



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:54 PM UTC

PDB ID : 9MTT / pdb_00009mtt
Title : Crystal structure of the wild-type *Thermus thermophilus* 70S ribosome in complex with mRNA, A-site Q230-N5-methylated Release Factor 1, and P-site deacylated-tRNA_{cys} at 2.60Å resolution
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Deposited on : 2025-01-12
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

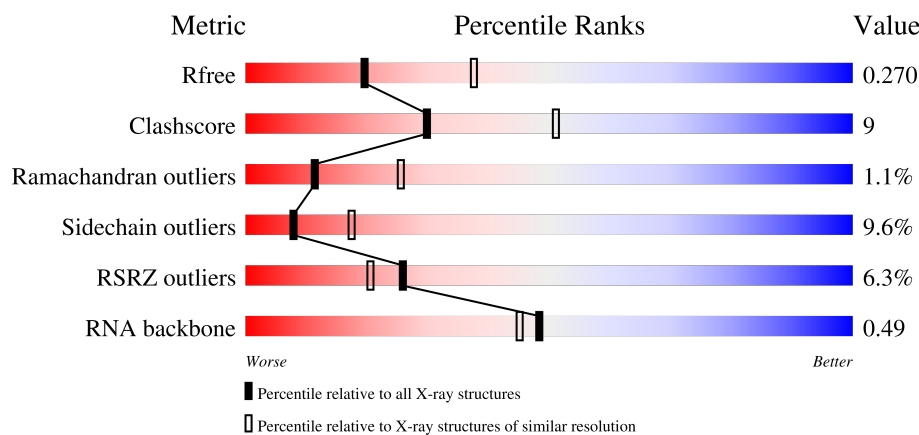
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)
RNA backbone	3983	1014 (2.84-2.36)

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	 5% 64% 27% 7% .
1	2A	2915	 3% 60% 30% 6% .
2	1B	121	 69% 28% ..

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Mol	Chain	Length	Quality of chain
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	
14	2S	112	

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Mol	Chain	Length	Quality of chain
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	
27	15	60	

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Mol	Chain	Length	Quality of chain
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	
39	2h	138	

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Mol	Chain	Length	Quality of chain
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	
52	1u	27	

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Mol	Chain	Length	Quality of chain
52	2u	27	
53	1v	24	
53	2v	24	
54	1w	354	
54	2w	354	
55	1x	74	
55	2x	74	

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	1733	-	-	-	X
56	MG	2a	1694	-	-	-	X
59	SF4	1d	302	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 296938 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
			1423	913	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	4			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	146	Total	C	N	O	S	0	0	0
			1097	701	191	204	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	1			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	154	Total	C	N	O	S	0	0	0
			1240	795	222	220	3			
21	2Z	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	76	Total	C	N	O	S	0	0	0
			604	373	128	102	1			
22	20	76	Total	C	N	O	S	0	0	0
			604	373	128	102	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	118	Total	C	N	O	S	0	0	0
			919	566	190	161	2			
44	2m	116	Total	C	N	O	S	0	0	0
			907	558	188	159	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			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 CYS-Stop mRNA.

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

- Molecule 54 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	1w	249	Total	C	N	O	S	0	0	0
			1939	1199	360	371	9			
54	2w	253	Total	C	N	O	S	0	0	0
			1957	1210	361	377	9			

- Molecule 55 is a RNA chain called P-site deacylated-tRNA_{cys}.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	1x	74	Total	C	N	O	P	S	0	0
			1577	704	280	518	74	1		
55	2x	74	Total	C	N	O	P	S	0	0
			1577	704	280	518	74	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	1083	Total	Mg	0	0
			1083	1083		
56	1B	37	Total	Mg	0	0
			37	37		
56	1D	14	Total	Mg	0	0
			14	14		
56	1E	17	Total	Mg	0	0
			17	17		
56	1F	14	Total	Mg	0	0
			14	14		
56	1G	4	Total	Mg	0	0
			4	4		
56	1I	1	Total	Mg	0	0
			1	1		
56	1N	8	Total	Mg	0	0
			8	8		
56	1O	5	Total	Mg	0	0
			5	5		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1P	6	Total 6	Mg 6	0	0
56	1Q	7	Total 7	Mg 7	0	0
56	1R	4	Total 4	Mg 4	0	0
56	1S	3	Total 3	Mg 3	0	0
56	1T	3	Total 3	Mg 3	0	0
56	1U	10	Total 10	Mg 10	0	0
56	1V	6	Total 6	Mg 6	0	0
56	1W	7	Total 7	Mg 7	0	0
56	1X	6	Total 6	Mg 6	0	0
56	1Y	3	Total 3	Mg 3	0	0
56	1Z	2	Total 2	Mg 2	0	0
56	10	6	Total 6	Mg 6	0	0
56	11	4	Total 4	Mg 4	0	0
56	12	3	Total 3	Mg 3	0	0
56	13	6	Total 6	Mg 6	0	0
56	14	1	Total 1	Mg 1	0	0
56	15	8	Total 8	Mg 8	0	0
56	16	2	Total 2	Mg 2	0	0
56	17	7	Total 7	Mg 7	0	0
56	18	4	Total 4	Mg 4	0	0
56	1a	224	Total 224	Mg 224	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1b	2	Total 2	Mg 2	0	0
56	1d	1	Total 1	Mg 1	0	0
56	1e	4	Total 4	Mg 4	0	0
56	1f	2	Total 2	Mg 2	0	0
56	1k	1	Total 1	Mg 1	0	0
56	1l	2	Total 2	Mg 2	0	0
56	1m	1	Total 1	Mg 1	0	0
56	1n	1	Total 1	Mg 1	0	0
56	1p	1	Total 1	Mg 1	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1v	4	Total 4	Mg 4	0	0
56	1w	1	Total 1	Mg 1	0	0
56	1x	13	Total 13	Mg 13	0	0
56	2A	870	Total 870	Mg 870	0	0
56	2B	20	Total 20	Mg 20	0	0
56	2D	6	Total 6	Mg 6	0	0
56	2E	7	Total 7	Mg 7	0	0
56	2F	6	Total 6	Mg 6	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

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2P	1	Total 1	Mg 1	0	0
56	2Q	4	Total 4	Mg 4	0	0
56	2R	3	Total 3	Mg 3	0	0
56	2T	3	Total 3	Mg 3	0	0
56	2U	2	Total 2	Mg 2	0	0
56	2V	2	Total 2	Mg 2	0	0
56	2W	4	Total 4	Mg 4	0	0
56	2X	2	Total 2	Mg 2	0	0
56	2Z	1	Total 1	Mg 1	0	0
56	20	1	Total 1	Mg 1	0	0
56	21	1	Total 1	Mg 1	0	0
56	23	3	Total 3	Mg 3	0	0
56	25	5	Total 5	Mg 5	0	0
56	26	1	Total 1	Mg 1	0	0
56	27	1	Total 1	Mg 1	0	0
56	28	3	Total 3	Mg 3	0	0
56	2a	176	Total 176	Mg 176	0	0
56	2d	2	Total 2	Mg 2	0	0
56	2e	1	Total 1	Mg 1	0	0
56	2f	1	Total 1	Mg 1	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 2 2	0	0
56	2l	2	Total Mg 2 2	0	0
56	2q	2	Total Mg 2 2	0	0
56	2r	2	Total Mg 2 2	0	0
56	2t	1	Total Mg 1 1	0	0
56	2v	2	Total Mg 2 2	0	0
56	2x	6	Total Mg 6 6	0	0

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1A	1	Total K 1 1	0	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

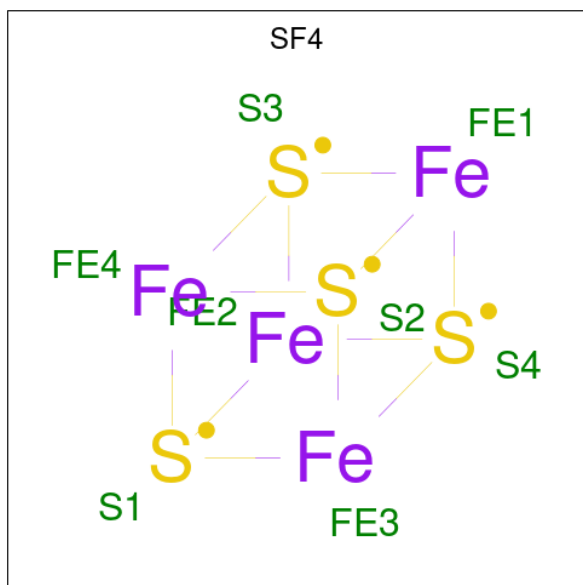
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1Y	1	Total Zn 1 1	0	0
58	14	1	Total Zn 1 1	0	0
58	15	1	Total Zn 1 1	0	0
58	16	1	Total Zn 1 1	0	0
58	19	1	Total Zn 1 1	0	0
58	1n	1	Total Zn 1 1	0	0
58	2Y	1	Total Zn 1 1	0	0
58	24	1	Total Zn 1 1	0	0
58	25	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	26	1	Total	Zn	0	0
			1	1		
58	29	1	Total	Zn	0	0
			1	1		
58	2n	1	Total	Zn	0	0
			1	1		

- Molecule 59 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
59	1d	1	Total	Fe	S	0	0
			8	4	4		
59	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 60 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1A	1841	Total	O	0	0
			1841	1841		
60	1B	66	Total	O	0	0
			66	66		
60	1D	24	Total	O	0	0
			24	24		
60	1E	27	Total	O	0	0
			27	27		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1F	16	Total 16	O 16	0	0
60	1G	3	Total 3	O 3	0	0
60	1H	2	Total 2	O 2	0	0
60	1N	5	Total 5	O 5	0	0
60	1O	5	Total 5	O 5	0	0
60	1P	20	Total 20	O 20	0	0
60	1Q	5	Total 5	O 5	0	0
60	1R	15	Total 15	O 15	0	0
60	1S	4	Total 4	O 4	0	0
60	1T	5	Total 5	O 5	0	0
60	1U	15	Total 15	O 15	0	0
60	1V	7	Total 7	O 7	0	0
60	1W	12	Total 12	O 12	0	0
60	1X	7	Total 7	O 7	0	0
60	1Y	1	Total 1	O 1	0	0
60	1Z	1	Total 1	O 1	0	0
60	10	10	Total 10	O 10	0	0
60	11	9	Total 9	O 9	0	0
60	12	4	Total 4	O 4	0	0
60	13	5	Total 5	O 5	0	0
60	15	5	Total 5	O 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	16	1	Total O 1 1	0	0
60	17	8	Total O 8 8	0	0
60	18	13	Total O 13 13	0	0
60	1a	274	Total O 274 274	0	0
60	1b	1	Total O 1 1	0	0
60	1g	1	Total O 1 1	0	0
60	1l	2	Total O 2 2	0	0
60	1n	1	Total O 1 1	0	0
60	1o	1	Total O 1 1	0	0
60	1q	1	Total O 1 1	0	0
60	1u	1	Total O 1 1	0	0
60	1v	3	Total O 3 3	0	0
60	1w	2	Total O 2 2	0	0
60	1x	15	Total O 15 15	0	0
60	2A	1163	Total O 1163 1163	0	0
60	2B	25	Total O 25 25	0	0
60	2D	22	Total O 22 22	0	0
60	2E	15	Total O 15 15	0	0
60	2F	11	Total O 11 11	0	0
60	2I	1	Total O 1 1	0	0
60	2N	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	2O	2	Total 2	O 2	0	0
60	2P	11	Total 11	O 11	0	0
60	2Q	1	Total 1	O 1	0	0
60	2R	5	Total 5	O 5	0	0
60	2T	5	Total 5	O 5	0	0
60	2U	2	Total 2	O 2	0	0
60	2V	2	Total 2	O 2	0	0
60	2W	4	Total 4	O 4	0	0
60	2X	3	Total 3	O 3	0	0
60	2Z	1	Total 1	O 1	0	0
60	20	5	Total 5	O 5	0	0
60	21	10	Total 10	O 10	0	0
60	23	2	Total 2	O 2	0	0
60	25	2	Total 2	O 2	0	0
60	27	6	Total 6	O 6	0	0
60	28	3	Total 3	O 3	0	0
60	29	1	Total 1	O 1	0	0
60	2a	138	Total 138	O 138	0	0
60	2d	1	Total 1	O 1	0	0
60	2e	1	Total 1	O 1	0	0
60	2g	1	Total 1	O 1	0	0

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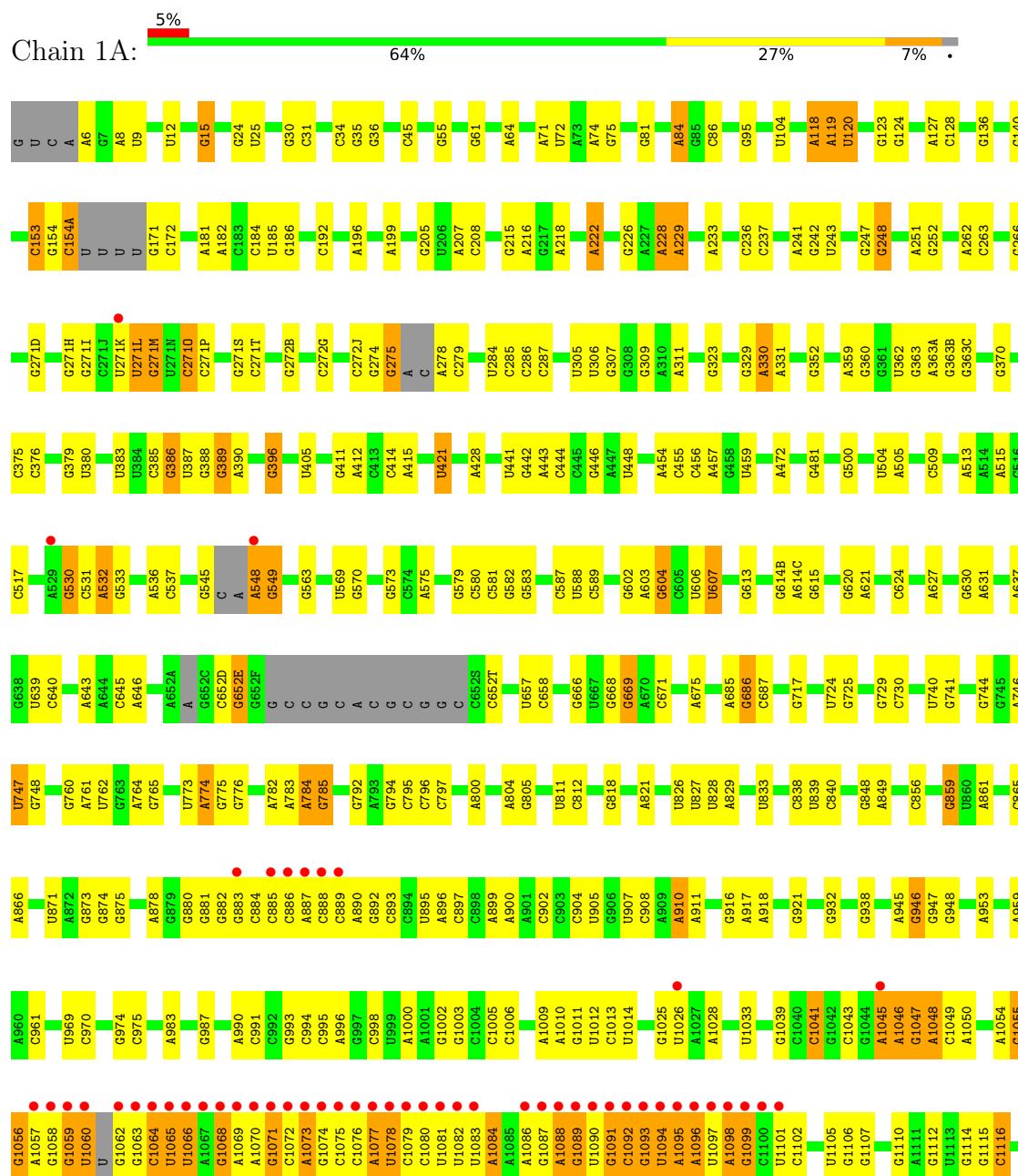
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	2j	3	Total 3	O 3	0	0
60	2l	3	Total 3	O 3	0	0
60	2q	1	Total 1	O 1	0	0
60	2t	2	Total 2	O 2	0	0
60	2v	1	Total 1	O 1	0	0
60	2w	3	Total 3	O 3	0	0
60	2x	8	Total 8	O 8	0	0

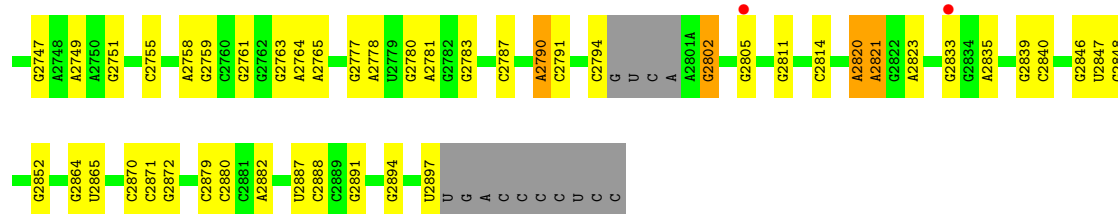
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

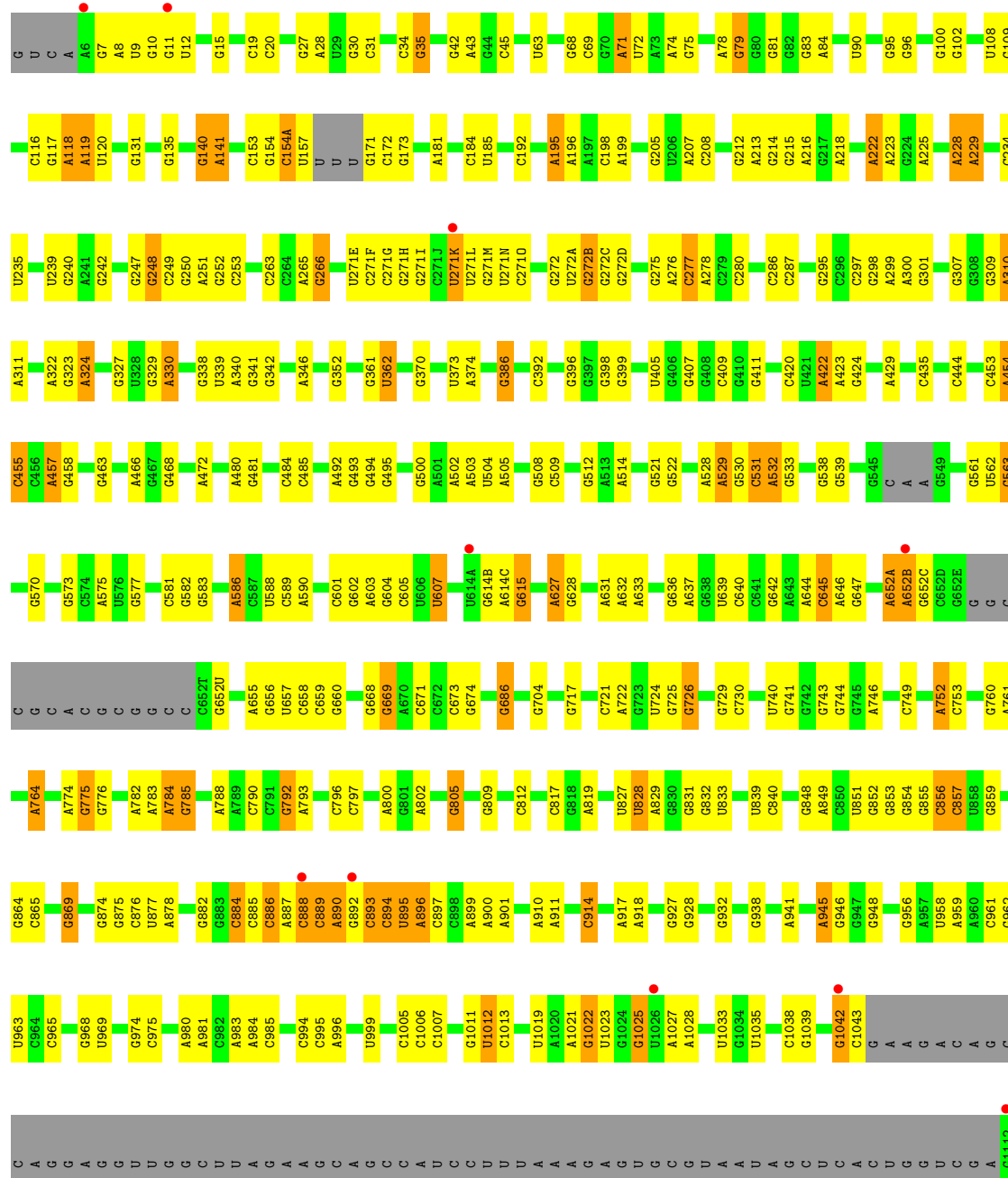
• Molecule 1: 23S Ribosomal RNA



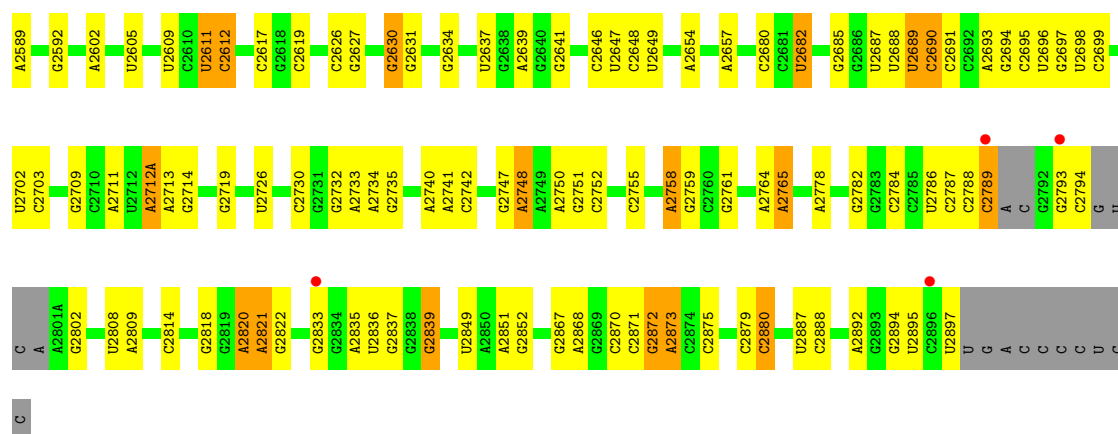
G125	A1241	A1359	G1459	G1607	G1763	C1881	C1996	C2108	C2168	G2217	G2383	U2506	G2618
A1128	G1252	A1360	G1460	A1608	G1764	C1882	G1997	U2109	A2169	A2278	G2384	C2507	C2619
G1132	A1253	G1364	G1461	A1609	G1769	G1883	A2001	C2111	A2171	G2279	G2385	G2508	C2626
G1135	G1256	A1365	C1467	A1610	A1773	A1889	G2002	G2112	A2172	C2283	U2390	G2512	G2627
G1136	U1283	C1370	C1468	A1637	U1778	A1890	A2013	G2113	A2173	C2284	G2396	A2518	G2628
G1137	U1283	G1371	G1473	A1641	U1779	G1891	A2014	G2115	C2175	C2285	U2396	A2523	A2623
G1138	U1284	A1373	G1473	A1642	U1780	C1892	A2015	G2116	A2176	A2286	G2400	C2521	G2630
A1142A	A1285	A1373	G1482	G1647	C1781	G1899	A2020	G2117	A2177	A2287	G2400	U2522	A2632
C1152	A1266	C1376	G1484	C1648	C1782	A1901	U2022	G2119	C2178	C2288	U2406	G2529	C2646
A1155	U1267	A1379	G1485	G1651	A1784	C1902	G2023	G2120	U2180	G2290	G2409	G2647	U2647
C1158	A1268	G1380	A1486	A1652	A1785	G1906	G2029	G2121	G2181	U2291	G2410	A2530	A2654
G1164	G1271	A1384	G1487	A1653	A1786	G1911	A2030	U2122	G2182	C2292	G2422	A2531	U2654
U1165	A1272	G1385	G1488	A1654	C1790	U1915	A2031	G2123	C2185	C2293	A2423	G2535	C2658
C1166	U1273	A1385	A1489	A1654	A1791	U1916	A2032	G2124	U2189	C2294	U2424	U2537	G2663
G1171	A1274	C1399	A1490	A1665	A1800	U1917	A2033	G2125	G2190	A2298	A2425	C2538	U2663
A1174	U1282	G1400	C1493	A1668	C1800	U1918	G2038	C2127	G2191	G2299	A2426	C2538	C2681
U1175	C1293	G1401	A1508	A1669	U1796	U1919	C2039	C2128	G2192	G2303	G2427	G2549	U2682
G1176	U1284	U1405	C1509	A1671	C1797	G1929	C2043	U2130	G2193	G2304	G2428	G2550	C2683
A1177	U1284	U1406	A1509A	U1673	U1798	G1930	U2047	G2131	G2198	A2305	A2429	U2551	U2687
C1178	A1301	U1407	A1509B	U1674	C1799	U1931	G2048	G2132	A2198	G2306	A2430	U2552	U2688
U1179	G1303	A1412	U1512	G1675	C1800	U1932	G2049	G2133	U2203	G2307	U2431	G2553	U2689
C1185	U1293	G1413	C1513	A1676	A1802	A1936	G2050	C2134	G2205	U2312	A2435	U2562	U2690
G1186	C1293	G1413	G1525	A1677	A1803	A1937	A2051	G2135	G2206	G2313	G2436	U2563	C2691
U1188	A1302	G1415	G1528A	A1677	C1804	A1938	G2052	C2136	G2207	C2314	A2439	A2564	A2693
C1188	G1303	C1417	U1528A	U1692	U1805	U1939	G2053	C2138	A2208	G2315	G2440	A2565	G2694
G1186	U1309	U1420	C1532	U1693	A1812	C1942	A2054	C2139	G2224	G2319	C2441	U2567	U2702
G1187	G1310	G1421	G1532	G1696	G1813	G1949	G2055	C2140	G2225	A2320	G2447	C2568	C2703
U1188	G1311	U1312	U	A1700	A1814	G1950	G2056	C2141	A2226	A2321	A2448	A2572	C2704
A1194	U1313	G1424	A	G1703	A1815	U1951	A2059	C2143	A2227	G2326	G2454	C2573	G2705
U1198	C1315	G1425	C	U1712	A1816	U1955	A2060	G2144	G2228	C2326	C2461	G2574	A2711
U1199	U1321	A1427	G1537	U1713	G1817	U1956	A2061	C2145	G2238	A2327	U2462	G2578	U2712
C1200	A1322	C1428	C1547	U1714	U1818	C1957	A2062	G2146	G2239	A2328	U2467	A2713	A2712A
C1201	U1332	G1429	C1548	G1714	G1824	C1958	G2069	G2147	G2240	A2329	U2478	G2591	A2713
G1203	G1332	U1431	A1558	G1721	G1828	C1962	U2074	G2148	U2243	G2330	A2476	G2592	G2714
A1210	C1333	C1437	G1559	A1722	A1829	U1963	U2075	G2150	U2244	U2331	A2477	G2595	G2718
U1211	U1335	A1439	G1560	A1723	U1833	G1964	G2093	G2151	U2245	U2332	C2477	A2602	A2721
C1217	A1336	U1442	A1569	G1740	U1833	C1965	U2096	G2152	G2246	A2333	A2478	G2603	G2722
G1223	G1337	G1442	U1578	C1743	G1839	C1967	G2097	G2153	G2248	A2336	A2478	U2604	C2723
G1223	A1342	A1445	A1579	U1745A	A1847	G1968	U2098	G2154	G2251	C2347	G2490	U2605	U2726
A1226	G1343	A1448	A1580	G1746	G1858	A1969	U2099	G2155	G2255	U2348	U2491	C2609	U2726
G1227	C1345	G1448	C1584	G1746	U1858	A1970	G2100	G2156	G2255	G2349	C2498	U2610	G2732
G1235	U1352	G1450	A1586	G1753	G1866	A1972	G2101	C2161	A2268	C2350	C2499	U2611	A2733
G1239	G1356	A1452	G1593	C1754	A1876	A1986	U2102	G2162	G2271	C2364	G2502	U2612	A2740
U1240	U1453	U1452	G1594	A1755	A1877	G1992	G2104	C2163	A2274	G2365	U2503	A2614	A2741
		G1455	G1595	G1756	G1878	U1993	C2105	C2164	G2275	A2377	U2504	G2617	G2744
				A1762			C2107	U2167	G2276	A2378	G2505		



• Molecule 1: 23S Ribosomal RNA



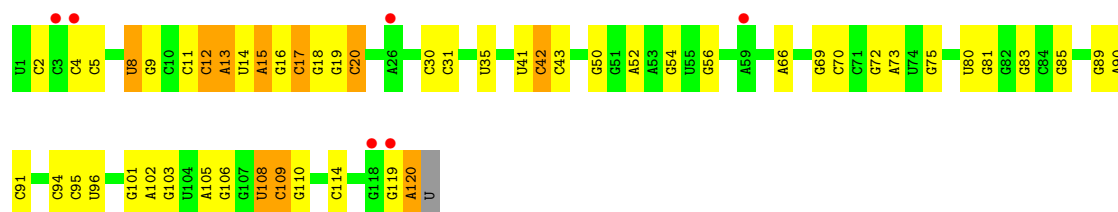
U2493	G2405	C2317	G2186	A2126	C2040	A1927	A1786	G1647	U	G1429	G1315	U1211	U1113
G2494	U2406	G2318	G2187	G2127	U2041	A1928	A1789	C1648	A	C1430	U1316	A1220	G1114
G2496	C2319	C2128	C2188	C2128	C2042	G1929	G1789	G1651	C1536	U1431	C1318	A1221	G1115
A2497	G2321	U2130	U2189	U2130	A2043	G1930	A1791	G1652	G1537	A1434	G1539	G1223	C1116
C2498	A2322	G2131	G2190	G2131	G2049	U1937	U1794	G1653	G1538	C1437	C1320	A1226	C1123
C2499	G2325	U2132	C2050	U2132	A2051	A1938	U1795	A1654	U1540	A1445	C1333	A1227	C1124
G2502	C2326	G2133	G2052	G2133	G2052	U1939	U1796	C1657	C1547	A1446	C1336	G1229	G1125
A2503	A2327	A2135	C2055	A2135	C2055	U1940	U1797	C1658	A1554	C1448	A1337	A1229	A1129
U2504	G2328	C2136	C2056	C2136	G2056	U1941	U1798	A1659	A1555	A1449	G1338	A1230	U1130
G2505	G2329	C2137	G2057	C2137	G2057	U1942	U1799	A1664	A1558	G1447	G1339	A1231	G1131
U2506	G2330	C2138	A2060	C2138	A2060	U1943	C1800	G1666	G1559	G1448	U1341	G1232	A1132
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A2518	G2238	U2144	C2065	U2144	C2065	G1815	A1815	U1671	A1569	G1455	U1353	C1237	C1140
G2524	G2239	C2145	C2066	C2145	C2066	U1963	G1816	A1674	U1578	A1460	A1354	U1238	U1141
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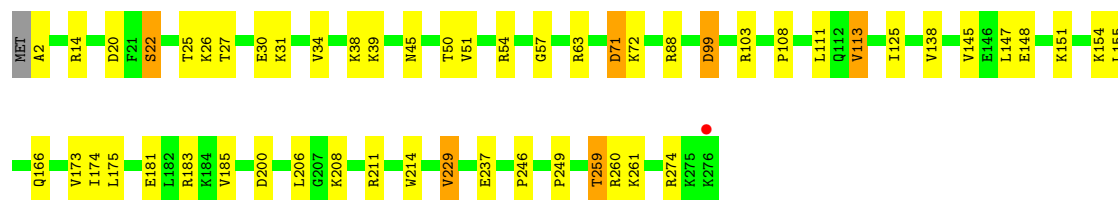
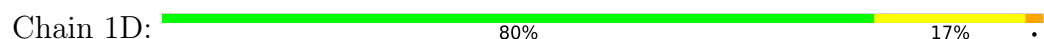
- Molecule 2: 5S Ribosomal RNA



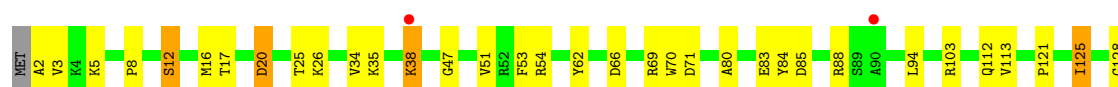
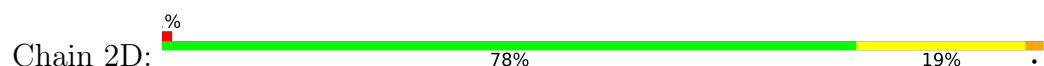
- Molecule 2: 5S Ribosomal RNA



- Molecule 3: 50S ribosomal protein L2



- Molecule 3: 50S ribosomal protein L2





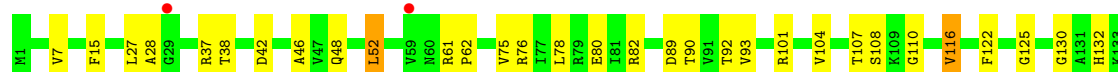
- Molecule 4: 50S ribosomal protein L3

Chain 1E: 84% 14% ..



- Molecule 4: 50S ribosomal protein L3

Chain 2E: 2% 76% 21% ..



- Molecule 5: 50S ribosomal protein L4

Chain 1F: 73% 21% ..



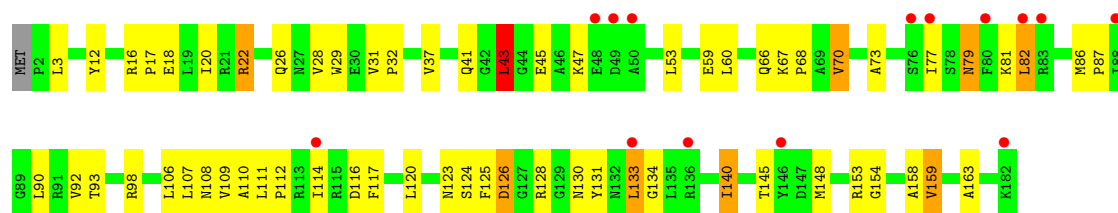
- Molecule 5: 50S ribosomal protein L4

Chain 2F: 68% 24% 5% .

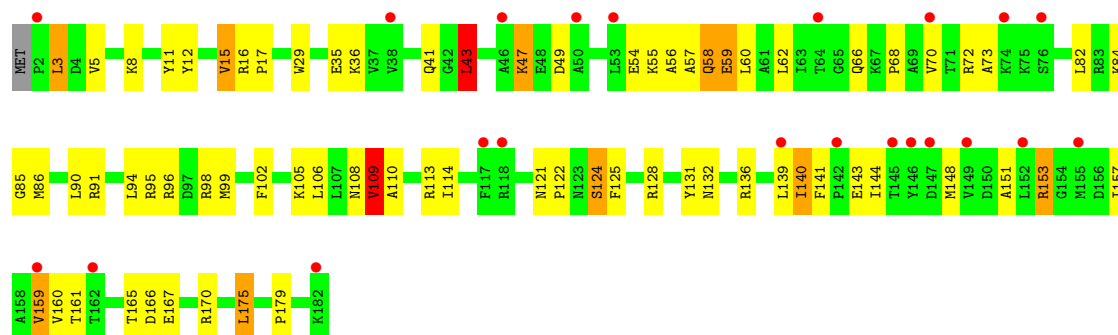


- Molecule 6: 50S ribosomal protein L5

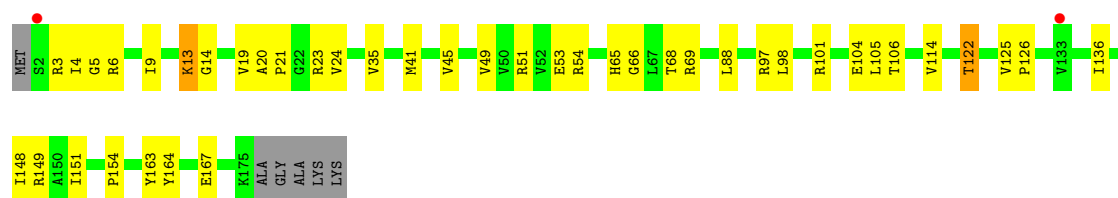
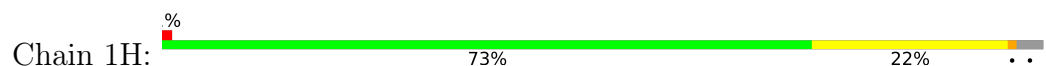
Chain 1G: 8% 65% 30% ..



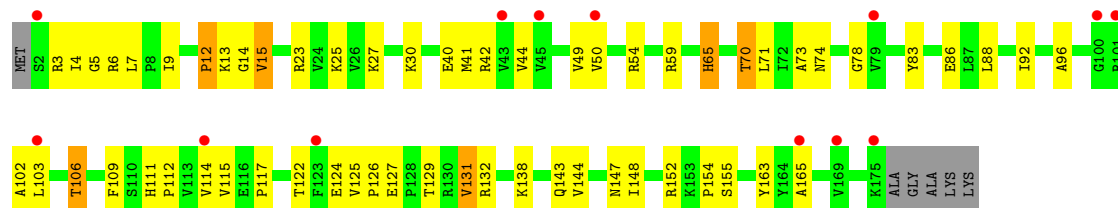
• Molecule 6: 50S ribosomal protein L5



• Molecule 7: 50S ribosomal protein L6



• Molecule 7: 50S ribosomal protein L6

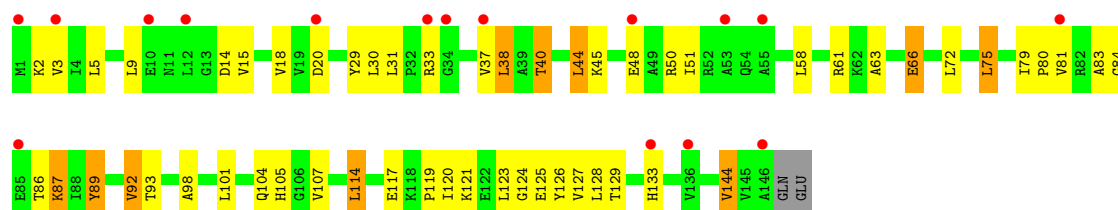


• Molecule 8: 50S ribosomal protein L9

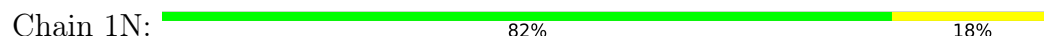




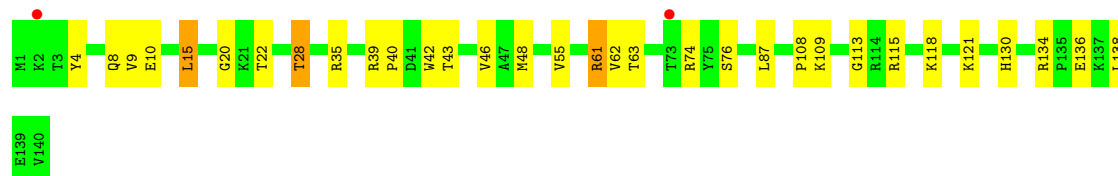
• Molecule 8: 50S ribosomal protein L9



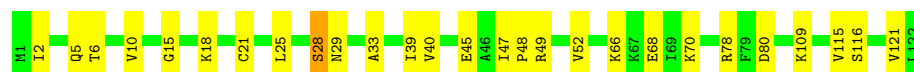
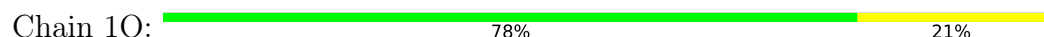
• Molecule 9: 50S ribosomal protein L13



• Molecule 9: 50S ribosomal protein L13



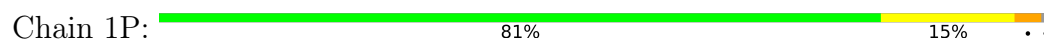
• Molecule 10: 50S ribosomal protein L14

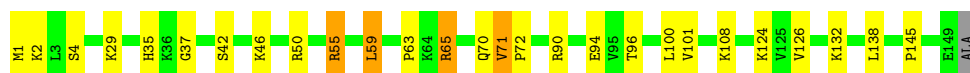


• Molecule 10: 50S ribosomal protein L14

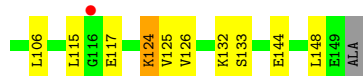


• Molecule 11: 50S ribosomal protein L15

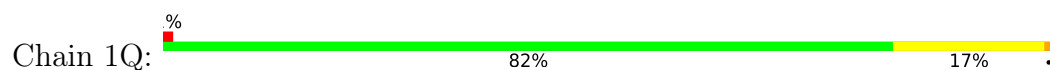




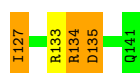
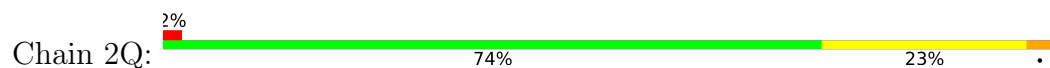
- Molecule 11: 50S ribosomal protein L15



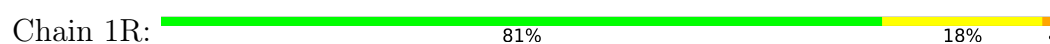
- Molecule 12: 50S ribosomal protein L16



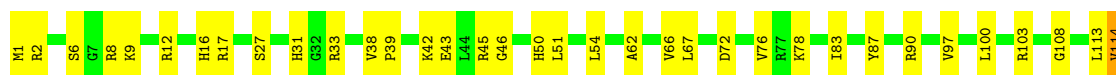
- Molecule 12: 50S ribosomal protein L16



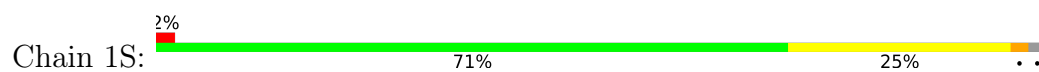
- Molecule 13: 50S ribosomal protein L17



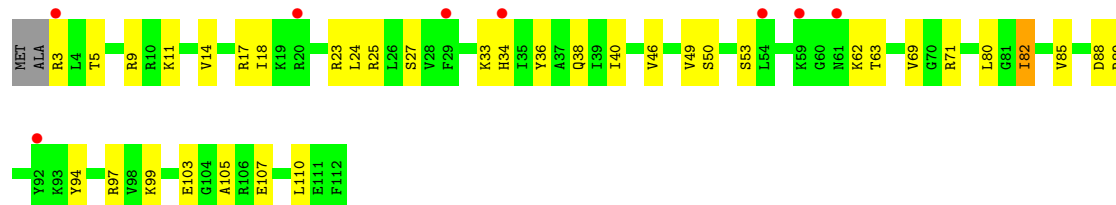
- Molecule 13: 50S ribosomal protein L17



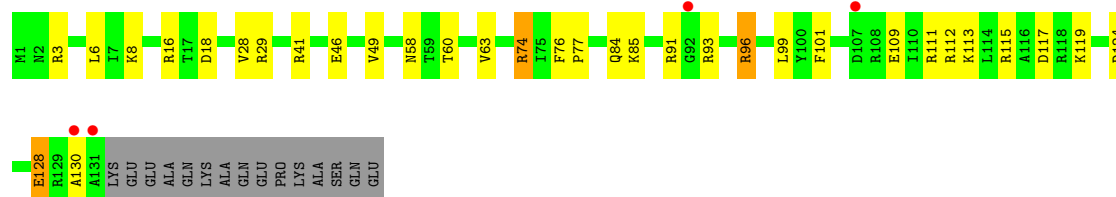
- Molecule 14: 50S ribosomal protein L18



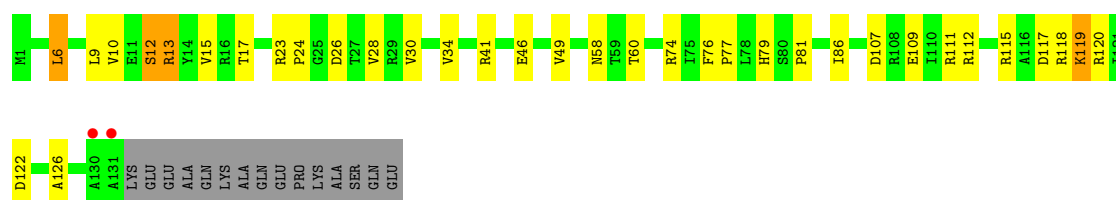
- Molecule 14: 50S ribosomal protein L18



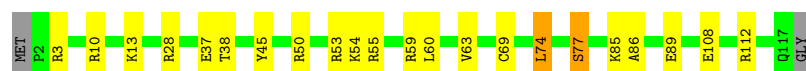
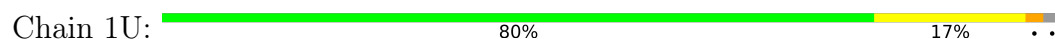
- Molecule 15: 50S ribosomal protein L19



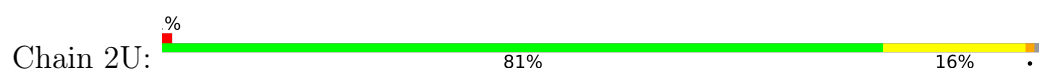
- Molecule 15: 50S ribosomal protein L19

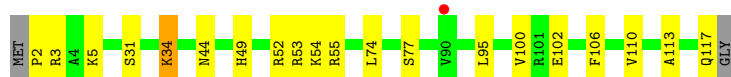


- Molecule 16: 50S ribosomal protein L20

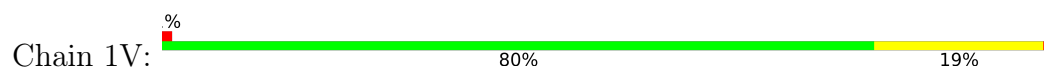


- Molecule 16: 50S ribosomal protein L20





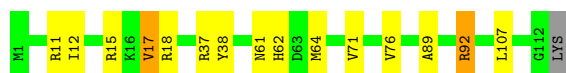
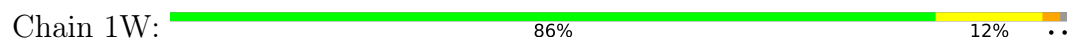
- Molecule 17: 50S ribosomal protein L21



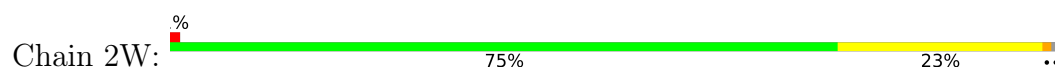
- Molecule 17: 50S ribosomal protein L21



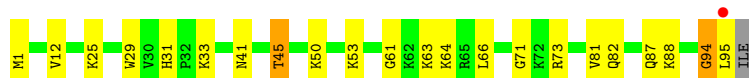
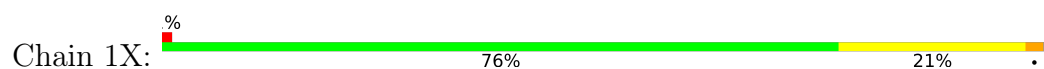
- Molecule 18: 50S ribosomal protein L22



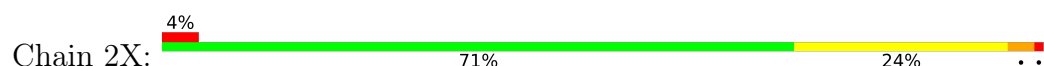
- Molecule 18: 50S ribosomal protein L22



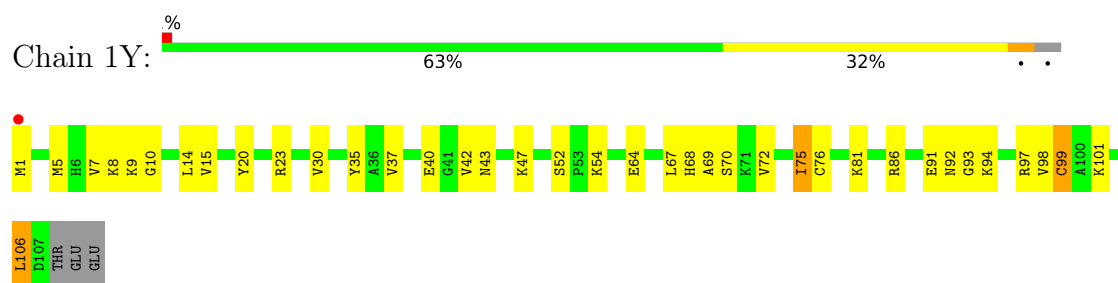
- Molecule 19: 50S ribosomal protein L23



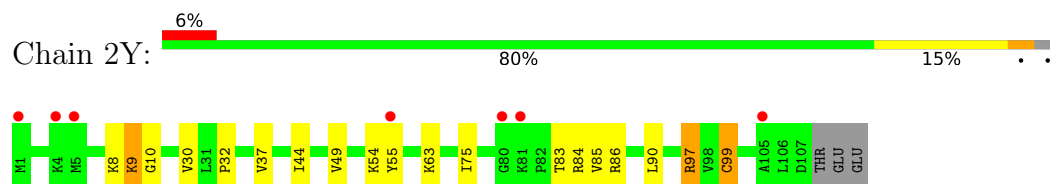
- Molecule 19: 50S ribosomal protein L23



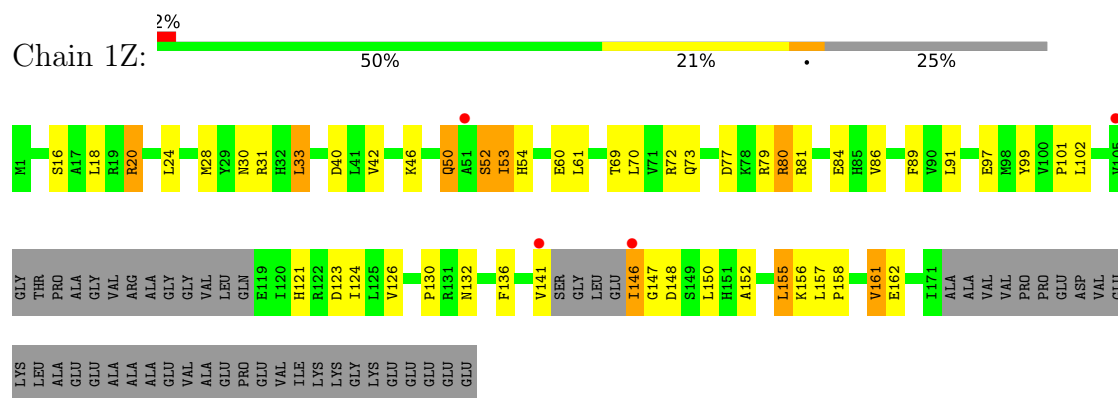
- Molecule 20: 50S ribosomal protein L24



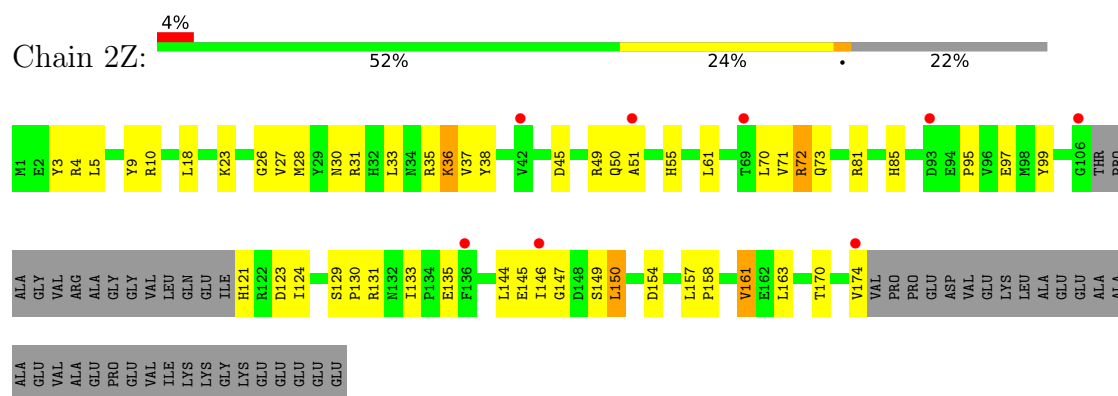
- Molecule 20: 50S ribosomal protein L24



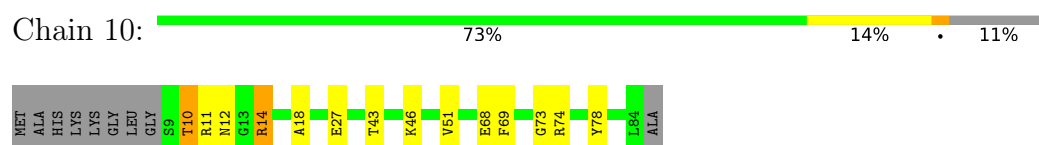
- Molecule 21: 50S ribosomal protein L25



- Molecule 21: 50S ribosomal protein L25



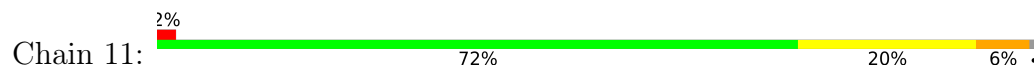
- Molecule 22: 50S ribosomal protein L27



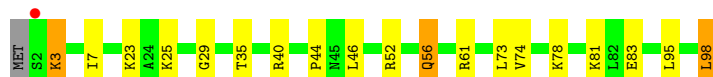
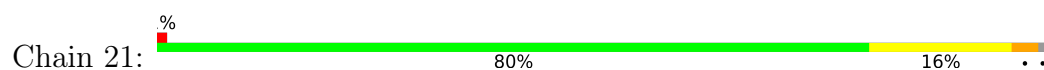
- Molecule 22: 50S ribosomal protein L27



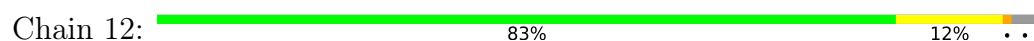
- Molecule 23: 50S ribosomal protein L28



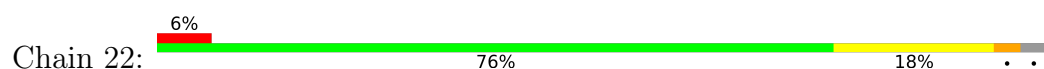
- Molecule 23: 50S ribosomal protein L28



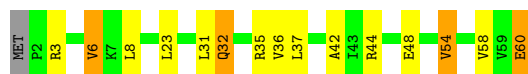
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29



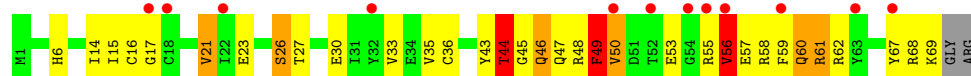
- Molecule 25: 50S ribosomal protein L30



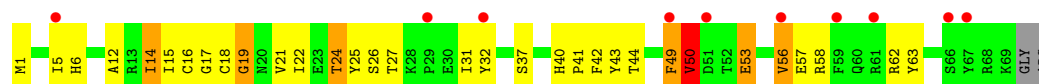
- Molecule 25: 50S ribosomal protein L30



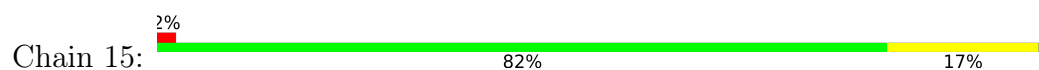
- Molecule 26: 50S ribosomal protein L31



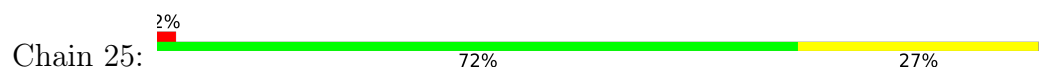
- Molecule 26: 50S ribosomal protein L31



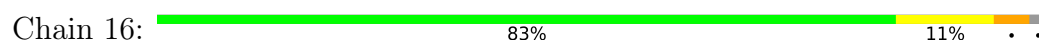
- Molecule 27: 50S ribosomal protein L32



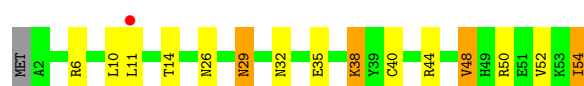
- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



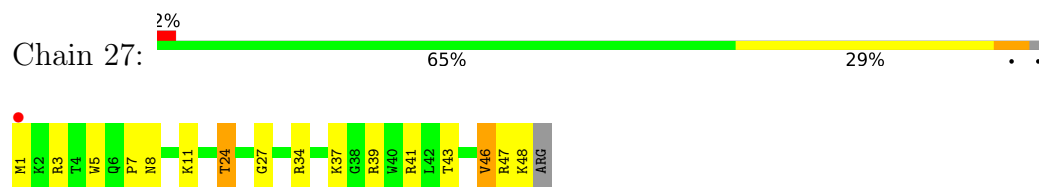
- Molecule 28: 50S ribosomal protein L33



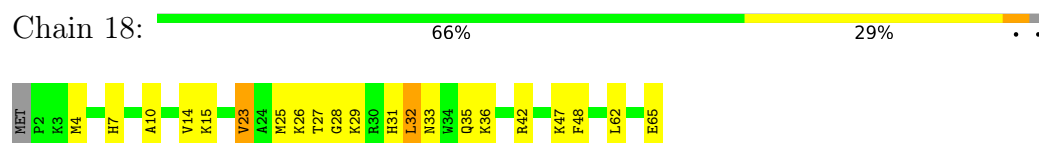
- Molecule 29: 50S ribosomal protein L34



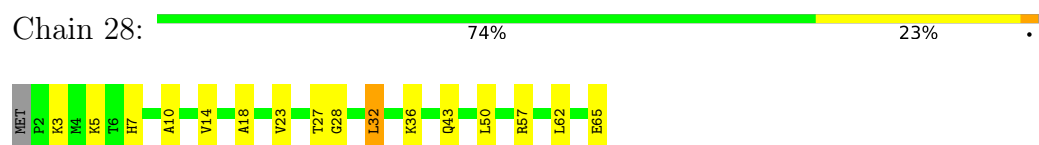
- Molecule 29: 50S ribosomal protein L34



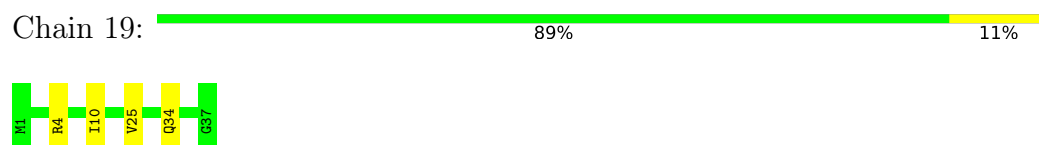
- Molecule 30: 50S ribosomal protein L35



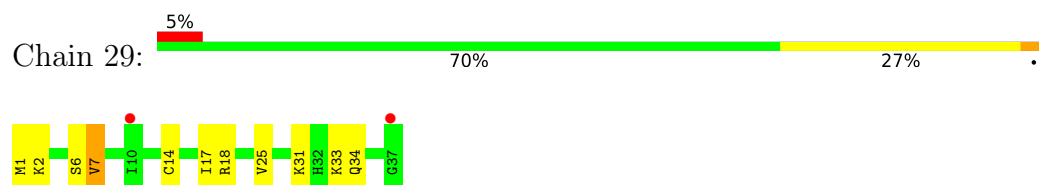
- Molecule 30: 50S ribosomal protein L35



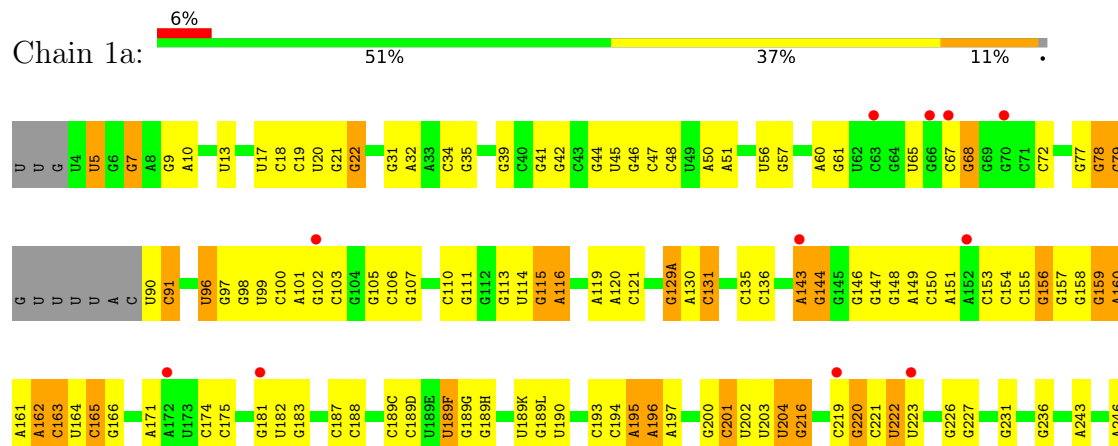
- Molecule 31: 50S ribosomal protein L36

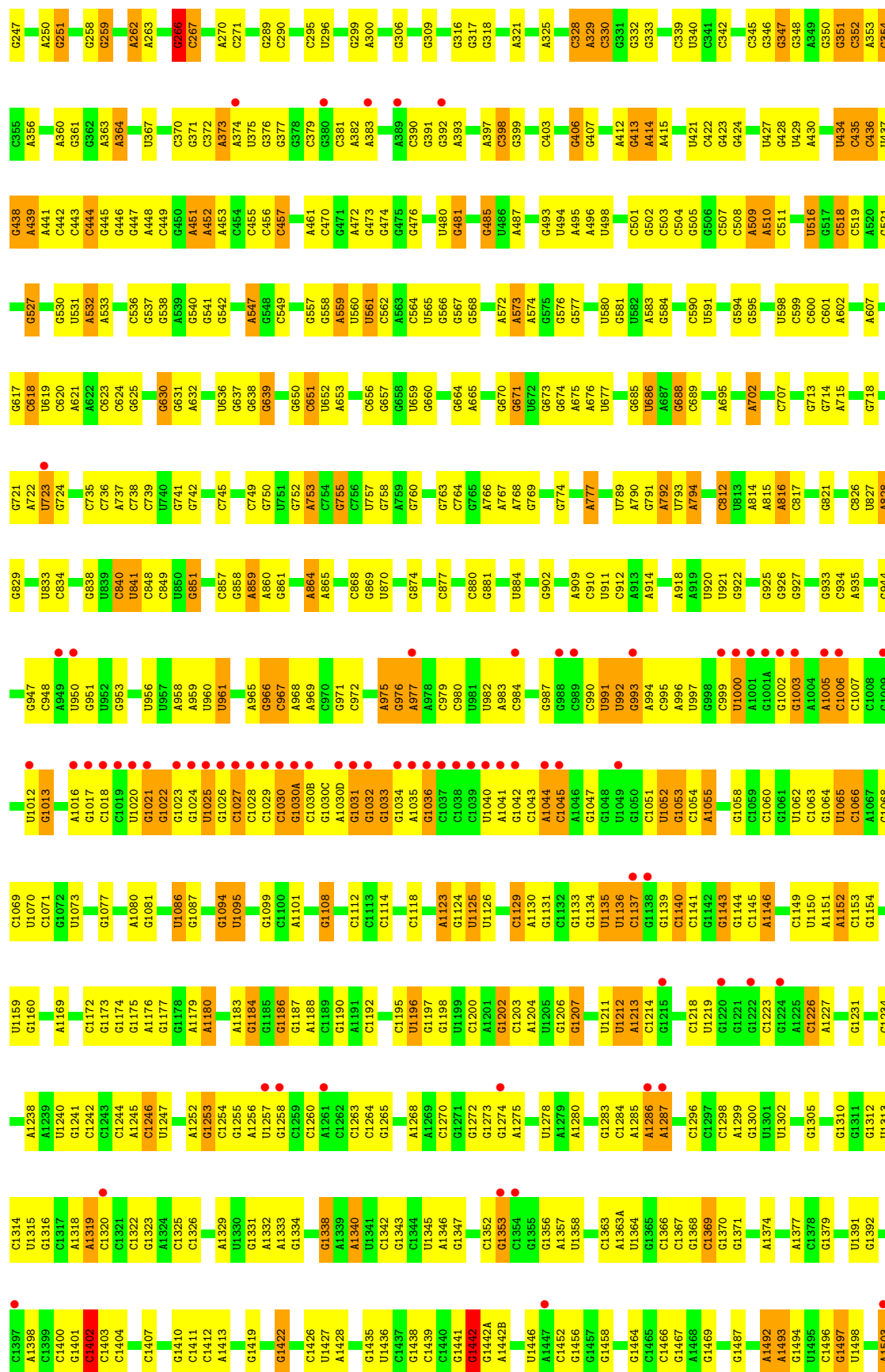


- Molecule 31: 50S ribosomal protein L36



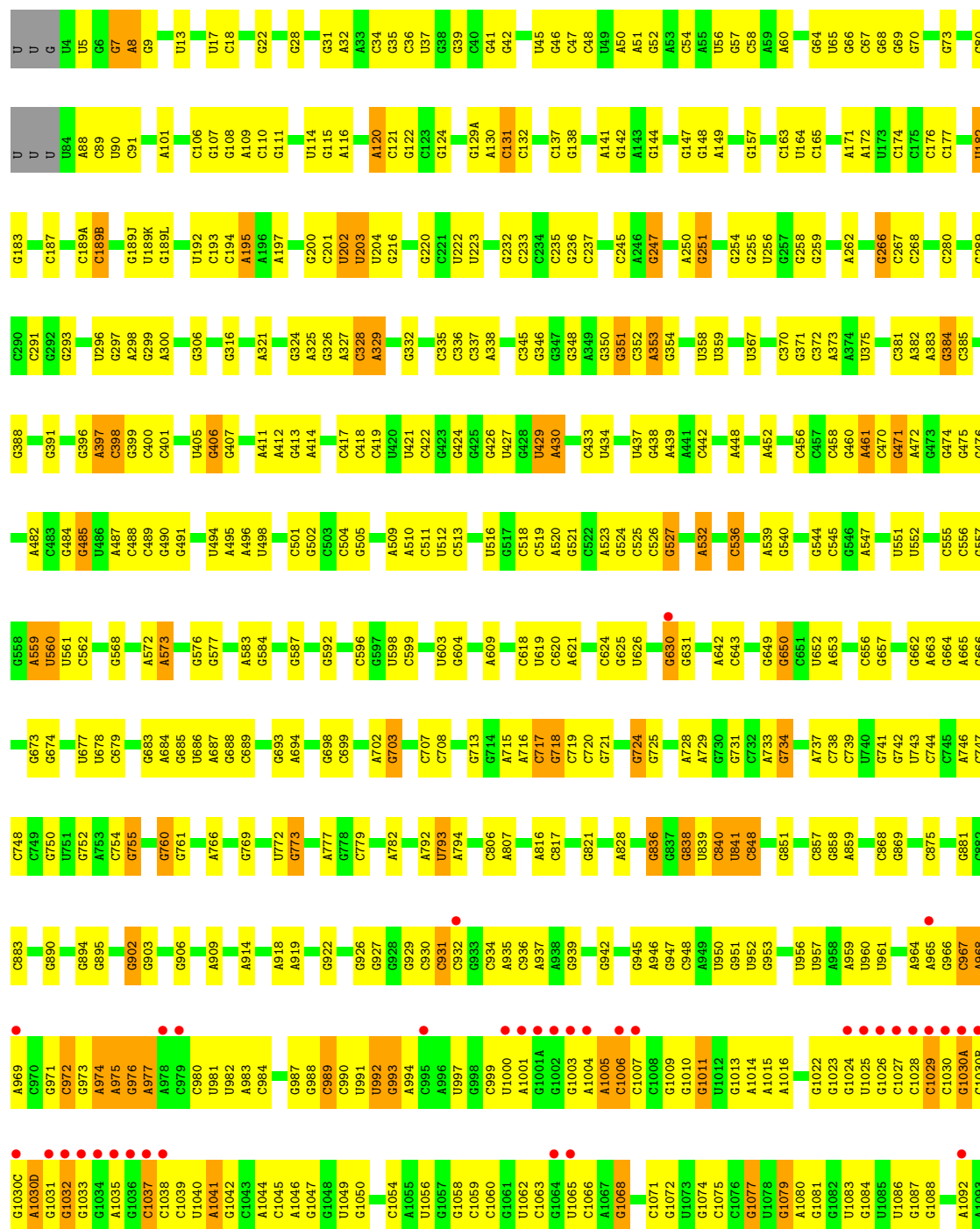
- Molecule 32: 16S Ribosomal RNA

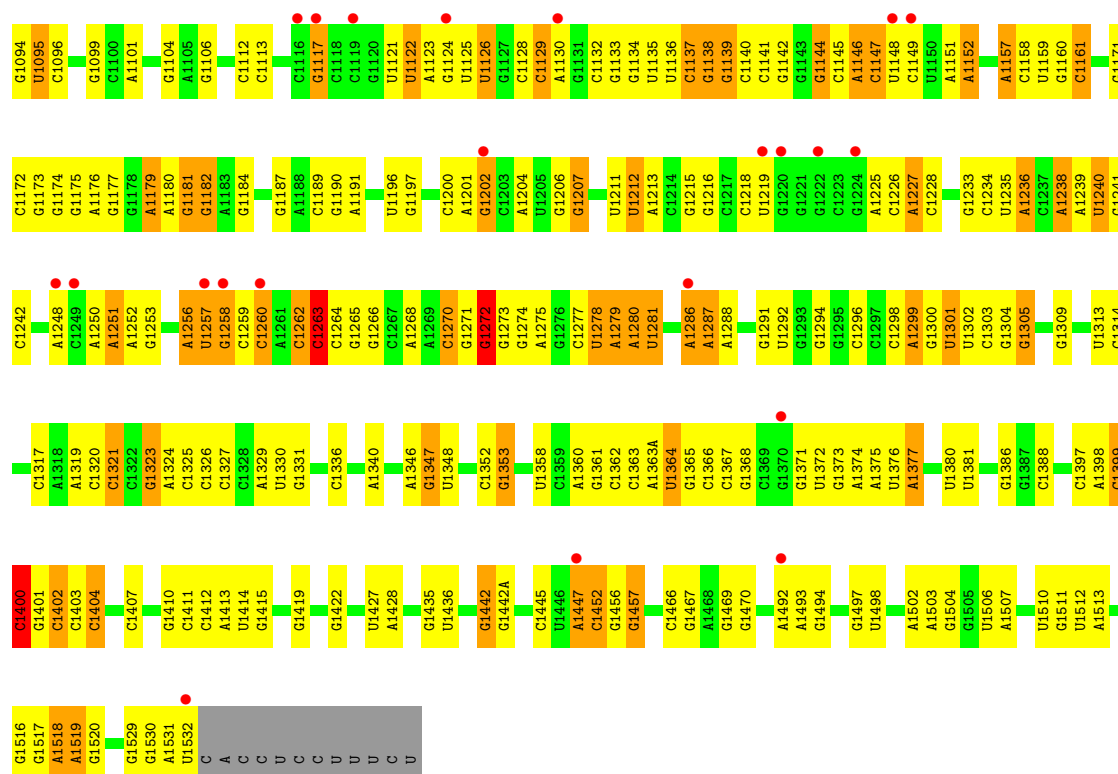




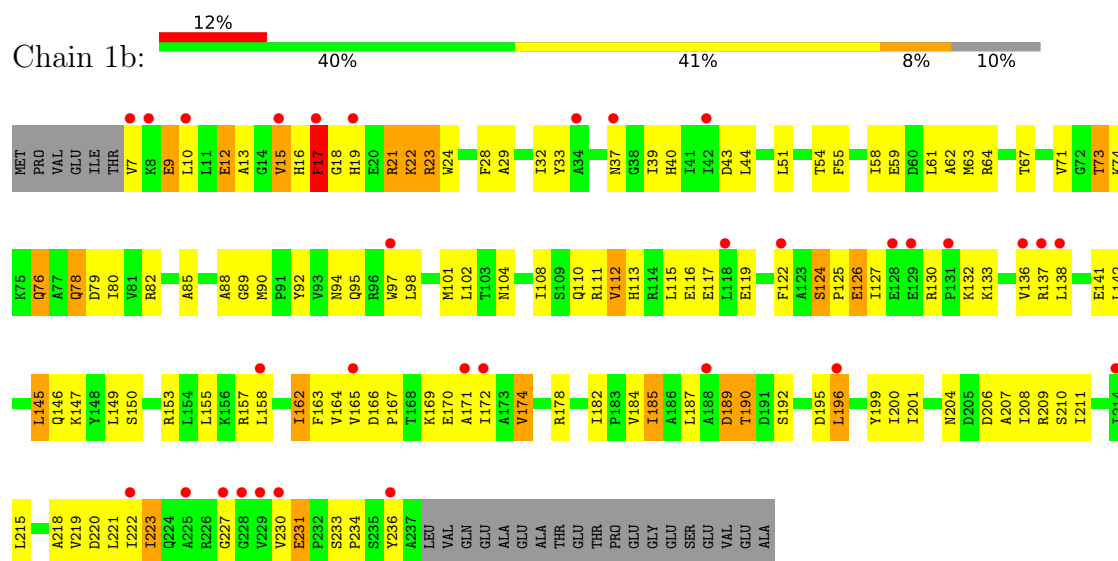


• Molecule 32: 16S Ribosomal RNA

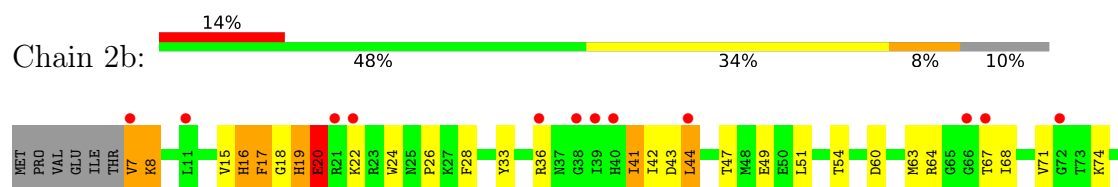


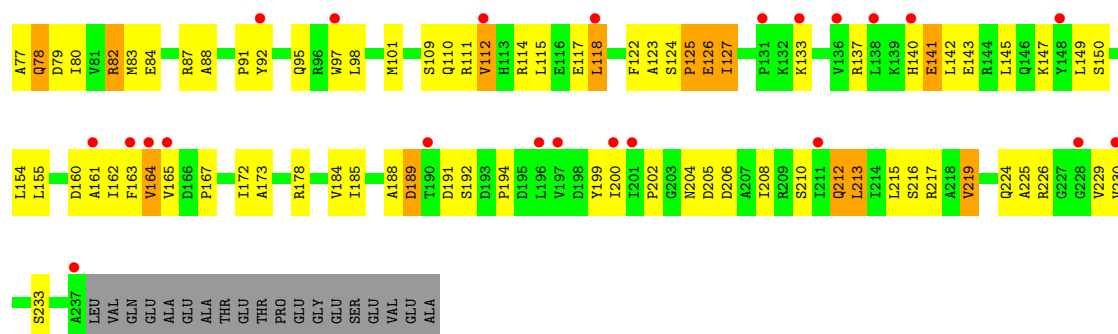


• Molecule 33: 30S ribosomal protein S2

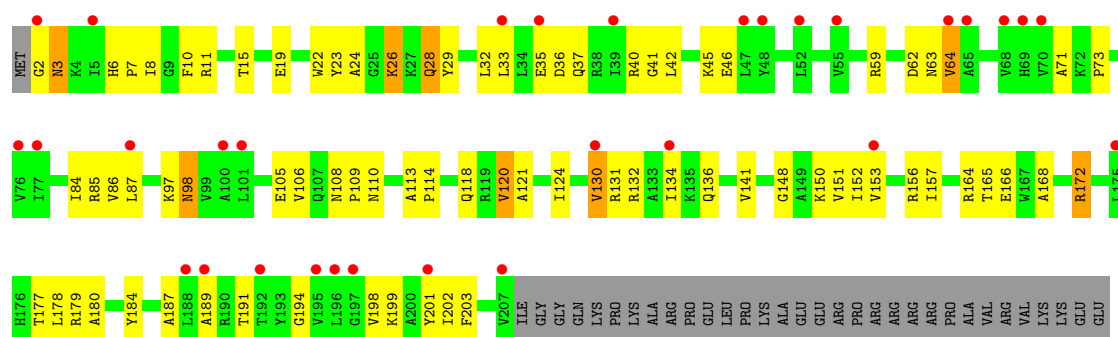


• Molecule 33: 30S ribosomal protein S2

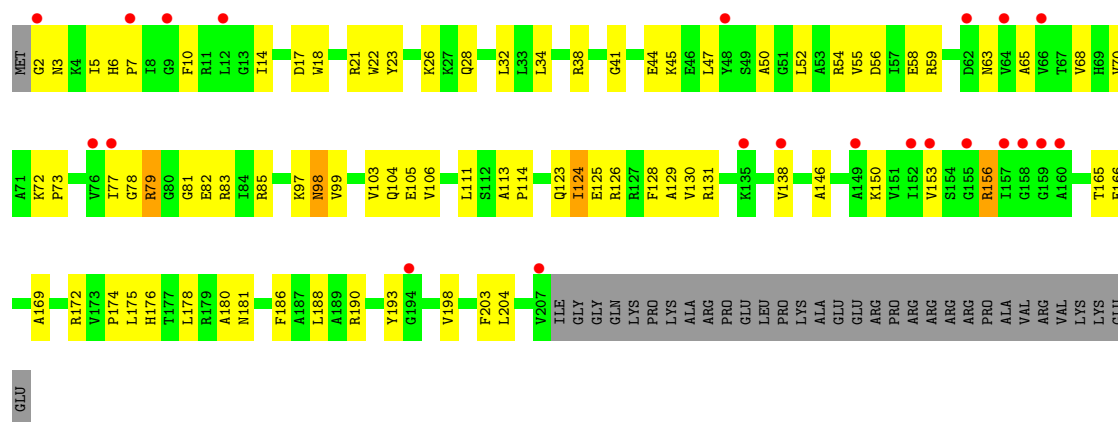




• Molecule 34: 30S ribosomal protein S3

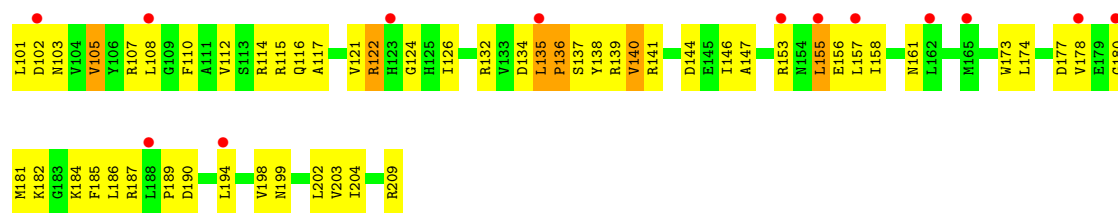


• Molecule 34: 30S ribosomal protein S3

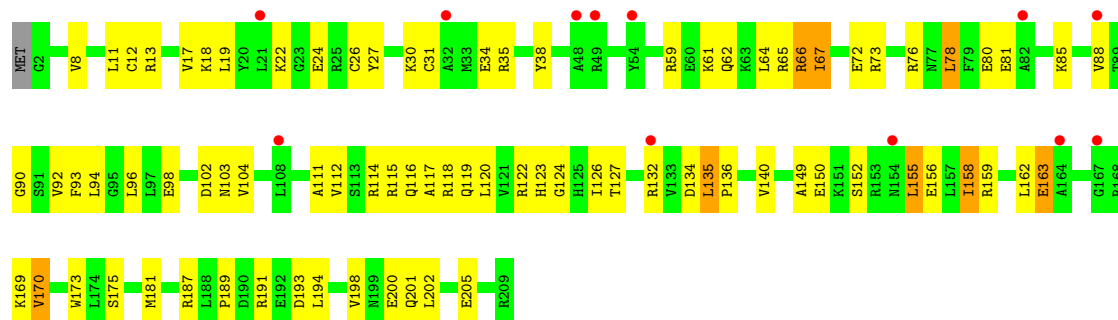


• Molecule 35: 30S ribosomal protein S4

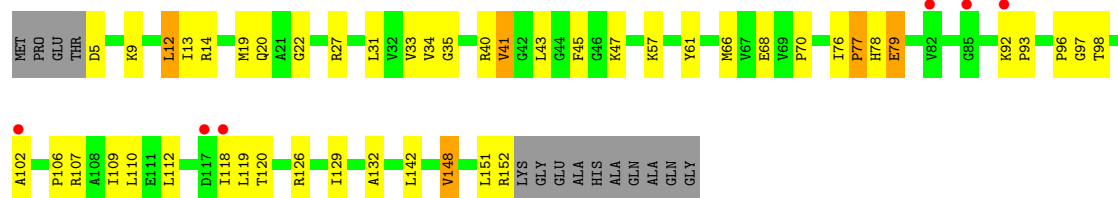




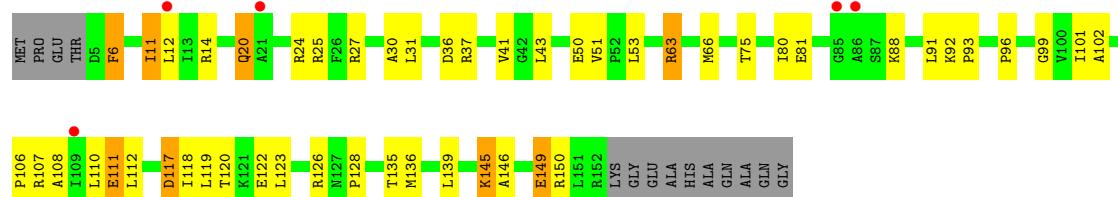
• Molecule 35: 30S ribosomal protein S4



• Molecule 36: 30S ribosomal protein S5



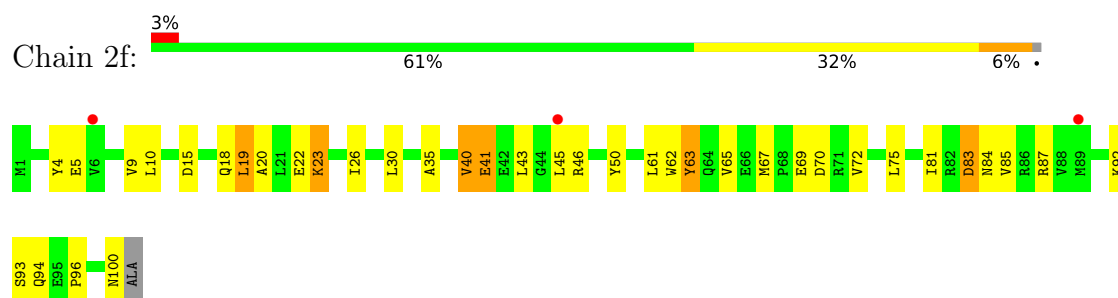
• Molecule 36: 30S ribosomal protein S5



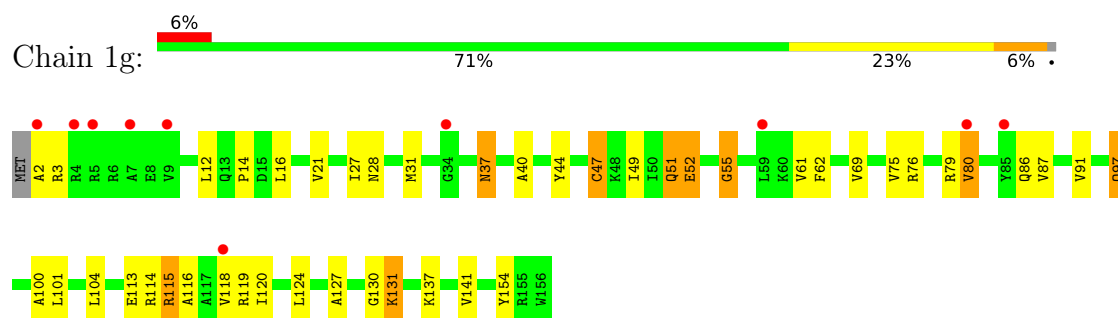
• Molecule 37: 30S ribosomal protein S6



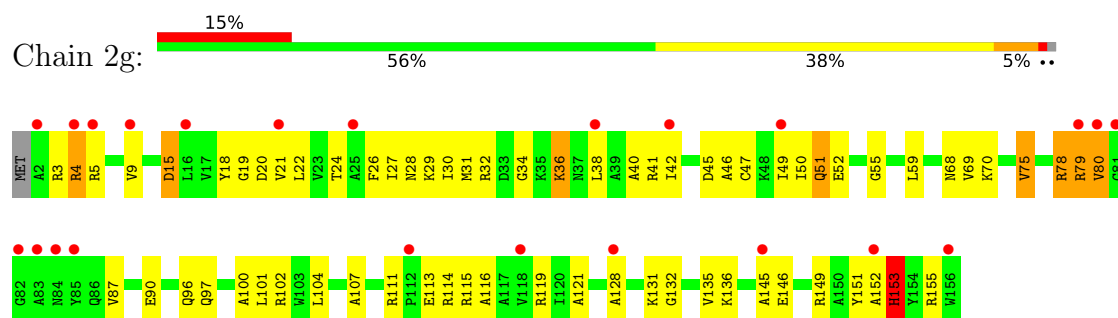
- Molecule 37: 30S ribosomal protein S6



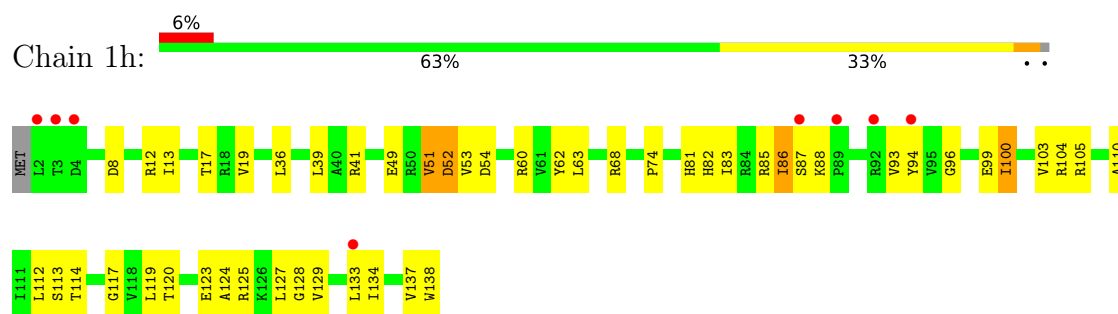
- Molecule 38: 30S ribosomal protein S7



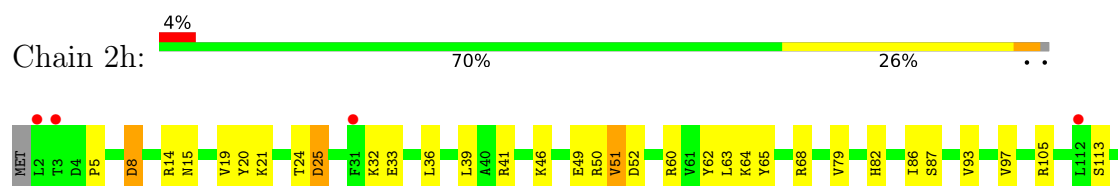
- Molecule 38: 30S ribosomal protein S7

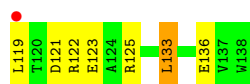


- Molecule 39: 30S ribosomal protein S8

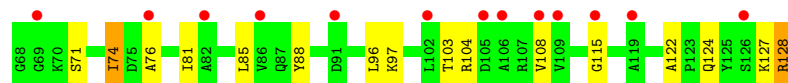
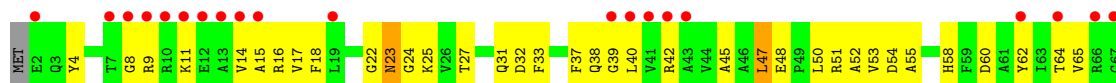


- Molecule 39: 30S ribosomal protein S8

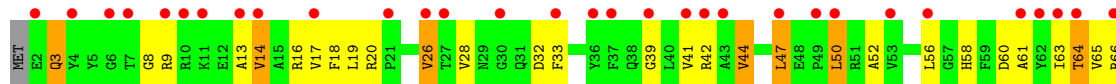
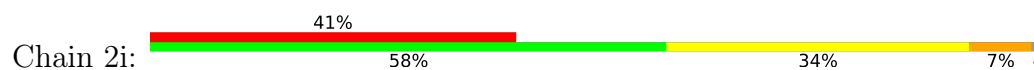




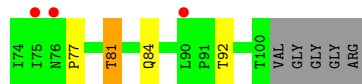
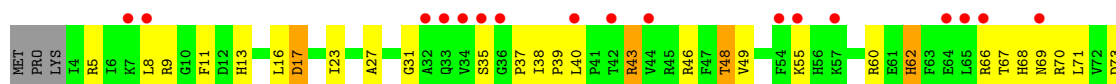
• Molecule 40: 30S ribosomal protein S9



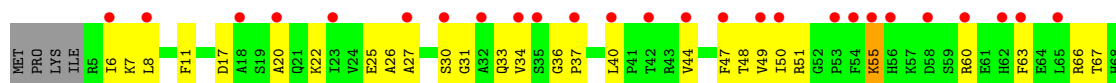
• Molecule 40: 30S ribosomal protein S9



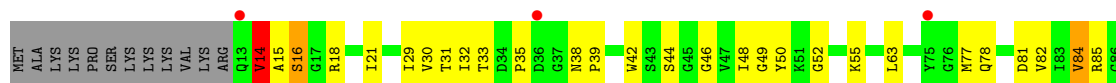
• Molecule 41: 30S ribosomal protein S10



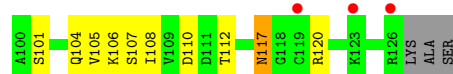
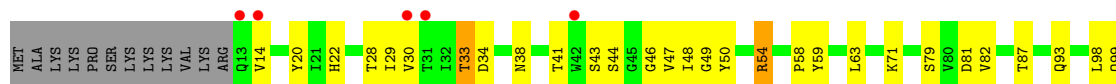
• Molecule 41: 30S ribosomal protein S10



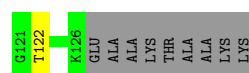
• Molecule 42: 30S ribosomal protein S11



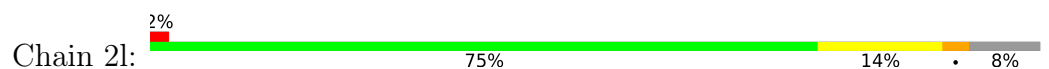
- Molecule 42: 30S ribosomal protein S11



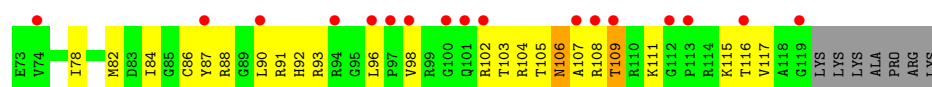
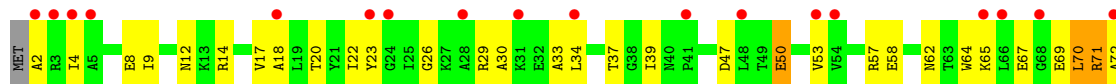
- Molecule 43: 30S ribosomal protein S12



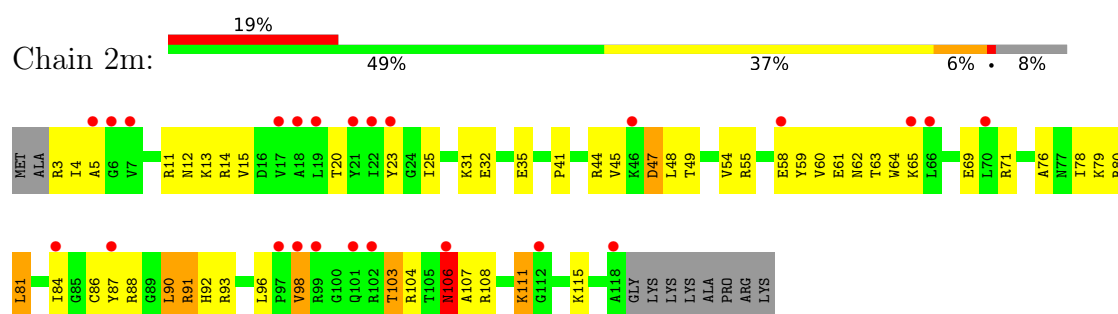
- Molecule 43: 30S ribosomal protein S12



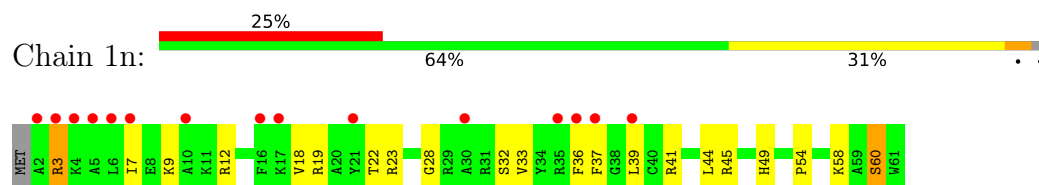
- Molecule 44: 30S ribosomal protein S13



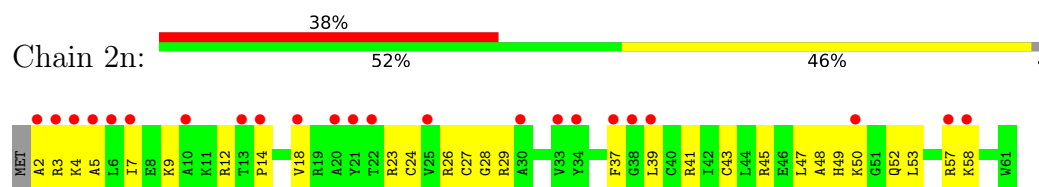
- Molecule 44: 30S ribosomal protein S13



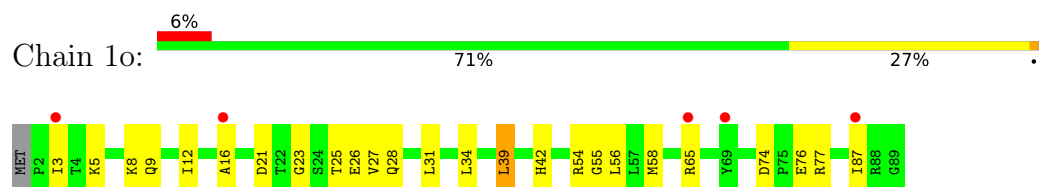
- Molecule 45: 30S ribosomal protein S14 type Z



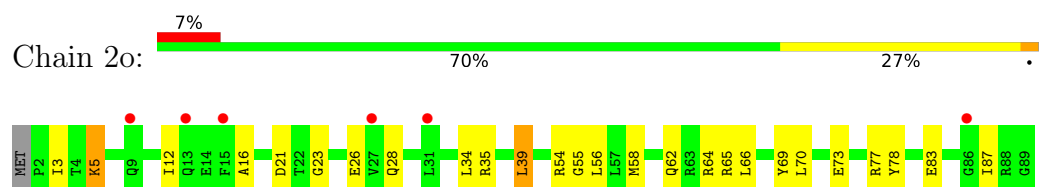
- Molecule 45: 30S ribosomal protein S14 type Z



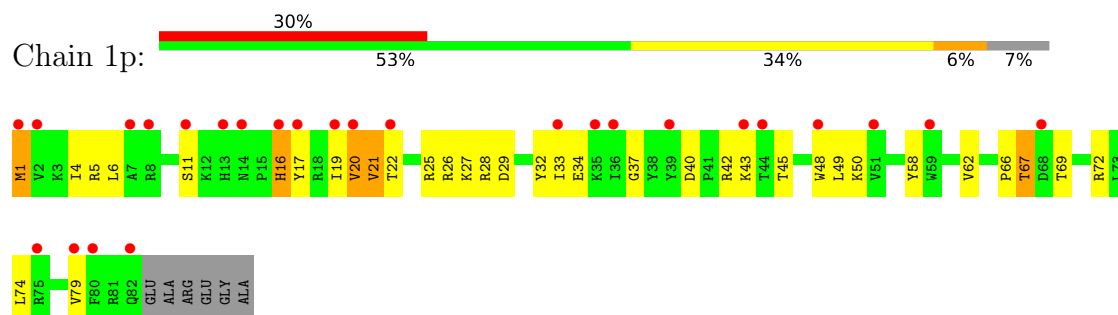
- Molecule 46: 30S ribosomal protein S15



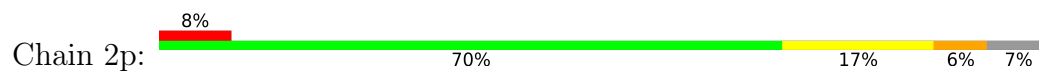
- Molecule 46: 30S ribosomal protein S15



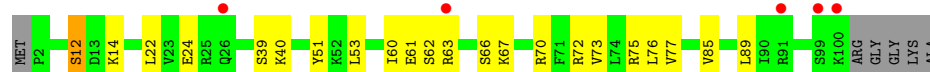
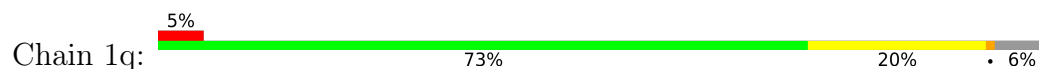
- Molecule 47: 30S ribosomal protein S16



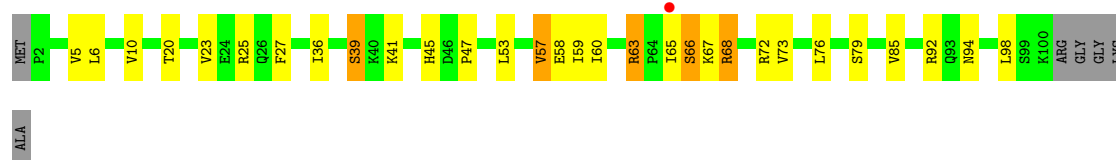
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17



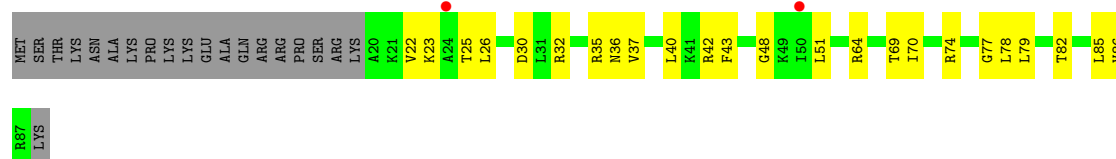
- Molecule 48: 30S ribosomal protein S17



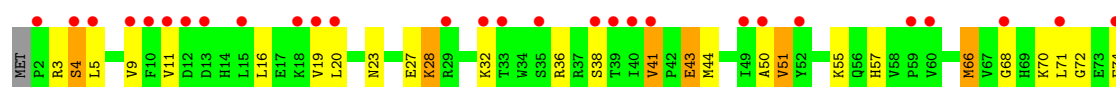
- Molecule 49: 30S ribosomal protein S18

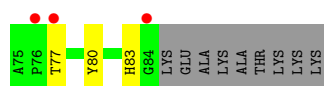


- Molecule 49: 30S ribosomal protein S18



- Molecule 50: 30S ribosomal protein S19





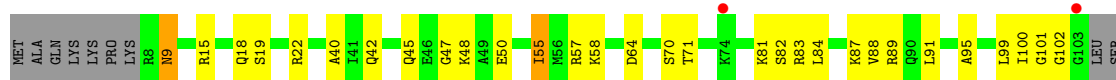
- Molecule 50: 30S ribosomal protein S19



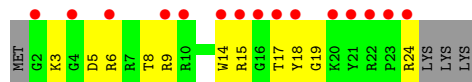
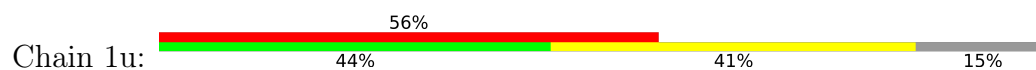
- Molecule 51: 30S ribosomal protein S20



