4'	2.15	0.46
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.49	0.46
32:1a:1124:G:H5''	41:1j:35:SER:OG	2.15	0.46
32:1a:1162:C:N4	32:1a:1174:G:H1	2.14	0.46
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.50	0.46
38:1g:23:VAL:O	38:1g:27:ILE:HG12	2.15	0.46
1:2A:272(H):C:H2'	1:2A:272(I):U:C6	2.51	0.46
1:2A:568:U:O4	62:2A:9746:HOH:O	2.18	0.46
1:2A:571:A:N6	1:2A:2499:C:O3'	2.48	0.46
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.50	0.46
1:2A:2125:G:H21	1:2A:2173:A:H62	1.62	0.46
32:2a:302:G:N3	32:2a:556:C:H4'	2.30	0.46
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.51	0.46
47:2p:68:ASP:O	47:2p:71:ARG:HB3	2.16	0.46
1:1A:715:G:C2	46:1o:56:LEU:HD21	2.51	0.46
1:1A:1047:G:O2'	1:1A:1048:A:H8	1.99	0.46
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.15	0.46
1:1A:2160:G:O6	1:1A:2161:C:N4	2.49	0.46
5:1F:123:LEU:HD13	5:1F:192:LEU:HD13	1.96	0.46
24:12:1:MET:HE3	24:12:5:GLU:HB3	1.96	0.46
32:1a:1429:C:H2'	32:1a:1430:C:C6	2.51	0.46
33:1b:146:GLN:O	33:1b:150:SER:HB3	2.15	0.46
34:1c:131:ARG:NH1	34:1c:166:GLU:OE2	2.48	0.46
45:1n:48:ALA:HB2	45:1n:53:LEU:HD12	1.97	0.46
1:2A:1403:C:OP1	1:2A:1520:G:N2	2.23	0.46
1:2A:2287:A:N6	1:2A:2344:U:H3	2.07	0.46
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.16	0.46
5:2F:130:ALA:H	5:2F:142:TRP:CD1	2.33	0.46
6:2G:125:PHE:CE2	6:2G:170:ARG:HB2	2.50	0.46
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.16	0.46
23:21:64:ALA:HA	23:21:67:ILE:HG13	1.96	0.46
26:24:16:CYS:SG	26:24:17:GLY:N	2.88	0.46
32:2a:828:A:OP1	39:2h:21:LYS:NZ	2.49	0.46
32:2a:1314:C:N4	50:2s:2:PRO:O	2.42	0.46
33:2b:178:ARG:NH2	39:2h:71:GLY:O	2.47	0.46
34:2c:125:GLU:C	34:2c:127:ARG:H	2.24	0.46
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1055:G:H3'	1:1A:1056:G:H8	1.81	0.46
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.77	0.46
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.50	0.46
19:1X:94:GLY:CA	19:1X:95:LEU:HB2	2.45	0.46
32:1a:840:C:H4'	32:1a:841:U:OP1	2.16	0.46
32:1a:1169:A:H2'	32:1a:1170:A:C8	2.50	0.46
33:1b:178:ARG:HB3	39:1h:72:PRO:HA	1.97	0.46
1:2A:307:G:N1	1:2A:310:A:OP2	2.47	0.46
1:2A:686:G:N2	1:2A:788:A:H61	2.13	0.46
1:2A:1005:C:O2'	9:2N:28:THR:HG21	2.16	0.46
1:2A:1006:C:C2	1:2A:1138:G:N2	2.84	0.46
3:2D:8:PRO:HB3	3:2D:14:ARG:HB2	1.97	0.46
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.96	0.46
32:2a:1133:G:C4	32:2a:1134:G:C8	3.04	0.46
32:2a:1388:C:H2'	32:2a:1389:C:H6	1.79	0.46
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.51	0.46
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.16	0.46
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.98	0.46
38:2g:97:GLN:HE21	38:2g:101:LEU:HD11	1.80	0.46
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.96	0.46
39:2h:37:ARG:NH2	39:2h:38:ILE:HD11	2.31	0.46
44:2m:3:ARG:HH22	44:2m:11:ARG:HG2	1.81	0.46
54:2w:41:C:H2'	54:2w:42:C:C6	2.50	0.46
54:2y:49:C:N3	54:2y:65:G:N2	2.63	0.46
1:1A:303:U:H2'	1:1A:304:G:C8	2.50	0.46
1:1A:559:G:H22	16:1U:49:HIS:CE1	2.34	0.46
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.15	0.46
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.63	0.46
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.97	0.46
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.76	0.46
32:1a:1162:C:H42	32:1a:1174:G:H1	1.62	0.46
33:1b:15:VAL:HG21	33:1b:213:LEU:HD13	1.98	0.46
39:1h:81:HIS:N	39:1h:138:TRP:O	2.48	0.46
1:2A:390:A:N6	62:2A:9925:HOH:O	2.48	0.46
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.16	0.46
1:2A:895:U:O3'	1:2A:896:A:H3'	2.16	0.46
1:2A:954:G:H5''	12:2Q:13:GLN:HB3	1.97	0.46
1:2A:2126:A:N3	1:2A:2127:G:H1'	2.31	0.46
2:2B:32:C:C2	2:2B:51:G:C2	3.04	0.46
5:2F:102:PRO:HB2	5:2F:105:VAL:HG23	1.97	0.46
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.74	0.46
32:2a:80:G:H1	32:2a:89:C:H42	1.63	0.46
32:2a:153:C:H2'	32:2a:154:C:C6	2.51	0.46
32:2a:491:G:H2'	32:2a:492:G:O4'	2.16	0.46
32:2a:1425:U:H2'	32:2a:1426:C:C6	2.51	0.46
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.96	0.46
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.97	0.46
1:1A:1252:G:N2	16:1U:37:GLU:OE2	2.43	0.46
1:1A:1759:A:H1'	1:1A:2711:A:C2	2.50	0.46
1:1A:2267:A:H5''	1:1A:2268:A:H5'	1.97	0.46
1:1A:2570:G:H2'	1:1A:2571:C:O4'	2.16	0.46
1:1A:2612:C:OP2	27:15:2:ALA:N	2.49	0.46
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.16	0.46
29:17:24:THR:O	29:17:28:ARG:HG3	2.15	0.46
32:1a:62:U:O2'	32:1a:379:C:O2	2.26	0.46
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.31	0.46
32:1a:445:G:H2'	32:1a:446:G:H8	1.80	0.46
48:1q:62:SER:HB3	48:1q:72:ARG:NH1	2.30	0.46
1:2A:407:G:H2'	1:2A:408:G:H8	1.81	0.46
1:2A:705:A:C2	1:2A:727:A:H1'	2.50	0.46
1:2A:925:C:H2'	1:2A:926:A:H8	1.81	0.46
1:2A:974:G:C4	1:2A:989:G:C2	3.04	0.46
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.47	0.46
1:2A:1297:C:H2'	1:2A:1298:C:C6	2.51	0.46
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.32	0.46
1:2A:2134:A:H3'	1:2A:2135:A:C8	2.50	0.46
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.50	0.46
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.16	0.46
6:2G:123:ASN:C	6:2G:125:PHE:H	2.23	0.46
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE2	1.97	0.46
32:2a:293:G:H5'	32:2a:610:G:N2	2.31	0.46
32:2a:924:C:H42	32:2a:1392:G:H1	1.63	0.46
32:2a:986:A:H1'	50:2s:55:LYS:HA	1.97	0.46
32:2a:1038:C:C2	32:2a:1039:C:C5	3.03	0.46
54:2y:69:G:H2'	54:2y:70:G:O4'	2.16	0.46
1:1A:422:A:H2'	1:1A:423:A:C8	2.51	0.46
1:1A:1710:C:O2'	1:1A:2858:C:N3	2.41	0.46
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.29	0.46
5:1F:164:ARG:O	5:1F:168:ARG:HB2	2.15	0.46
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.97	0.46
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.56	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:74:LYS:NZ	33:1b:205:ASP:OD2	2.49	0.46
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.51	0.46
40:1i:4:TYR:CZ	40:1i:88:TYR:HD1	2.34	0.46
1:2A:576:U:H2'	1:2A:577:G:C8	2.51	0.46
1:2A:625:G:N7	11:2P:107:LYS:NZ	2.55	0.46
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.51	0.46
2:2B:80:U:O2'	2:2B:81:G:H8	1.99	0.46
11:2P:21:ARG:HA	11:2P:21:ARG:HD3	1.72	0.46
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.16	0.46
33:2b:8:LYS:HA	33:2b:217:ARG:HH11	1.81	0.46
38:2g:152:ALA:O	38:2g:155:ARG:NH1	2.49	0.46
50:2s:27:GLU:HG2	50:2s:47:HIS:CE1	2.51	0.46
54:2w:1:G:N2	54:2w:72:C:H42	2.15	0.46
1:1A:562:U:C2	1:1A:572:A:C8	3.04	0.45
1:1A:784:A:H5'	1:1A:785:G:OP1	2.16	0.45
1:1A:882:G:H1	1:1A:894:C:N4	2.08	0.45
1:1A:1063:G:H1	1:1A:1075:C:N4	2.13	0.45
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.51	0.45
1:1A:2120:G:O2'	1:1A:2121:G:H5'	2.16	0.45
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.16	0.45
3:1D:242:ARG:HG3	3:1D:242:ARG:NH1	2.16	0.45
33:1b:47:THR:HA	33:1b:202:PRO:HG2	1.97	0.45
37:1f:97:PHE:CD2	49:1r:31:LEU:HD11	2.51	0.45
1:2A:83:G:N2	1:2A:102:G:H1'	2.31	0.45
1:2A:171:G:H2'	1:2A:172:C:C6	2.50	0.45
1:2A:718:A:H3'	1:2A:719:C:H6	1.80	0.45
1:2A:886:C:O2	1:2A:890:A:N6	2.49	0.45
1:2A:898:C:H2'	1:2A:899:A:H5'	1.96	0.45
1:2A:921:G:H2'	1:2A:922:U:C6	2.51	0.45
1:2A:1198:U:H2'	1:2A:1199:U:C6	2.51	0.45
1:2A:1929:G:H4'	1:2A:1930:G:OP1	2.16	0.45
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.51	0.45
6:2G:176:LEU:HD23	6:2G:176:LEU:HA	1.78	0.45
32:2a:192:U:H2'	32:2a:193:C:C6	2.51	0.45
32:2a:472:A:H4'	47:2p:80:PHE:O	2.16	0.45
34:2c:14:ILE:HG22	34:2c:15:THR:HG23	1.98	0.45
42:2k:73:MET:HG2	42:2k:103:LEU:HD21	1.98	0.45
43:2l:124:LYS:HD2	43:2l:125:PRO:HD2	1.97	0.45
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.16	0.45
50:2s:27:GLU:HB3	50:2s:28:LYS:HA	1.98	0.45
1:1A:754:C:O2'	1:1A:1272:A:N1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1178:C:O5'	1:1A:1178:C:H6	1.99	0.45
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.99	0.45
1:1A:1985:G:OP2	62:1A:4049:HOH:O	2.21	0.45
1:1A:2632:A:O2'	1:1A:2811:G:O2'	2.24	0.45
8:1I:77:LEU:HG	8:1I:101:LEU:HD13	1.98	0.45
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.16	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.68	0.45
32:1a:58:C:O2'	32:1a:388:G:N7	2.33	0.45
32:1a:405:U:O4	35:1d:2:GLY:N	2.49	0.45
39:1h:124:ALA:O	39:1h:128:GLY:N	2.49	0.45
47:1p:43:LYS:HG2	47:1p:48:TRP:CD2	2.52	0.45
48:1q:45:HIS:NE2	48:1q:47:PRO:HG3	2.30	0.45
1:2A:139:G:H2'	1:2A:140:G:N7	2.31	0.45
1:2A:446:G:OP1	16:2U:3:ARG:NH1	2.49	0.45
1:2A:494:G:OP1	18:2W:8:ARG:NH1	2.44	0.45
1:2A:746:A:H2'	1:2A:2612:C:H5''	1.98	0.45
1:2A:1695:G:N7	3:2D:14:ARG:NH2	2.64	0.45
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.51	0.45
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.98	0.45
6:2G:54:GLU:O	6:2G:58:GLN:N	2.42	0.45
16:2U:113:ALA:O	16:2U:117:GLN:HG2	2.15	0.45
17:2V:62:LEU:HD22	17:2V:93:GLU:HG2	1.98	0.45
24:22:35:LEU:HD12	24:22:53:LEU:HD12	1.98	0.45
32:2a:397:A:N7	32:2a:547:A:O2'	2.47	0.45
32:2a:537:G:H5''	43:2I:113:ARG:HH12	1.82	0.45
32:2a:653:A:C8	39:2h:56:LYS:HG2	2.51	0.45
32:2a:1006:C:O2	32:2a:1023:G:N1	2.46	0.45
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.51	0.45
33:2b:81:VAL:HG22	33:2b:215:LEU:HD11	1.97	0.45
35:2d:74:GLN:HA	35:2d:77:ASN:HB2	1.98	0.45
39:2h:12:ARG:HD2	39:2h:26:VAL:HB	1.98	0.45
1:1A:624:C:O2'	1:1A:657:U:OP1	2.31	0.45
1:1A:684:G:OP1	29:17:16:HIS:ND1	2.46	0.45
1:1A:2019:A:O4'	16:1U:34:LYS:HE3	2.16	0.45
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.52	0.45
3:1D:142:VAL:CG1	3:1D:191:ALA:HB1	2.46	0.45
4:1E:121:ASN:ND2	62:1E:402:HOH:O	2.38	0.45
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.32	0.45
13:1R:97:VAL:HG22	13:1R:114:VAL:HG22	1.98	0.45
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.97	0.45
32:1a:973:G:O3'	45:1n:41:ARG:NH1	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1202:G:O2'	45:1n:29:ARG:HG3	2.16	0.45
37:1f:68:PRO:HB2	37:1f:70:ASP:OD1	2.17	0.45
44:1m:15:VAL:HG21	44:1m:48:LEU:HD21	1.98	0.45
46:1o:18:PHE:CZ	46:1o:21:ASP:HB3	2.50	0.45
1:2A:117:G:C6	1:2A:119:A:C6	3.05	0.45
1:2A:863:A:P	12:2Q:22:LYS:HG3	2.56	0.45
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.24	0.45
1:2A:2135:A:C6	1:2A:2136:C:N4	2.84	0.45
27:25:16:ARG:HG3	27:25:17:ASP:N	2.29	0.45
32:2a:113:G:H2'	32:2a:114:U:C6	2.51	0.45
32:2a:130:A:N3	32:2a:263:A:O2'	2.41	0.45
32:2a:421:U:O2'	32:2a:423:G:N7	2.49	0.45
32:2a:833:U:H2'	32:2a:834:C:C6	2.51	0.45
34:2c:117:ALA:HB2	34:2c:200:ALA:HB3	1.99	0.45
34:2c:152:ILE:O	34:2c:152:ILE:HG13	2.16	0.45
37:2f:35:ALA:HB2	37:2f:67:MET:HE2	1.98	0.45
40:2i:3:GLN:HG3	40:2i:20:ARG:HE	1.80	0.45
40:2i:53:VAL:C	40:2i:55:ALA:H	2.23	0.45
44:2m:29:ARG:HD3	44:2m:64:TRP:CE3	2.51	0.45
52:2u:6:ARG:NH2	52:2u:15:ARG:HH22	2.13	0.45
1:1A:245:G:O6	30:18:8:LYS:NZ	2.39	0.45
1:1A:1913:A:H4'	1:1A:1914:C:H5''	1.98	0.45
7:1H:144:VAL:O	7:1H:148:ILE:HG13	2.17	0.45
12:1Q:112:GLU:HG3	12:1Q:113:GLN:N	2.30	0.45
19:1X:29:TRP:CZ3	19:1X:76:ARG:HD2	2.51	0.45
32:1a:294:U:OP1	32:1a:610:G:O2'	2.33	0.45
32:1a:811:C:O2'	32:1a:901:A:N1	2.46	0.45
32:1a:848:C:H2'	32:1a:849:C:C6	2.52	0.45
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.82	0.45
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.49	0.45
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.21	0.45
1:2A:536:A:H2'	1:2A:537:C:C6	2.52	0.45
1:2A:570:G:H2'	1:2A:2030:A:C5	2.52	0.45
1:2A:918:A:N3	2:2B:80:U:H4'	2.32	0.45
1:2A:1204:A:N6	1:2A:1240:U:H2'	2.32	0.45
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.27	0.45
1:2A:2059:A:C8	1:2A:2503:2MA:HM22	2.51	0.45
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.51	0.45
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.39	0.45
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.14	0.45
6:2G:11:TYR:O	6:2G:16:ARG:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:57:LEU:HD11	19:2X:78:LYS:HE2	1.99	0.45
32:2a:54:C:N4	32:2a:353:A:OP2	2.43	0.45
32:2a:707:C:H2'	32:2a:708:C:C6	2.52	0.45
32:2a:1034:G:H3'	32:2a:1035:A:C8	2.52	0.45
32:2a:1072:G:O6	32:2a:1102:A:N6	2.50	0.45
33:2b:28:PHE:CE1	33:2b:31:TYR:HD2	2.35	0.45
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	1.98	0.45
36:2e:31:LEU:HD21	36:2e:43:LEU:HD11	1.99	0.45
1:1A:121:G:H4'	1:1A:149:A:H5'	1.99	0.45
1:1A:221:A:N1	1:1A:265:A:O2'	2.49	0.45
1:1A:223:A:O4'	1:1A:422:A:H5'	2.16	0.45
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.51	0.45
1:1A:1059:G:H2'	1:1A:1060:U:C5	2.51	0.45
1:1A:1188:U:H2'	1:1A:1189:A:H5'	1.99	0.45
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.51	0.45
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.98	0.45
5:1F:167:ALA:HB1	5:1F:173:VAL:HG11	1.98	0.45
26:14:53:GLU:HB2	26:14:56:VAL:N	2.32	0.45
32:1a:269:C:H2'	32:1a:270:A:H8	1.78	0.45
32:1a:434:U:H2'	32:1a:435:C:C6	2.51	0.45
32:1a:1063:C:H3'	32:1a:1064:G:H2'	1.99	0.45
33:1b:93:VAL:HG21	33:1b:97:TRP:CD1	2.40	0.45
37:1f:92:LYS:HE3	37:1f:92:LYS:HB2	1.77	0.45
1:2A:329:G:N7	20:2Y:71:LYS:NZ	2.63	0.45
1:2A:414:C:H2'	1:2A:415:A:C8	2.51	0.45
1:2A:466:A:N3	1:2A:683:C:H1'	2.32	0.45
1:2A:868:U:C4	1:2A:869:G:N7	2.85	0.45
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.17	0.45
1:2A:1630:G:H2'	1:2A:1631:C:C6	2.50	0.45
1:2A:1775:U:OP1	62:2A:9759:HOH:O	2.21	0.45
1:2A:2155:G:H2'	1:2A:2156:G:H5'	1.99	0.45
24:22:16:LEU:HB3	24:22:20:GLU:HG3	1.98	0.45
28:26:19:ARG:HH21	28:26:52:VAL:HG11	1.82	0.45
28:26:23:THR:OG1	28:26:24:GLU:N	2.49	0.45
32:2a:827:U:H2'	32:2a:859:A:H61	1.81	0.45
32:2a:986:A:H1'	50:2s:54:GLY:O	2.17	0.45
32:2a:1278:U:H5'	32:2a:1279:A:O4'	2.16	0.45
36:2e:105:VAL:HB	36:2e:106:PRO:HD3	1.99	0.45
44:2m:3:ARG:HE	44:2m:3:ARG:HB2	1.46	0.45
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.30	0.45
54:2y:25:C:H2'	54:2y:26:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2y:51:U:H3	54:2y:63:G:H1	1.65	0.45
54:2y:52:G:C2	54:2y:63:G:C6	3.04	0.45
1:1A:596:G:H2'	1:1A:597:U:O4'	2.17	0.45
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.17	0.45
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.99	0.45
1:1A:1310:G:OP2	29:17:9:ARG:NE	2.41	0.45
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.16	0.45
5:1F:123:LEU:HD13	5:1F:192:LEU:HB3	1.99	0.45
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.52	0.45
21:1Z:120:ILE:H	21:1Z:171:ILE:C	2.23	0.45
32:1a:28:G:O2'	32:1a:296:U:OP1	2.29	0.45
37:1f:91:VAL:HG11	49:1r:72:ARG:NH1	2.31	0.45
47:1p:5:ARG:O	47:1p:20:VAL:N	2.43	0.45
54:1y:20:U:H1'	54:1y:21:A:O4'	2.16	0.45
1:2A:108:U:H2'	1:2A:109:G:C8	2.52	0.45
1:2A:858:U:OP1	22:20:44:ARG:NH2	2.48	0.45
1:2A:1029:A:N1	1:2A:2465:C:O2'	2.46	0.45
1:2A:1598:C:O3'	19:2X:35:THR:HG23	2.17	0.45
1:2A:1632:A:H8	1:2A:1632:A:O5'	2.00	0.45
1:2A:2354:G:H2'	1:2A:2355:C:H6	1.81	0.45
6:2G:129:GLY:HA3	6:2G:163:ALA:O	2.17	0.45
6:2G:146:TYR:CD2	44:2m:8:GLU:HG2	2.51	0.45
7:2H:17:VAL:O	7:2H:45:VAL:HG11	2.16	0.45
21:2Z:151:HIS:ND1	21:2Z:168:GLU:O	2.50	0.45
32:2a:628:G:H2'	32:2a:629:G:C8	2.52	0.45
32:2a:1428:A:H2'	32:2a:1429:C:C6	2.51	0.45
1:1A:127:A:H5''	1:1A:128:C:C6	2.52	0.45
1:1A:673:C:OP1	5:1F:54:ARG:NH1	2.48	0.45
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.32	0.45
1:1A:2352:A:N6	1:1A:2365:G:O2'	2.49	0.45
1:1A:2390:U:P	30:18:35:GLN:HE22	2.39	0.45
2:1B:7:G:H5''	2:1B:7:G:H8	1.82	0.45
32:1a:460:G:H8	32:1a:460:G:O5'	2.00	0.45
32:1a:943:U:H1'	40:1i:124:GLN:HE22	1.82	0.45
32:1a:1028:C:C4	32:1a:1029:C:C2	3.05	0.45
33:1b:231:GLU:HB3	33:1b:232:PRO:HD3	1.98	0.45
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.17	0.45
1:2A:817:C:O2'	1:2A:839:U:OP1	2.29	0.45
1:2A:1114:G:H2'	1:2A:1115:G:H8	1.81	0.45
1:2A:1366:A:H2'	1:2A:1367:A:O4'	2.17	0.45
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:42:C:C4	2:2B:43:C:C4	3.04	0.45
6:2G:136:ARG:HG3	6:2G:137:GLU:HG3	1.99	0.45
11:2P:122:PRO:HB3	11:2P:141:ALA:O	2.16	0.45
13:2R:44:LEU:HD23	13:2R:44:LEU:HA	1.76	0.45
24:22:16:LEU:O	24:22:67:LYS:NZ	2.49	0.45
32:2a:646:U:H2'	32:2a:647:C:C6	2.51	0.45
32:2a:1313:U:O4	32:2a:1324:A:N1	2.49	0.45
38:2g:18:TYR:HB3	38:2g:59:LEU:HD13	1.99	0.45
1:1A:381:G:O6	62:1A:4047:HOH:O	2.21	0.45
1:1A:515:A:H1'	1:1A:581:C:H1'	1.98	0.45
1:1A:957:A:N1	1:1A:2458:G:H4'	2.32	0.45
6:1G:16:ARG:HH21	6:1G:31:VAL:CG1	2.29	0.45
27:15:49:CYS:SG	27:15:51:TYR:HB2	2.57	0.45
32:1a:1131:G:OP1	40:1i:20:ARG:NH2	2.50	0.45
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.51	0.45
51:1t:82:SER:O	51:1t:86:ARG:HG3	2.16	0.45
54:1y:24:G:H2'	54:1y:25:C:C6	2.51	0.45
1:2A:79:G:O2'	1:2A:346:A:N3	2.42	0.45
1:2A:290:G:H2'	1:2A:291:C:C6	2.52	0.45
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.27	0.45
1:2A:639:U:H2'	1:2A:640:C:C6	2.51	0.45
1:2A:1011:G:H1	1:2A:1150:C:H42	1.65	0.45
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.50	0.45
1:2A:1468:C:H2'	1:2A:1469:A:C8	2.52	0.45
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	1.99	0.45
1:2A:2264:C:N4	22:20:15:ASP:OD2	2.49	0.45
32:2a:736:C:OP1	49:2r:72:ARG:NH2	2.31	0.45
32:2a:779:C:H2'	32:2a:780:A:O4'	2.16	0.45
32:2a:1095:U:C4	32:2a:1096:C:C4	3.05	0.45
32:2a:1165:C:H2'	32:2a:1166:G:H5'	1.99	0.45
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.17	0.45
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.50	0.45
35:2d:108:LEU:HD12	35:2d:174:LEU:HD13	1.98	0.45
44:2m:87:TYR:O	44:2m:91:ARG:HG2	2.17	0.45
54:2y:19:G:N3	54:2y:57:G:N1	2.65	0.45
1:1A:34:C:H5''	1:1A:35:G:OP2	2.17	0.45
1:1A:1903:G:OP1	3:1D:241:PRO:HB2	2.17	0.45
1:1A:2117:A:O2'	1:1A:2118:U:H5''	2.17	0.45
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	1.98	0.45
32:1a:264:U:O2'	48:1q:64:PRO:O	2.34	0.45
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:61:GLU:HA	48:1q:71:PHE:CD1	2.51	0.45
1:2A:983:A:C6	1:2A:984:A:N1	2.85	0.45
1:2A:1941:C:C5	1:2A:1942:5MC:HM52	2.52	0.45
1:2A:2400:G:H2'	1:2A:2401:U:H6	1.81	0.45
3:2D:76:PRO:CB	3:2D:116:GLN:HE21	2.29	0.45
3:2D:96:HIS:CD2	3:2D:102:LYS:HG2	2.52	0.45
6:2G:41:GLN:HG2	6:2G:154:GLY:O	2.17	0.45
8:2I:31:LEU:HD21	8:2I:38:LEU:HD11	1.99	0.45
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.23	0.45
32:2a:756:C:H2'	32:2a:757:U:O4'	2.17	0.45
32:2a:865:A:H5'	32:2a:1078:U:O4	2.17	0.45
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.51	0.45
33:2b:230:VAL:HG22	33:2b:231:GLU:H	1.81	0.45
34:2c:12:LEU:O	45:2n:57:ARG:NH2	2.50	0.45
34:2c:37:GLN:NE2	45:2n:52:GLN:OE1	2.36	0.45
37:2f:23:LYS:NZ	37:2f:42:GLU:OE1	2.46	0.45
39:2h:20:TYR:HA	39:2h:65:TYR:OH	2.15	0.45
40:2i:27:THR:HG23	40:2i:31:GLN:O	2.16	0.45
47:2p:67:THR:O	47:2p:71:ARG:N	2.46	0.45
1:1A:647:G:H8	1:1A:647:G:O5'	2.00	0.45
1:1A:800:A:H8	1:1A:800:A:OP1	2.00	0.45
1:1A:1837:C:OP1	32:1a:784:C:H4'	2.17	0.45
8:1I:27:ARG:HD3	23:11:71:TYR:CE2	2.52	0.45
8:1I:75:LEU:HD13	8:1I:105:HIS:CE1	2.52	0.45
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.77	0.45
32:1a:187:C:H2'	32:1a:188:C:H6	1.82	0.45
32:1a:272:C:H2'	32:1a:273:A:H8	1.81	0.45
32:1a:790:A:C6	32:1a:791:G:C6	3.05	0.45
33:1b:115:LEU:HD11	33:1b:146:GLN:HG3	1.98	0.45
42:1k:45:GLY:O	42:1k:50:TYR:HB2	2.17	0.45
1:2A:1029:A:N6	1:2A:1125:G:O2'	2.48	0.45
1:2A:1040:C:H2'	1:2A:1041:C:C6	2.52	0.45
1:2A:2750:A:H1'	1:2A:2752:C:N4	2.32	0.45
1:2A:2803:C:H2'	1:2A:2804:C:C6	2.52	0.45
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.83	0.45
6:2G:108:ASN:O	26:24:37:SER:N	2.49	0.45
24:22:20:GLU:O	24:22:24:LEU:N	2.47	0.45
32:2a:1187:G:C5'	40:2i:113:LYS:HE2	2.47	0.45
32:2a:1287:A:H2	32:2a:1353:G:H1'	1.82	0.45
32:2a:1468:A:H2'	32:2a:1469:G:O4'	2.17	0.45
55:2x:75:C:H2'	55:2x:76:A:H1'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:414:C:H2'	1:1A:415:A:C8	2.53	0.44
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.52	0.44
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.50	0.44
25:13:10:LYS:HB3	25:13:53:LEU:HA	1.99	0.44
26:14:16:CYS:SG	26:14:17:GLY:N	2.90	0.44
26:14:62:ARG:HB2	26:14:63:TYR:CD1	2.52	0.44
32:1a:165:C:H2'	32:1a:166:G:H8	1.82	0.44
32:1a:757:U:O2'	32:1a:879:C:O2	2.35	0.44
33:1b:133:LYS:HE3	33:1b:133:LYS:HB2	1.84	0.44
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.99	0.44
41:1j:30:SER:O	41:1j:81:THR:OG1	2.35	0.44
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.51	0.44
49:1r:38:GLU:HA	49:1r:41:LYS:HD3	1.99	0.44
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.42	0.44
54:1w:22:G:H2'	54:1w:23:A:C8	2.52	0.44
1:2A:492:A:H2'	1:2A:493:G:O4'	2.17	0.44
1:2A:910:A:N3	1:2A:2264:C:O2'	2.48	0.44
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.38	0.44
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.52	0.44
1:2A:2663:G:H2'	1:2A:2664:G:O4'	2.17	0.44
7:2H:43:VAL:HA	7:2H:52:VAL:HG22	1.99	0.44
7:2H:52:VAL:O	7:2H:65:HIS:NE2	2.45	0.44
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.17	0.44
13:2R:100:LEU:HD23	13:2R:111:LEU:HB3	1.99	0.44
21:2Z:93:ASP:CB	21:2Z:131:ARG:HH22	2.28	0.44
32:2a:429:U:OP2	35:2d:36:ARG:NH2	2.47	0.44
32:2a:584:G:C5'	48:2q:91:ARG:HH22	2.30	0.44
33:2b:55:PHE:HA	33:2b:58:ILE:HB	2.00	0.44
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.82	0.44
36:2e:33:VAL:HG22	36:2e:112:LEU:HD12	1.99	0.44
42:2k:14:VAL:HG12	42:2k:16:SER:H	1.82	0.44
44:2m:19:LEU:HD11	44:2m:56:LEU:HD21	1.98	0.44
47:2p:22:THR:HA	47:2p:33:ILE:HG13	1.98	0.44
51:2t:56:MET:HE3	51:2t:85:MET:HG2	1.99	0.44
1:1A:30:G:H2'	1:1A:31:C:C6	2.52	0.44
1:1A:887:A:H1'	1:1A:889:C:OP2	2.17	0.44
1:1A:902:C:H2'	1:1A:903:C:C6	2.53	0.44
1:1A:1342:A:O2'	1:1A:1344:G:OP2	2.32	0.44
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.82	0.44
3:1D:43:ARG:HA	3:1D:48:ARG:O	2.16	0.44
8:1I:110:ASP:HA	8:1I:111:PRO:HD2	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:102:VAL:HB	10:1O:106:LEU:HD12	1.98	0.44
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.98	0.44
34:1c:131:ARG:HH11	34:1c:166:GLU:CG	2.30	0.44
35:1d:196:LEU:C	35:1d:198:VAL:H	2.26	0.44
36:1e:68:GLU:HG3	36:1e:70:PRO:HD3	2.00	0.44
38:1g:100:ALA:O	38:1g:104:LEU:HB2	2.17	0.44
39:1h:34:GLU:HB3	39:1h:118:VAL:HG21	1.99	0.44
41:1j:21:GLN:HG2	41:1j:25:GLU:CD	2.42	0.44
54:1y:53:G:H2'	54:1y:54:5MU:H73	1.98	0.44
1:2A:384:U:H2'	1:2A:385:C:H6	1.82	0.44
1:2A:971:C:H2'	1:2A:972:G:O4'	2.17	0.44
1:2A:1538:G:H2'	1:2A:1539:G:H8	1.82	0.44
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.17	0.44
13:2R:87:TYR:OH	13:2R:116:LEU:HB3	2.17	0.44
32:2a:1248:A:N3	40:2i:70:LYS:HE2	2.33	0.44
35:2d:108:LEU:HD23	35:2d:110:PHE:CE2	2.52	0.44
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.53	0.44
50:2s:27:GLU:HG2	50:2s:47:HIS:NE2	2.32	0.44
54:2w:21:A:N6	54:2w:46:7MG:N3	2.65	0.44
1:1A:299:A:OP2	62:1A:4051:HOH:O	2.21	0.44
1:1A:411:G:C5	11:1P:72:PRO:HB3	2.53	0.44
1:1A:637:A:H8	11:1P:117:GLU:HG3	1.82	0.44
1:1A:896:A:H4'	1:1A:897:C:OP1	2.17	0.44
1:1A:1035:U:H2'	1:1A:1036:G:C8	2.52	0.44
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.53	0.44
1:1A:2321:G:H5''	1:1A:2322:A:OP2	2.16	0.44
3:1D:29:PRO:HB3	3:1D:63:ARG:NE	2.31	0.44
3:1D:37:LEU:HD13	3:1D:87:ASN:ND2	2.32	0.44
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.52	0.44
9:1N:130:HIS:HB3	9:1N:133:GLN:HG2	1.99	0.44
17:1V:46:VAL:HG22	17:1V:52:VAL:HG11	2.00	0.44
32:1a:397:A:H3'	32:1a:397:A:N3	2.32	0.44
33:1b:122:PHE:C	33:1b:124:SER:H	2.23	0.44
54:1y:7:A:O2'	54:1y:49:C:OP2	2.22	0.44
1:2A:686:G:H21	1:2A:788:A:H61	1.64	0.44
1:2A:1144:G:H2'	1:2A:1145:C:H6	1.81	0.44
1:2A:1993:U:H4'	4:2E:128:SER:OG	2.17	0.44
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.98	0.44
1:2A:2158:A:H4'	1:2A:2159:G:OP1	2.17	0.44
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.51	0.44
3:2D:10:THR:OG1	3:2D:13:ARG:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:145:VAL:HB	3:2D:155:LEU:HB2	1.98	0.44
21:2Z:23:LYS:HB3	21:2Z:38:TYR:CD1	2.53	0.44
32:2a:114:U:O2'	32:2a:115:G:H5'	2.17	0.44
32:2a:176:C:H2'	32:2a:177:C:H6	1.83	0.44
32:2a:509:A:H5'	35:2d:54:TYR:HD2	1.82	0.44
32:2a:557:G:C6	32:2a:558:G:C6	3.05	0.44
32:2a:957:U:H2'	32:2a:959:A:OP2	2.17	0.44
33:2b:21:ARG:HA	33:2b:39:ILE:HD13	1.98	0.44
47:2p:72:ARG:HH21	47:2p:73:LEU:HD21	1.83	0.44
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.99	0.44
54:2w:19:G:N2	54:2w:56:C:N3	2.65	0.44
1:1A:226:G:N2	1:1A:228:A:H62	2.16	0.44
1:1A:1007:C:H5''	9:1N:35:ARG:NH1	2.32	0.44
1:1A:1062:G:H5''	1:1A:1070:A:C4'	2.48	0.44
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.52	0.44
1:1A:1878:G:H2'	1:1A:1879:C:C6	2.53	0.44
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.32	0.44
2:1B:11:C:H3'	2:1B:12:C:H6	1.83	0.44
3:1D:61:LEU:O	3:1D:63:ARG:NH1	2.50	0.44
28:16:14:THR:HB	28:16:48:VAL:O	2.17	0.44
32:1a:1028:C:H2'	32:1a:1029:C:H4'	1.99	0.44
37:1f:97:PHE:HB2	49:1r:32:ARG:HD2	1.99	0.44
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.50	0.44
1:2A:1899:G:O2'	1:2A:1900:A:OP2	2.22	0.44
1:2A:2335:A:O2'	1:2A:2337:G:N7	2.32	0.44
1:2A:2366:A:H3'	1:2A:2367:G:H8	1.82	0.44
57:2A:3670:4M2:H31	57:2A:3670:4M2:CAD	2.48	0.44
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.18	0.44
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.52	0.44
16:2U:83:LEU:O	16:2U:87:GLY:N	2.51	0.44
32:2a:417:C:H2'	32:2a:418:C:C6	2.52	0.44
32:2a:985:C:N4	32:2a:1220:G:H1	2.12	0.44
32:2a:1005:A:O5'	32:2a:1005:A:H8	2.00	0.44
32:2a:1216:G:H5''	45:2n:5:ALA:HB2	1.99	0.44
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.53	0.44
38:2g:70:LYS:O	38:2g:138:LYS:HD2	2.17	0.44
39:2h:35:ILE:O	39:2h:39:LEU:HD13	2.17	0.44
44:2m:81:LEU:HD13	44:2m:88:ARG:HD2	2.00	0.44
1:1A:315:G:H2'	1:1A:316:C:C6	2.53	0.44
1:1A:897:C:C2	1:1A:898:C:C5	3.05	0.44
1:1A:1087:G:H2'	1:1A:1089:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1094:U:H2'	1:1A:1095:A:C8	2.53	0.44
1:1A:2422:A:O4'	54:1y:76:A:N6	2.51	0.44
6:1G:47:LYS:HD2	6:1G:80:PHE:O	2.18	0.44
26:14:56:VAL:HB	26:14:60:GLN:HG3	1.99	0.44
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.32	0.44
32:1a:408:A:H2'	32:1a:409:G:O4'	2.18	0.44
38:1g:76:ARG:N	38:1g:87:VAL:O	2.39	0.44
39:1h:17:THR:HG22	39:1h:63:LEU:HD23	2.00	0.44
39:1h:51:VAL:HG11	39:1h:60:ARG:HE	1.82	0.44
42:1k:16:SER:HA	42:1k:79:SER:O	2.18	0.44
44:1m:78:ILE:HA	44:1m:81:LEU:HD12	1.99	0.44
46:1o:39:LEU:HD22	46:1o:56:LEU:HD13	2.00	0.44
54:1w:24:G:H2'	54:1w:25:C:O4'	2.18	0.44
1:2A:566:U:H5''	11:2P:29:LYS:HE3	2.00	0.44
1:2A:966:G:H2'	1:2A:967:C:H6	1.81	0.44
1:2A:2166:G:H3'	1:2A:2167:U:H5''	2.00	0.44
1:2A:2370:G:C6	1:2A:2371:G:C6	3.06	0.44
1:2A:2400:G:H2'	1:2A:2401:U:C6	2.53	0.44
1:2A:2839:G:O2'	13:2R:49:ASP:OD2	2.27	0.44
7:2H:57:ASP:O	7:2H:62:LYS:HD2	2.17	0.44
32:2a:390:C:H4'	47:2p:28:ARG:HH21	1.83	0.44
32:2a:509:A:H2'	32:2a:510:A:C8	2.52	0.44
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.38	0.44
32:2a:975:A:N1	41:2j:48:THR:HB	2.33	0.44
36:2e:57:LYS:HG2	36:2e:61:TYR:CE2	2.52	0.44
38:2g:80:VAL:HB	38:2g:85:TYR:HE2	1.83	0.44
55:2x:9:G:O2'	55:2x:10:G:N7	2.45	0.44
1:1A:764:A:O4'	3:1D:213:ARG:HG3	2.17	0.44
1:1A:902:C:H2'	1:1A:903:C:H6	1.82	0.44
1:1A:2119:A:O2'	1:1A:2120:G:H5''	2.18	0.44
11:1P:135:LEU:HD23	11:1P:135:LEU:HA	1.73	0.44
32:1a:310:G:H5''	47:1p:31:LYS:HB2	1.99	0.44
32:1a:353:A:H5'	32:1a:353:A:H8	1.82	0.44
32:1a:599:C:H4'	39:1h:130:GLY:C	2.42	0.44
32:1a:737:A:H2'	32:1a:738:C:C6	2.52	0.44
35:1d:73:ARG:HD2	35:1d:73:ARG:HA	1.66	0.44
42:1k:48:ILE:O	42:1k:50:TYR:N	2.46	0.44
50:1s:29:ARG:O	50:1s:31:ILE:HG13	2.16	0.44
1:2A:262:A:H2'	1:2A:263:C:O4'	2.17	0.44
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.53	0.44
1:2A:2715:C:H2'	1:2A:2716:U:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:2:C:H2'	2:2B:3:C:C6	2.53	0.44
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.16	0.44
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.50	0.44
32:2a:408:A:H2'	32:2a:409:G:O4'	2.17	0.44
32:2a:688:G:H2'	32:2a:689:C:H6	1.81	0.44
32:2a:737:A:H2'	32:2a:738:C:C6	2.52	0.44
32:2a:748:C:H4'	32:2a:749:C:O5'	2.18	0.44
32:2a:1004:A:C4	32:2a:1038:C:C2	3.05	0.44
32:2a:1518:MA6:N6	32:2a:1519:MA6:H103	2.32	0.44
33:2b:15:VAL:HG23	33:2b:16:HIS:CD2	2.52	0.44
44:2m:67:GLU:HG3	44:2m:68:GLY:H	1.83	0.44
48:2q:22:LEU:HD13	48:2q:41:LYS:HG3	1.99	0.44
54:2y:43:C:O2'	54:2y:44:G:H5'	2.17	0.44
1:1A:1054:A:C6	1:1A:1055:G:C6	3.06	0.44
1:1A:1082:U:C4	1:1A:1086:A:N1	2.78	0.44
4:1E:51:PHE:HB3	4:1E:77:ILE:HD11	1.99	0.44
7:1H:88:LEU:HD22	7:1H:165:ALA:HA	1.99	0.44
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.53	0.44
32:1a:216:G:H2'	32:1a:217:C:C6	2.53	0.44
32:1a:1095:U:P	32:1a:1108:G:H1	2.40	0.44
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.50	0.44
50:1s:63:THR:OG1	50:1s:66:MET:HE3	2.18	0.44
1:2A:460:A:H2'	1:2A:461:C:O4'	2.18	0.44
1:2A:551:G:O2'	1:2A:1220:A:N3	2.45	0.44
1:2A:1638:C:O3'	1:2A:2709:G:N2	2.51	0.44
2:2B:11:C:OP2	2:2B:12:C:H5	2.01	0.44
6:2G:43:LEU:HB3	6:2G:44:GLY:H	1.57	0.44
7:2H:149:ARG:NH1	7:2H:163:TYR:HA	2.32	0.44
8:2I:27:ARG:HG3	23:21:71:TYR:CZ	2.52	0.44
12:2Q:137:TYR:CE2	21:2Z:49:ARG:HD3	2.52	0.44
32:2a:56:U:H2'	32:2a:57:G:H8	1.82	0.44
32:2a:160:A:H1'	32:2a:344:A:N7	2.32	0.44
32:2a:983:A:H2	32:2a:984:C:C6	2.35	0.44
32:2a:1122:U:N3	32:2a:1123:A:N7	2.66	0.44
34:2c:111:LEU:HD11	34:2c:144:SER:O	2.17	0.44
1:1A:2553:G:H22	54:1w:76:A:N6	2.14	0.44
1:1A:2640:G:P	9:1N:97:ARG:HH22	2.41	0.44
7:1H:98:LEU:HD12	7:1H:125:VAL:HG23	2.00	0.44
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.50	0.44
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.51	0.44
38:1g:50:ILE:HD11	38:1g:125:MET:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:90:LEU:HA	41:1j:91:PRO:HD3	1.90	0.44
47:1p:15:PRO:O	47:1p:16:HIS:ND1	2.51	0.44
1:2A:656:G:H2'	1:2A:657:U:O4'	2.18	0.44
1:2A:667:U:O2	30:28:2:PRO:HD2	2.18	0.44
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.01	0.44
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.53	0.44
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.52	0.44
3:2D:69:ARG:HE	3:2D:130:ALA:HB3	1.82	0.44
12:2Q:58:PHE:CE1	12:2Q:109:VAL:HG21	2.53	0.44
32:2a:328:C:H4'	32:2a:329:A:H5'	1.99	0.44
32:2a:653:A:O4'	39:2h:56:LYS:HE2	2.17	0.44
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.18	0.44
32:2a:996:A:N1	32:2a:1045:C:O2'	2.45	0.44
32:2a:1118:C:H2'	32:2a:1119:C:C6	2.53	0.44
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.52	0.44
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.17	0.44
46:2o:39:LEU:HD23	46:2o:39:LEU:HA	1.81	0.44
50:2s:44:MET:HA	50:2s:47:HIS:HD1	1.83	0.44
51:2t:53:LEU:HB2	51:2t:100:ILE:HG13	2.00	0.44
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.53	0.44
1:1A:1495:A:H2'	1:1A:1496:A:C8	2.52	0.44
1:1A:2138:C:C2	1:1A:2154:G:C2	3.06	0.44
6:1G:45:GLU:C	6:1G:47:LYS:H	2.25	0.44
14:1S:36:TYR:N	14:1S:36:TYR:CD2	2.86	0.44
32:1a:16:A:N1	32:1a:919:A:H2	2.16	0.44
32:1a:109:A:C6	32:1a:326:G:C6	3.06	0.44
32:1a:254:G:OP1	48:1q:67:LYS:O	2.36	0.44
32:1a:371:G:H2'	32:1a:372:C:O4'	2.18	0.44
32:1a:986:A:H2'	32:1a:987:G:O4'	2.17	0.44
32:1a:1036:G:H3'	32:1a:1037:C:C6	2.53	0.44
33:1b:70:PHE:HD2	33:1b:85:ALA:HB2	1.82	0.44
33:1b:178:ARG:NH2	39:1h:74:PRO:HB3	2.33	0.44
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.18	0.44
54:1y:36:A:H2'	54:1y:37:MIA:O4'	2.18	0.44
1:2A:183:C:N4	1:2A:213:A:H61	2.16	0.44
1:2A:1462:C:H4'	1:2A:2703:C:H5'	1.99	0.44
1:2A:1468:C:H2'	1:2A:1469:A:H8	1.82	0.44
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.18	0.44
2:2B:13:A:O2'	2:2B:14:U:H3'	2.17	0.44
2:2B:78:A:C2	2:2B:100:A:C4	3.05	0.44
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.84	0.44
7:2H:97:ARG:HA	7:2H:125:VAL:HG21	2.00	0.44
32:2a:670:G:H2'	32:2a:671:G:O4'	2.18	0.44
32:2a:1226:C:N4	44:2m:104:ARG:HG2	2.33	0.44
33:2b:192:SER:O	33:2b:194:PRO:HD3	2.17	0.44
45:2n:26:ARG:HD3	45:2n:43:CYS:SG	2.57	0.44
1:1A:667:U:O2	30:18:2:PRO:HD2	2.18	0.43
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.53	0.43
1:1A:2660:A:H2'	1:1A:2661:G:O4'	2.17	0.43
1:1A:2793:G:H22	1:1A:2804:C:H1'	1.82	0.43
4:1E:98:PRO:HD3	4:1E:175:VAL:HG13	2.00	0.43
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.33	0.43
32:1a:67:C:O2'	32:1a:171:A:H1'	2.18	0.43
32:1a:78:G:C6	32:1a:91:C:N4	2.86	0.43
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.18	0.43
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.53	0.43
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.82	0.43
38:1g:116:ALA:O	38:1g:120:ILE:HG12	2.18	0.43
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.53	0.43
45:1n:4:LYS:O	45:1n:7:ILE:HG13	2.18	0.43
1:2A:534:U:H2'	1:2A:535:C:C6	2.53	0.43
1:2A:1161:C:H2'	1:2A:1162:G:H8	1.83	0.43
1:2A:2116:G:N7	1:2A:2166:G:N2	2.66	0.43
1:2A:2154:G:C2	1:2A:2155:G:C8	3.06	0.43
1:2A:2498:C:H3'	62:2A:9704:HOH:O	2.17	0.43
7:2H:96:ALA:HB2	7:2H:105:LEU:HD23	2.00	0.43
11:2P:39:LYS:HA	11:2P:44:GLY:HA2	2.00	0.43
12:2Q:137:TYR:O	12:2Q:141:GLN:HG2	2.18	0.43
20:2Y:7:VAL:HG21	20:2Y:72:VAL:HG12	1.99	0.43
21:2Z:70:LEU:O	21:2Z:89:PHE:N	2.42	0.43
21:2Z:98:MET:HE2	21:2Z:100:VAL:HG22	2.00	0.43
26:24:48:ARG:HA	26:24:48:ARG:HD3	1.82	0.43
32:2a:446:G:H2'	32:2a:447:G:O4'	2.18	0.43
32:2a:767:A:H2'	32:2a:768:A:O4'	2.18	0.43
34:2c:151:VAL:HG22	34:2c:200:ALA:HA	1.98	0.43
48:2q:95:TYR:HA	48:2q:98:LEU:HD12	2.00	0.43
54:2w:43:C:H2'	54:2w:44:G:C8	2.53	0.43
1:1A:403:U:H4'	1:1A:404:C:H5'	2.00	0.43
1:1A:534:U:H2'	1:1A:535:C:C6	2.54	0.43
1:1A:1754:C:H5	15:1T:96:ARG:NH2	2.09	0.43
1:1A:1790:C:H5''	1:1A:1791:A:OP1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:96:HIS:CD2	3:1D:102:LYS:HG2	2.53	0.43
4:1E:117:MET:HE2	4:1E:117:MET:HB3	1.90	0.43
4:1E:170:LEU:HG	4:1E:185:LYS:O	2.17	0.43
11:1P:39:LYS:HD2	11:1P:45:LEU:HD11	2.00	0.43
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	2.00	0.43
12:1Q:85:LYS:HD3	22:10:7:LEU:HD13	2.00	0.43
13:1R:14:SER:OG	13:1R:15:SER:N	2.51	0.43
17:1V:55:ALA:HB2	17:1V:101:GLY:HA2	1.99	0.43
32:1a:277:C:H5''	48:1q:68:ARG:NH2	2.33	0.43
33:1b:164:VAL:O	33:1b:186:ALA:HA	2.18	0.43
34:1c:47:LEU:HD13	34:1c:68:VAL:HG11	2.01	0.43
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.99	0.43
36:1e:31:LEU:HD23	36:1e:31:LEU:HA	1.86	0.43
51:1t:100:ILE:HB	51:1t:101:GLY:H	1.62	0.43
1:2A:297:C:H2'	1:2A:298:G:O4'	2.19	0.43
1:2A:721:C:H2'	1:2A:722:A:C8	2.53	0.43
1:2A:729:G:H5'	1:2A:730:C:H5''	2.00	0.43
1:2A:831:G:O2'	11:2P:38:GLN:OE1	2.36	0.43
1:2A:1006:C:OP1	62:2A:9761:HOH:O	2.21	0.43
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.53	0.43
1:2A:2323:G:O6	62:2A:9752:HOH:O	2.20	0.43
1:2A:2579:C:OP1	62:2A:9753:HOH:O	2.20	0.43
1:2A:2639:A:C2	1:2A:2778:A:C8	3.07	0.43
2:2B:73:A:C4	2:2B:105:A:C2	3.06	0.43
5:2F:123:LEU:HD12	5:2F:124:LEU:H	1.83	0.43
16:2U:74:LEU:HD13	16:2U:79:PHE:HB2	2.00	0.43
32:2a:1228:C:H2'	32:2a:1229:A:H8	1.83	0.43
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.53	0.43
35:2d:88:VAL:O	35:2d:92:VAL:HG23	2.18	0.43
1:1A:652(C):G:N2	1:1A:653:A:H1'	2.34	0.43
1:1A:857:C:H4'	22:10:23:VAL:HG21	2.00	0.43
1:1A:1709:U:H2'	1:1A:1710:C:C6	2.53	0.43
1:1A:2108:C:H2'	1:1A:2109:U:C6	2.53	0.43
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.54	0.43
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.18	0.43
9:1N:28:THR:HG22	9:1N:29:LYS:N	2.33	0.43
32:1a:841:U:OP1	32:1a:841:U:H6	2.01	0.43
1:2A:144:C:C2	1:2A:145:G:C8	3.06	0.43
1:2A:579:G:H2'	1:2A:580:C:C6	2.54	0.43
1:2A:848:G:C2	1:2A:933:A:H1'	2.53	0.43
1:2A:1589:C:H2'	1:2A:1590:U:H6	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1600:C:OP1	19:2X:58:HIS:NE2	2.33	0.43
1:2A:2317:C:C4	1:2A:2318:G:N7	2.85	0.43
1:2A:2635:C:O2'	4:2E:80:GLU:OE2	2.28	0.43
2:2B:15:A:O4'	2:2B:110:G:C8	2.71	0.43
6:2G:11:TYR:OH	6:2G:33:ARG:HG2	2.18	0.43
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.19	0.43
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.50	0.43
21:2Z:97:GLU:HA	21:2Z:126:VAL:O	2.18	0.43
32:2a:7:G:H21	36:2e:121:LYS:HG2	1.84	0.43
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.53	0.43
33:2b:43:ASP:OD2	33:2b:45:GLN:HG3	2.19	0.43
34:2c:6:HIS:HA	34:2c:7:PRO:HD3	1.71	0.43
38:2g:116:ALA:O	38:2g:120:ILE:HG13	2.19	0.43
44:2m:72:ALA:O	44:2m:76:ALA:N	2.51	0.43
45:2n:52:GLN:O	45:2n:53:LEU:HD23	2.18	0.43
1:1A:207:A:H2'	1:1A:208:C:O4'	2.17	0.43
1:1A:359:A:H2'	1:1A:360:G:O4'	2.19	0.43
1:1A:1166:C:H2'	1:1A:1167:U:C6	2.53	0.43
1:1A:2319:G:H1	14:1S:3:ARG:HA	1.83	0.43
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.53	0.43
6:1G:108:ASN:HB3	26:14:22:ILE:HD13	1.99	0.43
24:12:35:LEU:HD12	24:12:53:LEU:HD12	2.00	0.43
32:1a:236:G:H5''	48:1q:42:TYR:OH	2.18	0.43
32:1a:1203:C:H2'	32:1a:1204:A:O4'	2.18	0.43
34:1c:32:LEU:HD23	34:1c:32:LEU:HA	1.89	0.43
35:1d:108:LEU:HD11	35:1d:174:LEU:HD22	1.99	0.43
35:1d:194:LEU:HD13	35:1d:194:LEU:HA	1.73	0.43
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.18	0.43
1:2A:1527:G:H5''	1:2A:1528:A:OP1	2.19	0.43
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.18	0.43
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.18	0.43
11:2P:55:ARG:HA	62:2P:303:HOH:O	2.18	0.43
16:2U:34:LYS:HA	16:2U:34:LYS:HD3	1.72	0.43
25:23:6:VAL:HG22	25:23:56:VAL:HG13	2.01	0.43
30:28:33:ASN:HA	30:28:36:LYS:HD2	2.00	0.43
32:2a:137:C:C2	32:2a:227:G:C2	3.06	0.43
32:2a:352:C:O2'	32:2a:354:G:OP1	2.28	0.43
32:2a:939:G:H1	32:2a:1344:C:N4	2.14	0.43
39:2h:98:LYS:HA	39:2h:98:LYS:HD3	1.85	0.43
48:2q:56:VAL:O	48:2q:77:VAL:HB	2.19	0.43
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.33	0.43
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.18	0.43
1:1A:2441:C:OP2	1:1A:2586:C:O2'	2.34	0.43
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.99	0.43
10:1O:64:ARG:HD2	10:1O:81:ASP:OD1	2.17	0.43
32:1a:392:G:H2'	32:1a:393:A:H8	1.83	0.43
32:1a:437:U:H5''	35:1d:155:LEU:HD11	2.00	0.43
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.52	0.43
36:1e:43:LEU:HD21	36:1e:132:ALA:HB1	2.00	0.43
39:1h:30:ARG:O	39:1h:34:GLU:HG2	2.18	0.43
48:1q:45:HIS:CD2	48:1q:47:PRO:HG3	2.54	0.43
1:2A:192:C:O2'	1:2A:802:A:N3	2.47	0.43
1:2A:250:G:C6	1:2A:251:A:C6	3.06	0.43
1:2A:658:C:H2'	1:2A:659:C:C6	2.53	0.43
1:2A:706:A:H2'	1:2A:707:G:O4'	2.18	0.43
1:2A:858:U:O2	1:2A:2268:A:H2'	2.18	0.43
1:2A:1378:A:O2'	1:2A:1379:A:H5''	2.18	0.43
1:2A:2274:A:C5	1:2A:2276:G:C8	3.07	0.43
1:2A:2744:G:N2	7:2H:143:GLN:OE1	2.49	0.43
3:2D:124:PRO:HG2	3:2D:129:ASN:ND2	2.34	0.43
3:2D:264:LYS:HA	3:2D:265:PRO:HD3	1.92	0.43
6:2G:125:PHE:CD1	6:2G:131:TYR:HD1	2.35	0.43
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.83	0.43
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.19	0.43
12:2Q:21:THR:CG2	12:2Q:101:ARG:HG2	2.47	0.43
13:2R:33:ARG:HH22	27:25:58:LEU:HA	1.84	0.43
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.50	0.43
28:26:13:CYS:SG	28:26:47:THR:HG21	2.58	0.43
32:2a:16:A:O2'	36:2e:16:THR:HB	2.19	0.43
32:2a:359:U:H2'	32:2a:360:A:H8	1.83	0.43
32:2a:1349:A:H2'	32:2a:1350:A:H8	1.82	0.43
33:2b:92:TYR:CD1	33:2b:151:GLY:HA3	2.53	0.43
1:1A:44:G:H5''	1:1A:45:C:OP1	2.18	0.43
1:1A:196:A:H2'	1:1A:196:A:N3	2.32	0.43
1:1A:524:U:H2'	1:1A:525:U:C6	2.53	0.43
1:1A:573:G:O2'	1:1A:574:C:H3'	2.19	0.43
1:1A:721:C:H2'	1:1A:722:A:H8	1.83	0.43
1:1A:1999:C:H5''	1:1A:2723:C:O2'	2.19	0.43
1:1A:2295:C:OP1	14:1S:10:ARG:NH1	2.51	0.43
12:1Q:16:ARG:HE	12:1Q:18:LYS:HD3	1.83	0.43
32:1a:719:C:O2'	49:1r:49:LYS:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:73:MET:HG2	42:1k:103:LEU:HD21	2.00	0.43
1:2A:141:A:C8	1:2A:1408:C:O2'	2.67	0.43
1:2A:480:A:O2'	20:2Y:46:LYS:O	2.30	0.43
1:2A:522:G:C6	1:2A:523:C:C4	3.07	0.43
1:2A:855:G:C6	1:2A:856:C:C4	3.06	0.43
8:2I:63:ALA:HA	8:2I:66:GLU:HB3	2.00	0.43
17:2V:74:LYS:HB2	17:2V:83:ARG:HB2	2.00	0.43
20:2Y:82:PRO:O	20:2Y:101:LYS:NZ	2.46	0.43
24:22:32:LEU:HD23	24:22:36:ARG:HH11	1.84	0.43
32:2a:42:G:O2'	32:2a:622:A:N1	2.44	0.43
32:2a:141:A:H1'	32:2a:182:U:O2	2.19	0.43
32:2a:179:A:H2'	32:2a:180:U:H6	1.83	0.43
32:2a:942:G:C2	32:2a:1342:C:C2	3.06	0.43
32:2a:1306:A:H2'	32:2a:1307:U:O4'	2.19	0.43
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	1.99	0.43
43:2l:8:ASN:O	43:2l:12:ARG:HG3	2.19	0.43
47:2p:47:ASP:OD1	47:2p:47:ASP:N	2.51	0.43
47:2p:51:VAL:HG12	47:2p:53:VAL:N	2.24	0.43
55:2x:23:C:H2'	55:2x:24:U:C6	2.52	0.43
1:1A:388:G:O2'	1:1A:389:G:N7	2.47	0.43
1:1A:1041:C:H42	1:1A:1114:G:H1	1.66	0.43
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.52	0.43
57:1A:3894:4M2:H28	57:1A:3894:4M2:H27	1.86	0.43
4:1E:111:ARG:HD2	4:1E:160:TYR:CD2	2.54	0.43
10:1O:34:THR:OG1	10:1O:35:VAL:N	2.51	0.43
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.33	0.43
24:12:32:LEU:HD11	24:12:54:LYS:CG	2.48	0.43
32:1a:165:C:H2'	32:1a:166:G:C8	2.54	0.43
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.45	0.43
32:1a:765:G:N1	32:1a:812:C:O2'	2.43	0.43
33:1b:74:LYS:O	33:1b:78:GLN:HG2	2.19	0.43
35:1d:162:LEU:CD1	35:1d:181:MET:HG2	2.49	0.43
55:1x:17:C:H5'	55:1x:61:C:OP1	2.18	0.43
1:2A:740:U:H2'	1:2A:741:G:C8	2.54	0.43
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.83	0.43
1:2A:2636:U:H1'	1:2A:2783:G:N2	2.34	0.43
16:2U:69:CYS:HB3	16:2U:74:LEU:HD12	2.00	0.43
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.49	0.43
31:29:2:LYS:NZ	31:29:31:LYS:O	2.37	0.43
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.84	0.43
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1352:C:N3	32:2a:1370:G:N2	2.58	0.43
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.45	0.43
32:2a:1524:C:H2'	32:2a:1525:G:C8	2.53	0.43
35:2d:173:TRP:CD2	35:2d:189:PRO:HG3	2.53	0.43
37:2f:12:PRO:HG2	37:2f:13:ASN:ND2	2.34	0.43
44:2m:90:LEU:HD23	44:2m:93:ARG:NE	2.34	0.43
46:2o:48:LYS:HA	46:2o:48:LYS:HD3	1.70	0.43
1:1A:657:U:H2'	1:1A:658:C:C6	2.54	0.43
1:1A:2131:G:H2'	1:1A:2131:G:N3	2.34	0.43
3:1D:68:LYS:O	3:1D:69:ARG:HB2	2.18	0.43
3:1D:242:ARG:HD2	3:1D:246:PRO:HG3	2.00	0.43
5:1F:56:GLU:OE2	5:1F:93:LYS:NZ	2.52	0.43
8:1I:106:GLY:HA2	8:1I:107:VAL:O	2.18	0.43
12:1Q:65:PHE:HB2	12:1Q:105:GLU:HB2	2.00	0.43
14:1S:28:VAL:HG11	14:1S:98:VAL:HG13	1.99	0.43
19:1X:50:LYS:HE2	62:1X:201:HOH:O	2.18	0.43
21:1Z:4:ARG:HH21	21:1Z:60:GLU:HG2	1.84	0.43
32:1a:184:G:H2'	32:1a:185:A:C8	2.53	0.43
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.88	0.43
1:2A:108:U:H2'	1:2A:109:G:H8	1.82	0.43
1:2A:264:C:O2'	1:2A:265:A:H2'	2.19	0.43
1:2A:794:G:H2'	1:2A:795:C:H6	1.83	0.43
1:2A:1133:U:O2'	1:2A:1137:G:OP1	2.36	0.43
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.18	0.43
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.67	0.43
15:2T:78:LEU:O	15:2T:78:LEU:HD23	2.18	0.43
31:29:29:ASN:HA	31:29:30:PRO:HD3	1.88	0.43
32:2a:142:G:H2'	32:2a:143:A:C8	2.53	0.43
32:2a:660:G:OP1	46:2o:5:LYS:HD2	2.19	0.43
32:2a:993:G:N3	32:2a:993:G:H2'	2.34	0.43
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.53	0.43
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.54	0.43
54:2w:51:U:H2'	54:2w:52:G:H8	1.84	0.43
55:2x:15:G:H2'	55:2x:59:A:N1	2.33	0.43
1:1A:455:C:N3	1:1A:473:G:H5'	2.33	0.43
1:1A:479:A:N3	1:1A:481:G:H5''	2.33	0.43
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.53	0.43
5:1F:89:VAL:HG12	5:1F:90:PHE:CD2	2.54	0.43
6:1G:43:LEU:HD12	6:1G:43:LEU:HA	1.80	0.43
14:1S:20:ARG:HA	14:1S:20:ARG:HD2	1.91	0.43
19:1X:12:VAL:HG21	19:1X:27:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:399:G:H2'	32:1a:400:C:C6	2.54	0.43
32:1a:841:U:C5	32:1a:848:C:H1'	2.53	0.43
35:1d:178:VAL:O	35:1d:179:GLU:HB2	2.18	0.43
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.07	0.43
1:2A:2203:U:O4'	3:2D:151:LYS:HE2	2.19	0.43
1:2A:2505:G:H4'	57:2A:3670:4M2:H23	2.01	0.43
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.19	0.43
7:2H:4:ILE:O	7:2H:69:ARG:HD2	2.19	0.43
12:2Q:81:VAL:HB	22:20:7:LEU:HD22	2.01	0.43
32:2a:16:A:N3	32:2a:1080:A:O2'	2.50	0.43
32:2a:671:G:H1	32:2a:735:C:H42	1.66	0.43
32:2a:1110:A:N6	32:2a:1111:A:N1	2.67	0.43
33:2b:91:PRO:HA	33:2b:151:GLY:O	2.18	0.43
33:2b:119:GLU:HG3	33:2b:153:ARG:HH22	1.83	0.43
34:2c:111:LEU:HD23	34:2c:111:LEU:HA	1.86	0.43
35:2d:82:ALA:HB2	35:2d:96:LEU:HD22	2.01	0.43
39:2h:29:SER:HB3	39:2h:32:LYS:CG	2.48	0.43
45:2n:21:TYR:HE1	45:2n:23:ARG:HE	1.67	0.43
1:1A:217:G:H2'	1:1A:218:A:O4'	2.19	0.43
1:1A:245:G:O5'	11:1P:73:GLY:HA2	2.19	0.43
1:1A:876:C:H2'	1:1A:877:U:O4'	2.19	0.43
1:1A:1051:G:H2'	1:1A:1052:C:O4'	2.19	0.43
1:1A:1753:G:N1	1:1A:1756:G:OP2	2.49	0.43
4:1E:97:LYS:HB3	4:1E:97:LYS:HE2	1.68	0.43
12:1Q:10:ARG:NH1	12:1Q:90:VAL:H	2.16	0.43
32:1a:189(A):C:H2'	32:1a:189(B):C:H6	1.84	0.43
32:1a:955:U:O2'	50:1s:83:HIS:HD2	2.02	0.43
32:1a:963:G:H5'	62:1a:1997:HOH:O	2.19	0.43
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.58	0.43
38:1g:74:GLU:OE2	38:1g:95:ARG:NE	2.49	0.43
40:1i:55:ALA:HB1	40:1i:59:PHE:CE2	2.54	0.43
1:2A:154(A):C:N4	1:2A:171:G:H1	2.17	0.43
1:2A:196:A:C4	1:2A:805:G:C6	3.07	0.43
1:2A:598:G:H2'	1:2A:599:G:O4'	2.19	0.43
1:2A:2279:G:OP2	22:20:11:ARG:NH1	2.50	0.43
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.34	0.43
5:2F:46:ARG:HB3	5:2F:48:THR:HG23	2.01	0.43
5:2F:164:ARG:O	5:2F:168:ARG:HB2	2.19	0.43
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.19	0.43
14:2S:87:PHE:CZ	14:2S:102:ALA:HB2	2.54	0.43
32:2a:302:G:O2'	32:2a:556:C:H5''	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:358:U:H2'	32:2a:359:U:H6	1.84	0.43
32:2a:1285:A:H4'	32:2a:1286:A:O5'	2.18	0.43
33:2b:29:ALA:HA	33:2b:32:ILE:HD12	2.00	0.43
55:2x:15:G:H21	55:2x:21:A:H1'	1.84	0.43
1:1A:620:G:N3	1:1A:620:G:H5'	2.34	0.42
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.54	0.42
8:1I:77:LEU:HD23	8:1I:104:GLN:NE2	2.34	0.42
13:1R:33:ARG:NH2	27:15:57:VAL:O	2.23	0.42
14:1S:11:LYS:HD3	14:1S:15:ARG:NH1	2.34	0.42
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.42	0.42
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.34	0.42
32:1a:356:A:N3	32:1a:368:U:O2'	2.43	0.42
32:1a:814:A:H2'	32:1a:816:A:H5''	2.01	0.42
51:1t:43:LEU:O	51:1t:47:GLY:N	2.52	0.42
51:1t:54:LYS:HA	51:1t:57:ARG:NH2	2.34	0.42
1:2A:448:U:C4	1:2A:583:G:H1'	2.54	0.42
1:2A:500:G:N1	1:2A:503:A:OP2	2.46	0.42
1:2A:866:A:N6	1:2A:914:C:C4	2.87	0.42
1:2A:996:A:O3'	16:2U:91:ASP:HB2	2.19	0.42
1:2A:1336:A:H2'	1:2A:1337:G:H8	1.83	0.42
1:2A:2019:A:O4'	16:2U:34:LYS:HE3	2.19	0.42
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.46	0.42
4:2E:119:ARG:HG3	4:2E:160:TYR:CG	2.54	0.42
6:2G:131:TYR:CE2	6:2G:133:LEU:HB3	2.54	0.42
8:2I:79:ILE:HA	8:2I:80:PRO:HD2	1.94	0.42
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	1.99	0.42
32:2a:116:A:H61	32:2a:313:A:H1'	1.84	0.42
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.54	0.42
32:2a:1065:U:H1'	32:2a:1066:C:OP2	2.19	0.42
32:2a:1255:G:O3'	32:2a:1258:G:H1'	2.18	0.42
33:2b:144:ARG:O	33:2b:147:LYS:HB3	2.19	0.42
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	2.01	0.42
49:2r:56:THR:HB	49:2r:58:LEU:HD13	2.01	0.42
