



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 04:54 AM UTC

PDB ID : 8EV7 / pdb_00008ev7
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome in complex with kanamycin, mRNA, and A-, P-, and E-site tRNAs
Authors : Seely, S.M.; Gagnon, M.G.
Deposited on : 2022-10-19
Resolution : 2.89 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

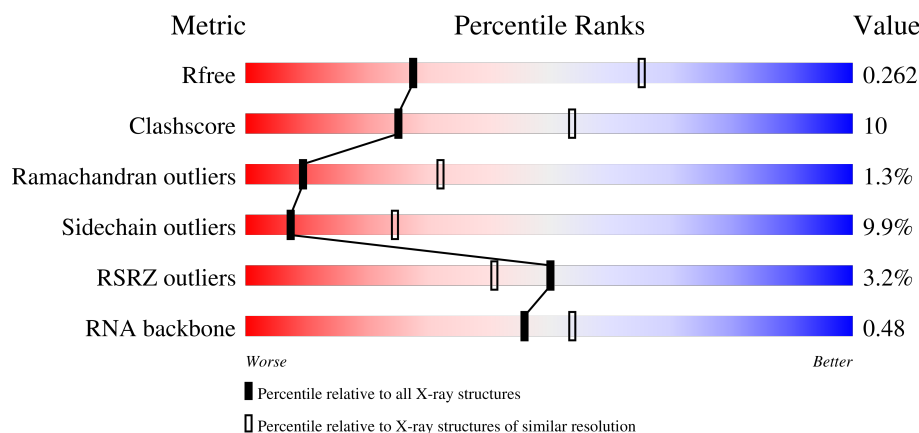
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)
RNA backbone	3983	1120 (3.10-2.70)

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	62% 30% 6% .
1	2A	2915	54% 34% 7% .
2	1B	121	75% 21% ..
2	2B	121	31% 55% 13% .

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

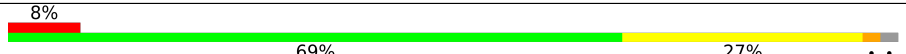
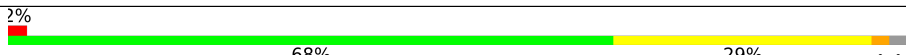
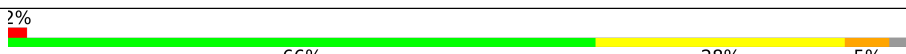
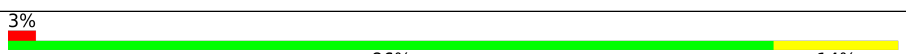
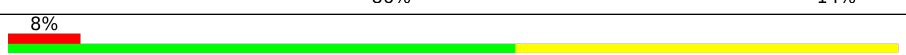
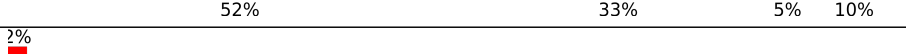
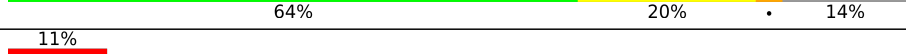
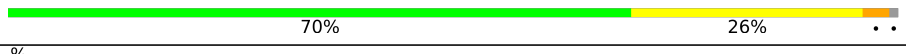
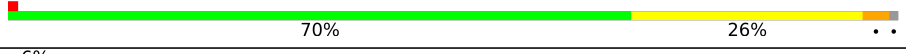
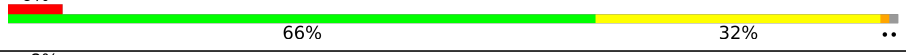
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Mol	Chain	Length	Quality of chain
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	
27	25	60	

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

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

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Mol	Chain	Length	Quality of chain
53	1v	24	
53	2v	24	
54	1w	76	
54	1y	76	
54	2w	76	
54	2y	76	
55	1x	77	
55	2x	77	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	PSU	2y	55	-	-	X	-
56	MG	1A	3532	-	-	-	X
56	MG	1a	1709	-	-	-	X
56	MG	1v	101	-	-	-	X

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 297628 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	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
22	20	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1503	Total	C	N	O	P	0	0	0
			32327	14396	5990	10438	1503			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1548	973	301	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1655	1038	326	284	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			810	514	144	149	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			983	623	193	167			
40	2i	127	Total	C	N	O	0	0	0
			978	619	190	169			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			709	440	138	131			
41	2j	96	Total	C	N	O	0	0	0
			714	445	138	131			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			829	516	155	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	2l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	123	Total	C	N	O	S	0	0	0
			958	592	198	166	2			
44	2m	122	Total	C	N	O	S	0	0	0
			950	586	197	165	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
50	2s	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
51	2t	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

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

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

- Molecule 53 is a RNA chain called mRNA.

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

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

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
54	1w	74	Total	C	N	O	P	S	0	0	0
			1592	713	285	518	74	2			
54	1y	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
54	2w	72	Total	C	N	O	P	S	0	0	0
			1544	690	278	502	72	2			
54	2y	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	1			

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

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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1A	932	Total	Mg	0	0
			932	932		
56	1B	29	Total	Mg	0	0
			29	29		
56	1D	4	Total	Mg	0	0
			4	4		
56	1E	4	Total	Mg	0	0
			4	4		
56	1F	3	Total	Mg	0	0
			3	3		
56	1G	2	Total	Mg	0	0
			2	2		
56	1N	2	Total	Mg	0	0
			2	2		
56	1O	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1P	2	Total 2	Mg 2	0	0
56	1Q	3	Total 3	Mg 3	0	0
56	1R	1	Total 1	Mg 1	0	0
56	1T	1	Total 1	Mg 1	0	0
56	1U	2	Total 2	Mg 2	0	0
56	1V	2	Total 2	Mg 2	0	0
56	1W	2	Total 2	Mg 2	0	0
56	1X	1	Total 1	Mg 1	0	0
56	1Y	1	Total 1	Mg 1	0	0
56	10	1	Total 1	Mg 1	0	0
56	11	1	Total 1	Mg 1	0	0
56	12	1	Total 1	Mg 1	0	0
56	13	4	Total 4	Mg 4	0	0
56	14	1	Total 1	Mg 1	0	0
56	15	3	Total 3	Mg 3	0	0
56	16	1	Total 1	Mg 1	0	0
56	17	1	Total 1	Mg 1	0	0
56	18	4	Total 4	Mg 4	0	0
56	19	3	Total 3	Mg 3	0	0
56	1a	354	Total 354	Mg 354	0	0
56	1d	2	Total 2	Mg 2	0	0

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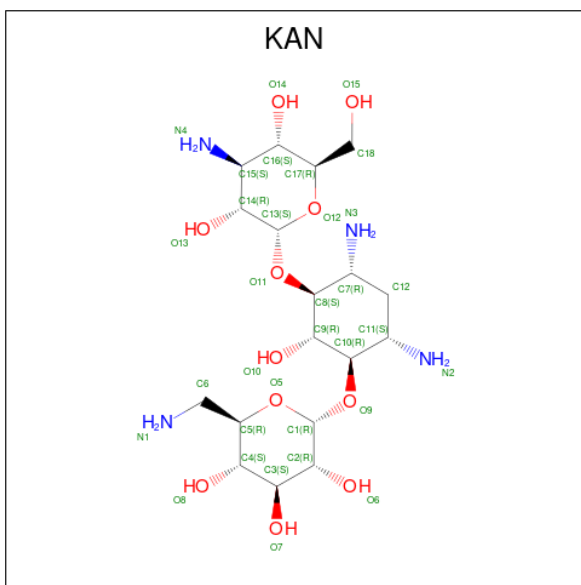
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1e	1	Total 1	Mg 1	0	0
56	1i	1	Total 1	Mg 1	0	0
56	1k	1	Total 1	Mg 1	0	0
56	1l	3	Total 3	Mg 3	0	0
56	1m	2	Total 2	Mg 2	0	0
56	1o	3	Total 3	Mg 3	0	0
56	1q	2	Total 2	Mg 2	0	0
56	1r	1	Total 1	Mg 1	0	0
56	1v	3	Total 3	Mg 3	0	0
56	1w	5	Total 5	Mg 5	0	0
56	1x	24	Total 24	Mg 24	0	0
56	1y	1	Total 1	Mg 1	0	0
56	2A	567	Total 567	Mg 567	0	0
56	2B	13	Total 13	Mg 13	0	0
56	2D	3	Total 3	Mg 3	0	0
56	2E	2	Total 2	Mg 2	0	0
56	2F	4	Total 4	Mg 4	0	0
56	2G	1	Total 1	Mg 1	0	0
56	2Q	2	Total 2	Mg 2	0	0
56	2T	2	Total 2	Mg 2	0	0
56	2W	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	20	2	Total 2	Mg 2	0	0
56	21	1	Total 1	Mg 1	0	0
56	23	1	Total 1	Mg 1	0	0
56	26	1	Total 1	Mg 1	0	0
56	28	2	Total 2	Mg 2	0	0
56	2a	227	Total 227	Mg 227	0	0
56	2e	1	Total 1	Mg 1	0	0
56	2g	1	Total 1	Mg 1	0	0
56	2q	1	Total 1	Mg 1	0	0
56	2t	1	Total 1	Mg 1	0	0
56	2v	2	Total 2	Mg 2	0	0
56	2w	1	Total 1	Mg 1	0	0
56	2x	7	Total 7	Mg 7	0	0

- Molecule 57 is KANAMYCIN A (CCD ID: KAN) (formula: C₁₈H₃₆N₄O₁₁) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	1A	1	Total	C	N	O	0	0
			33	18	4	11		
57	1A	1	Total	C	N	O	0	0
			33	18	4	11		
57	1A	1	Total	C	N	O	0	0
			33	18	4	11		
57	1a	1	Total	C	N	O	0	0
			33	18	4	11		
57	2A	1	Total	C	N	O	0	0
			33	18	4	11		
57	2A	1	Total	C	N	O	0	0
			33	18	4	11		
57	2a	1	Total	C	N	O	0	0
			33	18	4	11		

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

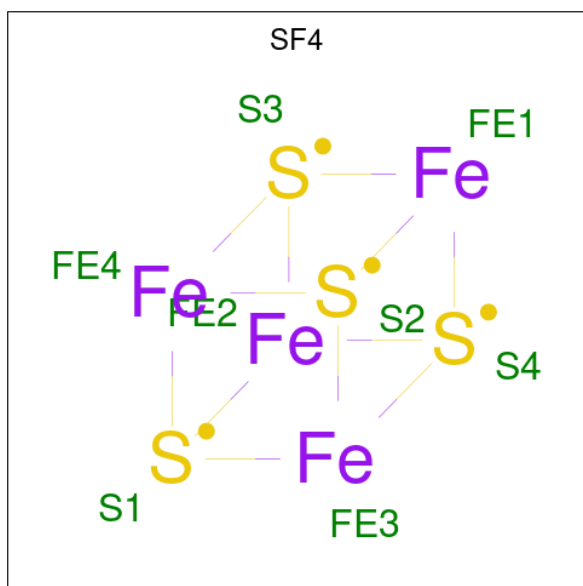
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1Y	1	Total	Zn	0	0
			1	1		
58	14	1	Total	Zn	0	0
			1	1		
58	15	1	Total	Zn	0	0
			1	1		
58	16	1	Total	Zn	0	0
			1	1		
58	19	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1n	1	Total	Zn	0	0
			1	1		
58	2Y	1	Total	Zn	0	0
			1	1		
58	24	1	Total	Zn	0	0
			1	1		
58	25	1	Total	Zn	0	0
			1	1		
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	938	Total O 938 938	0	0
60	1B	25	Total O 25 25	0	0
60	1D	9	Total O 9 9	0	0
60	1E	7	Total O 7 7	0	0
60	1F	9	Total O 9 9	0	0
60	1G	1	Total O 1 1	0	0
60	1H	1	Total O 1 1	0	0
60	1N	2	Total O 2 2	0	0
60	1O	4	Total O 4 4	0	0
60	1P	12	Total O 12 12	0	0
60	1Q	4	Total O 4 4	0	0
60	1R	5	Total O 5 5	0	0
60	1S	2	Total O 2 2	0	0
60	1T	8	Total O 8 8	0	0
60	1U	5	Total O 5 5	0	0
60	1V	4	Total O 4 4	0	0
60	1W	5	Total O 5 5	0	0
60	1X	4	Total O 4 4	0	0
60	1Y	5	Total O 5 5	0	0
60	1Z	1	Total O 1 1	0	0
60	10	4	Total O 4 4	0	0
60	11	4	Total O 4 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	12	2	Total 2	O 2	0	0
60	13	1	Total 1	O 1	0	0
60	14	1	Total 1	O 1	0	0
60	15	1	Total 1	O 1	0	0
60	16	3	Total 3	O 3	0	0
60	17	3	Total 3	O 3	0	0
60	18	2	Total 2	O 2	0	0
60	19	1	Total 1	O 1	0	0
60	1a	371	Total 371	O 371	0	0
60	1d	4	Total 4	O 4	0	0
60	1e	4	Total 4	O 4	0	0
60	1f	2	Total 2	O 2	0	0
60	1h	1	Total 1	O 1	0	0
60	1i	2	Total 2	O 2	0	0
60	1j	1	Total 1	O 1	0	0
60	1k	1	Total 1	O 1	0	0
60	1l	3	Total 3	O 3	0	0
60	1m	2	Total 2	O 2	0	0
60	1n	1	Total 1	O 1	0	0
60	1o	3	Total 3	O 3	0	0
60	1p	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1s	1	Total O 1 1	0	0
60	1t	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	16	Total O 16 16	0	0
60	2A	401	Total O 401 401	0	0
60	2B	18	Total O 18 18	0	0
60	2D	6	Total O 6 6	0	0
60	2E	3	Total O 3 3	0	0
60	2F	3	Total O 3 3	0	0
60	2O	1	Total O 1 1	0	0
60	2P	5	Total O 5 5	0	0
60	2R	2	Total O 2 2	0	0
60	2U	2	Total O 2 2	0	0
60	2W	1	Total O 1 1	0	0
60	2X	2	Total O 2 2	0	0
60	2Y	1	Total O 1 1	0	0
60	20	3	Total O 3 3	0	0
60	21	4	Total O 4 4	0	0
60	25	1	Total O 1 1	0	0
60	26	1	Total O 1 1	0	0

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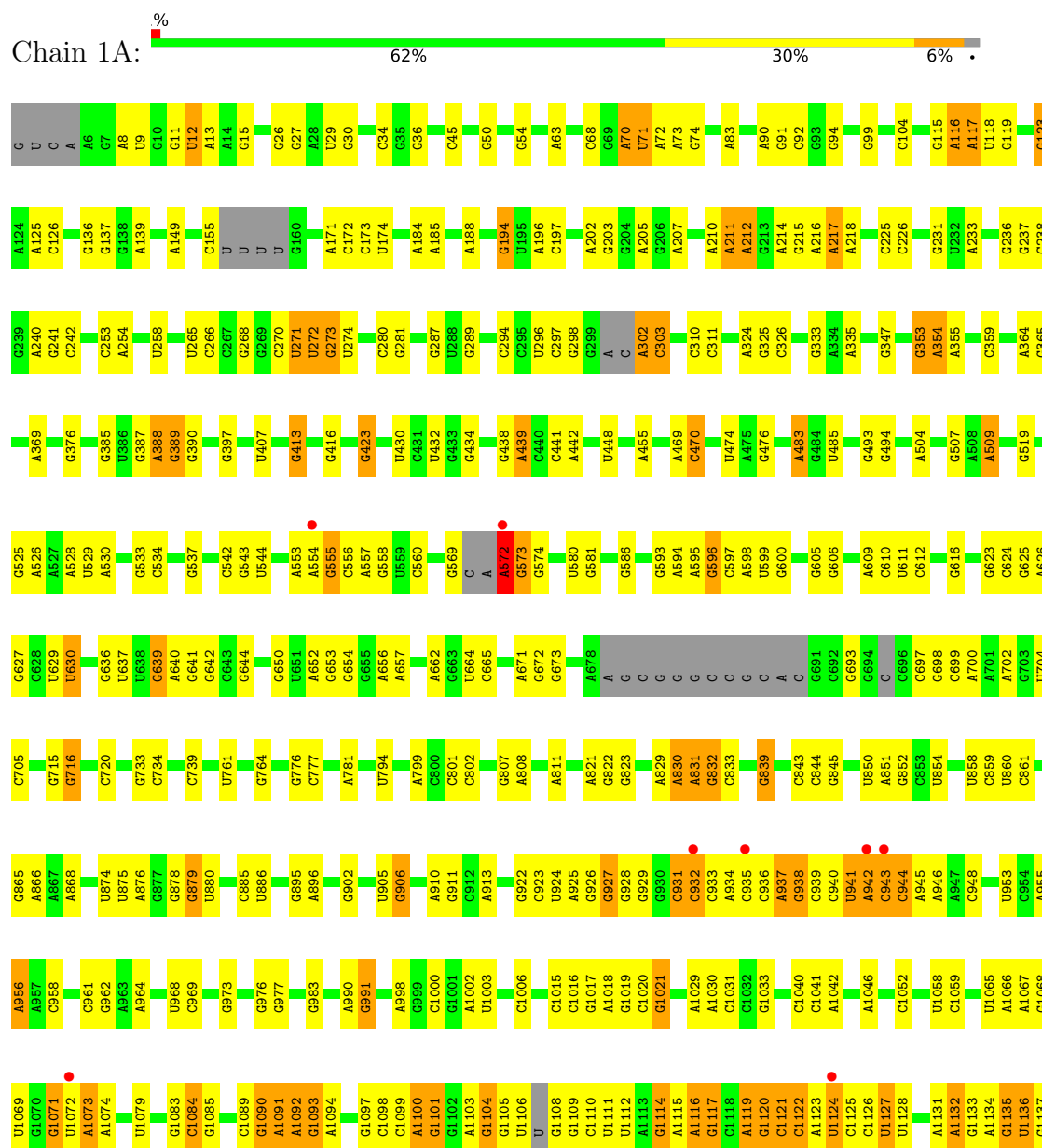
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	27	1	Total 1	O 1	0	0
60	28	3	Total 3	O 3	0	0
60	29	1	Total 1	O 1	0	0
60	2a	160	Total 160	O 160	0	0
60	2e	2	Total 2	O 2	0	0
60	2i	1	Total 1	O 1	0	0
60	2l	2	Total 2	O 2	0	0
60	2m	2	Total 2	O 2	0	0
60	2o	1	Total 1	O 1	0	0
60	2t	3	Total 3	O 3	0	0
60	2w	1	Total 1	O 1	0	0
60	2x	2	Total 2	O 2	0	0

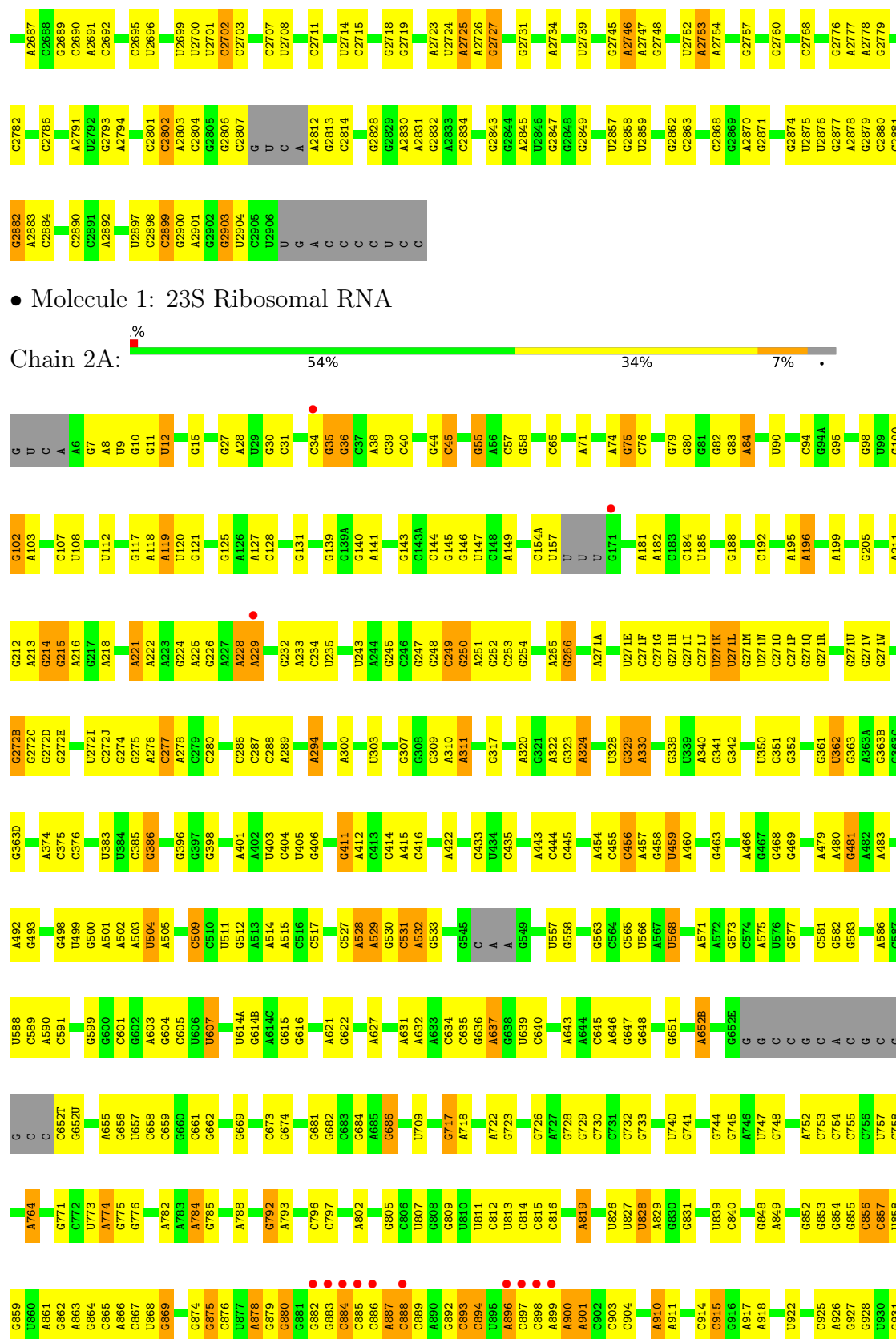
3 Residue-property plots

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.

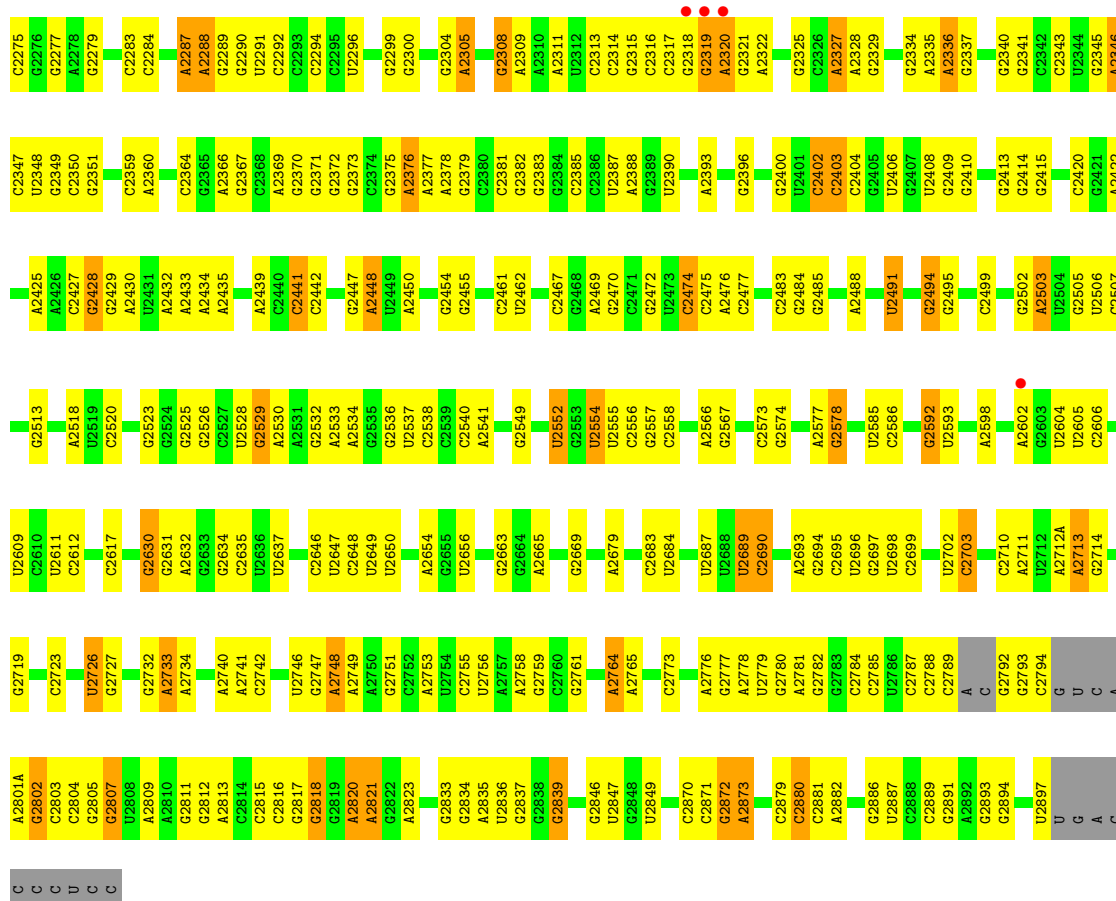
• Molecule 1: 23S Ribosomal RNA



U2564	G2335	G2227	C2158	C1335	C1733	U1346	A1219	C1138
G2565	C2336	G2228	C2159	U1336	G1734	A1347	U1220	G1139
U2566	G2337	A2229	C2160	A1843	U1735	G1355	G1221	U1140
C2338	U2230	A2264	C2161	A1943	G1740	G1356	A1222	A1141
A2339	A2237	G2071	G2162	G1944	G1743	C1361	C1223	A1142
A2340	A2341	G2074	G2163	G1945	A1747	U1362	C1224	U1143
C2342	G2343	G2077	C2164	A1946	A1748	A1363	G1228	U1147
C2343	G2344	C2077	U2166	G1947	U1749	U1362	G1231	C1148
G2346	G2347	C2078	C2167	U1948	G1750	C1366	G1232	A1149
C2347	A2348	A2082	G2168	G1854	G1757	A1367	G1236	C1150
A2349	U2356	G2083	G2169	A1860	G1787	A1368	G1246	U1151
G2350	U2357	A2084	G2170	G1870	G1788	U1379	C1246	G1152
C2353	C2357	G2091	U2172	G1870	G1789	U1383	A1246	G1153
A2354	A2358	G2091	G2173	G1870	A1787	G1384	A1255	U1154
G2359	C2359	G2096	G2174	A1878	G1775	U1391	A1265	C1155
C2362	C2362	U2097	G2175	G1888	G1775	U1391	G1263	A1157
C2363	A2364	G2102	G2176	G1889	G1781	U1398	G1264	U1158
G2365	G2365	G2115	G2177	G1892	G1785	U1399	A1265	U1159
C2366	C2366	U2120	G2178	G1897	A1786	A1400	C1270	G1161
A2372	A2373	U2121	C2180	A1898	G1787	G1401	G1275	G1163
C2376	C2376	U2122	G2181	A1899	U1788	G1404	G1282	G1168
G2387	C2387	G2127	G2182	G1900	A1790	U1411	A1283	G1171
A2388	A2388	G2128	G2183	G1904	G1794	A1412	A1405	A1172
G2390	A2390	C2129	C2184	G1905	G1795	A1413	A1406	A1173
G2391	G2391	G2130	A2185	A1911	A1804	U1418	A1293	A1174
C2392	C2392	U2131	U2015	A1912	G1807	A1419	G1296	A1175
C2393	C2393	G2132	G2019	A1921	U1808	A1425	C1297	U1176
G2394	G2394	C2133	G2025	G1925	U1809	G1426	G1298	G1177
G2395	C2395	U2135	U2033	G1928	U1810	A1430	A1299	G1180
C2396	C2396	A2136	G2034	G1928	A1811	U1431	G1302	G1181
C2397	C2397	G2137	A2035	G1928	A1812	A1438	G1310	G1182
A2405	A2405	U2140	U2038	G1933	C1812	A1439	G1312	G1183
C2414	C2414	U2141	U2039	U1933	C1813	U1560	U1312	U1186
G2415	G2415	G2142	G2040	A1935	A1814	A1441	U1314	U1187
C2416	C2416	U2143	A2041	C1935	A1815	A1315	A1315	A1188
G2417	G2417	U2144	A2042	U1937	A1816	C1316	C1316	A1189
G2418	U2418	G2145	C2043	U1938	A1817	U1562	A1317	G1190
G2419	G2419	G2146	U2044	A1938	C1821	U1566	A1318	G1197
U2420	U2420	G2147	G2045	A1940	A1822	U1567	U1319	C1198
C2422	C2422	A2148	U2050	A1941	U1825	G1572	A1320	C1199
A2434	A2434	G2149	G2051	C1942	C1826	G1573	A1321	G1200
G2435	G2435	C2150	A2052	G1943	U1827	A1574	A1324	A1201
C2436	C2436	C2151	G2053	G1951	C1828	A1575	A1327	A1202
A2437	A2437	U2152	U2054	G1952	U1829	G1579	G1327	G1210
G2440	G2440	G2153	A2055	U1953	G1830	G	U1338	U1211
U2441	U2441	U2154	G2056	A1954	C1831	U	U1339	C1212
C2442	C2442	A2155	G2060	U1955	G1832	A	C1341	G1216
G2443	G2443	A2156	C2061	C1956	A1833	C	G1459	G1217
U2444	U2444	A2157			A1834	G1584	G1460	G1218







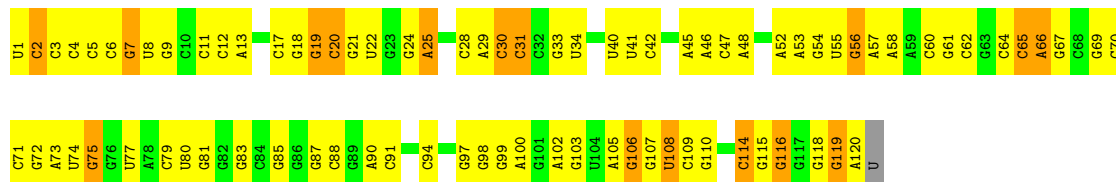
• Molecule 2: 5S Ribosomal RNA

Chain 1B: 75% 21%



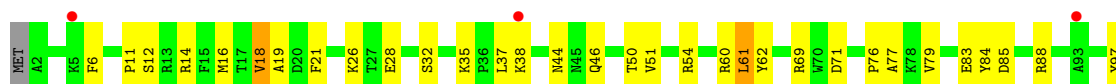
• Molecule 2: 5S Ribosomal RNA

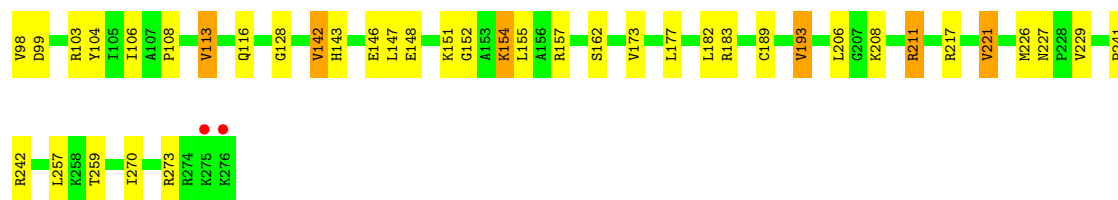
Chain 2B: 31% 55% 13%



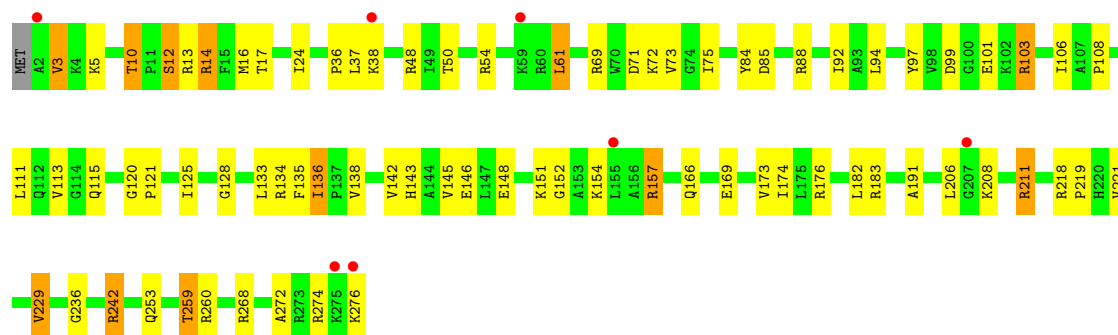
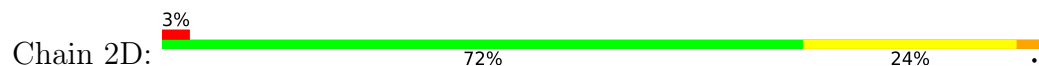
• Molecule 3: 50S ribosomal protein L2

Chain 1D: 2% 74% 23%

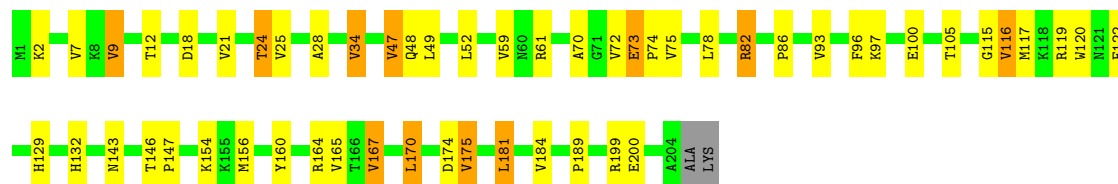




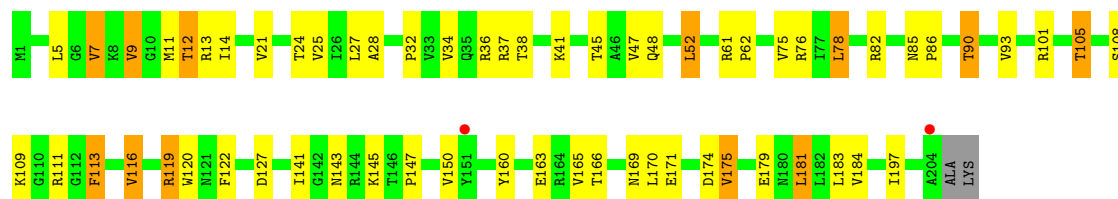
• Molecule 3: 50S ribosomal protein L2



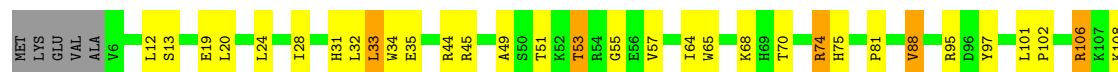
• Molecule 4: 50S ribosomal protein L3

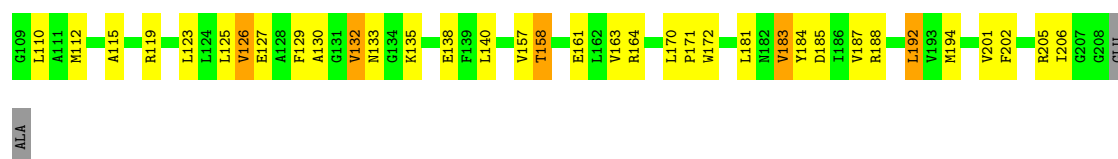


• Molecule 4: 50S ribosomal protein L3

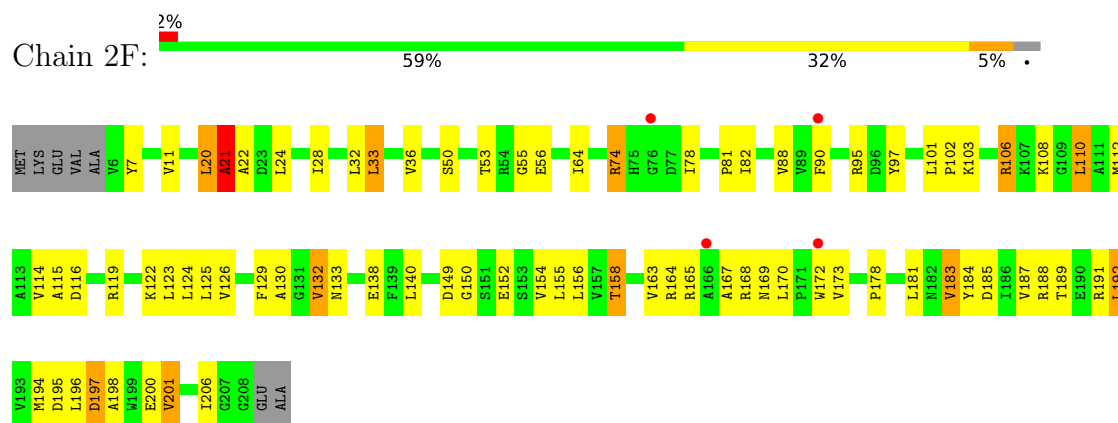


• Molecule 5: 50S ribosomal protein L4

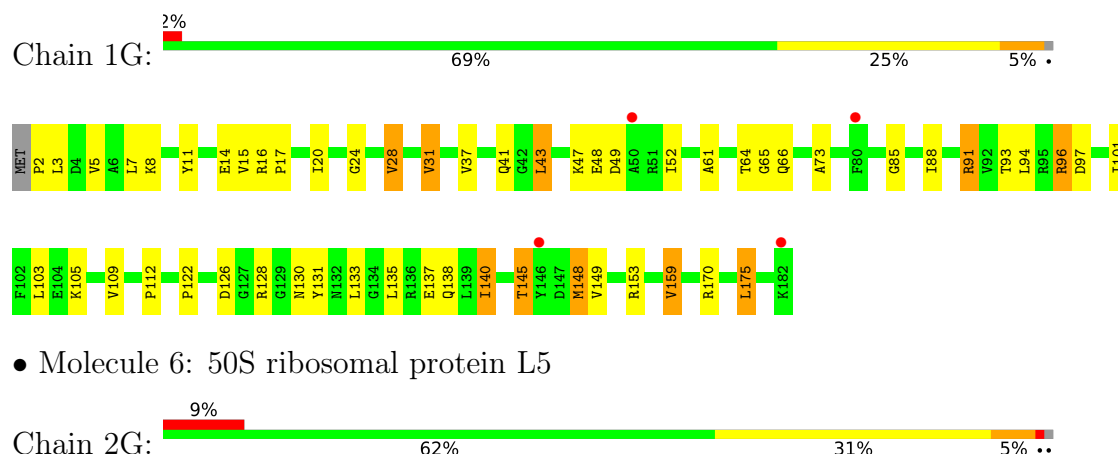




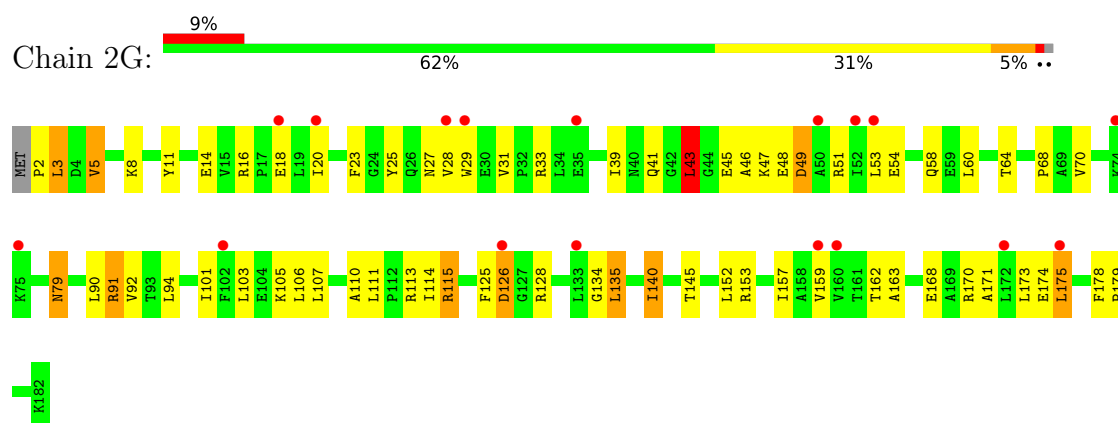
• Molecule 5: 50S ribosomal protein L4



• Molecule 6: 50S ribosomal protein L5

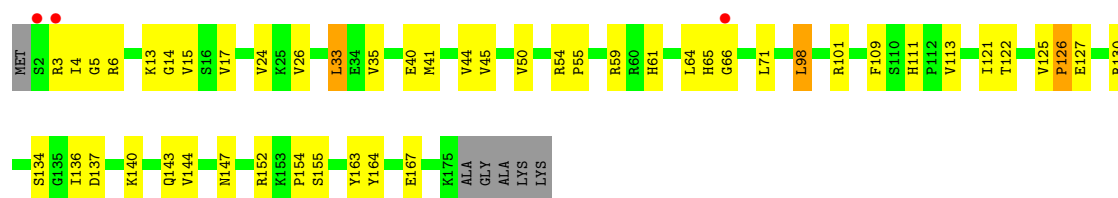


• Molecule 6: 50S ribosomal protein L5

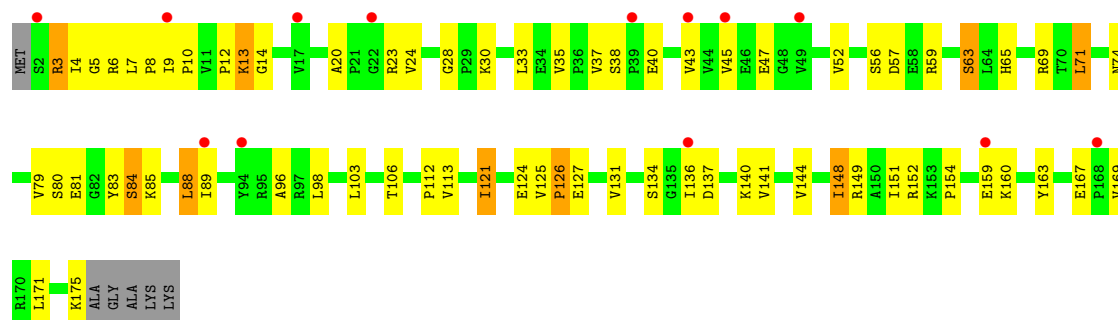


• Molecule 7: 50S ribosomal protein L6

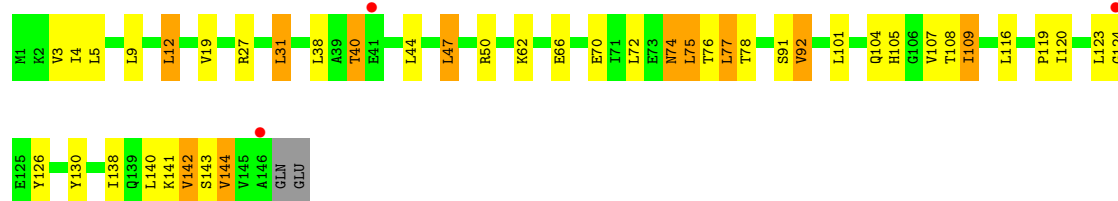




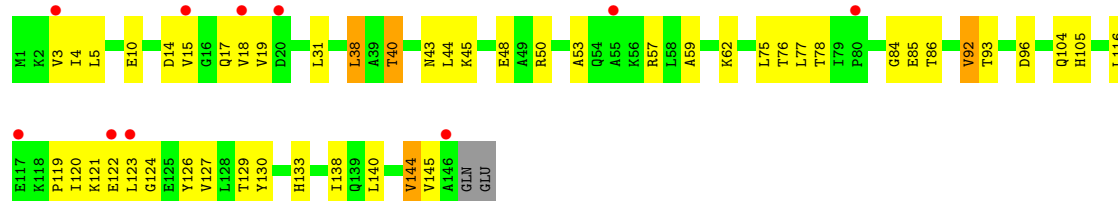
• Molecule 7: 50S ribosomal protein L6



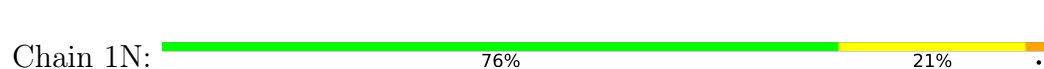
• Molecule 8: 50S ribosomal protein L9



• Molecule 8: 50S ribosomal protein L9



• Molecule 9: 50S ribosomal protein L13

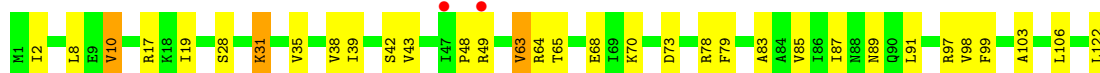
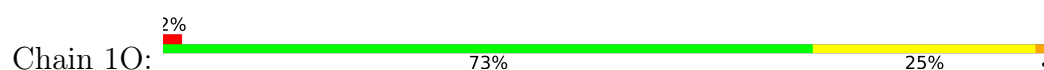




- Molecule 9: 50S ribosomal protein L13



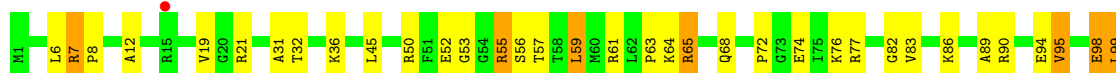
- Molecule 10: 50S ribosomal protein L14



- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

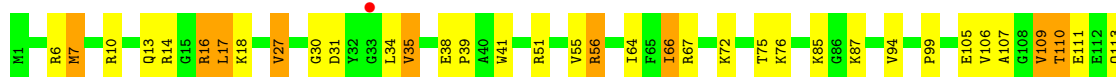
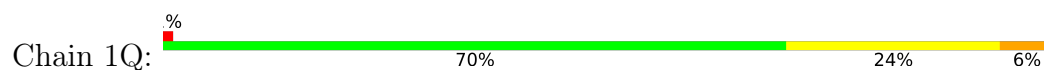


- Molecule 11: 50S ribosomal protein L15

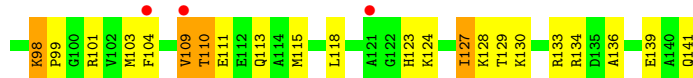
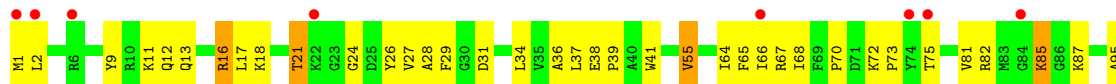




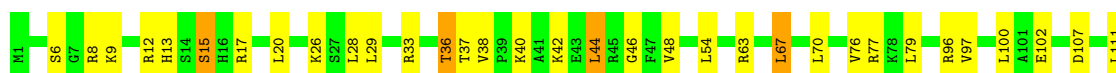
- Molecule 12: 50S ribosomal protein L16



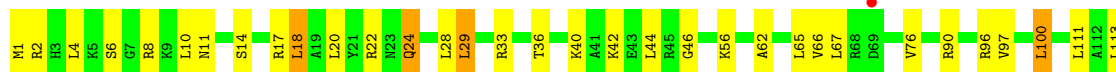
- Molecule 12: 50S ribosomal protein L16



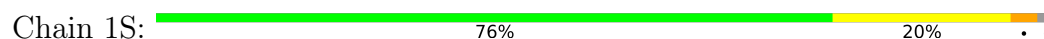
- Molecule 13: 50S ribosomal protein L17



- Molecule 13: 50S ribosomal protein L17

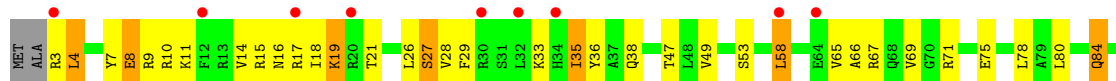


- Molecule 14: 50S ribosomal protein L18





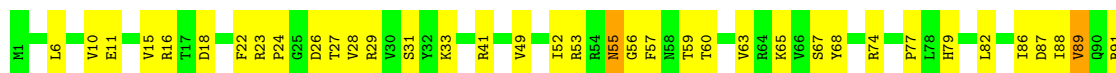
- Molecule 14: 50S ribosomal protein L18



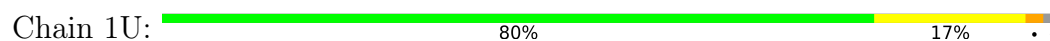
- Molecule 15: 50S ribosomal protein L19



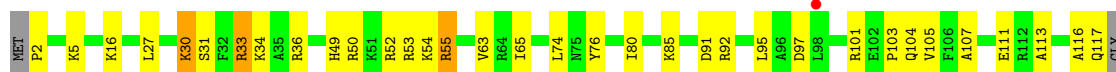
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20

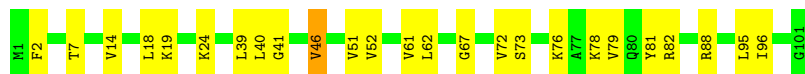


- Molecule 16: 50S ribosomal protein L20



- Molecule 17: 50S ribosomal protein L21

Chain 1V:  75% 24%



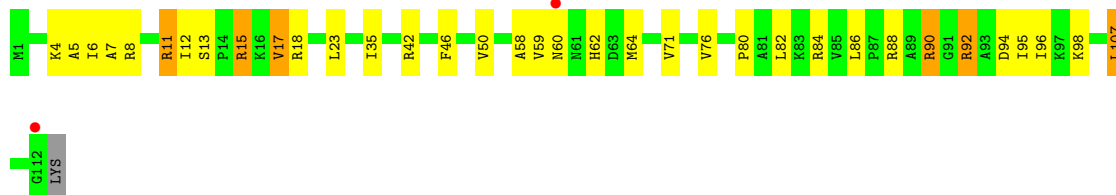
- Molecule 17: 50S ribosomal protein L21

Chain 2V:  72% 21% 6%



- Molecule 18: 50S ribosomal protein L22

Chain 1W:  68% 26% 5%



- Molecule 18: 50S ribosomal protein L22

Chain 2W:  75% 21%



- Molecule 19: 50S ribosomal protein L23

Chain 1X:  72% 25%

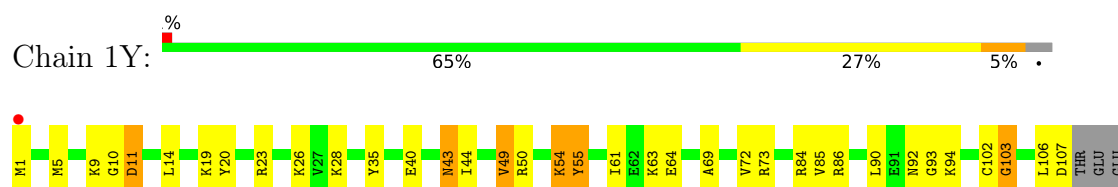


- Molecule 19: 50S ribosomal protein L23

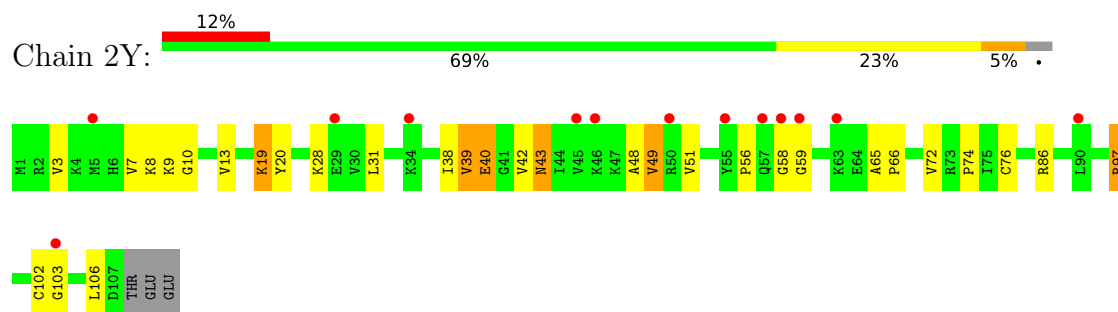
Chain 2X:  77% 21% 5%



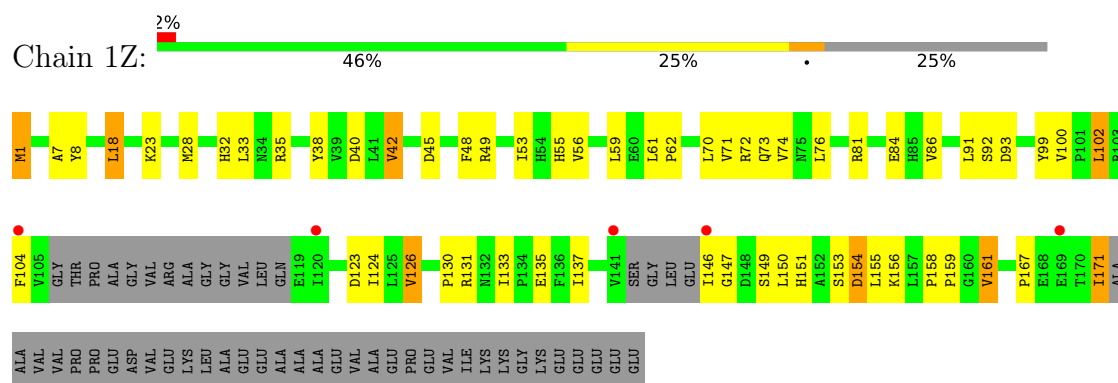
- Molecule 20: 50S ribosomal protein L24



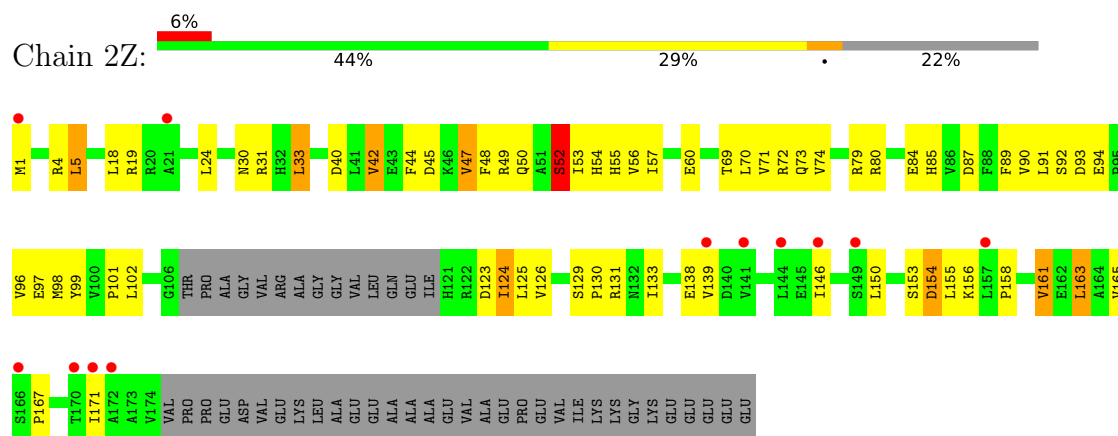
• Molecule 20: 50S ribosomal protein L24



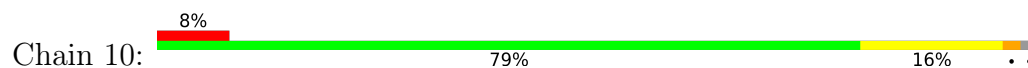
• Molecule 21: 50S ribosomal protein L25

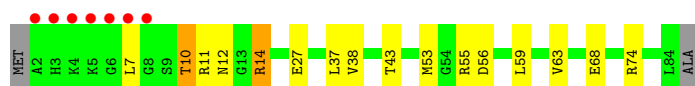


• Molecule 21: 50S ribosomal protein L25

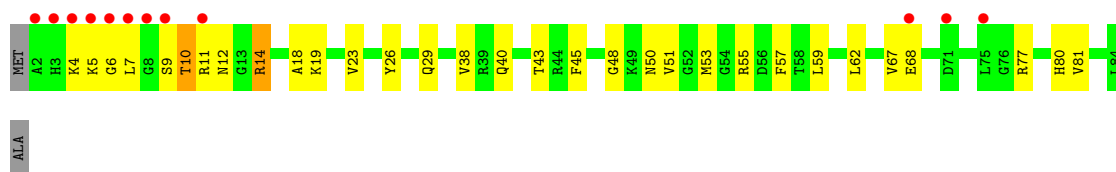


• Molecule 22: 50S ribosomal protein L27

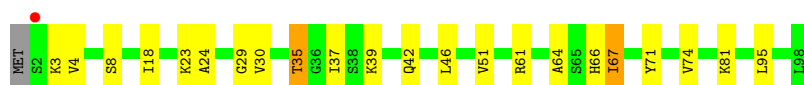
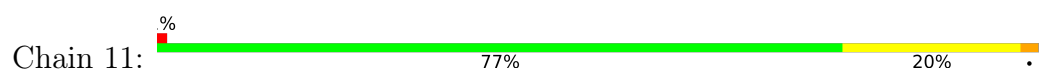




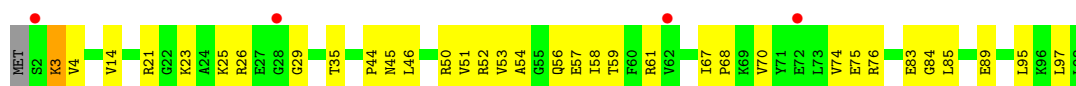
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



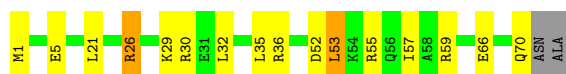
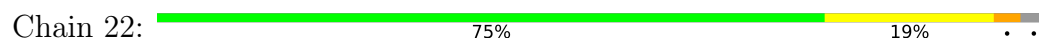
- Molecule 23: 50S ribosomal protein L28



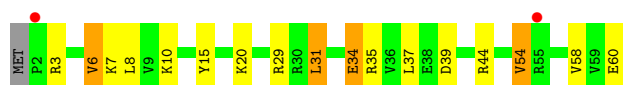
- Molecule 24: 50S ribosomal protein L29



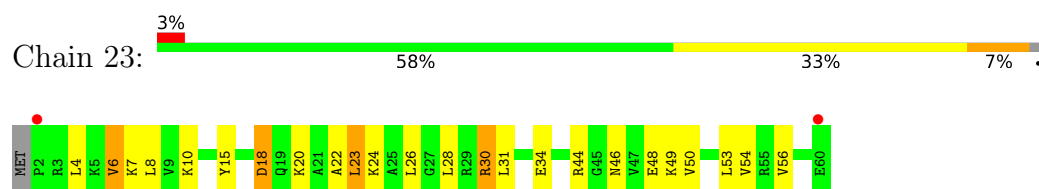
- Molecule 24: 50S ribosomal protein L29



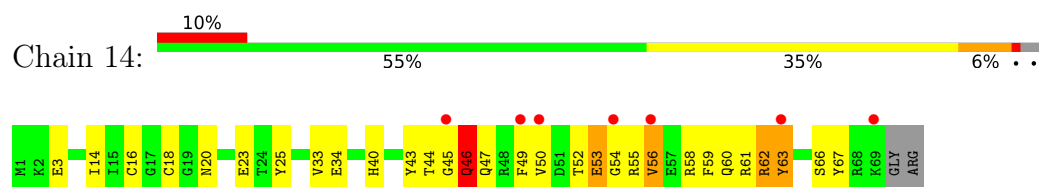
- Molecule 25: 50S ribosomal protein L30



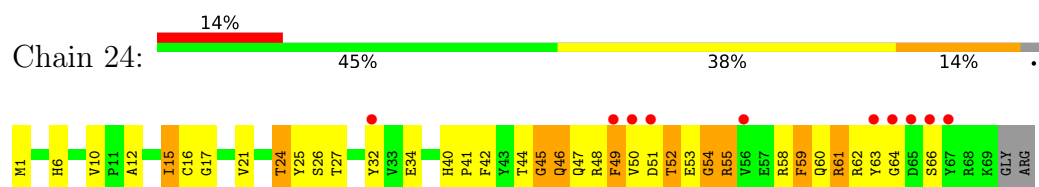
• Molecule 25: 50S ribosomal protein L30



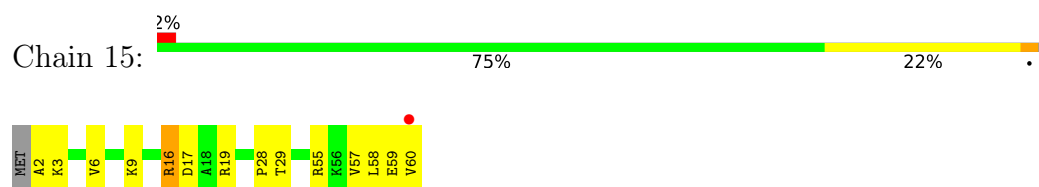
• Molecule 26: 50S ribosomal protein L31



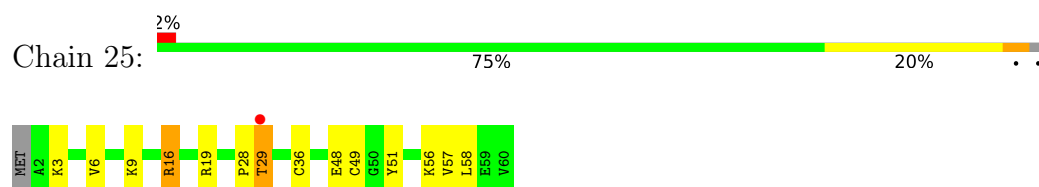
• Molecule 26: 50S ribosomal protein L31



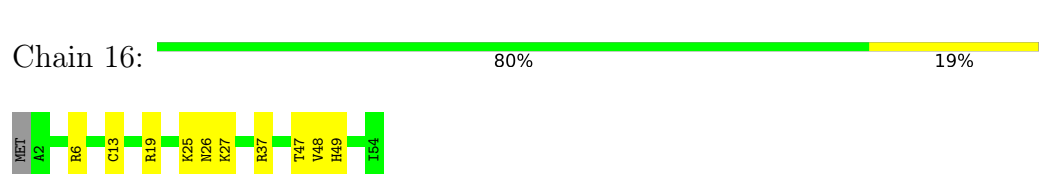
• Molecule 27: 50S ribosomal protein L32



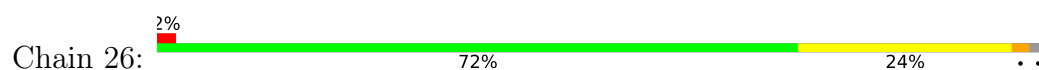
• Molecule 27: 50S ribosomal protein L32

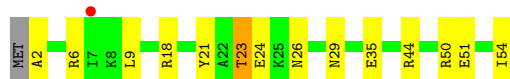


• Molecule 28: 50S ribosomal protein L33



• Molecule 28: 50S ribosomal protein L33

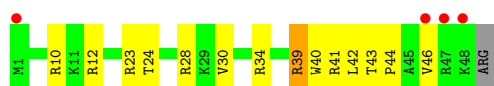




- Molecule 29: 50S ribosomal protein L34



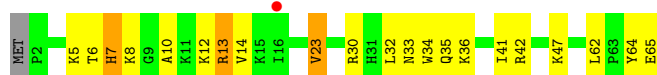
- Molecule 29: 50S ribosomal protein L34



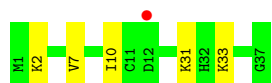
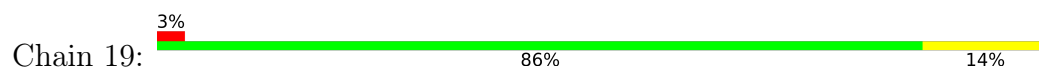
- Molecule 30: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L35



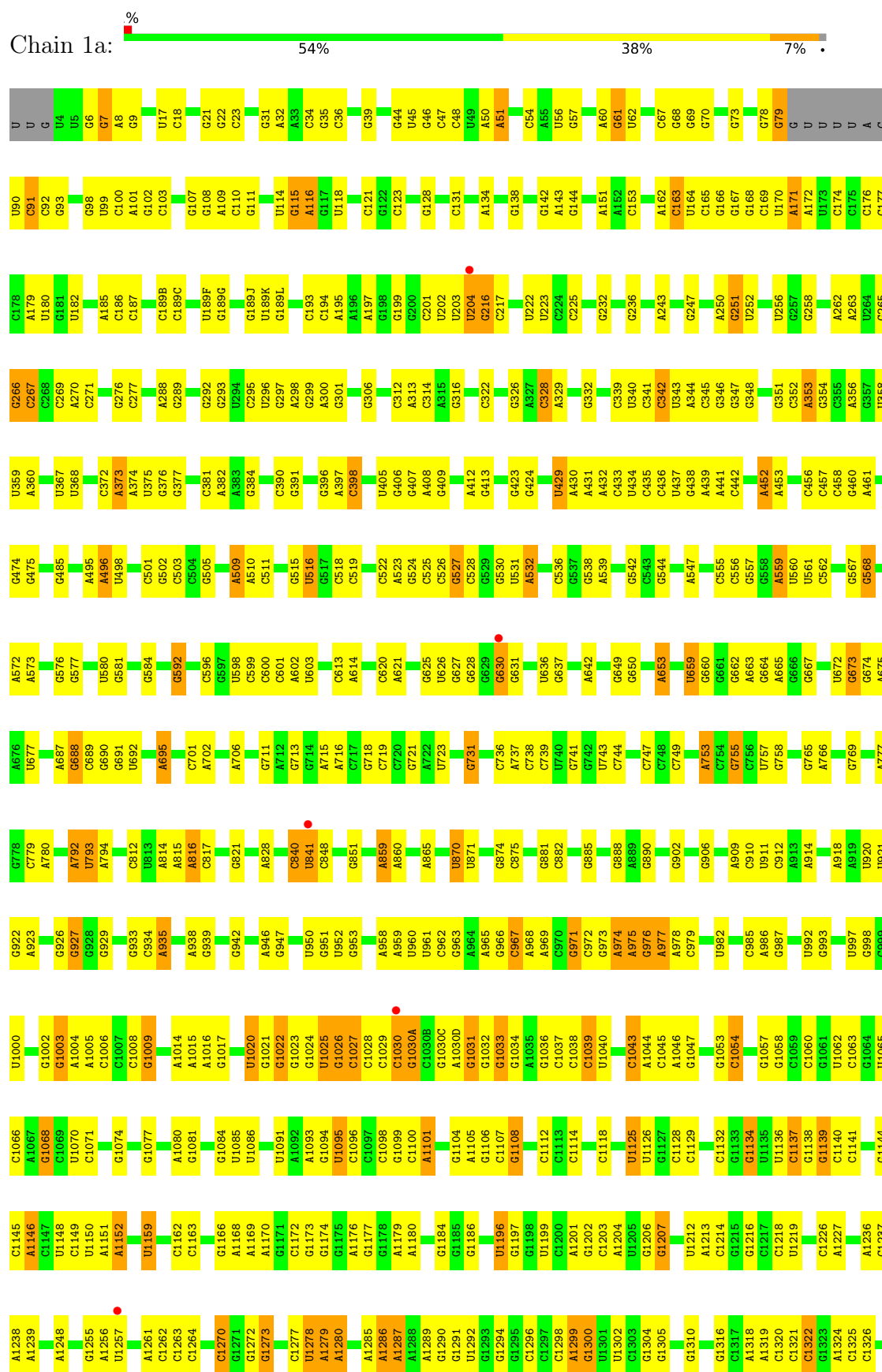
- Molecule 31: 50S ribosomal protein L36

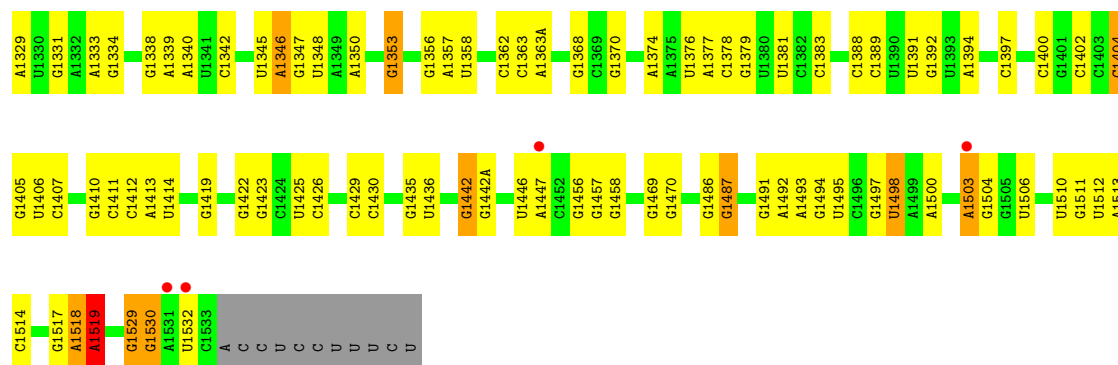


- Molecule 31: 50S ribosomal protein L36

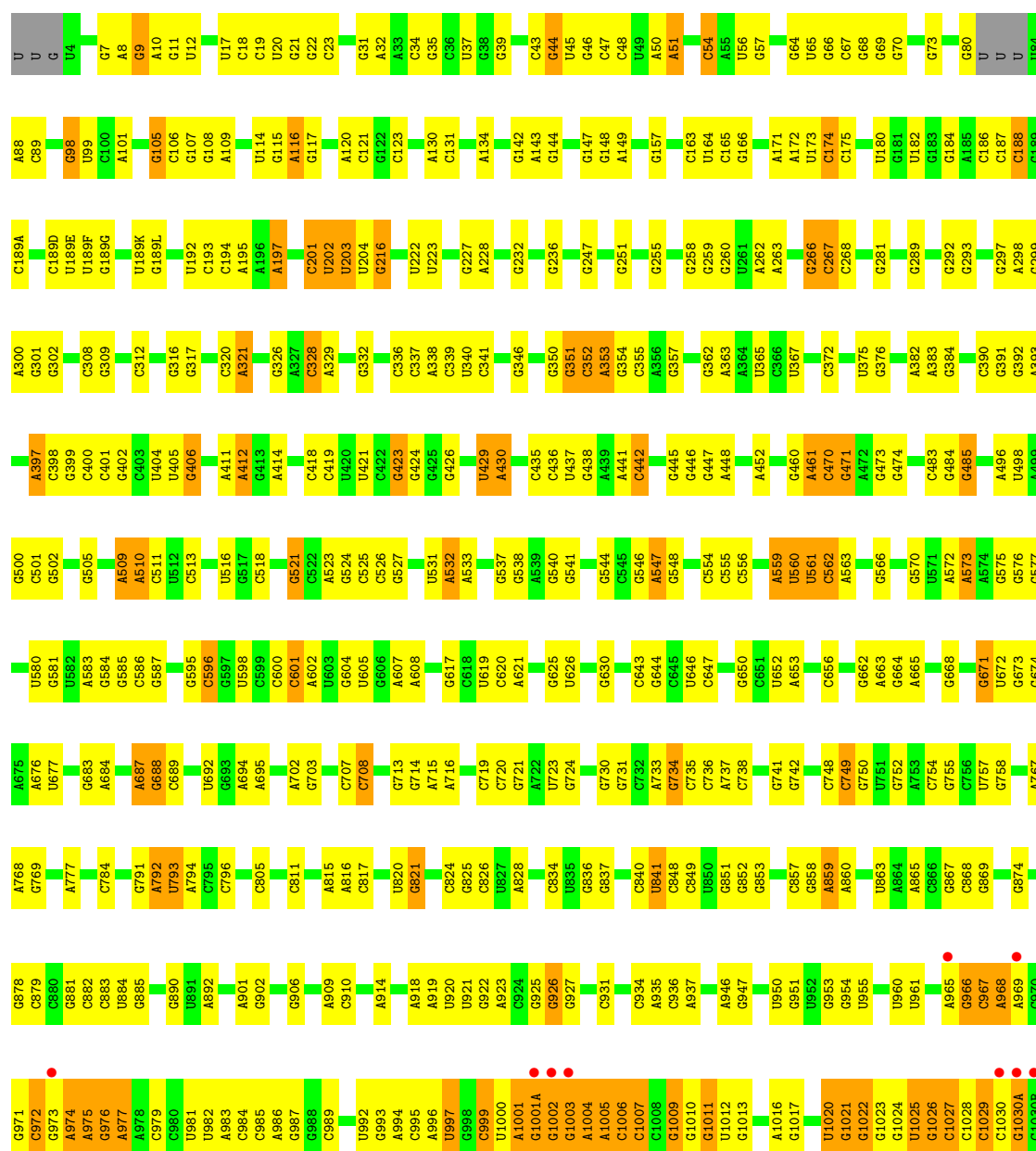


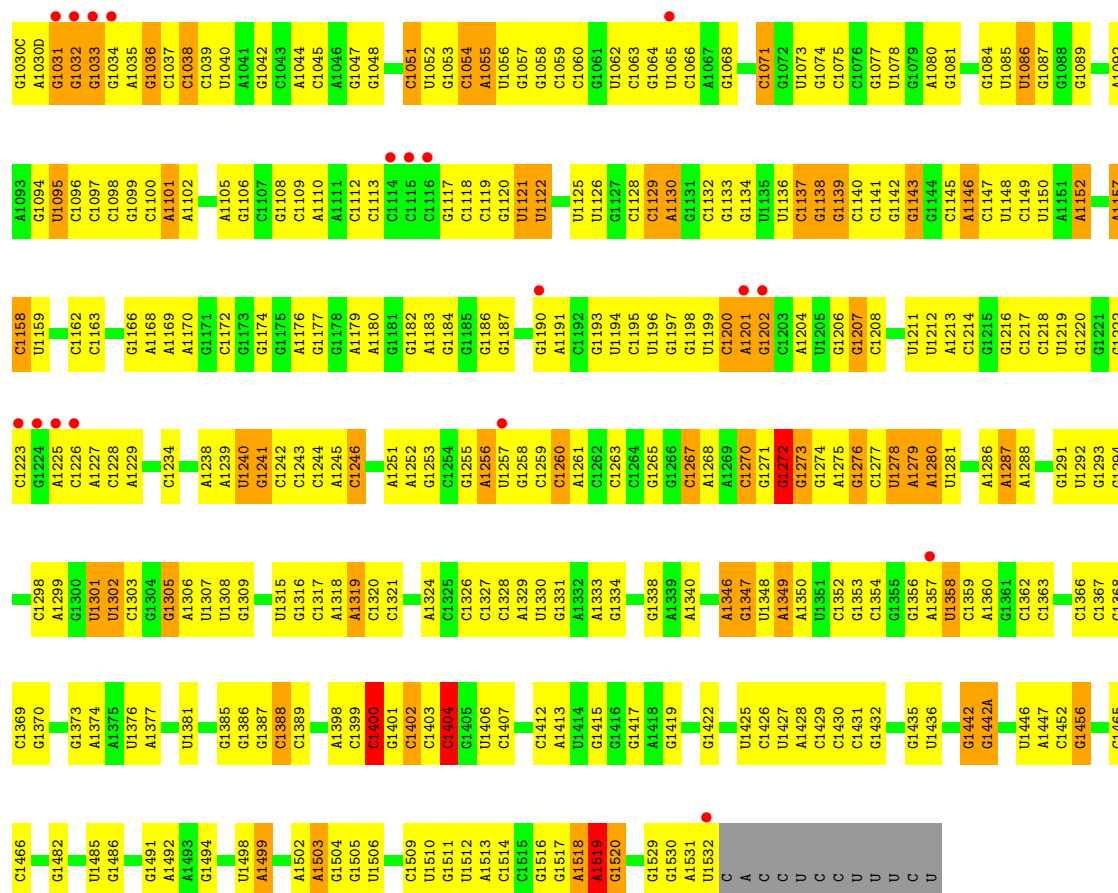
- Molecule 32: 16S Ribosomal RNA



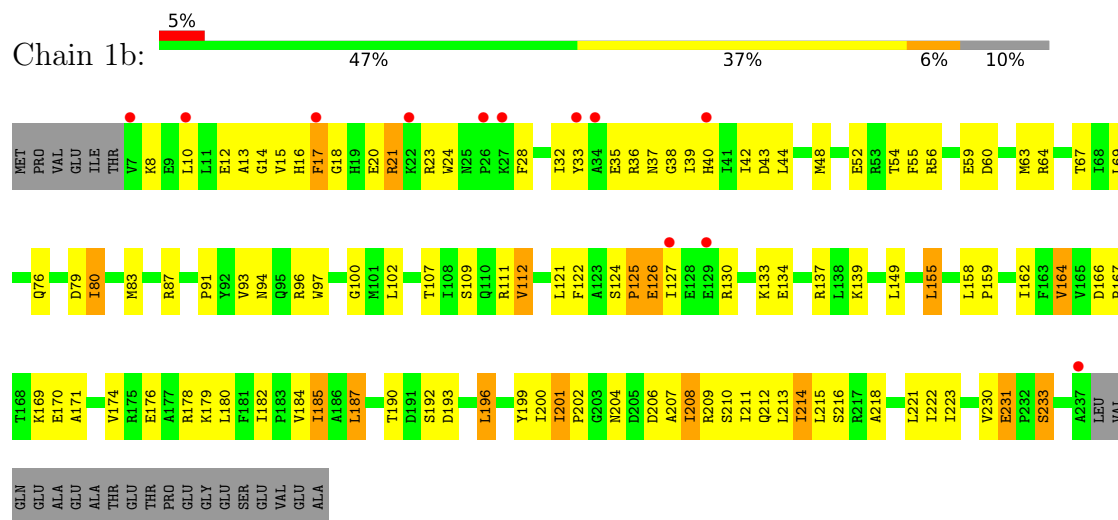


• Molecule 32: 16S Ribosomal RNA

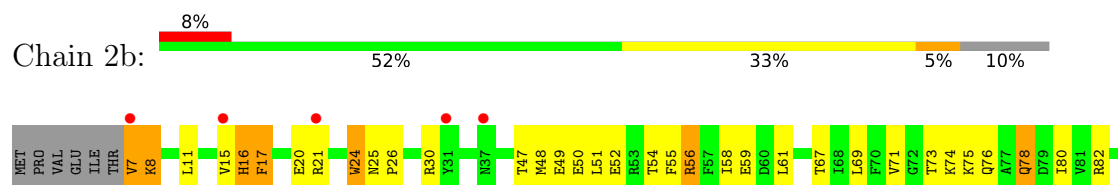


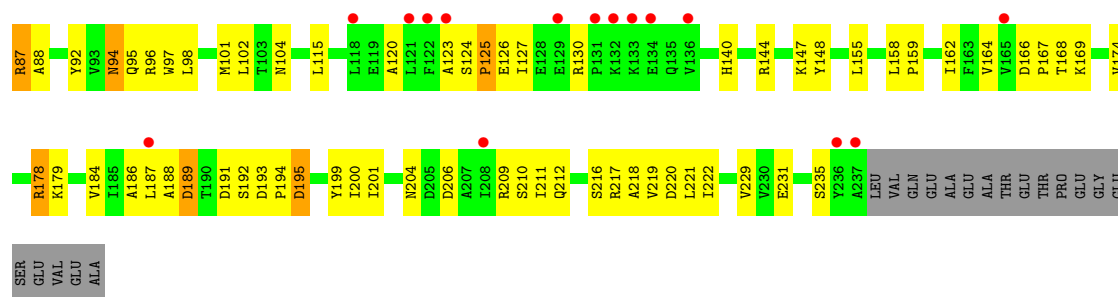


• Molecule 33: 30S ribosomal protein S2

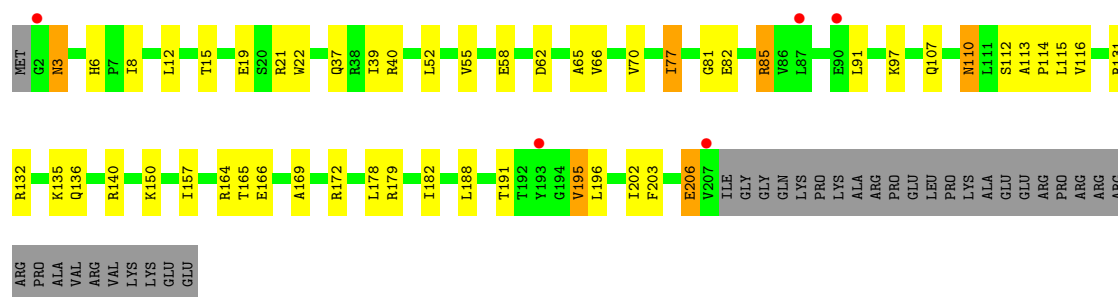


• Molecule 33: 30S ribosomal protein S2

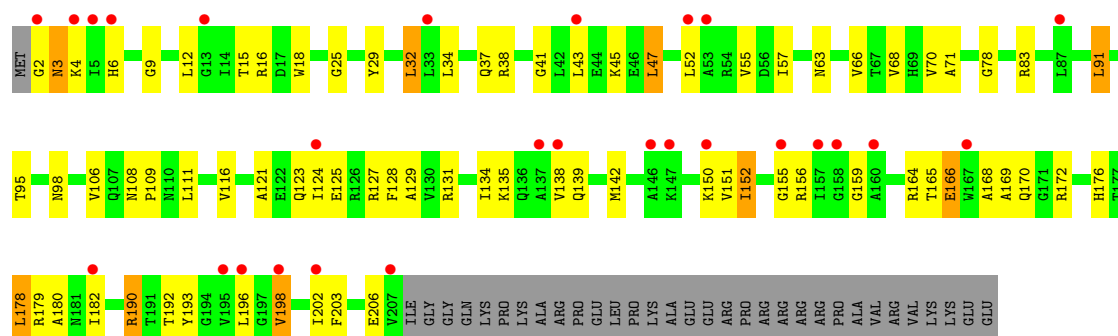




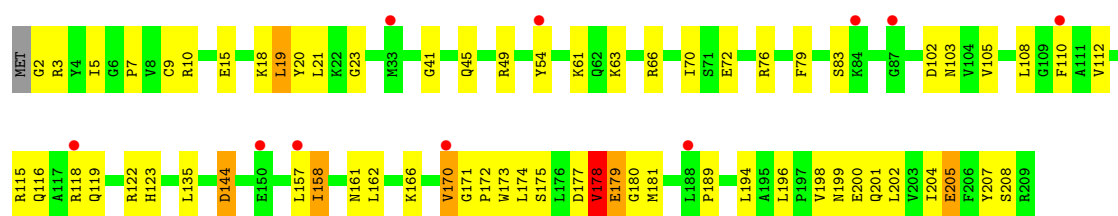
• Molecule 34: 30S ribosomal protein S3



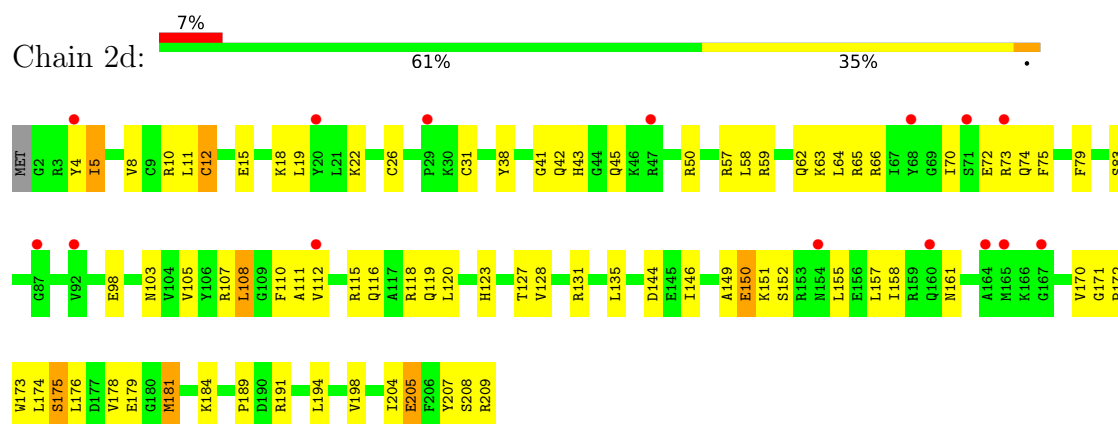
• Molecule 34: 30S ribosomal protein S3



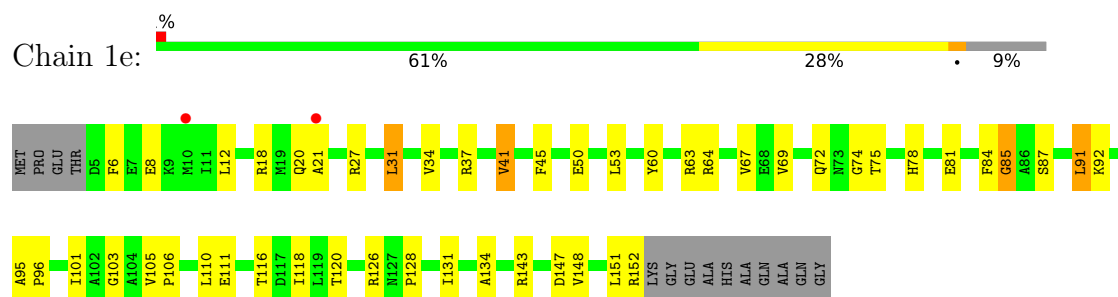
• Molecule 35: 30S ribosomal protein S4



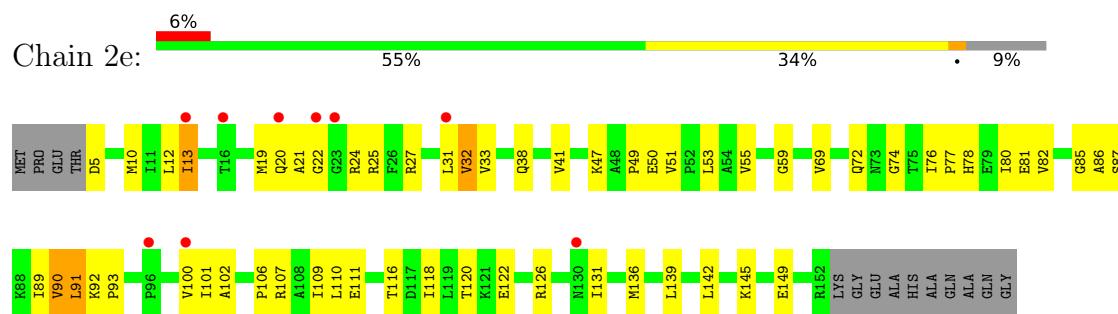
• Molecule 35: 30S ribosomal protein S4



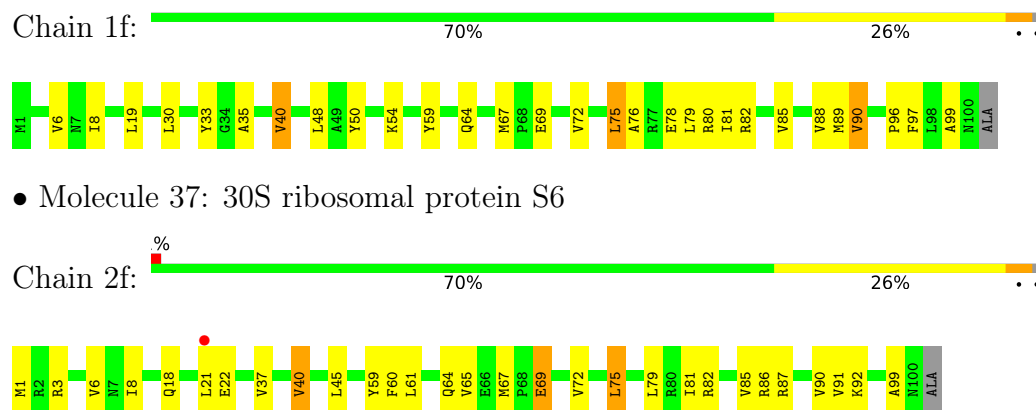
- Molecule 36: 30S ribosomal protein S5



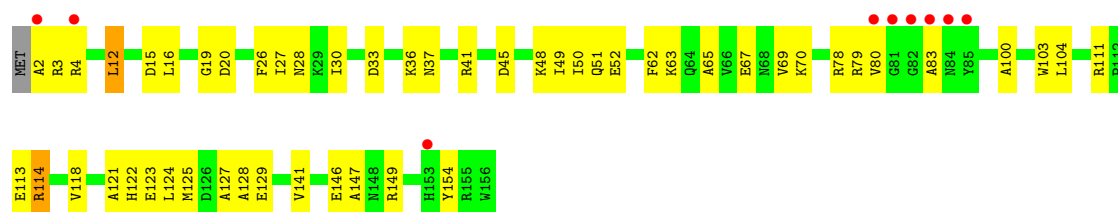
- Molecule 36: 30S ribosomal protein S5



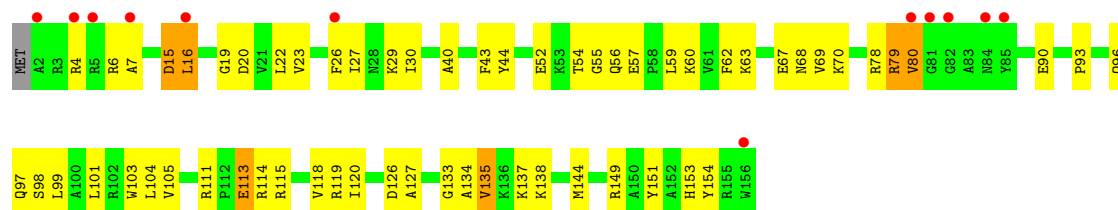
- Molecule 37: 30S ribosomal protein S6



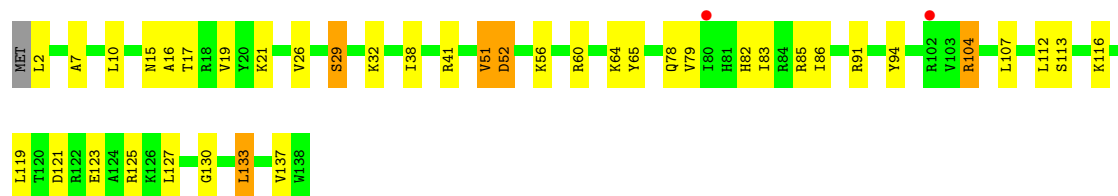
- Molecule 38: 30S ribosomal protein S7



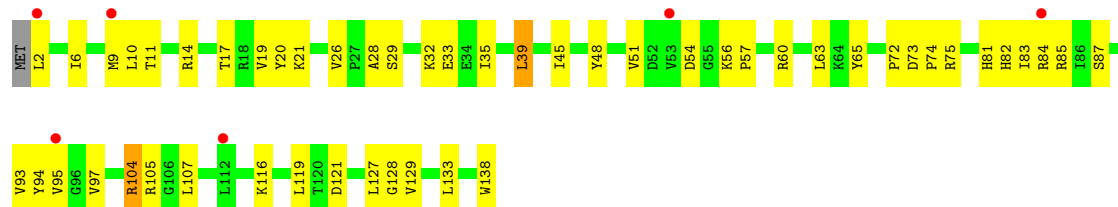
• Molecule 38: 30S ribosomal protein S7



• Molecule 39: 30S ribosomal protein S8



• Molecule 39: 30S ribosomal protein S8

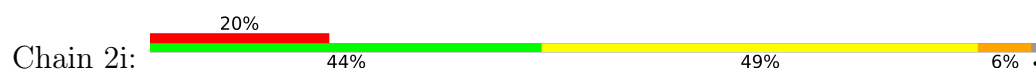


• Molecule 40: 30S ribosomal protein S9

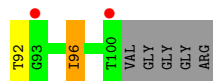




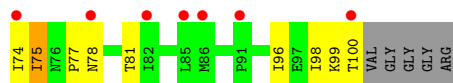
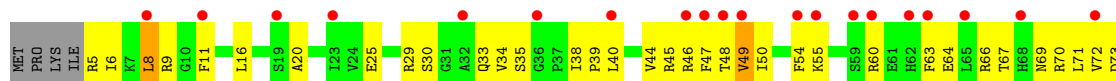
• Molecule 40: 30S ribosomal protein S9



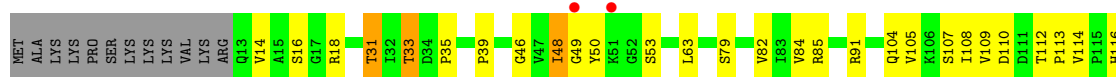
• Molecule 41: 30S ribosomal protein S10



• Molecule 41: 30S ribosomal protein S10

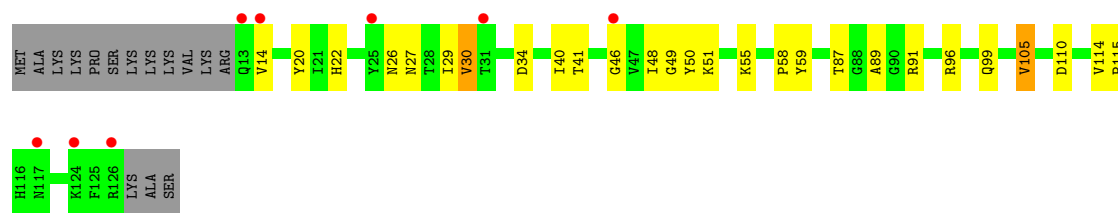


• Molecule 42: 30S ribosomal protein S11

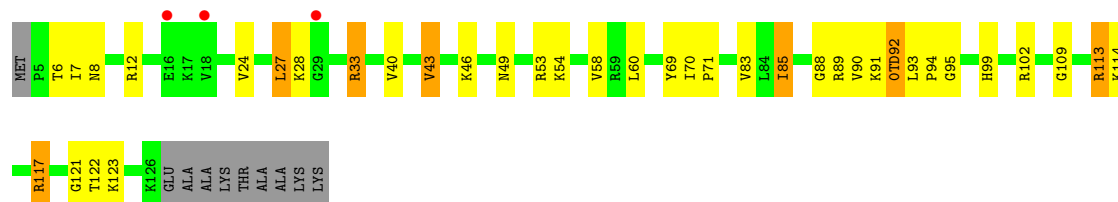


• Molecule 42: 30S ribosomal protein S11

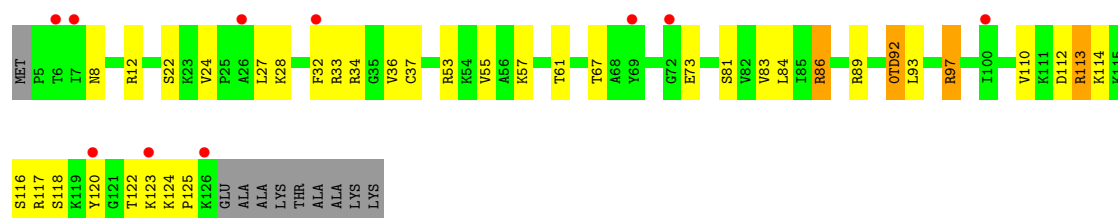




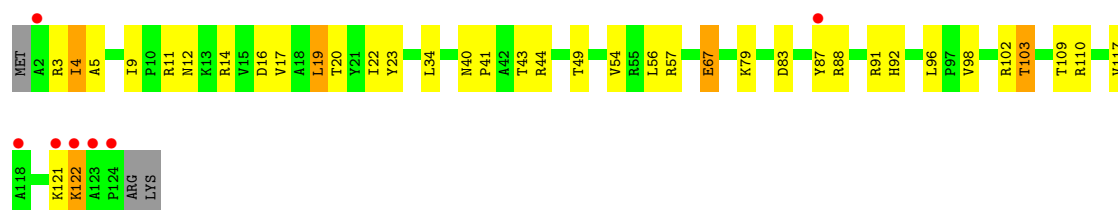
• Molecule 43: 30S ribosomal protein S12



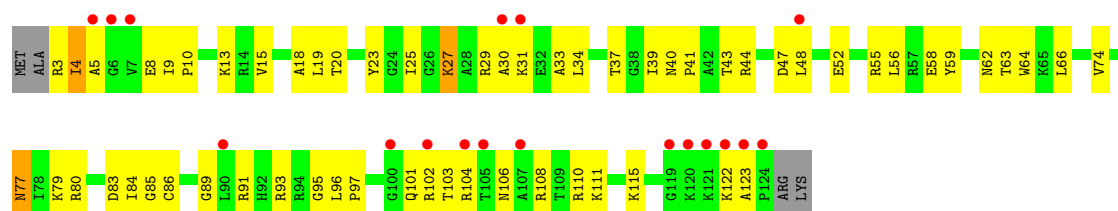
• Molecule 43: 30S ribosomal protein S12



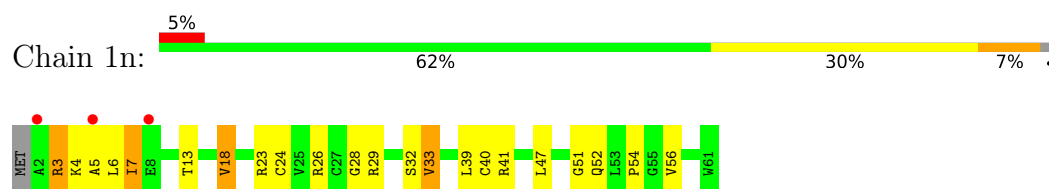
• Molecule 44: 30S ribosomal protein S13



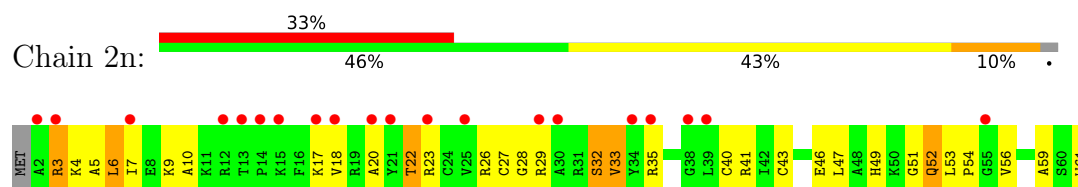
• Molecule 44: 30S ribosomal protein S13



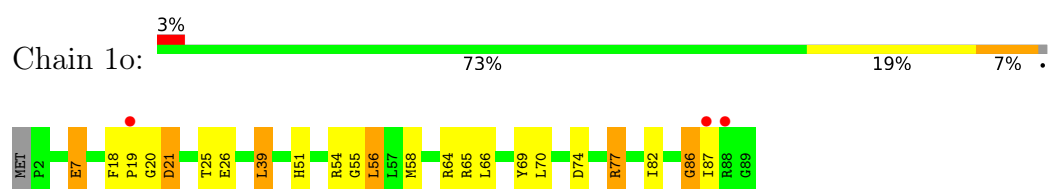
- Molecule 45: 30S ribosomal protein S14 type Z



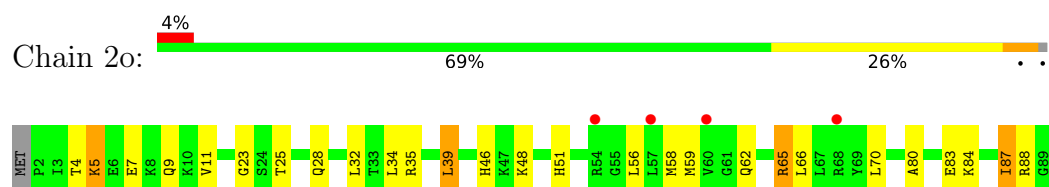
- Molecule 45: 30S ribosomal protein S14 type Z



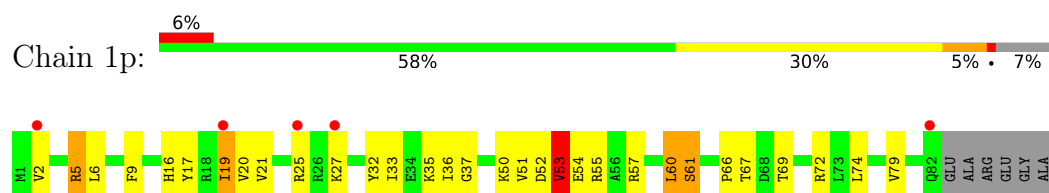
- Molecule 46: 30S ribosomal protein S15



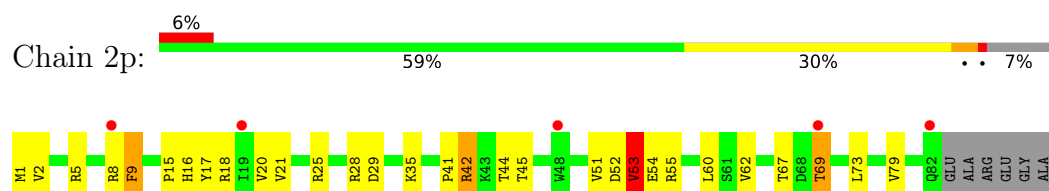
- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16

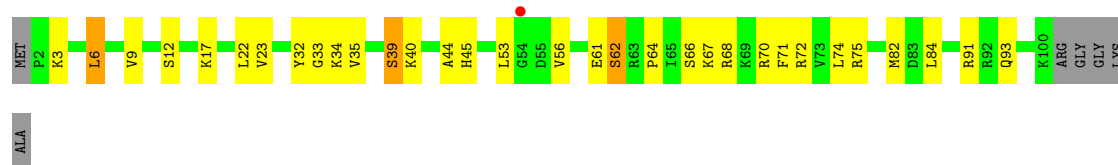


- Molecule 47: 30S ribosomal protein S16

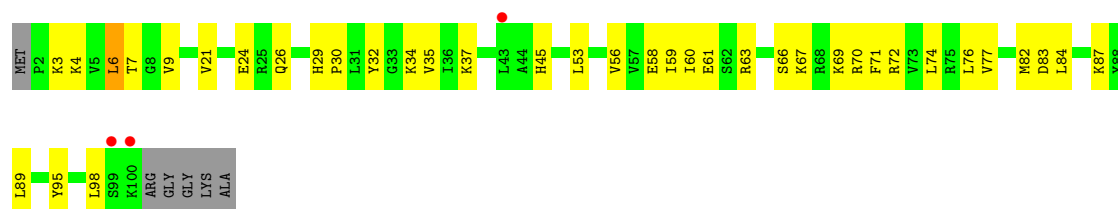


- Molecule 48: 30S ribosomal protein S17

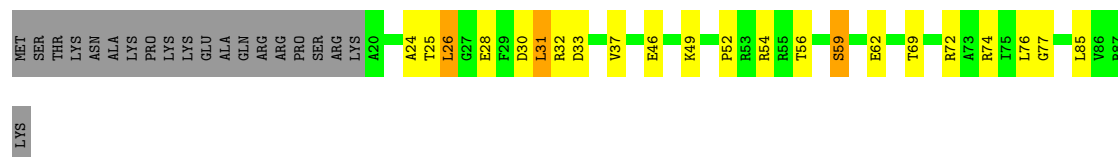




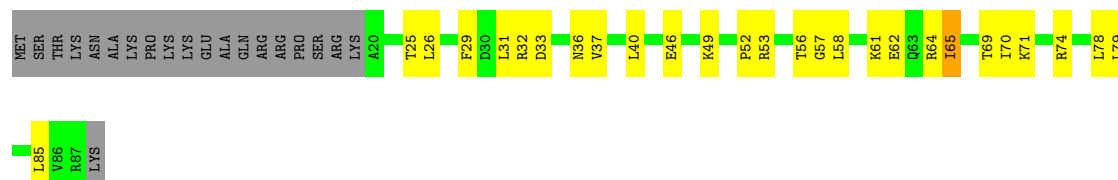
- Molecule 48: 30S ribosomal protein S17



- Molecule 49: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S18

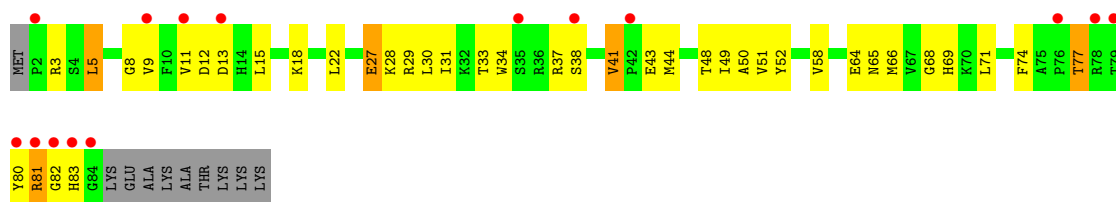


- Molecule 50: 30S ribosomal protein S19

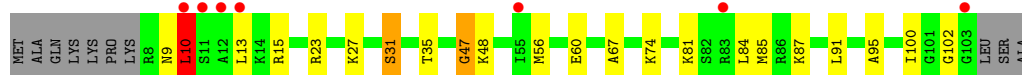


- Molecule 50: 30S ribosomal protein S19

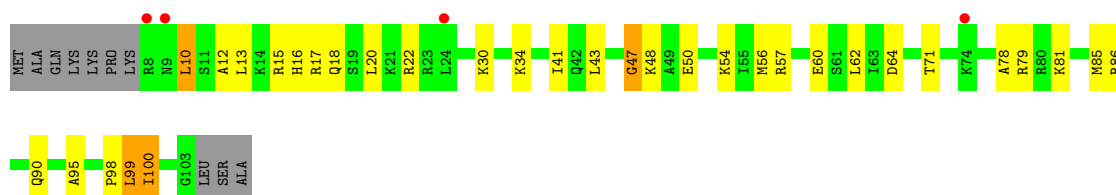




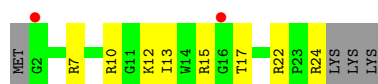
- Molecule 51: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S20



- Molecule 52: 30S ribosomal protein Thx



- Molecule 52: 30S ribosomal protein Thx



- Molecule 53: mRNA



- Molecule 53: mRNA





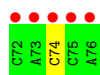
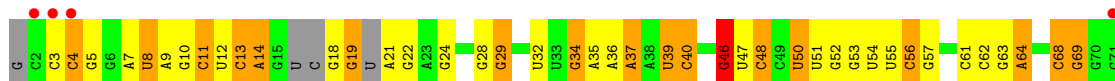
- Molecule 54: A-site and E-site tRNAs