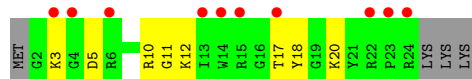
- Molecule 51: 30S ribosomal protein S20



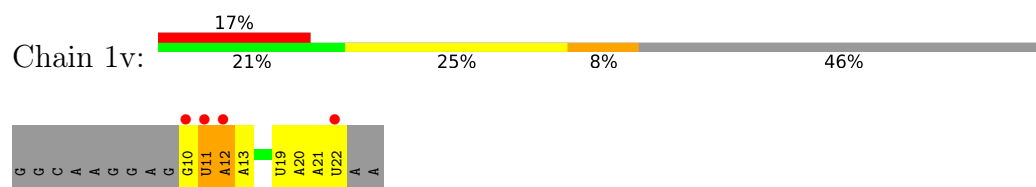
- Molecule 52: 30S ribosomal protein Thx



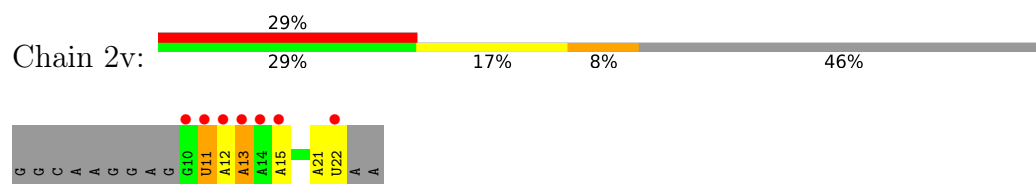
- Molecule 52: 30S ribosomal protein Thx



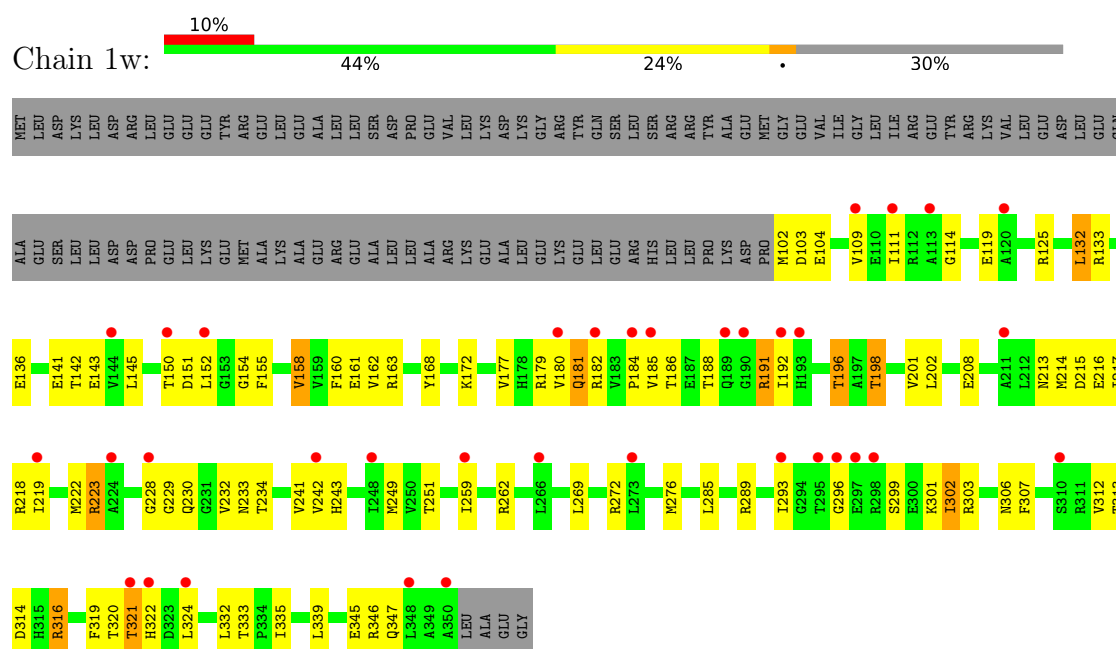
- Molecule 53: CYS-Stop mRNA



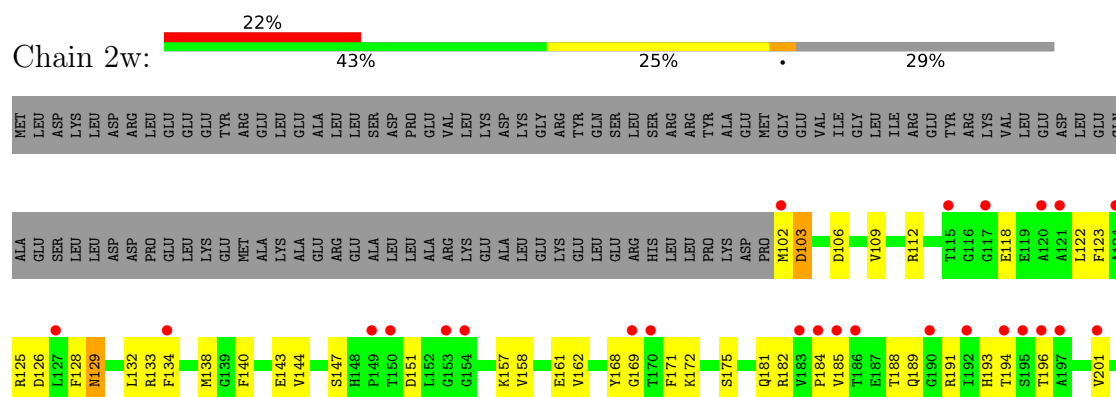
- Molecule 53: CYS-Stop mRNA

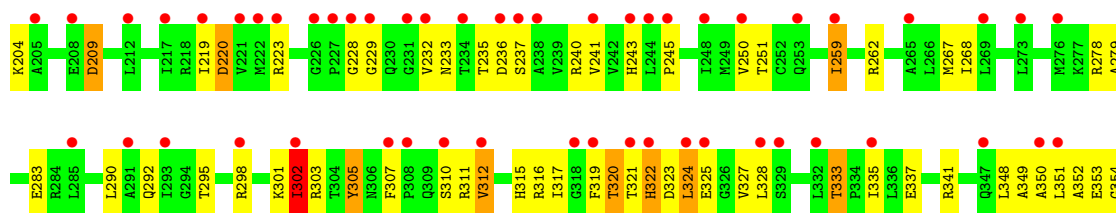


- Molecule 54: Peptide chain release factor 1



- Molecule 54: Peptide chain release factor 1





● Molecule 55: P-site deacylated-tRNAcys



● Molecule 55: P-site deacylated-tRNAcys



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.05Å 450.80Å 622.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	188.39 – 2.60 188.39 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (188.39-2.60) 99.8 (188.39-2.60)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.62Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.224 , 0.271 0.224 , 0.270	Depositor DCC
R_{free} test set	89459 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	296938	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 1.65% 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: 4OC, OMG, 2MG, 5MC, UR3, SF4, MA6, 2MA, ZN, M2G, OMU, 0TD, MG, MIA, MEQ, PSU, 5MU, 4SU, K, G7M, H2U, OMC

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	0.29	0/69011	0.47	2/107720 (0.0%)
1	2A	0.22	0/67295	0.41	1/105042 (0.0%)
2	1B	0.21	0/2882	0.40	0/4494
2	2B	0.18	0/2879	0.34	0/4487
3	1D	0.26	0/2186	0.51	0/2944
3	2D	0.24	0/2186	0.47	0/2944
4	1E	0.26	0/1592	0.49	0/2149
4	2E	0.22	0/1592	0.43	0/2149
5	1F	0.26	0/1619	0.48	0/2193
5	2F	0.20	0/1615	0.42	0/2188
6	1G	0.21	0/1448	0.45	0/1957
6	2G	0.20	0/1453	0.44	0/1963
7	1H	0.23	0/1356	0.44	0/1834
7	2H	0.19	0/1356	0.37	0/1834
8	1I	0.20	0/1112	0.47	0/1514
8	2I	0.19	0/1079	0.42	1/1475 (0.1%)
9	1N	0.25	0/1144	0.47	0/1543
9	2N	0.19	0/1144	0.40	0/1543
10	1O	0.25	0/943	0.48	0/1269
10	2O	0.21	0/943	0.46	0/1269
11	1P	0.26	0/1152	0.50	0/1533
11	2P	0.21	0/1152	0.48	1/1533 (0.1%)
12	1Q	0.26	0/1143	0.49	0/1527
12	2Q	0.20	0/1143	0.43	0/1527
13	1R	0.28	0/982	0.50	0/1312
13	2R	0.22	0/982	0.44	0/1312
14	1S	0.22	0/883	0.48	0/1176
14	2S	0.20	0/880	0.41	0/1172
15	1T	0.25	0/1105	0.48	0/1477
15	2T	0.20	0/1097	0.43	0/1468
16	1U	0.30	0/977	0.48	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.21	0/977	0.40	0/1301
17	1V	0.25	0/782	0.47	0/1049
17	2V	0.20	0/782	0.41	0/1049
18	1W	0.29	0/897	0.44	0/1205
18	2W	0.21	0/897	0.40	0/1205
19	1X	0.28	0/764	0.54	2/1025 (0.2%)
19	2X	0.20	0/764	0.47	2/1025 (0.2%)
20	1Y	0.23	0/819	0.46	0/1095
20	2Y	0.19	0/819	0.45	0/1095
21	1Z	0.23	0/1267	0.54	0/1717
21	2Z	0.21	0/1299	0.46	0/1763
22	10	0.28	0/612	0.51	0/816
22	20	0.21	0/612	0.46	0/816
23	11	0.26	0/762	0.45	0/1014
23	21	0.23	0/762	0.39	0/1014
24	12	0.24	0/590	0.41	0/781
24	22	0.19	0/590	0.38	0/781
25	13	0.27	0/474	0.47	0/635
25	23	0.20	0/469	0.47	0/630
26	14	0.24	0/565	0.51	0/761
26	24	0.24	0/545	0.50	0/737
27	15	0.30	0/469	0.51	0/635
27	25	0.22	0/469	0.43	0/635
28	16	0.27	0/460	0.50	0/613
28	26	0.20	0/456	0.42	0/608
29	17	0.32	0/426	0.57	0/561
29	27	0.25	0/426	0.50	0/561
30	18	0.28	0/525	0.50	0/691
30	28	0.20	0/525	0.41	0/691
31	19	0.25	0/310	0.61	1/407 (0.2%)
31	29	0.20	0/310	0.47	0/407
32	1a	0.20	1/35795 (0.0%)	0.38	3/55864 (0.0%)
32	2a	0.20	1/35886 (0.0%)	0.38	4/56005 (0.0%)
33	1b	0.24	0/1881	0.52	0/2542
33	2b	0.22	0/1860	0.49	0/2518
34	1c	0.21	0/1572	0.41	0/2126
34	2c	0.21	0/1566	0.45	0/2119
35	1d	0.23	0/1685	0.47	0/2262
35	2d	0.19	0/1704	0.44	0/2284
36	1e	0.22	0/1145	0.49	0/1543
36	2e	0.21	0/1149	0.45	0/1548
37	1f	0.20	0/823	0.44	0/1115
37	2f	0.21	0/829	0.43	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.21	0/1250	0.44	0/1679
38	2g	0.20	0/1254	0.47	0/1683
39	1h	0.19	0/1108	0.43	0/1494
39	2h	0.19	0/1108	0.41	0/1494
40	1i	0.20	0/1002	0.44	0/1346
40	2i	0.22	0/997	0.47	1/1343 (0.1%)
41	1j	0.20	0/722	0.45	0/982
41	2j	0.21	0/727	0.46	0/988
42	1k	0.19	0/844	0.43	0/1145
42	2k	0.19	0/848	0.40	0/1149
43	1l	0.21	0/937	0.46	0/1260
43	2l	0.21	0/937	0.43	0/1260
44	1m	0.22	0/929	0.48	0/1250
44	2m	0.21	0/917	0.47	0/1234
45	1n	0.20	0/501	0.46	0/664
45	2n	0.21	0/501	0.46	0/664
46	1o	0.20	0/739	0.39	0/985
46	2o	0.18	0/739	0.37	0/985
47	1p	0.19	0/697	0.47	0/939
47	2p	0.21	0/693	0.44	0/935
48	1q	0.19	0/836	0.40	0/1117
48	2q	0.19	0/836	0.44	0/1117
49	1r	0.20	0/560	0.39	0/746
49	2r	0.18	0/560	0.39	0/746
50	1s	0.24	0/667	0.52	0/900
50	2s	0.20	0/661	0.43	0/893
51	1t	0.18	0/730	0.44	0/965
51	2t	0.19	0/729	0.43	0/965
52	1u	0.20	0/203	0.43	0/266
52	2u	0.24	0/203	0.50	0/266
53	1v	0.25	0/310	0.40	0/480
53	2v	0.24	0/310	0.42	0/480
54	1w	0.21	0/1956	0.41	1/2634 (0.0%)
54	2w	0.23	0/1974	0.43	1/2657 (0.0%)
55	1x	0.22	0/1580	0.34	0/2458
55	2x	0.22	1/1580 (0.1%)	0.33	0/2458
All	All	0.23	3/313795 (0.0%)	0.43	20/468848 (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
11	1P	0	1
11	2P	0	1
21	1Z	0	1
33	1b	0	2
38	1g	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2x	8	4SU	O3'-P	5.46	1.61	1.56
32	2a	527	G7M	O3'-P	5.23	1.61	1.56
32	1a	527	G7M	O3'-P	5.03	1.61	1.56

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1992	G	C2'-C3'-O3'	6.54	119.30	109.50
54	2w	302	ILE	N-CA-C	-6.47	106.49	112.96
32	2a	1272	G	N1-C2-N2	-6.42	96.93	116.20
32	2a	1263	C	N1-C2-O2	6.16	137.39	118.90
1	2A	1992	G	C2'-C3'-O3'	6.02	118.54	109.50
32	2a	1272	G	N3-C2-N2	5.94	137.72	119.90
8	2I	124	GLY	N-CA-C	5.50	117.86	110.43
31	19	10	ILE	N-CA-C	-5.49	107.47	112.96
32	1a	266	G	C2'-C3'-O3'	5.46	117.69	109.50
32	1a	1442	G	P-O3'-C3'	5.40	126.17	119.70
32	1a	266	G	P-O3'-C3'	5.30	128.15	120.20
19	2X	94	GLY	CA-C-N	5.25	131.15	121.70
19	2X	94	GLY	C-N-CA	5.25	131.15	121.70
40	2i	44	VAL	N-CA-C	-5.22	106.46	112.98
54	1w	345	GLU	N-CA-C	-5.17	107.27	113.21
32	2a	1272	G	C5-C6-O6	5.16	144.07	128.60
11	2P	44	GLY	N-CA-C	5.11	120.53	111.02
1	1A	1210	A	C4'-C3'-O3'	5.11	117.06	109.40
19	1X	94	GLY	CA-C-N	5.05	130.79	121.70
19	1X	94	GLY	C-N-CA	5.05	130.79	121.70