50:2s:70:LYS:HB2	50:2s:73:GLU:HG3	2.01	0.42
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.49	0.42
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.52	0.42
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.19	0.42
23:11:93:GLU:O	23:11:97:LEU:HG	2.18	0.42
30:18:62:LEU:HB3	30:18:65:GLU:CG	2.49	0.42
32:1a:228:A:H2'	32:1a:229:U:O4'	2.20	0.42
32:1a:302:G:O2'	32:1a:556:C:H5''	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:337:C:H2'	32:1a:338:A:C8	2.54	0.42
33:1b:74:LYS:HB3	33:1b:169:LYS:HD3	2.01	0.42
41:1j:38:ILE:HA	41:1j:39:PRO:HD3	1.80	0.42
1:2A:747:U:O2	1:2A:2014:A:H1'	2.18	0.42
1:2A:1000:A:C4	1:2A:1155:A:C6	3.07	0.42
1:2A:1003:G:N2	1:2A:1153:C:C2	2.87	0.42
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.54	0.42
1:2A:1859:A:N6	1:2A:1883:G:O2'	2.52	0.42
1:2A:2265:U:H4'	12:2Q:13:GLN:HE22	1.84	0.42
1:2A:2850:A:OP2	1:2A:2866:U:H5	2.02	0.42
2:2B:23:G:C2	2:2B:61:G:C2	3.08	0.42
25:23:23:LEU:HD13	25:23:50:VAL:HG11	2.02	0.42
27:25:48:GLU:O	27:25:60:VAL:HG11	2.20	0.42
32:2a:437:U:O2'	35:2d:125:HIS:HE1	2.02	0.42
32:2a:626:U:H2'	32:2a:627:G:C8	2.54	0.42
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.34	0.42
32:2a:1386:G:C2	32:2a:1387:G:C8	3.07	0.42
32:2a:1503:A:N6	53:2v:12:A:H2	2.16	0.42
37:2f:3:ARG:HB3	37:2f:93:SER:HB2	2.00	0.42
38:2g:78:ARG:HH21	38:2g:79:ARG:HH12	1.66	0.42
39:2h:2:LEU:HD21	39:2h:5:PRO:HA	2.01	0.42
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.17	0.42
44:2m:107:ALA:HB3	44:2m:111:LYS:HD3	2.01	0.42
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.52	0.42
1:1A:2168:G:C6	1:1A:2171:A:C8	3.07	0.42
1:1A:2235:G:H2'	1:1A:2236:C:C6	2.54	0.42
1:1A:2576:G:H1'	62:1A:4364:HOH:O	2.19	0.42
4:1E:48:GLN:NE2	4:1E:66:HIS:NE2	2.67	0.42
11:1P:126:VAL:HG12	11:1P:148:LEU:CD2	2.49	0.42
14:1S:87:PHE:HZ	14:1S:98:VAL:HG12	1.84	0.42
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.54	0.42
22:10:17:GLN:O	22:10:19:LYS:NZ	2.52	0.42
32:1a:186:C:H2'	32:1a:187:C:C6	2.54	0.42
32:1a:233:C:H2'	32:1a:234:C:H6	1.84	0.42
35:1d:122:ARG:HA	35:1d:122:ARG:HD2	1.81	0.42
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	2.01	0.42
37:1f:6:VAL:HG22	37:1f:90:VAL:HG22	2.00	0.42
1:2A:848:G:H2'	1:2A:849:A:C8	2.55	0.42
1:2A:1999:C:H4'	1:2A:2723:C:O2	2.20	0.42
1:2A:2184:G:O2'	1:2A:2185:C:H5'	2.20	0.42
4:2E:125:GLY:O	62:2E:401:HOH:O	2.21	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.84	0.42
32:2a:6:G:C4	36:2e:119:LEU:HD11	2.54	0.42
32:2a:184:G:H2'	32:2a:185:A:C8	2.53	0.42
32:2a:833:U:H2'	32:2a:834:C:H6	1.83	0.42
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.19	0.42
38:2g:78:ARG:HE	38:2g:79:ARG:NH2	2.17	0.42
41:2j:8:LEU:HD22	41:2j:96:ILE:HG12	2.01	0.42
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	2.01	0.42
50:2s:28:LYS:HD2	50:2s:28:LYS:N	2.34	0.42
51:2t:77:ALA:O	51:2t:81:LYS:HG3	2.19	0.42
1:1A:27:G:N2	1:1A:512:G:H1'	2.35	0.42
1:1A:286:C:H2'	1:1A:287:C:H6	1.84	0.42
1:1A:729:G:C8	3:1D:208:LYS:HD2	2.54	0.42
1:1A:880:G:H2'	1:1A:881:G:H8	1.84	0.42
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.20	0.42
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.39	0.42
1:1A:1914:C:H2'	1:1A:1915:5MU:O4'	2.19	0.42
1:1A:2123:G:H1	1:1A:2175:C:H42	1.66	0.42
1:1A:2124:G:H1	1:1A:2174:C:N4	2.16	0.42
1:1A:2134:A:H62	1:1A:2157:G:H1'	1.84	0.42
4:1E:4:ILE:HD12	4:1E:91:VAL:HG12	2.00	0.42
32:1a:134:A:H1'	32:1a:325:A:C5	2.54	0.42
32:1a:250:A:H4'	32:1a:251:G:O5'	2.19	0.42
32:1a:848:C:H2'	32:1a:849:C:H6	1.85	0.42
32:1a:934:C:OP1	62:1a:1913:HOH:O	2.21	0.42
32:1a:1186:G:O3'	40:1i:113:LYS:HE2	2.20	0.42
34:1c:23:TYR:HE1	41:1j:67:THR:HG23	1.83	0.42
46:1o:43:LEU:HD13	46:1o:53:HIS:HD2	1.83	0.42
54:1y:22:G:H2'	54:1y:23:A:C8	2.54	0.42
1:2A:27:G:N2	1:2A:512:G:H1'	2.33	0.42
1:2A:39:C:O2	5:2F:46:ARG:NH2	2.52	0.42
1:2A:271(H):G:O6	1:2A:271(Q):G:C6	2.73	0.42
1:2A:1188:U:C4'	17:2V:79:VAL:HG22	2.46	0.42
1:2A:1494:A:H2'	1:2A:1495:A:H8	1.85	0.42
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.55	0.42
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	2.01	0.42
6:2G:111:LEU:HD23	6:2G:117:PHE:CZ	2.54	0.42
12:2Q:52:VAL:HA	12:2Q:55:VAL:HG12	2.02	0.42
25:23:31:LEU:HD23	25:23:31:LEU:HA	1.92	0.42
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.52	0.42
32:2a:429:U:H1'	32:2a:430:A:H5''	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:901:A:O2'	32:2a:1513:A:OP1	2.33	0.42
32:2a:1002:G:C4	32:2a:1003:G:H8	2.38	0.42
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.54	0.42
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.51	0.42
32:2a:1358:U:H5'	45:2n:34:TYR:CD1	2.55	0.42
33:2b:58:ILE:HD13	33:2b:58:ILE:HA	1.92	0.42
34:2c:151:VAL:HG13	34:2c:199:LYS:O	2.19	0.42
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.59	0.42
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	2.01	0.42
35:2d:158:ILE:HD12	35:2d:158:ILE:H	1.84	0.42
35:2d:200:GLU:O	35:2d:204:ILE:HG12	2.19	0.42
51:2t:50:GLU:O	51:2t:100:ILE:HD11	2.20	0.42
1:1A:910:A:C6	1:1A:911:A:C6	3.07	0.42
1:1A:1815:A:H8	1:1A:1815:A:OP1	2.01	0.42
6:1G:114:ILE:HB	6:1G:117:PHE:HB2	2.02	0.42
27:15:8:LYS:O	27:15:9:LYS:HD2	2.19	0.42
32:1a:113:G:H2'	32:1a:114:U:C6	2.54	0.42
32:1a:560:U:H4'	32:1a:561:U:O5'	2.20	0.42
32:1a:674:G:H2'	32:1a:675:A:C8	2.54	0.42
32:1a:690:G:C6	32:1a:691:G:C6	3.08	0.42
32:1a:1005:A:H2	32:1a:1025:U:H1'	1.82	0.42
44:1m:122:LYS:HA	44:1m:122:LYS:HD2	1.88	0.42
55:1x:25:C:H2'	55:1x:26:G:O4'	2.19	0.42
1:2A:422:A:H2'	1:2A:423:A:C8	2.55	0.42
1:2A:718:A:H3'	1:2A:719:C:C6	2.55	0.42
1:2A:854:G:H2'	1:2A:855:G:H8	1.84	0.42
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.54	0.42
2:2B:90:A:N7	2:2B:91:C:H1'	2.34	0.42
32:2a:731:G:H5'	32:2a:766:A:H4'	2.01	0.42
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.53	0.42
32:2a:1518:MA6:C6	32:2a:1519:MA6:H103	2.49	0.42
33:2b:162:ILE:O	33:2b:185:ILE:HG12	2.20	0.42
41:2j:6:ILE:HA	41:2j:97:GLU:O	2.19	0.42
44:2m:33:ALA:HA	44:2m:59:TYR:HE2	1.83	0.42
47:2p:60:LEU:HD12	47:2p:60:LEU:HA	1.89	0.42
1:1A:897:C:H2'	1:1A:898:C:C6	2.54	0.42
1:1A:1401:G:H2'	1:1A:1402:C:O4'	2.20	0.42
1:1A:1791:A:H5'	3:1D:206:LEU:HD12	2.02	0.42
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.44	0.42
7:1H:98:LEU:HD23	7:1H:100:GLY:O	2.20	0.42
10:1O:63:VAL:HB	10:1O:102:VAL:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:87:LYS:HG3	20:1Y:95:LYS:HD2	2.01	0.42
32:1a:255:G:H1'	48:1q:16:GLN:OE1	2.19	0.42
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.54	0.42
32:1a:713:G:H2'	32:1a:714:G:C8	2.54	0.42
32:1a:1186:G:H21	45:1n:61:TRP:C	2.27	0.42
39:1h:34:GLU:O	39:1h:38:ILE:HG12	2.19	0.42
40:1i:97:LYS:HB3	40:1i:98:PRO:HD3	2.02	0.42
46:1o:68:ARG:HG2	46:1o:72:ARG:NH2	2.35	0.42
49:1r:37:VAL:HG12	49:1r:78:LEU:HB3	2.01	0.42
54:1w:75:C:OP1	54:1w:76:A:O2'	2.22	0.42
54:1y:26:A:N1	54:1y:44:G:N2	2.68	0.42
1:2A:212:G:H2'	1:2A:213:A:O4'	2.20	0.42
1:2A:271(X):G:C2	1:2A:271(Y):U:O4	2.72	0.42
1:2A:469:G:H2'	1:2A:470:A:H5''	2.01	0.42
1:2A:515:A:H1'	1:2A:581:C:H1'	2.02	0.42
1:2A:638:G:H2'	1:2A:639:U:O4'	2.19	0.42
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.19	0.42
1:2A:1786:A:C4	1:2A:1938:A:C6	3.08	0.42
1:2A:2445:G:P	5:2F:74:ARG:HH22	2.39	0.42
12:2Q:27:VAL:O	12:2Q:29:PHE:N	2.53	0.42
21:2Z:14:LYS:HA	21:2Z:15:PRO:HD3	1.84	0.42
23:21:98:LEU:HD23	23:21:98:LEU:HA	1.89	0.42
30:28:34:TRP:CG	30:28:35:GLN:N	2.88	0.42
32:2a:921:U:O2	36:2e:19:MET:HB2	2.18	0.42
34:2c:181:ASN:N	34:2c:205:GLY:O	2.49	0.42
38:2g:74:GLU:OE2	38:2g:95:ARG:NE	2.41	0.42
44:2m:16:ASP:OD1	44:2m:16:ASP:N	2.52	0.42
54:2w:73:A:H3'	54:2w:74:C:C5'	2.48	0.42
1:1A:625:G:O6	11:1P:107:LYS:NZ	2.48	0.42
1:1A:755:C:H2'	1:1A:756:C:C6	2.55	0.42
1:1A:1853:A:H2'	1:1A:1854:A:C8	2.55	0.42
3:1D:8:PRO:HB3	3:1D:14:ARG:NE	2.35	0.42
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.20	0.42
8:1I:109:ILE:HG23	8:1I:130:TYR:CZ	2.55	0.42
26:14:63:TYR:N	26:14:63:TYR:CD1	2.86	0.42
32:1a:8:A:H5'	36:1e:101:ILE:HG22	2.00	0.42
32:1a:313:A:H2'	32:1a:314:C:C6	2.55	0.42
32:1a:1065:U:H4'	32:1a:1066:C:O5'	2.19	0.42
32:1a:1229:A:O2'	55:1x:30:G:OP1	2.33	0.42
32:1a:1249:C:O2'	40:1i:73:GLN:NE2	2.53	0.42
35:1d:188:LEU:HA	35:1d:189:PRO:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271:A:N3	1:2A:365:C:O2'	2.50	0.42
1:2A:307:G:N7	62:2A:9850:HOH:O	2.36	0.42
1:2A:909:A:C6	1:2A:912:C:C2	3.07	0.42
1:2A:1179:C:H2'	1:2A:1180:C:C6	2.55	0.42
1:2A:2050:C:C4	1:2A:2051:A:C6	3.08	0.42
3:2D:274:ARG:N	62:2D:405:HOH:O	2.50	0.42
4:2E:72:VAL:HA	4:2E:73:GLU:CB	2.48	0.42
10:2O:35:VAL:HG23	10:2O:65:THR:HG23	2.02	0.42
10:2O:104:ARG:NH1	10:2O:104:ARG:HB2	2.35	0.42
15:2T:127:ALA:C	15:2T:129:ARG:N	2.78	0.42
32:2a:580:U:H5''	46:2o:58:MET:HG2	2.02	0.42
32:2a:872:A:C8	32:2a:874:G:C8	3.08	0.42
32:2a:1226:C:H2'	44:2m:103:THR:HB	2.00	0.42
32:2a:1348:U:O2'	40:2i:120:ARG:HD2	2.19	0.42
34:2c:112:SER:HB3	34:2c:115:LEU:HD22	2.01	0.42
52:2u:9:ARG:HH12	52:2u:10:ARG:NH2	2.17	0.42
1:1A:228:A:C8	1:1A:229:A:H5'	2.51	0.42
1:1A:236:C:H2'	1:1A:237:C:C6	2.55	0.42
1:1A:1054:A:N6	1:1A:1055:G:O6	2.53	0.42
1:1A:1786:A:H8	62:1A:4341:HOH:O	2.02	0.42
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.20	0.42
1:1A:2181:G:O2'	1:1A:2182:G:OP1	2.34	0.42
15:1T:116:ALA:HB1	15:1T:121:ILE:HD11	2.02	0.42
15:1T:127:ALA:C	15:1T:129:ARG:N	2.76	0.42
26:14:49:PHE:HB3	26:14:50:VAL:HG12	2.02	0.42
32:1a:1226:C:H2'	44:1m:103:THR:HB	2.02	0.42
35:1d:166:LYS:HA	35:1d:166:LYS:HD2	1.81	0.42
40:1i:53:VAL:C	40:1i:55:ALA:H	2.25	0.42
41:1j:38:ILE:HG12	41:1j:71:LEU:O	2.19	0.42
47:1p:14:ASN:OD1	47:1p:42:ARG:NH2	2.53	0.42
1:2A:196:A:N3	1:2A:196:A:H2'	2.35	0.42
1:2A:221:A:N1	1:2A:265:A:O2'	2.50	0.42
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.54	0.42
1:2A:669:G:C2	1:2A:801:G:C6	3.08	0.42
1:2A:848:G:N9	1:2A:933:A:H8	2.17	0.42
1:2A:920:G:H2'	1:2A:921:G:H8	1.85	0.42
1:2A:997:G:OP2	16:2U:58:ARG:NH1	2.51	0.42
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.55	0.42
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.52	0.42
1:2A:1810:A:H8	1:2A:1810:A:O5'	2.03	0.42
1:2A:1895:C:H2'	1:2A:1896:G:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1999:C:H2'	1:2A:2000:G:O4'	2.19	0.42
1:2A:2393:A:H2'	1:2A:2394:C:O4'	2.19	0.42
1:2A:2503:2MA:H4'	1:2A:2504:U:OP1	2.20	0.42
1:2A:2886:G:H2'	1:2A:2887:U:C6	2.54	0.42
57:2A:3670:4M2:H28	57:2A:3670:4M2:H27	1.73	0.42
3:2D:275:LYS:HA	3:2D:275:LYS:HD2	1.85	0.42
6:2G:76:SER:CB	6:2G:84:LYS:H	2.33	0.42
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.51	0.42
32:2a:1084:G:C5	32:2a:1085:U:C4	3.08	0.42
32:2a:1502:A:C8	32:2a:1505:G:N2	2.87	0.42
34:2c:6:HIS:CG	45:2n:49:HIS:HB3	2.55	0.42
34:2c:159:GLY:HA2	34:2c:193:TYR:CD1	2.55	0.42
35:2d:63:LYS:O	35:2d:67:ILE:HG13	2.20	0.42
35:2d:128:VAL:HG12	35:2d:129:ASN:ND2	2.35	0.42
40:2i:115:GLY:O	40:2i:116:LYS:HD3	2.20	0.42
41:2j:16:LEU:O	41:2j:20:ALA:N	2.53	0.42
1:1A:615:G:OP1	5:1F:40:GLN:NE2	2.27	0.42
1:1A:2168:G:C6	1:1A:2171:A:H8	2.38	0.42
1:1A:2319:G:C2	14:1S:3:ARG:HA	2.54	0.42
1:1A:2689:U:H4'	1:1A:2690:C:O5'	2.20	0.42
1:1A:2788:C:P	4:1E:61:ARG:HH21	2.42	0.42
57:1A:3894:4M2:H31	57:1A:3894:4M2:CAD	2.48	0.42
6:1G:150:ASP:OD1	6:1G:150:ASP:N	2.53	0.42
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.19	0.42
8:1I:109:ILE:HG23	8:1I:130:TYR:OH	2.20	0.42
9:1N:4:TYR:CE2	16:1U:100:VAL:HG11	2.55	0.42
15:1T:65:LYS:HE3	15:1T:67:SER:HB2	2.02	0.42
32:1a:189(L):G:H2'	32:1a:190:U:C6	2.55	0.42
32:1a:328:C:H4'	32:1a:329:A:H5'	2.01	0.42
32:1a:976:G:H22	32:1a:1363:C:C5'	2.33	0.42
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	2.01	0.42
47:1p:68:ASP:O	47:1p:71:ARG:HB3	2.20	0.42
50:1s:41:VAL:HG13	50:1s:42:PRO:HD2	2.02	0.42
1:2A:890:A:N6	1:2A:893:C:H42	2.18	0.42
1:2A:1406:U:H2'	1:2A:1407:C:H6	1.85	0.42
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	2.01	0.42
1:2A:2232:U:OP2	23:21:40:ARG:NH2	2.52	0.42
1:2A:2298:A:H1'	1:2A:2321:G:N2	2.34	0.42
1:2A:2485:G:C2	1:2A:2486:G:C8	3.08	0.42
1:2A:2589:A:OP1	62:2A:9763:HOH:O	2.22	0.42
1:2A:2848:G:H1'	1:2A:2867:G:N2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:42:C:C6	6:2G:69:ALA:HB2	2.54	0.42
30:28:23:VAL:CG1	30:28:47:LYS:HB3	2.50	0.42
32:2a:520:A:N1	32:2a:536:C:H1'	2.35	0.42
32:2a:1204:A:OP1	45:2n:3:ARG:NH1	2.29	0.42
55:2x:19:G:C4	55:2x:57:A:C2	3.07	0.42
1:1A:90:U:H1'	1:1A:92:A:C8	2.54	0.42
1:1A:776:G:H4'	1:1A:777:A:O5'	2.20	0.42
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.53	0.42
1:1A:2032:G:H1'	4:1E:145:LYS:HD3	2.02	0.42
1:1A:2346:A:N1	62:1A:4132:HOH:O	2.37	0.42
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.01	0.42
6:1G:122:PRO:HD3	6:1G:181:ARG:HG2	2.01	0.42
19:1X:26:TYR:HB3	19:1X:92:LEU:HD22	2.02	0.42
21:1Z:4:ARG:NE	21:1Z:60:GLU:OE2	2.38	0.42
22:10:18:ALA:HB3	22:10:20:ARG:NH1	2.35	0.42
32:1a:266:G:H2'	32:1a:266:G:N3	2.34	0.42
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.18	0.42
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.46	0.42
34:1c:45:LYS:HB2	34:1c:45:LYS:HE3	1.80	0.42
50:1s:35:SER:OG	50:1s:38:SER:OG	2.22	0.42
55:1x:50:U:H2'	55:1x:51:C:H6	1.84	0.42
55:1x:54:5MU:H2'	55:1x:55:PSU:O4'	2.20	0.42
1:2A:234:C:H2'	1:2A:235:U:C6	2.55	0.42
1:2A:1115:G:C2	1:2A:1116:C:C2	3.07	0.42
1:2A:1340:U:OP1	19:2X:16:LYS:NZ	2.41	0.42
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.28	0.42
1:2A:1589:C:H2'	1:2A:1590:U:C6	2.55	0.42
1:2A:2111:C:H6	1:2A:2111:C:OP2	2.02	0.42
1:2A:2114:A:N6	1:2A:2119:A:N7	2.67	0.42
1:2A:2125:G:N2	1:2A:2173:A:H62	2.17	0.42
1:2A:2815:C:H2'	1:2A:2816:C:H6	1.84	0.42
2:2B:11:C:H3'	2:2B:12:C:C6	2.55	0.42
7:2H:44:VAL:HG12	7:2H:46:GLU:HG3	2.02	0.42
9:2N:73:THR:OG1	9:2N:82:LEU:HD11	2.20	0.42
15:2T:24:PRO:HD3	15:2T:52:ILE:HD12	2.01	0.42
17:2V:40:LEU:HB2	17:2V:46:VAL:HG22	2.01	0.42
23:21:62:VAL:HG22	23:21:63:ALA:O	2.19	0.42
29:27:26:GLY:O	29:27:30:VAL:HG23	2.19	0.42
32:2a:736:C:H2'	32:2a:737:A:C8	2.55	0.42
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.19	0.42
32:2a:1103:C:H2'	32:2a:1104:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.02	0.42
35:2d:52:SER:O	35:2d:56:VAL:HG23	2.20	0.42
35:2d:155:LEU:O	35:2d:159:ARG:HG3	2.20	0.42
35:2d:176:LEU:HD12	35:2d:182:LYS:O	2.19	0.42
36:2e:30:ALA:O	36:2e:45:PHE:HA	2.20	0.42
48:2q:74:LEU:HD23	48:2q:75:ARG:HG2	2.02	0.42
54:2y:4:C:C2	54:2y:70:G:C2	3.07	0.42
1:1A:630:G:OP2	30:18:15:LYS:NZ	2.44	0.41
1:1A:775:G:O5'	1:1A:777:A:H1'	2.19	0.41
1:1A:908:C:OP1	12:1Q:22:LYS:HB3	2.20	0.41
1:1A:2059:A:H2'	1:1A:2503:2MA:HM23	2.02	0.41
1:1A:2398:U:H2'	1:1A:2399:G:H8	1.84	0.41
1:1A:2629:A:HO2'	1:1A:2630:G:P	2.38	0.41
4:1E:31:CYS:HA	4:1E:32:PRO:HD2	1.94	0.41
9:1N:39:ARG:HA	9:1N:40:PRO:HD3	1.93	0.41
32:1a:308:C:H2'	32:1a:309:G:H8	1.85	0.41
32:1a:1004:A:N7	32:1a:1036:G:N2	2.67	0.41
40:1i:50:LEU:HD22	40:1i:56:LEU:HD12	2.02	0.41
44:1m:16:ASP:N	44:1m:16:ASP:OD1	2.53	0.41
1:2A:18:C:H4'	16:2U:23:GLY:O	2.20	0.41
1:2A:251:A:C5	1:2A:252:G:H1'	2.55	0.41
1:2A:565:C:H2'	1:2A:566:U:O4'	2.19	0.41
1:2A:885:C:O2'	1:2A:892:G:O6	2.35	0.41
1:2A:903:C:O2'	1:2A:904:C:H5'	2.19	0.41
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.20	0.41
1:2A:1710:C:H5'	1:2A:2859:G:H1'	2.01	0.41
1:2A:2193:G:H2'	1:2A:2194:G:O4'	2.20	0.41
1:2A:2238:G:N3	1:2A:2238:G:H2'	2.35	0.41
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.19	0.41
1:2A:2558:C:H2'	1:2A:2559:C:O4'	2.20	0.41
1:2A:2690:C:N4	1:2A:2713:A:H1'	2.34	0.41
5:2F:9:ILE:HD13	5:2F:123:LEU:HD23	2.02	0.41
6:2G:61:ALA:HA	6:2G:66:GLN:O	2.20	0.41
7:2H:12:PRO:O	7:2H:15:VAL:HG12	2.19	0.41
25:23:50:VAL:O	25:23:54:VAL:HB	2.19	0.41
32:2a:1004:A:C2	32:2a:1038:C:C4	3.08	0.41
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.35	0.41
32:2a:1104:G:H2'	32:2a:1105:A:O4'	2.20	0.41
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.54	0.41
34:2c:66:VAL:O	34:2c:102:ASN:N	2.47	0.41
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:81:THR:O	41:2j:85:LEU:HG	2.20	0.41
43:2l:53:ARG:HB3	43:2l:69:TYR:HE1	1.84	0.41
44:2m:4:ILE:HG22	44:2m:7:VAL:O	2.19	0.41
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.22	0.41
50:2s:18:LYS:O	50:2s:22:LEU:HD13	2.20	0.41
50:2s:30:LEU:HA	50:2s:48:THR:O	2.19	0.41
1:1A:631:A:H2'	1:1A:632:A:O4'	2.19	0.41
1:1A:1949:G:C6	1:1A:1950:G:C6	3.09	0.41
1:1A:2332:U:O4	62:1A:4029:HOH:O	2.17	0.41
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.56	0.41
20:1Y:92:ASN:HB3	20:1Y:94:LYS:N	2.18	0.41
22:10:82:ARG:HA	22:10:83:PRO:HD3	1.93	0.41
32:1a:427:U:OP2	35:1d:36:ARG:NH1	2.51	0.41
32:1a:567:G:H2'	32:1a:568:G:O4'	2.20	0.41
32:1a:1027:C:N4	32:1a:1033:G:O6	2.53	0.41
34:1c:22:TRP:CD1	34:1c:59:ARG:HD2	2.54	0.41
35:1d:107:ARG:NH2	35:1d:194:LEU:HD11	2.35	0.41
36:1e:59:GLY:O	36:1e:63:ARG:NH1	2.53	0.41
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	2.02	0.41
1:2A:81:G:O2'	1:2A:295:G:O2'	2.23	0.41
1:2A:330:A:H2	1:2A:1210:A:O2'	2.03	0.41
1:2A:357:A:H8	1:2A:357:A:O5'	2.03	0.41
1:2A:717:G:H2'	1:2A:718:A:O4'	2.20	0.41
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.55	0.41
1:2A:2296:U:H4'	1:2A:2297:C:OP1	2.20	0.41
1:2A:2504:U:OP2	62:2A:9762:HOH:O	2.22	0.41
1:2A:2602:A:H4'	1:2A:2603:G:C5'	2.50	0.41
1:2A:2654:A:N1	1:2A:2665:A:H5''	2.35	0.41
2:2B:40:U:N3	2:2B:44:G:OP2	2.45	0.41
3:2D:69:ARG:C	3:2D:71:ASP:N	2.78	0.41
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.43	0.41
6:2G:44:GLY:O	6:2G:47:LYS:HB2	2.20	0.41
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.35	0.41
21:2Z:161:VAL:HG13	21:2Z:161:VAL:O	2.20	0.41
32:2a:110:C:H2'	32:2a:111:G:O4'	2.20	0.41
32:2a:358:U:H2'	32:2a:359:U:C6	2.55	0.41
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.34	0.41
32:2a:1222:G:H2'	32:2a:1223:C:O4'	2.20	0.41
32:2a:1517:G:N7	32:2a:1518:MA6:H103	2.35	0.41
35:2d:58:LEU:O	35:2d:62:GLN:HG2	2.20	0.41
38:2g:65:ALA:O	38:2g:69:VAL:HG23	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:45:SER:OG	49:2r:47:THR:HG22	2.20	0.41
50:2s:41:VAL:HG13	50:2s:42:PRO:HD2	2.01	0.41
1:1A:890:A:H2'	1:1A:892:G:O4'	2.20	0.41
1:1A:1038:C:N4	1:1A:1117:G:H1	2.17	0.41
1:1A:1227:G:OP1	16:1U:13:LYS:HG2	2.20	0.41
1:1A:1860:G:H2'	1:1A:1861:G:O4'	2.20	0.41
1:1A:2170:A:H8	1:1A:2170:A:O5'	2.03	0.41
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.19	0.41
32:1a:266:G:O3'	48:1q:67:LYS:HB2	2.20	0.41
32:1a:1147:C:O2'	40:1i:5:TYR:OH	2.30	0.41
39:1h:44:PHE:HB3	39:1h:80:ILE:HG12	2.02	0.41
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.85	0.41
1:2A:217:G:H2'	1:2A:218:A:O4'	2.19	0.41
1:2A:776:G:P	62:2A:9717:HOH:O	2.76	0.41
1:2A:1334:G:C6	1:2A:1335:U:C4	3.08	0.41
1:2A:1359:A:C2	1:2A:1372:U:O4	2.73	0.41
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.55	0.41
1:2A:1703:G:H2'	1:2A:1704:G:C8	2.55	0.41
1:2A:2475:C:H42	1:2A:2529:G:H22	1.67	0.41
5:2F:129:PHE:HB3	5:2F:132:VAL:HG11	2.03	0.41
8:2I:44:LEU:HD12	8:2I:44:LEU:HA	1.94	0.41
23:21:67:ILE:N	23:21:68:PRO:HD2	2.36	0.41
28:26:7:ILE:HG21	28:26:27:LYS:HD3	2.03	0.41
32:2a:163:C:H2'	32:2a:164:U:C6	2.54	0.41
32:2a:376:G:H4'	47:2p:5:ARG:HD3	2.02	0.41
32:2a:583:A:H2'	32:2a:584:G:O4'	2.20	0.41
32:2a:908:A:H2'	32:2a:909:A:C8	2.55	0.41
32:2a:1098:C:OP1	33:2b:144:ARG:NH2	2.53	0.41
34:2c:131:ARG:NH2	36:2e:50:GLU:HG2	2.35	0.41
34:2c:164:ARG:HG2	34:2c:165:THR:N	2.35	0.41
35:2d:47:ARG:HH12	35:2d:49:ARG:HG2	1.84	0.41
41:2j:7:LYS:HB2	41:2j:97:GLU:HB2	2.01	0.41
49:2r:53:ARG:HA	49:2r:56:THR:OG1	2.20	0.41
52:2u:3:LYS:HB3	52:2u:14:TRP:CG	2.55	0.41
52:2u:18:TYR:CE1	52:2u:24:ARG:HB3	2.56	0.41
54:2y:51:U:C2	54:2y:64:A:C2	3.09	0.41
1:1A:784:A:OP1	1:1A:2588:G:H5''	2.21	0.41
1:1A:2124:G:H2'	1:1A:2125:G:O4'	2.21	0.41
1:1A:2206:G:H5''	1:1A:2207:G:C5	2.56	0.41
1:1A:2259:G:C6	1:1A:2260:C:C4	3.08	0.41
6:1G:43:LEU:HB2	6:1G:89:GLY:HA2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:167:GLU:HA	7:1H:168:PRO:HD3	1.86	0.41
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	2.02	0.41
30:18:52:LYS:N	30:18:53:PRO:HD2	2.36	0.41
32:1a:22:G:H4'	32:1a:885:G:C8	2.55	0.41
32:1a:46:G:O2'	32:1a:365:U:H1'	2.20	0.41
32:1a:310:G:H4'	47:1p:31:LYS:HD2	2.02	0.41
32:1a:986:A:H1'	50:1s:54:GLY:O	2.20	0.41
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.20	0.41
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.42	0.41
32:1a:1227:A:OP2	44:1m:96:LEU:HD21	2.19	0.41
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.54	0.41
45:1n:23:ARG:HD2	45:1n:28:GLY:O	2.21	0.41
1:2A:375:C:H2'	1:2A:376:C:C6	2.56	0.41
1:2A:886:C:H2'	1:2A:887:A:H1'	2.02	0.41
1:2A:910:A:C6	1:2A:911:A:C6	3.09	0.41
1:2A:1021:A:C2	1:2A:1023:U:C2	3.08	0.41
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.19	0.41
1:2A:2417:C:C4	1:2A:2418:A:N7	2.88	0.41
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.52	0.41
8:2I:65:ALA:HB1	8:2I:132:PRO:HG2	2.02	0.41
21:2Z:73:GLN:HB3	21:2Z:87:ASP:OD2	2.21	0.41
24:22:12:GLU:O	24:22:16:LEU:HG	2.20	0.41
28:26:10:LEU:HD13	28:26:19:ARG:HD3	2.01	0.41
32:2a:1424:C:H2'	32:2a:1425:U:O4'	2.20	0.41
40:2i:85:LEU:O	40:2i:89:ASN:N	2.53	0.41
44:2m:14:ARG:HG3	44:2m:44:ARG:CZ	2.50	0.41
44:2m:91:ARG:O	44:2m:96:LEU:N	2.53	0.41
47:2p:5:ARG:HH21	47:2p:24:ALA:HA	1.84	0.41
55:2x:21:A:N6	55:2x:46:G:H2'	2.35	0.41
55:2x:55:PSU:O2'	55:2x:57:A:N7	2.45	0.41
1:1A:27:G:C2	1:1A:512:G:N3	2.88	0.41
1:1A:1071:G:O2'	1:1A:1089:G:H2'	2.21	0.41
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.35	0.41
1:1A:1466:G:H2'	1:1A:1547:C:H41	1.85	0.41
1:1A:2577:A:H5'	27:15:3:LYS:HE3	2.01	0.41
1:1A:2626:C:H2'	1:1A:2627:G:O4'	2.20	0.41
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.37	0.41
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	2.02	0.41
13:1R:36:THR:HG22	13:1R:37:THR:N	2.35	0.41
17:1V:81:TYR:C	17:1V:82:ARG:HG3	2.46	0.41
18:1W:1:MET:HG3	18:1W:64:MET:SD	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.50	0.41
32:1a:381:C:H2'	32:1a:382:A:O4'	2.20	0.41
32:1a:868:C:H2'	32:1a:869:G:O4'	2.21	0.41
32:1a:909:A:H2'	32:1a:910:C:O4'	2.19	0.41
37:1f:48:LEU:HD22	49:1r:77:GLY:HA3	2.02	0.41
38:1g:50:ILE:HD13	38:1g:50:ILE:HA	1.87	0.41
39:1h:118:VAL:O	39:1h:119:LEU:HD23	2.20	0.41
44:1m:3:ARG:CD	44:1m:9:ILE:HG12	2.46	0.41
51:1t:88:VAL:O	51:1t:92:LEU:HG	2.21	0.41
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.56	0.41
1:2A:702:G:C2	1:2A:731:C:C2	3.09	0.41
1:2A:855:G:H2'	1:2A:856:C:C6	2.56	0.41
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.86	0.41
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.21	0.41
1:2A:1885:A:H2'	1:2A:1886:C:O4'	2.20	0.41
1:2A:2064:C:H2'	1:2A:2065:C:C6	2.56	0.41
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.53	0.41
1:2A:2639:A:H2'	1:2A:2640:G:O4'	2.20	0.41
5:2F:196:LEU:HD23	5:2F:196:LEU:HA	1.92	0.41
6:2G:131:TYR:HE2	6:2G:133:LEU:HB3	1.84	0.41
12:2Q:85:LYS:HD2	12:2Q:85:LYS:N	2.35	0.41
32:2a:722:A:C8	32:2a:724:G:H1'	2.56	0.41
32:2a:735:C:H2'	32:2a:736:C:C6	2.55	0.41
32:2a:1518:MA6:H8	32:2a:1518:MA6:O5'	2.21	0.41
35:2d:53:ASP:HB3	35:2d:57:ARG:NH1	2.33	0.41
47:2p:53:VAL:HG22	47:2p:79:VAL:HG22	2.01	0.41
1:1A:987:G:O2'	1:1A:1000:A:N3	2.47	0.41
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.32	0.41
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	2.03	0.41
4:1E:14:ILE:HG13	4:1E:21:VAL:HG13	2.03	0.41
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.55	0.41
22:10:43:THR:O	22:10:43:THR:HG23	2.21	0.41
32:1a:1003:G:C2	32:1a:1004:A:C2	3.09	0.41
32:1a:1097:C:O2'	32:1a:1169:A:N3	2.48	0.41
32:1a:1399:C:C4'	32:1a:1400:5MC:H5''	2.45	0.41
34:1c:164:ARG:HG2	34:1c:165:THR:N	2.35	0.41
37:1f:94:GLN:CD	49:1r:32:ARG:HE	2.28	0.41
38:1g:54:THR:O	38:1g:56:GLN:N	2.48	0.41
43:1l:124:LYS:HA	43:1l:125:PRO:HD3	1.91	0.41
54:1y:49:C:N4	54:1y:65:G:N1	2.37	0.41
1:2A:271(S):G:C6	1:2A:271(T):C:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1816:G:H8	3:2D:62:TYR:CZ	2.39	0.41
3:2D:206:LEU:HA	3:2D:206:LEU:HD23	1.77	0.41
8:2I:77:LEU:HB3	8:2I:142:VAL:HG13	2.02	0.41
10:2O:2:ILE:HG21	10:2O:8:LEU:HD11	2.01	0.41
14:2S:87:PHE:CE1	14:2S:102:ALA:HB2	2.55	0.41
19:2X:35:THR:HG22	19:2X:37:THR:H	1.85	0.41
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.21	0.41
32:2a:22:G:H2'	32:2a:23:C:C6	2.56	0.41
32:2a:194:C:C2'	32:2a:195:A:H5''	2.50	0.41
32:2a:345:C:H5'	32:2a:346:G:C5	2.55	0.41
32:2a:551:U:H2'	32:2a:552:U:C6	2.55	0.41
32:2a:936:C:H2'	32:2a:937:A:O4'	2.21	0.41
32:2a:1287:A:N3	32:2a:1353:G:O2'	2.48	0.41
32:2a:1394:A:N1	32:2a:1500:A:O2'	2.45	0.41
34:2c:131:ARG:HH21	36:2e:50:GLU:HG2	1.85	0.41
44:2m:4:ILE:HG23	44:2m:5:ALA:N	2.35	0.41
54:2w:2:C:H2'	54:2w:3:C:C6	2.55	0.41
1:1A:361:G:N1	1:1A:362:U:O4	2.53	0.41
1:1A:1654:A:C1'	1:1A:2823:A:H5'	2.51	0.41
1:1A:2110:G:H2'	1:1A:2110:G:OP2	2.21	0.41
1:1A:2590:A:H2'	1:1A:2591:C:H6	1.85	0.41
2:1B:4:C:H2'	2:1B:5:C:O4'	2.21	0.41
2:1B:48:A:H4'	14:1S:95:HIS:CD2	2.53	0.41
5:1F:102:PRO:HB2	5:1F:105:VAL:HG23	2.01	0.41
6:1G:121:ASN:HA	6:1G:122:PRO:HD3	1.91	0.41
12:1Q:42:ILE:HG12	12:1Q:103:MET:HE1	2.03	0.41
32:1a:441:A:H8	32:1a:441:A:OP2	2.04	0.41
32:1a:542:G:P	35:1d:10:ARG:HH22	2.43	0.41
32:1a:838:G:H2'	32:1a:839:U:H2'	2.03	0.41
39:1h:85:ARG:NH2	39:1h:87:SER:O	2.53	0.41
40:1i:4:TYR:CE1	40:1i:88:TYR:HA	2.56	0.41
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.21	0.41
50:1s:44:MET:HB3	50:1s:62:ILE:HD13	2.02	0.41
55:1x:6:G:N2	55:1x:67:C:N3	2.56	0.41
1:2A:459:U:OP2	29:27:39:ARG:NH1	2.54	0.41
1:2A:631:A:H2'	1:2A:632:A:O4'	2.20	0.41
1:2A:947:G:H2'	1:2A:948:G:C8	2.55	0.41
1:2A:2078:C:H2'	1:2A:2079:U:C6	2.55	0.41
1:2A:2159:G:N1	1:2A:2160:G:O6	2.54	0.41
1:2A:2165:G:H2'	1:2A:2166:G:C4'	2.51	0.41
1:2A:2228:G:C5	1:2A:2229:C:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2230:G:H1'	23:21:45:ASN:CG	2.46	0.41
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.20	0.41
5:2F:116:ASP:OD2	5:2F:117:ARG:NH1	2.53	0.41
11:2P:44:GLY:CA	11:2P:45:LEU:HB2	2.50	0.41
20:2Y:77:PRO:HD2	20:2Y:106:LEU:HD23	2.03	0.41
28:26:10:LEU:HG	28:26:54:ILE:HG13	2.01	0.41
32:2a:21:G:H2'	32:2a:22:G:C8	2.56	0.41
32:2a:586:C:O2'	32:2a:878:G:H4'	2.20	0.41
32:2a:814:A:N7	32:2a:816:A:C4	2.88	0.41
32:2a:933:G:OP2	38:2g:3:ARG:HB2	2.20	0.41
32:2a:975:A:N6	32:2a:1367:C:O4'	2.54	0.41
32:2a:1003:G:H2'	32:2a:1004:A:H1'	2.03	0.41
32:2a:1239:A:O2'	32:2a:1298:C:N4	2.44	0.41
32:2a:1431:C:H2'	32:2a:1432:G:O4'	2.19	0.41
44:2m:19:LEU:HD23	44:2m:30:ALA:HA	2.03	0.41
1:1A:192:C:O2'	1:1A:802:A:N3	2.51	0.41
1:1A:312:G:H5'	1:1A:331:A:O2'	2.20	0.41
1:1A:1094:U:C4	1:1A:1096:A:H5''	2.56	0.41
1:1A:1590:U:H2'	1:1A:1591:G:H8	1.86	0.41
1:1A:1665:A:H2'	1:1A:1666:G:O4'	2.20	0.41
1:1A:1843:C:H5'	3:1D:253:GLN:OE1	2.21	0.41
1:1A:2105:C:H2'	1:1A:2106:G:C8	2.55	0.41
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	2.01	0.41
10:1O:1:MET:HE3	10:1O:32:TYR:CZ	2.55	0.41
12:1Q:85:LYS:HD2	12:1Q:85:LYS:N	2.35	0.41
32:1a:404:U:H2'	32:1a:405:U:C6	2.56	0.41
32:1a:662:G:H2'	32:1a:663:A:C8	2.54	0.41
32:1a:864:A:H2'	32:1a:865:A:C8	2.56	0.41
32:1a:1028:C:H2'	32:1a:1029:C:C4'	2.51	0.41
32:1a:1239:A:O2'	38:1g:114:ARG:O	2.32	0.41
33:1b:111:ARG:HH12	33:1b:114:ARG:HD3	1.86	0.41
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.29	0.41
38:1g:111:ARG:HG2	38:1g:113:GLU:OE1	2.19	0.41
39:1h:51:VAL:HG21	39:1h:60:ARG:HD2	2.02	0.41
42:1k:32:ILE:HG22	42:1k:77:MET:HE3	2.02	0.41
44:1m:81:LEU:O	44:1m:89:GLY:HA3	2.20	0.41
46:1o:56:LEU:O	46:1o:60:VAL:HG23	2.20	0.41
54:1w:23:A:H2'	54:1w:24:G:H8	1.86	0.41
1:2A:1418:G:H8	1:2A:1418:G:O5'	2.04	0.41
1:2A:1422:G:C6	1:2A:1423:G:C5	3.09	0.41
1:2A:1906:G:OP2	1:2A:1929:G:O2'	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:66:GLU:OE2	8:2I:69:LYS:HD3	2.20	0.41
9:2N:48:MET:HE3	9:2N:48:MET:HB2	1.81	0.41
24:22:53:LEU:HD23	24:22:53:LEU:HA	1.86	0.41
27:25:16:ARG:HH11	27:25:17:ASP:CG	2.27	0.41
32:2a:1039:C:N4	32:2a:1040:U:C4	2.88	0.41
32:2a:1509:C:H2'	32:2a:1510:U:O4'	2.20	0.41
33:2b:51:LEU:HD23	33:2b:201:ILE:HD12	2.03	0.41
33:2b:163:PHE:HA	33:2b:185:ILE:O	2.21	0.41
40:2i:23:ASN:ND2	40:2i:25:LYS:HG2	2.35	0.41
54:2y:9:A:H5'	54:2y:46:7MG:N3	2.35	0.41
1:1A:184:C:H2'	1:1A:185:U:H6	1.83	0.41
1:1A:324:A:H2'	1:1A:325:G:O4'	2.21	0.41
1:1A:363(C):G:H2'	1:1A:363(D):G:C8	2.55	0.41
1:1A:428:A:H8	1:1A:428:A:OP2	2.04	0.41
1:1A:493:G:H2'	1:1A:494:G:O4'	2.19	0.41
1:1A:1111:A:N3	1:1A:1112:G:H1'	2.36	0.41
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	2.02	0.41
1:1A:1203:G:H5'	11:1P:3:LEU:HD23	2.02	0.41
1:1A:2097:C:H2'	1:1A:2098:U:O4'	2.21	0.41
1:1A:2106:G:H2'	1:1A:2107:C:C6	2.56	0.41
1:1A:2807:G:C2	1:1A:2808:U:C2	3.08	0.41
5:1F:11:VAL:HB	5:1F:18:ARG:HG3	2.03	0.41
5:1F:34:TRP:HA	11:1P:6:LEU:HD13	2.03	0.41
6:1G:48:GLU:O	6:1G:51:ARG:HG3	2.21	0.41
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.56	0.41
6:1G:126:ASP:OD2	6:1G:130:ASN:ND2	2.47	0.41
7:1H:88:LEU:HD12	7:1H:130:ARG:HG2	2.02	0.41
11:1P:126:VAL:HG12	11:1P:148:LEU:HD22	2.02	0.41
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	2.02	0.41
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	2.02	0.41
30:18:6:THR:HG23	30:18:64:TYR:HD2	1.85	0.41
32:1a:114:U:H1'	32:1a:353:A:H1'	2.03	0.41
32:1a:272:C:H2'	32:1a:273:A:C8	2.56	0.41
32:1a:1003:G:C2	32:1a:1004:A:H2	2.39	0.41
32:1a:1113:C:H1'	34:1c:178:LEU:HD22	2.01	0.41
32:1a:1159:U:OP1	33:1b:133:LYS:NZ	2.54	0.41
32:1a:1191:A:OP2	34:1c:3:ASN:ND2	2.54	0.41
32:1a:1417:G:H22	32:1a:1482:G:H2'	1.86	0.41
33:1b:189:ASP:O	33:1b:192:SER:OG	2.35	0.41
46:1o:55:GLY:O	46:1o:59:MET:HG3	2.21	0.41
50:1s:12:ASP:OD1	50:1s:37:ARG:NH2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:22:G:H2'	54:1w:23:A:H8	1.85	0.41
54:1w:26:A:N6	54:1w:44:G:H1	2.18	0.41
1:2A:225:A:N6	1:2A:226:G:C2	2.89	0.41
1:2A:287:C:H2'	1:2A:288:C:C6	2.56	0.41
1:2A:315:G:H2'	1:2A:316:C:C6	2.56	0.41
1:2A:647:G:H2'	1:2A:648:G:O4'	2.21	0.41
1:2A:826:U:H4'	11:2P:55:ARG:HB3	2.03	0.41
1:2A:980:A:N3	1:2A:2037:G:O2'	2.49	0.41
1:2A:1006:C:H5'	9:2N:28:THR:HG23	2.03	0.41
1:2A:1227:G:H2'	1:2A:1228:G:O4'	2.21	0.41
1:2A:1262:A:H2	27:25:10:LYS:HD2	1.86	0.41
1:2A:1301:A:C8	1:2A:1303:G:C8	3.09	0.41
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.55	0.41
1:2A:1751:C:O2'	1:2A:2861:G:O2'	2.25	0.41
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.20	0.41
1:2A:2104:G:N2	1:2A:2185:C:N3	2.65	0.41
1:2A:2189:U:H5'	1:2A:2190:G:OP2	2.21	0.41
1:2A:2287:A:C4	1:2A:2289:G:C8	3.09	0.41
1:2A:2436:G:C5	1:2A:2437:U:C5	3.09	0.41
1:2A:2691:C:O3'	1:2A:2871:C:H4'	2.20	0.41
1:2A:2836:U:C4	1:2A:2883:A:N6	2.88	0.41
3:2D:69:ARG:C	3:2D:71:ASP:H	2.29	0.41
7:2H:24:VAL:HG13	7:2H:37:VAL:HG21	2.02	0.41
9:2N:112:LEU:O	9:2N:116:LEU:HG	2.21	0.41
10:2O:7:TYR:CZ	10:2O:44:LYS:HG3	2.56	0.41
10:2O:108:GLU:H	10:2O:108:GLU:HG2	1.56	0.41
17:2V:14:VAL:HA	17:2V:18:LEU:HD12	2.03	0.41
19:2X:50:LYS:HB3	19:2X:84:ALA:HB2	2.02	0.41
20:2Y:30:VAL:O	20:2Y:32:PRO:HD3	2.20	0.41
21:2Z:121:HIS:HB3	21:2Z:123:ASP:O	2.21	0.41
30:28:32:LEU:HD12	30:28:32:LEU:HA	1.89	0.41
32:2a:258:G:H1	32:2a:268:C:H42	1.68	0.41
32:2a:620:C:H2'	32:2a:621:A:O4'	2.21	0.41
32:2a:738:C:H2'	32:2a:739:C:H6	1.86	0.41
32:2a:986:A:H2'	32:2a:987:G:O4'	2.20	0.41
32:2a:1006:C:N3	32:2a:1023:G:C6	2.88	0.41
32:2a:1047:G:H1	32:2a:1210:C:N4	2.15	0.41
32:2a:1332:A:H2'	32:2a:1333:A:C8	2.55	0.41
33:2b:58:ILE:HD11	33:2b:185:ILE:HD12	2.02	0.41
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	2.02	0.41
33:2b:171:ALA:HA	33:2b:174:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:119:ARG:HG3	34:2c:120:VAL:N	2.36	0.41
34:2c:156:ARG:HG2	34:2c:163:ALA:HB2	2.02	0.41
36:2e:122:GLU:HB2	36:2e:126:ARG:NH1	2.34	0.41
37:2f:9:VAL:HG22	37:2f:60:PHE:CD1	2.56	0.41
37:2f:76:ALA:O	37:2f:80:ARG:HG3	2.20	0.41
40:2i:20:ARG:HA	40:2i:21:PRO:HD3	1.93	0.41
44:2m:3:ARG:HH11	44:2m:45:VAL:HG11	1.86	0.41
47:2p:15:PRO:O	47:2p:16:HIS:ND1	2.53	0.41
50:2s:27:GLU:C	50:2s:28:LYS:HD2	2.46	0.41
53:2v:16:A:H2'	53:2v:17:U:O4'	2.20	0.41
54:2y:31:A:H2'	54:2y:32:PSU:O4'	2.21	0.41
54:2y:58:A:H4'	54:2y:59:U:OP1	2.20	0.41
1:1A:817:C:H4'	1:1A:932:G:C5	2.56	0.41
1:1A:1184:G:H5'	25:13:29:ARG:HH11	1.86	0.41
1:1A:1368:G:C2	1:1A:1369:G:C8	3.09	0.41
1:1A:1470:G:H5''	1:1A:1471:A:OP1	2.21	0.41
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.20	0.41
1:1A:2061:G:N2	61:1x:115:FME:O1	2.47	0.41
1:1A:2430:A:H5'	1:1A:2431:U:OP2	2.21	0.41
32:1a:501:C:H2'	32:1a:502:G:H8	1.85	0.41
32:1a:673:G:H2'	32:1a:674:G:C8	2.56	0.41
55:1x:75:C:H2'	55:1x:76:A:H1'	2.02	0.41
1:2A:38:A:H2'	1:2A:39:C:C6	2.56	0.41
1:2A:79:G:H2'	1:2A:80:G:C8	2.55	0.41
1:2A:614:U:H5'	1:2A:614(C):A:N6	2.36	0.41
1:2A:2119:A:C5	1:2A:2170:A:C6	3.09	0.41
1:2A:2712:U:OP1	1:2A:2714:G:H4'	2.20	0.41
8:2I:52:ARG:HE	8:2I:52:ARG:HB2	1.67	0.41
8:2I:84:GLY:O	8:2I:86:THR:N	2.51	0.41
13:2R:28:LEU:HD13	13:2R:48:VAL:HG21	2.03	0.41
17:2V:21:ARG:HD3	17:2V:91:TYR:CD1	2.55	0.41
22:20:39:ARG:HA	22:20:39:ARG:HD3	1.90	0.41
22:20:43:THR:HG23	22:20:43:THR:O	2.21	0.41
32:2a:93:G:C6	32:2a:96:U:C4	3.09	0.41
32:2a:250:A:H4'	32:2a:251:G:O5'	2.20	0.41
32:2a:457:C:H2'	32:2a:458:C:H6	1.86	0.41
33:2b:15:VAL:HG23	33:2b:16:HIS:HD2	1.85	0.41
35:2d:112:VAL:HG22	35:2d:116:GLN:OE1	2.21	0.41
39:2h:111:ILE:HD12	39:2h:135:CYS:SG	2.61	0.41
42:2k:79:SER:HA	42:2k:104:GLN:HB3	2.02	0.41
55:2x:61:C:H2'	55:2x:62:C:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:228:A:H2'	1:1A:230:U:O4'	2.20	0.40
1:1A:1065:U:H1'	1:1A:1074:G:C2	2.55	0.40
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.35	0.40
1:1A:2529:G:H5''	1:1A:2530:A:H5''	2.02	0.40
1:1A:2851:A:H2'	1:1A:2852:G:O4'	2.21	0.40
3:1D:6:PHE:HB3	3:1D:13:ARG:HG3	2.03	0.40
8:1I:73:GLU:HG3	8:1I:139:GLN:HB2	2.03	0.40
13:1R:52:ILE:HD11	13:1R:116:LEU:HD22	2.01	0.40
26:14:44:THR:O	26:14:45:GLY:C	2.64	0.40
32:1a:107:G:H2'	32:1a:108:G:O4'	2.20	0.40
32:1a:109:A:H2'	32:1a:326:G:N2	2.35	0.40
32:1a:427:U:OP1	35:1d:13:ARG:NH1	2.51	0.40
32:1a:502:G:C2	32:1a:503:C:C2	3.09	0.40
32:1a:626:U:C2	32:1a:627:G:C8	3.09	0.40
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.21	0.40
32:1a:1342:C:H4'	40:1i:125:TYR:O	2.21	0.40
33:1b:158:LEU:HD12	33:1b:158:LEU:HA	1.85	0.40
38:1g:78:ARG:HD2	38:1g:156:TRP:CE3	2.56	0.40
41:1j:35:SER:CB	41:1j:73:ASP:HB2	2.51	0.40
45:1n:37:PHE:C	45:1n:39:LEU:H	2.28	0.40
48:1q:45:HIS:HB3	48:1q:72:ARG:HG2	2.03	0.40
54:1y:44:G:H3'	54:1y:45:U:C6	2.56	0.40
1:2A:261:G:O2'	1:2A:610:G:O2'	2.32	0.40
1:2A:322:A:H3'	5:2F:169:ASN:OD1	2.21	0.40
1:2A:427:U:O3'	1:2A:428:A:H8	2.03	0.40
1:2A:537:C:H2'	1:2A:538:G:H8	1.86	0.40
1:2A:900:A:H2'	1:2A:901:A:H8	1.86	0.40
1:2A:1449:A:H5'	1:2A:1450:G:OP2	2.21	0.40
1:2A:2547:U:C5	1:2A:2566:A:C5	3.08	0.40
1:2A:2886:G:H2'	1:2A:2887:U:H6	1.86	0.40
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.55	0.40
26:24:59:PHE:N	26:24:59:PHE:CD2	2.89	0.40
32:2a:284:G:H2'	32:2a:285:G:H8	1.86	0.40
32:2a:1291:G:C6	32:2a:1292:U:C4	3.09	0.40
44:2m:122:LYS:HA	44:2m:122:LYS:HD2	1.87	0.40
54:2w:27:G:H2'	54:2w:28:G:O4'	2.21	0.40
1:1A:309:G:N3	1:1A:329:G:O2'	2.46	0.40
1:1A:588:U:H1'	5:1F:90:PHE:CG	2.56	0.40
1:1A:2141:G:C5	1:1A:2142:C:C2	3.09	0.40
1:1A:2584:U:H4'	57:1A:3894:4M2:H46	2.04	0.40
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.56	0.40
32:1a:1072:G:C6	32:1a:1073:U:C4	3.09	0.40
40:1i:49:PRO:HG2	40:1i:82:ALA:HB2	2.03	0.40
40:1i:63:ILE:HG22	40:1i:65:VAL:HG23	2.04	0.40
40:1i:112:LYS:HE2	40:1i:117:HIS:O	2.21	0.40
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.52	0.40
54:1y:11:C:H42	54:1y:24:G:H1	1.68	0.40
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.57	0.40
1:2A:271(U):G:N7	62:2A:9859:HOH:O	2.37	0.40
1:2A:500:G:N2	1:2A:502:A:H3'	2.36	0.40
1:2A:608:A:C6	1:2A:609:A:C6	3.09	0.40
1:2A:643:A:C8	28:26:44:ARG:NH1	2.89	0.40
1:2A:1114:G:H2'	1:2A:1115:G:C8	2.56	0.40
1:2A:2149:G:C6	1:2A:2150:U:C2	3.09	0.40
1:2A:2577:A:H5''	1:2A:2578:G:H5'	2.03	0.40
2:2B:49:C:H2'	2:2B:50:G:C8	2.56	0.40
5:2F:170:LEU:HA	5:2F:171:PRO:HD3	1.94	0.40
13:2R:33:ARG:NH1	27:25:57:VAL:O	2.54	0.40
13:2R:83:ILE:O	13:2R:86:ARG:HG2	2.21	0.40
26:24:62:ARG:HA	26:24:62:ARG:HD3	1.87	0.40
32:2a:155:C:H2'	32:2a:156:G:O4'	2.22	0.40
32:2a:728:A:H2'	32:2a:729:A:C8	2.56	0.40
32:2a:1004:A:C8	32:2a:1038:C:H1'	2.55	0.40
34:2c:130:VAL:HG11	34:2c:153:VAL:HG11	2.03	0.40
44:2m:19:LEU:HB3	44:2m:25:ILE:HG21	2.04	0.40
48:2q:81:ARG:HH21	48:2q:84:LEU:HD21	1.86	0.40
1:1A:360:G:H2'	1:1A:361:G:O4'	2.21	0.40
1:1A:370:G:H4'	1:1A:371:A:OP2	2.21	0.40
1:1A:764:A:N3	3:1D:213:ARG:NH1	2.67	0.40
1:1A:857:C:N4	1:1A:858:U:O4	2.55	0.40
3:1D:145:VAL:HB	3:1D:155:LEU:HB2	2.03	0.40
3:1D:223:GLY:HA3	3:1D:231:HIS:CE1	2.57	0.40
5:1F:12:LEU:HB3	5:1F:126:VAL:HG12	2.04	0.40
8:1I:124:GLY:H	8:1I:144:VAL:HG23	1.86	0.40
9:1N:14:VAL:HG11	9:1N:138:LEU:HD12	2.03	0.40
19:1X:27:THR:OG1	19:1X:80:ILE:HG12	2.22	0.40
21:1Z:93:ASP:N	21:1Z:93:ASP:OD1	2.54	0.40
32:1a:1162:C:H2'	32:1a:1163:C:C6	2.56	0.40
32:1a:1164:G:H2'	32:1a:1165:C:H6	1.86	0.40
38:1g:66:VAL:HG12	38:1g:70:LYS:HE3	2.02	0.40
40:1i:40:LEU:HD11	40:1i:70:LYS:HD2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	2.03	0.40
54:1w:52:G:H2'	54:1w:53:G:O4'	2.22	0.40
54:1y:5:G:C6	54:1y:6:G:C5	3.08	0.40
1:2A:753:C:H2'	1:2A:754:C:H6	1.86	0.40
1:2A:1269:A:O2'	1:2A:1325:G:O6	2.39	0.40
1:2A:2160:G:H2'	1:2A:2161:C:O4'	2.22	0.40
1:2A:2419:U:H2'	1:2A:2420:C:C6	2.57	0.40
1:2A:2430:A:H5'	1:2A:2431:U:OP2	2.21	0.40
1:2A:2521:C:C4	1:2A:2522:U:C4	3.10	0.40
1:2A:2848:G:C8	15:2T:97:ALA:HB2	2.56	0.40
3:2D:232:PRO:HG2	3:2D:248:SER:O	2.20	0.40
11:2P:36:LYS:HB3	11:2P:37:GLY:H	1.76	0.40
15:2T:51:ARG:HB3	15:2T:62:THR:HB	2.02	0.40
16:2U:48:ALA:O	16:2U:52:ARG:HB2	2.21	0.40
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.86	0.40
28:26:6:ARG:HH12	28:26:26:ASN:HB2	1.85	0.40
30:28:62:LEU:HB3	30:28:65:GLU:CG	2.51	0.40
31:29:27:CYS:SG	31:29:28:GLU:N	2.94	0.40
32:2a:1316:G:H4'	45:2n:18:VAL:HG13	2.04	0.40
34:2c:42:LEU:O	34:2c:46:GLU:HB2	2.21	0.40
35:2d:78:LEU:HD23	35:2d:96:LEU:HB3	2.03	0.40
37:2f:89:MET:HE1	49:2r:72:ARG:HG2	2.03	0.40
43:2l:24:VAL:HG12	43:2l:98:TYR:CE1	2.56	0.40
46:2o:36:ILE:HG23	46:2o:56:LEU:HD11	2.02	0.40
48:2q:5:VAL:C	48:2q:6:LEU:HD12	2.47	0.40
54:2y:64:A:H2'	54:2y:65:G:H8	1.86	0.40
1:1A:271(E):U:H2'	1:1A:271(F):C:H6	1.86	0.40
1:1A:631:A:HO2'	11:1P:67:MET:H	1.70	0.40
1:1A:904:C:O2'	21:1Z:169:GLU:OE2	2.30	0.40
1:1A:1231:G:H2'	1:1A:1232:G:H8	1.86	0.40
1:1A:2030:A:H4'	1:1A:2031:A:C8	2.57	0.40
1:1A:2126:A:H4'	1:1A:2127:G:OP1	2.20	0.40
1:1A:2740:A:C6	1:1A:2764:A:C8	3.09	0.40
4:1E:126:PRO:HB2	4:1E:131:ALA:HB2	2.03	0.40
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.53	0.40
6:1G:49:ASP:O	6:1G:51:ARG:N	2.54	0.40
6:1G:133:LEU:HG	6:1G:157:ILE:HB	2.03	0.40
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.22	0.40
8:1I:129:THR:HG22	8:1I:139:GLN:NE2	2.35	0.40
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.57	0.40
14:1S:65:VAL:O	14:1S:69:VAL:HG12	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:161:VAL:HG22	21:1Z:162:GLU:H	1.85	0.40
32:1a:392:G:H2'	32:1a:393:A:C8	2.56	0.40
32:1a:595:G:N3	32:1a:596:C:N4	2.70	0.40
32:1a:1509:C:H2'	32:1a:1510:U:O4'	2.21	0.40
36:1e:57:LYS:HG2	36:1e:61:TYR:HE2	1.84	0.40
39:1h:87:SER:CB	39:1h:93:VAL:H	2.34	0.40
40:1i:28:VAL:HA	40:1i:63:ILE:O	2.22	0.40
1:2A:277:C:HO2'	1:2A:278:A:P	2.44	0.40
1:2A:579:G:C8	1:2A:2017:U:C4	3.10	0.40
1:2A:637:A:H8	11:2P:117:GLU:HG3	1.87	0.40
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.21	0.40
1:2A:1508:A:H5'	1:2A:1509(A):A:N7	2.36	0.40
1:2A:1993:U:H2'	1:2A:1994:C:O4'	2.20	0.40
1:2A:2056:G:N2	27:25:5:PRO:HA	2.37	0.40
1:2A:2126:A:C2	1:2A:2127:G:H1'	2.57	0.40
1:2A:2336:A:H61	22:20:43:THR:HG22	1.87	0.40
1:2A:2516:G:C6	1:2A:2517:C:C4	3.09	0.40
7:2H:38:SER:HA	7:2H:39:PRO:HD3	1.91	0.40
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.21	0.40
32:2a:46:G:H2'	32:2a:366:C:C5	2.57	0.40
32:2a:362:G:N2	32:2a:365:U:OP2	2.54	0.40
32:2a:1123:A:H4'	41:2j:36:GLY:HA3	2.02	0.40
40:2i:127:LYS:O	40:2i:128:ARG:HB3	2.21	0.40
49:2r:65:ILE:H	49:2r:65:ILE:HG12	1.64	0.40
54:2w:47:U:H3'	54:2w:48:C:C5'	2.52	0.40
1:1A:1062:G:C8	1:1A:1088:A:H2'	2.56	0.40
1:1A:1826:G:H2'	1:1A:1827:C:O4'	2.20	0.40
1:1A:2137:C:H2'	1:1A:2138:C:H6	1.87	0.40
1:1A:2702:U:H4'	1:1A:2703:C:OP1	2.20	0.40
1:1A:2871:C:N3	62:1A:4142:HOH:O	2.37	0.40
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.22	0.40
6:1G:53:LEU:HA	6:1G:53:LEU:HD23	1.84	0.40
6:1G:140:ILE:HD13	6:1G:140:ILE:HA	1.81	0.40
10:1O:70:LYS:HB3	10:1O:70:LYS:HE2	1.92	0.40
16:1U:48:ALA:O	16:1U:52:ARG:HB2	2.22	0.40
24:12:23:LYS:O	24:12:27:GLU:HG3	2.22	0.40
32:1a:79:G:N2	32:1a:90:U:O2	2.55	0.40
32:1a:1038:C:O2'	32:1a:1039:C:H5'	2.21	0.40
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.57	0.40
36:1e:90:VAL:O	36:1e:120:THR:HA	2.22	0.40
39:1h:94:TYR:HE1	39:1h:132:GLU:HB2	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.54	0.40
48:1q:50:LYS:HE3	48:1q:51:TYR:CE2	2.56	0.40
1:2A:614(A):U:H4'	1:2A:614(B):G:H5''	2.03	0.40
1:2A:860:U:H1'	1:2A:2268:A:H5'	2.03	0.40
1:2A:1296:G:OP1	1:2A:2709:G:O2'	2.29	0.40
1:2A:1538:G:H2'	1:2A:1539:G:C8	2.56	0.40
1:2A:2637:U:H5''	4:2E:82:ARG:NH1	2.37	0.40
2:2B:58:A:C5	2:2B:59:A:C8	3.09	0.40
2:2B:103:G:N2	21:2Z:73:GLN:HE22	2.18	0.40
11:2P:85:LEU:HD13	11:2P:120:ALA:HB2	2.03	0.40
15:2T:8:LYS:HD2	15:2T:8:LYS:HA	1.94	0.40
16:2U:108:GLU:O	16:2U:112:ARG:HG3	2.21	0.40
22:20:10:THR:HG22	22:20:12:ASN:N	2.16	0.40
32:2a:23:C:H5	32:2a:561:U:O4	2.04	0.40
32:2a:45:U:OP1	32:2a:307:C:O2'	2.37	0.40
32:2a:397:A:H3'	32:2a:397:A:N3	2.36	0.40
32:2a:613:C:H2'	32:2a:614:A:H8	1.87	0.40
32:2a:1150:U:H2'	32:2a:1151:A:H5'	2.02	0.40
32:2a:1298:C:H1'	32:2a:1299:A:C2	2.56	0.40
33:2b:40:HIS:HB2	33:2b:190:THR:HG21	2.04	0.40
34:2c:124:ILE:HD11	34:2c:189:ALA:HB1	2.03	0.40
38:2g:78:ARG:HG2	38:2g:79:ARG:N	2.37	0.40
41:2j:23:ILE:HD13	41:2j:23:ILE:HA	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	260 (95%)	12 (4%)	1 (0%)	30	45
3	2D	273/276 (99%)	263 (96%)	9 (3%)	1 (0%)	30	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	1E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	24	39
4	2E	202/206 (98%)	193 (96%)	7 (4%)	2 (1%)	12	20
5	1F	201/210 (96%)	198 (98%)	2 (1%)	1 (0%)	24	39
5	2F	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	12	20
6	1G	179/182 (98%)	167 (93%)	9 (5%)	3 (2%)	7	12
6	2G	179/182 (98%)	167 (93%)	9 (5%)	3 (2%)	7	12
7	1H	172/180 (96%)	156 (91%)	15 (9%)	1 (1%)	21	34
7	2H	172/180 (96%)	157 (91%)	14 (8%)	1 (1%)	21	34
8	1I	144/148 (97%)	130 (90%)	11 (8%)	3 (2%)	5	9
8	2I	144/148 (97%)	130 (90%)	13 (9%)	1 (1%)	18	30
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	18	30
10	1O	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	1P	147/150 (98%)	139 (95%)	7 (5%)	1 (1%)	18	30
11	2P	147/150 (98%)	136 (92%)	10 (7%)	1 (1%)	18	30
12	1Q	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
12	2Q	139/141 (99%)	135 (97%)	3 (2%)	1 (1%)	18	30
13	1R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
13	2R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
14	1S	108/112 (96%)	103 (95%)	5 (5%)	0	100	100
14	2S	108/112 (96%)	101 (94%)	7 (6%)	0	100	100
15	1T	129/146 (88%)	119 (92%)	10 (8%)	0	100	100
15	2T	129/146 (88%)	119 (92%)	10 (8%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	114 (100%)	0	0	100	100
17	1V	99/101 (98%)	94 (95%)	4 (4%)	1 (1%)	12	20
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%)	108 (98%)	2 (2%)	0	100	100
19	1X	93/96 (97%)	92 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	2X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	19
20	1Y	105/110 (96%)	100 (95%)	3 (3%)	2 (2%)	6	10
20	2Y	105/110 (96%)	102 (97%)	3 (3%)	0	100	100
21	1Z	148/206 (72%)	131 (88%)	16 (11%)	1 (1%)	18	30
21	2Z	156/206 (76%)	133 (85%)	23 (15%)	0	100	100
22	10	81/85 (95%)	79 (98%)	2 (2%)	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%)	92 (97%)	2 (2%)	1 (1%)	11	19
24	12	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
24	22	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	14	67/71 (94%)	54 (81%)	10 (15%)	3 (4%)	2	2
26	24	67/71 (94%)	51 (76%)	10 (15%)	6 (9%)	0	0
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
28	16	51/54 (94%)	51 (100%)	0	0	100	100
28	26	51/54 (94%)	51 (100%)	0	0	100	100
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
29	27	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	5	9
30	18	62/65 (95%)	62 (100%)	0	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%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	200 (87%)	20 (9%)	9 (4%)	2	3
33	2b	229/256 (90%)	201 (88%)	20 (9%)	8 (4%)	3	4
34	1c	204/239 (85%)	185 (91%)	17 (8%)	2 (1%)	12	20
34	2c	204/239 (85%)	187 (92%)	15 (7%)	2 (1%)	12	20
35	1d	206/209 (99%)	195 (95%)	10 (5%)	1 (0%)	24	39
35	2d	206/209 (99%)	194 (94%)	11 (5%)	1 (0%)	24	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	1e	146/162 (90%)	134 (92%)	11 (8%)	1 (1%)	18	30
36	2e	146/162 (90%)	136 (93%)	10 (7%)	0	100	100
37	1f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
37	2f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	1g	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
38	2g	153/156 (98%)	146 (95%)	6 (4%)	1 (1%)	18	30
39	1h	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
39	2h	135/138 (98%)	131 (97%)	3 (2%)	1 (1%)	18	30
40	1i	125/128 (98%)	107 (86%)	17 (14%)	1 (1%)	16	27
40	2i	125/128 (98%)	108 (86%)	15 (12%)	2 (2%)	7	12
41	1j	95/105 (90%)	83 (87%)	8 (8%)	4 (4%)	2	3
41	2j	94/105 (90%)	81 (86%)	8 (8%)	5 (5%)	1	2
42	1k	112/129 (87%)	103 (92%)	5 (4%)	4 (4%)	2	4
42	2k	112/129 (87%)	104 (93%)	4 (4%)	4 (4%)	2	4
43	1l	119/132 (90%)	113 (95%)	6 (5%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	8 (7%)	0	100	100
44	1m	121/126 (96%)	112 (93%)	9 (7%)	0	100	100
44	2m	120/126 (95%)	110 (92%)	7 (6%)	3 (2%)	4	7
45	1n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
46	1o	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
46	2o	86/89 (97%)	82 (95%)	3 (4%)	1 (1%)	10	17
47	1p	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	9	16
47	2p	80/88 (91%)	75 (94%)	4 (5%)	1 (1%)	9	16
48	1q	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
48	2q	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
49	1r	66/88 (75%)	62 (94%)	4 (6%)	0	100	100
49	2r	66/88 (75%)	62 (94%)	4 (6%)	0	100	100
50	1s	81/93 (87%)	73 (90%)	8 (10%)	0	100	100
50	2s	81/93 (87%)	74 (91%)	6 (7%)	1 (1%)	10	17
51	1t	94/106 (89%)	86 (92%)	3 (3%)	5 (5%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	2t	94/106 (89%)	86 (92%)	3 (3%)	5 (5%)	1	2
52	1u	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	2u	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
All	All	11370/12128 (94%)	10690 (94%)	575 (5%)	105 (1%)	14	24