- Molecule 54: A-site and E-site tRNAs



- Molecule 54: A-site and E-site tRNAs

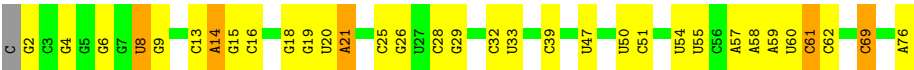


- Molecule 54: A-site and E-site tRNAs

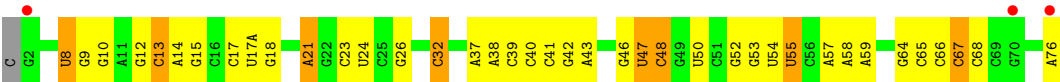


- Molecule 55: P-site tRNA





• Molecule 55: P-site tRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.36Å 447.53Å 617.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	152.88 – 2.89 152.88 – 2.89	Depositor EDS
% Data completeness (in resolution range)	98.5 (152.88-2.89) 98.5 (152.88-2.89)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.216 , 0.263 0.217 , 0.262	Depositor DCC
R_{free} test set	63210 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	69.3	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	297628	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.46% 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: 5MU, 4SU, OMG, MIA, MG, M2G, SF4, 2MG, KAN, UR3, PSU, ZN, 5MC, 2MU, MA6, 4OC, 7MG, 2MA, 0TD

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1A	0.28	0/69009	0.44	2/107712 (0.0%)
1	2A	0.21	0/67293	0.40	1/105034 (0.0%)
2	1B	0.22	0/2882	0.40	0/4494
2	2B	0.20	0/2879	0.38	0/4487
3	1D	0.28	0/2186	0.52	0/2944
3	2D	0.25	0/2186	0.51	0/2944
4	1E	0.27	0/1592	0.50	0/2149
4	2E	0.30	1/1592 (0.1%)	0.44	0/2149
5	1F	0.27	0/1619	0.50	0/2193
5	2F	0.22	0/1615	0.49	2/2188 (0.1%)
6	1G	0.23	0/1448	0.51	1/1957 (0.1%)
6	2G	0.26	0/1453	0.51	2/1963 (0.1%)
7	1H	0.24	0/1356	0.42	0/1834
7	2H	0.22	0/1356	0.41	0/1834
8	1I	0.19	0/1112	0.39	0/1514
8	2I	0.20	0/1079	0.42	0/1475
9	1N	0.25	0/1144	0.46	0/1543
9	2N	0.19	0/1144	0.41	0/1543
10	1O	0.26	0/943	0.48	0/1269
10	2O	0.22	0/943	0.48	0/1269
11	1P	0.26	0/1152	0.50	0/1533
11	2P	0.24	0/1152	0.52	2/1533 (0.1%)
12	1Q	0.28	0/1143	0.49	0/1527
12	2Q	0.21	0/1143	0.44	0/1527
13	1R	0.27	0/982	0.48	0/1312
13	2R	0.22	0/982	0.49	0/1312
14	1S	0.21	0/883	0.45	0/1176
14	2S	0.21	0/880	0.46	0/1172
15	1T	0.24	0/1105	0.51	0/1477
15	2T	0.23	0/1097	0.44	0/1468
16	1U	0.29	0/977	0.48	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.20	0/977	0.40	0/1301
17	1V	0.25	0/782	0.48	0/1049
17	2V	0.19	0/782	0.44	0/1049
18	1W	0.28	0/897	0.47	0/1205
18	2W	0.20	0/897	0.40	0/1205
19	1X	0.30	0/764	0.54	2/1025 (0.2%)
19	2X	0.19	0/764	0.45	0/1025
20	1Y	0.23	0/819	0.46	0/1095
20	2Y	0.19	0/819	0.44	0/1095
21	1Z	0.23	0/1267	0.52	0/1717
21	2Z	0.23	0/1299	0.44	1/1763 (0.1%)
22	10	0.28	0/662	0.54	0/881
22	20	0.23	0/662	0.45	0/881
23	11	0.32	1/762 (0.1%)	0.47	0/1014
23	21	0.23	0/762	0.43	0/1014
24	12	0.31	0/590	0.50	1/781 (0.1%)
24	22	0.20	0/590	0.40	0/781
25	13	0.28	0/474	0.48	0/635
25	23	0.19	0/469	0.41	0/630
26	14	0.25	0/565	0.61	0/761
26	24	0.28	0/545	0.65	1/737 (0.1%)
27	15	0.27	0/469	0.47	0/635
27	25	0.24	0/469	0.45	0/635
28	16	0.26	0/460	0.49	0/613
28	26	0.21	0/456	0.45	0/608
29	17	0.29	0/426	0.47	0/561
29	27	0.26	0/426	0.57	0/561
30	18	0.26	0/525	0.49	0/691
30	28	0.22	0/525	0.39	0/691
31	19	0.28	0/310	0.51	0/407
31	29	0.20	0/310	0.47	0/407
32	1a	0.21	0/35795	0.40	5/55864 (0.0%)
32	2a	0.20	0/35886	0.38	1/56005 (0.0%)
33	1b	0.22	0/1881	0.50	0/2542
33	2b	0.23	0/1860	0.52	2/2518 (0.1%)
34	1c	0.20	0/1572	0.41	0/2126
34	2c	0.22	0/1566	0.45	0/2119
35	1d	0.21	0/1685	0.45	0/2262
35	2d	0.19	0/1704	0.47	0/2284
36	1e	0.22	0/1145	0.47	0/1543
36	2e	0.22	0/1149	0.49	0/1548
37	1f	0.22	0/823	0.41	0/1115
37	2f	0.19	0/829	0.38	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.20	0/1250	0.42	1/1679 (0.1%)
38	2g	0.19	0/1254	0.38	0/1683
39	1h	0.21	0/1108	0.43	0/1494
39	2h	0.19	0/1108	0.42	0/1494
40	1i	0.21	0/1002	0.50	0/1346
40	2i	0.23	0/997	0.52	0/1343
41	1j	0.21	0/722	0.45	0/982
41	2j	0.34	0/727	0.50	0/988
42	1k	0.21	0/844	0.42	0/1145
42	2k	0.23	0/848	0.46	0/1149
43	1l	0.22	0/937	0.46	0/1260
43	2l	0.21	0/937	0.49	1/1260 (0.1%)
44	1m	0.22	0/969	0.48	0/1302
44	2m	0.20	0/961	0.46	0/1291
45	1n	0.21	0/501	0.44	0/664
45	2n	0.25	0/501	0.47	0/664
46	1o	0.19	0/739	0.40	0/985
46	2o	0.18	0/739	0.39	0/985
47	1p	0.20	0/697	0.50	0/939
47	2p	0.19	0/693	0.45	0/935
48	1q	0.20	0/836	0.43	0/1117
48	2q	0.19	0/836	0.38	0/1117
49	1r	0.19	0/560	0.41	0/746
49	2r	0.20	0/560	0.41	0/746
50	1s	0.20	0/667	0.50	0/900
50	2s	0.25	0/661	0.58	0/893
51	1t	0.23	0/730	0.51	0/965
51	2t	0.24	0/729	0.49	0/965
52	1u	0.24	0/203	0.55	0/266
52	2u	0.27	0/203	0.56	0/266
53	1v	0.18	0/310	0.31	0/480
53	2v	0.25	0/310	0.39	0/480
54	1w	0.27	1/1606 (0.1%)	0.45	0/2497
54	1y	0.29	1/1606 (0.1%)	0.44	0/2497
54	2w	0.27	1/1556 (0.1%)	0.41	0/2418
54	2y	0.31	0/1583	0.48	0/2459
55	1x	0.26	0/1725	0.41	0/2689
55	2x	0.26	1/1725 (0.1%)	0.41	0/2689
All	All	0.23	6/316686 (0.0%)	0.43	25/474113 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
33	1b	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	2E	109	LYS	C-N	-8.64	1.29	1.33
54	1y	8	4SU	O3'-P	5.29	1.61	1.56
54	1w	8	4SU	O3'-P	5.17	1.61	1.56
54	2w	8	4SU	O3'-P	5.05	1.61	1.56
55	2x	8	4SU	O3'-P	5.04	1.61	1.56
23	11	67	ILE	CA-CB	-5.01	1.51	1.54