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	1P	35	HIS	Peptide
21	1Z	136	PHE	Peptide
33	1b	122	PHE	Peptide
33	1b	9	GLU	Peptide
38	1g	79	ARG	Peptide
11	2P	35	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31193	603	0
1	2A	60322	0	30424	632	0
2	1B	2577	0	1305	20	0
2	2B	2575	0	1303	39	0
3	1D	2136	0	2218	44	0
3	2D	2136	0	2218	51	0
4	1E	1559	0	1618	22	0
4	2E	1559	0	1618	32	0
5	1F	1584	0	1625	26	0
5	2F	1580	0	1619	39	0
6	1G	1423	0	1436	40	0
6	2G	1428	0	1438	56	0
7	1H	1330	0	1407	28	0
7	2H	1330	0	1407	32	0
8	1I	1097	0	1140	24	0
8	2I	1064	0	1082	28	0
9	1N	1117	0	1184	14	0
9	2N	1117	0	1184	17	0
10	1O	933	0	996	15	0
10	2O	933	0	996	22	0
11	1P	1135	0	1212	19	0
11	2P	1135	0	1212	31	0
12	1Q	1122	0	1179	15	0
12	2Q	1122	0	1179	21	0
13	1R	968	0	1033	18	0
13	2R	968	0	1033	24	0
14	1S	873	0	927	16	0
14	2S	870	0	923	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	1T	1091	0	1151	22	0
15	2T	1083	0	1136	21	0
16	1U	959	0	1019	17	0
16	2U	959	0	1019	13	0
17	1V	771	0	830	11	0
17	2V	771	0	830	16	0
18	1W	886	0	940	9	0
18	2W	886	0	940	11	0
19	1X	750	0	814	14	0
19	2X	750	0	814	17	0
20	1Y	806	0	881	19	0
20	2Y	806	0	881	8	0
21	1Z	1240	0	1240	22	0
21	2Z	1271	0	1273	34	0
22	10	604	0	619	12	0
22	20	604	0	619	14	0
23	11	755	0	826	19	0
23	21	755	0	826	10	0
24	12	588	0	643	4	0
24	22	588	0	643	7	0
25	13	469	0	518	8	0
25	23	464	0	514	10	0
26	14	552	0	533	24	0
26	24	532	0	503	28	0
27	15	455	0	465	7	0
27	25	455	0	465	10	0
28	16	453	0	472	4	0
28	26	449	0	469	8	0
29	17	418	0	467	14	0
29	27	418	0	467	12	0
30	18	517	0	582	15	0
30	28	517	0	582	13	0
31	19	307	0	335	1	0
31	29	307	0	335	6	0
32	1a	32246	0	16294	480	0
32	2a	32327	0	16338	448	0
33	1b	1846	0	1867	88	0
33	2b	1825	0	1828	67	0
34	1c	1548	0	1535	53	0
34	2c	1542	0	1517	53	0
35	1d	1655	0	1672	60	0
35	2d	1674	0	1714	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	1e	1129	0	1185	36	0
36	2e	1133	0	1191	29	0
37	1f	810	0	804	18	0
37	2f	816	0	808	27	0
38	1g	1231	0	1238	31	0
38	2g	1235	0	1249	53	0
39	1h	1088	0	1126	33	0
39	2h	1088	0	1126	25	0
40	1i	983	0	986	37	0
40	2i	978	0	966	37	0
41	1j	709	0	650	29	0
41	2j	714	0	672	23	0
42	1k	829	0	825	25	0
42	2k	833	0	836	26	0
43	1l	932	0	981	18	0
43	2l	932	0	981	13	0
44	1m	919	0	951	38	0
44	2m	907	0	934	43	0
45	1n	492	0	529	16	0
45	2n	492	0	529	22	0
46	1o	728	0	760	14	0
46	2o	728	0	760	17	0
47	1p	681	0	697	26	0
47	2p	677	0	686	14	0
48	1q	823	0	891	15	0
48	2q	823	0	891	19	0
49	1r	555	0	618	14	0
49	2r	555	0	618	18	0
50	1s	652	0	662	24	0
50	2s	646	0	644	30	0
51	1t	728	0	798	22	0
51	2t	727	0	796	17	0
52	1u	199	0	208	7	0
52	2u	199	0	208	7	0
53	1v	277	0	140	8	0
53	2v	277	0	140	5	0
54	1w	1939	0	1922	54	0
54	2w	1957	0	1935	53	0
55	1x	1577	0	802	14	0
55	2x	1577	0	802	13	0
56	10	6	0	0	0	0
56	11	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	12	3	0	0	0	0
56	13	6	0	0	0	0
56	14	1	0	0	0	0
56	15	8	0	0	0	0
56	16	2	0	0	0	0
56	17	7	0	0	0	0
56	18	4	0	0	0	0
56	1A	1083	0	0	0	0
56	1B	37	0	0	0	0
56	1D	14	0	0	0	0
56	1E	17	0	0	0	0
56	1F	14	0	0	0	0
56	1G	4	0	0	0	0
56	1I	1	0	0	0	0
56	1N	8	0	0	0	0
56	1O	5	0	0	0	0
56	1P	6	0	0	0	0
56	1Q	7	0	0	0	0
56	1R	4	0	0	0	0
56	1S	3	0	0	0	0
56	1T	3	0	0	0	0
56	1U	10	0	0	0	0
56	1V	6	0	0	0	0
56	1W	7	0	0	0	0
56	1X	6	0	0	0	0
56	1Y	3	0	0	0	0
56	1Z	2	0	0	0	0
56	1a	224	0	0	0	0
56	1b	2	0	0	0	0
56	1d	1	0	0	0	0
56	1e	4	0	0	0	0
56	1f	2	0	0	0	0
56	1k	1	0	0	0	0
56	1l	2	0	0	0	0
56	1m	1	0	0	0	0
56	1n	1	0	0	0	0
56	1p	1	0	0	0	0
56	1t	1	0	0	0	0
56	1v	4	0	0	0	0
56	1w	1	0	0	0	0
56	1x	13	0	0	0	0
56	20	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	21	1	0	0	0	0
56	23	3	0	0	0	0
56	25	5	0	0	0	0
56	26	1	0	0	0	0
56	27	1	0	0	0	0
56	28	3	0	0	0	0
56	2A	870	0	0	0	0
56	2B	20	0	0	0	0
56	2D	6	0	0	0	0
56	2E	7	0	0	0	0
56	2F	6	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	2P	1	0	0	0	0
56	2Q	4	0	0	0	0
56	2R	3	0	0	0	0
56	2T	3	0	0	0	0
56	2U	2	0	0	0	0
56	2V	2	0	0	0	0
56	2W	4	0	0	0	0
56	2X	2	0	0	0	0
56	2Z	1	0	0	0	0
56	2a	176	0	0	0	0
56	2d	2	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	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	2q	2	0	0	0	0
56	2r	2	0	0	0	0
56	2t	1	0	0	0	0
56	2v	2	0	0	0	0
56	2x	6	0	0	0	0
57	1A	1	0	0	0	0
58	14	1	0	0	0	0
58	15	1	0	0	0	0
58	16	1	0	0	0	0
58	19	1	0	0	0	0
58	1Y	1	0	0	0	0
58	1n	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	24	1	0	0	0	0
58	25	1	0	0	0	0
58	26	1	0	0	0	0
58	29	1	0	0	0	0
58	2Y	1	0	0	0	0
58	2n	1	0	0	0	0
59	1d	8	0	0	2	0
59	2d	8	0	0	0	0
60	10	10	0	0	0	0
60	11	9	0	0	0	0
60	12	4	0	0	0	0
60	13	5	0	0	0	0
60	15	5	0	0	1	0
60	16	1	0	0	0	0
60	17	8	0	0	0	0
60	18	13	0	0	1	0
60	1A	1841	0	0	93	0
60	1B	66	0	0	2	0
60	1D	24	0	0	2	0
60	1E	27	0	0	2	0
60	1F	16	0	0	0	0
60	1G	3	0	0	3	0
60	1H	2	0	0	0	0
60	1N	5	0	0	0	0
60	1O	5	0	0	0	0
60	1P	20	0	0	2	0
60	1Q	5	0	0	0	0
60	1R	15	0	0	2	0
60	1S	4	0	0	1	0
60	1T	5	0	0	0	0
60	1U	15	0	0	1	0
60	1V	7	0	0	0	0
60	1W	12	0	0	0	0
60	1X	7	0	0	0	0
60	1Y	1	0	0	0	0
60	1Z	1	0	0	0	0
60	1a	274	0	0	17	0
60	1b	1	0	0	1	0
60	1g	1	0	0	0	0
60	1l	2	0	0	0	0
60	1n	1	0	0	0	0
60	1o	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1q	1	0	0	0	0
60	1u	1	0	0	0	0
60	1v	3	0	0	0	0
60	1w	2	0	0	0	0
60	1x	15	0	0	2	0
60	20	5	0	0	1	0
60	21	10	0	0	0	0
60	23	2	0	0	0	0
60	25	2	0	0	1	0
60	27	6	0	0	0	0
60	28	3	0	0	0	0
60	29	1	0	0	0	0
60	2A	1163	0	0	90	0
60	2B	25	0	0	2	0
60	2D	22	0	0	4	0
60	2E	15	0	0	1	0
60	2F	11	0	0	0	0
60	2I	1	0	0	0	0
60	2N	1	0	0	0	0
60	2O	2	0	0	1	0
60	2P	11	0	0	1	0
60	2Q	1	0	0	0	0
60	2R	5	0	0	2	0
60	2T	5	0	0	0	0
60	2U	2	0	0	0	0
60	2V	2	0	0	0	0
60	2W	4	0	0	0	0
60	2X	3	0	0	0	0
60	2Z	1	0	0	0	0
60	2a	138	0	0	10	0
60	2d	1	0	0	0	0
60	2e	1	0	0	0	0
60	2g	1	0	0	0	0
60	2j	3	0	0	0	0
60	2l	3	0	0	0	0
60	2q	1	0	0	0	0
60	2t	2	0	0	0	0
60	2v	1	0	0	0	0
60	2w	3	0	0	1	0
60	2x	8	0	0	0	0
All	All	296938	0	197070	4056	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 (4056) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:H3	1:1A:1086:A:H61	1.02	1.00
1:1A:1082:U:H3	1:1A:1086:A:N6	1.59	1.00
1:2A:2104:G:H1	1:2A:2185:C:H42	1.05	0.98
1:1A:2427:C:OP1	60:1A:4104:HOH:O	1.81	0.96
1:1A:2138:C:H42	1:1A:2153:G:H1	1.11	0.96
29:27:24:THR:HG22	29:27:27:GLY:H	1.30	0.95
1:1A:1082:U:O4	1:1A:1086:A:N1	2.03	0.91
1:2A:2589:A:OP1	60:2A:3907:HOH:O	1.89	0.91
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.53	0.90
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.19	0.90
29:17:24:THR:HG22	29:17:27:GLY:H	1.39	0.87
1:2A:784:A:OP2	60:2A:3907:HOH:O	1.93	0.86
1:2A:2504:U:OP2	60:2A:3908:HOH:O	1.93	0.86
15:1T:41:ARG:NH2	32:1a:346:G:OP1	2.08	0.86
1:2A:195:A:N7	60:2A:3920:HOH:O	2.07	0.86
22:10:11:ARG:O	22:10:14:ARG:NH2	2.09	0.86
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.09	0.85
32:2a:1086:U:H3	32:2a:1099:G:H22	1.26	0.84
1:1A:2467:C:OP2	60:1A:4105:HOH:O	1.93	0.84
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.58	0.84
1:1A:762:U:OP1	60:1A:4106:HOH:O	1.96	0.83
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.11	0.83
14:1S:61:ASN:HD22	14:1S:64:GLU:H	1.26	0.82
1:2A:2127:G:N1	1:2A:2161:C:C4	2.48	0.82
1:2A:1689:A:H62	1:2A:1698:A:H2	1.23	0.82
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.15	0.82
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.42	0.82
1:2A:805:G:OP1	60:2A:3909:HOH:O	1.98	0.81
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.60	0.81
10:1O:48:PRO:HB3	32:1a:1422:G:H5'	1.62	0.81
1:1A:2499:C:OP1	60:1A:4108:HOH:O	1.99	0.81
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.61	0.81
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.63	0.81
1:1A:1315:C:OP2	60:1A:4109:HOH:O	1.99	0.81
32:2a:975:A:H4'	32:2a:976:G:H5''	1.61	0.80
38:2g:70:LYS:HG3	38:2g:100:ALA:HB2	1.62	0.80
1:1A:1647:G:OP1	60:1A:4107:HOH:O	1.98	0.80
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:975:A:H4'	32:1a:976:G:H5''	1.64	0.80
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.63	0.80
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.63	0.79
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	1.63	0.79
1:1A:2469:A:O3'	12:1Q:56:ARG:NH2	2.15	0.79
32:1a:573:A:OP2	60:1a:1902:HOH:O	2.01	0.79
1:2A:2127:G:N2	1:2A:2161:C:C2	2.51	0.79
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.63	0.79
15:2T:107:ASP:OD2	15:2T:111:ARG:NH1	2.15	0.79
1:1A:1072:C:H2'	1:1A:1094:U:H3	1.47	0.79
7:2H:124:GLU:HB2	7:2H:132:ARG:HB3	1.65	0.79
1:1A:2138:C:N4	1:1A:2153:G:H1	1.80	0.79
1:1A:1670:C:OP1	60:1A:4110:HOH:O	2.01	0.79
1:2A:2592:G:OP1	60:2A:3910:HOH:O	2.00	0.79
1:2A:1021:A:H62	1:2A:1141:U:H3	1.29	0.78
32:1a:1035:A:H2'	32:1a:1036:G:H21	1.47	0.78
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.15	0.78
1:2A:2104:G:H1	1:2A:2185:C:N4	1.79	0.78
1:1A:1648:C:OP1	60:1A:4107:HOH:O	2.00	0.78
1:2A:1647:G:OP1	60:2A:3912:HOH:O	2.02	0.78
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.66	0.78
54:1w:229:GLY:HA3	55:1x:76:A:H3'	1.65	0.78
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.17	0.78
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.66	0.78
1:1A:1093:G:H3'	1:1A:1094:U:H5''	1.65	0.78
1:2A:2129:C:H42	1:2A:2159:G:H1	1.31	0.78
1:1A:1082:U:C4	1:1A:1086:A:N1	2.52	0.77
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.18	0.77
1:1A:1185:C:OP2	60:1A:4111:HOH:O	2.02	0.77
1:1A:2276:G:N7	60:1A:4145:HOH:O	2.16	0.77
1:2A:1226:A:OP1	17:2V:84:LYS:NZ	2.17	0.77
1:2A:1253:A:OP1	60:2A:3911:HOH:O	2.00	0.77
32:1a:519:C:OP1	54:1w:179:ARG:NH1	2.17	0.77
1:2A:1648:C:OP1	60:2A:3912:HOH:O	2.02	0.77
26:14:55:ARG:O	26:14:57:GLU:N	2.17	0.77
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.17	0.77
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.65	0.77
41:2j:51:ARG:HH11	45:2n:45:ARG:HH21	1.32	0.77
4:1E:110:GLY:O	60:1R:301:HOH:O	2.01	0.76
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.65	0.76
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:962:G:OP1	60:2A:3913:HOH:O	2.02	0.76
1:2A:2127:G:C6	1:2A:2161:C:N4	2.53	0.76
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.68	0.76
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.18	0.76
1:1A:2121:G:O6	1:1A:2176:A:N6	2.18	0.76
1:2A:1204:A:H2	1:2A:1241:A:H62	1.31	0.76
2:2B:103:G:O6	60:2B:301:HOH:O	2.04	0.76
1:1A:998:C:OP1	60:1A:4112:HOH:O	2.03	0.76
37:1f:35:ALA:HB1	37:1f:65:VAL:HG11	1.66	0.76
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.18	0.76
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.18	0.76
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.34	0.75
1:2A:2448:A:OP1	60:2A:3915:HOH:O	2.05	0.75
1:1A:1865:G:OP1	60:1A:4114:HOH:O	2.04	0.75
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.68	0.75
33:2b:54:THR:HG22	33:2b:199:TYR:HB3	1.68	0.75
54:2w:219:ILE:HG12	54:2w:241:VAL:HG12	1.67	0.75
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.20	0.75
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.19	0.75
50:1s:41:VAL:HG23	50:1s:43:GLU:H	1.52	0.75
32:1a:664:G:H22	32:1a:741:G:H1	1.32	0.75
1:1A:995:C:OP2	16:1U:54:LYS:NZ	2.17	0.75
1:2A:1664:A:OP1	60:2A:3916:HOH:O	2.05	0.75
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.19	0.75
1:2A:2127:G:C2	1:2A:2161:C:N3	2.55	0.74
32:1a:1108:G:O6	60:1a:1903:HOH:O	2.04	0.74
38:2g:22:LEU:HD12	38:2g:97:GLN:HE22	1.51	0.74
1:1A:1670:C:OP2	60:1A:4113:HOH:O	2.03	0.74
32:1a:1366:C:O2'	41:1j:60:ARG:NH1	2.20	0.74
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.18	0.74
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.69	0.74
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.52	0.74
39:1h:113:SER:HB2	39:1h:134:ILE:HD11	1.69	0.74
1:1A:991:C:OP2	60:1A:4115:HOH:O	2.05	0.74
32:1a:838:G:OP2	32:1a:840:C:N4	2.21	0.74
36:2e:99:GLY:H	36:2e:117:ASP:HB3	1.52	0.74
1:1A:1637:A:OP1	60:1A:4117:HOH:O	2.05	0.74
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.21	0.73
42:1k:15:ALA:HA	42:1k:77:MET:HA	1.71	0.73
1:2A:749:C:OP2	60:2A:3919:HOH:O	2.06	0.73
1:2A:2492:U:OP1	60:2A:3918:HOH:O	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:382:A:H2'	32:1a:383:A:C8	2.23	0.73
2:2B:66:A:H61	2:2B:109:C:H5'	1.53	0.73
1:1A:2718:G:O6	60:1A:4120:HOH:O	2.07	0.73
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.70	0.73
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.22	0.73
1:2A:1865:G:OP1	60:2A:3917:HOH:O	2.05	0.73
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.70	0.73
33:2b:91:PRO:HG2	33:2b:155:LEU:HD13	1.71	0.73
32:1a:557:G:OP1	60:1a:1904:HOH:O	2.06	0.73
25:23:5:LYS:NZ	25:23:34:GLU:OE2	2.20	0.73
1:1A:833:U:O2	11:1P:55:ARG:NH2	2.21	0.73
35:1d:122:ARG:NH1	35:1d:134:ASP:O	2.22	0.73
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.21	0.73
1:1A:1041:C:H42	1:1A:1114:G:H1	1.33	0.72
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.69	0.72
1:2A:1271:G:OP2	60:2A:3912:HOH:O	2.06	0.72
39:2h:51:VAL:HG11	39:2h:60:ARG:HH21	1.54	0.72
41:1j:13:HIS:HB3	41:1j:68:HIS:HD2	1.53	0.72
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.21	0.72
1:2A:752:A:H3'	29:27:1:MET:HE1	1.70	0.72
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.23	0.72
1:2A:198:C:OP2	60:2A:3920:HOH:O	2.06	0.72
8:2I:63:ALA:HA	8:2I:66:GLU:HG3	1.70	0.72
32:2a:953:G:H5'	32:2a:965:A:H61	1.53	0.72
1:1A:1010:A:OP2	60:1A:4118:HOH:O	2.06	0.72
1:1A:248:G:OP1	60:1A:4116:HOH:O	2.05	0.72
1:1A:1439:A:OP1	60:1A:4122:HOH:O	2.08	0.72
6:2G:122:PRO:HB3	6:2G:170:ARG:HH22	1.55	0.72
33:2b:95:GLN:HE22	33:2b:147:LYS:HB3	1.54	0.72
1:1A:2107:C:H42	1:1A:2182:G:H1	1.37	0.72
1:1A:2632:A:HO2'	1:1A:2811:G:HO2'	1.34	0.72
32:1a:1030:C:H42	32:1a:1031:G:H1	1.37	0.72
1:1A:1284:A:N7	60:1A:4164:HOH:O	2.21	0.71
32:1a:618:C:H5'	32:1a:619:U:H5''	1.72	0.71
1:2A:154(A):C:H42	1:2A:171:G:H1	1.37	0.71
1:2A:2518:A:OP2	60:2A:3924:HOH:O	2.08	0.71
26:24:16:CYS:SG	26:24:17:GLY:N	2.64	0.71
32:2a:544:G:OP1	35:2d:62:GLN:NE2	2.21	0.71
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.55	0.71
21:1Z:46:LYS:O	21:1Z:50:GLN:NE2	2.24	0.71
1:1A:2255:G:OP2	60:1A:4121:HOH:O	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.72	0.71
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.54	0.71
1:1A:1453:U:OP1	13:1R:77:ARG:NH1	2.23	0.71
26:24:12:ALA:HB3	26:24:24:THR:HG23	1.72	0.71
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.24	0.71
37:2f:43:LEU:HD11	49:2r:35:ARG:HH21	1.53	0.71
17:1V:60:GLU:HB2	17:1V:97:LYS:HE2	1.73	0.71
32:1a:1521:G:N3	60:1a:1918:HOH:O	2.22	0.71
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.19	0.71
49:1r:26:LEU:HD22	49:1r:39:VAL:HG13	1.73	0.71
1:2A:948:G:OP1	60:2A:3913:HOH:O	2.09	0.71
1:2A:1355:G:O6	60:2A:3914:HOH:O	2.04	0.71
1:2A:2150:U:H2'	1:2A:2151:G:H8	1.55	0.71
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.24	0.71
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.73	0.71
32:2a:677:U:H3	32:2a:713:G:H22	1.37	0.71
2:2B:81:G:OP2	60:2B:302:HOH:O	2.09	0.71
32:2a:972:C:O2'	41:2j:55:LYS:O	2.08	0.71
1:1A:1754:C:OP1	15:1T:96:ARG:NH1	2.24	0.70
1:2A:1970:A:OP1	60:2A:3921:HOH:O	2.07	0.70
1:2A:792:G:O6	60:2A:3925:HOH:O	2.08	0.70
32:2a:1327:C:H5''	52:2u:20:LYS:HB3	1.72	0.70
5:1F:181:LEU:O	5:1F:205:ARG:NH2	2.24	0.70
1:2A:135:G:N7	60:2A:3986:HOH:O	2.25	0.70
32:1a:330:C:O2	60:1a:1905:HOH:O	2.08	0.70
33:1b:15:VAL:HB	33:1b:209:ARG:HG2	1.72	0.70
1:2A:2821:A:OP2	60:2R:301:HOH:O	2.10	0.70
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.55	0.70
40:2i:17:VAL:HG22	40:2i:63:ILE:HG12	1.74	0.70
1:1A:2189:U:H2'	1:1A:2190:G:H8	1.54	0.70
1:1A:2384:G:O6	60:1A:4119:HOH:O	2.07	0.70
1:1A:1352:U:OP2	60:1A:4124:HOH:O	2.09	0.70
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.25	0.70
35:1d:20:TYR:HA	35:1d:26:CYS:SG	2.31	0.70
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.25	0.70
1:2A:2711:A:OP1	60:2A:3922:HOH:O	2.08	0.70
40:1i:53:VAL:O	40:1i:55:ALA:N	2.21	0.70
54:1w:114:GLY:HA3	54:1w:196:THR:HG22	1.71	0.70
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.38	0.70
1:2A:2171:A:N3	1:2A:2172:U:N3	2.39	0.70
50:2s:18:LYS:HA	50:2s:21:GLU:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:764:A:H5'	3:2D:210:GLY:HA2	1.73	0.70
1:2A:521:G:H2'	1:2A:522:G:H8	1.57	0.69
10:2O:54:GLU:OE1	60:2O:301:HOH:O	2.09	0.69
36:1e:35:GLY:HA3	36:1e:112:LEU:HB3	1.73	0.69
1:2A:2822:G:OP2	60:2A:3926:HOH:O	2.08	0.69
8:1I:72:LEU:HD23	8:1I:75:LEU:HD21	1.73	0.69
32:1a:316:G:OP2	32:1a:351:G:O2'	2.10	0.69
32:1a:437:U:H5'	35:1d:155:LEU:HD11	1.73	0.69
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.27	0.69
5:2F:195:ASP:OD1	5:2F:196:LEU:N	2.24	0.69
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	1.74	0.69
54:2w:312:VAL:HG23	54:2w:321:THR:HG23	1.74	0.69
1:1A:1971:A:OP1	60:1A:4127:HOH:O	2.09	0.69
1:1A:1986:A:OP1	60:1A:4125:HOH:O	2.09	0.69
1:2A:370:G:N7	60:2A:3992:HOH:O	2.26	0.69
1:2A:965:C:OP2	60:2A:3927:HOH:O	2.10	0.69
6:2G:60:LEU:HD23	6:2G:68:PRO:HG3	1.74	0.69
54:2w:228:GLY:HA3	54:2w:232:VAL:HB	1.74	0.69
1:1A:271(L):U:H4'	8:1I:50:ARG:HH22	1.56	0.69
1:1A:1673:U:OP1	60:1A:4123:HOH:O	2.09	0.69
1:1A:2038:G:O6	60:1A:4126:HOH:O	2.09	0.69
38:1g:37:ASN:HD21	40:1i:40:LEU:HA	1.58	0.69
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.74	0.69
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.56	0.69
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.23	0.69
27:15:17:ASP:OD2	60:15:6601:HOH:O	2.11	0.69
32:1a:583:A:OP2	60:1a:1907:HOH:O	2.10	0.69
41:2j:6:ILE:HG12	41:2j:98:ILE:HD12	1.74	0.69
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.56	0.69
1:1A:2702:U:OP2	60:1A:4130:HOH:O	2.11	0.69
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.73	0.69
14:2S:71:ARG:NH1	14:2S:107:GLU:OE2	2.26	0.69
37:2f:15:ASP:OD1	37:2f:18:GLN:N	2.24	0.69
1:1A:1671:U:OP2	60:1A:4110:HOH:O	2.11	0.69
32:1a:56:U:H2'	32:1a:57:G:C8	2.28	0.69
32:1a:375:U:O2	47:1p:28:ARG:NH1	2.26	0.69
1:2A:1035:U:O4	60:2A:3923:HOH:O	2.08	0.69
32:2a:1272:G:N2	32:2a:1273:G:C5	2.61	0.69
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.73	0.68
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.76	0.68
1:1A:153:C:OP1	23:11:92:LYS:NZ	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.57	0.68
1:1A:583:G:N7	60:1A:4191:HOH:O	2.26	0.68
1:1A:1970:A:OP1	60:1A:4127:HOH:O	2.11	0.68
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.74	0.68
54:1w:181:GLN:HG3	54:1w:306:ASN:HD22	1.59	0.68
1:1A:1253:A:OP1	60:1A:4128:HOH:O	2.10	0.68
38:2g:24:THR:O	38:2g:28:ASN:ND2	2.26	0.68
10:1O:21:CYS:HB2	10:1O:39:ILE:HD12	1.73	0.68
33:1b:112:VAL:HG12	33:1b:149:LEU:HD13	1.75	0.68
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.26	0.68
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.08	0.68
1:1A:1082:U:N3	1:1A:1086:A:N6	2.28	0.68
32:1a:979:C:OP1	60:1a:1908:HOH:O	2.12	0.68
1:2A:1633:G:OP2	60:2A:3934:HOH:O	2.12	0.68
1:2A:2127:G:C2	1:2A:2161:C:C4	2.81	0.68
4:2E:110:GLY:O	60:2R:301:HOH:O	2.11	0.68
54:2w:106:ASP:HB2	54:2w:204:LYS:HD2	1.75	0.68
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.24	0.68
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.11	0.68
32:1a:1027:C:C2	32:1a:1034:G:N2	2.59	0.68
1:2A:783:A:OP2	60:2A:3907:HOH:O	2.11	0.68
1:2A:945:A:OP2	60:2A:3935:HOH:O	2.12	0.68
1:2A:1762:A:N1	60:2A:4001:HOH:O	2.27	0.68
32:2a:1226:C:H2'	44:2m:103:THR:HB	1.74	0.68
1:1A:500:G:N7	60:1A:4192:HOH:O	2.26	0.68
32:1a:299:G:O6	60:1a:1906:HOH:O	2.09	0.68
38:1g:69:VAL:HG21	38:1g:104:LEU:HD21	1.76	0.68
44:2m:47:ASP:N	44:2m:47:ASP:OD1	2.24	0.68
54:2w:229:GLY:HA3	55:2x:76:A:H3'	1.73	0.68
1:2A:2268:A:OP1	60:2A:3929:HOH:O	2.11	0.68
1:2A:2879:C:OP2	60:2A:3936:HOH:O	2.12	0.68
32:2a:673:G:H2'	32:2a:674:G:C8	2.28	0.68
8:2I:114:LEU:HD11	8:2I:128:LEU:HD13	1.75	0.67
32:2a:1083:U:OP2	60:2a:1802:HOH:O	2.12	0.67
40:2i:128:ARG:NH2	55:2x:33:U:OP2	2.26	0.67
32:1a:451:A:H61	32:1a:481:G:H5'	1.60	0.67
33:1b:24:TRP:HZ3	33:1b:29:ALA:HB2	1.59	0.67
54:1w:119:GLU:HG3	54:1w:184:PRO:HB3	1.75	0.67
32:2a:8:A:N6	35:2d:205:GLU:O	2.26	0.67
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.37	0.67
1:2A:1568:G:N7	60:2D:403:HOH:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:1S:4:LEU:O	60:1S:301:HOH:O	2.13	0.67
42:1k:52:GLY:H	42:1k:55:LYS:HE2	1.58	0.67
1:2A:963:U:OP2	60:2A:3913:HOH:O	2.13	0.67
1:2A:1124:C:OP1	60:2A:3928:HOH:O	2.10	0.67
1:2A:1604:C:OP1	60:2A:3932:HOH:O	2.12	0.67
32:2a:937:A:OP2	60:2a:1801:HOH:O	2.11	0.67
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.28	0.67
1:2A:2759:G:OP2	60:2A:3933:HOH:O	2.12	0.67
32:2a:13:U:OP1	60:2a:1803:HOH:O	2.12	0.67
44:2m:45:VAL:HA	44:2m:48:LEU:HD12	1.76	0.67
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.76	0.67
50:1s:51:VAL:HG11	50:1s:71:LEU:HB3	1.77	0.67
1:2A:848:G:OP1	60:2A:3930:HOH:O	2.11	0.67
1:2A:1023:U:OP2	60:2A:3937:HOH:O	2.13	0.67
32:2a:461:A:O2'	32:2a:471:G:N7	2.26	0.67
54:2w:235:THR:OG1	60:2w:401:HOH:O	2.11	0.67
37:2f:5:GLU:HG3	37:2f:93:SER:HB3	1.77	0.67
1:1A:154(A):C:H42	1:1A:171:G:H1	1.42	0.67
1:2A:1449:A:O2'	1:2A:1529:G:N2	2.20	0.67
1:2A:2198:A:OP1	8:2I:33:ARG:NH2	2.27	0.67
8:2I:37:VAL:HG13	8:2I:38:LEU:HD12	1.77	0.67
1:1A:15:G:OP1	60:1A:4129:HOH:O	2.11	0.67
1:1A:1014:U:OP2	60:1A:4134:HOH:O	2.13	0.67
32:1a:1240:U:OP1	38:1g:119:ARG:NH2	2.28	0.67
35:2d:76:ARG:NH2	35:2d:80:GLU:OE2	2.27	0.67
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.30	0.66
32:2a:959:A:O2'	32:2a:984:C:O2'	2.07	0.66
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.76	0.66
32:1a:7:G:O2'	36:1e:120:THR:O	2.13	0.66
34:1c:187:ALA:HB3	34:1c:198:VAL:HB	1.75	0.66
54:1w:242:VAL:HG22	54:1w:249:MET:HB3	1.77	0.66
1:2A:869:G:O3'	12:2Q:6:ARG:NH1	2.28	0.66
1:2A:1312:U:OP2	19:2X:63:LYS:NZ	2.27	0.66
25:13:3:ARG:NH1	25:13:60:GLU:OE2	2.25	0.66
1:1A:1186:G:OP2	60:1A:4115:HOH:O	2.14	0.66
1:1A:2447:G:OP2	60:1A:4133:HOH:O	2.12	0.66
32:2a:176:C:H2'	32:2a:177:C:H6	1.60	0.66
32:2a:956:U:OP2	54:2w:133:ARG:NH2	2.27	0.66
48:2q:53:LEU:HD23	48:2q:85:VAL:HG11	1.76	0.66
1:1A:2303:G:O6	60:1A:4131:HOH:O	2.12	0.66
41:1j:23:ILE:O	41:1j:27:ALA:N	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:125:GLY:O	60:2E:401:HOH:O	2.12	0.66
1:2A:531:C:OP1	1:2A:561:G:N1	2.27	0.66
23:21:44:PRO:HB2	23:21:46:LEU:HD13	1.76	0.66
6:1G:123:ASN:O	60:1G:301:HOH:O	2.14	0.66
1:2A:299:A:N1	1:2A:322:A:O2'	2.26	0.66
32:2a:1271:G:N2	32:2a:1272:G:N7	2.44	0.66
39:2h:24:THR:HG22	39:2h:63:LEU:HD21	1.76	0.66
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.78	0.66
54:2w:259:ILE:HG13	54:2w:262:ARG:HH12	1.61	0.66
1:2A:2129:C:N4	1:2A:2159:G:H1	1.94	0.66
1:1A:441:U:O2	5:1F:46:ARG:NH2	2.26	0.66
1:1A:1332:G:OP1	60:1A:4109:HOH:O	2.13	0.66
1:1A:2289:G:OP1	60:1A:4136:HOH:O	2.14	0.66
1:1A:2552:OMU:OP2	60:1A:4123:HOH:O	2.13	0.66
33:1b:127:ILE:HG22	33:1b:130:ARG:H	1.60	0.66
1:2A:875:G:H5''	21:2Z:149:SER:HB3	1.78	0.66
38:2g:70:LYS:HG2	38:2g:96:GLN:HB3	1.77	0.66
43:2l:70:ILE:HD13	43:2l:77:LEU:HD12	1.78	0.66
6:1G:41:GLN:HB2	6:1G:90:LEU:HB2	1.77	0.65
1:2A:424:G:N7	60:2A:4022:HOH:O	2.30	0.65
33:2b:95:GLN:HE22	33:2b:147:LYS:HE2	1.61	0.65
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.77	0.65
1:2A:2447:G:OP2	60:2A:3938:HOH:O	2.14	0.65
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.78	0.65
23:21:3:LYS:HB2	23:21:61:ARG:HH22	1.60	0.65
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.77	0.65
40:2i:14:VAL:HG23	40:2i:66:ARG:HG3	1.78	0.65
51:2t:57:ARG:NH1	51:2t:101:GLY:O	2.29	0.65
32:1a:536:C:OP2	60:1a:1912:HOH:O	2.14	0.65
38:1g:49:ILE:HA	38:1g:52:GLU:HG3	1.76	0.65
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.78	0.65
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.28	0.65
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.78	0.65
45:1n:23:ARG:NH1	45:1n:28:GLY:O	2.30	0.65
51:1t:33:ILE:O	51:1t:37:SER:OG	2.14	0.65
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.78	0.65
11:1P:42:SER:O	60:1P:302:HOH:O	2.14	0.65
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.28	0.65
32:1a:702:A:OP2	60:1a:1911:HOH:O	2.14	0.65
1:1A:990:A:OP2	60:1A:4115:HOH:O	2.14	0.65
1:1A:2206:G:H5''	1:1A:2207:G:N7	2.11	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2763:G:OP2	60:1A:4138:HOH:O	2.14	0.65
32:1a:1135:U:H4'	32:1a:1136:U:H5	1.61	0.65
1:2A:775:G:O3'	60:2A:3943:HOH:O	2.15	0.65
1:2A:1299:G:N7	60:2A:4013:HOH:O	2.28	0.65
1:2A:2134:A:O2'	1:2A:2159:G:N2	2.28	0.65
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.77	0.65
1:1A:588:U:H2'	1:1A:589:C:C6	2.31	0.65
1:1A:2350:C:OP2	60:1A:4139:HOH:O	2.14	0.65
32:1a:21:G:OP1	60:1a:1910:HOH:O	2.13	0.65
1:2A:563:G:OP2	60:2A:3939:HOH:O	2.14	0.65
26:24:50:VAL:HG11	44:2m:65:LYS:HB2	1.79	0.65
8:1I:114:LEU:HD13	8:1I:130:TYR:HD1	1.61	0.65
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.78	0.65
1:2A:1184:G:OP1	25:23:30:ARG:NH1	2.30	0.65
32:2a:251:G:N7	60:2a:1812:HOH:O	2.30	0.65
1:1A:2162:G:H4'	1:1A:2172:U:H5'	1.79	0.65
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.30	0.65
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.78	0.65
32:1a:789:U:O2'	60:1a:1909:HOH:O	2.13	0.65
32:2a:1047:G:H5''	45:2n:4:LYS:HD2	1.79	0.65
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.13	0.65
1:1A:1072:C:H1'	1:1A:1092:C:H41	1.62	0.65
13:1R:98:LEU:HB2	13:1R:113:LEU:HD11	1.78	0.65
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	1.78	0.65
50:1s:41:VAL:HG22	50:1s:44:MET:HG3	1.77	0.65
32:1a:110:C:O2'	47:1p:25:ARG:O	2.16	0.64
1:2A:2127:G:O2'	1:2A:2173:A:N3	2.30	0.64
1:1A:2499:C:N3	60:1A:4212:HOH:O	2.30	0.64
26:24:15:ILE:HD12	26:24:21:VAL:HG12	1.79	0.64
39:2h:49:GLU:HG3	39:2h:62:TYR:HE2	1.62	0.64
32:1a:195:A:O5'	51:1t:68:LYS:NZ	2.28	0.64
32:1a:976:G:H5'	32:1a:1358:U:O2'	1.97	0.64
51:1t:10:LEU:HG	51:1t:12:ALA:H	1.62	0.64
1:2A:272(B):G:H2'	1:2A:272(C):G:H8	1.62	0.64
1:2A:1670:C:OP1	60:2A:3941:HOH:O	2.14	0.64
32:2a:1228:C:OP1	44:2m:115:LYS:N	2.23	0.64
49:2r:26:LEU:HD11	49:2r:42:ARG:HD3	1.80	0.64
1:1A:1056:G:H5''	1:1A:1057:A:O4'	1.98	0.64
1:1A:2759:G:N7	60:1A:4203:HOH:O	2.29	0.64
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.79	0.64
32:2a:1000:U:O4	32:2a:1001:A:N6	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:219:ILE:HG12	54:1w:241:VAL:HG12	1.77	0.64
1:2A:642:G:N2	1:2A:645:C:OP2	2.29	0.64
6:1G:131:TYR:HE2	6:1G:133:LEU:HD23	1.61	0.64
32:1a:67:C:H2'	32:1a:68:G:C8	2.32	0.64
1:1A:2189:U:H2'	1:1A:2190:G:C8	2.32	0.64
40:1i:23:ASN:O	40:1i:25:LYS:NZ	2.31	0.64
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.31	0.64
16:2U:44:ASN:HD21	17:2V:75:PHE:HB3	1.63	0.64
1:1A:2059:A:OP1	60:1A:4137:HOH:O	2.14	0.64
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.80	0.64
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.15	0.64
38:1g:115:ARG:HG2	38:1g:118:VAL:HG12	1.78	0.64
54:1w:259:ILE:HD13	54:1w:262:ARG:HH11	1.63	0.64
1:2A:1223:G:N2	1:2A:1226:A:OP2	2.26	0.64
33:1b:124:SER:O	33:1b:126:GLU:N	2.31	0.64
1:2A:272(D):G:O6	60:2A:3942:HOH:O	2.15	0.64
7:2H:96:ALA:HB1	7:2H:103:LEU:HD11	1.80	0.64
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.98	0.64
50:2s:27:GLU:HB2	50:2s:28:LYS:HB3	1.80	0.64
55:2x:23:U:H2'	55:2x:24:G:H8	1.63	0.64
32:2a:1314:C:OP2	50:2s:4:SER:OG	2.14	0.64
32:1a:1129:C:H5''	40:1i:16:ARG:HH12	1.61	0.63
1:1A:1072:C:N4	1:1A:1098:A:OP2	2.31	0.63
2:1B:58:A:OP2	60:1B:301:HOH:O	2.15	0.63
32:1a:652:U:O4	32:1a:752:G:O2'	2.15	0.63
32:2a:1238:A:OP2	60:2a:1805:HOH:O	2.16	0.63
35:2d:102:ASP:OD2	35:2d:118:ARG:NH1	2.30	0.63
36:1e:78:HIS:HE1	36:1e:142:LEU:HA	1.63	0.63
32:2a:624:C:H2'	32:2a:625:G:H8	1.63	0.63
41:2j:50:ILE:HA	41:2j:60:ARG:HG2	1.80	0.63
32:1a:1226:C:H3'	44:1m:96:LEU:HD21	1.80	0.63
37:1f:97:PHE:O	49:1r:31:LEU:N	2.28	0.63
5:2F:148:LEU:HD21	5:2F:191:ARG:HE	1.63	0.63
32:2a:254:G:OP1	48:2q:66:SER:OG	2.17	0.63
1:1A:2879:C:OP2	60:1A:4142:HOH:O	2.15	0.63
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.80	0.63
1:2A:2100:G:H1	1:2A:2189:U:H3	1.47	0.63
34:2c:52:LEU:HD13	34:2c:68:VAL:HG13	1.79	0.63
43:2l:40:VAL:HG21	43:2l:78:GLN:HA	1.79	0.63
49:2r:48:GLY:O	49:2r:74:ARG:NH2	2.32	0.63
1:1A:1309:G:H4'	29:17:7:PRO:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2682:U:O2'	15:1T:58:ASN:ND2	2.32	0.63
40:1i:50:LEU:HD23	40:1i:85:LEU:HD11	1.81	0.63
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.17	0.63
1:1A:1056:G:H4'	1:1A:1086:A:H8	1.64	0.63
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.81	0.63
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.34	0.63
49:2r:37:VAL:HG22	49:2r:78:LEU:HB3	1.80	0.63
32:2a:17:U:H2'	32:2a:18:C:C6	2.34	0.63
36:2e:12:LEU:HD12	36:2e:128:PRO:HB2	1.80	0.63
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.80	0.62
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.16	0.62
26:14:16:CYS:SG	26:14:17:GLY:N	2.72	0.62
40:2i:26:VAL:HG12	40:2i:61:ALA:HB3	1.80	0.62
1:2A:796:C:H2'	1:2A:797:C:C6	2.33	0.62
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.32	0.62
32:1a:600:C:H2'	32:1a:601:C:C6	2.34	0.62
1:2A:981:A:OP1	60:2A:3948:HOH:O	2.16	0.62
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.81	0.62
1:2A:2755:C:OP1	60:2A:3944:HOH:O	2.16	0.62
1:1A:1174:A:H4'	1:1A:1175:U:OP1	1.99	0.62
1:1A:1271:G:OP2	60:1A:4107:HOH:O	2.16	0.62
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.34	0.62
32:1a:130:A:N3	32:1a:263:A:O2'	2.31	0.62
32:1a:976:G:OP1	45:1n:32:SER:N	2.28	0.62
32:2a:1320:C:H1'	50:2s:73:GLU:HG3	1.81	0.62
38:2g:114:ARG:HB2	38:2g:115:ARG:NH2	2.15	0.62
40:2i:88:TYR:HD2	40:2i:89:ASN:HD22	1.44	0.62
1:1A:1064:C:N3	1:1A:1074:G:O6	2.31	0.62
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.31	0.62
43:2l:9:GLN:HG2	43:2l:12:ARG:HH21	1.63	0.62
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.80	0.62
33:1b:127:ILE:HG21	33:1b:130:ARG:HG3	1.82	0.62
1:2A:1533:G:H1'	1:2A:1537:G:H22	1.65	0.62
5:2F:33:LEU:HD21	5:2F:112:MET:HB3	1.80	0.62
34:2c:70:VAL:HG12	34:2c:72:LYS:H	1.64	0.62
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.80	0.62
1:1A:2181:G:O2'	1:1A:2182:G:OP1	2.13	0.62
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.80	0.62
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.17	0.62
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.33	0.62
34:2c:73:PRO:HD3	34:2c:105:GLU:HG3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:125:ARG:HG3	54:1w:154:GLY:HA2	1.82	0.62
1:2A:2110:G:H1	1:2A:2179:C:H42	1.48	0.62
7:2H:41:MET:HE2	7:2H:65:HIS:HA	1.82	0.62
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.82	0.62
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.15	0.62
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.33	0.62
15:1T:84:GLN:HG2	15:1T:85:LYS:HG2	1.82	0.62
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.30	0.62
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.82	0.62
22:20:14:ARG:NH1	60:20:201:HOH:O	2.32	0.62
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.33	0.62
54:2w:175:SER:HB2	54:2w:201:VAL:HG22	1.80	0.62
26:14:58:ARG:HH21	50:1s:68:GLY:HA3	1.65	0.61
33:1b:82:ARG:HH11	33:1b:92:TYR:HH	1.44	0.61
35:1d:189:PRO:HB2	35:1d:194:LEU:HD21	1.82	0.61
1:2A:1973:G:OP1	60:2A:3945:HOH:O	2.16	0.61
1:1A:271(H):G:H2'	1:1A:271(I):G:H8	1.65	0.61
3:1D:39:LYS:NZ	3:1D:57:GLY:O	2.33	0.61
7:1H:148:ILE:HA	7:1H:151:ILE:HD12	1.82	0.61
32:1a:501:C:H1'	32:1a:549:C:H1'	1.82	0.61
1:2A:2104:G:N2	1:2A:2185:C:N3	2.47	0.61
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.65	0.61
35:1d:105:VAL:HG23	35:1d:110:PHE:HB2	1.81	0.61
54:2w:302:ILE:HG13	54:2w:316:ARG:HD3	1.81	0.61
1:1A:848:G:H2'	1:1A:849:A:C8	2.35	0.61
1:2A:2110:G:H1	1:2A:2179:C:N4	1.98	0.61
1:2A:2782:G:OP2	60:2A:3949:HOH:O	2.16	0.61
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.33	0.61
36:2e:37:ARG:HH12	36:2e:111:GLU:HG2	1.65	0.61
44:2m:60:VAL:HG13	44:2m:64:TRP:HE3	1.64	0.61
1:1A:271(H):G:H2'	1:1A:271(I):G:C8	2.35	0.61
11:2P:20:GLY:O	11:2P:21:ARG:NH1	2.33	0.61
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.66	0.61
33:2b:112:VAL:HG12	33:2b:149:LEU:HD13	1.83	0.61
34:1c:63:ASN:HA	34:1c:98:ASN:HB2	1.80	0.61
41:1j:13:HIS:HB3	41:1j:68:HIS:CD2	2.36	0.61
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.35	0.61
32:2a:664:G:H22	32:2a:741:G:H1	1.48	0.61
36:2e:11:ILE:HD11	36:2e:108:ALA:HB3	1.82	0.61
43:2l:74:GLY:O	43:2l:102:ARG:NH2	2.31	0.61
32:1a:1298:C:H2'	38:1g:114:ARG:NH2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:21:ARG:O	33:1b:23:ARG:N	2.33	0.61
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.24	0.61
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.83	0.61
26:24:24:THR:OG1	26:24:25:TYR:N	2.34	0.61
40:2i:28:VAL:HG12	40:2i:63:ILE:HB	1.83	0.61
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.66	0.61
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.65	0.61
1:2A:2685:G:O6	60:2A:3940:HOH:O	2.14	0.61
32:2a:1129:C:OP1	40:2i:66:ARG:NH1	2.29	0.61
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.65	0.61
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.82	0.61
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.35	0.61
1:1A:2508:G:OP1	54:1w:223:ARG:NH2	2.34	0.61
6:1G:18:GLU:OE2	6:1G:22:ARG:NH1	2.34	0.61
26:14:50:VAL:HG22	44:1m:65:LYS:HE3	1.81	0.61
32:1a:950:U:H2'	32:1a:951:G:H8	1.66	0.61
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.34	0.61
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.83	0.61
1:1A:2243:U:OP1	60:1A:4144:HOH:O	2.16	0.61
1:2A:2576:G:OP1	60:2A:3950:HOH:O	2.16	0.61
6:2G:59:GLU:OE2	6:2G:153:ARG:NH2	2.34	0.61
19:2X:31:HIS:HD2	19:2X:33:LYS:H	1.49	0.61
36:1e:68:GLU:HG3	36:1e:70:PRO:HD3	1.83	0.60
1:2A:2499:C:O2	60:2A:3951:HOH:O	2.16	0.60
10:2O:77:ILE:HB	15:2T:74:ARG:HD2	1.83	0.60
42:2k:79:SER:HB2	42:2k:106:LYS:HD3	1.83	0.60
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.34	0.60
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.36	0.60
33:1b:178:ARG:HH22	39:1h:68:ARG:HH12	1.49	0.60
34:1c:157:ILE:HD12	34:1c:164:ARG:HB3	1.82	0.60
1:2A:81:G:O2'	1:2A:295:G:O2'	2.17	0.60
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.26	0.60
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.36	0.60
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.65	0.60
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.83	0.60
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.66	0.60
18:2W:25:ARG:NH2	18:2W:74:ALA:O	2.32	0.60
32:2a:1030(A):G:H1'	32:2a:1030(C):G:N7	2.16	0.60
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.37	0.60
34:2c:10:PHE:HA	45:2n:58:LYS:HE2	1.83	0.60
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:1I:14:ASP:O	8:1I:17:GLN:HB2	2.02	0.60
18:1W:12:ILE:HD13	18:1W:17:VAL:HG13	1.84	0.60
1:2A:1683:C:O2'	60:2A:3946:HOH:O	2.16	0.60
14:2S:99:LYS:NZ	14:2S:103:GLU:OE2	2.25	0.60
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.35	0.60
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.82	0.60
32:2a:630:G:H2'	32:2a:631:G:H8	1.66	0.60
35:2d:17:VAL:HG12	35:2d:18:LYS:H	1.66	0.60
32:1a:1131:G:H1	32:1a:1143:G:H21	1.49	0.60
33:1b:115:LEU:C	33:1b:117:GLU:H	2.09	0.60
32:2a:1132:C:H2'	32:2a:1133:G:C8	2.37	0.60
1:1A:630:G:OP2	30:18:15:LYS:NZ	2.30	0.60
1:1A:1399:C:OP1	19:1X:25:LYS:NZ	2.34	0.60
3:1D:147:LEU:HD13	3:1D:155:LEU:HD21	1.83	0.60
6:1G:68:PRO:HB3	6:1G:92:VAL:HB	1.82	0.60
1:2A:1333:C:OP2	60:2A:3952:HOH:O	2.16	0.60
1:2A:1452:A:OP2	60:2A:3953:HOH:O	2.16	0.60
14:2S:34:HIS:ND1	14:2S:53:SER:OG	2.32	0.60
26:24:58:ARG:HH21	50:2s:68:GLY:HA3	1.66	0.60
32:2a:405:U:H5''	32:2a:495:A:H2	1.65	0.60
32:2a:881:G:P	43:2l:12:ARG:HH22	2.24	0.60
31:19:25:VAL:HB	31:19:34:GLN:HB2	1.83	0.60
32:1a:258:G:H2'	32:1a:259:G:H8	1.65	0.60
32:1a:448:A:OP2	32:1a:485:G:N1	2.25	0.60
32:2a:110:C:H2'	32:2a:111:G:O4'	2.02	0.60
44:2m:81:LEU:HA	44:2m:84:ILE:HG12	1.82	0.60
1:1A:383:U:O4	60:1A:4141:HOH:O	2.15	0.60
1:1A:1951:U:O4	60:1A:4132:HOH:O	2.12	0.60
6:1G:125:PHE:N	60:1G:301:HOH:O	2.34	0.60
1:1A:630:G:OP1	30:18:47:LYS:NZ	2.34	0.60
1:1A:1448:G:N7	60:1A:4214:HOH:O	2.30	0.60
3:1D:206:LEU:O	3:1D:211:ARG:HD3	2.01	0.60
32:1a:673:G:H2'	32:1a:674:G:C8	2.37	0.60
40:1i:24:GLY:N	40:1i:60:ASP:OD1	2.35	0.60
1:2A:832:G:OP1	60:2A:3954:HOH:O	2.17	0.60
54:2w:103:ASP:OD2	54:2w:172:LYS:NZ	2.27	0.60
32:2a:266:G:H5''	32:2a:268:C:H41	1.67	0.60
32:2a:642:A:N3	39:2h:113:SER:OG	2.35	0.60
49:2r:25:THR:HG23	49:2r:26:LEU:HG	1.83	0.60
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.02	0.59
3:1D:166:GLN:HB2	3:1D:174:ILE:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:146:ILE:N	21:1Z:147:GLY:HA2	2.17	0.59
32:1a:1005:A:H5''	32:1a:1006:C:C5	2.36	0.59
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.20	0.59
34:1c:130:VAL:HG12	34:1c:134:ILE:HD11	1.84	0.59
44:1m:82:MET:O	44:1m:93:ARG:NH2	2.33	0.59
1:2A:562:U:OP1	60:2A:3947:HOH:O	2.16	0.59
1:2A:848:G:H2'	1:2A:849:A:C8	2.36	0.59
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.67	0.59
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.17	0.59
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	1.84	0.59
44:2m:91:ARG:HH21	44:2m:96:LEU:HD12	1.64	0.59
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.36	0.59
45:2n:47:LEU:HD22	45:2n:52:GLN:HB2	1.84	0.59
38:1g:97:GLN:HE21	38:1g:101:LEU:HD11	1.67	0.59
42:1k:14:VAL:HG22	42:1k:16:SER:H	1.66	0.59
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.35	0.59
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.38	0.59
32:2a:1239:A:H62	32:2a:1299:A:H62	1.50	0.59
34:1c:121:ALA:HB2	34:1c:187:ALA:HB1	1.85	0.59
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.03	0.59
3:2D:71:ASP:HB3	3:2D:103:ARG:HH12	1.67	0.59
41:2j:8:LEU:HD11	41:2j:20:ALA:HB2	1.84	0.59
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.37	0.59
34:1c:59:ARG:HG2	34:1c:64:VAL:HB	1.85	0.59
39:1h:36:LEU:HD23	39:1h:39:LEU:HD12	1.84	0.59
32:2a:407:G:H5''	35:2d:115:ARG:HB3	1.85	0.59
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.84	0.59
32:2a:782:A:OP1	60:2a:1806:HOH:O	2.17	0.59
32:2a:1172:C:H2'	32:2a:1173:G:C8	2.38	0.59
1:1A:2163:C:OP1	1:1A:2165:G:N2	2.35	0.59
35:1d:132:ARG:HH12	35:1d:134:ASP:HB3	1.67	0.59
1:2A:272(B):G:H2'	1:2A:272(C):G:C8	2.38	0.59
1:2A:888:C:OP1	44:2m:93:ARG:NH2	2.35	0.59
3:1D:125:ILE:HB	37:1f:81:ILE:HD11	1.85	0.59
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.38	0.59
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.09	0.59
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.37	0.59
1:2A:724:U:O4	60:2A:3931:HOH:O	2.11	0.59
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.84	0.59
26:24:14:ILE:HD11	26:24:24:THR:HG21	1.85	0.59
32:2a:903:G:OP1	60:2a:1804:HOH:O	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:883:G:H21	1:1A:893:C:H42	1.50	0.59
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.03	0.59
1:2A:586:A:N1	1:2A:809:G:O2'	2.31	0.59
32:2a:280:C:N3	48:2q:39:SER:OG	2.35	0.59
5:1F:9:ILE:HD12	5:1F:123:LEU:HD23	1.85	0.59
8:1I:4:ILE:HG12	8:1I:18:VAL:HG12	1.85	0.59
26:14:61:ARG:HG2	26:14:62:ARG:N	2.16	0.59
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.38	0.59
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.26	0.59
32:1a:1086:U:H3	32:1a:1099:G:H22	1.50	0.59
32:1a:1144:G:H21	32:1a:1146:A:H62	1.49	0.59
1:2A:959:A:N3	1:2A:2457:U:O2'	2.34	0.59
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.22	0.59
1:2A:2135:A:N1	1:2A:2156:G:O2'	2.35	0.59
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.84	0.59
32:2a:1141:C:H2'	32:2a:1142:G:H8	1.68	0.59
54:2w:317:ILE:HG13	54:2w:319:PHE:HB2	1.85	0.59
1:1A:184:C:H2'	1:1A:185:U:C6	2.38	0.59
1:1A:1235:G:O6	60:1A:4140:HOH:O	2.15	0.59
36:1e:5:ASP:OD1	36:1e:5:ASP:N	2.35	0.59
42:1k:21:ILE:HG12	42:1k:30:VAL:HG22	1.85	0.59
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.14	0.59
32:2a:1256:A:N6	32:2a:1278:U:H1'	2.17	0.59
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.85	0.59
54:2w:348:LEU:HA	54:2w:352:ALA:HB3	1.84	0.59
1:1A:1420:U:O2'	1:1A:1421:G:OP1	2.17	0.58
1:2A:911:A:OP1	60:2A:3955:HOH:O	2.17	0.58
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.66	0.58
8:2I:89:TYR:O	8:2I:121:LYS:NZ	2.36	0.58
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.43	0.58
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.35	0.58
1:2A:1971:A:OP1	60:2A:3921:HOH:O	2.17	0.58
50:2s:49:ILE:HD13	50:2s:71:LEU:HD11	1.85	0.58
6:1G:120:LEU:HD22	6:1G:133:LEU:HD22	1.85	0.58
14:1S:83:LYS:HB3	14:1S:111:GLU:HG3	1.84	0.58
41:1j:17:ASP:N	41:1j:17:ASP:OD1	2.35	0.58
32:2a:222:U:H2'	32:2a:223:U:C6	2.39	0.58
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.68	0.58
44:2m:91:ARG:HB2	44:2m:98:VAL:HG13	1.84	0.58
1:1A:192:C:OP1	60:1A:4144:HOH:O	2.17	0.58
1:1A:2681:C:OP2	4:1E:109:LYS:NZ	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:128:ARG:NH1	55:1x:35:C:OP1	2.37	0.58
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.69	0.58
1:2A:223:A:O2'	1:2A:420:C:O2	2.20	0.58
1:2A:890:A:H2'	1:2A:892:G:C8	2.38	0.58
1:2A:2849:U:O4	15:2T:23:ARG:NH1	2.33	0.58
2:2B:9:G:P	14:2S:25:ARG:HH22	2.26	0.58
6:2G:36:LYS:HZ3	6:2G:95:ARG:HH12	1.52	0.58
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.30	0.58
32:2a:41:G:H2'	32:2a:42:G:C8	2.38	0.58
32:2a:946:A:H2'	32:2a:947:G:C8	2.39	0.58
32:1a:956:U:OP2	54:1w:133:ARG:NH1	2.34	0.58
54:1w:321:THR:OG1	54:1w:322:HIS:N	2.37	0.58
1:2A:521:G:H2'	1:2A:522:G:C8	2.38	0.58
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.85	0.58
50:1s:36:ARG:HB3	50:1s:72:GLY:HA3	1.86	0.58
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.39	0.58
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.84	0.58
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.84	0.58
32:2a:1227:A:OP2	44:2m:111:LYS:HD2	2.04	0.58
34:2c:124:ILE:HG22	34:2c:130:VAL:HG22	1.85	0.58
1:1A:671:C:N4	60:1A:4261:HOH:O	2.36	0.58
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.30	0.58
33:1b:115:LEU:HB2	33:1b:145:LEU:HD22	1.85	0.58
42:1k:48:ILE:O	42:1k:50:TYR:N	2.29	0.58
1:2A:2114:A:H2	1:2A:2171:A:H61	1.52	0.58
5:2F:120:GLU:HB3	5:2F:122:LYS:HG2	1.86	0.58
33:2b:178:ARG:HH22	39:2h:68:ARG:HH12	1.52	0.58
1:1A:226:G:H21	1:1A:228:A:H62	1.51	0.58
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.36	0.58
20:1Y:92:ASN:HB3	20:1Y:94:LYS:HG3	1.85	0.58
32:1a:1005:A:OP2	32:1a:1006:C:N4	2.37	0.58
37:2f:4:TYR:HD1	37:2f:92:LYS:HA	1.69	0.58
1:1A:530:G:N1	1:1A:2023:G:OP1	2.26	0.58
1:1A:1071:G:H1'	1:1A:1089:G:C6	2.38	0.58
32:1a:328:C:H4'	32:1a:329:A:H5''	1.84	0.58
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.19	0.58
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.50	0.58
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.39	0.58
38:2g:69:VAL:HG12	38:2g:135:VAL:HG13	1.86	0.58
38:2g:149:ARG:HD3	42:2k:59:TYR:CE1	2.39	0.58
36:1e:31:LEU:HD11	36:1e:129:ILE:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.39	0.58
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.86	0.58
32:2a:41:G:H2'	32:2a:42:G:H8	1.69	0.58
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.39	0.58
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.39	0.58
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	1.85	0.57
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.86	0.57
32:1a:382:A:H2'	32:1a:383:A:H8	1.67	0.57
33:1b:74:LYS:NZ	33:1b:206:ASP:OD1	2.37	0.57
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.37	0.57
40:1i:11:LYS:H	40:1i:104:ARG:HH21	1.51	0.57
1:2A:686:G:N2	1:2A:788:A:H61	2.02	0.57
3:2D:69:ARG:NH1	3:2D:128:GLY:O	2.37	0.57
32:2a:931:C:H42	32:2a:1386:G:H1	1.52	0.57
36:2e:12:LEU:HB3	36:2e:31:LEU:HB2	1.86	0.57
1:1A:1060:U:H3	1:1A:1088:A:H8	1.50	0.57
1:1A:2121:G:H1	1:1A:2177:C:H42	1.50	0.57
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.39	0.57
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.52	0.57
1:2A:19:C:H2'	1:2A:20:C:C6	2.39	0.57
1:2A:247:G:H4'	1:2A:386:G:C5	2.39	0.57
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.86	0.57
1:1A:2155:G:H3'	1:1A:2156:G:C8	2.39	0.57
1:1A:2505:G:N2	1:1A:2506:U:O4	2.28	0.57
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.85	0.57
32:1a:17:U:H2'	32:1a:18:C:C6	2.39	0.57
35:1d:98:GLU:OE2	35:1d:107:ARG:NH1	2.37	0.57
1:2A:2198:A:H5'	8:2I:33:ARG:HH21	1.69	0.57
1:2A:2758:A:OP2	60:2A:3933:HOH:O	2.18	0.57
32:2a:373:A:H61	32:2a:391:G:H1'	1.70	0.57
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.37	0.57
32:1a:1030:C:N4	32:1a:1031:G:H1	2.02	0.57
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.86	0.57
54:1w:319:PHE:HE2	54:1w:335:ILE:HG12	1.70	0.57
1:2A:774:A:H2'	1:2A:774:A:N3	2.18	0.57
1:2A:864:G:H1'	1:2A:914:C:H42	1.69	0.57
1:2A:2134:A:H2	1:2A:2159:G:H1'	1.70	0.57
12:2Q:135:ASP:OD2	21:2Z:81:ARG:NH1	2.37	0.57
32:2a:1141:C:H2'	32:2a:1142:G:C8	2.40	0.57
33:2b:20:GLU:HG2	33:2b:191:ASP:HB3	1.86	0.57
1:1A:583:G:OP2	16:1U:10:ARG:NH1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2821:A:OP2	60:1R:301:HOH:O	2.18	0.57
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.39	0.57
1:2A:2430:A:H2'	1:2A:2430:A:N3	2.19	0.57
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.85	0.57
32:2a:527:G7M:OP1	60:2a:1807:HOH:O	2.17	0.57
32:2a:838:G:H3'	32:2a:840:C:H41	1.69	0.57
1:1A:1696:G:N7	60:1A:4235:HOH:O	2.33	0.57
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.17	0.57
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.87	0.57
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.87	0.57
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.35	0.57
33:1b:145:LEU:HD23	33:1b:149:LEU:HD12	1.85	0.57
21:2Z:145:GLU:HG3	21:2Z:146:ILE:H	1.68	0.57
32:2a:686:U:O2'	32:2a:703:G:N2	2.37	0.57
38:2g:42:ILE:HD12	38:2g:116:ALA:HB3	1.86	0.57
42:2k:48:ILE:O	42:2k:50:TYR:N	2.35	0.57
1:1A:2116:G:H2'	1:1A:2117:A:C6	2.39	0.57
1:1A:2155:G:H3'	1:1A:2156:G:H8	1.69	0.57
1:1A:2840:C:OP2	60:1A:4146:HOH:O	2.18	0.57
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.05	0.57
38:1g:113:GLU:HB3	38:1g:118:VAL:HG13	1.86	0.57
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.39	0.57
3:2D:242:ARG:O	60:2D:401:HOH:O	2.17	0.57
32:2a:939:G:OP1	38:2g:102:ARG:NH1	2.31	0.57
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.38	0.57
33:2b:15:VAL:HG11	33:2b:213:LEU:HD23	1.87	0.57
39:2h:33:GLU:OE2	39:2h:50:ARG:NH1	2.37	0.57
41:2j:22:LYS:O	41:2j:26:ALA:N	2.38	0.57
20:1Y:81:LYS:HD3	20:1Y:101:LYS:HD3	1.86	0.57
32:1a:1055:A:H2'	34:1c:156:ARG:HD2	1.87	0.57
32:2a:325:A:OP2	51:2t:70:SER:OG	2.22	0.57
32:2a:1372:U:H2'	32:2a:1373:G:O4'	2.05	0.57
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.86	0.57
1:1A:1064:C:O2	1:1A:1074:G:N1	2.35	0.57
33:1b:17:PHE:HA	33:1b:44:LEU:HD21	1.86	0.57
34:1c:62:ASP:O	34:1c:97:LYS:HB3	2.05	0.57
36:1e:35:GLY:HA2	36:1e:40:ARG:O	2.04	0.57
44:1m:9:ILE:HB	44:1m:18:ALA:HB1	1.86	0.57
24:22:61:LEU:HD23	24:22:64:LEU:HD23	1.85	0.57
32:2a:1399:C:H4'	32:2a:1400:5MC:H5''	1.86	0.57
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:2:ALA:N	3:2D:200:ASP:OD2	2.38	0.57
32:2a:840:C:H6	32:2a:840:C:H5'	1.70	0.57
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.40	0.57
45:2n:9:LYS:HA	45:2n:12:ARG:HD3	1.87	0.57
1:1A:136:G:N7	60:1A:4229:HOH:O	2.32	0.56
1:1A:1267:U:OP1	60:1A:4148:HOH:O	2.18	0.56
35:1d:138:TYR:OH	35:1d:141:ARG:NH2	2.38	0.56
1:2A:800:A:H8	1:2A:800:A:OP1	1.88	0.56
6:2G:59:GLU:HB2	6:2G:144:ILE:HD12	1.87	0.56
32:2a:56:U:H2'	32:2a:57:G:C8	2.40	0.56
40:2i:32:ASP:OD1	40:2i:33:PHE:N	2.37	0.56
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.38	0.56
1:1A:2099:U:H3	1:1A:2190:G:H1	1.53	0.56
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.86	0.56
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.39	0.56
32:1a:164:U:H2'	32:1a:165:C:C6	2.39	0.56
34:1c:7:PRO:HG2	34:1c:184:TYR:HB2	1.87	0.56
1:2A:1890:A:OP2	60:2A:3956:HOH:O	2.17	0.56
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.32	0.56
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.70	0.56
1:1A:1069:A:H2'	1:1A:1073:A:C8	2.40	0.56
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.86	0.56
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.39	0.56
32:1a:56:U:H2'	32:1a:57:G:H8	1.69	0.56
32:1a:560:U:O2'	32:1a:561:U:OP2	2.21	0.56
32:1a:966:M2G:HM13	32:1a:967:5MC:H1'	1.87	0.56
33:1b:95:GLN:NE2	33:1b:147:LYS:HB2	2.20	0.56
35:1d:177:ASP:O	35:1d:180:GLY:N	2.36	0.56
36:1e:78:HIS:HD2	39:1h:104:ARG:HD2	1.69	0.56
51:1t:11:SER:O	51:1t:15:ARG:N	2.35	0.56
1:2A:627:A:H62	11:2P:84:ASN:HD21	1.53	0.56
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.35	0.56
1:2A:892:G:H2'	1:2A:893:C:H4'	1.86	0.56
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.39	0.56
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.34	0.56
34:2c:32:LEU:HD23	34:2c:59:ARG:HD3	1.87	0.56
34:2c:180:ALA:HB1	34:2c:203:PHE:CE1	2.39	0.56
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.87	0.56
23:11:44:PRO:HB2	23:11:46:LEU:HD13	1.87	0.56
32:1a:1030:C:N3	32:1a:1031:G:N2	2.53	0.56
33:1b:76:GLN:HE21	33:1b:206:ASP:HA	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:101:MET:HA	33:1b:108:ILE:HG13	1.86	0.56
1:2A:586:A:H5'	5:2F:89:VAL:HG21	1.86	0.56
1:2A:1628:G:H2'	1:2A:1629:U:C6	2.40	0.56
1:2A:2049:G:N7	60:2A:4038:HOH:O	2.33	0.56
1:2A:2096:U:H2'	1:2A:2097:C:C6	2.40	0.56
17:2V:56:SER:H	17:2V:100:ARG:HB2	1.71	0.56
20:2Y:85:VAL:HG13	20:2Y:97:ARG:HB3	1.87	0.56
22:20:11:ARG:O	22:20:14:ARG:NH2	2.38	0.56
32:2a:539:A:H2'	32:2a:540:G:C8	2.40	0.56
53:2v:21:A:N6	54:2w:181:GLN:HE21	2.04	0.56
1:1A:1056:G:N1	1:1A:1102:C:OP2	2.26	0.56
1:1A:1336:A:OP2	19:1X:64:LYS:NZ	2.38	0.56
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.39	0.56
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	1.86	0.56
26:14:26:SER:OG	26:14:27:THR:N	2.36	0.56
32:1a:1131:G:H1	32:1a:1143:G:N2	2.04	0.56
1:2A:2121:G:H1	1:2A:2177:C:H42	1.53	0.56
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.88	0.56
6:2G:15:VAL:HG23	6:2G:175:LEU:HD23	1.87	0.56
15:2T:41:ARG:NH1	32:2a:346:G:OP1	2.39	0.56
54:2w:350:ALA:HA	54:2w:354:GLY:HA3	1.87	0.56
6:1G:12:TYR:HA	6:1G:16:ARG:HG3	1.86	0.56
11:1P:94:GLU:HG3	11:1P:124:LYS:HD2	1.88	0.56
40:1i:127:LYS:NZ	55:1x:34:G:OP2	2.37	0.56
41:1j:9:ARG:HG2	41:1j:69:ASN:HD22	1.70	0.56
1:2A:644:A:H4'	1:2A:645:C:C5	2.40	0.56
32:2a:953:G:H5'	32:2a:965:A:N6	2.20	0.56
46:2o:5:LYS:NZ	46:2o:5:LYS:H	2.02	0.56
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.41	0.56
1:1A:1056:G:H4'	1:1A:1086:A:C8	2.40	0.56
8:1I:31:LEU:HD21	8:1I:38:LEU:HG	1.87	0.56
34:1c:8:ILE:HG12	34:1c:184:TYR:HB3	1.87	0.56
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.86	0.56
42:1k:18:ARG:NH2	42:1k:35:PRO:O	2.39	0.56
47:1p:40:ASP:HB3	47:1p:48:TRP:HB3	1.88	0.56
1:2A:154(A):C:N4	1:2A:171:G:H1	2.04	0.56
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.88	0.56
32:2a:1263:C:N3	32:2a:1272:G:O6	2.39	0.56
34:2c:47:LEU:HB3	34:2c:52:LEU:HB2	1.87	0.56
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.06	0.56
54:2w:171:PHE:HB3	54:2w:201:VAL:HG11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:28:SER:OG	35:1d:30:LYS:HG2	2.05	0.56
1:2A:1628:G:H2'	1:2A:1629:U:H6	1.69	0.56
6:2G:110:ALA:HB1	6:2G:140:ILE:HG23	1.87	0.56
9:2N:15:LEU:N	9:2N:136:GLU:O	2.38	0.56
11:2P:1:MET:HG3	11:2P:5:ASP:HB2	1.88	0.56
32:2a:1239:A:H4'	32:2a:1240:U:H5''	1.87	0.56
32:2a:1320:C:N4	50:2s:36:ARG:HB2	2.21	0.56
1:1A:2161:C:HO2'	1:1A:2162:G:H8	1.53	0.56
32:1a:392:G:H2'	32:1a:393:A:H8	1.71	0.56
32:1a:757:U:H2'	32:1a:758:G:O4'	2.06	0.56
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.88	0.56
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.41	0.56
1:2A:886:C:HO2'	1:2A:889:C:H41	1.52	0.56
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.41	0.56
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.21	0.56
1:2A:2154:G:N7	1:2A:2156:G:N2	2.53	0.56
2:2B:52:A:C6	14:2S:33:LYS:HE3	2.41	0.56
17:2V:40:LEU:HB2	17:2V:46:VAL:HG23	1.86	0.56
32:2a:64:G:H4'	32:2a:65:U:H3'	1.86	0.56
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.88	0.56
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.39	0.56
32:1a:41:G:H2'	32:1a:42:G:C8	2.41	0.56
32:1a:339:C:H2'	32:1a:340:U:C6	2.41	0.56
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	1.87	0.56
1:2A:2345:G:OP2	28:26:38:LYS:NZ	2.39	0.56
34:2c:153:VAL:HG22	34:2c:198:VAL:HG12	1.88	0.56
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.26	0.55
9:1N:15:LEU:HD23	9:1N:137:LYS:HG2	1.87	0.55
14:1S:31:SER:O	14:1S:97:ARG:NH2	2.34	0.55
32:1a:972:C:O2'	41:1j:55:LYS:O	2.24	0.55
32:1a:1144:G:N2	32:1a:1146:A:H62	2.05	0.55
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.41	0.55
1:2A:1141:U:OP2	9:2N:63:THR:OG1	2.18	0.55
1:2A:2116:G:N7	1:2A:2166:G:N2	2.53	0.55
3:2D:38:LYS:HD3	3:2D:38:LYS:H	1.70	0.55
12:2Q:17:LEU:HD21	12:2Q:41:TRP:HE1	1.70	0.55
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.42	0.55
32:1a:601:C:H2'	32:1a:602:A:C8	2.42	0.55
32:1a:707:C:OP1	42:1k:85:ARG:NH1	2.39	0.55
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.88	0.55
32:1a:1298:C:OP2	38:1g:114:ARG:NH2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2127:G:C6	1:2A:2161:C:C4	2.95	0.55
1:2A:2577:A:OP1	60:2A:3950:HOH:O	2.18	0.55
32:2a:90:U:H2'	32:2a:91:C:H6	1.71	0.55
39:2h:41:ARG:NH2	39:2h:123:GLU:OE2	2.40	0.55
1:1A:1057:A:C8	1:1A:1086:A:H2'	2.41	0.55
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.42	0.55
28:16:14:THR:HB	28:16:48:VAL:O	2.06	0.55
39:1h:112:LEU:HD13	39:1h:133:LEU:HA	1.88	0.55
1:2A:1187:G:H5''	17:2V:81:TYR:CE1	2.40	0.55
40:2i:44:VAL:HA	40:2i:47:LEU:HD12	1.88	0.55
46:2o:70:LEU:HG	46:2o:78:TYR:HB2	1.88	0.55
55:2x:23:U:H2'	55:2x:24:G:C8	2.41	0.55
1:1A:624:C:O2'	1:1A:657:U:OP1	2.23	0.55
1:1A:1084:A:N3	1:1A:1105:U:O2'	2.39	0.55
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.22	0.55
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.40	0.55
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	1.88	0.55
3:2D:20:ASP:OD1	3:2D:20:ASP:N	2.29	0.55
8:2I:79:ILE:HB	8:2I:144:VAL:HG13	1.87	0.55
30:28:62:LEU:HB3	30:28:65:GLU:HG3	1.88	0.55
32:2a:411:A:OP1	35:2d:30:LYS:NZ	2.30	0.55
33:2b:7:VAL:O	33:2b:217:ARG:NE	2.37	0.55
33:2b:84:GLU:HA	33:2b:87:ARG:HB2	1.89	0.55
3:1D:211:ARG:HG2	3:1D:214:TRP:CZ3	2.41	0.55
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.40	0.55
47:1p:6:LEU:HB3	47:1p:17:TYR:HB3	1.87	0.55
6:2G:151:ALA:O	6:2G:153:ARG:NH1	2.40	0.55
32:1a:455:C:H42	32:1a:476:G:H1	1.54	0.55
32:1a:950:U:H2'	32:1a:951:G:C8	2.41	0.55
1:2A:171:G:H2'	1:2A:172:C:C6	2.41	0.55
1:2A:538:G:H2'	1:2A:539:G:H8	1.70	0.55
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.71	0.55
33:2b:162:ILE:O	33:2b:185:ILE:HG12	2.06	0.55
25:13:44:ARG:O	25:13:48:GLU:HG3	2.07	0.55
32:1a:262:A:H2'	32:1a:263:A:C8	2.42	0.55
32:1a:447:G:O6	32:1a:485:G:O2'	2.18	0.55
33:1b:178:ARG:NH1	33:1b:196:LEU:O	2.40	0.55
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.42	0.55
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.42	0.55
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.07	0.55
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:5:VAL:HG12	26:24:25:TYR:HE2	1.72	0.55
32:2a:259:G:OP2	51:2t:83:ARG:NH1	2.37	0.55
35:2d:149:ALA:O	35:2d:152:SER:OG	2.21	0.55
38:2g:15:ASP:OD1	38:2g:20:ASP:N	2.32	0.55
32:1a:848:C:H2'	32:1a:849:C:C6	2.42	0.55
42:1k:109:VAL:HG21	49:1r:84:LYS:HD2	1.88	0.55
1:2A:581:C:H2'	1:2A:582:G:C8	2.42	0.55
1:2A:668:G:H5'	1:2A:669:G:OP2	2.07	0.55
32:2a:131:C:H2'	32:2a:132:C:C6	2.42	0.55
33:2b:167:PRO:HG2	33:2b:192:SER:HB3	1.89	0.55
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.37	0.55
32:1a:737:A:H2'	32:1a:738:C:C6	2.42	0.55
35:1d:157:LEU:O	35:1d:161:ASN:ND2	2.40	0.55
38:1g:113:GLU:HB2	38:1g:119:ARG:HG2	1.89	0.55
53:1v:10:G:H2'	53:1v:11:U:H4'	1.89	0.55
54:1w:150:THR:HG22	54:1w:152:LEU:H	1.71	0.55
32:2a:56:U:H2'	32:2a:57:G:H8	1.72	0.55
39:2h:25:ASP:OD1	39:2h:60:ARG:HG3	2.07	0.55
45:2n:37:PHE:HB3	45:2n:39:LEU:HD12	1.89	0.55
1:1A:536:A:H2'	1:1A:537:C:C6	2.42	0.55
32:1a:721:G:H4'	32:1a:722:A:O4'	2.07	0.55
33:1b:92:TYR:HE1	33:1b:94:ASN:HB2	1.71	0.55
1:2A:529:A:H62	1:2A:2041:U:H3	1.55	0.55
32:2a:176:C:H2'	32:2a:177:C:C6	2.41	0.55
54:2w:320:THR:O	54:2w:320:THR:OG1	2.25	0.55
1:1A:744:G:OP1	4:1E:132:HIS:ND1	2.37	0.54
1:1A:1651:G:OP1	13:1R:40:LYS:NZ	2.40	0.54
32:1a:507:C:OP2	32:1a:508:C:O2'	2.20	0.54
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.42	0.54
1:2A:72:U:OP1	60:2A:3957:HOH:O	2.17	0.54
34:2c:123:GLN:HB3	34:2c:128:PHE:HD2	1.71	0.54
34:2c:131:ARG:HH21	36:2e:50:GLU:HG3	1.72	0.54
47:2p:40:ASP:OD2	47:2p:44:THR:OG1	2.23	0.54
1:1A:222:A:H3'	1:1A:421:U:H5'	1.89	0.54
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.41	0.54
1:1A:821:A:H2'	1:1A:946:G:H5''	1.89	0.54
1:1A:1045:A:H1'	1:1A:1047:G:C4	2.42	0.54
1:1A:1082:U:O4	1:1A:1086:A:C6	2.60	0.54
36:1e:45:PHE:CD2	36:1e:47:LYS:HE2	2.43	0.54
42:1k:84:VAL:HG23	42:1k:110:ASP:HA	1.89	0.54
2:2B:13:A:O2'	2:2B:15:A:OP2	2.24	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:44:ASN:ND2	17:2V:75:PHE:HB3	2.22	0.54
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.42	0.54
44:2m:23:TYR:CZ	44:2m:71:ARG:HG3	2.43	0.54
1:1A:1009:A:OP2	60:1A:4118:HOH:O	2.17	0.54
1:1A:1071:G:H1'	1:1A:1089:G:N1	2.22	0.54
1:1A:2180:U:N3	1:1A:2181:G:N7	2.55	0.54
6:1G:107:LEU:HA	6:1G:111:LEU:HD12	1.89	0.54
32:1a:193:C:H2'	32:1a:194:C:C6	2.42	0.54
32:1a:1268:A:N3	32:1a:1326:C:O2'	2.40	0.54
54:1w:285:LEU:HG	54:1w:289:ARG:HH12	1.73	0.54
1:2A:500:G:N1	1:2A:503:A:OP2	2.41	0.54
1:2A:2321:G:H5''	1:2A:2322:A:OP2	2.06	0.54
21:2Z:45:ASP:O	21:2Z:49:ARG:HG2	2.06	0.54
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.89	0.54
25:23:23:LEU:HD12	25:23:50:VAL:HG11	1.90	0.54
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.89	0.54
32:2a:662:G:H2'	32:2a:663:A:C8	2.42	0.54
32:2a:1262:C:C2'	32:2a:1263:C:H5'	2.37	0.54
44:2m:84:ILE:HB	50:2s:66:MET:HE2	1.89	0.54
54:2w:184:PRO:HG3	54:2w:193:HIS:HB2	1.89	0.54
1:1A:1068:G:C8	1:1A:1096:A:H1'	2.43	0.54
1:1A:1426:G:N7	3:1D:31:LYS:NZ	2.48	0.54
2:1B:23:G:O6	60:1B:302:HOH:O	2.17	0.54
32:1a:812:C:N3	60:1a:1934:HOH:O	2.33	0.54
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.41	0.54
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.07	0.54
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.41	0.54
47:2p:8:ARG:HB2	47:2p:28:ARG:HE	1.73	0.54
54:2w:324:LEU:HA	54:2w:327:VAL:HG22	1.89	0.54
1:1A:686:G:OP1	29:17:11:LYS:NZ	2.40	0.54
1:1A:883:G:N2	1:1A:893:C:H42	2.06	0.54
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.43	0.54
1:1A:2882:A:H5'	13:1R:96:ARG:HG3	1.89	0.54
32:1a:617:G:H1	32:1a:623:C:H42	1.54	0.54
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.40	0.54
33:1b:21:ARG:HA	33:1b:39:ILE:HA	1.89	0.54
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.87	0.54
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.08	0.54
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.08	0.54
1:2A:2750:A:O2'	1:2A:2752:C:N4	2.32	0.54
34:2c:34:LEU:HD11	34:2c:38:ARG:HH21	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.89	0.54
1:1A:2865:U:OP2	15:1T:119:LYS:NZ	2.38	0.54
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.73	0.54
32:1a:1060:C:OP1	45:1n:45:ARG:NH2	2.40	0.54
32:1a:1172:C:H2'	32:1a:1173:G:H8	1.73	0.54
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.22	0.54
54:1w:111:ILE:HB	54:1w:158:VAL:HG23	1.89	0.54
1:2A:1296:G:OP1	1:2A:2709:G:O2'	2.20	0.54
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.73	0.54
32:2a:406:G:N3	35:2d:119:GLN:NE2	2.47	0.54
32:2a:587:G:N2	32:2a:754:C:OP2	2.34	0.54
32:2a:1296:C:OP1	44:2m:44:ARG:NH2	2.40	0.54
50:2s:80:TYR:CZ	50:2s:82:GLY:HA2	2.43	0.54
1:1A:387:U:OP2	23:11:20:ARG:NH1	2.33	0.54
1:1A:2550:G:OP1	60:1A:4113:HOH:O	2.18	0.54
7:1H:9:ILE:HD11	7:1H:69:ARG:HG2	1.90	0.54
32:1a:100:C:H2'	32:1a:101:A:C8	2.42	0.54
32:1a:143:A:H5''	32:1a:144:G:H5'	1.90	0.54
32:1a:532:A:H61	32:1a:1206:G:HO2'	1.54	0.54
1:2A:956:G:OP2	12:2Q:14:ARG:NH1	2.38	0.54
1:2A:2639:A:OP2	60:2A:3958:HOH:O	2.19	0.54
21:2Z:55:HIS:HE1	21:2Z:135:GLU:HA	1.72	0.54
32:2a:932:C:H5'	38:2g:4:ARG:HG2	1.90	0.54
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.39	0.54
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.40	0.54
41:1j:11:PHE:HA	41:1j:66:ARG:O	2.08	0.54
1:2A:893:C:H2'	1:2A:894:C:C5	2.43	0.54
1:2A:1434:A:H61	1:2A:1558:A:H62	1.55	0.54
2:2B:54:G:H21	6:2G:29:TRP:HE1	1.56	0.54
2:2B:90:A:C5	2:2B:91:C:H1'	2.43	0.54
20:1Y:30:VAL:HG13	20:1Y:37:VAL:HG12	1.90	0.54
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.41	0.54
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.20	0.54
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.21	0.54
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.43	0.54
1:2A:602:G:O2'	1:2A:655:A:N6	2.41	0.54
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.16	0.54
1:2A:2169:A:H2'	1:2A:2170:A:C8	2.43	0.54
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.90	0.54
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.43	0.54
33:2b:74:LYS:O	33:2b:78:GLN:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2r:70:ILE:HG22	49:2r:74:ARG:HD2	1.89	0.54
51:2t:50:GLU:HG3	51:2t:100:ILE:HD13	1.89	0.54
1:1A:272(G):C:H42	1:1A:363(C):G:H1	1.54	0.53
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.08	0.53
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.43	0.53
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.07	0.53
1:1A:2053:G:OP2	60:1A:4150:HOH:O	2.18	0.53
3:1D:211:ARG:HG2	3:1D:214:TRP:CE3	2.43	0.53
32:1a:911:U:H2'	32:1a:912:C:C6	2.43	0.53
32:1a:1325:C:H4'	52:1u:17:THR:HG21	1.90	0.53
1:2A:323:G:O2'	1:2A:1205:U:N3	2.29	0.53
6:2G:36:LYS:HZ2	6:2G:95:ARG:HH22	1.56	0.53
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.89	0.53
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.22	0.53
38:2g:18:TYR:HB3	38:2g:59:LEU:HD22	1.90	0.53
51:2t:18:GLN:O	51:2t:22:ARG:HG2	2.08	0.53
1:1A:185:U:H2'	1:1A:186:G:H8	1.73	0.53
1:1A:1420:U:HO2'	1:1A:1421:G:P	2.31	0.53
1:1A:2144:U:HO2'	1:1A:2145:C:H5	1.57	0.53
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.41	0.53
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.89	0.53
33:1b:138:LEU:O	33:1b:142:LEU:N	2.40	0.53
44:1m:50:GLU:HA	44:1m:53:VAL:HB	1.90	0.53
44:1m:88:ARG:O	44:1m:92:HIS:ND1	2.41	0.53
1:2A:276:A:H5''	1:2A:277:C:H5'	1.91	0.53
1:2A:2127:G:C2	1:2A:2161:C:C2	2.96	0.53
1:2A:2138:C:H42	1:2A:2153:G:H1	1.54	0.53
4:2E:7:VAL:HG12	4:2E:27:LEU:HB3	1.90	0.53
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.91	0.53
34:2c:32:LEU:HD23	34:2c:59:ARG:HH11	1.73	0.53
42:2k:99:GLN:HG3	42:2k:105:VAL:HG11	1.90	0.53
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.89	0.53
1:2A:1123:C:H1'	31:29:18:ARG:HH21	1.72	0.53
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.08	0.53
32:2a:991:U:O2'	32:2a:992:U:H5'	2.09	0.53
32:2a:1179:A:O2'	40:2i:103:THR:OG1	2.18	0.53
34:2c:123:GLN:HA	34:2c:126:ARG:HB2	1.89	0.53
35:2d:61:LYS:NZ	35:2d:72:GLU:OE1	2.28	0.53
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	1.88	0.53
32:1a:129(A):G:H4'	32:1a:130:A:H5''	1.90	0.53
32:1a:160:A:H2'	32:1a:161:A:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.25	0.53
1:2A:2478:A:OP2	31:29:2:LYS:NZ	2.33	0.53
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.55	0.53
44:2m:60:VAL:HG13	44:2m:64:TRP:CE3	2.41	0.53
54:2w:129:ASN:HA	54:2w:132:LEU:HB2	1.90	0.53
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.43	0.53
32:1a:300:A:O2'	32:1a:564:C:N3	2.40	0.53
38:1g:86:GLN:HA	38:1g:86:GLN:HE21	1.74	0.53
1:2A:361:G:O2'	1:2A:362:U:H5'	2.08	0.53
1:2A:2524:G:N7	60:2A:4044:HOH:O	2.34	0.53
32:2a:523:A:H61	43:2l:92:0TD:CG	2.21	0.53
32:2a:1257:U:H5'	32:2a:1258:G:H5'	1.90	0.53
32:2a:1414:U:H2'	32:2a:1415:G:H8	1.72	0.53
33:2b:33:TYR:HB2	33:2b:43:ASP:HA	1.90	0.53
34:2c:18:TRP:O	34:2c:54:ARG:NH2	2.41	0.53
35:2d:103:ASN:OD1	35:2d:114:ARG:NH2	2.35	0.53
38:2g:68:ASN:HD22	38:2g:128:ALA:HA	1.74	0.53
1:1A:222:A:H5''	1:1A:421:U:OP1	2.09	0.53
1:1A:2134:A:H1'	1:1A:2159:G:H1'	1.89	0.53
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.43	0.53
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.89	0.53
32:1a:266:G:O2'	32:1a:267:C:OP2	2.25	0.53
35:1d:121:VAL:O	35:1d:134:ASP:HA	2.09	0.53
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.90	0.53
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.72	0.53
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.09	0.53
8:2I:29:TYR:HD2	8:2I:30:LEU:HD23	1.72	0.53
21:2Z:28:MET:O	21:2Z:35:ARG:N	2.35	0.53
32:2a:67:C:H2'	32:2a:68:G:C8	2.43	0.53
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.91	0.53
53:2v:11:U:H3'	53:2v:12:A:C8	2.43	0.53
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.90	0.53
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.09	0.53
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.56	0.53
1:2A:656:G:H2'	1:2A:657:U:O4'	2.09	0.53
8:2I:5:LEU:HD22	8:2I:9:LEU:HD23	1.90	0.53
13:2R:38:VAL:HG12	13:2R:42:LYS:HD2	1.91	0.53
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.23	0.53
32:2a:1138:G:C6	32:2a:1140:C:H1'	2.44	0.53
41:2j:30:SER:HB2	41:2j:81:THR:HB	1.91	0.53
54:2w:125:ARG:HA	54:2w:128:PHE:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.91	0.53
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.24	0.53
32:1a:164:U:H2'	32:1a:165:C:H6	1.72	0.53
32:1a:1036:G:OP2	32:1a:1036:G:N2	2.41	0.53
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.44	0.53
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.43	0.53
32:2a:171:A:H2'	32:2a:172:A:C8	2.44	0.53
32:2a:559:A:H4'	32:2a:560:U:H5''	1.91	0.53
32:2a:760:G:H3'	32:2a:761:G:H8	1.74	0.53
32:2a:929:G:H1	32:2a:1388:C:H42	1.55	0.53
1:1A:226:G:N2	1:1A:228:A:H62	2.07	0.53
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.43	0.53
1:1A:1805:U:O2	3:1D:50:THR:HB	2.08	0.53
37:1f:15:ASP:OD1	37:1f:18:GLN:N	2.28	0.53
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.08	0.53
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.55	0.53
1:2A:657:U:H2'	1:2A:658:C:C6	2.43	0.53
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.43	0.53
1:2A:2116:G:N2	1:2A:2162:G:OP1	2.42	0.53
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.43	0.53
44:2m:81:LEU:HD22	44:2m:88:ARG:HH12	1.73	0.53
1:1A:1902:C:H5'	3:1D:246:PRO:HD3	1.90	0.53
1:1A:2167:U:H3	1:1A:2171:A:N6	2.07	0.53
60:1A:4272:HOH:O	11:1P:37:GLY:HA3	2.09	0.53
3:1D:72:LYS:NZ	3:1D:99:ASP:OD2	2.32	0.53
32:1a:826:C:H2'	32:1a:827:U:C6	2.44	0.53
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.37	0.53
1:2A:2391:G:O6	1:2A:2425:A:H8	1.91	0.53
1:2A:2867:G:OP2	15:2T:119:LYS:NZ	2.41	0.53
3:2D:69:ARG:C	3:2D:71:ASP:H	2.17	0.53
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.42	0.53
15:2T:74:ARG:HG2	15:2T:76:PHE:CZ	2.43	0.53
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.90	0.53
1:1A:2181:G:H2'	1:1A:2182:G:C8	2.44	0.52
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.74	0.52
26:14:69:LYS:HD3	50:1s:20:LEU:HD13	1.90	0.52
32:1a:881:G:P	43:1l:12:ARG:HH22	2.32	0.52
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.26	0.52
32:1a:1492:A:N3	53:1v:20:A:O2'	2.39	0.52
35:1d:11:LEU:HD22	35:1d:66:ARG:HD3	1.91	0.52
37:1f:37:VAL:HA	37:1f:65:VAL:HG13	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:1x:48:G:N2	60:1x:204:HOH:O	2.42	0.52
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.91	0.52
28:26:10:LEU:HG	28:26:54:ILE:HG13	1.91	0.52
32:2a:718:G:C5'	42:2k:117:ASN:HD21	2.23	0.52
32:2a:975:A:H5'	32:2a:975:A:H8	1.73	0.52
32:2a:1326:C:H5''	52:2u:18:TYR:O	2.09	0.52
54:2w:219:ILE:HD13	54:2w:262:ARG:HD2	1.90	0.52
1:1A:1669:A:OP2	60:1A:4113:HOH:O	2.19	0.52
32:1a:13:U:O2'	60:1a:1913:HOH:O	2.15	0.52
32:1a:159:G:H21	32:1a:162:A:H62	1.57	0.52
32:1a:1310:G:OP2	44:1m:88:ARG:NH2	2.37	0.52
43:1l:28:LYS:HD3	43:1l:62:SER:HB2	1.91	0.52
1:2A:307:G:H21	1:2A:330:A:H62	1.55	0.52
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.56	0.52
1:2A:1311:G:H2'	29:27:47:ARG:HH22	1.73	0.52
3:2D:182:LEU:HB2	3:2D:272:ALA:HB3	1.90	0.52
10:2O:35:VAL:HG13	10:2O:65:THR:HG23	1.91	0.52
32:2a:1124:G:N7	32:2a:1145:C:O2'	2.41	0.52
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.82	0.52
1:1A:185:U:H2'	1:1A:186:G:C8	2.45	0.52
1:1A:446:G:OP1	16:1U:3:ARG:NH1	2.40	0.52
1:1A:859:G:O2'	1:1A:916:G:O6	2.20	0.52
1:1A:2794:C:H42	1:1A:2802:G:H1	1.57	0.52
32:1a:195:A:O2'	32:1a:222:U:O2'	2.25	0.52
33:1b:98:LEU:HB2	33:1b:101:MET:HE3	1.92	0.52
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.92	0.52
44:1m:14:ARG:HB2	44:1m:17:VAL:HG23	1.91	0.52
1:2A:140:G:N2	1:2A:1596:A:H4'	2.24	0.52
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.91	0.52
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.41	0.52
33:2b:115:LEU:HA	33:2b:118:LEU:HB2	1.90	0.52
1:1A:2114:A:O2'	1:1A:2167:U:O2'	2.21	0.52
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.44	0.52
1:1A:2619:C:H4'	4:1E:151:TYR:O	2.10	0.52
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.08	0.52
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.09	0.52
32:1a:41:G:H2'	32:1a:42:G:H8	1.74	0.52
32:1a:439:A:C5	32:1a:441:A:H1'	2.44	0.52
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.44	0.52
36:1e:148:VAL:O	36:1e:152:ARG:HG2	2.09	0.52
1:2A:2104:G:H2'	1:2A:2105:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.44	0.52
33:2b:60:ASP:O	33:2b:64:ARG:HG2	2.09	0.52
37:2f:96:PRO:HB3	49:2r:30:ASP:OD2	2.10	0.52
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.25	0.52
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.07	0.52
26:14:43:TYR:O	26:14:45:GLY:N	2.42	0.52
26:14:46:GLN:HB3	26:14:48:ARG:HE	1.74	0.52
54:1w:228:GLY:HA3	54:1w:232:VAL:HB	1.92	0.52
1:2A:1446:C:H42	1:2A:1465:G:H1	1.57	0.52
1:2A:2612:C:OP2	27:25:2:ALA:N	2.42	0.52
6:2G:5:VAL:HG12	26:24:25:TYR:CE2	2.44	0.52
21:2Z:70:LEU:HD12	21:2Z:71:VAL:H	1.72	0.52
32:2a:335:C:H2'	32:2a:336:C:C6	2.45	0.52
32:2a:474:G:H2'	32:2a:475:G:H8	1.74	0.52
33:2b:115:LEU:HD13	33:2b:145:LEU:HB2	1.91	0.52
38:2g:78:ARG:HB2	38:2g:87:VAL:HG21	1.92	0.52
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.91	0.52
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.09	0.52
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.26	0.52
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.09	0.52
15:1T:16:ARG:NH2	15:1T:18:ASP:OD2	2.40	0.52
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.92	0.52
26:14:58:ARG:HE	50:1s:68:GLY:H	1.57	0.52
32:1a:444:C:H2'	32:1a:445:G:H8	1.73	0.52
32:1a:1241:G:H1	32:1a:1296:C:H42	1.56	0.52
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.91	0.52
36:1e:76:ILE:HD11	36:1e:93:PRO:HD3	1.91	0.52
54:1w:213:ASN:O	54:1w:216:GLU:HG2	2.10	0.52
54:1w:243:HIS:HB2	54:1w:269:LEU:HD11	1.90	0.52
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.07	0.52
32:2a:630:G:H2'	32:2a:631:G:C8	2.44	0.52
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.24	0.52
50:2s:11:VAL:HG11	50:2s:16:LEU:HD13	1.90	0.52
54:2w:220:ASP:OD1	54:2w:220:ASP:N	2.42	0.52
1:1A:2711:A:N3	60:1A:4250:HOH:O	2.34	0.52
1:1A:2747:G:O6	1:1A:2755:C:H5''	2.10	0.52
2:1B:55:U:H2'	2:1B:56:G:O4'	2.10	0.52
32:1a:547:A:OP2	35:1d:2:GLY:N	2.43	0.52
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.42	0.52
32:1a:1352:C:OP1	52:1u:3:LYS:NZ	2.30	0.52
34:1c:73:PRO:HD3	34:1c:105:GLU:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.92	0.52
1:2A:1761:C:H2'	1:2A:1762:A:H5''	1.91	0.52
7:2H:74:ASN:O	7:2H:78:GLY:N	2.43	0.52
32:2a:472:A:OP1	47:2p:75:ARG:NH2	2.42	0.52
35:2d:19:LEU:HG	35:2d:67:ILE:HG13	1.92	0.52
1:1A:579:G:H2'	1:1A:580:C:C6	2.45	0.52
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.38	0.52
1:2A:171:G:H2'	1:2A:172:C:H6	1.74	0.52
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.38	0.52
32:2a:625:G:H2'	32:2a:626:U:C6	2.44	0.52
32:2a:715:A:H2'	32:2a:716:A:C8	2.45	0.52
32:2a:1259:C:N4	32:2a:1260:C:O2	2.43	0.52
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.24	0.52
38:2g:46:ALA:HB1	38:2g:121:ALA:HB2	1.92	0.52
39:2h:119:LEU:HB3	39:2h:123:GLU:HB2	1.91	0.52
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.24	0.52
1:1A:2117:A:O2'	1:1A:2118:U:H5''	2.10	0.52
17:1V:1:MET:HG3	17:1V:99:ILE:HD12	1.91	0.52
45:1n:45:ARG:HG3	45:1n:49:HIS:CD2	2.44	0.52
54:1w:103:ASP:HA	54:1w:168:TYR:HB3	1.92	0.52
1:2A:218:A:OP2	60:2A:3961:HOH:O	2.19	0.52
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.44	0.52
32:2a:35:G:O2'	43:2l:118:SER:O	2.27	0.52
32:2a:840:C:H4'	32:2a:841:U:OP1	2.09	0.52
42:2k:41:THR:HG21	42:2k:71:LYS:HB3	1.91	0.52
46:2o:70:LEU:HD11	46:2o:77:ARG:HB2	1.92	0.52
1:1A:800:A:H8	1:1A:800:A:OP1	1.93	0.52
1:1A:1773:A:N1	60:1A:4249:HOH:O	2.34	0.52
19:1X:63:LYS:O	19:1X:64:LYS:HD3	2.09	0.52
32:1a:565:U:H3'	32:1a:566:G:H2'	1.92	0.52
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.45	0.52
40:1i:50:LEU:O	40:1i:53:VAL:N	2.26	0.52
50:1s:27:GLU:CB	50:1s:28:LYS:HA	2.39	0.52
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.44	0.52
15:2T:122:ASP:O	15:2T:126:ALA:N	2.39	0.52
53:2v:11:U:H3'	53:2v:12:A:H8	1.74	0.52
1:1A:2155:G:H2'	1:1A:2156:G:H5'	1.92	0.51
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.92	0.51
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.92	0.51
32:1a:674:G:H2'	32:1a:675:A:H8	1.75	0.51
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1611:C:OP1	60:2A:3962:HOH:O	2.19	0.51
1:2A:2052:G:O2'	60:2A:3960:HOH:O	2.19	0.51
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.92	0.51
29:27:5:TRP:NE1	29:27:7:PRO:HG3	2.24	0.51
32:2a:991:U:N3	32:2a:1212:U:H1'	2.26	0.51
32:2a:1106:G:H5''	34:2c:172:ARG:HG2	1.92	0.51
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.45	0.51
32:2a:1380:U:C4	38:2g:3:ARG:HG2	2.45	0.51
33:2b:163:PHE:CD1	33:2b:185:ILE:HG13	2.45	0.51
34:2c:131:ARG:HD3	34:2c:166:GLU:CD	2.35	0.51
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.44	0.51
54:2w:102:MET:HG3	54:2w:103:ASP:H	1.74	0.51
1:1A:2115:G:N3	1:1A:2117:A:N6	2.58	0.51
32:1a:373:A:H2'	32:1a:374:A:H8	1.74	0.51
32:1a:664:G:N2	32:1a:741:G:H1	2.05	0.51
32:1a:1112:C:H1'	34:1c:179:ARG:HH11	1.75	0.51
33:1b:55:PHE:HE1	33:1b:218:ALA:HA	1.75	0.51
33:1b:95:GLN:HE22	33:1b:147:LYS:HB2	1.76	0.51
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.25	0.51
15:2T:9:LEU:O	15:2T:12:SER:OG	2.27	0.51
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.42	0.51
17:2V:66:ARG:O	17:2V:88:ARG:NH2	2.43	0.51
29:27:8:ASN:HB3	29:27:11:LYS:HB3	1.92	0.51
32:2a:624:C:H2'	32:2a:625:G:C8	2.44	0.51
32:2a:1071:C:H2'	32:2a:1072:G:H8	1.75	0.51
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.09	0.51
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.25	0.51
1:1A:242:G:OP1	60:1A:4155:HOH:O	2.19	0.51
1:1A:307:G:N7	60:1A:4233:HOH:O	2.32	0.51
1:1A:359:A:H2'	1:1A:360:G:O4'	2.10	0.51
1:1A:1824:G:O3'	3:1D:249:PRO:HD3	2.09	0.51
6:1G:41:GLN:NE2	6:1G:154:GLY:O	2.43	0.51
7:1H:105:LEU:HD11	7:1H:148:ILE:HG23	1.91	0.51
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.18	0.51
29:17:46:VAL:HG13	29:17:48:LYS:HZ2	1.74	0.51
32:1a:1025:U:O2	32:1a:1036:G:O6	2.28	0.51
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.45	0.51
35:1d:116:GLN:HE22	35:1d:157:LEU:HD23	1.75	0.51
38:1g:44:TYR:HA	38:1g:47:CYS:HB2	1.92	0.51
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.45	0.51
4:2E:37:ARG:HB2	4:2E:46:ALA:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.35	0.51
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.44	0.51
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.09	0.51
21:2Z:3:TYR:CD2	21:2Z:51:ALA:HB2	2.45	0.51
32:2a:141:A:H1'	32:2a:182:U:H1'	1.91	0.51
32:2a:973:G:H3'	32:2a:974:A:H5''	1.91	0.51
32:2a:1187:G:H4'	40:2i:111:ARG:HH11	1.74	0.51
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.91	0.51
1:1A:228:A:H3'	1:1A:229:A:C5'	2.40	0.51
1:1A:1056:G:H4'	1:1A:1086:A:H1'	1.92	0.51
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.46	0.51
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.46	0.51
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.91	0.51
32:1a:735:C:H2'	32:1a:736:C:H6	1.76	0.51
32:1a:1124:G:H5''	41:1j:35:SER:HG	1.75	0.51
32:1a:1284:C:H3'	32:1a:1285:A:H8	1.75	0.51
33:1b:138:LEU:HA	33:1b:141:GLU:HB3	1.92	0.51
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.11	0.51
1:2A:2135:A:OP1	1:2A:2159:G:N2	2.33	0.51
1:2A:2393:A:H5''	11:2P:63:PRO:HB3	1.92	0.51
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.43	0.51
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.45	0.51
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.45	0.51
6:2G:36:LYS:NZ	6:2G:95:ARG:HH12	2.09	0.51
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.10	0.51
44:2m:76:ALA:HA	44:2m:79:LYS:HB3	1.92	0.51
48:2q:41:LYS:NZ	48:2q:92:ARG:HH21	2.09	0.51
1:1A:2131:G:OP2	1:1A:2158:A:N6	2.44	0.51
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.91	0.51
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.93	0.51
32:1a:994:A:N1	32:1a:1047:G:H4'	2.25	0.51
33:1b:54:THR:HG22	33:1b:58:ILE:HD11	1.91	0.51
1:2A:19:C:H2'	1:2A:20:C:H6	1.76	0.51
1:2A:1155:A:H5''	16:2U:55:ARG:HD3	1.93	0.51
5:2F:130:ALA:H	5:2F:142:TRP:CD1	2.29	0.51
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.11	0.51
1:1A:796:C:H2'	1:1A:797:C:C6	2.45	0.51
1:1A:1093:G:H1	1:1A:1097:U:H3'	1.75	0.51
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.26	0.51
1:1A:2206:G:H3'	1:1A:2207:G:H8	1.74	0.51
3:1D:274:ARG:HD3	60:1D:411:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:1T:29:ARG:HG3	15:1T:46:GLU:HB2	1.93	0.51
26:14:57:GLU:OE1	26:14:58:ARG:NH1	2.44	0.51
32:1a:434:U:H2'	32:1a:435:C:C6	2.45	0.51
32:1a:1377:A:HO2'	38:1g:2:ALA:N	2.08	0.51
33:1b:13:ALA:HA	33:1b:17:PHE:HB3	1.93	0.51
1:2A:1472:A:H2'	1:2A:1473:G:O4'	2.11	0.51
1:2A:2131:G:O6	1:2A:2157:G:O2'	2.22	0.51
25:23:7:LYS:NZ	25:23:34:GLU:OE1	2.44	0.51
32:2a:539:A:H2'	32:2a:540:G:H8	1.75	0.51
32:2a:717:C:O3'	42:2k:117:ASN:ND2	2.44	0.51
32:2a:1041:A:H2'	32:2a:1042:G:O4'	2.11	0.51
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.75	0.51
32:2a:1375:A:H4'	38:2g:29:LYS:HE3	1.93	0.51
42:2k:98:LEU:O	42:2k:101:SER:OG	2.18	0.51
1:1A:286:C:H2'	1:1A:287:C:C6	2.46	0.51
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.11	0.51
3:1D:26:LYS:NZ	3:1D:30:GLU:HG2	2.25	0.51
6:1G:70:VAL:HG11	6:1G:87:PRO:HB3	1.93	0.51
32:1a:10:A:OP2	36:1e:126:ARG:HD2	2.10	0.51
32:1a:376:G:H5''	47:1p:5:ARG:HB2	1.91	0.51
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.92	0.51
32:1a:1095:U:P	32:1a:1108:G:H1	2.34	0.51
35:1d:147:ALA:HA	35:1d:182:LYS:HA	1.93	0.51
1:2A:984:A:H5''	1:2A:985:C:H5	1.75	0.51
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.11	0.51
32:2a:952:U:H4'	32:2a:964:A:N1	2.26	0.51
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.43	0.51
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.92	0.51
48:2q:45:HIS:HB2	48:2q:65:ILE:HD13	1.93	0.51
1:1A:2723:C:OP1	13:1R:3:HIS:ND1	2.44	0.51
6:1G:41:GLN:HB3	6:1G:43:LEU:HD22	1.91	0.51
32:1a:130:A:O2'	32:1a:131:C:O5'	2.24	0.51
32:1a:165:C:H2'	32:1a:166:G:H8	1.75	0.51
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.92	0.51
1:2A:2135:A:C4	1:2A:2136:C:H5	2.29	0.51
11:2P:44:GLY:O	60:2P:302:HOH:O	2.19	0.51
17:2V:69:LYS:HA	17:2V:88:ARG:HG2	1.93	0.51
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	1.92	0.51
22:20:43:THR:HG23	22:20:43:THR:O	2.11	0.51
35:2d:158:ILE:HG23	35:2d:162:LEU:HD12	1.93	0.51
1:1A:64:A:C5	19:1X:66:LEU:HD13	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1226:C:O2'	44:1m:111:LYS:NZ	2.44	0.51
38:1g:62:PHE:HA	38:1g:124:LEU:HD23	1.91	0.51
54:1w:198:THR:HG21	54:1w:293:ILE:HG23	1.92	0.51
1:2A:458:G:O2'	29:27:39:ARG:HD3	2.11	0.51
1:2A:833:U:O2	11:2P:55:ARG:NH2	2.44	0.51
16:2U:113:ALA:O	16:2U:117:GLN:NE2	2.41	0.51
32:2a:512:U:H2'	32:2a:513:C:C6	2.46	0.51
32:2a:520:A:N1	32:2a:536:C:H1'	2.26	0.51
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.46	0.51
1:1A:1753:G:N1	1:1A:1756:G:OP2	2.40	0.51
1:1A:2612:C:OP2	27:15:2:ALA:N	2.43	0.51
1:1A:2777:G:O6	60:1A:4154:HOH:O	2.19	0.51
3:1D:71:ASP:CB	3:1D:103:ARG:HH12	2.23	0.51
30:18:33:ASN:HA	30:18:36:LYS:HD2	1.91	0.51
32:1a:718:G:H5'	42:1k:117:ASN:HB2	1.92	0.51
32:1a:868:C:H2'	32:1a:869:G:O4'	2.11	0.51
32:1a:1313:U:P	50:1s:5:LEU:HB3	2.51	0.51
35:1d:124:GLY:C	35:1d:126:ILE:H	2.17	0.51
44:1m:20:THR:C	44:1m:22:ILE:H	2.19	0.51
1:2A:2712(A):A:OP1	60:2A:3922:HOH:O	2.19	0.51
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.25	0.51
21:2Z:145:GLU:CG	21:2Z:146:ILE:H	2.23	0.51
32:2a:474:G:H2'	32:2a:475:G:C8	2.46	0.51
32:2a:652:U:O4	32:2a:752:G:O2'	2.25	0.51
32:2a:875:C:O2'	39:2h:14:ARG:HD2	2.11	0.51
54:2w:240:ARG:HG3	54:2w:251:THR:HG22	1.93	0.51
1:1A:2131:G:N2	1:1A:2158:A:N1	2.59	0.50
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	1.92	0.50
15:1T:93:ARG:HB2	15:1T:117:ASP:HB2	1.93	0.50
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.93	0.50
32:1a:953:G:H5'	32:1a:965:A:H61	1.75	0.50
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.39	0.50
34:1c:124:ILE:HD11	34:1c:189:ALA:HB1	1.92	0.50
48:1q:12:SER:HB2	48:1q:14:LYS:HE2	1.93	0.50
49:1r:54:ARG:O	49:1r:54:ARG:HD2	2.12	0.50
1:2A:324:A:N6	1:2A:338:G:O2'	2.44	0.50
1:2A:2255:G:O2'	55:2x:3:C:H5'	2.11	0.50
32:2a:838:G:H1	32:2a:848:C:H42	1.59	0.50
32:2a:890:G:O2'	32:2a:906:G:O6	2.29	0.50
32:2a:1265:G:C2	32:2a:1271:G:C2	2.99	0.50
32:2a:1288:A:N1	32:2a:1371:G:H1'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:64:LYS:HD2	39:2h:79:VAL:HG21	1.93	0.50
41:2j:44:VAL:HG21	41:2j:66:ARG:HH11	1.76	0.50
1:1A:375:C:H2'	1:1A:376:C:C6	2.46	0.50
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.46	0.50
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.46	0.50
33:1b:37:ASN:C	33:1b:39:ILE:H	2.19	0.50
33:1b:101:MET:HG2	33:1b:108:ILE:HG21	1.93	0.50
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.12	0.50
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.34	0.50
5:2F:25:PRO:HD2	5:2F:115:ALA:HB2	1.93	0.50
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.11	0.50
30:28:32:LEU:O	30:28:36:LYS:HE3	2.10	0.50
32:2a:487:A:H2'	32:2a:488:C:O4'	2.12	0.50
32:2a:1367:C:H5'	41:2j:60:ARG:CZ	2.42	0.50
34:2c:181:ASN:ND2	34:2c:204:LEU:HD12	2.26	0.50
54:2w:103:ASP:HA	54:2w:168:TYR:HB3	1.93	0.50
33:1b:12:GLU:HA	33:1b:15:VAL:HG22	1.93	0.50
1:2A:286:C:H2'	1:2A:287:C:H6	1.76	0.50
1:2A:2038:G:O6	60:2A:3959:HOH:O	2.19	0.50
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.75	0.50
32:2a:950:U:H2'	32:2a:951:G:H8	1.76	0.50
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.39	0.50
33:2b:109:SER:O	33:2b:112:VAL:N	2.44	0.50
36:2e:88:LYS:HB3	36:2e:123:LEU:HB2	1.94	0.50
43:2l:57:LYS:NZ	43:2l:65:GLU:OE2	2.29	0.50
49:2r:35:ARG:O	49:2r:37:VAL:N	2.45	0.50
54:2w:310:SER:HA	54:2w:324:LEU:HD12	1.92	0.50
55:2x:67:C:H2'	55:2x:68:G:H8	1.75	0.50
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.12	0.50
28:16:6:ARG:NE	28:16:24:GLU:OE2	2.26	0.50
32:1a:5:U:H3	35:1d:86:LYS:HZ3	1.60	0.50
32:1a:590:C:H2'	32:1a:591:U:C6	2.46	0.50
32:1a:745:C:H5'	32:1a:851:G:H21	1.77	0.50
32:1a:857:C:H2'	32:1a:858:G:O4'	2.11	0.50
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.92	0.50
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.46	0.50
51:1t:36:LEU:HD13	51:1t:58:LYS:HG3	1.93	0.50
51:1t:86:ARG:O	51:1t:90:GLN:NE2	2.44	0.50
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.12	0.50
11:2P:59:LEU:HD21	30:28:10:ALA:HA	1.93	0.50
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:58:HIS:CE1	19:2X:77:LYS:HE3	2.47	0.50
26:24:41:PRO:HG3	26:24:49:PHE:CD1	2.46	0.50
32:2a:418:C:H2'	32:2a:419:C:C6	2.46	0.50
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.26	0.50
34:2c:77:ILE:O	34:2c:82:GLU:N	2.45	0.50
38:2g:146:GLU:O	38:2g:149:ARG:HB2	2.11	0.50
40:2i:97:LYS:HA	40:2i:102:LEU:HD22	1.94	0.50
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.92	0.50
1:1A:1364:G:OP1	23:11:2:SER:HA	2.12	0.50
1:1A:2110:G:H5'	1:1A:2145:C:H42	1.76	0.50
5:1F:136:THR:HA	5:1F:166:ALA:O	2.12	0.50
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.91	0.50
32:1a:414:A:H2'	32:1a:415:A:H8	1.77	0.50
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.27	0.50
34:1c:42:LEU:HA	34:1c:45:LYS:HG2	1.93	0.50
1:2A:500:G:N2	1:2A:502:A:H3'	2.25	0.50
1:2A:2138:C:N4	1:2A:2153:G:H1	2.10	0.50
2:2B:17:C:H2'	2:2B:18:G:O4'	2.11	0.50
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.93	0.50
33:2b:63:MET:HG3	33:2b:225:ALA:HB1	1.93	0.50
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.47	0.50
1:1A:921:G:O6	60:1A:4143:HOH:O	2.16	0.50
1:1A:1268:A:C2	1:1A:2013:A:C4	3.00	0.50
1:1A:2098:U:H3	1:1A:2191:G:H1	1.60	0.50
1:1A:2733:A:OP1	60:1A:4149:HOH:O	2.18	0.50
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.44	0.50
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.93	0.50
32:1a:1211:U:H4'	32:1a:1213:A:O4'	2.12	0.50
32:1a:1244:C:H2'	32:1a:1245:A:C8	2.46	0.50
34:1c:164:ARG:HG2	34:1c:165:THR:H	1.76	0.50
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.46	0.50
1:2A:463:G:N2	1:2A:466:A:OP2	2.35	0.50
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.77	0.50
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.30	0.50
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.94	0.50
19:2X:11:PRO:HB3	19:2X:92:LEU:HD11	1.94	0.50
26:24:12:ALA:HB2	26:24:26:SER:HB3	1.94	0.50
32:2a:743:U:H2'	32:2a:744:C:C6	2.47	0.50
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.46	0.50
32:2a:1128:C:H1'	32:2a:1147:C:N3	2.27	0.50
33:2b:137:ARG:O	33:2b:141:GLU:HB2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:6:PHE:HB2	36:2e:63:ARG:HH21	1.77	0.50
38:2g:69:VAL:HG11	38:2g:104:LEU:HD21	1.94	0.50
1:1A:2122:U:H3	1:1A:2176:A:H61	1.59	0.50
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.27	0.50
32:1a:155:C:H2'	32:1a:156:G:H8	1.76	0.50
33:1b:166:ASP:OD2	60:1b:401:HOH:O	2.20	0.50
35:1d:12:CYS:SG	35:1d:19:LEU:N	2.84	0.50
36:1e:92:LYS:N	36:1e:119:LEU:O	2.44	0.50
40:1i:53:VAL:C	40:1i:55:ALA:H	2.16	0.50
32:2a:930:C:H2'	32:2a:931:C:O4'	2.11	0.50
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.93	0.50
34:2c:41:GLY:O	34:2c:45:LYS:HG2	2.11	0.50
36:2e:136:MET:HA	36:2e:139:LEU:HD12	1.93	0.50
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	1.94	0.50
38:2g:22:LEU:HD12	38:2g:97:GLN:NE2	2.23	0.50
1:1A:668:G:H5'	1:1A:669:G:OP2	2.12	0.50
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.47	0.50
3:1D:145:VAL:HG11	3:1D:175:LEU:HD11	1.94	0.50
14:1S:71:ARG:NH1	14:1S:107:GLU:OE1	2.45	0.50
32:1a:250:A:H4'	32:1a:251:G:O5'	2.11	0.50
32:1a:1030(D):A:C8	32:1a:1031:G:H1'	2.47	0.50
32:1a:1070:U:H2'	32:1a:1071:C:H6	1.76	0.50
39:1h:114:THR:OG1	39:1h:117:GLY:O	2.29	0.50
55:1x:7:U:O2'	55:1x:49:U:OP2	2.28	0.50
1:2A:2162:G:H2'	1:2A:2163:C:O4'	2.11	0.50
2:2B:95:C:H2'	2:2B:96:U:C6	2.47	0.50
11:2P:48:PRO:O	30:28:57:ARG:NH2	2.43	0.50
19:2X:94:GLY:H	19:2X:95:LEU:C	2.20	0.50
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.11	0.50
52:2u:5:ASP:O	52:2u:11:GLY:HA3	2.12	0.50
1:1A:839:U:H2'	1:1A:840:C:C6	2.47	0.50
1:1A:1115:G:H2'	1:1A:1116:C:O4'	2.12	0.50
1:1A:1364:G:N7	23:11:3:LYS:HD2	2.27	0.50
1:1A:1818:U:O4	3:1D:154:LYS:HD2	2.12	0.50
1:1A:2096:U:H3	1:1A:2193:G:H1	1.60	0.50
1:1A:2336:A:H61	22:10:43:THR:CG2	2.25	0.50
32:1a:620:C:H2'	32:1a:621:A:O4'	2.12	0.50
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.11	0.50
32:1a:1053:G:N7	32:1a:1200:C:H5''	2.25	0.50
40:1i:55:ALA:HA	40:1i:58:HIS:CD2	2.47	0.50
1:2A:212:G:H2'	1:2A:213:A:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1210:A:H5'	1:2A:1210:A:N3	2.27	0.50
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.26	0.50
2:2B:114:C:H4'	14:2S:46:VAL:HG12	1.93	0.50
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.93	0.50
24:22:10:LEU:HD22	24:22:14:ARG:NH1	2.27	0.50
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.93	0.50
38:2g:151:TYR:OH	42:2k:54:ARG:NH1	2.45	0.50
54:2w:134:PHE:HE1	54:2w:333:THR:HG23	1.77	0.50
1:1A:414:C:H2'	1:1A:415:A:C8	2.46	0.49
1:1A:2409:G:N7	60:1A:4251:HOH:O	2.34	0.49
20:1Y:97:ARG:HB3	20:1Y:106:LEU:HD12	1.93	0.49
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.77	0.49
44:1m:84:ILE:HB	50:1s:74:PHE:HE1	1.77	0.49
47:1p:58:TYR:O	47:1p:62:VAL:HG23	2.12	0.49
48:1q:51:TYR:CE2	48:1q:73:VAL:HG21	2.46	0.49
1:2A:852:G:H2'	1:2A:853:G:H8	1.77	0.49
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.47	0.49
2:2B:14:U:OP2	2:2B:70:C:O2'	2.28	0.49
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.47	0.49
21:2Z:23:LYS:HB3	21:2Z:38:TYR:CD1	2.47	0.49
32:2a:164:U:H2'	32:2a:165:C:C6	2.47	0.49
32:2a:438:G:H5'	35:2d:123:HIS:HD2	1.77	0.49
32:2a:737:A:H2'	32:2a:738:C:C6	2.47	0.49
41:2j:63:PHE:HE1	45:2n:58:LYS:HG2	1.77	0.49
49:2r:22:VAL:O	49:2r:25:THR:HG22	2.11	0.49
1:1A:236:C:H2'	1:1A:237:C:C6	2.47	0.49
26:14:16:CYS:HB2	26:14:36:CYS:HB3	1.94	0.49
32:1a:21:G:H2'	32:1a:22:G:C8	2.47	0.49
32:1a:221:C:H2'	32:1a:222:U:H6	1.77	0.49
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.94	0.49
36:1e:45:PHE:HD2	36:1e:47:LYS:HE2	1.77	0.49
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.94	0.49
1:2A:918:A:C2	2:2B:80:U:H4'	2.47	0.49
38:2g:152:ALA:O	38:2g:155:ARG:HD3	2.11	0.49
54:2w:321:THR:HG21	54:2w:335:ILE:HD11	1.94	0.49
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.93	0.49
14:1S:61:ASN:HD21	14:1S:63:THR:HB	1.76	0.49
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.26	0.49
34:1c:85:ARG:HG3	34:1c:86:VAL:N	2.27	0.49
38:1g:16:LEU:HD11	40:1i:45:ALA:HB2	1.93	0.49
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.94	0.49
4:2E:52:LEU:HB3	4:2E:76:ARG:HD3	1.94	0.49
22:20:23:VAL:HA	22:20:38:VAL:HG22	1.93	0.49
32:2a:384:G:H2'	32:2a:385:C:C6	2.47	0.49
32:2a:489:C:H2'	32:2a:490:G:C8	2.47	0.49
32:2a:1325:C:H5''	52:2u:17:THR:HG21	1.94	0.49
54:2w:182:ARG:HB3	54:2w:307:PHE:HB2	1.93	0.49
6:1G:109:VAL:HG11	26:14:14:ILE:HD13	1.94	0.49
32:1a:193:C:H2'	32:1a:194:C:H6	1.76	0.49
32:1a:392:G:H2'	32:1a:393:A:C8	2.47	0.49
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.31	0.49
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.12	0.49
32:1a:1343:G:H4'	40:1i:122:ALA:HB3	1.94	0.49
33:1b:73:THR:OG1	33:1b:170:GLU:OE2	2.29	0.49
35:1d:81:GLU:OE2	35:1d:139:ARG:NH1	2.44	0.49
41:1j:49:VAL:HG12	45:1n:41:ARG:HB2	1.94	0.49
1:2A:1448:G:H2'	1:2A:1449:A:C8	2.48	0.49
1:2A:2134:A:C6	1:2A:2135:A:H1'	2.48	0.49
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.47	0.49
7:2H:103:LEU:HB3	7:2H:115:VAL:HB	1.95	0.49
9:2N:20:GLY:HA2	9:2N:61:ARG:HG2	1.95	0.49
21:2Z:10:ARG:NH2	21:2Z:26:GLY:O	2.46	0.49
32:2a:370:C:H2'	32:2a:371:G:H8	1.76	0.49
32:2a:381:C:H2'	32:2a:382:A:O4'	2.13	0.49
32:2a:977:A:O2'	32:2a:981:U:N3	2.39	0.49
32:2a:1381:U:H1'	38:2g:79:ARG:HG2	1.94	0.49
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.94	0.49
42:2k:79:SER:HA	42:2k:104:GLN:HB3	1.93	0.49
44:2m:59:TYR:CE1	44:2m:63:THR:HG21	2.47	0.49
1:1A:2181:G:H2'	1:1A:2182:G:N7	2.28	0.49
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.47	0.49
11:1P:71:VAL:HG22	11:1P:72:PRO:HA	1.94	0.49
13:1R:103:ARG:HD3	13:1R:108:GLY:O	2.12	0.49
20:1Y:14:LEU:HB2	20:1Y:75:ILE:HD11	1.94	0.49
35:1d:98:GLU:OE1	35:1d:103:ASN:ND2	2.45	0.49
38:1g:120:ILE:O	38:1g:124:LEU:HD12	2.12	0.49
45:1n:45:ARG:HG3	45:1n:49:HIS:HD2	1.77	0.49
1:2A:398:G:H2'	1:2A:399:G:C8	2.47	0.49
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.47	0.49
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.42	0.49
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:9:ILE:HB	7:2H:50:VAL:HG12	1.94	0.49
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.47	0.49
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.96	0.49
32:2a:1273:G:C6	32:2a:1274:G:C4	3.01	0.49
35:2d:11:LEU:HD22	35:2d:66:ARG:NH2	2.26	0.49
1:1A:747:U:O2	1:1A:2014:A:H1'	2.11	0.49
1:1A:773:U:H2'	1:1A:774:A:H5'	1.95	0.49
1:1A:1996:C:H4'	1:1A:1997:G:OP1	2.11	0.49
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.48	0.49
4:1E:9:VAL:HG13	15:1T:3:ARG:HG2	1.93	0.49
6:1G:37:VAL:HA	6:1G:158:ALA:O	2.13	0.49
7:1H:97:ARG:NH1	7:1H:104:GLU:OE1	2.45	0.49
16:1U:28:ARG:NH1	16:1U:38:THR:OG1	2.39	0.49
35:1d:23:GLY:HA3	35:1d:112:VAL:HG12	1.94	0.49
36:1e:57:LYS:HG2	36:1e:61:TYR:HE2	1.77	0.49
1:2A:2122:U:H2'	1:2A:2123:G:C8	2.47	0.49
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.27	0.49
1:2A:2356:C:P	22:20:24:LYS:HZ2	2.35	0.49
6:2G:102:PHE:HZ	6:2G:157:ILE:HD13	1.75	0.49
8:2I:45:LYS:HA	8:2I:48:GLU:HG2	1.95	0.49
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.12	0.49
32:2a:1240:U:OP2	38:2g:116:ALA:N	2.46	0.49
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.35	0.49
34:2c:52:LEU:HD11	34:2c:55:VAL:HG23	1.94	0.49
1:1A:185:U:H4'	1:1A:218:A:H4'	1.95	0.49
1:1A:687:C:H1'	29:17:4:THR:HG22	1.95	0.49
1:1A:1342:A:OP2	60:1A:4158:HOH:O	2.20	0.49
1:1A:1721:G:H2'	1:1A:1722:A:H2'	1.94	0.49
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.77	0.49
32:1a:189(C):C:H2'	32:1a:189(D):C:O4'	2.12	0.49
32:1a:430:A:H4'	35:1d:7:PRO:HG3	1.94	0.49
32:1a:600:C:H2'	32:1a:601:C:H6	1.77	0.49
36:1e:12:LEU:HD11	36:1e:14:ARG:HB3	1.95	0.49
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.12	0.49
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.28	0.49
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.47	0.49
6:2G:167:GLU:H	6:2G:167:GLU:CD	2.21	0.49
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.93	0.49
41:2j:17:ASP:OD1	41:2j:70:ARG:NE	2.45	0.49
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.95	0.49
32:1a:920:U:H2'	32:1a:921:U:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:993:G:H2'	32:1a:993:G:N3	2.28	0.49
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.47	0.49
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.60	0.49
32:1a:1438:G:H2'	32:1a:1439:C:C6	2.48	0.49
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.95	0.49
46:1o:8:LYS:HD2	46:1o:31:LEU:HD22	1.94	0.49
1:2A:531:C:H4'	1:2A:532:A:H5''	1.95	0.49
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	1.95	0.49
15:2T:26:ASP:O	15:2T:49:VAL:HG22	2.12	0.49
32:2a:1228:C:P	44:2m:108:ARG:HH22	2.36	0.49
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.46	0.49
51:2t:87:LYS:O	51:2t:91:LEU:HG	2.13	0.49
1:1A:1365:A:O4'	23:11:41:ARG:NH2	2.46	0.49
6:1G:43:LEU:HD23	6:1G:53:LEU:HD22	1.94	0.49
6:1G:82:LEU:HB2	6:1G:86:MET:SD	2.53	0.49
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.94	0.49
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.48	0.49
32:1a:1064:G:H4'	32:1a:1065:U:OP1	2.13	0.49
33:1b:119:GLU:OE2	33:1b:153:ARG:NH1	2.45	0.49
38:1g:127:ALA:HA	38:1g:131:LYS:O	2.13	0.49
54:1w:302:ILE:HG13	54:1w:316:ARG:NE	2.28	0.49
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.13	0.49
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.28	0.49
1:2A:1399:C:OP1	19:2X:25:LYS:NZ	2.40	0.49
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.12	0.49
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	1.94	0.49
21:2Z:10:ARG:NE	21:2Z:37:VAL:O	2.41	0.49
32:2a:316:G:OP2	32:2a:351:G:O2'	2.31	0.49
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.28	0.49
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.46	0.49
38:2g:90:GLU:OE1	38:2g:90:GLU:N	2.38	0.49
1:1A:2846:G:H2'	1:1A:2847:U:O4'	2.13	0.49
4:1E:79:ARG:NE	60:1E:403:HOH:O	2.31	0.49
14:1S:18:ILE:O	14:1S:21:THR:OG1	2.31	0.49
32:1a:509:A:O2'	32:1a:510:A:OP1	2.30	0.49
32:1a:568:G:O2'	32:1a:574:A:N1	2.45	0.49
32:1a:1426:C:H2'	32:1a:1427:U:H6	1.76	0.49
51:1t:78:ALA:HA	51:1t:81:LYS:HD3	1.94	0.49
1:2A:646:A:H2'	1:2A:647:G:O4'	2.13	0.49
1:2A:2680:C:H5'	4:2E:189:PRO:HA	1.94	0.49
2:2B:11:C:H3'	2:2B:12:C:H6	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.59	0.49
29:27:1:MET:HE3	29:27:3:ARG:NH2	2.28	0.49
32:2a:707:C:H2'	32:2a:708:C:H6	1.78	0.49
35:2d:169:LYS:HG2	35:2d:170:VAL:H	1.77	0.49
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.46	0.49
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.77	0.49
45:2n:26:ARG:HB3	45:2n:43:CYS:SG	2.53	0.49
1:1A:1876:A:H2'	1:1A:1877:A:C8	2.48	0.48
10:1O:2:ILE:HB	10:1O:33:ALA:HB3	1.95	0.48
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.19	0.48
34:1c:26:LYS:HB2	45:1n:36:PHE:HE1	1.77	0.48
34:1c:84:ILE:HA	34:1c:87:LEU:HD12	1.94	0.48
35:1d:108:LEU:HD23	35:1d:174:LEU:HD13	1.95	0.48
42:1k:84:VAL:HG11	42:1k:95:ILE:HD11	1.94	0.48
12:2Q:133:ARG:HG2	12:2Q:134:ARG:N	2.28	0.48
32:2a:222:U:H2'	32:2a:223:U:H6	1.78	0.48
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.46	0.48
32:2a:1225:A:H2'	32:2a:1225:A:N3	2.28	0.48
33:2b:44:LEU:HD23	33:2b:44:LEU:H	1.77	0.48
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.28	0.48
1:1A:2107:C:N4	1:1A:2182:G:H1	2.06	0.48
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.78	0.48
10:1O:18:LYS:HB2	10:1O:45:GLU:HB3	1.95	0.48
35:1d:138:TYR:HD2	35:1d:140:VAL:HG22	1.77	0.48
1:2A:35:G:H1'	1:2A:454:A:C4	2.48	0.48
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.94	0.48
1:2A:2365:G:O6	30:28:43:GLN:NE2	2.39	0.48
1:2A:2487:G:H2'	1:2A:2488:A:C8	2.48	0.48
13:2R:12:ARG:HE	13:2R:16:HIS:CE1	2.31	0.48
13:2R:33:ARG:NH2	13:2R:115:GLU:OE1	2.38	0.48
32:2a:28:G:O2'	32:2a:296:U:OP1	2.19	0.48
34:2c:77:ILE:O	34:2c:83:ARG:N	2.46	0.48
1:1A:2106:G:H2'	1:1A:2107:C:C6	2.48	0.48
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.28	0.48
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.95	0.48
6:1G:108:ASN:O	6:1G:112:PRO:HG2	2.13	0.48
17:1V:74:LYS:HB2	17:1V:83:ARG:HB2	1.94	0.48
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG22	2.13	0.48
32:1a:828:A:H2'	32:1a:829:G:O4'	2.13	0.48
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.49	0.48
32:1a:1508:G:H2'	32:1a:1509:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1e:102:ALA:HB1	36:1e:106:PRO:HB2	1.93	0.48
37:1f:99:ALA:O	49:1r:28:GLU:HA	2.13	0.48
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.78	0.48
44:1m:4:ILE:HG23	44:1m:22:ILE:HD11	1.93	0.48
51:1t:47:GLY:N	51:1t:48:LYS:HB2	2.27	0.48
1:2A:222:A:OP1	60:2A:3964:HOH:O	2.20	0.48
1:2A:422:A:H2'	1:2A:423:A:C8	2.48	0.48
5:2F:9:ILE:HG12	5:2F:123:LEU:HD23	1.95	0.48
7:2H:41:MET:HE1	7:2H:54:ARG:HB3	1.95	0.48
10:2O:58:VAL:HG21	10:2O:86:ILE:HD13	1.95	0.48
32:2a:1240:U:C2	38:2g:32:ARG:HD3	2.48	0.48
1:1A:2133:G:O2'	1:1A:2157:G:N2	2.47	0.48
1:1A:2529:G:H5''	1:1A:2530:A:H5''	1.95	0.48
2:1B:13:A:N1	2:1B:69:G:O2'	2.42	0.48
2:1B:90:A:C5	2:1B:91:C:H1'	2.49	0.48
20:1Y:5:MET:HG2	20:1Y:30:VAL:HG11	1.95	0.48
32:1a:516:PSU:O2	60:1a:1914:HOH:O	2.19	0.48
32:1a:814:A:H2'	32:1a:816:A:H5''	1.96	0.48
51:1t:42:GLN:NE2	51:1t:46:GLU:OE2	2.45	0.48
1:2A:828:U:H4'	1:2A:831:G:N1	2.28	0.48
1:2A:1161:C:H2'	1:2A:1162:G:C8	2.48	0.48
1:2A:2814:C:HO2'	27:25:29:THR:HG1	1.61	0.48
13:2R:8:ARG:HE	13:2R:43:GLU:HG2	1.79	0.48
17:2V:40:LEU:HD11	17:2V:101:GLY:HA3	1.94	0.48
32:2a:489:C:H2'	32:2a:490:G:H8	1.78	0.48
32:2a:1004:A:H2'	32:2a:1005:A:H5'	1.95	0.48
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.49	0.48
1:1A:8:A:H2'	1:1A:9:U:C6	2.49	0.48
1:1A:331:A:N1	60:1A:4259:HOH:O	2.35	0.48
1:1A:1006:C:O2'	9:1N:106:MET:HB3	2.13	0.48
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.48	0.48
1:1A:2462:U:H1'	1:1A:2491:U:O4	2.12	0.48
3:1D:20:ASP:OD1	3:1D:20:ASP:N	2.44	0.48
5:1F:95:ARG:HD3	5:1F:97:TYR:CZ	2.49	0.48
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	1.96	0.48
32:1a:1064:G:H1'	32:1a:1190:G:N2	2.29	0.48
33:1b:215:LEU:O	33:1b:219:VAL:HG23	2.14	0.48
34:1c:113:ALA:HA	34:1c:202:ILE:HD12	1.95	0.48
41:1j:49:VAL:HG11	45:1n:44:LEU:HD22	1.96	0.48
1:2A:1288:U:OP1	1:2A:1289:C:N4	2.43	0.48
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2611:U:H3'	1:2A:2611:U:OP2	2.14	0.48
5:2F:179:GLU:O	5:2F:205:ARG:NH2	2.42	0.48
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	1.94	0.48
32:2a:683:G:H2'	32:2a:684:A:C8	2.49	0.48
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.28	0.48
32:2a:1347:G:H22	32:2a:1374:A:P	2.36	0.48
33:2b:8:LYS:HG3	33:2b:51:LEU:HD13	1.95	0.48
33:2b:188:ALA:HB1	33:2b:192:SER:HB2	1.94	0.48
34:2c:79:ARG:N	34:2c:82:GLU:HB3	2.28	0.48
35:2d:78:LEU:HB3	35:2d:93:PHE:HE1	1.79	0.48
38:2g:101:LEU:HA	38:2g:104:LEU:HD12	1.96	0.48
40:2i:3:GLN:HB3	40:2i:20:ARG:HH21	1.77	0.48
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.28	0.48
1:1A:2312:U:OP1	6:1G:73:ALA:HA	2.13	0.48
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	1.94	0.48
32:1a:1060:C:P	45:1n:45:ARG:HH22	2.37	0.48
48:1q:51:TYR:HE1	48:1q:76:LEU:HB2	1.78	0.48
1:2A:271(G):C:O2'	23:21:81:LYS:HE2	2.13	0.48
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.48	0.48
1:2A:2101:G:N1	1:2A:2187:G:O6	2.47	0.48
27:25:35:GLU:HG2	27:25:51:TYR:CG	2.49	0.48
32:2a:1234:C:H1'	32:2a:1364:U:O2	2.14	0.48
34:2c:23:TYR:HA	41:2j:11:PHE:CD2	2.49	0.48
1:1A:1949:G:O6	60:1A:4153:HOH:O	2.19	0.48
32:1a:96:U:H2'	32:1a:97:G:H8	1.78	0.48
32:1a:735:C:H2'	32:1a:736:C:C6	2.49	0.48
32:1a:789:U:O2'	32:1a:791:G:N7	2.45	0.48
32:1a:790:A:OP1	55:1x:38:A:O2'	2.28	0.48
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.49	0.48
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.48	0.48
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.48	0.48
15:2T:15:VAL:HG13	15:2T:79:HIS:CE1	2.49	0.48
32:2a:337:C:H2'	32:2a:338:A:C8	2.49	0.48
32:2a:1320:C:O2	50:2s:36:ARG:NH2	2.44	0.48
33:2b:114:ARG:O	33:2b:118:LEU:N	2.46	0.48
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.13	0.48
1:1A:271(D):G:H1	1:1A:271(T):C:H42	1.60	0.48
1:1A:271(L):U:H4'	8:1I:50:ARG:NH2	2.26	0.48
1:1A:1452:A:OP2	60:1A:4160:HOH:O	2.20	0.48
1:1A:2166:G:H2'	1:1A:2167:U:C5	2.49	0.48
8:1I:93:THR:O	8:1I:97:ILE:HG13	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:944:G:N1	32:1a:1338:G:OP2	2.42	0.48
32:1a:958:A:N6	32:1a:959:A:N1	2.62	0.48
32:1a:1118:C:H1'	32:1a:1179:A:C5	2.49	0.48
1:2A:673:C:O2'	60:2A:3965:HOH:O	2.20	0.48
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.95	0.48
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	1.94	0.48
27:25:41:PRO:O	27:25:44:THR:OG1	2.22	0.48
32:2a:7:G:H5'	32:2a:298:A:O4'	2.14	0.48
32:2a:266:G:H2'	32:2a:266:G:N3	2.29	0.48
32:2a:662:G:O2'	32:2a:836:G:OP1	2.31	0.48
34:2c:103:VAL:HG22	34:2c:104:GLN:H	1.77	0.48
37:2f:62:TRP:C	37:2f:63:TYR:HD2	2.20	0.48
37:2f:83:ASP:N	37:2f:83:ASP:OD1	2.46	0.48
1:1A:2406:U:H2'	1:1A:2406:U:OP2	2.13	0.48
3:1D:25:THR:HG21	3:1D:113:VAL:HG11	1.96	0.48
8:1I:72:LEU:HD22	8:1I:101:LEU:HD21	1.94	0.48
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.96	0.48
32:1a:413:G:N2	32:1a:428:G:H1'	2.29	0.48
32:1a:504:C:OP1	60:1a:1915:HOH:O	2.20	0.48
32:1a:833:U:H2'	32:1a:834:C:H6	1.79	0.48
32:1a:1086:U:H2'	32:1a:1087:G:H8	1.79	0.48
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.47	0.48
38:1g:80:VAL:HG11	38:1g:154:TYR:CG	2.48	0.48
39:1h:49:GLU:HG2	39:1h:62:TYR:HE2	1.78	0.48
54:1w:151:ASP:OD1	54:1w:151:ASP:N	2.47	0.48
1:2A:855:G:C5	1:2A:856:C:C4	3.01	0.48
1:2A:882:G:H1	1:2A:894:C:H42	1.62	0.48
1:2A:895:U:O3'	1:2A:896:A:H3'	2.14	0.48
1:2A:1428:C:O2'	1:2A:1569:A:OP2	2.25	0.48
1:2A:2317:C:H2'	1:2A:2318:G:H5'	1.96	0.48
1:2A:2397:G:N2	1:2A:2420:C:H1'	2.29	0.48
6:2G:12:TYR:HA	6:2G:16:ARG:HD3	1.96	0.48
32:2a:202:U:H3'	32:2a:203:U:C6	2.49	0.48
32:2a:1112:C:N3	34:2c:178:LEU:HD12	2.28	0.48
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.13	0.48
39:2h:86:ILE:HG21	39:2h:133:LEU:HD23	1.96	0.48
42:2k:20:TYR:O	42:2k:30:VAL:HA	2.13	0.48
50:2s:28:LYS:HD3	50:2s:47:HIS:HA	1.95	0.48
54:2w:143:GLU:HB3	54:2w:161:GLU:HG2	1.96	0.48
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.29	0.48
21:1Z:46:LYS:HB3	21:1Z:46:LYS:HE2	1.74	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:739:C:HO2'	46:1o:42:HIS:HD1	1.56	0.48
32:1a:1298:C:H2'	38:1g:114:ARG:HH22	1.78	0.48
33:1b:32:ILE:HD13	33:1b:40:HIS:CD2	2.48	0.48
33:1b:95:GLN:OE1	33:1b:147:LYS:NZ	2.47	0.48
38:1g:137:LYS:O	38:1g:141:VAL:HG23	2.14	0.48
1:2A:746:A:H2'	1:2A:2612:C:H5''	1.96	0.48
1:2A:2475:C:H42	1:2A:2529:G:H22	1.61	0.48
4:2E:48:GLN:HE21	4:2E:78:LEU:HD22	1.78	0.48
10:2O:63:VAL:HG12	10:2O:106:LEU:HD11	1.96	0.48
28:26:14:THR:OG1	28:26:48:VAL:HG13	2.13	0.48
32:2a:1077:G:N2	32:2a:1080:A:OP2	2.38	0.48
32:2a:1117:G:N2	32:2a:1180:A:O2'	2.46	0.48
35:2d:111:ALA:HB2	35:2d:120:LEU:HD22	1.95	0.48
38:2g:113:GLU:HB2	38:2g:119:ARG:HG2	1.96	0.48
1:1A:272(J):C:H2'	1:1A:274:G:H8	1.79	0.47
1:1A:579:G:OP1	60:1A:4159:HOH:O	2.20	0.47
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.37	0.47