All (105) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	1D	275	LYS
5	1F	130	ALA
6	1G	47	LYS
6	1G	51	ARG
7	1H	126	PRO
21	1Z	152	ALA
33	1b	17	PHE
33	1b	22	LYS
34	1c	65	ALA
42	1k	89	ALA
47	1p	53	VAL
5	2F	130	ALA
6	2G	47	LYS
6	2G	51	ARG
7	2H	126	PRO
11	2P	45	LEU
23	21	3	LYS
26	24	48	ARG
26	24	55	ARG
26	24	62	ARG
29	27	46	VAL
33	2b	16	HIS
33	2b	123	ALA
34	2c	107	GLN
34	2c	108	ASN
42	2k	89	ALA
42	2k	90	GLY
44	2m	107	ALA
47	2p	53	VAL
51	2t	10	LEU
8	1I	105	HIS
8	1I	106	GLY
23	11	3	LYS

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Mol	Chain	Res	Type
26	14	45	GLY
41	1j	31	GLY
41	1j	77	PRO
42	1k	49	GLY
51	1t	10	LEU
51	1t	47	GLY
51	1t	96	GLY
51	1t	100	ILE
3	2D	3	VAL
4	2E	52	LEU
12	2Q	28	ALA
17	2V	79	VAL
26	24	45	GLY
33	2b	17	PHE
33	2b	21	ARG
33	2b	128	GLU
41	2j	29	ARG
44	2m	4	ILE
51	2t	47	GLY
6	1G	43	LEU
17	1V	79	VAL
20	1Y	53	PRO
26	14	56	VAL
33	1b	9	GLU
33	1b	20	GLU
33	1b	231	GLU
36	1e	86	ALA
41	1j	29	ARG
41	1j	78	ASN
6	2G	43	LEU
19	2X	2	LYS
26	24	47	GLN
26	24	65	ASP
33	2b	20	GLU
33	2b	231	GLU
38	2g	7	ALA
41	2j	30	SER
41	2j	78	ASN
44	2m	6	GLY
50	2s	29	ARG
51	2t	102	GLY
4	1E	52	LEU

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Mol	Chain	Res	Type
34	1c	66	VAL
40	1i	56	LEU
51	1t	95	ALA
4	2E	73	GLU
5	2F	21	ALA
8	2I	10	GLU
42	2k	49	GLY
46	2o	88	ARG
51	2t	95	ALA
51	2t	100	ILE
20	1Y	54	LYS
33	1b	16	HIS
33	1b	125	PRO
33	1b	126	GLU
35	1d	167	GLY
42	1k	90	GLY
35	2d	167	GLY
40	2i	54	ASP
40	2i	56	LEU
42	2k	105	VAL
8	1I	107	VAL
26	14	46	GLN
33	1b	10	LEU
9	2N	2	LYS
39	2h	73	ASP
41	2j	77	PRO
42	1k	105	VAL
41	2j	37	PRO
11	1P	122	PRO
33	2b	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%)	202 (94%)	13 (6%)	17 30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2D	215/218 (99%)	205 (95%)	10 (5%)	23	40
4	1E	164/166 (99%)	149 (91%)	15 (9%)	9	14
4	2E	164/166 (99%)	150 (92%)	14 (8%)	10	17
5	1F	160/166 (96%)	143 (89%)	17 (11%)	6	10
5	2F	159/166 (96%)	147 (92%)	12 (8%)	12	21
6	1G	144/156 (92%)	132 (92%)	12 (8%)	10	18
6	2G	143/156 (92%)	137 (96%)	6 (4%)	26	45
7	1H	144/148 (97%)	141 (98%)	3 (2%)	47	69
7	2H	144/148 (97%)	140 (97%)	4 (3%)	38	60
8	1I	113/124 (91%)	105 (93%)	8 (7%)	13	23
8	2I	105/124 (85%)	99 (94%)	6 (6%)	18	32
9	1N	118/119 (99%)	111 (94%)	7 (6%)	18	30
9	2N	118/119 (99%)	111 (94%)	7 (6%)	18	30
10	1O	100/100 (100%)	99 (99%)	1 (1%)	68	81
10	2O	100/100 (100%)	97 (97%)	3 (3%)	36	57
11	1P	115/116 (99%)	106 (92%)	9 (8%)	11	20
11	2P	115/116 (99%)	109 (95%)	6 (5%)	21	36
12	1Q	111/111 (100%)	109 (98%)	2 (2%)	51	72
12	2Q	111/111 (100%)	107 (96%)	4 (4%)	31	51
13	1R	101/101 (100%)	93 (92%)	8 (8%)	11	19
13	2R	101/101 (100%)	94 (93%)	7 (7%)	14	24
14	1S	86/88 (98%)	81 (94%)	5 (6%)	18	31
14	2S	85/88 (97%)	82 (96%)	3 (4%)	32	52
15	1T	115/127 (91%)	110 (96%)	5 (4%)	26	44
15	2T	113/127 (89%)	109 (96%)	4 (4%)	32	52
16	1U	93/94 (99%)	90 (97%)	3 (3%)	34	55
16	2U	93/94 (99%)	92 (99%)	1 (1%)	65	80
17	1V	80/82 (98%)	75 (94%)	5 (6%)	16	29
17	2V	80/82 (98%)	76 (95%)	4 (5%)	22	37
18	1W	90/92 (98%)	85 (94%)	5 (6%)	19	32
18	2W	90/92 (98%)	84 (93%)	6 (7%)	15	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	1X	77/78 (99%)	76 (99%)	1 (1%)	61	77
19	2X	77/78 (99%)	76 (99%)	1 (1%)	61	77
20	1Y	85/91 (93%)	81 (95%)	4 (5%)	23	40
20	2Y	85/91 (93%)	84 (99%)	1 (1%)	63	79
21	1Z	135/179 (75%)	130 (96%)	5 (4%)	30	50
21	2Z	137/179 (76%)	131 (96%)	6 (4%)	25	43
22	10	65/67 (97%)	62 (95%)	3 (5%)	24	41
22	20	65/67 (97%)	64 (98%)	1 (2%)	57	75
23	11	80/83 (96%)	75 (94%)	5 (6%)	16	29
23	21	80/83 (96%)	75 (94%)	5 (6%)	16	29
24	12	65/67 (97%)	65 (100%)	0	100	100
24	22	65/67 (97%)	64 (98%)	1 (2%)	57	75
25	13	51/52 (98%)	49 (96%)	2 (4%)	28	48
25	23	50/52 (96%)	48 (96%)	2 (4%)	28	47
26	14	59/63 (94%)	57 (97%)	2 (3%)	32	53
26	24	53/63 (84%)	49 (92%)	4 (8%)	12	21
27	15	50/52 (96%)	47 (94%)	3 (6%)	17	30
27	25	50/52 (96%)	46 (92%)	4 (8%)	11	19
28	16	51/52 (98%)	49 (96%)	2 (4%)	28	48
28	26	50/52 (96%)	48 (96%)	2 (4%)	28	47
29	17	41/42 (98%)	40 (98%)	1 (2%)	43	65
29	27	41/42 (98%)	41 (100%)	0	100	100
30	18	54/55 (98%)	52 (96%)	2 (4%)	30	50
30	28	54/55 (98%)	52 (96%)	2 (4%)	30	50
31	19	34/34 (100%)	34 (100%)	0	100	100
31	29	34/34 (100%)	34 (100%)	0	100	100
33	1b	192/220 (87%)	187 (97%)	5 (3%)	40	63
33	2b	187/220 (85%)	183 (98%)	4 (2%)	47	69
34	1c	142/188 (76%)	140 (99%)	2 (1%)	59	76
34	2c	140/188 (74%)	137 (98%)	3 (2%)	47	69
35	1d	169/181 (93%)	164 (97%)	5 (3%)	36	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	2d	173/181 (96%)	168 (97%)	5 (3%)	37	58
36	1e	113/123 (92%)	110 (97%)	3 (3%)	39	61
36	2e	114/123 (93%)	112 (98%)	2 (2%)	51	72
37	1f	84/90 (93%)	81 (96%)	3 (4%)	31	51
37	2f	85/90 (94%)	83 (98%)	2 (2%)	43	65
38	1g	119/127 (94%)	118 (99%)	1 (1%)	73	85
38	2g	120/127 (94%)	120 (100%)	0	100	100
39	1h	114/119 (96%)	111 (97%)	3 (3%)	40	63
39	2h	114/119 (96%)	111 (97%)	3 (3%)	40	63
40	1i	90/99 (91%)	86 (96%)	4 (4%)	25	43
40	2i	89/99 (90%)	87 (98%)	2 (2%)	45	67
41	1j	66/92 (72%)	64 (97%)	2 (3%)	36	57
41	2j	69/92 (75%)	66 (96%)	3 (4%)	26	44
42	1k	82/99 (83%)	80 (98%)	2 (2%)	43	65
42	2k	83/99 (84%)	81 (98%)	2 (2%)	43	65
43	1l	96/108 (89%)	94 (98%)	2 (2%)	47	69
43	2l	96/108 (89%)	93 (97%)	3 (3%)	35	56
44	1m	93/101 (92%)	90 (97%)	3 (3%)	34	55
44	2m	92/101 (91%)	89 (97%)	3 (3%)	33	55
45	1n	49/50 (98%)	47 (96%)	2 (4%)	27	46
45	2n	49/50 (98%)	46 (94%)	3 (6%)	17	30
46	1o	78/80 (98%)	77 (99%)	1 (1%)	61	77
46	2o	78/80 (98%)	76 (97%)	2 (3%)	40	63
47	1p	69/74 (93%)	62 (90%)	7 (10%)	7	11
47	2p	68/74 (92%)	61 (90%)	7 (10%)	7	10
48	1q	94/97 (97%)	94 (100%)	0	100	100
48	2q	94/97 (97%)	93 (99%)	1 (1%)	65	80
49	1r	59/77 (77%)	57 (97%)	2 (3%)	32	53
49	2r	59/77 (77%)	57 (97%)	2 (3%)	32	53
50	1s	69/80 (86%)	69 (100%)	0	100	100
50	2s	67/80 (84%)	66 (98%)	1 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	1t	70/82 (85%)	67 (96%)	3 (4%)	26	44
51	2t	70/82 (85%)	68 (97%)	2 (3%)	37	58
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	18 (100%)	0	100	100
All	All	9304/10064 (92%)	8930 (96%)	374 (4%)	28	47

All (374) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	14	ARG
3	1D	61	LEU
3	1D	94	LEU
3	1D	113	VAL
3	1D	122	ASP
3	1D	173	VAL
3	1D	193	VAL
3	1D	211	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	14	ILE
4	1E	21	VAL
4	1E	24	THR
4	1E	33	VAL
4	1E	47	VAL
4	1E	75	VAL
4	1E	116	VAL
4	1E	144	ARG
4	1E	170	LEU
4	1E	175	VAL
4	1E	181	LEU
4	1E	188	VAL
5	1F	18	ARG
5	1F	24	LEU
5	1F	33	LEU
5	1F	53	THR

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Mol	Chain	Res	Type
5	1F	57	VAL
5	1F	60	SER
5	1F	70	THR
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	125	LEU
5	1F	132	VAL
5	1F	170	LEU
5	1F	175	THR
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	3	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	43	LEU
6	1G	82	LEU
6	1G	133	LEU
6	1G	139	LEU
6	1G	140	ILE
6	1G	159	VAL
6	1G	161	THR
6	1G	174	GLU
6	1G	175	LEU
7	1H	71	LEU
7	1H	88	LEU
7	1H	98	LEU
8	1I	38	LEU
8	1I	47	LEU
8	1I	92	VAL
8	1I	108	THR
8	1I	109	ILE
8	1I	123	LEU
8	1I	127	VAL
8	1I	142	VAL
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	48	MET
9	1N	62	VAL

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Mol	Chain	Res	Type
9	1N	73	THR
10	1O	10	VAL
11	1P	59	LEU
11	1P	79	ARG
11	1P	83	VAL
11	1P	95	VAL
11	1P	106	LEU
11	1P	112	LEU
11	1P	125	VAL
11	1P	126	VAL
11	1P	148	LEU
12	1Q	75	THR
12	1Q	109	VAL
13	1R	29	LEU
13	1R	33	ARG
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	65	LEU
13	1R	100	LEU
13	1R	111	LEU
14	1S	13	ARG
14	1S	36	TYR
14	1S	49	VAL
14	1S	69	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	49	VAL
15	1T	89	VAL
15	1T	128	GLU
16	1U	8	VAL
16	1U	95	LEU
16	1U	108	GLU
17	1V	46	VAL
17	1V	51	VAL
17	1V	61	VAL
17	1V	72	VAL
17	1V	79	VAL
18	1W	11	ARG
18	1W	17	VAL
18	1W	19	LEU

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Mol	Chain	Res	Type
18	1W	23	LEU
18	1W	107	LEU
19	1X	52	VAL
20	1Y	43	ASN
20	1Y	72	VAL
20	1Y	87	LYS
20	1Y	90	LEU
21	1Z	42	VAL
21	1Z	76	LEU
21	1Z	126	VAL
21	1Z	132	ASN
21	1Z	148	ASP
22	10	14	ARG
22	10	39	ARG
22	10	55	ARG
23	11	11	ARG
23	11	30	VAL
23	11	35	THR
23	11	51	VAL
23	11	95	LEU
25	13	23	LEU
25	13	54	VAL
26	14	50	VAL
26	14	56	VAL
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
28	16	14	THR
28	16	48	VAL
29	17	24	THR
30	18	14	VAL
30	18	32	LEU
33	1b	7	VAL
33	1b	8	LYS
33	1b	112	VAL
33	1b	158	LEU
33	1b	200	ILE
34	1c	70	VAL
34	1c	115	LEU
35	1d	31	CYS
35	1d	112	VAL
35	1d	135	LEU

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Mol	Chain	Res	Type
35	1d	158	ILE
35	1d	194	LEU
36	1e	20	GLN
36	1e	38	GLN
36	1e	41	VAL
37	1f	72	VAL
37	1f	74	ASP
37	1f	75	LEU
38	1g	50	ILE
39	1h	26	VAL
39	1h	112	LEU
39	1h	133	LEU
40	1i	23	ASN
40	1i	42	ARG
40	1i	50	LEU
40	1i	86	VAL
41	1j	5	ARG
41	1j	72	VAL
42	1k	48	ILE
42	1k	114	VAL
43	1l	27	LEU
43	1l	83	VAL
44	1m	4	ILE
44	1m	19	LEU
44	1m	32	GLU
45	1n	18	VAL
45	1n	33	VAL
46	1o	66	LEU
47	1p	2	VAL
47	1p	19	ILE
47	1p	20	VAL
47	1p	42	ARG
47	1p	60	LEU
47	1p	67	THR
47	1p	69	THR
49	1r	31	LEU
49	1r	35	ARG
51	1t	10	LEU
51	1t	15	ARG
51	1t	24	LEU
3	2D	3	VAL
3	2D	12	SER

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Mol	Chain	Res	Type
3	2D	61	LEU
3	2D	94	LEU
3	2D	113	VAL
3	2D	173	VAL
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	257	LEU
4	2E	7	VAL
4	2E	9	VAL
4	2E	14	ILE
4	2E	21	VAL
4	2E	33	VAL
4	2E	38	THR
4	2E	52	LEU
4	2E	75	VAL
4	2E	77	ILE
4	2E	116	VAL
4	2E	170	LEU
4	2E	175	VAL
4	2E	181	LEU
4	2E	195	LEU
5	2F	24	LEU
5	2F	33	LEU
5	2F	70	THR
5	2F	74	ARG
5	2F	88	VAL
5	2F	106	ARG
5	2F	132	VAL
5	2F	170	LEU
5	2F	183	VAL
5	2F	191	ARG
5	2F	192	LEU
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	43	LEU
6	2G	79	ASN
6	2G	140	ILE
6	2G	159	VAL
7	2H	15	VAL
7	2H	84	SER

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Mol	Chain	Res	Type
7	2H	129	THR
7	2H	134	SER
8	2I	47	LEU
8	2I	50	ARG
8	2I	92	VAL
8	2I	123	LEU
8	2I	127	VAL
8	2I	140	LEU
9	2N	10	GLU
9	2N	14	VAL
9	2N	28	THR
9	2N	33	LEU
9	2N	34	LEU
9	2N	62	VAL
9	2N	99	LEU
10	2O	10	VAL
10	2O	78	ARG
10	2O	108	GLU
11	2P	59	LEU
11	2P	95	VAL
11	2P	112	LEU
11	2P	125	VAL
11	2P	126	VAL
11	2P	148	LEU
12	2Q	2	LEU
12	2Q	10	ARG
12	2Q	75	THR
12	2Q	110	THR
13	2R	29	LEU
13	2R	33	ARG
13	2R	44	LEU
13	2R	54	LEU
13	2R	65	LEU
13	2R	100	LEU
13	2R	111	LEU
14	2S	13	ARG
14	2S	69	VAL
14	2S	110	LEU
15	2T	28	VAL
15	2T	49	VAL
15	2T	89	VAL
15	2T	95	ARG

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Mol	Chain	Res	Type
16	2U	92	ARG
17	2V	46	VAL
17	2V	61	VAL
17	2V	72	VAL
17	2V	79	VAL
18	2W	11	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	100	THR
18	2W	107	LEU
19	2X	70	LEU
20	2Y	72	VAL
21	2Z	42	VAL
21	2Z	76	LEU
21	2Z	126	VAL
21	2Z	135	GLU
21	2Z	142	SER
21	2Z	171	ILE
22	20	39	ARG
23	21	11	ARG
23	21	30	VAL
23	21	51	VAL
23	21	56	GLN
23	21	95	LEU
24	22	52	ASP
25	23	23	LEU
25	23	54	VAL
26	24	34	GLU
26	24	50	VAL
26	24	56	VAL
26	24	59	PHE
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	35	GLU
28	26	14	THR
28	26	48	VAL
30	28	14	VAL
30	28	32	LEU
33	2b	7	VAL
33	2b	94	ASN

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Mol	Chain	Res	Type
33	2b	185	ILE
33	2b	235	SER
34	2c	14	ILE
34	2c	115	LEU
34	2c	152	ILE
35	2d	31	CYS
35	2d	135	LEU
35	2d	150	GLU
35	2d	158	ILE
35	2d	194	LEU
36	2e	41	VAL
36	2e	51	VAL
37	2f	21	LEU
37	2f	72	VAL
39	2h	26	VAL
39	2h	84	ARG
39	2h	133	LEU
40	2i	102	LEU
40	2i	108	VAL
41	2j	67	THR
41	2j	72	VAL
41	2j	89	ASP
42	2k	48	ILE
42	2k	114	VAL
43	2l	27	LEU
43	2l	33	ARG
43	2l	83	VAL
44	2m	15	VAL
44	2m	19	LEU
44	2m	104	ARG
45	2n	7	ILE
45	2n	18	VAL
45	2n	33	VAL
46	2o	39	LEU
46	2o	66	LEU
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	45	THR
47	2p	60	LEU
47	2p	62	VAL
47	2p	69	THR

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Mol	Chain	Res	Type
48	2q	53	LEU
49	2r	35	ARG
49	2r	37	VAL
50	2s	77	THR
51	2t	10	LEU
51	2t	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (122) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
4	1E	48	GLN
4	1E	121	ASN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	79	ASN
6	1G	132	ASN
9	1N	94	HIS
12	1Q	57	HIS
13	1R	13	HIS
13	1R	71	GLN
14	1S	95	HIS
18	1W	60	ASN
18	1W	111	HIS
19	1X	31	HIS
19	1X	82	GLN
20	1Y	43	ASN
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	132	ASN
21	1Z	151	HIS
22	10	3	HIS
23	11	19	GLN
24	12	9	GLN
24	12	46	GLN
24	12	65	ASN
30	18	35	GLN
33	1b	113	HIS
34	1c	6	HIS
34	1c	31	HIS
34	1c	102	ASN

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Mol	Chain	Res	Type
34	1c	139	GLN
34	1c	176	HIS
35	1d	77	ASN
35	1d	123	HIS
35	1d	161	ASN
38	1g	13	GLN
38	1g	28	ASN
39	1h	82	HIS
40	1i	23	ASN
40	1i	34	ASN
40	1i	58	HIS
40	1i	73	GLN
40	1i	124	GLN
41	1j	56	HIS
42	1k	99	GLN
42	1k	116	HIS
43	1l	99	HIS
45	1n	49	HIS
47	1p	13	HIS
50	1s	23	ASN
50	1s	57	HIS
50	1s	83	HIS
51	1t	73	HIS
3	2D	87	ASN
3	2D	116	GLN
3	2D	126	GLN
5	2F	69	HIS
6	2G	40	ASN
7	2H	111	HIS
8	2I	104	GLN
8	2I	105	HIS
9	2N	38	HIS
9	2N	101	HIS
9	2N	131	GLN
10	2O	3	GLN
12	2Q	12	GLN
12	2Q	13	GLN
13	2R	71	GLN
13	2R	91	GLN
14	2S	38	GLN
14	2S	84	GLN
14	2S	95	HIS

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Mol	Chain	Res	Type
16	2U	81	HIS
16	2U	94	ASN
17	2V	64	HIS
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
21	2Z	32	HIS
21	2Z	34	ASN
21	2Z	55	HIS
21	2Z	73	GLN
21	2Z	75	ASN
21	2Z	132	ASN
24	22	9	GLN
24	22	65	ASN
33	2b	40	HIS
33	2b	78	GLN
33	2b	94	ASN
33	2b	95	GLN
34	2c	6	HIS
34	2c	31	HIS
34	2c	123	GLN
34	2c	162	GLN
35	2d	77	ASN
35	2d	125	HIS
35	2d	161	ASN
36	2e	73	ASN
37	2f	13	ASN
37	2f	100	ASN
38	2g	28	ASN
38	2g	37	ASN
38	2g	64	GLN
38	2g	86	GLN
38	2g	97	GLN
38	2g	148	ASN
40	2i	58	HIS
40	2i	73	GLN
40	2i	117	HIS
40	2i	124	GLN
41	2j	21	GLN
42	2k	93	GLN
43	2l	99	HIS
46	2o	28	GLN

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Mol	Chain	Res	Type
46	2o	62	GLN
47	2p	13	HIS
50	2s	65	ASN
50	2s	69	HIS
50	2s	83	HIS
51	2t	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	440 (15%)	28 (0%)
1	2A	2791/2915 (95%)	462 (16%)	26 (0%)
2	1B	120/121 (99%)	9 (7%)	1 (0%)
2	2B	118/121 (97%)	27 (22%)	0
32	1a	1497/1521 (98%)	220 (14%)	0
32	2a	1501/1521 (98%)	226 (15%)	0
53	1v	12/27 (44%)	3 (25%)	0
53	2v	12/27 (44%)	3 (25%)	0
54	1w	72/76 (94%)	27 (37%)	0
54	1y	72/76 (94%)	24 (33%)	0
54	2w	70/76 (92%)	21 (30%)	0
54	2y	70/76 (92%)	16 (22%)	0
55	1x	75/77 (97%)	12 (16%)	0
55	2x	75/77 (97%)	13 (17%)	0
All	All	9349/9626 (97%)	1503 (16%)	55 (0%)

All (1503) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	55	G
1	1A	58	G
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	84	A
1	1A	93	G
1	1A	94	C
1	1A	95	G

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Mol	Chain	Res	Type
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	181	A
1	1A	182	A
1	1A	196	A
1	1A	198	C
1	1A	199	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	269	U
1	1A	271(C)	C
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(O)	C
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	282	A
1	1A	283	A
1	1A	306	U
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	352	G
1	1A	360	G
1	1A	362	U
1	1A	363	G
1	1A	363(B)	G
1	1A	386	G
1	1A	389	G
1	1A	396	G
1	1A	405	U
1	1A	407	G
1	1A	411	G
1	1A	412	A

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Mol	Chain	Res	Type
1	1A	418	G
1	1A	421	U
1	1A	428	A
1	1A	444	C
1	1A	448	U
1	1A	451	C
1	1A	454	A
1	1A	455	C
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	491	G
1	1A	494	G
1	1A	505	A
1	1A	509	C
1	1A	512	G
1	1A	529	A
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	534	U
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	574	C
1	1A	575	A
1	1A	586	A
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	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(E)	G
1	1A	668	G
1	1A	669	G
1	1A	686	G

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Mol	Chain	Res	Type
1	1A	730	C
1	1A	740	U
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	801	G
1	1A	805	G
1	1A	811	U
1	1A	812	C
1	1A	819	A
1	1A	827	U
1	1A	828	U
1	1A	830	G
1	1A	859	G
1	1A	866	A
1	1A	877	U
1	1A	879	G
1	1A	880	G
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	890	A
1	1A	892	G
1	1A	895	U
1	1A	896	A
1	1A	897	C
1	1A	898	C
1	1A	910	A
1	1A	932	G
1	1A	941	A
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	963	U

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Mol	Chain	Res	Type
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	995	C
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1022	G
1	1A	1026	U
1	1A	1033	U
1	1A	1038	C
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	1066	U
1	1A	1070	A
1	1A	1071	G
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1080	C
1	1A	1083	U
1	1A	1085	A
1	1A	1088	A
1	1A	1090	U
1	1A	1092	C
1	1A	1094	U
1	1A	1101	U
1	1A	1106	G
1	1A	1109	C
1	1A	1110	G
1	1A	1111	A
1	1A	1112	G
1	1A	1129	A

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Mol	Chain	Res	Type
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1155	A
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	1189	A
1	1A	1210	A
1	1A	1211	U
1	1A	1218	C
1	1A	1220	A
1	1A	1244	G
1	1A	1253	A
1	1A	1256	G
1	1A	1267	U
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	1308	A
1	1A	1315	C
1	1A	1320	C
1	1A	1345	C
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1379	A
1	1A	1384	A
1	1A	1385	G
1	1A	1386	C
1	1A	1416	G
1	1A	1417	C
1	1A	1419	A

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Mol	Chain	Res	Type
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	1459	G
1	1A	1461	G
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1493	C
1	1A	1496	A
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1509(B)	A
1	1A	1531	C
1	1A	1543	C
1	1A	1554	A
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	1653	G
1	1A	1654	A
1	1A	1664	A
1	1A	1667	G
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	1739	U
1	1A	1748	G

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Mol	Chain	Res	Type
1	1A	1749	A
1	1A	1756	G
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	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1929	G
1	1A	1930	G
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1984	G
1	1A	1992	G
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
1	1A	2035	G
1	1A	2039	C
1	1A	2043	C
1	1A	2055	C

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Mol	Chain	Res	Type
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2099	U
1	1A	2110	G
1	1A	2113	U
1	1A	2116	G
1	1A	2118	U
1	1A	2119	A
1	1A	2121	G
1	1A	2122	U
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	2140	C
1	1A	2142	C
1	1A	2143	C
1	1A	2144	U
1	1A	2145	C
1	1A	2146	C
1	1A	2147	G
1	1A	2148	G
1	1A	2151	G
1	1A	2152	G
1	1A	2155	G
1	1A	2157	G
1	1A	2159	G
1	1A	2162	G
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2174	C
1	1A	2178	C

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Mol	Chain	Res	Type
1	1A	2181	G
1	1A	2182	G
1	1A	2184	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2219	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2269	A
1	1A	2275	C
1	1A	2283	C
1	1A	2287	A
1	1A	2305	A
1	1A	2308	G
1	1A	2320	A
1	1A	2321	G
1	1A	2325	G
1	1A	2334	G
1	1A	2335	A
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2361	A
1	1A	2379	G
1	1A	2383	G
1	1A	2385	C
1	1A	2396	G
1	1A	2406	U
1	1A	2407	G
1	1A	2410	G
1	1A	2422	A
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C

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Mol	Chain	Res	Type
1	1A	2448	A
1	1A	2476	A
1	1A	2477	C
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	2524	G
1	1A	2529	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2584	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	2689	U
1	1A	2690	C
1	1A	2691	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2761	G
1	1A	2764	A
1	1A	2765	A
1	1A	2778	A
1	1A	2780	G
1	1A	2789	C
1	1A	2790	A
1	1A	2791	C
1	1A	2793	G
1	1A	2794	C
1	1A	2802	G
1	1A	2818	G

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Mol	Chain	Res	Type
1	1A	2820	A
1	1A	2821	A
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	7	G
2	1B	13	A
2	1B	52	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	78	G
32	1a	91	C
32	1a	96	U
32	1a	98	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	146	G
32	1a	156	G
32	1a	163	C
32	1a	174	C
32	1a	182	U
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A

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Mol	Chain	Res	Type
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	217	C
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	316	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	344	A
32	1a	348	G
32	1a	352	C
32	1a	353	A
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	424	G
32	1a	429	U
32	1a	430	A
32	1a	439	A
32	1a	441	A
32	1a	442	C
32	1a	452	A
32	1a	461	A
32	1a	470	C
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G

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Mol	Chain	Res	Type
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	527	7MG
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	564	C
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	630	G
32	1a	653	A
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	749	C
32	1a	755	G
32	1a	759	A
32	1a	773	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	838	G
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	859	A
32	1a	874	G
32	1a	902	G

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Mol	Chain	Res	Type
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	960	U
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	982	U
32	1a	992	U
32	1a	993	G
32	1a	1002	G
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1008	C
32	1a	1020	U
32	1a	1022	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1031	G
32	1a	1032	G
32	1a	1033	G
32	1a	1036	G
32	1a	1037	C
32	1a	1039	C
32	1a	1044	A
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G

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Mol	Chain	Res	Type
32	1a	1081	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1104	G
32	1a	1133	G
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1146	A
32	1a	1152	A
32	1a	1157	A
32	1a	1159	U
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1240	U
32	1a	1250	A
32	1a	1256	A
32	1a	1257	U
32	1a	1260	C
32	1a	1270	C
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1281	U
32	1a	1282	C
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U

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Mol	Chain	Res	Type
32	1a	1305	G
32	1a	1320	C
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1400	5MC
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1456	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	1519	MA6
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
32	1a	1532	U
53	1v	13	A
53	1v	14	A
53	1v	24	A
54	1w	2	C
54	1w	4	C
54	1w	9	A
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	22	G
54	1w	23	A
54	1w	24	G
54	1w	29	G
54	1w	42	C
54	1w	43	C

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Mol	Chain	Res	Type
54	1w	45	U
54	1w	46	7MG
54	1w	47	U
54	1w	48	C
54	1w	49	C
54	1w	56	C
54	1w	61	C
54	1w	68	C
54	1w	69	G
54	1w	70	G
54	1w	72	C
54	1w	73	A
54	1w	74	C
54	1w	75	C
54	1w	76	A
55	1x	6	G
55	1x	9	G
55	1x	19	G
55	1x	20	U
55	1x	21	A
55	1x	48	C
55	1x	56	C
55	1x	58	A
55	1x	61	C
55	1x	67	C
55	1x	69	C
55	1x	76	A
54	1y	2	C
54	1y	5	G
54	1y	9	A
54	1y	13	C
54	1y	19	G
54	1y	20	U
54	1y	21	A
54	1y	22	G
54	1y	26	A
54	1y	33	U
54	1y	37	MIA
54	1y	40	C
54	1y	45	U
54	1y	46	7MG
54	1y	47	U

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Mol	Chain	Res	Type
54	1y	48	C
54	1y	50	U
54	1y	57	G
54	1y	59	U
54	1y	60	U
54	1y	65	G
54	1y	68	C
54	1y	70	G
54	1y	73	A
1	2A	9	U
1	2A	10	G
1	2A	11	G
1	2A	15	G
1	2A	34	C
1	2A	45	C
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	95	G
1	2A	96	G
1	2A	102	G
1	2A	118	A
1	2A	120	U
1	2A	131	G
1	2A	140	G
1	2A	141	A
1	2A	154(A)	C
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	216	A
1	2A	222	A
1	2A	228	A
1	2A	229	A
1	2A	233	A

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Mol	Chain	Res	Type
1	2A	248	G
1	2A	250	G
1	2A	271(I)	G
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	289	A
1	2A	308	G
1	2A	311	A
1	2A	317	G
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	338	G
1	2A	342	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	363(A)	A
1	2A	386	G
1	2A	396	G
1	2A	404	C
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	422	A
1	2A	427	U
1	2A	443	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	494	G
1	2A	505	A

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Mol	Chain	Res	Type
1	2A	508	G
1	2A	509	C
1	2A	518	G
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	556	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	587	C
1	2A	588	U
1	2A	592	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	651	G
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	668	G
1	2A	669	G
1	2A	686	G
1	2A	709	U
1	2A	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	775	G
1	2A	776	G
1	2A	782	A

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Mol	Chain	Res	Type
1	2A	784	A
1	2A	785	G
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	848	G
1	2A	857	C
1	2A	859	G
1	2A	864	G
1	2A	866	A
1	2A	874	G
1	2A	875	G
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	893	C
1	2A	894	C
1	2A	896	A
1	2A	897	C
1	2A	900	A
1	2A	901	A
1	2A	904	C
1	2A	910	A
1	2A	912	C
1	2A	917	A
1	2A	932	G
1	2A	936	C
1	2A	941	A
1	2A	944	G
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	957	A
1	2A	959	A

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Mol	Chain	Res	Type
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	982	C
1	2A	983	A
1	2A	996	A
1	2A	1005	C
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1027	A
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1043	C
1	2A	1113	U
1	2A	1116	C
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142(A)	A
1	2A	1144	G
1	2A	1171	G
1	2A	1188	U
1	2A	1210	A
1	2A	1211	U
1	2A	1220	A
1	2A	1229	G
1	2A	1248	G
1	2A	1250	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1289	C
1	2A	1300	U
1	2A	1301	A

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Mol	Chain	Res	Type
1	2A	1303	G
1	2A	1314	C
1	2A	1320	C
1	2A	1345	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	1379	A
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1395	A
1	2A	1411	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1436	G
1	2A	1437	C
1	2A	1444	G
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
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

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Mol	Chain	Res	Type
1	2A	1542	A
1	2A	1543	C
1	2A	1545	A
1	2A	1547	C
1	2A	1548	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1582	C
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1593	G
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1640	C
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1695	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1721	G
1	2A	1722	A
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	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1829	A
1	2A	1835	G

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Mol	Chain	Res	Type
1	2A	1847	A
1	2A	1848	A
1	2A	1857	G
1	2A	1860	G
1	2A	1876	A
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
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	1931	U
1	2A	1936	A
1	2A	1938	A
1	2A	1952	A
1	2A	1955	U
1	2A	1963	U
1	2A	1964	G
1	2A	1966	A
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1984	G
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	2069	G
1	2A	2111	C

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Mol	Chain	Res	Type
1	2A	2116	G
1	2A	2119	A
1	2A	2122	U
1	2A	2125	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
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	2139	C
1	2A	2140	C
1	2A	2142	C
1	2A	2144	U
1	2A	2146	C
1	2A	2148	G
1	2A	2149	G
1	2A	2150	U
1	2A	2154	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2160	G
1	2A	2166	G
1	2A	2167	U
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2178	C
1	2A	2185	C
1	2A	2189	U
1	2A	2190	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2225	A
1	2A	2235	G

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Mol	Chain	Res	Type
1	2A	2238	G
1	2A	2239	G
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2312	U
1	2A	2313	C
1	2A	2319	G
1	2A	2320	A
1	2A	2322	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	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2410	G
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	2445	G
1	2A	2448	A
1	2A	2459	A
1	2A	2465	C
1	2A	2469	A
1	2A	2476	A
1	2A	2487	G
1	2A	2490	G
1	2A	2491	U
1	2A	2494	G
1	2A	2502	G

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Mol	Chain	Res	Type
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2582	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2630	G
1	2A	2646	C
1	2A	2654	A
1	2A	2669	G
1	2A	2679	A
1	2A	2689	U
1	2A	2690	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2741	A
1	2A	2751	G
1	2A	2752	C
1	2A	2754	U
1	2A	2757	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2793	G
1	2A	2802	G
1	2A	2818	G
1	2A	2820	A

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Mol	Chain	Res	Type
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2879	C
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	8	U
2	2B	16	G
2	2B	17	C
2	2B	20	C
2	2B	23	G
2	2B	25	A
2	2B	30	C
2	2B	42	C
2	2B	45	A
2	2B	53	A
2	2B	56	G
2	2B	58	A
2	2B	64	C
2	2B	69	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	90	A
2	2B	91	C
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	112	U
2	2B	116	G
2	2B	120	A
32	2a	6	G
32	2a	7	G
32	2a	9	G
32	2a	32	A
32	2a	39	G
32	2a	47	C

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Mol	Chain	Res	Type
32	2a	48	C
32	2a	51	A
32	2a	52	G
32	2a	66	G
32	2a	73	G
32	2a	78	G
32	2a	88	A
32	2a	89	C
32	2a	91	C
32	2a	96	U
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	144	G
32	2a	146	G
32	2a	156	G
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	189(J)	G
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	217	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	301	G
32	2a	316	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	344	A
32	2a	348	G

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Mol	Chain	Res	Type
32	2a	352	C
32	2a	353	A
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	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	441	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
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	7MG
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
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C

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Mol	Chain	Res	Type
32	2a	630	G
32	2a	653	A
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	723	U
32	2a	731	G
32	2a	749	C
32	2a	755	G
32	2a	759	A
32	2a	773	G
32	2a	777	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	838	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	859	A
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	960	U
32	2a	961	U
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	992	U
32	2a	993	G
32	2a	1001(A)	G

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Mol	Chain	Res	Type
32	2a	1002	G
32	2a	1003	G
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1008	C
32	2a	1009	G
32	2a	1020	U
32	2a	1022	G
32	2a	1024	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1033	G
32	2a	1037	C
32	2a	1038	C
32	2a	1039	C
32	2a	1044	A
32	2a	1046	A
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1104	G
32	2a	1117	G
32	2a	1125	U
32	2a	1129	C
32	2a	1133	G
32	2a	1134	G
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1146	A
32	2a	1152	A

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Mol	Chain	Res	Type
32	2a	1157	A
32	2a	1159	U
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1227	A
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1281	U
32	2a	1282	C
32	2a	1287	A
32	2a	1299	A
32	2a	1305	G
32	2a	1320	C
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	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1456	G
32	2a	1492	A

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Mol	Chain	Res	Type
32	2a	1494	G
32	2a	1498	UR3
32	2a	1503	A
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	13	A
53	2v	14	A
53	2v	24	A
54	2w	2	C
54	2w	4	C
54	2w	8	4SU
54	2w	19	G
54	2w	24	G
54	2w	29	G
54	2w	42	C
54	2w	43	C
54	2w	47	U
54	2w	48	C
54	2w	49	C
54	2w	56	C
54	2w	61	C
54	2w	62	C
54	2w	68	C
54	2w	69	G
54	2w	70	G
54	2w	73	A
54	2w	74	C
54	2w	75	C
54	2w	76	A
55	2x	9	G
55	2x	13	C
55	2x	16	C
55	2x	19	G
55	2x	34	C
55	2x	47	U
55	2x	48	C
55	2x	52	G

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Mol	Chain	Res	Type
55	2x	56	C
55	2x	60	U
55	2x	67	C
55	2x	68	C
55	2x	76	A
54	2y	2	C
54	2y	9	A
54	2y	13	C
54	2y	19	G
54	2y	22	G
54	2y	26	A
54	2y	33	U
54	2y	37	MIA
54	2y	40	C
54	2y	46	7MG
54	2y	47	U
54	2y	48	C
54	2y	50	U
54	2y	57	G
54	2y	68	C
54	2y	70	G

All (55) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	90	U
1	1A	196	A
1	1A	266	G
1	1A	278	A
1	1A	548	A
1	1A	746	A
1	1A	800	A
1	1A	827	U
1	1A	1036	G
1	1A	1047	G
1	1A	1065	U
1	1A	1067	A
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1210	A
1	1A	1442	G

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Mol	Chain	Res	Type
1	1A	1508	A
1	1A	1653	G
1	1A	1992	G
1	1A	2134	A
1	1A	2181	G
1	1A	2183	C
1	1A	2238	G
1	1A	2406	U
1	1A	2422	A
1	1A	2629	A
1	1A	2689	U
2	1B	1	U
1	2A	195	A
1	2A	196	A
1	2A	228	A
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	587	C
1	2A	752	A
1	2A	774	A
1	2A	856	C
1	2A	883	G
1	2A	900	A
1	2A	1026	U
1	2A	1210	A
1	2A	1300	U
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2126	A
1	2A	2406	U
1	2A	2689	U
1	2A	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
54	MIA	1w	37	54	28,31,32	2.41	6 (21%)	38,44,47	2.68	13 (34%)
54	PSU	2y	55	54	18,21,22	1.41	2 (11%)	21,30,33	2.10	3 (14%)
54	7MG	2w	46	54	23,26,27	1.30	2 (8%)	27,39,42	2.65	8 (29%)
1	PSU	1A	2605	1	18,21,22	1.40	3 (16%)	21,30,33	2.07	4 (19%)
32	5MC	1a	1404	32	19,22,23	1.53	2 (10%)	26,32,35	1.11	2 (7%)
1	5MU	2A	1939	1,56	19,22,23	1.42	5 (26%)	27,32,35	2.10	6 (22%)
54	PSU	1w	39	54	18,21,22	1.36	2 (11%)	21,30,33	2.14	4 (19%)
55	4SU	1x	8	55	18,21,22	2.02	5 (27%)	25,30,33	1.30	4 (16%)
54	4SU	1y	8	54	18,21,22	1.82	5 (27%)	25,30,33	1.92	5 (20%)
43	0TD	1l	92	43	8,9,10	4.74	1 (12%)	6,11,13	7.33	2 (33%)
54	5MU	1y	54	54	19,22,23	1.44	5 (26%)	27,32,35	1.96	5 (18%)
55	PSU	2x	55	55	18,21,22	1.36	2 (11%)	21,30,33	2.05	4 (19%)
32	5MC	2a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.17	3 (11%)
32	5MC	1a	1400	32	19,22,23	1.61	3 (15%)	26,32,35	1.09	3 (11%)
54	PSU	2y	32	54	18,21,22	1.40	2 (11%)	21,30,33	1.99	4 (19%)
1	PSU	2A	1917	1	18,21,22	1.38	2 (11%)	21,30,33	2.07	4 (19%)
32	UR3	2a	1498	32	19,22,23	1.13	1 (5%)	26,32,35	1.78	3 (11%)
55	5MC	2x	32	55	19,22,23	1.57	3 (15%)	26,32,35	1.23	4 (15%)
32	UR3	1a	1498	32	19,22,23	1.00	1 (5%)	26,32,35	1.67	3 (11%)
1	2MU	2A	2552	1,56	19,22,24	1.27	3 (15%)	25,31,36	1.73	6 (24%)
54	5MU	1w	54	54	19,22,23	1.37	5 (26%)	27,32,35	1.93	6 (22%)
1	PSU	1A	1911	1	18,21,22	1.40	2 (11%)	21,30,33	2.06	4 (19%)
55	5MU	2x	54	55	19,22,23	1.39	4 (21%)	27,32,35	1.94	7 (25%)
32	M2G	2a	966	32	24,27,28	1.31	4 (16%)	33,40,43	1.89	5 (15%)
1	5MC	2A	1962	1,56	19,22,23	1.78	3 (15%)	26,32,35	1.20	3 (11%)
1	4OC	2A	1920	1	19,22,24	0.76	0	25,31,35	0.92	1 (4%)
32	PSU	1a	516	32,56	18,21,22	1.40	3 (16%)	21,30,33	2.12	5 (23%)
54	PSU	2w	55	54	18,21,22	1.38	2 (11%)	21,30,33	1.97	4 (19%)
1	OMG	2A	2251	1,56,55	23,26,27	1.22	3 (13%)	32,38,41	2.04	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	PSU	1y	39	54	18,21,22	1.40	2 (11%)	21,30,33	2.08	3 (14%)
32	MA6	1a	1519	32	23,26,27	1.52	4 (17%)	33,38,41	2.37	12 (36%)
54	MIA	2w	37	54	21,24,32	1.61	3 (14%)	30,35,47	2.10	7 (23%)
1	5MC	1A	1962	1,56	19,22,23	1.56	3 (15%)	26,32,35	1.17	3 (11%)
32	5MC	2a	967	32	19,22,23	1.77	3 (15%)	26,32,35	1.15	3 (11%)
54	PSU	2y	39	54	18,21,22	1.39	3 (16%)	21,30,33	2.10	4 (19%)
54	4SU	1w	8	54	18,21,22	1.80	5 (27%)	25,30,33	2.07	4 (16%)
1	5MU	1A	1939	1	19,22,23	1.46	5 (26%)	27,32,35	2.22	5 (18%)
43	0TD	2l	92	43	8,9,10	4.48	1 (12%)	6,11,13	2.43	3 (50%)
32	5MC	2a	1407	32	19,22,23	1.65	3 (15%)	26,32,35	1.13	3 (11%)
1	2MU	1A	2552	1,56	19,22,24	1.27	2 (10%)	25,31,36	2.06	6 (24%)
32	MA6	2a	1518	32	23,26,27	1.59	4 (17%)	33,38,41	2.30	13 (39%)
54	PSU	1y	32	54	18,21,22	1.33	2 (11%)	21,30,33	1.99	4 (19%)
54	7MG	1y	46	54	23,26,27	1.33	5 (21%)	27,39,42	2.70	7 (25%)
1	2MA	1A	2503	1,56	22,25,26	1.38	3 (13%)	32,37,40	2.42	9 (28%)
32	M2G	1a	966	32	24,27,28	1.26	4 (16%)	33,40,43	1.80	6 (18%)
32	2MG	2a	1207	32	23,26,27	1.20	2 (8%)	33,38,41	2.28	8 (24%)
32	MA6	2a	1519	32	23,26,27	1.59	4 (17%)	33,38,41	2.37	13 (39%)
32	5MC	2a	1404	32	19,22,23	1.71	3 (15%)	26,32,35	1.15	3 (11%)
32	7MG	2a	527	32,56	23,26,27	1.36	4 (17%)	27,39,42	2.57	6 (22%)
55	PSU	1x	55	55	18,21,22	1.30	2 (11%)	21,30,33	2.11	4 (19%)
1	5MU	2A	1915	1	19,22,23	1.44	6 (31%)	27,32,35	2.19	6 (22%)
55	5MU	1x	54	56,55	19,22,23	1.39	6 (31%)	27,32,35	1.83	6 (22%)
1	5MU	1A	1915	1	19,22,23	1.31	5 (26%)	27,32,35	2.21	6 (22%)
54	PSU	2w	32	54	18,21,22	1.36	2 (11%)	21,30,33	1.96	3 (14%)
54	PSU	1w	32	56,54	18,21,22	1.35	2 (11%)	21,30,33	2.06	4 (19%)
1	4OC	1A	1920	1	19,22,24	0.79	0	25,31,35	0.98	1 (4%)
54	PSU	1w	55	54	18,21,22	1.40	2 (11%)	21,30,33	2.05	3 (14%)
32	4OC	1a	1402	32	20,23,24	0.74	0	25,32,35	0.95	1 (4%)
54	7MG	1w	46	54	23,26,27	1.34	3 (13%)	27,39,42	2.67	7 (25%)
1	5MC	2A	1942	1	19,22,23	1.82	3 (15%)	26,32,35	1.23	3 (11%)
32	MA6	1a	1518	32	23,26,27	1.57	4 (17%)	33,38,41	2.29	13 (39%)
54	7MG	2y	46	54	23,26,27	1.35	4 (17%)	27,39,42	2.70	7 (25%)
54	PSU	2w	39	54	18,21,22	1.38	2 (11%)	21,30,33	1.67	4 (19%)
32	4OC	2a	1402	32	20,23,24	0.75	1 (5%)	25,32,35	1.04	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	5MC	1a	1407	32	19,22,23	1.62	3 (15%)	26,32,35	1.10	2 (7%)
54	PSU	1y	55	54	18,21,22	1.42	2 (11%)	21,30,33	2.03	3 (14%)
1	PSU	1A	1917	1	18,21,22	1.40	2 (11%)	21,30,33	2.06	3 (14%)
54	MIA	1y	37	54	21,24,32	1.60	4 (19%)	30,35,47	2.11	7 (23%)
32	2MG	1a	1207	32	23,26,27	1.24	3 (13%)	33,38,41	2.30	9 (27%)
32	7MG	1a	527	32,56	23,26,27	1.40	4 (17%)	27,39,42	2.59	7 (25%)
54	5MU	2w	54	54	19,22,23	1.42	5 (26%)	27,32,35	1.79	6 (22%)
32	PSU	2a	516	32	18,21,22	1.32	3 (16%)	21,30,33	2.04	5 (23%)
32	5MC	1a	967	32	19,22,23	1.53	3 (15%)	26,32,35	1.08	2 (7%)
54	4SU	2w	8	54	18,21,22	1.74	5 (27%)	25,30,33	1.88	4 (16%)
55	5MC	1x	32	55	19,22,23	1.69	3 (15%)	26,32,35	1.19	2 (7%)
1	OMG	1A	2251	1,56,55	23,26,27	1.21	3 (13%)	32,38,41	2.05	6 (18%)
1	2MA	2A	2503	1,56	22,25,26	1.49	6 (27%)	32,37,40	2.33	9 (28%)
54	MIA	2y	37	54	21,24,32	1.62	4 (19%)	30,35,47	2.07	9 (30%)
54	4SU	2y	8	54	18,21,22	1.80	4 (22%)	25,30,33	2.27	5 (20%)
55	4SU	2x	8	55	18,21,22	2.08	6 (33%)	25,30,33	1.61	4 (16%)
54	5MU	2y	54	54	19,22,23	1.47	4 (21%)	27,32,35	2.04	8 (29%)
1	PSU	2A	2605	1	18,21,22	1.31	2 (11%)	21,30,33	2.12	5 (23%)
1	5MC	1A	1942	1,56	19,22,23	1.60	3 (15%)	26,32,35	1.15	2 (7%)
1	PSU	2A	1911	1	18,21,22	1.32	2 (11%)	21,30,33	1.94	4 (19%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	MIA	1w	37	54	-	1/15/33/34	0/3/3/3
54	PSU	2y	55	54	-	1/7/25/26	0/2/2/2
54	7MG	2w	46	54	-	3/7/37/38	0/3/3/3
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1,56	-	0/7/25/26	0/2/2/2
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
54	4SU	1y	8	54	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	1/7/12/14	-
54	5MU	1y	54	54	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	4/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
54	PSU	2y	32	54	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	2/7/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	1,56	-	1/9/27/28	0/2/2/2
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	5MC	2A	1962	1,56	-	0/7/25/26	0/2/2/2
1	4OC	2A	1920	1	-	1/9/27/30	0/2/2/2
32	PSU	1a	516	32,56	-	0/7/25/26	0/2/2/2
54	PSU	2w	55	54	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,56,55	-	1/9/27/28	0/3/3/3
54	PSU	1y	39	54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
54	MIA	2w	37	54	-	0/7/25/34	0/3/3/3
1	5MC	1A	1962	1,56	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
54	PSU	2y	39	54	-	0/7/25/26	0/2/2/2
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	2/7/12/14	-
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	2MU	1A	2552	1,56	-	0/9/27/28	0/2/2/2
32	MA6	2a	1518	32	-	3/11/29/30	0/3/3/3
54	PSU	1y	32	54	-	0/7/25/26	0/2/2/2
54	7MG	1y	46	54	-	5/7/37/38	0/3/3/3
1	2MA	1A	2503	1,56	-	0/7/25/26	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	7MG	2a	527	32,56	-	3/7/37/38	0/3/3/3
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	5MU	1x	54	56,55	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	0/7/25/26	0/2/2/2
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	56,54	-	0/7/25/26	0/2/2/2
1	4OC	1A	1920	1	-	1/9/27/30	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
54	7MG	1w	46	54	-	2/7/37/38	0/3/3/3
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	1/11/29/30	0/3/3/3
54	7MG	2y	46	54	-	4/7/37/38	0/3/3/3
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	2/9/29/30	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
54	PSU	1y	55	54	-	2/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
54	MIA	1y	37	54	-	2/7/25/34	0/3/3/3
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	7MG	1a	527	32,56	-	2/7/37/38	0/3/3/3
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	0/7/25/26	0/2/2/2
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	1,56,55	-	0/9/27/28	0/3/3/3
1	2MA	2A	2503	1,56	-	0/7/25/26	0/3/3/3
54	MIA	2y	37	54	-	2/7/25/34	0/3/3/3
54	4SU	2y	8	54	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	1/7/25/26	0/2/2/2
54	5MU	2y	54	54	-	3/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1,56	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	1/7/25/26	0/2/2/2

All (262) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.99	1.69	1.82
43	2l	92	0TD	CB-SB	-12.34	1.69	1.82
54	1w	37	MIA	C2-S10	-7.60	1.69	1.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	37	MIA	C13-C14	6.96	1.53	1.32
1	2A	1942	5MC	C5-C4	6.71	1.49	1.44
32	2a	967	5MC	C5-C4	6.54	1.49	1.44
1	2A	1962	5MC	C5-C4	6.53	1.49	1.44
32	2a	1404	5MC	C5-C4	6.17	1.48	1.44
32	2a	1400	5MC	C5-C4	6.16	1.48	1.44
55	1x	32	5MC	C5-C4	5.92	1.48	1.44
32	1a	1407	5MC	C5-C4	5.83	1.48	1.44
32	2a	1407	5MC	C5-C4	5.75	1.48	1.44
1	1A	1942	5MC	C5-C4	5.72	1.48	1.44
32	1a	1400	5MC	C5-C4	5.63	1.48	1.44
1	1A	1962	5MC	C5-C4	5.56	1.48	1.44
55	2x	32	5MC	C5-C4	5.53	1.48	1.44
32	1a	967	5MC	C5-C4	5.36	1.48	1.44
32	1a	1404	5MC	C5-C4	5.15	1.48	1.44
54	2w	37	MIA	C5-C4	5.11	1.48	1.39
54	2y	37	MIA	C5-C4	5.04	1.48	1.39
55	2x	8	4SU	C4-S4	-5.01	1.59	1.68
54	1y	37	MIA	C5-C4	4.98	1.48	1.39
54	1w	8	4SU	C4-S4	-4.88	1.60	1.68
32	2a	1519	MA6	C5-C4	4.85	1.47	1.39
54	1w	37	MIA	C5-C4	4.83	1.47	1.39
32	2a	1518	MA6	C5-C4	4.81	1.47	1.39
54	2y	8	4SU	C4-S4	-4.80	1.60	1.68
54	1y	8	4SU	C4-S4	-4.77	1.60	1.68
32	1a	1518	MA6	C5-C4	4.76	1.47	1.39
32	1a	1519	MA6	C5-C4	4.67	1.47	1.39
55	1x	8	4SU	C4-N3	-4.66	1.32	1.37
55	2x	8	4SU	C4-N3	-4.63	1.32	1.37
54	2w	8	4SU	C4-S4	-4.47	1.60	1.68
1	2A	2503	2MA	C5-C4	4.20	1.46	1.39
54	2y	55	PSU	C6-C5	4.06	1.39	1.35
54	1y	55	PSU	C6-C5	4.04	1.39	1.35
55	1x	8	4SU	C4-S4	-4.00	1.61	1.68
54	2y	32	PSU	C6-C5	3.94	1.39	1.35
54	2w	39	PSU	C6-C5	3.89	1.39	1.35
54	1w	55	PSU	C6-C5	3.87	1.39	1.35
1	1A	1917	PSU	C6-C5	3.86	1.39	1.35
54	1y	39	PSU	C6-C5	3.86	1.39	1.35
1	1A	2503	2MA	C5-C4	3.82	1.45	1.39
55	2x	55	PSU	C6-C5	3.74	1.39	1.35
54	2y	39	PSU	C6-C5	3.69	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	32	PSU	C6-C5	3.68	1.39	1.35
54	2w	55	PSU	C6-C5	3.68	1.39	1.35
55	1x	8	4SU	C2-N3	-3.58	1.31	1.38
54	2y	46	7MG	C5-C4	3.54	1.48	1.37
54	1y	46	7MG	C5-C4	3.52	1.48	1.37
54	1y	32	PSU	C6-C5	3.45	1.39	1.35
32	1a	1404	5MC	C6-C5	3.44	1.40	1.34
1	1A	1911	PSU	C6-C5	3.43	1.39	1.35
54	1w	46	7MG	C5-C4	3.43	1.48	1.37
54	1y	8	4SU	C4-N3	-3.41	1.34	1.37
32	1a	516	PSU	C6-C5	3.41	1.39	1.35
54	2w	46	7MG	C4-N9	-3.40	1.33	1.37
54	1w	32	PSU	C6-C5	3.37	1.39	1.35
32	2a	966	M2G	C5-C4	3.36	1.48	1.38
32	1a	527	7MG	C5-C4	3.34	1.47	1.37
55	1x	55	PSU	C6-C5	3.34	1.39	1.35
1	2A	2605	PSU	C6-C5	3.32	1.39	1.35
54	2w	8	4SU	C4-N3	-3.32	1.34	1.37
32	2a	1518	MA6	C5-C6	3.31	1.49	1.41
32	2a	516	PSU	C6-C5	3.27	1.38	1.35
55	2x	8	4SU	C5-C4	-3.27	1.38	1.42
1	2A	1917	PSU	C6-C5	3.26	1.38	1.35
32	2a	527	7MG	C5-C4	3.26	1.47	1.37
32	2a	527	7MG	C4-N9	-3.26	1.33	1.37
1	1A	2251	OMG	C5-C4	3.25	1.47	1.38
54	1w	39	PSU	C6-C5	3.24	1.38	1.35
54	1w	46	7MG	C4-N9	-3.20	1.33	1.37
54	1w	8	4SU	C4-N3	-3.15	1.34	1.37
54	2y	54	5MU	C2-N1	3.14	1.43	1.38
32	1a	1518	MA6	C5-C6	3.13	1.49	1.41
55	1x	8	4SU	C5-C4	-3.12	1.38	1.42
54	2w	46	7MG	C5-C4	3.11	1.47	1.37
32	1a	1400	5MC	C6-C5	3.11	1.39	1.34
1	1A	2605	PSU	C6-C5	3.11	1.38	1.35
32	2a	1207	2MG	C5-C4	3.09	1.47	1.38
32	2a	1519	MA6	C5-C6	3.09	1.49	1.41
1	1A	1939	5MU	C6-C5	3.08	1.39	1.34
1	2A	1911	PSU	C6-C5	3.08	1.38	1.35
32	1a	966	M2G	C5-C4	3.05	1.47	1.38
32	2a	1407	5MC	C6-C5	3.04	1.39	1.34
1	1A	1939	5MU	C4-N3	-3.04	1.33	1.38
32	1a	527	7MG	C4-N9	-3.03	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2y	8	4SU	C4-N3	-3.02	1.34	1.37
1	2A	1942	5MC	C6-C5	3.02	1.39	1.34
55	1x	32	5MC	C6-C5	3.01	1.39	1.34
1	1A	2605	PSU	C4-N3	-3.00	1.33	1.38
32	1a	1207	2MG	C5-C4	2.98	1.46	1.38
54	2w	37	MIA	C5-C6	2.97	1.49	1.41
1	2A	2251	OMG	C5-C4	2.96	1.46	1.38
1	2A	1917	PSU	C4-N3	-2.96	1.33	1.38
32	2a	1404	5MC	C6-C5	2.95	1.39	1.34
32	1a	967	5MC	C6-C5	2.92	1.39	1.34
54	2y	37	MIA	C5-C6	2.92	1.49	1.41
32	2a	1400	5MC	C6-C5	2.89	1.39	1.34
32	1a	1407	5MC	C6-C5	2.84	1.39	1.34
1	1A	2552	2MU	C4-N3	-2.84	1.33	1.38
55	2x	54	5MU	C6-C5	2.83	1.39	1.34
54	2y	54	5MU	C6-C5	2.83	1.39	1.34
54	1y	54	5MU	C6-C5	2.82	1.39	1.34
54	1y	37	MIA	C5-C6	2.82	1.48	1.41
1	1A	1942	5MC	C6-C5	2.81	1.39	1.34
54	2w	54	5MU	C6-C5	2.80	1.39	1.34
1	2A	1915	5MU	C4-N3	-2.79	1.33	1.38
32	2a	966	M2G	C2-N2	2.79	1.40	1.35
54	2y	8	4SU	C2-N1	2.78	1.42	1.38
32	1a	516	PSU	C4-N3	-2.76	1.33	1.38
54	1w	32	PSU	C4-N3	-2.75	1.33	1.38
54	1w	39	PSU	C4-N3	-2.73	1.33	1.38
54	1w	54	5MU	C6-C5	2.73	1.39	1.34
1	2A	1939	5MU	C6-C5	2.73	1.39	1.34
1	2A	2251	OMG	C6-N1	-2.73	1.33	1.38
54	1w	37	MIA	C5-C6	2.73	1.48	1.41
1	1A	1911	PSU	C4-N3	-2.73	1.33	1.38
55	1x	54	5MU	C4-N3	-2.71	1.33	1.38
32	1a	1519	MA6	C5-C6	2.71	1.48	1.41
1	2A	1915	5MU	C6-C5	2.69	1.39	1.34
55	2x	32	5MC	C6-C5	2.67	1.39	1.34
54	1y	54	5MU	C4-N3	-2.65	1.33	1.38
1	2A	2552	2MU	C4-N3	-2.65	1.34	1.38
55	1x	54	5MU	C6-C5	2.64	1.38	1.34
32	2a	967	5MC	C6-C5	2.63	1.38	1.34
1	1A	2503	2MA	C5-C6	2.63	1.48	1.41
1	2A	1962	5MC	C6-C5	2.62	1.38	1.34
1	1A	1962	5MC	C6-C5	2.61	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2y	54	5MU	C4-C5	2.60	1.49	1.44
1	2A	1911	PSU	C4-N3	-2.59	1.34	1.38
1	1A	1915	5MU	C6-C5	2.58	1.38	1.34
54	1w	37	MIA	C8-N7	2.57	1.36	1.31
55	2x	55	PSU	C4-N3	-2.57	1.34	1.38
54	1w	54	5MU	C4-N3	-2.57	1.34	1.38
54	1y	54	5MU	C2-N3	-2.57	1.33	1.38
54	2w	54	5MU	C4-N3	-2.56	1.34	1.38
1	1A	1939	5MU	C2-N3	-2.55	1.33	1.38
1	2A	1962	5MC	C6-N1	-2.54	1.33	1.38
1	2A	2605	PSU	C4-N3	-2.53	1.34	1.38
32	1a	1519	MA6	C5-N7	-2.53	1.34	1.39
55	1x	32	5MC	C6-N1	-2.52	1.33	1.38
32	1a	966	M2G	C6-N1	-2.52	1.34	1.38
54	1w	8	4SU	C5-C4	-2.51	1.39	1.42
54	1y	8	4SU	C5-C4	-2.51	1.39	1.42
54	1y	32	PSU	C4-N3	-2.51	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.49	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.49	1.34	1.38
1	2A	2503	2MA	C5-C6	2.48	1.47	1.41
32	2a	1498	UR3	C2-N1	2.47	1.41	1.38
54	2w	39	PSU	C4-N3	-2.46	1.34	1.38
54	2y	8	4SU	C5-C4	-2.46	1.39	1.42
1	1A	1917	PSU	C4-N3	-2.46	1.34	1.38
1	2A	1915	5MU	C2-N1	2.45	1.42	1.38
55	2x	54	5MU	C4-C5	2.44	1.48	1.44
1	1A	1915	5MU	C2-N1	2.44	1.42	1.38
1	2A	2503	2MA	C8-N7	2.44	1.36	1.31
1	1A	2605	PSU	C2-N3	-2.44	1.33	1.37
54	2y	55	PSU	C4-N3	-2.43	1.34	1.38
1	2A	1939	5MU	C2-N1	2.43	1.42	1.38
1	1A	2503	2MA	C5-N7	-2.42	1.34	1.39
54	1y	54	5MU	C2-N1	2.42	1.42	1.38
54	1y	55	PSU	C4-N3	-2.41	1.34	1.38
55	2x	54	5MU	C4-N3	-2.41	1.34	1.38
32	2a	516	PSU	C4-N3	-2.40	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.40	1.33	1.38
1	1A	1962	5MC	C6-N1	-2.40	1.33	1.38
54	2w	54	5MU	C2-N1	2.40	1.42	1.38
54	2y	37	MIA	C8-N7	2.39	1.36	1.31
1	2A	1939	5MU	C4-N3	-2.39	1.34	1.38
32	1a	527	7MG	C6-N1	-2.39	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	37	MIA	C8-N7	2.39	1.36	1.31
1	1A	2552	2MU	C5-C4	2.39	1.48	1.43
32	1a	966	M2G	C2-N2	2.39	1.39	1.35
32	2a	1519	MA6	C8-N7	2.37	1.36	1.31
54	2y	46	7MG	C6-N1	-2.37	1.34	1.38
55	2x	8	4SU	C2-N3	-2.36	1.33	1.38
54	1y	37	MIA	C8-N7	2.36	1.36	1.31
54	1y	8	4SU	C2-N1	2.36	1.42	1.38
1	2A	2503	2MA	C5-N7	-2.36	1.34	1.39
54	2y	32	PSU	C4-N3	-2.35	1.34	1.38
55	2x	54	5MU	C2-N1	2.35	1.42	1.38
32	2a	527	7MG	C6-N1	-2.35	1.34	1.38
32	2a	966	M2G	C6-N1	-2.35	1.34	1.38
54	2w	54	5MU	C4-C5	2.34	1.48	1.44
54	2y	54	5MU	C4-N3	-2.34	1.34	1.38
32	1a	1519	MA6	C8-N7	2.34	1.36	1.31
32	2a	1518	MA6	C8-N7	2.34	1.36	1.31
55	2x	32	5MC	C6-N1	-2.34	1.34	1.38
54	2w	8	4SU	C2-N3	-2.34	1.33	1.38
54	2w	55	PSU	C4-N3	-2.33	1.34	1.38
54	2y	46	7MG	C8-N9	2.32	1.47	1.45
54	2w	32	PSU	C4-N3	-2.32	1.34	1.38
54	1w	37	MIA	C5-N7	-2.31	1.34	1.39
54	1w	55	PSU	C4-N3	-2.31	1.34	1.38
1	2A	1915	5MU	C4-C5	2.30	1.48	1.44
55	1x	55	PSU	C4-N3	-2.30	1.34	1.38
54	2w	8	4SU	C5-C4	-2.30	1.39	1.42
1	1A	1939	5MU	C2-N1	2.29	1.42	1.38
32	1a	1518	MA6	C8-N7	2.29	1.36	1.31
32	1a	527	7MG	C8-N9	2.27	1.47	1.45
32	1a	1518	MA6	C5-N7	-2.26	1.35	1.39
1	1A	1939	5MU	C6-N1	-2.25	1.34	1.38
55	2x	8	4SU	O2-C2	2.25	1.27	1.23
54	2y	46	7MG	C4-N9	-2.24	1.35	1.37
54	1w	46	7MG	C6-N1	-2.24	1.34	1.38
1	2A	1939	5MU	C4-C5	2.24	1.48	1.44
32	2a	1400	5MC	C6-N1	-2.23	1.34	1.38
54	1w	54	5MU	C4-C5	2.22	1.48	1.44
1	1A	1915	5MU	C4-N3	-2.22	1.34	1.38
1	2A	1915	5MU	C6-N1	-2.22	1.34	1.38
1	2A	1942	5MC	C6-N1	-2.21	1.34	1.38
54	1y	39	PSU	C4-N3	-2.20	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1207	2MG	C6-N1	-2.20	1.34	1.38
55	1x	8	4SU	O2-C2	2.20	1.27	1.23
1	1A	1942	5MC	C6-N1	-2.20	1.34	1.38
54	2y	39	PSU	C4-N3	-2.20	1.34	1.38
54	1w	8	4SU	C2-N3	-2.19	1.34	1.38
32	2a	527	7MG	C8-N9	2.19	1.47	1.45
55	1x	54	5MU	C6-N1	-2.18	1.34	1.38
54	1y	46	7MG	C8-N9	2.18	1.47	1.45
32	2a	1407	5MC	C6-N1	-2.18	1.34	1.38
54	1y	37	MIA	C5-N7	-2.17	1.35	1.39
1	2A	2251	OMG	C5-N7	-2.17	1.34	1.39
32	1a	966	M2G	C5-N7	-2.17	1.34	1.39
1	1A	2251	OMG	C5-N7	-2.16	1.34	1.39
55	2x	8	4SU	C2-N1	2.16	1.41	1.38
32	2a	1404	5MC	C6-N1	-2.16	1.34	1.38
54	1y	8	4SU	C2-N3	-2.16	1.34	1.38
32	2a	1519	MA6	C5-N7	-2.15	1.35	1.39
55	1x	54	5MU	C2-N3	-2.14	1.34	1.38
54	2w	54	5MU	C2-N3	-2.13	1.34	1.38
1	2A	2552	2MU	C2-N3	-2.13	1.34	1.38
54	1w	8	4SU	C2-N1	2.12	1.41	1.38
54	1y	46	7MG	C6-N1	-2.11	1.34	1.38
1	2A	2503	2MA	C4-N9	-2.11	1.33	1.37
32	2a	967	5MC	C6-N1	-2.11	1.34	1.38
54	2w	8	4SU	C6-C5	2.10	1.40	1.35
1	1A	1915	5MU	C6-N1	-2.10	1.34	1.38
55	1x	54	5MU	C4-C5	2.10	1.48	1.44
54	2y	39	PSU	C4-C5	2.09	1.50	1.44
54	1y	46	7MG	C4-N9	-2.09	1.35	1.37
32	1a	1400	5MC	C6-N1	-2.08	1.34	1.38
1	2A	2552	2MU	C5-C4	2.08	1.48	1.43
54	1w	54	5MU	C2-N3	-2.08	1.34	1.38
32	1a	967	5MC	C6-N1	-2.08	1.34	1.38
54	1y	54	5MU	C4-C5	2.07	1.48	1.44
32	1a	516	PSU	C2-N3	-2.06	1.34	1.37
1	1A	1915	5MU	C4-C5	2.06	1.48	1.44
54	2y	37	MIA	C5-N7	-2.05	1.35	1.39
32	1a	1207	2MG	C4-N9	-2.05	1.32	1.38
32	2a	966	M2G	C5-N7	-2.05	1.35	1.39
32	1a	1407	5MC	C6-N1	-2.05	1.34	1.38
32	2a	1518	MA6	C6-N6	2.04	1.42	1.36
1	2A	1915	5MU	C2-N3	-2.03	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1402	4OC	C6-C5	2.03	1.39	1.35
54	1y	46	7MG	C5-C6	2.02	1.48	1.43
54	1w	54	5MU	C2-N1	2.02	1.41	1.38
1	2A	2503	2MA	C8-N9	-2.01	1.34	1.37
32	1a	1498	UR3	C2-N1	2.01	1.41	1.38
55	1x	54	5MU	C2-N1	2.01	1.41	1.38
32	2a	516	PSU	O4'-C1'	-2.00	1.41	1.43