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	359	U	OP1-P-OP2	-14.11	77.28	119.60
32	1a	359	U	O5'-P-OP1	-11.14	74.58	108.00
32	1a	358	U	OP2-P-O3'	-10.54	76.39	108.00
32	1a	358	U	OP1-P-O3'	8.76	134.28	108.00
32	1a	359	U	O5'-P-OP2	7.88	131.63	108.00
6	2G	43	LEU	CA-C-N	-6.78	112.56	122.46
6	2G	43	LEU	C-N-CA	-6.78	112.56	122.46
43	2l	28	LYS	N-CA-C	6.01	118.53	111.02
6	1G	52	ILE	N-CA-C	-5.81	105.71	112.98
1	1A	2014	G	C2'-C3'-O3'	5.76	118.14	109.50
38	1g	128	ALA	N-CA-C	-5.69	106.42	113.19
33	2b	24	TRP	CA-C-N	5.63	129.05	122.52
33	2b	24	TRP	C-N-CA	5.63	129.05	122.52
24	12	7	ARG	NE-CZ-NH2	5.54	124.19	119.20
26	24	54	GLY	N-CA-C	-5.50	108.14	115.40
1	1A	572	A	P-O3'-C3'	5.46	128.40	120.20
11	2P	44	GLY	CA-C-N	5.36	131.35	121.70
11	2P	44	GLY	C-N-CA	5.36	131.35	121.70
21	2Z	52	SER	CB-CA-C	-5.27	110.51	116.63
19	1X	94	GLY	CA-C-N	5.14	130.94	121.70
19	1X	94	GLY	C-N-CA	5.14	130.94	121.70
32	2a	1272	G	N1-C2-N2	-5.10	100.89	116.20
5	2F	21	ALA	CA-C-N	5.04	130.78	121.70
5	2F	21	ALA	C-N-CA	5.04	130.78	121.70
1	2A	1992	G	C2'-C3'-O3'	5.01	117.02	109.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	1b	8	LYS	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	31194	621	0
1	2A	60322	0	30423	738	0
2	1B	2577	0	1305	20	0
2	2B	2575	0	1303	62	0
3	1D	2136	0	2218	49	0
3	2D	2136	0	2218	46	0
4	1E	1559	0	1618	35	0
4	2E	1559	0	1618	43	0
5	1F	1584	0	1625	45	0
5	2F	1580	0	1619	55	0
6	1G	1423	0	1436	36	0
6	2G	1428	0	1438	48	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	41	0
8	1I	1097	0	1140	28	0
8	2I	1064	0	1082	30	0
9	1N	1117	0	1184	19	0
9	2N	1117	0	1184	29	0
10	1O	933	0	996	26	0
10	2O	933	0	996	25	0
11	1P	1135	0	1212	44	0
11	2P	1135	0	1212	43	0
12	1Q	1122	0	1179	33	0
12	2Q	1122	0	1179	41	0
13	1R	968	0	1033	21	0
13	2R	968	0	1033	26	0
14	1S	873	0	927	17	0
14	2S	870	0	923	34	0
15	1T	1091	0	1151	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	2T	1083	0	1136	37	0
16	1U	959	0	1019	14	0
16	2U	959	0	1019	24	0
17	1V	771	0	830	11	0
17	2V	771	0	830	15	0
18	1W	886	0	940	24	0
18	2W	886	0	940	14	0
19	1X	750	0	814	21	0
19	2X	750	0	814	13	0
20	1Y	806	0	881	22	0
20	2Y	806	0	881	18	0
21	1Z	1240	0	1240	35	0
21	2Z	1271	0	1273	49	0
22	10	653	0	674	13	0
22	20	653	0	674	20	0
23	11	755	0	826	15	0
23	21	755	0	826	23	0
24	12	588	0	643	15	0
24	22	588	0	643	9	0
25	13	469	0	518	9	0
25	23	464	0	514	16	0
26	14	552	0	533	18	0
26	24	532	0	503	32	0
27	15	455	0	465	9	0
27	25	455	0	465	9	0
28	16	453	0	473	6	0
28	26	449	0	469	9	0
29	17	418	0	467	16	0
29	27	418	0	467	12	0
30	18	517	0	582	17	0
30	28	517	0	582	20	0
31	19	307	0	335	2	0
31	29	307	0	335	12	0
32	1a	32246	0	16296	447	0
32	2a	32327	0	16336	557	0
33	1b	1846	0	1867	68	0
33	2b	1825	0	1828	71	0
34	1c	1548	0	1535	31	0
34	2c	1542	0	1517	55	0
35	1d	1655	0	1672	47	0
35	2d	1674	0	1714	54	0
36	1e	1129	0	1185	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	2e	1133	0	1191	40	0
37	1f	810	0	804	18	0
37	2f	816	0	808	17	0
38	1g	1231	0	1238	35	0
38	2g	1235	0	1249	50	0
39	1h	1088	0	1126	31	0
39	2h	1088	0	1126	36	0
40	1i	983	0	986	27	0
40	2i	978	0	966	61	0
41	1j	709	0	650	20	0
41	2j	714	0	672	34	0
42	1k	829	0	825	15	0
42	2k	833	0	836	18	0
43	1l	932	0	981	26	0
43	2l	932	0	981	23	0
44	1m	958	0	1002	22	0
44	2m	950	0	988	55	0
45	1n	492	0	529	20	0
45	2n	492	0	529	37	0
46	1o	728	0	760	15	0
46	2o	728	0	760	20	0
47	1p	681	0	697	24	0
47	2p	677	0	686	22	0
48	1q	823	0	891	24	0
48	2q	823	0	891	25	0
49	1r	555	0	618	13	0
49	2r	555	0	618	17	0
50	1s	652	0	662	16	0
50	2s	646	0	644	30	0
51	1t	728	0	798	13	0
51	2t	727	0	796	18	0
52	1u	199	0	208	8	0
52	2u	199	0	208	9	0
53	1v	277	0	140	3	0
53	2v	277	0	140	7	0
54	1w	1592	0	819	32	0
54	1y	1585	0	804	38	0
54	2w	1544	0	788	31	0
54	2y	1565	0	795	46	0
55	1x	1625	0	829	20	0
55	2x	1625	0	829	23	0
56	10	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	11	1	0	0	0	0
56	12	1	0	0	0	0
56	13	4	0	0	0	0
56	14	1	0	0	0	0
56	15	3	0	0	0	0
56	16	1	0	0	0	0
56	17	1	0	0	0	0
56	18	4	0	0	0	0
56	19	3	0	0	0	0
56	1A	932	0	0	0	0
56	1B	29	0	0	0	0
56	1D	4	0	0	0	0
56	1E	4	0	0	0	0
56	1F	3	0	0	0	0
56	1G	2	0	0	0	0
56	1N	2	0	0	0	0
56	1O	2	0	0	0	0
56	1P	2	0	0	0	0
56	1Q	3	0	0	0	0
56	1R	1	0	0	0	0
56	1T	1	0	0	0	0
56	1U	2	0	0	0	0
56	1V	2	0	0	0	0
56	1W	2	0	0	0	0
56	1X	1	0	0	0	0
56	1Y	1	0	0	0	0
56	1a	354	0	0	0	0
56	1d	2	0	0	0	0
56	1e	1	0	0	0	0
56	1i	1	0	0	0	0
56	1k	1	0	0	0	0
56	1l	3	0	0	0	0
56	1m	2	0	0	0	0
56	1o	3	0	0	0	0
56	1q	2	0	0	0	0
56	1r	1	0	0	0	0
56	1v	3	0	0	0	0
56	1w	5	0	0	0	0
56	1x	24	0	0	0	0
56	1y	1	0	0	0	0
56	20	2	0	0	0	0
56	21	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	23	1	0	0	0	0
56	26	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	567	0	0	0	0
56	2B	13	0	0	0	0
56	2D	3	0	0	0	0
56	2E	2	0	0	0	0
56	2F	4	0	0	0	0
56	2G	1	0	0	0	0
56	2Q	2	0	0	0	0
56	2T	2	0	0	0	0
56	2W	1	0	0	0	0
56	2a	227	0	0	0	0
56	2e	1	0	0	0	0
56	2g	1	0	0	0	0
56	2q	1	0	0	0	0
56	2t	1	0	0	0	0
56	2v	2	0	0	0	0
56	2w	1	0	0	0	0
56	2x	7	0	0	0	0
57	1A	99	0	108	6	0
57	1a	33	0	36	3	0
57	2A	66	0	72	4	0
57	2a	33	0	36	2	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
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	1	0
59	2d	8	0	0	1	0
60	10	4	0	0	0	0
60	11	4	0	0	1	0
60	12	2	0	0	0	0
60	13	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	14	1	0	0	1	0
60	15	1	0	0	0	0
60	16	3	0	0	1	0
60	17	3	0	0	0	0
60	18	2	0	0	0	0
60	19	1	0	0	0	0
60	1A	938	0	0	27	0
60	1B	25	0	0	0	0
60	1D	9	0	0	1	0
60	1E	7	0	0	1	0
60	1F	9	0	0	0	0
60	1G	1	0	0	0	0
60	1H	1	0	0	0	0
60	1N	2	0	0	0	0
60	1O	4	0	0	0	0
60	1P	12	0	0	4	0
60	1Q	4	0	0	1	0
60	1R	5	0	0	2	0
60	1S	2	0	0	1	0
60	1T	8	0	0	3	0
60	1U	5	0	0	0	0
60	1V	4	0	0	0	0
60	1W	5	0	0	1	0
60	1X	4	0	0	1	0
60	1Y	5	0	0	0	0
60	1Z	1	0	0	0	0
60	1a	371	0	0	12	0
60	1d	4	0	0	0	0
60	1e	4	0	0	0	0
60	1f	2	0	0	0	0
60	1h	1	0	0	1	0
60	1i	2	0	0	0	0
60	1j	1	0	0	0	0
60	1k	1	0	0	0	0
60	1l	3	0	0	0	0
60	1m	2	0	0	0	0
60	1n	1	0	0	0	0
60	1o	3	0	0	1	0
60	1p	1	0	0	0	0
60	1s	1	0	0	0	0
60	1t	1	0	0	0	0
60	1v	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1w	2	0	0	0	0
60	1x	16	0	0	2	0
60	20	3	0	0	0	0
60	21	4	0	0	0	0
60	25	1	0	0	0	0
60	26	1	0	0	0	0
60	27	1	0	0	0	0
60	28	3	0	0	0	0
60	29	1	0	0	0	0
60	2A	401	0	0	20	0
60	2B	18	0	0	2	0
60	2D	6	0	0	0	0
60	2E	3	0	0	1	0
60	2F	3	0	0	0	0
60	2O	1	0	0	0	0
60	2P	5	0	0	0	0
60	2R	2	0	0	0	0
60	2U	2	0	0	0	0
60	2W	1	0	0	0	0
60	2X	2	0	0	1	0
60	2Y	1	0	0	0	0
60	2a	160	0	0	11	0
60	2e	2	0	0	0	0
60	2i	1	0	0	0	0
60	2l	2	0	0	0	0
60	2m	2	0	0	0	0
60	2o	1	0	0	0	0
60	2t	3	0	0	0	0
60	2w	1	0	0	0	0
60	2x	2	0	0	0	0
All	All	297628	0	196941	4569	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (4569) 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:1128:U:H3	1:1A:1132:A:N6	1.28	1.31
32:2a:1399:C:H4'	32:2a:1400:5MC:H5'	1.35	1.07
32:1a:998:G:H1	32:1a:1043:C:N4	1.52	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1128:U:O4	1:1A:1132:A:N1	1.88	1.06
1:2A:2138:C:N4	1:2A:2153:G:H1	1.55	1.03
32:2a:997:U:H3	32:2a:1044:A:N6	1.56	1.03
32:2a:1002:G:H1	32:2a:1038:C:N4	1.59	1.01
54:2y:5:G:H1	54:2y:68:C:H42	1.01	0.94
32:2a:1025:U:H3	32:2a:1036:G:H1	1.12	0.93
21:2Z:52:SER:OG	21:2Z:53:ILE:N	1.99	0.93
1:1A:2331:G:N7	60:1A:4006:HOH:O	2.02	0.93
54:1w:6:G:H1	54:1w:67:C:N4	1.65	0.93
32:2a:953:G:H5'	32:2a:965:A:H61	1.33	0.93
54:2y:55:PSU:HN1	54:2y:57:G:H5''	1.30	0.92
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.51	0.92
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.52	0.91
55:1x:4:G:H1	55:1x:69:C:H42	1.04	0.91
1:1A:2146:G:H1	1:1A:2196:C:H42	1.14	0.91
1:1A:2587:C:OP2	60:1A:4005:HOH:O	1.89	0.91
54:1w:6:G:H1	54:1w:67:C:H42	0.92	0.91
1:1A:1108:G:H1	1:1A:1123:A:H61	1.17	0.90
54:2y:50:U:H3	54:2y:64:A:H61	1.17	0.90
54:2y:15:G:H22	54:2y:48:C:H42	1.16	0.89
32:1a:559:A:H4'	32:1a:560:U:H3'	1.52	0.89
1:1A:929:G:H1	1:1A:940:C:H42	1.17	0.89
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.05	0.89
20:1Y:92:ASN:HB3	20:1Y:94:LYS:H	1.37	0.88
1:2A:1689:A:H62	1:2A:1698:A:H2	1.18	0.87
54:1w:7:A:H61	54:1w:66:U:H3	1.21	0.86
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.58	0.85
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.58	0.85
32:2a:559:A:H4'	32:2a:560:U:H3'	1.57	0.85
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.09	0.85
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.25	0.85
54:2y:5:G:H1	54:2y:68:C:N4	1.74	0.85
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.10	0.84
1:2A:2136:C:N4	1:2A:2155:G:H1	1.75	0.84
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.09	0.84
32:2a:1002:G:H1	32:2a:1038:C:H42	0.84	0.84
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.60	0.84
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.24	0.84
1:2A:2129:C:H42	1:2A:2159:G:H1	1.20	0.84
1:1A:2695:C:O2	10:1O:70:LYS:NZ	2.11	0.84
55:1x:4:G:H1	55:1x:69:C:N4	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:998:G:N2	32:1a:1043:C:N3	2.26	0.83
42:2k:51:LYS:HA	42:2k:55:LYS:HE3	1.61	0.82
36:1e:78:HIS:HE1	36:1e:143:ARG:H	1.27	0.82
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.44	0.81
1:1A:1085:G:H1	1:1A:1162:C:H42	1.26	0.81
1:2A:2138:C:N3	1:2A:2153:G:N2	2.29	0.81
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.45	0.81
32:2a:975:A:H4'	32:2a:976:G:H5''	1.61	0.81
50:1s:27:GLU:HB2	50:1s:28:LYS:HA	1.63	0.81
1:1A:1100:A:H61	1:1A:1151:U:H3	1.29	0.81
32:1a:953:G:H5'	32:1a:965:A:H61	1.45	0.81
4:1E:34:VAL:HG22	4:1E:48:GLN:HE21	1.46	0.81
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.14	0.81
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.61	0.80
1:1A:1111:U:O2	1:1A:1119:A:N6	2.13	0.80
32:2a:64:G:H4'	32:2a:65:U:H3'	1.63	0.80
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.62	0.80
34:2c:131:ARG:HH21	34:2c:135:LYS:HE3	1.47	0.80
38:1g:50:ILE:HD13	38:1g:125:MET:HG2	1.62	0.80
1:2A:854:G:H2'	1:2A:855:G:H8	1.47	0.80
1:1A:2157:A:H5'	1:1A:2182:G:H4'	1.63	0.79
47:1p:51:VAL:HG12	47:1p:53:VAL:H	1.47	0.79
1:2A:2345:G:H4'	1:2A:2346:A:H5''	1.62	0.79
2:2B:66:A:H61	2:2B:109:C:H5''	1.47	0.79
32:1a:664:G:H22	32:1a:741:G:H1	1.30	0.79
1:2A:2138:C:H42	1:2A:2153:G:H1	0.81	0.79
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.65	0.79
12:2Q:85:LYS:HD3	22:20:7:LEU:HD12	1.62	0.79
47:2p:51:VAL:HG12	47:2p:53:VAL:H	1.47	0.79
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.65	0.79
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.63	0.79
32:2a:596:C:O2	32:2a:644:G:N2	2.15	0.79
55:1x:15:G:OP2	60:1x:201:HOH:O	2.00	0.79
37:2f:67:MET:HE1	37:2f:75:LEU:HD22	1.65	0.79
1:1A:1151:U:H2'	1:1A:1152:G:H8	1.48	0.79
1:1A:294:C:H42	1:1A:390:G:H1	1.29	0.78
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.65	0.78
54:2y:18:G:N2	54:2y:55:PSU:N3	2.26	0.78
1:1A:880:U:O2	11:1P:55:ARG:NH2	2.16	0.78
1:1A:927:G:H2'	1:1A:928:G:H8	1.47	0.78
3:1D:37:LEU:HD13	3:1D:62:TYR:HB2	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:407:G:H5''	35:1d:115:ARG:HG2	1.66	0.77
32:1a:1129:C:H5''	40:1i:16:ARG:HH12	1.48	0.77
37:2f:60:PHE:HE2	49:2r:78:LEU:HD21	1.50	0.77
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.66	0.77
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.63	0.77
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.48	0.77
54:1w:7:A:N6	54:1w:66:U:H3	1.81	0.77
1:2A:2227:A:OP2	60:2A:3605:HOH:O	2.02	0.77
1:1A:2757:G:N3	60:1A:4013:HOH:O	2.18	0.77
32:1a:975:A:H4'	32:1a:976:G:H5''	1.66	0.77
32:1a:1030:C:H42	32:1a:1031:G:H1	1.31	0.77
54:2y:15:G:H22	54:2y:48:C:N4	1.83	0.77
49:1r:32:ARG:HA	49:1r:69:THR:HG21	1.67	0.77
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.18	0.77
11:2P:39:LYS:HB2	11:2P:45:LEU:HG	1.66	0.77
41:2j:8:LEU:HB2	41:2j:96:ILE:HG12	1.66	0.77
32:2a:1030:C:H42	32:2a:1031:G:H1	1.33	0.77
8:1I:38:LEU:HG	8:1I:40:THR:HG22	1.67	0.76
1:2A:1434:A:H61	1:2A:1558:A:H62	1.32	0.76
1:1A:2140:U:O4	1:1A:2170:G:N2	2.18	0.76
23:11:3:LYS:HB2	23:11:61:ARG:HH12	1.50	0.76
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.18	0.76
54:2y:10:G:H1	54:2y:25:C:H42	1.30	0.76
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.67	0.76
32:2a:357:G:O6	60:2a:1903:HOH:O	2.04	0.76
40:2i:3:GLN:HE21	40:2i:20:ARG:HH21	1.33	0.76
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.19	0.76
48:1q:9:VAL:HG12	48:1q:56:VAL:HG22	1.68	0.76
54:1y:50:U:O4	54:1y:64:A:N1	2.19	0.76
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.03	0.76
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.18	0.76
32:2a:1029:C:C4	32:2a:1032:G:N1	2.54	0.75
32:1a:1027:C:C2	32:1a:1034:G:N2	2.54	0.75
33:2b:52:GLU:HG2	33:2b:56:ARG:HH12	1.50	0.75
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.66	0.75
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.22	0.75
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.19	0.75
1:1A:297:C:H2'	1:1A:298:G:H8	1.51	0.75
32:2a:148:G:H2'	32:2a:149:A:H8	1.49	0.75
32:1a:972:C:OP1	60:1a:2001:HOH:O	2.03	0.75
32:1a:1009:G:O6	32:1a:1020:U:O2	2.04	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2114:A:H62	1:2A:2115:G:H21	1.35	0.74
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.68	0.74
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	1.68	0.74
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.20	0.74
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.67	0.74
32:2a:1002:G:N2	32:2a:1038:C:N3	2.33	0.74
1:2A:2127:G:N2	1:2A:2161:C:C2	2.55	0.74
1:1A:1310:G:OP1	27:15:19:ARG:NH2	2.19	0.74
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.69	0.74
54:2w:11:C:H42	54:2w:24:G:H1	1.35	0.74
1:1A:2227:G:H3'	1:1A:2228:G:C8	2.23	0.74
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.52	0.74
54:2y:15:G:N2	54:2y:48:C:H42	1.86	0.74
54:1w:51:U:H3	54:1w:63:G:H1	1.34	0.74
17:2V:40:LEU:HB2	17:2V:46:VAL:HG13	1.68	0.74
32:2a:673:G:H2'	32:2a:674:G:C8	2.23	0.74
1:1A:964:A:N3	2:1B:80:U:O2'	2.20	0.73
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.68	0.73
32:2a:656:C:O2'	46:2o:28:GLN:NE2	2.20	0.73
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.21	0.73
1:1A:973:G:N7	60:1A:4017:HOH:O	2.20	0.73
32:2a:947:G:H1	32:2a:1234:C:H42	1.35	0.73
54:2y:50:U:H3	54:2y:64:A:N6	1.86	0.73
1:2A:2317:C:N4	1:2A:2318:G:O6	2.22	0.73
39:2h:9:MET:HG3	39:2h:26:VAL:HG11	1.71	0.73
1:1A:1956:C:N4	60:1A:4018:HOH:O	2.21	0.73
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.71	0.73
32:2a:1055:A:N7	32:2a:1200:C:N4	2.36	0.73
39:1h:29:SER:HB3	39:1h:32:LYS:HZ3	1.53	0.73
1:1A:2180:A:O2'	1:1A:2181:G:OP2	2.06	0.73
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.60	0.73
36:1e:18:ARG:HD3	36:1e:27:ARG:HH12	1.54	0.73
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.21	0.73
8:2I:124:GLY:H	8:2I:144:VAL:HG23	1.54	0.73
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.22	0.73
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.69	0.72
9:2N:123:TYR:OH	9:2N:130:HIS:NE2	2.18	0.72
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.20	0.72
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.55	0.72
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.69	0.72
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:509:C:OP1	60:2A:3606:HOH:O	2.07	0.72
1:2A:1204:A:H2	1:2A:1241:A:H62	1.36	0.72
1:1A:194:G:O6	23:11:39:LYS:NZ	2.18	0.72
32:1a:1173:G:OP2	60:1a:2002:HOH:O	2.06	0.72
33:1b:17:PHE:HB3	33:1b:44:LEU:HD11	1.70	0.72
32:2a:997:U:H3	32:2a:1044:A:H61	0.81	0.72
39:2h:21:LYS:O	39:2h:65:TYR:OH	2.07	0.72
1:1A:1101:G:H1	1:1A:1150:C:H42	1.38	0.72
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.05	0.72
1:2A:2807:G:N1	1:2A:2893:G:O6	2.17	0.72
35:2d:149:ALA:HB3	35:2d:152:SER:HB2	1.72	0.72
30:18:6:THR:HG22	30:18:63:PRO:HD2	1.70	0.71
33:1b:174:VAL:HG13	33:1b:184:VAL:HG11	1.69	0.71
1:2A:1031:G:H5''	31:29:8:LYS:HE3	1.72	0.71
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.72	0.71
21:2Z:93:ASP:HA	21:2Z:131:ARG:HH22	1.54	0.71
1:1A:2146:G:H1	1:1A:2196:C:N4	1.85	0.71
1:1A:2801:C:OP1	4:1E:61:ARG:NH2	2.23	0.71
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.72	0.71
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.24	0.71
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.26	0.71
48:2q:26:GLN:HG2	48:2q:37:LYS:HG2	1.71	0.71
55:1x:28:C:H2'	55:1x:29:G:H8	1.56	0.71
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.06	0.71
1:2A:1882:C:H5''	23:21:26:ARG:HH21	1.53	0.71
11:2P:121:LYS:HG2	11:2P:123:LEU:HG	1.72	0.71
54:2w:53:G:H1	54:2w:61:C:H42	1.38	0.71
1:2A:2849:U:OP2	15:2T:95:ARG:NH1	2.23	0.71
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.71	0.71
1:1A:1016:C:OP2	60:1A:4007:HOH:O	2.08	0.71
1:1A:2641:A:O2'	1:1A:2642:G:OP2	2.08	0.71
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.72	0.71
32:1a:642:A:N3	39:1h:113:SER:OG	2.23	0.71
32:1a:1030:C:N4	32:1a:1031:G:N1	2.38	0.71
47:1p:52:ASP:O	47:1p:54:GLU:N	2.24	0.71
1:1A:1151:U:H2'	1:1A:1152:G:C8	2.26	0.70
40:1i:53:VAL:O	40:1i:55:ALA:N	2.24	0.70
32:2a:966:M2G:HM23	32:2a:967:5MC:H1'	1.73	0.70
8:1I:78:THR:O	8:1I:104:GLN:NE2	2.22	0.70
32:1a:1030:C:N3	32:1a:1031:G:N2	2.39	0.70
33:1b:201:ILE:HG21	33:1b:214:ILE:HG21	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2646:G:N7	60:1A:4023:HOH:O	2.24	0.70
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.24	0.70
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.57	0.70
3:2D:101:GLU:OE2	3:2D:103:ARG:NH1	2.24	0.70
32:1a:405:U:O4	35:1d:2:GLY:N	2.25	0.70
32:2a:1030:C:N4	32:2a:1031:G:H1	1.88	0.70
32:2a:1347:G:H22	32:2a:1373:G:H2'	1.56	0.70
38:2g:151:TYR:HB3	38:2g:154:TYR:HD2	1.57	0.70
43:2l:57:LYS:HG2	43:2l:67:THR:HG22	1.73	0.70
32:1a:1151:A:HO2'	32:1a:1152:A:H8	1.40	0.70
1:2A:855:G:H1	1:2A:922:U:H3	1.40	0.70
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.24	0.70
12:2Q:12:GLN:HE21	12:2Q:73:PRO:HD2	1.57	0.70
32:2a:1329:A:OP2	52:2u:7:ARG:NH1	2.25	0.70
1:1A:2025:G:OP2	60:1A:4008:HOH:O	2.10	0.70
44:1m:3:ARG:NH2	44:1m:9:ILE:O	2.23	0.70
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.27	0.70
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.24	0.70
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.24	0.70
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.40	0.70
1:1A:1131:A:O2'	1:1A:1150:C:O2'	2.10	0.69
1:1A:1613:A:OP1	3:1D:211:ARG:NH1	2.25	0.69
32:1a:376:G:H5''	47:1p:5:ARG:HG2	1.72	0.69
1:2A:2014:A:H4'	18:2W:92:ARG:HH21	1.57	0.69
1:2A:2036:C:OP1	60:2A:3607:HOH:O	2.10	0.69
1:2A:2313:C:H4'	6:2G:91:ARG:HG3	1.73	0.69
1:1A:2457:G:OP1	5:1F:74:ARG:NH2	2.25	0.69
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.07	0.69
46:1o:18:PHE:O	46:1o:20:GLY:N	2.25	0.69
3:2D:71:ASP:OD2	3:2D:103:ARG:NH2	2.25	0.69
1:1A:1098:C:N4	60:1A:4028:HOH:O	2.25	0.69
18:1W:92:ARG:NH2	60:1W:301:HOH:O	2.25	0.69
1:2A:1721:G:N2	60:2A:3621:HOH:O	2.25	0.69
32:2a:1251:A:HO2'	32:2a:1369:C:HO2'	1.38	0.69
1:1A:928:G:N2	1:1A:943:C:O2	2.26	0.69
1:1A:1099:C:H42	1:1A:1152:G:H1	1.38	0.69
3:1D:69:ARG:NH1	3:1D:128:GLY:O	2.25	0.69
4:1E:167:VAL:HG22	4:1E:170:LEU:HD21	1.75	0.69
10:1O:87:ILE:HD12	10:1O:91:LEU:HA	1.74	0.69
25:13:10:LYS:NZ	25:13:15:TYR:OH	2.25	0.69
32:1a:1086:U:H3	32:1a:1099:G:H22	1.40	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	1.91	0.69
1:2A:459:U:H5''	29:27:40:TRP:CD2	2.26	0.69
1:2A:2513:G:N2	4:2E:143:ASN:OD1	2.25	0.69
7:2H:125:VAL:HG12	7:2H:131:VAL:HG22	1.75	0.69
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.73	0.69
54:2w:8:4SU:S4	54:2w:13:C:O2'	2.50	0.69
35:1d:178:VAL:O	35:1d:180:GLY:N	2.25	0.69
22:20:11:ARG:O	22:20:14:ARG:NH2	2.26	0.69
32:2a:35:G:O2'	43:2l:118:SER:O	2.09	0.69
32:1a:998:G:H1	32:1a:1043:C:H42	0.76	0.69
32:1a:1381:U:H1'	38:1g:79:ARG:HG2	1.74	0.69
1:2A:2127:G:N1	1:2A:2161:C:C4	2.61	0.69
32:2a:1086:U:H3	32:2a:1099:G:H22	1.39	0.69
40:2i:105:ASP:HB2	40:2i:107:ARG:HG3	1.75	0.69
42:2k:22:HIS:HB3	42:2k:29:ILE:HB	1.75	0.69
12:1Q:85:LYS:HG2	22:10:7:LEU:HB3	1.75	0.68
13:1R:63:ARG:NH1	60:1R:301:HOH:O	2.25	0.68
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.58	0.68
17:2V:76:LYS:HB2	17:2V:81:TYR:HB3	1.75	0.68
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.75	0.68
36:2e:20:GLN:NE2	36:2e:21:ALA:O	2.25	0.68
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.73	0.68
1:1A:1391:C:OP2	60:1A:4009:HOH:O	2.11	0.68
34:1c:82:GLU:OE2	34:1c:85:ARG:NH1	2.25	0.68
6:2G:41:GLN:HB3	6:2G:43:LEU:HD22	1.74	0.68
54:2y:10:G:H1	54:2y:25:C:N4	1.92	0.68
32:2a:363:A:OP2	43:2l:34:ARG:NH1	2.26	0.68
38:2g:78:ARG:HH21	38:2g:79:ARG:HH12	1.39	0.68
1:1A:1123:A:H2'	1:1A:1124:U:H4'	1.76	0.68
1:1A:1140:U:H1'	1:1A:1143:U:H5	1.57	0.68
32:1a:1030:C:N4	32:1a:1031:G:H1	1.90	0.68
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.39	0.68
1:2A:2099:U:H3	1:2A:2190:G:H1	1.42	0.68
32:2a:1316:G:H22	32:2a:1319:A:H5''	1.58	0.68
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.59	0.68
1:2A:253:C:OP2	30:28:5:LYS:NZ	2.26	0.68
1:2A:2129:C:N4	1:2A:2159:G:H1	1.90	0.68
1:2A:2534:A:N7	60:2A:3622:HOH:O	2.25	0.68
32:1a:67:C:H2'	32:1a:68:G:C8	2.29	0.68
1:2A:466:A:OP1	29:27:34:ARG:NH1	2.25	0.68
39:2h:20:TYR:HE2	39:2h:75:ARG:HD2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.75	0.68
33:1b:91:PRO:HG2	33:1b:155:LEU:HD13	1.76	0.68
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.59	0.68
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.26	0.68
54:1y:7:A:O2'	54:1y:49:C:OP2	2.09	0.68
1:2A:952:G:OP1	12:2Q:16:ARG:NH2	2.26	0.68
1:1A:739:C:O2'	3:1D:38:LYS:NZ	2.26	0.68
1:1A:2185:C:OP1	1:1A:2187:G:N2	2.27	0.68
5:1F:34:TRP:HA	11:1P:6:LEU:HD13	1.75	0.67
1:2A:1818:U:OP2	3:2D:157:ARG:NH1	2.28	0.67
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.65	0.67
32:2a:976:G:H5'	32:2a:1358:U:O2'	1.94	0.67
32:2a:1029:C:N3	32:2a:1032:G:N2	2.42	0.67
32:2a:1032:G:H2'	32:2a:1033:G:C8	2.30	0.67
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.59	0.67
46:2o:80:ALA:HA	46:2o:83:GLU:HG2	1.74	0.67
32:1a:1027:C:C4	32:1a:1034:G:C2	2.83	0.67
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.76	0.67
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.76	0.67
32:1a:1348:U:H4'	40:1i:120:ARG:HD2	1.76	0.67
1:2A:245:G:O6	30:28:8:LYS:NZ	2.27	0.67
32:1a:1491:G:C5	57:1a:1955:KAN:H2	2.29	0.67
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.75	0.67
32:2a:263:A:OP1	51:2t:79:ARG:NH1	2.28	0.67
32:2a:585:G:OP1	48:2q:37:LYS:NZ	2.27	0.67
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.77	0.67
26:24:24:THR:OG1	26:24:25:TYR:N	2.28	0.67
32:2a:297:G:N2	32:2a:300:A:OP2	2.27	0.67
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.76	0.67
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.76	0.67
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.60	0.67
2:2B:22:U:H3	2:2B:61:G:H1	1.43	0.67
50:2s:27:GLU:HB2	50:2s:28:LYS:HA	1.76	0.67
29:17:24:THR:HG22	29:17:27:GLY:H	1.60	0.67
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.30	0.67
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.76	0.67
47:2p:52:ASP:O	47:2p:54:GLU:N	2.27	0.67
1:1A:2324:U:H5'	6:1G:88:ILE:HD11	1.77	0.67
31:29:29:ASN:HD22	31:29:32:HIS:CE1	2.13	0.67
1:1A:1041:C:OP2	16:1U:54:LYS:NZ	2.26	0.66
1:1A:2336:C:H41	57:1A:3934:KAN:HN11	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:897:C:H1'	54:2w:56:C:C5	2.29	0.66
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.75	0.66
11:2P:60:MET:SD	30:28:13:ARG:NH1	2.66	0.66
38:2g:27:ILE:HD13	38:2g:40:ALA:HA	1.77	0.66
32:1a:67:C:O2'	32:1a:171:A:N3	2.27	0.66
32:2a:266:G:H5''	32:2a:268:C:H41	1.60	0.66
44:2m:25:ILE:HD11	44:2m:66:LEU:HD13	1.76	0.66
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.77	0.66
4:1E:119:ARG:HD2	4:1E:160:TYR:HB2	1.77	0.66
25:13:39:ASP:OD1	25:13:44:ARG:NH1	2.28	0.66
32:1a:1060:C:H5''	41:1j:51:ARG:HG2	1.77	0.66
1:2A:1183:G:H5''	25:23:30:ARG:HH22	1.59	0.66
1:2A:1793:C:OP1	60:2A:3608:HOH:O	2.11	0.66
41:2j:30:SER:O	41:2j:81:THR:OG1	2.13	0.66
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.76	0.66
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.78	0.66
54:2y:55:PSU:N1	54:2y:57:G:H5''	2.08	0.66
1:1A:1040:C:OP1	16:1U:53:ARG:NH2	2.29	0.66
40:1i:128:ARG:NH2	55:1x:33:U:OP2	2.28	0.66
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.24	0.66
6:2G:135:LEU:HD21	6:2G:157:ILE:HD12	1.78	0.66
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.76	0.66
1:1A:943:C:N3	1:1A:944:C:N4	2.43	0.66
1:2A:882:G:H2'	1:2A:883:G:C8	2.30	0.66
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.60	0.66
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.75	0.66
1:1A:1100:A:N6	1:1A:1151:U:H3	1.94	0.66
1:2A:900:A:O2'	1:2A:901:A:OP1	2.13	0.66
1:1A:1110:C:N3	1:1A:1120:G:O6	2.29	0.66
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.11	0.66
4:2E:48:GLN:HE21	4:2E:78:LEU:HG	1.61	0.66
32:2a:643:C:H2'	32:2a:644:G:H8	1.61	0.66
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.77	0.66
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.76	0.66
26:14:58:ARG:NH2	60:14:601:HOH:O	2.28	0.66
32:1a:1199:U:OP1	60:1a:2004:HOH:O	2.13	0.66
15:2T:27:THR:HB	15:2T:89:VAL:HG22	1.78	0.66
32:2a:376:G:H5''	47:2p:5:ARG:HD2	1.78	0.66
32:2a:677:U:H3	32:2a:713:G:H22	1.41	0.66
1:1A:303:C:H42	1:1A:385:G:H1	1.44	0.65
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.29	0.65
54:1w:51:U:H2'	54:1w:52:G:C8	2.31	0.65
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.78	0.65
7:2H:7:LEU:HD12	7:2H:8:PRO:HD2	1.77	0.65
36:2e:74:GLY:HA3	36:2e:116:THR:HG22	1.79	0.65
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.29	0.65
1:2A:2632:A:HO2'	1:2A:2811:G:HO2'	1.36	0.65
1:1A:2585:C:OP1	60:1A:4005:HOH:O	2.13	0.65
32:1a:78:G:C6	32:1a:91:C:N4	2.64	0.65
2:2B:102:A:N7	60:2B:301:HOH:O	2.29	0.65
3:1D:221:VAL:HG22	3:1D:226:MET:HE2	1.79	0.65
32:1a:677:U:H3	32:1a:713:G:H22	1.45	0.65
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.29	0.65
32:2a:1075:C:OP1	33:2b:179:LYS:NZ	2.21	0.65
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.79	0.65
1:2A:2126:A:N6	1:2A:2162:G:O2'	2.23	0.65
32:1a:118:U:H3'	32:1a:288:A:H61	1.61	0.65
1:2A:2393:A:H5''	11:2P:63:PRO:HB3	1.79	0.65
1:1A:927:G:H2'	1:1A:928:G:C8	2.32	0.65
38:1g:78:ARG:HG2	38:1g:79:ARG:H	1.61	0.65
1:2A:918:A:O2'	2:2B:97:G:N2	2.27	0.65
44:2m:85:GLY:HA2	44:2m:93:ARG:HH22	1.62	0.65
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.30	0.65
33:2b:179:LYS:HA	39:2h:72:PRO:HG3	1.78	0.65
1:1A:238:C:O2	30:18:12:LYS:NZ	2.28	0.65
1:1A:2158:C:N3	1:1A:2177:G:N2	2.45	0.65
1:2A:2116:G:N2	1:2A:2162:G:OP1	2.30	0.65
1:1A:1117:G:H1'	1:1A:1135:G:H2'	1.79	0.65
2:2B:7:G:H21	14:2S:38:GLN:NE2	1.94	0.65
41:1j:27:ALA:HB2	41:1j:81:THR:HG21	1.78	0.64
32:2a:1004:A:N6	32:2a:1037:C:O2	2.24	0.64
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.62	0.64
55:2x:40:C:H2'	55:2x:41:C:H6	1.62	0.64
1:2A:1033:U:OP1	31:29:9:ARG:NH2	2.25	0.64
24:22:1:MET:N	24:22:52:ASP:OD1	2.30	0.64
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.79	0.64
32:1a:68:G:H1	32:1a:101:A:H61	1.45	0.64
1:2A:568:U:H5'	1:2A:945:A:N1	2.12	0.64
1:2A:2526:G:O2'	31:29:33:LYS:NZ	2.29	0.64
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.14	0.64
1:2A:2789:C:O3'	60:2A:3609:HOH:O	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:7:G:N2	14:2S:38:GLN:HE22	1.96	0.64
10:2O:49:ARG:NH1	32:2a:1422:G:O3'	2.29	0.64
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.29	0.64
54:1y:8:4SU:H4'	54:1y:48:C:H4'	1.80	0.64
1:2A:2746:U:OP1	7:2H:85:LYS:NZ	2.31	0.64
32:2a:983:A:N1	32:2a:1222:G:N2	2.45	0.64
1:1A:1312:G:O2'	1:1A:2034:G:O6	2.08	0.64
5:1F:108:LYS:HG2	5:1F:112:MET:HE2	1.79	0.64
32:1a:316:G:OP2	32:1a:351:G:O2'	2.16	0.64
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.33	0.64
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.79	0.64
50:1s:28:LYS:NZ	50:1s:46:GLY:O	2.31	0.64
32:2a:975:A:N1	41:2j:48:THR:HB	2.12	0.64
32:2a:1274:G:N2	32:2a:1275:A:N7	2.42	0.64
33:2b:174:VAL:HG13	33:2b:184:VAL:HG11	1.79	0.64
1:1A:1139:G:H3'	1:1A:1140:U:H5''	1.79	0.64
4:1E:132:HIS:NE2	60:1E:401:HOH:O	2.29	0.64
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.62	0.64
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.79	0.64
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.16	0.64
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	1.79	0.64
50:2s:3:ARG:NE	50:2s:8:GLY:O	2.29	0.64
54:1w:5:G:H2'	54:1w:6:G:C8	2.33	0.64
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.33	0.64
1:1A:625:G:O2'	1:1A:702:A:N6	2.29	0.64
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.31	0.64
21:2Z:47:VAL:O	21:2Z:50:GLN:NE2	2.30	0.64
41:2j:5:ARG:N	41:2j:99:LYS:O	2.31	0.64
12:1Q:14:ARG:HG2	12:1Q:41:TRP:HH2	1.62	0.64
21:1Z:150:LEU:HG	21:1Z:151:HIS:H	1.62	0.64
32:1a:888:G:O6	60:1a:2003:HOH:O	2.11	0.64
26:24:53:GLU:HG2	26:24:54:GLY:H	1.62	0.64
32:2a:186:C:H5'	51:2t:78:ALA:HB1	1.80	0.64
54:2y:67:C:H2'	54:2y:68:C:H6	1.63	0.64
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.79	0.63
40:2i:50:LEU:HD13	40:2i:56:LEU:HA	1.80	0.63
1:1A:2153:G:H5''	1:1A:2154:U:H3'	1.80	0.63
8:1I:76:THR:HG22	8:1I:141:LYS:HE2	1.79	0.63
1:2A:1183:G:H5''	25:23:30:ARG:NH2	2.13	0.63
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.33	0.63
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.32	0.63
38:2g:79:ARG:HD2	38:2g:80:VAL:H	1.62	0.63
54:2y:6:G:H1	54:2y:67:C:H42	1.44	0.63
1:2A:861:A:N3	2:2B:79:C:O2'	2.31	0.63
21:2Z:154:ASP:OD1	21:2Z:154:ASP:N	2.19	0.63
34:2c:41:GLY:O	34:2c:45:LYS:NZ	2.29	0.63
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.33	0.63
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.79	0.63
40:1i:23:ASN:HB2	40:1i:25:LYS:HD3	1.79	0.63
1:2A:249:C:O2	30:28:12:LYS:NZ	2.30	0.63
1:2A:2136:C:N4	1:2A:2155:G:N1	2.45	0.63
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.63	0.63
32:2a:986:A:N3	50:2s:52:TYR:OH	2.30	0.63
33:2b:217:ARG:HA	33:2b:220:ASP:HB2	1.80	0.63
34:2c:179:ARG:NH1	34:2c:206:GLU:OE1	2.31	0.63
32:1a:1008:C:N3	32:1a:1021:G:O6	2.32	0.63
6:2G:126:ASP:HB3	6:2G:128:ARG:H	1.63	0.63
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.80	0.63
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.80	0.63
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.81	0.63
32:2a:1400:5MC:H6	32:2a:1400:5MC:H5''	1.63	0.63
32:1a:356:A:N3	32:1a:368:U:O2'	2.29	0.63
32:1a:972:C:O2'	41:1j:55:LYS:O	2.15	0.63
1:2A:852:G:H2'	1:2A:853:G:H8	1.62	0.63
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.15	0.63
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.13	0.63
14:2S:28:VAL:HG11	14:2S:98:VAL:HG13	1.79	0.63
50:2s:28:LYS:HB3	50:2s:29:ARG:CB	2.28	0.63
3:1D:60:ARG:NH1	60:1D:401:HOH:O	2.32	0.63
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.81	0.63
1:2A:2144:U:O2'	1:2A:2147:G:O6	2.15	0.63
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.80	0.63
1:1A:2434:A:O4'	54:1y:76:A:N6	2.32	0.63
32:2a:1047:G:H5''	45:2n:4:LYS:HD3	1.81	0.63
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.81	0.63
1:1A:2335:G:O6	57:1A:3934:KAN:O7	2.15	0.63
6:1G:15:VAL:HG22	6:1G:175:LEU:HB3	1.81	0.63
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.81	0.63
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.99	0.63
26:24:16:CYS:SG	26:24:17:GLY:N	2.71	0.63
32:2a:999:C:H42	32:2a:1042:G:H1	1.47	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1225:A:OP1	44:2m:103:THR:OG1	2.16	0.63
32:2a:1518:MA6:N6	32:2a:1519:MA6:H103	2.13	0.63
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.31	0.63
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.14	0.62
32:1a:1027:C:N4	32:1a:1034:G:C6	2.67	0.62
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.81	0.62
32:2a:573:A:N3	32:2a:883:C:O2'	2.32	0.62
35:2d:157:LEU:O	35:2d:161:ASN:ND2	2.32	0.62
1:1A:922:G:H1	1:1A:948:C:H42	1.44	0.62
1:1A:2158:C:N4	1:1A:2177:G:N1	2.47	0.62
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.32	0.62
1:2A:83:G:H1	1:2A:102:G:HO2'	1.47	0.62
54:2y:18:G:H22	54:2y:55:PSU:HN3	1.42	0.62
1:1A:325:G:OP2	20:1Y:84:ARG:NH2	2.33	0.62
1:1A:1405:A:H2	1:1A:1418:U:O4	1.82	0.62
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.34	0.62
36:1e:78:HIS:CE1	36:1e:143:ARG:H	2.13	0.62
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.13	0.62
4:2E:7:VAL:HG13	4:2E:27:LEU:HB3	1.82	0.62
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.81	0.62
21:2Z:153:SER:HB2	21:2Z:167:PRO:HB3	1.81	0.62
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.32	0.62
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.33	0.62
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.81	0.62
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.81	0.62
42:1k:79:SER:HA	42:1k:104:GLN:HB3	1.81	0.62
1:2A:2422:A:O4'	54:2y:76:A:N6	2.33	0.62
10:2O:77:ILE:HD12	15:2T:74:ARG:HD2	1.81	0.62
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.32	0.62
55:2x:40:C:H2'	55:2x:41:C:C6	2.33	0.62
5:1F:13:SER:OG	5:1F:127:GLU:OE1	2.15	0.62
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.33	0.62
1:2A:2637:U:H5''	4:2E:82:ARG:HH12	1.63	0.62
10:2O:97:ARG:HA	10:2O:117:LEU:HD22	1.81	0.62
32:1a:256:U:OP1	48:1q:17:LYS:NZ	2.32	0.62
1:2A:987:G:O2'	1:2A:1000:A:N3	2.33	0.62
1:2A:2171:A:N3	1:2A:2172:U:N3	2.47	0.62
7:2H:80:SER:OG	7:2H:81:GLU:OE1	2.18	0.62
32:2a:236:G:O2'	48:2q:4:LYS:NZ	2.33	0.62
34:2c:43:LEU:HD21	34:2c:91:LEU:HD13	1.80	0.62
1:1A:99:G:H21	24:12:7:ARG:HH22	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:297:C:H2'	1:1A:298:G:C8	2.34	0.62
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.31	0.62
14:2S:84:GLN:H	14:2S:111:GLU:HB2	1.65	0.62
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.82	0.62
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.28	0.62
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	1.82	0.62
1:2A:2284:C:OP2	28:26:2:ALA:N	2.33	0.62
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.63	0.62
34:2c:182:ILE:HG12	34:2c:203:PHE:HD1	1.64	0.62
54:2y:7:A:O2'	54:2y:49:C:O4'	2.16	0.62
1:1A:2416:C:O3'	11:1P:77:ARG:NH2	2.33	0.62
51:1t:67:ALA:HB1	51:1t:74:LYS:HD2	1.82	0.62
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.35	0.62
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.34	0.62
32:2a:134:A:H61	47:2p:25:ARG:NH1	1.98	0.62
60:2a:1906:HOH:O	44:2m:104:ARG:NH2	2.33	0.62
1:1A:1219:A:H4'	1:1A:1220:U:OP1	1.98	0.61
9:2N:30:ILE:HG23	9:2N:52:VAL:HG11	1.82	0.61
9:2N:42:TRP:HA	9:2N:48:MET:HE1	1.82	0.61
44:2m:3:ARG:HG2	44:2m:9:ILE:H	1.66	0.61
46:2o:4:THR:OG1	46:2o:7:GLU:OE1	2.16	0.61
1:1A:1223:C:H2'	1:1A:1224:C:H6	1.64	0.61
1:1A:2405:A:H5''	11:1P:63:PRO:HB3	1.81	0.61
32:1a:1292:U:OP1	38:1g:41:ARG:NH2	2.33	0.61
1:2A:2299:G:N1	1:2A:2318:G:N7	2.48	0.61
21:1Z:99:TYR:HB3	21:1Z:123:ASP:OD2	2.00	0.61
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.33	0.61
44:2m:37:THR:HG21	44:2m:56:LEU:HA	1.82	0.61
1:1A:1445:C:OP1	19:1X:25:LYS:NZ	2.33	0.61
32:2a:222:U:H2'	32:2a:223:U:C6	2.35	0.61
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.81	0.61
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.83	0.61
1:1A:555:G:N1	1:1A:2045:G:OP1	2.27	0.61
1:1A:1296:G:N3	60:1A:4049:HOH:O	2.31	0.61
1:1A:2013:U:H2'	1:1A:2014:G:H5''	1.83	0.61
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.82	0.61
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.35	0.61
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.82	0.61
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.82	0.61
32:2a:1491:G:C5	57:2a:1828:KAN:H2	2.35	0.61
32:1a:166:G:H2'	32:1a:167:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.33	0.61
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.00	0.61
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.82	0.61
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.34	0.61
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.15	0.61
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.34	0.61
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.36	0.61
32:2a:1190:G:H5''	34:2c:176:HIS:CE1	2.36	0.61
32:2a:1385:G:H2'	32:2a:1386:G:H8	1.66	0.61
35:2d:22:LYS:HG2	59:2d:501:SF4:S4	2.41	0.61
1:1A:906:G:O2'	1:1A:962:G:O6	2.18	0.61
32:1a:719:C:H1'	49:1r:49:LYS:HB3	1.83	0.61
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.36	0.61
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.33	0.61
1:2A:643:A:N1	1:2A:2369:A:O2'	2.32	0.61
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.82	0.61
9:2N:104:LYS:HA	9:2N:107:LEU:HD12	1.83	0.61
54:2y:18:G:N2	54:2y:55:PSU:C4	2.68	0.61
5:1F:185:ASP:OD1	5:1F:188:ARG:NH1	2.32	0.60
34:1c:62:ASP:HA	34:1c:97:LYS:HG2	1.83	0.60
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.82	0.60
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	1.82	0.60
32:2a:953:G:H5'	32:2a:965:A:N6	2.11	0.60
32:2a:987:G:H1	32:2a:1218:C:H42	1.48	0.60
1:1A:2290:A:OP2	22:10:12:ASN:ND2	2.35	0.60
1:1A:2877:G:OP2	15:1T:119:LYS:NZ	2.23	0.60
12:1Q:31:ASP:HA	12:1Q:134:ARG:HH11	1.65	0.60
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.83	0.60
1:1A:2156:A:O2'	1:1A:2157:A:OP1	2.18	0.60
1:1A:2641:A:OP2	60:1A:4010:HOH:O	2.17	0.60
12:1Q:109:VAL:HG13	12:1Q:113:GLN:HB3	1.83	0.60
2:2B:103:G:H21	21:2Z:73:GLN:HE22	1.49	0.60
32:2a:1324:A:OP2	60:2a:1905:HOH:O	2.16	0.60
15:1T:127:ALA:C	15:1T:129:ARG:H	2.09	0.60
32:1a:1458:G:OP1	51:1t:35:THR:OG1	2.18	0.60
33:1b:121:LEU:HD11	33:1b:130:ARG:HH22	1.64	0.60
1:2A:1015:G:H2'	1:2A:1016:G:C8	2.37	0.60
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.34	0.60
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.82	0.60
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.35	0.60
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.34	0.60
32:2a:1271:G:C2	32:2a:1272:G:N7	2.69	0.60
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.66	0.60
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.84	0.60
32:2a:620:C:H2'	32:2a:621:A:O4'	2.02	0.60
34:2c:131:ARG:HH11	34:2c:166:GLU:HG2	1.67	0.60
1:1A:231:G:C8	30:18:5:LYS:HG2	2.35	0.60
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.35	0.60
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.36	0.60
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.37	0.60
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.67	0.60
1:1A:2149:G:H1	1:1A:2183:C:H42	1.49	0.60
21:1Z:1:MET:HG2	21:1Z:55:HIS:ND1	2.16	0.60
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.36	0.60
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.20	0.60
1:2A:2184:G:H2'	1:2A:2185:C:C6	2.37	0.60
1:1A:2658:C:OP2	1:1A:2745:G:O2'	2.18	0.60
32:2a:1005:A:H5''	32:2a:1006:C:C5	2.37	0.60
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.84	0.60
12:1Q:67:ARG:NH1	12:1Q:105:GLU:OE2	2.34	0.60
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.35	0.60
39:1h:10:LEU:HD12	39:1h:85:ARG:HG2	1.83	0.60
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.34	0.60
2:2B:54:G:H21	6:2G:29:TRP:HE1	1.49	0.60
32:2a:1187:G:H5'	40:2i:113:LYS:HE2	1.84	0.60
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.84	0.60
41:2j:74:ILE:HD13	41:2j:81:THR:HG21	1.84	0.60
54:2y:55:PSU:HN1	54:2y:57:G:C5'	2.12	0.60
1:1A:324:A:OP1	20:1Y:86:ARG:NH2	2.34	0.59
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	1.84	0.59
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.34	0.59
54:2w:14:A:H61	54:2w:21:A:H2	1.49	0.59
1:1A:2348:A:H61	22:10:43:THR:HG22	1.67	0.59
23:11:18:ILE:HG12	23:11:37:ILE:HG12	1.84	0.59
32:2a:148:G:H2'	32:2a:149:A:C8	2.35	0.59
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.35	0.59
32:1a:1029:C:H41	32:1a:1030(A):G:N2	2.00	0.59
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.66	0.59
35:1d:7:PRO:HB2	35:1d:10:ARG:HD2	1.83	0.59
54:1y:19:G:N2	54:1y:56:C:N3	2.50	0.59
7:2H:149:ARG:NH1	7:2H:167:GLU:OE2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:2y:7:A:H61	54:2y:66:U:H3	1.50	0.59
54:2y:67:C:H2'	54:2y:68:C:C6	2.37	0.59
1:1A:1942:4OC:HM22	1:1A:1943:G:H5'	1.83	0.59
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.84	0.59
12:1Q:35:VAL:HG13	12:1Q:130:LYS:HB3	1.83	0.59
21:1Z:137:ILE:HA	21:1Z:156:LYS:HZ1	1.67	0.59
32:2a:1190:G:H5''	34:2c:176:HIS:HE1	1.67	0.59
43:2l:117:ARG:HG2	43:2l:122:THR:HB	1.84	0.59
1:1A:265:U:H2'	1:1A:266:C:C6	2.37	0.59
1:1A:1085:G:H1	1:1A:1162:C:N4	1.97	0.59
1:1A:1775:C:N4	60:1A:4058:HOH:O	2.34	0.59
55:1x:28:C:H2'	55:1x:29:G:C8	2.36	0.59
1:2A:2127:G:C2	1:2A:2161:C:N3	2.71	0.59
38:2g:68:ASN:ND2	38:2g:127:ALA:O	2.32	0.59
49:2r:58:LEU:HD22	49:2r:62:GLU:HB3	1.85	0.59
1:1A:1140:U:H1'	1:1A:1143:U:C5	2.36	0.59
54:1w:51:U:H2'	54:1w:52:G:H8	1.66	0.59
1:2A:251:A:C5	1:2A:252:G:H1'	2.37	0.59
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.34	0.59
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.36	0.59
32:2a:362:G:N2	32:2a:365:U:OP2	2.36	0.59
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.17	0.59
8:1I:4:ILE:HD11	8:1I:44:LEU:HD12	1.84	0.59
26:14:54:GLY:N	26:14:55:ARG:HA	2.17	0.59
32:1a:1068:G:H8	32:1a:1068:G:OP2	1.86	0.59
51:2t:56:MET:HE3	51:2t:85:MET:HG2	1.85	0.59
11:1P:7:ARG:HD3	60:1P:301:HOH:O	2.03	0.59
32:1a:69:G:H2'	32:1a:70:G:C8	2.37	0.59
32:1a:673:G:H2'	32:1a:674:G:C8	2.37	0.59
54:1w:43:C:H2'	54:1w:44:G:C8	2.38	0.59
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.20	0.59
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.18	0.59
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.36	0.59
1:2A:2734:A:OP2	60:2A:3610:HOH:O	2.17	0.59
26:24:46:GLN:C	26:24:48:ARG:H	2.10	0.59
1:1A:610:C:OP2	11:1P:21:ARG:NH2	2.36	0.59
32:1a:1498:UR3:O2'	53:1v:17:U:OP1	2.19	0.59
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.35	0.59
35:1d:18:LYS:HG2	59:1d:303:SF4:S1	2.42	0.59
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.35	0.59
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.85	0.59
25:23:6:VAL:HG13	25:23:56:VAL:HG22	1.85	0.59
45:2n:59:ALA:HB1	45:2n:61:TRP:HZ3	1.66	0.59
47:2p:15:PRO:HD2	47:2p:42:ARG:HD3	1.84	0.59
1:1A:2160:C:H42	1:1A:2175:G:H1	1.51	0.59
40:1i:9:ARG:HG2	40:1i:14:VAL:HG12	1.85	0.59
1:2A:854:G:H2'	1:2A:855:G:C8	2.34	0.59
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.38	0.59
5:2F:28:ILE:HG23	5:2F:112:MET:HE3	1.85	0.59
1:1A:1121:C:H2'	1:1A:1122:C:H5'	1.84	0.58
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.21	0.58
37:1f:35:ALA:HA	37:1f:67:MET:HB3	1.85	0.58
11:2P:37:GLY:O	11:2P:40:SER:OG	2.20	0.58
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.35	0.58
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.84	0.58
32:2a:1029:C:N4	32:2a:1032:G:N1	2.50	0.58
6:1G:5:VAL:HG11	6:1G:101:ILE:HG12	1.85	0.58
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.38	0.58
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.84	0.58
14:2S:3:ARG:NH1	14:2S:4:LEU:H	2.01	0.58
54:2y:9:A:H4'	54:2y:46:7MG:H5'	1.85	0.58
1:1A:650:G:N7	11:1P:107:LYS:NZ	2.51	0.58
1:1A:2158:C:N4	1:1A:2177:G:C6	2.72	0.58
1:1A:2690:C:OP2	60:1A:4011:HOH:O	2.17	0.58
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.38	0.58
21:1Z:48:PHE:HE1	21:1Z:71:VAL:HG11	1.68	0.58
34:1c:52:LEU:HD21	34:1c:55:VAL:HG23	1.84	0.58
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.21	0.58
1:2A:2143:C:H2'	1:2A:2144:U:O4'	2.03	0.58
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.36	0.58
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.04	0.58
25:23:23:LEU:HD13	25:23:50:VAL:HG11	1.85	0.58
45:2n:27:CYS:SG	45:2n:28:GLY:N	2.76	0.58
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.37	0.58
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.85	0.58
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.84	0.58
1:2A:848:G:H2'	1:2A:849:A:C8	2.38	0.58
1:2A:1412:A:H2'	1:2A:1413:G:H8	1.68	0.58
1:2A:2224:G:OP1	3:2D:268:ARG:NE	2.37	0.58
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.86	0.58
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:316:G:OP2	32:2a:351:G:O2'	2.21	0.58
8:1I:126:TYR:HB2	8:1I:142:VAL:HG23	1.85	0.58
11:1P:89:ALA:HA	11:1P:121:LYS:HD3	1.85	0.58
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.86	0.58
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.86	0.58
13:2R:20:LEU:HD21	13:2R:40:LYS:HD3	1.85	0.58
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.85	0.58
33:2b:76:GLN:HE21	33:2b:206:ASP:HA	1.68	0.58
1:1A:1384:G:N7	19:1X:62:LYS:NZ	2.43	0.58
1:1A:2564:2MU:O5'	1:1A:2564:2MU:H6	2.04	0.58
1:1A:2692:C:H5'	4:1E:189:PRO:HA	1.86	0.58
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.19	0.58
37:1f:30:LEU:HD23	37:1f:75:LEU:HD11	1.84	0.58
54:1w:60:U:H5''	54:1w:61:C:H5	1.68	0.58
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.34	0.58
1:2A:2136:C:N3	1:2A:2155:G:N2	2.43	0.58
2:2B:7:G:H1	2:2B:114:C:H42	1.51	0.58
6:2G:39:ILE:HG12	6:2G:157:ILE:HG12	1.86	0.58
32:2a:447:G:O6	32:2a:485:G:O2'	2.14	0.58
38:2g:111:ARG:NH2	38:2g:126:ASP:OD2	2.36	0.58
54:2y:58:A:N3	54:2y:60:U:N3	2.52	0.58
1:1A:1361:C:O2'	1:1A:1438:A:N3	2.34	0.58
1:2A:884:C:H3'	1:2A:885:C:C6	2.38	0.58
1:2A:1999:C:O2	1:2A:2687:U:O2'	2.20	0.58
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.69	0.58
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.37	0.58
1:1A:2127:C:H2'	1:1A:2128:G:C8	2.39	0.58
5:1F:51:THR:HB	5:1F:88:VAL:HG11	1.86	0.58
6:1G:122:PRO:HB3	6:1G:170:ARG:HH12	1.69	0.58
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.36	0.58
1:2A:2319:G:H22	14:2S:3:ARG:HH11	1.51	0.58
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.85	0.58
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.84	0.58
10:2O:24:VAL:HG12	10:2O:33:ALA:HB2	1.85	0.58
10:2O:98:VAL:HG22	10:2O:117:LEU:HB3	1.85	0.58
12:2Q:29:PHE:HB3	12:2Q:65:PHE:CD2	2.39	0.58
32:2a:513:C:N4	60:2a:1904:HOH:O	2.36	0.58
19:1X:60:ARG:HH12	29:17:47:ARG:HH12	1.51	0.58
35:1d:170:VAL:HG12	35:1d:171:GLY:H	1.69	0.58
51:1t:9:ASN:O	51:1t:10:LEU:HB2	2.02	0.58
1:2A:2144:U:H1'	1:2A:2148:G:N2	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.03	0.58
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.69	0.58
5:1F:101:LEU:O	5:1F:106:ARG:NH1	2.35	0.57
12:1Q:16:ARG:HG3	12:1Q:18:LYS:HG3	1.86	0.57
12:1Q:16:ARG:O	12:1Q:18:LYS:N	2.37	0.57
36:1e:148:VAL:HG21	39:1h:107:LEU:HB3	1.84	0.57
1:2A:307:G:H21	1:2A:330:A:H62	1.51	0.57
32:2a:34:C:H2'	32:2a:35:G:H8	1.69	0.57
38:2g:57:GLU:HG3	38:2g:60:LYS:H	1.69	0.57
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.84	0.57
54:2w:28:G:H2'	54:2w:29:G:O4'	2.04	0.57
1:1A:831:A:O4'	3:1D:227:ASN:ND2	2.37	0.57
32:1a:171:A:H2'	32:1a:172:A:C8	2.40	0.57
1:2A:2818:G:OP2	13:2R:42:LYS:NZ	2.37	0.57
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.85	0.57
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.04	0.57
38:2g:54:THR:O	38:2g:56:GLN:N	2.32	0.57
1:1A:572:A:H61	17:1V:19:LYS:H	1.51	0.57
1:1A:1740:U:H1'	3:1D:14:ARG:NH2	2.19	0.57
32:1a:1030:C:N3	32:1a:1031:G:C2	2.72	0.57
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	1.86	0.57
1:2A:958:U:O2	2:2B:90:A:O2'	2.19	0.57
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.37	0.57
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.33	0.57
32:2a:662:G:H2'	32:2a:663:A:C8	2.39	0.57
40:2i:23:ASN:HD21	40:2i:25:LYS:HG2	1.69	0.57
51:2t:10:LEU:HG	51:2t:12:ALA:H	1.69	0.57
1:1A:1634:C:H2'	1:1A:1635:C:H6	1.69	0.57
1:1A:2130:C:H2'	1:1A:2131:U:H6	1.70	0.57
1:1A:2133:C:N3	1:1A:2167:C:O2'	2.31	0.57
32:1a:1310:G:OP2	44:1m:88:ARG:NH2	2.37	0.57
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.39	0.57
1:2A:910:A:H62	12:2Q:12:GLN:HA	1.68	0.57
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.40	0.57
1:2A:2032:G:N7	60:2A:3629:HOH:O	2.32	0.57
6:2G:103:LEU:HD23	6:2G:106:LEU:HD23	1.86	0.57
11:2P:88:LEU:HD22	11:2P:95:VAL:HG21	1.86	0.57
23:21:83:GLU:OE1	23:21:83:GLU:N	2.37	0.57
27:25:51:TYR:CE2	27:25:56:LYS:HD2	2.39	0.57
32:2a:34:C:H2'	32:2a:35:G:C8	2.39	0.57
33:2b:144:ARG:NH2	33:2b:148:TYR:OH	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:2m:10:PRO:HD2	44:2m:18:ALA:HA	1.85	0.57
1:1A:1513:G:O2'	1:1A:1593:C:O2'	2.19	0.57
1:1A:1834:A:O2'	3:1D:259:THR:HG21	2.04	0.57
20:1Y:92:ASN:HB3	20:1Y:94:LYS:N	2.14	0.57
42:1k:91:ARG:NH1	42:1k:110:ASP:OD2	2.37	0.57
48:1q:62:SER:OG	48:1q:72:ARG:HG2	2.05	0.57
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.03	0.57
1:2A:774:A:H2'	1:2A:774:A:N3	2.20	0.57
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.40	0.57
7:2H:28:GLY:HA3	7:2H:79:VAL:HB	1.86	0.57
30:28:62:LEU:HB3	30:28:65:GLU:HG2	1.86	0.57
38:2g:15:ASP:OD1	38:2g:19:GLY:N	2.37	0.57
1:1A:910:A:H2'	1:1A:911:G:C8	2.39	0.57
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.39	0.57
32:1a:7:G:H5'	32:1a:298:A:O4'	2.04	0.57
36:1e:78:HIS:HD2	39:1h:104:ARG:HD2	1.69	0.57
1:2A:2820:A:OP1	13:2R:2:ARG:NH2	2.37	0.57
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.22	0.57
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.69	0.57
34:2c:71:ALA:HA	34:2c:106:VAL:HB	1.86	0.57
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.86	0.57
1:1A:2158:C:N3	1:1A:2177:G:C2	2.73	0.57
15:1T:29:ARG:HG3	15:1T:46:GLU:HB2	1.85	0.57
21:1Z:93:ASP:HB3	21:1Z:131:ARG:HH22	1.70	0.57
32:1a:21:G:H2'	32:1a:22:G:C8	2.40	0.57
32:1a:532:A:H2	32:1a:1206:G:H21	1.53	0.57
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.38	0.57
1:2A:637:A:OP1	11:2P:133:SER:OG	2.13	0.57
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.38	0.57
32:2a:1251:A:N1	32:2a:1354:C:O2'	2.32	0.57
32:2a:1251:A:O2'	32:2a:1369:C:O2'	2.10	0.57
32:2a:1288:A:N3	32:2a:1352:C:O2'	2.32	0.57
55:2x:47:U:N3	55:2x:50:U:OP1	2.38	0.57
1:1A:910:A:H2'	1:1A:911:G:H8	1.69	0.57
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.86	0.57
1:1A:2279:A:H5''	1:1A:2280:A:H5'	1.86	0.57
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.85	0.57
21:1Z:23:LYS:HD3	21:1Z:40:ASP:HA	1.87	0.57
35:1d:61:LYS:NZ	35:1d:72:GLU:OE1	2.37	0.57
51:1t:60:GLU:HG3	51:1t:81:LYS:HD2	1.87	0.57
1:2A:1149:G:H2'	1:2A:1150:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:66:ALA:O	14:2S:69:VAL:HG12	2.04	0.57
44:2m:59:TYR:O	44:2m:63:THR:OG1	2.23	0.57
1:1A:2262:G:OP1	12:1Q:85:LYS:NZ	2.29	0.57
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.87	0.57
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.36	0.57
5:2F:185:ASP:OD1	5:2F:188:ARG:NH1	2.37	0.57
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.04	0.57
9:2N:55:VAL:HG23	9:2N:56:ASN:HD22	1.70	0.57
32:2a:538:G:O6	60:2a:1904:HOH:O	2.16	0.57
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.40	0.57
55:2x:40:C:H4'	54:2y:36:A:OP1	2.04	0.57
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.69	0.57
1:2A:878:A:H61	1:2A:899:A:H1'	1.70	0.57
33:2b:15:VAL:HB	33:2b:209:ARG:HB3	1.87	0.57
54:2w:12:U:H3'	54:2w:13:C:H5''	1.85	0.57
32:1a:1002:G:H3'	32:1a:1003:G:C4'	2.31	0.56
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.87	0.56
34:1c:39:ILE:HG23	34:1c:91:LEU:HD11	1.85	0.56
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.68	0.56
55:1x:61:C:H2'	55:1x:62:C:H6	1.68	0.56
1:2A:307:G:N1	1:2A:310:A:OP2	2.35	0.56
1:2A:1021:A:H62	1:2A:1141:U:H3	1.52	0.56
19:2X:1:MET:HE1	24:22:26:ARG:HH21	1.68	0.56
1:1A:2482:G:P	12:1Q:56:ARG:HH12	2.27	0.56
39:1h:51:VAL:HG11	39:1h:60:ARG:HH12	1.70	0.56
44:1m:96:LEU:C	44:1m:110:ARG:HG2	2.30	0.56
49:1r:59:SER:H	49:1r:62:GLU:HB2	1.70	0.56
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.40	0.56
32:2a:17:U:H2'	32:2a:18:C:C6	2.40	0.56
32:2a:601:C:H2'	32:2a:602:A:C8	2.41	0.56
54:2y:2:C:H2'	54:2y:3:C:H6	1.68	0.56
1:1A:1501:U:O2'	1:1A:1502:G:N7	2.34	0.56
1:1A:1814:A:OP1	60:1A:4012:HOH:O	2.17	0.56
10:1O:49:ARG:HH12	32:1a:1423:G:P	2.29	0.56
21:1Z:1:MET:HE1	21:1Z:133:ILE:HG22	1.87	0.56
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.38	0.56
44:1m:40:ASN:HD22	44:1m:43:THR:HG23	1.70	0.56
1:2A:2193:G:H2'	1:2A:2194:G:H8	1.70	0.56
1:2A:2637:U:H5''	4:2E:82:ARG:NH1	2.19	0.56
17:2V:72:VAL:HG13	17:2V:85:LYS:HB2	1.88	0.56
32:2a:975:A:H5'	32:2a:975:A:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:73:ASP:OD2	39:2h:75:ARG:NH2	2.37	0.56
44:2m:4:ILE:HG23	44:2m:5:ALA:H	1.70	0.56
53:2v:14:A:H2'	53:2v:14:A:N3	2.20	0.56
1:1A:11:G:H2'	1:1A:12:U:H5''	1.87	0.56
5:1F:95:ARG:HD3	5:1F:97:TYR:CZ	2.39	0.56
41:1j:5:ARG:NH1	41:1j:71:LEU:HD21	2.19	0.56
1:2A:972:G:OP2	1:2A:973:A:O2'	2.22	0.56
32:2a:130:A:H5'	48:2q:63:ARG:HH11	1.71	0.56
32:2a:157:G:H1	32:2a:164:U:H3	1.53	0.56
32:2a:1026:G:O6	32:2a:1036:G:N2	2.39	0.56
34:2c:52:LEU:HD11	34:2c:55:VAL:HG22	1.86	0.56
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.87	0.56
32:1a:1149:C:H2'	32:1a:1150:U:H6	1.71	0.56
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.06	0.56
2:2B:54:G:H21	6:2G:29:TRP:NE1	2.04	0.56
2:2B:57:A:C4	6:2G:29:TRP:HB3	2.40	0.56
5:2F:155:LEU:HB2	5:2F:189:THR:HG21	1.87	0.56
1:1A:2053:A:C6	1:1A:2510:C:H1'	2.41	0.56
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	1.87	0.56
32:1a:1457:G:H5''	51:1t:35:THR:HG21	1.87	0.56
33:1b:174:VAL:O	33:1b:178:ARG:HG2	2.06	0.56
37:1f:19:LEU:HD11	37:1f:59:TYR:CE1	2.41	0.56
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.05	0.56
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.22	0.56
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.88	0.56
5:2F:95:ARG:HD3	5:2F:97:TYR:CZ	2.41	0.56
32:2a:1009:G:H22	32:2a:1021:G:H1'	1.71	0.56
33:2b:55:PHE:O	33:2b:59:GLU:N	2.36	0.56
33:2b:74:LYS:HG2	33:2b:169:LYS:HG2	1.87	0.56
34:2c:47:LEU:HD12	34:2c:68:VAL:HG11	1.87	0.56
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.40	0.56
32:1a:958:A:C2	50:1s:55:LYS:HB2	2.40	0.56
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.41	0.56
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.40	0.56
45:1n:33:VAL:HA	45:1n:40:CYS:HA	1.86	0.56
1:2A:674:G:H1'	5:2F:74:ARG:HD3	1.88	0.56
1:2A:1823:G:OP1	3:2D:54:ARG:NH1	2.37	0.56
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.41	0.56
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.39	0.56
26:24:53:GLU:H	26:24:53:GLU:CD	2.14	0.56
33:2b:178:ARG:HG2	33:2b:184:VAL:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:34:LEU:HD11	34:2c:38:ARG:HH21	1.70	0.56
34:2c:125:GLU:HB2	34:2c:190:ARG:HH21	1.71	0.56
1:1A:397:G:OP1	1:1A:430:U:N3	2.24	0.56
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	1.87	0.56
32:1a:45:U:H2'	32:1a:46:G:C8	2.41	0.56
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.88	0.56
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.88	0.56
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.17	0.56
1:2A:2540:C:O2'	1:2A:2740:A:N3	2.37	0.56
2:2B:17:C:H2'	2:2B:18:G:O4'	2.05	0.56
22:20:10:THR:HG22	22:20:12:ASN:H	1.70	0.56
40:2i:4:TYR:HB3	40:2i:84:ALA:HB1	1.88	0.56
1:1A:2858:G:C8	15:1T:97:ALA:HB2	2.41	0.56
19:1X:44:GLU:HG3	19:1X:51:VAL:HG23	1.88	0.56
22:10:11:ARG:O	22:10:14:ARG:NH2	2.37	0.56
1:2A:2557:G:H2'	1:2A:2558:C:H6	1.70	0.56
32:2a:1191:A:OP2	34:2c:3:ASN:ND2	2.39	0.56
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.38	0.56
41:2j:8:LEU:HD21	41:2j:20:ALA:HB2	1.88	0.56
44:2m:39:ILE:HD13	44:2m:52:GLU:HB3	1.86	0.56
44:2m:85:GLY:HA2	44:2m:93:ARG:NH2	2.20	0.56
1:1A:9:U:H3	1:1A:2641:A:H2	1.53	0.56
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	1.88	0.56
32:1a:390:C:H2'	32:1a:391:G:C8	2.41	0.56
32:1a:736:C:H2'	32:1a:737:A:C8	2.41	0.56
54:1y:55:PSU:N1	54:1y:57:G:OP2	2.40	0.56
1:2A:27:G:N2	1:2A:512:G:H1'	2.21	0.56
6:2G:115:ARG:HB2	6:2G:115:ARG:HH11	1.70	0.56
32:2a:841:U:C5	32:2a:848:C:H1'	2.41	0.56
32:2a:972:C:O2'	41:2j:55:LYS:O	2.24	0.56
38:2g:133:GLY:O	38:2g:137:LYS:N	2.37	0.56
39:2h:6:ILE:HB	39:2h:85:ARG:HH11	1.71	0.56
1:1A:173:C:H2'	1:1A:174:U:C6	2.41	0.55
5:1F:24:LEU:HD23	5:1F:115:ALA:HA	1.87	0.55
8:1I:31:LEU:HD21	8:1I:38:LEU:HD22	1.87	0.55
15:1T:64:ARG:NH1	15:1T:73:GLU:OE2	2.39	0.55
34:1c:58:GLU:H	34:1c:65:ALA:HB3	1.70	0.55
1:2A:2773:C:OP1	4:2E:166:THR:OG1	2.25	0.55
32:2a:1272:G:N2	32:2a:1273:G:C8	2.72	0.55
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	1.87	0.55
33:2b:96:ARG:HD3	33:2b:98:LEU:HG	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.21	0.55
8:1I:116:LEU:HD21	8:1I:119:PRO:HA	1.88	0.55
12:1Q:138:ASP:OD2	21:1Z:81:ARG:NH1	2.39	0.55
32:1a:765:G:N1	32:1a:812:C:O2'	2.30	0.55
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.03	0.55
32:1a:1379:G:O6	38:1g:2:ALA:N	2.39	0.55
48:1q:45:HIS:H	48:1q:72:ARG:HA	1.71	0.55
1:2A:981:A:N1	1:2A:2027:G:O2'	2.35	0.55
1:2A:1024:G:HO2'	1:2A:1144:G:HO2'	1.45	0.55
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.41	0.55
4:2E:48:GLN:NE2	4:2E:78:LEU:HG	2.20	0.55
18:2W:79:GLY:HA3	18:2W:100:THR:HG22	1.89	0.55
32:2a:920:U:H2'	32:2a:921:U:C6	2.40	0.55
33:2b:95:GLN:HG3	33:2b:147:LYS:HE2	1.88	0.55
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.89	0.55
1:1A:2147:G:N1	1:1A:2194:U:OP1	2.19	0.55
1:1A:2356:U:OP1	28:16:37:ARG:NH1	2.39	0.55
4:1E:119:ARG:HG2	4:1E:120:TRP:CE2	2.42	0.55
36:1e:60:TYR:OH	36:1e:64:ARG:NH2	2.37	0.55
54:1y:15:G:H22	54:1y:48:C:H42	1.54	0.55
1:2A:492:A:H2'	1:2A:493:G:O4'	2.07	0.55
1:2A:855:G:H2'	1:2A:856:C:C6	2.40	0.55
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.39	0.55
33:2b:195:ASP:OD1	33:2b:195:ASP:N	2.38	0.55
40:2i:85:LEU:HB3	40:2i:92:TYR:HD2	1.70	0.55
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.88	0.55
1:1A:359:C:H4'	20:1Y:73:ARG:HD2	1.88	0.55
1:1A:720:C:H5''	5:1F:81:PRO:HD2	1.88	0.55
1:1A:939:C:H2'	1:1A:940:C:C6	2.42	0.55
1:1A:1228:G:O2'	25:13:29:ARG:NH1	2.39	0.55
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.38	0.55
1:2A:2127:G:C6	1:2A:2161:C:N4	2.74	0.55
1:2A:2781:A:H5''	1:2A:2782:G:H5'	1.89	0.55
34:2c:6:HIS:HB3	45:2n:49:HIS:ND1	2.22	0.55
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.41	0.55
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.07	0.55
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.19	0.55
11:1P:59:LEU:HD21	30:18:10:ALA:HA	1.88	0.55
1:2A:2336:A:H61	22:20:43:THR:HG22	1.72	0.55
32:2a:1385:G:H2'	32:2a:1386:G:C8	2.42	0.55
54:2y:8:4SU:H1'	54:2y:48:C:H1'	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:166:LYS:NZ	35:1d:179:GLU:OE2	2.37	0.55
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.71	0.55
47:1p:57:ARG:O	47:1p:61:SER:N	2.36	0.55
32:2a:67:C:H2'	32:2a:68:G:C8	2.41	0.55
37:2f:45:LEU:HD12	37:2f:59:TYR:HD1	1.71	0.55
54:2w:36:A:H2'	54:2w:37:MIA:H8	1.89	0.55
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.41	0.55
7:1H:41:MET:HE1	7:1H:54:ARG:HB3	1.88	0.55
55:1x:8:4SU:O5'	55:1x:8:4SU:H6	2.06	0.55
1:2A:468:G:N7	29:27:39:ARG:NH2	2.54	0.55
1:2A:479:A:N3	1:2A:481:G:H5''	2.21	0.55
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.87	0.55
7:2H:159:GLU:HG2	7:2H:169:VAL:HG11	1.88	0.55
11:2P:95:VAL:HG13	11:2P:125:VAL:HA	1.89	0.55
32:2a:825:G:H21	39:2h:11:THR:HG21	1.71	0.55
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.06	0.55
38:2g:16:LEU:HD21	40:2i:45:ALA:HB2	1.88	0.55
38:2g:27:ILE:HA	38:2g:30:ILE:HD12	1.88	0.55
38:2g:78:ARG:HH21	38:2g:79:ARG:NH1	2.05	0.55
8:1I:5:LEU:HD11	8:1I:19:VAL:HG22	1.89	0.55
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.42	0.55
34:2c:121:ALA:HB2	34:2c:198:VAL:HG21	1.88	0.55
43:2l:24:VAL:HB	43:2l:27:LEU:HD22	1.89	0.55
43:2l:113:ARG:HH21	43:2l:116:SER:HB2	1.72	0.55
54:2w:11:C:N4	54:2w:24:G:H1	2.04	0.55
1:1A:1108:G:H1	1:1A:1123:A:N6	1.97	0.55
1:1A:2786:C:H5''	4:1E:164:ARG:HG2	1.89	0.55
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.42	0.55
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	1.89	0.55
54:1y:36:A:H2'	54:1y:37:MIA:O4'	2.07	0.55
54:1y:48:C:C2	54:1y:59:U:H1'	2.42	0.55
1:2A:1426:G:OP2	1:2A:1427:A:O2'	2.23	0.55
1:2A:2096:U:H3	1:2A:2193:G:H1	1.54	0.55
15:2T:26:ASP:OD1	15:2T:120:ARG:NH2	2.34	0.55
15:2T:94:ALA:HB1	15:2T:99:LEU:HD21	1.89	0.55
32:2a:601:C:H2'	32:2a:602:A:H8	1.70	0.55
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.30	0.55
41:2j:25:GLU:OE2	41:2j:29:ARG:NH2	2.40	0.55
1:1A:210:A:N1	1:1A:254:A:O2'	2.40	0.55
1:1A:1099:C:N4	1:1A:1152:G:H1	2.05	0.55
1:1A:1501:U:OP1	13:1R:77:ARG:NH1	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1897:C:H2'	1:1A:1898:A:O4'	2.07	0.55
1:1A:2495:C:N3	12:1Q:124:LYS:NZ	2.52	0.55
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.07	0.55
32:1a:1316:G:H4'	45:1n:18:VAL:HG11	1.89	0.55
32:1a:1458:G:H5''	51:1t:31:SER:HB2	1.88	0.55
33:1b:200:ILE:HG22	33:1b:202:PRO:HD3	1.87	0.55
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.88	0.55
32:2a:859:A:H2'	32:2a:860:A:O4'	2.07	0.55
32:2a:865:A:H5'	32:2a:1078:U:H5	1.72	0.55
1:1A:572:A:N6	17:1V:19:LYS:H	2.04	0.54
32:1a:373:A:H2'	32:1a:374:A:H8	1.70	0.54
1:2A:234:C:H2'	1:2A:235:U:H6	1.71	0.54
32:2a:1027:C:O2'	32:2a:1034:G:N2	2.40	0.54
1:1A:1108:G:P	1:1A:1116:A:H1'	2.47	0.54
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.54	0.54
54:1w:6:G:N2	54:1w:67:C:N3	2.42	0.54
1:2A:646:A:H2'	1:2A:647:G:O4'	2.07	0.54
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.32	0.54
26:24:60:GLN:O	26:24:62:ARG:NH1	2.39	0.54
28:26:23:THR:OG1	28:26:24:GLU:N	2.40	0.54
32:2a:974:A:P	45:2n:41:ARG:HH12	2.30	0.54
32:2a:1275:A:H3'	32:2a:1276:G:H8	1.72	0.54
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.75	0.54
33:2b:218:ALA:O	33:2b:222:ILE:HG23	2.07	0.54
40:2i:77:ILE:O	40:2i:81:ILE:HG12	2.07	0.54
55:2x:21:A:H62	55:2x:46:G:H2'	1.72	0.54
54:2y:35:A:H2'	54:2y:36:A:O4'	2.07	0.54
1:1A:553:A:O2'	1:1A:554:A:H5'	2.08	0.54
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.89	0.54
32:1a:935:A:O2'	32:1a:1383:C:N3	2.38	0.54
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.89	0.54
1:2A:648:G:O2'	1:2A:2351:G:OP1	2.20	0.54
7:2H:20:ALA:HB3	7:2H:23:ARG:HG3	1.88	0.54
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.23	0.54
21:2Z:5:LEU:HB2	21:2Z:47:VAL:HG21	1.88	0.54
1:1A:273:G:N2	8:1I:50:ARG:HH12	2.04	0.54
1:1A:2122:G:H1	1:1A:2211:U:H3	1.53	0.54
10:1O:64:ARG:HG2	10:1O:83:ALA:HB3	1.90	0.54
21:1Z:7:ALA:HB2	21:1Z:59:LEU:HD22	1.88	0.54
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.73	0.54
32:1a:997:U:H3	32:1a:1044:A:H61	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2387:U:O2'	22:20:19:LYS:NZ	2.41	0.54
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.08	0.54
16:2U:49:HIS:HA	16:2U:52:ARG:HB2	1.89	0.54
32:2a:692:U:O2'	32:2a:694:A:N7	2.30	0.54
1:1A:2802:C:O2	1:1A:2903:G:N2	2.25	0.54
7:1H:127:GLU:HG3	7:1H:130:ARG:HE	1.72	0.54
12:1Q:10:ARG:NH1	60:1Q:301:HOH:O	2.27	0.54
51:1t:87:LYS:O	51:1t:91:LEU:HG	2.08	0.54
1:2A:243:U:OP1	30:28:6:THR:OG1	2.17	0.54
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.73	0.54
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.43	0.54
32:2a:448:A:P	32:2a:485:G:H22	2.30	0.54
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.07	0.54
1:1A:642:G:H5'	5:1F:205:ARG:HD3	1.89	0.54
1:1A:1452:U:H2'	1:1A:1453:C:C6	2.42	0.54
7:1H:17:VAL:HG13	7:1H:26:VAL:HG22	1.89	0.54
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.88	0.54
18:1W:58:ALA:HB1	18:1W:64:MET:HB2	1.89	0.54
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.35	0.54
33:1b:21:ARG:HB3	33:1b:39:ILE:HG13	1.88	0.54
33:1b:60:ASP:HA	33:1b:63:MET:HE3	1.90	0.54
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.23	0.54
1:2A:2261:C:H1'	1:2A:2388:A:N3	2.22	0.54
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.43	0.54
14:2S:7:TYR:CZ	14:2S:91:PRO:HG3	2.43	0.54
15:2T:118:ARG:HG2	32:2a:1442(A):G:C8	2.42	0.54
32:2a:1000:U:H2'	32:2a:1001:A:C8	2.43	0.54
32:2a:1503:A:H1'	53:2v:13:A:N6	2.23	0.54
40:2i:3:GLN:HE21	40:2i:20:ARG:NH2	2.04	0.54
54:2y:18:G:N1	54:2y:55:PSU:C4	2.71	0.54
1:1A:294:C:N4	1:1A:390:G:H1	2.04	0.54
1:1A:1160:G:H2'	1:1A:1161:G:O4'	2.07	0.54
1:1A:1634:C:H2'	1:1A:1635:C:C6	2.42	0.54
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.40	0.54
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.33	0.54
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.88	0.54
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.88	0.54
45:1n:4:LYS:HA	45:1n:7:ILE:HG22	1.89	0.54
1:2A:2305:A:H5''	6:2G:134:GLY:HA3	1.89	0.54
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.41	0.54
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:375:U:OP1	47:2p:69:THR:HG21	2.08	0.54
32:2a:664:G:P	49:2r:64:ARG:HH21	2.30	0.54
1:1A:698:G:H2'	1:1A:699:C:C6	2.42	0.54
2:1B:113:G:N2	14:1S:45:GLY:O	2.40	0.54
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.42	0.54
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.90	0.54
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.90	0.54
21:1Z:1:MET:N	21:1Z:135:GLU:OE2	2.38	0.54
32:1a:1025:U:O2	32:1a:1036:G:O6	2.26	0.54
55:1x:16:C:O2	55:1x:60:U:H4'	2.08	0.54
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.08	0.54
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.41	0.54
1:2A:2343:C:O2'	1:2A:2373:G:O2'	2.26	0.54
32:2a:931:C:H42	32:2a:1386:G:H1	1.55	0.54
32:2a:1228:C:OP1	44:2m:115:LYS:NZ	2.39	0.54
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.22	0.54
39:2h:32:LYS:HA	39:2h:35:ILE:HD12	1.89	0.54
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.42	0.54
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.42	0.54
11:1P:98:GLU:O	11:1P:101:VAL:HG12	2.07	0.54
32:1a:1144:G:N2	32:1a:1146:A:H62	2.05	0.54
32:1a:1414:U:H3	32:1a:1486:G:H1	1.56	0.54
44:1m:19:LEU:HD11	44:1m:56:LEU:HD21	1.89	0.54
1:2A:729:G:O5'	3:2D:208:LYS:NZ	2.41	0.54
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.88	0.54
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.23	0.54
43:2l:8:ASN:O	43:2l:12:ARG:HG3	2.08	0.54
1:1A:1513:G:HO2'	1:1A:1593:C:HO2'	1.48	0.54
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.90	0.54
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.43	0.54
39:1h:121:ASP:OD2	39:1h:125:ARG:NH2	2.41	0.54
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.73	0.54
2:2B:107:G:H2'	2:2B:108:U:H5''	1.91	0.54
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.89	0.54
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.48	0.54
21:2Z:97:GLU:HA	21:2Z:126:VAL:O	2.07	0.54
32:2a:689:C:OP1	42:2k:27:ASN:ND2	2.37	0.54
32:2a:947:G:H1	32:2a:1234:C:N4	2.04	0.54
33:1b:230:VAL:HG22	33:1b:231:GLU:H	1.72	0.53
1:2A:2104:G:H2'	1:2A:2105:C:C6	2.43	0.53
32:2a:881:G:H2'	32:2a:882:C:O4'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1204:A:P	45:2n:3:ARG:HH22	2.31	0.53
41:2j:47:PHE:HB2	41:2j:63:PHE:HB2	1.89	0.53
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.41	0.53
32:1a:128:G:O2'	48:1q:3:LYS:NZ	2.31	0.53
32:1a:166:G:H2'	32:1a:167:G:C8	2.43	0.53
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.07	0.53
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.73	0.53
32:2a:742:G:P	46:2o:35:ARG:HH22	2.31	0.53
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.43	0.53
32:2a:1085:U:H3'	32:2a:1086:U:C5	2.43	0.53
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.08	0.53
36:2e:76:ILE:HD12	36:2e:142:LEU:HD21	1.90	0.53
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.89	0.53
54:2y:42:C:H2'	54:2y:43:C:H6	1.73	0.53
10:1O:63:VAL:HG11	10:1O:85:VAL:HG23	1.89	0.53
32:1a:1346:A:N1	32:1a:1374:A:H5''	2.24	0.53
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.90	0.53
41:1j:5:ARG:HH11	41:1j:71:LEU:HD21	1.74	0.53
1:2A:878:A:N6	1:2A:899:A:O2'	2.42	0.53
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.71	0.53
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.43	0.53
26:24:58:ARG:HD2	50:2s:68:GLY:H	1.74	0.53
32:1a:971:G:N2	32:1a:1363(A):A:OP2	2.39	0.53
54:1y:40:C:H2'	54:1y:41:C:H6	1.73	0.53
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.42	0.53
1:2A:2552:2MU:H2'	1:2A:2554:U:H5''	1.90	0.53
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.43	0.53
9:2N:32:THR:HG23	9:2N:37:LYS:HB2	1.89	0.53
12:2Q:82:ARG:H	22:20:7:LEU:HD11	1.74	0.53
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	1.91	0.53
44:2m:33:ALA:HB1	44:2m:56:LEU:HD11	1.90	0.53
1:1A:1084:C:H42	1:1A:1163:G:H1	1.56	0.53
1:1A:2481:A:O3'	12:1Q:56:ARG:NH1	2.41	0.53
1:1A:2484:G:OP2	60:1A:4014:HOH:O	2.19	0.53
32:1a:920:U:H2'	32:1a:921:U:C6	2.43	0.53
48:1q:9:VAL:HG11	48:1q:84:LEU:HD12	1.89	0.53
1:2A:287:C:H2'	1:2A:288:C:C6	2.44	0.53
1:2A:588:U:H2'	1:2A:589:C:C6	2.43	0.53
1:2A:819:A:OP2	1:2A:1187:G:N2	2.33	0.53
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.22	0.53
3:2D:166:GLN:HB2	3:2D:174:ILE:HG22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:837:G:H1	32:2a:849:C:H42	1.56	0.53
32:2a:1053:G:N7	32:2a:1200:C:H5'	2.24	0.53
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.43	0.53
32:2a:1456:G:O6	51:2t:54:LYS:NZ	2.30	0.53
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.91	0.53
34:2c:127:ARG:NH2	34:2c:192:THR:OG1	2.41	0.53
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.22	0.53
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.90	0.53
1:1A:1115:A:H1'	1:1A:1142:A:H4'	1.90	0.53
1:1A:1735:U:O2	1:1A:1747:A:H5'	2.08	0.53
1:1A:1846:A:OP2	3:1D:54:ARG:NH2	2.41	0.53
1:1A:2347:A:O2'	1:1A:2348:A:OP2	2.25	0.53
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.43	0.53
32:1a:1345:U:OP1	40:1i:120:ARG:NH1	2.42	0.53
55:1x:19:G:H4'	55:1x:20:U:OP2	2.07	0.53
2:2B:55:U:H1'	6:2G:29:TRP:HD1	1.74	0.53
2:2B:87:G:N2	2:2B:90:A:OP2	2.36	0.53
7:2H:43:VAL:HA	7:2H:52:VAL:HG22	1.91	0.53
12:2Q:24:GLY:HA2	12:2Q:67:ARG:NH2	2.24	0.53
32:2a:56:U:H2'	32:2a:57:G:C8	2.44	0.53
32:2a:664:G:H22	32:2a:741:G:H1	1.56	0.53
35:2d:108:LEU:HD11	35:2d:174:LEU:HB3	1.90	0.53
45:2n:6:LEU:O	45:2n:10:ALA:N	2.39	0.53
48:2q:70:ARG:C	48:2q:71:PHE:HD1	2.17	0.53
1:1A:71:U:H5'	24:12:61:LEU:HD12	1.90	0.53
32:1a:44:G:C2	32:1a:45:U:H1'	2.44	0.53
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.44	0.53
1:2A:459:U:H2'	1:2A:460:A:H8	1.73	0.53
1:2A:882:G:H2'	1:2A:883:G:H8	1.70	0.53
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.56	0.53
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.73	0.53
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.91	0.53
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.23	0.53
32:2a:7:G:H5'	32:2a:298:A:O4'	2.09	0.53
32:2a:1243:C:H42	32:2a:1294:G:H1	1.55	0.53
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.91	0.53
32:1a:381:C:H2'	32:1a:382:A:O4'	2.09	0.53
32:1a:1037:C:H2'	32:1a:1038:C:H6	1.74	0.53
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.90	0.53
37:1f:97:PHE:HD2	49:1r:31:LEU:HD11	1.74	0.53
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:116:ASP:OD1	5:2F:119:ARG:NH2	2.41	0.53
26:24:47:GLN:C	26:24:49:PHE:H	2.17	0.53
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.74	0.53
33:2b:16:HIS:CB	33:2b:210:SER:HB2	2.39	0.53
54:2y:6:G:N2	54:2y:67:C:N3	2.56	0.53
1:1A:1101:G:H1	1:1A:1150:C:N4	2.06	0.53
1:1A:1552:C:H2'	1:1A:1553:A:H8	1.74	0.53
1:1A:1785:C:OP1	15:1T:96:ARG:NH1	2.42	0.53
2:1B:90:A:N7	2:1B:91:C:H1'	2.24	0.53
32:1a:17:U:H2'	32:1a:18:C:C6	2.44	0.53
50:1s:27:GLU:OE1	50:1s:27:GLU:N	2.39	0.53
1:2A:323:G:O2'	1:2A:1205:U:N3	2.38	0.53
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.09	0.53
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.09	0.53
32:2a:997:U:O2	32:2a:1044:A:N1	2.41	0.53
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.24	0.53
38:2g:15:ASP:OD2	38:2g:44:TYR:OH	2.26	0.53
42:2k:48:ILE:O	42:2k:50:TYR:N	2.39	0.53
1:1A:63:A:O3'	19:1X:71:GLY:HA3	2.09	0.53
3:1D:155:LEU:HD23	3:1D:177:LEU:HD22	1.91	0.53
4:1E:170:LEU:HB3	4:1E:184:VAL:HG22	1.89	0.53
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.90	0.53
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.43	0.53
21:1Z:100:VAL:O	21:1Z:123:ASP:HB2	2.09	0.53
32:1a:51:A:N7	32:1a:114:U:O2'	2.42	0.53
32:1a:532:A:N6	32:1a:1206:G:O2'	2.42	0.53
1:2A:271(A):A:N7	1:2A:271(W):G:N2	2.56	0.53
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.89	0.53
2:2B:3:C:H2'	2:2B:4:C:C6	2.44	0.53
4:2E:12:THR:HG22	4:2E:13:ARG:H	1.73	0.53
5:2F:133:ASN:N	5:2F:138:GLU:OE1	2.42	0.53
29:27:30:VAL:O	29:27:34:ARG:HG2	2.09	0.53
35:2d:150:GLU:OE1	35:2d:151:LYS:N	2.40	0.53
40:2i:19:LEU:HD12	40:2i:84:ALA:HB3	1.90	0.53
54:2w:68:C:H2'	54:2w:69:G:H8	1.74	0.53
1:1A:1473:A:H4'	1:1A:1474:C:O4'	2.09	0.52
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.06	0.52
32:1a:56:U:H2'	32:1a:57:G:C8	2.43	0.52
32:1a:715:A:H2'	32:1a:716:A:C8	2.44	0.52
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.91	0.52
43:1l:28:LYS:HB2	43:1l:33:ARG:HH21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.43	0.52
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	1.89	0.52
26:24:15:ILE:HB	26:24:32:TYR:HD1	1.74	0.52
32:2a:595:G:N3	32:2a:596:C:N4	2.53	0.52
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.09	0.52
44:2m:79:LYS:NZ	44:2m:83:ASP:OD2	2.37	0.52
1:1A:125:A:H5''	1:1A:126:C:C6	2.44	0.52
1:1A:715:G:H5'	1:1A:716:G:OP2	2.09	0.52
1:1A:2166:U:H3	1:1A:2169:G:H22	1.56	0.52
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.43	0.52
28:16:13:CYS:SG	28:16:47:THR:HG21	2.49	0.52
32:1a:179:A:H2'	32:1a:180:U:H6	1.74	0.52
32:1a:1368:G:OP1	40:1i:111:ARG:NH2	2.43	0.52
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.43	0.52
1:2A:586:A:N1	1:2A:809:G:O2'	2.35	0.52
1:2A:994:C:O2'	1:2A:996:A:OP1	2.17	0.52
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.73	0.52
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.45	0.52
7:2H:113:VAL:HG11	7:2H:151:ILE:HG21	1.91	0.52
26:24:64:GLY:C	26:24:66:SER:H	2.17	0.52
32:2a:1255:G:OP1	41:2j:45:ARG:NH2	2.42	0.52
38:2g:78:ARG:HG2	38:2g:79:ARG:H	1.74	0.52
1:1A:879:G:H5'	11:1P:45:LEU:HD21	1.91	0.52
1:1A:1469:G:OP1	1:1A:1538:G:O2'	2.26	0.52
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.08	0.52
5:1F:135:LYS:HB2	5:1F:138:GLU:CD	2.35	0.52
6:1G:61:ALA:O	6:1G:65:GLY:N	2.43	0.52
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.08	0.52
32:1a:1179:A:H2'	32:1a:1180:A:O4'	2.10	0.52
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.32	0.52
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.42	0.52
40:1i:31:GLN:HE21	40:1i:36:TYR:HD1	1.57	0.52
54:1y:23:A:H2'	54:1y:24:G:C8	2.44	0.52
1:2A:188:G:H5'	23:21:14:VAL:HG21	1.89	0.52
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.10	0.52
2:2B:11:C:OP2	2:2B:12:C:N4	2.30	0.52
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.41	0.52
32:2a:1244:C:H42	32:2a:1293:G:H1	1.56	0.52
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.08	0.52
36:2e:102:ALA:HB1	36:2e:106:PRO:HB2	1.89	0.52
1:1A:68:C:O2	1:1A:72:A:O2'	2.19	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2130:C:H2'	1:1A:2131:U:C6	2.44	0.52
9:1N:112:LEU:O	9:1N:116:LEU:HG	2.09	0.52
16:1U:28:ARG:NH1	16:1U:38:THR:OG1	2.39	0.52
32:1a:116:A:H61	32:1a:313:A:H1'	1.75	0.52
32:1a:1304:G:C6	32:1a:1305:G:N1	2.78	0.52
41:1j:55:LYS:O	41:1j:57:LYS:N	2.43	0.52
1:2A:568:U:H5'	1:2A:945:A:C6	2.44	0.52
1:2A:955:C:OP1	12:2Q:87:LYS:HE3	2.09	0.52
3:2D:72:LYS:HB3	3:2D:75:ILE:HD12	1.90	0.52
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.42	0.52
26:24:15:ILE:HB	26:24:32:TYR:CD1	2.45	0.52
32:2a:646:U:H2'	32:2a:647:C:C6	2.44	0.52
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.90	0.52
1:1A:494:G:OP2	29:17:37:LYS:NZ	2.42	0.52
1:1A:1068:G:OP2	9:1N:65:LYS:NZ	2.43	0.52
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.38	0.52
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.91	0.52
32:1a:526:C:OP2	43:1I:91:LYS:HE3	2.08	0.52
32:1a:1004:A:C5'	32:1a:1024:G:H1	2.23	0.52
32:1a:1162:C:N4	32:1a:1174:G:H1	2.08	0.52
2:2B:83:G:N2	2:2B:94:C:O2	2.33	0.52
32:2a:1109:C:H2'	32:2a:1110:A:O4'	2.09	0.52
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.25	0.52
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	1.90	0.52
45:2n:43:CYS:HA	45:2n:46:GLU:HG3	1.92	0.52
48:2q:76:LEU:HD12	48:2q:77:VAL:H	1.73	0.52
1:1A:734:C:H1'	29:17:4:THR:HG22	1.92	0.52
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.45	0.52
12:1Q:51:ARG:HG3	12:1Q:66:ILE:HD11	1.92	0.52
15:1T:112:ARG:NH2	60:1T:303:HOH:O	2.42	0.52
32:1a:437:U:OP2	60:1a:2006:HOH:O	2.19	0.52
32:1a:580:U:H2'	32:1a:581:G:O4'	2.09	0.52
33:1b:112:VAL:HG12	33:1b:149:LEU:HD22	1.91	0.52
44:1m:3:ARG:HB2	44:1m:57:ARG:HH21	1.74	0.52
45:1n:23:ARG:HD2	45:1n:28:GLY:O	2.09	0.52
1:2A:271(G):C:H2'	1:2A:271(H):G:H8	1.74	0.52
2:2B:115:G:H2'	2:2B:116:G:O4'	2.09	0.52
32:2a:946:A:H2'	32:2a:947:G:C8	2.44	0.52
32:2a:1027:C:N4	32:2a:1036:G:O6	2.43	0.52
32:2a:1129:C:O2'	32:2a:1130:A:N7	2.39	0.52
32:2a:1193:G:O2'	36:2e:25:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.44	0.52
33:2b:216:SER:O	33:2b:220:ASP:N	2.29	0.52
35:2d:12:CYS:HB3	35:2d:19:LEU:H	1.75	0.52
36:2e:78:HIS:HB2	39:2h:104:ARG:HD2	1.92	0.52
1:1A:594:A:O2'	17:1V:78:LYS:HE2	2.10	0.52
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.10	0.52
24:12:52:ASP:O	24:12:56:GLN:HG3	2.09	0.52
32:1a:737:A:H2'	32:1a:738:C:C6	2.45	0.52
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.45	0.52
36:1e:85:GLY:C	36:1e:87:SER:H	2.16	0.52
1:2A:2803:C:H2'	1:2A:2804:C:C6	2.45	0.52
2:2B:19:G:H2'	2:2B:20:C:O4'	2.10	0.52
8:2I:43:ASN:ND2	23:21:75:GLU:OE2	2.43	0.52
21:2Z:45:ASP:O	21:2Z:49:ARG:HG2	2.10	0.52
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.90	0.52
32:2a:714:G:H2'	32:2a:715:A:C8	2.45	0.52
32:2a:1207:2MG:H2'	32:2a:1208:C:H6	1.75	0.52
32:2a:1305:G:H5'	52:2u:4:GLY:HA3	1.91	0.52
32:2a:1367:C:OP1	40:2i:115:GLY:N	2.38	0.52
40:2i:4:TYR:O	40:2i:18:PHE:HA	2.09	0.52
55:2x:50:U:H3	55:2x:64:G:H1	1.57	0.52
54:2y:14:A:O2'	54:2y:15:G:OP1	2.24	0.52
1:1A:653:G:H2'	1:1A:654:G:C8	2.45	0.52
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.43	0.52
32:1a:1029:C:H41	32:1a:1030(A):G:H21	1.56	0.52
35:1d:119:GLN:HG3	35:1d:123:HIS:CD2	2.45	0.52
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.09	0.52
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.91	0.52
54:1y:51:U:H2'	54:1y:52:G:C8	2.45	0.52
1:2A:212:G:H2'	1:2A:213:A:O4'	2.10	0.52
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.09	0.52
22:20:50:ASN:HB2	22:20:81:VAL:HB	1.91	0.52
32:2a:815:A:N7	32:2a:1509:C:O2'	2.42	0.52
32:2a:1348:U:H2'	32:2a:1349:A:H8	1.74	0.52
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.43	0.52
41:2j:38:ILE:HG12	41:2j:71:LEU:O	2.10	0.52
1:1A:905:U:O2	1:1A:2280:A:H2'	2.09	0.52
10:1O:49:ARG:NH1	32:1a:1422:G:O3'	2.38	0.52
24:12:17:SER:N	24:12:20:GLU:OE1	2.39	0.52
1:2A:309:G:N3	1:2A:329:G:O2'	2.43	0.52
1:2A:863:A:H2'	1:2A:864:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:884:C:H3'	1:2A:885:C:H6	1.73	0.52
1:2A:979:G:N7	60:2A:3633:HOH:O	2.33	0.52
1:2A:1639:U:H2'	1:2A:1640:C:H5''	1.92	0.52
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.45	0.52
1:2A:2689:U:P	1:2A:2719:G:H22	2.32	0.52
2:2B:55:U:H1'	6:2G:29:TRP:CD1	2.44	0.52
9:2N:15:LEU:HD12	9:2N:53:VAL:HB	1.92	0.52
25:23:18:ASP:OD1	25:23:18:ASP:N	2.38	0.52
32:2a:757:U:H2'	32:2a:758:G:O4'	2.10	0.52
32:2a:1318:A:O2'	50:2s:37:ARG:HB2	2.10	0.52
1:1A:2348:A:H61	22:10:43:THR:CG2	2.22	0.52
6:1G:101:ILE:HG22	6:1G:105:LYS:HE2	1.91	0.52
32:1a:718:G:H5'	42:1k:117:ASN:HB2	1.92	0.52
39:1h:119:LEU:HD11	39:1h:127:LEU:HD23	1.92	0.52
11:2P:50:ARG:HH21	30:28:7:HIS:HD2	1.57	0.52
32:2a:560:U:H4'	32:2a:561:U:O5'	2.10	0.52
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.45	0.52
40:2i:28:VAL:HA	40:2i:63:ILE:O	2.10	0.52
40:2i:88:TYR:HD2	40:2i:89:ASN:HB2	1.75	0.52
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.44	0.52
1:1A:1312:G:O4'	18:1W:15:ARG:NH2	2.43	0.51
1:1A:1814:A:H5'	1:1A:2620:G:H4'	1.92	0.51
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.10	0.51
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.92	0.51
32:1a:688:G:H2'	32:1a:689:C:H6	1.75	0.51
32:1a:1015:A:N3	32:1a:1218:C:O2'	2.40	0.51
36:1e:95:ALA:HB1	36:1e:96:PRO:HD2	1.91	0.51
38:1g:28:ASN:HD21	38:1g:36:LYS:HZ1	1.57	0.51
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.43	0.51
1:2A:1472:A:H2'	1:2A:1473:G:O4'	2.11	0.51
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.92	0.51
1:2A:2156:G:H2'	1:2A:2157:G:C6	2.46	0.51
18:2W:35:ILE:HG23	27:25:28:PRO:HD2	1.92	0.51
32:2a:1366:C:O2'	41:2j:60:ARG:NH2	2.42	0.51
35:2d:11:LEU:HD23	35:2d:66:ARG:HB3	1.92	0.51
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.10	0.51
5:1F:31:HIS:NE2	5:1F:35:GLU:OE2	2.36	0.51
11:1P:7:ARG:NH2	60:1P:301:HOH:O	2.20	0.51
32:1a:967:5MC:H4'	40:1i:125:TYR:HE1	1.74	0.51
54:1y:5:G:H1'	54:1y:69:G:N2	2.25	0.51
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1590:U:H2'	1:2A:1591:G:C8	2.45	0.51
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.45	0.51
7:2H:3:ARG:HB3	7:2H:3:ARG:HH11	1.75	0.51
7:2H:74:ASN:OD1	7:2H:83:TYR:OH	2.23	0.51
10:2O:119:PRO:HB2	15:2T:68:TYR:CE2	2.44	0.51
32:2a:1036:G:H5''	32:2a:1037:C:OP2	2.10	0.51
32:2a:1399:C:H4'	32:2a:1400:5MC:C5'	2.24	0.51
12:1Q:31:ASP:OD1	12:1Q:134:ARG:NH1	2.44	0.51
16:1U:52:ARG:HA	16:1U:55:ARG:HG3	1.92	0.51
32:1a:1100:C:OP2	33:1b:96:ARG:HD2	2.11	0.51
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.91	0.51
1:2A:276:A:H5''	1:2A:277:C:H5'	1.92	0.51
1:2A:946:G:H2'	1:2A:947:G:H8	1.75	0.51
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.45	0.51
8:2I:75:LEU:HD22	8:2I:105:HIS:CD2	2.46	0.51
32:2a:865:A:H5'	32:2a:1078:U:C5	2.45	0.51
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.46	0.51
32:2a:1499:A:H1'	32:2a:1520:G:H5'	1.93	0.51
34:2c:37:GLN:HE22	45:2n:52:GLN:HB3	1.75	0.51
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	1.93	0.51
35:2d:111:ALA:HA	35:2d:116:GLN:HE21	1.74	0.51
38:2g:69:VAL:HG11	38:2g:134:ALA:HB1	1.91	0.51
38:2g:151:TYR:HB3	38:2g:154:TYR:CD2	2.43	0.51
1:1A:233:A:H4'	11:1P:74:GLU:HB2	1.93	0.51
1:1A:956:A:C5	12:1Q:13:GLN:HG3	2.44	0.51
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.46	0.51
12:1Q:38:GLU:HA	12:1Q:99:PRO:HG3	1.92	0.51
31:19:2:LYS:HE2	31:19:31:LYS:O	2.10	0.51
32:1a:169:C:H2'	32:1a:170:U:H6	1.76	0.51
32:1a:890:G:O2'	32:1a:906:G:O6	2.21	0.51
54:1y:67:C:H2'	54:1y:68:C:C6	2.45	0.51
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.26	0.51
1:2A:910:A:N1	1:2A:2277:G:H1'	2.25	0.51
1:2A:1300:U:H4'	1:2A:1301:A:H5''	1.91	0.51
1:2A:2382:G:OP2	60:2A:3611:HOH:O	2.19	0.51
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.10	0.51
32:2a:328:C:H4'	32:2a:329:A:H5'	1.92	0.51
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.50	0.51
1:1A:1106:U:N3	1:1A:1108:G:O2'	2.44	0.51
1:1A:1653:C:H4'	1:1A:1654:A:O5'	2.11	0.51
1:1A:2307:C:OP1	14:1S:10:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:41:MET:HE2	7:1H:65:HIS:HA	1.93	0.51
21:1Z:130:PRO:HA	21:1Z:133:ILE:HG13	1.92	0.51
25:13:8:LEU:HA	25:13:54:VAL:HG23	1.93	0.51
32:1a:600:C:H2'	32:1a:601:C:C6	2.46	0.51
32:1a:757:U:H2'	32:1a:758:G:O4'	2.10	0.51
33:1b:15:VAL:HG21	33:1b:213:LEU:HD13	1.92	0.51
15:2T:33:LYS:HD3	15:2T:82:LEU:HD23	1.92	0.51
32:2a:936:C:H2'	32:2a:937:A:O4'	2.10	0.51
43:2l:53:ARG:HG3	43:2l:93:LEU:HD21	1.92	0.51
47:2p:52:ASP:HB3	47:2p:55:ARG:HB2	1.93	0.51
54:2w:4:C:N3	54:2w:69:G:N2	2.58	0.51
1:1A:794:U:O2	1:1A:2036:A:H1'	2.10	0.51
13:1R:118:GLU:H	13:1R:118:GLU:CD	2.18	0.51
26:14:44:THR:O	26:14:46:GLN:N	2.44	0.51
1:2A:529:A:H62	1:2A:2041:U:H3	1.56	0.51
1:2A:2400:G:H4'	28:26:18:ARG:HG2	1.93	0.51
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.41	0.51
2:2B:52:A:N6	14:2S:33:LYS:HG2	2.26	0.51
21:2Z:99:TYR:HB3	21:2Z:123:ASP:CG	2.35	0.51
23:21:44:PRO:O	23:21:46:LEU:N	2.43	0.51
32:2a:1207:2MG:H2'	32:2a:1208:C:C6	2.45	0.51
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.46	0.51
33:2b:71:VAL:HB	33:2b:164:VAL:HA	1.92	0.51
33:2b:74:LYS:NZ	33:2b:206:ASP:OD1	2.44	0.51
36:2e:87:SER:HB3	36:2e:131:ILE:HD13	1.92	0.51
40:2i:20:ARG:O	40:2i:60:ASP:N	2.42	0.51
41:2j:5:ARG:HA	41:2j:73:ASP:OD1	2.10	0.51
44:2m:3:ARG:HB3	44:2m:8:GLU:HA	1.93	0.51
1:1A:1154:U:H2'	1:1A:1155:C:O4'	2.11	0.51
1:1A:1431:G:O2'	1:1A:1442:U:O2	2.23	0.51
6:1G:145:THR:HG23	6:1G:148:MET:SD	2.51	0.51
21:1Z:104:PHE:HE1	21:1Z:171:ILE:HD11	1.75	0.51
32:1a:1026:G:C8	32:1a:1027:C:O2	2.64	0.51
33:1b:54:THR:HG23	33:1b:199:TYR:HB3	1.91	0.51
36:1e:91:LEU:HG	36:1e:118:ILE:HD11	1.92	0.51
1:2A:925:C:H2'	1:2A:926:A:C8	2.45	0.51
1:2A:928:G:H8	1:2A:928:G:O5'	1.94	0.51
10:2O:88:ASN:HD21	10:2O:92:GLU:HB2	1.74	0.51
32:2a:8:A:H5'	36:2e:101:ILE:HG22	1.93	0.51
32:2a:1003:G:H2'	32:2a:1004:A:O4'	2.10	0.51
32:2a:1502:A:C8	32:2a:1505:G:N2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:112:VAL:H	35:2d:116:GLN:NE2	2.08	0.51
35:2d:175:SER:OG	35:2d:176:LEU:N	2.43	0.51
1:1A:1495:G:O2'	1:1A:1575:A:N1	2.40	0.51
23:11:3:LYS:H	23:11:46:LEU:HD12	1.76	0.51
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.08	0.51
32:1a:946:A:H2'	32:1a:947:G:C8	2.45	0.51
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.46	0.51
36:1e:105:VAL:HG21	36:1e:128:PRO:HB3	1.91	0.51
41:1j:38:ILE:HG12	41:1j:71:LEU:O	2.10	0.51
1:2A:658:C:H2'	1:2A:659:C:C6	2.45	0.51
1:2A:1411:C:H42	1:2A:1591:G:H1	1.58	0.51
4:2E:111:ARG:HD3	4:2E:160:TYR:CD2	2.46	0.51
4:2E:170:LEU:HB3	4:2E:184:VAL:CG2	2.41	0.51
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.92	0.51
26:24:48:ARG:HG3	26:24:51:ASP:O	2.11	0.51
32:2a:501:C:H2'	32:2a:502:G:H8	1.76	0.51
44:2m:31:LYS:HA	44:2m:34:LEU:HD12	1.92	0.51
1:1A:310:C:H2'	1:1A:311:C:C6	2.46	0.51
1:1A:878:G:N2	11:1P:53:GLY:O	2.44	0.51
1:1A:956:A:N1	1:1A:2289:G:H1'	2.25	0.51
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.45	0.51
4:1E:9:VAL:O	60:1T:301:HOH:O	2.19	0.51
6:1G:5:VAL:HG22	6:1G:8:LYS:HE2	1.93	0.51
32:1a:36:C:OP1	43:1l:123:LYS:NZ	2.30	0.51
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.73	0.51
33:1b:76:GLN:HB3	33:1b:208:ILE:HG23	1.93	0.51
37:1f:35:ALA:HB2	37:1f:67:MET:HE2	1.92	0.51
39:1h:112:LEU:HB3	39:1h:133:LEU:HA	1.93	0.51
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.93	0.51
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.29	0.51
32:2a:45:U:H2'	32:2a:46:G:C8	2.46	0.51
32:2a:796:C:N4	60:2a:1922:HOH:O	2.44	0.51
32:2a:984:C:H2'	32:2a:985:C:C6	2.45	0.51
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.46	0.51
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.41	0.51
47:2p:17:TYR:HE2	47:2p:41:PRO:HG3	1.74	0.51
53:2v:12:A:N3	53:2v:12:A:H2'	2.25	0.51
1:1A:469:A:H1'	1:1A:1246:C:O4'	2.11	0.51
1:1A:1121:C:O2	1:1A:1122:C:H2'	2.11	0.51
1:1A:1410:G:P	23:11:3:LYS:HG3	2.51	0.51
1:1A:2455:C:OP1	5:1F:68:LYS:HD3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:32:LEU:HD12	24:12:57:ILE:HD12	1.93	0.51
55:1x:50:U:H2'	55:1x:51:C:C6	2.46	0.51
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.46	0.51
1:2A:2167:U:H3'	1:2A:2168:G:H21	1.76	0.51
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.75	0.51
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.47	0.51
1:2A:2748:A:H2'	1:2A:2749:A:H8	1.76	0.51
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.93	0.51
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.10	0.51
16:2U:36:ARG:HH21	17:2V:82:ARG:HH21	1.59	0.51
32:2a:107:G:N7	51:2t:15:ARG:NH2	2.59	0.51
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.93	0.51
33:2b:167:PRO:HG2	33:2b:192:SER:HB2	1.92	0.51
33:2b:168:THR:OG1	33:2b:191:ASP:O	2.24	0.51
34:2c:116:VAL:HG21	34:2c:202:ILE:HD11	1.93	0.51
39:2h:33:GLU:HG2	39:2h:48:TYR:CE1	2.46	0.51
54:2w:50:U:H3	54:2w:64:A:H61	1.59	0.51
1:1A:310:C:H2'	1:1A:311:C:H6	1.76	0.50
1:1A:830:A:O2'	1:1A:832:G:OP1	2.22	0.50
1:1A:2145:G:H1	1:1A:2197:C:H42	1.58	0.50
2:1B:24:G:N7	2:1B:56:G:H2'	2.26	0.50
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.43	0.50
32:1a:438:G:H4'	35:1d:123:HIS:ND1	2.26	0.50
32:1a:627:G:H2'	32:1a:628:G:H8	1.76	0.50
32:1a:664:G:N2	32:1a:741:G:H1	2.03	0.50
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.23	0.50
54:1y:18:G:O2'	54:1y:57:G:O6	2.29	0.50
1:2A:324:A:N6	1:2A:338:G:O2'	2.43	0.50
1:2A:2287:A:C8	1:2A:2289:G:C8	2.99	0.50
12:2Q:68:ILE:HG22	12:2Q:101:ARG:HE	1.76	0.50
32:2a:20:U:H2'	32:2a:21:G:O4'	2.10	0.50
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.11	0.50
50:2s:15:LEU:HA	50:2s:18:LYS:HD2	1.91	0.50
1:1A:1464:G:O2'	1:1A:1627:A:N6	2.43	0.50
15:1T:73:GLU:OE2	15:1T:103:ARG:NE	2.44	0.50
32:1a:142:G:H2'	32:1a:143:A:H8	1.76	0.50
54:1w:5:G:H2'	54:1w:6:G:H8	1.73	0.50
1:2A:184:C:H2'	1:2A:185:U:C6	2.46	0.50
1:2A:483:A:H1'	20:2Y:59:GLY:O	2.12	0.50
1:2A:652(B):A:N6	1:2A:655:A:N3	2.58	0.50
1:2A:828:U:H4'	1:2A:831:G:N1	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.11	0.50
12:2Q:21:THR:HG21	12:2Q:101:ARG:HD2	1.94	0.50
25:23:4:LEU:HD22	25:23:56:VAL:HG11	1.92	0.50
32:2a:1051:C:H2'	32:2a:1052:U:H6	1.76	0.50
1:1A:54:G:O2'	1:1A:125:A:N1	2.43	0.50
1:1A:968:U:H2'	1:1A:969:C:C6	2.47	0.50
1:1A:2832:G:O2'	1:1A:2834:C:OP2	2.26	0.50
4:1E:154:LYS:HG2	4:1E:156:MET:HE3	1.93	0.50
5:1F:123:LEU:HD13	5:1F:192:LEU:HD13	1.93	0.50
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.12	0.50
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.93	0.50
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.11	0.50
7:2H:3:ARG:NH2	7:2H:5:GLY:H	2.10	0.50
21:2Z:156:LYS:HE3	21:2Z:158:PRO:HD3	1.93	0.50
32:2a:748:C:H4'	32:2a:749:C:O5'	2.11	0.50
32:2a:1054:C:H4'	32:2a:1055:A:O5'	2.12	0.50
32:2a:1326:C:H5''	52:2u:18:TYR:O	2.10	0.50
33:2b:95:GLN:HB2	33:2b:148:TYR:HD1	1.77	0.50
38:2g:113:GLU:CG	38:2g:119:ARG:HG2	2.40	0.50
44:2m:39:ILE:HD11	44:2m:55:ARG:HD2	1.94	0.50
44:2m:91:ARG:HD2	44:2m:96:LEU:HB2	1.92	0.50
1:1A:843:C:H2'	1:1A:844:C:C6	2.46	0.50
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.46	0.50
1:1A:1501:U:N3	60:1A:4048:HOH:O	2.31	0.50
1:1A:2545:A:H2'	1:1A:2546:A:O4'	2.11	0.50
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	1.92	0.50
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.94	0.50
15:1T:24:PRO:HA	15:1T:49:VAL:HG22	1.93	0.50
32:1a:92:C:H2'	32:1a:93:G:H8	1.77	0.50
35:1d:79:PHE:HE1	35:1d:204:ILE:HD13	1.76	0.50
1:2A:214:G:O2'	1:2A:215:G:O4'	2.16	0.50
1:2A:896:A:H1'	54:2w:56:C:H5'	1.94	0.50
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.35	0.50
21:2Z:138:GLU:HB2	21:2Z:156:LYS:HD3	1.93	0.50
32:2a:501:C:H2'	32:2a:502:G:C8	2.46	0.50
32:2a:767:A:H2'	32:2a:768:A:O4'	2.11	0.50
32:2a:1328:C:O2'	44:2m:29:ARG:NE	2.40	0.50
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.58	0.50
1:2A:582:G:H2'	1:2A:583:G:C8	2.46	0.50
1:2A:857:C:H2'	1:2A:858:U:C6	2.46	0.50
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:55:VAL:HG12	12:2Q:64:ILE:HD12	1.94	0.50
32:2a:390:C:H2'	32:2a:391:G:C8	2.47	0.50
32:2a:523:A:N1	43:2l:92:0TD:H6	2.27	0.50
32:2a:598:U:H4'	39:2h:94:TYR:CG	2.46	0.50
32:2a:1145:C:H4'	32:2a:1146:A:H5'	1.93	0.50
44:2m:3:ARG:HG2	44:2m:9:ILE:N	2.25	0.50
55:2x:39:C:O2'	54:2y:35:A:O2'	2.18	0.50
54:2y:5:G:N2	54:2y:68:C:N3	2.49	0.50
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.94	0.50
32:1a:50:A:N1	32:1a:360:A:O2'	2.41	0.50
32:1a:1159:U:OP1	33:1b:133:LYS:NZ	2.45	0.50
45:1n:32:SER:HB3	45:1n:41:ARG:HB3	1.94	0.50
46:1o:77:ARG:NH2	60:1o:201:HOH:O	2.42	0.50
47:1p:52:ASP:HB3	47:1p:55:ARG:HB2	1.94	0.50
1:2A:271(U):G:H2'	1:2A:271(V):G:H8	1.77	0.50
1:2A:2137:C:N4	1:2A:2155:G:O6	2.43	0.50
8:2I:5:LEU:HD11	8:2I:19:VAL:HG13	1.93	0.50
10:2O:71:ARG:C	10:2O:73:ASP:H	2.20	0.50
12:2Q:110:THR:HG23	12:2Q:113:GLN:HB2	1.94	0.50
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.25	0.50
21:2Z:44:PHE:O	21:2Z:48:PHE:N	2.39	0.50
23:21:76:ARG:HH22	23:21:97:LEU:HD22	1.76	0.50
32:2a:607:A:H2'	32:2a:608:A:O4'	2.11	0.50
32:2a:719:C:H42	49:2r:71:LYS:HE2	1.77	0.50
32:2a:868:C:H2'	32:2a:869:G:O4'	2.11	0.50
32:2a:1004:A:H5''	32:2a:1024:G:H22	1.77	0.50
32:2a:1004:A:H1'	32:2a:1038:C:O2	2.11	0.50
32:2a:1048:G:H1'	60:2a:1910:HOH:O	2.10	0.50
32:2a:1152:A:OP1	41:2j:70:ARG:NH2	2.44	0.50
36:2e:24:ARG:NH1	53:2v:24:A:OP2	2.45	0.50
39:2h:116:LYS:HG3	39:2h:129:VAL:HG11	1.93	0.50
45:2n:32:SER:O	45:2n:40:CYS:HA	2.11	0.50
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.47	0.50
1:1A:2227:G:H3'	1:1A:2228:G:N7	2.26	0.50
6:1G:41:GLN:HB3	6:1G:43:LEU:HD22	1.94	0.50
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.47	0.50
21:1Z:48:PHE:CE1	21:1Z:71:VAL:HG11	2.47	0.50
33:1b:80:ILE:HD11	33:1b:212:GLN:HA	1.94	0.50
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.12	0.50
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.76	0.50
1:2A:2882:A:H5'	13:2R:96:ARG:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:11:C:H3'	2:2B:12:C:C6	2.47	0.50
19:2X:48:LYS:NZ	24:22:30:ARG:HH22	2.09	0.50
26:24:60:GLN:O	26:24:62:ARG:N	2.45	0.50
32:2a:984:C:H2'	32:2a:985:C:H6	1.76	0.50
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.76	0.50
32:2a:1240:U:N3	38:2g:30:ILE:O	2.18	0.50
35:2d:146:ILE:HD12	35:2d:146:ILE:H	1.77	0.50
32:1a:343:U:O2'	32:1a:346:G:O6	2.23	0.50
32:1a:353:A:H5'	32:1a:353:A:H8	1.77	0.50
32:1a:584:G:H5'	48:1q:91:ARG:NH2	2.27	0.50
33:1b:93:VAL:HG21	33:1b:97:TRP:HD1	1.77	0.50
38:1g:121:ALA:O	38:1g:125:MET:HG3	2.11	0.50
1:2A:1405:U:H2'	1:2A:1406:U:H6	1.76	0.50
1:2A:1591:G:H2'	1:2A:1592:C:C6	2.47	0.50
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.76	0.50
1:2A:2137:C:N3	1:2A:2155:G:C6	2.80	0.50
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.28	0.50
1:2A:2748:A:H2'	1:2A:2749:A:C8	2.46	0.50
6:2G:11:TYR:OH	6:2G:16:ARG:NH1	2.45	0.50
8:2I:75:LEU:HD22	8:2I:105:HIS:HD2	1.75	0.50
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.92	0.50
26:24:41:PRO:HB3	26:24:49:PHE:CD1	2.46	0.50
32:2a:715:A:H2'	32:2a:716:A:C8	2.47	0.50
32:2a:852:G:H2'	32:2a:853:G:O4'	2.12	0.50
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.12	0.50
48:2q:60:ILE:HB	48:2q:74:LEU:HD12	1.94	0.50
1:1A:1128:U:C4	1:1A:1132:A:N1	2.75	0.50
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.44	0.50
3:1D:79:VAL:HG12	3:1D:113:VAL:HA	1.93	0.50
10:1O:122:LEU:HD13	15:1T:72:VAL:HG11	1.92	0.50
32:1a:262:A:H2'	32:1a:263:A:C8	2.47	0.50
37:1f:50:TYR:OH	49:1r:74:ARG:O	2.30	0.50
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.58	0.50
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.47	0.50
1:2A:1920:4OC:HM22	1:2A:1921:G:H5'	1.93	0.50
1:2A:2116:G:N7	1:2A:2166:G:N2	2.51	0.50
1:2A:2142:C:H2'	1:2A:2143:C:O4'	2.11	0.50
7:2H:96:ALA:HB1	7:2H:103:LEU:HD11	1.93	0.50
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.94	0.50
11:2P:19:VAL:HG12	11:2P:27:HIS:HB3	1.92	0.50
32:2a:397:A:H3'	32:2a:397:A:N3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:604:G:H2'	32:2a:605:U:O4'	2.12	0.50
32:2a:646:U:H2'	32:2a:647:C:H6	1.77	0.50
32:2a:1429:C:H2'	32:2a:1430:C:C6	2.47	0.50
36:2e:80:ILE:HG22	36:2e:91:LEU:HB2	1.94	0.50
39:2h:87:SER:HB2	39:2h:93:VAL:HB	1.94	0.50
41:2j:33:GLN:O	41:2j:75:ILE:N	2.36	0.50
3:1D:44:ASN:ND2	3:1D:46:GLN:HG3	2.27	0.49
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	1.94	0.49
18:1W:35:ILE:HG23	27:15:28:PRO:HD2	1.93	0.49
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.94	0.49
33:1b:21:ARG:HG2	33:1b:21:ARG:O	2.11	0.49
43:1l:117:ARG:HG2	43:1l:122:THR:HB	1.92	0.49
54:1y:23:A:H2'	54:1y:24:G:H8	1.77	0.49
1:2A:84:A:N1	1:2A:98:G:O2'	2.36	0.49
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.46	0.49
9:2N:34:LEU:HD23	9:2N:107:LEU:HD21	1.94	0.49
20:2Y:39:VAL:HB	20:2Y:42:VAL:HB	1.95	0.49
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.22	0.49
35:2d:8:VAL:HB	35:2d:115:ARG:HH22	1.77	0.49
1:1A:1831:C:OP2	3:1D:183:ARG:NH2	2.43	0.49
1:1A:2650:G:P	4:1E:82:ARG:HH22	2.34	0.49
10:1O:35:VAL:HG23	10:1O:65:THR:HG23	1.94	0.49
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	1.94	0.49
26:14:34:GLU:H	26:14:34:GLU:CD	2.19	0.49
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.42	0.49
32:1a:328:C:H4'	32:1a:329:A:H5'	1.93	0.49
32:1a:339:C:H2'	32:1a:340:U:C6	2.47	0.49
32:1a:841:U:OP2	32:1a:841:U:H6	1.96	0.49
1:2A:631:A:N3	1:2A:2415:G:O2'	2.37	0.49
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.46	0.49
1:2A:2649:U:H2'	1:2A:2650:U:C6	2.47	0.49
9:2N:38:HIS:NE2	9:2N:50:ASP:OD2	2.42	0.49
32:2a:509:A:O2'	32:2a:510:A:OP1	2.24	0.49
1:1A:172:C:N4	1:1A:202:A:H61	2.10	0.49
1:1A:895:G:H2'	1:1A:896:A:C8	2.47	0.49
1:1A:1018:A:H8	1:1A:1018:A:OP1	1.96	0.49
1:1A:2289:G:OP2	22:10:10:THR:HG21	2.13	0.49
32:1a:1162:C:H42	32:1a:1174:G:H1	1.58	0.49
55:1x:39:C:O2'	54:1y:35:A:O2'	2.30	0.49
1:2A:234:C:H2'	1:2A:235:U:C6	2.48	0.49
1:2A:1549:C:H2'	1:2A:1550:C:H6	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2080:G:H2'	1:2A:2081:C:H6	1.76	0.49
26:24:12:ALA:HB3	26:24:26:SER:HB3	1.93	0.49
32:2a:316:G:H2'	32:2a:317:G:H8	1.76	0.49
32:2a:555:C:H2'	32:2a:556:C:C6	2.47	0.49
32:2a:719:C:N4	49:2r:71:LYS:HE2	2.27	0.49
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.47	0.49
32:2a:1315:U:H2'	32:2a:1316:G:O4'	2.12	0.49
32:2a:1315:U:O2'	32:2a:1360:A:N3	2.42	0.49
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	1.93	0.49
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.94	0.49
51:2t:57:ARG:HH12	51:2t:100:ILE:HD12	1.76	0.49
1:1A:225:C:H2'	1:1A:226:C:C6	2.47	0.49
1:1A:1715:A:H4'	1:1A:1716:A:O5'	2.12	0.49
1:1A:1849:U:H2'	3:1D:157:ARG:HG3	1.94	0.49
1:1A:1954:A:H2'	1:1A:1955:G:O4'	2.12	0.49
32:1a:659:U:H2'	32:1a:660:G:C8	2.48	0.49
36:1e:78:HIS:CD2	39:1h:104:ARG:HH11	2.31	0.49
1:2A:796:C:H2'	1:2A:797:C:C6	2.47	0.49
1:2A:1638:C:H5''	1:2A:2710:C:O2'	2.12	0.49
1:2A:2469:A:H5'	1:2A:2470:G:OP2	2.12	0.49
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.47	0.49
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.48	0.49
32:2a:1263:C:N3	32:2a:1272:G:O6	2.46	0.49
33:2b:87:ARG:HG2	33:2b:219:VAL:HG11	1.95	0.49
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.94	0.49
41:2j:34:VAL:HA	41:2j:74:ILE:HA	1.92	0.49
1:1A:2623:U:H2'	27:15:2:ALA:O	2.12	0.49
32:1a:277:C:P	48:1q:68:ARG:HH12	2.35	0.49
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.48	0.49
41:1j:19:SER:OG	41:1j:91:PRO:HD2	2.13	0.49
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.41	0.49
2:2B:106:G:N7	60:2B:304:HOH:O	2.35	0.49
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.77	0.49
7:2H:33:LEU:HD11	7:2H:136:ILE:HG22	1.94	0.49
9:2N:121:LYS:HD3	9:2N:130:HIS:CE1	2.47	0.49
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE2	1.93	0.49
32:2a:583:A:H2'	32:2a:584:G:O4'	2.11	0.49
32:2a:1388:C:H2'	32:2a:1389:C:C6	2.47	0.49
33:2b:15:VAL:O	33:2b:17:PHE:N	2.45	0.49
33:2b:73:THR:HA	33:2b:94:ASN:O	2.13	0.49
35:2d:57:ARG:HD3	35:2d:205:GLU:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:100:VAL:O	36:2e:107:ARG:NH1	2.42	0.49
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	1.94	0.49
54:2w:51:U:H2'	54:2w:52:G:C8	2.47	0.49
55:2x:23:C:H2'	55:2x:24:U:C6	2.47	0.49
1:1A:29:U:H2'	1:1A:30:G:C8	2.47	0.49
1:1A:941:U:O2'	1:1A:942:A:OP1	2.30	0.49
1:1A:2204:G:C2	1:1A:2205:C:C2	3.00	0.49
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.44	0.49
1:1A:2858:G:H1'	1:1A:2877:G:N2	2.28	0.49
18:1W:11:ARG:HH11	18:1W:11:ARG:C	2.20	0.49
32:1a:102:G:O2'	32:1a:151:A:N3	2.40	0.49
32:1a:625:G:H2'	32:1a:626:U:C6	2.47	0.49
32:1a:1149:C:OP1	40:1i:9:ARG:NH2	2.45	0.49
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.48	0.49
45:1n:39:LEU:HD11	45:1n:47:LEU:HD12	1.95	0.49
49:1r:52:PRO:HB2	49:1r:54:ARG:HG2	1.95	0.49
50:1s:63:THR:O	50:1s:66:MET:HG2	2.11	0.49
1:2A:445:C:OP1	16:2U:2:PRO:HA	2.12	0.49
6:2G:171:ALA:O	6:2G:175:LEU:HB2	2.12	0.49
25:23:8:LEU:HG	25:23:31:LEU:HD23	1.94	0.49
32:2a:826:C:H42	32:2a:874:G:H1	1.59	0.49
32:2a:1321:C:O2'	50:2s:77:THR:HG21	2.12	0.49
1:1A:225:C:H2'	1:1A:226:C:H6	1.76	0.49
1:1A:533:G:N2	18:1W:80:PRO:HG2	2.28	0.49
1:1A:1639:G:H2'	1:1A:1640:G:C8	2.47	0.49
1:1A:2024:G:OP2	13:1R:9:LYS:NZ	2.45	0.49
1:1A:2331:G:N1	14:1S:3:ARG:HA	2.28	0.49
1:1A:2372:A:H8	1:1A:2372:A:O5'	1.96	0.49
9:1N:4:TYR:HB2	16:1U:101:ARG:NH1	2.27	0.49
32:1a:204:U:H4'	32:1a:216:G:O5'	2.12	0.49
32:1a:509:A:H5'	35:1d:54:TYR:HD2	1.76	0.49
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.94	0.49
32:1a:1004:A:H5''	32:1a:1024:G:H1	1.77	0.49
32:1a:1126:U:O2	32:1a:1280:A:H2'	2.13	0.49
32:1a:1413:A:H2	32:1a:1487:G:H22	1.60	0.49
48:1q:53:LEU:HB3	48:1q:82:MET:HE1	1.94	0.49
54:1y:38:A:H2'	54:1y:39:PSU:O4'	2.12	0.49
1:2A:2454:G:H1'	60:2A:3629:HOH:O	2.12	0.49
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.47	0.49
7:2H:88:LEU:HD23	7:2H:88:LEU:H	1.78	0.49
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:73:GLN:H	21:2Z:87:ASP:HB2	1.78	0.49
28:26:35:GLU:HG2	28:26:50:ARG:HD3	1.94	0.49
28:26:44:ARG:HG2	28:26:44:ARG:HH11	1.78	0.49
32:2a:1362:C:N4	60:2a:1921:HOH:O	2.46	0.49
44:2m:123:ALA:HB2	54:2w:39:PSU:H1'	1.95	0.49
47:2p:15:PRO:O	47:2p:16:HIS:ND1	2.46	0.49
1:1A:211:A:H5''	1:1A:448:U:OP1	2.13	0.49
1:1A:2168:C:H4'	1:1A:2169:G:C4	2.47	0.49
1:1A:2339:A:H2'	1:1A:2340:A:H8	1.76	0.49
1:1A:2745:G:H3'	1:1A:2746:A:O4'	2.12	0.49
5:1F:34:TRP:CE2	11:1P:8:PRO:HD3	2.47	0.49
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.93	0.49
32:1a:79:G:C6	32:1a:90:U:O2	2.66	0.49
32:1a:598:U:H4'	39:1h:94:TYR:CD2	2.47	0.49
32:1a:974:A:OP2	45:1n:29:ARG:NH2	2.45	0.49
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.46	0.49
34:1c:157:ILE:HD13	34:1c:166:GLU:HB2	1.95	0.49
55:1x:25:C:H2'	55:1x:26:G:O4'	2.12	0.49
1:2A:11:G:C2'	1:2A:12:U:H5'	2.42	0.49
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.48	0.49
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.12	0.49
6:2G:70:VAL:HA	6:2G:90:LEU:HD23	1.95	0.49
21:2Z:31:ARG:NH1	21:2Z:94:GLU:HG2	2.27	0.49
32:2a:1080:A:OP1	36:2e:47:LYS:HD3	2.13	0.49
36:2e:93:PRO:HG2	39:2h:105:ARG:HE	1.78	0.49
51:2t:98:PRO:O	51:2t:99:LEU:HB2	2.13	0.49
1:1A:119:G:H4'	1:1A:149:A:H5'	1.95	0.49
1:1A:636:G:N2	1:1A:640:A:O2'	2.46	0.49
1:1A:1757:C:O2'	1:1A:2868:C:N3	2.45	0.49
1:1A:2724:U:OP1	1:1A:2727:G:H4'	2.12	0.49
3:1D:76:PRO:O	3:1D:98:VAL:HG22	2.12	0.49
4:1E:143:ASN:HD22	4:1E:147:PRO:HD2	1.78	0.49
32:1a:176:C:H2'	32:1a:177:C:H6	1.78	0.49
32:1a:295:C:H2'	32:1a:296:U:O4'	2.13	0.49
32:1a:814:A:H2'	32:1a:816:A:H5''	1.95	0.49
2:2B:66:A:N6	2:2B:109:C:H5''	2.20	0.49
3:2D:145:VAL:HG13	3:2D:191:ALA:HB2	1.95	0.49
17:2V:2:PHE:CZ	17:2V:41:GLY:HA3	2.47	0.49
32:2a:437:U:O2	35:2d:119:GLN:NE2	2.45	0.49
32:2a:521:G:H4'	43:2l:73:GLU:HG2	1.94	0.49
32:2a:890:G:O2'	32:2a:906:G:O6	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:953:G:OP2	60:2a:1906:HOH:O	2.19	0.49
33:2b:78:GLN:NE2	33:2b:95:GLN:OE1	2.46	0.49
36:2e:32:VAL:HG11	36:2e:59:GLY:HA2	1.95	0.49
38:2g:115:ARG:HH11	38:2g:118:VAL:HG21	1.78	0.49
54:2y:65:G:H2'	54:2y:66:U:C6	2.48	0.49
1:1A:1105:G:H2'	1:1A:1106:U:C5	2.48	0.49
1:1A:2143:G:H2'	1:1A:2144:U:C6	2.48	0.49
11:1P:112:LEU:HD22	11:1P:113:LYS:H	1.78	0.49
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.48	0.49
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.95	0.49
32:1a:779:C:H2'	32:1a:780:A:O4'	2.13	0.49
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.24	0.49
33:1b:59:GLU:HB2	33:1b:221:LEU:HD21	1.95	0.49
34:1c:12:LEU:HD11	45:1n:51:GLY:HA2	1.95	0.49
1:2A:30:G:H2'	1:2A:31:C:C6	2.48	0.49
6:2G:114:ILE:HA	6:2G:140:ILE:HD11	1.95	0.49
32:2a:173:U:H5''	32:2a:197:A:O4'	2.13	0.49
32:2a:201:C:H42	32:2a:216:G:H1	1.60	0.49
32:2a:1064:G:OP1	32:2a:1386:G:H4'	2.11	0.49
38:2g:79:ARG:HD2	38:2g:80:VAL:N	2.26	0.49
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.93	0.49
54:2y:36:A:H2'	54:2y:37:MIA:O4'	2.13	0.49
1:1A:943:C:H2'	1:1A:944:C:C6	2.48	0.48
1:1A:1733:C:H2'	1:1A:1734:G:O4'	2.13	0.48
1:1A:2142:G:C2'	1:1A:2143:G:H5'	2.43	0.48
1:1A:2193:A:O2'	1:1A:2194:U:H5''	2.13	0.48
1:1A:2387:G:N2	1:1A:2390:A:OP2	2.43	0.48
6:1G:109:VAL:HG11	26:14:14:ILE:HG21	1.95	0.48
32:1a:1503:A:O2'	53:1v:13:A:N1	2.46	0.48
44:1m:11:ARG:O	44:1m:12:ASN:HB2	2.11	0.48
54:1y:68:C:H2'	54:1y:69:G:H5''	1.95	0.48
1:2A:249:C:H4'	1:2A:250:G:O5'	2.13	0.48
1:2A:856:C:H2'	1:2A:857:C:C6	2.48	0.48
1:2A:2390:U:P	30:28:35:GLN:HE22	2.35	0.48
2:2B:60:C:H2'	2:2B:61:G:C8	2.48	0.48
6:2G:5:VAL:HG23	6:2G:8:LYS:HB2	1.95	0.48
8:2I:53:ALA:O	8:2I:57:ARG:HG2	2.13	0.48
8:2I:62:LYS:HE2	8:2I:133:HIS:CE1	2.48	0.48
14:2S:94:TYR:CE2	14:2S:99:LYS:HG3	2.48	0.48
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.48	0.48
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.48	0.48
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.29	0.48
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.48	0.48
1:1A:1232:G:H5''	17:1V:81:TYR:CE1	2.48	0.48
1:1A:2575:U:H4'	10:1O:28:SER:HA	1.95	0.48
7:1H:55:PRO:HG2	7:1H:61:HIS:CE1	2.48	0.48
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.47	0.48
32:1a:933:G:OP2	38:1g:3:ARG:HB2	2.13	0.48
32:1a:1054:C:C4	54:1w:34:G:H1'	2.48	0.48
35:1d:112:VAL:HG23	35:1d:116:GLN:HE22	1.78	0.48
1:2A:38:A:H2'	1:2A:39:C:C6	2.48	0.48
1:2A:1549:C:H2'	1:2A:1550:C:C6	2.47	0.48
12:2Q:18:LYS:O	12:2Q:98:LYS:NZ	2.36	0.48
32:2a:355:C:H3'	60:2a:1914:HOH:O	2.12	0.48
32:2a:1004:A:C8	32:2a:1005:A:H4'	2.47	0.48
32:2a:1128:C:O2'	32:2a:1129:C:OP1	2.31	0.48
33:2b:80:ILE:HD13	33:2b:211:ILE:HG22	1.96	0.48
34:2c:131:ARG:NH2	34:2c:135:LYS:HE3	2.20	0.48
38:2g:79:ARG:HH21	38:2g:80:VAL:H	1.61	0.48
1:1A:1182:G:O6	57:1A:3935:KAN:O13	2.26	0.48
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.95	0.48
11:1P:59:LEU:HG	30:18:58:ILE:HD13	1.95	0.48
12:1Q:6:ARG:C	12:1Q:7:MET:HG2	2.38	0.48
32:1a:1261:A:H3'	32:1a:1262:C:H6	1.78	0.48
33:1b:36:ARG:C	33:1b:38:GLY:H	2.21	0.48
39:1h:7:ALA:HB2	39:1h:85:ARG:HG3	1.96	0.48
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.37	0.48
1:2A:1449:A:O2'	1:2A:1529:G:N2	2.40	0.48
1:2A:2103:C:H2'	1:2A:2104:G:C8	2.48	0.48
1:2A:2126:A:N3	1:2A:2127:G:H1'	2.29	0.48
1:2A:2495:G:H5''	12:2Q:82:ARG:HG2	1.95	0.48
2:2B:30:C:H2'	2:2B:31:C:H5'	1.94	0.48
2:2B:33:G:H5'	6:2G:2:PRO:HD3	1.94	0.48
5:2F:7:TYR:O	5:2F:22:ALA:N	2.47	0.48
8:2I:3:VAL:O	8:2I:18:VAL:HA	2.12	0.48
32:2a:1016:A:H2'	32:2a:1017:G:O4'	2.12	0.48
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.48	0.48
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.48	0.48
33:2b:178:ARG:NH1	39:2h:74:PRO:HG3	2.28	0.48
36:2e:78:HIS:ND1	39:2h:107:LEU:HD12	2.29	0.48
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:630:U:OP1	5:1F:102:PRO:HA	2.14	0.48
1:1A:925:A:N6	1:1A:945:A:O2'	2.46	0.48
1:1A:2033:U:OP1	18:1W:42:ARG:NH1	2.42	0.48
1:1A:2096:U:H2'	1:1A:2097:U:C6	2.47	0.48
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.11	0.48
6:1G:112:PRO:HG3	26:14:43:TYR:CE2	2.48	0.48
32:1a:78:G:C2	32:1a:91:C:N3	2.82	0.48
32:1a:431:A:H2'	32:1a:432:A:O4'	2.13	0.48
32:1a:1172:C:H3'	60:1a:2002:HOH:O	2.13	0.48
33:1b:12:GLU:O	33:1b:15:VAL:HG22	2.13	0.48
1:2A:717:G:H2'	1:2A:718:A:O4'	2.13	0.48
1:2A:1798:U:OP2	3:2D:274:ARG:NH2	2.35	0.48
1:2A:1908:C:O2	55:2x:12:G:H4'	2.13	0.48
7:2H:38:SER:C	7:2H:40:GLU:H	2.22	0.48
7:2H:59:ARG:O	7:2H:63:SER:OG	2.30	0.48
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.13	0.48
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.13	0.48
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.96	0.48
37:2f:69:GLU:CD	37:2f:69:GLU:H	2.21	0.48
42:2k:87:THR:HG22	42:2k:91:ARG:HH12	1.78	0.48
44:2m:74:VAL:HA	44:2m:77:ASN:HB2	1.95	0.48
48:2q:4:LYS:HE2	48:2q:6:LEU:HD11	1.95	0.48
1:1A:215:G:H21	1:1A:217:A:H62	1.61	0.48
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.49	0.48
1:1A:2148:A:N1	1:1A:2184:G:O2'	2.43	0.48
1:1A:2707:C:H2'	1:1A:2708:U:H6	1.77	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.52	0.48
32:1a:909:A:H2'	32:1a:910:C:O4'	2.13	0.48
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.13	0.48
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.38	0.48
39:1h:91:ARG:HD3	48:1q:32:TYR:O	2.13	0.48
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.78	0.48
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.13	0.48
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.49	0.48
1:2A:2265:U:H4'	12:2Q:13:GLN:HE22	1.78	0.48
1:2A:2370:G:C6	1:2A:2371:G:C6	3.02	0.48
8:2I:5:LEU:H	8:2I:5:LEU:HD12	1.78	0.48
15:2T:22:PHE:CE1	15:2T:52:ILE:HD11	2.48	0.48
24:22:1:MET:HE3	24:22:5:GLU:HB3	1.95	0.48
32:2a:7:G:N7	36:2e:92:LYS:HD2	2.29	0.48
32:2a:109:A:C6	32:2a:326:G:C6	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:742:G:OP2	46:2o:35:ARG:NH2	2.46	0.48
32:2a:1349:A:H2'	32:2a:1350:A:H8	1.79	0.48
46:2o:28:GLN:HE21	46:2o:66:LEU:HD21	1.78	0.48
50:2s:51:VAL:O	50:2s:58:VAL:N	2.24	0.48
54:2w:4:C:N4	54:2w:69:G:H1	2.11	0.48
55:2x:37:A:H2'	55:2x:38:A:O4'	2.13	0.48
1:1A:91:G:H2'	1:1A:92:C:C6	2.48	0.48
1:1A:173:C:H2'	1:1A:174:U:H6	1.78	0.48
1:1A:543:G:H2'	1:1A:544:U:C6	2.49	0.48
1:1A:2724:U:H1'	1:1A:2725:A:C8	2.48	0.48
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.12	0.48
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.74	0.48
11:1P:95:VAL:HG13	11:1P:125:VAL:HA	1.95	0.48
21:1Z:93:ASP:HB2	21:1Z:131:ARG:HH12	1.79	0.48
32:1a:662:G:H2'	32:1a:663:A:C8	2.49	0.48
32:1a:691:G:H2'	32:1a:692:U:C6	2.49	0.48
54:1w:37:MIA:H162	54:1w:37:MIA:H121	1.73	0.48
54:1w:66:U:H2'	54:1w:67:C:H6	1.79	0.48
1:2A:480:A:N3	1:2A:499:U:O2'	2.40	0.48
1:2A:1924:C:H4'	55:2x:13:C:O2'	2.14	0.48
1:2A:1999:C:H5''	1:2A:2723:C:O2'	2.13	0.48
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.42	0.48
6:2G:170:ARG:NH1	6:2G:174:GLU:OE1	2.47	0.48
15:2T:16:ARG:NH2	15:2T:18:ASP:OD2	2.46	0.48
32:2a:232:G:H1'	32:2a:262:A:N1	2.29	0.48
32:2a:537:G:H5''	43:2l:113:ARG:NH1	2.28	0.48
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.45	0.48
38:2g:149:ARG:HD2	42:2k:59:TYR:CE1	2.49	0.48
40:2i:18:PHE:HD2	40:2i:62:TYR:HD2	1.62	0.48
48:2q:3:LYS:HB3	48:2q:61:GLU:HB3	1.95	0.48
1:1A:2149:G:H1	1:1A:2183:C:N4	2.10	0.48
2:1B:45:A:OP2	6:1G:96:ARG:NH2	2.44	0.48
11:1P:64:LYS:NZ	60:1P:302:HOH:O	2.37	0.48
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.49	0.48
34:1c:164:ARG:HG2	34:1c:165:THR:H	1.78	0.48
35:1d:102:ASP:OD1	35:1d:103:ASN:N	2.46	0.48
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	1.94	0.48
1:2A:139:G:H2'	1:2A:140:G:N7	2.28	0.48
1:2A:947:G:H2'	1:2A:948:G:C8	2.49	0.48
1:2A:2095:C:H2'	1:2A:2096:U:O4'	2.14	0.48
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.95	0.48
29:27:34:ARG:HB2	29:27:42:LEU:HD22	1.95	0.48
32:2a:730:G:O6	46:2o:51:HIS:NE2	2.38	0.48
32:2a:1271:G:N2	32:2a:1272:G:N7	2.62	0.48
32:2a:1494:G:N7	57:2a:1828:KAN:N2	2.61	0.48
41:2j:8:LEU:HG	41:2j:70:ARG:HB2	1.95	0.48
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	1.96	0.48
44:2m:95:GLY:HA2	44:2m:110:ARG:HH21	1.78	0.48
1:1A:26:G:C6	1:1A:27:G:N1	2.82	0.48
1:1A:1554:A:O2'	1:1A:1555:C:OP1	2.22	0.48
1:1A:2041:A:N7	27:15:9:LYS:HE2	2.29	0.48
3:1D:142:VAL:HG23	3:1D:193:VAL:HA	1.95	0.48
8:1I:27:ARG:HD3	23:11:71:TYR:CE2	2.48	0.48
26:14:59:PHE:CE2	50:1s:64:GLU:HB3	2.49	0.48
32:1a:1027:C:C4	32:1a:1034:G:N1	2.81	0.48
43:1l:109:GLY:HA3	43:1l:121:GLY:O	2.14	0.48
1:2A:864:G:C6	1:2A:865:C:N4	2.82	0.48
1:2A:946:G:H2'	1:2A:947:G:C8	2.48	0.48
1:2A:1857:G:O2'	1:2A:1885:A:N6	2.45	0.48
7:2H:3:ARG:HD3	7:2H:6:ARG:HH21	1.79	0.48
7:2H:9:ILE:HG12	7:2H:69:ARG:HG3	1.95	0.48
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.96	0.48
34:2c:25:GLY:O	34:2c:29:TYR:HB2	2.13	0.48
35:2d:10:ARG:HG3	35:2d:11:LEU:HD12	1.96	0.48
42:2k:48:ILE:C	42:2k:50:TYR:H	2.22	0.48
1:1A:929:G:H4'	54:1w:19:G:C6	2.49	0.48
1:1A:1091:A:O2'	1:1A:1093:G:C4	2.67	0.48
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.78	0.48
1:1A:1898:A:H2'	1:1A:1899:A:C8	2.49	0.48
1:1A:1974:A:C6	1:1A:1975:A:N1	2.82	0.48
1:1A:2177:G:H2'	1:1A:2177:G:N3	2.29	0.48
60:1A:4262:HOH:O	5:1F:53:THR:HG21	2.14	0.48
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.49	0.48
34:1c:37:GLN:HE22	45:1n:52:GLN:HB3	1.78	0.48
1:2A:340:A:H2'	1:2A:341:G:O4'	2.13	0.48
1:2A:500:G:N1	1:2A:503:A:OP2	2.45	0.48
1:2A:925:C:H2'	1:2A:926:A:H8	1.78	0.48
1:2A:1590:U:H2'	1:2A:1591:G:H8	1.78	0.48
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.28	0.48
1:2A:2137:C:N3	1:2A:2155:G:N1	2.62	0.48
1:2A:2168:G:H8	1:2A:2170:A:N7	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.49	0.48
1:2A:2689:U:H4'	1:2A:2690:C:H5'	1.96	0.48
14:2S:14:VAL:HG21	14:2S:90:GLY:O	2.14	0.48
32:2a:353:A:H5'	32:2a:353:A:H8	1.78	0.48
32:2a:1194:U:H4'	36:2e:22:GLY:CA	2.44	0.48
33:2b:76:GLN:NE2	33:2b:206:ASP:HA	2.28	0.48
45:2n:6:LEU:HB3	45:2n:23:ARG:HH21	1.79	0.48
1:1A:596:G:O2'	1:1A:597:C:H3'	2.13	0.48
1:1A:653:G:H2'	1:1A:654:G:H8	1.79	0.48
1:1A:1210:G:H2'	1:1A:1211:U:C6	2.49	0.48
1:1A:1717:C:O2	4:1E:129:HIS:NE2	2.38	0.48
32:1a:69:G:H2'	32:1a:70:G:H8	1.76	0.48
32:1a:653:A:OP1	39:1h:56:LYS:NZ	2.47	0.48
32:1a:1261:A:H3'	32:1a:1262:C:C6	2.49	0.48
37:1f:8:ILE:HD11	37:1f:79:LEU:HD13	1.95	0.48
38:1g:67:GLU:HA	38:1g:70:LYS:HD2	1.96	0.48
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.13	0.48
55:1x:4:G:N2	55:1x:69:C:N3	2.50	0.48
54:1y:14:A:N6	54:1y:15:G:C6	2.82	0.48
1:2A:459:U:H2'	1:2A:460:A:C8	2.49	0.48
1:2A:631:A:H2'	1:2A:632:A:O4'	2.14	0.48
1:2A:1138:G:O6	57:2A:3569:KAN:N4	2.47	0.48
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.94	0.48
12:2Q:26:TYR:O	12:2Q:67:ARG:NH1	2.47	0.48
13:2R:100:LEU:HD11	13:2R:113:LEU:HD23	1.96	0.48
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.59	0.48
29:27:24:THR:O	29:27:28:ARG:HG3	2.14	0.48
32:2a:301:G:H2'	32:2a:302:G:H8	1.78	0.48
32:2a:302:G:N3	32:2a:556:C:H4'	2.28	0.48
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.49	0.48
32:2a:1095:U:H2'	32:2a:1096:C:C6	2.49	0.48
32:2a:1239:A:H62	32:2a:1299:A:N6	2.12	0.48
37:2f:99:ALA:HB3	49:2r:29:PHE:CE2	2.49	0.48
38:2g:6:ARG:HB3	38:2g:6:ARG:HH11	1.79	0.48
1:1A:611:U:H2'	1:1A:612:C:C6	2.48	0.47
1:1A:2481:A:O2'	12:1Q:56:ARG:NH1	2.45	0.47
6:1G:11:TYR:O	6:1G:16:ARG:HG3	2.14	0.47
8:1I:124:GLY:H	8:1I:144:VAL:HG23	1.79	0.47
18:1W:90:ARG:HE	18:1W:90:ARG:HB3	1.39	0.47
32:1a:1294:G:N7	60:1a:2030:HOH:O	2.36	0.47
38:1g:118:VAL:HG13	38:1g:122:HIS:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2019:A:H4'	16:2U:34:LYS:HD2	1.96	0.47
1:2A:2732:G:H3'	1:2A:2733:A:O4'	2.13	0.47
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.14	0.47
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.13	0.47
15:2T:88:ILE:HG21	15:2T:91:ARG:NE	2.29	0.47
32:2a:382:A:H2'	32:2a:383:A:C8	2.49	0.47
32:2a:575:G:O2'	32:2a:821:G:H5'	2.14	0.47
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.49	0.47
44:2m:20:THR:HG21	44:2m:27:LYS:HD2	1.95	0.47
46:2o:62:GLN:NE2	46:2o:65:ARG:HD2	2.29	0.47
1:1A:241:G:P	11:1P:50:ARG:HH12	2.37	0.47
1:1A:831:A:C8	1:1A:839:G:C5	3.02	0.47
1:1A:2304:C:OP1	14:1S:17:ARG:NH2	2.37	0.47
3:1D:44:ASN:HD21	3:1D:46:GLN:HG3	1.78	0.47
4:1E:18:ASP:HB3	15:1T:82:LEU:HD21	1.97	0.47
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.33	0.47
32:1a:1239:A:H62	32:1a:1299:A:N6	2.12	0.47
48:1q:22:LEU:HD11	48:1q:39:SER:HB2	1.95	0.47
1:2A:744:G:H2'	1:2A:745:G:O4'	2.13	0.47
1:2A:747:U:O2	1:2A:2014:A:H1'	2.14	0.47
1:2A:1366:A:OP1	23:21:3:LYS:NZ	2.38	0.47
1:2A:2349:G:OP2	30:28:42:ARG:NE	2.43	0.47
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.45	0.47
26:24:45:GLY:O	26:24:47:GLN:N	2.43	0.47
32:2a:586:C:O2'	32:2a:878:G:H4'	2.14	0.47
32:2a:1030:C:N3	32:2a:1031:G:N2	2.61	0.47
32:2a:1306:A:OP2	52:2u:6:ARG:NH1	2.42	0.47
38:2g:113:GLU:HG3	38:2g:118:VAL:HG12	1.95	0.47
40:2i:53:VAL:O	40:2i:55:ALA:N	2.47	0.47
1:1A:1462:G:O2'	1:1A:1463:C:OP2	2.22	0.47
1:1A:1552:C:H2'	1:1A:1553:A:C8	2.50	0.47
1:1A:1727:U:O2'	1:1A:1794:G:N7	2.40	0.47
1:1A:2178:G:OP2	1:1A:2178:G:H8	1.97	0.47
20:1Y:55:TYR:CD2	20:1Y:55:TYR:N	2.82	0.47
32:1a:322:C:O2'	51:1t:23:ARG:HD2	2.14	0.47
33:1b:134:GLU:HA	33:1b:137:ARG:HE	1.80	0.47
35:1d:173:TRP:CZ3	35:1d:174:LEU:HG	2.49	0.47
54:1w:26:A:H61	54:1w:44:G:H1	1.62	0.47
1:2A:887:A:H4'	1:2A:888:C:C5	2.49	0.47
1:2A:893:C:H2'	1:2A:894:C:C5	2.49	0.47