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.14	0.47
1:1A:2563:U:H4'	10:1O:28:SER:HA	1.96	0.47
3:1D:237:GLU:OE2	60:1D:401:HOH:O	2.20	0.47
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.95	0.47
32:1a:266:G:N3	32:1a:266:G:H5''	2.29	0.47
32:1a:685:G:O2'	32:1a:686:U:H5'	2.13	0.47
32:1a:909:A:H2'	32:1a:910:C:O4'	2.14	0.47
32:1a:1426:C:H2'	32:1a:1427:U:C6	2.49	0.47
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.49	0.47
1:2A:192:C:O2'	1:2A:802:A:N3	2.44	0.47
1:2A:307:G:N1	1:2A:310:A:OP2	2.47	0.47
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.29	0.47
10:2O:16:ALA:HB2	10:2O:52:VAL:HG21	1.95	0.47
33:2b:118:LEU:HD12	33:2b:142:LEU:HB2	1.95	0.47
1:1A:305:U:H2'	1:1A:306:U:C6	2.49	0.47
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.49	0.47
12:1Q:32:TYR:OH	12:1Q:111:GLU:OE2	2.32	0.47
32:1a:865:A:H2	32:1a:918:A:H4'	1.78	0.47
33:1b:162:ILE:HD11	33:1b:184:VAL:HG13	1.96	0.47
54:1w:319:PHE:CE2	54:1w:335:ILE:HG12	2.49	0.47
1:2A:1858:G:N2	1:2A:1883:G:H2'	2.29	0.47
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.31	0.47
23:21:7:ILE:HG23	23:21:98:LEU:HD11	1.96	0.47
32:2a:148:G:H2'	32:2a:149:A:C8	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:728:A:H2'	32:2a:729:A:C8	2.49	0.47
32:2a:1326:C:H2'	32:2a:1327:C:C6	2.50	0.47
38:2g:149:ARG:HB3	42:2k:59:TYR:CE2	2.49	0.47
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.49	0.47
45:2n:47:LEU:HD23	45:2n:47:LEU:HA	1.74	0.47
1:1A:1203:G:O6	60:1A:4151:HOH:O	2.18	0.47
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.49	0.47
16:1U:108:GLU:O	16:1U:112:ARG:HG2	2.14	0.47
32:1a:1051:C:H2'	32:1a:1052:U:H6	1.78	0.47
38:1g:28:ASN:HA	38:1g:31:MET:HE2	1.95	0.47
48:1q:66:SER:OG	48:1q:67:LYS:N	2.47	0.47
54:1w:303:ARG:HA	54:1w:313:THR:O	2.14	0.47
1:2A:493:G:H2'	1:2A:494:G:O4'	2.15	0.47
19:2X:57:LEU:HD11	19:2X:78:LYS:HE2	1.95	0.47
27:25:2:ALA:N	60:25:201:HOH:O	2.46	0.47
32:2a:232:G:H2'	32:2a:233:C:O4'	2.13	0.47
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.50	0.47
39:2h:82:HIS:NE2	39:2h:136:GLU:OE2	2.47	0.47
1:1A:274:G:H2'	1:1A:275:G:C8	2.49	0.47
1:1A:826:U:OP1	60:1A:4104:HOH:O	2.20	0.47
1:1A:829:A:N7	1:1A:2248:C:H5'	2.30	0.47
32:1a:735:C:H5'	49:1r:71:LYS:HD3	1.95	0.47
44:1m:84:ILE:HG13	44:1m:86:CYS:H	1.78	0.47
48:1q:62:SER:OG	48:1q:72:ARG:NE	2.41	0.47
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.39	0.47
3:2D:5:LYS:HG2	3:2D:17:THR:HG22	1.96	0.47
10:2O:88:ASN:ND2	10:2O:90:GLN:OE1	2.47	0.47
32:2a:1516:G:N2	32:2a:1519:MA6:OP2	2.47	0.47
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.49	0.47
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.14	0.47
51:2t:84:LEU:O	51:2t:88:VAL:HG23	2.15	0.47
1:1A:987:G:O2'	1:1A:1000:A:N3	2.43	0.47
1:1A:1322:A:N1	1:1A:1333:C:O2'	2.41	0.47
10:1O:25:LEU:HG	10:1O:40:VAL:HG23	1.96	0.47
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.97	0.47
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.49	0.47
1:2A:1364:G:P	23:21:3:LYS:HG3	2.53	0.47
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.33	0.47
1:2A:2478:A:H5'	31:29:31:LYS:HD2	1.97	0.47
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.13	0.47
3:2D:242:ARG:HD3	3:2D:242:ARG:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:50:HIS:CE1	13:2R:54:LEU:HD11	2.50	0.47
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.78	0.47
33:2b:28:PHE:CD1	33:2b:194:PRO:HG3	2.50	0.47
35:2d:24:GLU:HA	35:2d:27:TYR:HD2	1.80	0.47
35:2d:150:GLU:C	35:2d:152:SER:H	2.21	0.47
1:1A:207:A:H2'	1:1A:208:C:O4'	2.14	0.47
1:1A:639:U:H2'	1:1A:640:C:C6	2.49	0.47
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	2.15	0.47
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.14	0.47
1:1A:2721:A:H2'	1:1A:2722:G:O4'	2.14	0.47
10:1O:15:GLY:O	10:1O:47:ILE:HG12	2.14	0.47
32:1a:1368:G:O2'	41:1j:46:ARG:NH1	2.48	0.47
39:1h:103:VAL:HG21	39:1h:110:ALA:HB2	1.96	0.47
39:1h:124:ALA:O	39:1h:128:GLY:N	2.44	0.47
1:2A:652(A):A:H2'	1:2A:652(A):A:N3	2.29	0.47
1:2A:740:U:H2'	1:2A:741:G:C8	2.50	0.47
1:2A:1200:C:H1'	16:2U:2:PRO:HG3	1.96	0.47
1:2A:1668:A:O2'	1:2A:1674:G:N7	2.38	0.47
1:2A:2164:C:C5	1:2A:2165:G:H1'	2.50	0.47
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.96	0.47
8:2I:14:ASP:OD1	8:2I:15:VAL:N	2.47	0.47
8:2I:83:ALA:HB1	8:2I:123:LEU:HD11	1.97	0.47
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.50	0.47
24:22:32:LEU:HA	24:22:53:LEU:HD13	1.96	0.47
32:2a:707:C:H2'	32:2a:708:C:C6	2.49	0.47
32:2a:1134:G:C2	32:2a:1135:U:H1'	2.50	0.47
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.95	0.47
33:2b:95:GLN:NE2	33:2b:147:LYS:HB3	2.26	0.47
34:2c:70:VAL:O	34:2c:106:VAL:N	2.32	0.47
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.96	0.47
46:2o:39:LEU:HB3	46:2o:56:LEU:HD12	1.97	0.47
54:2w:223:ARG:HG3	54:2w:236:ASP:OD1	2.14	0.47
1:1A:81:G:H21	20:1Y:1:MET:HE1	1.79	0.47
1:1A:119:A:H4'	1:1A:120:U:OP1	2.14	0.47
1:1A:389:G:O6	11:1P:70:GLN:HB2	2.15	0.47
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.96	0.47
8:1I:4:ILE:HD11	8:1I:44:LEU:HD23	1.97	0.47
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.15	0.47
14:1S:25:ARG:HD3	14:1S:42:ASP:OD1	2.15	0.47
26:14:46:GLN:HE21	26:14:46:GLN:HB2	1.53	0.47
32:1a:347:G:C5	32:1a:348:G:C8	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:185:ILE:HG22	33:1b:199:TYR:HD2	1.79	0.47
41:1j:48:THR:HG23	41:1j:62:HIS:CE1	2.50	0.47
44:1m:84:ILE:HG21	50:1s:66:MET:HB3	1.97	0.47
47:1p:28:ARG:HG3	47:1p:29:ASP:N	2.29	0.47
47:1p:37:GLY:HA3	47:1p:50:LYS:O	2.14	0.47
54:1w:141:GLU:HG3	54:1w:163:ARG:HE	1.80	0.47
55:1x:49:U:H3	55:1x:65:A:H61	1.61	0.47
1:2A:253:C:OP2	30:28:5:LYS:NZ	2.33	0.47
1:2A:514:A:N3	1:2A:581:C:O2'	2.45	0.47
1:2A:1035:U:H5''	7:2H:59:ARG:HD3	1.96	0.47
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.15	0.47
1:2A:1359:A:H2'	1:2A:1360:A:H5'	1.97	0.47
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.97	0.47
1:2A:2196:C:OP2	60:2A:3966:HOH:O	2.20	0.47
1:2A:2765:A:OP2	60:2A:3969:HOH:O	2.21	0.47
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.15	0.47
6:2G:70:VAL:HG22	6:2G:90:LEU:HD22	1.97	0.47
10:2O:34:THR:OG1	10:2O:69:ILE:HD11	2.14	0.47
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.14	0.47
32:2a:110:C:O2'	47:2p:25:ARG:O	2.31	0.47
32:2a:187:C:O2'	51:2t:89:ARG:HD3	2.15	0.47
32:2a:1327:C:OP1	52:2u:12:LYS:NZ	2.31	0.47
40:2i:73:GLN:O	40:2i:77:ILE:HG13	2.15	0.47
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.15	0.47
51:2t:57:ARG:HH12	51:2t:100:ILE:HG13	1.78	0.47
55:2x:55:PSU:O2'	55:2x:57:G:N7	2.43	0.47
55:2x:61:C:H2'	55:2x:62:C:H6	1.79	0.47
1:1A:517:C:OP2	27:15:13:LYS:HE2	2.15	0.47
1:1A:1062:G:H8	1:1A:1070:A:H4'	1.78	0.47
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.80	0.47
21:1Z:30:ASN:OD1	21:1Z:33:LEU:HD23	2.15	0.47
32:1a:580:U:H2'	32:1a:581:G:O4'	2.14	0.47
32:1a:1124:G:H5''	41:1j:35:SER:OG	2.15	0.47
32:1a:1371:G:OP2	40:1i:11:LYS:HE2	2.15	0.47
33:1b:61:LEU:HA	33:1b:64:ARG:HD2	1.95	0.47
1:2A:81:G:N7	60:2A:4056:HOH:O	2.35	0.47
1:2A:652(B):A:N3	1:2A:652(B):A:H2'	2.30	0.47
5:2F:148:LEU:HD11	5:2F:193:VAL:HG21	1.97	0.47
6:2G:35:GLU:HG3	6:2G:36:LYS:HG3	1.96	0.47
17:2V:65:GLY:HA3	17:2V:91:TYR:CZ	2.49	0.47
32:2a:237:C:H5''	48:2q:25:ARG:CZ	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:555:C:H2'	32:2a:556:C:C6	2.50	0.47
32:2a:1004:A:C6	32:2a:1037:C:H1'	2.49	0.47
32:2a:1236:A:O2'	32:2a:1304:G:H4'	2.15	0.47
44:2m:25:ILE:HD11	44:2m:60:VAL:HG11	1.97	0.47
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.50	0.47
32:1a:189(F):U:C4	48:1q:72:ARG:NH2	2.83	0.47
32:1a:583:A:H2'	32:1a:584:G:O4'	2.15	0.47
32:1a:880:C:OP1	43:1l:8:ASN:ND2	2.46	0.47
32:1a:1187:G:N3	45:1n:60:SER:OG	2.48	0.47
34:1c:134:ILE:HG23	34:1c:151:VAL:HG13	1.96	0.47
42:1k:78:GLN:O	42:1k:104:GLN:N	2.45	0.47
44:1m:91:ARG:NH2	44:1m:96:LEU:HD13	2.29	0.47
55:1x:76:A:H1'	60:1x:206:HOH:O	2.14	0.47
1:2A:884:C:H2'	1:2A:885:C:O4'	2.15	0.47
1:2A:1669:A:H5''	1:2A:2550:G:OP1	2.15	0.47
1:2A:1779:U:H2'	60:2A:4592:HOH:O	2.14	0.47
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.50	0.47
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.49	0.47
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.80	0.47
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.58	0.47
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	1.97	0.47
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.13	0.47
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.52	0.47
32:2a:137:C:H2'	32:2a:138:G:H8	1.80	0.47
32:2a:1445:C:O2'	32:2a:1447:A:N6	2.48	0.47
54:2w:189:GLN:HB3	54:2w:191:ARG:HG3	1.97	0.47
1:1A:1095:A:H2'	1:1A:1096:A:O4'	2.14	0.47
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.49	0.47
2:1B:57:A:H1'	6:1G:29:TRP:HB2	1.97	0.47
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.96	0.47
9:1N:30:ILE:HG23	9:1N:52:VAL:HG11	1.97	0.47
15:1T:8:LYS:HE3	15:1T:8:LYS:HB3	1.81	0.47
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.49	0.47
32:1a:60:A:N1	32:1a:107:G:O2'	2.36	0.47
32:1a:598:U:H2'	32:1a:599:C:C6	2.49	0.47
32:1a:1065:U:H1'	32:1a:1066:C:OP2	2.15	0.47
33:1b:71:VAL:HG23	33:1b:164:VAL:HA	1.97	0.47
37:1f:10:LEU:HD21	37:1f:26:ILE:HD11	1.97	0.47
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.50	0.47
1:2A:1906:G:OP2	1:2A:1929:G:O2'	2.33	0.47
1:2A:2165:G:H2'	1:2A:2166:G:H5''	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.15	0.47
3:2D:70:TRP:CD1	3:2D:70:TRP:H	2.33	0.47
11:2P:84:ASN:HD22	11:2P:117:GLU:HB3	1.80	0.47
31:29:7:VAL:HG12	31:29:34:GLN:HB3	1.97	0.47
32:2a:448:A:OP2	32:2a:485:G:N2	2.42	0.47
32:2a:717:C:H2'	32:2a:734:G:OP2	2.15	0.47
44:2m:80:ARG:O	44:2m:84:ILE:HG23	2.15	0.47
1:1A:284:U:H2'	1:1A:285:C:C6	2.50	0.46
1:1A:1091:G:C5	1:1A:1092:C:N4	2.83	0.46
1:1A:2271:G:OP1	22:10:18:ALA:HB1	2.14	0.46
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.49	0.46
36:1e:77:PRO:HG2	36:1e:142:LEU:HD22	1.97	0.46
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	1.98	0.46
41:1j:39:PRO:HB3	41:1j:70:ARG:CZ	2.44	0.46
1:2A:8:A:H2'	1:2A:9:U:C6	2.50	0.46
1:2A:398:G:H2'	1:2A:399:G:H8	1.80	0.46
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.16	0.46
1:2A:2405:G:H5'	11:2P:75:ILE:HD13	1.97	0.46
1:2A:2586:C:H1'	60:2A:4813:HOH:O	2.15	0.46
6:2G:56:ALA:O	6:2G:60:LEU:HB2	2.15	0.46
19:2X:44:GLU:O	19:2X:48:LYS:N	2.45	0.46
26:24:15:ILE:HB	26:24:32:TYR:HD1	1.79	0.46
32:2a:108:G:N1	51:2t:15:ARG:HG2	2.30	0.46
32:2a:620:C:H2'	32:2a:621:A:O4'	2.15	0.46
32:2a:1006:C:H2'	32:2a:1007:C:O4'	2.16	0.46
54:2w:112:ARG:CZ	54:2w:157:LYS:HD2	2.45	0.46
1:1A:1055:G:H2'	1:1A:1056:G:O4'	2.15	0.46
22:10:10:THR:CG2	22:10:12:ASN:H	2.28	0.46
32:1a:456:C:H2'	32:1a:457:C:C6	2.50	0.46
32:1a:1024:G:H2'	32:1a:1025:U:H5''	1.97	0.46
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.50	0.46
32:1a:1298:C:C4	38:1g:114:ARG:HD2	2.50	0.46
38:1g:14:PRO:HG3	38:1g:21:VAL:HG22	1.97	0.46
54:1w:161:GLU:OE1	54:1w:163:ARG:HD3	2.14	0.46
1:2A:42:G:H2'	1:2A:43:A:O4'	2.15	0.46
1:2A:659:C:H2'	1:2A:660:G:H8	1.79	0.46
1:2A:884:C:N4	1:2A:893:C:N3	2.63	0.46
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.15	0.46
2:2B:14:U:H1'	2:2B:108:U:O2'	2.15	0.46
5:2F:165:ARG:HG2	5:2F:168:ARG:NH2	2.30	0.46
14:2S:23:ARG:NH1	14:2S:85:VAL:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:22:3:LEU:O	24:22:7:ARG:HG3	2.16	0.46
32:2a:1466:C:H2'	32:2a:1467:G:O4'	2.16	0.46
35:2d:65:ARG:HB3	35:2d:65:ARG:HH11	1.81	0.46
1:1A:1043:C:HO2'	1:1A:1048:A:HO2'	1.60	0.46
1:1A:2126:A:C5	1:1A:2163:C:H1'	2.50	0.46
3:1D:108:PRO:HD2	3:1D:111:LEU:HD22	1.97	0.46
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.16	0.46
26:14:49:PHE:HB3	26:14:50:VAL:H	1.55	0.46
32:1a:155:C:H2'	32:1a:156:G:C8	2.50	0.46
32:1a:501:C:H2'	32:1a:502:G:C8	2.50	0.46
32:1a:975:A:H4'	32:1a:976:G:C5'	2.40	0.46
32:1a:1149:C:H2'	32:1a:1150:U:O4'	2.15	0.46
39:1h:51:VAL:HG21	39:1h:60:ARG:HB2	1.97	0.46
41:1j:70:ARG:HA	41:1j:70:ARG:HD3	1.71	0.46
50:1s:36:ARG:HB3	50:1s:72:GLY:CA	2.45	0.46
54:1w:314:ASP:OD2	54:1w:339:LEU:HD11	2.15	0.46
1:2A:632:A:H2'	1:2A:633:A:C8	2.50	0.46
1:2A:1279:G:H4'	13:2R:31:HIS:CD2	2.50	0.46
1:2A:2128:C:H42	1:2A:2160:G:H1	1.64	0.46
7:2H:15:VAL:HG12	7:2H:27:LYS:O	2.15	0.46
8:2I:2:LYS:HG2	8:2I:20:ASP:OD1	2.16	0.46
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.97	0.46
13:2R:54:LEU:HB3	13:2R:62:ALA:HB1	1.98	0.46
32:2a:504:C:OP1	60:2a:1810:HOH:O	2.20	0.46
32:2a:1157:A:H5'	32:2a:1158:C:C6	2.50	0.46
32:2a:1277:C:H1'	32:2a:1279:A:C8	2.50	0.46
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.51	0.46
41:2j:27:ALA:HA	41:2j:81:THR:OG1	2.15	0.46
1:1A:881:G:H2'	1:1A:882:G:O4'	2.16	0.46
1:1A:1101:U:H2'	1:1A:1102:C:C5	2.50	0.46
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.50	0.46
1:1A:2127:G:H21	1:1A:2173:A:H1'	1.81	0.46
3:1D:206:LEU:HD23	3:1D:206:LEU:HA	1.75	0.46
35:1d:146:ILE:H	35:1d:146:ILE:HD12	1.80	0.46
44:1m:87:TYR:O	44:1m:91:ARG:HG3	2.16	0.46
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.13	0.46
1:2A:228:A:O2'	1:2A:229:A:H4'	2.15	0.46
2:2B:66:A:N6	2:2B:109:C:H5'	2.26	0.46
2:2B:75:G:H21	21:2Z:85:HIS:CE1	2.33	0.46
6:2G:121:ASN:O	6:2G:131:TYR:OH	2.29	0.46
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2T:13:ARG:H	15:2T:13:ARG:HG3	1.44	0.46
21:2Z:146:ILE:HA	21:2Z:147:GLY:HA2	1.70	0.46
33:2b:163:PHE:HA	33:2b:185:ILE:O	2.15	0.46
35:2d:191:ARG:HE	35:2d:200:GLU:CD	2.23	0.46
38:2g:27:ILE:HA	38:2g:30:ILE:HD12	1.97	0.46
42:2k:58:PRO:HB3	42:2k:93:GLN:HG2	1.97	0.46
1:1A:284:U:H2'	1:1A:285:C:H6	1.80	0.46
1:1A:865:C:N3	1:1A:908:C:N4	2.64	0.46
1:1A:947:G:OP2	60:1A:4161:HOH:O	2.21	0.46
1:1A:1138:G:N3	9:1N:106:MET:HE2	2.31	0.46
1:1A:1300:U:H4'	1:1A:1301:A:H5'	1.98	0.46
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.15	0.46
5:1F:52:LYS:HD3	5:1F:56:GLU:O	2.14	0.46
30:18:62:LEU:HB3	30:18:65:GLU:HG3	1.96	0.46
32:1a:638:G:H2'	32:1a:639:G:O4'	2.15	0.46
1:2A:588:U:H2'	1:2A:589:C:C6	2.50	0.46
1:2A:1539:G:H2'	1:2A:1540:U:O4'	2.16	0.46
1:2A:2123:G:H2'	1:2A:2124:G:C8	2.51	0.46
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.51	0.46
1:2A:2536:G:H2'	1:2A:2537:U:H6	1.81	0.46
5:2F:23:ASP:O	5:2F:24:LEU:HD23	2.16	0.46
6:2G:108:ASN:HA	26:24:37:SER:HB2	1.96	0.46
21:2Z:144:LEU:HD23	21:2Z:144:LEU:HA	1.71	0.46
32:2a:45:U:H2'	32:2a:46:G:C8	2.50	0.46
32:2a:370:C:H2'	32:2a:371:G:C8	2.50	0.46
32:2a:433:C:H2'	32:2a:434:U:H6	1.80	0.46
32:2a:1158:C:N4	32:2a:1160:G:N3	2.64	0.46
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.51	0.46
32:2a:1271:G:N2	32:2a:1272:G:C8	2.83	0.46
45:2n:37:PHE:CE1	45:2n:53:LEU:HD13	2.50	0.46
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.50	0.46
33:1b:132:LYS:O	33:1b:136:VAL:HG13	2.15	0.46
35:1d:22:LYS:HG2	59:1d:302:SF4:S4	2.56	0.46
35:1d:88:VAL:O	35:1d:92:VAL:HG23	2.15	0.46
1:2A:793:A:OP2	1:2A:2071:A:O2'	2.30	0.46
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.50	0.46
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.15	0.46
60:2A:3954:HOH:O	11:2P:37:GLY:HA3	2.14	0.46
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.15	0.46
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.48	0.46
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:24:14:ILE:HA	26:24:31:ILE:O	2.15	0.46
32:2a:90:U:H2'	32:2a:91:C:C6	2.49	0.46
32:2a:977:A:O3'	32:2a:980:C:N4	2.49	0.46
42:2k:48:ILE:HG12	42:2k:63:LEU:HB3	1.97	0.46
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	1.97	0.46
1:1A:1091:G:H2'	1:1A:1092:C:C6	2.51	0.46
1:1A:2127:G:N2	1:1A:2173:A:H1'	2.30	0.46
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.31	0.46
1:1A:2507:C:O4'	54:1w:233:ASN:HB3	2.16	0.46
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.50	0.46
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.43	0.46
21:1Z:146:ILE:N	21:1Z:148:ASP:H	2.13	0.46
32:1a:196:A:N3	32:1a:222:U:H1'	2.30	0.46
32:1a:364:A:H8	32:1a:364:A:OP2	1.98	0.46
32:1a:1041:A:H2'	32:1a:1042:G:O4'	2.15	0.46
32:1a:1179:A:H4'	40:1i:103:THR:HA	1.98	0.46
33:1b:133:LYS:O	33:1b:136:VAL:HG22	2.15	0.46
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.97	0.46
44:1m:30:ALA:O	44:1m:34:LEU:HG	2.15	0.46
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.50	0.46
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.31	0.46
3:2D:47:GLY:O	60:2D:402:HOH:O	2.21	0.46
3:2D:206:LEU:O	3:2D:211:ARG:HD3	2.16	0.46
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.80	0.46
14:2S:62:LYS:HB3	14:2S:97:ARG:NE	2.31	0.46
32:2a:192:U:H2'	32:2a:193:C:H6	1.80	0.46
32:2a:957:U:H2'	32:2a:959:A:OP2	2.16	0.46
32:2a:1228:C:N4	44:2m:104:ARG:O	2.47	0.46
32:2a:1412:C:H2'	32:2a:1413:A:H8	1.80	0.46
33:2b:71:VAL:HG23	33:2b:164:VAL:HA	1.97	0.46
33:2b:97:TRP:CH2	33:2b:173:ALA:HA	2.51	0.46
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	1.96	0.46
35:2d:92:VAL:O	35:2d:96:LEU:HG	2.16	0.46
35:2d:159:ARG:O	35:2d:163:GLU:N	2.46	0.46
50:2s:39:THR:OG1	50:2s:70:LYS:NZ	2.49	0.46
54:2w:279:ALA:O	54:2w:283:GLU:HB2	2.15	0.46
55:2x:67:C:H2'	55:2x:68:G:C8	2.51	0.46
1:1A:948:G:H5'	60:1A:4640:HOH:O	2.14	0.46
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.81	0.46
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.96	0.46
20:1Y:7:VAL:HG11	20:1Y:72:VAL:HG23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1058:G:H5''	34:1c:199:LYS:HE3	1.98	0.46
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.31	0.46
38:1g:12:LEU:HD12	38:1g:21:VAL:HG12	1.98	0.46
1:2A:1515:G:H2'	1:2A:1516:C:C6	2.51	0.46
1:2A:2127:G:N1	1:2A:2161:C:C5	2.83	0.46
1:2A:2270:G:H2'	1:2A:2271:G:O4'	2.16	0.46
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.13	0.46
7:2H:12:PRO:HD2	7:2H:15:VAL:HG21	1.98	0.46
10:2O:70:LYS:HB3	10:2O:70:LYS:HE2	1.70	0.46
34:2c:156:ARG:NH1	34:2c:193:TYR:O	2.48	0.46
37:2f:45:LEU:O	37:2f:46:ARG:HG3	2.16	0.46
38:2g:78:ARG:HH21	38:2g:79:ARG:HH11	1.64	0.46
44:2m:106:ASN:HB2	44:2m:107:ALA:H	1.50	0.46
1:1A:55:G:O2'	1:1A:127:A:N1	2.45	0.46
1:1A:1364:G:P	23:11:3:LYS:HG3	2.56	0.46
1:1A:1957:C:H2'	1:1A:1958:C:C6	2.51	0.46
18:1W:71:VAL:HA	18:1W:107:LEU:HD23	1.98	0.46
32:1a:222:U:H2'	32:1a:223:U:C6	2.51	0.46
32:1a:1268:A:O2'	52:1u:19:GLY:HA2	2.16	0.46
33:1b:51:LEU:HD22	33:1b:55:PHE:HE2	1.81	0.46
34:1c:8:ILE:C	34:1c:10:PHE:H	2.22	0.46
40:1i:23:ASN:ND2	40:1i:60:ASP:OD2	2.49	0.46
1:2A:68:G:H2'	1:2A:69:C:O4'	2.16	0.46
1:2A:2461:C:H2'	1:2A:2462:U:H6	1.80	0.46
6:2G:82:LEU:HA	6:2G:86:MET:SD	2.56	0.46
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.97	0.46
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.16	0.46
32:2a:1235:U:O2'	32:2a:1305:G:O5'	2.33	0.46
32:2a:1360:A:H8	32:2a:1360:A:OP1	1.99	0.46
32:2a:1507:A:OP2	53:2v:13:A:N6	2.45	0.46
48:2q:27:PHE:CE1	48:2q:36:ILE:HD11	2.51	0.46
54:2w:303:ARG:HH21	54:2w:316:ARG:HH22	1.64	0.46
1:1A:1790:C:H5''	1:1A:1791:A:OP1	2.16	0.46
8:1I:135:GLU:O	8:1I:137:PRO:HD3	2.15	0.46
26:14:56:VAL:O	26:14:60:GLN:HB2	2.16	0.46
32:1a:106:C:O2'	32:1a:379:C:H5''	2.16	0.46
32:1a:414:A:H2'	32:1a:415:A:C8	2.51	0.46
32:1a:1530:G:H4'	32:1a:1530:G:OP1	2.15	0.46
54:1w:196:THR:HG21	54:1w:296:GLY:O	2.16	0.46
54:1w:307:PHE:CD1	54:1w:324:LEU:HD21	2.51	0.46
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:34:TRP:CZ3	11:2P:8:PRO:HB3	2.50	0.46
7:2H:42:ARG:HG2	7:2H:44:VAL:HG13	1.98	0.46
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.98	0.46
32:2a:130:A:H5'	48:2q:63:ARG:HH21	1.80	0.46
32:2a:131:C:H2'	32:2a:132:C:H6	1.81	0.46
32:2a:358:U:H2'	32:2a:359:U:C6	2.51	0.46
32:2a:1029:C:H42	32:2a:1032:G:H1	1.64	0.46
33:2b:133:LYS:O	33:2b:137:ARG:HG2	2.15	0.46
37:2f:20:ALA:HA	37:2f:23:LYS:HG3	1.97	0.46
45:2n:39:LEU:HD22	45:2n:43:CYS:HB3	1.98	0.46
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.97	0.46
1:1A:1359:A:C2	1:1A:1372:U:O4	2.69	0.45
1:1A:2047:U:O2'	1:1A:2823:A:N1	2.48	0.45
1:1A:2138:C:N3	1:1A:2153:G:N2	2.52	0.45
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.49	0.45
12:1Q:115:MET:HE3	12:1Q:115:MET:HB3	1.74	0.45
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.45	0.45
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.62	0.45
21:1Z:152:ALA:HA	21:1Z:155:LEU:HD22	1.98	0.45
23:11:71:TYR:O	23:11:74:VAL:HG22	2.16	0.45
32:1a:435:C:H2'	32:1a:436:C:C6	2.52	0.45
40:1i:22:GLY:N	40:1i:58:HIS:O	2.40	0.45
1:2A:601:C:OP1	5:2F:108:LYS:NZ	2.46	0.45
1:2A:784:A:C8	1:2A:792:G:C5	3.04	0.45
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.79	0.45
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.47	0.45
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.31	0.45
6:2G:56:ALA:HB2	6:2G:153:ARG:HE	1.81	0.45
32:2a:34:C:H2'	32:2a:35:G:C8	2.50	0.45
32:2a:1137:C:O2	32:2a:1138:G:N2	2.49	0.45
39:2h:5:PRO:HA	39:2h:8:ASP:HB3	1.98	0.45
51:2t:58:LYS:HD2	51:2t:58:LYS:HA	1.71	0.45
1:1A:1372:U:H2'	1:1A:1373:A:O4'	2.16	0.45
1:1A:2436:G:O2'	60:1A:4156:HOH:O	2.20	0.45
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	1.98	0.45
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.52	0.45
28:16:38:LYS:HB3	28:16:38:LYS:HE3	1.78	0.45
32:1a:78:G:N2	32:1a:91:C:N3	2.65	0.45
32:1a:1025:U:O2	32:1a:1036:G:C6	2.69	0.45
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.49	0.45
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:110:GLN:HA	33:1b:113:HIS:CD2	2.52	0.45
34:1c:132:ARG:HG2	34:1c:136:GLN:NE2	2.32	0.45
48:1q:24:GLU:HG2	48:1q:39:SER:HB3	1.98	0.45
1:2A:455:C:N3	1:2A:472:A:H2'	2.31	0.45
1:2A:852:G:H2'	1:2A:853:G:C8	2.51	0.45
1:2A:1011:G:H5''	16:2U:77:SER:OG	2.16	0.45
1:2A:1818:U:O4	3:2D:154:LYS:HD2	2.16	0.45
1:2A:2626:C:H2'	1:2A:2627:G:O4'	2.17	0.45
2:2B:72:G:O2'	2:2B:105:A:N6	2.50	0.45
7:2H:102:ALA:HA	7:2H:117:PRO:HD3	1.98	0.45
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.99	0.45
32:2a:1030(D):A:H8	32:2a:1031:G:C8	2.33	0.45
32:2a:1176:A:H2'	32:2a:1177:G:H8	1.80	0.45
32:2a:1469:G:H2'	32:2a:1470:G:C8	2.51	0.45
48:2q:6:LEU:HD22	48:2q:23:VAL:HG11	1.99	0.45
55:2x:21:H2U:OP2	55:2x:21:H2U:H4'	2.13	0.45
55:2x:43:U:H2'	55:2x:44:C:H6	1.81	0.45
1:1A:620:G:N3	1:1A:620:G:H5'	2.30	0.45
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.51	0.45
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.45	0.45
1:1A:1412:A:H2'	1:1A:1413:G:C8	2.51	0.45
6:1G:111:LEU:HB3	6:1G:117:PHE:CE2	2.51	0.45
32:1a:113:G:H2'	32:1a:114:U:C6	2.51	0.45
32:1a:601:C:H2'	32:1a:602:A:H8	1.78	0.45
33:1b:16:HIS:HD2	33:1b:18:GLY:H	1.65	0.45
35:1d:98:GLU:HA	35:1d:103:ASN:HD22	1.81	0.45
35:1d:122:ARG:HD2	35:1d:122:ARG:HA	1.56	0.45
1:2A:639:U:H2'	1:2A:640:C:C6	2.51	0.45
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.33	0.45
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.50	0.45
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.52	0.45
1:2A:2176:A:H2'	1:2A:2177:C:H6	1.82	0.45
1:2A:2788:C:N3	1:2A:2789:C:N4	2.64	0.45
2:2B:8:U:O3'	14:2S:25:ARG:NH2	2.49	0.45
11:2P:124:LYS:HA	11:2P:144:GLU:O	2.16	0.45
22:20:70:GLN:HG2	22:20:72:ARG:HG3	1.98	0.45
26:24:57:GLU:CB	26:24:58:ARG:HA	2.46	0.45
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.49	0.45
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.52	0.45
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.26	0.45
42:2k:43:SER:HA	42:2k:47:VAL:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:86:C:H4'	1:1A:104:U:H1'	1.98	0.45
1:1A:748:G:C8	18:1W:89:ALA:HB1	2.51	0.45
1:1A:2314:C:H2'	1:1A:2315:G:C8	2.50	0.45
1:1A:2703:C:H2'	1:1A:2704:C:H6	1.81	0.45
5:1F:195:ASP:HB2	5:1F:198:ALA:H	1.82	0.45
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.64	0.45
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	1.99	0.45
21:1Z:54:HIS:ND1	21:1Z:101:PRO:HG3	2.32	0.45
26:14:49:PHE:HD1	26:14:49:PHE:HA	1.68	0.45
33:1b:62:ALA:C	33:1b:64:ARG:H	2.23	0.45
34:1c:28:GLN:HE21	34:1c:28:GLN:HB3	1.67	0.45
35:1d:19:LEU:O	35:1d:21:LEU:N	2.49	0.45
37:1f:19:LEU:HD21	37:1f:59:TYR:CZ	2.51	0.45
38:1g:51:GLN:NE2	38:1g:55:GLY:O	2.38	0.45
50:1s:41:VAL:HG23	50:1s:43:GLU:N	2.25	0.45
53:1v:20:A:N6	54:1w:186:THR:OG1	2.49	0.45
1:2A:601:C:O2'	1:2A:605:C:H5''	2.17	0.45
1:2A:1268:A:C2	1:2A:2013:A:C4	3.05	0.45
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.16	0.45
1:2A:2097:C:H2'	1:2A:2098:U:C6	2.50	0.45
2:2B:119:G:H5'	2:2B:120:A:OP2	2.17	0.45
4:2E:89:ASP:OD1	4:2E:89:ASP:N	2.40	0.45
12:2Q:54:MET:HE1	12:2Q:104:PHE:HB3	1.99	0.45
16:2U:34:LYS:HA	16:2U:34:LYS:HD2	1.62	0.45
32:2a:946:A:H2'	32:2a:947:G:H8	1.81	0.45
33:2b:74:LYS:NZ	33:2b:205:ASP:O	2.35	0.45
34:2c:44:GLU:HA	34:2c:52:LEU:HD23	1.99	0.45
36:2e:93:PRO:HG2	39:2h:105:ARG:NH1	2.31	0.45
37:2f:26:ILE:O	37:2f:30:LEU:HG	2.17	0.45
39:2h:36:LEU:HA	39:2h:39:LEU:HD12	1.98	0.45
39:2h:51:VAL:HG21	39:2h:60:ARG:HB2	1.99	0.45
41:2j:37:PRO:HA	41:2j:72:VAL:HG13	1.98	0.45
54:2w:311:ARG:HB2	54:2w:322:HIS:CE1	2.51	0.45
21:1Z:79:ARG:HD2	21:1Z:80:ARG:HH12	1.81	0.45
21:1Z:91:LEU:HD22	21:1Z:130:PRO:HG3	1.99	0.45
32:1a:1202:G:H2'	32:1a:1203:C:O4'	2.16	0.45
39:1h:82:HIS:O	39:1h:137:VAL:HA	2.17	0.45
52:1u:6:ARG:HG2	52:1u:15:ARG:HD2	1.99	0.45
55:1x:13:A:H2'	55:1x:14:A:H5''	1.98	0.45
1:2A:615:G:OP1	5:2F:40:GLN:NE2	2.45	0.45
1:2A:1012:U:H5	9:2N:28:THR:HG21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1773:A:OP2	60:2A:3970:HOH:O	2.21	0.45
1:2A:1877:A:C5	1:2A:1878:G:H1'	2.51	0.45
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.52	0.45
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.98	0.45
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.97	0.45
54:2w:194:THR:HB	54:2w:298:ARG:HD3	1.99	0.45
1:1A:657:U:H2'	1:1A:658:C:C6	2.51	0.45
1:1A:784:A:H5'	1:1A:785:G:OP1	2.17	0.45
12:1Q:7:MET:HE3	12:1Q:7:MET:HB3	1.63	0.45
26:14:15:ILE:HD13	26:14:21:VAL:HB	1.98	0.45
32:1a:452:A:H4'	47:1p:72:ARG:HH21	1.80	0.45
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.51	0.45
38:1g:100:ALA:O	38:1g:104:LEU:HG	2.17	0.45
54:1w:132:LEU:HD22	54:1w:142:THR:HG21	1.99	0.45
1:2A:1815:A:P	3:2D:54:ARG:HH22	2.39	0.45
2:2B:89:G:H2'	2:2B:90:A:C8	2.52	0.45
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.99	0.45
7:2H:7:LEU:HD12	7:2H:7:LEU:HA	1.87	0.45
32:2a:109:A:C6	32:2a:326:G:C6	3.05	0.45
32:2a:573:A:N3	32:2a:883:C:O2'	2.46	0.45
32:2a:1181:G:H1'	32:2a:1182:G:C5	2.52	0.45
33:2b:115:LEU:HB2	33:2b:145:LEU:HD13	1.99	0.45
44:2m:14:ARG:HB3	44:2m:41:PRO:O	2.16	0.45
48:2q:10:VAL:HA	48:2q:20:THR:O	2.17	0.45
1:1A:455:C:N3	1:1A:472:A:H2'	2.32	0.45
1:1A:624:C:OP1	60:1A:4162:HOH:O	2.21	0.45
1:1A:875:G:H1	1:1A:902:C:H42	1.63	0.45
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.82	0.45
1:1A:2161:C:O2'	1:1A:2162:G:H8	1.98	0.45
1:1A:2390:U:P	30:18:35:GLN:HE22	2.40	0.45
1:1A:2848:G:O6	60:1A:4157:HOH:O	2.20	0.45
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.39	0.45
7:1H:3:ARG:CG	7:1H:6:ARG:HG2	2.47	0.45
17:1V:28:GLU:HG3	17:1V:29:PRO:HD2	1.98	0.45
32:1a:119:A:H4'	32:1a:120:A:C8	2.52	0.45
32:1a:1466:C:H2'	32:1a:1467:G:O4'	2.16	0.45
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.82	0.45
47:1p:26:ARG:HG3	47:1p:27:LYS:O	2.17	0.45
1:2A:1405:U:H2'	1:2A:1406:U:H6	1.82	0.45
1:2A:2206:G:H3'	1:2A:2207:G:N7	2.29	0.45
1:2A:2386:C:H2'	1:2A:2387:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:211:ARG:HG2	3:2D:214:TRP:CE3	2.52	0.45
4:2E:108:SER:HB3	4:2E:165:VAL:HG21	1.99	0.45
9:2N:115:ARG:HG3	9:2N:118:LYS:HE3	1.98	0.45
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.49	0.45
19:2X:94:GLY:N	19:2X:95:LEU:HB2	2.32	0.45
36:2e:102:ALA:O	36:2e:107:ARG:NH2	2.50	0.45
36:2e:145:LYS:O	36:2e:149:GLU:HB2	2.16	0.45
42:2k:29:ILE:HA	42:2k:44:SER:HB3	1.99	0.45
42:2k:82:VAL:HB	42:2k:108:ILE:HD13	1.99	0.45
44:2m:20:THR:HA	44:2m:25:ILE:O	2.16	0.45
50:2s:48:THR:HG22	50:2s:61:TYR:HA	1.99	0.45
1:1A:1799:G:O2'	3:1D:181:GLU:OE2	2.23	0.45
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.17	0.45
2:1B:44:G:OP1	6:1G:98:ARG:NH2	2.47	0.45
6:1G:59:GLU:OE2	6:1G:153:ARG:NH2	2.46	0.45
7:1H:54:ARG:HB3	7:1H:65:HIS:CD2	2.52	0.45
32:1a:34:C:H2'	32:1a:35:G:C8	2.52	0.45
32:1a:538:G:H5''	43:1l:114:LYS:HB2	1.99	0.45
32:1a:625:G:H4'	47:1p:16:HIS:CG	2.52	0.45
32:1a:659:U:H2'	32:1a:660:G:C8	2.52	0.45
32:1a:1264:C:H2'	32:1a:1265:G:H8	1.82	0.45
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.16	0.45
40:1i:50:LEU:O	40:1i:52:ALA:N	2.50	0.45
42:1k:87:THR:O	42:1k:87:THR:OG1	2.26	0.45
54:1w:143:GLU:OE1	54:1w:163:ARG:NH2	2.50	0.45
1:2A:628:G:H5''	30:28:18:ALA:HB2	1.99	0.45
1:2A:1290:C:H2'	1:2A:1291:C:H6	1.82	0.45
2:2B:75:G:H1'	21:2Z:27:VAL:HG11	1.97	0.45
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	1.99	0.45
7:2H:125:VAL:HG22	7:2H:131:VAL:HG22	1.99	0.45
21:2Z:36:LYS:HB2	21:2Z:36:LYS:HE3	1.85	0.45
26:24:26:SER:OG	26:24:27:THR:N	2.50	0.45
29:27:46:VAL:HG13	29:27:48:LYS:NZ	2.32	0.45
34:2c:3:ASN:N	34:2c:3:ASN:OD1	2.50	0.45
40:2i:16:ARG:HB2	40:2i:64:THR:HG23	1.99	0.45
1:1A:1509(A):A:H3'	1:1A:1509(B):A:H8	1.81	0.45
1:1A:1714:G:H1	1:1A:1745(A):C:H42	1.65	0.45
1:1A:2595:G:N7	60:1A:4265:HOH:O	2.36	0.45
5:1F:7:TYR:CD2	5:1F:24:LEU:HB2	2.51	0.45
8:1I:1:MET:N	8:1I:21:VAL:O	2.41	0.45
12:1Q:110:THR:HG23	12:1Q:113:GLN:OE1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:76:CYS:HB2	20:1Y:99:CYS:HB2	1.98	0.45
32:1a:115:G:H4'	32:1a:116:A:O5'	2.16	0.45
44:1m:84:ILE:HD12	50:1s:74:PHE:CZ	2.52	0.45
54:1w:346:ARG:HB3	54:1w:347:GLN:NE2	2.32	0.45
1:2A:743:G:OP1	4:2E:130:GLY:HA2	2.16	0.45
1:2A:2189:U:H2'	1:2A:2190:G:H8	1.82	0.45
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.52	0.45
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.16	0.45
32:2a:1320:C:C1'	50:2s:73:GLU:HG3	2.45	0.45
32:2a:1469:G:H2'	32:2a:1470:G:H8	1.82	0.45
1:1A:513:A:O2'	1:1A:1217:C:OP1	2.33	0.45
1:1A:1762:A:H2'	60:1A:5724:HOH:O	2.16	0.45
30:18:42:ARG:HD2	60:18:203:HOH:O	2.16	0.45
32:1a:1123:A:O2'	41:1j:37:PRO:O	2.28	0.45
42:1k:93:GLN:HA	42:1k:93:GLN:HE21	1.82	0.45
43:1l:119:LYS:HB2	43:1l:120:TYR:CD2	2.52	0.45
1:2A:207:A:H2'	1:2A:208:C:O4'	2.17	0.45
1:2A:784:A:H5'	1:2A:785:G:OP1	2.17	0.45
1:2A:1665:A:H4'	10:2O:67:LYS:HB2	1.99	0.45
1:2A:2641:G:H5''	9:2N:76:SER:HB3	1.99	0.45
7:2H:3:ARG:HG2	7:2H:6:ARG:NE	2.32	0.45
8:2I:75:LEU:HD11	8:2I:105:HIS:ND1	2.32	0.45
32:2a:114:U:H1'	32:2a:353:A:H1'	1.98	0.45
32:2a:806:C:H2'	32:2a:807:A:C8	2.52	0.45
33:2b:98:LEU:HB2	33:2b:101:MET:HG3	1.99	0.45
40:2i:3:GLN:HB3	40:2i:20:ARG:NH2	2.32	0.45
1:1A:871:U:OP1	12:1Q:5:ARG:HG3	2.18	0.44
1:1A:1059:G:OP2	1:1A:1060:U:H5''	2.17	0.44
1:1A:1449:A:H2'	1:1A:1450:G:O4'	2.17	0.44
1:1A:2149:G:H2'	1:1A:2150:U:O4'	2.17	0.44
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.52	0.44
20:1Y:14:LEU:HD12	20:1Y:23:ARG:O	2.17	0.44
25:13:6:VAL:HG12	25:13:54:VAL:HG21	1.98	0.44
32:1a:925:G:H1	32:1a:1391:U:H3	1.65	0.44
32:1a:948:C:OP1	44:1m:108:ARG:N	2.50	0.44
32:1a:1456:G:N2	51:1t:43:LEU:HD21	2.31	0.44
44:1m:4:ILE:HG13	44:1m:57:ARG:HG3	1.99	0.44
48:1q:72:ARG:HE	48:1q:72:ARG:HB2	1.64	0.44
1:2A:856:C:H2'	1:2A:857:C:C6	2.52	0.44
1:2A:2375:G:O2'	1:2A:2377:A:N7	2.38	0.44
1:2A:2697:G:H2'	1:2A:2698:U:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.17	0.44
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.52	0.44
6:2G:36:LYS:NZ	6:2G:95:ARG:HH22	2.14	0.44
9:2N:138:LEU:HD23	9:2N:138:LEU:HA	1.84	0.44
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.32	0.44
21:2Z:163:LEU:HD23	21:2Z:163:LEU:HA	1.77	0.44
26:24:62:ARG:HA	26:24:62:ARG:NE	2.32	0.44
29:27:34:ARG:NH2	29:27:41:ARG:O	2.46	0.44
32:2a:297:G:H4'	32:2a:557:G:H4'	1.99	0.44
32:2a:325:A:H2'	32:2a:326:G:O4'	2.17	0.44
32:2a:1121:U:H2'	32:2a:1122:U:C6	2.52	0.44
32:2a:1265:G:C6	32:2a:1266:G:C5	3.05	0.44
32:2a:1327:C:P	52:2u:12:LYS:HZ1	2.35	0.44
32:2a:1372:U:OP1	40:2i:72:GLY:N	2.49	0.44
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.48	0.44
55:2x:48:G:C4	55:2x:59:C:H1'	2.53	0.44
1:1A:181:A:H5''	29:17:36:GLN:NE2	2.33	0.44
1:1A:1424:G:H2'	1:1A:1425:G:O4'	2.17	0.44
1:1A:2626:C:H2'	1:1A:2627:G:O4'	2.17	0.44
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.98	0.44
32:1a:1114:C:H42	32:1a:1186:G:H1	1.65	0.44
32:1a:1519:MA6:H8	32:1a:1519:MA6:O5'	2.17	0.44
40:1i:15:ALA:HB2	40:1i:65:VAL:HG23	1.99	0.44
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.52	0.44
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.17	0.44
1:2A:2127:G:H2'	1:2A:2128:C:C5	2.52	0.44
1:2A:2153:G:H2'	1:2A:2154:G:H8	1.82	0.44
12:2Q:2:LEU:HD22	12:2Q:69:PHE:CE1	2.53	0.44
13:2R:100:LEU:HD21	13:2R:113:LEU:HD23	1.99	0.44
15:2T:26:ASP:OD1	15:2T:120:ARG:NH2	2.39	0.44
23:21:52:ARG:HG3	23:21:56:GLN:O	2.17	0.44
32:2a:164:U:H2'	32:2a:165:C:H6	1.83	0.44
32:2a:235:C:H2'	32:2a:236:G:H8	1.83	0.44
32:2a:397:A:H3'	32:2a:397:A:N3	2.32	0.44
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.16	0.44
32:2a:1218:C:OP2	45:2n:9:LYS:NZ	2.50	0.44
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.32	0.44
38:2g:146:GLU:OE1	38:2g:149:ARG:HD2	2.17	0.44
44:2m:88:ARG:O	44:2m:92:HIS:ND1	2.50	0.44
54:2w:169:GLY:HA2	54:2w:172:LYS:HE3	1.99	0.44
1:1A:2305:A:N1	6:1G:154:GLY:N	2.54	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2314:C:H2'	1:1A:2315:G:H8	1.83	0.44
5:1F:168:ARG:H	5:1F:168:ARG:HG3	1.46	0.44
6:1G:82:LEU:HD12	6:1G:86:MET:HB2	1.98	0.44
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	1.98	0.44
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.79	0.44
32:1a:181:G:N2	32:1a:183:G:C2	2.85	0.44
32:1a:448:A:H2'	32:1a:449:C:C6	2.52	0.44
32:1a:741:G:H2'	32:1a:742:G:O4'	2.17	0.44
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.52	0.44
33:1b:170:GLU:O	33:1b:174:VAL:HG13	2.18	0.44
34:1c:114:PRO:C	34:1c:118:GLN:HE21	2.25	0.44
35:1d:135:LEU:O	35:1d:137:SER:N	2.49	0.44
41:1j:35:SER:HB3	41:1j:73:ASP:CB	2.42	0.44
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.73	0.44
32:2a:375:U:H5''	47:2p:6:LEU:HD22	2.00	0.44
34:2c:21:ARG:HH22	34:2c:56:ASP:CG	2.26	0.44
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.52	0.44
41:2j:74:ILE:HD12	41:2j:74:ILE:HA	1.68	0.44
51:2t:64:ASP:OD2	51:2t:81:LYS:NZ	2.42	0.44
1:1A:184:C:H2'	1:1A:185:U:H6	1.80	0.44
1:1A:652(D):C:H2'	1:1A:652(E):G:O4'	2.17	0.44
1:1A:1002:G:H2'	1:1A:1003:G:O4'	2.17	0.44
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.53	0.44
1:1A:2203:U:O4'	3:1D:151:LYS:HE2	2.16	0.44
1:1A:2428:G:H5''	1:1A:2429:G:OP1	2.17	0.44
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	1.99	0.44
13:1R:67:LEU:HG	13:1R:76:VAL:HG21	2.00	0.44
21:1Z:16:SER:HB2	21:1Z:20:ARG:HH21	1.81	0.44
32:1a:444:C:H2'	32:1a:445:G:C8	2.52	0.44
32:1a:977:A:H1'	32:1a:982:U:O4	2.17	0.44
32:1a:1017:G:H2'	32:1a:1018:C:C6	2.52	0.44
34:1c:71:ALA:HB2	34:1c:109:PRO:HB3	2.00	0.44
35:1d:9:CYS:O	35:1d:13:ARG:HG3	2.17	0.44
35:1d:57:ARG:HH22	36:1e:107:ARG:HD3	1.83	0.44
39:1h:124:ALA:HB1	39:1h:129:VAL:O	2.17	0.44
41:1j:27:ALA:HA	41:1j:81:THR:HG21	1.99	0.44
43:1l:23:LYS:HE2	43:1l:23:LYS:HB3	1.85	0.44
54:1w:125:ARG:HG2	54:1w:155:PHE:CD2	2.53	0.44
54:1w:285:LEU:HG	54:1w:289:ARG:NH1	2.31	0.44
1:2A:876:C:H2'	1:2A:877:U:O4'	2.17	0.44
1:2A:2207:G:H2'	1:2A:2208:A:C2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:109:VAL:HG22	12:2Q:113:GLN:OE1	2.18	0.44
27:25:40:LYS:HD3	27:25:46:CYS:HB2	1.98	0.44
32:2a:189(A):C:H2'	32:2a:189(B):C:H6	1.82	0.44
32:2a:526:C:OP2	43:2l:91:LYS:HE3	2.17	0.44
32:2a:1004:A:N6	32:2a:1037:C:O2	2.51	0.44
32:2a:1123:A:H4'	41:2j:36:GLY:HA3	2.00	0.44
38:2g:97:GLN:NE2	38:2g:101:LEU:HD11	2.31	0.44
38:2g:111:ARG:NH2	38:2g:113:GLU:OE2	2.31	0.44
42:2k:22:HIS:O	42:2k:28:THR:HA	2.17	0.44
54:2w:235:THR:HG22	54:2w:237:SER:HB3	1.99	0.44
1:1A:1778:U:OP2	60:1A:4163:HOH:O	2.21	0.44
1:1A:2627:G:O2'	1:1A:2781:A:N1	2.33	0.44
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.52	0.44
23:11:82:LEU:HA	23:11:85:LEU:HD12	1.99	0.44
32:1a:659:U:H2'	32:1a:660:G:H8	1.82	0.44
32:1a:1329:A:H5''	44:1m:26:GLY:H	1.82	0.44
35:1d:135:LEU:C	35:1d:137:SER:H	2.26	0.44
47:1p:22:THR:HA	47:1p:33:ILE:HG13	1.98	0.44
47:1p:74:LEU:O	47:1p:79:VAL:HG22	2.18	0.44
51:1t:8:ARG:HD3	51:1t:8:ARG:HA	1.72	0.44
1:2A:271(F):C:H2'	1:2A:271(G):C:O4'	2.18	0.44
1:2A:686:G:H21	1:2A:788:A:H61	1.65	0.44
1:2A:724:U:H2'	1:2A:725:G:O4'	2.17	0.44
32:2a:664:G:P	49:2r:64:ARG:HH21	2.41	0.44
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.17	0.44
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.52	0.44
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.32	0.44
48:2q:5:VAL:HA	48:2q:59:ILE:O	2.17	0.44
1:1A:1263:U:H2'	1:1A:1264:G:C8	2.53	0.44
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.50	0.44
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.15	0.44
21:1Z:69:THR:HA	21:1Z:89:PHE:O	2.18	0.44
26:14:61:ARG:HH12	50:1s:41:VAL:HA	1.83	0.44
32:1a:147:G:H1	32:1a:175:C:H42	1.64	0.44
32:1a:390:C:H2'	32:1a:391:G:C8	2.52	0.44
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.53	0.44
44:1m:115:LYS:O	44:1m:117:VAL:HG13	2.17	0.44
1:2A:79:G:O2'	1:2A:346:A:N3	2.45	0.44
1:2A:1269:A:H2'	1:2A:1270:C:C6	2.52	0.44
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.28	0.44
1:2A:2111:C:N4	1:2A:2144:U:O2'	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.18	0.44
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.18	0.44
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.53	0.44
4:2E:104:VAL:HA	4:2E:197:ILE:O	2.18	0.44
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.17	0.44
8:2I:3:VAL:O	8:2I:18:VAL:HA	2.17	0.44
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.98	0.44
21:2Z:157:LEU:HG	21:2Z:161:VAL:HG22	1.99	0.44
32:2a:524:G:H2'	32:2a:525:C:C6	2.52	0.44
32:2a:936:C:H2'	32:2a:937:A:O4'	2.18	0.44
33:2b:147:LYS:HB3	33:2b:147:LYS:HE2	1.83	0.44
38:2g:97:GLN:HE21	38:2g:101:LEU:HD11	1.82	0.44
40:2i:19:LEU:HD23	40:2i:61:ALA:HB2	1.99	0.44
1:1A:379:G:N2	23:11:42:GLN:OE1	2.36	0.44
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.33	0.44
2:1B:113:G:H2'	2:1B:114:C:C6	2.53	0.44
4:1E:181:LEU:HD21	15:1T:6:LEU:HD12	2.00	0.44
7:1H:98:LEU:HG	7:1H:125:VAL:HG23	1.99	0.44
17:1V:43:GLU:OE1	17:1V:43:GLU:N	2.50	0.44
17:1V:81:TYR:C	17:1V:82:ARG:HD2	2.43	0.44
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.52	0.44
32:1a:19:C:H2'	32:1a:20:U:H6	1.83	0.44
32:1a:407:G:H5''	35:1d:115:ARG:HB3	1.99	0.44
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.17	0.44
34:1c:131:ARG:HA	34:1c:134:ILE:HD12	1.99	0.44
42:1k:31:THR:HG22	42:1k:42:TRP:CB	2.48	0.44
43:1l:60:LEU:HB2	43:1l:64:TYR:O	2.18	0.44
44:1m:70:LEU:HD23	44:1m:70:LEU:HA	1.82	0.44
1:2A:453:C:O2	1:2A:457:A:O2'	2.34	0.44
1:2A:1263:U:C4	1:2A:1264:G:C6	3.06	0.44
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.45	0.44
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.53	0.44
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.15	0.44
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.52	0.44
6:2G:73:ALA:HB3	6:2G:85:GLY:H	1.83	0.44
9:2N:61:ARG:HD3	9:2N:61:ARG:HA	1.58	0.44
21:2Z:95:PRO:HA	21:2Z:129:SER:HA	2.00	0.44
26:24:41:PRO:HG3	26:24:49:PHE:CE1	2.53	0.44
32:2a:67:C:H2'	32:2a:68:G:H8	1.82	0.44
32:2a:298:A:H8	32:2a:298:A:OP1	2.00	0.44
32:2a:975:A:N1	41:2j:48:THR:HB	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:990:C:H2'	32:2a:991:U:O4'	2.16	0.44
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.52	0.44
33:2b:163:PHE:HD1	33:2b:185:ILE:HG13	1.82	0.44
35:2d:59:ARG:NH2	35:2d:62:GLN:HG3	2.33	0.44
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.52	0.44
39:2h:32:LYS:O	39:2h:36:LEU:HG	2.18	0.44
50:2s:14:HIS:CG	50:2s:15:LEU:N	2.86	0.44
50:2s:27:GLU:HA	50:2s:28:LYS:HA	1.85	0.44
1:1A:1093:G:H1'	1:1A:1098:A:N6	2.32	0.44
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.53	0.44
8:1I:140:LEU:HD23	8:1I:140:LEU:HA	1.67	0.44
17:1V:22:VAL:HG23	17:1V:23:GLU:O	2.18	0.44
21:1Z:99:TYR:HB3	21:1Z:123:ASP:HB2	1.99	0.44
26:14:68:ARG:HH21	26:14:68:ARG:HA	1.82	0.44
32:1a:453:A:H4'	47:1p:72:ARG:HB2	2.00	0.44
32:1a:503:C:H2'	32:1a:504:C:H6	1.82	0.44
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.40	0.44
32:1a:1368:G:C2'	32:1a:1369:C:H5'	2.48	0.44
1:2A:10:G:H2'	1:2A:11:G:C8	2.52	0.44
1:2A:857:C:H4'	22:20:23:VAL:HG21	2.00	0.44
1:2A:2336:A:H61	22:20:43:THR:CG2	2.30	0.44
3:2D:70:TRP:HB3	3:2D:190:TYR:CE2	2.53	0.44
5:2F:7:TYR:CD2	5:2F:24:LEU:HB2	2.53	0.44
5:2F:158:THR:OG1	5:2F:159:GLY:N	2.51	0.44
12:2Q:16:ARG:HG2	12:2Q:18:LYS:HE3	2.00	0.44
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	2.00	0.44
22:20:12:ASN:HA	22:20:14:ARG:HH21	1.83	0.44
32:2a:417:C:H2'	32:2a:418:C:C6	2.53	0.44
32:2a:839:U:H3'	32:2a:840:C:H5'	1.99	0.44
32:2a:918:A:H2'	32:2a:919:A:C8	2.53	0.44
32:2a:1452:C:H5'	32:2a:1457:G:C4	2.53	0.44
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	2.00	0.44
33:2b:109:SER:O	33:2b:111:ARG:N	2.51	0.44
37:2f:45:LEU:HD12	37:2f:45:LEU:H	1.83	0.44
54:2w:175:SER:OG	54:2w:292:GLN:HB3	2.18	0.44
1:1A:228:A:H8	1:1A:229:A:H5'	1.82	0.44
1:1A:385:C:O2'	1:1A:388:G:N2	2.50	0.44
1:1A:582:G:H2'	1:1A:583:G:C8	2.53	0.44
1:1A:1489:U:HO2'	1:1A:1490:A:H8	1.65	0.44
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.53	0.44
2:1B:12:C:H2'	22:10:73:GLY:HA3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:86:ARG:HB3	20:1Y:98:VAL:HG23	2.00	0.44
32:1a:201:C:H42	32:1a:216:G:H1	1.66	0.44
32:1a:221:C:H2'	32:1a:222:U:C6	2.52	0.44
32:1a:226:G:H2'	32:1a:227:G:C8	2.53	0.44
32:1a:473:G:H2'	32:1a:474:G:C8	2.53	0.44
32:1a:656:C:O2'	46:1o:28:GLN:OE1	2.20	0.44
32:1a:688:G:H2'	32:1a:689:C:C6	2.52	0.44
32:1a:865:A:C2	32:1a:918:A:H4'	2.53	0.44
32:1a:1332:A:H2'	32:1a:1333:A:C8	2.53	0.44
32:1a:1340:A:O2'	55:1x:31:A:O3'	2.35	0.44
35:1d:8:VAL:HG13	59:1d:302:SF4:S4	2.58	0.44
1:2A:27:G:O2'	1:2A:28:A:OP2	2.33	0.44
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.33	0.44
1:2A:2680:C:H1'	4:2E:187:ALA:HB1	1.99	0.44
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.29	0.44
6:2G:11:TYR:HA	6:2G:15:VAL:CG1	2.48	0.44
18:2W:30:GLU:O	18:2W:34:ASN:ND2	2.51	0.44
19:2X:44:GLU:HG2	19:2X:49:VAL:O	2.18	0.44
32:2a:203:U:H2'	32:2a:203:U:OP2	2.17	0.44
32:2a:324:G:N2	32:2a:327:A:C8	2.86	0.44
32:2a:875:C:H1'	39:2h:15:ASN:HD21	1.83	0.44
32:2a:1216:G:H5''	45:2n:5:ALA:HB2	1.99	0.44
32:2a:1264:C:C4	32:2a:1272:G:O6	2.71	0.44
32:2a:1309:G:C6	32:2a:1329:A:C6	3.06	0.44
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	2.00	0.44
40:2i:111:ARG:O	40:2i:113:LYS:HD2	2.17	0.44
45:2n:9:LYS:HE3	45:2n:9:LYS:HB2	1.86	0.44
50:2s:36:ARG:HA	50:2s:71:LEU:HB3	2.00	0.44
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.48	0.43
1:1A:1056:G:C5'	1:1A:1086:A:H8	2.30	0.43
1:1A:1071:G:OP1	1:1A:1071:G:H3'	2.18	0.43
1:1A:2203:U:O2'	1:1A:2205:C:H5'	2.18	0.43
1:1A:2319:G:H22	14:1S:3:ARG:NE	2.16	0.43
32:1a:363:A:C5	43:1l:31:PRO:HD2	2.53	0.43
32:1a:536:C:N4	32:1a:537:G:O6	2.50	0.43
32:1a:1035:A:H2'	32:1a:1036:G:N2	2.23	0.43
32:1a:1044:A:C5	32:1a:1045:C:H1'	2.53	0.43
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.18	0.43
35:1d:50:ARG:HH22	36:1e:9:LYS:NZ	2.16	0.43
35:1d:101:LEU:HG	35:1d:121:VAL:HG21	2.00	0.43
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.88	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:721:C:H2'	1:2A:722:A:C8	2.52	0.43
1:2A:1157:G:O6	60:2A:3971:HOH:O	2.21	0.43
1:2A:2536:G:H2'	1:2A:2537:U:C6	2.53	0.43
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	1.99	0.43
6:2G:105:LYS:O	6:2G:109:VAL:HG13	2.18	0.43
8:2I:104:GLN:HB3	8:2I:105:HIS:CD2	2.52	0.43
22:20:31:VAL:HB	22:20:35:ASN:HB2	2.00	0.43
25:23:22:ALA:O	25:23:26:LEU:HG	2.18	0.43
26:24:14:ILE:HG13	26:24:22:ILE:HB	2.00	0.43
32:2a:438:G:O2'	32:2a:494:U:O4	2.28	0.43
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.53	0.43
32:2a:1058:G:C2	32:2a:1059:C:C2	3.06	0.43
32:2a:1228:C:OP2	44:2m:111:LYS:HE3	2.18	0.43
32:2a:1263:C:C4	32:2a:1272:G:O6	2.71	0.43
33:2b:41:ILE:O	33:2b:41:ILE:HG13	2.17	0.43
33:2b:82:ARG:HB2	33:2b:92:TYR:CE1	2.53	0.43
37:2f:15:ASP:O	37:2f:19:LEU:HB2	2.18	0.43
37:2f:22:GLU:OE2	37:2f:84:ASN:ND2	2.51	0.43
38:2g:107:ALA:O	38:2g:111:ARG:HG3	2.18	0.43
46:2o:62:GLN:O	46:2o:66:LEU:HG	2.18	0.43
48:2q:45:HIS:CD2	48:2q:47:PRO:HD3	2.53	0.43
1:1A:569:U:C4	1:1A:570:G:C6	3.06	0.43
1:1A:602:G:O6	60:1A:4152:HOH:O	2.18	0.43
1:1A:2146:C:H5''	1:1A:2147:G:C4	2.53	0.43
9:1N:47:ALA:HB3	9:1N:115:ARG:HH21	1.83	0.43
18:1W:92:ARG:HB3	18:1W:92:ARG:HH21	1.83	0.43
32:1a:96:U:H2'	32:1a:97:G:C8	2.52	0.43
32:1a:162:A:C5	32:1a:163:C:H1'	2.54	0.43
32:1a:398:C:H2'	32:1a:399:G:H8	1.83	0.43
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.49	0.43
35:1d:153:ARG:CB	35:1d:181:MET:HE1	2.48	0.43
37:1f:27:GLN:HA	37:1f:30:LEU:HD12	2.00	0.43
40:1i:32:ASP:OD1	40:1i:33:PHE:N	2.51	0.43
1:2A:242:G:C8	30:28:5:LYS:HG2	2.54	0.43
1:2A:272:G:H4'	1:2A:272(A):U:H5''	2.00	0.43
1:2A:538:G:H2'	1:2A:539:G:C8	2.52	0.43
1:2A:729:G:C8	3:2D:208:LYS:HD2	2.54	0.43
1:2A:1654:A:OP1	13:2R:1:MET:N	2.44	0.43
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.54	0.43
1:2A:1847:A:H3'	1:2A:1848:A:H5'	1.98	0.43
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:34:TRP:CH2	11:2P:8:PRO:HB3	2.53	0.43
5:2F:170:LEU:HG	5:2F:172:TRP:NE1	2.33	0.43
12:2Q:17:LEU:HD21	12:2Q:41:TRP:NE1	2.32	0.43
12:2Q:43:THR:HG22	12:2Q:94:VAL:HG12	2.00	0.43
32:2a:328:C:H4'	32:2a:329:A:H5'	1.99	0.43
32:2a:1125:U:H6	32:2a:1126:U:O2'	2.02	0.43
32:2a:1144:G:N2	32:2a:1146:A:H62	2.16	0.43
32:2a:1263:C:O2	32:2a:1273:G:C2	2.72	0.43
38:2g:79:ARG:NH2	38:2g:80:VAL:HA	2.33	0.43
40:2i:8:GLY:HA2	40:2i:79:LEU:HB3	2.01	0.43
44:2m:11:ARG:C	44:2m:13:LYS:H	2.26	0.43
44:2m:11:ARG:O	44:2m:13:LYS:N	2.51	0.43
1:1A:251:A:C5	1:1A:252:G:H1'	2.54	0.43
1:1A:1311:G:OP2	29:17:47:ARG:NH2	2.52	0.43
1:1A:1336:A:H2'	1:1A:1337:G:C8	2.53	0.43
1:1A:2306:C:H3'	1:1A:2307:G:H8	1.83	0.43
13:1R:1:MET:HE3	13:1R:1:MET:HB2	1.92	0.43
15:1T:128:GLU:C	15:1T:130:ALA:H	2.25	0.43
20:1Y:68:HIS:ND1	20:1Y:70:SER:HB3	2.33	0.43
32:1a:35:G:N2	43:1l:118:SER:OG	2.39	0.43
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.53	0.43
32:1a:375:U:OP1	47:1p:69:THR:HG21	2.18	0.43
32:1a:1456:G:N2	51:1t:51:GLU:OE2	2.49	0.43
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.54	0.43
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.50	0.43
36:1e:12:LEU:HD22	36:1e:13:ILE:H	1.83	0.43
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.44	0.43
44:1m:2:ALA:N	44:1m:8:GLU:HB2	2.33	0.43
44:1m:105:THR:HG22	44:1m:106:ASN:H	1.82	0.43
54:1w:177:VAL:HG13	54:1w:198:THR:HG23	2.00	0.43
1:2A:659:C:H2'	1:2A:660:G:C8	2.54	0.43
1:2A:1287:A:C5	1:2A:1288:U:C4	3.06	0.43
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.18	0.43
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.43
1:2A:2107:C:H2'	1:2A:2108:C:O4'	2.19	0.43
6:2G:98:ARG:NH1	26:24:1:MET:SD	2.91	0.43
32:2a:429:U:H1'	32:2a:430:A:H5''	2.01	0.43
32:2a:456:C:C2	32:2a:476:G:C2	3.06	0.43
32:2a:1014:A:H1'	50:2s:34:TRP:HB2	2.00	0.43
35:2d:98:GLU:CD	35:2d:103:ASN:HD21	2.26	0.43
37:2f:100:ASN:HD21	49:2r:23:LYS:HG2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:87:SER:HB2	39:2h:93:VAL:HB	2.00	0.43
46:2o:26:GLU:CD	46:2o:77:ARG:HH21	2.26	0.43
48:2q:76:LEU:HD21	48:2q:79:SER:HB2	2.00	0.43
1:1A:127:A:H5''	1:1A:128:C:C6	2.54	0.43
1:1A:1065:U:C4	1:1A:1066:U:C2	3.06	0.43
1:1A:1580:A:OP2	1:1A:1580:A:H8	2.01	0.43
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.18	0.43
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.18	0.43
1:1A:2336:A:H61	22:10:43:THR:HG22	1.83	0.43
10:1O:109:LYS:HE2	10:1O:109:LYS:HB3	1.88	0.43
15:1T:49:VAL:HG22	15:1T:63:VAL:HG22	1.99	0.43
29:17:5:TRP:NE1	29:17:7:PRO:HG3	2.34	0.43
32:1a:299:G:H2'	32:1a:300:A:C8	2.53	0.43
32:1a:406:G:C2	32:1a:407:G:C8	3.07	0.43
32:1a:530:G:C6	53:1v:21:A:C4	3.07	0.43
32:1a:600:C:N3	32:1a:639:G:C2	2.86	0.43
32:1a:677:U:H3	32:1a:713:G:H22	1.65	0.43
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.18	0.43
35:1d:64:LEU:HB2	35:1d:198:VAL:HG11	2.00	0.43
35:1d:190:ASP:O	35:1d:194:LEU:HD23	2.18	0.43
37:1f:35:ALA:HA	37:1f:67:MET:HB3	2.01	0.43
37:1f:67:MET:HB2	37:1f:68:PRO:HD2	2.01	0.43
1:2A:297:C:H2'	1:2A:298:G:O4'	2.19	0.43
1:2A:298:G:H5''	1:2A:299:A:OP1	2.19	0.43
1:2A:1696:G:N7	60:2A:4058:HOH:O	2.36	0.43
1:2A:2305:A:O2'	6:2G:136:ARG:HD3	2.19	0.43
1:2A:2689:U:H4'	1:2A:2690:C:H5'	2.01	0.43
5:2F:160:ASN:ND2	5:2F:163:VAL:HG23	2.33	0.43
6:2G:179:PRO:HB2	26:24:42:PHE:CE2	2.53	0.43
9:2N:121:LYS:HD3	9:2N:130:HIS:CE1	2.53	0.43
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.18	0.43
32:2a:583:A:H2'	32:2a:584:G:O4'	2.18	0.43
45:2n:3:ARG:HD3	45:2n:3:ARG:HA	1.80	0.43
54:2w:123:PHE:HA	54:2w:126:ASP:HB2	2.00	0.43
1:1A:532:A:OP1	16:1U:45:TYR:OH	2.27	0.43
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.18	0.43
27:15:16:ARG:O	27:15:20:ARG:HG3	2.19	0.43
29:17:24:THR:O	29:17:28:ARG:HG3	2.18	0.43
32:1a:598:U:H4'	39:1h:94:TYR:CG	2.52	0.43
32:1a:1283:G:H2'	32:1a:1284:C:C6	2.54	0.43
34:1c:191:THR:OG1	34:1c:194:GLY:O	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:102:ASP:N	35:1d:102:ASP:OD1	2.50	0.43
35:1d:140:VAL:HG11	35:1d:146:ILE:HD11	2.01	0.43
37:1f:95:GLU:O	49:1r:32:ARG:NH1	2.51	0.43
42:1k:16:SER:O	42:1k:35:PRO:HD3	2.18	0.43
1:2A:589:C:H2'	1:2A:590:A:C8	2.53	0.43
1:2A:1790:C:H4'	3:2D:209:ALA:HB2	2.00	0.43
1:2A:2336:A:H61	22:20:43:THR:HG22	1.83	0.43
1:2A:2619:C:H4'	4:2E:151:TYR:O	2.17	0.43
1:2A:2786:U:O2'	4:2E:62:PRO:O	2.30	0.43
3:2D:274:ARG:N	60:2D:406:HOH:O	2.46	0.43
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.19	0.43
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.88	0.43
24:22:32:LEU:HD13	24:22:53:LEU:HB3	2.00	0.43
25:23:46:ASN:O	25:23:50:VAL:HG22	2.19	0.43
32:2a:689:C:P	42:2k:46:GLY:HA3	2.59	0.43
32:2a:806:C:H2'	32:2a:807:A:H8	1.84	0.43
35:2d:17:VAL:HG12	35:2d:18:LYS:N	2.31	0.43
1:1A:61:G:OP1	24:12:51:ARG:NH2	2.52	0.43
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.54	0.43
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	2.00	0.43
1:1A:1547:C:H2'	1:1A:1548:C:C6	2.54	0.43
32:1a:102:G:H2'	32:1a:103:C:H6	1.84	0.43
32:1a:189(F):U:O4	48:1q:72:ARG:NH2	2.52	0.43
32:1a:1152:A:H2'	32:1a:1153:C:C6	2.54	0.43
32:1a:1245:A:H2'	32:1a:1246:C:O4'	2.17	0.43
32:1a:1264:C:H2'	32:1a:1265:G:C8	2.54	0.43
33:1b:146:GLN:O	33:1b:150:SER:N	2.50	0.43
33:1b:163:PHE:HA	33:1b:185:ILE:O	2.17	0.43
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	2.00	0.43
34:1c:22:TRP:CG	34:1c:59:ARG:HB2	2.54	0.43
34:1c:33:LEU:O	34:1c:37:GLN:HG2	2.19	0.43
54:1w:214:MET:HG2	54:1w:217:ILE:HD12	1.99	0.43
1:2A:251:A:C5	1:2A:252:G:H1'	2.53	0.43
1:2A:1345:C:OP2	60:2A:3968:HOH:O	2.20	0.43
1:2A:2507:C:O4'	54:2w:233:ASN:HB3	2.19	0.43
1:2A:2851:A:H2'	1:2A:2852:G:O4'	2.18	0.43
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.53	0.43
3:2D:85:ASP:OD2	3:2D:88:ARG:NH1	2.41	0.43
16:2U:106:PHE:O	16:2U:110:VAL:HG23	2.18	0.43
32:2a:988:G:C2	32:2a:989:C:H1'	2.54	0.43
32:2a:1104:G:H4'	33:2b:111:ARG:CZ	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:4:ARG:HB2	38:2g:5:ARG:H	1.65	0.43
54:2w:323:ASP:O	54:2w:327:VAL:HG13	2.19	0.43
1:1A:271(M):G:H21	8:1I:50:ARG:HH11	1.67	0.43
1:1A:548:A:H1'	1:1A:549:G:OP1	2.18	0.43
1:1A:2051:A:H5'	1:1A:2578:G:O4'	2.18	0.43
1:1A:2100:G:H2'	1:1A:2101:G:O4'	2.19	0.43
1:1A:2274:A:O2'	1:1A:2276:G:OP1	2.33	0.43
1:1A:2573:C:N4	54:1w:234:THR:O	2.51	0.43
8:1I:101:LEU:HG	8:1I:107:VAL:HB	2.01	0.43
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.72	0.43
21:1Z:24:LEU:HD21	21:1Z:86:VAL:HG13	2.01	0.43
32:1a:102:G:H2'	32:1a:103:C:C6	2.53	0.43
32:1a:987:G:H1	32:1a:1218:C:H42	1.66	0.43
32:1a:1064:G:H1'	32:1a:1190:G:H21	1.84	0.43
32:1a:1318:A:H5''	50:1s:3:ARG:NH1	2.34	0.43
32:1a:1367:C:OP1	40:1i:115:GLY:N	2.46	0.43
40:1i:8:GLY:O	40:1i:76:ALA:HB1	2.19	0.43
45:1n:58:LYS:HE2	45:1n:58:LYS:HB3	1.58	0.43
1:2A:239:U:H2'	1:2A:240:G:O4'	2.19	0.43
1:2A:340:A:H2'	1:2A:341:G:O4'	2.18	0.43
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.51	0.43
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.18	0.43
14:2S:27:SER:HA	14:2S:88:ASP:HB3	2.00	0.43
26:24:40:HIS:CD2	26:24:41:PRO:HD2	2.53	0.43
32:2a:189(A):C:H2'	32:2a:189(B):C:C6	2.54	0.43
32:2a:1134:G:N1	32:2a:1135:U:H1'	2.32	0.43
40:2i:3:GLN:OE1	40:2i:20:ARG:NH2	2.52	0.43
42:2k:81:ASP:OD1	42:2k:106:LYS:HB2	2.17	0.43
1:1A:969:U:H2'	1:1A:970:C:C6	2.54	0.43
1:1A:1087:G:H8	1:1A:1087:G:O5'	2.02	0.43
1:1A:1356:G:N2	1:1A:1376:C:C2	2.87	0.43
1:1A:1891:G:C6	1:1A:1892:C:C4	3.07	0.43
1:1A:2298:A:H2'	1:1A:2299:G:O4'	2.19	0.43
1:1A:2319:G:C2	14:1S:3:ARG:HA	2.54	0.43
1:1A:2794:C:N4	1:1A:2802:G:H1	2.15	0.43
2:1B:16:G:C6	2:1B:69:G:C2	3.06	0.43
4:1E:59:VAL:O	4:1E:64:LYS:HE3	2.19	0.43
32:1a:153:C:H2'	32:1a:154:C:C6	2.54	0.43
32:1a:165:C:H2'	32:1a:166:G:C8	2.54	0.43
32:1a:448:A:C4	32:1a:487:A:C2	3.07	0.43
32:1a:1226:C:H5'	50:1s:80:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1518:MA6:C9	32:1a:1519:MA6:H92	2.47	0.43
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	2.00	0.43
37:1f:19:LEU:HD11	37:1f:59:TYR:CE1	2.53	0.43
43:1l:69:TYR:HB2	43:1l:90:VAL:HG21	2.01	0.43
1:2A:30:G:H2'	1:2A:31:C:C6	2.53	0.43
1:2A:704:G:H1'	1:2A:726:G:N2	2.34	0.43
1:2A:1042:G:H4'	1:2A:1042:G:OP1	2.19	0.43
1:2A:1509:C:OP1	1:2A:1509:C:H2'	2.19	0.43
1:2A:2038:G:C6	1:2A:2039:C:C4	3.07	0.43
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.19	0.43
1:2A:2552:OMU:H2'	1:2A:2554:U:OP2	2.19	0.43
3:2D:66:ASP:OD2	3:2D:103:ARG:NH1	2.48	0.43
4:2E:101:ARG:HA	4:2E:170:LEU:O	2.19	0.43
6:2G:102:PHE:HE1	6:2G:141:PHE:CZ	2.37	0.43
7:2H:106:THR:HG23	7:2H:112:PRO:HB3	2.00	0.43
10:2O:68:GLU:HA	10:2O:78:ARG:HB2	2.01	0.43
10:2O:98:VAL:O	10:2O:119:PRO:HD3	2.19	0.43
32:2a:418:C:H2'	32:2a:419:C:H6	1.83	0.43
32:2a:551:U:H2'	32:2a:552:U:C6	2.53	0.43
32:2a:1175:G:H2'	32:2a:1176:A:C8	2.54	0.43
32:2a:1271:G:C2	32:2a:1272:G:N7	2.87	0.43
32:2a:1323:G:O2'	32:2a:1362:C:O2'	2.34	0.43
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.59	0.43
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.19	0.43
40:2i:42:ARG:O	40:2i:74:ILE:HD13	2.19	0.43
44:2m:86:CYS:O	44:2m:90:LEU:N	2.51	0.43
1:1A:153:C:H2'	1:1A:154:G:C8	2.54	0.43
1:1A:1342:A:O2'	1:1A:1344:G:OP2	2.31	0.43
1:1A:1453:U:P	13:1R:77:ARG:NH1	2.92	0.43
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.17	0.43
1:1A:2814:C:HO2'	27:15:29:THR:HG1	1.66	0.43
5:1F:178:PRO:HB2	5:1F:201:VAL:CG2	2.49	0.43
32:1a:148:G:H2'	32:1a:149:A:C8	2.53	0.43
32:1a:370:C:H2'	32:1a:371:G:C8	2.53	0.43
32:1a:598:U:H2'	32:1a:599:C:H6	1.83	0.43
32:1a:676:A:H2'	32:1a:677:U:C6	2.54	0.43
32:1a:767:A:H2'	32:1a:768:A:O4'	2.17	0.43
32:1a:840:C:H4'	32:1a:841:U:OP1	2.19	0.43
33:1b:23:ARG:H	33:1b:23:ARG:HG3	1.57	0.43
33:1b:178:ARG:HH21	39:1h:74:PRO:HB3	1.83	0.43
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:100:ARG:NH1	35:1d:137:SER:OG	2.52	0.43
38:1g:113:GLU:OE1	38:1g:113:GLU:N	2.50	0.43
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.43
1:2A:141:A:H8	1:2A:1408:C:O2'	2.01	0.43
1:2A:1290:C:H2'	1:2A:1291:C:C6	2.54	0.43
4:2E:52:LEU:O	4:2E:76:ARG:N	2.43	0.43
6:2G:3:LEU:O	6:2G:8:LYS:NZ	2.47	0.43
6:2G:54:GLU:HA	6:2G:57:ALA:HB3	2.01	0.43
7:2H:70:THR:HA	7:2H:73:ALA:HB3	2.01	0.43
18:2W:72:LYS:HB3	18:2W:106:ILE:HG22	2.01	0.43
26:24:53:GLU:H	26:24:53:GLU:HG3	1.51	0.43
32:2a:603:U:H2'	32:2a:604:G:C8	2.54	0.43
32:2a:693:G:H2'	32:2a:694:A:C8	2.54	0.43
33:2b:77:ALA:HB2	33:2b:165:VAL:HG11	2.01	0.43
36:2e:93:PRO:HG2	39:2h:105:ARG:CZ	2.49	0.43
44:2m:106:ASN:OD1	44:2m:106:ASN:N	2.50	0.43
1:1A:1049:C:C4	1:1A:1050:A:N7	2.87	0.43
1:1A:1448:G:O2'	1:1A:1528(A):A:N1	2.46	0.43
6:1G:45:GLU:OE2	60:1G:302:HOH:O	2.21	0.43
32:1a:398:C:H2'	32:1a:399:G:C8	2.54	0.43
32:1a:739:C:O2'	46:1o:42:HIS:ND1	2.47	0.43
32:1a:1252:A:H2'	32:1a:1253:G:O4'	2.19	0.43
32:1a:1496:C:H2'	32:1a:1497:G:O4'	2.19	0.43
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.54	0.43
36:1e:9:LYS:HB3	36:1e:33:VAL:HG12	2.01	0.43
39:1h:53:VAL:HG12	39:1h:54:ASP:OD1	2.19	0.43
40:1i:23:ASN:ND2	40:1i:23:ASN:H	2.17	0.43
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.54	0.43
1:2A:263:C:O2'	1:2A:429:A:N3	2.47	0.43
1:2A:999:U:H5''	1:2A:1154:G:O6	2.19	0.43
1:2A:2579:C:H2'	1:2A:2580:U:O4'	2.19	0.43
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.51	0.43
3:2D:80:ALA:N	3:2D:94:LEU:O	2.45	0.43
15:2T:34:VAL:O	15:2T:41:ARG:N	2.45	0.43
18:2W:71:VAL:HA	18:2W:107:LEU:HD23	2.01	0.43
22:20:50:ASN:HB3	22:20:63:VAL:HG22	2.01	0.43
32:2a:137:C:H2'	32:2a:138:G:C8	2.54	0.43
32:2a:841:U:H6	32:2a:841:U:P	2.42	0.43
40:2i:96:LEU:HD23	40:2i:96:LEU:HA	1.87	0.43
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.18	0.43
1:1A:247:G:H4'	1:1A:386:G:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.54	0.42
1:1A:838:C:H2'	1:1A:839:U:C6	2.54	0.42
1:1A:873:G:H2'	1:1A:874:G:C8	2.54	0.42
1:1A:918:A:H5''	2:1B:98:G:O2'	2.19	0.42
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.19	0.42
1:1A:1098:A:C8	1:1A:1099:G:H1'	2.53	0.42
1:1A:1676:A:H2'	1:1A:1677:A:O4'	2.19	0.42
1:1A:2102:U:H2'	1:1A:2103:C:C6	2.53	0.42
2:1B:2:C:H2'	2:1B:3:C:C6	2.54	0.42
2:1B:24:G:N7	2:1B:56:G:H2'	2.34	0.42
2:1B:28:C:H2'	2:1B:29:A:O4'	2.18	0.42
2:1B:49:C:H2'	2:1B:50:G:C8	2.54	0.42
3:1D:34:VAL:HG12	3:1D:63:ARG:HG3	2.01	0.42
5:1F:102:PRO:O	5:1F:106:ARG:HG3	2.18	0.42
15:1T:99:LEU:HD22	15:1T:101:PHE:HE2	1.83	0.42
18:1W:62:HIS:O	18:1W:64:MET:HG3	2.19	0.42
19:1X:94:GLY:N	19:1X:95:LEU:HB2	2.33	0.42
25:13:3:ARG:HD3	25:13:60:GLU:CD	2.44	0.42
29:17:46:VAL:HG13	29:17:48:LYS:NZ	2.33	0.42
32:1a:135:C:H2'	32:1a:136:C:H5'	2.01	0.42
32:1a:295:C:H2'	32:1a:296:U:O4'	2.19	0.42
32:1a:346:G:H3'	32:1a:346:G:N3	2.34	0.42
32:1a:493:G:H2'	32:1a:494:U:C5	2.54	0.42
32:1a:794:A:OP2	60:1a:1916:HOH:O	2.21	0.42
32:1a:1137:C:O5'	32:1a:1137:C:H6	2.01	0.42
32:1a:1226:C:P	44:1m:91:ARG:HH22	2.41	0.42
36:1e:41:VAL:O	36:1e:66:MET:HA	2.19	0.42
42:1k:81:ASP:OD2	42:1k:81:ASP:N	2.52	0.42
1:2A:373:U:H2'	1:2A:374:A:H8	1.84	0.42
1:2A:995:C:OP2	16:2U:54:LYS:NZ	2.36	0.42
1:2A:2120:G:H2'	1:2A:2121:G:H8	1.84	0.42
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	2.01	0.42
2:2B:83:G:H1	2:2B:94:C:H42	1.67	0.42
3:2D:137:PRO:O	3:2D:140:THR:OG1	2.30	0.42
6:2G:41:GLN:HB3	6:2G:43:LEU:HD22	2.00	0.42
8:2I:87:LYS:HE2	8:2I:87:LYS:HB2	1.82	0.42
13:2R:38:VAL:HB	13:2R:39:PRO:HD3	2.00	0.42
21:2Z:9:TYR:OH	21:2Z:61:LEU:HD23	2.19	0.42
21:2Z:150:LEU:HD23	21:2Z:150:LEU:HA	1.79	0.42
32:2a:255:G:C6	32:2a:256:U:C4	3.07	0.42
32:2a:401:C:P	35:2d:73:ARG:HH21	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1130:A:H5'	40:2i:18:PHE:CE2	2.54	0.42
32:2a:1360:A:H2'	32:2a:1361:G:O4'	2.19	0.42
34:2c:97:LYS:O	34:2c:99:VAL:N	2.52	0.42
37:2f:65:VAL:HG21	37:2f:67:MET:HE2	2.01	0.42
48:2q:59:ILE:HG22	48:2q:73:VAL:HA	2.00	0.42
1:1A:724:U:H2'	1:1A:725:G:O4'	2.19	0.42
1:1A:856:C:H5'	22:10:27:GLU:OE2	2.19	0.42
1:1A:1173:G:N1	1:1A:1176:G:OP2	2.52	0.42
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.54	0.42
1:1A:2121:G:H1	1:1A:2177:C:N4	2.16	0.42
1:1A:2127:G:O2'	1:1A:2173:A:H2	2.01	0.42
1:1A:2287:A:C8	1:1A:2289:G:C8	3.07	0.42
8:1I:2:LYS:HB3	8:1I:39:ALA:HB3	2.00	0.42
32:1a:31:G:H5'	32:1a:306:G:N2	2.34	0.42
32:1a:1240:U:P	38:1g:116:ALA:HB2	2.59	0.42
33:1b:223:ILE:H	33:1b:223:ILE:HG13	1.65	0.42
34:1c:134:ILE:HG22	34:1c:168:ALA:HB3	2.00	0.42
34:1c:178:LEU:HA	34:1c:178:LEU:HD23	1.78	0.42
1:2A:223:A:N1	1:2A:407:G:O2'	2.43	0.42
1:2A:2129:C:N3	1:2A:2159:G:N2	2.57	0.42
1:2A:2139:C:N4	1:2A:2140:C:N3	2.67	0.42
32:2a:194:C:H2'	32:2a:195:A:H5''	2.01	0.42
32:2a:399:G:H2'	32:2a:400:C:C6	2.54	0.42
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.54	0.42
34:2c:81:GLY:O	34:2c:85:ARG:HD3	2.19	0.42
36:2e:146:ALA:O	36:2e:150:ARG:HG2	2.19	0.42
38:2g:47:CYS:HA	38:2g:50:ILE:HG22	1.99	0.42
38:2g:75:VAL:HG13	38:2g:145:ALA:HA	2.00	0.42
54:2w:243:HIS:CD2	54:2w:245:PRO:HD2	2.54	0.42
1:1A:908:C:OP1	12:1Q:22:LYS:HD3	2.19	0.42
1:1A:2507:C:H4'	54:1w:233:ASN:O	2.19	0.42
5:1F:178:PRO:HB2	5:1F:201:VAL:HG22	2.01	0.42
7:1H:97:ARG:HD3	7:1H:104:GLU:OE2	2.19	0.42
9:1N:10:GLU:HG2	9:1N:11:PRO:HD2	2.00	0.42
32:1a:403:C:H5''	35:1d:136:PRO:HD2	2.00	0.42
32:1a:557:G:C6	32:1a:558:G:C6	3.07	0.42
32:1a:948:C:P	44:1m:108:ARG:H	2.42	0.42
32:1a:1044:A:H5'	32:1a:1045:C:OP2	2.19	0.42
36:1e:93:PRO:HG2	39:1h:105:ARG:NH1	2.35	0.42
39:1h:100:ILE:H	39:1h:100:ILE:HG13	1.54	0.42
41:1j:23:ILE:HD13	41:1j:23:ILE:HA	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:87:TYR:CE2	44:1m:91:ARG:HD2	2.54	0.42
46:1o:5:LYS:HE2	46:1o:5:LYS:HB2	1.85	0.42
52:1u:18:TYR:CE1	52:1u:24:ARG:HB3	2.54	0.42
54:1w:182:ARG:O	54:1w:184:PRO:HD3	2.20	0.42
1:2A:250:G:C6	1:2A:251:A:C6	3.08	0.42
1:2A:636:G:OP1	11:2P:132:LYS:HE2	2.19	0.42
1:2A:1257:C:O5'	1:2A:1257:C:H6	2.02	0.42
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.31	0.42
1:2A:1651:G:N2	1:2A:2007:C:C2	2.88	0.42
1:2A:1803:A:HO2'	3:2D:259:THR:HG21	1.84	0.42
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	2.01	0.42
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.84	0.42
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.53	0.42
13:2R:72:ASP:O	13:2R:76:VAL:HG23	2.19	0.42
27:25:31:VAL:HG22	27:25:42:PRO:HD3	2.00	0.42
30:28:50:LEU:HD23	30:28:50:LEU:HA	1.77	0.42
32:2a:36:C:H2'	32:2a:37:U:O4'	2.19	0.42
32:2a:519:C:O5'	54:2w:301:LYS:NZ	2.52	0.42
32:2a:642:A:C6	32:2a:643:C:C4	3.07	0.42
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	2.01	0.42
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	2.00	0.42
35:2d:90:GLY:O	35:2d:94:LEU:HG	2.18	0.42
35:2d:111:ALA:HB1	35:2d:116:GLN:HG2	2.01	0.42
37:2f:61:LEU:HD22	37:2f:63:TYR:HE2	1.83	0.42
40:2i:20:ARG:O	40:2i:60:ASP:N	2.43	0.42
46:2o:69:TYR:O	46:2o:73:GLU:HG2	2.18	0.42
47:2p:43:LYS:HG2	47:2p:48:TRP:CE2	2.53	0.42
1:1A:35:G:H2'	1:1A:36:G:O4'	2.19	0.42
1:1A:880:G:C2	1:1A:881:G:C8	3.07	0.42
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.55	0.42
1:1A:1653:G:H3'	13:1R:2:ARG:HD3	2.01	0.42
1:1A:2683:C:H5'	15:1T:58:ASN:HD22	1.84	0.42
7:1H:101:ARG:NH2	7:1H:122:THR:OG1	2.52	0.42
16:1U:85:LYS:HE2	16:1U:85:LYS:HB3	1.83	0.42
23:11:73:LEU:HD22	23:11:97:LEU:HB2	2.01	0.42
32:1a:473:G:H2'	32:1a:474:G:H8	1.85	0.42
32:1a:598:U:H4'	39:1h:94:TYR:CD2	2.54	0.42
32:1a:1063:C:OP2	32:1a:1064:G:O2'	2.27	0.42
39:1h:13:ILE:O	39:1h:17:THR:HG23	2.19	0.42
39:1h:96:GLY:H	39:1h:99:GLU:CD	2.28	0.42
47:1p:43:LYS:HA	47:1p:48:TRP:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:1w:150:THR:N	54:1w:154:GLY:O	2.51	0.42
1:2A:184:C:H2'	1:2A:185:U:C6	2.54	0.42
1:2A:1992:G:H1'	60:2A:4199:HOH:O	2.19	0.42
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	2.00	0.42
33:2b:16:HIS:CD2	33:2b:18:GLY:H	2.38	0.42
33:2b:42:ILE:HG21	33:2b:202:PRO:O	2.19	0.42
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.54	0.42
1:1A:1335:U:H2'	1:1A:1336:A:O4'	2.20	0.42
1:1A:1693:U:H1'	3:1D:14:ARG:NH2	2.34	0.42
1:1A:2130:U:H2'	1:1A:2158:A:N6	2.34	0.42
1:1A:2521:C:C4	1:1A:2522:U:C4	3.08	0.42
1:1A:2563:U:O2	1:1A:2565:A:H8	2.02	0.42
2:1B:108:U:H2'	2:1B:109:C:H5''	1.99	0.42
11:1P:4:SER:HB2	60:1P:314:HOH:O	2.20	0.42
26:14:44:THR:O	26:14:47:GLN:HB2	2.20	0.42
26:14:46:GLN:HB3	26:14:48:ARG:NE	2.34	0.42
32:1a:1012:U:H2'	32:1a:1013:G:C8	2.54	0.42
32:1a:1077:G:O6	36:1e:47:LYS:NZ	2.51	0.42
36:1e:96:PRO:O	36:1e:98:THR:N	2.50	0.42
44:1m:29:ARG:HD3	44:1m:64:TRP:CE2	2.54	0.42
50:1s:20:LEU:HD21	50:1s:43:GLU:HG2	2.01	0.42
54:1w:142:THR:HA	54:1w:161:GLU:O	2.19	0.42
54:1w:219:ILE:HD13	54:1w:262:ARG:HD3	2.01	0.42
1:2A:275:G:H2'	1:2A:276:A:O4'	2.20	0.42
1:2A:631:A:OP1	11:2P:65:ARG:HD3	2.19	0.42
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.02	0.42
1:2A:1600:C:OP1	19:2X:58:HIS:NE2	2.47	0.42
4:2E:15:PHE:CD2	15:2T:81:PRO:HD3	2.54	0.42
4:2E:181:LEU:HD12	4:2E:181:LEU:HA	1.77	0.42
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.19	0.42
23:21:73:LEU:HA	23:21:73:LEU:HD23	1.81	0.42
28:26:40:CYS:O	28:26:44:ARG:N	2.52	0.42
32:2a:620:C:C2	35:2d:135:LEU:HG	2.54	0.42
32:2a:993:G:N3	32:2a:993:G:H2'	2.35	0.42
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.54	0.42
33:2b:18:GLY:HA3	33:2b:42:ILE:H	1.85	0.42
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.44	0.42
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.83	0.42
1:1A:2175:C:O2'	1:1A:2176:A:O5'	2.34	0.42
3:1D:20:ASP:OD2	3:1D:22:SER:OG	2.37	0.42
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:122:PHE:O	60:1E:401:HOH:O	2.21	0.42
8:1I:61:ARG:HD3	8:1I:61:ARG:HA	1.80	0.42
13:1R:29:LEU:HD23	13:1R:29:LEU:HA	1.85	0.42
32:1a:45:U:H2'	32:1a:46:G:C8	2.55	0.42
32:1a:859:A:H2'	32:1a:860:A:O4'	2.19	0.42
32:1a:1130:A:OP1	40:1i:16:ARG:NH2	2.52	0.42
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.81	0.42
32:1a:1206:G:H3'	32:1a:1207:2MG:H8	1.85	0.42
33:1b:167:PRO:HD3	33:1b:187:LEU:O	2.19	0.42
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.52	0.42
35:1d:100:ARG:NH2	35:1d:102:ASP:OD2	2.51	0.42
35:1d:174:LEU:HD23	35:1d:185:PHE:HA	2.01	0.42
42:1k:18:ARG:O	42:1k:32:ILE:HG23	2.20	0.42
44:1m:106:ASN:HB2	44:1m:107:ALA:H	1.54	0.42
54:1w:181:GLN:HE21	54:1w:181:GLN:HB3	1.60	0.42
1:2A:108:U:H2'	1:2A:109:G:C8	2.55	0.42
1:2A:581:C:H2'	1:2A:582:G:H8	1.85	0.42
1:2A:1319:G:C6	1:2A:1320:C:N4	2.88	0.42
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.54	0.42
1:2A:1991:U:H2'	1:2A:1992:G:H5''	2.00	0.42
1:2A:2740:A:H2'	1:2A:2741:A:C8	2.54	0.42
2:2B:52:A:N6	14:2S:33:LYS:HG3	2.35	0.42
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.59	0.42
32:2a:724:G:C2	32:2a:725:G:C8	3.08	0.42
32:2a:779:C:O2'	42:2k:120:ARG:HD3	2.20	0.42
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.26	0.42
34:2c:111:LEU:HD22	34:2c:146:ALA:HB2	2.02	0.42
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.75	0.42
1:1A:1101:U:H2'	1:1A:1102:C:H5	1.85	0.42
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.19	0.42
19:1X:50:LYS:N	19:1X:87:GLN:OE1	2.45	0.42
30:18:28:GLY:O	30:18:36:LYS:NZ	2.50	0.42
32:1a:651:C:N4	32:1a:753:A:OP2	2.49	0.42
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.35	0.42
32:1a:990:C:C2	32:1a:991:U:C5	3.08	0.42
32:1a:999:C:H2'	32:1a:1000:U:O4'	2.19	0.42
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.19	0.42
32:1a:1401:G:C2	32:1a:1402:4OC:H1'	2.55	0.42
33:1b:21:ARG:H	33:1b:21:ARG:HH21	1.67	0.42
33:1b:22:LYS:H	33:1b:22:LYS:HG2	1.65	0.42
46:1o:9:GLN:HA	46:1o:12:ILE:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:31:SER:O	51:1t:35:THR:OG1	2.38	0.42
51:1t:53:LEU:HA	51:1t:56:MET:HE2	2.02	0.42
1:2A:484:C:H2'	1:2A:485:C:H6	1.84	0.42
1:2A:570:G:H2'	1:2A:2030:A:C5	2.54	0.42
1:2A:760:G:H2'	1:2A:761:A:O4'	2.18	0.42
1:2A:1419:A:C8	1:2A:1421:G:C6	3.08	0.42
1:2A:1510:G:H2'	1:2A:1511:C:C6	2.55	0.42
1:2A:2006:C:H6	1:2A:2006:C:O5'	2.03	0.42
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.54	0.42
1:2A:2134:A:N1	1:2A:2135:A:H1'	2.34	0.42
7:2H:127:GLU:OE1	7:2H:129:THR:OG1	2.38	0.42
13:2R:38:VAL:O	13:2R:42:LYS:HG3	2.18	0.42
13:2R:67:LEU:HG	13:2R:76:VAL:HG21	2.01	0.42
32:2a:490:G:H2'	32:2a:491:G:H8	1.84	0.42
32:2a:698:G:H2'	32:2a:699:C:C6	2.55	0.42
32:2a:1004:A:N1	32:2a:1037:C:C2	2.88	0.42
33:2b:24:TRP:CE3	33:2b:26:PRO:HA	2.55	0.42
35:2d:64:LEU:HD13	35:2d:198:VAL:HG21	2.02	0.42
36:2e:6:PHE:HE1	36:2e:36:ASP:HB3	1.84	0.42
40:2i:67:GLY:O	40:2i:73:GLN:NE2	2.50	0.42
49:2r:43:PHE:C	49:2r:51:LEU:HD12	2.45	0.42
1:1A:1400:G:H2'	1:1A:1401:G:C8	2.54	0.42
1:1A:1812:A:O2'	3:1D:45:ASN:N	2.52	0.42
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.50	0.42
1:1A:2104:G:H2'	1:1A:2105:C:O4'	2.20	0.42
1:1A:2400:G:O6	60:1A:4147:HOH:O	2.18	0.42
7:1H:13:LYS:H	7:1H:13:LYS:HG2	1.61	0.42
15:1T:96:ARG:CZ	15:1T:96:ARG:HB3	2.49	0.42
32:1a:347:G:C6	32:1a:348:G:C4	3.07	0.42
32:1a:438:G:O2'	32:1a:494:U:O4	2.34	0.42
32:1a:501:C:H2'	32:1a:502:G:H8	1.85	0.42
32:1a:518:C:C4	32:1a:530:G:C5	3.07	0.42
32:1a:921:U:O2	36:1e:19:MET:HB2	2.19	0.42
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.54	0.42
33:1b:167:PRO:HG2	33:1b:192:SER:HB3	2.01	0.42
34:1c:132:ARG:NH1	34:1c:136:GLN:HE22	2.18	0.42
41:1j:5:ARG:HD3	41:1j:71:LEU:HD11	2.02	0.42
1:2A:7:G:H2'	1:2A:8:A:O4'	2.19	0.42
1:2A:1019:U:O2'	1:2A:1021:A:H2	2.03	0.42
1:2A:1338:G:N3	1:2A:1393:A:H2	2.18	0.42
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:13:A:N1	2:2B:69:G:O2'	2.47	0.42
3:2D:242:ARG:HG2	3:2D:246:PRO:HG3	2.00	0.42
7:2H:25:LYS:HZ2	7:2H:27:LYS:HD2	1.85	0.42
8:2I:93:THR:HG22	8:2I:119:PRO:HG3	2.01	0.42
32:2a:1095:U:H2'	32:2a:1096:C:O4'	2.19	0.42
32:2a:1291:G:O3'	40:2i:39:GLY:HA3	2.20	0.42
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.55	0.42
33:2b:95:GLN:NE2	33:2b:147:LYS:HE2	2.31	0.42
37:2f:41:GLU:CD	49:2r:35:ARG:HH22	2.27	0.42
1:1A:643:A:H5'	60:1A:5326:HOH:O	2.20	0.42
1:1A:794:G:H2'	1:1A:795:C:C6	2.55	0.42
1:1A:1077:A:H2'	1:1A:1078:U:H4'	2.02	0.42
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.20	0.42
1:1A:1558:A:C2	1:1A:1560:G:C8	3.08	0.42
1:1A:2135:A:C2	1:1A:2136:C:H1'	2.54	0.42
2:1B:66:A:H61	2:1B:108:U:H2'	1.85	0.42
32:1a:472:A:N6	32:1a:473:G:C2	2.88	0.42
32:1a:624:C:H5'	47:1p:11:SER:HB3	2.01	0.42
40:1i:27:THR:OG1	40:1i:31:GLN:O	2.33	0.42
44:1m:23:TYR:CE2	44:1m:71:ARG:HG2	2.55	0.42
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.32	0.42
45:1n:3:ARG:HD3	45:1n:3:ARG:HA	1.66	0.42
48:1q:75:ARG:CZ	48:1q:77:VAL:HG22	2.49	0.42
49:1r:25:THR:HG23	49:1r:26:LEU:HG	2.02	0.42
1:2A:154:G:C6	1:2A:154(A):C:C4	3.08	0.42
1:2A:1025:G:O2'	60:2A:3937:HOH:O	2.14	0.42
1:2A:2110:G:H3'	1:2A:2111:C:C5'	2.50	0.42
1:2A:2164:C:H41	1:2A:2165:G:H21	1.67	0.42
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.55	0.42
1:2A:2526:G:C6	1:2A:2527:C:C4	3.08	0.42
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.55	0.42
6:2G:124:SER:HB2	6:2G:131:TYR:CE1	2.55	0.42
7:2H:71:LEU:HD23	7:2H:71:LEU:HA	1.90	0.42
7:2H:152:ARG:HA	7:2H:152:ARG:HD3	1.68	0.42
32:2a:293:G:H4'	32:2a:609:A:N1	2.35	0.42
32:2a:337:C:H2'	32:2a:338:A:H8	1.84	0.42
32:2a:1084:G:H5''	32:2a:1086:U:C4	2.55	0.42
32:2a:1145:C:H4'	32:2a:1146:A:H8	1.83	0.42
38:2g:32:ARG:C	38:2g:34:GLY:H	2.28	0.42
44:2m:86:CYS:SG	50:2s:73:GLU:HB3	2.60	0.42
1:1A:124:G:OP1	1:1A:1376:C:O2'	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:262:A:H2'	1:1A:263:C:O4'	2.20	0.42
1:1A:309:G:C5	1:1A:330:A:C6	3.08	0.42
1:1A:581:C:H5''	60:1U:307:HOH:O	2.20	0.42
1:1A:1256:G:H1'	5:1F:82:ILE:HD11	2.01	0.42
1:1A:1508:A:O2'	1:1A:1509:C:OP1	2.24	0.42
1:1A:1784:A:H4'	1:1A:1785:A:O5'	2.20	0.42
1:1A:2051:A:H4'	4:1E:141:ILE:HG12	2.02	0.42
1:1A:2131:G:H5'	1:1A:2133:G:N9	2.35	0.42
1:1A:2160:G:O6	1:1A:2161:C:N4	2.53	0.42
1:1A:2740:A:H2'	1:1A:2741:A:C8	2.55	0.42
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	2.02	0.42
5:1F:110:LEU:HD11	5:1F:181:LEU:HG	2.02	0.42
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HD3	2.02	0.42
18:1W:61:ASN:HB2	18:1W:62:HIS:CD2	2.55	0.42
21:1Z:102:LEU:HD11	21:1Z:124:ILE:HB	2.01	0.42
25:13:35:ARG:HH21	25:13:37:LEU:HD21	1.85	0.42
32:1a:187:C:H2'	32:1a:188:C:O4'	2.20	0.42
32:1a:243:A:C2	32:1a:246:A:C8	3.08	0.42
34:1c:106:VAL:HG12	34:1c:108:ASN:H	1.85	0.42
34:1c:141:VAL:HG11	34:1c:202:ILE:HG12	2.02	0.42
34:1c:150:LYS:O	34:1c:201:TYR:N	2.50	0.42
37:1f:21:LEU:O	37:1f:25:ILE:HG13	2.20	0.42
47:1p:21:VAL:HG22	47:1p:33:ILE:HD12	2.02	0.42
49:1r:71:LYS:O	49:1r:75:ILE:HG13	2.20	0.42
1:2A:309:G:C5	1:2A:330:A:C6	3.07	0.42
1:2A:492:A:H2'	1:2A:493:G:O4'	2.20	0.42
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.55	0.42
1:2A:2390:U:O2'	1:2A:2391:G:H5'	2.20	0.42
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.53	0.42
21:2Z:130:PRO:HB2	21:2Z:131:ARG:NH1	2.35	0.42
22:20:51:VAL:N	22:20:62:LEU:HD12	2.35	0.42
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.20	0.42
32:2a:1363(A):A:H1'	32:2a:1365:G:N7	2.35	0.42
33:2b:162:ILE:HG13	33:2b:184:VAL:HA	2.01	0.42
37:2f:30:LEU:HD11	37:2f:63:TYR:HD1	1.84	0.42
44:2m:5:ALA:HA	44:2m:61:GLU:HG2	2.01	0.42
1:1A:8:A:H2'	1:1A:9:U:H6	1.83	0.41
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.20	0.41
1:1A:604:G:OP2	11:1P:90:ARG:NH1	2.53	0.41
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.20	0.41
1:1A:1652:A:C2'	1:1A:1653:G:H5'	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1784:A:H4'	1:1A:1785:A:C5'	2.50	0.41
1:1A:2283:C:H2'	1:1A:2284:C:O4'	2.20	0.41
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.20	0.41
7:1H:41:MET:HE1	7:1H:65:HIS:HD2	1.85	0.41
9:1N:42:TRP:CE3	16:1U:63:VAL:HG11	2.54	0.41
9:1N:75:TYR:HA	9:1N:81:GLY:O	2.20	0.41
15:1T:91:ARG:NE	15:1T:124:ASP:OD2	2.53	0.41
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.20	0.41
21:1Z:146:ILE:N	21:1Z:147:GLY:CA	2.84	0.41
32:1a:636:U:H2'	32:1a:637:G:H8	1.84	0.41
32:1a:864:A:H2'	32:1a:865:A:C8	2.55	0.41
32:1a:1287:A:H2	32:1a:1353:G:N3	2.18	0.41
33:1b:92:TYR:CE1	33:1b:94:ASN:HB2	2.54	0.41
34:1c:23:TYR:CG	34:1c:24:ALA:N	2.88	0.41
36:1e:79:GLU:H	36:1e:79:GLU:HG3	1.50	0.41
45:1n:37:PHE:HB3	45:1n:39:LEU:HD12	2.01	0.41
55:1x:61:C:H2'	55:1x:62:C:H6	1.85	0.41
1:2A:582:G:H2'	1:2A:583:G:C8	2.55	0.41
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.55	0.41
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.19	0.41
1:2A:1558:A:H4'	1:2A:1559:G:O5'	2.20	0.41
1:2A:1886:C:H2'	1:2A:1887:C:C6	2.55	0.41
2:2B:54:G:H21	6:2G:29:TRP:NE1	2.17	0.41
18:2W:68:ARG:O	18:2W:109:GLU:HA	2.19	0.41
20:2Y:30:VAL:O	20:2Y:32:PRO:HD3	2.20	0.41
32:2a:382:A:H2'	32:2a:383:A:C8	2.55	0.41
32:2a:458:C:H2'	32:2a:460:G:O4'	2.20	0.41
32:2a:983:A:H1'	32:2a:1049:U:O2	2.20	0.41
32:2a:1319:A:H4'	32:2a:1320:C:OP1	2.19	0.41
35:2d:81:GLU:OE2	35:2d:85:LYS:NZ	2.53	0.41
38:2g:31:MET:HG3	38:2g:36:LYS:HA	2.01	0.41
1:1A:390:A:OP2	23:11:26:ARG:NH2	2.53	0.41
1:1A:459:U:H4'	29:17:40:TRP:CZ3	2.55	0.41
1:1A:515:A:H1'	1:1A:581:C:H1'	2.03	0.41
1:1A:1062:G:C2	1:1A:1088:A:H2'	2.54	0.41
1:1A:1301:A:C8	1:1A:1303:G:C8	3.08	0.41
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.54	0.41
2:1B:21:G:H2'	2:1B:22:U:O4'	2.20	0.41
29:17:9:ARG:HG2	29:17:46:VAL:HG23	2.02	0.41
32:1a:110:C:H2'	32:1a:111:G:O4'	2.19	0.41
32:1a:136:C:H1'	47:1p:1:MET:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:204:U:H4'	32:1a:216:G:O5'	2.20	0.41
32:1a:325:A:OP2	51:1t:70:SER:OG	2.30	0.41
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.55	0.41
32:1a:958:A:C2	50:1s:55:LYS:HB2	2.54	0.41
32:1a:1438:G:H2'	32:1a:1439:C:H6	1.86	0.41
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.34	0.41
33:1b:141:GLU:O	33:1b:145:LEU:HB2	2.20	0.41
33:1b:171:ALA:O	33:1b:174:VAL:HG22	2.19	0.41
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	2.01	0.41
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	2.03	0.41
46:1o:5:LYS:H	46:1o:5:LYS:HD3	1.85	0.41
47:1p:4:ILE:O	47:1p:66:PRO:HA	2.20	0.41
55:1x:61:C:H2'	55:1x:62:C:C6	2.55	0.41
1:2A:484:C:H2'	1:2A:485:C:C6	2.55	0.41
1:2A:945:A:C4	1:2A:2448:A:C2	3.07	0.41
1:2A:2443:C:H2'	1:2A:2444:G:C8	2.55	0.41
1:2A:2637:U:OP1	4:2E:82:ARG:NH1	2.53	0.41
1:2A:2641:G:P	9:2N:74:ARG:HH21	2.44	0.41
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.55	0.41
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	2.02	0.41
11:2P:52:GLU:HB3	11:2P:55:ARG:NH1	2.35	0.41
11:2P:83:VAL:O	11:2P:115:LEU:N	2.42	0.41
19:2X:59:VAL:N	19:2X:76:ARG:O	2.34	0.41
32:2a:1265:G:C4	32:2a:1271:G:N2	2.88	0.41
34:2c:5:ILE:HD12	34:2c:5:ILE:HA	1.86	0.41
34:2c:186:PHE:HD1	34:2c:198:VAL:O	2.03	0.41
38:2g:15:ASP:OD1	38:2g:19:GLY:N	2.53	0.41
1:1A:154(A):C:N4	1:1A:171:G:H1	2.14	0.41
1:1A:1152:C:H4'	16:1U:77:SER:HA	2.02	0.41
1:1A:1754:C:H2'	1:1A:1755:A:O4'	2.20	0.41
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.56	0.41
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.56	0.41
4:1E:101:ARG:NH2	4:1E:171:GLU:HB2	2.35	0.41
6:1G:111:LEU:HD22	6:1G:120:LEU:HD21	2.01	0.41
6:1G:126:ASP:OD2	6:1G:130:ASN:HB2	2.20	0.41
12:1Q:4:PRO:HD3	12:1Q:70:PRO:O	2.20	0.41
32:1a:630:G:H2'	32:1a:631:G:C8	2.55	0.41
32:1a:714:G:H2'	32:1a:715:A:C8	2.55	0.41
32:1a:1032:G:H2'	32:1a:1033:G:C8	2.56	0.41
32:1a:1068:G:N7	32:1a:1094:G:H2'	2.35	0.41
39:1h:87:SER:HB2	39:1h:93:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:1x:19:G:C4	55:1x:57:G:N2	2.88	0.41
1:2A:658:C:H2'	1:2A:659:C:C6	2.54	0.41
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.50	0.41
1:2A:1607:C:H5''	1:2A:1608:A:H5'	2.02	0.41
1:2A:1689:A:H2'	1:2A:1690:A:H8	1.85	0.41
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.28	0.41
2:2B:42:C:O2'	6:2G:66:GLN:HG2	2.20	0.41
6:2G:11:TYR:OH	6:2G:16:ARG:NH1	2.54	0.41
7:2H:83:TYR:CE2	7:2H:138:LYS:HB2	2.54	0.41
11:2P:47:ASP:HA	11:2P:48:PRO:HD3	1.95	0.41
11:2P:86:LYS:HG2	11:2P:117:GLU:O	2.21	0.41
13:2R:78:LYS:HE2	13:2R:83:ILE:HD11	2.01	0.41
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.20	0.41
32:2a:945:G:C2	32:2a:946:A:C8	3.08	0.41
32:2a:1148:U:O2'	40:2i:66:ARG:HD2	2.21	0.41
32:2a:1160:G:H2'	32:2a:1161:C:C6	2.54	0.41
32:2a:1206:G:C6	32:2a:1207:2MG:C5	3.08	0.41
33:2b:212:GLN:O	33:2b:216:SER:N	2.51	0.41
47:2p:8:ARG:HG2	47:2p:17:TYR:CE1	2.55	0.41
47:2p:69:THR:HG23	47:2p:72:ARG:HH12	1.85	0.41
1:1A:1158:C:H4'	25:13:32:GLN:HB2	2.02	0.41
1:1A:2122:U:H2'	1:1A:2123:G:O4'	2.20	0.41
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.55	0.41
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.56	0.41
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	2.03	0.41
22:10:46:LYS:HB2	22:10:78:TYR:CE1	2.55	0.41
30:18:31:HIS:CE1	30:18:32:LEU:HD22	2.55	0.41
32:1a:226:G:H2'	32:1a:227:G:H8	1.84	0.41
32:1a:270:A:H2'	32:1a:271:C:O4'	2.20	0.41
32:1a:1005:A:C2	32:1a:1025:U:H1'	2.56	0.41
32:1a:1212:U:H4'	32:1a:1213:A:C8	2.56	0.41
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.88	0.41
33:1b:115:LEU:O	33:1b:117:GLU:N	2.54	0.41
34:1c:41:GLY:C	34:1c:45:LYS:HE3	2.46	0.41
39:1h:85:ARG:NH1	39:1h:87:SER:O	2.54	0.41
39:1h:86:ILE:HG22	39:1h:93:VAL:HG21	2.02	0.41
54:1w:192:ILE:H	54:1w:192:ILE:HG13	1.68	0.41
1:2A:234:C:H2'	1:2A:235:U:C6	2.55	0.41
1:2A:817:C:O2'	1:2A:839:U:OP1	2.29	0.41
1:2A:1021:A:C8	1:2A:1021:A:H3'	2.56	0.41
1:2A:1886:C:H2'	1:2A:1887:C:H6	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1005:A:H3'	32:2a:1006:C:C6	2.55	0.41
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.28	0.41
37:2f:70:ASP:OD1	37:2f:70:ASP:N	2.46	0.41
39:2h:51:VAL:CG2	39:2h:60:ARG:HB2	2.51	0.41
44:2m:3:ARG:HB3	44:2m:4:ILE:HD12	2.03	0.41
46:2o:35:ARG:O	46:2o:39:LEU:HB2	2.21	0.41
47:2p:5:ARG:HH21	47:2p:28:ARG:HA	1.86	0.41
47:2p:26:ARG:HE	47:2p:26:ARG:HB2	1.51	0.41
1:1A:675:A:C8	1:1A:804:A:C6	3.09	0.41
1:1A:687:C:H5''	29:17:2:LYS:HE2	2.03	0.41
1:1A:1227:G:OP1	16:1U:13:LYS:NZ	2.42	0.41
1:1A:1668:A:O4'	1:1A:1669:A:C2	2.73	0.41
1:1A:1779:U:H2'	60:1A:4288:HOH:O	2.20	0.41
1:1A:2105:C:H2'	1:1A:2106:G:O4'	2.21	0.41
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.56	0.41
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.56	0.41
11:1P:132:LYS:HB2	11:1P:132:LYS:HE2	1.79	0.41
14:1S:61:ASN:ND2	14:1S:63:THR:HB	2.34	0.41
14:1S:67:ARG:HD2	14:1S:71:ARG:NH2	2.36	0.41
24:12:52:ASP:O	24:12:56:GLN:HG3	2.19	0.41
30:18:26:LYS:HD2	30:18:48:PHE:CD2	2.55	0.41
32:1a:427:U:C4	32:1a:428:G:C6	3.09	0.41
32:1a:1034:G:H3'	32:1a:1035:A:H8	1.86	0.41
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.54	0.41
32:1a:1286:A:N3	52:1u:18:TYR:OH	2.52	0.41
33:1b:76:GLN:NE2	33:1b:206:ASP:OD1	2.54	0.41
34:1c:148:GLY:HA3	34:1c:172:ARG:O	2.19	0.41
43:1l:34:ARG:HB2	43:1l:105:TYR:HE2	1.85	0.41
49:1r:37:VAL:CG2	49:1r:78:LEU:HB3	2.51	0.41
50:1s:38:SER:O	50:1s:70:LYS:HA	2.20	0.41
54:1w:109:VAL:HB	54:1w:160:PHE:CZ	2.56	0.41
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.85	0.41
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.43	0.41
1:2A:2526:G:H5'	1:2A:2742:C:O2'	2.20	0.41
1:2A:2528:U:O2'	1:2A:2529:G:H3'	2.20	0.41
25:23:26:LEU:HD13	25:23:47:VAL:HG22	2.03	0.41
35:2d:127:THR:HG22	35:2d:132:ARG:HA	2.02	0.41
38:2g:45:ASP:O	38:2g:49:ILE:HG13	2.20	0.41
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.55	0.41
44:2m:108:ARG:HA	44:2m:108:ARG:HD3	1.80	0.41
1:1A:396:G:H1'	23:11:42:GLN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.20	0.41
1:1A:1313:U:H2'	1:1A:1610:A:C2	2.56	0.41
1:1A:1745(A):C:H5'	1:1A:1746:G:OP2	2.20	0.41
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	2.03	0.41
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.18	0.41
5:1F:116:ASP:OD2	11:1P:1:MET:HB3	2.21	0.41
32:1a:360:A:N6	32:1a:361:G:C6	2.89	0.41
32:1a:381:C:H2'	32:1a:382:A:O4'	2.21	0.41
32:1a:676:A:H1'	42:1k:115:PRO:HB3	2.03	0.41
32:1a:792:A:H1'	32:1a:794:A:N7	2.35	0.41
32:1a:959:A:O2'	32:1a:984:C:O2'	2.33	0.41
32:1a:1174:G:H2'	32:1a:1175:G:H8	1.86	0.41
33:1b:187:LEU:HD23	33:1b:201:ILE:O	2.21	0.41
33:1b:233:SER:HA	33:1b:234:PRO:HD3	1.91	0.41
34:1c:120:VAL:HG23	34:1c:198:VAL:HG11	2.02	0.41
34:1c:153:VAL:O	34:1c:166:GLU:N	2.53	0.41
35:1d:116:GLN:NE2	35:1d:157:LEU:HD23	2.36	0.41
38:1g:80:VAL:HG11	38:1g:154:TYR:CD2	2.55	0.41
1:2A:2532:G:O2'	1:2A:2657:A:N6	2.52	0.41
2:2B:19:G:H2'	2:2B:20:C:O4'	2.21	0.41
2:2B:101:G:H2'	2:2B:102:A:C8	2.56	0.41
4:2E:37:ARG:NH1	4:2E:42:ASP:OD1	2.47	0.41
10:2O:10:VAL:HG21	10:2O:16:ALA:HB3	2.03	0.41
12:2Q:72:LYS:HB3	12:2Q:94:VAL:HG23	2.02	0.41
14:2S:24:LEU:HD23	14:2S:24:LEU:HA	1.90	0.41
26:24:18:CYS:SG	26:24:19:GLY:N	2.94	0.41
29:27:46:VAL:HG13	29:27:48:LYS:HZ2	1.85	0.41
32:2a:598:U:H2'	32:2a:599:C:C6	2.56	0.41
32:2a:1005:A:N3	32:2a:1005:A:H2'	2.35	0.41
32:2a:1014:A:H5'	50:2s:14:HIS:CE1	2.56	0.41
33:2b:87:ARG:NH2	33:2b:233:SER:HB2	2.35	0.41
37:2f:10:LEU:HD23	37:2f:85:VAL:HA	2.02	0.41
40:2i:9:ARG:HA	40:2i:13:ALA:O	2.21	0.41
48:2q:94:ASN:O	48:2q:98:LEU:HD13	2.20	0.41
54:2w:312:VAL:HG21	54:2w:327:VAL:HG21	2.02	0.41
1:1A:666:G:H1'	30:18:4:MET:HE3	2.02	0.41
1:1A:2578:G:OP1	1:1A:2614:A:N6	2.50	0.41
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.55	0.41
6:1G:41:GLN:HG3	6:1G:60:LEU:HD22	2.02	0.41
11:1P:100:LEU:HA	11:1P:100:LEU:HD23	1.82	0.41
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.36	0.41
32:1a:540:G:C6	32:1a:541:G:C5	3.09	0.41
32:1a:688:G:H5'	42:1k:46:GLY:C	2.45	0.41
32:1a:980:C:H1'	45:1n:19:ARG:HA	2.03	0.41
32:1a:1069:C:O2'	32:1a:1192:C:H1'	2.21	0.41
32:1a:1144:G:C6	32:1a:1145:C:N4	2.88	0.41
32:1a:1314:C:H2'	32:1a:1315:U:C6	2.55	0.41
32:1a:1508:G:H2'	32:1a:1509:C:H6	1.86	0.41
33:1b:71:VAL:HG11	33:1b:97:TRP:HE1	1.86	0.41
35:1d:63:LYS:HB2	35:1d:63:LYS:HE3	1.83	0.41
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	2.00	0.41
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.69	0.41
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.56	0.41
1:2A:1927:A:H2'	1:2A:1928:A:C8	2.56	0.41
1:2A:2400:G:N2	1:2A:2417:C:C2	2.89	0.41
1:2A:2416:C:H2'	1:2A:2417:C:H6	1.86	0.41
1:2A:2514:U:H2'	1:2A:2515:C:C6	2.55	0.41
2:2B:16:G:C2'	2:2B:17:C:H5'	2.51	0.41
7:2H:144:VAL:O	7:2H:148:ILE:HG13	2.20	0.41
30:28:28:GLY:O	30:28:36:LYS:NZ	2.51	0.41
32:2a:31:G:H5'	32:2a:306:G:C2	2.56	0.41
32:2a:200:G:H2'	32:2a:201:C:O4'	2.21	0.41
32:2a:532:A:N6	32:2a:1206:G:O2'	2.53	0.41
32:2a:718:G:H5'	42:2k:117:ASN:HD21	1.86	0.41
32:2a:772:U:H2'	32:2a:773:G:O4'	2.20	0.41
32:2a:1296:C:H5''	44:2m:44:ARG:HH22	1.85	0.41
33:2b:125:PRO:O	33:2b:126:GLU:HB2	2.20	0.41
46:2o:34:LEU:HD12	46:2o:34:LEU:HA	1.88	0.41
49:2r:40:LEU:HB3	49:2r:79:LEU:HD11	2.02	0.41
55:2x:43:U:H2'	55:2x:44:C:C6	2.55	0.41
1:1A:30:G:H2'	1:1A:31:C:O4'	2.21	0.41
1:1A:228:A:C8	1:1A:229:A:H5'	2.55	0.41
1:1A:606:U:H4'	1:1A:658:C:H4'	2.02	0.41
1:1A:861:A:C2	1:1A:917:A:C4	3.09	0.41
1:1A:1692:U:O2'	1:1A:1693:U:H2'	2.20	0.41
1:1A:2029:G:H2'	1:1A:2031:A:OP1	2.21	0.41
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.55	0.41
1:1A:2712:U:H1'	1:1A:2712(A):A:C8	2.55	0.41
1:1A:2864:G:H2'	1:1A:2865:U:C6	2.56	0.41
18:1W:37:ARG:HD2	18:1W:38:TYR:CE2	2.56	0.41
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:352:C:O2'	32:1a:354:G:OP1	2.34	0.41
32:1a:376:G:OP2	47:1p:67:THR:HG21	2.21	0.41
32:1a:449:C:O2	47:1p:42:ARG:HD2	2.21	0.41
32:1a:769:G:H4'	32:1a:1513:A:H4'	2.02	0.41
32:1a:861:G:O2'	32:1a:874:G:O2'	2.38	0.41
32:1a:1006:C:H2'	32:1a:1007:C:O4'	2.21	0.41
33:1b:85:ALA:O	33:1b:89:GLY:N	2.54	0.41
34:1c:132:ARG:HH11	34:1c:136:GLN:HE22	1.69	0.41
39:1h:100:ILE:HB	39:1h:125:ARG:HH12	1.86	0.41
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	2.03	0.41
48:1q:53:LEU:HD22	48:1q:85:VAL:HG11	2.03	0.41
53:1v:21:A:H3'	54:1w:191:ARG:NH1	2.36	0.41
1:2A:271(K):U:O2	8:2I:50:ARG:HD3	2.20	0.41
1:2A:1309:G:H4'	29:27:7:PRO:HB2	2.03	0.41
1:2A:1745(A):C:H5'	1:2A:1746:G:OP2	2.21	0.41
1:2A:2121:G:H1	1:2A:2177:C:N4	2.18	0.41
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.20	0.41
4:2E:48:GLN:HA	4:2E:80:GLU:HA	2.03	0.41
4:2E:170:LEU:HB3	4:2E:184:VAL:CG2	2.51	0.41
32:2a:247:G:OP1	32:2a:247:G:H4'	2.20	0.41
32:2a:358:U:H2'	32:2a:359:U:H6	1.85	0.41
32:2a:792:A:H4'	32:2a:793:U:C5'	2.51	0.41
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.36	0.41
32:2a:1365:G:C6	32:2a:1366:C:C4	3.09	0.41
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.82	0.41
47:2p:8:ARG:HB2	47:2p:28:ARG:NE	2.35	0.41
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	2.03	0.41
49:2r:74:ARG:HA	49:2r:79:LEU:O	2.21	0.41
1:1A:171:G:H2'	1:1A:172:C:C6	2.56	0.41
1:1A:271(M):G:H8	1:1A:271(M):G:H2'	1.76	0.41
1:1A:884:C:H42	1:1A:892:G:H1	1.69	0.41
1:1A:1252:G:N1	16:1U:37:GLU:OE2	2.51	0.41
1:1A:1359:A:H2	1:1A:1372:U:O4	2.04	0.41
1:1A:1468:C:OP1	60:1A:4122:HOH:O	2.22	0.41
1:1A:2134:A:H4'	1:1A:2159:G:H21	1.86	0.41
1:1A:2146:C:H5''	1:1A:2147:G:C5	2.56	0.41
1:1A:2531:A:N3	1:1A:2658:C:O2'	2.48	0.41
1:1A:2702:U:H4'	1:1A:2703:C:OP1	2.20	0.41
1:1A:2703:C:H2'	1:1A:2704:C:C6	2.56	0.41
1:1A:2705:A:H2'	1:1A:2706:G:O4'	2.21	0.41
7:1H:105:LEU:HD12	7:1H:151:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:138:LEU:HD23	9:1N:138:LEU:HA	1.82	0.41
10:1O:25:LEU:HD23	10:1O:25:LEU:HA	1.79	0.41
21:1Z:77:ASP:O	21:1Z:81:ARG:N	2.47	0.41
26:14:35:VAL:HG22	26:14:36:CYS:H	1.86	0.41
28:16:25:LYS:NZ	28:16:51:GLU:OE2	2.54	0.41
32:1a:567:G:H2'	32:1a:568:G:O4'	2.20	0.41
32:1a:670:G:H2'	32:1a:671:G:O4'	2.21	0.41
32:1a:714:G:N3	32:1a:777:A:H1'	2.36	0.41
32:1a:951:G:C6	32:1a:1231:G:C6	3.09	0.41
32:1a:976:G:C8	32:1a:1358:U:C2	3.08	0.41
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.21	0.41
32:1a:1195:C:H5''	32:1a:1196:U:OP2	2.21	0.41
33:1b:74:LYS:O	33:1b:78:GLN:HG2	2.20	0.41
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.56	0.41
36:1e:43:LEU:HD21	36:1e:132:ALA:HB1	2.03	0.41
39:1h:8:ASP:O	39:1h:12:ARG:N	2.39	0.41
40:1i:45:ALA:O	40:1i:48:GLU:HB2	2.21	0.41
44:1m:33:ALA:O	44:1m:37:THR:OG1	2.23	0.41
48:1q:51:TYR:HE2	48:1q:73:VAL:HG21	1.86	0.41
54:1w:109:VAL:HG13	54:1w:201:VAL:HG22	2.02	0.41
1:2A:27:G:N2	1:2A:512:G:H1'	2.35	0.41
1:2A:458:G:C8	29:27:37:LYS:HG2	2.55	0.41
1:2A:829:A:N7	1:2A:2248:C:H5'	2.36	0.41
1:2A:839:U:H2'	1:2A:840:C:C6	2.56	0.41
1:2A:1530:C:H6	1:2A:1530:C:H2'	1.74	0.41
1:2A:2198:A:H5'	8:2I:33:ARG:NH2	2.36	0.41
1:2A:2250:G:O2'	1:2A:2496:C:OP1	2.28	0.41
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.54	0.41
1:2A:2443:C:H2'	1:2A:2444:G:H8	1.86	0.41
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.20	0.41
1:2A:2695:C:H2'	1:2A:2696:U:H6	1.86	0.41
2:2B:80:U:O2'	2:2B:81:G:H8	2.03	0.41
3:2D:34:VAL:HA	3:2D:62:TYR:O	2.21	0.41
3:2D:69:ARG:C	3:2D:71:ASP:N	2.77	0.41
5:2F:120:GLU:HB3	5:2F:122:LYS:CG	2.51	0.41
5:2F:170:LEU:HG	5:2F:172:TRP:HE1	1.85	0.41
7:2H:88:LEU:HD11	7:2H:165:ALA:HA	2.02	0.41
10:2O:48:PRO:CB	32:2a:1422:G:H5''	2.42	0.41
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	2.03	0.41
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	2.02	0.41
18:2W:18:ARG:HG2	18:2W:76:VAL:HB	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:145:GLU:HG3	21:2Z:146:ILE:N	2.36	0.41
22:20:45:PHE:HE1	22:20:77:ARG:CZ	2.33	0.41
24:22:21:LEU:HD11	24:22:63:VAL:HG12	2.03	0.41
26:24:1:MET:HB3	26:24:6:HIS:CD2	2.56	0.41
32:2a:124:G:H4'	32:2a:291:C:O2'	2.21	0.41
32:2a:678:U:H2'	32:2a:679:C:C6	2.55	0.41
32:2a:894:G:C6	32:2a:895:G:C5	3.09	0.41
32:2a:983:A:H2	32:2a:984:C:C6	2.39	0.41
32:2a:1201:A:H1'	32:2a:1202:G:OP2	2.20	0.41
32:2a:1346:A:H5'	32:2a:1348:U:H1'	2.02	0.41
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.56	0.41
32:2a:1404:5MC:HN41	32:2a:1497:G:H1	1.69	0.41
33:2b:200:ILE:HG22	33:2b:202:PRO:HD3	2.03	0.41
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	2.03	0.41
34:2c:50:ALA:HB1	34:2c:72:LYS:O	2.21	0.41
35:2d:124:GLY:C	35:2d:126:ILE:H	2.28	0.41
38:2g:131:LYS:HG2	38:2g:132:GLY:H	1.85	0.41
44:2m:31:LYS:O	44:2m:35:GLU:N	2.51	0.41
51:2t:40:ALA:HB2	51:2t:55:ILE:HG22	2.03	0.41
54:2w:118:GLU:O	54:2w:122:LEU:HG	2.21	0.41
54:2w:305:TYR:HA	54:2w:312:VAL:HG12	2.03	0.41
54:2w:337:GLU:O	54:2w:341:ARG:HG3	2.21	0.41
1:1A:6:A:H61	1:1A:2897:U:H3	1.68	0.41
1:1A:774:A:H2'	1:1A:774:A:N3	2.36	0.41
1:1A:904:C:H2'	1:1A:905:U:C6	2.56	0.41
1:1A:2160:G:C6	1:1A:2161:C:C4	3.09	0.41
1:1A:2396:G:H1'	23:11:30:VAL:HG12	2.03	0.41
20:1Y:5:MET:HE2	20:1Y:5:MET:HB2	1.79	0.41
24:12:64:LEU:O	24:12:68:ARG:HG2	2.21	0.41
32:1a:674:G:H2'	32:1a:675:A:C8	2.55	0.41
32:1a:723:U:O2'	32:1a:724:G:H5'	2.21	0.41
32:1a:1493:A:H4'	53:1v:19:U:O2	2.21	0.41
32:1a:1503:A:C6	53:1v:12:A:C2	3.09	0.41
35:1d:114:ARG:HA	35:1d:117:ALA:HB3	2.01	0.41
40:1i:37:PHE:CE1	40:1i:74:ILE:HG13	2.56	0.41
49:1r:51:LEU:O	49:1r:63:GLN:NE2	2.54	0.41
54:1w:332:LEU:HD23	54:1w:332:LEU:HA	1.87	0.41
1:2A:265:A:C8	1:2A:266:G:H1'	2.55	0.41
1:2A:338:G:H2'	1:2A:339:U:H6	1.86	0.41
1:2A:764:A:N1	1:2A:1789:A:O2'	2.49	0.41
1:2A:1676:A:H2'	1:2A:1677:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1942:5MC:C4	1:2A:1943:U:C4	3.09	0.41
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.56	0.41
5:2F:135:LYS:HD2	5:2F:135:LYS:N	2.36	0.41
6:2G:11:TYR:O	6:2G:16:ARG:HG3	2.20	0.41
7:2H:109:PHE:C	7:2H:111:HIS:H	2.29	0.41
32:2a:69:G:H2'	32:2a:70:G:H8	1.86	0.41
32:2a:375:U:O3'	47:2p:6:LEU:HB2	2.21	0.41
32:2a:427:U:OP1	35:2d:13:ARG:NH1	2.51	0.41
32:2a:1092:A:H8	32:2a:1092:A:OP1	2.04	0.41
32:2a:1233:G:H2'	32:2a:1234:C:C6	2.56	0.41
35:2d:102:ASP:HB3	35:2d:136:PRO:HB3	2.03	0.41
36:2e:41:VAL:O	36:2e:66:MET:HA	2.21	0.41
39:2h:86:ILE:HG21	39:2h:133:LEU:CD2	2.51	0.41
39:2h:121:ASP:O	39:2h:125:ARG:HB2	2.20	0.41
50:2s:74:PHE:O	50:2s:76:PRO:HD3	2.21	0.41
54:2w:223:ARG:NH1	54:2w:236:ASP:OD1	2.54	0.41
1:1A:12:U:O2	1:1A:12:U:H2'	2.20	0.40
1:1A:24:G:H2'	1:1A:25:U:O4'	2.21	0.40
1:1A:1584:C:O2'	1:1A:1586:A:H5'	2.20	0.40
1:1A:2032:G:OP2	1:1A:2454:G:O2'	2.26	0.40
1:1A:2144:U:O2'	1:1A:2145:C:H5	2.04	0.40
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.03	0.40
22:10:10:THR:HG23	22:10:12:ASN:H	1.86	0.40
32:1a:77:G:H2'	32:1a:78:G:O4'	2.21	0.40
32:1a:445:G:H2'	32:1a:446:G:C8	2.56	0.40
32:1a:1030:C:C4	32:1a:1030(A):G:H1'	2.56	0.40
32:1a:1218:C:OP2	45:1n:9:LYS:NZ	2.53	0.40
32:1a:1226:C:C5	44:1m:104:ARG:HA	2.56	0.40
33:1b:211:ILE:HG13	33:1b:211:ILE:H	1.74	0.40
35:1d:60:GLU:OE1	35:1d:199:ASN:N	2.43	0.40
35:1d:184:LYS:HB3	35:1d:184:LYS:HE2	1.93	0.40
37:1f:25:ILE:HG13	37:1f:25:ILE:H	1.63	0.40
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.56	0.40
1:2A:1253:A:H4'	60:2A:4188:HOH:O	2.19	0.40
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.53	0.40
3:2D:53:PHE:C	3:2D:218:ARG:HB2	2.46	0.40
14:2S:105:ALA:HB1	14:2S:110:LEU:HD23	2.03	0.40
32:2a:57:G:H2'	32:2a:58:C:O4'	2.21	0.40
32:2a:649:G:H2'	32:2a:650:G:O4'	2.21	0.40
32:2a:685:G:C2	32:2a:686:U:C4	3.10	0.40
32:2a:1137:C:H1'	32:2a:1138:G:C2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.35	0.40
33:2b:18:GLY:HA2	33:2b:42:ILE:HD12	2.04	0.40
33:2b:87:ARG:CZ	33:2b:233:SER:HB2	2.51	0.40
34:2c:175:LEU:H	34:2c:175:LEU:HD12	1.86	0.40
37:2f:22:GLU:H	37:2f:22:GLU:HG2	1.74	0.40
40:2i:118:LYS:H	40:2i:121:ARG:HB3	1.85	0.40
50:2s:30:LEU:HD23	50:2s:31:ILE:N	2.35	0.40
50:2s:63:THR:OG1	50:2s:66:MET:HE3	2.21	0.40
1:1A:241:A:O4'	1:1A:243:U:C6	2.74	0.40
1:1A:760:G:H2'	1:1A:761:A:O4'	2.20	0.40
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.37	0.40
1:1A:1069:A:H2'	1:1A:1073:A:N7	2.36	0.40
1:1A:1094:U:O3'	1:1A:1095:A:H8	2.03	0.40
1:1A:1198:U:H2'	1:1A:1199:U:C6	2.57	0.40
1:1A:1486:A:H2'	1:1A:1487:G:H8	1.86	0.40
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.20	0.40
1:1A:2246:G:H2'	1:1A:2247:A:C8	2.56	0.40
3:1D:45:ASN:N	3:1D:45:ASN:OD1	2.53	0.40
4:1E:92:THR:O	4:1E:95:ILE:HG12	2.21	0.40
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.39	0.40
8:1I:101:LEU:HD12	8:1I:105:HIS:HB2	2.03	0.40
32:1a:219:C:H2'	32:1a:220:G:O4'	2.21	0.40
32:1a:443:C:C2'	32:1a:444:C:H5'	2.51	0.40
34:1c:32:LEU:HD22	34:1c:59:ARG:HD3	2.02	0.40
35:1d:173:TRP:CZ3	35:1d:174:LEU:HG	2.56	0.40
54:1w:312:VAL:HG22	54:1w:324:LEU:HD12	2.02	0.40
1:2A:1695:G:H1'	3:2D:8:PRO:O	2.22	0.40
1:2A:2466:C:H5''	31:29:6:SER:HB2	2.03	0.40
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.56	0.40
3:2D:26:LYS:O	3:2D:83:GLU:HG2	2.22	0.40
6:2G:62:LEU:O	6:2G:143:GLU:HG2	2.21	0.40
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.19	0.40
9:2N:109:LYS:HA	9:2N:109:LYS:HD3	1.90	0.40
17:2V:62:LEU:HD12	17:2V:93:GLU:HG2	2.03	0.40
28:26:11:LEU:HA	28:26:11:LEU:HD23	1.78	0.40
32:2a:868:C:H2'	32:2a:869:G:O4'	2.21	0.40
32:2a:902:G:H2'	32:2a:903:G:H8	1.86	0.40
32:2a:909:A:N3	32:2a:1413:A:O2'	2.50	0.40
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.21	0.40
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.89	0.40
33:2b:60:ASP:O	33:2b:64:ARG:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:6:HIS:HD2	34:2c:7:PRO:HD2	1.85	0.40
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	2.03	0.40
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.56	0.40
38:2g:40:ALA:HB3	40:2i:41:VAL:HG21	2.02	0.40
42:2k:33:THR:OG1	42:2k:34:ASP:O	2.38	0.40
54:2w:140:PHE:HB3	54:2w:162:VAL:CG1	2.51	0.40
54:2w:259:ILE:HG13	54:2w:262:ARG:NH1	2.32	0.40
1:1A:84:A:OP2	20:1Y:8:LYS:NZ	2.28	0.40
1:1A:740:U:H2'	1:1A:741:G:C8	2.56	0.40
1:1A:818:G:H5'	1:1A:839:U:OP1	2.21	0.40
1:1A:1712:C:H2'	1:1A:1713:U:O4'	2.21	0.40
1:1A:2177:C:H2'	1:1A:2178:C:O4'	2.21	0.40
1:1A:2180:U:C2	1:1A:2181:G:C8	3.10	0.40
1:1A:2820:A:C8	4:1E:109:LYS:HE2	2.56	0.40
2:1B:78:A:C2	2:1B:100:A:C4	3.09	0.40
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.19	0.40
7:1H:51:ARG:NH2	7:1H:53:GLU:OE2	2.50	0.40
11:1P:46:LYS:HE3	11:1P:46:LYS:HB3	1.96	0.40
32:1a:262:A:C6	32:1a:263:A:C6	3.09	0.40
32:1a:631:G:H2'	32:1a:632:A:C8	2.56	0.40
32:1a:947:G:H1	32:1a:1234:C:H42	1.68	0.40
32:1a:1125:U:H5'	41:1j:5:ARG:HH22	1.86	0.40
32:1a:1254:C:H41	41:1j:43:ARG:HH12	1.69	0.40
32:1a:1342:C:H1'	40:1i:124:GLN:HG3	2.04	0.40
33:1b:145:LEU:O	33:1b:149:LEU:HB2	2.21	0.40
39:1h:117:GLY:O	39:1h:119:LEU:HG	2.21	0.40
40:1i:4:TYR:CZ	40:1i:88:TYR:HD1	2.39	0.40
40:1i:47:LEU:H	40:1i:47:LEU:HD12	1.86	0.40
40:1i:50:LEU:HG	40:1i:81:ILE:HG21	2.03	0.40
42:1k:48:ILE:HG21	42:1k:63:LEU:HD12	2.03	0.40
43:1l:117:ARG:HB3	43:1l:122:THR:HB	2.04	0.40
44:1m:69:GLU:HA	44:1m:72:ALA:HB3	2.02	0.40
49:1r:70:ILE:HG22	49:1r:74:ARG:HD2	2.03	0.40
53:1v:21:A:H3'	54:1w:191:ARG:HH12	1.85	0.40
1:2A:118:A:C8	1:2A:119:A:C8	3.09	0.40
1:2A:248:G:C2	1:2A:2431:U:H4'	2.56	0.40
1:2A:265:A:H1'	1:2A:266:G:O4'	2.22	0.40
1:2A:280:C:C2	1:2A:361:G:C2	3.10	0.40
1:2A:927:G:H2'	1:2A:928:G:O4'	2.20	0.40
1:2A:969:U:O3'	25:23:14:GLY:HA2	2.21	0.40
1:2A:2788:C:O2'	1:2A:2809:A:N3	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:30:LYS:HE3	7:2H:30:LYS:HB3	1.86	0.40
8:2I:29:TYR:CD2	8:2I:30:LEU:HD23	2.54	0.40
8:2I:84:GLY:C	8:2I:86:THR:H	2.29	0.40
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.21	0.40
14:2S:11:LYS:HB3	14:2S:11:LYS:HE2	1.78	0.40
14:2S:38:GLN:HG3	14:2S:40:ILE:HD11	2.02	0.40
21:2Z:129:SER:C	21:2Z:131:ARG:H	2.30	0.40
28:26:29:ASN:OD1	28:26:29:ASN:N	2.54	0.40
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.56	0.40
32:2a:947:G:H2'	32:2a:948:C:O4'	2.22	0.40
32:2a:1074:G:C6	32:2a:1075:C:C4	3.09	0.40
33:2b:143:GLU:O	33:2b:147:LYS:HG3	2.22	0.40
34:2c:113:ALA:HB3	34:2c:114:PRO:HD3	2.03	0.40
53:2v:15:A:O5'	53:2v:15:A:H8	2.04	0.40
1:1A:1041:C:N4	1:1A:1114:G:H1	2.09	0.40
1:1A:1223:G:N2	1:1A:1226:A:OP2	2.51	0.40
1:1A:2562:U:H4'	10:1O:25:LEU:HD21	2.02	0.40
10:1O:68:GLU:OE1	10:1O:78:ARG:NH1	2.50	0.40
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.86	0.40
23:11:50:ARG:HG2	23:11:59:THR:OG1	2.22	0.40
32:1a:763:G:H2'	32:1a:764:C:C6	2.56	0.40
32:1a:947:G:H5''	44:1m:109:THR:HG23	2.04	0.40
32:1a:991:U:H4'	32:1a:992:U:O5'	2.21	0.40
32:1a:995:C:O2'	32:1a:996:A:H5'	2.22	0.40
32:1a:1241:G:H1	32:1a:1296:C:N4	2.18	0.40
32:1a:1284:C:H3'	32:1a:1285:A:C8	2.55	0.40
33:1b:102:LEU:HD23	33:1b:182:ILE:HD12	2.03	0.40
35:1d:96:LEU:HA	35:1d:99:SER:HB2	2.02	0.40
40:1i:38:GLN:HG2	40:1i:39:GLY:N	2.34	0.40
41:1j:13:HIS:HA	41:1j:16:LEU:HB3	2.04	0.40
54:1w:272:ARG:O	54:1w:276:MET:HG3	2.21	0.40
1:2A:361:G:C2'	1:2A:362:U:H5'	2.51	0.40
1:2A:958:U:OP1	12:2Q:74:TYR:OH	2.33	0.40
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.56	0.40
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.31	0.40
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.86	0.40
1:2A:2502:G:H5''	1:2A:2503:2MA:H5''	2.02	0.40
1:2A:2583:G:OP2	60:2A:3973:HOH:O	2.22	0.40
8:2I:120:ILE:HG21	8:2I:126:TYR:CE2	2.56	0.40
9:2N:39:ARG:HA	9:2N:40:PRO:HD3	1.95	0.40
11:2P:84:ASN:ND2	11:2P:117:GLU:HB3	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:84:ASN:HB3	11:2P:117:GLU:O	2.21	0.40
32:2a:106:C:N4	60:2a:1835:HOH:O	2.55	0.40
32:2a:120:A:C6	32:2a:122:G:C2	3.10	0.40
32:2a:299:G:H2'	32:2a:300:A:C8	2.57	0.40
32:2a:738:C:H2'	32:2a:739:C:C6	2.56	0.40
32:2a:1211:U:H1'	32:2a:1213:A:C2	2.57	0.40
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.39	0.40
32:2a:1292:U:OP2	38:2g:41:ARG:NH2	2.55	0.40
35:2d:94:LEU:O	35:2d:98:GLU:N	2.47	0.40
41:2j:81:THR:C	41:2j:83:GLU:N	2.79	0.40
44:2m:87:TYR:N	50:2s:73:GLU:O	2.49	0.40
1:1A:118:A:C8	1:1A:119:A:C8	3.09	0.40
1:1A:1047:G:C2	1:1A:1110:G:C4	3.09	0.40
1:1A:1665:A:OP1	10:1O:66:LYS:NZ	2.53	0.40
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.83	0.40
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.22	0.40
1:1A:2512:C:H2'	1:1A:2513:G:O4'	2.22	0.40
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.57	0.40
20:1Y:91:GLU:C	20:1Y:93:GLY:H	2.30	0.40
32:1a:79:G:H22	32:1a:90:U:H1'	1.87	0.40
32:1a:377:G:H5'	47:1p:5:ARG:HH12	1.87	0.40
32:1a:670:G:C6	32:1a:671:G:C5	3.10	0.40
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	2.03	0.40
33:1b:85:ALA:O	33:1b:90:MET:N	2.50	0.40
39:1h:81:HIS:N	39:1h:138:TRP:O	2.53	0.40
44:1m:92:HIS:NE2	44:1m:98:VAL:HG21	2.37	0.40
49:1r:31:LEU:HD23	49:1r:31:LEU:HA	1.92	0.40
1:2A:392:C:H5''	1:2A:409:C:H5''	2.03	0.40
1:2A:851:U:H5'	25:23:49:LYS:HD2	2.03	0.40
1:2A:864:G:C6	1:2A:865:C:N4	2.89	0.40
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.52	0.40
5:2F:93:LYS:HD3	5:2F:93:LYS:HA	1.80	0.40
8:2I:98:ALA:HA	8:2I:101:LEU:HB3	2.04	0.40
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.57	0.40
21:2Z:158:PRO:O	21:2Z:161:VAL:HG13	2.21	0.40
32:2a:60:A:N1	32:2a:107:G:O2'	2.53	0.40
32:2a:396:G:O2'	32:2a:398:C:OP1	2.26	0.40
32:2a:501:C:H2'	32:2a:502:G:C8	2.56	0.40
32:2a:1270:C:O2'	32:2a:1313:U:O2'	2.30	0.40
40:2i:50:LEU:HD11	40:2i:81:ILE:HG21	2.04	0.40
50:2s:63:THR:HG1	50:2s:66:MET:HE3	1.86	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%)	257 (94%)	16 (6%)	0	100	100
3	2D	273/276 (99%)	260 (95%)	12 (4%)	1 (0%)	30	51
4	1E	202/206 (98%)	190 (94%)	11 (5%)	1 (0%)	24	46
4	2E	202/206 (98%)	192 (95%)	9 (4%)	1 (0%)	24	46
5	1F	201/210 (96%)	193 (96%)	7 (4%)	1 (0%)	24	46
5	2F	201/210 (96%)	187 (93%)	10 (5%)	4 (2%)	6	12
6	1G	179/182 (98%)	158 (88%)	18 (10%)	3 (2%)	7	15
6	2G	179/182 (98%)	144 (80%)	29 (16%)	6 (3%)	3	4
7	1H	172/180 (96%)	159 (92%)	12 (7%)	1 (1%)	21	42
7	2H	172/180 (96%)	154 (90%)	14 (8%)	4 (2%)	5	9
8	1I	144/148 (97%)	126 (88%)	18 (12%)	0	100	100
8	2I	144/148 (97%)	124 (86%)	17 (12%)	3 (2%)	5	11
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
10	1O	120/122 (98%)	110 (92%)	7 (6%)	3 (2%)	4	8
10	2O	120/122 (98%)	112 (93%)	7 (6%)	1 (1%)	16	34
11	1P	147/150 (98%)	139 (95%)	7 (5%)	1 (1%)	18	38
11	2P	147/150 (98%)	135 (92%)	11 (8%)	1 (1%)	18	38
12	1Q	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
12	2Q	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
13	1R	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
13	2R	116/118 (98%)	110 (95%)	5 (4%)	1 (1%)	14	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	1S	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	14	30
14	2S	108/112 (96%)	97 (90%)	9 (8%)	2 (2%)	6	13
15	1T	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
15	2T	129/146 (88%)	121 (94%)	8 (6%)	0	100	100
16	1U	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
16	2U	114/118 (97%)	110 (96%)	4 (4%)	0	100	100
17	1V	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	12	28
17	2V	99/101 (98%)	90 (91%)	7 (7%)	2 (2%)	6	12
18	1W	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
18	2W	110/113 (97%)	106 (96%)	3 (3%)	1 (1%)	14	30
19	1X	93/96 (97%)	89 (96%)	4 (4%)	0	100	100
19	2X	93/96 (97%)	87 (94%)	4 (4%)	2 (2%)	5	10
20	1Y	105/110 (96%)	96 (91%)	8 (8%)	1 (1%)	12	28
20	2Y	105/110 (96%)	97 (92%)	6 (6%)	2 (2%)	6	13
21	1Z	148/206 (72%)	127 (86%)	18 (12%)	3 (2%)	6	12
21	2Z	156/206 (76%)	139 (89%)	16 (10%)	1 (1%)	21	42
22	10	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
22	20	74/85 (87%)	70 (95%)	4 (5%)	0	100	100
23	11	95/98 (97%)	91 (96%)	3 (3%)	1 (1%)	11	25
23	21	95/98 (97%)	90 (95%)	4 (4%)	1 (1%)	11	25
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	65 (96%)	3 (4%)	0	100	100
25	13	57/60 (95%)	52 (91%)	4 (7%)	1 (2%)	6	14
25	23	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
26	14	67/71 (94%)	55 (82%)	9 (13%)	3 (4%)	2	2
26	24	67/71 (94%)	49 (73%)	15 (22%)	3 (4%)	2	2
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
27	25	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
28	16	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
28	26	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	27	46/49 (94%)	46 (100%)	0	0	100	100
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%)	33 (94%)	2 (6%)	0	100	100
33	1b	229/256 (90%)	185 (81%)	31 (14%)	13 (6%)	1	1
33	2b	229/256 (90%)	187 (82%)	30 (13%)	12 (5%)	1	2
34	1c	204/239 (85%)	173 (85%)	30 (15%)	1 (0%)	24	46
34	2c	204/239 (85%)	176 (86%)	23 (11%)	5 (2%)	4	8
35	1d	206/209 (99%)	173 (84%)	30 (15%)	3 (2%)	8	18
35	2d	206/209 (99%)	192 (93%)	13 (6%)	1 (0%)	24	46
36	1e	146/162 (90%)	127 (87%)	16 (11%)	3 (2%)	5	11
36	2e	146/162 (90%)	131 (90%)	15 (10%)	0	100	100
37	1f	98/101 (97%)	90 (92%)	8 (8%)	0	100	100
37	2f	98/101 (97%)	90 (92%)	7 (7%)	1 (1%)	12	28
38	1g	153/156 (98%)	139 (91%)	12 (8%)	2 (1%)	9	21
38	2g	153/156 (98%)	127 (83%)	23 (15%)	3 (2%)	6	12
39	1h	135/138 (98%)	122 (90%)	12 (9%)	1 (1%)	18	38
39	2h	135/138 (98%)	126 (93%)	9 (7%)	0	100	100
40	1i	125/128 (98%)	103 (82%)	20 (16%)	2 (2%)	7	16
40	2i	125/128 (98%)	104 (83%)	20 (16%)	1 (1%)	16	34
41	1j	95/105 (90%)	81 (85%)	12 (13%)	2 (2%)	5	11
41	2j	94/105 (90%)	80 (85%)	12 (13%)	2 (2%)	5	11
42	1k	112/129 (87%)	97 (87%)	12 (11%)	3 (3%)	4	7
42	2k	112/129 (87%)	95 (85%)	15 (13%)	2 (2%)	6	14
43	1l	119/132 (90%)	107 (90%)	12 (10%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	8 (7%)	0	100	100
44	1m	116/126 (92%)	105 (90%)	10 (9%)	1 (1%)	14	30
44	2m	114/126 (90%)	96 (84%)	16 (14%)	2 (2%)	6	14
45	1n	58/61 (95%)	53 (91%)	4 (7%)	1 (2%)	7	15
45	2n	58/61 (95%)	52 (90%)	4 (7%)	2 (3%)	3	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	1o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	2o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
47	1p	80/88 (91%)	62 (78%)	18 (22%)	0	100	100
47	2p	80/88 (91%)	68 (85%)	11 (14%)	1 (1%)	9	21
48	1q	97/105 (92%)	92 (95%)	4 (4%)	1 (1%)	12	28
48	2q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12	28
49	1r	66/88 (75%)	62 (94%)	4 (6%)	0	100	100
49	2r	66/88 (75%)	62 (94%)	3 (4%)	1 (2%)	8	18
50	1s	81/93 (87%)	64 (79%)	17 (21%)	0	100	100
50	2s	81/93 (87%)	68 (84%)	11 (14%)	2 (2%)	4	8
51	1t	94/106 (89%)	81 (86%)	9 (10%)	4 (4%)	2	2
51	2t	94/106 (89%)	83 (88%)	9 (10%)	2 (2%)	5	11
52	1u	21/27 (78%)	19 (90%)	1 (5%)	1 (5%)	2	2
52	2u	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
54	1w	246/354 (70%)	229 (93%)	16 (6%)	1 (0%)	30	51
54	2w	250/354 (71%)	223 (89%)	25 (10%)	2 (1%)	16	34
All	All	11841/12836 (92%)	10743 (91%)	962 (8%)	136 (1%)	11	25