All (424) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	1l	92	0TD	CSB-SB-CB	17.51	133.84	102.36
54	2y	46	7MG	N9-C4-N3	9.55	139.45	125.46
54	1y	46	7MG	N9-C4-N3	9.47	139.33	125.46
54	1w	46	7MG	N9-C4-N3	9.20	138.94	125.46
32	1a	527	7MG	N9-C4-N3	8.99	138.64	125.46
54	1w	37	MIA	C12-C13-C14	-8.58	111.61	127.01
32	2a	527	7MG	N9-C4-N3	8.46	137.86	125.46
1	1A	2503	2MA	C5-C4-N3	-8.27	118.47	127.18
54	2w	46	7MG	N9-C4-N3	8.20	137.47	125.46
1	2A	2503	2MA	C5-C4-N3	-7.96	118.79	127.18
54	1w	37	MIA	C5-C4-N3	-7.61	119.17	127.18
32	2a	1498	UR3	C4-N3-C2	-7.12	118.85	124.58
32	2a	1207	2MG	C2-N3-C4	7.04	120.81	112.00
32	1a	1207	2MG	C2-N3-C4	6.90	120.64	112.00
32	1a	516	PSU	N1-C2-N3	6.64	122.18	115.17
1	2A	2605	PSU	N1-C2-N3	6.60	122.13	115.17
1	1A	2251	OMG	C5-C4-N3	-6.60	117.89	128.39
54	1w	39	PSU	N1-C2-N3	6.59	122.12	115.17
32	1a	1498	UR3	C4-N3-C2	-6.56	119.30	124.58
1	2A	1917	PSU	N1-C2-N3	6.53	122.05	115.17
54	2y	55	PSU	N1-C2-N3	6.51	122.04	115.17
54	2y	8	4SU	C4-N3-C2	-6.47	121.11	127.31
1	1A	2605	PSU	N1-C2-N3	6.47	121.99	115.17
54	2y	39	PSU	N1-C2-N3	6.45	121.98	115.17
54	1w	32	PSU	N1-C2-N3	6.43	121.95	115.17
1	1A	1917	PSU	N1-C2-N3	6.42	121.94	115.17
32	2a	966	M2G	C5-C4-N3	-6.42	118.18	128.39
54	1y	55	PSU	N1-C2-N3	6.40	121.92	115.17
55	2x	55	PSU	N1-C2-N3	6.39	121.91	115.17
54	1y	39	PSU	N1-C2-N3	6.38	121.90	115.17
1	1A	2503	2MA	N3-C4-N9	6.33	135.02	126.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	55	PSU	N1-C2-N3	6.31	121.83	115.17
1	1A	1911	PSU	N1-C2-N3	6.31	121.82	115.17
32	1a	1519	MA6	C5-C4-N3	-6.26	118.09	126.72
54	1w	55	PSU	N1-C2-N3	6.25	121.76	115.17
1	2A	2503	2MA	N3-C4-N9	6.24	134.91	126.99
54	2w	55	PSU	N1-C2-N3	6.24	121.75	115.17
1	2A	2251	OMG	C5-C4-N3	-6.23	118.48	128.39
54	1y	37	MIA	C5-C4-N3	-6.23	118.14	126.72
32	2a	516	PSU	N1-C2-N3	6.20	121.71	115.17
54	2w	37	MIA	C5-C4-N3	-6.10	118.31	126.72
54	2w	32	PSU	N1-C2-N3	6.10	121.60	115.17
54	1y	32	PSU	N1-C2-N3	6.08	121.58	115.17
54	2y	32	PSU	N1-C2-N3	6.04	121.54	115.17
54	1w	8	4SU	C5-C4-N3	5.95	120.29	114.75
32	1a	966	M2G	C5-C4-N3	-5.90	119.00	128.39
1	1A	2552	2MU	N3-C2-N1	5.87	122.53	114.89
54	1w	8	4SU	C4-N3-C2	-5.82	121.73	127.31
32	2a	527	7MG	N9-C8-N7	-5.81	95.15	103.37
1	2A	1911	PSU	N1-C2-N3	5.79	121.28	115.17
32	2a	1519	MA6	C5-C4-N3	-5.79	118.75	126.72
54	1y	46	7MG	C5-C4-N3	-5.77	117.31	128.13
54	2w	46	7MG	N9-C8-N7	-5.76	95.22	103.37
54	2y	37	MIA	C5-C4-N3	-5.76	118.79	126.72
32	1a	1207	2MG	C5-C4-N3	-5.74	119.26	128.39
54	2y	46	7MG	C5-C4-N3	-5.70	117.43	128.13
32	1a	1518	MA6	C5-C4-N3	-5.62	118.98	126.72
32	2a	1207	2MG	C5-C4-N3	-5.57	119.53	128.39
54	1w	37	MIA	N3-C4-N9	5.53	134.01	126.99
32	1a	527	7MG	C5-C4-N3	-5.53	117.76	128.13
54	1w	46	7MG	N9-C8-N7	-5.48	95.61	103.37
54	2w	8	4SU	C4-N3-C2	-5.43	122.11	127.31
32	2a	1518	MA6	C5-C4-N3	-5.43	119.24	126.72
54	2y	8	4SU	C5-C4-N3	5.41	119.79	114.75
1	1A	1915	5MU	O4-C4-C5	-5.39	118.75	124.92
1	2A	1915	5MU	C4-N3-C2	-5.39	120.28	127.34
1	1A	1939	5MU	C5-C4-N3	5.34	119.97	115.32
1	1A	1915	5MU	C4-N3-C2	-5.33	120.35	127.34
54	1w	46	7MG	C5-C4-N3	-5.32	118.15	128.13
1	1A	2251	OMG	C2-N3-C4	5.31	121.44	112.30
54	1y	8	4SU	C5-C4-N3	5.28	119.66	114.75
54	1y	8	4SU	C4-N3-C2	-5.25	122.29	127.31
1	1A	1939	5MU	C4-N3-C2	-5.23	120.49	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1939	5MU	C4-N3-C2	-5.11	120.64	127.34
1	2A	1915	5MU	C5-C4-N3	5.09	119.75	115.32
32	2a	527	7MG	C5-C4-N3	-5.08	118.59	128.13
54	1y	37	MIA	N3-C4-N9	5.07	135.80	127.17
1	2A	2251	OMG	C2-N3-C4	5.03	120.97	112.30
54	2w	46	7MG	C5-C4-N3	-5.03	118.68	128.13
1	1A	1915	5MU	N3-C2-N1	4.98	121.38	114.89
32	1a	527	7MG	N9-C8-N7	-4.98	96.33	103.37
1	1A	2251	OMG	N9-C4-N3	4.95	135.84	125.95
54	1y	46	7MG	N9-C8-N7	-4.94	96.38	103.37
1	1A	1939	5MU	O4-C4-C5	-4.90	119.31	124.92
1	1A	1939	5MU	N3-C2-N1	4.90	121.27	114.89
54	2w	37	MIA	N3-C4-N9	4.90	135.49	127.17
54	2y	46	7MG	N9-C8-N7	-4.87	96.48	103.37
55	2x	54	5MU	N3-C2-N1	4.86	121.21	114.89
54	1y	54	5MU	O4-C4-C5	-4.84	119.38	124.92
1	2A	1915	5MU	N3-C2-N1	4.84	121.19	114.89
54	2w	39	PSU	N1-C2-N3	4.82	120.25	115.17
1	1A	2552	2MU	C4-N3-C2	-4.81	120.64	126.61
54	2y	37	MIA	N3-C4-N9	4.79	135.31	127.17
32	2a	966	M2G	N9-C4-N3	4.75	135.45	125.95
1	2A	1939	5MU	N3-C2-N1	4.74	121.06	114.89
32	1a	1519	MA6	N3-C4-N9	4.72	135.19	127.17
54	2w	8	4SU	C5-C4-N3	4.69	119.11	114.75
1	2A	2552	2MU	N3-C2-N1	4.69	120.99	114.89
1	2A	2251	OMG	N9-C4-N3	4.68	135.30	125.95
54	2w	46	7MG	C2-N3-C4	4.67	120.35	112.30
1	1A	1915	5MU	C5-C4-N3	4.67	119.38	115.32
54	2y	46	7MG	C2-N3-C4	4.60	120.22	112.30
54	1y	46	7MG	C2-N3-C4	4.57	120.17	112.30
54	1w	54	5MU	C4-N3-C2	-4.57	121.35	127.34
54	1y	54	5MU	C5-C4-N3	4.56	119.29	115.32
54	2y	54	5MU	C4-N3-C2	-4.53	121.40	127.34
32	2a	966	M2G	C2-N3-C4	4.53	120.88	112.51
32	2a	1518	MA6	C2-N1-C6	4.50	122.81	111.83
55	2x	54	5MU	C4-N3-C2	-4.50	121.44	127.34
54	1w	54	5MU	C5-C4-N3	4.46	119.20	115.32
32	2a	1519	MA6	N3-C4-N9	4.46	134.75	127.17
1	2A	2605	PSU	C4-N3-C2	-4.45	120.24	126.37
32	2a	1518	MA6	C4-C5-N7	-4.44	105.50	110.58
1	1A	2605	PSU	C4-N3-C2	-4.41	120.30	126.37
55	2x	8	4SU	C5-C4-N3	4.41	118.85	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2y	54	5MU	C5-C4-N3	4.40	119.15	115.32
32	2a	1518	MA6	C9-N6-C6	-4.39	109.35	120.52
1	2A	1939	5MU	O4-C4-C5	-4.39	119.89	124.92
54	1w	39	PSU	C4-N3-C2	-4.37	120.36	126.37
54	2y	54	5MU	N3-C2-N1	4.34	120.54	114.89
54	1y	54	5MU	C4-N3-C2	-4.34	121.65	127.34
32	1a	516	PSU	C4-N3-C2	-4.33	120.40	126.37
54	1w	54	5MU	N3-C2-N1	4.32	120.52	114.89
32	1a	1518	MA6	C4-C5-N7	-4.32	105.64	110.58
54	1y	39	PSU	O2-C2-N1	-4.32	118.33	122.79
32	1a	1519	MA6	C9-N6-C6	-4.31	109.55	120.52
55	2x	55	PSU	C4-N3-C2	-4.30	120.44	126.37
54	1w	32	PSU	C4-N3-C2	-4.28	120.47	126.37
32	1a	527	7MG	C2-N3-C4	4.28	119.67	112.30
32	2a	1519	MA6	C4-C5-N7	-4.28	105.69	110.58
1	2A	1917	PSU	C4-N3-C2	-4.24	120.53	126.37
1	1A	1911	PSU	C4-N3-C2	-4.23	120.54	126.37
32	1a	1518	MA6	C2-N1-C6	4.22	122.15	111.83
1	2A	1915	5MU	O4-C4-C5	-4.22	120.09	124.92
1	2A	2552	2MU	C4-N3-C2	-4.21	121.38	126.61
55	1x	55	PSU	C4-N3-C2	-4.21	120.57	126.37
55	1x	55	PSU	O2-C2-N1	-4.21	118.45	122.79
54	1y	54	5MU	N3-C2-N1	4.21	120.37	114.89
54	2y	39	PSU	O2-C2-N1	-4.21	118.45	122.79
32	2a	527	7MG	C2-N3-C4	4.21	119.54	112.30
32	1a	966	M2G	C2-N3-C4	4.21	120.29	112.51
32	2a	1519	MA6	C2-N1-C6	4.19	122.08	111.83
54	2y	8	4SU	N3-C2-N1	4.19	120.35	114.89
1	2A	1939	5MU	C5-C4-N3	4.19	118.96	115.32
54	1w	55	PSU	O2-C2-N1	-4.19	118.47	122.79
55	1x	54	5MU	C4-N3-C2	-4.18	121.86	127.34
32	1a	966	M2G	N9-C4-N3	4.17	134.29	125.95
55	1x	54	5MU	N3-C2-N1	4.16	120.31	114.89
54	1w	46	7MG	C2-N3-C4	4.16	119.46	112.30
32	2a	516	PSU	C4-N3-C2	-4.16	120.65	126.37
54	2y	55	PSU	O2-C2-N1	-4.15	118.51	122.79
1	1A	2552	2MU	O2-C2-N1	-4.14	117.41	122.80
54	2y	8	4SU	C5-C4-S4	-4.12	119.59	124.31
1	1A	1917	PSU	C4-N3-C2	-4.12	120.69	126.37
54	2y	39	PSU	C4-N3-C2	-4.09	120.73	126.37
54	1y	32	PSU	C4-N3-C2	-4.09	120.73	126.37
43	2l	92	0TD	CSB-SB-CB	-4.08	95.04	102.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1519	MA6	C9-N6-C6	-4.07	110.16	120.52
1	2A	1911	PSU	C4-N3-C2	-4.07	120.76	126.37
55	2x	8	4SU	C1'-N1-C2	4.07	124.90	117.59
32	1a	1518	MA6	C9-N6-C6	-4.05	110.22	120.52
54	1y	39	PSU	C4-N3-C2	-4.05	120.80	126.37
1	1A	1939	5MU	C5-C6-N1	-4.04	118.93	123.31
54	1w	54	5MU	O4-C4-C5	-4.03	120.31	124.92
54	2y	54	5MU	O4-C4-C5	-4.01	120.33	124.92
54	2y	55	PSU	C4-N3-C2	-4.00	120.86	126.37
54	2w	54	5MU	C4-N3-C2	-4.00	122.10	127.34
54	1w	37	MIA	C15-C14-C13	-3.99	110.69	122.66
32	1a	1518	MA6	N3-C4-N9	3.99	133.95	127.17
54	2w	54	5MU	N3-C2-N1	3.98	120.07	114.89
1	1A	2503	2MA	C4-C5-N7	-3.97	106.04	110.58
54	1w	39	PSU	O2-C2-N1	-3.97	118.70	122.79
55	1x	54	5MU	C5-C4-N3	3.97	118.77	115.32
54	2w	8	4SU	N3-C2-N1	3.96	120.04	114.89
54	2w	54	5MU	C5-C4-N3	3.95	118.76	115.32
54	2y	32	PSU	C4-N3-C2	-3.94	120.94	126.37
32	1a	1519	MA6	C2-N1-C6	3.92	121.40	111.83
32	1a	1519	MA6	C4-C5-N7	-3.91	106.11	110.58
32	2a	1207	2MG	C6-C5-N7	3.91	137.40	130.29
1	2A	1915	5MU	C5-C6-N1	-3.90	119.08	123.31
55	1x	54	5MU	O4-C4-C5	-3.89	120.47	124.92
32	2a	1518	MA6	N3-C4-N9	3.89	133.78	127.17
1	2A	1939	5MU	C5-C6-N1	-3.88	119.10	123.31
32	1a	1207	2MG	C6-C5-N7	3.86	137.32	130.29
1	2A	1962	5MC	C5-C6-N1	-3.85	119.13	123.31
54	2w	37	MIA	C2-N3-C4	3.84	121.21	111.83
54	1y	37	MIA	C2-N3-C4	3.83	121.19	111.83
54	1y	55	PSU	O2-C2-N1	-3.83	118.84	122.79
54	1y	55	PSU	C4-N3-C2	-3.80	121.13	126.37
1	1A	1911	PSU	O2-C2-N1	-3.79	118.88	122.79
32	2a	1518	MA6	C2-N3-C4	3.77	121.05	111.83
54	2w	55	PSU	C4-N3-C2	-3.75	121.21	126.37
32	1a	1519	MA6	C2-N3-C4	3.74	120.98	111.83
32	2a	516	PSU	O2-C2-N1	-3.73	118.94	122.79
54	2w	32	PSU	C4-N3-C2	-3.73	121.24	126.37
54	2w	55	PSU	O2-C2-N1	-3.72	118.95	122.79
32	2a	1519	MA6	C2-N3-C4	3.72	120.91	111.83
54	1w	55	PSU	C4-N3-C2	-3.71	121.27	126.37
54	2y	37	MIA	C2-N3-C4	3.70	120.87	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1400	5MC	C5-C6-N1	-3.70	119.30	123.31
54	2w	32	PSU	O2-C2-N1	-3.68	118.99	122.79
32	1a	1207	2MG	N1-C2-N2	3.67	120.31	116.56
55	1x	32	5MC	C5-C6-N1	-3.67	119.33	123.31
32	1a	1207	2MG	N9-C4-N3	3.65	133.26	125.95
54	1w	37	MIA	C11-S10-C2	-3.65	99.51	102.25
55	2x	54	5MU	C5-C4-N3	3.65	118.50	115.32
32	2a	1207	2MG	N1-C2-N2	3.64	120.28	116.56
1	2A	1942	5MC	C5-C6-N1	-3.64	119.36	123.31
32	2a	1207	2MG	N9-C4-N3	3.62	133.20	125.95
54	2y	37	MIA	N3-C2-N1	-3.62	123.10	128.58
54	2w	37	MIA	C4-C5-N7	-3.61	106.46	110.58
1	1A	1917	PSU	O2-C2-N1	-3.60	119.07	122.79
32	1a	1518	MA6	C2-N3-C4	3.60	120.63	111.83
1	2A	2503	2MA	C4-C5-N7	-3.60	106.47	110.58
54	2y	32	PSU	O2-C2-N1	-3.58	119.09	122.79
32	1a	1498	UR3	C5-C4-N3	3.58	119.75	115.04
54	2w	54	5MU	O4-C4-C5	-3.58	120.83	124.92
32	2a	1518	MA6	N1-C2-N3	-3.58	123.17	128.58
55	2x	54	5MU	O4-C4-C5	-3.56	120.85	124.92
54	1w	37	MIA	C16-C14-C13	-3.53	112.06	122.66
54	2w	37	MIA	N3-C2-N1	-3.53	123.24	128.58
54	1y	32	PSU	O2-C2-N1	-3.52	119.15	122.79
54	1w	8	4SU	C5-C4-S4	-3.51	120.30	124.31
32	2a	967	5MC	C5-C6-N1	-3.48	119.53	123.31
54	2y	37	MIA	C4-C5-N7	-3.47	106.62	110.58
1	2A	2251	OMG	C6-C5-N7	3.46	136.58	130.29
54	1y	37	MIA	C4-C5-N7	-3.45	106.64	110.58
54	1w	37	MIA	C6-C5-N7	3.45	136.19	132.43
54	1w	37	MIA	C4-C5-N7	-3.43	106.66	110.58
54	1y	37	MIA	N3-C2-N1	-3.42	123.41	128.58
32	1a	1400	5MC	C5-C6-N1	-3.41	119.61	123.31
54	1w	32	PSU	O2-C2-N1	-3.41	119.28	122.79
1	2A	1911	PSU	O2-C2-N1	-3.39	119.30	122.79
54	1w	8	4SU	N3-C2-N1	3.38	119.30	114.89
54	1y	54	5MU	C5-C6-N1	-3.38	119.64	123.31
54	1y	8	4SU	N3-C2-N1	3.36	119.27	114.89
54	1w	54	5MU	C5-C6-N1	-3.36	119.67	123.31
32	1a	1407	5MC	C5-C6-N1	-3.36	119.67	123.31
1	1A	1942	5MC	C5-C6-N1	-3.33	119.70	123.31
55	2x	32	5MC	C5-C6-N1	-3.33	119.70	123.31
54	1w	37	MIA	C2-N3-C4	3.30	120.92	112.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1498	UR3	C5-C4-N3	3.27	119.34	115.04
32	2a	1519	MA6	N1-C2-N3	-3.26	123.64	128.58
32	1a	1404	5MC	C5-C6-N1	-3.26	119.77	123.31
1	2A	1917	PSU	O2-C2-N1	-3.25	119.44	122.79
32	2a	1404	5MC	C5-C6-N1	-3.24	119.80	123.31
1	2A	2503	2MA	C4-N9-C8	3.23	109.13	105.74
32	1a	516	PSU	O2-C2-N1	-3.23	119.46	122.79
1	1A	1942	5MC	C5-C4-N3	-3.23	118.44	121.75
54	2w	39	PSU	C4-N3-C2	-3.20	121.96	126.37
55	2x	55	PSU	O2-C2-N1	-3.20	119.49	122.79
43	2l	92	0TD	OD2-CG-CB	3.19	120.04	113.15
1	1A	2503	2MA	C5-N7-C8	3.18	108.44	103.45
32	1a	1207	2MG	C4-C5-N7	-3.15	105.68	110.67
32	1a	1207	2MG	N2-C2-N3	-3.14	116.50	120.51
32	1a	1518	MA6	N1-C2-N3	-3.14	123.84	128.58
32	2a	1519	MA6	C5-N7-C8	3.13	108.37	103.45
32	1a	967	5MC	C5-C6-N1	-3.12	119.92	123.31
32	1a	1518	MA6	C10-N6-C6	-3.08	112.68	120.52
1	2A	2605	PSU	O2-C2-N1	-3.08	119.61	122.79
55	1x	8	4SU	C6-C5-C4	-3.07	117.29	119.95
32	1a	966	M2G	C6-C5-N7	3.07	135.88	130.29
54	2w	54	5MU	C5-C6-N1	-3.07	119.98	123.31
32	2a	1518	MA6	C5-N7-C8	3.05	108.25	103.45
55	1x	54	5MU	C5-C6-N1	-3.05	120.00	123.31
54	1y	8	4SU	C5-C4-S4	-3.05	120.83	124.31
1	1A	1915	5MU	C5-C6-N1	-3.04	120.02	123.31
54	2w	46	7MG	C5-C6-N1	3.03	116.28	110.94
43	1l	92	0TD	OD2-CG-CB	3.03	119.71	113.15
1	1A	2503	2MA	C4-N9-C8	3.03	108.92	105.74
32	1a	1404	5MC	C5-C4-N3	-3.03	118.65	121.75
32	2a	1407	5MC	C5-C4-N3	-3.02	118.66	121.75
1	2A	2552	2MU	C5-C4-N3	2.99	118.99	114.80
32	1a	1519	MA6	N1-C2-N3	-2.99	124.05	128.58
32	1a	1407	5MC	C5-C4-N3	-2.97	118.71	121.75
32	2a	1519	MA6	C4-N9-C8	2.96	108.85	105.74
54	2y	37	MIA	C4-N9-C8	2.96	108.84	105.74
32	2a	1207	2MG	C4-C5-N7	-2.95	105.99	110.67
32	1a	1518	MA6	C5-N7-C8	2.95	108.08	103.45
1	2A	2503	2MA	N6-C6-N1	2.93	120.98	117.03
32	1a	1519	MA6	C5-N7-C8	2.93	108.05	103.45
32	2a	966	M2G	C6-C5-N7	2.91	135.59	130.29
55	1x	32	5MC	C5-C4-N3	-2.87	118.81	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2552	2MU	C2'-C1'-N1	-2.87	108.80	114.24
55	2x	8	4SU	C6-C5-C4	-2.87	117.47	119.95
1	1A	2251	OMG	C6-C5-N7	2.84	135.47	130.29
55	2x	32	5MC	C5-C4-N3	-2.83	118.85	121.75
1	1A	1920	4OC	O2-C2-N3	-2.81	117.91	122.33
32	2a	1407	5MC	C5-C6-N1	-2.81	120.27	123.31
32	2a	527	7MG	C5-C6-N1	2.80	115.86	110.94
32	1a	1519	MA6	N1-C6-N6	2.78	120.24	116.86
32	1a	1207	2MG	CM2-N2-C2	-2.77	117.70	123.65
32	2a	1207	2MG	N2-C2-N3	-2.76	116.99	120.51
32	2a	1402	4OC	C6-C5-C4	2.74	120.30	117.00
54	2w	37	MIA	C5-N7-C8	2.72	107.73	103.45
1	1A	2503	2MA	N9-C8-N7	-2.72	110.08	113.94
54	2y	54	5MU	C5-C6-N1	-2.72	120.36	123.31
1	1A	1915	5MU	O2-C2-N1	-2.71	119.28	122.80
1	2A	2251	OMG	C4-C5-N7	-2.70	106.39	110.67
1	1A	2605	PSU	O2-C2-N3	-2.70	117.06	121.86
32	1a	1400	5MC	C5-C4-N3	-2.69	119.00	121.75
54	1y	37	MIA	C5-N7-C8	2.69	107.68	103.45
55	1x	8	4SU	O2-C2-N1	2.68	126.29	122.80
54	2w	8	4SU	C5-C4-S4	-2.68	121.25	124.31
55	2x	54	5MU	C5-C6-N1	-2.68	120.41	123.31
54	1w	46	7MG	C5-C4-N9	-2.68	102.91	106.33
54	1w	46	7MG	C5-C6-N1	2.67	115.64	110.94
1	1A	1962	5MC	C5-C4-N3	-2.67	119.02	121.75
32	1a	1519	MA6	C10-N6-C6	-2.67	113.73	120.52
32	2a	1518	MA6	C6-C5-N7	2.66	137.69	133.43
1	1A	2503	2MA	C6-C5-N7	2.66	137.22	132.09
1	2A	2503	2MA	C5-N7-C8	2.66	107.62	103.45
1	1A	1962	5MC	C5-C6-N1	-2.64	120.45	123.31
32	1a	1402	4OC	C6-C5-C4	2.63	120.17	117.00
32	2a	1404	5MC	C5-C4-N3	-2.62	119.07	121.75
54	2y	37	MIA	C5-N7-C8	2.62	107.56	103.45
1	2A	2552	2MU	O4-C4-C5	-2.61	120.66	125.16
32	2a	1518	MA6	C4-N9-C8	2.61	108.48	105.74
1	2A	2605	PSU	C5-C6-N1	-2.60	118.53	122.14
32	2a	1400	5MC	C5-C4-N3	-2.60	119.09	121.75
54	1y	37	MIA	C4-N9-C8	2.59	108.46	105.74
54	1y	46	7MG	C5-C6-N1	2.59	115.49	110.94
32	1a	967	5MC	C5-C4-N3	-2.57	119.12	121.75
54	2y	8	4SU	C1'-N1-C2	2.56	122.19	117.59
54	2w	39	PSU	C6-C5-C4	-2.55	116.45	118.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1498	UR3	C3U-N3-C2	2.55	121.77	117.33
54	2w	46	7MG	O4'-C1'-N9	-2.55	105.83	109.30
32	2a	967	5MC	C5-C4-N3	-2.53	119.16	121.75
32	2a	966	M2G	C4-C5-N7	-2.53	106.66	110.67
54	1w	37	MIA	C2-N1-C6	2.53	122.34	117.54
1	2A	1917	PSU	C5-C6-N1	-2.52	118.64	122.14
1	2A	2503	2MA	C2-N1-C6	2.52	121.97	118.10
54	2y	46	7MG	C5-C4-N9	-2.51	103.12	106.33
32	1a	527	7MG	C5-C6-N1	2.51	115.36	110.94
43	2l	92	0TD	OD1-CG-CB	-2.51	117.19	122.44
32	1a	966	M2G	C4-C5-N7	-2.51	106.70	110.67
54	2w	37	MIA	C4-N9-C8	2.50	108.37	105.74
54	2y	54	5MU	C1'-N1-C2	2.50	122.09	117.59
1	1A	2605	PSU	C5-C6-N1	-2.50	118.67	122.14
1	2A	1942	5MC	O2-C2-N3	-2.48	118.42	122.33
1	1A	2251	OMG	C4-C5-N7	-2.48	106.75	110.67
1	2A	1962	5MC	C5-C4-N3	-2.48	119.22	121.75
54	2y	54	5MU	C5M-C5-C4	2.46	121.41	118.78
1	2A	2503	2MA	N9-C8-N7	-2.45	110.46	113.94
54	2y	46	7MG	C5-C6-N1	2.43	115.22	110.94
32	2a	1519	MA6	N1-C6-N6	2.43	119.81	116.86
1	2A	1939	5MU	O2-C2-N1	-2.42	119.65	122.80
32	2a	1404	5MC	O2-C2-N3	-2.41	118.53	122.33
1	1A	2503	2MA	C2-N1-C6	2.41	121.80	118.10
55	2x	32	5MC	O2-C2-N3	-2.40	118.54	122.33
55	1x	8	4SU	C1'-N1-C2	2.40	121.91	117.59
55	2x	54	5MU	O2-C2-N1	-2.40	119.68	122.80
32	2a	1519	MA6	C10-N6-C6	-2.39	114.45	120.52
32	2a	1519	MA6	N9-C8-N7	-2.38	110.56	113.94
32	1a	1518	MA6	C6-C5-N7	2.36	137.19	133.43
1	1A	2503	2MA	N6-C6-N1	2.35	120.20	117.03
55	1x	8	4SU	C5-C4-N3	2.35	116.94	114.75
32	1a	1518	MA6	C4-N9-C8	2.35	108.20	105.74
55	2x	8	4SU	C1'-N1-C6	-2.33	115.81	120.78
54	1y	46	7MG	C5-C4-N9	-2.32	103.36	106.33
32	2a	1207	2MG	CM2-N2-C2	-2.32	118.66	123.65
55	2x	54	5MU	C5M-C5-C4	2.32	121.26	118.78
1	1A	2552	2MU	C5-C4-N3	2.31	118.03	114.80
1	2A	1942	5MC	C5-C4-N3	-2.31	119.39	121.75
54	1w	39	PSU	C5-C6-N1	-2.31	118.94	122.14
54	2w	46	7MG	O6-C6-C5	-2.30	121.98	127.62
54	1w	37	MIA	N3-C2-N1	-2.29	122.82	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1400	5MC	O2-C2-N3	-2.27	118.76	122.33
32	1a	1498	UR3	C3U-N3-C2	2.27	121.28	117.33
1	1A	2552	2MU	O4-C4-C5	-2.26	121.26	125.16
32	2a	1519	MA6	C6-C5-N7	2.26	137.04	133.43
54	1w	32	PSU	C5-C6-N1	-2.26	119.01	122.14
54	1w	46	7MG	O6-C6-C5	-2.26	122.08	127.62
1	2A	2552	2MU	O2-C2-N1	-2.26	119.86	122.80
32	2a	1518	MA6	C10-N6-C9	-2.25	108.95	116.18
1	2A	1920	4OC	O2-C2-N3	-2.25	118.79	122.33
54	1w	37	MIA	C5-N7-C8	2.24	106.98	103.45
32	2a	1407	5MC	O2-C2-N3	-2.24	118.79	122.33
54	1y	32	PSU	C5-C6-N1	-2.23	119.04	122.14
1	2A	2503	2MA	C6-C5-N7	2.22	136.38	132.09
54	2y	54	5MU	C1'-N1-C6	-2.22	117.50	121.15
32	2a	1518	MA6	N9-C8-N7	-2.22	110.79	113.94
1	1A	1911	PSU	C5-C6-N1	-2.21	119.07	122.14
55	1x	55	PSU	C5-C6-N1	-2.21	119.07	122.14
54	1y	8	4SU	C1'-N1-C2	2.21	121.56	117.59
32	2a	516	PSU	O4'-C1'-C2'	2.19	108.18	105.15
32	2a	527	7MG	C5-C4-N9	-2.19	103.53	106.33
32	2a	516	PSU	C5-C6-N1	-2.18	119.11	122.14
32	1a	516	PSU	O4'-C1'-C2'	2.17	108.15	105.15
1	1A	2251	OMG	O6-C6-C5	-2.16	120.83	126.53
55	2x	55	PSU	C5-C6-N1	-2.16	119.15	122.14
32	1a	1519	MA6	C5-C6-N6	-2.16	121.92	125.33
32	2a	1518	MA6	C10-N6-C6	-2.16	115.04	120.52
32	1a	1518	MA6	C10-N6-C9	-2.15	109.26	116.18
32	1a	527	7MG	O6-C6-C5	-2.15	122.34	127.62
1	2A	1915	5MU	O2-C2-N1	-2.14	120.01	122.80
32	1a	527	7MG	C5-C4-N9	-2.13	103.60	106.33
32	1a	1519	MA6	C4-N9-C8	2.13	107.97	105.74
55	1x	54	5MU	O2-C2-N1	-2.13	120.03	122.80
54	2w	54	5MU	C5M-C5-C4	2.12	121.05	118.78
54	2w	46	7MG	C6-C5-C4	-2.10	118.71	122.40
1	2A	2552	2MU	C2'-C1'-N1	-2.10	110.26	114.24
54	2w	55	PSU	C5-C6-N1	-2.09	119.24	122.14
1	2A	1962	5MC	CM5-C5-C6	-2.09	120.03	122.85
1	2A	2251	OMG	C5-C6-N1	2.08	118.55	113.25
32	2a	1400	5MC	O2-C2-N3	-2.08	119.06	122.33
32	1a	1518	MA6	N9-C8-N7	-2.07	111.00	113.94
54	2y	37	MIA	C2-N1-C6	2.06	122.11	118.73
32	1a	516	PSU	C5-C6-N1	-2.06	119.28	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1911	PSU	C5-C6-N1	-2.06	119.29	122.14
32	2a	967	5MC	CM5-C5-C6	-2.05	120.08	122.85
32	1a	966	M2G	O6-C6-C5	-2.05	121.13	126.53
54	2y	46	7MG	O6-C6-C5	-2.04	122.61	127.62
55	2x	32	5MC	C1'-N1-C6	-2.04	117.79	121.15
54	1y	46	7MG	O6-C6-C5	-2.04	122.62	127.62
54	2w	39	PSU	O2-C2-N1	-2.03	120.69	122.79
54	2y	39	PSU	C6-C5-C4	-2.03	116.80	118.17
1	2A	2605	PSU	O2-C2-N3	-2.03	118.26	121.86
54	2y	37	MIA	N9-C8-N7	-2.02	111.07	113.94
1	1A	1962	5MC	O2-C2-N3	-2.02	119.15	122.33
54	2y	32	PSU	C6-C5-C4	-2.02	116.81	118.17
32	1a	1207	2MG	C8-N7-C5	2.01	107.84	104.26
54	1w	37	MIA	C4-N9-C8	2.01	107.85	105.74
54	1w	54	5MU	O2-C2-N1	-2.00	120.19	122.80

There are no chirality outliers.

All (62) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	1a	1400	5MC	O4'-C4'-C5'-O5'
32	1a	1400	5MC	C3'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
1	2A	2251	OMG	C1'-C2'-O2'-CM2
32	2a	1498	UR3	O4'-C4'-C5'-O5'
32	2a	1498	UR3	C3'-C4'-C5'-O5'
32	2a	1518	MA6	C5-C6-N6-C9
43	2l	92	0TD	O-C-CA-CB
54	1w	37	MIA	C12-C13-C14-C16
54	1y	46	7MG	C4'-C5'-O5'-P
54	2y	46	7MG	O4'-C4'-C5'-O5'
54	1y	55	PSU	C2'-C1'-C5-C4
54	2y	55	PSU	C2'-C1'-C5-C4
32	1a	527	7MG	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
54	1y	37	MIA	C3'-C4'-C5'-O5'
54	2y	37	MIA	C3'-C4'-C5'-O5'
54	2y	46	7MG	C3'-C4'-C5'-O5'
54	2y	54	5MU	C3'-C4'-C5'-O5'
54	2y	54	5MU	O4'-C4'-C5'-O5'
32	1a	527	7MG	O4'-C4'-C5'-O5'
32	2a	527	7MG	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	2a	1402	4OC	O4'-C4'-C5'-O5'
54	1y	37	MIA	O4'-C4'-C5'-O5'
32	2a	1518	MA6	N1-C6-N6-C9
32	1a	1519	MA6	C3'-C4'-C5'-O5'
54	1y	46	7MG	C3'-C4'-C5'-O5'
32	2a	1400	5MC	C2'-C1'-N1-C6
32	2a	527	7MG	O4'-C4'-C5'-O5'
54	2y	37	MIA	O4'-C4'-C5'-O5'
54	2w	46	7MG	O4'-C1'-N9-C4
32	2a	1519	MA6	C5-C6-N6-C10
54	1w	46	7MG	C3'-C4'-C5'-O5'
54	2y	46	7MG	C2'-C1'-N9-C8
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	1a	1518	MA6	C5-C6-N6-C10
54	1y	46	7MG	C2'-C1'-N9-C8
54	2w	46	7MG	C2'-C1'-N9-C8
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
32	2a	1400	5MC	O4'-C1'-N1-C6
32	2a	1400	5MC	C2'-C1'-N1-C2
54	1y	55	PSU	O4'-C1'-C5-C4
32	1a	1519	MA6	C5-C6-N6-C10
32	2a	1518	MA6	C5-C6-N6-C10
32	2a	527	7MG	C4'-C5'-O5'-P
32	1a	967	5MC	O4'-C4'-C5'-O5'
54	2w	46	7MG	O4'-C1'-N9-C8
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C1'-N1-C2
54	1y	46	7MG	O4'-C1'-N9-C8
32	2a	1519	MA6	C4'-C5'-O5'-P
1	2A	1911	PSU	O4'-C4'-C5'-O5'
54	1y	46	7MG	O4'-C4'-C5'-O5'
1	1A	1920	4OC	C2'-C1'-N1-C2
54	2y	46	7MG	O4'-C1'-N9-C8
1	2A	2552	2MU	O4'-C4'-C5'-O5'
54	1w	46	7MG	C4'-C5'-O5'-P
1	2A	1920	4OC	C2'-C1'-N1-C2
54	2y	54	5MU	C2'-C1'-N1-C2
55	2x	8	4SU	C2'-C1'-N1-C2

There are no ring outliers.

34 monomers are involved in 44 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	1w	37	MIA	1	0
54	2w	46	7MG	2	0
1	2A	1939	5MU	1	0
54	1w	39	PSU	1	0
55	1x	8	4SU	2	0
43	1l	92	0TD	1	0
54	1y	54	5MU	1	0
55	2x	55	PSU	1	0
32	1a	1400	5MC	2	0
54	2y	32	PSU	1	0
55	2x	32	5MC	1	0
1	2A	2552	2MU	2	0
1	2A	2251	OMG	2	0
32	1a	1519	MA6	1	0
32	2a	967	5MC	1	0
1	1A	1939	5MU	1	0
43	2l	92	0TD	1	0
32	2a	1518	MA6	5	0
1	1A	2503	2MA	1	0
32	2a	1207	2MG	1	0
32	2a	1519	MA6	2	0
55	1x	55	PSU	1	0
55	1x	54	5MU	1	0
1	1A	1915	5MU	1	0
32	1a	1402	4OC	2	0
54	1w	46	7MG	1	0
1	2A	1942	5MC	1	0
32	1a	1518	MA6	1	0
54	2y	46	7MG	1	0
32	2a	1402	4OC	2	0
1	1A	1917	PSU	1	0
54	1y	37	MIA	1	0
54	2w	8	4SU	1	0
1	2A	2503	2MA	3	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2312 ligands modelled in this entry, 2306 are monoatomic - leaving 6 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
60	SF4	2d	501	35	0,12,12	-	-	-		
57	4M2	1A	3894	-	62,62,62	3.24	13 (20%)	73,90,90	2.34	22 (30%)
61	FME	2x	3003	55	8,9,10	0.45	0	8,9,11	1.30	1 (12%)
60	SF4	1d	501	35	0,12,12	-	-	-		
57	4M2	2A	3670	-	62,62,62	3.21	15 (24%)	73,90,90	2.28	22 (30%)
61	FME	1x	115	55	8,9,10	0.36	0	8,9,11	1.50	1 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	SF4	2d	501	35	-	-	0/6/5/5
57	4M2	1A	3894	-	-	14/36/93/93	0/6/6/6
61	FME	2x	3003	55	-	4/7/9/11	-
60	SF4	1d	501	35	-	-	0/6/5/5
57	4M2	2A	3670	-	-	8/36/93/93	0/6/6/6
61	FME	1x	115	55	-	4/7/9/11	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	1A	3894	4M2	CAN-CBI	21.86	1.56	1.34
57	2A	3670	4M2	CAN-CBI	21.61	1.56	1.34
57	2A	3670	4M2	CBS-CBL	-7.46	1.41	1.51
57	1A	3894	4M2	CBS-CBL	-6.96	1.42	1.51
57	1A	3894	4M2	CBX-CBT	-4.31	1.47	1.52
57	1A	3894	4M2	OBF-CBX	-4.03	1.35	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	2A	3670	4M2	CAV-CBK	3.21	1.52	1.48
57	2A	3670	4M2	CBM-CAN	-3.17	1.41	1.46
57	1A	3894	4M2	C2-N1	3.09	1.39	1.33
57	2A	3670	4M2	C2-N3	3.07	1.39	1.33
57	1A	3894	4M2	CBM-CAN	-2.87	1.41	1.46
57	2A	3670	4M2	C2-N1	2.86	1.39	1.33
57	2A	3670	4M2	C8-N9	-2.81	1.32	1.37
57	1A	3894	4M2	C8-N9	-2.66	1.33	1.37
57	1A	3894	4M2	C2-N3	2.63	1.38	1.33
57	2A	3670	4M2	C5-C4	-2.62	1.34	1.39
57	1A	3894	4M2	C5-N7	-2.60	1.34	1.39
57	2A	3670	4M2	CBX-CBT	-2.49	1.49	1.52
57	2A	3670	4M2	C5-N7	-2.48	1.34	1.39
57	1A	3894	4M2	C5-C6	-2.41	1.35	1.41
57	1A	3894	4M2	C5-C4	-2.37	1.34	1.39
57	2A	3670	4M2	CBK-CBL	-2.30	1.32	1.34
57	2A	3670	4M2	C5-C6	-2.20	1.36	1.41
57	2A	3670	4M2	C4-N9	-2.15	1.33	1.37
57	1A	3894	4M2	CAV-CBK	2.12	1.51	1.48
57	2A	3670	4M2	OBF-CBX	-2.12	1.38	1.41
57	2A	3670	4M2	CBV-CBZ	-2.06	1.50	1.53
57	1A	3894	4M2	OBE-CBX	-2.03	1.42	1.45

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	1A	3894	4M2	CBN-OBF-CBX	-7.66	107.03	117.82
57	2A	3670	4M2	N3-C2-N1	-7.57	117.12	128.58
57	2A	3670	4M2	CBN-OBF-CBX	-7.55	107.18	117.82
57	1A	3894	4M2	N3-C2-N1	-7.02	117.96	128.58
57	1A	3894	4M2	OBH-CCC-N9	-6.04	96.49	108.09
57	2A	3670	4M2	N9-C8-N7	-5.15	106.62	113.94
57	1A	3894	4M2	N9-C8-N7	-4.67	107.31	113.94
57	2A	3670	4M2	C4-C5-N7	-4.53	105.41	110.58
57	1A	3894	4M2	OBF-CBX-CBT	4.40	113.84	106.69
57	2A	3670	4M2	OBF-CBX-CBT	4.30	113.67	106.69
57	2A	3670	4M2	C5-N7-C8	4.28	110.17	103.45
57	1A	3894	4M2	OBH-CBW-CBZ	-4.24	97.97	104.13
57	2A	3670	4M2	CAA-OBA-CBK	-3.99	110.56	119.19
57	1A	3894	4M2	C5-N7-C8	3.94	109.64	103.45
57	1A	3894	4M2	C4-C5-N7	-3.88	106.15	110.58
57	1A	3894	4M2	C5-C4-N3	-3.78	121.52	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	1A	3894	4M2	C4-C5-C6	3.69	119.73	115.91
57	2A	3670	4M2	C2-N1-C6	3.56	120.52	111.83
57	2A	3670	4M2	OBH-CBW-CBZ	-3.55	98.97	104.13
57	1A	3894	4M2	C2-N1-C6	3.52	120.44	111.83
57	2A	3670	4M2	C5-C4-N3	-3.52	121.88	126.72
57	2A	3670	4M2	C2-N3-C4	3.48	120.34	111.83
57	1A	3894	4M2	CBT-CBS-CBL	-3.44	98.78	102.05
57	1A	3894	4M2	CAA-OBA-CBK	-3.40	111.84	119.19
57	1A	3894	4M2	CAC-OBC-CCB	-3.29	106.03	114.47
57	2A	3670	4M2	C4-N9-CCC	-3.26	119.00	126.63
61	1x	115	FME	CA-N-CN	-3.23	117.85	122.82
57	1A	3894	4M2	C2-N3-C4	3.22	119.69	111.83
57	1A	3894	4M2	CBM-CAN-CBI	-3.15	123.72	129.43
57	2A	3670	4M2	C4-N9-C8	2.96	108.84	105.74
57	2A	3670	4M2	C5-C4-N9	2.88	108.95	105.81
57	1A	3894	4M2	CAE-CBR-CCA	-2.85	109.15	113.39
57	2A	3670	4M2	C4-C5-C6	2.84	118.85	115.91
57	1A	3894	4M2	C4-N9-C8	2.76	108.63	105.74
57	2A	3670	4M2	OBH-CCC-N9	-2.60	103.10	108.09
57	2A	3670	4M2	CBM-CAN-CBI	-2.59	124.73	129.43
57	1A	3894	4M2	CBW-OBH-CCC	-2.48	104.00	109.47
57	2A	3670	4M2	CCC-N9-C8	2.27	132.14	127.09
57	1A	3894	4M2	C5-C4-N9	2.26	108.27	105.81
57	1A	3894	4M2	C5-C6-N6	-2.24	121.78	125.33
57	1A	3894	4M2	CCC-N9-C8	-2.21	122.19	127.09
57	2A	3670	4M2	CBW-OBH-CCC	-2.17	104.67	109.47
61	2x	3003	FME	CA-N-CN	-2.16	119.49	122.82
57	2A	3670	4M2	OBG-CBY-OB	-2.16	104.94	110.04
57	2A	3670	4M2	CAE-CBR-CCA	-2.09	110.28	113.39
57	2A	3670	4M2	CBT-CBS-CBL	-2.00	100.15	102.05

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	1A	3894	4M2	C5-C6-N6-CAF
57	1A	3894	4M2	CAV-CBK-OBA-CAA
57	1A	3894	4M2	CBL-CBK-OBA-CAA
57	2A	3670	4M2	CAV-CBK-OBA-CAA
61	1x	115	FME	O1-CN-N-CA
61	1x	115	FME	C-CA-CB-CG
61	2x	3003	FME	O1-CN-N-CA

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Mol	Chain	Res	Type	Atoms
61	2x	3003	FME	C-CA-CB-CG
61	1x	115	FME	CA-CB-CG-SD
57	1A	3894	4M2	OAI-CAU-CBW-OBH
61	2x	3003	FME	N-CA-CB-CG
57	1A	3894	4M2	OBD-CAV-CBK-OBA
57	1A	3894	4M2	CAN-CBI-CBJ-OAH
57	1A	3894	4M2	CAN-CBI-CBJ-NAZ
57	2A	3670	4M2	CAN-CBI-CBJ-OAH
57	2A	3670	4M2	CAN-CBI-CBJ-NAZ
57	1A	3894	4M2	CAR-CBN-OBF-CBX
61	2x	3003	FME	CB-CA-N-CN
57	1A	3894	4M2	CAD-CBI-CBJ-NAZ
57	2A	3670	4M2	CAD-CBI-CBJ-NAZ
57	2A	3670	4M2	OBD-CAV-CBK-OBA
57	1A	3894	4M2	CAS-CBN-OBF-CBX
57	1A	3894	4M2	CAD-CBI-CBJ-OAH
57	2A	3670	4M2	CAD-CBI-CBJ-OAH
61	1x	115	FME	N-CA-CB-CG
57	1A	3894	4M2	OAI-CAU-CBW-CBZ
57	1A	3894	4M2	C5-C6-N6-CAG
57	1A	3894	4M2	N1-C6-N6-CAF
57	2A	3670	4M2	CAR-CBN-OBF-CBX
57	2A	3670	4M2	CBL-CBK-OBA-CAA

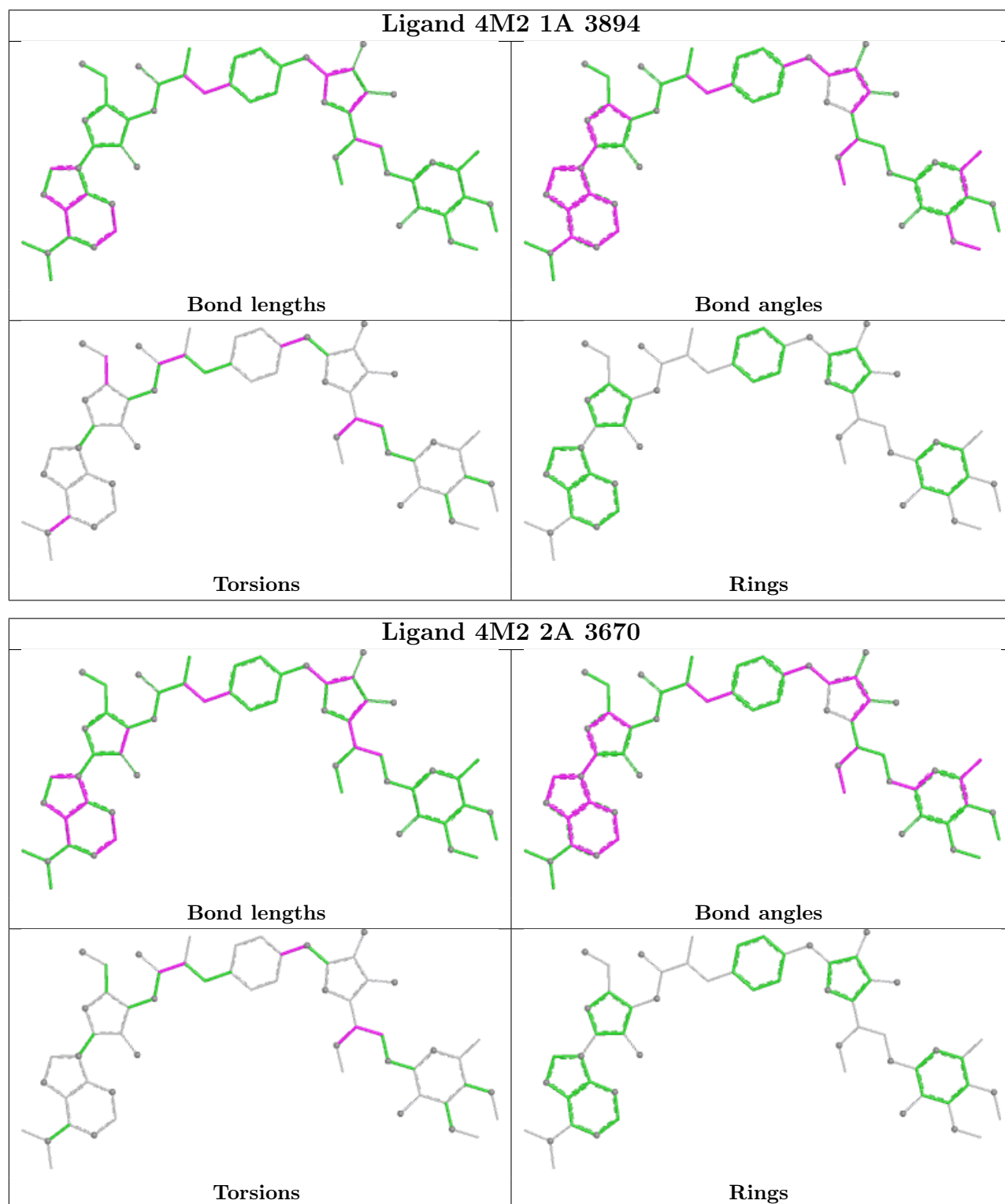
There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	1A	3894	4M2	6	0
57	2A	3670	4M2	6	0
61	1x	115	FME	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	0.02	172 (6%) 27 21	22, 42, 92, 106	0
1	2A	2789/2915 (95%)	0.13	129 (4%) 37 29	26, 46, 90, 104	0
2	1B	120/121 (99%)	0.47	2 (1%) 69 64	37, 59, 71, 89	0
2	2B	120/121 (99%)	1.28	15 (12%) 8 6	46, 66, 77, 90	0
3	1D	275/276 (99%)	0.19	7 (2%) 58 52	21, 42, 59, 79	0
3	2D	275/276 (99%)	0.32	6 (2%) 62 56	23, 44, 61, 80	0
4	1E	204/206 (99%)	0.36	6 (2%) 53 46	20, 45, 65, 78	0
4	2E	204/206 (99%)	0.40	8 (3%) 43 35	21, 49, 68, 79	0
5	1F	203/210 (96%)	0.60	8 (3%) 43 35	23, 51, 73, 89	0
5	2F	203/210 (96%)	0.61	4 (1%) 65 59	25, 56, 75, 91	0
6	1G	181/182 (99%)	1.21	28 (15%) 5 4	48, 67, 80, 92	0
6	2G	181/182 (99%)	1.55	39 (21%) 2 1	52, 71, 82, 95	0
7	1H	174/180 (96%)	1.18	18 (10%) 12 9	48, 65, 75, 82	0
7	2H	174/180 (96%)	1.54	46 (26%) 1 1	52, 70, 80, 83	0
8	1I	146/148 (98%)	1.09	13 (8%) 15 12	47, 74, 83, 89	0
8	2I	146/148 (98%)	1.39	26 (17%) 4 2	49, 74, 84, 86	0
9	1N	140/140 (100%)	0.73	6 (4%) 40 32	31, 48, 69, 79	0
9	2N	140/140 (100%)	0.66	5 (3%) 46 38	36, 53, 72, 80	0
10	1O	122/122 (100%)	-0.13	1 (0%) 82 79	25, 38, 58, 63	0
10	2O	122/122 (100%)	0.65	4 (3%) 49 40	39, 57, 72, 76	0
11	1P	149/150 (99%)	0.70	10 (6%) 24 18	23, 52, 75, 81	0
11	2P	149/150 (99%)	0.73	5 (3%) 48 40	26, 58, 78, 83	0
12	1Q	141/141 (100%)	0.64	8 (5%) 29 23	30, 49, 64, 80	0
12	2Q	141/141 (100%)	0.97	15 (10%) 11 9	37, 54, 68, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	0.20	0 100 100	30, 40, 55, 67	0
13	2R	118/118 (100%)	0.17	1 (0%) 82 79	32, 43, 57, 69	0
14	1S	110/112 (98%)	0.89	4 (3%) 46 38	45, 59, 71, 75	0
14	2S	110/112 (98%)	1.65	33 (30%) 1 0	52, 64, 74, 77	0
15	1T	131/146 (89%)	0.70	10 (7%) 20 15	37, 50, 73, 84	0
15	2T	131/146 (89%)	0.62	6 (4%) 37 29	41, 53, 74, 84	0
16	1U	116/118 (98%)	0.35	3 (2%) 57 51	26, 42, 58, 75	0
16	2U	116/118 (98%)	0.53	2 (1%) 69 64	32, 47, 62, 77	0
17	1V	101/101 (100%)	0.61	7 (6%) 23 17	29, 51, 66, 77	0
17	2V	101/101 (100%)	0.78	2 (1%) 65 59	33, 58, 70, 77	0
18	1W	112/113 (99%)	-0.08	1 (0%) 81 78	25, 37, 59, 86	0
18	2W	112/113 (99%)	0.19	2 (1%) 67 63	29, 40, 61, 88	0
19	1X	95/96 (98%)	0.02	5 (5%) 32 25	22, 35, 60, 84	0
19	2X	95/96 (98%)	0.78	7 (7%) 20 15	40, 60, 75, 82	0
20	1Y	107/110 (97%)	0.99	5 (4%) 36 28	44, 59, 72, 85	0
20	2Y	107/110 (97%)	1.14	12 (11%) 10 8	49, 62, 75, 87	0
21	1Z	154/206 (74%)	1.29	26 (16%) 4 3	46, 71, 88, 93	0
21	2Z	160/206 (77%)	1.82	58 (36%) 1 0	52, 76, 90, 94	0
22	10	83/85 (97%)	0.24	8 (9%) 13 11	25, 36, 66, 88	0
22	20	83/85 (97%)	1.44	18 (21%) 2 1	47, 65, 77, 91	0
23	11	97/98 (98%)	0.50	5 (5%) 33 25	30, 47, 69, 79	0
23	21	97/98 (98%)	0.68	3 (3%) 51 43	30, 51, 72, 80	0
24	12	70/72 (97%)	0.85	4 (5%) 29 23	39, 56, 67, 77	0
24	22	70/72 (97%)	0.76	2 (2%) 53 46	45, 61, 69, 77	0
25	13	59/60 (98%)	0.50	3 (5%) 33 26	33, 46, 68, 76	0
25	23	59/60 (98%)	0.80	3 (5%) 33 26	38, 52, 70, 79	0
26	14	69/71 (97%)	1.05	9 (13%) 7 6	47, 72, 90, 94	0
26	24	69/71 (97%)	1.93	28 (40%) 0 0	73, 86, 96, 98	0
27	15	59/60 (98%)	-0.25	0 100 100	19, 32, 51, 62	0
27	25	59/60 (98%)	0.24	0 100 100	32, 49, 66, 73	0
28	16	53/54 (98%)	-0.16	0 100 100	28, 39, 56, 61	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.89	4 (7%)	20	15	41, 58, 70, 77	0
29	17	48/49 (97%)	-0.01	3 (6%)	26	19	24, 30, 58, 73	0
29	27	48/49 (97%)	0.10	3 (6%)	26	19	25, 33, 60, 75	0
30	18	64/65 (98%)	0.38	0	100	100	30, 41, 49, 58	0
30	28	64/65 (98%)	0.39	0	100	100	35, 45, 53, 59	0
31	19	37/37 (100%)	0.79	1 (2%)	56	49	39, 49, 63, 67	0
31	29	37/37 (100%)	0.96	3 (8%)	18	13	43, 55, 65, 70	0
32	1a	1488/1521 (97%)	0.91	98 (6%)	24	18	41, 69, 92, 105	0
32	2a	1491/1521 (98%)	1.20	288 (19%)	3	2	45, 72, 93, 104	0
33	1b	231/256 (90%)	1.57	65 (28%)	1	1	67, 82, 90, 96	0
33	2b	231/256 (90%)	2.11	121 (52%)	0	0	70, 84, 90, 96	0
34	1c	206/239 (86%)	1.32	33 (16%)	5	3	64, 76, 85, 95	0
34	2c	206/239 (86%)	1.88	85 (41%)	0	0	68, 79, 86, 95	0
35	1d	208/209 (99%)	1.42	44 (21%)	2	1	55, 70, 80, 86	0
35	2d	208/209 (99%)	1.69	62 (29%)	1	0	58, 71, 81, 86	0
36	1e	148/162 (91%)	1.17	17 (11%)	9	8	58, 70, 79, 91	0
36	2e	148/162 (91%)	1.64	40 (27%)	1	1	61, 73, 82, 90	0
37	1f	100/101 (99%)	0.81	3 (3%)	52	45	54, 66, 77, 83	0
37	2f	100/101 (99%)	1.04	9 (9%)	15	12	54, 68, 77, 83	0
38	1g	155/156 (99%)	1.23	23 (14%)	5	4	63, 73, 85, 97	0
38	2g	155/156 (99%)	1.69	40 (25%)	1	1	66, 75, 87, 98	0
39	1h	137/138 (99%)	1.25	17 (12%)	8	7	61, 72, 79, 85	0
39	2h	137/138 (99%)	1.60	34 (24%)	2	1	62, 75, 81, 86	0
40	1i	127/128 (99%)	1.39	22 (17%)	4	3	49, 75, 83, 92	0
40	2i	127/128 (99%)	2.45	85 (66%)	0	0	73, 84, 92, 96	0
41	1j	97/105 (92%)	1.46	21 (21%)	2	1	45, 75, 86, 93	0
41	2j	96/105 (91%)	2.78	74 (77%)	0	0	72, 85, 93, 98	0
42	1k	114/129 (88%)	0.97	8 (7%)	22	17	46, 68, 80, 86	0
42	2k	114/129 (88%)	1.25	17 (14%)	5	4	48, 70, 81, 89	0
43	1l	121/132 (91%)	0.79	10 (8%)	17	12	44, 58, 70, 74	0
43	2l	121/132 (91%)	0.93	7 (5%)	29	22	47, 61, 72, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	123/126 (97%)	1.03	9 (7%) 21 15	51, 67, 77, 85	0
44	2m	122/126 (96%)	2.05	56 (45%) 0 0	70, 83, 88, 92	0
45	1n	60/61 (98%)	1.07	7 (11%) 9 7	50, 62, 74, 76	0
45	2n	60/61 (98%)	3.20	55 (91%) 0 0	75, 83, 90, 93	0
46	1o	88/89 (98%)	1.20	14 (15%) 5 3	50, 68, 79, 82	0
46	2o	88/89 (98%)	1.23	8 (9%) 15 11	53, 69, 80, 83	0
47	1p	82/88 (93%)	1.92	40 (48%) 0 0	58, 70, 77, 82	0
47	2p	82/88 (93%)	1.56	20 (24%) 2 1	57, 70, 78, 84	0
48	1q	99/105 (94%)	1.28	13 (13%) 7 6	59, 71, 79, 83	0
48	2q	99/105 (94%)	1.35	20 (20%) 3 1	59, 73, 80, 83	0
49	1r	68/88 (77%)	0.84	7 (10%) 12 9	52, 64, 78, 81	0
49	2r	68/88 (77%)	1.34	8 (11%) 9 7	60, 74, 83, 87	0
50	1s	83/93 (89%)	1.10	7 (8%) 17 12	66, 75, 83, 95	0
50	2s	83/93 (89%)	2.11	41 (49%) 0 0	70, 78, 85, 96	0
51	1t	96/106 (90%)	1.42	20 (20%) 2 1	57, 70, 82, 88	0
51	2t	96/106 (90%)	1.29	17 (17%) 4 2	59, 70, 83, 85	0
52	1u	23/27 (85%)	1.97	10 (43%) 0 0	64, 70, 77, 79	0
52	2u	23/27 (85%)	2.18	14 (60%) 0 0	68, 74, 78, 81	0
53	1v	14/27 (51%)	1.08	2 (14%) 6 5	51, 71, 93, 96	0
53	2v	13/27 (48%)	1.71	4 (30%) 1 0	56, 68, 87, 96	0
54	1w	67/76 (88%)	1.25	12 (17%) 3 2	62, 87, 96, 105	0
54	1y	67/76 (88%)	1.25	10 (14%) 5 4	41, 93, 98, 100	0
54	2w	66/76 (86%)	1.55	11 (16%) 4 3	66, 88, 96, 99	0
54	2y	66/76 (86%)	1.58	18 (27%) 1 1	44, 94, 99, 100	0
55	1x	72/77 (93%)	0.30	2 (2%) 55 48	25, 59, 82, 92	0
55	2x	72/77 (93%)	0.92	3 (4%) 40 32	43, 79, 90, 94	0
All	All	20877/21754 (95%)	0.78	2513 (12%) 9 7	19, 62, 88, 106	0

