Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2026 – 02:57 PM EDT

PDB ID	:	8EKB / pdb_00008ekb
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with mRNA, deacylated P-site tRNAmet, and thermorubin at 2.70A resolution
Authors	:	Paranjpe, M.N.; Polikanov, Y.S.
Deposited on	:	2022-09-20
Resolution	:	2.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

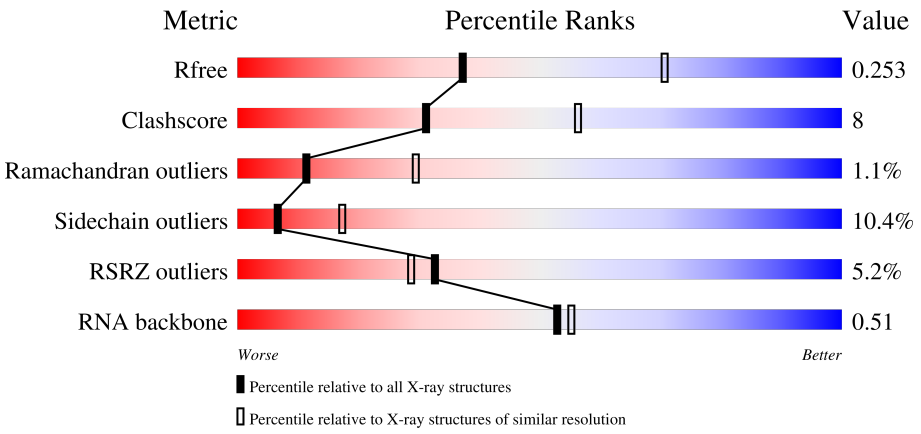
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.70 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	1A	2915	4% 67% 26% 6% •
1	2A	2915	3% 60% 30% 6% •
2	1B	121	74% 23% • •
2	2B	121	8% 48% 40% 12% •

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Mol	Chain	Length	Quality of chain
3	1D	276	%, 81%, 17%
3	2D	276	%, 80%, 17%
4	1E	206	%, 72%, 22%, 5%
4	2E	206	%, 71%, 25%
5	1F	210	74%, 19%
5	2F	210	%, 60%, 31%, 5%
6	1G	182	2%, 71%, 25%
6	2G	182	16%, 58%, 35%, 6%
7	1H	180	2%, 69%, 25%
7	2H	180	7%, 68%, 27%
8	1I	148	%, 63%, 32%
8	2I	148	6%, 61%, 30%, 6%
9	1N	140	%, 79%, 16%, 5%
9	2N	140	2%, 71%, 24%
10	1O	122	81%, 18%
10	2O	122	69%, 29%
11	1P	150	%, 75%, 21%
11	2P	150	%, 71%, 24%
12	1Q	141	%, 79%, 18%
12	2Q	141	4%, 70%, 27%
13	1R	118	81%, 16%
13	2R	118	%, 77%, 20%
14	1S	112	70%, 25%
14	2S	112	17%, 66%, 29%
15	1T	146	2%, 71%, 18%, 10%

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Mol	Chain	Length	Quality of chain
15	2T	146	%, 60%, 27%, 10%
16	1U	118	%, 80%, 17%
16	2U	118	%, 77%, 20%
17	1V	101	80%, 16%
17	2V	101	%, 72%, 27%
18	1W	113	88%, 10%
18	2W	113	4%, 76%, 19%
19	1X	96	2%, 82%, 16%
19	2X	96	3%, 68%, 30%
20	1Y	110	3%, 72%, 21%, 5%
20	2Y	110	10%, 70%, 22%, 5%
21	1Z	206	4%, 52%, 20%, 25%
21	2Z	206	11%, 47%, 27%, 22%
22	10	85	%, 79%, 8%, 12%
22	20	85	7%, 64%, 24%, 9%
23	11	98	%, 79%, 19%
23	21	98	%, 65%, 32%
24	12	72	%, 72%, 24%
24	22	72	3%, 75%, 19%
25	13	60	2%, 73%, 22%
25	23	60	68%, 25%, 5%
26	14	71	7%, 54%, 35%, 7%
26	24	71	28%, 49%, 35%, 11%
27	15	60	85%, 13%
27	25	60	2%, 80%, 17%

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Mol	Chain	Length	Quality of chain
28	16	54	59% 35%
28	26	54	2% 70% 22% 6%
29	17	49	8% 76% 20%
29	27	49	4% 69% 27%
30	18	65	72% 25%
30	28	65	75% 23%
31	19	37	78% 19%
31	29	37	5% 76% 24%
32	1a	1521	3% 56% 35% 8%
32	2a	1521	4% 53% 37% 9%
33	1b	256	9% 52% 33% 5% 10%
33	2b	256	23% 46% 39% 5% 10%
34	1c	239	10% 55% 30% 14%
34	2c	239	13% 55% 26% 5% 14%
35	1d	209	11% 68% 25% 6%
35	2d	209	5% 59% 33% 7%
36	1e	162	% 56% 32% 9%
36	2e	162	10% 63% 24% 9%
37	1f	101	4% 65% 30%
37	2f	101	3% 81% 16%
38	1g	156	7% 76% 20%
38	2g	156	11% 68% 26% 5%
39	1h	138	% 67% 28%
39	2h	138	9% 71% 26%
40	1i	128	12% 67% 27% 5%

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Mol	Chain	Length	Quality of chain
40	2i	128	30% 65% 30%
41	1j	105	23% 54% 31% 7% 8%
41	2j	105	20% 55% 29% 7% 9%
42	1k	129	2% 67% 19% 12%
42	2k	129	6% 61% 25% 12%
43	1l	132	5% 70% 19% 8%
43	2l	132	3% 72% 18% 8%
44	1m	126	6% 64% 25% 8%
44	2m	126	27% 56% 37% 5%
45	1n	61	5% 61% 31% 7%
45	2n	61	41% 57% 39%
46	1o	89	2% 79% 17%
46	2o	89	4% 65% 29%
47	1p	88	19% 52% 39% 7%
47	2p	88	5% 59% 31% 7%
48	1q	105	5% 75% 15% 6%
48	2q	105	4% 67% 25% 6%
49	1r	88	5% 48% 28% 23%
49	2r	88	% 50% 26% 23%
50	1s	93	8% 55% 32% 11%
50	2s	93	34% 43% 40% 6% 11%
51	1t	106	14% 69% 18% 9%
51	2t	106	8% 66% 21% 9%
52	1u	27	52% 30% 15%
52	2u	27	19% 63% 19% 15%

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Mol	Chain	Length	Quality of chain
53	1v	21	10% 19% 5% 76%
53	2v	21	10% 14% 10% 76%
54	1x	77	74% 18% 6%
54	2x	77	3% 69% 25% 5%

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
55	MG	1A	3517	-	-	-	X
55	MG	1W	207	-	-	-	X
55	MG	1a	1647	-	-	-	X
55	MG	2a	1708	-	-	-	X
55	MG	2a	1761	-	-	-	X

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 292790 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
			Total	C	N	O	P			
1	1A	2871	61852	27531	11572	19878	2871	0	0	0
1	2A	2800	60322	26848	11284	19390	2800	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	1B	120	2577	1146	476	835	120	0	0	0
2	2B	120	2575	1146	476	833	120	0	0	0

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	1G	181	1423	913	253	253	4	0	0	0
6	2G	181	1428	913	258	253	4	0	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
22	10	75	598	370	127	100	1	0	0	0
22	20	77	608	375	129	103	1	0	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 53 is a RNA chain called M-Stop-mRNA.

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

- Molecule 54 is a RNA chain called P-site deacylated tRNAmet.

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

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
55	1A	1052	1052	1052	0	0
55	1B	38	38	38	0	0
55	1D	11	11	11	0	0
55	1E	13	13	13	0	0
55	1F	11	11	11	0	0
55	1G	5	5	5	0	0
55	1I	1	1	1	0	0
55	1N	6	6	6	0	0
55	1O	5	5	5	0	0
55	1P	6	6	6	0	0
55	1Q	7	7	7	0	0
55	1R	5	5	5	0	0
55	1S	3	3	3	0	0
55	1T	2	2	2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
55	1U	13	13	13	0	0
55	1V	8	8	8	0	0
55	1W	7	7	7	0	0
55	1X	6	6	6	0	0
55	1Y	2	2	2	0	0
55	1Z	3	3	3	0	0
55	10	7	7	7	0	0
55	11	4	4	4	0	0
55	12	2	2	2	0	0
55	13	3	3	3	0	0
55	14	1	1	1	0	0
55	15	7	7	7	0	0
55	16	1	1	1	0	0
55	17	6	6	6	0	0
55	18	8	8	8	0	0
55	1a	198	198	198	0	0
55	1b	1	1	1	0	0
55	1d	1	1	1	0	0
55	1e	1	1	1	0	0
55	1f	1	1	1	0	0
55	1l	2	2	2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
55	1m	2	2	2	0	0
55	1n	1	1	1	0	0
55	1p	1	1	1	0	0
55	1r	1	1	1	0	0
55	1t	1	1	1	0	0
55	1v	1	1	1	0	0
55	1x	15	15	15	0	0
55	2A	716	716	716	0	0
55	2B	17	17	17	0	0
55	2D	7	7	7	0	0
55	2E	6	6	6	0	0
55	2F	3	3	3	0	0
55	2G	1	1	1	0	0
55	2N	1	1	1	0	0
55	2O	1	1	1	0	0
55	2P	1	1	1	0	0
55	2Q	4	4	4	0	0
55	2R	2	2	2	0	0
55	2T	2	2	2	0	0
55	2U	1	1	1	0	0
55	2V	2	2	2	0	0

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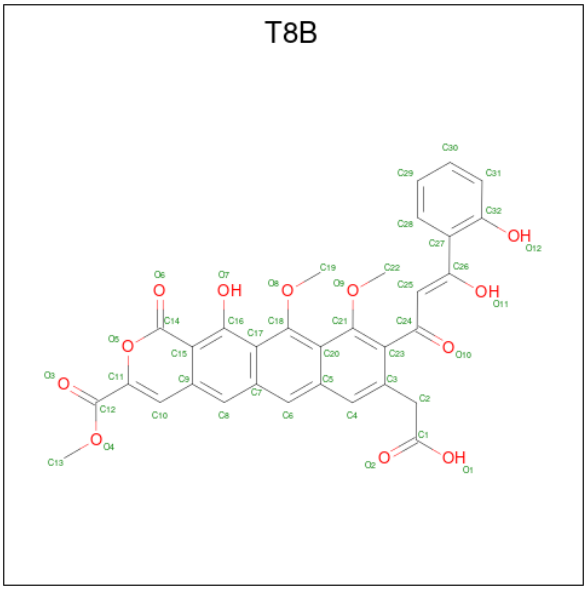
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
55	2W	3	3	3	0	0
55	2Y	1	1	1	0	0
55	2Z	1	1	1	0	0
55	20	1	1	1	0	0
55	21	1	1	1	0	0
55	23	1	1	1	0	0
55	25	1	1	1	0	0
55	27	3	3	3	0	0
55	28	3	3	3	0	0
55	2a	197	197	197	0	0
55	2e	1	1	1	0	0
55	2f	2	2	2	0	0
55	2j	1	1	1	0	0
55	2k	1	1	1	0	0
55	2l	4	4	4	0	0
55	2q	2	2	2	0	0
55	2r	1	1	1	0	0
55	2t	1	1	1	0	0
55	2x	5	5	5	0	0

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1A	1	Total K 1 1	0	0
56	2A	1	Total K 1 1	0	0

- Molecule 57 is Thermorubin (CCD ID: T8B) (formula: $C_{32}H_{24}O_{12}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1A	1	Total C O 44 32 12	0	0
57	2A	1	Total C O 44 32 12	0	0

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

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

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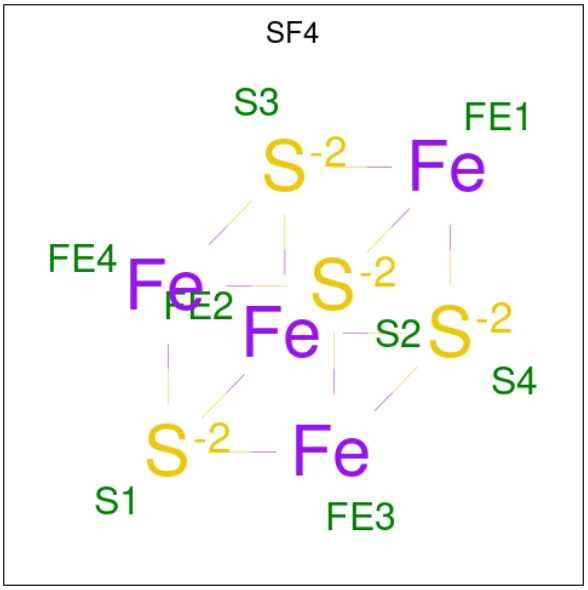
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	1n	1	Total Zn 1 1	0	0
58	2Y	1	Total Zn 1 1	0	0
58	24	1	Total Zn 1 1	0	0
58	25	1	Total Zn 1 1	0	0
58	26	1	Total Zn 1 1	0	0
58	29	1	Total Zn 1 1	0	0
58	2n	1	Total Zn 1 1	0	0

- 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 8 4 4	0	0
59	2d	1	Total Fe S 8 4 4	0	0

- Molecule 60 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	2039	Total O 2039 2039	0	0
60	1B	63	Total O 63 63	0	0
60	1D	24	Total O 24 24	0	0
60	1E	27	Total O 27 27	0	0
60	1F	14	Total O 14 14	0	0
60	1G	2	Total O 2 2	0	0
60	1H	3	Total O 3 3	0	0
60	1I	1	Total O 1 1	0	0
60	1N	5	Total O 5 5	0	0
60	1O	5	Total O 5 5	0	0
60	1P	21	Total O 21 21	0	0
60	1Q	7	Total O 7 7	0	0
60	1R	13	Total O 13 13	0	0
60	1S	4	Total O 4 4	0	0
60	1T	7	Total O 7 7	0	0
60	1U	13	Total O 13 13	0	0
60	1V	8	Total O 8 8	0	0
60	1W	8	Total O 8 8	0	0
60	1X	5	Total O 5 5	0	0
60	1Y	2	Total O 2 2	0	0
60	1Z	1	Total O 1 1	0	0
60	10	11	Total O 11 11	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	11	12	Total O 12 12	0	0
60	12	4	Total O 4 4	0	0
60	13	5	Total O 5 5	0	0
60	14	1	Total O 1 1	0	0
60	15	6	Total O 6 6	0	0
60	16	2	Total O 2 2	0	0
60	17	11	Total O 11 11	0	0
60	18	10	Total O 10 10	0	0
60	1a	297	Total O 297 297	0	0
60	1d	1	Total O 1 1	0	0
60	1e	1	Total O 1 1	0	0
60	1f	1	Total O 1 1	0	0
60	1g	1	Total O 1 1	0	0
60	1l	8	Total O 8 8	0	0
60	1m	1	Total O 1 1	0	0
60	1o	2	Total O 2 2	0	0
60	1p	1	Total O 1 1	0	0
60	1q	2	Total O 2 2	0	0
60	1v	3	Total O 3 3	0	0
60	1x	15	Total O 15 15	0	0
60	2A	971	Total O 971 971	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	2B	15	Total O 15 15	0	0
60	2D	18	Total O 18 18	0	0
60	2E	10	Total O 10 10	0	0
60	2F	11	Total O 11 11	0	0
60	2N	3	Total O 3 3	0	0
60	2O	2	Total O 2 2	0	0
60	2P	11	Total O 11 11	0	0
60	2Q	2	Total O 2 2	0	0
60	2R	3	Total O 3 3	0	0
60	2T	3	Total O 3 3	0	0
60	2U	2	Total O 2 2	0	0
60	2V	1	Total O 1 1	0	0
60	2W	3	Total O 3 3	0	0
60	2X	4	Total O 4 4	0	0
60	2Z	1	Total O 1 1	0	0
60	20	4	Total O 4 4	0	0
60	21	3	Total O 3 3	0	0
60	23	2	Total O 2 2	0	0
60	26	1	Total O 1 1	0	0
60	27	2	Total O 2 2	0	0
60	28	3	Total O 3 3	0	0

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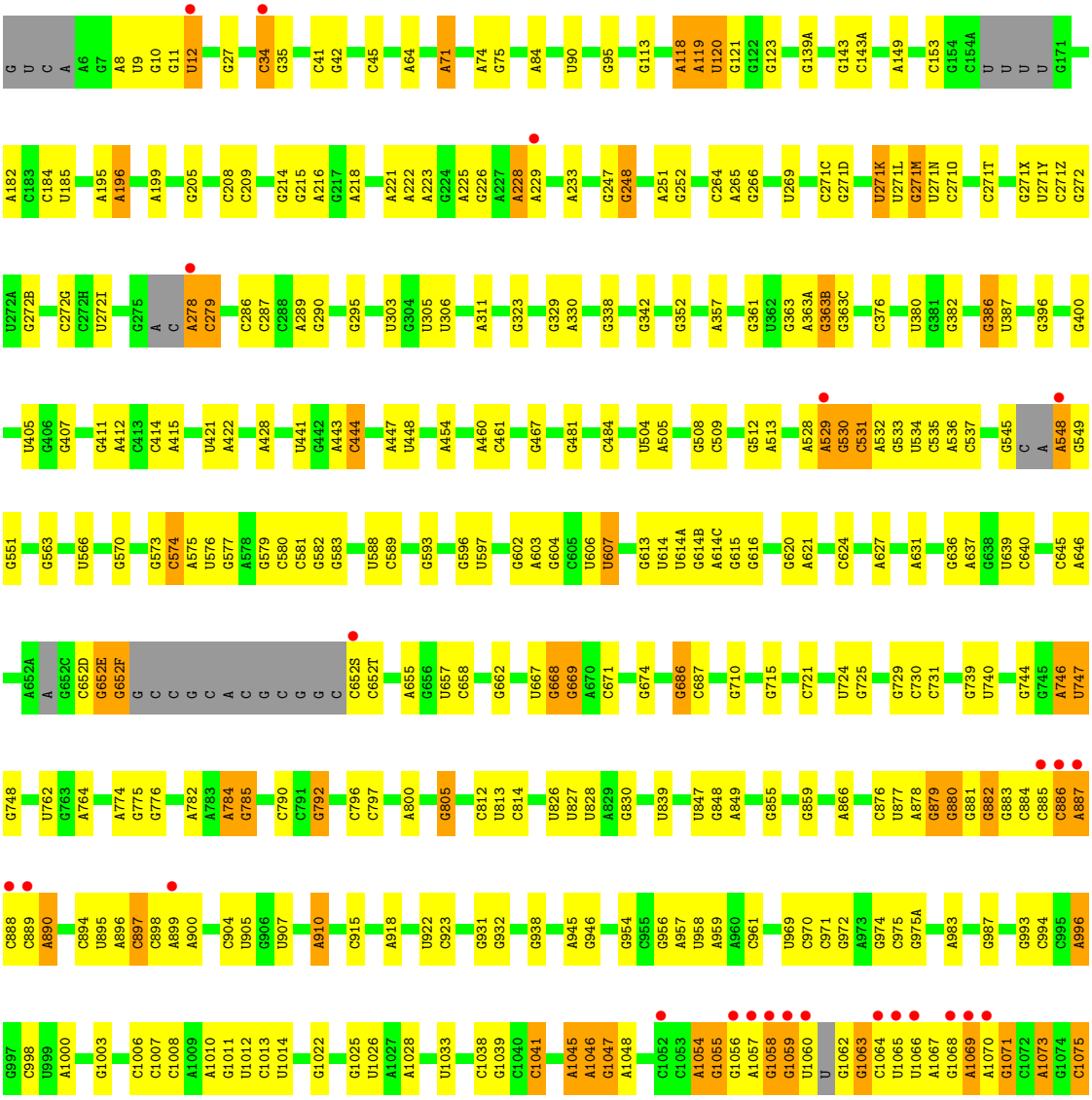
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	29	1	Total O 1 1	0	0
60	2a	176	Total O 176 176	0	0
60	2c	1	Total O 1 1	0	0
60	2d	1	Total O 1 1	0	0
60	2e	1	Total O 1 1	0	0
60	2f	1	Total O 1 1	0	0
60	2j	2	Total O 2 2	0	0
60	2l	2	Total O 2 2	0	0
60	2n	1	Total O 1 1	0	0
60	2p	3	Total O 3 3	0	0
60	2q	2	Total O 2 2	0	0
60	2r	3	Total O 3 3	0	0
60	2t	6	Total O 6 6	0	0
60	2v	1	Total O 1 1	0	0
60	2x	3	Total O 3 3	0	0

3 Residue-property plots (i)

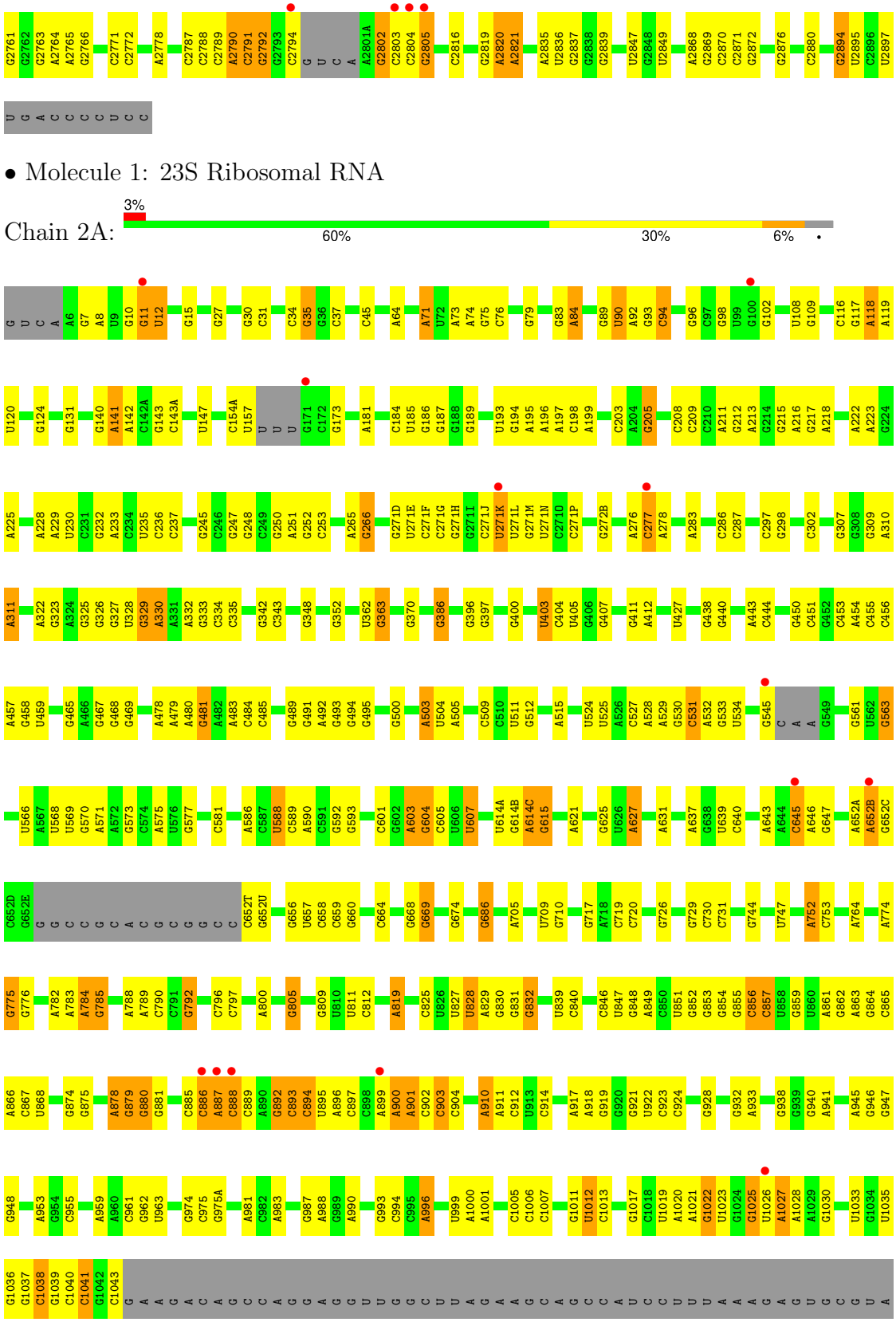
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: 23S Ribosomal RNA

Chain 1A:

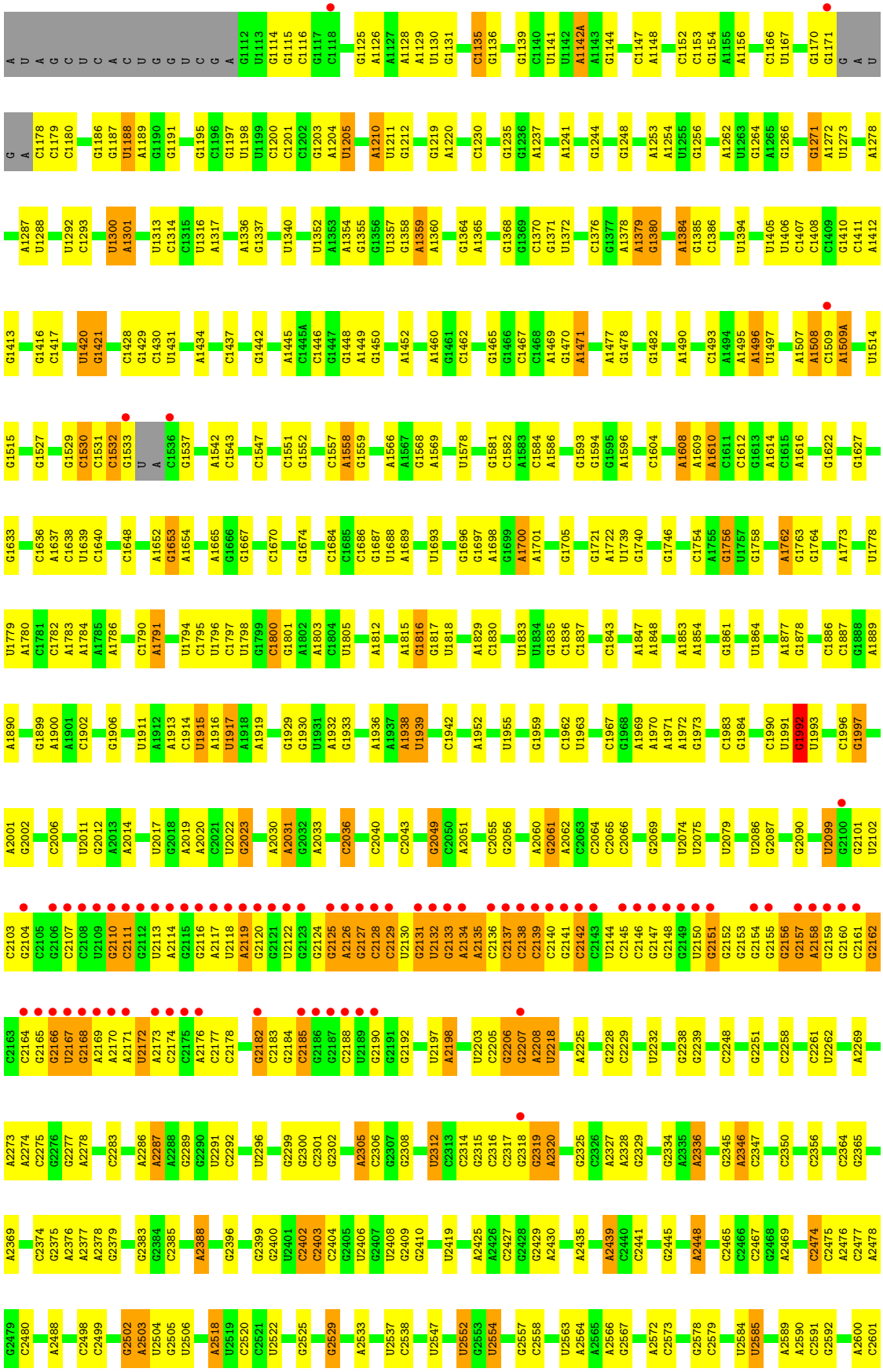


C1076 A1077 U1078 C1079 C1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 G1089 U1090 G1091 C1092 G1093 U1094 A1095 A1096 U1097 A1098 G1099 C1100 U1101 C1102 A1103 C1104 U1105 G1106 G1110 A1111 G1112 U1113 G1114 G1115 C1116 G1120 G1125 U1130 C1135 G1136 G1137 G1138 U1141 U1142 A1142A A1143 G1144 G1149 C1153
G1154 A1155 G1164 U1165 C1166 G1170 G1171 G1173 A1174 U1175 G1176 A1177 C1178 C1179 C1180 G1183 G1186 G1187 U1188 G1191 C1201 A1220 G1227 G1243 G1248 A1253 A1254 U1255 G1256 U1263 G1264 A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1274 A1278 G1281 U1292 C1293
C1297 U1300 A1301 A1302 G1303 C1315 G1332 A1342 U1352 A1353 A1354 U1357 G1358 A1359 A1360 G1364 A1365 G1371 U1372 A1373 A1379 G1380 A1384 G1385 C1386 U1396 U1405 U1406 C1407 C1408 G1416 C1417 G1418 A1419 U1420 G1421 G1424 G1425 G1426 A1427 C1428 G1429 C1430 U1431
G1442 A1445 G1448 A1449 G1450 A1452 U1453 G1455 G1461 G1466 C1467 C1468 G1482 A1486 G1487 G1488 U1489 A1490 C1493 A1494 A1495 A1496 U1503 C1504 C1505 A1508 C1509 A1509A U1518 G1519 C1532 G U A C G1537 U1540 G1541 A1542 C1543 C1547 C1548 A1554 A1558
G1559 G1560 A1566 A1569 U1578 A1579 A1580 G1581 C1584 A1586 A1587 C1588 C1589 G1593 G1594 G1595 U1602 A1603 G1606 C1607 A1608 A1609 A1614 G1622 G1630 C1631 A1634 G1635 C1636 A1637 C1638 U1639 C1640 G1647 C1648 G1651 A1654 C1657 C1658 A1669 C1670 U1671 G1674
U1688 U1693 G1697 A1698 G1699 A1700 A1701 G1702 G1703 G1704 G1705 U1706 U1720 G1721 A1722 U1739 G1740 A1741 G1742 G1746 G1753 G1756 A1759 A1762 G1763 G1764 A1773 U1778 U1779 A1780 A1783 A1784 A1791 U1794 C1795 U1796 C1797 U1798 G1799 C1800 G1801 A1802 A1803 A1815 G1816
G1817 A1829 G1839 A1847 A1859 G1865 G1878 C1882 G1883 A1889 A1890 G1899 A1900 G1903 G1906 U1911 C1914 U1915 A1916 U1917 A1918 A1919 C1920 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 C1942 A1952 A1953 G1954 U1955 G1959 C1962 U1963 G1964
C1965 A1966 C1967 G1968 A1969 A1970 A1971 A1972 G1984 G1985 A1986 U1991 G1992 U1993 G1997 A2001 G2002 G2010 A2013 A2014 A2019 A2020 C2021 U2022 G2023 U2028 G2029 A2030 A2031 G2032 A2033 C2039 C2043 G2049 G2053 A2054 C2055 G2056 A2060 G2061 A2062 C2063 G2069 G2070 A2071 G2072
G2080 G2093 U2096 U2099 G2100 G2101 U2102 C2105 G2106 C2107 C2108 U2109 G2110 C2111 U2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 C2128 C2129 U2130 G2131 U2132 G2133 A2134 A2135 C2136 C2137 C2138 C2139 C2140 G2141 C2142 C2143 U2144 C2145 C2146 G2147 G2148 G2149 U2150 G2151
G2154 G2155 G2156 G2157 A2158 G2159 G2160 C2161 G2162 C2163 C2164 G2165 G2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 U2180 G2181 G2182 C2183 U2189 G2190 G2193 A2198 G2206 G2207 G2219 G2224 A2225 C2226 A2227 G2228 U2232 U2233 G2234 G2235 G2238 G2239 U2243 U2244
G2251 U2262 A2268 A2269 A2273 A2274 G2277 A2278 G2279 C2283 C2284 C2285 A2286 A2287 A2288 G2289 G2290 U2291 A2292 C2293 C2294 G2295 U2296 A2305 C2306 G2307 G2308 U2312 G2319 A2320 G2325 C2326 A2327 A2328 G2329 G2334 A2335 A2336 G2337 U2344 C2347 U2348 G2349 C2350 C2364 G2372
G2373 C2374 G2375 G2383 G2384 C2385 U2390 A2393 C2394 C2395 G2396 C2404 G2405 U2406 G2407 G2410 G2415 C2416 C2417 A2418 U2419 A2422 U2423 C2424 A2425 A2426 C2427 G2428 G2429 A2430 U2431 A2432 A2435 A2439 C2440 C2441 G2445 G2446 G2447 A2448 G2458 C2466 C2467 G2468 A2469 G2470 C2471
A2476 C2477 C2483 C2499 G2502 A2503 U2504 G2505 U2506 A2518 G2525 G2529 G2535 G2536 U2537 C2538 G2549 G2550 C2551 U2552 G2553 U2554 A2564 A2565 A2566 G2567 C2568 G2569 A2572 C2575 G2582 A2602 G2603 U2604 U2605 G2608 U2609 C2610 U2611 C2612 U2613 C2617 C2626 G2627
C2628 A2629 G2630 C2635 C2646 U2647 C2648 U2649 A2654 G2661 A2662 C2667 G2685 G2686 U2687 U2688 U2689 C2690 A2693 G2694 U2702 C2703 G2706 A2711 U2712 A2712A A2713 G2714 G2718 U2726 G2729 G2732 A2733 A2741 C2742 A2748 A2749 C2755 U2756 A2757 A2758 G2759 C2760



• Molecule 1: 23S Ribosomal RNA

Chain 2A: 3% 60% 30% 6% •


A U A G C U C A C U G G U C G A
G A C1178 C1179 C1180 G1186 G1187 U1188 A1189 G1190 G1191 G1195 C1196 G1197 U1198 U1199 C1200 C1201 C1202 G1203 A1204 U1205 A1210 U1211 G1212 G1219 A1220 C1230 G1235 G1236 A1237 A1241 G1244 G1248 A1253 A1254 U1255 G1256 A1262 U1263 G1264 A1265 G1266 G1271 A1272 U1273 A1278
A1287 U1288 U1292 C1293 U1300 A1301 U1313 C1314 C1315 U1316 A1317 A1336 G1337 U1340 U1352 A1353 A1354 G1355 G1356 U1357 G1358 A1359 A1360 G1364 A1365 G1368 G1369 C1370 G1371 U1372 C1376 G1377 A1378 A1379 G1380 A1384 G1385 C1386 U1394 U1405 U1406 C1407 C1408 C1409 G1410 C1411 A1412
G1413 G1416 C1417 U1420 G1421 C1428 G1429 C1430 U1431 A1434 C1437 G1442 A1445 C1445A C1446 G1447 G1448 A1449 G1450 A1452 A1460 G1461 C1462 G1465 G1466 C1467 C1468 A1469 G1470 A1471 A1477 G1478 G1482 A1490 C1493 A1494 A1495 A1496 U1497 A1507 A1508 C1509 A1509A U1514
G1515 G1527 G1529 C1530 C1531 C1532 G1533 U A C1536 G1537 A1542 C1543 C1547 C1551 G1552 C1557 A1558 G1559 A1566 A1567 G1568 A1569 U1578 G1581 C1582 A1583 C1584 A1586 G1593 G1594 G1595 A1596 C1604 A1608 A1609 A1610 C1611 C1612 G1613 A1614 C1615 A1616 G1622 G1627
G1633 C1636 A1637 C1638 U1639 C1640 C1648 A1652 G1653 A1654 A1665 G1666 G1667 C1670 G1674 C1684 C1685 C1686 G1687 U1688 A1689 U1693 G1696 G1697 A1698 G1699 A1700 A1701 G1705 G1721 A1722 U1739 G1740 G1746 C1754 A1755 G1756 U1757 G1758 A1762 G1763 G1764 A1773 U1778
U1779 A1780 C1781 C1782 A1783 A1784 A1785 A1786 C1790 A1791 U1794 C1795 U1796 C1797 U1798 G1799 C1800 G1801 A1802 A1803 C1804 U1805 A1812 A1815 G1816 G1817 U1818 A1829 C1830 U1833 U1834 G1835 C1836 C1837 C1843 A1847 A1848 A1853 A1854 G1861 U1864 A1877 G1878 C1886 C1887 G1888 A1889
A1890 G1899 A1900 A1901 C1902 G1906 U1911 A1912 A1913 C1914 U1915 A1916 U1917 A1918 A1919 G1929 G1930 U1931 A1932 G1933 A1936 A1937 A1938 U1939 C1942 A1952 U1955 G1959 C1962 U1963 C1967 G1968 A1969 A1970 A1971 A1972 G1973 C1983 G1984 C1990 U1991 G1992 U1993 C1996 G1997
A2001 G2002 C2006 U2011 G2012 A2013 A2014 U2017 G2018 A2019 A2020 C2021 U2022 G2023 A2030 A2031 G2032 A2033 C2036 C2040 C2043 G2049 C2050 A2051 C2055 G2056 A2060 G2061 A2062 C2063 C2064 C2065 C2066 G2069 U2074 U2075 U2079 U2086 G2087 G2090 U2099 G2100 G2101 U2102
C2103 C2104 C2105 G2106 C2107 C2108 U2109 G2110 C2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 C2123 G2124 G2125 A2126 G2127 C2128 C2129 U2130 G2131 U2132 G2133 A2134 A2135 C2136 C2137 C2138 C2139 C2140 G2141 C2142 C2143 U2144 C2145 C2146 G2147 G2148 G2149 U2150 G2151 G2152 G2153 G2154 G2155 G2156 G2157 A2158 G2159 G2160 C2161 G2162
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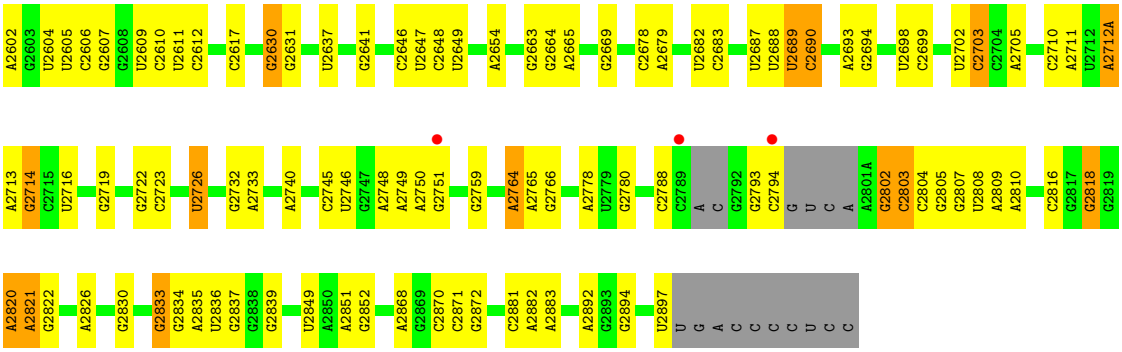
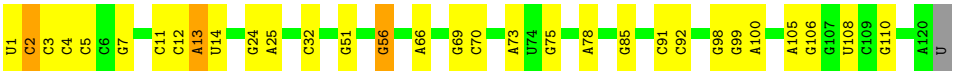


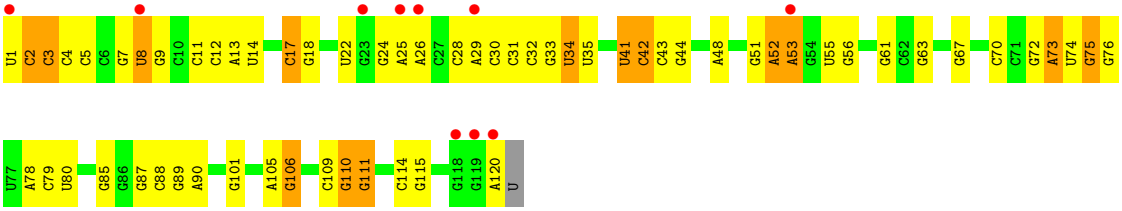
- Molecule 2: 5S Ribosomal RNA

Chain 1B:



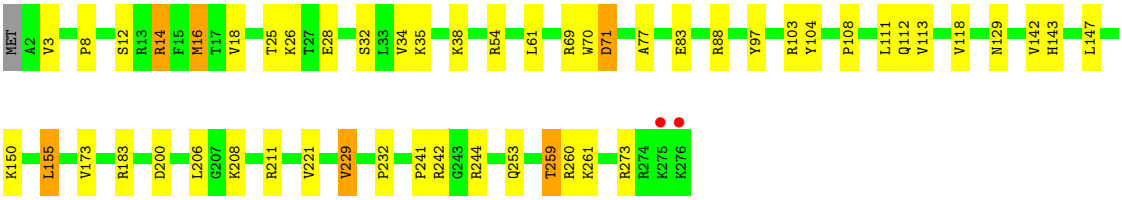
- Molecule 2: 5S Ribosomal RNA

Chain 2B:



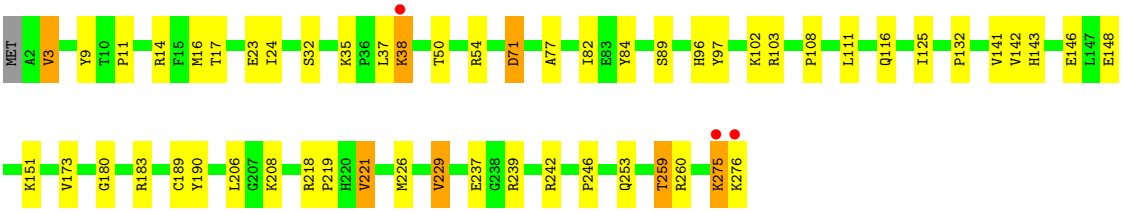
- Molecule 3: 50S ribosomal protein L2

Chain 1D:



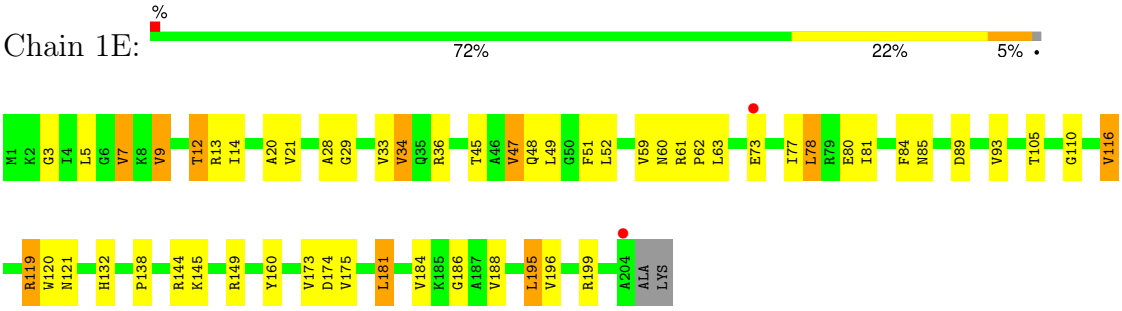
- Molecule 3: 50S ribosomal protein L2

Chain 2D:



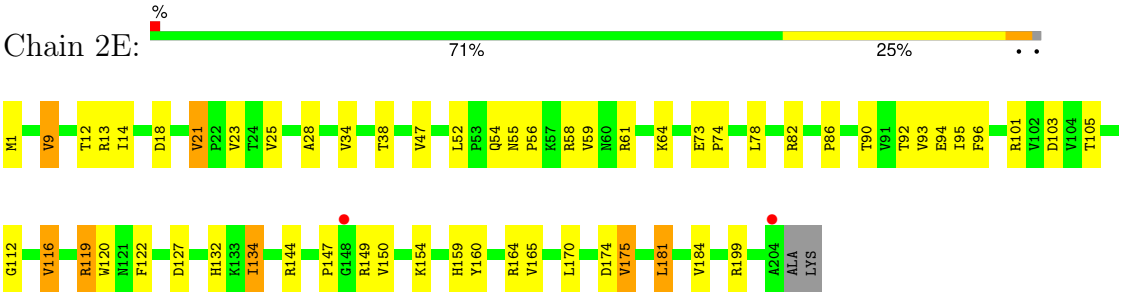
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



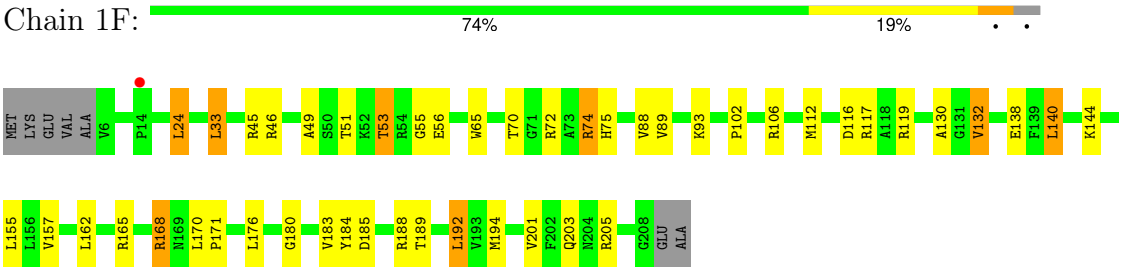
• Molecule 4: 50S ribosomal protein L3

Chain 2E:



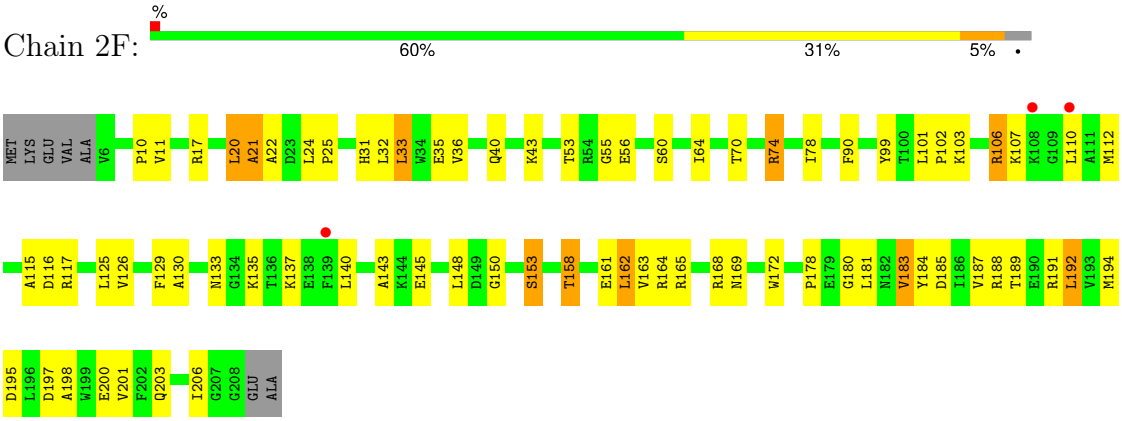
• Molecule 5: 50S ribosomal protein L4

Chain 1F:



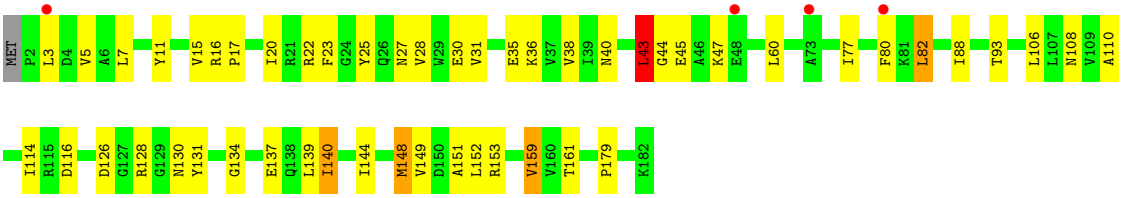
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



• Molecule 6: 50S ribosomal protein L5

Chain 1G:

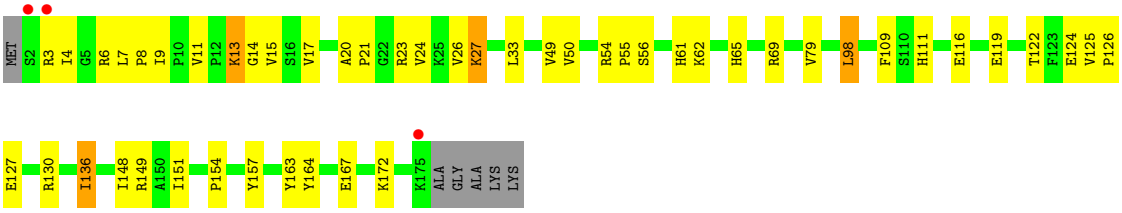


• Molecule 6: 50S ribosomal protein L5

Chain 2G:

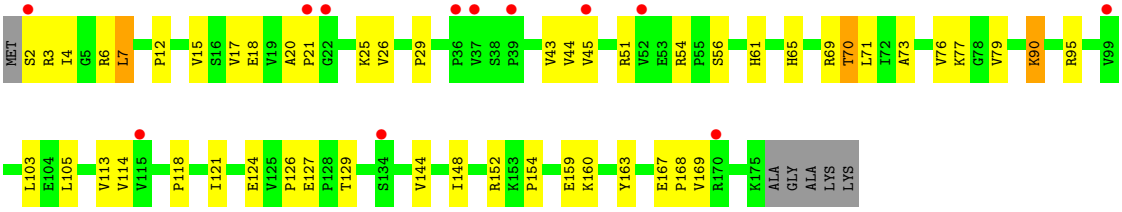
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



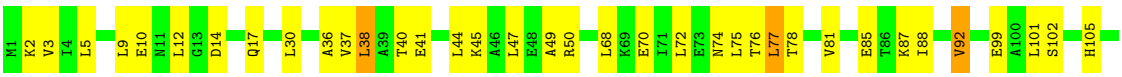
• Molecule 7: 50S ribosomal protein L6

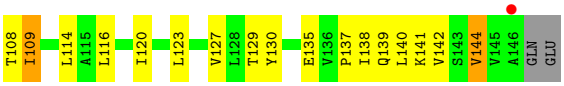
Chain 2H:



• Molecule 8: 50S ribosomal protein L9

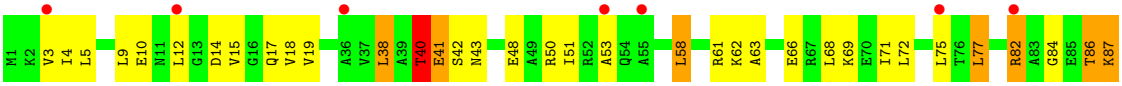
Chain 1I:





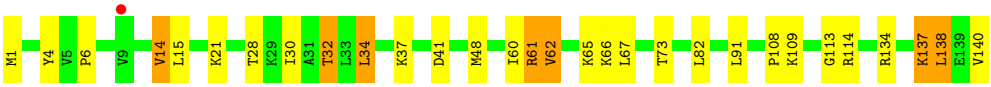
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



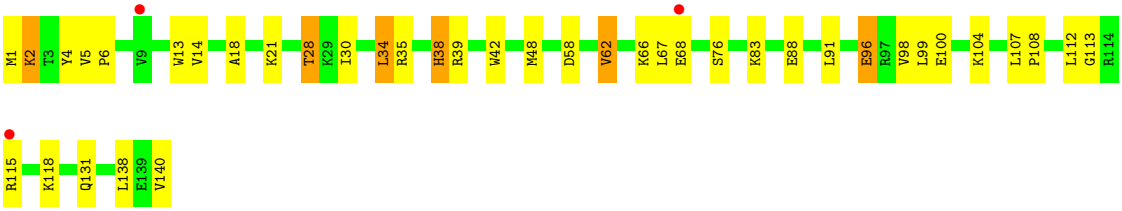
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



• Molecule 9: 50S ribosomal protein L13

Chain 2N:

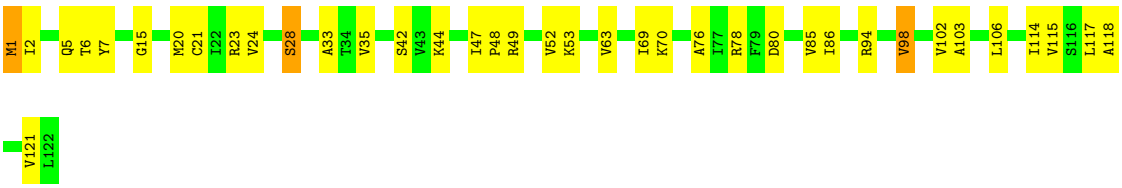


• Molecule 10: 50S ribosomal protein L14

Chain 1O:

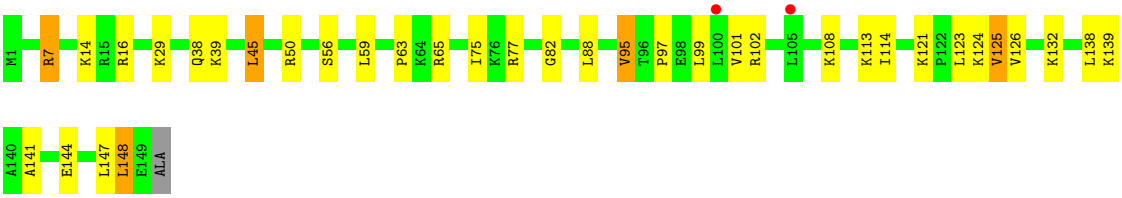
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



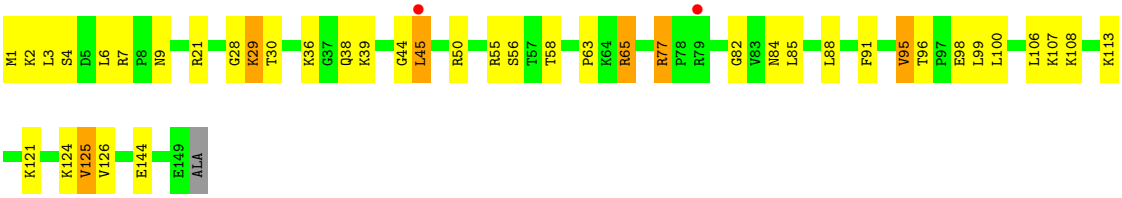
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



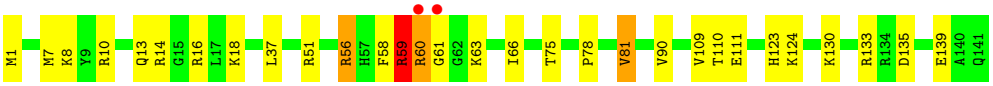
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



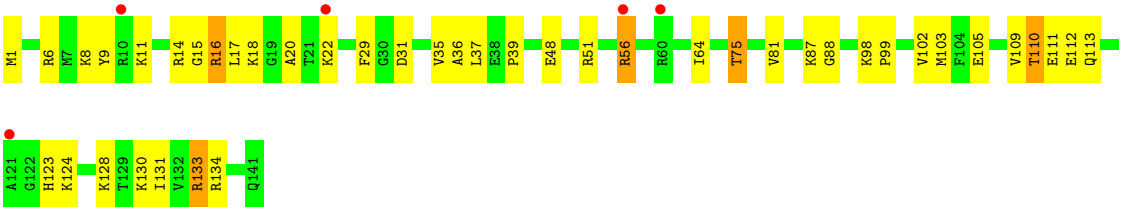
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



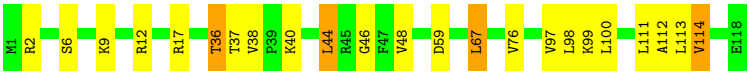
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



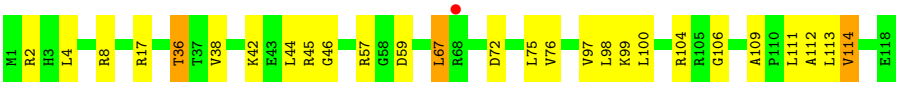
• Molecule 13: 50S ribosomal protein L17

Chain 1R:



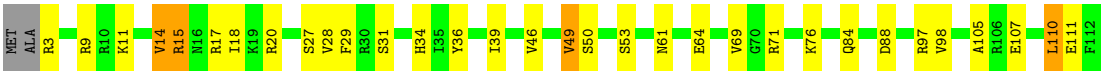
• Molecule 13: 50S ribosomal protein L17

Chain 2R:



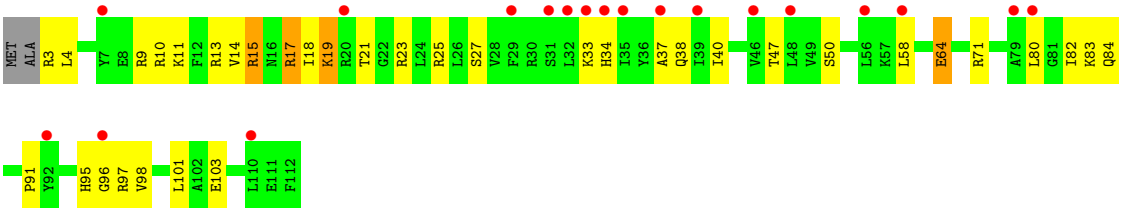
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



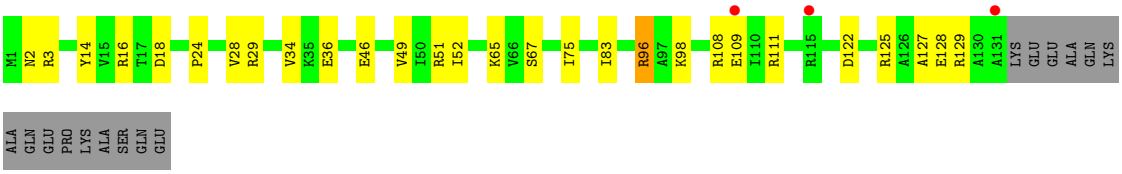
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



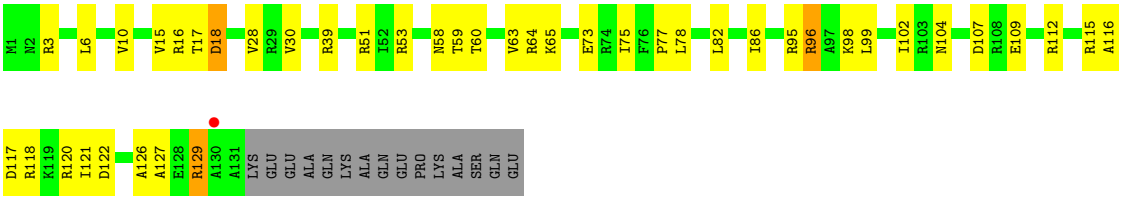
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



• Molecule 15: 50S ribosomal protein L19

Chain 2T:



• Molecule 16: 50S ribosomal protein L20

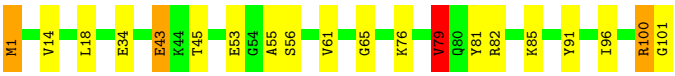
Chain 1U:

• Molecule 16: 50S ribosomal protein L20

Chain 2U:

• Molecule 17: 50S ribosomal protein L21

Chain 1V:

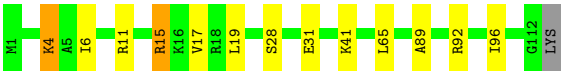


• Molecule 17: 50S ribosomal protein L21

Chain 2V:

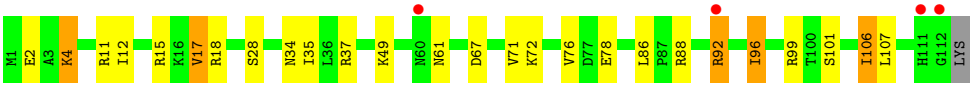
• Molecule 18: 50S ribosomal protein L22

Chain 1W:



• Molecule 18: 50S ribosomal protein L22

Chain 2W:



• Molecule 19: 50S ribosomal protein L23

Chain 1X:

• Molecule 19: 50S ribosomal protein L23

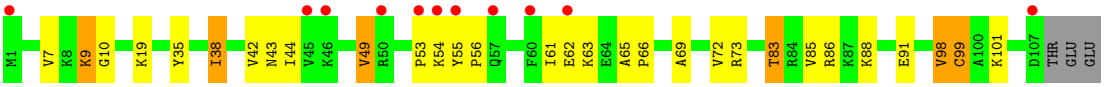
Chain 2X:

• Molecule 20: 50S ribosomal protein L24

Chain 1Y:

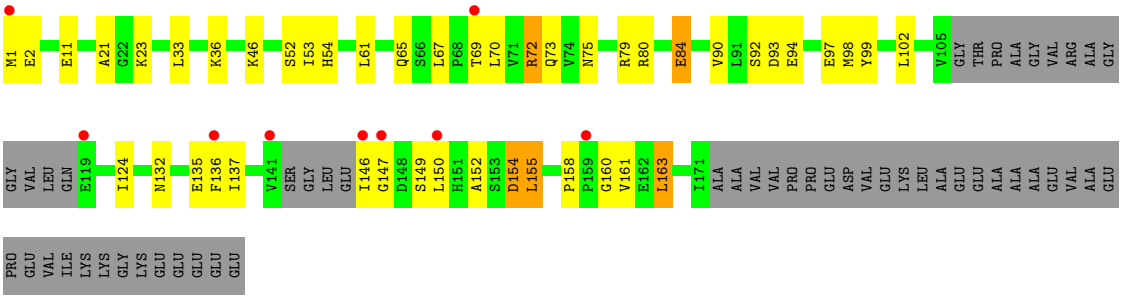
• Molecule 20: 50S ribosomal protein L24

Chain 2Y:



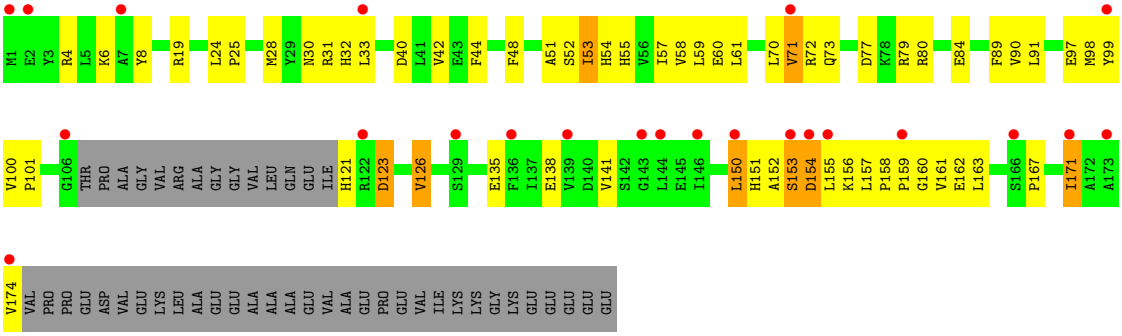
• Molecule 21: 50S ribosomal protein L25

Chain 1Z:



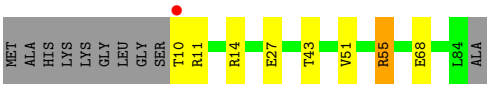
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



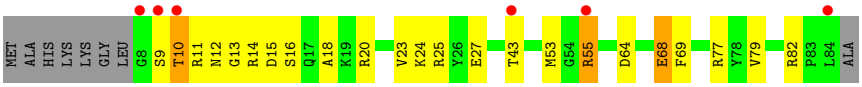
• Molecule 22: 50S ribosomal protein L27

Chain 10:



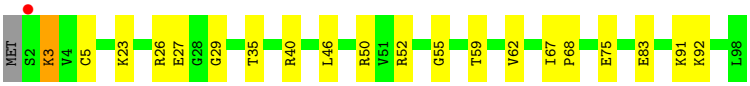
• Molecule 22: 50S ribosomal protein L27

Chain 20:



• Molecule 23: 50S ribosomal protein L28

Chain 11:

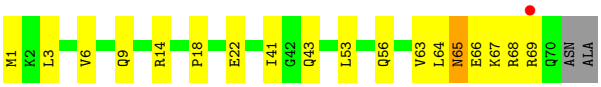


• Molecule 23: 50S ribosomal protein L28

Chain 21:

• Molecule 24: 50S ribosomal protein L29

Chain 12:

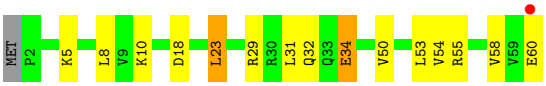


• Molecule 24: 50S ribosomal protein L29

Chain 22:

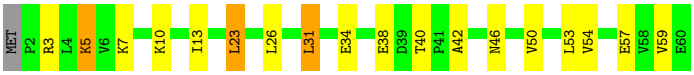
• Molecule 25: 50S ribosomal protein L30

Chain 13:



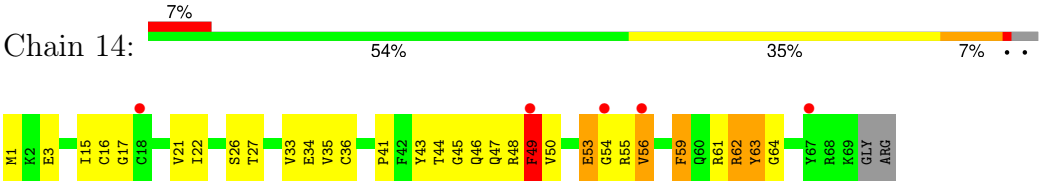
• Molecule 25: 50S ribosomal protein L30

Chain 23:



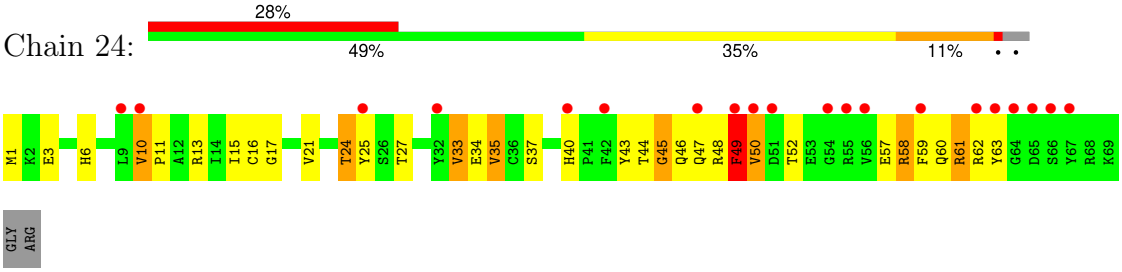
• Molecule 26: 50S ribosomal protein L31

Chain 14:



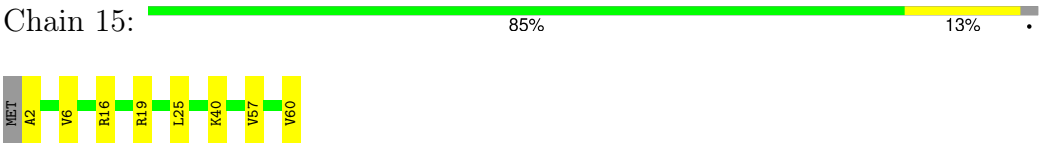
• Molecule 26: 50S ribosomal protein L31

Chain 24:



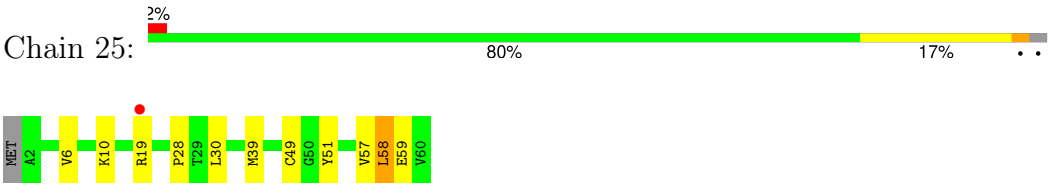
• Molecule 27: 50S ribosomal protein L32

Chain 15:



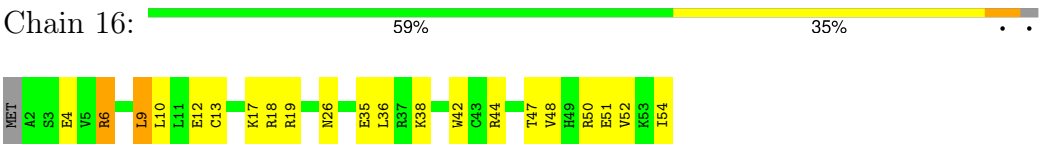
• Molecule 27: 50S ribosomal protein L32

Chain 25:



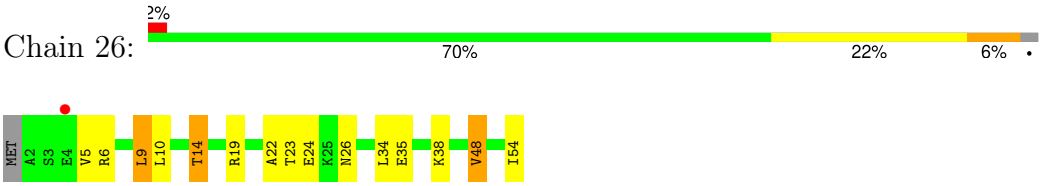
• Molecule 28: 50S ribosomal protein L33

Chain 16:



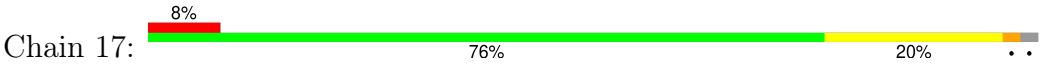
• Molecule 28: 50S ribosomal protein L33

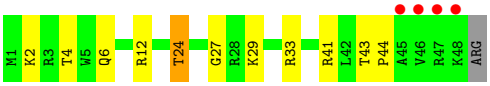
Chain 26:



• Molecule 29: 50S ribosomal protein L34

Chain 17:



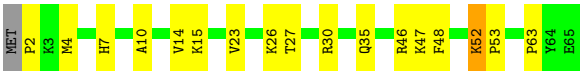


- Molecule 29: 50S ribosomal protein L34

Chain 27:

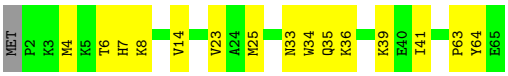
- Molecule 30: 50S ribosomal protein L35

Chain 18:



- Molecule 30: 50S ribosomal protein L35

Chain 28:

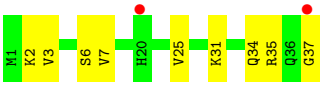


- Molecule 31: 50S ribosomal protein L36

Chain 19:

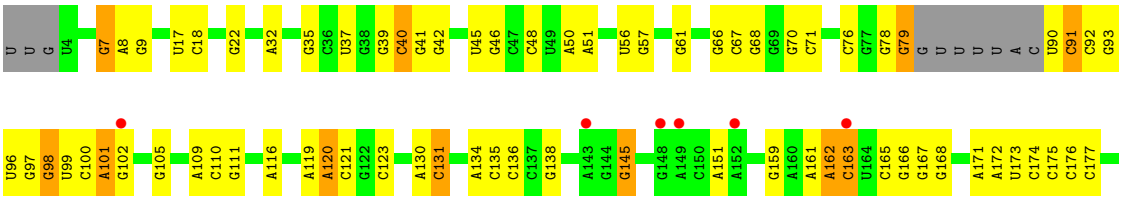
- Molecule 31: 50S ribosomal protein L36

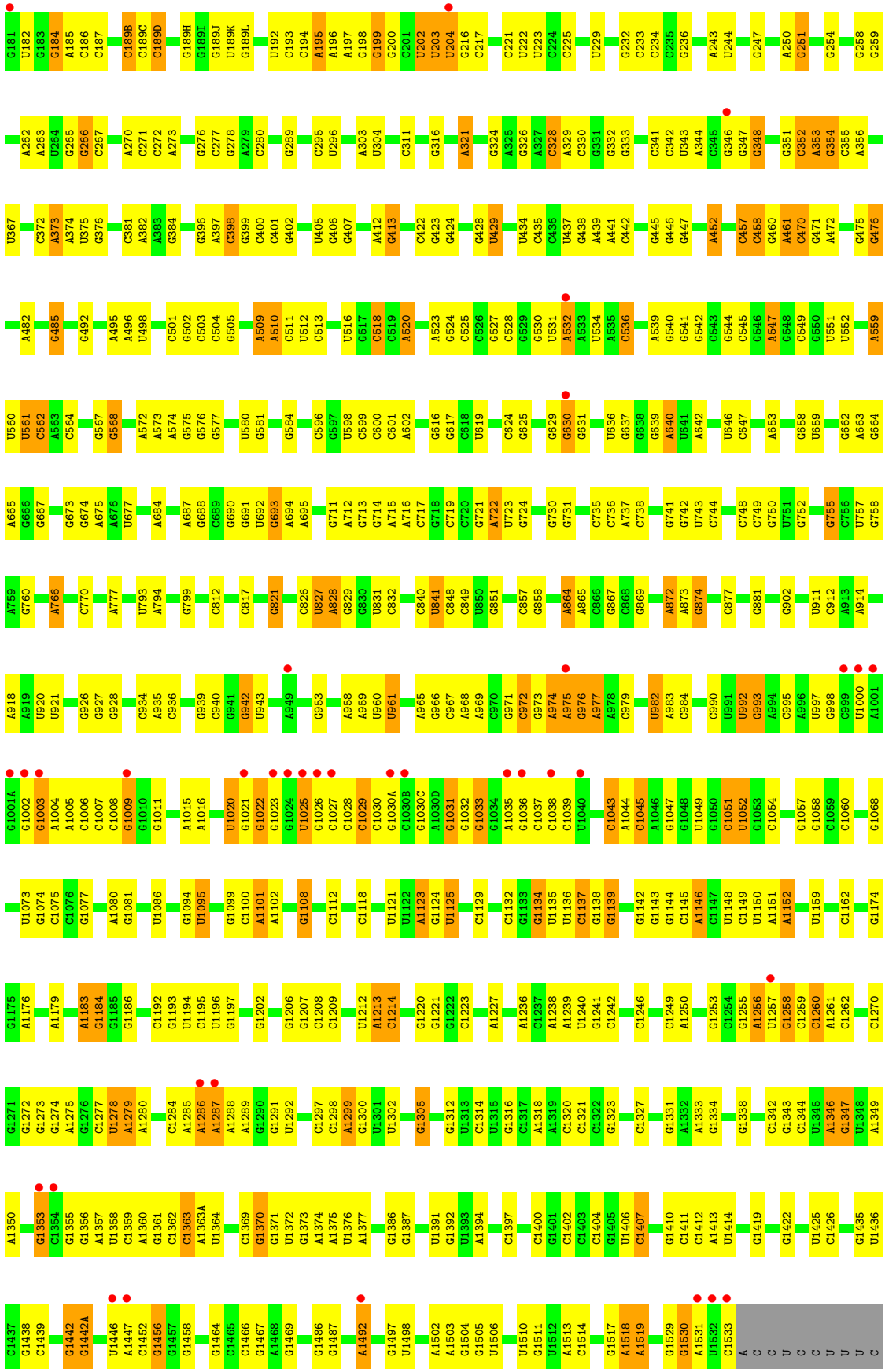
Chain 29:



- Molecule 32: 16S Ribosomal RNA

Chain 1a:

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A262 A263 U264 G265 G266 C267 A270 C271 C272 A273 G276 C277 G278 A279 C280 G289 C295 U296 A303 U304 C311 G316 A321 G324 A325 G326 A327 C328 A329 C330 G331 G332 G333 C341 C342 U343 A344 C345 G346 G347 G348 G351 C352 A353 G354 C355 A356
U367 C372 A373 A374 U375 G376 C381 A382 A383 G384 G396 A397 C398 G399 C400 C401 G402 U405 G406 G407 A412 G413 C422 G423 G424 C428 U429 U434 C435 C436 U437 G438 A439 A441 C442 G445 G446 G447 A452 C457 G458 G460 A461 C470 G471 A472 G475 G476
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U560 U561 C562 A563 C564 G567 G568 A572 A573 A574 G575 G576 G577 U580 G581 G584 C596 G597 U598 C599 C600 C601 A602 G616 G617 C618 U619 C624 G625 G629 G630 G631 U636 G637 G638 G639 A640 U641 A642 U646 C647 A653 G658 U659 G662 A663 G664
A665 G666 G667 G673 G674 A675 A676 U677 A684 A687 G688 C689 G690 G691 U692 G693 A694 A695 G711 A712 G713 G714 A715 A716 C717 G718 C719 C720 G721 A722 U723 G724 G730 G731 C735 C736 A737 C738 G741 G742 U743 C744 C748 C749 G750 U751 G752 G755 C756 U757 G758
A759 G760 A766 C770 A777 U793 A794 G799 C812 C817 G821 C826 U827 A828 G829 G830 U831 C832 C840 U841 C848 C849 U850 G851 C857 G858 A864 A865 C866 G867 C868 G869 A872 A873 G874 C877 G881 G902 U911 C912 A913 A914
A918 A919 U920 U921 G926 G927 G928 C934 A935 C936 G939 C940 G941 G942 U943 A949 G953 A958 A959 U960 U961 A965 G966 C967 A968 A969 C970 G971 G972 G973 A974 A975 G976 A977 A978 C979 U982 A983 C984 C990 U991 U992 G993 A994 C995 A996 U997 G998 C999 U1000 A1001
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U1073 G1074 C1075 C1076 G1077 A1080 G1081 U1086 G1094 U1095 G1099 C1100 A1101 A1102 G1108 C1112 C1118 U1121 U1122 A1123 G1124 U1125 C1129 C1132 G1133 G1134 U1135 U1136 C1137 G1138 G1139 G1142 G1143 G1144 C1145 A1146 C1147 U1148 C1149 U1150 A1151 A1152 U1159 C1162 G1174
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C1437 G1438 C1439 G1442 G1442A U1446 A1447 C1452 G1456 G1457 G1458 G1464 C1465 C1466 G1467 A1468 G1469 G1486 G1487 A1492 G1497 U1498 A1502 A1503 G1504 G1505 U1506 U1510 G1511 U1512 A1513 C1514 G1517 A1518 A1519 G1529 G1530 A1531 U1532 C1533 A C C U C C U U U C

U

- Molecule 32: 16S Ribosomal RNA

Chain 2a: 4% 53% 37% 9%

U U U G U4 U5 G6 G7 A8 G9 G15 A16 U17 C18 G21 G22 A32 A33 C34 G35 C36 G39 C40 C41 G42 U45 G46 C47 C48 U49 A50 A51 C54 A55 U56 G57 G64 U65 G66 C67 G68 G73 G80 U U U U84 A88 C89 A101 G102

C103 G107 G108 A109 G113 A116 G117 C121 U125 G126 G129A A130 C131 C132 U133 A134 G144 G147 G148 A149 C150 G157 G158 G159 A162 C163 U164 C175 C176 C177 U182 C187 C189A C189B C189C C189D U189E U189F U189K G189L U190 G191 U192 C193 C194

A195 A196 C201 U202 U203 U204 G216 C217 U222 U223 C224 C225 G231 C245 A246 A247 G251 U252 G259 G260 U261 A262 A263 G266 C267 C268 C280 G281 A282 C283 G289 G297 A298 G299 A300 G301 G302 A303 U304 G305 G306 G316 A321 G324 A325 G326 A327

C328 A329 C330 G331 G332 A349 G350 G351 C352 A353 G354 U367 C372 A373 G376 G377 G384 G388 A389 C390 A397 C398 C401 U404 U405 G406 G407 A408 G409 G410 A411 A412 C418 U421 C422 G423 G424 G425 G426 U427 G428 U429 A430 C433 U434 C435 C436 U437