All (136) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
7	1H	126	PRO
23	11	3	LYS
26	14	56	VAL
33	1b	17	PHE
40	1i	54	ASP
44	1m	67	GLU
5	2F	130	ALA
5	2F	133	ASN
6	2G	47	LYS
7	2H	126	PRO
33	2b	17	PHE
33	2b	22	LYS
38	2g	4	ARG
38	2g	80	VAL

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Mol	Chain	Res	Type
6	1G	43	LEU
6	1G	126	ASP
26	14	49	PHE
33	1b	124	SER
33	1b	126	GLU
42	1k	49	GLY
51	1t	99	LEU
51	1t	100	ILE
5	2F	195	ASP
7	2H	92	ILE
8	2I	117	GLU
17	2V	100	ARG
26	24	56	VAL
34	2c	98	ASN
34	2c	129	ALA
41	2j	31	GLY
49	2r	36	ASN
50	2s	13	ASP
17	1V	79	VAL
20	1Y	54	LYS
26	14	44	THR
33	1b	9	GLU
33	1b	22	LYS
33	1b	78	GLN
33	1b	116	GLU
40	1i	51	ARG
45	1n	60	SER
51	1t	10	LEU
6	2G	84	LYS
7	2H	12	PRO
7	2H	65	HIS
11	2P	29	LYS
19	2X	94	GLY
33	2b	20	GLU
33	2b	78	GLN
33	2b	226	ARG
34	2c	79	ARG
37	2f	40	VAL
40	2i	52	ALA
42	2k	49	GLY
45	2n	27	CYS
54	2w	209	ASP

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Mol	Chain	Res	Type
54	2w	349	ALA
4	1E	52	LEU
10	1O	49	ARG
11	1P	29	LYS
21	1Z	52	SER
33	1b	125	PRO
39	1h	83	ILE
48	1q	61	GLU
4	2E	52	LEU
5	2F	89	VAL
6	2G	72	ARG
8	2I	89	TYR
10	2O	5	GLN
21	2Z	31	ARG
23	2l	3	LYS
33	2b	19	HIS
33	2b	36	ARG
33	2b	123	ALA
34	2c	156	ARG
48	2q	68	ARG
50	2s	12	ASP
51	2t	95	ALA
51	2t	102	GLY
6	1G	47	LYS
10	1O	29	ASN
21	1Z	53	ILE
25	13	42	ALA
33	1b	63	MET
33	1b	155	LEU
33	1b	220	ASP
33	1b	227	GLY
34	1c	98	ASN
35	1d	136	PRO
35	1d	156	GLU
36	1e	22	GLY
36	1e	77	PRO
41	1j	77	PRO
42	1k	104	GLN
52	1u	5	ASP
54	1w	299	SER
6	2G	43	LEU
6	2G	124	SER

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Mol	Chain	Res	Type
17	2V	79	VAL
18	2W	58	ALA
33	2b	16	HIS
35	2d	156	GLU
38	2g	153	HIS
42	2k	54	ARG
44	2m	12	ASN
44	2m	106	ASN
45	2n	14	PRO
10	1O	5	GLN
21	1Z	157	LEU
41	1j	31	GLY
3	2D	125	ILE
8	2I	80	PRO
13	2R	45	ARG
14	2S	94	TYR
19	2X	93	GLU
20	2Y	54	LYS
20	2Y	55	TYR
33	2b	110	GLN
41	2j	33	GLN
47	2p	67	THR
42	1k	14	VAL
6	2G	109	VAL
26	24	50	VAL
35	1d	178	VAL
51	1t	47	GLY
26	24	19	GLY
33	2b	125	PRO
14	1S	96	GLY
36	1e	97	GLY
38	1g	130	GLY
34	2c	174	PRO
33	1b	231	GLU
38	1g	55	GLY
14	2S	82	ILE
33	2b	127	ILE

5.3.2 Protein sidechains [i](#)

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	204 (95%)	11 (5%)	21	45
3	2D	215/218 (99%)	204 (95%)	11 (5%)	21	45
4	1E	164/166 (99%)	159 (97%)	5 (3%)	36	64
4	2E	164/166 (99%)	153 (93%)	11 (7%)	15	33
5	1F	160/166 (96%)	144 (90%)	16 (10%)	7	16
5	2F	159/166 (96%)	140 (88%)	19 (12%)	5	10
6	1G	143/156 (92%)	126 (88%)	17 (12%)	5	10
6	2G	143/156 (92%)	126 (88%)	17 (12%)	5	10
7	1H	144/148 (97%)	133 (92%)	11 (8%)	12	27
7	2H	144/148 (97%)	134 (93%)	10 (7%)	14	32
8	1I	113/124 (91%)	96 (85%)	17 (15%)	3	5
8	2I	105/124 (85%)	88 (84%)	17 (16%)	2	4
9	1N	118/119 (99%)	113 (96%)	5 (4%)	26	52
9	2N	118/119 (99%)	105 (89%)	13 (11%)	6	13
10	1O	100/100 (100%)	95 (95%)	5 (5%)	22	46
10	2O	100/100 (100%)	94 (94%)	6 (6%)	17	37
11	1P	115/116 (99%)	107 (93%)	8 (7%)	14	31
11	2P	115/116 (99%)	101 (88%)	14 (12%)	5	10
12	1Q	111/111 (100%)	107 (96%)	4 (4%)	31	58
12	2Q	111/111 (100%)	102 (92%)	9 (8%)	11	24
13	1R	101/101 (100%)	98 (97%)	3 (3%)	36	64
13	2R	101/101 (100%)	98 (97%)	3 (3%)	36	64
14	1S	86/88 (98%)	76 (88%)	10 (12%)	5	11
14	2S	85/88 (97%)	78 (92%)	7 (8%)	10	24
15	1T	115/127 (91%)	111 (96%)	4 (4%)	32	59
15	2T	113/127 (89%)	104 (92%)	9 (8%)	11	25
16	1U	93/94 (99%)	88 (95%)	5 (5%)	20	42
16	2U	93/94 (99%)	87 (94%)	6 (6%)	15	35
17	1V	80/82 (98%)	76 (95%)	4 (5%)	22	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	2V	80/82 (98%)	74 (92%)	6 (8%)	12	28
18	1W	90/92 (98%)	87 (97%)	3 (3%)	33	61
18	2W	90/92 (98%)	83 (92%)	7 (8%)	11	26
19	1X	77/78 (99%)	73 (95%)	4 (5%)	21	44
19	2X	77/78 (99%)	71 (92%)	6 (8%)	11	26
20	1Y	85/91 (93%)	77 (91%)	8 (9%)	8	18
20	2Y	85/91 (93%)	78 (92%)	7 (8%)	10	24
21	1Z	135/179 (75%)	113 (84%)	22 (16%)	2	4
21	2Z	137/179 (76%)	122 (89%)	15 (11%)	6	13
22	10	61/67 (91%)	57 (93%)	4 (7%)	15	34
22	20	61/67 (91%)	58 (95%)	3 (5%)	22	47
23	11	80/83 (96%)	73 (91%)	7 (9%)	9	21
23	21	80/83 (96%)	72 (90%)	8 (10%)	7	16
24	12	65/67 (97%)	61 (94%)	4 (6%)	16	36
24	22	65/67 (97%)	59 (91%)	6 (9%)	8	19
25	13	51/52 (98%)	44 (86%)	7 (14%)	3	7
25	23	50/52 (96%)	45 (90%)	5 (10%)	7	16
26	14	59/63 (94%)	44 (75%)	15 (25%)	0	1
26	24	53/63 (84%)	44 (83%)	9 (17%)	2	4
27	15	50/52 (96%)	48 (96%)	2 (4%)	28	55
27	25	50/52 (96%)	47 (94%)	3 (6%)	17	37
28	16	51/52 (98%)	48 (94%)	3 (6%)	18	38
28	26	50/52 (96%)	44 (88%)	6 (12%)	5	10
29	17	41/42 (98%)	38 (93%)	3 (7%)	13	29
29	27	41/42 (98%)	38 (93%)	3 (7%)	13	29
30	18	54/55 (98%)	50 (93%)	4 (7%)	13	29
30	28	54/55 (98%)	50 (93%)	4 (7%)	13	29
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	65
31	29	34/34 (100%)	29 (85%)	5 (15%)	3	6
33	1b	192/220 (87%)	158 (82%)	34 (18%)	2	3
33	2b	187/220 (85%)	152 (81%)	35 (19%)	1	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	1c	142/188 (76%)	131 (92%)	11 (8%)	12	27
34	2c	140/188 (74%)	130 (93%)	10 (7%)	13	31
35	1d	169/181 (93%)	151 (89%)	18 (11%)	6	14
35	2d	173/181 (96%)	157 (91%)	16 (9%)	8	19
36	1e	113/123 (92%)	106 (94%)	7 (6%)	16	36
36	2e	114/123 (93%)	96 (84%)	18 (16%)	2	4
37	1f	84/90 (93%)	75 (89%)	9 (11%)	6	14
37	2f	85/90 (94%)	76 (89%)	9 (11%)	6	14
38	1g	119/127 (94%)	106 (89%)	13 (11%)	6	13
38	2g	120/127 (94%)	109 (91%)	11 (9%)	8	19
39	1h	114/119 (96%)	107 (94%)	7 (6%)	17	37
39	2h	114/119 (96%)	104 (91%)	10 (9%)	9	21
40	1i	90/99 (91%)	80 (89%)	10 (11%)	6	12
40	2i	89/99 (90%)	76 (85%)	13 (15%)	3	6
41	1j	66/92 (72%)	57 (86%)	9 (14%)	3	7
41	2j	69/92 (75%)	59 (86%)	10 (14%)	3	6
42	1k	82/99 (83%)	73 (89%)	9 (11%)	6	13
42	2k	83/99 (84%)	76 (92%)	7 (8%)	10	23
43	1l	96/108 (89%)	87 (91%)	9 (9%)	8	18
43	2l	96/108 (89%)	86 (90%)	10 (10%)	7	14
44	1m	89/101 (88%)	76 (85%)	13 (15%)	3	6
44	2m	88/101 (87%)	73 (83%)	15 (17%)	2	4
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5	10
45	2n	49/50 (98%)	45 (92%)	4 (8%)	10	24
46	1o	78/80 (98%)	70 (90%)	8 (10%)	7	15
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9	20
47	1p	69/74 (93%)	60 (87%)	9 (13%)	4	8
47	2p	68/74 (92%)	58 (85%)	10 (15%)	3	6
48	1q	94/97 (97%)	90 (96%)	4 (4%)	26	51
48	2q	94/97 (97%)	89 (95%)	5 (5%)	20	43
49	1r	59/77 (77%)	51 (86%)	8 (14%)	3	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	2r	59/77 (77%)	57 (97%)	2 (3%)	32 60
50	1s	69/80 (86%)	57 (83%)	12 (17%)	2 3
50	2s	67/80 (84%)	62 (92%)	5 (8%)	12 28
51	1t	70/82 (85%)	62 (89%)	8 (11%)	5 11
51	2t	70/82 (85%)	62 (89%)	8 (11%)	5 11
52	1u	18/22 (82%)	16 (89%)	2 (11%)	6 12
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19 40
54	1w	203/298 (68%)	175 (86%)	28 (14%)	3 7
54	2w	203/298 (68%)	171 (84%)	32 (16%)	2 4
All	All	9693/10660 (91%)	8764 (90%)	929 (10%)	8 17

All (929) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	22	SER
3	1D	27	THR
3	1D	38	LYS
3	1D	71	ASP
3	1D	99	ASP
3	1D	113	VAL
3	1D	138	VAL
3	1D	173	VAL
3	1D	183	ARG
3	1D	229	VAL
3	1D	259	THR
4	1E	27	LEU
4	1E	73	GLU
4	1E	75	VAL
4	1E	116	VAL
4	1E	181	LEU
5	1F	24	LEU
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	70	THR
5	1F	137	LYS
5	1F	140	LEU
5	1F	154	VAL
5	1F	162	LEU

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Mol	Chain	Res	Type
5	1F	168	ARG
5	1F	183	VAL
5	1F	192	LEU
5	1F	196	LEU
5	1F	201	VAL
5	1F	204	ASN
5	1F	205	ARG
6	1G	3	LEU
6	1G	22	ARG
6	1G	26	GLN
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	70	VAL
6	1G	77	ILE
6	1G	79	ASN
6	1G	81	LYS
6	1G	82	LEU
6	1G	116	ASP
6	1G	133	LEU
6	1G	140	ILE
6	1G	145	THR
6	1G	148	MET
6	1G	159	VAL
7	1H	13	LYS
7	1H	19	VAL
7	1H	23	ARG
7	1H	45	VAL
7	1H	49	VAL
7	1H	68	THR
7	1H	88	LEU
7	1H	106	THR
7	1H	114	VAL
7	1H	122	THR
7	1H	136	ILE
8	1I	9	LEU
8	1I	12	LEU
8	1I	15	VAL
8	1I	20	ASP
8	1I	21	VAL
8	1I	38	LEU
8	1I	68	LEU

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Mol	Chain	Res	Type
8	1I	78	THR
8	1I	87	LYS
8	1I	92	VAL
8	1I	103	ARG
8	1I	104	GLN
8	1I	109	ILE
8	1I	116	LEU
8	1I	122	GLU
8	1I	127	VAL
8	1I	140	LEU
9	1N	9	VAL
9	1N	14	VAL
9	1N	28	THR
9	1N	73	THR
9	1N	87	LEU
10	1O	10	VAL
10	1O	28	SER
10	1O	52	VAL
10	1O	80	ASP
10	1O	116	SER
11	1P	2	LYS
11	1P	55	ARG
11	1P	59	LEU
11	1P	65	ARG
11	1P	71	VAL
11	1P	96	THR
11	1P	101	VAL
11	1P	126	VAL
12	1Q	7	MET
12	1Q	35	VAL
12	1Q	75	THR
12	1Q	109	VAL
13	1R	74	LYS
13	1R	114	VAL
13	1R	118	GLU
14	1S	26	LEU
14	1S	46	VAL
14	1S	48	LEU
14	1S	50	SER
14	1S	68	GLN
14	1S	69	VAL
14	1S	73	LEU

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Mol	Chain	Res	Type
14	1S	83	LYS
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	74	ARG
15	1T	96	ARG
15	1T	128	GLU
16	1U	59	ARG
16	1U	60	LEU
16	1U	74	LEU
16	1U	77	SER
16	1U	89	GLU
17	1V	32	THR
17	1V	46	VAL
17	1V	53	GLU
17	1V	79	VAL
18	1W	11	ARG
18	1W	17	VAL
18	1W	92	ARG
19	1X	1	MET
19	1X	45	THR
19	1X	81	VAL
19	1X	88	LYS
20	1Y	40	GLU
20	1Y	47	LYS
20	1Y	52	SER
20	1Y	64	GLU
20	1Y	67	LEU
20	1Y	75	ILE
20	1Y	99	CYS
20	1Y	106	LEU
21	1Z	18	LEU
21	1Z	20	ARG
21	1Z	28	MET
21	1Z	31	ARG
21	1Z	33	LEU
21	1Z	50	GLN
21	1Z	60	GLU
21	1Z	61	LEU
21	1Z	70	LEU
21	1Z	73	GLN
21	1Z	80	ARG

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Mol	Chain	Res	Type
21	1Z	84	GLU
21	1Z	121	HIS
21	1Z	126	VAL
21	1Z	132	ASN
21	1Z	141	VAL
21	1Z	146	ILE
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	156	LYS
21	1Z	161	VAL
21	1Z	162	GLU
22	10	10	THR
22	10	14	ARG
22	10	68	GLU
22	10	74	ARG
23	11	21	ARG
23	11	35	THR
23	11	40	ARG
23	11	46	LEU
23	11	67	ILE
23	11	74	VAL
23	11	95	LEU
24	12	5	GLU
24	12	19	VAL
24	12	53	LEU
24	12	65	ASN
25	13	6	VAL
25	13	23	LEU
25	13	32	GLN
25	13	36	VAL
25	13	54	VAL
25	13	58	VAL
25	13	60	GLU
26	14	21	VAL
26	14	23	GLU
26	14	26	SER
26	14	30	GLU
26	14	33	VAL
26	14	44	THR
26	14	46	GLN
26	14	49	PHE
26	14	50	VAL

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Mol	Chain	Res	Type
26	14	53	GLU
26	14	56	VAL
26	14	59	PHE
26	14	60	GLN
26	14	61	ARG
26	14	67	TYR
27	15	6	VAL
27	15	55	ARG
28	16	14	THR
28	16	48	VAL
28	16	52	VAL
29	17	24	THR
29	17	43	THR
29	17	46	VAL
30	18	14	VAL
30	18	23	VAL
30	18	29	LYS
30	18	32	LEU
31	19	4	ARG
33	1b	7	VAL
33	1b	10	LEU
33	1b	12	GLU
33	1b	15	VAL
33	1b	17	PHE
33	1b	19	HIS
33	1b	21	ARG
33	1b	23	ARG
33	1b	67	THR
33	1b	73	THR
33	1b	76	GLN
33	1b	79	ASP
33	1b	80	ILE
33	1b	111	ARG
33	1b	112	VAL
33	1b	137	ARG
33	1b	145	LEU
33	1b	157	ARG
33	1b	158	LEU
33	1b	162	ILE
33	1b	165	VAL
33	1b	172	ILE
33	1b	174	VAL

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Mol	Chain	Res	Type
33	1b	185	ILE
33	1b	189	ASP
33	1b	190	THR
33	1b	196	LEU
33	1b	200	ILE
33	1b	208	ILE
33	1b	222	ILE
33	1b	223	ILE
33	1b	230	VAL
33	1b	231	GLU
33	1b	236	TYR
34	1c	3	ASN
34	1c	15	THR
34	1c	26	LYS
34	1c	28	GLN
34	1c	36	ASP
34	1c	46	GLU
34	1c	64	VAL
34	1c	110	ASN
34	1c	120	VAL
34	1c	130	VAL
34	1c	172	ARG
35	1d	3	ARG
35	1d	26	CYS
35	1d	34	GLU
35	1d	86	LYS
35	1d	88	VAL
35	1d	105	VAL
35	1d	122	ARG
35	1d	135	LEU
35	1d	140	VAL
35	1d	144	ASP
35	1d	155	LEU
35	1d	158	ILE
35	1d	186	LEU
35	1d	187	ARG
35	1d	202	LEU
35	1d	203	VAL
35	1d	204	ILE
35	1d	209	ARG
36	1e	12	LEU
36	1e	27	ARG

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Mol	Chain	Res	Type
36	1e	34	VAL
36	1e	41	VAL
36	1e	79	GLU
36	1e	148	VAL
36	1e	151	LEU
37	1f	37	VAL
37	1f	45	LEU
37	1f	54	LYS
37	1f	55	ASP
37	1f	65	VAL
37	1f	66	GLU
37	1f	72	VAL
37	1f	73	ASN
37	1f	98	LEU
38	1g	37	ASN
38	1g	47	CYS
38	1g	51	GLN
38	1g	52	GLU
38	1g	61	VAL
38	1g	75	VAL
38	1g	76	ARG
38	1g	80	VAL
38	1g	87	VAL
38	1g	91	VAL
38	1g	97	GLN
38	1g	115	ARG
38	1g	131	LYS
39	1h	19	VAL
39	1h	51	VAL
39	1h	52	ASP
39	1h	63	LEU
39	1h	86	ILE
39	1h	100	ILE
39	1h	127	LEU
40	1i	9	ARG
40	1i	14	VAL
40	1i	17	VAL
40	1i	23	ASN
40	1i	47	LEU
40	1i	74	ILE
40	1i	96	LEU
40	1i	97	LYS

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Mol	Chain	Res	Type
40	1i	108	VAL
40	1i	128	ARG
41	1j	8	LEU
41	1j	17	ASP
41	1j	38	ILE
41	1j	43	ARG
41	1j	48	THR
41	1j	62	HIS
41	1j	81	THR
41	1j	84	GLN
41	1j	92	THR
42	1k	14	VAL
42	1k	16	SER
42	1k	33	THR
42	1k	82	VAL
42	1k	84	VAL
42	1k	87	THR
42	1k	93	GLN
42	1k	114	VAL
42	1k	117	ASN
43	1l	18	VAL
43	1l	22	SER
43	1l	24	VAL
43	1l	34	ARG
43	1l	40	VAL
43	1l	41	ARG
43	1l	84	LEU
43	1l	86	ARG
43	1l	119	LYS
44	1m	12	ASN
44	1m	39	ILE
44	1m	47	ASP
44	1m	50	GLU
44	1m	70	LEU
44	1m	71	ARG
44	1m	78	ILE
44	1m	90	LEU
44	1m	102	ARG
44	1m	103	THR
44	1m	106	ASN
44	1m	109	THR
44	1m	116	THR

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Mol	Chain	Res	Type
45	1n	3	ARG
45	1n	7	ILE
45	1n	12	ARG
45	1n	18	VAL
45	1n	22	THR
45	1n	33	VAL
46	1o	3	ILE
46	1o	25	THR
46	1o	26	GLU
46	1o	27	VAL
46	1o	34	LEU
46	1o	39	LEU
46	1o	76	GLU
46	1o	87	ILE
47	1p	1	MET
47	1p	16	HIS
47	1p	19	ILE
47	1p	20	VAL
47	1p	21	VAL
47	1p	34	GLU
47	1p	45	THR
47	1p	49	LEU
47	1p	67	THR
48	1q	12	SER
48	1q	60	ILE
48	1q	63	ARG
48	1q	89	LEU
49	1r	25	THR
49	1r	26	LEU
49	1r	28	GLU
49	1r	37	VAL
49	1r	54	ARG
49	1r	65	ILE
49	1r	85	LEU
49	1r	86	VAL
50	1s	4	SER
50	1s	9	VAL
50	1s	19	VAL
50	1s	23	ASN
50	1s	28	LYS
50	1s	32	LYS
50	1s	41	VAL

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Mol	Chain	Res	Type
50	1s	43	GLU
50	1s	51	VAL
50	1s	66	MET
50	1s	77	THR
50	1s	83	HIS
51	1t	17	ARG
51	1t	24	LEU
51	1t	37	SER
51	1t	60	GLU
51	1t	62	LEU
51	1t	70	SER
51	1t	80	ARG
51	1t	100	ILE
52	1u	8	THR
52	1u	9	ARG
54	1w	102	MET
54	1w	104	GLU
54	1w	132	LEU
54	1w	136	GLU
54	1w	145	LEU
54	1w	158	VAL
54	1w	162	VAL
54	1w	172	LYS
54	1w	180	VAL
54	1w	181	GLN
54	1w	185	VAL
54	1w	188	THR
54	1w	191	ARG
54	1w	196	THR
54	1w	198	THR
54	1w	202	LEU
54	1w	208	GLU
54	1w	215	ASP
54	1w	218	ARG
54	1w	222	MET
54	1w	223	ARG
54	1w	251	THR
54	1w	301	LYS
54	1w	302	ILE
54	1w	316	ARG
54	1w	320	THR
54	1w	321	THR

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Mol	Chain	Res	Type
54	1w	333	THR
3	2D	3	VAL
3	2D	12	SER
3	2D	20	ASP
3	2D	25	THR
3	2D	38	LYS
3	2D	112	GLN
3	2D	113	VAL
3	2D	173	VAL
3	2D	183	ARG
3	2D	229	VAL
3	2D	259	THR
4	2E	38	THR
4	2E	75	VAL
4	2E	90	THR
4	2E	92	THR
4	2E	107	THR
4	2E	116	VAL
4	2E	134	ILE
4	2E	154	LYS
4	2E	181	LEU
4	2E	188	VAL
4	2E	195	LEU
5	2F	19	GLU
5	2F	23	ASP
5	2F	57	VAL
5	2F	74	ARG
5	2F	112	MET
5	2F	114	VAL
5	2F	124	LEU
5	2F	133	ASN
5	2F	135	LYS
5	2F	153	SER
5	2F	158	THR
5	2F	161	GLU
5	2F	162	LEU
5	2F	170	LEU
5	2F	183	VAL
5	2F	188	ARG
5	2F	196	LEU
5	2F	197	ASP
5	2F	201	VAL

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Mol	Chain	Res	Type
6	2G	3	LEU
6	2G	15	VAL
6	2G	43	LEU
6	2G	47	LYS
6	2G	49	ASP
6	2G	58	GLN
6	2G	59	GLU
6	2G	94	LEU
6	2G	109	VAL
6	2G	140	ILE
6	2G	148	MET
6	2G	153	ARG
6	2G	159	VAL
6	2G	160	VAL
6	2G	161	THR
6	2G	165	THR
6	2G	175	LEU
7	2H	15	VAL
7	2H	23	ARG
7	2H	40	GLU
7	2H	49	VAL
7	2H	70	THR
7	2H	106	THR
7	2H	114	VAL
7	2H	122	THR
7	2H	131	VAL
7	2H	155	SER
8	2I	38	LEU
8	2I	40	THR
8	2I	44	LEU
8	2I	51	ILE
8	2I	58	LEU
8	2I	61	ARG
8	2I	66	GLU
8	2I	75	LEU
8	2I	81	VAL
8	2I	87	LYS
8	2I	92	VAL
8	2I	114	LEU
8	2I	125	GLU
8	2I	127	VAL
8	2I	129	THR

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Mol	Chain	Res	Type
8	2I	133	HIS
8	2I	144	VAL
9	2N	8	GLN
9	2N	9	VAL
9	2N	10	GLU
9	2N	15	LEU
9	2N	22	THR
9	2N	28	THR
9	2N	43	THR
9	2N	46	VAL
9	2N	55	VAL
9	2N	61	ARG
9	2N	62	VAL
9	2N	87	LEU
9	2N	134	ARG
10	2O	1	MET
10	2O	10	VAL
10	2O	21	CYS
10	2O	52	VAL
10	2O	69	ILE
10	2O	86	ILE
11	2P	2	LYS
11	2P	3	LEU
11	2P	30	THR
11	2P	55	ARG
11	2P	56	SER
11	2P	59	LEU
11	2P	96	THR
11	2P	101	VAL
11	2P	102	ARG
11	2P	106	LEU
11	2P	124	LYS
11	2P	125	VAL
11	2P	133	SER
11	2P	148	LEU
12	2Q	35	VAL
12	2Q	60	ARG
12	2Q	75	THR
12	2Q	77	LYS
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	127	ILE

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Mol	Chain	Res	Type
12	2Q	134	ARG
12	2Q	135	ASP
13	2R	6	SER
13	2R	27	SER
13	2R	114	VAL
14	2S	5	THR
14	2S	36	TYR
14	2S	49	VAL
14	2S	50	SER
14	2S	69	VAL
14	2S	80	LEU
14	2S	82	ILE
15	2T	6	LEU
15	2T	12	SER
15	2T	13	ARG
15	2T	17	THR
15	2T	28	VAL
15	2T	46	GLU
15	2T	115	ARG
15	2T	118	ARG
15	2T	119	LYS
16	2U	5	LYS
16	2U	31	SER
16	2U	34	LYS
16	2U	74	LEU
16	2U	95	LEU
16	2U	102	GLU
17	2V	28	GLU
17	2V	46	VAL
17	2V	53	GLU
17	2V	56	SER
17	2V	73	SER
17	2V	79	VAL
18	2W	1	MET
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	65	LEU
18	2W	86	LEU
18	2W	92	ARG
19	2X	38	GLU
19	2X	49	VAL

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Mol	Chain	Res	Type
19	2X	75	ASP
19	2X	80	ILE
19	2X	92	LEU
19	2X	93	GLU
20	2Y	9	LYS
20	2Y	37	VAL
20	2Y	49	VAL
20	2Y	75	ILE
20	2Y	90	LEU
20	2Y	97	ARG
20	2Y	99	CYS
21	2Z	4	ARG
21	2Z	5	LEU
21	2Z	18	LEU
21	2Z	30	ASN
21	2Z	33	LEU
21	2Z	36	LYS
21	2Z	50	GLN
21	2Z	72	ARG
21	2Z	121	HIS
21	2Z	133	ILE
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	161	VAL
21	2Z	170	THR
21	2Z	174	VAL
22	20	10	THR
22	20	36	ILE
22	20	74	ARG
23	21	35	THR
23	21	40	ARG
23	21	56	GLN
23	21	74	VAL
23	21	78	LYS
23	21	83	GLU
23	21	95	LEU
23	21	98	LEU
24	22	3	LEU
24	22	17	SER
24	22	19	VAL
24	22	53	LEU
24	22	62	THR

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Mol	Chain	Res	Type
24	22	70	GLN
25	23	31	LEU
25	23	34	GLU
25	23	54	VAL
25	23	56	VAL
25	23	59	VAL
26	24	5	ILE
26	24	14	ILE
26	24	24	THR
26	24	44	THR
26	24	49	PHE
26	24	50	VAL
26	24	53	GLU
26	24	56	VAL
26	24	63	TYR
27	25	6	VAL
27	25	26	THR
27	25	58	LEU
28	26	29	ASN
28	26	32	ASN
28	26	38	LYS
28	26	48	VAL
28	26	52	VAL
28	26	54	ILE
29	27	24	THR
29	27	43	THR
29	27	46	VAL
30	28	3	LYS
30	28	14	VAL
30	28	23	VAL
30	28	32	LEU
31	29	1	MET
31	29	7	VAL
31	29	14	CYS
31	29	17	ILE
31	29	33	LYS
33	2b	7	VAL
33	2b	8	LYS
33	2b	19	HIS
33	2b	20	GLU
33	2b	41	ILE
33	2b	44	LEU

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Mol	Chain	Res	Type
33	2b	47	THR
33	2b	49	GLU
33	2b	67	THR
33	2b	79	ASP
33	2b	82	ARG
33	2b	83	MET
33	2b	112	VAL
33	2b	117	GLU
33	2b	118	LEU
33	2b	122	PHE
33	2b	124	SER
33	2b	126	GLU
33	2b	127	ILE
33	2b	140	HIS
33	2b	141	GLU
33	2b	150	SER
33	2b	154	LEU
33	2b	160	ASP
33	2b	164	VAL
33	2b	172	ILE
33	2b	189	ASP
33	2b	208	ILE
33	2b	212	GLN
33	2b	213	LEU
33	2b	215	LEU
33	2b	219	VAL
33	2b	224	GLN
33	2b	229	VAL
33	2b	230	VAL
34	2c	14	ILE
34	2c	17	ASP
34	2c	26	LYS
34	2c	28	GLN
34	2c	124	ILE
34	2c	125	GLU
34	2c	138	VAL
34	2c	165	THR
34	2c	188	LEU
34	2c	190	ARG
35	2d	8	VAL
35	2d	12	CYS
35	2d	34	GLU

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Mol	Chain	Res	Type
35	2d	66	ARG
35	2d	67	ILE
35	2d	78	LEU
35	2d	135	LEU
35	2d	155	LEU
35	2d	158	ILE
35	2d	163	GLU
35	2d	170	VAL
35	2d	175	SER
35	2d	181	MET
35	2d	194	LEU
35	2d	201	GLN
35	2d	202	LEU
36	2e	6	PHE
36	2e	11	ILE
36	2e	20	GLN
36	2e	24	ARG
36	2e	25	ARG
36	2e	27	ARG
36	2e	51	VAL
36	2e	53	LEU
36	2e	63	ARG
36	2e	75	THR
36	2e	81	GLU
36	2e	111	GLU
36	2e	112	LEU
36	2e	117	ASP
36	2e	120	THR
36	2e	135	THR
36	2e	145	LYS
36	2e	149	GLU
37	2f	19	LEU
37	2f	23	LYS
37	2f	40	VAL
37	2f	41	GLU
37	2f	63	TYR
37	2f	69	GLU
37	2f	72	VAL
37	2f	83	ASP
37	2f	94	GLN
38	2g	9	VAL
38	2g	15	ASP

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Mol	Chain	Res	Type
38	2g	21	VAL
38	2g	36	LYS
38	2g	38	LEU
38	2g	51	GLN
38	2g	52	GLU
38	2g	75	VAL
38	2g	78	ARG
38	2g	79	ARG
38	2g	153	HIS
39	2h	8	ASP
39	2h	19	VAL
39	2h	21	LYS
39	2h	25	ASP
39	2h	46	LYS
39	2h	51	VAL
39	2h	52	ASP
39	2h	97	VAL
39	2h	122	ARG
39	2h	133	LEU
40	2i	3	GLN
40	2i	14	VAL
40	2i	26	VAL
40	2i	47	LEU
40	2i	50	LEU
40	2i	56	LEU
40	2i	58	HIS
40	2i	64	THR
40	2i	65	VAL
40	2i	74	ILE
40	2i	108	VAL
40	2i	124	GLN
40	2i	128	ARG
41	2j	7	LYS
41	2j	25	GLU
41	2j	34	VAL
41	2j	47	PHE
41	2j	55	LYS
41	2j	67	THR
41	2j	69	ASN
41	2j	72	VAL
41	2j	74	ILE
41	2j	94	VAL

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Mol	Chain	Res	Type
42	2k	14	VAL
42	2k	33	THR
42	2k	38	ASN
42	2k	87	THR
42	2k	107	SER
42	2k	112	THR
42	2k	117	ASN
43	2l	11	VAL
43	2l	28	LYS
43	2l	36	VAL
43	2l	39	VAL
43	2l	57	LYS
43	2l	70	ILE
43	2l	78	GLN
43	2l	89	ARG
43	2l	104	VAL
43	2l	117	ARG
44	2m	15	VAL
44	2m	32	GLU
44	2m	47	ASP
44	2m	49	THR
44	2m	54	VAL
44	2m	55	ARG
44	2m	69	GLU
44	2m	78	ILE
44	2m	81	LEU
44	2m	90	LEU
44	2m	91	ARG
44	2m	98	VAL
44	2m	103	THR
44	2m	106	ASN
44	2m	111	LYS
45	2n	7	ILE
45	2n	18	VAL
45	2n	50	LYS
45	2n	57	ARG
46	2o	3	ILE
46	2o	5	LYS
46	2o	12	ILE
46	2o	39	LEU
46	2o	64	ARG
46	2o	83	GLU

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Mol	Chain	Res	Type
46	2o	87	ILE
47	2p	1	MET
47	2p	2	VAL
47	2p	5	ARG
47	2p	20	VAL
47	2p	21	VAL
47	2p	26	ARG
47	2p	44	THR
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
48	2q	39	SER
48	2q	57	VAL
48	2q	60	ILE
48	2q	63	ARG
48	2q	66	SER
49	2r	82	THR
49	2r	86	VAL
50	2s	37	ARG
50	2s	41	VAL
50	2s	43	GLU
50	2s	49	ILE
50	2s	69	HIS
51	2t	9	ASN
51	2t	19	SER
51	2t	42	GLN
51	2t	45	GLN
51	2t	55	ILE
51	2t	71	THR
51	2t	82	SER
51	2t	99	LEU
52	2u	10	ARG
54	2w	103	ASP
54	2w	109	VAL
54	2w	129	ASN
54	2w	138	MET
54	2w	144	VAL
54	2w	147	SER
54	2w	151	ASP
54	2w	158	VAL
54	2w	185	VAL
54	2w	188	THR

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Mol	Chain	Res	Type
54	2w	196	THR
54	2w	209	ASP
54	2w	220	ASP
54	2w	250	VAL
54	2w	259	ILE
54	2w	267	MET
54	2w	268	ILE
54	2w	278	ARG
54	2w	290	LEU
54	2w	295	THR
54	2w	302	ILE
54	2w	305	TYR
54	2w	312	VAL
54	2w	315	HIS
54	2w	320	THR
54	2w	322	HIS
54	2w	324	LEU
54	2w	325	GLU
54	2w	328	LEU
54	2w	333	THR
54	2w	351	LEU
54	2w	353	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	126	GLN
4	1E	48	GLN
4	1E	121	ASN
5	1F	8	GLN
5	1F	203	GLN
6	1G	26	GLN
6	1G	41	GLN
8	1I	74	ASN
8	1I	139	GLN
9	1N	94	HIS
9	1N	131	GLN
11	1P	84	ASN
12	1Q	12	GLN
12	1Q	13	GLN
12	1Q	57	HIS

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Mol	Chain	Res	Type
12	1Q	123	HIS
13	1R	71	GLN
13	1R	91	GLN
14	1S	61	ASN
15	1T	58	ASN
15	1T	84	GLN
16	1U	94	ASN
18	1W	60	ASN
19	1X	31	HIS
19	1X	82	GLN
21	1Z	32	HIS
21	1Z	73	GLN
23	11	56	GLN
26	14	46	GLN
29	17	36	GLN
30	18	35	GLN
33	1b	16	HIS
33	1b	40	HIS
33	1b	76	GLN
33	1b	140	HIS
34	1c	6	HIS
34	1c	28	GLN
34	1c	31	HIS
34	1c	136	GLN
35	1d	77	ASN
35	1d	123	HIS
36	1e	78	HIS
36	1e	141	GLN
37	1f	73	ASN
37	1f	100	ASN
38	1g	28	ASN
38	1g	37	ASN
38	1g	86	GLN
38	1g	97	GLN
38	1g	122	HIS
39	1h	15	ASN
39	1h	81	HIS
40	1i	23	ASN
40	1i	58	HIS
40	1i	89	ASN
40	1i	124	GLN
41	1j	56	HIS

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Mol	Chain	Res	Type
41	1j	62	HIS
41	1j	69	ASN
42	1k	93	GLN
43	1l	99	HIS
47	1p	16	HIS
47	1p	76	GLN
50	1s	47	HIS
51	1t	16	HIS
51	1t	75	ASN
54	1w	129	ASN
54	1w	148	HIS
54	1w	344	GLN
54	1w	347	GLN
3	2D	112	GLN
4	2E	48	GLN
4	2E	121	ASN
4	2E	180	ASN
5	2F	69	HIS
5	2F	160	ASN
5	2F	203	GLN
6	2G	79	ASN
7	2H	143	GLN
8	2I	11	ASN
9	2N	94	HIS
10	2O	5	GLN
10	2O	89	ASN
11	2P	27	HIS
11	2P	84	ASN
12	2Q	12	GLN
12	2Q	123	HIS
13	2R	50	HIS
13	2R	91	GLN
15	2T	58	ASN
16	2U	94	ASN
18	2W	111	HIS
19	2X	31	HIS
21	2Z	55	HIS
21	2Z	73	GLN
23	21	56	GLN
24	22	48	HIS
24	22	70	GLN
26	24	40	HIS

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Mol	Chain	Res	Type
28	26	20	ASN
28	26	32	ASN
30	28	35	GLN
33	2b	16	HIS
33	2b	78	GLN
33	2b	95	GLN
33	2b	135	GLN
33	2b	212	GLN
34	2c	37	GLN
34	2c	98	ASN
34	2c	102	ASN
34	2c	139	GLN
34	2c	181	ASN
35	2d	77	ASN
35	2d	116	GLN
35	2d	199	ASN
35	2d	201	GLN
37	2f	11	ASN
37	2f	84	ASN
37	2f	100	ASN
38	2g	28	ASN
38	2g	68	ASN
38	2g	97	GLN
38	2g	109	ASN
38	2g	148	ASN
39	2h	15	ASN
40	2i	31	GLN
41	2j	56	HIS
42	2k	99	GLN
42	2k	117	ASN
43	2l	8	ASN
43	2l	78	GLN
44	2m	62	ASN
44	2m	77	ASN
47	2p	13	HIS
48	2q	45	HIS
50	2s	57	HIS
50	2s	65	ASN
50	2s	83	HIS
51	2t	18	GLN
51	2t	42	GLN
51	2t	45	GLN

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Mol	Chain	Res	Type
51	2t	75	ASN
54	2w	189	GLN
54	2w	193	HIS
54	2w	261	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	449 (15%)	36 (1%)
1	2A	2791/2915 (95%)	461 (16%)	22 (0%)
2	1B	119/121 (98%)	10 (8%)	0
2	2B	118/121 (97%)	21 (17%)	0
32	1a	1497/1521 (98%)	319 (21%)	0
32	2a	1501/1521 (98%)	309 (20%)	0
53	1v	10/24 (41%)	4 (40%)	0
53	2v	10/24 (41%)	3 (30%)	0
55	1x	73/74 (98%)	10 (13%)	0
55	2x	73/74 (98%)	13 (17%)	0
All	All	9056/9310 (97%)	1599 (17%)	58 (0%)

All (1599) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	72	U
1	1A	74	A
1	1A	75	G
1	1A	84	A
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	123	G
1	1A	140	G
1	1A	153	C
1	1A	154(A)	C
1	1A	182	A
1	1A	196	A

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Mol	Chain	Res	Type
1	1A	199	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(O)	C
1	1A	271(S)	G
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	352	G
1	1A	362	U
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	370	G
1	1A	380	U
1	1A	386	G
1	1A	389	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	428	A
1	1A	442	G
1	1A	444	C
1	1A	448	U
1	1A	454	A
1	1A	456	C
1	1A	457	A
1	1A	481	G

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Mol	Chain	Res	Type
1	1A	504	U
1	1A	505	A
1	1A	509	C
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	575	A
1	1A	587	C
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	652(T)	C
1	1A	669	G
1	1A	685	A
1	1A	686	G
1	1A	717	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	764	A
1	1A	765	G
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	783	A
1	1A	784	A
1	1A	785	G
1	1A	792	G
1	1A	805	G
1	1A	811	U

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Mol	Chain	Res	Type
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G
1	1A	866	A
1	1A	878	A
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	895	U
1	1A	896	A
1	1A	897	C
1	1A	899	A
1	1A	900	A
1	1A	907	U
1	1A	910	A
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1005	C
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1041	C
1	1A	1045	A
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A

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Mol	Chain	Res	Type
1	1A	1055	G
1	1A	1056	G
1	1A	1058	G
1	1A	1059	G
1	1A	1060	U
1	1A	1063	G
1	1A	1064	C
1	1A	1066	U
1	1A	1068	G
1	1A	1071	G
1	1A	1073	A
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	1081	U
1	1A	1083	U
1	1A	1084	A
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1092	C
1	1A	1093	G
1	1A	1094	U
1	1A	1095	A
1	1A	1096	A
1	1A	1098	A
1	1A	1099	G
1	1A	1107	G
1	1A	1112	G
1	1A	1116	C
1	1A	1128	A
1	1A	1132	A
1	1A	1135	C
1	1A	1136	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U

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Mol	Chain	Res	Type
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1194	A
1	1A	1210	A
1	1A	1211	U
1	1A	1241	A
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1276	A
1	1A	1281	G
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1321	A
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	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1437	C
1	1A	1445	A
1	1A	1450	G
1	1A	1453	U
1	1A	1455	G
1	1A	1459	G
1	1A	1461	G
1	1A	1467	C
1	1A	1473	G
1	1A	1482	G

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Mol	Chain	Res	Type
1	1A	1485	G
1	1A	1493	C
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1509(B)	A
1	1A	1525	G
1	1A	1558	A
1	1A	1569	A
1	1A	1578	U
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1647	G
1	1A	1648	C
1	1A	1654	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1703	G
1	1A	1740	G
1	1A	1743	C
1	1A	1746	G
1	1A	1756	G
1	1A	1763	G
1	1A	1764	G
1	1A	1769	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	1828	G
1	1A	1829	A
1	1A	1839	G
1	1A	1847	A
1	1A	1858	G
1	1A	1878	G
1	1A	1881	C

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Mol	Chain	Res	Type
1	1A	1882	C
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1915	5MU
1	1A	1929	G
1	1A	1930	G
1	1A	1931	U
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	1992	G
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2039	C
1	1A	2043	C
1	1A	2049	G
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2069	G
1	1A	2093	G
1	1A	2099	U
1	1A	2102	U
1	1A	2105	C
1	1A	2108	C
1	1A	2110	G
1	1A	2112	G
1	1A	2113	U
1	1A	2116	G

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Mol	Chain	Res	Type
1	1A	2117	A
1	1A	2120	G
1	1A	2122	U
1	1A	2123	G
1	1A	2124	G
1	1A	2126	A
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2138	C
1	1A	2142	C
1	1A	2144	U
1	1A	2145	C
1	1A	2146	C
1	1A	2147	G
1	1A	2149	G
1	1A	2151	G
1	1A	2155	G
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2160	G
1	1A	2162	G
1	1A	2163	C
1	1A	2164	C
1	1A	2165	G
1	1A	2166	G
1	1A	2168	G
1	1A	2170	A
1	1A	2171	A
1	1A	2172	U
1	1A	2175	C
1	1A	2176	A
1	1A	2178	C
1	1A	2180	U
1	1A	2182	G
1	1A	2184	G

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Mol	Chain	Res	Type
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2278	A
1	1A	2280	G
1	1A	2283	C
1	1A	2286	A
1	1A	2287	A
1	1A	2294	C
1	1A	2305	A
1	1A	2307	G
1	1A	2308	G
1	1A	2320	A
1	1A	2321	G
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2383	G
1	1A	2385	C
1	1A	2400	G
1	1A	2406	U
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	2431	U
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2476	A

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Mol	Chain	Res	Type
1	1A	2478	A
1	1A	2490	G
1	1A	2498	C
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2529	G
1	1A	2535	G
1	1A	2549	G
1	1A	2554	U
1	1A	2562	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2663	G
1	1A	2689	U
1	1A	2690	C
1	1A	2691	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2744	G
1	1A	2758	A
1	1A	2761	G
1	1A	2764	A
1	1A	2765	A
1	1A	2778	A
1	1A	2780	G
1	1A	2783	G

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Mol	Chain	Res	Type
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2805	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2872	G
1	1A	2880	C
1	1A	2894	G
2	1B	13	A
2	1B	15	A
2	1B	45	A
2	1B	56	G
2	1B	73	A
2	1B	85	G
2	1B	91	C
2	1B	106	G
2	1B	110	G
2	1B	120	A
32	1a	5	U
32	1a	7	G
32	1a	9	G
32	1a	22	G
32	1a	32	A
32	1a	39	G
32	1a	44	G
32	1a	47	C
32	1a	48	C
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	65	U
32	1a	68	G
32	1a	72	C
32	1a	78	G
32	1a	79	G
32	1a	91	C
32	1a	96	U
32	1a	98	G
32	1a	99	U

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Mol	Chain	Res	Type
32	1a	105	G
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	129(A)	G
32	1a	131	C
32	1a	143	A
32	1a	144	G
32	1a	146	G
32	1a	150	C
32	1a	151	A
32	1a	156	G
32	1a	157	G
32	1a	158	G
32	1a	159	G
32	1a	160	A
32	1a	162	A
32	1a	163	C
32	1a	165	C
32	1a	171	A
32	1a	174	C
32	1a	182	U
32	1a	189(F)	U
32	1a	189(G)	G
32	1a	189(H)	G
32	1a	190	U
32	1a	195	A
32	1a	196	A
32	1a	197	A
32	1a	200	G
32	1a	201	C
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	220	G
32	1a	222	U
32	1a	231	G
32	1a	247	G
32	1a	251	G
32	1a	259	G
32	1a	262	A

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Mol	Chain	Res	Type
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	290	C
32	1a	309	G
32	1a	317	G
32	1a	318	G
32	1a	321	A
32	1a	328	C
32	1a	329	A
32	1a	330	C
32	1a	332	G
32	1a	342	C
32	1a	345	C
32	1a	347	G
32	1a	350	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	364	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	414	A
32	1a	421	U
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	434	U
32	1a	435	C
32	1a	436	C
32	1a	438	G
32	1a	439	A
32	1a	442	C

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Mol	Chain	Res	Type
32	1a	444	C
32	1a	451	A
32	1a	452	A
32	1a	457	C
32	1a	461	A
32	1a	470	C
32	1a	480	U
32	1a	481	G
32	1a	485	G
32	1a	495	A
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	527	G7M
32	1a	531	U
32	1a	532	A
32	1a	533	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	594	G
32	1a	595	G
32	1a	607	A
32	1a	618	C
32	1a	630	G
32	1a	639	G
32	1a	650	G
32	1a	651	C
32	1a	653	A
32	1a	657	G
32	1a	665	A
32	1a	671	G
32	1a	686	U

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Mol	Chain	Res	Type
32	1a	688	G
32	1a	695	A
32	1a	702	A
32	1a	723	U
32	1a	749	C
32	1a	753	A
32	1a	755	G
32	1a	760	G
32	1a	766	A
32	1a	774	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	812	C
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	859	A
32	1a	864	A
32	1a	870	U
32	1a	884	U
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	983	A

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Mol	Chain	Res	Type
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1013	G
32	1a	1020	U
32	1a	1021	G
32	1a	1022	G
32	1a	1023	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1032	G
32	1a	1033	G
32	1a	1036	G
32	1a	1040	U
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
32	1a	1052	U
32	1a	1053	G
32	1a	1054	C
32	1a	1055	A
32	1a	1065	U
32	1a	1066	C
32	1a	1081	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G

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Mol	Chain	Res	Type
32	1a	1123	A
32	1a	1125	U
32	1a	1126	U
32	1a	1129	C
32	1a	1133	G
32	1a	1134	G
32	1a	1135	U
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G
32	1a	1140	C
32	1a	1143	G
32	1a	1146	A
32	1a	1151	A
32	1a	1152	A
32	1a	1154	G
32	1a	1159	U
32	1a	1160	G
32	1a	1169	A
32	1a	1180	A
32	1a	1184	G
32	1a	1186	G
32	1a	1188	A
32	1a	1196	U
32	1a	1197	G
32	1a	1198	G
32	1a	1202	G
32	1a	1204	A
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1226	C
32	1a	1227	A
32	1a	1238	A
32	1a	1246	C
32	1a	1247	U
32	1a	1253	G
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C

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Mol	Chain	Res	Type
32	1a	1275	A
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1312	G
32	1a	1319	A
32	1a	1320	C
32	1a	1322	C
32	1a	1323	G
32	1a	1338	G
32	1a	1340	A
32	1a	1345	U
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1364	U
32	1a	1369	C
32	1a	1370	G
32	1a	1379	G
32	1a	1398	A
32	1a	1402	4OC
32	1a	1419	G
32	1a	1422	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1442(B)	A
32	1a	1446	U
32	1a	1452	C
32	1a	1469	G
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U

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Mol	Chain	Res	Type
32	1a	1517	G
32	1a	1529	G
32	1a	1530	G
32	1a	1532	U
53	1v	11	U
53	1v	12	A
53	1v	13	A
53	1v	22	U
55	1x	14	A
55	1x	18	G
55	1x	20	H2U
55	1x	21	H2U
55	1x	26	A
55	1x	46	A
55	1x	48	G
55	1x	54	5MU
55	1x	64	G
55	1x	76	A
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	63	U
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	78	A
1	2A	79	G
1	2A	83	G
1	2A	84	A
1	2A	90	U
1	2A	95	G
1	2A	100	G
1	2A	102	G
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	140	G
1	2A	141	A
1	2A	153	C

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Mol	Chain	Res	Type
1	2A	154(A)	C
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	248	G
1	2A	249	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	310	A
1	2A	311	A
1	2A	324	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	342	G
1	2A	352	G
1	2A	362	U
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	411	G
1	2A	422	A
1	2A	435	C
1	2A	444	C
1	2A	454	A
1	2A	455	C

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Mol	Chain	Res	Type
1	2A	457	A
1	2A	480	A
1	2A	481	G
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	652(A)	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	669	G
1	2A	671	C
1	2A	686	G
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G

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Mol	Chain	Res	Type
1	2A	790	C
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	854	G
1	2A	857	C
1	2A	859	G
1	2A	869	G
1	2A	874	G
1	2A	878	A
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	894	C
1	2A	895	U
1	2A	896	A
1	2A	897	C
1	2A	899	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	961	C
1	2A	968	G
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	996	A

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Mol	Chain	Res	Type
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1025	G
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1042	G
1	2A	1043	C
1	2A	1114	G
1	2A	1116	C
1	2A	1129	A
1	2A	1130	U
1	2A	1133	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142(A)	A
1	2A	1151	G
1	2A	1167	U
1	2A	1180	C
1	2A	1206	G
1	2A	1210	A
1	2A	1211	U
1	2A	1220	A
1	2A	1229	G
1	2A	1248	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1284	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1342	A
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A

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Mol	Chain	Res	Type
1	2A	1370	C
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1403	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	1461	G
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1495	A
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1532	C
1	2A	1547	C
1	2A	1554	A
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1579	A
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A

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Mol	Chain	Res	Type
1	2A	1587	A
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1616	A
1	2A	1647	G
1	2A	1648	C
1	2A	1654	A
1	2A	1671	U
1	2A	1674	G
1	2A	1675	C
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	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
1	2A	1847	A
1	2A	1848	A
1	2A	1861	G
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1940	U
1	2A	1955	U
1	2A	1963	U

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Mol	Chain	Res	Type
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2035	G
1	2A	2036	C
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2063	C
1	2A	2069	G
1	2A	2080	G
1	2A	2108	C
1	2A	2111	C
1	2A	2116	G
1	2A	2117	A
1	2A	2122	U
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2140	C
1	2A	2142	C

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Mol	Chain	Res	Type
1	2A	2145	C
1	2A	2146	C
1	2A	2149	G
1	2A	2150	U
1	2A	2153	G
1	2A	2154	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2162	G
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2170	A
1	2A	2172	U
1	2A	2174	C
1	2A	2175	C
1	2A	2176	A
1	2A	2178	C
1	2A	2181	G
1	2A	2182	G
1	2A	2183	C
1	2A	2185	C
1	2A	2186	G
1	2A	2188	C
1	2A	2189	U
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2219	G
1	2A	2225	A
1	2A	2239	G
1	2A	2274	A
1	2A	2275	C
1	2A	2279	G
1	2A	2280	G
1	2A	2283	C

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Mol	Chain	Res	Type
1	2A	2287	A
1	2A	2288	A
1	2A	2305	A
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2325	G
1	2A	2327	A
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2341	G
1	2A	2343	C
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2376	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2388	A
1	2A	2396	G
1	2A	2402	C
1	2A	2406	U
1	2A	2410	G
1	2A	2414	G
1	2A	2422	A
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2431	U
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2458	G
1	2A	2468	G
1	2A	2476	A
1	2A	2478	A
1	2A	2480	C
1	2A	2490	G

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Mol	Chain	Res	Type
1	2A	2494	G
1	2A	2497	A
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2513	G
1	2A	2518	A
1	2A	2529	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2574	G
1	2A	2578	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2630	G
1	2A	2634	G
1	2A	2654	A
1	2A	2682	U
1	2A	2689	U
1	2A	2690	C
1	2A	2691	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2730	C
1	2A	2733	A
1	2A	2748	A
1	2A	2751	G
1	2A	2758	A
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2789	C
1	2A	2793	G

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Mol	Chain	Res	Type
1	2A	2794	C
1	2A	2802	G
1	2A	2808	U
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2839	G
1	2A	2872	G
1	2A	2873	A
1	2A	2875	C
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	2	C
2	2B	4	C
2	2B	5	C
2	2B	8	U
2	2B	12	C
2	2B	13	A
2	2B	15	A
2	2B	17	C
2	2B	20	C
2	2B	30	C
2	2B	35	U
2	2B	41	U
2	2B	42	C
2	2B	56	G
2	2B	73	A
2	2B	85	G
2	2B	106	G
2	2B	108	U
2	2B	109	C
2	2B	110	G
2	2B	120	A
32	2a	5	U
32	2a	7	G
32	2a	8	A
32	2a	9	G

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Mol	Chain	Res	Type
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	52	G
32	2a	54	C
32	2a	66	G
32	2a	73	G
32	2a	80	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	115	G
32	2a	116	A
32	2a	120	A
32	2a	121	C
32	2a	129(A)	G
32	2a	131	C
32	2a	142	G
32	2a	144	G
32	2a	147	G
32	2a	157	G
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	183	G
32	2a	189(B)	C
32	2a	189(J)	G
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	220	G
32	2a	245	C
32	2a	247	G
32	2a	250	A
32	2a	251	G

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Mol	Chain	Res	Type
32	2a	258	G
32	2a	262	A
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	329	A
32	2a	332	G
32	2a	345	C
32	2a	348	G
32	2a	350	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	384	G
32	2a	388	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	414	A
32	2a	421	U
32	2a	422	C
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U

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Mol	Chain	Res	Type
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
32	2a	532	A
32	2a	536	C
32	2a	545	C
32	2a	547	A
32	2a	559	A
32	2a	560	U
32	2a	561	U
32	2a	568	G
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	592	G
32	2a	596	C
32	2a	618	C
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	657	G
32	2a	665	A
32	2a	666	G
32	2a	687	A
32	2a	688	G
32	2a	702	A
32	2a	703	G
32	2a	717	C
32	2a	718	G
32	2a	719	C
32	2a	720	C
32	2a	721	G
32	2a	724	G
32	2a	731	G
32	2a	733	A
32	2a	734	G
32	2a	746	A
32	2a	747	C

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Mol	Chain	Res	Type
32	2a	748	C
32	2a	755	G
32	2a	760	G
32	2a	766	A
32	2a	773	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	836	G
32	2a	838	G
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	851	G
32	2a	857	C
32	2a	858	G
32	2a	859	A
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	935	A
32	2a	942	G
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	987	G
32	2a	989	C

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Mol	Chain	Res	Type
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	997	U
32	2a	999	C
32	2a	1003	G
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1011	G
32	2a	1013	G
32	2a	1022	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(D)	A
32	2a	1032	G
32	2a	1033	G
32	2a	1035	A
32	2a	1037	C
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1041	A
32	2a	1044	A
32	2a	1045	C
32	2a	1046	A
32	2a	1050	G
32	2a	1054	C
32	2a	1056	U
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1079	G
32	2a	1081	G
32	2a	1087	G

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Mol	Chain	Res	Type
32	2a	1088	G
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1113	C
32	2a	1117	G
32	2a	1122	U
32	2a	1126	U
32	2a	1129	C
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1144	G
32	2a	1146	A
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1161	C
32	2a	1171	G
32	2a	1174	G
32	2a	1179	A
32	2a	1181	G
32	2a	1182	G
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1200	C
32	2a	1202	G
32	2a	1204	A
32	2a	1212	U
32	2a	1215	G
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1240	U
32	2a	1248	A
32	2a	1250	A
32	2a	1251	A
32	2a	1256	A
32	2a	1257	U

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Mol	Chain	Res	Type
32	2a	1258	G
32	2a	1260	C
32	2a	1262	C
32	2a	1263	C
32	2a	1268	A
32	2a	1270	C
32	2a	1272	G
32	2a	1275	A
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1281	U
32	2a	1286	A
32	2a	1287	A
32	2a	1294	G
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U
32	2a	1303	C
32	2a	1305	G
32	2a	1317	C
32	2a	1321	C
32	2a	1323	G
32	2a	1336	C
32	2a	1340	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1364	U
32	2a	1368	G
32	2a	1377	A
32	2a	1397	C
32	2a	1398	A
32	2a	1399	C
32	2a	1400	5MC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1457	G

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Mol	Chain	Res	Type
32	2a	1492	A
32	2a	1493	A
32	2a	1494	G
32	2a	1503	A
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	11	U
53	2v	13	A
53	2v	22	U
55	2x	6	G
55	2x	9	A
55	2x	18	G
55	2x	19	G
55	2x	20	H2U
55	2x	21	H2U
55	2x	22	A
55	2x	26	A
55	2x	37	MIA
55	2x	42	G
55	2x	46	A
55	2x	48	G
55	2x	76	A

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	266	G
1	1A	278	A
1	1A	548	A
1	1A	573	G
1	1A	685	A
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	776	G
1	1A	974	G

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Mol	Chain	Res	Type
1	1A	1047	G
1	1A	1065	U
1	1A	1142(A)	A
1	1A	1174	A
1	1A	1176	G
1	1A	1210	A
1	1A	1275	A
1	1A	1379	A
1	1A	1420	U
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1653	G
1	1A	1992	G
1	1A	2126	A
1	1A	2134	A
1	1A	2158	A
1	1A	2181	G
1	1A	2183	C
1	1A	2333	A
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2439	A
1	1A	2689	U
1	2A	34	C
1	2A	195	A
1	2A	196	A
1	2A	266	G
1	2A	277	C
1	2A	310	A
1	2A	528	A
1	2A	752	A
1	2A	827	U
1	2A	856	C
1	2A	896	A
1	2A	900	A
1	2A	1210	A
1	2A	1379	A
1	2A	1530	C
1	2A	1653	G
1	2A	1992	G

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Mol	Chain	Res	Type
1	2A	2062	A
1	2A	2126	A
1	2A	2406	U
1	2A	2430	A
1	2A	2689	U

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

66 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
32	UR3	1a	1498	32	19,22,23	1.04	1 (5%)	26,32,35	1.67	4 (15%)
32	4OC	1a	1402	56,32	20,23,24	0.76	0	25,32,35	1.04	2 (8%)
55	PSU	1x	55	55	18,21,22	1.31	2 (11%)	21,30,33	1.97	3 (14%)
1	PSU	2A	2605	1	18,21,22	1.35	3 (16%)	21,30,33	2.11	5 (23%)
1	PSU	1A	1911	1	18,21,22	1.39	3 (16%)	21,30,33	1.95	4 (19%)
32	5MC	2a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.23	2 (7%)
1	5MC	2A	1962	1,56	19,22,23	1.62	3 (15%)	26,32,35	1.08	2 (7%)
32	5MC	2a	967	56,32	19,22,23	1.68	3 (15%)	26,32,35	1.11	2 (7%)
32	M2G	2a	966	32	24,27,28	1.32	3 (12%)	33,40,43	1.91	6 (18%)
55	H2U	1x	21	55	18,21,22	0.87	2 (11%)	19,30,33	0.91	0
55	PSU	2x	32	55	18,21,22	1.35	2 (11%)	21,30,33	2.00	3 (14%)
55	PSU	2x	55	55	18,21,22	1.37	2 (11%)	21,30,33	2.01	4 (19%)
1	PSU	2A	1911	1	18,21,22	1.36	3 (16%)	21,30,33	2.00	4 (19%)
1	OMG	1A	2251	55,1,56	23,26,27	1.25	3 (13%)	32,38,41	2.05	6 (18%)
32	PSU	1a	516	56,32	18,21,22	1.37	2 (11%)	21,30,33	2.07	4 (19%)
1	OMG	2A	2251	55,1,56	23,26,27	1.22	3 (13%)	32,38,41	1.92	6 (18%)
32	5MC	1a	1404	32	19,22,23	1.77	3 (15%)	26,32,35	1.24	4 (15%)
1	5MU	1A	1939	1	19,22,23	1.47	4 (21%)	27,32,35	2.16	6 (22%)
32	MA6	1a	1519	32	23,26,27	0.39	0	33,38,41	2.11	9 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	1A	1920	1	19,22,23	0.84	0	25,31,34	0.94	0
55	MIA	1x	37	55	21,24,32	1.61	4 (19%)	30,35,47	2.06	7 (23%)
32	M2G	1a	966	32	24,27,28	1.34	3 (12%)	33,40,43	1.85	6 (18%)
32	MA6	2a	1518	32	23,26,27	0.42	0	33,38,41	2.09	9 (27%)
43	0TD	1l	92	43	8,9,10	4.63	2 (25%)	6,11,13	8.09	2 (33%)
54	MEQ	1w	230	54	8,9,10	0.60	0	5,10,12	1.27	1 (20%)
1	OMC	2A	1920	1	19,22,23	0.80	0	25,31,34	0.95	0
1	OMU	2A	2552	1,56	19,22,23	1.18	3 (15%)	25,31,34	1.81	5 (20%)
43	0TD	2l	92	43	8,9,10	4.69	2 (25%)	6,11,13	4.03	2 (33%)
55	H2U	2x	20	55	18,21,22	0.87	2 (11%)	19,30,33	1.01	1 (5%)
1	5MC	2A	1942	1,56	19,22,23	1.72	3 (15%)	26,32,35	1.13	2 (7%)
32	UR3	2a	1498	32	19,22,23	1.00	1 (5%)	26,32,35	1.79	3 (11%)
54	MEQ	2w	230	54	8,9,10	0.62	0	5,10,12	0.54	0
32	5MC	2a	1404	32	19,22,23	1.64	3 (15%)	26,32,35	1.19	2 (7%)
32	MA6	1a	1518	32	23,26,27	0.40	0	33,38,41	2.08	9 (27%)
55	4SU	1x	8	55	18,21,22	1.84	4 (22%)	25,30,33	1.89	4 (16%)
32	4OC	2a	1402	56,32	20,23,24	0.79	0	25,32,35	1.02	3 (12%)
32	5MC	1a	1407	32	19,22,23	1.72	3 (15%)	26,32,35	1.17	4 (15%)
1	2MA	2A	2503	1,56	22,25,26	1.43	3 (13%)	32,37,40	2.40	8 (25%)
55	H2U	2x	21	55	18,21,22	0.87	2 (11%)	19,30,33	0.77	0
55	4SU	2x	8	55	18,21,22	1.78	4 (22%)	25,30,33	1.95	5 (20%)
1	PSU	1A	1917	1	18,21,22	1.41	3 (16%)	21,30,33	2.13	4 (19%)
32	G7M	1a	527	56,32	23,26,27	1.51	3 (13%)	34,39,42	1.73	5 (14%)
1	5MC	1A	1962	1,56	19,22,23	1.73	3 (15%)	26,32,35	1.16	3 (11%)
32	G7M	2a	527	32	23,26,27	1.53	3 (13%)	34,39,42	1.74	5 (14%)
32	MA6	2a	1519	32	23,26,27	0.43	0	33,38,41	2.18	10 (30%)
1	PSU	2A	1917	1,56	18,21,22	1.38	2 (11%)	21,30,33	2.06	4 (19%)
32	5MC	1a	1400	32	19,22,23	1.71	3 (15%)	26,32,35	1.18	3 (11%)
1	5MC	1A	1942	1,56	19,22,23	1.55	2 (10%)	26,32,35	1.20	4 (15%)
32	5MC	1a	967	32	19,22,23	1.47	2 (10%)	26,32,35	1.06	2 (7%)
55	5MU	1x	54	55	19,22,23	1.45	4 (21%)	27,32,35	1.91	6 (22%)
1	5MU	2A	1939	1,56	19,22,23	1.47	5 (26%)	27,32,35	2.24	7 (25%)
1	PSU	1A	2605	1,56	18,21,22	1.46	4 (22%)	21,30,33	2.17	4 (19%)
32	2MG	1a	1207	32	23,26,27	1.27	4 (17%)	33,38,41	2.24	8 (24%)
32	2MG	2a	1207	32	23,26,27	1.30	4 (17%)	33,38,41	2.11	5 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MU	2A	1915	1	19,22,23	1.53	6 (31%)	27,32,35	2.13	6 (22%)
55	5MU	2x	54	55	19,22,23	1.39	4 (21%)	27,32,35	2.06	6 (22%)
1	5MU	1A	1915	1	19,22,23	1.40	6 (31%)	27,32,35	2.06	7 (25%)
1	2MA	1A	2503	1,56	22,25,26	1.42	5 (22%)	32,37,40	2.33	11 (34%)
55	H2U	1x	20	55	18,21,22	0.90	1 (5%)	19,30,33	1.11	1 (5%)
32	PSU	2a	516	32	18,21,22	1.36	3 (16%)	21,30,33	1.96	5 (23%)
1	OMU	1A	2552	1,56	19,22,23	1.29	4 (21%)	25,31,34	1.92	5 (20%)
55	MIA	2x	37	55	21,24,32	1.61	3 (14%)	30,35,47	2.05	9 (30%)
32	5MC	2a	1407	56,32	19,22,23	1.70	3 (15%)	26,32,35	1.25	3 (11%)
55	PSU	2x	39	55	18,21,22	1.40	2 (11%)	21,30,33	1.82	4 (19%)
55	PSU	1x	39	55	18,21,22	1.45	2 (11%)	21,30,33	1.74	3 (14%)
55	PSU	1x	32	55	18,21,22	1.31	2 (11%)	21,30,33	1.94	3 (14%)

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
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	56,32	-	2/9/29/30	0/2/2/2
55	PSU	1x	55	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	2/7/25/26	0/2/2/2
1	5MC	2A	1962	1,56	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	56,32	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
55	H2U	1x	21	55	-	5/7/38/39	0/2/2/2
55	PSU	2x	32	55	-	0/7/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	55,1,56	-	0/9/27/28	0/3/3/3
32	PSU	1a	516	56,32	-	1/7/25/26	0/2/2/2
1	OMG	2A	2251	55,1,56	-	0/9/27/28	0/3/3/3
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
1	OMC	1A	1920	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	MIA	1x	37	55	-	1/7/25/34	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
54	MEQ	1w	230	54	-	5/8/9/11	-
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	OMU	2A	2552	1,56	-	0/9/27/28	0/2/2/2
43	0TD	2l	92	43	-	1/7/12/14	-
55	H2U	2x	20	55	-	2/7/38/39	0/2/2/2
1	5MC	2A	1942	1,56	-	0/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
54	MEQ	2w	230	54	-	7/8/9/11	-
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	56,32	-	2/9/29/30	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	2MA	2A	2503	1,56	-	2/7/25/26	0/3/3/3
55	H2U	2x	21	55	-	5/7/38/39	0/2/2/2
55	4SU	2x	8	55	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	56,32	-	2/7/25/26	0/3/3/3
1	5MC	1A	1962	1,56	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	32	-	0/7/25/26	0/3/3/3
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
1	PSU	2A	1917	1,56	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	1,56	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
55	5MU	1x	54	55	-	2/7/25/26	0/2/2/2
1	5MU	2A	1939	1,56	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	1,56	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	1/9/27/28	0/3/3/3
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
1	2MA	1A	2503	1,56	-	1/7/25/26	0/3/3/3
55	H2U	1x	20	55	-	2/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
1	OMU	1A	2552	1,56	-	0/9/27/28	0/2/2/2
55	MIA	2x	37	55	-	2/7/25/34	0/3/3/3
32	5MC	2a	1407	56,32	-	0/7/25/26	0/2/2/2
55	PSU	2x	39	55	-	0/7/25/26	0/2/2/2
55	PSU	1x	39	55	-	0/7/25/26	0/2/2/2
55	PSU	1x	32	55	-	0/7/25/26	0/2/2/2

All (167) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.57	1.69	1.82
43	1l	92	0TD	CB-SB	-12.53	1.69	1.82
32	1a	1404	5MC	C5-C4	6.55	1.49	1.44
32	1a	1407	5MC	C5-C4	6.39	1.49	1.44
1	2A	1942	5MC	C5-C4	6.28	1.48	1.44
1	1A	1962	5MC	C5-C4	6.27	1.48	1.44
32	2a	967	5MC	C5-C4	6.24	1.48	1.44
32	1a	1400	5MC	C5-C4	6.19	1.48	1.44
32	2a	1400	5MC	C5-C4	6.16	1.48	1.44
32	2a	1407	5MC	C5-C4	6.10	1.48	1.44
32	2a	1404	5MC	C5-C4	5.92	1.48	1.44
1	2A	1962	5MC	C5-C4	5.74	1.48	1.44
1	1A	1942	5MC	C5-C4	5.35	1.48	1.44
32	1a	967	5MC	C5-C4	5.12	1.48	1.44
55	2x	37	MIA	C5-C4	4.95	1.47	1.39
55	1x	37	MIA	C5-C4	4.92	1.47	1.39
55	1x	8	4SU	C4-S4	-4.83	1.60	1.68
32	2a	527	G7M	C5-N7	-4.82	1.33	1.39
32	1a	527	G7M	C5-N7	-4.70	1.33	1.39
55	2x	8	4SU	C4-S4	-4.65	1.60	1.68
1	2A	2503	2MA	C5-C4	4.16	1.46	1.39
1	1A	2503	2MA	C5-C4	3.96	1.46	1.39
55	2x	39	PSU	C6-C5	3.93	1.39	1.35
55	1x	39	PSU	C6-C5	3.88	1.39	1.35
55	2x	55	PSU	C6-C5	3.87	1.39	1.35
1	1A	1911	PSU	C6-C5	3.60	1.39	1.35
55	1x	55	PSU	C6-C5	3.58	1.39	1.35
55	2x	32	PSU	C6-C5	3.55	1.39	1.35
55	1x	8	4SU	C4-N3	-3.54	1.34	1.37
32	1a	516	PSU	C6-C5	3.50	1.39	1.35
32	2a	516	PSU	C6-C5	3.48	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1207	2MG	C5-C4	3.43	1.48	1.38
32	2a	966	M2G	C5-C4	3.37	1.48	1.38
1	2A	1917	PSU	C6-C5	3.33	1.39	1.35
32	1a	966	M2G	C5-C4	3.32	1.47	1.38
1	1A	1917	PSU	C6-C5	3.29	1.38	1.35
32	1a	1207	2MG	C5-C4	3.24	1.47	1.38
32	1a	527	G7M	C5-C4	3.23	1.46	1.38
32	2a	527	G7M	C5-C4	3.21	1.46	1.38
32	1a	966	M2G	C2-N2	3.20	1.41	1.35
1	2A	2605	PSU	C6-C5	3.16	1.38	1.35
55	1x	54	5MU	C6-C5	3.14	1.39	1.34
55	1x	32	PSU	C6-C5	3.12	1.38	1.35
1	1A	2251	OMG	C6-N1	-3.12	1.33	1.38
43	2l	92	0TD	CB-CA	-3.09	1.53	1.54
1	2A	2251	OMG	C5-C4	3.09	1.47	1.38
1	1A	2605	PSU	C4-N3	-3.07	1.33	1.38
1	1A	1942	5MC	C6-C5	3.06	1.39	1.34
1	1A	2251	OMG	C5-C4	3.06	1.47	1.38
55	2x	37	MIA	C5-C6	3.05	1.49	1.41
1	2A	1911	PSU	C6-C5	3.00	1.38	1.35
1	2A	1915	5MU	C6-C5	2.99	1.39	1.34
1	1A	1939	5MU	C4-N3	-2.97	1.33	1.38
32	1a	1400	5MC	C6-C5	2.96	1.39	1.34
55	2x	8	4SU	C4-N3	-2.95	1.34	1.37
1	1A	1915	5MU	C4-N3	-2.93	1.33	1.38
1	1A	1939	5MU	C6-C5	2.91	1.39	1.34
1	2A	1939	5MU	C4-C5	2.90	1.49	1.44
55	2x	54	5MU	C6-C5	2.90	1.39	1.34
1	2A	1962	5MC	C6-C5	2.88	1.39	1.34
32	2a	1400	5MC	C6-C5	2.87	1.39	1.34
1	1A	1962	5MC	C6-C5	2.86	1.39	1.34
1	2A	1915	5MU	C2-N1	2.86	1.42	1.38
32	1a	967	5MC	C6-C5	2.85	1.39	1.34
55	1x	39	PSU	C4-N3	-2.82	1.33	1.38
1	2A	2251	OMG	C6-N1	-2.80	1.33	1.38
55	1x	37	MIA	C5-C6	2.79	1.48	1.41
1	1A	1917	PSU	C4-N3	-2.79	1.33	1.38
32	1a	1404	5MC	C6-C5	2.75	1.39	1.34
32	2a	1407	5MC	C6-C5	2.74	1.39	1.34
32	2a	966	M2G	C2-N2	2.73	1.40	1.35
55	1x	8	4SU	C5-C4	-2.73	1.39	1.42
1	2A	2605	PSU	C4-N3	-2.72	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	1939	5MU	C4-N3	-2.72	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.72	1.33	1.38
1	2A	1942	5MC	C6-C5	2.71	1.39	1.34
1	1A	1911	PSU	C4-N3	-2.71	1.33	1.38
55	2x	8	4SU	C5-C4	-2.70	1.39	1.42
32	2a	1404	5MC	C6-C5	2.70	1.39	1.34
1	1A	2605	PSU	C6-C5	2.69	1.38	1.35
1	2A	1915	5MU	C4-N3	-2.69	1.33	1.38
1	2A	1915	5MU	C4-C5	2.67	1.49	1.44
1	1A	2503	2MA	C5-N7	-2.64	1.34	1.39
1	1A	2552	OMU	C4-N3	-2.63	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.63	1.33	1.38
32	1a	516	PSU	C4-N3	-2.62	1.33	1.38
55	2x	8	4SU	C2-N1	2.60	1.42	1.38
55	1x	54	5MU	C4-N3	-2.58	1.34	1.38
32	2a	967	5MC	C6-C5	2.57	1.38	1.34
55	2x	39	PSU	C4-N3	-2.57	1.34	1.38
55	2x	32	PSU	C4-N3	-2.56	1.34	1.38
1	2A	2552	OMU	C4-N3	-2.56	1.34	1.38
55	2x	37	MIA	C8-N7	2.55	1.36	1.31
55	2x	54	5MU	C4-C5	2.54	1.49	1.44
1	2A	1917	PSU	C4-N3	-2.54	1.34	1.38
1	2A	1939	5MU	C6-C5	2.54	1.38	1.34
32	2a	1207	2MG	C6-N1	-2.53	1.34	1.38
1	1A	2552	OMU	C2-N3	-2.52	1.33	1.38
32	1a	1207	2MG	C6-N1	-2.52	1.34	1.38
1	2A	2503	2MA	C5-N7	-2.51	1.34	1.39
32	2a	966	M2G	C6-N1	-2.51	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.48	1.33	1.38
32	2a	527	G7M	C6-N1	-2.48	1.34	1.38
32	2a	516	PSU	C4-N3	-2.47	1.34	1.38
1	1A	2503	2MA	C4-N9	-2.44	1.32	1.37
55	2x	55	PSU	C4-N3	-2.43	1.34	1.38
55	2x	20	H2U	C4-N3	-2.42	1.33	1.37
32	1a	1207	2MG	C2-N3	2.42	1.36	1.32
1	2A	1939	5MU	C2-N3	-2.42	1.33	1.38
32	1a	1404	5MC	C6-N1	-2.42	1.33	1.38
1	2A	1939	5MU	C6-N1	-2.41	1.33	1.38
1	1A	2552	OMU	C2-N1	2.41	1.42	1.38
1	1A	1915	5MU	C6-C5	2.41	1.38	1.34
55	1x	37	MIA	C5-N7	-2.40	1.34	1.39
32	1a	1498	UR3	C2-N1	2.39	1.41	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1x	37	MIA	C8-N7	2.39	1.36	1.31
1	1A	1962	5MC	C6-N1	-2.39	1.33	1.38
55	1x	21	H2U	C4-N3	-2.38	1.33	1.37
1	2A	1962	5MC	C6-N1	-2.37	1.34	1.38
32	2a	1207	2MG	C2-N3	2.37	1.36	1.32
55	1x	54	5MU	C2-N1	2.37	1.42	1.38
32	1a	527	G7M	C6-N1	-2.37	1.34	1.38
55	1x	54	5MU	C4-C5	2.37	1.48	1.44
1	1A	2605	PSU	C2-N3	-2.36	1.33	1.37
55	1x	55	PSU	C4-N3	-2.36	1.34	1.38
55	2x	54	5MU	C4-N3	-2.35	1.34	1.38
55	1x	32	PSU	C4-N3	-2.35	1.34	1.38
32	1a	1407	5MC	C6-C5	2.34	1.38	1.34
32	2a	1407	5MC	C6-N1	-2.34	1.34	1.38
1	1A	2605	PSU	C2-N1	-2.34	1.33	1.36
32	1a	1400	5MC	C6-N1	-2.34	1.34	1.38
55	2x	20	H2U	C2-N3	-2.34	1.33	1.38
55	2x	21	H2U	C2-N3	-2.33	1.33	1.38
55	1x	20	H2U	C2-N3	-2.32	1.33	1.38
32	1a	1407	5MC	C6-N1	-2.29	1.34	1.38
32	1a	966	M2G	C6-N1	-2.29	1.34	1.38
1	2A	2251	OMG	C5-N7	-2.29	1.34	1.39
55	1x	21	H2U	C2-N3	-2.28	1.34	1.38
1	1A	1915	5MU	C2-N1	2.28	1.42	1.38
32	2a	1400	5MC	C6-N1	-2.28	1.34	1.38
1	1A	1917	PSU	C2-N3	-2.27	1.33	1.37
1	2A	1942	5MC	C6-N1	-2.26	1.34	1.38
1	1A	2503	2MA	C8-N7	2.25	1.36	1.31
55	2x	54	5MU	C2-N1	2.23	1.42	1.38
1	2A	2503	2MA	C5-C6	2.22	1.47	1.41
1	1A	1939	5MU	C2-N3	-2.22	1.34	1.38
32	2a	967	5MC	C6-N1	-2.20	1.34	1.38
55	1x	8	4SU	C2-N3	-2.19	1.34	1.38
1	1A	1915	5MU	C6-N1	-2.17	1.34	1.38
1	1A	2552	OMU	C5-C4	-2.15	1.39	1.43
1	1A	2503	2MA	C5-C6	2.15	1.47	1.41
55	2x	21	H2U	C4-N3	-2.14	1.34	1.37
1	1A	2251	OMG	C5-N7	-2.11	1.34	1.39
1	2A	1915	5MU	C6-N1	-2.08	1.34	1.38
32	2a	516	PSU	O4'-C1'	-2.08	1.41	1.43
1	1A	1915	5MU	C4-C5	2.08	1.48	1.44
1	1A	1915	5MU	C2-N3	-2.08	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	OMU	C2-N3	-2.08	1.34	1.38
32	1a	1207	2MG	C5-N7	-2.07	1.34	1.39
1	1A	1911	PSU	C2-N3	-2.07	1.34	1.37
1	2A	1915	5MU	C2-N3	-2.06	1.34	1.38
32	2a	1498	UR3	C2-N1	2.05	1.41	1.38
32	2a	1207	2MG	C5-N7	-2.05	1.35	1.39
1	2A	2552	OMU	C5-C4	-2.03	1.39	1.43
1	2A	1911	PSU	C2-N3	-2.03	1.34	1.37
1	2A	2605	PSU	C2-N3	-2.03	1.34	1.37
43	1l	92	0TD	CB-CG	2.02	1.55	1.52