All (2513) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
38	2g	81	GLY	7.6
1	1A	885	C	7.4

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Mol	Chain	Res	Type	RSRZ
38	1g	82	GLY	7.4
23	2l	2	SER	7.4
38	2g	82	GLY	7.3
44	2m	123	ALA	7.1
44	2m	122	LYS	7.1
41	2j	65	LEU	6.6
32	2a	1034	G	6.6
45	2n	39	LEU	6.4
6	2G	2	PRO	6.2
32	2a	1033	G	6.2
1	1A	884	C	6.1
1	1A	1064	C	6.0
38	2g	83	ALA	6.0
45	2n	38	GLY	5.9
40	2i	102	LEU	5.9
44	1m	124	PRO	5.9
44	2m	102	ARG	5.8
22	10	3	HIS	5.8
40	2i	106	ALA	5.7
1	1A	1078	U	5.7
1	1A	1097	U	5.7
40	2i	105	ASP	5.7
45	2n	2	ALA	5.6
1	1A	1095	A	5.6
23	1l	2	SER	5.6
1	1A	883	G	5.5
38	2g	84	ASN	5.5
1	2A	2154	G	5.4
52	1u	24	ARG	5.4
1	2A	1536	C	5.4
41	2j	35	SER	5.3
1	1A	1509	C	5.3
45	1n	2	ALA	5.2
22	10	5	LYS	5.2
1	1A	1059	G	5.2
1	1A	896	A	5.1
1	1A	1060	U	5.1
1	1A	1508	A	5.1
47	1p	38	TYR	5.1
32	1a	1531	A	5.0
1	2A	2155	G	5.0
26	24	56	VAL	5.0

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Mol	Chain	Res	Type	RSRZ
22	10	7	LEU	5.0
1	1A	1094	U	5.0
45	2n	34	TYR	5.0
50	2s	2	PRO	4.9
32	1a	1024	G	4.9
41	2j	40	LEU	4.9
1	1A	888	C	4.9
26	24	57	GLU	4.9
21	2Z	173	ALA	4.8
32	2a	1030(B)	C	4.8
44	2m	124	PRO	4.8
39	2h	2	LEU	4.8
22	20	2	ALA	4.8
38	1g	80	VAL	4.8
20	1Y	1	MET	4.8
45	2n	25	VAL	4.8
32	1a	1030(B)	C	4.8
1	1A	1063	G	4.8
1	1A	2115	G	4.8
32	2a	1150	U	4.7
1	1A	887	A	4.7
3	2D	262	ARG	4.7
41	2j	46	ARG	4.6
54	2w	75	C	4.6
1	1A	1077	A	4.6
1	2A	2153	G	4.6
18	2W	112	GLY	4.6
22	10	6	GLY	4.6
32	1a	1023	G	4.6
1	1A	1081	U	4.6
45	2n	18	VAL	4.6
33	2b	237	ALA	4.6
35	2d	152	SER	4.6
41	2j	34	VAL	4.6
15	1T	130	ALA	4.5
54	1w	75	C	4.5
1	1A	1068	G	4.5
8	2I	146	ALA	4.5
22	10	2	ALA	4.5
33	2b	200	ILE	4.5
1	2A	229	A	4.5
26	24	63	TYR	4.5

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Mol	Chain	Res	Type	RSRZ
21	2Z	144	LEU	4.5
41	2j	41	PRO	4.5
1	1A	1080	C	4.4
45	2n	21	TYR	4.4
40	1i	126	SER	4.4
38	1g	81	GLY	4.4
44	2m	120	LYS	4.4
1	1A	1066	U	4.4
45	2n	30	ALA	4.4
32	2a	1003	G	4.4
32	1a	1532	U	4.3
1	1A	1070	A	4.3
1	2A	1847	A	4.3
36	2e	85	GLY	4.3
47	2p	48	TRP	4.3
38	2g	80	VAL	4.3
32	1a	1030(A)	G	4.3
32	1a	1030	C	4.3
32	2a	1030	C	4.3
41	2j	78	ASN	4.3
40	2i	10	ARG	4.3
36	2e	74	GLY	4.3
50	2s	79	THR	4.3
33	2b	187	LEU	4.3
38	2g	5	ARG	4.3
1	1A	614(B)	G	4.3
32	2a	1001	A	4.3
3	1D	275	LYS	4.3
36	2e	22	GLY	4.3
51	2t	103	GLY	4.3
12	2Q	28	ALA	4.2
15	1T	131	ALA	4.2
36	2e	17	ALA	4.2
22	20	3	HIS	4.2
1	1A	886	C	4.2
40	2i	39	GLY	4.2
41	2j	10	GLY	4.2
33	1b	129	GLU	4.2
33	2b	165	VAL	4.2
33	2b	121	LEU	4.2
45	2n	29	ARG	4.2
32	2a	1000	U	4.2

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Mol	Chain	Res	Type	RSRZ
32	1a	1503	A	4.2
54	2w	76	A	4.2
1	2A	2802	G	4.2
32	2a	1001(A)	G	4.2
33	1b	133	LYS	4.2
33	1b	126	GLU	4.2
7	1H	2	SER	4.2
32	1a	1447	A	4.2
54	2w	1	G	4.2
38	2g	85	TYR	4.1
40	2i	36	TYR	4.1
41	2j	77	PRO	4.1
6	1G	182	LYS	4.1
34	2c	2	GLY	4.1
46	1o	89	GLY	4.1
1	1A	2113	U	4.1
32	2a	1532	U	4.1
33	2b	67	THR	4.1
25	23	2	PRO	4.1
33	2b	236	TYR	4.1
50	2s	80	TYR	4.1
32	2a	1030(A)	G	4.1
54	1y	18	G	4.1
42	2k	49	GLY	4.1
45	2n	33	VAL	4.1
33	2b	161	ALA	4.1
41	2j	58	ASP	4.1
50	2s	72	GLY	4.1
46	1o	87	ILE	4.1
1	2A	2156	G	4.1
40	2i	14	VAL	4.1
32	1a	204	U	4.1
40	1i	2	GLU	4.1
44	2m	64	TRP	4.1
1	1A	1096	A	4.1
1	2A	896	A	4.1
54	1w	74	C	4.1
40	2i	41	VAL	4.1
1	1A	1058	G	4.0
32	1a	1001(A)	G	4.0
1	1A	1076	C	4.0
32	1a	1036	G	4.0

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Mol	Chain	Res	Type	RSRZ
41	2j	32	ALA	4.0
44	2m	5	ALA	4.0
21	2Z	146	ILE	4.0
52	2u	14	TRP	4.0
19	1X	95	LEU	4.0
32	1a	163	C	4.0
35	2d	160	GLN	4.0
33	1b	237	ALA	4.0
34	2c	52	LEU	4.0
35	2d	173	TRP	4.0
44	2m	100	GLY	4.0
33	1b	19	HIS	4.0
33	1b	28	PHE	4.0
3	1D	276	LYS	4.0
41	2j	30	SER	4.0
45	2n	5	ALA	4.0
50	2s	71	LEU	4.0
9	2N	9	VAL	4.0
41	2j	44	VAL	4.0
50	2s	77	THR	3.9
32	2a	1002	G	3.9
33	2b	175	ARG	3.9
45	2n	53	LEU	3.9
1	1A	1088	A	3.9
32	1a	1030(D)	A	3.9
26	24	50	VAL	3.9
41	2j	76	ASN	3.9
41	2j	42	THR	3.9
32	1a	630	G	3.9
32	2a	976	G	3.9
32	2a	1202	G	3.9
34	2c	8	ILE	3.9
7	1H	66	GLY	3.9
51	1t	69	GLY	3.9
39	2h	4	ASP	3.9
50	2s	13	ASP	3.9
45	2n	14	PRO	3.9
32	1a	1025	U	3.9
45	2n	59	ALA	3.9
41	2j	93	GLY	3.9
41	2j	47	PHE	3.9
1	1A	882	G	3.9

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Mol	Chain	Res	Type	RSRZ
33	2b	199	TYR	3.9
42	1k	25	TYR	3.9
43	2l	18	VAL	3.9
45	2n	54	PRO	3.9
32	2a	1248	A	3.9
12	1Q	112	GLU	3.9
45	2n	15	LYS	3.9
47	1p	19	ILE	3.9
51	1t	103	GLY	3.9
42	1k	14	VAL	3.9
1	1A	1176	G	3.8
1	2A	2157	G	3.8
1	2A	2126	A	3.8
6	1G	139	LEU	3.8
32	2a	1035	A	3.8
36	1e	119	LEU	3.8
33	1b	34	ALA	3.8
21	2Z	143	GLY	3.8
32	1a	1027	C	3.8
1	1A	1026	U	3.8
32	1a	1257	U	3.8
33	2b	152	PHE	3.8
35	2d	110	PHE	3.8
40	2i	104	ARG	3.8
41	2j	43	ARG	3.8
6	1G	146	TYR	3.8
45	2n	49	HIS	3.8
38	2g	117	ALA	3.8
1	1A	2207	G	3.8
32	1a	1003	G	3.8
1	1A	1069	A	3.8
1	2A	2173	A	3.8
21	2Z	174	VAL	3.8
32	2a	1358	U	3.8
44	2m	121	LYS	3.8
4	2E	204	ALA	3.8
33	1b	188	ALA	3.8
33	2b	17	PHE	3.8
45	2n	31	ARG	3.8
50	2s	9	VAL	3.8
1	2A	1171	G	3.8
32	2a	1224	G	3.8

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Mol	Chain	Res	Type	RSRZ
33	1b	26	PRO	3.8
32	1a	345	C	3.8
40	2i	63	ILE	3.8
50	2s	69	HIS	3.8
54	2w	74	C	3.8
45	2n	12	ARG	3.8
41	2j	48	THR	3.7
1	1A	2117	A	3.7
32	1a	1001	A	3.7
35	2d	176	LEU	3.7
54	1w	73	A	3.7
32	1a	1031	G	3.7
32	2a	1190	G	3.7
41	1j	4	ILE	3.7
21	2Z	21	ALA	3.7
41	2j	27	ALA	3.7
45	2n	3	ARG	3.7
33	1b	17	PHE	3.7
33	2b	71	VAL	3.7
41	2j	23	ILE	3.7
1	1A	1098	A	3.7
32	2a	1531	A	3.7
1	1A	1087	G	3.7
1	1A	2190	G	3.7
32	1a	1030(C)	G	3.7
26	24	49	PHE	3.7
33	2b	163	PHE	3.7
6	1G	53	LEU	3.7
21	2Z	170	THR	3.7
41	2j	88	LEU	3.7
53	2v	12	A	3.7
20	2Y	57	GLN	3.7
1	1A	2112	G	3.7
41	2j	56	HIS	3.7
45	2n	22	THR	3.7
21	2Z	122	ARG	3.7
29	27	45	ALA	3.7
34	2c	155	GLY	3.7
52	2u	16	GLY	3.7
1	1A	229	A	3.6
33	2b	140	HIS	3.6
33	2b	215	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
44	2m	106	ASN	3.6
32	2a	630	G	3.6
32	2a	1024	G	3.6
32	2a	1032	G	3.6
1	2A	2136	C	3.6
32	2a	1029	C	3.6
50	2s	54	GLY	3.6
22	20	68	GLU	3.6
34	1c	2	GLY	3.6
1	2A	883	G	3.6
41	2j	63	PHE	3.6
6	2G	35	GLU	3.6
22	20	84	LEU	3.6
51	1t	10	LEU	3.6
1	1A	1065	U	3.6
1	2A	2119	A	3.6
32	1a	344	A	3.6
32	2a	1030(D)	A	3.6
32	2a	1286	A	3.6
8	2I	8	PRO	3.6
21	1Z	100	VAL	3.6
40	2i	64	THR	3.6
50	1s	13	ASP	3.6
32	2a	1040	U	3.6
14	2S	35	ILE	3.5
1	2A	2146	C	3.5
32	2a	1363	C	3.5
32	1a	1002	G	3.5
54	1w	1	G	3.5
38	1g	83	ALA	3.5
38	2g	152	ALA	3.5
21	1Z	141	VAL	3.5
40	2i	28	VAL	3.5
44	2m	23	TYR	3.5
38	2g	16	LEU	3.5
33	1b	127	ILE	3.5
36	2e	107	ARG	3.5
20	2Y	1	MET	3.5
33	2b	123	ALA	3.5
33	2b	188	ALA	3.5
1	1A	897	C	3.5
1	2A	34	C	3.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2174	C	3.5
5	1F	14	PRO	3.5
1	1A	1093	G	3.5
1	2A	2133	G	3.5
7	2H	2	SER	3.5
33	2b	53	ARG	3.5
50	2s	29	ARG	3.5
17	1V	42	GLY	3.5
49	2r	60	ALA	3.5
8	2I	18	VAL	3.5
33	2b	112	VAL	3.5
32	2a	1038	C	3.5
38	2g	32	ARG	3.5
1	1A	2157	G	3.5
32	2a	1220	G	3.5
22	10	4	LYS	3.5
1	1A	2790	A	3.5
54	1w	76	A	3.5
44	2m	67	GLU	3.5
33	2b	93	VAL	3.5
36	2e	115	VAL	3.5
47	1p	5	ARG	3.5
7	1H	92	ILE	3.4
40	1i	114	TYR	3.4
1	1A	2145	C	3.4
32	2a	973	G	3.4
32	2a	1036	G	3.4
35	1d	23	GLY	3.4
42	2k	36	ASP	3.4
54	2w	15	G	3.4
21	1Z	168	GLU	3.4
11	1P	99	LEU	3.4
35	2d	157	LEU	3.4
21	2Z	121	HIS	3.4
33	2b	57	PHE	3.4
34	2c	182	ILE	3.4
35	2d	20	TYR	3.4
21	1Z	170	THR	3.4
32	2a	980	C	3.4
21	2Z	150	LEU	3.4
33	2b	19	HIS	3.4
34	2c	30	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
41	2j	5	ARG	3.4
47	1p	81	ARG	3.4
32	1a	1021	G	3.4
32	2a	1117	G	3.4
34	2c	14	ILE	3.4
35	2d	158	ILE	3.4
32	2a	965	A	3.4
54	2y	35	A	3.4
26	14	54	GLY	3.4
35	1d	167	GLY	3.4
51	1t	47	GLY	3.4
14	2S	54	LEU	3.4
40	2i	66	ARG	3.4
41	2j	66	ARG	3.4
32	2a	1192	C	3.4
38	2g	21	VAL	3.4
39	2h	9	MET	3.4
35	2d	166	LYS	3.4
32	2a	983	A	3.4
41	1j	100	THR	3.4
6	2G	48	GLU	3.4
22	20	6	GLY	3.4
33	2b	221	LEU	3.4
35	2d	155	LEU	3.4
38	1g	2	ALA	3.4
40	2i	13	ALA	3.4
47	1p	82	GLN	3.4
39	2h	15	ASN	3.4
21	2Z	141	VAL	3.4
32	2a	999	C	3.3
32	2a	1116	C	3.3
26	14	63	TYR	3.3
40	2i	5	TYR	3.3
25	23	60	GLU	3.3
33	1b	12	GLU	3.3
39	1h	2	LEU	3.3
33	2b	177	ALA	3.3
40	2i	8	GLY	3.3
40	2i	67	GLY	3.3
51	2t	86	ARG	3.3
1	2A	2159	G	3.3
32	1a	1033	G	3.3

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Mol	Chain	Res	Type	RSRZ
51	2t	74	LYS	3.3
1	1A	2189	U	3.3
26	24	67	TYR	3.3
38	1g	85	TYR	3.3
43	2l	64	TYR	3.3
1	1A	2136	C	3.3
1	1A	2146	C	3.3
24	12	69	ARG	3.3
48	2q	80	GLY	3.3
6	2G	28	VAL	3.3
50	1s	9	VAL	3.3
21	2Z	171	ILE	3.3
41	1j	75	ILE	3.3
1	1A	2100	G	3.3
1	1A	2793	G	3.3
32	2a	963	G	3.3
32	2a	993	G	3.3
34	1c	179	ARG	3.3
35	2d	106	TYR	3.3
40	2i	103	THR	3.3
41	2j	59	SER	3.3
23	11	98	LEU	3.3
40	2i	19	LEU	3.3
40	2i	30	GLY	3.3
41	2j	36	GLY	3.3
33	1b	22	LYS	3.3
45	2n	17	LYS	3.3
26	14	59	PHE	3.3
21	2Z	140	ASP	3.3
36	2e	105	VAL	3.3
1	1A	548	A	3.3
1	1A	1073	A	3.3
1	2A	2117	A	3.3
32	2a	1004	A	3.3
22	20	72	ARG	3.3
45	1n	3	ARG	3.3
1	2A	652(U)	G	3.3
32	1a	306	G	3.3
32	2a	1031	G	3.3
33	1b	213	LEU	3.3
38	2g	77	SER	3.3
40	2i	7	THR	3.3

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Mol	Chain	Res	Type	RSRZ
45	2n	13	THR	3.3
14	2S	36	TYR	3.3
40	2i	127	LYS	3.3
44	1m	27	LYS	3.3
8	1I	146	ALA	3.3
33	2b	225	ALA	3.3
1	1A	271(K)	U	3.3
39	2h	134	ILE	3.3
41	2j	49	VAL	3.3
44	2m	4	ILE	3.3
6	1G	49	ASP	3.3
7	1H	3	ARG	3.2
40	1i	66	ARG	3.2
40	2i	107	ARG	3.2
1	1A	1067	A	3.2
21	2Z	168	GLU	3.2
32	1a	1005	A	3.2
33	2b	154	LEU	3.2
37	2f	21	LEU	3.2
41	2j	62	HIS	3.2
36	2e	20	GLN	3.2
48	1q	99	SER	3.2
50	2s	52	TYR	3.2
6	2G	50	ALA	3.2
4	1E	77	ILE	3.2
8	2I	15	VAL	3.2
33	2b	136	VAL	3.2
35	2d	154	ASN	3.2
40	2i	75	ASP	3.2
45	2n	27	CYS	3.2
7	2H	60	ARG	3.2
32	2a	1112	C	3.2
32	2a	1321	C	3.2
34	1c	87	LEU	3.2
34	2c	188	LEU	3.2
45	2n	47	LEU	3.2
33	2b	190	THR	3.2
36	2e	75	THR	3.2
1	1A	2114	A	3.2
1	1A	2158	A	3.2
32	2a	1183	A	3.2
32	2a	1447	A	3.2

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Mol	Chain	Res	Type	RSRZ
54	1y	35	A	3.2
35	1d	70	ILE	3.2
1	1A	879	G	3.2
1	2A	2793	G	3.2
40	2i	9	ARG	3.2
1	2A	271(K)	U	3.2
34	2c	4	LYS	3.2
54	1w	20	U	3.2
55	1x	47	U	3.2
41	2j	85	LEU	3.2
50	2s	68	GLY	3.2
25	23	51	ALA	3.2
32	2a	962	C	3.2
32	2a	995	C	3.2
44	2m	87	TYR	3.2
33	1b	7	VAL	3.2
41	2j	50	ILE	3.2
45	2n	37	PHE	3.2
46	1o	60	VAL	3.2
1	1A	1057	A	3.2
32	1a	1035	A	3.2
32	2a	1179	A	3.2
44	2m	104	ARG	3.2
33	2b	48	MET	3.2
14	1S	48	LEU	3.2
40	2i	12	GLU	3.2
1	1A	2897	U	3.2
1	2A	2149	G	3.2
32	1a	79	G	3.2
54	1y	20	U	3.2
11	2P	118	GLY	3.2
6	1G	76	SER	3.2
12	1Q	81	VAL	3.2
21	2Z	136	PHE	3.2
35	2d	4	TYR	3.2
32	2a	1027	C	3.1
29	17	47	ARG	3.1
35	2d	76	ARG	3.1
52	1u	15	ARG	3.1
3	2D	275	LYS	3.1
33	1b	27	LYS	3.1
32	2a	994	A	3.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1041	A	3.1
45	2n	44	LEU	3.1
34	2c	22	TRP	3.1
34	2c	185	GLY	3.1
45	2n	7	ILE	3.1
36	2e	100	VAL	3.1
32	1a	1034	G	3.1
32	2a	1042	G	3.1
32	2a	1182	G	3.1
32	2a	1323	G	3.1
12	1Q	10	ARG	3.1
33	2b	22	LYS	3.1
44	2m	71	ARG	3.1
38	2g	37	ASN	3.1
1	1A	2142	C	3.1
32	2a	1039	C	3.1
32	2a	1149	C	3.1
33	1b	11	LEU	3.1
50	2s	15	LEU	3.1
16	1U	117	GLN	3.1
1	1A	278	A	3.1
32	1a	1183	A	3.1
32	2a	974	A	3.1
8	1I	124	GLY	3.1
31	29	37	GLY	3.1
14	2S	49	VAL	3.1
33	2b	197	VAL	3.1
14	1S	3	ARG	3.1
42	2k	124	LYS	3.1
6	2G	12	TYR	3.1
7	2H	41	MET	3.1
38	2g	154	TYR	3.1
42	2k	25	TYR	3.1
40	2i	29	ASN	3.1
39	2h	112	LEU	3.1
40	1i	105	ASP	3.1
1	2A	2893	G	3.1
1	2A	271(J)	C	3.1
1	2A	2175	C	3.1
40	2i	27	THR	3.1
51	2t	47	GLY	3.1
33	2b	162	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
49	2r	20	ALA	3.1
14	2S	11	LYS	3.1
19	2X	68	ARG	3.1
41	2j	72	VAL	3.1
49	2r	43	PHE	3.1
8	2I	38	LEU	3.1
32	2a	981	U	3.1
32	2a	1121	U	3.1
26	24	65	ASP	3.1
38	2g	33	ASP	3.1
47	1p	13	HIS	3.1
1	1A	1074	G	3.1
1	2A	2792	G	3.1
32	1a	346	G	3.1
32	2a	1048	G	3.1
34	2c	171	GLY	3.1
50	1s	48	THR	3.1
52	2u	11	GLY	3.1
33	2b	207	ALA	3.1
40	2i	15	ALA	3.1
44	1m	2	ALA	3.1
45	2n	50	LYS	3.1
51	1t	95	ALA	3.1
21	2Z	1	MET	3.1
21	2Z	4	ARG	3.1
33	2b	24	TRP	3.1
1	1A	652(S)	C	3.1
1	1A	1075	C	3.1
32	2a	1028	C	3.1
1	2A	2114	A	3.0
32	1a	161	A	3.0
33	1b	9	GLU	3.0
44	2m	61	GLU	3.0
1	1A	1082	U	3.0
32	2a	17	U	3.0
32	2a	952	U	3.0
6	2G	74	LYS	3.0
35	1d	166	LYS	3.0
35	2d	124	GLY	3.0
39	2h	11	THR	3.0
41	2j	87	THR	3.0
47	2p	69	THR	3.0

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Mol	Chain	Res	Type	RSRZ
21	1Z	146	ILE	3.0
45	2n	42	ILE	3.0
36	2e	24	ARG	3.0
40	1i	106	ALA	3.0
52	1u	6	ARG	3.0
33	2b	122	PHE	3.0
40	2i	18	PHE	3.0
1	2A	10	G	3.0
32	2a	1316	G	3.0
35	2d	188	LEU	3.0
36	2e	12	LEU	3.0
1	2A	884	C	3.0
32	2a	1249	C	3.0
15	1T	104	ASN	3.0
21	2Z	159	PRO	3.0
1	1A	2135	A	3.0
32	2a	1324	A	3.0
47	2p	82	GLN	3.0
14	2S	3	ARG	3.0
21	1Z	1	MET	3.0
34	2c	190	ARG	3.0
36	2e	114	GLY	3.0
46	1o	88	ARG	3.0
47	2p	81	ARG	3.0
33	2b	120	ALA	3.0
34	2c	137	ALA	3.0
34	2c	149	ALA	3.0
34	2c	160	ALA	3.0
34	2c	10	PHE	3.0
8	1I	38	LEU	3.0
26	24	25	TYR	3.0
34	2c	193	TYR	3.0
52	1u	23	PRO	3.0
1	1A	1062	G	3.0
1	1A	2110	G	3.0
26	24	51	ASP	3.0
32	2a	1030(C)	G	3.0
32	2a	1047	G	3.0
51	1t	74	LYS	3.0
1	1A	898	C	3.0
32	2a	1045	C	3.0
32	2a	1260	C	3.0

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Mol	Chain	Res	Type	RSRZ
54	2w	2	C	3.0
55	1x	67	C	3.0
14	2S	17	ARG	3.0
32	2a	1357	A	3.0
34	1c	14	ILE	3.0
41	2j	60	ARG	3.0
41	2j	86	MET	3.0
52	2u	24	ARG	3.0
12	2Q	19	GLY	3.0
45	2n	28	GLY	3.0
34	2c	189	ALA	3.0
1	1A	614(A)	U	3.0
46	1o	57	LEU	3.0
47	1p	73	LEU	3.0
20	1Y	91	GLU	3.0
7	2H	128	PRO	3.0
3	2D	38	LYS	3.0
6	2G	146	TYR	3.0
34	2c	23	TYR	3.0
39	1h	65	TYR	3.0
47	2p	38	TYR	3.0
46	1o	68	ARG	3.0
33	2b	185	ILE	3.0
12	2Q	21	THR	3.0
33	2b	66	GLY	3.0
52	1u	2	GLY	3.0
1	1A	2165	G	3.0
1	1A	2138	C	3.0
6	1G	73	ALA	3.0
32	2a	1283	G	3.0
41	1j	32	ALA	3.0
42	2k	23	ALA	3.0
54	2y	57	G	3.0
55	2x	70	G	3.0
32	2a	1114	C	3.0
1	1A	1174	A	3.0
1	1A	2173	A	3.0
39	2h	53	VAL	3.0
54	1y	36	A	3.0
6	2G	3	LEU	2.9
21	2Z	91	LEU	2.9
44	2m	19	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
33	2b	75	LYS	2.9
35	2d	51	PRO	2.9
41	2j	37	PRO	2.9
44	2m	27	LYS	2.9
47	1p	46	PRO	2.9
51	2t	8	ARG	2.9
52	2u	10	ARG	2.9
41	1j	74	ILE	2.9
40	2i	100	GLY	2.9
8	2I	53	ALA	2.9
20	2Y	78	ALA	2.9
36	2e	21	ALA	2.9
7	2H	26	VAL	2.9
7	2H	37	VAL	2.9
33	2b	230	VAL	2.9
35	1d	110	PHE	2.9
35	2d	88	VAL	2.9
45	2n	36	PHE	2.9
22	20	7	LEU	2.9
26	24	9	LEU	2.9
1	1A	1089	G	2.9
1	1A	2191	G	2.9
32	2a	979	C	2.9
32	2a	1115	C	2.9
32	2a	1397	C	2.9
1	2A	2158	A	2.9
1	2A	2169	A	2.9
44	1m	122	LYS	2.9
41	1j	77	PRO	2.9
41	2j	39	PRO	2.9
52	1u	14	TRP	2.9
1	2A	2113	U	2.9
41	2j	19	SER	2.9
33	2b	135	GLN	2.9
40	2i	124	GLN	2.9
4	1E	1	MET	2.9
36	2e	18	ARG	2.9
38	1g	84	ASN	2.9
40	2i	111	ARG	2.9
33	2b	214	ILE	2.9
7	2H	15	VAL	2.9
7	2H	45	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
14	2S	65	VAL	2.9
34	2c	55	VAL	2.9
35	2d	178	VAL	2.9
46	1o	66	LEU	2.9
1	1A	889	C	2.9
1	1A	1100	C	2.9
1	1A	2803	C	2.9
32	1a	1029	C	2.9
1	1A	881	G	2.9
1	1A	1173	G	2.9
1	2A	271(L)	U	2.9
1	2A	2112	G	2.9
32	1a	1032	G	2.9
54	2y	33	U	2.9
6	1G	77	ILE	2.9
34	1c	182	ILE	2.9
52	2u	18	TYR	2.9
7	2H	22	GLY	2.9
21	2Z	147	GLY	2.9
42	1k	90	GLY	2.9
43	1l	63	GLY	2.9
33	2b	218	ALA	2.9
45	2n	20	ALA	2.9
6	1G	80	PHE	2.9
14	2S	32	LEU	2.9
22	20	30	VAL	2.9
39	1h	112	LEU	2.9
48	2q	100	LYS	2.9
33	2b	86	GLU	2.9
11	1P	15	ARG	2.9
35	1d	3	ARG	2.9
35	2d	115	ARG	2.9
38	2g	49	ILE	2.9
44	2m	22	ILE	2.9
6	2G	126	ASP	2.9
47	1p	68	ASP	2.9
1	1A	12	U	2.9
1	1A	2164	C	2.9
1	2A	2139	C	2.9
1	2A	2163	C	2.9
14	2S	7	TYR	2.9
32	2a	1113	C	2.9

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Mol	Chain	Res	Type	RSRZ
32	2a	1213	A	2.9
34	2c	13	GLY	2.9
40	2i	62	TYR	2.9
44	2m	68	GLY	2.9
1	1A	880	G	2.9
1	1A	1171	G	2.9
1	2A	2110	G	2.9
21	1Z	152	ALA	2.9
22	20	5	LYS	2.9
47	1p	43	LYS	2.9
14	2S	85	VAL	2.9
35	2d	112	VAL	2.9
41	2j	94	VAL	2.9
54	2y	19	G	2.9
7	2H	39	PRO	2.8
21	2Z	95	PRO	2.8
33	1b	23	ARG	2.8
33	2b	96	ARG	2.8
7	2H	72	ILE	2.8
26	24	14	ILE	2.8
46	2o	3	ILE	2.8
5	1F	208	GLY	2.8
7	2H	100	GLY	2.8
33	2b	189	ASP	2.8
35	1d	102	ASP	2.8
33	1b	156	LYS	2.8
40	2i	125	TYR	2.8
34	2c	61	ALA	2.8
34	2c	192	THR	2.8
36	1e	151	LEU	2.8
6	2G	38	VAL	2.8
21	2Z	104	PHE	2.8
35	1d	140	VAL	2.8
1	1A	878	A	2.8
1	1A	2794	C	2.8
1	2A	897	C	2.8
1	2A	2804	C	2.8
11	1P	149	GLU	2.8
32	1a	342	C	2.8
54	1y	56	C	2.8
21	2Z	68	PRO	2.8
1	2A	2168	G	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	1094	G	2.8
40	1i	104	ARG	2.8
54	1w	15	G	2.8
54	2y	18	G	2.8
54	2y	34	G	2.8
35	1d	71	SER	2.8
12	2Q	22	LYS	2.8
10	2O	81	ASP	2.8
6	2G	53	LEU	2.8
8	2I	68	LEU	2.8
21	1Z	150	LEU	2.8
33	1b	187	LEU	2.8
35	1d	157	LEU	2.8
40	2i	96	LEU	2.8
41	2j	100	THR	2.8
42	2k	75	TYR	2.8
50	2s	22	LEU	2.8
51	1t	13	LEU	2.8
21	2Z	172	ALA	2.8
38	2g	2	ALA	2.8
40	2i	43	ALA	2.8
33	1b	230	VAL	2.8
33	2b	129	GLU	2.8
1	2A	2172	U	2.8
32	2a	992	U	2.8
32	2a	1020	U	2.8
38	1g	115	ARG	2.8
41	1j	60	ARG	2.8
44	2m	29	ARG	2.8
1	2A	899	A	2.8
32	1a	160	A	2.8
32	1a	1286	A	2.8
32	2a	968	A	2.8
44	2m	101	GLN	2.8
54	2y	36	A	2.8
1	1A	1079	C	2.8
1	2A	1043	C	2.8
32	1a	1028	C	2.8
3	2D	276	LYS	2.8
6	2G	20	ILE	2.8
6	2G	88	ILE	2.8
41	2j	57	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
32	1a	625	G	2.8
32	2a	631	G	2.8
32	2a	971	G	2.8
32	2a	1021	G	2.8
54	1w	44	G	2.8
22	20	75	LEU	2.8
40	1i	19	LEU	2.8
44	2m	119	GLY	2.8
45	2n	51	GLY	2.8
52	2u	4	GLY	2.8
7	2H	169	VAL	2.8
33	2b	31	TYR	2.8
40	1i	13	ALA	2.8
33	2b	126	GLU	2.8
40	2i	65	VAL	2.8
40	2i	101	PHE	2.8
41	2j	61	GLU	2.8
41	2j	64	GLU	2.8
43	1l	64	TYR	2.8
45	2n	10	ALA	2.8
50	2s	24	ALA	2.8
35	1d	33	MET	2.8
33	2b	114	ARG	2.8
36	2e	25	ARG	2.8
40	2i	128	ARG	2.8
45	1n	14	PRO	2.8
41	2j	84	GLN	2.8
32	2a	982	U	2.8
32	2a	1122	U	2.8
34	2c	45	LYS	2.8
1	1A	655	A	2.8
1	1A	1045	A	2.8
32	2a	977	A	2.8
32	2a	996	A	2.8
41	2j	75	ILE	2.8
53	2v	24	A	2.8
32	2a	1119	C	2.8
32	2a	1217	C	2.8
32	2a	1322	C	2.8
37	1f	17	SER	2.8
7	1H	67	LEU	2.8
7	2H	64	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
17	1V	101	GLY	2.8
21	1Z	160	GLY	2.8
34	1c	196	LEU	2.8
35	1d	87	GLY	2.8
40	2i	6	GLY	2.8
41	2j	90	LEU	2.8
46	2o	20	GLY	2.8
7	2H	61	HIS	2.8
33	2b	205	ASP	2.8
4	1E	204	ALA	2.8
6	2G	161	THR	2.8
8	1I	70	GLU	2.8
8	2I	41	GLU	2.8
33	2b	184	VAL	2.8
34	2c	76	VAL	2.8
36	2e	33	VAL	2.8
40	2i	2	GLU	2.8
40	2i	119	ALA	2.8
41	2j	24	VAL	2.8
45	2n	56	VAL	2.8
47	1p	2	VAL	2.8
52	2u	17	THR	2.8
26	24	59	PHE	2.8
1	1A	2125	G	2.8
32	1a	1026	G	2.8
32	2a	1053	G	2.8
39	1h	48	TYR	2.8
40	1i	51	ARG	2.8
35	1d	37	PRO	2.7
42	2k	13	GLN	2.7
14	2S	57	LYS	2.7
1	1A	895	U	2.7
1	2A	272(A)	U	2.7
1	2A	895	U	2.7
32	1a	560	U	2.7
32	2a	4	U	2.7
33	1b	24	TRP	2.7
33	2b	69	LEU	2.7
34	1c	52	LEU	2.7
39	1h	10	LEU	2.7
41	2j	71	LEU	2.7
45	2n	61	TRP	2.7

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Mol	Chain	Res	Type	RSRZ
3	1D	203	ASN	2.7
1	1A	899	A	2.7
2	2B	53	A	2.7
32	2a	1151	A	2.7
32	2a	1363(A)	A	2.7
35	1d	6	GLY	2.7
34	2c	6	HIS	2.7
34	2c	176	HIS	2.7
1	1A	2140	C	2.7
2	2B	20	C	2.7
3	2D	2	ALA	2.7
32	2a	824	C	2.7
32	2a	1118	C	2.7
33	2b	77	ALA	2.7
34	1c	100	ALA	2.7
40	2i	46	ALA	2.7
41	2j	83	GLU	2.7
38	2g	79	ARG	2.7
40	1i	59	PHE	2.7
42	2k	54	ARG	2.7
44	2m	88	ARG	2.7
47	1p	80	PHE	2.7
48	1q	11	VAL	2.7
50	2s	10	PHE	2.7
54	2y	56	C	2.7
33	1b	202	PRO	2.7
36	2e	61	TYR	2.7
39	2h	89	PRO	2.7
38	1g	86	GLN	2.7
1	2A	2148	G	2.7
1	2A	2152	G	2.7
2	2B	119	G	2.7
32	2a	1154	G	2.7
54	2w	19	G	2.7
21	2Z	57	ILE	2.7
39	2h	80	ILE	2.7
7	1H	71	LEU	2.7
7	1H	105	LEU	2.7
19	2X	92	LEU	2.7
34	1c	94	LEU	2.7
34	2c	91	LEU	2.7
39	2h	39	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
39	2h	23	SER	2.7
48	2q	97	SER	2.7
32	2a	1194	U	2.7
15	1T	111	ARG	2.7
21	2Z	2	GLU	2.7
29	27	47	ARG	2.7
35	2d	179	GLU	2.7
33	1b	15	VAL	2.7
33	2b	70	PHE	2.7
34	2c	15	THR	2.7
35	2d	187	ARG	2.7
38	2g	4	ARG	2.7
40	2i	42	ARG	2.7
47	1p	25	ARG	2.7
52	2u	6	ARG	2.7
45	2n	16	PHE	2.7
32	2a	969	A	2.7
32	2a	1275	A	2.7
35	2d	189	PRO	2.7
53	2v	14	A	2.7
35	2d	86	LYS	2.7
40	2i	11	LYS	2.7
51	1t	38	LYS	2.7
1	2A	885	C	2.7
32	1a	1008	C	2.7
33	2b	211	ILE	2.7
34	2c	124	ILE	2.7
51	2t	63	ILE	2.7
14	2S	58	LEU	2.7
34	1c	43	LEU	2.7
40	2i	99	LEU	2.7
41	1j	86	MET	2.7
48	2q	74	LEU	2.7
1	1A	2131	G	2.7
1	2A	882	G	2.7
32	2a	953	G	2.7
32	2a	1373	G	2.7
34	2c	78	GLY	2.7
35	2d	183	GLY	2.7
36	1e	85	GLY	2.7
40	2i	68	GLY	2.7
50	2s	82	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
54	1y	19	G	2.7
54	2y	22	G	2.7
5	1F	15	SER	2.7
38	1g	32	ARG	2.7
47	2p	18	ARG	2.7
50	2s	78	ARG	2.7
8	2I	36	ALA	2.7
21	2Z	88	PHE	2.7
22	20	43	THR	2.7
26	14	49	PHE	2.7
33	1b	225	ALA	2.7
34	1c	65	ALA	2.7
48	2q	77	VAL	2.7
39	2h	25	ASP	2.7
6	2G	17	PRO	2.7
8	2I	137	PRO	2.7
20	2Y	63	LYS	2.7
32	2a	1126	U	2.7
39	2h	67	PRO	2.7
41	2j	91	PRO	2.7
11	2P	70	GLN	2.7
34	2c	29	TYR	2.7
35	1d	38	TYR	2.7
40	1i	125	TYR	2.7
1	1A	529	A	2.7
1	1A	2119	A	2.7
32	2a	1180	A	2.7
33	2b	108	ILE	2.7
51	2t	55	ILE	2.7
1	1A	2137	C	2.7
1	1A	2804	C	2.7
32	2a	1006	C	2.7
32	2a	1195	C	2.7
32	2a	1234	C	2.7
6	2G	19	LEU	2.7
11	1P	147	LEU	2.7
20	2Y	90	LEU	2.7
21	2Z	157	LEU	2.7
33	2b	213	LEU	2.7
34	2c	204	LEU	2.7
35	2d	194	LEU	2.7
51	2t	10	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
47	1p	16	HIS	2.7
11	1P	79	ARG	2.7
33	2b	99	GLY	2.7
35	1d	168	ARG	2.7
45	2n	35	ARG	2.7
21	2Z	149	SER	2.7
35	1d	137	SER	2.7
12	2Q	104	PHE	2.7
14	2S	12	PHE	2.7
15	2T	131	ALA	2.7
33	2b	7	VAL	2.7
36	1e	21	ALA	2.7
40	1i	14	VAL	2.7
45	1n	4	LYS	2.7
45	2n	11	LYS	2.7
49	1r	20	ALA	2.7
51	1t	68	LYS	2.7
1	1A	1071	G	2.6
1	1A	2159	G	2.6
1	2A	171	G	2.6
1	2A	2131	G	2.6
32	2a	1058	G	2.6
32	2a	1131	G	2.6
32	2a	1181	G	2.6
54	2y	15	G	2.6
1	1A	9	U	2.6
32	2a	1062	U	2.6
33	2b	201	ILE	2.6
33	2b	222	ILE	2.6
34	2c	39	ILE	2.6
36	2e	118	ILE	2.6
41	2j	38	ILE	2.6
32	1a	614	A	2.6
32	2a	1130	A	2.6
37	1f	21	LEU	2.6
44	2m	90	LEU	2.6
39	1h	85	ARG	2.6
49	1r	42	ARG	2.6
4	2E	73	GLU	2.6
17	1V	43	GLU	2.6
32	2a	970	C	2.6
32	2a	1018	C	2.6

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Mol	Chain	Res	Type	RSRZ
32	2a	1019	C	2.6
32	2a	1218	C	2.6
37	2f	92	LYS	2.6
40	2i	109	VAL	2.6
50	2s	4	SER	2.6
50	2s	35	SER	2.6
33	2b	55	PHE	2.6
33	2b	194	PRO	2.6
33	2b	76	GLN	2.6
34	2c	62	ASP	2.6
39	2h	48	TYR	2.6
40	2i	114	TYR	2.6
1	1A	2116	G	2.6
32	1a	181	G	2.6
32	1a	1196	U	2.6
32	2a	960	U	2.6
54	1w	70	G	2.6
54	2y	5	G	2.6
8	2I	72	LEU	2.6
33	2b	61	LEU	2.6
41	2j	9	ARG	2.6
45	2n	41	ARG	2.6
33	1b	134	GLU	2.6
38	1g	90	GLU	2.6
39	2h	43	GLY	2.6
41	2j	14	LYS	2.6
47	2p	37	GLY	2.6
2	2B	26	A	2.6
32	1a	162	A	2.6
54	2y	58	A	2.6
40	2i	90	PRO	2.6
41	1j	20	ALA	2.6
41	2j	20	ALA	2.6
44	2m	77	ASN	2.6
12	2Q	65	PHE	2.6
33	1b	190	THR	2.6
33	2b	54	THR	2.6
35	1d	173	TRP	2.6
44	2m	103	THR	2.6
51	2t	98	PRO	2.6
1	2A	1040	C	2.6
6	2G	52	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
41	1j	98	ILE	2.6
48	2q	59	ILE	2.6
7	2H	67	LEU	2.6
39	2h	65	TYR	2.6
33	2b	21	ARG	2.6
41	1j	46	ARG	2.6
43	1l	89	ARG	2.6
1	2A	2150	U	2.6
50	2s	70	LYS	2.6
55	2x	47	U	2.6
35	2d	24	GLU	2.6
36	2e	97	GLY	2.6
45	2n	55	GLY	2.6
1	1A	275	G	2.6
32	2a	1106	G	2.6
32	2a	1127	G	2.6
32	2a	1193	G	2.6
7	2H	44	VAL	2.6
21	2Z	42	VAL	2.6
33	2b	34	ALA	2.6
33	2b	202	PRO	2.6
36	1e	94	ALA	2.6
44	2m	72	ALA	2.6
49	1r	60	ALA	2.6
51	2t	9	ASN	2.6
6	1G	29	TRP	2.6
9	1N	8	GLN	2.6
50	2s	38	SER	2.6
1	2A	878	A	2.6
1	2A	2801(A)	A	2.6
32	2a	975	A	2.6
32	2a	1503	A	2.6
33	1b	193	ASP	2.6
41	2j	73	ASP	2.6
17	1V	99	ILE	2.6
1	2A	894	C	2.6
6	2G	139	LEU	2.6
32	2a	403	C	2.6
32	2a	972	C	2.6
32	2a	1007	C	2.6
33	1b	221	LEU	2.6
33	2b	11	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
34	2c	175	LEU	2.6
44	2m	66	LEU	2.6
15	1T	125	ARG	2.6
19	2X	69	TYR	2.6
35	2d	209	ARG	2.6
51	1t	80	ARG	2.6
40	2i	112	LYS	2.6
21	1Z	138	GLU	2.6
34	2c	9	GLY	2.6
52	2u	2	GLY	2.6
1	2A	2144	U	2.6
7	1H	44	VAL	2.6
7	2H	49	VAL	2.6
33	1b	93	VAL	2.6
33	2b	29	ALA	2.6
33	2b	125	PRO	2.6
34	2c	73	PRO	2.6
34	2c	75	VAL	2.6
40	2i	33	PHE	2.6
36	2e	116	THR	2.5
47	1p	76	GLN	2.6
1	1A	652(U)	G	2.5
1	1A	2124	G	2.5
1	2A	2319	G	2.5
32	2a	944	G	2.5
32	2a	1050	G	2.5
32	2a	1084	G	2.5
32	2a	1120	G	2.5
32	2a	1276	G	2.5
33	2b	83	MET	2.5
7	2H	136	ILE	2.5
42	2k	40	ILE	2.5
1	2A	917	A	2.5
1	2A	2134	A	2.5
32	2a	1016	A	2.5
32	2a	1123	A	2.5
34	2c	33	LEU	2.5
40	2i	40	LEU	2.5
47	2p	6	LEU	2.5
9	1N	115	ARG	2.5
35	1d	59	ARG	2.5
45	2n	26	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
48	1q	68	ARG	2.5
48	2q	3	LYS	2.5
40	2i	117	HIS	2.5
9	1N	72	TYR	2.5
34	2c	184	TYR	2.5
48	2q	24	GLU	2.5
1	1A	154(A)	C	2.5
1	2A	2143	C	2.5
1	2A	2789	C	2.5
32	2a	1223	C	2.5
54	2y	13	C	2.5
26	14	45	GLY	2.5
34	2c	194	GLY	2.5
35	2d	2	GLY	2.5
38	2g	34	GLY	2.5
6	2G	87	PRO	2.5
21	2Z	105	VAL	2.5
21	2Z	161	VAL	2.5
34	2c	68	VAL	2.5
34	2c	207	VAL	2.5
39	1h	26	VAL	2.5
14	2S	55	ALA	2.5
15	2T	130	ALA	2.5
22	20	18	ALA	2.5
35	2d	45	GLN	2.5
42	2k	117	ASN	2.5
1	1A	1963	U	2.5
1	1A	2167	U	2.5
14	2S	52	SER	2.5
32	1a	841	U	2.5
32	2a	1205	U	2.5
34	2c	20	SER	2.5
45	2n	60	SER	2.5
31	19	12	ASP	2.5
39	2h	13	ILE	2.5
41	2j	82	ILE	2.5
6	1G	75	LYS	2.5
14	2S	80	LEU	2.5
21	2Z	33	LEU	2.5
24	22	69	ARG	2.5
33	2b	147	LYS	2.5
36	2e	71	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
40	2i	79	LEU	2.5
43	1l	23	LYS	2.5
48	1q	100	LYS	2.5
1	2A	2124	G	2.5
1	2A	2165	G	2.5
1	2A	2166	G	2.5
32	1a	610	G	2.5
32	2a	1124	G	2.5
1	1A	1084	A	2.5
1	1A	1086	A	2.5
33	1b	33	TYR	2.5
34	1c	193	TYR	2.5
34	2c	201	TYR	2.5
36	2e	60	TYR	2.5
46	1o	78	TYR	2.5
53	1v	13	A	2.5
36	1e	114	GLY	2.5
43	1l	95	GLY	2.5
40	2i	49	PRO	2.5
7	2H	115	VAL	2.5
21	2Z	139	VAL	2.5
38	1g	141	VAL	2.5
43	1l	18	VAL	2.5
46	2o	60	VAL	2.5
35	1d	45	GLN	2.5
38	2g	116	ALA	2.5
40	1i	76	ALA	2.5
40	2i	37	PHE	2.5
45	2n	48	ALA	2.5
50	2s	74	PHE	2.5
1	1A	34	C	2.5
17	1V	1	MET	2.5
9	2N	73	THR	2.5
38	2g	109	ASN	2.5
43	2l	8	ASN	2.5
8	1I	131	LYS	2.5
33	1b	200	ILE	2.5
33	2b	195	ASP	2.5
33	2b	208	ILE	2.5
38	2g	156	TRP	2.5
40	2i	78	LYS	2.5
45	1n	17	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	1A	2130	U	2.5
6	2G	51	ARG	2.5
7	2H	88	LEU	2.5
7	2H	98	LEU	2.5
15	2T	108	ARG	2.5
35	1d	135	LEU	2.5
40	1i	111	ARG	2.5
42	2k	126	ARG	2.5
45	2n	23	ARG	2.5
47	2p	74	LEU	2.5
51	1t	8	ARG	2.5
33	2b	113	HIS	2.5
20	2Y	91	GLU	2.5
12	1Q	32	TYR	2.5
33	2b	33	TYR	2.5
44	1m	21	TYR	2.5
44	2m	59	TYR	2.5
12	2Q	33	GLY	2.5
1	1A	2833	G	2.5
1	2A	652(B)	A	2.5
1	2A	2115	G	2.5
1	2A	2116	G	2.5
1	2A	2308	G	2.5
32	1a	1004	A	2.5
32	2a	1087	G	2.5
32	2a	1157	A	2.5
32	2a	1221	G	2.5
32	2a	1252	A	2.5
32	2a	1280	A	2.5
32	2a	1396	A	2.5
35	2d	111	ALA	2.5
40	2i	31	GLN	2.5
40	2i	86	VAL	2.5
8	1I	65	ALA	2.5
14	2S	5	THR	2.5
34	2c	181	ASN	2.5
44	2m	105	THR	2.5
35	2d	9	CYS	2.5
40	2i	70	LYS	2.5
45	2n	4	LYS	2.5
49	2r	21	LYS	2.5
6	2G	82	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
9	2N	115	ARG	2.5
33	1b	21	ARG	2.5
39	2h	63	LEU	2.5
44	1m	102	ARG	2.5
44	2m	78	ILE	2.5
49	2r	54	ARG	2.5
51	1t	11	SER	2.5
32	1a	100	C	2.5
32	1a	290	C	2.5
32	1a	1039	C	2.5
42	1k	36	ASP	2.5
50	2s	14	HIS	2.5
32	1a	223	U	2.5
32	1a	343	U	2.5
32	2a	991	U	2.5
32	2a	1025	U	2.5
32	2a	1125	U	2.5
32	2a	1148	U	2.5
32	2a	1212	U	2.5
33	1b	236	TYR	2.5
35	2d	6	GLY	2.5
21	2Z	71	VAL	2.5
34	1c	68	VAL	2.5
34	1c	198	VAL	2.5
36	1e	20	GLN	2.5
37	2f	16	GLN	2.5
41	1j	34	VAL	2.5
36	2e	86	ALA	2.5
46	2o	18	PHE	2.5
33	2b	179	LYS	2.4
34	2c	150	LYS	2.4
43	1l	91	LYS	2.4
47	1p	22	THR	2.4
47	1p	69	THR	2.4
14	2S	61	ASN	2.4
32	1a	975	A	2.4
32	2a	1245	A	2.4
34	2c	3	ASN	2.4
41	2j	45	ARG	2.4
21	1Z	171	ILE	2.4
21	2Z	102	LEU	2.4
28	26	11	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
33	2b	44	LEU	2.4
36	1e	13	ILE	2.4
39	2h	83	ILE	2.4
1	2A	2151	G	2.4
32	2a	654	G	2.4
32	2a	1026	G	2.4
32	2a	1064	G	2.4
41	2j	68	HIS	2.4
1	1A	2896	C	2.4
1	2A	2111	C	2.4
2	2B	5	C	2.4
32	1a	311	C	2.4
32	1a	1452	C	2.4
32	2a	1369	C	2.4
1	2A	614(A)	U	2.4
4	2E	56	PRO	2.4
7	2H	135	GLY	2.4
8	2I	1	MET	2.4
16	2U	73	GLY	2.4
32	2a	1446	U	2.4
36	2e	10	MET	2.4
38	2g	132	GLY	2.4
47	1p	78	GLY	2.4
50	2s	84	GLY	2.4
8	2I	145	VAL	2.4
21	2Z	165	VAL	2.4
33	2b	156	LYS	2.4
35	1d	201	GLN	2.4
35	2d	128	VAL	2.4
41	2j	33	GLN	2.4
5	2F	21	ALA	2.4
6	1G	50	ALA	2.4
21	1Z	104	PHE	2.4
48	1q	37	LYS	2.4
35	1d	82	ALA	2.4
15	1T	129	ARG	2.4
33	2b	111	ARG	2.4
38	1g	79	ARG	2.4
46	1o	22	THR	2.4
8	2I	5	LEU	2.4
8	2I	9	LEU	2.4
21	2Z	70	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
36	2e	13	ILE	2.4
39	2h	10	LEU	2.4
44	2m	25	ILE	2.4
50	2s	62	ILE	2.4
41	1j	35	SER	2.4
1	1A	2801(A)	A	2.4
32	1a	152	A	2.4
32	1a	609	A	2.4
32	2a	1005	A	2.4
32	2a	1046	A	2.4
32	2a	1287	A	2.4
45	2n	40	CYS	2.4
1	1A	2120	G	2.4
32	1a	78	G	2.4
32	2a	1272	G	2.4
35	2d	165	MET	2.4
5	2F	131	GLY	2.4
7	1H	14	GLY	2.4
21	1Z	159	PRO	2.4
26	24	7	PRO	2.4
33	1b	38	GLY	2.4
40	1i	30	GLY	2.4
42	1k	49	GLY	2.4
44	2m	112	GLY	2.4
8	2I	112	LYS	2.4
21	1Z	156	LYS	2.4
46	2o	5	LYS	2.4
1	2A	886	C	2.4
1	2A	888	C	2.4
1	2A	2896	C	2.4
1	1A	2132	U	2.4
1	2A	9	U	2.4
10	2O	7	TYR	2.4
32	1a	1054	C	2.4
32	2a	934	C	2.4
33	2b	15	VAL	2.4
34	2c	48	TYR	2.4
40	2i	53	VAL	2.4
44	2m	7	VAL	2.4
7	2H	145	ALA	2.4
15	1T	45	PHE	2.4
21	2Z	164	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
32	1a	1446	U	2.4
48	2q	95	TYR	2.4
26	14	55	ARG	2.4
33	1b	62	ALA	2.4
48	1q	91	ARG	2.4
4	2E	77	ILE	2.4
21	2Z	41	LEU	2.4
34	2c	77	ILE	2.4
50	2s	5	LEU	2.4
35	2d	137	SER	2.4
40	2i	126	SER	2.4
48	2q	99	SER	2.4
6	1G	167	GLU	2.4
6	2G	29	TRP	2.4
8	1I	10	GLU	2.4
35	2d	163	GLU	2.4
39	2h	8	ASP	2.4
45	2n	24	CYS	2.4
48	2q	96	GLU	2.4
1	1A	1177	A	2.4
3	1D	38	LYS	2.4
29	27	48	LYS	2.4
32	2a	946	A	2.4
32	2a	1092	A	2.4
32	2a	1188	A	2.4
32	2a	1250	A	2.4
40	2i	118	LYS	2.4
41	2j	55	LYS	2.4
47	1p	35	LYS	2.4
50	2s	18	LYS	2.4
7	1H	174	GLY	2.4
21	1Z	147	GLY	2.4
21	2Z	26	GLY	2.4
22	10	13	GLY	2.4
41	2j	52	GLY	2.4
14	1S	14	VAL	2.4
22	20	79	VAL	2.4
33	1b	229	VAL	2.4
39	1h	61	VAL	2.4
1	1A	2156	G	2.4
1	1A	2319	G	2.4
6	2G	163	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
7	2H	6	ARG	2.4
12	2Q	29	PHE	2.4
14	2S	29	PHE	2.4
20	2Y	55	TYR	2.4
32	2a	80	G	2.4
32	2a	942	G	2.4
32	2a	987	G	2.4
32	2a	1356	G	2.4
32	2a	1370	G	2.4
36	1e	95	ALA	2.4
38	2g	46	ALA	2.4
39	1h	44	PHE	2.4
39	1h	60	ARG	2.4
43	1l	26	ALA	2.4
47	2p	64	ALA	2.4
51	1t	12	ALA	2.4
33	2b	51	LEU	2.4
34	2c	5	ILE	2.4
35	2d	70	ILE	2.4
41	1j	8	LEU	2.4
41	1j	88	LEU	2.4
41	2j	8	LEU	2.4
1	1A	1072	C	2.4
1	2A	1744	C	2.4
32	2a	1063	C	2.4
32	2a	1070	U	2.4
32	2a	1257	U	2.4
51	1t	100	ILE	2.4
32	2a	1277	C	2.4
32	2a	1359	C	2.4
6	1G	35	GLU	2.4
21	1Z	166	SER	2.4
33	2b	210	SER	2.4
34	2c	18	TRP	2.4
37	2f	89	MET	2.4
25	13	2	PRO	2.4
36	2e	96	PRO	2.4
7	2H	52	VAL	2.4
7	2H	114	VAL	2.4
34	1c	172	ARG	2.4
34	2c	198	VAL	2.4
35	1d	141	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
38	2g	9	VAL	2.4
38	2g	135	VAL	2.4
42	2k	14	VAL	2.4
44	2m	15	VAL	2.4
49	2r	39	VAL	2.4
50	2s	3	ARG	2.4
20	2Y	89	PHE	2.4
22	20	69	PHE	2.4
32	2a	964	A	2.4
12	2Q	121	ALA	2.4
34	2c	129	ALA	2.4
36	1e	86	ALA	2.4
44	2m	28	ALA	2.4
48	2q	71	PHE	2.4
40	2i	50	LEU	2.3
48	1q	95	TYR	2.3
49	2r	58	LEU	2.3
33	2b	68	ILE	2.3
34	1c	39	ILE	2.3
35	1d	5	ILE	2.3
35	2d	204	ILE	2.3
39	2h	38	ILE	2.3
1	1A	2101	G	2.3
1	1A	2147	G	2.3
1	1A	2148	G	2.3
1	2A	614(B)	G	2.3
1	2A	864	G	2.3
1	2A	880	G	2.3
1	2A	892	G	2.3
32	2a	84	U	2.3
32	2a	1017	G	2.3
32	2a	1061	G	2.3
32	2a	1290	G	2.3
32	2a	1351	U	2.3
32	2a	1361	G	2.3
12	1Q	80	GLU	2.3
1	2A	1509	C	2.3
7	1H	13	LYS	2.3
32	1a	48	C	2.3
32	1a	1006	C	2.3
32	2a	1069	C	2.3
32	2a	1214	C	2.3

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Mol	Chain	Res	Type	RSRZ
32	2a	1320	C	2.3
33	1b	195	ASP	2.3
37	2f	55	ASP	2.3
40	2i	97	LYS	2.3
45	2n	9	LYS	2.3
47	1p	12	LYS	2.3
47	1p	47	ASP	2.3
47	1p	48	TRP	2.3
21	2Z	167	PRO	2.3
33	2b	131	PRO	2.3
8	2I	16	GLY	2.3
33	1b	89	GLY	2.3
34	1c	41	GLY	2.3
34	2c	158	GLY	2.3
35	2d	23	GLY	2.3
38	1g	130	GLY	2.3
18	1W	68	ARG	2.3
20	1Y	2	ARG	2.3
26	24	61	ARG	2.3
40	2i	38	GLN	2.3
8	1I	107	VAL	2.3
21	2Z	86	VAL	2.3
33	2b	229	VAL	2.3
43	1l	11	VAL	2.3
47	1p	79	VAL	2.3
6	1G	175	LEU	2.3
7	2H	165	ALA	2.3
9	1N	87	LEU	2.3
34	2c	50	ALA	2.3
34	2c	94	LEU	2.3
44	2m	118	ALA	2.3
47	2p	4	ILE	2.3
32	2a	653	A	2.3
32	2a	1044	A	2.3
32	2a	1201	A	2.3
39	2h	82	HIS	2.3
50	2s	63	THR	2.3
35	2d	161	ASN	2.3
42	2k	38	ASN	2.3
26	24	2	LYS	2.3
33	2b	50	GLU	2.3
35	2d	98	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
7	2H	56	SER	2.3
21	1Z	66	SER	2.3
32	2a	950	U	2.3
37	1f	70	ASP	2.3
1	1A	2141	G	2.3
1	1A	2151	G	2.3
1	2A	2751	G	2.3
32	2a	1009	G	2.3
1	2A	893	C	2.3
7	2H	3	ARG	2.3
8	2I	13	GLY	2.3
14	2S	97	ARG	2.3
17	1V	41	GLY	2.3
21	1Z	122	ARG	2.3
32	2a	307	C	2.3
32	2a	1043	C	2.3
34	2c	11	ARG	2.3
47	1p	42	ARG	2.3
51	2t	42	GLN	2.3
52	1u	9	ARG	2.3
7	2H	79	VAL	2.3
44	2m	60	VAL	2.3
47	2p	20	VAL	2.3
49	1r	86	VAL	2.3
4	1E	78	LEU	2.3
8	1I	75	LEU	2.3
21	2Z	125	LEU	2.3
33	2b	105	PHE	2.3
34	1c	34	LEU	2.3
34	2c	71	ALA	2.3
35	1d	194	LEU	2.3
41	2j	54	PHE	2.3
45	2n	6	LEU	2.3
35	1d	204	ILE	2.3
48	2q	90	ILE	2.3
18	2W	111	HIS	2.3
12	2Q	32	TYR	2.3
40	2i	4	TYR	2.3
24	12	11	GLU	2.3
36	1e	81	GLU	2.3
1	1A	2169	A	2.3
1	2A	863	A	2.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2171	A	2.3
32	1a	946	A	2.3
32	2a	250	A	2.3
21	2Z	166	SER	2.3
48	2q	2	PRO	2.3
50	1s	12	ASP	2.3
16	1U	36	ARG	2.3
33	2b	30	ARG	2.3
34	1c	190	ARG	2.3
35	2d	49	ARG	2.3
36	2e	14	ARG	2.3
44	2m	57	ARG	2.3
4	2E	115	GLY	2.3
17	2V	8	GLY	2.3
39	2h	78	GLN	2.3
46	2o	71	GLN	2.3
2	2B	1	U	2.3
32	2a	1012	U	2.3
32	2a	1313	U	2.3
54	1y	45	U	2.3
6	2G	31	VAL	2.3
12	2Q	52	VAL	2.3
14	2S	14	VAL	2.3
34	2c	151	VAL	2.3
44	2m	54	VAL	2.3
45	1n	25	VAL	2.3
47	1p	21	VAL	2.3
6	1G	178	PHE	2.3
35	2d	174	LEU	2.3
36	1e	84	PHE	2.3
44	2m	48	LEU	2.3
50	1s	5	LEU	2.3
1	1A	652(F)	G	2.3
6	2G	140	ILE	2.3
7	1H	4	ILE	2.3
33	1b	214	ILE	2.3
35	1d	195	ALA	2.3
39	2h	28	ALA	2.3
40	2i	52	ALA	2.3
1	1A	1532	C	2.3
1	1A	2166	G	2.3
1	2A	1041	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2321	G	2.3
2	2B	118	G	2.3
32	2a	470	C	2.3
32	2a	849	C	2.3
32	2a	951	G	2.3
32	2a	998	G	2.3
32	2a	1023	G	2.3
32	2a	1071	C	2.3
32	2a	1178	G	2.3
32	2a	1282	C	2.3
32	2a	1344	C	2.3
32	2a	1365	G	2.3
41	2j	74	ILE	2.3
43	2l	7	ILE	2.3
54	1w	2	C	2.3
47	1p	27	LYS	2.3
36	2e	133	TYR	2.3
40	2i	92	TYR	2.3
50	2s	61	TYR	2.3
7	2H	58	GLU	2.3
26	24	53	GLU	2.3
40	2i	110	GLU	2.3
43	2l	16	GLU	2.3
12	1Q	60	ARG	2.3
23	21	68	PRO	2.3
33	2b	234	PRO	2.3
34	2c	17	ASP	2.3
35	1d	73	ARG	2.3
35	2d	47	ARG	2.3
50	2s	76	PRO	2.3
11	1P	70	GLN	2.3
24	12	70	GLN	2.3
20	2Y	80	GLY	2.3
32	1a	228	A	2.3
32	1a	1256	A	2.3
32	1a	1299	A	2.3
32	2a	959	A	2.3
32	2a	1102	A	2.3
33	1b	45	GLN	2.3
40	2i	73	GLN	2.3
33	1b	18	GLY	2.3
33	2b	227	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
44	2m	6	GLY	2.3
50	2s	34	TRP	2.3
5	1F	154	VAL	2.3
7	1H	103	LEU	2.3
9	1N	140	VAL	2.3
10	2O	98	VAL	2.3
11	2P	135	LEU	2.3
14	1S	46	VAL	2.3
33	2b	164	VAL	2.3
40	2i	47	LEU	2.3
43	1l	60	LEU	2.3
44	2m	98	VAL	2.3
47	1p	74	LEU	2.3
50	2s	16	LEU	2.3
1	1A	1101	U	2.2
1	1A	2150	U	2.2
1	2A	157	U	2.2
7	2H	9	ILE	2.2
19	2X	91	ALA	2.2
32	2a	202	U	2.2
34	1c	60	ALA	2.2
34	2c	187	ALA	2.2
50	2s	31	ILE	2.2
51	1t	66	ALA	2.2
54	1w	45	U	2.2
54	2w	45	U	2.2
33	2b	16	HIS	2.2
51	2t	73	HIS	2.2
34	2c	199	LYS	2.2
40	1i	25	LYS	2.2
41	2j	22	LYS	2.2
19	1X	35	THR	2.2
21	1Z	69	THR	2.2
36	2e	120	THR	2.2
47	1p	44	THR	2.2
49	1r	47	THR	2.2
51	1t	71	THR	2.2
6	1G	45	GLU	2.2
25	13	60	GLU	2.2
33	1b	20	GLU	2.2
41	1j	83	GLU	2.2
14	2S	92	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
19	1X	69	TYR	2.2
34	1c	184	TYR	2.2
38	1g	151	TYR	2.2
47	1p	39	TYR	2.2
1	2A	1712	C	2.2
32	1a	984	C	2.2
32	1a	1132	C	2.2
32	2a	985	C	2.2
32	2a	1145	C	2.2
32	2a	1262	C	2.2
1	1A	2133	G	2.2
1	2A	1719	G	2.2
32	2a	189(I)	G	2.2
32	2a	988	G	2.2
32	2a	1138	G	2.2
32	2a	1273	G	2.2
32	2a	1310	G	2.2
54	1y	57	G	2.2
54	2w	22	G	2.2
23	11	26	ARG	2.2
26	24	13	ARG	2.2
35	1d	47	ARG	2.2
35	1d	139	ARG	2.2
39	2h	30	ARG	2.2
45	2n	45	ARG	2.2
45	2n	57	ARG	2.2
6	2G	49	ASP	2.2
26	24	66	SER	2.2
36	2e	23	GLY	2.2
36	2e	39	GLY	2.2
47	1p	37	GLY	2.2
4	1E	75	VAL	2.2
6	2G	7	LEU	2.2
8	2I	92	VAL	2.2
22	20	66	VAL	2.2
33	1b	174	VAL	2.2
39	2h	19	VAL	2.2
40	2i	44	VAL	2.2
47	2p	73	LEU	2.2
50	2s	41	VAL	2.2
1	1A	1762	A	2.2
1	2A	8	A	2.2