G438 A439 A441 C442 C443 C444 G445 A448 A451 A452 C456 C457 C458 G460 A461 C470 G471 C483 G484 G485 G492 A496 U498 C501 G502 C503 C504 G505 A509 A510 C511 U512 C513 U516 G517 C518 A523 G524 C525 C526 G527 G530 U531 A532 A533 G537 G538 A539

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G750 A753 C754 G755 G756 U757 G758 A759 G763 A767 A768 G769 C770 A777 G785 A792 U793 A794 A807 C808 A814 A815 A816 C817 G818 G821 C824 G825 C826 U827 A828 G829 C834 U835 G836 G837 G838 U839 C840 U841 C848 G853 G854 G855 C856 C857 G858 A859

A860 U863 A864 A865 G869 A873 G881 G890 U891 A892 G902 G906 A913 A914 A915 A918 A919 U920 U921 G922 A923 C924 G925 G926 G927 C931 G932 G933 C934 A935 C936 A937 A938 G942 U943 G944 G945 A946 G947 C948 A949 U950 G951 U952 G953 A959 U960 U961

A965 G966 C967 A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 C979 C980 U981 U982 A983 C984 C985 G988 C989 C990 U991 U992 G993 A994 C995 A996 U997 G998 C999 U1000 A1001 G1001A G1002 G1003 A1004 A1005 C1006 C1007 C1008 G1009 G1010 G1011 U1012 G1013 A1014 A1015 A1016 G1017 C1018 C1019 U1020 G1021 G1022 G1023

G1024 U1025 G1026 C1027 C1028 C1029 C1030 G1030A C1030B G1030C A1030D G1031 G1032 G1033 G1034 A1035 G1036 C1037 C1038 C1039 U1040 A1041 G1042 C1043 A1044 C1045 G1048 C1051 U1052 G1053 C1054 A1055 G1058 C1059 U1062 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 G1077 U1078 G1079 A1080 G1081 G1084 U1085 U1086

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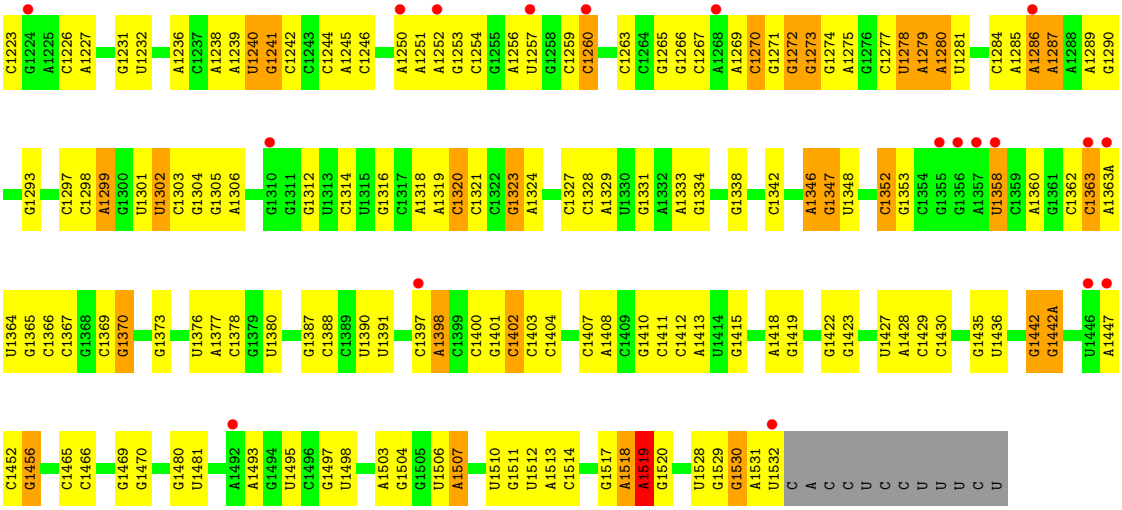
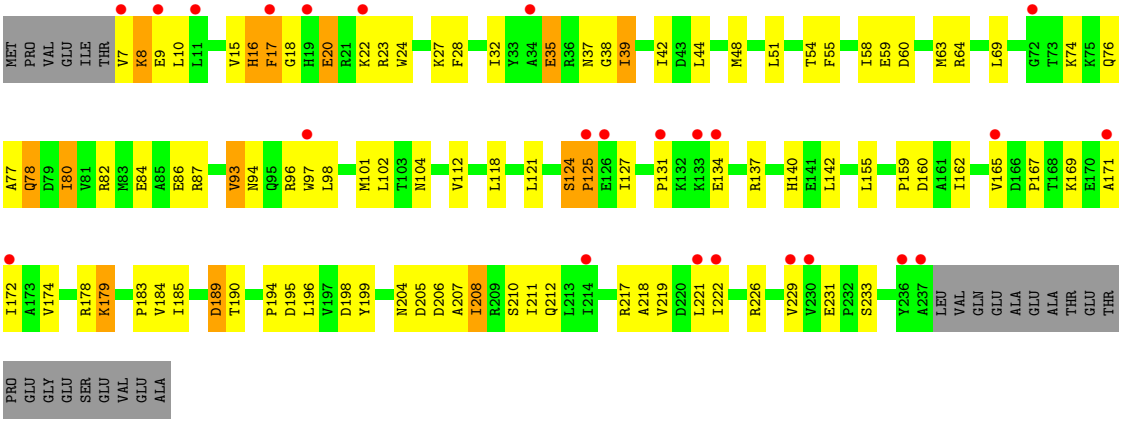
A1151 A1152 A1157 C1158 U1159 G1166 A1168 A1169 A1170 G1171 C1172 G1173 G1174 G1175 A1176 G1177 G1178 A1179 A1180 G1181 G1182 A1183 G1184 G1185 G1186 G1187 A1188 C1189 G1190 A1191 C1192 U1196 G1197 C1200 A1201 G1202 C1203 A1204 U1205 G1206 G1207 C1208 C1209 C1210 U1211 U1212 A1213 C1214 G1215 G1216 C1217 C1218 U1219 G1220 G1221 G1222



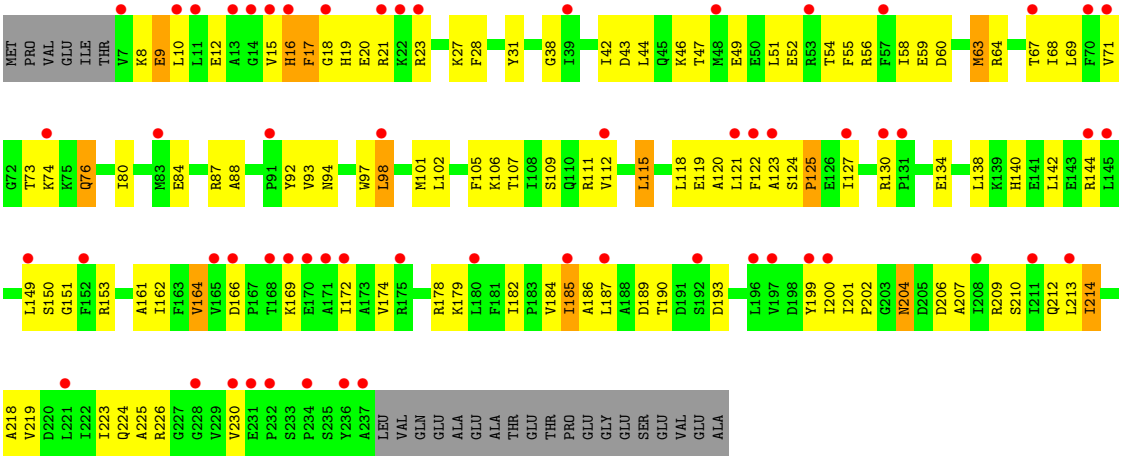
- Molecule 33: 30S ribosomal protein S2

Chain 1b:



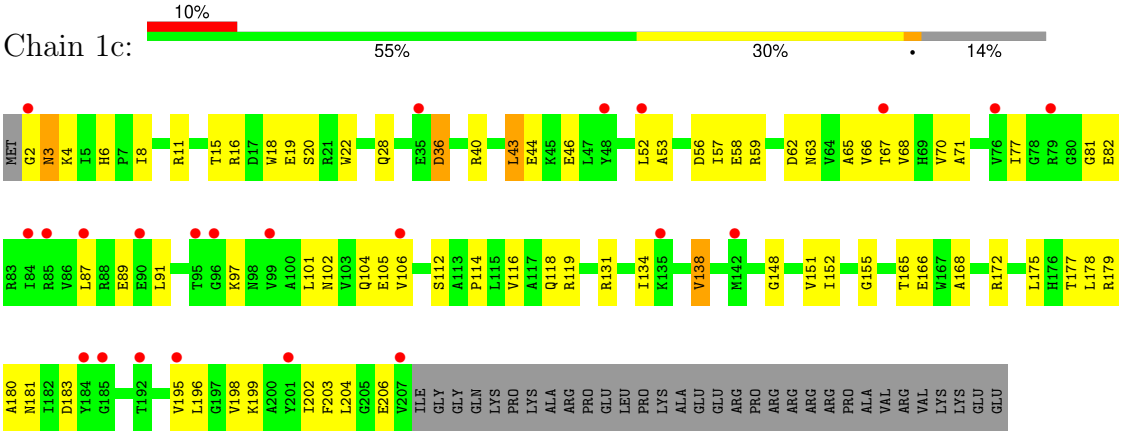
- Molecule 33: 30S ribosomal protein S2

Chain 2b:



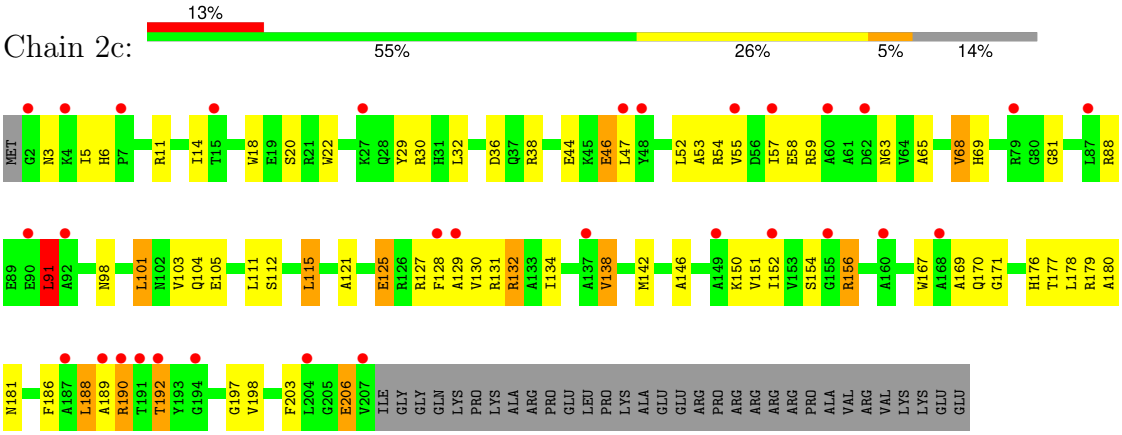
- Molecule 34: 30S ribosomal protein S3

Chain 1c:



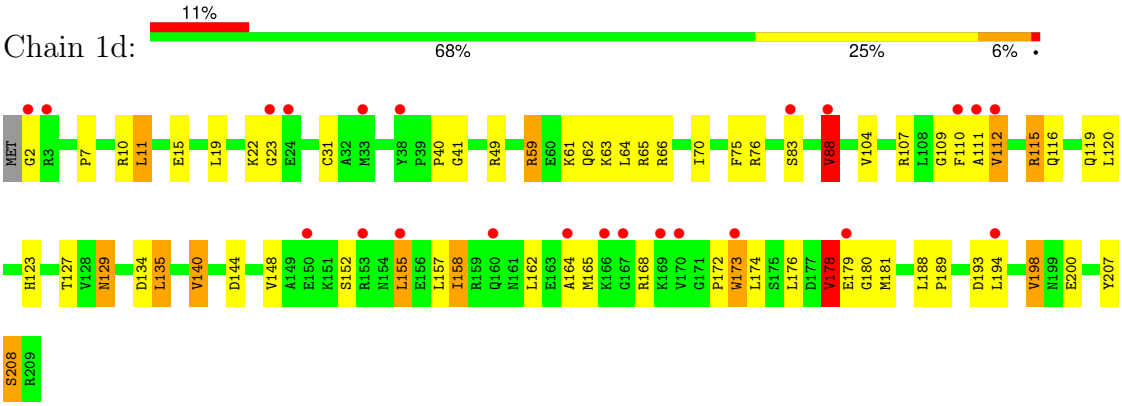
- Molecule 34: 30S ribosomal protein S3

Chain 2c:



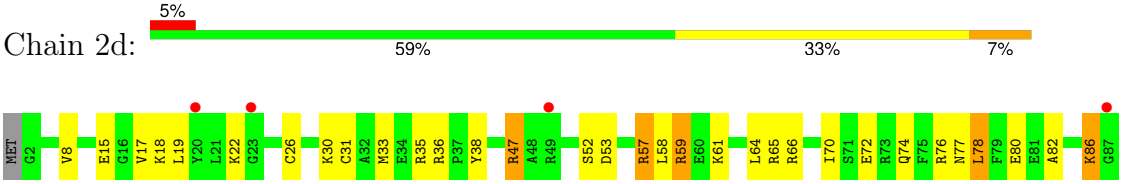
- Molecule 35: 30S ribosomal protein S4

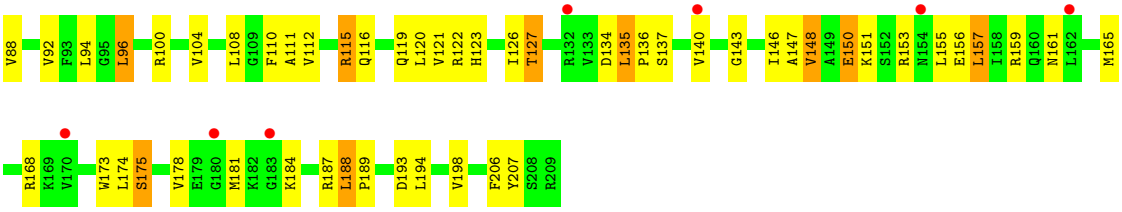
Chain 1d:



- Molecule 35: 30S ribosomal protein S4

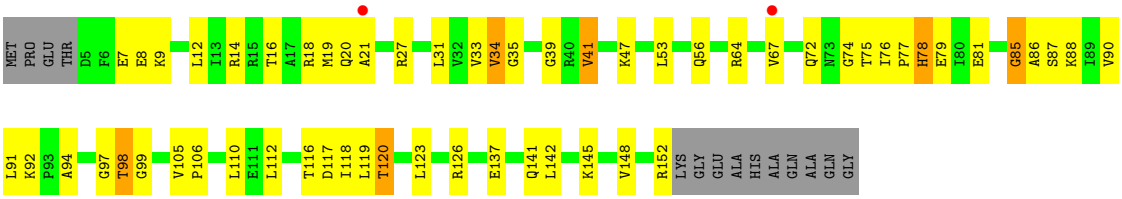
Chain 2d:





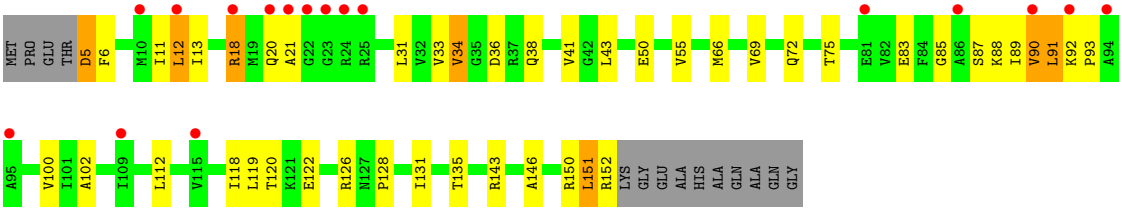
- Molecule 36: 30S ribosomal protein S5

Chain 1e:



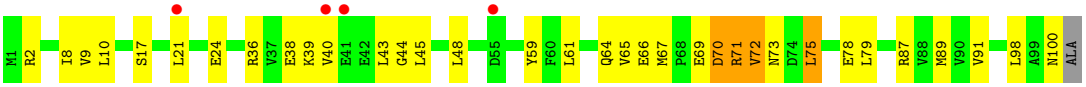
- Molecule 36: 30S ribosomal protein S5

Chain 2e:



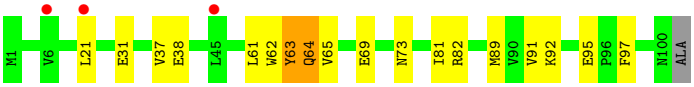
- Molecule 37: 30S ribosomal protein S6

Chain 1f:



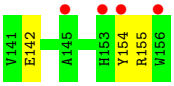
- Molecule 37: 30S ribosomal protein S6

Chain 2f:



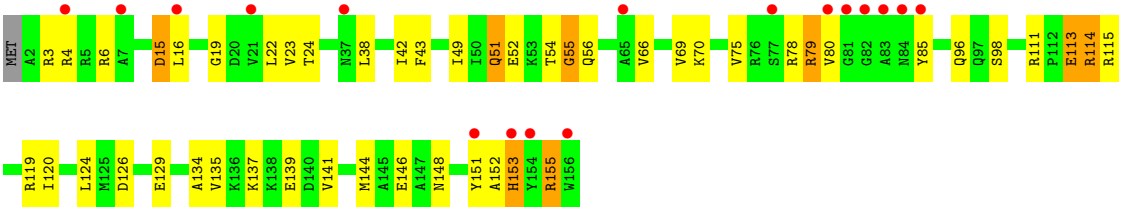
- Molecule 38: 30S ribosomal protein S7

Chain 1g:



• Molecule 38: 30S ribosomal protein S7

Chain 2g:

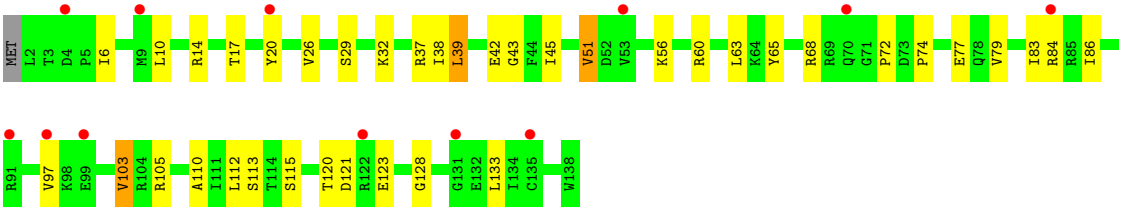


• Molecule 39: 30S ribosomal protein S8

Chain 1h:

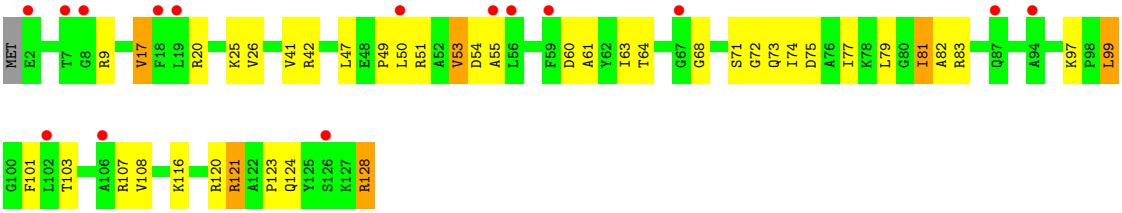
• Molecule 39: 30S ribosomal protein S8

Chain 2h:



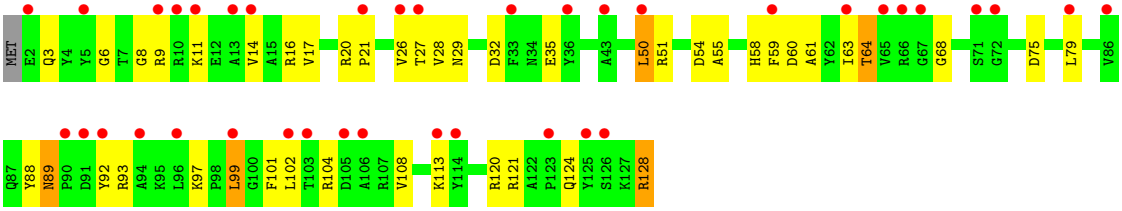
• Molecule 40: 30S ribosomal protein S9

Chain 1i:



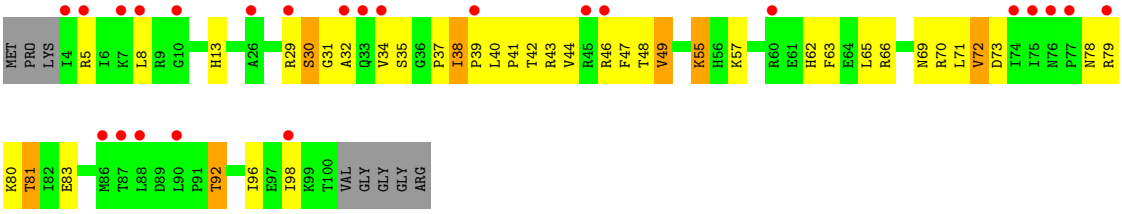
• Molecule 40: 30S ribosomal protein S9

Chain 2i:



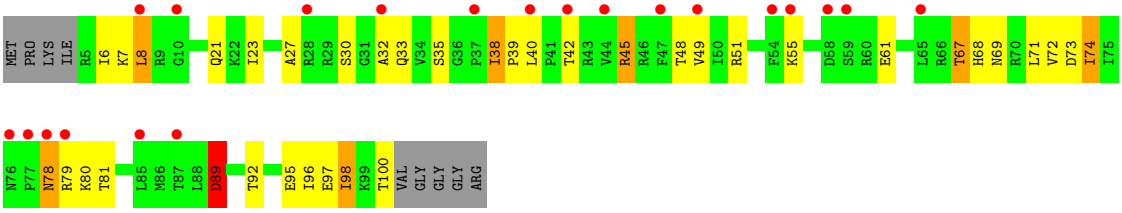
- Molecule 41: 30S ribosomal protein S10

Chain 1j:



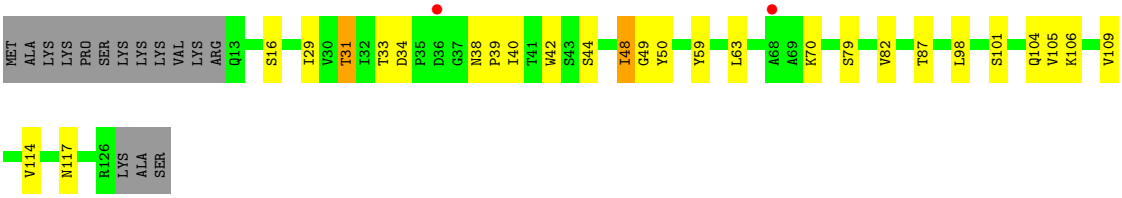
- Molecule 41: 30S ribosomal protein S10

Chain 2j:



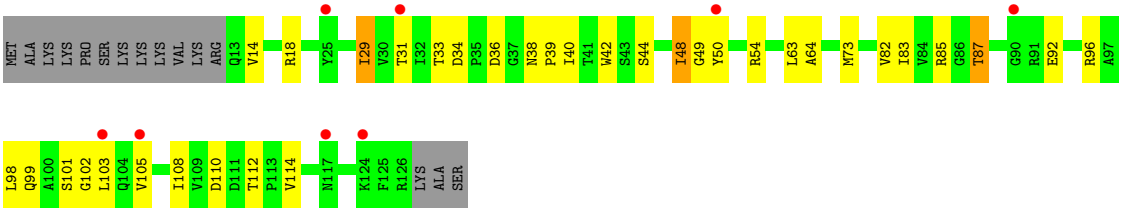
- Molecule 42: 30S ribosomal protein S11

Chain 1k:



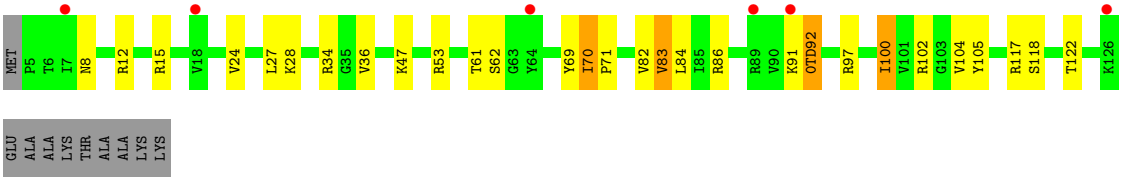
- Molecule 42: 30S ribosomal protein S11

Chain 2k:



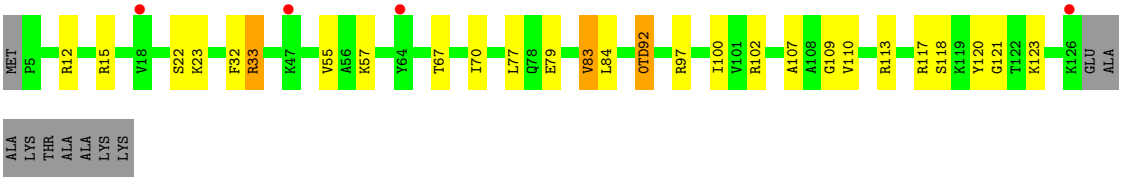
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



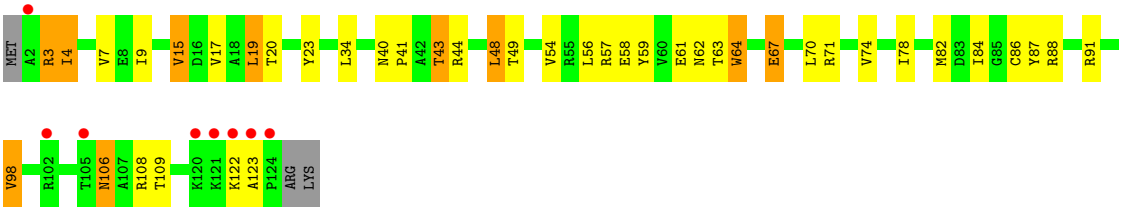
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



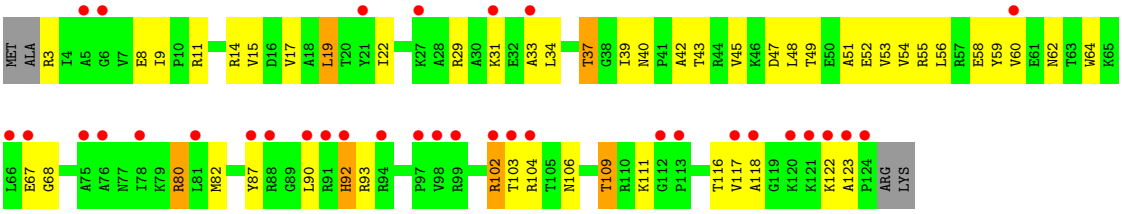
• Molecule 44: 30S ribosomal protein S13

Chain 1m:



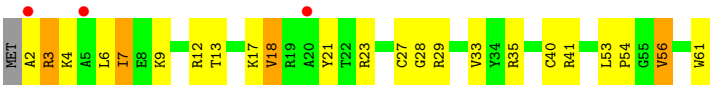
• Molecule 44: 30S ribosomal protein S13

Chain 2m:



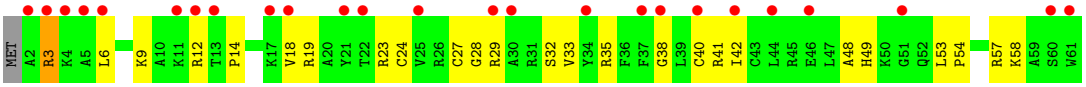
• Molecule 45: 30S ribosomal protein S14 type Z

Chain 1n:



• Molecule 45: 30S ribosomal protein S14 type Z

Chain 2n:

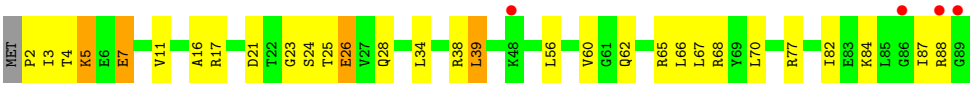


- Molecule 46: 30S ribosomal protein S15

Chain 1o:

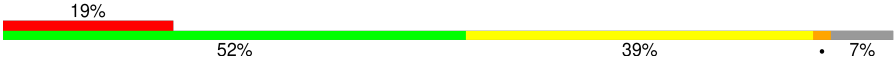
- Molecule 46: 30S ribosomal protein S15

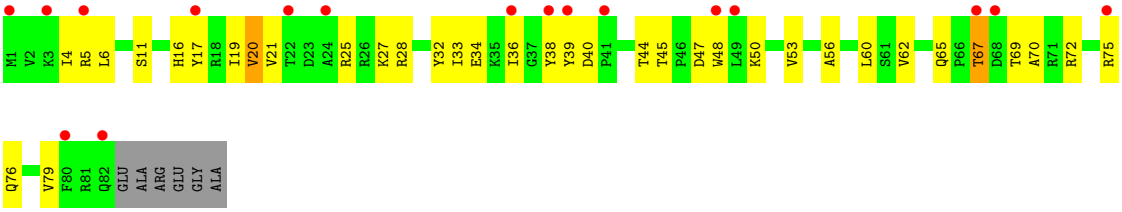
Chain 2o:



- Molecule 47: 30S ribosomal protein S16

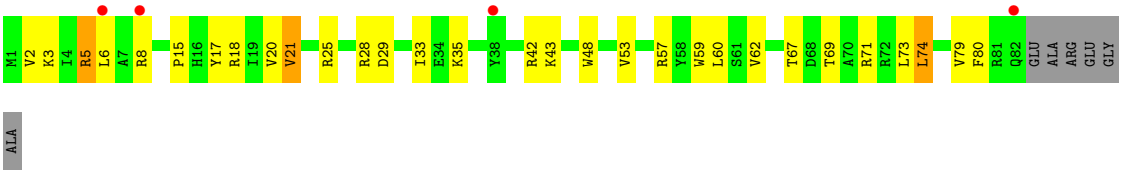
Chain 1p:





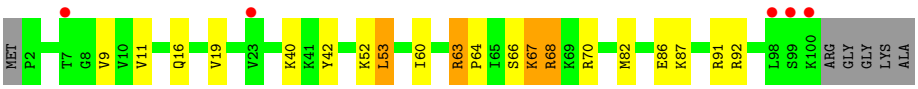
- Molecule 47: 30S ribosomal protein S16

Chain 2p:



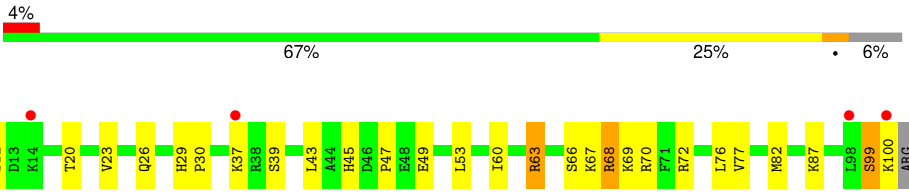
- Molecule 48: 30S ribosomal protein S17

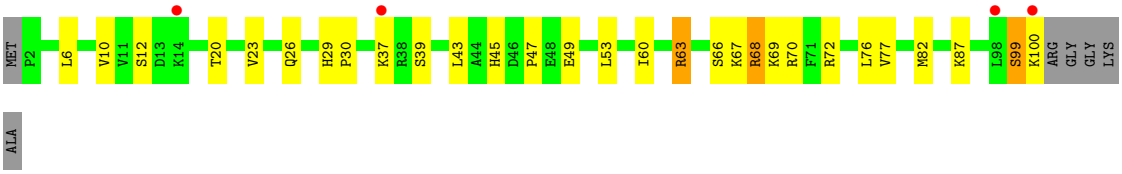
Chain 1q:



- Molecule 48: 30S ribosomal protein S17

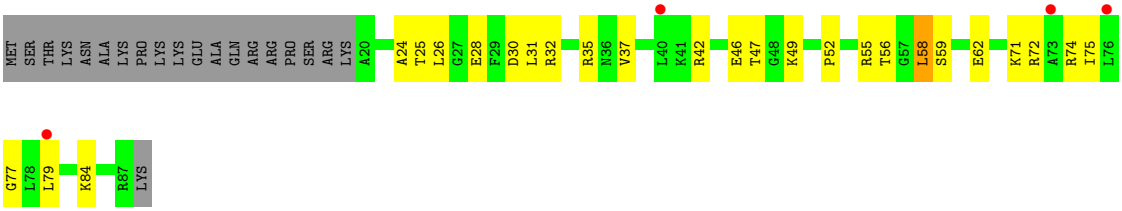
Chain 2q:





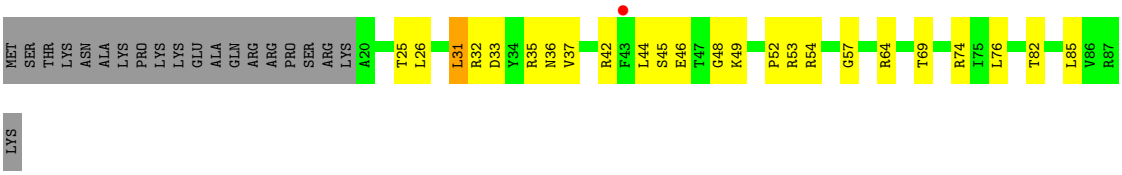
- Molecule 49: 30S ribosomal protein S18

Chain 1r:



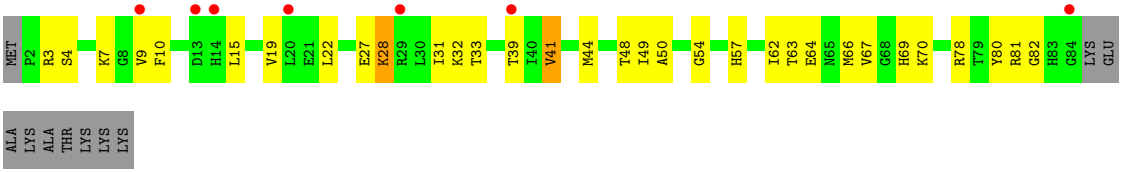
- Molecule 49: 30S ribosomal protein S18

Chain 2r:



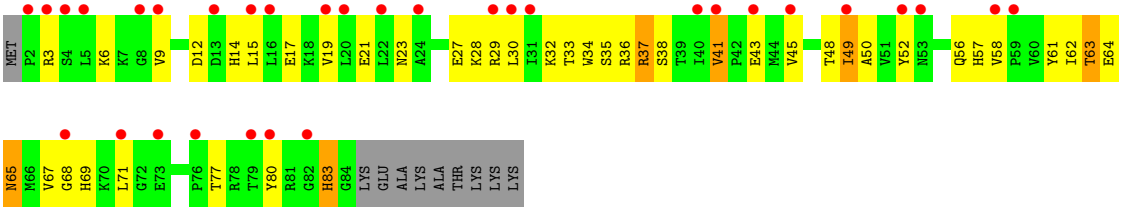
- Molecule 50: 30S ribosomal protein S19

Chain 1s:



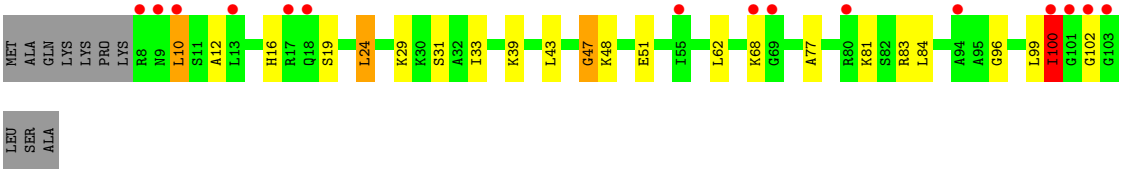
- Molecule 50: 30S ribosomal protein S19

Chain 2s:



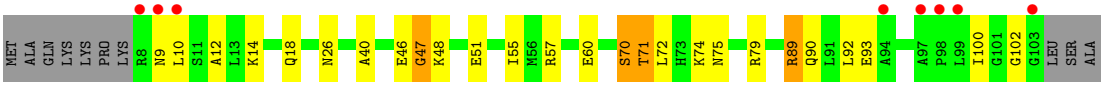
- Molecule 51: 30S ribosomal protein S20

Chain 1t:



- Molecule 51: 30S ribosomal protein S20

Chain 2t:

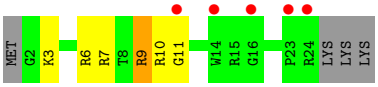


- Molecule 52: 30S ribosomal protein Thx

Chain 1u:

- Molecule 52: 30S ribosomal protein Thx

Chain 2u:



- Molecule 53: M-Stop-mRNA

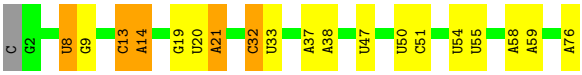
Chain 1v:

- Molecule 53: M-Stop-mRNA

Chain 2v:

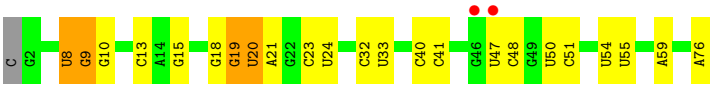
- Molecule 54: P-site deacylated tRNAmet

Chain 1x:



• Molecule 54: P-site deacylated tRNAmet

Chain 2x:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	209.51Å 449.73Å 622.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	155.54 – 2.70 155.54 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.8 (155.54-2.70) 96.8 (155.54-2.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.18 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.17.1	Depositor
R, R_{free}	0.209 , 0.257 0.207 , 0.253	Depositor DCC
R_{free} test set	77099 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	56.8	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 67.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	292790	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.73% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, UR3, 4OC, OMU, 2MG, 5MC, M2G, 4SU, G7M, 0TD, SF4, MA6, OMC, T8B, PSU, OMG, 5MU, K, ZN, 2MA

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	0.30	1/69011 (0.0%)	0.47	1/107720 (0.0%)
1	2A	0.23	0/67295	0.42	1/105042 (0.0%)
2	1B	0.23	0/2882	0.41	0/4494
2	2B	0.21	0/2879	0.39	0/4487
3	1D	0.29	0/2186	0.51	0/2944
3	2D	0.24	0/2186	0.48	0/2944
4	1E	0.27	0/1592	0.50	0/2149
4	2E	0.23	0/1592	0.45	0/2149
5	1F	0.28	0/1619	0.50	0/2193
5	2F	0.22	0/1615	0.46	2/2188 (0.1%)
6	1G	0.22	0/1448	0.43	0/1957
6	2G	0.21	0/1453	0.45	0/1963
7	1H	0.23	0/1356	0.45	0/1834
7	2H	0.21	0/1356	0.40	0/1834
8	1I	0.20	0/1112	0.42	0/1514
8	2I	0.20	0/1079	0.43	0/1475
9	1N	0.25	0/1144	0.47	0/1543
9	2N	0.21	0/1144	0.39	0/1543
10	1O	0.27	0/943	0.46	0/1269
10	2O	0.22	0/943	0.46	0/1269
11	1P	0.25	0/1152	0.50	0/1533
11	2P	0.24	0/1152	0.53	0/1533
12	1Q	0.30	0/1143	0.51	0/1527
12	2Q	0.22	0/1143	0.45	0/1527
13	1R	0.27	0/982	0.50	0/1312
13	2R	0.21	0/982	0.47	0/1312
14	1S	0.22	0/883	0.47	0/1176
14	2S	0.24	0/880	0.46	0/1172
15	1T	0.25	0/1105	0.50	0/1477
15	2T	0.22	0/1097	0.43	0/1468
16	1U	0.30	0/977	0.47	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.21	0/977	0.39	0/1301
17	1V	0.24	0/782	0.47	0/1049
17	2V	0.19	0/782	0.39	0/1049
18	1W	0.29	0/897	0.47	0/1205
18	2W	0.23	0/897	0.40	0/1205
19	1X	0.26	0/764	0.50	2/1025 (0.2%)
19	2X	0.21	0/764	0.49	2/1025 (0.2%)
20	1Y	0.23	0/819	0.46	0/1095
20	2Y	0.21	0/819	0.46	0/1095
21	1Z	0.24	0/1267	0.49	0/1717
21	2Z	0.25	0/1299	0.44	0/1763
22	10	0.28	0/606	0.57	0/808
22	20	0.21	0/616	0.46	0/821
23	11	0.27	0/762	0.46	0/1014
23	21	0.26	0/762	0.44	0/1014
24	12	0.25	0/590	0.46	0/781
24	22	0.20	0/590	0.36	0/781
25	13	0.29	0/474	0.49	0/635
25	23	0.19	0/469	0.45	0/630
26	14	0.26	0/565	0.56	0/761
26	24	0.26	0/545	0.55	0/737
27	15	0.26	0/469	0.47	0/635
27	25	0.23	0/469	0.46	0/635
28	16	0.28	0/460	0.50	0/613
28	26	0.22	0/456	0.44	0/608
29	17	0.33	0/426	0.54	0/561
29	27	0.25	0/426	0.50	0/561
30	18	0.28	0/525	0.51	0/691
30	28	0.21	0/525	0.41	0/691
31	19	0.26	0/310	0.50	0/407
31	29	0.21	0/310	0.45	0/407
32	1a	0.21	1/35795 (0.0%)	0.39	1/55864 (0.0%)
32	2a	0.20	0/35886	0.39	0/56005
33	1b	0.23	0/1881	0.51	1/2542 (0.0%)
33	2b	0.25	0/1860	0.51	0/2518
34	1c	0.20	0/1572	0.39	0/2126
34	2c	0.26	0/1566	0.46	0/2119
35	1d	0.22	0/1685	0.48	0/2262
35	2d	0.22	0/1704	0.44	0/2284
36	1e	0.22	0/1145	0.46	0/1543
36	2e	0.24	0/1149	0.45	0/1548
37	1f	0.21	0/823	0.41	0/1115
37	2f	0.20	0/829	0.42	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.20	0/1250	0.41	0/1679
38	2g	0.22	0/1254	0.42	0/1683
39	1h	0.19	0/1108	0.43	0/1494
39	2h	0.19	0/1108	0.41	0/1494
40	1i	0.23	0/1002	0.50	0/1346
40	2i	0.23	0/997	0.47	0/1343
41	1j	0.21	0/722	0.43	0/982
41	2j	0.23	0/727	0.44	0/988
42	1k	0.21	0/844	0.41	0/1145
42	2k	0.19	0/848	0.40	0/1149
43	1l	0.22	0/937	0.42	0/1260
43	2l	0.21	0/937	0.44	0/1260
44	1m	0.21	0/969	0.50	0/1302
44	2m	0.26	0/961	0.46	0/1291
45	1n	0.21	0/501	0.46	0/664
45	2n	0.21	0/501	0.41	0/664
46	1o	0.20	0/739	0.41	0/985
46	2o	0.20	0/739	0.38	0/985
47	1p	0.24	0/697	0.48	0/939
47	2p	0.20	0/693	0.45	0/935
48	1q	0.20	0/836	0.41	0/1117
48	2q	0.18	0/836	0.41	0/1117
49	1r	0.20	0/560	0.41	0/746
49	2r	0.21	0/560	0.40	0/746
50	1s	0.22	0/667	0.50	0/900
50	2s	0.26	0/661	0.56	0/893
51	1t	0.26	0/730	0.48	0/965
51	2t	0.21	0/729	0.43	0/965
52	1u	0.22	0/203	0.46	0/266
52	2u	0.20	0/203	0.44	0/266
53	1v	0.28	0/122	0.46	0/188
53	2v	0.24	0/122	0.46	0/188
54	1x	0.28	0/1725	0.42	0/2689
54	2x	0.24	0/1725	0.39	0/2689
All	All	0.24	2/309861 (0.0%)	0.44	10/463541 (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
26	24	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	2552	OMU	O3'-P	5.27	1.61	1.56
32	1a	527	G7M	O3'-P	5.23	1.61	1.56

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1992	G	C2'-C3'-O3'	6.68	119.52	109.50
33	1b	38	GLY	N-CA-C	-6.41	107.46	115.08
1	2A	1992	G	C2'-C3'-O3'	5.76	118.15	109.50
19	2X	94	GLY	CA-C-N	5.44	131.50	121.70
19	2X	94	GLY	C-N-CA	5.44	131.50	121.70
32	1a	266	G	C2'-C3'-O3'	5.34	117.51	109.50
19	1X	94	GLY	CA-C-N	5.33	131.30	121.70
19	1X	94	GLY	C-N-CA	5.33	131.30	121.70
5	2F	21	ALA	CA-C-N	5.11	130.90	121.70
5	2F	21	ALA	C-N-CA	5.11	130.90	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	24	61	ARG	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31195	547	0
1	2A	60322	0	30425	648	0
2	1B	2577	0	1305	18	0
2	2B	2575	0	1303	44	0
3	1D	2136	0	2218	34	0
3	2D	2136	0	2218	38	0
4	1E	1559	0	1618	35	0
4	2E	1559	0	1618	35	0
5	1F	1584	0	1625	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	2F	1580	0	1619	55	0
6	1G	1423	0	1436	26	0
6	2G	1428	0	1438	52	0
7	1H	1330	0	1407	25	0
7	2H	1330	0	1407	25	0
8	1I	1097	0	1140	25	0
8	2I	1064	0	1082	41	0
9	1N	1117	0	1184	17	0
9	2N	1117	0	1184	21	0
10	1O	933	0	996	15	0
10	2O	933	0	996	24	0
11	1P	1135	0	1212	24	0
11	2P	1135	0	1212	29	0
12	1Q	1122	0	1179	17	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	15	0
13	2R	968	0	1033	16	0
14	1S	873	0	927	17	0
14	2S	870	0	923	23	0
15	1T	1091	0	1151	17	0
15	2T	1083	0	1136	26	0
16	1U	959	0	1019	16	0
16	2U	959	0	1019	16	0
17	1V	771	0	830	9	0
17	2V	771	0	830	16	0
18	1W	886	0	940	6	0
18	2W	886	0	940	17	0
19	1X	750	0	814	10	0
19	2X	750	0	814	19	0
20	1Y	806	0	881	14	0
20	2Y	806	0	881	14	0
21	1Z	1240	0	1240	27	0
21	2Z	1271	0	1273	39	0
22	10	598	0	614	9	0
22	20	608	0	622	14	0
23	11	755	0	826	13	0
23	21	755	0	826	21	0
24	12	588	0	643	8	0
24	22	588	0	643	10	0
25	13	469	0	518	7	0
25	23	464	0	514	9	0
26	14	552	0	533	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	24	532	0	503	29	0
27	15	455	0	465	4	0
27	25	455	0	465	7	0
28	16	453	0	473	11	0
28	26	449	0	469	7	0
29	17	418	0	467	6	0
29	27	418	0	467	12	0
30	18	517	0	582	13	0
30	28	517	0	582	11	0
31	19	307	0	335	5	0
31	29	307	0	335	6	0
32	1a	32246	0	16294	406	0
32	2a	32327	0	16338	477	0
33	1b	1846	0	1867	59	0
33	2b	1825	0	1828	70	0
34	1c	1548	0	1535	44	0
34	2c	1542	0	1517	51	0
35	1d	1655	0	1672	48	0
35	2d	1674	0	1714	56	0
36	1e	1129	0	1185	33	0
36	2e	1133	0	1191	29	0
37	1f	810	0	804	19	0
37	2f	816	0	808	12	0
38	1g	1231	0	1238	21	0
38	2g	1235	0	1249	27	0
39	1h	1088	0	1126	29	0
39	2h	1088	0	1126	29	0
40	1i	983	0	986	26	0
40	2i	978	0	966	31	0
41	1j	709	0	650	27	0
41	2j	714	0	672	26	0
42	1k	829	0	825	13	0
42	2k	833	0	836	20	0
43	1l	932	0	981	20	0
43	2l	932	0	981	18	0
44	1m	958	0	1002	30	0
44	2m	950	0	988	36	0
45	1n	492	0	529	20	0
45	2n	492	0	529	18	0
46	1o	728	0	760	13	0
46	2o	728	0	760	20	0
47	1p	681	0	697	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	2p	677	0	686	24	0
48	1q	823	0	891	14	0
48	2q	823	0	891	15	0
49	1r	555	0	618	17	0
49	2r	555	0	618	11	0
50	1s	652	0	662	22	0
50	2s	646	0	644	43	0
51	1t	728	0	798	16	0
51	2t	727	0	796	18	0
52	1u	199	0	208	5	0
52	2u	199	0	208	8	0
53	1v	109	0	55	1	0
53	2v	109	0	55	1	0
54	1x	1625	0	829	9	0
54	2x	1625	0	829	10	0
55	10	7	0	0	0	0
55	11	4	0	0	0	0
55	12	2	0	0	0	0
55	13	3	0	0	0	0
55	14	1	0	0	0	0
55	15	7	0	0	0	0
55	16	1	0	0	0	0
55	17	6	0	0	0	0
55	18	8	0	0	0	0
55	1A	1052	0	0	0	0
55	1B	38	0	0	0	0
55	1D	11	0	0	0	0
55	1E	13	0	0	0	0
55	1F	11	0	0	0	0
55	1G	5	0	0	0	0
55	1I	1	0	0	0	0
55	1N	6	0	0	0	0
55	1O	5	0	0	0	0
55	1P	6	0	0	0	0
55	1Q	7	0	0	0	0
55	1R	5	0	0	0	0
55	1S	3	0	0	0	0
55	1T	2	0	0	0	0
55	1U	13	0	0	0	0
55	1V	8	0	0	0	0
55	1W	7	0	0	0	0
55	1X	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	1Y	2	0	0	0	0
55	1Z	3	0	0	0	0
55	1a	198	0	0	0	0
55	1b	1	0	0	0	0
55	1d	1	0	0	0	0
55	1e	1	0	0	0	0
55	1f	1	0	0	0	0
55	1l	2	0	0	0	0
55	1m	2	0	0	0	0
55	1n	1	0	0	0	0
55	1p	1	0	0	0	0
55	1r	1	0	0	0	0
55	1t	1	0	0	0	0
55	1v	1	0	0	0	0
55	1x	15	0	0	0	0
55	20	1	0	0	0	0
55	21	1	0	0	0	0
55	23	1	0	0	0	0
55	25	1	0	0	0	0
55	27	3	0	0	0	0
55	28	3	0	0	0	0
55	2A	716	0	0	0	0
55	2B	17	0	0	0	0
55	2D	7	0	0	0	0
55	2E	6	0	0	0	0
55	2F	3	0	0	0	0
55	2G	1	0	0	0	0
55	2N	1	0	0	0	0
55	2O	1	0	0	0	0
55	2P	1	0	0	0	0
55	2Q	4	0	0	0	0
55	2R	2	0	0	0	0
55	2T	2	0	0	0	0
55	2U	1	0	0	0	0
55	2V	2	0	0	0	0
55	2W	3	0	0	0	0
55	2Y	1	0	0	0	0
55	2Z	1	0	0	0	0
55	2a	197	0	0	0	0
55	2e	1	0	0	0	0
55	2f	2	0	0	0	0
55	2j	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	2k	1	0	0	0	0
55	2l	4	0	0	0	0
55	2q	2	0	0	0	0
55	2r	1	0	0	0	0
55	2t	1	0	0	0	0
55	2x	5	0	0	0	0
56	1A	1	0	0	0	0
56	2A	1	0	0	0	0
57	1A	44	0	20	0	0
57	2A	44	0	20	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	0	0
59	2d	8	0	0	0	0
60	10	11	0	0	0	0
60	11	12	0	0	0	0
60	12	4	0	0	0	0
60	13	5	0	0	0	0
60	14	1	0	0	0	0
60	15	6	0	0	0	0
60	16	2	0	0	0	0
60	17	11	0	0	0	0
60	18	10	0	0	0	0
60	1A	2039	0	0	81	0
60	1B	63	0	0	1	0
60	1D	24	0	0	0	0
60	1E	27	0	0	3	0
60	1F	14	0	0	1	0
60	1G	2	0	0	0	0
60	1H	3	0	0	0	0
60	1I	1	0	0	0	0
60	1N	5	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1O	5	0	0	0	0
60	1P	21	0	0	0	0
60	1Q	7	0	0	0	0
60	1R	13	0	0	2	0
60	1S	4	0	0	0	0
60	1T	7	0	0	0	0
60	1U	13	0	0	0	0
60	1V	8	0	0	0	0
60	1W	8	0	0	1	0
60	1X	5	0	0	0	0
60	1Y	2	0	0	1	0
60	1Z	1	0	0	0	0
60	1a	297	0	0	15	0
60	1d	1	0	0	0	0
60	1e	1	0	0	0	0
60	1f	1	0	0	0	0
60	1g	1	0	0	0	0
60	1l	8	0	0	0	0
60	1m	1	0	0	0	0
60	1o	2	0	0	0	0
60	1p	1	0	0	0	0
60	1q	2	0	0	0	0
60	1v	3	0	0	0	0
60	1x	15	0	0	0	0
60	20	4	0	0	0	0
60	21	3	0	0	1	0
60	23	2	0	0	1	0
60	26	1	0	0	0	0
60	27	2	0	0	0	0
60	28	3	0	0	0	0
60	29	1	0	0	0	0
60	2A	971	0	0	87	0
60	2B	15	0	0	3	0
60	2D	18	0	0	1	0
60	2E	10	0	0	1	0
60	2F	11	0	0	0	0
60	2N	3	0	0	0	0
60	2O	2	0	0	0	0
60	2P	11	0	0	0	0
60	2Q	2	0	0	0	0
60	2R	3	0	0	0	0
60	2T	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	2U	2	0	0	0	0
60	2V	1	0	0	0	0
60	2W	3	0	0	0	0
60	2X	4	0	0	0	0
60	2Z	1	0	0	0	0
60	2a	176	0	0	8	0
60	2c	1	0	0	0	0
60	2d	1	0	0	0	0
60	2e	1	0	0	0	0
60	2f	1	0	0	0	0
60	2j	2	0	0	0	0
60	2l	2	0	0	1	0
60	2n	1	0	0	0	0
60	2p	3	0	0	0	0
60	2q	2	0	0	1	0
60	2r	3	0	0	0	0
60	2t	6	0	0	2	0
60	2v	1	0	0	0	0
60	2x	3	0	0	0	0
All	All	292790	0	193244	3779	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 8.