All (282) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	1l	92	0TD	CSB-SB-CB	-19.43	67.44	102.36
43	2l	92	0TD	CSB-SB-CB	-9.09	86.02	102.36
1	2A	2503	2MA	C5-C4-N3	-8.22	118.52	127.18
1	1A	2503	2MA	C5-C4-N3	-7.71	119.06	127.18
32	2a	1498	UR3	C4-N3-C2	-7.32	118.69	124.58
32	1a	1207	2MG	C2-N3-C4	7.19	120.99	112.00
32	2a	1207	2MG	C2-N3-C4	7.06	120.83	112.00
1	2A	2503	2MA	N3-C4-N9	7.06	135.95	126.99
1	1A	2605	PSU	N1-C2-N3	6.87	122.41	115.17
1	1A	1917	PSU	N1-C2-N3	6.68	122.22	115.17
1	1A	2251	OMG	C5-C4-N3	-6.55	117.96	128.39
1	2A	2605	PSU	N1-C2-N3	6.53	122.05	115.17
32	1a	1207	2MG	C5-C4-N3	-6.51	118.03	128.39
32	1a	516	PSU	N1-C2-N3	6.48	122.00	115.17
32	2a	966	M2G	C5-C4-N3	-6.45	118.12	128.39
1	2A	1917	PSU	N1-C2-N3	6.38	121.90	115.17
32	2a	1207	2MG	C5-C4-N3	-6.38	118.24	128.39
32	1a	1498	UR3	C4-N3-C2	-6.36	119.47	124.58
55	2x	55	PSU	N1-C2-N3	6.21	121.72	115.17
32	1a	966	M2G	C5-C4-N3	-6.19	118.53	128.39
1	1A	2503	2MA	N3-C4-N9	6.12	134.76	126.99
1	2A	1911	PSU	N1-C2-N3	6.12	121.62	115.17
55	2x	32	PSU	N1-C2-N3	6.07	121.57	115.17
1	1A	1911	PSU	N1-C2-N3	6.02	121.52	115.17
1	2A	2251	OMG	C5-C4-N3	-6.02	118.80	128.39
55	1x	37	MIA	C5-C4-N3	-6.02	118.43	126.72
55	1x	55	PSU	N1-C2-N3	6.01	121.51	115.17
55	1x	32	PSU	N1-C2-N3	5.82	121.31	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	37	MIA	C5-C4-N3	-5.82	118.70	126.72
32	2a	516	PSU	N1-C2-N3	5.73	121.22	115.17
1	2A	1939	5MU	C4-N3-C2	-5.66	119.92	127.34
55	1x	39	PSU	N1-C2-N3	5.64	121.11	115.17
55	1x	8	4SU	C5-C4-N3	5.60	119.96	114.75
55	2x	39	PSU	N1-C2-N3	5.59	121.06	115.17
32	1a	527	G7M	N9-C4-N3	5.49	136.94	125.95
1	2A	1915	5MU	N3-C2-N1	5.47	122.01	114.89
32	2a	527	G7M	N9-C4-N3	5.45	136.85	125.95
55	2x	54	5MU	N3-C2-N1	5.45	121.98	114.89
1	2A	1939	5MU	N3-C2-N1	5.40	121.92	114.89
32	2a	527	G7M	C5-C4-N3	-5.38	117.98	128.15
1	1A	2251	OMG	C2-N3-C4	5.24	121.32	112.30
1	1A	2552	OMU	C4-N3-C2	-5.23	120.12	126.61
32	1a	527	G7M	C5-C4-N3	-5.22	118.28	128.15
55	1x	8	4SU	C4-N3-C2	-5.22	122.31	127.31
1	2A	1915	5MU	C4-N3-C2	-5.21	120.51	127.34
55	2x	8	4SU	C4-N3-C2	-5.19	122.34	127.31
1	1A	1939	5MU	C4-N3-C2	-5.12	120.62	127.34
55	2x	8	4SU	C5-C4-N3	5.08	119.48	114.75
55	2x	54	5MU	C4-N3-C2	-5.05	120.72	127.34
32	1a	1518	MA6	N1-C2-N3	-5.03	120.97	128.58
1	1A	1915	5MU	N3-C2-N1	5.00	121.40	114.89
32	1a	1519	MA6	C5-C4-N3	-4.98	119.86	126.72
1	1A	1915	5MU	C4-N3-C2	-4.97	120.82	127.34
32	2a	966	M2G	N9-C4-N3	4.97	135.88	125.95
32	2a	1519	MA6	N1-C2-N3	-4.96	121.08	128.58
32	2a	1518	MA6	C5-C4-N3	-4.89	119.98	126.72
1	1A	1939	5MU	C5-C4-N3	4.84	119.53	115.32
1	1A	2251	OMG	N9-C4-N3	4.84	135.63	125.95
1	2A	2251	OMG	N9-C4-N3	4.81	135.57	125.95
32	2a	527	G7M	C2-N3-C4	4.79	120.54	112.30
1	2A	2552	OMU	C4-N3-C2	-4.78	120.68	126.61
32	1a	966	M2G	N9-C4-N3	4.76	135.48	125.95
32	2a	1518	MA6	N1-C2-N3	-4.76	121.37	128.58
1	2A	1939	5MU	C5-C6-N1	-4.75	118.16	123.31
1	1A	1939	5MU	O4-C4-C5	-4.73	119.50	124.92
55	1x	54	5MU	N3-C2-N1	4.73	121.04	114.89
1	2A	2251	OMG	C2-N3-C4	4.72	120.43	112.30
32	1a	1207	2MG	N9-C4-N3	4.71	135.37	125.95
32	2a	1207	2MG	N9-C4-N3	4.70	135.34	125.95
32	2a	1519	MA6	C5-C4-N3	-4.62	120.35	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1519	MA6	N1-C2-N3	-4.59	121.63	128.58
32	1a	527	G7M	C2-N3-C4	4.58	120.19	112.30
55	1x	37	MIA	N3-C4-N9	4.57	134.94	127.17
1	1A	1939	5MU	N3-C2-N1	4.56	120.83	114.89
1	1A	1915	5MU	C5-C4-N3	4.53	119.26	115.32
32	2a	966	M2G	C2-N3-C4	4.47	120.78	112.51
32	1a	966	M2G	C2-N3-C4	4.45	120.75	112.51
55	1x	54	5MU	C4-N3-C2	-4.45	121.50	127.34
1	2A	2605	PSU	C4-N3-C2	-4.41	120.30	126.37
1	2A	1939	5MU	C5-C4-N3	4.36	119.11	115.32
1	1A	1917	PSU	C4-N3-C2	-4.36	120.37	126.37
1	1A	2605	PSU	C4-N3-C2	-4.33	120.40	126.37
1	2A	2552	OMU	N3-C2-N1	4.33	120.53	114.89
1	2A	1915	5MU	C5-C4-N3	4.31	119.07	115.32
32	1a	1518	MA6	C5-C4-N3	-4.29	120.81	126.72
32	2a	1519	MA6	C4-C5-N7	-4.29	105.67	110.58
32	1a	516	PSU	C4-N3-C2	-4.28	120.47	126.37
1	2A	1911	PSU	C4-N3-C2	-4.26	120.50	126.37
1	1A	1939	5MU	C5-C6-N1	-4.26	118.68	123.31
1	2A	1917	PSU	C4-N3-C2	-4.23	120.54	126.37
55	2x	55	PSU	C4-N3-C2	-4.21	120.57	126.37
1	1A	2552	OMU	N3-C2-N1	4.21	120.37	114.89
55	2x	37	MIA	C4-C5-N7	-4.20	105.78	110.58
32	2a	1400	5MC	C5-C6-N1	-4.20	118.75	123.31
32	2a	1519	MA6	C5-N7-C8	4.18	110.02	103.45
55	2x	37	MIA	N3-C4-N9	4.14	134.21	127.17
1	1A	1911	PSU	C4-N3-C2	-4.11	120.70	126.37
1	1A	2552	OMU	C5-C4-N3	4.10	120.54	114.80
55	2x	32	PSU	C4-N3-C2	-4.07	120.76	126.37
1	1A	2605	PSU	O2-C2-N1	-3.99	118.67	122.79
32	1a	1518	MA6	C5-N7-C8	3.99	109.71	103.45
32	1a	1518	MA6	C2-N1-C6	3.98	121.56	111.83
55	1x	54	5MU	C5-C4-N3	3.98	118.78	115.32
55	1x	54	5MU	O4-C4-C5	-3.94	120.41	124.92
32	2a	516	PSU	C4-N3-C2	-3.94	120.95	126.37
32	1a	1519	MA6	C2-N1-C6	3.93	121.44	111.83
55	1x	32	PSU	C4-N3-C2	-3.93	120.96	126.37
32	2a	1519	MA6	C2-N1-C6	3.93	121.42	111.83
55	1x	55	PSU	C4-N3-C2	-3.92	120.97	126.37
1	1A	2503	2MA	N6-C6-N1	3.90	122.29	117.03
32	2a	1518	MA6	C2-N1-C6	3.89	121.32	111.83
32	2a	1518	MA6	C5-N7-C8	3.88	109.55	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1518	MA6	N9-C8-N7	-3.88	108.43	113.94
32	2a	1518	MA6	C4-C5-N7	-3.85	106.19	110.58
55	2x	54	5MU	O4-C4-C5	-3.79	120.58	124.92
55	1x	37	MIA	C4-C5-N7	-3.79	106.25	110.58
55	2x	54	5MU	C5-C4-N3	3.77	118.60	115.32
1	2A	1917	PSU	O2-C2-N1	-3.74	118.93	122.79
55	1x	32	PSU	O2-C2-N1	-3.73	118.94	122.79
32	2a	1404	5MC	C5-C6-N1	-3.71	119.28	123.31
55	1x	37	MIA	C2-N3-C4	3.71	120.89	111.83
55	2x	37	MIA	C2-N3-C4	3.68	120.82	111.83
1	1A	1915	5MU	O4-C4-C5	-3.68	120.70	124.92
55	2x	32	PSU	O2-C2-N1	-3.68	118.99	122.79
1	1A	1962	5MC	C5-C6-N1	-3.66	119.34	123.31
55	2x	8	4SU	C5-C4-S4	-3.65	120.14	124.31
32	1a	1519	MA6	C5-N7-C8	3.60	109.11	103.45
32	2a	1519	MA6	N9-C8-N7	-3.60	108.83	113.94
32	2a	1519	MA6	C2-N3-C4	3.58	120.56	111.83
32	2a	1518	MA6	C2-N3-C4	3.53	120.45	111.83
32	1a	1400	5MC	C5-C6-N1	-3.51	119.50	123.31
1	2A	2503	2MA	N6-C6-N1	3.51	121.77	117.03
1	2A	1915	5MU	O4-C4-C5	-3.50	120.91	124.92
32	1a	1518	MA6	C4-C5-N7	-3.48	106.61	110.58
32	1a	1518	MA6	C2-N3-C4	3.47	120.30	111.83
55	2x	39	PSU	C4-N3-C2	-3.47	121.60	126.37
32	1a	1519	MA6	C4-C5-N7	-3.46	106.62	110.58
1	2A	2552	OMU	C5-C4-N3	3.43	119.61	114.80
32	1a	516	PSU	O2-C2-N1	-3.42	119.26	122.79
32	1a	1519	MA6	C2-N3-C4	3.41	120.17	111.83
1	2A	1915	5MU	C5-C6-N1	-3.39	119.63	123.31
1	1A	1917	PSU	O2-C2-N1	-3.39	119.29	122.79
1	1A	1942	5MC	C5-C6-N1	-3.38	119.64	123.31
55	1x	37	MIA	N3-C2-N1	-3.37	123.49	128.58
55	2x	8	4SU	N3-C2-N1	3.36	119.27	114.89
32	2a	516	PSU	O2-C2-N1	-3.36	119.32	122.79
32	2a	1518	MA6	N9-C8-N7	-3.34	109.19	113.94
32	1a	1519	MA6	C4-C5-C6	3.34	119.36	115.91
32	1a	1519	MA6	N3-C4-N9	3.29	132.77	127.17
55	1x	55	PSU	O2-C2-N1	-3.29	119.39	122.79
1	2A	2503	2MA	C4-N9-C8	3.28	109.18	105.74
55	2x	37	MIA	N3-C2-N1	-3.28	123.62	128.58
32	2a	967	5MC	C5-C6-N1	-3.27	119.76	123.31
1	2A	2552	OMU	O2-C2-N1	-3.27	118.55	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1911	PSU	O2-C2-N1	-3.26	119.43	122.79
1	1A	2251	OMG	C6-C5-N7	3.25	136.21	130.29
32	2a	1498	UR3	C5-C4-N3	3.24	119.30	115.04
1	2A	1939	5MU	O4-C4-C5	-3.21	121.24	124.92
55	1x	8	4SU	C5-C4-S4	-3.21	120.64	124.31
1	1A	2552	OMU	O4-C4-C5	-3.21	119.63	125.16
32	2a	1407	5MC	C5-C4-N3	-3.19	118.48	121.75
32	1a	1519	MA6	N9-C8-N7	-3.19	109.42	113.94
32	2a	1407	5MC	C5-C6-N1	-3.14	119.90	123.31
1	2A	1942	5MC	C5-C6-N1	-3.14	119.91	123.31
55	1x	54	5MU	C5-C6-N1	-3.13	119.92	123.31
55	2x	54	5MU	C5-C6-N1	-3.12	119.93	123.31
1	2A	1962	5MC	C5-C6-N1	-3.12	119.93	123.31
32	1a	1207	2MG	C6-C5-N7	3.11	135.95	130.29
55	2x	54	5MU	O2-C2-N1	-3.10	118.76	122.80
55	1x	39	PSU	C4-N3-C2	-3.09	122.11	126.37
1	1A	2503	2MA	C4-N9-C8	3.07	108.96	105.74
1	1A	2503	2MA	C4-C5-N7	-3.06	107.08	110.58
32	1a	1518	MA6	N3-C4-N9	3.06	132.37	127.17
32	1a	1498	UR3	C5-C4-N3	3.04	119.04	115.04
55	1x	20	H2U	C5-C6-N1	-3.03	102.35	111.52
32	2a	1518	MA6	N3-C4-N9	3.03	132.32	127.17
32	1a	1404	5MC	C5-C4-N3	-3.02	118.66	121.75
32	2a	1207	2MG	C6-C5-N7	3.00	135.76	130.29
1	2A	2605	PSU	O2-C2-N1	-3.00	119.69	122.79
43	1l	92	0TD	OD2-CG-CB	2.98	119.58	113.15
55	2x	55	PSU	O2-C2-N1	-2.98	119.72	122.79
1	2A	2503	2MA	C4-C5-N7	-2.95	107.21	110.58
43	2l	92	0TD	OD2-CG-CB	2.94	119.49	113.15
32	1a	966	M2G	C6-C5-N7	2.93	135.63	130.29
55	2x	37	MIA	C5-N7-C8	2.92	108.04	103.45
1	1A	1915	5MU	C5-C6-N1	-2.91	120.15	123.31
55	2x	39	PSU	O2-C2-N1	-2.89	119.81	122.79
32	1a	1407	5MC	C5-C6-N1	-2.88	120.19	123.31
32	2a	1518	MA6	C4-C5-C6	2.87	118.88	115.91
55	1x	8	4SU	N3-C2-N1	2.87	118.62	114.89
1	2A	1939	5MU	O2-C2-N1	-2.85	119.08	122.80
32	1a	1400	5MC	C5-C4-N3	-2.84	118.84	121.75
32	1a	1404	5MC	C5-C6-N1	-2.84	120.23	123.31
32	1a	1407	5MC	C5-C4-N3	-2.84	118.85	121.75
32	2a	966	M2G	C6-C5-N7	2.83	135.43	130.29
55	2x	8	4SU	C1'-N1-C2	2.81	122.64	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	1942	5MC	C5-C4-N3	-2.77	118.91	121.75
55	1x	37	MIA	C5-N7-C8	2.76	107.78	103.45
32	1a	1402	4OC	C6-C5-C4	2.75	120.31	117.00
1	2A	1962	5MC	C5-C4-N3	-2.73	118.95	121.75
1	1A	1942	5MC	C5-C4-N3	-2.71	118.97	121.75
1	2A	2552	OMU	O4-C4-C5	-2.70	120.50	125.16
1	2A	2251	OMG	C6-C5-N7	2.70	135.20	130.29
32	2a	1404	5MC	C5-C4-N3	-2.69	119.00	121.75
1	1A	1939	5MU	O2-C2-N1	-2.68	119.31	122.80
32	1a	1207	2MG	C4-C5-N7	-2.66	106.46	110.67
1	1A	2251	OMG	C4-C5-N7	-2.65	106.47	110.67
32	1a	527	G7M	O6-C6-C5	-2.63	122.14	128.01
32	1a	1404	5MC	CM5-C5-C6	-2.62	119.30	122.85
32	1a	967	5MC	C5-C6-N1	-2.62	120.47	123.31
32	2a	1519	MA6	N3-C4-N9	2.61	131.60	127.17
1	2A	2251	OMG	O6-C6-C5	-2.60	119.68	126.53
32	2a	1400	5MC	C5-C4-N3	-2.59	119.10	121.75
32	2a	1498	UR3	C3U-N3-C4	2.58	121.45	117.87
1	1A	1911	PSU	O2-C2-N1	-2.58	120.13	122.79
1	1A	1917	PSU	C5-C6-N1	-2.58	118.56	122.14
1	1A	1962	5MC	C5-C4-N3	-2.57	119.12	121.75
1	2A	2503	2MA	C5-N7-C8	2.57	107.49	103.45
32	1a	1518	MA6	C4-N9-C8	2.55	108.42	105.74
1	1A	2503	2MA	C2-N1-C6	2.54	122.01	118.10
32	1a	966	M2G	C4-C5-N7	-2.47	106.76	110.67
32	1a	1407	5MC	CM5-C5-C6	-2.47	119.51	122.85
32	1a	967	5MC	C5-C4-N3	-2.46	119.24	121.75
32	2a	1207	2MG	C4-C5-N7	-2.45	106.78	110.67
1	1A	2605	PSU	C5-C6-N1	-2.45	118.73	122.14
32	2a	1407	5MC	O2-C2-N3	-2.43	118.50	122.33
32	2a	527	G7M	O6-C6-C5	-2.41	122.62	128.01
32	1a	1404	5MC	O2-C2-N3	-2.41	118.53	122.33
55	2x	37	MIA	C6-C5-N7	2.41	136.74	132.09
1	2A	2503	2MA	C2-N1-C6	2.40	121.79	118.10
32	2a	516	PSU	O4'-C1'-C2'	2.40	108.47	105.15
54	1w	230	MEQ	CB-CG-CD	-2.39	107.74	113.06
32	1a	1207	2MG	C2-N1-C6	-2.37	121.68	124.55
32	1a	1498	UR3	C6-N1-C2	-2.37	119.86	121.80
32	2a	966	M2G	C4-C5-N7	-2.37	106.91	110.67
1	1A	2503	2MA	C5-N7-C8	2.37	107.17	103.45
1	1A	1915	5MU	O2-C2-N1	-2.36	119.73	122.80
1	2A	2503	2MA	N9-C8-N7	-2.36	110.59	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2503	2MA	N9-C8-N7	-2.35	110.60	113.94
1	1A	1911	PSU	C5-C6-N1	-2.35	118.89	122.14
32	2a	1402	4OC	CM4-N4-C4	-2.33	117.89	122.45
1	1A	2552	OMU	C1'-N1-C2	2.29	121.70	117.59
32	1a	1402	4OC	O2-C2-N3	-2.29	118.73	122.33
32	2a	967	5MC	C5-C4-N3	-2.28	119.42	121.75
32	2a	1519	MA6	C4-C5-C6	2.28	118.27	115.91
55	1x	54	5MU	O2-C2-N1	-2.28	119.83	122.80
1	2A	2605	PSU	C5-C6-N1	-2.27	118.98	122.14
32	2a	1402	4OC	C6-C5-C4	2.27	119.74	117.00
32	1a	1400	5MC	O2-C2-N3	-2.26	118.77	122.33
32	1a	1407	5MC	O2-C2-N3	-2.25	118.79	122.33
1	1A	2503	2MA	C6-C5-N7	2.24	136.41	132.09
32	1a	1207	2MG	CM2-N2-C2	-2.24	118.83	123.65
32	2a	527	G7M	C5-C6-N1	2.24	116.47	111.84
1	1A	1942	5MC	O2-C2-N3	-2.23	118.81	122.33
1	1A	1915	5MU	C5M-C5-C4	2.23	121.17	118.78
55	2x	37	MIA	C4-N9-C8	2.22	108.07	105.74
1	1A	1942	5MC	N1-C2-N3	2.21	122.64	118.80
1	2A	1911	PSU	C5-C6-N1	-2.17	119.13	122.14
55	2x	55	PSU	C5-C6-N1	-2.17	119.13	122.14
32	1a	527	G7M	C5-C6-N1	2.16	116.30	111.84
55	2x	20	H2U	O4-C4-N3	2.15	123.61	120.30
32	1a	1498	UR3	C1'-N1-C2	2.12	120.51	117.04
1	2A	1917	PSU	C5-C6-N1	-2.11	119.21	122.14
55	1x	37	MIA	C4-N9-C8	2.10	107.95	105.74
1	1A	2503	2MA	CM2-C2-N1	2.10	120.27	117.13
1	1A	1962	5MC	CM5-C5-C6	-2.09	120.02	122.85
55	1x	39	PSU	O2-C2-N3	-2.09	118.14	121.86
1	2A	1915	5MU	O2-C2-N1	-2.09	120.07	122.80
32	1a	516	PSU	C5-C6-N1	-2.09	119.24	122.14
32	1a	1207	2MG	O6-C6-C5	-2.08	121.04	126.53
32	2a	1402	4OC	O2-C2-N3	-2.08	119.05	122.33
32	2a	516	PSU	C5-C6-N1	-2.06	119.28	122.14
32	2a	1519	MA6	C5-C4-N9	2.05	108.05	105.81
32	2a	966	M2G	O6-C6-C5	-2.05	121.12	126.53
55	2x	37	MIA	N9-C8-N7	-2.05	111.03	113.94
1	2A	1939	5MU	C5M-C5-C6	-2.04	120.09	122.85
1	2A	2605	PSU	O2-C2-N3	-2.03	118.25	121.86
32	1a	966	M2G	O6-C6-C5	-2.03	121.16	126.53
1	1A	2251	OMG	C5-C6-N1	2.03	118.43	113.25
1	2A	2251	OMG	C5-C6-N1	2.03	118.41	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	2x	39	PSU	C6-C5-C4	-2.02	116.81	118.17
1	1A	2503	2MA	N3-C2-N1	-2.02	122.20	125.77

There are no chirality outliers.

All (54) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
43	1l	92	0TD	CG-CB-SB-CSB
54	1w	230	MEQ	CG-CD-NE2-CE
32	2a	1400	5MC	O4'-C4'-C5'-O5'
54	2w	230	MEQ	N-CA-CB-CG
54	2w	230	MEQ	C-CA-CB-CG
54	2w	230	MEQ	CG-CD-NE2-CE
55	1x	21	H2U	C3'-C4'-C5'-O5'
55	1x	21	H2U	O4'-C1'-N1-C6
55	2x	21	H2U	C4'-C5'-O5'-P
55	2x	21	H2U	O4'-C1'-N1-C6
32	1a	527	G7M	C3'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1400	5MC	C3'-C4'-C5'-O5'
55	2x	20	H2U	O4'-C4'-C5'-O5'
55	2x	20	H2U	C3'-C4'-C5'-O5'
55	2x	21	H2U	C3'-C4'-C5'-O5'
55	2x	37	MIA	O4'-C4'-C5'-O5'
54	1w	230	MEQ	CA-CB-CG-CD
55	2x	21	H2U	O4'-C1'-N1-C2
1	1A	1915	5MU	O4'-C4'-C5'-O5'
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
55	1x	21	H2U	O4'-C4'-C5'-O5'
54	2w	230	MEQ	OE1-CD-NE2-CE
54	2w	230	MEQ	NE2-CD-CG-CB
54	2w	230	MEQ	OE1-CD-CG-CB
32	1a	1402	4OC	C3'-C4'-C5'-O5'
55	2x	37	MIA	C3'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
55	1x	20	H2U	O4'-C4'-C5'-O5'
55	1x	20	H2U	C3'-C4'-C5'-O5'
55	1x	54	5MU	O4'-C4'-C5'-O5'
55	1x	21	H2U	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
54	1w	230	MEQ	OE1-CD-NE2-CE
55	2x	21	H2U	O4'-C4'-C5'-O5'
55	1x	54	5MU	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
55	1x	21	H2U	O4'-C1'-N1-C2
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	2w	230	MEQ	CA-CB-CG-CD
32	2a	1519	MA6	C4'-C5'-O5'-P
1	2A	2503	2MA	O4'-C4'-C5'-O5'
54	1w	230	MEQ	OE1-CD-CG-CB
1	1A	1915	5MU	C3'-C4'-C5'-O5'
32	1a	516	PSU	O4'-C4'-C5'-O5'
43	1l	92	0TD	CA-CB-SB-CSB
54	1w	230	MEQ	NE2-CD-CG-CB
55	1x	37	MIA	O4'-C4'-C5'-O5'
43	2l	92	0TD	CG-CB-SB-CSB
1	1A	2503	2MA	C4'-C5'-O5'-P
32	1a	1207	2MG	C4'-C5'-O5'-P
1	2A	2503	2MA	C4'-C5'-O5'-P

There are no ring outliers.

24 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1402	4OC	2	0
32	2a	1400	5MC	1	0
32	2a	967	5MC	1	0
55	2x	55	PSU	1	0
32	1a	516	PSU	1	0
1	1A	1939	5MU	1	0
32	1a	1519	MA6	3	0
32	1a	966	M2G	1	0
32	2a	1518	MA6	1	0
1	2A	2552	OMU	1	0
43	2l	92	0TD	1	0
1	2A	1942	5MC	1	0
32	2a	1404	5MC	3	0
32	1a	1518	MA6	2	0
32	2a	1402	4OC	2	0
1	2A	2503	2MA	1	0
55	2x	21	H2U	1	0
32	2a	527	G7M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	2a	1519	MA6	3	0
32	1a	967	5MC	1	0
32	1a	1207	2MG	1	0
32	2a	1207	2MG	1	0
1	2A	1915	5MU	1	0
1	1A	2552	OMU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2702 ligands modelled in this entry, 2700 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	SF4	1d	302	35	0,12,12	-	-	-		
59	SF4	2d	303	35	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	SF4	1d	302	35	-	-	0/6/5/5
59	SF4	2d	303	35	-	-	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	1d	302	SF4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1A	2860/2915 (98%)	-0.53	139 (4%) 35 29	18, 36, 93, 105	0
1	2A	2789/2915 (95%)	-0.14	102 (3%) 45 39	31, 55, 88, 103	0
2	1B	120/121 (99%)	-0.36	0 100 100	30, 52, 64, 84	0
2	2B	120/121 (99%)	0.54	6 (5%) 34 28	61, 74, 82, 87	0
3	1D	275/276 (99%)	-0.22	1 (0%) 88 86	20, 38, 54, 71	0
3	2D	275/276 (99%)	0.08	3 (1%) 78 74	27, 49, 60, 75	0
4	1E	204/206 (99%)	-0.20	0 100 100	20, 41, 59, 74	0
4	2E	204/206 (99%)	0.17	4 (1%) 65 60	32, 57, 72, 77	0
5	1F	203/210 (96%)	-0.19	0 100 100	17, 42, 66, 81	0
5	2F	203/210 (96%)	0.35	1 (0%) 87 85	34, 63, 75, 85	0
6	1G	181/182 (99%)	0.89	14 (7%) 19 15	48, 68, 78, 86	0
6	2G	181/182 (99%)	1.10	22 (12%) 8 6	67, 78, 84, 91	0
7	1H	174/180 (96%)	0.25	2 (1%) 78 74	39, 55, 66, 73	0
7	2H	174/180 (96%)	1.00	13 (7%) 20 16	66, 77, 84, 91	0
8	1I	146/148 (98%)	0.52	1 (0%) 84 82	40, 69, 76, 78	0
8	2I	146/148 (98%)	1.02	16 (10%) 10 8	57, 75, 80, 83	0
9	1N	140/140 (100%)	-0.18	0 100 100	25, 39, 61, 69	0
9	2N	140/140 (100%)	0.44	2 (1%) 73 69	46, 62, 75, 80	0
10	1O	122/122 (100%)	-0.15	0 100 100	29, 41, 58, 63	0
10	2O	122/122 (100%)	0.19	1 (0%) 82 80	40, 54, 65, 73	0
11	1P	149/150 (99%)	-0.12	0 100 100	20, 43, 66, 75	0
11	2P	149/150 (99%)	0.45	6 (4%) 42 37	36, 64, 77, 83	0
12	1Q	141/141 (100%)	-0.02	2 (1%) 73 69	26, 41, 53, 62	0
12	2Q	141/141 (100%)	0.56	3 (2%) 63 58	44, 62, 70, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.33	0 100 100	23, 36, 48, 58	0
13	2R	118/118 (100%)	0.13	0 100 100	40, 52, 61, 70	0
14	1S	110/112 (98%)	0.13	2 (1%) 67 63	38, 52, 63, 67	0
14	2S	110/112 (98%)	0.92	8 (7%) 21 17	60, 70, 79, 84	0
15	1T	131/146 (89%)	0.07	4 (3%) 51 45	34, 46, 67, 80	0
15	2T	131/146 (89%)	0.24	2 (1%) 72 68	48, 57, 72, 77	0
16	1U	116/118 (98%)	-0.38	0 100 100	22, 32, 48, 58	0
16	2U	116/118 (98%)	0.29	1 (0%) 81 78	41, 56, 70, 74	0
17	1V	101/101 (100%)	-0.24	1 (0%) 79 76	21, 43, 58, 67	0
17	2V	101/101 (100%)	0.60	2 (1%) 65 60	44, 65, 76, 81	0
18	1W	112/113 (99%)	-0.33	0 100 100	22, 31, 53, 76	0
18	2W	112/113 (99%)	0.08	1 (0%) 81 78	38, 50, 66, 80	0
19	1X	95/96 (98%)	-0.21	1 (1%) 78 74	24, 37, 56, 68	0
19	2X	95/96 (98%)	0.43	4 (4%) 40 35	46, 58, 74, 79	0
20	1Y	107/110 (97%)	0.16	1 (0%) 81 78	35, 49, 69, 73	0
20	2Y	107/110 (97%)	0.81	7 (6%) 25 19	56, 68, 80, 85	0
21	1Z	154/206 (74%)	0.36	4 (2%) 57 51	39, 57, 72, 79	0
21	2Z	160/206 (77%)	0.87	8 (5%) 34 28	62, 74, 80, 85	0
22	10	76/85 (89%)	-0.15	0 100 100	28, 38, 53, 57	0
22	20	76/85 (89%)	0.58	4 (5%) 32 26	43, 61, 70, 75	0
23	11	97/98 (98%)	0.07	2 (2%) 63 58	26, 42, 67, 72	0
23	21	97/98 (98%)	0.25	1 (1%) 79 76	40, 54, 72, 76	0
24	12	70/72 (97%)	0.01	0 100 100	33, 48, 58, 73	0
24	22	70/72 (97%)	0.65	4 (5%) 29 24	58, 68, 75, 83	0
25	13	59/60 (98%)	-0.40	0 100 100	25, 36, 62, 73	0
25	23	59/60 (98%)	0.31	0 100 100	49, 60, 72, 78	0
26	14	69/71 (97%)	1.07	12 (17%) 4 3	63, 79, 87, 94	0
26	24	69/71 (97%)	1.23	10 (14%) 6 4	75, 84, 90, 96	0
27	15	59/60 (98%)	-0.31	1 (1%) 69 64	18, 35, 62, 70	0
27	25	59/60 (98%)	0.05	1 (1%) 69 64	39, 50, 67, 77	0
28	16	53/54 (98%)	-0.18	0 100 100	31, 43, 54, 58	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.42	1 (1%) 66 61	49, 59, 67, 68	0
29	17	48/49 (97%)	-0.29	1 (2%) 63 58	19, 26, 56, 62	0
29	27	48/49 (97%)	0.07	1 (2%) 63 58	30, 40, 65, 70	0
30	18	64/65 (98%)	-0.26	0 100 100	25, 34, 43, 51	0
30	28	64/65 (98%)	0.39	0 100 100	44, 53, 62, 66	0
31	19	37/37 (100%)	-0.04	0 100 100	32, 43, 56, 59	0
31	29	37/37 (100%)	0.93	2 (5%) 31 26	56, 64, 71, 71	0
32	1a	1488/1521 (97%)	0.61	85 (5%) 29 24	38, 76, 93, 102	0
32	2a	1491/1521 (98%)	0.46	58 (3%) 43 38	45, 75, 92, 104	0
33	1b	231/256 (90%)	1.17	32 (13%) 6 5	70, 78, 86, 91	0
33	2b	231/256 (90%)	1.13	35 (15%) 5 4	68, 80, 85, 90	0
34	1c	206/239 (86%)	1.20	31 (15%) 5 4	68, 79, 86, 91	0
34	2c	206/239 (86%)	1.08	22 (10%) 11 9	72, 79, 85, 90	0
35	1d	208/209 (99%)	1.13	21 (10%) 12 9	57, 75, 82, 87	0
35	2d	208/209 (99%)	0.92	12 (5%) 29 23	58, 70, 79, 84	0
36	1e	148/162 (91%)	0.63	6 (4%) 41 36	52, 68, 75, 78	0
36	2e	148/162 (91%)	0.69	5 (3%) 48 42	61, 70, 77, 84	0
37	1f	100/101 (99%)	0.65	4 (4%) 42 37	61, 69, 75, 78	0
37	2f	100/101 (99%)	0.71	3 (3%) 52 47	62, 71, 78, 81	0
38	1g	155/156 (99%)	0.99	10 (6%) 25 19	67, 77, 83, 86	0
38	2g	155/156 (99%)	1.09	23 (14%) 5 4	71, 79, 85, 87	0
39	1h	137/138 (99%)	0.78	8 (5%) 29 23	62, 72, 78, 83	0
39	2h	137/138 (99%)	0.75	5 (3%) 46 40	60, 70, 77, 79	0
40	1i	127/128 (99%)	1.55	33 (25%) 1 1	68, 79, 84, 86	0
40	2i	127/128 (99%)	1.94	53 (41%) 0 0	72, 83, 88, 91	0
41	1j	97/105 (92%)	1.44	20 (20%) 2 2	67, 81, 86, 87	0
41	2j	96/105 (91%)	1.79	39 (40%) 0 0	74, 83, 88, 90	0
42	1k	114/129 (88%)	0.60	4 (3%) 47 41	50, 70, 78, 79	0
42	2k	114/129 (88%)	0.78	8 (7%) 22 18	56, 73, 81, 85	0
43	1l	121/132 (91%)	0.57	4 (3%) 49 43	54, 64, 71, 77	0
43	2l	121/132 (91%)	0.57	3 (2%) 58 52	53, 64, 72, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	118/126 (93%)	1.59	35 (29%) 1 1	70, 80, 85, 87	0
44	2m	116/126 (92%)	1.44	24 (20%) 2 2	73, 80, 86, 91	0
45	1n	60/61 (98%)	1.57	15 (25%) 2 1	72, 80, 84, 86	0
45	2n	60/61 (98%)	2.18	23 (38%) 1 0	72, 81, 86, 90	0
46	1o	88/89 (98%)	0.83	5 (5%) 29 24	51, 70, 80, 86	0
46	2o	88/89 (98%)	0.79	6 (6%) 23 19	61, 70, 78, 80	0
47	1p	82/88 (93%)	1.69	26 (31%) 1 1	65, 77, 83, 87	0
47	2p	82/88 (93%)	1.03	7 (8%) 16 13	62, 70, 77, 81	0
48	1q	99/105 (94%)	0.89	5 (5%) 33 28	59, 70, 77, 83	0
48	2q	99/105 (94%)	0.63	1 (1%) 79 76	56, 69, 76, 80	0
49	1r	68/88 (77%)	0.62	0 100 100	59, 68, 76, 82	0
49	2r	68/88 (77%)	0.78	2 (2%) 53 48	65, 73, 78, 84	0
50	1s	83/93 (89%)	1.81	31 (37%) 1 0	75, 82, 86, 87	0
50	2s	83/93 (89%)	1.69	30 (36%) 1 0	77, 84, 89, 92	0
51	1t	96/106 (90%)	1.17	13 (13%) 7 5	64, 75, 79, 85	0
51	2t	96/106 (90%)	0.68	2 (2%) 63 58	57, 69, 77, 81	0
52	1u	23/27 (85%)	2.37	15 (65%) 0 0	76, 79, 83, 84	0
52	2u	23/27 (85%)	1.85	10 (43%) 0 0	76, 80, 83, 84	0
53	1v	13/24 (54%)	1.61	4 (30%) 1 1	57, 81, 93, 94	0
53	2v	13/24 (54%)	1.76	7 (53%) 0 0	68, 85, 96, 98	0
54	1w	248/354 (70%)	1.09	35 (14%) 6 5	57, 78, 85, 91	0
54	2w	252/354 (71%)	1.68	77 (30%) 1 1	71, 83, 90, 92	0
55	1x	66/74 (89%)	0.17	1 (1%) 72 68	43, 74, 85, 88	0
55	2x	66/74 (89%)	0.40	1 (1%) 72 68	55, 78, 88, 90	0
All	All	21073/22146 (95%)	0.34	1323 (6%) 26 20	17, 64, 87, 105	0

All (1323) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	6	GLY	9.3
1	2A	2147	G	8.2
45	1n	2	ALA	7.3
1	2A	2145	C	7.3
1	2A	2146	C	6.8

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Mol	Chain	Res	Type	RSRZ
1	1A	1093	G	6.6
1	2A	2133	G	6.3
45	2n	2	ALA	6.3
1	1A	2113	U	6.1
1	1A	2129	C	6.1
54	2w	185	VAL	6.1
1	2A	2117	A	6.0
1	1A	2141	G	6.0
1	2A	2111	C	5.7
1	1A	2108	C	5.7
40	2i	10	ARG	5.6
1	1A	2130	U	5.6
40	2i	105	ASP	5.6
45	2n	5	ALA	5.5
1	1A	2112	G	5.5
44	2m	7	VAL	5.4
45	2n	22	THR	5.4
44	1m	107	ALA	5.3
1	1A	2115	G	5.2
1	2A	2112	G	5.2
1	1A	2117	A	5.0
40	2i	102	LEU	5.0
1	1A	1098	A	5.0
21	2Z	174	VAL	5.0
54	1w	185	VAL	5.0
1	2A	2115	G	5.0
1	1A	1064	C	5.0
50	1s	9	VAL	5.0
40	1i	15	ALA	4.9
1	1A	2145	C	4.9
54	2w	232	VAL	4.9
1	2A	2144	U	4.9
54	2w	183	VAL	4.9
1	1A	1072	C	4.9
1	2A	2138	C	4.8
1	1A	1094	U	4.8
32	1a	1532	U	4.8
1	1A	2116	G	4.8
32	1a	1027	C	4.7
54	2w	190	GLY	4.7
1	1A	2124	G	4.7
1	1A	2131	G	4.7

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Mol	Chain	Res	Type	RSRZ
32	1a	1257	U	4.6
1	1A	2114	A	4.6
1	1A	2159	G	4.6
1	1A	2160	G	4.6
32	1a	1029	C	4.5
1	1A	2120	G	4.5
34	1c	2	GLY	4.5
1	1A	2174	C	4.5
1	1A	1058	G	4.5
1	1A	2154	G	4.5
1	2A	2155	G	4.5
32	2a	1034	G	4.5
45	2n	7	ILE	4.4
54	2w	234	THR	4.4
33	1b	7	VAL	4.4
1	2A	2105	C	4.4
39	2h	2	LEU	4.4
1	1A	1088	A	4.4
45	1n	5	ALA	4.4
1	1A	2133	G	4.4
52	1u	23	PRO	4.4
1	1A	2128	C	4.4
1	2A	2130	U	4.3
1	2A	2113	U	4.3
1	1A	2132	U	4.3
32	1a	1531	A	4.3
40	2i	108	VAL	4.3
54	2w	328	LEU	4.3
45	1n	7	ILE	4.3
1	1A	2139	C	4.3
1	1A	2178	C	4.3
32	1a	1286	A	4.3
6	1G	82	LEU	4.2
33	1b	230	VAL	4.2
1	1A	1100	C	4.2
1	2A	2104	G	4.2
40	1i	8	GLY	4.2
1	1A	2109	U	4.2
1	1A	2125	G	4.2
1	1A	2127	G	4.2
1	1A	2148	G	4.2
32	1a	1034	G	4.2

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Mol	Chain	Res	Type	RSRZ
40	2i	14	VAL	4.1
1	1A	1068	G	4.1
1	1A	1071	G	4.1
1	1A	2147	G	4.1
44	2m	5	ALA	4.1
1	1A	2110	G	4.1
50	1s	71	LEU	4.1
32	1a	1224	G	4.0
50	2s	2	PRO	4.0
12	2Q	104	PHE	4.0
1	1A	2158	A	4.0
1	2A	2139	C	4.0
54	2w	237	SER	4.0
23	2l	2	SER	4.0
1	1A	1077	A	4.0
1	1A	2122	U	4.0
1	1A	2169	A	4.0
1	1A	2173	A	4.0
1	1A	2175	C	4.0
1	2A	2174	C	4.0
32	1a	1028	C	4.0
1	2A	2159	G	3.9
1	1A	2179	C	3.9
1	2A	2137	C	3.9
45	2n	13	THR	3.9
1	1A	2167	U	3.9
33	1b	227	GLY	3.9
46	2o	86	GLY	3.9
40	2i	11	LYS	3.9
1	2A	2127	G	3.9
40	2i	109	VAL	3.9
1	2A	2134	A	3.9
40	2i	2	GLU	3.9
45	2n	4	LYS	3.9
32	1a	1030	C	3.9
32	2a	1030(B)	C	3.9
1	2A	2131	G	3.8
1	2A	2158	A	3.8
1	1A	2107	C	3.8
26	14	59	PHE	3.8
33	1b	229	VAL	3.8
54	1w	295	THR	3.8

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Mol	Chain	Res	Type	RSRZ
15	1T	131	ALA	3.8
40	2i	7	THR	3.8
51	1t	103	GLY	3.8
1	1A	2121	G	3.8
21	2Z	93	ASP	3.8
50	1s	39	THR	3.8
1	2A	2132	U	3.8
41	2j	75	ILE	3.8
8	2I	146	ALA	3.7
40	2i	13	ALA	3.7
32	1a	1036	G	3.7
54	2w	307	PHE	3.7
45	2n	18	VAL	3.7
20	2Y	1	MET	3.7
6	2G	152	LEU	3.7
35	1d	155	LEU	3.7
52	1u	22	ARG	3.7
1	2A	2120	G	3.7
32	1a	380	G	3.7
1	1A	2142	C	3.7
1	2A	2183	C	3.7
45	2n	21	TYR	3.7
33	2b	136	VAL	3.7
1	1A	2135	A	3.6
1	1A	2111	C	3.6
54	2w	153	GLY	3.6
41	2j	34	VAL	3.6
7	2H	100	GLY	3.6
1	2A	2110	G	3.6
1	2A	2154	G	3.6
33	1b	131	PRO	3.6
1	1A	2134	A	3.6
1	1A	2170	A	3.6
32	1a	1035	A	3.6
47	1p	17	TYR	3.6
41	2j	47	PHE	3.6
26	24	56	VAL	3.6
54	2w	221	VAL	3.6
34	1c	52	LEU	3.6
40	1i	19	LEU	3.6
43	1l	91	LYS	3.6
54	1w	192	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
54	2w	231	GLY	3.6
1	1A	1060	U	3.6
1	2A	2140	C	3.5
1	2A	2143	C	3.5
26	24	51	ASP	3.5
1	2A	2148	G	3.5
1	2A	2165	G	3.5
1	2A	2182	G	3.5
44	1m	100	GLY	3.5
52	2u	14	TRP	3.5
40	1i	2	GLU	3.5
32	1a	1503	A	3.5
1	1A	1092	C	3.5
1	1A	2140	C	3.5
1	2A	2128	C	3.5
1	1A	1063	G	3.5
32	1a	1353	G	3.5
39	1h	92	ARG	3.5
40	1i	105	ASP	3.5
17	2V	42	GLY	3.5
54	2w	228	GLY	3.5
27	15	60	VAL	3.5
1	1A	1059	G	3.5
1	2A	2153	G	3.5
52	1u	17	THR	3.5
38	1g	7	ALA	3.5
47	1p	7	ALA	3.5
45	2n	14	PRO	3.5
47	1p	16	HIS	3.5
23	11	2	SER	3.4
26	24	49	PHE	3.4
22	20	68	GLU	3.4
34	2c	2	GLY	3.4
51	2t	103	GLY	3.4
54	2w	236	ASP	3.4
1	1A	2150	U	3.4
38	1g	9	VAL	3.4
1	2A	2160	G	3.4
1	1A	1057	A	3.4
1	2A	2114	A	3.4
1	2A	2135	A	3.4
4	2E	204	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	2A	2142	C	3.4
1	1A	1082	U	3.4
41	2j	74	ILE	3.4
41	2j	35	SER	3.4
1	1A	2157	G	3.4
1	2A	2119	A	3.4
32	1a	1447	A	3.4
44	1m	97	PRO	3.4
38	2g	2	ALA	3.4
45	2n	39	LEU	3.4
20	2Y	5	MET	3.4
1	1A	1097	U	3.3
32	1a	1037	C	3.3
47	1p	14	ASN	3.3
40	1i	126	SER	3.3
1	1A	2143	C	3.3
1	2A	2175	C	3.3
32	1a	1354	C	3.3
38	2g	4	ARG	3.3
45	2n	3	ARG	3.3
54	1w	184	PRO	3.3
34	1c	207	VAL	3.3
41	1j	55	LYS	3.3
1	1A	2119	A	3.3
1	1A	1099	G	3.3
1	1A	2181	G	3.3
32	1a	1030(A)	G	3.3
12	1Q	60	ARG	3.3
1	1A	1078	U	3.3
38	1g	118	VAL	3.3
38	2g	42	ILE	3.3
1	1A	1062	G	3.3
1	1A	2104	G	3.3
1	2A	2106	G	3.3
22	20	10	THR	3.3
38	2g	16	LEU	3.3
7	2H	165	ALA	3.3
1	2A	2126	A	3.2
32	2a	965	A	3.2
44	2m	70	LEU	3.2
54	2w	310	SER	3.2
1	1A	2149	G	3.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2156	G	3.2
26	14	56	VAL	3.2
34	1c	64	VAL	3.2
34	1c	130	VAL	3.2
50	1s	13	ASP	3.2
1	2A	2167	U	3.2
1	1A	1075	C	3.2
54	2w	226	GLY	3.2
36	2e	86	ALA	3.2
45	2n	33	VAL	3.2
1	1A	2166	G	3.2
1	2A	2157	G	3.2
6	1G	83	ARG	3.2
42	2k	126	ARG	3.2
41	2j	55	LYS	3.2
35	2d	167	GLY	3.2
40	1i	39	GLY	3.2
41	2j	32	ALA	3.2
46	1o	87	ILE	3.2
1	2A	2169	A	3.2
47	1p	1	MET	3.2
41	2j	37	PRO	3.2
1	2A	2125	G	3.2
1	2A	2166	G	3.2
7	2H	2	SER	3.2
1	2A	2129	C	3.1
3	1D	276	LYS	3.1
8	2I	20	ASP	3.1
41	2j	65	LEU	3.1
44	1m	90	LEU	3.1
51	1t	10	LEU	3.1
54	2w	150	THR	3.1
1	1A	2189	U	3.1
54	2w	197	ALA	3.1
33	2b	200	ILE	3.1
1	2A	2149	G	3.1
40	2i	47	LEU	3.1
51	1t	18	GLN	3.1
53	1v	12	A	3.1
54	1w	219	ILE	3.1
6	1G	76	SER	3.1
33	2b	7	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
41	2j	63	PHE	3.1
50	1s	4	SER	3.1
38	2g	5	ARG	3.1
1	1A	2123	G	3.1
1	1A	2165	G	3.1
1	2A	2116	G	3.1
32	1a	1021	G	3.1
32	2a	1030(A)	G	3.1
1	1A	2146	C	3.1
9	2N	73	THR	3.1
34	1c	39	ILE	3.1
44	2m	118	ALA	3.1
45	1n	30	ALA	3.1
54	2w	124	ALA	3.1
1	1A	1073	A	3.1
40	2i	9	ARG	3.1
40	2i	36	TYR	3.1
52	1u	21	TYR	3.1
1	2A	2118	U	3.1
1	1A	2155	G	3.1
32	1a	1003	G	3.1
41	2j	93	GLY	3.1
50	1s	77	THR	3.1
34	1c	189	ALA	3.1
43	1l	89	ARG	3.1
32	2a	1035	A	3.0
33	2b	11	LEU	3.0
37	1f	55	ASP	3.0
32	2a	1257	U	3.0
40	2i	63	ILE	3.0
40	1i	42	ARG	3.0
45	2n	10	ALA	3.0
27	25	60	VAL	3.0
42	2k	119	CYS	3.0
1	1A	1087	G	3.0
1	2A	2168	G	3.0
32	1a	1024	G	3.0
32	2a	1002	G	3.0
1	2A	2108	C	3.0
6	2G	2	PRO	3.0
32	1a	1041	A	3.0
21	2Z	106	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
15	2T	131	ALA	3.0
21	1Z	51	ALA	3.0
40	1i	13	ALA	3.0
33	1b	136	VAL	3.0
40	1i	41	VAL	3.0
40	2i	96	LEU	3.0
40	2i	21	PRO	3.0
1	1A	2151	G	3.0
1	2A	2141	G	3.0
32	2a	1033	G	3.0
32	2a	1149	C	3.0
1	1A	1069	A	3.0
1	1A	1086	A	3.0
14	2S	3	ARG	3.0
20	2Y	80	GLY	3.0
46	1o	3	ILE	3.0
54	2w	293	ILE	3.0
33	2b	161	ALA	3.0
38	1g	80	VAL	3.0
40	1i	14	VAL	3.0
54	1w	152	LEU	3.0
54	2w	285	LEU	3.0
52	1u	24	ARG	3.0
50	2s	84	GLY	3.0
1	1A	888	C	3.0
1	2A	2136	C	3.0
35	2d	48	ALA	3.0
41	1j	34	VAL	3.0
44	1m	53	VAL	3.0
1	1A	2118	U	2.9
1	1A	2180	U	2.9
1	2A	2109	U	2.9
50	2s	69	HIS	2.9
7	1H	2	SER	2.9
50	1s	18	LYS	2.9
38	2g	84	ASN	2.9
52	2u	22	ARG	2.9
34	2c	158	GLY	2.9
38	2g	80	VAL	2.9
41	1j	44	VAL	2.9
1	2A	2123	G	2.9
1	2A	2177	C	2.9

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Mol	Chain	Res	Type	RSRZ
1	1A	887	A	2.9
1	2A	2319	G	2.9
32	1a	1001(A)	G	2.9
1	1A	1081	U	2.9
32	1a	1040	U	2.9
50	1s	35	SER	2.9
53	1v	11	U	2.9
41	1j	33	GLN	2.9
44	1m	101	GLN	2.9
35	1d	102	ASP	2.9
34	1c	65	ALA	2.9
34	2c	160	ALA	2.9
40	2i	106	ALA	2.9
44	1m	72	ALA	2.9
54	2w	205	ALA	2.9
44	1m	96	LEU	2.9
54	1w	324	LEU	2.9
47	1p	82	GLN	2.9
1	1A	2136	C	2.9
1	2A	2170	A	2.9
32	1a	1030(D)	A	2.9
44	2m	102	ARG	2.9
54	2w	223	ARG	2.9
1	1A	1026	U	2.9
1	1A	2168	G	2.9
26	14	63	TYR	2.9
47	1p	19	ILE	2.9
40	2i	67	GLY	2.9
35	2d	164	ALA	2.9
8	2l	3	VAL	2.9
41	2j	49	VAL	2.9
50	1s	60	VAL	2.9
40	2i	118	LYS	2.9
54	1w	348	LEU	2.9
41	2j	62	HIS	2.9
44	1m	102	ARG	2.9
52	1u	14	TRP	2.9
18	2W	60	ASN	2.9
54	2w	248	ILE	2.9
32	1a	999	C	2.9
44	2m	87	TYR	2.9
44	1m	2	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
44	1m	28	ALA	2.9
34	1c	195	VAL	2.9
54	2w	227	PRO	2.8
33	1b	137	ARG	2.8
21	1Z	146	ILE	2.8
33	1b	172	ILE	2.8
35	1d	69	GLY	2.8
40	2i	4	TYR	2.8
45	1n	4	LYS	2.8
46	1o	69	TYR	2.8
50	1s	5	LEU	2.8
50	2s	24	ALA	2.8
34	1c	68	VAL	2.8
1	1A	2164	C	2.8
32	2a	1030	C	2.8
54	2w	149	PRO	2.8
26	14	52	THR	2.8
33	1b	171	ALA	2.8
44	1m	5	ALA	2.8
33	1b	165	VAL	2.8
37	2f	6	VAL	2.8
47	1p	20	VAL	2.8
1	1A	1083	U	2.8
32	1a	1000	U	2.8
38	1g	5	ARG	2.8
1	1A	548	A	2.8
32	2a	979	C	2.8
20	2Y	4	LYS	2.8
1	1A	2156	G	2.8
41	2j	76	ASN	2.8
54	2w	154	GLY	2.8
34	1c	192	THR	2.8
21	1Z	141	VAL	2.8
46	2o	13	GLN	2.8
1	1A	2144	U	2.8
32	1a	1020	U	2.8
53	1v	22	U	2.8
53	2v	22	U	2.8
14	2S	59	LYS	2.8
51	1t	74	LYS	2.8
32	1a	374	A	2.8
53	2v	12	A	2.8

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Mol	Chain	Res	Type	RSRZ
37	2f	45	LEU	2.8
44	1m	66	LEU	2.8
15	1T	107	ASP	2.8
6	2G	149	VAL	2.8
33	2b	197	VAL	2.8
35	2d	32	ALA	2.8
38	2g	152	ALA	2.8
41	2j	44	VAL	2.8
54	2w	196	THR	2.8
2	2B	119	G	2.8
40	1i	9	ARG	2.8
52	1u	18	TYR	2.8
7	2H	103	LEU	2.7
34	2c	12	LEU	2.7
39	1h	2	LEU	2.7
50	2s	38	SER	2.7
54	2w	244	LEU	2.7
1	1A	1067	A	2.7
8	2I	34	GLY	2.7
32	1a	172	A	2.7
51	1t	69	GLY	2.7
6	2G	147	ASP	2.7
38	2g	118	VAL	2.7
40	1i	106	ALA	2.7
14	2S	29	PHE	2.7
54	2w	241	VAL	2.7
39	1h	94	TYR	2.7
50	2s	52	TYR	2.7
26	14	18	CYS	2.7
6	2G	53	LEU	2.7
50	1s	84	GLY	2.7
1	1A	1066	U	2.7
1	2A	271(K)	U	2.7
6	1G	49	ASP	2.7
47	1p	2	VAL	2.7
47	1p	79	VAL	2.7
52	1u	15	ARG	2.7
33	1b	17	PHE	2.7
32	2a	1001	A	2.7
33	1b	42	ILE	2.7
54	2w	192	ILE	2.7
35	1d	21	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
31	29	37	GLY	2.7
26	14	55	ARG	2.7
35	2d	154	ASN	2.7
38	2g	156	TRP	2.7
40	1i	10	ARG	2.7
41	2j	30	SER	2.7
54	2w	195	SER	2.7
41	2j	20	ALA	2.7
41	2j	54	PHE	2.7
54	1w	144	VAL	2.7
54	2w	121	ALA	2.7
53	2v	11	U	2.7
54	2w	184	PRO	2.7
26	24	67	TYR	2.7
47	1p	39	TYR	2.7
32	2a	1130	A	2.7
53	2v	14	A	2.7
40	2i	81	ILE	2.7
54	2w	335	ILE	2.7
32	1a	1039	C	2.7
6	1G	133	LEU	2.7
50	1s	20	LEU	2.7
35	1d	3	ARG	2.7
40	1i	66	ARG	2.7
40	2i	30	GLY	2.7
52	1u	9	ARG	2.7
26	24	66	SER	2.7
3	2D	90	ALA	2.7
7	2H	169	VAL	2.7
8	2I	81	VAL	2.7
34	1c	55	VAL	2.7
40	2i	86	VAL	2.7
45	2n	25	VAL	2.7
54	2w	291	ALA	2.7
50	2s	76	PRO	2.7
6	2G	146	TYR	2.6
32	2a	1219	U	2.6
32	2a	1532	U	2.6
6	1G	114	ILE	2.6
1	2A	2173	A	2.6
42	1k	98	LEU	2.6
54	2w	332	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
51	1t	80	ARG	2.6
26	14	17	GLY	2.6
33	1b	129	GLU	2.6
1	2A	2178	C	2.6
32	2a	1249	C	2.6
6	2G	50	ALA	2.6
7	2H	123	PHE	2.6
16	2U	90	VAL	2.6
34	2c	153	VAL	2.6
34	2c	207	VAL	2.6
42	1k	36	ASP	2.6
54	2w	217	ILE	2.6
33	2b	138	LEU	2.6
39	2h	119	LEU	2.6
11	2P	15	ARG	2.6
52	1u	6	ARG	2.6
50	2s	45	VAL	2.6
54	1w	211	ALA	2.6
54	2w	321	THR	2.6
1	2A	2107	C	2.6
1	2A	2896	C	2.6
32	2a	1027	C	2.6
33	2b	201	ILE	2.6
35	1d	194	LEU	2.6
45	2n	34	TYR	2.6
35	1d	73	ARG	2.6
35	2d	49	ARG	2.6
35	2d	132	ARG	2.6
40	2i	107	ARG	2.6
1	2A	1026	U	2.6
54	2w	325	GLU	2.6
34	2c	194	GLY	2.6
50	1s	68	GLY	2.6
50	2s	8	GLY	2.6
52	2u	4	GLY	2.6
54	2w	318	GLY	2.6
1	2A	2152	G	2.6
32	1a	66	G	2.6
32	2a	1032	G	2.6
6	2G	159	VAL	2.6
40	1i	76	ALA	2.6
43	2l	94	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
44	2m	98	VAL	2.6
54	1w	120	ALA	2.6
33	1b	97	TRP	2.6
35	1d	71	SER	2.6
50	1s	38	SER	2.6
54	2w	222	MET	2.6
6	1G	88	ILE	2.6
38	2g	38	LEU	2.6
40	2i	50	LEU	2.6
41	1j	40	LEU	2.6
50	2s	3	ARG	2.6
54	1w	296	GLY	2.6
32	1a	1025	U	2.6
15	2T	130	ALA	2.6
34	1c	76	VAL	2.6
38	2g	83	ALA	2.6
38	2g	128	ALA	2.6
39	1h	89	PRO	2.6
40	2i	17	VAL	2.6
45	2n	30	ALA	2.6
42	2k	13	GLN	2.6
42	2k	42	TRP	2.5
1	1A	1074	G	2.5
1	1A	1176	G	2.5
32	1a	392	G	2.5
32	1a	1026	G	2.5
32	2a	1036	G	2.5
53	1v	10	G	2.5
6	1G	77	ILE	2.5
44	1m	4	ILE	2.5
54	1w	111	ILE	2.5
1	1A	2176	A	2.5
32	1a	1044	A	2.5
35	1d	162	LEU	2.5
47	2p	12	LYS	2.5
54	2w	298	ARG	2.5
33	2b	140	HIS	2.5
40	1i	12	GLU	2.5
44	2m	58	GLU	2.5
1	2A	1536	C	2.5
44	1m	68	GLY	2.5
50	1s	41	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
50	1s	76	PRO	2.5
50	2s	41	VAL	2.5
52	2u	23	PRO	2.5
54	2w	201	VAL	2.5
6	1G	50	ALA	2.5
1	1A	2102	U	2.5
50	1s	12	ASP	2.5
31	29	10	ILE	2.5
44	2m	84	ILE	2.5
44	1m	3	ARG	2.5
52	2u	6	ARG	2.5
54	2w	273	LEU	2.5
47	1p	13	HIS	2.5
1	2A	2162	G	2.5
32	1a	1023	G	2.5
1	1A	1070	A	2.5
20	2Y	55	TYR	2.5
32	1a	143	A	2.5
32	1a	1001	A	2.5
54	1w	297	GLU	2.5
40	1i	69	GLY	2.5
44	1m	112	GLY	2.5
33	1b	15	VAL	2.5
33	2b	165	VAL	2.5
43	1l	18	VAL	2.5
50	2s	11	VAL	2.5
47	1p	80	PHE	2.5
1	1A	2105	C	2.5
1	2A	2103	C	2.5
32	2a	1038	C	2.5
33	2b	190	THR	2.5
41	1j	75	ILE	2.5
45	2n	58	LYS	2.5
50	2s	7	LYS	2.5
44	2m	19	LEU	2.5
45	2n	57	ARG	2.5
50	2s	5	LEU	2.5
40	2i	117	HIS	2.5
6	1G	48	GLU	2.5
24	22	5	GLU	2.5
38	2g	85	TYR	2.5
40	2i	125	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1089	G	2.5
1	1A	2126	A	2.5
1	1A	2162	G	2.5
1	2A	2121	G	2.5
8	2I	37	VAL	2.5
32	1a	70	G	2.5
32	2a	1003	G	2.5
54	1w	180	VAL	2.5
54	2w	312	VAL	2.5
38	2g	25	ALA	2.5
45	1n	16	PHE	2.5
49	2r	24	ALA	2.5
54	2w	186	THR	2.5
12	2Q	60	ARG	2.5
34	1c	188	LEU	2.5
35	1d	135	LEU	2.5
40	1i	40	LEU	2.5
50	1s	40	ILE	2.5
54	1w	259	ILE	2.5
1	1A	2138	C	2.5
1	1A	2185	C	2.5
32	1a	219	C	2.5
32	1a	1018	C	2.5
50	2s	13	ASP	2.5
1	2A	2180	U	2.5
32	1a	723	U	2.5
32	1a	1012	U	2.5
54	2w	208	GLU	2.5
35	2d	54	TYR	2.5
44	1m	87	TYR	2.5
52	1u	16	GLY	2.5
40	1i	86	VAL	2.5
6	2G	46	ALA	2.5
15	1T	130	ALA	2.5
40	1i	43	ALA	2.5
40	2i	119	ALA	2.5
54	1w	224	ALA	2.5
54	2w	120	ALA	2.5
3	2D	38	LYS	2.4
52	2u	17	THR	2.4
54	1w	321	THR	2.4
32	1a	152	A	2.4

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Mol	Chain	Res	Type	RSRZ
32	2a	1004	A	2.4
32	2a	1248	A	2.4
26	24	5	ILE	2.4
33	1b	214	ILE	2.4
50	1s	15	LEU	2.4
50	2s	15	LEU	2.4
54	2w	219	ILE	2.4
54	2w	269	LEU	2.4
1	1A	2106	G	2.4
1	1A	2153	G	2.4
1	1A	2182	G	2.4
1	2A	2181	G	2.4
2	2B	118	G	2.4
32	2a	1202	G	2.4
47	1p	48	TRP	2.4
47	1p	59	TRP	2.4
54	2w	243	HIS	2.4
1	2A	2179	C	2.4
32	1a	984	C	2.4
32	1a	989	C	2.4
32	2a	1037	C	2.4
6	2G	142	PRO	2.4
33	2b	131	PRO	2.4
33	2b	228	GLY	2.4
34	2c	7	PRO	2.4
38	2g	81	GLY	2.4
43	2l	72	GLY	2.4
42	1k	13	GLN	2.4
47	2p	82	GLN	2.4
50	1s	19	VAL	2.4
50	1s	10	PHE	2.4
50	1s	32	LYS	2.4
41	1j	32	ALA	2.4
50	1s	74	PHE	2.4
45	1n	3	ARG	2.4
52	2u	15	ARG	2.4
34	1c	196	LEU	2.4
36	1e	118	ILE	2.4
54	2w	212	LEU	2.4
54	2w	259	ILE	2.4
2	2B	59	A	2.4
32	1a	1287	A	2.4

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Mol	Chain	Res	Type	RSRZ
1	1A	1091	G	2.4
1	1A	2152	G	2.4
1	1A	2190	G	2.4
26	14	54	GLY	2.4
50	2s	59	PRO	2.4
33	1b	8	LYS	2.4
7	1H	133	VAL	2.4
7	2H	114	VAL	2.4
32	2a	995	C	2.4
34	1c	70	VAL	2.4
40	2i	92	TYR	2.4
54	1w	242	VAL	2.4
1	2A	1113	U	2.4
1	2A	2150	U	2.4
12	1Q	107	ALA	2.4
40	2i	66	ARG	2.4
41	1j	42	THR	2.4
44	2m	22	ILE	2.4
14	2S	61	ASN	2.4
47	1p	68	ASP	2.4
32	2a	969	A	2.4
32	2a	978	A	2.4
44	1m	65	LYS	2.4
33	2b	38	GLY	2.4
45	2n	38	GLY	2.4
7	2H	45	VAL	2.4
40	2i	41	VAL	2.4
50	2s	67	VAL	2.4
1	1A	883	G	2.4
1	1A	2805	G	2.4
1	2A	892	G	2.4
1	2A	1042	G	2.4
1	2A	2318	G	2.4
32	1a	102	G	2.4
32	1a	1009	G	2.4
32	1a	1032	G	2.4
34	1c	100	ALA	2.4
40	1i	119	ALA	2.4
40	2i	61	ALA	2.4
44	2m	21	TYR	2.4
45	1n	21	TYR	2.4
52	2u	24	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
55	2x	70	G	2.4
8	2I	12	LEU	2.4
33	1b	158	LEU	2.4
34	2c	157	ILE	2.4
35	2d	108	LEU	2.4
41	2j	8	LEU	2.4
45	2n	6	LEU	2.4
1	1A	2161	C	2.4
1	1A	2177	C	2.4
32	1a	1038	C	2.4
32	2a	1148	U	2.4
41	1j	76	ASN	2.4
39	1h	4	ASP	2.4
40	1i	91	ASP	2.4
3	2D	276	LYS	2.4
20	2Y	81	LYS	2.4
40	1i	11	LYS	2.4
41	1j	57	LYS	2.4
34	1c	197	GLY	2.4
34	2c	155	GLY	2.4
44	2m	112	GLY	2.4
54	2w	229	GLY	2.4
6	2G	38	VAL	2.4
8	2I	33	ARG	2.4
37	1f	90	VAL	2.4
41	2j	60	ARG	2.4
48	1q	91	ARG	2.4
1	2A	6	A	2.4
1	2A	652(B)	A	2.4
32	1a	1016	A	2.4
33	2b	237	ALA	2.4
40	2i	43	ALA	2.4
45	1n	37	PHE	2.4
35	1d	4	TYR	2.3
35	1d	157	LEU	2.3
41	1j	8	LEU	2.3
41	2j	40	LEU	2.3
45	1n	6	LEU	2.3
34	2c	77	ILE	2.3
47	1p	36	ILE	2.3
33	2b	67	THR	2.3
54	2w	170	THR	2.3

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Mol	Chain	Res	Type	RSRZ
33	1b	19	HIS	2.3
1	1A	2833	G	2.3
1	2A	11	G	2.3
32	1a	1031	G	2.3
32	2a	1001(A)	G	2.3
32	2a	1024	G	2.3
32	2a	1030(C)	G	2.3
8	2I	85	GLU	2.3
32	1a	1320	C	2.3
54	2w	245	PRO	2.3
11	2P	116	GLY	2.3
11	2P	65	ARG	2.3
54	2w	347	GLN	2.3
34	2c	76	VAL	2.3
44	1m	98	VAL	2.3
33	1b	122	PHE	2.3
33	1b	118	LEU	2.3
39	2h	112	LEU	2.3
49	2r	50	ILE	2.3
51	1t	100	ILE	2.3
14	2S	92	TYR	2.3
32	1a	383	A	2.3
41	2j	42	THR	2.3
41	2j	81	THR	2.3
41	2j	100	THR	2.3
50	1s	33	THR	2.3
51	1t	9	ASN	2.3
54	2w	102	MET	2.3
39	1h	87	SER	2.3
1	1A	1101	U	2.3
32	1a	988	G	2.3
32	1a	1002	G	2.3
32	2a	1220	G	2.3
40	2i	49	PRO	2.3
41	2j	53	PRO	2.3
1	1A	889	C	2.3
32	1a	1045	C	2.3
33	2b	21	ARG	2.3
38	1g	4	ARG	2.3
40	1i	67	GLY	2.3
52	1u	10	ARG	2.3
40	1i	108	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
20	2Y	105	ALA	2.3
33	1b	34	ALA	2.3
33	2b	44	LEU	2.3
9	2N	2	LYS	2.3
33	2b	133	LYS	2.3
44	2m	46	LYS	2.3
44	2m	65	LYS	2.3
51	2t	74	LYS	2.3
11	2P	84	ASN	2.3
26	24	29	PRO	2.3
35	1d	153	ARG	2.3
47	1p	75	ARG	2.3
54	1w	182	ARG	2.3
35	1d	178	VAL	2.3
36	1e	82	VAL	2.3
6	2G	117	PHE	2.3
21	2Z	136	PHE	2.3
33	2b	163	PHE	2.3
33	2b	196	LEU	2.3
1	2A	2151	G	2.3
26	14	22	ILE	2.3
34	1c	77	ILE	2.3
36	2e	109	ILE	2.3
41	2j	27	ALA	2.3
45	1n	10	ALA	2.3
45	2n	20	ALA	2.3
54	2w	265	ALA	2.3
1	2A	2164	C	2.3
1	2A	2207	G	2.3
1	2A	2833	G	2.3
14	2S	34	HIS	2.3
32	1a	1019	C	2.3
32	1a	1138	G	2.3
32	2a	1029	C	2.3
32	2a	1260	C	2.3
35	1d	123	HIS	2.3
54	2w	322	HIS	2.3
21	2Z	69	THR	2.3
40	2i	70	LYS	2.3
40	2i	62	TYR	2.3
41	2j	78	ASN	2.3
7	2H	101	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
40	2i	42	ARG	2.3
40	2i	104	ARG	2.3
44	1m	108	ARG	2.3
50	1s	2	PRO	2.3
54	1w	298	ARG	2.3
32	1a	1005	A	2.3
35	1d	180	GLY	2.3
36	2e	85	GLY	2.3
8	1I	38	LEU	2.3
19	1X	95	LEU	2.3
21	1Z	105	VAL	2.3
24	22	63	VAL	2.3
28	26	11	LEU	2.3
47	1p	51	VAL	2.3
47	2p	79	VAL	2.3
54	2w	250	VAL	2.3
1	1A	1090	U	2.2
34	2c	149	ALA	2.2
38	2g	49	ILE	2.2
41	2j	23	ILE	2.2
44	2m	18	ALA	2.2
47	1p	33	ILE	2.2
50	1s	50	ALA	2.2
6	2G	182	LYS	2.2
8	2I	1	MET	2.2
20	1Y	1	MET	2.2
34	2c	135	LYS	2.2
45	1n	17	LYS	2.2
45	2n	50	LYS	2.2
8	2I	48	GLU	2.2
34	1c	201	TYR	2.2
43	2l	64	TYR	2.2
50	2s	80	TYR	2.2
1	1A	885	C	2.2
1	1A	886	C	2.2
1	1A	2103	C	2.2
1	2A	2188	C	2.2
2	2B	3	C	2.2
32	1a	1006	C	2.2
32	1a	993	G	2.2
32	2a	1222	G	2.2
44	2m	101	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	66	GLY	2.2
40	1i	115	GLY	2.2
40	2i	6	GLY	2.2
50	2s	68	GLY	2.2
52	1u	2	GLY	2.2
54	2w	117	GLY	2.2
6	2G	139	LEU	2.2
40	2i	53	VAL	2.2
44	1m	48	LEU	2.2
44	1m	74	VAL	2.2
6	1G	80	PHE	2.2
29	17	48	LYS	2.2
32	1a	389	A	2.2
32	2a	1092	A	2.2
40	2i	37	PHE	2.2
40	2i	127	LYS	2.2
52	2u	13	ILE	2.2
54	1w	248	ILE	2.2
54	2w	319	PHE	2.2
1	2A	2122	U	2.2
34	1c	35	GLU	2.2
40	1i	7	THR	2.2
40	2i	64	THR	2.2
44	1m	109	THR	2.2
50	2s	64	GLU	2.2
54	2w	115	THR	2.2
26	24	32	TYR	2.2
6	2G	118	ARG	2.2
44	1m	41	PRO	2.2
1	1A	2163	C	2.2
11	2P	68	GLN	2.2
32	1a	63	C	2.2
36	1e	117	ASP	2.2
1	2A	2793	G	2.2
32	1a	1042	G	2.2
32	1a	1274	G	2.2
32	2a	1026	G	2.2
32	2a	1031	G	2.2
54	1w	190	GLY	2.2
34	1c	101	LEU	2.2
44	2m	66	LEU	2.2
45	1n	39	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
47	2p	60	LEU	2.2
33	2b	230	VAL	2.2
36	1e	92	LYS	2.2
40	2i	26	VAL	2.2
41	2j	80	LYS	2.2
44	1m	54	VAL	2.2
50	1s	11	VAL	2.2
21	2Z	146	ILE	2.2
39	2h	31	PHE	2.2
54	2w	276	MET	2.2
54	2w	350	ALA	2.2
6	2G	145	THR	2.2
8	2I	10	GLU	2.2
1	1A	529	A	2.2
32	2a	1286	A	2.2
32	1a	223	U	2.2
33	2b	36	ARG	2.2
44	2m	99	ARG	2.2
48	1q	63	ARG	2.2
44	1m	23	TYR	2.2
50	2s	53	ASN	2.2
7	2H	175	LYS	2.2
14	1S	4	LEU	2.2
24	22	24	LEU	2.2
33	1b	196	LEU	2.2
33	2b	22	LYS	2.2
34	1c	47	LEU	2.2
40	1i	102	LEU	2.2
41	2j	58	ASP	2.2
4	2E	59	VAL	2.2
5	2F	89	VAL	2.2
6	2G	155	MET	2.2
21	2Z	42	VAL	2.2
26	14	50	VAL	2.2
38	2g	21	VAL	2.2
44	2m	17	VAL	2.2
54	1w	109	VAL	2.2
1	1A	1080	C	2.2
8	2I	133	HIS	2.2
26	24	59	PHE	2.2
32	2a	1028	C	2.2
32	2a	1116	C	2.2