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Mol	Chain	Res	Type	RSRZ
3	2D	270	ILE	2.2
6	1G	86	MET	2.2
7	1H	165	ALA	2.2
20	2Y	94	LYS	2.2
21	2Z	54	HIS	2.2
23	1I	81	LYS	2.2
32	2a	1225	A	2.2
32	2a	1318	A	2.2
32	2a	1319	A	2.2
34	2c	128	PHE	2.2
35	2d	22	LYS	2.2
39	1h	45	ILE	2.2
40	1i	37	PHE	2.2
34	2c	60	ALA	2.2
47	2p	1	MET	2.2
47	2p	16	HIS	2.2
1	2A	1113	U	2.2
32	2a	90	U	2.2
32	2a	863	U	2.2
32	2a	961	U	2.2
32	2a	997	U	2.2
34	1c	95	THR	2.2
35	1d	150	GLU	2.2
45	2n	46	GLU	2.2
26	24	32	TYR	2.2
33	1b	31	TYR	2.2
14	2S	13	ARG	2.2
34	2c	126	ARG	2.2
42	1k	117	ASN	2.2
50	2s	53	ASN	2.2
52	2u	15	ARG	2.2
21	2Z	101	PRO	2.2
1	1A	2111	C	2.2
1	1A	2139	C	2.2
1	2A	652(V)	C	2.2
1	2A	889	C	2.2
1	2A	2138	C	2.2
32	1a	91	C	2.2
32	2a	92	C	2.2
32	2a	840	C	2.2
32	2a	1037	C	2.2
1	2A	271(M)	G	2.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2206	G	2.2
2	2B	24	G	2.2
14	2S	70	GLY	2.2
19	1X	94	GLY	2.2
21	1Z	92	SER	2.2
26	24	54	GLY	2.2
33	2b	38	GLY	2.2
35	1d	124	GLY	2.2
41	2j	17	ASP	2.2
43	2l	63	GLY	2.2
5	2F	24	LEU	2.2
21	2Z	163	LEU	2.2
35	2d	64	LEU	2.2
35	2d	186	LEU	2.2
36	1e	91	LEU	2.2
48	1q	84	LEU	2.2
54	2w	70	G	2.2
55	2x	46	G	2.2
6	2G	5	VAL	2.2
7	2H	138	LYS	2.2
9	2N	140	VAL	2.2
12	2Q	106	VAL	2.2
14	2S	93	LYS	2.2
35	1d	88	VAL	2.2
42	2k	114	VAL	2.2
44	2m	31	LYS	2.2
47	1p	3	LYS	2.2
3	1D	15	PHE	2.2
33	2b	58	ILE	2.2
38	1g	50	ILE	2.2
38	1g	62	PHE	2.2
39	2h	111	ILE	2.2
40	2i	81	ILE	2.2
46	1o	3	ILE	2.2
47	1p	1	MET	2.2
47	1p	36	ILE	2.2
47	2p	19	ILE	2.2
48	1q	71	PHE	2.2
51	2t	100	ILE	2.2
33	1b	186	ALA	2.2
36	1e	30	ALA	2.2
44	1m	123	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
51	1t	67	ALA	2.2
2	2B	120	A	2.2
6	2G	162	THR	2.2
34	1c	15	THR	2.2
44	2m	69	GLU	2.2
32	1a	1110	A	2.2
32	2a	1256	A	2.2
32	2a	1285	A	2.2
53	2v	23	A	2.2
21	2Z	131	ARG	2.2
26	24	58	ARG	2.2
5	2F	7	TYR	2.2
6	2G	25	TYR	2.2
21	2Z	99	TYR	2.2
32	2a	1281	U	2.2
34	1c	164	ARG	2.2
38	2g	76	ARG	2.2
51	2t	80	ARG	2.2
28	26	20	ASN	2.2
31	29	29	ASN	2.2
33	2b	148	TYR	2.2
35	1d	138	TYR	2.2
37	2f	100	ASN	2.2
38	2g	148	ASN	2.2
52	1u	18	TYR	2.2
8	2I	132	PRO	2.2
33	2b	167	PRO	2.2
33	2b	183	PRO	2.2
39	1h	101	PRO	2.2
46	1o	19	PRO	2.2
5	1F	125	LEU	2.2
9	2N	84	LYS	2.2
11	1P	124	LYS	2.2
21	2Z	106	GLY	2.2
22	20	76	GLY	2.2
26	14	51	ASP	2.2
34	1c	80	GLY	2.2
34	1c	185	GLY	2.2
34	2c	196	LEU	2.2
35	1d	11	LEU	2.2
35	1d	152	SER	2.2
37	2f	75	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
42	1k	123	LYS	2.2
46	1o	23	GLY	2.2
46	1o	61	GLY	2.2
47	1p	30	GLY	2.2
48	1q	79	SER	2.2
48	2q	22	LEU	2.2
51	2t	24	LEU	2.2
6	1G	160	VAL	2.2
14	2S	69	VAL	2.2
15	1T	89	VAL	2.2
50	2s	11	VAL	2.2
1	1A	645	C	2.2
1	1A	894	C	2.2
1	1A	1104	C	2.2
1	1A	2175	C	2.2
1	1A	2178	C	2.2
14	2S	34	HIS	2.2
14	2S	87	PHE	2.2
32	1a	92	C	2.2
32	1a	1066	C	2.2
32	2a	174	C	2.2
33	1b	223	ILE	2.2
38	1g	153	HIS	2.2
44	2m	84	ILE	2.2
3	1D	2	ALA	2.2
12	2Q	49	ALA	2.2
33	1b	13	ALA	2.2
1	1A	545	G	2.2
1	1A	2121	G	2.2
1	2A	906	G	2.2
1	2A	916	G	2.2
1	2A	2125	G	2.2
1	2A	2160	G	2.2
1	2A	2805	G	2.2
2	2B	18	G	2.2
24	22	66	GLU	2.2
32	1a	69	G	2.2
32	1a	380	G	2.2
32	2a	189(J)	G	2.2
32	2a	588	G	2.2
32	2a	1077	G	2.2
32	2a	1156	G	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1271	G	2.2
32	2a	1312	G	2.2
34	2c	206	GLU	2.2
36	2e	81	GLU	2.2
54	2y	52	G	2.2
33	2b	47	THR	2.2
36	1e	98	THR	2.2
3	1D	262	ARG	2.2
6	1G	113	ARG	2.2
6	2G	115	ARG	2.2
7	1H	95	ARG	2.2
15	2T	115	ARG	2.2
33	1b	36	ARG	2.2
33	2b	130	ARG	2.2
38	1g	76	ARG	2.2
39	2h	12	ARG	2.2
40	1i	121	ARG	2.2
1	1A	900	A	2.2
26	14	67	TYR	2.2
32	1a	532	A	2.2
32	2a	655	A	2.2
32	2a	978	A	2.2
32	2a	1014	A	2.2
32	2a	1105	A	2.2
32	2a	1261	A	2.2
38	1g	109	ASN	2.2
38	2g	14	PRO	2.2
48	1q	88	TYR	2.2
52	2u	23	PRO	2.2
53	1v	12	A	2.2
54	2y	21	A	2.2
1	1A	1175	U	2.2
1	1A	2118	U	2.2
1	1A	2172	U	2.2
1	2A	2130	U	2.2
2	1B	1	U	2.2
29	17	48	LYS	2.2
32	2a	1219	U	2.2
46	1o	5	LYS	2.2
7	2H	103	LEU	2.2
14	2S	45	GLY	2.2
19	2X	86	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	14	GLY	2.2
34	1c	175	LEU	2.2
38	1g	16	LEU	2.2
40	1i	102	LEU	2.2
44	2m	96	LEU	2.2
33	2b	166	ASP	2.2
5	1F	9	ILE	2.2
6	1G	149	VAL	2.2
8	2I	37	VAL	2.2
21	1Z	105	VAL	2.2
21	2Z	153	SER	2.2
26	24	10	VAL	2.2
33	1b	165	VAL	2.2
34	1c	49	SER	2.2
26	24	40	HIS	2.2
35	1d	170	VAL	2.2
35	2d	5	ILE	2.2
35	2d	146	ILE	2.2
38	2g	42	ILE	2.2
21	1Z	136	PHE	2.2
21	2Z	152	ALA	2.1
34	2c	180	ALA	2.1
35	1d	48	ALA	2.1
38	1g	156	TRP	2.1
42	2k	42	TRP	2.1
44	1m	30	ALA	2.1
4	1E	73	GLU	2.1
1	2A	914	C	2.1
6	1G	51	ARG	2.1
6	1G	83	ARG	2.1
8	1I	108	THR	2.1
32	1a	1038	C	2.1
32	2a	1209	C	2.1
32	2a	1244	C	2.1
32	2a	1326	C	2.1
34	1c	127	ARG	2.1
35	1d	153	ARG	2.1
35	2d	107	ARG	2.1
44	2m	109	THR	2.1
49	2r	42	ARG	2.1
1	1A	652(E)	G	2.1
1	1A	892	G	2.1

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Mol	Chain	Res	Type	RSRZ
1	2A	1042	G	2.1
1	2A	1533	G	2.1
1	2A	2141	G	2.1
2	2B	23	G	2.1
32	1a	1323	G	2.1
32	2a	587	G	2.1
32	2a	954	G	2.1
32	2a	1022	G	2.1
32	2a	1311	G	2.1
13	2R	5	LYS	2.1
14	2S	38	GLN	2.1
37	2f	54	LYS	2.1
52	2u	3	LYS	2.1
6	2G	111	LEU	2.1
6	2G	175	LEU	2.1
33	2b	145	LEU	2.1
34	1c	91	LEU	2.1
1	1A	890	A	2.1
1	1A	1085	A	2.1
1	1A	1103	A	2.1
2	2B	25	A	2.1
5	1F	131	GLY	2.1
7	2H	28	GLY	2.1
14	2S	96	GLY	2.1
32	1a	134	A	2.1
32	2a	1191	A	2.1
41	1j	10	GLY	2.1
43	2l	29	GLY	2.1
46	2o	86	GLY	2.1
1	1A	2144	U	2.1
1	2A	2897	U	2.1
6	2G	147	ASP	2.1
7	2H	50	VAL	2.1
8	1I	145	VAL	2.1
11	2P	95	VAL	2.1
21	1Z	137	ILE	2.1
21	2Z	124	ILE	2.1
32	1a	1040	U	2.1
32	2a	723	U	2.1
32	2a	1159	U	2.1
32	2a	1315	U	2.1
21	2Z	142	SER	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	80	ILE	2.1
33	2b	40	HIS	2.1
34	2c	138	VAL	2.1
39	1h	80	ILE	2.1
48	2q	73	VAL	2.1
54	2y	45	U	2.1
22	20	45	PHE	2.1
6	1G	169	ALA	2.1
41	2j	26	ALA	2.1
8	1I	117	GLU	2.1
33	1b	231	GLU	2.1
35	1d	34	GLU	2.1
15	1T	96	ARG	2.1
26	14	68	ARG	2.1
33	1b	30	ARG	2.1
35	1d	35	ARG	2.1
47	1p	75	ARG	2.1
47	2p	5	ARG	2.1
8	2I	86	THR	2.1
9	1N	73	THR	2.1
4	2E	74	PRO	2.1
7	2H	36	PRO	2.1
7	2H	153	LYS	2.1
10	2O	66	LYS	2.1
17	2V	85	LYS	2.1
19	2X	33	LYS	2.1
21	1Z	167	PRO	2.1
41	2j	80	LYS	2.1
45	2n	58	LYS	2.1
47	2p	35	LYS	2.1
48	1q	87	LYS	2.1
1	2A	652(T)	C	2.1
16	1U	104	GLN	2.1
32	1a	174	C	2.1
32	1a	221	C	2.1
32	2a	612	C	2.1
32	2a	984	C	2.1
32	2a	1059	C	2.1
32	2a	1103	C	2.1
32	2a	1109	C	2.1
32	2a	1259	C	2.1
10	1O	112	MET	2.1

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Mol	Chain	Res	Type	RSRZ
6	1G	12	TYR	2.1
12	2Q	37	LEU	2.1
19	2X	66	LEU	2.1
20	2Y	92	ASN	2.1
38	2g	12	LEU	2.1
40	2i	56	LEU	2.1
41	2j	69	ASN	2.1
40	2i	88	TYR	2.1
44	2m	70	LEU	2.1
48	2q	6	LEU	2.1
48	2q	42	TYR	2.1
8	2I	84	GLY	2.1
34	2c	31	HIS	2.1
1	1A	2154	G	2.1
1	1A	2162	G	2.1
7	2H	57	ASP	2.1
8	2I	144	VAL	2.1
32	1a	1523	G	2.1
32	2a	9	G	2.1
32	2a	1099	G	2.1
32	2a	1171	G	2.1
34	1c	55	VAL	2.1
34	2c	141	VAL	2.1
36	2e	5	ASP	2.1
36	2e	90	VAL	2.1
40	2i	17	VAL	2.1
47	1p	51	VAL	2.1
47	2p	53	VAL	2.1
52	2u	13	ILE	2.1
54	1w	10	G	2.1
7	2H	38	SER	2.1
7	2H	123	PHE	2.1
1	2A	278	A	2.1
1	2A	405	U	2.1
1	2A	887	A	2.1
1	2A	1026	U	2.1
1	2A	2118	U	2.1
32	1a	65	U	2.1
32	2a	1080	A	2.1
32	2a	1236	A	2.1
44	1m	28	ALA	2.1
44	2m	18	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
54	1y	21	A	2.1
7	2H	51	ARG	2.1
11	1P	90	ARG	2.1
12	2Q	59	ARG	2.1
15	2T	125	ARG	2.1
33	2b	144	ARG	2.1
34	2c	40	ARG	2.1
39	2h	69	ARG	2.1
33	1b	168	THR	2.1
35	2d	89	THR	2.1
7	1H	175	LYS	2.1
26	24	8	LYS	2.1
7	2H	29	PRO	2.1
33	1b	234	PRO	2.1
38	2g	112	PRO	2.1
35	2d	201	GLN	2.1
36	2e	136	MET	2.1
40	1i	124	GLN	2.1
6	2G	34	LEU	2.1
6	2G	172	LEU	2.1
7	1H	7	LEU	2.1
33	2b	10	LEU	2.1
33	2b	118	LEU	2.1
39	1h	63	LEU	2.1
41	1j	85	LEU	2.1
51	1t	75	ASN	2.1
21	2Z	29	TYR	2.1
26	24	19	GLY	2.1
33	1b	227	GLY	2.1
39	1h	62	TYR	2.1
41	1j	36	GLY	2.1
44	2m	92	HIS	2.1
1	1A	2129	C	2.1
1	2A	645	C	2.1
1	2A	2145	C	2.1
1	2A	2161	C	2.1
1	2A	2803	C	2.1
7	2H	43	VAL	2.1
11	1P	71	VAL	2.1
32	1a	307	C	2.1
32	2a	1054	C	2.1
32	2a	1097	C	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1384	C	2.1
36	2e	41	VAL	2.1
36	2e	82	VAL	2.1
48	1q	23	VAL	2.1
54	2y	62	C	2.1
24	12	37	PHE	2.1
42	2k	125	PHE	2.1
6	2G	76	SER	2.1
12	1Q	6	ARG	2.1
15	1T	39	ARG	2.1
22	10	82	ARG	2.1
33	2b	13	ALA	2.1
33	2b	186	ALA	2.1
34	2c	24	ALA	2.1
34	2c	53	ALA	2.1
34	2c	90	GLU	2.1
35	1d	164	ALA	2.1
36	1e	126	ARG	2.1
38	1g	155	ARG	2.1
40	1i	42	ARG	2.1
40	2i	84	ALA	2.1
41	2j	79	ARG	2.1
50	2s	81	ARG	2.1
1	1A	1047	G	2.1
1	1A	1117	G	2.1
1	1A	2127	G	2.1
1	1A	2182	G	2.1
32	2a	945	G	2.1
32	2a	1072	G	2.1
32	2a	1081	G	2.1
32	2a	1177	G	2.1
32	2a	1216	G	2.1
32	2a	1253	G	2.1
33	2b	97	TRP	2.1
1	1A	272(A)	U	2.1
1	1A	1083	U	2.1
1	2A	652(A)	A	2.1
1	2A	1963	U	2.1
2	1B	120	A	2.1
32	2a	65	U	2.1
32	2a	1146	A	2.1
32	2a	1292	U	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	132	LYS	2.1
34	2c	191	THR	2.1
35	2d	136	PRO	2.1
39	2h	101	PRO	2.1
33	2b	101	MET	2.1
33	1b	110	GLN	2.1
28	26	34	LEU	2.1
33	1b	180	LEU	2.1
35	2d	21	LEU	2.1
36	2e	43	LEU	2.1
49	1r	76	LEU	2.1
44	2m	40	ASN	2.1
22	20	80	HIS	2.1
35	2d	123	HIS	2.1
36	2e	29	GLY	2.1
42	2k	76	GLY	2.1
21	1Z	99	TYR	2.1
26	24	15	ILE	2.1
34	1c	48	TYR	2.1
35	2d	126	ILE	2.1
4	2E	72	VAL	2.1
12	1Q	55	VAL	2.1
26	24	33	VAL	2.1
29	17	46	VAL	2.1
6	1G	126	ASP	2.0
40	2i	59	PHE	2.1
15	2T	112	ARG	2.0
19	1X	68	ARG	2.0
28	26	19	ARG	2.0
35	2d	118	ARG	2.0
40	2i	83	ARG	2.0
41	1j	25	GLU	2.0
48	2q	58	GLU	2.0
50	1s	81	ARG	2.0
5	1F	22	ALA	2.0
8	2I	55	ALA	2.0
34	2c	65	ALA	2.0
34	2c	92	ALA	2.0
40	2i	45	ALA	2.0
1	1A	652(T)	C	2.0
1	1A	1052	C	2.0
1	2A	279	C	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2137	C	2.0
32	1a	136	C	2.0
32	1a	1007	C	2.0
32	1a	1363	C	2.0
32	1a	1369	C	2.0
32	2a	1284	C	2.0
32	2a	1382	C	2.0
41	1j	99	LYS	2.0
54	2y	68	C	2.0
7	1H	70	THR	2.0
41	2j	81	THR	2.0
47	1p	45	THR	2.0
33	1b	125	PRO	2.0
38	2g	89	MET	2.0
39	2h	27	PRO	2.0
42	1k	35	PRO	2.0
1	1A	405	U	2.0
4	2E	195	LEU	2.0
21	1Z	70	LEU	2.0
23	21	46	LEU	2.0
32	1a	723	U	2.0
32	2a	1078	U	2.0
33	1b	51	LEU	2.0
34	1c	111	LEU	2.0
34	2c	87	LEU	2.0
35	2d	202	LEU	2.0
38	2g	124	LEU	2.0
46	2o	31	LEU	2.0
48	2q	31	LEU	2.0
54	1y	33	U	2.0
1	1A	11	G	2.0
1	1A	1099	G	2.0
1	1A	1509(A)	A	2.0
1	1A	2152	G	2.0
1	2A	881	G	2.0
2	2B	21	G	2.0
32	1a	914	A	2.0
32	1a	1461	G	2.0
32	2a	629	G	2.0
32	2a	1101	A	2.0
51	1t	73	HIS	2.0
6	2G	77	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
8	1I	79	ILE	2.0
14	2S	60	GLY	2.0
16	2U	43	GLY	2.0
33	2b	42	ILE	2.0
36	1e	80	ILE	2.0
38	2g	27	ILE	2.0
51	2t	102	GLY	2.0
8	2I	19	VAL	2.0
20	2Y	45	VAL	2.0
33	1b	136	VAL	2.0
34	2c	70	VAL	2.0
35	1d	104	VAL	2.0
35	2d	198	VAL	2.0
39	1h	20	TYR	2.0
47	1p	62	VAL	2.0
25	13	55	ARG	2.0
7	2H	159	GLU	2.0
11	1P	74	GLU	2.0
26	24	42	PHE	2.0
33	1b	137	ARG	2.0
34	2c	127	ARG	2.0
44	2m	55	ARG	2.0
52	1u	10	ARG	2.0
20	1Y	11	ASP	2.0
33	2b	193	ASP	2.0
33	2b	231	GLU	2.0
34	2c	36	ASP	2.0
20	1Y	47	LYS	2.0
39	2h	64	LYS	2.0
51	2t	11	SER	2.0
21	2Z	130	PRO	2.0
33	2b	26	PRO	2.0
33	2b	91	PRO	2.0
40	2i	21	PRO	2.0
52	1u	8	THR	2.0
2	2B	2	C	2.0
6	1G	3	LEU	2.0
11	2P	148	LEU	2.0
17	1V	35	LEU	2.0
32	1a	848	C	2.0
32	2a	848	C	2.0
32	2a	1189	C	2.0