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2402:C:H1'	1:2A:2403:C:H5	1.79	0.47
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.48	0.47
10:2O:2:ILE:HB	10:2O:33:ALA:HB3	1.96	0.47
13:2R:24:GLN:HB3	13:2R:44:LEU:HD11	1.96	0.47
32:2a:46:G:O2'	32:2a:365:U:H1'	2.15	0.47
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.30	0.47
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.14	0.47
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.50	0.47
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.49	0.47
33:2b:7:VAL:HG12	33:2b:8:LYS:H	1.79	0.47
36:2e:19:MET:SD	36:2e:24:ARG:HB3	2.53	0.47
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.08	0.47
52:2u:18:TYR:CE1	52:2u:24:ARG:HB3	2.48	0.47
1:1A:494:G:N7	29:17:39:ARG:NH2	2.62	0.47
1:1A:1942:4OC:O5'	1:1A:1942:4OC:H6	2.14	0.47
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.95	0.47
32:1a:1039:C:H2'	32:1a:1040:U:C6	2.49	0.47
32:1a:1054:C:C4	32:1a:1196:U:H5	2.32	0.47
34:1c:150:LYS:HG3	34:1c:169:ALA:HB2	1.96	0.47
34:1c:203:PHE:HZ	34:1c:206:GLU:HG2	1.80	0.47
35:1d:108:LEU:HD23	35:1d:110:PHE:CZ	2.49	0.47
35:1d:199:ASN:O	35:1d:201:GLN:N	2.47	0.47
54:1y:40:C:H2'	54:1y:41:C:C6	2.50	0.47
1:2A:375:C:H2'	1:2A:376:C:C6	2.49	0.47
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.49	0.47
1:2A:1187:G:H8	1:2A:1187:G:OP2	1.97	0.47
1:2A:2136:C:H42	1:2A:2155:G:H1	1.49	0.47
1:2A:2408:U:H2'	1:2A:2409:G:H8	1.80	0.47
1:2A:2817:G:O2'	1:2A:2836:U:O2	2.26	0.47
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.11	0.47
32:2a:320:C:H2'	32:2a:321:A:O4'	2.15	0.47
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.96	0.47
32:2a:950:U:H2'	32:2a:951:G:C8	2.49	0.47
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.49	0.47
32:2a:1369:C:OP2	40:2i:112:LYS:N	2.38	0.47
38:2g:22:LEU:HG	38:2g:62:PHE:HE2	1.79	0.47
40:2i:55:ALA:HA	40:2i:58:HIS:HD2	1.79	0.47
55:2x:66:C:H2'	55:2x:67:C:O4'	2.14	0.47
54:2y:6:G:H1	54:2y:67:C:N4	2.12	0.47
1:1A:1679:A:N7	60:1A:4060:HOH:O	2.36	0.47
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:176:C:H2'	32:1a:177:C:C6	2.50	0.47
32:1a:269:C:H2'	32:1a:270:A:C8	2.50	0.47
35:1d:23:GLY:HA3	35:1d:112:VAL:HG12	1.97	0.47
40:1i:6:GLY:HA3	40:1i:83:ARG:HB3	1.97	0.47
1:2A:403:U:H4'	1:2A:404:C:H5'	1.95	0.47
1:2A:2408:U:H2'	1:2A:2409:G:C8	2.49	0.47
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.47	0.47
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.15	0.47
11:2P:50:ARG:HH21	30:28:7:HIS:CD2	2.33	0.47
20:2Y:76:CYS:HA	20:2Y:106:LEU:HD21	1.95	0.47
1:1A:441:C:H2'	1:1A:442:A:C8	2.50	0.47
1:1A:1091:A:OP1	1:1A:1092:A:H3'	2.14	0.47
1:1A:1368:A:N1	1:1A:1379:C:O2'	2.45	0.47
1:1A:1854:G:OP1	3:1D:54:ARG:NH1	2.47	0.47
1:1A:2128:G:H2'	1:1A:2129:C:C6	2.50	0.47
1:1A:2331:G:C2	14:1S:3:ARG:HA	2.50	0.47
1:1A:2489:C:N4	31:19:10:ILE:HG23	2.29	0.47
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.14	0.47
54:1w:9:A:O2'	54:1w:10:G:N7	2.48	0.47
1:2A:2078:C:C4	1:2A:2079:U:C4	3.03	0.47
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.48	0.47
4:2E:108:SER:HB3	4:2E:165:VAL:HG21	1.97	0.47
11:2P:59:LEU:HD21	30:28:10:ALA:HA	1.96	0.47
14:2S:67:ARG:NH1	14:2S:107:GLU:OE2	2.47	0.47
32:2a:1330:U:H4'	44:2m:23:TYR:CZ	2.50	0.47
35:2d:189:PRO:HB2	35:2d:194:LEU:HD11	1.97	0.47
38:2g:67:GLU:HA	38:2g:70:LYS:HD2	1.96	0.47
1:1A:1115:A:H2'	1:1A:1119:A:N7	2.29	0.47
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.15	0.47
1:1A:1921:G:N3	1:1A:1921:G:H2'	2.30	0.47
1:1A:2060:G:H2'	1:1A:2061:C:O4'	2.14	0.47
1:1A:2291:G:O6	22:10:14:ARG:HG3	2.13	0.47
1:1A:2418:U:C2	11:1P:72:PRO:HG2	2.50	0.47
1:1A:2623:U:C4	27:15:3:LYS:HG2	2.49	0.47
1:1A:2661:U:H2'	1:1A:2662:U:C6	2.50	0.47
5:1F:28:ILE:HD13	5:1F:119:ARG:HH21	1.80	0.47
6:1G:20:ILE:O	6:1G:24:GLY:N	2.38	0.47
7:1H:143:GLN:HG3	7:1H:147:ASN:HD21	1.80	0.47
15:1T:51:ARG:HB2	15:1T:98:LYS:HD3	1.97	0.47
32:1a:438:G:H4'	35:1d:123:HIS:CE1	2.49	0.47
32:1a:523:A:N1	43:1l:92:0TD:H6	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1003:G:C4	32:1a:1004:A:H2	2.33	0.47
32:1a:1144:G:H21	32:1a:1146:A:H62	1.63	0.47
33:1b:208:ILE:H	33:1b:208:ILE:HG12	1.52	0.47
35:1d:105:VAL:HG13	35:1d:110:PHE:HB2	1.96	0.47
43:1l:46:LYS:HD2	43:1l:94:PRO:HG3	1.96	0.47
1:2A:458:G:O2'	29:27:39:ARG:HD2	2.14	0.47
1:2A:557:U:H2'	1:2A:558:G:H8	1.79	0.47
1:2A:1580:A:H5'	1:2A:1581:G:OP2	2.15	0.47
1:2A:1805:U:O2	3:2D:50:THR:HB	2.15	0.47
1:2A:2308:G:OP2	60:2A:3612:HOH:O	2.20	0.47
1:2A:2577:A:OP2	27:25:3:LYS:NZ	2.46	0.47
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.50	0.47
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.51	0.47
9:2N:123:TYR:CZ	9:2N:129:PRO:HD2	2.49	0.47
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.14	0.47
21:2Z:92:SER:O	21:2Z:130:PRO:HG3	2.15	0.47
26:24:40:HIS:CE1	26:24:42:PHE:HB3	2.50	0.47
32:2a:54:C:N4	32:2a:353:A:OP2	2.41	0.47
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.15	0.47
32:2a:1060:C:C5	34:2c:2:GLY:HA3	2.49	0.47
32:2a:1120:G:C6	32:2a:1121:U:C4	3.03	0.47
32:2a:1126:U:H6	32:2a:1281:U:C2	2.32	0.47
32:2a:1359:C:H3'	45:2n:35:ARG:HH22	1.79	0.47
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.50	0.47
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.49	0.47
40:2i:97:LYS:HA	40:2i:102:LEU:HG	1.96	0.47
45:2n:23:ARG:HD2	45:2n:28:GLY:O	2.14	0.47
48:2q:95:TYR:O	48:2q:98:LEU:HB2	2.14	0.47
55:2x:15:G:H2'	55:2x:59:A:N1	2.29	0.47
54:2y:52:G:H5'	54:2y:53:G:OP2	2.15	0.47
1:1A:423:G:H1'	23:11:42:GLN:HB3	1.97	0.47
1:1A:2050:U:H2'	1:1A:2051:G:O4'	2.14	0.47
1:1A:2121:U:H3	1:1A:2212:G:H1	1.61	0.47
3:1D:6:PHE:HE2	3:1D:18:VAL:HG13	1.80	0.47
3:1D:16:MET:HE3	3:1D:16:MET:HB2	1.83	0.47
32:1a:1329:A:N7	52:1u:7:ARG:NH2	2.63	0.47
33:1b:60:ASP:O	33:1b:64:ARG:HG2	2.14	0.47
43:1l:33:ARG:HD3	43:1l:33:ARG:HA	1.61	0.47
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.47	0.47
1:2A:995:C:O2	9:2N:3:THR:OG1	2.28	0.47
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.30	0.47
6:2G:79:ASN:OD1	6:2G:79:ASN:N	2.26	0.47
32:2a:308:C:H2'	32:2a:309:G:C8	2.49	0.47
32:2a:689:C:P	42:2k:46:GLY:HA3	2.54	0.47
32:2a:1219:U:H2'	32:2a:1220:G:O4'	2.15	0.47
32:2a:1265:G:C4	32:2a:1271:G:N2	2.83	0.47
35:2d:70:ILE:HD11	35:2d:74:GLN:HB3	1.95	0.47
1:1A:137:G:N7	60:1X:201:HOH:O	2.36	0.47
1:1A:2812:A:H1'	1:1A:2904:U:H1'	1.97	0.47
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.50	0.47
6:1G:101:ILE:HD13	26:14:25:TYR:HB2	1.97	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.66	0.47
32:1a:938:A:C6	32:1a:939:G:C5	3.03	0.47
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.47	0.47
35:1d:199:ASN:O	35:1d:202:LEU:N	2.44	0.47
36:1e:85:GLY:O	36:1e:87:SER:N	2.40	0.47
38:1g:69:VAL:HG21	38:1g:104:LEU:HD13	1.96	0.47
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.97	0.47
54:1y:67:C:H2'	54:1y:68:C:H6	1.78	0.47
1:2A:565:C:H2'	1:2A:566:U:O4'	2.15	0.47
1:2A:566:U:H5''	11:2P:29:LYS:HE3	1.97	0.47
5:2F:164:ARG:O	5:2F:168:ARG:HB2	2.15	0.47
12:2Q:17:LEU:HD21	12:2Q:41:TRP:HE1	1.80	0.47
14:2S:10:ARG:NE	14:2S:91:PRO:O	2.48	0.47
32:2a:174:C:H2'	32:2a:175:C:H6	1.80	0.47
32:2a:1097:C:H2'	32:2a:1098:C:H6	1.80	0.47
32:2a:1270:C:H2'	32:2a:1271:G:C8	2.49	0.47
32:2a:1305:G:O2'	32:2a:1331:G:N2	2.48	0.47
33:2b:219:VAL:HA	33:2b:222:ILE:HG12	1.97	0.47
34:2c:108:ASN:HB3	34:2c:111:LEU:HB2	1.96	0.47
36:2e:93:PRO:HG2	39:2h:105:ARG:NE	2.29	0.47
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.40	0.47
1:1A:2171:G:C6	1:1A:2172:U:C2	3.03	0.47
2:1B:1:U:O2'	2:1B:2:C:OP1	2.30	0.47
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.96	0.47
34:1c:110:ASN:N	34:1c:110:ASN:OD1	2.47	0.47
34:1c:110:ASN:HD22	34:1c:140:ARG:HB3	1.79	0.47
36:1e:31:LEU:HD23	36:1e:45:PHE:CD1	2.50	0.47
38:1g:20:ASP:OD2	38:1g:63:LYS:NZ	2.47	0.47
55:1x:13:C:H2'	55:1x:14:A:H5''	1.97	0.47
1:2A:271(Q):G:H2'	1:2A:271(R):G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.36	0.47
1:2A:2741:A:H2'	1:2A:2742:C:O4'	2.14	0.47
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.97	0.47
8:2I:5:LEU:HD13	8:2I:17:GLN:HB3	1.97	0.47
12:2Q:34:LEU:HD13	12:2Q:118:LEU:HB3	1.97	0.47
32:2a:925:G:H1'	32:2a:1502:A:C4	2.50	0.47
32:2a:1256:A:N1	32:2a:1278:U:H1'	2.30	0.47
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.30	0.47
33:2b:16:HIS:HB2	33:2b:204:ASN:CB	2.41	0.47
33:2b:188:ALA:HB1	33:2b:192:SER:OG	2.15	0.47
36:2e:102:ALA:O	36:2e:107:ARG:NH2	2.48	0.47
44:2m:13:LYS:HA	44:2m:44:ARG:NH1	2.28	0.47
50:2s:80:TYR:O	50:2s:82:GLY:N	2.44	0.47
54:2y:15:G:N1	54:2y:48:C:N3	2.53	0.47
1:1A:574:G:O2'	1:1A:1265:A:N3	2.43	0.46
1:1A:1730:C:H2'	1:1A:1731:C:C6	2.50	0.46
2:1B:8:U:O3'	14:1S:25:ARG:NH2	2.48	0.46
12:1Q:17:LEU:HD21	12:1Q:41:TRP:CD1	2.50	0.46
32:1a:138:G:H1	32:1a:225:C:H42	1.62	0.46
32:1a:250:A:H4'	32:1a:251:G:O5'	2.15	0.46
32:1a:865:A:H2	32:1a:918:A:H4'	1.80	0.46
32:1a:950:U:H2'	32:1a:951:G:C8	2.50	0.46
32:1a:1169:A:H2'	32:1a:1170:A:C8	2.50	0.46
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.48	0.46
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.23	0.46
1:2A:247:G:H4'	1:2A:386:G:C5	2.50	0.46
1:2A:932:G:H4'	1:2A:933:A:O5'	2.15	0.46
1:2A:1016:G:H2'	1:2A:1017:G:O4'	2.15	0.46
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.14	0.46
1:2A:1462:C:H4'	1:2A:2703:C:H5'	1.97	0.46
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.51	0.46
1:2A:2823:A:OP1	4:2E:113:PHE:HB2	2.15	0.46
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.15	0.46
11:2P:47:ASP:OD2	11:2P:49:ARG:NH2	2.46	0.46
21:2Z:40:ASP:OD2	21:2Z:42:VAL:HG13	2.15	0.46
32:2a:43:C:H2'	32:2a:44:G:O4'	2.15	0.46
32:2a:792:A:H4'	32:2a:793:U:H5''	1.97	0.46
32:2a:976:G:P	45:2n:32:SER:H	2.36	0.46
32:2a:1092:A:H5''	38:2g:4:ARG:CZ	2.45	0.46
33:2b:76:GLN:OE1	33:2b:76:GLN:N	2.42	0.46
40:2i:81:ILE:O	40:2i:85:LEU:HG	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:2j:33:GLN:HG3	41:2j:34:VAL:N	2.30	0.46
1:1A:240:A:C5	1:1A:241:G:H1'	2.50	0.46
1:1A:2225:U:O4'	3:1D:151:LYS:HE2	2.15	0.46
4:1E:9:VAL:HG13	4:1E:25:VAL:O	2.16	0.46
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.96	0.46
32:1a:185:A:H2'	32:1a:186:C:C6	2.50	0.46
32:1a:292:G:N7	32:1a:293:G:H1'	2.30	0.46
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.30	0.46
32:1a:555:C:H2'	32:1a:556:C:C6	2.50	0.46
32:1a:688:G:H2'	32:1a:689:C:C6	2.50	0.46
32:1a:1168:A:H8	32:1a:1168:A:OP1	1.98	0.46
33:1b:37:ASN:O	33:1b:39:ILE:HD12	2.15	0.46
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.80	0.46
54:1y:26:A:H61	54:1y:44:G:H1	1.62	0.46
54:1y:52:G:H2'	54:1y:53:G:C8	2.51	0.46
1:2A:271(G):C:H2'	1:2A:271(H):G:C8	2.50	0.46
1:2A:681:G:H2'	1:2A:682:G:O4'	2.15	0.46
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.15	0.46
1:2A:1479:G:H5''	1:2A:1560:G:H4'	1.97	0.46
1:2A:2756:U:H5''	31:29:19:ARG:HA	1.97	0.46
32:2a:867:G:OP2	32:2a:867:G:H8	1.98	0.46
54:2w:19:G:H1	54:2w:56:C:H42	1.62	0.46
1:1A:302:A:H2'	1:1A:303:C:C6	2.50	0.46
1:1A:599:U:H2'	1:1A:600:G:C8	2.51	0.46
1:1A:1221:G:N2	1:1A:1223:C:OP2	2.48	0.46
2:1B:2:C:H2'	2:1B:3:C:C6	2.51	0.46
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.51	0.46
11:1P:63:PRO:HB2	30:18:30:ARG:NH2	2.30	0.46
32:1a:672:U:O2'	32:1a:673:G:O5'	2.27	0.46
32:1a:1125:U:H4'	41:1j:5:ARG:HH12	1.80	0.46
36:1e:41:VAL:HG23	36:1e:67:VAL:HG13	1.96	0.46
40:1i:5:TYR:HD1	40:1i:17:VAL:O	1.99	0.46
54:1w:50:U:O4	54:1w:64:A:N1	2.49	0.46
1:2A:1252:G:N3	16:2U:33:ARG:HG2	2.30	0.46
1:2A:2376:A:H3'	1:2A:2377:A:H8	1.80	0.46
1:2A:2809:A:H62	1:2A:2891:G:H2'	1.79	0.46
2:2B:24:G:N7	2:2B:56:G:H2'	2.29	0.46
4:2E:5:LEU:HD22	4:2E:197:ILE:HG12	1.97	0.46
32:2a:671:G:H1	32:2a:735:C:H42	1.63	0.46
32:2a:951:G:OP2	44:2m:102:ARG:NH1	2.49	0.46
32:2a:1028:C:N3	32:2a:1033:G:O6	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1075:C:H5''	33:2b:179:LYS:NZ	2.30	0.46
32:2a:1101:A:H4'	32:2a:1102:A:O5'	2.15	0.46
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.16	0.46
33:2b:74:LYS:HD2	33:2b:166:ASP:CB	2.46	0.46
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.79	0.46
1:1A:196:A:H2'	1:1A:197:C:O4'	2.15	0.46
1:1A:1355:G:P	29:17:9:ARG:HD2	2.56	0.46
1:1A:1463:C:H2'	1:1A:1464:G:O4'	2.15	0.46
1:1A:1470:G:H2'	1:1A:1471:G:O4'	2.14	0.46
1:1A:1954:A:OP2	60:1A:4015:HOH:O	2.20	0.46
1:1A:2389:A:H2'	1:1A:2390:A:C8	2.50	0.46
57:1A:3934:KAN:HN11	57:1A:3934:KAN:H4	1.58	0.46
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.15	0.46
25:13:6:VAL:HG12	25:13:54:VAL:HG21	1.97	0.46
29:17:24:THR:O	29:17:28:ARG:HG3	2.16	0.46
32:1a:792:A:H4'	32:1a:793:U:O5'	2.16	0.46
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.50	0.46
54:1y:19:G:N1	54:1y:56:C:N4	2.62	0.46
1:2A:80:G:O2'	1:2A:294:A:N1	2.46	0.46
1:2A:515:A:H1'	1:2A:581:C:H1'	1.97	0.46
1:2A:773:U:O2'	3:2D:48:ARG:HD3	2.16	0.46
1:2A:997:G:H5''	16:2U:92:ARG:NH1	2.30	0.46
1:2A:1584:C:O2'	1:2A:1586:A:O5'	2.29	0.46
1:2A:2156:G:H2'	1:2A:2157:G:N1	2.31	0.46
1:2A:2491:U:OP2	60:2A:3613:HOH:O	2.20	0.46
2:2B:105:A:H5'	2:2B:106:G:OP2	2.15	0.46
2:2B:106:G:H5'	21:2Z:31:ARG:HG2	1.97	0.46
25:23:15:TYR:O	25:23:20:LYS:NZ	2.49	0.46
32:2a:983:A:H3'	32:2a:983:A:N3	2.30	0.46
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.96	0.46
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.97	0.46
43:2l:110:VAL:HB	43:2l:113:ARG:HG2	1.96	0.46
1:1A:91:G:H2'	1:1A:92:C:H6	1.81	0.46
1:1A:509:A:O2'	20:1Y:49:VAL:O	2.31	0.46
1:1A:1845:G:H4'	3:1D:51:VAL:HG21	1.98	0.46
5:1F:32:LEU:HD13	5:1F:112:MET:HE1	1.98	0.46
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.63	0.46
26:14:16:CYS:HA	26:14:33:VAL:O	2.15	0.46
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.15	0.46
33:1b:93:VAL:HG21	33:1b:97:TRP:CD1	2.50	0.46
44:1m:122:LYS:HA	44:1m:122:LYS:HD2	1.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:19:ILE:HG22	47:1p:37:GLY:C	2.41	0.46
1:2A:1401:G:H2'	1:2A:1402:C:C6	2.51	0.46
2:2B:19:G:H8	2:2B:19:G:OP2	1.99	0.46
3:2D:10:THR:HG23	3:2D:13:ARG:HG3	1.96	0.46
3:2D:146:GLU:HG2	3:2D:152:GLY:C	2.41	0.46
16:2U:65:ILE:HD11	16:2U:95:LEU:HB3	1.96	0.46
21:2Z:50:GLN:H	21:2Z:50:GLN:CD	2.24	0.46
32:2a:266:G:H2'	32:2a:266:G:N3	2.31	0.46
33:2b:15:VAL:HG23	33:2b:16:HIS:HD2	1.79	0.46
34:2c:63:ASN:HA	34:2c:98:ASN:H	1.81	0.46
34:2c:152:ILE:O	34:2c:152:ILE:HG13	2.15	0.46
35:2d:8:VAL:HA	35:2d:11:LEU:HD13	1.97	0.46
45:2n:22:THR:HB	45:2n:33:VAL:HB	1.97	0.46
50:2s:38:SER:HB2	50:2s:71:LEU:HD22	1.98	0.46
54:2w:68:C:H2'	54:2w:69:G:C8	2.50	0.46
55:2x:58:A:H4'	55:2x:59:A:OP1	2.14	0.46
1:1A:116:A:C8	1:1A:117:A:C8	3.03	0.46
1:1A:931:C:C4	1:1A:932:C:H1'	2.50	0.46
1:1A:2331:G:H22	14:1S:3:ARG:NE	2.14	0.46
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.16	0.46
6:1G:73:ALA:HB3	6:1G:85:GLY:H	1.81	0.46
14:1S:61:ASN:HB3	14:1S:64:GLU:HB2	1.98	0.46
17:1V:67:GLY:O	17:1V:88:ARG:HG2	2.15	0.46
32:1a:8:A:H5'	36:1e:101:ILE:HG22	1.97	0.46
32:1a:189(B):C:H2'	32:1a:189(C):C:C6	2.51	0.46
32:1a:435:C:H2'	32:1a:436:C:H6	1.80	0.46
32:1a:1112:C:H1'	34:1c:179:ARG:HH11	1.81	0.46
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.51	0.46
33:1b:21:ARG:HB2	33:1b:38:GLY:O	2.15	0.46
33:1b:164:VAL:HG23	33:1b:185:ILE:O	2.16	0.46
47:1p:21:VAL:HG13	47:1p:33:ILE:HB	1.97	0.46
47:1p:50:LYS:HA	47:1p:50:LYS:HD2	1.68	0.46
54:1w:22:G:N7	54:1w:46:7MG:N2	2.56	0.46
1:2A:887:A:H4'	1:2A:888:C:H5	1.79	0.46
1:2A:1003:G:O2'	1:2A:1010:A:N1	2.46	0.46
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.49	0.46
1:2A:1615:C:H2'	1:2A:1617:C:C5	2.50	0.46
12:2Q:21:THR:HG21	12:2Q:101:ARG:HB2	1.98	0.46
21:2Z:138:GLU:H	21:2Z:156:LYS:HE2	1.80	0.46
32:2a:193:C:H2'	32:2a:194:C:H6	1.80	0.46
32:2a:406:G:H4'	35:2d:5:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.28	0.46
32:2a:429:U:H1'	32:2a:430:A:H5''	1.98	0.46
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.49	0.46
32:2a:1485:U:H2'	32:2a:1486:G:C8	2.50	0.46
33:2b:120:ALA:O	33:2b:125:PRO:HD2	2.15	0.46
34:2c:18:TRP:HE3	34:2c:18:TRP:H	1.63	0.46
37:2f:8:ILE:HD11	37:2f:79:LEU:HD13	1.96	0.46
38:2g:99:LEU:HD22	38:2g:103:TRP:CZ2	2.50	0.46
41:2j:54:PHE:O	41:2j:55:LYS:HG2	2.16	0.46
50:2s:64:GLU:CD	50:2s:64:GLU:H	2.24	0.46
1:1A:1127:U:H2'	1:1A:1128:U:C6	2.50	0.46
1:1A:1173:A:N1	1:1A:2475:C:O2'	2.40	0.46
1:1A:1790:A:H1'	1:1A:2723:A:C2	2.51	0.46
1:1A:1979:C:H2'	1:1A:1980:C:C6	2.51	0.46
60:1A:4036:HOH:O	11:1P:19:VAL:HG22	2.16	0.46
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.49	0.46
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.51	0.46
32:1a:109:A:C6	32:1a:326:G:C6	3.03	0.46
32:1a:193:C:H2'	32:1a:194:C:C6	2.50	0.46
32:1a:501:C:H2'	32:1a:502:G:C8	2.50	0.46
32:1a:976:G:OP1	45:1n:32:SER:N	2.47	0.46
1:2A:398:G:OP1	1:2A:2090:G:O2'	2.33	0.46
1:2A:1507:A:O2'	1:2A:1508:A:H8	1.98	0.46
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.16	0.46
15:2T:26:ASP:O	15:2T:49:VAL:HG22	2.15	0.46
32:2a:37:U:O2'	32:2a:500:G:H4'	2.16	0.46
32:2a:338:A:H2	32:2a:351:G:H22	1.64	0.46
32:2a:668:G:H21	46:2o:46:HIS:CE1	2.33	0.46
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.50	0.46
32:2a:1239:A:H4'	32:2a:1240:U:H5''	1.98	0.46
40:2i:45:ALA:O	40:2i:48:GLU:HB2	2.16	0.46
44:2m:89:GLY:O	44:2m:93:ARG:HG3	2.16	0.46
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.30	0.46
54:2w:39:PSU:H2'	54:2w:40:C:H6	1.81	0.46
55:2x:17:C:H2'	55:2x:17(A):U:H5	1.81	0.46
1:1A:8:A:H2'	1:1A:9:U:C6	2.51	0.46
1:1A:1104:G:H1	1:1A:1126:C:H42	1.62	0.46
1:1A:2160:C:N4	1:1A:2175:G:H1	2.14	0.46
1:1A:2731:G:O2'	1:1A:2857:U:OP1	2.30	0.46
3:1D:83:GLU:OE1	3:1D:104:TYR:OH	2.20	0.46
18:1W:12:ILE:HD13	18:1W:17:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:163:C:H2'	32:1a:164:U:C6	2.50	0.46
32:1a:299:G:C6	32:1a:300:A:C6	3.04	0.46
32:1a:1028:C:H2'	32:1a:1029:C:O4'	2.16	0.46
32:1a:1318:A:H5''	50:1s:3:ARG:HH12	1.81	0.46
33:1b:162:ILE:O	33:1b:185:ILE:HG12	2.15	0.46
35:1d:19:LEU:HB3	35:1d:21:LEU:HD21	1.96	0.46
48:1q:6:LEU:HG	48:1q:23:VAL:HG11	1.98	0.46
1:2A:754:C:H2'	1:2A:755:C:C6	2.50	0.46
1:2A:1141:U:OP2	9:2N:63:THR:OG1	2.27	0.46
1:2A:1301:A:O2'	1:2A:1303:G:N7	2.42	0.46
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.51	0.46
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.16	0.46
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.51	0.46
1:2A:2427:C:H5''	1:2A:2428:G:OP1	2.16	0.46
1:2A:2556:C:H2'	1:2A:2557:G:O4'	2.16	0.46
1:2A:2656:U:OP2	60:2A:3614:HOH:O	2.21	0.46
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.44	0.46
10:2O:26:LYS:O	10:2O:30:ALA:HB2	2.15	0.46
14:2S:87:PHE:CZ	14:2S:102:ALA:HB2	2.51	0.46
19:2X:44:GLU:OE1	60:2X:101:HOH:O	2.21	0.46
32:2a:11:G:H1	32:2a:23:C:H42	1.62	0.46
32:2a:202:U:H3'	32:2a:203:U:C6	2.51	0.46
32:2a:435:C:H2'	32:2a:436:C:H6	1.81	0.46
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.50	0.46
32:2a:1425:U:H2'	32:2a:1426:C:C6	2.51	0.46
34:2c:12:LEU:HD23	34:2c:16:ARG:HB3	1.98	0.46
1:1A:36:G:N3	1:1A:476:G:O2'	2.48	0.46
1:1A:1299:A:OP1	60:1A:4016:HOH:O	2.20	0.46
2:1B:6:C:H2'	2:1B:7:G:O4'	2.16	0.46
32:1a:396:G:O2'	32:1a:398:C:OP1	2.27	0.46
32:1a:690:G:C6	32:1a:691:G:C6	3.04	0.46
32:1a:701:C:OP1	32:1a:702:A:O2'	2.32	0.46
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.51	0.46
32:1a:1084:G:C5	32:1a:1085:U:C4	3.04	0.46
32:1a:1495:U:O4	57:1a:1955:KAN:N3	2.47	0.46
38:1g:45:ASP:O	38:1g:49:ILE:HG13	2.16	0.46
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.15	0.46
1:2A:1033:U:P	31:29:9:ARG:HH22	2.35	0.46
1:2A:1528(A):A:H2'	1:2A:1529:G:O4'	2.16	0.46
6:2G:125:PHE:CE2	6:2G:170:ARG:HD3	2.50	0.46
9:2N:17:ASP:O	9:2N:21:LYS:HE2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.50	0.46
32:2a:435:C:H2'	32:2a:436:C:C6	2.51	0.46
32:2a:538:G:H5''	43:2l:114:LYS:HB2	1.97	0.46
32:2a:583:A:N6	32:2a:758:G:O2'	2.49	0.46
34:2c:138:VAL:HG11	34:2c:169:ALA:HA	1.98	0.46
43:2l:37:CYS:SG	43:2l:81:SER:HB2	2.56	0.46
1:1A:595:A:H5''	1:1A:596:G:OP2	2.16	0.46
1:1A:1404:G:O2'	1:1A:1419:A:N6	2.48	0.46
1:1A:1615:G:H5'	3:1D:60:ARG:HA	1.98	0.46
11:1P:57:THR:O	11:1P:61:ARG:HG3	2.17	0.46
24:12:51:ARG:HD3	24:12:55:ARG:NH1	2.31	0.46
32:1a:458:C:H2'	32:1a:460:G:O4'	2.16	0.46
32:1a:601:C:H2'	32:1a:602:A:C8	2.51	0.46
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.51	0.46
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.98	0.46
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.98	0.46
1:2A:27:G:O2'	1:2A:28:A:OP2	2.31	0.46
1:2A:121:G:H4'	1:2A:149:A:H5'	1.98	0.46
1:2A:945:A:C4	1:2A:2448:A:C2	3.04	0.46
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.31	0.46
4:2E:127:ASP:OD2	60:2E:401:HOH:O	2.20	0.46
7:2H:30:LYS:HD2	7:2H:30:LYS:HA	1.79	0.46
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.97	0.46
17:2V:57:VAL:HG22	17:2V:99:ILE:HG23	1.98	0.46
29:27:12:ARG:CZ	29:27:44:PRO:HB3	2.46	0.46
32:2a:399:G:H2'	32:2a:400:C:C6	2.50	0.46
32:2a:1267:C:H5	32:2a:1268:A:C5	2.34	0.46
34:2c:9:GLY:HA2	34:2c:12:LEU:HG	1.98	0.46
37:2f:99:ALA:HB2	49:2r:31:LEU:HD11	1.98	0.46
38:2g:23:VAL:O	38:2g:27:ILE:HG13	2.16	0.46
1:1A:1821:C:H5''	1:1A:1822:A:OP1	2.15	0.45
8:1I:70:GLU:O	8:1I:74:ASN:HB2	2.16	0.45
20:1Y:11:ASP:OD1	20:1Y:11:ASP:N	2.46	0.45
32:1a:841:U:C4	32:1a:848:C:H1'	2.51	0.45
32:1a:1206:G:H2'	32:1a:1207:2MG:O4'	2.15	0.45
32:1a:1216:G:H5''	45:1n:5:ALA:CB	2.46	0.45
32:1a:1320:C:OP1	50:1s:70:LYS:NZ	2.40	0.45
38:1g:12:LEU:HD12	38:1g:12:LEU:H	1.80	0.45
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.31	0.45
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.16	0.45
1:2A:320:A:H4'	1:2A:322:A:N7	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:813:U:H2'	1:2A:814:C:C6	2.52	0.45
1:2A:903:C:H2'	1:2A:904:C:C6	2.51	0.45
1:2A:2067:G:O2'	1:2A:2069:G:H5'	2.17	0.45
1:2A:2152:G:C2	1:2A:2153:G:H1'	2.51	0.45
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	1.98	0.45
16:2U:97:ASP:OD1	16:2U:101:ARG:HD2	2.16	0.45
18:2W:65:LEU:HD12	18:2W:68:ARG:HD2	1.98	0.45
26:24:26:SER:OG	26:24:27:THR:N	2.48	0.45
27:25:36:CYS:HB3	27:25:49:CYS:HB3	1.98	0.45
32:2a:931:C:N4	32:2a:1386:G:H1	2.14	0.45
37:2f:3:ARG:HD3	37:2f:64:GLN:HE21	1.81	0.45
53:2v:13:A:H8	53:2v:13:A:OP2	1.98	0.45
1:1A:27:G:N2	1:1A:537:G:H1'	2.32	0.45
1:1A:280:C:H2'	1:1A:281:G:H8	1.81	0.45
1:1A:354:A:N7	1:1A:1255:A:O2'	2.38	0.45
5:1F:132:VAL:CG2	5:1F:163:VAL:HG22	2.46	0.45
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.14	0.45
21:1Z:126:VAL:HG13	21:1Z:161:VAL:HG23	1.99	0.45
29:17:46:VAL:HG13	29:17:48:LYS:NZ	2.32	0.45
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.17	0.45
32:1a:1047:G:H5''	45:1n:4:LYS:HD3	1.98	0.45
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.38	0.45
54:1y:9:A:O3'	54:1y:45:U:O2'	2.33	0.45
1:2A:993:G:N2	17:2V:23:GLU:OE2	2.49	0.45
1:2A:2125:G:N1	1:2A:2172:U:OP1	2.39	0.45
1:2A:2849:U:O4	15:2T:23:ARG:NH2	2.41	0.45
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.16	0.45
32:2a:142:G:H2'	32:2a:143:A:C8	2.51	0.45
32:2a:692:U:H5	42:2k:26:ASN:OD1	1.98	0.45
32:2a:1010:G:N1	32:2a:1020:U:H1'	2.31	0.45
32:2a:1516:G:H2'	32:2a:1518:MA6:OP2	2.16	0.45
33:2b:30:ARG:HH21	33:2b:194:PRO:HB2	1.80	0.45
55:2x:10:G:N2	55:2x:26:G:H1'	2.31	0.45
1:1A:1400:A:H2'	1:1A:1401:G:O4'	2.16	0.45
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.17	0.45
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.98	0.45
12:1Q:106:VAL:HG21	12:1Q:114:ALA:HB1	1.96	0.45
32:1a:266:G:H2'	32:1a:266:G:N3	2.30	0.45
32:1a:567:G:H2'	32:1a:568:G:O4'	2.16	0.45
32:1a:1095:U:P	32:1a:1108:G:H1	2.39	0.45
32:1a:1104:G:H2'	32:1a:1105:A:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:49:VAL:HG21	45:1n:41:ARG:O	2.16	0.45
42:1k:33:THR:HA	42:1k:39:PRO:HA	1.98	0.45
46:1o:26:GLU:OE2	46:1o:77:ARG:NE	2.49	0.45
54:1y:64:A:H2'	54:1y:65:G:C8	2.52	0.45
1:2A:839:U:H2'	1:2A:840:C:C6	2.51	0.45
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	1.96	0.45
1:2A:2137:C:O2'	1:2A:2138:C:OP2	2.32	0.45
1:2A:2414:G:N7	57:2A:3568:KAN:N4	2.61	0.45
2:2B:21:G:H1	2:2B:62:C:H42	1.64	0.45
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.98	0.45
7:2H:35:VAL:HG13	7:2H:71:LEU:HD22	1.98	0.45
11:2P:97:PRO:HG3	11:2P:112:LEU:HD12	1.99	0.45
15:2T:122:ASP:O	15:2T:126:ALA:N	2.44	0.45
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.99	0.45
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.51	0.45
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.16	0.45
38:2g:59:LEU:O	38:2g:63:LYS:HG3	2.16	0.45
1:1A:593:G:H2'	1:1A:2052:A:C5	2.51	0.45
1:1A:699:C:H2'	1:1A:700:A:O4'	2.17	0.45
1:1A:2023:A:H2'	1:1A:2024:G:C8	2.51	0.45
1:1A:2153:G:H5'	1:1A:2155:G:C8	2.51	0.45
1:1A:2568:C:H2'	1:1A:2569:G:O4'	2.17	0.45
2:1B:1:U:HO2'	2:1B:2:C:P	2.38	0.45
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.99	0.45
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.81	0.45
10:1O:68:GLU:OE1	10:1O:78:ARG:NH1	2.50	0.45
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.51	0.45
32:1a:711:G:OP1	37:1f:54:LYS:NZ	2.34	0.45
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.98	0.45
32:1a:1350:A:O2'	38:1g:33:ASP:OD1	2.31	0.45
1:2A:656:G:H2'	1:2A:657:U:O4'	2.16	0.45
1:2A:984:A:H5''	1:2A:985:C:H5	1.81	0.45
1:2A:1926:U:O2'	1:2A:1928:A:N7	2.44	0.45
1:2A:2340:G:H2'	1:2A:2341:G:H8	1.82	0.45
1:2A:2679:A:H4'	4:2E:165:VAL:HG11	1.98	0.45
1:2A:2812:G:H2'	1:2A:2813:A:C8	2.52	0.45
6:2G:3:LEU:H	6:2G:3:LEU:HG	1.40	0.45
7:2H:98:LEU:HB2	7:2H:125:VAL:HG22	1.97	0.45
15:2T:26:ASP:OD2	15:2T:120:ARG:NH1	2.40	0.45
16:2U:101:ARG:O	16:2U:103:PRO:HD3	2.16	0.45
16:2U:113:ALA:O	16:2U:117:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:2Y:43:ASN:ND2	20:2Y:65:ALA:HB3	2.31	0.45
25:23:7:LYS:HG3	25:23:34:GLU:HG3	1.98	0.45
26:24:44:THR:O	26:24:46:GLN:N	2.49	0.45
32:2a:560:U:H6	32:2a:560:U:H2'	1.58	0.45
32:2a:791:G:H2'	32:2a:792:A:H5'	1.99	0.45
32:2a:824:C:H2'	32:2a:825:G:C8	2.51	0.45
32:2a:1417:G:C6	32:2a:1482:G:C6	3.05	0.45
38:2g:29:LYS:HB2	38:2g:105:VAL:HG21	1.98	0.45
41:2j:64:GLU:OE2	41:2j:66:ARG:NH1	2.49	0.45
51:2t:86:ARG:O	51:2t:90:GLN:HB2	2.16	0.45
1:1A:271:U:H4'	1:1A:272:U:OP2	2.16	0.45
1:1A:704:U:H2'	1:1A:705:C:C6	2.52	0.45
2:1B:7:G:H5'	14:1S:29:PHE:CE2	2.51	0.45
10:1O:64:ARG:NH2	10:1O:99:PHE:O	2.50	0.45
29:17:22:MET:HA	29:17:28:ARG:HG2	1.99	0.45
32:1a:456:C:H2'	32:1a:457:C:C6	2.51	0.45
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.98	0.45
54:1y:19:G:C4'	54:1y:57:G:H22	2.29	0.45
1:2A:415:A:H2'	1:2A:416:C:O4'	2.16	0.45
1:2A:571:A:N6	1:2A:2499:C:O3'	2.46	0.45
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.81	0.45
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.51	0.45
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.51	0.45
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.51	0.45
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.31	0.45
12:2Q:26:TYR:HD1	12:2Q:28:ALA:HB2	1.82	0.45
32:2a:974:A:OP2	45:2n:41:ARG:NH1	2.48	0.45
32:2a:1302:U:OP1	44:2m:13:LYS:NZ	2.32	0.45
40:2i:3:GLN:HG3	40:2i:20:ARG:HE	1.80	0.45
40:2i:6:GLY:HA3	40:2i:80:GLY:O	2.15	0.45
50:2s:80:TYR:O	50:2s:81:ARG:HG2	2.16	0.45
1:1A:865:G:H4'	1:1A:885:C:O3'	2.17	0.45
1:1A:1138:C:H2'	1:1A:1139:G:O4'	2.17	0.45
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.50	0.45
1:1A:2150:C:H2'	1:1A:2151:C:O4'	2.17	0.45
60:1A:4524:HOH:O	19:1X:65:ARG:HD2	2.17	0.45
13:1R:26:LYS:HE2	13:1R:70:LEU:O	2.16	0.45
25:13:7:LYS:HB2	25:13:34:GLU:HG3	1.98	0.45
32:1a:299:G:H2'	32:1a:300:A:C8	2.51	0.45
32:1a:342:C:H2'	32:1a:343:U:C6	2.52	0.45
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:111:ARG:HD2	38:1g:123:GLU:HB2	1.98	0.45
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.34	0.45
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.98	0.45
54:1w:70:G:C2	54:1w:71:G:H1'	2.52	0.45
1:2A:196:A:N3	1:2A:196:A:H2'	2.31	0.45
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.52	0.45
5:2F:196:LEU:HD23	5:2F:196:LEU:HA	1.81	0.45
6:2G:23:PHE:HB2	6:2G:25:TYR:CZ	2.51	0.45
6:2G:33:ARG:NH2	6:2G:162:THR:HG21	2.32	0.45
6:2G:51:ARG:HA	6:2G:51:ARG:HD3	1.81	0.45
7:2H:3:ARG:HH22	7:2H:5:GLY:H	1.63	0.45
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.78	0.45
11:2P:60:MET:HA	30:28:13:ARG:NH1	2.32	0.45
13:2R:33:ARG:HA	13:2R:114:VAL:O	2.17	0.45
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.49	0.45
22:20:26:TYR:O	22:20:29:GLN:HB2	2.16	0.45
32:2a:227:G:H2'	32:2a:228:A:H8	1.81	0.45
32:2a:1001(A):G:H3'	32:2a:1002:G:O4'	2.17	0.45
32:2a:1133:G:H1	32:2a:1141:C:H42	1.65	0.45
32:2a:1149:C:P	40:2i:9:ARG:HH21	2.39	0.45
35:2d:57:ARG:CD	35:2d:205:GLU:HB3	2.47	0.45
36:2e:110:LEU:HD13	36:2e:118:ILE:HD13	1.99	0.45
44:2m:64:TRP:HB2	44:2m:66:LEU:HD21	1.99	0.45
48:2q:84:LEU:HA	48:2q:87:LYS:HZ2	1.80	0.45
1:1A:294:C:N3	1:1A:390:G:N2	2.46	0.45
1:1A:854:U:OP2	11:1P:36:LYS:HD3	2.17	0.45
1:1A:943:C:H5'	54:1w:56:C:OP1	2.17	0.45
1:1A:1183:G:N3	9:1N:106:MET:HE2	2.32	0.45
1:1A:1231:G:H2'	1:1A:1232:G:O4'	2.16	0.45
1:1A:1312:G:O6	18:1W:13:SER:OG	2.14	0.45
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.28	0.45
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	1.99	0.45
18:1W:4:LYS:HD2	18:1W:6:ILE:HD11	1.98	0.45
25:13:31:LEU:HD23	25:13:31:LEU:HA	1.80	0.45
32:1a:99:U:H2'	32:1a:100:C:C6	2.52	0.45
32:1a:841:U:C5	32:1a:848:C:H1'	2.51	0.45
32:1a:1095:U:OP1	32:1a:1108:G:N2	2.43	0.45
32:1a:1166:G:N2	32:1a:1170:A:OP2	2.49	0.45
38:1g:146:GLU:O	38:1g:149:ARG:HB2	2.17	0.45
39:1h:104:ARG:HA	39:1h:104:ARG:HD3	1.65	0.45
42:1k:18:ARG:NH2	42:1k:35:PRO:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:20:THR:C	44:1m:22:ILE:H	2.25	0.45
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.17	0.45
1:2A:528:A:C2	1:2A:2043:C:H4'	2.52	0.45
1:2A:634:C:H2'	1:2A:635:C:C6	2.52	0.45
1:2A:732:C:H2'	1:2A:733:G:O4'	2.17	0.45
1:2A:2690:C:N4	1:2A:2713:A:H1'	2.31	0.45
1:2A:2788:C:H5''	4:2E:61:ARG:HH21	1.82	0.45
12:2Q:70:PRO:HA	12:2Q:95:ALA:HB2	1.98	0.45
15:2T:127:ALA:C	15:2T:129:ARG:H	2.24	0.45
21:2Z:130:PRO:HA	21:2Z:133:ILE:HG13	1.99	0.45
31:29:3:VAL:HA	31:29:35:ARG:O	2.17	0.45
32:2a:147:G:H1	32:2a:175:C:H42	1.64	0.45
32:2a:587:G:N2	32:2a:754:C:OP2	2.48	0.45
32:2a:683:G:H2'	32:2a:684:A:C8	2.52	0.45
32:2a:1279:A:OP2	41:2j:9:ARG:NH2	2.50	0.45
34:2c:66:VAL:HG12	34:2c:68:VAL:HG23	1.98	0.45
1:1A:253:C:O2'	1:1A:254:A:H2'	2.17	0.45
1:1A:945:A:H2'	1:1A:945:A:N3	2.32	0.45
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.17	0.45
1:1A:2859:U:OP2	15:1T:95:ARG:NH1	2.50	0.45
32:1a:78:G:N1	32:1a:91:C:C4	2.85	0.45
49:1r:52:PRO:O	49:1r:56:THR:HG23	2.16	0.45
1:2A:182:A:N3	1:2A:433:C:O2'	2.44	0.45
1:2A:643:A:C8	28:26:44:ARG:NH1	2.85	0.45
1:2A:1278:A:H2'	1:2A:1279:G:C8	2.52	0.45
1:2A:1278:A:H5''	13:2R:36:THR:HG22	1.98	0.45
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.79	0.45
1:2A:2031:A:N3	1:2A:2455:G:O2'	2.36	0.45
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.99	0.45
5:2F:158:THR:HA	5:2F:195:ASP:HB2	1.99	0.45
5:2F:184:TYR:HE1	11:2P:3:LEU:HD21	1.82	0.45
21:2Z:57:ILE:HD12	21:2Z:71:VAL:HG23	1.98	0.45
32:2a:411:A:H2'	32:2a:412:A:H4'	1.99	0.45
32:2a:836:G:C6	32:2a:851:G:C6	3.04	0.45
32:2a:1130:A:O2'	40:2i:3:GLN:NE2	2.45	0.45
34:2c:125:GLU:HB2	34:2c:190:ARG:NH2	2.30	0.45
37:2f:45:LEU:HD12	37:2f:59:TYR:CD1	2.51	0.45
44:2m:96:LEU:O	44:2m:110:ARG:NE	2.50	0.45
54:2w:56:C:H2'	54:2w:57:G:O4'	2.16	0.45
1:1A:1199:C:H2'	1:1A:1200:G:O4'	2.17	0.45
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2180:A:HO2'	1:1A:2181:G:P	2.36	0.45
1:1A:2549:U:H2'	1:1A:2550:C:C6	2.52	0.45
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.17	0.45
7:1H:152:ARG:HD3	7:1H:152:ARG:HA	1.65	0.45
14:1S:51:ALA:HB3	14:1S:73:LEU:HB2	1.99	0.45
15:1T:127:ALA:C	15:1T:129:ARG:N	2.74	0.45
32:1a:22:G:H2'	32:1a:23:C:H6	1.82	0.45
32:1a:911:U:H2'	32:1a:912:C:C6	2.52	0.45
32:1a:1511:G:H2'	32:1a:1512:U:O4'	2.16	0.45
33:1b:33:TYR:HB2	33:1b:43:ASP:HB2	1.98	0.45
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.98	0.45
36:1e:87:SER:HB3	36:1e:131:ILE:HD13	1.98	0.45
39:1h:83:ILE:HG13	39:1h:137:VAL:HG22	1.98	0.45
46:1o:7:GLU:H	46:1o:7:GLU:HG3	1.59	0.45
1:2A:265:A:H1'	1:2A:266:G:O4'	2.17	0.45
1:2A:271(K):U:H4'	1:2A:271(L):U:OP2	2.17	0.45
1:2A:1029:A:N6	1:2A:1125:G:O2'	2.50	0.45
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.16	0.45
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.82	0.45
8:2I:84:GLY:O	8:2I:86:THR:N	2.50	0.45
19:2X:29:TRP:CZ3	19:2X:76:ARG:HG3	2.52	0.45
32:2a:1216:G:H5''	45:2n:5:ALA:HB2	1.97	0.45
32:2a:1259:C:C4	32:2a:1260:C:H1'	2.52	0.45
32:2a:1268:A:H4'	52:2u:19:GLY:HA2	1.99	0.45
34:2c:182:ILE:HG12	34:2c:203:PHE:CD1	2.50	0.45
35:2d:171:GLY:HA2	35:2d:172:PRO:HD3	1.81	0.45
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.52	0.45
1:1A:1000:C:OP1	12:1Q:87:LYS:HE2	2.15	0.45
1:1A:1133:G:H2'	1:1A:1135:G:C8	2.52	0.45
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.52	0.45
1:1A:1515:C:H2'	1:1A:1516:A:C8	2.51	0.45
1:1A:1904:C:H2'	1:1A:1905:G:O4'	2.16	0.45
1:1A:2227:G:H5''	1:1A:2228:G:C5	2.52	0.45
1:1A:2718:G:H2'	1:1A:2719:G:O4'	2.17	0.45
6:1G:126:ASP:HB2	6:1G:130:ASN:O	2.17	0.45
9:1N:14:VAL:HG11	9:1N:138:LEU:HD12	1.98	0.45
15:1T:16:ARG:HH21	15:1T:19:LEU:HD21	1.81	0.45
32:1a:1136:U:H5''	32:1a:1137:C:C4	2.51	0.45
32:1a:1248:A:N3	40:1i:70:LYS:HE2	2.32	0.45
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.17	0.45
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:100:ALA:O	38:1g:104:LEU:HB2	2.17	0.45
38:1g:147:ALA:C	38:1g:149:ARG:H	2.25	0.45
54:1w:63:G:H2'	54:1w:64:A:C8	2.52	0.45
54:1y:56:C:C2	54:1y:57:G:C8	3.05	0.45
54:1y:58:A:O2'	54:1y:59:U:OP1	2.33	0.45
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.60	0.45
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.50	0.45
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.16	0.45
6:2G:25:TYR:C	6:2G:27:ASN:H	2.25	0.45
11:2P:7:ARG:HG3	11:2P:8:PRO:HD2	1.98	0.45
20:2Y:28:LYS:HB2	20:2Y:40:GLU:HG2	1.99	0.45
21:2Z:102:LEU:HD23	21:2Z:139:VAL:HG21	1.99	0.45
32:2a:187:C:H2'	32:2a:188:C:C6	2.51	0.45
32:2a:1347:G:H5''	40:2i:107:ARG:HB3	1.99	0.45
36:2e:24:ARG:HD2	53:2v:24:A:OP2	2.17	0.45
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.32	0.45
45:2n:18:VAL:C	45:2n:20:ALA:H	2.24	0.45
1:1A:580:U:H2'	1:1A:581:G:C8	2.52	0.44
6:1G:14:GLU:O	6:1G:17:PRO:HD2	2.17	0.44
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.98	0.44
19:1X:24:GLY:O	19:1X:83:VAL:HG22	2.17	0.44
32:1a:222:U:H2'	32:1a:223:U:C6	2.52	0.44
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.18	0.44
32:1a:1325:C:OP1	52:1u:15:ARG:NH2	2.50	0.44
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.35	0.44
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.17	0.44
47:1p:60:LEU:HD11	47:1p:66:PRO:HD3	1.97	0.44
50:1s:43:GLU:OE1	50:1s:43:GLU:N	2.42	0.44
1:2A:1803:A:N1	1:2A:1822:G:O2'	2.35	0.44
1:2A:2193:G:H2'	1:2A:2194:G:C8	2.50	0.44
1:2A:2299:G:H2'	1:2A:2300:G:C8	2.52	0.44
3:2D:133:LEU:HA	3:2D:136:ILE:HG13	1.99	0.44
6:2G:46:ALA:HA	6:2G:49:ASP:O	2.17	0.44
16:2U:52:ARG:HA	16:2U:55:ARG:HG3	1.99	0.44
19:2X:35:THR:HG22	19:2X:37:THR:N	2.32	0.44
20:2Y:8:LYS:HD3	20:2Y:97:ARG:NH1	2.32	0.44
26:24:48:ARG:HG3	26:24:52:THR:HA	1.99	0.44
32:2a:757:U:O2'	32:2a:879:C:O2	2.33	0.44
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.16	0.44
32:2a:1162:C:H2'	32:2a:1163:C:C6	2.51	0.44
36:2e:51:VAL:O	36:2e:55:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2o:48:LYS:HD3	46:2o:48:LYS:HA	1.74	0.44
1:1A:2219:U:H1'	1:1A:2220:A:C8	2.52	0.44
1:1A:2224:C:H2'	1:1A:2225:U:O4'	2.17	0.44
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.52	0.44
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	1.99	0.44
32:1a:962:C:H2'	32:1a:963:G:O4'	2.17	0.44
48:1q:74:LEU:HD23	48:1q:75:ARG:HG2	1.98	0.44
55:1x:16:C:H5	60:1x:201:HOH:O	2.00	0.44
1:2A:221:A:N1	1:2A:265:A:O2'	2.49	0.44
1:2A:829:A:N7	1:2A:2248:C:H5'	2.32	0.44
1:2A:918:A:C2	2:2B:81:G:H5'	2.52	0.44
1:2A:1027:A:C6	1:2A:1126:A:C4	3.05	0.44
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.18	0.44
1:2A:1532:C:H42	1:2A:1537:G:H1	1.66	0.44
1:2A:2684:U:OP1	15:2T:53:ARG:HD3	2.16	0.44
5:2F:108:LYS:HE2	5:2F:108:LYS:HB2	1.85	0.44
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.52	0.44
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.31	0.44
32:2a:404:U:H2'	32:2a:405:U:C6	2.52	0.44
32:2a:922:G:C6	32:2a:923:A:C6	3.06	0.44
32:2a:979:C:OP1	32:2a:1223:C:N4	2.50	0.44
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.18	0.44
33:2b:24:TRP:CD1	33:2b:24:TRP:H	2.35	0.44
33:2b:130:ARG:HD3	33:2b:130:ARG:HA	1.72	0.44
54:2w:18:G:O2'	54:2w:57:G:N2	2.40	0.44
54:2w:34:G:H2'	54:2w:35:A:H8	1.83	0.44
1:1A:287:G:O2'	1:1A:448:U:OP2	2.15	0.44
1:1A:333:G:N3	1:1A:353:G:O2'	2.44	0.44
1:1A:931:C:H42	1:1A:938:G:H1	1.66	0.44
1:1A:1115:A:H4'	1:1A:1116:A:H8	1.82	0.44
1:1A:1314:A:H2'	1:1A:1315:A:O4'	2.18	0.44
1:1A:1686:U:O2'	1:1A:1687:C:H5'	2.18	0.44
1:1A:2054:G:OP2	1:1A:2466:G:O2'	2.27	0.44
8:1I:75:LEU:HD22	8:1I:105:HIS:HD2	1.82	0.44
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.83	0.44
32:1a:538:G:H5''	43:1I:114:LYS:HB2	2.00	0.44
33:1b:12:GLU:C	33:1b:14:GLY:H	2.26	0.44
34:1c:188:LEU:HD11	34:1c:195:VAL:HG13	1.98	0.44
1:2A:374:A:C2	1:2A:401:A:C4	3.05	0.44
1:2A:635:C:H2'	1:2A:636:G:O4'	2.18	0.44
1:2A:1598:C:H2'	1:2A:1599:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1942:5MC:OP2	1:2A:1943:U:O2'	2.23	0.44
1:2A:2111:C:N4	1:2A:2144:U:O2'	2.42	0.44
15:2T:55:ASN:H	15:2T:59:THR:HB	1.83	0.44
16:2U:50:ARG:O	16:2U:54:LYS:NZ	2.51	0.44
16:2U:107:ALA:O	16:2U:111:GLU:HG2	2.18	0.44
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.52	0.44
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.82	0.44
32:2a:1329:A:H5'	44:2m:29:ARG:NE	2.32	0.44
54:2w:10:G:N2	54:2w:11:C:N3	2.66	0.44
1:1A:799:A:H3'	29:17:1:MET:HE1	1.99	0.44
1:1A:1121:C:C2'	1:1A:1122:C:H5'	2.48	0.44
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.18	0.44
1:1A:2874:G:OP1	15:1T:119:LYS:HD2	2.17	0.44
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.82	0.44
15:1T:118:ARG:HD3	15:1T:118:ARG:HA	1.67	0.44
21:1Z:74:VAL:HG22	21:1Z:86:VAL:HG12	2.00	0.44
32:1a:374:A:C6	32:1a:375:U:C4	3.06	0.44
32:1a:408:A:H2'	32:1a:409:G:O4'	2.17	0.44
32:1a:524:G:H2'	32:1a:525:C:C6	2.52	0.44
32:1a:636:U:H2'	32:1a:637:G:C8	2.52	0.44
32:1a:1290:G:C4	32:1a:1291:G:C8	3.05	0.44
35:1d:3:ARG:HD3	35:1d:118:ARG:HD2	1.99	0.44
38:1g:16:LEU:HD22	40:1i:42:ARG:HA	1.99	0.44
38:1g:48:LYS:O	38:1g:52:GLU:HG3	2.18	0.44
39:1h:51:VAL:HG21	39:1h:60:ARG:NH1	2.32	0.44
45:1n:24:CYS:HB2	45:1n:40:CYS:HB3	1.99	0.44
51:1t:48:LYS:HD3	51:1t:48:LYS:HA	1.83	0.44
1:2A:330:A:H2	1:2A:1210:A:O2'	2.01	0.44
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.53	0.44
1:2A:1170:G:O6	1:2A:1180:C:N4	2.51	0.44
1:2A:2080:G:H2'	1:2A:2081:C:C6	2.52	0.44
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.29	0.44
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.16	0.44
1:2A:2740:A:H2'	1:2A:2741:A:C8	2.53	0.44
1:2A:2820:A:C5	13:2R:4:LEU:HD11	2.52	0.44
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	2.00	0.44
11:2P:81:GLN:HB3	11:2P:106:LEU:HD12	1.98	0.44
18:2W:72:LYS:HB3	18:2W:106:ILE:HG22	1.99	0.44
32:2a:393:A:H5'	32:2a:483:C:O2'	2.18	0.44
32:2a:673:G:O3'	37:2f:87:ARG:NH2	2.50	0.44
32:2a:1020:U:H2'	32:2a:1021:G:H8	1.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1097:C:H1'	32:2a:1170:A:H1'	2.00	0.44
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	1.98	0.44
40:2i:50:LEU:H	40:2i:50:LEU:HG	1.66	0.44
41:2j:46:ARG:HG2	41:2j:64:GLU:HB3	1.99	0.44
44:2m:33:ALA:HA	44:2m:59:TYR:CE2	2.53	0.44
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.51	0.44
45:2n:51:GLY:C	45:2n:53:LEU:H	2.25	0.44
51:2t:50:GLU:O	51:2t:100:ILE:HD11	2.18	0.44
1:1A:940:C:N4	60:1A:4121:HOH:O	2.49	0.44
1:1A:1140:U:H2'	1:1A:1141:A:C8	2.52	0.44
1:1A:1152:G:H2'	1:1A:1153:G:O4'	2.17	0.44
1:1A:2703:C:O3'	1:1A:2881:C:H4'	2.17	0.44
2:1B:33:G:H5'	6:1G:2:PRO:HD3	2.00	0.44
11:1P:124:LYS:HA	11:1P:144:GLU:HB3	2.00	0.44
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.99	0.44
27:15:16:ARG:HD2	27:15:17:ASP:OD1	2.17	0.44
32:1a:435:C:H2'	32:1a:436:C:C6	2.53	0.44
32:1a:625:G:H4'	47:1p:16:HIS:CG	2.52	0.44
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.50	0.44
32:1a:1129:C:OP1	40:1i:66:ARG:NH1	2.51	0.44
32:1a:1486:G:H2'	32:1a:1487:G:C8	2.52	0.44
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.53	0.44
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.42	0.44
36:1e:103:GLY:O	36:1e:106:PRO:HD2	2.17	0.44
1:2A:361:G:O2'	1:2A:362:U:H5'	2.16	0.44
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.99	0.44
2:2B:64:C:H2'	2:2B:65:C:C6	2.52	0.44
3:2D:182:LEU:HB2	3:2D:272:ALA:H	1.82	0.44
6:2G:163:ALA:HB1	6:2G:168:GLU:HB2	2.00	0.44
32:2a:1191:A:OP1	34:2c:4:LYS:HG3	2.16	0.44
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	1.99	0.44
40:2i:23:ASN:ND2	40:2i:25:LYS:HG2	2.33	0.44
47:2p:9:PHE:N	47:2p:9:PHE:CD1	2.85	0.44
48:2q:3:LYS:HD3	48:2q:61:GLU:O	2.18	0.44
54:2w:8:4SU:H1'	54:2w:48:C:H1'	2.00	0.44
1:1A:664:U:H2'	1:1A:665:C:C6	2.53	0.44
1:1A:2159:C:H2'	1:1A:2160:C:C6	2.53	0.44
3:1D:152:GLY:O	3:1D:154:LYS:HG2	2.18	0.44
4:1E:119:ARG:HG2	4:1E:120:TRP:NE1	2.32	0.44
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.98	0.44
26:14:63:TYR:N	26:14:63:TYR:CD1	2.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:8:A:N6	35:1d:205:GLU:O	2.50	0.44
32:1a:165:C:H2'	32:1a:166:G:C8	2.52	0.44
32:1a:1030(D):A:H2'	32:1a:1031:G:H4'	1.99	0.44
32:1a:1285:A:H8	32:1a:1285:A:O5'	2.00	0.44
1:2A:286:C:H2'	1:2A:287:C:C6	2.53	0.44
1:2A:880:G:N1	1:2A:898:C:O2	2.48	0.44
1:2A:1637:A:H4'	1:2A:2711:A:O2'	2.17	0.44
1:2A:2886:G:H2'	1:2A:2887:U:H6	1.83	0.44
2:2B:24:G:H4'	2:2B:25:A:C8	2.52	0.44
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.98	0.44
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	2.00	0.44
8:2I:78:THR:O	8:2I:104:GLN:NE2	2.51	0.44
9:2N:28:THR:HG22	9:2N:29:LYS:N	2.32	0.44
11:2P:126:VAL:HG22	11:2P:146:VAL:HB	2.00	0.44
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.18	0.44
17:2V:18:LEU:HD21	17:2V:20:LEU:HB2	1.99	0.44
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.71	0.44
32:2a:625:G:H2'	32:2a:626:U:H6	1.82	0.44
32:2a:688:G:H5'	42:2k:46:GLY:C	2.42	0.44
32:2a:950:U:H2'	32:2a:951:G:H8	1.83	0.44
32:2a:1010:G:N2	32:2a:1020:U:O2'	2.50	0.44
38:2g:144:MET:HE2	38:2g:144:MET:HB3	1.77	0.44
39:2h:11:THR:HA	39:2h:14:ARG:NH1	2.33	0.44
40:2i:99:LEU:HB3	40:2i:101:PHE:HE2	1.81	0.44
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.17	0.44
1:1A:326:C:OP2	20:1Y:73:ARG:NH2	2.49	0.44
1:1A:858:U:H2'	11:1P:21:ARG:HA	2.00	0.44
1:1A:1223:C:H2'	1:1A:1224:C:C6	2.48	0.44
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.18	0.44
1:1A:2343:G:O2'	22:10:43:THR:HG22	2.18	0.44
1:1A:2707:C:H2'	1:1A:2708:U:C6	2.53	0.44
5:1F:106:ARG:H	5:1F:106:ARG:HG2	1.52	0.44
18:1W:5:ALA:C	18:1W:6:ILE:HG13	2.43	0.44
20:1Y:54:LYS:HA	20:1Y:55:TYR:HA	1.78	0.44
21:1Z:102:LEU:HD12	21:1Z:137:ILE:HB	1.99	0.44
32:1a:60:A:N1	32:1a:107:G:O2'	2.45	0.44
32:1a:61:G:H2'	32:1a:62:U:O4'	2.17	0.44
32:1a:186:C:H2'	32:1a:187:C:C6	2.52	0.44
32:1a:232:G:H1'	32:1a:262:A:N1	2.33	0.44
32:1a:377:G:P	47:1p:5:ARG:HD2	2.57	0.44
32:1a:1322:C:N4	60:1a:2075:HOH:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:59:GLU:HG2	33:1b:63:MET:HE2	1.99	0.44
35:1d:144:ASP:N	35:1d:144:ASP:OD1	2.49	0.44
37:1f:33:TYR:OH	37:1f:78:GLU:HG3	2.18	0.44
44:1m:16:ASP:N	44:1m:16:ASP:OD1	2.50	0.44
1:2A:557:U:H2'	1:2A:558:G:C8	2.53	0.44
1:2A:1519:G:H2'	60:2A:3697:HOH:O	2.18	0.44
1:2A:1842:G:O2'	3:2D:253:GLN:OE1	2.35	0.44
1:2A:2032:G:H1'	4:2E:145:LYS:HD3	2.00	0.44
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.52	0.44
2:2B:91:C:OP1	12:2Q:16:ARG:HG3	2.18	0.44
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.99	0.44
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HA	1.83	0.44
12:2Q:31:ASP:HA	12:2Q:134:ARG:NH1	2.33	0.44
21:2Z:79:ARG:HB2	21:2Z:80:ARG:NH1	2.33	0.44
32:2a:825:G:N2	39:2h:11:THR:HG21	2.33	0.44
32:2a:999:C:N4	32:2a:1042:G:H1	2.13	0.44
32:2a:1055:A:C6	32:2a:1206:G:C5	3.06	0.44
32:2a:1307:U:H2'	32:2a:1308:U:C6	2.52	0.44
32:2a:1330:U:H2'	32:2a:1331:G:H5'	2.00	0.44
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.51	0.44
38:2g:20:ASP:HB3	38:2g:23:VAL:HB	2.00	0.44
38:2g:22:LEU:HG	38:2g:62:PHE:CE2	2.52	0.44
40:2i:94:ALA:C	40:2i:96:LEU:H	2.25	0.44
49:2r:70:ILE:HG22	49:2r:74:ARG:HD2	2.00	0.44
1:1A:270:C:O3'	1:1A:271:U:H3'	2.18	0.44
1:1A:485:U:OP2	29:17:39:ARG:NH1	2.49	0.44
1:1A:1002:A:N1	1:1A:2470:G:H4'	2.32	0.44
1:1A:1071:G:OP1	57:1A:3935:KAN:H3	2.18	0.44
1:1A:1093:G:H2'	1:1A:1156:G:N2	2.32	0.44
1:1A:1136:U:N3	1:1A:1148:C:H1'	2.33	0.44
1:1A:1362:U:H2'	1:1A:1363:A:C8	2.52	0.44
1:1A:2376:C:H4'	22:10:56:ASP:OD1	2.18	0.44
1:1A:2639:G:O2'	1:1A:2794:A:N1	2.40	0.44
3:1D:6:PHE:CE2	3:1D:18:VAL:HG13	2.52	0.44
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.76	0.44
32:1a:341:C:H2'	32:1a:342:C:C6	2.53	0.44
32:1a:1237:C:O2'	32:1a:1300:G:N2	2.41	0.44
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.85	0.44
35:1d:173:TRP:CE2	35:1d:189:PRO:HG3	2.53	0.44
52:1u:13:ILE:HG13	52:1u:22:ARG:HD2	1.99	0.44
1:2A:76:C:O3'	24:22:59:ARG:HG3	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:952:G:C6	1:2A:966:G:C6	3.06	0.44
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.33	0.44
1:2A:2160:G:H2'	1:2A:2161:C:H5''	2.00	0.44
1:2A:2375:G:O2'	1:2A:2377:A:N7	2.31	0.44
7:2H:152:ARG:HD3	7:2H:152:ARG:HA	1.82	0.44
19:2X:27:THR:HG23	19:2X:80:ILE:HG12	2.00	0.44
20:2Y:19:LYS:HE2	20:2Y:19:LYS:HB3	1.81	0.44
26:24:62:ARG:HD3	26:24:62:ARG:HA	1.76	0.44
32:2a:51:A:N7	32:2a:114:U:O2'	2.50	0.44
32:2a:438:G:H4'	35:2d:123:HIS:CE1	2.53	0.44
32:2a:523:A:H61	43:2l:92:OTD:CG	2.31	0.44
32:2a:922:G:H2'	32:2a:923:A:C8	2.53	0.44
32:2a:983:A:H2	32:2a:984:C:C6	2.36	0.44
34:2c:32:LEU:HD23	34:2c:32:LEU:HA	1.85	0.44
39:2h:104:ARG:HA	39:2h:104:ARG:HD3	1.75	0.44
54:2w:19:G:N2	54:2w:56:C:N3	2.63	0.44
1:1A:123:G:N2	29:17:48:LYS:HG2	2.32	0.44
1:1A:580:U:H2'	1:1A:581:G:H8	1.82	0.44
1:1A:1177:G:O6	1:1A:2062:C:H1'	2.18	0.44
1:1A:2641:A:HO2'	1:1A:2642:G:P	2.37	0.44
6:1G:37:VAL:HG21	6:1G:103:LEU:HD11	1.99	0.44
6:1G:91:ARG:HE	6:1G:91:ARG:HB3	1.53	0.44
32:1a:433:C:H2'	32:1a:434:U:C6	2.53	0.44
32:1a:620:C:H2'	32:1a:621:A:O4'	2.18	0.44
32:1a:870:U:H4'	32:1a:871:U:H5''	2.00	0.44
43:1l:43:VAL:HG12	43:1l:93:LEU:HD22	2.00	0.44
55:1x:2:G:H2'	55:1x:2:G:N3	2.33	0.44
1:2A:458:G:O2'	1:2A:469:G:O6	2.27	0.44
1:2A:852:G:H2'	1:2A:853:G:C8	2.48	0.44
1:2A:918:A:N3	2:2B:80:U:O2'	2.49	0.44
1:2A:984:A:H5''	1:2A:985:C:C5	2.53	0.44
4:2E:183:LEU:HD21	15:2T:10:VAL:HG11	2.00	0.44
6:2G:170:ARG:HH12	6:2G:174:GLU:CD	2.26	0.44
18:2W:60:ASN:HD22	18:2W:60:ASN:N	2.16	0.44
21:2Z:45:ASP:OD1	21:2Z:49:ARG:HD3	2.18	0.44
32:2a:445:G:H2'	32:2a:446:G:C8	2.53	0.44
32:2a:554:C:H2'	32:2a:555:C:C6	2.52	0.44
32:2a:733:A:O2'	32:2a:734:G:OP2	2.33	0.44
32:2a:811:C:O2'	32:2a:901:A:N1	2.47	0.44
32:2a:954:G:H2'	32:2a:955:U:O4'	2.18	0.44
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.83	0.44
38:2g:6:ARG:HB3	38:2g:6:ARG:NH1	2.32	0.44
39:2h:81:HIS:N	39:2h:138:TRP:O	2.51	0.44
45:2n:26:ARG:NH2	45:2n:47:LEU:HD21	2.33	0.44
50:2s:5:LEU:H	50:2s:5:LEU:HG	1.59	0.44
1:1A:174:U:H4'	1:1A:207:A:H4'	1.99	0.43
1:1A:364:A:H2'	1:1A:365:G:O4'	2.18	0.43
32:1a:769:G:H4'	32:1a:1513:A:H4'	2.00	0.43
32:1a:1394:A:N1	32:1a:1500:A:O2'	2.48	0.43
40:1i:26:VAL:HG22	40:1i:61:ALA:HB3	1.99	0.43
54:1y:52:G:H2'	54:1y:53:G:H8	1.83	0.43
1:2A:211:A:H2'	1:2A:212:G:O4'	2.18	0.43
1:2A:530:G:C5	1:2A:2022:U:H5''	2.53	0.43
1:2A:2006:C:O2'	1:2A:2823:A:N3	2.49	0.43
10:2O:17:ARG:HA	10:2O:17:ARG:HD3	1.35	0.43
12:2Q:2:LEU:HD22	12:2Q:2:LEU:H	1.83	0.43
16:2U:27:LEU:HB3	16:2U:31:SER:HB3	2.00	0.43
16:2U:105:VAL:HG22	17:2V:45:THR:HG21	2.00	0.43
23:21:52:ARG:HA	23:21:56:GLN:O	2.18	0.43
26:24:59:PHE:CD2	50:2s:64:GLU:HB2	2.52	0.43
30:28:23:VAL:HG11	30:28:47:LYS:HD3	2.00	0.43
32:2a:56:U:H2'	32:2a:57:G:H8	1.79	0.43
32:2a:192:U:H2'	32:2a:193:C:C6	2.53	0.43
32:2a:973:G:H3'	32:2a:974:A:H5''	1.99	0.43
32:2a:1228:C:H2'	32:2a:1229:A:H8	1.83	0.43
32:2a:1381:U:H1'	38:2g:79:ARG:HG2	2.00	0.43
35:2d:128:VAL:HG13	35:2d:144:ASP:HB3	2.00	0.43
49:2r:40:LEU:HB3	49:2r:79:LEU:HD11	2.00	0.43
1:1A:868:A:O2'	1:1A:991:G:OP2	2.30	0.43
1:1A:2274:U:H4'	1:1A:2340:A:C2	2.53	0.43
1:1A:2642:G:H2'	1:1A:2643:G:C8	2.53	0.43
1:1A:2892:A:OP1	13:1R:96:ARG:NE	2.30	0.43
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.52	0.43
15:1T:59:THR:HG23	15:1T:78:LEU:HB3	2.01	0.43
17:1V:24:LYS:HE2	17:1V:24:LYS:HB3	1.85	0.43
21:1Z:45:ASP:CG	21:1Z:49:ARG:HE	2.26	0.43
32:1a:560:U:H6	32:1a:560:U:H2'	1.63	0.43
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.33	0.43
32:1a:1038:C:C2'	32:1a:1039:C:H5'	2.48	0.43
33:1b:17:PHE:CB	33:1b:44:LEU:HD11	2.44	0.43
36:1e:147:ASP:O	36:1e:151:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:53:VAL:HG21	40:1i:85:LEU:HD13	2.00	0.43
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.83	0.43
1:2A:1847:A:H3'	1:2A:1848:A:H5'	2.00	0.43
1:2A:2131:G:N7	1:2A:2133:G:C2	2.86	0.43
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.53	0.43
2:2B:28:C:H2'	2:2B:29:A:O4'	2.18	0.43
3:2D:121:PRO:HB3	3:2D:135:PHE:CE2	2.53	0.43
9:2N:103:VAL:HG11	9:2N:120:LEU:HD22	2.01	0.43
26:24:61:ARG:HH21	50:2s:9:VAL:HG21	1.83	0.43
32:2a:391:G:C6	32:2a:392:G:C5	3.06	0.43
32:2a:736:C:H2'	32:2a:737:A:C8	2.53	0.43
32:2a:1074:G:O2'	32:2a:1101:A:N1	2.41	0.43
32:2a:1106:G:H5''	34:2c:172:ARG:HB3	2.00	0.43
32:2a:1431:C:H2'	32:2a:1432:G:O4'	2.17	0.43
33:2b:95:GLN:HB2	33:2b:148:TYR:CD1	2.53	0.43
37:2f:6:VAL:HG22	37:2f:90:VAL:HG22	1.99	0.43
38:2g:93:PRO:HA	38:2g:96:GLN:HB2	2.01	0.43
43:2l:34:ARG:O	43:2l:61:THR:HG23	2.18	0.43
45:2n:6:LEU:HB3	45:2n:23:ARG:NH2	2.33	0.43
50:2s:22:LEU:HD22	50:2s:31:ILE:HD11	2.00	0.43
51:2t:16:HIS:CE1	51:2t:20:LEU:HD11	2.53	0.43
54:2y:18:G:O6	54:2y:55:PSU:H1'	2.18	0.43
54:2y:63:G:H2'	54:2y:64:A:O4'	2.18	0.43
1:1A:2033:U:H2'	1:1A:2034:G:O4'	2.17	0.43
1:1A:2036:A:H2'	1:1A:2037:A:C8	2.53	0.43
1:1A:2163:G:C6	1:1A:2164:C:C2	3.06	0.43
1:1A:2812:A:N3	1:1A:2904:U:H1'	2.33	0.43
7:1H:109:PHE:C	7:1H:111:HIS:H	2.25	0.43
13:1R:13:HIS:HE1	13:1R:15:SER:OG	2.00	0.43
15:1T:35:LYS:HG3	15:1T:40:THR:HG22	2.01	0.43
24:12:3:LEU:O	24:12:7:ARG:HG3	2.18	0.43
30:18:52:LYS:N	30:18:53:PRO:HD2	2.33	0.43
32:1a:34:C:H2'	32:1a:35:G:C8	2.53	0.43
32:1a:602:A:H2'	32:1a:603:U:C6	2.53	0.43
32:1a:649:G:H2'	32:1a:650:G:C8	2.54	0.43
39:1h:2:LEU:N	60:1h:201:HOH:O	2.51	0.43
51:1t:27:LYS:O	51:1t:31:SER:OG	2.36	0.43
1:2A:307:G:N2	1:2A:309:G:H3'	2.33	0.43
1:2A:463:G:N2	1:2A:466:A:OP2	2.47	0.43
1:2A:648:G:O2'	1:2A:2351:G:H5''	2.18	0.43
1:2A:1125:G:H5'	31:29:37:GLY:HA2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1283:G:N2	1:2A:1285:G:H3'	2.33	0.43
1:2A:2125:G:H1'	1:2A:2173:A:H61	1.83	0.43
1:2A:2494:G:C5	1:2A:2495:G:N7	2.86	0.43
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.33	0.43
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.18	0.43
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.17	0.43
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.53	0.43
18:2W:82:LEU:HD22	18:2W:84:ARG:HH22	1.83	0.43
22:20:48:GLY:HA3	22:20:80:HIS:ND1	2.33	0.43
26:24:58:ARG:HD2	50:2s:68:GLY:N	2.33	0.43
32:2a:1073:U:O2	33:2b:104:ASN:ND2	2.48	0.43
32:2a:1149:C:H2'	32:2a:1150:U:O4'	2.18	0.43
32:2a:1201:A:H4'	32:2a:1202:G:O5'	2.18	0.43
32:2a:1317:C:OP2	45:2n:17:LYS:HD3	2.18	0.43
38:2g:97:GLN:O	38:2g:101:LEU:HG	2.17	0.43
42:2k:58:PRO:HG3	42:2k:89:ALA:O	2.19	0.43
45:2n:23:ARG:HA	45:2n:29:ARG:O	2.18	0.43
1:1A:271:U:H1'	8:1I:50:ARG:CZ	2.49	0.43
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.52	0.43
1:1A:2148:A:N3	1:1A:2149:G:H1'	2.33	0.43
4:1E:24:THR:HG23	4:1E:184:VAL:HG12	2.00	0.43
4:1E:96:PHE:O	4:1E:175:VAL:HG11	2.18	0.43
5:1F:133:ASN:N	5:1F:138:GLU:OE1	2.30	0.43
8:1I:78:THR:HA	8:1I:143:SER:OG	2.18	0.43
20:1Y:26:LYS:HD2	20:1Y:26:LYS:HA	1.83	0.43
32:1a:530:G:H1'	54:1w:35:A:O2'	2.18	0.43
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.53	0.43
32:1a:1318:A:H5''	50:1s:3:ARG:NH1	2.33	0.43
32:1a:1388:C:H2'	32:1a:1389:C:C6	2.53	0.43
37:1f:8:ILE:HG12	37:1f:88:VAL:HG22	2.00	0.43
40:1i:50:LEU:HD23	40:1i:81:ILE:HD11	1.99	0.43
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.53	0.43
54:1y:41:C:H2'	54:1y:42:C:C6	2.52	0.43
1:2A:35:G:H2'	1:2A:36:G:O4'	2.18	0.43
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.82	0.43
1:2A:1274:A:N3	1:2A:1297:C:H1'	2.33	0.43
1:2A:1530:C:H1'	1:2A:1531:C:OP1	2.18	0.43
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.52	0.43
1:2A:2318:G:H21	14:2S:3:ARG:CD	2.31	0.43
1:2A:2432:A:C6	1:2A:2433:A:C6	3.06	0.43
60:2A:3693:HOH:O	18:2W:11:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:70:C:H2'	2:2B:71:C:H6	1.83	0.43
5:2F:11:VAL:HG22	5:2F:125:LEU:HD12	2.01	0.43
12:2Q:81:VAL:HG12	22:20:5:LYS:HD3	1.98	0.43
16:2U:27:LEU:HA	16:2U:30:LYS:HB2	2.00	0.43
32:2a:298:A:C6	32:2a:299:G:C2	3.07	0.43
32:2a:392:G:H2'	32:2a:393:A:H8	1.84	0.43
32:2a:401:C:H2'	32:2a:402:G:C8	2.53	0.43
32:2a:461:A:O2'	32:2a:470:C:H5'	2.18	0.43
32:2a:532:A:N6	32:2a:1206:G:O2'	2.52	0.43
32:2a:560:U:H5'	32:2a:566:G:N2	2.34	0.43
32:2a:1092:A:H5''	38:2g:4:ARG:NH1	2.32	0.43
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.83	0.43
35:2d:191:ARG:NH1	35:2d:191:ARG:O	2.49	0.43
36:2e:12:LEU:HD23	36:2e:13:ILE:N	2.33	0.43
43:2l:89:ARG:HA	43:2l:97:ARG:HA	2.00	0.43
43:2l:124:LYS:HA	43:2l:125:PRO:HD3	1.89	0.43
44:2m:80:ARG:HH21	50:2s:69:HIS:HE1	1.66	0.43
49:2r:52:PRO:O	49:2r:56:THR:HG23	2.18	0.43
1:1A:94:G:O2'	24:12:48:HIS:ND1	2.40	0.43
1:1A:605:G:H2'	1:1A:606:G:C8	2.54	0.43
1:1A:1137:G:C6	1:1A:1138:C:C4	3.05	0.43
1:1A:1356:G:OP2	29:17:9:ARG:NH2	2.51	0.43
1:1A:1662:A:H4'	1:1A:1663:C:OP2	2.17	0.43
6:1G:97:ASP:O	6:1G:101:ILE:HG13	2.18	0.43
21:1Z:28:MET:HE2	21:1Z:35:ARG:HB2	2.00	0.43
32:1a:6:G:H4'	32:1a:298:A:H4'	2.00	0.43
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.53	0.43
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.53	0.43
33:1b:87:ARG:NH2	33:1b:233:SER:HB3	2.33	0.43
41:1j:78:ASN:O	41:1j:80:LYS:N	2.52	0.43
1:2A:7:G:H2'	1:2A:8:A:O4'	2.19	0.43
1:2A:1359:A:C2	1:2A:1372:U:O4	2.72	0.43
1:2A:1639:U:C2'	1:2A:1640:C:H5''	2.48	0.43
1:2A:1680:U:O2'	1:2A:1763:G:N7	2.41	0.43
4:2E:181:LEU:HD11	15:2T:6:LEU:HD23	2.00	0.43
9:2N:38:HIS:ND1	9:2N:39:ARG:HG3	2.33	0.43
17:2V:24:LYS:HA	17:2V:92:THR:OG1	2.17	0.43
25:23:8:LEU:HD23	25:23:30:ARG:O	2.18	0.43
25:23:22:ALA:HB2	25:23:49:LYS:HD3	2.00	0.43
29:27:34:ARG:HH21	29:27:39:ARG:HG2	1.83	0.43
32:2a:922:G:N3	32:2a:1398:A:H2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1098:C:H2'	32:2a:1099:G:O4'	2.18	0.43
40:2i:8:GLY:O	40:2i:14:VAL:HA	2.19	0.43
40:2i:9:ARG:HA	40:2i:13:ALA:O	2.18	0.43
40:2i:31:GLN:HB2	40:2i:35:GLU:OE1	2.18	0.43
45:2n:3:ARG:O	45:2n:7:ILE:HG12	2.19	0.43
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.18	0.43
47:2p:1:MET:HE2	47:2p:1:MET:HB3	1.89	0.43
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	2.00	0.43
48:2q:3:LYS:HD2	48:2q:60:ILE:HD11	1.99	0.43
50:2s:34:TRP:HA	50:2s:52:TYR:HB3	2.01	0.43
54:2w:10:G:N2	54:2w:11:C:C2	2.87	0.43
1:1A:844:C:H2'	1:1A:845:G:O4'	2.18	0.43
1:1A:1825:U:H2'	1:1A:1826:C:H6	1.84	0.43
1:1A:2193:A:HO2'	1:1A:2194:U:H6	1.67	0.43
2:1B:94:C:H2'	2:1B:95:C:H6	1.84	0.43
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.00	0.43
9:1N:96:GLU:H	9:1N:96:GLU:CD	2.26	0.43
9:1N:99:LEU:HD23	9:1N:99:LEU:HA	1.88	0.43
15:1T:3:ARG:NH2	60:1T:301:HOH:O	2.19	0.43
16:1U:50:ARG:HB2	16:1U:53:ARG:NH2	2.33	0.43
32:1a:162:A:N7	32:1a:163:C:H1'	2.34	0.43
32:1a:376:G:O3'	47:1p:5:ARG:HD2	2.18	0.43
32:1a:1036:G:H5''	32:1a:1037:C:C5	2.53	0.43
32:1a:1091:U:H2'	32:1a:1093:A:OP2	2.19	0.43
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.18	0.43
32:1a:1296:C:OP1	44:1m:44:ARG:NH2	2.51	0.43
34:1c:182:ILE:HG12	34:1c:203:PHE:HD1	1.82	0.43
47:1p:37:GLY:HA3	47:1p:50:LYS:O	2.18	0.43
1:2A:2117:A:O2'	1:2A:2118:U:H5''	2.19	0.43
1:2A:2809:A:N6	1:2A:2891:G:H2'	2.33	0.43
4:2E:179:GLU:HB2	4:2E:181:LEU:HD22	2.00	0.43
6:2G:41:GLN:HE21	6:2G:153:ARG:HB3	1.82	0.43
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.84	0.43
8:2I:59:ALA:HA	8:2I:62:LYS:HB2	2.00	0.43
10:2O:105:GLU:OE1	10:2O:105:GLU:N	2.39	0.43
15:2T:57:PHE:HA	15:2T:79:HIS:HD2	1.84	0.43
32:2a:105:G:H5'	32:2a:106:C:OP2	2.19	0.43
32:2a:262:A:H2'	32:2a:263:A:C8	2.54	0.43
32:2a:1239:A:H62	32:2a:1299:A:H62	1.65	0.43
33:2b:50:GLU:HB3	33:2b:200:ILE:O	2.19	0.43
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:19:VAL:HG23	39:2h:21:LYS:HG3	2.00	0.43
43:2l:110:VAL:HG23	43:2l:120:TYR:HB3	2.00	0.43
48:2q:59:ILE:HG13	48:2q:71:PHE:HD2	1.83	0.43
50:2s:22:LEU:O	50:2s:27:GLU:N	2.52	0.43
51:2t:64:ASP:OD2	51:2t:81:LYS:NZ	2.36	0.43
1:1A:116:A:H3'	1:1A:117:A:H5''	2.01	0.43
1:1A:1197:G:H5''	16:1U:81:HIS:CD2	2.53	0.43
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.18	0.43
1:1A:2190:G:C6	1:1A:2193:A:C8	3.07	0.43
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.54	0.43
1:1A:2754:A:H61	1:1A:2776:G:H1'	1.84	0.43
23:11:3:LYS:HB3	23:11:4:VAL:H	1.38	0.43
32:1a:79:G:H1'	32:1a:91:C:O2	2.19	0.43
32:1a:111:G:H5''	47:1p:27:LYS:HB3	2.01	0.43
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.18	0.43
32:1a:1494:G:N7	57:1a:1955:KAN:H122	2.34	0.43
33:1b:15:VAL:HG23	33:1b:16:HIS:ND1	2.34	0.43
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.16	0.43
42:1k:48:ILE:O	42:1k:50:TYR:N	2.52	0.43
50:1s:11:VAL:HG11	50:1s:16:LEU:HB2	2.00	0.43
54:1w:24:G:C6	54:1w:25:C:C4	3.06	0.43
54:1y:18:G:H1	54:1y:55:PSU:H1'	1.82	0.43
1:2A:272(B):G:H2'	1:2A:272(C):G:H8	1.84	0.43
1:2A:764:A:N1	1:2A:1789:A:O2'	2.49	0.43
1:2A:918:A:HO2'	2:2B:97:G:H22	1.62	0.43
1:2A:1364:G:P	23:21:3:LYS:HG3	2.58	0.43
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.19	0.43
1:2A:2207:G:H3'	1:2A:2208:A:H5''	2.01	0.43
5:2F:122:LYS:NZ	5:2F:152:GLU:OE2	2.46	0.43
6:2G:5:VAL:HG23	6:2G:8:LYS:CB	2.49	0.43
10:2O:7:TYR:CE1	10:2O:20:MET:HB2	2.54	0.43
21:2Z:72:ARG:HD3	21:2Z:72:ARG:HA	1.71	0.43
32:2a:227:G:H2'	32:2a:228:A:C8	2.54	0.43
32:2a:301:G:H2'	32:2a:302:G:C8	2.53	0.43
32:2a:340:U:H2'	32:2a:341:C:C6	2.54	0.43
32:2a:926:G:H22	53:2v:16:A:P	2.42	0.43
32:2a:1000:U:H2'	32:2a:1001:A:H8	1.84	0.43
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.34	0.43
34:2c:29:TYR:HE1	41:2j:11:PHE:HE2	1.67	0.43
34:2c:134:ILE:HG22	34:2c:168:ALA:HB3	2.00	0.43
35:2d:41:GLY:O	35:2d:43:HIS:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2x:8:4SU:H1'	55:2x:48:C:O2	2.19	0.43
1:1A:572:A:O2'	1:1A:573:G:OP1	2.29	0.43
1:1A:1097:G:H2'	1:1A:1098:C:O4'	2.19	0.43
1:1A:1836:U:O2	3:1D:50:THR:HB	2.18	0.43
1:1A:2146:G:N2	1:1A:2196:C:N3	2.53	0.43
1:1A:2332:A:H2'	1:1A:2332:A:N3	2.34	0.43
1:1A:2453:C:OP2	1:1A:2598:C:O2'	2.37	0.43
7:1H:3:ARG:HG2	7:1H:6:ARG:HG2	2.00	0.43
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.53	0.43
11:1P:113:LYS:HA	11:1P:129:ALA:O	2.19	0.43
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.18	0.43
17:1V:2:PHE:CE2	17:1V:41:GLY:HA3	2.54	0.43
32:1a:313:A:H2'	32:1a:314:C:C6	2.54	0.43
32:1a:630:G:H2'	32:1a:631:G:H8	1.84	0.43
32:1a:1002:G:C5	32:1a:1003:G:H1'	2.54	0.43
37:1f:76:ALA:O	37:1f:80:ARG:HG3	2.18	0.43
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	2.00	0.43
42:1k:84:VAL:HG11	42:1k:91:ARG:HH11	1.84	0.43
43:1l:60:LEU:HD11	43:1l:85:ILE:HD13	1.99	0.43
54:1w:62:C:H5'	54:1w:63:G:OP2	2.18	0.43
1:2A:55:G:O2'	1:2A:127:A:N1	2.51	0.43
1:2A:383:U:H2'	1:2A:385:C:H5	1.83	0.43
1:2A:1264:G:H2'	1:2A:2014:A:N6	2.34	0.43
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.19	0.43
34:2c:71:ALA:HB2	34:2c:109:PRO:HB3	2.01	0.43
35:2d:108:LEU:HB3	35:2d:110:PHE:CD1	2.54	0.43
35:2d:108:LEU:HB3	35:2d:110:PHE:CE1	2.54	0.43
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.99	0.43
1:1A:925:A:H61	1:1A:945:A:C2'	2.32	0.43
1:1A:2204:G:N2	1:1A:2205:C:O2	2.52	0.43
1:1A:2849:G:H5'	13:1R:46:GLY:CA	2.48	0.43
1:1A:2858:G:H8	15:1T:97:ALA:HB2	1.82	0.43
2:1B:75:G:H22	21:1Z:73:GLN:HE21	1.66	0.43
3:1D:11:PRO:O	3:1D:14:ARG:HG3	2.19	0.43
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.99	0.43
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.33	0.43
32:1a:179:A:H2'	32:1a:180:U:C6	2.52	0.43
32:1a:262:A:C6	32:1a:263:A:C6	3.07	0.43
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.54	0.43
33:1b:16:HIS:CD2	33:1b:204:ASN:H	2.37	0.43
1:2A:82:G:N1	1:2A:103:A:OP2	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:647:G:H2'	1:2A:648:G:O4'	2.18	0.43
1:2A:757:U:H2'	1:2A:758:C:O4'	2.19	0.43
1:2A:1021:A:H8	1:2A:1021:A:H3'	1.84	0.43
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.54	0.43
1:2A:1354:A:H2'	1:2A:1355:G:O4'	2.19	0.43
1:2A:1474:C:H42	1:2A:1517:G:H1	1.67	0.43
1:2A:2375:G:H2'	1:2A:2377:A:OP2	2.18	0.43
2:2B:41:U:H5	6:2G:70:VAL:H	1.64	0.43
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.82	0.43
5:2F:110:LEU:HD11	5:2F:181:LEU:HD23	2.01	0.43
5:2F:132:VAL:HA	5:2F:138:GLU:HB3	2.01	0.43
10:2O:19:ILE:HG22	10:2O:43:VAL:HA	2.01	0.43
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.19	0.43
32:2a:418:C:H2'	32:2a:419:C:C6	2.54	0.43
33:2b:97:TRP:CH2	33:2b:101:MET:HB2	2.54	0.43
39:2h:48:TYR:HA	39:2h:60:ARG:O	2.18	0.43
44:2m:48:LEU:HD22	44:2m:52:GLU:OE1	2.18	0.43
1:1A:8:A:H2'	1:1A:9:U:H6	1.84	0.43
1:1A:2198:A:H2'	1:1A:2199:C:C6	2.54	0.43
1:1A:2311:G:N2	1:1A:2330:G:H1'	2.34	0.43
1:1A:2760:G:O6	1:1A:2768:C:H5''	2.19	0.43
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	2.01	0.43
7:1H:121:ILE:HG13	7:1H:144:VAL:HG21	1.99	0.43
13:1R:38:VAL:HG12	13:1R:42:LYS:HE3	2.00	0.43
20:1Y:19:LYS:HE2	20:1Y:20:TYR:CE2	2.54	0.43
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.54	0.43
21:1Z:8:TYR:HB2	21:1Z:38:TYR:CZ	2.54	0.43
24:12:16:LEU:HB3	24:12:20:GLU:HB2	2.01	0.43
24:12:23:LYS:O	24:12:27:GLU:HG3	2.19	0.43
32:1a:341:C:H2'	32:1a:342:C:H6	1.83	0.43
32:1a:1027:C:N4	32:1a:1034:G:N1	2.66	0.43
32:1a:1204:A:OP1	60:1a:2008:HOH:O	2.21	0.43
32:1a:1429:C:H2'	32:1a:1430:C:H6	1.84	0.43
38:1g:103:TRP:CH2	38:1g:141:VAL:HG21	2.54	0.43
42:1k:48:ILE:HD12	42:1k:63:LEU:HB2	2.00	0.43
46:1o:18:PHE:CE2	46:1o:21:ASP:HB2	2.54	0.43
54:1w:64:A:H2'	54:1w:65:G:O4'	2.19	0.43
1:2A:621:A:H3'	1:2A:622:G:H8	1.84	0.43
1:2A:1889:A:N1	1:2A:2234:G:H1'	2.34	0.43
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.19	0.43
1:2A:2082:A:H2'	1:2A:2083:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2114:A:O2'	1:2A:2167:U:H1'	2.19	0.43
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.19	0.43
5:2F:156:LEU:HD21	5:2F:163:VAL:HG12	2.00	0.43
9:2N:48:MET:HB3	9:2N:48:MET:HE2	1.69	0.43
12:2Q:109:VAL:HG22	12:2Q:113:GLN:OE1	2.19	0.43
14:2S:16:ASN:HA	14:2S:19:LYS:HG3	2.01	0.43
20:2Y:20:TYR:CE2	20:2Y:43:ASN:HA	2.53	0.43
21:2Z:4:ARG:NH2	21:2Z:60:GLU:OE2	2.31	0.43
21:2Z:138:GLU:HG2	21:2Z:156:LYS:NZ	2.34	0.43
32:2a:1100:C:H2'	32:2a:1102:A:O5'	2.18	0.43
33:2b:58:ILE:HA	33:2b:61:LEU:HB3	2.00	0.43
33:2b:82:ARG:HG3	33:2b:92:TYR:OH	2.19	0.43
39:2h:39:LEU:HB3	39:2h:45:ILE:HG12	2.01	0.43
54:2w:34:G:H2'	54:2w:35:A:C8	2.54	0.43
1:1A:1468:G:C6	1:1A:1469:G:C5	3.07	0.42
1:1A:1572:G:C6	1:1A:1573:G:C2	3.06	0.42
1:1A:2040:G:O2'	16:1U:34:LYS:HE2	2.19	0.42
1:1A:2139:A:O2'	1:1A:2140:U:H5''	2.19	0.42
6:1G:137:GLU:HB2	6:1G:140:ILE:HD13	2.01	0.42
8:1I:62:LYS:O	8:1I:66:GLU:HG2	2.19	0.42
11:1P:68:GLN:HG3	60:1P:302:HOH:O	2.19	0.42
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.19	0.42
32:1a:974:A:H8	32:1a:974:A:OP1	2.02	0.42
32:1a:977:A:H1'	32:1a:982:U:O4	2.19	0.42
32:1a:985:C:H2'	32:1a:986:A:C8	2.54	0.42
32:1a:1030(A):G:H1'	32:1a:1031:G:H1	1.84	0.42
44:1m:121:LYS:HE2	44:1m:121:LYS:HB2	1.87	0.42
1:2A:57:C:H2'	1:2A:58:G:O4'	2.19	0.42
1:2A:75:G:N2	1:2A:112:U:O2	2.46	0.42
1:2A:107:C:H2'	1:2A:108:U:H6	1.84	0.42
1:2A:927:G:H2'	1:2A:928:G:O4'	2.18	0.42
1:2A:1043:C:H3'	1:2A:1043:C:OP2	2.19	0.42
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.19	0.42
1:2A:2335:A:C8	1:2A:2337:G:C5	3.07	0.42
57:2A:3568:KAN:H1	57:2A:3568:KAN:H11	1.73	0.42
2:2B:98:G:H3'	2:2B:99:G:H8	1.84	0.42
8:2I:14:ASP:N	8:2I:17:GLN:OE1	2.51	0.42
15:2T:60:THR:HG22	15:2T:77:PRO:HA	2.01	0.42
21:2Z:54:HIS:CD2	21:2Z:101:PRO:HG3	2.54	0.42
21:2Z:124:ILE:HD13	21:2Z:163:LEU:HD11	2.00	0.42
26:24:59:PHE:HD2	50:2s:64:GLU:HB2	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.54	0.42
32:2a:768:A:N3	32:2a:1512:U:O2'	2.49	0.42
32:2a:1085:U:H3'	32:2a:1086:U:C6	2.54	0.42
32:2a:1089:G:H1	32:2a:1096:C:H42	1.67	0.42
34:2c:150:LYS:HB2	34:2c:150:LYS:HE3	1.91	0.42
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.19	0.42
44:2m:108:ARG:HD3	44:2m:108:ARG:HA	1.67	0.42
48:2q:84:LEU:HA	48:2q:87:LYS:NZ	2.34	0.42
1:1A:242:C:OP2	30:18:5:LYS:NZ	2.39	0.42
1:1A:273:G:O2'	1:1A:274:U:H5''	2.19	0.42
1:1A:639:G:N2	5:1F:44:ARG:O	2.49	0.42
1:1A:931:C:O5'	1:1A:931:C:H6	2.01	0.42
1:1A:1560:U:H2'	1:1A:1561:C:H6	1.84	0.42
1:1A:1781:G:O2'	1:1A:2870:A:N1	2.44	0.42
1:1A:2182:G:O6	1:1A:2183:C:N4	2.52	0.42
1:1A:2372:A:H2'	1:1A:2373:A:O4'	2.19	0.42
3:1D:37:LEU:CD1	3:1D:62:TYR:HB2	2.43	0.42
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	2.01	0.42
15:1T:15:VAL:HG13	15:1T:79:HIS:CE1	2.55	0.42
18:1W:82:LEU:HD22	18:1W:84:ARG:HH22	1.83	0.42
19:1X:35:THR:HG22	19:1X:38:GLU:N	2.27	0.42
32:1a:297:G:H4'	32:1a:557:G:H4'	2.00	0.42
32:1a:1298:C:C4	38:1g:114:ARG:HD2	2.54	0.42
35:1d:19:LEU:O	35:1d:21:LEU:HG	2.19	0.42
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	2.00	0.42
1:2A:250:G:C6	1:2A:251:A:C6	3.07	0.42
1:2A:511:U:O4	1:2A:512:G:N1	2.52	0.42
4:2E:11:MET:HG2	4:2E:24:THR:HB	2.02	0.42
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.84	0.42
6:2G:107:LEU:HA	6:2G:111:LEU:HD13	2.02	0.42
13:2R:97:VAL:HG22	13:2R:114:VAL:HG22	2.01	0.42
20:2Y:31:LEU:HD23	20:2Y:31:LEU:HA	1.82	0.42
25:23:28:LEU:HD23	25:23:28:LEU:HA	1.90	0.42
30:28:62:LEU:HB3	30:28:65:GLU:CG	2.49	0.42
32:2a:857:C:H2'	32:2a:858:G:O4'	2.19	0.42
32:2a:918:A:H2'	32:2a:919:A:C8	2.54	0.42
32:2a:994:A:N3	32:2a:994:A:H2'	2.34	0.42
32:2a:1129:C:OP2	40:2i:66:ARG:NH1	2.52	0.42
35:2d:112:VAL:HG22	35:2d:116:GLN:NE2	2.34	0.42
36:2e:76:ILE:O	36:2e:93:PRO:HB3	2.19	0.42
1:1A:554:A:H62	1:1A:2063:U:H3	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:734:C:C1'	29:17:4:THR:HG22	2.48	0.42
1:1A:832:G:C6	1:1A:833:C:C4	3.08	0.42
1:1A:1105:G:OP2	1:1A:1106:U:H3'	2.19	0.42
1:1A:1383:G:H2'	1:1A:1384:G:O4'	2.19	0.42
6:1G:101:ILE:HG21	26:14:25:TYR:HB2	2.00	0.42
8:1I:72:LEU:HD21	8:1I:107:VAL:HG11	1.99	0.42
12:1Q:34:LEU:HD11	12:1Q:129:THR:HB	2.00	0.42
26:14:62:ARG:HD3	26:14:62:ARG:HA	1.75	0.42
32:1a:706:A:N3	42:1k:31:THR:HG21	2.34	0.42
32:1a:1503:A:C6	53:1v:12:A:H2	2.37	0.42
33:1b:55:PHE:CE1	33:1b:218:ALA:HA	2.55	0.42
54:1y:8:4SU:H4'	54:1y:48:C:C4'	2.49	0.42
1:2A:65:C:O2'	1:2A:456:C:N3	2.49	0.42
1:2A:459:U:H5''	29:27:40:TRP:CG	2.54	0.42
1:2A:639:U:H2'	1:2A:640:C:C6	2.54	0.42
1:2A:647:G:H8	1:2A:647:G:O5'	2.02	0.42
1:2A:915:C:H1'	60:2A:3700:HOH:O	2.19	0.42
1:2A:931:G:O2'	25:23:24:LYS:HD3	2.19	0.42
1:2A:1003:G:N2	1:2A:1153:C:C2	2.87	0.42
1:2A:1019:U:H3	1:2A:1142(A):A:N6	2.13	0.42
1:2A:2290:G:H4'	1:2A:2381:C:O2'	2.19	0.42
9:2N:69:GLN:O	9:2N:71:ILE:HG13	2.19	0.42
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.33	0.42
21:2Z:163:LEU:HG	21:2Z:165:VAL:HG22	2.01	0.42
22:20:38:VAL:HG11	22:20:45:PHE:HD2	1.84	0.42
26:24:15:ILE:O	26:24:32:TYR:HA	2.20	0.42
32:2a:67:C:H2'	32:2a:68:G:H8	1.83	0.42
32:2a:142:G:H2'	32:2a:143:A:H8	1.84	0.42
32:2a:987:G:H1	32:2a:1218:C:N4	2.14	0.42
32:2a:1097:C:H2'	32:2a:1098:C:C6	2.54	0.42
32:2a:1291:G:C6	32:2a:1292:U:C4	3.07	0.42
34:2c:131:ARG:NH1	34:2c:166:GLU:HG2	2.32	0.42
40:2i:112:LYS:HE2	40:2i:117:HIS:O	2.19	0.42
40:2i:117:HIS:HB2	40:2i:121:ARG:HG2	2.01	0.42
1:1A:70:A:N7	19:1X:31:HIS:HE1	2.18	0.42
1:1A:519:G:OP1	18:1W:8:ARG:HD3	2.18	0.42
1:1A:656:A:H2'	1:1A:657:A:O4'	2.19	0.42
1:1A:1073:A:C2	1:1A:2500:A:H5'	2.55	0.42
1:1A:2675:G:C6	1:1A:2676:G:C4	3.08	0.42
5:1F:110:LEU:HD11	5:1F:181:LEU:HG	2.01	0.42
18:1W:7:ALA:HB2	18:1W:50:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:94:GLY:H	19:1X:95:LEU:C	2.27	0.42
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.84	0.42
23:11:24:ALA:HB1	60:11:204:HOH:O	2.19	0.42
26:14:61:ARG:O	26:14:62:ARG:C	2.62	0.42
32:1a:950:U:H2'	32:1a:951:G:H8	1.84	0.42
32:1a:1304:G:C5	32:1a:1305:G:C6	3.08	0.42
34:1c:157:ILE:HB	34:1c:164:ARG:HH21	1.84	0.42
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.54	0.42
1:2A:1291:C:H2'	1:2A:1292:U:H6	1.84	0.42
1:2A:2127:G:C2	1:2A:2161:C:C4	3.06	0.42
1:2A:2148:G:H2'	1:2A:2149:G:C8	2.54	0.42
1:2A:2697:G:H2'	1:2A:2698:U:O4'	2.19	0.42
2:2B:1:U:H2'	2:2B:2:C:C6	2.54	0.42
5:2F:123:LEU:HD12	5:2F:124:LEU:N	2.34	0.42
6:2G:68:PRO:HB3	6:2G:92:VAL:HB	2.01	0.42
25:23:44:ARG:O	25:23:48:GLU:HG3	2.19	0.42
32:2a:707:C:O2'	32:2a:708:C:H5'	2.19	0.42
32:2a:1007:C:N3	32:2a:1022:G:O6	2.52	0.42
32:2a:1030(A):G:N2	32:2a:1030(C):G:H3'	2.35	0.42
32:2a:1057:G:H2'	32:2a:1058:G:O4'	2.19	0.42
32:2a:1317:C:P	45:2n:17:LYS:HG2	2.59	0.42
40:2i:102:LEU:HD13	40:2i:103:THR:HB	2.02	0.42
43:2l:114:LYS:NZ	43:2l:125:PRO:HG2	2.35	0.42
47:2p:9:PHE:N	47:2p:9:PHE:HD1	2.16	0.42
1:1A:807:G:H2'	1:1A:808:A:O4'	2.20	0.42
1:1A:2212:G:H2'	1:1A:2213:G:H8	1.84	0.42
1:1A:2691:A:H4'	4:1E:165:VAL:HG11	2.01	0.42
1:1A:2752:U:C2'	1:1A:2753:A:H5'	2.49	0.42
15:1T:108:ARG:HG3	15:1T:109:GLU:N	2.34	0.42
32:1a:265:G:O3'	48:1q:66:SER:HA	2.20	0.42
34:1c:12:LEU:HD23	34:1c:12:LEU:HA	1.79	0.42
35:1d:174:LEU:HD23	35:1d:174:LEU:HA	1.75	0.42
46:1o:74:ASP:OD2	46:1o:77:ARG:HB2	2.19	0.42
1:2A:1242:A:N1	11:2P:4:SER:OG	2.41	0.42
1:2A:2528:U:O2'	1:2A:2530:A:OP1	2.33	0.42
1:2A:2532:G:H1'	1:2A:2663:G:N2	2.35	0.42
3:2D:14:ARG:HE	3:2D:14:ARG:HB3	1.49	0.42
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	2.01	0.42
8:2I:45:LYS:O	8:2I:48:GLU:N	2.52	0.42
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.84	0.42
26:24:15:ILE:HG23	26:24:21:VAL:HG22	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:8:A:N6	35:2d:209:ARG:HB2	2.34	0.42
32:2a:98:G:H5'	32:2a:99:U:OP2	2.19	0.42
32:2a:441:A:H3'	32:2a:442:C:C6	2.54	0.42
32:2a:546:G:OP1	35:2d:73:ARG:HG2	2.19	0.42
33:2b:51:LEU:HD22	33:2b:55:PHE:CE2	2.54	0.42
36:2e:109:ILE:H	36:2e:109:ILE:HG13	1.71	0.42
43:2l:32:PHE:CE1	43:2l:86:ARG:HB3	2.54	0.42
45:2n:3:ARG:HG3	45:2n:4:LYS:H	1.85	0.42
45:2n:27:CYS:SG	45:2n:29:ARG:HG3	2.60	0.42
54:2w:4:C:H42	54:2w:69:G:H1	1.66	0.42
54:2y:7:A:N6	54:2y:66:U:H3	2.15	0.42
1:1A:1430:A:N3	1:1A:1451:U:H1'	2.34	0.42
1:1A:1925:G:OP1	3:1D:241:PRO:HB2	2.19	0.42
1:1A:2173:G:C6	1:1A:2174:G:C6	3.07	0.42
1:1A:2189:U:O2	1:1A:2189:U:H2'	2.18	0.42
9:1N:12:ARG:HG2	9:1N:14:VAL:HG23	2.01	0.42
11:1P:86:LYS:HB3	11:1P:118:GLY:HA3	2.01	0.42
11:1P:94:GLU:OE1	11:1P:124:LYS:HD3	2.20	0.42
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	2.01	0.42
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.01	0.42
32:1a:922:G:C6	32:1a:923:A:C6	3.06	0.42
60:1a:2145:HOH:O	45:1n:3:ARG:HG2	2.19	0.42
36:1e:6:PHE:HB3	36:1e:34:VAL:HG22	2.01	0.42
1:2A:722:A:H2'	1:2A:723:G:C8	2.54	0.42
1:2A:728:G:H5''	3:2D:13:ARG:NH2	2.35	0.42
1:2A:784:A:N6	3:2D:229:VAL:HG11	2.34	0.42
1:2A:826:U:H5''	1:2A:2428:G:O3'	2.19	0.42
1:2A:1219:G:H1	1:2A:1230:C:H42	1.67	0.42
1:2A:1506:C:H2'	1:2A:1507:A:H5'	2.00	0.42
1:2A:1668:A:O2'	1:2A:1674:G:N7	2.45	0.42
1:2A:2592:G:H2'	1:2A:2593:U:O4'	2.19	0.42
2:2B:118:G:C2	2:2B:119:G:H1'	2.55	0.42
7:2H:3:ARG:HH12	7:2H:6:ARG:H	1.67	0.42
7:2H:169:VAL:HG12	7:2H:171:LEU:HD23	2.01	0.42
22:20:40:GLN:HE21	22:20:57:PHE:HB3	1.84	0.42
23:21:67:ILE:N	23:21:68:PRO:HD2	2.35	0.42
32:2a:976:G:OP1	45:2n:32:SER:N	2.36	0.42
32:2a:977:A:O2'	32:2a:981:U:N3	2.53	0.42
32:2a:1198:G:H2'	32:2a:1199:U:C6	2.54	0.42
32:2a:1263:C:C4	32:2a:1272:G:O6	2.71	0.42
35:2d:38:TYR:CE1	35:2d:45:GLN:HG3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:18:GLN:O	37:2f:22:GLU:HG2	2.20	0.42
40:2i:8:GLY:N	40:2i:15:ALA:O	2.49	0.42
51:2t:13:LEU:O	51:2t:17:ARG:HG3	2.20	0.42
1:1A:673:G:O2'	1:1A:2363:G:OP1	2.31	0.42
1:1A:2178:G:H2'	1:1A:2179:G:C2	2.54	0.42
3:1D:79:VAL:CG1	3:1D:113:VAL:HA	2.49	0.42
3:1D:206:LEU:HD23	3:1D:206:LEU:HA	1.78	0.42
10:1O:70:LYS:HB3	10:1O:70:LYS:HE2	1.88	0.42
21:1Z:40:ASP:OD2	21:1Z:42:VAL:HG13	2.19	0.42
28:16:6:ARG:NH2	60:16:201:HOH:O	2.47	0.42
32:1a:153:C:H42	32:1a:168:G:H1	1.66	0.42
32:1a:276:G:OP1	48:1q:12:SER:OG	2.33	0.42
32:1a:592:G:O6	60:1a:2005:HOH:O	2.19	0.42
32:1a:1134:G:N3	32:1a:1134:G:H2'	2.35	0.42
32:1a:1353:G:OP1	52:1u:10:ARG:NH1	2.50	0.42
33:1b:122:PHE:HE2	33:1b:139:LYS:HB2	1.84	0.42
35:1d:172:PRO:C	35:1d:174:LEU:H	2.27	0.42
36:1e:84:PHE:HB2	36:1e:134:ALA:HB2	2.01	0.42
37:1f:99:ALA:O	49:1r:28:GLU:HA	2.18	0.42
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	2.02	0.42
48:1q:3:LYS:HD3	48:1q:61:GLU:O	2.18	0.42
54:1y:66:U:C4	54:1y:67:C:C4	3.07	0.42
1:2A:307:G:H22	1:2A:310:A:P	2.43	0.42
1:2A:590:A:H2'	1:2A:591:C:C6	2.54	0.42
1:2A:942:G:H4'	1:2A:1190:G:H5'	2.01	0.42
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.34	0.42
1:2A:1741:A:H2'	1:2A:1742:G:O4'	2.20	0.42
1:2A:2070:G:C2	1:2A:2442:C:C2	3.07	0.42
1:2A:2507:C:H5''	1:2A:2573:C:N4	2.35	0.42
1:2A:2647:U:H2'	1:2A:2648:C:C6	2.55	0.42
3:2D:5:LYS:HB3	3:2D:5:LYS:HE3	1.83	0.42
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	2.01	0.42
7:2H:121:ILE:HD13	7:2H:121:ILE:HA	1.82	0.42
19:2X:32:PRO:HA	19:2X:77:LYS:HB2	2.02	0.42
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.52	0.42
32:2a:193:C:H2'	32:2a:194:C:C6	2.55	0.42
32:2a:595:G:H1'	32:2a:596:C:C5	2.55	0.42
32:2a:617:G:H4'	47:2p:44:THR:O	2.19	0.42
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.52	0.42
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.82	0.42
32:2a:1121:U:C4	32:2a:1122:U:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:82:ARG:HB2	37:2f:85:VAL:HG23	2.02	0.42
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.20	0.42
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	2.02	0.42
1:1A:104:C:H1'	20:1Y:1:MET:HE2	2.00	0.42
1:1A:483:A:H5''	60:1A:4149:HOH:O	2.20	0.42
1:1A:923:C:H2'	1:1A:924:U:O4'	2.19	0.42
1:1A:1112:U:H2'	1:1A:1114:G:OP2	2.19	0.42
1:1A:1702:A:O2'	4:1E:115:GLY:HA2	2.20	0.42
2:1B:88:C:H2'	2:1B:89:G:O4'	2.20	0.42
20:1Y:44:ILE:HA	20:1Y:63:LYS:O	2.19	0.42
20:1Y:92:ASN:CG	20:1Y:94:LYS:HG2	2.44	0.42
22:10:38:VAL:HB	22:10:59:LEU:HB2	2.01	0.42
32:1a:599:C:H4'	39:1h:130:GLY:C	2.44	0.42
32:1a:674:G:H2'	32:1a:675:A:C8	2.55	0.42
32:1a:859:A:H2'	32:1a:860:A:O4'	2.19	0.42
32:1a:929:G:H1	32:1a:1388:C:H42	1.66	0.42
32:1a:1037:C:H2'	32:1a:1038:C:C6	2.52	0.42
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.19	0.42
32:1a:1226:C:H2'	44:1m:103:THR:HB	2.01	0.42
37:1f:48:LEU:HD22	49:1r:77:GLY:HA3	2.01	0.42
43:1l:92:0TD:OD2	43:1l:92:0TD:C	2.68	0.42
46:1o:82:ILE:O	46:1o:86:GLY:N	2.52	0.42
55:1x:19:G:C2	55:1x:57:A:N3	2.88	0.42
1:2A:514:A:N3	1:2A:581:C:O2'	2.45	0.42
1:2A:1124:C:H2'	1:2A:1125:G:O4'	2.20	0.42
1:2A:1485:G:H2'	1:2A:1486:A:C8	2.55	0.42
1:2A:2135:A:C8	1:2A:2136:C:H5	2.37	0.42
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.19	0.42
1:2A:2348:U:H5'	28:26:21:TYR:CE1	2.55	0.42
1:2A:2523:G:N2	1:2A:2764:A:N3	2.67	0.42
1:2A:2740:A:C6	1:2A:2741:A:C6	3.08	0.42
2:2B:24:G:H4'	2:2B:25:A:N7	2.34	0.42
3:2D:97:TYR:C	3:2D:99:ASP:N	2.78	0.42
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.77	0.42
5:2F:149:ASP:OD1	5:2F:149:ASP:N	2.51	0.42
8:2I:86:THR:O	8:2I:123:LEU:HB2	2.19	0.42
16:2U:16:LYS:HE2	16:2U:16:LYS:HB3	1.82	0.42
16:2U:85:LYS:HB2	16:2U:116:ALA:HB1	2.00	0.42
32:2a:171:A:H2'	32:2a:172:A:C8	2.54	0.42
32:2a:375:U:O2'	47:2p:28:ARG:HD2	2.20	0.42
32:2a:438:G:H4'	35:2d:123:HIS:ND1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:562:C:H4'	32:2a:563:A:O5'	2.20	0.42
32:2a:863:U:H2'	32:2a:865:A:OP2	2.19	0.42
32:2a:1222:G:H2'	32:2a:1223:C:O4'	2.19	0.42
35:2d:11:LEU:O	35:2d:15:GLU:HG2	2.19	0.42
39:2h:10:LEU:HD13	39:2h:83:ILE:HG12	2.01	0.42
40:2i:63:ILE:HD13	40:2i:77:ILE:HG23	2.02	0.42
40:2i:128:ARG:NE	55:2x:32:5MC:OP2	2.53	0.42
1:1A:236:G:H4'	1:1A:413:G:C5	2.54	0.42
1:1A:1069:U:O2'	1:1A:1168:G:H5'	2.20	0.42
1:1A:1074:A:N6	1:1A:1171:G:H2'	2.35	0.42
1:1A:1412:A:H2'	1:1A:1413:A:O4'	2.20	0.42
1:1A:2687:A:H5''	10:1O:31:LYS:HE2	2.01	0.42
1:1A:2862:G:H2'	1:1A:2863:C:O4'	2.20	0.42
2:1B:78:A:C2	2:1B:100:A:C4	3.08	0.42
10:1O:49:ARG:NH2	32:1a:1423:G:OP1	2.45	0.42
18:1W:11:ARG:NE	18:1W:98:LYS:HB3	2.35	0.42
32:1a:79:G:C6	32:1a:90:U:C2	3.08	0.42
32:1a:688:G:H5'	42:1k:46:GLY:C	2.44	0.42
32:1a:753:A:OP1	46:1o:69:TYR:OH	2.29	0.42
32:1a:1529:G:H4'	32:1a:1530:G:OP2	2.19	0.42
36:1e:92:LYS:O	36:1e:118:ILE:HG13	2.20	0.42
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	2.01	0.42
45:1n:32:SER:O	45:1n:41:ARG:N	2.53	0.42
54:1w:48:C:C2	54:1w:59:U:H1'	2.55	0.42
1:2A:875:G:C2	1:2A:903:C:C2	3.08	0.42
1:2A:978:G:H2'	1:2A:979:G:O4'	2.20	0.42
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.55	0.42
1:2A:1232:G:C6	1:2A:1233:C:C4	3.08	0.42
1:2A:1638:C:H2'	1:2A:1639:U:O4'	2.20	0.42
1:2A:1685:C:H2'	1:2A:1686:C:C6	2.54	0.42
4:2E:141:ILE:HD12	4:2E:150:VAL:HG21	2.02	0.42
6:2G:179:PRO:HB2	26:24:42:PHE:CE2	2.49	0.42
8:2I:123:LEU:HD12	8:2I:144:VAL:HB	2.02	0.42
10:2O:24:VAL:CG1	10:2O:33:ALA:HB2	2.50	0.42
11:2P:135:LEU:HD23	11:2P:135:LEU:HA	1.83	0.42
12:2Q:12:GLN:HG2	12:2Q:73:PRO:HD2	2.02	0.42
16:2U:91:ASP:H	17:2V:11:GLN:CD	2.27	0.42
25:23:26:LEU:HD21	25:23:46:ASN:HB2	2.00	0.42
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.35	0.42
32:2a:737:A:H2'	32:2a:738:C:C6	2.54	0.42
32:2a:1058:G:H2'	32:2a:1059:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.20	0.42
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.47	0.42
32:2a:1112:C:C4	34:2c:178:LEU:HD12	2.55	0.42
32:2a:1206:G:O2'	34:2c:193:TYR:HA	2.19	0.42
32:2a:1309:G:C6	32:2a:1329:A:C6	3.08	0.42
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.55	0.42
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.54	0.42
33:2b:87:ARG:HH11	33:2b:219:VAL:HG12	1.85	0.42
34:2c:135:LYS:HZ3	36:2e:53:LEU:HD12	1.85	0.42
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.55	0.42
44:2m:80:ARG:HH21	50:2s:69:HIS:CE1	2.38	0.42
48:2q:32:TYR:O	48:2q:34:LYS:N	2.50	0.42
1:1A:637:U:H5'	1:1A:640:A:N6	2.35	0.42
1:1A:1015:C:O2	1:1A:1030:A:O2'	2.37	0.42
1:1A:1405:A:C2	1:1A:1418:U:O4	2.68	0.42
1:1A:1604:C:H5''	1:1A:1605:A:OP2	2.20	0.42
1:1A:2331:G:H22	14:1S:3:ARG:CD	2.32	0.42
1:1A:2528:G:C6	1:1A:2529:C:C4	3.08	0.42
1:1A:2689:G:H2'	1:1A:2690:C:C6	2.55	0.42
5:1F:33:LEU:HD12	5:1F:33:LEU:HA	1.82	0.42
7:1H:3:ARG:NH1	7:1H:4:ILE:H	2.18	0.42
19:1X:11:PRO:HD3	24:12:37:PHE:CD2	2.55	0.42
19:1X:60:ARG:HH12	29:17:47:ARG:NH1	2.18	0.42
21:1Z:53:ILE:HG22	21:1Z:71:VAL:HG12	2.01	0.42
32:1a:695:A:OP2	42:1k:53:SER:N	2.52	0.42
32:1a:927:G:OP2	32:1a:927:G:H4'	2.19	0.42
32:1a:977:A:H2'	32:1a:978:A:H5''	2.01	0.42
32:1a:1289:A:OP1	52:1u:10:ARG:NH2	2.53	0.42
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.88	0.42
38:1g:79:ARG:O	38:1g:83:ALA:HB3	2.20	0.42
48:1q:44:ALA:HA	48:1q:71:PHE:O	2.19	0.42
1:2A:947:G:H2'	1:2A:948:G:H8	1.85	0.42
1:2A:971:C:O2'	1:2A:983:A:N3	2.50	0.42
1:2A:2061:G:H5''	1:2A:2503:2MA:C2	2.50	0.42
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.35	0.42
1:2A:2792:G:H2'	1:2A:2792:G:N3	2.35	0.42
2:2B:6:C:H2'	2:2B:7:G:O4'	2.20	0.42
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	2.02	0.42
14:2S:71:ARG:H	14:2S:71:ARG:HG3	1.55	0.42
32:2a:460:G:N2	32:2a:471:G:N7	2.67	0.42
32:2a:547:A:H4'	32:2a:548:G:O5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1029:C:N4	32:2a:1032:G:C6	2.88	0.42
35:2d:128:VAL:O	35:2d:131:ARG:N	2.53	0.42
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.55	0.42
45:2n:6:LEU:HD12	45:2n:6:LEU:HA	1.82	0.42
46:2o:87:ILE:O	46:2o:88:ARG:HB3	2.19	0.42
55:2x:23:C:H2'	55:2x:24:U:H6	1.84	0.42
54:2y:58:A:H4'	54:2y:59:U:OP1	2.20	0.42
1:1A:416:G:O5'	1:1A:416:G:H8	2.02	0.41
1:1A:560:C:O3'	16:1U:53:ARG:NH1	2.51	0.41
1:1A:572:A:O2'	1:1A:573:G:H5'	2.20	0.41
8:1I:47:LEU:HD23	8:1I:47:LEU:HA	1.78	0.41
9:1N:32:THR:HG23	9:1N:37:LYS:HB2	2.01	0.41
21:1Z:18:LEU:HD12	21:1Z:18:LEU:HA	1.88	0.41
32:1a:528:C:H41	43:1l:49:ASN:CG	2.28	0.41
32:1a:625:G:H2'	32:1a:626:U:H6	1.84	0.41
32:1a:659:U:H2'	32:1a:660:G:H8	1.85	0.41
32:1a:675:A:H1'	42:1k:116:HIS:CG	2.56	0.41
32:1a:922:G:H4'	36:1e:20:GLN:HA	2.02	0.41
32:1a:1106:G:C6	32:1a:1107:C:C4	3.08	0.41
32:1a:1270:C:OP2	52:1u:24:ARG:NH2	2.53	0.41
36:1e:91:LEU:HD12	36:1e:120:THR:HG22	2.02	0.41
38:1g:62:PHE:HD1	38:1g:124:LEU:HD21	1.85	0.41
1:2A:8:A:H2'	1:2A:9:U:H6	1.85	0.41
1:2A:11:G:H2'	1:2A:12:U:H5'	2.01	0.41
1:2A:500:G:N2	1:2A:502:A:H3'	2.35	0.41
1:2A:601:C:O2	1:2A:605:C:H4'	2.20	0.41
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.35	0.41
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.53	0.41
2:2B:7:G:H1	2:2B:114:C:N4	2.15	0.41
3:2D:37:LEU:HD12	3:2D:37:LEU:HA	1.81	0.41
11:2P:90:ARG:NH1	11:2P:105:LEU:HD11	2.35	0.41
13:2R:44:LEU:HD23	13:2R:44:LEU:HA	1.78	0.41
14:2S:11:LYS:HE3	14:2S:15:ARG:NH1	2.35	0.41
21:2Z:97:GLU:HB3	21:2Z:125:LEU:HD11	2.02	0.41
21:2Z:126:VAL:CG1	21:2Z:161:VAL:HG23	2.50	0.41
23:21:50:ARG:HD2	23:21:57:GLU:OE2	2.19	0.41
23:21:70:VAL:O	23:21:74:VAL:HG23	2.20	0.41
32:2a:9:G:H2'	32:2a:10:A:H8	1.85	0.41
32:2a:259:G:H2'	32:2a:260:G:O4'	2.20	0.41
32:2a:351:G:H4'	32:2a:352:C:OP1	2.20	0.41
32:2a:1002:G:C2	32:2a:1003:G:H8	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1194:U:H2'	32:2a:1195:C:C6	2.55	0.41
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.35	0.41
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	2.02	0.41
36:2e:89:ILE:HD12	36:2e:89:ILE:HA	1.90	0.41
38:2g:26:PHE:CD2	38:2g:62:PHE:HE1	2.38	0.41
40:2i:86:VAL:HA	40:2i:89:ASN:O	2.20	0.41
45:2n:53:LEU:HD23	45:2n:53:LEU:HA	1.77	0.41
50:2s:41:VAL:HG13	50:2s:43:GLU:OE1	2.20	0.41
50:2s:66:MET:HB2	50:2s:74:PHE:CZ	2.55	0.41
1:1A:212:A:N1	1:1A:434:G:O2'	2.49	0.41
1:1A:861:C:H4'	1:1A:1270:C:O2	2.20	0.41
1:1A:937:A:H2'	1:1A:938:G:O4'	2.20	0.41
1:1A:1021:G:O2'	1:1A:1202:A:N1	2.46	0.41
1:1A:1147:U:H2'	1:1A:1148:C:O4'	2.21	0.41
3:1D:61:LEU:HD12	3:1D:61:LEU:HA	1.81	0.41
6:1G:3:LEU:O	6:1G:8:LYS:NZ	2.36	0.41
10:1O:2:ILE:HG13	10:1O:8:LEU:HD21	2.02	0.41
26:14:18:CYS:SG	26:14:20:ASN:HB2	2.60	0.41
32:1a:559:A:P	36:1e:126:ARG:HH22	2.43	0.41
32:1a:1027:C:N3	32:1a:1034:G:N2	2.68	0.41
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	2.03	0.41
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.55	0.41
46:1o:18:PHE:C	46:1o:20:GLY:H	2.21	0.41
49:1r:25:THR:O	49:1r:26:LEU:HD12	2.20	0.41
1:2A:483:A:O4'	20:2Y:48:ALA:HB1	2.19	0.41
1:2A:652(B):A:N6	1:2A:655:A:H1'	2.35	0.41
1:2A:684:G:O2'	1:2A:788:A:N7	2.52	0.41
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.41
1:2A:1598:C:H2'	1:2A:1599:C:H6	1.85	0.41
1:2A:1786:A:C4	1:2A:1938:A:C6	3.08	0.41
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.19	0.41
1:2A:1857:G:C6	1:2A:1858:G:N1	2.88	0.41
7:2H:140:LYS:HE3	7:2H:140:LYS:HB2	1.81	0.41
10:2O:98:VAL:HG23	10:2O:118:ALA:HA	2.02	0.41
11:2P:44:GLY:HA3	11:2P:45:LEU:O	2.20	0.41
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.53	0.41
20:2Y:20:TYR:CZ	20:2Y:43:ASN:HA	2.55	0.41
23:21:52:ARG:HH21	23:21:57:GLU:HB2	1.86	0.41
32:2a:108:G:C6	51:2t:15:ARG:HG2	2.55	0.41
32:2a:292:G:N7	32:2a:293:G:H1'	2.35	0.41
32:2a:376:G:H5''	47:2p:5:ARG:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:652:U:O4	32:2a:752:G:O2'	2.31	0.41
32:2a:1168:A:H2'	32:2a:1169:A:C8	2.55	0.41
32:2a:1268:A:N3	32:2a:1326:C:O2'	2.53	0.41
34:2c:131:ARG:NH2	36:2e:50:GLU:HG3	2.35	0.41
35:2d:58:LEU:O	35:2d:62:GLN:HG2	2.20	0.41
36:2e:90:VAL:O	36:2e:120:THR:HA	2.19	0.41
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.20	0.41
1:1A:504:A:N1	1:1A:525:G:H4'	2.34	0.41
1:1A:623:G:H2'	1:1A:624:C:O4'	2.20	0.41
1:1A:672:G:H2'	1:1A:673:G:O4'	2.20	0.41
1:1A:821:A:H2'	1:1A:821:A:N3	2.35	0.41
1:1A:2132:G:H2'	1:1A:2132:G:OP2	2.21	0.41
1:1A:2695:C:H2'	1:1A:2696:U:H6	1.86	0.41
9:1N:30:ILE:HG23	9:1N:52:VAL:HG11	2.01	0.41
10:1O:106:LEU:HD23	10:1O:106:LEU:HA	1.86	0.41
15:1T:66:VAL:HA	15:1T:71:GLY:HA2	2.01	0.41
19:1X:43:VAL:HG21	19:1X:81:VAL:HG11	2.02	0.41
21:1Z:102:LEU:HB2	21:1Z:123:ASP:HA	2.02	0.41
22:10:53:MET:HG3	22:10:59:LEU:HD23	2.02	0.41
26:14:61:ARG:HG3	26:14:62:ARG:N	2.35	0.41
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.35	0.41
28:16:47:THR:O	28:16:49:HIS:ND1	2.47	0.41
32:1a:123:C:OP1	32:1a:312:C:H5'	2.20	0.41
32:1a:515:G:H2'	32:1a:516:PSU:O4'	2.20	0.41
32:1a:737:A:H2'	32:1a:738:C:H6	1.84	0.41
32:1a:986:A:H2'	32:1a:987:G:O4'	2.20	0.41
32:1a:1339:A:H2'	32:1a:1340:A:O4'	2.20	0.41
32:1a:1404:5MC:H2'	32:1a:1405:G:C8	2.55	0.41
33:1b:32:ILE:HD13	33:1b:40:HIS:CD2	2.55	0.41
34:1c:131:ARG:HE	34:1c:135:LYS:HE3	1.85	0.41
35:1d:63:LYS:HB2	35:1d:63:LYS:HE3	1.86	0.41
38:1g:15:ASP:OD1	38:1g:19:GLY:N	2.53	0.41
51:1t:56:MET:HE3	51:1t:85:MET:HG2	2.02	0.41
1:2A:288:C:H2'	1:2A:289:A:H8	1.84	0.41
1:2A:311:A:C6	1:2A:328:U:C4	3.08	0.41
1:2A:673:C:H5''	5:2F:81:PRO:HD2	2.02	0.41
1:2A:686:G:N2	1:2A:788:A:H61	2.19	0.41
1:2A:1473:G:C6	1:2A:1474:C:C4	3.08	0.41
1:2A:2420:C:H5'	28:26:54:ILE:HD11	2.02	0.41
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.20	0.41
9:2N:45:ASN:OD1	9:2N:46:VAL:HG22	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	2.02	0.41
13:2R:10:LEU:HD23	13:2R:10:LEU:HA	1.91	0.41
14:2S:58:LEU:HD12	14:2S:65:VAL:HG22	2.02	0.41
15:2T:119:LYS:HB2	32:2a:1442(A):G:N2	2.35	0.41
22:20:6:GLY:C	22:20:7:LEU:HD23	2.45	0.41
32:2a:676:A:H1'	42:2k:115:PRO:HB3	2.03	0.41
32:2a:741:G:H2'	32:2a:742:G:O4'	2.21	0.41
32:2a:909:A:H2'	32:2a:910:C:O4'	2.20	0.41
32:2a:1005:A:OP1	32:2a:1006:C:N4	2.53	0.41
32:2a:1317:C:N3	50:2s:37:ARG:NH2	2.69	0.41
33:2b:25:ASN:ND2	33:2b:193:ASP:HA	2.35	0.41
35:2d:15:GLU:HB3	35:2d:63:LYS:HG3	2.01	0.41
37:2f:91:VAL:HG12	37:2f:92:LYS:O	2.20	0.41
42:2k:20:TYR:O	42:2k:30:VAL:HA	2.20	0.41
44:2m:84:ILE:HG13	44:2m:86:CYS:H	1.85	0.41
49:2r:53:ARG:O	49:2r:57:GLY:N	2.40	0.41
49:2r:61:LYS:O	49:2r:65:ILE:HG12	2.20	0.41
52:2u:6:ARG:O	52:2u:12:LYS:HE3	2.20	0.41
54:2w:10:G:H2'	54:2w:11:C:C6	2.55	0.41
54:2y:3:C:N3	54:2y:70:G:O6	2.53	0.41
1:1A:439:A:O5'	1:1A:439:A:H8	2.04	0.41
1:1A:1614:A:OP2	3:1D:84:TYR:OH	2.28	0.41
1:1A:2039:U:O2'	1:1A:2041:A:OP2	2.38	0.41
1:1A:2482:G:O6	1:1A:2488:A:O2'	2.18	0.41
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	2.03	0.41
11:1P:98:GLU:HG3	11:1P:99:LEU:N	2.35	0.41
12:1Q:17:LEU:HB3	12:1Q:39:PRO:HB2	2.02	0.41
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.55	0.41
32:1a:731:G:H5'	32:1a:766:A:H4'	2.02	0.41
32:1a:985:C:H2'	32:1a:986:A:H8	1.84	0.41
33:1b:207:ALA:HB3	33:1b:210:SER:CB	2.50	0.41
34:1c:19:GLU:HB3	34:1c:40:ARG:HH21	1.85	0.41
34:1c:131:ARG:NE	34:1c:135:LYS:HE3	2.35	0.41
35:1d:196:LEU:C	35:1d:198:VAL:H	2.29	0.41
37:1f:6:VAL:HG22	37:1f:90:VAL:HG13	2.03	0.41
39:1h:16:ALA:HB1	39:1h:21:LYS:HB2	2.02	0.41
41:1j:65:LEU:HD13	45:1n:56:VAL:HG22	2.02	0.41
47:1p:6:LEU:HB3	47:1p:17:TYR:CD1	2.55	0.41
54:1w:75:C:H2'	54:1w:76:A:C4	2.55	0.41
54:1y:22:G:C2	54:1y:23:A:C5	3.08	0.41
1:2A:729:G:O4'	3:2D:208:LYS:NZ	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.55	0.41
1:2A:2484:G:C2	1:2A:2485:G:C8	3.08	0.41
4:2E:52:LEU:HB3	4:2E:76:ARG:HD3	2.03	0.41
32:2a:12:U:O2'	32:2a:526:C:H4'	2.21	0.41
32:2a:392:G:H2'	32:2a:393:A:C8	2.55	0.41
32:2a:404:U:P	35:2d:118:ARG:HH21	2.43	0.41
32:2a:544:G:OP1	35:2d:62:GLN:NE2	2.54	0.41
32:2a:1253:G:H5'	41:2j:44:VAL:O	2.20	0.41
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	2.03	0.41
34:2c:155:GLY:HA3	34:2c:196:LEU:HD22	2.03	0.41
36:2e:136:MET:HA	36:2e:139:LEU:HD12	2.01	0.41
40:2i:32:ASP:HB3	40:2i:35:GLU:HB2	2.01	0.41
41:2j:47:PHE:N	41:2j:63:PHE:O	2.33	0.41
44:2m:101:GLN:OE1	44:2m:101:GLN:N	2.54	0.41
1:1A:273:G:H21	8:1I:50:ARG:HH12	1.66	0.41
1:1A:854:U:P	11:1P:36:LYS:HD3	2.60	0.41
1:1A:876:A:N7	1:1A:2260:C:H5'	2.36	0.41
1:1A:955:A:H2'	1:1A:958:C:C5	2.55	0.41
1:1A:1089:C:H2'	1:1A:1090:G:H5''	2.02	0.41
1:1A:1848:G:OP1	3:1D:88:ARG:NH2	2.53	0.41
1:1A:1911:A:H2'	1:1A:1912:A:C8	2.55	0.41
1:1A:2162:C:O2	1:1A:2174:G:N2	2.54	0.41
5:1F:161:GLU:HG2	5:1F:164:ARG:NH2	2.36	0.41
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.36	0.41
12:1Q:51:ARG:O	12:1Q:55:VAL:HG23	2.20	0.41
13:1R:28:LEU:HD23	13:1R:48:VAL:HG21	2.02	0.41
16:1U:16:LYS:HE2	16:1U:16:LYS:HB3	1.75	0.41
25:13:15:TYR:O	25:13:20:LYS:NZ	2.53	0.41
26:14:55:ARG:N	26:14:56:VAL:CA	2.83	0.41
32:1a:8:A:N7	35:1d:208:SER:OG	2.42	0.41
32:1a:743:U:H2'	32:1a:744:C:C6	2.55	0.41
32:1a:875:C:H1'	39:1h:15:ASN:OD1	2.20	0.41
32:1a:881:G:H2'	32:1a:882:C:O4'	2.21	0.41
32:1a:942:G:C2	32:1a:1342:C:C2	3.09	0.41
33:1b:15:VAL:HB	33:1b:209:ARG:HG3	2.02	0.41
33:1b:44:LEU:O	33:1b:48:MET:HG2	2.20	0.41
35:1d:112:VAL:HG23	35:1d:116:GLN:NE2	2.36	0.41
39:1h:119:LEU:HB3	39:1h:123:GLU:HB2	2.03	0.41
43:1l:7:ILE:HD13	43:1l:7:ILE:HA	1.90	0.41
1:2A:527:C:H6	60:2A:3976:HOH:O	2.03	0.41
1:2A:740:U:H2'	1:2A:741:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:848:G:OP1	60:2A:3615:HOH:O	2.22	0.41
1:2A:1263:U:C4	1:2A:1264:G:C6	3.08	0.41
1:2A:1988:C:H2'	1:2A:1989:G:O4'	2.20	0.41
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.20	0.41
11:2P:38:GLN:C	11:2P:40:SER:H	2.29	0.41
13:2R:1:MET:HE3	13:2R:1:MET:HB2	1.97	0.41
13:2R:33:ARG:HD2	13:2R:115:GLU:HB3	2.01	0.41
14:2S:27:SER:HA	14:2S:88:ASP:HB3	2.01	0.41
21:2Z:52:SER:OG	21:2Z:54:HIS:ND1	2.49	0.41
22:20:51:VAL:N	22:20:62:LEU:HD12	2.36	0.41
32:2a:116:A:C4	32:2a:117:G:C8	3.09	0.41
32:2a:741:G:H5''	46:2o:59:MET:HE1	2.01	0.41
32:2a:1330:U:H4'	44:2m:23:TYR:CE1	2.55	0.41
33:2b:75:LYS:O	33:2b:78:GLN:HG2	2.21	0.41
34:2c:178:LEU:C	34:2c:180:ALA:H	2.28	0.41
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.54	0.41
48:2q:29:HIS:CG	48:2q:30:PRO:HD2	2.55	0.41
55:2x:17:C:H2'	55:2x:17(A):U:C5	2.56	0.41
54:2y:59:U:H3'	54:2y:60:U:O2	2.20	0.41
1:1A:493:G:OP1	29:17:33:ARG:NH1	2.53	0.41
1:1A:801:C:H2'	1:1A:802:C:C6	2.56	0.41
1:1A:850:U:C4	1:1A:851:A:N7	2.88	0.41
1:1A:943:C:C2	1:1A:944:C:C4	3.08	0.41
1:1A:1140:U:H3	1:1A:1142:A:H5'	1.85	0.41
1:1A:1495:G:H1'	1:1A:1574:A:N1	2.35	0.41
1:1A:1888:G:C6	1:1A:1889:G:C6	3.09	0.41
1:1A:2619:G:H2'	1:1A:2620:G:O4'	2.20	0.41
3:1D:147:LEU:HD13	3:1D:155:LEU:HD11	2.03	0.41
12:1Q:31:ASP:HA	12:1Q:134:ARG:NH1	2.34	0.41
18:1W:88:ARG:NH1	18:1W:94:ASP:OD2	2.53	0.41
21:1Z:154:ASP:N	21:1Z:154:ASP:OD1	2.36	0.41
32:1a:1025:U:O2	32:1a:1036:G:C6	2.74	0.41
32:1a:1176:A:H2'	32:1a:1177:G:O4'	2.21	0.41
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.21	0.41
34:1c:116:VAL:HG21	34:1c:202:ILE:HD11	2.03	0.41
35:1d:122:ARG:HD2	35:1d:122:ARG:HA	1.86	0.41
35:1d:162:LEU:HD13	35:1d:181:MET:HB3	2.02	0.41
54:1y:41:C:H2'	54:1y:42:C:H6	1.86	0.41
1:2A:224:G:H2'	1:2A:225:A:O4'	2.20	0.41
1:2A:275:G:H2'	1:2A:276:A:O4'	2.20	0.41
1:2A:792:G:H5''	1:2A:793:A:H5'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.21	0.41
1:2A:1312:U:OP2	19:2X:63:LYS:HD2	2.21	0.41
1:2A:1653:G:O6	13:2R:11:ASN:ND2	2.53	0.41
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.53	0.41
1:2A:2536:G:C6	1:2A:2537:U:C4	3.08	0.41
1:2A:2776:A:H4'	1:2A:2777:G:H5''	2.02	0.41
5:2F:53:THR:HG22	5:2F:56:GLU:CD	2.45	0.41
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	2.01	0.41
11:2P:44:GLY:HA2	11:2P:45:LEU:HB2	2.02	0.41
13:2R:18:LEU:HD21	13:2R:22:ARG:CZ	2.50	0.41
13:2R:29:LEU:HD12	13:2R:29:LEU:HA	1.84	0.41
26:24:53:GLU:C	26:24:55:ARG:H	2.27	0.41
32:2a:423:G:H3'	32:2a:423:G:N3	2.36	0.41
32:2a:1272:G:N2	32:2a:1273:G:C5	2.88	0.41
35:2d:50:ARG:NH1	36:2e:10:MET:HE3	2.36	0.41
40:2i:54:ASP:C	40:2i:56:LEU:H	2.28	0.41
45:2n:3:ARG:HG3	45:2n:4:LYS:N	2.36	0.41
50:2s:11:VAL:HG12	50:2s:13:ASP:H	1.86	0.41
52:2u:6:ARG:H	52:2u:6:ARG:HG3	1.65	0.41
55:2x:47:U:H3'	55:2x:48:C:C5'	2.51	0.41
1:1A:136:G:H1'	19:1X:41:ASN:ND2	2.35	0.41
1:1A:469:A:C6	5:1F:45:ARG:HD2	2.55	0.41
1:1A:2328:C:O2'	6:1G:128:ARG:NH2	2.54	0.41
2:1B:90:A:C5	2:1B:91:C:H1'	2.55	0.41
30:18:8:LYS:O	30:18:12:LYS:HG3	2.20	0.41
32:1a:115:G:H4'	32:1a:116:A:O5'	2.19	0.41
32:1a:250:A:H5'	32:1a:252:U:O4'	2.21	0.41
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.51	0.41
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.56	0.41
32:1a:1286:A:H8	32:1a:1287:A:H4'	1.82	0.41
34:1c:132:ARG:O	34:1c:136:GLN:HG3	2.20	0.41
35:1d:116:GLN:HE22	35:1d:161:ASN:HD21	1.67	0.41
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.89	0.41
48:1q:64:PRO:HB3	48:1q:70:ARG:NH1	2.35	0.41
1:2A:479:A:O2'	1:2A:481:G:H5'	2.21	0.41
1:2A:531:C:H4'	1:2A:532:A:H5''	2.03	0.41
1:2A:815:C:H2'	1:2A:816:C:H6	1.85	0.41
1:2A:1449:A:HO2'	1:2A:1529:G:H21	1.64	0.41
1:2A:2055:C:OP1	1:2A:2056:G:H4'	2.20	0.41
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.62	0.41
2:2B:75:G:N3	21:2Z:85:HIS:CE1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	2.03	0.41
5:2F:197:ASP:O	5:2F:200:GLU:HB3	2.20	0.41
26:24:46:GLN:C	26:24:48:ARG:N	2.78	0.41
32:2a:267:C:OP1	48:2q:67:LYS:HG3	2.20	0.41
32:2a:1003:G:N2	32:2a:1025:U:O4	2.53	0.41
34:2c:135:LYS:O	34:2c:139:GLN:HB2	2.21	0.41
39:2h:95:VAL:HG11	39:2h:133:LEU:HD12	2.03	0.41
46:2o:83:GLU:HG3	46:2o:84:LYS:N	2.34	0.41
1:1A:116:A:H3'	1:1A:117:A:C5'	2.50	0.41
1:1A:470:C:H4'	5:1F:49:ALA:HB2	2.02	0.41
1:1A:1186:U:H4'	1:1A:1188:A:O4'	2.20	0.41
1:1A:1218:G:O2'	1:1A:1219:A:O4'	2.39	0.41
1:1A:1787:G:H4'	1:1A:1789:G:O4'	2.21	0.41
1:1A:2583:C:O2'	4:1E:146:THR:O	2.33	0.41
3:1D:19:ALA:HB3	3:1D:21:PHE:CE1	2.56	0.41
4:1E:70:ALA:O	4:1E:72:VAL:HG23	2.21	0.41
5:1F:172:TRP:CD1	5:1F:172:TRP:H	2.38	0.41
24:12:32:LEU:HD11	24:12:54:LYS:HG2	2.02	0.41
32:1a:34:C:H2'	32:1a:35:G:H8	1.86	0.41
32:1a:958:A:C6	32:1a:959:A:C6	3.09	0.41
32:1a:1128:C:H4'	32:1a:1148:U:O2	2.21	0.41
32:1a:1162:C:H2'	32:1a:1163:C:O4'	2.20	0.41
33:1b:109:SER:HA	33:1b:112:VAL:HG13	2.03	0.41
33:1b:167:PRO:O	33:1b:171:ALA:N	2.53	0.41
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.46	0.41
50:1s:66:MET:HB2	50:1s:74:PHE:CZ	2.56	0.41
1:2A:75:G:H4'	24:22:55:ARG:NH1	2.35	0.41
1:2A:862:G:H21	2:2B:100:A:H2	1.68	0.41
1:2A:1515:G:H2'	1:2A:1516:C:C6	2.56	0.41
1:2A:1607:C:H5''	1:2A:1608:A:H5'	2.03	0.41
1:2A:2168:G:C8	1:2A:2170:A:N7	2.89	0.41
1:2A:2483:C:H2'	1:2A:2484:G:O4'	2.20	0.41
4:2E:101:ARG:HD2	4:2E:169:ASN:ND2	2.36	0.41
6:2G:16:ARG:HA	6:2G:16:ARG:HD2	1.89	0.41
6:2G:173:LEU:HB3	6:2G:178:PHE:CG	2.55	0.41
9:2N:91:LEU:HD23	9:2N:91:LEU:HA	1.85	0.41
13:2R:62:ALA:O	13:2R:66:VAL:HG23	2.20	0.41
21:2Z:54:HIS:HB3	21:2Z:101:PRO:HD3	2.02	0.41
32:2a:600:C:H2'	32:2a:601:C:C6	2.56	0.41
32:2a:1318:A:H5''	50:2s:3:ARG:NH2	2.36	0.41
33:2b:78:GLN:O	33:2b:94:ASN:ND2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:114:LYS:HA	43:2l:114:LYS:HD3	1.88	0.41
44:2m:48:LEU:HD23	44:2m:48:LEU:HA	1.92	0.41
44:2m:91:ARG:HH12	44:2m:103:THR:HG21	1.86	0.41
45:2n:53:LEU:HA	45:2n:54:PRO:HD3	1.91	0.41
51:2t:30:LYS:O	51:2t:34:LYS:HG3	2.20	0.41
55:2x:14:A:N6	55:2x:21:A:C2	2.86	0.41
1:1A:268:G:H4'	23:11:81:LYS:HG2	2.03	0.41
1:1A:388:A:H2'	1:1A:389:G:C8	2.56	0.41
1:1A:525:G:N1	1:1A:528:A:OP2	2.54	0.41
1:1A:629:U:H4'	1:1A:705:C:H4'	2.02	0.41
1:1A:776:G:C6	3:1D:208:LYS:HB2	2.55	0.41
1:1A:781:A:O2'	1:1A:1682:G:H5'	2.20	0.41
1:1A:1103:A:N7	1:1A:1132:A:H2'	2.36	0.41
1:1A:1188:A:C4	1:1A:1190:G:N7	2.89	0.41
1:1A:1452:U:H2'	1:1A:1453:C:H6	1.84	0.41
1:1A:2325:C:H4'	6:1G:91:ARG:HG3	2.02	0.41
1:1A:2357:G:N3	1:1A:2393:C:H2'	2.36	0.41
1:1A:2376:C:OP1	22:10:55:ARG:HD3	2.21	0.41
1:1A:2702:C:H5''	1:1A:2882:G:N2	2.36	0.41
1:1A:2747:A:H2'	1:1A:2748:G:O4'	2.21	0.41
1:1A:2899:C:H2'	1:1A:2900:G:O4'	2.21	0.41
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.21	0.41
4:1E:2:LYS:HG3	4:1E:200:GLU:HB2	2.03	0.41
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.33	0.41
5:1F:126:VAL:HG21	5:1F:129:PHE:CZ	2.56	0.41
5:1F:158:THR:O	5:1F:164:ARG:NH1	2.49	0.41
5:1F:202:PHE:CZ	5:1F:206:ILE:HD13	2.56	0.41
7:1H:126:PRO:HB2	7:1H:127:GLU:H	1.67	0.41
9:1N:39:ARG:NH2	9:1N:41:ASP:OD2	2.53	0.41
10:1O:10:VAL:HG13	10:1O:17:ARG:C	2.45	0.41
11:1P:50:ARG:HD3	30:18:7:HIS:HD2	1.82	0.41
12:1Q:27:VAL:HG23	12:1Q:138:ASP:OD1	2.21	0.41
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.21	0.41
18:1W:11:ARG:HE	18:1W:98:LYS:HB3	1.86	0.41
20:1Y:5:MET:HE2	20:1Y:5:MET:HB2	1.87	0.41
27:15:59:GLU:HG2	27:15:60:VAL:N	2.36	0.41
28:16:25:LYS:HE3	28:16:27:LYS:HA	2.03	0.41
32:1a:270:A:H2'	32:1a:271:C:O4'	2.21	0.41
32:1a:456:C:H2'	32:1a:457:C:H6	1.84	0.41
32:1a:495:A:H4'	32:1a:496:A:OP1	2.20	0.41
32:1a:538:G:H2'	32:1a:539:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:626:U:C2	32:1a:627:G:C8	3.09	0.41
32:1a:738:C:H2'	32:1a:739:C:H6	1.86	0.41
32:1a:935:A:N6	38:1g:3:ARG:HG3	2.36	0.41
32:1a:952:U:H2'	32:1a:953:G:H8	1.86	0.41
32:1a:1070:U:H2'	32:1a:1071:C:C6	2.56	0.41
32:1a:1324:A:O4'	32:1a:1362:C:H4'	2.21	0.41
34:1c:113:ALA:HB3	34:1c:114:PRO:HD3	2.01	0.41
36:1e:27:ARG:NH1	36:1e:27:ARG:HB2	2.36	0.41
39:1h:116:LYS:HD2	39:1h:127:LEU:HG	2.02	0.41
44:1m:79:LYS:NZ	44:1m:83:ASP:OD2	2.52	0.41
45:1n:6:LEU:HG	45:1n:23:ARG:HH22	1.85	0.41
48:1q:32:TYR:O	48:1q:34:LYS:N	2.52	0.41
49:1r:24:ALA:C	49:1r:26:LEU:H	2.29	0.41
54:1w:18:G:H4'	54:1w:60:U:C6	2.56	0.41
54:1w:66:U:H2'	54:1w:67:C:C6	2.55	0.41
54:1w:71:G:H2'	54:1w:71:G:N3	2.36	0.41
1:2A:127:A:H5''	1:2A:128:C:C6	2.56	0.41
1:2A:146:G:H2'	1:2A:147:U:O4'	2.21	0.41
1:2A:184:C:H2'	1:2A:185:U:H6	1.84	0.41
1:2A:228:A:O2'	1:2A:229:A:H4'	2.21	0.41
1:2A:272(D):G:C2	1:2A:272(E):G:C8	3.09	0.41
1:2A:503:A:H4'	1:2A:504:U:H5''	2.03	0.41
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.55	0.41
1:2A:868:U:C4	1:2A:869:G:N7	2.89	0.41
1:2A:1131:G:H8	1:2A:2025:C:H4'	1.86	0.41
1:2A:1685:C:H2'	1:2A:1686:C:H6	1.86	0.41
1:2A:2073:C:O2'	1:2A:2598:A:O2'	2.34	0.41
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.56	0.41
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.56	0.41
1:2A:2494:G:C4	1:2A:2495:G:C8	3.09	0.41
1:2A:2815:C:H2'	1:2A:2816:C:C6	2.55	0.41
3:2D:85:ASP:HB2	3:2D:92:ILE:HD13	2.03	0.41
5:2F:24:LEU:HD21	5:2F:114:VAL:HG12	2.02	0.41
7:2H:98:LEU:HD22	7:2H:124:GLU:HA	2.03	0.41
15:2T:88:ILE:HG21	15:2T:91:ARG:CZ	2.51	0.41
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.36	0.41
21:2Z:1:MET:O	21:2Z:55:HIS:ND1	2.54	0.41
30:28:8:LYS:HD3	30:28:8:LYS:HA	1.84	0.41
30:28:34:TRP:CG	30:28:35:GLN:N	2.89	0.41
31:29:1:MET:SD	31:29:35:ARG:N	2.94	0.41
32:2a:123:C:OP1	32:2a:312:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:662:G:H2'	32:2a:663:A:H8	1.83	0.41
32:2a:687:A:H4'	32:2a:688:G:O5'	2.21	0.41
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.56	0.41
32:2a:975:A:N6	41:2j:60:ARG:HH12	2.19	0.41
32:2a:999:C:N4	60:2a:1935:HOH:O	2.54	0.41
32:2a:1021:G:C6	32:2a:1022:G:C8	3.09	0.41
32:2a:1137:C:H5''	32:2a:1138:G:OP1	2.21	0.41
32:2a:1217:C:H2'	32:2a:1218:C:O4'	2.20	0.41
32:2a:1327:C:H2'	32:2a:1328:C:H6	1.86	0.41
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	2.03	0.41
46:2o:5:LYS:HE2	46:2o:5:LYS:HB2	1.86	0.41
47:2p:69:THR:O	47:2p:73:LEU:HG	2.21	0.41
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.54	0.41
54:2w:21:A:N6	54:2w:46:7MG:C4	2.88	0.41
1:1A:860:U:H2'	1:1A:861:C:C6	2.56	0.41
1:1A:1016:C:H2'	1:1A:1017:G:O4'	2.21	0.41
1:1A:1052:C:O2'	9:1N:106:MET:HB3	2.21	0.41
1:1A:1103:A:N6	1:1A:1133:G:OP2	2.52	0.41
11:1P:31:ALA:O	11:1P:32:THR:OG1	2.36	0.41
32:1a:68:G:H1	32:1a:101:A:N6	2.14	0.41
32:1a:110:C:H2'	32:1a:111:G:O4'	2.21	0.41
32:1a:452:A:O2'	32:1a:453:A:OP2	2.36	0.41
32:1a:731:G:OP1	32:1a:766:A:H1'	2.21	0.41
32:1a:1098:C:C2	32:1a:1099:G:C8	3.09	0.41
38:1g:50:ILE:HD13	38:1g:125:MET:CG	2.44	0.41
38:1g:65:ALA:O	38:1g:69:VAL:HG23	2.21	0.41
39:1h:17:THR:HB	39:1h:78:GLN:OE1	2.20	0.41
43:1l:69:TYR:HB2	43:1l:90:VAL:HG21	2.02	0.41
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.56	0.41
1:2A:875:G:C6	1:2A:876:C:C2	3.09	0.41
1:2A:892:G:H3'	1:2A:893:C:H5''	2.02	0.41
1:2A:953:A:C2	1:2A:954:G:C8	3.09	0.41
1:2A:1580:A:H3'	1:2A:1581:G:H8	1.85	0.41
1:2A:1983:C:H4'	1:2A:2606:C:H4'	2.02	0.41
1:2A:2129:C:N3	1:2A:2159:G:N2	2.61	0.41
2:2B:46:A:H2'	2:2B:47:C:C6	2.56	0.41
2:2B:57:A:N3	6:2G:29:TRP:HB3	2.36	0.41
2:2B:60:C:H2'	2:2B:61:G:H8	1.85	0.41
4:2E:11:MET:HB3	4:2E:11:MET:HE2	1.74	0.41
5:2F:184:TYR:CE1	11:2P:3:LEU:HD21	2.56	0.41
7:2H:84:SER:OG	7:2H:134:SER:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:126:PRO:HB2	7:2H:127:GLU:H	1.68	0.41
15:2T:41:ARG:NH1	32:2a:346:G:OP1	2.53	0.41
22:20:53:MET:HG3	22:20:59:LEU:CD2	2.51	0.41
30:28:6:THR:HG23	30:28:64:TYR:HD2	1.85	0.41
32:2a:336:C:H2'	32:2a:337:C:C6	2.56	0.41
32:2a:338:A:H2'	32:2a:339:C:C6	2.56	0.41
32:2a:852:G:C6	32:2a:853:G:C5	3.08	0.41
32:2a:1242:C:H2'	32:2a:1243:C:O4'	2.21	0.41
32:2a:1306:A:H2'	32:2a:1307:U:O4'	2.21	0.41
35:2d:179:GLU:C	35:2d:181:MET:H	2.28	0.41
41:2j:69:ASN:O	41:2j:70:ARG:NH1	2.42	0.41
48:2q:9:VAL:O	48:2q:21:VAL:HA	2.22	0.41
54:2y:60:U:O2'	54:2y:61:C:H5'	2.21	0.41
1:1A:1033:G:O2'	1:1A:1046:A:N3	2.49	0.40
1:1A:1293:A:OP1	5:1F:95:ARG:NH1	2.41	0.40
4:1E:73:GLU:H	4:1E:73:GLU:HG3	1.65	0.40
10:1O:48:PRO:CB	32:1a:1422:G:H5''	2.50	0.40
13:1R:33:ARG:NH1	13:1R:115:GLU:OE1	2.48	0.40
14:1S:8:GLU:H	14:1S:8:GLU:HG2	1.59	0.40
16:1U:105:VAL:HG11	17:1V:39:LEU:HD21	2.04	0.40
23:11:8:SER:HB3	23:11:66:HIS:CD2	2.56	0.40
25:13:35:ARG:HE	25:13:37:LEU:HD21	1.85	0.40
32:1a:840:C:H4'	32:1a:841:U:OP1	2.20	0.40
32:1a:977:A:O2'	32:1a:979:C:OP2	2.36	0.40
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.37	0.40
32:1a:1203:C:H2'	32:1a:1204:A:O4'	2.22	0.40
33:1b:193:ASP:HB3	33:1b:196:LEU:HD22	2.03	0.40
36:1e:37:ARG:HH12	36:1e:111:GLU:HB3	1.86	0.40
44:1m:3:ARG:NH2	44:1m:9:ILE:HG13	2.36	0.40
1:2A:117:G:C6	1:2A:119:A:C6	3.09	0.40
1:2A:192:C:O2'	1:2A:802:A:N3	2.42	0.40
1:2A:253:C:H2'	1:2A:254:G:O4'	2.20	0.40
1:2A:350:U:H2'	1:2A:351:G:O4'	2.21	0.40
1:2A:819:A:C4	1:2A:1189:A:C2	3.09	0.40
1:2A:1291:C:H2'	1:2A:1292:U:C6	2.56	0.40
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.57	0.40
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.21	0.40
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.20	0.40
2:2B:40:U:H1'	2:2B:45:A:H61	1.86	0.40
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.56	0.40
6:2G:54:GLU:O	6:2G:58:GLN:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:137:ASP:O	7:2H:141:VAL:HG23	2.22	0.40
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	2.03	0.40
22:20:53:MET:HG2	22:20:57:PHE:HA	2.03	0.40
23:21:23:LYS:HB3	23:21:29:GLY:HA3	2.03	0.40
24:22:35:LEU:HD12	24:22:53:LEU:HD12	2.03	0.40
32:2a:165:C:H2'	32:2a:166:G:H8	1.85	0.40
32:2a:401:C:H2'	32:2a:402:G:H8	1.86	0.40
32:2a:473:G:H2'	32:2a:474:G:H8	1.86	0.40
32:2a:1071:C:H5''	36:2e:49:PRO:HG3	2.02	0.40
33:2b:51:LEU:HD22	33:2b:55:PHE:HE2	1.87	0.40
35:2d:4:TYR:O	35:2d:5:ILE:HG22	2.21	0.40
44:2m:43:THR:OG1	44:2m:48:LEU:HD21	2.21	0.40
54:2w:39:PSU:H2'	54:2w:40:C:C6	2.55	0.40
1:1A:354:A:HO2'	1:1A:355:A:H8	1.69	0.40
1:1A:1066:A:N1	1:1A:1186:U:O2'	2.47	0.40
1:1A:1100:A:H3'	1:1A:1101:G:H8	1.86	0.40
1:1A:1321:A:N1	1:1A:1341:C:O2'	2.47	0.40
1:1A:1589:A:H8	1:1A:1589:A:OP1	2.04	0.40
1:1A:1686:U:H4'	1:1A:2711:C:H4'	2.03	0.40
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.56	0.40
1:1A:2875:U:C4	1:1A:2876:U:C4	3.09	0.40
4:1E:117:MET:HE2	4:1E:117:MET:HB3	1.71	0.40
6:1G:138:GLN:OE1	6:1G:138:GLN:N	2.46	0.40
10:1O:19:ILE:HG22	10:1O:43:VAL:HG22	2.03	0.40
14:1S:35:ILE:HB	60:1S:201:HOH:O	2.20	0.40
15:1T:27:THR:HB	15:1T:90:GLN:HB3	2.03	0.40
19:1X:41:ASN:O	19:1X:45:THR:HG23	2.21	0.40
32:1a:474:G:H5'	32:1a:475:G:OP2	2.20	0.40
32:1a:911:U:OP1	43:1l:95:GLY:HA2	2.21	0.40
32:1a:1114:C:H42	32:1a:1186:G:H1	1.70	0.40
43:1l:113:ARG:HA	43:1l:113:ARG:HD2	1.64	0.40
1:2A:956:G:H2'	1:2A:957:A:H2'	2.03	0.40
1:2A:1711:C:H2'	1:2A:1712:C:C6	2.56	0.40
1:2A:2148:G:N1	1:2A:2149:G:O6	2.54	0.40
1:2A:2154:G:H2'	1:2A:2155:G:H5'	2.02	0.40
1:2A:2461:C:H2'	1:2A:2462:U:H6	1.86	0.40
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.40	0.40
14:2S:29:PHE:O	14:2S:35:ILE:HA	2.20	0.40
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	2.03	0.40
32:2a:19:C:H5''	36:2e:86:ALA:CB	2.51	0.40
32:2a:524:G:H2'	32:2a:525:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:51:LEU:O	33:2b:55:PHE:HB2	2.21	0.40
38:2g:79:ARG:H	38:2g:79:ARG:HG3	1.52	0.40
44:2m:30:ALA:O	44:2m:34:LEU:HG	2.21	0.40
44:2m:97:PRO:HA	44:2m:110:ARG:HD3	2.03	0.40
46:2o:32:LEU:HD23	46:2o:32:LEU:HA	1.83	0.40
48:2q:89:LEU:HA	48:2q:89:LEU:HD23	1.87	0.40
1:1A:1298:G:C2	1:1A:1299:A:C2	3.10	0.40
1:1A:2132:G:C5	1:1A:2142:G:C8	3.10	0.40
1:1A:2333:G:H5'	57:1A:3934:KAN:HN21	1.86	0.40
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.39	0.40
7:1H:64:LEU:HD23	7:1H:64:LEU:HA	1.91	0.40
9:1N:39:ARG:HH21	9:1N:41:ASP:CG	2.29	0.40
9:1N:121:LYS:HD3	9:1N:130:HIS:CE1	2.56	0.40
13:1R:20:LEU:HD21	13:1R:40:LYS:HD3	2.04	0.40
13:1R:33:ARG:NH2	27:15:57:VAL:O	2.49	0.40
13:1R:63:ARG:NH2	60:1R:303:HOH:O	2.35	0.40
14:1S:5:THR:OG1	14:1S:8:GLU:HG2	2.21	0.40
16:1U:8:VAL:O	16:1U:12:ARG:HG3	2.22	0.40
18:1W:62:HIS:O	18:1W:64:MET:HG3	2.22	0.40
30:18:26:LYS:HB2	30:18:44:LYS:O	2.21	0.40
32:1a:31:G:N2	60:1a:2063:HOH:O	2.55	0.40
32:1a:973:G:H3'	32:1a:974:A:H5''	2.04	0.40
33:1b:16:HIS:CD2	33:1b:17:PHE:N	2.89	0.40
33:1b:52:GLU:HG2	33:1b:56:ARG:HH12	1.86	0.40
33:1b:212:GLN:O	33:1b:216:SER:OG	2.29	0.40
35:1d:116:GLN:NE2	35:1d:157:LEU:HD21	2.37	0.40
38:1g:127:ALA:C	38:1g:129:GLU:H	2.28	0.40
43:1l:90:VAL:O	43:1l:92:OTD:N	2.54	0.40
47:1p:74:LEU:HG	47:1p:79:VAL:HG21	2.03	0.40
55:1x:58:A:H4'	55:1x:59:A:OP1	2.21	0.40
1:2A:661:C:H2'	1:2A:662:G:C8	2.56	0.40
1:2A:1139:G:N2	57:2A:3569:KAN:O14	2.54	0.40
1:2A:2635:C:H5''	4:2E:78:LEU:O	2.22	0.40
1:2A:2872:G:O2'	1:2A:2873:A:H5'	2.22	0.40
4:2E:105:THR:HG23	4:2E:166:THR:OG1	2.21	0.40
9:2N:102:ALA:O	9:2N:106:MET:HG3	2.22	0.40
14:2S:105:ALA:HB1	14:2S:110:LEU:HD23	2.03	0.40
14:2S:110:LEU:HD12	14:2S:110:LEU:HA	1.82	0.40
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.57	0.40
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.55	0.40
38:2g:54:THR:C	38:2g:56:GLN:H	2.26	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:2h:54:ASP:O	39:2h:56:LYS:HG2	2.22	0.40
39:2h:82:HIS:CE1	39:2h:84:ARG:HD3	2.56	0.40
42:2k:87:THR:HG22	42:2k:91:ARG:NH1	2.36	0.40
45:2n:9:LYS:O	45:2n:9:LYS:HG2	2.21	0.40
1:1A:216:A:H5''	11:1P:76:LYS:HE2	2.02	0.40
1:1A:1440:U:C4	1:1A:1441:A:C6	3.10	0.40
1:1A:2801:C:P	4:1E:61:ARG:HH21	2.42	0.40
21:1Z:156:LYS:HE3	21:1Z:158:PRO:HD3	2.04	0.40
32:1a:103:C:O2'	32:1a:172:A:N1	2.47	0.40
32:1a:429:U:H3'	35:1d:9:CYS:SG	2.62	0.40
32:1a:502:G:H2'	32:1a:503:C:O4'	2.21	0.40
32:1a:613:C:H2'	32:1a:614:A:C8	2.57	0.40
32:1a:667:G:H4'	46:1o:51:HIS:ND1	2.37	0.40
32:1a:997:U:H3	32:1a:1044:A:N6	2.20	0.40
32:1a:1239:A:C4	32:1a:1298:C:N4	2.89	0.40
34:1c:77:ILE:H	34:1c:77:ILE:HG12	1.72	0.40
40:1i:49:PRO:HD3	40:1i:78:LYS:HG3	2.03	0.40
47:1p:9:PHE:HB2	47:1p:16:HIS:O	2.21	0.40
55:1x:8:4SU:O2	55:1x:21:A:H2	2.03	0.40
54:1y:7:A:OP1	54:1y:8:4SU:H5	2.21	0.40
1:2A:39:C:H2'	1:2A:40:C:C6	2.57	0.40
1:2A:44:G:O3'	1:2A:45:C:H4'	2.22	0.40
1:2A:144:C:H2'	1:2A:145:G:H8	1.87	0.40
1:2A:218:A:C2	1:2A:235:U:H4'	2.56	0.40
1:2A:320:A:H4'	1:2A:322:A:C8	2.57	0.40
1:2A:729:G:H2'	1:2A:1775:U:H1'	2.03	0.40
1:2A:900:A:H3'	1:2A:901:A:C8	2.56	0.40
1:2A:1517:G:C6	1:2A:1518:U:C4	3.10	0.40
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.21	0.40
1:2A:2294:C:OP1	14:2S:10:ARG:HD2	2.21	0.40
1:2A:2726:U:O2'	1:2A:2727:G:H8	2.04	0.40
3:2D:12:SER:O	3:2D:16:MET:HE3	2.21	0.40
4:2E:32:PRO:HA	4:2E:90:THR:HA	2.03	0.40
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	2.04	0.40
7:2H:10:PRO:O	7:2H:12:PRO:HD3	2.21	0.40
8:2I:40:THR:O	8:2I:44:LEU:HB2	2.22	0.40
12:2Q:66:ILE:HG12	12:2Q:104:PHE:CD1	2.56	0.40
12:2Q:136:ALA:HB1	21:2Z:52:SER:HB2	2.03	0.40
14:2S:8:GLU:HA	14:2S:11:LYS:HB2	2.03	0.40
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.29	0.40
23:21:54:ALA:HB1	23:21:83:GLU:HG3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:21:85:LEU:HD23	23:21:89:GLU:CD	2.47	0.40
32:2a:540:G:H2'	32:2a:541:G:O4'	2.21	0.40
32:2a:580:U:H2'	32:2a:581:G:O4'	2.21	0.40
32:2a:1022:G:C6	32:2a:1023:G:C6	3.09	0.40
32:2a:1186:G:H4'	40:2i:110:GLU:OE2	2.22	0.40
33:2b:178:ARG:HE	33:2b:178:ARG:HB3	1.69	0.40
34:2c:159:GLY:HA2	34:2c:193:TYR:CD1	2.57	0.40
36:2e:145:LYS:O	36:2e:149:GLU:HB2	2.22	0.40
37:2f:86:ARG:O	37:2f:87:ARG:HG2	2.22	0.40
38:2g:68:ASN:O	38:2g:135:VAL:HG13	2.21	0.40
38:2g:69:VAL:HG13	38:2g:134:ALA:O	2.22	0.40
39:2h:17:THR:HA	39:2h:65:TYR:HE1	1.87	0.40
40:2i:43:ALA:HA	40:2i:74:ILE:HD13	2.03	0.40
55:2x:55:PSU:O2'	55:2x:57:A:N7	2.50	0.40
54:2y:4:C:H2'	54:2y:5:G:H5'	2.03	0.40
1:1A:886:U:H1'	1:1A:1236:G:H1'	2.04	0.40
1:1A:1446:G:H2'	1:1A:1447:G:C8	2.57	0.40
1:1A:1459:G:H2'	1:1A:1460:G:O4'	2.20	0.40
1:1A:1628:G:N7	60:1A:4066:HOH:O	2.37	0.40
1:1A:2102:G:OP1	23:11:35:THR:HG21	2.22	0.40
1:1A:2373:A:H5'	30:18:27:THR:OG1	2.22	0.40
1:1A:2485:U:O2	1:1A:2485:U:H2'	2.21	0.40
1:1A:2734:A:O2'	1:1A:2884:C:H5'	2.21	0.40
12:1Q:72:LYS:HB3	12:1Q:94:VAL:HG23	2.03	0.40
12:1Q:85:LYS:HD2	12:1Q:85:LYS:N	2.37	0.40
18:1W:46:PHE:O	18:1W:50:VAL:HG23	2.21	0.40
32:1a:90:U:H2'	32:1a:91:C:C6	2.57	0.40
32:1a:266:G:H4'	32:1a:267:C:C5	2.56	0.40
32:1a:522:C:OP2	43:1l:69:TYR:OH	2.37	0.40
33:1b:79:ASP:O	33:1b:83:MET:HG2	2.21	0.40
33:1b:204:ASN:OD1	33:1b:206:ASP:N	2.54	0.40
35:1d:18:LYS:HD2	35:1d:20:TYR:CZ	2.57	0.40
38:1g:27:ILE:HA	38:1g:30:ILE:HD12	2.04	0.40
44:1m:54:VAL:HA	44:1m:57:ARG:HB3	2.03	0.40
50:1s:16:LEU:HD12	50:1s:16:LEU:HA	1.82	0.40
1:2A:10:G:H1'	1:2A:2801(A):A:N7	2.37	0.40
1:2A:30:G:C6	1:2A:31:C:C4	3.10	0.40
1:2A:271(P):C:OP1	8:2I:45:LYS:HE2	2.20	0.40
1:2A:414:C:H4'	1:2A:1879:C:O2	2.22	0.40
1:2A:588:U:H1'	5:2F:90:PHE:HB3	2.02	0.40
1:2A:863:A:H2'	1:2A:864:G:H8	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1507:A:O2'	1:2A:1508:A:C8	2.74	0.40
1:2A:2271:G:OP1	22:20:18:ALA:HB1	2.21	0.40
1:2A:2474:C:H5''	1:2A:2475:C:OP2	2.21	0.40
3:2D:36:PRO:HA	3:2D:61:LEU:HD12	2.03	0.40
6:2G:175:LEU:HD12	6:2G:175:LEU:HA	1.90	0.40
9:2N:39:ARG:NH2	9:2N:41:ASP:OD1	2.54	0.40
12:2Q:36:ALA:HB1	12:2Q:127:ILE:HD12	2.04	0.40
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.51	0.40
32:2a:69:G:C2	32:2a:70:G:C8	3.09	0.40
32:2a:570:G:H1'	32:2a:820:U:C4	2.57	0.40
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.37	0.40
35:2d:65:ARG:HG3	35:2d:75:PHE:CD1	2.57	0.40
40:2i:127:LYS:O	40:2i:128:ARG:HB3	2.21	0.40
44:2m:122:LYS:HA	44:2m:122:LYS:HD2	1.72	0.40
45:2n:18:VAL:O	45:2n:20:ALA:N	2.48	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	255 (93%)	18 (7%)	0	100	100
3	2D	273/276 (99%)	252 (92%)	19 (7%)	2 (1%)	18	48
4	1E	202/206 (98%)	188 (93%)	12 (6%)	2 (1%)	12	39
4	2E	202/206 (98%)	190 (94%)	10 (5%)	2 (1%)	12	39
5	1F	201/210 (96%)	195 (97%)	5 (2%)	1 (0%)	24	54
5	2F	201/210 (96%)	185 (92%)	13 (6%)	3 (2%)	8	28
6	1G	179/182 (98%)	163 (91%)	14 (8%)	2 (1%)	11	36
6	2G	179/182 (98%)	168 (94%)	10 (6%)	1 (1%)	21	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	1H	172/180 (96%)	163 (95%)	8 (5%)	1 (1%)	21	51
7	2H	172/180 (96%)	150 (87%)	19 (11%)	3 (2%)	7	26
8	1I	144/148 (97%)	130 (90%)	14 (10%)	0	100	100
8	2I	144/148 (97%)	121 (84%)	20 (14%)	3 (2%)	5	21
9	1N	138/140 (99%)	129 (94%)	9 (6%)	0	100	100
9	2N	138/140 (99%)	128 (93%)	8 (6%)	2 (1%)	9	30
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	109 (91%)	9 (8%)	2 (2%)	7	26
11	1P	147/150 (98%)	137 (93%)	10 (7%)	0	100	100
11	2P	147/150 (98%)	130 (88%)	13 (9%)	4 (3%)	4	16
12	1Q	139/141 (99%)	132 (95%)	5 (4%)	2 (1%)	9	30
12	2Q	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	18	48
13	1R	116/118 (98%)	109 (94%)	6 (5%)	1 (1%)	14	41
13	2R	116/118 (98%)	103 (89%)	12 (10%)	1 (1%)	14	41
14	1S	108/112 (96%)	102 (94%)	6 (6%)	0	100	100
14	2S	108/112 (96%)	99 (92%)	7 (6%)	2 (2%)	6	23
15	1T	129/146 (88%)	118 (92%)	10 (8%)	1 (1%)	16	44
15	2T	129/146 (88%)	120 (93%)	6 (5%)	3 (2%)	5	19
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%)	90 (91%)	9 (9%)	0	100	100
17	2V	99/101 (98%)	91 (92%)	7 (7%)	1 (1%)	12	39
18	1W	110/113 (97%)	108 (98%)	2 (2%)	0	100	100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
19	1X	93/96 (97%)	89 (96%)	3 (3%)	1 (1%)	11	36
19	2X	93/96 (97%)	87 (94%)	6 (6%)	0	100	100
20	1Y	105/110 (96%)	94 (90%)	8 (8%)	3 (3%)	3	15
20	2Y	105/110 (96%)	92 (88%)	11 (10%)	2 (2%)	6	23
21	1Z	148/206 (72%)	128 (86%)	19 (13%)	1 (1%)	18	48
21	2Z	156/206 (76%)	127 (81%)	26 (17%)	3 (2%)	6	23
22	10	81/85 (95%)	80 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	20	81/85 (95%)	75 (93%)	5 (6%)	1 (1%)	10	34
23	11	95/98 (97%)	92 (97%)	3 (3%)	0	100	100
23	21	95/98 (97%)	92 (97%)	1 (1%)	2 (2%)	5	21
24	12	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
24	22	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
25	13	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
25	23	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
26	14	67/71 (94%)	53 (79%)	9 (13%)	5 (8%)	1	2
26	24	67/71 (94%)	52 (78%)	10 (15%)	5 (8%)	1	2
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
29	17	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
29	27	46/49 (94%)	45 (98%)	0	1 (2%)	5	20
30	18	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
30	28	62/65 (95%)	60 (97%)	1 (2%)	1 (2%)	7	27
31	19	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	198 (86%)	23 (10%)	8 (4%)	3	12
33	2b	229/256 (90%)	200 (87%)	20 (9%)	9 (4%)	2	10
34	1c	204/239 (85%)	181 (89%)	20 (10%)	3 (2%)	8	28
34	2c	204/239 (85%)	172 (84%)	27 (13%)	5 (2%)	4	17
35	1d	206/209 (99%)	192 (93%)	11 (5%)	3 (2%)	8	28
35	2d	206/209 (99%)	182 (88%)	20 (10%)	4 (2%)	6	23
36	1e	146/162 (90%)	133 (91%)	10 (7%)	3 (2%)	5	21
36	2e	146/162 (90%)	131 (90%)	11 (8%)	4 (3%)	4	16
37	1f	98/101 (97%)	92 (94%)	5 (5%)	1 (1%)	12	39
37	2f	98/101 (97%)	91 (93%)	6 (6%)	1 (1%)	12	39
38	1g	153/156 (98%)	142 (93%)	9 (6%)	2 (1%)	9	32
38	2g	153/156 (98%)	137 (90%)	13 (8%)	3 (2%)	6	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	1h	135/138 (98%)	128 (95%)	7 (5%)	0	100	100
39	2h	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
40	1i	125/128 (98%)	109 (87%)	15 (12%)	1 (1%)	16	44
40	2i	125/128 (98%)	107 (86%)	17 (14%)	1 (1%)	16	44
41	1j	95/105 (90%)	76 (80%)	15 (16%)	4 (4%)	2	9
41	2j	94/105 (90%)	79 (84%)	10 (11%)	5 (5%)	1	5
42	1k	112/129 (87%)	102 (91%)	7 (6%)	3 (3%)	4	16
42	2k	112/129 (87%)	100 (89%)	10 (9%)	2 (2%)	6	25
43	1l	119/132 (90%)	109 (92%)	10 (8%)	0	100	100
43	2l	119/132 (90%)	107 (90%)	12 (10%)	0	100	100
44	1m	121/126 (96%)	110 (91%)	10 (8%)	1 (1%)	16	44
44	2m	120/126 (95%)	106 (88%)	13 (11%)	1 (1%)	16	44
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	26
46	1o	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5	19
46	2o	86/89 (97%)	76 (88%)	10 (12%)	0	100	100
47	1p	80/88 (91%)	67 (84%)	12 (15%)	1 (1%)	9	32
47	2p	80/88 (91%)	74 (92%)	5 (6%)	1 (1%)	9	32
48	1q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12	39
48	2q	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
49	1r	66/88 (75%)	61 (92%)	4 (6%)	1 (2%)	8	28
49	2r	66/88 (75%)	61 (92%)	5 (8%)	0	100	100
50	1s	81/93 (87%)	69 (85%)	9 (11%)	3 (4%)	2	11
50	2s	81/93 (87%)	66 (82%)	13 (16%)	2 (2%)	4	17
51	1t	94/106 (89%)	84 (89%)	5 (5%)	5 (5%)	1	5
51	2t	94/106 (89%)	83 (88%)	6 (6%)	5 (5%)	1	5
52	1u	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
52	2u	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
All	All	11370/12128 (94%)	10373 (91%)	846 (7%)	151 (1%)	9	32