All (3779) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1082:U:H3	1:1A:1086:A:N6	1.30	1.28
1:2A:2136:C:N4	1:2A:2155:G:H1	1.49	1.10
32:2a:1133:G:H1	32:2a:1141:C:N4	1.52	1.07
32:2a:1002:G:H1	32:2a:1038:C:N4	1.52	1.05
1:2A:2138:C:N4	1:2A:2153:G:H1	1.61	0.99
1:1A:1082:U:O4	1:1A:1086:A:N1	1.96	0.98
1:2A:2136:C:H42	1:2A:2155:G:H1	1.03	0.95
1:1A:1057:A:H61	1:1A:1081:U:H3	1.14	0.95
1:1A:2100:G:H1	1:1A:2189:U:H3	0.96	0.93
1:2A:2714:G:OP2	60:2A:3805:HOH:O	1.85	0.93
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.01	0.93
29:17:24:THR:HG22	29:17:27:GLY:H	1.33	0.92
1:2A:2104:G:H1	1:2A:2185:C:H42	1.12	0.92
25:23:13:ILE:O	60:23:201:HOH:O	1.87	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.52	0.91
33:2b:16:HIS:HB2	33:2b:204:ASN:HB3	1.50	0.90
1:1A:2427:C:OP1	60:1A:4105:HOH:O	1.88	0.89
1:2A:2137:C:N4	1:2A:2154:G:H1	1.70	0.89
1:2A:2589:A:OP1	60:2A:3806:HOH:O	1.90	0.89
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.55	0.88
1:2A:784:A:OP2	60:2A:3806:HOH:O	1.89	0.87
1:1A:1041:C:H42	1:1A:1114:G:H1	1.23	0.87
1:1A:1062:G:H1	1:1A:1077:A:H61	1.16	0.87
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.56	0.86
33:2b:52:GLU:HG3	33:2b:56:ARG:HH22	1.40	0.86
1:2A:783:A:OP2	60:2A:3806:HOH:O	1.93	0.86
1:2A:1187:G:OP2	60:2A:3807:HOH:O	1.94	0.84
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.10	0.84
1:2A:2712(A):A:OP2	60:2A:3805:HOH:O	1.95	0.83
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.59	0.83
1:2A:2136:C:N3	1:2A:2155:G:N2	2.26	0.83
1:2A:1689:A:H62	1:2A:1698:A:H2	1.26	0.83
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.61	0.83
1:1A:1670:C:OP2	60:1A:4106:HOH:O	1.96	0.82
32:2a:1002:G:N2	32:2a:1038:C:N3	2.28	0.82
1:2A:1041:C:O2	1:2A:1114:G:N2	2.12	0.82
1:1A:1865:G:OP1	60:1A:4107:HOH:O	1.97	0.82
1:1A:1993:U:OP2	60:1A:4108:HOH:O	1.97	0.82
1:1A:975(A):G:OP1	60:1A:4109:HOH:O	1.97	0.81
32:2a:1133:G:N2	32:2a:1141:C:N3	2.29	0.81
1:1A:1253:A:OP1	60:1A:4111:HOH:O	1.98	0.81
1:1A:1271:G:OP2	60:1A:4110:HOH:O	1.97	0.81
1:2A:1204:A:H2	1:2A:1241:A:H62	1.27	0.81
17:1V:55:ALA:HA	17:1V:101:GLY:HA2	1.61	0.81
1:1A:1082:U:N3	1:1A:1086:A:N6	2.04	0.81
1:2A:2134:A:H62	1:2A:2157:G:H4'	1.45	0.81
1:2A:2138:C:H42	1:2A:2153:G:H1	0.86	0.81
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.11	0.81
1:1A:1065:U:O2	1:1A:1073:A:N6	2.13	0.80
1:1A:1602:U:O4	60:1A:4113:HOH:O	1.99	0.80
1:2A:847:U:OP2	60:2A:3808:HOH:O	1.99	0.80
36:2e:122:GLU:O	36:2e:126:ARG:NH1	2.14	0.80
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.14	0.80
1:2A:988:A:N7	60:2A:3834:HOH:O	2.13	0.80
44:2m:40:ASN:HD22	44:2m:43:THR:HG23	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1603:A:OP1	60:1A:4114:HOH:O	2.00	0.80
1:1A:2499:C:OP1	60:1A:4112:HOH:O	1.98	0.80
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.14	0.80
42:2k:48:ILE:O	42:2k:50:TYR:N	2.15	0.80
8:2I:40:THR:OG1	8:2I:41:GLU:N	2.10	0.80
1:2A:2711:A:OP2	60:2A:3805:HOH:O	2.00	0.79
1:2A:500:G:N1	1:2A:503:A:OP2	2.15	0.79
1:1A:2448:A:OP1	60:1A:4112:HOH:O	2.00	0.79
1:1A:975(A):G:H5"	60:1A:4109:HOH:O	1.82	0.79
1:2A:846:C:O2'	60:2A:3809:HOH:O	2.00	0.79
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.16	0.79
32:2a:664:G:H22	32:2a:741:G:H1	1.31	0.79
1:1A:1058:G:H1	1:1A:1080:C:H42	1.31	0.78
1:1A:2096:U:H3	1:1A:2193:G:H1	1.32	0.78
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.65	0.78
1:2A:792:G:O6	60:2A:3810:HOH:O	2.02	0.78
32:2a:1252:A:H61	32:2a:1285:A:H61	1.30	0.78
2:2B:22:U:H3	2:2B:61:G:H1	1.32	0.78
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.65	0.78
1:2A:2104:G:H1	1:2A:2185:C:N4	1.82	0.77
1:2A:2345:G:H4'	1:2A:2346:A:H5"	1.64	0.77
1:1A:762:U:OP1	60:1A:4115:HOH:O	2.01	0.77
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.50	0.77
3:2D:275:LYS:HD2	3:2D:276:LYS:HB2	1.66	0.77
30:28:33:ASN:HA	30:28:36:LYS:HD2	1.67	0.77
32:1a:76:C:H42	32:1a:93:G:H1	1.33	0.77
40:2i:16:ARG:HB2	40:2i:64:THR:HG22	1.67	0.77
8:1I:75:LEU:HD22	8:1I:105:HIS:HD2	1.48	0.77
32:2a:737:A:H1'	37:2f:73:ASN:HD21	1.49	0.77
1:2A:2171:A:N3	1:2A:2172:U:N3	2.32	0.77
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.65	0.77
32:2a:1133:G:H1	32:2a:1141:C:H42	0.81	0.77
1:1A:11:G:H2'	1:1A:12:U:H5'	1.67	0.77
33:2b:88:ALA:HB2	33:2b:219:VAL:HG13	1.67	0.77
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.19	0.77
1:1A:2128:C:N3	1:1A:2160:G:N2	2.33	0.77
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.66	0.77
1:2A:962:G:OP1	60:2A:3811:HOH:O	2.02	0.76
32:2a:998:G:H1	32:2a:1043:C:H42	1.29	0.76
32:1a:1021:G:O2'	32:1a:1022:G:O5'	2.04	0.76
1:2A:89:G:H3'	1:2A:90:U:H5"	1.68	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1212:U:H5"	32:1a:1213:A:H5'	1.67	0.76
1:2A:2099:U:H3	1:2A:2190:G:H1	1.32	0.76
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.66	0.76
35:2d:188:LEU:HD12	35:2d:189:PRO:HD2	1.67	0.76
1:1A:993:G:OP1	16:1U:50:ARG:NH2	2.19	0.76
1:1A:2142:C:N3	1:1A:2149:G:O6	2.19	0.76
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.18	0.76
1:1A:2128:C:N4	1:1A:2160:G:N1	2.35	0.75
32:1a:221:C:H2'	32:1a:222:U:H6	1.51	0.75
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.66	0.75
1:2A:2049:G:N7	60:2A:3848:HOH:O	2.18	0.75
1:1A:998:C:OP1	60:1A:4118:HOH:O	2.05	0.75
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.17	0.75
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.50	0.75
1:2A:570:G:O6	60:2A:3812:HOH:O	2.03	0.75
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.19	0.75
1:1A:1693:U:O2'	3:1D:14:ARG:NH2	2.19	0.74
34:1c:131:ARG:HH11	34:1c:166:GLU:HG3	1.51	0.74
6:2G:7:LEU:HB2	6:2G:104:GLU:HG3	1.69	0.74
1:1A:2136:C:N3	1:1A:2155:G:C2	2.55	0.74
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.21	0.74
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.19	0.74
48:2q:12:SER:HB3	48:2q:20:THR:HB	1.69	0.74
32:1a:1125:U:H4'	41:1j:5:ARG:HH22	1.51	0.74
1:2A:928:G:O6	60:2A:3808:HOH:O	2.03	0.74
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.18	0.74
41:2j:8:LEU:HB3	41:2j:96:ILE:HG23	1.69	0.74
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.60	0.74
38:1g:79:ARG:HD2	38:1g:80:VAL:H	1.51	0.74
1:1A:956:G:O6	60:1A:4116:HOH:O	2.04	0.74
1:2A:1670:C:OP1	60:2A:3814:HOH:O	2.05	0.74
33:2b:16:HIS:HB3	33:2b:210:SER:HB2	1.68	0.74
1:2A:1604:C:OP2	60:2A:3813:HOH:O	2.04	0.74
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.68	0.74
32:2a:331:G:OP2	60:2a:1805:HOH:O	2.05	0.74
32:2a:975:A:H4'	32:2a:976:G:H5"	1.69	0.74
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.52	0.73
34:1c:19:GLU:O	34:1c:40:ARG:NH2	2.21	0.73
1:2A:912:C:OP1	12:2Q:8:LYS:NZ	2.20	0.73
1:2A:1021:A:H62	1:2A:1141:U:H3	1.34	0.73
1:1A:826:U:OP1	60:1A:4105:HOH:O	2.05	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1604:C:OP1	60:2A:3815:HOH:O	2.06	0.73
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.21	0.73
1:1A:668:G:OP2	60:1A:4117:HOH:O	2.05	0.73
32:2a:407:G:H5"	35:2d:115:ARG:HB3	1.71	0.73
1:1A:2028:U:O4	60:1A:4119:HOH:O	2.06	0.73
50:2s:19:VAL:O	50:2s:23:ASN:ND2	2.21	0.73
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.71	0.73
1:2A:652(A):A:H3'	1:2A:652(B):A:H5"	1.71	0.73
1:1A:1315:C:OP2	60:1A:4120:HOH:O	2.06	0.72
1:2A:450:G:O6	60:2A:3816:HOH:O	2.06	0.72
40:2i:128:ARG:NH2	54:2x:33:U:OP2	2.22	0.72
8:1I:76:THR:HG22	8:1I:141:LYS:HE2	1.70	0.72
1:2A:832:G:H5'	11:2P:45:LEU:HD11	1.71	0.72
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.24	0.72
4:2E:119:ARG:HD3	4:2E:160:TYR:HB2	1.69	0.72
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.54	0.72
44:2m:37:THR:O	44:2m:55:ARG:NH1	2.22	0.72
32:1a:316:G:OP2	32:1a:351:G:O2'	2.06	0.72
32:1a:542:G:OP1	35:1d:10:ARG:NH2	2.21	0.72
1:2A:854:G:H2'	1:2A:855:G:H8	1.54	0.72
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.70	0.72
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.53	0.72
32:2a:1105:A:H2'	32:2a:1106:G:H8	1.55	0.72
1:1A:2099:U:H3	1:1A:2190:G:H1	1.38	0.72
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.72	0.72
36:1e:92:LYS:HB3	36:1e:119:LEU:HB2	1.71	0.72
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.70	0.72
32:2a:1278:U:H5'	32:2a:1279:A:H5'	1.71	0.72
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.23	0.72
1:2A:2518:A:OP2	60:2A:3817:HOH:O	2.08	0.72
34:2c:129:ALA:HB3	34:2c:132:ARG:HD2	1.72	0.71
50:2s:49:ILE:HG22	50:2s:62:ILE:HD11	1.69	0.71
1:1A:2131:G:H5"	1:1A:2132:U:H3'	1.71	0.71
1:2A:948:G:OP1	60:2A:3811:HOH:O	2.07	0.71
32:2a:504:C:OP1	60:2a:1806:HOH:O	2.06	0.71
1:1A:1669:A:OP2	60:1A:4106:HOH:O	2.08	0.71
1:2A:2448:A:OP1	60:2A:3812:HOH:O	2.08	0.71
1:2A:2504:U:OP2	60:2A:3818:HOH:O	2.08	0.71
1:1A:2821:A:OP2	60:1R:301:HOH:O	2.08	0.71
32:2a:642:A:N3	39:2h:113:SER:OG	2.23	0.71
1:2A:531:C:OP1	1:2A:561:G:N1	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.73	0.71
1:1A:2794:C:H42	1:1A:2802:G:H22	1.38	0.71
32:1a:353:A:N7	60:1a:1817:HOH:O	2.24	0.71
11:2P:29:LYS:HG3	11:2P:30:THR:H	1.54	0.71
17:2V:40:LEU:HB2	17:2V:46:VAL:HG12	1.72	0.71
19:2X:65:ARG:HB2	19:2X:70:LEU:HD23	1.73	0.71
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.73	0.71
1:1A:1055:G:H1	1:1A:1104:C:H42	1.39	0.71
1:2A:31:C:OP1	60:2A:3819:HOH:O	2.09	0.71
1:2A:500:G:H22	1:2A:503:A:H5'	1.53	0.71
1:1A:279:C:H42	1:1A:361:G:H1	1.39	0.71
32:1a:567:G:N3	60:1a:1816:HOH:O	2.23	0.71
32:1a:975:A:H4'	32:1a:976:G:H5"	1.72	0.71
40:1i:53:VAL:O	40:1i:55:ALA:N	2.24	0.71
32:2a:1277:C:HO2'	32:2a:1279:A:H8	1.39	0.71
1:1A:602:G:O2'	1:1A:655:A:N6	2.24	0.70
1:1A:1778:U:OP1	60:1A:4126:HOH:O	2.09	0.70
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.06	0.70
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.72	0.70
32:2a:1023:G:H3'	32:2a:1024:G:H8	1.55	0.70
1:1A:422:A:OP2	60:1A:4124:HOH:O	2.09	0.70
32:1a:532:A:N6	32:1a:1206:G:O2'	2.25	0.70
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.71	0.70
32:2a:785:G:OP2	60:2a:1807:HOH:O	2.08	0.70
1:2A:2552:OMU:OP2	60:2A:3822:HOH:O	2.09	0.70
1:1A:1637:A:OP2	60:1A:4122:HOH:O	2.08	0.70
1:1A:2128:C:N4	1:1A:2160:G:H1	1.89	0.70
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.23	0.70
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.25	0.70
1:2A:2319:G:H22	14:2S:3:ARG:HH11	1.38	0.70
4:2E:127:ASP:OD2	60:2E:401:HOH:O	2.09	0.70
26:14:15:ILE:HG12	26:14:21:VAL:HG22	1.74	0.70
32:1a:375:U:OP1	47:1p:69:THR:OG1	2.09	0.70
32:2a:1147:C:O2	40:2i:16:ARG:NH1	2.24	0.70
44:2m:33:ALA:O	44:2m:37:THR:OG1	2.10	0.70
33:1b:59:GLU:HG2	33:1b:63:MET:HE2	1.74	0.70
51:2t:70:SER:O	60:2t:301:HOH:O	2.09	0.70
1:1A:1918:A:N6	60:1A:4173:HOH:O	2.25	0.70
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.74	0.70
45:2n:23:ARG:NH1	45:2n:28:GLY:O	2.24	0.70
1:2A:2036:C:OP1	60:2A:3821:HOH:O	2.09	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:752:A:H3'	29:27:1:MET:HE1	1.73	0.69
1:1A:792:G:O6	60:1A:4121:HOH:O	2.08	0.69
1:1A:1452:A:OP2	60:1A:4127:HOH:O	2.10	0.69
3:1D:8:PRO:HB3	3:1D:14:ARG:HG2	1.73	0.69
26:24:24:THR:OG1	26:24:25:TYR:N	2.25	0.69
32:2a:1250:A:H4'	40:2i:68:GLY:H	1.57	0.69
1:1A:441:U:O2	5:1F:46:ARG:NH2	2.23	0.69
34:1c:11:ARG:NH2	34:1c:177:THR:O	2.25	0.69
1:2A:1633:G:OP2	60:2A:3820:HOH:O	2.09	0.69
32:2a:1272:G:N2	32:2a:1273:G:N7	2.40	0.69
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.75	0.69
1:1A:120:U:OP2	60:1A:4123:HOH:O	2.09	0.69
1:1A:1332:G:OP1	60:1A:4120:HOH:O	2.10	0.69
1:1A:1784:A:OP2	60:1A:4125:HOH:O	2.09	0.69
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.73	0.69
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.74	0.69
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.58	0.69
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.24	0.69
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.25	0.69
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.73	0.69
26:24:16:CYS:SG	26:24:17:GLY:N	2.64	0.69
1:1A:2206:G:H3'	1:1A:2207:G:C8	2.28	0.69
32:1a:1002:G:H3'	32:1a:1003:G:H4'	1.73	0.69
44:1m:3:ARG:HD2	44:1m:9:ILE:HG12	1.75	0.69
1:2A:981:A:OP1	60:2A:3823:HOH:O	2.10	0.69
1:2A:2499:C:OP2	60:2A:3825:HOH:O	2.10	0.69
1:2A:1622:G:OP2	60:2A:3829:HOH:O	2.11	0.69
1:1A:1986:A:OP1	60:1A:4128:HOH:O	2.10	0.69
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.25	0.69
33:2b:87:ARG:HH11	33:2b:219:VAL:HG12	1.58	0.69
26:24:44:THR:O	26:24:46:GLN:N	2.26	0.68
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	1.75	0.68
1:2A:253:C:O2'	60:2A:3824:HOH:O	2.10	0.68
3:2D:237:GLU:OE2	60:2D:401:HOH:O	2.10	0.68
34:1c:56:ASP:HB2	34:1c:67:THR:HB	1.75	0.68
24:22:13:ALA:HB1	24:22:21:LEU:HD21	1.76	0.68
1:1A:1671:U:O4	60:1A:4106:HOH:O	2.09	0.68
1:1A:1890:A:OP2	60:1A:4130:HOH:O	2.11	0.68
32:1a:1314:C:OP2	50:1s:4:SER:OG	2.10	0.68
1:2A:1023:U:OP2	60:2A:3827:HOH:O	2.11	0.68
1:2A:1434:A:H61	1:2A:1558:A:H62	1.40	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2138:C:N3	1:2A:2153:G:N2	2.37	0.68
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.75	0.68
32:1a:324:G:N7	60:1a:1822:HOH:O	2.26	0.68
1:2A:805:G:OP1	60:2A:3826:HOH:O	2.10	0.68
1:2A:2135:A:N1	1:2A:2156:G:O2'	2.27	0.68
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.75	0.68
49:1r:26:LEU:HD11	49:1r:42:ARG:HD3	1.76	0.68
1:2A:1568:G:N7	60:2A:3872:HOH:O	2.26	0.68
32:2a:1002:G:H1	32:2a:1038:C:H42	0.77	0.68
33:2b:223:ILE:HA	33:2b:226:ARG:HG2	1.76	0.68
1:2A:1452:A:OP2	60:2A:3828:HOH:O	2.11	0.68
1:1A:2033:A:OP1	60:1A:4119:HOH:O	2.12	0.67
26:14:16:CYS:SG	26:14:17:GLY:N	2.66	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.76	0.67
1:2A:1762:A:N1	60:2A:3878:HOH:O	2.27	0.67
1:2A:2136:C:N4	1:2A:2155:G:N1	2.32	0.67
12:2Q:35:VAL:HG22	12:2Q:102:VAL:HG22	1.75	0.67
1:1A:1105:U:H2'	1:1A:1106:G:H8	1.60	0.67
10:2O:2:ILE:HD12	10:2O:6:THR:HG21	1.77	0.67
11:1P:39:LYS:HB2	11:1P:45:LEU:HD13	1.76	0.67
32:1a:642:A:N3	39:1h:113:SER:OG	2.25	0.67
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.75	0.67
6:2G:121:ASN:HD21	6:2G:123:ASN:HB2	1.59	0.67
15:1T:16:ARG:NH1	15:1T:83:ILE:O	2.24	0.67
41:1j:30:SER:HB3	41:1j:81:THR:HG23	1.76	0.67
32:2a:1010:G:N2	32:2a:1020:U:O2'	2.28	0.67
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.30	0.67
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.42	0.67
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.28	0.67
48:2q:49:GLU:OE1	60:2q:301:HOH:O	2.12	0.67
1:1A:2819:G:OP1	60:1A:4134:HOH:O	2.12	0.67
3:1D:147:LEU:HD13	3:1D:155:LEU:HD21	1.77	0.67
32:2a:953:G:H5'	32:2a:965:A:H61	1.59	0.67
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.77	0.67
1:1A:400:G:N7	60:1A:4181:HOH:O	2.27	0.67
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.76	0.67
39:1h:34:GLU:OE1	39:1h:37:ARG:NH1	2.28	0.67
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD11	1.76	0.67
1:1A:2763:G:OP2	60:1A:4137:HOH:O	2.13	0.67
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.30	0.67
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:95:VAL:HG13	11:2P:125:VAL:HA	1.76	0.67
32:2a:1321:C:H4'	44:2m:87:TYR:HE2	1.60	0.67
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	1.77	0.66
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	1.75	0.66
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.76	0.66
1:1A:1915:5MU:OP2	60:1A:4136:HOH:O	2.13	0.66
1:1A:2447:G:OP2	60:1A:4132:HOH:O	2.12	0.66
1:2A:987:G:OP2	60:2A:3832:HOH:O	2.13	0.66
1:1A:1058:G:H1	1:1A:1080:C:N4	1.92	0.66
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.13	0.66
1:2A:775:G:O3'	60:2A:3833:HOH:O	2.13	0.66
1:1A:2759:G:N7	60:1A:4184:HOH:O	2.28	0.66
34:2c:20:SER:HB3	34:2c:22:TRP:HE1	1.61	0.66
32:1a:664:G:H22	32:1a:741:G:H1	1.44	0.66
36:1e:78:HIS:HE1	36:1e:142:LEU:HA	1.61	0.66
36:1e:81:GLU:HG2	36:1e:90:VAL:HG22	1.76	0.66
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.78	0.66
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.31	0.66
34:2c:6:HIS:HB3	45:2n:49:HIS:CD2	2.31	0.66
47:2p:21:VAL:HG22	47:2p:33:ILE:HB	1.77	0.66
34:1c:172:ARG:NH2	34:1c:206:GLU:OE2	2.29	0.66
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.27	0.66
1:1A:2235:G:N7	60:1A:4186:HOH:O	2.29	0.66
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.30	0.66
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.78	0.66
35:2d:140:VAL:HG11	35:2d:146:ILE:HD11	1.76	0.66
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.78	0.66
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.41	0.66
1:2A:586:A:N1	1:2A:809:G:O2'	2.27	0.66
1:2A:879:G:H3'	1:2A:880:G:H8	1.61	0.66
32:2a:406:G:H21	35:2d:119:GLN:HE22	1.44	0.66
11:2P:29:LYS:HG3	11:2P:30:THR:N	2.11	0.65
32:2a:297:G:N2	32:2a:300:A:OP2	2.30	0.65
32:2a:1129:C:O2'	32:2a:1130:A:N7	2.29	0.65
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.77	0.65
48:2q:66:SER:HB3	48:2q:69:LYS:HB2	1.78	0.65
1:1A:2123:G:H2'	1:1A:2124:G:H8	1.60	0.65
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.77	0.65
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.29	0.65
5:2F:192:LEU:HD13	5:2F:194:MET:HE2	1.79	0.65
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:504:C:OP1	60:1a:1804:HOH:O	2.14	0.65
1:2A:1012:U:O4	9:2N:28:THR:HG21	1.96	0.65
1:2A:2114:A:N6	1:2A:2119:A:N7	2.45	0.65
39:2h:29:SER:HB3	39:2h:32:LYS:HG3	1.78	0.65
1:1A:1057:A:N6	1:1A:1081:U:H3	1.90	0.65
2:1B:99:G:OP2	60:1B:301:HOH:O	2.14	0.65
33:2b:120:ALA:O	33:2b:125:PRO:HD2	1.97	0.65
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.79	0.65
4:1E:119:ARG:HD3	4:1E:160:TYR:HB2	1.79	0.65
1:2A:2705:A:OP2	60:2A:3838:HOH:O	2.14	0.65
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.31	0.65
32:2a:117:G:OP2	60:2a:1810:HOH:O	2.15	0.65
33:2b:97:TRP:HH2	33:2b:102:LEU:HD13	1.61	0.65
1:1A:740:U:OP2	60:1A:4125:HOH:O	2.15	0.65
1:1A:1187:G:H5"	17:1V:81:TYR:CE1	2.32	0.65
1:2A:140:G:N3	1:2A:142:A:N6	2.45	0.65
1:2A:397:G:N7	60:2A:3881:HOH:O	2.30	0.65
7:2H:3:ARG:HG2	7:2H:6:ARG:HE	1.62	0.65
32:2a:1321:C:H4'	44:2m:87:TYR:CE2	2.32	0.65
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.70	0.65
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.79	0.65
32:2a:838:G:H1	32:2a:848:C:H42	1.44	0.65
1:1A:1014:U:OP2	60:1A:4139:HOH:O	2.14	0.65
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.32	0.65
1:1A:1120:G:O6	60:1A:4129:HOH:O	2.10	0.65
1:1A:1468:C:OP1	60:1A:4140:HOH:O	2.15	0.65
32:1a:812:C:N3	60:1a:1826:HOH:O	2.30	0.65
48:1q:67:LYS:HA	48:1q:70:ARG:HH12	1.62	0.65
1:2A:2816:C:O3'	13:2R:99:LYS:NZ	2.29	0.65
32:2a:998:G:H1	32:2a:1043:C:N4	1.95	0.65
4:1E:29:GLY:HA3	60:1E:409:HOH:O	1.97	0.65
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.77	0.65
1:2A:217:G:OP2	60:2A:3837:HOH:O	2.14	0.65
2:2B:24:G:N3	2:2B:26:A:N6	2.45	0.65
26:14:34:GLU:HG2	26:14:35:VAL:HG12	1.80	0.64
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	1.79	0.64
1:2A:1973:G:OP1	60:2A:3836:HOH:O	2.14	0.64
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.78	0.64
32:2a:922:G:H4'	36:2e:20:GLN:HA	1.78	0.64
1:1A:2243:U:OP1	60:1A:4142:HOH:O	2.15	0.64
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:584:G:H5'	48:1q:91:ARG:HH22	1.62	0.64
1:2A:1627:G:OP1	60:2A:3839:HOH:O	2.14	0.64
32:2a:944:G:OP1	60:2a:1809:HOH:O	2.14	0.64
1:1A:2336:A:H61	22:10:43:THR:HG22	1.62	0.64
5:2F:31:HIS:HD2	11:2P:9:ASN:H	1.45	0.64
8:2I:130:TYR:HD2	8:2I:138:ILE:HD12	1.62	0.64
32:2a:1279:A:H4'	32:2a:1280:A:OP1	1.98	0.64
41:2j:35:SER:HB3	41:2j:73:ASP:HB2	1.78	0.64
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.30	0.64
1:2A:2131:G:H4'	1:2A:2132:U:H3'	1.79	0.64
2:2B:7:G:H21	14:2S:38:GLN:NE2	1.86	0.64
1:1A:1342:A:OP2	60:1A:4113:HOH:O	2.14	0.64
1:2A:963:U:OP2	60:2A:3811:HOH:O	2.14	0.64
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.15	0.64
33:1b:74:LYS:NZ	33:1b:205:ASP:O	2.27	0.64
1:2A:1355:G:O6	60:2A:3830:HOH:O	2.11	0.64
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.77	0.64
33:2b:178:ARG:HH12	39:2h:68:ARG:HH22	1.43	0.64
46:2o:82:ILE:HB	46:2o:87:ILE:HB	1.79	0.64
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.44	0.64
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.31	0.64
15:2T:16:ARG:NH2	15:2T:18:ASP:OD2	2.31	0.64
32:2a:1023:G:H3'	32:2a:1024:G:C8	2.32	0.64
8:2I:77:LEU:HB3	8:2I:142:VAL:HG13	1.80	0.64
1:1A:1076:C:O2'	1:1A:1077:A:N7	2.29	0.64
32:2a:975:A:N1	41:2j:48:THR:HB	2.13	0.64
15:1T:51:ARG:HG3	15:1T:98:LYS:HD2	1.78	0.63
1:2A:643:A:N1	1:2A:2369:A:O2'	2.31	0.63
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.16	0.63
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.12	0.63
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.31	0.63
1:2A:1864:U:OP1	1:2A:2410:G:O2'	2.16	0.63
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.62	0.63
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.80	0.63
15:2T:118:ARG:HG2	32:2a:1442(A):G:C8	2.33	0.63
36:2e:11:ILE:HD11	36:2e:33:VAL:HB	1.80	0.63
44:2m:3:ARG:NH2	44:2m:9:ILE:O	2.32	0.63
32:1a:330:C:O2	60:1a:1805:HOH:O	2.15	0.63
1:2A:2133:G:O2'	1:2A:2157:G:N2	2.32	0.63
22:20:11:ARG:O	22:20:14:ARG:NH2	2.30	0.63
1:1A:2552:OMU:OP2	60:1A:4141:HOH:O	2.15	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:972:C:O2'	41:1j:55:LYS:O	2.17	0.63
32:2a:532:A:N1	34:2c:156:ARG:NH2	2.44	0.63
51:2t:57:ARG:HH12	51:2t:100:ILE:HD12	1.63	0.63
1:1A:467:G:OP1	29:17:33:ARG:NH1	2.31	0.63
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.29	0.63
32:1a:1458:G:H5"	51:1t:31:SER:HB2	1.78	0.63
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.30	0.63
1:1A:387:U:O4	60:1A:4133:HOH:O	2.12	0.63
7:1H:3:ARG:HG2	7:1H:6:ARG:HG3	1.81	0.63
32:2a:1004:A:H5"	32:2a:1024:G:H22	1.63	0.63
32:2a:1040:U:H2'	32:2a:1041:A:H8	1.62	0.63
10:2O:49:ARG:NH2	32:2a:1423:G:OP1	2.27	0.63
38:2g:111:ARG:NH1	38:2g:113:GLU:OE2	2.32	0.63
1:2A:947:G:O6	60:2A:3840:HOH:O	2.14	0.63
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.15	0.63
15:2T:127:ALA:C	15:2T:129:ARG:H	2.07	0.63
32:2a:662:G:O2'	32:2a:836:G:OP1	2.16	0.63
34:2c:58:GLU:HB2	34:2c:65:ALA:HB3	1.79	0.63
1:1A:530:G:N1	1:1A:2023:G:OP1	2.30	0.62
11:1P:126:VAL:HG12	11:1P:148:LEU:HD13	1.81	0.62
32:1a:457:C:H2'	32:1a:458:C:H6	1.64	0.62
8:2I:5:LEU:HD23	8:2I:9:LEU:HD12	1.81	0.62
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.32	0.62
1:1A:1354:A:H5"	3:1D:38:LYS:HD3	1.81	0.62
1:2A:2207:G:H3'	1:2A:2208:A:H5"	1.81	0.62
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.31	0.62
41:1j:38:ILE:HG13	41:1j:71:LEU:HB3	1.81	0.62
1:2A:1203:G:O6	60:2A:3835:HOH:O	2.13	0.62
35:2d:65:ARG:NH1	35:2d:70:ILE:O	2.32	0.62
36:2e:20:GLN:NE2	36:2e:21:ALA:O	2.32	0.62
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.13	0.62
33:2b:119:GLU:CD	33:2b:153:ARG:HH12	2.06	0.62
21:2Z:77:ASP:OD2	21:2Z:80:ARG:NH1	2.32	0.62
50:2s:49:ILE:HD13	50:2s:71:LEU:HD11	1.80	0.62
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.34	0.62
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.35	0.62
1:2A:1300:U:H4'	1:2A:1301:A:H5"	1.82	0.62
33:1b:80:ILE:HD12	33:1b:212:GLN:HA	1.82	0.62
1:2A:1278:A:OP1	13:2R:36:THR:HG23	1.98	0.62
1:2A:1959:G:N7	60:2A:3884:HOH:O	2.31	0.62
6:2G:5:VAL:HG22	6:2G:8:LYS:HE2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:53:ILE:HA	21:2Z:71:VAL:HG23	1.82	0.62
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.34	0.62
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.82	0.62
1:1A:2790:A:H3'	1:1A:2790:A:N3	2.14	0.62
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.80	0.62
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.32	0.62
16:2U:85:LYS:HB2	16:2U:116:ALA:HB1	1.81	0.62
12:2Q:11:LYS:NZ	12:2Q:88:GLY:O	2.28	0.62
21:1Z:52:SER:O	21:1Z:54:HIS:N	2.33	0.62
26:14:44:THR:O	26:14:46:GLN:N	2.33	0.62
1:2A:286:C:H2'	1:2A:287:C:C6	2.35	0.62
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.82	0.62
1:1A:878:A:N6	1:1A:899:A:O2'	2.31	0.61
5:2F:33:LEU:HD22	5:2F:112:MET:HE3	1.82	0.61
32:2a:1259:C:N4	32:2a:1260:C:O2	2.33	0.61
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.81	0.61
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.35	0.61
25:13:5:LYS:NZ	25:13:34:GLU:OE2	2.33	0.61
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.16	0.61
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.32	0.61
6:2G:33:ARG:HH21	6:2G:162:THR:HG21	1.65	0.61
7:2H:15:VAL:HG12	7:2H:29:PRO:HD3	1.82	0.61
20:2Y:86:ARG:HB2	20:2Y:98:VAL:HG22	1.80	0.61
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.66	0.61
32:1a:145:G:H1	32:1a:177:C:H42	1.46	0.61
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.48	0.61
1:2A:2127:G:N1	1:2A:2160:G:O6	2.32	0.61
1:2A:2137:C:H42	1:2A:2154:G:H1	1.48	0.61
32:2a:130:A:H5'	48:2q:63:ARG:HE	1.65	0.61
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.83	0.61
28:16:13:CYS:SG	28:16:47:THR:HG21	2.40	0.61
32:1a:171:A:H2'	32:1a:172:A:C8	2.34	0.61
44:1m:15:VAL:HG11	44:1m:48:LEU:HD11	1.82	0.61
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.35	0.61
20:2Y:83:THR:HG21	20:2Y:99:CYS:HB2	1.83	0.61
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.34	0.61
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.35	0.61
32:2a:1209:C:O2'	32:2a:1214:C:N4	2.34	0.61
1:1A:528:A:O2'	1:1A:529:A:H5'	2.00	0.61
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.81	0.61
34:1c:181:ASN:HB3	34:1c:204:LEU:HB2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:128:ARG:NH2	54:1x:33:U:OP2	2.33	0.61
1:1A:382:G:O6	60:1A:4145:HOH:O	2.16	0.61
5:1F:89:VAL:O	60:1F:401:HOH:O	2.16	0.61
35:1d:7:PRO:HB2	35:1d:10:ARG:HD2	1.81	0.61
54:1x:8:4SU:O5'	54:1x:8:4SU:H6	2.01	0.61
1:2A:2478:A:OP2	31:29:2:LYS:NZ	2.29	0.61
32:2a:56:U:H2'	32:2a:57:G:C8	2.36	0.61
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.35	0.61
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.35	0.61
32:1a:161:A:H2'	32:1a:162:A:C8	2.36	0.61
41:1j:47:PHE:HB2	41:1j:63:PHE:HB2	1.83	0.61
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.65	0.61
13:2R:104:ARG:HD2	13:2R:109:ALA:HB3	1.82	0.61
32:2a:1263:C:C4	32:2a:1272:G:O6	2.54	0.61
1:1A:1300:U:H4'	1:1A:1301:A:H5"	1.83	0.61
1:1A:2134:A:O2'	1:1A:2135:A:OP1	2.17	0.61
1:1A:2816:C:O3'	13:1R:99:LYS:NZ	2.33	0.61
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.83	0.61
32:1a:405:U:O4	35:1d:2:GLY:N	2.33	0.61
47:1p:38:TYR:OH	47:1p:47:ASP:OD2	2.18	0.61
42:2k:29:ILE:HG23	42:2k:44:SER:HB3	1.81	0.61
24:12:14:ARG:O	24:12:67:LYS:NZ	2.30	0.60
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.33	0.60
32:1a:509:A:OP2	60:1a:1807:HOH:O	2.16	0.60
32:1a:1291:G:OP1	38:1g:37:ASN:ND2	2.34	0.60
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.15	0.60
1:2A:2006:C:OP2	60:2A:3842:HOH:O	2.16	0.60
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.18	0.60
19:2X:60:ARG:HH12	29:27:47:ARG:HH22	1.48	0.60
32:2a:1086:U:H3	32:2a:1099:G:H22	1.47	0.60
54:2x:40:C:H2'	54:2x:41:C:H6	1.66	0.60
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.34	0.60
26:14:55:ARG:N	26:14:56:VAL:HA	2.16	0.60
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.01	0.60
1:2A:2110:G:H3'	1:2A:2111:C:H5'	1.82	0.60
1:2A:2144:U:O2'	1:2A:2147:G:O6	2.18	0.60
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.29	0.60
1:1A:1173:G:N1	1:1A:1176:G:OP2	2.34	0.60
21:1Z:52:SER:C	21:1Z:54:HIS:H	2.10	0.60
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.84	0.60
1:2A:2134:A:OP2	1:2A:2157:G:N2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:673:G:H2'	32:2a:674:G:C8	2.36	0.60
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.84	0.60
32:2a:1277:C:O2'	32:2a:1279:A:H8	1.83	0.60
28:16:35:GLU:OE2	28:16:50:ARG:NH1	2.32	0.60
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.29	0.60
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.83	0.60
37:1f:9:VAL:HB	37:1f:87:ARG:HB2	1.84	0.60
1:2A:1507:A:O2'	1:2A:1508:A:O4'	2.18	0.60
32:2a:933:G:N2	32:2a:935:A:O4'	2.34	0.60
18:1W:92:ARG:NH1	60:1W:301:HOH:O	2.34	0.60
32:1a:67:C:H2'	32:1a:68:G:C8	2.37	0.60
41:1j:78:ASN:O	41:1j:80:LYS:N	2.35	0.60
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.82	0.60
1:2A:2127:G:N2	1:2A:2161:C:N3	2.50	0.60
7:2H:18:GLU:HB3	7:2H:25:LYS:HB2	1.82	0.60
32:2a:537:G:H5"	43:2l:113:ARG:NH1	2.16	0.60
34:2c:91:LEU:HD21	34:2c:101:LEU:HD23	1.84	0.60
35:2d:153:ARG:HD3	35:2d:181:MET:HG3	1.83	0.60
1:1A:1058:G:N2	1:1A:1081:U:O2	2.34	0.60
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.84	0.60
32:1a:510:A:OP2	35:1d:49:ARG:NH1	2.35	0.60
32:1a:719:C:H1'	49:1r:49:LYS:HB3	1.83	0.60
32:1a:1145:C:H4'	32:1a:1146:A:H5'	1.82	0.60
40:1i:20:ARG:O	40:1i:60:ASP:N	2.22	0.60
1:2A:854:G:H2'	1:2A:855:G:C8	2.36	0.60
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.84	0.60
6:2G:15:VAL:HG21	6:2G:176:LEU:HD23	1.84	0.60
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.02	0.60
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.37	0.60
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.83	0.60
1:1A:271(K):U:H1'	8:1I:50:ARG:CZ	2.31	0.60
1:1A:2010:G:O6	60:1A:4143:HOH:O	2.16	0.60
4:1E:149:ARG:O	60:1E:401:HOH:O	2.16	0.60
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.84	0.60
36:1e:33:VAL:HG13	36:1e:112:LEU:HD12	1.84	0.60
32:2a:45:U:H2'	32:2a:46:G:C8	2.37	0.60
32:2a:653:A:OP1	39:2h:56:LYS:NZ	2.26	0.60
32:2a:1183:A:O2'	32:2a:1185:G:OP2	2.19	0.60
35:2d:86:LYS:H	35:2d:86:LYS:HD2	1.67	0.60
32:1a:70:G:H1	32:1a:99:U:H3	1.50	0.60
32:1a:429:U:O2'	35:1d:22:LYS:NZ	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:828:A:H2'	32:1a:829:G:O4'	2.02	0.60
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.01	0.60
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.84	0.60
35:1d:62:GLN:OE1	35:1d:65:ARG:NH1	2.35	0.60
1:2A:271(G):C:H2'	1:2A:271(H):G:H8	1.67	0.60
1:2A:453:C:OP1	60:2A:3816:HOH:O	2.16	0.60
1:2A:2780:G:OP2	9:2N:118:LYS:HD3	2.02	0.60
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.66	0.60
5:2F:117:ARG:HH12	11:2P:1:MET:H3	1.49	0.60
32:2a:280:C:N3	48:2q:39:SER:OG	2.27	0.60
32:2a:1273:G:H3'	32:2a:1274:G:C8	2.36	0.60
33:2b:15:VAL:HB	33:2b:209:ARG:HB3	1.84	0.60
50:2s:32:LYS:HA	50:2s:50:ALA:HB3	1.83	0.60
1:1A:1045:A:OP1	1:1A:1045:A:H4'	2.00	0.60
1:1A:2306:C:O2	60:1A:4135:HOH:O	2.12	0.60
1:1A:2364:C:OP1	22:10:55:ARG:NH1	2.31	0.60
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.83	0.60
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.35	0.60
32:1a:102:G:O2'	32:1a:151:A:N3	2.29	0.60
1:1A:847:U:OP2	60:1A:4144:HOH:O	2.16	0.59
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.84	0.59
1:2A:614(C):A:C4	5:2F:180:GLY:HA2	2.37	0.59
2:2B:3:C:H2'	2:2B:4:C:C6	2.37	0.59
9:2N:21:LYS:NZ	9:2N:140:VAL:OXT	2.30	0.59
29:27:24:THR:HG22	29:27:27:GLY:H	1.65	0.59
34:1c:138:VAL:HG23	34:1c:151:VAL:HG23	1.84	0.59
1:1A:1274:A:N3	1:1A:1297:C:H1'	2.17	0.59
1:1A:2305:A:H5"	6:1G:134:GLY:HA3	1.84	0.59
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.18	0.59
32:2a:539:A:H2'	32:2a:540:G:C8	2.37	0.59
32:2a:1033:G:H2'	32:2a:1034:G:H8	1.67	0.59
1:1A:668:G:H5'	1:1A:669:G:OP2	2.02	0.59
1:1A:2142:C:O2	1:1A:2149:G:N1	2.30	0.59
1:2A:30:G:H2'	1:2A:31:C:C6	2.37	0.59
1:2A:83:G:H1	1:2A:102:G:HO2'	1.50	0.59
1:2A:1952:A:OP1	10:2O:42:SER:OG	2.20	0.59
8:2I:87:LYS:HE2	8:2I:87:LYS:H	1.67	0.59
32:2a:1189:C:OP1	41:2j:51:ARG:NH2	2.35	0.59
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.85	0.59
32:1a:373:A:H2'	32:1a:374:A:H8	1.67	0.59
32:1a:1456:G:O3'	51:1t:39:LYS:NZ	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.67	0.59
32:2a:433:C:H2'	32:2a:434:U:H6	1.67	0.59
1:1A:1762:A:H2'	60:1A:5350:HOH:O	2.02	0.59
23:11:52:ARG:NH1	23:11:55:GLY:O	2.36	0.59
25:13:50:VAL:HB	25:13:53:LEU:HD12	1.84	0.59
32:1a:509:A:OP2	60:1a:1806:HOH:O	2.16	0.59
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.38	0.59
1:2A:27:G:N2	1:2A:512:G:H1'	2.18	0.59
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.18	0.59
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.38	0.59
14:2S:34:HIS:O	14:2S:97:ARG:NH2	2.36	0.59
49:2r:26:LEU:HD11	49:2r:42:ARG:HD3	1.84	0.59
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.36	0.59
15:1T:16:ARG:NH2	15:1T:18:ASP:OD2	2.33	0.59
32:1a:221:C:H2'	32:1a:222:U:C6	2.37	0.59
1:2A:1114:G:H2'	1:2A:1115:G:H8	1.67	0.59
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.83	0.59
28:26:14:THR:OG1	28:26:48:VAL:O	2.19	0.59
32:2a:187:C:O2'	51:2t:89:ARG:NH2	2.36	0.59
32:2a:1104:G:H4'	33:2b:111:ARG:HH21	1.68	0.59
1:1A:1054:A:H61	1:1A:1105:U:H3	1.51	0.59
15:1T:65:LYS:HE2	15:1T:67:SER:HB2	1.85	0.59
35:1d:64:LEU:HD13	35:1d:198:VAL:HG11	1.85	0.59
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.84	0.59
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.84	0.59
40:2i:3:GLN:HE21	40:2i:20:ARG:HE	1.51	0.59
1:1A:1959:G:N7	60:1A:4205:HOH:O	2.32	0.59
1:1A:2296:U:OP2	14:1S:9:ARG:NH2	2.34	0.59
19:1X:94:GLY:H	19:1X:95:LEU:C	2.11	0.59
51:1t:10:LEU:HB3	51:1t:12:ALA:H	1.67	0.59
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.38	0.59
1:2A:2498:C:OP2	60:2A:3825:HOH:O	2.17	0.59
8:2I:38:LEU:H	8:2I:38:LEU:HD12	1.68	0.59
32:2a:757:U:H2'	32:2a:758:G:O4'	2.03	0.59
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.85	0.59
3:2D:71:ASP:OD2	3:2D:103:ARG:NH1	2.25	0.59
18:2W:88:ARG:HB2	18:2W:92:ARG:HB3	1.85	0.59
32:2a:1244:C:H42	32:2a:1293:G:H1	1.50	0.59
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.83	0.59
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.38	0.58
32:1a:1221:G:OP1	32:1a:1320:C:N4	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:43:LEU:HD22	51:1t:48:LYS:HD2	1.85	0.58
1:2A:2637:U:H5"	4:2E:82:ARG:HH12	1.67	0.58
32:2a:1166:G:N2	32:2a:1170:A:OP2	2.34	0.58
33:2b:63:MET:HG2	33:2b:225:ALA:HB1	1.83	0.58
32:1a:76:C:N4	32:1a:93:G:H1	2.01	0.58
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.18	0.58
1:2A:1378:A:O2'	1:2A:1380:G:N7	2.28	0.58
1:2A:2445:G:OP1	5:2F:74:ARG:NH2	2.33	0.58
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.85	0.58
32:2a:148:G:H2'	32:2a:149:A:H8	1.69	0.58
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.18	0.58
2:1B:14:U:OP2	2:1B:70:C:O2'	2.21	0.58
32:1a:343:U:O2'	32:1a:346:G:O6	2.16	0.58
32:1a:472:A:OP2	47:1p:75:ARG:NH2	2.36	0.58
37:1f:10:LEU:HD23	37:1f:61:LEU:HD13	1.85	0.58
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.85	0.58
1:2A:147:U:O4	60:2A:3841:HOH:O	2.15	0.58
11:2P:39:LYS:HB2	11:2P:45:LEU:HD13	1.84	0.58
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.17	0.58
1:1A:11:G:C2'	1:1A:12:U:H5'	2.34	0.58
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.36	0.58
9:1N:15:LEU:HD23	9:1N:137:LYS:HG2	1.86	0.58
37:1f:8:ILE:HD11	37:1f:79:LEU:HD13	1.85	0.58
1:2A:1022:G:H22	1:2A:1142(A):A:H2	1.49	0.58
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.39	0.58
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.09	0.58
32:1a:56:U:H2'	32:1a:57:G:C8	2.37	0.58
32:1a:799:G:OP2	60:1a:1808:HOH:O	2.17	0.58
32:1a:1031:G:H2'	32:1a:1032:G:C8	2.39	0.58
37:1f:100:ASN:HB2	49:1r:28:GLU:HA	1.84	0.58
1:2A:863:A:H2'	1:2A:864:G:H8	1.68	0.58
50:2s:61:TYR:CE2	50:2s:63:THR:HG22	2.38	0.58
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.84	0.58
2:2B:55:U:O3'	6:2G:27:ASN:ND2	2.36	0.58
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.69	0.58
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.86	0.58
9:1N:73:THR:HB	9:1N:82:LEU:HD11	1.84	0.58
51:1t:43:LEU:O	51:1t:47:GLY:N	2.28	0.58
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.21	0.58
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.37	0.58
8:2I:38:LEU:HB2	8:2I:40:THR:HG22	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:11:ARG:NH2	34:2c:177:THR:O	2.37	0.58
3:1D:12:SER:HB3	3:1D:208:LYS:HB3	1.85	0.58
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.36	0.58
26:14:16:CYS:HB2	26:14:36:CYS:HB3	1.86	0.58
1:2A:2592:G:OP1	60:2A:3844:HOH:O	2.17	0.58
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.04	0.58
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.38	0.58
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.85	0.58
4:1E:110:GLY:O	60:1R:301:HOH:O	2.16	0.58
32:1a:560:U:O2'	32:1a:561:U:OP2	2.16	0.58
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.84	0.58
33:1b:48:MET:HA	33:1b:51:LEU:HB2	1.86	0.58
49:1r:31:LEU:HD23	49:1r:31:LEU:H	1.68	0.58
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.38	0.58
33:2b:204:ASN:HD21	33:2b:207:ALA:HB3	1.69	0.58
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.84	0.58
1:1A:1418:G:OP2	60:1A:4146:HOH:O	2.17	0.58
32:1a:1025:U:O2	32:1a:1036:G:O6	2.22	0.58
32:1a:1406:U:H3'	32:1a:1407:5MC:HM53	1.85	0.58
35:1d:112:VAL:HG23	35:1d:116:GLN:HE22	1.69	0.58
46:1o:70:LEU:HD11	46:1o:77:ARG:HB3	1.86	0.58
34:2c:53:ALA:HB2	34:2c:115:LEU:HD13	1.85	0.58
8:1I:37:VAL:HG13	8:1I:38:LEU:HD23	1.85	0.57
9:1N:6:PRO:HG3	9:1N:41:ASP:HB2	1.86	0.57
32:1a:1223:C:OP2	50:1s:78:ARG:NH2	2.35	0.57
1:2A:302:C:OP1	20:2Y:101:LYS:NZ	2.36	0.57
32:2a:222:U:H2'	32:2a:223:U:C6	2.39	0.57
32:2a:1316:G:N2	32:2a:1319:A:OP2	2.37	0.57
32:2a:1512:U:H2'	32:2a:1513:A:C8	2.39	0.57
38:2g:70:LYS:HG2	38:2g:96:GLN:HB3	1.85	0.57
32:1a:1136:U:H5"	32:1a:1137:C:C4	2.39	0.57
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.04	0.57
26:24:58:ARG:HG3	50:2s:65:ASN:HA	1.86	0.57
1:1A:1011:G:OP1	16:1U:77:SER:OG	2.22	0.57
15:1T:127:ALA:C	15:1T:129:ARG:H	2.13	0.57
32:1a:624:C:H2'	32:1a:625:G:H8	1.70	0.57
32:1a:1036:G:H5"	32:1a:1037:C:C5	2.39	0.57
1:2A:307:G:N1	1:2A:310:A:OP2	2.33	0.57
5:2F:33:LEU:HB3	11:2P:6:LEU:HD21	1.86	0.57
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.28	0.57
32:2a:951:G:N7	44:2m:102:ARG:NH2	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2279:G:O6	22:10:14:ARG:HG3	2.04	0.57
1:1A:2469:A:O3'	12:1Q:56:ARG:NH1	2.38	0.57
2:1B:11:C:OP2	2:1B:12:C:N4	2.29	0.57
3:1D:108:PRO:HD2	3:1D:111:LEU:HD22	1.86	0.57
17:1V:34:GLU:HB3	17:1V:56:SER:HB2	1.85	0.57
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.86	0.57
32:1a:636:U:H2'	32:1a:637:G:H8	1.70	0.57
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.85	0.57
23:21:32:LYS:O	60:21:201:HOH:O	2.17	0.57
25:23:40:THR:HG22	25:23:42:ALA:H	1.68	0.57
26:24:46:GLN:HE21	26:24:48:ARG:HB2	1.68	0.57
32:2a:1271:G:C2	32:2a:1272:G:N7	2.72	0.57
35:2d:165:MET:HE2	35:2d:168:ARG:HD2	1.86	0.57
1:1A:1054:A:N6	1:1A:1105:U:H3	2.03	0.57
52:1u:17:THR:O	52:1u:22:ARG:NH1	2.37	0.57
1:2A:400:G:N7	60:2A:3889:HOH:O	2.32	0.57
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.03	0.57
4:2E:61:ARG:HA	4:2E:64:LYS:HB2	1.85	0.57
26:24:60:GLN:O	26:24:62:ARG:NH1	2.37	0.57
32:2a:129(A):G:C6	32:2a:189(E):U:H4'	2.40	0.57
32:2a:1026:G:H5'	32:2a:1027:C:O5'	2.05	0.57
32:2a:1219:U:OP1	45:2n:19:ARG:NH1	2.36	0.57
1:1A:1243:G:O2'	11:1P:7:ARG:NH2	2.37	0.57
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.38	0.57
1:1A:2537:U:H2'	1:1A:2538:C:C6	2.40	0.57
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.36	0.57
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.85	0.57
40:2i:88:TYR:HD2	40:2i:89:ASN:HB2	1.70	0.57
33:2b:12:GLU:HA	33:2b:213:LEU:HD11	1.86	0.57
9:1N:109:LYS:HE2	60:1N:302:HOH:O	2.04	0.57
32:1a:445:G:H2'	32:1a:446:G:C8	2.40	0.57
1:2A:1665:A:H1'	10:2O:1:MET:HG3	1.85	0.57
1:2A:1890:A:OP2	60:2A:3843:HOH:O	2.17	0.57
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.37	0.57
26:24:62:ARG:HA	26:24:62:ARG:CZ	2.35	0.57
32:2a:262:A:H4'	51:2t:75:ASN:HB2	1.87	0.57
32:2a:1507:A:N6	32:2a:1528:U:O4	2.20	0.57
41:2j:30:SER:O	41:2j:81:THR:OG1	2.15	0.57
1:1A:2137:C:H2'	1:1A:2138:C:C6	2.40	0.57
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	1.86	0.57
1:2A:323:G:HO2'	1:2A:1205:U:H3	1.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.53	0.57
21:2Z:55:HIS:HE1	21:2Z:135:GLU:HB2	1.69	0.57
32:2a:192:U:O2'	51:2t:60:GLU:OE1	2.21	0.57
1:1A:1263:U:OP1	27:15:16:ARG:NH1	2.36	0.57
1:1A:1783:A:N7	60:1A:4203:HOH:O	2.32	0.57
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.38	0.57
32:1a:258:G:H2'	32:1a:259:G:H8	1.68	0.57
32:1a:640:A:O2'	39:1h:115:SER:O	2.22	0.57
6:2G:41:GLN:O	6:2G:43:LEU:N	2.38	0.57
6:2G:83:ARG:O	6:2G:85:GLY:N	2.38	0.57
8:2I:43:ASN:ND2	23:21:75:GLU:OE2	2.38	0.57
19:2X:32:PRO:HA	19:2X:77:LYS:HB2	1.85	0.57
21:2Z:72:ARG:NH1	21:2Z:97:GLU:O	2.34	0.57
34:2c:125:GLU:O	34:2c:190:ARG:NH2	2.38	0.57
1:1A:588:U:H2'	1:1A:589:C:C6	2.40	0.56
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.70	0.56
34:1c:71:ALA:HA	34:1c:106:VAL:HG21	1.85	0.56
51:1t:43:LEU:HD13	51:1t:51:GLU:HB3	1.86	0.56
1:2A:2127:G:N1	1:2A:2161:C:N4	2.53	0.56
32:2a:972:C:O2'	41:2j:55:LYS:O	2.23	0.56
33:2b:122:PHE:O	33:2b:127:ILE:HB	2.05	0.56
32:1a:1108:G:O6	60:1a:1809:HOH:O	2.17	0.56
1:2A:2130:U:O2	1:2A:2134:A:O2'	2.19	0.56
32:2a:707:C:OP1	42:2k:85:ARG:NH1	2.38	0.56
32:2a:1118:C:OP1	40:2i:104:ARG:NH1	2.37	0.56
33:2b:43:ASP:OD2	33:2b:46:LYS:N	2.35	0.56
41:2j:67:THR:O	41:2j:67:THR:OG1	2.21	0.56
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.41	0.56
32:1a:1318:A:OP1	50:1s:7:LYS:NZ	2.27	0.56
32:1a:1456:G:N2	51:1t:51:GLU:OE2	2.37	0.56
1:2A:668:G:H5'	1:2A:669:G:OP2	2.04	0.56
1:2A:888:C:OP1	44:2m:93:ARG:NH1	2.34	0.56
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.41	0.56
1:2A:2206:G:H3'	1:2A:2207:G:N7	2.20	0.56
32:2a:1263:C:N3	32:2a:1272:G:O6	2.39	0.56
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.20	0.56
1:1A:2285:C:OP2	28:16:6:ARG:NH1	2.39	0.56
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.40	0.56
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.38	0.56
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.86	0.56
17:2V:56:SER:H	17:2V:100:ARG:HB2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.38	0.56
35:2d:121:VAL:HG22	35:2d:126:ILE:HG13	1.86	0.56
46:2o:11:VAL:HG21	46:2o:34:LEU:HD22	1.88	0.56
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.40	0.56
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.88	0.56
32:1a:1035:A:H2'	32:1a:1036:G:H21	1.69	0.56
1:2A:286:C:H2'	1:2A:287:C:H6	1.71	0.56
1:2A:848:G:H2'	1:2A:849:A:C8	2.40	0.56
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.40	0.56
6:2G:7:LEU:HD13	6:2G:104:GLU:HA	1.87	0.56
18:2W:4:LYS:HB2	18:2W:106:ILE:HG12	1.87	0.56
23:21:3:LYS:HB2	23:21:61:ARG:HH12	1.70	0.56
32:2a:707:C:H2'	32:2a:708:C:C6	2.40	0.56
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.40	0.56
34:2c:29:TYR:OH	45:2n:54:PRO:O	2.23	0.56
35:2d:15:GLU:OE2	35:2d:66:ARG:NH1	2.39	0.56
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.40	0.56
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.05	0.56
32:1a:276:G:O3'	48:1q:68:ARG:NH1	2.34	0.56
32:1a:1008:C:N3	32:1a:1021:G:O6	2.39	0.56
1:2A:839:U:H2'	1:2A:840:C:C6	2.40	0.56
32:2a:663:A:O3'	49:2r:64:ARG:NH2	2.35	0.56
1:1A:2161:C:O2'	1:1A:2162:G:H5"	2.06	0.56
32:1a:1531:A:H8	32:1a:1531:A:O5'	1.87	0.56
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.20	0.56
1:2A:2138:C:H2'	1:2A:2139:C:O4'	2.05	0.56
15:2T:64:ARG:HB2	15:2T:73:GLU:HG2	1.87	0.56
32:2a:17:U:H2'	32:2a:18:C:C6	2.41	0.56
1:1A:2106:G:H1	1:1A:2183:C:H42	1.53	0.56
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.88	0.56
32:1a:438:G:N1	32:1a:495:A:OP2	2.26	0.56
1:2A:1186:G:OP2	60:2A:3845:HOH:O	2.18	0.56
26:24:48:ARG:NH2	26:24:52:THR:O	2.38	0.56
3:1D:70:TRP:CE2	3:1D:150:LYS:HD2	2.40	0.56
1:2A:919:G:N2	1:2A:2269:A:OP2	2.34	0.56
1:2A:1410:G:H2'	1:2A:1411:C:H6	1.71	0.56
1:2A:2232:U:P	23:21:40:ARG:HH12	2.29	0.56
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.41	0.56
32:2a:959:A:HO2'	32:2a:984:C:HO2'	1.50	0.56
33:2b:60:ASP:O	33:2b:64:ARG:HG2	2.06	0.56
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:13:18:ASP:OD1	25:13:18:ASP:N	2.37	0.56
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.20	0.56
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.41	0.56
32:2a:1518:MA6:H93	32:2a:1519:MA6:H92	1.87	0.56
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	1.87	0.56
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.87	0.56
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.40	0.55
32:1a:995:C:O2	45:1n:4:LYS:NZ	2.38	0.55
32:1a:1223:C:P	50:1s:78:ARG:HH21	2.29	0.55
41:1j:65:LEU:HD13	45:1n:56:VAL:HG22	1.88	0.55
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.88	0.55
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.41	0.55
32:2a:157:G:H1	32:2a:164:U:H3	1.52	0.55
32:2a:999:C:H2'	32:2a:1000:U:C6	2.42	0.55
32:2a:1105:A:H2'	32:2a:1106:G:C8	2.40	0.55
1:1A:512:G:OP2	60:1A:4147:HOH:O	2.18	0.55
1:1A:1062:G:P	1:1A:1070:A:H1'	2.46	0.55
1:1A:2136:C:C2	1:1A:2155:G:N2	2.74	0.55
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.22	0.55
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.70	0.55
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	1.87	0.55
33:1b:24:TRP:CD1	33:1b:24:TRP:H	2.24	0.55
36:1e:152:ARG:NH2	39:1h:107:LEU:O	2.39	0.55
2:2B:5:C:OP1	2:2B:61:G:O2'	2.23	0.55
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.21	0.55
32:2a:828:A:N6	32:2a:858:G:O2'	2.39	0.55
32:2a:1176:A:H2'	32:2a:1177:G:C8	2.42	0.55
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.88	0.55
50:2s:48:THR:HG22	50:2s:61:TYR:HA	1.88	0.55
32:1a:1075:C:OP1	33:1b:179:LYS:NZ	2.39	0.55
49:1r:52:PRO:HD2	49:1r:55:ARG:HB2	1.88	0.55
1:2A:863:A:H2'	1:2A:864:G:C8	2.42	0.55
20:2Y:49:VAL:HG21	20:2Y:61:ILE:HG23	1.88	0.55
38:2g:23:VAL:HG13	38:2g:43:PHE:CE2	2.41	0.55
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.42	0.55
1:1A:1041:C:N4	1:1A:1114:G:H1	2.00	0.55
1:1A:1991:U:H2'	1:1A:1992:G:H5"	1.88	0.55
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.07	0.55
33:1b:82:ARG:NH1	33:1b:86:GLU:OE2	2.39	0.55
1:2A:2689:U:OP2	1:2A:2719:G:N2	2.31	0.55
5:2F:32:LEU:HD22	5:2F:112:MET:HE2	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.40	0.55
36:2e:31:LEU:HD22	36:2e:43:LEU:HD11	1.88	0.55
1:1A:739:G:OP1	60:1A:4149:HOH:O	2.18	0.55
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.42	0.55
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.88	0.55
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.15	0.55
42:1k:34:ASP:HB3	42:1k:40:ILE:HD11	1.89	0.55
32:2a:1183:A:H3'	32:2a:1184:G:H5"	1.88	0.55
46:2o:26:GLU:OE1	46:2o:77:ARG:NH2	2.39	0.55
1:1A:639:U:H2'	1:1A:640:C:C6	2.41	0.55
1:1A:1580:A:OP2	1:1A:1580:A:H8	1.90	0.55
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.21	0.55
1:1A:2114:A:H2	1:1A:2168:G:H1'	1.71	0.55
23:11:23:LYS:HB3	23:11:29:GLY:HA3	1.87	0.55
1:2A:1697:G:OP2	1:2A:1698:A:O2'	2.18	0.55
1:2A:2258:C:O2'	1:2A:2427:C:OP2	2.22	0.55
32:2a:1122:U:H2'	32:2a:1123:A:H8	1.70	0.55
1:1A:747:U:O2	1:1A:2014:A:H1'	2.07	0.55
1:1A:1903:G:OP1	3:1D:241:PRO:HB2	2.07	0.55
32:1a:984:C:H42	32:1a:1221:G:H1	1.52	0.55
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.21	0.55
33:2b:185:ILE:HG22	33:2b:199:TYR:HB2	1.89	0.55
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.71	0.55
37:2f:62:TRP:CH2	37:2f:64:GLN:HB2	2.41	0.55
50:2s:64:GLU:CD	50:2s:64:GLU:H	2.15	0.55
1:1A:34:C:H5"	1:1A:35:G:OP2	2.07	0.55
1:1A:2612:C:OP2	27:15:2:ALA:N	2.40	0.55
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.89	0.55
10:1O:7:TYR:HE2	10:1O:20:MET:HE3	1.72	0.55
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.88	0.55
1:2A:796:C:H2'	1:2A:797:C:C6	2.41	0.55
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.39	0.55
5:2F:117:ARG:HH12	11:2P:1:MET:N	2.04	0.55
21:2Z:99:TYR:HB3	21:2Z:123:ASP:HB2	1.88	0.55
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.41	0.55
1:1A:529:A:OP2	9:1N:114:ARG:NH2	2.37	0.55
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.42	0.55
32:1a:45:U:H2'	32:1a:46:G:C8	2.41	0.55
32:1a:721:G:H4'	32:1a:722:A:O4'	2.07	0.55
32:1a:1255:G:N7	41:1j:43:ARG:NH2	2.55	0.55
34:1c:43:LEU:HD21	34:1c:91:LEU:HD13	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:44:VAL:HG22	41:1j:66:ARG:HG2	1.89	0.55
21:2Z:98:MET:HE2	21:2Z:100:VAL:HG22	1.88	0.55
32:1a:601:C:H2'	32:1a:602:A:C8	2.41	0.55
32:1a:973:G:OP1	41:1j:57:LYS:NZ	2.30	0.55
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.89	0.55
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.07	0.55
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.40	0.55
34:2c:111:LEU:HD21	34:2c:146:ALA:HB2	1.87	0.55
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.21	0.54
1:2A:867:C:H2'	1:2A:868:U:H6	1.72	0.54
1:2A:2012:G:H4'	18:2W:96:ILE:HD13	1.88	0.54
19:2X:26:TYR:HB3	19:2X:92:LEU:HD22	1.87	0.54
24:22:35:LEU:HD11	24:22:49:LYS:HE2	1.88	0.54
32:2a:130:A:N3	32:2a:263:A:O2'	2.30	0.54
32:2a:708:C:H2'	32:2a:709:G:H8	1.73	0.54
32:1a:757:U:H2'	32:1a:758:G:O4'	2.07	0.54
35:1d:165:MET:HE2	35:1d:176:LEU:HD23	1.88	0.54
1:2A:1313:U:OP1	60:2A:3849:HOH:O	2.18	0.54
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.88	0.54
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.29	0.54
32:2a:64:G:H4'	32:2a:65:U:H3'	1.89	0.54
35:2d:143:GLY:HA2	35:2d:184:LYS:HE3	1.89	0.54
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.06	0.54
32:1a:376:G:O3'	47:1p:5:ARG:NH1	2.40	0.54
34:1c:8:ILE:HD12	34:1c:16:ARG:HG3	1.90	0.54
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.25	0.54
44:1m:91:ARG:HB2	44:1m:98:VAL:HG13	1.89	0.54
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.89	0.54
4:2E:119:ARG:HG2	4:2E:120:TRP:CD1	2.42	0.54
6:2G:69:ALA:HB3	6:2G:91:ARG:HH21	1.72	0.54
10:2O:98:VAL:HG11	10:2O:114:ILE:HG23	1.90	0.54
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	1.89	0.54
22:20:27:GLU:HG3	22:20:68:GLU:HA	1.89	0.54
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.43	0.54
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.40	0.54
52:2u:9:ARG:HH21	52:2u:10:ARG:HH21	1.54	0.54
1:1A:1800:C:OP2	3:1D:183:ARG:NH2	2.40	0.54
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.42	0.54
11:1P:38:GLN:O	11:1P:39:LYS:HB3	2.06	0.54
26:14:50:VAL:HG21	44:1m:64:TRP:C	2.33	0.54
32:1a:1007:C:N3	32:1a:1022:G:O6	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1047:G:H5"	45:1n:4:LYS:HD3	1.89	0.54
2:2B:101:G:OP2	60:2B:301:HOH:O	2.19	0.54
6:2G:124:SER:O	6:2G:124:SER:OG	2.24	0.54
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE2	1.88	0.54
32:2a:545:C:O2'	32:2a:549:C:OP1	2.22	0.54
43:2l:32:PHE:O	43:2l:33:ARG:HD3	2.07	0.54
1:1A:652(F):G:H1	1:1A:652(S):C:H42	1.55	0.54
33:1b:60:ASP:HA	33:1b:63:MET:HE3	1.89	0.54
44:1m:15:VAL:HG22	44:1m:43:THR:O	2.07	0.54
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.05	0.54
35:2d:150:GLU:OE1	35:2d:151:LYS:N	2.38	0.54
54:2x:8:4SU:O5'	54:2x:8:4SU:H6	2.07	0.54
1:1A:2136:C:N4	1:1A:2155:G:C6	2.76	0.54
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.37	0.54
32:1a:200:G:H1	32:1a:217:C:H42	1.56	0.54
1:2A:2110:G:OP1	1:2A:2118:U:N3	2.36	0.54
32:2a:302:G:N3	32:2a:556:C:H4'	2.23	0.54
32:2a:1033:G:H2'	32:2a:1034:G:C8	2.43	0.54
32:2a:1347:G:HO2'	32:2a:1373:G:H1	1.54	0.54
35:2d:82:ALA:HB1	35:2d:92:VAL:HG13	1.89	0.54
4:1E:7:VAL:HG12	4:1E:51:PHE:HE2	1.72	0.54
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.43	0.54
32:1a:130:A:O2'	32:1a:131:C:O5'	2.26	0.54
32:1a:376:G:H5"	47:1p:5:ARG:HB3	1.89	0.54
32:1a:598:U:H4'	39:1h:94:TYR:CG	2.43	0.54
34:1c:134:ILE:HG23	34:1c:151:VAL:HB	1.89	0.54
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	1.90	0.54
1:2A:646:A:H2'	1:2A:647:G:O4'	2.08	0.54
1:2A:987:G:P	60:2A:3832:HOH:O	2.66	0.54
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.90	0.54
2:2B:2:C:H2'	2:2B:3:C:C6	2.42	0.54
32:2a:1314:C:OP1	50:2s:6:LYS:NZ	2.33	0.54
36:2e:152:ARG:HG3	39:2h:43:GLY:O	2.08	0.54
1:1A:414:C:H2'	1:1A:415:A:C8	2.43	0.54
4:1E:116:VAL:HG11	4:1E:138:PRO:HB3	1.89	0.54
32:1a:510:A:OP2	60:1a:1810:HOH:O	2.18	0.54
33:1b:78:GLN:HA	33:1b:78:GLN:HE21	1.72	0.54
1:2A:143:G:H2'	1:2A:143(A):C:C6	2.43	0.54
1:2A:2552:OMU:H2'	1:2A:2554:U:OP2	2.07	0.54
6:2G:152:LEU:H	6:2G:152:LEU:HD12	1.72	0.54
41:2j:89:ASP:OD1	41:2j:89:ASP:N	2.33	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:118:A:C8	1:1A:119:A:C8	2.95	0.54
1:1A:271(Z):C:N4	60:1A:4260:HOH:O	2.40	0.54
1:1A:278:A:H2'	1:1A:279:C:C6	2.43	0.54
1:1A:2550:G:OP1	60:1A:4106:HOH:O	2.19	0.54
36:1e:94:ALA:HB1	36:1e:98:THR:HG21	1.89	0.54
1:2A:184:C:H2'	1:2A:185:U:C6	2.43	0.54
1:2A:1022:G:N2	1:2A:1023:U:O4	2.41	0.54
1:2A:1805:U:O2	3:2D:50:THR:HB	2.08	0.54
5:2F:116:ASP:OD2	11:2P:1:MET:N	2.37	0.54
8:2I:129:THR:HG22	8:2I:139:GLN:HE21	1.72	0.54
10:2O:80:ASP:OD1	15:2T:64:ARG:NH2	2.40	0.54
14:2S:37:ALA:HB2	14:2S:101:LEU:HD11	1.89	0.54
26:24:58:ARG:HH21	44:2m:80:ARG:NH2	2.06	0.54
1:1A:1371:G:H2'	1:1A:1372:U:H5	1.73	0.54
1:1A:2072:G:N2	60:1A:4266:HOH:O	2.41	0.54
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.90	0.54
32:1a:684:A:H1'	42:1k:39:PRO:HD2	1.90	0.54
35:1d:178:VAL:HG12	35:1d:179:GLU:H	1.74	0.54
1:2A:247:G:H4'	1:2A:386:G:C5	2.43	0.54
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.42	0.54
12:2Q:75:THR:HG21	12:2Q:87:LYS:HE3	1.88	0.54
32:2a:404:U:H2'	32:2a:405:U:C6	2.43	0.54
32:2a:953:G:N7	44:2m:104:ARG:NH2	2.56	0.54
32:2a:1030(A):G:N3	32:2a:1030(C):G:H8	2.06	0.54
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.43	0.54
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.74	0.53
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.40	0.53
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	1.90	0.53
49:1r:58:LEU:HB3	49:1r:62:GLU:HB3	1.89	0.53
1:2A:894:C:O2'	1:2A:895:U:H5"	2.08	0.53
1:2A:1271:G:OP2	60:2A:3846:HOH:O	2.18	0.53
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.06	0.53
32:2a:148:G:H2'	32:2a:149:A:C8	2.42	0.53
32:2a:501:C:H2'	32:2a:502:G:C8	2.42	0.53
35:2d:31:CYS:SG	35:2d:33:MET:HB3	2.48	0.53
1:1A:1622:G:OP2	60:1A:4150:HOH:O	2.18	0.53
24:12:64:LEU:HD11	24:12:68:ARG:HE	1.72	0.53
32:1a:1186:G:H21	45:1n:61:TRP:C	2.17	0.53
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.44	0.53
1:2A:2154:G:N7	1:2A:2156:G:N2	2.56	0.53
8:2I:117:GLU:H	8:2I:117:GLU:CD	2.15	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:728:A:H2'	32:2a:729:A:C8	2.43	0.53
32:2a:952:U:H2'	32:2a:953:G:H8	1.72	0.53
34:2c:127:ARG:NH2	34:2c:192:THR:OG1	2.41	0.53
44:2m:14:ARG:HB2	44:2m:17:VAL:HG22	1.90	0.53
1:1A:8:A:H2'	1:1A:9:U:H6	1.73	0.53
35:1d:189:PRO:HB3	35:1d:193:ASP:HB3	1.90	0.53
54:1x:50:U:H2'	54:1x:51:C:C6	2.43	0.53
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.44	0.53
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.89	0.53
32:2a:131:C:H2'	32:2a:132:C:H6	1.73	0.53
32:2a:863:U:O2'	32:2a:865:A:N7	2.36	0.53
32:2a:1127:G:H5'	32:2a:1280:A:O2'	2.08	0.53
34:2c:54:ARG:HB2	34:2c:69:HIS:CG	2.43	0.53
1:1A:2155:G:H2'	1:1A:2155:G:N3	2.24	0.53
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.40	0.53
15:1T:29:ARG:HG3	15:1T:46:GLU:HB2	1.91	0.53
26:14:61:ARG:HG3	26:14:62:ARG:N	2.24	0.53
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.23	0.53
32:2a:890:G:O2'	32:2a:906:G:O6	2.16	0.53
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.44	0.53
33:2b:178:ARG:NH1	39:2h:68:ARG:HH22	2.06	0.53
35:2d:59:ARG:NH1	35:2d:59:ARG:HA	2.22	0.53
50:2s:17:GLU:HG2	50:2s:21:GLU:HG3	1.89	0.53
6:1G:137:GLU:HG2	6:1G:152:LEU:HD22	1.89	0.53
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.41	0.53
32:1a:662:G:H2'	32:1a:663:A:C8	2.43	0.53
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.42	0.53
1:2A:403:U:H4'	1:2A:404:C:H5'	1.90	0.53
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.44	0.53
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.44	0.53
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.77	0.53
39:2h:10:LEU:HD13	39:2h:83:ILE:HG12	1.91	0.53
44:2m:45:VAL:HA	44:2m:48:LEU:HD12	1.90	0.53
1:1A:2467:C:H4'	12:1Q:123:HIS:CD2	2.43	0.53
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.44	0.53
33:1b:134:GLU:HA	33:1b:137:ARG:HE	1.72	0.53
1:2A:527:C:H5	60:2A:4361:HOH:O	1.91	0.53
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.43	0.53
18:2W:2:GLU:OE2	18:2W:72:LYS:NZ	2.28	0.53
32:2a:545:C:OP1	35:2d:61:LYS:NZ	2.42	0.53
32:2a:922:G:N3	32:2a:1398:A:H2	2.06	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.07	0.53
33:2b:166:ASP:OD1	33:2b:169:LYS:HB2	2.08	0.53
32:1a:123:C:OP1	32:1a:311:C:O2'	2.20	0.53
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.38	0.53
1:2A:2137:C:N3	1:2A:2154:G:N2	2.44	0.53
1:2A:2396:G:OP1	23:21:25:LYS:NZ	2.29	0.53
7:2H:70:THR:HA	7:2H:73:ALA:HB3	1.90	0.53
26:24:61:ARG:O	26:24:61:ARG:NH1	2.41	0.53
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.91	0.53
32:2a:1352:C:OP1	52:2u:3:LYS:NZ	2.33	0.53
34:2c:18:TRP:CD1	45:2n:54:PRO:HA	2.44	0.53
24:12:9:GLN:HE22	24:12:56:GLN:HG2	1.74	0.53
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.56	0.53
1:2A:2803:C:H2'	1:2A:2804:C:C6	2.44	0.53
32:2a:1239:A:H62	32:2a:1299:A:N6	2.07	0.53
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.89	0.53
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.91	0.53
42:1k:48:ILE:HD12	42:1k:63:LEU:HB2	1.91	0.53
46:1o:82:ILE:HD12	46:1o:88:ARG:HG3	1.89	0.53
1:2A:307:G:H21	1:2A:330:A:H62	1.56	0.53
5:2F:126:VAL:HG21	5:2F:129:PHE:CZ	2.44	0.53
1:1A:484:C:OP1	20:1Y:51:VAL:HG22	2.09	0.53
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.09	0.53
1:1A:2129:C:N3	1:1A:2159:G:O6	2.42	0.53
32:1a:1249:C:O2'	40:1i:73:GLN:NE2	2.42	0.53
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.24	0.53
1:2A:784:A:H5'	1:2A:785:G:OP1	2.09	0.53
26:24:45:GLY:C	26:24:47:GLN:H	2.18	0.53
28:26:9:LEU:HA	28:26:54:ILE:HB	1.91	0.53
32:2a:952:U:H2'	32:2a:953:G:C8	2.44	0.53
32:2a:1092:A:H5"	38:2g:4:ARG:CZ	2.39	0.53
35:2d:64:LEU:HB2	35:2d:198:VAL:HG21	1.91	0.53
44:2m:82:MET:HE3	44:2m:92:HIS:HB3	1.90	0.53
23:11:50:ARG:HG2	23:11:59:THR:HG22	1.90	0.52
32:1a:96:U:H2'	32:1a:97:G:C8	2.44	0.52
32:1a:96:U:H2'	32:1a:97:G:H8	1.74	0.52
32:1a:518:C:O2'	32:1a:530:G:N2	2.43	0.52
1:2A:893:C:H2'	1:2A:894:C:C5	2.44	0.52
48:2q:10:VAL:HG12	48:2q:53:LEU:HD12	1.90	0.52
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.44	0.52
1:1A:1176:G:H21	1:1A:1178:C:P	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1354:A:H4'	3:1D:38:LYS:HE3	1.91	0.52
6:1G:44:GLY:N	6:1G:88:ILE:O	2.43	0.52
14:1S:105:ALA:HB1	14:1S:110:LEU:HD23	1.91	0.52
32:1a:973:G:H3'	32:1a:974:A:H5"	1.91	0.52
32:1a:1192:C:P	34:1c:4:LYS:HZ1	2.33	0.52
34:1c:114:PRO:O	34:1c:118:GLN:NE2	2.41	0.52
1:2A:479:A:N3	1:2A:481:G:H5"	2.24	0.52
8:2I:123:LEU:HD21	8:2I:145:VAL:HA	1.91	0.52
28:26:10:LEU:HG	28:26:54:ILE:HG13	1.91	0.52
32:2a:948:C:H2'	32:2a:949:A:H8	1.73	0.52
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.30	0.52
51:2t:10:LEU:HG	51:2t:12:ALA:H	1.74	0.52
6:1G:114:ILE:HG12	6:1G:140:ILE:HG12	1.91	0.52
11:1P:95:VAL:HG22	11:1P:125:VAL:HB	1.91	0.52
31:19:27:CYS:SG	31:19:28:GLU:N	2.82	0.52
32:1a:92:C:H2'	32:1a:93:G:C8	2.44	0.52
34:1c:152:ILE:HB	34:1c:199:LYS:HB2	1.91	0.52
45:1n:21:TYR:HE1	45:1n:23:ARG:HE	1.58	0.52
1:2A:990:A:OP2	60:2A:3845:HOH:O	2.19	0.52
1:2A:2552:OMU:H6	1:2A:2552:OMU:O5'	2.10	0.52
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.90	0.52
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.42	0.52
32:2a:1427:U:H2'	32:2a:1428:A:C8	2.45	0.52
36:2e:5:ASP:N	36:2e:5:ASP:OD1	2.42	0.52
1:1A:2131:G:H5'	1:1A:2133:G:C8	2.44	0.52
33:1b:28:PHE:HD1	33:1b:194:PRO:HG3	1.74	0.52
1:2A:459:U:H5"	29:27:40:TRP:CD2	2.45	0.52
1:2A:2722:G:H5'	13:2R:4:LEU:HD12	1.91	0.52
32:2a:620:C:C2	35:2d:135:LEU:HG	2.45	0.52
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.09	0.52
33:2b:15:VAL:HG12	33:2b:209:ARG:HD2	1.91	0.52
34:2c:125:GLU:HB3	34:2c:190:ARG:O	2.10	0.52
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.92	0.52
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.08	0.52
32:1a:673:G:H2'	32:1a:674:G:C8	2.44	0.52
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.38	0.52
1:2A:947:G:OP2	60:2A:3847:HOH:O	2.18	0.52
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.89	0.52
1:2A:2683:C:O2	10:2O:70:LYS:NZ	2.31	0.52
26:24:46:GLN:NE2	26:24:48:ARG:HD3	2.25	0.52
32:2a:376:G:H5"	47:2p:5:ARG:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:180:ALA:HB1	34:2c:203:PHE:HE1	1.75	0.52
47:2p:18:ARG:HD3	47:2p:35:LYS:HD2	1.90	0.52
1:1A:400:G:O6	60:1A:4148:HOH:O	2.18	0.52
11:1P:99:LEU:HD13	11:1P:102:ARG:HH21	1.75	0.52
26:14:41:PRO:HA	26:14:47:GLN:HB3	1.91	0.52
32:1a:184:G:H2'	32:1a:185:A:H8	1.73	0.52
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.44	0.52
32:1a:1273:G:H3'	32:1a:1274:G:H8	1.74	0.52
41:1j:40:LEU:HB2	41:1j:69:ASN:HB2	1.90	0.52
44:1m:78:ILE:HG22	44:1m:82:MET:HE2	1.92	0.52
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.44	0.52
1:2A:2759:G:OP2	60:2A:3850:HOH:O	2.19	0.52
6:2G:117:PHE:CE2	6:2G:119:GLY:HA2	2.45	0.52
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.42	0.52
32:2a:973:G:H3'	32:2a:974:A:H5"	1.92	0.52
32:2a:1279:A:O2'	32:2a:1281:U:OP2	2.26	0.52
48:2q:45:HIS:CD2	48:2q:47:PRO:HD3	2.45	0.52
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.91	0.52
32:1a:1278:U:H5'	32:1a:1279:A:O4'	2.10	0.52
33:1b:204:ASN:OD1	33:1b:206:ASP:N	2.35	0.52
1:2A:400:G:O6	60:2A:3831:HOH:O	2.13	0.52
10:2O:98:VAL:HG13	10:2O:117:LEU:HB3	1.92	0.52
32:2a:976:G:N2	32:2a:1363:C:OP2	2.37	0.52
37:2f:38:GLU:HB2	37:2f:64:GLN:HE22	1.75	0.52
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.91	0.52
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.44	0.52
32:1a:165:C:H2'	32:1a:166:G:C8	2.44	0.52
32:1a:1035:A:N3	32:1a:1036:G:N2	2.58	0.52
35:1d:173:TRP:CZ3	35:1d:174:LEU:HG	2.45	0.52
1:2A:1019:U:OP1	1:2A:1035:U:O2'	2.21	0.52
8:2I:5:LEU:HD21	8:2I:12:LEU:HB3	1.92	0.52
10:2O:98:VAL:HG22	10:2O:118:ALA:HA	1.91	0.52
36:2e:143:ARG:NE	39:2h:77:GLU:OE2	2.31	0.52
54:2x:50:U:H2'	54:2x:51:C:C6	2.45	0.52
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.25	0.52
1:1A:2319:G:H22	14:1S:3:ARG:HA	1.74	0.52
32:1a:920:U:H2'	32:1a:921:U:C6	2.45	0.52
36:1e:137:GLU:OE2	36:1e:141:GLN:NE2	2.39	0.52
5:2F:31:HIS:CD2	11:2P:9:ASN:H	2.28	0.52
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.10	0.52
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1099:G:OP2	33:2b:144:ARG:NH2	2.43	0.52
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.45	0.52
1:1A:2108:C:H2'	1:1A:2109:U:H6	1.75	0.52
21:1Z:150:LEU:HD21	21:1Z:154:ASP:HB2	1.92	0.52
32:1a:175:C:H2'	32:1a:176:C:C6	2.44	0.52
32:1a:328:C:H4'	32:1a:329:A:H5'	1.92	0.52
32:1a:864:A:H2'	32:1a:865:A:C8	2.45	0.52
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.39	0.52
36:1e:85:GLY:C	36:1e:87:SER:H	2.17	0.52
37:1f:39:LYS:HB2	37:1f:64:GLN:HB3	1.92	0.52
37:1f:67:MET:SD	37:1f:75:LEU:HD12	2.50	0.52
39:1h:28:ALA:HA	39:1h:59:LEU:HG	1.92	0.52
40:1i:42:ARG:NH1	40:1i:71:SER:OG	2.36	0.52
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.92	0.52
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.42	0.52
1:2A:2022:U:OP1	60:2A:3803:HOH:O	2.19	0.52
15:2T:6:LEU:O	15:2T:10:VAL:HG23	2.09	0.52
15:2T:51:ARG:HG3	15:2T:98:LYS:HD2	1.90	0.52
54:2x:50:U:H2'	54:2x:51:C:H6	1.75	0.52
1:1A:184:C:H2'	1:1A:185:U:C6	2.45	0.51
1:1A:2176:A:H2'	1:1A:2177:C:C6	2.44	0.51
1:1A:2393:A:H2'	1:1A:2394:C:H6	1.75	0.51
9:1N:62:VAL:HG22	9:1N:66:LYS:HD2	1.92	0.51
17:1V:1:MET:HG2	17:1V:43:GLU:OE1	2.10	0.51
32:1a:1372:U:OP1	40:1i:72:GLY:N	2.40	0.51
35:1d:112:VAL:HG23	35:1d:116:GLN:NE2	2.26	0.51
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.43	0.51
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.92	0.51
32:2a:1122:U:H2'	32:2a:1123:A:C8	2.45	0.51
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.72	0.51
33:2b:164:VAL:HG23	33:2b:186:ALA:HB2	1.92	0.51
34:2c:180:ALA:HA	34:2c:206:GLU:HA	1.92	0.51
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.42	0.51
1:1A:880:G:H1	1:1A:898:C:H42	1.58	0.51
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.92	0.51
32:1a:222:U:H2'	32:1a:223:U:C6	2.45	0.51
32:1a:1152:A:H5'	41:1j:13:HIS:ND1	2.25	0.51
42:1k:48:ILE:O	42:1k:50:TYR:N	2.43	0.51
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	1.92	0.51
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.45	0.51
1:2A:2110:G:H3'	1:2A:2111:C:C5'	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.39	0.51
12:2Q:110:THR:HB	12:2Q:113:GLN:H	1.74	0.51
32:2a:427:U:OP2	35:2d:36:ARG:NH2	2.39	0.51
32:2a:736:C:H2'	32:2a:737:A:C8	2.46	0.51
33:2b:19:HIS:HB2	33:2b:204:ASN:HB2	1.92	0.51
15:1T:122:ASP:OD2	32:1a:1442(A):G:O2'	2.23	0.51
23:11:59:THR:O	23:11:91:LYS:NZ	2.43	0.51
2:2B:32:C:H2'	2:2B:33:G:O4'	2.11	0.51
7:2H:7:LEU:HB3	7:2H:69:ARG:HH21	1.75	0.51
32:2a:984:C:H2'	32:2a:985:C:H6	1.76	0.51
32:2a:1189:C:H5'	34:2c:5:ILE:HD12	1.92	0.51
33:2b:15:VAL:O	33:2b:17:PHE:N	2.44	0.51
33:2b:124:SER:HB3	33:2b:125:PRO:HD3	1.92	0.51
38:2g:54:THR:O	38:2g:56:GLN:N	2.43	0.51
39:2h:20:TYR:HA	39:2h:65:TYR:CE1	2.45	0.51
32:1a:262:A:C6	32:1a:263:A:C6	2.98	0.51
32:1a:1376:U:H2'	32:1a:1377:A:C8	2.46	0.51
34:1c:62:ASP:HA	34:1c:97:LYS:HD3	1.92	0.51
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.11	0.51
36:1e:88:LYS:HB3	36:1e:123:LEU:HB2	1.93	0.51
1:2A:370:G:OP2	60:2A:3853:HOH:O	2.19	0.51
21:2Z:53:ILE:HD11	21:2Z:99:TYR:HB2	1.92	0.51
26:24:46:GLN:C	26:24:48:ARG:H	2.18	0.51
32:2a:35:G:O2'	43:2l:118:SER:O	2.24	0.51
32:2a:1014:A:H1'	50:2s:34:TRP:HB2	1.91	0.51
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.11	0.51
34:2c:69:HIS:CD2	34:2c:104:GLN:HG2	2.46	0.51
34:2c:131:ARG:HH21	36:2e:50:GLU:HG3	1.74	0.51
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.93	0.51
50:2s:33:THR:HG21	50:2s:49:ILE:HD11	1.92	0.51
1:1A:574:C:N3	4:1E:145:LYS:NZ	2.57	0.51
26:14:26:SER:OG	26:14:27:THR:N	2.43	0.51
28:16:9:LEU:HD13	28:16:51:GLU:HG3	1.92	0.51
30:18:26:LYS:HD2	30:18:48:PHE:CD2	2.46	0.51
32:1a:259:G:OP2	51:1t:83:ARG:NH2	2.42	0.51
32:1a:1112:C:H1'	34:1c:179:ARG:HH11	1.76	0.51
32:1a:1220:G:N2	50:1s:54:GLY:O	2.36	0.51
32:1a:1291:G:H2'	32:1a:1292:U:C6	2.46	0.51
32:1a:1492:A:N3	43:1l:47:LYS:HE3	2.26	0.51
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.43	0.51
34:1c:155:GLY:HA3	34:1c:196:LEU:HD22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:38:GLU:HB2	37:1f:64:GLN:HG3	1.92	0.51
39:1h:51:VAL:HG21	39:1h:60:ARG:HH11	1.76	0.51
45:1n:9:LYS:HG3	45:1n:12:ARG:HH21	1.74	0.51
1:2A:143:G:H2'	1:2A:143(A):C:H6	1.73	0.51
2:2B:7:G:H2'	2:2B:8:U:O4'	2.10	0.51
32:2a:147:G:H1	32:2a:175:C:H42	1.58	0.51
32:2a:373:A:O2'	32:2a:451:A:N7	2.43	0.51
32:2a:401:C:O2'	32:2a:621:A:N3	2.40	0.51
47:2p:8:ARG:HH21	47:2p:15:PRO:HG3	1.76	0.51
50:2s:38:SER:HB2	50:2s:71:LEU:HD22	1.91	0.51
1:1A:1176:G:H1'	1:1A:1177:A:H5"	1.92	0.51
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.11	0.51
32:1a:79:G:O6	32:1a:90:U:C2	2.63	0.51
32:1a:79:G:C6	32:1a:90:U:O2	2.63	0.51
6:2G:114:ILE:HB	6:2G:117:PHE:HD1	1.74	0.51
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.30	0.51
32:2a:1429:C:H2'	32:2a:1430:C:C6	2.46	0.51
33:2b:119:GLU:HG2	33:2b:142:LEU:HD11	1.93	0.51
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.10	0.51
35:1d:59:ARG:HH12	35:1d:62:GLN:HB2	1.74	0.51
1:2A:852:G:H2'	1:2A:853:G:C8	2.46	0.51
1:2A:1371:G:H2'	1:2A:1372:U:H5	1.75	0.51
5:2F:148:LEU:HD21	5:2F:191:ARG:HD2	1.93	0.51
17:2V:16:PRO:HD3	17:2V:99:ILE:HD11	1.92	0.51
26:24:15:ILE:HG23	26:24:21:VAL:HG22	1.93	0.51
35:2d:76:ARG:NE	35:2d:80:GLU:OE2	2.39	0.51
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.10	0.51
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.11	0.51
32:1a:624:C:H2'	32:1a:625:G:C8	2.46	0.51
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.46	0.51
35:1d:10:ARG:HB2	35:1d:40:PRO:HG3	1.93	0.51
37:1f:69:GLU:O	37:1f:71:ARG:N	2.42	0.51
1:2A:212:G:H2'	1:2A:213:A:O4'	2.11	0.51
1:2A:880:G:H2'	1:2A:881:G:H8	1.75	0.51
21:2Z:55:HIS:CE1	21:2Z:135:GLU:HB2	2.46	0.51
34:2c:47:LEU:HB3	34:2c:52:LEU:HB2	1.92	0.51
47:2p:74:LEU:HD13	47:2p:79:VAL:HG21	1.93	0.51
1:1A:1007:C:OP1	9:1N:37:LYS:HE2	2.11	0.51
1:1A:2336:A:H61	22:10:43:THR:CG2	2.24	0.51
33:1b:24:TRP:H	33:1b:24:TRP:HD1	1.58	0.51
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:10:ARG:NE	14:2S:91:PRO:O	2.37	0.51
32:2a:1002:G:C6	32:2a:1003:G:H8	2.27	0.51
32:2a:1092:A:N3	32:2a:1183:A:N6	2.59	0.51
32:2a:1272:G:N2	32:2a:1273:G:C5	2.79	0.51
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.11	0.51
1:1A:2105:C:H2'	1:1A:2106:G:C8	2.46	0.51
1:1A:2404:C:O3'	11:1P:77:ARG:NH2	2.44	0.51
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.11	0.51
7:1H:33:LEU:HD21	7:1H:136:ILE:HG13	1.92	0.51
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.93	0.51
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.93	0.51
21:1Z:92:SER:O	21:1Z:94:GLU:N	2.44	0.51
32:1a:130:A:OP2	48:1q:63:ARG:NE	2.40	0.51
32:1a:619:U:C2	35:1d:135:LEU:HD22	2.46	0.51
32:1a:1327:C:OP2	52:1u:12:LYS:NZ	2.44	0.51
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.26	0.51
1:2A:11:G:C2'	1:2A:12:U:H5'	2.41	0.51
4:2E:18:ASP:HB3	15:2T:82:LEU:HD21	1.93	0.51
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.91	0.51
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.43	0.51
22:20:12:ASN:O	22:20:14:ARG:N	2.38	0.51
23:21:19:GLN:HB3	23:21:35:THR:HG23	1.92	0.51
32:2a:157:G:H2'	32:2a:158:G:H8	1.75	0.51
32:2a:501:C:H2'	32:2a:502:G:H8	1.75	0.51
32:2a:532:A:H2'	32:2a:532:A:N3	2.25	0.51
32:2a:735:C:H2'	32:2a:736:C:H6	1.75	0.51
32:2a:976:G:OP2	32:2a:1358:U:O2'	2.28	0.51
33:2b:12:GLU:O	33:2b:15:VAL:HG22	2.11	0.51
33:2b:52:GLU:HG3	33:2b:56:ARG:NH2	2.18	0.51
35:2d:47:ARG:NH1	35:2d:47:ARG:HB2	2.26	0.51
1:1A:2140:C:N3	1:1A:2151:G:O6	2.44	0.50
1:2A:603:A:H4'	1:2A:604:G:H5'	1.93	0.50
1:2A:639:U:H2'	1:2A:640:C:C6	2.46	0.50
1:2A:861:A:N3	2:2B:79:C:O2'	2.40	0.50
2:2B:14:U:OP2	2:2B:70:C:O2'	2.25	0.50
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.92	0.50
16:2U:29:SER:OG	16:2U:30:LYS:NZ	2.37	0.50
23:21:83:GLU:OE1	23:21:83:GLU:N	2.45	0.50
40:2i:11:LYS:HA	40:2i:108:VAL:HG12	1.94	0.50
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.76	0.50
1:1A:2787:C:H1'	4:1E:62:PRO:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:66:A:H61	2:1B:108:U:H2'	1.77	0.50
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.44	0.50
12:1Q:59:ARG:O	12:1Q:61:GLY:N	2.30	0.50
32:1a:166:G:H2'	32:1a:167:G:C8	2.46	0.50
32:1a:715:A:H2'	32:1a:716:A:C8	2.46	0.50
32:1a:1134:G:H5'	32:1a:1135:U:OP2	2.10	0.50
39:1h:26:VAL:O	39:1h:59:LEU:N	2.40	0.50
1:2A:271(G):C:H2'	1:2A:271(H):G:C8	2.45	0.50
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.46	0.50
5:2F:178:PRO:HB3	5:2F:198:ALA:HA	1.94	0.50
32:2a:54:C:N4	32:2a:353:A:OP2	2.43	0.50
32:2a:537:G:H5"	43:2l:113:ARG:HH12	1.76	0.50
35:2d:173:TRP:CD2	35:2d:189:PRO:HB3	2.46	0.50
1:1A:303:U:O4	60:1A:4151:HOH:O	2.19	0.50
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.92	0.50
32:1a:911:U:H2'	32:1a:912:C:C6	2.46	0.50
35:1d:88:VAL:HA	36:1e:97:GLY:HA3	1.93	0.50
1:2A:484:C:H2'	1:2A:485:C:C6	2.46	0.50
1:2A:568:U:O4	60:2A:3851:HOH:O	2.19	0.50
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.77	0.50
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.47	0.50
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.92	0.50
32:2a:1072:G:H2'	32:2a:1073:U:C6	2.47	0.50
41:2j:38:ILE:HG12	41:2j:71:LEU:O	2.10	0.50
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.09	0.50
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.44	0.50
26:14:61:ARG:HG3	26:14:62:ARG:H	1.77	0.50
32:1a:953:G:H5'	32:1a:965:A:H61	1.76	0.50
35:1d:119:GLN:HG2	35:1d:123:HIS:CD2	2.47	0.50
35:1d:178:VAL:C	35:1d:180:GLY:H	2.18	0.50
1:2A:386:G:O2'	60:2A:3855:HOH:O	2.19	0.50
1:2A:531:C:OP2	60:2A:3821:HOH:O	2.19	0.50
1:2A:1938:A:OP2	60:2A:3852:HOH:O	2.19	0.50
1:2A:2137:C:N4	1:2A:2154:G:N1	2.50	0.50
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.47	0.50
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.93	0.50
7:2H:7:LEU:HB3	7:2H:69:ARG:NH2	2.27	0.50
7:2H:144:VAL:O	7:2H:148:ILE:HG13	2.12	0.50
32:2a:189(L):G:H2'	32:2a:190:U:C6	2.46	0.50
34:2c:154:SER:O	34:2c:197:GLY:N	2.42	0.50
1:1A:534:U:H2'	1:1A:535:C:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.12	0.50
1:1A:1489:U:HO2'	1:1A:1490:A:H8	1.60	0.50
1:1A:2139:C:H2'	1:1A:2140:C:O4'	2.12	0.50
10:1O:63:VAL:HG12	10:1O:106:LEU:HD21	1.93	0.50
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.47	0.50
8:2I:82:ARG:CZ	8:2I:82:ARG:H	2.25	0.50
9:2N:18:ALA:HA	9:2N:21:LYS:HD2	1.93	0.50
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	1.94	0.50
32:2a:664:G:P	49:2r:64:ARG:HH21	2.35	0.50
32:2a:947:G:O3'	44:2m:109:THR:OG1	2.30	0.50
32:2a:1250:A:H4'	40:2i:68:GLY:N	2.24	0.50
32:2a:1252:A:N6	32:2a:1285:A:H61	2.06	0.50
32:2a:1376:U:OP1	38:2g:98:SER:OG	2.25	0.50
1:1A:800:A:H8	1:1A:800:A:OP1	1.95	0.50
1:1A:1364:G:OP2	23:11:3:LYS:HG3	2.12	0.50
1:1A:1779:U:H2'	60:1A:4203:HOH:O	2.10	0.50
1:1A:2233:U:H2'	1:1A:2234:G:C8	2.47	0.50
32:1a:195:A:OP1	51:1t:68:LYS:NZ	2.43	0.50
32:1a:1349:A:H5"	40:1i:121:ARG:HB2	1.94	0.50
44:1m:19:LEU:HD21	44:1m:56:LEU:HD11	1.93	0.50
47:1p:53:VAL:HG13	47:1p:79:VAL:HG22	1.92	0.50
17:2V:14:VAL:HA	17:2V:18:LEU:HD23	1.94	0.50
32:2a:444:C:H2'	32:2a:445:G:H8	1.76	0.50
32:2a:560:U:H5'	32:2a:566:G:N2	2.26	0.50
32:2a:1289:A:OP1	52:2u:9:ARG:NH2	2.43	0.50
35:2d:155:LEU:HD23	35:2d:156:GLU:N	2.27	0.50
37:2f:97:PHE:HD2	49:2r:31:LEU:HD11	1.77	0.50
47:2p:5:ARG:HH21	47:2p:28:ARG:HA	1.77	0.50
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.12	0.50
4:1E:119:ARG:HG2	4:1E:120:TRP:CD1	2.47	0.50
1:2A:342:G:H2'	1:2A:343:C:H6	1.76	0.50
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.47	0.50
3:2D:3:VAL:HG13	3:2D:17:THR:HB	1.93	0.50
4:2E:14:ILE:HG13	4:2E:21:VAL:HG13	1.93	0.50
6:2G:122:PRO:O	6:2G:125:PHE:HD2	1.95	0.50
13:2R:57:ARG:NE	13:2R:59:ASP:OD1	2.42	0.50
22:20:15:ASP:OD1	22:20:16:SER:N	2.43	0.50
32:2a:41:G:H2'	32:2a:42:G:H8	1.76	0.50
32:2a:618:C:N4	32:2a:621:A:N7	2.59	0.50
38:2g:113:GLU:CG	38:2g:119:ARG:HG2	2.41	0.50
44:2m:3:ARG:HH22	44:2m:11:ARG:HG2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:536:A:H2'	1:1A:537:C:C6	2.46	0.50
32:1a:262:A:H2'	32:1a:263:A:C8	2.47	0.50
32:1a:458:C:H2'	32:1a:460:G:O4'	2.12	0.50
33:1b:16:HIS:HD2	33:1b:204:ASN:H	1.59	0.50
33:1b:93:VAL:HG11	33:1b:97:TRP:CD1	2.47	0.50
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.47	0.50
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.76	0.50
2:2B:11:C:H3'	2:2B:12:C:C6	2.46	0.50
2:2B:42:C:O2'	6:2G:67:LYS:O	2.15	0.50
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.93	0.50
7:2H:3:ARG:HH12	7:2H:65:HIS:HD1	1.60	0.50
11:2P:2:LYS:HG2	11:2P:4:SER:H	1.76	0.50
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.45	0.50
19:2X:32:PRO:O	19:2X:77:LYS:NZ	2.40	0.50
23:21:50:ARG:HG2	23:21:59:THR:HG23	1.92	0.50
30:28:34:TRP:CG	30:28:35:GLN:N	2.80	0.50
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.60	0.50
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.95	0.50
32:2a:1081:G:OP1	36:2e:18:ARG:HG2	2.11	0.50
1:1A:1227:G:OP1	16:1U:13:LYS:NZ	2.45	0.50
2:1B:1:U:H2'	2:1B:2:C:C6	2.47	0.50
11:1P:97:PRO:HD3	11:1P:126:VAL:O	2.11	0.50
32:1a:40:C:H2'	32:1a:41:G:H8	1.77	0.50
32:1a:881:G:P	43:1l:12:ARG:HH22	2.34	0.50
32:1a:998:G:H1	32:1a:1043:C:H42	1.58	0.50
32:1a:1080:A:H5'	36:1e:14:ARG:NH2	2.27	0.50
32:1a:1086:U:H3	32:1a:1099:G:H22	1.58	0.50
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.94	0.50
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.47	0.50
3:2D:180:GLY:HA3	3:2D:275:LYS:HE2	1.94	0.50
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.77	0.50
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.94	0.50
32:2a:741:G:H2'	32:2a:742:G:O4'	2.12	0.50
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.27	0.50
33:2b:76:GLN:HG3	33:2b:206:ASP:O	2.12	0.50
1:1A:1359:A:H2'	1:1A:1360:A:H5'	1.93	0.49
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.47	0.49
4:1E:47:VAL:HG22	4:1E:84:PHE:O	2.11	0.49
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.43	0.49
32:1a:186:C:H2'	32:1a:187:C:C6	2.46	0.49
35:1d:110:PHE:CE1	35:1d:148:VAL:HG23	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:49:PRO:HG3	40:1i:82:ALA:HB2	1.94	0.49
43:1l:28:LYS:HG3	43:1l:62:SER:HB2	1.93	0.49
1:2A:993:G:N2	17:2V:23:GLU:OE2	2.45	0.49
1:2A:1219:G:H1	1:2A:1230:C:H42	1.60	0.49
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.47	0.49
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.12	0.49
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.12	0.49
11:2P:124:LYS:HG3	11:2P:144:GLU:HB3	1.92	0.49
12:2Q:48:GLU:OE1	12:2Q:51:ARG:NH2	2.44	0.49
17:2V:56:SER:HB3	17:2V:100:ARG:HG3	1.94	0.49
32:2a:429:U:H1'	32:2a:430:A:H5"	1.93	0.49
32:2a:839:U:H3'	32:2a:840:C:H5'	1.93	0.49
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.27	0.49
46:2o:4:THR:OG1	46:2o:7:GLU:HG3	2.12	0.49
1:1A:652(F):G:H1	1:1A:652(S):C:N4	2.10	0.49
1:1A:667:U:O2	30:18:2:PRO:HD2	2.13	0.49
8:1I:14:ASP:O	8:1I:17:GLN:HB3	2.11	0.49
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.47	0.49
21:1Z:136:PHE:O	21:1Z:137:ILE:HG13	2.12	0.49
32:1a:110:C:H2'	32:1a:111:G:O4'	2.11	0.49
32:1a:1162:C:H42	32:1a:1174:G:H1	1.60	0.49
32:1a:1414:U:H3	32:1a:1486:G:H1	1.60	0.49
1:2A:10:G:H2'	1:2A:11:G:C8	2.47	0.49
1:2A:276:A:H5"	1:2A:277:C:H5'	1.94	0.49
1:2A:524:U:H2'	1:2A:525:U:C6	2.47	0.49
1:2A:887:A:H4'	1:2A:888:C:C5	2.47	0.49
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.28	0.49
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.12	0.49
1:2A:2101:G:H2'	1:2A:2102:U:O4'	2.12	0.49
1:2A:2166:G:H3'	1:2A:2167:U:H5"	1.94	0.49
1:2A:2306:C:N4	6:2G:42:GLY:O	2.42	0.49
26:24:34:GLU:OE1	44:2m:3:ARG:HA	2.12	0.49
29:27:24:THR:HG22	29:27:26:GLY:N	2.27	0.49
32:2a:316:G:OP2	32:2a:351:G:O2'	2.30	0.49
32:2a:627:G:H2'	32:2a:628:G:H8	1.76	0.49
40:2i:6:GLY:HA3	40:2i:17:VAL:HB	1.93	0.49
48:2q:45:HIS:HB3	48:2q:72:ARG:HG2	1.94	0.49
50:2s:64:GLU:O	50:2s:67:VAL:HG23	2.12	0.49
1:1A:922:U:H2'	1:1A:923:C:C6	2.47	0.49
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.45	0.49
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.93	0.49
4:1E:89:ASP:OD1	4:1E:89:ASP:N	2.44	0.49
18:1W:41:LYS:HE2	27:15:25:LEU:HD21	1.93	0.49
32:1a:524:G:H2'	32:1a:525:C:C6	2.47	0.49
34:1c:148:GLY:HA3	34:1c:172:ARG:H	1.78	0.49
1:2A:2689:U:P	1:2A:2719:G:H22	2.33	0.49
8:2I:71:ILE:O	8:2I:75:LEU:HG	2.11	0.49
14:2S:25:ARG:HB3	14:2S:40:ILE:HB	1.93	0.49
18:2W:18:ARG:HG2	18:2W:76:VAL:HB	1.93	0.49
19:2X:60:ARG:NH1	29:27:47:ARG:HH22	2.10	0.49
32:2a:922:G:C6	32:2a:923:A:C6	2.99	0.49
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.47	0.49
1:1A:8:A:H2'	1:1A:9:U:C6	2.47	0.49
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.47	0.49
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.46	0.49
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.47	0.49
32:1a:584:G:O6	60:1a:1811:HOH:O	2.19	0.49
32:1a:684:A:N6	60:1a:1839:HOH:O	2.44	0.49
32:1a:977:A:H1'	32:1a:982:U:O4	2.12	0.49
33:1b:174:VAL:HG13	33:1b:184:VAL:HG11	1.93	0.49
36:1e:8:GLU:HG3	36:1e:34:VAL:HG23	1.94	0.49
41:1j:48:THR:OG1	41:1j:62:HIS:ND1	2.45	0.49
1:2A:195:A:N7	60:2A:3867:HOH:O	2.34	0.49
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.12	0.49
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.77	0.49
3:2D:221:VAL:HG22	3:2D:226:MET:HE3	1.95	0.49
5:2F:143:ALA:HB1	5:2F:148:LEU:HB2	1.94	0.49
19:2X:35:THR:HB	19:2X:38:GLU:HB3	1.94	0.49
26:24:50:VAL:HG11	44:2m:64:TRP:C	2.37	0.49
32:2a:601:C:H2'	32:2a:602:A:C8	2.48	0.49
32:2a:624:C:H2'	32:2a:625:G:H8	1.77	0.49
32:2a:1220:G:O3'	50:2s:36:ARG:HD3	2.12	0.49
38:2g:23:VAL:HG13	38:2g:43:PHE:HE2	1.76	0.49
39:2h:97:VAL:HG21	39:2h:128:GLY:HA2	1.93	0.49
1:1A:579:G:H2'	1:1A:580:C:C6	2.48	0.49
1:1A:2116:G:H2'	1:1A:2117:A:C6	2.47	0.49
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.45	0.49
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.13	0.49
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.94	0.49
32:1a:171:A:H2'	32:1a:172:A:H8	1.74	0.49
32:1a:551:U:H2'	32:1a:552:U:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.45	0.49
53:1v:14:A:H3'	53:1v:14:A:N3	2.27	0.49
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.47	0.49
1:2A:2679:A:H4'	4:2E:165:VAL:HG11	1.95	0.49
3:2D:77:ALA:HA	3:2D:97:TYR:HA	1.94	0.49
23:21:2:SER:HB3	23:21:46:LEU:HD12	1.94	0.49
32:2a:130:A:O2'	32:2a:131:C:O5'	2.28	0.49
32:2a:1203:C:H2'	32:2a:1204:A:H8	1.77	0.49
32:2a:1226:C:H4'	50:2s:80:TYR:CZ	2.48	0.49
35:2d:112:VAL:HG22	35:2d:116:GLN:HE22	1.77	0.49
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.93	0.49
50:2s:49:ILE:HD11	50:2s:71:LEU:HD21	1.93	0.49
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.46	0.49
1:1A:1077:A:H2'	1:1A:1078:U:H4'	1.94	0.49
1:1A:2134:A:N3	1:1A:2159:G:O2'	2.41	0.49
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.13	0.49
28:16:12:GLU:OE1	28:16:52:VAL:HG11	2.13	0.49
32:1a:1346:A:OP1	40:1i:120:ARG:NH1	2.34	0.49
42:1k:31:THR:HA	42:1k:42:TRP:HA	1.95	0.49
45:1n:7:ILE:HD11	45:1n:28:GLY:HA3	1.94	0.49
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.31	0.49
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.93	0.49
8:2I:5:LEU:H	8:2I:5:LEU:HD12	1.76	0.49
38:2g:78:ARG:HD3	38:2g:79:ARG:N	2.28	0.49
47:2p:28:ARG:HG2	47:2p:29:ASP:OD1	2.12	0.49
1:1A:886:C:OP1	1:1A:886:C:H4'	2.09	0.49
1:1A:2206:G:H3'	1:1A:2207:G:H8	1.75	0.49
7:1H:157:TYR:CE1	7:1H:172:LYS:HG3	2.48	0.49
16:1U:82:GLY:HA3	16:1U:113:ALA:HB1	1.94	0.49
32:1a:189(B):C:H2'	32:1a:189(C):C:C6	2.48	0.49
33:1b:98:LEU:HG	33:1b:101:MET:HE3	1.93	0.49
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.77	0.49
52:1u:15:ARG:HB3	52:1u:15:ARG:HH11	1.77	0.49
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.77	0.49
1:2A:1667:G:O2'	1:2A:1991:U:O4	2.27	0.49
3:2D:11:PRO:O	3:2D:14:ARG:HG3	2.11	0.49
11:2P:28:GLY:O	11:2P:30:THR:N	2.45	0.49
19:2X:50:LYS:N	19:2X:87:GLN:OE1	2.35	0.49
32:2a:67:C:H2'	32:2a:68:G:C8	2.48	0.49
32:2a:580:U:H2'	32:2a:581:G:O4'	2.12	0.49
32:2a:946:A:H2'	32:2a:947:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1252:A:H2'	32:2a:1253:G:O4'	2.13	0.49
32:2a:1328:C:O2'	44:2m:29:ARG:NH2	2.40	0.49
33:2b:27:LYS:HD3	33:2b:193:ASP:OD1	2.12	0.49
1:1A:1055:G:H1	1:1A:1104:C:N4	2.06	0.49
32:1a:277:C:P	48:1q:68:ARG:HH12	2.35	0.49
32:1a:942:G:H21	40:1i:124:GLN:NE2	2.11	0.49
32:1a:1346:A:H61	32:1a:1374:A:H3'	1.77	0.49
39:1h:39:LEU:HB3	39:1h:45:ILE:HG12	1.93	0.49
42:1k:98:LEU:O	42:1k:101:SER:OG	2.24	0.49
1:2A:563:G:OP2	60:2A:3856:HOH:O	2.20	0.49
1:2A:910:A:N1	1:2A:2277:G:H1'	2.27	0.49
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.45	0.49
1:2A:2114:A:H1'	1:2A:2168:G:H1'	1.94	0.49
1:2A:2134:A:H2'	1:2A:2134:A:N3	2.28	0.49
5:2F:107:LYS:HG3	5:2F:206:ILE:HA	1.94	0.49
8:2I:40:THR:HG1	8:2I:41:GLU:H	1.57	0.49
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.94	0.49
32:2a:261:U:OP2	51:2t:79:ARG:NH2	2.46	0.49
32:2a:437:U:H5"	35:2d:155:LEU:HD11	1.95	0.49
32:2a:1109:C:H2'	32:2a:1110:A:O4'	2.13	0.49
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.28	0.49
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.40	0.49
1:1A:271(M):G:O2'	1:1A:271(N):U:H5"	2.13	0.49
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.48	0.49
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.12	0.49
32:1a:162:A:C8	32:1a:163:C:H1'	2.48	0.49
32:1a:175:C:H2'	32:1a:176:C:H6	1.78	0.49
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.48	0.49
1:2A:2698:U:H2'	1:2A:2699:C:C6	2.48	0.49
8:2I:62:LYS:HG2	8:2I:133:HIS:CE1	2.48	0.49
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.94	0.49
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.48	0.49
32:2a:600:C:H2'	32:2a:601:C:C6	2.47	0.49
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.47	0.49
47:2p:28:ARG:NH1	47:2p:29:ASP:OD1	2.45	0.49
50:2s:12:ASP:HB3	50:2s:14:HIS:CD2	2.48	0.49
1:1A:248:G:OP1	60:1A:4152:HOH:O	2.19	0.49
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.13	0.49
32:1a:977:A:O2'	32:1a:979:C:OP2	2.26	0.49
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.48	0.49
34:1c:134:ILE:HG22	34:1c:168:ALA:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:297:C:H2'	1:2A:298:G:O4'	2.13	0.49
1:2A:322:A:OP1	5:2F:168:ARG:HD2	2.12	0.49
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.94	0.49
6:2G:44:GLY:N	6:2G:88:ILE:O	2.44	0.49
8:2I:129:THR:HG22	8:2I:139:GLN:NE2	2.28	0.49
32:2a:551:U:H2'	32:2a:552:U:C6	2.47	0.49
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.94	0.49
40:2i:3:GLN:HG3	40:2i:20:ARG:HG2	1.95	0.49
46:2o:82:ILE:HD12	46:2o:88:ARG:HB2	1.95	0.49
48:2q:6:LEU:HB3	48:2q:23:VAL:HG11	1.94	0.49
1:1A:593:G:H4'	30:18:4:MET:HE2	1.95	0.48
1:1A:855:G:O2'	22:10:27:GLU:OE2	2.24	0.48
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.94	0.48
32:1a:575:G:O2'	32:1a:821:G:H5'	2.13	0.48
38:1g:50:ILE:HD11	38:1g:125:MET:HG2	1.95	0.48
1:2A:1266:G:O4'	18:2W:15:ARG:NH2	2.43	0.48
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.47	0.48
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.48	0.48
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.13	0.48
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.48	0.48
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.13	0.48
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.48	0.48
15:1T:125:ARG:HG2	15:1T:129:ARG:HH21	1.78	0.48
32:1a:321:A:N7	32:1a:328:C:O2'	2.40	0.48
1:2A:203:C:OP2	60:2A:3854:HOH:O	2.19	0.48
1:2A:645:C:H5"	1:2A:646:A:OP2	2.13	0.48
1:2A:987:G:O2'	1:2A:1000:A:N3	2.42	0.48
1:2A:1527:G:H2'	1:2A:1542:A:N1	2.28	0.48
1:2A:2128:C:H2'	1:2A:2129:C:O4'	2.13	0.48
4:2E:59:VAL:HG21	4:2E:74:PRO:HB3	1.95	0.48
32:2a:189(C):C:H2'	32:2a:189(D):C:O4'	2.13	0.48
32:2a:562:C:H1'	43:2l:15:ARG:HB3	1.94	0.48
33:2b:55:PHE:O	33:2b:59:GLU:N	2.36	0.48
34:2c:138:VAL:HG23	34:2c:151:VAL:HG23	1.94	0.48
42:2k:73:MET:HG2	42:2k:103:LEU:HD21	1.95	0.48
1:1A:1075:C:H2'	1:1A:1076:C:H5'	1.95	0.48
1:1A:1429:G:H2'	1:1A:1430:C:H6	1.78	0.48
11:1P:121:LYS:O	11:1P:123:LEU:N	2.46	0.48
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.45	0.48
32:1a:396:G:O2'	32:1a:398:C:OP1	2.20	0.48
32:1a:1029:C:N4	32:1a:1031:G:O6	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1289:A:N1	32:1a:1371:G:O2'	2.41	0.48
33:1b:20:GLU:HG2	33:1b:23:ARG:HH11	1.78	0.48
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.94	0.48
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.49	0.48
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.95	0.48
39:1h:121:ASP:HB2	39:1h:125:ARG:HH21	1.78	0.48
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.13	0.48
1:2A:186:G:H2'	1:2A:187:G:H8	1.78	0.48
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.31	0.48
44:2m:90:LEU:HA	44:2m:93:ARG:HE	1.77	0.48
1:1A:1057:A:H62	1:1A:1087:G:P	2.36	0.48
1:1A:1371:G:H2'	1:1A:1372:U:C5	2.48	0.48
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.28	0.48
1:1A:2154:G:C2	1:1A:2155:G:H1'	2.48	0.48
2:1B:24:G:N7	2:1B:56:G:H2'	2.28	0.48
32:1a:37:U:O2'	32:1a:547:A:N1	2.40	0.48
32:1a:243:A:H4'	32:1a:244:U:H5"	1.95	0.48
32:1a:743:U:H2'	32:1a:744:C:C6	2.48	0.48
32:1a:1100:C:OP2	33:1b:96:ARG:HD2	2.14	0.48
32:1a:1239:A:H62	32:1a:1299:A:N6	2.11	0.48
33:1b:54:THR:O	33:1b:58:ILE:HG13	2.14	0.48
34:1c:52:LEU:HD13	34:1c:68:VAL:HG13	1.94	0.48
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.78	0.48
44:1m:88:ARG:HG2	44:1m:98:VAL:HG12	1.96	0.48
1:2A:947:G:H2'	1:2A:948:G:C8	2.48	0.48
1:2A:2818:G:OP1	1:2A:2837:G:O2'	2.20	0.48
6:2G:19:LEU:HD12	6:2G:175:LEU:HD12	1.95	0.48
9:2N:115:ARG:HA	9:2N:118:LYS:HE3	1.96	0.48
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.94	0.48
32:2a:838:G:N2	32:2a:840:C:H5"	2.28	0.48
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.13	0.48
37:2f:38:GLU:HB2	37:2f:64:GLN:NE2	2.28	0.48
1:1A:185:U:H4'	1:1A:218:A:H4'	1.96	0.48
1:1A:376:C:OP2	60:1A:4154:HOH:O	2.20	0.48
1:1A:2291:U:O2'	1:1A:2374:C:O2	2.31	0.48
3:1D:83:GLU:OE1	3:1D:104:TYR:OH	2.28	0.48
7:1H:111:HIS:CD2	7:1H:111:HIS:H	2.30	0.48
21:1Z:132:ASN:HD22	21:1Z:160:GLY:HA3	1.77	0.48
22:10:43:THR:O	22:10:43:THR:HG23	2.14	0.48
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.78	0.48
47:1p:19:ILE:HG22	47:1p:36:ILE:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2299:G:N1	1:2A:2318:G:N7	2.60	0.48
1:2A:2833:G:H4'	1:2A:2834:G:OP2	2.12	0.48
5:2F:188:ARG:HG2	11:2P:3:LEU:HD11	1.95	0.48
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.28	0.48
32:2a:56:U:H2'	32:2a:57:G:H8	1.77	0.48
32:2a:814:A:N7	32:2a:816:A:C4	2.81	0.48
32:2a:1086:U:H2'	32:2a:1087:G:H8	1.78	0.48
35:2d:135:LEU:C	35:2d:137:SER:H	2.21	0.48
1:1A:27:G:N2	1:1A:512:G:H1'	2.29	0.48
1:1A:636:G:OP1	11:1P:132:LYS:HE2	2.14	0.48
18:1W:4:LYS:HD3	18:1W:6:ILE:HD11	1.95	0.48
21:1Z:132:ASN:ND2	21:1Z:160:GLY:HA3	2.28	0.48
32:1a:270:A:H2'	32:1a:271:C:C6	2.48	0.48
1:2A:484:C:H2'	1:2A:485:C:H6	1.79	0.48
1:2A:901:A:H2'	1:2A:902:C:C6	2.49	0.48
1:2A:1288:U:O4	13:2R:106:GLY:HA3	2.13	0.48
1:2A:1495:A:H2'	1:2A:1496:A:C8	2.48	0.48
1:2A:2127:G:C2	1:2A:2161:C:N3	2.81	0.48
1:2A:2305:A:H1'	6:2G:136:ARG:HG2	1.94	0.48
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.13	0.48
13:2R:98:LEU:HB2	13:2R:113:LEU:HD11	1.95	0.48
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.13	0.48
32:2a:950:U:OP2	44:2m:102:ARG:HD3	2.14	0.48
32:2a:1097:C:O2'	32:2a:1169:A:N3	2.41	0.48
34:2c:59:ARG:NH1	34:2c:63:ASN:O	2.46	0.48
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.31	0.48
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.13	0.48
7:1H:17:VAL:HG22	7:1H:26:VAL:HG22	1.96	0.48
32:1a:447:G:O6	32:1a:485:G:O2'	2.25	0.48
32:1a:1260:C:O5'	32:1a:1284:C:H4'	2.14	0.48
33:1b:69:LEU:HD13	33:1b:155:LEU:HD22	1.96	0.48
1:2A:789:A:N1	60:2A:3906:HOH:O	2.35	0.48
1:2A:1037:G:H2'	1:2A:1038:C:O4'	2.12	0.48
1:2A:2849:U:OP2	15:2T:95:ARG:NH1	2.46	0.48
8:2I:63:ALA:HA	8:2I:66:GLU:HB3	1.95	0.48
21:2Z:30:ASN:HA	21:2Z:89:PHE:HE1	1.78	0.48
32:2a:1169:A:H2'	32:2a:1170:A:O4'	2.14	0.48
50:2s:35:SER:O	50:2s:71:LEU:HD23	2.13	0.48
1:1A:1062:G:C5	1:1A:1088:A:H2'	2.49	0.48
1:1A:1651:G:OP1	13:1R:40:LYS:HE3	2.13	0.48
1:1A:2101:G:H2'	1:1A:2102:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2224:G:H4'	1:1A:2226:C:C2	2.49	0.48
32:1a:667:G:H4'	46:1o:51:HIS:ND1	2.29	0.48
32:1a:928:G:O2'	32:1a:1533:C:OP1	2.32	0.48
34:1c:57:ILE:HG12	34:1c:66:VAL:HG12	1.96	0.48
39:1h:121:ASP:HB2	39:1h:125:ARG:NH2	2.29	0.48
49:1r:74:ARG:HG3	49:1r:79:LEU:HB2	1.96	0.48
1:2A:923:C:H2'	1:2A:924:C:H6	1.78	0.48
1:2A:2317:C:N4	1:2A:2318:G:O6	2.46	0.48
9:2N:42:TRP:HA	9:2N:48:MET:SD	2.54	0.48
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.49	0.48
15:2T:30:VAL:HG22	15:2T:86:ILE:HG12	1.95	0.48
32:2a:1187:G:OP1	40:2i:113:LYS:NZ	2.46	0.48
36:2e:146:ALA:O	36:2e:150:ARG:HG2	2.14	0.48
39:2h:14:ARG:HH21	39:2h:84:ARG:HA	1.79	0.48
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.49	0.48
45:2n:24:CYS:O	45:2n:28:GLY:N	2.40	0.48
47:2p:3:LYS:O	47:2p:21:VAL:HA	2.14	0.48
48:2q:26:GLN:OE1	48:2q:37:LYS:NZ	2.46	0.48
1:1A:1058:G:N2	1:1A:1080:C:N3	2.54	0.48
1:1A:2118:U:O4	1:1A:2149:G:H1'	2.14	0.48
1:1A:2238:G:N3	1:1A:2238:G:H2'	2.27	0.48
1:1A:2706:G:N7	60:1A:4221:HOH:O	2.35	0.48
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.13	0.48
20:1Y:30:VAL:HG13	20:1Y:37:VAL:HG12	1.94	0.48
44:1m:17:VAL:O	44:1m:20:THR:OG1	2.32	0.48
1:2A:615:G:OP1	5:2F:40:GLN:NE2	2.47	0.48
1:2A:903:C:H2'	1:2A:904:C:C6	2.49	0.48
2:2B:105:A:H5'	2:2B:106:G:OP2	2.14	0.48
6:2G:41:GLN:O	6:2G:43:LEU:HD22	2.14	0.48
16:2U:104:GLN:HE21	16:2U:105:VAL:HG23	1.77	0.48
19:2X:1:MET:HE2	19:2X:3:THR:HG22	1.94	0.48
32:2a:1182:G:H4'	32:2a:1183:A:H5"	1.96	0.48
1:1A:295:G:H4'	20:1Y:1:MET:HE3	1.95	0.48
1:1A:1039:G:H1	1:1A:1116:C:H42	1.62	0.48
1:1A:1057:A:N6	1:1A:1087:G:OP1	2.46	0.48
1:1A:1066:U:H2'	1:1A:1068:G:OP2	2.12	0.48
19:1X:54:VAL:HG22	19:1X:81:VAL:HG12	1.95	0.48
32:1a:56:U:H2'	32:1a:57:G:H8	1.79	0.48
32:1a:434:U:H2'	32:1a:435:C:C6	2.49	0.48
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.49	0.48
32:1a:1241:G:H2'	32:1a:1242:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:656:G:H2'	1:2A:657:U:O4'	2.14	0.48
1:2A:867:C:H2'	1:2A:868:U:C6	2.48	0.48
1:2A:1237:A:OP1	60:2A:3858:HOH:O	2.20	0.48
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.49	0.48
2:2B:11:C:H3'	2:2B:12:C:H6	1.78	0.48
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.13	0.48
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.95	0.48
32:2a:107:G:H2'	32:2a:108:G:O4'	2.13	0.48
32:2a:826:C:H2'	32:2a:827:U:C6	2.48	0.48
32:2a:1512:U:H2'	32:2a:1513:A:H8	1.78	0.48
44:2m:29:ARG:HD3	44:2m:64:TRP:CE2	2.48	0.48
50:2s:63:THR:OG1	50:2s:64:GLU:N	2.47	0.48
1:1A:2337:G:OP1	60:1A:4153:HOH:O	2.20	0.47
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.48	0.47
32:1a:229:U:H5"	47:1p:33:ILE:HD13	1.94	0.47
32:1a:1149:C:H2'	32:1a:1150:U:C6	2.49	0.47
43:1l:84:LEU:HB3	43:1l:104:VAL:HG11	1.95	0.47
1:2A:71:A:H5"	1:2A:73:A:C8	2.49	0.47
1:2A:322:A:OP2	5:2F:169:ASN:HB2	2.14	0.47
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.95	0.47
2:2B:52:A:N6	14:2S:33:LYS:HG2	2.29	0.47
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.96	0.47
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.13	0.47
32:2a:442:C:H42	32:2a:492:G:H1	1.62	0.47
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.95	0.47
36:2e:6:PHE:HB3	36:2e:34:VAL:HG22	1.95	0.47
38:2g:152:ALA:O	38:2g:155:ARG:HD3	2.14	0.47
46:2o:5:LYS:H	46:2o:5:LYS:HD3	1.79	0.47
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.94	0.47
1:1A:9:U:H3	1:1A:2629:A:H2	1.60	0.47
4:1E:13:ARG:HD2	4:1E:20:ALA:HB1	1.95	0.47
32:1a:236:G:H5"	48:1q:42:TYR:OH	2.15	0.47
32:1a:341:C:H2'	32:1a:342:C:C6	2.49	0.47
32:1a:983:A:H1'	32:1a:1049:U:O2	2.14	0.47
33:1b:16:HIS:CD2	33:1b:204:ASN:H	2.32	0.47
52:1u:3:LYS:HB3	52:1u:14:TRP:CD1	2.49	0.47
1:2A:271(K):U:O2	8:2I:50:ARG:HD3	2.13	0.47
1:2A:1384:A:N3	1:2A:1405:U:H1'	2.28	0.47
1:2A:1693:U:H1'	3:2D:14:ARG:NH2	2.29	0.47
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.48	0.47