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Mol	Chain	Res	Type	RSRZ
37	2f	94	GLN	2.0
41	2j	21	GLN	2.0
45	1n	6	LEU	2.0
49	1r	58	LEU	2.0
50	1s	15	LEU	2.0
54	2w	13	C	2.0
38	2g	153	HIS	2.0
32	2a	955	U	2.0
32	2a	1136	U	2.0
32	2a	1247	U	2.0
32	2a	1341	U	2.0
6	1G	140	ILE	2.0
31	29	21	GLY	2.0
33	1b	228	GLY	2.0
33	2b	127	ILE	2.0
39	1h	111	ILE	2.0
40	2i	115	GLY	2.0
41	2j	31	GLY	2.0
47	2p	14	ASN	2.0
51	1t	55	ILE	2.0
1	2A	2170	A	2.0
2	2B	58	A	2.0
21	2Z	80	ARG	2.0
23	11	51	VAL	2.0
32	1a	1041	A	2.0
32	2a	1268	A	2.0
38	2g	75	VAL	2.0
38	2g	118	VAL	2.0
44	2m	3	ARG	2.0
47	1p	20	VAL	2.0
50	2s	67	VAL	2.0
35	2d	207	TYR	2.0
47	1p	17	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	PSU	2y	55	20/21	0.40	0.22	83,99,115,129	0
54	PSU	1y	55	20/21	0.49	0.18	82,98,110,129	0
54	5MU	2y	54	21/22	0.50	0.20	87,93,116,137	0
54	7MG	2y	46	24/25	0.66	0.17	82,95,104,125	0
54	MIA	2y	37	22/30	0.66	0.16	68,80,89,112	0
54	5MU	1y	54	21/22	0.68	0.15	80,93,103,130	0
54	PSU	2y	32	20/21	0.68	0.16	79,88,94,98	0
54	7MG	1y	46	24/25	0.69	0.14	81,93,105,133	0
54	7MG	2w	46	24/25	0.70	0.15	69,93,102,115	0
54	4SU	2y	8	20/21	0.74	0.14	87,95,107,114	0
54	4SU	1y	8	20/21	0.77	0.12	84,90,107,112	0
54	PSU	2y	39	20/21	0.78	0.16	75,87,93,93	0
54	MIA	1y	37	22/30	0.79	0.13	74,81,87,100	0
54	5MU	2w	54	21/22	0.80	0.15	60,71,83,85	0
54	7MG	1w	46	24/25	0.80	0.13	71,81,95,125	0
32	2MG	2a	1207	24/25	0.82	0.16	72,87,94,98	0
54	PSU	2w	55	20/21	0.82	0.13	57,80,90,92	0
54	4SU	2w	8	20/21	0.82	0.14	64,91,96,98	0
32	M2G	2a	966	25/26	0.85	0.18	45,64,88,101	0
54	PSU	2w	32	20/21	0.85	0.17	63,79,90,93	0
55	4SU	2x	8	20/21	0.85	0.12	66,80,86,89	0
54	PSU	1y	32	20/21	0.86	0.13	75,86,94,98	0
54	PSU	1y	39	20/21	0.87	0.14	73,85,90,93	0
32	5MC	2a	967	21/22	0.88	0.15	60,75,80,91	0
54	MIA	2w	37	22/30	0.88	0.16	49,73,85,86	0
43	0TD	2l	92	10/11	0.88	0.12	50,61,67,77	0
54	4SU	1w	8	20/21	0.88	0.11	70,77,91,94	0
55	5MU	2x	54	21/22	0.89	0.12	69,81,87,96	0
55	PSU	2x	55	20/21	0.90	0.11	63,78,85,86	0
1	5MU	2A	1915	21/22	0.91	0.11	56,63,68,75	0
32	PSU	2a	516	20/21	0.91	0.11	56,64,70,74	0
32	7MG	2a	527	24/25	0.91	0.12	53,64,78,82	0
32	5MC	2a	1400	21/22	0.91	0.14	61,72,78,82	0
32	4OC	2a	1402	22/23	0.91	0.12	49,66,75,76	0
54	PSU	1w	55	20/21	0.91	0.10	55,77,90,90	0
1	4OC	2A	1920	21/23	0.92	0.10	45,51,56,64	0
43	0TD	1l	92	10/11	0.92	0.15	44,58,62,69	0
32	5MC	2a	1404	21/22	0.92	0.13	52,59,71,74	0
32	MA6	2a	1518	24/25	0.92	0.14	53,67,73,75	0
32	MA6	2a	1519	24/25	0.92	0.14	45,65,75,82	0
54	PSU	2w	39	20/21	0.92	0.13	63,72,81,83	0
1	PSU	2A	1917	20/21	0.92	0.09	47,56,61,63	0
32	5MC	2a	1407	21/22	0.93	0.11	36,55,59,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	PSU	2A	1911	20/21	0.93	0.09	40,51,56,58	0
54	PSU	1w	32	20/21	0.93	0.12	59,74,84,92	0
55	5MC	2x	32	21/22	0.93	0.13	66,71,79,82	0
55	5MU	1x	54	21/22	0.93	0.10	52,64,69,72	0
1	5MC	2A	1962	21/22	0.93	0.10	34,40,48,53	0
55	PSU	1x	55	20/21	0.93	0.09	51,62,74,75	0
54	5MU	1w	54	21/22	0.93	0.09	51,64,74,75	0
32	UR3	2a	1498	21/22	0.94	0.12	41,54,63,70	0
1	5MU	1A	1915	21/22	0.94	0.11	50,58,65,70	0
1	5MC	2A	1942	21/22	0.94	0.11	44,47,58,74	0
54	PSU	1w	39	20/21	0.94	0.11	58,68,76,78	0
32	2MG	1a	1207	24/25	0.94	0.10	48,66,70,78	0
55	4SU	1x	8	20/21	0.95	0.09	43,54,68,74	0
32	PSU	1a	516	20/21	0.95	0.11	53,61,67,70	0
55	5MC	1x	32	21/22	0.95	0.11	35,48,56,75	0
1	5MU	2A	1939	21/22	0.95	0.10	26,34,39,41	0
32	4OC	1a	1402	22/23	0.96	0.10	33,44,54,59	0
32	5MC	1a	1407	21/22	0.96	0.10	27,38,45,47	0
1	OMG	2A	2251	24/25	0.96	0.08	27,33,39,39	0
1	PSU	2A	2605	20/21	0.96	0.08	25,32,38,39	0
1	5MC	1A	1942	21/22	0.96	0.10	38,47,55,63	0
54	MIA	1w	37	29/30	0.96	0.11	44,56,67,77	0
1	PSU	1A	1917	20/21	0.96	0.12	47,53,60,62	0
32	7MG	1a	527	24/25	0.96	0.08	33,43,56,62	0
32	M2G	1a	966	25/26	0.96	0.10	37,51,54,61	0
32	5MC	1a	967	21/22	0.96	0.10	42,51,61,68	0
1	4OC	1A	1920	21/23	0.96	0.10	38,47,52,61	0
32	5MC	1a	1400	21/22	0.97	0.09	36,44,55,65	0
1	2MU	1A	2552	21/23	0.97	0.07	25,34,40,43	0
1	2MA	2A	2503	23/24	0.97	0.06	21,25,31,36	0
1	2MU	2A	2552	21/23	0.97	0.07	27,37,41,43	0
32	5MC	1a	1404	21/22	0.97	0.09	23,37,50,52	0
1	5MU	1A	1939	21/22	0.97	0.08	21,29,37,41	0
32	UR3	1a	1498	21/22	0.97	0.09	30,40,45,52	0
32	MA6	1a	1518	24/25	0.97	0.09	32,41,49,57	0
32	MA6	1a	1519	24/25	0.97	0.10	27,43,51,60	0
1	PSU	1A	1911	20/21	0.98	0.07	41,47,54,55	0
1	PSU	1A	2605	20/21	0.98	0.07	21,29,35,36	0
1	5MC	1A	1962	21/22	0.98	0.08	29,38,43,46	0
1	OMG	1A	2251	24/25	0.98	0.07	19,30,34,37	0
1	2MA	1A	2503	23/24	0.98	0.07	17,22,30,33	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1793	1/1	0.46	0.22	86,86,86,86	0
56	MG	2A	3547	1/1	0.47	0.21	70,70,70,70	0
56	MG	2a	1745	1/1	0.48	0.40	72,72,72,72	0
56	MG	2B	3021	1/1	0.52	0.21	76,76,76,76	0
56	MG	2a	1623	1/1	0.53	0.28	80,80,80,80	0
56	MG	1B	218	1/1	0.55	0.22	64,64,64,64	0
56	MG	2a	1751	1/1	0.56	0.34	70,70,70,70	0
56	MG	2A	3285	1/1	0.56	0.29	68,68,68,68	0
56	MG	2a	1760	1/1	0.59	0.41	79,79,79,79	0
56	MG	2A	3541	1/1	0.61	0.26	67,67,67,67	0
56	MG	2a	1705	1/1	0.61	0.34	69,69,69,69	0
56	MG	2A	3544	1/1	0.62	0.24	75,75,75,75	0
56	MG	15	104	1/1	0.62	0.26	55,55,55,55	0
56	MG	1a	1754	1/1	0.62	0.27	84,84,84,84	0
56	MG	2a	1797	1/1	0.62	0.14	89,89,89,89	0
56	MG	1a	1716	1/1	0.63	0.25	81,81,81,81	0
56	MG	1A	3487	1/1	0.63	0.18	48,48,48,48	0
56	MG	2a	1691	1/1	0.63	0.43	80,80,80,80	0
56	MG	1A	3242	1/1	0.64	0.36	83,83,83,83	0
56	MG	2R	201	1/1	0.65	0.22	58,58,58,58	0
56	MG	2A	3590	1/1	0.65	0.23	65,65,65,65	0
56	MG	2A	3568	1/1	0.65	0.27	74,74,74,74	0
56	MG	2A	3321	1/1	0.66	0.13	59,59,59,59	0
56	MG	2A	3479	1/1	0.67	0.20	53,53,53,53	0
56	MG	2A	3104	1/1	0.67	0.26	72,72,72,72	0
56	MG	2a	1782	1/1	0.67	0.21	90,90,90,90	0
56	MG	1A	3840	1/1	0.67	0.21	65,65,65,65	0
56	MG	1A	3845	1/1	0.67	0.38	68,68,68,68	0
56	MG	2Z	8001	1/1	0.68	0.16	90,90,90,90	0
56	MG	2A	3116	1/1	0.68	0.21	67,67,67,67	0
56	MG	2A	3641	1/1	0.68	0.31	57,57,57,57	0
56	MG	2A	3556	1/1	0.68	0.21	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1794	1/1	0.68	0.23	94,94,94,94	0
56	MG	1y	3006	1/1	0.68	0.15	82,82,82,82	0
56	MG	2A	3505	1/1	0.69	0.20	72,72,72,72	0
56	MG	1a	1745	1/1	0.69	0.24	81,81,81,81	0
56	MG	1A	3741	1/1	0.69	0.17	63,63,63,63	0
56	MG	2a	1684	1/1	0.70	0.20	76,76,76,76	0
56	MG	2a	1800	1/1	0.70	0.28	82,82,82,82	0
56	MG	2f	3002	1/1	0.70	0.24	85,85,85,85	0
56	MG	2j	8002	1/1	0.70	0.11	92,92,92,92	0
56	MG	2a	1710	1/1	0.71	0.33	65,65,65,65	0
56	MG	2A	3236	1/1	0.71	0.23	65,65,65,65	0
56	MG	2A	3537	1/1	0.71	0.22	67,67,67,67	0
56	MG	2a	1752	1/1	0.71	0.22	78,78,78,78	0
56	MG	1A	3934	1/1	0.71	0.19	84,84,84,84	0
56	MG	2a	1621	1/1	0.71	0.28	80,80,80,80	0
56	MG	2a	1682	1/1	0.72	0.26	64,64,64,64	0
56	MG	2a	1768	1/1	0.72	0.22	79,79,79,79	0
56	MG	1a	1804	1/1	0.72	0.34	65,65,65,65	0
56	MG	1a	1820	1/1	0.72	0.22	72,72,72,72	0
56	MG	1B	222	1/1	0.72	0.21	78,78,78,78	0
56	MG	1A	3516	1/1	0.72	0.12	65,65,65,65	0
56	MG	2A	3481	1/1	0.72	0.20	62,62,62,62	0
56	MG	1a	1615	1/1	0.72	0.36	60,60,60,60	0
56	MG	2A	3574	1/1	0.72	0.18	62,62,62,62	0
56	MG	2a	1786	1/1	0.73	0.27	64,64,64,64	0
56	MG	2A	3411	1/1	0.73	0.21	57,57,57,57	0
56	MG	1A	3498	1/1	0.73	0.34	58,58,58,58	0
56	MG	1A	3799	1/1	0.73	0.16	64,64,64,64	0
56	MG	2a	1729	1/1	0.73	0.18	75,75,75,75	0
56	MG	2a	1769	1/1	0.73	0.16	65,65,65,65	0
56	MG	2A	3608	1/1	0.73	0.20	64,64,64,64	0
56	MG	1A	3466	1/1	0.74	0.18	64,64,64,64	0
56	MG	2A	3526	1/1	0.74	0.19	60,60,60,60	0
56	MG	2A	3597	1/1	0.74	0.24	65,65,65,65	0
56	MG	2A	3533	1/1	0.74	0.17	73,73,73,73	0
56	MG	1A	3686	1/1	0.74	0.24	62,62,62,62	0
56	MG	1y	3007	1/1	0.74	0.21	79,79,79,79	0
56	MG	2A	3086	1/1	0.74	0.12	51,51,51,51	0
56	MG	2A	3447	1/1	0.74	0.19	68,68,68,68	0
56	MG	1A	3720	1/1	0.74	0.18	66,66,66,66	0
56	MG	2j	8001	1/1	0.74	0.13	76,76,76,76	0
56	MG	1a	1704	1/1	0.74	0.23	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3413	1/1	0.75	0.25	56,56,56,56	0
56	MG	2A	3614	1/1	0.75	0.24	47,47,47,47	0
56	MG	2A	3625	1/1	0.75	0.16	62,62,62,62	0
56	MG	2A	3529	1/1	0.75	0.19	58,58,58,58	0
56	MG	2A	3681	1/1	0.75	0.15	50,50,50,50	0
56	MG	2a	1716	1/1	0.75	0.31	69,69,69,69	0
56	MG	2A	3257	1/1	0.75	0.19	61,61,61,61	0
56	MG	1a	1708	1/1	0.75	0.38	60,60,60,60	0
56	MG	2A	3219	1/1	0.75	0.37	69,69,69,69	0
56	MG	2A	3596	1/1	0.75	0.26	76,76,76,76	0
56	MG	1A	3216	1/1	0.75	0.44	65,65,65,65	0
56	MG	2A	3575	1/1	0.76	0.13	62,62,62,62	0
56	MG	2B	3011	1/1	0.76	0.41	72,72,72,72	0
56	MG	1A	3575	1/1	0.76	0.16	31,31,31,31	0
56	MG	2a	1788	1/1	0.76	0.15	81,81,81,81	0
56	MG	1A	3635	1/1	0.76	0.28	66,66,66,66	0
56	MG	1A	3652	1/1	0.76	0.30	65,65,65,65	0
56	MG	1A	3827	1/1	0.76	0.19	68,68,68,68	0
56	MG	2A	3403	1/1	0.76	0.21	25,25,25,25	0
56	MG	1A	3550	1/1	0.76	0.20	49,49,49,49	0
56	MG	1A	3699	1/1	0.76	0.15	65,65,65,65	0
56	MG	2a	1686	1/1	0.76	0.20	82,82,82,82	0
56	MG	1A	3855	1/1	0.77	0.30	69,69,69,69	0
56	MG	2a	1662	1/1	0.77	0.21	67,67,67,67	0
56	MG	2A	3067	1/1	0.77	0.20	51,51,51,51	0
56	MG	1A	3640	1/1	0.77	0.34	82,82,82,82	0
56	MG	2A	3096	1/1	0.77	0.19	57,57,57,57	0
56	MG	1a	1604	1/1	0.77	0.24	64,64,64,64	0
56	MG	2a	1693	1/1	0.77	0.27	69,69,69,69	0
56	MG	1a	1828	1/1	0.77	0.31	83,83,83,83	0
56	MG	1A	3235	1/1	0.77	0.20	64,64,64,64	0
56	MG	2A	3423	1/1	0.78	0.17	36,36,36,36	0
56	MG	1a	1750	1/1	0.78	0.28	69,69,69,69	0
56	MG	2a	1709	1/1	0.78	0.15	92,92,92,92	0
56	MG	1A	3662	1/1	0.78	0.20	45,45,45,45	0
56	MG	2a	1711	1/1	0.78	0.28	69,69,69,69	0
56	MG	1a	1787	1/1	0.78	0.29	71,71,71,71	0
56	MG	2A	3497	1/1	0.78	0.18	64,64,64,64	0
56	MG	2A	3126	1/1	0.78	0.14	59,59,59,59	0
56	MG	2A	3163	1/1	0.78	0.17	59,59,59,59	0
56	MG	1a	1789	1/1	0.78	0.19	75,75,75,75	0
56	MG	2B	3010	1/1	0.78	0.19	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3756	1/1	0.78	0.27	67,67,67,67	0
56	MG	1A	3520	1/1	0.78	0.18	56,56,56,56	0
56	MG	2A	3538	1/1	0.78	0.18	82,82,82,82	0
56	MG	1A	3936	1/1	0.78	0.22	61,61,61,61	0
56	MG	2A	3294	1/1	0.78	0.15	60,60,60,60	0
56	MG	1A	3514	1/1	0.78	0.17	66,66,66,66	0
56	MG	2A	3396	1/1	0.78	0.16	50,50,50,50	0
56	MG	2a	1668	1/1	0.78	0.09	66,66,66,66	0
56	MG	2A	3557	1/1	0.78	0.15	55,55,55,55	0
56	MG	1A	3440	1/1	0.78	0.17	61,61,61,61	0
56	MG	1a	1726	1/1	0.78	0.14	87,87,87,87	0
56	MG	10	105	1/1	0.78	0.17	63,63,63,63	0
56	MG	2a	1731	1/1	0.79	0.39	87,87,87,87	0
56	MG	2a	1743	1/1	0.79	0.31	92,92,92,92	0
56	MG	2A	3508	1/1	0.79	0.13	44,44,44,44	0
56	MG	1A	3781	1/1	0.79	0.13	69,69,69,69	0
56	MG	2a	1657	1/1	0.79	0.27	76,76,76,76	0
56	MG	1a	1617	1/1	0.79	0.32	71,71,71,71	0
56	MG	2A	3531	1/1	0.79	0.18	66,66,66,66	0
56	MG	1A	3059	1/1	0.79	0.41	66,66,66,66	0
56	MG	2a	1781	1/1	0.79	0.28	64,64,64,64	0
56	MG	1a	1818	1/1	0.79	0.28	72,72,72,72	0
56	MG	1A	3166	1/1	0.79	0.30	65,65,65,65	0
56	MG	1A	3837	1/1	0.79	0.14	56,56,56,56	0
56	MG	1F	308	1/1	0.79	0.26	63,63,63,63	0
56	MG	1A	3746	1/1	0.79	0.16	31,31,31,31	0
56	MG	2A	3279	1/1	0.79	0.11	46,46,46,46	0
56	MG	1A	3752	1/1	0.79	0.23	62,62,62,62	0
56	MG	2F	305	1/1	0.79	0.14	48,48,48,48	0
56	MG	1A	3706	1/1	0.79	0.14	55,55,55,55	0
56	MG	2A	3507	1/1	0.79	0.17	63,63,63,63	0
56	MG	2A	3419	1/1	0.80	0.16	60,60,60,60	0
56	MG	1a	1611	1/1	0.80	0.25	62,62,62,62	0
56	MG	2A	3602	1/1	0.80	0.17	63,63,63,63	0
56	MG	2a	1746	1/1	0.80	0.12	55,55,55,55	0
56	MG	2A	3282	1/1	0.80	0.17	41,41,41,41	0
56	MG	2A	3539	1/1	0.80	0.14	63,63,63,63	0
56	MG	2a	1671	1/1	0.80	0.16	86,86,86,86	0
56	MG	2a	1675	1/1	0.80	0.22	64,64,64,64	0
56	MG	2A	3624	1/1	0.80	0.13	58,58,58,58	0
56	MG	1A	3425	1/1	0.80	0.16	52,52,52,52	0
56	MG	2A	3286	1/1	0.80	0.15	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3696	1/1	0.80	0.18	50,50,50,50	0
56	MG	2A	3301	1/1	0.80	0.12	58,58,58,58	0
56	MG	2a	1702	1/1	0.80	0.26	64,64,64,64	0
56	MG	1a	1731	1/1	0.80	0.35	79,79,79,79	0
56	MG	2a	1795	1/1	0.80	0.27	76,76,76,76	0
56	MG	2A	3217	1/1	0.80	0.23	68,68,68,68	0
56	MG	2A	3070	1/1	0.80	0.29	52,52,52,52	0
56	MG	2e	201	1/1	0.80	0.26	67,67,67,67	0
56	MG	1a	1621	1/1	0.80	0.19	70,70,70,70	0
56	MG	1A	3134	1/1	0.80	0.21	56,56,56,56	0
56	MG	2a	1604	1/1	0.80	0.14	76,76,76,76	0
56	MG	1a	1706	1/1	0.81	0.17	72,72,72,72	0
56	MG	2A	3632	1/1	0.81	0.38	66,66,66,66	0
56	MG	1A	3438	1/1	0.81	0.20	40,40,40,40	0
56	MG	2A	3672	1/1	0.81	0.17	34,34,34,34	0
56	MG	1a	1711	1/1	0.81	0.27	68,68,68,68	0
56	MG	2a	1722	1/1	0.81	0.19	59,59,59,59	0
56	MG	10	103	1/1	0.81	0.18	61,61,61,61	0
56	MG	1A	3604	1/1	0.81	0.23	32,32,32,32	0
56	MG	2A	3343	1/1	0.81	0.13	40,40,40,40	0
56	MG	1A	3670	1/1	0.81	0.13	66,66,66,66	0
56	MG	1A	3885	1/1	0.81	0.14	64,64,64,64	0
56	MG	2a	1749	1/1	0.81	0.16	59,59,59,59	0
56	MG	1a	1605	1/1	0.81	0.21	71,71,71,71	0
56	MG	2a	1602	1/1	0.81	0.22	70,70,70,70	0
56	MG	2a	1756	1/1	0.81	0.17	78,78,78,78	0
56	MG	1A	3290	1/1	0.81	0.32	68,68,68,68	0
56	MG	2a	1611	1/1	0.81	0.28	68,68,68,68	0
56	MG	1a	1762	1/1	0.81	0.18	64,64,64,64	0
56	MG	2A	3421	1/1	0.81	0.19	51,51,51,51	0
56	MG	2a	1626	1/1	0.81	0.25	63,63,63,63	0
56	MG	2a	1783	1/1	0.81	0.22	68,68,68,68	0
56	MG	1A	3813	1/1	0.81	0.16	63,63,63,63	0
56	MG	2A	3175	1/1	0.81	0.22	47,47,47,47	0
56	MG	2A	3587	1/1	0.81	0.17	59,59,59,59	0
56	MG	2A	3213	1/1	0.81	0.13	58,58,58,58	0
56	MG	1A	3233	1/1	0.81	0.22	60,60,60,60	0
56	MG	1a	1790	1/1	0.81	0.26	62,62,62,62	0
56	MG	1A	3750	1/1	0.81	0.11	51,51,51,51	0
56	MG	1a	1814	1/1	0.81	0.26	74,74,74,74	0
56	MG	1a	1632	1/1	0.81	0.17	78,78,78,78	0
56	MG	2A	3620	1/1	0.81	0.19	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	223	1/1	0.81	0.16	58,58,58,58	0
56	MG	1S	8001	1/1	0.82	0.13	67,67,67,67	0
56	MG	2a	1703	1/1	0.82	0.29	76,76,76,76	0
56	MG	1a	1658	1/1	0.82	0.26	59,59,59,59	0
56	MG	2A	3521	1/1	0.82	0.15	52,52,52,52	0
56	MG	2A	3077	1/1	0.82	0.18	51,51,51,51	0
56	MG	2A	3643	1/1	0.82	0.14	63,63,63,63	0
56	MG	2A	3644	1/1	0.82	0.10	45,45,45,45	0
56	MG	2A	3290	1/1	0.82	0.23	50,50,50,50	0
56	MG	1A	3767	1/1	0.82	0.14	63,63,63,63	0
56	MG	1A	3771	1/1	0.82	0.23	63,63,63,63	0
56	MG	2A	3311	1/1	0.82	0.15	46,46,46,46	0
56	MG	2a	1744	1/1	0.82	0.23	56,56,56,56	0
56	MG	1A	3581	1/1	0.82	0.18	42,42,42,42	0
56	MG	2A	3339	1/1	0.82	0.14	42,42,42,42	0
56	MG	2A	3112	1/1	0.82	0.14	58,58,58,58	0
56	MG	2A	3374	1/1	0.82	0.11	47,47,47,47	0
56	MG	2a	1601	1/1	0.82	0.28	82,82,82,82	0
56	MG	2A	3546	1/1	0.82	0.13	72,72,72,72	0
56	MG	1a	1792	1/1	0.82	0.14	82,82,82,82	0
56	MG	2a	1608	1/1	0.82	0.17	73,73,73,73	0
56	MG	2A	3124	1/1	0.82	0.24	50,50,50,50	0
56	MG	2A	3405	1/1	0.82	0.27	58,58,58,58	0
56	MG	1a	1803	1/1	0.82	0.17	69,69,69,69	0
56	MG	2a	1625	1/1	0.82	0.26	72,72,72,72	0
56	MG	1A	3310	1/1	0.82	0.21	52,52,52,52	0
56	MG	1A	3630	1/1	0.82	0.21	62,62,62,62	0
56	MG	2A	3200	1/1	0.82	0.27	56,56,56,56	0
56	MG	1a	1720	1/1	0.82	0.14	57,57,57,57	0
56	MG	2A	3425	1/1	0.82	0.23	76,76,76,76	0
56	MG	1A	3825	1/1	0.82	0.20	64,64,64,64	0
56	MG	1A	3256	1/1	0.82	0.14	53,53,53,53	0
56	MG	1a	1829	1/1	0.82	0.22	59,59,59,59	0
56	MG	1A	3755	1/1	0.82	0.13	32,32,32,32	0
56	MG	1A	3676	1/1	0.82	0.14	52,52,52,52	0
56	MG	2A	3621	1/1	0.82	0.15	48,48,48,48	0
56	MG	1A	3823	1/1	0.83	0.18	67,67,67,67	0
56	MG	1A	3182	1/1	0.83	0.23	52,52,52,52	0
56	MG	1y	3005	1/1	0.83	0.17	78,78,78,78	0
56	MG	1A	3429	1/1	0.83	0.20	49,49,49,49	0
56	MG	1a	1727	1/1	0.83	0.28	64,64,64,64	0
56	MG	2A	3050	1/1	0.83	0.20	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3433	1/1	0.83	0.20	54,54,54,54	0
56	MG	1A	3612	1/1	0.83	0.14	43,43,43,43	0
56	MG	1A	3843	1/1	0.83	0.23	47,47,47,47	0
56	MG	1a	1752	1/1	0.83	0.34	66,66,66,66	0
56	MG	2A	3087	1/1	0.83	0.22	69,69,69,69	0
56	MG	1A	3623	1/1	0.83	0.15	59,59,59,59	0
56	MG	1A	3847	1/1	0.83	0.13	51,51,51,51	0
56	MG	1a	1769	1/1	0.83	0.24	58,58,58,58	0
56	MG	1A	3162	1/1	0.83	0.25	39,39,39,39	0
56	MG	1A	3768	1/1	0.83	0.11	61,61,61,61	0
56	MG	2a	1612	1/1	0.83	0.13	66,66,66,66	0
56	MG	2a	1618	1/1	0.83	0.17	68,68,68,68	0
56	MG	1a	1625	1/1	0.83	0.12	48,48,48,48	0
56	MG	1A	3357	1/1	0.83	0.20	60,60,60,60	0
56	MG	1A	3715	1/1	0.83	0.21	69,69,69,69	0
56	MG	2a	1774	1/1	0.83	0.20	70,70,70,70	0
56	MG	1A	3796	1/1	0.83	0.14	66,66,66,66	0
56	MG	1a	1805	1/1	0.83	0.12	58,58,58,58	0
56	MG	2A	3427	1/1	0.83	0.22	65,65,65,65	0
56	MG	2a	1784	1/1	0.83	0.17	87,87,87,87	0
56	MG	2a	1665	1/1	0.83	0.32	66,66,66,66	0
56	MG	2a	1667	1/1	0.83	0.19	57,57,57,57	0
56	MG	1a	1810	1/1	0.83	0.17	77,77,77,77	0
56	MG	2A	3466	1/1	0.83	0.39	49,49,49,49	0
56	MG	1A	3360	1/1	0.83	0.15	52,52,52,52	0
56	MG	2A	3222	1/1	0.83	0.22	46,46,46,46	0
56	MG	2A	3482	1/1	0.83	0.14	77,77,77,77	0
56	MG	1A	3810	1/1	0.83	0.24	63,63,63,63	0
56	MG	2a	1690	1/1	0.83	0.26	69,69,69,69	0
56	MG	2A	3246	1/1	0.83	0.15	61,61,61,61	0
56	MG	1A	3555	1/1	0.83	0.21	40,40,40,40	0
56	MG	1A	3535	1/1	0.84	0.14	40,40,40,40	0
56	MG	1a	1643	1/1	0.84	0.34	61,61,61,61	0
56	MG	1a	1791	1/1	0.84	0.17	73,73,73,73	0
56	MG	1a	1645	1/1	0.84	0.36	63,63,63,63	0
56	MG	2a	1680	1/1	0.84	0.27	72,72,72,72	0
56	MG	1A	3398	1/1	0.84	0.13	36,36,36,36	0
56	MG	1a	1688	1/1	0.84	0.23	57,57,57,57	0
56	MG	2A	3426	1/1	0.84	0.19	44,44,44,44	0
56	MG	1B	213	1/1	0.84	0.12	49,49,49,49	0
56	MG	1A	3036	1/1	0.84	0.14	54,54,54,54	0
56	MG	2A	3463	1/1	0.84	0.12	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3646	1/1	0.84	0.26	68,68,68,68	0
56	MG	1a	1816	1/1	0.84	0.16	83,83,83,83	0
56	MG	1A	3489	1/1	0.84	0.12	31,31,31,31	0
56	MG	2A	3642	1/1	0.84	0.13	65,65,65,65	0
56	MG	1A	3241	1/1	0.84	0.12	50,50,50,50	0
56	MG	2A	3245	1/1	0.84	0.18	55,55,55,55	0
56	MG	2A	3646	1/1	0.84	0.12	46,46,46,46	0
56	MG	1a	1719	1/1	0.84	0.14	62,62,62,62	0
56	MG	2a	1725	1/1	0.84	0.18	58,58,58,58	0
56	MG	1A	3583	1/1	0.84	0.11	64,64,64,64	0
56	MG	1r	3001	1/1	0.84	0.27	67,67,67,67	0
56	MG	1v	3001	1/1	0.84	0.18	58,58,58,58	0
56	MG	2B	3018	1/1	0.84	0.18	62,62,62,62	0
56	MG	2A	3525	1/1	0.84	0.10	64,64,64,64	0
56	MG	2E	304	1/1	0.84	0.14	43,43,43,43	0
56	MG	1x	103	1/1	0.84	0.11	54,54,54,54	0
56	MG	1y	3004	1/1	0.84	0.10	73,73,73,73	0
56	MG	1A	3593	1/1	0.84	0.14	38,38,38,38	0
56	MG	20	101	1/1	0.84	0.14	68,68,68,68	0
56	MG	1A	3761	1/1	0.84	0.21	71,71,71,71	0
56	MG	1A	3314	1/1	0.84	0.36	68,68,68,68	0
56	MG	1A	3227	1/1	0.84	0.20	63,63,63,63	0
56	MG	1A	3622	1/1	0.84	0.11	55,55,55,55	0
56	MG	2A	3337	1/1	0.84	0.14	48,48,48,48	0
56	MG	1A	3775	1/1	0.84	0.16	43,43,43,43	0
56	MG	2A	3545	1/1	0.84	0.09	66,66,66,66	0
56	MG	1A	3860	1/1	0.84	0.21	58,58,58,58	0
56	MG	2A	3350	1/1	0.84	0.09	30,30,30,30	0
56	MG	1A	3869	1/1	0.84	0.19	52,52,52,52	0
56	MG	1A	3184	1/1	0.84	0.15	59,59,59,59	0
56	MG	2a	1629	1/1	0.84	0.19	66,66,66,66	0
56	MG	2a	1643	1/1	0.84	0.23	60,60,60,60	0
56	MG	2a	1646	1/1	0.84	0.30	68,68,68,68	0
56	MG	2a	1648	1/1	0.84	0.18	55,55,55,55	0
56	MG	2a	1649	1/1	0.84	0.24	65,65,65,65	0
56	MG	1a	1770	1/1	0.84	0.28	44,44,44,44	0
56	MG	1A	3905	1/1	0.84	0.20	46,46,46,46	0
56	MG	2A	3406	1/1	0.84	0.19	58,58,58,58	0
56	MG	1A	3870	1/1	0.85	0.12	49,49,49,49	0
56	MG	2A	3356	1/1	0.85	0.18	48,48,48,48	0
56	MG	2A	3369	1/1	0.85	0.20	64,64,64,64	0
56	MG	2A	3571	1/1	0.85	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
56	MG	2A	3080	1/1	0.85	0.14	45,45,45,45	0
56	MG	1A	3442	1/1	0.85	0.14	54,54,54,54	0
56	MG	2a	1666	1/1	0.85	0.27	63,63,63,63	0
56	MG	2A	3577	1/1	0.85	0.18	62,62,62,62	0
56	MG	1a	1785	1/1	0.85	0.19	71,71,71,71	0
56	MG	1A	3891	1/1	0.85	0.14	57,57,57,57	0
56	MG	1A	3153	1/1	0.85	0.17	52,52,52,52	0
56	MG	1A	3717	1/1	0.85	0.33	56,56,56,56	0
56	MG	1A	3485	1/1	0.85	0.23	51,51,51,51	0
56	MG	2A	3416	1/1	0.85	0.16	54,54,54,54	0
56	MG	1a	1667	1/1	0.85	0.35	76,76,76,76	0
56	MG	1a	1796	1/1	0.85	0.32	80,80,80,80	0
56	MG	1a	1679	1/1	0.85	0.23	67,67,67,67	0
56	MG	1A	3347	1/1	0.85	0.17	46,46,46,46	0
56	MG	1a	1694	1/1	0.85	0.20	55,55,55,55	0
56	MG	1A	3565	1/1	0.85	0.13	29,29,29,29	0
56	MG	2a	1704	1/1	0.85	0.14	50,50,50,50	0
56	MG	1A	3230	1/1	0.85	0.14	55,55,55,55	0
56	MG	2a	1706	1/1	0.85	0.11	68,68,68,68	0
56	MG	1A	3577	1/1	0.85	0.17	43,43,43,43	0
56	MG	1A	3830	1/1	0.85	0.20	60,60,60,60	0
56	MG	2A	3230	1/1	0.85	0.23	60,60,60,60	0
56	MG	1O	8001	1/1	0.85	0.17	63,63,63,63	0
56	MG	2A	3661	1/1	0.85	0.20	61,61,61,61	0
56	MG	2A	3239	1/1	0.85	0.09	58,58,58,58	0
56	MG	2a	1726	1/1	0.85	0.13	68,68,68,68	0
56	MG	2A	3486	1/1	0.85	0.21	58,58,58,58	0
56	MG	2B	3007	1/1	0.85	0.34	74,74,74,74	0
56	MG	2a	1734	1/1	0.85	0.18	64,64,64,64	0
56	MG	1a	1822	1/1	0.85	0.12	79,79,79,79	0
56	MG	2A	3501	1/1	0.85	0.10	42,42,42,42	0
56	MG	2B	3012	1/1	0.85	0.13	65,65,65,65	0
56	MG	1A	3834	1/1	0.85	0.18	60,60,60,60	0
56	MG	1A	3495	1/1	0.85	0.17	48,48,48,48	0
56	MG	2D	302	1/1	0.85	0.14	70,70,70,70	0
56	MG	2A	3260	1/1	0.85	0.14	27,27,27,27	0
56	MG	2A	3513	1/1	0.85	0.20	56,56,56,56	0
56	MG	2G	3001	1/1	0.85	0.17	58,58,58,58	0
56	MG	2Q	3002	1/1	0.85	0.13	52,52,52,52	0
56	MG	1a	1833	1/1	0.85	0.20	61,61,61,61	0
56	MG	2A	3523	1/1	0.85	0.15	46,46,46,46	0
56	MG	2a	1776	1/1	0.85	0.11	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3249	1/1	0.85	0.36	69,69,69,69	0
56	MG	1A	3502	1/1	0.85	0.14	71,71,71,71	0
56	MG	1A	3365	1/1	0.85	0.14	45,45,45,45	0
56	MG	1y	3002	1/1	0.85	0.19	72,72,72,72	0
56	MG	1a	1744	1/1	0.85	0.27	63,63,63,63	0
56	MG	2A	3299	1/1	0.85	0.20	54,54,54,54	0
56	MG	2a	1789	1/1	0.85	0.14	62,62,62,62	0
56	MG	2a	1790	1/1	0.85	0.21	72,72,72,72	0
56	MG	1A	3388	1/1	0.85	0.16	55,55,55,55	0
56	MG	2a	1616	1/1	0.85	0.24	64,64,64,64	0
56	MG	1a	1749	1/1	0.85	0.15	56,56,56,56	0
56	MG	1A	3615	1/1	0.85	0.17	34,34,34,34	0
56	MG	2A	3324	1/1	0.85	0.20	45,45,45,45	0
56	MG	1A	3700	1/1	0.85	0.17	71,71,71,71	0
56	MG	1a	1616	1/1	0.85	0.37	68,68,68,68	0
56	MG	1A	3778	1/1	0.85	0.23	65,65,65,65	0
56	MG	2A	3552	1/1	0.85	0.17	53,53,53,53	0
56	MG	2w	3002	1/1	0.85	0.35	75,75,75,75	0
56	MG	2A	3363	1/1	0.86	0.13	65,65,65,65	0
56	MG	2a	1658	1/1	0.86	0.27	81,81,81,81	0
56	MG	2A	3364	1/1	0.86	0.17	55,55,55,55	0
56	MG	1A	3666	1/1	0.86	0.17	45,45,45,45	0
56	MG	1A	3229	1/1	0.86	0.21	56,56,56,56	0
56	MG	2A	3384	1/1	0.86	0.12	61,61,61,61	0
56	MG	1A	3826	1/1	0.86	0.18	55,55,55,55	0
56	MG	2a	1670	1/1	0.86	0.17	66,66,66,66	0
56	MG	2A	3137	1/1	0.86	0.22	62,62,62,62	0
56	MG	2A	3146	1/1	0.86	0.09	47,47,47,47	0
56	MG	1A	3296	1/1	0.86	0.25	56,56,56,56	0
56	MG	2A	3605	1/1	0.86	0.14	58,58,58,58	0
56	MG	2A	3174	1/1	0.86	0.20	63,63,63,63	0
56	MG	1a	1823	1/1	0.86	0.19	58,58,58,58	0
56	MG	2A	3199	1/1	0.86	0.28	60,60,60,60	0
56	MG	1a	1827	1/1	0.86	0.31	63,63,63,63	0
56	MG	1A	3453	1/1	0.86	0.18	34,34,34,34	0
56	MG	2a	1699	1/1	0.86	0.12	49,49,49,49	0
56	MG	1A	3213	1/1	0.86	0.22	55,55,55,55	0
56	MG	1A	3540	1/1	0.86	0.19	55,55,55,55	0
56	MG	1a	1760	1/1	0.86	0.18	59,59,59,59	0
56	MG	2A	3223	1/1	0.86	0.17	56,56,56,56	0
56	MG	2A	3444	1/1	0.86	0.14	57,57,57,57	0
56	MG	1a	1665	1/1	0.86	0.28	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3234	1/1	0.86	0.21	56,56,56,56	0
56	MG	1x	102	1/1	0.86	0.17	62,62,62,62	0
56	MG	2A	3470	1/1	0.86	0.11	53,53,53,53	0
56	MG	2A	3237	1/1	0.86	0.20	63,63,63,63	0
56	MG	2a	1724	1/1	0.86	0.16	77,77,77,77	0
56	MG	2B	3004	1/1	0.86	0.19	50,50,50,50	0
56	MG	1A	3085	1/1	0.86	0.15	52,52,52,52	0
56	MG	1x	110	1/1	0.86	0.19	55,55,55,55	0
56	MG	2A	3485	1/1	0.86	0.13	47,47,47,47	0
56	MG	2a	1732	1/1	0.86	0.14	77,77,77,77	0
56	MG	1y	3001	1/1	0.86	0.22	73,73,73,73	0
56	MG	2a	1739	1/1	0.86	0.13	64,64,64,64	0
56	MG	2A	3248	1/1	0.86	0.11	43,43,43,43	0
56	MG	2A	3498	1/1	0.86	0.23	56,56,56,56	0
56	MG	2A	3500	1/1	0.86	0.13	56,56,56,56	0
56	MG	2A	3249	1/1	0.86	0.15	45,45,45,45	0
56	MG	2E	307	1/1	0.86	0.29	51,51,51,51	0
56	MG	1I	3001	1/1	0.86	0.16	65,65,65,65	0
56	MG	1A	3417	1/1	0.86	0.10	36,36,36,36	0
56	MG	2A	3262	1/1	0.86	0.20	59,59,59,59	0
56	MG	2A	3263	1/1	0.86	0.17	44,44,44,44	0
56	MG	1A	3712	1/1	0.86	0.17	36,36,36,36	0
56	MG	1A	3713	1/1	0.86	0.20	71,71,71,71	0
56	MG	1A	3852	1/1	0.86	0.18	70,70,70,70	0
56	MG	2A	3045	1/1	0.86	0.09	38,38,38,38	0
56	MG	2a	1778	1/1	0.86	0.26	78,78,78,78	0
56	MG	2a	1780	1/1	0.86	0.22	69,69,69,69	0
56	MG	1A	3323	1/1	0.86	0.25	55,55,55,55	0
56	MG	2A	3292	1/1	0.86	0.15	47,47,47,47	0
56	MG	1A	3788	1/1	0.86	0.23	61,61,61,61	0
56	MG	1A	3335	1/1	0.86	0.33	63,63,63,63	0
56	MG	2a	1615	1/1	0.86	0.19	60,60,60,60	0
56	MG	1A	3196	1/1	0.86	0.14	61,61,61,61	0
56	MG	1a	1614	1/1	0.86	0.28	59,59,59,59	0
56	MG	2A	3085	1/1	0.86	0.25	56,56,56,56	0
56	MG	1a	1722	1/1	0.86	0.18	64,64,64,64	0
56	MG	2A	3328	1/1	0.86	0.17	47,47,47,47	0
56	MG	1A	3500	1/1	0.86	0.20	62,62,62,62	0
56	MG	1a	1811	1/1	0.86	0.14	58,58,58,58	0
56	MG	2a	1637	1/1	0.86	0.16	60,60,60,60	0
56	MG	2a	1638	1/1	0.86	0.09	68,68,68,68	0
56	MG	1a	1813	1/1	0.86	0.21	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3105	1/1	0.86	0.21	52,52,52,52	0
56	MG	1A	3282	1/1	0.86	0.26	58,58,58,58	0
56	MG	2r	3001	1/1	0.86	0.28	84,84,84,84	0
56	MG	2w	3001	1/1	0.86	0.21	58,58,58,58	0
56	MG	2A	3358	1/1	0.86	0.14	50,50,50,50	0
56	MG	1A	3542	1/1	0.87	0.13	33,33,33,33	0
56	MG	1A	3348	1/1	0.87	0.10	33,33,33,33	0
56	MG	1A	3848	1/1	0.87	0.25	66,66,66,66	0
56	MG	1A	3252	1/1	0.87	0.23	47,47,47,47	0
56	MG	1A	3560	1/1	0.87	0.13	19,19,19,19	0
56	MG	1A	3859	1/1	0.87	0.15	40,40,40,40	0
56	MG	2a	1651	1/1	0.87	0.30	69,69,69,69	0
56	MG	2a	1656	1/1	0.87	0.20	54,54,54,54	0
56	MG	1A	3469	1/1	0.87	0.10	48,48,48,48	0
56	MG	1a	1635	1/1	0.87	0.12	62,62,62,62	0
56	MG	2A	3565	1/1	0.87	0.20	45,45,45,45	0
56	MG	2A	3115	1/1	0.87	0.13	62,62,62,62	0
56	MG	1A	3572	1/1	0.87	0.16	41,41,41,41	0
56	MG	2A	3121	1/1	0.87	0.09	60,60,60,60	0
56	MG	1A	3476	1/1	0.87	0.21	36,36,36,36	0
56	MG	1A	3689	1/1	0.87	0.19	53,53,53,53	0
56	MG	2A	3582	1/1	0.87	0.13	46,46,46,46	0
56	MG	1A	3886	1/1	0.87	0.16	58,58,58,58	0
56	MG	1a	1812	1/1	0.87	0.28	65,65,65,65	0
56	MG	1A	3127	1/1	0.87	0.27	62,62,62,62	0
56	MG	2A	3386	1/1	0.87	0.12	33,33,33,33	0
56	MG	2A	3600	1/1	0.87	0.16	45,45,45,45	0
56	MG	2A	3170	1/1	0.87	0.32	68,68,68,68	0
56	MG	2A	3402	1/1	0.87	0.21	62,62,62,62	0
56	MG	1A	3698	1/1	0.87	0.32	65,65,65,65	0
56	MG	2a	1697	1/1	0.87	0.17	64,64,64,64	0
56	MG	1a	1684	1/1	0.87	0.26	64,64,64,64	0
56	MG	2A	3616	1/1	0.87	0.14	64,64,64,64	0
56	MG	2A	3188	1/1	0.87	0.34	59,59,59,59	0
56	MG	2A	3407	1/1	0.87	0.10	24,24,24,24	0
56	MG	1A	3259	1/1	0.87	0.19	37,37,37,37	0
56	MG	1a	1819	1/1	0.87	0.09	91,91,91,91	0
56	MG	2A	3211	1/1	0.87	0.23	48,48,48,48	0
56	MG	2A	3639	1/1	0.87	0.08	44,44,44,44	0
56	MG	1A	3173	1/1	0.87	0.15	41,41,41,41	0
56	MG	1B	202	1/1	0.87	0.20	61,61,61,61	0
56	MG	2a	1720	1/1	0.87	0.21	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3805	1/1	0.87	0.12	52,52,52,52	0
56	MG	1A	3236	1/1	0.87	0.16	58,58,58,58	0
56	MG	1A	3596	1/1	0.87	0.16	51,51,51,51	0
56	MG	2A	3650	1/1	0.87	0.10	55,55,55,55	0
56	MG	1A	3294	1/1	0.87	0.27	63,63,63,63	0
56	MG	2A	3436	1/1	0.87	0.14	54,54,54,54	0
56	MG	2A	3678	1/1	0.87	0.54	49,49,49,49	0
56	MG	1A	3423	1/1	0.87	0.15	62,62,62,62	0
56	MG	1A	3237	1/1	0.87	0.17	57,57,57,57	0
56	MG	2a	1742	1/1	0.87	0.21	70,70,70,70	0
56	MG	1A	3239	1/1	0.87	0.19	63,63,63,63	0
56	MG	2B	3008	1/1	0.87	0.12	61,61,61,61	0
56	MG	2A	3238	1/1	0.87	0.41	61,61,61,61	0
56	MG	1Q	3005	1/1	0.87	0.18	58,58,58,58	0
56	MG	2A	3243	1/1	0.87	0.30	66,66,66,66	0
56	MG	2B	3017	1/1	0.87	0.20	59,59,59,59	0
56	MG	1A	3734	1/1	0.87	0.18	58,58,58,58	0
56	MG	1V	203	1/1	0.87	0.13	64,64,64,64	0
56	MG	1Y	502	1/1	0.87	0.32	60,60,60,60	0
56	MG	2a	1761	1/1	0.87	0.13	71,71,71,71	0
56	MG	2a	1763	1/1	0.87	0.13	75,75,75,75	0
56	MG	1A	3041	1/1	0.87	0.15	43,43,43,43	0
56	MG	1A	3025	1/1	0.87	0.22	34,34,34,34	0
56	MG	12	101	1/1	0.87	0.13	54,54,54,54	0
56	MG	1A	3838	1/1	0.87	0.12	40,40,40,40	0
56	MG	1a	1753	1/1	0.87	0.21	67,67,67,67	0
56	MG	2A	3273	1/1	0.87	0.12	47,47,47,47	0
56	MG	2A	3278	1/1	0.87	0.13	40,40,40,40	0
56	MG	15	105	1/1	0.87	0.11	55,55,55,55	0
56	MG	1a	1603	1/1	0.87	0.30	60,60,60,60	0
56	MG	2A	3516	1/1	0.87	0.13	46,46,46,46	0
56	MG	2a	1603	1/1	0.87	0.16	64,64,64,64	0
56	MG	2A	3059	1/1	0.87	0.16	66,66,66,66	0
56	MG	2a	1605	1/1	0.87	0.19	54,54,54,54	0
56	MG	2A	3522	1/1	0.87	0.13	44,44,44,44	0
56	MG	2A	3065	1/1	0.87	0.11	47,47,47,47	0
56	MG	2A	3288	1/1	0.87	0.18	56,56,56,56	0
56	MG	1A	3243	1/1	0.87	0.32	66,66,66,66	0
56	MG	2A	3528	1/1	0.87	0.10	73,73,73,73	0
56	MG	1A	3842	1/1	0.87	0.20	56,56,56,56	0
56	MG	2A	3293	1/1	0.87	0.15	54,54,54,54	0
56	MG	2A	3072	1/1	0.87	0.10	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3295	1/1	0.87	0.19	42,42,42,42	0
56	MG	2A	3296	1/1	0.87	0.17	52,52,52,52	0
56	MG	2a	1627	1/1	0.87	0.18	61,61,61,61	0
56	MG	2v	3001	1/1	0.87	0.27	60,60,60,60	0
56	MG	1A	3015	1/1	0.87	0.32	58,58,58,58	0
56	MG	2a	1633	1/1	0.87	0.20	71,71,71,71	0
56	MG	1A	3250	1/1	0.88	0.14	57,57,57,57	0
56	MG	2a	1613	1/1	0.88	0.20	59,59,59,59	0
56	MG	1A	3616	1/1	0.88	0.12	45,45,45,45	0
56	MG	1P	203	1/1	0.88	0.29	48,48,48,48	0
56	MG	2a	1617	1/1	0.88	0.21	51,51,51,51	0
56	MG	1x	112	1/1	0.88	0.20	68,68,68,68	0
56	MG	1x	113	1/1	0.88	0.18	68,68,68,68	0
56	MG	1a	1723	1/1	0.88	0.19	61,61,61,61	0
56	MG	1a	1725	1/1	0.88	0.18	63,63,63,63	0
56	MG	1Q	3002	1/1	0.88	0.18	43,43,43,43	0
56	MG	1A	3522	1/1	0.88	0.11	50,50,50,50	0
56	MG	1a	1728	1/1	0.88	0.15	67,67,67,67	0
56	MG	1R	202	1/1	0.88	0.21	71,71,71,71	0
56	MG	2a	1635	1/1	0.88	0.21	61,61,61,61	0
56	MG	2A	3033	1/1	0.88	0.12	53,53,53,53	0
56	MG	1a	1740	1/1	0.88	0.15	60,60,60,60	0
56	MG	2a	1639	1/1	0.88	0.12	54,54,54,54	0
56	MG	2a	1641	1/1	0.88	0.12	55,55,55,55	0
56	MG	1A	3533	1/1	0.88	0.14	55,55,55,55	0
56	MG	2A	3542	1/1	0.88	0.11	48,48,48,48	0
56	MG	1A	3297	1/1	0.88	0.26	62,62,62,62	0
56	MG	1A	3459	1/1	0.88	0.16	42,42,42,42	0
56	MG	2A	3066	1/1	0.88	0.08	39,39,39,39	0
56	MG	1A	3462	1/1	0.88	0.19	58,58,58,58	0
56	MG	2A	3307	1/1	0.88	0.10	42,42,42,42	0
56	MG	1A	3543	1/1	0.88	0.19	54,54,54,54	0
56	MG	2A	3315	1/1	0.88	0.09	36,36,36,36	0
56	MG	2a	1664	1/1	0.88	0.19	60,60,60,60	0
56	MG	2A	3562	1/1	0.88	0.12	60,60,60,60	0
56	MG	1A	3651	1/1	0.88	0.17	62,62,62,62	0
56	MG	1A	3463	1/1	0.88	0.17	57,57,57,57	0
56	MG	2A	3569	1/1	0.88	0.11	43,43,43,43	0
56	MG	1A	3661	1/1	0.88	0.15	51,51,51,51	0
56	MG	1a	1761	1/1	0.88	0.14	51,51,51,51	0
56	MG	16	103	1/1	0.88	0.15	51,51,51,51	0
56	MG	2a	1677	1/1	0.88	0.21	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1678	1/1	0.88	0.28	60,60,60,60	0
56	MG	2A	3341	1/1	0.88	0.13	41,41,41,41	0
56	MG	1A	3165	1/1	0.88	0.17	51,51,51,51	0
56	MG	2A	3095	1/1	0.88	0.37	65,65,65,65	0
56	MG	1A	3394	1/1	0.88	0.18	43,43,43,43	0
56	MG	2A	3591	1/1	0.88	0.13	54,54,54,54	0
56	MG	1a	1774	1/1	0.88	0.20	81,81,81,81	0
56	MG	2a	1692	1/1	0.88	0.15	72,72,72,72	0
56	MG	1A	3854	1/1	0.88	0.20	67,67,67,67	0
56	MG	2A	3599	1/1	0.88	0.12	78,78,78,78	0
56	MG	1A	3005	1/1	0.88	0.18	59,59,59,59	0
56	MG	1A	3402	1/1	0.88	0.11	27,27,27,27	0
56	MG	1A	3773	1/1	0.88	0.18	48,48,48,48	0
56	MG	2A	3375	1/1	0.88	0.09	51,51,51,51	0
56	MG	2A	3612	1/1	0.88	0.20	56,56,56,56	0
56	MG	1A	3861	1/1	0.88	0.18	58,58,58,58	0
56	MG	2A	3615	1/1	0.88	0.12	69,69,69,69	0
56	MG	1A	3862	1/1	0.88	0.14	54,54,54,54	0
56	MG	2A	3617	1/1	0.88	0.12	49,49,49,49	0
56	MG	1A	3677	1/1	0.88	0.16	68,68,68,68	0
56	MG	2A	3401	1/1	0.88	0.18	64,64,64,64	0
56	MG	2A	3131	1/1	0.88	0.25	55,55,55,55	0
56	MG	1a	1800	1/1	0.88	0.12	56,56,56,56	0
56	MG	2A	3626	1/1	0.88	0.13	51,51,51,51	0
56	MG	2A	3145	1/1	0.88	0.07	50,50,50,50	0
56	MG	2a	1727	1/1	0.88	0.11	54,54,54,54	0
56	MG	1A	3776	1/1	0.88	0.12	48,48,48,48	0
56	MG	2A	3153	1/1	0.88	0.30	59,59,59,59	0
56	MG	1A	3680	1/1	0.88	0.23	54,54,54,54	0
56	MG	1A	3414	1/1	0.88	0.12	52,52,52,52	0
56	MG	1A	3687	1/1	0.88	0.12	63,63,63,63	0
56	MG	2A	3645	1/1	0.88	0.12	72,72,72,72	0
56	MG	2A	3417	1/1	0.88	0.19	51,51,51,51	0
56	MG	2A	3648	1/1	0.88	0.13	43,43,43,43	0
56	MG	1A	3901	1/1	0.88	0.13	36,36,36,36	0
56	MG	1a	1655	1/1	0.88	0.15	57,57,57,57	0
56	MG	2A	3664	1/1	0.88	0.09	43,43,43,43	0
56	MG	2A	3194	1/1	0.88	0.16	53,53,53,53	0
56	MG	2A	3676	1/1	0.88	0.10	50,50,50,50	0
56	MG	2a	1754	1/1	0.88	0.13	73,73,73,73	0
56	MG	1A	3790	1/1	0.88	0.15	48,48,48,48	0
56	MG	1A	3316	1/1	0.88	0.23	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	3002	1/1	0.88	0.19	67,67,67,67	0
56	MG	2A	3207	1/1	0.88	0.08	33,33,33,33	0
56	MG	1A	3322	1/1	0.88	0.19	57,57,57,57	0
56	MG	1a	1668	1/1	0.88	0.08	44,44,44,44	0
56	MG	2a	1770	1/1	0.88	0.26	67,67,67,67	0
56	MG	2A	3446	1/1	0.88	0.10	41,41,41,41	0
56	MG	1A	3210	1/1	0.88	0.15	45,45,45,45	0
56	MG	2A	3461	1/1	0.88	0.19	57,57,57,57	0
56	MG	1B	210	1/1	0.88	0.11	53,53,53,53	0
56	MG	1a	1687	1/1	0.88	0.15	57,57,57,57	0
56	MG	1A	3275	1/1	0.88	0.18	48,48,48,48	0
56	MG	1a	1826	1/1	0.88	0.18	60,60,60,60	0
56	MG	2A	3231	1/1	0.88	0.25	59,59,59,59	0
56	MG	1B	216	1/1	0.88	0.10	58,58,58,58	0
56	MG	2F	301	1/1	0.88	0.12	54,54,54,54	0
56	MG	1A	3101	1/1	0.88	0.22	61,61,61,61	0
56	MG	1A	3815	1/1	0.88	0.17	31,31,31,31	0
56	MG	2A	3490	1/1	0.88	0.09	51,51,51,51	0
56	MG	1A	3215	1/1	0.88	0.18	43,43,43,43	0
56	MG	1a	1834	1/1	0.88	0.08	63,63,63,63	0
56	MG	1b	3001	1/1	0.88	0.19	68,68,68,68	0
56	MG	25	502	1/1	0.88	0.16	51,51,51,51	0
56	MG	28	101	1/1	0.88	0.27	57,57,57,57	0
56	MG	1c	3001	1/1	0.88	0.38	61,61,61,61	0
56	MG	2A	3504	1/1	0.88	0.12	55,55,55,55	0
56	MG	1E	306	1/1	0.88	0.11	61,61,61,61	0
56	MG	2A	3506	1/1	0.88	0.14	57,57,57,57	0
56	MG	1A	3022	1/1	0.88	0.13	52,52,52,52	0
56	MG	2v	3002	1/1	0.88	0.18	60,60,60,60	0
56	MG	1w	3001	1/1	0.88	0.18	52,52,52,52	0
56	MG	1w	3005	1/1	0.88	0.14	65,65,65,65	0
56	MG	1A	3822	1/1	0.89	0.25	56,56,56,56	0
56	MG	1A	3386	1/1	0.89	0.08	42,42,42,42	0
56	MG	1A	3484	1/1	0.89	0.16	46,46,46,46	0
56	MG	2A	3063	1/1	0.89	0.16	48,48,48,48	0
56	MG	1A	3009	1/1	0.89	0.20	44,44,44,44	0
56	MG	2A	3540	1/1	0.89	0.13	53,53,53,53	0
56	MG	1A	3287	1/1	0.89	0.33	57,57,57,57	0
56	MG	1A	3170	1/1	0.89	0.31	64,64,64,64	0
56	MG	1A	3831	1/1	0.89	0.14	23,23,23,23	0
56	MG	2a	1636	1/1	0.89	0.20	62,62,62,62	0
56	MG	10	106	1/1	0.89	0.09	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3491	1/1	0.89	0.14	46,46,46,46	0
56	MG	2A	3303	1/1	0.89	0.13	48,48,48,48	0
56	MG	2A	3551	1/1	0.89	0.10	33,33,33,33	0
56	MG	2A	3078	1/1	0.89	0.09	51,51,51,51	0
56	MG	2A	3309	1/1	0.89	0.10	39,39,39,39	0
56	MG	1A	3399	1/1	0.89	0.15	59,59,59,59	0
56	MG	1A	3087	1/1	0.89	0.23	63,63,63,63	0
56	MG	1a	1768	1/1	0.89	0.10	66,66,66,66	0
56	MG	2A	3322	1/1	0.89	0.14	50,50,50,50	0
56	MG	1A	3839	1/1	0.89	0.19	61,61,61,61	0
56	MG	1A	3499	1/1	0.89	0.10	49,49,49,49	0
56	MG	1A	3719	1/1	0.89	0.12	48,48,48,48	0
56	MG	2A	3100	1/1	0.89	0.15	52,52,52,52	0
56	MG	2A	3103	1/1	0.89	0.10	46,46,46,46	0
56	MG	1a	1780	1/1	0.89	0.24	74,74,74,74	0
56	MG	2A	3586	1/1	0.89	0.18	73,73,73,73	0
56	MG	1A	3620	1/1	0.89	0.22	43,43,43,43	0
56	MG	2A	3106	1/1	0.89	0.22	55,55,55,55	0
56	MG	1A	3412	1/1	0.89	0.11	44,44,44,44	0
56	MG	2A	3359	1/1	0.89	0.12	54,54,54,54	0
56	MG	1A	3739	1/1	0.89	0.28	43,43,43,43	0
56	MG	1A	3176	1/1	0.89	0.08	47,47,47,47	0
56	MG	2a	1679	1/1	0.89	0.20	66,66,66,66	0
56	MG	2A	3117	1/1	0.89	0.24	52,52,52,52	0
56	MG	2a	1681	1/1	0.89	0.13	84,84,84,84	0
56	MG	1A	3626	1/1	0.89	0.12	44,44,44,44	0
56	MG	1A	3627	1/1	0.89	0.14	66,66,66,66	0
56	MG	2A	3607	1/1	0.89	0.09	55,55,55,55	0
56	MG	2a	1688	1/1	0.89	0.15	65,65,65,65	0
56	MG	2A	3377	1/1	0.89	0.09	40,40,40,40	0
56	MG	1A	3099	1/1	0.89	0.16	44,44,44,44	0
56	MG	2A	3613	1/1	0.89	0.19	71,71,71,71	0
56	MG	1A	3856	1/1	0.89	0.09	41,41,41,41	0
56	MG	1a	1629	1/1	0.89	0.24	69,69,69,69	0
56	MG	1A	3754	1/1	0.89	0.14	26,26,26,26	0
56	MG	2a	1700	1/1	0.89	0.12	57,57,57,57	0
56	MG	1a	1633	1/1	0.89	0.20	66,66,66,66	0
56	MG	2A	3619	1/1	0.89	0.22	47,47,47,47	0
56	MG	2A	3147	1/1	0.89	0.12	55,55,55,55	0
56	MG	2A	3148	1/1	0.89	0.24	59,59,59,59	0
56	MG	1A	3420	1/1	0.89	0.15	46,46,46,46	0
56	MG	1a	1642	1/1	0.89	0.28	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3168	1/1	0.89	0.12	59,59,59,59	0
56	MG	1A	3302	1/1	0.89	0.35	65,65,65,65	0
56	MG	1A	3759	1/1	0.89	0.14	43,43,43,43	0
56	MG	1A	3641	1/1	0.89	0.11	57,57,57,57	0
56	MG	2A	3418	1/1	0.89	0.11	41,41,41,41	0
56	MG	1a	1656	1/1	0.89	0.26	57,57,57,57	0
56	MG	2A	3190	1/1	0.89	0.22	37,37,37,37	0
56	MG	1A	3763	1/1	0.89	0.16	63,63,63,63	0
56	MG	1A	3018	1/1	0.89	0.28	53,53,53,53	0
56	MG	1A	3649	1/1	0.89	0.16	67,67,67,67	0
56	MG	2A	3204	1/1	0.89	0.30	55,55,55,55	0
56	MG	2A	3651	1/1	0.89	0.13	54,54,54,54	0
56	MG	2A	3656	1/1	0.89	0.25	58,58,58,58	0
56	MG	2A	3428	1/1	0.89	0.14	34,34,34,34	0
56	MG	2a	1741	1/1	0.89	0.12	65,65,65,65	0
56	MG	1A	3190	1/1	0.89	0.08	47,47,47,47	0
56	MG	2A	3666	1/1	0.89	0.11	47,47,47,47	0
56	MG	2A	3439	1/1	0.89	0.11	60,60,60,60	0
56	MG	1A	3104	1/1	0.89	0.27	71,71,71,71	0
56	MG	1a	1824	1/1	0.89	0.15	69,69,69,69	0
56	MG	1a	1681	1/1	0.89	0.12	58,58,58,58	0
56	MG	2A	3453	1/1	0.89	0.19	64,64,64,64	0
56	MG	2A	3454	1/1	0.89	0.09	34,34,34,34	0
56	MG	2A	3455	1/1	0.89	0.13	39,39,39,39	0
56	MG	1A	3656	1/1	0.89	0.18	38,38,38,38	0
56	MG	1A	3919	1/1	0.89	0.12	46,46,46,46	0
56	MG	2A	3464	1/1	0.89	0.11	55,55,55,55	0
56	MG	1A	3206	1/1	0.89	0.19	40,40,40,40	0
56	MG	1A	3014	1/1	0.89	0.12	46,46,46,46	0
56	MG	1a	1699	1/1	0.89	0.29	68,68,68,68	0
56	MG	2A	3233	1/1	0.89	0.08	48,48,48,48	0
56	MG	2a	1772	1/1	0.89	0.23	76,76,76,76	0
56	MG	1a	1701	1/1	0.89	0.07	50,50,50,50	0
56	MG	1a	1702	1/1	0.89	0.15	67,67,67,67	0
56	MG	1A	3051	1/1	0.89	0.22	58,58,58,58	0
56	MG	1A	3787	1/1	0.89	0.17	62,62,62,62	0
56	MG	1A	3341	1/1	0.89	0.38	68,68,68,68	0
56	MG	1a	1709	1/1	0.89	0.14	62,62,62,62	0
56	MG	2A	3499	1/1	0.89	0.19	35,35,35,35	0
56	MG	1A	3674	1/1	0.89	0.10	48,48,48,48	0
56	MG	2X	101	1/1	0.89	0.10	42,42,42,42	0
56	MG	2a	1787	1/1	0.89	0.15	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3024	1/1	0.89	0.18	57,57,57,57	0
56	MG	1A	3797	1/1	0.89	0.15	67,67,67,67	0
56	MG	20	103	1/1	0.89	0.20	65,65,65,65	0
56	MG	1A	3154	1/1	0.89	0.16	53,53,53,53	0
56	MG	2A	3251	1/1	0.89	0.15	59,59,59,59	0
56	MG	2A	3253	1/1	0.89	0.12	57,57,57,57	0
56	MG	1A	3802	1/1	0.89	0.11	56,56,56,56	0
56	MG	2a	1799	1/1	0.89	0.23	51,51,51,51	0
56	MG	2A	3511	1/1	0.89	0.13	62,62,62,62	0
56	MG	1A	3804	1/1	0.89	0.10	61,61,61,61	0
56	MG	1A	3060	1/1	0.89	0.16	44,44,44,44	0
56	MG	1A	3566	1/1	0.89	0.14	32,32,32,32	0
56	MG	2A	3269	1/1	0.89	0.13	53,53,53,53	0
56	MG	1O	8003	1/1	0.89	0.21	54,54,54,54	0
56	MG	2t	3001	1/1	0.89	0.12	57,57,57,57	0
56	MG	1A	3269	1/1	0.89	0.16	57,57,57,57	0
56	MG	1A	3076	1/1	0.89	0.15	66,66,66,66	0
56	MG	2A	3022	1/1	0.89	0.09	53,53,53,53	0
56	MG	1a	1736	1/1	0.89	0.22	58,58,58,58	0
56	MG	1A	3747	1/1	0.90	0.09	30,30,30,30	0
56	MG	2A	3304	1/1	0.90	0.14	59,59,59,59	0
56	MG	2A	3094	1/1	0.90	0.11	50,50,50,50	0
56	MG	1A	3163	1/1	0.90	0.12	43,43,43,43	0
56	MG	1A	3545	1/1	0.90	0.15	49,49,49,49	0
56	MG	1A	3851	1/1	0.90	0.11	50,50,50,50	0
56	MG	1a	1610	1/1	0.90	0.24	59,59,59,59	0
56	MG	2a	1628	1/1	0.90	0.19	66,66,66,66	0
56	MG	1a	1781	1/1	0.90	0.21	76,76,76,76	0
56	MG	1A	3472	1/1	0.90	0.11	37,37,37,37	0
56	MG	2A	3325	1/1	0.90	0.14	49,49,49,49	0
56	MG	1A	3270	1/1	0.90	0.19	48,48,48,48	0
56	MG	2A	3329	1/1	0.90	0.13	35,35,35,35	0
56	MG	2A	3331	1/1	0.90	0.09	53,53,53,53	0
56	MG	2A	3111	1/1	0.90	0.10	51,51,51,51	0
56	MG	1A	3410	1/1	0.90	0.10	43,43,43,43	0
56	MG	1A	3272	1/1	0.90	0.10	39,39,39,39	0
56	MG	1A	3273	1/1	0.90	0.32	59,59,59,59	0
56	MG	1A	3762	1/1	0.90	0.33	68,68,68,68	0
56	MG	2A	3352	1/1	0.90	0.10	47,47,47,47	0
56	MG	1A	3568	1/1	0.90	0.10	31,31,31,31	0
56	MG	2a	1653	1/1	0.90	0.21	62,62,62,62	0
56	MG	2a	1655	1/1	0.90	0.23	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3181	1/1	0.90	0.12	56,56,56,56	0
56	MG	1a	1801	1/1	0.90	0.20	59,59,59,59	0
56	MG	2A	3362	1/1	0.90	0.23	58,58,58,58	0
56	MG	1a	1802	1/1	0.90	0.18	54,54,54,54	0
56	MG	2a	1663	1/1	0.90	0.30	55,55,55,55	0
56	MG	1A	3863	1/1	0.90	0.12	56,56,56,56	0
56	MG	2A	3139	1/1	0.90	0.09	47,47,47,47	0
56	MG	2A	3371	1/1	0.90	0.11	41,41,41,41	0
56	MG	2A	3593	1/1	0.90	0.08	41,41,41,41	0
56	MG	1A	3865	1/1	0.90	0.11	50,50,50,50	0
56	MG	1A	3247	1/1	0.90	0.23	52,52,52,52	0
56	MG	1A	3667	1/1	0.90	0.11	51,51,51,51	0
56	MG	2a	1673	1/1	0.90	0.26	55,55,55,55	0
56	MG	1A	3871	1/1	0.90	0.21	69,69,69,69	0
56	MG	2A	3150	1/1	0.90	0.10	54,54,54,54	0
56	MG	1A	3493	1/1	0.90	0.18	53,53,53,53	0
56	MG	2A	3400	1/1	0.90	0.14	61,61,61,61	0
56	MG	1a	1652	1/1	0.90	0.28	63,63,63,63	0
56	MG	2A	3610	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3672	1/1	0.90	0.10	48,48,48,48	0
56	MG	2a	1683	1/1	0.90	0.14	82,82,82,82	0
56	MG	1A	3283	1/1	0.90	0.14	44,44,44,44	0
56	MG	2a	1685	1/1	0.90	0.35	62,62,62,62	0
56	MG	1A	3893	1/1	0.90	0.15	71,71,71,71	0
56	MG	1a	1663	1/1	0.90	0.30	68,68,68,68	0
56	MG	2A	3184	1/1	0.90	0.19	51,51,51,51	0
56	MG	1A	3142	1/1	0.90	0.15	47,47,47,47	0
56	MG	2A	3618	1/1	0.90	0.11	45,45,45,45	0
56	MG	1A	3589	1/1	0.90	0.16	64,64,64,64	0
56	MG	2A	3193	1/1	0.90	0.13	48,48,48,48	0
56	MG	1A	3122	1/1	0.90	0.15	51,51,51,51	0
56	MG	2A	3623	1/1	0.90	0.12	52,52,52,52	0
56	MG	1a	1670	1/1	0.90	0.14	56,56,56,56	0
56	MG	1a	1677	1/1	0.90	0.14	51,51,51,51	0
56	MG	1A	3293	1/1	0.90	0.29	60,60,60,60	0
56	MG	1A	3599	1/1	0.90	0.07	46,46,46,46	0
56	MG	2A	3633	1/1	0.90	0.16	62,62,62,62	0
56	MG	2A	3634	1/1	0.90	0.14	56,56,56,56	0
56	MG	2A	3209	1/1	0.90	0.13	44,44,44,44	0
56	MG	1A	3792	1/1	0.90	0.30	34,34,34,34	0
56	MG	1a	1686	1/1	0.90	0.19	53,53,53,53	0
56	MG	1A	3688	1/1	0.90	0.12	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3429	1/1	0.90	0.14	55,55,55,55	0
56	MG	2A	3434	1/1	0.90	0.12	34,34,34,34	0
56	MG	2A	3218	1/1	0.90	0.14	53,53,53,53	0
56	MG	1A	3435	1/1	0.90	0.11	29,29,29,29	0
56	MG	2A	3220	1/1	0.90	0.17	56,56,56,56	0
56	MG	2a	1728	1/1	0.90	0.20	75,75,75,75	0
56	MG	1A	3691	1/1	0.90	0.17	60,60,60,60	0
56	MG	2A	3653	1/1	0.90	0.08	46,46,46,46	0
56	MG	1a	1697	1/1	0.90	0.28	51,51,51,51	0
56	MG	2a	1733	1/1	0.90	0.16	78,78,78,78	0
56	MG	2A	3448	1/1	0.90	0.12	33,33,33,33	0
56	MG	2a	1737	1/1	0.90	0.08	55,55,55,55	0
56	MG	1A	3606	1/1	0.90	0.18	62,62,62,62	0
56	MG	1B	220	1/1	0.90	0.11	56,56,56,56	0
56	MG	1A	3608	1/1	0.90	0.21	60,60,60,60	0
56	MG	1A	3031	1/1	0.90	0.08	42,42,42,42	0
56	MG	1A	3379	1/1	0.90	0.09	48,48,48,48	0
56	MG	1x	109	1/1	0.90	0.12	57,57,57,57	0
56	MG	1F	306	1/1	0.90	0.11	46,46,46,46	0
56	MG	2a	1748	1/1	0.90	0.17	59,59,59,59	0
56	MG	2B	3003	1/1	0.90	0.12	69,69,69,69	0
56	MG	2a	1750	1/1	0.90	0.19	66,66,66,66	0
56	MG	1A	3812	1/1	0.90	0.16	61,61,61,61	0
56	MG	2A	3471	1/1	0.90	0.16	48,48,48,48	0
56	MG	2a	1753	1/1	0.90	0.14	72,72,72,72	0
56	MG	2A	3474	1/1	0.90	0.15	41,41,41,41	0
56	MG	2B	3009	1/1	0.90	0.21	60,60,60,60	0
56	MG	2a	1757	1/1	0.90	0.29	71,71,71,71	0
56	MG	2a	1758	1/1	0.90	0.11	59,59,59,59	0
56	MG	1A	3705	1/1	0.90	0.09	32,32,32,32	0
56	MG	1N	3001	1/1	0.90	0.27	51,51,51,51	0
56	MG	1A	3194	1/1	0.90	0.09	55,55,55,55	0
56	MG	2a	1767	1/1	0.90	0.13	55,55,55,55	0
56	MG	2B	3014	1/1	0.90	0.21	68,68,68,68	0
56	MG	1O	8002	1/1	0.90	0.11	63,63,63,63	0
56	MG	1A	3257	1/1	0.90	0.21	48,48,48,48	0
56	MG	2B	3020	1/1	0.90	0.09	66,66,66,66	0
56	MG	1A	3070	1/1	0.90	0.29	60,60,60,60	0
56	MG	1A	3714	1/1	0.90	0.16	56,56,56,56	0
56	MG	1A	3395	1/1	0.90	0.13	58,58,58,58	0
56	MG	2A	3023	1/1	0.90	0.14	43,43,43,43	0
56	MG	2A	3024	1/1	0.90	0.23	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3536	1/1	0.90	0.08	24,24,24,24	0
56	MG	1A	3538	1/1	0.90	0.11	45,45,45,45	0
56	MG	2O	202	1/1	0.90	0.13	52,52,52,52	0
56	MG	1U	202	1/1	0.90	0.27	40,40,40,40	0
56	MG	2A	3054	1/1	0.90	0.14	50,50,50,50	0
56	MG	2T	3001	1/1	0.90	0.16	45,45,45,45	0
56	MG	2V	3002	1/1	0.90	0.40	57,57,57,57	0
56	MG	1U	204	1/1	0.90	0.25	55,55,55,55	0
56	MG	2a	1791	1/1	0.90	0.20	75,75,75,75	0
56	MG	2A	3060	1/1	0.90	0.10	49,49,49,49	0
56	MG	2A	3284	1/1	0.90	0.08	47,47,47,47	0
56	MG	1A	3396	1/1	0.90	0.12	42,42,42,42	0
56	MG	1W	3001	1/1	0.90	0.14	48,48,48,48	0
56	MG	2A	3520	1/1	0.90	0.24	56,56,56,56	0
56	MG	1A	3723	1/1	0.90	0.13	58,58,58,58	0
56	MG	1A	3633	1/1	0.90	0.12	50,50,50,50	0
56	MG	1A	3634	1/1	0.90	0.16	57,57,57,57	0
56	MG	1A	3268	1/1	0.90	0.19	63,63,63,63	0
56	MG	1A	3743	1/1	0.90	0.26	52,52,52,52	0
56	MG	15	101	1/1	0.90	0.12	48,48,48,48	0
56	MG	1A	3744	1/1	0.90	0.11	40,40,40,40	0
56	MG	1A	3639	1/1	0.90	0.18	61,61,61,61	0
56	MG	2A	3532	1/1	0.90	0.20	57,57,57,57	0
56	MG	16	102	1/1	0.90	0.07	41,41,41,41	0
56	MG	2A	3536	1/1	0.90	0.12	53,53,53,53	0
61	FME	2x	3003	10/11	0.90	0.20	43,53,58,59	10
56	MG	1A	3217	1/1	0.91	0.18	54,54,54,54	0
56	MG	1A	3820	1/1	0.91	0.13	52,52,52,52	0
56	MG	2V	3001	1/1	0.91	0.23	62,62,62,62	0
56	MG	2A	3189	1/1	0.91	0.22	54,54,54,54	0
56	MG	1A	3320	1/1	0.91	0.10	52,52,52,52	0
56	MG	1a	1798	1/1	0.91	0.22	67,67,67,67	0
56	MG	2A	3467	1/1	0.91	0.15	51,51,51,51	0
56	MG	20	102	1/1	0.91	0.20	61,61,61,61	0
56	MG	2A	3469	1/1	0.91	0.37	53,53,53,53	0
56	MG	1A	3058	1/1	0.91	0.16	53,53,53,53	0
56	MG	2A	3198	1/1	0.91	0.11	52,52,52,52	0
56	MG	1A	3547	1/1	0.91	0.25	55,55,55,55	0
56	MG	1A	3001	1/1	0.91	0.17	60,60,60,60	0
56	MG	1A	3327	1/1	0.91	0.09	49,49,49,49	0
56	MG	2A	3205	1/1	0.91	0.20	46,46,46,46	0
56	MG	2A	3484	1/1	0.91	0.07	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1606	1/1	0.91	0.08	60,60,60,60	0
56	MG	2a	1607	1/1	0.91	0.25	67,67,67,67	0
56	MG	1A	3828	1/1	0.91	0.14	43,43,43,43	0
56	MG	2A	3208	1/1	0.91	0.08	52,52,52,52	0
56	MG	1A	3556	1/1	0.91	0.16	62,62,62,62	0
56	MG	2A	3495	1/1	0.91	0.14	50,50,50,50	0
56	MG	2a	1614	1/1	0.91	0.34	58,58,58,58	0
56	MG	1A	3558	1/1	0.91	0.13	43,43,43,43	0
56	MG	1a	1608	1/1	0.91	0.19	56,56,56,56	0
56	MG	2A	3214	1/1	0.91	0.09	57,57,57,57	0
56	MG	1A	3690	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	3437	1/1	0.91	0.08	24,24,24,24	0
56	MG	1A	3264	1/1	0.91	0.08	53,53,53,53	0
56	MG	1A	3439	1/1	0.91	0.08	54,54,54,54	0
56	MG	1A	3567	1/1	0.91	0.12	48,48,48,48	0
56	MG	1A	3336	1/1	0.91	0.20	28,28,28,28	0
56	MG	2A	3224	1/1	0.91	0.11	49,49,49,49	0
56	MG	2A	3509	1/1	0.91	0.08	35,35,35,35	0
56	MG	2A	3226	1/1	0.91	0.10	60,60,60,60	0
56	MG	2a	1634	1/1	0.91	0.09	59,59,59,59	0
56	MG	1a	1619	1/1	0.91	0.11	71,71,71,71	0
56	MG	2A	3515	1/1	0.91	0.10	45,45,45,45	0
56	MG	1A	3092	1/1	0.91	0.11	49,49,49,49	0
56	MG	1a	1622	1/1	0.91	0.10	59,59,59,59	0
56	MG	1A	3844	1/1	0.91	0.10	54,54,54,54	0
56	MG	1A	3342	1/1	0.91	0.15	48,48,48,48	0
56	MG	1A	3457	1/1	0.91	0.10	35,35,35,35	0
56	MG	1A	3152	1/1	0.91	0.14	43,43,43,43	0
56	MG	1A	3234	1/1	0.91	0.18	50,50,50,50	0
56	MG	1a	1830	1/1	0.91	0.28	61,61,61,61	0
56	MG	1a	1637	1/1	0.91	0.09	44,44,44,44	0
56	MG	2a	1652	1/1	0.91	0.17	57,57,57,57	0
56	MG	1a	1640	1/1	0.91	0.07	47,47,47,47	0
56	MG	2a	1654	1/1	0.91	0.21	69,69,69,69	0
56	MG	1a	1641	1/1	0.91	0.08	49,49,49,49	0
56	MG	1b	3002	1/1	0.91	0.07	85,85,85,85	0
56	MG	2A	3535	1/1	0.91	0.08	55,55,55,55	0
56	MG	1A	3584	1/1	0.91	0.19	70,70,70,70	0
56	MG	2a	1659	1/1	0.91	0.09	55,55,55,55	0
56	MG	2A	3252	1/1	0.91	0.22	48,48,48,48	0
56	MG	1A	3853	1/1	0.91	0.10	37,37,37,37	0
56	MG	2A	3255	1/1	0.91	0.23	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3356	1/1	0.91	0.10	26,26,26,26	0
56	MG	1a	1651	1/1	0.91	0.29	56,56,56,56	0
56	MG	1A	3042	1/1	0.91	0.08	40,40,40,40	0
56	MG	1A	3359	1/1	0.91	0.11	22,22,22,22	0
56	MG	2A	3268	1/1	0.91	0.09	49,49,49,49	0
56	MG	1A	3722	1/1	0.91	0.10	46,46,46,46	0
56	MG	1x	107	1/1	0.91	0.13	75,75,75,75	0
56	MG	2A	3550	1/1	0.91	0.10	70,70,70,70	0
56	MG	1a	1657	1/1	0.91	0.11	50,50,50,50	0
56	MG	1A	3187	1/1	0.91	0.18	44,44,44,44	0
56	MG	1x	111	1/1	0.91	0.12	61,61,61,61	0
56	MG	1A	3475	1/1	0.91	0.14	42,42,42,42	0
56	MG	2A	3559	1/1	0.91	0.11	52,52,52,52	0
56	MG	1A	3605	1/1	0.91	0.16	45,45,45,45	0
56	MG	1a	1666	1/1	0.91	0.18	46,46,46,46	0
56	MG	1A	3361	1/1	0.91	0.16	55,55,55,55	0
56	MG	1A	3478	1/1	0.91	0.09	29,29,29,29	0
56	MG	1A	3868	1/1	0.91	0.11	37,37,37,37	0
56	MG	1A	3611	1/1	0.91	0.12	22,22,22,22	0
56	MG	1A	3482	1/1	0.91	0.09	35,35,35,35	0
56	MG	2A	3576	1/1	0.91	0.12	42,42,42,42	0
56	MG	2A	3005	1/1	0.91	0.14	50,50,50,50	0
56	MG	2A	3006	1/1	0.91	0.17	58,58,58,58	0
56	MG	2A	3583	1/1	0.91	0.13	70,70,70,70	0
56	MG	2A	3015	1/1	0.91	0.10	62,62,62,62	0
56	MG	1A	3614	1/1	0.91	0.12	23,23,23,23	0
56	MG	1A	3749	1/1	0.91	0.13	39,39,39,39	0
56	MG	1A	3483	1/1	0.91	0.12	27,27,27,27	0
56	MG	2A	3306	1/1	0.91	0.08	30,30,30,30	0
56	MG	2A	3031	1/1	0.91	0.14	50,50,50,50	0
56	MG	1A	3363	1/1	0.91	0.14	49,49,49,49	0
56	MG	2A	3310	1/1	0.91	0.11	36,36,36,36	0
56	MG	2A	3035	1/1	0.91	0.11	45,45,45,45	0
56	MG	2A	3036	1/1	0.91	0.12	50,50,50,50	0
56	MG	2a	1714	1/1	0.91	0.15	56,56,56,56	0
56	MG	2A	3604	1/1	0.91	0.07	44,44,44,44	0
56	MG	2a	1717	1/1	0.91	0.15	63,63,63,63	0
56	MG	2A	3320	1/1	0.91	0.18	51,51,51,51	0
56	MG	2a	1721	1/1	0.91	0.15	54,54,54,54	0
56	MG	1A	3063	1/1	0.91	0.10	52,52,52,52	0
56	MG	1a	1689	1/1	0.91	0.14	39,39,39,39	0
56	MG	1A	3898	1/1	0.91	0.25	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3057	1/1	0.91	0.21	54,54,54,54	0
56	MG	1A	3192	1/1	0.91	0.17	42,42,42,42	0
56	MG	1A	3385	1/1	0.91	0.09	68,68,68,68	0
56	MG	1a	1700	1/1	0.91	0.19	57,57,57,57	0
56	MG	1A	3913	1/1	0.91	0.20	54,54,54,54	0
56	MG	1A	3624	1/1	0.91	0.07	32,32,32,32	0
56	MG	1A	3102	1/1	0.91	0.29	58,58,58,58	0
56	MG	1A	3284	1/1	0.91	0.23	54,54,54,54	0
56	MG	2a	1736	1/1	0.91	0.18	66,66,66,66	0
56	MG	1A	3045	1/1	0.91	0.19	46,46,46,46	0
56	MG	2A	3075	1/1	0.91	0.11	47,47,47,47	0
56	MG	1B	207	1/1	0.91	0.12	44,44,44,44	0
56	MG	1A	3766	1/1	0.91	0.08	31,31,31,31	0
56	MG	1A	3116	1/1	0.91	0.17	51,51,51,51	0
56	MG	2A	3084	1/1	0.91	0.16	59,59,59,59	0
56	MG	2A	3627	1/1	0.91	0.12	49,49,49,49	0
56	MG	2A	3628	1/1	0.91	0.18	49,49,49,49	0
56	MG	2A	3630	1/1	0.91	0.14	56,56,56,56	0
56	MG	1B	214	1/1	0.91	0.11	41,41,41,41	0
56	MG	1A	3291	1/1	0.91	0.12	52,52,52,52	0
56	MG	1A	3770	1/1	0.91	0.20	63,63,63,63	0
56	MG	1A	3244	1/1	0.91	0.12	52,52,52,52	0
56	MG	1A	3029	1/1	0.91	0.34	40,40,40,40	0
56	MG	1A	3503	1/1	0.91	0.19	57,57,57,57	0
56	MG	1D	305	1/1	0.91	0.09	38,38,38,38	0
56	MG	1D	308	1/1	0.91	0.20	51,51,51,51	0
56	MG	1A	3510	1/1	0.91	0.17	52,52,52,52	0
56	MG	2A	3390	1/1	0.91	0.09	51,51,51,51	0
56	MG	1A	3777	1/1	0.91	0.08	43,43,43,43	0
56	MG	1A	3248	1/1	0.91	0.15	63,63,63,63	0
56	MG	2a	1764	1/1	0.91	0.16	67,67,67,67	0
56	MG	1G	3005	1/1	0.91	0.09	40,40,40,40	0
56	MG	1A	3779	1/1	0.91	0.19	70,70,70,70	0
56	MG	1a	1746	1/1	0.91	0.09	52,52,52,52	0
56	MG	1A	3647	1/1	0.91	0.12	59,59,59,59	0
56	MG	2A	3663	1/1	0.91	0.11	53,53,53,53	0
56	MG	1A	3404	1/1	0.91	0.14	52,52,52,52	0
56	MG	1A	3518	1/1	0.91	0.14	57,57,57,57	0
56	MG	2A	3668	1/1	0.91	0.17	44,44,44,44	0
56	MG	2A	3409	1/1	0.91	0.17	46,46,46,46	0
56	MG	2A	3410	1/1	0.91	0.10	56,56,56,56	0
56	MG	1A	3789	1/1	0.91	0.24	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3167	1/1	0.91	0.26	50,50,50,50	0
56	MG	2A	3129	1/1	0.91	0.12	47,47,47,47	0
56	MG	2a	1785	1/1	0.91	0.18	58,58,58,58	0
56	MG	1A	3411	1/1	0.91	0.08	37,37,37,37	0
56	MG	2A	3134	1/1	0.91	0.20	54,54,54,54	0
56	MG	1A	3793	1/1	0.91	0.10	38,38,38,38	0
56	MG	1A	3658	1/1	0.91	0.18	52,52,52,52	0
56	MG	1a	1765	1/1	0.91	0.15	51,51,51,51	0
56	MG	2A	3424	1/1	0.91	0.11	54,54,54,54	0
56	MG	2a	1792	1/1	0.91	0.11	76,76,76,76	0
56	MG	1A	3659	1/1	0.91	0.09	41,41,41,41	0
56	MG	1A	3527	1/1	0.91	0.12	69,69,69,69	0
56	MG	1A	3169	1/1	0.91	0.13	60,60,60,60	0
56	MG	2a	1796	1/1	0.91	0.22	64,64,64,64	0
56	MG	2B	3015	1/1	0.91	0.14	53,53,53,53	0
56	MG	1A	3309	1/1	0.91	0.30	66,66,66,66	0
56	MG	2A	3152	1/1	0.91	0.19	50,50,50,50	0
56	MG	1A	3415	1/1	0.91	0.09	53,53,53,53	0
56	MG	2A	3435	1/1	0.91	0.11	45,45,45,45	0
56	MG	2A	3158	1/1	0.91	0.08	47,47,47,47	0
56	MG	1X	103	1/1	0.91	0.10	40,40,40,40	0
56	MG	1A	3123	1/1	0.91	0.15	42,42,42,42	0
56	MG	10	102	1/1	0.91	0.09	47,47,47,47	0
56	MG	2A	3173	1/1	0.91	0.33	60,60,60,60	0
56	MG	1A	3671	1/1	0.91	0.19	40,40,40,40	0
56	MG	1A	3254	1/1	0.91	0.18	54,54,54,54	0
56	MG	2Q	3001	1/1	0.91	0.11	47,47,47,47	0
59	ZN	24	501	1/1	0.91	0.09	185,185,185,185	0
61	FME	1x	115	10/11	0.91	0.21	38,46,53,57	10
56	MG	2A	3180	1/1	0.91	0.18	54,54,54,54	0
56	MG	1A	3285	1/1	0.92	0.15	57,57,57,57	0
56	MG	1A	3846	1/1	0.92	0.08	39,39,39,39	0
56	MG	1a	1607	1/1	0.92	0.27	52,52,52,52	0
56	MG	1A	3351	1/1	0.92	0.20	55,55,55,55	0
56	MG	1A	3355	1/1	0.92	0.19	51,51,51,51	0
56	MG	1a	1808	1/1	0.92	0.06	40,40,40,40	0
56	MG	1A	3850	1/1	0.92	0.10	54,54,54,54	0
56	MG	2A	3206	1/1	0.92	0.20	48,48,48,48	0
56	MG	2A	3475	1/1	0.92	0.08	53,53,53,53	0
56	MG	21	101	1/1	0.92	0.11	43,43,43,43	0
56	MG	2A	3476	1/1	0.92	0.14	41,41,41,41	0
56	MG	2A	3478	1/1	0.92	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1612	1/1	0.92	0.07	56,56,56,56	0
56	MG	1A	3625	1/1	0.92	0.18	55,55,55,55	0
56	MG	1A	3728	1/1	0.92	0.14	40,40,40,40	0
56	MG	2A	3483	1/1	0.92	0.09	56,56,56,56	0
56	MG	1A	3732	1/1	0.92	0.10	55,55,55,55	0
56	MG	2A	3212	1/1	0.92	0.09	66,66,66,66	0
56	MG	1A	3251	1/1	0.92	0.10	47,47,47,47	0
56	MG	2A	3489	1/1	0.92	0.16	73,73,73,73	0
56	MG	2a	1610	1/1	0.92	0.32	53,53,53,53	0
56	MG	1A	3736	1/1	0.92	0.19	49,49,49,49	0
56	MG	1A	3232	1/1	0.92	0.10	55,55,55,55	0
56	MG	1A	3150	1/1	0.92	0.32	55,55,55,55	0
56	MG	1a	1821	1/1	0.92	0.18	65,65,65,65	0
56	MG	1a	1623	1/1	0.92	0.16	54,54,54,54	0
56	MG	1A	3632	1/1	0.92	0.26	40,40,40,40	0
56	MG	1A	3118	1/1	0.92	0.16	50,50,50,50	0
56	MG	1a	1825	1/1	0.92	0.12	66,66,66,66	0
56	MG	1A	3046	1/1	0.92	0.19	28,28,28,28	0
56	MG	1A	3086	1/1	0.92	0.31	51,51,51,51	0
56	MG	1A	3178	1/1	0.92	0.18	38,38,38,38	0
56	MG	2A	3232	1/1	0.92	0.17	51,51,51,51	0
56	MG	1A	3866	1/1	0.92	0.19	63,63,63,63	0
56	MG	2A	3510	1/1	0.92	0.17	46,46,46,46	0
56	MG	1A	3546	1/1	0.92	0.13	46,46,46,46	0
56	MG	2A	3512	1/1	0.92	0.10	45,45,45,45	0