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Mol	Chain	Res	Type	RSRZ
37	1f	60	PHE	2.2
41	1j	54	PHE	2.2
51	1t	55	ILE	2.2
54	1w	193	HIS	2.2
8	2I	53	ALA	2.2
33	1b	188	ALA	2.2
44	1m	18	ALA	2.2
54	1w	350	ALA	2.2
1	2A	1112	G	2.2
1	2A	2100	G	2.2
32	1a	181	G	2.2
32	2a	630	G	2.2
32	2a	1117	G	2.2
41	1j	64	GLU	2.2
40	2i	103	THR	2.2
50	2s	77	THR	2.2
38	2g	79	ARG	2.2
2	2B	26	A	2.2
38	1g	85	TYR	2.2
40	1i	62	TYR	2.2
41	1j	69	ASN	2.2
44	1m	113	PRO	2.2
44	2m	23	TYR	2.2
44	2m	106	ASN	2.2
53	2v	13	A	2.2
24	22	70	GLN	2.2
48	1q	100	LYS	2.2
34	1c	33	LEU	2.2
36	1e	85	GLY	2.2
44	1m	24	GLY	2.2
51	1t	62	LEU	2.2
54	1w	228	GLY	2.2
54	1w	266	LEU	2.2
54	2w	351	LEU	2.2
34	2c	138	VAL	2.2
40	1i	109	VAL	2.2
41	1j	35	SER	2.2
50	1s	49	ILE	2.2
50	2s	9	VAL	2.2
54	1w	322	HIS	2.2
45	2n	37	PHE	2.2
46	2o	15	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
8	2I	55	ALA	2.1
21	2Z	51	ALA	2.1
38	2g	145	ALA	2.1
40	1i	82	ALA	2.1
41	2j	18	ALA	2.1
51	1t	76	ALA	2.1
1	2A	888	C	2.1
1	2A	2163	C	2.1
2	2B	4	C	2.1
44	1m	116	THR	2.1
41	2j	91	PRO	2.1
44	2m	97	PRO	2.1
33	1b	37	ASN	2.1
6	1G	146	TYR	2.1
26	14	67	TYR	2.1
33	2b	148	TYR	2.1
40	2i	112	LYS	2.1
50	2s	70	LYS	2.1
52	2u	3	LYS	2.1
14	2S	54	LEU	2.1
33	1b	10	LEU	2.1
41	1j	90	LEU	2.1
54	2w	127	LEU	2.1
54	2w	324	LEU	2.1
1	1A	1095	A	2.1
32	1a	949	A	2.1
32	2a	1447	A	2.1
34	2c	9	GLY	2.1
6	2G	76	SER	2.1
34	1c	153	VAL	2.1
34	2c	152	ILE	2.1
47	1p	11	SER	2.1
50	2s	74	PHE	2.1
33	1b	128	GLU	2.1
19	2X	68	ARG	2.1
45	1n	35	ARG	2.1
6	2G	64	THR	2.1
40	1i	64	THR	2.1
47	1p	22	THR	2.1
42	2k	123	LYS	2.1
44	1m	31	LYS	2.1
1	1A	1076	C	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1006	C	2.1
54	1w	189	GLN	2.1
29	27	1	MET	2.1
33	1b	236	TYR	2.1
33	2b	92	TYR	2.1
33	2b	118	LEU	2.1
37	2f	89	MET	2.1
34	2c	48	TYR	2.1
41	1j	65	LEU	2.1
42	1k	75	TYR	2.1
50	2s	16	LEU	2.1
19	2X	86	GLY	2.1
33	2b	72	GLY	2.1
40	2i	39	GLY	2.1
41	1j	36	GLY	2.1
54	2w	169	GLY	2.1
6	2G	70	VAL	2.1
8	2I	136	VAL	2.1
10	2O	58	VAL	2.1
32	1a	1220	G	2.1
32	2a	1064	G	2.1
32	2a	1370	G	2.1
34	1c	5	ILE	2.1
34	2c	62	ASP	2.1
35	1d	8	VAL	2.1
42	2k	14	VAL	2.1
53	2v	10	G	2.1
54	2w	302	ILE	2.1
40	2i	33	PHE	2.1
45	1n	36	PHE	2.1
48	1q	99	SER	2.1
54	1w	310	SER	2.1
54	2w	134	PHE	2.1
1	1A	1045	A	2.1
32	1a	977	A	2.1
32	2a	1492	A	2.1
36	1e	102	ALA	2.1
53	2v	15	A	2.1
54	1w	113	ALA	2.1
14	1S	3	ARG	2.1
26	24	61	ARG	2.1
51	1t	8	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	162	THR	2.1
39	1h	3	THR	2.1
54	2w	194	THR	2.1
6	2G	74	LYS	2.1
34	1c	87	LEU	2.1
35	1d	188	LEU	2.1
36	2e	12	LEU	2.1
39	1h	133	LEU	2.1
41	2j	71	LEU	2.1
50	2s	71	LEU	2.1
54	1w	273	LEU	2.1
33	1b	228	GLY	2.1
38	2g	82	GLY	2.1
41	2j	56	HIS	2.1
47	2p	16	HIS	2.1
52	1u	4	GLY	2.1
1	1A	1079	C	2.1
7	2H	79	VAL	2.1
32	1a	67	C	2.1
32	2a	1007	C	2.1
32	2a	1119	C	2.1
35	1d	5	ILE	2.1
55	1x	44	C	2.1
11	2P	79	ARG	2.1
19	2X	65	ARG	2.1
33	1b	225	ALA	2.1
35	2d	82	ALA	2.1
36	2e	21	ALA	2.1
54	2w	238	ALA	2.1
54	2w	329	SER	2.1
1	2A	2191	G	2.1
32	1a	1215	G	2.1
32	1a	1222	G	2.1
32	1a	1258	G	2.1
32	2a	1224	G	2.1
32	2a	1258	G	2.1
1	2A	2102	U	2.1
32	2a	1000	U	2.1
32	2a	1065	U	2.1
41	1j	7	LYS	2.1
38	2g	112	PRO	2.1
19	2X	92	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	138	LEU	2.1
34	1c	175	LEU	2.1
38	1g	59	LEU	2.1
44	1m	34	LEU	2.1
4	2E	29	GLY	2.1
17	2V	8	GLY	2.1
33	2b	40	HIS	2.1
34	2c	159	GLY	2.1
4	2E	151	TYR	2.1
33	1b	222	ILE	2.1
33	2b	39	ILE	2.1
50	1s	52	TYR	2.1
7	2H	50	VAL	2.1
35	2d	88	VAL	2.1
6	1G	136	ARG	2.0
23	11	26	ARG	2.0
40	2i	91	ASP	2.0
41	1j	66	ARG	2.0
41	2j	73	ASP	2.0
41	2j	79	ARG	2.0
47	1p	8	ARG	2.0
47	2p	8	ARG	2.0
47	2p	28	ARG	2.0
38	1g	2	ALA	2.0
40	2i	126	SER	2.0
46	1o	16	ALA	2.0
51	1t	70	SER	2.0
1	1A	1509	C	2.0
6	1G	182	LYS	2.0
32	1a	1030(B)	C	2.0
32	2a	932	C	2.0
33	2b	97	TRP	2.0
39	2h	3	THR	2.0
40	2i	27	THR	2.0
47	1p	44	THR	2.0
54	1w	150	THR	2.0
41	2j	77	PRO	2.0
50	1s	59	PRO	2.0
1	1A	271(K)	U	2.0
1	2A	614(A)	U	2.0
32	1a	950	U	2.0
32	1a	1049	U	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1025	U	2.0
35	1d	108	LEU	2.0
35	2d	21	LEU	2.0
46	2o	9	GLN	2.0
54	2w	253	GLN	2.0
1	2A	2101	G	2.0
32	1a	1017	G	2.0
32	2a	1124	G	2.0
34	1c	69	HIS	2.0
12	2Q	61	GLY	2.0
15	1T	92	GLY	2.0
33	2b	211	ILE	2.0
44	1m	119	GLY	2.0
48	2q	65	ILE	2.0
54	1w	293	ILE	2.0
33	2b	164	VAL	2.0
34	1c	48	TYR	2.0
37	1f	88	VAL	2.0
46	2o	27	VAL	2.0
14	2S	20	ARG	2.0
46	1o	65	ARG	2.0
50	1s	29	ARG	2.0
43	1l	47	LYS	2.0
47	1p	35	LYS	2.0
47	1p	43	LYS	2.0
52	1u	20	LYS	2.0
22	20	9	SER	2.0
50	2s	4	SER	2.0
35	1d	165	MET	2.0
42	2k	31	THR	2.0
54	2w	308	PRO	2.0
1	1A	2137	C	2.0
1	2A	2161	C	2.0
1	2A	2789	C	2.0
32	1a	1137	C	2.0
32	1a	1397	C	2.0
40	2i	56	LEU	2.0
46	2o	31	LEU	2.0
48	1q	26	GLN	2.0
1	1A	1065	U	2.0
17	1V	101	GLY	2.0
34	1c	134	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
38	1g	34	GLY	2.0
41	2j	6	ILE	2.0
41	2j	50	ILE	2.0
1	1A	1096	A	2.0
1	2A	2176	A	2.0
7	2H	43	VAL	2.0
22	20	11	ARG	2.0
32	1a	1261	A	2.0
33	2b	112	VAL	2.0
34	2c	64	VAL	2.0
34	2c	66	VAL	2.0
38	2g	9	VAL	2.0
42	2k	30	VAL	2.0
44	1m	94	ARG	2.0
50	2s	60	VAL	2.0
26	14	32	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
55	H2U	2x	21	20/21	0.64	0.15	85,95,104,117	0
55	H2U	2x	20	20/21	0.68	0.13	80,92,100,105	0
55	H2U	1x	21	20/21	0.74	0.15	90,94,100,109	0
55	PSU	2x	55	20/21	0.79	0.11	77,82,86,90	0
55	H2U	1x	20	20/21	0.80	0.11	78,87,93,97	0
55	5MU	2x	54	21/22	0.83	0.12	79,84,89,101	0
55	PSU	1x	55	20/21	0.86	0.11	74,78,85,92	0
55	5MU	1x	54	21/22	0.87	0.12	72,81,84,92	0
55	4SU	2x	8	20/21	0.87	0.11	79,83,87,88	0
1	5MU	2A	1915	21/22	0.88	0.11	67,76,83,92	0
55	MIA	2x	37	22/30	0.88	0.12	70,77,80,83	0
43	0TD	1l	92	10/11	0.89	0.13	55,62,65,75	0
32	2MG	1a	1207	24/25	0.89	0.13	73,81,90,91	0
55	PSU	1x	32	20/21	0.89	0.11	67,75,79,79	0
32	2MG	2a	1207	24/25	0.89	0.11	76,81,85,90	0
32	PSU	2a	516	20/21	0.90	0.10	66,78,82,82	0
55	PSU	2x	39	20/21	0.91	0.09	67,76,80,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MEQ	1w	230	10/11	0.91	0.16	38,56,64,64	0
54	MEQ	2w	230	10/11	0.91	0.20	56,71,75,84	0
55	PSU	2x	32	20/21	0.91	0.10	71,75,80,81	0
32	M2G	2a	966	25/26	0.91	0.16	62,71,84,88	0
32	5MC	2a	967	21/22	0.92	0.14	61,69,77,87	0
1	PSU	2A	1911	20/21	0.92	0.10	56,61,68,69	0
32	4OC	2a	1402	22/23	0.93	0.12	56,65,70,76	0
1	5MU	1A	1915	21/22	0.93	0.10	52,63,68,74	0
55	4SU	1x	8	20/21	0.93	0.10	62,71,78,84	0
32	M2G	1a	966	25/26	0.93	0.10	59,66,75,79	0
32	5MC	1a	967	21/22	0.93	0.12	61,67,75,77	0
55	MIA	1x	37	22/30	0.93	0.10	59,65,70,73	0
32	G7M	2a	527	24/25	0.94	0.10	59,64,67,72	0
43	0TD	2l	92	10/11	0.94	0.10	61,66,68,84	0
32	5MC	1a	1400	21/22	0.94	0.12	53,61,68,69	0
32	G7M	1a	527	24/25	0.94	0.11	53,61,68,70	0
32	PSU	1a	516	20/21	0.94	0.09	65,74,78,81	0
32	5MC	2a	1400	21/22	0.94	0.12	68,71,75,78	0
1	PSU	1A	1911	20/21	0.95	0.09	41,54,60,62	0
32	5MC	2a	1404	21/22	0.95	0.09	52,56,63,69	0
32	MA6	2a	1518	24/25	0.95	0.10	47,63,66,69	0
32	5MC	1a	1404	21/22	0.95	0.10	44,49,54,57	0
32	4OC	1a	1402	22/23	0.96	0.09	48,54,58,60	0
1	PSU	1A	1917	20/21	0.96	0.07	48,56,60,61	0
1	OMC	2A	1920	21/22	0.96	0.09	56,61,66,69	0
55	PSU	1x	39	20/21	0.96	0.07	55,64,70,71	0
32	5MC	2a	1407	21/22	0.96	0.09	47,56,59,63	0
32	UR3	2a	1498	21/22	0.96	0.09	49,57,60,67	0
1	5MC	2A	1942	21/22	0.96	0.09	48,54,58,60	0
32	MA6	2a	1519	24/25	0.96	0.12	51,62,68,70	0
1	5MC	2A	1962	21/22	0.96	0.08	38,48,53,58	0
1	OMG	2A	2251	24/25	0.97	0.08	32,42,46,48	0
1	2MA	2A	2503	23/24	0.97	0.08	26,38,41,45	0
1	PSU	2A	2605	20/21	0.97	0.07	27,37,43,46	0
1	PSU	1A	2605	20/21	0.97	0.07	25,29,34,41	0
32	5MC	1a	1407	21/22	0.97	0.09	38,46,52,55	0
32	UR3	1a	1498	21/22	0.97	0.07	45,51,53,54	0
1	PSU	2A	1917	20/21	0.97	0.06	57,65,71,76	0
32	MA6	1a	1518	24/25	0.97	0.09	41,47,50,52	0
1	5MU	2A	1939	21/22	0.97	0.08	31,40,44,45	0
32	MA6	1a	1519	24/25	0.97	0.09	41,46,49,54	0
1	5MC	1A	1942	21/22	0.97	0.08	33,39,45,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	OMG	1A	2251	24/25	0.98	0.06	23,27,29,31	0
1	2MA	1A	2503	23/24	0.98	0.06	15,20,23,26	0
1	OMU	1A	2552	21/22	0.98	0.07	25,30,33,36	0
1	OMU	2A	2552	21/22	0.98	0.07	33,41,46,50	0
1	5MU	1A	1939	21/22	0.98	0.06	22,27,32,32	0
1	OMC	1A	1920	21/22	0.98	0.07	42,50,53,53	0
1	5MC	1A	1962	21/22	0.98	0.06	26,33,40,54	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	235	1/1	0.56	0.21	70,70,70,70	0
56	MG	1a	1781	1/1	0.57	0.18	91,91,91,91	0
56	MG	2A	3723	1/1	0.57	0.23	75,75,75,75	0
56	MG	2B	220	1/1	0.57	0.25	80,80,80,80	0
56	MG	2A	3656	1/1	0.62	0.21	79,79,79,79	0
56	MG	1A	4006	1/1	0.63	0.18	74,74,74,74	0
56	MG	2j	201	1/1	0.64	0.15	78,78,78,78	0
56	MG	1a	1664	1/1	0.65	0.19	83,83,83,83	0
56	MG	1a	1824	1/1	0.65	0.24	80,80,80,80	0
56	MG	1a	1813	1/1	0.66	0.16	89,89,89,89	0
56	MG	1a	1643	1/1	0.69	0.34	78,78,78,78	0
56	MG	2a	1750	1/1	0.69	0.22	92,92,92,92	0
56	MG	1l	202	1/1	0.69	0.11	75,75,75,75	0
56	MG	2A	3867	1/1	0.70	0.15	79,79,79,79	0
56	MG	1A	3028	1/1	0.70	0.20	69,69,69,69	0
56	MG	1a	1786	1/1	0.71	0.16	85,85,85,85	0
56	MG	1O	201	1/1	0.71	0.20	64,64,64,64	0
56	MG	1a	1676	1/1	0.72	0.24	73,73,73,73	0
56	MG	1a	1681	1/1	0.72	0.16	76,76,76,76	0
56	MG	1A	3829	1/1	0.72	0.18	54,54,54,54	0
56	MG	2A	3740	1/1	0.72	0.17	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	1a	1700	1/1	0.73	0.29	76,76,76,76	0
56	MG	2A	3759	1/1	0.73	0.21	52,52,52,52	0
56	MG	1a	1734	1/1	0.73	0.28	90,90,90,90	0
56	MG	2A	3678	1/1	0.73	0.23	69,69,69,69	0
56	MG	2A	3707	1/1	0.73	0.18	57,57,57,57	0
56	MG	2g	201	1/1	0.73	0.15	78,78,78,78	0
56	MG	1A	3255	1/1	0.73	0.25	66,66,66,66	0
56	MG	1a	1733	1/1	0.74	0.56	87,87,87,87	0
56	MG	2A	3366	1/1	0.74	0.23	78,78,78,78	0
56	MG	2a	1657	1/1	0.74	0.30	64,64,64,64	0
56	MG	2a	1678	1/1	0.74	0.33	73,73,73,73	0
56	MG	2a	1694	1/1	0.74	0.44	76,76,76,76	0
56	MG	2A	3453	1/1	0.74	0.23	67,67,67,67	0
56	MG	2A	3464	1/1	0.74	0.34	83,83,83,83	0
56	MG	1A	3989	1/1	0.74	0.16	42,42,42,42	0
56	MG	1V	201	1/1	0.75	0.36	53,53,53,53	0
56	MG	2A	3216	1/1	0.75	0.18	67,67,67,67	0
56	MG	2A	3568	1/1	0.75	0.23	86,86,86,86	0
56	MG	2a	1681	1/1	0.75	0.21	78,78,78,78	0
56	MG	2A	3622	1/1	0.75	0.32	70,70,70,70	0
56	MG	1A	3344	1/1	0.75	0.20	70,70,70,70	0
56	MG	2A	3673	1/1	0.75	0.19	69,69,69,69	0
56	MG	2B	209	1/1	0.75	0.24	69,69,69,69	0
56	MG	1a	1778	1/1	0.76	0.27	64,64,64,64	0
56	MG	2A	3869	1/1	0.76	0.19	80,80,80,80	0
56	MG	1A	3984	1/1	0.76	0.23	69,69,69,69	0
56	MG	1a	1711	1/1	0.76	0.35	74,74,74,74	0
56	MG	2a	1634	1/1	0.76	0.23	69,69,69,69	0
56	MG	1a	1796	1/1	0.76	0.14	64,64,64,64	0
56	MG	1A	3082	1/1	0.77	0.17	64,64,64,64	0
56	MG	1A	3515	1/1	0.77	0.21	73,73,73,73	0
56	MG	2A	3119	1/1	0.77	0.19	64,64,64,64	0
56	MG	2A	3853	1/1	0.77	0.24	76,76,76,76	0
56	MG	1a	1696	1/1	0.77	0.14	67,67,67,67	0
56	MG	2A	3360	1/1	0.77	0.14	68,68,68,68	0
56	MG	1a	1810	1/1	0.77	0.12	76,76,76,76	0
56	MG	1A	3647	1/1	0.77	0.21	74,74,74,74	0
56	MG	2j	202	1/1	0.77	0.10	76,76,76,76	0
56	MG	1A	3206	1/1	0.78	0.14	57,57,57,57	0
56	MG	1a	1607	1/1	0.78	0.12	80,80,80,80	0
56	MG	1a	1702	1/1	0.78	0.36	75,75,75,75	0
56	MG	2B	211	1/1	0.78	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	2B	215	1/1	0.78	0.19	70,70,70,70	0
56	MG	1A	3716	1/1	0.78	0.23	76,76,76,76	0
56	MG	1a	1714	1/1	0.78	0.13	65,65,65,65	0
56	MG	1a	1652	1/1	0.78	0.36	77,77,77,77	0
56	MG	1v	102	1/1	0.78	0.16	81,81,81,81	0
56	MG	2A	3099	1/1	0.78	0.30	75,75,75,75	0
56	MG	2A	3713	1/1	0.78	0.26	69,69,69,69	0
56	MG	2a	1722	1/1	0.78	0.18	71,71,71,71	0
56	MG	2a	1735	1/1	0.78	0.18	84,84,84,84	0
56	MG	1A	3303	1/1	0.78	0.18	53,53,53,53	0
56	MG	1a	1769	1/1	0.78	0.24	73,73,73,73	0
56	MG	1A	3850	1/1	0.78	0.14	62,62,62,62	0
56	MG	1A	3968	1/1	0.78	0.18	72,72,72,72	0
56	MG	1G	204	1/1	0.79	0.13	61,61,61,61	0
56	MG	2B	207	1/1	0.79	0.18	72,72,72,72	0
56	MG	1A	3916	1/1	0.79	0.12	25,25,25,25	0
56	MG	1A	3752	1/1	0.79	0.19	51,51,51,51	0
56	MG	2A	3504	1/1	0.79	0.20	57,57,57,57	0
56	MG	1A	3409	1/1	0.79	0.38	53,53,53,53	0
56	MG	1A	3843	1/1	0.79	0.15	55,55,55,55	0
56	MG	1a	1645	1/1	0.79	0.18	78,78,78,78	0
56	MG	1A	3298	1/1	0.79	0.26	63,63,63,63	0
56	MG	1B	230	1/1	0.79	0.23	65,65,65,65	0
56	MG	1a	1775	1/1	0.79	0.19	73,73,73,73	0
56	MG	1B	231	1/1	0.79	0.26	67,67,67,67	0
56	MG	2A	3280	1/1	0.79	0.14	48,48,48,48	0
56	MG	2A	3283	1/1	0.79	0.13	69,69,69,69	0
56	MG	2A	3290	1/1	0.79	0.20	56,56,56,56	0
56	MG	2A	3304	1/1	0.79	0.21	63,63,63,63	0
56	MG	1A	3888	1/1	0.79	0.19	52,52,52,52	0
56	MG	1A	3465	1/1	0.80	0.20	64,64,64,64	0
56	MG	1A	3869	1/1	0.80	0.21	64,64,64,64	0
56	MG	2A	3586	1/1	0.80	0.21	71,71,71,71	0
56	MG	2A	3267	1/1	0.80	0.18	81,81,81,81	0
56	MG	2A	3655	1/1	0.80	0.18	80,80,80,80	0
56	MG	1A	3199	1/1	0.80	0.20	56,56,56,56	0
56	MG	2A	3666	1/1	0.80	0.20	68,68,68,68	0
56	MG	2W	202	1/1	0.80	0.19	63,63,63,63	0
56	MG	1a	1760	1/1	0.80	0.28	77,77,77,77	0
56	MG	1A	4064	1/1	0.80	0.21	58,58,58,58	0
56	MG	2A	3298	1/1	0.80	0.24	73,73,73,73	0
56	MG	1A	3908	1/1	0.80	0.11	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3524	1/1	0.80	0.13	72,72,72,72	0
56	MG	2a	1717	1/1	0.80	0.20	74,74,74,74	0
56	MG	2A	3737	1/1	0.80	0.15	64,64,64,64	0
56	MG	2A	3087	1/1	0.80	0.25	63,63,63,63	0
56	MG	2A	3750	1/1	0.80	0.19	71,71,71,71	0
56	MG	2A	3089	1/1	0.80	0.15	69,69,69,69	0
56	MG	2A	3781	1/1	0.80	0.16	78,78,78,78	0
56	MG	1A	3327	1/1	0.80	0.25	58,58,58,58	0
56	MG	2r	102	1/1	0.80	0.31	80,80,80,80	0
56	MG	1O	205	1/1	0.81	0.16	73,73,73,73	0
56	MG	1A	4000	1/1	0.81	0.12	31,31,31,31	0
56	MG	1a	1708	1/1	0.81	0.20	70,70,70,70	0
56	MG	2A	3760	1/1	0.81	0.17	69,69,69,69	0
56	MG	2A	3379	1/1	0.81	0.30	69,69,69,69	0
56	MG	2A	3789	1/1	0.81	0.14	85,85,85,85	0
56	MG	2A	3815	1/1	0.81	0.15	53,53,53,53	0
56	MG	2A	3391	1/1	0.81	0.31	54,54,54,54	0
56	MG	2A	3393	1/1	0.81	0.13	67,67,67,67	0
56	MG	2A	3451	1/1	0.81	0.36	80,80,80,80	0
56	MG	1Y	201	1/1	0.81	0.14	62,62,62,62	0
56	MG	1A	3759	1/1	0.81	0.22	66,66,66,66	0
56	MG	2A	3502	1/1	0.81	0.18	66,66,66,66	0
56	MG	1x	112	1/1	0.81	0.15	77,77,77,77	0
56	MG	2A	3535	1/1	0.81	0.17	65,65,65,65	0
56	MG	2A	3030	1/1	0.81	0.27	55,55,55,55	0
56	MG	1a	1728	1/1	0.81	0.27	75,75,75,75	0
56	MG	1a	1637	1/1	0.81	0.29	87,87,87,87	0
56	MG	2A	3650	1/1	0.81	0.20	59,59,59,59	0
56	MG	2A	3653	1/1	0.81	0.27	67,67,67,67	0
56	MG	1A	4023	1/1	0.81	0.17	60,60,60,60	0
56	MG	1A	3811	1/1	0.81	0.27	64,64,64,64	0
56	MG	2A	3197	1/1	0.81	0.27	69,69,69,69	0
56	MG	2a	1730	1/1	0.81	0.25	69,69,69,69	0
56	MG	1A	3661	1/1	0.81	0.17	57,57,57,57	0
56	MG	2a	1746	1/1	0.81	0.29	74,74,74,74	0
56	MG	1a	1653	1/1	0.81	0.24	81,81,81,81	0
56	MG	2a	1757	1/1	0.81	0.27	66,66,66,66	0
56	MG	1A	3934	1/1	0.81	0.11	21,21,21,21	0
56	MG	1A	3614	1/1	0.81	0.11	29,29,29,29	0
56	MG	1A	3717	1/1	0.81	0.23	61,61,61,61	0
56	MG	1A	3498	1/1	0.81	0.26	75,75,75,75	0
56	MG	2x	101	1/1	0.81	0.35	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1602	1/1	0.82	0.38	75,75,75,75	0
56	MG	2A	3565	1/1	0.82	0.15	53,53,53,53	0
56	MG	1A	4059	1/1	0.82	0.15	46,46,46,46	0
56	MG	2A	3239	1/1	0.82	0.09	46,46,46,46	0
56	MG	2A	3589	1/1	0.82	0.26	74,74,74,74	0
56	MG	1A	3341	1/1	0.82	0.24	74,74,74,74	0
56	MG	1A	3535	1/1	0.82	0.09	61,61,61,61	0
56	MG	1A	3586	1/1	0.82	0.25	61,61,61,61	0
56	MG	2A	3286	1/1	0.82	0.19	76,76,76,76	0
56	MG	1A	3728	1/1	0.82	0.18	54,54,54,54	0
56	MG	2a	1654	1/1	0.82	0.28	79,79,79,79	0
56	MG	1A	3133	1/1	0.82	0.14	68,68,68,68	0
56	MG	2a	1665	1/1	0.82	0.28	62,62,62,62	0
56	MG	1A	3873	1/1	0.82	0.12	26,26,26,26	0
56	MG	2a	1679	1/1	0.82	0.42	68,68,68,68	0
56	MG	2A	3353	1/1	0.82	0.19	72,72,72,72	0
56	MG	2A	3699	1/1	0.82	0.18	69,69,69,69	0
56	MG	1a	1753	1/1	0.82	0.19	79,79,79,79	0
56	MG	2A	3020	1/1	0.82	0.19	55,55,55,55	0
56	MG	2A	3024	1/1	0.82	0.20	62,62,62,62	0
56	MG	1A	3184	1/1	0.82	0.22	59,59,59,59	0
56	MG	2A	3739	1/1	0.82	0.12	42,42,42,42	0
56	MG	1A	3787	1/1	0.82	0.14	72,72,72,72	0
56	MG	1a	1682	1/1	0.82	0.41	74,74,74,74	0
56	MG	1A	4050	1/1	0.82	0.11	64,64,64,64	0
56	MG	1a	1780	1/1	0.82	0.23	76,76,76,76	0
56	MG	2A	3151	1/1	0.82	0.22	61,61,61,61	0
56	MG	2l	202	1/1	0.82	0.10	74,74,74,74	0
56	MG	2A	3170	1/1	0.82	0.22	80,80,80,80	0
56	MG	2A	3505	1/1	0.82	0.13	35,35,35,35	0
56	MG	1a	1741	1/1	0.83	0.18	58,58,58,58	0
56	MG	1A	3854	1/1	0.83	0.30	43,43,43,43	0
56	MG	1a	1679	1/1	0.83	0.21	72,72,72,72	0
56	MG	1A	3338	1/1	0.83	0.28	66,66,66,66	0
56	MG	1A	3644	1/1	0.83	0.17	52,52,52,52	0
56	MG	1B	217	1/1	0.83	0.14	54,54,54,54	0
56	MG	2a	1630	1/1	0.83	0.43	72,72,72,72	0
56	MG	2A	3100	1/1	0.83	0.34	66,66,66,66	0
56	MG	2A	3105	1/1	0.83	0.26	73,73,73,73	0
56	MG	1A	3512	1/1	0.83	0.16	65,65,65,65	0
56	MG	1a	1609	1/1	0.83	0.29	85,85,85,85	0
56	MG	2A	3167	1/1	0.83	0.14	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3375	1/1	0.83	0.36	77,77,77,77	0
56	MG	1A	3909	1/1	0.83	0.13	63,63,63,63	0
56	MG	1E	312	1/1	0.83	0.21	52,52,52,52	0
56	MG	2A	3528	1/1	0.83	0.16	60,60,60,60	0
56	MG	1a	1727	1/1	0.83	0.32	75,75,75,75	0
56	MG	2A	3263	1/1	0.83	0.24	63,63,63,63	0
56	MG	1A	4015	1/1	0.83	0.21	75,75,75,75	0
56	MG	2A	3814	1/1	0.83	0.20	75,75,75,75	0
56	MG	1l	201	1/1	0.83	0.16	72,72,72,72	0
56	MG	2A	3842	1/1	0.83	0.23	70,70,70,70	0
56	MG	2a	1764	1/1	0.83	0.13	58,58,58,58	0
56	MG	2a	1774	1/1	0.83	0.11	65,65,65,65	0
56	MG	2A	3845	1/1	0.83	0.14	85,85,85,85	0
56	MG	2A	3851	1/1	0.83	0.17	50,50,50,50	0
56	MG	1A	3703	1/1	0.83	0.11	22,22,22,22	0
56	MG	1O	204	1/1	0.83	0.14	56,56,56,56	0
56	MG	1a	1737	1/1	0.83	0.43	73,73,73,73	0
56	MG	2B	202	1/1	0.83	0.16	67,67,67,67	0
56	MG	1a	1678	1/1	0.84	0.20	72,72,72,72	0
56	MG	2A	3680	1/1	0.84	0.24	67,67,67,67	0
56	MG	1A	3256	1/1	0.84	0.12	56,56,56,56	0
56	MG	2D	302	1/1	0.84	0.20	46,46,46,46	0
56	MG	1A	3714	1/1	0.84	0.27	65,65,65,65	0
56	MG	2a	1615	1/1	0.84	0.24	58,58,58,58	0
56	MG	2A	3712	1/1	0.84	0.13	75,75,75,75	0
56	MG	1A	3076	1/1	0.84	0.16	66,66,66,66	0
56	MG	1a	1694	1/1	0.84	0.22	63,63,63,63	0
56	MG	2A	3735	1/1	0.84	0.19	75,75,75,75	0
56	MG	1a	1614	1/1	0.84	0.16	75,75,75,75	0
56	MG	1a	1626	1/1	0.84	0.27	64,64,64,64	0
56	MG	2A	3282	1/1	0.84	0.10	66,66,66,66	0
56	MG	1A	3804	1/1	0.84	0.13	59,59,59,59	0
56	MG	2a	1692	1/1	0.84	0.40	73,73,73,73	0
56	MG	1A	3980	1/1	0.84	0.20	70,70,70,70	0
56	MG	2a	1715	1/1	0.84	0.18	68,68,68,68	0
56	MG	2A	3561	1/1	0.84	0.14	60,60,60,60	0
56	MG	2A	3764	1/1	0.84	0.21	71,71,71,71	0
56	MG	2A	3287	1/1	0.84	0.17	66,66,66,66	0
56	MG	1A	3393	1/1	0.84	0.10	67,67,67,67	0
56	MG	2A	3577	1/1	0.84	0.18	61,61,61,61	0
56	MG	1A	3827	1/1	0.84	0.21	45,45,45,45	0
56	MG	2A	3301	1/1	0.84	0.28	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	1725	1/1	0.84	0.34	80,80,80,80	0
56	MG	1B	229	1/1	0.84	0.20	67,67,67,67	0
56	MG	2A	3356	1/1	0.84	0.16	63,63,63,63	0
56	MG	2A	3358	1/1	0.84	0.29	70,70,70,70	0
56	MG	1A	3663	1/1	0.84	0.09	27,27,27,27	0
56	MG	2A	3164	1/1	0.84	0.28	52,52,52,52	0
56	MG	16	102	1/1	0.84	0.27	54,54,54,54	0
56	MG	2A	3675	1/1	0.84	0.23	79,79,79,79	0
56	MG	2A	3050	1/1	0.85	0.29	75,75,75,75	0
56	MG	2A	3581	1/1	0.85	0.22	61,61,61,61	0
56	MG	2A	3063	1/1	0.85	0.27	75,75,75,75	0
56	MG	2A	3296	1/1	0.85	0.12	61,61,61,61	0
56	MG	1A	3812	1/1	0.85	0.14	43,43,43,43	0
56	MG	1a	1766	1/1	0.85	0.20	68,68,68,68	0
56	MG	1A	3415	1/1	0.85	0.32	68,68,68,68	0
56	MG	2B	204	1/1	0.85	0.21	76,76,76,76	0
56	MG	2A	3330	1/1	0.85	0.15	74,74,74,74	0
56	MG	1B	202	1/1	0.85	0.23	62,62,62,62	0
56	MG	2A	3664	1/1	0.85	0.16	49,49,49,49	0
56	MG	2A	3665	1/1	0.85	0.15	54,54,54,54	0
56	MG	1B	211	1/1	0.85	0.24	53,53,53,53	0
56	MG	2A	3672	1/1	0.85	0.28	76,76,76,76	0
56	MG	2N	201	1/1	0.85	0.11	81,81,81,81	0
56	MG	1A	3541	1/1	0.85	0.29	68,68,68,68	0
56	MG	1A	3971	1/1	0.85	0.10	69,69,69,69	0
56	MG	2A	3362	1/1	0.85	0.13	65,65,65,65	0
56	MG	2A	3152	1/1	0.85	0.22	65,65,65,65	0
56	MG	2A	3692	1/1	0.85	0.17	82,82,82,82	0
56	MG	2A	3160	1/1	0.85	0.31	75,75,75,75	0
56	MG	1A	3979	1/1	0.85	0.09	28,28,28,28	0
56	MG	1A	3542	1/1	0.85	0.16	61,61,61,61	0
56	MG	2A	3396	1/1	0.85	0.10	71,71,71,71	0
56	MG	2A	3717	1/1	0.85	0.16	62,62,62,62	0
56	MG	2A	3720	1/1	0.85	0.22	68,68,68,68	0
56	MG	1A	3569	1/1	0.85	0.19	75,75,75,75	0
56	MG	2A	3731	1/1	0.85	0.14	48,48,48,48	0
56	MG	1A	3683	1/1	0.85	0.13	74,74,74,74	0
56	MG	1F	310	1/1	0.85	0.10	58,58,58,58	0
56	MG	2a	1723	1/1	0.85	0.16	74,74,74,74	0
56	MG	2A	3491	1/1	0.85	0.14	58,58,58,58	0
56	MG	1A	3775	1/1	0.85	0.17	59,59,59,59	0
56	MG	1A	3684	1/1	0.85	0.14	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3753	1/1	0.85	0.14	74,74,74,74	0
56	MG	1a	1668	1/1	0.85	0.26	71,71,71,71	0
56	MG	1a	1735	1/1	0.85	0.40	69,69,69,69	0
56	MG	1A	3794	1/1	0.85	0.27	57,57,57,57	0
56	MG	2A	3773	1/1	0.85	0.20	59,59,59,59	0
56	MG	2A	3778	1/1	0.85	0.12	60,60,60,60	0
56	MG	2A	3551	1/1	0.85	0.24	75,75,75,75	0
56	MG	1A	3401	1/1	0.85	0.13	48,48,48,48	0
56	MG	2A	3284	1/1	0.85	0.13	65,65,65,65	0
56	MG	2v	101	1/1	0.85	0.35	70,70,70,70	0
56	MG	1A	3029	1/1	0.85	0.16	71,71,71,71	0
56	MG	1A	3233	1/1	0.86	0.17	57,57,57,57	0
56	MG	2A	3266	1/1	0.86	0.19	79,79,79,79	0
56	MG	1a	1821	1/1	0.86	0.13	68,68,68,68	0
56	MG	2A	3821	1/1	0.86	0.08	80,80,80,80	0
56	MG	2A	3570	1/1	0.86	0.15	72,72,72,72	0
56	MG	2A	3276	1/1	0.86	0.31	71,71,71,71	0
56	MG	1A	3905	1/1	0.86	0.12	43,43,43,43	0
56	MG	1A	3480	1/1	0.86	0.12	52,52,52,52	0
56	MG	2A	3855	1/1	0.86	0.15	56,56,56,56	0
56	MG	1A	3135	1/1	0.86	0.10	32,32,32,32	0
56	MG	1a	1723	1/1	0.86	0.09	71,71,71,71	0
56	MG	1v	103	1/1	0.86	0.13	61,61,61,61	0
56	MG	1a	1624	1/1	0.86	0.32	71,71,71,71	0
56	MG	1A	3167	1/1	0.86	0.29	68,68,68,68	0
56	MG	1a	1633	1/1	0.86	0.28	66,66,66,66	0
56	MG	1a	1732	1/1	0.86	0.11	75,75,75,75	0
56	MG	1A	3358	1/1	0.86	0.12	48,48,48,48	0
56	MG	2B	216	1/1	0.86	0.12	70,70,70,70	0
56	MG	1B	224	1/1	0.86	0.10	57,57,57,57	0
56	MG	2A	3671	1/1	0.86	0.12	51,51,51,51	0
56	MG	2A	3073	1/1	0.86	0.24	69,69,69,69	0
56	MG	2A	3341	1/1	0.86	0.17	63,63,63,63	0
56	MG	2W	203	1/1	0.86	0.19	45,45,45,45	0
56	MG	2a	1603	1/1	0.86	0.29	81,81,81,81	0
56	MG	1A	3264	1/1	0.86	0.18	71,71,71,71	0
56	MG	2a	1624	1/1	0.86	0.35	72,72,72,72	0
56	MG	2A	3677	1/1	0.86	0.14	49,49,49,49	0
56	MG	1a	1736	1/1	0.86	0.30	65,65,65,65	0
56	MG	2a	1650	1/1	0.86	0.21	66,66,66,66	0
56	MG	2a	1651	1/1	0.86	0.23	69,69,69,69	0
56	MG	1A	3097	1/1	0.86	0.17	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	3689	1/1	0.86	0.17	58,58,58,58	0
56	MG	1A	3690	1/1	0.86	0.14	69,69,69,69	0
56	MG	1A	3694	1/1	0.86	0.11	27,27,27,27	0
56	MG	2A	3114	1/1	0.86	0.30	63,63,63,63	0
56	MG	1A	3982	1/1	0.86	0.14	54,54,54,54	0
56	MG	2a	1690	1/1	0.86	0.45	78,78,78,78	0
56	MG	2A	3388	1/1	0.86	0.18	60,60,60,60	0
56	MG	1a	1670	1/1	0.86	0.20	78,78,78,78	0
56	MG	2a	1713	1/1	0.86	0.24	56,56,56,56	0
56	MG	1A	3103	1/1	0.86	0.22	64,64,64,64	0
56	MG	1A	3709	1/1	0.86	0.13	33,33,33,33	0
56	MG	1A	3063	1/1	0.86	0.23	54,54,54,54	0
56	MG	2A	3732	1/1	0.86	0.11	57,57,57,57	0
56	MG	2A	3733	1/1	0.86	0.15	70,70,70,70	0
56	MG	1A	3337	1/1	0.86	0.21	57,57,57,57	0
56	MG	2a	1737	1/1	0.86	0.30	69,69,69,69	0
56	MG	2a	1738	1/1	0.86	0.12	71,71,71,71	0
56	MG	1A	4012	1/1	0.86	0.15	62,62,62,62	0
56	MG	2A	3484	1/1	0.86	0.19	63,63,63,63	0
56	MG	1A	3421	1/1	0.86	0.14	69,69,69,69	0
56	MG	2a	1759	1/1	0.86	0.28	58,58,58,58	0
56	MG	2a	1761	1/1	0.86	0.20	75,75,75,75	0
56	MG	2a	1763	1/1	0.86	0.19	70,70,70,70	0
56	MG	1A	3603	1/1	0.86	0.13	59,59,59,59	0
56	MG	2A	3221	1/1	0.86	0.17	75,75,75,75	0
56	MG	2A	3754	1/1	0.86	0.17	68,68,68,68	0
56	MG	1A	4048	1/1	0.86	0.12	55,55,55,55	0
56	MG	2A	3517	1/1	0.86	0.37	81,81,81,81	0
56	MG	2A	3249	1/1	0.86	0.18	69,69,69,69	0
56	MG	2A	3255	1/1	0.86	0.19	62,62,62,62	0
56	MG	2A	3259	1/1	0.86	0.34	65,65,65,65	0
56	MG	2A	3554	1/1	0.86	0.15	38,38,38,38	0
56	MG	2x	104	1/1	0.86	0.12	77,77,77,77	0
56	MG	1A	3608	1/1	0.87	0.11	43,43,43,43	0
56	MG	2A	3367	1/1	0.87	0.14	70,70,70,70	0
56	MG	2B	213	1/1	0.87	0.27	67,67,67,67	0
56	MG	1a	1782	1/1	0.87	0.25	80,80,80,80	0
56	MG	1A	3837	1/1	0.87	0.13	39,39,39,39	0
56	MG	1a	1795	1/1	0.87	0.14	55,55,55,55	0
56	MG	1a	1707	1/1	0.87	0.20	58,58,58,58	0
56	MG	1A	3382	1/1	0.87	0.20	61,61,61,61	0
56	MG	2R	203	1/1	0.87	0.14	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	3694	1/1	0.87	0.20	67,67,67,67	0
56	MG	2A	3430	1/1	0.87	0.31	60,60,60,60	0
56	MG	1a	1638	1/1	0.87	0.25	74,74,74,74	0
56	MG	2a	1608	1/1	0.87	0.09	75,75,75,75	0
56	MG	2a	1612	1/1	0.87	0.26	67,67,67,67	0
56	MG	2A	3711	1/1	0.87	0.09	64,64,64,64	0
56	MG	2a	1616	1/1	0.87	0.18	56,56,56,56	0
56	MG	2a	1623	1/1	0.87	0.17	64,64,64,64	0
56	MG	2A	3242	1/1	0.87	0.21	74,74,74,74	0
56	MG	2A	3454	1/1	0.87	0.15	57,57,57,57	0
56	MG	1a	1641	1/1	0.87	0.34	61,61,61,61	0
56	MG	2a	1649	1/1	0.87	0.21	72,72,72,72	0
56	MG	2A	3719	1/1	0.87	0.12	55,55,55,55	0
56	MG	1A	4062	1/1	0.87	0.11	44,44,44,44	0
56	MG	1A	3534	1/1	0.87	0.12	38,38,38,38	0
56	MG	1a	1649	1/1	0.87	0.19	63,63,63,63	0
56	MG	2a	1664	1/1	0.87	0.26	58,58,58,58	0
56	MG	1A	4067	1/1	0.87	0.09	68,68,68,68	0
56	MG	2a	1667	1/1	0.87	0.21	66,66,66,66	0
56	MG	1a	1730	1/1	0.87	0.46	70,70,70,70	0
56	MG	2A	3273	1/1	0.87	0.15	70,70,70,70	0
56	MG	2A	3519	1/1	0.87	0.25	68,68,68,68	0
56	MG	1A	3853	1/1	0.87	0.14	59,59,59,59	0
56	MG	1a	1663	1/1	0.87	0.15	71,71,71,71	0
56	MG	2A	3747	1/1	0.87	0.23	66,66,66,66	0
56	MG	2A	3748	1/1	0.87	0.15	76,76,76,76	0
56	MG	1W	202	1/1	0.87	0.13	42,42,42,42	0
56	MG	1A	3917	1/1	0.87	0.10	45,45,45,45	0
56	MG	2A	3557	1/1	0.87	0.18	47,47,47,47	0
56	MG	13	105	1/1	0.87	0.10	28,28,28,28	0
56	MG	2a	1725	1/1	0.87	0.15	52,52,52,52	0
56	MG	1A	3387	1/1	0.87	0.14	55,55,55,55	0
56	MG	1a	1738	1/1	0.87	0.30	69,69,69,69	0
56	MG	1a	1601	1/1	0.87	0.35	72,72,72,72	0
56	MG	1a	1744	1/1	0.87	0.17	76,76,76,76	0
56	MG	1a	1747	1/1	0.87	0.11	60,60,60,60	0
56	MG	2a	1748	1/1	0.87	0.14	61,61,61,61	0
56	MG	1A	4009	1/1	0.87	0.17	62,62,62,62	0
56	MG	2a	1754	1/1	0.87	0.14	74,74,74,74	0
56	MG	1A	3963	1/1	0.87	0.16	54,54,54,54	0
56	MG	2A	3618	1/1	0.87	0.14	37,37,37,37	0
56	MG	2A	3315	1/1	0.87	0.14	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	3322	1/1	0.87	0.34	65,65,65,65	0
56	MG	2A	3109	1/1	0.87	0.19	60,60,60,60	0
56	MG	2a	1770	1/1	0.87	0.12	63,63,63,63	0
56	MG	2A	3332	1/1	0.87	0.22	66,66,66,66	0
56	MG	1A	3815	1/1	0.87	0.17	62,62,62,62	0
56	MG	2A	3659	1/1	0.87	0.14	59,59,59,59	0
56	MG	1A	3419	1/1	0.87	0.27	60,60,60,60	0
56	MG	2A	3149	1/1	0.87	0.17	58,58,58,58	0
56	MG	1a	1695	1/1	0.87	0.21	70,70,70,70	0
56	MG	1A	4045	1/1	0.87	0.17	57,57,57,57	0
56	MG	2B	205	1/1	0.87	0.22	59,59,59,59	0
56	MG	2x	103	1/1	0.87	0.27	75,75,75,75	0
56	MG	1a	1697	1/1	0.87	0.18	63,63,63,63	0
56	MG	2A	3115	1/1	0.88	0.33	64,64,64,64	0
56	MG	2A	3761	1/1	0.88	0.14	68,68,68,68	0
56	MG	2A	3401	1/1	0.88	0.17	68,68,68,68	0
56	MG	2A	3423	1/1	0.88	0.24	66,66,66,66	0
56	MG	2A	3427	1/1	0.88	0.33	63,63,63,63	0
56	MG	2A	3429	1/1	0.88	0.29	60,60,60,60	0
56	MG	2A	3785	1/1	0.88	0.16	72,72,72,72	0
56	MG	1A	4033	1/1	0.88	0.16	45,45,45,45	0
56	MG	2A	3794	1/1	0.88	0.14	55,55,55,55	0
56	MG	2A	3431	1/1	0.88	0.31	58,58,58,58	0
56	MG	2A	3438	1/1	0.88	0.23	57,57,57,57	0
56	MG	2A	3133	1/1	0.88	0.10	52,52,52,52	0
56	MG	2A	3832	1/1	0.88	0.18	66,66,66,66	0
56	MG	2A	3144	1/1	0.88	0.30	64,64,64,64	0
56	MG	1a	1661	1/1	0.88	0.10	70,70,70,70	0
56	MG	1a	1740	1/1	0.88	0.11	62,62,62,62	0
56	MG	1A	3302	1/1	0.88	0.28	56,56,56,56	0
56	MG	1A	3487	1/1	0.88	0.17	64,64,64,64	0
56	MG	2A	3860	1/1	0.88	0.12	49,49,49,49	0
56	MG	1a	1746	1/1	0.88	0.13	57,57,57,57	0
56	MG	1a	1666	1/1	0.88	0.19	75,75,75,75	0
56	MG	1A	3494	1/1	0.88	0.15	68,68,68,68	0
56	MG	2A	3182	1/1	0.88	0.21	56,56,56,56	0
56	MG	1A	3962	1/1	0.88	0.10	68,68,68,68	0
56	MG	2B	206	1/1	0.88	0.22	70,70,70,70	0
56	MG	2A	3198	1/1	0.88	0.16	52,52,52,52	0
56	MG	2A	3531	1/1	0.88	0.20	49,49,49,49	0
56	MG	2A	3200	1/1	0.88	0.18	65,65,65,65	0
56	MG	2A	3210	1/1	0.88	0.14	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	1a	1672	1/1	0.88	0.10	70,70,70,70	0
56	MG	2A	3219	1/1	0.88	0.13	62,62,62,62	0
56	MG	2B	219	1/1	0.88	0.30	68,68,68,68	0
56	MG	1a	1675	1/1	0.88	0.28	69,69,69,69	0
56	MG	2A	3235	1/1	0.88	0.15	49,49,49,49	0
56	MG	2F	301	1/1	0.88	0.18	46,46,46,46	0
56	MG	10	105	1/1	0.88	0.17	63,63,63,63	0
56	MG	1A	3578	1/1	0.88	0.14	69,69,69,69	0
56	MG	2A	3571	1/1	0.88	0.11	53,53,53,53	0
56	MG	2A	3247	1/1	0.88	0.08	59,59,59,59	0
56	MG	2Z	301	1/1	0.88	0.15	69,69,69,69	0
56	MG	25	101	1/1	0.88	0.11	54,54,54,54	0
56	MG	2A	3578	1/1	0.88	0.22	71,71,71,71	0
56	MG	1a	1779	1/1	0.88	0.19	95,95,95,95	0
56	MG	2a	1610	1/1	0.88	0.29	70,70,70,70	0
56	MG	14	101	1/1	0.88	0.17	61,61,61,61	0
56	MG	2A	3588	1/1	0.88	0.14	62,62,62,62	0
56	MG	1A	3392	1/1	0.88	0.32	74,74,74,74	0
56	MG	2A	3605	1/1	0.88	0.13	61,61,61,61	0
56	MG	2A	3610	1/1	0.88	0.12	35,35,35,35	0
56	MG	2A	3260	1/1	0.88	0.37	73,73,73,73	0
56	MG	2a	1631	1/1	0.88	0.17	77,77,77,77	0
56	MG	1A	3599	1/1	0.88	0.25	61,61,61,61	0
56	MG	1a	1690	1/1	0.88	0.26	67,67,67,67	0
56	MG	1a	1692	1/1	0.88	0.14	62,62,62,62	0
56	MG	2A	3269	1/1	0.88	0.20	60,60,60,60	0
56	MG	1A	4083	1/1	0.88	0.17	66,66,66,66	0
56	MG	1A	3504	1/1	0.88	0.23	69,69,69,69	0
56	MG	2a	1658	1/1	0.88	0.43	69,69,69,69	0
56	MG	2a	1659	1/1	0.88	0.21	63,63,63,63	0
56	MG	2A	3660	1/1	0.88	0.12	69,69,69,69	0
56	MG	1a	1608	1/1	0.88	0.12	70,70,70,70	0
56	MG	1A	3430	1/1	0.88	0.08	45,45,45,45	0
56	MG	2a	1668	1/1	0.88	0.29	60,60,60,60	0
56	MG	1A	3514	1/1	0.88	0.15	53,53,53,53	0
56	MG	1a	1615	1/1	0.88	0.12	75,75,75,75	0
56	MG	1A	3638	1/1	0.88	0.16	74,74,74,74	0
56	MG	2a	1684	1/1	0.88	0.32	66,66,66,66	0
56	MG	2a	1689	1/1	0.88	0.29	71,71,71,71	0
56	MG	1A	3866	1/1	0.88	0.22	49,49,49,49	0
56	MG	1a	1710	1/1	0.88	0.11	78,78,78,78	0
56	MG	1x	104	1/1	0.88	0.36	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	2a	1707	1/1	0.88	0.17	72,72,72,72	0
56	MG	1a	1631	1/1	0.88	0.19	62,62,62,62	0
56	MG	2A	3299	1/1	0.88	0.25	49,49,49,49	0
56	MG	2A	3683	1/1	0.88	0.10	48,48,48,48	0
56	MG	1A	3443	1/1	0.88	0.28	62,62,62,62	0
56	MG	2A	3691	1/1	0.88	0.14	74,74,74,74	0
56	MG	1a	1717	1/1	0.88	0.14	64,64,64,64	0
56	MG	2A	3305	1/1	0.88	0.30	61,61,61,61	0
56	MG	1A	3454	1/1	0.88	0.21	62,62,62,62	0
56	MG	2A	3317	1/1	0.88	0.19	60,60,60,60	0
56	MG	2A	3033	1/1	0.88	0.18	52,52,52,52	0
56	MG	2A	3329	1/1	0.88	0.29	79,79,79,79	0
56	MG	1A	3781	1/1	0.88	0.10	33,33,33,33	0
56	MG	1A	3094	1/1	0.88	0.20	53,53,53,53	0
56	MG	2A	3071	1/1	0.88	0.15	44,44,44,44	0
56	MG	1F	303	1/1	0.88	0.09	61,61,61,61	0
56	MG	1a	1644	1/1	0.88	0.18	68,68,68,68	0
56	MG	2a	1760	1/1	0.88	0.33	64,64,64,64	0
56	MG	1a	1731	1/1	0.88	0.40	66,66,66,66	0
56	MG	2A	3095	1/1	0.88	0.14	62,62,62,62	0
56	MG	1A	3467	1/1	0.88	0.14	68,68,68,68	0
56	MG	1a	1646	1/1	0.88	0.18	72,72,72,72	0
56	MG	2A	3101	1/1	0.88	0.20	58,58,58,58	0
56	MG	2d	301	1/1	0.88	0.27	64,64,64,64	0
56	MG	2A	3373	1/1	0.88	0.25	60,60,60,60	0
56	MG	2A	3377	1/1	0.88	0.32	66,66,66,66	0
56	MG	2A	3746	1/1	0.88	0.13	69,69,69,69	0
56	MG	1a	1648	1/1	0.88	0.26	67,67,67,67	0
56	MG	2r	101	1/1	0.88	0.21	82,82,82,82	0
56	MG	2A	3383	1/1	0.88	0.23	72,72,72,72	0
56	MG	2A	3385	1/1	0.88	0.11	60,60,60,60	0
56	MG	1A	3538	1/1	0.88	0.17	55,55,55,55	0
56	MG	2A	3110	1/1	0.88	0.17	53,53,53,53	0
56	MG	1A	4024	1/1	0.88	0.17	72,72,72,72	0
57	K	1A	3557	1/1	0.88	0.26	89,89,89,89	0
56	MG	1B	205	1/1	0.89	0.22	66,66,66,66	0
56	MG	2A	3132	1/1	0.89	0.14	59,59,59,59	0
56	MG	1A	3326	1/1	0.89	0.09	49,49,49,49	0
56	MG	2A	3336	1/1	0.89	0.09	76,76,76,76	0
56	MG	1A	3051	1/1	0.89	0.14	43,43,43,43	0
56	MG	2B	217	1/1	0.89	0.16	71,71,71,71	0
56	MG	1a	1616	1/1	0.89	0.10	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1620	1/1	0.89	0.11	58,58,58,58	0
56	MG	1B	221	1/1	0.89	0.17	53,53,53,53	0
56	MG	2A	3663	1/1	0.89	0.13	62,62,62,62	0
56	MG	1a	1785	1/1	0.89	0.18	67,67,67,67	0
56	MG	1A	3658	1/1	0.89	0.12	62,62,62,62	0
56	MG	2A	3166	1/1	0.89	0.20	62,62,62,62	0
56	MG	1B	226	1/1	0.89	0.16	61,61,61,61	0
56	MG	1A	3771	1/1	0.89	0.10	38,38,38,38	0
56	MG	1a	1803	1/1	0.89	0.22	63,63,63,63	0
56	MG	2A	3378	1/1	0.89	0.20	54,54,54,54	0
56	MG	1a	1804	1/1	0.89	0.11	58,58,58,58	0
56	MG	1A	3161	1/1	0.89	0.09	66,66,66,66	0
56	MG	2A	3199	1/1	0.89	0.21	61,61,61,61	0
56	MG	1a	1811	1/1	0.89	0.19	73,73,73,73	0
56	MG	2A	3204	1/1	0.89	0.12	64,64,64,64	0
56	MG	1A	3026	1/1	0.89	0.12	44,44,44,44	0
56	MG	2A	3212	1/1	0.89	0.24	58,58,58,58	0
56	MG	2A	3214	1/1	0.89	0.11	59,59,59,59	0
56	MG	2A	3416	1/1	0.89	0.30	61,61,61,61	0
56	MG	2A	3421	1/1	0.89	0.41	62,62,62,62	0
56	MG	2a	1637	1/1	0.89	0.23	56,56,56,56	0
56	MG	2a	1640	1/1	0.89	0.22	75,75,75,75	0
56	MG	2a	1643	1/1	0.89	0.17	64,64,64,64	0
56	MG	1a	1818	1/1	0.89	0.10	72,72,72,72	0
56	MG	1A	3223	1/1	0.89	0.20	60,60,60,60	0
56	MG	1a	1712	1/1	0.89	0.20	59,59,59,59	0
56	MG	1e	204	1/1	0.89	0.21	83,83,83,83	0
56	MG	1A	4010	1/1	0.89	0.14	64,64,64,64	0
56	MG	1A	3172	1/1	0.89	0.29	57,57,57,57	0
56	MG	2A	3439	1/1	0.89	0.17	61,61,61,61	0
56	MG	2A	3724	1/1	0.89	0.12	54,54,54,54	0
56	MG	2A	3727	1/1	0.89	0.11	72,72,72,72	0
56	MG	2A	3446	1/1	0.89	0.41	64,64,64,64	0
56	MG	2A	3246	1/1	0.89	0.19	65,65,65,65	0
56	MG	1A	3802	1/1	0.89	0.08	35,35,35,35	0
56	MG	1A	4022	1/1	0.89	0.14	56,56,56,56	0
56	MG	1A	3517	1/1	0.89	0.10	66,66,66,66	0
56	MG	1A	3520	1/1	0.89	0.18	44,44,44,44	0
56	MG	2A	3008	1/1	0.89	0.14	52,52,52,52	0
56	MG	1a	1650	1/1	0.89	0.18	58,58,58,58	0
56	MG	1A	3697	1/1	0.89	0.11	59,59,59,59	0
56	MG	1P	206	1/1	0.89	0.36	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1696	1/1	0.89	0.18	80,80,80,80	0
56	MG	2A	3507	1/1	0.89	0.15	69,69,69,69	0
56	MG	2A	3514	1/1	0.89	0.16	60,60,60,60	0
56	MG	2A	3516	1/1	0.89	0.13	58,58,58,58	0
56	MG	1a	1660	1/1	0.89	0.21	68,68,68,68	0
56	MG	2a	1719	1/1	0.89	0.17	54,54,54,54	0
56	MG	2A	3043	1/1	0.89	0.26	72,72,72,72	0
56	MG	1S	203	1/1	0.89	0.10	54,54,54,54	0
56	MG	2a	1724	1/1	0.89	0.16	82,82,82,82	0
56	MG	2A	3279	1/1	0.89	0.13	52,52,52,52	0
56	MG	2A	3767	1/1	0.89	0.17	67,67,67,67	0
56	MG	2a	1732	1/1	0.89	0.24	61,61,61,61	0
56	MG	2a	1734	1/1	0.89	0.14	68,68,68,68	0
56	MG	2A	3058	1/1	0.89	0.18	66,66,66,66	0
56	MG	2A	3536	1/1	0.89	0.18	71,71,71,71	0
56	MG	2A	3542	1/1	0.89	0.11	42,42,42,42	0
56	MG	2a	1740	1/1	0.89	0.19	66,66,66,66	0
56	MG	2a	1745	1/1	0.89	0.21	67,67,67,67	0
56	MG	1A	4038	1/1	0.89	0.11	20,20,20,20	0
56	MG	1A	4039	1/1	0.89	0.11	57,57,57,57	0
56	MG	2A	3792	1/1	0.89	0.12	55,55,55,55	0
56	MG	1A	3601	1/1	0.89	0.24	45,45,45,45	0
56	MG	2A	3795	1/1	0.89	0.13	58,58,58,58	0
56	MG	1Y	202	1/1	0.89	0.07	60,60,60,60	0
56	MG	1A	3935	1/1	0.89	0.11	61,61,61,61	0
56	MG	1A	3942	1/1	0.89	0.12	65,65,65,65	0
56	MG	2A	3096	1/1	0.89	0.22	72,72,72,72	0
56	MG	2A	3834	1/1	0.89	0.11	41,41,41,41	0
56	MG	1A	3954	1/1	0.89	0.12	55,55,55,55	0
56	MG	1A	3253	1/1	0.89	0.08	57,57,57,57	0
56	MG	2a	1775	1/1	0.89	0.11	60,60,60,60	0
56	MG	1A	3527	1/1	0.89	0.27	60,60,60,60	0
56	MG	2d	302	1/1	0.89	0.07	73,73,73,73	0
56	MG	1A	3835	1/1	0.89	0.09	39,39,39,39	0
56	MG	1A	3531	1/1	0.89	0.36	70,70,70,70	0
56	MG	2A	3859	1/1	0.89	0.11	47,47,47,47	0
56	MG	1a	1761	1/1	0.89	0.18	69,69,69,69	0
56	MG	2q	202	1/1	0.89	0.23	77,77,77,77	0
56	MG	1A	3313	1/1	0.89	0.11	49,49,49,49	0
56	MG	2A	3595	1/1	0.89	0.14	65,65,65,65	0
56	MG	2t	201	1/1	0.89	0.23	60,60,60,60	0
56	MG	2A	3599	1/1	0.89	0.11	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	3600	1/1	0.89	0.28	59,59,59,59	0
56	MG	2A	3318	1/1	0.89	0.25	74,74,74,74	0
56	MG	1a	1687	1/1	0.89	0.32	70,70,70,70	0
56	MG	2A	3617	1/1	0.89	0.24	77,77,77,77	0
56	MG	2A	3094	1/1	0.90	0.16	41,41,41,41	0
56	MG	1A	3516	1/1	0.90	0.17	84,84,84,84	0
56	MG	2A	3306	1/1	0.90	0.24	39,39,39,39	0
56	MG	2A	3308	1/1	0.90	0.16	59,59,59,59	0
56	MG	2A	3311	1/1	0.90	0.09	57,57,57,57	0
56	MG	1D	312	1/1	0.90	0.19	50,50,50,50	0
56	MG	1E	309	1/1	0.90	0.27	74,74,74,74	0
56	MG	1A	3844	1/1	0.90	0.23	60,60,60,60	0
56	MG	2E	305	1/1	0.90	0.07	30,30,30,30	0
56	MG	2A	3620	1/1	0.90	0.24	64,64,64,64	0
56	MG	1A	3845	1/1	0.90	0.12	58,58,58,58	0
56	MG	2R	202	1/1	0.90	0.15	53,53,53,53	0
56	MG	2A	3326	1/1	0.90	0.23	63,63,63,63	0
56	MG	2T	203	1/1	0.90	0.15	72,72,72,72	0
56	MG	1F	304	1/1	0.90	0.13	50,50,50,50	0
56	MG	1A	3598	1/1	0.90	0.23	59,59,59,59	0
56	MG	1F	314	1/1	0.90	0.20	59,59,59,59	0
56	MG	2A	3333	1/1	0.90	0.15	73,73,73,73	0
56	MG	28	101	1/1	0.90	0.18	67,67,67,67	0
56	MG	2a	1601	1/1	0.90	0.20	60,60,60,60	0
56	MG	1G	201	1/1	0.90	0.09	54,54,54,54	0
56	MG	2A	3339	1/1	0.90	0.08	65,65,65,65	0
56	MG	1A	3332	1/1	0.90	0.12	64,64,64,64	0
56	MG	1A	3404	1/1	0.90	0.10	54,54,54,54	0
56	MG	2a	1614	1/1	0.90	0.16	55,55,55,55	0
56	MG	2A	3122	1/1	0.90	0.16	66,66,66,66	0
56	MG	1a	1763	1/1	0.90	0.08	64,64,64,64	0
56	MG	1O	203	1/1	0.90	0.28	69,69,69,69	0
56	MG	1A	3361	1/1	0.90	0.10	45,45,45,45	0
56	MG	1A	3212	1/1	0.90	0.17	61,61,61,61	0
56	MG	1A	3872	1/1	0.90	0.09	45,45,45,45	0
56	MG	2a	1632	1/1	0.90	0.21	58,58,58,58	0
56	MG	1Q	204	1/1	0.90	0.08	52,52,52,52	0
56	MG	2a	1636	1/1	0.90	0.26	56,56,56,56	0
56	MG	1A	3315	1/1	0.90	0.22	46,46,46,46	0
56	MG	1A	3884	1/1	0.90	0.16	72,72,72,72	0
56	MG	2A	3165	1/1	0.90	0.17	43,43,43,43	0
56	MG	2a	1647	1/1	0.90	0.22	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	1V	206	1/1	0.90	0.06	51,51,51,51	0
56	MG	1A	3625	1/1	0.90	0.10	36,36,36,36	0
56	MG	2A	3168	1/1	0.90	0.26	67,67,67,67	0
56	MG	2a	1653	1/1	0.90	0.23	59,59,59,59	0
56	MG	1A	3249	1/1	0.90	0.16	65,65,65,65	0
56	MG	2A	3704	1/1	0.90	0.11	36,36,36,36	0
56	MG	2A	3171	1/1	0.90	0.16	48,48,48,48	0
56	MG	2A	3395	1/1	0.90	0.11	60,60,60,60	0
56	MG	1a	1792	1/1	0.90	0.16	56,56,56,56	0
56	MG	1A	3422	1/1	0.90	0.10	55,55,55,55	0
56	MG	2A	3403	1/1	0.90	0.10	56,56,56,56	0
56	MG	1a	1685	1/1	0.90	0.14	50,50,50,50	0
56	MG	2A	3419	1/1	0.90	0.17	45,45,45,45	0
56	MG	1a	1686	1/1	0.90	0.27	72,72,72,72	0
56	MG	1A	3645	1/1	0.90	0.07	15,15,15,15	0
56	MG	2A	3201	1/1	0.90	0.20	55,55,55,55	0
56	MG	2A	3428	1/1	0.90	0.32	63,63,63,63	0
56	MG	12	101	1/1	0.90	0.09	48,48,48,48	0
56	MG	13	101	1/1	0.90	0.13	35,35,35,35	0
56	MG	1A	3783	1/1	0.90	0.13	37,37,37,37	0
56	MG	2A	3434	1/1	0.90	0.30	55,55,55,55	0
56	MG	2a	1703	1/1	0.90	0.11	45,45,45,45	0
56	MG	2A	3437	1/1	0.90	0.33	59,59,59,59	0
56	MG	1A	3424	1/1	0.90	0.13	59,59,59,59	0
56	MG	16	101	1/1	0.90	0.17	41,41,41,41	0
56	MG	2A	3217	1/1	0.90	0.08	56,56,56,56	0
56	MG	1A	4052	1/1	0.90	0.11	62,62,62,62	0
56	MG	1b	301	1/1	0.90	0.12	75,75,75,75	0
56	MG	2A	3231	1/1	0.90	0.30	65,65,65,65	0
56	MG	2A	3462	1/1	0.90	0.17	59,59,59,59	0
56	MG	1A	3928	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3508	1/1	0.90	0.28	35,35,35,35	0
56	MG	2A	3487	1/1	0.90	0.15	59,59,59,59	0
56	MG	2a	1733	1/1	0.90	0.11	70,70,70,70	0
56	MG	1a	1706	1/1	0.90	0.25	67,67,67,67	0
56	MG	1a	1605	1/1	0.90	0.18	68,68,68,68	0
56	MG	2A	3503	1/1	0.90	0.15	58,58,58,58	0
56	MG	1a	1606	1/1	0.90	0.19	56,56,56,56	0
56	MG	1A	3085	1/1	0.90	0.24	43,43,43,43	0
56	MG	2A	3252	1/1	0.90	0.23	59,59,59,59	0
56	MG	2A	3786	1/1	0.90	0.25	61,61,61,61	0
56	MG	1x	105	1/1	0.90	0.22	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3936	1/1	0.90	0.12	65,65,65,65	0
56	MG	2a	1751	1/1	0.90	0.21	68,68,68,68	0
56	MG	2a	1752	1/1	0.90	0.14	76,76,76,76	0
56	MG	2A	3002	1/1	0.90	0.32	55,55,55,55	0
56	MG	2A	3005	1/1	0.90	0.33	69,69,69,69	0
56	MG	2A	3524	1/1	0.90	0.09	37,37,37,37	0
56	MG	2A	3007	1/1	0.90	0.18	55,55,55,55	0
56	MG	2A	3820	1/1	0.90	0.11	51,51,51,51	0
56	MG	1A	4073	1/1	0.90	0.09	19,19,19,19	0
56	MG	2A	3268	1/1	0.90	0.10	78,78,78,78	0
56	MG	2A	3018	1/1	0.90	0.33	60,60,60,60	0
56	MG	2A	3841	1/1	0.90	0.17	55,55,55,55	0
56	MG	1A	3554	1/1	0.90	0.10	71,71,71,71	0
56	MG	2A	3547	1/1	0.90	0.13	57,57,57,57	0
56	MG	1A	3667	1/1	0.90	0.10	50,50,50,50	0
56	MG	1A	3442	1/1	0.90	0.15	59,59,59,59	0
56	MG	1A	3352	1/1	0.90	0.13	61,61,61,61	0
56	MG	1A	3688	1/1	0.90	0.08	42,42,42,42	0
56	MG	2A	3045	1/1	0.90	0.32	69,69,69,69	0
56	MG	1B	220	1/1	0.90	0.11	64,64,64,64	0
56	MG	1A	3579	1/1	0.90	0.09	49,49,49,49	0
56	MG	1A	3977	1/1	0.90	0.12	25,25,25,25	0
56	MG	1A	3833	1/1	0.90	0.17	58,58,58,58	0
56	MG	2A	3072	1/1	0.90	0.10	56,56,56,56	0
56	MG	1A	3580	1/1	0.90	0.12	59,59,59,59	0
56	MG	1A	3981	1/1	0.90	0.10	48,48,48,48	0
56	MG	1A	3584	1/1	0.90	0.11	50,50,50,50	0
56	MG	2B	210	1/1	0.90	0.08	68,68,68,68	0
56	MG	2A	3192	1/1	0.91	0.12	69,69,69,69	0
56	MG	1A	3499	1/1	0.91	0.17	61,61,61,61	0
56	MG	2A	3440	1/1	0.91	0.24	53,53,53,53	0
56	MG	2A	3798	1/1	0.91	0.17	57,57,57,57	0
56	MG	1A	3921	1/1	0.91	0.15	48,48,48,48	0
56	MG	1A	3923	1/1	0.91	0.10	64,64,64,64	0
56	MG	1A	3745	1/1	0.91	0.17	44,44,44,44	0
56	MG	1A	3748	1/1	0.91	0.12	46,46,46,46	0
56	MG	2A	3460	1/1	0.91	0.13	59,59,59,59	0
56	MG	2A	3461	1/1	0.91	0.25	55,55,55,55	0
56	MG	1A	3500	1/1	0.91	0.07	29,29,29,29	0
56	MG	1A	3754	1/1	0.91	0.14	48,48,48,48	0
56	MG	2A	3479	1/1	0.91	0.23	65,65,65,65	0
56	MG	2A	3850	1/1	0.91	0.08	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	3757	1/1	0.91	0.23	52,52,52,52	0
56	MG	1A	3944	1/1	0.91	0.18	60,60,60,60	0
56	MG	1D	304	1/1	0.91	0.29	41,41,41,41	0
56	MG	2A	3497	1/1	0.91	0.16	46,46,46,46	0
56	MG	1A	3952	1/1	0.91	0.08	51,51,51,51	0
56	MG	2A	3866	1/1	0.91	0.13	47,47,47,47	0
56	MG	1a	1806	1/1	0.91	0.15	57,57,57,57	0
56	MG	1A	3953	1/1	0.91	0.35	50,50,50,50	0
56	MG	2A	3870	1/1	0.91	0.10	72,72,72,72	0
56	MG	2B	201	1/1	0.91	0.20	68,68,68,68	0
56	MG	1A	3501	1/1	0.91	0.11	61,61,61,61	0
56	MG	1A	3769	1/1	0.91	0.09	25,25,25,25	0
56	MG	1A	3503	1/1	0.91	0.08	47,47,47,47	0
56	MG	1A	3296	1/1	0.91	0.09	42,42,42,42	0
56	MG	1A	3507	1/1	0.91	0.19	45,45,45,45	0
56	MG	1a	1674	1/1	0.91	0.16	70,70,70,70	0
56	MG	1e	201	1/1	0.91	0.29	58,58,58,58	0
56	MG	2A	3526	1/1	0.91	0.07	33,33,33,33	0
56	MG	1e	203	1/1	0.91	0.11	57,57,57,57	0
56	MG	1A	3975	1/1	0.91	0.11	38,38,38,38	0
56	MG	1A	3091	1/1	0.91	0.14	48,48,48,48	0
56	MG	1N	203	1/1	0.91	0.07	43,43,43,43	0
56	MG	1n	101	1/1	0.91	0.22	59,59,59,59	0
56	MG	1N	208	1/1	0.91	0.12	35,35,35,35	0
56	MG	1A	3509	1/1	0.91	0.12	56,56,56,56	0
56	MG	1A	3366	1/1	0.91	0.10	43,43,43,43	0
56	MG	1A	3801	1/1	0.91	0.11	23,23,23,23	0
56	MG	2A	3271	1/1	0.91	0.37	67,67,67,67	0
56	MG	1x	107	1/1	0.91	0.20	72,72,72,72	0
56	MG	1A	3613	1/1	0.91	0.09	62,62,62,62	0
56	MG	2T	202	1/1	0.91	0.10	59,59,59,59	0
56	MG	1A	3368	1/1	0.91	0.36	60,60,60,60	0
56	MG	1a	1688	1/1	0.91	0.30	72,72,72,72	0
56	MG	1A	3425	1/1	0.91	0.14	55,55,55,55	0
56	MG	1A	3998	1/1	0.91	0.09	28,28,28,28	0
56	MG	23	102	1/1	0.91	0.17	59,59,59,59	0
56	MG	1A	3299	1/1	0.91	0.19	53,53,53,53	0
56	MG	1A	3643	1/1	0.91	0.10	48,48,48,48	0
56	MG	1A	3818	1/1	0.91	0.08	37,37,37,37	0
56	MG	1A	3333	1/1	0.91	0.19	49,49,49,49	0
56	MG	2a	1604	1/1	0.91	0.33	67,67,67,67	0
56	MG	2A	3592	1/1	0.91	0.17	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3594	1/1	0.91	0.13	58,58,58,58	0
56	MG	2A	3292	1/1	0.91	0.13	62,62,62,62	0
56	MG	2A	3031	1/1	0.91	0.10	64,64,64,64	0
56	MG	1A	3335	1/1	0.91	0.15	54,54,54,54	0
56	MG	2A	3042	1/1	0.91	0.27	66,66,66,66	0
56	MG	2A	3606	1/1	0.91	0.08	54,54,54,54	0
56	MG	2A	3607	1/1	0.91	0.13	66,66,66,66	0
56	MG	2a	1625	1/1	0.91	0.29	67,67,67,67	0
56	MG	2a	1626	1/1	0.91	0.16	55,55,55,55	0
56	MG	10	102	1/1	0.91	0.12	55,55,55,55	0
56	MG	2A	3303	1/1	0.91	0.10	49,49,49,49	0
56	MG	1A	3448	1/1	0.91	0.18	66,66,66,66	0
56	MG	1A	4020	1/1	0.91	0.17	72,72,72,72	0
56	MG	1A	3648	1/1	0.91	0.13	67,67,67,67	0
56	MG	2A	3635	1/1	0.91	0.12	41,41,41,41	0
56	MG	2A	3648	1/1	0.91	0.17	66,66,66,66	0
56	MG	2a	1642	1/1	0.91	0.27	67,67,67,67	0
56	MG	1A	3449	1/1	0.91	0.09	51,51,51,51	0
56	MG	1A	3064	1/1	0.91	0.11	44,44,44,44	0
56	MG	2A	3654	1/1	0.91	0.17	70,70,70,70	0
56	MG	1A	3464	1/1	0.91	0.18	63,63,63,63	0
56	MG	1A	4034	1/1	0.91	0.10	49,49,49,49	0
56	MG	2A	3084	1/1	0.91	0.18	53,53,53,53	0
56	MG	2A	3319	1/1	0.91	0.18	62,62,62,62	0
56	MG	2a	1655	1/1	0.91	0.29	55,55,55,55	0
56	MG	18	103	1/1	0.91	0.09	54,54,54,54	0
56	MG	2A	3324	1/1	0.91	0.10	69,69,69,69	0
56	MG	2A	3325	1/1	0.91	0.39	72,72,72,72	0
56	MG	2a	1660	1/1	0.91	0.16	59,59,59,59	0
56	MG	1A	3248	1/1	0.91	0.13	56,56,56,56	0
56	MG	2A	3090	1/1	0.91	0.23	68,68,68,68	0
56	MG	2A	3093	1/1	0.91	0.12	53,53,53,53	0
56	MG	2A	3331	1/1	0.91	0.08	65,65,65,65	0
56	MG	2a	1674	1/1	0.91	0.20	65,65,65,65	0
56	MG	2a	1676	1/1	0.91	0.16	61,61,61,61	0
56	MG	1A	3679	1/1	0.91	0.12	22,22,22,22	0
56	MG	2A	3676	1/1	0.91	0.15	64,64,64,64	0
56	MG	1a	1726	1/1	0.91	0.12	59,59,59,59	0
56	MG	2A	3334	1/1	0.91	0.28	70,70,70,70	0
56	MG	2a	1685	1/1	0.91	0.21	76,76,76,76	0
56	MG	1a	1603	1/1	0.91	0.10	55,55,55,55	0
56	MG	1A	3398	1/1	0.91	0.18	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	1691	1/1	0.91	0.32	59,59,59,59	0
56	MG	1A	4047	1/1	0.91	0.11	64,64,64,64	0
56	MG	2a	1693	1/1	0.91	0.17	67,67,67,67	0
56	MG	2A	3344	1/1	0.91	0.25	51,51,51,51	0
56	MG	1A	3540	1/1	0.91	0.11	57,57,57,57	0
56	MG	2a	1699	1/1	0.91	0.23	61,61,61,61	0
56	MG	2a	1701	1/1	0.91	0.16	64,64,64,64	0
56	MG	2A	3103	1/1	0.91	0.24	54,54,54,54	0
56	MG	2A	3695	1/1	0.91	0.22	61,61,61,61	0
56	MG	2a	1708	1/1	0.91	0.15	53,53,53,53	0
56	MG	1A	3855	1/1	0.91	0.12	48,48,48,48	0
56	MG	1A	4051	1/1	0.91	0.11	36,36,36,36	0
56	MG	2A	3706	1/1	0.91	0.13	48,48,48,48	0
56	MG	1a	1610	1/1	0.91	0.15	73,73,73,73	0
56	MG	2A	3709	1/1	0.91	0.17	57,57,57,57	0
56	MG	2A	3364	1/1	0.91	0.16	72,72,72,72	0
56	MG	1a	1611	1/1	0.91	0.22	61,61,61,61	0
56	MG	1A	3306	1/1	0.91	0.14	49,49,49,49	0
56	MG	2A	3368	1/1	0.91	0.08	62,62,62,62	0
56	MG	2A	3369	1/1	0.91	0.11	48,48,48,48	0
56	MG	1A	3187	1/1	0.91	0.14	70,70,70,70	0
56	MG	2A	3721	1/1	0.91	0.11	54,54,54,54	0
56	MG	1A	3543	1/1	0.91	0.11	69,69,69,69	0
56	MG	2A	3126	1/1	0.91	0.07	55,55,55,55	0
56	MG	2A	3726	1/1	0.91	0.13	51,51,51,51	0
56	MG	1a	1739	1/1	0.91	0.07	68,68,68,68	0
56	MG	2a	1742	1/1	0.91	0.21	56,56,56,56	0
56	MG	1a	1618	1/1	0.91	0.10	72,72,72,72	0
56	MG	1A	3266	1/1	0.91	0.12	53,53,53,53	0
56	MG	1a	1621	1/1	0.91	0.17	48,48,48,48	0
56	MG	1a	1623	1/1	0.91	0.21	63,63,63,63	0
56	MG	2A	3736	1/1	0.91	0.12	67,67,67,67	0
56	MG	1A	3566	1/1	0.91	0.10	39,39,39,39	0
56	MG	2A	3155	1/1	0.91	0.16	59,59,59,59	0
56	MG	2A	3158	1/1	0.91	0.11	47,47,47,47	0
56	MG	2A	3744	1/1	0.91	0.26	46,46,46,46	0
56	MG	2A	3397	1/1	0.91	0.11	72,72,72,72	0
56	MG	2A	3399	1/1	0.91	0.14	64,64,64,64	0
56	MG	1A	3495	1/1	0.91	0.13	54,54,54,54	0
56	MG	2A	3163	1/1	0.91	0.40	71,71,71,71	0
56	MG	2A	3751	1/1	0.91	0.11	58,58,58,58	0
56	MG	2a	1772	1/1	0.91	0.20	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	2A	3404	1/1	0.91	0.22	65,65,65,65	0
56	MG	2A	3405	1/1	0.91	0.17	61,61,61,61	0
56	MG	2a	1776	1/1	0.91	0.14	71,71,71,71	0
56	MG	2A	3755	1/1	0.91	0.14	66,66,66,66	0
56	MG	1a	1627	1/1	0.91	0.25	63,63,63,63	0
56	MG	1a	1630	1/1	0.91	0.14	61,61,61,61	0
56	MG	1A	3712	1/1	0.91	0.12	43,43,43,43	0
56	MG	1A	3572	1/1	0.91	0.20	58,58,58,58	0
56	MG	2l	201	1/1	0.91	0.11	70,70,70,70	0
56	MG	1A	3575	1/1	0.91	0.10	43,43,43,43	0
56	MG	2A	3768	1/1	0.91	0.18	76,76,76,76	0
56	MG	1a	1772	1/1	0.91	0.12	64,64,64,64	0
56	MG	2A	3774	1/1	0.91	0.09	81,81,81,81	0
56	MG	1B	209	1/1	0.91	0.16	44,44,44,44	0
56	MG	2A	3173	1/1	0.91	0.10	48,48,48,48	0
56	MG	2A	3176	1/1	0.91	0.13	68,68,68,68	0
56	MG	1A	3353	1/1	0.91	0.22	68,68,68,68	0
56	MG	2A	3185	1/1	0.91	0.08	53,53,53,53	0
56	MG	2A	3790	1/1	0.91	0.10	53,53,53,53	0
56	MG	2A	3782	1/1	0.92	0.16	70,70,70,70	0
56	MG	1A	3896	1/1	0.92	0.12	52,52,52,52	0
56	MG	1a	1771	1/1	0.92	0.23	67,67,67,67	0
56	MG	2A	3787	1/1	0.92	0.10	67,67,67,67	0
56	MG	1A	3726	1/1	0.92	0.27	66,66,66,66	0
56	MG	1a	1774	1/1	0.92	0.12	63,63,63,63	0
56	MG	2A	3791	1/1	0.92	0.11	55,55,55,55	0
56	MG	1A	3098	1/1	0.92	0.18	56,56,56,56	0
56	MG	2A	3436	1/1	0.92	0.14	52,52,52,52	0
56	MG	1B	203	1/1	0.92	0.22	51,51,51,51	0
56	MG	1A	3731	1/1	0.92	0.13	58,58,58,58	0
56	MG	2A	3806	1/1	0.92	0.14	70,70,70,70	0
56	MG	2A	3187	1/1	0.92	0.13	63,63,63,63	0
56	MG	1A	3915	1/1	0.92	0.09	56,56,56,56	0
56	MG	2A	3195	1/1	0.92	0.08	56,56,56,56	0
56	MG	2A	3447	1/1	0.92	0.23	56,56,56,56	0
56	MG	2A	3822	1/1	0.92	0.17	40,40,40,40	0
56	MG	1B	210	1/1	0.92	0.08	46,46,46,46	0
56	MG	1a	1640	1/1	0.92	0.28	70,70,70,70	0
56	MG	2A	3838	1/1	0.92	0.15	52,52,52,52	0
56	MG	2A	3840	1/1	0.92	0.08	74,74,74,74	0
56	MG	1a	1784	1/1	0.92	0.14	65,65,65,65	0
56	MG	1A	3151	1/1	0.92	0.23	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	3090	1/1	0.92	0.21	39,39,39,39	0
56	MG	2A	3849	1/1	0.92	0.10	70,70,70,70	0
56	MG	1a	1788	1/1	0.92	0.06	81,81,81,81	0
56	MG	2A	3205	1/1	0.92	0.09	46,46,46,46	0
56	MG	2A	3852	1/1	0.92	0.08	57,57,57,57	0
56	MG	2A	3478	1/1	0.92	0.12	70,70,70,70	0
56	MG	1A	3751	1/1	0.92	0.14	53,53,53,53	0
56	MG	2A	3483	1/1	0.92	0.16	60,60,60,60	0
56	MG	2A	3211	1/1	0.92	0.16	64,64,64,64	0
56	MG	1a	1793	1/1	0.92	0.20	56,56,56,56	0
56	MG	1A	3457	1/1	0.92	0.11	69,69,69,69	0
56	MG	2A	3868	1/1	0.92	0.13	35,35,35,35	0
56	MG	2A	3494	1/1	0.92	0.20	62,62,62,62	0
56	MG	2A	3495	1/1	0.92	0.23	57,57,57,57	0
56	MG	1A	3462	1/1	0.92	0.20	56,56,56,56	0
56	MG	1B	225	1/1	0.92	0.08	46,46,46,46	0
56	MG	1A	3399	1/1	0.92	0.17	51,51,51,51	0
56	MG	1A	3113	1/1	0.92	0.06	40,40,40,40	0
56	MG	2A	3225	1/1	0.92	0.11	50,50,50,50	0
56	MG	2A	3230	1/1	0.92	0.11	52,52,52,52	0
56	MG	2B	208	1/1	0.92	0.33	66,66,66,66	0
56	MG	1a	1809	1/1	0.92	0.08	71,71,71,71	0
56	MG	2A	3232	1/1	0.92	0.17	68,68,68,68	0
56	MG	1a	1651	1/1	0.92	0.07	54,54,54,54	0
56	MG	2B	212	1/1	0.92	0.25	67,67,67,67	0
56	MG	1A	3403	1/1	0.92	0.09	51,51,51,51	0
56	MG	2A	3241	1/1	0.92	0.23	64,64,64,64	0
56	MG	2A	3525	1/1	0.92	0.09	45,45,45,45	0
56	MG	1A	3469	1/1	0.92	0.18	58,58,58,58	0
56	MG	2A	3243	1/1	0.92	0.14	52,52,52,52	0
56	MG	2A	3244	1/1	0.92	0.28	57,57,57,57	0
56	MG	1a	1816	1/1	0.92	0.08	64,64,64,64	0
56	MG	2E	302	1/1	0.92	0.26	57,57,57,57	0
56	MG	1a	1657	1/1	0.92	0.09	44,44,44,44	0
56	MG	2E	306	1/1	0.92	0.08	52,52,52,52	0
56	MG	1B	234	1/1	0.92	0.08	33,33,33,33	0
56	MG	2F	305	1/1	0.92	0.19	40,40,40,40	0
56	MG	1A	3470	1/1	0.92	0.23	46,46,46,46	0
56	MG	2P	201	1/1	0.92	0.10	56,56,56,56	0
56	MG	2Q	203	1/1	0.92	0.11	62,62,62,62	0
56	MG	1A	3947	1/1	0.92	0.12	56,56,56,56	0
56	MG	1A	3780	1/1	0.92	0.15	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	2T	201	1/1	0.92	0.11	53,53,53,53	0
56	MG	1A	3131	1/1	0.92	0.14	51,51,51,51	0
56	MG	2A	3558	1/1	0.92	0.14	55,55,55,55	0
56	MG	1a	1667	1/1	0.92	0.22	78,78,78,78	0
56	MG	2A	3564	1/1	0.92	0.10	46,46,46,46	0
56	MG	1f	201	1/1	0.92	0.17	52,52,52,52	0
56	MG	2A	3566	1/1	0.92	0.07	44,44,44,44	0
56	MG	1k	201	1/1	0.92	0.13	56,56,56,56	0
56	MG	1E	310	1/1	0.92	0.11	29,29,29,29	0
56	MG	1A	3482	1/1	0.92	0.21	61,61,61,61	0
56	MG	2A	3576	1/1	0.92	0.17	58,58,58,58	0
56	MG	1E	314	1/1	0.92	0.10	61,61,61,61	0
56	MG	2a	1606	1/1	0.92	0.20	54,54,54,54	0
56	MG	2a	1607	1/1	0.92	0.38	59,59,59,59	0
56	MG	1A	3539	1/1	0.92	0.22	55,55,55,55	0
56	MG	2A	3275	1/1	0.92	0.25	65,65,65,65	0
56	MG	1A	3790	1/1	0.92	0.14	60,60,60,60	0
56	MG	1x	101	1/1	0.92	0.08	64,64,64,64	0
56	MG	1x	102	1/1	0.92	0.09	68,68,68,68	0
56	MG	2A	3281	1/1	0.92	0.11	55,55,55,55	0
56	MG	2a	1618	1/1	0.92	0.16	64,64,64,64	0
56	MG	2a	1621	1/1	0.92	0.11	60,60,60,60	0
56	MG	2A	3593	1/1	0.92	0.14	57,57,57,57	0
56	MG	1F	306	1/1	0.92	0.08	33,33,33,33	0
56	MG	1A	3965	1/1	0.92	0.07	72,72,72,72	0
56	MG	2A	3598	1/1	0.92	0.20	62,62,62,62	0
56	MG	1A	3486	1/1	0.92	0.18	57,57,57,57	0
56	MG	1A	3654	1/1	0.92	0.10	61,61,61,61	0
56	MG	2A	3602	1/1	0.92	0.16	53,53,53,53	0
56	MG	1A	3972	1/1	0.92	0.08	54,54,54,54	0
56	MG	2a	1635	1/1	0.92	0.24	52,52,52,52	0
56	MG	2A	3289	1/1	0.92	0.27	69,69,69,69	0
56	MG	2A	3004	1/1	0.92	0.23	49,49,49,49	0
56	MG	1N	201	1/1	0.92	0.10	53,53,53,53	0
56	MG	2A	3612	1/1	0.92	0.08	48,48,48,48	0
56	MG	1A	3312	1/1	0.92	0.09	38,38,38,38	0
56	MG	2a	1645	1/1	0.92	0.21	69,69,69,69	0
56	MG	2A	3297	1/1	0.92	0.22	71,71,71,71	0
56	MG	1A	3414	1/1	0.92	0.21	53,53,53,53	0
56	MG	2A	3621	1/1	0.92	0.07	37,37,37,37	0
56	MG	1A	3807	1/1	0.92	0.06	22,22,22,22	0
56	MG	2A	3629	1/1	0.92	0.18	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3662	1/1	0.92	0.15	47,47,47,47	0
56	MG	2A	3637	1/1	0.92	0.14	54,54,54,54	0
56	MG	2a	1656	1/1	0.92	0.40	72,72,72,72	0
56	MG	1A	3257	1/1	0.92	0.12	63,63,63,63	0
56	MG	1A	3665	1/1	0.92	0.06	19,19,19,19	0
56	MG	1A	3545	1/1	0.92	0.32	38,38,38,38	0
56	MG	1A	3986	1/1	0.92	0.09	38,38,38,38	0
56	MG	2A	3307	1/1	0.92	0.10	48,48,48,48	0
56	MG	2A	3039	1/1	0.92	0.18	62,62,62,62	0
56	MG	2a	1666	1/1	0.92	0.19	56,56,56,56	0
56	MG	2A	3041	1/1	0.92	0.18	54,54,54,54	0
56	MG	2A	3312	1/1	0.92	0.17	72,72,72,72	0
56	MG	2a	1669	1/1	0.92	0.12	68,68,68,68	0
56	MG	1S	201	1/1	0.92	0.28	46,46,46,46	0
56	MG	1a	1699	1/1	0.92	0.26	56,56,56,56	0
56	MG	2a	1677	1/1	0.92	0.34	66,66,66,66	0
56	MG	1S	202	1/1	0.92	0.11	59,59,59,59	0
56	MG	1a	1701	1/1	0.92	0.47	70,70,70,70	0
56	MG	2a	1680	1/1	0.92	0.13	63,63,63,63	0
56	MG	2A	3053	1/1	0.92	0.22	60,60,60,60	0
56	MG	2A	3056	1/1	0.92	0.19	66,66,66,66	0
56	MG	1A	3988	1/1	0.92	0.07	32,32,32,32	0
56	MG	2a	1686	1/1	0.92	0.29	61,61,61,61	0
56	MG	1A	3674	1/1	0.92	0.07	33,33,33,33	0
56	MG	2A	3328	1/1	0.92	0.13	53,53,53,53	0
56	MG	2A	3065	1/1	0.92	0.20	47,47,47,47	0
56	MG	1A	3678	1/1	0.92	0.05	21,21,21,21	0
56	MG	1A	3552	1/1	0.92	0.12	45,45,45,45	0
56	MG	1A	3834	1/1	0.92	0.12	35,35,35,35	0
56	MG	2A	3684	1/1	0.92	0.11	62,62,62,62	0
56	MG	1A	3497	1/1	0.92	0.13	36,36,36,36	0
56	MG	2a	1700	1/1	0.92	0.22	59,59,59,59	0
56	MG	1A	3563	1/1	0.92	0.16	53,53,53,53	0
56	MG	1A	4011	1/1	0.92	0.11	42,42,42,42	0
56	MG	2A	3338	1/1	0.92	0.12	73,73,73,73	0
56	MG	1A	3838	1/1	0.92	0.10	46,46,46,46	0
56	MG	2A	3696	1/1	0.92	0.08	74,74,74,74	0
56	MG	2A	3698	1/1	0.92	0.09	58,58,58,58	0
56	MG	2A	3340	1/1	0.92	0.20	61,61,61,61	0
56	MG	1a	1718	1/1	0.92	0.31	66,66,66,66	0
56	MG	2A	3705	1/1	0.92	0.10	46,46,46,46	0
56	MG	1a	1720	1/1	0.92	0.12	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3346	1/1	0.92	0.28	46,46,46,46	0
56	MG	2A	3350	1/1	0.92	0.12	54,54,54,54	0
56	MG	2a	1727	1/1	0.92	0.11	81,81,81,81	0
56	MG	2A	3352	1/1	0.92	0.19	60,60,60,60	0
56	MG	1A	4013	1/1	0.92	0.07	50,50,50,50	0
56	MG	1a	1724	1/1	0.92	0.14	64,64,64,64	0
56	MG	1A	3841	1/1	0.92	0.15	54,54,54,54	0
56	MG	2A	3359	1/1	0.92	0.21	60,60,60,60	0
56	MG	1A	3263	1/1	0.92	0.25	52,52,52,52	0
56	MG	2A	3361	1/1	0.92	0.26	51,51,51,51	0
56	MG	15	108	1/1	0.92	0.09	49,49,49,49	0
56	MG	1A	3226	1/1	0.92	0.20	51,51,51,51	0
56	MG	2a	1743	1/1	0.92	0.17	63,63,63,63	0
56	MG	2A	3104	1/1	0.92	0.15	65,65,65,65	0
56	MG	1A	3367	1/1	0.92	0.20	53,53,53,53	0
56	MG	1A	3848	1/1	0.92	0.18	41,41,41,41	0
56	MG	2a	1749	1/1	0.92	0.23	56,56,56,56	0
56	MG	1A	3231	1/1	0.92	0.10	33,33,33,33	0
56	MG	2A	3371	1/1	0.92	0.20	61,61,61,61	0
56	MG	1A	3701	1/1	0.92	0.09	43,43,43,43	0
56	MG	2a	1753	1/1	0.92	0.13	66,66,66,66	0
56	MG	2A	3375	1/1	0.92	0.07	62,62,62,62	0
56	MG	2a	1756	1/1	0.92	0.12	59,59,59,59	0
56	MG	1A	4036	1/1	0.92	0.12	33,33,33,33	0
56	MG	2A	3738	1/1	0.92	0.12	56,56,56,56	0
56	MG	2A	3118	1/1	0.92	0.18	58,58,58,58	0
56	MG	1A	3267	1/1	0.92	0.27	48,48,48,48	0
56	MG	2A	3121	1/1	0.92	0.12	52,52,52,52	0
56	MG	1A	3291	1/1	0.92	0.10	44,44,44,44	0
56	MG	2a	1767	1/1	0.92	0.11	57,57,57,57	0
56	MG	1A	4043	1/1	0.92	0.10	56,56,56,56	0
56	MG	2a	1771	1/1	0.92	0.20	59,59,59,59	0
56	MG	2A	3129	1/1	0.92	0.12	62,62,62,62	0
56	MG	2a	1773	1/1	0.92	0.29	75,75,75,75	0
56	MG	2A	3392	1/1	0.92	0.26	71,71,71,71	0
56	MG	1A	3440	1/1	0.92	0.09	53,53,53,53	0
56	MG	1A	3867	1/1	0.92	0.16	31,31,31,31	0
56	MG	1A	3713	1/1	0.92	0.08	56,56,56,56	0
56	MG	1A	3870	1/1	0.92	0.10	37,37,37,37	0
56	MG	2A	3756	1/1	0.92	0.12	52,52,52,52	0
56	MG	2A	3757	1/1	0.92	0.10	46,46,46,46	0
56	MG	1A	3871	1/1	0.92	0.11	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3583	1/1	0.92	0.11	39,39,39,39	0
56	MG	1A	3385	1/1	0.92	0.29	24,24,24,24	0
56	MG	1A	3067	1/1	0.92	0.11	56,56,56,56	0
56	MG	1a	1756	1/1	0.92	0.20	71,71,71,71	0
56	MG	1A	4063	1/1	0.92	0.08	22,22,22,22	0
56	MG	1A	3885	1/1	0.92	0.18	44,44,44,44	0
56	MG	1a	1762	1/1	0.92	0.21	78,78,78,78	0
56	MG	2A	3777	1/1	0.92	0.08	58,58,58,58	0
56	MG	1A	3724	1/1	0.92	0.10	43,43,43,43	0
56	MG	2A	3779	1/1	0.92	0.12	62,62,62,62	0
56	MG	1A	4069	1/1	0.92	0.13	56,56,56,56	0
56	MG	2A	3435	1/1	0.93	0.20	59,59,59,59	0
56	MG	1A	3483	1/1	0.93	0.18	49,49,49,49	0
56	MG	1A	4017	1/1	0.93	0.08	41,41,41,41	0
56	MG	1A	4018	1/1	0.93	0.09	73,73,73,73	0
56	MG	2A	3188	1/1	0.93	0.15	75,75,75,75	0
56	MG	2A	3796	1/1	0.93	0.12	81,81,81,81	0
56	MG	1A	3270	1/1	0.93	0.21	59,59,59,59	0
56	MG	2A	3801	1/1	0.93	0.09	57,57,57,57	0
56	MG	2A	3803	1/1	0.93	0.13	56,56,56,56	0
56	MG	2A	3194	1/1	0.93	0.32	68,68,68,68	0
56	MG	2A	3809	1/1	0.93	0.12	55,55,55,55	0
56	MG	1A	3272	1/1	0.93	0.27	55,55,55,55	0
56	MG	2A	3450	1/1	0.93	0.11	48,48,48,48	0
56	MG	1A	3839	1/1	0.93	0.10	70,70,70,70	0
56	MG	1A	3491	1/1	0.93	0.09	41,41,41,41	0
56	MG	1A	4025	1/1	0.93	0.07	38,38,38,38	0
56	MG	2A	3457	1/1	0.93	0.07	54,54,54,54	0
56	MG	1A	4030	1/1	0.93	0.09	48,48,48,48	0
56	MG	1A	4032	1/1	0.93	0.08	32,32,32,32	0
56	MG	1A	3339	1/1	0.93	0.06	33,33,33,33	0
56	MG	1A	3410	1/1	0.93	0.16	53,53,53,53	0
56	MG	2A	3466	1/1	0.93	0.08	51,51,51,51	0
56	MG	2A	3844	1/1	0.93	0.07	62,62,62,62	0
56	MG	2A	3469	1/1	0.93	0.12	72,72,72,72	0
56	MG	2A	3473	1/1	0.93	0.09	68,68,68,68	0
56	MG	2A	3477	1/1	0.93	0.18	60,60,60,60	0
56	MG	2A	3208	1/1	0.93	0.08	65,65,65,65	0
56	MG	1A	3700	1/1	0.93	0.07	35,35,35,35	0
56	MG	1A	3340	1/1	0.93	0.06	38,38,38,38	0
56	MG	2A	3854	1/1	0.93	0.10	35,35,35,35	0
56	MG	1A	3274	1/1	0.93	0.09	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	3704	1/1	0.93	0.10	54,54,54,54	0
56	MG	1A	3286	1/1	0.93	0.32	34,34,34,34	0
56	MG	2A	3864	1/1	0.93	0.11	54,54,54,54	0
56	MG	1A	3350	1/1	0.93	0.24	54,54,54,54	0
56	MG	2A	3218	1/1	0.93	0.07	47,47,47,47	0
56	MG	1A	3859	1/1	0.93	0.10	39,39,39,39	0
56	MG	2A	3220	1/1	0.93	0.12	49,49,49,49	0
56	MG	1A	3863	1/1	0.93	0.10	34,34,34,34	0
56	MG	2A	3223	1/1	0.93	0.17	69,69,69,69	0
56	MG	1A	3864	1/1	0.93	0.10	40,40,40,40	0
56	MG	1a	1798	1/1	0.93	0.16	53,53,53,53	0
56	MG	2A	3510	1/1	0.93	0.13	25,25,25,25	0
56	MG	1a	1800	1/1	0.93	0.19	62,62,62,62	0
56	MG	1a	1628	1/1	0.93	0.14	56,56,56,56	0
56	MG	1A	3016	1/1	0.93	0.15	40,40,40,40	0
56	MG	1A	3502	1/1	0.93	0.12	55,55,55,55	0
56	MG	2A	3520	1/1	0.93	0.09	46,46,46,46	0
56	MG	1A	3715	1/1	0.93	0.17	53,53,53,53	0
56	MG	1A	3423	1/1	0.93	0.11	44,44,44,44	0
56	MG	1A	3099	1/1	0.93	0.19	41,41,41,41	0
56	MG	2B	214	1/1	0.93	0.21	65,65,65,65	0
56	MG	1A	3587	1/1	0.93	0.26	48,48,48,48	0
56	MG	2A	3529	1/1	0.93	0.06	32,32,32,32	0
56	MG	2A	3530	1/1	0.93	0.10	62,62,62,62	0
56	MG	2B	218	1/1	0.93	0.08	65,65,65,65	0
56	MG	1A	3589	1/1	0.93	0.12	45,45,45,45	0
56	MG	1a	1642	1/1	0.93	0.17	60,60,60,60	0
56	MG	1a	1820	1/1	0.93	0.23	62,62,62,62	0
56	MG	2A	3539	1/1	0.93	0.10	34,34,34,34	0
56	MG	1A	4072	1/1	0.93	0.09	58,58,58,58	0
56	MG	2A	3543	1/1	0.93	0.09	44,44,44,44	0
56	MG	2A	3544	1/1	0.93	0.10	41,41,41,41	0
56	MG	2A	3546	1/1	0.93	0.07	34,34,34,34	0
56	MG	2A	3253	1/1	0.93	0.10	57,57,57,57	0
56	MG	2O	201	1/1	0.93	0.13	58,58,58,58	0
56	MG	1A	3878	1/1	0.93	0.11	47,47,47,47	0
56	MG	2Q	201	1/1	0.93	0.17	59,59,59,59	0
56	MG	1A	4074	1/1	0.93	0.13	49,49,49,49	0
56	MG	1b	302	1/1	0.93	0.17	80,80,80,80	0
56	MG	1A	4080	1/1	0.93	0.10	36,36,36,36	0
56	MG	1a	1647	1/1	0.93	0.12	73,73,73,73	0
56	MG	1A	3590	1/1	0.93	0.17	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3729	1/1	0.93	0.12	46,46,46,46	0
56	MG	2W	201	1/1	0.93	0.34	52,52,52,52	0
56	MG	1A	3591	1/1	0.93	0.08	32,32,32,32	0
56	MG	2A	3567	1/1	0.93	0.10	52,52,52,52	0
56	MG	2A	3270	1/1	0.93	0.10	58,58,58,58	0
56	MG	20	101	1/1	0.93	0.13	75,75,75,75	0
56	MG	23	101	1/1	0.93	0.41	62,62,62,62	0
56	MG	2A	3569	1/1	0.93	0.07	45,45,45,45	0
56	MG	1A	3889	1/1	0.93	0.10	49,49,49,49	0
56	MG	25	103	1/1	0.93	0.15	60,60,60,60	0
56	MG	1A	3892	1/1	0.93	0.13	43,43,43,43	0
56	MG	2A	3575	1/1	0.93	0.11	34,34,34,34	0
56	MG	2a	1602	1/1	0.93	0.12	67,67,67,67	0
56	MG	1A	3736	1/1	0.93	0.18	60,60,60,60	0
56	MG	1A	3898	1/1	0.93	0.11	55,55,55,55	0
56	MG	2a	1605	1/1	0.93	0.11	60,60,60,60	0
56	MG	1A	3904	1/1	0.93	0.10	36,36,36,36	0
56	MG	1A	3739	1/1	0.93	0.09	53,53,53,53	0
56	MG	2A	3583	1/1	0.93	0.18	57,57,57,57	0
56	MG	1A	3743	1/1	0.93	0.10	51,51,51,51	0
56	MG	2a	1611	1/1	0.93	0.10	46,46,46,46	0
56	MG	1B	223	1/1	0.93	0.11	53,53,53,53	0
56	MG	1A	3593	1/1	0.93	0.10	37,37,37,37	0
56	MG	1A	3237	1/1	0.93	0.07	59,59,59,59	0
56	MG	1x	111	1/1	0.93	0.15	64,64,64,64	0
56	MG	1A	3429	1/1	0.93	0.17	49,49,49,49	0
56	MG	1A	3600	1/1	0.93	0.15	52,52,52,52	0
56	MG	2a	1622	1/1	0.93	0.33	49,49,49,49	0
56	MG	1a	1671	1/1	0.93	0.21	59,59,59,59	0
56	MG	1A	3192	1/1	0.93	0.28	35,35,35,35	0
56	MG	2A	3294	1/1	0.93	0.09	73,73,73,73	0
56	MG	1A	3198	1/1	0.93	0.25	31,31,31,31	0
56	MG	2A	3604	1/1	0.93	0.14	69,69,69,69	0
56	MG	1A	3093	1/1	0.93	0.08	43,43,43,43	0
56	MG	2A	3013	1/1	0.93	0.07	43,43,43,43	0
56	MG	2a	1633	1/1	0.93	0.19	62,62,62,62	0
56	MG	2A	3017	1/1	0.93	0.13	50,50,50,50	0
56	MG	2A	3300	1/1	0.93	0.14	52,52,52,52	0
56	MG	2A	3611	1/1	0.93	0.12	50,50,50,50	0
56	MG	1A	3933	1/1	0.93	0.11	26,26,26,26	0
56	MG	2A	3615	1/1	0.93	0.16	62,62,62,62	0
56	MG	2A	3302	1/1	0.93	0.08	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	1A	3760	1/1	0.93	0.21	44,44,44,44	0
56	MG	2A	3023	1/1	0.93	0.33	57,57,57,57	0
56	MG	2a	1646	1/1	0.93	0.35	59,59,59,59	0
56	MG	1D	310	1/1	0.93	0.06	40,40,40,40	0
56	MG	1A	3765	1/1	0.93	0.11	22,22,22,22	0
56	MG	1D	314	1/1	0.93	0.11	31,31,31,31	0
56	MG	2A	3630	1/1	0.93	0.12	41,41,41,41	0
56	MG	1a	1684	1/1	0.93	0.23	58,58,58,58	0
56	MG	2A	3310	1/1	0.93	0.33	62,62,62,62	0
56	MG	2A	3639	1/1	0.93	0.10	40,40,40,40	0
56	MG	1A	3612	1/1	0.93	0.10	23,23,23,23	0
56	MG	1A	3088	1/1	0.93	0.15	28,28,28,28	0
56	MG	2A	3313	1/1	0.93	0.11	60,60,60,60	0
56	MG	1E	311	1/1	0.93	0.09	26,26,26,26	0
56	MG	1A	3209	1/1	0.93	0.13	59,59,59,59	0
56	MG	1A	3776	1/1	0.93	0.09	26,26,26,26	0
56	MG	2A	3657	1/1	0.93	0.09	59,59,59,59	0
56	MG	1E	316	1/1	0.93	0.07	58,58,58,58	0
56	MG	1A	3379	1/1	0.93	0.07	45,45,45,45	0
56	MG	2A	3661	1/1	0.93	0.09	64,64,64,64	0
56	MG	2A	3662	1/1	0.93	0.13	43,43,43,43	0
56	MG	2a	1671	1/1	0.93	0.10	59,59,59,59	0
56	MG	2a	1672	1/1	0.93	0.19	69,69,69,69	0
56	MG	2a	1673	1/1	0.93	0.21	56,56,56,56	0
56	MG	2A	3323	1/1	0.93	0.10	53,53,53,53	0
56	MG	2A	3055	1/1	0.93	0.08	48,48,48,48	0
56	MG	1A	3210	1/1	0.93	0.10	34,34,34,34	0
56	MG	1A	3258	1/1	0.93	0.09	60,60,60,60	0
56	MG	2A	3059	1/1	0.93	0.23	54,54,54,54	0
56	MG	2A	3061	1/1	0.93	0.08	46,46,46,46	0
56	MG	1F	307	1/1	0.93	0.09	40,40,40,40	0
56	MG	2a	1682	1/1	0.93	0.18	62,62,62,62	0
56	MG	1a	1698	1/1	0.93	0.16	62,62,62,62	0
56	MG	1A	3958	1/1	0.93	0.09	39,39,39,39	0
56	MG	1A	3786	1/1	0.93	0.11	27,27,27,27	0
56	MG	2a	1687	1/1	0.93	0.24	58,58,58,58	0
56	MG	1A	3526	1/1	0.93	0.21	43,43,43,43	0
56	MG	2A	3335	1/1	0.93	0.17	63,63,63,63	0
56	MG	2A	3682	1/1	0.93	0.13	51,51,51,51	0
56	MG	2A	3078	1/1	0.93	0.15	46,46,46,46	0
56	MG	2A	3082	1/1	0.93	0.14	54,54,54,54	0
56	MG	1A	3461	1/1	0.93	0.09	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	1695	1/1	0.93	0.23	62,62,62,62	0
56	MG	1a	1703	1/1	0.93	0.31	67,67,67,67	0
56	MG	2a	1698	1/1	0.93	0.25	64,64,64,64	0
56	MG	1a	1704	1/1	0.93	0.28	52,52,52,52	0
56	MG	2A	3693	1/1	0.93	0.07	68,68,68,68	0
56	MG	1A	3528	1/1	0.93	0.17	43,43,43,43	0
56	MG	1A	3969	1/1	0.93	0.14	65,65,65,65	0
56	MG	2A	3347	1/1	0.93	0.20	57,57,57,57	0
56	MG	2A	3697	1/1	0.93	0.14	35,35,35,35	0
56	MG	1A	3796	1/1	0.93	0.14	47,47,47,47	0
56	MG	1a	1709	1/1	0.93	0.26	69,69,69,69	0
56	MG	2A	3701	1/1	0.93	0.10	55,55,55,55	0
56	MG	1A	3800	1/1	0.93	0.10	16,16,16,16	0
56	MG	2A	3355	1/1	0.93	0.12	62,62,62,62	0
56	MG	1O	202	1/1	0.93	0.17	56,56,56,56	0
56	MG	1A	3122	1/1	0.93	0.10	49,49,49,49	0
56	MG	1A	3390	1/1	0.93	0.09	54,54,54,54	0
56	MG	2a	1726	1/1	0.93	0.12	62,62,62,62	0
56	MG	2A	3102	1/1	0.93	0.08	29,29,29,29	0
56	MG	2a	1728	1/1	0.93	0.17	54,54,54,54	0