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2137:C:C2	1:2A:2154:G:N2	2.76	0.47
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.49	0.47
1:2A:2809:A:H2'	1:2A:2810:A:C8	2.49	0.47
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.28	0.47
32:2a:1263:C:H1'	32:2a:1273:G:N2	2.29	0.47
32:2a:1266:G:N2	32:2a:1269:A:OP2	2.34	0.47
32:2a:1298:C:H2'	38:2g:114:ARG:NH2	2.28	0.47
40:2i:99:LEU:HB3	40:2i:101:PHE:CE2	2.49	0.47
44:2m:67:GLU:HB3	44:2m:68:GLY:H	1.55	0.47
1:1A:731:C:OP1	60:1A:4155:HOH:O	2.20	0.47
1:1A:2836:U:H2'	1:1A:2837:G:C8	2.50	0.47
6:1G:23:PHE:HB2	6:1G:25:TYR:CE2	2.50	0.47
6:1G:126:ASP:OD2	6:1G:130:ASN:ND2	2.45	0.47
26:14:61:ARG:NH2	50:1s:9:VAL:HG21	2.30	0.47
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.96	0.47
1:2A:218:A:C2	1:2A:235:U:H4'	2.49	0.47
1:2A:839:U:H2'	1:2A:840:C:H6	1.79	0.47
1:2A:2182:G:H2'	1:2A:2183:C:C6	2.48	0.47
1:2A:2498:C:H3'	60:2A:3825:HOH:O	2.14	0.47
2:2B:1:U:H2'	2:2B:2:C:C6	2.49	0.47
2:2B:24:G:H4'	2:2B:25:A:N7	2.29	0.47
3:2D:108:PRO:HD2	3:2D:111:LEU:HD22	1.95	0.47
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.94	0.47
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.54	0.47
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.49	0.47
32:2a:631:G:H2'	32:2a:632:A:H8	1.79	0.47
33:2b:106:LYS:HA	33:2b:109:SER:HB2	1.96	0.47
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.96	0.47
36:2e:90:VAL:O	36:2e:120:THR:HA	2.15	0.47
42:2k:18:ARG:HD2	42:2k:83:ILE:HD11	1.96	0.47
42:2k:110:ASP:HB3	49:2r:85:LEU:HB3	1.96	0.47
1:1A:882:G:H1	1:1A:894:C:H42	1.61	0.47
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.13	0.47
24:12:1:MET:HE2	24:12:6:VAL:HG22	1.96	0.47
32:1a:1192:C:OP2	34:1c:4:LYS:NZ	2.33	0.47
34:1c:87:LEU:O	34:1c:91:LEU:N	2.34	0.47
35:1d:172:PRO:C	35:1d:174:LEU:H	2.21	0.47
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.50	0.47
1:2A:994:C:O2'	1:2A:996:A:OP1	2.32	0.47
2:2B:9:G:P	14:2S:25:ARG:HH22	2.37	0.47
7:2H:90:LYS:HG2	7:2H:159:GLU:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:60:GLU:HB2	17:2V:97:LYS:HE2	1.96	0.47
26:24:61:ARG:HH21	50:2s:9:VAL:HG11	1.78	0.47
27:25:57:VAL:HG12	27:25:58:LEU:HD13	1.96	0.47
32:2a:685:G:C2	32:2a:686:U:C4	3.03	0.47
32:2a:688:G:H2'	32:2a:689:C:H6	1.79	0.47
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.14	0.47
35:2d:104:VAL:HG21	35:2d:140:VAL:HG21	1.97	0.47
44:2m:33:ALA:HB1	44:2m:60:VAL:HG22	1.95	0.47
47:2p:6:LEU:HD23	47:2p:17:TYR:CG	2.50	0.47
54:2x:40:C:H2'	54:2x:41:C:C6	2.47	0.47
1:1A:2029:G:H2'	1:1A:2031:A:OP1	2.13	0.47
1:1A:2483:C:N3	12:1Q:124:LYS:NZ	2.60	0.47
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.79	0.47
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	1.97	0.47
34:1c:104:GLN:HG3	34:1c:105:GLU:N	2.30	0.47
47:1p:67:THR:H	47:1p:70:ALA:HB3	1.80	0.47
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.13	0.47
2:2B:2:C:H2'	2:2B:3:C:H6	1.80	0.47
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.48	0.47
6:2G:33:ARG:O	6:2G:34:LEU:HD23	2.14	0.47
12:2Q:20:ALA:HB2	21:2Z:79:ARG:HG3	1.96	0.47
14:2S:11:LYS:O	14:2S:15:ARG:HB2	2.14	0.47
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.96	0.47
18:2W:35:ILE:HG23	27:25:28:PRO:HD2	1.97	0.47
32:2a:1004:A:N6	32:2a:1037:C:H1'	2.30	0.47
32:2a:1346:A:H5"	40:2i:120:ARG:HH12	1.80	0.47
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.96	0.47
34:2c:69:HIS:HA	34:2c:104:GLN:HB3	1.96	0.47
1:1A:889:C:O2'	1:1A:890:A:O4'	2.33	0.47
1:1A:1176:G:N2	1:1A:1178:C:OP2	2.47	0.47
1:1A:1364:G:P	23:11:3:LYS:HG3	2.55	0.47
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.96	0.47
5:1F:51:THR:O	5:1F:93:LYS:NZ	2.43	0.47
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.30	0.47
32:1a:540:G:H2'	32:1a:541:G:O4'	2.15	0.47
33:1b:77:ALA:HB2	33:1b:211:ILE:HG21	1.96	0.47
36:1e:110:LEU:HD13	36:1e:118:ILE:HD13	1.96	0.47
40:1i:49:PRO:C	40:1i:51:ARG:H	2.23	0.47
47:1p:6:LEU:HB3	47:1p:17:TYR:CD1	2.49	0.47
1:2A:1178:C:H2'	1:2A:1179:C:H6	1.79	0.47
1:2A:2135:A:C8	1:2A:2136:C:H5	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2291:U:O2'	1:2A:2374:C:O2	2.31	0.47
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.30	0.47
6:2G:126:ASP:O	6:2G:128:ARG:N	2.45	0.47
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.56	0.47
32:2a:456:C:H2'	32:2a:457:C:C6	2.49	0.47
42:2k:98:LEU:O	42:2k:101:SER:OG	2.31	0.47
1:1A:264:C:O2'	1:1A:265:A:H2'	2.15	0.47
1:1A:576:U:H2'	1:1A:577:G:C8	2.49	0.47
1:1A:969:U:H2'	1:1A:970:C:C6	2.50	0.47
1:1A:2287:A:O2'	1:1A:2289:G:N7	2.45	0.47
1:1A:2292:C:OP1	14:1S:17:ARG:NH2	2.46	0.47
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.50	0.47
26:14:53:GLU:CD	26:14:54:GLY:H	2.23	0.47
26:14:55:ARG:H	26:14:56:VAL:HA	1.78	0.47
32:1a:138:G:H1	32:1a:225:C:H42	1.61	0.47
44:1m:34:LEU:HD13	44:1m:41:PRO:HA	1.97	0.47
44:1m:84:ILE:HG13	44:1m:86:CYS:H	1.80	0.47
45:1n:27:CYS:SG	45:1n:29:ARG:HB2	2.54	0.47
46:1o:74:ASP:HB3	46:1o:77:ARG:HB2	1.97	0.47
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.15	0.47
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.50	0.47
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.15	0.47
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.14	0.47
1:2A:2064:C:H2'	1:2A:2065:C:C6	2.50	0.47
1:2A:2316:C:H2'	1:2A:2317:C:H6	1.80	0.47
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.14	0.47
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.97	0.47
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.96	0.47
5:2F:11:VAL:HG22	5:2F:125:LEU:HD12	1.95	0.47
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.96	0.47
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.50	0.47
16:2U:76:TYR:O	16:2U:80:ILE:HG12	2.14	0.47
32:2a:196:A:N3	32:2a:222:U:H1'	2.29	0.47
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.97	0.47
35:2d:61:LYS:NZ	35:2d:72:GLU:OE1	2.33	0.47
35:2d:78:LEU:HD23	35:2d:96:LEU:HB3	1.96	0.47
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.79	0.47
35:2d:119:GLN:HG3	35:2d:123:HIS:CD2	2.50	0.47
35:2d:127:THR:HG23	35:2d:147:ALA:HB3	1.97	0.47
41:2j:6:ILE:HG12	41:2j:98:ILE:HG13	1.97	0.47
43:2l:113:ARG:NH2	60:2l:301:HOH:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:2p:8:ARG:HB3	47:2p:28:ARG:NH1	2.30	0.47
51:2t:47:GLY:HA2	51:2t:48:LYS:C	2.40	0.47
3:1D:38:LYS:HA	3:1D:38:LYS:HD2	1.76	0.47
9:1N:4:TYR:HB2	16:1U:101:ARG:NH1	2.29	0.47
20:1Y:55:TYR:CE1	20:1Y:61:ILE:HG21	2.50	0.47
32:1a:17:U:H2'	32:1a:18:C:C6	2.50	0.47
32:1a:35:G:O2'	43:1l:118:SER:O	2.24	0.47
32:1a:1037:C:H2'	32:1a:1038:C:H6	1.79	0.47
36:1e:145:LYS:O	36:1e:148:VAL:HG22	2.15	0.47
36:1e:148:VAL:O	36:1e:152:ARG:HG3	2.15	0.47
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.95	0.47
1:2A:571:A:N6	1:2A:2499:C:O3'	2.48	0.47
1:2A:878:A:H61	1:2A:899:A:H1'	1.80	0.47
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.80	0.47
32:2a:656:C:O2'	46:2o:28:GLN:OE1	2.18	0.47
32:2a:892:A:O2'	32:2a:1415:G:H4'	2.15	0.47
39:2h:6:ILE:O	39:2h:10:LEU:HG	2.14	0.47
48:2q:29:HIS:CD2	48:2q:30:PRO:HD2	2.49	0.47
1:1A:223:A:N1	1:1A:407:G:O2'	2.47	0.47
1:1A:1424:G:H2'	1:1A:1425:G:O4'	2.15	0.47
1:1A:2116:G:H2'	1:1A:2117:A:C5	2.49	0.47
32:1a:272:C:H2'	32:1a:273:A:H8	1.80	0.47
32:1a:961:U:OP2	32:1a:1223:C:O2'	2.25	0.47
40:1i:99:LEU:HD23	40:1i:101:PHE:CE2	2.49	0.47
1:2A:1040:C:H2'	1:2A:1041:C:C6	2.49	0.47
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.50	0.47
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.12	0.47
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.97	0.47
17:2V:66:ARG:O	17:2V:88:ARG:NH2	2.48	0.47
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG21	1.80	0.47
32:2a:149:A:H2'	32:2a:150:C:C6	2.50	0.47
32:2a:936:C:H2'	32:2a:937:A:O4'	2.14	0.47
33:2b:55:PHE:HE1	33:2b:218:ALA:HA	1.79	0.47
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.97	0.47
1:1A:715:G:C4	46:1o:56:LEU:HD21	2.50	0.47
1:1A:1056:G:H5"	1:1A:1057:A:H5'	1.97	0.47
1:1A:2159:G:H4'	1:1A:2159:G:OP1	2.14	0.47
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.50	0.47
2:1B:78:A:C2	2:1B:100:A:C4	3.02	0.47
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.97	0.47
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.15	0.47
34:1c:104:GLN:HG3	34:1c:105:GLU:H	1.80	0.47
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.50	0.47
13:2R:67:LEU:HD13	13:2R:76:VAL:HG21	1.96	0.47
28:26:23:THR:OG1	28:26:24:GLU:N	2.45	0.47
32:2a:67:C:H2'	32:2a:68:G:H8	1.79	0.47
32:2a:409:G:H1	32:2a:433:C:H42	1.62	0.47
32:2a:707:C:H5"	42:2k:85:ARG:HH12	1.80	0.47
32:2a:1176:A:H2'	32:2a:1177:G:H8	1.77	0.47
54:2x:19:G:H4'	54:2x:20:U:OP2	2.15	0.47
1:1A:620:G:N3	1:1A:620:G:H5'	2.29	0.46
1:1A:1268:A:C2	1:1A:2013:A:C4	3.04	0.46
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.51	0.46
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.50	0.46
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.51	0.46
1:1A:1594:G:H2'	1:1A:1595:G:O4'	2.15	0.46
1:1A:2469:A:O2'	12:1Q:56:ARG:HD3	2.15	0.46
1:2A:141:A:H8	1:2A:1408:C:O2'	1.98	0.46
1:2A:2336:A:H61	22:20:43:THR:CG2	2.28	0.46
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.96	0.46
21:2Z:159:PRO:HA	21:2Z:160:GLY:HA2	1.62	0.46
32:2a:448:A:P	32:2a:485:G:H22	2.37	0.46
32:2a:532:A:N6	32:2a:1206:G:O2'	2.48	0.46
32:2a:840:C:H4'	32:2a:841:U:OP1	2.15	0.46
32:2a:977:A:O2'	32:2a:981:U:N3	2.48	0.46
32:2a:1002:G:C2	32:2a:1003:G:H1'	2.50	0.46
32:2a:1122:U:C4	32:2a:1123:A:N7	2.83	0.46
34:2c:32:LEU:O	34:2c:36:ASP:HB2	2.14	0.46
39:2h:51:VAL:HG11	39:2h:60:ARG:HH12	1.80	0.46
44:2m:117:VAL:HG22	44:2m:118:ALA:H	1.81	0.46
50:2s:28:LYS:HB3	50:2s:29:ARG:HA	1.97	0.46
1:1A:2131:G:N2	1:1A:2158:A:N1	2.63	0.46
1:1A:2876:G:H4'	15:1T:2:ASN:ND2	2.30	0.46
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.97	0.46
32:1a:119:A:H4'	32:1a:120:A:C8	2.50	0.46
32:1a:636:U:H2'	32:1a:637:G:C8	2.50	0.46
32:1a:848:C:H2'	32:1a:849:C:H6	1.81	0.46
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.48	0.46
1:2A:208:C:H2'	1:2A:209:C:C6	2.51	0.46
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.15	0.46
1:2A:1836:C:H2'	1:2A:1837:C:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.80	0.46
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.15	0.46
12:2Q:31:ASP:HA	12:2Q:134:ARG:HH11	1.79	0.46
32:2a:1219:U:O2'	50:2s:34:TRP:HB3	2.16	0.46
45:2n:48:ALA:HB2	45:2n:53:LEU:HD12	1.97	0.46
1:1A:1071:G:H1'	1:1A:1089:G:H2'	1.97	0.46
1:1A:1427:A:H4'	1:1A:1428:C:O4'	2.15	0.46
1:1A:2206:G:H5"	1:1A:2207:G:N7	2.31	0.46
1:1A:2469:A:H2'	1:1A:2470:G:O4'	2.16	0.46
4:1E:181:LEU:HD12	4:1E:181:LEU:HA	1.79	0.46
32:1a:198:G:H2'	32:1a:199:G:H8	1.80	0.46
32:1a:1442:G:O2'	32:1a:1442(A):G:H5'	2.15	0.46
33:1b:10:LEU:HA	33:1b:48:MET:HE1	1.97	0.46
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.15	0.46
1:2A:885:C:H1'	1:2A:892:G:O6	2.14	0.46
1:2A:903:C:H2'	1:2A:904:C:H6	1.80	0.46
1:2A:1125:G:H5'	31:29:37:GLY:HA2	1.97	0.46
1:2A:1532:C:H42	1:2A:1537:G:H1	1.62	0.46
1:2A:2090:G:N2	23:21:45:ASN:OD1	2.35	0.46
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.50	0.46
2:2B:41:U:H5	6:2G:70:VAL:H	1.63	0.46
4:2E:12:THR:HG22	4:2E:13:ARG:N	2.30	0.46
4:2E:103:ASP:N	4:2E:199:ARG:O	2.44	0.46
6:2G:33:ARG:O	6:2G:161:THR:HG23	2.15	0.46
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.98	0.46
32:2a:1427:U:H2'	32:2a:1428:A:H8	1.80	0.46
36:2e:12:LEU:HD22	36:2e:128:PRO:HB2	1.96	0.46
40:2i:55:ALA:HA	40:2i:58:HIS:CD2	2.50	0.46
12:1Q:58:PHE:HB3	12:1Q:61:GLY:O	2.14	0.46
32:1a:258:G:H2'	32:1a:259:G:C8	2.49	0.46
32:1a:271:C:H2'	32:1a:272:C:C6	2.50	0.46
32:1a:995:C:H1'	45:1n:4:LYS:HE2	1.98	0.46
32:1a:1250:A:H4'	40:1i:68:GLY:N	2.30	0.46
34:1c:6:HIS:CD2	34:1c:8:ILE:H	2.28	0.46
1:2A:218:A:OP2	60:2A:3859:HOH:O	2.21	0.46
1:2A:975(A):G:O2'	1:2A:1156:A:N1	2.41	0.46
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.50	0.46
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.15	0.46
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.97	0.46
32:2a:1226:C:O2	50:2s:83:HIS:HE1	1.99	0.46
34:2c:177:THR:HG22	34:2c:179:ARG:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:2k:92:GLU:O	42:2k:96:ARG:HG2	2.15	0.46
43:2l:110:VAL:HG23	43:2l:120:TYR:HB3	1.97	0.46
1:1A:272(G):C:H42	1:1A:363(C):G:H1	1.63	0.46
1:1A:1406:U:H2'	1:1A:1407:C:H6	1.79	0.46
1:1A:2319:G:N2	14:1S:3:ARG:HA	2.30	0.46
5:1F:140:LEU:HD21	5:1F:170:LEU:HD21	1.97	0.46
14:1S:28:VAL:HG11	14:1S:98:VAL:HG13	1.96	0.46
32:1a:1150:U:H4'	41:1j:41:PRO:HG3	1.98	0.46
33:1b:37:ASN:C	33:1b:39:ILE:H	2.24	0.46
34:1c:58:GLU:HB2	34:1c:65:ALA:HB3	1.97	0.46
1:2A:265:A:C8	1:2A:266:G:H1'	2.51	0.46
1:2A:625:G:N7	11:2P:107:LYS:NZ	2.60	0.46
1:2A:800:A:H8	1:2A:800:A:OP1	1.98	0.46
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.81	0.46
5:2F:164:ARG:O	5:2F:168:ARG:HB2	2.15	0.46
8:2I:50:ARG:HA	8:2I:53:ALA:HB3	1.97	0.46
32:2a:547:A:OP1	60:2a:1811:HOH:O	2.20	0.46
41:2j:78:ASN:O	41:2j:81:THR:N	2.44	0.46
42:2k:82:VAL:HB	42:2k:108:ILE:HD13	1.96	0.46
1:1A:887:A:C2	1:1A:889:C:H3'	2.51	0.46
1:1A:2394:C:P	30:18:30:ARG:HH21	2.39	0.46
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.96	0.46
21:1Z:158:PRO:O	21:1Z:161:VAL:HG22	2.15	0.46
32:1a:598:U:H2'	32:1a:599:C:H6	1.80	0.46
40:1i:77:ILE:O	40:1i:81:ILE:HG23	2.16	0.46
47:1p:56:ALA:O	47:1p:60:LEU:HB2	2.15	0.46
54:1x:19:G:H4'	54:1x:20:U:OP2	2.16	0.46
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.50	0.46
18:2W:71:VAL:HA	18:2W:107:LEU:HD23	1.97	0.46
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.98	0.46
32:2a:1030(A):G:N2	32:2a:1030(C):G:H3'	2.31	0.46
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.51	0.46
47:2p:43:LYS:HG2	47:2p:48:TRP:CG	2.51	0.46
1:1A:796:C:H2'	1:1A:797:C:C6	2.51	0.46
1:1A:2123:G:H2'	1:1A:2124:G:C8	2.46	0.46
1:1A:2390:U:P	30:18:35:GLN:HE22	2.38	0.46
5:1F:33:LEU:HD13	5:1F:112:MET:HE2	1.97	0.46
8:1I:109:ILE:HD13	8:1I:109:ILE:HA	1.74	0.46
32:1a:195:A:H2'	32:1a:196:A:C4	2.51	0.46
32:1a:858:G:O6	32:1a:869:G:H3'	2.15	0.46
32:1a:1051:C:H2'	32:1a:1052:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.98	0.46
40:1i:79:LEU:HD11	40:1i:83:ARG:HH11	1.81	0.46
1:2A:588:U:H1'	5:2F:90:PHE:CG	2.49	0.46
1:2A:774:A:H2'	1:2A:774:A:N3	2.31	0.46
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.42	0.46
1:2A:1027:A:C2	1:2A:2488:A:H5'	2.51	0.46
1:2A:1446:C:H42	1:2A:1465:G:H1	1.62	0.46
6:2G:117:PHE:HE2	6:2G:119:GLY:HA2	1.80	0.46
15:2T:99:LEU:O	15:2T:102:ILE:HG12	2.16	0.46
21:2Z:31:ARG:HG3	21:2Z:32:HIS:CD2	2.51	0.46
21:2Z:54:HIS:CG	21:2Z:101:PRO:HG3	2.51	0.46
32:2a:134:A:H61	47:2p:25:ARG:NH1	2.13	0.46
32:2a:434:U:H2'	32:2a:435:C:C6	2.50	0.46
32:2a:457:C:H2'	32:2a:458:C:H6	1.80	0.46
32:2a:859:A:H2'	32:2a:860:A:O4'	2.16	0.46
32:2a:1014:A:H2'	32:2a:1015:A:C4	2.50	0.46
32:2a:1260:C:P	32:2a:1284:C:H4'	2.56	0.46
47:2p:15:PRO:HD2	47:2p:42:ARG:HD3	1.98	0.46
1:1A:247:G:H4'	1:1A:386:G:C5	2.51	0.46
1:1A:1164:G:H2'	1:1A:1165:U:C6	2.51	0.46
1:1A:1916:A:H2'	1:1A:1917:PSU:O4'	2.16	0.46
2:1B:7:G:H5'	14:1S:29:PHE:CE2	2.50	0.46
15:1T:127:ALA:C	15:1T:129:ARG:N	2.74	0.46
32:1a:1123:A:C2	41:1j:39:PRO:HD2	2.51	0.46
32:1a:1333:A:H2'	32:1a:1334:G:O4'	2.16	0.46
1:2A:362:U:O2'	1:2A:363:G:H5'	2.15	0.46
1:2A:1853:A:H2'	1:2A:1854:A:C8	2.51	0.46
1:2A:2011:U:H2'	1:2A:2012:G:O4'	2.16	0.46
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.79	0.46
1:2A:2821:A:O2'	1:2A:2826:A:N1	2.49	0.46
2:2B:33:G:C6	2:2B:34:U:C4	3.04	0.46
17:2V:24:LYS:HE3	17:2V:24:LYS:HB3	1.69	0.46
22:20:18:ALA:O	22:20:20:ARG:NH1	2.49	0.46
24:22:53:LEU:O	24:22:57:ILE:HG13	2.16	0.46
32:2a:460:G:N2	32:2a:471:G:N7	2.64	0.46
32:2a:643:C:H2'	32:2a:644:G:H8	1.81	0.46
32:2a:858:G:O6	32:2a:869:G:H3'	2.16	0.46
32:2a:1239:A:H4'	32:2a:1240:U:H5'	1.98	0.46
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.98	0.46
40:2i:21:PRO:HG3	40:2i:59:PHE:CE1	2.51	0.46
44:2m:37:THR:HG22	44:2m:55:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:2s:28:LYS:HA	50:2s:28:LYS:HD3	1.84	0.46
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.15	0.46
1:1A:1753:G:N1	1:1A:1756:G:OP2	2.47	0.46
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.81	0.46
8:1I:81:VAL:HG21	8:1I:88:ILE:HD13	1.98	0.46
23:11:26:ARG:HG3	23:11:27:GLU:HG3	1.98	0.46
24:12:18:PRO:O	24:12:22:GLU:HG3	2.16	0.46
32:1a:90:U:H4'	32:1a:91:C:OP1	2.14	0.46
42:1k:34:ASP:OD1	42:1k:38:ASN:N	2.49	0.46
49:1r:56:THR:HB	49:1r:58:LEU:HD12	1.98	0.46
51:1t:47:GLY:HA2	51:1t:48:LYS:C	2.41	0.46
1:2A:1886:C:H2'	1:2A:1887:C:H6	1.80	0.46
1:2A:2119:A:N6	1:2A:2170:A:N7	2.64	0.46
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.31	0.46
7:2H:127:GLU:C	7:2H:129:THR:H	2.24	0.46
32:2a:131:C:H2'	32:2a:132:C:C6	2.50	0.46
32:2a:1118:C:H1'	32:2a:1179:A:C5	2.51	0.46
33:2b:179:LYS:HA	39:2h:72:PRO:HG3	1.98	0.46
34:2c:186:PHE:HE1	34:2c:197:GLY:HA2	1.80	0.46
39:2h:39:LEU:HB3	39:2h:45:ILE:HG12	1.97	0.46
48:2q:10:VAL:HG12	48:2q:53:LEU:HA	1.98	0.46
1:1A:1059:G:H1	1:1A:1079:C:H42	1.64	0.46
4:1E:119:ARG:HG2	4:1E:120:TRP:NE1	2.30	0.46
8:1I:114:LEU:HD13	8:1I:130:TYR:HD1	1.81	0.46
32:1a:580:U:H2'	32:1a:581:G:O4'	2.16	0.46
32:1a:691:G:H2'	32:1a:692:U:C6	2.50	0.46
32:1a:1286:A:C8	32:1a:1287:A:H4'	2.51	0.46
35:1d:111:ALA:HB1	35:1d:116:GLN:HE21	1.81	0.46
39:1h:51:VAL:HG21	39:1h:60:ARG:NH1	2.31	0.46
41:1j:8:LEU:HD22	41:1j:96:ILE:HG22	1.97	0.46
51:1t:77:ALA:O	51:1t:81:LYS:HG3	2.16	0.46
1:2A:864:G:OP2	12:2Q:22:LYS:HE3	2.16	0.46
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.16	0.46
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.98	0.46
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.51	0.46
1:2A:2830:G:O2'	1:2A:2883:A:N1	2.42	0.46
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.38	0.46
20:2Y:43:ASN:ND2	20:2Y:65:ALA:HB3	2.31	0.46
22:20:69:PHE:CE2	22:20:79:VAL:HG22	2.51	0.46
23:21:5:CYS:SG	23:21:62:VAL:HG23	2.56	0.46
40:2i:20:ARG:O	40:2i:60:ASP:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:50:LEU:HD12	40:2i:51:ARG:HG3	1.97	0.46
42:2k:87:THR:O	42:2k:87:THR:OG1	2.31	0.46
52:2u:9:ARG:HH21	52:2u:10:ARG:NH2	2.14	0.46
1:1A:1741:A:H2'	1:1A:1742:G:O4'	2.16	0.45
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.97	0.45
7:1H:27:LYS:HB3	7:1H:27:LYS:HE2	1.75	0.45
9:1N:14:VAL:HG13	9:1N:138:LEU:HG	1.98	0.45
32:1a:1080:A:H5'	36:1e:14:ARG:HH21	1.79	0.45
32:1a:1355:G:H2'	32:1a:1356:G:C8	2.51	0.45
32:1a:1358:U:OP2	32:1a:1359:C:N4	2.45	0.45
34:1c:112:SER:O	34:1c:116:VAL:HG23	2.16	0.45
38:1g:62:PHE:HA	38:1g:124:LEU:HD22	1.98	0.45
38:1g:111:ARG:HD2	38:1g:123:GLU:HB2	1.98	0.45
1:2A:2522:U:O2'	1:2A:2647:U:OP1	2.29	0.45
1:2A:2663:G:H3'	1:2A:2664:G:H8	1.81	0.45
2:2B:26:A:O2'	60:2B:302:HOH:O	2.21	0.45
21:2Z:6:LYS:HD2	21:2Z:8:TYR:OH	2.16	0.45
32:2a:523:A:N1	43:2l:92:0TD:H6	2.31	0.45
32:2a:942:G:C2	32:2a:1342:C:C2	3.03	0.45
32:2a:1190:G:O2'	34:2c:3:ASN:HB2	2.16	0.45
32:2a:1212:U:H5'	32:2a:1213:A:C8	2.51	0.45
32:2a:1265:G:C6	32:2a:1266:G:C6	3.04	0.45
32:2a:1274:G:N2	32:2a:1275:A:H62	2.13	0.45
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.49	0.45
33:2b:118:LEU:HD23	33:2b:142:LEU:HB2	1.98	0.45
34:2c:6:HIS:ND1	45:2n:49:HIS:HB3	2.31	0.45
46:2o:56:LEU:O	46:2o:60:VAL:HG23	2.17	0.45
47:2p:53:VAL:O	47:2p:57:ARG:HG3	2.17	0.45
54:2x:23:C:H2'	54:2x:24:U:C6	2.51	0.45
1:1A:784:A:H5'	1:1A:785:G:OP1	2.16	0.45
1:1A:881:G:N2	1:1A:897:C:C2	2.82	0.45
1:1A:2626:C:H2'	1:1A:2627:G:O4'	2.15	0.45
1:1A:2712:U:OP1	1:1A:2714:G:H4'	2.16	0.45
4:1E:195:LEU:HG	4:1E:196:VAL:N	2.32	0.45
7:1H:3:ARG:HH21	7:1H:65:HIS:HB3	1.81	0.45
9:1N:32:THR:HG22	9:1N:37:LYS:HB2	1.98	0.45
32:1a:265:G:H5'	48:1q:64:PRO:O	2.17	0.45
32:1a:512:U:H2'	32:1a:513:C:C6	2.51	0.45
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.50	0.45
33:1b:97:TRP:CZ2	33:1b:102:LEU:HD13	2.51	0.45
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:122:LYS:HG2	44:1m:123:ALA:H	1.80	0.45
49:1r:58:LEU:HB3	49:1r:62:GLU:CB	2.47	0.45
49:1r:71:LYS:O	49:1r:75:ILE:HG13	2.15	0.45
1:2A:468:G:H5"	5:2F:60:SER:HB2	1.97	0.45
32:2a:328:C:H4'	32:2a:329:A:H5'	1.98	0.45
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.81	0.45
32:2a:1134:G:C6	32:2a:1135:U:H1'	2.51	0.45
32:2a:1299:A:H2'	32:2a:1299:A:N3	2.32	0.45
41:2j:42:THR:HG23	41:2j:68:HIS:HA	1.99	0.45
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.98	0.45
1:1A:2022:U:HO2'	1:1A:2617:C:H5'	1.80	0.45
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.52	0.45
32:1a:736:C:H2'	32:1a:737:A:C8	2.51	0.45
32:1a:1194:U:H2'	32:1a:1195:C:C6	2.51	0.45
39:1h:86:ILE:HD12	39:1h:133:LEU:HD22	1.97	0.45
1:2A:1638:C:H5"	1:2A:2710:C:O2'	2.16	0.45
1:2A:2126:A:C2	1:2A:2173:A:H1'	2.52	0.45
1:2A:2647:U:H2'	1:2A:2648:C:C6	2.51	0.45
2:2B:17:C:H2'	2:2B:18:G:O4'	2.16	0.45
7:2H:54:ARG:HG2	7:2H:65:HIS:CE1	2.52	0.45
7:2H:56:SER:HB3	7:2H:61:HIS:ND1	2.31	0.45
32:2a:1007:C:N3	32:2a:1022:G:O6	2.50	0.45
32:2a:1119:C:OP2	40:2i:9:ARG:NH2	2.45	0.45
34:2c:134:ILE:HG23	34:2c:151:VAL:HB	1.99	0.45
36:2e:87:SER:HB3	36:2e:131:ILE:HD13	1.98	0.45
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.97	0.45
40:2i:17:VAL:HA	40:2i:63:ILE:HG12	1.98	0.45
1:1A:1301:A:O2'	1:1A:1302:A:H3'	2.16	0.45
1:1A:2136:C:C2	1:1A:2155:G:C2	3.04	0.45
1:1A:2375:G:O6	60:1A:4156:HOH:O	2.21	0.45
10:1O:76:ALA:HB3	15:1T:75:ILE:HD12	1.98	0.45
12:1Q:16:ARG:HG2	12:1Q:18:LYS:HD3	1.98	0.45
12:1Q:51:ARG:HD3	12:1Q:66:ILE:HD11	1.98	0.45
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.51	0.45
32:1a:598:U:H2'	32:1a:599:C:C6	2.51	0.45
32:1a:982:U:H5"	45:1n:6:LEU:HD21	1.99	0.45
32:1a:1343:G:H2'	32:1a:1344:C:C6	2.52	0.45
33:1b:183:PRO:HA	33:1b:198:ASP:OD2	2.16	0.45
36:1e:27:ARG:NH1	36:1e:27:ARG:HB2	2.31	0.45
40:1i:116:LYS:HA	40:1i:123:PRO:HD3	1.98	0.45
44:1m:108:ARG:HD3	44:1m:108:ARG:HA	1.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2113:U:N3	1:2A:2114:A:N7	2.64	0.45
16:2U:34:LYS:NZ	16:2U:37:GLU:OE1	2.39	0.45
22:20:9:SER:OG	22:20:10:THR:N	2.49	0.45
32:2a:36:C:O2'	43:2l:117:ARG:NH2	2.49	0.45
32:2a:1369:C:H2'	32:2a:1370:G:C8	2.51	0.45
38:2g:22:LEU:HD11	38:2g:66:VAL:HG11	1.98	0.45
42:2k:34:ASP:OD1	42:2k:36:ASP:N	2.48	0.45
50:2s:52:TYR:HB2	50:2s:57:HIS:CE1	2.51	0.45
1:1A:123:G:OP2	60:1A:4158:HOH:O	2.21	0.45
1:1A:662:G:H5"	11:1P:16:ARG:HG2	1.98	0.45
1:1A:1090:U:C2	1:1A:1102:C:H1'	2.51	0.45
1:1A:1466:G:H2'	1:1A:1547:C:N4	2.32	0.45
5:1F:155:LEU:HD11	5:1F:176:LEU:HD12	1.97	0.45
30:18:26:LYS:HG2	30:18:46:ARG:O	2.16	0.45
6:2G:45:GLU:H	6:2G:45:GLU:HG2	1.45	0.45
32:2a:975:A:H5"	32:2a:1363(A):A:N6	2.31	0.45
32:2a:1067:A:O2'	32:2a:1068:G:OP2	2.34	0.45
32:2a:1352:C:H2'	32:2a:1353:G:C8	2.51	0.45
34:2c:30:ARG:HE	45:2n:38:GLY:HA3	1.82	0.45
35:2d:155:LEU:O	35:2d:159:ARG:HG3	2.16	0.45
50:2s:71:LEU:HD12	50:2s:71:LEU:HA	1.70	0.45
1:1A:1508:A:O2'	1:1A:1509:C:H5"	2.17	0.45
1:1A:2667:C:H1'	7:1H:109:PHE:CD1	2.52	0.45
2:1B:75:G:H22	21:1Z:73:GLN:NE2	2.13	0.45
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.50	0.45
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.52	0.45
32:1a:457:C:H2'	32:1a:458:C:C6	2.48	0.45
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.17	0.45
35:1d:23:GLY:HA3	35:1d:112:VAL:HG12	1.98	0.45
39:1h:10:LEU:HB3	39:1h:83:ILE:HG12	1.97	0.45
39:1h:124:ALA:O	39:1h:128:GLY:N	2.46	0.45
44:1m:40:ASN:HB3	44:1m:43:THR:OG1	2.17	0.45
50:1s:39:THR:OG1	50:1s:70:LYS:HE2	2.17	0.45
1:2A:627:A:N7	11:2P:84:ASN:ND2	2.62	0.45
1:2A:1853:A:N1	1:2A:2087:G:H1'	2.31	0.45
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.31	0.45
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.51	0.45
15:2T:127:ALA:C	15:2T:129:ARG:N	2.74	0.45
32:2a:33:A:N3	43:2l:32:PHE:HE2	2.14	0.45
32:2a:512:U:H2'	32:2a:513:C:H6	1.82	0.45
32:2a:967:5MC:H2'	32:2a:968:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1245:A:H2'	32:2a:1246:C:O4'	2.17	0.45
33:2b:92:TYR:N	33:2b:151:GLY:O	2.42	0.45
34:2c:88:ARG:HA	34:2c:91:LEU:HB2	1.99	0.45
38:2g:78:ARG:HD3	38:2g:79:ARG:H	1.80	0.45
39:2h:51:VAL:HG11	39:2h:60:ARG:NH1	2.31	0.45
41:2j:49:VAL:HG12	41:2j:61:GLU:O	2.16	0.45
42:2k:31:THR:HG23	42:2k:42:TRP:HB3	1.99	0.45
51:2t:74:LYS:N	60:2t:303:HOH:O	2.49	0.45
1:1A:606:U:H4'	1:1A:658:C:H4'	1.97	0.45
1:1A:1547:C:H2'	1:1A:1548:C:C6	2.51	0.45
7:1H:26:VAL:HG12	7:1H:79:VAL:HG21	1.98	0.45
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.77	0.45
29:17:29:LYS:O	29:17:33:ARG:HB2	2.16	0.45
32:1a:461:A:O2'	32:1a:470:C:H5'	2.17	0.45
32:1a:520:A:N1	32:1a:536:C:H1'	2.32	0.45
32:1a:539:A:H2'	32:1a:540:G:C8	2.52	0.45
34:1c:183:ASP:HB3	34:1c:202:ILE:HB	1.97	0.45
35:1d:61:LYS:HD2	35:1d:207:TYR:OH	2.17	0.45
36:1e:20:GLN:NE2	36:1e:21:ALA:O	2.50	0.45
43:1l:117:ARG:HB3	43:1l:122:THR:HB	1.98	0.45
1:2A:955:C:OP2	12:2Q:14:ARG:HG3	2.16	0.45
1:2A:2167:U:H3'	1:2A:2168:G:H21	1.81	0.45
6:2G:11:TYR:OH	6:2G:16:ARG:HD3	2.17	0.45
10:2O:7:TYR:CZ	10:2O:44:LYS:HG3	2.52	0.45
21:2Z:28:MET:SD	21:2Z:59:LEU:HD12	2.57	0.45
32:2a:109:A:C6	32:2a:326:G:C6	3.05	0.45
34:2c:14:ILE:HD12	34:2c:178:LEU:HD22	1.99	0.45
1:1A:848:G:H2'	1:1A:849:A:C8	2.52	0.45
1:1A:957:A:N1	1:1A:2458:G:H4'	2.32	0.45
14:1S:71:ARG:NH1	14:1S:107:GLU:OE1	2.49	0.45
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.49	0.45
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.99	0.45
32:1a:475:G:C2'	32:1a:476:G:H5'	2.47	0.45
32:1a:501:C:H1'	32:1a:549:C:H1'	1.97	0.45
32:1a:1386:G:H2'	32:1a:1387:G:H8	1.82	0.45
41:1j:31:GLY:HA3	41:1j:32:ALA:HA	1.51	0.45
50:1s:27:GLU:CD	50:1s:27:GLU:H	2.21	0.45
1:2A:236:C:H2'	1:2A:237:C:C6	2.52	0.45
1:2A:511:U:H4'	1:2A:1235:G:H4'	1.99	0.45
1:2A:515:A:H1'	1:2A:581:C:H1'	1.99	0.45
1:2A:1357:U:H2'	1:2A:1358:G:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.32	0.45
2:2B:28:C:H2'	2:2B:29:A:O4'	2.16	0.45
3:2D:16:MET:HG3	3:2D:206:LEU:O	2.17	0.45
4:2E:150:VAL:HG13	4:2E:154:LYS:HD2	1.98	0.45
5:2F:31:HIS:HE1	5:2F:35:GLU:OE2	1.99	0.45
25:23:23:LEU:HD13	25:23:50:VAL:HG11	1.99	0.45
26:24:58:ARG:O	26:24:61:ARG:HB2	2.17	0.45
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.50	0.45
32:2a:857:C:H2'	32:2a:858:G:O4'	2.16	0.45
32:2a:1020:U:H2'	32:2a:1021:G:C8	2.52	0.45
32:2a:1095:U:C4	32:2a:1096:C:C4	3.05	0.45
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.52	0.45
33:2b:80:ILE:HD11	33:2b:212:GLN:HA	1.99	0.45
38:2g:115:ARG:O	38:2g:119:ARG:HG3	2.17	0.45
51:2t:9:ASN:OD1	51:2t:9:ASN:N	2.49	0.45
1:1A:566:U:H5"	11:1P:29:LYS:HE3	1.98	0.45
22:10:11:ARG:O	22:10:14:ARG:NH2	2.31	0.45
32:1a:1347:G:H5"	40:1i:107:ARG:HB3	1.98	0.45
37:1f:17:SER:O	37:1f:21:LEU:HG	2.17	0.45
1:2A:27:G:H22	1:2A:512:G:H1'	1.80	0.45
1:2A:236:C:H2'	1:2A:237:C:H6	1.81	0.45
1:2A:309:G:N3	1:2A:329:G:O2'	2.47	0.45
1:2A:2104:G:N2	1:2A:2185:C:N3	2.48	0.45
1:2A:2572:A:C8	4:2E:144:ARG:HD3	2.52	0.45
32:2a:1121:U:C2'	32:2a:1122:U:H5'	2.47	0.45
32:2a:1202:G:O4'	45:2n:29:ARG:NH1	2.49	0.45
41:2j:32:ALA:HA	41:2j:33:GLN:HA	1.76	0.45
50:2s:37:ARG:H	50:2s:37:ARG:HG3	1.56	0.45
1:1A:34:C:N4	1:1A:447:A:H61	2.15	0.45
1:1A:631:A:N3	1:1A:2415:G:O2'	2.46	0.45
1:1A:671:C:N4	60:1A:4332:HOH:O	2.49	0.45
1:1A:1952:A:C6	1:1A:1953:A:N1	2.85	0.45
14:1S:31:SER:O	14:1S:97:ARG:NH2	2.43	0.45
32:1a:194:C:H2'	32:1a:195:A:H5"	1.99	0.45
38:1g:15:ASP:OD2	38:1g:18:TYR:N	2.50	0.45
39:1h:116:LYS:HD3	39:1h:127:LEU:HD22	1.99	0.45
43:1l:70:ILE:HG12	43:1l:100:ILE:HD13	1.99	0.45
44:1m:57:ARG:HG2	44:1m:61:GLU:OE1	2.16	0.45
1:2A:660:G:H5'	5:2F:99:TYR:CE1	2.53	0.45
1:2A:1019:U:O2'	1:2A:1021:A:H2	2.00	0.45
1:2A:1340:U:OP1	19:2X:16:LYS:NZ	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2051:A:H8	1:2A:2051:A:OP2	2.00	0.45
1:2A:2119:A:N6	1:2A:2171:A:C6	2.85	0.45
1:2A:2161:C:H2'	1:2A:2162:G:O4'	2.16	0.45
1:2A:2316:C:H2'	1:2A:2317:C:C6	2.51	0.45
1:2A:2375:G:N2	1:2A:2378:A:OP2	2.44	0.45
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.52	0.45
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.17	0.45
2:2B:43:C:OP1	26:24:6:HIS:NE2	2.42	0.45
5:2F:53:THR:HG22	5:2F:56:GLU:CD	2.42	0.45
6:2G:25:TYR:CZ	6:2G:32:PRO:HD3	2.51	0.45
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.71	0.45
32:2a:149:A:H2'	32:2a:150:C:H6	1.82	0.45
32:2a:1012:U:H2'	32:2a:1013:G:C8	2.51	0.45
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.17	0.45
46:2o:21:ASP:OD2	46:2o:24:SER:HB3	2.18	0.45
1:1A:1179:C:H2'	1:1A:1180:C:H6	1.83	0.44
1:1A:1359:A:N1	1:1A:1372:U:C4	2.85	0.44
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.50	0.44
21:1Z:99:TYR:HA	21:1Z:124:ILE:O	2.17	0.44
32:1a:193:C:H2'	32:1a:194:C:C6	2.52	0.44
32:1a:711:G:H2'	32:1a:712:A:C8	2.52	0.44
32:1a:748:C:O5'	32:1a:748:C:H6	1.99	0.44
32:1a:1209:C:O2'	32:1a:1214:C:N4	2.45	0.44
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.85	0.44
1:2A:686:G:N2	1:2A:788:A:H61	2.15	0.44
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.52	0.44
4:2E:101:ARG:HA	4:2E:170:LEU:O	2.17	0.44
32:2a:412:A:O4'	35:2d:35:ARG:NH2	2.51	0.44
34:2c:112:SER:HB3	34:2c:115:LEU:HD22	1.99	0.44
1:1A:580:C:H2'	1:1A:581:C:C6	2.51	0.44
1:1A:686:G:H8	29:17:6:GLN:O	1.99	0.44
1:1A:1075:C:O2	1:1A:1076:C:H2'	2.17	0.44
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.17	0.44
4:1E:60:ASN:OD1	4:1E:63:LEU:HG	2.17	0.44
5:1F:24:LEU:HD12	5:1F:24:LEU:HA	1.87	0.44
12:1Q:78:PRO:HG2	12:1Q:81:VAL:HG11	1.99	0.44
32:1a:7:G:O2'	36:1e:120:THR:O	2.35	0.44
32:1a:1129:C:O2'	32:1a:1139:G:N7	2.41	0.44
32:1a:1438:G:H2'	32:1a:1439:C:C6	2.52	0.44
36:1e:77:PRO:HD2	36:1e:142:LEU:HD13	1.99	0.44
1:2A:342:G:H2'	1:2A:343:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1186:G:C2	1:2A:1187:G:H1'	2.52	0.44
13:2R:72:ASP:HB3	13:2R:75:LEU:HB3	1.98	0.44
32:2a:1270:C:H2'	32:2a:1271:G:C8	2.53	0.44
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.17	0.44
38:2g:15:ASP:OD1	38:2g:19:GLY:N	2.50	0.44
39:2h:120:THR:OG1	39:2h:123:GLU:HG3	2.17	0.44
41:2j:40:LEU:HB2	41:2j:69:ASN:HB3	1.99	0.44
54:2x:15:G:H2'	54:2x:59:A:N1	2.33	0.44
1:1A:551:G:O2'	1:1A:1220:A:N3	2.47	0.44
1:1A:1048:A:N1	1:1A:1112:G:O2'	2.43	0.44
1:1A:1141:U:H4'	1:1A:1142(A):A:O4'	2.17	0.44
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.33	0.44
2:1B:2:C:H2'	2:1B:3:C:C6	2.52	0.44
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.82	0.44
13:1R:36:THR:HG22	13:1R:37:THR:H	1.82	0.44
13:1R:44:LEU:HD23	13:1R:44:LEU:HA	1.85	0.44
30:18:4:MET:HE3	30:18:63:PRO:HG3	2.00	0.44
44:1m:87:TYR:O	44:1m:91:ARG:HG2	2.18	0.44
1:2A:592:G:O2'	30:28:4:MET:HG3	2.18	0.44
1:2A:1919:A:N1	32:2a:1495:U:O2'	2.41	0.44
1:2A:2203:U:O4'	3:2D:151:LYS:HE2	2.17	0.44
1:2A:2726:U:H4'	10:2O:1:MET:HE1	2.00	0.44
1:2A:2745:C:C4	1:2A:2746:U:C4	3.04	0.44
2:2B:73:A:C4	2:2B:105:A:C2	3.04	0.44
10:2O:102:VAL:HB	10:2O:106:LEU:HD12	1.98	0.44
19:2X:14:SER:C	19:2X:16:LYS:H	2.25	0.44
21:2Z:157:LEU:HD21	21:2Z:163:LEU:HB2	2.00	0.44
26:24:10:VAL:HG22	26:24:11:PRO:HD2	1.99	0.44
32:2a:7:G:H5'	32:2a:298:A:O4'	2.17	0.44
32:2a:620:C:H2'	32:2a:621:A:O4'	2.17	0.44
32:2a:1318:A:OP1	50:2s:3:ARG:NH1	2.51	0.44
33:2b:55:PHE:CE1	33:2b:218:ALA:HA	2.52	0.44
35:2d:150:GLU:HA	35:2d:153:ARG:HG3	1.98	0.44
38:2g:151:TYR:OH	42:2k:54:ARG:HD3	2.17	0.44
40:2i:93:ARG:HD3	40:2i:93:ARG:HA	1.63	0.44
44:2m:122:LYS:HG3	44:2m:123:ALA:H	1.83	0.44
1:1A:2232:U:P	23:11:40:ARG:HH12	2.40	0.44
5:1F:165:ARG:HA	5:1F:168:ARG:HD2	2.00	0.44
32:1a:600:C:H2'	32:1a:601:C:H6	1.82	0.44
32:1a:737:A:H2'	32:1a:738:C:C6	2.52	0.44
32:1a:993:G:H1	32:1a:1045:C:H42	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.42	0.44
36:1e:18:ARG:HH11	36:1e:27:ARG:HH12	1.65	0.44
39:1h:97:VAL:HA	39:1h:100:ILE:HD11	1.98	0.44
42:1k:104:GLN:O	42:1k:106:LYS:N	2.50	0.44
49:1r:59:SER:H	49:1r:62:GLU:HB2	1.81	0.44
1:2A:7:G:H4'	9:2N:13:TRP:CH2	2.52	0.44
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.18	0.44
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.17	0.44
1:2A:2314:C:H2'	1:2A:2315:G:H8	1.80	0.44
1:2A:2356:C:OP1	22:20:24:LYS:NZ	2.40	0.44
5:2F:153:SER:HB2	5:2F:189:THR:HA	1.99	0.44
15:2T:116:ALA:HB1	15:2T:121:ILE:HD11	2.00	0.44
22:20:68:GLU:HG3	22:20:82:ARG:HH21	1.81	0.44
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.53	0.44
36:2e:11:ILE:HB	36:2e:31:LEU:HB3	1.98	0.44
38:2g:137:LYS:O	38:2g:141:VAL:HG23	2.18	0.44
38:2g:148:ASN:HD22	38:2g:151:TYR:HE2	1.64	0.44
40:2i:26:VAL:HG22	40:2i:61:ALA:HB3	1.99	0.44
42:2k:33:THR:HA	42:2k:39:PRO:HA	1.99	0.44
50:2s:28:LYS:HB3	50:2s:29:ARG:CA	2.47	0.44
50:2s:41:VAL:HG13	50:2s:43:GLU:H	1.82	0.44
1:1A:1045:A:OP1	1:1A:1046:A:H3'	2.17	0.44
1:1A:1639:U:O2'	1:1A:1640:C:H5'	2.17	0.44
1:1A:2080:G:OP1	23:11:35:THR:HG21	2.18	0.44
12:1Q:135:ASP:O	12:1Q:139:GLU:HG3	2.18	0.44
14:1S:11:LYS:HD2	14:1S:15:ARG:NH1	2.32	0.44
21:1Z:155:LEU:HD12	21:1Z:155:LEU:HA	1.86	0.44
32:1a:70:G:H2'	32:1a:71:C:C6	2.52	0.44
32:1a:1004:A:H5"	32:1a:1025:U:C5	2.52	0.44
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.52	0.44
41:1j:81:THR:C	41:1j:83:GLU:H	2.24	0.44
1:2A:93:G:H2'	1:2A:94:C:C6	2.53	0.44
1:2A:784:A:N6	3:2D:229:VAL:HG11	2.32	0.44
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.18	0.44
1:2A:2125:G:N1	1:2A:2172:U:OP1	2.48	0.44
1:2A:2127:G:C6	1:2A:2161:C:N4	2.85	0.44
1:2A:2261:C:H1'	1:2A:2388:A:N3	2.33	0.44
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	1.98	0.44
4:2E:1:MET:HE3	4:2E:199:ARG:HB3	1.99	0.44
32:2a:1271:G:C2	32:2a:1272:G:C8	3.05	0.44
34:2c:52:LEU:HD13	34:2c:68:VAL:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:74:GLN:O	35:2d:78:LEU:HD12	2.17	0.44
46:2o:62:GLN:O	46:2o:66:LEU:HG	2.18	0.44
47:2p:43:LYS:HA	47:2p:48:TRP:HB3	2.00	0.44
1:1A:271(D):G:H1	1:1A:271(T):C:H42	1.65	0.44
1:1A:583:G:OP2	16:1U:10:ARG:HD2	2.17	0.44
1:1A:887:A:H2	1:1A:889:C:H3'	1.82	0.44
4:1E:121:ASN:ND2	60:1E:408:HOH:O	2.51	0.44
8:1I:129:THR:HG22	8:1I:139:GLN:NE2	2.27	0.44
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.17	0.44
10:1O:10:VAL:HG11	10:1O:16:ALA:HB3	2.00	0.44
24:12:63:VAL:HA	24:12:66:GLU:HG2	1.99	0.44
32:1a:501:C:H2'	32:1a:502:G:C8	2.52	0.44
41:1j:29:ARG:O	41:1j:31:GLY:N	2.51	0.44
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.98	0.44
5:2F:137:LYS:HA	5:2F:140:LEU:HD12	2.00	0.44
7:2H:26:VAL:HG12	7:2H:79:VAL:HG11	1.98	0.44
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.99	0.44
30:28:63:PRO:HG2	30:28:64:TYR:CE2	2.53	0.44
32:2a:324:G:N1	32:2a:327:A:OP2	2.51	0.44
32:2a:1318:A:H1'	50:2s:37:ARG:HH21	1.81	0.44
32:2a:1469:G:H2'	32:2a:1470:G:C8	2.53	0.44
1:1A:1111:A:N3	1:1A:1112:G:H1'	2.32	0.44
1:1A:1697:G:OP2	1:1A:1698:A:O2'	2.31	0.44
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.32	0.44
8:1I:116:LEU:HD11	8:1I:120:ILE:HG13	1.99	0.44
11:1P:124:LYS:HA	11:1P:144:GLU:HB3	2.00	0.44
44:1m:67:GLU:HG3	44:1m:71:ARG:NH2	2.33	0.44
50:1s:41:VAL:N	50:1s:44:MET:SD	2.82	0.44
50:1s:80:TYR:C	50:1s:82:GLY:H	2.25	0.44
54:1x:20:U:O2'	54:1x:21:A:OP1	2.33	0.44
1:2A:96:G:H4'	24:22:48:HIS:NE2	2.33	0.44
1:2A:864:G:C6	1:2A:865:C:N4	2.86	0.44
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.35	0.44
1:2A:1354:A:O3'	3:2D:38:LYS:HE3	2.18	0.44
8:2I:86:THR:HG23	8:2I:87:LYS:HE2	1.99	0.44
12:2Q:56:ARG:HB3	12:2Q:56:ARG:HH11	1.83	0.44
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.17	0.44
16:2U:75:ASN:OD1	16:2U:78:THR:N	2.48	0.44
32:2a:691:G:H2'	32:2a:692:U:C6	2.53	0.44
32:2a:976:G:C8	32:2a:1358:U:C2	3.05	0.44
32:2a:1327:C:H2'	32:2a:1328:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.83	0.44
1:1A:1915:5MU:H2'	1:1A:1916:A:O4'	2.17	0.44
1:1A:2168:G:O6	1:1A:2171:A:H5"	2.18	0.44
7:1H:9:ILE:HD11	7:1H:69:ARG:HG2	2.00	0.44
10:1O:68:GLU:OE1	10:1O:78:ARG:NH1	2.47	0.44
19:1X:31:HIS:CD2	19:1X:33:LYS:HB2	2.53	0.44
21:1Z:67:LEU:HD23	21:1Z:67:LEU:HA	1.84	0.44
32:1a:352:C:O2'	32:1a:354:G:OP1	2.30	0.44
33:1b:16:HIS:HB2	33:1b:204:ASN:CB	2.45	0.44
36:1e:7:GLU:N	36:1e:35:GLY:O	2.41	0.44
37:1f:39:LYS:HE3	37:1f:39:LYS:HB3	1.80	0.44
44:1m:4:ILE:HB	44:1m:57:ARG:HG3	2.00	0.44
1:2A:37:C:H4'	1:2A:451:C:OP1	2.18	0.44
1:2A:76:C:O3'	24:22:59:ARG:HG3	2.17	0.44
1:2A:438:G:H2'	1:2A:440:G:C8	2.53	0.44
1:2A:601:C:O2'	1:2A:605:C:H5"	2.17	0.44
1:2A:1779:U:H2'	60:2A:4021:HOH:O	2.17	0.44
1:2A:2127:G:O2'	1:2A:2173:A:N3	2.51	0.44
9:2N:62:VAL:CG1	9:2N:66:LYS:HB2	2.47	0.44
21:2Z:51:ALA:O	21:2Z:52:SER:HB3	2.17	0.44
25:23:7:LYS:HB2	25:23:34:GLU:HG3	2.00	0.44
32:2a:671:G:H2'	32:2a:672:U:O4'	2.18	0.44
32:2a:1055:A:H2'	34:2c:156:ARG:HD2	2.00	0.44
32:2a:1298:C:H4'	32:2a:1299:A:C4	2.52	0.44
33:2b:214:ILE:HD13	33:2b:214:ILE:HA	1.67	0.44
51:2t:90:GLN:O	51:2t:93:GLU:HG3	2.17	0.44
1:1A:10:G:N2	1:1A:2802:G:OP1	2.49	0.44
1:1A:2718:G:O2'	1:1A:2847:U:OP1	2.31	0.44
7:1H:62:LYS:HB3	7:1H:62:LYS:HE2	1.84	0.44
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	2.00	0.44
20:1Y:106:LEU:O	20:1Y:107:ASP:HB2	2.17	0.44
32:1a:865:A:C2	32:1a:918:A:H4'	2.53	0.44
32:1a:1318:A:H5"	50:1s:3:ARG:HH12	1.83	0.44
33:1b:8:LYS:HB3	33:1b:9:GLU:H	1.67	0.44
35:1d:59:ARG:HA	35:1d:59:ARG:NH1	2.33	0.44
35:1d:109:GLY:HA3	35:1d:165:MET:CG	2.48	0.44
35:1d:158:ILE:H	35:1d:158:ILE:HG13	1.42	0.44
42:1k:33:THR:HG22	42:1k:39:PRO:HA	2.00	0.44
47:1p:4:ILE:N	47:1p:65:GLN:O	2.49	0.44
50:1s:15:LEU:HD13	50:1s:33:THR:HB	2.00	0.44
1:2A:589:C:H2'	1:2A:590:A:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.57	0.44
2:2B:31:C:H4'	6:2G:29:TRP:CH2	2.53	0.44
14:2S:3:ARG:HH11	14:2S:3:ARG:HA	1.82	0.44
21:2Z:171:ILE:H	21:2Z:171:ILE:HG13	1.65	0.44
32:2a:377:G:OP1	47:2p:3:LYS:HE2	2.18	0.44
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.18	0.44
32:2a:991:U:C4	32:2a:1212:U:H1'	2.53	0.44
32:2a:998:G:H2'	32:2a:999:C:O4'	2.18	0.44
32:2a:1048:G:OP1	45:2n:3:ARG:HG3	2.18	0.44
32:2a:1151:A:O2'	32:2a:1152:A:H8	2.00	0.44
32:2a:1329:A:N7	52:2u:7:ARG:NH2	2.66	0.44
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.53	0.44
34:2c:121:ALA:HB1	34:2c:188:LEU:O	2.17	0.44
36:2e:100:VAL:HG22	36:2e:118:ILE:HG22	2.00	0.44
39:2h:38:ILE:O	39:2h:42:GLU:HB2	2.18	0.44
51:2t:40:ALA:HB2	51:2t:55:ILE:HB	2.00	0.44
1:1A:813:U:H2'	1:1A:814:C:C6	2.53	0.43
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.53	0.43
1:1A:2748:A:H5'	7:1H:4:ILE:HD12	1.99	0.43
2:1B:4:C:H2'	2:1B:5:C:C6	2.53	0.43
5:1F:117:ARG:NH2	5:1F:189:THR:O	2.48	0.43
31:19:8:LYS:O	31:19:34:GLN:NE2	2.44	0.43
32:1a:735:C:H2'	32:1a:736:C:H6	1.83	0.43
32:1a:1009:G:O6	32:1a:1020:U:O2	2.36	0.43
32:1a:1318:A:H5"	50:1s:3:ARG:NH1	2.32	0.43
36:1e:152:ARG:HB3	39:1h:43:GLY:HA3	1.99	0.43
41:1j:37:PRO:HA	41:1j:72:VAL:HG23	2.00	0.43
1:2A:251:A:C5	1:2A:252:G:H1'	2.53	0.43
1:2A:325:G:H2'	1:2A:326:G:O4'	2.18	0.43
6:2G:18:GLU:HG2	6:2G:21:ARG:NH2	2.33	0.43
10:2O:70:LYS:HB3	10:2O:70:LYS:HE2	1.84	0.43
32:2a:32:A:C2	32:2a:33:A:C4	3.06	0.43
32:2a:722:A:N6	32:2a:724:G:C2	2.85	0.43
32:2a:1000:U:C2'	32:2a:1001:A:H5'	2.48	0.43
32:2a:1129:C:H2'	32:2a:1139:G:O6	2.18	0.43
32:2a:1173:G:H2'	32:2a:1174:G:H8	1.83	0.43
33:2b:174:VAL:HG13	33:2b:184:VAL:HG11	1.99	0.43
33:2b:185:ILE:CG2	33:2b:199:TYR:HB2	2.48	0.43
43:2l:83:VAL:HG23	43:2l:107:ALA:HB2	2.00	0.43
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.18	0.43
1:1A:444:C:H4'	5:1F:49:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:744:G:OP1	4:1E:132:HIS:ND1	2.43	0.43
1:1A:1063:G:H2'	1:1A:1064:C:C6	2.53	0.43
1:1A:1971:A:C4	3:1D:241:PRO:HD3	2.53	0.43
1:1A:2789:C:O2	1:1A:2894:G:N1	2.45	0.43
13:1R:9:LYS:O	13:1R:17:ARG:HD3	2.17	0.43
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.67	0.43
21:1Z:152:ALA:HB1	21:1Z:163:LEU:HD21	1.99	0.43
32:1a:97:G:H2'	32:1a:98:G:O4'	2.18	0.43
32:1a:192:U:H2'	32:1a:193:C:H6	1.82	0.43
32:1a:881:G:OP2	43:1l:12:ARG:NH2	2.51	0.43
32:1a:1220:G:H2'	32:1a:1221:G:O4'	2.18	0.43
32:1a:1318:A:H4'	50:1s:10:PHE:CE2	2.53	0.43
40:1i:47:LEU:HB3	40:1i:50:LEU:HD11	2.00	0.43
46:1o:17:ARG:HH11	46:1o:17:ARG:HG3	1.82	0.43
51:1t:99:LEU:HA	51:1t:100:ILE:O	2.18	0.43
1:2A:265:A:N6	1:2A:427:U:O2'	2.45	0.43
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.17	0.43
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.83	0.43
3:2D:96:HIS:CD2	3:2D:102:LYS:HG2	2.53	0.43
7:2H:17:VAL:HG13	7:2H:26:VAL:HG22	2.00	0.43
7:2H:105:LEU:HB2	7:2H:113:VAL:HB	2.00	0.43
7:2H:167:GLU:HA	7:2H:168:PRO:HD3	1.87	0.43
32:2a:41:G:H2'	32:2a:42:G:C8	2.53	0.43
32:2a:770:C:OP1	60:2a:1812:HOH:O	2.21	0.43
32:2a:1040:U:H2'	32:2a:1041:A:C8	2.48	0.43
33:2b:121:LEU:HD21	33:2b:130:ARG:HH12	1.83	0.43
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	2.00	0.43
50:2s:61:TYR:HE2	50:2s:63:THR:HG22	1.81	0.43
1:1A:1083:U:C2	1:1A:1085:A:H5"	2.52	0.43
1:1A:1634:A:OP2	60:1A:4159:HOH:O	2.21	0.43
1:1A:2070:G:N3	60:1A:4231:HOH:O	2.36	0.43
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.19	0.43
26:14:49:PHE:HB3	26:14:50:VAL:H	1.45	0.43
1:2A:830:G:H5"	60:2A:4363:HOH:O	2.18	0.43
1:2A:922:U:H2'	1:2A:923:C:C6	2.53	0.43
1:2A:2134:A:H1'	1:2A:2158:A:C6	2.53	0.43
2:2B:43:C:H5"	26:24:1:MET:HG2	2.00	0.43
2:2B:110:G:O2'	2:2B:111:G:H5'	2.17	0.43
32:2a:1241:G:H2'	32:2a:1242:C:C6	2.53	0.43
33:2b:47:THR:O	33:2b:51:LEU:N	2.51	0.43
35:2d:157:LEU:HG	35:2d:161:ASN:ND2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:97:LYS:C	40:2i:99:LEU:H	2.27	0.43
45:2n:3:ARG:CZ	45:2n:3:ARG:HB2	2.48	0.43
1:1A:226:G:H21	1:1A:228:A:H62	1.66	0.43
1:1A:1357:U:H2'	1:1A:1358:G:O4'	2.18	0.43
3:1D:16:MET:HE2	3:1D:16:MET:HB2	1.90	0.43
6:1G:80:PHE:HB2	6:1G:82:LEU:HB2	2.00	0.43
9:1N:4:TYR:HB2	16:1U:101:ARG:HH12	1.84	0.43
32:1a:78:G:HO2'	32:1a:79:G:C5'	2.31	0.43
37:1f:89:MET:HE1	49:1r:72:ARG:HB3	2.01	0.43
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.53	0.43
44:1m:59:TYR:O	44:1m:63:THR:OG1	2.33	0.43
1:2A:465:G:OP1	29:27:12:ARG:NH2	2.48	0.43
1:2A:819:A:C4	1:2A:1189:A:C2	3.07	0.43
1:2A:1364:G:P	23:21:3:LYS:HG3	2.58	0.43
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.19	0.43
1:2A:2563:U:H4'	10:2O:28:SER:HA	1.99	0.43
1:2A:2740:A:C6	1:2A:2764:A:C8	3.06	0.43
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.44	0.43
9:2N:6:PRO:HG2	9:2N:48:MET:HE1	1.99	0.43
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.99	0.43
36:2e:36:ASP:C	36:2e:38:GLN:H	2.27	0.43
39:2h:39:LEU:HD12	39:2h:39:LEU:HA	1.81	0.43
39:2h:103:VAL:HG21	39:2h:110:ALA:HB2	2.01	0.43
1:1A:113:G:H5'	60:1A:4313:HOH:O	2.18	0.43
1:1A:271(X):G:C2	1:1A:271(Y):U:O4	2.71	0.43
1:1A:996:A:H4'	16:1U:91:ASP:OD2	2.18	0.43
12:1Q:10:ARG:NH2	12:1Q:90:VAL:H	2.16	0.43
12:1Q:37:LEU:HD21	12:1Q:130:LYS:HE2	2.00	0.43
32:1a:1530:G:H2'	32:1a:1531:A:C8	2.53	0.43
60:1a:2054:HOH:O	43:1l:61:THR:HG22	2.18	0.43
39:1h:82:HIS:CE1	39:1h:84:ARG:HB2	2.54	0.43
47:1p:50:LYS:HA	47:1p:50:LYS:HD2	1.70	0.43
1:2A:479:A:H4'	1:2A:480:A:OP1	2.17	0.43
1:2A:784:A:C8	1:2A:792:G:C5	3.07	0.43
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.18	0.43
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.18	0.43
1:2A:2134:A:N6	1:2A:2157:G:H4'	2.23	0.43
1:2A:2408:U:H2'	1:2A:2409:G:C8	2.53	0.43
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.51	0.43
1:2A:2881:C:H2'	1:2A:2882:A:O4'	2.19	0.43
8:2I:87:LYS:HE2	8:2I:87:LYS:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:23:ARG:NH2	14:2S:84:GLN:HG2	2.33	0.43
32:2a:828:A:H2'	32:2a:829:G:O4'	2.19	0.43
32:2a:1104:G:C6	32:2a:1105:A:C5	3.06	0.43
33:2b:68:ILE:HG12	33:2b:161:ALA:HB3	2.01	0.43
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.78	0.43
36:2e:93:PRO:HG2	39:2h:105:ARG:CZ	2.48	0.43
44:2m:80:ARG:NH2	50:2s:69:HIS:HE1	2.16	0.43
50:2s:21:GLU:C	50:2s:23:ASN:H	2.27	0.43
1:1A:879:G:N1	1:1A:899:A:H1'	2.33	0.43
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.52	0.43
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.18	0.43
1:1A:2771:C:H2'	1:1A:2772:C:C6	2.52	0.43
1:1A:2791:C:H2'	1:1A:2792:G:H8	1.84	0.43
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.18	0.43
4:1E:34:VAL:HG13	4:1E:48:GLN:HE21	1.83	0.43
18:1W:28:SER:O	18:1W:31:GLU:N	2.51	0.43
28:16:17:LYS:HE3	28:16:17:LYS:HB3	1.61	0.43
32:1a:159:G:O2'	32:1a:161:A:N7	2.47	0.43
32:1a:192:U:H2'	32:1a:193:C:C6	2.53	0.43
32:1a:233:C:H2'	32:1a:234:C:H6	1.84	0.43
32:1a:250:A:H4'	32:1a:251:G:O5'	2.18	0.43
32:1a:509:A:O2'	32:1a:510:A:OP1	2.33	0.43
32:1a:872:A:C8	32:1a:874:G:C8	3.06	0.43
34:1c:52:LEU:HD12	34:1c:53:ALA:H	1.82	0.43
34:1c:101:LEU:HD12	34:1c:102:ASN:H	1.82	0.43
47:1p:20:VAL:HG22	47:1p:34:GLU:O	2.19	0.43
50:1s:62:ILE:HA	50:1s:66:MET:SD	2.59	0.43
1:2A:467:G:OP1	29:27:33:ARG:HD2	2.18	0.43
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.32	0.43
1:2A:2474:C:H5"	1:2A:2475:C:OP2	2.19	0.43
1:2A:2600:A:H2'	1:2A:2601:C:C6	2.54	0.43
21:2Z:53:ILE:O	21:2Z:70:LEU:HD11	2.19	0.43
32:2a:1252:A:H61	32:2a:1285:A:N6	2.06	0.43
40:2i:32:ASP:O	40:2i:35:GLU:N	2.51	0.43
42:2k:102:GLY:O	42:2k:103:LEU:HD23	2.19	0.43
44:2m:55:ARG:O	44:2m:59:TYR:HB3	2.18	0.43
1:1A:27:G:C2	1:1A:512:G:N3	2.87	0.43
1:1A:1062:G:O5'	1:1A:1070:A:O2'	2.35	0.43
1:1A:1142(A):A:C4	1:1A:1144:G:N7	2.86	0.43
1:1A:1358:G:N2	1:1A:1372:U:C5	2.86	0.43
1:1A:2105:C:H2'	1:1A:2106:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:43:LEU:C	6:1G:45:GLU:H	2.27	0.43
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	2.00	0.43
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.43	0.43
26:14:63:TYR:CD1	26:14:63:TYR:N	2.87	0.43
32:1a:100:C:H2'	32:1a:101:A:C8	2.54	0.43
32:1a:353:A:H5'	32:1a:353:A:H8	1.82	0.43
32:1a:742:G:OP2	46:1o:35:ARG:NH2	2.33	0.43
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.18	0.43
32:1a:841:U:O2	32:1a:841:U:H2'	2.18	0.43
32:1a:877:C:OP1	39:1h:88:LYS:NZ	2.36	0.43
32:1a:1004:A:H5"	32:1a:1025:U:H5	1.84	0.43
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.54	0.43
39:1h:6:ILE:HD11	39:1h:31:PHE:CD2	2.54	0.43
50:1s:67:VAL:O	50:1s:69:HIS:N	2.51	0.43
1:2A:918:A:N3	2:2B:80:U:O2'	2.47	0.43
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.40	0.43
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.54	0.43
7:2H:152:ARG:HA	7:2H:152:ARG:HD3	1.79	0.43
12:2Q:130:LYS:HE2	12:2Q:130:LYS:HB3	1.78	0.43
26:24:58:ARG:HD3	50:2s:68:GLY:H	1.84	0.43
32:2a:201:C:H5'	32:2a:202:U:OP2	2.19	0.43
32:2a:824:C:H2'	32:2a:825:G:C8	2.53	0.43
32:2a:1418:A:O5'	32:2a:1418:A:H8	2.02	0.43
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	2.00	0.43
47:2p:71:ARG:HG3	47:2p:80:PHE:HE2	1.84	0.43
1:1A:1648:C:OP1	60:1A:4110:HOH:O	2.22	0.43
1:1A:2128:C:N4	1:1A:2160:G:C6	2.85	0.43
6:1G:151:ALA:HB3	6:1G:153:ARG:NH1	2.34	0.43
20:1Y:5:MET:HE2	20:1Y:5:MET:HB2	1.63	0.43
32:1a:374:A:C6	32:1a:375:U:C4	3.07	0.43
32:1a:690:G:C6	32:1a:691:G:C6	3.07	0.43
32:1a:1288:A:N1	32:1a:1371:G:H1'	2.34	0.43
32:1a:1369:C:H2'	32:1a:1370:G:C8	2.54	0.43
1:2A:493:G:H2'	1:2A:494:G:O4'	2.19	0.43
1:2A:566:U:P	17:2V:80:GLN:HE21	2.42	0.43
1:2A:918:A:C5	1:2A:919:G:H1'	2.54	0.43
1:2A:1170:G:O6	1:2A:1180:C:N4	2.52	0.43
1:2A:1902:C:H5'	3:2D:246:PRO:HD3	2.00	0.43
1:2A:2402:C:H1'	1:2A:2403:C:H5	1.83	0.43
5:2F:185:ASP:OD1	5:2F:188:ARG:NH1	2.43	0.43
7:2H:118:PRO:HD2	7:2H:121:ILE:HB	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:54:HIS:ND1	21:2Z:101:PRO:HG3	2.34	0.43
32:2a:15:G:C4	32:2a:16:A:C8	3.06	0.43
32:2a:1265:G:C4	32:2a:1271:G:N2	2.87	0.43
34:2c:98:ASN:ND2	34:2c:98:ASN:H	2.16	0.43
41:2j:7:LYS:HB2	41:2j:71:LEU:HD13	2.00	0.43
44:2m:122:LYS:HG3	44:2m:123:ALA:N	2.33	0.43
1:1A:272:G:N7	1:1A:421:U:H2'	2.34	0.43
1:1A:657:U:H2'	1:1A:658:C:C6	2.54	0.43
1:1A:748:G:C8	18:1W:89:ALA:HB1	2.52	0.43
1:1A:904:C:H2'	1:1A:905:U:C6	2.53	0.43
1:1A:1062:G:N2	1:1A:1088:A:C6	2.87	0.43
1:1A:1095:A:C8	1:1A:1096:A:C8	3.07	0.43
1:1A:1630:G:H2'	1:1A:1631:C:C6	2.54	0.43
1:1A:1930:G:O2'	1:1A:1968:G:O6	2.36	0.43
1:1A:2019:A:O4'	16:1U:34:LYS:HE2	2.18	0.43
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.35	0.43
17:1V:65:GLY:HA3	17:1V:91:TYR:CZ	2.54	0.43
25:13:23:LEU:HD13	25:13:50:VAL:HG11	2.01	0.43
32:1a:401:C:H2'	32:1a:402:G:C8	2.53	0.43
32:1a:542:G:H5'	35:1d:41:GLY:HA3	2.01	0.43
32:1a:831:U:H2'	32:1a:832:C:C6	2.53	0.43
32:1a:979:C:N4	45:1n:18:VAL:O	2.36	0.43
32:1a:1297:C:OP2	44:1m:44:ARG:NH2	2.49	0.43
32:1a:1316:G:H5"	45:1n:17:LYS:HE3	2.01	0.43
32:1a:1350:A:OP1	40:1i:121:ARG:HD3	2.19	0.43
37:1f:38:GLU:N	37:1f:64:GLN:O	2.51	0.43
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	2.01	0.43
1:2A:194:G:H2'	1:2A:195:A:O4'	2.19	0.43
1:2A:705:A:H1'	3:2D:9:TYR:CE2	2.54	0.43
1:2A:709:U:H2'	1:2A:710:G:C8	2.54	0.43
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.53	0.43
2:2B:55:U:H1'	6:2G:29:TRP:CD1	2.54	0.43
5:2F:25:PRO:HD2	5:2F:115:ALA:HB2	2.01	0.43
21:2Z:150:LEU:O	21:2Z:171:ILE:HG13	2.18	0.43
32:2a:109:A:H2'	32:2a:326:G:N2	2.33	0.43
32:2a:824:C:H2'	32:2a:825:G:H8	1.84	0.43
32:2a:1058:G:H2'	32:2a:1059:C:O4'	2.19	0.43
32:2a:1171:G:N2	32:2a:1172:C:O2	2.52	0.43
33:2b:97:TRP:HE1	33:2b:172:ILE:HG22	1.84	0.43
34:2c:188:LEU:HG	34:2c:189:ALA:H	1.83	0.43
35:2d:108:LEU:HD21	35:2d:174:LEU:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2g:16:LEU:HD12	38:2g:16:LEU:H	1.84	0.43
45:2n:32:SER:O	45:2n:40:CYS:HA	2.19	0.43
50:2s:17:GLU:O	50:2s:21:GLU:N	2.39	0.43
50:2s:64:GLU:HG2	50:2s:65:ASN:H	1.84	0.43
1:1A:1647:G:OP1	60:1A:4110:HOH:O	2.21	0.43
1:1A:1936:A:OP1	1:1A:1937:A:H5'	2.18	0.43
5:1F:53:THR:HB	5:1F:56:GLU:OE1	2.19	0.43
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.59	0.43
9:1N:60:ILE:O	9:1N:61:ARG:HD3	2.19	0.43
9:1N:91:LEU:HD23	9:1N:91:LEU:HA	1.90	0.43
13:1R:38:VAL:HG22	13:1R:112:ALA:HB2	1.99	0.43
32:1a:111:G:H5"	47:1p:27:LYS:HB3	2.00	0.43
32:1a:135:C:H2'	32:1a:136:C:H5'	2.00	0.43
32:1a:381:C:H2'	32:1a:382:A:O4'	2.18	0.43
32:1a:867:G:O2'	32:1a:873:A:N1	2.51	0.43
35:1d:129:ASN:N	35:1d:129:ASN:OD1	2.52	0.43
47:1p:20:VAL:HG21	47:1p:32:TYR:CD2	2.54	0.43
1:2A:731:C:H5"	60:2A:4040:HOH:O	2.18	0.43
1:2A:1991:U:H2'	1:2A:1992:G:H5"	2.00	0.43
12:2Q:16:ARG:HG3	12:2Q:18:LYS:HG3	2.01	0.43
14:2S:3:ARG:NH1	14:2S:4:LEU:H	2.17	0.43
18:2W:34:ASN:ND2	27:25:39:MET:HG3	2.34	0.43
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.19	0.43
32:2a:971:G:H1'	32:2a:1365:G:O2'	2.18	0.43
32:2a:994:A:C5	32:2a:1216:G:H4'	2.54	0.43
32:2a:1020:U:H2'	32:2a:1021:G:H8	1.84	0.43
32:2a:1113:C:H2'	32:2a:1114:C:H6	1.84	0.43
33:2b:15:VAL:HG23	33:2b:16:HIS:HD2	1.84	0.43
33:2b:169:LYS:O	33:2b:169:LYS:HD3	2.18	0.43
35:2d:135:LEU:O	35:2d:137:SER:N	2.52	0.43
38:2g:120:ILE:O	38:2g:124:LEU:HB2	2.19	0.43
1:1A:121:G:H4'	1:1A:149:A:H5'	2.01	0.42
1:1A:338:G:OP2	60:1A:4160:HOH:O	2.22	0.42
1:1A:1636:C:H2'	1:1A:1637:A:C8	2.54	0.42
1:1A:1720:U:H2'	1:1A:1721:G:O4'	2.19	0.42
1:1A:2635:C:O2'	4:1E:80:GLU:OE2	2.37	0.42
24:12:41:ILE:HG13	24:12:43:GLN:HG3	2.01	0.42
28:16:38:LYS:HE3	28:16:38:LYS:HB3	1.77	0.42
32:1a:271:C:H2'	32:1a:272:C:H6	1.84	0.42
32:1a:413:G:N2	32:1a:428:G:H1'	2.33	0.42
32:1a:730:G:H2'	32:1a:766:A:H5"	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1032:G:H2'	32:1a:1033:G:O4'	2.19	0.42
33:1b:97:TRP:HZ2	33:1b:102:LEU:HD13	1.83	0.42
35:1d:63:LYS:HE3	35:1d:63:LYS:HB2	1.82	0.42
46:1o:39:LEU:O	46:1o:42:HIS:N	2.52	0.42
1:2A:940:G:N3	1:2A:1191:G:H4'	2.34	0.42
1:2A:996:A:H1'	17:2V:9:GLY:O	2.19	0.42
1:2A:1830:C:OP2	60:2A:3860:HOH:O	2.22	0.42
1:2A:2017:U:OP2	60:2A:3857:HOH:O	2.20	0.42
1:2A:2103:C:H2'	1:2A:2104:G:O4'	2.19	0.42
8:2I:130:TYR:CE2	8:2I:132:PRO:HB3	2.54	0.42
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	2.01	0.42
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	2.00	0.42
27:25:49:CYS:SG	27:25:51:TYR:HB2	2.59	0.42
32:2a:982:U:N3	32:2a:1223:C:N3	2.66	0.42
32:2a:1041:A:H2'	32:2a:1042:G:O4'	2.18	0.42
32:2a:1071:C:H2'	32:2a:1072:G:C8	2.54	0.42
47:2p:57:ARG:NH2	47:2p:79:VAL:O	2.52	0.42
51:2t:57:ARG:NH1	51:2t:100:ILE:HD12	2.33	0.42
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.52	0.42
1:1A:886:C:O2'	1:1A:890:A:N6	2.53	0.42
7:1H:98:LEU:HD12	7:1H:125:VAL:HG23	2.00	0.42
10:1O:108:GLU:H	10:1O:108:GLU:HG3	1.70	0.42
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.34	0.42
31:19:17:ILE:HD13	31:19:26:ILE:HD13	2.00	0.42
32:1a:236:G:OP1	48:1q:40:LYS:NZ	2.48	0.42
32:1a:1112:C:O2	34:1c:179:ARG:HG2	2.19	0.42
32:1a:1342:C:O2'	40:1i:124:GLN:HG3	2.18	0.42
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.54	0.42
35:1d:164:ALA:O	35:1d:168:ARG:HG3	2.19	0.42
36:1e:105:VAL:HB	36:1e:106:PRO:HD3	2.01	0.42
38:1g:104:LEU:HD13	38:1g:104:LEU:HA	1.78	0.42
44:1m:54:VAL:HG12	44:1m:57:ARG:HH12	1.84	0.42
1:2A:1612:C:O2'	29:27:5:TRP:O	2.37	0.42
1:2A:1686:C:H2'	1:2A:1687:G:O4'	2.18	0.42
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	2.00	0.42
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.19	0.42
20:2Y:44:ILE:HG23	20:2Y:62:GLU:HB3	2.01	0.42
23:21:64:ALA:HA	23:21:67:ILE:HG13	2.01	0.42
31:29:3:VAL:HA	31:29:35:ARG:O	2.19	0.42
32:2a:224:C:H2'	32:2a:225:C:C6	2.53	0.42
32:2a:259:G:H2'	32:2a:260:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:739:C:OP1	46:2o:2:PRO:HD3	2.19	0.42
32:2a:938:A:N3	32:2a:1376:U:O2'	2.44	0.42
32:2a:1210:C:H2'	32:2a:1211:U:H5"	2.00	0.42
32:2a:1380:U:C4	38:2g:3:ARG:HG2	2.54	0.42
32:2a:1518:MA6:H93	32:2a:1519:MA6:C9	2.49	0.42
33:2b:42:ILE:HG21	33:2b:202:PRO:O	2.20	0.42
41:2j:68:HIS:CD2	41:2j:68:HIS:H	2.35	0.42
1:1A:41:C:H2'	1:1A:42:G:O4'	2.19	0.42
1:1A:196:A:O2'	1:1A:805:G:O6	2.29	0.42
1:1A:746:A:H2'	1:1A:2612:C:H5"	2.01	0.42
1:1A:1069:A:H4'	1:1A:1070:A:H5"	2.00	0.42
1:1A:1183:G:O2'	25:13:29:ARG:NH1	2.51	0.42
1:1A:1359:A:C2	1:1A:1372:U:O4	2.73	0.42
1:1A:1508:A:H4'	1:1A:1509:C:OP1	2.19	0.42
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.84	0.42
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.19	0.42
16:1U:34:LYS:NZ	16:1U:37:GLU:OE1	2.51	0.42
16:1U:95:LEU:HD12	16:1U:95:LEU:HA	1.82	0.42
32:1a:165:C:H2'	32:1a:166:G:H8	1.83	0.42
35:1d:178:VAL:O	35:1d:180:GLY:N	2.46	0.42
36:1e:78:HIS:CD2	39:1h:104:ARG:HD2	2.54	0.42
42:1k:59:TYR:CE2	42:1k:63:LEU:HD11	2.55	0.42
1:2A:1200:C:H5'	60:2A:3880:HOH:O	2.19	0.42
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.52	0.42
1:2A:2314:C:H5'	6:2G:38:VAL:HG11	2.01	0.42
2:2B:72:G:O2'	2:2B:105:A:N6	2.53	0.42
6:2G:39:ILE:O	6:2G:91:ARG:HA	2.19	0.42
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	2.01	0.42
8:2I:87:LYS:HD2	8:2I:87:LYS:O	2.19	0.42
32:2a:266:G:H5"	32:2a:268:C:H41	1.83	0.42
32:2a:1226:C:O2'	44:2m:111:LYS:NZ	2.40	0.42
32:2a:1244:C:N4	32:2a:1293:G:H1	2.16	0.42
32:2a:1353:G:OP1	52:2u:10:ARG:NH1	2.53	0.42
36:2e:33:VAL:HG22	36:2e:34:VAL:H	1.83	0.42
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.20	0.42
1:1A:1006:C:C2	1:1A:1138:G:N2	2.87	0.42
1:1A:2648:C:H2'	1:1A:2649:U:C6	2.54	0.42
12:1Q:1:MET:HE3	12:1Q:1:MET:HB2	1.77	0.42
21:1Z:21:ALA:O	21:1Z:23:LYS:NZ	2.50	0.42
23:11:67:ILE:N	23:11:68:PRO:HD2	2.33	0.42
30:18:23:VAL:HG13	30:18:47:LYS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:629:G:H2'	32:1a:630:G:O4'	2.19	0.42
32:1a:857:C:H2'	32:1a:858:G:O4'	2.19	0.42
32:1a:1073:U:O2'	33:1b:104:ASN:OD1	2.25	0.42
32:1a:1361:G:H2'	32:1a:1362:C:O4'	2.19	0.42
33:1b:22:LYS:HE3	33:1b:35:GLU:OE2	2.19	0.42
33:1b:93:VAL:HG11	33:1b:97:TRP:HD1	1.83	0.42
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.52	0.42
33:1b:208:ILE:H	33:1b:208:ILE:HD13	1.85	0.42
34:1c:22:TRP:CZ2	45:1n:54:PRO:HG2	2.55	0.42
50:1s:32:LYS:HA	50:1s:50:ALA:HB3	2.01	0.42
1:2A:189:G:H2'	1:2A:205:G:N2	2.35	0.42
1:2A:223:A:N1	1:2A:407:G:O2'	2.46	0.42
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.54	0.42
1:2A:747:U:O2	1:2A:2014:A:H1'	2.18	0.42
1:2A:879:G:H3'	1:2A:880:G:C8	2.48	0.42
1:2A:1462:C:H4'	1:2A:2703:C:H5'	2.02	0.42
1:2A:2218:U:N3	23:21:55:GLY:O	2.37	0.42
1:2A:2641:G:H5"	9:2N:76:SER:HB3	2.01	0.42
1:2A:2750:A:H8	1:2A:2750:A:OP1	2.02	0.42
2:2B:34:U:O4	2:2B:44:G:O2'	2.31	0.42
4:2E:59:VAL:HG21	4:2E:74:PRO:CB	2.50	0.42
10:2O:86:ILE:HG22	10:2O:94:ARG:HD3	2.00	0.42
18:2W:86:LEU:HD23	18:2W:88:ARG:HD3	2.02	0.42
32:2a:562:C:H4'	32:2a:563:A:O5'	2.19	0.42
32:2a:881:G:P	43:2l:12:ARG:HH22	2.43	0.42
32:2a:1004:A:C8	32:2a:1025:U:O4	2.73	0.42
32:2a:1304:G:C6	32:2a:1305:G:N1	2.88	0.42
43:2l:22:SER:OG	43:2l:23:LYS:N	2.53	0.42
45:2n:24:CYS:HB2	45:2n:40:CYS:HB3	2.02	0.42
1:1A:570:G:H2'	1:1A:2030:A:C5	2.55	0.42
1:1A:1372:U:H2'	1:1A:1373:A:O4'	2.20	0.42
2:1B:13:A:N1	2:1B:69:G:O2'	2.43	0.42
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.20	0.42
19:1X:61:GLY:HA3	19:1X:73:ARG:O	2.19	0.42
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.54	0.42
38:1g:28:ASN:HD22	38:1g:28:ASN:HA	1.70	0.42
54:1x:13:C:H2'	54:1x:14:A:H5"	2.02	0.42
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.25	0.42
1:2A:534:U:O2'	16:2U:49:HIS:ND1	2.50	0.42
1:2A:719:C:H2'	1:2A:720:C:H6	1.84	0.42
1:2A:900:A:O2'	1:2A:901:A:OP1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1684:C:C2	1:2A:1705:G:N2	2.88	0.42
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.55	0.42
1:2A:2127:G:N2	1:2A:2161:C:C2	2.88	0.42
1:2A:2141:G:C6	1:2A:2151:G:C5	3.08	0.42
5:2F:162:LEU:HD12	5:2F:162:LEU:HA	1.79	0.42
32:2a:646:U:H2'	32:2a:647:C:C6	2.55	0.42
32:2a:959:A:O2'	32:2a:984:C:O2'	2.23	0.42
32:2a:1072:G:H2'	32:2a:1073:U:H6	1.83	0.42
32:2a:1111:A:H2'	32:2a:1112:C:H6	1.84	0.42
34:2c:142:MET:HG3	34:2c:170:GLN:HB3	2.02	0.42
36:2e:91:LEU:HG	36:2e:118:ILE:HD11	2.02	0.42
1:1A:305:U:H2'	1:1A:306:U:C6	2.54	0.42
1:1A:1495:A:C6	1:1A:1496:A:C6	3.08	0.42
1:1A:1815:A:OP2	3:1D:54:ARG:NH2	2.41	0.42
1:1A:2154:G:N1	1:1A:2155:G:H1'	2.34	0.42
1:1A:2820:A:P	13:1R:2:ARG:HH22	2.43	0.42
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.20	0.42
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.19	0.42
21:1Z:54:HIS:HD2	21:1Z:99:TYR:O	2.02	0.42
21:1Z:79:ARG:HB3	21:1Z:80:ARG:NH1	2.35	0.42
28:16:10:LEU:HG	28:16:54:ILE:HG13	2.02	0.42
32:1a:204:U:P	32:1a:204:U:H3'	2.59	0.42
32:1a:295:C:H2'	32:1a:296:U:O4'	2.20	0.42
32:1a:714:G:H2'	32:1a:715:A:C8	2.54	0.42
37:1f:44:GLY:HA2	37:1f:59:TYR:CZ	2.55	0.42
38:1g:72:ARG:HD3	38:1g:142:GLU:OE2	2.20	0.42
47:1p:53:VAL:HG22	47:1p:79:VAL:HG22	2.01	0.42
1:2A:491:G:H2'	1:2A:492:A:C8	2.55	0.42
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.84	0.42
1:2A:2156:G:H2'	1:2A:2157:G:C6	2.55	0.42
1:2A:2164:C:C5	1:2A:2165:G:H1'	2.54	0.42
6:2G:110:ALA:O	6:2G:140:ILE:HG23	2.19	0.42
7:2H:12:PRO:O	7:2H:15:VAL:HG22	2.19	0.42
7:2H:90:LYS:HB3	7:2H:160:LYS:HA	2.00	0.42
8:2I:48:GLU:HA	8:2I:51:ILE:HG22	2.02	0.42
21:2Z:153:SER:HB3	21:2Z:167:PRO:HA	2.02	0.42
32:2a:583:A:H2'	32:2a:584:G:O4'	2.20	0.42
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.20	0.42
32:2a:1151:A:O2'	32:2a:1152:A:O5'	2.36	0.42
32:2a:1286:A:H2'	32:2a:1287:A:H5'	2.00	0.42
32:2a:1530:G:OP1	32:2a:1530:G:H4'	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:22:LYS:HB2	35:2d:26:CYS:SG	2.60	0.42
35:2d:31:CYS:O	35:2d:35:ARG:HG3	2.19	0.42
37:2f:64:GLN:HE21	37:2f:64:GLN:HB3	1.63	0.42
38:2g:38:LEU:O	38:2g:42:ILE:HG13	2.19	0.42
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	2.02	0.42
1:1A:548:A:H61	17:1V:18:LEU:HA	1.84	0.42
1:1A:1171:G:H3'	1:1A:1173:G:H5'	2.02	0.42
1:1A:1171:G:OP2	1:1A:1174:A:N6	2.53	0.42
1:1A:1186:G:H2'	1:1A:1187:G:O4'	2.19	0.42
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.54	0.42
5:1F:132:VAL:HA	5:1F:138:GLU:HB3	2.01	0.42
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	2.01	0.42
8:1I:38:LEU:HD21	23:11:75:GLU:CD	2.44	0.42
26:14:16:CYS:HA	26:14:33:VAL:O	2.20	0.42
26:14:53:GLU:HB2	26:14:55:ARG:C	2.45	0.42
32:1a:90:U:O2	32:1a:90:U:H2'	2.19	0.42
32:1a:617:G:H4'	47:1p:44:THR:O	2.20	0.42
32:1a:1002:G:C5	32:1a:1003:G:H1'	2.55	0.42
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	2.01	0.42
48:1q:66:SER:O	48:1q:70:ARG:NH1	2.53	0.42
54:1x:37:A:H2'	54:1x:38:A:O4'	2.19	0.42
1:2A:184:C:H2'	1:2A:185:U:H6	1.85	0.42
1:2A:593:G:H4'	30:28:4:MET:HE2	2.00	0.42
1:2A:862:G:H2'	1:2A:863:A:O4'	2.20	0.42
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.55	0.42
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.55	0.42
1:2A:2197:U:H1'	1:2A:2198:A:C8	2.54	0.42
1:2A:2228:G:C5	1:2A:2229:C:C4	3.07	0.42
4:2E:92:THR:O	4:2E:95:ILE:HG12	2.19	0.42
32:2a:918:A:H2'	32:2a:919:A:O4'	2.20	0.42
32:2a:953:G:H5'	32:2a:965:A:N6	2.32	0.42
32:2a:988:G:H2'	32:2a:989:C:O4'	2.20	0.42
32:2a:1221:G:O3'	50:2s:77:THR:OG1	2.36	0.42
34:2c:125:GLU:OE1	34:2c:190:ARG:HB3	2.19	0.42
41:2j:6:ILE:HG22	41:2j:8:LEU:HD22	2.00	0.42
1:1A:910:A:N1	1:1A:2277:G:H1'	2.35	0.42
4:1E:9:VAL:HB	15:1T:3:ARG:HG2	2.02	0.42
7:1H:7:LEU:HA	7:1H:8:PRO:HD3	1.93	0.42
23:11:5:CYS:SG	23:11:62:VAL:HG23	2.60	0.42
25:13:10:LYS:HB3	25:13:53:LEU:HA	2.02	0.42
32:1a:958:A:C6	32:1a:959:A:N1	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	2.00	0.42
51:1t:16:HIS:O	51:1t:19:SER:OG	2.38	0.42
51:1t:29:LYS:O	51:1t:33:ILE:HG13	2.19	0.42
1:2A:84:A:N1	1:2A:98:G:O2'	2.41	0.42
1:2A:1152:C:H4'	16:2U:77:SER:HA	2.02	0.42
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.19	0.42
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.20	0.42
57:2A:3717:T8B:H18	57:2A:3717:T8B:O12	2.20	0.42
8:2I:14:ASP:O	8:2I:17:GLN:HB2	2.20	0.42
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.19	0.42
15:2T:65:LYS:HE3	15:2T:65:LYS:HB3	1.76	0.42
25:23:26:LEU:HD21	25:23:46:ASN:HB2	2.01	0.42
26:24:40:HIS:HB3	26:24:43:TYR:HB2	2.02	0.42
32:2a:807:A:H2'	32:2a:808:C:C6	2.55	0.42
32:2a:1106:G:H4'	34:2c:171:GLY:O	2.19	0.42
32:2a:1129:C:O2'	32:2a:1130:A:C8	2.70	0.42
32:2a:1410:G:H2'	32:2a:1411:C:C6	2.55	0.42
45:2n:57:ARG:HG2	45:2n:58:LYS:H	1.85	0.42
47:2p:59:TRP:HA	47:2p:62:VAL:HG22	2.01	0.42
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.19	0.42
5:1F:140:LEU:HD13	5:1F:140:LEU:HA	1.86	0.42
6:1G:44:GLY:HA2	6:1G:88:ILE:HG22	2.00	0.42
6:1G:179:PRO:HG3	26:14:43:TYR:CZ	2.54	0.42
32:1a:232:G:H1'	32:1a:262:A:N1	2.35	0.42
32:1a:1144:G:N2	32:1a:1146:A:H62	2.18	0.42
33:1b:27:LYS:HB2	33:1b:194:PRO:HD2	2.01	0.42
33:1b:167:PRO:O	33:1b:171:ALA:N	2.53	0.42
35:1d:104:VAL:HG21	35:1d:140:VAL:HG11	2.02	0.42
37:1f:65:VAL:HG21	37:1f:67:MET:HE2	2.02	0.42
38:1g:121:ALA:O	38:1g:125:MET:HG3	2.20	0.42
45:1n:2:ALA:O	45:1n:6:LEU:HD22	2.20	0.42
1:2A:185:U:H4'	1:2A:218:A:H4'	2.02	0.42
1:2A:186:G:H2'	1:2A:187:G:C8	2.54	0.42
1:2A:311:A:C6	1:2A:328:U:C4	3.08	0.42
1:2A:887:A:H4'	1:2A:888:C:H5	1.85	0.42
1:2A:899:A:C2'	1:2A:900:A:H5"	2.50	0.42
1:2A:1614:A:P	1:2A:1614:A:H8	2.42	0.42
1:2A:2502:G:N7	60:2A:3908:HOH:O	2.37	0.42
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.84	0.42
9:2N:104:LYS:HA	9:2N:107:LEU:HD12	2.02	0.42
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:21:56:GLN:HE21	23:21:87:PRO:HG3	1.84	0.42
32:2a:920:U:H2'	32:2a:921:U:C6	2.55	0.42
32:2a:1027:C:H3'	32:2a:1028:C:C6	2.55	0.42
32:2a:1168:A:C6	32:2a:1169:A:C6	3.07	0.42
32:2a:1321:C:O2'	50:2s:77:THR:HG21	2.20	0.42
34:2c:131:ARG:NH1	34:2c:167:TRP:O	2.49	0.42
1:1A:208:C:H2'	1:1A:209:C:C6	2.55	0.42
1:1A:289:A:H2'	1:1A:290:G:O4'	2.20	0.42
1:1A:652(E):G:C6	1:1A:652(F):G:C6	3.08	0.42
1:1A:1064:C:H1'	1:1A:1076:C:H5	1.85	0.42
32:1a:68:G:H5'	32:1a:171:A:O2'	2.20	0.42
32:1a:568:G:O2'	32:1a:574:A:N1	2.48	0.42
32:1a:625:G:H4'	47:1p:16:HIS:CG	2.55	0.42
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.35	0.42
32:1a:943:U:OP2	60:1a:1813:HOH:O	2.21	0.42
47:1p:40:ASP:O	47:1p:48:TRP:HB2	2.19	0.42
1:2A:784:A:H3'	60:2A:4401:HOH:O	2.20	0.42
1:2A:829:A:N7	1:2A:2248:C:H5'	2.34	0.42
1:2A:900:A:H3'	1:2A:901:A:C8	2.55	0.42
1:2A:1843:C:H5'	3:2D:253:GLN:OE1	2.20	0.42
1:2A:2678:C:H2'	1:2A:2679:A:O4'	2.19	0.42
57:2A:3717:T8B:H5	32:2a:1408:A:C2	2.55	0.42
7:2H:76:VAL:O	7:2H:79:VAL:HG22	2.20	0.42
26:24:57:GLU:CB	26:24:58:ARG:HA	2.49	0.42
32:2a:4:U:H3	39:2h:105:ARG:NE	2.17	0.42
32:2a:925:G:H5"	32:2a:926:G:OP1	2.19	0.42
32:2a:1040:U:C2	32:2a:1041:A:C8	3.08	0.42
32:2a:1232:U:OP1	40:2i:124:GLN:HG2	2.20	0.42
37:2f:82:ARG:HE	37:2f:82:ARG:HB3	1.67	0.42
40:2i:26:VAL:HG13	40:2i:61:ALA:HB3	2.01	0.42
41:2j:27:ALA:HB1	41:2j:74:ILE:HD11	2.02	0.42
43:2l:109:GLY:HA3	43:2l:121:GLY:O	2.20	0.42
1:1A:143:G:H2'	1:1A:143(A):C:C6	2.55	0.41
1:1A:286:C:H2'	1:1A:287:C:H6	1.85	0.41
1:1A:971:C:H2'	1:1A:972:G:O4'	2.19	0.41
1:1A:1010:A:N3	1:1A:1153:C:H1'	2.35	0.41
1:1A:1060:U:O2	1:1A:1062:G:H1'	2.20	0.41
4:1E:3:GLY:HA3	4:1E:81:ILE:HD12	2.02	0.41
8:1I:72:LEU:HD23	8:1I:72:LEU:HA	1.81	0.41
13:1R:98:LEU:HB2	13:1R:113:LEU:HD11	2.01	0.41
32:1a:162:A:H2	32:1a:348:G:H5'	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:625:G:H4'	47:1p:16:HIS:CD2	2.55	0.41
32:1a:1273:G:H3'	32:1a:1274:G:C8	2.54	0.41
47:1p:72:ARG:O	47:1p:76:GLN:N	2.44	0.41
1:2A:478:A:N1	1:2A:500:G:H4'	2.35	0.41
1:2A:1262:A:H2	27:25:10:LYS:HD2	1.85	0.41
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.55	0.41
1:2A:1990:C:H2'	1:2A:1991:U:O4'	2.20	0.41
1:2A:2851:A:H2'	1:2A:2852:G:O4'	2.20	0.41
2:2B:114:C:H2'	2:2B:115:G:C8	2.55	0.41
3:2D:132:PRO:HG3	3:2D:190:TYR:CE2	2.54	0.41
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.54	0.41
5:2F:158:THR:HB	5:2F:195:ASP:HB2	2.02	0.41
15:2T:117:ASP:O	15:2T:121:ILE:HG13	2.20	0.41
21:2Z:24:LEU:HD12	21:2Z:25:PRO:HD2	2.02	0.41
21:2Z:152:ALA:C	21:2Z:154:ASP:H	2.29	0.41
31:29:6:SER:O	31:29:6:SER:OG	2.33	0.41
32:2a:353:A:H5'	32:2a:353:A:H8	1.84	0.41
32:2a:418:C:H1'	32:2a:540:G:O2'	2.20	0.41
32:2a:631:G:H2'	32:2a:632:A:C8	2.54	0.41
32:2a:664:G:N2	32:2a:741:G:H1	2.10	0.41
32:2a:1104:G:H4'	33:2b:111:ARG:HE	1.85	0.41
32:2a:1129:C:H5"	32:2a:1130:A:OP1	2.20	0.41
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.19	0.41
33:2b:60:ASP:HA	33:2b:63:MET:HE2	2.02	0.41
36:2e:89:ILE:HG13	36:2e:91:LEU:HD13	2.01	0.41
49:2r:53:ARG:O	49:2r:57:GLY:N	2.48	0.41
51:2t:72:LEU:HD12	51:2t:72:LEU:HA	1.84	0.41
53:2v:14:A:H2'	53:2v:14:A:N3	2.34	0.41
1:1A:196:A:H2'	1:1A:196:A:N3	2.35	0.41
1:1A:414:C:H2'	1:1A:415:A:H8	1.84	0.41
1:1A:614(C):A:C4	5:1F:180:GLY:HA2	2.56	0.41
1:1A:918:A:H5"	2:1B:98:G:O2'	2.20	0.41
1:1A:1359:A:N6	1:1A:1372:U:H3	2.18	0.41
1:1A:2053:G:OP1	4:1E:144:ARG:HG3	2.20	0.41
1:1A:2804:C:H2'	1:1A:2805:G:O4'	2.20	0.41
8:1I:45:LYS:O	8:1I:49:ALA:N	2.49	0.41
10:1O:68:GLU:HB3	10:1O:78:ARG:HB2	2.02	0.41
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.20	0.41
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	2.02	0.41
28:16:18:ARG:HD2	28:16:42:TRP:CD1	2.55	0.41
32:1a:185:A:H2'	32:1a:186:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:674:G:H2'	32:1a:675:A:H8	1.85	0.41
32:1a:1142:G:H2'	32:1a:1143:G:O4'	2.20	0.41
32:1a:1353:G:C2	32:1a:1370:G:C2	3.09	0.41
34:1c:44:GLU:HA	34:1c:52:LEU:HD23	2.02	0.41
43:1l:34:ARG:O	43:1l:61:THR:HG23	2.20	0.41
44:1m:23:TYR:CE2	44:1m:71:ARG:HG3	2.55	0.41
1:2A:193:U:OP2	60:2A:3861:HOH:O	2.22	0.41
1:2A:271(P):C:O3'	8:2I:42:SER:OG	2.36	0.41
1:2A:479:A:O2'	1:2A:481:G:H5'	2.20	0.41
1:2A:856:C:HO2'	1:2A:857:C:P	2.43	0.41
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.53	0.41
1:2A:1000:A:C6	1:2A:1001:A:C6	3.08	0.41
1:2A:1817:G:C6	1:2A:1818:U:C4	3.08	0.41
1:2A:2114:A:H2'	1:2A:2114:A:N3	2.34	0.41
4:2E:181:LEU:HA	4:2E:181:LEU:HD12	1.76	0.41
6:2G:73:ALA:HB3	6:2G:85:GLY:H	1.85	0.41
14:2S:64:GLU:H	14:2S:64:GLU:HG3	1.63	0.41
16:2U:102:GLU:HB3	16:2U:104:GLN:HE22	1.85	0.41
32:2a:540:G:H2'	32:2a:541:G:C8	2.54	0.41
41:2j:74:ILE:HD12	41:2j:74:ILE:HA	1.68	0.41
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	2.02	0.41
48:2q:99:SER:HB2	48:2q:100:LYS:H	1.74	0.41
1:1A:226:G:N2	1:1A:228:A:H62	2.19	0.41
1:1A:251:A:C5	1:1A:252:G:H1'	2.55	0.41
1:1A:784:A:C8	1:1A:792:G:C5	3.08	0.41
1:1A:987:G:O2'	1:1A:1000:A:N3	2.45	0.41
1:1A:1705:G:C6	1:1A:1706:U:C4	3.08	0.41
1:1A:2093:G:C6	1:1A:2225:A:C8	3.09	0.41
14:1S:61:ASN:HB3	14:1S:64:GLU:HB2	2.02	0.41
21:1Z:46:LYS:HB3	21:1Z:46:LYS:HE2	1.70	0.41
26:14:46:GLN:O	26:14:48:ARG:N	2.52	0.41
32:1a:278:G:OP2	48:1q:92:ARG:NH2	2.53	0.41
32:1a:373:A:C2	32:1a:482:A:C6	3.08	0.41
32:1a:692:U:O2'	32:1a:694:A:N7	2.34	0.41
32:1a:1261:A:H3'	32:1a:1262:C:C6	2.54	0.41
36:1e:76:ILE:HD12	36:1e:78:HIS:O	2.19	0.41
41:1j:40:LEU:HB2	41:1j:69:ASN:CB	2.50	0.41
42:1k:16:SER:HA	42:1k:79:SER:O	2.20	0.41
48:1q:87:LYS:HA	48:1q:87:LYS:HD3	1.82	0.41
54:1x:58:A:H4'	54:1x:59:A:OP1	2.20	0.41
1:2A:118:A:C8	1:2A:119:A:C8	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:124:G:OP1	1:2A:1376:C:O2'	2.36	0.41
1:2A:886:C:H2'	1:2A:887:A:H1'	2.03	0.41
1:2A:1913:A:C2	32:2a:1493:A:H8	2.38	0.41
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	2.02	0.41
23:21:23:LYS:HE3	23:21:23:LYS:HB2	1.88	0.41
28:26:10:LEU:HD23	28:26:22:ALA:HB2	2.02	0.41
32:2a:21:G:H2'	32:2a:22:G:C8	2.55	0.41
32:2a:303:A:H2'	32:2a:304:U:O4'	2.20	0.41
32:2a:951:G:C6	32:2a:1231:G:C6	3.08	0.41
32:2a:983:A:H2	32:2a:984:C:C6	2.38	0.41
32:2a:1184:G:OP1	32:2a:1184:G:H3'	2.20	0.41
32:2a:1456:G:N1	51:2t:51:GLU:OE2	2.50	0.41
34:2c:46:GLU:H	34:2c:46:GLU:HG2	1.50	0.41
35:2d:57:ARG:HB3	35:2d:206:PHE:HB2	2.02	0.41
43:2l:92:0TD:H8	43:2l:92:0TD:H4	1.76	0.41
44:2m:51:ALA:HA	44:2m:54:VAL:HG22	2.02	0.41
1:1A:1540:U:H2'	1:1A:1541:G:O4'	2.21	0.41
1:1A:1614:A:P	1:1A:1614:A:H8	2.43	0.41
1:1A:1791:A:OP2	1:1A:1791:A:H8	2.04	0.41
2:1B:2:C:H2'	2:1B:3:C:H6	1.85	0.41
6:1G:108:ASN:HD22	26:14:22:ILE:HD13	1.85	0.41
20:1Y:89:PHE:HA	20:1Y:94:LYS:O	2.21	0.41
30:18:52:LYS:N	30:18:53:PRO:HD2	2.35	0.41
32:1a:865:A:H2	32:1a:918:A:H4'	1.86	0.41
1:2A:828:U:H4'	1:2A:831:G:N1	2.35	0.41
1:2A:862:G:O2'	2:2B:78:A:N3	2.53	0.41
1:2A:888:C:OP1	44:2m:93:ARG:HD3	2.20	0.41
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.55	0.41
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.56	0.41
1:2A:2286:A:H4'	1:2A:2287:A:O5'	2.20	0.41
8:2I:62:LYS:HE2	8:2I:133:HIS:CE1	2.55	0.41
21:2Z:156:LYS:NZ	21:2Z:158:PRO:HD3	2.34	0.41
23:21:52:ARG:HD3	23:21:56:GLN:O	2.21	0.41
32:2a:1390:U:H2'	32:2a:1391:U:C6	2.55	0.41
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.36	0.41
37:2f:89:MET:HG2	37:2f:91:VAL:HG23	2.01	0.41
51:2t:26:ASN:HA	51:2t:71:THR:HG23	2.02	0.41
1:1A:577:G:O2'	1:1A:1254:A:OP1	2.37	0.41
1:1A:581:C:H2'	1:1A:582:G:C8	2.56	0.41
1:1A:1069:A:H2'	1:1A:1073:A:N7	2.35	0.41
1:1A:1779:U:OP2	60:1A:4157:HOH:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2180:U:H2'	1:1A:2181:G:O4'	2.20	0.41
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.45	0.41
1:1A:2262:U:H4'	1:1A:2328:A:C2	2.55	0.41
1:1A:2741:A:H2'	1:1A:2742:C:O4'	2.21	0.41
14:1S:84:GLN:HA	14:1S:111:GLU:HB2	2.02	0.41
16:1U:16:LYS:HB3	16:1U:16:LYS:HE3	1.79	0.41
20:1Y:6:HIS:H	20:1Y:6:HIS:CD2	2.38	0.41
26:14:50:VAL:HG22	44:1m:62:ASN:O	2.21	0.41
32:1a:167:G:H2'	32:1a:168:G:C8	2.56	0.41
32:1a:189(C):C:H2'	32:1a:189(D):C:O4'	2.20	0.41
32:1a:921:U:O2	36:1e:19:MET:HB2	2.21	0.41
35:1d:134:ASP:OD1	35:1d:134:ASP:N	2.52	0.41
50:1s:19:VAL:HA	50:1s:22:LEU:HD12	2.02	0.41
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.56	0.41
1:2A:2061:G:H5"	1:2A:2503:2MA:C2	2.51	0.41
1:2A:2065:C:H2'	1:2A:2066:C:H6	1.84	0.41
1:2A:2203:U:H2'	1:2A:2205:C:H6	1.83	0.41
9:2N:30:ILE:O	9:2N:34:LEU:HD22	2.19	0.41
21:2Z:98:MET:O	21:2Z:126:VAL:N	2.52	0.41
24:22:10:LEU:HD21	24:22:59:ARG:HG2	2.03	0.41
26:24:49:PHE:HB3	26:24:50:VAL:H	1.74	0.41
29:27:1:MET:HE3	29:27:3:ARG:NH2	2.36	0.41
32:2a:553:A:H2'	32:2a:554:C:C6	2.56	0.41
32:2a:692:U:O2'	32:2a:694:A:N7	2.49	0.41
32:2a:1122:U:C2	32:2a:1123:A:C8	3.08	0.41
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.82	0.41
36:2e:151:LEU:HB3	39:2h:79:VAL:HG22	2.01	0.41
41:2j:78:ASN:O	41:2j:80:LYS:N	2.54	0.41
46:2o:7:GLU:OE1	46:2o:38:ARG:NH2	2.53	0.41
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.55	0.41
1:1A:1082:U:C4	1:1A:1086:A:N1	2.83	0.41
1:1A:1448:G:H4'	1:1A:1542:A:OP1	2.20	0.41
1:1A:2106:G:H1	1:1A:2183:C:N4	2.17	0.41
1:1A:2147:G:H3'	1:1A:2147:G:N3	2.36	0.41
1:1A:2168:G:N1	1:1A:2171:A:C8	2.89	0.41
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.50	0.41
11:1P:125:VAL:HG13	11:1P:138:LEU:HD21	2.02	0.41
32:1a:693:G:H2'	32:1a:694:A:C8	2.56	0.41
32:1a:1049:U:OP1	45:1n:3:ARG:HB3	2.20	0.41
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.21	0.41
32:1a:1272:G:H2'	32:1a:1273:G:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1375:A:H4'	38:1g:29:LYS:HD3	2.01	0.41
35:1d:65:ARG:HG3	35:1d:75:PHE:CD1	2.56	0.41
37:1f:69:GLU:O	37:1f:72:VAL:HG13	2.20	0.41
49:1r:26:LEU:HD11	49:1r:42:ARG:HH21	1.85	0.41
49:1r:30:ASP:C	49:1r:32:ARG:H	2.28	0.41
50:1s:27:GLU:HB2	50:1s:28:LYS:HB3	2.03	0.41
1:2A:195:A:H61	1:2A:198:C:H3'	1.86	0.41
1:2A:330:A:H2	1:2A:1210:A:H2'	1.84	0.41
1:2A:1754:C:N3	1:2A:2716:U:O2'	2.51	0.41
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.56	0.41
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.56	0.41
8:2I:58:LEU:HD21	8:2I:62:LYS:HE3	2.03	0.41
16:2U:50:ARG:NH1	17:2V:71:LEU:O	2.53	0.41
18:2W:12:ILE:O	18:2W:101:SER:OG	2.32	0.41
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	2.02	0.41
32:2a:125:U:H2'	32:2a:126:G:C8	2.55	0.41
32:2a:245:C:O2	32:2a:283:C:N3	2.54	0.41
32:2a:426:G:H2'	32:2a:427:U:C6	2.56	0.41
32:2a:737:A:H2'	32:2a:738:C:C6	2.56	0.41
32:2a:1023:G:H5'	32:2a:1024:G:OP2	2.20	0.41
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.86	0.41
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.21	0.41
33:2b:182:ILE:H	33:2b:182:ILE:HG13	1.66	0.41
45:2n:9:LYS:HG3	45:2n:12:ARG:HH21	1.86	0.41
46:2o:67:LEU:HD23	46:2o:67:LEU:HA	1.89	0.41
1:1A:1003:G:O2'	1:1A:1010:A:N1	2.51	0.41
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.56	0.41
1:1A:1606:G:H5"	1:1A:1607:C:OP1	2.21	0.41
1:1A:1657:C:H2'	1:1A:1658:C:C6	2.56	0.41
1:1A:2138:C:N3	1:1A:2154:G:C6	2.88	0.41
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.36	0.41
1:1A:2344:U:O2'	28:16:36:LEU:HB3	2.20	0.41
7:1H:148:ILE:HA	7:1H:151:ILE:HD12	2.02	0.41
10:1O:16:ALA:HB2	10:1O:52:VAL:HG21	2.03	0.41
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	2.02	0.41
21:1Z:54:HIS:O	21:1Z:98:MET:HE1	2.21	0.41
26:14:63:TYR:N	26:14:64:GLY:HA2	2.36	0.41
32:1a:8:A:N7	35:1d:208:SER:OG	2.53	0.41
32:1a:741:G:H2'	32:1a:742:G:O4'	2.20	0.41
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.36	0.41
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1466:C:H2'	32:1a:1467:G:O4'	2.21	0.41
34:1c:36:ASP:N	34:1c:36:ASP:OD1	2.51	0.41
36:1e:41:VAL:HG23	36:1e:67:VAL:CG1	2.51	0.41
1:2A:108:U:H2'	1:2A:109:G:C8	2.56	0.41
1:2A:140:G:N2	1:2A:1596:A:H4'	2.36	0.41
1:2A:245:G:O6	30:28:8:LYS:NZ	2.36	0.41
1:2A:458:G:O2'	1:2A:469:G:O6	2.27	0.41
1:2A:1639:U:H4'	1:2A:2699:C:H4'	2.02	0.41
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.86	0.41
1:2A:2172:U:H4'	1:2A:2173:A:OP2	2.20	0.41
1:2A:2722:G:H2'	1:2A:2723:C:C6	2.55	0.41
13:2R:42:LYS:HB3	13:2R:45:ARG:NH2	2.36	0.41
32:2a:102:G:C6	32:2a:103:C:C4	3.08	0.41
32:2a:193:C:H2'	32:2a:194:C:C6	2.55	0.41
32:2a:289:G:OP2	60:2a:1810:HOH:O	2.22	0.41
32:2a:818:G:N2	32:2a:873:A:OP1	2.54	0.41
32:2a:1367:C:H4'	41:2j:48:THR:HG21	2.02	0.41
35:2d:100:ARG:NH1	35:2d:137:SER:OG	2.54	0.41
1:1A:460:A:H2'	1:1A:461:C:O4'	2.20	0.41
1:1A:687:C:H5"	29:17:2:LYS:HE2	2.02	0.41
1:1A:954:G:OP1	12:1Q:14:ARG:O	2.39	0.41
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.86	0.41
1:1A:2243:U:H2'	1:1A:2244:U:H6	1.80	0.41
1:1A:2661:G:H2'	1:1A:2662:A:C8	2.56	0.41
32:1a:79:G:N2	32:1a:90:U:O2'	2.54	0.41
32:1a:399:G:H2'	32:1a:400:C:C6	2.55	0.41
32:1a:735:C:H2'	32:1a:736:C:C6	2.55	0.41
32:1a:939:G:H2'	32:1a:940:C:C6	2.56	0.41
32:1a:976:G:N2	32:1a:1363:C:OP2	2.44	0.41
32:1a:1057:G:H2'	32:1a:1058:G:O4'	2.21	0.41
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.56	0.41
33:1b:55:PHE:HA	33:1b:58:ILE:HD12	2.01	0.41
38:1g:29:LYS:HA	38:1g:29:LYS:HD2	1.92	0.41
49:1r:24:ALA:C	49:1r:26:LEU:H	2.28	0.41
50:1s:31:ILE:HD12	50:1s:49:ILE:HG12	2.02	0.41
1:2A:90:U:H1'	1:2A:92:A:C8	2.55	0.41
1:2A:116:C:H2'	1:2A:117:G:O4'	2.21	0.41
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.56	0.41
1:2A:1508:A:H5'	1:2A:1509(A):A:C8	2.56	0.41
1:2A:1551:C:H2'	1:2A:1552:G:O4'	2.21	0.41
1:2A:1790:C:H5"	1:2A:1791:A:OP1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2129:C:N4	1:2A:2159:G:H1	2.19	0.41
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	2.03	0.41
21:2Z:138:GLU:H	21:2Z:156:LYS:HE2	1.85	0.41
32:2a:458:C:H2'	32:2a:460:G:O4'	2.21	0.41
32:2a:767:A:H2'	32:2a:768:A:O4'	2.21	0.41
32:2a:1026:G:H5'	32:2a:1027:C:P	2.61	0.41
32:2a:1329:A:OP2	52:2u:7:ARG:NH1	2.53	0.41
34:2c:130:VAL:O	34:2c:134:ILE:HG12	2.21	0.41
1:1A:363(A):A:H2'	1:1A:363(B):G:C8	2.56	0.41
1:1A:530:G:H4'	1:1A:531:C:OP1	2.21	0.41
1:1A:616:G:H5'	5:1F:205:ARG:HD3	2.03	0.41
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.55	0.41
1:1A:1759:A:H1'	1:1A:2711:A:C2	2.56	0.41
1:1A:2155:G:H5"	1:1A:2156:G:C8	2.56	0.41
1:1A:2466:C:H5"	31:19:6:SER:HB2	2.02	0.41
1:1A:2575:C:OP2	60:1A:4161:HOH:O	2.22	0.41
3:1D:118:VAL:N	3:1D:129:ASN:OD1	2.50	0.41
7:1H:55:PRO:HG2	7:1H:61:HIS:ND1	2.36	0.41
15:1T:96:ARG:CZ	15:1T:96:ARG:HB3	2.51	0.41
15:1T:108:ARG:HG3	15:1T:109:GLU:N	2.36	0.41
21:1Z:132:ASN:OD1	21:1Z:132:ASN:N	2.53	0.41
32:1a:67:C:H4'	32:1a:172:A:O4'	2.20	0.41
32:1a:303:A:H2'	32:1a:304:U:O4'	2.21	0.41
32:1a:502:G:C2	32:1a:503:C:C2	3.08	0.41
32:1a:646:U:H2'	32:1a:647:C:C6	2.56	0.41
32:1a:658:G:H2'	32:1a:659:U:H6	1.85	0.41
32:1a:711:G:H2'	32:1a:712:A:H8	1.86	0.41
32:1a:848:C:H2'	32:1a:849:C:C6	2.56	0.41
32:1a:1095:U:P	32:1a:1108:G:H1	2.44	0.41
32:1a:1284:C:H3'	32:1a:1285:A:H8	1.86	0.41
32:1a:1299:A:H5"	32:1a:1299:A:N3	2.36	0.41
33:1b:172:ILE:H	33:1b:172:ILE:HG13	1.63	0.41
33:1b:174:VAL:O	33:1b:178:ARG:HG3	2.21	0.41
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.21	0.41
35:1d:11:LEU:O	35:1d:15:GLU:HG2	2.21	0.41
38:1g:37:ASN:OD1	40:1i:41:VAL:HG23	2.21	0.41
44:1m:74:VAL:O	44:1m:78:ILE:HG13	2.20	0.41
44:1m:91:ARG:HA	44:1m:91:ARG:HD2	1.96	0.41
1:2A:35:G:H1'	1:2A:454:A:C4	2.56	0.41
1:2A:438:G:H2'	1:2A:440:G:H8	1.86	0.41
1:2A:719:C:H2'	1:2A:720:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:744:G:OP1	4:2E:132:HIS:ND1	2.50	0.41
1:2A:921:G:C6	1:2A:922:U:C4	3.09	0.41
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.35	0.41
1:2A:1586:A:H8	1:2A:1586:A:O5'	2.04	0.41
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.18	0.41
1:2A:1783:A:O2'	1:2A:2607:G:O2'	2.28	0.41
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.56	0.41
8:2I:84:GLY:C	8:2I:86:THR:H	2.29	0.41
9:2N:91:LEU:HG	9:2N:98:VAL:HG21	2.01	0.41
12:2Q:29:PHE:HB2	12:2Q:105:GLU:OE1	2.20	0.41
14:2S:19:LYS:HG2	14:2S:19:LYS:H	1.52	0.41
15:2T:122:ASP:O	15:2T:126:ALA:N	2.54	0.41
20:2Y:54:LYS:C	20:2Y:56:PRO:HD3	2.46	0.41
21:2Z:4:ARG:NH2	21:2Z:58:VAL:HG11	2.36	0.41
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	2.03	0.41
25:23:5:LYS:HB3	25:23:57:GLU:HG2	2.03	0.41
26:24:33:VAL:HG13	26:24:35:VAL:H	1.86	0.41
29:27:24:THR:HG22	29:27:26:GLY:H	1.85	0.41
32:2a:524:G:H2'	32:2a:525:C:C6	2.55	0.41
32:2a:714:G:H2'	32:2a:715:A:C8	2.55	0.41
32:2a:826:C:H2'	32:2a:827:U:H6	1.86	0.41
32:2a:977:A:H2'	32:2a:977:A:N3	2.36	0.41
32:2a:980:C:H3'	32:2a:981:U:C6	2.56	0.41
32:2a:1051:C:H2'	32:2a:1052:U:C6	2.55	0.41
32:2a:1066:C:H2'	32:2a:1067:A:C8	2.55	0.41
32:2a:1297:C:H4'	32:2a:1298:C:H5'	2.02	0.41
33:2b:28:PHE:CG	33:2b:190:THR:HA	2.55	0.41
33:2b:56:ARG:HA	33:2b:59:GLU:HB3	2.02	0.41
33:2b:115:LEU:HD13	33:2b:153:ARG:NH1	2.36	0.41
33:2b:134:GLU:O	33:2b:138:LEU:N	2.31	0.41
35:2d:88:VAL:O	35:2d:92:VAL:HG12	2.21	0.41
35:2d:108:LEU:HD23	35:2d:108:LEU:HA	1.88	0.41
38:2g:49:ILE:HA	38:2g:52:GLU:OE2	2.21	0.41
38:2g:69:VAL:HG11	38:2g:134:ALA:HB1	2.02	0.41
42:2k:34:ASP:OD2	42:2k:38:ASN:HB2	2.21	0.41
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.21	0.41
51:2t:92:LEU:HD23	51:2t:92:LEU:HA	1.86	0.41
1:1A:208:C:H2'	1:1A:209:C:H6	1.86	0.41
1:1A:876:C:H2'	1:1A:877:U:O4'	2.21	0.41
1:1A:1068:G:H1'	1:1A:1096:A:N3	2.36	0.41
1:1A:1170:G:C2	1:1A:1180:C:C2	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1B:32:C:C2	2:1B:51:G:N2	2.89	0.41
3:1D:25:THR:HG21	3:1D:113:VAL:HG21	2.03	0.41
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.03	0.41
6:1G:35:GLU:HG2	6:1G:36:LYS:HG2	2.04	0.41
8:1I:70:GLU:O	8:1I:74:ASN:HB2	2.21	0.41
11:1P:139:LYS:C	11:1P:141:ALA:H	2.29	0.41
32:1a:202:U:H5"	32:1a:203:U:H5	1.86	0.41
32:1a:1151:A:O2'	32:1a:1152:A:O5'	2.35	0.41
32:1a:1250:A:H4'	40:1i:68:GLY:H	1.85	0.41
33:1b:76:GLN:CD	33:1b:76:GLN:H	2.29	0.41
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.47	0.41
37:1f:69:GLU:HG2	37:1f:70:ASP:H	1.86	0.41
45:1n:53:LEU:O	45:1n:56:VAL:HG23	2.21	0.41
47:1p:5:ARG:NH2	47:1p:28:ARG:HA	2.36	0.41
1:2A:658:C:H2'	1:2A:659:C:C6	2.56	0.41
1:2A:887:A:O2'	1:2A:888:C:H3'	2.21	0.41
1:2A:1756:G:H4'	1:2A:1758:G:O4'	2.21	0.41
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.21	0.41
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.53	0.41
9:2N:138:LEU:HD23	9:2N:138:LEU:HA	1.70	0.41
21:2Z:70:LEU:HD12	21:2Z:71:VAL:H	1.85	0.41
28:26:38:LYS:HB3	28:26:38:LYS:HE3	1.81	0.41
30:28:34:TRP:CE2	30:28:35:GLN:HB3	2.56	0.41
32:2a:1081:G:H5"	36:2e:18:ARG:HD2	2.03	0.41
33:2b:118:LEU:O	33:2b:122:PHE:HB3	2.20	0.41
36:2e:83:GLU:HG2	36:2e:88:LYS:HG3	2.02	0.41
54:2x:9:G:O2'	54:2x:10:G:N7	2.46	0.41
1:1A:1047:G:H2'	1:1A:1110:G:N2	2.35	0.40
1:1A:1062:G:H2'	1:1A:1063:G:C8	2.55	0.40
1:1A:2131:G:N2	1:1A:2133:G:N3	2.69	0.40
1:1A:2251:OMG:H1'	1:1A:2251:OMG:HM23	1.65	0.40
3:1D:69:ARG:C	3:1D:71:ASP:H	2.29	0.40
8:1I:30:LEU:HB3	8:1I:36:ALA:HB3	2.03	0.40
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.54	0.40
26:14:50:VAL:HG11	44:1m:64:TRP:HA	2.02	0.40
26:14:59:PHE:HE2	50:1s:64:GLU:HB3	1.87	0.40
32:1a:134:A:H61	47:1p:25:ARG:HH12	1.70	0.40
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.56	0.40
32:1a:523:A:H61	43:1l:92:0TD:CG	2.34	0.40
32:1a:523:A:N1	43:1l:92:0TD:H6	2.36	0.40
32:1a:677:U:H3	32:1a:713:G:H22	1.67	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:18:TRP:H	34:1c:18:TRP:HE3	1.68	0.40
34:1c:22:TRP:CD1	34:1c:59:ARG:HD2	2.56	0.40
34:1c:63:ASN:OD1	34:1c:63:ASN:N	2.55	0.40
37:1f:48:LEU:HD22	49:1r:77:GLY:HA3	2.02	0.40
38:1g:78:ARG:HB3	38:1g:79:ARG:H	1.74	0.40
43:1l:36:VAL:HG12	43:1l:82:VAL:HG22	2.03	0.40
44:1m:84:ILE:HD11	44:1m:86:CYS:HB2	2.03	0.40
1:2A:83:G:N1	1:2A:102:G:O2'	2.45	0.40
1:2A:1359:A:N6	1:2A:1372:U:H3	2.19	0.40
1:2A:2301:C:H2'	1:2A:2302:G:H8	1.85	0.40
2:2B:76:G:N7	60:2B:304:HOH:O	2.37	0.40
3:2D:96:HIS:HD2	3:2D:102:LYS:HG2	1.85	0.40
4:2E:112:GLY:O	4:2E:159:HIS:HA	2.21	0.40
21:2Z:19:ARG:HG3	21:2Z:25:PRO:HD3	2.03	0.40
22:20:25:ARG:HD3	22:20:25:ARG:HA	1.90	0.40
26:24:46:GLN:HE22	26:24:48:ARG:HH11	1.68	0.40
32:2a:113:G:N3	32:2a:353:A:O2'	2.48	0.40
32:2a:1039:C:C2	32:2a:1040:U:H1'	2.56	0.40
32:2a:1480:G:H2'	32:2a:1481:U:H6	1.86	0.40
33:2b:58:ILE:HD13	33:2b:58:ILE:HA	1.87	0.40
43:2l:77:LEU:HD21	43:2l:107:ALA:HA	2.02	0.40
44:2m:31:LYS:HA	44:2m:34:LEU:HD12	2.03	0.40
49:2r:48:GLY:O	49:2r:74:ARG:NH2	2.54	0.40
1:1A:614:U:H2'	1:1A:614(A):U:O4'	2.22	0.40
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.57	0.40
1:1A:1142(A):A:C8	1:1A:1144:G:C8	3.09	0.40
1:1A:1155:A:OP1	16:1U:55:ARG:HD2	2.21	0.40
1:1A:1408:C:C2	1:1A:1595:G:N2	2.89	0.40
1:1A:2155:G:C3'	1:1A:2156:G:H5'	2.51	0.40
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.22	0.40
1:1A:2729:G:O2'	4:1E:186:GLY:HA3	2.21	0.40
32:1a:1148:U:H2'	32:1a:1149:C:O4'	2.20	0.40
33:1b:124:SER:HA	33:1b:125:PRO:HA	1.80	0.40
35:1d:107:ARG:HG3	35:1d:173:TRP:HH2	1.86	0.40
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	2.03	0.40
38:1g:58:PRO:O	38:1g:61:VAL:HG12	2.21	0.40
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.54	0.40
54:1x:32:5MC:HM52	54:1x:33:U:O4	2.21	0.40
1:2A:2399:G:H2'	1:2A:2400:G:O4'	2.21	0.40
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.56	0.40
3:2D:23:GLU:O	3:2D:82:ILE:HB	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:2E:147:PRO:O	4:2E:149:ARG:HG2	2.21	0.40
15:2T:59:THR:HG23	15:2T:78:LEU:HB3	2.02	0.40
20:2Y:35:TYR:CE2	20:2Y:69:ALA:HB3	2.56	0.40
32:2a:190:U:H2'	32:2a:191:G:H8	1.86	0.40
32:2a:735:C:H2'	32:2a:736:C:C6	2.55	0.40
32:2a:1084:G:OP1	32:2a:1086:U:C2	2.74	0.40
33:2b:31:TYR:CE2	33:2b:200:ILE:HG21	2.57	0.40
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.37	0.40
1:1A:596:G:H2'	1:1A:597:U:O4'	2.20	0.40
1:1A:710:G:H1	1:1A:721:C:H42	1.70	0.40
1:1A:839:U:H1'	1:1A:1191:G:H1'	2.03	0.40
1:1A:1056:G:N2	1:1A:1102:C:C5	2.89	0.40
3:1D:206:LEU:HD23	3:1D:206:LEU:HA	1.85	0.40
4:1E:5:LEU:HD12	4:1E:51:PHE:HB2	2.04	0.40
4:1E:14:ILE:HB	15:1T:14:TYR:CZ	2.57	0.40
4:1E:48:GLN:NE2	4:1E:78:LEU:HG	2.36	0.40
6:1G:144:ILE:HA	6:1G:148:MET:HE1	2.02	0.40
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.68	0.40
20:1Y:34:LYS:NZ	60:1Y:301:HOH:O	2.31	0.40
32:1a:343:U:H1'	32:1a:347:G:N2	2.37	0.40
32:1a:990:C:O5'	32:1a:990:C:H6	2.05	0.40
33:1b:118:LEU:HB3	33:1b:142:LEU:HD12	2.03	0.40
41:1j:49:VAL:CG2	45:1n:41:ARG:HB2	2.50	0.40
42:1k:38:ASN:HA	42:1k:39:PRO:HD3	1.97	0.40
43:1l:83:VAL:HG21	43:1l:100:ILE:HG12	2.03	0.40
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.56	0.40
1:2A:569:U:C4	1:2A:570:G:C6	3.09	0.40
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.57	0.40
1:2A:1983:C:H4'	1:2A:2606:C:H4'	2.03	0.40
1:2A:2467:C:O2	12:2Q:124:LYS:HE2	2.21	0.40
2:2B:53:A:H8	2:2B:53:A:O5'	2.05	0.40
2:2B:87:G:N2	2:2B:90:A:OP2	2.50	0.40
4:2E:56:PRO:C	4:2E:58:ARG:H	2.29	0.40
4:2E:96:PHE:O	4:2E:175:VAL:HG21	2.21	0.40
4:2E:105:THR:HG21	4:2E:164:ARG:CZ	2.52	0.40
5:2F:10:PRO:HB3	5:2F:17:ARG:NH1	2.37	0.40
5:2F:197:ASP:O	5:2F:200:GLU:HB3	2.21	0.40
8:2I:3:VAL:O	8:2I:18:VAL:HA	2.21	0.40
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.56	0.40
32:2a:1269:A:H2	32:2a:1312:G:N3	2.20	0.40
32:2a:1380:U:C5	38:2g:3:ARG:HG2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2u:6:ARG:HA	52:2u:11:GLY:HA3	2.03	0.40
1:1A:662:G:H5'	11:1P:14:LYS:O	2.20	0.40
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.56	0.40
1:1A:2477:C:O2	31:19:4:ARG:NH2	2.46	0.40
2:1B:92:C:OP1	21:1Z:79:ARG:NH1	2.55	0.40
6:1G:148:MET:HB2	6:1G:148:MET:HE2	1.86	0.40
8:1I:109:ILE:HG23	8:1I:130:TYR:CZ	2.56	0.40
8:1I:135:GLU:C	8:1I:137:PRO:HD3	2.47	0.40
10:1O:35:VAL:HG23	10:1O:65:THR:HG23	2.03	0.40
32:1a:664:G:N2	32:1a:741:G:H1	2.15	0.40
32:1a:826:C:H2'	32:1a:827:U:C6	2.57	0.40
32:1a:1502:A:C8	32:1a:1505:G:N2	2.89	0.40
33:1b:169:LYS:HD3	33:1b:169:LYS:O	2.21	0.40
36:1e:99:GLY:N	36:1e:117:ASP:OD1	2.48	0.40
37:1f:2:ARG:HD2	37:1f:69:GLU:HB3	2.02	0.40
45:1n:29:ARG:HB3	45:1n:40:CYS:HB3	2.02	0.40
51:1t:24:LEU:HD13	51:1t:24:LEU:HA	1.89	0.40
1:2A:211:A:H2'	1:2A:212:G:O4'	2.21	0.40
1:2A:332:A:O2'	1:2A:334:C:OP2	2.30	0.40
1:2A:1197:G:H2'	1:2A:1198:U:H6	1.86	0.40
1:2A:1394:U:OP1	60:2A:3815:HOH:O	2.22	0.40
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.57	0.40
6:2G:108:ASN:HA	26:24:37:SER:HB3	2.02	0.40
20:2Y:53:PRO:C	20:2Y:55:TYR:H	2.29	0.40
21:2Z:44:PHE:O	21:2Z:48:PHE:N	2.35	0.40
25:23:31:LEU:HD22	25:23:31:LEU:HA	1.93	0.40
32:2a:1183:A:H3'	32:2a:1184:G:C5'	2.50	0.40
35:2d:92:VAL:O	35:2d:96:LEU:HD22	2.21	0.40
35:2d:110:PHE:CD2	35:2d:148:VAL:HG23	2.56	0.40
39:2h:17:THR:HG22	39:2h:63:LEU:HD13	2.04	0.40
46:2o:17:ARG:HD3	46:2o:77:ARG:HH21	1.86	0.40
1:1A:624:C:H6	1:1A:624:C:O5'	2.05	0.40
1:1A:657:U:H2'	1:1A:658:C:H6	1.87	0.40
1:1A:724:U:H2'	1:1A:725:G:O4'	2.21	0.40
1:1A:899:A:H2'	1:1A:899:A:N3	2.37	0.40
1:1A:1466:G:H2'	1:1A:1547:C:H41	1.86	0.40
1:1A:2418:A:H2'	1:1A:2419:U:C6	2.57	0.40
1:1A:2611:U:H6	1:1A:2611:U:H5'	1.86	0.40
20:1Y:7:VAL:HG21	20:1Y:72:VAL:CG1	2.52	0.40
21:1Z:75:ASN:O	21:1Z:84:GLU:HG3	2.21	0.40
32:1a:109:A:C6	32:1a:326:G:C6	3.10	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:254:G:O2'	48:1q:16:GLN:O	2.39	0.40
32:1a:616:G:O2'	32:1a:617:G:H5'	2.21	0.40
32:1a:992:U:H4'	32:1a:993:G:H5"	2.03	0.40
32:1a:1149:C:P	40:1i:9:ARG:HH21	2.44	0.40
32:1a:1256:A:N7	32:1a:1278:U:H1'	2.37	0.40
36:1e:85:GLY:O	36:1e:87:SER:N	2.55	0.40
38:1g:20:ASP:OD2	38:1g:23:VAL:HG23	2.21	0.40
38:1g:120:ILE:H	38:1g:120:ILE:HG12	1.72	0.40
39:1h:73:ASP:OD1	39:1h:75:ARG:NE	2.53	0.40
43:1l:8:ASN:O	43:1l:12:ARG:HG3	2.21	0.40
44:1m:3:ARG:HG3	44:1m:7:VAL:O	2.21	0.40
49:1r:55:ARG:HD2	49:1r:55:ARG:HA	1.97	0.40
1:2A:851:U:O2'	25:23:42:ALA:O	2.37	0.40
1:2A:875:G:O2'	21:2Z:151:HIS:NE2	2.54	0.40
1:2A:1114:G:H2'	1:2A:1115:G:C8	2.52	0.40
1:2A:1470:G:H5"	1:2A:1471:A:OP1	2.22	0.40
1:2A:1529:G:O6	1:2A:1530:C:N4	2.55	0.40
1:2A:2019:A:O4'	16:2U:34:LYS:HE2	2.22	0.40
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.21	0.40
1:2A:2287:A:C8	1:2A:2289:G:C8	3.10	0.40
1:2A:2439:A:C8	1:2A:2439:A:H5'	2.56	0.40
1:2A:2748:A:C4	1:2A:2749:A:C8	3.10	0.40
3:2D:77:ALA:HB2	3:2D:97:TYR:CD1	2.56	0.40
7:2H:44:VAL:HG22	7:2H:51:ARG:HB2	2.03	0.40
27:25:30:LEU:HD23	27:25:30:LEU:HA	1.92	0.40
29:27:24:THR:O	29:27:28:ARG:HG3	2.22	0.40
32:2a:176:C:H2'	32:2a:177:C:H6	1.85	0.40
32:2a:736:C:H2'	32:2a:737:A:H8	1.85	0.40
32:2a:913:A:H4'	32:2a:914:A:O5'	2.21	0.40
32:2a:1029:C:C4	32:2a:1032:G:N1	2.86	0.40
32:2a:1254:C:OP1	41:2j:45:ARG:HG3	2.21	0.40
32:2a:1272:G:H5'	32:2a:1273:G:OP2	2.20	0.40
36:2e:102:ALA:HA	36:2e:120:THR:OG1	2.22	0.40
44:2m:49:THR:OG1	44:2m:52:GLU:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	257 (94%)	16 (6%)	0	100	100
3	2D	273/276 (99%)	257 (94%)	16 (6%)	0	100	100
4	1E	202/206 (98%)	189 (94%)	12 (6%)	1 (0%)	24	48
4	2E	202/206 (98%)	191 (95%)	10 (5%)	1 (0%)	24	48
5	1F	201/210 (96%)	198 (98%)	2 (1%)	1 (0%)	24	48
5	2F	201/210 (96%)	187 (93%)	13 (6%)	1 (0%)	24	48
6	1G	179/182 (98%)	167 (93%)	10 (6%)	2 (1%)	11	29
6	2G	179/182 (98%)	152 (85%)	22 (12%)	5 (3%)	4	9
7	1H	172/180 (96%)	161 (94%)	10 (6%)	1 (1%)	21	44
7	2H	172/180 (96%)	149 (87%)	22 (13%)	1 (1%)	21	44
8	1I	144/148 (97%)	130 (90%)	14 (10%)	0	100	100
8	2I	144/148 (97%)	118 (82%)	22 (15%)	4 (3%)	4	9
9	1N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
9	2N	138/140 (99%)	129 (94%)	8 (6%)	1 (1%)	18	41
10	1O	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
10	2O	120/122 (98%)	110 (92%)	9 (8%)	1 (1%)	16	37
11	1P	147/150 (98%)	132 (90%)	15 (10%)	0	100	100
11	2P	147/150 (98%)	129 (88%)	15 (10%)	3 (2%)	6	16
12	1Q	139/141 (99%)	131 (94%)	6 (4%)	2 (1%)	9	23
12	2Q	139/141 (99%)	127 (91%)	10 (7%)	2 (1%)	9	23
13	1R	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
13	2R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	1S	108/112 (96%)	104 (96%)	4 (4%)	0	100	100
14	2S	108/112 (96%)	100 (93%)	7 (6%)	1 (1%)	14	35
15	1T	129/146 (88%)	120 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	2T	129/146 (88%)	123 (95%)	6 (5%)	0	100	100
16	1U	114/118 (97%)	112 (98%)	2 (2%)	0	100	100
16	2U	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
17	1V	99/101 (98%)	93 (94%)	2 (2%)	4 (4%)	2	5
17	2V	99/101 (98%)	91 (92%)	7 (7%)	1 (1%)	12	32
18	1W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
18	2W	110/113 (97%)	107 (97%)	3 (3%)	0	100	100
19	1X	93/96 (97%)	90 (97%)	1 (1%)	2 (2%)	5	14
19	2X	93/96 (97%)	87 (94%)	3 (3%)	3 (3%)	3	7
20	1Y	105/110 (96%)	93 (89%)	10 (10%)	2 (2%)	6	17
20	2Y	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
21	1Z	148/206 (72%)	131 (88%)	15 (10%)	2 (1%)	9	23
21	2Z	156/206 (76%)	129 (83%)	26 (17%)	1 (1%)	21	44
22	10	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
22	20	75/85 (88%)	67 (89%)	7 (9%)	1 (1%)	9	25
23	11	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	29
23	21	95/98 (97%)	94 (99%)	0	1 (1%)	11	29
24	12	68/72 (94%)	66 (97%)	2 (3%)	0	100	100
24	22	68/72 (94%)	64 (94%)	4 (6%)	0	100	100
25	13	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
25	23	57/60 (95%)	51 (90%)	5 (9%)	1 (2%)	6	18
26	14	67/71 (94%)	49 (73%)	15 (22%)	3 (4%)	2	4
26	24	67/71 (94%)	54 (81%)	11 (16%)	2 (3%)	3	8
27	15	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	50 (98%)	1 (2%)	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%)	1 (2%)	0	100	100
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	62 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	195 (85%)	27 (12%)	7 (3%)	3	8
33	2b	229/256 (90%)	176 (77%)	42 (18%)	11 (5%)	2	3
34	1c	204/239 (85%)	184 (90%)	19 (9%)	1 (0%)	24	48
34	2c	204/239 (85%)	167 (82%)	32 (16%)	5 (2%)	4	11
35	1d	206/209 (99%)	184 (89%)	19 (9%)	3 (2%)	8	22
35	2d	206/209 (99%)	186 (90%)	19 (9%)	1 (0%)	24	48
36	1e	146/162 (90%)	130 (89%)	13 (9%)	3 (2%)	5	15
36	2e	146/162 (90%)	133 (91%)	11 (8%)	2 (1%)	9	23
37	1f	98/101 (97%)	87 (89%)	8 (8%)	3 (3%)	3	8
37	2f	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
38	1g	153/156 (98%)	139 (91%)	10 (6%)	4 (3%)	4	11
38	2g	153/156 (98%)	137 (90%)	13 (8%)	3 (2%)	6	16
39	1h	135/138 (98%)	125 (93%)	9 (7%)	1 (1%)	18	41
39	2h	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
40	1i	125/128 (98%)	106 (85%)	18 (14%)	1 (1%)	16	37
40	2i	125/128 (98%)	103 (82%)	21 (17%)	1 (1%)	16	37
41	1j	95/105 (90%)	83 (87%)	10 (10%)	2 (2%)	5	15
41	2j	94/105 (90%)	79 (84%)	12 (13%)	3 (3%)	3	7
42	1k	112/129 (87%)	102 (91%)	8 (7%)	2 (2%)	6	18
42	2k	112/129 (87%)	98 (88%)	13 (12%)	1 (1%)	14	35
43	1l	119/132 (90%)	113 (95%)	4 (3%)	2 (2%)	7	19
43	2l	119/132 (90%)	112 (94%)	7 (6%)	0	100	100
44	1m	121/126 (96%)	107 (88%)	12 (10%)	2 (2%)	7	19
44	2m	120/126 (95%)	94 (78%)	24 (20%)	2 (2%)	7	19
45	1n	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
45	2n	58/61 (95%)	55 (95%)	1 (2%)	2 (3%)	3	7
46	1o	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
46	2o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
47	1p	80/88 (91%)	70 (88%)	9 (11%)	1 (1%)	9	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	2p	80/88 (91%)	69 (86%)	11 (14%)	0	100	100
48	1q	97/105 (92%)	89 (92%)	7 (7%)	1 (1%)	12	32
48	2q	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	12	32
49	1r	66/88 (75%)	59 (89%)	6 (9%)	1 (2%)	8	22
49	2r	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
50	1s	81/93 (87%)	68 (84%)	12 (15%)	1 (1%)	10	27
50	2s	81/93 (87%)	59 (73%)	21 (26%)	1 (1%)	10	27
51	1t	94/106 (89%)	87 (93%)	3 (3%)	4 (4%)	2	4
51	2t	94/106 (89%)	86 (92%)	6 (6%)	2 (2%)	5	15
52	1u	21/27 (78%)	18 (86%)	3 (14%)	0	100	100
52	2u	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
All	All	11356/12128 (94%)	10330 (91%)	901 (8%)	125 (1%)	11	29