56	MG	1A	3371	1/1	0.92	0.12	49,49,49,49	0
56	MG	1A	3643	1/1	0.92	0.10	55,55,55,55	0
56	MG	1A	3301	1/1	0.92	0.12	45,45,45,45	0
56	MG	1A	3877	1/1	0.92	0.28	58,58,58,58	0
56	MG	1A	3878	1/1	0.92	0.11	43,43,43,43	0
56	MG	1l	202	1/1	0.92	0.19	50,50,50,50	0
56	MG	1A	3265	1/1	0.92	0.09	41,41,41,41	0
56	MG	1a	1653	1/1	0.92	0.22	50,50,50,50	0
56	MG	1a	1654	1/1	0.92	0.20	46,46,46,46	0
56	MG	1w	3003	1/1	0.92	0.21	50,50,50,50	0
56	MG	1A	3648	1/1	0.92	0.19	69,69,69,69	0
56	MG	1A	3888	1/1	0.92	0.11	46,46,46,46	0
56	MG	1A	3890	1/1	0.92	0.09	42,42,42,42	0
56	MG	1x	104	1/1	0.92	0.22	50,50,50,50	0
56	MG	1A	3305	1/1	0.92	0.19	55,55,55,55	0
56	MG	1A	3306	1/1	0.92	0.22	62,62,62,62	0
56	MG	1a	1664	1/1	0.92	0.28	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3390	1/1	0.92	0.16	64,64,64,64	0
56	MG	1A	3900	1/1	0.92	0.23	35,35,35,35	0
56	MG	1A	3654	1/1	0.92	0.10	27,27,27,27	0
56	MG	1x	114	1/1	0.92	0.07	57,57,57,57	0
56	MG	1A	3655	1/1	0.92	0.08	28,28,28,28	0
56	MG	2A	3280	1/1	0.92	0.09	25,25,25,25	0
56	MG	1a	1669	1/1	0.92	0.15	49,49,49,49	0
56	MG	2A	3283	1/1	0.92	0.13	50,50,50,50	0
56	MG	1A	3910	1/1	0.92	0.18	38,38,38,38	0
56	MG	1a	1672	1/1	0.92	0.19	55,55,55,55	0
56	MG	1a	1673	1/1	0.92	0.29	52,52,52,52	0
56	MG	1A	3561	1/1	0.92	0.13	43,43,43,43	0
56	MG	1A	3267	1/1	0.92	0.24	63,63,63,63	0
56	MG	1A	3049	1/1	0.92	0.19	42,42,42,42	0
56	MG	1a	1683	1/1	0.92	0.07	64,64,64,64	0
56	MG	2A	3017	1/1	0.92	0.16	42,42,42,42	0
56	MG	2A	3019	1/1	0.92	0.18	47,47,47,47	0
56	MG	2A	3566	1/1	0.92	0.11	41,41,41,41	0
56	MG	1A	3480	1/1	0.92	0.11	36,36,36,36	0
56	MG	1a	1685	1/1	0.92	0.29	57,57,57,57	0
56	MG	1B	201	1/1	0.92	0.11	53,53,53,53	0
56	MG	1A	3311	1/1	0.92	0.12	54,54,54,54	0
56	MG	1A	3663	1/1	0.92	0.14	43,43,43,43	0
56	MG	1A	3665	1/1	0.92	0.21	59,59,59,59	0
56	MG	1A	3313	1/1	0.92	0.09	56,56,56,56	0
56	MG	2A	3044	1/1	0.92	0.19	46,46,46,46	0
56	MG	1A	3573	1/1	0.92	0.11	43,43,43,43	0
56	MG	2A	3585	1/1	0.92	0.16	64,64,64,64	0
56	MG	1a	1698	1/1	0.92	0.43	72,72,72,72	0
56	MG	2a	1694	1/1	0.92	0.19	62,62,62,62	0
56	MG	2a	1696	1/1	0.92	0.14	66,66,66,66	0
56	MG	1A	3669	1/1	0.92	0.11	58,58,58,58	0
56	MG	2A	3317	1/1	0.92	0.11	48,48,48,48	0
56	MG	1A	3089	1/1	0.92	0.18	54,54,54,54	0
56	MG	2A	3592	1/1	0.92	0.07	54,54,54,54	0
56	MG	1B	219	1/1	0.92	0.12	49,49,49,49	0
56	MG	1A	3013	1/1	0.92	0.11	33,33,33,33	0
56	MG	2A	3062	1/1	0.92	0.07	41,41,41,41	0
56	MG	2A	3598	1/1	0.92	0.16	52,52,52,52	0
56	MG	1B	221	1/1	0.92	0.08	48,48,48,48	0
56	MG	1A	3579	1/1	0.92	0.15	27,27,27,27	0
56	MG	2A	3601	1/1	0.92	0.10	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1712	1/1	0.92	0.10	58,58,58,58	0
56	MG	1A	3673	1/1	0.92	0.10	45,45,45,45	0
56	MG	1B	224	1/1	0.92	0.14	63,63,63,63	0
56	MG	2A	3069	1/1	0.92	0.11	52,52,52,52	0
56	MG	2a	1718	1/1	0.92	0.12	71,71,71,71	0
56	MG	2A	3606	1/1	0.92	0.22	40,40,40,40	0
56	MG	1a	1710	1/1	0.92	0.26	51,51,51,51	0
56	MG	1A	3486	1/1	0.92	0.15	27,27,27,27	0
56	MG	1a	1712	1/1	0.92	0.08	61,61,61,61	0
56	MG	2A	3611	1/1	0.92	0.13	57,57,57,57	0
56	MG	2A	3345	1/1	0.92	0.07	45,45,45,45	0
56	MG	2A	3346	1/1	0.92	0.07	31,31,31,31	0
56	MG	1a	1715	1/1	0.92	0.26	62,62,62,62	0
56	MG	1A	3319	1/1	0.92	0.10	51,51,51,51	0
56	MG	2a	1730	1/1	0.92	0.16	56,56,56,56	0
56	MG	2A	3079	1/1	0.92	0.12	42,42,42,42	0
56	MG	1a	1717	1/1	0.92	0.12	60,60,60,60	0
56	MG	1A	3405	1/1	0.92	0.12	62,62,62,62	0
56	MG	2A	3361	1/1	0.92	0.09	54,54,54,54	0
56	MG	1E	307	1/1	0.92	0.22	36,36,36,36	0
56	MG	1A	3678	1/1	0.92	0.08	46,46,46,46	0
56	MG	2a	1738	1/1	0.92	0.37	70,70,70,70	0
56	MG	1A	3587	1/1	0.92	0.09	40,40,40,40	0
56	MG	1a	1724	1/1	0.92	0.17	46,46,46,46	0
56	MG	1A	3681	1/1	0.92	0.09	37,37,37,37	0
56	MG	2A	3372	1/1	0.92	0.12	54,54,54,54	0
56	MG	1A	3803	1/1	0.92	0.10	65,65,65,65	0
56	MG	1A	3682	1/1	0.92	0.16	47,47,47,47	0
56	MG	2A	3101	1/1	0.92	0.16	58,58,58,58	0
56	MG	2A	3382	1/1	0.92	0.15	40,40,40,40	0
56	MG	1N	3002	1/1	0.92	0.20	45,45,45,45	0
56	MG	1A	3685	1/1	0.92	0.09	49,49,49,49	0
56	MG	2A	3635	1/1	0.92	0.12	54,54,54,54	0
56	MG	2A	3638	1/1	0.92	0.13	53,53,53,53	0
56	MG	2A	3389	1/1	0.92	0.08	39,39,39,39	0
56	MG	1a	1732	1/1	0.92	0.19	60,60,60,60	0
56	MG	2A	3394	1/1	0.92	0.16	56,56,56,56	0
56	MG	2A	3395	1/1	0.92	0.13	53,53,53,53	0
56	MG	1A	3806	1/1	0.92	0.14	67,67,67,67	0
56	MG	2A	3399	1/1	0.92	0.16	58,58,58,58	0
56	MG	1A	3409	1/1	0.92	0.12	33,33,33,33	0
56	MG	1A	3219	1/1	0.92	0.08	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3226	1/1	0.92	0.30	57,57,57,57	0
56	MG	1Q	3004	1/1	0.92	0.10	56,56,56,56	0
56	MG	2A	3404	1/1	0.92	0.10	39,39,39,39	0
56	MG	1A	3144	1/1	0.92	0.18	51,51,51,51	0
56	MG	2A	3658	1/1	0.92	0.10	44,44,44,44	0
56	MG	1A	3277	1/1	0.92	0.12	49,49,49,49	0
56	MG	2a	1773	1/1	0.92	0.13	57,57,57,57	0
56	MG	1a	1751	1/1	0.92	0.09	65,65,65,65	0
56	MG	1A	3821	1/1	0.92	0.19	60,60,60,60	0
56	MG	1T	201	1/1	0.92	0.17	62,62,62,62	0
56	MG	2A	3667	1/1	0.92	0.12	64,64,64,64	0
56	MG	1A	3334	1/1	0.92	0.21	49,49,49,49	0
56	MG	2A	3412	1/1	0.92	0.07	27,27,27,27	0
56	MG	1A	3693	1/1	0.92	0.09	62,62,62,62	0
56	MG	2A	3136	1/1	0.92	0.20	53,53,53,53	0
56	MG	1V	202	1/1	0.92	0.27	59,59,59,59	0
56	MG	1A	3278	1/1	0.92	0.32	61,61,61,61	0
56	MG	2A	3144	1/1	0.92	0.09	49,49,49,49	0
56	MG	1A	3697	1/1	0.92	0.31	64,64,64,64	0
56	MG	1A	3281	1/1	0.92	0.21	52,52,52,52	0
56	MG	1A	3508	1/1	0.92	0.09	41,41,41,41	0
56	MG	1A	3422	1/1	0.92	0.14	45,45,45,45	0
56	MG	1a	1772	1/1	0.92	0.11	50,50,50,50	0
56	MG	1A	3613	1/1	0.92	0.11	34,34,34,34	0
56	MG	1a	1775	1/1	0.92	0.24	58,58,58,58	0
56	MG	1A	3833	1/1	0.92	0.15	66,66,66,66	0
56	MG	2A	3430	1/1	0.92	0.14	58,58,58,58	0
56	MG	2B	3016	1/1	0.92	0.23	61,61,61,61	0
56	MG	2a	1798	1/1	0.92	0.09	43,43,43,43	0
56	MG	1A	3149	1/1	0.92	0.23	50,50,50,50	0
56	MG	2A	3164	1/1	0.92	0.21	40,40,40,40	0
56	MG	2B	3019	1/1	0.92	0.22	44,44,44,44	0
56	MG	1l	101	1/1	0.92	0.16	44,44,44,44	0
56	MG	1A	3711	1/1	0.92	0.09	54,54,54,54	0
56	MG	1A	3168	1/1	0.92	0.14	44,44,44,44	0
56	MG	2p	3001	1/1	0.92	0.22	74,74,74,74	0
56	MG	2E	302	1/1	0.92	0.16	51,51,51,51	0
56	MG	1A	3231	1/1	0.92	0.36	61,61,61,61	0
56	MG	1A	3619	1/1	0.92	0.20	44,44,44,44	0
56	MG	1A	3431	1/1	0.92	0.11	34,34,34,34	0
56	MG	1a	1795	1/1	0.92	0.20	50,50,50,50	0
56	MG	1A	3716	1/1	0.92	0.14	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	4M2	2A	3670	57/57	0.92	0.13	26,50,69,76	0
56	MG	1a	1601	1/1	0.92	0.11	68,68,68,68	0
59	ZN	2n	501	1/1	0.92	0.12	152,152,152,152	0
56	MG	2A	3456	1/1	0.92	0.10	42,42,42,42	0
56	MG	1A	3621	1/1	0.92	0.10	56,56,56,56	0
56	MG	1A	3785	1/1	0.93	0.12	65,65,65,65	0
56	MG	2a	1620	1/1	0.93	0.24	55,55,55,55	0
56	MG	13	101	1/1	0.93	0.14	46,46,46,46	0
56	MG	1A	3874	1/1	0.93	0.15	27,27,27,27	0
56	MG	1t	3001	1/1	0.93	0.22	49,49,49,49	0
56	MG	2A	3563	1/1	0.93	0.10	62,62,62,62	0
56	MG	2A	3370	1/1	0.93	0.10	44,44,44,44	0
56	MG	1a	1714	1/1	0.93	0.35	61,61,61,61	0
56	MG	1A	3225	1/1	0.93	0.07	36,36,36,36	0
56	MG	1A	3084	1/1	0.93	0.16	60,60,60,60	0
56	MG	1A	3364	1/1	0.93	0.10	35,35,35,35	0
56	MG	1A	3702	1/1	0.93	0.12	26,26,26,26	0
56	MG	1A	3703	1/1	0.93	0.21	60,60,60,60	0
56	MG	2A	3183	1/1	0.93	0.09	29,29,29,29	0
56	MG	1A	3419	1/1	0.93	0.09	53,53,53,53	0
56	MG	2A	3580	1/1	0.93	0.10	50,50,50,50	0
56	MG	2a	1640	1/1	0.93	0.16	48,48,48,48	0
56	MG	1x	105	1/1	0.93	0.17	57,57,57,57	0
56	MG	1A	3642	1/1	0.93	0.09	42,42,42,42	0
56	MG	2A	3392	1/1	0.93	0.14	51,51,51,51	0
56	MG	2a	1647	1/1	0.93	0.16	68,68,68,68	0
56	MG	1A	3709	1/1	0.93	0.15	50,50,50,50	0
56	MG	1a	1606	1/1	0.93	0.27	57,57,57,57	0
56	MG	2A	3588	1/1	0.93	0.13	55,55,55,55	0
56	MG	2A	3589	1/1	0.93	0.09	49,49,49,49	0
56	MG	1A	3798	1/1	0.93	0.10	27,27,27,27	0
56	MG	2A	3398	1/1	0.93	0.12	45,45,45,45	0
56	MG	1A	3318	1/1	0.93	0.28	60,60,60,60	0
56	MG	1A	3801	1/1	0.93	0.09	43,43,43,43	0
56	MG	2A	3595	1/1	0.93	0.12	47,47,47,47	0
56	MG	1A	3048	1/1	0.93	0.16	32,32,32,32	0
56	MG	2A	3201	1/1	0.93	0.12	42,42,42,42	0
56	MG	2a	1660	1/1	0.93	0.22	52,52,52,52	0
56	MG	2A	3203	1/1	0.93	0.27	42,42,42,42	0
56	MG	1A	3373	1/1	0.93	0.07	29,29,29,29	0
56	MG	1a	1735	1/1	0.93	0.10	66,66,66,66	0
56	MG	1a	1613	1/1	0.93	0.31	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3424	1/1	0.93	0.14	51,51,51,51	0
56	MG	1A	3376	1/1	0.93	0.23	51,51,51,51	0
56	MG	1A	3426	1/1	0.93	0.14	53,53,53,53	0
56	MG	2A	3001	1/1	0.93	0.13	63,63,63,63	0
56	MG	2A	3003	1/1	0.93	0.15	31,31,31,31	0
56	MG	1A	3807	1/1	0.93	0.09	63,63,63,63	0
56	MG	1A	3578	1/1	0.93	0.07	56,56,56,56	0
56	MG	2a	1676	1/1	0.93	0.12	58,58,58,58	0
56	MG	2A	3215	1/1	0.93	0.17	53,53,53,53	0
56	MG	2A	3009	1/1	0.93	0.17	45,45,45,45	0
56	MG	1A	3653	1/1	0.93	0.07	31,31,31,31	0
56	MG	1A	3428	1/1	0.93	0.14	39,39,39,39	0
56	MG	1A	3143	1/1	0.93	0.29	48,48,48,48	0
56	MG	1B	212	1/1	0.93	0.15	50,50,50,50	0
56	MG	1A	3817	1/1	0.93	0.12	54,54,54,54	0
56	MG	1a	1757	1/1	0.93	0.13	57,57,57,57	0
56	MG	2A	3026	1/1	0.93	0.28	41,41,41,41	0
56	MG	1A	3430	1/1	0.93	0.09	47,47,47,47	0
56	MG	1A	3725	1/1	0.93	0.10	49,49,49,49	0
56	MG	2A	3034	1/1	0.93	0.07	34,34,34,34	0
56	MG	2A	3431	1/1	0.93	0.09	54,54,54,54	0
56	MG	1B	217	1/1	0.93	0.09	56,56,56,56	0
56	MG	1A	3726	1/1	0.93	0.08	38,38,38,38	0
56	MG	1A	3501	1/1	0.93	0.15	62,62,62,62	0
56	MG	1A	3730	1/1	0.93	0.10	58,58,58,58	0
56	MG	2A	3443	1/1	0.93	0.07	45,45,45,45	0
56	MG	2A	3048	1/1	0.93	0.11	46,46,46,46	0
56	MG	1A	3381	1/1	0.93	0.08	47,47,47,47	0
56	MG	2A	3240	1/1	0.93	0.16	45,45,45,45	0
56	MG	2A	3051	1/1	0.93	0.11	53,53,53,53	0
56	MG	2A	3637	1/1	0.93	0.12	58,58,58,58	0
56	MG	1A	3733	1/1	0.93	0.17	48,48,48,48	0
56	MG	2A	3055	1/1	0.93	0.13	47,47,47,47	0
56	MG	2A	3640	1/1	0.93	0.12	40,40,40,40	0
56	MG	1A	3660	1/1	0.93	0.09	54,54,54,54	0
56	MG	1a	1650	1/1	0.93	0.31	57,57,57,57	0
56	MG	2A	3457	1/1	0.93	0.08	45,45,45,45	0
56	MG	2A	3250	1/1	0.93	0.12	52,52,52,52	0
56	MG	1a	1778	1/1	0.93	0.12	65,65,65,65	0
56	MG	2A	3061	1/1	0.93	0.10	56,56,56,56	0
56	MG	1A	3016	1/1	0.93	0.08	39,39,39,39	0
56	MG	2A	3649	1/1	0.93	0.07	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3254	1/1	0.93	0.13	36,36,36,36	0
56	MG	1A	3507	1/1	0.93	0.14	60,60,60,60	0
56	MG	1a	1782	1/1	0.93	0.12	60,60,60,60	0
56	MG	2A	3655	1/1	0.93	0.08	41,41,41,41	0
56	MG	1A	3113	1/1	0.93	0.25	47,47,47,47	0
56	MG	2A	3472	1/1	0.93	0.08	47,47,47,47	0
56	MG	2A	3659	1/1	0.93	0.10	31,31,31,31	0
56	MG	2A	3473	1/1	0.93	0.08	47,47,47,47	0
56	MG	2A	3662	1/1	0.93	0.20	37,37,37,37	0
56	MG	1a	1786	1/1	0.93	0.11	55,55,55,55	0
56	MG	2A	3068	1/1	0.93	0.09	47,47,47,47	0
56	MG	2A	3264	1/1	0.93	0.22	52,52,52,52	0
56	MG	2A	3477	1/1	0.93	0.18	52,52,52,52	0
56	MG	2A	3266	1/1	0.93	0.08	53,53,53,53	0
56	MG	2A	3671	1/1	0.93	0.12	52,52,52,52	0
56	MG	1E	301	1/1	0.93	0.24	43,43,43,43	0
56	MG	1A	3598	1/1	0.93	0.20	61,61,61,61	0
56	MG	2A	3677	1/1	0.93	0.42	49,49,49,49	0
56	MG	1A	3195	1/1	0.93	0.23	46,46,46,46	0
56	MG	2A	3680	1/1	0.93	0.13	57,57,57,57	0
56	MG	1E	308	1/1	0.93	0.08	49,49,49,49	0
56	MG	2B	3001	1/1	0.93	0.15	59,59,59,59	0
56	MG	1A	3512	1/1	0.93	0.13	66,66,66,66	0
56	MG	1a	1793	1/1	0.93	0.12	74,74,74,74	0
56	MG	1A	3668	1/1	0.93	0.18	45,45,45,45	0
56	MG	2A	3488	1/1	0.93	0.09	50,50,50,50	0
56	MG	1G	3001	1/1	0.93	0.25	59,59,59,59	0
56	MG	2A	3083	1/1	0.93	0.22	41,41,41,41	0
56	MG	1a	1797	1/1	0.93	0.15	51,51,51,51	0
56	MG	2A	3496	1/1	0.93	0.10	54,54,54,54	0
56	MG	2a	1755	1/1	0.93	0.19	67,67,67,67	0
56	MG	1A	3003	1/1	0.93	0.12	32,32,32,32	0
56	MG	2B	3013	1/1	0.93	0.06	54,54,54,54	0
56	MG	2A	3287	1/1	0.93	0.06	29,29,29,29	0
56	MG	1A	3393	1/1	0.93	0.10	52,52,52,52	0
56	MG	1A	3197	1/1	0.93	0.10	44,44,44,44	0
56	MG	2A	3291	1/1	0.93	0.07	28,28,28,28	0
56	MG	2A	3089	1/1	0.93	0.18	58,58,58,58	0
56	MG	2a	1766	1/1	0.93	0.08	48,48,48,48	0
56	MG	2A	3093	1/1	0.93	0.19	55,55,55,55	0
56	MG	1A	3198	1/1	0.93	0.11	43,43,43,43	0
56	MG	1N	3006	1/1	0.93	0.09	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3444	1/1	0.93	0.12	26,26,26,26	0
56	MG	2D	304	1/1	0.93	0.20	38,38,38,38	0
56	MG	1A	3171	1/1	0.93	0.23	56,56,56,56	0
56	MG	2A	3300	1/1	0.93	0.17	45,45,45,45	0
56	MG	2E	305	1/1	0.93	0.11	39,39,39,39	0
56	MG	1A	3758	1/1	0.93	0.08	33,33,33,33	0
56	MG	2A	3102	1/1	0.93	0.29	60,60,60,60	0
56	MG	1a	1675	1/1	0.93	0.07	41,41,41,41	0
56	MG	1A	3531	1/1	0.93	0.12	61,61,61,61	0
56	MG	2O	201	1/1	0.93	0.09	54,54,54,54	0
56	MG	1a	1678	1/1	0.93	0.12	54,54,54,54	0
56	MG	2A	3518	1/1	0.93	0.17	57,57,57,57	0
56	MG	2A	3308	1/1	0.93	0.09	38,38,38,38	0
56	MG	1A	3455	1/1	0.93	0.09	25,25,25,25	0
56	MG	1A	3172	1/1	0.93	0.19	41,41,41,41	0
56	MG	2U	202	1/1	0.93	0.09	44,44,44,44	0
56	MG	1A	3458	1/1	0.93	0.09	26,26,26,26	0
56	MG	1a	1817	1/1	0.93	0.15	64,64,64,64	0
56	MG	1R	201	1/1	0.93	0.11	45,45,45,45	0
56	MG	1A	3212	1/1	0.93	0.12	41,41,41,41	0
56	MG	2A	3119	1/1	0.93	0.10	54,54,54,54	0
56	MG	1A	3069	1/1	0.93	0.24	52,52,52,52	0
56	MG	1A	3214	1/1	0.93	0.11	54,54,54,54	0
56	MG	1T	202	1/1	0.93	0.11	43,43,43,43	0
56	MG	23	101	1/1	0.93	0.19	62,62,62,62	0
56	MG	2A	3534	1/1	0.93	0.10	58,58,58,58	0
56	MG	1A	3465	1/1	0.93	0.11	35,35,35,35	0
56	MG	1A	3858	1/1	0.93	0.14	45,45,45,45	0
56	MG	1A	3544	1/1	0.93	0.23	35,35,35,35	0
56	MG	1A	3055	1/1	0.93	0.15	45,45,45,45	0
56	MG	1A	3407	1/1	0.93	0.07	38,38,38,38	0
56	MG	2I	201	1/1	0.93	0.13	77,77,77,77	0
56	MG	1A	3095	1/1	0.93	0.25	56,56,56,56	0
56	MG	2q	202	1/1	0.93	0.12	80,80,80,80	0
56	MG	2q	203	1/1	0.93	0.08	59,59,59,59	0
56	MG	2A	3141	1/1	0.93	0.17	49,49,49,49	0
56	MG	2A	3143	1/1	0.93	0.19	56,56,56,56	0
56	MG	1A	3124	1/1	0.93	0.12	46,46,46,46	0
56	MG	1A	3007	1/1	0.93	0.12	29,29,29,29	0
56	MG	1a	1832	1/1	0.93	0.29	57,57,57,57	0
56	MG	1A	3279	1/1	0.93	0.28	57,57,57,57	0
56	MG	2A	3548	1/1	0.93	0.09	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3780	1/1	0.93	0.11	62,62,62,62	0
56	MG	1A	3413	1/1	0.93	0.11	62,62,62,62	0
56	MG	1A	3784	1/1	0.93	0.10	45,45,45,45	0
56	MG	2A	3554	1/1	0.93	0.09	44,44,44,44	0
56	MG	2A	3573	1/1	0.94	0.07	52,52,52,52	0
56	MG	1x	106	1/1	0.94	0.15	59,59,59,59	0
56	MG	19	503	1/1	0.94	0.07	37,37,37,37	0
56	MG	2A	3376	1/1	0.94	0.10	41,41,41,41	0
56	MG	2a	1631	1/1	0.94	0.12	65,65,65,65	0
56	MG	2a	1632	1/1	0.94	0.24	63,63,63,63	0
56	MG	1x	108	1/1	0.94	0.10	55,55,55,55	0
56	MG	1A	3344	1/1	0.94	0.13	40,40,40,40	0
56	MG	2A	3179	1/1	0.94	0.23	56,56,56,56	0
56	MG	1A	3133	1/1	0.94	0.17	52,52,52,52	0
56	MG	1A	3103	1/1	0.94	0.09	44,44,44,44	0
56	MG	1A	3138	1/1	0.94	0.25	36,36,36,36	0
56	MG	1A	3926	1/1	0.94	0.11	44,44,44,44	0
56	MG	2A	3393	1/1	0.94	0.07	51,51,51,51	0
56	MG	1A	3354	1/1	0.94	0.10	42,42,42,42	0
56	MG	1a	1729	1/1	0.94	0.23	67,67,67,67	0
56	MG	2a	1644	1/1	0.94	0.10	61,61,61,61	0
56	MG	2A	3191	1/1	0.94	0.12	52,52,52,52	0
56	MG	1a	1730	1/1	0.94	0.12	63,63,63,63	0
56	MG	1A	3140	1/1	0.94	0.22	47,47,47,47	0
56	MG	1a	1609	1/1	0.94	0.17	56,56,56,56	0
56	MG	1a	1733	1/1	0.94	0.15	51,51,51,51	0
56	MG	1A	3253	1/1	0.94	0.13	33,33,33,33	0
56	MG	1A	3569	1/1	0.94	0.08	38,38,38,38	0
56	MG	1a	1737	1/1	0.94	0.11	51,51,51,51	0
56	MG	2A	3004	1/1	0.94	0.19	50,50,50,50	0
56	MG	1B	203	1/1	0.94	0.07	33,33,33,33	0
56	MG	1B	205	1/1	0.94	0.14	43,43,43,43	0
56	MG	1A	3650	1/1	0.94	0.10	38,38,38,38	0
56	MG	1B	209	1/1	0.94	0.06	42,42,42,42	0
56	MG	2A	3016	1/1	0.94	0.08	38,38,38,38	0
56	MG	1a	1747	1/1	0.94	0.08	53,53,53,53	0
56	MG	1A	3421	1/1	0.94	0.14	60,60,60,60	0
56	MG	2A	3609	1/1	0.94	0.09	52,52,52,52	0
56	MG	2A	3414	1/1	0.94	0.15	59,59,59,59	0
56	MG	2A	3415	1/1	0.94	0.13	44,44,44,44	0
56	MG	1A	3040	1/1	0.94	0.09	38,38,38,38	0
56	MG	1A	3574	1/1	0.94	0.18	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1669	1/1	0.94	0.07	67,67,67,67	0
56	MG	1A	3727	1/1	0.94	0.06	39,39,39,39	0
56	MG	2A	3216	1/1	0.94	0.28	57,57,57,57	0
56	MG	2A	3025	1/1	0.94	0.19	60,60,60,60	0
56	MG	1A	3299	1/1	0.94	0.07	41,41,41,41	0
56	MG	2A	3028	1/1	0.94	0.24	40,40,40,40	0
56	MG	2A	3030	1/1	0.94	0.27	48,48,48,48	0
56	MG	1A	3106	1/1	0.94	0.17	47,47,47,47	0
56	MG	2A	3032	1/1	0.94	0.14	44,44,44,44	0
56	MG	1A	3497	1/1	0.94	0.07	26,26,26,26	0
56	MG	2A	3225	1/1	0.94	0.22	49,49,49,49	0
56	MG	1a	1628	1/1	0.94	0.23	43,43,43,43	0
56	MG	1A	3108	1/1	0.94	0.14	36,36,36,36	0
56	MG	1A	3111	1/1	0.94	0.10	45,45,45,45	0
56	MG	2A	3043	1/1	0.94	0.08	44,44,44,44	0
56	MG	1A	3112	1/1	0.94	0.07	44,44,44,44	0
56	MG	2A	3438	1/1	0.94	0.09	39,39,39,39	0
56	MG	1A	3308	1/1	0.94	0.16	39,39,39,39	0
56	MG	2A	3442	1/1	0.94	0.09	29,29,29,29	0
56	MG	2A	3046	1/1	0.94	0.28	50,50,50,50	0
56	MG	2A	3047	1/1	0.94	0.17	50,50,50,50	0
56	MG	1A	3740	1/1	0.94	0.11	34,34,34,34	0
56	MG	1a	1638	1/1	0.94	0.17	55,55,55,55	0
56	MG	1A	3185	1/1	0.94	0.10	41,41,41,41	0
56	MG	2A	3450	1/1	0.94	0.09	39,39,39,39	0
56	MG	2A	3451	1/1	0.94	0.14	40,40,40,40	0
56	MG	2a	1701	1/1	0.94	0.12	55,55,55,55	0
56	MG	2A	3452	1/1	0.94	0.13	32,32,32,32	0
56	MG	1D	301	1/1	0.94	0.11	40,40,40,40	0
56	MG	1D	303	1/1	0.94	0.26	49,49,49,49	0
56	MG	1A	3079	1/1	0.94	0.16	38,38,38,38	0
56	MG	2A	3058	1/1	0.94	0.09	50,50,50,50	0
56	MG	2a	1707	1/1	0.94	0.11	43,43,43,43	0
56	MG	1a	1644	1/1	0.94	0.20	48,48,48,48	0
56	MG	2A	3458	1/1	0.94	0.14	37,37,37,37	0
56	MG	2A	3460	1/1	0.94	0.14	47,47,47,47	0
56	MG	1A	3189	1/1	0.94	0.14	47,47,47,47	0
56	MG	2A	3654	1/1	0.94	0.21	42,42,42,42	0
56	MG	1A	3594	1/1	0.94	0.10	52,52,52,52	0
56	MG	1E	303	1/1	0.94	0.15	48,48,48,48	0
56	MG	1A	3377	1/1	0.94	0.09	42,42,42,42	0
56	MG	1A	3597	1/1	0.94	0.12	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1788	1/1	0.94	0.19	50,50,50,50	0
56	MG	1A	3436	1/1	0.94	0.15	40,40,40,40	0
56	MG	1F	301	1/1	0.94	0.07	49,49,49,49	0
56	MG	1A	3081	1/1	0.94	0.19	35,35,35,35	0
56	MG	1A	3600	1/1	0.94	0.09	38,38,38,38	0
56	MG	2A	3071	1/1	0.94	0.07	34,34,34,34	0
56	MG	1A	3117	1/1	0.94	0.08	44,44,44,44	0
56	MG	2A	3073	1/1	0.94	0.18	53,53,53,53	0
56	MG	2A	3074	1/1	0.94	0.10	50,50,50,50	0
56	MG	2A	3673	1/1	0.94	0.12	47,47,47,47	0
56	MG	2A	3675	1/1	0.94	0.25	57,57,57,57	0
56	MG	1a	1659	1/1	0.94	0.36	59,59,59,59	0
56	MG	2A	3275	1/1	0.94	0.07	31,31,31,31	0
56	MG	2a	1735	1/1	0.94	0.11	56,56,56,56	0
56	MG	2A	3277	1/1	0.94	0.06	38,38,38,38	0
56	MG	1a	1660	1/1	0.94	0.30	56,56,56,56	0
56	MG	1a	1661	1/1	0.94	0.24	61,61,61,61	0
56	MG	1A	3384	1/1	0.94	0.13	41,41,41,41	0
56	MG	2A	3281	1/1	0.94	0.17	52,52,52,52	0
56	MG	1a	1799	1/1	0.94	0.08	46,46,46,46	0
56	MG	2A	3081	1/1	0.94	0.07	45,45,45,45	0
56	MG	2B	3005	1/1	0.94	0.17	64,64,64,64	0
56	MG	2A	3082	1/1	0.94	0.09	40,40,40,40	0
56	MG	1A	3156	1/1	0.94	0.12	50,50,50,50	0
56	MG	1A	3441	1/1	0.94	0.10	50,50,50,50	0
56	MG	1A	3094	1/1	0.94	0.17	41,41,41,41	0
56	MG	1N	3005	1/1	0.94	0.10	40,40,40,40	0
56	MG	1A	3083	1/1	0.94	0.12	37,37,37,37	0
56	MG	1A	3679	1/1	0.94	0.14	61,61,61,61	0
56	MG	2A	3091	1/1	0.94	0.07	45,45,45,45	0
56	MG	1a	1806	1/1	0.94	0.10	62,62,62,62	0
56	MG	1A	3764	1/1	0.94	0.09	47,47,47,47	0
56	MG	1a	1809	1/1	0.94	0.10	60,60,60,60	0
56	MG	1A	3528	1/1	0.94	0.08	53,53,53,53	0
56	MG	1P	201	1/1	0.94	0.08	51,51,51,51	0
56	MG	1a	1674	1/1	0.94	0.32	59,59,59,59	0
56	MG	1A	3067	1/1	0.94	0.30	42,42,42,42	0
56	MG	2a	1762	1/1	0.94	0.14	64,64,64,64	0
56	MG	1A	3532	1/1	0.94	0.12	59,59,59,59	0
56	MG	1A	3769	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3683	1/1	0.94	0.11	53,53,53,53	0
56	MG	1A	3684	1/1	0.94	0.15	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1682	1/1	0.94	0.15	43,43,43,43	0
56	MG	1A	3321	1/1	0.94	0.10	48,48,48,48	0
56	MG	1A	3617	1/1	0.94	0.07	41,41,41,41	0
56	MG	2F	302	1/1	0.94	0.11	53,53,53,53	0
56	MG	2A	3519	1/1	0.94	0.17	64,64,64,64	0
56	MG	1A	3238	1/1	0.94	0.15	31,31,31,31	0
56	MG	2A	3312	1/1	0.94	0.10	54,54,54,54	0
56	MG	2A	3313	1/1	0.94	0.13	55,55,55,55	0
56	MG	2a	1779	1/1	0.94	0.09	54,54,54,54	0
56	MG	1A	3026	1/1	0.94	0.07	43,43,43,43	0
56	MG	1A	3537	1/1	0.94	0.12	28,28,28,28	0
56	MG	2A	3318	1/1	0.94	0.09	33,33,33,33	0
56	MG	2A	3120	1/1	0.94	0.24	57,57,57,57	0
56	MG	1A	3324	1/1	0.94	0.25	53,53,53,53	0
56	MG	1A	3200	1/1	0.94	0.10	48,48,48,48	0
56	MG	2A	3323	1/1	0.94	0.10	47,47,47,47	0
56	MG	2V	3003	1/1	0.94	0.11	48,48,48,48	0
56	MG	1A	3328	1/1	0.94	0.30	61,61,61,61	0
56	MG	2X	102	1/1	0.94	0.08	63,63,63,63	0
56	MG	1A	3694	1/1	0.94	0.09	27,27,27,27	0
56	MG	1A	3872	1/1	0.94	0.12	50,50,50,50	0
56	MG	1A	3333	1/1	0.94	0.18	40,40,40,40	0
56	MG	2A	3330	1/1	0.94	0.11	49,49,49,49	0
56	MG	1Z	303	1/1	0.94	0.31	59,59,59,59	0
56	MG	2A	3334	1/1	0.94	0.07	35,35,35,35	0
56	MG	2A	3335	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3336	1/1	0.94	0.06	30,30,30,30	0
56	MG	1A	3204	1/1	0.94	0.12	38,38,38,38	0
56	MG	2A	3543	1/1	0.94	0.08	54,54,54,54	0
56	MG	1A	3125	1/1	0.94	0.06	34,34,34,34	0
56	MG	1A	3884	1/1	0.94	0.13	40,40,40,40	0
56	MG	1A	3629	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3344	1/1	0.94	0.10	31,31,31,31	0
56	MG	1a	1707	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3470	1/1	0.94	0.22	58,58,58,58	0
56	MG	2l	202	1/1	0.94	0.12	54,54,54,54	0
56	MG	2a	1609	1/1	0.94	0.10	47,47,47,47	0
56	MG	1l	102	1/1	0.94	0.07	54,54,54,54	0
56	MG	1A	3701	1/1	0.94	0.07	58,58,58,58	0
56	MG	1A	3207	1/1	0.94	0.08	50,50,50,50	0
56	MG	2A	3149	1/1	0.94	0.11	41,41,41,41	0
56	MG	1A	3338	1/1	0.94	0.15	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3554	1/1	0.94	0.09	42,42,42,42	0
56	MG	1A	3039	1/1	0.94	0.12	49,49,49,49	0
56	MG	1A	3637	1/1	0.94	0.12	54,54,54,54	0
56	MG	2w	3003	1/1	0.94	0.12	58,58,58,58	0
56	MG	2x	3001	1/1	0.94	0.10	49,49,49,49	0
56	MG	2A	3161	1/1	0.94	0.18	53,53,53,53	0
58	K	1A	3931	1/1	0.94	0.14	71,71,71,71	0
58	K	2A	3242	1/1	0.94	0.10	65,65,65,65	0
59	ZN	16	101	1/1	0.94	0.20	91,91,91,91	0
56	MG	1A	3128	1/1	0.94	0.14	47,47,47,47	0
56	MG	18	101	1/1	0.94	0.16	37,37,37,37	0
56	MG	2A	3167	1/1	0.94	0.09	43,43,43,43	0
56	MG	19	502	1/1	0.94	0.16	49,49,49,49	0
56	MG	1A	3451	1/1	0.95	0.07	21,21,21,21	0
56	MG	1A	3186	1/1	0.95	0.22	36,36,36,36	0
56	MG	2A	3342	1/1	0.95	0.10	43,43,43,43	0
56	MG	2A	3156	1/1	0.95	0.11	50,50,50,50	0
56	MG	2A	3157	1/1	0.95	0.07	55,55,55,55	0
56	MG	1A	3139	1/1	0.95	0.29	45,45,45,45	0
56	MG	2A	3159	1/1	0.95	0.12	44,44,44,44	0
56	MG	2a	1622	1/1	0.95	0.07	42,42,42,42	0
56	MG	2A	3160	1/1	0.95	0.07	36,36,36,36	0
56	MG	2a	1624	1/1	0.95	0.20	62,62,62,62	0
56	MG	2A	3558	1/1	0.95	0.14	64,64,64,64	0
56	MG	1A	3325	1/1	0.95	0.07	43,43,43,43	0
56	MG	2A	3353	1/1	0.95	0.09	35,35,35,35	0
56	MG	2A	3162	1/1	0.95	0.24	45,45,45,45	0
56	MG	2A	3564	1/1	0.95	0.21	34,34,34,34	0
56	MG	1A	3791	1/1	0.95	0.21	34,34,34,34	0
56	MG	1a	1721	1/1	0.95	0.14	47,47,47,47	0
56	MG	2A	3567	1/1	0.95	0.09	54,54,54,54	0
56	MG	2A	3166	1/1	0.95	0.07	45,45,45,45	0
56	MG	1A	3053	1/1	0.95	0.22	48,48,48,48	0
56	MG	2A	3570	1/1	0.95	0.11	51,51,51,51	0
56	MG	1A	3037	1/1	0.95	0.12	32,32,32,32	0
56	MG	1A	3461	1/1	0.95	0.10	23,23,23,23	0
56	MG	2A	3367	1/1	0.95	0.14	44,44,44,44	0
56	MG	2A	3171	1/1	0.95	0.22	47,47,47,47	0
56	MG	1A	3906	1/1	0.95	0.06	34,34,34,34	0
56	MG	2a	1642	1/1	0.95	0.28	61,61,61,61	0
56	MG	1A	3329	1/1	0.95	0.15	54,54,54,54	0
56	MG	1y	3003	1/1	0.95	0.07	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3330	1/1	0.95	0.16	39,39,39,39	0
56	MG	1A	3332	1/1	0.95	0.21	50,50,50,50	0
56	MG	2A	3181	1/1	0.95	0.28	55,55,55,55	0
56	MG	2A	3182	1/1	0.95	0.17	39,39,39,39	0
56	MG	2a	1650	1/1	0.95	0.12	39,39,39,39	0
56	MG	1A	3921	1/1	0.95	0.09	38,38,38,38	0
56	MG	1A	3924	1/1	0.95	0.09	49,49,49,49	0
56	MG	2A	3185	1/1	0.95	0.31	50,50,50,50	0
56	MG	2A	3387	1/1	0.95	0.09	47,47,47,47	0
56	MG	2A	3388	1/1	0.95	0.11	46,46,46,46	0
56	MG	2A	3186	1/1	0.95	0.05	51,51,51,51	0
56	MG	2A	3187	1/1	0.95	0.13	42,42,42,42	0
56	MG	2A	3594	1/1	0.95	0.13	52,52,52,52	0
56	MG	2A	3391	1/1	0.95	0.07	40,40,40,40	0
56	MG	1A	3056	1/1	0.95	0.15	43,43,43,43	0
56	MG	2a	1661	1/1	0.95	0.20	62,62,62,62	0
56	MG	1A	3928	1/1	0.95	0.07	40,40,40,40	0
56	MG	1A	3707	1/1	0.95	0.19	38,38,38,38	0
56	MG	1A	3288	1/1	0.95	0.13	42,42,42,42	0
56	MG	1A	3937	1/1	0.95	0.16	40,40,40,40	0
56	MG	1A	3636	1/1	0.95	0.17	51,51,51,51	0
56	MG	2A	3197	1/1	0.95	0.07	42,42,42,42	0
56	MG	2A	3603	1/1	0.95	0.08	47,47,47,47	0
56	MG	1a	1738	1/1	0.95	0.12	36,36,36,36	0
56	MG	1a	1739	1/1	0.95	0.24	70,70,70,70	0
56	MG	1A	3553	1/1	0.95	0.07	44,44,44,44	0
56	MG	1A	3401	1/1	0.95	0.08	38,38,38,38	0
56	MG	2A	3202	1/1	0.95	0.12	51,51,51,51	0
56	MG	1A	3221	1/1	0.95	0.17	30,30,30,30	0
56	MG	1A	3808	1/1	0.95	0.12	46,46,46,46	0
56	MG	1a	1618	1/1	0.95	0.13	48,48,48,48	0
56	MG	2A	3408	1/1	0.95	0.07	54,54,54,54	0
56	MG	1A	3809	1/1	0.95	0.06	50,50,50,50	0
56	MG	1A	3030	1/1	0.95	0.08	36,36,36,36	0
56	MG	1A	3557	1/1	0.95	0.10	22,22,22,22	0
56	MG	1A	3292	1/1	0.95	0.09	33,33,33,33	0
56	MG	1A	3814	1/1	0.95	0.13	39,39,39,39	0
56	MG	1A	3644	1/1	0.95	0.10	51,51,51,51	0
56	MG	1A	3406	1/1	0.95	0.11	27,27,27,27	0
56	MG	2a	1687	1/1	0.95	0.33	50,50,50,50	0
56	MG	1A	3819	1/1	0.95	0.10	43,43,43,43	0
56	MG	2a	1689	1/1	0.95	0.08	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3721	1/1	0.95	0.07	50,50,50,50	0
56	MG	1a	1634	1/1	0.95	0.21	45,45,45,45	0
56	MG	2A	3038	1/1	0.95	0.06	34,34,34,34	0
56	MG	2A	3041	1/1	0.95	0.19	29,29,29,29	0
56	MG	1A	3340	1/1	0.95	0.18	48,48,48,48	0
56	MG	2a	1695	1/1	0.95	0.23	66,66,66,66	0
56	MG	1A	3563	1/1	0.95	0.10	30,30,30,30	0
56	MG	2A	3221	1/1	0.95	0.11	35,35,35,35	0
56	MG	2a	1698	1/1	0.95	0.11	64,64,64,64	0
56	MG	2A	3629	1/1	0.95	0.08	53,53,53,53	0
56	MG	1A	3408	1/1	0.95	0.12	36,36,36,36	0
56	MG	2A	3631	1/1	0.95	0.07	57,57,57,57	0
56	MG	1A	3145	1/1	0.95	0.14	37,37,37,37	0
56	MG	1A	3147	1/1	0.95	0.15	36,36,36,36	0
56	MG	1A	3295	1/1	0.95	0.18	49,49,49,49	0
56	MG	1A	3729	1/1	0.95	0.12	47,47,47,47	0
56	MG	2A	3636	1/1	0.95	0.12	52,52,52,52	0
56	MG	2A	3228	1/1	0.95	0.12	42,42,42,42	0
56	MG	2A	3432	1/1	0.95	0.10	37,37,37,37	0
56	MG	2A	3229	1/1	0.95	0.17	41,41,41,41	0
56	MG	1D	304	1/1	0.95	0.07	22,22,22,22	0
56	MG	2A	3052	1/1	0.95	0.49	58,58,58,58	0
56	MG	2A	3437	1/1	0.95	0.08	36,36,36,36	0
56	MG	1a	1779	1/1	0.95	0.19	52,52,52,52	0
56	MG	1A	3829	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3056	1/1	0.95	0.07	23,23,23,23	0
56	MG	2A	3235	1/1	0.95	0.11	53,53,53,53	0
56	MG	1a	1646	1/1	0.95	0.09	52,52,52,52	0
56	MG	1a	1647	1/1	0.95	0.08	49,49,49,49	0
56	MG	2a	1723	1/1	0.95	0.23	56,56,56,56	0
56	MG	1a	1648	1/1	0.95	0.07	48,48,48,48	0
56	MG	1a	1649	1/1	0.95	0.31	58,58,58,58	0
56	MG	2A	3449	1/1	0.95	0.05	34,34,34,34	0
56	MG	1A	3346	1/1	0.95	0.10	56,56,56,56	0
56	MG	2A	3241	1/1	0.95	0.06	59,59,59,59	0
56	MG	1A	3228	1/1	0.95	0.26	51,51,51,51	0
56	MG	2A	3657	1/1	0.95	0.10	59,59,59,59	0
56	MG	1A	3105	1/1	0.95	0.23	39,39,39,39	0
56	MG	1E	305	1/1	0.95	0.10	26,26,26,26	0
56	MG	1A	3350	1/1	0.95	0.15	40,40,40,40	0
56	MG	1A	3657	1/1	0.95	0.10	35,35,35,35	0
56	MG	1A	3492	1/1	0.95	0.08	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3002	1/1	0.95	0.07	32,32,32,32	0
56	MG	2A	3665	1/1	0.95	0.10	41,41,41,41	0
56	MG	2A	3459	1/1	0.95	0.15	44,44,44,44	0
56	MG	1F	302	1/1	0.95	0.19	32,32,32,32	0
56	MG	1A	3494	1/1	0.95	0.12	34,34,34,34	0
56	MG	2A	3669	1/1	0.95	0.14	68,68,68,68	0
56	MG	1A	3352	1/1	0.95	0.10	56,56,56,56	0
56	MG	1A	3580	1/1	0.95	0.14	36,36,36,36	0
56	MG	1a	1662	1/1	0.95	0.06	25,25,25,25	0
56	MG	2A	3258	1/1	0.95	0.12	35,35,35,35	0
56	MG	2a	1747	1/1	0.95	0.12	46,46,46,46	0
56	MG	2A	3468	1/1	0.95	0.08	43,43,43,43	0
56	MG	1G	3003	1/1	0.95	0.11	50,50,50,50	0
56	MG	1A	3353	1/1	0.95	0.17	46,46,46,46	0
56	MG	1A	3199	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	3151	1/1	0.95	0.09	36,36,36,36	0
56	MG	1A	3585	1/1	0.95	0.10	34,34,34,34	0
56	MG	1N	3004	1/1	0.95	0.07	41,41,41,41	0
56	MG	1A	3266	1/1	0.95	0.14	50,50,50,50	0
56	MG	2A	3271	1/1	0.95	0.09	53,53,53,53	0
56	MG	2A	3272	1/1	0.95	0.07	47,47,47,47	0
56	MG	1A	3849	1/1	0.95	0.06	46,46,46,46	0
56	MG	1A	3032	1/1	0.95	0.09	47,47,47,47	0
56	MG	2A	3276	1/1	0.95	0.11	51,51,51,51	0
56	MG	1A	3591	1/1	0.95	0.06	69,69,69,69	0
56	MG	1A	3205	1/1	0.95	0.36	41,41,41,41	0
56	MG	1A	3017	1/1	0.95	0.30	53,53,53,53	0
56	MG	2A	3088	1/1	0.95	0.09	38,38,38,38	0
56	MG	1a	1676	1/1	0.95	0.30	53,53,53,53	0
56	MG	1P	202	1/1	0.95	0.11	30,30,30,30	0
56	MG	2A	3092	1/1	0.95	0.14	36,36,36,36	0
56	MG	1A	3096	1/1	0.95	0.44	52,52,52,52	0
56	MG	2A	3492	1/1	0.95	0.20	59,59,59,59	0
56	MG	1A	3208	1/1	0.95	0.21	42,42,42,42	0
56	MG	1a	1680	1/1	0.95	0.13	48,48,48,48	0
56	MG	2a	1775	1/1	0.95	0.14	56,56,56,56	0
56	MG	1A	3675	1/1	0.95	0.11	50,50,50,50	0
56	MG	2D	301	1/1	0.95	0.16	46,46,46,46	0
56	MG	1A	3312	1/1	0.95	0.33	60,60,60,60	0
56	MG	2D	303	1/1	0.95	0.12	36,36,36,36	0
56	MG	1A	3209	1/1	0.95	0.22	55,55,55,55	0
56	MG	1A	3367	1/1	0.95	0.14	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3515	1/1	0.95	0.11	58,58,58,58	0
56	MG	1A	3370	1/1	0.95	0.07	43,43,43,43	0
56	MG	1A	3097	1/1	0.95	0.14	26,26,26,26	0
56	MG	1A	3276	1/1	0.95	0.22	47,47,47,47	0
56	MG	2A	3108	1/1	0.95	0.28	37,37,37,37	0
56	MG	2F	303	1/1	0.95	0.14	51,51,51,51	0
56	MG	1A	3240	1/1	0.95	0.15	55,55,55,55	0
56	MG	1a	1690	1/1	0.95	0.11	35,35,35,35	0
56	MG	2N	8001	1/1	0.95	0.07	53,53,53,53	0
56	MG	1a	1693	1/1	0.95	0.17	44,44,44,44	0
56	MG	1A	3523	1/1	0.95	0.14	33,33,33,33	0
56	MG	1A	3526	1/1	0.95	0.16	52,52,52,52	0
56	MG	2A	3305	1/1	0.95	0.07	43,43,43,43	0
56	MG	2A	3514	1/1	0.95	0.09	59,59,59,59	0
56	MG	2A	3118	1/1	0.95	0.18	33,33,33,33	0
56	MG	1A	3211	1/1	0.95	0.13	44,44,44,44	0
56	MG	1W	3002	1/1	0.95	0.21	53,53,53,53	0
56	MG	1A	3378	1/1	0.95	0.10	45,45,45,45	0
56	MG	2A	3122	1/1	0.95	0.15	47,47,47,47	0
56	MG	1A	3529	1/1	0.95	0.09	60,60,60,60	0
56	MG	2g	8001	1/1	0.95	0.06	65,65,65,65	0
56	MG	1d	502	1/1	0.95	0.34	58,58,58,58	0
56	MG	1e	3001	1/1	0.95	0.09	71,71,71,71	0
56	MG	2A	3314	1/1	0.95	0.08	39,39,39,39	0
56	MG	1Z	301	1/1	0.95	0.11	46,46,46,46	0
56	MG	2A	3132	1/1	0.95	0.18	51,51,51,51	0
56	MG	2q	201	1/1	0.95	0.16	55,55,55,55	0
56	MG	1l	203	1/1	0.95	0.14	52,52,52,52	0
56	MG	2l	102	1/1	0.95	0.06	45,45,45,45	0
56	MG	2A	3135	1/1	0.95	0.14	36,36,36,36	0
56	MG	1A	3873	1/1	0.95	0.08	13,13,13,13	0
56	MG	1a	1705	1/1	0.95	0.07	40,40,40,40	0
56	MG	2A	3138	1/1	0.95	0.10	29,29,29,29	0
56	MG	1A	3530	1/1	0.95	0.08	53,53,53,53	0
56	MG	1A	3876	1/1	0.95	0.19	46,46,46,46	0
56	MG	1w	3002	1/1	0.95	0.07	37,37,37,37	0
56	MG	1A	3159	1/1	0.95	0.13	29,29,29,29	0
57	4M2	1A	3894	57/57	0.95	0.10	21,37,55,60	0
56	MG	1A	3280	1/1	0.95	0.18	44,44,44,44	0
56	MG	1x	101	1/1	0.95	0.09	55,55,55,55	0
56	MG	2A	3332	1/1	0.95	0.14	57,57,57,57	0
56	MG	1A	3881	1/1	0.95	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
56	MG	1A	3783	1/1	0.95	0.10	51,51,51,51	0
56	MG	1A	3692	1/1	0.95	0.13	52,52,52,52	0
56	MG	1A	3064	1/1	0.95	0.26	38,38,38,38	0
56	MG	2A	3338	1/1	0.95	0.12	43,43,43,43	0
56	MG	10	104	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3899	1/1	0.96	0.15	50,50,50,50	0
56	MG	1n	502	1/1	0.96	0.10	42,42,42,42	0
56	MG	1A	3027	1/1	0.96	0.16	35,35,35,35	0
56	MG	1s	3001	1/1	0.96	0.08	57,57,57,57	0
56	MG	1A	3708	1/1	0.96	0.20	55,55,55,55	0
56	MG	1A	3903	1/1	0.96	0.16	39,39,39,39	0
56	MG	2A	3127	1/1	0.96	0.15	47,47,47,47	0
56	MG	1A	3218	1/1	0.96	0.06	44,44,44,44	0
56	MG	12	102	1/1	0.96	0.10	49,49,49,49	0
56	MG	1A	3800	1/1	0.96	0.18	46,46,46,46	0
56	MG	2A	3133	1/1	0.96	0.17	49,49,49,49	0
56	MG	1A	3908	1/1	0.96	0.16	43,43,43,43	0
56	MG	2A	3289	1/1	0.96	0.06	37,37,37,37	0
56	MG	15	102	1/1	0.96	0.07	39,39,39,39	0
56	MG	2a	1672	1/1	0.96	0.09	64,64,64,64	0
56	MG	1A	3343	1/1	0.96	0.14	34,34,34,34	0
56	MG	1A	3034	1/1	0.96	0.26	44,44,44,44	0
56	MG	1A	3915	1/1	0.96	0.17	36,36,36,36	0
56	MG	1a	1718	1/1	0.96	0.07	49,49,49,49	0
56	MG	2A	3140	1/1	0.96	0.13	37,37,37,37	0
56	MG	1A	3916	1/1	0.96	0.09	41,41,41,41	0
56	MG	2A	3142	1/1	0.96	0.08	44,44,44,44	0
56	MG	1A	3477	1/1	0.96	0.09	18,18,18,18	0
56	MG	1A	3920	1/1	0.96	0.25	34,34,34,34	0
56	MG	2A	3480	1/1	0.96	0.09	52,52,52,52	0
56	MG	1A	3345	1/1	0.96	0.13	45,45,45,45	0
56	MG	1A	3923	1/1	0.96	0.16	43,43,43,43	0
56	MG	1A	3479	1/1	0.96	0.06	53,53,53,53	0
56	MG	1A	3255	1/1	0.96	0.09	44,44,44,44	0
56	MG	1A	3927	1/1	0.96	0.16	40,40,40,40	0
56	MG	1A	3645	1/1	0.96	0.07	58,58,58,58	0
56	MG	1A	3929	1/1	0.96	0.17	39,39,39,39	0
56	MG	1A	3930	1/1	0.96	0.17	41,41,41,41	0
56	MG	1A	3718	1/1	0.96	0.08	23,23,23,23	0
56	MG	1A	3935	1/1	0.96	0.18	40,40,40,40	0
56	MG	2A	3494	1/1	0.96	0.08	53,53,53,53	0
56	MG	1A	3481	1/1	0.96	0.13	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3300	1/1	0.96	0.04	24,24,24,24	0
56	MG	1A	3120	1/1	0.96	0.14	39,39,39,39	0
56	MG	2A	3316	1/1	0.96	0.06	31,31,31,31	0
56	MG	1A	3349	1/1	0.96	0.06	43,43,43,43	0
56	MG	1A	3222	1/1	0.96	0.22	38,38,38,38	0
56	MG	2A	3319	1/1	0.96	0.09	40,40,40,40	0
56	MG	2A	3674	1/1	0.96	0.06	39,39,39,39	0
56	MG	1A	3304	1/1	0.96	0.09	39,39,39,39	0
56	MG	1A	3223	1/1	0.96	0.12	36,36,36,36	0
56	MG	1A	3570	1/1	0.96	0.14	31,31,31,31	0
56	MG	2A	3008	1/1	0.96	0.07	42,42,42,42	0
56	MG	2A	3679	1/1	0.96	0.14	46,46,46,46	0
56	MG	2a	1708	1/1	0.96	0.09	61,61,61,61	0
56	MG	1A	3121	1/1	0.96	0.24	38,38,38,38	0
56	MG	2A	3169	1/1	0.96	0.15	41,41,41,41	0
56	MG	1A	3098	1/1	0.96	0.15	24,24,24,24	0
56	MG	1A	3082	1/1	0.96	0.19	42,42,42,42	0
56	MG	2a	1713	1/1	0.96	0.20	52,52,52,52	0
56	MG	1A	3191	1/1	0.96	0.12	27,27,27,27	0
56	MG	2A	3018	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	3576	1/1	0.96	0.16	24,24,24,24	0
56	MG	2A	3176	1/1	0.96	0.20	37,37,37,37	0
56	MG	2A	3177	1/1	0.96	0.15	40,40,40,40	0
56	MG	2A	3517	1/1	0.96	0.11	55,55,55,55	0
56	MG	2A	3178	1/1	0.96	0.08	41,41,41,41	0
56	MG	2A	3020	1/1	0.96	0.09	30,30,30,30	0
56	MG	1a	1626	1/1	0.96	0.24	61,61,61,61	0
56	MG	1A	3020	1/1	0.96	0.05	40,40,40,40	0
56	MG	2A	3340	1/1	0.96	0.06	51,51,51,51	0
56	MG	1A	3735	1/1	0.96	0.15	52,52,52,52	0
56	MG	1a	1631	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3358	1/1	0.96	0.05	45,45,45,45	0
56	MG	2A	3527	1/1	0.96	0.10	34,34,34,34	0
56	MG	1A	3052	1/1	0.96	0.14	40,40,40,40	0
56	MG	2A	3029	1/1	0.96	0.05	26,26,26,26	0
56	MG	1A	3126	1/1	0.96	0.07	36,36,36,36	0
56	MG	1A	3043	1/1	0.96	0.07	34,34,34,34	0
56	MG	1a	1636	1/1	0.96	0.16	53,53,53,53	0
56	MG	1a	1764	1/1	0.96	0.09	47,47,47,47	0
56	MG	1A	3742	1/1	0.96	0.15	54,54,54,54	0
56	MG	1A	3664	1/1	0.96	0.16	50,50,50,50	0
56	MG	2E	303	1/1	0.96	0.06	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1740	1/1	0.96	0.14	66,66,66,66	0
56	MG	1A	3315	1/1	0.96	0.08	46,46,46,46	0
56	MG	2A	3195	1/1	0.96	0.05	32,32,32,32	0
56	MG	2A	3196	1/1	0.96	0.08	47,47,47,47	0
56	MG	1A	3745	1/1	0.96	0.07	64,64,64,64	0
56	MG	1a	1771	1/1	0.96	0.15	40,40,40,40	0
56	MG	2A	3366	1/1	0.96	0.13	34,34,34,34	0
56	MG	1A	3068	1/1	0.96	0.10	17,17,17,17	0
56	MG	1A	3317	1/1	0.96	0.23	43,43,43,43	0
56	MG	1A	3274	1/1	0.96	0.26	49,49,49,49	0
56	MG	1a	1776	1/1	0.96	0.15	53,53,53,53	0
56	MG	1a	1777	1/1	0.96	0.05	57,57,57,57	0
56	MG	1A	3505	1/1	0.96	0.08	55,55,55,55	0
56	MG	1A	3751	1/1	0.96	0.12	44,44,44,44	0
56	MG	2Q	3003	1/1	0.96	0.06	48,48,48,48	0
56	MG	1A	3590	1/1	0.96	0.10	24,24,24,24	0
56	MG	1A	3506	1/1	0.96	0.10	53,53,53,53	0
56	MG	2A	3553	1/1	0.96	0.06	45,45,45,45	0
56	MG	1A	3164	1/1	0.96	0.19	53,53,53,53	0
56	MG	2A	3555	1/1	0.96	0.08	47,47,47,47	0
56	MG	2A	3383	1/1	0.96	0.10	52,52,52,52	0
56	MG	1A	3130	1/1	0.96	0.05	40,40,40,40	0
56	MG	2A	3210	1/1	0.96	0.20	58,58,58,58	0
56	MG	1A	3757	1/1	0.96	0.05	23,23,23,23	0
56	MG	2A	3560	1/1	0.96	0.06	47,47,47,47	0
56	MG	1A	3509	1/1	0.96	0.17	48,48,48,48	0
56	MG	1F	304	1/1	0.96	0.07	50,50,50,50	0
56	MG	1F	305	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3044	1/1	0.96	0.07	22,22,22,22	0
56	MG	2a	1771	1/1	0.96	0.12	53,53,53,53	0
56	MG	1A	3088	1/1	0.96	0.14	22,22,22,22	0
56	MG	1A	3135	1/1	0.96	0.19	30,30,30,30	0
56	MG	1G	3002	1/1	0.96	0.05	34,34,34,34	0
56	MG	1A	3137	1/1	0.96	0.13	45,45,45,45	0
56	MG	1A	3012	1/1	0.96	0.13	33,33,33,33	0
56	MG	1A	3765	1/1	0.96	0.12	66,66,66,66	0
56	MG	1A	3380	1/1	0.96	0.07	26,26,26,26	0
56	MG	1A	3519	1/1	0.96	0.10	51,51,51,51	0
56	MG	1N	3003	1/1	0.96	0.07	40,40,40,40	0
56	MG	1A	3110	1/1	0.96	0.11	38,38,38,38	0
56	MG	1A	3383	1/1	0.96	0.08	31,31,31,31	0
56	MG	2A	3579	1/1	0.96	0.06	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3091	1/1	0.96	0.17	42,42,42,42	0
56	MG	1A	3072	1/1	0.96	0.07	35,35,35,35	0
56	MG	1A	3864	1/1	0.96	0.17	38,38,38,38	0
56	MG	1A	3772	1/1	0.96	0.06	33,33,33,33	0
56	MG	1a	1807	1/1	0.96	0.16	58,58,58,58	0
56	MG	1a	1671	1/1	0.96	0.21	48,48,48,48	0
56	MG	1A	3448	1/1	0.96	0.14	39,39,39,39	0
56	MG	1A	3774	1/1	0.96	0.14	61,61,61,61	0
56	MG	1A	3449	1/1	0.96	0.06	27,27,27,27	0
56	MG	1A	3175	1/1	0.96	0.13	47,47,47,47	0
56	MG	1A	3387	1/1	0.96	0.07	18,18,18,18	0
56	MG	1A	3454	1/1	0.96	0.08	24,24,24,24	0
56	MG	1A	3245	1/1	0.96	0.09	48,48,48,48	0
56	MG	1A	3246	1/1	0.96	0.19	40,40,40,40	0
56	MG	1A	3391	1/1	0.96	0.12	30,30,30,30	0
56	MG	2A	3244	1/1	0.96	0.06	46,46,46,46	0
56	MG	2d	502	1/1	0.96	0.06	64,64,64,64	0
56	MG	1A	3023	1/1	0.96	0.07	42,42,42,42	0
56	MG	2e	202	1/1	0.96	0.05	71,71,71,71	0
56	MG	1A	3460	1/1	0.96	0.07	28,28,28,28	0
56	MG	1U	201	1/1	0.96	0.13	48,48,48,48	0
56	MG	1A	3114	1/1	0.96	0.08	41,41,41,41	0
56	MG	1A	3882	1/1	0.96	0.11	41,41,41,41	0
56	MG	1V	201	1/1	0.96	0.23	55,55,55,55	0
56	MG	1A	3883	1/1	0.96	0.14	33,33,33,33	0
56	MG	2A	3099	1/1	0.96	0.10	50,50,50,50	0
56	MG	1A	3539	1/1	0.96	0.10	17,17,17,17	0
56	MG	1A	3180	1/1	0.96	0.13	40,40,40,40	0
56	MG	2A	3256	1/1	0.96	0.14	46,46,46,46	0
56	MG	1A	3077	1/1	0.96	0.19	47,47,47,47	0
56	MG	1A	3464	1/1	0.96	0.11	57,57,57,57	0
56	MG	2A	3259	1/1	0.96	0.08	30,30,30,30	0
56	MG	1A	3397	1/1	0.96	0.06	17,17,17,17	0
56	MG	1a	1696	1/1	0.96	0.15	47,47,47,47	0
56	MG	1Y	503	1/1	0.96	0.08	56,56,56,56	0
56	MG	1A	3339	1/1	0.96	0.20	32,32,32,32	0
56	MG	1Z	302	1/1	0.96	0.20	48,48,48,48	0
56	MG	2x	3002	1/1	0.96	0.08	72,72,72,72	0
56	MG	2A	3267	1/1	0.96	0.10	34,34,34,34	0
56	MG	1A	3467	1/1	0.96	0.12	41,41,41,41	0
56	MG	2A	3113	1/1	0.96	0.06	46,46,46,46	0
56	MG	2A	3270	1/1	0.96	0.06	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	ZN	14	501	1/1	0.96	0.05	90,90,90,90	0
56	MG	2A	3114	1/1	0.96	0.12	49,49,49,49	0
56	MG	1A	3895	1/1	0.96	0.07	39,39,39,39	0
56	MG	1A	3146	1/1	0.96	0.08	38,38,38,38	0
60	SF4	2d	501	8/8	0.96	0.06	58,71,79,93	0
56	MG	2A	3274	1/1	0.96	0.07	43,43,43,43	0
56	MG	1a	1703	1/1	0.96	0.09	49,49,49,49	0
56	MG	1A	3909	1/1	0.97	0.14	42,42,42,42	0
56	MG	2A	3039	1/1	0.97	0.09	37,37,37,37	0
56	MG	2A	3040	1/1	0.97	0.17	36,36,36,36	0
56	MG	1A	3548	1/1	0.97	0.10	54,54,54,54	0
56	MG	2A	3042	1/1	0.97	0.13	48,48,48,48	0
56	MG	1U	203	1/1	0.97	0.36	40,40,40,40	0
56	MG	1A	3911	1/1	0.97	0.10	31,31,31,31	0
56	MG	1A	3912	1/1	0.97	0.14	37,37,37,37	0
56	MG	2A	3647	1/1	0.97	0.07	42,42,42,42	0
56	MG	1A	3496	1/1	0.97	0.06	47,47,47,47	0
56	MG	2a	1674	1/1	0.97	0.22	62,62,62,62	0
56	MG	1a	1794	1/1	0.97	0.11	54,54,54,54	0
56	MG	1A	3914	1/1	0.97	0.14	37,37,37,37	0
56	MG	1A	3131	1/1	0.97	0.19	40,40,40,40	0
56	MG	2A	3652	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3618	1/1	0.97	0.10	29,29,29,29	0
56	MG	1W	3004	1/1	0.97	0.06	41,41,41,41	0
56	MG	2A	3053	1/1	0.97	0.17	45,45,45,45	0
56	MG	2A	3326	1/1	0.97	0.09	35,35,35,35	0
56	MG	2A	3327	1/1	0.97	0.07	48,48,48,48	0
56	MG	1A	3917	1/1	0.97	0.12	32,32,32,32	0
56	MG	1A	3074	1/1	0.97	0.06	40,40,40,40	0
56	MG	1A	3093	1/1	0.97	0.26	59,59,59,59	0
56	MG	1A	3753	1/1	0.97	0.10	33,33,33,33	0
56	MG	2A	3192	1/1	0.97	0.09	46,46,46,46	0
56	MG	2A	3333	1/1	0.97	0.05	38,38,38,38	0
56	MG	1A	3922	1/1	0.97	0.07	41,41,41,41	0
56	MG	1A	3452	1/1	0.97	0.09	26,26,26,26	0
56	MG	10	101	1/1	0.97	0.04	45,45,45,45	0
56	MG	2A	3503	1/1	0.97	0.06	47,47,47,47	0
56	MG	1A	3119	1/1	0.97	0.07	44,44,44,44	0
56	MG	1A	3925	1/1	0.97	0.18	44,44,44,44	0
56	MG	1A	3220	1/1	0.97	0.18	31,31,31,31	0
56	MG	2A	3064	1/1	0.97	0.07	50,50,50,50	0
56	MG	1A	3366	1/1	0.97	0.09	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3504	1/1	0.97	0.06	13,13,13,13	0
56	MG	1A	3835	1/1	0.97	0.09	36,36,36,36	0
56	MG	1a	1692	1/1	0.97	0.07	45,45,45,45	0
56	MG	1A	3562	1/1	0.97	0.10	29,29,29,29	0
56	MG	1A	3456	1/1	0.97	0.07	23,23,23,23	0
56	MG	2A	3347	1/1	0.97	0.06	54,54,54,54	0
56	MG	2A	3349	1/1	0.97	0.07	36,36,36,36	0
56	MG	1A	3564	1/1	0.97	0.14	52,52,52,52	0
56	MG	2A	3351	1/1	0.97	0.07	39,39,39,39	0
56	MG	1A	3075	1/1	0.97	0.07	36,36,36,36	0
56	MG	1A	3841	1/1	0.97	0.10	33,33,33,33	0
56	MG	2A	3354	1/1	0.97	0.04	30,30,30,30	0
56	MG	2A	3355	1/1	0.97	0.04	22,22,22,22	0
56	MG	1A	3038	1/1	0.97	0.09	33,33,33,33	0
56	MG	2A	3357	1/1	0.97	0.05	35,35,35,35	0
56	MG	2A	3524	1/1	0.97	0.09	24,24,24,24	0
56	MG	2a	1715	1/1	0.97	0.09	59,59,59,59	0
56	MG	1A	3303	1/1	0.97	0.17	28,28,28,28	0
56	MG	2A	3076	1/1	0.97	0.28	60,60,60,60	0
56	MG	2A	3360	1/1	0.97	0.06	19,19,19,19	0
56	MG	2a	1719	1/1	0.97	0.08	47,47,47,47	0
56	MG	1A	3372	1/1	0.97	0.14	41,41,41,41	0
56	MG	1B	204	1/1	0.97	0.12	42,42,42,42	0
56	MG	2A	3530	1/1	0.97	0.07	50,50,50,50	0
56	MG	1A	3179	1/1	0.97	0.20	26,26,26,26	0
56	MG	17	101	1/1	0.97	0.07	55,55,55,55	0
56	MG	2A	3365	1/1	0.97	0.14	52,52,52,52	0
56	MG	1B	206	1/1	0.97	0.19	44,44,44,44	0
56	MG	1A	3511	1/1	0.97	0.10	52,52,52,52	0
56	MG	1B	208	1/1	0.97	0.06	56,56,56,56	0
56	MG	1A	3571	1/1	0.97	0.13	33,33,33,33	0
56	MG	1a	1602	1/1	0.97	0.26	60,60,60,60	0
56	MG	1A	3638	1/1	0.97	0.07	34,34,34,34	0
56	MG	2E	301	1/1	0.97	0.09	39,39,39,39	0
56	MG	1B	211	1/1	0.97	0.10	43,43,43,43	0
56	MG	1A	3337	1/1	0.97	0.30	34,34,34,34	0
56	MG	1a	1713	1/1	0.97	0.07	34,34,34,34	0
56	MG	2A	3090	1/1	0.97	0.15	37,37,37,37	0
56	MG	2E	306	1/1	0.97	0.10	47,47,47,47	0
56	MG	2A	3380	1/1	0.97	0.08	48,48,48,48	0
56	MG	2A	3381	1/1	0.97	0.08	42,42,42,42	0
56	MG	1A	3416	1/1	0.97	0.06	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3227	1/1	0.97	0.14	42,42,42,42	0
56	MG	2F	304	1/1	0.97	0.08	49,49,49,49	0
56	MG	1A	3201	1/1	0.97	0.08	45,45,45,45	0
56	MG	1A	3203	1/1	0.97	0.15	45,45,45,45	0
56	MG	1A	3517	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	3307	1/1	0.97	0.06	33,33,33,33	0
56	MG	1f	3001	1/1	0.97	0.09	42,42,42,42	0
56	MG	2A	3097	1/1	0.97	0.16	42,42,42,42	0
56	MG	2A	3098	1/1	0.97	0.06	32,32,32,32	0
56	MG	1g	3001	1/1	0.97	0.23	54,54,54,54	0
56	MG	1A	3158	1/1	0.97	0.07	39,39,39,39	0
56	MG	1A	3107	1/1	0.97	0.06	24,24,24,24	0
56	MG	2U	201	1/1	0.97	0.09	35,35,35,35	0
56	MG	1A	3857	1/1	0.97	0.04	25,25,25,25	0
56	MG	1A	3057	1/1	0.97	0.27	43,43,43,43	0
56	MG	1A	3141	1/1	0.97	0.20	44,44,44,44	0
56	MG	1A	3582	1/1	0.97	0.08	42,42,42,42	0
56	MG	1A	3524	1/1	0.97	0.08	32,32,32,32	0
56	MG	2a	1759	1/1	0.97	0.09	75,75,75,75	0
56	MG	1D	302	1/1	0.97	0.06	32,32,32,32	0
56	MG	2A	3109	1/1	0.97	0.04	40,40,40,40	0
56	MG	2A	3110	1/1	0.97	0.05	31,31,31,31	0
56	MG	2A	3247	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	3078	1/1	0.97	0.11	47,47,47,47	0
56	MG	2a	1765	1/1	0.97	0.08	61,61,61,61	0
56	MG	1A	3071	1/1	0.97	0.11	27,27,27,27	0
56	MG	1A	3786	1/1	0.97	0.14	59,59,59,59	0
56	MG	1A	3586	1/1	0.97	0.08	27,27,27,27	0
56	MG	1a	1624	1/1	0.97	0.05	45,45,45,45	0
56	MG	1D	309	1/1	0.97	0.29	28,28,28,28	0
56	MG	1A	3427	1/1	0.97	0.10	45,45,45,45	0
56	MG	1a	1627	1/1	0.97	0.08	42,42,42,42	0
56	MG	1E	302	1/1	0.97	0.23	35,35,35,35	0
56	MG	1A	3050	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3100	1/1	0.97	0.23	55,55,55,55	0
56	MG	1A	3090	1/1	0.97	0.05	43,43,43,43	0
56	MG	2A	3123	1/1	0.97	0.13	52,52,52,52	0
56	MG	1A	3286	1/1	0.97	0.06	39,39,39,39	0
56	MG	1a	1741	1/1	0.97	0.10	47,47,47,47	0
56	MG	2A	3420	1/1	0.97	0.04	36,36,36,36	0
56	MG	1a	1742	1/1	0.97	0.04	20,20,20,20	0
56	MG	2A	3422	1/1	0.97	0.06	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3129	1/1	0.97	0.17	41,41,41,41	0
56	MG	2A	3130	1/1	0.97	0.10	66,66,66,66	0
56	MG	1A	3795	1/1	0.97	0.04	32,32,32,32	0
56	MG	1A	3724	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	3875	1/1	0.97	0.05	22,22,22,22	0
56	MG	1A	3595	1/1	0.97	0.10	48,48,48,48	0
56	MG	1A	3434	1/1	0.97	0.09	25,25,25,25	0
56	MG	1A	3260	1/1	0.97	0.17	37,37,37,37	0
56	MG	1A	3879	1/1	0.97	0.11	34,34,34,34	0
56	MG	1A	3289	1/1	0.97	0.12	44,44,44,44	0
56	MG	1A	3261	1/1	0.97	0.14	36,36,36,36	0
56	MG	1a	1755	1/1	0.97	0.11	44,44,44,44	0
56	MG	1a	1756	1/1	0.97	0.06	40,40,40,40	0
56	MG	1G	3004	1/1	0.97	0.05	51,51,51,51	0
56	MG	1A	3262	1/1	0.97	0.25	31,31,31,31	0
56	MG	2A	3007	1/1	0.97	0.07	34,34,34,34	0
56	MG	2a	1630	1/1	0.97	0.23	62,62,62,62	0
56	MG	2A	3440	1/1	0.97	0.13	37,37,37,37	0
56	MG	2A	3441	1/1	0.97	0.13	48,48,48,48	0
56	MG	1A	3731	1/1	0.97	0.13	52,52,52,52	0
56	MG	2f	3001	1/1	0.97	0.11	47,47,47,47	0
56	MG	1A	3601	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3602	1/1	0.97	0.12	33,33,33,33	0
56	MG	2A	3445	1/1	0.97	0.17	53,53,53,53	0
56	MG	1A	3887	1/1	0.97	0.04	27,27,27,27	0
56	MG	1A	3603	1/1	0.97	0.23	54,54,54,54	0
56	MG	1A	3889	1/1	0.97	0.05	40,40,40,40	0
56	MG	1A	3488	1/1	0.97	0.12	32,32,32,32	0
56	MG	1A	3541	1/1	0.97	0.07	58,58,58,58	0
56	MG	2A	3155	1/1	0.97	0.29	46,46,46,46	0
56	MG	1A	3892	1/1	0.97	0.22	34,34,34,34	0
56	MG	1a	1773	1/1	0.97	0.07	44,44,44,44	0
56	MG	2a	1645	1/1	0.97	0.14	47,47,47,47	0
56	MG	1A	3737	1/1	0.97	0.11	40,40,40,40	0
56	MG	2A	3622	1/1	0.97	0.23	49,49,49,49	0
56	MG	1A	3738	1/1	0.97	0.15	39,39,39,39	0
56	MG	1A	3896	1/1	0.97	0.27	41,41,41,41	0
56	MG	2A	3027	1/1	0.97	0.27	45,45,45,45	0
56	MG	2A	3298	1/1	0.97	0.11	56,56,56,56	0
56	MG	1A	3263	1/1	0.97	0.12	42,42,42,42	0
56	MG	1A	3607	1/1	0.97	0.08	48,48,48,48	0
56	MG	1A	3073	1/1	0.97	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
56	MG	2A	3302	1/1	0.97	0.07	33,33,33,33	0
56	MG	2A	3165	1/1	0.97	0.15	31,31,31,31	0
56	MG	1A	3400	1/1	0.97	0.07	35,35,35,35	0
56	MG	1A	3902	1/1	0.97	0.08	40,40,40,40	0
56	MG	1A	3193	1/1	0.97	0.14	40,40,40,40	0
56	MG	1A	3818	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	3326	1/1	0.97	0.10	44,44,44,44	0
56	MG	1A	3445	1/1	0.97	0.06	26,26,26,26	0
56	MG	2A	3172	1/1	0.97	0.14	36,36,36,36	0
56	MG	1a	1630	1/1	0.98	0.06	27,27,27,27	0
56	MG	1A	3880	1/1	0.98	0.14	23,23,23,23	0
56	MG	2A	3002	1/1	0.98	0.14	29,29,29,29	0
56	MG	1A	3418	1/1	0.98	0.10	54,54,54,54	0
56	MG	1A	3157	1/1	0.98	0.06	41,41,41,41	0
56	MG	1A	3035	1/1	0.98	0.06	41,41,41,41	0
56	MG	2A	3297	1/1	0.98	0.06	36,36,36,36	0
56	MG	1A	3362	1/1	0.98	0.14	60,60,60,60	0
56	MG	1A	3392	1/1	0.98	0.07	31,31,31,31	0
56	MG	1A	3080	1/1	0.98	0.19	41,41,41,41	0
56	MG	1A	3628	1/1	0.98	0.06	46,46,46,46	0
56	MG	2A	3010	1/1	0.98	0.06	34,34,34,34	0
56	MG	2A	3011	1/1	0.98	0.04	35,35,35,35	0
56	MG	2A	3012	1/1	0.98	0.06	43,43,43,43	0
56	MG	2A	3107	1/1	0.98	0.05	42,42,42,42	0
56	MG	2A	3014	1/1	0.98	0.09	41,41,41,41	0
56	MG	1a	1639	1/1	0.98	0.06	43,43,43,43	0
56	MG	1A	3832	1/1	0.98	0.07	23,23,23,23	0
56	MG	1A	3177	1/1	0.98	0.16	52,52,52,52	0
56	MG	2a	1619	1/1	0.98	0.11	40,40,40,40	0
56	MG	1A	3160	1/1	0.98	0.10	24,24,24,24	0
56	MG	1W	3003	1/1	0.98	0.11	34,34,34,34	0
56	MG	1A	3631	1/1	0.98	0.12	36,36,36,36	0
56	MG	2A	3021	1/1	0.98	0.07	29,29,29,29	0
56	MG	1X	101	1/1	0.98	0.12	38,38,38,38	0
56	MG	1X	102	1/1	0.98	0.08	38,38,38,38	0
56	MG	1A	3836	1/1	0.98	0.06	48,48,48,48	0
56	MG	1A	3161	1/1	0.98	0.11	32,32,32,32	0
56	MG	1A	3258	1/1	0.98	0.24	29,29,29,29	0
56	MG	1A	3369	1/1	0.98	0.19	37,37,37,37	0
56	MG	1A	3897	1/1	0.98	0.12	30,30,30,30	0
56	MG	1B	225	1/1	0.98	0.07	41,41,41,41	0
56	MG	1A	3588	1/1	0.98	0.06	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3065	1/1	0.98	0.14	29,29,29,29	0
56	MG	1A	3136	1/1	0.98	0.24	36,36,36,36	0
56	MG	2A	3660	1/1	0.98	0.13	47,47,47,47	0
56	MG	2A	3128	1/1	0.98	0.11	33,33,33,33	0
56	MG	1A	3148	1/1	0.98	0.23	35,35,35,35	0
56	MG	2A	3433	1/1	0.98	0.08	34,34,34,34	0
56	MG	1A	3592	1/1	0.98	0.12	43,43,43,43	0
56	MG	1D	306	1/1	0.98	0.12	36,36,36,36	0
56	MG	1a	1734	1/1	0.98	0.06	53,53,53,53	0
56	MG	2A	3037	1/1	0.98	0.07	51,51,51,51	0
56	MG	1D	307	1/1	0.98	0.12	40,40,40,40	0
56	MG	1A	3432	1/1	0.98	0.05	29,29,29,29	0
56	MG	1A	3904	1/1	0.98	0.06	27,27,27,27	0
56	MG	1A	3468	1/1	0.98	0.08	30,30,30,30	0
56	MG	1A	3549	1/1	0.98	0.05	40,40,40,40	0
56	MG	1A	3907	1/1	0.98	0.11	34,34,34,34	0
56	MG	1A	3183	1/1	0.98	0.21	36,36,36,36	0
56	MG	1A	3403	1/1	0.98	0.07	15,15,15,15	0
56	MG	1a	1743	1/1	0.98	0.07	38,38,38,38	0
56	MG	1A	3471	1/1	0.98	0.07	28,28,28,28	0
56	MG	1A	3374	1/1	0.98	0.09	32,32,32,32	0
56	MG	2A	3049	1/1	0.98	0.06	41,41,41,41	0
56	MG	1a	1831	1/1	0.98	0.08	37,37,37,37	0
56	MG	1A	3473	1/1	0.98	0.12	36,36,36,36	0
56	MG	1A	3695	1/1	0.98	0.06	45,45,45,45	0
56	MG	1a	1748	1/1	0.98	0.06	38,38,38,38	0
56	MG	1F	303	1/1	0.98	0.13	41,41,41,41	0
56	MG	2a	1777	1/1	0.98	0.19	53,53,53,53	0
56	MG	2A	3348	1/1	0.98	0.06	40,40,40,40	0
56	MG	2B	3006	1/1	0.98	0.11	59,59,59,59	0
56	MG	2A	3151	1/1	0.98	0.26	44,44,44,44	0
56	MG	1A	3474	1/1	0.98	0.09	26,26,26,26	0
56	MG	2A	3572	1/1	0.98	0.04	49,49,49,49	0
56	MG	1A	3513	1/1	0.98	0.04	25,25,25,25	0
56	MG	1A	3375	1/1	0.98	0.06	31,31,31,31	0
56	MG	1F	307	1/1	0.98	0.12	43,43,43,43	0
56	MG	1A	3115	1/1	0.98	0.08	46,46,46,46	0
56	MG	2A	3462	1/1	0.98	0.04	37,37,37,37	0
56	MG	2A	3578	1/1	0.98	0.08	51,51,51,51	0
56	MG	1A	3918	1/1	0.98	0.24	39,39,39,39	0
56	MG	1l	201	1/1	0.98	0.15	40,40,40,40	0
56	MG	2A	3581	1/1	0.98	0.04	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3465	1/1	0.98	0.06	33,33,33,33	0
56	MG	1A	3028	1/1	0.98	0.21	19,19,19,19	0
56	MG	1A	3054	1/1	0.98	0.09	32,32,32,32	0
56	MG	1a	1759	1/1	0.98	0.09	48,48,48,48	0
56	MG	1A	3010	1/1	0.98	0.05	32,32,32,32	0
56	MG	2A	3261	1/1	0.98	0.04	56,56,56,56	0
56	MG	1A	3331	1/1	0.98	0.10	37,37,37,37	0
56	MG	1A	3609	1/1	0.98	0.11	31,31,31,31	0
56	MG	1a	1763	1/1	0.98	0.06	49,49,49,49	0
56	MG	2A	3265	1/1	0.98	0.04	33,33,33,33	0
56	MG	1A	3610	1/1	0.98	0.08	30,30,30,30	0
56	MG	1A	3188	1/1	0.98	0.19	28,28,28,28	0
56	MG	2A	3368	1/1	0.98	0.06	41,41,41,41	0
56	MG	1a	1766	1/1	0.98	0.05	48,48,48,48	0
56	MG	1w	3004	1/1	0.98	0.04	57,57,57,57	0
56	MG	1a	1767	1/1	0.98	0.06	50,50,50,50	0
56	MG	1A	3521	1/1	0.98	0.09	41,41,41,41	0
56	MG	2A	3373	1/1	0.98	0.05	39,39,39,39	0
56	MG	1A	3811	1/1	0.98	0.06	46,46,46,46	0
56	MG	1A	3867	1/1	0.98	0.08	76,76,76,76	0
56	MG	1A	3382	1/1	0.98	0.05	54,54,54,54	0
56	MG	1A	3760	1/1	0.98	0.05	19,19,19,19	0
56	MG	2A	3487	1/1	0.98	0.16	53,53,53,53	0
56	MG	2A	3378	1/1	0.98	0.05	40,40,40,40	0
56	MG	2A	3379	1/1	0.98	0.04	35,35,35,35	0
56	MG	1A	3932	1/1	0.98	0.20	26,26,26,26	0
56	MG	2A	3491	1/1	0.98	0.05	49,49,49,49	0
56	MG	1a	1691	1/1	0.98	0.14	47,47,47,47	0
56	MG	1A	3710	1/1	0.98	0.06	45,45,45,45	0
56	MG	1A	3109	1/1	0.98	0.05	28,28,28,28	0
56	MG	1a	1620	1/1	0.98	0.13	37,37,37,37	0
56	MG	2A	3385	1/1	0.98	0.05	45,45,45,45	0
56	MG	1A	3446	1/1	0.98	0.06	26,26,26,26	0
56	MG	1A	3447	1/1	0.98	0.11	20,20,20,20	0
56	MG	1A	3061	1/1	0.98	0.12	38,38,38,38	0
56	MG	1Q	3003	1/1	0.98	0.04	41,41,41,41	0
56	MG	2A	3502	1/1	0.98	0.05	51,51,51,51	0
56	MG	1A	3155	1/1	0.98	0.14	36,36,36,36	0
59	ZN	2Y	501	1/1	0.98	0.04	85,85,85,85	0
56	MG	1a	1784	1/1	0.98	0.11	45,45,45,45	0
59	ZN	29	501	1/1	0.98	0.05	64,64,64,64	0
56	MG	1A	3271	1/1	0.98	0.07	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	SF4	1d	501	8/8	0.98	0.07	51,62,75,79	0
56	MG	1A	3011	1/1	0.98	0.20	32,32,32,32	0
56	MG	1A	3490	1/1	0.98	0.04	9,9,9,9	0
56	MG	1A	3824	1/1	0.98	0.09	53,53,53,53	0
56	MG	1A	3559	1/1	0.99	0.09	40,40,40,40	0
56	MG	2A	3561	1/1	0.99	0.07	34,34,34,34	0
56	MG	1A	3132	1/1	0.99	0.07	17,17,17,17	0
56	MG	1B	215	1/1	0.99	0.04	26,26,26,26	0
56	MG	1A	3006	1/1	0.99	0.04	42,42,42,42	0
56	MG	1A	3368	1/1	0.99	0.11	37,37,37,37	0
56	MG	1a	1815	1/1	0.99	0.06	49,49,49,49	0
56	MG	1A	3816	1/1	0.99	0.07	25,25,25,25	0
56	MG	1a	1783	1/1	0.99	0.08	58,58,58,58	0
56	MG	1A	3298	1/1	0.99	0.23	53,53,53,53	0
56	MG	1A	3450	1/1	0.99	0.05	36,36,36,36	0
56	MG	2A	3154	1/1	0.99	0.06	49,49,49,49	0
56	MG	2A	3013	1/1	0.99	0.04	33,33,33,33	0
56	MG	2A	3493	1/1	0.99	0.04	39,39,39,39	0
56	MG	1A	3174	1/1	0.99	0.06	39,39,39,39	0
56	MG	1A	3047	1/1	0.99	0.12	28,28,28,28	0
56	MG	1A	3794	1/1	0.99	0.03	21,21,21,21	0
56	MG	1A	3062	1/1	0.99	0.04	31,31,31,31	0
56	MG	1A	3933	1/1	0.99	0.07	44,44,44,44	0
56	MG	1A	3019	1/1	0.99	0.06	38,38,38,38	0
56	MG	2A	3125	1/1	0.99	0.08	40,40,40,40	0
56	MG	1A	3389	1/1	0.99	0.10	23,23,23,23	0
56	MG	1a	1695	1/1	0.99	0.16	42,42,42,42	0
56	MG	1A	3748	1/1	0.99	0.07	33,33,33,33	0
56	MG	2A	3584	1/1	0.99	0.04	36,36,36,36	0
56	MG	1A	3224	1/1	0.99	0.16	32,32,32,32	0
56	MG	1A	3004	1/1	0.99	0.07	47,47,47,47	0
56	MG	1A	3704	1/1	0.99	0.10	26,26,26,26	0
56	MG	1A	3021	1/1	0.99	0.15	17,17,17,17	0
56	MG	1A	3551	1/1	0.99	0.03	35,35,35,35	0
56	MG	1A	3552	1/1	0.99	0.05	20,20,20,20	0
56	MG	2A	3549	1/1	0.99	0.07	62,62,62,62	0
59	ZN	1Y	501	1/1	0.99	0.04	71,71,71,71	0
56	MG	1A	3202	1/1	0.99	0.07	46,46,46,46	0
59	ZN	15	103	1/1	0.99	0.14	81,81,81,81	0
56	MG	1A	3066	1/1	0.99	0.14	17,17,17,17	0
59	ZN	1n	501	1/1	0.99	0.03	56,56,56,56	0
56	MG	2A	3397	1/1	0.99	0.04	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3534	1/1	0.99	0.04	40,40,40,40	0
59	ZN	25	501	1/1	0.99	0.03	54,54,54,54	0
59	ZN	26	501	1/1	0.99	0.04	63,63,63,63	0
56	MG	1E	304	1/1	0.99	0.12	23,23,23,23	0
56	MG	1Q	3001	1/1	0.99	0.08	36,36,36,36	0
56	MG	1A	3782	1/1	0.99	0.08	45,45,45,45	0
56	MG	1A	3443	1/1	0.99	0.08	31,31,31,31	0
56	MG	1A	3008	1/1	0.99	0.04	29,29,29,29	0
56	MG	1A	3033	1/1	0.99	0.12	20,20,20,20	0
59	ZN	19	501	1/1	1.00	0.04	42,42,42,42	0
56	MG	1a	1758	1/1	1.00	0.04	29,29,29,29	0
56	MG	1A	3525	1/1	1.00	0.09	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.