All (151) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	49	ASP
15	1T	118	ARG
26	14	62	ARG
33	1b	10	LEU
33	1b	17	PHE
40	1i	54	ASP
51	1t	10	LEU
5	2F	130	ALA
7	2H	126	PRO
10	2O	5	GLN
26	24	45	GLY
29	27	46	VAL
33	2b	16	HIS
33	2b	123	ALA
35	2d	42	GLN
47	2p	53	VAL
51	2t	10	LEU
4	1E	100	GLU
7	1H	126	PRO
12	1Q	17	LEU
26	14	45	GLY
33	1b	126	GLU
34	1c	107	GLN
35	1d	178	VAL
35	1d	200	GLU
37	1f	40	VAL
47	1p	53	VAL
49	1r	33	ASP
50	1s	29	ARG
51	1t	100	ILE
8	2I	85	GLU
12	2Q	27	VAL
17	2V	79	VAL
26	24	55	ARG
26	24	61	ARG
33	2b	17	PHE
33	2b	125	PRO
34	2c	95	THR
34	2c	156	ARG
35	2d	181	MET
36	2e	77	PRO
40	2i	54	ASP

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Mol	Chain	Res	Type
41	2j	75	ILE
42	2k	49	GLY
50	2s	27	GLU
51	2t	47	GLY
51	2t	95	ALA
20	1Y	54	LYS
20	1Y	103	GLY
21	1Z	159	PRO
26	14	46	GLN
26	14	47	GLN
26	14	53	GLU
33	1b	155	LEU
33	1b	231	GLU
34	1c	81	GLY
41	1j	77	PRO
41	1j	79	ARG
42	1k	49	GLY
50	1s	27	GLU
51	1t	47	GLY
3	2D	3	VAL
4	2E	52	LEU
4	2E	113	PHE
7	2H	47	GLU
8	2I	40	THR
11	2P	38	GLN
13	2R	14	SER
14	2S	84	GLN
20	2Y	43	ASN
21	2Z	163	LEU
23	21	3	LYS
26	24	46	GLN
30	28	7	HIS
38	2g	7	ALA
38	2g	55	GLY
41	2j	78	ASN
44	2m	4	ILE
51	2t	99	LEU
51	2t	100	ILE
4	1E	52	LEU
20	1Y	40	GLU
33	1b	13	ALA
33	1b	20	GLU

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Mol	Chain	Res	Type
35	1d	179	GLU
36	1e	21	ALA
36	1e	85	GLY
41	1j	78	ASN
51	1t	95	ALA
51	1t	102	GLY
6	2G	110	ALA
8	2I	10	GLU
9	2N	2	LYS
15	2T	127	ALA
15	2T	128	GLU
22	20	4	LYS
23	21	45	ASN
26	24	52	THR
33	2b	231	GLU
34	2c	129	ALA
35	2d	18	LYS
36	2e	27	ARG
41	2j	39	PRO
42	2k	105	VAL
45	2n	52	GLN
50	2s	81	ARG
12	1Q	16	ARG
36	1e	69	VAL
38	1g	4	ARG
42	1k	107	SER
48	1q	33	GLY
50	1s	81	ARG
5	2F	21	ALA
11	2P	29	LYS
11	2P	45	LEU
11	2P	140	ALA
15	2T	55	ASN
21	2Z	161	VAL
33	2b	8	LYS
33	2b	20	GLU
33	2b	21	ARG
33	2b	78	GLN
34	2c	3	ASN
38	2g	80	VAL
6	1G	96	ARG
13	1R	107	ASP

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Mol	Chain	Res	Type
19	1X	94	GLY
44	1m	67	GLU
46	1o	19	PRO
7	2H	65	HIS
9	2N	48	MET
21	2Z	146	ILE
34	2c	91	LEU
37	2f	40	VAL
41	2j	77	PRO
34	1c	66	VAL
36	2e	69	VAL
38	1g	80	VAL
42	1k	105	VAL
46	1o	86	GLY
20	2Y	51	VAL
35	2d	5	ILE
36	2e	85	GLY
41	2j	50	ILE
41	1j	91	PRO
3	2D	236	GLY
5	2F	206	ILE
10	2O	72	PRO
14	2S	35	ILE
33	1b	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	193 (90%)	22 (10%)	7	23
3	2D	215/218 (99%)	186 (86%)	29 (14%)	4	12
4	1E	164/166 (99%)	146 (89%)	18 (11%)	6	20
4	2E	164/166 (99%)	147 (90%)	17 (10%)	7	23
5	1F	160/166 (96%)	140 (88%)	20 (12%)	4	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	2F	159/166 (96%)	144 (91%)	15 (9%)	8	26
6	1G	143/156 (92%)	130 (91%)	13 (9%)	9	28
6	2G	143/156 (92%)	121 (85%)	22 (15%)	2	9
7	1H	144/148 (97%)	131 (91%)	13 (9%)	9	28
7	2H	144/148 (97%)	129 (90%)	15 (10%)	7	23
8	1I	113/124 (91%)	96 (85%)	17 (15%)	3	10
8	2I	105/124 (85%)	92 (88%)	13 (12%)	4	15
9	1N	118/119 (99%)	106 (90%)	12 (10%)	7	23
9	2N	118/119 (99%)	103 (87%)	15 (13%)	4	14
10	1O	100/100 (100%)	92 (92%)	8 (8%)	11	34
10	2O	100/100 (100%)	92 (92%)	8 (8%)	11	34
11	1P	115/116 (99%)	100 (87%)	15 (13%)	4	13
11	2P	115/116 (99%)	105 (91%)	10 (9%)	9	30
12	1Q	111/111 (100%)	101 (91%)	10 (9%)	9	28
12	2Q	111/111 (100%)	96 (86%)	15 (14%)	4	12
13	1R	101/101 (100%)	87 (86%)	14 (14%)	3	11
13	2R	101/101 (100%)	92 (91%)	9 (9%)	9	28
14	1S	86/88 (98%)	74 (86%)	12 (14%)	3	11
14	2S	85/88 (97%)	71 (84%)	14 (16%)	2	8
15	1T	115/127 (91%)	108 (94%)	7 (6%)	17	46
15	2T	113/127 (89%)	108 (96%)	5 (4%)	25	59
16	1U	93/94 (99%)	87 (94%)	6 (6%)	15	44
16	2U	93/94 (99%)	87 (94%)	6 (6%)	15	44
17	1V	80/82 (98%)	68 (85%)	12 (15%)	3	10
17	2V	80/82 (98%)	67 (84%)	13 (16%)	2	8
18	1W	90/92 (98%)	80 (89%)	10 (11%)	6	20
18	2W	90/92 (98%)	81 (90%)	9 (10%)	7	24
19	1X	77/78 (99%)	75 (97%)	2 (3%)	40	73
19	2X	77/78 (99%)	74 (96%)	3 (4%)	28	63
20	1Y	85/91 (93%)	71 (84%)	14 (16%)	2	8
20	2Y	85/91 (93%)	77 (91%)	8 (9%)	8	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	1Z	135/179 (75%)	116 (86%)	19 (14%)	3	11
21	2Z	137/179 (76%)	119 (87%)	18 (13%)	4	13
22	10	65/67 (97%)	60 (92%)	5 (8%)	12	35
22	20	65/67 (97%)	60 (92%)	5 (8%)	12	35
23	11	80/83 (96%)	77 (96%)	3 (4%)	29	64
23	21	80/83 (96%)	75 (94%)	5 (6%)	16	45
24	12	65/67 (97%)	61 (94%)	4 (6%)	16	46
24	22	65/67 (97%)	59 (91%)	6 (9%)	8	27
25	13	51/52 (98%)	44 (86%)	7 (14%)	3	12
25	23	50/52 (96%)	45 (90%)	5 (10%)	7	24
26	14	59/63 (94%)	47 (80%)	12 (20%)	1	4
26	24	53/63 (84%)	45 (85%)	8 (15%)	3	10
27	15	50/52 (96%)	45 (90%)	5 (10%)	7	24
27	25	50/52 (96%)	45 (90%)	5 (10%)	7	24
28	16	51/52 (98%)	49 (96%)	2 (4%)	28	63
28	26	50/52 (96%)	46 (92%)	4 (8%)	11	34
29	17	41/42 (98%)	37 (90%)	4 (10%)	7	25
29	27	41/42 (98%)	37 (90%)	4 (10%)	7	25
30	18	54/55 (98%)	51 (94%)	3 (6%)	19	50
30	28	54/55 (98%)	48 (89%)	6 (11%)	6	20
31	19	34/34 (100%)	32 (94%)	2 (6%)	18	48
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	48
33	1b	192/220 (87%)	166 (86%)	26 (14%)	4	12
33	2b	187/220 (85%)	166 (89%)	21 (11%)	6	19
34	1c	142/188 (76%)	127 (89%)	15 (11%)	6	22
34	2c	140/188 (74%)	129 (92%)	11 (8%)	11	34
35	1d	169/181 (93%)	153 (90%)	16 (10%)	8	26
35	2d	173/181 (96%)	157 (91%)	16 (9%)	8	27
36	1e	113/123 (92%)	108 (96%)	5 (4%)	25	59
36	2e	114/123 (93%)	103 (90%)	11 (10%)	8	26
37	1f	84/90 (93%)	78 (93%)	6 (7%)	13	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	2f	85/90 (94%)	78 (92%)	7 (8%)	10	32
38	1g	119/127 (94%)	114 (96%)	5 (4%)	26	60
38	2g	120/127 (94%)	109 (91%)	11 (9%)	8	27
39	1h	114/119 (96%)	105 (92%)	9 (8%)	11	34
39	2h	114/119 (96%)	107 (94%)	7 (6%)	17	46
40	1i	90/99 (91%)	78 (87%)	12 (13%)	4	12
40	2i	89/99 (90%)	77 (86%)	12 (14%)	4	12
41	1j	66/92 (72%)	62 (94%)	4 (6%)	17	46
41	2j	69/92 (75%)	64 (93%)	5 (7%)	13	39
42	1k	82/99 (83%)	73 (89%)	9 (11%)	6	20
42	2k	83/99 (84%)	78 (94%)	5 (6%)	17	47
43	1l	96/108 (89%)	84 (88%)	12 (12%)	4	15
43	2l	96/108 (89%)	86 (90%)	10 (10%)	7	23
44	1m	93/101 (92%)	84 (90%)	9 (10%)	8	25
44	2m	92/101 (91%)	86 (94%)	6 (6%)	15	44
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5	16
45	2n	49/50 (98%)	43 (88%)	6 (12%)	5	16
46	1o	78/80 (98%)	70 (90%)	8 (10%)	7	23
46	2o	78/80 (98%)	73 (94%)	5 (6%)	16	44
47	1p	69/74 (93%)	61 (88%)	8 (12%)	5	18
47	2p	68/74 (92%)	57 (84%)	11 (16%)	2	8
48	1q	94/97 (97%)	89 (95%)	5 (5%)	20	52
48	2q	94/97 (97%)	88 (94%)	6 (6%)	16	44
49	1r	59/77 (77%)	52 (88%)	7 (12%)	5	16
49	2r	59/77 (77%)	54 (92%)	5 (8%)	10	31
50	1s	69/80 (86%)	64 (93%)	5 (7%)	13	39
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4	12
51	1t	70/82 (85%)	66 (94%)	4 (6%)	18	49
51	2t	70/82 (85%)	66 (94%)	4 (6%)	18	49
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9303/10064 (92%)	8378 (90%)	925 (10%)	7 24

All (925) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	18	VAL
3	1D	32	SER
3	1D	35	LYS
3	1D	61	LEU
3	1D	99	ASP
3	1D	106	ILE
3	1D	113	VAL
3	1D	116	GLN
3	1D	142	VAL
3	1D	154	LYS
3	1D	162	SER
3	1D	173	VAL
3	1D	182	LEU
3	1D	193	VAL
3	1D	211	ARG
3	1D	217	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	257	LEU
3	1D	270	ILE
3	1D	273	ARG
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	21	VAL
4	1E	24	THR
4	1E	34	VAL
4	1E	47	VAL
4	1E	49	LEU
4	1E	73	GLU
4	1E	75	VAL
4	1E	78	LEU
4	1E	82	ARG
4	1E	97	LYS
4	1E	116	VAL
4	1E	167	VAL

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Mol	Chain	Res	Type
4	1E	170	LEU
4	1E	175	VAL
4	1E	181	LEU
5	1F	12	LEU
5	1F	19	GLU
5	1F	20	LEU
5	1F	33	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	64	ILE
5	1F	70	THR
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	125	LEU
5	1F	126	VAL
5	1F	132	VAL
5	1F	140	LEU
5	1F	158	THR
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	91	ARG
6	1G	133	LEU
6	1G	135	LEU
6	1G	140	ILE
6	1G	145	THR
6	1G	148	MET
6	1G	149	VAL
6	1G	159	VAL
6	1G	175	LEU
7	1H	15	VAL
7	1H	33	LEU
7	1H	44	VAL
7	1H	45	VAL
7	1H	50	VAL
7	1H	59	ARG

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Mol	Chain	Res	Type
7	1H	71	LEU
7	1H	98	LEU
7	1H	101	ARG
7	1H	113	VAL
7	1H	122	THR
7	1H	134	SER
7	1H	155	SER
8	1I	9	LEU
8	1I	12	LEU
8	1I	31	LEU
8	1I	40	THR
8	1I	47	LEU
8	1I	74	ASN
8	1I	75	LEU
8	1I	77	LEU
8	1I	91	SER
8	1I	92	VAL
8	1I	101	LEU
8	1I	108	THR
8	1I	109	ILE
8	1I	123	LEU
8	1I	140	LEU
8	1I	142	VAL
8	1I	144	VAL
9	1N	28	THR
9	1N	30	ILE
9	1N	33	LEU
9	1N	34	LEU
9	1N	43	THR
9	1N	46	VAL
9	1N	62	VAL
9	1N	67	LEU
9	1N	73	THR
9	1N	87	LEU
9	1N	99	LEU
9	1N	112	LEU
10	1O	10	VAL
10	1O	31	LYS
10	1O	38	VAL
10	1O	39	ILE
10	1O	42	SER
10	1O	63	VAL

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Mol	Chain	Res	Type
10	1O	89	ASN
10	1O	98	VAL
11	1P	7	ARG
11	1P	55	ARG
11	1P	56	SER
11	1P	59	LEU
11	1P	65	ARG
11	1P	83	VAL
11	1P	95	VAL
11	1P	98	GLU
11	1P	99	LEU
11	1P	101	VAL
11	1P	112	LEU
11	1P	125	VAL
11	1P	126	VAL
11	1P	133	SER
11	1P	148	LEU
12	1Q	7	MET
12	1Q	27	VAL
12	1Q	35	VAL
12	1Q	56	ARG
12	1Q	64	ILE
12	1Q	66	ILE
12	1Q	75	THR
12	1Q	76	LYS
12	1Q	109	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	8	ARG
13	1R	15	SER
13	1R	29	LEU
13	1R	36	THR
13	1R	37	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	67	LEU
13	1R	79	LEU
13	1R	100	LEU
13	1R	102	GLU
13	1R	111	LEU
13	1R	114	VAL
14	1S	8	GLU

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Mol	Chain	Res	Type
14	1S	13	ARG
14	1S	14	VAL
14	1S	19	LYS
14	1S	25	ARG
14	1S	36	TYR
14	1S	49	VAL
14	1S	69	VAL
14	1S	71	ARG
14	1S	80	LEU
14	1S	85	VAL
14	1S	110	LEU
15	1T	6	LEU
15	1T	28	VAL
15	1T	49	VAL
15	1T	89	VAL
15	1T	111	ARG
15	1T	118	ARG
15	1T	128	GLU
16	1U	8	VAL
16	1U	31	SER
16	1U	74	LEU
16	1U	83	LEU
16	1U	90	VAL
16	1U	95	LEU
17	1V	7	THR
17	1V	18	LEU
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	73	SER
17	1V	79	VAL
17	1V	82	ARG
17	1V	95	LEU
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	23	LEU
18	1W	59	VAL
18	1W	60	ASN

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Mol	Chain	Res	Type
18	1W	90	ARG
18	1W	92	ARG
18	1W	95	ILE
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
20	1Y	11	ASP
20	1Y	14	LEU
20	1Y	28	LYS
20	1Y	43	ASN
20	1Y	49	VAL
20	1Y	50	ARG
20	1Y	55	TYR
20	1Y	61	ILE
20	1Y	64	GLU
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
20	1Y	106	LEU
20	1Y	107	ASP
21	1Z	1	MET
21	1Z	18	LEU
21	1Z	32	HIS
21	1Z	33	LEU
21	1Z	42	VAL
21	1Z	56	VAL
21	1Z	61	LEU
21	1Z	70	LEU
21	1Z	76	LEU
21	1Z	84	GLU
21	1Z	91	LEU
21	1Z	102	LEU
21	1Z	124	ILE
21	1Z	126	VAL
21	1Z	149	SER
21	1Z	154	ASP
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	171	ILE
22	10	10	THR
22	10	14	ARG
22	10	37	LEU

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Mol	Chain	Res	Type
22	10	63	VAL
22	10	74	ARG
23	11	30	VAL
23	11	35	THR
23	11	95	LEU
24	12	19	VAL
24	12	45	SER
24	12	53	LEU
24	12	69	ARG
25	13	3	ARG
25	13	6	VAL
25	13	31	LEU
25	13	34	GLU
25	13	54	VAL
25	13	58	VAL
25	13	60	GLU
26	14	3	GLU
26	14	23	GLU
26	14	46	GLN
26	14	49	PHE
26	14	50	VAL
26	14	52	THR
26	14	53	GLU
26	14	56	VAL
26	14	60	GLN
26	14	63	TYR
26	14	66	SER
26	14	67	TYR
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
27	15	55	ARG
27	15	58	LEU
28	16	19	ARG
28	16	48	VAL
29	17	1	MET
29	17	4	THR
29	17	24	THR
29	17	43	THR
30	18	14	VAL
30	18	23	VAL
30	18	32	LEU

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Mol	Chain	Res	Type
31	19	7	VAL
31	19	33	LYS
33	1b	21	ARG
33	1b	23	ARG
33	1b	35	GLU
33	1b	67	THR
33	1b	80	ILE
33	1b	94	ASN
33	1b	107	THR
33	1b	111	ARG
33	1b	112	VAL
33	1b	126	GLU
33	1b	127	ILE
33	1b	158	LEU
33	1b	164	VAL
33	1b	170	GLU
33	1b	179	LYS
33	1b	182	ILE
33	1b	185	ILE
33	1b	187	LEU
33	1b	192	SER
33	1b	196	LEU
33	1b	201	ILE
33	1b	208	ILE
33	1b	214	ILE
33	1b	215	LEU
33	1b	223	ILE
33	1b	233	SER
34	1c	3	ASN
34	1c	15	THR
34	1c	21	ARG
34	1c	70	VAL
34	1c	77	ILE
34	1c	85	ARG
34	1c	110	ASN
34	1c	112	SER
34	1c	115	LEU
34	1c	172	ARG
34	1c	178	LEU
34	1c	191	THR
34	1c	195	VAL
34	1c	196	LEU

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Mol	Chain	Res	Type
34	1c	206	GLU
35	1d	5	ILE
35	1d	19	LEU
35	1d	45	GLN
35	1d	49	ARG
35	1d	70	ILE
35	1d	76	ARG
35	1d	83	SER
35	1d	135	LEU
35	1d	144	ASP
35	1d	158	ILE
35	1d	170	VAL
35	1d	175	SER
35	1d	177	ASP
35	1d	178	VAL
35	1d	194	LEU
35	1d	205	GLU
36	1e	12	LEU
36	1e	31	LEU
36	1e	41	VAL
36	1e	81	GLU
36	1e	91	LEU
37	1f	40	VAL
37	1f	64	GLN
37	1f	72	VAL
37	1f	75	LEU
37	1f	81	ILE
37	1f	90	VAL
38	1g	12	LEU
38	1g	37	ASN
38	1g	51	GLN
38	1g	113	GLU
38	1g	114	ARG
39	1h	19	VAL
39	1h	26	VAL
39	1h	29	SER
39	1h	38	ILE
39	1h	51	VAL
39	1h	52	ASP
39	1h	82	HIS
39	1h	104	ARG
39	1h	133	LEU

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Mol	Chain	Res	Type
40	1i	9	ARG
40	1i	23	ASN
40	1i	42	ARG
40	1i	54	ASP
40	1i	64	THR
40	1i	65	VAL
40	1i	74	ILE
40	1i	83	ARG
40	1i	92	TYR
40	1i	108	VAL
40	1i	109	VAL
40	1i	128	ARG
41	1j	8	LEU
41	1j	38	ILE
41	1j	49	VAL
41	1j	96	ILE
42	1k	14	VAL
42	1k	16	SER
42	1k	31	THR
42	1k	33	THR
42	1k	48	ILE
42	1k	109	VAL
42	1k	112	THR
42	1k	114	VAL
42	1k	126	ARG
43	1l	6	THR
43	1l	27	LEU
43	1l	33	ARG
43	1l	40	VAL
43	1l	43	VAL
43	1l	58	VAL
43	1l	70	ILE
43	1l	83	VAL
43	1l	85	ILE
43	1l	89	ARG
43	1l	113	ARG
43	1l	117	ARG
44	1m	4	ILE
44	1m	14	ARG
44	1m	19	LEU
44	1m	49	THR
44	1m	102	ARG

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Mol	Chain	Res	Type
44	1m	103	THR
44	1m	109	THR
44	1m	117	VAL
44	1m	122	LYS
45	1n	3	ARG
45	1n	7	ILE
45	1n	13	THR
45	1n	18	VAL
45	1n	26	ARG
45	1n	33	VAL
46	1o	7	GLU
46	1o	21	ASP
46	1o	39	LEU
46	1o	56	LEU
46	1o	64	ARG
46	1o	66	LEU
46	1o	77	ARG
46	1o	87	ILE
47	1p	2	VAL
47	1p	5	ARG
47	1p	19	ILE
47	1p	53	VAL
47	1p	60	LEU
47	1p	61	SER
47	1p	67	THR
47	1p	69	THR
48	1q	6	LEU
48	1q	35	VAL
48	1q	39	SER
48	1q	62	SER
48	1q	93	GLN
49	1r	26	LEU
49	1r	31	LEU
49	1r	37	VAL
49	1r	46	GLU
49	1r	59	SER
49	1r	76	LEU
49	1r	85	LEU
50	1s	12	ASP
50	1s	41	VAL
50	1s	48	THR
50	1s	51	VAL

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Mol	Chain	Res	Type
50	1s	79	THR
51	1t	10	LEU
51	1t	13	LEU
51	1t	31	SER
51	1t	84	LEU
3	2D	3	VAL
3	2D	10	THR
3	2D	12	SER
3	2D	14	ARG
3	2D	24	ILE
3	2D	38	LYS
3	2D	61	LEU
3	2D	88	ARG
3	2D	94	LEU
3	2D	103	ARG
3	2D	106	ILE
3	2D	113	VAL
3	2D	115	GLN
3	2D	134	ARG
3	2D	136	ILE
3	2D	138	VAL
3	2D	142	VAL
3	2D	157	ARG
3	2D	169	GLU
3	2D	173	VAL
3	2D	176	ARG
3	2D	183	ARG
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	260	ARG
3	2D	276	LYS
4	2E	7	VAL
4	2E	9	VAL
4	2E	12	THR
4	2E	14	ILE
4	2E	21	VAL
4	2E	34	VAL
4	2E	38	THR
4	2E	45	THR

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Mol	Chain	Res	Type
4	2E	75	VAL
4	2E	78	LEU
4	2E	90	THR
4	2E	105	THR
4	2E	116	VAL
4	2E	119	ARG
4	2E	163	GLU
4	2E	175	VAL
4	2E	181	LEU
5	2F	20	LEU
5	2F	33	LEU
5	2F	50	SER
5	2F	74	ARG
5	2F	82	ILE
5	2F	88	VAL
5	2F	106	ARG
5	2F	110	LEU
5	2F	132	VAL
5	2F	158	THR
5	2F	165	ARG
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	3	LEU
6	2G	5	VAL
6	2G	14	GLU
6	2G	18	GLU
6	2G	28	VAL
6	2G	31	VAL
6	2G	43	LEU
6	2G	45	GLU
6	2G	49	ASP
6	2G	53	LEU
6	2G	60	LEU
6	2G	79	ASN
6	2G	91	ARG
6	2G	113	ARG
6	2G	115	ARG
6	2G	126	ASP
6	2G	135	LEU
6	2G	140	ILE

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Mol	Chain	Res	Type
6	2G	145	THR
6	2G	152	LEU
6	2G	159	VAL
6	2G	175	LEU
7	2H	3	ARG
7	2H	13	LYS
7	2H	37	VAL
7	2H	45	VAL
7	2H	56	SER
7	2H	57	ASP
7	2H	63	SER
7	2H	71	LEU
7	2H	84	SER
7	2H	88	LEU
7	2H	89	ILE
7	2H	121	ILE
7	2H	148	ILE
7	2H	160	LYS
7	2H	175	LYS
8	2I	15	VAL
8	2I	38	LEU
8	2I	50	ARG
8	2I	76	THR
8	2I	77	LEU
8	2I	92	VAL
8	2I	116	LEU
8	2I	121	LYS
8	2I	127	VAL
8	2I	129	THR
8	2I	140	LEU
8	2I	144	VAL
8	2I	145	VAL
9	2N	5	VAL
9	2N	14	VAL
9	2N	22	THR
9	2N	34	LEU
9	2N	38	HIS
9	2N	43	THR
9	2N	46	VAL
9	2N	58	ASP
9	2N	62	VAL
9	2N	85	ILE

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Mol	Chain	Res	Type
9	2N	99	LEU
9	2N	112	LEU
9	2N	120	LEU
9	2N	131	GLN
9	2N	140	VAL
10	2O	17	ARG
10	2O	18	LYS
10	2O	24	VAL
10	2O	35	VAL
10	2O	47	ILE
10	2O	69	ILE
10	2O	70	LYS
10	2O	106	LEU
11	2P	42	SER
11	2P	45	LEU
11	2P	56	SER
11	2P	83	VAL
11	2P	95	VAL
11	2P	99	LEU
11	2P	100	LEU
11	2P	112	LEU
11	2P	125	VAL
11	2P	148	LEU
12	2Q	1	MET
12	2Q	11	LYS
12	2Q	16	ARG
12	2Q	21	THR
12	2Q	38	GLU
12	2Q	55	VAL
12	2Q	75	THR
12	2Q	85	LYS
12	2Q	98	LYS
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	127	ILE
12	2Q	129	THR
12	2Q	133	ARG
12	2Q	139	GLU
13	2R	6	SER
13	2R	18	LEU
13	2R	24	GLN
13	2R	28	LEU

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Mol	Chain	Res	Type
13	2R	29	LEU
13	2R	65	LEU
13	2R	100	LEU
13	2R	111	LEU
13	2R	118	GLU
14	2S	4	LEU
14	2S	8	GLU
14	2S	19	LYS
14	2S	21	THR
14	2S	26	LEU
14	2S	27	SER
14	2S	36	TYR
14	2S	49	VAL
14	2S	53	SER
14	2S	58	LEU
14	2S	75	GLU
14	2S	78	LEU
14	2S	80	LEU
14	2S	110	LEU
15	2T	31	SER
15	2T	63	VAL
15	2T	89	VAL
15	2T	96	ARG
15	2T	108	ARG
16	2U	5	LYS
16	2U	30	LYS
16	2U	33	ARG
16	2U	55	ARG
16	2U	63	VAL
16	2U	74	LEU
17	2V	7	THR
17	2V	32	THR
17	2V	43	GLU
17	2V	46	VAL
17	2V	51	VAL
17	2V	61	VAL
17	2V	62	LEU
17	2V	72	VAL
17	2V	73	SER
17	2V	79	VAL
17	2V	82	ARG
17	2V	85	LYS

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Mol	Chain	Res	Type
17	2V	99	ILE
18	2W	11	ARG
18	2W	15	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	67	ASP
18	2W	96	ILE
18	2W	100	THR
18	2W	109	GLU
19	2X	1	MET
19	2X	56	THR
19	2X	57	LEU
20	2Y	3	VAL
20	2Y	7	VAL
20	2Y	19	LYS
20	2Y	39	VAL
20	2Y	40	GLU
20	2Y	49	VAL
20	2Y	72	VAL
20	2Y	97	ARG
21	2Z	5	LEU
21	2Z	18	LEU
21	2Z	24	LEU
21	2Z	33	LEU
21	2Z	42	VAL
21	2Z	47	VAL
21	2Z	52	SER
21	2Z	56	VAL
21	2Z	70	LEU
21	2Z	91	LEU
21	2Z	96	VAL
21	2Z	98	MET
21	2Z	124	ILE
21	2Z	129	SER
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	155	LEU
21	2Z	171	ILE
22	20	9	SER
22	20	10	THR
22	20	14	ARG

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Mol	Chain	Res	Type
22	20	67	VAL
22	20	68	GLU
23	21	4	VAL
23	21	58	ILE
23	21	59	THR
23	21	61	ARG
23	21	95	LEU
24	22	21	LEU
24	22	26	ARG
24	22	32	LEU
24	22	53	LEU
24	22	66	GLU
24	22	70	GLN
25	23	6	VAL
25	23	18	ASP
25	23	23	LEU
25	23	30	ARG
25	23	54	VAL
26	24	10	VAL
26	24	15	ILE
26	24	24	THR
26	24	34	GLU
26	24	49	PHE
26	24	50	VAL
26	24	59	PHE
26	24	63	TYR
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	48	GLU
27	25	58	LEU
28	26	9	LEU
28	26	23	THR
28	26	29	ASN
28	26	51	GLU
29	27	23	ARG
29	27	39	ARG
29	27	41	ARG
29	27	43	THR
30	28	13	ARG
30	28	14	VAL
30	28	23	VAL

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Mol	Chain	Res	Type
30	28	30	ARG
30	28	32	LEU
30	28	41	ILE
31	29	7	VAL
31	29	26	ILE
33	2b	7	VAL
33	2b	11	LEU
33	2b	47	THR
33	2b	48	MET
33	2b	49	GLU
33	2b	56	ARG
33	2b	67	THR
33	2b	87	ARG
33	2b	94	ASN
33	2b	102	LEU
33	2b	115	LEU
33	2b	126	GLU
33	2b	127	ILE
33	2b	140	HIS
33	2b	158	LEU
33	2b	178	ARG
33	2b	189	ASP
33	2b	195	ASP
33	2b	221	LEU
33	2b	229	VAL
33	2b	235	SER
34	2c	15	THR
34	2c	32	LEU
34	2c	47	LEU
34	2c	57	ILE
34	2c	70	VAL
34	2c	124	ILE
34	2c	152	ILE
34	2c	166	GLU
34	2c	178	LEU
34	2c	190	ARG
34	2c	198	VAL
35	2d	12	CYS
35	2d	31	CYS
35	2d	59	ARG
35	2d	83	SER
35	2d	107	ARG

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Mol	Chain	Res	Type
35	2d	108	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	150	GLU
35	2d	155	LEU
35	2d	158	ILE
35	2d	170	VAL
35	2d	175	SER
35	2d	178	VAL
35	2d	205	GLU
35	2d	208	SER
36	2e	13	ILE
36	2e	31	LEU
36	2e	32	VAL
36	2e	38	GLN
36	2e	41	VAL
36	2e	72	GLN
36	2e	81	GLU
36	2e	82	VAL
36	2e	90	VAL
36	2e	91	LEU
36	2e	111	GLU
37	2f	1	MET
37	2f	21	LEU
37	2f	40	VAL
37	2f	61	LEU
37	2f	69	GLU
37	2f	72	VAL
37	2f	75	LEU
38	2g	15	ASP
38	2g	16	LEU
38	2g	52	GLU
38	2g	79	ARG
38	2g	90	GLU
38	2g	98	SER
38	2g	104	LEU
38	2g	113	GLU
38	2g	120	ILE
38	2g	135	VAL
38	2g	138	LYS
39	2h	2	LEU
39	2h	39	LEU

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Mol	Chain	Res	Type
39	2h	51	VAL
39	2h	63	LEU
39	2h	104	ARG
39	2h	119	LEU
39	2h	127	LEU
40	2i	27	THR
40	2i	50	LEU
40	2i	53	VAL
40	2i	64	THR
40	2i	65	VAL
40	2i	86	VAL
40	2i	89	ASN
40	2i	93	ARG
40	2i	102	LEU
40	2i	108	VAL
40	2i	125	TYR
40	2i	128	ARG
41	2j	8	LEU
41	2j	16	LEU
41	2j	49	VAL
41	2j	98	ILE
41	2j	100	THR
42	2k	14	VAL
42	2k	30	VAL
42	2k	41	THR
42	2k	96	ARG
42	2k	114	VAL
43	2l	22	SER
43	2l	33	ARG
43	2l	36	VAL
43	2l	55	VAL
43	2l	83	VAL
43	2l	86	ARG
43	2l	97	ARG
43	2l	112	ASP
43	2l	113	ARG
43	2l	123	LYS
44	2m	15	VAL
44	2m	19	LEU
44	2m	27	LYS
44	2m	47	ASP
44	2m	77	ASN

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Mol	Chain	Res	Type
44	2m	106	ASN
45	2n	3	ARG
45	2n	6	LEU
45	2n	22	THR
45	2n	32	SER
45	2n	33	VAL
45	2n	56	VAL
46	2o	5	LYS
46	2o	39	LEU
46	2o	58	MET
46	2o	65	ARG
46	2o	87	ILE
47	2p	2	VAL
47	2p	9	PHE
47	2p	20	VAL
47	2p	21	VAL
47	2p	42	ARG
47	2p	45	THR
47	2p	53	VAL
47	2p	60	LEU
47	2p	62	VAL
47	2p	67	THR
47	2p	69	THR
48	2q	6	LEU
48	2q	7	THR
48	2q	24	GLU
48	2q	35	VAL
48	2q	56	VAL
48	2q	83	ASP
49	2r	25	THR
49	2r	26	LEU
49	2r	37	VAL
49	2r	46	GLU
49	2r	65	ILE
50	2s	5	LEU
50	2s	12	ASP
50	2s	33	THR
50	2s	41	VAL
50	2s	48	THR
50	2s	49	ILE
50	2s	65	ASN
50	2s	77	THR

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Mol	Chain	Res	Type
50	2s	83	HIS
51	2t	41	ILE
51	2t	43	LEU
51	2t	62	LEU
51	2t	71	THR
52	2u	7	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	126	GLN
4	1E	48	GLN
4	1E	180	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	58	GLN
7	1H	147	ASN
10	1O	89	ASN
12	1Q	12	GLN
12	1Q	57	HIS
13	1R	13	HIS
13	1R	71	GLN
13	1R	91	GLN
15	1T	90	GLN
16	1U	81	HIS
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
21	1Z	32	HIS
21	1Z	73	GLN
21	1Z	121	HIS
21	1Z	151	HIS
23	11	56	GLN
24	12	9	GLN
25	13	32	GLN
27	15	23	HIS
28	16	20	ASN
33	1b	40	HIS
33	1b	78	GLN

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Mol	Chain	Res	Type
33	1b	94	ASN
33	1b	140	HIS
34	1c	6	HIS
34	1c	37	GLN
34	1c	162	GLN
35	1d	42	GLN
35	1d	43	HIS
35	1d	77	ASN
35	1d	116	GLN
35	1d	123	HIS
36	1e	38	GLN
36	1e	78	HIS
37	1f	57	GLN
37	1f	73	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	51	GLN
38	1g	122	HIS
38	1g	148	ASN
40	1i	23	ASN
40	1i	124	GLN
41	1j	56	HIS
42	1k	62	GLN
43	1l	99	HIS
44	1m	40	ASN
46	1o	46	HIS
46	1o	50	HIS
47	1p	13	HIS
47	1p	14	ASN
47	1p	76	GLN
48	1q	26	GLN
48	1q	45	HIS
50	1s	23	ASN
50	1s	83	HIS
51	1t	42	GLN
51	1t	75	ASN
3	2D	87	ASN
3	2D	116	GLN
3	2D	143	HIS
4	2E	169	ASN
5	2F	69	HIS
5	2F	160	ASN

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Mol	Chain	Res	Type
6	2G	41	GLN
6	2G	132	ASN
9	2N	131	GLN
12	2Q	12	GLN
12	2Q	13	GLN
12	2Q	89	ASN
13	2R	13	HIS
13	2R	71	GLN
14	2S	38	GLN
16	2U	94	ASN
18	2W	61	ASN
19	2X	31	HIS
19	2X	82	GLN
21	2Z	73	GLN
22	20	35	ASN
23	21	56	GLN
30	28	35	GLN
30	28	43	GLN
31	29	20	HIS
33	2b	19	HIS
33	2b	40	HIS
33	2b	78	GLN
33	2b	94	ASN
34	2c	37	GLN
34	2c	108	ASN
34	2c	176	HIS
34	2c	181	ASN
35	2d	77	ASN
35	2d	116	GLN
35	2d	125	HIS
35	2d	199	ASN
36	2e	38	GLN
36	2e	141	GLN
37	2f	73	ASN
38	2g	28	ASN
38	2g	148	ASN
40	2i	3	GLN
40	2i	58	HIS
40	2i	124	GLN
41	2j	13	HIS
44	2m	40	ASN
44	2m	62	ASN

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Mol	Chain	Res	Type
46	2o	28	GLN
46	2o	50	HIS
46	2o	62	GLN
50	2s	23	ASN
50	2s	47	HIS
50	2s	56	GLN
50	2s	69	HIS
51	2t	16	HIS
51	2t	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	459 (16%)	29 (1%)
1	2A	2791/2915 (95%)	494 (17%)	23 (0%)
2	1B	120/121 (99%)	9 (7%)	1 (0%)
2	2B	118/121 (97%)	33 (27%)	0
32	1a	1497/1521 (98%)	237 (15%)	0
32	2a	1501/1521 (98%)	290 (19%)	0
53	1v	12/24 (50%)	1 (8%)	0
53	2v	12/24 (50%)	4 (33%)	0
54	1w	72/76 (94%)	21 (29%)	0
54	1y	72/76 (94%)	24 (33%)	0
54	2w	69/76 (90%)	24 (34%)	0
54	2y	70/76 (92%)	24 (34%)	0
55	1x	75/77 (97%)	9 (12%)	0
55	2x	75/77 (97%)	14 (18%)	0
All	All	9348/9620 (97%)	1643 (17%)	53 (0%)

All (1643) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	50	G
1	1A	70	A
1	1A	71	U
1	1A	73	A

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Mol	Chain	Res	Type
1	1A	74	G
1	1A	83	A
1	1A	90	A
1	1A	116	A
1	1A	117	A
1	1A	118	U
1	1A	123	G
1	1A	139	A
1	1A	155	C
1	1A	171	A
1	1A	185	A
1	1A	188	A
1	1A	194	G
1	1A	203	G
1	1A	205	A
1	1A	211	A
1	1A	212	A
1	1A	214	A
1	1A	217	A
1	1A	218	A
1	1A	237	G
1	1A	258	U
1	1A	271	U
1	1A	272	U
1	1A	273	G
1	1A	289	G
1	1A	296	U
1	1A	303	C
1	1A	335	A
1	1A	353	G
1	1A	354	A
1	1A	369	A
1	1A	376	G
1	1A	387	G
1	1A	388	A
1	1A	389	G
1	1A	407	U
1	1A	413	G
1	1A	423	G
1	1A	432	U
1	1A	438	G
1	1A	439	A

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Mol	Chain	Res	Type
1	1A	455	A
1	1A	470	C
1	1A	474	U
1	1A	483	A
1	1A	507	G
1	1A	526	A
1	1A	529	U
1	1A	530	A
1	1A	534	C
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	586	G
1	1A	596	G
1	1A	598	A
1	1A	609	A
1	1A	616	G
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	639	G
1	1A	641	G
1	1A	644	G
1	1A	652	A
1	1A	662	A
1	1A	671	A
1	1A	693	G
1	1A	697	C
1	1A	716	G
1	1A	733	G
1	1A	761	U
1	1A	764	G
1	1A	777	C
1	1A	811	A
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	830	A
1	1A	831	A

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Mol	Chain	Res	Type
1	1A	832	G
1	1A	839	G
1	1A	852	G
1	1A	859	C
1	1A	866	A
1	1A	874	U
1	1A	875	U
1	1A	879	G
1	1A	902	G
1	1A	906	G
1	1A	913	A
1	1A	926	G
1	1A	927	G
1	1A	931	C
1	1A	932	C
1	1A	933	C
1	1A	934	A
1	1A	935	C
1	1A	936	C
1	1A	937	A
1	1A	938	G
1	1A	942	A
1	1A	943	C
1	1A	944	C
1	1A	946	A
1	1A	953	U
1	1A	956	A
1	1A	961	C
1	1A	976	G
1	1A	977	G
1	1A	983	G
1	1A	990	A
1	1A	991	G
1	1A	998	A
1	1A	1003	U
1	1A	1006	C
1	1A	1019	G
1	1A	1020	C
1	1A	1021	G
1	1A	1029	A
1	1A	1031	C
1	1A	1042	A

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Mol	Chain	Res	Type
1	1A	1058	U
1	1A	1059	C
1	1A	1071	G
1	1A	1072	U
1	1A	1073	A
1	1A	1079	U
1	1A	1083	G
1	1A	1084	C
1	1A	1090	G
1	1A	1091	A
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1100	A
1	1A	1101	G
1	1A	1104	G
1	1A	1109	G
1	1A	1114	G
1	1A	1116	A
1	1A	1117	G
1	1A	1119	A
1	1A	1120	G
1	1A	1121	C
1	1A	1122	C
1	1A	1124	U
1	1A	1125	C
1	1A	1127	U
1	1A	1132	A
1	1A	1134	A
1	1A	1135	G
1	1A	1136	U
1	1A	1140	U
1	1A	1142	A
1	1A	1147	U
1	1A	1149	A
1	1A	1154	U
1	1A	1156	G
1	1A	1157	A
1	1A	1158	G
1	1A	1162	C
1	1A	1175	A
1	1A	1176	U

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Mol	Chain	Res	Type
1	1A	1180	C
1	1A	1181	G
1	1A	1187	U
1	1A	1201	A
1	1A	1216	G
1	1A	1217	G
1	1A	1218	G
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1222	A
1	1A	1223	C
1	1A	1263	C
1	1A	1275	G
1	1A	1282	G
1	1A	1283	A
1	1A	1296	G
1	1A	1299	A
1	1A	1302	G
1	1A	1314	A
1	1A	1317	G
1	1A	1318	A
1	1A	1319	U
1	1A	1327	G
1	1A	1346	U
1	1A	1347	A
1	1A	1366	C
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1430	A
1	1A	1431	G
1	1A	1441	A
1	1A	1442	U
1	1A	1462	G
1	1A	1463	C
1	1A	1466	U
1	1A	1467	G
1	1A	1474	C
1	1A	1475	G
1	1A	1491	A

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Mol	Chain	Res	Type
1	1A	1497	G
1	1A	1502	G
1	1A	1514	C
1	1A	1529	G
1	1A	1539	C
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1562	U
1	1A	1605	A
1	1A	1606	G
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1627	A
1	1A	1628	G
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1655	A
1	1A	1656	A
1	1A	1695	C
1	1A	1721	G
1	1A	1743	G
1	1A	1747	A
1	1A	1748	A
1	1A	1750	G
1	1A	1764	G
1	1A	1767	A
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1807	G
1	1A	1811	A
1	1A	1813	C
1	1A	1822	A
1	1A	1828	C
1	1A	1831	C
1	1A	1832	G
1	1A	1833	A
1	1A	1843	A

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Mol	Chain	Res	Type
1	1A	1847	G
1	1A	1860	A
1	1A	1870	G
1	1A	1878	A
1	1A	1892	G
1	1A	1899	A
1	1A	1900	G
1	1A	1911	A
1	1A	1922	A
1	1A	1928	G
1	1A	1935	A
1	1A	1940	A
1	1A	1941	A
1	1A	1951	G
1	1A	1952	G
1	1A	1956	C
1	1A	1959	A
1	1A	1960	A
1	1A	1977	U
1	1A	1985	U
1	1A	1988	A
1	1A	1989	C
1	1A	1992	A
1	1A	1993	A
1	1A	1994	A
1	1A	2005	C
1	1A	2014	G
1	1A	2015	U
1	1A	2019	G
1	1A	2042	A
1	1A	2045	G
1	1A	2053	A
1	1A	2055	A
1	1A	2061	C
1	1A	2065	C
1	1A	2071	G
1	1A	2074	G
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2084	A

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Mol	Chain	Res	Type
1	1A	2091	G
1	1A	2115	G
1	1A	2120	U
1	1A	2128	G
1	1A	2132	G
1	1A	2135	U
1	1A	2136	A
1	1A	2138	G
1	1A	2143	G
1	1A	2148	A
1	1A	2149	G
1	1A	2151	C
1	1A	2152	U
1	1A	2153	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2157	A
1	1A	2158	C
1	1A	2162	C
1	1A	2164	C
1	1A	2166	U
1	1A	2168	C
1	1A	2169	G
1	1A	2170	G
1	1A	2172	U
1	1A	2173	G
1	1A	2178	G
1	1A	2179	G
1	1A	2180	A
1	1A	2181	G
1	1A	2184	G
1	1A	2188	G
1	1A	2189	U
1	1A	2193	A
1	1A	2194	U
1	1A	2195	A
1	1A	2196	C
1	1A	2200	C
1	1A	2204	G
1	1A	2206	G
1	1A	2214	G

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Mol	Chain	Res	Type
1	1A	2220	A
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2230	U
1	1A	2237	A
1	1A	2247	G
1	1A	2250	G
1	1A	2251	G
1	1A	2280	A
1	1A	2291	G
1	1A	2292	G
1	1A	2295	C
1	1A	2298	A
1	1A	2299	A
1	1A	2306	C
1	1A	2308	U
1	1A	2317	A
1	1A	2319	G
1	1A	2320	G
1	1A	2324	U
1	1A	2326	C
1	1A	2332	A
1	1A	2333	G
1	1A	2334	A
1	1A	2337	G
1	1A	2346	G
1	1A	2348	A
1	1A	2359	C
1	1A	2362	C
1	1A	2365	G
1	1A	2366	G
1	1A	2373	A
1	1A	2389	A
1	1A	2391	G
1	1A	2395	G
1	1A	2397	C
1	1A	2414	C
1	1A	2418	U
1	1A	2419	G
1	1A	2422	G
1	1A	2436	C

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Mol	Chain	Res	Type
1	1A	2437	A
1	1A	2440	G
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U
1	1A	2446	A
1	1A	2447	A
1	1A	2451	A
1	1A	2452	C
1	1A	2453	C
1	1A	2460	A
1	1A	2483	C
1	1A	2488	A
1	1A	2493	G
1	1A	2502	G
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2532	C
1	1A	2541	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	C
1	1A	2586	G
1	1A	2594	G
1	1A	2597	U
1	1A	2614	A
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2640	C
1	1A	2641	A
1	1A	2642	G
1	1A	2666	A
1	1A	2701	U
1	1A	2702	C
1	1A	2714	U
1	1A	2715	C
1	1A	2725	A
1	1A	2726	A

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Mol	Chain	Res	Type
1	1A	2727	G
1	1A	2739	U
1	1A	2746	A
1	1A	2753	A
1	1A	2777	A
1	1A	2778	A
1	1A	2779	G
1	1A	2782	C
1	1A	2791	A
1	1A	2793	G
1	1A	2802	C
1	1A	2803	A
1	1A	2804	C
1	1A	2806	G
1	1A	2807	C
1	1A	2813	G
1	1A	2814	C
1	1A	2828	G
1	1A	2830	A
1	1A	2831	A
1	1A	2843	G
1	1A	2845	A
1	1A	2847	G
1	1A	2871	G
1	1A	2882	G
1	1A	2883	A
1	1A	2890	C
1	1A	2899	C
1	1A	2901	A
1	1A	2903	G
2	1B	2	C
2	1B	24	G
2	1B	35	U
2	1B	42	C
2	1B	56	G
2	1B	67	G
2	1B	73	A
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A

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Mol	Chain	Res	Type
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	54	C
32	1a	61	G
32	1a	73	G
32	1a	79	G
32	1a	91	C
32	1a	98	G
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	163	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(J)	G
32	1a	195	A
32	1a	197	A
32	1a	199	G
32	1a	201	C
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	217	C
32	1a	243	A
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	306	G
32	1a	328	C
32	1a	332	G

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Mol	Chain	Res	Type
32	1a	342	C
32	1a	344	A
32	1a	345	C
32	1a	347	G
32	1a	348	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	430	A
32	1a	439	A
32	1a	441	A
32	1a	442	C
32	1a	452	A
32	1a	461	A
32	1a	485	G
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	519	C
32	1a	527	7MG
32	1a	531	U
32	1a	532	A
32	1a	536	C
32	1a	544	G
32	1a	547	A
32	1a	559	A

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Mol	Chain	Res	Type
32	1a	561	U
32	1a	562	C
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	592	G
32	1a	596	C
32	1a	630	G
32	1a	653	A
32	1a	659	U
32	1a	665	A
32	1a	673	G
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	721	G
32	1a	723	U
32	1a	731	G
32	1a	747	C
32	1a	749	C
32	1a	753	A
32	1a	755	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	859	A
32	1a	870	U
32	1a	874	G
32	1a	885	G
32	1a	902	G
32	1a	914	A

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Mol	Chain	Res	Type
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	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1020	U
32	1a	1022	G
32	1a	1023	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1039	C
32	1a	1043	C
32	1a	1045	C
32	1a	1046	A
32	1a	1053	G
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G

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Mol	Chain	Res	Type
32	1a	1095	U
32	1a	1096	C
32	1a	1101	A
32	1a	1108	G
32	1a	1125	U
32	1a	1132	C
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1141	C
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1201	A
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1270	C
32	1a	1273	G
32	1a	1278	U
32	1a	1279	A
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	1322	C
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G

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Mol	Chain	Res	Type
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1378	C
32	1a	1397	C
32	1a	1406	U
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1456	G
32	1a	1487	G
32	1a	1492	A
32	1a	1493	A
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1517	G
32	1a	1519	MA6
32	1a	1529	G
32	1a	1530	G
32	1a	1532	U
53	1v	13	A
54	1w	2	C
54	1w	6	G
54	1w	8	4SU
54	1w	14	A
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	23	A
54	1w	24	G
54	1w	45	U
54	1w	46	7MG
54	1w	47	U
54	1w	48	C
54	1w	50	U
54	1w	62	C
54	1w	64	A
54	1w	68	C

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Mol	Chain	Res	Type
54	1w	69	G
54	1w	70	G
54	1w	73	A
54	1w	74	C
55	1x	6	G
55	1x	9	G
55	1x	14	A
55	1x	18	G
55	1x	21	A
55	1x	47	U
55	1x	61	C
55	1x	69	C
55	1x	76	A
54	1y	5	G
54	1y	6	G
54	1y	8	4SU
54	1y	9	A
54	1y	13	C
54	1y	19	G
54	1y	20	U
54	1y	21	A
54	1y	23	A
54	1y	35	A
54	1y	44	G
54	1y	45	U
54	1y	46	7MG
54	1y	47	U
54	1y	48	C
54	1y	49	C
54	1y	53	G
54	1y	54	5MU
54	1y	56	C
54	1y	59	U
54	1y	61	C
54	1y	65	G
54	1y	69	G
54	1y	70	G
1	2A	12	U
1	2A	15	G
1	2A	35	G
1	2A	36	G
1	2A	45	C

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Mol	Chain	Res	Type
1	2A	55	G
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	79	G
1	2A	84	A
1	2A	90	U
1	2A	94	C
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	125	G
1	2A	131	G
1	2A	154(A)	C
1	2A	157	U
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	226	G
1	2A	228	A
1	2A	229	A
1	2A	232	G
1	2A	233	A
1	2A	248	G
1	2A	249	C
1	2A	250	G
1	2A	271(J)	C
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G

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Mol	Chain	Res	Type
1	2A	272(I)	U
1	2A	272(J)	C
1	2A	274	G
1	2A	277	C
1	2A	278	A
1	2A	280	C
1	2A	294	A
1	2A	303	U
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	329	G
1	2A	330	A
1	2A	342	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	363(B)	G
1	2A	363(D)	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	406	G
1	2A	411	G
1	2A	412	A
1	2A	422	A
1	2A	435	C
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	459	U
1	2A	481	G
1	2A	498	G
1	2A	501	A
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	528	A
1	2A	529	A
1	2A	531	C

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Mol	Chain	Res	Type
1	2A	532	A
1	2A	533	G
1	2A	563	G
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	599	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(A)	U
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	651	G
1	2A	652(B)	A
1	2A	669	G
1	2A	686	G
1	2A	709	U
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	771	G
1	2A	774	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	857	C

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Mol	Chain	Res	Type
1	2A	859	G
1	2A	866	A
1	2A	867	C
1	2A	869	G
1	2A	874	G
1	2A	875	G
1	2A	878	A
1	2A	879	G
1	2A	880	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	893	C
1	2A	894	C
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	933	A
1	2A	941	A
1	2A	944	G
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	958	U
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	982	C
1	2A	983	A
1	2A	990	A
1	2A	996	A
1	2A	997	G
1	2A	998	C
1	2A	1005	C

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Mol	Chain	Res	Type
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1043	C
1	2A	1114	G
1	2A	1116	C
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142(A)	A
1	2A	1169	G
1	2A	1170	G
1	2A	1171	G
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1237	A
1	2A	1250	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1284	A
1	2A	1300	U
1	2A	1301	A
1	2A	1306	C
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A

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Mol	Chain	Res	Type
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1411	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1435	G
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1455	G
1	2A	1460	A
1	2A	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	1541	G
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1559	G
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A

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Mol	Chain	Res	Type
1	2A	1582	C
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1616	A
1	2A	1639	U
1	2A	1640	C
1	2A	1648	C
1	2A	1654	A
1	2A	1663	C
1	2A	1664	A
1	2A	1669	A
1	2A	1670	C
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1739	U
1	2A	1740	G
1	2A	1746	G
1	2A	1756	G
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1812	A
1	2A	1816	G
1	2A	1819	A
1	2A	1835	G
1	2A	1839	G

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Mol	Chain	Res	Type
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1896	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1936	A
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1981	A
1	2A	1983	C
1	2A	1984	G
1	2A	1993	U
1	2A	1996	C
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2027	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2096	U
1	2A	2105	C
1	2A	2110	G

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Mol	Chain	Res	Type
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2124	G
1	2A	2126	A
1	2A	2127	G
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
1	2A	2146	C
1	2A	2150	U
1	2A	2151	G
1	2A	2153	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2159	G
1	2A	2161	C
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2172	U
1	2A	2174	C
1	2A	2178	C
1	2A	2182	G
1	2A	2185	C
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G

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Mol	Chain	Res	Type
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2236	C
1	2A	2238	G
1	2A	2239	G
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2288	A
1	2A	2304	G
1	2A	2305	A
1	2A	2308	G
1	2A	2309	A
1	2A	2311	A
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2327	A
1	2A	2334	G
1	2A	2336	A
1	2A	2346	A
1	2A	2347	C
1	2A	2350	C
1	2A	2372	G
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2402	C
1	2A	2403	C
1	2A	2406	U
1	2A	2410	G
1	2A	2413	G
1	2A	2425	A
1	2A	2428	G
1	2A	2429	G
1	2A	2430	A
1	2A	2434	A

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Mol	Chain	Res	Type
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2477	C
1	2A	2491	U
1	2A	2494	G
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2541	A
1	2A	2549	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2574	G
1	2A	2578	G
1	2A	2585	U
1	2A	2592	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	2669	G
1	2A	2689	U
1	2A	2690	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

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Mol	Chain	Res	Type
1	2A	2733	A
1	2A	2748	A
1	2A	2751	G
1	2A	2761	G
1	2A	2764	A
1	2A	2765	A
1	2A	2778	A
1	2A	2779	U
1	2A	2780	G
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2834	G
1	2A	2835	A
1	2A	2837	G
1	2A	2839	G
1	2A	2872	G
1	2A	2873	A
1	2A	2879	C
1	2A	2880	C
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	5	C
2	2B	7	G
2	2B	8	U
2	2B	9	G
2	2B	13	A
2	2B	19	G
2	2B	20	C
2	2B	25	A
2	2B	30	C
2	2B	31	C
2	2B	34	U
2	2B	42	C
2	2B	53	A
2	2B	56	G

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Mol	Chain	Res	Type
2	2B	58	A
2	2B	65	C
2	2B	66	A
2	2B	67	G
2	2B	69	G
2	2B	72	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	88	C
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	114	C
2	2B	116	G
2	2B	119	G
2	2B	120	A
32	2a	9	G
32	2a	22	G
32	2a	31	G
32	2a	32	A
32	2a	39	G
32	2a	44	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
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	98	G
32	2a	101	A
32	2a	105	G
32	2a	115	G
32	2a	116	A
32	2a	120	A
32	2a	121	C
32	2a	131	C

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Mol	Chain	Res	Type
32	2a	144	G
32	2a	163	C
32	2a	174	C
32	2a	180	U
32	2a	182	U
32	2a	184	G
32	2a	188	C
32	2a	189(A)	C
32	2a	189(F)	U
32	2a	189(G)	G
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	281	G
32	2a	289	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	350	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	384	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	414	A
32	2a	421	U
32	2a	423	G

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Mol	Chain	Res	Type
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	521	G
32	2a	531	U
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	560	U
32	2a	561	U
32	2a	562	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	601	C
32	2a	619	U
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	665	A
32	2a	671	G
32	2a	672	U
32	2a	687	A
32	2a	688	G
32	2a	695	A

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Mol	Chain	Res	Type
32	2a	702	A
32	2a	703	G
32	2a	708	C
32	2a	720	C
32	2a	721	G
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	734	G
32	2a	749	C
32	2a	755	G
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	805	C
32	2a	816	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	834	C
32	2a	840	C
32	2a	841	U
32	2a	859	A
32	2a	884	U
32	2a	885	G
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	935	A
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

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Mol	Chain	Res	Type
32	2a	982	U
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	995	C
32	2a	996	A
32	2a	997	U
32	2a	999	C
32	2a	1001	A
32	2a	1001(A)	G
32	2a	1002	G
32	2a	1003	G
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1007	C
32	2a	1009	G
32	2a	1011	G
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1032	G
32	2a	1033	G
32	2a	1035	A
32	2a	1036	G
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1051	C
32	2a	1054	C
32	2a	1055	A
32	2a	1056	U
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G

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Mol	Chain	Res	Type
32	2a	1071	C
32	2a	1077	G
32	2a	1081	G
32	2a	1086	U
32	2a	1087	G
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1113	C
32	2a	1117	G
32	2a	1121	U
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1143	G
32	2a	1146	A
32	2a	1152	A
32	2a	1157	A
32	2a	1158	C
32	2a	1159	U
32	2a	1172	C
32	2a	1174	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1200	C
32	2a	1201	A
32	2a	1202	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1214	C
32	2a	1227	A

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Mol	Chain	Res	Type
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1246	C
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1261	A
32	2a	1267	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1276	G
32	2a	1277	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1287	A
32	2a	1301	U
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1319	A
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1349	A
32	2a	1358	U
32	2a	1363	C
32	2a	1368	G
32	2a	1370	G
32	2a	1388	C
32	2a	1400	5MC
32	2a	1404	5MC
32	2a	1406	U
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A

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Mol	Chain	Res	Type
32	2a	1452	C
32	2a	1456	G
32	2a	1492	A
32	2a	1499	A
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1519	MA6
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	13	A
53	2v	14	A
53	2v	15	A
53	2v	24	A
54	2w	3	C
54	2w	4	C
54	2w	5	G
54	2w	7	A
54	2w	9	A
54	2w	11	C
54	2w	13	C
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	29	G
54	2w	34	G
54	2w	40	C
54	2w	46	7MG
54	2w	47	U
54	2w	48	C
54	2w	50	U
54	2w	56	C
54	2w	62	C
54	2w	63	G
54	2w	64	A
54	2w	68	C
54	2w	69	G
54	2w	74	C

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Mol	Chain	Res	Type
55	2x	9	G
55	2x	13	C
55	2x	18	G
55	2x	21	A
55	2x	42	G
55	2x	43	A
55	2x	47	U
55	2x	48	C
55	2x	52	G
55	2x	53	G
55	2x	65	C
55	2x	67	C
55	2x	68	C
55	2x	76	A
54	2y	15	G
54	2y	19	G
54	2y	23	A
54	2y	24	G
54	2y	25	C
54	2y	27	G
54	2y	34	G
54	2y	37	MIA
54	2y	45	U
54	2y	49	C
54	2y	52	G
54	2y	53	G
54	2y	55	PSU
54	2y	56	C
54	2y	57	G
54	2y	58	A
54	2y	59	U
54	2y	61	C
54	2y	62	C
54	2y	63	G
54	2y	65	G
54	2y	69	G
54	2y	70	G
54	2y	73	A

All (53) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	1A	115	G
1	1A	184	A
1	1A	271	U
1	1A	302	A
1	1A	509	A
1	1A	572	A
1	1A	913	A
1	1A	941	U
1	1A	1065	U
1	1A	1067	A
1	1A	1093	G
1	1A	1124	U
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1466	U
1	1A	1554	A
1	1A	1654	A
1	1A	2014	G
1	1A	2156	A
1	1A	2180	A
1	1A	2192	A
1	1A	2203	G
1	1A	2205	C
1	1A	2418	U
1	1A	2442	A
1	1A	2641	A
1	1A	2701	U
2	1B	1	U
1	2A	34	C
1	2A	195	A
1	2A	228	A
1	2A	266	G
1	2A	271(K)	U
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	752	A
1	2A	827	U
1	2A	856	C

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Mol	Chain	Res	Type
1	2A	900	A
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1653	G
1	2A	1695	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A
1	2A	2126	A
1	2A	2689	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	PSU	1A	2617	1	18,21,22	1.40	4 (22%)	21,30,33	1.95	4 (19%)
32	5MC	1a	1400	32	19,22,23	1.76	3 (15%)	26,32,35	1.20	3 (11%)
54	PSU	2w	39	54	18,21,22	1.43	2 (11%)	21,30,33	1.73	4 (19%)
55	5MC	1x	32	55	19,22,23	1.71	3 (15%)	26,32,35	1.12	3 (11%)
32	MA6	2a	1518	32	23,26,27	1.58	4 (17%)	33,38,41	2.28	10 (30%)
1	5MC	1A	1984	1	19,22,23	1.54	3 (15%)	26,32,35	1.22	3 (11%)
1	5MC	2A	1942	1	19,22,23	1.66	3 (15%)	26,32,35	1.08	2 (7%)
54	PSU	1y	55	54	18,21,22	1.34	2 (11%)	21,30,33	2.11	5 (23%)
32	4OC	1a	1402	32,56	20,23,24	0.75	0	25,32,35	0.92	1 (4%)
1	5MU	1A	1961	1,56	19,22,23	1.36	4 (21%)	27,32,35	2.20	6 (22%)
32	5MC	1a	1404	32,56	19,22,23	1.78	3 (15%)	26,32,35	1.10	3 (11%)
32	2MG	1a	1207	32	23,26,27	1.24	3 (13%)	33,38,41	2.25	9 (27%)
1	4OC	2A	1920	1	19,22,24	0.78	0	25,31,35	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MA	2A	2503	1,56	22,25,26	1.37	5 (22%)	32,37,40	2.38	9 (28%)
32	5MC	2a	1407	32	19,22,23	1.50	2 (10%)	26,32,35	1.27	3 (11%)
32	5MC	1a	967	32	19,22,23	1.72	3 (15%)	26,32,35	1.16	3 (11%)
1	PSU	2A	1917	1,56	18,21,22	1.41	2 (11%)	21,30,33	2.09	4 (19%)
55	5MU	1x	54	55	19,22,23	1.43	6 (31%)	27,32,35	1.93	7 (25%)
32	M2G	1a	966	32	24,27,28	1.30	3 (12%)	33,40,43	1.89	6 (18%)
54	PSU	2y	39	54	18,21,22	1.37	2 (11%)	21,30,33	1.91	3 (14%)
32	7MG	1a	527	32	23,26,27	1.44	4 (17%)	27,39,42	2.57	5 (18%)
1	PSU	1A	1933	1	18,21,22	1.40	2 (11%)	21,30,33	2.15	3 (14%)
1	5MU	1A	1937	1	19,22,23	1.38	6 (31%)	27,32,35	2.23	6 (22%)
54	PSU	1w	55	54	18,21,22	1.38	2 (11%)	21,30,33	2.04	3 (14%)
54	5MU	2y	54	54	19,22,23	1.51	4 (21%)	27,32,35	2.13	9 (33%)
32	UR3	2a	1498	32	19,22,23	1.06	1 (5%)	26,32,35	1.79	3 (11%)
54	5MU	1y	54	54	19,22,23	1.57	6 (31%)	27,32,35	1.99	6 (22%)
54	5MU	1w	54	54	19,22,23	1.48	5 (26%)	27,32,35	1.85	6 (22%)
54	PSU	2y	32	54	18,21,22	1.34	2 (11%)	21,30,33	1.94	4 (19%)
54	PSU	1y	32	54	18,21,22	1.41	3 (16%)	21,30,33	1.87	4 (19%)
54	4SU	1w	8	54	18,21,22	1.71	4 (22%)	25,30,33	2.11	4 (16%)
54	PSU	1w	32	54	18,21,22	1.36	2 (11%)	21,30,33	1.97	3 (14%)
55	5MU	2x	54	55	19,22,23	1.42	5 (26%)	27,32,35	2.31	6 (22%)
54	7MG	1y	46	54	23,26,27	1.34	4 (17%)	27,39,42	2.59	6 (22%)
54	PSU	2w	55	54	18,21,22	1.38	2 (11%)	21,30,33	2.14	4 (19%)
54	PSU	1y	39	54	18,21,22	1.42	2 (11%)	21,30,33	1.85	4 (19%)
54	7MG	1w	46	54	23,26,27	1.43	4 (17%)	27,39,42	2.50	5 (18%)
55	4SU	1x	8	55	18,21,22	2.12	4 (22%)	25,30,33	1.43	5 (20%)
32	4OC	2a	1402	32,56	20,23,24	0.78	0	25,32,35	1.18	2 (8%)
54	PSU	1w	39	54	18,21,22	1.36	2 (11%)	21,30,33	1.96	3 (14%)
1	OMG	2A	2251	1,55	23,26,27	1.25	3 (13%)	32,38,41	2.06	6 (18%)
43	0TD	1l	92	43	8,9,10	4.60	1 (12%)	6,11,13	3.70	3 (50%)
54	PSU	2y	55	54	18,21,22	1.31	3 (16%)	21,30,33	1.90	5 (23%)
1	5MU	2A	1915	1	19,22,23	1.52	5 (26%)	27,32,35	2.14	8 (29%)
1	PSU	1A	1939	1	18,21,22	1.45	4 (22%)	21,30,33	2.07	3 (14%)
32	PSU	1a	516	32,56	18,21,22	1.33	2 (11%)	21,30,33	2.02	5 (23%)
1	4OC	1A	1942	1,56	19,22,24	0.80	0	25,31,35	0.88	0
43	0TD	2l	92	43	8,9,10	4.48	1 (12%)	6,11,13	1.74	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	PSU	2x	55	55	18,21,22	1.35	2 (11%)	21,30,33	1.99	4 (19%)
32	MA6	2a	1519	32	23,26,27	1.59	4 (17%)	33,38,41	2.24	11 (33%)
32	MA6	1a	1519	32	23,26,27	1.55	4 (17%)	33,38,41	2.30	12 (36%)
32	5MC	1a	1407	32	19,22,23	1.41	3 (15%)	26,32,35	1.20	2 (7%)
1	5MC	2A	1962	1,56	19,22,23	1.50	3 (15%)	26,32,35	1.20	2 (7%)
54	MIA	1y	37	54	21,24,32	1.61	3 (14%)	30,35,47	2.01	10 (33%)
1	5MU	2A	1939	1	19,22,23	1.43	5 (26%)	27,32,35	2.37	6 (22%)
55	5MC	2x	32	55	19,22,23	1.78	2 (10%)	26,32,35	1.16	3 (11%)
54	4SU	2y	8	54	18,21,22	1.88	5 (27%)	25,30,33	2.27	5 (20%)
32	UR3	1a	1498	32	19,22,23	1.09	1 (5%)	26,32,35	1.83	3 (11%)
54	MIA	2w	37	54	24,27,32	2.11	5 (20%)	32,39,47	2.37	11 (34%)
54	MIA	1w	37	54	28,31,32	2.42	7 (25%)	38,44,47	2.75	14 (36%)
54	7MG	2w	46	54	23,26,27	1.34	5 (21%)	27,39,42	2.66	7 (25%)
55	4SU	2x	8	55,56	18,21,22	1.98	4 (22%)	25,30,33	1.43	4 (16%)
1	OMG	1A	2263	1,55,56	23,26,27	1.24	3 (13%)	32,38,41	2.05	5 (15%)
54	7MG	2y	46	54	23,26,27	1.47	4 (17%)	27,39,42	2.79	6 (22%)
54	MIA	2y	37	54,32	21,24,32	1.60	4 (19%)	30,35,47	2.10	9 (30%)
1	5MC	1A	1964	1	19,22,23	1.44	3 (15%)	26,32,35	1.16	3 (11%)
54	4SU	1y	8	54	18,21,22	1.71	3 (16%)	25,30,33	1.91	6 (24%)
32	M2G	2a	966	32	24,27,28	1.32	3 (12%)	33,40,43	1.85	6 (18%)
1	2MU	2A	2552	1,56	19,22,24	1.23	2 (10%)	25,31,36	1.92	5 (20%)
32	7MG	2a	527	32	23,26,27	1.36	3 (13%)	27,39,42	2.62	6 (22%)
32	5MC	2a	1404	32	19,22,23	1.82	3 (15%)	26,32,35	1.20	3 (11%)
32	2MG	2a	1207	32	23,26,27	1.24	2 (8%)	33,38,41	2.18	7 (21%)
1	PSU	2A	2605	1	18,21,22	1.34	3 (16%)	21,30,33	2.12	4 (19%)
32	PSU	2a	516	32	18,21,22	1.35	2 (11%)	21,30,33	1.93	5 (23%)
1	2MA	1A	2515	1,56	22,25,26	1.46	4 (18%)	32,37,40	2.42	8 (25%)
32	MA6	1a	1518	32	23,26,27	1.49	5 (21%)	33,38,41	2.28	13 (39%)
54	PSU	2w	32	54	18,21,22	1.36	2 (11%)	21,30,33	1.94	3 (14%)
1	PSU	2A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	1.95	3 (14%)
55	PSU	1x	55	55	18,21,22	1.29	2 (11%)	21,30,33	2.01	4 (19%)
54	4SU	2w	8	54	18,21,22	1.74	4 (22%)	25,30,33	2.37	5 (20%)
32	5MC	2a	967	32	19,22,23	1.75	3 (15%)	26,32,35	1.19	3 (11%)
1	2MU	1A	2564	1,56	19,22,24	1.21	2 (10%)	25,31,36	2.16	6 (24%)
54	5MU	2w	54	54	19,22,23	1.34	4 (21%)	27,32,35	1.82	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	5MC	2a	1400	32	19,22,23	1.58	3 (15%)	26,32,35	1.07	2 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1A	2617	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	2/7/25/26	0/2/2/2
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
55	5MC	1x	32	55	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	2/11/29/30	0/3/3/3
1	5MC	1A	1984	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
54	PSU	1y	55	54	-	1/7/25/26	0/2/2/2
32	4OC	1a	1402	32,56	-	1/9/29/30	0/2/2/2
1	5MU	1A	1961	1,56	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32,56	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
1	4OC	2A	1920	1	-	0/9/27/30	0/2/2/2
1	2MA	2A	2503	1,56	-	1/7/25/26	0/3/3/3
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
1	PSU	2A	1917	1,56	-	2/7/25/26	0/2/2/2
55	5MU	1x	54	55	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
54	PSU	2y	39	54	-	0/7/25/26	0/2/2/2
32	7MG	1a	527	32	-	3/7/37/38	0/3/3/3
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1937	1	-	0/7/25/26	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
54	5MU	2y	54	54	-	2/7/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
54	5MU	1y	54	54	-	3/7/25/26	0/2/2/2
54	5MU	1w	54	54	-	0/7/25/26	0/2/2/2
54	PSU	2y	32	54	-	1/7/25/26	0/2/2/2
54	PSU	1y	32	54	-	0/7/25/26	0/2/2/2
54	4SU	1w	8	54	-	0/7/25/26	0/2/2/2
54	PSU	1w	32	54	-	0/7/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	7MG	1y	46	54	-	2/7/37/38	0/3/3/3
54	PSU	2w	55	54	-	0/7/25/26	0/2/2/2
54	PSU	1y	39	54	-	0/7/25/26	0/2/2/2
54	7MG	1w	46	54	-	3/7/37/38	0/3/3/3
55	4SU	1x	8	55	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32,56	-	2/9/29/30	0/2/2/2
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,55	-	0/9/27/28	0/3/3/3
43	0TD	1l	92	43	-	2/7/12/14	-
54	PSU	2y	55	54	-	2/7/25/26	0/2/2/2
1	5MU	2A	1915	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1939	1	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32,56	-	0/7/25/26	0/2/2/2
1	4OC	1A	1942	1,56	-	1/9/27/30	0/2/2/2
43	0TD	2l	92	43	-	1/7/12/14	-
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
32	MA6	2a	1519	32	-	4/11/29/30	0/3/3/3
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1,56	-	0/7/25/26	0/2/2/2
54	MIA	1y	37	54	-	1/7/25/34	0/3/3/3
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/7/25/26	0/2/2/2
54	4SU	2y	8	54	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
54	MIA	2w	37	54	-	2/11/29/34	0/3/3/3
54	MIA	1w	37	54	-	1/15/33/34	0/3/3/3
54	7MG	2w	46	54	-	4/7/37/38	0/3/3/3
55	4SU	2x	8	55,56	-	1/7/25/26	0/2/2/2
1	OMG	1A	2263	1,55,56	-	1/9/27/28	0/3/3/3
54	7MG	2y	46	54	-	3/7/37/38	0/3/3/3
54	MIA	2y	37	54,32	-	3/7/25/34	0/3/3/3
1	5MC	1A	1964	1	-	0/7/25/26	0/2/2/2
54	4SU	1y	8	54	-	3/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
1	2MU	2A	2552	1,56	-	1/9/27/28	0/2/2/2
32	7MG	2a	527	32	-	3/7/37/38	0/3/3/3
32	5MC	2a	1404	32	-	1/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
1	2MA	1A	2515	1,56	-	1/7/25/26	0/3/3/3
32	MA6	1a	1518	32	-	1/11/29/30	0/3/3/3
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
55	PSU	1x	55	55	-	2/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	2/7/25/26	0/2/2/2
1	2MU	1A	2564	1,56	-	0/9/27/28	0/2/2/2
54	5MU	2w	54	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2