All (125) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
7	1H	126	PRO
12	1Q	60	ARG
17	1V	100	ARG
21	1Z	53	ILE
21	1Z	93	ASP
23	11	3	LYS
26	14	45	GLY
26	14	49	PHE
26	14	62	ARG
33	1b	17	PHE
33	1b	125	PRO
38	1g	80	VAL
40	1i	54	ASP
41	1j	79	ARG
42	1k	105	VAL
43	1l	91	LYS
44	1m	67	GLU
44	1m	106	ASN
50	1s	81	ARG
6	2G	51	ARG
6	2G	84	LYS

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Mol	Chain	Res	Type
7	2H	126	PRO
10	2O	5	GLN
11	2P	29	LYS
11	2P	36	LYS
33	2b	16	HIS
33	2b	17	PHE
42	2k	49	GLY
35	1d	173	TRP
36	1e	85	GLY
48	1q	68	ARG
5	2F	130	ALA
6	2G	42	GLY
8	2I	10	GLU
8	2I	40	THR
8	2I	41	GLU
11	2P	44	GLY
17	2V	79	VAL
19	2X	94	GLY
26	24	45	GLY
33	2b	20	GLU
33	2b	123	ALA
38	2g	55	GLY
38	2g	80	VAL
40	2i	121	ARG
44	2m	8	GLU
48	2q	68	ARG
51	2t	47	GLY
6	1G	47	LYS
17	1V	79	VAL
19	1X	94	GLY
33	1b	8	LYS
37	1f	71	ARG
41	1j	30	SER
42	1k	49	GLY
47	1p	39	TYR
51	1t	47	GLY
12	2Q	16	ARG
26	24	49	PHE
33	2b	10	LEU
33	2b	21	ARG
34	2c	91	LEU
34	2c	156	ARG