56	MG	2a	1729	1/1	0.93	0.11	62,62,62,62	0
56	MG	1A	3391	1/1	0.93	0.09	49,49,49,49	0
56	MG	2a	1731	1/1	0.93	0.15	66,66,66,66	0
56	MG	1A	3536	1/1	0.93	0.22	59,59,59,59	0
56	MG	2A	3715	1/1	0.93	0.15	62,62,62,62	0
56	MG	2A	3363	1/1	0.93	0.08	68,68,68,68	0
56	MG	1Q	201	1/1	0.93	0.23	37,37,37,37	0
56	MG	2a	1736	1/1	0.93	0.17	61,61,61,61	0
56	MG	1A	3466	1/1	0.93	0.27	62,62,62,62	0
56	MG	1A	3222	1/1	0.93	0.10	43,43,43,43	0
56	MG	2A	3113	1/1	0.93	0.23	62,62,62,62	0
56	MG	1A	3983	1/1	0.93	0.10	51,51,51,51	0
56	MG	1A	3813	1/1	0.93	0.06	42,42,42,42	0
56	MG	2a	1744	1/1	0.93	0.27	59,59,59,59	0
56	MG	2A	3116	1/1	0.93	0.32	60,60,60,60	0
56	MG	2A	3117	1/1	0.93	0.17	48,48,48,48	0
56	MG	1T	202	1/1	0.93	0.14	63,63,63,63	0
56	MG	1U	203	1/1	0.93	0.14	43,43,43,43	0
56	MG	1a	1729	1/1	0.93	0.09	54,54,54,54	0
56	MG	2A	3380	1/1	0.93	0.12	53,53,53,53	0
56	MG	1A	3265	1/1	0.93	0.15	74,74,74,74	0
56	MG	2A	3123	1/1	0.93	0.10	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	3386	1/1	0.93	0.11	52,52,52,52	0
56	MG	2A	3387	1/1	0.93	0.23	50,50,50,50	0
56	MG	1A	3987	1/1	0.93	0.07	64,64,64,64	0
56	MG	2A	3390	1/1	0.93	0.11	51,51,51,51	0
56	MG	1A	3817	1/1	0.93	0.24	61,61,61,61	0
56	MG	1W	207	1/1	0.93	0.10	49,49,49,49	0
56	MG	1A	3050	1/1	0.93	0.11	15,15,15,15	0
56	MG	1A	3991	1/1	0.93	0.13	27,27,27,27	0
56	MG	1Z	302	1/1	0.93	0.13	49,49,49,49	0
56	MG	1A	3822	1/1	0.93	0.07	27,27,27,27	0
56	MG	2A	3398	1/1	0.93	0.09	54,54,54,54	0
56	MG	1A	3825	1/1	0.93	0.16	42,42,42,42	0
56	MG	1l	104	1/1	0.93	0.12	57,57,57,57	0
56	MG	1A	4004	1/1	0.93	0.07	35,35,35,35	0
56	MG	1A	3826	1/1	0.93	0.14	41,41,41,41	0
56	MG	2A	3162	1/1	0.93	0.12	46,46,46,46	0
56	MG	2A	3413	1/1	0.93	0.15	46,46,46,46	0
56	MG	2A	3414	1/1	0.93	0.18	50,50,50,50	0
56	MG	1a	1742	1/1	0.93	0.22	62,62,62,62	0
56	MG	2A	3771	1/1	0.93	0.08	68,68,68,68	0
56	MG	2A	3417	1/1	0.93	0.31	56,56,56,56	0
56	MG	13	104	1/1	0.93	0.14	44,44,44,44	0
56	MG	2A	3775	1/1	0.93	0.08	61,61,61,61	0
56	MG	2q	201	1/1	0.93	0.08	69,69,69,69	0
56	MG	2A	3420	1/1	0.93	0.10	50,50,50,50	0
56	MG	1A	3668	1/1	0.93	0.09	49,49,49,49	0
56	MG	1A	3175	1/1	0.93	0.06	35,35,35,35	0
56	MG	1a	1748	1/1	0.93	0.11	65,65,65,65	0
56	MG	1A	3831	1/1	0.93	0.14	62,62,62,62	0
56	MG	1A	3336	1/1	0.93	0.22	46,46,46,46	0
56	MG	2x	102	1/1	0.93	0.26	61,61,61,61	0
56	MG	1a	1759	1/1	0.93	0.11	40,40,40,40	0
56	MG	1A	3544	1/1	0.93	0.18	63,63,63,63	0
56	MG	18	101	1/1	0.93	0.21	55,55,55,55	0
56	MG	1A	3428	1/1	0.94	0.17	44,44,44,44	0
56	MG	1A	3345	1/1	0.94	0.19	45,45,45,45	0
56	MG	2A	3175	1/1	0.94	0.16	48,48,48,48	0
56	MG	1A	3518	1/1	0.94	0.27	47,47,47,47	0
56	MG	1A	3519	1/1	0.94	0.16	55,55,55,55	0
56	MG	2A	3184	1/1	0.94	0.27	63,63,63,63	0
56	MG	1a	1765	1/1	0.94	0.08	67,67,67,67	0
56	MG	2A	3442	1/1	0.94	0.10	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	3799	1/1	0.94	0.15	77,77,77,77	0
56	MG	2A	3443	1/1	0.94	0.35	54,54,54,54	0
56	MG	2A	3444	1/1	0.94	0.12	46,46,46,46	0
56	MG	2A	3804	1/1	0.94	0.13	67,67,67,67	0
56	MG	2A	3805	1/1	0.94	0.06	44,44,44,44	0
56	MG	2A	3445	1/1	0.94	0.33	59,59,59,59	0
56	MG	1A	3006	1/1	0.94	0.12	48,48,48,48	0
56	MG	2A	3811	1/1	0.94	0.10	54,54,54,54	0
56	MG	2A	3813	1/1	0.94	0.07	42,42,42,42	0
56	MG	1a	1768	1/1	0.94	0.11	66,66,66,66	0
56	MG	2A	3449	1/1	0.94	0.27	54,54,54,54	0
56	MG	1A	3431	1/1	0.94	0.06	51,51,51,51	0
56	MG	1a	1770	1/1	0.94	0.07	70,70,70,70	0
56	MG	2A	3452	1/1	0.94	0.24	48,48,48,48	0
56	MG	1A	3434	1/1	0.94	0.18	62,62,62,62	0
56	MG	2A	3196	1/1	0.94	0.26	60,60,60,60	0
56	MG	2A	3835	1/1	0.94	0.08	48,48,48,48	0
56	MG	2A	3456	1/1	0.94	0.07	39,39,39,39	0
56	MG	1A	3671	1/1	0.94	0.07	26,26,26,26	0
56	MG	1A	3435	1/1	0.94	0.08	37,37,37,37	0
56	MG	1A	3436	1/1	0.94	0.17	29,29,29,29	0
56	MG	1a	1777	1/1	0.94	0.17	63,63,63,63	0
56	MG	2A	3463	1/1	0.94	0.09	55,55,55,55	0
56	MG	2A	3846	1/1	0.94	0.10	56,56,56,56	0
56	MG	1A	3529	1/1	0.94	0.23	42,42,42,42	0
56	MG	1a	1604	1/1	0.94	0.14	74,74,74,74	0
56	MG	2A	3467	1/1	0.94	0.14	51,51,51,51	0
56	MG	2A	3468	1/1	0.94	0.12	46,46,46,46	0
56	MG	1A	3152	1/1	0.94	0.14	31,31,31,31	0
56	MG	2A	3206	1/1	0.94	0.10	43,43,43,43	0
56	MG	2A	3474	1/1	0.94	0.21	57,57,57,57	0
56	MG	1A	3009	1/1	0.94	0.10	28,28,28,28	0
56	MG	2A	3209	1/1	0.94	0.11	48,48,48,48	0
56	MG	2A	3861	1/1	0.94	0.08	35,35,35,35	0
56	MG	1A	4031	1/1	0.94	0.09	45,45,45,45	0
56	MG	2A	3480	1/1	0.94	0.14	47,47,47,47	0
56	MG	2A	3481	1/1	0.94	0.11	49,49,49,49	0
56	MG	1A	3356	1/1	0.94	0.08	50,50,50,50	0
56	MG	1A	3445	1/1	0.94	0.07	45,45,45,45	0
56	MG	2A	3485	1/1	0.94	0.08	40,40,40,40	0
56	MG	1A	3290	1/1	0.94	0.13	48,48,48,48	0
56	MG	1A	3052	1/1	0.94	0.09	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	3493	1/1	0.94	0.25	61,61,61,61	0
56	MG	1A	3856	1/1	0.94	0.08	47,47,47,47	0
56	MG	1A	3168	1/1	0.94	0.12	34,34,34,34	0
56	MG	1A	4041	1/1	0.94	0.13	40,40,40,40	0
56	MG	2A	3500	1/1	0.94	0.13	55,55,55,55	0
56	MG	1a	1617	1/1	0.94	0.11	59,59,59,59	0
56	MG	1A	3861	1/1	0.94	0.11	51,51,51,51	0
56	MG	1A	3862	1/1	0.94	0.10	34,34,34,34	0
56	MG	2A	3224	1/1	0.94	0.09	48,48,48,48	0
56	MG	1A	3455	1/1	0.94	0.24	59,59,59,59	0
56	MG	2A	3229	1/1	0.94	0.29	44,44,44,44	0
56	MG	1A	3105	1/1	0.94	0.27	64,64,64,64	0
56	MG	1A	3234	1/1	0.94	0.06	42,42,42,42	0
56	MG	1a	1808	1/1	0.94	0.09	52,52,52,52	0
56	MG	1A	3708	1/1	0.94	0.06	23,23,23,23	0
56	MG	2A	3237	1/1	0.94	0.12	58,58,58,58	0
56	MG	2A	3522	1/1	0.94	0.08	35,35,35,35	0
56	MG	1A	3868	1/1	0.94	0.10	26,26,26,26	0
56	MG	2D	303	1/1	0.94	0.09	53,53,53,53	0
56	MG	2E	301	1/1	0.94	0.12	61,61,61,61	0
56	MG	1A	4057	1/1	0.94	0.07	54,54,54,54	0
56	MG	2E	303	1/1	0.94	0.21	61,61,61,61	0
56	MG	1a	1629	1/1	0.94	0.10	56,56,56,56	0
56	MG	1A	3372	1/1	0.94	0.09	46,46,46,46	0
56	MG	2E	307	1/1	0.94	0.10	31,31,31,31	0
56	MG	1A	3235	1/1	0.94	0.08	56,56,56,56	0
56	MG	2F	304	1/1	0.94	0.15	56,56,56,56	0
56	MG	1A	3547	1/1	0.94	0.12	50,50,50,50	0
56	MG	1A	3550	1/1	0.94	0.14	41,41,41,41	0
56	MG	2A	3248	1/1	0.94	0.06	60,60,60,60	0
56	MG	1a	1822	1/1	0.94	0.08	58,58,58,58	0
56	MG	2A	3251	1/1	0.94	0.18	63,63,63,63	0
56	MG	1A	3173	1/1	0.94	0.18	45,45,45,45	0
56	MG	2R	201	1/1	0.94	0.20	64,64,64,64	0
56	MG	1a	1639	1/1	0.94	0.21	56,56,56,56	0
56	MG	1A	3875	1/1	0.94	0.13	30,30,30,30	0
56	MG	2A	3258	1/1	0.94	0.14	69,69,69,69	0
56	MG	1A	4070	1/1	0.94	0.10	51,51,51,51	0
56	MG	2A	3548	1/1	0.94	0.09	42,42,42,42	0
56	MG	2A	3550	1/1	0.94	0.17	49,49,49,49	0
56	MG	1e	202	1/1	0.94	0.10	59,59,59,59	0
56	MG	1A	3876	1/1	0.94	0.11	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2X	101	1/1	0.94	0.10	72,72,72,72	0
56	MG	1A	3244	1/1	0.94	0.23	35,35,35,35	0
56	MG	1A	3879	1/1	0.94	0.12	25,25,25,25	0
56	MG	1f	202	1/1	0.94	0.26	64,64,64,64	0
56	MG	1A	3561	1/1	0.94	0.11	33,33,33,33	0
56	MG	1A	4081	1/1	0.94	0.09	55,55,55,55	0
56	MG	1A	4082	1/1	0.94	0.07	42,42,42,42	0
56	MG	25	105	1/1	0.94	0.07	42,42,42,42	0
56	MG	1A	3311	1/1	0.94	0.08	48,48,48,48	0
56	MG	28	102	1/1	0.94	0.23	61,61,61,61	0
56	MG	28	103	1/1	0.94	0.16	57,57,57,57	0
56	MG	1A	3246	1/1	0.94	0.17	39,39,39,39	0
56	MG	1A	3053	1/1	0.94	0.16	28,28,28,28	0
56	MG	2A	3277	1/1	0.94	0.26	56,56,56,56	0
56	MG	1A	3570	1/1	0.94	0.21	44,44,44,44	0
56	MG	1B	207	1/1	0.94	0.11	40,40,40,40	0
56	MG	1A	3730	1/1	0.94	0.17	52,52,52,52	0
56	MG	1A	3471	1/1	0.94	0.12	48,48,48,48	0
56	MG	1A	3900	1/1	0.94	0.25	39,39,39,39	0
56	MG	1x	110	1/1	0.94	0.12	66,66,66,66	0
56	MG	2A	3285	1/1	0.94	0.14	67,67,67,67	0
56	MG	2A	3584	1/1	0.94	0.12	43,43,43,43	0
56	MG	2a	1613	1/1	0.94	0.15	62,62,62,62	0
56	MG	1A	3574	1/1	0.94	0.24	37,37,37,37	0
56	MG	1A	3476	1/1	0.94	0.08	63,63,63,63	0
56	MG	1A	3907	1/1	0.94	0.17	42,42,42,42	0
56	MG	2a	1617	1/1	0.94	0.15	60,60,60,60	0
56	MG	2A	3003	1/1	0.94	0.25	53,53,53,53	0
56	MG	2A	3291	1/1	0.94	0.07	53,53,53,53	0
56	MG	1a	1665	1/1	0.94	0.14	70,70,70,70	0
56	MG	1B	222	1/1	0.94	0.09	54,54,54,54	0
56	MG	1A	3576	1/1	0.94	0.20	48,48,48,48	0
56	MG	1A	3577	1/1	0.94	0.12	39,39,39,39	0
56	MG	2A	3011	1/1	0.94	0.13	42,42,42,42	0
56	MG	2a	1629	1/1	0.94	0.16	58,58,58,58	0
56	MG	1a	1669	1/1	0.94	0.10	65,65,65,65	0
56	MG	1A	3479	1/1	0.94	0.20	50,50,50,50	0
56	MG	1A	3750	1/1	0.94	0.17	56,56,56,56	0
56	MG	1A	3314	1/1	0.94	0.22	52,52,52,52	0
56	MG	1a	1673	1/1	0.94	0.09	80,80,80,80	0
56	MG	2A	3609	1/1	0.94	0.06	33,33,33,33	0
56	MG	1A	3920	1/1	0.94	0.07	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3481	1/1	0.94	0.19	48,48,48,48	0
56	MG	1B	233	1/1	0.94	0.14	54,54,54,54	0
56	MG	2A	3032	1/1	0.94	0.07	40,40,40,40	0
56	MG	1A	3117	1/1	0.94	0.07	38,38,38,38	0
56	MG	2A	3036	1/1	0.94	0.15	47,47,47,47	0
56	MG	1A	3755	1/1	0.94	0.07	61,61,61,61	0
56	MG	1A	3932	1/1	0.94	0.06	43,43,43,43	0
56	MG	1A	3316	1/1	0.94	0.20	52,52,52,52	0
56	MG	2A	3627	1/1	0.94	0.20	51,51,51,51	0
56	MG	1a	1683	1/1	0.94	0.11	61,61,61,61	0
56	MG	2a	1652	1/1	0.94	0.31	53,53,53,53	0
56	MG	2A	3316	1/1	0.94	0.14	53,53,53,53	0
56	MG	2A	3631	1/1	0.94	0.06	32,32,32,32	0
56	MG	2A	3634	1/1	0.94	0.09	40,40,40,40	0
56	MG	2A	3044	1/1	0.94	0.10	45,45,45,45	0
56	MG	2A	3636	1/1	0.94	0.10	51,51,51,51	0
56	MG	1A	3485	1/1	0.94	0.07	49,49,49,49	0
56	MG	2A	3048	1/1	0.94	0.15	50,50,50,50	0
56	MG	2A	3641	1/1	0.94	0.16	62,62,62,62	0
56	MG	2a	1663	1/1	0.94	0.19	62,62,62,62	0
56	MG	2A	3646	1/1	0.94	0.22	57,57,57,57	0
56	MG	1A	3395	1/1	0.94	0.15	35,35,35,35	0
56	MG	2A	3649	1/1	0.94	0.12	61,61,61,61	0
56	MG	1E	305	1/1	0.94	0.12	29,29,29,29	0
56	MG	1A	3764	1/1	0.94	0.18	42,42,42,42	0
56	MG	1A	3939	1/1	0.94	0.11	54,54,54,54	0
56	MG	2a	1670	1/1	0.94	0.21	55,55,55,55	0
56	MG	2A	3057	1/1	0.94	0.28	69,69,69,69	0
56	MG	1A	3396	1/1	0.94	0.17	52,52,52,52	0
56	MG	1a	1691	1/1	0.94	0.10	74,74,74,74	0
56	MG	1A	3943	1/1	0.94	0.07	46,46,46,46	0
56	MG	2a	1675	1/1	0.94	0.27	58,58,58,58	0
56	MG	2A	3062	1/1	0.94	0.15	64,64,64,64	0
56	MG	1A	3488	1/1	0.94	0.30	51,51,51,51	0
56	MG	1A	3318	1/1	0.94	0.07	29,29,29,29	0
56	MG	1A	3948	1/1	0.94	0.07	50,50,50,50	0
56	MG	1A	3949	1/1	0.94	0.06	32,32,32,32	0
56	MG	1A	3774	1/1	0.94	0.08	17,17,17,17	0
56	MG	2A	3075	1/1	0.94	0.11	46,46,46,46	0
56	MG	1A	3492	1/1	0.94	0.26	50,50,50,50	0
56	MG	2A	3081	1/1	0.94	0.21	54,54,54,54	0
56	MG	1A	3596	1/1	0.94	0.23	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	3342	1/1	0.94	0.26	51,51,51,51	0
56	MG	2a	1688	1/1	0.94	0.27	68,68,68,68	0
56	MG	1F	311	1/1	0.94	0.14	45,45,45,45	0
56	MG	2A	3345	1/1	0.94	0.11	56,56,56,56	0
56	MG	1F	312	1/1	0.94	0.14	39,39,39,39	0
56	MG	1A	3777	1/1	0.94	0.05	18,18,18,18	0
56	MG	2A	3348	1/1	0.94	0.08	63,63,63,63	0
56	MG	1A	3961	1/1	0.94	0.07	53,53,53,53	0
56	MG	1a	1705	1/1	0.94	0.26	61,61,61,61	0
56	MG	2A	3685	1/1	0.94	0.11	32,32,32,32	0
56	MG	1A	3493	1/1	0.94	0.08	64,64,64,64	0
56	MG	2A	3690	1/1	0.94	0.09	57,57,57,57	0
56	MG	2A	3354	1/1	0.94	0.09	57,57,57,57	0
56	MG	1A	3323	1/1	0.94	0.08	51,51,51,51	0
56	MG	2a	1702	1/1	0.94	0.12	71,71,71,71	0
56	MG	1A	3325	1/1	0.94	0.07	42,42,42,42	0
56	MG	2a	1704	1/1	0.94	0.12	62,62,62,62	0
56	MG	2a	1705	1/1	0.94	0.16	68,68,68,68	0
56	MG	2A	3357	1/1	0.94	0.13	50,50,50,50	0
56	MG	1N	206	1/1	0.94	0.10	48,48,48,48	0
56	MG	2a	1710	1/1	0.94	0.12	40,40,40,40	0
56	MG	2a	1711	1/1	0.94	0.20	71,71,71,71	0
56	MG	1A	3251	1/1	0.94	0.07	45,45,45,45	0
56	MG	2a	1714	1/1	0.94	0.22	58,58,58,58	0
56	MG	1A	3186	1/1	0.94	0.14	51,51,51,51	0
56	MG	1A	3408	1/1	0.94	0.18	51,51,51,51	0
56	MG	1A	3004	1/1	0.94	0.13	34,34,34,34	0
56	MG	2a	1720	1/1	0.94	0.15	57,57,57,57	0
56	MG	1a	1715	1/1	0.94	0.38	70,70,70,70	0
56	MG	1A	3191	1/1	0.94	0.16	52,52,52,52	0
56	MG	2A	3107	1/1	0.94	0.08	49,49,49,49	0
56	MG	1A	3030	1/1	0.94	0.17	32,32,32,32	0
56	MG	1a	1719	1/1	0.94	0.15	69,69,69,69	0
56	MG	1A	3617	1/1	0.94	0.14	49,49,49,49	0
56	MG	1A	3195	1/1	0.94	0.07	45,45,45,45	0
56	MG	1A	3626	1/1	0.94	0.09	34,34,34,34	0
56	MG	1Q	207	1/1	0.94	0.14	38,38,38,38	0
56	MG	1A	3636	1/1	0.94	0.07	32,32,32,32	0
56	MG	2A	3716	1/1	0.94	0.10	52,52,52,52	0
56	MG	1A	3810	1/1	0.94	0.21	24,24,24,24	0
56	MG	1A	3637	1/1	0.94	0.07	24,24,24,24	0
56	MG	1T	201	1/1	0.94	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3036	1/1	0.94	0.23	33,33,33,33	0
56	MG	1T	203	1/1	0.94	0.28	59,59,59,59	0
56	MG	1A	3642	1/1	0.94	0.12	44,44,44,44	0
56	MG	1U	209	1/1	0.94	0.10	51,51,51,51	0
56	MG	1A	3047	1/1	0.94	0.05	27,27,27,27	0
56	MG	2A	3729	1/1	0.94	0.17	62,62,62,62	0
56	MG	2A	3389	1/1	0.94	0.07	70,70,70,70	0
56	MG	1A	3201	1/1	0.94	0.18	40,40,40,40	0
56	MG	2A	3134	1/1	0.94	0.10	48,48,48,48	0
56	MG	2A	3135	1/1	0.94	0.09	42,42,42,42	0
56	MG	2A	3136	1/1	0.94	0.19	53,53,53,53	0
56	MG	2A	3394	1/1	0.94	0.11	54,54,54,54	0
56	MG	2A	3138	1/1	0.94	0.07	41,41,41,41	0
56	MG	2A	3140	1/1	0.94	0.12	53,53,53,53	0
56	MG	1A	3990	1/1	0.94	0.08	13,13,13,13	0
56	MG	2A	3741	1/1	0.94	0.12	65,65,65,65	0
56	MG	2A	3145	1/1	0.94	0.14	61,61,61,61	0
56	MG	2A	3147	1/1	0.94	0.28	50,50,50,50	0
56	MG	1W	205	1/1	0.94	0.19	39,39,39,39	0
56	MG	2A	3402	1/1	0.94	0.11	43,43,43,43	0
56	MG	2A	3749	1/1	0.94	0.16	59,59,59,59	0
56	MG	2a	1762	1/1	0.94	0.14	71,71,71,71	0
56	MG	1A	3139	1/1	0.94	0.17	28,28,28,28	0
56	MG	1A	3995	1/1	0.94	0.21	64,64,64,64	0
56	MG	2A	3752	1/1	0.94	0.09	52,52,52,52	0
56	MG	2a	1768	1/1	0.94	0.25	64,64,64,64	0
56	MG	2A	3153	1/1	0.94	0.12	60,60,60,60	0
56	MG	2A	3407	1/1	0.94	0.21	51,51,51,51	0
56	MG	2A	3408	1/1	0.94	0.20	41,41,41,41	0
56	MG	2A	3409	1/1	0.94	0.23	45,45,45,45	0
56	MG	2A	3411	1/1	0.94	0.20	55,55,55,55	0
56	MG	2A	3154	1/1	0.94	0.08	42,42,42,42	0
56	MG	1A	3142	1/1	0.94	0.25	36,36,36,36	0
56	MG	1Y	203	1/1	0.94	0.22	47,47,47,47	0
56	MG	2A	3763	1/1	0.94	0.14	55,55,55,55	0
56	MG	2A	3159	1/1	0.94	0.21	63,63,63,63	0
56	MG	2A	3418	1/1	0.94	0.17	34,34,34,34	0
56	MG	1Z	301	1/1	0.94	0.12	52,52,52,52	0
56	MG	2A	3769	1/1	0.94	0.17	68,68,68,68	0
56	MG	1A	3999	1/1	0.94	0.07	19,19,19,19	0
56	MG	1A	3824	1/1	0.94	0.09	35,35,35,35	0
56	MG	2A	3422	1/1	0.94	0.27	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	10	103	1/1	0.94	0.10	37,37,37,37	0
56	MG	2A	3424	1/1	0.94	0.29	52,52,52,52	0
56	MG	2A	3426	1/1	0.94	0.15	55,55,55,55	0
56	MG	1A	3145	1/1	0.94	0.14	49,49,49,49	0
56	MG	2v	102	1/1	0.94	0.10	60,60,60,60	0
56	MG	1a	1752	1/1	0.94	0.06	40,40,40,40	0
56	MG	1A	3652	1/1	0.94	0.07	21,21,21,21	0
56	MG	1A	4008	1/1	0.94	0.13	40,40,40,40	0
56	MG	1A	3427	1/1	0.94	0.09	46,46,46,46	0
56	MG	2x	105	1/1	0.94	0.15	71,71,71,71	0
56	MG	2A	3433	1/1	0.94	0.17	58,58,58,58	0
58	ZN	14	102	1/1	0.94	0.12	125,125,125,125	0
56	MG	1A	3733	1/1	0.95	0.07	47,47,47,47	0
56	MG	1A	4079	1/1	0.95	0.05	38,38,38,38	0
56	MG	2A	3492	1/1	0.95	0.14	52,52,52,52	0
56	MG	2A	3245	1/1	0.95	0.13	70,70,70,70	0
56	MG	1A	3397	1/1	0.95	0.09	48,48,48,48	0
56	MG	2A	3843	1/1	0.95	0.07	61,61,61,61	0
56	MG	1A	3897	1/1	0.95	0.09	44,44,44,44	0
56	MG	1v	101	1/1	0.95	0.11	64,64,64,64	0
56	MG	2A	3499	1/1	0.95	0.13	47,47,47,47	0
56	MG	2A	3847	1/1	0.95	0.06	55,55,55,55	0
56	MG	1A	3240	1/1	0.95	0.07	42,42,42,42	0
56	MG	2A	3250	1/1	0.95	0.12	55,55,55,55	0
56	MG	1A	3741	1/1	0.95	0.07	52,52,52,52	0
56	MG	1A	4084	1/1	0.95	0.09	49,49,49,49	0
56	MG	1B	201	1/1	0.95	0.09	59,59,59,59	0
56	MG	2A	3506	1/1	0.95	0.16	45,45,45,45	0
56	MG	1x	103	1/1	0.95	0.05	58,58,58,58	0
56	MG	2A	3857	1/1	0.95	0.06	37,37,37,37	0
56	MG	2A	3508	1/1	0.95	0.08	34,34,34,34	0
56	MG	2A	3256	1/1	0.95	0.10	54,54,54,54	0
56	MG	2A	3257	1/1	0.95	0.12	62,62,62,62	0
56	MG	1A	3588	1/1	0.95	0.15	33,33,33,33	0
56	MG	2A	3865	1/1	0.95	0.07	62,62,62,62	0
56	MG	1A	3242	1/1	0.95	0.24	37,37,37,37	0
56	MG	1A	3906	1/1	0.95	0.12	54,54,54,54	0
56	MG	2A	3262	1/1	0.95	0.06	40,40,40,40	0
56	MG	2A	3521	1/1	0.95	0.09	56,56,56,56	0
56	MG	1x	109	1/1	0.95	0.12	67,67,67,67	0
56	MG	2A	3265	1/1	0.95	0.08	56,56,56,56	0
56	MG	1A	3243	1/1	0.95	0.19	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2B	203	1/1	0.95	0.15	57,57,57,57	0
56	MG	1A	3115	1/1	0.95	0.12	48,48,48,48	0
56	MG	1A	3018	1/1	0.95	0.16	32,32,32,32	0
56	MG	1x	113	1/1	0.95	0.17	78,78,78,78	0
56	MG	1A	3912	1/1	0.95	0.10	39,39,39,39	0
56	MG	1A	3913	1/1	0.95	0.07	57,57,57,57	0
56	MG	1B	218	1/1	0.95	0.12	48,48,48,48	0
56	MG	2A	3274	1/1	0.95	0.14	52,52,52,52	0
56	MG	1B	219	1/1	0.95	0.17	40,40,40,40	0
56	MG	2A	3541	1/1	0.95	0.12	40,40,40,40	0
56	MG	2A	3006	1/1	0.95	0.26	61,61,61,61	0
56	MG	1A	3405	1/1	0.95	0.10	53,53,53,53	0
56	MG	1a	1662	1/1	0.95	0.13	66,66,66,66	0
56	MG	1A	3247	1/1	0.95	0.20	58,58,58,58	0
56	MG	1A	3120	1/1	0.95	0.13	28,28,28,28	0
56	MG	2A	3016	1/1	0.95	0.20	65,65,65,65	0
56	MG	1A	3919	1/1	0.95	0.07	43,43,43,43	0
56	MG	1A	3319	1/1	0.95	0.15	50,50,50,50	0
56	MG	2D	301	1/1	0.95	0.11	38,38,38,38	0
56	MG	2A	3019	1/1	0.95	0.04	32,32,32,32	0
56	MG	1A	3758	1/1	0.95	0.10	24,24,24,24	0
56	MG	1A	3185	1/1	0.95	0.19	47,47,47,47	0
56	MG	2A	3288	1/1	0.95	0.35	65,65,65,65	0
56	MG	1A	3602	1/1	0.95	0.09	35,35,35,35	0
56	MG	2A	3027	1/1	0.95	0.14	44,44,44,44	0
56	MG	1A	3929	1/1	0.95	0.07	35,35,35,35	0
56	MG	1A	3763	1/1	0.95	0.14	40,40,40,40	0
56	MG	2A	3293	1/1	0.95	0.17	59,59,59,59	0
56	MG	1B	232	1/1	0.95	0.07	50,50,50,50	0
56	MG	2A	3295	1/1	0.95	0.11	53,53,53,53	0
56	MG	2F	306	1/1	0.95	0.21	48,48,48,48	0
56	MG	1A	3031	1/1	0.95	0.07	32,32,32,32	0
56	MG	2A	3034	1/1	0.95	0.09	56,56,56,56	0
56	MG	1A	3127	1/1	0.95	0.16	38,38,38,38	0
56	MG	1A	3768	1/1	0.95	0.09	37,37,37,37	0
56	MG	2A	3040	1/1	0.95	0.09	49,49,49,49	0
56	MG	1B	236	1/1	0.95	0.12	41,41,41,41	0
56	MG	2A	3582	1/1	0.95	0.20	59,59,59,59	0
56	MG	1A	3254	1/1	0.95	0.16	49,49,49,49	0
56	MG	1D	306	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3330	1/1	0.95	0.13	45,45,45,45	0
56	MG	1A	3772	1/1	0.95	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	2U	202	1/1	0.95	0.12	54,54,54,54	0
56	MG	2V	201	1/1	0.95	0.25	46,46,46,46	0
56	MG	1D	313	1/1	0.95	0.16	31,31,31,31	0
56	MG	1A	3511	1/1	0.95	0.06	40,40,40,40	0
56	MG	1E	302	1/1	0.95	0.13	39,39,39,39	0
56	MG	1A	3001	1/1	0.95	0.08	31,31,31,31	0
56	MG	1E	306	1/1	0.95	0.15	48,48,48,48	0
56	MG	1A	3945	1/1	0.95	0.13	54,54,54,54	0
56	MG	1a	1689	1/1	0.95	0.16	57,57,57,57	0
56	MG	1A	3621	1/1	0.95	0.11	9,9,9,9	0
56	MG	23	103	1/1	0.95	0.07	41,41,41,41	0
56	MG	1A	3623	1/1	0.95	0.10	42,42,42,42	0
56	MG	25	102	1/1	0.95	0.13	42,42,42,42	0
56	MG	1A	3624	1/1	0.95	0.09	42,42,42,42	0
56	MG	1A	3951	1/1	0.95	0.05	15,15,15,15	0
56	MG	26	101	1/1	0.95	0.16	55,55,55,55	0
56	MG	1A	3132	1/1	0.95	0.17	39,39,39,39	0
56	MG	2A	3066	1/1	0.95	0.27	56,56,56,56	0
56	MG	2A	3068	1/1	0.95	0.06	44,44,44,44	0
56	MG	1A	3334	1/1	0.95	0.16	54,54,54,54	0
56	MG	1A	3632	1/1	0.95	0.08	59,59,59,59	0
56	MG	1A	3956	1/1	0.95	0.07	24,24,24,24	0
56	MG	1A	3633	1/1	0.95	0.05	27,27,27,27	0
56	MG	1F	309	1/1	0.95	0.19	30,30,30,30	0
56	MG	2A	3080	1/1	0.95	0.10	46,46,46,46	0
56	MG	1A	3789	1/1	0.95	0.07	31,31,31,31	0
56	MG	1A	3635	1/1	0.95	0.05	24,24,24,24	0
56	MG	2a	1609	1/1	0.95	0.07	51,51,51,51	0
56	MG	1A	3791	1/1	0.95	0.10	46,46,46,46	0
56	MG	2A	3624	1/1	0.95	0.12	61,61,61,61	0
56	MG	2A	3625	1/1	0.95	0.09	39,39,39,39	0
56	MG	2A	3626	1/1	0.95	0.09	50,50,50,50	0
56	MG	1F	313	1/1	0.95	0.12	57,57,57,57	0
56	MG	2A	3628	1/1	0.95	0.09	35,35,35,35	0
56	MG	1A	3792	1/1	0.95	0.05	38,38,38,38	0
56	MG	1A	3966	1/1	0.95	0.08	57,57,57,57	0
56	MG	2A	3337	1/1	0.95	0.11	45,45,45,45	0
56	MG	2a	1619	1/1	0.95	0.12	52,52,52,52	0
56	MG	2a	1620	1/1	0.95	0.06	61,61,61,61	0
56	MG	2A	3632	1/1	0.95	0.12	43,43,43,43	0
56	MG	2A	3633	1/1	0.95	0.10	44,44,44,44	0
56	MG	1A	3426	1/1	0.95	0.17	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3043	1/1	0.95	0.16	43,43,43,43	0
56	MG	1A	3134	1/1	0.95	0.10	40,40,40,40	0
56	MG	1N	205	1/1	0.95	0.21	40,40,40,40	0
56	MG	2a	1628	1/1	0.95	0.22	58,58,58,58	0
56	MG	2A	3097	1/1	0.95	0.13	45,45,45,45	0
56	MG	2A	3343	1/1	0.95	0.09	69,69,69,69	0
56	MG	2A	3642	1/1	0.95	0.19	38,38,38,38	0
56	MG	2A	3645	1/1	0.95	0.17	52,52,52,52	0
56	MG	1A	3640	1/1	0.95	0.06	22,22,22,22	0
56	MG	1N	207	1/1	0.95	0.10	49,49,49,49	0
56	MG	1A	3262	1/1	0.95	0.13	49,49,49,49	0
56	MG	1A	3976	1/1	0.95	0.09	38,38,38,38	0
56	MG	1A	3046	1/1	0.95	0.05	39,39,39,39	0
56	MG	2a	1638	1/1	0.95	0.33	60,60,60,60	0
56	MG	1A	3806	1/1	0.95	0.10	48,48,48,48	0
56	MG	2A	3351	1/1	0.95	0.15	56,56,56,56	0
56	MG	1A	3054	1/1	0.95	0.10	46,46,46,46	0
56	MG	2A	3106	1/1	0.95	0.05	46,46,46,46	0
56	MG	1A	3140	1/1	0.95	0.29	29,29,29,29	0
56	MG	1a	1722	1/1	0.95	0.29	45,45,45,45	0
56	MG	1A	3100	1/1	0.95	0.06	40,40,40,40	0
56	MG	2A	3112	1/1	0.95	0.10	47,47,47,47	0
56	MG	1A	3342	1/1	0.95	0.09	40,40,40,40	0
56	MG	1A	3102	1/1	0.95	0.07	46,46,46,46	0
56	MG	1Q	205	1/1	0.95	0.09	49,49,49,49	0
56	MG	1A	3269	1/1	0.95	0.14	48,48,48,48	0
56	MG	2A	3667	1/1	0.95	0.12	35,35,35,35	0
56	MG	2A	3668	1/1	0.95	0.07	48,48,48,48	0
56	MG	1A	3657	1/1	0.95	0.08	35,35,35,35	0
56	MG	1A	3086	1/1	0.95	0.17	37,37,37,37	0
56	MG	1A	3821	1/1	0.95	0.11	41,41,41,41	0
56	MG	2A	3674	1/1	0.95	0.07	52,52,52,52	0
56	MG	2a	1661	1/1	0.95	0.15	51,51,51,51	0
56	MG	2A	3365	1/1	0.95	0.10	52,52,52,52	0
56	MG	1A	3660	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3351	1/1	0.95	0.10	52,52,52,52	0
56	MG	1A	3213	1/1	0.95	0.07	36,36,36,36	0
56	MG	2A	3679	1/1	0.95	0.18	56,56,56,56	0
56	MG	2A	3124	1/1	0.95	0.24	68,68,68,68	0
56	MG	2A	3125	1/1	0.95	0.31	57,57,57,57	0
56	MG	1A	3220	1/1	0.95	0.36	39,39,39,39	0
56	MG	2A	3127	1/1	0.95	0.10	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3376	1/1	0.95	0.22	52,52,52,52	0
56	MG	2A	3686	1/1	0.95	0.08	61,61,61,61	0
56	MG	2A	3128	1/1	0.95	0.21	58,58,58,58	0
56	MG	1A	3450	1/1	0.95	0.11	46,46,46,46	0
56	MG	2A	3131	1/1	0.95	0.08	45,45,45,45	0
56	MG	1A	3452	1/1	0.95	0.16	43,43,43,43	0
56	MG	2A	3382	1/1	0.95	0.10	53,53,53,53	0
56	MG	1V	205	1/1	0.95	0.10	39,39,39,39	0
56	MG	2A	3384	1/1	0.95	0.15	50,50,50,50	0
56	MG	1A	3830	1/1	0.95	0.19	47,47,47,47	0
56	MG	1W	201	1/1	0.95	0.07	34,34,34,34	0
56	MG	1A	3277	1/1	0.95	0.06	43,43,43,43	0
56	MG	1W	203	1/1	0.95	0.06	38,38,38,38	0
56	MG	2A	3700	1/1	0.95	0.20	61,61,61,61	0
56	MG	2A	3139	1/1	0.95	0.17	61,61,61,61	0
56	MG	1A	4007	1/1	0.95	0.11	47,47,47,47	0
56	MG	2A	3141	1/1	0.95	0.26	50,50,50,50	0
56	MG	2A	3142	1/1	0.95	0.15	40,40,40,40	0
56	MG	2A	3143	1/1	0.95	0.15	48,48,48,48	0
56	MG	1W	206	1/1	0.95	0.12	29,29,29,29	0
56	MG	1A	3280	1/1	0.95	0.08	39,39,39,39	0
56	MG	1A	3360	1/1	0.95	0.13	53,53,53,53	0
56	MG	1A	3676	1/1	0.95	0.05	19,19,19,19	0
56	MG	1A	3459	1/1	0.95	0.07	43,43,43,43	0
56	MG	1A	3282	1/1	0.95	0.13	34,34,34,34	0
56	MG	2A	3400	1/1	0.95	0.06	59,59,59,59	0
56	MG	1A	3681	1/1	0.95	0.08	34,34,34,34	0
56	MG	1A	3363	1/1	0.95	0.11	37,37,37,37	0
56	MG	1A	3283	1/1	0.95	0.51	44,44,44,44	0
56	MG	10	104	1/1	0.95	0.17	61,61,61,61	0
56	MG	1A	3685	1/1	0.95	0.08	27,27,27,27	0
56	MG	11	101	1/1	0.95	0.20	33,33,33,33	0
56	MG	1A	4019	1/1	0.95	0.10	55,55,55,55	0
56	MG	2A	3728	1/1	0.95	0.07	49,49,49,49	0
56	MG	1A	3686	1/1	0.95	0.13	55,55,55,55	0
56	MG	2A	3410	1/1	0.95	0.21	47,47,47,47	0
56	MG	2a	1712	1/1	0.95	0.09	56,56,56,56	0
56	MG	1a	1767	1/1	0.95	0.18	49,49,49,49	0
56	MG	2A	3412	1/1	0.95	0.21	44,44,44,44	0
56	MG	12	102	1/1	0.95	0.08	49,49,49,49	0
56	MG	2a	1716	1/1	0.95	0.30	53,53,53,53	0
56	MG	1A	3846	1/1	0.95	0.15	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	2a	1718	1/1	0.95	0.11	54,54,54,54	0
56	MG	1A	3104	1/1	0.95	0.10	51,51,51,51	0
56	MG	1A	3553	1/1	0.95	0.23	33,33,33,33	0
56	MG	1A	3155	1/1	0.95	0.10	45,45,45,45	0
56	MG	15	103	1/1	0.95	0.32	44,44,44,44	0
56	MG	15	106	1/1	0.95	0.15	45,45,45,45	0
56	MG	1a	1776	1/1	0.95	0.06	59,59,59,59	0
56	MG	1A	4028	1/1	0.95	0.10	57,57,57,57	0
56	MG	2A	3179	1/1	0.95	0.27	60,60,60,60	0
56	MG	2A	3181	1/1	0.95	0.12	38,38,38,38	0
56	MG	1A	3555	1/1	0.95	0.31	51,51,51,51	0
56	MG	2A	3183	1/1	0.95	0.12	54,54,54,54	0
56	MG	1A	3699	1/1	0.95	0.08	36,36,36,36	0
56	MG	17	104	1/1	0.95	0.09	39,39,39,39	0
56	MG	17	106	1/1	0.95	0.12	53,53,53,53	0
56	MG	1A	3556	1/1	0.95	0.22	44,44,44,44	0
56	MG	2A	3189	1/1	0.95	0.07	58,58,58,58	0
56	MG	1A	3559	1/1	0.95	0.19	33,33,33,33	0
56	MG	18	104	1/1	0.95	0.14	46,46,46,46	0
56	MG	1A	3702	1/1	0.95	0.11	38,38,38,38	0
56	MG	2a	1739	1/1	0.95	0.09	50,50,50,50	0
56	MG	1A	4035	1/1	0.95	0.07	45,45,45,45	0
56	MG	2a	1741	1/1	0.95	0.13	53,53,53,53	0
56	MG	1a	1789	1/1	0.95	0.12	70,70,70,70	0
56	MG	1A	3370	1/1	0.95	0.16	51,51,51,51	0
56	MG	1A	3562	1/1	0.95	0.35	41,41,41,41	0
56	MG	2A	3766	1/1	0.95	0.11	56,56,56,56	0
56	MG	2A	3441	1/1	0.95	0.19	50,50,50,50	0
56	MG	2a	1747	1/1	0.95	0.18	65,65,65,65	0
56	MG	1A	3705	1/1	0.95	0.08	29,29,29,29	0
56	MG	1A	4040	1/1	0.95	0.11	37,37,37,37	0
56	MG	1a	1797	1/1	0.95	0.10	68,68,68,68	0
56	MG	1A	3865	1/1	0.95	0.10	36,36,36,36	0
56	MG	1A	4042	1/1	0.95	0.10	47,47,47,47	0
56	MG	1A	3371	1/1	0.95	0.11	58,58,58,58	0
56	MG	2A	3448	1/1	0.95	0.24	56,56,56,56	0
56	MG	1A	4044	1/1	0.95	0.09	22,22,22,22	0
56	MG	1a	1805	1/1	0.95	0.18	71,71,71,71	0
56	MG	2a	1758	1/1	0.95	0.23	56,56,56,56	0
56	MG	1A	3158	1/1	0.95	0.12	33,33,33,33	0
56	MG	1a	1807	1/1	0.95	0.14	57,57,57,57	0
56	MG	2A	3213	1/1	0.95	0.17	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	1a	1612	1/1	0.95	0.17	58,58,58,58	0
56	MG	1A	3711	1/1	0.95	0.09	32,32,32,32	0
56	MG	2A	3788	1/1	0.95	0.17	41,41,41,41	0
56	MG	2a	1766	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	3229	1/1	0.95	0.11	43,43,43,43	0
56	MG	1A	3297	1/1	0.95	0.07	45,45,45,45	0
56	MG	2a	1769	1/1	0.95	0.10	70,70,70,70	0
56	MG	1A	3060	1/1	0.95	0.10	38,38,38,38	0
56	MG	1A	3107	1/1	0.95	0.15	34,34,34,34	0
56	MG	2A	3793	1/1	0.95	0.07	72,72,72,72	0
56	MG	1A	4055	1/1	0.95	0.09	62,62,62,62	0
56	MG	2A	3222	1/1	0.95	0.25	40,40,40,40	0
56	MG	1A	3300	1/1	0.95	0.10	47,47,47,47	0
56	MG	1A	3389	1/1	0.95	0.19	37,37,37,37	0
56	MG	1A	3719	1/1	0.95	0.18	53,53,53,53	0
56	MG	2A	3800	1/1	0.95	0.07	53,53,53,53	0
56	MG	2A	3228	1/1	0.95	0.23	44,44,44,44	0
56	MG	2A	3471	1/1	0.95	0.16	62,62,62,62	0
56	MG	2A	3472	1/1	0.95	0.23	48,48,48,48	0
56	MG	1a	1625	1/1	0.95	0.10	57,57,57,57	0
56	MG	1A	3110	1/1	0.95	0.16	36,36,36,36	0
56	MG	1A	3171	1/1	0.95	0.28	43,43,43,43	0
56	MG	1A	3883	1/1	0.95	0.06	14,14,14,14	0
56	MG	2A	3812	1/1	0.95	0.06	41,41,41,41	0
56	MG	1A	4068	1/1	0.95	0.10	29,29,29,29	0
56	MG	1A	3305	1/1	0.95	0.29	40,40,40,40	0
56	MG	2A	3238	1/1	0.95	0.08	44,44,44,44	0
56	MG	2A	3816	1/1	0.95	0.07	37,37,37,37	0
56	MG	2A	3482	1/1	0.95	0.17	66,66,66,66	0
56	MG	1A	3062	1/1	0.95	0.09	31,31,31,31	0
56	MG	1A	3308	1/1	0.95	0.10	30,30,30,30	0
56	MG	2A	3823	1/1	0.95	0.09	28,28,28,28	0
56	MG	1A	3309	1/1	0.95	0.14	36,36,36,36	0
56	MG	2x	106	1/1	0.95	0.10	76,76,76,76	0
56	MG	2A	3833	1/1	0.95	0.14	63,63,63,63	0
56	MG	2A	3486	1/1	0.95	0.11	48,48,48,48	0
58	ZN	24	501	1/1	0.95	0.17	131,131,131,131	0
56	MG	1A	3400	1/1	0.96	0.08	38,38,38,38	0
56	MG	2A	3515	1/1	0.96	0.08	46,46,46,46	0
56	MG	2A	3001	1/1	0.96	0.43	60,60,60,60	0
56	MG	1A	3740	1/1	0.96	0.08	55,55,55,55	0
56	MG	1A	3594	1/1	0.96	0.16	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3264	1/1	0.96	0.09	49,49,49,49	0
56	MG	1B	214	1/1	0.96	0.05	48,48,48,48	0
56	MG	1A	3595	1/1	0.96	0.12	49,49,49,49	0
56	MG	2A	3523	1/1	0.96	0.14	52,52,52,52	0
56	MG	1A	3329	1/1	0.96	0.22	49,49,49,49	0
56	MG	1A	3746	1/1	0.96	0.05	21,21,21,21	0
56	MG	1A	3597	1/1	0.96	0.11	44,44,44,44	0
56	MG	1A	3402	1/1	0.96	0.23	43,43,43,43	0
56	MG	1A	3128	1/1	0.96	0.37	33,33,33,33	0
56	MG	2A	3272	1/1	0.96	0.11	59,59,59,59	0
56	MG	2A	3858	1/1	0.96	0.05	48,48,48,48	0
56	MG	2A	3014	1/1	0.96	0.12	47,47,47,47	0
56	MG	2A	3533	1/1	0.96	0.13	44,44,44,44	0
56	MG	2A	3015	1/1	0.96	0.06	42,42,42,42	0
56	MG	2A	3863	1/1	0.96	0.06	60,60,60,60	0
56	MG	1a	1658	1/1	0.96	0.06	49,49,49,49	0
56	MG	2A	3538	1/1	0.96	0.14	61,61,61,61	0
56	MG	1A	3918	1/1	0.96	0.10	45,45,45,45	0
56	MG	1A	3496	1/1	0.96	0.06	45,45,45,45	0
56	MG	2A	3278	1/1	0.96	0.08	38,38,38,38	0
56	MG	1A	3753	1/1	0.96	0.07	43,43,43,43	0
56	MG	1A	3331	1/1	0.96	0.21	41,41,41,41	0
56	MG	2A	3022	1/1	0.96	0.14	31,31,31,31	0
56	MG	1A	3922	1/1	0.96	0.06	15,15,15,15	0
56	MG	1A	3066	1/1	0.96	0.12	43,43,43,43	0
56	MG	2A	3025	1/1	0.96	0.43	48,48,48,48	0
56	MG	1A	3924	1/1	0.96	0.10	56,56,56,56	0
56	MG	2A	3553	1/1	0.96	0.09	34,34,34,34	0
56	MG	2A	3029	1/1	0.96	0.14	58,58,58,58	0
56	MG	2A	3555	1/1	0.96	0.09	50,50,50,50	0
56	MG	2A	3556	1/1	0.96	0.10	33,33,33,33	0
56	MG	1A	3224	1/1	0.96	0.07	38,38,38,38	0
56	MG	1A	3605	1/1	0.96	0.07	40,40,40,40	0
56	MG	2A	3559	1/1	0.96	0.06	37,37,37,37	0
56	MG	2A	3560	1/1	0.96	0.08	34,34,34,34	0
56	MG	1A	3169	1/1	0.96	0.20	40,40,40,40	0
56	MG	1A	3049	1/1	0.96	0.07	31,31,31,31	0
56	MG	1A	3411	1/1	0.96	0.07	51,51,51,51	0
56	MG	2A	3035	1/1	0.96	0.14	42,42,42,42	0
56	MG	1D	302	1/1	0.96	0.08	43,43,43,43	0
56	MG	1A	3070	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3615	1/1	0.96	0.09	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	1D	307	1/1	0.96	0.14	37,37,37,37	0
56	MG	1D	308	1/1	0.96	0.15	38,38,38,38	0
56	MG	2A	3572	1/1	0.96	0.10	39,39,39,39	0
56	MG	2A	3573	1/1	0.96	0.08	37,37,37,37	0
56	MG	2A	3574	1/1	0.96	0.10	25,25,25,25	0
56	MG	1a	1677	1/1	0.96	0.15	55,55,55,55	0
56	MG	1D	309	1/1	0.96	0.22	44,44,44,44	0
56	MG	1A	3092	1/1	0.96	0.12	37,37,37,37	0
56	MG	2A	3046	1/1	0.96	0.08	45,45,45,45	0
56	MG	2A	3579	1/1	0.96	0.09	24,24,24,24	0
56	MG	2F	303	1/1	0.96	0.06	43,43,43,43	0
56	MG	2A	3580	1/1	0.96	0.06	52,52,52,52	0
56	MG	1a	1680	1/1	0.96	0.07	82,82,82,82	0
56	MG	2A	3049	1/1	0.96	0.05	29,29,29,29	0
56	MG	2G	201	1/1	0.96	0.13	66,66,66,66	0
56	MG	1A	3940	1/1	0.96	0.11	83,83,83,83	0
56	MG	2A	3051	1/1	0.96	0.15	55,55,55,55	0
56	MG	1A	3618	1/1	0.96	0.13	52,52,52,52	0
56	MG	1A	3770	1/1	0.96	0.08	28,28,28,28	0
56	MG	2Q	202	1/1	0.96	0.22	53,53,53,53	0
56	MG	1E	301	1/1	0.96	0.17	49,49,49,49	0
56	MG	1A	3619	1/1	0.96	0.07	19,19,19,19	0
56	MG	1A	3620	1/1	0.96	0.05	37,37,37,37	0
56	MG	1A	3946	1/1	0.96	0.08	49,49,49,49	0
56	MG	1A	3506	1/1	0.96	0.11	33,33,33,33	0
56	MG	2A	3597	1/1	0.96	0.06	36,36,36,36	0
56	MG	1A	3416	1/1	0.96	0.13	37,37,37,37	0
56	MG	2U	201	1/1	0.96	0.16	59,59,59,59	0
56	MG	1A	3418	1/1	0.96	0.13	53,53,53,53	0
56	MG	2A	3064	1/1	0.96	0.12	49,49,49,49	0
56	MG	1A	3279	1/1	0.96	0.05	40,40,40,40	0
56	MG	2A	3603	1/1	0.96	0.06	52,52,52,52	0
56	MG	1A	3420	1/1	0.96	0.10	52,52,52,52	0
56	MG	2W	204	1/1	0.96	0.04	53,53,53,53	0
56	MG	2A	3067	1/1	0.96	0.09	42,42,42,42	0
56	MG	1a	1693	1/1	0.96	0.34	62,62,62,62	0
56	MG	2A	3069	1/1	0.96	0.14	50,50,50,50	0
56	MG	2I	101	1/1	0.96	0.10	60,60,60,60	0
56	MG	2A	3608	1/1	0.96	0.11	55,55,55,55	0
56	MG	2A	3070	1/1	0.96	0.21	52,52,52,52	0
56	MG	1A	3628	1/1	0.96	0.09	36,36,36,36	0
56	MG	1A	3782	1/1	0.96	0.04	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3955	1/1	0.96	0.10	41,41,41,41	0
56	MG	2A	3614	1/1	0.96	0.15	48,48,48,48	0
56	MG	25	104	1/1	0.96	0.05	41,41,41,41	0
56	MG	1A	3630	1/1	0.96	0.11	40,40,40,40	0
56	MG	2A	3616	1/1	0.96	0.09	44,44,44,44	0
56	MG	1A	3784	1/1	0.96	0.11	50,50,50,50	0
56	MG	2A	3079	1/1	0.96	0.13	55,55,55,55	0
56	MG	1F	308	1/1	0.96	0.18	23,23,23,23	0
56	MG	1A	3073	1/1	0.96	0.08	30,30,30,30	0
56	MG	1A	3513	1/1	0.96	0.08	45,45,45,45	0
56	MG	2A	3623	1/1	0.96	0.07	36,36,36,36	0
56	MG	1A	3634	1/1	0.96	0.07	34,34,34,34	0
56	MG	2A	3086	1/1	0.96	0.14	56,56,56,56	0
56	MG	1A	3136	1/1	0.96	0.06	46,46,46,46	0
56	MG	2A	3088	1/1	0.96	0.07	52,52,52,52	0
56	MG	1A	3236	1/1	0.96	0.11	43,43,43,43	0
56	MG	1A	3967	1/1	0.96	0.11	59,59,59,59	0
56	MG	2A	3092	1/1	0.96	0.37	52,52,52,52	0
56	MG	1A	3284	1/1	0.96	0.24	31,31,31,31	0
56	MG	1G	203	1/1	0.96	0.07	80,80,80,80	0
56	MG	1A	3793	1/1	0.96	0.11	21,21,21,21	0
56	MG	1A	3970	1/1	0.96	0.08	67,67,67,67	0
56	MG	1A	3343	1/1	0.96	0.23	44,44,44,44	0
56	MG	2A	3098	1/1	0.96	0.09	53,53,53,53	0
56	MG	2A	3349	1/1	0.96	0.14	62,62,62,62	0
56	MG	1N	204	1/1	0.96	0.07	45,45,45,45	0
56	MG	2A	3640	1/1	0.96	0.08	49,49,49,49	0
56	MG	1A	3639	1/1	0.96	0.11	33,33,33,33	0
56	MG	1A	3973	1/1	0.96	0.09	55,55,55,55	0
56	MG	2A	3644	1/1	0.96	0.07	51,51,51,51	0
56	MG	1A	3061	1/1	0.96	0.19	48,48,48,48	0
56	MG	1a	1716	1/1	0.96	0.17	57,57,57,57	0
56	MG	2A	3647	1/1	0.96	0.10	57,57,57,57	0
56	MG	1A	3287	1/1	0.96	0.11	39,39,39,39	0
56	MG	2a	1627	1/1	0.96	0.20	56,56,56,56	0
56	MG	1A	3288	1/1	0.96	0.10	40,40,40,40	0
56	MG	1A	3803	1/1	0.96	0.05	32,32,32,32	0
56	MG	2A	3651	1/1	0.96	0.06	59,59,59,59	0
56	MG	2A	3652	1/1	0.96	0.06	61,61,61,61	0
56	MG	1A	3522	1/1	0.96	0.24	41,41,41,41	0
56	MG	1a	1721	1/1	0.96	0.08	45,45,45,45	0
56	MG	1A	3805	1/1	0.96	0.15	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3238	1/1	0.96	0.17	32,32,32,32	0
56	MG	1P	202	1/1	0.96	0.23	30,30,30,30	0
56	MG	2A	3658	1/1	0.96	0.06	38,38,38,38	0
56	MG	1P	203	1/1	0.96	0.20	31,31,31,31	0
56	MG	2a	1639	1/1	0.96	0.20	55,55,55,55	0
56	MG	1A	3646	1/1	0.96	0.07	16,16,16,16	0
56	MG	1A	3239	1/1	0.96	0.09	20,20,20,20	0
56	MG	1A	3985	1/1	0.96	0.05	43,43,43,43	0
56	MG	1A	3292	1/1	0.96	0.07	35,35,35,35	0
56	MG	1A	3649	1/1	0.96	0.10	25,25,25,25	0
56	MG	1R	202	1/1	0.96	0.18	43,43,43,43	0
56	MG	2a	1648	1/1	0.96	0.13	64,64,64,64	0
56	MG	1A	3354	1/1	0.96	0.13	33,33,33,33	0
56	MG	1A	3653	1/1	0.96	0.07	24,24,24,24	0
56	MG	1A	3816	1/1	0.96	0.19	47,47,47,47	0
56	MG	2A	3669	1/1	0.96	0.13	55,55,55,55	0
56	MG	2A	3670	1/1	0.96	0.25	77,77,77,77	0
56	MG	1A	3114	1/1	0.96	0.11	38,38,38,38	0
56	MG	1A	3655	1/1	0.96	0.14	44,44,44,44	0
56	MG	1A	3656	1/1	0.96	0.08	35,35,35,35	0
56	MG	1A	3530	1/1	0.96	0.21	49,49,49,49	0
56	MG	1U	205	1/1	0.96	0.05	35,35,35,35	0
56	MG	2A	3381	1/1	0.96	0.11	55,55,55,55	0
56	MG	1A	3077	1/1	0.96	0.05	27,27,27,27	0
56	MG	1A	4003	1/1	0.96	0.10	55,55,55,55	0
56	MG	2a	1662	1/1	0.96	0.17	58,58,58,58	0
56	MG	1V	202	1/1	0.96	0.08	34,34,34,34	0
56	MG	1A	3532	1/1	0.96	0.24	49,49,49,49	0
56	MG	2A	3681	1/1	0.96	0.07	58,58,58,58	0
56	MG	1a	1745	1/1	0.96	0.23	55,55,55,55	0
56	MG	1A	3437	1/1	0.96	0.08	47,47,47,47	0
56	MG	1A	3439	1/1	0.96	0.13	31,31,31,31	0
56	MG	1A	3011	1/1	0.96	0.10	33,33,33,33	0
56	MG	1a	1751	1/1	0.96	0.10	38,38,38,38	0
56	MG	2A	3687	1/1	0.96	0.06	62,62,62,62	0
56	MG	1A	3664	1/1	0.96	0.09	21,21,21,21	0
56	MG	1A	3537	1/1	0.96	0.18	42,42,42,42	0
56	MG	1a	1754	1/1	0.96	0.06	60,60,60,60	0
56	MG	1a	1755	1/1	0.96	0.10	55,55,55,55	0
56	MG	1A	3146	1/1	0.96	0.12	54,54,54,54	0
56	MG	1a	1758	1/1	0.96	0.07	41,41,41,41	0
56	MG	1A	3362	1/1	0.96	0.15	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	3150	1/1	0.96	0.11	51,51,51,51	0
56	MG	1X	101	1/1	0.96	0.05	23,23,23,23	0
56	MG	1X	103	1/1	0.96	0.14	40,40,40,40	0
56	MG	1X	105	1/1	0.96	0.20	41,41,41,41	0
56	MG	2a	1683	1/1	0.96	0.09	63,63,63,63	0
56	MG	1A	3670	1/1	0.96	0.05	26,26,26,26	0
56	MG	1A	4014	1/1	0.96	0.09	47,47,47,47	0
56	MG	2A	3702	1/1	0.96	0.07	45,45,45,45	0
56	MG	1A	3245	1/1	0.96	0.15	46,46,46,46	0
56	MG	1A	3673	1/1	0.96	0.09	30,30,30,30	0
56	MG	1A	3446	1/1	0.96	0.09	45,45,45,45	0
56	MG	1A	3447	1/1	0.96	0.09	43,43,43,43	0
56	MG	1A	3364	1/1	0.96	0.13	45,45,45,45	0
56	MG	1A	3150	1/1	0.96	0.09	40,40,40,40	0
56	MG	1A	3197	1/1	0.96	0.14	25,25,25,25	0
56	MG	1A	3451	1/1	0.96	0.10	53,53,53,53	0
56	MG	2A	3714	1/1	0.96	0.07	35,35,35,35	0
56	MG	1l	103	1/1	0.96	0.06	36,36,36,36	0
56	MG	1A	3118	1/1	0.96	0.12	34,34,34,34	0
56	MG	2A	3415	1/1	0.96	0.21	39,39,39,39	0
56	MG	1A	3551	1/1	0.96	0.12	27,27,27,27	0
56	MG	1A	3851	1/1	0.96	0.06	17,17,17,17	0
56	MG	2A	3172	1/1	0.96	0.09	57,57,57,57	0
56	MG	2A	3722	1/1	0.96	0.18	64,64,64,64	0
56	MG	1A	3453	1/1	0.96	0.27	62,62,62,62	0
56	MG	2A	3174	1/1	0.96	0.12	37,37,37,37	0
56	MG	2A	3725	1/1	0.96	0.12	53,53,53,53	0
56	MG	1A	3687	1/1	0.96	0.05	20,20,20,20	0
56	MG	2a	1709	1/1	0.96	0.06	53,53,53,53	0
56	MG	1A	3084	1/1	0.96	0.09	43,43,43,43	0
56	MG	2A	3178	1/1	0.96	0.10	45,45,45,45	0
56	MG	1A	3153	1/1	0.96	0.25	35,35,35,35	0
56	MG	1a	1783	1/1	0.96	0.11	54,54,54,54	0
56	MG	15	102	1/1	0.96	0.27	29,29,29,29	0
56	MG	1A	3857	1/1	0.96	0.09	43,43,43,43	0
56	MG	1A	3693	1/1	0.96	0.08	36,36,36,36	0
56	MG	1A	4037	1/1	0.96	0.09	27,27,27,27	0
56	MG	2A	3186	1/1	0.96	0.05	60,60,60,60	0
56	MG	1A	3860	1/1	0.96	0.06	23,23,23,23	0
56	MG	1a	1790	1/1	0.96	0.08	76,76,76,76	0
56	MG	1a	1791	1/1	0.96	0.18	61,61,61,61	0
56	MG	2A	3191	1/1	0.96	0.06	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3742	1/1	0.96	0.06	33,33,33,33	0
56	MG	1A	3252	1/1	0.96	0.12	40,40,40,40	0
56	MG	2A	3193	1/1	0.96	0.10	55,55,55,55	0
56	MG	17	103	1/1	0.96	0.17	45,45,45,45	0
56	MG	1A	3373	1/1	0.96	0.23	39,39,39,39	0
56	MG	17	105	1/1	0.96	0.11	39,39,39,39	0
56	MG	1A	3558	1/1	0.96	0.07	49,49,49,49	0
56	MG	1A	3374	1/1	0.96	0.12	34,34,34,34	0
56	MG	18	102	1/1	0.96	0.10	33,33,33,33	0
56	MG	1a	1801	1/1	0.96	0.13	57,57,57,57	0
56	MG	1a	1802	1/1	0.96	0.06	68,68,68,68	0
56	MG	2A	3202	1/1	0.96	0.16	56,56,56,56	0
56	MG	1A	3310	1/1	0.96	0.11	45,45,45,45	0
56	MG	1A	3463	1/1	0.96	0.06	65,65,65,65	0
56	MG	1A	3376	1/1	0.96	0.07	42,42,42,42	0
56	MG	1A	3378	1/1	0.96	0.19	40,40,40,40	0
56	MG	1A	3205	1/1	0.96	0.07	33,33,33,33	0
56	MG	2A	3762	1/1	0.96	0.07	62,62,62,62	0
56	MG	1A	3381	1/1	0.96	0.10	53,53,53,53	0
56	MG	1A	3154	1/1	0.96	0.10	35,35,35,35	0
56	MG	1A	3035	1/1	0.96	0.17	23,23,23,23	0
56	MG	1A	4054	1/1	0.96	0.07	15,15,15,15	0
56	MG	2A	3458	1/1	0.96	0.20	44,44,44,44	0
56	MG	1A	3126	1/1	0.96	0.13	49,49,49,49	0
56	MG	2A	3770	1/1	0.96	0.05	46,46,46,46	0
56	MG	1a	1815	1/1	0.96	0.16	63,63,63,63	0
56	MG	1A	4056	1/1	0.96	0.05	40,40,40,40	0
56	MG	1A	3388	1/1	0.96	0.23	45,45,45,45	0
56	MG	1A	3477	1/1	0.96	0.06	48,48,48,48	0
56	MG	2A	3776	1/1	0.96	0.06	32,32,32,32	0
56	MG	1A	4060	1/1	0.96	0.05	11,11,11,11	0
56	MG	2a	1755	1/1	0.96	0.19	68,68,68,68	0
56	MG	1A	3160	1/1	0.96	0.07	36,36,36,36	0
56	MG	1A	3055	1/1	0.96	0.07	51,51,51,51	0
56	MG	2A	3780	1/1	0.96	0.07	57,57,57,57	0
56	MG	1A	3881	1/1	0.96	0.08	22,22,22,22	0
56	MG	2A	3470	1/1	0.96	0.15	53,53,53,53	0
56	MG	1A	3259	1/1	0.96	0.10	25,25,25,25	0
56	MG	1A	3261	1/1	0.96	0.05	29,29,29,29	0
56	MG	2A	3226	1/1	0.96	0.07	30,30,30,30	0
56	MG	1A	3723	1/1	0.96	0.14	47,47,47,47	0
56	MG	2A	3475	1/1	0.96	0.15	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	3476	1/1	0.96	0.09	69,69,69,69	0
56	MG	1A	3886	1/1	0.96	0.15	39,39,39,39	0
56	MG	1A	3887	1/1	0.96	0.07	46,46,46,46	0
56	MG	1A	3320	1/1	0.96	0.18	59,59,59,59	0
56	MG	1A	3585	1/1	0.96	0.14	41,41,41,41	0
56	MG	1A	4075	1/1	0.96	0.09	50,50,50,50	0
56	MG	2A	3236	1/1	0.96	0.06	49,49,49,49	0
56	MG	1A	3890	1/1	0.96	0.14	43,43,43,43	0
56	MG	1A	3322	1/1	0.96	0.23	37,37,37,37	0
56	MG	1m	3001	1/1	0.96	0.06	74,74,74,74	0
56	MG	2A	3240	1/1	0.96	0.07	68,68,68,68	0
56	MG	1A	3894	1/1	0.96	0.04	35,35,35,35	0
56	MG	2e	201	1/1	0.96	0.06	57,57,57,57	0
56	MG	2f	201	1/1	0.96	0.11	51,51,51,51	0
56	MG	2A	3490	1/1	0.96	0.16	46,46,46,46	0
56	MG	1p	101	1/1	0.96	0.23	61,61,61,61	0
56	MG	1A	3895	1/1	0.96	0.16	44,44,44,44	0
56	MG	1A	3216	1/1	0.96	0.09	38,38,38,38	0
56	MG	1a	1632	1/1	0.96	0.18	64,64,64,64	0
56	MG	1v	104	1/1	0.96	0.10	70,70,70,70	0
56	MG	1w	401	1/1	0.96	0.08	59,59,59,59	0
56	MG	1A	3218	1/1	0.96	0.12	50,50,50,50	0
56	MG	1a	1636	1/1	0.96	0.25	62,62,62,62	0
56	MG	2A	3501	1/1	0.96	0.11	41,41,41,41	0
56	MG	2A	3817	1/1	0.96	0.08	56,56,56,56	0
56	MG	1A	3166	1/1	0.96	0.04	40,40,40,40	0
56	MG	1A	3490	1/1	0.96	0.24	34,34,34,34	0
56	MG	1A	3901	1/1	0.96	0.07	28,28,28,28	0
56	MG	1B	204	1/1	0.96	0.15	46,46,46,46	0
56	MG	1A	3221	1/1	0.96	0.26	68,68,68,68	0
56	MG	1B	206	1/1	0.96	0.06	40,40,40,40	0
56	MG	1A	3738	1/1	0.96	0.06	44,44,44,44	0
56	MG	1B	208	1/1	0.96	0.10	69,69,69,69	0
56	MG	2A	3511	1/1	0.96	0.12	56,56,56,56	0
56	MG	2A	3512	1/1	0.96	0.17	35,35,35,35	0
56	MG	2A	3370	1/1	0.97	0.24	56,56,56,56	0
56	MG	2A	3146	1/1	0.97	0.21	46,46,46,46	0
56	MG	2A	3372	1/1	0.97	0.05	41,41,41,41	0
56	MG	1A	3193	1/1	0.97	0.21	23,23,23,23	0
56	MG	2A	3374	1/1	0.97	0.08	43,43,43,43	0
56	MG	2A	3148	1/1	0.97	0.09	38,38,38,38	0
56	MG	1A	3137	1/1	0.97	0.09	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2D	304	1/1	0.97	0.04	29,29,29,29	0
56	MG	2D	305	1/1	0.97	0.17	37,37,37,37	0
56	MG	2D	306	1/1	0.97	0.07	48,48,48,48	0
56	MG	1A	3024	1/1	0.97	0.08	33,33,33,33	0
56	MG	1A	3045	1/1	0.97	0.09	32,32,32,32	0
56	MG	1A	3761	1/1	0.97	0.08	43,43,43,43	0
56	MG	1A	3762	1/1	0.97	0.07	15,15,15,15	0
56	MG	1A	3141	1/1	0.97	0.09	36,36,36,36	0
56	MG	1a	1794	1/1	0.97	0.13	60,60,60,60	0
56	MG	1A	3627	1/1	0.97	0.09	22,22,22,22	0
56	MG	1A	3200	1/1	0.97	0.09	33,33,33,33	0
56	MG	1A	3766	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3767	1/1	0.97	0.04	20,20,20,20	0
56	MG	1a	1799	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	3025	1/1	0.97	0.14	30,30,30,30	0
56	MG	1A	3202	1/1	0.97	0.16	47,47,47,47	0
56	MG	1A	3204	1/1	0.97	0.06	35,35,35,35	0
56	MG	1A	3144	1/1	0.97	0.07	16,16,16,16	0
56	MG	1a	1613	1/1	0.97	0.10	29,29,29,29	0
56	MG	2A	3169	1/1	0.97	0.08	58,58,58,58	0
56	MG	1A	3068	1/1	0.97	0.12	37,37,37,37	0
56	MG	2Q	204	1/1	0.97	0.12	46,46,46,46	0
56	MG	2A	3643	1/1	0.97	0.07	42,42,42,42	0
56	MG	1A	3523	1/1	0.97	0.18	43,43,43,43	0
56	MG	1A	3208	1/1	0.97	0.12	35,35,35,35	0
56	MG	1A	3007	1/1	0.97	0.08	37,37,37,37	0
56	MG	1B	212	1/1	0.97	0.16	31,31,31,31	0
56	MG	1a	1619	1/1	0.97	0.10	50,50,50,50	0
56	MG	1B	213	1/1	0.97	0.08	46,46,46,46	0
56	MG	2A	3177	1/1	0.97	0.08	65,65,65,65	0
56	MG	1a	1812	1/1	0.97	0.06	69,69,69,69	0
56	MG	2V	202	1/1	0.97	0.20	59,59,59,59	0
56	MG	1A	3931	1/1	0.97	0.06	53,53,53,53	0
56	MG	1A	3148	1/1	0.97	0.13	28,28,28,28	0
56	MG	1A	3778	1/1	0.97	0.06	31,31,31,31	0
56	MG	2A	3406	1/1	0.97	0.10	40,40,40,40	0
56	MG	1A	3211	1/1	0.97	0.06	51,51,51,51	0
56	MG	1A	3641	1/1	0.97	0.05	47,47,47,47	0
56	MG	1A	3271	1/1	0.97	0.11	45,45,45,45	0
56	MG	1A	3937	1/1	0.97	0.07	37,37,37,37	0
56	MG	1a	1823	1/1	0.97	0.09	50,50,50,50	0
56	MG	1A	3347	1/1	0.97	0.19	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3048	1/1	0.97	0.06	32,32,32,32	0
56	MG	2A	3190	1/1	0.97	0.33	59,59,59,59	0
56	MG	1A	3785	1/1	0.97	0.09	56,56,56,56	0
56	MG	1d	301	1/1	0.97	0.19	39,39,39,39	0
56	MG	1A	3273	1/1	0.97	0.12	38,38,38,38	0
56	MG	1A	3533	1/1	0.97	0.11	23,23,23,23	0
56	MG	1a	1634	1/1	0.97	0.13	49,49,49,49	0
56	MG	1A	3108	1/1	0.97	0.06	36,36,36,36	0
56	MG	1A	3275	1/1	0.97	0.07	39,39,39,39	0
56	MG	1A	3214	1/1	0.97	0.07	41,41,41,41	0
56	MG	1A	3650	1/1	0.97	0.07	29,29,29,29	0
56	MG	1A	3651	1/1	0.97	0.06	25,25,25,25	0
56	MG	2A	3425	1/1	0.97	0.11	49,49,49,49	0
56	MG	1A	3950	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	3441	1/1	0.97	0.09	32,32,32,32	0
56	MG	2A	3203	1/1	0.97	0.06	56,56,56,56	0
56	MG	1D	301	1/1	0.97	0.07	33,33,33,33	0
56	MG	1A	3278	1/1	0.97	0.13	35,35,35,35	0
56	MG	1t	201	1/1	0.97	0.16	62,62,62,62	0
56	MG	2A	3432	1/1	0.97	0.11	57,57,57,57	0
56	MG	1D	303	1/1	0.97	0.04	38,38,38,38	0
56	MG	1A	3798	1/1	0.97	0.07	24,24,24,24	0
56	MG	1A	3799	1/1	0.97	0.10	26,26,26,26	0
56	MG	1A	3357	1/1	0.97	0.07	50,50,50,50	0
56	MG	1A	3444	1/1	0.97	0.20	34,34,34,34	0
56	MG	1A	3957	1/1	0.97	0.05	30,30,30,30	0
56	MG	2A	3688	1/1	0.97	0.10	48,48,48,48	0
56	MG	1A	3215	1/1	0.97	0.23	31,31,31,31	0
56	MG	2A	3215	1/1	0.97	0.19	56,56,56,56	0
56	MG	1A	3959	1/1	0.97	0.07	49,49,49,49	0
56	MG	1A	3960	1/1	0.97	0.08	41,41,41,41	0
56	MG	1a	1654	1/1	0.97	0.11	56,56,56,56	0
56	MG	1x	106	1/1	0.97	0.16	45,45,45,45	0
56	MG	1a	1656	1/1	0.97	0.07	62,62,62,62	0
56	MG	1A	3359	1/1	0.97	0.07	48,48,48,48	0
56	MG	1A	3074	1/1	0.97	0.19	32,32,32,32	0
56	MG	1A	3659	1/1	0.97	0.06	32,32,32,32	0
56	MG	1E	303	1/1	0.97	0.08	32,32,32,32	0
56	MG	1E	304	1/1	0.97	0.14	34,34,34,34	0
56	MG	1A	3964	1/1	0.97	0.09	33,33,33,33	0
56	MG	1A	3217	1/1	0.97	0.07	49,49,49,49	0
56	MG	1A	3111	1/1	0.97	0.22	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	3546	1/1	0.97	0.16	31,31,31,31	0
56	MG	2A	3455	1/1	0.97	0.07	62,62,62,62	0
56	MG	1A	3219	1/1	0.97	0.22	39,39,39,39	0
56	MG	2A	3708	1/1	0.97	0.17	61,61,61,61	0
56	MG	1A	3549	1/1	0.97	0.16	32,32,32,32	0
56	MG	1E	313	1/1	0.97	0.10	20,20,20,20	0
56	MG	1A	3027	1/1	0.97	0.10	40,40,40,40	0
56	MG	2A	3010	1/1	0.97	0.10	50,50,50,50	0
56	MG	1A	3666	1/1	0.97	0.04	21,21,21,21	0
56	MG	1E	317	1/1	0.97	0.05	50,50,50,50	0
56	MG	2a	1644	1/1	0.97	0.11	36,36,36,36	0
56	MG	1F	301	1/1	0.97	0.18	28,28,28,28	0
56	MG	2A	3465	1/1	0.97	0.11	22,22,22,22	0
56	MG	1F	302	1/1	0.97	0.12	28,28,28,28	0
56	MG	1A	3365	1/1	0.97	0.10	52,52,52,52	0
56	MG	1A	3013	1/1	0.97	0.08	22,22,22,22	0
56	MG	1A	3974	1/1	0.97	0.10	27,27,27,27	0
56	MG	1A	3156	1/1	0.97	0.09	34,34,34,34	0
56	MG	1A	3819	1/1	0.97	0.04	47,47,47,47	0
56	MG	2A	3021	1/1	0.97	0.06	24,24,24,24	0
56	MG	1A	3157	1/1	0.97	0.17	38,38,38,38	0
56	MG	1A	3672	1/1	0.97	0.08	22,22,22,22	0
56	MG	1A	3369	1/1	0.97	0.11	55,55,55,55	0
56	MG	1A	3458	1/1	0.97	0.15	40,40,40,40	0
56	MG	2A	3730	1/1	0.97	0.05	69,69,69,69	0
56	MG	1A	3079	1/1	0.97	0.15	54,54,54,54	0
56	MG	2A	3028	1/1	0.97	0.13	51,51,51,51	0
56	MG	1A	3460	1/1	0.97	0.17	44,44,44,44	0
56	MG	2A	3734	1/1	0.97	0.10	29,29,29,29	0
56	MG	1A	3828	1/1	0.97	0.06	38,38,38,38	0
56	MG	1A	3560	1/1	0.97	0.04	21,21,21,21	0
56	MG	1A	3225	1/1	0.97	0.04	28,28,28,28	0
56	MG	1A	3294	1/1	0.97	0.14	42,42,42,42	0
56	MG	1N	202	1/1	0.97	0.19	37,37,37,37	0
56	MG	2A	3261	1/1	0.97	0.13	52,52,52,52	0
56	MG	1A	3832	1/1	0.97	0.11	52,52,52,52	0
56	MG	1A	3015	1/1	0.97	0.15	25,25,25,25	0
56	MG	2A	3488	1/1	0.97	0.15	44,44,44,44	0
56	MG	2A	3745	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3565	1/1	0.97	0.22	32,32,32,32	0
56	MG	1A	3228	1/1	0.97	0.12	44,44,44,44	0
56	MG	1A	3567	1/1	0.97	0.19	36,36,36,36	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	0.97	0.10	43,43,43,43	0
56	MG	1A	3689	1/1	0.97	0.06	28,28,28,28	0
56	MG	1A	3840	1/1	0.97	0.10	56,56,56,56	0
56	MG	1A	4001	1/1	0.97	0.11	23,23,23,23	0
56	MG	1A	3230	1/1	0.97	0.09	40,40,40,40	0
56	MG	2A	3047	1/1	0.97	0.21	50,50,50,50	0
56	MG	1A	3165	1/1	0.97	0.19	33,33,33,33	0
56	MG	1A	3468	1/1	0.97	0.16	48,48,48,48	0
56	MG	1A	3695	1/1	0.97	0.06	19,19,19,19	0
56	MG	2A	3758	1/1	0.97	0.11	32,32,32,32	0
56	MG	1P	205	1/1	0.97	0.10	41,41,41,41	0
56	MG	2A	3052	1/1	0.97	0.09	54,54,54,54	0
56	MG	1A	3696	1/1	0.97	0.06	21,21,21,21	0
56	MG	1A	3847	1/1	0.97	0.06	14,14,14,14	0
56	MG	1Q	202	1/1	0.97	0.10	33,33,33,33	0
56	MG	2A	3509	1/1	0.97	0.09	56,56,56,56	0
56	MG	1Q	203	1/1	0.97	0.05	37,37,37,37	0
56	MG	1A	3301	1/1	0.97	0.09	36,36,36,36	0
56	MG	1A	3232	1/1	0.97	0.28	31,31,31,31	0
56	MG	2A	3060	1/1	0.97	0.12	54,54,54,54	0
56	MG	1A	3119	1/1	0.97	0.11	38,38,38,38	0
56	MG	2a	1697	1/1	0.97	0.19	66,66,66,66	0
56	MG	1R	201	1/1	0.97	0.06	40,40,40,40	0
56	MG	2A	3772	1/1	0.97	0.06	54,54,54,54	0
56	MG	1a	1713	1/1	0.97	0.11	47,47,47,47	0
56	MG	1A	3852	1/1	0.97	0.10	23,23,23,23	0
56	MG	1R	204	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3472	1/1	0.97	0.07	37,37,37,37	0
56	MG	1A	3474	1/1	0.97	0.16	35,35,35,35	0
56	MG	1A	4016	1/1	0.97	0.06	54,54,54,54	0
56	MG	1A	3383	1/1	0.97	0.14	39,39,39,39	0
56	MG	1A	3581	1/1	0.97	0.08	23,23,23,23	0
56	MG	1A	3582	1/1	0.97	0.04	31,31,31,31	0
56	MG	2A	3527	1/1	0.97	0.14	67,67,67,67	0
56	MG	2A	3783	1/1	0.97	0.06	34,34,34,34	0
56	MG	1U	202	1/1	0.97	0.35	35,35,35,35	0
56	MG	1A	3858	1/1	0.97	0.09	43,43,43,43	0
56	MG	1U	204	1/1	0.97	0.18	37,37,37,37	0
56	MG	2A	3076	1/1	0.97	0.07	42,42,42,42	0
56	MG	1A	4021	1/1	0.97	0.09	39,39,39,39	0
56	MG	2A	3534	1/1	0.97	0.20	58,58,58,58	0
56	MG	1U	207	1/1	0.97	0.32	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1U	208	1/1	0.97	0.10	29,29,29,29	0
56	MG	1A	3384	1/1	0.97	0.35	24,24,24,24	0
56	MG	2a	1721	1/1	0.97	0.09	48,48,48,48	0
56	MG	1U	210	1/1	0.97	0.21	32,32,32,32	0
56	MG	2A	3540	1/1	0.97	0.05	60,60,60,60	0
56	MG	2A	3083	1/1	0.97	0.13	55,55,55,55	0
56	MG	1A	3304	1/1	0.97	0.18	31,31,31,31	0
56	MG	2A	3085	1/1	0.97	0.06	49,49,49,49	0
56	MG	1A	3386	1/1	0.97	0.17	21,21,21,21	0
56	MG	2A	3545	1/1	0.97	0.14	44,44,44,44	0
56	MG	2A	3309	1/1	0.97	0.07	54,54,54,54	0
56	MG	1V	204	1/1	0.97	0.09	49,49,49,49	0
56	MG	1A	3017	1/1	0.97	0.08	62,62,62,62	0
56	MG	2A	3549	1/1	0.97	0.08	36,36,36,36	0
56	MG	2A	3807	1/1	0.97	0.08	47,47,47,47	0
56	MG	1A	3032	1/1	0.97	0.17	30,30,30,30	0
56	MG	1A	3124	1/1	0.97	0.13	48,48,48,48	0
56	MG	2A	3552	1/1	0.97	0.05	46,46,46,46	0
56	MG	1A	3125	1/1	0.97	0.18	29,29,29,29	0
56	MG	1A	3010	1/1	0.97	0.09	33,33,33,33	0
56	MG	1A	3056	1/1	0.97	0.05	46,46,46,46	0
56	MG	1A	3718	1/1	0.97	0.04	14,14,14,14	0
56	MG	1A	3174	1/1	0.97	0.09	49,49,49,49	0
56	MG	2A	3819	1/1	0.97	0.04	32,32,32,32	0
56	MG	2A	3320	1/1	0.97	0.05	49,49,49,49	0
56	MG	2A	3321	1/1	0.97	0.10	53,53,53,53	0
56	MG	1A	3720	1/1	0.97	0.08	29,29,29,29	0
56	MG	1A	3394	1/1	0.97	0.16	40,40,40,40	0
56	MG	2A	3825	1/1	0.97	0.04	43,43,43,43	0
56	MG	2A	3830	1/1	0.97	0.05	44,44,44,44	0
56	MG	2A	3831	1/1	0.97	0.08	49,49,49,49	0
56	MG	2A	3562	1/1	0.97	0.04	36,36,36,36	0
56	MG	1a	1743	1/1	0.97	0.16	63,63,63,63	0
56	MG	1A	3241	1/1	0.97	0.13	35,35,35,35	0
56	MG	1X	106	1/1	0.97	0.08	43,43,43,43	0
56	MG	1A	3057	1/1	0.97	0.07	24,24,24,24	0
56	MG	1A	3179	1/1	0.97	0.06	25,25,25,25	0
56	MG	1A	3180	1/1	0.97	0.13	29,29,29,29	0
56	MG	1a	1749	1/1	0.97	0.10	45,45,45,45	0
56	MG	1A	3317	1/1	0.97	0.17	48,48,48,48	0
56	MG	1A	3058	1/1	0.97	0.16	44,44,44,44	0
56	MG	2A	3108	1/1	0.97	0.07	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	10	101	1/1	0.97	0.04	45,45,45,45	0
56	MG	1A	3880	1/1	0.97	0.08	27,27,27,27	0
56	MG	2A	3111	1/1	0.97	0.17	51,51,51,51	0
56	MG	1A	3059	1/1	0.97	0.08	17,17,17,17	0
56	MG	2a	1765	1/1	0.97	0.11	68,68,68,68	0
56	MG	1A	4046	1/1	0.97	0.04	16,16,16,16	0
56	MG	1a	1757	1/1	0.97	0.08	59,59,59,59	0
56	MG	1A	3882	1/1	0.97	0.12	30,30,30,30	0
56	MG	1A	3735	1/1	0.97	0.09	23,23,23,23	0
56	MG	1A	4049	1/1	0.97	0.05	37,37,37,37	0
56	MG	2A	3856	1/1	0.97	0.11	52,52,52,52	0
56	MG	1A	3019	1/1	0.97	0.07	47,47,47,47	0
56	MG	1A	3321	1/1	0.97	0.11	25,25,25,25	0
56	MG	1A	3604	1/1	0.97	0.08	46,46,46,46	0
56	MG	2A	3587	1/1	0.97	0.09	58,58,58,58	0
56	MG	1a	1764	1/1	0.97	0.07	64,64,64,64	0
56	MG	2A	3862	1/1	0.97	0.14	60,60,60,60	0
56	MG	12	103	1/1	0.97	0.08	44,44,44,44	0
56	MG	1A	3037	1/1	0.97	0.05	39,39,39,39	0
56	MG	13	102	1/1	0.97	0.11	34,34,34,34	0
56	MG	1A	3188	1/1	0.97	0.04	40,40,40,40	0
56	MG	1A	3609	1/1	0.97	0.12	44,44,44,44	0
56	MG	2A	3596	1/1	0.97	0.16	59,59,59,59	0
56	MG	13	106	1/1	0.97	0.09	51,51,51,51	0
56	MG	1A	3744	1/1	0.97	0.12	42,42,42,42	0
56	MG	1A	3406	1/1	0.97	0.18	46,46,46,46	0
56	MG	1a	1773	1/1	0.97	0.08	60,60,60,60	0
56	MG	2A	3601	1/1	0.97	0.06	57,57,57,57	0
56	MG	1A	3324	1/1	0.97	0.09	31,31,31,31	0
56	MG	15	105	1/1	0.97	0.19	36,36,36,36	0
56	MG	1A	3250	1/1	0.97	0.26	30,30,30,30	0
56	MG	1A	3505	1/1	0.97	0.18	21,21,21,21	0
56	MG	2A	3137	1/1	0.97	0.09	26,26,26,26	0
56	MG	1A	3616	1/1	0.97	0.06	32,32,32,32	0
56	MG	1A	3189	1/1	0.97	0.06	42,42,42,42	0
56	MG	1A	3899	1/1	0.97	0.13	29,29,29,29	0
56	MG	1A	3040	1/1	0.97	0.09	35,35,35,35	0
56	MG	1A	3413	1/1	0.97	0.06	52,52,52,52	0
56	MG	1A	3903	1/1	0.97	0.06	20,20,20,20	0
56	MG	17	107	1/1	0.97	0.05	45,45,45,45	0
56	MG	1A	3042	1/1	0.97	0.04	39,39,39,39	0
56	MG	1a	1622	1/1	0.98	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	2A	3227	1/1	0.98	0.07	49,49,49,49	0
56	MG	1A	3432	1/1	0.98	0.15	41,41,41,41	0
56	MG	1A	3710	1/1	0.98	0.05	31,31,31,31	0
56	MG	1A	3433	1/1	0.98	0.20	34,34,34,34	0
56	MG	1A	4027	1/1	0.98	0.05	50,50,50,50	0
56	MG	1A	3910	1/1	0.98	0.09	53,53,53,53	0
56	MG	2A	3233	1/1	0.98	0.08	48,48,48,48	0
56	MG	2A	3234	1/1	0.98	0.06	40,40,40,40	0
56	MG	1A	4029	1/1	0.98	0.05	50,50,50,50	0
56	MG	2A	3765	1/1	0.98	0.06	60,60,60,60	0
56	MG	1A	3911	1/1	0.98	0.11	33,33,33,33	0
56	MG	1A	3183	1/1	0.98	0.03	25,25,25,25	0
56	MG	1A	3081	1/1	0.98	0.05	44,44,44,44	0
56	MG	1G	202	1/1	0.98	0.10	55,55,55,55	0
56	MG	2A	3074	1/1	0.98	0.11	44,44,44,44	0
56	MG	1A	3914	1/1	0.98	0.04	53,53,53,53	0
56	MG	1A	3631	1/1	0.98	0.07	17,17,17,17	0
56	MG	2A	3077	1/1	0.98	0.07	26,26,26,26	0
56	MG	2A	3591	1/1	0.98	0.04	38,38,38,38	0
56	MG	1a	1635	1/1	0.98	0.10	34,34,34,34	0
56	MG	1A	3293	1/1	0.98	0.04	47,47,47,47	0
56	MG	1A	3814	1/1	0.98	0.05	38,38,38,38	0
56	MG	1A	3071	1/1	0.98	0.11	23,23,23,23	0
56	MG	1A	3438	1/1	0.98	0.15	32,32,32,32	0
56	MG	1A	3295	1/1	0.98	0.15	28,28,28,28	0
56	MG	1A	3095	1/1	0.98	0.05	40,40,40,40	0
56	MG	1A	3130	1/1	0.98	0.18	31,31,31,31	0
56	MG	1a	1787	1/1	0.98	0.14	63,63,63,63	0
56	MG	2A	3784	1/1	0.98	0.04	51,51,51,51	0
56	MG	1A	3820	1/1	0.98	0.30	29,29,29,29	0
56	MG	2A	3254	1/1	0.98	0.04	49,49,49,49	0
56	MG	1A	3721	1/1	0.98	0.10	46,46,46,46	0
56	MG	1A	3927	1/1	0.98	0.05	32,32,32,32	0
56	MG	1A	3564	1/1	0.98	0.10	23,23,23,23	0
56	MG	2A	3091	1/1	0.98	0.12	39,39,39,39	0
56	MG	1A	3823	1/1	0.98	0.04	25,25,25,25	0
56	MG	2a	1641	1/1	0.98	0.12	52,52,52,52	0
56	MG	1A	3930	1/1	0.98	0.03	50,50,50,50	0
56	MG	1P	201	1/1	0.98	0.20	29,29,29,29	0
56	MG	1A	3096	1/1	0.98	0.12	23,23,23,23	0
56	MG	1A	3112	1/1	0.98	0.17	32,32,32,32	0
56	MG	1P	204	1/1	0.98	0.26	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3797	1/1	0.98	0.12	61,61,61,61	0
56	MG	2A	3613	1/1	0.98	0.10	46,46,46,46	0
56	MG	1A	3021	1/1	0.98	0.03	16,16,16,16	0
56	MG	1A	3568	1/1	0.98	0.14	34,34,34,34	0
56	MG	1a	1655	1/1	0.98	0.09	48,48,48,48	0
56	MG	1A	3260	1/1	0.98	0.03	32,32,32,32	0
56	MG	1A	4053	1/1	0.98	0.03	32,32,32,32	0
56	MG	2A	3619	1/1	0.98	0.06	33,33,33,33	0
56	MG	1A	3227	1/1	0.98	0.05	42,42,42,42	0
56	MG	1a	1659	1/1	0.98	0.06	72,72,72,72	0
56	MG	2A	3808	1/1	0.98	0.08	60,60,60,60	0
56	MG	1A	3732	1/1	0.98	0.07	43,43,43,43	0
56	MG	2A	3810	1/1	0.98	0.07	53,53,53,53	0
56	MG	1A	3938	1/1	0.98	0.04	46,46,46,46	0
56	MG	1A	3571	1/1	0.98	0.14	36,36,36,36	0
56	MG	1A	3039	1/1	0.98	0.09	15,15,15,15	0
56	MG	1A	3941	1/1	0.98	0.11	58,58,58,58	0
56	MG	1R	203	1/1	0.98	0.12	41,41,41,41	0
56	MG	1A	3573	1/1	0.98	0.16	30,30,30,30	0
56	MG	1A	3346	1/1	0.98	0.21	38,38,38,38	0
56	MG	2A	3818	1/1	0.98	0.07	46,46,46,46	0
56	MG	1A	3005	1/1	0.98	0.05	35,35,35,35	0
56	MG	1a	1814	1/1	0.98	0.07	68,68,68,68	0
56	MG	1A	4065	1/1	0.98	0.08	41,41,41,41	0
56	MG	1A	4066	1/1	0.98	0.04	30,30,30,30	0
56	MG	1a	1817	1/1	0.98	0.08	70,70,70,70	0
56	MG	2A	3824	1/1	0.98	0.04	44,44,44,44	0
56	MG	1A	3836	1/1	0.98	0.18	53,53,53,53	0
56	MG	2A	3826	1/1	0.98	0.05	44,44,44,44	0
56	MG	2A	3827	1/1	0.98	0.10	46,46,46,46	0
56	MG	2A	3828	1/1	0.98	0.04	65,65,65,65	0
56	MG	2A	3829	1/1	0.98	0.04	44,44,44,44	0
56	MG	1A	3348	1/1	0.98	0.14	33,33,33,33	0
56	MG	2A	3120	1/1	0.98	0.07	31,31,31,31	0
56	MG	2A	3638	1/1	0.98	0.08	42,42,42,42	0
56	MG	1U	201	1/1	0.98	0.14	32,32,32,32	0
56	MG	1A	3510	1/1	0.98	0.13	27,27,27,27	0
56	MG	1A	3742	1/1	0.98	0.05	58,58,58,58	0
56	MG	2A	3836	1/1	0.98	0.04	36,36,36,36	0
56	MG	2A	3837	1/1	0.98	0.06	50,50,50,50	0
56	MG	2A	3459	1/1	0.98	0.17	51,51,51,51	0
56	MG	1A	4071	1/1	0.98	0.05	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	3349	1/1	0.98	0.12	39,39,39,39	0
56	MG	1A	3194	1/1	0.98	0.18	32,32,32,32	0
56	MG	1A	3842	1/1	0.98	0.07	44,44,44,44	0
56	MG	1A	3116	1/1	0.98	0.05	28,28,28,28	0
56	MG	1A	4077	1/1	0.98	0.03	42,42,42,42	0
56	MG	2A	3130	1/1	0.98	0.04	47,47,47,47	0
56	MG	1A	3307	1/1	0.98	0.12	28,28,28,28	0
56	MG	1A	3041	1/1	0.98	0.19	30,30,30,30	0
56	MG	1A	3749	1/1	0.98	0.06	15,15,15,15	0
56	MG	1A	3456	1/1	0.98	0.08	34,34,34,34	0
56	MG	1A	3162	1/1	0.98	0.17	33,33,33,33	0
56	MG	1A	3849	1/1	0.98	0.14	51,51,51,51	0
56	MG	1A	3355	1/1	0.98	0.21	61,61,61,61	0
56	MG	1A	3163	1/1	0.98	0.19	38,38,38,38	0
56	MG	1A	3164	1/1	0.98	0.21	33,33,33,33	0
56	MG	1A	3521	1/1	0.98	0.14	38,38,38,38	0
56	MG	1A	3756	1/1	0.98	0.04	45,45,45,45	0
56	MG	2a	1706	1/1	0.98	0.03	44,44,44,44	0
56	MG	1A	3138	1/1	0.98	0.06	43,43,43,43	0
56	MG	1X	102	1/1	0.98	0.24	42,42,42,42	0
56	MG	1A	3407	1/1	0.98	0.08	47,47,47,47	0
56	MG	1X	104	1/1	0.98	0.08	45,45,45,45	0
56	MG	1A	3101	1/1	0.98	0.11	17,17,17,17	0
56	MG	2A	3314	1/1	0.98	0.06	54,54,54,54	0
56	MG	1A	3592	1/1	0.98	0.16	33,33,33,33	0
56	MG	1A	3525	1/1	0.98	0.19	38,38,38,38	0
56	MG	1A	3089	1/1	0.98	0.27	35,35,35,35	0
56	MG	1A	3078	1/1	0.98	0.04	31,31,31,31	0
56	MG	1A	3121	1/1	0.98	0.07	39,39,39,39	0
56	MG	2A	3489	1/1	0.98	0.08	32,32,32,32	0
56	MG	1A	3276	1/1	0.98	0.15	32,32,32,32	0
56	MG	1B	215	1/1	0.98	0.06	40,40,40,40	0
56	MG	1x	108	1/1	0.98	0.25	48,48,48,48	0
56	MG	1A	3143	1/1	0.98	0.08	17,17,17,17	0
56	MG	2A	3156	1/1	0.98	0.10	31,31,31,31	0
56	MG	2A	3157	1/1	0.98	0.08	47,47,47,47	0
56	MG	1A	3020	1/1	0.98	0.11	40,40,40,40	0
56	MG	2A	3327	1/1	0.98	0.11	46,46,46,46	0
56	MG	1A	3675	1/1	0.98	0.05	37,37,37,37	0
56	MG	1A	3123	1/1	0.98	0.11	33,33,33,33	0
56	MG	2A	3161	1/1	0.98	0.12	52,52,52,52	0
56	MG	10	106	1/1	0.98	0.07	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3677	1/1	0.98	0.06	19,19,19,19	0
56	MG	1I	102	1/1	0.98	0.11	39,39,39,39	0
56	MG	1A	3978	1/1	0.98	0.05	29,29,29,29	0
56	MG	1A	3417	1/1	0.98	0.05	38,38,38,38	0
56	MG	1A	3080	1/1	0.98	0.10	30,30,30,30	0
56	MG	1A	3773	1/1	0.98	0.07	32,32,32,32	0
56	MG	1A	3680	1/1	0.98	0.05	26,26,26,26	0
56	MG	1B	228	1/1	0.98	0.04	35,35,35,35	0
56	MG	1A	3473	1/1	0.98	0.09	43,43,43,43	0
56	MG	2A	3513	1/1	0.98	0.09	43,43,43,43	0
56	MG	13	103	1/1	0.98	0.04	37,37,37,37	0
56	MG	2A	3012	1/1	0.98	0.08	41,41,41,41	0
56	MG	1A	3874	1/1	0.98	0.08	28,28,28,28	0
56	MG	1A	3281	1/1	0.98	0.13	23,23,23,23	0
56	MG	2A	3518	1/1	0.98	0.10	34,34,34,34	0
56	MG	1A	3475	1/1	0.98	0.15	50,50,50,50	0
56	MG	1A	3877	1/1	0.98	0.11	62,62,62,62	0
56	MG	2E	304	1/1	0.98	0.13	31,31,31,31	0
56	MG	15	101	1/1	0.98	0.15	26,26,26,26	0
56	MG	1A	3606	1/1	0.98	0.11	39,39,39,39	0
56	MG	1A	3779	1/1	0.98	0.10	64,64,64,64	0
56	MG	1A	3607	1/1	0.98	0.08	25,25,25,25	0
56	MG	2F	302	1/1	0.98	0.06	55,55,55,55	0
56	MG	1A	3147	1/1	0.98	0.05	24,24,24,24	0
56	MG	15	107	1/1	0.98	0.15	45,45,45,45	0
56	MG	1A	3992	1/1	0.98	0.07	17,17,17,17	0
56	MG	1A	3994	1/1	0.98	0.04	58,58,58,58	0
56	MG	1A	3176	1/1	0.98	0.08	27,27,27,27	0
56	MG	2A	3026	1/1	0.98	0.13	40,40,40,40	0
56	MG	17	101	1/1	0.98	0.07	34,34,34,34	0
56	MG	2O	202	1/1	0.98	0.06	52,52,52,52	0
56	MG	2A	3532	1/1	0.98	0.11	42,42,42,42	0
56	MG	17	102	1/1	0.98	0.15	31,31,31,31	0
56	MG	1A	3996	1/1	0.98	0.11	43,43,43,43	0
56	MG	1A	3997	1/1	0.98	0.05	34,34,34,34	0
56	MG	1A	3610	1/1	0.98	0.13	28,28,28,28	0
56	MG	2A	3537	1/1	0.98	0.07	51,51,51,51	0
56	MG	1A	3611	1/1	0.98	0.07	36,36,36,36	0
56	MG	1A	3692	1/1	0.98	0.06	25,25,25,25	0
56	MG	1D	311	1/1	0.98	0.20	23,23,23,23	0
56	MG	1A	3478	1/1	0.98	0.12	50,50,50,50	0
56	MG	1A	4002	1/1	0.98	0.06	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3037	1/1	0.98	0.03	35,35,35,35	0
56	MG	2A	3038	1/1	0.98	0.14	28,28,28,28	0
56	MG	1A	3177	1/1	0.98	0.22	20,20,20,20	0
56	MG	1A	3285	1/1	0.98	0.09	30,30,30,30	0
56	MG	1A	4005	1/1	0.98	0.08	31,31,31,31	0
56	MG	1A	3106	1/1	0.98	0.08	27,27,27,27	0
56	MG	1A	3328	1/1	0.98	0.14	44,44,44,44	0
56	MG	1A	3891	1/1	0.98	0.07	39,39,39,39	0
56	MG	2A	3207	1/1	0.98	0.06	46,46,46,46	0
56	MG	2X	102	1/1	0.98	0.11	46,46,46,46	0
56	MG	1A	3698	1/1	0.98	0.10	25,25,25,25	0
56	MG	1a	1750	1/1	0.98	0.06	39,39,39,39	0
56	MG	1A	3893	1/1	0.98	0.09	50,50,50,50	0
56	MG	1A	3149	1/1	0.98	0.11	23,23,23,23	0
56	MG	1A	3181	1/1	0.98	0.04	16,16,16,16	0
56	MG	1A	3795	1/1	0.98	0.07	51,51,51,51	0
56	MG	1A	3377	1/1	0.98	0.17	27,27,27,27	0
56	MG	1A	3797	1/1	0.98	0.07	56,56,56,56	0
56	MG	1E	315	1/1	0.98	0.21	46,46,46,46	0
56	MG	2A	3054	1/1	0.98	0.04	51,51,51,51	0
56	MG	1A	3548	1/1	0.98	0.10	33,33,33,33	0
56	MG	1A	3289	1/1	0.98	0.13	38,38,38,38	0
56	MG	27	101	1/1	0.98	0.13	39,39,39,39	0
56	MG	1A	3182	1/1	0.98	0.12	35,35,35,35	0
56	MG	1A	3489	1/1	0.98	0.09	31,31,31,31	0
56	MG	1A	3706	1/1	0.98	0.04	19,19,19,19	0
56	MG	1A	3707	1/1	0.98	0.04	10,10,10,10	0
56	MG	1F	305	1/1	0.98	0.11	31,31,31,31	0
58	ZN	1n	102	1/1	0.98	0.04	89,89,89,89	0
56	MG	1A	3380	1/1	0.98	0.12	36,36,36,36	0
59	SF4	2d	303	8/8	0.98	0.04	64,76,84,86	0
56	MG	1A	3170	1/1	0.99	0.03	26,26,26,26	0
56	MG	2A	3180	1/1	0.99	0.10	47,47,47,47	0
56	MG	1B	227	1/1	0.99	0.03	37,37,37,37	0
56	MG	2A	3710	1/1	0.99	0.07	39,39,39,39	0
56	MG	1A	4061	1/1	0.99	0.09	22,22,22,22	0
56	MG	1W	204	1/1	0.99	0.17	33,33,33,33	0
56	MG	1A	3190	1/1	0.99	0.04	30,30,30,30	0
56	MG	1A	3075	1/1	0.99	0.06	9,9,9,9	0
56	MG	1A	3012	1/1	0.99	0.04	28,28,28,28	0
56	MG	1I	201	1/1	0.99	0.04	64,64,64,64	0
56	MG	1A	3808	1/1	0.99	0.04	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3718	1/1	0.99	0.03	42,42,42,42	0
56	MG	1A	3809	1/1	0.99	0.04	18,18,18,18	0
56	MG	1A	3008	1/1	0.99	0.09	23,23,23,23	0
56	MG	1A	3734	1/1	0.99	0.06	27,27,27,27	0
56	MG	1A	3669	1/1	0.99	0.06	36,36,36,36	0
56	MG	1B	237	1/1	0.99	0.06	30,30,30,30	0
56	MG	1A	3065	1/1	0.99	0.20	42,42,42,42	0
56	MG	1A	3737	1/1	0.99	0.05	36,36,36,36	0
56	MG	2A	3585	1/1	0.99	0.09	34,34,34,34	0
56	MG	1A	3038	1/1	0.99	0.06	23,23,23,23	0
56	MG	1A	4026	1/1	0.99	0.03	25,25,25,25	0
56	MG	1D	305	1/1	0.99	0.03	17,17,17,17	0
56	MG	2A	3802	1/1	0.99	0.03	55,55,55,55	0
56	MG	2A	3009	1/1	0.99	0.04	39,39,39,39	0
56	MG	2A	3590	1/1	0.99	0.04	33,33,33,33	0
56	MG	1A	3484	1/1	0.99	0.12	31,31,31,31	0
56	MG	1A	3196	1/1	0.99	0.23	35,35,35,35	0
56	MG	1A	4076	1/1	0.99	0.02	43,43,43,43	0
56	MG	1A	3003	1/1	0.99	0.02	23,23,23,23	0
56	MG	1A	4078	1/1	0.99	0.04	39,39,39,39	0
56	MG	1A	3159	1/1	0.99	0.08	27,27,27,27	0
56	MG	1A	3412	1/1	0.99	0.08	41,41,41,41	0
56	MG	1A	3268	1/1	0.99	0.12	32,32,32,32	0
56	MG	1A	3902	1/1	0.99	0.03	35,35,35,35	0
56	MG	1A	3178	1/1	0.99	0.12	29,29,29,29	0
56	MG	1A	3622	1/1	0.99	0.09	36,36,36,36	0
56	MG	2A	3743	1/1	0.99	0.04	45,45,45,45	0
56	MG	1A	3747	1/1	0.99	0.04	25,25,25,25	0
56	MG	1A	3022	1/1	0.99	0.07	38,38,38,38	0
56	MG	1Q	206	1/1	0.99	0.17	39,39,39,39	0
56	MG	1a	1819	1/1	0.99	0.02	55,55,55,55	0
56	MG	1A	3993	1/1	0.99	0.04	34,34,34,34	0
56	MG	1A	3069	1/1	0.99	0.07	35,35,35,35	0
56	MG	1E	307	1/1	0.99	0.13	45,45,45,45	0
56	MG	1E	308	1/1	0.99	0.03	27,27,27,27	0
56	MG	1A	3682	1/1	0.99	0.04	26,26,26,26	0
56	MG	1A	3788	1/1	0.99	0.04	42,42,42,42	0
56	MG	1A	3129	1/1	0.99	0.08	29,29,29,29	0
56	MG	1A	3203	1/1	0.99	0.10	23,23,23,23	0
56	MG	15	104	1/1	0.99	0.21	24,24,24,24	0
56	MG	1A	3083	1/1	0.99	0.10	32,32,32,32	0
56	MG	1A	3033	1/1	0.99	0.04	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3629	1/1	0.99	0.06	55,55,55,55	0
56	MG	1A	3034	1/1	0.99	0.10	27,27,27,27	0
56	MG	1A	3207	1/1	0.99	0.04	20,20,20,20	0
56	MG	1A	3072	1/1	0.99	0.04	18,18,18,18	0
56	MG	1A	3722	1/1	0.99	0.05	42,42,42,42	0
56	MG	1B	216	1/1	0.99	0.05	43,43,43,43	0
56	MG	1U	206	1/1	0.99	0.09	30,30,30,30	0
56	MG	2A	3839	1/1	0.99	0.04	29,29,29,29	0
56	MG	1A	3691	1/1	0.99	0.03	25,25,25,25	0
56	MG	1A	3087	1/1	0.99	0.05	25,25,25,25	0
56	MG	1A	3725	1/1	0.99	0.06	23,23,23,23	0
56	MG	1A	3023	1/1	0.99	0.05	15,15,15,15	0
56	MG	1A	3727	1/1	0.99	0.06	43,43,43,43	0
56	MG	1A	3044	1/1	0.99	0.06	24,24,24,24	0
56	MG	1V	203	1/1	0.99	0.15	29,29,29,29	0
56	MG	2A	3496	1/1	0.99	0.07	74,74,74,74	0
56	MG	2A	3848	1/1	0.99	0.03	23,23,23,23	0
56	MG	2A	3563	1/1	0.99	0.06	33,33,33,33	0
58	ZN	1Y	204	1/1	0.99	0.04	63,63,63,63	0
56	MG	1A	3925	1/1	0.99	0.05	30,30,30,30	0
58	ZN	15	109	1/1	0.99	0.03	57,57,57,57	0
56	MG	2A	3498	1/1	0.99	0.04	61,61,61,61	0
58	ZN	2Y	501	1/1	0.99	0.03	85,85,85,85	0
56	MG	1A	4058	1/1	0.99	0.05	36,36,36,36	0
58	ZN	25	106	1/1	0.99	0.03	62,62,62,62	0
58	ZN	26	102	1/1	0.99	0.05	61,61,61,61	0
58	ZN	29	501	1/1	0.99	0.04	71,71,71,71	0
58	ZN	2n	501	1/1	0.99	0.05	85,85,85,85	0
59	SF4	1d	302	8/8	0.99	0.04	67,80,86,86	0
56	MG	1A	3926	1/1	0.99	0.04	33,33,33,33	0
58	ZN	19	501	1/1	1.00	0.03	42,42,42,42	0
56	MG	2A	3703	1/1	1.00	0.04	22,22,22,22	0
56	MG	1A	3014	1/1	1.00	0.03	23,23,23,23	0
56	MG	1A	3109	1/1	1.00	0.09	27,27,27,27	0
58	ZN	16	103	1/1	1.00	0.03	39,39,39,39	0

6.5 Other polymers

There are no such residues in this entry.