All (259) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.58	1.69	1.82
43	2l	92	0TD	CB-SB	-12.36	1.69	1.82
54	1w	37	MIA	C2-S10	-7.87	1.69	1.75
54	2w	37	MIA	C2-S10	-7.10	1.69	1.75
32	2a	1404	5MC	C5-C4	6.80	1.49	1.44
54	1w	37	MIA	C13-C14	6.72	1.52	1.32
32	1a	1404	5MC	C5-C4	6.54	1.49	1.44
32	1a	1400	5MC	C5-C4	6.50	1.49	1.44
55	2x	32	5MC	C5-C4	6.41	1.49	1.44
32	2a	967	5MC	C5-C4	6.39	1.49	1.44
32	1a	967	5MC	C5-C4	6.37	1.48	1.44
55	1x	32	5MC	C5-C4	6.03	1.48	1.44
1	2A	1942	5MC	C5-C4	6.03	1.48	1.44
32	2a	1400	5MC	C5-C4	5.65	1.48	1.44
1	1A	1984	5MC	C5-C4	5.52	1.48	1.44
1	2A	1962	5MC	C5-C4	5.25	1.48	1.44
32	2a	1518	MA6	C5-C4	5.08	1.48	1.39
32	2a	1407	5MC	C5-C4	5.01	1.47	1.44
54	1y	37	MIA	C5-C4	5.00	1.48	1.39
54	2y	8	4SU	C4-S4	-5.00	1.59	1.68
54	2y	37	MIA	C5-C4	4.99	1.48	1.39
32	2a	1519	MA6	C5-C4	4.90	1.47	1.39
1	1A	1964	5MC	C5-C4	4.87	1.47	1.44
54	2w	37	MIA	C5-C4	4.84	1.47	1.39
54	2w	8	4SU	C4-S4	-4.82	1.60	1.68
55	1x	8	4SU	C4-N3	-4.80	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1407	5MC	C5-C4	4.76	1.47	1.44
32	1a	1519	MA6	C5-C4	4.69	1.47	1.39
54	1w	37	MIA	C5-C4	4.64	1.47	1.39
55	1x	8	4SU	C4-S4	-4.52	1.60	1.68
54	1w	8	4SU	C4-S4	-4.45	1.60	1.68
55	2x	8	4SU	C4-S4	-4.44	1.60	1.68
32	1a	1518	MA6	C5-C4	4.43	1.47	1.39
55	2x	8	4SU	C4-N3	-4.35	1.33	1.37
1	1A	2515	2MA	C5-C4	4.34	1.46	1.39
54	1y	8	4SU	C4-S4	-4.32	1.61	1.68
54	1y	32	PSU	C6-C5	4.15	1.39	1.35
54	1y	39	PSU	C6-C5	4.01	1.39	1.35
54	2w	39	PSU	C6-C5	4.01	1.39	1.35
54	1w	55	PSU	C6-C5	3.97	1.39	1.35
54	2w	55	PSU	C6-C5	3.93	1.39	1.35
55	1x	8	4SU	C2-N3	-3.84	1.31	1.38
55	2x	55	PSU	C6-C5	3.82	1.39	1.35
1	2A	2503	2MA	C5-C4	3.78	1.45	1.39
54	2y	46	7MG	C5-C4	3.76	1.49	1.37
54	2y	32	PSU	C6-C5	3.74	1.39	1.35
54	1w	39	PSU	C6-C5	3.72	1.39	1.35
32	2a	516	PSU	C6-C5	3.64	1.39	1.35
54	2y	39	PSU	C6-C5	3.63	1.39	1.35
54	1w	32	PSU	C6-C5	3.63	1.39	1.35
1	2A	1911	PSU	C6-C5	3.57	1.39	1.35
54	1y	55	PSU	C6-C5	3.54	1.39	1.35
1	1A	1933	PSU	C6-C5	3.53	1.39	1.35
54	1w	46	7MG	C5-C4	3.48	1.48	1.37
54	2w	32	PSU	C6-C5	3.48	1.39	1.35
54	1y	46	7MG	C5-C4	3.46	1.48	1.37
32	1a	527	7MG	C5-C4	3.42	1.48	1.37
54	2y	54	5MU	C2-N1	3.42	1.43	1.38
54	1w	46	7MG	C4-N9	-3.41	1.33	1.37
54	2w	46	7MG	C5-C4	3.40	1.48	1.37
54	1y	8	4SU	C4-N3	-3.37	1.34	1.37
32	1a	527	7MG	C4-N9	-3.33	1.33	1.37
32	1a	516	PSU	C6-C5	3.31	1.39	1.35
32	2a	527	7MG	C4-N9	-3.30	1.33	1.37
55	2x	8	4SU	C2-N3	-3.30	1.32	1.38
32	2a	966	M2G	C5-C4	3.30	1.47	1.38
32	2a	527	7MG	C5-C4	3.24	1.47	1.37
1	1A	1939	PSU	C6-C5	3.24	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1x	8	4SU	C5-C4	-3.23	1.38	1.42
32	2a	1207	2MG	C5-C4	3.21	1.47	1.38
54	1y	54	5MU	C6-C5	3.18	1.39	1.34
1	1A	2617	PSU	C6-C5	3.17	1.38	1.35
32	2a	1518	MA6	C5-C6	3.16	1.49	1.41
1	2A	1917	PSU	C6-C5	3.16	1.38	1.35
55	2x	32	5MC	C6-C5	3.11	1.39	1.34
54	2y	8	4SU	C4-N3	-3.08	1.34	1.37
32	1a	966	M2G	C2-N2	3.08	1.40	1.35
32	1a	1207	2MG	C5-C4	3.07	1.47	1.38
1	2A	2251	OMG	C5-C4	3.07	1.47	1.38
32	2a	1407	5MC	C6-C5	3.07	1.39	1.34
55	1x	55	PSU	C6-C5	3.06	1.38	1.35
55	1x	32	5MC	C6-C5	3.06	1.39	1.34
32	1a	966	M2G	C5-C4	3.06	1.47	1.38
1	2A	2605	PSU	C6-C5	3.05	1.38	1.35
1	1A	2263	OMG	C5-C4	3.04	1.47	1.38
54	1y	37	MIA	C5-C6	3.00	1.49	1.41
1	1A	2564	2MU	C4-N3	-2.99	1.33	1.38
1	2A	1915	5MU	C2-N1	2.98	1.43	1.38
54	1y	54	5MU	C2-N1	2.94	1.43	1.38
32	2a	966	M2G	C2-N2	2.94	1.40	1.35
54	1w	54	5MU	C6-C5	2.94	1.39	1.34
55	1x	54	5MU	C6-C5	2.93	1.39	1.34
1	2A	2251	OMG	C6-N1	-2.93	1.33	1.38
32	2a	1519	MA6	C5-C6	2.91	1.48	1.41
1	2A	1915	5MU	C6-C5	2.90	1.39	1.34
54	2w	37	MIA	C5-C6	2.89	1.48	1.41
32	1a	1518	MA6	C5-C6	2.88	1.48	1.41
1	1A	1961	5MU	C4-N3	-2.87	1.33	1.38
54	2w	8	4SU	C4-N3	-2.87	1.34	1.37
54	2w	46	7MG	C4-N9	-2.87	1.34	1.37
32	1a	1519	MA6	C5-C6	2.86	1.48	1.41
32	2a	1404	5MC	C6-C5	2.86	1.39	1.34
55	2x	54	5MU	C6-C5	2.85	1.39	1.34
32	2a	967	5MC	C6-C5	2.82	1.39	1.34
1	2A	1915	5MU	C4-C5	2.82	1.49	1.44
1	2A	1939	5MU	C4-N3	-2.82	1.33	1.38
54	2y	46	7MG	C8-N9	2.82	1.47	1.45
54	1w	54	5MU	C4-C5	2.81	1.49	1.44
54	2y	37	MIA	C5-C6	2.81	1.48	1.41
1	1A	2617	PSU	C4-N3	-2.80	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1404	5MC	C6-C5	2.79	1.39	1.34
54	2y	8	4SU	C2-N1	2.79	1.42	1.38
1	2A	1939	5MU	C6-C5	2.79	1.39	1.34
54	1w	8	4SU	C4-N3	-2.78	1.34	1.37
1	1A	2263	OMG	C6-N1	-2.78	1.33	1.38
1	2A	1942	5MC	C6-C5	2.77	1.39	1.34
55	2x	54	5MU	C4-C5	2.77	1.49	1.44
1	1A	1937	5MU	C4-N3	-2.75	1.33	1.38
54	2y	55	PSU	C6-C5	2.75	1.38	1.35
54	2y	8	4SU	C5-C4	-2.75	1.39	1.42
1	2A	1917	PSU	C4-N3	-2.73	1.33	1.38
54	1y	54	5MU	C4-N3	-2.70	1.33	1.38
32	1a	967	5MC	C6-C5	2.69	1.39	1.34
55	2x	8	4SU	C5-C4	-2.67	1.39	1.42
54	2w	39	PSU	C4-N3	-2.67	1.33	1.38
1	1A	1939	PSU	C4-N3	-2.65	1.33	1.38
32	2a	1400	5MC	C6-C5	2.63	1.38	1.34
1	1A	1933	PSU	C4-N3	-2.63	1.33	1.38
1	2A	2605	PSU	C4-N3	-2.62	1.33	1.38
54	1y	39	PSU	C4-N3	-2.62	1.33	1.38
1	2A	1962	5MC	C6-N1	-2.62	1.33	1.38
54	2y	54	5MU	C6-C5	2.61	1.38	1.34
54	1y	54	5MU	C4-C5	2.61	1.49	1.44
1	2A	2503	2MA	C5-N7	-2.60	1.34	1.39
32	1a	1400	5MC	C6-C5	2.60	1.38	1.34
1	1A	1984	5MC	C6-N1	-2.59	1.33	1.38
1	1A	1964	5MC	C6-C5	2.58	1.38	1.34
55	1x	55	PSU	C4-N3	-2.58	1.34	1.38
1	2A	1915	5MU	C4-N3	-2.58	1.34	1.38
54	2y	54	5MU	C4-C5	2.58	1.49	1.44
54	1w	37	MIA	C5-C6	2.57	1.48	1.41
1	1A	1937	5MU	C6-C5	2.57	1.38	1.34
54	1w	54	5MU	C4-N3	-2.56	1.34	1.38
54	1y	37	MIA	C8-N7	2.56	1.36	1.31
54	1w	37	MIA	C5-N7	-2.55	1.34	1.39
1	2A	1911	PSU	C4-N3	-2.54	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.54	1.33	1.38
55	1x	54	5MU	C4-C5	2.54	1.49	1.44
54	1w	32	PSU	C4-N3	-2.53	1.34	1.38
1	1A	2515	2MA	C5-C6	2.52	1.48	1.41
54	2y	46	7MG	C6-N1	-2.52	1.34	1.38
32	1a	527	7MG	C6-N1	-2.51	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2w	54	5MU	C6-C5	2.51	1.38	1.34
55	1x	54	5MU	C4-N3	-2.50	1.34	1.38
54	2y	39	PSU	C4-N3	-2.50	1.34	1.38
54	2w	55	PSU	C4-N3	-2.49	1.34	1.38
54	1w	8	4SU	C2-N1	2.48	1.42	1.38
54	2w	8	4SU	C2-N1	2.47	1.42	1.38
54	1w	46	7MG	C6-N1	-2.47	1.34	1.38
1	1A	1961	5MU	C6-C5	2.46	1.38	1.34
1	1A	1961	5MU	C6-N1	-2.46	1.33	1.38
32	2a	1519	MA6	C5-N7	-2.46	1.34	1.39
54	1w	55	PSU	C4-N3	-2.45	1.34	1.38
54	1y	55	PSU	C4-N3	-2.45	1.34	1.38
1	1A	1961	5MU	C2-N3	-2.45	1.33	1.38
32	1a	1400	5MC	C6-N1	-2.45	1.33	1.38
1	1A	2515	2MA	C5-N7	-2.44	1.34	1.39
54	1w	54	5MU	C2-N1	2.44	1.42	1.38
32	1a	1207	2MG	C6-N1	-2.43	1.34	1.38
1	1A	1939	PSU	C2-N1	-2.43	1.33	1.36
54	1y	8	4SU	C5-C4	-2.43	1.39	1.42
55	2x	55	PSU	C4-N3	-2.42	1.34	1.38
32	1a	1519	MA6	C5-N7	-2.41	1.34	1.39
54	1w	39	PSU	C4-N3	-2.41	1.34	1.38
32	2a	516	PSU	C4-N3	-2.41	1.34	1.38
1	2A	2552	2MU	C5-C4	2.41	1.48	1.43
1	1A	1964	5MC	C6-N1	-2.40	1.33	1.38
32	1a	1498	UR3	C2-N1	2.40	1.41	1.38
54	2y	55	PSU	C4-N3	-2.39	1.34	1.38
54	1w	8	4SU	C5-C4	-2.39	1.39	1.42
54	2y	54	5MU	C4-N3	-2.39	1.34	1.38
55	1x	32	5MC	C6-N1	-2.38	1.34	1.38
32	1a	966	M2G	C6-N1	-2.37	1.34	1.38
32	1a	516	PSU	C4-N3	-2.36	1.34	1.38
1	2A	1939	5MU	C4-C5	2.35	1.48	1.44
32	2a	966	M2G	C6-N1	-2.35	1.34	1.38
54	2w	54	5MU	C4-C5	2.35	1.48	1.44
32	2a	1519	MA6	C8-N7	2.35	1.36	1.31
54	2y	37	MIA	C8-N7	2.34	1.36	1.31
32	1a	1407	5MC	C6-C5	2.34	1.38	1.34
32	2a	1498	UR3	C2-N1	2.34	1.41	1.38
54	2w	32	PSU	C4-N3	-2.34	1.34	1.38
54	2y	32	PSU	C4-N3	-2.32	1.34	1.38
54	2w	8	4SU	C5-C4	-2.32	1.39	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	1w	37	MIA	C4-N9	-2.31	1.32	1.37
54	1y	46	7MG	C8-N9	2.31	1.47	1.45
32	2a	527	7MG	C6-N1	-2.31	1.34	1.38
32	2a	1518	MA6	C8-N7	2.31	1.36	1.31
32	1a	1404	5MC	C6-N1	-2.30	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.30	1.34	1.38
1	1A	2515	2MA	C8-N7	2.30	1.36	1.31
55	2x	54	5MU	C4-N3	-2.28	1.34	1.38
1	2A	2552	2MU	C4-N3	-2.28	1.34	1.38
1	1A	2263	OMG	C5-N7	-2.28	1.34	1.39
55	1x	54	5MU	C2-N1	2.27	1.42	1.38
1	2A	1962	5MC	C6-C5	2.27	1.38	1.34
55	2x	54	5MU	C2-N1	2.27	1.42	1.38
54	2w	54	5MU	C4-N3	-2.26	1.34	1.38
54	2w	37	MIA	C5-N7	-2.26	1.35	1.39
1	1A	1937	5MU	C2-N1	2.26	1.42	1.38
32	1a	1407	5MC	C6-N1	-2.25	1.34	1.38
54	1y	46	7MG	C4-N9	-2.24	1.35	1.37
54	1w	37	MIA	C8-N7	2.24	1.36	1.31
54	2w	37	MIA	C8-N7	2.24	1.36	1.31
54	1y	46	7MG	C6-N1	-2.24	1.34	1.38
55	2x	54	5MU	C6-N1	-2.24	1.34	1.38
54	1y	32	PSU	C4-N3	-2.23	1.34	1.38
32	1a	1518	MA6	C8-N7	2.23	1.36	1.31
1	1A	1937	5MU	C2-N3	-2.22	1.34	1.38
32	1a	1518	MA6	C5-N7	-2.22	1.35	1.39
54	2w	46	7MG	C5-C6	2.20	1.49	1.43
32	2a	1404	5MC	C6-N1	-2.20	1.34	1.38
32	1a	1518	MA6	C4-N9	-2.19	1.33	1.37
54	1y	54	5MU	C2-N3	-2.19	1.34	1.38
1	1A	2617	PSU	C2-N1	-2.18	1.33	1.36
1	1A	1939	PSU	C2-N3	-2.18	1.33	1.37
1	2A	1942	5MC	C6-N1	-2.17	1.34	1.38
32	1a	967	5MC	C6-N1	-2.15	1.34	1.38
32	2a	967	5MC	C6-N1	-2.15	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.15	1.34	1.38
1	1A	1984	5MC	C6-C5	2.15	1.38	1.34
32	1a	1519	MA6	C8-N7	2.14	1.35	1.31
1	1A	2564	2MU	C5-C4	2.13	1.48	1.43
54	2w	54	5MU	C2-N1	2.13	1.41	1.38
32	1a	1207	2MG	C4-N9	-2.13	1.32	1.38
32	2a	1518	MA6	C5-N7	-2.13	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1400	5MC	C6-N1	-2.12	1.34	1.38
1	1A	2617	PSU	C2-N3	-2.11	1.34	1.37
54	2y	55	PSU	C2-N1	-2.11	1.33	1.36
1	2A	2503	2MA	C8-N7	2.11	1.35	1.31
1	2A	2251	OMG	C5-N7	-2.10	1.34	1.39
1	2A	1915	5MU	C6-N1	-2.10	1.34	1.38
54	2w	46	7MG	C8-N9	2.10	1.47	1.45
54	2y	46	7MG	C2-N3	2.10	1.38	1.33
1	2A	2503	2MA	C5-C6	2.09	1.46	1.41
1	1A	1937	5MU	C6-N1	-2.08	1.34	1.38
54	1w	46	7MG	C8-N9	2.07	1.47	1.45
55	1x	54	5MU	C6-N1	-2.06	1.34	1.38
1	2A	2605	PSU	C2-N3	-2.06	1.34	1.37
54	2y	37	MIA	C5-N7	-2.05	1.35	1.39
1	2A	2503	2MA	C4-N9	-2.05	1.33	1.37
1	1A	1937	5MU	C4-C5	2.04	1.48	1.44
54	2y	8	4SU	C2-N3	-2.03	1.34	1.38
54	2w	46	7MG	C6-N1	-2.02	1.35	1.38
55	1x	54	5MU	C2-N3	-2.01	1.34	1.38
54	1w	54	5MU	C2-N3	-2.01	1.34	1.38
32	1a	527	7MG	C8-N9	2.01	1.47	1.45
54	1y	54	5MU	C6-N1	-2.01	1.34	1.38
54	1y	32	PSU	C4-C5	2.00	1.49	1.44

All (423) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2y	46	7MG	N9-C4-N3	10.02	140.14	125.46
54	1w	37	MIA	C12-C13-C14	-9.24	110.43	127.01
54	1y	46	7MG	N9-C4-N3	9.05	138.72	125.46
54	2w	46	7MG	N9-C4-N3	8.97	138.60	125.46
32	2a	527	7MG	N9-C4-N3	8.81	138.38	125.46
32	1a	527	7MG	N9-C4-N3	8.77	138.31	125.46
54	1w	46	7MG	N9-C4-N3	8.62	138.09	125.46
1	1A	2515	2MA	C5-C4-N3	-8.41	118.32	127.18
1	2A	2503	2MA	C5-C4-N3	-8.07	118.68	127.18
43	1l	92	0TD	CSB-SB-CB	-7.96	88.06	102.36
54	2w	37	MIA	C5-C4-N3	-7.91	118.85	127.18
54	1w	37	MIA	C5-C4-N3	-7.32	119.47	127.18
54	2w	8	4SU	C4-N3-C2	-7.24	120.38	127.31
32	1a	1498	UR3	C4-N3-C2	-7.12	118.85	124.58
32	2a	1498	UR3	C4-N3-C2	-7.01	118.94	124.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1207	2MG	C2-N3-C4	6.87	120.59	112.00
1	1A	2515	2MA	N3-C4-N9	6.71	135.51	126.99
32	2a	1207	2MG	C2-N3-C4	6.69	120.37	112.00
1	2A	2503	2MA	N3-C4-N9	6.69	135.48	126.99
1	2A	1917	PSU	N1-C2-N3	6.68	122.22	115.17
54	2w	55	PSU	N1-C2-N3	6.64	122.18	115.17
1	1A	1933	PSU	N1-C2-N3	6.63	122.16	115.17
54	1y	55	PSU	N1-C2-N3	6.52	122.05	115.17
1	1A	1939	PSU	N1-C2-N3	6.50	122.02	115.17
1	1A	2263	OMG	C5-C4-N3	-6.48	118.08	128.39
1	2A	2251	OMG	C5-C4-N3	-6.47	118.10	128.39
1	2A	2605	PSU	N1-C2-N3	6.35	121.86	115.17
54	1w	8	4SU	C4-N3-C2	-6.25	121.32	127.31
54	2y	8	4SU	C4-N3-C2	-6.21	121.36	127.31
1	2A	1911	PSU	N1-C2-N3	6.15	121.66	115.17
32	2a	966	M2G	C5-C4-N3	-6.14	118.62	128.39
55	2x	55	PSU	N1-C2-N3	6.12	121.63	115.17
54	1w	55	PSU	N1-C2-N3	6.11	121.61	115.17
54	2w	37	MIA	N3-C4-N9	6.11	134.74	126.99
54	2w	32	PSU	N1-C2-N3	6.10	121.61	115.17
55	1x	55	PSU	N1-C2-N3	6.09	121.60	115.17
54	1w	39	PSU	N1-C2-N3	6.09	121.59	115.17
32	1a	966	M2G	C5-C4-N3	-6.06	118.74	128.39
54	2y	8	4SU	C5-C4-N3	6.06	120.38	114.75
54	1w	32	PSU	N1-C2-N3	6.04	121.54	115.17
54	2y	32	PSU	N1-C2-N3	6.00	121.50	115.17
1	2A	1939	5MU	C4-N3-C2	-5.96	119.53	127.34
32	2a	516	PSU	N1-C2-N3	5.91	121.40	115.17
54	1y	39	PSU	N1-C2-N3	5.90	121.39	115.17
32	2a	1518	MA6	C5-C4-N3	-5.89	118.61	126.72
54	2y	39	PSU	N1-C2-N3	5.88	121.37	115.17
1	1A	2564	2MU	N3-C2-N1	5.88	122.54	114.89
55	2x	54	5MU	C4-N3-C2	-5.79	119.75	127.34
54	1y	32	PSU	N1-C2-N3	5.77	121.25	115.17
54	2w	8	4SU	C5-C4-N3	5.76	120.11	114.75
32	1a	516	PSU	N1-C2-N3	5.76	121.24	115.17
54	2y	46	7MG	C5-C4-N3	-5.74	117.35	128.13
55	2x	54	5MU	N3-C2-N1	5.67	122.28	114.89
54	1y	8	4SU	C4-N3-C2	-5.64	121.91	127.31
32	2a	1207	2MG	C5-C4-N3	-5.64	119.41	128.39
32	2a	1519	MA6	C5-C4-N3	-5.63	118.97	126.72
54	1w	37	MIA	N3-C4-N9	5.61	134.11	126.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	2617	PSU	N1-C2-N3	5.59	121.07	115.17
54	2w	46	7MG	N9-C8-N7	-5.55	95.51	103.37
54	2y	37	MIA	C5-C4-N3	-5.54	119.08	126.72
54	1w	46	7MG	N9-C8-N7	-5.52	95.56	103.37
32	1a	527	7MG	C5-C4-N3	-5.50	117.81	128.13
32	2a	527	7MG	N9-C8-N7	-5.47	95.63	103.37
1	2A	1939	5MU	N3-C2-N1	5.43	121.95	114.89
1	1A	2564	2MU	C4-N3-C2	-5.42	119.88	126.61
1	1A	2263	OMG	C2-N3-C4	5.42	121.64	112.30
54	1y	37	MIA	C5-C4-N3	-5.41	119.26	126.72
54	1w	8	4SU	C5-C4-N3	5.41	119.79	114.75
1	1A	1937	5MU	C4-N3-C2	-5.41	120.25	127.34
32	1a	1519	MA6	C5-C4-N3	-5.41	119.27	126.72
54	2w	46	7MG	C5-C4-N3	-5.39	118.00	128.13
54	2w	39	PSU	N1-C2-N3	5.36	120.82	115.17
1	2A	2552	2MU	N3-C2-N1	5.35	121.86	114.89
1	1A	1937	5MU	C5-C4-N3	5.34	119.97	115.32
1	1A	1961	5MU	C4-N3-C2	-5.33	120.35	127.34
54	2y	55	PSU	N1-C2-N3	5.30	120.76	115.17
32	1a	1207	2MG	C5-C4-N3	-5.28	119.98	128.39
1	2A	1915	5MU	C4-N3-C2	-5.27	120.42	127.34
32	2a	527	7MG	C5-C4-N3	-5.27	118.25	128.13
32	1a	1518	MA6	C5-C4-N3	-5.25	119.49	126.72
54	1y	46	7MG	N9-C8-N7	-5.22	95.97	103.37
1	2A	1915	5MU	N3-C2-N1	5.22	121.69	114.89
1	2A	1939	5MU	C5-C4-N3	5.14	119.79	115.32
55	1x	54	5MU	N3-C2-N1	5.13	121.57	114.89
54	1y	46	7MG	C5-C4-N3	-5.11	118.53	128.13
1	1A	1961	5MU	C5-C4-N3	5.06	119.72	115.32
1	1A	1937	5MU	N3-C2-N1	5.05	121.47	114.89
1	1A	1961	5MU	O4-C4-C5	-5.02	119.17	124.92
1	2A	2251	OMG	C2-N3-C4	5.01	120.92	112.30
32	1a	527	7MG	N9-C8-N7	-4.94	96.37	103.37
54	1y	54	5MU	N3-C2-N1	4.94	121.32	114.89
54	2y	37	MIA	N3-C4-N9	4.93	135.55	127.17
1	2A	2251	OMG	N9-C4-N3	4.86	135.68	125.95
1	1A	1937	5MU	O4-C4-C5	-4.85	119.37	124.92
54	2y	46	7MG	C2-N3-C4	4.83	120.61	112.30
1	1A	1961	5MU	N3-C2-N1	4.83	121.17	114.89
54	1y	54	5MU	C4-N3-C2	-4.77	121.08	127.34
32	1a	966	M2G	C2-N3-C4	4.71	121.21	112.51
54	2y	46	7MG	N9-C8-N7	-4.68	96.75	103.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	966	M2G	N9-C4-N3	4.64	135.23	125.95
54	2y	8	4SU	C5-C4-S4	-4.62	119.03	124.31
54	1w	46	7MG	C5-C4-N3	-4.55	119.60	128.13
1	2A	2552	2MU	C4-N3-C2	-4.53	120.99	126.61
54	2y	54	5MU	C5-C4-N3	4.51	119.24	115.32
54	2w	46	7MG	C2-N3-C4	4.51	120.06	112.30
32	1a	527	7MG	C2-N3-C4	4.48	120.02	112.30
32	2a	966	M2G	C2-N3-C4	4.48	120.79	112.51
54	2y	54	5MU	C4-N3-C2	-4.45	121.51	127.34
32	2a	527	7MG	C2-N3-C4	4.42	119.91	112.30
54	2w	55	PSU	C4-N3-C2	-4.42	120.29	126.37
55	2x	54	5MU	C5-C4-N3	4.40	119.15	115.32
32	1a	966	M2G	N9-C4-N3	4.40	134.74	125.95
1	2A	1939	5MU	C5-C6-N1	-4.39	118.54	123.31
54	1w	54	5MU	N3-C2-N1	4.39	120.61	114.89
32	1a	1519	MA6	C2-N1-C6	4.38	122.53	111.83
1	2A	1939	5MU	O4-C4-C5	-4.37	119.92	124.92
32	1a	1518	MA6	C2-N1-C6	4.36	122.49	111.83
1	1A	2263	OMG	N9-C4-N3	4.36	134.68	125.95
1	2A	1915	5MU	C5-C4-N3	4.36	119.11	115.32
54	1y	8	4SU	N3-C2-N1	4.34	120.54	114.89
32	2a	1518	MA6	C9-N6-C6	-4.34	109.48	120.52
1	1A	2564	2MU	O2-C2-N1	-4.33	117.16	122.80
54	1y	46	7MG	C2-N3-C4	4.32	119.75	112.30
55	1x	54	5MU	C4-N3-C2	-4.32	121.67	127.34
54	1y	54	5MU	C5-C4-N3	4.31	119.07	115.32
32	2a	1518	MA6	C2-N1-C6	4.30	122.34	111.83
1	2A	2605	PSU	C4-N3-C2	-4.30	120.44	126.37
32	1a	1207	2MG	C6-C5-N7	4.30	138.12	130.29
32	1a	1519	MA6	N3-C4-N9	4.30	134.48	127.17
55	1x	55	PSU	C4-N3-C2	-4.29	120.46	126.37
1	1A	1933	PSU	C4-N3-C2	-4.29	120.46	126.37
32	2a	1518	MA6	N3-C4-N9	4.28	134.45	127.17
54	2w	8	4SU	N3-C2-N1	4.28	120.46	114.89
32	1a	1518	MA6	C4-C5-N7	-4.25	105.72	110.58
54	1y	37	MIA	N3-C4-N9	4.25	134.39	127.17
54	1w	37	MIA	C15-C14-C13	-4.24	109.93	122.66
55	2x	55	PSU	C4-N3-C2	-4.24	120.53	126.37
32	2a	1519	MA6	C2-N1-C6	4.23	122.16	111.83
32	2a	1519	MA6	C9-N6-C6	-4.22	109.78	120.52
32	2a	1519	MA6	C4-C5-N7	-4.22	105.76	110.58
32	1a	1518	MA6	C9-N6-C6	-4.18	109.90	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	516	PSU	O2-C2-N1	-4.17	118.49	122.79
54	1w	54	5MU	C4-N3-C2	-4.16	121.89	127.34
54	2w	54	5MU	C4-N3-C2	-4.13	121.92	127.34
54	2y	54	5MU	N3-C2-N1	4.13	120.27	114.89
54	1w	37	MIA	C11-S10-C2	-4.10	99.17	102.25
54	1w	55	PSU	C4-N3-C2	-4.10	120.72	126.37
1	1A	2515	2MA	N6-C6-N1	4.06	122.51	117.03
54	2y	54	5MU	O4-C4-C5	-4.06	120.28	124.92
54	1y	8	4SU	C5-C4-N3	4.05	118.51	114.75
55	2x	54	5MU	O4-C4-C5	-4.03	120.31	124.92
1	2A	1917	PSU	O2-C2-N1	-4.03	118.63	122.79
54	1w	8	4SU	C5-C4-S4	-4.03	119.70	124.31
54	2w	8	4SU	C5-C4-S4	-4.01	119.73	124.31
32	2a	516	PSU	C4-N3-C2	-4.00	120.85	126.37
54	1w	32	PSU	C4-N3-C2	-4.00	120.86	126.37
32	2a	1519	MA6	N3-C4-N9	4.00	133.96	127.17
1	1A	1933	PSU	O2-C2-N1	-3.99	118.67	122.79
54	1y	55	PSU	O2-C2-N1	-3.99	118.68	122.79
32	2a	1518	MA6	C4-C5-N7	-3.99	106.03	110.58
1	1A	1939	PSU	O2-C2-N1	-3.98	118.68	122.79
54	2w	54	5MU	O4-C4-C5	-3.98	120.36	124.92
54	2w	54	5MU	N3-C2-N1	3.96	120.05	114.89
32	1a	1207	2MG	N1-C2-N2	3.94	120.58	116.56
54	2w	54	5MU	C5-C4-N3	3.93	118.74	115.32
1	2A	1917	PSU	C4-N3-C2	-3.88	121.02	126.37
1	1A	1961	5MU	C5-C6-N1	-3.87	119.11	123.31
54	2y	55	PSU	O2-C2-N1	-3.87	118.80	122.79
54	2y	55	PSU	C4-N3-C2	-3.87	121.04	126.37
32	2a	1207	2MG	C6-C5-N7	3.86	137.32	130.29
54	1y	55	PSU	C4-N3-C2	-3.86	121.05	126.37
32	1a	516	PSU	C4-N3-C2	-3.86	121.06	126.37
1	1A	1939	PSU	C4-N3-C2	-3.84	121.09	126.37
54	2y	32	PSU	C4-N3-C2	-3.83	121.10	126.37
1	2A	1911	PSU	C4-N3-C2	-3.82	121.11	126.37
32	1a	1519	MA6	C4-C5-N7	-3.82	106.22	110.58
54	2y	37	MIA	N3-C2-N1	-3.81	122.82	128.58
54	1w	54	5MU	C5-C4-N3	3.79	118.62	115.32
54	1w	46	7MG	C2-N3-C4	3.79	118.83	112.30
32	1a	1519	MA6	C9-N6-C6	-3.77	110.93	120.52
54	2w	32	PSU	C4-N3-C2	-3.76	121.19	126.37
55	2x	54	5MU	O2-C2-N1	-3.75	117.91	122.80
1	1A	1984	5MC	C5-C6-N1	-3.74	119.25	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2y	39	PSU	C4-N3-C2	-3.73	121.24	126.37
54	1w	37	MIA	C16-C14-C13	-3.70	111.55	122.66
32	2a	1518	MA6	C2-N3-C4	3.70	120.87	111.83
32	1a	1518	MA6	N3-C4-N9	3.70	133.46	127.17
1	2A	2605	PSU	O2-C2-N1	-3.70	118.98	122.79
54	1y	37	MIA	N3-C2-N1	-3.69	123.00	128.58
54	1w	8	4SU	N3-C2-N1	3.67	119.67	114.89
54	1w	39	PSU	C4-N3-C2	-3.67	121.31	126.37
54	2y	37	MIA	C2-N3-C4	3.67	120.79	111.83
1	2A	1915	5MU	C5-C6-N1	-3.67	119.33	123.31
54	1w	39	PSU	O2-C2-N1	-3.66	119.01	122.79
54	1y	37	MIA	C4-C5-N7	-3.65	106.41	110.58
1	1A	2617	PSU	C4-N3-C2	-3.64	121.35	126.37
32	2a	1207	2MG	N9-C4-N3	3.64	133.22	125.95
54	1y	37	MIA	C2-N3-C4	3.63	120.71	111.83
55	2x	54	5MU	C5-C6-N1	-3.63	119.37	123.31
32	1a	1518	MA6	C2-N3-C4	3.62	120.68	111.83
54	2y	8	4SU	N3-C2-N1	3.60	119.57	114.89
54	2w	32	PSU	O2-C2-N1	-3.59	119.08	122.79
55	1x	8	4SU	C6-C5-C4	-3.58	116.85	119.95
54	2w	37	MIA	C4-C5-N7	-3.57	106.50	110.58
32	1a	1400	5MC	C5-C6-N1	-3.57	119.44	123.31
32	1a	967	5MC	C5-C6-N1	-3.55	119.45	123.31
1	1A	2617	PSU	O2-C2-N1	-3.55	119.13	122.79
54	1y	54	5MU	C5-C6-N1	-3.54	119.46	123.31
1	2A	1915	5MU	O4-C4-C5	-3.52	120.89	124.92
54	1w	32	PSU	O2-C2-N1	-3.52	119.16	122.79
55	2x	8	4SU	C5-C4-N3	3.50	118.01	114.75
1	2A	1939	5MU	O2-C2-N1	-3.50	118.24	122.80
54	1y	32	PSU	C4-N3-C2	-3.49	121.56	126.37
1	1A	2263	OMG	C6-C5-N7	3.49	136.63	130.29
32	1a	1519	MA6	C2-N3-C4	3.48	120.33	111.83
1	2A	2503	2MA	C4-N9-C8	3.47	109.38	105.74
54	1y	54	5MU	O4-C4-C5	-3.45	120.97	124.92
54	2y	54	5MU	C1'-N1-C2	3.45	123.78	117.59
54	2y	37	MIA	C4-N9-C8	3.44	109.35	105.74
55	1x	54	5MU	O4-C4-C5	-3.44	120.98	124.92
55	1x	8	4SU	C5-C4-N3	3.43	117.94	114.75
32	1a	1518	MA6	N1-C2-N3	-3.43	123.39	128.58
32	1a	1498	UR3	C5-C4-N3	3.43	119.55	115.04
54	1w	55	PSU	O2-C2-N1	-3.43	119.26	122.79
54	2w	55	PSU	O2-C2-N1	-3.42	119.27	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1519	MA6	C2-N3-C4	3.41	120.16	111.83
1	2A	2552	2MU	O2-C2-N1	-3.40	118.37	122.80
54	1y	39	PSU	C4-N3-C2	-3.40	121.69	126.37
54	2w	37	MIA	C2-N3-C4	3.39	121.17	112.29
1	2A	1962	5MC	C5-C6-N1	-3.39	119.63	123.31
32	2a	967	5MC	C5-C6-N1	-3.38	119.65	123.31
54	1w	37	MIA	C4-C5-N7	-3.37	106.73	110.58
54	2y	39	PSU	O2-C2-N1	-3.35	119.33	122.79
32	2a	1404	5MC	C5-C4-N3	-3.35	118.32	121.75
54	1y	32	PSU	O2-C2-N1	-3.35	119.34	122.79
1	1A	2515	2MA	C4-C5-N7	-3.35	106.76	110.58
32	1a	966	M2G	C6-C5-N7	3.34	136.36	130.29
54	2y	54	5MU	C1'-N1-C6	-3.31	115.69	121.15
54	2w	37	MIA	C6-C5-N7	3.28	136.00	132.43
1	2A	2503	2MA	N6-C6-N1	3.26	121.43	117.03
32	1a	1207	2MG	C4-C5-N7	-3.24	105.54	110.67
32	1a	1207	2MG	N9-C4-N3	3.23	132.42	125.95
1	1A	1937	5MU	C5-C6-N1	-3.22	119.82	123.31
43	1l	92	0TD	OD2-CG-CB	3.21	120.09	113.15
1	2A	2503	2MA	C4-C5-N7	-3.19	106.93	110.58
1	1A	2564	2MU	C5-C4-N3	3.19	119.27	114.80
32	1a	1519	MA6	N1-C6-N6	3.19	120.74	116.86
55	2x	32	5MC	C5-C6-N1	-3.18	119.86	123.31
55	1x	55	PSU	O2-C2-N1	-3.18	119.50	122.79
1	2A	2251	OMG	C6-C5-N7	3.18	136.07	130.29
1	2A	1911	PSU	O2-C2-N1	-3.18	119.51	122.79
32	1a	1519	MA6	N1-C2-N3	-3.17	123.79	128.58
54	1w	46	7MG	C5-C4-N9	-3.16	102.28	106.33
55	1x	32	5MC	C5-C6-N1	-3.16	119.88	123.31
32	2a	1404	5MC	C5-C6-N1	-3.15	119.89	123.31
32	2a	1498	UR3	C5-C4-N3	3.15	119.19	115.04
32	2a	1407	5MC	C5-C4-N3	-3.14	118.53	121.75
54	2y	32	PSU	O2-C2-N1	-3.14	119.55	122.79
32	1a	1404	5MC	C5-C6-N1	-3.12	119.93	123.31
54	1w	37	MIA	C2-N3-C4	3.12	120.45	112.29
55	1x	54	5MU	C5-C4-N3	3.11	118.03	115.32
32	2a	1518	MA6	N1-C2-N3	-3.11	123.88	128.58
32	2a	1407	5MC	C5-C6-N1	-3.09	119.95	123.31
54	2w	39	PSU	C4-N3-C2	-3.09	122.12	126.37
32	2a	1207	2MG	C4-C5-N7	-3.08	105.79	110.67
54	2y	37	MIA	C4-C5-N7	-3.08	107.06	110.58
55	2x	8	4SU	C1'-N1-C2	3.08	123.12	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1518	MA6	C10-N6-C6	-3.07	112.71	120.52
1	1A	2564	2MU	O4-C4-C5	-3.07	119.87	125.16
55	1x	8	4SU	O2-C2-N1	3.07	126.79	122.80
32	1a	1400	5MC	C5-C4-N3	-3.06	118.62	121.75
32	1a	1407	5MC	C5-C4-N3	-3.05	118.63	121.75
54	1w	37	MIA	C6-C5-N7	3.04	135.75	132.43
1	1A	1964	5MC	C5-C6-N1	-3.04	120.01	123.31
1	1A	1964	5MC	C5-C4-N3	-3.03	118.65	121.75
32	2a	966	M2G	C6-C5-N7	3.01	135.77	130.29
43	2l	92	0TD	OD2-CG-CB	3.01	119.65	113.15
1	2A	1942	5MC	C5-C6-N1	-3.00	120.06	123.31
54	2y	46	7MG	C5-C4-N9	-2.99	102.50	106.33
55	1x	32	5MC	C5-C4-N3	-2.99	118.69	121.75
1	1A	2263	OMG	C4-C5-N7	-2.98	105.95	110.67
54	1w	54	5MU	O4-C4-C5	-2.96	121.53	124.92
54	1w	54	5MU	C5-C6-N1	-2.94	120.12	123.31
32	1a	1407	5MC	C5-C6-N1	-2.93	120.13	123.31
32	1a	1518	MA6	C5-N7-C8	2.92	108.03	103.45
1	2A	2552	2MU	O4-C4-C5	-2.92	120.13	125.16
1	1A	2515	2MA	C4-N9-C8	2.89	108.78	105.74
32	1a	1519	MA6	C4-N9-C8	2.89	108.77	105.74
32	2a	527	7MG	C5-C6-N1	2.88	116.00	110.94
54	2w	46	7MG	C5-C6-N1	2.87	116.00	110.94
32	1a	1519	MA6	C5-N7-C8	2.85	107.93	103.45
1	2A	1942	5MC	C5-C4-N3	-2.84	118.84	121.75
1	2A	2503	2MA	C5-N7-C8	2.81	107.87	103.45
55	2x	32	5MC	C5-C4-N3	-2.81	118.87	121.75
54	1y	46	7MG	C5-C4-N9	-2.80	102.74	106.33
54	2w	8	4SU	C1'-N1-C2	2.79	122.61	117.59
1	2A	2503	2MA	N9-C8-N7	-2.79	109.98	113.94
32	1a	1207	2MG	N2-C2-N3	-2.78	116.97	120.51
32	2a	1519	MA6	C5-N7-C8	2.77	107.80	103.45
32	2a	1207	2MG	N1-C2-N2	2.76	119.38	116.56
54	1y	8	4SU	C5-C4-S4	-2.76	121.15	124.31
32	2a	1519	MA6	N1-C2-N3	-2.76	124.41	128.58
32	2a	516	PSU	O2-C2-N1	-2.75	119.95	122.79
32	2a	967	5MC	C5-C4-N3	-2.75	118.93	121.75
32	2a	1518	MA6	C10-N6-C6	-2.73	113.58	120.52
32	1a	1519	MA6	C10-N6-C6	-2.72	113.59	120.52
32	1a	1404	5MC	C5-C4-N3	-2.72	118.97	121.75
54	2w	54	5MU	C5-C6-N1	-2.71	120.37	123.31
55	2x	55	PSU	O2-C2-N1	-2.70	120.00	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	1y	37	MIA	C5-N7-C8	2.70	107.69	103.45
54	1w	54	5MU	C5M-C5-C4	2.69	121.66	118.78
54	2y	54	5MU	C5-C6-N1	-2.69	120.39	123.31
1	2A	2251	OMG	C4-C5-N7	-2.69	106.41	110.67
55	1x	54	5MU	C5-C6-N1	-2.69	120.39	123.31
54	1y	37	MIA	C4-N9-C8	2.66	108.53	105.74
32	2a	1519	MA6	C10-N6-C6	-2.66	113.75	120.52
32	2a	1400	5MC	C5-C4-N3	-2.65	119.04	121.75
54	2y	54	5MU	O2-C2-N3	-2.64	116.61	121.49
32	2a	1407	5MC	O2-C2-N3	-2.63	118.19	122.33
32	1a	527	7MG	C5-C6-N1	2.62	115.56	110.94
32	2a	1402	4OC	O2-C2-N3	-2.62	118.20	122.33
32	2a	1402	4OC	C6-C5-C4	2.62	120.15	117.00
32	1a	1518	MA6	C4-N9-C8	2.61	108.48	105.74
32	2a	1207	2MG	N2-C2-N3	-2.61	117.19	120.51
32	1a	966	M2G	C4-C5-N7	-2.60	106.55	110.67
1	1A	2515	2MA	C5-N7-C8	2.60	107.53	103.45
32	2a	1518	MA6	C5-N7-C8	2.56	107.48	103.45
54	2y	37	MIA	C5-N7-C8	2.55	107.45	103.45
32	1a	516	PSU	C6-C5-C4	-2.55	116.46	118.17
54	2w	37	MIA	C12-N6-C6	-2.54	120.49	122.85
32	2a	1518	MA6	C10-N6-C9	-2.54	108.01	116.18
54	2w	37	MIA	C11-S10-C2	-2.54	100.35	102.25
32	2a	1400	5MC	C5-C6-N1	-2.54	120.56	123.31
54	1w	37	MIA	C4-N9-C8	2.53	108.40	105.74
54	2w	37	MIA	C5-N7-C8	2.52	107.41	103.45
55	2x	32	5MC	O2-C2-N3	-2.51	118.37	122.33
1	2A	2552	2MU	C5-C4-N3	2.50	118.31	114.80
32	1a	1518	MA6	C6-C5-N7	2.49	137.42	133.43
1	1A	1984	5MC	CM5-C5-C6	-2.48	119.50	122.85
55	2x	8	4SU	O2-C2-N1	2.46	126.00	122.80
54	2w	37	MIA	C2-N1-C6	2.44	122.17	117.54
32	2a	967	5MC	O2-C2-N3	-2.42	118.51	122.33
54	2w	37	MIA	C4-N9-C8	2.42	108.28	105.74
55	2x	8	4SU	O2-C2-N3	-2.40	117.06	121.49
32	1a	1207	2MG	CM2-N2-C2	-2.40	118.50	123.65
32	2a	966	M2G	C4-C5-N7	-2.39	106.88	110.67
54	1w	37	MIA	C2-N1-C6	2.39	122.08	117.54
1	1A	2617	PSU	C6-C5-C4	-2.39	116.56	118.17
54	2w	55	PSU	C5-C6-N1	-2.37	118.85	122.14
54	2y	54	5MU	C5M-C5-C4	2.37	121.31	118.78
55	2x	55	PSU	C5-C6-N1	-2.36	118.86	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1402	4OC	C6-C5-C4	2.34	119.82	117.00
55	1x	55	PSU	C5-C6-N1	-2.34	118.90	122.14
54	2w	37	MIA	N3-C2-N1	-2.33	122.75	127.00
32	2a	1498	UR3	C1'-N1-C2	2.33	120.85	117.04
1	1A	1961	5MU	O2-C2-N1	-2.32	119.77	122.80
43	2l	92	0TD	OD1-CG-CB	-2.32	117.58	122.44
32	2a	527	7MG	C5-C4-N9	-2.32	103.36	106.33
54	2w	46	7MG	C5-C4-N9	-2.31	103.37	106.33
54	1y	39	PSU	O2-C2-N1	-2.30	120.42	122.79
32	1a	1498	UR3	C1'-N1-C2	2.30	120.80	117.04
54	1w	37	MIA	C5-N7-C8	2.30	107.06	103.45
54	1y	37	MIA	C6-C5-N7	2.29	136.50	132.09
54	1y	46	7MG	C5-C6-N1	2.28	114.96	110.94
1	1A	2515	2MA	C2-N1-C6	2.27	121.59	118.10
32	2a	1519	MA6	N1-C6-N6	2.27	119.62	116.86
32	1a	967	5MC	C5-C4-N3	-2.27	119.43	121.75
32	1a	1518	MA6	N9-C8-N7	-2.27	110.72	113.94
54	1w	37	MIA	N6-C6-N1	2.27	121.38	118.33
55	1x	54	5MU	O2-C2-N1	-2.27	119.85	122.80
32	1a	1518	MA6	C10-N6-C9	-2.25	108.94	116.18
1	1A	1964	5MC	O2-C2-N3	-2.25	118.78	122.33
1	1A	1937	5MU	O2-C2-N1	-2.24	119.88	122.80
1	2A	1962	5MC	C5-C4-N3	-2.24	119.46	121.75
1	1A	2515	2MA	N9-C8-N7	-2.24	110.76	113.94
54	2y	37	MIA	N9-C8-N7	-2.23	110.77	113.94
1	2A	2503	2MA	C2-N1-C6	2.23	121.52	118.10
54	2y	8	4SU	C1'-N1-C2	2.22	121.59	117.59
54	2w	54	5MU	C5M-C5-C4	2.22	121.16	118.78
54	2w	39	PSU	O2-C2-N1	-2.22	120.50	122.79
32	2a	516	PSU	O4'-C1'-C2'	2.21	108.21	105.15
54	1y	54	5MU	O2-C2-N3	-2.21	117.42	121.49
32	1a	1519	MA6	N9-C8-N7	-2.20	110.81	113.94
54	2y	37	MIA	C2-N1-C6	2.19	122.33	118.73
54	2y	46	7MG	C5-C6-N1	2.18	114.78	110.94
54	2w	39	PSU	C6-C5-C4	-2.17	116.71	118.17
43	1l	92	0TD	OD1-CG-CB	-2.16	117.91	122.44
54	1y	55	PSU	O4'-C1'-C2'	2.16	108.14	105.15
1	1A	2564	2MU	C2'-C1'-N1	-2.15	110.16	114.24
55	1x	54	5MU	C5M-C5-C4	2.14	121.07	118.78
32	1a	966	M2G	O6-C6-C5	-2.14	120.88	126.53
32	2a	516	PSU	C5-C6-N1	-2.14	119.17	122.14
54	1w	37	MIA	N3-C2-N1	-2.13	123.11	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	32	5MC	O2-C2-N3	-2.13	118.97	122.33
54	2y	55	PSU	O4'-C1'-C2'	2.12	108.09	105.15
54	2w	46	7MG	O6-C6-C5	-2.12	122.42	127.62
1	1A	1984	5MC	C5-C4-N3	-2.12	119.58	121.75
55	1x	8	4SU	C1'-N1-C2	2.11	121.39	117.59
54	2y	55	PSU	C6-C5-C4	-2.11	116.75	118.17
1	2A	1915	5MU	C5M-C5-C4	2.11	121.03	118.78
54	1y	8	4SU	C1'-N1-C2	2.10	121.36	117.59
54	2y	32	PSU	O4'-C1'-C2'	2.10	108.05	105.15
1	2A	2251	OMG	CM2-O2'-C2'	-2.10	109.09	114.47
1	2A	1915	5MU	C5M-C5-C6	-2.09	120.02	122.85
55	1x	8	4SU	O2-C2-N3	-2.08	117.65	121.49
54	1y	37	MIA	C2-N1-C6	2.08	122.14	118.73
1	2A	2605	PSU	C5-C6-N1	-2.07	119.26	122.14
32	1a	1400	5MC	CM5-C5-C6	-2.07	120.05	122.85
32	2a	966	M2G	O6-C6-C5	-2.06	121.08	126.53
54	1y	39	PSU	O2-C2-N3	-2.06	118.20	121.86
32	1a	516	PSU	O4'-C1'-C2'	2.06	108.01	105.15
32	2a	1404	5MC	O2-C2-N3	-2.06	119.08	122.33
54	1y	37	MIA	N9-C8-N7	-2.06	111.02	113.94
54	1y	8	4SU	C6-N1-C2	-2.05	118.50	121.00
32	2a	1519	MA6	C4-N9-C8	2.05	107.89	105.74
1	2A	2503	2MA	C6-C5-N7	2.04	136.02	132.09
1	2A	1917	PSU	C5-C6-N1	-2.04	119.31	122.14
32	1a	1207	2MG	C8-N7-C5	2.04	107.89	104.26
32	1a	1404	5MC	CM5-C5-C6	-2.03	120.11	122.85
54	1y	32	PSU	C6-C5-C4	-2.03	116.81	118.17
54	1y	55	PSU	C5-C6-N1	-2.02	119.34	122.14
1	2A	1915	5MU	O2-C2-N1	-2.01	120.18	122.80
32	1a	967	5MC	O2-C2-N3	-2.01	119.16	122.33

There are no chirality outliers.

All (70) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	2263	OMG	C1'-C2'-O2'-CM2
32	1a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	O-C-CA-CB
54	1w	37	MIA	C12-C13-C14-C16
54	1y	46	7MG	C4'-C5'-O5'-P
54	1y	54	5MU	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
54	2w	37	MIA	C5-C6-N6-C12
54	2w	37	MIA	N1-C6-N6-C12
54	2w	46	7MG	O4'-C4'-C5'-O5'
54	2y	55	PSU	C2'-C1'-C5-C6
54	2y	55	PSU	O4'-C1'-C5-C6
32	1a	527	7MG	C3'-C4'-C5'-O5'
32	2a	967	5MC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
54	2w	46	7MG	C3'-C4'-C5'-O5'
54	2y	37	MIA	C3'-C4'-C5'-O5'
54	1y	8	4SU	C3'-C4'-C5'-O5'
54	1y	8	4SU	O4'-C4'-C5'-O5'
54	1y	54	5MU	C3'-C4'-C5'-O5'
1	2A	1917	PSU	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	7MG	O4'-C4'-C5'-O5'
55	1x	55	PSU	O4'-C4'-C5'-O5'
54	2y	37	MIA	O4'-C4'-C5'-O5'
54	2y	46	7MG	O4'-C1'-N9-C4
32	1a	1518	MA6	C5-C6-N6-C10
32	2a	1518	MA6	C5-C6-N6-C10
32	2a	1519	MA6	C5-C6-N6-C10
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	527	7MG	C3'-C4'-C5'-O5'
32	2a	967	5MC	C3'-C4'-C5'-O5'
32	1a	1400	5MC	O4'-C4'-C5'-O5'
1	2A	2552	2MU	O4'-C4'-C5'-O5'
54	2y	32	PSU	O4'-C4'-C5'-O5'
32	1a	1519	MA6	C5-C6-N6-C10
54	1w	46	7MG	C2'-C1'-N9-C8
54	2w	46	7MG	C2'-C1'-N9-C8
54	2y	46	7MG	C2'-C1'-N9-C8
43	2l	92	0TD	CG-CB-SB-CSB
1	1A	1942	4OC	C3'-C2'-O2'-CM2
32	2a	1519	MA6	C4'-C5'-O5'-P
54	1y	55	PSU	O4'-C1'-C5-C4
54	1y	46	7MG	C2'-C1'-N9-C8
54	2y	46	7MG	O4'-C1'-N9-C8
32	2a	1518	MA6	C5-C6-N6-C9
32	1a	527	7MG	C4'-C5'-O5'-P
1	2A	1917	PSU	C3'-C4'-C5'-O5'
32	2a	527	7MG	C4'-C5'-O5'-P

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Mol	Chain	Res	Type	Atoms
54	2y	37	MIA	C4'-C5'-O5'-P
32	1a	967	5MC	O4'-C4'-C5'-O5'
54	1w	46	7MG	C4'-C5'-O5'-P
54	1y	8	4SU	C4'-C5'-O5'-P
32	2a	1207	2MG	O4'-C4'-C5'-O5'
54	2y	54	5MU	C2'-C1'-N1-C6
54	2y	54	5MU	C2'-C1'-N1-C2
54	1w	46	7MG	O4'-C1'-N9-C8
32	2a	1404	5MC	C3'-C4'-C5'-O5'
1	1A	2515	2MA	C4'-C5'-O5'-P
43	1l	92	0TD	CG-CB-SB-CSB
32	1a	1400	5MC	C3'-C4'-C5'-O5'
32	2a	527	7MG	O4'-C4'-C5'-O5'
32	1a	1402	4OC	O4'-C4'-C5'-O5'
55	1x	55	PSU	C3'-C4'-C5'-O5'
32	2a	1402	4OC	C3'-C4'-C5'-O5'
54	1y	54	5MU	C4'-C5'-O5'-P
54	2w	46	7MG	O4'-C1'-N9-C8
55	2x	8	4SU	C2'-C1'-N1-C2
54	1y	37	MIA	C3'-C4'-C5'-O5'
1	2A	2503	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

44 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	2w	39	PSU	3	0
32	2a	1518	MA6	3	0
1	2A	1942	5MC	1	0
54	1y	55	PSU	2	0
1	1A	1961	5MU	1	0
32	1a	1404	5MC	1	0
32	1a	1207	2MG	1	0
1	2A	1920	4OC	1	0
1	2A	2503	2MA	1	0
32	1a	967	5MC	1	0
54	1y	39	PSU	1	0
54	1w	46	7MG	1	0
55	1x	8	4SU	2	0
32	2a	1402	4OC	2	0
43	1l	92	0TD	3	0
54	2y	55	PSU	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	1915	5MU	1	0
32	1a	516	PSU	1	0
1	1A	1942	4OC	2	0
43	2l	92	0TD	2	0
55	2x	55	PSU	1	0
32	2a	1519	MA6	2	0
32	1a	1519	MA6	1	0
54	1y	37	MIA	1	0
1	2A	1939	5MU	1	0
55	2x	32	5MC	1	0
54	2y	8	4SU	1	0
32	1a	1498	UR3	1	0
54	2w	37	MIA	1	0
54	1w	37	MIA	1	0
54	2w	46	7MG	1	0
55	2x	8	4SU	1	0
54	2y	46	7MG	1	0
54	2y	37	MIA	1	0
54	1y	8	4SU	3	0
32	2a	966	M2G	1	0
1	2A	2552	2MU	2	0
32	2a	1404	5MC	1	0
32	2a	1207	2MG	2	0
32	1a	1518	MA6	1	0
54	2w	8	4SU	2	0
32	2a	967	5MC	2	0
1	1A	2564	2MU	1	0
32	2a	1400	5MC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2280 ligands modelled in this entry, 2271 are monoatomic - leaving 9 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	$\# Z > 2$
57	KAN	2a	1828	-	34,35,35	1.63	6 (17%)	47,52,52	1.50	8 (17%)
59	SF4	2d	501	35	0,12,12	-	-	-	-	-
57	KAN	2A	3569	56	34,35,35	1.57	6 (17%)	47,52,52	1.98	15 (31%)
57	KAN	1a	1955	-	34,35,35	1.62	6 (17%)	47,52,52	1.10	5 (10%)
57	KAN	2A	3568	56	34,35,35	1.52	5 (14%)	47,52,52	1.68	6 (12%)
57	KAN	1A	3935	56	34,35,35	1.66	6 (17%)	47,52,52	1.76	12 (25%)
57	KAN	1A	3934	-	34,35,35	1.48	5 (14%)	47,52,52	1.63	11 (23%)
57	KAN	1A	3933	-	34,35,35	1.69	6 (17%)	47,52,52	1.29	5 (10%)
59	SF4	1d	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
57	KAN	2a	1828	-	-	1/12/72/72	0/3/3/3
59	SF4	2d	501	35	-	-	0/6/5/5
57	KAN	2A	3569	56	-	2/12/72/72	0/3/3/3
57	KAN	1a	1955	-	-	3/12/72/72	0/3/3/3
57	KAN	2A	3568	56	-	4/12/72/72	0/3/3/3
57	KAN	1A	3935	56	-	2/12/72/72	0/3/3/3
57	KAN	1A	3934	-	-	4/12/72/72	0/3/3/3
57	KAN	1A	3933	-	-	4/12/72/72	0/3/3/3
59	SF4	1d	303	35	-	-	0/6/5/5

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	1A	3933	KAN	C14-C15	-5.68	1.46	1.53
57	2a	1828	KAN	C14-C15	-5.67	1.46	1.53
57	1A	3935	KAN	C14-C15	-5.25	1.46	1.53
57	1a	1955	KAN	C14-C15	-5.24	1.47	1.53
57	2A	3568	KAN	C14-C15	-5.12	1.47	1.53
57	1A	3934	KAN	C14-C15	-4.16	1.48	1.53
57	1A	3933	KAN	C16-C15	-4.07	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	1A	3935	KAN	C16-C15	-4.01	1.48	1.53
57	2A	3569	KAN	C14-C15	-3.98	1.48	1.53
57	2A	3569	KAN	O12-C13	3.85	1.51	1.41
57	1A	3934	KAN	C15-N4	3.64	1.52	1.47
57	1a	1955	KAN	C16-C15	-3.61	1.49	1.53
57	2A	3569	KAN	C16-C15	-3.52	1.49	1.53
57	2A	3569	KAN	C15-N4	3.43	1.52	1.47
57	1a	1955	KAN	O12-C13	3.18	1.50	1.41
57	2A	3568	KAN	C15-N4	3.17	1.52	1.47
57	1A	3935	KAN	C15-N4	3.14	1.52	1.47
57	2a	1828	KAN	O12-C13	3.11	1.49	1.41
57	1a	1955	KAN	C15-N4	3.10	1.52	1.47
57	2A	3568	KAN	C16-C15	-3.08	1.49	1.53
57	1A	3934	KAN	C16-C15	-3.07	1.49	1.53
57	2A	3568	KAN	O12-C13	3.06	1.49	1.41
57	1A	3933	KAN	C15-N4	2.98	1.51	1.47
57	1A	3935	KAN	O12-C13	2.94	1.49	1.41
57	2a	1828	KAN	C16-C15	-2.90	1.49	1.53
57	1A	3934	KAN	O12-C13	2.88	1.49	1.41
57	2a	1828	KAN	C15-N4	2.81	1.51	1.47
57	1A	3933	KAN	O12-C13	2.74	1.48	1.41
57	1A	3935	KAN	O11-C13	-2.48	1.34	1.41
57	2a	1828	KAN	O5-C1	2.46	1.48	1.41
57	2A	3569	KAN	O5-C1	2.45	1.48	1.41
57	2a	1828	KAN	O5-C5	2.44	1.50	1.44
57	1A	3933	KAN	O5-C5	2.41	1.50	1.44
57	1A	3933	KAN	O5-C1	2.35	1.47	1.41
57	1A	3934	KAN	O5-C5	2.27	1.49	1.44
57	2A	3569	KAN	O5-C5	2.24	1.49	1.44
57	1A	3935	KAN	O9-C1	-2.22	1.35	1.41
57	1a	1955	KAN	O5-C1	2.17	1.47	1.41
57	1a	1955	KAN	O5-C5	2.10	1.49	1.44
57	2A	3568	KAN	O5-C1	2.09	1.47	1.41

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	2A	3568	KAN	C17-C16-C15	5.82	117.11	110.67
57	2A	3568	KAN	O12-C17-C16	5.04	118.78	109.70
57	2A	3568	KAN	C13-O11-C8	-4.78	106.66	117.98
57	2a	1828	KAN	O12-C17-C16	4.68	118.14	109.70
57	2a	1828	KAN	C17-C16-C15	4.57	115.72	110.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	2A	3569	KAN	C4-C3-C2	4.46	118.66	110.83
57	1A	3933	KAN	C10-C9-C8	4.43	118.08	109.11
57	2A	3569	KAN	C11-C12-C7	4.01	117.90	111.02
57	1A	3934	KAN	C13-O12-C17	-3.92	106.06	113.72
57	1A	3934	KAN	O11-C8-C9	3.77	116.80	107.23
57	2A	3569	KAN	C3-C4-C5	3.67	116.89	110.23
57	1A	3935	KAN	O9-C1-O5	-3.59	101.24	110.69
57	1A	3935	KAN	C13-O11-C8	-3.56	109.53	117.98
57	1A	3935	KAN	C1-O9-C10	-3.50	109.68	117.98
57	2A	3569	KAN	O5-C1-C2	3.48	117.52	110.37
57	1A	3935	KAN	C13-C14-C15	-3.47	105.74	110.40
57	1A	3934	KAN	O9-C10-C9	3.39	115.86	107.23
57	2A	3569	KAN	C1-O9-C10	-3.34	110.06	117.98
57	2A	3569	KAN	O12-C17-C16	3.29	115.63	109.70
57	1A	3933	KAN	O12-C17-C16	3.29	115.62	109.70
57	2A	3569	KAN	C1-C2-C3	3.27	116.90	110.01
57	2a	1828	KAN	C13-C14-C15	-3.26	106.01	110.40
57	1A	3935	KAN	O12-C17-C16	3.20	115.46	109.70
57	2A	3569	KAN	O5-C5-C6	3.19	112.20	106.07
57	1A	3935	KAN	C10-C9-C8	3.14	115.48	109.11
57	2a	1828	KAN	C13-O11-C8	-3.06	110.72	117.98
57	1A	3935	KAN	C4-C3-C2	3.05	116.18	110.83
57	1A	3934	KAN	C3-C4-C5	3.04	115.74	110.23
57	1A	3934	KAN	C10-C9-C8	-3.02	102.99	109.11
57	1a	1955	KAN	C13-O11-C8	-2.95	110.98	117.98
57	2A	3569	KAN	C17-C16-C15	2.92	113.91	110.67
57	2A	3569	KAN	C13-C14-C15	2.91	114.31	110.40
57	2A	3569	KAN	O11-C8-C7	-2.88	102.31	109.18
57	1A	3935	KAN	O5-C1-C2	2.88	116.28	110.37
57	2A	3569	KAN	C12-C11-C10	2.72	116.17	109.50
57	1A	3935	KAN	C1-C2-C3	2.58	115.44	110.01
57	1A	3934	KAN	C4-C3-C2	2.58	115.36	110.83
57	1a	1955	KAN	C18-C17-C16	-2.55	106.76	113.02
57	1A	3935	KAN	C18-C17-C16	-2.54	106.77	113.02
57	2A	3569	KAN	O12-C13-C14	2.53	115.58	110.37
57	1A	3935	KAN	C1-O5-C5	-2.48	108.88	113.72
57	1A	3933	KAN	C13-O11-C8	-2.43	112.21	117.98
57	2a	1828	KAN	O9-C1-C2	-2.43	102.10	108.09
57	1A	3934	KAN	O5-C5-C4	2.34	113.92	109.70
57	2A	3568	KAN	C1-O9-C10	-2.33	112.46	117.98
57	2A	3569	KAN	C10-C9-C8	2.31	113.78	109.11
57	2a	1828	KAN	O5-C5-C6	2.30	110.49	106.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	1A	3934	KAN	C6-C5-C4	-2.26	107.51	112.80
57	1A	3934	KAN	O9-C10-C11	2.14	114.30	109.18
57	2A	3568	KAN	C1-O5-C5	-2.13	109.56	113.72
57	2A	3568	KAN	O14-C16-C15	-2.12	106.42	110.22
57	1A	3934	KAN	C17-C16-C15	-2.11	108.33	110.67
57	1A	3935	KAN	C16-C15-C14	-2.09	106.52	111.06
57	1a	1955	KAN	O12-C17-C16	2.09	113.47	109.70
57	1A	3933	KAN	C12-C11-C10	2.09	114.61	109.50
57	1a	1955	KAN	C10-C9-C8	2.07	113.30	109.11
57	1A	3933	KAN	C18-C17-C16	-2.05	107.98	113.02
57	2a	1828	KAN	C6-C5-C4	-2.04	108.03	112.80
57	2A	3569	KAN	C12-C7-C8	2.04	114.50	109.50
57	2a	1828	KAN	C1-O9-C10	-2.04	113.15	117.98
57	1A	3934	KAN	C11-C12-C7	2.02	114.49	111.02
57	1a	1955	KAN	O9-C10-C11	-2.02	104.37	109.18

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	2A	3568	KAN	C11-C10-O9-C1
57	1A	3934	KAN	C9-C8-O11-C13
57	1A	3935	KAN	O12-C17-C18-O15
57	1A	3935	KAN	C16-C17-C18-O15
57	1A	3933	KAN	O12-C17-C18-O15
57	1a	1955	KAN	O12-C17-C18-O15
57	2A	3568	KAN	O12-C17-C18-O15
57	1A	3934	KAN	C9-C10-O9-C1
57	1a	1955	KAN	C16-C17-C18-O15
57	2a	1828	KAN	O12-C17-C18-O15
57	1A	3933	KAN	O5-C1-O9-C10
57	1A	3934	KAN	O12-C17-C18-O15
57	2A	3569	KAN	O12-C17-C18-O15
57	1A	3933	KAN	C2-C1-O9-C10
57	2A	3568	KAN	C9-C10-O9-C1
57	2A	3568	KAN	C16-C17-C18-O15
57	1A	3933	KAN	C16-C17-C18-O15
57	1a	1955	KAN	C9-C10-O9-C1
57	2A	3569	KAN	O12-C13-O11-C8
57	1A	3934	KAN	C4-C5-C6-N1

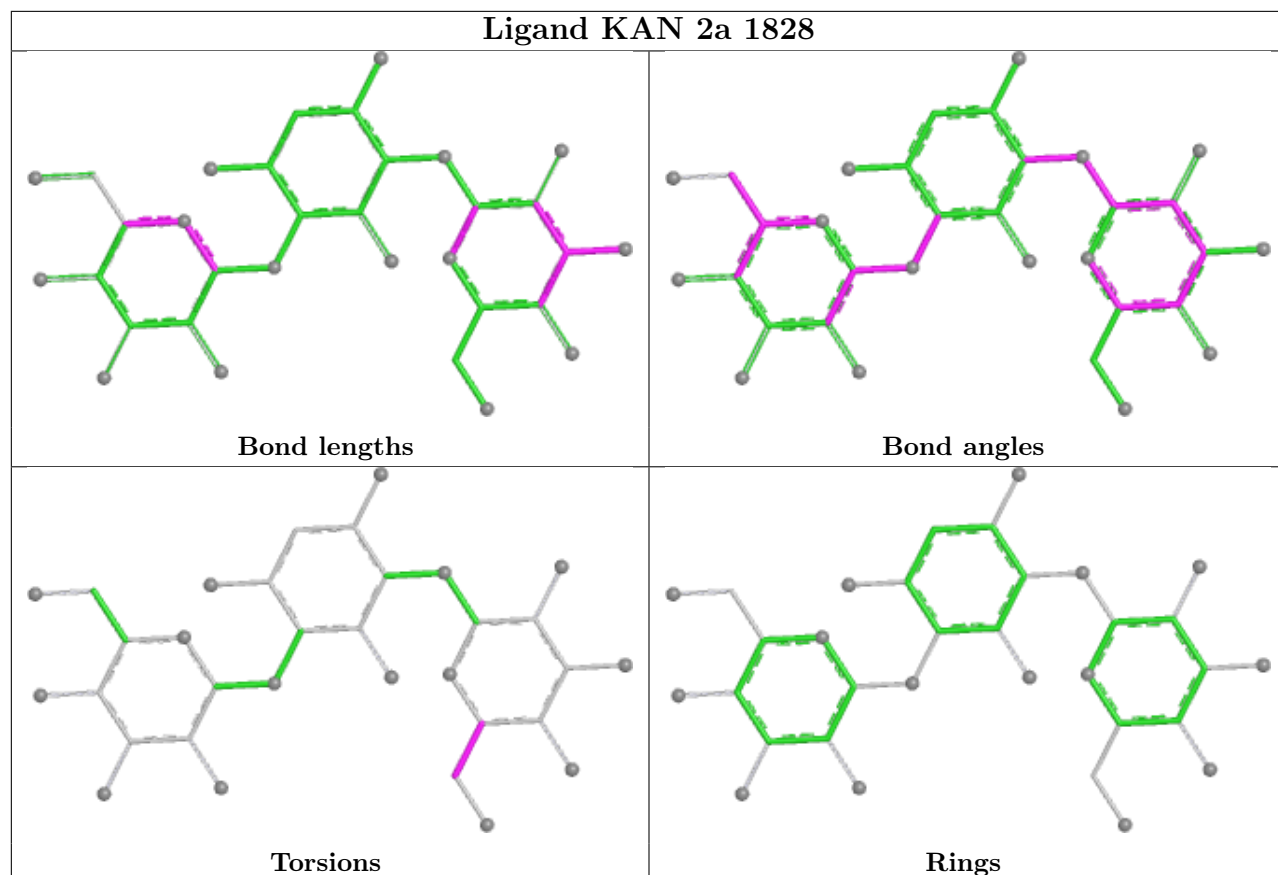
There are no ring outliers.

8 monomers are involved in 17 short contacts:

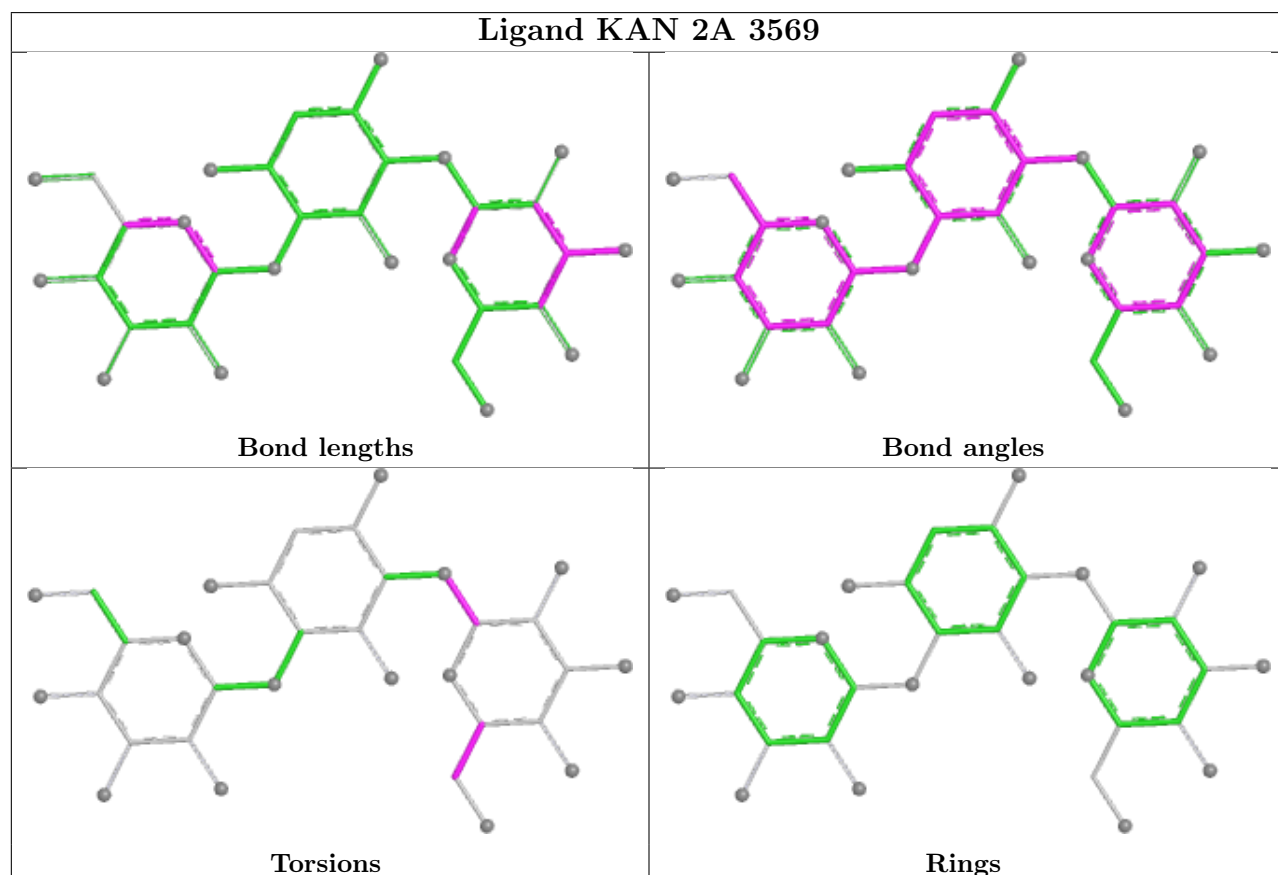
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	2a	1828	KAN	2	0
59	2d	501	SF4	1	0
57	2A	3569	KAN	2	0
57	1a	1955	KAN	3	0
57	2A	3568	KAN	2	0
57	1A	3935	KAN	2	0
57	1A	3934	KAN	4	0
59	1d	303	SF4	1	0

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

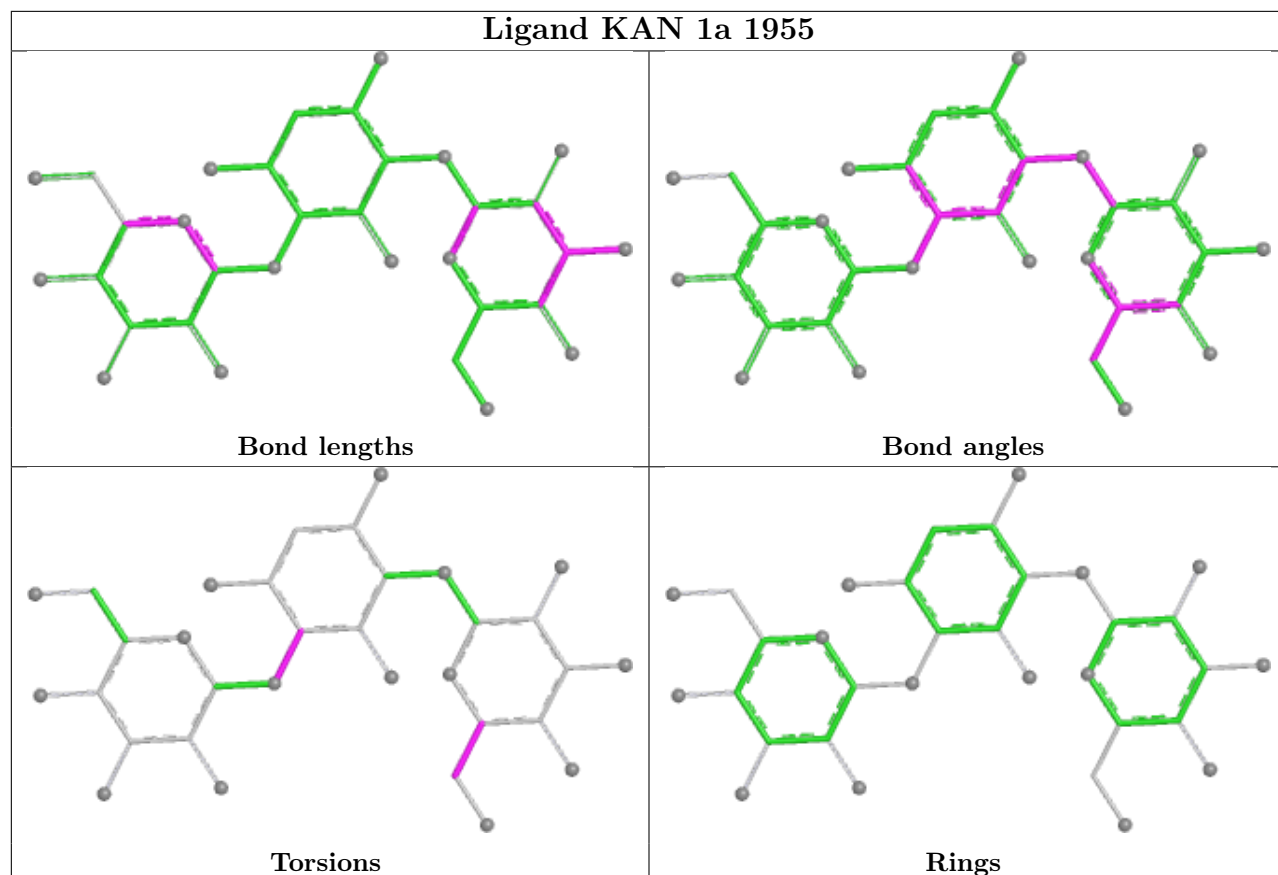
Ligand KAN 2a 1828



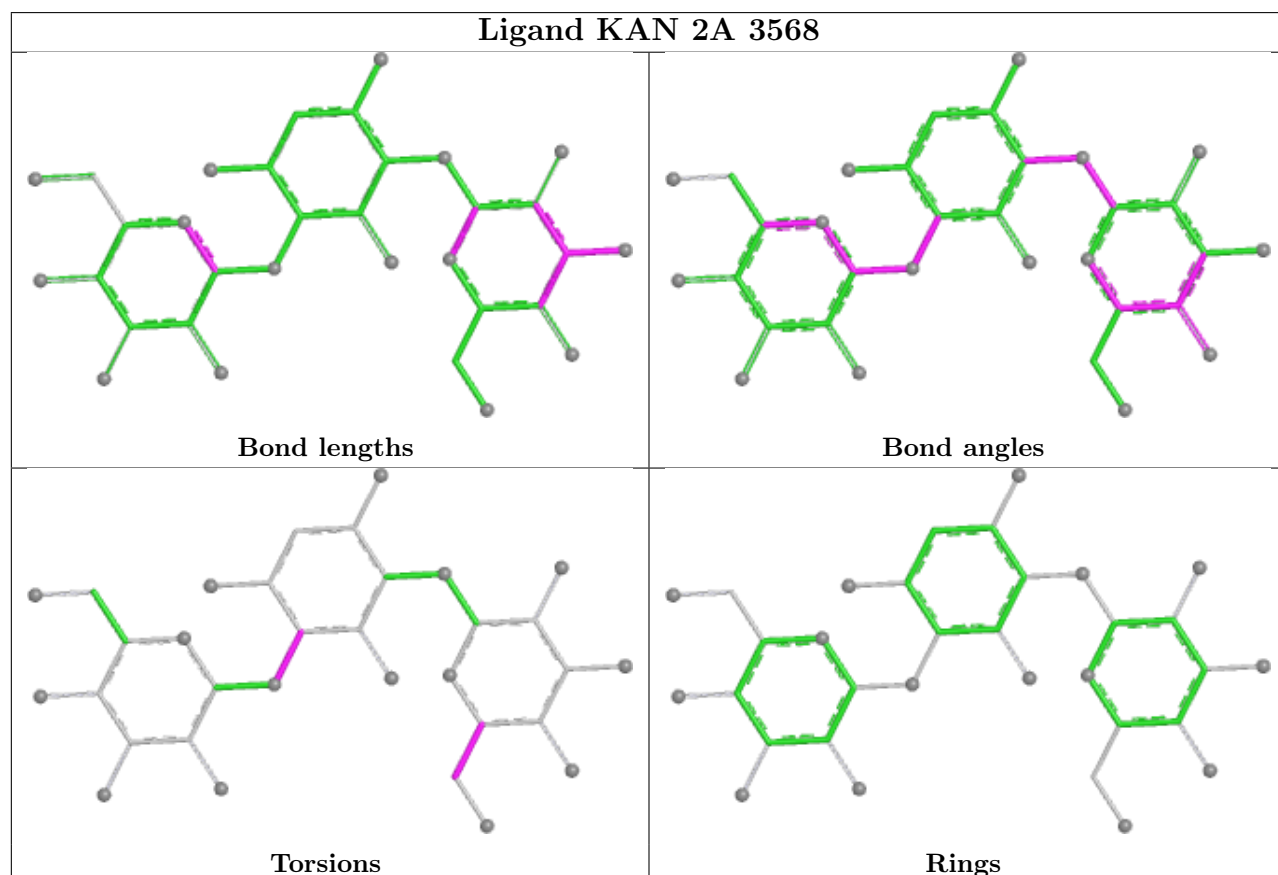
Ligand KAN 2A 3569



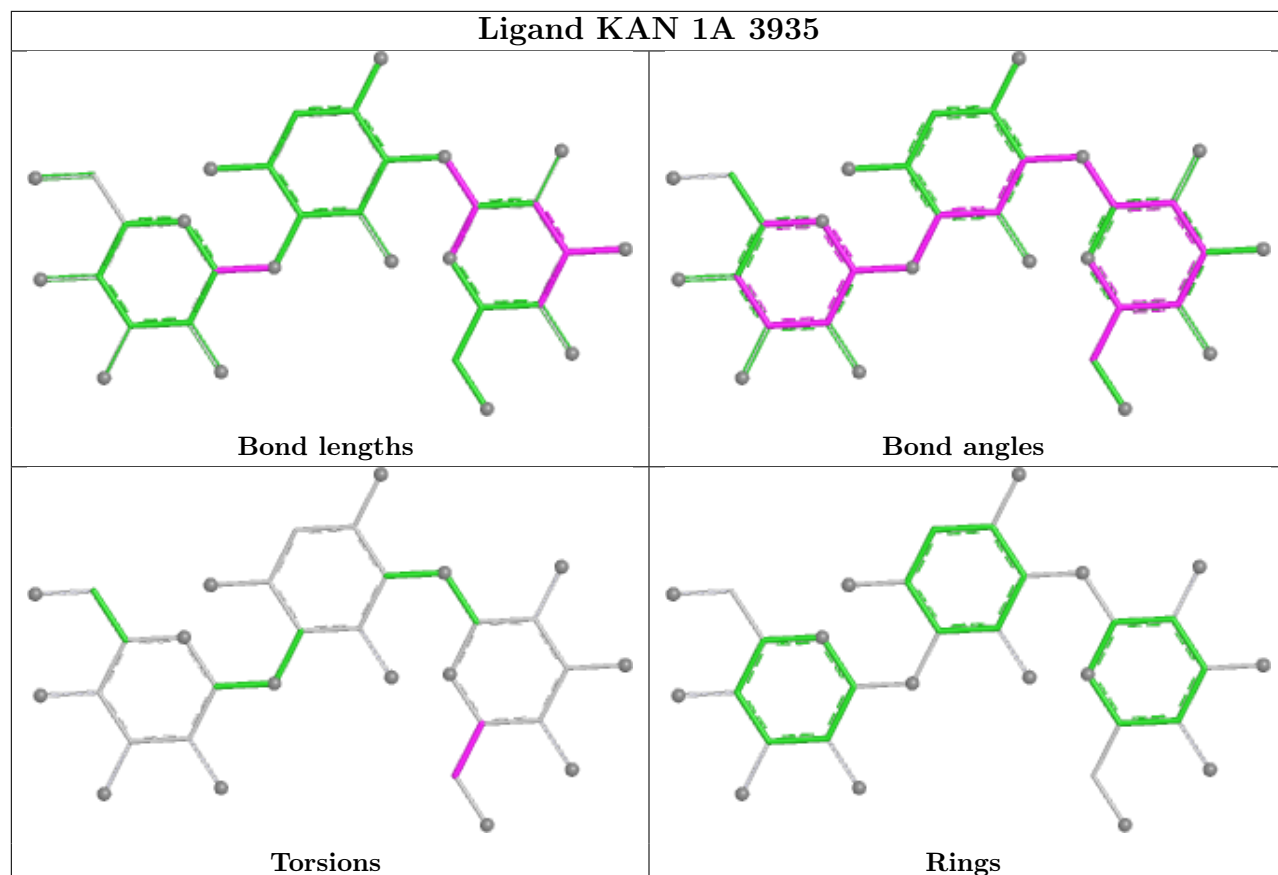
Ligand KAN 1a 1955



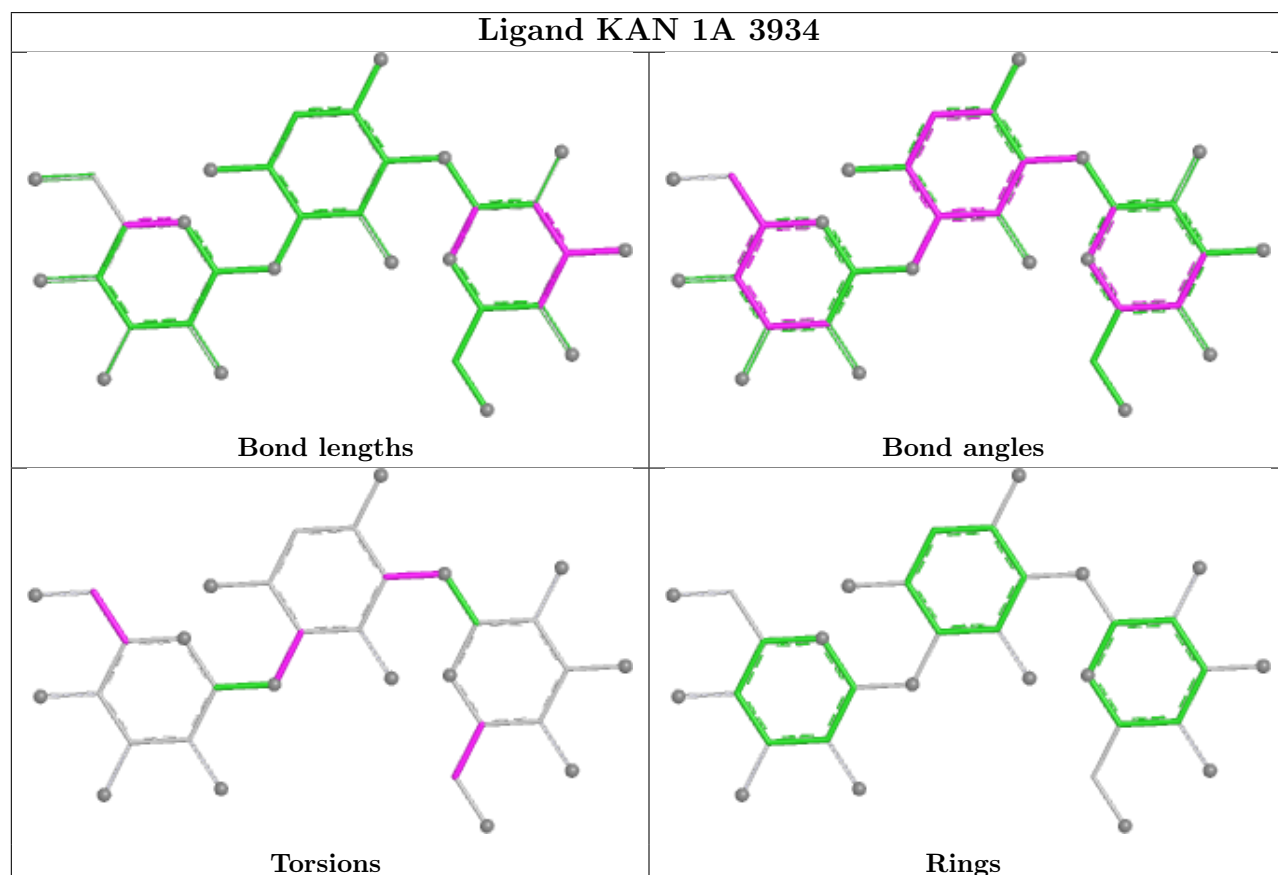
Ligand KAN 2A 3568

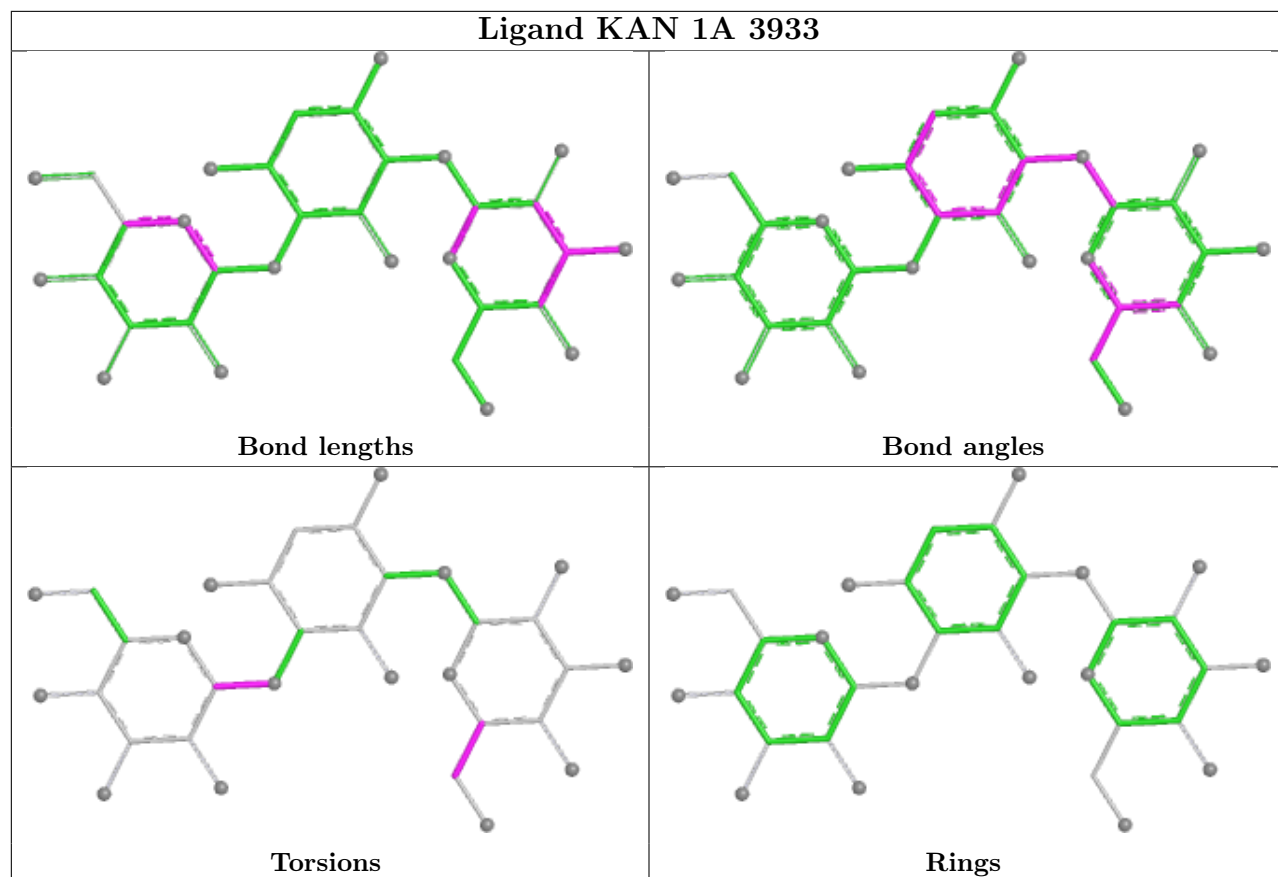


Ligand KAN 1A 3935



Ligand KAN 1A 3934





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%)	-0.56	21 (0%) 84 79	23, 43, 106, 122	0
1	2A	2789/2915 (95%)	-0.22	28 (1%) 79 73	38, 65, 105, 122	0
2	1B	120/121 (99%)	-0.53	0 100 100	37, 56, 75, 100	0
2	2B	120/121 (99%)	0.26	0 100 100	69, 87, 98, 111	0
3	1D	275/276 (99%)	-0.02	5 (1%) 67 59	25, 44, 60, 83	0
3	2D	275/276 (99%)	0.22	7 (2%) 58 48	36, 56, 69, 83	0
4	1E	204/206 (99%)	-0.18	0 100 100	27, 46, 67, 86	0
4	2E	204/206 (99%)	0.15	2 (0%) 79 73	39, 68, 80, 91	0
5	1F	203/210 (96%)	-0.12	0 100 100	24, 49, 75, 96	0
5	2F	203/210 (96%)	0.33	4 (1%) 65 56	43, 75, 91, 103	0
6	1G	181/182 (99%)	0.38	4 (2%) 62 53	46, 64, 81, 96	0
6	2G	181/182 (99%)	0.89	17 (9%) 14 12	74, 88, 97, 104	0
7	1H	174/180 (96%)	0.09	3 (1%) 69 61	45, 62, 75, 81	0
7	2H	174/180 (96%)	0.87	13 (7%) 20 16	77, 91, 102, 106	0
8	1I	146/148 (98%)	0.33	3 (2%) 63 54	51, 82, 93, 97	0
8	2I	146/148 (98%)	0.83	10 (6%) 23 18	65, 86, 96, 101	0
9	1N	140/140 (100%)	-0.06	0 100 100	34, 46, 69, 79	0
9	2N	140/140 (100%)	0.49	4 (2%) 53 45	55, 73, 88, 93	0
10	1O	122/122 (100%)	0.09	2 (1%) 70 62	33, 46, 64, 70	0
10	2O	122/122 (100%)	0.26	1 (0%) 82 77	52, 64, 78, 86	0
11	1P	149/150 (99%)	0.06	3 (2%) 65 56	23, 51, 76, 86	0
11	2P	149/150 (99%)	0.30	3 (2%) 65 56	46, 76, 92, 100	0
12	1Q	141/141 (100%)	-0.13	1 (0%) 84 79	34, 47, 60, 86	0
12	2Q	141/141 (100%)	0.80	11 (7%) 19 16	58, 76, 88, 98	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.26	0 100 100	29, 40, 53, 64	0
13	2R	118/118 (100%)	0.02	1 (0%) 82 77	47, 59, 70, 77	0
14	1S	110/112 (98%)	-0.01	0 100 100	42, 56, 68, 76	0
14	2S	110/112 (98%)	0.95	10 (9%) 15 12	70, 81, 90, 94	0
15	1T	131/146 (89%)	0.11	3 (2%) 61 52	39, 50, 76, 95	0
15	2T	131/146 (89%)	0.51	3 (2%) 61 52	56, 68, 88, 96	0
16	1U	116/118 (98%)	-0.29	0 100 100	27, 37, 54, 71	0
16	2U	116/118 (98%)	0.30	1 (0%) 81 75	49, 70, 82, 89	0
17	1V	101/101 (100%)	-0.32	0 100 100	28, 46, 62, 79	0
17	2V	101/101 (100%)	0.49	2 (1%) 65 56	50, 79, 90, 93	0
18	1W	112/113 (99%)	-0.18	2 (1%) 67 59	26, 38, 59, 92	0
18	2W	112/113 (99%)	0.19	1 (0%) 81 75	45, 56, 75, 96	0
19	1X	95/96 (98%)	-0.16	1 (1%) 78 71	30, 44, 66, 87	0
19	2X	95/96 (98%)	0.47	5 (5%) 32 25	48, 67, 81, 90	0
20	1Y	107/110 (97%)	0.03	1 (0%) 81 75	47, 57, 80, 89	0
20	2Y	107/110 (97%)	1.02	13 (12%) 8 7	69, 81, 94, 95	0
21	1Z	154/206 (74%)	0.28	5 (3%) 50 41	50, 67, 93, 100	0
21	2Z	160/206 (77%)	0.71	12 (7%) 20 16	77, 92, 105, 111	0
22	10	83/85 (97%)	0.26	7 (8%) 17 14	33, 44, 72, 89	0
22	20	83/85 (97%)	1.09	12 (14%) 6 4	52, 72, 86, 95	0
23	11	97/98 (98%)	0.22	1 (1%) 79 73	28, 45, 76, 80	0
23	21	97/98 (98%)	0.68	4 (4%) 41 33	46, 62, 84, 97	0
24	12	70/72 (97%)	-0.10	2 (2%) 53 45	42, 54, 65, 94	0
24	22	70/72 (97%)	0.48	0 100 100	61, 78, 87, 89	0
25	13	59/60 (98%)	-0.13	2 (3%) 48 39	30, 42, 66, 84	0
25	23	59/60 (98%)	0.64	2 (3%) 48 39	65, 74, 90, 102	0
26	14	69/71 (97%)	0.64	7 (10%) 12 10	57, 81, 99, 107	0
26	24	69/71 (97%)	1.04	10 (14%) 6 4	87, 95, 106, 110	0
27	15	59/60 (98%)	-0.15	1 (1%) 69 61	26, 39, 57, 70	0
27	25	59/60 (98%)	0.25	1 (1%) 69 61	46, 60, 75, 79	0
28	16	53/54 (98%)	-0.33	0 100 100	34, 46, 61, 68	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.41	1 (1%) 66 58	57, 65, 77, 82	0
29	17	48/49 (97%)	-0.05	1 (2%) 63 54	30, 34, 65, 72	0
29	27	48/49 (97%)	0.22	4 (8%) 17 14	37, 46, 70, 82	0
30	18	64/65 (98%)	-0.06	1 (1%) 70 62	31, 39, 48, 65	0
30	28	64/65 (98%)	0.65	1 (1%) 70 62	48, 63, 70, 76	0
31	19	37/37 (100%)	-0.01	1 (2%) 56 47	39, 46, 66, 70	0
31	29	37/37 (100%)	0.83	3 (8%) 18 15	67, 78, 90, 92	0
32	1a	1488/1521 (97%)	-0.18	9 (0%) 85 81	42, 71, 104, 121	0
32	2a	1491/1521 (98%)	0.17	27 (1%) 67 59	55, 85, 106, 122	0
33	1b	231/256 (90%)	0.59	12 (5%) 33 26	72, 89, 104, 110	0
33	2b	231/256 (90%)	0.89	20 (8%) 16 13	84, 97, 104, 110	0
34	1c	206/239 (86%)	0.26	5 (2%) 59 50	60, 76, 89, 94	0
34	2c	206/239 (86%)	1.14	27 (13%) 7 6	84, 94, 100, 107	0
35	1d	208/209 (99%)	0.70	10 (4%) 35 28	58, 74, 88, 98	0
35	2d	208/209 (99%)	0.93	15 (7%) 21 17	67, 80, 93, 101	0
36	1e	148/162 (91%)	0.21	2 (1%) 73 65	58, 69, 81, 94	0
36	2e	148/162 (91%)	0.82	9 (6%) 27 21	78, 86, 94, 102	0
37	1f	100/101 (99%)	0.07	0 100 100	57, 72, 83, 86	0
37	2f	100/101 (99%)	0.17	1 (1%) 79 73	64, 77, 86, 96	0
38	1g	155/156 (99%)	0.48	9 (5%) 29 22	63, 75, 91, 102	0
38	2g	155/156 (99%)	0.58	12 (7%) 19 16	76, 87, 98, 113	0
39	1h	137/138 (99%)	0.47	2 (1%) 72 64	62, 74, 82, 89	0
39	2h	137/138 (99%)	0.87	6 (4%) 39 30	74, 86, 93, 97	0
40	1i	127/128 (99%)	0.87	8 (6%) 26 20	59, 81, 91, 94	0
40	2i	127/128 (99%)	1.40	26 (20%) 2 2	79, 94, 101, 105	0
41	1j	97/105 (92%)	1.13	16 (16%) 4 3	58, 83, 96, 101	0
41	2j	96/105 (91%)	1.59	27 (28%) 1 1	84, 95, 104, 110	0
42	1k	114/129 (88%)	0.37	2 (1%) 67 59	52, 72, 83, 87	0
42	2k	114/129 (88%)	0.76	8 (7%) 22 18	63, 81, 90, 93	0
43	1l	121/132 (91%)	0.16	3 (2%) 58 48	47, 56, 73, 82	0
43	2l	121/132 (91%)	0.75	10 (8%) 17 14	60, 73, 84, 87	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	123/126 (97%)	0.58	7 (5%) 29 23	60, 72, 85, 98	0
44	2m	122/126 (96%)	1.21	18 (14%) 5 4	78, 92, 98, 105	0
45	1n	60/61 (98%)	0.51	3 (5%) 34 27	61, 70, 77, 82	0
45	2n	60/61 (98%)	1.94	20 (33%) 1 1	83, 92, 98, 99	0
46	1o	88/89 (98%)	0.47	3 (3%) 48 39	57, 69, 83, 91	0
46	2o	88/89 (98%)	0.54	4 (4%) 38 30	64, 81, 89, 95	0
47	1p	82/88 (93%)	0.96	5 (6%) 27 21	62, 74, 85, 96	0
47	2p	82/88 (93%)	0.81	5 (6%) 27 21	64, 76, 86, 92	0
48	1q	99/105 (94%)	0.54	1 (1%) 79 73	57, 73, 84, 89	0
48	2q	99/105 (94%)	0.60	3 (3%) 52 43	68, 80, 89, 95	0
49	1r	68/88 (77%)	0.01	0 100 100	61, 72, 85, 88	0
49	2r	68/88 (77%)	0.31	0 100 100	64, 81, 90, 96	0
50	1s	83/93 (89%)	0.38	2 (2%) 59 50	62, 75, 84, 94	0
50	2s	83/93 (89%)	1.21	15 (18%) 3 3	87, 94, 102, 107	0
51	1t	96/106 (90%)	0.82	7 (7%) 21 17	64, 77, 88, 96	0
51	2t	96/106 (90%)	0.61	4 (4%) 40 32	65, 77, 91, 94	0
52	1u	23/27 (85%)	0.70	2 (8%) 16 13	64, 72, 77, 80	0
52	2u	23/27 (85%)	2.14	14 (60%) 0 0	80, 89, 93, 94	0
53	1v	13/24 (54%)	0.49	1 (7%) 19 16	50, 62, 88, 105	0
53	2v	13/24 (54%)	1.68	4 (30%) 1 1	75, 95, 115, 118	0
54	1w	67/76 (88%)	0.42	3 (4%) 38 30	60, 98, 112, 115	0
54	1y	67/76 (88%)	0.57	2 (2%) 52 43	44, 104, 112, 121	0
54	2w	65/76 (85%)	0.77	9 (13%) 6 5	85, 108, 116, 120	0
54	2y	66/76 (86%)	1.02	4 (6%) 27 21	62, 113, 118, 119	0
55	1x	72/77 (93%)	-0.04	0 100 100	45, 72, 93, 99	0
55	2x	72/77 (93%)	0.27	3 (4%) 40 32	61, 86, 100, 106	0
All	All	20875/21748 (95%)	0.15	668 (3%) 50 41	23, 70, 100, 122	0