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Mol	Chain	Res	Type
34	2c	181	ASN
34	2c	188	LEU
38	2g	153	HIS
4	1E	52	LEU
17	1V	43	GLU
19	1X	2	LYS
20	1Y	54	LYS
33	1b	16	HIS
33	1b	20	GLU
38	1g	54	THR
49	1r	25	THR
51	1t	102	GLY
4	2E	52	LEU
6	2G	43	LEU
6	2G	72	ARG
8	2I	117	GLU
19	2X	15	GLU
21	2Z	153	SER
33	2b	38	GLY
33	2b	74	LYS
33	2b	105	PHE
33	2b	125	PRO
34	2c	81	GLY
41	2j	79	ARG
45	2n	27	CYS
50	2s	65	ASN
6	1G	43	LEU
12	1Q	59	ARG
17	1V	53	GLU
33	1b	131	PRO
35	1d	88	VAL
37	1f	70	ASP
51	1t	100	ILE
9	2N	2	LYS
23	21	3	LYS
25	23	38	GLU
33	2b	9	GLU
36	2e	69	VAL
41	2j	78	ASN
44	2m	42	ALA
45	2n	14	PRO
33	1b	231	GLU

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Mol	Chain	Res	Type
34	1c	81	GLY
36	1e	86	ALA
38	1g	17	VAL
43	1l	105	TYR
51	1t	96	GLY
19	2X	48	LYS
41	2j	89	ASP
37	1f	40	VAL
22	20	13	GLY
36	2e	85	GLY
20	1Y	103	GLY
38	1g	82	GLY
35	2d	136	PRO
39	1h	73	ASP
12	2Q	15	GLY
51	2t	102	GLY
35	1d	178	VAL
14	2S	96	GLY
36	1e	39	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	1D	215/218 (99%)	196 (91%)	19 (9%)	9 23
3	2D	215/218 (99%)	199 (93%)	16 (7%)	13 32
4	1E	164/166 (99%)	144 (88%)	20 (12%)	5 12
4	2E	164/166 (99%)	149 (91%)	15 (9%)	9 22
5	1F	160/166 (96%)	143 (89%)	17 (11%)	6 17
5	2F	159/166 (96%)	141 (89%)	18 (11%)	5 14
6	1G	143/156 (92%)	126 (88%)	17 (12%)	5 13
6	2G	143/156 (92%)	122 (85%)	21 (15%)	3 8
7	1H	144/148 (97%)	129 (90%)	15 (10%)	7 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	2H	144/148 (97%)	131 (91%)	13 (9%)	9	23
8	1I	113/124 (91%)	90 (80%)	23 (20%)	1	3
8	2I	105/124 (85%)	87 (83%)	18 (17%)	2	6
9	1N	118/119 (99%)	105 (89%)	13 (11%)	6	15
9	2N	118/119 (99%)	103 (87%)	15 (13%)	4	11
10	1O	100/100 (100%)	97 (97%)	3 (3%)	36	66
10	2O	100/100 (100%)	92 (92%)	8 (8%)	11	28
11	1P	115/116 (99%)	106 (92%)	9 (8%)	11	29
11	2P	115/116 (99%)	101 (88%)	14 (12%)	5	12
12	1Q	111/111 (100%)	101 (91%)	10 (9%)	9	23
12	2Q	111/111 (100%)	99 (89%)	12 (11%)	6	16
13	1R	101/101 (100%)	94 (93%)	7 (7%)	14	34
13	2R	101/101 (100%)	95 (94%)	6 (6%)	18	42
14	1S	86/88 (98%)	77 (90%)	9 (10%)	6	17
14	2S	85/88 (97%)	70 (82%)	15 (18%)	2	5
15	1T	115/127 (91%)	109 (95%)	6 (5%)	21	47
15	2T	113/127 (89%)	102 (90%)	11 (10%)	8	20
16	1U	93/94 (99%)	86 (92%)	7 (8%)	12	31
16	2U	93/94 (99%)	87 (94%)	6 (6%)	15	37
17	1V	80/82 (98%)	73 (91%)	7 (9%)	9	23
17	2V	80/82 (98%)	73 (91%)	7 (9%)	9	23
18	1W	90/92 (98%)	83 (92%)	7 (8%)	11	29
18	2W	90/92 (98%)	82 (91%)	8 (9%)	9	23
19	1X	77/78 (99%)	75 (97%)	2 (3%)	40	70
19	2X	77/78 (99%)	76 (99%)	1 (1%)	61	83
20	1Y	85/91 (93%)	76 (89%)	9 (11%)	6	17
20	2Y	85/91 (93%)	72 (85%)	13 (15%)	3	7
21	1Z	135/179 (75%)	123 (91%)	12 (9%)	9	23
21	2Z	137/179 (76%)	119 (87%)	18 (13%)	4	10
22	10	60/67 (90%)	58 (97%)	2 (3%)	33	63
22	20	61/67 (91%)	56 (92%)	5 (8%)	10	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	11	80/83 (96%)	78 (98%)	2 (2%)	42	71
23	21	80/83 (96%)	72 (90%)	8 (10%)	7	19
24	12	65/67 (97%)	62 (95%)	3 (5%)	24	51
24	22	65/67 (97%)	59 (91%)	6 (9%)	8	22
25	13	51/52 (98%)	44 (86%)	7 (14%)	3	9
25	23	50/52 (96%)	44 (88%)	6 (12%)	5	12
26	14	59/63 (94%)	52 (88%)	7 (12%)	5	13
26	24	53/63 (84%)	41 (77%)	12 (23%)	1	3
27	15	50/52 (96%)	46 (92%)	4 (8%)	11	28
27	25	50/52 (96%)	47 (94%)	3 (6%)	17	41
28	16	51/52 (98%)	45 (88%)	6 (12%)	5	13
28	26	50/52 (96%)	43 (86%)	7 (14%)	3	9
29	17	41/42 (98%)	37 (90%)	4 (10%)	7	19
29	27	41/42 (98%)	37 (90%)	4 (10%)	7	19
30	18	54/55 (98%)	51 (94%)	3 (6%)	19	44
30	28	54/55 (98%)	51 (94%)	3 (6%)	19	44
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	67
31	29	34/34 (100%)	33 (97%)	1 (3%)	37	67
33	1b	192/220 (87%)	165 (86%)	27 (14%)	3	9
33	2b	187/220 (85%)	162 (87%)	25 (13%)	4	9
34	1c	142/188 (76%)	124 (87%)	18 (13%)	4	11
34	2c	140/188 (74%)	120 (86%)	20 (14%)	3	8
35	1d	169/181 (93%)	144 (85%)	25 (15%)	3	8
35	2d	173/181 (96%)	148 (86%)	25 (14%)	3	8
36	1e	113/123 (92%)	98 (87%)	15 (13%)	4	10
36	2e	114/123 (93%)	100 (88%)	14 (12%)	4	12
37	1f	84/90 (93%)	73 (87%)	11 (13%)	4	10
37	2f	85/90 (94%)	78 (92%)	7 (8%)	10	27
38	1g	119/127 (94%)	109 (92%)	10 (8%)	10	26
38	2g	120/127 (94%)	103 (86%)	17 (14%)	3	8
39	1h	114/119 (96%)	105 (92%)	9 (8%)	11	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	2h	114/119 (96%)	107 (94%)	7 (6%)	17	40
40	1i	90/99 (91%)	77 (86%)	13 (14%)	3	8
40	2i	89/99 (90%)	78 (88%)	11 (12%)	4	11
41	1j	66/92 (72%)	56 (85%)	10 (15%)	3	7
41	2j	69/92 (75%)	56 (81%)	13 (19%)	1	4
42	1k	82/99 (83%)	74 (90%)	8 (10%)	7	19
42	2k	83/99 (84%)	76 (92%)	7 (8%)	10	26
43	1l	96/108 (89%)	91 (95%)	5 (5%)	21	47
43	2l	96/108 (89%)	87 (91%)	9 (9%)	8	21
44	1m	93/101 (92%)	81 (87%)	12 (13%)	4	10
44	2m	92/101 (91%)	78 (85%)	14 (15%)	3	7
45	1n	49/50 (98%)	43 (88%)	6 (12%)	5	12
45	2n	49/50 (98%)	44 (90%)	5 (10%)	7	18
46	1o	78/80 (98%)	72 (92%)	6 (8%)	12	30
46	2o	78/80 (98%)	72 (92%)	6 (8%)	12	30
47	1p	69/74 (93%)	63 (91%)	6 (9%)	9	24
47	2p	68/74 (92%)	59 (87%)	9 (13%)	4	10
48	1q	94/97 (97%)	85 (90%)	9 (10%)	8	20
48	2q	94/97 (97%)	86 (92%)	8 (8%)	10	25
49	1r	59/77 (77%)	53 (90%)	6 (10%)	7	18
49	2r	59/77 (77%)	50 (85%)	9 (15%)	3	7
50	1s	69/80 (86%)	65 (94%)	4 (6%)	18	42
50	2s	67/80 (84%)	58 (87%)	9 (13%)	4	9
51	1t	70/82 (85%)	65 (93%)	5 (7%)	13	33
51	2t	70/82 (85%)	66 (94%)	4 (6%)	18	43
52	1u	18/22 (82%)	16 (89%)	2 (11%)	6	15
52	2u	18/22 (82%)	17 (94%)	1 (6%)	19	44
All	All	9294/10064 (92%)	8326 (90%)	968 (10%)	7	17

All (968) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL

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Mol	Chain	Res	Type
3	1D	14	ARG
3	1D	16	MET
3	1D	18	VAL
3	1D	32	SER
3	1D	34	VAL
3	1D	61	LEU
3	1D	71	ASP
3	1D	112	GLN
3	1D	142	VAL
3	1D	155	LEU
3	1D	173	VAL
3	1D	200	ASP
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	253	GLN
3	1D	259	THR
3	1D	273	ARG
4	1E	7	VAL
4	1E	9	VAL
4	1E	12	THR
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	45	THR
4	1E	47	VAL
4	1E	49	LEU
4	1E	59	VAL
4	1E	73	GLU
4	1E	77	ILE
4	1E	78	LEU
4	1E	116	VAL
4	1E	119	ARG
4	1E	173	VAL
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
4	1E	195	LEU
5	1F	24	LEU
5	1F	33	LEU
5	1F	53	THR
5	1F	70	THR

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Mol	Chain	Res	Type
5	1F	72	ARG
5	1F	74	ARG
5	1F	88	VAL
5	1F	106	ARG
5	1F	132	VAL
5	1F	140	LEU
5	1F	144	LYS
5	1F	162	LEU
5	1F	168	ARG
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
5	1F	203	GLN
6	1G	3	LEU
6	1G	5	VAL
6	1G	7	LEU
6	1G	22	ARG
6	1G	28	VAL
6	1G	31	VAL
6	1G	40	ASN
6	1G	43	LEU
6	1G	60	LEU
6	1G	82	LEU
6	1G	116	ASP
6	1G	139	LEU
6	1G	140	ILE
6	1G	148	MET
6	1G	149	VAL
6	1G	159	VAL
6	1G	161	THR
7	1H	13	LYS
7	1H	15	VAL
7	1H	23	ARG
7	1H	24	VAL
7	1H	27	LYS
7	1H	49	VAL
7	1H	56	SER
7	1H	98	LEU
7	1H	116	GLU
7	1H	119	GLU
7	1H	122	THR
7	1H	124	GLU

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Mol	Chain	Res	Type
7	1H	127	GLU
7	1H	130	ARG
7	1H	136	ILE
8	1I	2	LYS
8	1I	5	LEU
8	1I	9	LEU
8	1I	10	GLU
8	1I	12	LEU
8	1I	38	LEU
8	1I	41	GLU
8	1I	47	LEU
8	1I	68	LEU
8	1I	77	LEU
8	1I	78	THR
8	1I	85	GLU
8	1I	87	LYS
8	1I	92	VAL
8	1I	99	GLU
8	1I	101	LEU
8	1I	102	SER
8	1I	108	THR
8	1I	109	ILE
8	1I	123	LEU
8	1I	127	VAL
8	1I	140	LEU
8	1I	144	VAL
9	1N	1	MET
9	1N	14	VAL
9	1N	28	THR
9	1N	32	THR
9	1N	34	LEU
9	1N	48	MET
9	1N	61	ARG
9	1N	62	VAL
9	1N	65	LYS
9	1N	67	LEU
9	1N	134	ARG
9	1N	137	LYS
9	1N	138	LEU
10	1O	52	VAL
10	1O	69	ILE
10	1O	98	VAL

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Mol	Chain	Res	Type
11	1P	7	ARG
11	1P	45	LEU
11	1P	56	SER
11	1P	75	ILE
11	1P	95	VAL
11	1P	101	VAL
11	1P	125	VAL
11	1P	147	LEU
11	1P	148	LEU
12	1Q	7	MET
12	1Q	8	LYS
12	1Q	56	ARG
12	1Q	59	ARG
12	1Q	60	ARG
12	1Q	63	LYS
12	1Q	75	THR
12	1Q	81	VAL
12	1Q	109	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	36	THR
13	1R	44	LEU
13	1R	67	LEU
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	14	VAL
14	1S	15	ARG
14	1S	36	TYR
14	1S	46	VAL
14	1S	49	VAL
14	1S	50	SER
14	1S	69	VAL
14	1S	76	LYS
14	1S	110	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	36	GLU
15	1T	49	VAL
15	1T	96	ARG
15	1T	128	GLU
16	1U	8	VAL

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Mol	Chain	Res	Type
16	1U	27	LEU
16	1U	31	SER
16	1U	74	LEU
16	1U	77	SER
16	1U	83	LEU
16	1U	95	LEU
17	1V	1	MET
17	1V	45	THR
17	1V	61	VAL
17	1V	79	VAL
17	1V	82	ARG
17	1V	85	LYS
17	1V	100	ARG
18	1W	4	LYS
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	65	LEU
18	1W	96	ILE
19	1X	35	THR
19	1X	38	GLU
20	1Y	7	VAL
20	1Y	9	LYS
20	1Y	23	ARG
20	1Y	28	LYS
20	1Y	47	LYS
20	1Y	61	ILE
20	1Y	67	LEU
20	1Y	72	VAL
20	1Y	99	CYS
21	1Z	33	LEU
21	1Z	61	LEU
21	1Z	65	GLN
21	1Z	70	LEU
21	1Z	72	ARG
21	1Z	84	GLU
21	1Z	102	LEU
21	1Z	135	GLU
21	1Z	149	SER
21	1Z	154	ASP
21	1Z	155	LEU

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Mol	Chain	Res	Type
21	1Z	163	LEU
22	10	10	THR
22	10	55	ARG
23	11	46	LEU
23	11	83	GLU
24	12	3	LEU
24	12	53	LEU
24	12	65	ASN
25	13	23	LEU
25	13	32	GLN
25	13	34	GLU
25	13	54	VAL
25	13	55	ARG
25	13	58	VAL
25	13	60	GLU
26	14	1	MET
26	14	3	GLU
26	14	49	PHE
26	14	53	GLU
26	14	56	VAL
26	14	59	PHE
26	14	63	TYR
27	15	6	VAL
27	15	40	LYS
27	15	57	VAL
27	15	60	VAL
28	16	4	GLU
28	16	6	ARG
28	16	9	LEU
28	16	19	ARG
28	16	44	ARG
28	16	48	VAL
29	17	4	THR
29	17	24	THR
29	17	41	ARG
29	17	43	THR
30	18	14	VAL
30	18	15	LYS
30	18	52	LYS
31	19	4	ARG
33	1b	7	VAL
33	1b	15	VAL

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Mol	Chain	Res	Type
33	1b	32	ILE
33	1b	35	GLU
33	1b	39	ILE
33	1b	44	LEU
33	1b	64	ARG
33	1b	78	GLN
33	1b	80	ILE
33	1b	93	VAL
33	1b	94	ASN
33	1b	112	VAL
33	1b	121	LEU
33	1b	124	SER
33	1b	127	ILE
33	1b	140	HIS
33	1b	160	ASP
33	1b	165	VAL
33	1b	179	LYS
33	1b	189	ASP
33	1b	196	LEU
33	1b	208	ILE
33	1b	217	ARG
33	1b	221	LEU
33	1b	226	ARG
33	1b	229	VAL
33	1b	233	SER
34	1c	3	ASN
34	1c	15	THR
34	1c	20	SER
34	1c	28	GLN
34	1c	36	ASP
34	1c	43	LEU
34	1c	46	GLU
34	1c	70	VAL
34	1c	77	ILE
34	1c	82	GLU
34	1c	89	GLU
34	1c	119	ARG
34	1c	138	VAL
34	1c	165	THR
34	1c	175	LEU
34	1c	178	LEU
34	1c	195	VAL

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Mol	Chain	Res	Type
34	1c	198	VAL
35	1d	11	LEU
35	1d	19	LEU
35	1d	31	CYS
35	1d	59	ARG
35	1d	70	ILE
35	1d	76	ARG
35	1d	83	SER
35	1d	88	VAL
35	1d	112	VAL
35	1d	115	ARG
35	1d	127	THR
35	1d	129	ASN
35	1d	135	LEU
35	1d	140	VAL
35	1d	144	ASP
35	1d	152	SER
35	1d	155	LEU
35	1d	157	LEU
35	1d	158	ILE
35	1d	178	VAL
35	1d	188	LEU
35	1d	194	LEU
35	1d	198	VAL
35	1d	200	GLU
35	1d	208	SER
36	1e	9	LYS
36	1e	12	LEU
36	1e	16	THR
36	1e	31	LEU
36	1e	34	VAL
36	1e	41	VAL
36	1e	47	LYS
36	1e	53	LEU
36	1e	56	GLN
36	1e	64	ARG
36	1e	78	HIS
36	1e	79	GLU
36	1e	91	LEU
36	1e	98	THR
36	1e	120	THR
37	1f	24	GLU

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Mol	Chain	Res	Type
37	1f	36	ARG
37	1f	43	LEU
37	1f	45	LEU
37	1f	66	GLU
37	1f	72	VAL
37	1f	73	ASN
37	1f	75	LEU
37	1f	78	GLU
37	1f	91	VAL
37	1f	98	LEU
38	1g	12	LEU
38	1g	50	ILE
38	1g	61	VAL
38	1g	78	ARG
38	1g	104	LEU
38	1g	110	GLN
38	1g	113	GLU
38	1g	115	ARG
38	1g	140	ASP
38	1g	155	ARG
39	1h	29	SER
39	1h	37	ARG
39	1h	49	GLU
39	1h	51	VAL
39	1h	112	LEU
39	1h	115	SER
39	1h	121	ASP
39	1h	122	ARG
39	1h	133	LEU
40	1i	17	VAL
40	1i	25	LYS
40	1i	53	VAL
40	1i	64	THR
40	1i	74	ILE
40	1i	75	ASP
40	1i	81	ILE
40	1i	97	LYS
40	1i	99	LEU
40	1i	103	THR
40	1i	108	VAL
40	1i	121	ARG
40	1i	128	ARG

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Mol	Chain	Res	Type
41	1j	34	VAL
41	1j	38	ILE
41	1j	42	THR
41	1j	46	ARG
41	1j	49	VAL
41	1j	55	LYS
41	1j	72	VAL
41	1j	81	THR
41	1j	92	THR
41	1j	98	ILE
42	1k	31	THR
42	1k	48	ILE
42	1k	70	LYS
42	1k	82	VAL
42	1k	87	THR
42	1k	109	VAL
42	1k	114	VAL
42	1k	117	ASN
43	1l	70	ILE
43	1l	83	VAL
43	1l	86	ARG
43	1l	97	ARG
43	1l	100	ILE
44	1m	3	ARG
44	1m	4	ILE
44	1m	15	VAL
44	1m	19	LEU
44	1m	43	THR
44	1m	48	LEU
44	1m	49	THR
44	1m	64	TRP
44	1m	70	LEU
44	1m	98	VAL
44	1m	106	ASN
44	1m	109	THR
45	1n	3	ARG
45	1n	7	ILE
45	1n	13	THR
45	1n	18	VAL
45	1n	33	VAL
45	1n	56	VAL
46	1o	3	ILE

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Mol	Chain	Res	Type
46	1o	39	LEU
46	1o	47	LYS
46	1o	56	LEU
46	1o	84	LYS
46	1o	87	ILE
47	1p	11	SER
47	1p	20	VAL
47	1p	21	VAL
47	1p	45	THR
47	1p	62	VAL
47	1p	67	THR
48	1q	9	VAL
48	1q	11	VAL
48	1q	19	VAL
48	1q	52	LYS
48	1q	53	LEU
48	1q	60	ILE
48	1q	63	ARG
48	1q	67	LYS
48	1q	86	GLU
49	1r	35	ARG
49	1r	37	VAL
49	1r	46	GLU
49	1r	47	THR
49	1r	58	LEU
49	1r	84	LYS
50	1s	28	LYS
50	1s	41	VAL
50	1s	48	THR
50	1s	63	THR
51	1t	10	LEU
51	1t	24	LEU
51	1t	62	LEU
51	1t	84	LEU
51	1t	100	ILE
52	1u	15	ARG
52	1u	20	LYS
3	2D	3	VAL
3	2D	32	SER
3	2D	37	LEU
3	2D	38	LYS
3	2D	71	ASP

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Mol	Chain	Res	Type
3	2D	89	SER
3	2D	116	GLN
3	2D	141	VAL
3	2D	142	VAL
3	2D	173	VAL
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	260	ARG
3	2D	275	LYS
4	2E	9	VAL
4	2E	21	VAL
4	2E	23	VAL
4	2E	34	VAL
4	2E	38	THR
4	2E	73	GLU
4	2E	78	LEU
4	2E	90	THR
4	2E	94	GLU
4	2E	116	VAL
4	2E	119	ARG
4	2E	134	ILE
4	2E	175	VAL
4	2E	181	LEU
4	2E	184	VAL
5	2F	20	LEU
5	2F	33	LEU
5	2F	43	LYS
5	2F	70	THR
5	2F	74	ARG
5	2F	106	ARG
5	2F	133	ASN
5	2F	135	LYS
5	2F	145	GLU
5	2F	153	SER
5	2F	158	THR
5	2F	161	GLU
5	2F	162	LEU
5	2F	165	ARG
5	2F	183	VAL
5	2F	192	LEU

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Mol	Chain	Res	Type
5	2F	201	VAL
5	2F	203	GLN
6	2G	3	LEU
6	2G	7	LEU
6	2G	18	GLU
6	2G	19	LEU
6	2G	26	GLN
6	2G	28	VAL
6	2G	31	VAL
6	2G	43	LEU
6	2G	45	GLU
6	2G	51	ARG
6	2G	59	GLU
6	2G	70	VAL
6	2G	91	ARG
6	2G	124	SER
6	2G	130	ASN
6	2G	135	LEU
6	2G	139	LEU
6	2G	140	ILE
6	2G	152	LEU
6	2G	159	VAL
6	2G	165	THR
7	2H	2	SER
7	2H	7	LEU
7	2H	43	VAL
7	2H	45	VAL
7	2H	70	THR
7	2H	71	LEU
7	2H	77	LYS
7	2H	90	LYS
7	2H	95	ARG
7	2H	103	LEU
7	2H	114	VAL
7	2H	124	GLU
7	2H	169	VAL
8	2I	15	VAL
8	2I	38	LEU
8	2I	40	THR
8	2I	58	LEU
8	2I	61	ARG
8	2I	68	LEU

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Mol	Chain	Res	Type
8	2I	69	LYS
8	2I	77	LEU
8	2I	82	ARG
8	2I	86	THR
8	2I	87	LYS
8	2I	92	VAL
8	2I	117	GLU
8	2I	121	LYS
8	2I	123	LEU
8	2I	125	GLU
8	2I	127	VAL
8	2I	144	VAL
9	2N	1	MET
9	2N	2	LYS
9	2N	5	VAL
9	2N	14	VAL
9	2N	28	THR
9	2N	34	LEU
9	2N	38	HIS
9	2N	62	VAL
9	2N	68	GLU
9	2N	83	LYS
9	2N	96	GLU
9	2N	99	LEU
9	2N	100	GLU
9	2N	112	LEU
9	2N	131	GLN
10	2O	1	MET
10	2O	21	CYS
10	2O	28	SER
10	2O	52	VAL
10	2O	53	LYS
10	2O	69	ILE
10	2O	78	ARG
10	2O	98	VAL
11	2P	7	ARG
11	2P	45	LEU
11	2P	56	SER
11	2P	58	THR
11	2P	65	ARG
11	2P	77	ARG
11	2P	95	VAL

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Mol	Chain	Res	Type
11	2P	96	THR
11	2P	98	GLU
11	2P	99	LEU
11	2P	100	LEU
11	2P	106	LEU
11	2P	125	VAL
11	2P	126	VAL
12	2Q	1	MET
12	2Q	6	ARG
12	2Q	56	ARG
12	2Q	64	ILE
12	2Q	75	THR
12	2Q	81	VAL
12	2Q	98	LYS
12	2Q	109	VAL
12	2Q	110	THR
12	2Q	112	GLU
12	2Q	131	ILE
12	2Q	133	ARG
13	2R	36	THR
13	2R	44	LEU
13	2R	67	LEU
13	2R	100	LEU
13	2R	111	LEU
13	2R	114	VAL
14	2S	13	ARG
14	2S	15	ARG
14	2S	17	ARG
14	2S	19	LYS
14	2S	21	THR
14	2S	27	SER
14	2S	50	SER
14	2S	58	LEU
14	2S	64	GLU
14	2S	71	ARG
14	2S	80	LEU
14	2S	82	ILE
14	2S	83	LYS
14	2S	98	VAL
14	2S	103	GLU
15	2T	15	VAL
15	2T	17	THR

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Mol	Chain	Res	Type
15	2T	18	ASP
15	2T	28	VAL
15	2T	39	ARG
15	2T	63	VAL
15	2T	96	ARG
15	2T	104	ASN
15	2T	107	ASP
15	2T	115	ARG
15	2T	129	ARG
16	2U	8	VAL
16	2U	17	ILE
16	2U	31	SER
16	2U	74	LEU
16	2U	77	SER
16	2U	117	GLN
17	2V	1	MET
17	2V	7	THR
17	2V	25	LEU
17	2V	38	LEU
17	2V	61	VAL
17	2V	79	VAL
17	2V	82	ARG
18	2W	4	LYS
18	2W	11	ARG
18	2W	17	VAL
18	2W	28	SER
18	2W	67	ASP
18	2W	92	ARG
18	2W	96	ILE
18	2W	106	ILE
19	2X	81	VAL
20	2Y	7	VAL
20	2Y	9	LYS
20	2Y	19	LYS
20	2Y	38	ILE
20	2Y	42	VAL
20	2Y	49	VAL
20	2Y	72	VAL
20	2Y	83	THR
20	2Y	85	VAL
20	2Y	88	LYS
20	2Y	91	GLU

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Mol	Chain	Res	Type
20	2Y	98	VAL
20	2Y	99	CYS
21	2Z	40	ASP
21	2Z	42	VAL
21	2Z	53	ILE
21	2Z	57	ILE
21	2Z	60	GLU
21	2Z	71	VAL
21	2Z	91	LEU
21	2Z	121	HIS
21	2Z	123	ASP
21	2Z	126	VAL
21	2Z	141	VAL
21	2Z	150	LEU
21	2Z	154	ASP
21	2Z	155	LEU
21	2Z	161	VAL
21	2Z	162	GLU
21	2Z	171	ILE
21	2Z	174	VAL
22	20	10	THR
22	20	53	MET
22	20	55	ARG
22	20	64	ASP
22	20	68	GLU
23	21	21	ARG
23	21	26	ARG
23	21	30	VAL
23	21	59	THR
23	21	65	SER
23	21	78	LYS
23	21	81	LYS
23	21	98	LEU
24	22	30	ARG
24	22	35	LEU
24	22	38	GLN
24	22	46	GLN
24	22	59	ARG
24	22	62	THR
25	23	3	ARG
25	23	5	LYS
25	23	23	LEU

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Mol	Chain	Res	Type
25	23	31	LEU
25	23	54	VAL
25	23	59	VAL
26	24	3	GLU
26	24	10	VAL
26	24	13	ARG
26	24	24	THR
26	24	27	THR
26	24	33	VAL
26	24	35	VAL
26	24	49	PHE
26	24	50	VAL
26	24	58	ARG
26	24	59	PHE
26	24	63	TYR
27	25	6	VAL
27	25	58	LEU
27	25	59	GLU
28	26	5	VAL
28	26	9	LEU
28	26	14	THR
28	26	19	ARG
28	26	34	LEU
28	26	35	GLU
28	26	48	VAL
29	27	1	MET
29	27	4	THR
29	27	29	LYS
29	27	43	THR
30	28	14	VAL
30	28	23	VAL
30	28	41	ILE
31	29	7	VAL
33	2b	8	LYS
33	2b	9	GLU
33	2b	23	ARG
33	2b	44	LEU
33	2b	49	GLU
33	2b	63	MET
33	2b	67	THR
33	2b	71	VAL
33	2b	73	THR

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Mol	Chain	Res	Type
33	2b	76	GLN
33	2b	93	VAL
33	2b	94	ASN
33	2b	98	LEU
33	2b	107	THR
33	2b	112	VAL
33	2b	115	LEU
33	2b	140	HIS
33	2b	149	LEU
33	2b	150	SER
33	2b	164	VAL
33	2b	185	ILE
33	2b	204	ASN
33	2b	214	ILE
33	2b	224	GLN
33	2b	230	VAL
34	2c	38	ARG
34	2c	44	GLU
34	2c	46	GLU
34	2c	55	VAL
34	2c	57	ILE
34	2c	68	VAL
34	2c	91	LEU
34	2c	101	LEU
34	2c	103	VAL
34	2c	105	GLU
34	2c	115	LEU
34	2c	125	GLU
34	2c	128	PHE
34	2c	132	ARG
34	2c	138	VAL
34	2c	152	ILE
34	2c	190	ARG
34	2c	192	THR
34	2c	198	VAL
34	2c	206	GLU
35	2d	8	VAL
35	2d	17	VAL
35	2d	19	LEU
35	2d	47	ARG
35	2d	52	SER
35	2d	53	ASP

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Mol	Chain	Res	Type
35	2d	57	ARG
35	2d	58	LEU
35	2d	59	ARG
35	2d	77	ASN
35	2d	78	LEU
35	2d	86	LYS
35	2d	94	LEU
35	2d	96	LEU
35	2d	115	ARG
35	2d	120	LEU
35	2d	127	THR
35	2d	135	LEU
35	2d	148	VAL
35	2d	150	GLU
35	2d	157	LEU
35	2d	175	SER
35	2d	178	VAL
35	2d	188	LEU
35	2d	194	LEU
36	2e	5	ASP
36	2e	12	LEU
36	2e	13	ILE
36	2e	18	ARG
36	2e	34	VAL
36	2e	41	VAL
36	2e	55	VAL
36	2e	66	MET
36	2e	72	GLN
36	2e	75	THR
36	2e	90	VAL
36	2e	91	LEU
36	2e	135	THR
36	2e	151	LEU
37	2f	21	LEU
37	2f	31	GLU
37	2f	63	TYR
37	2f	64	GLN
37	2f	69	GLU
37	2f	92	LYS
37	2f	95	GLU
38	2g	6	ARG
38	2g	15	ASP

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Mol	Chain	Res	Type
38	2g	24	THR
38	2g	51	GLN
38	2g	75	VAL
38	2g	79	ARG
38	2g	85	TYR
38	2g	113	GLU
38	2g	114	ARG
38	2g	126	ASP
38	2g	129	GLU
38	2g	135	VAL
38	2g	139	GLU
38	2g	144	MET
38	2g	146	GLU
38	2g	153	HIS
38	2g	155	ARG
39	2h	26	VAL
39	2h	37	ARG
39	2h	39	LEU
39	2h	51	VAL
39	2h	103	VAL
39	2h	112	LEU
39	2h	115	SER
40	2i	27	THR
40	2i	29	ASN
40	2i	50	LEU
40	2i	54	ASP
40	2i	64	THR
40	2i	75	ASP
40	2i	89	ASN
40	2i	92	TYR
40	2i	99	LEU
40	2i	102	LEU
40	2i	128	ARG
41	2j	8	LEU
41	2j	21	GLN
41	2j	23	ILE
41	2j	38	ILE
41	2j	45	ARG
41	2j	67	THR
41	2j	72	VAL
41	2j	74	ILE
41	2j	89	ASP

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Mol	Chain	Res	Type
41	2j	95	GLU
41	2j	97	GLU
41	2j	98	ILE
41	2j	100	THR
42	2k	14	VAL
42	2k	29	ILE
42	2k	48	ILE
42	2k	63	LEU
42	2k	87	THR
42	2k	112	THR
42	2k	114	VAL
43	2l	33	ARG
43	2l	55	VAL
43	2l	57	LYS
43	2l	67	THR
43	2l	79	GLU
43	2l	83	VAL
43	2l	97	ARG
43	2l	102	ARG
43	2l	123	LYS
44	2m	15	VAL
44	2m	19	LEU
44	2m	22	ILE
44	2m	37	THR
44	2m	39	ILE
44	2m	47	ASP
44	2m	53	VAL
44	2m	80	ARG
44	2m	92	HIS
44	2m	102	ARG
44	2m	103	THR
44	2m	106	ASN
44	2m	109	THR
44	2m	116	THR
45	2n	3	ARG
45	2n	6	LEU
45	2n	18	VAL
45	2n	33	VAL
45	2n	42	ILE
46	2o	3	ILE
46	2o	5	LYS
46	2o	7	GLU

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Mol	Chain	Res	Type
46	2o	26	GLU
46	2o	39	LEU
46	2o	84	LYS
47	2p	2	VAL
47	2p	5	ARG
47	2p	20	VAL
47	2p	21	VAL
47	2p	60	LEU
47	2p	67	THR
47	2p	69	THR
47	2p	73	LEU
47	2p	74	LEU
48	2q	43	LEU
48	2q	60	ILE
48	2q	63	ARG
48	2q	70	ARG
48	2q	76	LEU
48	2q	77	VAL
48	2q	87	LYS
48	2q	99	SER
49	2r	25	THR
49	2r	31	LEU
49	2r	35	ARG
49	2r	37	VAL
49	2r	44	LEU
49	2r	45	SER
49	2r	46	GLU
49	2r	76	LEU
49	2r	82	THR
50	2s	15	LEU
50	2s	27	GLU
50	2s	37	ARG
50	2s	41	VAL
50	2s	45	VAL
50	2s	49	ILE
50	2s	56	GLN
50	2s	63	THR
50	2s	83	HIS
51	2t	46	GLU
51	2t	70	SER
51	2t	71	THR
51	2t	89	ARG

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Mol	Chain	Res	Type
52	2u	9	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (126) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	87	ASN
3	1D	116	GLN
3	1D	126	GLN
3	1D	201	HIS
4	1E	48	GLN
4	1E	121	ASN
5	1F	69	HIS
5	1F	133	ASN
6	1G	26	GLN
6	1G	108	ASN
9	1N	8	GLN
9	1N	94	HIS
12	1Q	123	HIS
13	1R	31	HIS
13	1R	71	GLN
14	1S	95	HIS
16	1U	94	ASN
19	1X	31	HIS
19	1X	82	GLN
21	1Z	54	HIS
21	1Z	65	GLN
21	1Z	73	GLN
21	1Z	151	HIS
23	11	56	GLN
25	13	32	GLN
28	16	20	ASN
30	18	35	GLN
33	1b	16	HIS
33	1b	40	HIS
33	1b	94	ASN
34	1c	6	HIS
34	1c	69	HIS
35	1d	42	GLN
35	1d	45	GLN
35	1d	116	GLN
35	1d	123	HIS
35	1d	125	HIS

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Mol	Chain	Res	Type
35	1d	161	ASN
36	1e	78	HIS
37	1f	57	GLN
37	1f	73	ASN
37	1f	100	ASN
38	1g	13	GLN
38	1g	28	ASN
38	1g	148	ASN
40	1i	3	GLN
40	1i	31	GLN
40	1i	34	ASN
40	1i	73	GLN
40	1i	89	ASN
40	1i	124	GLN
43	1l	99	HIS
44	1m	77	ASN
44	1m	92	HIS
46	1o	9	GLN
47	1p	13	HIS
47	1p	76	GLN
50	1s	57	HIS
50	1s	83	HIS
51	1t	16	HIS
51	1t	73	HIS
51	1t	75	ASN
51	1t	90	GLN
3	2D	87	ASN
3	2D	166	GLN
4	2E	48	GLN
4	2E	55	ASN
5	2F	31	HIS
6	2G	58	GLN
7	2H	139	GLN
8	2I	139	GLN
12	2Q	123	HIS
13	2R	50	HIS
14	2S	38	GLN
14	2S	68	GLN
15	2T	58	ASN
16	2U	94	ASN
18	2W	62	HIS
19	2X	31	HIS

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Mol	Chain	Res	Type
19	2X	82	GLN
21	2Z	32	HIS
21	2Z	55	HIS
21	2Z	73	GLN
21	2Z	75	ASN
22	20	35	ASN
23	21	56	GLN
24	22	56	GLN
26	24	46	GLN
30	28	43	GLN
33	2b	25	ASN
33	2b	76	GLN
33	2b	94	ASN
33	2b	135	GLN
34	2c	98	ASN
34	2c	181	ASN
35	2d	45	GLN
35	2d	74	GLN
35	2d	77	ASN
35	2d	116	GLN
35	2d	119	GLN
36	2e	72	GLN
36	2e	141	GLN
37	2f	64	GLN
37	2f	73	ASN
38	2g	28	ASN
38	2g	86	GLN
38	2g	96	GLN
38	2g	148	ASN
40	2i	3	GLN
40	2i	38	GLN
40	2i	58	HIS
40	2i	117	HIS
41	2j	13	HIS
41	2j	62	HIS
42	2k	104	GLN
42	2k	117	ASN
44	2m	40	ASN
45	2n	49	HIS
47	2p	13	HIS
47	2p	16	HIS
49	2r	63	GLN

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Mol	Chain	Res	Type
50	2s	47	HIS
50	2s	69	HIS
50	2s	83	HIS
51	2t	16	HIS
51	2t	90	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2864/2915 (98%)	421 (14%)	30 (1%)
1	2A	2791/2915 (95%)	433 (15%)	23 (0%)
2	1B	119/121 (98%)	8 (6%)	0
2	2B	118/121 (97%)	27 (22%)	0
32	1a	1497/1521 (98%)	263 (17%)	0
32	2a	1501/1521 (98%)	279 (18%)	0
53	1v	4/21 (19%)	0	0
53	2v	4/21 (19%)	1 (25%)	0
54	1x	75/77 (97%)	6 (8%)	0
54	2x	75/77 (97%)	9 (12%)	0
All	All	9048/9310 (97%)	1447 (15%)	53 (0%)

All (1447) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	84	A
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	139(A)	G
1	1A	182	A
1	1A	196	A
1	1A	199	A
1	1A	205	G
1	1A	214	G

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Mol	Chain	Res	Type
1	1A	215	G
1	1A	216	A
1	1A	221	A
1	1A	222	A
1	1A	225	A
1	1A	228	A
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	269	U
1	1A	271(C)	C
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(O)	C
1	1A	272(B)	G
1	1A	272(I)	U
1	1A	279	C
1	1A	311	A
1	1A	329	G
1	1A	330	A
1	1A	342	G
1	1A	352	G
1	1A	357	A
1	1A	363	G
1	1A	363(B)	G
1	1A	380	U
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	428	A
1	1A	444	C
1	1A	448	U
1	1A	454	A
1	1A	481	G
1	1A	504	U
1	1A	505	A
1	1A	508	G
1	1A	509	C
1	1A	513	A

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Mol	Chain	Res	Type
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	574	C
1	1A	575	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(D)	C
1	1A	652(E)	G
1	1A	652(F)	G
1	1A	652(T)	C
1	1A	668	G
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	764	A
1	1A	774	A
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U

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Mol	Chain	Res	Type
1	1A	830	G
1	1A	859	G
1	1A	866	A
1	1A	879	G
1	1A	880	G
1	1A	882	G
1	1A	883	G
1	1A	884	C
1	1A	885	C
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	890	A
1	1A	895	U
1	1A	896	A
1	1A	897	C
1	1A	900	A
1	1A	907	U
1	1A	910	A
1	1A	915	C
1	1A	931	G
1	1A	932	G
1	1A	938	G
1	1A	945	A
1	1A	946	G
1	1A	958	U
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1008	C
1	1A	1012	U
1	1A	1013	C
1	1A	1022	G
1	1A	1026	U
1	1A	1033	U
1	1A	1038	C
1	1A	1041	C
1	1A	1045	A
1	1A	1046	A

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Mol	Chain	Res	Type
1	1A	1047	G
1	1A	1054	A
1	1A	1055	G
1	1A	1058	G
1	1A	1059	G
1	1A	1063	G
1	1A	1069	A
1	1A	1071	G
1	1A	1073	A
1	1A	1075	C
1	1A	1076	C
1	1A	1078	U
1	1A	1079	C
1	1A	1081	U
1	1A	1083	U
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1091	G
1	1A	1093	G
1	1A	1094	U
1	1A	1096	A
1	1A	1098	A
1	1A	1101	U
1	1A	1110	G
1	1A	1112	G
1	1A	1116	C
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1149	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1220	A
1	1A	1248	G
1	1A	1253	A
1	1A	1256	G

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Mol	Chain	Res	Type
1	1A	1271	G
1	1A	1272	A
1	1A	1273	U
1	1A	1281	G
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1352	U
1	1A	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1386	C
1	1A	1396	U
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1455	G
1	1A	1461	G
1	1A	1467	C
1	1A	1482	G
1	1A	1493	C
1	1A	1505	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1532	C
1	1A	1540	U
1	1A	1543	C
1	1A	1554	A
1	1A	1558	A
1	1A	1560	G
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1580	A

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Mol	Chain	Res	Type
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1648	C
1	1A	1654	A
1	1A	1674	G
1	1A	1700	A
1	1A	1701	A
1	1A	1703	G
1	1A	1722	A
1	1A	1739	U
1	1A	1746	G
1	1A	1756	G
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1816	G
1	1A	1829	A
1	1A	1839	G
1	1A	1847	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1914	C
1	1A	1919	A
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A

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Mol	Chain	Res	Type
1	1A	1972	A
1	1A	1984	G
1	1A	1992	G
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2039	C
1	1A	2043	C
1	1A	2049	G
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2063	C
1	1A	2069	G
1	1A	2108	C
1	1A	2112	G
1	1A	2113	U
1	1A	2114	A
1	1A	2116	G
1	1A	2121	G
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2136	C
1	1A	2137	C
1	1A	2138	C
1	1A	2142	C
1	1A	2144	U
1	1A	2146	C
1	1A	2149	G
1	1A	2150	U
1	1A	2151	G
1	1A	2155	G

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Mol	Chain	Res	Type
1	1A	2156	G
1	1A	2157	G
1	1A	2158	A
1	1A	2159	G
1	1A	2162	G
1	1A	2165	G
1	1A	2166	G
1	1A	2171	A
1	1A	2172	U
1	1A	2173	A
1	1A	2174	C
1	1A	2181	G
1	1A	2182	G
1	1A	2183	C
1	1A	2189	U
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2219	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2273	A
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2294	C
1	1A	2305	A
1	1A	2308	G
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2372	G
1	1A	2383	G
1	1A	2385	C
1	1A	2396	G
1	1A	2405	G

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Mol	Chain	Res	Type
1	1A	2406	U
1	1A	2407	G
1	1A	2410	G
1	1A	2422	A
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U
1	1A	2432	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2471	C
1	1A	2476	A
1	1A	2477	C
1	1A	2502	G
1	1A	2505	G
1	1A	2518	A
1	1A	2525	G
1	1A	2529	G
1	1A	2535	G
1	1A	2549	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2569	G
1	1A	2582	G
1	1A	2602	A
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2613	U
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A

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Mol	Chain	Res	Type
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2755	C
1	1A	2757	A
1	1A	2758	A
1	1A	2761	G
1	1A	2764	A
1	1A	2765	A
1	1A	2766	G
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2792	G
1	1A	2802	G
1	1A	2803	C
1	1A	2805	G
1	1A	2820	A
1	1A	2821	A
1	1A	2835	A
1	1A	2872	G
1	1A	2880	C
1	1A	2894	G
1	1A	2895	U
1	1A	2897	U
2	1B	2	C
2	1B	13	A
2	1B	25	A
2	1B	56	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	22	G
32	1a	32	A
32	1a	39	G
32	1a	40	C
32	1a	42	G
32	1a	48	C

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Mol	Chain	Res	Type
32	1a	50	A
32	1a	51	A
32	1a	61	G
32	1a	66	G
32	1a	79	G
32	1a	91	C
32	1a	98	G
32	1a	101	A
32	1a	105	G
32	1a	116	A
32	1a	120	A
32	1a	121	C
32	1a	131	C
32	1a	145	G
32	1a	162	A
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	184	G
32	1a	189(B)	C
32	1a	189(D)	C
32	1a	189(H)	G
32	1a	189(J)	G
32	1a	195	A
32	1a	197	A
32	1a	199	G
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	280	C
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	344	A
32	1a	348	G

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Mol	Chain	Res	Type
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	355	C
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	439	A
32	1a	441	A
32	1a	442	C
32	1a	452	A
32	1a	457	C
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	471	G
32	1a	476	G
32	1a	485	G
32	1a	492	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	520	A
32	1a	528	C
32	1a	531	U
32	1a	532	A
32	1a	534	U

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Mol	Chain	Res	Type
32	1a	536	C
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	562	C
32	1a	564	C
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	630	G
32	1a	631	G
32	1a	639	G
32	1a	640	A
32	1a	653	A
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	693	G
32	1a	695	A
32	1a	717	C
32	1a	722	A
32	1a	723	U
32	1a	724	G
32	1a	731	G
32	1a	749	C
32	1a	752	G
32	1a	755	G
32	1a	760	G
32	1a	766	A
32	1a	770	C
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G
32	1a	827	U
32	1a	828	A
32	1a	840	C
32	1a	841	U

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Mol	Chain	Res	Type
32	1a	851	G
32	1a	864	A
32	1a	872	A
32	1a	874	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	935	A
32	1a	936	C
32	1a	942	G
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	972	C
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	982	U
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1011	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	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G

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Mol	Chain	Res	Type
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1039	C
32	1a	1043	C
32	1a	1044	A
32	1a	1045	C
32	1a	1051	C
32	1a	1052	U
32	1a	1054	C
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G
32	1a	1121	U
32	1a	1123	A
32	1a	1124	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	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1176	A
32	1a	1183	A
32	1a	1184	G
32	1a	1193	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1213	A
32	1a	1214	C
32	1a	1227	A
32	1a	1236	A
32	1a	1238	A
32	1a	1246	C

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Mol	Chain	Res	Type
32	1a	1253	G
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C
32	1a	1275	A
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	1305	G
32	1a	1312	G
32	1a	1323	G
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1363(A)	A
32	1a	1364	U
32	1a	1370	G
32	1a	1394	A
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1469	G
32	1a	1487	G
32	1a	1492	A
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U

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Mol	Chain	Res	Type
32	1a	1517	G
32	1a	1529	G
32	1a	1530	G
54	1x	9	G
54	1x	13	C
54	1x	14	A
54	1x	21	A
54	1x	47	U
54	1x	76	A
1	2A	8	A
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
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	118	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	154(A)	C
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	197	A
1	2A	199	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	230	U

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Mol	Chain	Res	Type
1	2A	232	G
1	2A	233	A
1	2A	248	G
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	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	283	A
1	2A	311	A
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	348	G
1	2A	352	G
1	2A	363	G
1	2A	386	G
1	2A	396	G
1	2A	403	U
1	2A	405	U
1	2A	411	G
1	2A	412	A
1	2A	444	C
1	2A	455	C
1	2A	456	C
1	2A	457	A
1	2A	481	G
1	2A	503	A
1	2A	504	U
1	2A	505	A
1	2A	509	C
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G

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Mol	Chain	Res	Type
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	588	U
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(A)	U
1	2A	614(B)	G
1	2A	614(C)	A
1	2A	615	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	664	C
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	726	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	764	A
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	790	C
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	832	G
1	2A	857	C
1	2A	859	G
1	2A	866	A
1	2A	874	G

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Mol	Chain	Res	Type
1	2A	878	A
1	2A	879	G
1	2A	880	G
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	892	G
1	2A	893	C
1	2A	894	C
1	2A	896	A
1	2A	897	C
1	2A	900	A
1	2A	901	A
1	2A	903	C
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	933	A
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	999	U
1	2A	1012	U
1	2A	1013	C
1	2A	1017	G
1	2A	1020	A
1	2A	1022	G
1	2A	1025	G
1	2A	1027	A
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G

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Mol	Chain	Res	Type
1	2A	1041	C
1	2A	1043	C
1	2A	1116	C
1	2A	1126	A
1	2A	1128	A
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	1144	G
1	2A	1171	G
1	2A	1188	U
1	2A	1195	G
1	2A	1205	U
1	2A	1210	A
1	2A	1211	U
1	2A	1212	G
1	2A	1220	A
1	2A	1244	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A
1	2A	1300	U
1	2A	1301	A
1	2A	1314	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1380	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C

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Mol	Chain	Res	Type
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1531	C
1	2A	1532	C
1	2A	1533	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	1584	C
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1616	A
1	2A	1640	C
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1721	G
1	2A	1722	A

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Mol	Chain	Res	Type
1	2A	1739	U
1	2A	1740	G
1	2A	1746	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1812	A
1	2A	1816	G
1	2A	1829	A
1	2A	1835	G
1	2A	1847	A
1	2A	1848	A
1	2A	1861	G
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1915	5MU
1	2A	1929	G
1	2A	1930	G
1	2A	1936	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	1984	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A

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Mol	Chain	Res	Type
1	2A	2033	A
1	2A	2036	C
1	2A	2043	C
1	2A	2049	G
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	2099	U
1	2A	2107	C
1	2A	2110	G
1	2A	2111	C
1	2A	2116	G
1	2A	2117	A
1	2A	2120	G
1	2A	2122	U
1	2A	2124	G
1	2A	2125	G
1	2A	2126	A
1	2A	2127	G
1	2A	2128	C
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2137	C
1	2A	2138	C
1	2A	2139	C
1	2A	2140	C
1	2A	2142	C
1	2A	2145	C
1	2A	2146	C
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A

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Mol	Chain	Res	Type
1	2A	2162	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2172	U
1	2A	2174	C
1	2A	2176	A
1	2A	2177	C
1	2A	2178	C
1	2A	2182	G
1	2A	2185	C
1	2A	2188	C
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2275	C
1	2A	2278	A
1	2A	2283	C
1	2A	2287	A
1	2A	2305	A
1	2A	2308	G
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2346	A
1	2A	2347	C
1	2A	2350	C
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2388	A
1	2A	2402	C

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Mol	Chain	Res	Type
1	2A	2403	C
1	2A	2406	U
1	2A	2419	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2448	A
1	2A	2465	C
1	2A	2469	A
1	2A	2474	C
1	2A	2476	A
1	2A	2477	C
1	2A	2480	C
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	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2585	U
1	2A	2602	A
1	2A	2609	U
1	2A	2610	C
1	2A	2611	U
1	2A	2612	C
1	2A	2630	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

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Mol	Chain	Res	Type
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2751	G
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2793	G
1	2A	2794	C
1	2A	2802	G
1	2A	2803	C
1	2A	2808	U
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2872	G
1	2A	2892	A
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	3	C
2	2B	8	U
2	2B	13	A
2	2B	17	C
2	2B	30	C
2	2B	34	U
2	2B	35	U
2	2B	41	U
2	2B	42	C
2	2B	51	G
2	2B	52	A
2	2B	53	A
2	2B	56	G
2	2B	63	G
2	2B	67	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G

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Mol	Chain	Res	Type
2	2B	88	C
2	2B	89	G
2	2B	106	G
2	2B	109	C
2	2B	110	G
2	2B	111	G
2	2B	120	A
32	2a	6	G
32	2a	7	G
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A
32	2a	65	U
32	2a	66	G
32	2a	73	G
32	2a	80	G
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	129(A)	G
32	2a	131	C
32	2a	144	G
32	2a	159	G
32	2a	162	A
32	2a	163	C
32	2a	182	U
32	2a	189(A)	C
32	2a	189(E)	U
32	2a	189(F)	U
32	2a	195	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	217	C
32	2a	231	G

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Mol	Chain	Res	Type
32	2a	247	G
32	2a	251	G
32	2a	252	U
32	2a	266	G
32	2a	267	C
32	2a	281	G
32	2a	289	G
32	2a	306	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	349	A
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	373	A
32	2a	384	G
32	2a	388	G
32	2a	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	421	U
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	451	A
32	2a	452	A
32	2a	457	C
32	2a	470	C
32	2a	471	G
32	2a	483	C
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U

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Mol	Chain	Res	Type
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	531	U
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	553	A
32	2a	559	A
32	2a	560	U
32	2a	562	C
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	596	C
32	2a	618	C
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	723	U
32	2a	731	G
32	2a	742	G
32	2a	748	C
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	759	A
32	2a	763	G
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	807	A
32	2a	816	A
32	2a	817	C
32	2a	821	G

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Mol	Chain	Res	Type
32	2a	828	A
32	2a	834	C
32	2a	840	C
32	2a	841	U
32	2a	853	G
32	2a	855	G
32	2a	859	A
32	2a	902	G
32	2a	914	A
32	2a	915	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	935	A
32	2a	942	G
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	995	C
32	2a	997	U
32	2a	999	C
32	2a	1001	A
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	1010	G
32	2a	1011	G

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Mol	Chain	Res	Type
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1030(A)	G
32	2a	1030(D)	A
32	2a	1031	G
32	2a	1032	G
32	2a	1035	A
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1053	G
32	2a	1054	C
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1070	U
32	2a	1077	G
32	2a	1079	G
32	2a	1081	G
32	2a	1085	U
32	2a	1086	U
32	2a	1092	A
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1108	G
32	2a	1109	C
32	2a	1113	C
32	2a	1122	U
32	2a	1124	G
32	2a	1129	C
32	2a	1130	A
32	2a	1133	G
32	2a	1135	U
32	2a	1136	U

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Mol	Chain	Res	Type
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1146	A
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1158	C
32	2a	1159	U
32	2a	1171	G
32	2a	1172	C
32	2a	1181	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1189	C
32	2a	1196	U
32	2a	1197	G
32	2a	1201	A
32	2a	1202	G
32	2a	1211	U
32	2a	1213	A
32	2a	1227	A
32	2a	1236	A
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1267	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1286	A
32	2a	1287	A
32	2a	1290	G
32	2a	1299	A
32	2a	1302	U

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Mol	Chain	Res	Type
32	2a	1303	C
32	2a	1306	A
32	2a	1320	C
32	2a	1323	G
32	2a	1338	G
32	2a	1346	A
32	2a	1347	G
32	2a	1352	C
32	2a	1358	U
32	2a	1363	C
32	2a	1364	U
32	2a	1370	G
32	2a	1378	C
32	2a	1397	C
32	2a	1398	A
32	2a	1402	4OC
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1507	A
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	15	A
54	2x	9	G
54	2x	13	C
54	2x	18	G
54	2x	19	G
54	2x	20	U
54	2x	21	A
54	2x	47	U

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Mol	Chain	Res	Type
54	2x	48	C
54	2x	76	A

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	90	U
1	1A	195	A
1	1A	196	A
1	1A	266	G
1	1A	278	A
1	1A	529	A
1	1A	548	A
1	1A	746	A
1	1A	764	A
1	1A	774	A
1	1A	827	U
1	1A	958	U
1	1A	974	G
1	1A	1067	A
1	1A	1174	A
1	1A	1176	G
1	1A	1379	A
1	1A	1442	G
1	1A	1508	A
1	1A	1608	A
1	1A	1992	G
1	1A	2062	A
1	1A	2126	A
1	1A	2134	A
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2439	A
1	1A	2689	U
1	1A	2756	U
1	2A	196	A
1	2A	228	A
1	2A	266	G
1	2A	271(K)	U
1	2A	271(M)	G
1	2A	277	C

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Mol	Chain	Res	Type
1	2A	528	A
1	2A	752	A
1	2A	856	C
1	2A	896	A
1	2A	900	A
1	2A	974	G
1	2A	1026	U
1	2A	1210	A
1	2A	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1653	G
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 (i)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
32	UR3	1a	1498	32	19,22,23	1.09	2 (10%)	26,32,35	1.81	5 (19%)
32	M2G	1a	966	32	24,27,28	1.31	4 (16%)	33,40,43	1.84	6 (18%)
32	2MG	1a	1207	32	23,26,27	1.24	3 (13%)	33,38,41	2.22	7 (21%)
43	0TD	1l	92	43	8,9,10	4.42	2 (25%)	6,11,13	10.13	3 (50%)
32	5MC	1a	967	32	19,22,23	1.44	3 (15%)	26,32,35	1.06	2 (7%)
1	2MA	2A	2503	55,1	22,25,26	1.47	5 (22%)	32,37,40	2.28	9 (28%)
1	PSU	2A	1911	1	18,21,22	1.45	2 (11%)	21,30,33	1.89	4 (19%)
32	5MC	2a	1404	32	19,22,23	1.50	2 (10%)	26,32,35	1.09	2 (7%)
1	5MU	1A	1939	55,1	19,22,23	1.47	4 (21%)	27,32,35	2.22	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
32	MA6	2a	1518	32	23,26,27	0.39	0	33,38,41	2.03	9 (27%)
54	4SU	2x	8	54	18,21,22	1.97	5 (27%)	25,30,33	1.44	3 (12%)
32	PSU	2a	516	32	18,21,22	1.32	2 (11%)	21,30,33	1.94	5 (23%)
54	5MU	2x	54	54	19,22,23	1.43	5 (26%)	27,32,35	1.90	6 (22%)
32	4OC	1a	1402	32	20,23,24	0.72	0	25,32,35	1.03	3 (12%)
1	PSU	2A	1917	1	18,21,22	1.42	2 (11%)	21,30,33	2.12	4 (19%)
1	5MU	2A	1939	1	19,22,23	1.48	5 (26%)	27,32,35	2.20	6 (22%)
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	1.06	0
1	5MC	2A	1962	55,1	19,22,23	1.66	3 (15%)	26,32,35	1.16	2 (7%)
43	0TD	2l	92	43	8,9,10	4.61	1 (12%)	6,11,13	2.32	3 (50%)
1	OMG	1A	2251	55,1,54	23,26,27	1.21	3 (13%)	32,38,41	1.92	7 (21%)
32	5MC	2a	1400	32	19,22,23	1.60	3 (15%)	26,32,35	1.15	2 (7%)
32	5MC	2a	1407	32	19,22,23	1.52	3 (15%)	26,32,35	1.18	3 (11%)
1	OMU	2A	2552	55,1	19,22,23	1.24	3 (15%)	25,31,34	1.98	6 (24%)
1	OMG	2A	2251	1,54	23,26,27	1.17	3 (13%)	32,38,41	1.94	6 (18%)
32	MA6	2a	1519	32	23,26,27	0.42	0	33,38,41	2.15	10 (30%)
1	OMU	1A	2552	55,1	19,22,23	1.19	2 (10%)	25,31,34	1.93	6 (24%)
54	5MC	2x	32	54	19,22,23	1.63	3 (15%)	26,32,35	1.27	3 (11%)
1	2MA	1A	2503	55,1	22,25,26	1.48	5 (22%)	32,37,40	2.21	9 (28%)
32	UR3	2a	1498	32	19,22,23	1.02	2 (10%)	26,32,35	1.69	3 (11%)
32	5MC	1a	1404	32	19,22,23	1.74	3 (15%)	26,32,35	1.13	3 (11%)
1	OMC	2A	1920	1	19,22,23	0.76	0	25,31,34	0.94	0
32	MA6	1a	1518	32	23,26,27	0.40	0	33,38,41	2.05	10 (30%)
1	PSU	2A	2605	1	18,21,22	1.34	2 (11%)	21,30,33	2.01	4 (19%)
54	4SU	1x	8	54	18,21,22	2.10	6 (33%)	25,30,33	1.43	5 (20%)
54	PSU	2x	55	54	18,21,22	1.37	2 (11%)	21,30,33	2.00	4 (19%)
32	PSU	1a	516	32	18,21,22	1.39	2 (11%)	21,30,33	1.94	3 (14%)
32	G7M	2a	527	55,32	23,26,27	1.52	3 (13%)	34,39,42	1.72	5 (14%)
1	OMC	1A	1920	1	19,22,23	0.78	0	25,31,34	0.99	1 (4%)
1	PSU	1A	1917	1	18,21,22	1.44	3 (16%)	21,30,33	2.06	4 (19%)
54	5MC	1x	32	54	19,22,23	1.70	3 (15%)	26,32,35	1.40	4 (15%)
1	PSU	1A	1911	1	18,21,22	1.32	2 (11%)	21,30,33	2.04	3 (14%)
32	5MC	1a	1400	32	19,22,23	1.69	3 (15%)	26,32,35	1.25	4 (15%)
32	5MC	1a	1407	32	19,22,23	1.57	3 (15%)	26,32,35	1.18	4 (15%)
1	5MU	2A	1915	1,57	19,22,23	1.52	5 (26%)	27,32,35	2.10	6 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	5MC	2A	1942	1	19,22,23	1.61	3 (15%)	26,32,35	1.12	2 (7%)
32	G7M	1a	527	55,32	23,26,27	1.52	3 (13%)	34,39,42	1.77	5 (14%)
32	MA6	1a	1519	32	23,26,27	0.46	0	33,38,41	2.07	8 (24%)
54	PSU	1x	55	54	18,21,22	1.38	2 (11%)	21,30,33	2.02	4 (19%)
32	5MC	2a	967	32	19,22,23	1.67	3 (15%)	26,32,35	1.13	2 (7%)
1	5MU	1A	1915	1,57	19,22,23	1.49	5 (26%)	27,32,35	2.25	6 (22%)
1	5MC	1A	1942	55,1	19,22,23	1.45	3 (15%)	26,32,35	1.17	2 (7%)
32	2MG	2a	1207	32	23,26,27	1.26	3 (13%)	33,38,41	2.09	7 (21%)
32	M2G	2a	966	32	24,27,28	1.36	4 (16%)	33,40,43	1.98	5 (15%)
54	5MU	1x	54	54	19,22,23	1.46	5 (26%)	27,32,35	1.70	5 (18%)
1	PSU	1A	2605	55,1	18,21,22	1.43	3 (16%)	21,30,33	2.01	5 (23%)
1	5MC	1A	1962	55,1	19,22,23	1.76	3 (15%)	26,32,35	1.13	3 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
43	0TD	1l	92	43	-	3/7/12/14	-
32	5MC	1a	967	32	-	1/7/25/26	0/2/2/2
1	2MA	2A	2503	55,1	-	0/7/25/26	0/3/3/3
1	PSU	2A	1911	1	-	2/7/25/26	0/2/2/2
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	5MU	1A	1939	55,1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
54	4SU	2x	8	54	-	0/7/25/26	0/2/2/2
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
54	5MU	2x	54	54	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	1/9/29/30	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	5MU	2A	1939	1	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	3/9/29/30	0/2/2/2
1	5MC	2A	1962	55,1	-	0/7/25/26	0/2/2/2
43	0TD	2l	92	43	-	1/7/12/14	-
1	OMG	1A	2251	55,1,54	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	55,1	-	0/9/27/28	0/2/2/2
1	OMG	2A	2251	1,54	-	0/9/27/28	0/3/3/3
32	MA6	2a	1519	32	-	3/11/29/30	0/3/3/3
1	OMU	1A	2552	55,1	-	0/9/27/28	0/2/2/2
54	5MC	2x	32	54	-	1/7/25/26	0/2/2/2
1	2MA	1A	2503	55,1	-	0/7/25/26	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	1/9/27/28	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
54	4SU	1x	8	54	-	1/7/25/26	0/2/2/2
54	PSU	2x	55	54	-	0/7/25/26	0/2/2/2
32	PSU	1a	516	32	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	55,32	-	2/7/25/26	0/3/3/3
1	OMC	1A	1920	1	-	1/9/27/28	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
54	5MC	1x	32	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	5MU	2A	1915	1,57	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	G7M	1a	527	55,32	-	2/7/25/26	0/3/3/3
32	MA6	1a	1519	32	-	3/11/29/30	0/3/3/3
54	PSU	1x	55	54	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	1/7/25/26	0/2/2/2
1	5MU	1A	1915	1,57	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	55,1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
54	5MU	1x	54	54	-	0/7/25/26	0/2/2/2
1	PSU	1A	2605	55,1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	55,1	-	2/7/25/26	0/2/2/2

All (151) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.71	1.69	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-11.92	1.70	1.82
1	1A	1962	5MC	C5-C4	6.64	1.49	1.44
32	1a	1404	5MC	C5-C4	6.20	1.48	1.44
32	2a	967	5MC	C5-C4	6.15	1.48	1.44
32	1a	1400	5MC	C5-C4	6.12	1.48	1.44
54	1x	32	5MC	C5-C4	5.98	1.48	1.44
1	2A	1962	5MC	C5-C4	5.98	1.48	1.44
1	2A	1942	5MC	C5-C4	5.81	1.48	1.44
32	1a	1407	5MC	C5-C4	5.78	1.48	1.44
32	2a	1400	5MC	C5-C4	5.78	1.48	1.44
54	2x	32	5MC	C5-C4	5.66	1.48	1.44
32	2a	1404	5MC	C5-C4	5.35	1.48	1.44
32	2a	1407	5MC	C5-C4	5.24	1.48	1.44
54	1x	8	4SU	C4-N3	-4.96	1.32	1.37
32	1a	967	5MC	C5-C4	4.92	1.47	1.44
1	1A	1942	5MC	C5-C4	4.90	1.47	1.44
32	1a	527	G7M	C5-N7	-4.58	1.33	1.39
32	2a	527	G7M	C5-N7	-4.52	1.34	1.39
54	2x	8	4SU	C4-N3	-4.45	1.33	1.37
1	1A	2503	2MA	C5-C4	4.39	1.46	1.39
54	2x	8	4SU	C4-S4	-4.37	1.61	1.68
1	2A	2503	2MA	C5-C4	4.36	1.46	1.39
54	1x	8	4SU	C4-S4	-4.05	1.61	1.68
54	1x	8	4SU	C2-N3	-3.95	1.31	1.38
1	2A	2605	PSU	C6-C5	3.67	1.39	1.35
54	2x	55	PSU	C6-C5	3.65	1.39	1.35
54	1x	55	PSU	C6-C5	3.64	1.39	1.35
1	2A	1911	PSU	C6-C5	3.56	1.39	1.35
1	2A	1917	PSU	C6-C5	3.56	1.39	1.35
32	1a	516	PSU	C6-C5	3.49	1.39	1.35
1	1A	1939	5MU	C4-N3	-3.49	1.32	1.38
1	1A	1917	PSU	C6-C5	3.48	1.39	1.35
32	2a	966	M2G	C5-C4	3.45	1.48	1.38
32	1a	527	G7M	C5-C4	3.43	1.46	1.38
1	2A	1915	5MU	C6-C5	3.42	1.40	1.34
32	2a	527	G7M	C5-C4	3.39	1.46	1.38
32	2a	1207	2MG	C5-C4	3.27	1.47	1.38
54	1x	32	5MC	C6-C5	3.24	1.39	1.34
54	1x	8	4SU	C5-C4	-3.23	1.38	1.42
1	1A	1911	PSU	C6-C5	3.20	1.38	1.35
32	2a	516	PSU	C6-C5	3.17	1.38	1.35
1	1A	1915	5MU	C6-C5	3.15	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1404	5MC	C6-C5	3.14	1.39	1.34
32	1a	966	M2G	C5-C4	3.11	1.47	1.38
1	1A	2251	OMG	C5-C4	3.09	1.47	1.38
54	2x	8	4SU	C5-C4	-3.05	1.38	1.42
1	1A	2605	PSU	C4-N3	-3.04	1.33	1.38
1	2A	2251	OMG	C5-C4	3.04	1.47	1.38
54	1x	54	5MU	C6-C5	3.03	1.39	1.34
54	1x	54	5MU	C4-N3	-2.98	1.33	1.38
1	1A	1939	5MU	C2-N3	-2.98	1.32	1.38
32	1a	1207	2MG	C5-C4	2.97	1.46	1.38
54	2x	54	5MU	C6-C5	2.96	1.39	1.34
1	1A	1917	PSU	C4-N3	-2.93	1.33	1.38
54	2x	32	5MC	C6-C5	2.92	1.39	1.34
1	2A	1939	5MU	C4-N3	-2.90	1.33	1.38
32	2a	966	M2G	C2-N2	2.89	1.40	1.35
32	1a	966	M2G	C2-N2	2.87	1.40	1.35
1	2A	1915	5MU	C4-N3	-2.85	1.33	1.38
1	2A	1911	PSU	C4-N3	-2.85	1.33	1.38
1	2A	1939	5MU	C6-C5	2.85	1.39	1.34
1	1A	2552	OMU	C4-N3	-2.83	1.33	1.38
1	2A	1962	5MC	C6-C5	2.82	1.39	1.34
54	2x	54	5MU	C4-N3	-2.79	1.33	1.38
32	2a	1404	5MC	C6-C5	2.77	1.39	1.34
1	1A	1939	5MU	C6-C5	2.77	1.39	1.34
1	2A	2552	OMU	C4-N3	-2.76	1.33	1.38
1	2A	1942	5MC	C6-C5	2.74	1.39	1.34
1	1A	1915	5MU	C2-N1	2.72	1.42	1.38
32	2a	1400	5MC	C6-C5	2.71	1.39	1.34
1	1A	2605	PSU	C6-C5	2.70	1.38	1.35
54	2x	8	4SU	C2-N3	-2.69	1.33	1.38
1	1A	1962	5MC	C6-C5	2.69	1.39	1.34
1	2A	1939	5MU	C6-N1	-2.68	1.33	1.38
1	1A	1942	5MC	C6-C5	2.68	1.39	1.34
32	2a	967	5MC	C6-C5	2.67	1.39	1.34
32	1a	1400	5MC	C6-C5	2.67	1.39	1.34
1	1A	2251	OMG	C6-N1	-2.66	1.33	1.38
1	1A	1915	5MU	C4-C5	2.65	1.49	1.44
32	2a	1407	5MC	C6-C5	2.64	1.38	1.34
32	1a	967	5MC	C6-C5	2.63	1.38	1.34
1	1A	2552	OMU	C2-N3	-2.62	1.33	1.38
1	1A	2503	2MA	C5-C6	2.62	1.48	1.41
1	2A	1915	5MU	C4-C5	2.60	1.49	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	966	M2G	C6-N1	-2.59	1.34	1.38
1	1A	1915	5MU	C4-N3	-2.58	1.34	1.38
1	2A	1939	5MU	C4-C5	2.57	1.49	1.44
1	1A	1911	PSU	C4-N3	-2.55	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.55	1.34	1.38
1	2A	2503	2MA	C5-C6	2.55	1.48	1.41
32	1a	516	PSU	C4-N3	-2.55	1.34	1.38
32	2a	516	PSU	C4-N3	-2.52	1.34	1.38
1	1A	1942	5MC	C6-N1	-2.50	1.33	1.38
54	2x	55	PSU	C4-N3	-2.50	1.34	1.38
32	1a	527	G7M	C6-N1	-2.48	1.34	1.38
1	2A	1917	PSU	C4-N3	-2.47	1.34	1.38
32	1a	1498	UR3	C2-N1	2.43	1.41	1.38
1	1A	2605	PSU	C2-N3	-2.39	1.33	1.37
32	1a	1400	5MC	C6-N1	-2.38	1.34	1.38
32	2a	527	G7M	C6-N1	-2.37	1.34	1.38
43	1l	92	0TD	CB-CA	2.37	1.55	1.54
1	2A	2605	PSU	C4-N3	-2.37	1.34	1.38
32	2a	1207	2MG	C6-N1	-2.36	1.34	1.38
1	2A	2251	OMG	C6-N1	-2.35	1.34	1.38
1	1A	2503	2MA	C5-N7	-2.34	1.34	1.39
32	1a	1407	5MC	C6-C5	2.33	1.38	1.34
54	1x	55	PSU	C4-N3	-2.33	1.34	1.38
54	2x	54	5MU	C4-C5	2.33	1.48	1.44
32	1a	966	M2G	C6-N1	-2.32	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.30	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.29	1.34	1.38
54	1x	54	5MU	C2-N3	-2.29	1.34	1.38
1	1A	2503	2MA	C8-N7	2.28	1.36	1.31
1	2A	2251	OMG	C5-N7	-2.28	1.34	1.39
54	1x	32	5MC	C6-N1	-2.25	1.34	1.38
32	1a	967	5MC	C6-N1	-2.25	1.34	1.38
1	2A	2503	2MA	C8-N7	2.24	1.36	1.31
1	1A	2251	OMG	C5-N7	-2.24	1.34	1.39
1	2A	2503	2MA	C5-N7	-2.23	1.35	1.39
32	2a	1407	5MC	C6-N1	-2.22	1.34	1.38
1	2A	1915	5MU	C2-N1	2.22	1.41	1.38
1	2A	2552	OMU	C5-C4	2.21	1.48	1.43
32	1a	966	M2G	C5-N7	-2.20	1.34	1.39
1	1A	1917	PSU	C2-N3	-2.20	1.33	1.37
54	1x	54	5MU	C4-C5	2.19	1.48	1.44
1	2A	1915	5MU	C2-N3	-2.19	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	966	M2G	C5-N7	-2.19	1.34	1.39
1	1A	1962	5MC	C6-N1	-2.19	1.34	1.38
32	2a	1400	5MC	C6-N1	-2.19	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.19	1.34	1.38
32	1a	1207	2MG	C2-N3	2.18	1.36	1.32
1	2A	1942	5MC	C6-N1	-2.16	1.34	1.38
54	2x	8	4SU	O2-C2	2.16	1.26	1.23
32	2a	1498	UR3	C2-N1	2.16	1.41	1.38
54	1x	8	4SU	C6-C5	2.12	1.40	1.35
54	2x	54	5MU	C2-N3	-2.09	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.09	1.34	1.38
1	2A	2503	2MA	C4-N9	-2.09	1.33	1.37
54	1x	54	5MU	C2-N1	2.09	1.41	1.38
32	1a	1407	5MC	C6-N1	-2.08	1.34	1.38
32	2a	1498	UR3	C6-C5	2.08	1.39	1.35
1	1A	2503	2MA	C4-N9	-2.07	1.33	1.37
32	2a	967	5MC	C6-N1	-2.05	1.34	1.38
32	1a	1498	UR3	C5-C4	-2.04	1.38	1.43
54	2x	54	5MU	C6-N1	-2.03	1.34	1.38
1	1A	1915	5MU	C2-N3	-2.02	1.34	1.38
1	2A	2552	OMU	C2-N3	-2.02	1.34	1.38
54	2x	32	5MC	C6-N1	-2.02	1.34	1.38
32	2a	1207	2MG	C5-N7	-2.02	1.35	1.39
54	1x	8	4SU	O2-C2	2.02	1.26	1.23

All (254) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	24.39	146.21	102.36
1	2A	2503	2MA	C5-C4-N3	-7.95	118.81	127.18
1	1A	2503	2MA	C5-C4-N3	-7.46	119.32	127.18
32	1a	1207	2MG	C2-N3-C4	7.06	120.84	112.00
1	2A	1917	PSU	N1-C2-N3	6.84	122.39	115.17
32	2a	966	M2G	C5-C4-N3	-6.84	117.51	128.39
32	1a	1498	UR3	C4-N3-C2	-6.67	119.21	124.58
32	2a	1498	UR3	C4-N3-C2	-6.66	119.22	124.58
32	2a	1207	2MG	C2-N3-C4	6.64	120.30	112.00
1	1A	1917	PSU	N1-C2-N3	6.53	122.06	115.17
1	1A	2605	PSU	N1-C2-N3	6.47	122.00	115.17
54	1x	55	PSU	N1-C2-N3	6.41	121.93	115.17
54	2x	55	PSU	N1-C2-N3	6.38	121.90	115.17
1	1A	1911	PSU	N1-C2-N3	6.35	121.87	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2503	2MA	N3-C4-N9	6.22	134.89	126.99
32	1a	516	PSU	N1-C2-N3	6.20	121.70	115.17
32	1a	966	M2G	C5-C4-N3	-6.08	118.71	128.39
32	2a	516	PSU	N1-C2-N3	5.92	121.41	115.17
1	2A	2605	PSU	N1-C2-N3	5.90	121.39	115.17
1	2A	2251	OMG	C5-C4-N3	-5.88	119.03	128.39
32	1a	1207	2MG	C5-C4-N3	-5.87	119.05	128.39
1	1A	2503	2MA	N3-C4-N9	5.85	134.41	126.99
1	2A	1911	PSU	N1-C2-N3	5.84	121.33	115.17
1	2A	1915	5MU	N3-C2-N1	5.82	122.47	114.89
1	2A	1939	5MU	N3-C2-N1	5.73	122.35	114.89
32	2a	1207	2MG	C5-C4-N3	-5.70	119.33	128.39
1	1A	1915	5MU	C4-N3-C2	-5.64	119.94	127.34
32	1a	527	G7M	N9-C4-N3	5.57	137.08	125.95
1	2A	1939	5MU	C4-N3-C2	-5.56	120.05	127.34
32	1a	527	G7M	C5-C4-N3	-5.54	117.68	128.15
1	1A	2251	OMG	C5-C4-N3	-5.54	119.58	128.39
1	1A	1915	5MU	C5-C4-N3	5.51	120.11	115.32
1	1A	1939	5MU	C5-C4-N3	5.43	120.04	115.32
1	1A	1915	5MU	N3-C2-N1	5.42	121.94	114.89
32	2a	527	G7M	N9-C4-N3	5.38	136.72	125.95
32	2a	527	G7M	C5-C4-N3	-5.35	118.04	128.15
1	2A	2552	OMU	N3-C2-N1	5.25	121.72	114.89
32	1a	1519	MA6	N1-C2-N3	-5.24	120.64	128.58
32	2a	966	M2G	N9-C4-N3	5.24	136.43	125.95
1	2A	2552	OMU	C4-N3-C2	-5.12	120.25	126.61
1	1A	1939	5MU	C4-N3-C2	-5.10	120.65	127.34
1	2A	1915	5MU	C4-N3-C2	-5.06	120.70	127.34
1	1A	2552	OMU	N3-C2-N1	5.02	121.43	114.89
1	2A	2251	OMG	C2-N3-C4	4.88	120.71	112.30
54	2x	54	5MU	N3-C2-N1	4.87	121.23	114.89
1	1A	1939	5MU	O4-C4-C5	-4.86	119.35	124.92
32	1a	527	G7M	C2-N3-C4	4.84	120.63	112.30
32	2a	1519	MA6	C5-C4-N3	-4.83	120.06	126.72
32	2a	1519	MA6	N1-C2-N3	-4.83	121.28	128.58
32	1a	1518	MA6	N1-C2-N3	-4.78	121.34	128.58
1	1A	1939	5MU	N3-C2-N1	4.77	121.11	114.89
1	1A	2251	OMG	C2-N3-C4	4.71	120.41	112.30
32	2a	527	G7M	C2-N3-C4	4.67	120.34	112.30
32	2a	966	M2G	C2-N3-C4	4.60	121.02	112.51
1	1A	2552	OMU	C4-N3-C2	-4.58	120.93	126.61
1	2A	2251	OMG	N9-C4-N3	4.58	135.10	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	1518	MA6	C5-C4-N3	-4.57	120.42	126.72
32	1a	966	M2G	N9-C4-N3	4.56	135.06	125.95
54	1x	32	5MC	C5-C6-N1	-4.45	118.48	123.31
32	2a	1518	MA6	N1-C2-N3	-4.44	121.86	128.58
54	2x	54	5MU	C4-N3-C2	-4.44	121.52	127.34
1	1A	1939	5MU	C5-C6-N1	-4.42	118.52	123.31
32	1a	966	M2G	C2-N3-C4	4.38	120.61	112.51
1	1A	2251	OMG	N9-C4-N3	4.36	134.67	125.95
54	1x	54	5MU	N3-C2-N1	4.30	120.50	114.89
1	2A	2605	PSU	C4-N3-C2	-4.28	120.47	126.37
32	1a	1519	MA6	C2-N1-C6	4.28	122.28	111.83
32	2a	1519	MA6	C4-C5-N7	-4.27	105.70	110.58
1	1A	1911	PSU	C4-N3-C2	-4.21	120.57	126.37
32	1a	1518	MA6	C5-C4-N3	-4.20	120.94	126.72
1	2A	1915	5MU	C5-C4-N3	4.16	118.94	115.32
1	1A	1917	PSU	C4-N3-C2	-4.15	120.66	126.37
32	1a	1207	2MG	N9-C4-N3	4.14	134.24	125.95
1	2A	1939	5MU	C5-C6-N1	-4.12	118.83	123.31
32	2a	1519	MA6	C5-N7-C8	4.08	109.86	103.45
32	1a	1518	MA6	C2-N1-C6	4.05	121.72	111.83
32	1a	1518	MA6	C5-N7-C8	4.04	109.80	103.45
32	1a	1519	MA6	C5-C4-N3	-4.03	121.17	126.72
54	2x	55	PSU	C4-N3-C2	-4.03	120.83	126.37
1	2A	1917	PSU	O2-C2-N1	-4.00	118.66	122.79
32	2a	516	PSU	C4-N3-C2	-4.00	120.86	126.37
1	1A	1915	5MU	O4-C4-C5	-3.99	120.36	124.92
1	2A	1939	5MU	C5-C4-N3	3.97	118.78	115.32
1	2A	1917	PSU	C4-N3-C2	-3.95	120.93	126.37
32	2a	1518	MA6	C2-N1-C6	3.88	121.30	111.83
32	2a	1518	MA6	C4-C5-N7	-3.88	106.15	110.58
32	2a	1518	MA6	C5-N7-C8	3.88	109.54	103.45
32	2a	1207	2MG	N9-C4-N3	3.87	133.70	125.95
32	2a	1519	MA6	C2-N1-C6	3.86	121.26	111.83
1	1A	2605	PSU	C4-N3-C2	-3.83	121.10	126.37
32	1a	1518	MA6	C4-C5-N7	-3.81	106.23	110.58
54	1x	54	5MU	C4-N3-C2	-3.79	122.37	127.34
54	2x	54	5MU	C5-C4-N3	3.77	118.60	115.32
32	1a	1207	2MG	C6-C5-N7	3.75	137.11	130.29
32	1a	1519	MA6	C5-N7-C8	3.73	109.32	103.45
1	2A	2552	OMU	O2-C2-N1	-3.73	117.94	122.80
1	1A	1942	5MC	C5-C6-N1	-3.73	119.27	123.31
32	1a	1518	MA6	N9-C8-N7	-3.73	108.65	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1x	55	PSU	C4-N3-C2	-3.73	121.24	126.37
32	1a	516	PSU	C4-N3-C2	-3.71	121.26	126.37
54	2x	8	4SU	C1'-N1-C2	3.70	124.24	117.59
32	2a	1400	5MC	C5-C6-N1	-3.69	119.31	123.31
1	2A	1962	5MC	C5-C6-N1	-3.65	119.35	123.31
54	1x	8	4SU	C6-C5-C4	-3.63	116.81	119.95
54	1x	54	5MU	C5-C4-N3	3.60	118.45	115.32
32	2a	1519	MA6	C2-N3-C4	3.58	120.56	111.83
32	1a	1404	5MC	C5-C6-N1	-3.55	119.45	123.31
1	2A	2503	2MA	C4-C5-N7	-3.55	106.52	110.58
32	1a	1519	MA6	C4-C5-N7	-3.53	106.55	110.58
1	1A	1915	5MU	C5-C6-N1	-3.52	119.50	123.31
32	1a	1519	MA6	N9-C8-N7	-3.47	109.01	113.94
1	1A	1911	PSU	O2-C2-N1	-3.47	119.21	122.79
43	1l	92	0TD	OD2-CG-CB	3.45	120.61	113.15
1	2A	1911	PSU	C4-N3-C2	-3.45	121.62	126.37
32	2a	1519	MA6	N9-C8-N7	-3.45	109.04	113.94
1	1A	2251	OMG	C6-C5-N7	3.43	136.54	130.29
32	2a	1207	2MG	C6-C5-N7	3.42	136.51	130.29
43	2l	92	0TD	CSB-SB-CB	-3.39	96.27	102.36
1	1A	2503	2MA	C4-C5-N7	-3.39	106.71	110.58
1	2A	1911	PSU	O2-C2-N1	-3.38	119.31	122.79
32	1a	1519	MA6	C2-N3-C4	3.38	120.07	111.83
54	1x	55	PSU	O2-C2-N1	-3.37	119.32	122.79
43	2l	92	0TD	OD2-CG-CB	3.37	120.42	113.15
1	1A	2552	OMU	O2-C2-N1	-3.35	118.44	122.80
32	2a	1518	MA6	N9-C8-N7	-3.35	109.19	113.94
1	2A	1915	5MU	C5-C6-N1	-3.30	119.73	123.31
32	1a	967	5MC	C5-C6-N1	-3.29	119.74	123.31
54	2x	54	5MU	O4-C4-C5	-3.28	121.17	124.92
1	2A	1942	5MC	C5-C6-N1	-3.28	119.75	123.31
32	1a	1518	MA6	C2-N3-C4	3.27	119.81	111.83
1	1A	1962	5MC	C5-C6-N1	-3.27	119.76	123.31
32	2a	1518	MA6	C2-N3-C4	3.27	119.81	111.83
32	1a	1498	UR3	C5-C4-N3	3.26	119.33	115.04
32	2a	967	5MC	C5-C6-N1	-3.26	119.78	123.31
54	2x	8	4SU	C6-C5-C4	-3.24	117.14	119.95
54	2x	32	5MC	O2-C2-N3	-3.23	117.23	122.33
32	1a	1400	5MC	C5-C6-N1	-3.23	119.81	123.31
32	1a	516	PSU	O2-C2-N1	-3.23	119.46	122.79
1	2A	1915	5MU	O4-C4-C5	-3.22	121.23	124.92
32	2a	516	PSU	O2-C2-N1	-3.21	119.47	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1939	5MU	O2-C2-N1	-3.19	118.64	122.80
1	2A	1939	5MU	O4-C4-C5	-3.18	121.28	124.92
54	2x	54	5MU	C5-C6-N1	-3.18	119.86	123.31
54	2x	32	5MC	C5-C6-N1	-3.18	119.86	123.31
54	2x	55	PSU	O2-C2-N1	-3.17	119.52	122.79
54	1x	54	5MU	O4-C4-C5	-3.16	121.31	124.92
54	2x	8	4SU	C5-C4-N3	3.15	117.68	114.75
32	1a	1407	5MC	C5-C4-N3	-3.14	118.53	121.75
54	1x	32	5MC	C5-C4-N3	-3.13	118.55	121.75
54	1x	54	5MU	C5-C6-N1	-3.13	119.92	123.31
1	1A	2552	OMU	C5-C4-N3	3.12	119.17	114.80
1	1A	1917	PSU	O2-C2-N1	-3.12	119.57	122.79
32	2a	1404	5MC	C5-C6-N1	-3.10	119.94	123.31
1	2A	2552	OMU	C5-C4-N3	3.10	119.14	114.80
1	1A	2503	2MA	N6-C6-N1	3.09	121.20	117.03
1	2A	2251	OMG	C6-C5-N7	3.07	135.87	130.29
54	1x	8	4SU	O2-C2-N1	3.06	126.78	122.80
1	2A	2503	2MA	C4-N9-C8	3.04	108.94	105.74
32	2a	1498	UR3	C5-C4-N3	3.04	119.05	115.04
1	1A	2552	OMU	O4-C4-C5	-3.03	119.94	125.16
32	2a	1407	5MC	C5-C4-N3	-3.00	118.68	121.75
32	1a	1400	5MC	C5-C4-N3	-2.95	118.73	121.75
32	1a	1207	2MG	C4-C5-N7	-2.93	106.03	110.67
1	1A	2503	2MA	C2-N1-C6	2.92	122.60	118.10
32	2a	1407	5MC	C5-C6-N1	-2.89	120.18	123.31
1	1A	2503	2MA	C4-N9-C8	2.87	108.75	105.74
32	2a	1518	MA6	C4-C5-C6	2.86	118.87	115.91
32	1a	966	M2G	C6-C5-N7	2.84	135.47	130.29
1	2A	2605	PSU	O2-C2-N1	-2.81	119.89	122.79
1	1A	2605	PSU	O2-C2-N1	-2.78	119.92	122.79
32	2a	1518	MA6	N3-C4-N9	2.77	131.89	127.17
32	2a	1207	2MG	C4-C5-N7	-2.77	106.28	110.67
32	2a	1404	5MC	C5-C4-N3	-2.77	118.92	121.75
1	2A	1915	5MU	O2-C2-N1	-2.75	119.22	122.80
32	1a	967	5MC	C5-C4-N3	-2.73	118.95	121.75
32	2a	1519	MA6	N3-C4-N9	2.72	131.79	127.17
1	1A	2552	OMU	C2'-C1'-N1	-2.71	109.10	114.24
32	2a	1498	UR3	C3U-N3-C4	2.70	121.61	117.87
1	2A	2503	2MA	C5-N7-C8	2.70	107.69	103.45
1	2A	2552	OMU	O4-C4-C5	-2.70	120.51	125.16
1	2A	2503	2MA	N6-C6-N1	2.70	120.66	117.03
32	1a	1498	UR3	C3U-N3-C4	2.69	121.60	117.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	1518	MA6	N3-C4-N9	2.65	131.67	127.17
1	2A	1962	5MC	C5-C4-N3	-2.63	119.06	121.75
1	1A	1962	5MC	CM5-C5-C6	-2.63	119.30	122.85
1	1A	1915	5MU	O2-C2-N1	-2.63	119.38	122.80
1	1A	1942	5MC	C5-C4-N3	-2.61	119.08	121.75
32	2a	966	M2G	C6-C5-N7	2.61	135.04	130.29
32	2a	1519	MA6	C4-C5-C6	2.60	118.60	115.91
54	2x	32	5MC	C5-C4-N3	-2.58	119.11	121.75
32	2a	1207	2MG	N1-C2-N2	2.56	119.18	116.56
32	1a	1519	MA6	N3-C4-N9	2.56	131.51	127.17
43	2l	92	0TD	OD1-CG-CB	-2.52	117.17	122.44
1	1A	2503	2MA	C5-N7-C8	2.49	107.36	103.45
1	1A	2251	OMG	O6-C6-C5	-2.49	119.97	126.53
32	2a	966	M2G	C4-C5-N7	-2.48	106.73	110.67
1	2A	1942	5MC	C5-C4-N3	-2.48	119.21	121.75
32	1a	1498	UR3	C1'-N1-C2	2.47	121.08	117.04
1	1A	1920	OMC	O2-C2-N3	-2.45	118.47	122.33
32	2a	1400	5MC	C5-C4-N3	-2.44	119.25	121.75
1	2A	2503	2MA	C2-N1-C6	2.44	121.85	118.10
32	2a	1207	2MG	N2-C2-N3	-2.42	117.42	120.51
54	2x	54	5MU	O2-C2-N1	-2.42	119.64	122.80
32	1a	1404	5MC	C5-C4-N3	-2.42	119.27	121.75
32	2a	527	G7M	O6-C6-C5	-2.42	122.61	128.01
1	2A	2251	OMG	O6-C6-C5	-2.40	120.20	126.53
32	1a	966	M2G	O6-C6-C5	-2.39	120.21	126.53
1	2A	2503	2MA	N9-C8-N7	-2.39	110.54	113.94
1	2A	2552	OMU	C2'-C1'-N1	-2.39	109.70	114.24
32	1a	966	M2G	C4-C5-N7	-2.38	106.90	110.67
32	1a	527	G7M	O6-C6-C5	-2.36	122.75	128.01
43	1l	92	0TD	OD1-CG-CB	-2.36	117.51	122.44
54	1x	8	4SU	S4-C4-N3	-2.35	117.75	120.20
32	1a	1402	4OC	C6-C5-C4	2.34	119.83	117.00
32	2a	967	5MC	C5-C4-N3	-2.33	119.37	121.75
32	1a	1518	MA6	C4-C5-C6	2.32	118.31	115.91
1	2A	2251	OMG	C4-C5-N7	-2.32	107.00	110.67
1	1A	1962	5MC	C5-C4-N3	-2.29	119.40	121.75
32	1a	1207	2MG	N1-C2-N2	2.27	118.88	116.56
32	1a	1407	5MC	CM5-C5-C6	-2.26	119.79	122.85
1	2A	2605	PSU	C5-C6-N1	-2.26	119.01	122.14
32	1a	527	G7M	C5-C6-N1	2.25	116.50	111.84
32	1a	1400	5MC	O2-C2-N3	-2.25	118.78	122.33
1	1A	2605	PSU	C5-C6-N1	-2.25	119.02	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	2503	2MA	C6-C5-N7	2.23	136.40	132.09
54	1x	8	4SU	C4-N3-C2	2.21	129.43	127.31
32	1a	1407	5MC	O2-C2-N3	-2.20	118.85	122.33
1	1A	2251	OMG	C4-C5-N7	-2.19	107.21	110.67
54	1x	32	5MC	O2-C2-N3	-2.18	118.90	122.33
1	1A	2503	2MA	C6-C5-N7	2.18	136.28	132.09
1	2A	1911	PSU	C6-C5-C4	-2.18	116.71	118.17
32	2a	527	G7M	C5-C6-N1	2.17	116.33	111.84
1	1A	2251	OMG	C5-C6-N1	2.15	118.72	113.25
32	2a	1519	MA6	C5-C4-N9	2.14	108.15	105.81
1	1A	2503	2MA	N9-C8-N7	-2.13	110.91	113.94
54	2x	55	PSU	C5-C6-N1	-2.13	119.18	122.14
1	1A	2605	PSU	O2-C2-N3	-2.13	118.08	121.86
32	1a	1207	2MG	C8-N7-C5	2.13	108.05	104.26
32	1a	1402	4OC	C5-C6-N1	-2.11	118.41	121.84
32	1a	1407	5MC	C5-C6-N1	-2.10	121.03	123.31
32	1a	1404	5MC	O2-C2-N3	-2.09	119.03	122.33
32	2a	516	PSU	O4'-C1'-C2'	2.09	108.05	105.15
32	1a	1518	MA6	C4-N9-C8	2.08	107.92	105.74
1	1A	1917	PSU	C5-C6-N1	-2.06	119.27	122.14
32	1a	1402	4OC	CM4-N4-C4	-2.06	118.42	122.45
54	1x	32	5MC	N1-C2-N3	2.03	122.33	118.80
1	1A	1939	5MU	O2-C2-N3	-2.03	117.75	121.49
54	1x	8	4SU	C5-C4-N3	2.03	116.64	114.75
32	1a	1400	5MC	C1'-N1-C6	-2.03	117.81	121.15
1	2A	1917	PSU	C5-C6-N1	-2.02	119.33	122.14
32	2a	516	PSU	C5-C6-N1	-2.01	119.35	122.14
32	1a	1498	UR3	O4-C4-C5	-2.01	118.66	124.35
32	2a	1407	5MC	O2-C2-N3	-2.00	119.17	122.33
54	1x	55	PSU	C5-C6-N1	-2.00	119.36	122.14

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	2251	OMG	C1'-C2'-O2'-CM2
43	1l	92	0TD	SB-CB-CG-OD2
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
1	2A	1911	PSU	O4'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	527	G7M	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	G7M	O4'-C4'-C5'-O5'
32	1a	967	5MC	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
43	2l	92	0TD	CG-CB-SB-CSB
32	2a	527	G7M	O4'-C4'-C5'-O5'
43	1l	92	0TD	SB-CB-CG-OD1
1	1A	1962	5MC	C2'-C1'-N1-C6
32	1a	1519	MA6	C4'-C5'-O5'-P
32	2a	1519	MA6	C4'-C5'-O5'-P
32	1a	1402	4OC	O4'-C4'-C5'-O5'
1	2A	1911	PSU	C3'-C4'-C5'-O5'
32	2a	967	5MC	O4'-C4'-C5'-O5'
1	1A	1962	5MC	O4'-C1'-N1-C6
32	2a	1402	4OC	C2'-C1'-N1-C2
54	2x	32	5MC	C2'-C1'-N1-C2
54	1x	8	4SU	O4'-C4'-C5'-O5'
1	2A	1920	OMC	C2'-C1'-N1-C2
1	1A	1920	OMC	C2'-C1'-N1-C2

There are no ring outliers.

21 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
43	1l	92	0TD	2	0
1	2A	2503	2MA	1	0
1	1A	1939	5MU	2	0
32	2a	1518	MA6	2	0
54	2x	8	4SU	1	0
1	2A	1917	PSU	1	0
1	2A	1939	5MU	1	0
32	2a	1402	4OC	2	0
43	2l	92	0TD	2	0
1	1A	2251	OMG	1	0
1	2A	2552	OMU	3	0
32	2a	1519	MA6	2	0
1	1A	2552	OMU	2	0
32	1a	1518	MA6	1	0
54	1x	8	4SU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1A	1917	PSU	1	0
54	1x	32	5MC	1	0
32	1a	1407	5MC	1	0
32	1a	1519	MA6	1	0
32	2a	967	5MC	1	0
1	1A	1915	5MU	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2481 ligands modelled in this entry, 2477 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
57	T8B	1A	4052	55,1	48,48,48	2.60	11 (22%)	63,71,71	1.72	13 (20%)
59	SF4	2d	501	35	0,12,12	-	-	-		
57	T8B	2A	3717	55,1	48,48,48	2.62	11 (22%)	63,71,71	1.81	15 (23%)
59	SF4	1d	3202	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	T8B	1A	4052	55,1	-	4/26/26/26	0/5/5/5
59	SF4	2d	501	35	-	-	0/6/5/5
57	T8B	2A	3717	55,1	-	1/26/26/26	0/5/5/5
59	SF4	1d	3202	35	-	-	0/6/5/5

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	2A	3717	T8B	C27-C26	-9.83	1.40	1.48
57	1A	4052	T8B	C27-C26	-9.67	1.40	1.48
57	2A	3717	T8B	C25-C26	8.37	1.53	1.38
57	1A	4052	T8B	C2-C3	-7.98	1.40	1.51
57	1A	4052	T8B	C25-C26	7.95	1.53	1.38
57	2A	3717	T8B	C2-C3	-7.78	1.40	1.51
57	2A	3717	T8B	C10-C11	4.64	1.38	1.33
57	1A	4052	T8B	C10-C11	4.53	1.38	1.33
57	1A	4052	T8B	C11-C12	-4.26	1.39	1.48
57	2A	3717	T8B	C11-C12	-3.63	1.40	1.48
57	2A	3717	T8B	C23-C24	-3.31	1.40	1.49
57	1A	4052	T8B	C23-C24	-3.28	1.40	1.49
57	2A	3717	T8B	C25-C24	3.11	1.53	1.43
57	1A	4052	T8B	C25-C24	3.04	1.53	1.43
57	1A	4052	T8B	C9-C10	-2.79	1.38	1.43
57	1A	4052	T8B	C15-C14	-2.74	1.40	1.46
57	2A	3717	T8B	C15-C14	-2.70	1.40	1.46
57	2A	3717	T8B	C9-C10	-2.59	1.38	1.43
57	2A	3717	T8B	C15-C9	-2.33	1.38	1.42
57	1A	4052	T8B	C15-C9	-2.32	1.38	1.42
57	2A	3717	T8B	O11-C26	2.30	1.36	1.31
57	1A	4052	T8B	O11-C26	2.28	1.36	1.31

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	2A	3717	T8B	C26-C25-C24	-5.18	113.52	120.81
57	2A	3717	T8B	O5-C14-O6	4.71	122.06	116.45
57	1A	4052	T8B	C21-C23-C24	-4.67	119.73	125.09
57	2A	3717	T8B	C21-C23-C24	-4.57	119.84	125.09
57	2A	3717	T8B	C13-O4-C12	-4.42	107.66	115.85
57	1A	4052	T8B	C26-C25-C24	-4.29	114.78	120.81
57	1A	4052	T8B	O5-C14-O6	4.03	121.25	116.45
57	1A	4052	T8B	C13-O4-C12	-3.80	108.80	115.85
57	1A	4052	T8B	O11-C26-C27	3.23	118.78	113.95
57	2A	3717	T8B	C32-C27-C26	3.20	126.83	121.69
57	1A	4052	T8B	C11-O5-C14	-3.19	118.98	121.54
57	2A	3717	T8B	O4-C12-C11	3.14	116.17	111.77
57	1A	4052	T8B	C32-C27-C26	2.91	126.38	121.69
57	2A	3717	T8B	O5-C11-C12	2.90	117.81	112.19
57	2A	3717	T8B	O11-C26-C27	2.85	118.21	113.95
57	1A	4052	T8B	C4-C5-C6	-2.65	117.73	122.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	2A	3717	T8B	O11-C26-C25	-2.46	117.87	121.09
57	2A	3717	T8B	C11-O5-C14	-2.38	119.63	121.54
57	2A	3717	T8B	C15-C16-C17	2.37	122.99	121.13
57	1A	4052	T8B	C15-C16-C17	2.31	122.95	121.13
57	2A	3717	T8B	C4-C5-C6	-2.25	118.40	122.13
57	2A	3717	T8B	O2-C1-C2	-2.25	116.16	122.94
57	1A	4052	T8B	O10-C24-C23	2.24	123.09	119.31
57	2A	3717	T8B	C19-O8-C18	-2.20	109.25	113.92
57	1A	4052	T8B	O11-C26-C25	-2.17	118.24	121.09
57	2A	3717	T8B	O6-C14-C15	-2.08	119.17	124.45
57	1A	4052	T8B	O4-C12-C11	2.05	114.64	111.77
57	1A	4052	T8B	C9-C10-C11	-2.03	117.75	120.13

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	1A	4052	T8B	C11-C12-O4-C13
57	1A	4052	T8B	O3-C12-O4-C13
57	2A	3717	T8B	C11-C12-O4-C13
57	1A	4052	T8B	C25-C26-C27-C28
57	1A	4052	T8B	C25-C26-C27-C32

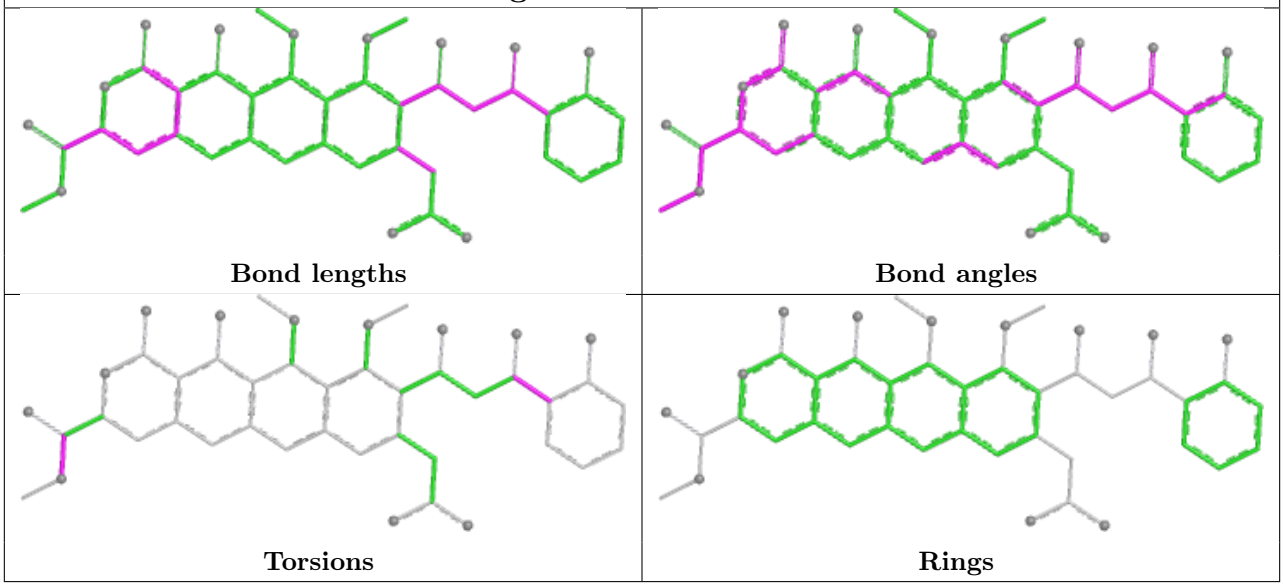
There are no ring outliers.

1 monomer is involved in 2 short contacts:

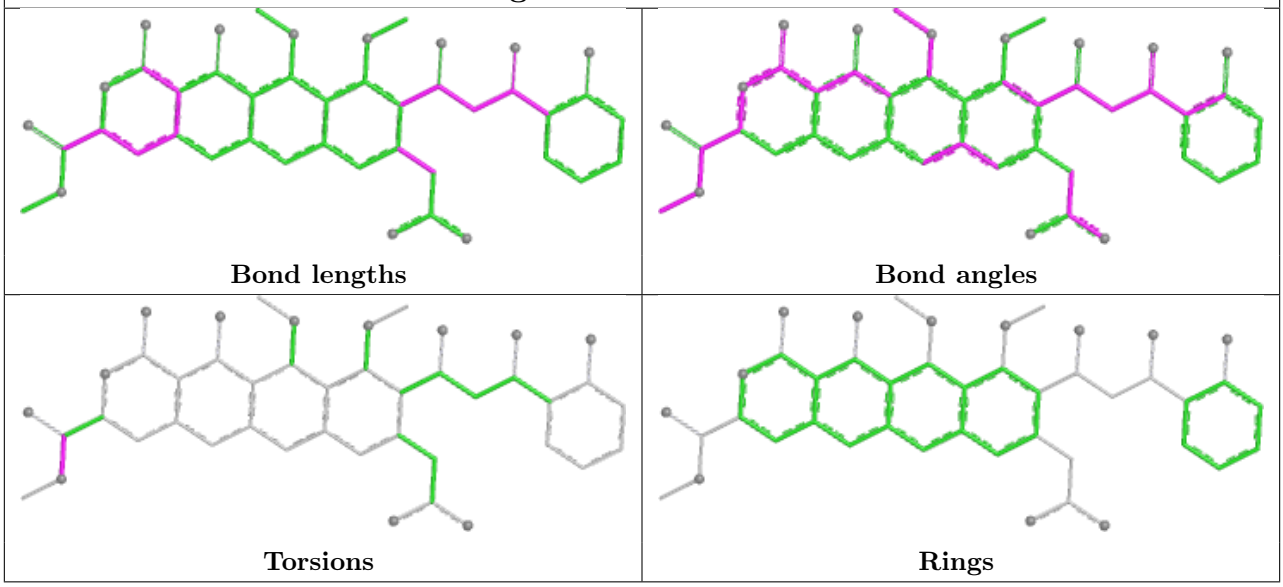
Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	2A	3717	T8B	2	0

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 then 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 T8B 1A 4052



Ligand T8B 2A 3717



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 (i)

6.1 Protein, DNA and RNA chains (i)

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%)	-0.62	106 (3%)	45	41	18, 34, 94, 109	0
1	2A	2789/2915 (95%)	-0.21	93 (3%)	49	45	29, 54, 92, 108	0
2	1B	120/121 (99%)	-0.50	0	100	100	27, 48, 64, 86	0
2	2B	120/121 (99%)	0.93	10 (8%)	17	14	57, 80, 90, 94	0
3	1D	275/276 (99%)	-0.30	2 (0%)	84	83	18, 33, 49, 78	0
3	2D	275/276 (99%)	0.10	3 (1%)	78	76	27, 46, 58, 75	0
4	1E	204/206 (99%)	-0.17	2 (0%)	79	78	16, 38, 60, 81	0
4	2E	204/206 (99%)	0.19	2 (0%)	79	78	29, 55, 68, 79	0
5	1F	203/210 (96%)	-0.25	1 (0%)	87	86	16, 40, 66, 87	0
5	2F	203/210 (96%)	0.33	3 (1%)	72	70	32, 64, 78, 85	0
6	1G	181/182 (99%)	0.23	4 (2%)	62	59	38, 55, 73, 87	0
6	2G	181/182 (99%)	1.30	30 (16%)	4	4	64, 79, 86, 92	0
7	1H	174/180 (96%)	0.05	3 (1%)	69	67	38, 53, 66, 70	0
7	2H	174/180 (96%)	0.97	12 (6%)	23	20	66, 80, 88, 94	0
8	1I	146/148 (98%)	0.41	1 (0%)	84	83	41, 68, 79, 84	0
8	2I	146/148 (98%)	0.96	9 (6%)	26	23	50, 72, 81, 89	0
9	1N	140/140 (100%)	-0.10	1 (0%)	84	83	26, 39, 59, 73	0
9	2N	140/140 (100%)	0.53	3 (2%)	63	61	41, 62, 77, 84	0
10	1O	122/122 (100%)	-0.20	0	100	100	25, 39, 56, 64	0
10	2O	122/122 (100%)	0.10	0	100	100	41, 52, 64, 72	0
11	1P	149/150 (99%)	-0.06	2 (1%)	75	73	19, 42, 65, 74	0
11	2P	149/150 (99%)	0.35	2 (1%)	75	73	33, 64, 80, 91	0
12	1Q	141/141 (100%)	-0.25	2 (1%)	73	72	24, 38, 52, 67	0
12	2Q	141/141 (100%)	0.52	5 (3%)	47	43	41, 60, 72, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	-0.34	0 100 100	22, 34, 50, 57	0
13	2R	118/118 (100%)	0.17	1 (0%) 82 81	37, 49, 59, 69	0
14	1S	110/112 (98%)	-0.02	0 100 100	34, 47, 59, 64	0
14	2S	110/112 (98%)	1.23	19 (17%) 4 3	60, 74, 82, 88	0
15	1T	131/146 (89%)	0.04	3 (2%) 61 58	31, 43, 68, 74	0
15	2T	131/146 (89%)	0.10	1 (0%) 82 81	47, 56, 73, 80	0
16	1U	116/118 (98%)	-0.43	1 (0%) 81 80	20, 31, 50, 68	0
16	2U	116/118 (98%)	0.24	1 (0%) 81 80	40, 57, 71, 79	0
17	1V	101/101 (100%)	-0.34	0 100 100	21, 41, 57, 66	0
17	2V	101/101 (100%)	0.41	1 (0%) 79 78	40, 68, 75, 79	0
18	1W	112/113 (99%)	-0.43	0 100 100	21, 31, 52, 80	0
18	2W	112/113 (99%)	0.21	4 (3%) 46 42	37, 48, 67, 83	0
19	1X	95/96 (98%)	-0.17	2 (2%) 63 61	24, 36, 60, 78	0
19	2X	95/96 (98%)	0.60	3 (3%) 50 46	45, 58, 74, 85	0
20	1Y	107/110 (97%)	0.28	3 (2%) 55 51	37, 50, 71, 78	0
20	2Y	107/110 (97%)	0.95	11 (10%) 12 10	54, 70, 80, 90	0
21	1Z	154/206 (74%)	0.45	9 (5%) 29 25	39, 58, 75, 81	0
21	2Z	160/206 (77%)	1.23	23 (14%) 6 5	65, 77, 87, 91	0
22	10	75/85 (88%)	-0.20	1 (1%) 75 73	24, 36, 54, 62	0
22	20	77/85 (90%)	0.75	6 (7%) 19 16	41, 60, 72, 73	0
23	11	97/98 (98%)	-0.04	1 (1%) 79 78	23, 42, 68, 72	0
23	21	97/98 (98%)	0.30	1 (1%) 79 78	39, 53, 74, 78	0
24	12	70/72 (97%)	-0.01	1 (1%) 73 72	31, 46, 58, 72	0
24	22	70/72 (97%)	0.64	2 (2%) 53 50	57, 68, 74, 76	0
25	13	59/60 (98%)	-0.36	1 (1%) 69 67	24, 36, 56, 68	0
25	23	59/60 (98%)	0.28	0 100 100	47, 60, 77, 83	0
26	14	69/71 (97%)	0.78	5 (7%) 21 18	53, 74, 88, 91	0
26	24	69/71 (97%)	1.66	20 (28%) 1 1	79, 86, 93, 95	0
27	15	59/60 (98%)	-0.45	0 100 100	20, 34, 60, 64	0
27	25	59/60 (98%)	0.09	1 (1%) 69 67	33, 51, 66, 84	0
28	16	53/54 (98%)	-0.24	0 100 100	29, 39, 56, 58	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	0.51	1 (1%) 66 63	46, 58, 67, 73	0
29	17	48/49 (97%)	-0.21	4 (8%) 17 14	20, 24, 49, 57	0
29	27	48/49 (97%)	-0.02	2 (4%) 40 37	30, 38, 63, 69	0
30	18	64/65 (98%)	-0.23	0 100 100	25, 31, 41, 47	0
30	28	64/65 (98%)	0.17	0 100 100	43, 52, 59, 63	0
31	19	37/37 (100%)	-0.36	0 100 100	29, 40, 56, 60	0
31	29	37/37 (100%)	0.79	2 (5%) 31 27	56, 63, 74, 78	0
32	1a	1488/1521 (97%)	0.27	43 (2%) 53 50	33, 68, 94, 106	0
32	2a	1491/1521 (98%)	0.44	67 (4%) 38 34	40, 75, 95, 107	0
33	1b	231/256 (90%)	0.93	24 (10%) 11 10	64, 79, 88, 91	0
33	2b	231/256 (90%)	1.55	60 (25%) 1 1	69, 83, 89, 95	0
34	1c	206/239 (86%)	1.03	23 (11%) 10 8	61, 75, 83, 87	0
34	2c	206/239 (86%)	1.35	31 (15%) 5 4	73, 82, 88, 90	0
35	1d	208/209 (99%)	1.04	23 (11%) 10 8	56, 70, 82, 86	0
35	2d	208/209 (99%)	0.87	11 (5%) 32 28	60, 71, 79, 89	0
36	1e	148/162 (91%)	0.53	2 (1%) 73 72	50, 63, 74, 82	0
36	2e	148/162 (91%)	0.98	17 (11%) 9 8	59, 72, 79, 86	0
37	1f	100/101 (99%)	0.75	4 (4%) 42 38	57, 68, 76, 80	0
37	2f	100/101 (99%)	0.65	3 (3%) 52 49	58, 69, 77, 80	0
38	1g	155/156 (99%)	0.64	11 (7%) 22 19	60, 71, 85, 93	0
38	2g	155/156 (99%)	0.85	17 (10%) 10 9	70, 78, 87, 92	0
39	1h	137/138 (99%)	0.58	1 (0%) 84 83	53, 66, 73, 78	0
39	2h	137/138 (99%)	1.04	12 (8%) 15 13	63, 72, 78, 83	0
40	1i	127/128 (99%)	1.01	15 (11%) 9 7	56, 78, 85, 87	0
40	2i	127/128 (99%)	1.63	38 (29%) 1 1	69, 84, 90, 93	0
41	1j	97/105 (92%)	1.41	24 (24%) 2 1	59, 80, 85, 89	0
41	2j	96/105 (91%)	1.47	21 (21%) 2 2	72, 85, 90, 91	0
42	1k	114/129 (88%)	0.54	2 (1%) 67 65	42, 65, 76, 80	0
42	2k	114/129 (88%)	0.75	8 (7%) 22 19	53, 71, 80, 85	0
43	1l	121/132 (91%)	0.44	6 (4%) 34 30	45, 55, 68, 72	0
43	2l	121/132 (91%)	0.49	4 (3%) 49 45	54, 62, 70, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
44	1m	123/126 (97%)	0.71	8 (6%) 25 22	56, 73, 81, 98	0
44	2m	122/126 (96%)	1.71	34 (27%) 1 1	71, 84, 90, 95	0
45	1n	60/61 (98%)	1.02	3 (5%) 34 30	61, 71, 78, 80	0
45	2n	60/61 (98%)	1.72	25 (41%) 0 0	74, 82, 86, 89	0
46	1o	88/89 (98%)	0.45	2 (2%) 61 58	47, 64, 75, 79	0
46	2o	88/89 (98%)	0.70	4 (4%) 38 34	57, 68, 76, 83	0
47	1p	82/88 (93%)	1.28	17 (20%) 2 2	58, 71, 81, 86	0
47	2p	82/88 (93%)	0.80	4 (4%) 35 31	59, 67, 77, 80	0
48	1q	99/105 (94%)	0.71	5 (5%) 33 29	54, 65, 74, 77	0
48	2q	99/105 (94%)	0.65	4 (4%) 42 38	58, 69, 76, 81	0
49	1r	68/88 (77%)	0.64	4 (5%) 28 25	56, 68, 77, 80	0
49	2r	68/88 (77%)	0.49	1 (1%) 72 70	62, 69, 79, 83	0
50	1s	83/93 (89%)	0.72	7 (8%) 17 14	66, 76, 84, 87	0
50	2s	83/93 (89%)	1.85	32 (38%) 1 0	78, 86, 92, 94	0
51	1t	96/106 (90%)	1.03	15 (15%) 5 4	61, 70, 77, 84	0
51	2t	96/106 (90%)	0.67	8 (8%) 17 14	58, 67, 78, 83	0
52	1u	23/27 (85%)	0.72	0 100 100	64, 68, 75, 78	0
52	2u	23/27 (85%)	1.64	5 (21%) 2 2	74, 81, 84, 86	0
53	1v	5/21 (23%)	0.74	2 (40%) 1 0	46, 49, 75, 81	0
53	2v	5/21 (23%)	1.65	2 (40%) 1 0	64, 70, 86, 93	0
54	1x	72/77 (93%)	-0.26	0 100 100	32, 55, 74, 86	0
54	2x	72/77 (93%)	0.44	2 (2%) 55 51	46, 74, 84, 96	0
All	All	20580/21438 (95%)	0.24	1077 (5%) 33 29	16, 61, 87, 109	0

All (1077) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
44	2m	124	PRO	12.0
44	1m	123	ALA	8.7
44	2m	123	ALA	8.6
44	2m	102	ARG	8.2
44	1m	124	PRO	6.4
26	24	65	ASP	6.2
33	2b	165	VAL	6.2

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Mol	Chain	Res	Type	RSRZ
21	1Z	146	ILE	6.0
45	1n	2	ALA	5.8
44	2m	122	LYS	5.7
21	2Z	174	VAL	5.3
1	1A	2115	G	5.2
32	1a	1447	A	5.1
34	2c	87	LEU	5.0
21	1Z	141	VAL	5.0
45	2n	2	ALA	4.8
3	2D	276	LYS	4.8
50	2s	24	ALA	4.8
1	2A	2117	A	4.7
34	2c	2	GLY	4.7
44	2m	90	LEU	4.7
38	1g	80	VAL	4.6
1	1A	1096	A	4.6
1	1A	2121	G	4.6
1	1A	899	A	4.5
1	1A	2117	A	4.5
32	1a	630	G	4.5
20	2Y	1	MET	4.5
26	24	66	SER	4.5
40	2i	10	ARG	4.5
38	2g	83	ALA	4.4
50	2s	16	LEU	4.4
1	2A	2155	G	4.4
1	2A	2133	G	4.4
43	1l	91	LYS	4.3
26	24	56	VAL	4.3
33	2b	168	THR	4.3
38	1g	154	TYR	4.3
1	2A	2174	C	4.3
1	1A	1078	U	4.3
1	1A	2167	U	4.3
6	1G	48	GLU	4.2
1	1A	1094	U	4.2
1	1A	2114	A	4.2
33	2b	234	PRO	4.2
37	1f	55	ASP	4.2
1	2A	1536	C	4.2
23	21	2	SER	4.2
38	2g	80	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
3	1D	276	LYS	4.2
44	1m	122	LYS	4.2
1	1A	2170	A	4.2
53	2v	14	A	4.2
40	2i	102	LEU	4.2
16	1U	117	GLN	4.1
44	2m	6	GLY	4.1
41	1j	98	ILE	4.1
40	2i	66	ARG	4.1
1	1A	2145	C	4.1
50	2s	9	VAL	4.1
41	2j	32	ALA	4.1
38	1g	79	ARG	4.0
1	2A	2139	C	4.0
35	1d	179	GLU	3.9
22	20	9	SER	3.9
19	2X	92	LEU	3.9
40	1i	19	LEU	3.9
32	1a	1001	A	3.9
1	2A	2159	G	3.9
1	1A	1095	A	3.9
1	2A	652(B)	A	3.9
41	2j	47	PHE	3.9
26	14	56	VAL	3.9
40	2i	105	ASP	3.9
32	2a	1030(B)	C	3.8
20	2Y	57	GLN	3.8
50	2s	71	LEU	3.8
1	2A	2112	G	3.8
51	1t	103	GLY	3.8
32	1a	1531	A	3.8
1	1A	2178	C	3.8
1	2A	2140	C	3.8
7	1H	2	SER	3.8
51	2t	103	GLY	3.8
1	1A	2159	G	3.8
1	2A	2111	C	3.8
38	2g	16	LEU	3.8
38	2g	82	GLY	3.8
6	2G	28	VAL	3.8
38	2g	84	ASN	3.7
33	2b	236	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
35	1d	164	ALA	3.7
1	1A	2146	C	3.7
47	1p	68	ASP	3.7
26	24	67	TYR	3.7
1	2A	1533	G	3.7
6	2G	20	ILE	3.7
2	2B	120	A	3.7
32	1a	1532	U	3.7
38	1g	85	TYR	3.7
1	1A	1099	G	3.6
1	2A	2138	C	3.6
34	1c	2	GLY	3.6
3	2D	38	LYS	3.6
32	2a	1363(A)	A	3.6
35	1d	23	GLY	3.6
6	2G	19	LEU	3.6
51	1t	69	GLY	3.6
21	2Z	150	LEU	3.6
1	2A	2109	U	3.6
26	24	49	PHE	3.6
54	2x	47	U	3.5
32	1a	1286	A	3.5
34	2c	190	ARG	3.5
33	2b	21	ARG	3.5
32	2a	1532	U	3.5
33	2b	22	LYS	3.5
7	2H	2	SER	3.5
41	1j	75	ILE	3.5
43	2l	64	TYR	3.4
1	2A	2157	G	3.4
41	2j	76	ASN	3.4
50	2s	2	PRO	3.4
1	1A	2135	A	3.4
2	2B	25	A	3.4
14	2S	58	LEU	3.4
1	1A	2119	A	3.4
44	2m	121	LYS	3.4
15	1T	131	ALA	3.4
22	20	8	GLY	3.4
1	2A	2118	U	3.4
1	1A	2156	G	3.4
44	2m	103	THR	3.4

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Mol	Chain	Res	Type	RSRZ
40	2i	123	PRO	3.4
33	1b	237	ALA	3.4
34	2c	137	ALA	3.4
33	1b	214	ILE	3.3
43	1l	89	ARG	3.3
32	2a	1035	A	3.3
51	1t	18	GLN	3.3
1	1A	1068	G	3.3
1	1A	2133	G	3.3
9	2N	9	VAL	3.3
1	1A	2122	U	3.3
21	2Z	155	LEU	3.3
35	1d	24	GLU	3.3
1	1A	2151	G	3.3
1	2A	2115	G	3.3
1	2A	2160	G	3.3
50	2s	80	TYR	3.3
1	1A	2113	U	3.3
1	2A	2113	U	3.3
41	2j	55	LYS	3.3
33	2b	57	PHE	3.3
1	2A	2170	A	3.3
32	2a	1036	G	3.3
40	2i	2	GLU	3.3
44	2m	87	TYR	3.3
36	2e	21	ALA	3.3
34	2c	207	VAL	3.3
39	2h	53	VAL	3.3
1	1A	2111	C	3.2
1	2A	2137	C	3.2
34	2c	160	ALA	3.2
40	2i	106	ALA	3.2
1	1A	888	C	3.2
1	1A	1064	C	3.2
1	2A	2128	C	3.2
50	2s	41	VAL	3.2
51	2t	9	ASN	3.2
1	1A	2112	G	3.2
50	2s	29	ARG	3.2
54	2x	46	G	3.2
6	2G	48	GLU	3.2
20	2Y	53	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
29	17	45	ALA	3.2
44	1m	2	ALA	3.2
26	24	63	TYR	3.2
21	2Z	154	ASP	3.2
44	2m	104	ARG	3.2
52	2u	24	ARG	3.2
40	1i	56	LEU	3.2
40	2i	96	LEU	3.2
1	1A	2169	A	3.1
24	22	66	GLU	3.1
33	2b	192	SER	3.1
44	2m	60	VAL	3.1
1	2A	2125	G	3.1
1	2A	2147	G	3.1
1	2A	2166	G	3.1
46	2o	88	ARG	3.1
26	24	51	ASP	3.1
36	2e	94	ALA	3.1
45	2n	5	ALA	3.1
26	24	59	PHE	3.1
38	2g	21	VAL	3.1
1	1A	1065	U	3.1
35	1d	169	LYS	3.1
1	2A	2110	G	3.1
33	2b	231	GLU	3.1
50	1s	84	GLY	3.1
53	1v	14	A	3.1
26	24	42	PHE	3.1
1	2A	2167	U	3.1
6	2G	4	ASP	3.1
20	1Y	91	GLU	3.1
1	2A	2318	G	3.1
32	2a	1030(A)	G	3.1
33	2b	169	LYS	3.1
40	2i	43	ALA	3.1
1	2A	2145	C	3.1
40	2i	21	PRO	3.0
1	2A	1026	U	3.0
1	1A	2157	G	3.0
1	2A	2168	G	3.0
32	2a	1224	G	3.0
41	2j	59	SER	3.0

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Mol	Chain	Res	Type	RSRZ
45	2n	21	TYR	3.0
50	2s	13	ASP	3.0
33	1b	134	GLU	3.0
35	2d	154	ASN	3.0
51	1t	9	ASN	3.0
1	1A	2120	G	3.0
1	1A	2125	G	3.0
1	2A	2116	G	3.0
44	2m	120	LYS	3.0
48	1q	100	LYS	3.0
1	1A	2173	A	3.0
40	2i	67	GLY	3.0
43	1l	18	VAL	3.0
33	2b	121	LEU	3.0
38	1g	153	HIS	3.0
20	2Y	55	TYR	3.0
12	1Q	60	ARG	3.0
45	2n	13	THR	3.0
1	1A	1087	G	3.0
1	1A	2141	G	3.0
1	1A	2140	C	3.0
6	1G	73	ALA	3.0
32	2a	530	G	3.0
32	2a	1001(A)	G	3.0
32	2a	1033	G	3.0
1	1A	2158	A	3.0
33	2b	197	VAL	3.0
33	2b	11	LEU	2.9
32	1a	1000	U	2.9
52	2u	14	TRP	2.9
21	1Z	159	PRO	2.9
41	1j	76	ASN	2.9
21	2Z	146	ILE	2.9
50	2s	40	ILE	2.9
52	2u	11	GLY	2.9
34	2c	189	ALA	2.9
33	1b	165	VAL	2.9
35	2d	140	VAL	2.9
1	1A	2160	G	2.9
1	2A	2121	G	2.9
1	2A	2164	C	2.9
1	2A	2175	C	2.9

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Mol	Chain	Res	Type	RSRZ
33	2b	131	PRO	2.9
1	1A	1060	U	2.9
1	1A	2150	U	2.9
24	12	69	ARG	2.9
34	2c	194	GLY	2.9
33	2b	237	ALA	2.9
19	1X	95	LEU	2.9
37	2f	21	LEU	2.9
20	2Y	54	LYS	2.9
41	1j	33	GLN	2.9
1	2A	2134	A	2.9
1	2A	2142	C	2.9
1	2A	2169	A	2.9
1	2A	2173	A	2.9
32	1a	1354	C	2.9
32	1a	1024	G	2.9
32	2a	1202	G	2.9
14	2S	7	TYR	2.9
36	2e	22	GLY	2.9
50	2s	68	GLY	2.9
21	1Z	150	LEU	2.9
43	2l	47	LYS	2.9
38	1g	156	TRP	2.9
44	2m	94	ARG	2.9
1	2A	2114	A	2.9
32	2a	1038	C	2.9
38	2g	154	TYR	2.9
1	2A	2127	G	2.9
44	1m	121	LYS	2.9
36	2e	10	MET	2.8
22	20	55	ARG	2.8
33	2b	172	ILE	2.8
3	2D	275	LYS	2.8
45	2n	38	GLY	2.8
32	2a	950	U	2.8
32	2a	1040	U	2.8
32	2a	1257	U	2.8
40	2i	14	VAL	2.8
32	2a	1116	C	2.8
21	2Z	1	MET	2.8
2	2B	118	G	2.8
34	2c	155	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
33	2b	149	LEU	2.8
33	2b	221	LEU	2.8
38	2g	85	TYR	2.8
33	1b	17	PHE	2.8
35	1d	150	GLU	2.8
32	1a	204	U	2.8
1	1A	1057	A	2.8
1	2A	899	A	2.8
33	2b	211	ILE	2.8
1	1A	2101	G	2.8
1	1A	2805	G	2.8
1	2A	2165	G	2.8
39	2h	4	ASP	2.8
26	14	67	TYR	2.8
26	24	40	HIS	2.8
44	1m	105	THR	2.8
35	1d	110	PHE	2.8
12	2Q	10	ARG	2.8
41	1j	79	ARG	2.8
1	1A	1081	U	2.8
2	2B	26	A	2.8
1	1A	2177	C	2.8
38	2g	156	TRP	2.8
42	2k	117	ASN	2.8
6	2G	172	LEU	2.8
33	2b	166	ASP	2.8
41	2j	58	ASP	2.8
20	1Y	1	MET	2.8
40	1i	106	ALA	2.8
44	2m	117	VAL	2.8
1	2A	2132	U	2.7
32	2a	1020	U	2.7
8	2I	75	LEU	2.7
14	2S	32	LEU	2.7
35	1d	167	GLY	2.7
44	2m	112	GLY	2.7
1	2A	2108	C	2.7
32	1a	999	C	2.7
34	2c	60	ALA	2.7
33	2b	70	PHE	2.7
36	1e	67	VAL	2.7
38	1g	2	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
41	1j	60	ARG	2.7
44	2m	98	VAL	2.7
6	2G	2	PRO	2.7
41	2j	77	PRO	2.7
5	2F	108	LYS	2.7
1	1A	1059	G	2.7
1	2A	1171	G	2.7
41	1j	4	ILE	2.7
19	2X	95	LEU	2.7
9	2N	68	GLU	2.7
41	2j	49	VAL	2.7
44	2m	76	ALA	2.7
33	2b	122	PHE	2.7
34	2c	128	PHE	2.7
53	2v	15	A	2.7
1	1A	886	C	2.7
1	1A	889	C	2.7
1	1A	2174	C	2.7
1	2A	2143	C	2.7
32	1a	1030(B)	C	2.7
32	2a	1260	C	2.7
33	2b	208	ILE	2.7
39	1h	2	LEU	2.7
41	1j	88	LEU	2.7
44	2m	66	LEU	2.7
1	1A	2110	G	2.7
1	2A	2104	G	2.7
1	2A	2131	G	2.7
1	2A	2190	G	2.7
19	1X	94	GLY	2.7
21	2Z	106	GLY	2.7
33	1b	97	TRP	2.7
38	2g	77	SER	2.7
6	2G	31	VAL	2.7
34	1c	95	THR	2.7
34	1c	192	THR	2.7
35	1d	170	VAL	2.7
44	2m	27	LYS	2.7
35	2d	20	TYR	2.7
32	2a	1030(D)	A	2.7
32	2a	1357	A	2.7
12	2Q	60	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
33	2b	112	VAL	2.7
41	1j	34	VAL	2.7
40	2i	103	THR	2.7
44	2m	5	ALA	2.7
45	2n	37	PHE	2.7
50	1s	9	VAL	2.7
50	2s	79	THR	2.7
1	2A	2123	G	2.6
32	1a	346	G	2.6
35	1d	160	GLN	2.6
1	1A	2132	U	2.6
40	2i	92	TYR	2.6
33	2b	48	MET	2.6
1	1A	2134	A	2.6
1	2A	2119	A	2.6
41	2j	65	LEU	2.6
11	2P	79	ARG	2.6
33	2b	175	ARG	2.6
35	1d	153	ARG	2.6
44	1m	102	ARG	2.6
44	2m	91	ARG	2.6
52	2u	16	GLY	2.6
1	1A	2129	C	2.6
1	1A	2179	C	2.6
8	2I	3	VAL	2.6
33	2b	13	ALA	2.6
40	2i	126	SER	2.6
14	2S	35	ILE	2.6
1	1A	1058	G	2.6
1	2A	2120	G	2.6
1	2A	2148	G	2.6
2	2B	23	G	2.6
32	1a	1002	G	2.6
32	2a	1002	G	2.6
6	2G	53	LEU	2.6
14	2S	80	LEU	2.6
41	1j	45	ARG	2.6
1	2A	2158	A	2.6
32	2a	1447	A	2.6
7	2H	115	VAL	2.6
8	2I	146	ALA	2.6
18	2W	60	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
34	2c	168	ALA	2.6
40	2i	26	VAL	2.6
41	1j	87	THR	2.6
52	2u	23	PRO	2.6
1	1A	2175	C	2.6
42	1k	36	ASP	2.6
50	2s	31	ILE	2.6
34	2c	48	TYR	2.6
40	2i	5	TYR	2.6
51	1t	10	LEU	2.6
51	2t	99	LEU	2.6
33	2b	53	ARG	2.6
21	1Z	147	GLY	2.6
38	1g	81	GLY	2.6
41	1j	10	GLY	2.6
50	2s	82	GLY	2.6
1	1A	1093	G	2.6
1	2A	2141	G	2.6
32	2a	630	G	2.6
41	2j	78	ASN	2.6
47	1p	22	THR	2.6
1	2A	2176	A	2.6
1	1A	1052	C	2.6
1	1A	2803	C	2.6
32	1a	163	C	2.6
32	1a	1027	C	2.6
49	1r	40	LEU	2.6
49	1r	79	LEU	2.6
39	2h	20	TYR	2.6
47	2p	38	TYR	2.6
45	2n	4	LYS	2.6
33	2b	170	GLU	2.6
1	2A	2150	U	2.6
9	1N	9	VAL	2.6
21	2Z	173	ALA	2.6
40	2i	71	SER	2.5
1	2A	2154	G	2.5
2	2B	119	G	2.5
32	2a	951	G	2.5
32	2a	1182	G	2.5
40	2i	91	ASP	2.5
33	1b	172	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	2126	A	2.5
21	2Z	144	LEU	2.5
32	2a	1183	A	2.5
35	1d	155	LEU	2.5
45	2n	44	LEU	2.5
7	1H	175	LYS	2.5
48	2q	100	LYS	2.5
33	2b	199	TYR	2.5
35	1d	38	TYR	2.5
1	1A	652(S)	C	2.5
7	2H	36	PRO	2.5
33	2b	230	VAL	2.5
36	2e	90	VAL	2.5
33	2b	171	ALA	2.5
1	1A	1066	U	2.5
34	2c	62	ASP	2.5
22	20	84	LEU	2.5
35	1d	194	LEU	2.5
50	1s	29	ARG	2.5
14	2S	34	HIS	2.5
32	2a	1131	G	2.5
32	2a	1220	G	2.5
25	13	60	GLU	2.5
43	1l	64	TYR	2.5
50	2s	43	GLU	2.5
50	2s	73	GLU	2.5
39	2h	131	GLY	2.5
34	2c	55	VAL	2.5
43	2l	18	VAL	2.5
12	2Q	121	ALA	2.5
40	2i	13	ALA	2.5
45	2n	30	ALA	2.5
1	1A	2136	C	2.5
1	2A	645	C	2.5
32	2a	1037	C	2.5
32	2a	1397	C	2.5
47	1p	1	MET	2.5
34	2c	15	THR	2.5
21	2Z	153	SER	2.5
14	2S	39	ILE	2.5
1	1A	1097	U	2.5
1	2A	2189	U	2.5

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Mol	Chain	Res	Type	RSRZ
27	25	19	ARG	2.5
34	2c	57	ILE	2.5
51	1t	55	ILE	2.5
50	2s	22	LEU	2.5
31	29	20	HIS	2.5
26	24	32	TYR	2.5
42	2k	25	TYR	2.5
46	2o	86	GLY	2.5
46	2o	89	GLY	2.5
1	1A	1077	A	2.5
1	2A	2149	G	2.5
32	1a	149	A	2.5
33	1b	229	VAL	2.5
33	2b	15	VAL	2.5
6	2G	50	ALA	2.5
8	1I	146	ALA	2.5
15	2T	130	ALA	2.5
33	2b	123	ALA	2.5
47	1p	24	ALA	2.5
47	2p	82	GLN	2.5
40	2i	27	THR	2.5
5	2F	110	LEU	2.5
33	2b	187	LEU	2.5
35	1d	3	ARG	2.5
50	2s	30	LEU	2.5
1	2A	2188	C	2.5
1	1A	12	U	2.5
32	2a	1025	U	2.5
7	2H	21	PRO	2.5
33	1b	236	TYR	2.5
33	2b	91	PRO	2.5
14	2S	79	ALA	2.5
34	2c	92	ALA	2.5
38	2g	65	ALA	2.5
14	2S	33	LYS	2.4
43	2l	126	LYS	2.4
32	2a	1492	A	2.4
47	1p	5	ARG	2.4
34	2c	204	LEU	2.4
15	1T	109	GLU	2.4
1	1A	1100	C	2.4
1	1A	2142	C	2.4

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Mol	Chain	Res	Type	RSRZ
1	1A	2804	C	2.4
1	2A	2789	C	2.4
4	2E	148	GLY	2.4
34	1c	96	GLY	2.4
34	2c	7	PRO	2.4
38	2g	81	GLY	2.4
50	2s	59	PRO	2.4
26	24	47	GLN	2.4
21	1Z	136	PHE	2.4
40	1i	18	PHE	2.4
22	10	10	THR	2.4
26	24	55	ARG	2.4
38	1g	78	ARG	2.4
41	2j	42	THR	2.4
47	2p	8	ARG	2.4
34	1c	87	LEU	2.4
1	1A	1070	A	2.4
28	26	4	GLU	2.4
32	2a	1034	G	2.4
35	1d	33	MET	2.4
6	2G	119	GLY	2.4
51	2t	98	PRO	2.4
3	1D	275	LYS	2.4
45	2n	17	LYS	2.4
1	1A	2138	C	2.4
1	1A	2161	C	2.4
6	2G	160	VAL	2.4
7	2H	52	VAL	2.4
20	2Y	45	VAL	2.4
21	2Z	71	VAL	2.4
32	2a	1149	C	2.4
32	2a	1363	C	2.4
34	1c	184	TYR	2.4
35	2d	170	VAL	2.4
36	2e	20	GLN	2.4
1	1A	2130	U	2.4
1	1A	2506	U	2.4
6	2G	23	PHE	2.4
9	2N	115	ARG	2.4
14	2S	37	ALA	2.4
32	1a	1025	U	2.4
32	1a	1257	U	2.4