All (668) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	123	ALA	9.6
44	1m	124	PRO	8.6

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Mol	Chain	Res	Type	RSRZ
23	2l	2	SER	8.1
44	2m	122	LYS	7.5
44	2m	124	PRO	6.8
44	2m	102	ARG	6.3
44	1m	123	ALA	6.1
22	10	3	HIS	5.8
23	11	2	SER	5.8
22	10	8	GLY	5.8
44	1m	122	LYS	5.7
22	20	5	LYS	5.4
50	2s	80	TYR	5.4
51	1t	103	GLY	5.3
1	2A	883	G	5.1
22	20	2	ALA	5.0
44	1m	121	LYS	4.9
15	1T	131	ALA	4.9
22	10	7	LEU	4.8
22	20	3	HIS	4.8
54	2y	34	G	4.8
50	1s	84	GLY	4.8
38	1g	82	GLY	4.7
45	2n	38	GLY	4.7
22	10	6	GLY	4.6
50	2s	9	VAL	4.6
7	1H	2	SER	4.5
45	2n	13	THR	4.4
45	2n	25	VAL	4.4
40	1i	106	ALA	4.3
38	2g	82	GLY	4.3
53	2v	14	A	4.3
31	29	37	GLY	4.3
45	2n	39	LEU	4.3
45	2n	34	TYR	4.3
20	1Y	1	MET	4.3
15	1T	130	ALA	4.3
26	14	45	GLY	4.2
22	20	4	LYS	4.2
26	24	66	SER	4.2
40	2i	102	LEU	4.2
3	1D	276	LYS	4.2
35	2d	47	ARG	4.2
32	1a	1531	A	4.1

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Mol	Chain	Res	Type	RSRZ
52	2u	11	GLY	4.1
21	1Z	141	VAL	4.1
12	1Q	33	GLY	4.1
53	2v	24	A	4.0
40	2i	122	ALA	4.0
3	2D	38	LYS	4.0
50	2s	82	GLY	4.0
9	2N	45	ASN	4.0
22	20	6	GLY	4.0
41	2j	47	PHE	4.0
35	2d	164	ALA	4.0
38	2g	84	ASN	4.0
1	2A	2319	G	4.0
41	2j	62	HIS	3.9
33	2b	237	ALA	3.8
41	2j	59	SER	3.8
38	1g	80	VAL	3.7
43	2l	100	ILE	3.7
6	2G	28	VAL	3.7
38	2g	80	VAL	3.7
42	2k	124	LYS	3.7
41	2j	65	LEU	3.7
44	2m	121	LYS	3.7
25	23	2	PRO	3.7
22	20	7	LEU	3.7
38	2g	81	GLY	3.7
50	2s	2	PRO	3.7
33	2b	121	LEU	3.7
45	1n	2	ALA	3.6
19	2X	92	LEU	3.6
11	1P	15	ARG	3.6
34	2c	158	GLY	3.6
36	2e	22	GLY	3.6
41	2j	55	LYS	3.5
45	2n	2	ALA	3.5
44	2m	119	GLY	3.5
50	2s	13	ASP	3.5
40	1i	114	TYR	3.5
42	2k	13	GLN	3.5
52	2u	14	TRP	3.5
9	2N	44	PRO	3.5
41	2j	8	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
51	1t	10	LEU	3.5
36	2e	13	ILE	3.4
21	2Z	144	LEU	3.4
33	2b	7	VAL	3.4
41	2j	85	LEU	3.4
46	2o	60	VAL	3.4
26	14	50	VAL	3.4
32	1a	1532	U	3.4
12	2Q	66	ILE	3.4
38	1g	85	TYR	3.4
52	2u	17	THR	3.4
34	2c	155	GLY	3.3
43	1l	16	GLU	3.3
32	2a	1030(B)	C	3.3
40	2i	127	LYS	3.3
43	2l	126	LYS	3.3
45	2n	18	VAL	3.3
26	24	67	TYR	3.3
33	2b	37	ASN	3.3
1	1A	554	A	3.3
54	2w	73	A	3.3
34	2c	198	VAL	3.3
53	2v	12	A	3.3
14	2S	17	ARG	3.3
21	2Z	170	THR	3.3
6	1G	182	LYS	3.2
32	1a	204	U	3.2
6	2G	20	ILE	3.2
26	24	65	ASP	3.2
1	2A	882	G	3.2
21	2Z	146	ILE	3.2
52	2u	13	ILE	3.2
22	10	2	ALA	3.2
27	15	60	VAL	3.2
5	2F	172	TRP	3.2
12	2Q	104	PHE	3.2
41	1j	4	ILE	3.2
26	14	49	PHE	3.2
35	1d	188	LEU	3.1
45	2n	21	TYR	3.1
40	2i	14	VAL	3.1
7	2H	159	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
32	2a	1202	G	3.1
35	1d	110	PHE	3.1
32	2a	1532	U	3.1
41	1j	33	GLN	3.1
20	2Y	58	GLY	3.1
52	2u	4	GLY	3.1
32	2a	1114	C	3.1
1	2A	171	G	3.1
32	2a	1030(A)	G	3.1
53	2v	13	A	3.1
1	2A	884	C	3.1
8	2I	146	ALA	3.0
40	2i	125	TYR	3.0
41	1j	76	ASN	3.0
47	2p	82	GLN	3.0
41	2j	91	PRO	3.0
32	2a	1033	G	3.0
11	2P	15	ARG	3.0
45	2n	29	ARG	3.0
47	1p	82	GLN	3.0
51	1t	55	ILE	3.0
40	2i	126	SER	3.0
36	1e	10	MET	3.0
26	24	56	VAL	3.0
1	2A	896	A	3.0
32	2a	1357	A	3.0
55	2x	76	A	3.0
34	2c	157	ILE	3.0
41	1j	29	ARG	3.0
45	2n	3	ARG	3.0
6	2G	133	LEU	3.0
44	2m	100	GLY	3.0
32	2a	1224	G	3.0
54	2w	72	C	3.0
41	1j	32	ALA	3.0
14	2S	20	ARG	2.9
41	2j	74	ILE	2.9
31	29	21	GLY	2.9
50	2s	38	SER	2.9
15	2T	131	ALA	2.9
45	2n	20	ALA	2.9
6	1G	80	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
3	2D	276	LYS	2.9
52	1u	16	GLY	2.9
25	23	60	GLU	2.9
26	14	56	VAL	2.9
6	2G	74	LYS	2.9
1	1A	932	C	2.9
35	2d	73	ARG	2.9
42	2k	25	TYR	2.9
54	1w	73	A	2.9
4	2E	204	ALA	2.9
20	2Y	45	VAL	2.9
33	1b	237	ALA	2.9
33	2b	165	VAL	2.9
41	2j	63	PHE	2.9
41	2j	48	THR	2.9
31	29	17	ILE	2.9
45	2n	7	ILE	2.9
32	1a	1257	U	2.9
20	2Y	29	GLU	2.9
35	2d	165	MET	2.9
12	2Q	22	LYS	2.9
20	2Y	63	LYS	2.9
29	17	48	LYS	2.9
48	2q	99	SER	2.9
52	2u	24	ARG	2.9
41	1j	93	GLY	2.8
45	2n	14	PRO	2.8
46	1o	19	PRO	2.8
33	2b	236	TYR	2.8
20	2Y	5	MET	2.8
14	2S	64	GLU	2.8
35	1d	150	GLU	2.8
20	2Y	55	TYR	2.8
46	1o	87	ILE	2.8
1	1A	942	A	2.8
29	27	48	LYS	2.8
33	1b	129	GLU	2.8
19	2X	18	TYR	2.8
1	1A	1140	U	2.8
41	2j	40	LEU	2.8
54	2w	2	C	2.8
52	2u	8	THR	2.8

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Mol	Chain	Res	Type	RSRZ
34	1c	2	GLY	2.8
48	1q	54	GLY	2.8
50	2s	11	VAL	2.8
1	2A	885	C	2.8
43	1l	29	GLY	2.8
41	1j	60	ARG	2.7
34	2c	138	VAL	2.7
34	2c	87	LEU	2.7
32	2a	1257	U	2.7
12	2Q	75	THR	2.7
22	20	9	SER	2.7
40	2i	10	ARG	2.7
40	1i	110	GLU	2.7
33	1b	17	PHE	2.7
4	2E	151	TYR	2.7
1	1A	1142	A	2.7
40	2i	11	LYS	2.7
34	2c	13	GLY	2.7
52	2u	2	GLY	2.7
8	2I	3	VAL	2.7
36	2e	100	VAL	2.7
6	2G	52	ILE	2.7
1	2A	2602	A	2.7
54	2w	76	A	2.7
33	2b	21	ARG	2.7
45	2n	55	GLY	2.7
50	2s	79	THR	2.7
36	2e	96	PRO	2.7
52	2u	23	PRO	2.7
20	2Y	57	GLN	2.7
32	2a	973	G	2.7
35	2d	92	VAL	2.7
35	1d	157	LEU	2.7
47	1p	19	ILE	2.7
33	1b	22	LYS	2.7
39	2h	9	MET	2.7
33	1b	40	HIS	2.7
38	2g	156	TRP	2.7
44	2m	104	ARG	2.7
1	1A	572	A	2.7
34	1c	207	VAL	2.7
34	2c	207	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
42	2k	14	VAL	2.7
41	2j	23	ILE	2.6
45	2n	17	LYS	2.6
48	2q	100	LYS	2.6
33	2b	123	ALA	2.6
1	2A	1171	G	2.6
23	2l	28	GLY	2.6
8	2I	123	LEU	2.6
12	2Q	2	LEU	2.6
20	2Y	46	LYS	2.6
34	2c	182	ILE	2.6
34	2c	146	ALA	2.6
44	1m	87	TYR	2.6
38	1g	84	ASN	2.6
23	2l	72	GLU	2.6
41	2j	82	ILE	2.6
40	2i	101	PHE	2.6
46	1o	88	ARG	2.6
22	10	5	LYS	2.6
41	2j	49	VAL	2.6
15	2T	130	ALA	2.6
26	24	51	ASP	2.6
10	1O	49	ARG	2.6
14	2S	3	ARG	2.6
38	2g	4	ARG	2.6
32	2a	969	A	2.6
3	2D	275	LYS	2.6
33	2b	131	PRO	2.6
35	1d	84	LYS	2.6
41	1j	77	PRO	2.6
19	2X	95	LEU	2.6
7	2H	43	VAL	2.6
40	2i	53	VAL	2.6
29	27	47	ARG	2.5
51	1t	83	ARG	2.5
1	1A	1555	C	2.5
32	2a	1116	C	2.5
32	1a	1503	A	2.5
26	24	63	TYR	2.5
40	2i	96	LEU	2.5
43	2l	69	TYR	2.5
34	2c	124	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
41	1j	75	ILE	2.5
34	2c	160	ALA	2.5
38	2g	2	ALA	2.5
38	2g	26	PHE	2.5
51	2t	9	ASN	2.5
7	1H	3	ARG	2.5
1	2A	1026	U	2.5
54	2w	3	C	2.5
14	2S	32	LEU	2.5
20	2Y	59	GLY	2.5
34	2c	167	TRP	2.5
39	2h	2	LEU	2.5
40	2i	99	LEU	2.5
29	27	46	VAL	2.5
33	1b	7	VAL	2.5
34	1c	193	TYR	2.5
35	1d	170	VAL	2.5
5	2F	90	PHE	2.5
41	1j	100	THR	2.5
45	2n	30	ALA	2.5
20	2Y	50	ARG	2.5
12	2Q	1	MET	2.5
21	2Z	1	MET	2.5
44	2m	90	LEU	2.5
26	24	64	GLY	2.5
30	28	16	ILE	2.5
36	2e	23	GLY	2.5
1	2A	2155	G	2.5
1	2A	2318	G	2.5
1	1A	1141	A	2.5
41	1j	46	ARG	2.5
54	1y	36	A	2.5
22	10	4	LYS	2.5
33	2b	133	LYS	2.5
42	1k	51	LYS	2.5
22	20	8	GLY	2.5
35	2d	167	GLY	2.5
34	2c	195	VAL	2.5
7	2H	94	TYR	2.5
19	2X	69	TYR	2.5
40	1i	13	ALA	2.5
3	1D	5	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
3	1D	38	LYS	2.5
37	2f	21	LEU	2.4
7	2H	89	ILE	2.4
43	2l	7	ILE	2.4
38	1g	81	GLY	2.4
22	20	68	GLU	2.4
43	2l	32	PHE	2.4
27	25	29	THR	2.4
42	2k	31	THR	2.4
32	2a	1223	C	2.4
35	2d	154	ASN	2.4
33	2b	118	LEU	2.4
50	1s	71	LEU	2.4
51	1t	13	LEU	2.4
1	2A	229	A	2.4
1	2A	899	A	2.4
1	1A	2178	G	2.4
32	1a	630	G	2.4
34	2c	5	ILE	2.4
3	2D	59	LYS	2.4
34	2c	4	LYS	2.4
40	1i	2	GLU	2.4
40	2i	116	LYS	2.4
6	2G	29	TRP	2.4
36	1e	21	ALA	2.4
39	2h	112	LEU	2.4
41	2j	78	ASN	2.4
1	2A	897	C	2.4
1	2A	2146	C	2.4
8	2I	80	PRO	2.4
8	2I	20	ASP	2.4
35	1d	87	GLY	2.4
40	2i	109	VAL	2.4
41	2j	72	VAL	2.4
19	2X	68	ARG	2.4
32	2a	1002	G	2.4
41	2j	19	SER	2.4
33	1b	34	ALA	2.4
41	2j	32	ALA	2.4
24	12	70	GLN	2.4
35	2d	20	TYR	2.4
41	1j	88	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
3	2D	207	GLY	2.4
34	2c	2	GLY	2.4
40	2i	108	VAL	2.4
43	1l	18	VAL	2.4
42	2k	126	ARG	2.4
1	1A	935	C	2.4
44	2m	5	ALA	2.4
32	2a	1034	G	2.4
35	2d	68	TYR	2.4
40	2i	27	THR	2.4
34	2c	43	LEU	2.4
38	1g	153	HIS	2.4
55	2x	70	G	2.4
20	2Y	90	LEU	2.4
7	2H	39	PRO	2.4
12	2Q	6	ARG	2.3
52	2u	10	ARG	2.3
3	2D	2	ALA	2.3
33	2b	134	GLU	2.3
32	2a	1115	C	2.3
54	2w	74	C	2.3
7	2H	2	SER	2.3
32	1a	1447	A	2.3
12	2Q	74	TYR	2.3
17	2V	94	LEU	2.3
41	1j	85	LEU	2.3
7	2H	136	ILE	2.3
21	1Z	146	ILE	2.3
6	2G	75	LYS	2.3
33	1b	26	PRO	2.3
7	2H	17	VAL	2.3
38	2g	5	ARG	2.3
39	2h	84	ARG	2.3
26	14	54	GLY	2.3
40	1i	30	GLY	2.3
6	2G	102	PHE	2.3
31	19	12	ASP	2.3
8	1I	146	ALA	2.3
38	1g	83	ALA	2.3
43	2l	26	ALA	2.3
36	2e	20	GLN	2.3
33	2b	187	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
40	1i	19	LEU	2.3
32	2a	1226	C	2.3
54	1y	35	A	2.3
54	2y	35	A	2.3
33	1b	27	LYS	2.3
15	1T	115	ARG	2.3
30	18	46	ARG	2.3
35	2d	112	VAL	2.3
7	1H	66	GLY	2.3
52	1u	2	GLY	2.3
34	2c	137	ALA	2.3
54	2w	71	G	2.3
13	2R	69	ASP	2.3
34	2c	33	LEU	2.3
33	1b	127	ILE	2.3
9	2N	73	THR	2.3
14	2S	30	ARG	2.3
22	20	11	ARG	2.3
33	1b	33	TYR	2.3
1	1A	2160	C	2.3
1	2A	1509	C	2.3
1	2A	1536	C	2.3
1	1A	1124	U	2.3
32	2a	1225	A	2.3
43	2l	72	GLY	2.3
36	2e	130	ASN	2.3
41	2j	11	PHE	2.3
40	2i	119	ALA	2.3
41	1j	26	ALA	2.3
6	2G	53	LEU	2.3
48	2q	43	LEU	2.3
20	2Y	34	LYS	2.3
45	2n	15	LYS	2.3
1	1A	1221	G	2.3
32	2a	1032	G	2.3
24	12	69	ARG	2.3
36	2e	16	THR	2.3
41	2j	60	ARG	2.3
47	2p	69	THR	2.3
6	2G	160	VAL	2.3
23	21	62	VAL	2.3
1	2A	34	C	2.2

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Mol	Chain	Res	Type	RSRZ
41	2j	86	MET	2.2
8	1I	41	GLU	2.2
8	2I	122	GLU	2.2
34	2c	53	ALA	2.2
40	2i	106	ALA	2.2
44	1m	2	ALA	2.2
44	2m	31	LYS	2.2
28	26	7	ILE	2.2
41	2j	46	ARG	2.2
46	2o	54	ARG	2.2
25	13	2	PRO	2.2
35	2d	71	SER	2.2
40	2i	49	PRO	2.2
6	1G	146	TYR	2.2
26	14	63	TYR	2.2
33	2b	31	TYR	2.2
1	1A	1584	G	2.2
1	1A	2163	G	2.2
1	2A	2127	G	2.2
32	2a	1190	G	2.2
50	2s	84	GLY	2.2
1	1A	2139	A	2.2
6	2G	175	LEU	2.2
8	2I	117	GLU	2.2
16	2U	98	LEU	2.2
21	1Z	169	GLU	2.2
32	2a	1030	C	2.2
40	2i	95	LYS	2.2
7	2H	9	ILE	2.2
40	2i	117	HIS	2.2
6	2G	159	VAL	2.2
50	2s	42	PRO	2.2
21	1Z	104	PHE	2.2
1	2A	2133	G	2.2
1	2A	2156	G	2.2
6	1G	50	ALA	2.2
11	1P	147	LEU	2.2
14	2S	58	LEU	2.2
47	1p	27	LYS	2.2
18	2W	30	GLU	2.2
32	2a	1031	G	2.2
54	1w	1	G	2.2

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Mol	Chain	Res	Type	RSRZ
55	2x	2	G	2.2
54	2y	33	U	2.2
35	1d	118	ARG	2.2
47	1p	25	ARG	2.2
50	2s	78	ARG	2.2
32	2a	965	A	2.2
54	2w	4	C	2.2
6	2G	126	ASP	2.2
10	2O	81	ASP	2.2
12	2Q	109	VAL	2.2
21	2Z	139	VAL	2.2
21	2Z	141	VAL	2.2
44	2m	7	VAL	2.2
47	1p	2	VAL	2.2
43	2l	6	THR	2.2
12	2Q	84	GLY	2.2
18	1W	112	GLY	2.2
38	2g	85	TYR	2.2
41	1j	86	MET	2.2
26	14	69	LYS	2.2
43	2l	123	LYS	2.2
34	1c	87	LEU	2.2
12	2Q	121	ALA	2.2
39	1h	102	ARG	2.2
45	2n	12	ARG	2.2
47	2p	19	ILE	2.2
32	1a	841	U	2.2
32	2a	1001(A)	G	2.2
32	2a	1003	G	2.2
22	20	71	ASP	2.2
32	2a	1201	A	2.2
39	2h	53	VAL	2.2
53	1v	12	A	2.2
35	1d	33	MET	2.2
47	2p	48	TRP	2.2
14	2S	92	TYR	2.2
26	24	32	TYR	2.2
43	2l	120	TYR	2.2
11	2P	45	LEU	2.2
19	1X	95	LEU	2.2
46	2o	57	LEU	2.2
8	2I	55	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
34	2c	202	ILE	2.1
46	2o	68	ARG	2.1
51	2t	8	ARG	2.1
35	2d	160	GLN	2.1
34	2c	6	HIS	2.1
7	2H	49	VAL	2.1
33	2b	136	VAL	2.1
35	2d	29	PRO	2.1
41	2j	100	THR	2.1
44	2m	105	THR	2.1
52	2u	3	LYS	2.1
1	2A	2062	A	2.1
54	1w	70	G	2.1
1	1A	2414	C	2.1
1	2A	888	C	2.1
26	24	49	PHE	2.1
33	1b	10	LEU	2.1
54	2w	75	C	2.1
44	1m	118	ALA	2.1
50	2s	35	SER	2.1
51	1t	11	SER	2.1
40	2i	128	ARG	2.1
21	2Z	171	ILE	2.1
41	2j	68	HIS	2.1
8	2I	18	VAL	2.1
32	2a	1065	U	2.1
34	2c	147	LYS	2.1
11	2P	109	GLY	2.1
20	2Y	103	GLY	2.1
35	2d	87	GLY	2.1
44	2m	6	GLY	2.1
22	20	75	LEU	2.1
33	2b	122	PHE	2.1
34	2c	52	LEU	2.1
38	2g	16	LEU	2.1
21	2Z	21	ALA	2.1
38	1g	2	ALA	2.1
38	1g	4	ARG	2.1
40	2i	114	TYR	2.1
45	2n	35	ARG	2.1
50	2s	81	ARG	2.1
21	2Z	149	SER	2.1

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Mol	Chain	Res	Type	RSRZ
34	1c	90	GLU	2.1
1	1A	2183	C	2.1
33	2b	132	LYS	2.1
34	2c	150	LYS	2.1
42	2k	117	ASN	2.1
5	2F	76	GLY	2.1
14	2S	12	PHE	2.1
41	2j	54	PHE	2.1
52	2u	5	ASP	2.1
41	1j	79	ARG	2.1
45	2n	23	ARG	2.1
47	2p	8	ARG	2.1
52	2u	6	ARG	2.1
5	2F	166	ALA	2.1
11	1P	119	GLU	2.1
33	2b	208	ILE	2.1
39	1h	80	ILE	2.1
45	1n	5	ALA	2.1
45	1n	8	GLU	2.1
21	2Z	166	SER	2.1
3	1D	275	LYS	2.1
32	1a	1030	C	2.1
6	2G	172	LEU	2.1
21	2Z	157	LEU	2.1
44	2m	48	LEU	2.1
51	2t	24	LEU	2.1
1	1A	1072	U	2.1
42	1k	49	GLY	2.1
15	2T	111	ARG	2.1
3	1D	93	ALA	2.1
21	1Z	120	ILE	2.1
44	2m	107	ALA	2.1
51	1t	12	ALA	2.1
17	2V	73	SER	2.0
29	27	1	MET	2.0
40	2i	97	LYS	2.0
44	2m	120	LYS	2.0
52	2u	20	LYS	2.0
1	2A	2320	A	2.0
33	2b	15	VAL	2.0
39	2h	95	VAL	2.0
40	2i	86	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
50	2s	76	PRO	2.0
36	2e	31	LEU	2.0
1	1A	1139	G	2.0
8	1I	124	GLY	2.0
41	2j	36	GLY	2.0
42	2k	46	GLY	2.0
6	2G	50	ALA	2.0
21	2Z	172	ALA	2.0
38	2g	7	ALA	2.0
40	2i	105	ASP	2.0
44	2m	30	ALA	2.0
6	2G	18	GLU	2.0
33	2b	129	GLU	2.0
35	2d	4	TYR	2.0
51	2t	74	LYS	2.0
8	2I	15	VAL	2.0
14	2S	34	HIS	2.0
50	2s	83	HIS	2.0
7	2H	168	PRO	2.0
3	2D	155	LEU	2.0
34	2c	196	LEU	2.0
54	2y	23	A	2.0
18	1W	60	ASN	2.0
25	13	55	ARG	2.0
7	2H	22	GLY	2.0
40	1i	18	PHE	2.0
1	1A	943	C	2.0
1	2A	886	C	2.0
1	2A	898	C	2.0
10	1O	47	ILE	2.0
9	2N	43	THR	2.0
1	2A	2154	G	2.0
6	2G	35	GLU	2.0
35	1d	54	TYR	2.0
7	2H	45	VAL	2.0
26	24	50	VAL	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column

labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	7MG	2y	46	24/25	0.53	0.14	108,115,122,143	0
54	5MU	2y	54	21/22	0.53	0.14	100,108,120,137	0
54	7MG	2w	46	24/25	0.54	0.12	104,113,124,141	0
54	7MG	1y	46	24/25	0.55	0.14	101,112,119,130	0
54	MIA	2y	37	22/30	0.55	0.16	92,104,116,129	0
54	4SU	2y	8	20/21	0.61	0.14	111,115,121,124	0
54	7MG	1w	46	24/25	0.62	0.13	88,103,119,135	0
54	PSU	2y	32	20/21	0.64	0.18	99,110,119,121	0
54	5MU	1y	54	21/22	0.65	0.15	97,103,113,129	0
54	PSU	2y	55	20/21	0.66	0.11	102,113,127,129	0
54	PSU	1y	55	20/21	0.70	0.14	101,108,115,126	0
54	4SU	2w	8	20/21	0.71	0.10	109,114,122,137	0
54	4SU	1y	8	20/21	0.71	0.10	101,107,113,113	0
54	MIA	1y	37	22/30	0.78	0.12	81,90,97,99	0
55	PSU	2x	55	20/21	0.78	0.12	80,89,100,105	0
54	4SU	1w	8	20/21	0.79	0.10	91,99,107,109	0
54	PSU	2y	39	20/21	0.81	0.12	91,101,110,111	0
54	PSU	1y	32	20/21	0.81	0.11	84,92,101,101	0
55	4SU	2x	8	20/21	0.82	0.11	77,88,93,93	0
32	2MG	2a	1207	24/25	0.83	0.13	86,91,99,102	0
55	5MU	2x	54	21/22	0.84	0.12	88,93,99,109	0
54	5MU	2w	54	21/22	0.84	0.09	79,91,95,99	0
54	PSU	1w	55	20/21	0.84	0.09	70,90,98,99	0
54	PSU	2w	32	20/21	0.85	0.13	87,95,100,102	0
54	PSU	2w	55	20/21	0.85	0.09	92,97,106,108	0
54	PSU	1w	32	20/21	0.88	0.12	68,78,82,83	0
1	5MU	2A	1915	21/22	0.88	0.10	76,83,88,89	0
54	PSU	1y	39	20/21	0.88	0.09	85,91,104,106	0
32	PSU	2a	516	20/21	0.89	0.10	76,83,89,89	0
1	PSU	2A	1917	20/21	0.90	0.08	72,78,88,88	0
55	5MU	1x	54	21/22	0.90	0.08	64,75,79,84	0
55	PSU	1x	55	20/21	0.90	0.08	66,70,78,83	0
32	7MG	2a	527	24/25	0.91	0.11	66,72,78,82	0
54	MIA	2w	37	25/30	0.91	0.11	79,89,94,97	0
55	5MC	2x	32	21/22	0.91	0.13	75,83,87,88	0
1	5MU	1A	1937	21/22	0.92	0.10	56,63,70,74	0
32	M2G	2a	966	25/26	0.92	0.15	68,79,87,92	0
32	5MC	2a	967	21/22	0.92	0.13	78,81,86,94	0
54	PSU	2w	39	20/21	0.92	0.11	82,94,99,99	0
55	4SU	1x	8	20/21	0.92	0.11	60,68,78,79	0
32	5MC	2a	1400	21/22	0.92	0.17	72,81,85,92	0
54	5MU	1w	54	21/22	0.93	0.08	62,76,84,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	5MC	2a	1407	21/22	0.93	0.10	60,65,71,82	0
1	5MC	2A	1942	21/22	0.94	0.09	56,70,78,85	0
32	UR3	2a	1498	21/22	0.94	0.10	60,64,69,78	0
43	0TD	2l	92	10/11	0.94	0.10	64,69,74,81	0
1	5MC	2A	1962	21/22	0.94	0.11	50,57,68,78	0
32	7MG	1a	527	24/25	0.94	0.09	47,53,57,59	0
1	4OC	2A	1920	21/23	0.94	0.08	67,72,75,78	0
32	4OC	2a	1402	22/23	0.94	0.10	64,71,75,78	0
1	PSU	2A	1911	20/21	0.95	0.07	66,72,75,75	0
32	5MC	2a	1404	21/22	0.95	0.09	54,63,68,70	0
43	0TD	1l	92	10/11	0.95	0.07	48,51,54,65	0
32	PSU	1a	516	20/21	0.95	0.08	54,64,71,71	0
32	MA6	2a	1519	24/25	0.95	0.12	57,69,76,82	0
1	OMG	2A	2251	24/25	0.95	0.10	45,51,56,60	0
1	2MA	2A	2503	23/24	0.95	0.13	34,44,50,54	0
1	PSU	2A	2605	20/21	0.95	0.09	34,47,51,52	0
1	PSU	1A	1933	20/21	0.96	0.08	44,51,56,58	0
54	MIA	1w	37	29/30	0.96	0.11	51,58,69,70	0
54	PSU	1w	39	20/21	0.96	0.09	53,72,76,78	0
1	PSU	1A	1939	20/21	0.96	0.08	40,57,64,66	0
32	2MG	1a	1207	24/25	0.96	0.06	54,70,73,76	0
32	5MC	1a	1400	21/22	0.96	0.10	43,54,62,67	0
1	5MU	1A	1961	21/22	0.96	0.08	36,39,43,51	0
55	5MC	1x	32	21/22	0.96	0.10	52,57,62,65	0
1	5MC	1A	1964	21/22	0.96	0.08	46,50,55,56	0
32	MA6	2a	1518	24/25	0.96	0.10	54,70,74,77	0
1	2MA	1A	2515	23/24	0.97	0.07	21,27,32,34	0
1	2MU	1A	2564	21/23	0.97	0.07	31,36,40,44	0
32	5MC	1a	1404	21/22	0.97	0.09	42,46,51,51	0
1	2MU	2A	2552	21/23	0.97	0.06	40,45,56,62	0
32	5MC	1a	1407	21/22	0.97	0.07	40,46,50,53	0
32	UR3	1a	1498	21/22	0.97	0.08	34,45,49,55	0
32	MA6	1a	1519	24/25	0.97	0.10	43,48,53,58	0
1	4OC	1A	1942	21/23	0.97	0.09	41,49,55,56	0
1	OMG	1A	2263	24/25	0.97	0.08	24,30,34,38	0
32	M2G	1a	966	25/26	0.97	0.10	56,61,69,70	0
1	5MU	2A	1939	21/22	0.97	0.07	47,51,55,58	0
32	5MC	1a	967	21/22	0.97	0.11	57,63,68,70	0
32	4OC	1a	1402	22/23	0.98	0.07	46,53,58,68	0
32	MA6	1a	1518	24/25	0.98	0.08	40,48,52,58	0
1	5MC	1A	1984	21/22	0.98	0.06	31,45,47,49	0
1	PSU	1A	2617	20/21	0.98	0.07	24,35,39,40	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3915	1/1	0.24	0.19	86,86,86,86	0
56	MG	2A	3456	1/1	0.33	0.29	97,97,97,97	0
56	MG	1x	123	1/1	0.36	0.16	85,85,85,85	0
56	MG	2A	3515	1/1	0.37	0.27	86,86,86,86	0
56	MG	2a	1642	1/1	0.40	0.36	84,84,84,84	0
56	MG	1a	1883	1/1	0.41	0.24	89,89,89,89	0
56	MG	1A	3920	1/1	0.42	0.16	95,95,95,95	0
56	MG	2a	1725	1/1	0.42	0.25	96,96,96,96	0
56	MG	1A	3838	1/1	0.43	0.29	84,84,84,84	0
56	MG	2l	101	1/1	0.43	0.22	82,82,82,82	0
56	MG	2v	102	1/1	0.43	0.36	89,89,89,89	0
56	MG	2A	3498	1/1	0.45	0.19	90,90,90,90	0
56	MG	1a	1832	1/1	0.45	0.18	78,78,78,78	0
56	MG	1A	3751	1/1	0.46	0.31	72,72,72,72	0
56	MG	1a	1853	1/1	0.47	0.21	81,81,81,81	0
56	MG	1A	3730	1/1	0.47	0.16	73,73,73,73	0
56	MG	2A	3464	1/1	0.47	0.27	82,82,82,82	0
56	MG	2a	1803	1/1	0.48	0.29	82,82,82,82	0
56	MG	2a	1817	1/1	0.50	0.20	75,75,75,75	0
56	MG	2A	3329	1/1	0.51	0.17	86,86,86,86	0
56	MG	1A	3865	1/1	0.52	0.14	79,79,79,79	0
56	MG	2A	3110	1/1	0.54	0.11	85,85,85,85	0
56	MG	1a	1918	1/1	0.54	0.19	86,86,86,86	0
56	MG	1a	1936	1/1	0.54	0.16	71,71,71,71	0
56	MG	1Q	203	1/1	0.54	0.18	63,63,63,63	0
56	MG	1A	3770	1/1	0.55	0.18	74,74,74,74	0
56	MG	2a	1685	1/1	0.56	0.30	81,81,81,81	0
56	MG	2a	1779	1/1	0.57	0.24	81,81,81,81	0
56	MG	1A	3175	1/1	0.57	0.16	83,83,83,83	0
56	MG	1a	1739	1/1	0.58	0.21	75,75,75,75	0
56	MG	1A	3892	1/1	0.58	0.15	69,69,69,69	0
56	MG	1A	3766	1/1	0.58	0.18	98,98,98,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1802	1/1	0.59	0.21	81,81,81,81	0
56	MG	1A	3803	1/1	0.59	0.23	55,55,55,55	0
56	MG	1B	220	1/1	0.59	0.32	81,81,81,81	0
56	MG	1a	1872	1/1	0.59	0.19	71,71,71,71	0
56	MG	1w	104	1/1	0.61	0.17	93,93,93,93	0
56	MG	2A	3197	1/1	0.61	0.34	66,66,66,66	0
56	MG	1A	3488	1/1	0.62	0.22	94,94,94,94	0
56	MG	2a	1798	1/1	0.62	0.17	89,89,89,89	0
56	MG	2a	1797	1/1	0.63	0.18	99,99,99,99	0
56	MG	2A	3061	1/1	0.63	0.28	79,79,79,79	0
56	MG	1A	3919	1/1	0.63	0.17	85,85,85,85	0
56	MG	1A	3627	1/1	0.63	0.21	56,56,56,56	0
56	MG	1a	1738	1/1	0.63	0.13	95,95,95,95	0
56	MG	2a	1827	1/1	0.63	0.16	74,74,74,74	0
56	MG	2A	3517	1/1	0.63	0.15	91,91,91,91	0
56	MG	2a	1700	1/1	0.64	0.23	77,77,77,77	0
56	MG	1a	1717	1/1	0.64	0.22	77,77,77,77	0
56	MG	2A	3333	1/1	0.64	0.20	79,79,79,79	0
56	MG	2A	3530	1/1	0.64	0.14	74,74,74,74	0
56	MG	1a	1746	1/1	0.64	0.15	85,85,85,85	0
56	MG	2a	1607	1/1	0.64	0.16	83,83,83,83	0
56	MG	1d	302	1/1	0.64	0.24	81,81,81,81	0
56	MG	2a	1663	1/1	0.64	0.28	85,85,85,85	0
56	MG	1a	1674	1/1	0.64	0.18	78,78,78,78	0
56	MG	2a	1699	1/1	0.64	0.11	81,81,81,81	0
56	MG	1A	3140	1/1	0.65	0.17	71,71,71,71	0
56	MG	1A	3855	1/1	0.65	0.16	69,69,69,69	0
56	MG	2a	1621	1/1	0.66	0.15	99,99,99,99	0
56	MG	2A	3513	1/1	0.66	0.21	82,82,82,82	0
56	MG	1A	3706	1/1	0.66	0.20	55,55,55,55	0
56	MG	2a	1800	1/1	0.66	0.16	86,86,86,86	0
56	MG	2a	1664	1/1	0.66	0.13	89,89,89,89	0
56	MG	2A	3075	1/1	0.66	0.37	81,81,81,81	0
56	MG	1A	3772	1/1	0.66	0.22	76,76,76,76	0
56	MG	2A	3144	1/1	0.66	0.16	91,91,91,91	0
56	MG	1a	1879	1/1	0.66	0.13	87,87,87,87	0
56	MG	1a	1831	1/1	0.67	0.15	102,102,102,102	0
56	MG	1a	1615	1/1	0.67	0.14	83,83,83,83	0
56	MG	1a	1691	1/1	0.67	0.17	75,75,75,75	0
56	MG	2a	1723	1/1	0.67	0.18	84,84,84,84	0
56	MG	2A	3524	1/1	0.67	0.29	79,79,79,79	0
56	MG	2A	3510	1/1	0.67	0.17	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2T	202	1/1	0.67	0.20	82,82,82,82	0
56	MG	2A	3346	1/1	0.68	0.25	69,69,69,69	0
56	MG	2A	3447	1/1	0.68	0.18	86,86,86,86	0
56	MG	2a	1764	1/1	0.68	0.22	75,75,75,75	0
56	MG	1a	1896	1/1	0.68	0.15	73,73,73,73	0
56	MG	2A	3065	1/1	0.68	0.20	79,79,79,79	0
56	MG	2a	1649	1/1	0.68	0.17	81,81,81,81	0
56	MG	2A	3548	1/1	0.69	0.22	58,58,58,58	0
56	MG	1o	103	1/1	0.69	0.17	75,75,75,75	0
56	MG	2a	1721	1/1	0.69	0.35	82,82,82,82	0
56	MG	1a	1609	1/1	0.69	0.33	81,81,81,81	0
56	MG	2A	3451	1/1	0.69	0.19	84,84,84,84	0
56	MG	1x	112	1/1	0.69	0.13	72,72,72,72	0
56	MG	2a	1778	1/1	0.69	0.10	87,87,87,87	0
56	MG	2a	1698	1/1	0.69	0.32	86,86,86,86	0
56	MG	1A	3866	1/1	0.70	0.25	69,69,69,69	0
56	MG	2a	1672	1/1	0.70	0.16	94,94,94,94	0
56	MG	2a	1811	1/1	0.70	0.12	79,79,79,79	0
56	MG	1A	3784	1/1	0.70	0.18	76,76,76,76	0
56	MG	2A	3361	1/1	0.70	0.32	67,67,67,67	0
56	MG	2A	3459	1/1	0.70	0.16	56,56,56,56	0
56	MG	2A	3500	1/1	0.71	0.09	80,80,80,80	0
56	MG	2a	1614	1/1	0.71	0.31	84,84,84,84	0
56	MG	2A	3063	1/1	0.71	0.26	69,69,69,69	0
56	MG	1A	3648	1/1	0.71	0.13	77,77,77,77	0
56	MG	2a	1644	1/1	0.71	0.17	83,83,83,83	0
56	MG	2A	3442	1/1	0.71	0.15	78,78,78,78	0
56	MG	2a	1787	1/1	0.71	0.18	84,84,84,84	0
56	MG	2a	1654	1/1	0.71	0.25	76,76,76,76	0
56	MG	1A	3085	1/1	0.71	0.24	73,73,73,73	0
56	MG	1A	3727	1/1	0.71	0.16	65,65,65,65	0
56	MG	1a	1912	1/1	0.71	0.20	71,71,71,71	0
56	MG	2A	3541	1/1	0.71	0.11	85,85,85,85	0
56	MG	2a	1686	1/1	0.71	0.18	80,80,80,80	0
56	MG	1a	1862	1/1	0.71	0.13	78,78,78,78	0
56	MG	2a	1821	1/1	0.71	0.34	67,67,67,67	0
56	MG	2A	3020	1/1	0.71	0.26	72,72,72,72	0
56	MG	1A	3185	1/1	0.71	0.25	73,73,73,73	0
56	MG	2a	1623	1/1	0.72	0.23	70,70,70,70	0
56	MG	1A	3868	1/1	0.72	0.10	83,83,83,83	0
56	MG	1a	1882	1/1	0.72	0.14	86,86,86,86	0
56	MG	1A	3658	1/1	0.72	0.21	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1782	1/1	0.72	0.36	65,65,65,65	0
56	MG	1a	1894	1/1	0.72	0.14	67,67,67,67	0
56	MG	1A	3900	1/1	0.72	0.17	75,75,75,75	0
56	MG	1A	3647	1/1	0.72	0.15	91,91,91,91	0
56	MG	1A	3253	1/1	0.72	0.17	73,73,73,73	0
56	MG	2A	3545	1/1	0.72	0.20	72,72,72,72	0
56	MG	1a	1859	1/1	0.72	0.12	79,79,79,79	0
56	MG	1A	3794	1/1	0.72	0.17	59,59,59,59	0
56	MG	2A	3140	1/1	0.72	0.18	71,71,71,71	0
56	MG	1A	3800	1/1	0.72	0.11	68,68,68,68	0
56	MG	1v	101	1/1	0.72	0.41	73,73,73,73	0
56	MG	2A	3503	1/1	0.72	0.12	89,89,89,89	0
56	MG	2a	1658	1/1	0.73	0.22	77,77,77,77	0
56	MG	2A	3496	1/1	0.73	0.23	91,91,91,91	0
56	MG	2A	3340	1/1	0.73	0.13	69,69,69,69	0
56	MG	2A	3086	1/1	0.73	0.21	67,67,67,67	0
56	MG	1A	3449	1/1	0.73	0.14	51,51,51,51	0
56	MG	2A	3435	1/1	0.73	0.15	74,74,74,74	0
56	MG	1a	1890	1/1	0.73	0.12	83,83,83,83	0
56	MG	1A	3151	1/1	0.73	0.14	68,68,68,68	0
56	MG	1a	1693	1/1	0.73	0.17	63,63,63,63	0
56	MG	2a	1717	1/1	0.73	0.21	77,77,77,77	0
56	MG	2A	3308	1/1	0.73	0.24	58,58,58,58	0
56	MG	2A	3526	1/1	0.73	0.14	76,76,76,76	0
56	MG	2a	1822	1/1	0.73	0.21	71,71,71,71	0
56	MG	1A	3752	1/1	0.73	0.16	71,71,71,71	0
56	MG	1a	1616	1/1	0.73	0.13	61,61,61,61	0
56	MG	2A	3441	1/1	0.74	0.18	85,85,85,85	0
56	MG	1A	3887	1/1	0.74	0.13	61,61,61,61	0
56	MG	1A	3761	1/1	0.74	0.13	79,79,79,79	0
56	MG	1a	1723	1/1	0.74	0.17	80,80,80,80	0
56	MG	1A	3929	1/1	0.74	0.34	69,69,69,69	0
56	MG	1x	102	1/1	0.74	0.14	80,80,80,80	0
56	MG	2A	3341	1/1	0.74	0.24	81,81,81,81	0
56	MG	1a	1666	1/1	0.74	0.18	90,90,90,90	0
56	MG	2a	1722	1/1	0.74	0.20	79,79,79,79	0
56	MG	2A	3353	1/1	0.74	0.22	81,81,81,81	0
56	MG	2a	1819	1/1	0.74	0.34	57,57,57,57	0
56	MG	1A	3631	1/1	0.74	0.16	77,77,77,77	0
56	MG	2a	1732	1/1	0.74	0.23	90,90,90,90	0
56	MG	2G	201	1/1	0.74	0.20	75,75,75,75	0
56	MG	1A	3856	1/1	0.74	0.21	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	2x	103	1/1	0.74	0.11	83,83,83,83	0
56	MG	2x	107	1/1	0.74	0.17	80,80,80,80	0
56	MG	1A	3922	1/1	0.75	0.14	67,67,67,67	0
56	MG	2A	3291	1/1	0.75	0.23	82,82,82,82	0
56	MG	2A	3458	1/1	0.75	0.23	73,73,73,73	0
56	MG	2a	1730	1/1	0.75	0.17	83,83,83,83	0
56	MG	1A	3313	1/1	0.75	0.21	75,75,75,75	0
56	MG	2a	1734	1/1	0.75	0.14	59,59,59,59	0
56	MG	1A	3208	1/1	0.75	0.22	84,84,84,84	0
56	MG	2a	1775	1/1	0.75	0.22	73,73,73,73	0
56	MG	2A	3471	1/1	0.75	0.20	78,78,78,78	0
56	MG	2A	3484	1/1	0.75	0.25	67,67,67,67	0
56	MG	2A	3055	1/1	0.75	0.28	69,69,69,69	0
56	MG	1a	1953	1/1	0.75	0.10	83,83,83,83	0
56	MG	1F	303	1/1	0.75	0.24	75,75,75,75	0
56	MG	2A	3342	1/1	0.75	0.13	77,77,77,77	0
56	MG	1l	203	1/1	0.75	0.23	71,71,71,71	0
56	MG	2A	3350	1/1	0.75	0.10	66,66,66,66	0
56	MG	1o	101	1/1	0.75	0.14	80,80,80,80	0
56	MG	2a	1667	1/1	0.75	0.20	81,81,81,81	0
56	MG	1A	3166	1/1	0.75	0.33	58,58,58,58	0
56	MG	2A	3370	1/1	0.75	0.26	60,60,60,60	0
56	MG	2A	3387	1/1	0.75	0.18	73,73,73,73	0
56	MG	1A	3726	1/1	0.75	0.23	63,63,63,63	0
56	MG	1a	1855	1/1	0.75	0.13	63,63,63,63	0
56	MG	2A	3543	1/1	0.75	0.13	88,88,88,88	0
56	MG	1A	3757	1/1	0.75	0.23	65,65,65,65	0
56	MG	2A	3151	1/1	0.75	0.26	65,65,65,65	0
56	MG	1A	3230	1/1	0.76	0.16	76,76,76,76	0
56	MG	1A	3654	1/1	0.76	0.13	76,76,76,76	0
56	MG	1A	3417	1/1	0.76	0.20	51,51,51,51	0
56	MG	2a	1695	1/1	0.76	0.23	80,80,80,80	0
56	MG	1a	1814	1/1	0.76	0.17	76,76,76,76	0
56	MG	1A	3024	1/1	0.76	0.23	74,74,74,74	0
56	MG	2A	3059	1/1	0.76	0.25	75,75,75,75	0
56	MG	1A	3880	1/1	0.76	0.19	66,66,66,66	0
56	MG	1a	1709	1/1	0.76	0.44	68,68,68,68	0
56	MG	1a	1610	1/1	0.76	0.17	71,71,71,71	0
56	MG	1A	3484	1/1	0.76	0.18	51,51,51,51	0
56	MG	2a	1724	1/1	0.76	0.21	77,77,77,77	0
56	MG	1a	1931	1/1	0.77	0.12	92,92,92,92	0
56	MG	2A	3047	1/1	0.77	0.24	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1724	1/1	0.77	0.29	75,75,75,75	0
56	MG	1a	1942	1/1	0.77	0.18	79,79,79,79	0
56	MG	1B	206	1/1	0.77	0.10	61,61,61,61	0
56	MG	1A	3409	1/1	0.77	0.17	69,69,69,69	0
56	MG	2a	1620	1/1	0.77	0.11	92,92,92,92	0
56	MG	1A	3218	1/1	0.77	0.15	75,75,75,75	0
56	MG	2A	3067	1/1	0.77	0.27	80,80,80,80	0
56	MG	1a	1757	1/1	0.77	0.12	69,69,69,69	0
56	MG	2A	3505	1/1	0.77	0.12	82,82,82,82	0
56	MG	2A	3509	1/1	0.77	0.20	57,57,57,57	0
56	MG	1a	1774	1/1	0.77	0.12	76,76,76,76	0
56	MG	2A	3511	1/1	0.77	0.21	87,87,87,87	0
56	MG	2A	3364	1/1	0.77	0.29	62,62,62,62	0
56	MG	1A	3668	1/1	0.77	0.26	69,69,69,69	0
56	MG	2A	3130	1/1	0.77	0.15	73,73,73,73	0
56	MG	1v	102	1/1	0.77	0.23	67,67,67,67	0
56	MG	2a	1804	1/1	0.77	0.26	78,78,78,78	0
56	MG	2a	1676	1/1	0.77	0.09	84,84,84,84	0
56	MG	2a	1815	1/1	0.77	0.22	71,71,71,71	0
56	MG	14	502	1/1	0.77	0.09	79,79,79,79	0
56	MG	2A	3529	1/1	0.77	0.12	82,82,82,82	0
56	MG	1A	3438	1/1	0.77	0.12	78,78,78,78	0
56	MG	2A	3538	1/1	0.77	0.18	66,66,66,66	0
56	MG	2A	3163	1/1	0.77	0.10	76,76,76,76	0
56	MG	1A	3782	1/1	0.77	0.23	76,76,76,76	0
56	MG	1A	3532	1/1	0.77	0.43	53,53,53,53	0
56	MG	2A	3547	1/1	0.77	0.11	81,81,81,81	0
56	MG	2a	1763	1/1	0.78	0.28	55,55,55,55	0
56	MG	1A	3755	1/1	0.78	0.15	54,54,54,54	0
56	MG	2A	3540	1/1	0.78	0.10	84,84,84,84	0
56	MG	1a	1781	1/1	0.78	0.08	75,75,75,75	0
56	MG	2A	3542	1/1	0.78	0.13	83,83,83,83	0
56	MG	2a	1781	1/1	0.78	0.21	73,73,73,73	0
56	MG	2A	3495	1/1	0.78	0.10	74,74,74,74	0
56	MG	1q	202	1/1	0.78	0.10	76,76,76,76	0
56	MG	2A	3307	1/1	0.78	0.20	75,75,75,75	0
56	MG	2A	3407	1/1	0.78	0.27	59,59,59,59	0
56	MG	2A	3413	1/1	0.78	0.18	47,47,47,47	0
56	MG	2a	1801	1/1	0.78	0.11	75,75,75,75	0
56	MG	2A	3433	1/1	0.78	0.25	51,51,51,51	0
56	MG	1a	1922	1/1	0.78	0.10	82,82,82,82	0
56	MG	1a	1923	1/1	0.78	0.13	81,81,81,81	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	0.78	0.14	72,72,72,72	0
56	MG	1a	1924	1/1	0.78	0.14	83,83,83,83	0
56	MG	1A	3642	1/1	0.78	0.12	63,63,63,63	0
56	MG	1A	3630	1/1	0.78	0.20	78,78,78,78	0
56	MG	13	104	1/1	0.78	0.20	70,70,70,70	0
56	MG	2a	1631	1/1	0.78	0.20	100,100,100,100	0
56	MG	1A	3817	1/1	0.78	0.18	49,49,49,49	0
56	MG	1B	204	1/1	0.78	0.13	63,63,63,63	0
56	MG	2A	3461	1/1	0.78	0.11	58,58,58,58	0
56	MG	1A	3537	1/1	0.78	0.19	57,57,57,57	0
56	MG	1A	3029	1/1	0.79	0.26	63,63,63,63	0
56	MG	1A	3331	1/1	0.79	0.12	55,55,55,55	0
56	MG	1A	3377	1/1	0.79	0.13	63,63,63,63	0
56	MG	2A	3563	1/1	0.79	0.18	78,78,78,78	0
56	MG	1a	1925	1/1	0.79	0.11	64,64,64,64	0
56	MG	1a	1891	1/1	0.79	0.16	78,78,78,78	0
56	MG	2A	3169	1/1	0.79	0.15	67,67,67,67	0
56	MG	1a	1934	1/1	0.79	0.16	57,57,57,57	0
56	MG	2A	3255	1/1	0.79	0.09	76,76,76,76	0
56	MG	2a	1616	1/1	0.79	0.19	81,81,81,81	0
56	MG	1A	3293	1/1	0.79	0.19	38,38,38,38	0
56	MG	1a	1868	1/1	0.79	0.15	68,68,68,68	0
56	MG	1x	111	1/1	0.79	0.09	70,70,70,70	0
56	MG	2a	1627	1/1	0.79	0.28	78,78,78,78	0
56	MG	2A	3489	1/1	0.79	0.11	72,72,72,72	0
56	MG	2A	3493	1/1	0.79	0.19	76,76,76,76	0
56	MG	1B	229	1/1	0.79	0.11	68,68,68,68	0
56	MG	2A	3417	1/1	0.79	0.19	68,68,68,68	0
56	MG	2a	1729	1/1	0.79	0.26	84,84,84,84	0
56	MG	2a	1652	1/1	0.79	0.21	76,76,76,76	0
56	MG	2a	1731	1/1	0.79	0.21	72,72,72,72	0
56	MG	2a	1823	1/1	0.79	0.10	88,88,88,88	0
56	MG	2a	1825	1/1	0.79	0.13	58,58,58,58	0
56	MG	2A	3332	1/1	0.79	0.34	80,80,80,80	0
56	MG	1a	1847	1/1	0.79	0.13	74,74,74,74	0
56	MG	2x	102	1/1	0.79	0.15	73,73,73,73	0
56	MG	2a	1739	1/1	0.79	0.14	79,79,79,79	0
56	MG	2a	1751	1/1	0.79	0.25	62,62,62,62	0
56	MG	2B	206	1/1	0.80	0.24	73,73,73,73	0
56	MG	1A	3138	1/1	0.80	0.29	65,65,65,65	0
56	MG	1B	218	1/1	0.80	0.17	76,76,76,76	0
56	MG	1A	3873	1/1	0.80	0.09	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	3229	1/1	0.80	0.20	72,72,72,72	0
56	MG	1A	3398	1/1	0.80	0.21	78,78,78,78	0
56	MG	2a	1737	1/1	0.80	0.14	72,72,72,72	0
56	MG	1w	103	1/1	0.80	0.13	81,81,81,81	0
56	MG	1A	3057	1/1	0.80	0.19	91,91,91,91	0
56	MG	1A	3635	1/1	0.80	0.12	69,69,69,69	0
56	MG	1A	3716	1/1	0.80	0.12	63,63,63,63	0
56	MG	1A	3904	1/1	0.80	0.21	41,41,41,41	0
56	MG	2a	1777	1/1	0.80	0.13	85,85,85,85	0
56	MG	1A	3909	1/1	0.80	0.13	75,75,75,75	0
56	MG	1A	3914	1/1	0.80	0.10	64,64,64,64	0
56	MG	2A	3043	1/1	0.80	0.13	53,53,53,53	0
56	MG	1a	1819	1/1	0.80	0.23	70,70,70,70	0
56	MG	1A	3494	1/1	0.80	0.15	69,69,69,69	0
56	MG	1A	3852	1/1	0.80	0.18	61,61,61,61	0
56	MG	1a	1929	1/1	0.80	0.11	87,87,87,87	0
56	MG	1A	3168	1/1	0.80	0.24	81,81,81,81	0
56	MG	1A	3771	1/1	0.80	0.10	64,64,64,64	0
56	MG	2A	3367	1/1	0.80	0.31	69,69,69,69	0
56	MG	2A	3369	1/1	0.80	0.25	68,68,68,68	0
56	MG	1a	1684	1/1	0.80	0.21	81,81,81,81	0
56	MG	2a	1805	1/1	0.80	0.09	95,95,95,95	0
56	MG	1A	3149	1/1	0.80	0.10	70,70,70,70	0
56	MG	1A	3932	1/1	0.80	0.22	65,65,65,65	0
56	MG	1a	1700	1/1	0.80	0.11	73,73,73,73	0
56	MG	2A	3127	1/1	0.80	0.15	76,76,76,76	0
56	MG	1l	202	1/1	0.80	0.31	70,70,70,70	0
56	MG	2A	3134	1/1	0.80	0.26	69,69,69,69	0
56	MG	1A	3749	1/1	0.80	0.14	66,66,66,66	0
56	MG	2a	1712	1/1	0.80	0.11	74,74,74,74	0
56	MG	1a	1876	1/1	0.80	0.23	83,83,83,83	0
56	MG	2A	3546	1/1	0.80	0.22	70,70,70,70	0
56	MG	2w	101	1/1	0.80	0.14	83,83,83,83	0
56	MG	2A	3150	1/1	0.80	0.31	65,65,65,65	0
56	MG	1o	102	1/1	0.80	0.15	76,76,76,76	0
56	MG	2A	3154	1/1	0.80	0.26	46,46,46,46	0
56	MG	2B	211	1/1	0.81	0.14	90,90,90,90	0
56	MG	2F	304	1/1	0.81	0.13	75,75,75,75	0
56	MG	2A	3294	1/1	0.81	0.36	64,64,64,64	0
56	MG	1A	3507	1/1	0.81	0.18	49,49,49,49	0
56	MG	1A	3194	1/1	0.81	0.08	58,58,58,58	0
56	MG	2A	3474	1/1	0.81	0.39	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	3314	1/1	0.81	0.27	67,67,67,67	0
56	MG	2A	3328	1/1	0.81	0.24	69,69,69,69	0
56	MG	2a	1746	1/1	0.81	0.26	77,77,77,77	0
56	MG	2a	1617	1/1	0.81	0.07	101,101,101,101	0
56	MG	1a	1726	1/1	0.81	0.08	75,75,75,75	0
56	MG	1A	3199	1/1	0.81	0.29	68,68,68,68	0
56	MG	1A	3105	1/1	0.81	0.28	41,41,41,41	0
56	MG	1a	1741	1/1	0.81	0.11	73,73,73,73	0
56	MG	1A	3741	1/1	0.81	0.14	49,49,49,49	0
56	MG	1a	1754	1/1	0.81	0.22	62,62,62,62	0
56	MG	1a	1877	1/1	0.81	0.17	70,70,70,70	0
56	MG	2a	1648	1/1	0.81	0.23	76,76,76,76	0
56	MG	1a	1680	1/1	0.81	0.38	83,83,83,83	0
56	MG	1A	3129	1/1	0.81	0.09	83,83,83,83	0
56	MG	1a	1775	1/1	0.81	0.16	62,62,62,62	0
56	MG	1a	1780	1/1	0.81	0.16	67,67,67,67	0
56	MG	1A	3882	1/1	0.81	0.10	72,72,72,72	0
56	MG	1a	1785	1/1	0.81	0.12	64,64,64,64	0
56	MG	1a	1787	1/1	0.81	0.16	83,83,83,83	0
56	MG	1a	1898	1/1	0.81	0.18	78,78,78,78	0
56	MG	2A	3527	1/1	0.81	0.23	73,73,73,73	0
56	MG	1a	1908	1/1	0.81	0.16	72,72,72,72	0
56	MG	1a	1800	1/1	0.81	0.32	80,80,80,80	0
56	MG	2a	1694	1/1	0.81	0.17	77,77,77,77	0
56	MG	1A	3146	1/1	0.81	0.11	69,69,69,69	0
56	MG	2A	3418	1/1	0.81	0.08	70,70,70,70	0
56	MG	1A	3186	1/1	0.81	0.16	68,68,68,68	0
56	MG	2A	3190	1/1	0.81	0.26	61,61,61,61	0
56	MG	1x	115	1/1	0.81	0.17	79,79,79,79	0
56	MG	2A	3223	1/1	0.81	0.27	38,38,38,38	0
56	MG	19	101	1/1	0.81	0.18	70,70,70,70	0
56	MG	1A	3898	1/1	0.81	0.14	41,41,41,41	0
56	MG	2A	3287	1/1	0.81	0.26	60,60,60,60	0
56	MG	2A	3290	1/1	0.81	0.18	55,55,55,55	0
56	MG	2A	3030	1/1	0.81	0.22	56,56,56,56	0
56	MG	1a	1902	1/1	0.82	0.08	85,85,85,85	0
56	MG	2A	3445	1/1	0.82	0.12	84,84,84,84	0
56	MG	1A	3312	1/1	0.82	0.30	65,65,65,65	0
56	MG	2A	3281	1/1	0.82	0.28	40,40,40,40	0
56	MG	2A	3561	1/1	0.82	0.22	64,64,64,64	0
56	MG	1A	3137	1/1	0.82	0.22	70,70,70,70	0
56	MG	1a	1686	1/1	0.82	0.17	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3215	1/1	0.82	0.10	67,67,67,67	0
56	MG	1A	3759	1/1	0.82	0.28	73,73,73,73	0
56	MG	1A	3217	1/1	0.82	0.41	63,63,63,63	0
56	MG	2Q	202	1/1	0.82	0.31	75,75,75,75	0
56	MG	1A	3187	1/1	0.82	0.16	81,81,81,81	0
56	MG	2A	3473	1/1	0.82	0.29	66,66,66,66	0
56	MG	2a	1606	1/1	0.82	0.26	87,87,87,87	0
56	MG	2A	3311	1/1	0.82	0.26	60,60,60,60	0
56	MG	2a	1749	1/1	0.82	0.18	62,62,62,62	0
56	MG	2A	3481	1/1	0.82	0.24	71,71,71,71	0
56	MG	2a	1756	1/1	0.82	0.26	68,68,68,68	0
56	MG	2a	1760	1/1	0.82	0.36	61,61,61,61	0
56	MG	2a	1762	1/1	0.82	0.43	62,62,62,62	0
56	MG	2a	1615	1/1	0.82	0.23	81,81,81,81	0
56	MG	1a	1711	1/1	0.82	0.18	75,75,75,75	0
56	MG	2a	1771	1/1	0.82	0.28	82,82,82,82	0
56	MG	1A	3768	1/1	0.82	0.17	71,71,71,71	0
56	MG	2a	1619	1/1	0.82	0.23	80,80,80,80	0
56	MG	2A	3490	1/1	0.82	0.10	68,68,68,68	0
56	MG	2A	3491	1/1	0.82	0.13	68,68,68,68	0
56	MG	2A	3062	1/1	0.82	0.23	59,59,59,59	0
56	MG	1A	3769	1/1	0.82	0.11	66,66,66,66	0
56	MG	1A	3876	1/1	0.82	0.12	59,59,59,59	0
56	MG	2a	1790	1/1	0.82	0.12	92,92,92,92	0
56	MG	2a	1795	1/1	0.82	0.11	85,85,85,85	0
56	MG	2a	1635	1/1	0.82	0.25	59,59,59,59	0
56	MG	2a	1637	1/1	0.82	0.22	64,64,64,64	0
56	MG	2A	3066	1/1	0.82	0.29	59,59,59,59	0
56	MG	1A	3403	1/1	0.82	0.13	56,56,56,56	0
56	MG	1A	3604	1/1	0.82	0.18	71,71,71,71	0
56	MG	1A	3176	1/1	0.82	0.35	77,77,77,77	0
56	MG	1e	201	1/1	0.82	0.11	77,77,77,77	0
56	MG	1A	3775	1/1	0.82	0.15	59,59,59,59	0
56	MG	1A	3161	1/1	0.82	0.19	67,67,67,67	0
56	MG	1A	3202	1/1	0.82	0.22	74,74,74,74	0
56	MG	1A	3298	1/1	0.82	0.16	58,58,58,58	0
56	MG	1A	3798	1/1	0.82	0.22	64,64,64,64	0
56	MG	1a	1888	1/1	0.82	0.13	75,75,75,75	0
56	MG	1A	3744	1/1	0.82	0.15	72,72,72,72	0
56	MG	1a	1778	1/1	0.82	0.21	53,53,53,53	0
56	MG	2A	3411	1/1	0.82	0.23	69,69,69,69	0
56	MG	1v	103	1/1	0.82	0.24	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1892	1/1	0.82	0.15	68,68,68,68	0
56	MG	1A	3641	1/1	0.82	0.14	66,66,66,66	0
56	MG	1A	3461	1/1	0.82	0.12	58,58,58,58	0
56	MG	2A	3208	1/1	0.82	0.29	42,42,42,42	0
56	MG	1a	1782	1/1	0.82	0.20	81,81,81,81	0
56	MG	1a	1764	1/1	0.83	0.22	69,69,69,69	0
56	MG	2a	1679	1/1	0.83	0.20	73,73,73,73	0
56	MG	2a	1776	1/1	0.83	0.12	80,80,80,80	0
56	MG	1A	3881	1/1	0.83	0.22	62,62,62,62	0
56	MG	1A	3452	1/1	0.83	0.09	52,52,52,52	0
56	MG	1A	3796	1/1	0.83	0.11	73,73,73,73	0
56	MG	1A	3130	1/1	0.83	0.18	54,54,54,54	0
56	MG	2a	1608	1/1	0.83	0.31	61,61,61,61	0
56	MG	2A	3522	1/1	0.83	0.11	81,81,81,81	0
56	MG	1A	3860	1/1	0.83	0.09	88,88,88,88	0
56	MG	1a	1613	1/1	0.83	0.15	74,74,74,74	0
56	MG	2A	3258	1/1	0.83	0.38	43,43,43,43	0
56	MG	1B	205	1/1	0.83	0.10	50,50,50,50	0
56	MG	2A	3082	1/1	0.83	0.22	63,63,63,63	0
56	MG	2A	3536	1/1	0.83	0.38	57,57,57,57	0
56	MG	1A	3113	1/1	0.83	0.17	69,69,69,69	0
56	MG	2A	3381	1/1	0.83	0.11	59,59,59,59	0
56	MG	2A	3382	1/1	0.83	0.10	84,84,84,84	0
56	MG	1a	1619	1/1	0.83	0.30	71,71,71,71	0
56	MG	2a	1809	1/1	0.83	0.10	74,74,74,74	0
56	MG	1a	1805	1/1	0.83	0.10	63,63,63,63	0
56	MG	1a	1659	1/1	0.83	0.23	40,40,40,40	0
56	MG	1A	3802	1/1	0.83	0.11	65,65,65,65	0
56	MG	2a	1646	1/1	0.83	0.37	58,58,58,58	0
56	MG	2A	3494	1/1	0.83	0.08	79,79,79,79	0
56	MG	1a	1947	1/1	0.83	0.16	81,81,81,81	0
56	MG	1A	3002	1/1	0.83	0.13	66,66,66,66	0
56	MG	1A	3591	1/1	0.83	0.23	53,53,53,53	0
56	MG	2a	1655	1/1	0.83	0.22	72,72,72,72	0
56	MG	1A	3640	1/1	0.83	0.14	68,68,68,68	0
56	MG	2B	209	1/1	0.83	0.10	76,76,76,76	0
56	MG	2A	3439	1/1	0.83	0.18	75,75,75,75	0
56	MG	1A	3846	1/1	0.83	0.09	42,42,42,42	0
56	MG	1a	1900	1/1	0.83	0.19	72,72,72,72	0
56	MG	1A	3453	1/1	0.84	0.30	56,56,56,56	0
56	MG	1a	1790	1/1	0.84	0.15	69,69,69,69	0
56	MG	1A	3296	1/1	0.84	0.26	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1713	1/1	0.84	0.14	72,72,72,72	0
56	MG	2a	1715	1/1	0.84	0.23	69,69,69,69	0
56	MG	1A	3418	1/1	0.84	0.13	55,55,55,55	0
56	MG	2A	3549	1/1	0.84	0.12	53,53,53,53	0
56	MG	2A	3552	1/1	0.84	0.15	70,70,70,70	0
56	MG	2A	3254	1/1	0.84	0.36	63,63,63,63	0
56	MG	1x	116	1/1	0.84	0.10	78,78,78,78	0
56	MG	2B	203	1/1	0.84	0.18	75,75,75,75	0
56	MG	2a	1727	1/1	0.84	0.09	97,97,97,97	0
56	MG	1A	3645	1/1	0.84	0.18	60,60,60,60	0
56	MG	2A	3261	1/1	0.84	0.30	71,71,71,71	0
56	MG	2A	3454	1/1	0.84	0.28	81,81,81,81	0
56	MG	2F	301	1/1	0.84	0.20	63,63,63,63	0
56	MG	2A	3270	1/1	0.84	0.25	64,64,64,64	0
56	MG	1A	3611	1/1	0.84	0.12	57,57,57,57	0
56	MG	1a	1823	1/1	0.84	0.16	69,69,69,69	0
56	MG	2A	3032	1/1	0.84	0.10	68,68,68,68	0
56	MG	1A	3806	1/1	0.84	0.14	58,58,58,58	0
56	MG	2a	1605	1/1	0.84	0.40	73,73,73,73	0
56	MG	2A	3469	1/1	0.84	0.14	71,71,71,71	0
56	MG	1A	3809	1/1	0.84	0.18	86,86,86,86	0
56	MG	2A	3303	1/1	0.84	0.31	56,56,56,56	0
56	MG	2a	1611	1/1	0.84	0.28	80,80,80,80	0
56	MG	1a	1844	1/1	0.84	0.14	53,53,53,53	0
56	MG	1A	3422	1/1	0.84	0.20	61,61,61,61	0
56	MG	1A	3254	1/1	0.84	0.20	45,45,45,45	0
56	MG	1a	1607	1/1	0.84	0.24	63,63,63,63	0
56	MG	2A	3327	1/1	0.84	0.21	86,86,86,86	0
56	MG	1A	3655	1/1	0.84	0.16	73,73,73,73	0
56	MG	1A	3850	1/1	0.84	0.21	59,59,59,59	0
56	MG	1a	1944	1/1	0.84	0.09	70,70,70,70	0
56	MG	1a	1611	1/1	0.84	0.14	64,64,64,64	0
56	MG	2a	1786	1/1	0.84	0.20	72,72,72,72	0
56	MG	1a	1745	1/1	0.84	0.26	71,71,71,71	0
56	MG	1a	1954	1/1	0.84	0.10	70,70,70,70	0
56	MG	2a	1793	1/1	0.84	0.16	73,73,73,73	0
56	MG	2a	1794	1/1	0.84	0.15	88,88,88,88	0
56	MG	1A	3851	1/1	0.84	0.16	61,61,61,61	0
56	MG	2A	3098	1/1	0.84	0.19	74,74,74,74	0
56	MG	1A	3142	1/1	0.84	0.13	60,60,60,60	0
56	MG	2a	1799	1/1	0.84	0.09	68,68,68,68	0
56	MG	1A	3665	1/1	0.84	0.11	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	2A	3354	1/1	0.84	0.13	84,84,84,84	0
56	MG	2A	3128	1/1	0.84	0.25	73,73,73,73	0
56	MG	1A	3666	1/1	0.84	0.14	80,80,80,80	0
56	MG	2A	3132	1/1	0.84	0.12	84,84,84,84	0
56	MG	1a	1621	1/1	0.84	0.20	39,39,39,39	0
56	MG	2a	1808	1/1	0.84	0.14	77,77,77,77	0
56	MG	2A	3136	1/1	0.84	0.23	55,55,55,55	0
56	MG	1a	1886	1/1	0.84	0.11	81,81,81,81	0
56	MG	1A	3858	1/1	0.84	0.15	71,71,71,71	0
56	MG	1a	1662	1/1	0.84	0.43	76,76,76,76	0
56	MG	2a	1669	1/1	0.84	0.09	91,91,91,91	0
56	MG	2A	3399	1/1	0.84	0.15	41,41,41,41	0
56	MG	1A	3785	1/1	0.84	0.17	73,73,73,73	0
56	MG	2A	3532	1/1	0.84	0.32	64,64,64,64	0
56	MG	2a	1824	1/1	0.84	0.19	73,73,73,73	0
56	MG	1A	3792	1/1	0.84	0.26	78,78,78,78	0
56	MG	1A	3793	1/1	0.84	0.21	65,65,65,65	0
56	MG	2g	201	1/1	0.84	0.15	88,88,88,88	0
56	MG	2a	1691	1/1	0.84	0.11	90,90,90,90	0
56	MG	1A	3412	1/1	0.84	0.10	49,49,49,49	0
56	MG	2x	101	1/1	0.84	0.33	58,58,58,58	0
56	MG	1a	1897	1/1	0.84	0.07	83,83,83,83	0
56	MG	2A	3426	1/1	0.84	0.17	56,56,56,56	0
56	MG	2A	3429	1/1	0.84	0.19	74,74,74,74	0
56	MG	2W	201	1/1	0.85	0.21	76,76,76,76	0
56	MG	20	102	1/1	0.85	0.40	68,68,68,68	0
56	MG	1a	1863	1/1	0.85	0.08	80,80,80,80	0
56	MG	28	102	1/1	0.85	0.13	69,69,69,69	0
56	MG	2A	3102	1/1	0.85	0.50	66,66,66,66	0
56	MG	1A	3428	1/1	0.85	0.19	69,69,69,69	0
56	MG	2A	3492	1/1	0.85	0.19	69,69,69,69	0
56	MG	1A	3508	1/1	0.85	0.17	63,63,63,63	0
56	MG	2a	1609	1/1	0.85	0.25	79,79,79,79	0
56	MG	2a	1738	1/1	0.85	0.41	75,75,75,75	0
56	MG	2a	1610	1/1	0.85	0.15	83,83,83,83	0
56	MG	1A	3048	1/1	0.85	0.27	46,46,46,46	0
56	MG	2A	3129	1/1	0.85	0.23	73,73,73,73	0
56	MG	1A	3121	1/1	0.85	0.19	49,49,49,49	0
56	MG	1a	1747	1/1	0.85	0.18	63,63,63,63	0
56	MG	1A	3329	1/1	0.85	0.10	47,47,47,47	0
56	MG	1A	3928	1/1	0.85	0.10	62,62,62,62	0
56	MG	2A	3504	1/1	0.85	0.16	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1763	1/1	0.85	0.14	73,73,73,73	0
56	MG	2a	1769	1/1	0.85	0.20	70,70,70,70	0
56	MG	1A	3646	1/1	0.85	0.08	64,64,64,64	0
56	MG	2a	1774	1/1	0.85	0.16	79,79,79,79	0
56	MG	1a	1626	1/1	0.85	0.12	75,75,75,75	0
56	MG	1a	1651	1/1	0.85	0.28	56,56,56,56	0
56	MG	1A	3869	1/1	0.85	0.12	65,65,65,65	0
56	MG	1a	1779	1/1	0.85	0.10	68,68,68,68	0
56	MG	2a	1640	1/1	0.85	0.28	64,64,64,64	0
56	MG	1A	3592	1/1	0.85	0.20	48,48,48,48	0
56	MG	2A	3183	1/1	0.85	0.25	61,61,61,61	0
56	MG	1A	3213	1/1	0.85	0.24	57,57,57,57	0
56	MG	2A	3196	1/1	0.85	0.27	57,57,57,57	0
56	MG	1A	3824	1/1	0.85	0.17	62,62,62,62	0
56	MG	1a	1899	1/1	0.85	0.18	77,77,77,77	0
56	MG	2A	3211	1/1	0.85	0.29	42,42,42,42	0
56	MG	1a	1679	1/1	0.85	0.24	70,70,70,70	0
56	MG	1a	1786	1/1	0.85	0.13	75,75,75,75	0
56	MG	2A	3237	1/1	0.85	0.13	55,55,55,55	0
56	MG	2A	3539	1/1	0.85	0.13	86,86,86,86	0
56	MG	2a	1666	1/1	0.85	0.27	75,75,75,75	0
56	MG	2A	3239	1/1	0.85	0.24	40,40,40,40	0
56	MG	2A	3007	1/1	0.85	0.16	72,72,72,72	0
56	MG	1B	209	1/1	0.85	0.10	67,67,67,67	0
56	MG	2a	1673	1/1	0.85	0.07	88,88,88,88	0
56	MG	2A	3023	1/1	0.85	0.10	65,65,65,65	0
56	MG	1A	3833	1/1	0.85	0.12	67,67,67,67	0
56	MG	1A	3649	1/1	0.85	0.11	65,65,65,65	0
56	MG	2A	3448	1/1	0.85	0.17	71,71,71,71	0
56	MG	2a	1814	1/1	0.85	0.10	73,73,73,73	0
56	MG	2a	1688	1/1	0.85	0.35	72,72,72,72	0
56	MG	1B	228	1/1	0.85	0.10	80,80,80,80	0
56	MG	2a	1693	1/1	0.85	0.11	85,85,85,85	0
56	MG	1A	3883	1/1	0.85	0.24	43,43,43,43	0
56	MG	1A	3842	1/1	0.85	0.23	63,63,63,63	0
56	MG	1A	3358	1/1	0.85	0.15	62,62,62,62	0
56	MG	1A	3617	1/1	0.85	0.13	50,50,50,50	0
56	MG	1a	1714	1/1	0.85	0.10	80,80,80,80	0
56	MG	1A	3080	1/1	0.85	0.12	57,57,57,57	0
56	MG	15	103	1/1	0.85	0.14	77,77,77,77	0
56	MG	1a	1938	1/1	0.85	0.14	84,84,84,84	0
56	MG	1A	3419	1/1	0.85	0.14	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3908	1/1	0.85	0.13	61,61,61,61	0
56	MG	2A	3475	1/1	0.85	0.14	62,62,62,62	0
56	MG	1a	1730	1/1	0.85	0.11	76,76,76,76	0
56	MG	2x	104	1/1	0.85	0.10	68,68,68,68	0
56	MG	2x	106	1/1	0.85	0.22	54,54,54,54	0
56	MG	1A	3378	1/1	0.85	0.16	56,56,56,56	0
56	MG	2A	3312	1/1	0.86	0.08	75,75,75,75	0
56	MG	1A	3180	1/1	0.86	0.11	56,56,56,56	0
56	MG	1A	3333	1/1	0.86	0.37	45,45,45,45	0
56	MG	2a	1684	1/1	0.86	0.17	74,74,74,74	0
56	MG	2A	3514	1/1	0.86	0.21	70,70,70,70	0
56	MG	1A	3522	1/1	0.86	0.22	30,30,30,30	0
56	MG	1A	3336	1/1	0.86	0.10	54,54,54,54	0
56	MG	2A	3330	1/1	0.86	0.15	62,62,62,62	0
56	MG	2A	3331	1/1	0.86	0.27	56,56,56,56	0
56	MG	1a	1771	1/1	0.86	0.15	63,63,63,63	0
56	MG	1A	3344	1/1	0.86	0.33	36,36,36,36	0
56	MG	1a	1620	1/1	0.86	0.15	72,72,72,72	0
56	MG	1A	3557	1/1	0.86	0.25	59,59,59,59	0
56	MG	1A	3141	1/1	0.86	0.14	75,75,75,75	0
56	MG	2a	1701	1/1	0.86	0.14	61,61,61,61	0
56	MG	2a	1702	1/1	0.86	0.13	84,84,84,84	0
56	MG	2a	1705	1/1	0.86	0.18	79,79,79,79	0
56	MG	2A	3533	1/1	0.86	0.12	64,64,64,64	0
56	MG	1a	1633	1/1	0.86	0.14	55,55,55,55	0
56	MG	1a	1641	1/1	0.86	0.21	67,67,67,67	0
56	MG	1A	3657	1/1	0.86	0.16	69,69,69,69	0
56	MG	1a	1653	1/1	0.86	0.25	60,60,60,60	0
56	MG	1A	3083	1/1	0.86	0.20	71,71,71,71	0
56	MG	2A	3363	1/1	0.86	0.12	65,65,65,65	0
56	MG	1A	3926	1/1	0.86	0.12	83,83,83,83	0
56	MG	1A	3300	1/1	0.86	0.22	43,43,43,43	0
56	MG	1a	1796	1/1	0.86	0.07	74,74,74,74	0
56	MG	2A	3115	1/1	0.86	0.29	67,67,67,67	0
56	MG	2A	3374	1/1	0.86	0.10	60,60,60,60	0
56	MG	2A	3378	1/1	0.86	0.49	57,57,57,57	0
56	MG	1a	1935	1/1	0.86	0.16	70,70,70,70	0
56	MG	1A	3607	1/1	0.86	0.27	46,46,46,46	0
56	MG	1A	3388	1/1	0.86	0.27	74,74,74,74	0
56	MG	2A	3565	1/1	0.86	0.08	64,64,64,64	0
56	MG	2A	3391	1/1	0.86	0.11	78,78,78,78	0
56	MG	2B	205	1/1	0.86	0.06	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2a	1744	1/1	0.86	0.29	68,68,68,68	0
56	MG	1A	3669	1/1	0.86	0.11	62,62,62,62	0
56	MG	2a	1747	1/1	0.86	0.40	72,72,72,72	0
56	MG	2B	207	1/1	0.86	0.16	65,65,65,65	0
56	MG	1A	3864	1/1	0.86	0.15	68,68,68,68	0
56	MG	2A	3408	1/1	0.86	0.20	58,58,58,58	0
56	MG	2D	302	1/1	0.86	0.13	68,68,68,68	0
56	MG	1A	3671	1/1	0.86	0.11	70,70,70,70	0
56	MG	1a	1826	1/1	0.86	0.11	74,74,74,74	0
56	MG	1A	3700	1/1	0.86	0.19	72,72,72,72	0
56	MG	2a	1767	1/1	0.86	0.28	59,59,59,59	0
56	MG	1a	1692	1/1	0.86	0.09	86,86,86,86	0
56	MG	1A	3154	1/1	0.86	0.05	67,67,67,67	0
56	MG	1a	1694	1/1	0.86	0.25	46,46,46,46	0
56	MG	1a	1852	1/1	0.86	0.20	72,72,72,72	0
56	MG	1A	3620	1/1	0.86	0.19	63,63,63,63	0
56	MG	2A	3164	1/1	0.86	0.27	42,42,42,42	0
56	MG	2a	1602	1/1	0.86	0.22	74,74,74,74	0
56	MG	1a	1854	1/1	0.86	0.18	83,83,83,83	0
56	MG	2A	3170	1/1	0.86	0.23	40,40,40,40	0
56	MG	1B	225	1/1	0.86	0.12	80,80,80,80	0
56	MG	1A	3722	1/1	0.86	0.20	54,54,54,54	0
56	MG	1a	1712	1/1	0.86	0.15	69,69,69,69	0
56	MG	1A	3454	1/1	0.86	0.09	59,59,59,59	0
56	MG	2A	3198	1/1	0.86	0.39	50,50,50,50	0
56	MG	2a	1612	1/1	0.86	0.15	68,68,68,68	0
56	MG	2A	3455	1/1	0.86	0.27	56,56,56,56	0
56	MG	1A	3039	1/1	0.86	0.13	50,50,50,50	0
56	MG	1O	3102	1/1	0.86	0.10	60,60,60,60	0
56	MG	1A	3480	1/1	0.86	0.14	74,74,74,74	0
56	MG	1l	101	1/1	0.86	0.18	69,69,69,69	0
56	MG	1x	104	1/1	0.86	0.33	76,76,76,76	0
56	MG	1A	3324	1/1	0.86	0.20	49,49,49,49	0
56	MG	1a	1880	1/1	0.86	0.11	81,81,81,81	0
56	MG	2a	1624	1/1	0.86	0.15	61,61,61,61	0
56	MG	2a	1625	1/1	0.86	0.32	51,51,51,51	0
56	MG	2a	1807	1/1	0.86	0.19	79,79,79,79	0
56	MG	1x	114	1/1	0.86	0.14	86,86,86,86	0
56	MG	1A	3486	1/1	0.86	0.09	50,50,50,50	0
56	MG	1A	3410	1/1	0.86	0.09	72,72,72,72	0
56	MG	2a	1812	1/1	0.86	0.15	96,96,96,96	0
56	MG	2A	3264	1/1	0.86	0.30	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	2A	3268	1/1	0.86	0.16	77,77,77,77	0
56	MG	2a	1816	1/1	0.86	0.07	89,89,89,89	0
56	MG	1x	119	1/1	0.86	0.08	78,78,78,78	0
56	MG	1x	120	1/1	0.86	0.14	80,80,80,80	0
56	MG	2A	3284	1/1	0.86	0.26	60,60,60,60	0
56	MG	1A	3888	1/1	0.86	0.07	68,68,68,68	0
56	MG	2A	3002	1/1	0.86	0.25	55,55,55,55	0
56	MG	1a	1742	1/1	0.86	0.12	69,69,69,69	0
56	MG	2A	3008	1/1	0.86	0.09	57,57,57,57	0
56	MG	2A	3296	1/1	0.86	0.36	52,52,52,52	0
56	MG	2A	3011	1/1	0.86	0.26	55,55,55,55	0
56	MG	2A	3304	1/1	0.86	0.17	56,56,56,56	0
56	MG	2A	3501	1/1	0.86	0.10	74,74,74,74	0
56	MG	2a	1665	1/1	0.86	0.28	61,61,61,61	0
56	MG	2A	3305	1/1	0.86	0.17	60,60,60,60	0
56	MG	1A	3891	1/1	0.86	0.19	69,69,69,69	0
56	MG	1A	3271	1/1	0.86	0.31	33,33,33,33	0
56	MG	2a	1670	1/1	0.86	0.10	74,74,74,74	0
56	MG	1A	3810	1/1	0.86	0.16	65,65,65,65	0
56	MG	1a	1856	1/1	0.87	0.21	56,56,56,56	0
56	MG	1A	3427	1/1	0.87	0.17	43,43,43,43	0
56	MG	1A	3008	1/1	0.87	0.09	61,61,61,61	0
56	MG	1A	3188	1/1	0.87	0.16	52,52,52,52	0
56	MG	2A	3179	1/1	0.87	0.23	51,51,51,51	0
56	MG	2A	3550	1/1	0.87	0.21	64,64,64,64	0
56	MG	2a	1708	1/1	0.87	0.12	80,80,80,80	0
56	MG	2A	3409	1/1	0.87	0.21	68,68,68,68	0
56	MG	2A	3557	1/1	0.87	0.14	62,62,62,62	0
56	MG	1a	1867	1/1	0.87	0.17	72,72,72,72	0
56	MG	1A	3558	1/1	0.87	0.29	58,58,58,58	0
56	MG	2A	3564	1/1	0.87	0.15	65,65,65,65	0
56	MG	2A	3414	1/1	0.87	0.10	55,55,55,55	0
56	MG	2A	3416	1/1	0.87	0.19	57,57,57,57	0
56	MG	1a	1869	1/1	0.87	0.09	64,64,64,64	0
56	MG	1a	1736	1/1	0.87	0.19	79,79,79,79	0
56	MG	1a	1737	1/1	0.87	0.07	89,89,89,89	0
56	MG	1A	3559	1/1	0.87	0.25	54,54,54,54	0
56	MG	1A	3827	1/1	0.87	0.22	39,39,39,39	0
56	MG	2A	3434	1/1	0.87	0.17	79,79,79,79	0
56	MG	2A	3214	1/1	0.87	0.32	41,41,41,41	0
56	MG	2A	3222	1/1	0.87	0.27	49,49,49,49	0
56	MG	1A	3578	1/1	0.87	0.36	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	3394	1/1	0.87	0.11	69,69,69,69	0
56	MG	2A	3443	1/1	0.87	0.12	70,70,70,70	0
56	MG	1A	3395	1/1	0.87	0.17	70,70,70,70	0
56	MG	1a	1618	1/1	0.87	0.06	75,75,75,75	0
56	MG	1A	3844	1/1	0.87	0.15	79,79,79,79	0
56	MG	23	101	1/1	0.87	0.16	73,73,73,73	0
56	MG	1a	1889	1/1	0.87	0.08	75,75,75,75	0
56	MG	2a	1754	1/1	0.87	0.36	63,63,63,63	0
56	MG	2a	1755	1/1	0.87	0.40	63,63,63,63	0
56	MG	1A	3327	1/1	0.87	0.30	62,62,62,62	0
56	MG	1a	1755	1/1	0.87	0.09	68,68,68,68	0
56	MG	2a	1761	1/1	0.87	0.16	69,69,69,69	0
56	MG	1A	3660	1/1	0.87	0.10	69,69,69,69	0
56	MG	1A	3400	1/1	0.87	0.21	66,66,66,66	0
56	MG	1A	3923	1/1	0.87	0.25	44,44,44,44	0
56	MG	2A	3025	1/1	0.87	0.26	54,54,54,54	0
56	MG	2A	3282	1/1	0.87	0.27	46,46,46,46	0
56	MG	2A	3026	1/1	0.87	0.13	39,39,39,39	0
56	MG	1A	3183	1/1	0.87	0.13	75,75,75,75	0
56	MG	2A	3288	1/1	0.87	0.23	74,74,74,74	0
56	MG	1a	1644	1/1	0.87	0.21	63,63,63,63	0
56	MG	2A	3034	1/1	0.87	0.26	55,55,55,55	0
56	MG	2A	3480	1/1	0.87	0.44	70,70,70,70	0
56	MG	2A	3037	1/1	0.87	0.14	59,59,59,59	0
56	MG	2A	3041	1/1	0.87	0.20	39,39,39,39	0
56	MG	2A	3300	1/1	0.87	0.20	53,53,53,53	0
56	MG	1A	3464	1/1	0.87	0.09	83,83,83,83	0
56	MG	2A	3046	1/1	0.87	0.16	76,76,76,76	0
56	MG	1A	3280	1/1	0.87	0.30	51,51,51,51	0
56	MG	1A	3780	1/1	0.87	0.09	70,70,70,70	0
56	MG	1A	3093	1/1	0.87	0.26	21,21,21,21	0
56	MG	2a	1633	1/1	0.87	0.21	55,55,55,55	0
56	MG	1a	1663	1/1	0.87	0.23	65,65,65,65	0
56	MG	1A	3694	1/1	0.87	0.15	39,39,39,39	0
56	MG	1a	1672	1/1	0.87	0.13	60,60,60,60	0
56	MG	1A	3061	1/1	0.87	0.11	72,72,72,72	0
56	MG	1A	3790	1/1	0.87	0.15	66,66,66,66	0
56	MG	1a	1789	1/1	0.87	0.11	77,77,77,77	0
56	MG	2A	3071	1/1	0.87	0.18	72,72,72,72	0
56	MG	1A	3414	1/1	0.87	0.18	54,54,54,54	0
56	MG	2A	3506	1/1	0.87	0.09	90,90,90,90	0
56	MG	1a	1683	1/1	0.87	0.17	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	1799	1/1	0.87	0.20	76,76,76,76	0
56	MG	2a	1656	1/1	0.87	0.09	85,85,85,85	0
56	MG	1A	3203	1/1	0.87	0.16	70,70,70,70	0
56	MG	1A	3636	1/1	0.87	0.14	62,62,62,62	0
56	MG	2a	1813	1/1	0.87	0.09	90,90,90,90	0
56	MG	1A	3874	1/1	0.87	0.16	65,65,65,65	0
56	MG	1a	1939	1/1	0.87	0.24	68,68,68,68	0
56	MG	1A	3638	1/1	0.87	0.16	73,73,73,73	0
56	MG	1A	3878	1/1	0.87	0.10	57,57,57,57	0
56	MG	1N	201	1/1	0.87	0.21	66,66,66,66	0
56	MG	2A	3525	1/1	0.87	0.16	81,81,81,81	0
56	MG	1a	1698	1/1	0.87	0.29	75,75,75,75	0
56	MG	1A	3347	1/1	0.87	0.23	31,31,31,31	0
56	MG	1A	3233	1/1	0.87	0.18	48,48,48,48	0
56	MG	1W	202	1/1	0.87	0.13	47,47,47,47	0
56	MG	1a	1850	1/1	0.87	0.09	73,73,73,73	0
56	MG	1A	3251	1/1	0.87	0.20	49,49,49,49	0
56	MG	2A	3372	1/1	0.87	0.18	60,60,60,60	0
56	MG	2a	1687	1/1	0.87	0.14	71,71,71,71	0
56	MG	1A	3644	1/1	0.87	0.18	57,57,57,57	0
56	MG	1a	1715	1/1	0.87	0.29	58,58,58,58	0
56	MG	2A	3379	1/1	0.87	0.10	59,59,59,59	0
56	MG	1A	3804	1/1	0.87	0.27	77,77,77,77	0
56	MG	2A	3161	1/1	0.87	0.33	61,61,61,61	0
56	MG	2A	3383	1/1	0.87	0.12	43,43,43,43	0
56	MG	2A	3553	1/1	0.88	0.12	67,67,67,67	0
56	MG	2A	3554	1/1	0.88	0.09	74,74,74,74	0
56	MG	2A	3421	1/1	0.88	0.26	59,59,59,59	0
56	MG	1B	215	1/1	0.88	0.16	53,53,53,53	0
56	MG	2A	3428	1/1	0.88	0.12	78,78,78,78	0
56	MG	2a	1711	1/1	0.88	0.06	81,81,81,81	0
56	MG	1A	3193	1/1	0.88	0.08	55,55,55,55	0
56	MG	1A	3637	1/1	0.88	0.15	61,61,61,61	0
56	MG	2A	3265	1/1	0.88	0.29	42,42,42,42	0
56	MG	2A	3266	1/1	0.88	0.18	39,39,39,39	0
56	MG	1A	3875	1/1	0.88	0.08	72,72,72,72	0
56	MG	1a	1675	1/1	0.88	0.25	68,68,68,68	0
56	MG	1A	3016	1/1	0.88	0.09	61,61,61,61	0
56	MG	1A	3174	1/1	0.88	0.09	63,63,63,63	0
56	MG	2A	3057	1/1	0.88	0.20	52,52,52,52	0
56	MG	1a	1681	1/1	0.88	0.43	64,64,64,64	0
56	MG	2F	302	1/1	0.88	0.15	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	1793	1/1	0.88	0.11	74,74,74,74	0
56	MG	2A	3449	1/1	0.88	0.29	61,61,61,61	0
56	MG	1D	303	1/1	0.88	0.06	65,65,65,65	0
56	MG	2A	3453	1/1	0.88	0.21	74,74,74,74	0
56	MG	1E	304	1/1	0.88	0.12	70,70,70,70	0
56	MG	1F	301	1/1	0.88	0.25	52,52,52,52	0
56	MG	1A	3144	1/1	0.88	0.27	72,72,72,72	0
56	MG	2a	1741	1/1	0.88	0.31	50,50,50,50	0
56	MG	2A	3298	1/1	0.88	0.21	50,50,50,50	0
56	MG	26	101	1/1	0.88	0.15	61,61,61,61	0
56	MG	1A	3421	1/1	0.88	0.12	61,61,61,61	0
56	MG	1A	3364	1/1	0.88	0.16	49,49,49,49	0
56	MG	2a	1603	1/1	0.88	0.12	67,67,67,67	0
56	MG	2a	1752	1/1	0.88	0.23	57,57,57,57	0
56	MG	2a	1753	1/1	0.88	0.33	46,46,46,46	0
56	MG	2a	1604	1/1	0.88	0.21	43,43,43,43	0
56	MG	2A	3462	1/1	0.88	0.23	48,48,48,48	0
56	MG	1a	1940	1/1	0.88	0.15	47,47,47,47	0
56	MG	2a	1758	1/1	0.88	0.24	61,61,61,61	0
56	MG	2A	3466	1/1	0.88	0.25	61,61,61,61	0
56	MG	1Q	202	1/1	0.88	0.15	62,62,62,62	0
56	MG	2A	3083	1/1	0.88	0.28	69,69,69,69	0
56	MG	1a	1696	1/1	0.88	0.24	46,46,46,46	0
56	MG	2A	3089	1/1	0.88	0.31	61,61,61,61	0
56	MG	1A	3032	1/1	0.88	0.18	69,69,69,69	0
56	MG	2A	3099	1/1	0.88	0.19	46,46,46,46	0
56	MG	2A	3315	1/1	0.88	0.25	57,57,57,57	0
56	MG	2A	3483	1/1	0.88	0.15	75,75,75,75	0
56	MG	2A	3317	1/1	0.88	0.26	38,38,38,38	0
56	MG	1V	201	1/1	0.88	0.12	43,43,43,43	0
56	MG	1a	1834	1/1	0.88	0.08	64,64,64,64	0
56	MG	1A	3204	1/1	0.88	0.15	61,61,61,61	0
56	MG	1Y	201	1/1	0.88	0.08	64,64,64,64	0
56	MG	1A	3821	1/1	0.88	0.14	30,30,30,30	0
56	MG	1A	3433	1/1	0.88	0.12	41,41,41,41	0
56	MG	2a	1785	1/1	0.88	0.12	60,60,60,60	0
56	MG	1A	3826	1/1	0.88	0.20	82,82,82,82	0
56	MG	1a	1716	1/1	0.88	0.23	70,70,70,70	0
56	MG	1A	3434	1/1	0.88	0.10	78,78,78,78	0
56	MG	1a	1720	1/1	0.88	0.08	80,80,80,80	0
56	MG	2A	3344	1/1	0.88	0.18	47,47,47,47	0
56	MG	1A	3585	1/1	0.88	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	1A	3590	1/1	0.88	0.34	55,55,55,55	0
56	MG	1A	3386	1/1	0.88	0.15	54,54,54,54	0
56	MG	1A	3177	1/1	0.88	0.17	65,65,65,65	0
56	MG	2A	3360	1/1	0.88	0.13	77,77,77,77	0
56	MG	1a	1735	1/1	0.88	0.20	80,80,80,80	0
56	MG	2A	3157	1/1	0.88	0.08	74,74,74,74	0
56	MG	2A	3159	1/1	0.88	0.23	69,69,69,69	0
56	MG	1A	3845	1/1	0.88	0.29	65,65,65,65	0
56	MG	2A	3368	1/1	0.88	0.14	80,80,80,80	0
56	MG	1A	3595	1/1	0.88	0.27	51,51,51,51	0
56	MG	2a	1661	1/1	0.88	0.14	79,79,79,79	0
56	MG	1A	3917	1/1	0.88	0.13	67,67,67,67	0
56	MG	2A	3371	1/1	0.88	0.13	62,62,62,62	0
56	MG	1A	3136	1/1	0.88	0.21	56,56,56,56	0
56	MG	1A	3068	1/1	0.88	0.20	62,62,62,62	0
56	MG	1A	3610	1/1	0.88	0.10	54,54,54,54	0
56	MG	1a	1743	1/1	0.88	0.15	66,66,66,66	0
56	MG	1A	3069	1/1	0.88	0.28	62,62,62,62	0
56	MG	1A	3614	1/1	0.88	0.15	73,73,73,73	0
56	MG	1x	121	1/1	0.88	0.08	57,57,57,57	0
56	MG	2a	1674	1/1	0.88	0.17	90,90,90,90	0
56	MG	1a	1625	1/1	0.88	0.12	72,72,72,72	0
56	MG	2A	3390	1/1	0.88	0.35	72,72,72,72	0
56	MG	1A	3053	1/1	0.88	0.15	40,40,40,40	0
56	MG	2A	3398	1/1	0.88	0.12	76,76,76,76	0
56	MG	1a	1627	1/1	0.88	0.12	70,70,70,70	0
56	MG	2A	3212	1/1	0.88	0.36	43,43,43,43	0
56	MG	1A	3401	1/1	0.88	0.10	61,61,61,61	0
56	MG	1A	3165	1/1	0.88	0.23	52,52,52,52	0
56	MG	1A	3704	1/1	0.88	0.11	49,49,49,49	0
56	MG	1A	3081	1/1	0.88	0.17	51,51,51,51	0
56	MG	1A	3192	1/1	0.88	0.12	41,41,41,41	0
56	MG	1A	3252	1/1	0.88	0.10	67,67,67,67	0
56	MG	1a	1660	1/1	0.88	0.18	47,47,47,47	0
56	MG	1B	210	1/1	0.88	0.24	35,35,35,35	0
57	KAN	2A	3568	33/33	0.88	0.09	51,58,63,65	0
57	KAN	2A	3569	33/33	0.88	0.13	56,65,71,73	0
56	MG	2a	1660	1/1	0.89	0.11	57,57,57,57	0
56	MG	1a	1860	1/1	0.89	0.15	73,73,73,73	0
56	MG	1A	3216	1/1	0.89	0.31	49,49,49,49	0
56	MG	1x	124	1/1	0.89	0.17	65,65,65,65	0
56	MG	1y	101	1/1	0.89	0.20	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1719	1/1	0.89	0.09	95,95,95,95	0
56	MG	1A	3691	1/1	0.89	0.19	37,37,37,37	0
56	MG	1A	3615	1/1	0.89	0.14	50,50,50,50	0
56	MG	1A	3357	1/1	0.89	0.38	31,31,31,31	0
56	MG	2A	3289	1/1	0.89	0.06	80,80,80,80	0
56	MG	1A	3885	1/1	0.89	0.21	53,53,53,53	0
56	MG	1a	1874	1/1	0.89	0.11	71,71,71,71	0
56	MG	2a	1675	1/1	0.89	0.08	94,94,94,94	0
56	MG	1a	1727	1/1	0.89	0.14	65,65,65,65	0
56	MG	2a	1677	1/1	0.89	0.10	67,67,67,67	0
56	MG	19	102	1/1	0.89	0.12	55,55,55,55	0
56	MG	2A	3027	1/1	0.89	0.20	58,58,58,58	0
56	MG	2A	3299	1/1	0.89	0.26	64,64,64,64	0
56	MG	2A	3029	1/1	0.89	0.18	67,67,67,67	0
56	MG	2A	3301	1/1	0.89	0.18	65,65,65,65	0
56	MG	1a	1734	1/1	0.89	0.21	76,76,76,76	0
56	MG	1a	1602	1/1	0.89	0.23	67,67,67,67	0
56	MG	1A	3886	1/1	0.89	0.16	39,39,39,39	0
56	MG	1A	3012	1/1	0.89	0.15	51,51,51,51	0
56	MG	1A	3501	1/1	0.89	0.07	51,51,51,51	0
56	MG	1a	1887	1/1	0.89	0.10	75,75,75,75	0
56	MG	2A	3516	1/1	0.89	0.06	78,78,78,78	0
56	MG	1A	3710	1/1	0.89	0.09	43,43,43,43	0
56	MG	2A	3519	1/1	0.89	0.26	56,56,56,56	0
56	MG	2A	3520	1/1	0.89	0.22	59,59,59,59	0
56	MG	2a	1703	1/1	0.89	0.19	67,67,67,67	0
56	MG	2A	3313	1/1	0.89	0.20	28,28,28,28	0
56	MG	1A	3711	1/1	0.89	0.07	46,46,46,46	0
56	MG	2A	3054	1/1	0.89	0.20	57,57,57,57	0
56	MG	1A	3172	1/1	0.89	0.07	79,79,79,79	0
56	MG	2A	3325	1/1	0.89	0.20	62,62,62,62	0
56	MG	1A	3368	1/1	0.89	0.30	24,24,24,24	0
56	MG	2A	3058	1/1	0.89	0.41	55,55,55,55	0
56	MG	2A	3531	1/1	0.89	0.13	57,57,57,57	0
56	MG	1A	3518	1/1	0.89	0.18	45,45,45,45	0
56	MG	1a	1893	1/1	0.89	0.07	79,79,79,79	0
56	MG	1A	3519	1/1	0.89	0.30	46,46,46,46	0
56	MG	1a	1895	1/1	0.89	0.36	51,51,51,51	0
56	MG	2A	3064	1/1	0.89	0.20	59,59,59,59	0
56	MG	2a	1726	1/1	0.89	0.33	65,65,65,65	0
56	MG	2A	3334	1/1	0.89	0.24	62,62,62,62	0
56	MG	1A	3229	1/1	0.89	0.11	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	1752	1/1	0.89	0.14	56,56,56,56	0
56	MG	1a	1753	1/1	0.89	0.14	58,58,58,58	0
56	MG	1A	3525	1/1	0.89	0.28	34,34,34,34	0
56	MG	1A	3200	1/1	0.89	0.12	66,66,66,66	0
56	MG	2a	1736	1/1	0.89	0.15	64,64,64,64	0
56	MG	1A	3747	1/1	0.89	0.23	66,66,66,66	0
56	MG	1a	1906	1/1	0.89	0.11	54,54,54,54	0
56	MG	1A	3302	1/1	0.89	0.37	61,61,61,61	0
56	MG	2A	3355	1/1	0.89	0.22	76,76,76,76	0
56	MG	1A	3750	1/1	0.89	0.11	67,67,67,67	0
56	MG	1a	1913	1/1	0.89	0.18	66,66,66,66	0
56	MG	1A	3834	1/1	0.89	0.14	68,68,68,68	0
56	MG	2A	3555	1/1	0.89	0.16	58,58,58,58	0
56	MG	1A	3835	1/1	0.89	0.11	59,59,59,59	0
56	MG	2A	3558	1/1	0.89	0.24	46,46,46,46	0
56	MG	2A	3105	1/1	0.89	0.30	56,56,56,56	0
56	MG	2A	3109	1/1	0.89	0.21	57,57,57,57	0
56	MG	1A	3837	1/1	0.89	0.18	51,51,51,51	0
56	MG	1A	3387	1/1	0.89	0.20	74,74,74,74	0
56	MG	2A	3567	1/1	0.89	0.09	67,67,67,67	0
56	MG	2A	3122	1/1	0.89	0.13	33,33,33,33	0
56	MG	2A	3124	1/1	0.89	0.20	45,45,45,45	0
56	MG	1A	3840	1/1	0.89	0.16	71,71,71,71	0
56	MG	1a	1927	1/1	0.89	0.14	70,70,70,70	0
56	MG	1a	1928	1/1	0.89	0.11	70,70,70,70	0
56	MG	2a	1765	1/1	0.89	0.37	59,59,59,59	0
56	MG	1A	3841	1/1	0.89	0.14	73,73,73,73	0
56	MG	1A	3309	1/1	0.89	0.28	42,42,42,42	0
56	MG	2A	3133	1/1	0.89	0.18	72,72,72,72	0
56	MG	2a	1773	1/1	0.89	0.13	91,91,91,91	0
56	MG	1A	3173	1/1	0.89	0.07	70,70,70,70	0
56	MG	1A	3577	1/1	0.89	0.28	51,51,51,51	0
56	MG	1B	208	1/1	0.89	0.09	61,61,61,61	0
56	MG	2Q	201	1/1	0.89	0.10	71,71,71,71	0
56	MG	1A	3241	1/1	0.89	0.26	36,36,36,36	0
56	MG	2T	201	1/1	0.89	0.19	55,55,55,55	0
56	MG	1A	3004	1/1	0.89	0.16	68,68,68,68	0
56	MG	1a	1676	1/1	0.89	0.17	73,73,73,73	0
56	MG	2a	1784	1/1	0.89	0.21	66,66,66,66	0
56	MG	1B	214	1/1	0.89	0.23	49,49,49,49	0
56	MG	1a	1795	1/1	0.89	0.10	55,55,55,55	0
56	MG	1A	3764	1/1	0.89	0.14	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1949	1/1	0.89	0.13	78,78,78,78	0
56	MG	2a	1792	1/1	0.89	0.24	59,59,59,59	0
56	MG	1A	3117	1/1	0.89	0.30	41,41,41,41	0
56	MG	1A	3023	1/1	0.89	0.10	55,55,55,55	0
56	MG	2A	3165	1/1	0.89	0.39	77,77,77,77	0
56	MG	2A	3167	1/1	0.89	0.24	64,64,64,64	0
56	MG	1B	221	1/1	0.89	0.28	58,58,58,58	0
56	MG	1a	1807	1/1	0.89	0.22	76,76,76,76	0
56	MG	2A	3171	1/1	0.89	0.36	51,51,51,51	0
56	MG	1A	3036	1/1	0.89	0.23	32,32,32,32	0
56	MG	1A	3656	1/1	0.89	0.09	71,71,71,71	0
56	MG	2A	3187	1/1	0.89	0.27	39,39,39,39	0
56	MG	1m	202	1/1	0.89	0.09	58,58,58,58	0
56	MG	2A	3192	1/1	0.89	0.32	36,36,36,36	0
56	MG	2A	3440	1/1	0.89	0.16	57,57,57,57	0
56	MG	1A	3859	1/1	0.89	0.09	69,69,69,69	0
56	MG	1a	1825	1/1	0.89	0.21	76,76,76,76	0
56	MG	1A	3263	1/1	0.89	0.19	31,31,31,31	0
56	MG	2A	3199	1/1	0.89	0.30	38,38,38,38	0
56	MG	1a	1827	1/1	0.89	0.20	68,68,68,68	0
56	MG	1A	3598	1/1	0.89	0.21	60,60,60,60	0
56	MG	1A	3774	1/1	0.89	0.06	83,83,83,83	0
56	MG	2A	3213	1/1	0.89	0.33	48,48,48,48	0
56	MG	1A	3601	1/1	0.89	0.15	43,43,43,43	0
56	MG	2A	3218	1/1	0.89	0.35	56,56,56,56	0
56	MG	1a	1841	1/1	0.89	0.11	72,72,72,72	0
56	MG	1a	1843	1/1	0.89	0.15	63,63,63,63	0
56	MG	2A	3224	1/1	0.89	0.19	45,45,45,45	0
56	MG	2a	1636	1/1	0.89	0.19	69,69,69,69	0
56	MG	1A	3662	1/1	0.89	0.12	60,60,60,60	0
56	MG	1a	1702	1/1	0.89	0.26	58,58,58,58	0
56	MG	1a	1707	1/1	0.89	0.32	41,41,41,41	0
56	MG	2A	3243	1/1	0.89	0.44	53,53,53,53	0
56	MG	2A	3245	1/1	0.89	0.31	63,63,63,63	0
56	MG	1A	3476	1/1	0.89	0.14	63,63,63,63	0
56	MG	1A	3478	1/1	0.89	0.11	60,60,60,60	0
56	MG	2a	1650	1/1	0.89	0.34	73,73,73,73	0
56	MG	1A	3269	1/1	0.89	0.22	33,33,33,33	0
56	MG	1A	3789	1/1	0.89	0.06	78,78,78,78	0
56	MG	2A	3262	1/1	0.89	0.17	65,65,65,65	0
56	MG	1A	3179	1/1	0.89	0.11	70,70,70,70	0
56	MG	1A	3791	1/1	0.89	0.22	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	1909	1/1	0.90	0.09	62,62,62,62	0
56	MG	1a	1671	1/1	0.90	0.18	69,69,69,69	0
56	MG	1A	3524	1/1	0.90	0.38	44,44,44,44	0
56	MG	1A	3171	1/1	0.90	0.06	61,61,61,61	0
56	MG	1B	223	1/1	0.90	0.08	63,63,63,63	0
56	MG	2A	3310	1/1	0.90	0.31	56,56,56,56	0
56	MG	1A	3529	1/1	0.90	0.24	33,33,33,33	0
56	MG	1A	3713	1/1	0.90	0.12	61,61,61,61	0
56	MG	2A	3085	1/1	0.90	0.17	67,67,67,67	0
56	MG	2a	1683	1/1	0.90	0.14	83,83,83,83	0
56	MG	1A	3530	1/1	0.90	0.34	43,43,43,43	0
56	MG	1a	1926	1/1	0.90	0.08	77,77,77,77	0
56	MG	1A	3717	1/1	0.90	0.14	62,62,62,62	0
56	MG	2A	3323	1/1	0.90	0.22	40,40,40,40	0
56	MG	1A	3396	1/1	0.90	0.15	61,61,61,61	0
56	MG	1A	3447	1/1	0.90	0.16	53,53,53,53	0
56	MG	1a	1685	1/1	0.90	0.12	79,79,79,79	0
56	MG	2A	3106	1/1	0.90	0.26	52,52,52,52	0
56	MG	1a	1933	1/1	0.90	0.11	74,74,74,74	0
56	MG	1A	3539	1/1	0.90	0.18	33,33,33,33	0
56	MG	1a	1688	1/1	0.90	0.20	72,72,72,72	0
56	MG	2A	3528	1/1	0.90	0.15	64,64,64,64	0
56	MG	1a	1811	1/1	0.90	0.19	63,63,63,63	0
56	MG	1a	1937	1/1	0.90	0.24	52,52,52,52	0
56	MG	2A	3125	1/1	0.90	0.23	69,69,69,69	0
56	MG	1A	3153	1/1	0.90	0.10	65,65,65,65	0
56	MG	1a	1816	1/1	0.90	0.10	81,81,81,81	0
56	MG	2A	3535	1/1	0.90	0.12	65,65,65,65	0
56	MG	1a	1818	1/1	0.90	0.13	64,64,64,64	0
56	MG	1A	3884	1/1	0.90	0.20	59,59,59,59	0
56	MG	1a	1821	1/1	0.90	0.08	88,88,88,88	0
56	MG	2a	1714	1/1	0.90	0.09	58,58,58,58	0
56	MG	1A	3232	1/1	0.90	0.19	58,58,58,58	0
56	MG	1A	3087	1/1	0.90	0.29	40,40,40,40	0
56	MG	1A	3564	1/1	0.90	0.22	43,43,43,43	0
56	MG	1A	3567	1/1	0.90	0.17	37,37,37,37	0
56	MG	2A	3142	1/1	0.90	0.21	73,73,73,73	0
56	MG	2A	3362	1/1	0.90	0.13	58,58,58,58	0
56	MG	1X	101	1/1	0.90	0.19	56,56,56,56	0
56	MG	2A	3149	1/1	0.90	0.08	75,75,75,75	0
56	MG	1A	3402	1/1	0.90	0.12	63,63,63,63	0
56	MG	1a	1706	1/1	0.90	0.25	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	3153	1/1	0.90	0.11	69,69,69,69	0
56	MG	1a	1839	1/1	0.90	0.10	75,75,75,75	0
56	MG	1A	3458	1/1	0.90	0.50	54,54,54,54	0
56	MG	1a	1842	1/1	0.90	0.20	55,55,55,55	0
56	MG	2a	1735	1/1	0.90	0.09	71,71,71,71	0
56	MG	1A	3354	1/1	0.90	0.32	25,25,25,25	0
56	MG	1A	3653	1/1	0.90	0.07	84,84,84,84	0
56	MG	2A	3560	1/1	0.90	0.14	82,82,82,82	0
56	MG	1A	3405	1/1	0.90	0.09	60,60,60,60	0
56	MG	2A	3562	1/1	0.90	0.13	73,73,73,73	0
56	MG	1A	3758	1/1	0.90	0.10	58,58,58,58	0
56	MG	1a	1851	1/1	0.90	0.10	64,64,64,64	0
56	MG	2A	3168	1/1	0.90	0.09	71,71,71,71	0
56	MG	2A	3386	1/1	0.90	0.13	66,66,66,66	0
56	MG	1A	3264	1/1	0.90	0.25	32,32,32,32	0
56	MG	2A	3388	1/1	0.90	0.14	53,53,53,53	0
56	MG	19	103	1/1	0.90	0.18	63,63,63,63	0
56	MG	1A	3912	1/1	0.90	0.13	61,61,61,61	0
56	MG	2A	3392	1/1	0.90	0.16	57,57,57,57	0
56	MG	1w	105	1/1	0.90	0.31	55,55,55,55	0
56	MG	2A	3181	1/1	0.90	0.29	50,50,50,50	0
56	MG	2a	1759	1/1	0.90	0.11	63,63,63,63	0
56	MG	2D	303	1/1	0.90	0.13	67,67,67,67	0
56	MG	1a	1604	1/1	0.90	0.20	62,62,62,62	0
56	MG	1A	3913	1/1	0.90	0.07	65,65,65,65	0
56	MG	2A	3189	1/1	0.90	0.18	55,55,55,55	0
56	MG	1a	1857	1/1	0.90	0.19	71,71,71,71	0
56	MG	1a	1608	1/1	0.90	0.12	65,65,65,65	0
56	MG	2A	3194	1/1	0.90	0.35	47,47,47,47	0
56	MG	1A	3310	1/1	0.90	0.15	53,53,53,53	0
56	MG	1A	3763	1/1	0.90	0.20	53,53,53,53	0
56	MG	1A	3267	1/1	0.90	0.32	40,40,40,40	0
56	MG	2A	3419	1/1	0.90	0.14	62,62,62,62	0
56	MG	1x	118	1/1	0.90	0.10	71,71,71,71	0
56	MG	2A	3205	1/1	0.90	0.33	49,49,49,49	0
56	MG	1a	1865	1/1	0.90	0.10	59,59,59,59	0
56	MG	28	101	1/1	0.90	0.16	47,47,47,47	0
56	MG	1A	3235	1/1	0.90	0.09	55,55,55,55	0
56	MG	1A	3659	1/1	0.90	0.12	65,65,65,65	0
56	MG	1A	3485	1/1	0.90	0.12	64,64,64,64	0
56	MG	2a	1783	1/1	0.90	0.26	60,60,60,60	0
56	MG	1a	1871	1/1	0.90	0.17	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1617	1/1	0.90	0.11	84,84,84,84	0
56	MG	2A	3219	1/1	0.90	0.36	35,35,35,35	0
56	MG	1a	1873	1/1	0.90	0.17	62,62,62,62	0
56	MG	2a	1788	1/1	0.90	0.26	62,62,62,62	0
56	MG	1A	3415	1/1	0.90	0.24	48,48,48,48	0
56	MG	1A	3371	1/1	0.90	0.15	60,60,60,60	0
56	MG	2A	3010	1/1	0.90	0.27	49,49,49,49	0
56	MG	2A	3236	1/1	0.90	0.34	33,33,33,33	0
56	MG	1A	3927	1/1	0.90	0.22	86,86,86,86	0
56	MG	2A	3015	1/1	0.90	0.10	51,51,51,51	0
56	MG	2A	3019	1/1	0.90	0.15	58,58,58,58	0
56	MG	1A	3375	1/1	0.90	0.27	25,25,25,25	0
56	MG	2A	3253	1/1	0.90	0.21	50,50,50,50	0
56	MG	2a	1618	1/1	0.90	0.07	129,129,129,129	0
56	MG	1a	1622	1/1	0.90	0.24	56,56,56,56	0
56	MG	2A	3024	1/1	0.90	0.22	48,48,48,48	0
56	MG	1A	3019	1/1	0.90	0.11	63,63,63,63	0
56	MG	1A	3325	1/1	0.90	0.20	41,41,41,41	0
56	MG	2a	1806	1/1	0.90	0.12	90,90,90,90	0
56	MG	1a	1885	1/1	0.90	0.07	71,71,71,71	0
56	MG	1B	203	1/1	0.90	0.13	74,74,74,74	0
56	MG	1A	3778	1/1	0.90	0.13	64,64,64,64	0
56	MG	2a	1629	1/1	0.90	0.20	55,55,55,55	0
56	MG	1a	1748	1/1	0.90	0.10	59,59,59,59	0
56	MG	2A	3468	1/1	0.90	0.14	73,73,73,73	0
56	MG	1a	1749	1/1	0.90	0.14	73,73,73,73	0
56	MG	1a	1634	1/1	0.90	0.18	61,61,61,61	0
56	MG	2A	3279	1/1	0.90	0.29	31,31,31,31	0
56	MG	2A	3038	1/1	0.90	0.12	57,57,57,57	0
56	MG	1A	3326	1/1	0.90	0.22	42,42,42,42	0
56	MG	2a	1820	1/1	0.90	0.28	58,58,58,58	0
56	MG	1A	3680	1/1	0.90	0.17	58,58,58,58	0
56	MG	1a	1645	1/1	0.90	0.14	71,71,71,71	0
56	MG	1a	1646	1/1	0.90	0.17	67,67,67,67	0
56	MG	1A	3682	1/1	0.90	0.09	41,41,41,41	0
56	MG	2A	3485	1/1	0.90	0.19	58,58,58,58	0
56	MG	1A	3861	1/1	0.90	0.07	81,81,81,81	0
56	MG	2e	201	1/1	0.90	0.09	74,74,74,74	0
56	MG	1a	1658	1/1	0.90	0.35	46,46,46,46	0
56	MG	2A	3292	1/1	0.90	0.33	50,50,50,50	0
56	MG	1A	3242	1/1	0.90	0.13	62,62,62,62	0
56	MG	2A	3295	1/1	0.90	0.30	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1B	213	1/1	0.90	0.21	40,40,40,40	0
56	MG	1A	3282	1/1	0.90	0.28	44,44,44,44	0
56	MG	1A	3625	1/1	0.90	0.10	57,57,57,57	0
56	MG	2A	3497	1/1	0.90	0.18	71,71,71,71	0
56	MG	1A	3224	1/1	0.90	0.27	23,23,23,23	0
56	MG	2A	3499	1/1	0.90	0.19	73,73,73,73	0
56	MG	1a	1670	1/1	0.90	0.12	62,62,62,62	0
56	MG	2A	3206	1/1	0.91	0.31	31,31,31,31	0
56	MG	2A	3207	1/1	0.91	0.27	34,34,34,34	0
56	MG	1A	3436	1/1	0.91	0.07	57,57,57,57	0
56	MG	2A	3210	1/1	0.91	0.31	44,44,44,44	0
56	MG	1A	3025	1/1	0.91	0.11	41,41,41,41	0
56	MG	1x	113	1/1	0.91	0.19	67,67,67,67	0
56	MG	2a	1653	1/1	0.91	0.17	49,49,49,49	0
56	MG	1B	216	1/1	0.91	0.10	67,67,67,67	0
56	MG	1a	1849	1/1	0.91	0.19	61,61,61,61	0
56	MG	2A	3216	1/1	0.91	0.27	38,38,38,38	0
56	MG	1A	3441	1/1	0.91	0.07	26,26,26,26	0
56	MG	2a	1659	1/1	0.91	0.14	69,69,69,69	0
56	MG	1A	3236	1/1	0.91	0.20	48,48,48,48	0
56	MG	2A	3220	1/1	0.91	0.40	59,59,59,59	0
56	MG	2a	1662	1/1	0.91	0.14	73,73,73,73	0
56	MG	1A	3593	1/1	0.91	0.34	55,55,55,55	0
56	MG	1A	3384	1/1	0.91	0.06	72,72,72,72	0
56	MG	1A	3597	1/1	0.91	0.23	45,45,45,45	0
56	MG	2A	3227	1/1	0.91	0.29	37,37,37,37	0
56	MG	2A	3470	1/1	0.91	0.10	68,68,68,68	0
56	MG	1A	3304	1/1	0.91	0.21	46,46,46,46	0
56	MG	2A	3235	1/1	0.91	0.44	47,47,47,47	0
56	MG	1A	3719	1/1	0.91	0.09	57,57,57,57	0
56	MG	1A	3720	1/1	0.91	0.14	66,66,66,66	0
56	MG	1A	3205	1/1	0.91	0.26	65,65,65,65	0
56	MG	2A	3003	1/1	0.91	0.17	60,60,60,60	0
56	MG	2A	3006	1/1	0.91	0.09	57,57,57,57	0
56	MG	2A	3247	1/1	0.91	0.45	41,41,41,41	0
56	MG	1A	3028	1/1	0.91	0.06	57,57,57,57	0
56	MG	2a	1680	1/1	0.91	0.16	67,67,67,67	0
56	MG	1a	1713	1/1	0.91	0.09	75,75,75,75	0
56	MG	1A	3853	1/1	0.91	0.11	59,59,59,59	0
56	MG	2A	3256	1/1	0.91	0.21	24,24,24,24	0
56	MG	1A	3391	1/1	0.91	0.17	62,62,62,62	0
56	MG	1A	3728	1/1	0.91	0.12	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	1A	3393	1/1	0.91	0.10	53,53,53,53	0
56	MG	1A	3732	1/1	0.91	0.09	68,68,68,68	0
56	MG	1A	3463	1/1	0.91	0.06	60,60,60,60	0
56	MG	1a	1721	1/1	0.91	0.07	81,81,81,81	0
56	MG	1a	1722	1/1	0.91	0.07	85,85,85,85	0
56	MG	2a	1696	1/1	0.91	0.08	52,52,52,52	0
56	MG	1A	3247	1/1	0.91	0.09	68,68,68,68	0
56	MG	2A	3271	1/1	0.91	0.30	34,34,34,34	0
56	MG	2A	3277	1/1	0.91	0.16	58,58,58,58	0
56	MG	1A	3470	1/1	0.91	0.27	43,43,43,43	0
56	MG	1a	1725	1/1	0.91	0.15	76,76,76,76	0
56	MG	1a	1878	1/1	0.91	0.10	77,77,77,77	0
56	MG	2a	1704	1/1	0.91	0.23	69,69,69,69	0
56	MG	2A	3031	1/1	0.91	0.28	47,47,47,47	0
56	MG	2A	3507	1/1	0.91	0.18	57,57,57,57	0
56	MG	1A	3210	1/1	0.91	0.35	47,47,47,47	0
56	MG	2a	1710	1/1	0.91	0.05	85,85,85,85	0
56	MG	1A	3318	1/1	0.91	0.19	64,64,64,64	0
56	MG	2A	3036	1/1	0.91	0.16	68,68,68,68	0
56	MG	1a	1881	1/1	0.91	0.11	70,70,70,70	0
56	MG	12	101	1/1	0.91	0.15	73,73,73,73	0
56	MG	1A	3622	1/1	0.91	0.27	44,44,44,44	0
56	MG	1a	1884	1/1	0.91	0.16	70,70,70,70	0
56	MG	2a	1718	1/1	0.91	0.11	68,68,68,68	0
56	MG	2A	3044	1/1	0.91	0.23	49,49,49,49	0
56	MG	1A	3397	1/1	0.91	0.07	60,60,60,60	0
56	MG	15	101	1/1	0.91	0.24	51,51,51,51	0
56	MG	1A	3872	1/1	0.91	0.22	61,61,61,61	0
56	MG	18	102	1/1	0.91	0.07	55,55,55,55	0
56	MG	1A	3626	1/1	0.91	0.33	47,47,47,47	0
56	MG	1a	1740	1/1	0.91	0.14	67,67,67,67	0
56	MG	1A	3322	1/1	0.91	0.29	58,58,58,58	0
56	MG	1A	3629	1/1	0.91	0.12	73,73,73,73	0
56	MG	1A	3006	1/1	0.91	0.08	59,59,59,59	0
56	MG	1A	3760	1/1	0.91	0.14	52,52,52,52	0
56	MG	2a	1733	1/1	0.91	0.11	74,74,74,74	0
56	MG	1A	3050	1/1	0.91	0.17	43,43,43,43	0
56	MG	1A	3632	1/1	0.91	0.25	71,71,71,71	0
56	MG	1A	3189	1/1	0.91	0.27	51,51,51,51	0
56	MG	1A	3489	1/1	0.91	0.07	45,45,45,45	0
56	MG	2A	3070	1/1	0.91	0.32	61,61,61,61	0
56	MG	1A	3493	1/1	0.91	0.11	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	3257	1/1	0.91	0.17	57,57,57,57	0
56	MG	2A	3076	1/1	0.91	0.24	47,47,47,47	0
56	MG	2a	1745	1/1	0.91	0.34	44,44,44,44	0
56	MG	1a	1901	1/1	0.91	0.12	76,76,76,76	0
56	MG	1A	3496	1/1	0.91	0.08	47,47,47,47	0
56	MG	1a	1904	1/1	0.91	0.10	70,70,70,70	0
56	MG	1A	3500	1/1	0.91	0.23	61,61,61,61	0
56	MG	2A	3088	1/1	0.91	0.20	49,49,49,49	0
56	MG	1A	3404	1/1	0.91	0.11	58,58,58,58	0
56	MG	2A	3092	1/1	0.91	0.21	55,55,55,55	0
56	MG	1a	1760	1/1	0.91	0.12	59,59,59,59	0
56	MG	1a	1761	1/1	0.91	0.14	69,69,69,69	0
56	MG	1A	3505	1/1	0.91	0.09	46,46,46,46	0
56	MG	1a	1914	1/1	0.91	0.12	74,74,74,74	0
56	MG	1A	3261	1/1	0.91	0.25	25,25,25,25	0
56	MG	2A	3343	1/1	0.91	0.22	67,67,67,67	0
56	MG	2A	3108	1/1	0.91	0.32	58,58,58,58	0
56	MG	1a	1920	1/1	0.91	0.08	66,66,66,66	0
56	MG	2A	3349	1/1	0.91	0.27	48,48,48,48	0
56	MG	1a	1768	1/1	0.91	0.16	75,75,75,75	0
56	MG	1A	3896	1/1	0.91	0.12	65,65,65,65	0
56	MG	2a	1768	1/1	0.91	0.31	71,71,71,71	0
56	MG	2A	3118	1/1	0.91	0.24	42,42,42,42	0
56	MG	1A	3407	1/1	0.91	0.07	85,85,85,85	0
56	MG	1A	3899	1/1	0.91	0.17	53,53,53,53	0
56	MG	1a	1623	1/1	0.91	0.13	66,66,66,66	0
56	MG	1A	3408	1/1	0.91	0.12	74,74,74,74	0
56	MG	2B	204	1/1	0.91	0.28	60,60,60,60	0
56	MG	1A	3074	1/1	0.91	0.15	50,50,50,50	0
56	MG	1A	3521	1/1	0.91	0.27	31,31,31,31	0
56	MG	1a	1930	1/1	0.91	0.12	72,72,72,72	0
56	MG	2a	1780	1/1	0.91	0.11	56,56,56,56	0
56	MG	2B	208	1/1	0.91	0.07	67,67,67,67	0
56	MG	1A	3079	1/1	0.91	0.11	54,54,54,54	0
56	MG	1a	1783	1/1	0.91	0.31	47,47,47,47	0
56	MG	1A	3158	1/1	0.91	0.20	41,41,41,41	0
56	MG	2A	3135	1/1	0.91	0.24	68,68,68,68	0
56	MG	1A	3225	1/1	0.91	0.29	40,40,40,40	0
56	MG	2A	3373	1/1	0.91	0.16	69,69,69,69	0
56	MG	1A	3007	1/1	0.91	0.06	60,60,60,60	0
56	MG	2a	1789	1/1	0.91	0.11	66,66,66,66	0
56	MG	2A	3376	1/1	0.91	0.11	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3353	1/1	0.91	0.21	27,27,27,27	0
56	MG	2A	3143	1/1	0.91	0.10	59,59,59,59	0
56	MG	2A	3380	1/1	0.91	0.28	54,54,54,54	0
56	MG	1A	3163	1/1	0.91	0.14	67,67,67,67	0
56	MG	2a	1796	1/1	0.91	0.16	68,68,68,68	0
56	MG	1a	1792	1/1	0.91	0.19	59,59,59,59	0
56	MG	20	101	1/1	0.91	0.14	52,52,52,52	0
56	MG	1A	3918	1/1	0.91	0.10	55,55,55,55	0
56	MG	1A	3231	1/1	0.91	0.12	51,51,51,51	0
56	MG	1A	3286	1/1	0.91	0.23	23,23,23,23	0
56	MG	1A	3921	1/1	0.91	0.21	43,43,43,43	0
56	MG	1A	3541	1/1	0.91	0.32	43,43,43,43	0
56	MG	1A	3663	1/1	0.91	0.13	54,54,54,54	0
56	MG	1A	3553	1/1	0.91	0.23	34,34,34,34	0
56	MG	2A	3396	1/1	0.91	0.29	63,63,63,63	0
56	MG	1d	301	1/1	0.91	0.24	62,62,62,62	0
56	MG	1A	3556	1/1	0.91	0.11	25,25,25,25	0
56	MG	2A	3403	1/1	0.91	0.16	61,61,61,61	0
56	MG	1a	1667	1/1	0.91	0.10	66,66,66,66	0
56	MG	1A	3363	1/1	0.91	0.16	34,34,34,34	0
56	MG	1A	3423	1/1	0.91	0.09	65,65,65,65	0
56	MG	1A	3931	1/1	0.91	0.13	74,74,74,74	0
56	MG	1A	3670	1/1	0.91	0.16	53,53,53,53	0
56	MG	1B	202	1/1	0.91	0.19	55,55,55,55	0
56	MG	2a	1613	1/1	0.91	0.30	81,81,81,81	0
56	MG	1A	3426	1/1	0.91	0.11	57,57,57,57	0
56	MG	1A	3679	1/1	0.91	0.11	40,40,40,40	0
56	MG	2A	3182	1/1	0.91	0.32	39,39,39,39	0
56	MG	1A	3054	1/1	0.91	0.19	40,40,40,40	0
56	MG	2A	3185	1/1	0.91	0.32	40,40,40,40	0
56	MG	2A	3423	1/1	0.91	0.15	88,88,88,88	0
56	MG	2A	3424	1/1	0.91	0.17	51,51,51,51	0
56	MG	2A	3186	1/1	0.91	0.34	38,38,38,38	0
56	MG	1A	3143	1/1	0.91	0.10	50,50,50,50	0
56	MG	2A	3188	1/1	0.91	0.32	30,30,30,30	0
56	MG	2v	101	1/1	0.91	0.19	61,61,61,61	0
56	MG	1A	3689	1/1	0.91	0.12	55,55,55,55	0
56	MG	1w	101	1/1	0.91	0.14	72,72,72,72	0
56	MG	1w	102	1/1	0.91	0.12	63,63,63,63	0
56	MG	2A	3437	1/1	0.91	0.16	58,58,58,58	0
56	MG	1A	3234	1/1	0.91	0.24	25,25,25,25	0
56	MG	1A	3299	1/1	0.91	0.29	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1a	1840	1/1	0.91	0.14	70,70,70,70	0
56	MG	1B	212	1/1	0.91	0.10	62,62,62,62	0
56	MG	1A	3697	1/1	0.91	0.09	55,55,55,55	0
56	MG	1x	107	1/1	0.91	0.14	71,71,71,71	0
56	MG	1A	3814	1/1	0.92	0.10	73,73,73,73	0
56	MG	1A	3303	1/1	0.92	0.10	42,42,42,42	0
56	MG	1A	3701	1/1	0.92	0.07	42,42,42,42	0
56	MG	2A	3087	1/1	0.92	0.13	76,76,76,76	0
56	MG	1A	3096	1/1	0.92	0.11	59,59,59,59	0
56	MG	1A	3608	1/1	0.92	0.33	57,57,57,57	0
56	MG	1A	3708	1/1	0.92	0.09	33,33,33,33	0
56	MG	1a	1932	1/1	0.92	0.27	72,72,72,72	0
56	MG	2a	1678	1/1	0.92	0.45	72,72,72,72	0
56	MG	1A	3170	1/1	0.92	0.18	73,73,73,73	0
56	MG	2A	3502	1/1	0.92	0.30	70,70,70,70	0
56	MG	1A	3145	1/1	0.92	0.10	52,52,52,52	0
56	MG	1a	1673	1/1	0.92	0.14	68,68,68,68	0
56	MG	1a	1801	1/1	0.92	0.12	53,53,53,53	0
56	MG	2A	3107	1/1	0.92	0.15	60,60,60,60	0
56	MG	1A	3260	1/1	0.92	0.27	25,25,25,25	0
56	MG	1A	3420	1/1	0.92	0.05	32,32,32,32	0
56	MG	2a	1690	1/1	0.92	0.10	90,90,90,90	0
56	MG	1a	1808	1/1	0.92	0.16	60,60,60,60	0
56	MG	1A	3104	1/1	0.92	0.27	39,39,39,39	0
56	MG	2A	3512	1/1	0.92	0.10	85,85,85,85	0
56	MG	2A	3116	1/1	0.92	0.22	42,42,42,42	0
56	MG	1a	1813	1/1	0.92	0.07	58,58,58,58	0
56	MG	2a	1697	1/1	0.92	0.09	69,69,69,69	0
56	MG	1A	3314	1/1	0.92	0.32	39,39,39,39	0
56	MG	1A	3621	1/1	0.92	0.07	78,78,78,78	0
56	MG	1A	3133	1/1	0.92	0.25	54,54,54,54	0
56	MG	2A	3126	1/1	0.92	0.18	53,53,53,53	0
56	MG	2A	3324	1/1	0.92	0.46	68,68,68,68	0
56	MG	1a	1682	1/1	0.92	0.17	62,62,62,62	0
56	MG	1A	3723	1/1	0.92	0.12	66,66,66,66	0
56	MG	1A	3321	1/1	0.92	0.20	27,27,27,27	0
56	MG	1A	3510	1/1	0.92	0.11	65,65,65,65	0
56	MG	2A	3131	1/1	0.92	0.28	58,58,58,58	0
56	MG	2a	1709	1/1	0.92	0.10	70,70,70,70	0
56	MG	1A	3514	1/1	0.92	0.22	34,34,34,34	0
56	MG	1k	201	1/1	0.92	0.10	74,74,74,74	0
56	MG	1A	3628	1/1	0.92	0.20	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3196	1/1	0.92	0.10	62,62,62,62	0
56	MG	1A	3739	1/1	0.92	0.08	48,48,48,48	0
56	MG	2A	3137	1/1	0.92	0.19	57,57,57,57	0
56	MG	2A	3534	1/1	0.92	0.15	57,57,57,57	0
56	MG	1A	3740	1/1	0.92	0.10	52,52,52,52	0
56	MG	1a	1838	1/1	0.92	0.13	74,74,74,74	0
56	MG	1A	3134	1/1	0.92	0.22	64,64,64,64	0
56	MG	2A	3345	1/1	0.92	0.15	69,69,69,69	0
56	MG	1A	3431	1/1	0.92	0.18	66,66,66,66	0
56	MG	2A	3347	1/1	0.92	0.30	42,42,42,42	0
56	MG	1A	3745	1/1	0.92	0.17	61,61,61,61	0
56	MG	1A	3389	1/1	0.92	0.29	65,65,65,65	0
56	MG	1a	1701	1/1	0.92	0.21	47,47,47,47	0
56	MG	1A	3390	1/1	0.92	0.11	54,54,54,54	0
56	MG	1a	1703	1/1	0.92	0.17	51,51,51,51	0
56	MG	1A	3862	1/1	0.92	0.14	70,70,70,70	0
56	MG	2A	3158	1/1	0.92	0.07	66,66,66,66	0
56	MG	1A	3001	1/1	0.92	0.21	39,39,39,39	0
56	MG	1A	3528	1/1	0.92	0.33	35,35,35,35	0
56	MG	1T	201	1/1	0.92	0.12	55,55,55,55	0
56	MG	1U	201	1/1	0.92	0.23	41,41,41,41	0
56	MG	1A	3106	1/1	0.92	0.21	31,31,31,31	0
56	MG	1x	109	1/1	0.92	0.15	56,56,56,56	0
56	MG	1V	202	1/1	0.92	0.12	47,47,47,47	0
56	MG	2a	1742	1/1	0.92	0.21	51,51,51,51	0
56	MG	1A	3274	1/1	0.92	0.25	43,43,43,43	0
56	MG	1A	3446	1/1	0.92	0.25	47,47,47,47	0
56	MG	1A	3870	1/1	0.92	0.12	61,61,61,61	0
56	MG	2A	3172	1/1	0.92	0.30	48,48,48,48	0
56	MG	2a	1748	1/1	0.92	0.13	69,69,69,69	0
56	MG	2A	3173	1/1	0.92	0.25	39,39,39,39	0
56	MG	2A	3174	1/1	0.92	0.27	48,48,48,48	0
56	MG	1a	1718	1/1	0.92	0.10	73,73,73,73	0
56	MG	2B	202	1/1	0.92	0.23	68,68,68,68	0
56	MG	1A	3534	1/1	0.92	0.31	32,32,32,32	0
56	MG	1A	3155	1/1	0.92	0.08	59,59,59,59	0
56	MG	1A	3538	1/1	0.92	0.29	53,53,53,53	0
56	MG	1A	3033	1/1	0.92	0.16	68,68,68,68	0
56	MG	1A	3540	1/1	0.92	0.17	32,32,32,32	0
56	MG	1A	3014	1/1	0.92	0.23	59,59,59,59	0
56	MG	1A	3548	1/1	0.92	0.07	54,54,54,54	0
56	MG	1A	3650	1/1	0.92	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3206	1/1	0.92	0.20	75,75,75,75	0
56	MG	1A	3554	1/1	0.92	0.27	54,54,54,54	0
56	MG	1a	1731	1/1	0.92	0.08	72,72,72,72	0
56	MG	2A	3397	1/1	0.92	0.21	74,74,74,74	0
56	MG	1a	1601	1/1	0.92	0.11	59,59,59,59	0
56	MG	1A	3207	1/1	0.92	0.08	59,59,59,59	0
56	MG	1A	3346	1/1	0.92	0.27	44,44,44,44	0
56	MG	2a	1772	1/1	0.92	0.31	52,52,52,52	0
56	MG	1a	1606	1/1	0.92	0.17	74,74,74,74	0
56	MG	2A	3014	1/1	0.92	0.08	51,51,51,51	0
56	MG	1A	3119	1/1	0.92	0.27	44,44,44,44	0
56	MG	2A	3017	1/1	0.92	0.12	53,53,53,53	0
56	MG	1A	3348	1/1	0.92	0.23	28,28,28,28	0
56	MG	1A	3351	1/1	0.92	0.39	36,36,36,36	0
56	MG	1A	3565	1/1	0.92	0.34	60,60,60,60	0
56	MG	1A	3466	1/1	0.92	0.10	45,45,45,45	0
56	MG	1a	1612	1/1	0.92	0.12	72,72,72,72	0
56	MG	1a	1744	1/1	0.92	0.15	64,64,64,64	0
56	MG	2A	3420	1/1	0.92	0.21	52,52,52,52	0
56	MG	1A	3783	1/1	0.92	0.09	56,56,56,56	0
56	MG	1A	3575	1/1	0.92	0.28	31,31,31,31	0
56	MG	1A	3664	1/1	0.92	0.09	59,59,59,59	0
56	MG	1A	3788	1/1	0.92	0.11	53,53,53,53	0
56	MG	1A	3901	1/1	0.92	0.21	53,53,53,53	0
56	MG	2A	3033	1/1	0.92	0.28	68,68,68,68	0
56	MG	2A	3430	1/1	0.92	0.13	47,47,47,47	0
56	MG	2A	3431	1/1	0.92	0.09	70,70,70,70	0
56	MG	1A	3352	1/1	0.92	0.31	32,32,32,32	0
56	MG	2A	3035	1/1	0.92	0.20	53,53,53,53	0
56	MG	1A	3472	1/1	0.92	0.15	60,60,60,60	0
56	MG	2A	3230	1/1	0.92	0.27	50,50,50,50	0
56	MG	1A	3475	1/1	0.92	0.07	64,64,64,64	0
56	MG	1A	3009	1/1	0.92	0.19	51,51,51,51	0
56	MG	1A	3124	1/1	0.92	0.08	56,56,56,56	0
56	MG	1a	1758	1/1	0.92	0.05	65,65,65,65	0
56	MG	2A	3240	1/1	0.92	0.17	50,50,50,50	0
56	MG	1A	3356	1/1	0.92	0.26	26,26,26,26	0
56	MG	1A	3677	1/1	0.92	0.10	56,56,56,56	0
56	MG	1A	3481	1/1	0.92	0.09	72,72,72,72	0
56	MG	2a	1622	1/1	0.92	0.11	92,92,92,92	0
56	MG	2A	3248	1/1	0.92	0.27	57,57,57,57	0
56	MG	2A	3249	1/1	0.92	0.27	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	3452	1/1	0.92	0.16	59,59,59,59	0
56	MG	2A	3252	1/1	0.92	0.21	59,59,59,59	0
56	MG	2a	1810	1/1	0.92	0.12	67,67,67,67	0
56	MG	1A	3799	1/1	0.92	0.15	67,67,67,67	0
56	MG	1a	1765	1/1	0.92	0.08	88,88,88,88	0
56	MG	1A	3482	1/1	0.92	0.12	55,55,55,55	0
56	MG	1A	3801	1/1	0.92	0.08	63,63,63,63	0
56	MG	1A	3596	1/1	0.92	0.23	25,25,25,25	0
56	MG	1a	1911	1/1	0.92	0.15	64,64,64,64	0
56	MG	1A	3688	1/1	0.92	0.14	37,37,37,37	0
56	MG	2A	3263	1/1	0.92	0.38	48,48,48,48	0
56	MG	1A	3301	1/1	0.92	0.17	42,42,42,42	0
56	MG	1a	1648	1/1	0.92	0.14	51,51,51,51	0
56	MG	1a	1916	1/1	0.92	0.08	70,70,70,70	0
56	MG	1a	1917	1/1	0.92	0.18	62,62,62,62	0
56	MG	1A	3411	1/1	0.92	0.07	54,54,54,54	0
56	MG	1a	1652	1/1	0.92	0.21	57,57,57,57	0
56	MG	1A	3167	1/1	0.92	0.30	46,46,46,46	0
56	MG	2A	3278	1/1	0.92	0.27	38,38,38,38	0
56	MG	2A	3477	1/1	0.92	0.20	58,58,58,58	0
56	MG	2t	201	1/1	0.92	0.19	55,55,55,55	0
56	MG	2A	3479	1/1	0.92	0.25	46,46,46,46	0
56	MG	2A	3074	1/1	0.92	0.14	51,51,51,51	0
56	MG	1a	1654	1/1	0.92	0.25	41,41,41,41	0
56	MG	1A	3602	1/1	0.92	0.09	48,48,48,48	0
56	MG	2A	3077	1/1	0.92	0.24	46,46,46,46	0
56	MG	2A	3285	1/1	0.92	0.44	39,39,39,39	0
56	MG	2A	3488	1/1	0.92	0.22	61,61,61,61	0
56	MG	2A	3286	1/1	0.92	0.29	50,50,50,50	0
56	MG	2A	3078	1/1	0.92	0.17	35,35,35,35	0
57	KAN	1A	3933	33/33	0.92	0.10	34,44,58,64	0
57	KAN	1A	3934	33/33	0.92	0.08	39,48,55,63	0
56	MG	2A	3079	1/1	0.92	0.12	74,74,74,74	0
56	MG	1A	3811	1/1	0.92	0.08	81,81,81,81	0
57	KAN	2a	1828	33/33	0.92	0.11	47,61,67,70	0
56	MG	2A	3096	1/1	0.93	0.18	44,44,44,44	0
56	MG	2A	3097	1/1	0.93	0.13	48,48,48,48	0
56	MG	1A	3240	1/1	0.93	0.28	49,49,49,49	0
56	MG	2a	1668	1/1	0.93	0.24	69,69,69,69	0
56	MG	1A	3568	1/1	0.93	0.28	42,42,42,42	0
56	MG	2A	3101	1/1	0.93	0.08	41,41,41,41	0
56	MG	1a	1809	1/1	0.93	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	2A	3103	1/1	0.93	0.11	59,59,59,59	0
56	MG	1A	3572	1/1	0.93	0.14	40,40,40,40	0
56	MG	1E	301	1/1	0.93	0.10	37,37,37,37	0
56	MG	1E	302	1/1	0.93	0.24	27,27,27,27	0
56	MG	1a	1941	1/1	0.93	0.10	55,55,55,55	0
56	MG	1a	1815	1/1	0.93	0.23	61,61,61,61	0
56	MG	1a	1687	1/1	0.93	0.10	69,69,69,69	0
56	MG	2A	3113	1/1	0.93	0.10	72,72,72,72	0
56	MG	1A	3573	1/1	0.93	0.13	57,57,57,57	0
56	MG	1A	3413	1/1	0.93	0.41	43,43,43,43	0
56	MG	1a	1950	1/1	0.93	0.20	92,92,92,92	0
56	MG	2A	3120	1/1	0.93	0.25	51,51,51,51	0
56	MG	1F	302	1/1	0.93	0.05	56,56,56,56	0
56	MG	1A	3101	1/1	0.93	0.28	45,45,45,45	0
56	MG	1G	202	1/1	0.93	0.11	47,47,47,47	0
56	MG	2A	3508	1/1	0.93	0.05	68,68,68,68	0
56	MG	1A	3132	1/1	0.93	0.20	33,33,33,33	0
56	MG	1O	3101	1/1	0.93	0.18	64,64,64,64	0
56	MG	1a	1828	1/1	0.93	0.09	66,66,66,66	0
56	MG	1A	3243	1/1	0.93	0.17	51,51,51,51	0
56	MG	1A	3765	1/1	0.93	0.19	60,60,60,60	0
56	MG	1A	3010	1/1	0.93	0.19	66,66,66,66	0
56	MG	1a	1836	1/1	0.93	0.15	72,72,72,72	0
56	MG	1A	3661	1/1	0.93	0.07	70,70,70,70	0
56	MG	1A	3181	1/1	0.93	0.19	60,60,60,60	0
56	MG	1A	3067	1/1	0.93	0.10	75,75,75,75	0
56	MG	1A	3135	1/1	0.93	0.16	48,48,48,48	0
56	MG	1A	3594	1/1	0.93	0.33	47,47,47,47	0
56	MG	2A	3523	1/1	0.93	0.09	63,63,63,63	0
56	MG	1A	3773	1/1	0.93	0.19	48,48,48,48	0
56	MG	1A	3214	1/1	0.93	0.22	55,55,55,55	0
56	MG	2A	3335	1/1	0.93	0.24	42,42,42,42	0
56	MG	2A	3338	1/1	0.93	0.23	53,53,53,53	0
56	MG	1a	1845	1/1	0.93	0.28	54,54,54,54	0
56	MG	1a	1846	1/1	0.93	0.14	42,42,42,42	0
56	MG	10	101	1/1	0.93	0.30	46,46,46,46	0
56	MG	1a	1848	1/1	0.93	0.26	56,56,56,56	0
56	MG	1A	3667	1/1	0.93	0.11	71,71,71,71	0
56	MG	1A	3777	1/1	0.93	0.12	63,63,63,63	0
56	MG	1A	3082	1/1	0.93	0.24	67,67,67,67	0
56	MG	2a	1719	1/1	0.93	0.22	70,70,70,70	0
56	MG	2a	1720	1/1	0.93	0.22	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3424	1/1	0.93	0.17	48,48,48,48	0
56	MG	1A	3380	1/1	0.93	0.10	67,67,67,67	0
56	MG	1A	3599	1/1	0.93	0.09	57,57,57,57	0
56	MG	2A	3352	1/1	0.93	0.11	70,70,70,70	0
56	MG	2A	3160	1/1	0.93	0.07	57,57,57,57	0
56	MG	17	101	1/1	0.93	0.12	54,54,54,54	0
56	MG	1A	3676	1/1	0.93	0.11	57,57,57,57	0
56	MG	2A	3356	1/1	0.93	0.21	54,54,54,54	0
56	MG	2A	3544	1/1	0.93	0.12	69,69,69,69	0
56	MG	2A	3359	1/1	0.93	0.09	54,54,54,54	0
56	MG	1A	3600	1/1	0.93	0.08	52,52,52,52	0
56	MG	1a	1858	1/1	0.93	0.10	68,68,68,68	0
56	MG	1x	117	1/1	0.93	0.13	57,57,57,57	0
56	MG	1A	3258	1/1	0.93	0.22	44,44,44,44	0
56	MG	1A	3385	1/1	0.93	0.20	59,59,59,59	0
56	MG	1a	1861	1/1	0.93	0.12	64,64,64,64	0
56	MG	1A	3603	1/1	0.93	0.15	65,65,65,65	0
56	MG	1x	122	1/1	0.93	0.09	63,63,63,63	0
56	MG	1A	3317	1/1	0.93	0.10	55,55,55,55	0
56	MG	1a	1729	1/1	0.93	0.21	53,53,53,53	0
56	MG	2a	1743	1/1	0.93	0.29	39,39,39,39	0
56	MG	1a	1603	1/1	0.93	0.12	61,61,61,61	0
56	MG	1A	3511	1/1	0.93	0.10	49,49,49,49	0
56	MG	1a	1605	1/1	0.93	0.20	63,63,63,63	0
56	MG	1A	3897	1/1	0.93	0.18	51,51,51,51	0
56	MG	2A	3377	1/1	0.93	0.23	59,59,59,59	0
56	MG	2A	3184	1/1	0.93	0.16	54,54,54,54	0
56	MG	2a	1750	1/1	0.93	0.19	61,61,61,61	0
56	MG	1A	3512	1/1	0.93	0.14	39,39,39,39	0
56	MG	1A	3693	1/1	0.93	0.09	53,53,53,53	0
56	MG	2A	3009	1/1	0.93	0.13	59,59,59,59	0
56	MG	1A	3795	1/1	0.93	0.09	69,69,69,69	0
56	MG	1A	3110	1/1	0.93	0.11	68,68,68,68	0
56	MG	2A	3012	1/1	0.93	0.21	33,33,33,33	0
56	MG	1A	3797	1/1	0.93	0.14	58,58,58,58	0
56	MG	1A	3905	1/1	0.93	0.09	70,70,70,70	0
56	MG	2A	3016	1/1	0.93	0.21	58,58,58,58	0
56	MG	1A	3907	1/1	0.93	0.07	45,45,45,45	0
56	MG	2B	210	1/1	0.93	0.11	74,74,74,74	0
56	MG	1A	3112	1/1	0.93	0.27	23,23,23,23	0
56	MG	2B	212	1/1	0.93	0.09	64,64,64,64	0
56	MG	2B	213	1/1	0.93	0.11	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3394	1/1	0.93	0.08	59,59,59,59	0
56	MG	1A	3139	1/1	0.93	0.13	68,68,68,68	0
56	MG	2E	302	1/1	0.93	0.25	36,36,36,36	0
56	MG	2A	3200	1/1	0.93	0.19	46,46,46,46	0
56	MG	2A	3202	1/1	0.93	0.23	38,38,38,38	0
56	MG	2F	303	1/1	0.93	0.10	65,65,65,65	0
56	MG	1A	3191	1/1	0.93	0.08	57,57,57,57	0
56	MG	2A	3401	1/1	0.93	0.19	59,59,59,59	0
56	MG	2A	3402	1/1	0.93	0.10	56,56,56,56	0
56	MG	1A	3026	1/1	0.93	0.06	32,32,32,32	0
56	MG	1A	3618	1/1	0.93	0.14	58,58,58,58	0
56	MG	1A	3227	1/1	0.93	0.24	54,54,54,54	0
56	MG	1A	3916	1/1	0.93	0.12	63,63,63,63	0
56	MG	1a	1751	1/1	0.93	0.21	62,62,62,62	0
56	MG	1A	3035	1/1	0.93	0.20	39,39,39,39	0
56	MG	1A	3273	1/1	0.93	0.26	21,21,21,21	0
56	MG	1A	3450	1/1	0.93	0.07	47,47,47,47	0
56	MG	2A	3215	1/1	0.93	0.27	35,35,35,35	0
56	MG	1A	3070	1/1	0.93	0.14	44,44,44,44	0
56	MG	1A	3275	1/1	0.93	0.38	39,39,39,39	0
56	MG	1A	3812	1/1	0.93	0.11	68,68,68,68	0
56	MG	1A	3334	1/1	0.93	0.11	45,45,45,45	0
56	MG	1A	3816	1/1	0.93	0.21	42,42,42,42	0
56	MG	2a	1791	1/1	0.93	0.13	68,68,68,68	0
56	MG	1A	3120	1/1	0.93	0.12	41,41,41,41	0
56	MG	2A	3039	1/1	0.93	0.13	41,41,41,41	0
56	MG	2A	3225	1/1	0.93	0.31	41,41,41,41	0
56	MG	2A	3226	1/1	0.93	0.28	52,52,52,52	0
56	MG	2A	3040	1/1	0.93	0.08	43,43,43,43	0
56	MG	1A	3460	1/1	0.93	0.07	53,53,53,53	0
56	MG	1A	3340	1/1	0.93	0.14	36,36,36,36	0
56	MG	2A	3234	1/1	0.93	0.28	43,43,43,43	0
56	MG	1a	1766	1/1	0.93	0.06	63,63,63,63	0
56	MG	1a	1767	1/1	0.93	0.12	60,60,60,60	0
56	MG	1A	3343	1/1	0.93	0.14	44,44,44,44	0
56	MG	2A	3238	1/1	0.93	0.36	48,48,48,48	0
56	MG	2A	3048	1/1	0.93	0.24	54,54,54,54	0
56	MG	1a	1769	1/1	0.93	0.18	79,79,79,79	0
56	MG	1A	3633	1/1	0.93	0.11	70,70,70,70	0
56	MG	1A	3828	1/1	0.93	0.11	49,49,49,49	0
56	MG	1a	1907	1/1	0.93	0.10	68,68,68,68	0
56	MG	1A	3015	1/1	0.93	0.15	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3543	1/1	0.93	0.22	26,26,26,26	0
56	MG	1a	1910	1/1	0.93	0.10	52,52,52,52	0
56	MG	1A	3547	1/1	0.93	0.25	42,42,42,42	0
56	MG	1A	3738	1/1	0.93	0.12	63,63,63,63	0
56	MG	2a	1628	1/1	0.93	0.10	69,69,69,69	0
56	MG	1B	207	1/1	0.93	0.08	52,52,52,52	0
56	MG	1A	3465	1/1	0.93	0.20	48,48,48,48	0
56	MG	1A	3551	1/1	0.93	0.23	28,28,28,28	0
56	MG	2A	3457	1/1	0.93	0.15	44,44,44,44	0
56	MG	1a	1784	1/1	0.93	0.06	67,67,67,67	0
56	MG	1A	3285	1/1	0.93	0.18	26,26,26,26	0
56	MG	2a	1639	1/1	0.93	0.17	71,71,71,71	0
56	MG	1A	3003	1/1	0.93	0.14	55,55,55,55	0
56	MG	1a	1668	1/1	0.93	0.07	62,62,62,62	0
56	MG	2a	1643	1/1	0.93	0.23	59,59,59,59	0
56	MG	1A	3843	1/1	0.93	0.07	69,69,69,69	0
56	MG	2A	3465	1/1	0.93	0.06	76,76,76,76	0
56	MG	1A	3471	1/1	0.93	0.17	66,66,66,66	0
56	MG	1a	1791	1/1	0.93	0.09	69,69,69,69	0
56	MG	1A	3746	1/1	0.93	0.16	54,54,54,54	0
56	MG	1A	3290	1/1	0.93	0.31	40,40,40,40	0
56	MG	2A	3274	1/1	0.93	0.29	32,32,32,32	0
56	MG	2A	3472	1/1	0.93	0.15	84,84,84,84	0
56	MG	1A	3291	1/1	0.93	0.18	31,31,31,31	0
56	MG	2A	3084	1/1	0.93	0.19	43,43,43,43	0
56	MG	2a	1657	1/1	0.93	0.26	60,60,60,60	0
56	MG	2x	105	1/1	0.93	0.21	61,61,61,61	0
56	MG	1B	219	1/1	0.93	0.22	59,59,59,59	0
56	MG	1A	3125	1/1	0.93	0.11	59,59,59,59	0
56	MG	1A	3099	1/1	0.93	0.22	44,44,44,44	0
56	MG	1A	3150	1/1	0.93	0.04	75,75,75,75	0
56	MG	1a	1804	1/1	0.93	0.08	57,57,57,57	0
56	MG	2A	3091	1/1	0.93	0.24	59,59,59,59	0
56	MG	1A	3753	1/1	0.93	0.07	57,57,57,57	0
56	MG	1A	3011	1/1	0.94	0.24	48,48,48,48	0
56	MG	1A	3294	1/1	0.94	0.26	40,40,40,40	0
56	MG	1a	1762	1/1	0.94	0.08	70,70,70,70	0
56	MG	2a	1681	1/1	0.94	0.13	64,64,64,64	0
56	MG	1A	3376	1/1	0.94	0.12	75,75,75,75	0
56	MG	2A	3177	1/1	0.94	0.18	47,47,47,47	0
56	MG	2A	3178	1/1	0.94	0.33	35,35,35,35	0
56	MG	1A	3209	1/1	0.94	0.32	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	2A	3518	1/1	0.94	0.08	59,59,59,59	0
56	MG	1A	3849	1/1	0.94	0.06	68,68,68,68	0
56	MG	2a	1689	1/1	0.94	0.09	72,72,72,72	0
56	MG	2A	3348	1/1	0.94	0.27	50,50,50,50	0
56	MG	1a	1656	1/1	0.94	0.21	53,53,53,53	0
56	MG	1a	1657	1/1	0.94	0.29	46,46,46,46	0
56	MG	1A	3328	1/1	0.94	0.21	46,46,46,46	0
56	MG	1A	3379	1/1	0.94	0.12	56,56,56,56	0
56	MG	1A	3762	1/1	0.94	0.11	57,57,57,57	0
56	MG	1a	1772	1/1	0.94	0.13	58,58,58,58	0
56	MG	1B	217	1/1	0.94	0.26	64,64,64,64	0
56	MG	1A	3467	1/1	0.94	0.16	29,29,29,29	0
56	MG	1a	1776	1/1	0.94	0.08	72,72,72,72	0
56	MG	1A	3297	1/1	0.94	0.10	63,63,63,63	0
56	MG	1A	3533	1/1	0.94	0.19	44,44,44,44	0
56	MG	2A	3195	1/1	0.94	0.24	53,53,53,53	0
56	MG	1A	3605	1/1	0.94	0.13	72,72,72,72	0
56	MG	2A	3366	1/1	0.94	0.07	66,66,66,66	0
56	MG	1a	1669	1/1	0.94	0.05	68,68,68,68	0
56	MG	1A	3058	1/1	0.94	0.11	35,35,35,35	0
56	MG	1a	1903	1/1	0.94	0.08	61,61,61,61	0
56	MG	1A	3675	1/1	0.94	0.09	52,52,52,52	0
56	MG	1A	3535	1/1	0.94	0.42	44,44,44,44	0
56	MG	2A	3204	1/1	0.94	0.15	38,38,38,38	0
56	MG	1A	3049	1/1	0.94	0.08	38,38,38,38	0
56	MG	1A	3474	1/1	0.94	0.08	45,45,45,45	0
56	MG	2A	3375	1/1	0.94	0.13	56,56,56,56	0
56	MG	2a	1716	1/1	0.94	0.09	85,85,85,85	0
56	MG	1A	3612	1/1	0.94	0.11	53,53,53,53	0
56	MG	1a	1788	1/1	0.94	0.09	71,71,71,71	0
56	MG	1A	3195	1/1	0.94	0.21	68,68,68,68	0
56	MG	1a	1677	1/1	0.94	0.09	56,56,56,56	0
56	MG	2A	3052	1/1	0.94	0.17	57,57,57,57	0
56	MG	2A	3551	1/1	0.94	0.15	59,59,59,59	0
56	MG	1a	1678	1/1	0.94	0.20	42,42,42,42	0
56	MG	1A	3684	1/1	0.94	0.12	53,53,53,53	0
56	MG	1A	3686	1/1	0.94	0.17	15,15,15,15	0
56	MG	1a	1794	1/1	0.94	0.08	40,40,40,40	0
56	MG	2A	3556	1/1	0.94	0.10	56,56,56,56	0
56	MG	2a	1728	1/1	0.94	0.24	60,60,60,60	0
56	MG	2A	3217	1/1	0.94	0.36	38,38,38,38	0
56	MG	1A	3169	1/1	0.94	0.15	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	3559	1/1	0.94	0.09	66,66,66,66	0
56	MG	1A	3237	1/1	0.94	0.12	56,56,56,56	0
56	MG	1a	1797	1/1	0.94	0.08	72,72,72,72	0
56	MG	2A	3221	1/1	0.94	0.34	35,35,35,35	0
56	MG	2A	3393	1/1	0.94	0.14	52,52,52,52	0
56	MG	1A	3182	1/1	0.94	0.05	53,53,53,53	0
56	MG	1A	3545	1/1	0.94	0.19	31,31,31,31	0
56	MG	1A	3546	1/1	0.94	0.25	33,33,33,33	0
56	MG	1A	3696	1/1	0.94	0.07	49,49,49,49	0
56	MG	2a	1740	1/1	0.94	0.27	58,58,58,58	0
56	MG	1A	3877	1/1	0.94	0.09	70,70,70,70	0
56	MG	1a	1806	1/1	0.94	0.18	62,62,62,62	0
56	MG	1A	3786	1/1	0.94	0.09	51,51,51,51	0
56	MG	1A	3879	1/1	0.94	0.12	68,68,68,68	0
56	MG	2A	3405	1/1	0.94	0.34	58,58,58,58	0
56	MG	2A	3231	1/1	0.94	0.27	54,54,54,54	0
56	MG	2A	3232	1/1	0.94	0.17	46,46,46,46	0
56	MG	1A	3787	1/1	0.94	0.10	57,57,57,57	0
56	MG	2A	3410	1/1	0.94	0.16	50,50,50,50	0
56	MG	1A	3027	1/1	0.94	0.07	28,28,28,28	0
56	MG	2A	3412	1/1	0.94	0.16	54,54,54,54	0
56	MG	1A	3345	1/1	0.94	0.28	36,36,36,36	0
56	MG	1A	3550	1/1	0.94	0.34	29,29,29,29	0
56	MG	1A	3392	1/1	0.94	0.14	49,49,49,49	0
56	MG	2A	3080	1/1	0.94	0.16	45,45,45,45	0
56	MG	1A	3308	1/1	0.94	0.13	46,46,46,46	0
56	MG	2a	1757	1/1	0.94	0.28	57,57,57,57	0
56	MG	1A	3272	1/1	0.94	0.16	27,27,27,27	0
56	MG	1A	3709	1/1	0.94	0.10	15,15,15,15	0
56	MG	1a	1820	1/1	0.94	0.15	47,47,47,47	0
56	MG	1A	3432	1/1	0.94	0.05	56,56,56,56	0
56	MG	1a	1705	1/1	0.94	0.18	54,54,54,54	0
56	MG	2A	3425	1/1	0.94	0.08	57,57,57,57	0
56	MG	1a	1824	1/1	0.94	0.06	80,80,80,80	0
56	MG	1A	3890	1/1	0.94	0.05	69,69,69,69	0
56	MG	1A	3108	1/1	0.94	0.22	27,27,27,27	0
56	MG	1A	3490	1/1	0.94	0.07	56,56,56,56	0
56	MG	2A	3093	1/1	0.94	0.23	69,69,69,69	0
56	MG	2a	1770	1/1	0.94	0.24	54,54,54,54	0
56	MG	1a	1710	1/1	0.94	0.28	43,43,43,43	0
56	MG	1a	1952	1/1	0.94	0.06	58,58,58,58	0
56	MG	1a	1829	1/1	0.94	0.07	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	3436	1/1	0.94	0.26	61,61,61,61	0
56	MG	2a	1601	1/1	0.94	0.10	76,76,76,76	0
56	MG	15	102	1/1	0.94	0.19	39,39,39,39	0
56	MG	2A	3438	1/1	0.94	0.16	63,63,63,63	0
56	MG	1A	3893	1/1	0.94	0.07	41,41,41,41	0
56	MG	1a	1833	1/1	0.94	0.11	59,59,59,59	0
56	MG	1A	3715	1/1	0.94	0.10	68,68,68,68	0
56	MG	1a	1835	1/1	0.94	0.12	83,83,83,83	0
56	MG	2A	3269	1/1	0.94	0.18	35,35,35,35	0
56	MG	1A	3492	1/1	0.94	0.11	44,44,44,44	0
56	MG	18	103	1/1	0.94	0.15	58,58,58,58	0
56	MG	2A	3272	1/1	0.94	0.14	58,58,58,58	0
56	MG	1A	3563	1/1	0.94	0.17	39,39,39,39	0
56	MG	1A	3350	1/1	0.94	0.19	30,30,30,30	0
56	MG	1A	3435	1/1	0.94	0.12	54,54,54,54	0
56	MG	1A	3311	1/1	0.94	0.20	42,42,42,42	0
56	MG	1A	3497	1/1	0.94	0.13	59,59,59,59	0
56	MG	1A	3805	1/1	0.94	0.10	74,74,74,74	0
56	MG	2A	3283	1/1	0.94	0.34	50,50,50,50	0
56	MG	2A	3117	1/1	0.94	0.21	32,32,32,32	0
56	MG	1A	3906	1/1	0.94	0.30	53,53,53,53	0
56	MG	1A	3724	1/1	0.94	0.10	47,47,47,47	0
56	MG	2A	3460	1/1	0.94	0.06	46,46,46,46	0
56	MG	1A	3221	1/1	0.94	0.08	55,55,55,55	0
56	MG	1A	3244	1/1	0.94	0.09	53,53,53,53	0
56	MG	1A	3503	1/1	0.94	0.25	36,36,36,36	0
56	MG	1A	3576	1/1	0.94	0.17	22,22,22,22	0
56	MG	1A	3445	1/1	0.94	0.26	51,51,51,51	0
56	MG	2A	3467	1/1	0.94	0.13	60,60,60,60	0
56	MG	1A	3815	1/1	0.94	0.09	45,45,45,45	0
56	MG	1A	3737	1/1	0.94	0.13	61,61,61,61	0
56	MG	1x	105	1/1	0.94	0.27	41,41,41,41	0
56	MG	1a	1732	1/1	0.94	0.21	53,53,53,53	0
56	MG	1x	108	1/1	0.94	0.15	42,42,42,42	0
56	MG	1A	3245	1/1	0.94	0.10	40,40,40,40	0
56	MG	1A	3819	1/1	0.94	0.20	47,47,47,47	0
56	MG	1A	3820	1/1	0.94	0.21	28,28,28,28	0
56	MG	2A	3302	1/1	0.94	0.14	41,41,41,41	0
56	MG	1A	3579	1/1	0.94	0.24	41,41,41,41	0
56	MG	2a	1645	1/1	0.94	0.15	56,56,56,56	0
56	MG	1A	3580	1/1	0.94	0.27	35,35,35,35	0
56	MG	1A	3581	1/1	0.94	0.34	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	3652	1/1	0.94	0.19	43,43,43,43	0
56	MG	1A	3583	1/1	0.94	0.23	39,39,39,39	0
56	MG	1A	3829	1/1	0.94	0.20	44,44,44,44	0
56	MG	2A	3487	1/1	0.94	0.19	41,41,41,41	0
56	MG	1A	3830	1/1	0.94	0.15	42,42,42,42	0
56	MG	1A	3832	1/1	0.94	0.10	53,53,53,53	0
56	MG	1A	3156	1/1	0.94	0.07	59,59,59,59	0
56	MG	2A	3152	1/1	0.94	0.10	54,54,54,54	0
56	MG	1A	3018	1/1	0.94	0.22	66,66,66,66	0
56	MG	1a	1632	1/1	0.94	0.11	54,54,54,54	0
56	MG	2A	3319	1/1	0.94	0.09	44,44,44,44	0
56	MG	2A	3322	1/1	0.94	0.33	54,54,54,54	0
56	MG	2q	201	1/1	0.94	0.27	72,72,72,72	0
56	MG	1A	3319	1/1	0.94	0.39	44,44,44,44	0
56	MG	1A	3361	1/1	0.94	0.22	30,30,30,30	0
56	MG	1a	1750	1/1	0.94	0.06	70,70,70,70	0
56	MG	1a	1875	1/1	0.94	0.13	60,60,60,60	0
56	MG	1a	1638	1/1	0.94	0.11	58,58,58,58	0
56	MG	1a	1639	1/1	0.94	0.16	35,35,35,35	0
56	MG	1a	1640	1/1	0.94	0.27	55,55,55,55	0
56	MG	1A	3043	1/1	0.94	0.37	58,58,58,58	0
56	MG	2A	3166	1/1	0.94	0.14	44,44,44,44	0
56	MG	2a	1671	1/1	0.94	0.08	88,88,88,88	0
56	MG	1A	3126	1/1	0.94	0.05	74,74,74,74	0
56	MG	1A	3128	1/1	0.94	0.11	62,62,62,62	0
56	MG	1A	3754	1/1	0.94	0.12	52,52,52,52	0
57	KAN	1a	1955	33/33	0.94	0.10	44,52,58,59	0
56	MG	2A	3336	1/1	0.94	0.11	68,68,68,68	0
56	MG	2A	3337	1/1	0.94	0.25	61,61,61,61	0
56	MG	2A	3013	1/1	0.94	0.16	60,60,60,60	0
56	MG	1A	3248	1/1	0.95	0.17	66,66,66,66	0
56	MG	1A	3250	1/1	0.95	0.09	59,59,59,59	0
56	MG	2A	3072	1/1	0.95	0.08	64,64,64,64	0
56	MG	1A	3818	1/1	0.95	0.27	52,52,52,52	0
56	MG	1A	3295	1/1	0.95	0.23	39,39,39,39	0
56	MG	1a	1830	1/1	0.95	0.07	70,70,70,70	0
56	MG	1A	3910	1/1	0.95	0.07	54,54,54,54	0
56	MG	2A	3385	1/1	0.95	0.14	51,51,51,51	0
56	MG	1A	3911	1/1	0.95	0.06	49,49,49,49	0
56	MG	1A	3651	1/1	0.95	0.09	58,58,58,58	0
56	MG	1a	1945	1/1	0.95	0.08	61,61,61,61	0
56	MG	2A	3389	1/1	0.95	0.13	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	1946	1/1	0.95	0.12	69,69,69,69	0
56	MG	1A	3742	1/1	0.95	0.17	41,41,41,41	0
56	MG	1A	3822	1/1	0.95	0.11	57,57,57,57	0
56	MG	2a	1706	1/1	0.95	0.11	57,57,57,57	0
56	MG	1A	3823	1/1	0.95	0.28	50,50,50,50	0
56	MG	1A	3190	1/1	0.95	0.12	55,55,55,55	0
56	MG	1A	3825	1/1	0.95	0.17	45,45,45,45	0
56	MG	1A	3056	1/1	0.95	0.07	55,55,55,55	0
56	MG	1A	3443	1/1	0.95	0.15	35,35,35,35	0
56	MG	1A	3097	1/1	0.95	0.32	55,55,55,55	0
56	MG	2A	3400	1/1	0.95	0.16	60,60,60,60	0
56	MG	1A	3582	1/1	0.95	0.25	49,49,49,49	0
56	MG	1i	201	1/1	0.95	0.10	84,84,84,84	0
56	MG	1A	3123	1/1	0.95	0.17	26,26,26,26	0
56	MG	2A	3404	1/1	0.95	0.23	41,41,41,41	0
56	MG	1l	201	1/1	0.95	0.09	58,58,58,58	0
56	MG	2A	3406	1/1	0.95	0.08	57,57,57,57	0
56	MG	1A	3584	1/1	0.95	0.15	28,28,28,28	0
56	MG	1A	3924	1/1	0.95	0.10	52,52,52,52	0
56	MG	1m	201	1/1	0.95	0.10	48,48,48,48	0
56	MG	1A	3256	1/1	0.95	0.21	43,43,43,43	0
56	MG	1A	3513	1/1	0.95	0.08	32,32,32,32	0
56	MG	1A	3098	1/1	0.95	0.18	48,48,48,48	0
56	MG	2B	201	1/1	0.95	0.07	75,75,75,75	0
56	MG	1A	3515	1/1	0.95	0.16	30,30,30,30	0
56	MG	2A	3257	1/1	0.95	0.12	37,37,37,37	0
56	MG	1A	3930	1/1	0.95	0.08	49,49,49,49	0
56	MG	1A	3756	1/1	0.95	0.13	67,67,67,67	0
56	MG	1A	3516	1/1	0.95	0.22	31,31,31,31	0
56	MG	1a	1628	1/1	0.95	0.06	55,55,55,55	0
56	MG	2A	3112	1/1	0.95	0.12	42,42,42,42	0
56	MG	1A	3517	1/1	0.95	0.32	41,41,41,41	0
56	MG	2A	3422	1/1	0.95	0.16	57,57,57,57	0
56	MG	2A	3114	1/1	0.95	0.07	60,60,60,60	0
56	MG	1A	3041	1/1	0.95	0.14	25,25,25,25	0
56	MG	1A	3349	1/1	0.95	0.27	26,26,26,26	0
56	MG	1A	3042	1/1	0.95	0.17	42,42,42,42	0
56	MG	2A	3427	1/1	0.95	0.20	67,67,67,67	0
56	MG	1A	3198	1/1	0.95	0.22	52,52,52,52	0
56	MG	1A	3455	1/1	0.95	0.15	41,41,41,41	0
56	MG	2A	3273	1/1	0.95	0.35	54,54,54,54	0
56	MG	2A	3121	1/1	0.95	0.23	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	2A	3432	1/1	0.95	0.22	44,44,44,44	0
56	MG	1A	3456	1/1	0.95	0.15	44,44,44,44	0
56	MG	2A	3123	1/1	0.95	0.12	33,33,33,33	0
56	MG	1a	1643	1/1	0.95	0.09	51,51,51,51	0
56	MG	1x	106	1/1	0.95	0.12	64,64,64,64	0
56	MG	1A	3526	1/1	0.95	0.24	28,28,28,28	0
56	MG	1A	3306	1/1	0.95	0.25	50,50,50,50	0
56	MG	1a	1866	1/1	0.95	0.14	73,73,73,73	0
56	MG	1A	3147	1/1	0.95	0.09	59,59,59,59	0
56	MG	1a	1647	1/1	0.95	0.12	54,54,54,54	0
56	MG	1A	3127	1/1	0.95	0.14	57,57,57,57	0
56	MG	1a	1870	1/1	0.95	0.07	62,62,62,62	0
56	MG	1a	1649	1/1	0.95	0.19	42,42,42,42	0
56	MG	1A	3854	1/1	0.95	0.11	39,39,39,39	0
56	MG	1A	3531	1/1	0.95	0.26	34,34,34,34	0
56	MG	1A	3355	1/1	0.95	0.10	23,23,23,23	0
56	MG	2A	3293	1/1	0.95	0.41	60,60,60,60	0
56	MG	1A	3022	1/1	0.95	0.14	57,57,57,57	0
56	MG	2A	3138	1/1	0.95	0.09	65,65,65,65	0
56	MG	1A	3063	1/1	0.95	0.12	39,39,39,39	0
56	MG	1A	3051	1/1	0.95	0.08	27,27,27,27	0
56	MG	2a	1766	1/1	0.95	0.19	73,73,73,73	0
56	MG	1A	3536	1/1	0.95	0.25	38,38,38,38	0
56	MG	1A	3613	1/1	0.95	0.13	52,52,52,52	0
56	MG	2A	3147	1/1	0.95	0.19	65,65,65,65	0
56	MG	1A	3863	1/1	0.95	0.08	60,60,60,60	0
56	MG	1A	3107	1/1	0.95	0.23	30,30,30,30	0
56	MG	1a	1770	1/1	0.95	0.14	60,60,60,60	0
56	MG	1B	226	1/1	0.95	0.10	53,53,53,53	0
56	MG	2A	3463	1/1	0.95	0.07	66,66,66,66	0
56	MG	2A	3306	1/1	0.95	0.13	74,74,74,74	0
56	MG	1A	3779	1/1	0.95	0.16	71,71,71,71	0
56	MG	1a	1773	1/1	0.95	0.13	59,59,59,59	0
56	MG	2A	3309	1/1	0.95	0.36	53,53,53,53	0
56	MG	2A	3156	1/1	0.95	0.08	47,47,47,47	0
56	MG	1A	3362	1/1	0.95	0.31	36,36,36,36	0
56	MG	1A	3044	1/1	0.95	0.20	34,34,34,34	0
56	MG	1A	3695	1/1	0.95	0.08	55,55,55,55	0
56	MG	1a	1777	1/1	0.95	0.24	71,71,71,71	0
56	MG	1A	3047	1/1	0.95	0.11	32,32,32,32	0
56	MG	2A	3162	1/1	0.95	0.13	59,59,59,59	0
56	MG	2A	3318	1/1	0.95	0.26	39,39,39,39	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	0.95	0.07	69,69,69,69	0
56	MG	2a	1630	1/1	0.95	0.14	57,57,57,57	0
56	MG	1A	3366	1/1	0.95	0.19	59,59,59,59	0
56	MG	2A	3321	1/1	0.95	0.40	54,54,54,54	0
56	MG	2a	1634	1/1	0.95	0.07	59,59,59,59	0
56	MG	1A	3091	1/1	0.95	0.07	64,64,64,64	0
56	MG	1A	3416	1/1	0.95	0.06	64,64,64,64	0
56	MG	2A	3482	1/1	0.95	0.10	60,60,60,60	0
56	MG	1A	3624	1/1	0.95	0.22	40,40,40,40	0
56	MG	1A	3477	1/1	0.95	0.23	44,44,44,44	0
56	MG	2a	1641	1/1	0.95	0.09	62,62,62,62	0
56	MG	2A	3018	1/1	0.95	0.06	32,32,32,32	0
56	MG	1A	3370	1/1	0.95	0.17	33,33,33,33	0
56	MG	1A	3479	1/1	0.95	0.13	38,38,38,38	0
56	MG	2A	3022	1/1	0.95	0.06	36,36,36,36	0
56	MG	1A	3276	1/1	0.95	0.25	52,52,52,52	0
56	MG	2a	1647	1/1	0.95	0.17	54,54,54,54	0
56	MG	1P	201	1/1	0.95	0.10	49,49,49,49	0
56	MG	1A	3372	1/1	0.95	0.22	36,36,36,36	0
56	MG	1A	3374	1/1	0.95	0.10	57,57,57,57	0
56	MG	2a	1651	1/1	0.95	0.21	46,46,46,46	0
56	MG	1R	201	1/1	0.95	0.14	27,27,27,27	0
56	MG	1A	3320	1/1	0.95	0.31	26,26,26,26	0
56	MG	1A	3277	1/1	0.95	0.25	43,43,43,43	0
56	MG	1U	202	1/1	0.95	0.11	43,43,43,43	0
56	MG	1A	3278	1/1	0.95	0.09	39,39,39,39	0
56	MG	1A	3718	1/1	0.95	0.11	32,32,32,32	0
56	MG	1W	201	1/1	0.95	0.23	57,57,57,57	0
56	MG	1A	3092	1/1	0.95	0.16	54,54,54,54	0
56	MG	1a	1798	1/1	0.95	0.06	75,75,75,75	0
56	MG	1A	3115	1/1	0.95	0.19	31,31,31,31	0
56	MG	1A	3721	1/1	0.95	0.09	33,33,33,33	0
56	MG	1A	3562	1/1	0.95	0.38	28,28,28,28	0
56	MG	2A	3191	1/1	0.95	0.13	50,50,50,50	0
56	MG	1a	1915	1/1	0.95	0.12	85,85,85,85	0
56	MG	1A	3211	1/1	0.95	0.23	31,31,31,31	0
56	MG	2A	3042	1/1	0.95	0.25	51,51,51,51	0
56	MG	1a	1697	1/1	0.95	0.16	67,67,67,67	0
56	MG	2a	1826	1/1	0.95	0.14	59,59,59,59	0
56	MG	1A	3116	1/1	0.95	0.13	24,24,24,24	0
56	MG	1a	1699	1/1	0.95	0.07	64,64,64,64	0
56	MG	1a	1921	1/1	0.95	0.09	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	13	101	1/1	0.95	0.30	26,26,26,26	0
56	MG	2A	3050	1/1	0.95	0.22	53,53,53,53	0
56	MG	2A	3203	1/1	0.95	0.21	48,48,48,48	0
56	MG	13	102	1/1	0.95	0.09	53,53,53,53	0
56	MG	2A	3053	1/1	0.95	0.14	37,37,37,37	0
56	MG	1A	3429	1/1	0.95	0.08	59,59,59,59	0
56	MG	1A	3055	1/1	0.95	0.11	41,41,41,41	0
56	MG	1a	1704	1/1	0.95	0.29	33,33,33,33	0
56	MG	1A	3807	1/1	0.95	0.11	51,51,51,51	0
56	MG	1A	3095	1/1	0.95	0.29	32,32,32,32	0
56	MG	2a	1682	1/1	0.95	0.07	80,80,80,80	0
56	MG	1A	3571	1/1	0.95	0.26	30,30,30,30	0
56	MG	16	101	1/1	0.95	0.21	52,52,52,52	0
56	MG	1A	3731	1/1	0.95	0.13	56,56,56,56	0
57	KAN	1A	3935	33/33	0.95	0.08	27,36,51,59	0
56	MG	1A	3292	1/1	0.95	0.14	36,36,36,36	0
56	MG	1A	3902	1/1	0.95	0.09	38,38,38,38	0
56	MG	1A	3733	1/1	0.95	0.14	32,32,32,32	0
56	MG	1A	3498	1/1	0.95	0.18	45,45,45,45	0
56	MG	2A	3175	1/1	0.96	0.20	52,52,52,52	0
56	MG	1A	3148	1/1	0.96	0.06	65,65,65,65	0
56	MG	1a	1756	1/1	0.96	0.13	55,55,55,55	0
56	MG	1a	1629	1/1	0.96	0.11	31,31,31,31	0
56	MG	2A	3180	1/1	0.96	0.29	30,30,30,30	0
56	MG	1A	3925	1/1	0.96	0.12	48,48,48,48	0
56	MG	1a	1759	1/1	0.96	0.06	62,62,62,62	0
56	MG	1A	3451	1/1	0.96	0.10	42,42,42,42	0
56	MG	2A	3351	1/1	0.96	0.18	58,58,58,58	0
56	MG	1A	3238	1/1	0.96	0.29	28,28,28,28	0
56	MG	1a	1635	1/1	0.96	0.07	56,56,56,56	0
56	MG	2A	3521	1/1	0.96	0.23	45,45,45,45	0
56	MG	1a	1636	1/1	0.96	0.14	55,55,55,55	0
56	MG	1a	1637	1/1	0.96	0.13	54,54,54,54	0
56	MG	1A	3279	1/1	0.96	0.21	45,45,45,45	0
56	MG	1A	3005	1/1	0.96	0.12	58,58,58,58	0
56	MG	1A	3623	1/1	0.96	0.26	49,49,49,49	0
56	MG	1A	3330	1/1	0.96	0.23	25,25,25,25	0
56	MG	1a	1642	1/1	0.96	0.08	68,68,68,68	0
56	MG	1A	3725	1/1	0.96	0.08	27,27,27,27	0
56	MG	1B	201	1/1	0.96	0.14	63,63,63,63	0
56	MG	2A	3365	1/1	0.96	0.16	51,51,51,51	0
56	MG	1A	3281	1/1	0.96	0.18	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	3457	1/1	0.96	0.13	46,46,46,46	0
56	MG	1A	3332	1/1	0.96	0.24	45,45,45,45	0
56	MG	1A	3062	1/1	0.96	0.27	53,53,53,53	0
56	MG	1A	3283	1/1	0.96	0.32	39,39,39,39	0
56	MG	2A	3537	1/1	0.96	0.11	63,63,63,63	0
56	MG	1A	3178	1/1	0.96	0.08	57,57,57,57	0
56	MG	1A	3542	1/1	0.96	0.16	40,40,40,40	0
56	MG	1A	3734	1/1	0.96	0.11	40,40,40,40	0
56	MG	1A	3735	1/1	0.96	0.10	37,37,37,37	0
56	MG	2A	3051	1/1	0.96	0.19	47,47,47,47	0
56	MG	1A	3337	1/1	0.96	0.20	42,42,42,42	0
56	MG	1A	3338	1/1	0.96	0.13	52,52,52,52	0
56	MG	1A	3634	1/1	0.96	0.10	64,64,64,64	0
56	MG	1A	3339	1/1	0.96	0.13	26,26,26,26	0
56	MG	2A	3056	1/1	0.96	0.15	58,58,58,58	0
56	MG	1A	3399	1/1	0.96	0.20	51,51,51,51	0
56	MG	1A	3034	1/1	0.96	0.19	32,32,32,32	0
56	MG	1a	1919	1/1	0.96	0.07	57,57,57,57	0
56	MG	2A	3060	1/1	0.96	0.12	48,48,48,48	0
56	MG	1A	3743	1/1	0.96	0.07	47,47,47,47	0
56	MG	1a	1664	1/1	0.96	0.15	53,53,53,53	0
56	MG	1a	1665	1/1	0.96	0.11	43,43,43,43	0
56	MG	1A	3549	1/1	0.96	0.17	26,26,26,26	0
56	MG	1A	3341	1/1	0.96	0.09	46,46,46,46	0
56	MG	1A	3342	1/1	0.96	0.18	51,51,51,51	0
56	MG	1A	3473	1/1	0.96	0.05	59,59,59,59	0
56	MG	2A	3068	1/1	0.96	0.23	44,44,44,44	0
56	MG	2A	3069	1/1	0.96	0.14	45,45,45,45	0
56	MG	2A	3395	1/1	0.96	0.16	50,50,50,50	0
56	MG	1B	224	1/1	0.96	0.06	39,39,39,39	0
56	MG	1A	3643	1/1	0.96	0.09	54,54,54,54	0
56	MG	2A	3228	1/1	0.96	0.22	28,28,28,28	0
56	MG	1A	3287	1/1	0.96	0.34	49,49,49,49	0
56	MG	2A	3566	1/1	0.96	0.18	43,43,43,43	0
56	MG	2A	3073	1/1	0.96	0.12	44,44,44,44	0
56	MG	1B	227	1/1	0.96	0.11	58,58,58,58	0
56	MG	1A	3555	1/1	0.96	0.12	42,42,42,42	0
56	MG	1A	3289	1/1	0.96	0.18	35,35,35,35	0
56	MG	1D	301	1/1	0.96	0.21	28,28,28,28	0
56	MG	1D	302	1/1	0.96	0.14	57,57,57,57	0
56	MG	1A	3131	1/1	0.96	0.21	52,52,52,52	0
56	MG	1A	3406	1/1	0.96	0.15	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3064	1/1	0.96	0.06	36,36,36,36	0
56	MG	1E	303	1/1	0.96	0.29	24,24,24,24	0
56	MG	2A	3242	1/1	0.96	0.41	35,35,35,35	0
56	MG	1A	3857	1/1	0.96	0.06	59,59,59,59	0
56	MG	2A	3244	1/1	0.96	0.46	59,59,59,59	0
56	MG	1A	3560	1/1	0.96	0.24	36,36,36,36	0
56	MG	1A	3246	1/1	0.96	0.10	41,41,41,41	0
56	MG	1a	1812	1/1	0.96	0.12	54,54,54,54	0
56	MG	1a	1943	1/1	0.96	0.06	69,69,69,69	0
56	MG	2A	3250	1/1	0.96	0.13	57,57,57,57	0
56	MG	2A	3251	1/1	0.96	0.29	48,48,48,48	0
56	MG	1A	3065	1/1	0.96	0.16	22,22,22,22	0
56	MG	2A	3090	1/1	0.96	0.06	54,54,54,54	0
56	MG	1G	201	1/1	0.96	0.12	38,38,38,38	0
56	MG	1A	3020	1/1	0.96	0.08	47,47,47,47	0
56	MG	1A	3249	1/1	0.96	0.16	42,42,42,42	0
56	MG	2A	3094	1/1	0.96	0.33	61,61,61,61	0
56	MG	1a	1948	1/1	0.96	0.07	69,69,69,69	0
56	MG	2A	3259	1/1	0.96	0.12	42,42,42,42	0
56	MG	2A	3260	1/1	0.96	0.17	43,43,43,43	0
56	MG	1a	1689	1/1	0.96	0.07	48,48,48,48	0
56	MG	1a	1690	1/1	0.96	0.18	53,53,53,53	0
56	MG	1A	3184	1/1	0.96	0.05	61,61,61,61	0
56	MG	2A	3100	1/1	0.96	0.18	37,37,37,37	0
56	MG	1A	3157	1/1	0.96	0.07	62,62,62,62	0
56	MG	1A	3090	1/1	0.96	0.07	54,54,54,54	0
56	MG	2A	3267	1/1	0.96	0.28	33,33,33,33	0
56	MG	1Q	201	1/1	0.96	0.09	26,26,26,26	0
56	MG	1a	1695	1/1	0.96	0.23	48,48,48,48	0
56	MG	1A	3487	1/1	0.96	0.14	52,52,52,52	0
56	MG	1A	3867	1/1	0.96	0.20	53,53,53,53	0
56	MG	1A	3160	1/1	0.96	0.06	76,76,76,76	0
56	MG	1A	3574	1/1	0.96	0.14	18,18,18,18	0
56	MG	1A	3767	1/1	0.96	0.12	34,34,34,34	0
56	MG	2A	3276	1/1	0.96	0.16	37,37,37,37	0
56	MG	2A	3444	1/1	0.96	0.12	55,55,55,55	0
56	MG	1A	3871	1/1	0.96	0.10	50,50,50,50	0
56	MG	2A	3446	1/1	0.96	0.11	60,60,60,60	0
56	MG	1A	3021	1/1	0.96	0.12	40,40,40,40	0
56	MG	1A	3255	1/1	0.96	0.40	44,44,44,44	0
56	MG	1A	3491	1/1	0.96	0.15	56,56,56,56	0
56	MG	2A	3450	1/1	0.96	0.17	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3045	1/1	0.96	0.16	37,37,37,37	0
56	MG	1A	3219	1/1	0.96	0.07	55,55,55,55	0
56	MG	1q	201	1/1	0.96	0.21	66,66,66,66	0
56	MG	2A	3119	1/1	0.96	0.26	45,45,45,45	0
56	MG	1A	3359	1/1	0.96	0.08	32,32,32,32	0
56	MG	1A	3164	1/1	0.96	0.22	38,38,38,38	0
56	MG	1A	3259	1/1	0.96	0.19	27,27,27,27	0
56	MG	1A	3776	1/1	0.96	0.08	43,43,43,43	0
56	MG	1A	3307	1/1	0.96	0.18	28,28,28,28	0
56	MG	1A	3037	1/1	0.96	0.15	32,32,32,32	0
56	MG	1A	3094	1/1	0.96	0.30	25,25,25,25	0
56	MG	1A	3672	1/1	0.96	0.15	48,48,48,48	0
56	MG	1A	3781	1/1	0.96	0.07	60,60,60,60	0
56	MG	1A	3588	1/1	0.96	0.42	46,46,46,46	0
56	MG	2a	1632	1/1	0.96	0.06	58,58,58,58	0
56	MG	1A	3367	1/1	0.96	0.16	52,52,52,52	0
56	MG	1A	3262	1/1	0.96	0.10	32,32,32,32	0
56	MG	1A	3226	1/1	0.96	0.13	61,61,61,61	0
56	MG	18	101	1/1	0.96	0.14	53,53,53,53	0
56	MG	1A	3072	1/1	0.96	0.25	45,45,45,45	0
56	MG	2a	1638	1/1	0.96	0.09	59,59,59,59	0
56	MG	1A	3509	1/1	0.96	0.14	52,52,52,52	0
56	MG	1A	3266	1/1	0.96	0.22	26,26,26,26	0
56	MG	1A	3373	1/1	0.96	0.18	52,52,52,52	0
56	MG	1A	3073	1/1	0.96	0.11	46,46,46,46	0
56	MG	2A	3139	1/1	0.96	0.28	41,41,41,41	0
56	MG	1A	3268	1/1	0.96	0.20	29,29,29,29	0
56	MG	1a	1728	1/1	0.96	0.06	77,77,77,77	0
56	MG	1A	3013	1/1	0.96	0.20	46,46,46,46	0
56	MG	2A	3478	1/1	0.96	0.16	64,64,64,64	0
56	MG	1A	3437	1/1	0.96	0.20	42,42,42,42	0
56	MG	2a	1818	1/1	0.96	0.06	86,86,86,86	0
56	MG	2A	3145	1/1	0.96	0.07	66,66,66,66	0
56	MG	2A	3146	1/1	0.96	0.27	59,59,59,59	0
56	MG	1A	3075	1/1	0.96	0.07	56,56,56,56	0
56	MG	1A	3439	1/1	0.96	0.05	44,44,44,44	0
56	MG	1a	1733	1/1	0.96	0.06	88,88,88,88	0
56	MG	1a	1864	1/1	0.96	0.07	55,55,55,55	0
56	MG	2A	3486	1/1	0.96	0.12	54,54,54,54	0
56	MG	1A	3440	1/1	0.96	0.09	54,54,54,54	0
56	MG	1A	3077	1/1	0.96	0.10	69,69,69,69	0
56	MG	2A	3320	1/1	0.96	0.13	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	3520	1/1	0.96	0.24	17,17,17,17	0
56	MG	1A	3606	1/1	0.96	0.18	66,66,66,66	0
56	MG	1A	3702	1/1	0.96	0.06	31,31,31,31	0
56	MG	1A	3703	1/1	0.96	0.10	38,38,38,38	0
56	MG	2A	3005	1/1	0.96	0.32	48,48,48,48	0
56	MG	1A	3442	1/1	0.96	0.12	54,54,54,54	0
56	MG	1A	3705	1/1	0.96	0.09	50,50,50,50	0
56	MG	1a	1614	1/1	0.96	0.05	47,47,47,47	0
56	MG	1A	3100	1/1	0.96	0.21	25,25,25,25	0
56	MG	1A	3707	1/1	0.96	0.08	50,50,50,50	0
56	MG	1A	3609	1/1	0.96	0.06	57,57,57,57	0
56	MG	1A	3523	1/1	0.96	0.12	43,43,43,43	0
56	MG	1A	3808	1/1	0.96	0.08	52,52,52,52	0
56	MG	1A	3444	1/1	0.96	0.09	38,38,38,38	0
56	MG	1A	3040	1/1	0.96	0.14	49,49,49,49	0
56	MG	1A	3712	1/1	0.96	0.10	37,37,37,37	0
56	MG	1A	3381	1/1	0.96	0.05	59,59,59,59	0
56	MG	1A	3201	1/1	0.96	0.07	52,52,52,52	0
56	MG	1A	3102	1/1	0.96	0.20	30,30,30,30	0
56	MG	1A	3616	1/1	0.96	0.11	48,48,48,48	0
56	MG	1A	3071	1/1	0.97	0.22	37,37,37,37	0
56	MG	1A	3813	1/1	0.97	0.05	42,42,42,42	0
56	MG	1A	3365	1/1	0.97	0.29	20,20,20,20	0
56	MG	2A	3104	1/1	0.97	0.11	45,45,45,45	0
56	MG	1A	3729	1/1	0.97	0.12	41,41,41,41	0
56	MG	1a	1905	1/1	0.97	0.05	73,73,73,73	0
56	MG	1A	3683	1/1	0.97	0.17	54,54,54,54	0
56	MG	1A	3162	1/1	0.97	0.12	49,49,49,49	0
56	MG	1A	3222	1/1	0.97	0.26	19,19,19,19	0
56	MG	1A	3060	1/1	0.97	0.06	29,29,29,29	0
56	MG	2A	3111	1/1	0.97	0.15	29,29,29,29	0
56	MG	1A	3504	1/1	0.97	0.10	37,37,37,37	0
56	MG	1A	3369	1/1	0.97	0.34	43,43,43,43	0
56	MG	2a	1692	1/1	0.97	0.12	67,67,67,67	0
56	MG	1A	3506	1/1	0.97	0.24	43,43,43,43	0
56	MG	1A	3103	1/1	0.97	0.10	62,62,62,62	0
56	MG	2A	3275	1/1	0.97	0.31	33,33,33,33	0
56	MG	2A	3193	1/1	0.97	0.12	51,51,51,51	0
56	MG	1A	3076	1/1	0.97	0.10	45,45,45,45	0
56	MG	1N	202	1/1	0.97	0.07	71,71,71,71	0
56	MG	1x	101	1/1	0.97	0.05	75,75,75,75	0
56	MG	2A	3280	1/1	0.97	0.17	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	2A	3045	1/1	0.97	0.06	41,41,41,41	0
56	MG	1A	3265	1/1	0.97	0.26	41,41,41,41	0
56	MG	1x	103	1/1	0.97	0.06	68,68,68,68	0
56	MG	1A	3239	1/1	0.97	0.17	23,23,23,23	0
56	MG	1A	3448	1/1	0.97	0.12	42,42,42,42	0
56	MG	1A	3089	1/1	0.97	0.10	32,32,32,32	0
56	MG	1A	3544	1/1	0.97	0.18	16,16,16,16	0
56	MG	1A	3315	1/1	0.97	0.28	42,42,42,42	0
56	MG	1a	1624	1/1	0.97	0.07	59,59,59,59	0
56	MG	1x	110	1/1	0.97	0.11	68,68,68,68	0
56	MG	1A	3335	1/1	0.97	0.25	27,27,27,27	0
56	MG	1A	3316	1/1	0.97	0.38	51,51,51,51	0
56	MG	1A	3748	1/1	0.97	0.07	47,47,47,47	0
56	MG	1a	1802	1/1	0.97	0.09	52,52,52,52	0
56	MG	1a	1803	1/1	0.97	0.04	59,59,59,59	0
56	MG	1A	3228	1/1	0.97	0.28	33,33,33,33	0
56	MG	2A	3297	1/1	0.97	0.22	41,41,41,41	0
56	MG	1A	3836	1/1	0.97	0.07	27,27,27,27	0
56	MG	2A	3384	1/1	0.97	0.23	42,42,42,42	0
56	MG	1a	1630	1/1	0.97	0.06	49,49,49,49	0
56	MG	1a	1631	1/1	0.97	0.09	64,64,64,64	0
56	MG	1A	3586	1/1	0.97	0.36	54,54,54,54	0
56	MG	1A	3122	1/1	0.97	0.24	40,40,40,40	0
56	MG	1a	1810	1/1	0.97	0.09	63,63,63,63	0
56	MG	2A	3141	1/1	0.97	0.11	40,40,40,40	0
56	MG	1A	3839	1/1	0.97	0.12	58,58,58,58	0
56	MG	1A	3159	1/1	0.97	0.07	54,54,54,54	0
56	MG	1A	3430	1/1	0.97	0.05	51,51,51,51	0
56	MG	2A	3001	1/1	0.97	0.06	88,88,88,88	0
56	MG	1A	3889	1/1	0.97	0.09	61,61,61,61	0
56	MG	1A	3552	1/1	0.97	0.17	34,34,34,34	0
56	MG	2A	3004	1/1	0.97	0.04	42,42,42,42	0
56	MG	1A	3017	1/1	0.97	0.07	64,64,64,64	0
56	MG	1A	3382	1/1	0.97	0.07	56,56,56,56	0
56	MG	1A	3714	1/1	0.97	0.07	34,34,34,34	0
56	MG	13	103	1/1	0.97	0.12	53,53,53,53	0
56	MG	1A	3894	1/1	0.97	0.06	53,53,53,53	0
56	MG	2A	3155	1/1	0.97	0.07	60,60,60,60	0
56	MG	1A	3895	1/1	0.97	0.08	57,57,57,57	0
56	MG	2A	3081	1/1	0.97	0.15	59,59,59,59	0
56	MG	1A	3383	1/1	0.97	0.08	59,59,59,59	0
56	MG	1A	3847	1/1	0.97	0.12	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3360	1/1	0.97	0.21	29,29,29,29	0
56	MG	1A	3462	1/1	0.97	0.09	59,59,59,59	0
56	MG	1A	3288	1/1	0.97	0.11	32,32,32,32	0
56	MG	1A	3197	1/1	0.97	0.10	37,37,37,37	0
56	MG	1A	3527	1/1	0.97	0.29	25,25,25,25	0
56	MG	1A	3903	1/1	0.97	0.16	39,39,39,39	0
56	MG	18	104	1/1	0.97	0.13	52,52,52,52	0
56	MG	2A	3415	1/1	0.97	0.23	43,43,43,43	0
56	MG	1A	3673	1/1	0.97	0.07	43,43,43,43	0
56	MG	2E	301	1/1	0.97	0.13	51,51,51,51	0
56	MG	2A	3021	1/1	0.97	0.16	48,48,48,48	0
56	MG	1A	3561	1/1	0.97	0.31	28,28,28,28	0
56	MG	1A	3495	1/1	0.97	0.04	47,47,47,47	0
56	MG	2A	3095	1/1	0.97	0.16	41,41,41,41	0
56	MG	1A	3639	1/1	0.97	0.08	29,29,29,29	0
56	MG	1A	3678	1/1	0.97	0.18	43,43,43,43	0
56	MG	1a	1661	1/1	0.97	0.41	57,57,57,57	0
56	MG	2A	3339	1/1	0.97	0.21	48,48,48,48	0
56	MG	1A	3305	1/1	0.97	0.27	53,53,53,53	0
56	MG	2A	3176	1/1	0.97	0.18	41,41,41,41	0
56	MG	2A	3028	1/1	0.97	0.18	57,57,57,57	0
58	ZN	24	501	1/1	0.97	0.08	126,126,126,126	0
58	ZN	2n	501	1/1	0.97	0.05	103,103,103,103	0
56	MG	1A	3114	1/1	0.98	0.22	33,33,33,33	0
56	MG	1A	3698	1/1	0.98	0.06	21,21,21,21	0
56	MG	1A	3212	1/1	0.98	0.05	52,52,52,52	0
56	MG	2D	301	1/1	0.98	0.08	34,34,34,34	0
56	MG	1A	3736	1/1	0.98	0.08	48,48,48,48	0
56	MG	2A	3316	1/1	0.98	0.32	27,27,27,27	0
56	MG	1A	3483	1/1	0.98	0.06	48,48,48,48	0
56	MG	1A	3046	1/1	0.98	0.25	46,46,46,46	0
56	MG	1A	3848	1/1	0.98	0.08	43,43,43,43	0
56	MG	1A	3270	1/1	0.98	0.17	31,31,31,31	0
56	MG	1A	3084	1/1	0.98	0.05	54,54,54,54	0
56	MG	1A	3031	1/1	0.98	0.06	36,36,36,36	0
56	MG	1D	304	1/1	0.98	0.06	57,57,57,57	0
56	MG	1A	3030	1/1	0.98	0.04	27,27,27,27	0
56	MG	1A	3468	1/1	0.98	0.12	40,40,40,40	0
56	MG	2A	3326	1/1	0.98	0.32	30,30,30,30	0
56	MG	1A	3469	1/1	0.98	0.08	37,37,37,37	0
56	MG	1A	3109	1/1	0.98	0.29	47,47,47,47	0
56	MG	1A	3587	1/1	0.98	0.31	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
56	MG	1A	3674	1/1	0.98	0.07	37,37,37,37	0
56	MG	1A	3088	1/1	0.98	0.10	43,43,43,43	0
56	MG	1A	3589	1/1	0.98	0.36	47,47,47,47	0
56	MG	1A	3152	1/1	0.98	0.16	55,55,55,55	0
56	MG	1A	3619	1/1	0.98	0.11	28,28,28,28	0
56	MG	1a	1817	1/1	0.98	0.06	53,53,53,53	0
56	MG	2A	3233	1/1	0.98	0.15	38,38,38,38	0
56	MG	1A	3323	1/1	0.98	0.21	49,49,49,49	0
56	MG	1A	3220	1/1	0.98	0.07	38,38,38,38	0
56	MG	1A	3681	1/1	0.98	0.06	57,57,57,57	0
56	MG	1A	3111	1/1	0.98	0.35	24,24,24,24	0
56	MG	1P	202	1/1	0.98	0.10	69,69,69,69	0
56	MG	1a	1650	1/1	0.98	0.12	38,38,38,38	0
56	MG	1A	3566	1/1	0.98	0.19	34,34,34,34	0
56	MG	2A	3241	1/1	0.98	0.41	39,39,39,39	0
56	MG	1A	3052	1/1	0.98	0.06	26,26,26,26	0
56	MG	1A	3685	1/1	0.98	0.09	47,47,47,47	0
56	MG	1B	211	1/1	0.98	0.30	42,42,42,42	0
56	MG	1A	3223	1/1	0.98	0.35	30,30,30,30	0
56	MG	2A	3148	1/1	0.98	0.06	51,51,51,51	0
56	MG	1A	3569	1/1	0.98	0.35	34,34,34,34	0
56	MG	1A	3570	1/1	0.98	0.35	25,25,25,25	0
56	MG	1A	3690	1/1	0.98	0.06	33,33,33,33	0
56	MG	1A	3499	1/1	0.98	0.11	38,38,38,38	0
56	MG	1r	101	1/1	0.98	0.05	64,64,64,64	0
56	MG	2A	3201	1/1	0.98	0.23	35,35,35,35	0
56	MG	1A	3692	1/1	0.98	0.09	29,29,29,29	0
56	MG	2A	3358	1/1	0.98	0.06	60,60,60,60	0
56	MG	1A	3066	1/1	0.98	0.07	38,38,38,38	0
56	MG	1A	3459	1/1	0.98	0.06	57,57,57,57	0
56	MG	1a	1837	1/1	0.98	0.18	44,44,44,44	0
56	MG	2a	1626	1/1	0.98	0.31	53,53,53,53	0
56	MG	1A	3502	1/1	0.98	0.06	52,52,52,52	0
56	MG	1A	3425	1/1	0.98	0.11	46,46,46,46	0
58	ZN	2Y	501	1/1	0.98	0.04	98,98,98,98	0
56	MG	1a	1708	1/1	0.98	0.25	49,49,49,49	0
56	MG	1B	222	1/1	0.98	0.04	59,59,59,59	0
56	MG	2A	3246	1/1	0.99	0.28	31,31,31,31	0
56	MG	1A	3118	1/1	0.99	0.03	37,37,37,37	0
56	MG	1A	3699	1/1	0.99	0.04	51,51,51,51	0
56	MG	2A	3209	1/1	0.99	0.30	35,35,35,35	0
56	MG	1A	3284	1/1	0.99	0.06	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	1A	3086	1/1	0.99	0.03	30,30,30,30	0
56	MG	1a	1655	1/1	0.99	0.07	56,56,56,56	0
56	MG	1A	3059	1/1	0.99	0.05	30,30,30,30	0
56	MG	1A	3078	1/1	0.99	0.10	14,14,14,14	0
56	MG	1A	3038	1/1	0.99	0.10	26,26,26,26	0
56	MG	1a	1951	1/1	0.99	0.04	64,64,64,64	0
56	MG	1A	3831	1/1	0.99	0.11	54,54,54,54	0
58	ZN	1Y	202	1/1	0.99	0.02	66,66,66,66	0
58	ZN	14	501	1/1	0.99	0.03	99,99,99,99	0
58	ZN	15	104	1/1	0.99	0.02	49,49,49,49	0
58	ZN	1n	501	1/1	0.99	0.03	64,64,64,64	0
56	MG	2A	3049	1/1	0.99	0.04	79,79,79,79	0
56	MG	2A	3357	1/1	0.99	0.05	51,51,51,51	0
58	ZN	25	501	1/1	0.99	0.05	66,66,66,66	0
58	ZN	26	102	1/1	0.99	0.03	63,63,63,63	0
58	ZN	29	501	1/1	0.99	0.03	88,88,88,88	0
56	MG	1a	1822	1/1	0.99	0.07	55,55,55,55	0
59	SF4	1d	303	8/8	0.99	0.03	60,65,69,72	0
59	SF4	2d	501	8/8	0.99	0.03	60,79,85,85	0
56	MG	1A	3687	1/1	1.00	0.04	33,33,33,33	0
58	ZN	16	102	1/1	1.00	0.04	48,48,48,48	0
58	ZN	19	104	1/1	1.00	0.07	52,52,52,52	0

6.5 Other polymers

There are no such residues in this entry.