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Mol	Chain	Res	Type	RSRZ
40	1i	59	PHE	2.4
41	2j	54	PHE	2.4
35	2d	49	ARG	2.4
40	2i	9	ARG	2.4
46	1o	88	ARG	2.4
6	2G	175	LEU	2.4
33	2b	200	ILE	2.4
34	1c	84	ILE	2.4
42	2k	31	THR	2.4
21	2Z	129	SER	2.4
33	1b	9	GLU	2.4
34	1c	90	GLU	2.4
47	1p	48	TRP	2.4
18	2W	112	GLY	2.4
35	2d	23	GLY	2.4
35	1d	112	VAL	2.4
6	2G	136	ARG	2.4
26	14	49	PHE	2.4
32	1a	1009	G	2.4
32	1a	1026	G	2.4
35	2d	132	ARG	2.4
41	1j	26	ALA	2.4
41	1j	46	ARG	2.4
47	1p	39	TYR	2.4
1	1A	2164	C	2.4
1	2A	2122	U	2.4
6	2G	88	ILE	2.4
14	2S	110	LEU	2.4
33	2b	39	ILE	2.4
33	2b	180	LEU	2.4
45	2n	6	LEU	2.4
50	2s	20	LEU	2.4
50	1s	39	THR	2.4
32	1a	1038	C	2.4
18	2W	111	HIS	2.4
21	2Z	166	SER	2.4
37	1f	41	GLU	2.4
40	1i	2	GLU	2.4
19	2X	1	MET	2.4
33	1b	22	LYS	2.4
41	2j	37	PRO	2.4
40	1i	8	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
7	2H	37	VAL	2.4
7	2H	170	ARG	2.4
20	2Y	50	ARG	2.4
26	24	62	ARG	2.4
41	2j	44	VAL	2.4
36	2e	86	ALA	2.4
44	2m	118	ALA	2.4
49	1r	73	ALA	2.4
6	2G	111	LEU	2.3
8	2I	12	LEU	2.3
21	2Z	33	LEU	2.3
41	2j	8	LEU	2.3
50	2s	15	LEU	2.3
21	1Z	69	THR	2.3
1	1A	1056	G	2.3
1	1A	2189	U	2.3
32	1a	1001(A)	G	2.3
32	1a	1003	G	2.3
32	2a	1181	G	2.3
32	2a	1190	G	2.3
34	1c	35	GLU	2.3
1	1A	1509	C	2.3
1	2A	886	C	2.3
6	2G	76	SER	2.3
7	2H	134	SER	2.3
33	1b	133	LYS	2.3
34	2c	4	LYS	2.3
35	1d	83	SER	2.3
40	2i	11	LYS	2.3
48	2q	37	LYS	2.3
51	1t	68	LYS	2.3
6	2G	129	GLY	2.3
18	2W	92	ARG	2.3
40	2i	86	VAL	2.3
6	2G	62	LEU	2.3
33	2b	10	LEU	2.3
40	2i	99	LEU	2.3
33	2b	185	ILE	2.3
1	1A	2171	A	2.3
32	2a	532	A	2.3
32	2a	1268	A	2.3
38	2g	37	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
29	27	48	LYS	2.3
44	1m	120	LYS	2.3
20	2Y	107	ASP	2.3
32	1a	1446	U	2.3
1	2A	2182	G	2.3
1	2A	2186	G	2.3
32	1a	102	G	2.3
32	1a	1023	G	2.3
32	2a	971	G	2.3
38	2g	4	ARG	2.3
41	2j	10	GLY	2.3
26	24	10	VAL	2.3
36	2e	115	VAL	2.3
36	1e	21	ALA	2.3
41	2j	85	LEU	2.3
42	2k	103	LEU	2.3
45	1n	20	ALA	2.3
40	2i	63	ILE	2.3
33	1b	19	HIS	2.3
6	2G	161	THR	2.3
34	2c	191	THR	2.3
45	2n	22	THR	2.3
48	1q	7	THR	2.3
39	2h	9	MET	2.3
39	2h	99	GLU	2.3
45	2n	11	LYS	2.3
53	1v	15	A	2.3
14	2S	20	ARG	2.3
33	2b	232	PRO	2.3
26	14	54	GLY	2.3
36	2e	23	GLY	2.3
7	2H	99	VAL	2.3
35	1d	88	VAL	2.3
50	2s	45	VAL	2.3
40	2i	33	PHE	2.3
45	1n	5	ALA	2.3
1	1A	885	C	2.3
1	1A	2123	G	2.3
1	1A	2124	G	2.3
1	1A	2165	G	2.3
1	2A	11	G	2.3
1	2A	277	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	2A	2207	G	2.3
32	1a	148	G	2.3
32	2a	1019	C	2.3
41	2j	87	THR	2.3
38	2g	151	TYR	2.3
20	2Y	62	GLU	2.3
34	2c	90	GLU	2.3
13	2R	68	ARG	2.3
36	2e	18	ARG	2.3
39	2h	91	ARG	2.3
44	2m	99	ARG	2.3
32	1a	1035	A	2.3
33	2b	14	GLY	2.3
33	2b	228	GLY	2.3
33	1b	11	LEU	2.3
14	2S	29	PHE	2.3
33	2b	127	ILE	2.2
44	2m	33	ALA	2.2
51	2t	97	ALA	2.2
40	2i	113	LYS	2.2
41	1j	86	MET	2.2
44	2m	31	LYS	2.2
1	2A	2161	C	2.2
1	1A	1176	G	2.2
1	1A	2116	G	2.2
1	1A	2147	G	2.2
1	2A	545	G	2.2
32	1a	1030(A)	G	2.2
8	2I	82	ARG	2.2
51	2t	8	ARG	2.2
21	2Z	159	PRO	2.2
47	1p	41	PRO	2.2
12	1Q	61	GLY	2.2
34	2c	47	LEU	2.2
37	2f	6	VAL	2.2
41	1j	8	LEU	2.2
45	2n	25	VAL	2.2
40	2i	59	PHE	2.2
42	2k	124	LYS	2.2
47	1p	3	LYS	2.2
39	2h	135	CYS	2.2
40	1i	7	THR	2.2

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Mol	Chain	Res	Type	RSRZ
40	2i	114	TYR	2.2
12	2Q	56	ARG	2.2
41	1j	5	ARG	2.2
45	2n	29	ARG	2.2
51	1t	17	ARG	2.2
46	1o	19	PRO	2.2
14	2S	31	SER	2.2
1	2A	2187	G	2.2
26	24	9	LEU	2.2
32	1a	1036	G	2.2
32	2a	1355	G	2.2
40	2i	72	GLY	2.2
47	1p	49	LEU	2.2
29	17	46	VAL	2.2
34	1c	195	VAL	2.2
43	1l	126	LYS	2.2
33	2b	83	MET	2.2
43	1l	7	ILE	2.2
8	2I	55	ALA	2.2
21	2Z	7	ALA	2.2
34	2c	129	ALA	2.2
35	1d	111	ALA	2.2
36	2e	95	ALA	2.2
41	1j	32	ALA	2.2
32	1a	949	A	2.2
32	1a	1287	A	2.2
34	1c	67	THR	2.2
29	17	47	ARG	2.2
34	1c	79	ARG	2.2
34	2c	79	ARG	2.2
41	2j	28	ARG	2.2
26	24	25	TYR	2.2
6	1G	3	LEU	2.2
14	2S	48	LEU	2.2
20	2Y	46	LYS	2.2
35	1d	166	LYS	2.2
37	1f	21	LEU	2.2
37	2f	45	LEU	2.2
48	1q	99	SER	2.2
50	2s	4	SER	2.2
21	2Z	139	VAL	2.2
26	24	50	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	1A	2163	C	2.2
1	2A	2107	C	2.2
1	2A	2185	C	2.2
6	1G	80	PHE	2.2
21	2Z	136	PHE	2.2
32	2a	1043	C	2.2
44	2m	78	ILE	2.2
47	1p	36	ILE	2.2
34	2c	149	ALA	2.2
1	2A	2106	G	2.2
1	2A	2151	G	2.2
1	2A	2751	G	2.2
32	1a	1353	G	2.2
32	2a	631	G	2.2
32	2a	1173	G	2.2
36	2e	81	GLU	2.2
22	20	10	THR	2.2
26	14	18	CYS	2.2
36	2e	25	ARG	2.2
39	2h	122	ARG	2.2
1	2A	2171	A	2.2
32	2a	1252	A	2.2
40	2i	36	TYR	2.2
29	17	48	LYS	2.2
41	1j	7	LYS	2.2
11	1P	105	LEU	2.2
33	1b	221	LEU	2.2
33	2b	196	LEU	2.2
34	1c	52	LEU	2.2
40	2i	50	LEU	2.2
50	1s	20	LEU	2.2
6	2G	126	ASP	2.2
50	1s	13	ASP	2.2
6	2G	15	VAL	2.2
34	1c	207	VAL	2.2
38	2g	153	HIS	2.2
40	2i	65	VAL	2.2
45	2n	60	SER	2.2
20	2Y	60	PHE	2.2
6	2G	46	ALA	2.1
40	1i	94	ALA	2.1
51	1t	94	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	1A	2128	C	2.1
32	2a	1029	C	2.1
51	1t	80	ARG	2.1
1	1A	2154	G	2.1
32	1a	181	G	2.1
32	2a	1356	G	2.1
41	1j	39	PRO	2.1
34	1c	135	LYS	2.1
50	2s	53	ASN	2.1
44	2m	21	TYR	2.1
29	27	1	MET	2.1
33	2b	98	LEU	2.1
50	2s	5	LEU	2.1
1	1A	278	A	2.1
1	1A	529	A	2.1
1	1A	1098	A	2.1
1	2A	887	A	2.1
7	2H	22	GLY	2.1
31	29	37	GLY	2.1
32	1a	143	A	2.1
32	1a	1492	A	2.1
34	1c	185	GLY	2.1
35	1d	2	GLY	2.1
35	2d	183	GLY	2.1
42	2k	90	GLY	2.1
51	1t	102	GLY	2.1
1	1A	2109	U	2.1
21	2Z	171	ILE	2.1
32	2a	1446	U	2.1
34	1c	76	VAL	2.1
34	2c	152	ILE	2.1
37	1f	40	VAL	2.1
41	1j	74	ILE	2.1
42	2k	105	VAL	2.1
44	2m	92	HIS	2.1
40	1i	126	SER	2.1
5	2F	139	PHE	2.1
6	2G	117	PHE	2.1
8	2I	36	ALA	2.1
34	2c	187	ALA	2.1
51	2t	94	ALA	2.1
21	2Z	2	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
33	1b	126	GLU	2.1
51	1t	8	ARG	2.1
22	20	43	THR	2.1
33	2b	67	THR	2.1
44	2m	97	PRO	2.1
1	1A	2794	C	2.1
1	2A	1509	C	2.1
1	2A	2794	C	2.1
32	1a	1533	C	2.1
32	2a	1030	C	2.1
6	2G	146	TYR	2.1
11	1P	100	LEU	2.1
40	2i	79	LEU	2.1
47	1p	38	TYR	2.1
14	2S	96	GLY	2.1
26	24	54	GLY	2.1
1	1A	2181	G	2.1
1	2A	171	G	2.1
32	1a	1021	G	2.1
32	2a	1030(C)	G	2.1
45	2n	42	ILE	2.1
23	11	2	SER	2.1
33	2b	152	PHE	2.1
49	2r	43	PHE	2.1
1	1A	887	A	2.1
2	2B	8	U	2.1
32	1a	1040	U	2.1
32	2a	1001	A	2.1
32	2a	1110	A	2.1
21	1Z	119	GLU	2.1
32	2a	1126	U	2.1
40	1i	55	ALA	2.1
35	1d	173	TRP	2.1
50	2s	3	ARG	2.1
48	2q	14	LYS	2.1
7	2H	39	PRO	2.1
41	1j	77	PRO	2.1
44	2m	113	PRO	2.1
6	2G	155	MET	2.1
21	1Z	1	MET	2.1
47	1p	82	GLN	2.1
40	1i	50	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
44	2m	81	LEU	2.1
45	2n	40	CYS	2.1
34	1c	48	TYR	2.1
35	2d	87	GLY	2.1
38	1g	82	GLY	2.1
45	2n	34	TYR	2.1
45	2n	51	GLY	2.1
50	1s	14	HIS	2.1
51	1t	101	GLY	2.1
1	1A	2137	C	2.1
1	2A	2136	C	2.1
6	2G	52	ILE	2.1
14	2S	46	VAL	2.1
24	22	63	VAL	2.1
32	2a	979	C	2.1
32	2a	999	C	2.1
33	2b	71	VAL	2.1
36	2e	109	ILE	2.1
50	2s	19	VAL	2.1
4	1E	73	GLU	2.1
33	2b	144	ARG	2.1
44	2m	75	ALA	2.1
45	2n	12	ARG	2.1
1	2A	2100	G	2.1
16	2U	51	LYS	2.1
32	2a	1017	G	2.1
32	2a	1286	A	2.1
34	2c	27	LYS	2.1
5	1F	14	PRO	2.1
33	1b	131	PRO	2.1
34	1c	142	MET	2.1
11	2P	45	LEU	2.1
33	2b	145	LEU	2.1
36	2e	12	LEU	2.1
40	1i	102	LEU	2.1
41	1j	90	LEU	2.1
47	2p	6	LEU	2.1
51	2t	10	LEU	2.1
33	1b	72	GLY	2.1
33	2b	18	GLY	2.1
35	2d	180	GLY	2.1
40	1i	67	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
50	2s	8	GLY	2.1
21	2Z	99	TYR	2.1
40	2i	125	TYR	2.1
42	2k	50	TYR	2.1
47	1p	17	TYR	2.1
7	2H	45	VAL	2.1
33	1b	7	VAL	2.1
45	2n	18	VAL	2.1
48	1q	23	VAL	2.1
6	2G	128	ARG	2.0
41	1j	29	ARG	2.0
42	1k	68	ALA	2.0
44	2m	67	GLU	2.0
44	2m	88	ARG	2.0
4	1E	204	ALA	2.0
38	2g	7	ALA	2.0
1	1A	34	C	2.0
1	2A	2129	C	2.0
1	2A	2146	C	2.0
12	2Q	22	LYS	2.0
32	2a	1137	C	2.0
32	2a	1192	C	2.0
33	2b	74	LYS	2.0
36	2e	92	LYS	2.0
46	2o	48	LYS	2.0
33	1b	125	PRO	2.0
40	2i	90	PRO	2.0
50	2s	76	PRO	2.0
32	2a	1358	U	2.0
33	2b	213	LEU	2.0
35	2d	162	LEU	2.0
39	2h	70	GLN	2.0
49	1r	76	LEU	2.0
1	1A	229	A	2.0
1	1A	1069	A	2.0
1	1A	2162	G	2.0
1	1A	2166	G	2.0
1	1A	2168	G	2.0
1	1A	2207	G	2.0
1	2A	100	G	2.0
2	2B	53	A	2.0
32	1a	532	A	2.0

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Mol	Chain	Res	Type	RSRZ
32	1a	975	A	2.0
32	2a	1024	G	2.0
32	2a	1031	G	2.0
32	2a	1250	A	2.0
32	2a	1310	G	2.0
33	2b	16	HIS	2.0
33	1b	222	ILE	2.0
50	2s	49	ILE	2.0
51	1t	100	ILE	2.0
14	2S	92	TYR	2.0
34	1c	201	TYR	2.0
6	2G	33	ARG	2.0
7	1H	3	ARG	2.0
21	2Z	122	ARG	2.0
39	2h	84	ARG	2.0
41	2j	79	ARG	2.0
45	2n	3	ARG	2.0
45	2n	46	GLU	2.0
47	1p	80	PHE	2.0
4	2E	204	ALA	2.0
8	2I	53	ALA	2.0
8	2I	115	ALA	2.0
20	1Y	107	ASP	2.0
33	1b	34	ALA	2.0
33	1b	171	ALA	2.0
38	1g	145	ALA	2.0
40	2i	94	ALA	2.0
34	2c	192	THR	2.0
45	2n	61	TRP	2.0
47	1p	67	THR	2.0
1	1A	1079	C	2.0
1	2A	888	C	2.0
1	2A	1118	C	2.0
14	2S	56	LEU	2.0
17	2V	38	LEU	2.0
32	2a	1214	C	2.0
40	1i	87	GLN	2.0
41	2j	40	LEU	2.0
48	1q	98	LEU	2.0
48	2q	98	LEU	2.0
51	1t	13	LEU	2.0
1	2A	271(K)	U	2.0

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Mol	Chain	Res	Type	RSRZ
2	2B	1	U	2.0
21	2Z	143	GLY	2.0
26	24	64	GLY	2.0
1	1A	548	A	2.0
2	2B	29	A	2.0
15	1T	115	ARG	2.0
32	1a	152	A	2.0
32	2a	968	A	2.0
33	1b	230	VAL	2.0
33	2b	7	VAL	2.0
33	2b	23	ARG	2.0
33	2b	130	ARG	2.0
34	1c	85	ARG	2.0
34	1c	99	VAL	2.0
34	1c	106	VAL	2.0
36	2e	24	ARG	2.0
39	2h	97	VAL	2.0
47	1p	75	ARG	2.0
50	2s	58	VAL	2.0
50	2s	52	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	2MG	2a	1207	24/25	0.83	0.13	72,84,90,96	0
54	PSU	2x	55	20/21	0.85	0.13	68,76,80,83	0
1	5MU	2A	1915	21/22	0.88	0.10	64,68,74,78	0
54	5MC	2x	32	21/22	0.89	0.14	68,73,77,85	0
32	M2G	2a	966	25/26	0.89	0.15	60,66,80,86	0
32	PSU	2a	516	20/21	0.90	0.10	66,76,86,86	0
32	5MC	2a	967	21/22	0.91	0.13	63,70,78,83	0
54	4SU	2x	8	20/21	0.91	0.12	69,75,80,82	0
54	PSU	1x	55	20/21	0.92	0.08	49,53,62,66	0
1	PSU	2A	1911	20/21	0.92	0.10	57,61,75,76	0
54	5MU	2x	54	21/22	0.92	0.10	70,75,81,84	0
32	G7M	2a	527	24/25	0.92	0.11	63,68,73,74	0
1	PSU	2A	1917	20/21	0.93	0.10	52,60,67,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
43	0TD	2l	92	10/11	0.93	0.10	60,63,64,77	0
54	5MU	1x	54	21/22	0.93	0.09	53,58,64,70	0
32	PSU	1a	516	20/21	0.93	0.08	60,67,70,71	0
32	2MG	1a	1207	24/25	0.93	0.11	65,76,80,83	0
54	5MC	1x	32	21/22	0.93	0.11	43,52,59,64	0
1	OMC	2A	1920	21/22	0.94	0.10	51,56,60,64	0
32	G7M	1a	527	24/25	0.94	0.11	45,50,59,65	0
1	5MU	1A	1915	21/22	0.94	0.08	49,53,63,66	0
32	5MC	2a	1400	21/22	0.94	0.10	64,70,73,75	0
32	4OC	2a	1402	22/23	0.94	0.09	54,60,66,70	0
32	M2G	1a	966	25/26	0.95	0.10	41,52,61,66	0
1	PSU	1A	1911	20/21	0.95	0.09	38,46,51,54	0
32	5MC	2a	1404	21/22	0.95	0.09	48,52,57,62	0
43	0TD	1l	92	10/11	0.95	0.10	49,54,59,67	0
1	2MA	2A	2503	23/24	0.96	0.09	20,33,38,42	0
32	5MC	1a	1400	21/22	0.96	0.09	44,50,53,54	0
32	5MC	2a	1407	21/22	0.96	0.08	45,49,53,59	0
32	UR3	2a	1498	21/22	0.96	0.10	44,53,58,63	0
32	MA6	2a	1518	24/25	0.96	0.09	46,56,62,65	0
1	PSU	1A	1917	20/21	0.96	0.07	39,50,57,60	0
54	4SU	1x	8	20/21	0.96	0.07	47,56,64,71	0
32	5MC	1a	967	21/22	0.96	0.08	44,52,63,66	0
1	5MC	1A	1942	21/22	0.96	0.08	36,40,42,50	0
1	5MC	2A	1962	21/22	0.96	0.08	32,42,46,61	0
1	OMU	1A	2552	21/22	0.97	0.07	21,26,31,35	0
32	5MC	1a	1404	21/22	0.97	0.07	28,35,41,42	0
32	MA6	1a	1518	24/25	0.97	0.07	34,39,43,44	0
32	MA6	2a	1519	24/25	0.97	0.10	46,56,60,66	0
1	5MU	2A	1939	21/22	0.97	0.07	29,34,38,40	0
1	5MC	2A	1942	21/22	0.97	0.07	42,47,52,59	0
32	MA6	1a	1519	24/25	0.97	0.10	34,40,47,50	0
1	OMG	2A	2251	24/25	0.97	0.08	31,35,41,42	0
1	OMC	1A	1920	21/22	0.97	0.08	34,43,47,51	0
1	PSU	2A	2605	20/21	0.98	0.06	28,35,38,39	0
1	OMG	1A	2251	24/25	0.98	0.07	16,23,27,27	0
32	4OC	1a	1402	22/23	0.98	0.07	39,42,48,58	0
1	5MU	1A	1939	21/22	0.98	0.05	20,24,29,32	0
32	5MC	1a	1407	21/22	0.98	0.07	34,38,42,44	0
32	UR3	1a	1498	21/22	0.98	0.05	32,37,41,43	0
1	PSU	1A	2605	20/21	0.98	0.06	20,24,28,33	0
1	5MC	1A	1962	21/22	0.98	0.07	25,33,38,38	0
1	OMU	2A	2552	21/22	0.98	0.06	29,36,39,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	2MA	1A	2503	23/24	0.99	0.05	16,20,24,28	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1647	1/1	0.39	0.47	81,81,81,81	0
55	MG	2a	1685	1/1	0.43	0.37	81,81,81,81	0
55	MG	2B	203	1/1	0.46	0.38	78,78,78,78	0
55	MG	2B	204	1/1	0.53	0.18	93,93,93,93	0
55	MG	2A	3085	1/1	0.53	0.30	82,82,82,82	0
55	MG	2a	1719	1/1	0.53	0.15	109,109,109,109	0
55	MG	18	108	1/1	0.57	0.30	72,72,72,72	0
55	MG	2A	3433	1/1	0.58	0.30	66,66,66,66	0
55	MG	2A	3580	1/1	0.58	0.16	74,74,74,74	0
55	MG	1A	3329	1/1	0.59	0.23	63,63,63,63	0
55	MG	1A	3733	1/1	0.60	0.16	64,64,64,64	0
55	MG	2A	3148	1/1	0.60	0.25	80,80,80,80	0
55	MG	1B	231	1/1	0.61	0.26	77,77,77,77	0
55	MG	1A	4041	1/1	0.62	0.27	68,68,68,68	0
55	MG	1W	207	1/1	0.63	0.47	47,47,47,47	0
55	MG	1a	1766	1/1	0.64	0.15	74,74,74,74	0
55	MG	2a	1708	1/1	0.65	0.44	72,72,72,72	0
55	MG	1A	3778	1/1	0.65	0.26	50,50,50,50	0
55	MG	1a	1796	1/1	0.66	0.31	85,85,85,85	0
55	MG	1A	3462	1/1	0.66	0.17	69,69,69,69	0
55	MG	2a	1763	1/1	0.66	0.25	77,77,77,77	0
55	MG	1a	1786	1/1	0.67	0.23	64,64,64,64	0
55	MG	1A	4024	1/1	0.67	0.23	73,73,73,73	0
55	MG	2a	1689	1/1	0.68	0.32	79,79,79,79	0
55	MG	2B	213	1/1	0.68	0.22	75,75,75,75	0
55	MG	2B	217	1/1	0.69	0.27	77,77,77,77	0
55	MG	1A	3984	1/1	0.69	0.22	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3704	1/1	0.69	0.26	76,76,76,76	0
55	MG	1A	3297	1/1	0.69	0.20	68,68,68,68	0
55	MG	1e	201	1/1	0.69	0.16	76,76,76,76	0
55	MG	2A	3551	1/1	0.69	0.21	70,70,70,70	0
55	MG	2A	3517	1/1	0.70	0.27	77,77,77,77	0
55	MG	2A	3081	1/1	0.70	0.38	80,80,80,80	0
55	MG	2A	3570	1/1	0.70	0.25	78,78,78,78	0
55	MG	1B	232	1/1	0.70	0.16	79,79,79,79	0
55	MG	2a	1755	1/1	0.70	0.23	65,65,65,65	0
55	MG	2A	3688	1/1	0.70	0.25	63,63,63,63	0
55	MG	1A	3916	1/1	0.71	0.18	79,79,79,79	0
55	MG	2A	3716	1/1	0.71	0.16	67,67,67,67	0
55	MG	1A	3514	1/1	0.71	0.14	85,85,85,85	0
55	MG	2A	3208	1/1	0.71	0.25	65,65,65,65	0
55	MG	2A	3468	1/1	0.72	0.21	61,61,61,61	0
55	MG	2A	3558	1/1	0.72	0.21	72,72,72,72	0
55	MG	2A	3483	1/1	0.72	0.15	70,70,70,70	0
55	MG	2a	1748	1/1	0.72	0.28	73,73,73,73	0
55	MG	2a	1604	1/1	0.72	0.17	71,71,71,71	0
55	MG	2a	1761	1/1	0.72	0.42	87,87,87,87	0
55	MG	2A	3194	1/1	0.72	0.29	74,74,74,74	0
55	MG	2A	3509	1/1	0.73	0.26	72,72,72,72	0
55	MG	2a	1752	1/1	0.73	0.35	65,65,65,65	0
55	MG	1a	1779	1/1	0.73	0.24	69,69,69,69	0
55	MG	1A	3309	1/1	0.73	0.17	54,54,54,54	0
55	MG	2A	3682	1/1	0.73	0.29	77,77,77,77	0
55	MG	2a	1786	1/1	0.73	0.24	76,76,76,76	0
55	MG	1A	3525	1/1	0.74	0.35	67,67,67,67	0
55	MG	1A	3392	1/1	0.74	0.10	64,64,64,64	0
55	MG	1A	3023	1/1	0.74	0.30	66,66,66,66	0
55	MG	1A	3783	1/1	0.74	0.21	56,56,56,56	0
55	MG	1A	3340	1/1	0.74	0.18	59,59,59,59	0
55	MG	1A	3950	1/1	0.74	0.13	74,74,74,74	0
55	MG	2a	1759	1/1	0.74	0.24	78,78,78,78	0
55	MG	2A	3475	1/1	0.74	0.24	69,69,69,69	0
55	MG	2a	1673	1/1	0.74	0.33	70,70,70,70	0
55	MG	1A	3954	1/1	0.74	0.18	76,76,76,76	0
55	MG	1A	3471	1/1	0.75	0.36	83,83,83,83	0
55	MG	2A	3080	1/1	0.75	0.35	73,73,73,73	0
55	MG	1A	3252	1/1	0.75	0.25	64,64,64,64	0
55	MG	2A	3358	1/1	0.75	0.20	71,71,71,71	0
55	MG	2a	1753	1/1	0.75	0.31	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3510	1/1	0.75	0.32	60,60,60,60	0
55	MG	2a	1646	1/1	0.75	0.24	68,68,68,68	0
55	MG	2A	3692	1/1	0.75	0.21	64,64,64,64	0
55	MG	1A	3278	1/1	0.75	0.12	62,62,62,62	0
55	MG	2A	3445	1/1	0.75	0.19	62,62,62,62	0
55	MG	1A	4028	1/1	0.76	0.18	58,58,58,58	0
55	MG	1a	1625	1/1	0.76	0.28	71,71,71,71	0
55	MG	1a	1627	1/1	0.76	0.29	78,78,78,78	0
55	MG	1A	3102	1/1	0.76	0.24	57,57,57,57	0
55	MG	2a	1691	1/1	0.76	0.29	83,83,83,83	0
55	MG	1a	1655	1/1	0.76	0.18	81,81,81,81	0
55	MG	2A	3136	1/1	0.76	0.21	74,74,74,74	0
55	MG	1a	1659	1/1	0.76	0.20	64,64,64,64	0
55	MG	1A	3526	1/1	0.76	0.21	55,55,55,55	0
55	MG	1A	3817	1/1	0.76	0.16	27,27,27,27	0
55	MG	2B	214	1/1	0.76	0.17	70,70,70,70	0
55	MG	2A	3337	1/1	0.76	0.26	71,71,71,71	0
55	MG	1A	3388	1/1	0.76	0.19	70,70,70,70	0
55	MG	2a	1608	1/1	0.76	0.21	75,75,75,75	0
55	MG	2a	1633	1/1	0.76	0.23	76,76,76,76	0
55	MG	2A	3496	1/1	0.77	0.14	69,69,69,69	0
55	MG	2A	3501	1/1	0.77	0.20	56,56,56,56	0
55	MG	1A	4042	1/1	0.77	0.23	61,61,61,61	0
55	MG	1A	4044	1/1	0.77	0.14	73,73,73,73	0
55	MG	2a	1606	1/1	0.77	0.17	62,62,62,62	0
55	MG	2A	3513	1/1	0.77	0.15	64,64,64,64	0
55	MG	2A	3178	1/1	0.77	0.17	63,63,63,63	0
55	MG	1A	3368	1/1	0.77	0.39	70,70,70,70	0
55	MG	2A	3556	1/1	0.77	0.16	78,78,78,78	0
55	MG	1A	3371	1/1	0.77	0.23	57,57,57,57	0
55	MG	2A	3559	1/1	0.77	0.15	59,59,59,59	0
55	MG	2A	3327	1/1	0.77	0.20	58,58,58,58	0
55	MG	1F	307	1/1	0.77	0.17	59,59,59,59	0
55	MG	2A	3602	1/1	0.77	0.13	79,79,79,79	0
55	MG	2a	1739	1/1	0.77	0.20	73,73,73,73	0
55	MG	2A	3604	1/1	0.77	0.19	61,61,61,61	0
55	MG	1A	3991	1/1	0.77	0.38	63,63,63,63	0
55	MG	1Y	201	1/1	0.77	0.12	64,64,64,64	0
55	MG	14	101	1/1	0.77	0.16	81,81,81,81	0
55	MG	1A	3632	1/1	0.77	0.18	58,58,58,58	0
55	MG	2A	3472	1/1	0.77	0.13	87,87,87,87	0
55	MG	1A	3680	1/1	0.77	0.19	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3445	1/1	0.77	0.21	63,63,63,63	0
55	MG	2q	202	1/1	0.77	0.12	81,81,81,81	0
55	MG	2x	102	1/1	0.77	0.29	71,71,71,71	0
55	MG	2a	1683	1/1	0.78	0.20	75,75,75,75	0
55	MG	2A	3380	1/1	0.78	0.22	53,53,53,53	0
55	MG	1A	3852	1/1	0.78	0.34	80,80,80,80	0
55	MG	2A	3186	1/1	0.78	0.11	60,60,60,60	0
55	MG	2B	205	1/1	0.78	0.24	66,66,66,66	0
55	MG	2B	206	1/1	0.78	0.28	68,68,68,68	0
55	MG	1A	3908	1/1	0.78	0.20	74,74,74,74	0
55	MG	2a	1745	1/1	0.78	0.16	69,69,69,69	0
55	MG	1a	1785	1/1	0.78	0.20	75,75,75,75	0
55	MG	2A	3651	1/1	0.78	0.25	74,74,74,74	0
55	MG	2A	3532	1/1	0.78	0.11	66,66,66,66	0
55	MG	2A	3686	1/1	0.78	0.17	59,59,59,59	0
55	MG	1A	3420	1/1	0.78	0.18	68,68,68,68	0
55	MG	2a	1620	1/1	0.78	0.31	67,67,67,67	0
55	MG	2a	1762	1/1	0.78	0.15	81,81,81,81	0
55	MG	1B	226	1/1	0.78	0.12	62,62,62,62	0
55	MG	2a	1635	1/1	0.78	0.18	71,71,71,71	0
55	MG	2A	3702	1/1	0.78	0.22	58,58,58,58	0
55	MG	1a	1797	1/1	0.78	0.39	84,84,84,84	0
55	MG	2A	3041	1/1	0.79	0.27	60,60,60,60	0
55	MG	2A	3403	1/1	0.79	0.16	55,55,55,55	0
55	MG	2A	3055	1/1	0.79	0.33	75,75,75,75	0
55	MG	2A	3512	1/1	0.79	0.12	65,65,65,65	0
55	MG	1A	3513	1/1	0.79	0.08	74,74,74,74	0
55	MG	2A	3608	1/1	0.79	0.14	71,71,71,71	0
55	MG	1B	227	1/1	0.79	0.26	69,69,69,69	0
55	MG	2A	3667	1/1	0.79	0.14	67,67,67,67	0
55	MG	2A	3326	1/1	0.79	0.34	67,67,67,67	0
55	MG	1A	3372	1/1	0.79	0.27	65,65,65,65	0
55	MG	2a	1703	1/1	0.79	0.26	65,65,65,65	0
55	MG	1x	108	1/1	0.79	0.11	61,61,61,61	0
55	MG	2A	3036	1/1	0.79	0.38	67,67,67,67	0
55	MG	2x	103	1/1	0.79	0.39	75,75,75,75	0
55	MG	1a	1713	1/1	0.80	0.17	71,71,71,71	0
55	MG	2a	1682	1/1	0.80	0.20	65,65,65,65	0
55	MG	1A	3517	1/1	0.80	0.40	68,68,68,68	0
55	MG	1A	3413	1/1	0.80	0.11	67,67,67,67	0
55	MG	2A	3341	1/1	0.80	0.17	62,62,62,62	0
55	MG	2A	3714	1/1	0.80	0.17	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3957	1/1	0.80	0.15	69,69,69,69	0
55	MG	1A	3373	1/1	0.80	0.19	64,64,64,64	0
55	MG	1A	3565	1/1	0.80	0.20	61,61,61,61	0
55	MG	2a	1736	1/1	0.80	0.38	80,80,80,80	0
55	MG	1A	3614	1/1	0.80	0.24	64,64,64,64	0
55	MG	1A	3428	1/1	0.80	0.25	49,49,49,49	0
55	MG	2A	3560	1/1	0.80	0.20	47,47,47,47	0
55	MG	2A	3462	1/1	0.80	0.12	70,70,70,70	0
55	MG	1A	3401	1/1	0.80	0.15	58,58,58,58	0
55	MG	2A	3004	1/1	0.80	0.31	67,67,67,67	0
55	MG	1a	1692	1/1	0.80	0.15	71,71,71,71	0
55	MG	2A	3477	1/1	0.80	0.19	70,70,70,70	0
55	MG	2A	3237	1/1	0.80	0.24	62,62,62,62	0
55	MG	2A	3299	1/1	0.80	0.33	64,64,64,64	0
55	MG	2a	1770	1/1	0.80	0.20	55,55,55,55	0
55	MG	2A	3304	1/1	0.80	0.34	76,76,76,76	0
55	MG	2a	1639	1/1	0.80	0.09	68,68,68,68	0
55	MG	2A	3305	1/1	0.80	0.30	55,55,55,55	0
55	MG	2a	1650	1/1	0.80	0.36	65,65,65,65	0
55	MG	2a	1638	1/1	0.81	0.21	54,54,54,54	0
55	MG	2A	3231	1/1	0.81	0.30	75,75,75,75	0
55	MG	2A	3669	1/1	0.81	0.14	60,60,60,60	0
55	MG	1A	4025	1/1	0.81	0.30	62,62,62,62	0
55	MG	1A	3887	1/1	0.81	0.13	65,65,65,65	0
55	MG	1A	3382	1/1	0.81	0.12	71,71,71,71	0
55	MG	2A	3689	1/1	0.81	0.23	69,69,69,69	0
55	MG	1A	3742	1/1	0.81	0.15	45,45,45,45	0
55	MG	2A	3697	1/1	0.81	0.24	60,60,60,60	0
55	MG	2A	3323	1/1	0.81	0.23	65,65,65,65	0
55	MG	1a	1637	1/1	0.81	0.43	69,69,69,69	0
55	MG	1A	3770	1/1	0.81	0.31	66,66,66,66	0
55	MG	1A	3104	1/1	0.81	0.15	68,68,68,68	0
55	MG	2a	1726	1/1	0.81	0.20	69,69,69,69	0
55	MG	2B	202	1/1	0.81	0.15	66,66,66,66	0
55	MG	1A	3639	1/1	0.81	0.18	60,60,60,60	0
55	MG	1A	3967	1/1	0.81	0.17	70,70,70,70	0
55	MG	1a	1698	1/1	0.81	0.22	66,66,66,66	0
55	MG	1a	1709	1/1	0.81	0.21	66,66,66,66	0
55	MG	1A	3970	1/1	0.81	0.14	45,45,45,45	0
55	MG	2A	3565	1/1	0.81	0.38	48,48,48,48	0
55	MG	2a	1756	1/1	0.81	0.19	68,68,68,68	0
55	MG	1A	3407	1/1	0.81	0.10	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2D	302	1/1	0.81	0.20	61,61,61,61	0
55	MG	1A	3829	1/1	0.81	0.28	81,81,81,81	0
55	MG	1A	3730	1/1	0.81	0.14	17,17,17,17	0
55	MG	1Z	302	1/1	0.81	0.11	57,57,57,57	0
55	MG	1a	1794	1/1	0.81	0.26	78,78,78,78	0
55	MG	2a	1628	1/1	0.81	0.38	69,69,69,69	0
55	MG	2A	3612	1/1	0.81	0.14	54,54,54,54	0
55	MG	2A	3216	1/1	0.81	0.17	74,74,74,74	0
55	MG	2A	3294	1/1	0.82	0.28	63,63,63,63	0
55	MG	2A	3487	1/1	0.82	0.17	60,60,60,60	0
55	MG	2A	3298	1/1	0.82	0.22	64,64,64,64	0
55	MG	2a	1655	1/1	0.82	0.16	71,71,71,71	0
55	MG	1G	204	1/1	0.82	0.12	61,61,61,61	0
55	MG	1N	205	1/1	0.82	0.25	54,54,54,54	0
55	MG	1a	1772	1/1	0.82	0.23	71,71,71,71	0
55	MG	1T	202	1/1	0.82	0.21	57,57,57,57	0
55	MG	1A	3451	1/1	0.82	0.16	60,60,60,60	0
55	MG	1a	1650	1/1	0.82	0.22	63,63,63,63	0
55	MG	2A	3518	1/1	0.82	0.14	71,71,71,71	0
55	MG	2A	3526	1/1	0.82	0.21	69,69,69,69	0
55	MG	2A	3527	1/1	0.82	0.11	54,54,54,54	0
55	MG	1A	3983	1/1	0.82	0.22	67,67,67,67	0
55	MG	2A	3173	1/1	0.82	0.29	61,61,61,61	0
55	MG	1A	3835	1/1	0.82	0.14	53,53,53,53	0
55	MG	1a	1664	1/1	0.82	0.20	70,70,70,70	0
55	MG	2B	211	1/1	0.82	0.15	76,76,76,76	0
55	MG	2A	3395	1/1	0.82	0.15	55,55,55,55	0
55	MG	1A	3204	1/1	0.82	0.20	65,65,65,65	0
55	MG	2A	3197	1/1	0.82	0.25	60,60,60,60	0
55	MG	2A	3198	1/1	0.82	0.15	67,67,67,67	0
55	MG	2A	3204	1/1	0.82	0.17	67,67,67,67	0
55	MG	2A	3584	1/1	0.82	0.16	54,54,54,54	0
55	MG	2a	1607	1/1	0.82	0.46	75,75,75,75	0
55	MG	1A	3923	1/1	0.82	0.11	29,29,29,29	0
55	MG	1a	1604	1/1	0.82	0.17	64,64,64,64	0
55	MG	2a	1779	1/1	0.82	0.23	71,71,71,71	0
55	MG	2A	3474	1/1	0.82	0.17	70,70,70,70	0
55	MG	2j	201	1/1	0.82	0.09	86,86,86,86	0
55	MG	2q	201	1/1	0.82	0.24	78,78,78,78	0
55	MG	2A	3014	1/1	0.82	0.39	65,65,65,65	0
55	MG	1a	1711	1/1	0.82	0.40	69,69,69,69	0
55	MG	2A	3481	1/1	0.82	0.11	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3315	1/1	0.83	0.30	79,79,79,79	0
55	MG	2A	3319	1/1	0.83	0.22	59,59,59,59	0
55	MG	1A	3328	1/1	0.83	0.15	61,61,61,61	0
55	MG	2a	1627	1/1	0.83	0.43	75,75,75,75	0
55	MG	1A	3618	1/1	0.83	0.26	63,63,63,63	0
55	MG	1A	4018	1/1	0.83	0.18	76,76,76,76	0
55	MG	2A	3577	1/1	0.83	0.21	55,55,55,55	0
55	MG	2a	1636	1/1	0.83	0.10	72,72,72,72	0
55	MG	1A	4020	1/1	0.83	0.31	75,75,75,75	0
55	MG	2A	3582	1/1	0.83	0.18	67,67,67,67	0
55	MG	1A	3839	1/1	0.83	0.32	28,28,28,28	0
55	MG	1A	3206	1/1	0.83	0.10	44,44,44,44	0
55	MG	1A	3479	1/1	0.83	0.24	60,60,60,60	0
55	MG	2a	1663	1/1	0.83	0.24	54,54,54,54	0
55	MG	1A	3900	1/1	0.83	0.17	46,46,46,46	0
55	MG	2A	3609	1/1	0.83	0.13	77,77,77,77	0
55	MG	1A	3658	1/1	0.83	0.23	66,66,66,66	0
55	MG	2A	3425	1/1	0.83	0.29	61,61,61,61	0
55	MG	1a	1654	1/1	0.83	0.53	72,72,72,72	0
55	MG	1A	3337	1/1	0.83	0.41	61,61,61,61	0
55	MG	2a	1696	1/1	0.83	0.36	62,62,62,62	0
55	MG	1A	3257	1/1	0.83	0.14	48,48,48,48	0
55	MG	1a	1661	1/1	0.83	0.24	71,71,71,71	0
55	MG	1A	3937	1/1	0.83	0.10	73,73,73,73	0
55	MG	1a	1667	1/1	0.83	0.20	52,52,52,52	0
55	MG	1a	1676	1/1	0.83	0.35	70,70,70,70	0
55	MG	1a	1683	1/1	0.83	0.29	73,73,73,73	0
55	MG	2A	3701	1/1	0.83	0.13	62,62,62,62	0
55	MG	1A	3386	1/1	0.83	0.23	64,64,64,64	0
55	MG	1A	3430	1/1	0.83	0.20	61,61,61,61	0
55	MG	1E	311	1/1	0.83	0.19	80,80,80,80	0
55	MG	1A	3347	1/1	0.83	0.23	77,77,77,77	0
55	MG	1A	3958	1/1	0.83	0.18	48,48,48,48	0
55	MG	1a	1735	1/1	0.83	0.11	69,69,69,69	0
55	MG	1A	3965	1/1	0.83	0.16	52,52,52,52	0
55	MG	1O	202	1/1	0.83	0.29	56,56,56,56	0
55	MG	2A	3245	1/1	0.83	0.30	74,74,74,74	0
55	MG	2A	3280	1/1	0.83	0.26	67,67,67,67	0
55	MG	2A	3284	1/1	0.83	0.23	44,44,44,44	0
55	MG	1a	1776	1/1	0.83	0.11	72,72,72,72	0
55	MG	1S	203	1/1	0.83	0.11	71,71,71,71	0
55	MG	1A	3272	1/1	0.83	0.25	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	27	103	1/1	0.83	0.10	56,56,56,56	0
55	MG	1A	3574	1/1	0.83	0.16	53,53,53,53	0
55	MG	1A	3582	1/1	0.83	0.12	55,55,55,55	0
55	MG	1A	3492	1/1	0.84	0.14	42,42,42,42	0
55	MG	1A	3575	1/1	0.84	0.16	75,75,75,75	0
55	MG	1A	3130	1/1	0.84	0.28	61,61,61,61	0
55	MG	1A	3241	1/1	0.84	0.25	59,59,59,59	0
55	MG	1N	203	1/1	0.84	0.12	52,52,52,52	0
55	MG	2A	3668	1/1	0.84	0.15	74,74,74,74	0
55	MG	1A	4021	1/1	0.84	0.19	96,96,96,96	0
55	MG	2a	1660	1/1	0.84	0.24	69,69,69,69	0
55	MG	1a	1660	1/1	0.84	0.28	56,56,56,56	0
55	MG	2A	3227	1/1	0.84	0.23	74,74,74,74	0
55	MG	2a	1677	1/1	0.84	0.27	70,70,70,70	0
55	MG	2A	3228	1/1	0.84	0.23	73,73,73,73	0
55	MG	2A	3230	1/1	0.84	0.20	57,57,57,57	0
55	MG	2A	3691	1/1	0.84	0.19	63,63,63,63	0
55	MG	1A	3780	1/1	0.84	0.11	65,65,65,65	0
55	MG	1A	3187	1/1	0.84	0.36	65,65,65,65	0
55	MG	2A	3242	1/1	0.84	0.16	71,71,71,71	0
55	MG	2a	1702	1/1	0.84	0.30	66,66,66,66	0
55	MG	1f	201	1/1	0.84	0.25	61,61,61,61	0
55	MG	2a	1706	1/1	0.84	0.24	56,56,56,56	0
55	MG	2A	3262	1/1	0.84	0.55	85,85,85,85	0
55	MG	2a	1716	1/1	0.84	0.13	79,79,79,79	0
55	MG	1x	101	1/1	0.84	0.30	75,75,75,75	0
55	MG	1x	107	1/1	0.84	0.20	67,67,67,67	0
55	MG	1A	3253	1/1	0.84	0.32	65,65,65,65	0
55	MG	1A	4034	1/1	0.84	0.12	63,63,63,63	0
55	MG	1a	1682	1/1	0.84	0.28	65,65,65,65	0
55	MG	1A	3365	1/1	0.84	0.17	61,61,61,61	0
55	MG	2a	1749	1/1	0.84	0.14	70,70,70,70	0
55	MG	1a	1684	1/1	0.84	0.31	65,65,65,65	0
55	MG	1A	3528	1/1	0.84	0.23	65,65,65,65	0
55	MG	1A	3666	1/1	0.84	0.18	53,53,53,53	0
55	MG	1A	3530	1/1	0.84	0.23	55,55,55,55	0
55	MG	2A	3082	1/1	0.84	0.19	63,63,63,63	0
55	MG	1A	3870	1/1	0.84	0.14	50,50,50,50	0
55	MG	2A	3108	1/1	0.84	0.18	52,52,52,52	0
55	MG	2a	1602	1/1	0.84	0.14	61,61,61,61	0
55	MG	1B	230	1/1	0.84	0.10	74,74,74,74	0
55	MG	2A	3350	1/1	0.84	0.16	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3138	1/1	0.84	0.21	68,68,68,68	0
55	MG	2e	201	1/1	0.84	0.13	79,79,79,79	0
55	MG	2f	202	1/1	0.84	0.20	81,81,81,81	0
55	MG	1A	3074	1/1	0.84	0.13	55,55,55,55	0
55	MG	2l	202	1/1	0.84	0.12	60,60,60,60	0
55	MG	1a	1746	1/1	0.84	0.09	54,54,54,54	0
55	MG	1a	1628	1/1	0.84	0.19	54,54,54,54	0
55	MG	2A	3603	1/1	0.84	0.14	48,48,48,48	0
55	MG	2A	3181	1/1	0.84	0.31	65,65,65,65	0
55	MG	2A	3324	1/1	0.85	0.12	68,68,68,68	0
55	MG	2A	3164	1/1	0.85	0.16	55,55,55,55	0
55	MG	2A	3574	1/1	0.85	0.14	54,54,54,54	0
55	MG	2A	3165	1/1	0.85	0.23	59,59,59,59	0
55	MG	1A	3307	1/1	0.85	0.34	25,25,25,25	0
55	MG	1A	3846	1/1	0.85	0.29	33,33,33,33	0
55	MG	2a	1637	1/1	0.85	0.20	65,65,65,65	0
55	MG	1a	1672	1/1	0.85	0.23	62,62,62,62	0
55	MG	2A	3185	1/1	0.85	0.25	60,60,60,60	0
55	MG	1A	3761	1/1	0.85	0.20	48,48,48,48	0
55	MG	1b	301	1/1	0.85	0.12	80,80,80,80	0
55	MG	2A	3399	1/1	0.85	0.16	61,61,61,61	0
55	MG	2A	3400	1/1	0.85	0.22	73,73,73,73	0
55	MG	1B	236	1/1	0.85	0.14	71,71,71,71	0
55	MG	2A	3639	1/1	0.85	0.21	58,58,58,58	0
55	MG	1A	3572	1/1	0.85	0.09	23,23,23,23	0
55	MG	2A	3199	1/1	0.85	0.06	69,69,69,69	0
55	MG	1a	1613	1/1	0.85	0.22	70,70,70,70	0
55	MG	2a	1684	1/1	0.85	0.20	68,68,68,68	0
55	MG	2A	3460	1/1	0.85	0.17	63,63,63,63	0
55	MG	2A	3677	1/1	0.85	0.16	54,54,54,54	0
55	MG	2A	3681	1/1	0.85	0.21	54,54,54,54	0
55	MG	1x	104	1/1	0.85	0.19	65,65,65,65	0
55	MG	1A	3646	1/1	0.85	0.28	68,68,68,68	0
55	MG	2A	3221	1/1	0.85	0.12	58,58,58,58	0
55	MG	1A	3470	1/1	0.85	0.11	73,73,73,73	0
55	MG	1N	202	1/1	0.85	0.14	52,52,52,52	0
55	MG	2a	1713	1/1	0.85	0.23	75,75,75,75	0
55	MG	2A	3229	1/1	0.85	0.14	59,59,59,59	0
55	MG	2A	3693	1/1	0.85	0.13	51,51,51,51	0
55	MG	1a	1635	1/1	0.85	0.20	59,59,59,59	0
55	MG	2a	1734	1/1	0.85	0.16	64,64,64,64	0
55	MG	1A	3969	1/1	0.85	0.23	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2a	1738	1/1	0.85	0.16	59,59,59,59	0
55	MG	1a	1717	1/1	0.85	0.15	63,63,63,63	0
55	MG	1a	1723	1/1	0.85	0.18	56,56,56,56	0
55	MG	2A	3074	1/1	0.85	0.16	71,71,71,71	0
55	MG	2A	3502	1/1	0.85	0.20	61,61,61,61	0
55	MG	1A	3260	1/1	0.85	0.14	55,55,55,55	0
55	MG	2A	3265	1/1	0.85	0.17	52,52,52,52	0
55	MG	2A	3266	1/1	0.85	0.24	75,75,75,75	0
55	MG	2A	3275	1/1	0.85	0.24	48,48,48,48	0
55	MG	1A	3314	1/1	0.85	0.27	63,63,63,63	0
55	MG	1a	1760	1/1	0.85	0.15	48,48,48,48	0
55	MG	2A	3519	1/1	0.85	0.28	61,61,61,61	0
55	MG	1A	3190	1/1	0.85	0.18	76,76,76,76	0
55	MG	2A	3093	1/1	0.85	0.20	78,78,78,78	0
55	MG	2a	1772	1/1	0.85	0.28	70,70,70,70	0
55	MG	1A	3419	1/1	0.85	0.10	51,51,51,51	0
55	MG	2E	306	1/1	0.85	0.12	64,64,64,64	0
55	MG	2V	202	1/1	0.85	0.16	63,63,63,63	0
55	MG	2f	201	1/1	0.85	0.17	57,57,57,57	0
55	MG	2A	3135	1/1	0.85	0.08	58,58,58,58	0
55	MG	2a	1601	1/1	0.85	0.14	72,72,72,72	0
55	MG	2A	3554	1/1	0.85	0.14	68,68,68,68	0
55	MG	1U	205	1/1	0.85	0.30	37,37,37,37	0
55	MG	1V	208	1/1	0.85	0.14	56,56,56,56	0
55	MG	1A	4015	1/1	0.85	0.28	53,53,53,53	0
55	MG	2A	3150	1/1	0.85	0.25	60,60,60,60	0
55	MG	2a	1631	1/1	0.86	0.26	67,67,67,67	0
55	MG	1A	3936	1/1	0.86	0.11	80,80,80,80	0
55	MG	2A	3432	1/1	0.86	0.10	35,35,35,35	0
55	MG	1I	201	1/1	0.86	0.10	71,71,71,71	0
55	MG	1A	3792	1/1	0.86	0.25	33,33,33,33	0
55	MG	2A	3624	1/1	0.86	0.12	49,49,49,49	0
55	MG	2A	3631	1/1	0.86	0.12	50,50,50,50	0
55	MG	1A	3989	1/1	0.86	0.11	49,49,49,49	0
55	MG	1a	1782	1/1	0.86	0.10	66,66,66,66	0
55	MG	2A	3652	1/1	0.86	0.09	63,63,63,63	0
55	MG	2A	3105	1/1	0.86	0.20	48,48,48,48	0
55	MG	1A	3668	1/1	0.86	0.13	60,60,60,60	0
55	MG	2A	3246	1/1	0.86	0.29	68,68,68,68	0
55	MG	2A	3673	1/1	0.86	0.34	70,70,70,70	0
55	MG	2A	3122	1/1	0.86	0.15	51,51,51,51	0
55	MG	2A	3130	1/1	0.86	0.40	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1O	201	1/1	0.86	0.11	64,64,64,64	0
55	MG	2A	3270	1/1	0.86	0.35	55,55,55,55	0
55	MG	2A	3271	1/1	0.86	0.17	56,56,56,56	0
55	MG	2A	3489	1/1	0.86	0.14	44,44,44,44	0
55	MG	1B	223	1/1	0.86	0.22	56,56,56,56	0
55	MG	2A	3498	1/1	0.86	0.20	57,57,57,57	0
55	MG	1a	1685	1/1	0.86	0.19	60,60,60,60	0
55	MG	1A	3640	1/1	0.86	0.17	35,35,35,35	0
55	MG	1a	1641	1/1	0.86	0.22	63,63,63,63	0
55	MG	1A	4017	1/1	0.86	0.13	63,63,63,63	0
55	MG	1A	3894	1/1	0.86	0.09	19,19,19,19	0
55	MG	2A	3303	1/1	0.86	0.31	77,77,77,77	0
55	MG	1A	3779	1/1	0.86	0.13	55,55,55,55	0
55	MG	2a	1727	1/1	0.86	0.07	82,82,82,82	0
55	MG	2A	3177	1/1	0.86	0.30	60,60,60,60	0
55	MG	1x	102	1/1	0.86	0.16	64,64,64,64	0
55	MG	1a	1715	1/1	0.86	0.21	59,59,59,59	0
55	MG	1A	3749	1/1	0.86	0.21	59,59,59,59	0
55	MG	2a	1740	1/1	0.86	0.19	65,65,65,65	0
55	MG	1a	1658	1/1	0.86	0.17	70,70,70,70	0
55	MG	2A	3187	1/1	0.86	0.20	57,57,57,57	0
55	MG	1x	109	1/1	0.86	0.17	66,66,66,66	0
55	MG	1A	3914	1/1	0.86	0.09	59,59,59,59	0
55	MG	1a	1745	1/1	0.86	0.07	48,48,48,48	0
55	MG	1A	3841	1/1	0.86	0.09	41,41,41,41	0
55	MG	2E	304	1/1	0.86	0.14	53,53,53,53	0
55	MG	1a	1750	1/1	0.86	0.08	61,61,61,61	0
55	MG	2A	3368	1/1	0.86	0.10	42,42,42,42	0
55	MG	2Z	301	1/1	0.86	0.15	71,71,71,71	0
55	MG	2A	3566	1/1	0.86	0.13	52,52,52,52	0
55	MG	2a	1767	1/1	0.86	0.13	85,85,85,85	0
55	MG	2a	1768	1/1	0.86	0.20	64,64,64,64	0
55	MG	2A	3046	1/1	0.86	0.25	65,65,65,65	0
55	MG	2A	3571	1/1	0.86	0.13	62,62,62,62	0
55	MG	2A	3391	1/1	0.86	0.18	62,62,62,62	0
55	MG	2a	1783	1/1	0.86	0.17	70,70,70,70	0
55	MG	2a	1785	1/1	0.86	0.19	82,82,82,82	0
55	MG	1a	1758	1/1	0.86	0.12	57,57,57,57	0
55	MG	2A	3058	1/1	0.86	0.12	52,52,52,52	0
55	MG	2A	3223	1/1	0.86	0.29	70,70,70,70	0
55	MG	2a	1609	1/1	0.86	0.26	78,78,78,78	0
55	MG	2a	1617	1/1	0.86	0.23	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2a	1619	1/1	0.86	0.28	69,69,69,69	0
55	MG	2A	3402	1/1	0.86	0.17	64,64,64,64	0
55	MG	1A	3557	1/1	0.86	0.19	52,52,52,52	0
55	MG	2A	3415	1/1	0.86	0.17	72,72,72,72	0
55	MG	2a	1630	1/1	0.86	0.30	58,58,58,58	0
55	MG	2A	3523	1/1	0.87	0.13	35,35,35,35	0
55	MG	1a	1727	1/1	0.87	0.10	57,57,57,57	0
55	MG	1a	1606	1/1	0.87	0.12	62,62,62,62	0
55	MG	1a	1736	1/1	0.87	0.26	71,71,71,71	0
55	MG	2A	3550	1/1	0.87	0.15	67,67,67,67	0
55	MG	1a	1612	1/1	0.87	0.10	69,69,69,69	0
55	MG	2A	3300	1/1	0.87	0.27	67,67,67,67	0
55	MG	2A	3117	1/1	0.87	0.27	68,68,68,68	0
55	MG	1A	3643	1/1	0.87	0.16	61,61,61,61	0
55	MG	2a	1616	1/1	0.87	0.17	67,67,67,67	0
55	MG	1A	3251	1/1	0.87	0.15	50,50,50,50	0
55	MG	1A	3039	1/1	0.87	0.09	37,37,37,37	0
55	MG	2A	3564	1/1	0.87	0.10	43,43,43,43	0
55	MG	1A	3571	1/1	0.87	0.18	54,54,54,54	0
55	MG	2A	3322	1/1	0.87	0.21	58,58,58,58	0
55	MG	1a	1764	1/1	0.87	0.09	51,51,51,51	0
55	MG	1a	1633	1/1	0.87	0.17	55,55,55,55	0
55	MG	2a	1632	1/1	0.87	0.42	65,65,65,65	0
55	MG	1A	3803	1/1	0.87	0.10	39,39,39,39	0
55	MG	2A	3153	1/1	0.87	0.16	68,68,68,68	0
55	MG	1A	3810	1/1	0.87	0.28	52,52,52,52	0
55	MG	1A	3961	1/1	0.87	0.32	65,65,65,65	0
55	MG	1a	1780	1/1	0.87	0.25	63,63,63,63	0
55	MG	2A	3594	1/1	0.87	0.11	41,41,41,41	0
55	MG	2a	1642	1/1	0.87	0.20	76,76,76,76	0
55	MG	2A	3597	1/1	0.87	0.22	79,79,79,79	0
55	MG	2a	1648	1/1	0.87	0.31	60,60,60,60	0
55	MG	2A	3175	1/1	0.87	0.15	63,63,63,63	0
55	MG	2A	3176	1/1	0.87	0.13	68,68,68,68	0
55	MG	2a	1659	1/1	0.87	0.17	53,53,53,53	0
55	MG	2A	3374	1/1	0.87	0.11	61,61,61,61	0
55	MG	1B	235	1/1	0.87	0.09	67,67,67,67	0
55	MG	2a	1665	1/1	0.87	0.15	72,72,72,72	0
55	MG	2a	1666	1/1	0.87	0.31	66,66,66,66	0
55	MG	2a	1671	1/1	0.87	0.22	61,61,61,61	0
55	MG	1A	3501	1/1	0.87	0.30	40,40,40,40	0
55	MG	1a	1652	1/1	0.87	0.25	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3616	1/1	0.87	0.15	55,55,55,55	0
55	MG	1D	301	1/1	0.87	0.24	43,43,43,43	0
55	MG	1A	3825	1/1	0.87	0.11	26,26,26,26	0
55	MG	2A	3634	1/1	0.87	0.08	70,70,70,70	0
55	MG	1A	3442	1/1	0.87	0.15	72,72,72,72	0
55	MG	1a	1798	1/1	0.87	0.22	74,74,74,74	0
55	MG	2a	1692	1/1	0.87	0.15	73,73,73,73	0
55	MG	2A	3408	1/1	0.87	0.14	66,66,66,66	0
55	MG	2A	3663	1/1	0.87	0.16	47,47,47,47	0
55	MG	1F	311	1/1	0.87	0.20	53,53,53,53	0
55	MG	1A	3830	1/1	0.87	0.09	38,38,38,38	0
55	MG	1A	3973	1/1	0.87	0.09	59,59,59,59	0
55	MG	2a	1712	1/1	0.87	0.22	75,75,75,75	0
55	MG	1r	101	1/1	0.87	0.35	69,69,69,69	0
55	MG	1A	3692	1/1	0.87	0.22	53,53,53,53	0
55	MG	2A	3449	1/1	0.87	0.14	50,50,50,50	0
55	MG	2a	1725	1/1	0.87	0.17	63,63,63,63	0
55	MG	2A	3459	1/1	0.87	0.11	50,50,50,50	0
55	MG	1A	3700	1/1	0.87	0.12	40,40,40,40	0
55	MG	1A	3703	1/1	0.87	0.12	18,18,18,18	0
55	MG	1A	3125	1/1	0.87	0.14	33,33,33,33	0
55	MG	2A	3690	1/1	0.87	0.07	68,68,68,68	0
55	MG	2A	3224	1/1	0.87	0.18	65,65,65,65	0
55	MG	1A	3255	1/1	0.87	0.16	61,61,61,61	0
55	MG	1A	3736	1/1	0.87	0.07	23,23,23,23	0
55	MG	2A	3695	1/1	0.87	0.26	62,62,62,62	0
55	MG	1A	3454	1/1	0.87	0.33	55,55,55,55	0
55	MG	2A	3699	1/1	0.87	0.18	61,61,61,61	0
55	MG	2A	3480	1/1	0.87	0.15	48,48,48,48	0
55	MG	1A	3349	1/1	0.87	0.13	50,50,50,50	0
55	MG	1V	207	1/1	0.87	0.12	63,63,63,63	0
55	MG	2A	3705	1/1	0.87	0.13	62,62,62,62	0
55	MG	2A	3708	1/1	0.87	0.12	74,74,74,74	0
55	MG	2A	3233	1/1	0.87	0.22	60,60,60,60	0
55	MG	1A	3759	1/1	0.87	0.09	37,37,37,37	0
55	MG	2A	3492	1/1	0.87	0.18	63,63,63,63	0
55	MG	2A	3042	1/1	0.87	0.13	52,52,52,52	0
55	MG	1A	3385	1/1	0.87	0.23	52,52,52,52	0
55	MG	2A	3049	1/1	0.87	0.17	51,51,51,51	0
55	MG	2a	1773	1/1	0.87	0.26	71,71,71,71	0
55	MG	2a	1777	1/1	0.87	0.11	77,77,77,77	0
55	MG	1A	3910	1/1	0.87	0.10	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2B	210	1/1	0.87	0.14	69,69,69,69	0
55	MG	1A	3765	1/1	0.87	0.19	52,52,52,52	0
55	MG	2A	3072	1/1	0.87	0.14	57,57,57,57	0
55	MG	2A	3511	1/1	0.87	0.13	77,77,77,77	0
55	MG	1A	3292	1/1	0.87	0.18	52,52,52,52	0
55	MG	1A	3543	1/1	0.87	0.14	55,55,55,55	0
55	MG	1a	1719	1/1	0.87	0.30	71,71,71,71	0
55	MG	2A	3276	1/1	0.87	0.26	64,64,64,64	0
55	MG	2G	201	1/1	0.87	0.16	67,67,67,67	0
55	MG	1A	3927	1/1	0.87	0.14	43,43,43,43	0
55	MG	2W	201	1/1	0.87	0.20	67,67,67,67	0
55	MG	2W	203	1/1	0.87	0.13	63,63,63,63	0
55	MG	2x	104	1/1	0.87	0.30	69,69,69,69	0
55	MG	2x	105	1/1	0.87	0.17	70,70,70,70	0
58	ZN	14	102	1/1	0.87	0.18	128,128,128,128	0
55	MG	2A	3094	1/1	0.88	0.26	51,51,51,51	0
55	MG	1A	3744	1/1	0.88	0.10	40,40,40,40	0
55	MG	1A	3748	1/1	0.88	0.16	40,40,40,40	0
55	MG	1a	1742	1/1	0.88	0.17	68,68,68,68	0
55	MG	2A	3301	1/1	0.88	0.21	62,62,62,62	0
55	MG	1A	3335	1/1	0.88	0.10	40,40,40,40	0
55	MG	2A	3123	1/1	0.88	0.21	65,65,65,65	0
55	MG	1A	3291	1/1	0.88	0.34	50,50,50,50	0
55	MG	1a	1747	1/1	0.88	0.16	72,72,72,72	0
55	MG	2a	1622	1/1	0.88	0.25	63,63,63,63	0
55	MG	1B	214	1/1	0.88	0.31	63,63,63,63	0
55	MG	2A	3568	1/1	0.88	0.12	63,63,63,63	0
55	MG	1A	3607	1/1	0.88	0.11	27,27,27,27	0
55	MG	2A	3141	1/1	0.88	0.12	47,47,47,47	0
55	MG	1A	3611	1/1	0.88	0.10	43,43,43,43	0
55	MG	2A	3149	1/1	0.88	0.25	66,66,66,66	0
55	MG	1a	1629	1/1	0.88	0.24	62,62,62,62	0
55	MG	2A	3581	1/1	0.88	0.16	67,67,67,67	0
55	MG	1A	3219	1/1	0.88	0.14	47,47,47,47	0
55	MG	2A	3161	1/1	0.88	0.10	51,51,51,51	0
55	MG	2A	3593	1/1	0.88	0.08	81,81,81,81	0
55	MG	1A	3034	1/1	0.88	0.21	61,61,61,61	0
55	MG	1A	3098	1/1	0.88	0.22	49,49,49,49	0
55	MG	2A	3359	1/1	0.88	0.11	67,67,67,67	0
55	MG	1A	3638	1/1	0.88	0.10	24,24,24,24	0
55	MG	1A	3781	1/1	0.88	0.15	50,50,50,50	0
55	MG	1A	3508	1/1	0.88	0.33	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3353	1/1	0.88	0.20	61,61,61,61	0
55	MG	1E	309	1/1	0.88	0.13	29,29,29,29	0
55	MG	1a	1792	1/1	0.88	0.12	66,66,66,66	0
55	MG	1A	3793	1/1	0.88	0.10	52,52,52,52	0
55	MG	1A	3359	1/1	0.88	0.32	66,66,66,66	0
55	MG	1A	3360	1/1	0.88	0.33	46,46,46,46	0
55	MG	2A	3191	1/1	0.88	0.08	67,67,67,67	0
55	MG	2a	1681	1/1	0.88	0.17	77,77,77,77	0
55	MG	1A	3427	1/1	0.88	0.12	61,61,61,61	0
55	MG	2A	3418	1/1	0.88	0.17	70,70,70,70	0
55	MG	2A	3422	1/1	0.88	0.16	54,54,54,54	0
55	MG	2A	3195	1/1	0.88	0.14	68,68,68,68	0
55	MG	2a	1686	1/1	0.88	0.26	63,63,63,63	0
55	MG	1A	3266	1/1	0.88	0.28	52,52,52,52	0
55	MG	1a	1663	1/1	0.88	0.22	69,69,69,69	0
55	MG	2A	3672	1/1	0.88	0.12	56,56,56,56	0
55	MG	2A	3438	1/1	0.88	0.20	71,71,71,71	0
55	MG	2a	1697	1/1	0.88	0.35	69,69,69,69	0
55	MG	2A	3442	1/1	0.88	0.14	59,59,59,59	0
55	MG	1A	3974	1/1	0.88	0.12	49,49,49,49	0
55	MG	2A	3201	1/1	0.88	0.19	66,66,66,66	0
55	MG	2A	3684	1/1	0.88	0.19	74,74,74,74	0
55	MG	2A	3458	1/1	0.88	0.12	32,32,32,32	0
55	MG	1a	1665	1/1	0.88	0.11	60,60,60,60	0
55	MG	1A	3015	1/1	0.88	0.32	57,57,57,57	0
55	MG	1a	1671	1/1	0.88	0.22	59,59,59,59	0
55	MG	1A	3440	1/1	0.88	0.17	74,74,74,74	0
55	MG	1A	3986	1/1	0.88	0.14	52,52,52,52	0
55	MG	1a	1677	1/1	0.88	0.12	58,58,58,58	0
55	MG	2A	3225	1/1	0.88	0.10	69,69,69,69	0
55	MG	1A	3315	1/1	0.88	0.14	59,59,59,59	0
55	MG	1R	205	1/1	0.88	0.14	45,45,45,45	0
55	MG	1A	3326	1/1	0.88	0.19	52,52,52,52	0
55	MG	1A	3163	1/1	0.88	0.08	45,45,45,45	0
55	MG	1a	1687	1/1	0.88	0.14	56,56,56,56	0
55	MG	1A	3569	1/1	0.88	0.10	40,40,40,40	0
55	MG	2A	3491	1/1	0.88	0.16	67,67,67,67	0
55	MG	2A	3710	1/1	0.88	0.13	70,70,70,70	0
55	MG	2A	3712	1/1	0.88	0.12	71,71,71,71	0
55	MG	1A	3282	1/1	0.88	0.13	70,70,70,70	0
55	MG	1a	1699	1/1	0.88	0.18	65,65,65,65	0
55	MG	2a	1758	1/1	0.88	0.18	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3497	1/1	0.88	0.16	53,53,53,53	0
55	MG	2A	3053	1/1	0.88	0.22	58,58,58,58	0
55	MG	2A	3500	1/1	0.88	0.11	45,45,45,45	0
55	MG	1a	1704	1/1	0.88	0.20	62,62,62,62	0
55	MG	2a	1765	1/1	0.88	0.21	76,76,76,76	0
55	MG	2A	3249	1/1	0.88	0.28	63,63,63,63	0
55	MG	2A	3257	1/1	0.88	0.35	58,58,58,58	0
55	MG	2A	3260	1/1	0.88	0.42	68,68,68,68	0
55	MG	1A	4019	1/1	0.88	0.14	68,68,68,68	0
55	MG	2A	3263	1/1	0.88	0.18	60,60,60,60	0
55	MG	1A	3859	1/1	0.88	0.12	24,24,24,24	0
55	MG	1A	3735	1/1	0.88	0.21	62,62,62,62	0
55	MG	2a	1782	1/1	0.88	0.08	75,75,75,75	0
55	MG	1A	3332	1/1	0.88	0.18	48,48,48,48	0
55	MG	2E	305	1/1	0.88	0.11	38,38,38,38	0
55	MG	10	107	1/1	0.88	0.09	54,54,54,54	0
55	MG	2a	1787	1/1	0.88	0.08	91,91,91,91	0
55	MG	2a	1793	1/1	0.88	0.11	81,81,81,81	0
55	MG	2a	1797	1/1	0.88	0.11	76,76,76,76	0
55	MG	1A	3741	1/1	0.88	0.29	57,57,57,57	0
55	MG	2A	3084	1/1	0.88	0.10	63,63,63,63	0
55	MG	18	106	1/1	0.88	0.25	49,49,49,49	0
55	MG	1A	3469	1/1	0.88	0.13	68,68,68,68	0
55	MG	2A	3533	1/1	0.88	0.14	58,58,58,58	0
55	MG	20	101	1/1	0.88	0.21	71,71,71,71	0
55	MG	27	102	1/1	0.88	0.21	54,54,54,54	0
55	MG	2A	3535	1/1	0.88	0.25	74,74,74,74	0
55	MG	28	3401	1/1	0.88	0.18	58,58,58,58	0
55	MG	28	3403	1/1	0.88	0.18	72,72,72,72	0
55	MG	2A	3544	1/1	0.88	0.12	49,49,49,49	0
55	MG	2A	3545	1/1	0.88	0.19	77,77,77,77	0
55	MG	1a	1756	1/1	0.89	0.12	63,63,63,63	0
55	MG	1A	4033	1/1	0.89	0.11	54,54,54,54	0
55	MG	1A	3861	1/1	0.89	0.13	53,53,53,53	0
55	MG	1A	3541	1/1	0.89	0.10	57,57,57,57	0
55	MG	2A	3329	1/1	0.89	0.23	37,37,37,37	0
55	MG	2A	3335	1/1	0.89	0.25	44,44,44,44	0
55	MG	1a	1632	1/1	0.89	0.29	77,77,77,77	0
55	MG	2A	3575	1/1	0.89	0.11	37,37,37,37	0
55	MG	2a	1623	1/1	0.89	0.33	68,68,68,68	0
55	MG	2A	3159	1/1	0.89	0.15	56,56,56,56	0
55	MG	1A	3439	1/1	0.89	0.17	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1774	1/1	0.89	0.17	63,63,63,63	0
55	MG	1A	3734	1/1	0.89	0.11	54,54,54,54	0
55	MG	2A	3360	1/1	0.89	0.16	56,56,56,56	0
55	MG	2A	3585	1/1	0.89	0.19	71,71,71,71	0
55	MG	2A	3168	1/1	0.89	0.19	37,37,37,37	0
55	MG	1a	1636	1/1	0.89	0.28	65,65,65,65	0
55	MG	2A	3377	1/1	0.89	0.12	31,31,31,31	0
55	MG	2A	3600	1/1	0.89	0.17	66,66,66,66	0
55	MG	1B	203	1/1	0.89	0.22	56,56,56,56	0
55	MG	2a	1640	1/1	0.89	0.11	64,64,64,64	0
55	MG	1A	3552	1/1	0.89	0.09	28,28,28,28	0
55	MG	2a	1644	1/1	0.89	0.16	65,65,65,65	0
55	MG	1a	1645	1/1	0.89	0.08	65,65,65,65	0
55	MG	1A	3279	1/1	0.89	0.14	59,59,59,59	0
55	MG	1B	225	1/1	0.89	0.12	52,52,52,52	0
55	MG	2A	3610	1/1	0.89	0.14	61,61,61,61	0
55	MG	2a	1657	1/1	0.89	0.12	52,52,52,52	0
55	MG	2a	1658	1/1	0.89	0.23	61,61,61,61	0
55	MG	2A	3183	1/1	0.89	0.12	62,62,62,62	0
55	MG	1A	3441	1/1	0.89	0.10	66,66,66,66	0
55	MG	1A	3194	1/1	0.89	0.17	37,37,37,37	0
55	MG	2a	1664	1/1	0.89	0.32	68,68,68,68	0
55	MG	1A	3443	1/1	0.89	0.10	71,71,71,71	0
55	MG	1A	3746	1/1	0.89	0.18	51,51,51,51	0
55	MG	1A	3925	1/1	0.89	0.13	62,62,62,62	0
55	MG	2A	3424	1/1	0.89	0.25	58,58,58,58	0
55	MG	2a	1675	1/1	0.89	0.29	72,72,72,72	0
55	MG	1A	3283	1/1	0.89	0.25	56,56,56,56	0
55	MG	2a	1678	1/1	0.89	0.16	55,55,55,55	0
55	MG	2A	3661	1/1	0.89	0.26	61,61,61,61	0
55	MG	2A	3196	1/1	0.89	0.23	57,57,57,57	0
55	MG	1A	3378	1/1	0.89	0.16	58,58,58,58	0
55	MG	1p	101	1/1	0.89	0.17	65,65,65,65	0
55	MG	1a	1662	1/1	0.89	0.16	57,57,57,57	0
55	MG	2A	3443	1/1	0.89	0.12	45,45,45,45	0
55	MG	1t	201	1/1	0.89	0.23	67,67,67,67	0
55	MG	1v	101	1/1	0.89	0.26	65,65,65,65	0
55	MG	2A	3678	1/1	0.89	0.12	67,67,67,67	0
55	MG	2a	1693	1/1	0.89	0.27	72,72,72,72	0
55	MG	2A	3680	1/1	0.89	0.15	60,60,60,60	0
55	MG	2A	3452	1/1	0.89	0.22	41,41,41,41	0
55	MG	2A	3457	1/1	0.89	0.11	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3334	1/1	0.89	0.28	62,62,62,62	0
55	MG	1A	3457	1/1	0.89	0.21	54,54,54,54	0
55	MG	2A	3218	1/1	0.89	0.18	58,58,58,58	0
55	MG	2a	1711	1/1	0.89	0.18	48,48,48,48	0
55	MG	1A	3953	1/1	0.89	0.15	63,63,63,63	0
55	MG	1A	3764	1/1	0.89	0.17	52,52,52,52	0
55	MG	1A	3209	1/1	0.89	0.13	51,51,51,51	0
55	MG	1A	3197	1/1	0.89	0.08	39,39,39,39	0
55	MG	1x	111	1/1	0.89	0.14	62,62,62,62	0
55	MG	1x	113	1/1	0.89	0.12	75,75,75,75	0
55	MG	1A	3226	1/1	0.89	0.26	61,61,61,61	0
55	MG	2a	1729	1/1	0.89	0.17	74,74,74,74	0
55	MG	1A	3616	1/1	0.89	0.10	47,47,47,47	0
55	MG	1A	3390	1/1	0.89	0.10	56,56,56,56	0
55	MG	1A	3968	1/1	0.89	0.11	45,45,45,45	0
55	MG	1A	3304	1/1	0.89	0.18	56,56,56,56	0
55	MG	1A	3636	1/1	0.89	0.17	45,45,45,45	0
55	MG	2A	3706	1/1	0.89	0.11	69,69,69,69	0
55	MG	2A	3244	1/1	0.89	0.25	68,68,68,68	0
55	MG	2A	3493	1/1	0.89	0.14	77,77,77,77	0
55	MG	1Q	204	1/1	0.89	0.10	64,64,64,64	0
55	MG	2A	3713	1/1	0.89	0.23	61,61,61,61	0
55	MG	1A	3398	1/1	0.89	0.12	54,54,54,54	0
55	MG	1A	3230	1/1	0.89	0.40	68,68,68,68	0
55	MG	1A	3503	1/1	0.89	0.13	41,41,41,41	0
55	MG	2A	3059	1/1	0.89	0.10	47,47,47,47	0
55	MG	1a	1703	1/1	0.89	0.13	63,63,63,63	0
55	MG	2A	3503	1/1	0.89	0.08	64,64,64,64	0
55	MG	1A	3240	1/1	0.89	0.24	52,52,52,52	0
55	MG	2A	3264	1/1	0.89	0.32	57,57,57,57	0
55	MG	1A	3816	1/1	0.89	0.16	57,57,57,57	0
55	MG	1A	3356	1/1	0.89	0.15	76,76,76,76	0
55	MG	2a	1769	1/1	0.89	0.21	52,52,52,52	0
55	MG	1A	3357	1/1	0.89	0.15	46,46,46,46	0
55	MG	2a	1771	1/1	0.89	0.26	61,61,61,61	0
55	MG	2B	216	1/1	0.89	0.32	68,68,68,68	0
55	MG	1A	4004	1/1	0.89	0.12	55,55,55,55	0
55	MG	2A	3272	1/1	0.89	0.19	57,57,57,57	0
55	MG	2a	1778	1/1	0.89	0.14	63,63,63,63	0
55	MG	2E	303	1/1	0.89	0.08	30,30,30,30	0
55	MG	1a	1716	1/1	0.89	0.27	69,69,69,69	0
55	MG	1A	3200	1/1	0.89	0.24	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	10	105	1/1	0.89	0.17	61,61,61,61	0
55	MG	2A	3102	1/1	0.89	0.14	68,68,68,68	0
55	MG	2Q	203	1/1	0.89	0.14	54,54,54,54	0
55	MG	1A	3425	1/1	0.89	0.12	45,45,45,45	0
55	MG	2a	1795	1/1	0.89	0.09	84,84,84,84	0
55	MG	1A	3273	1/1	0.89	0.23	56,56,56,56	0
55	MG	2A	3112	1/1	0.89	0.21	63,63,63,63	0
55	MG	2A	3541	1/1	0.89	0.12	69,69,69,69	0
55	MG	2A	3115	1/1	0.89	0.17	50,50,50,50	0
55	MG	1A	3682	1/1	0.89	0.11	41,41,41,41	0
55	MG	1A	3316	1/1	0.89	0.24	43,43,43,43	0
55	MG	1A	3079	1/1	0.89	0.22	54,54,54,54	0
55	MG	28	3402	1/1	0.89	0.14	44,44,44,44	0
55	MG	2r	101	1/1	0.89	0.10	84,84,84,84	0
55	MG	1A	3851	1/1	0.89	0.20	39,39,39,39	0
55	MG	2A	3308	1/1	0.89	0.23	52,52,52,52	0
55	MG	1A	3534	1/1	0.89	0.21	60,60,60,60	0
55	MG	1A	3718	1/1	0.89	0.10	33,33,33,33	0
56	K	1A	3482	1/1	0.89	0.15	90,90,90,90	0
55	MG	1A	4032	1/1	0.89	0.10	39,39,39,39	0
55	MG	2A	3107	1/1	0.90	0.19	43,43,43,43	0
55	MG	1A	3463	1/1	0.90	0.28	66,66,66,66	0
55	MG	2A	3110	1/1	0.90	0.20	64,64,64,64	0
55	MG	2A	3561	1/1	0.90	0.10	64,64,64,64	0
55	MG	17	106	1/1	0.90	0.08	49,49,49,49	0
55	MG	2A	3306	1/1	0.90	0.29	43,43,43,43	0
55	MG	1A	3919	1/1	0.90	0.09	25,25,25,25	0
55	MG	2A	3313	1/1	0.90	0.19	56,56,56,56	0
55	MG	2a	1625	1/1	0.90	0.40	52,52,52,52	0
55	MG	1A	3338	1/1	0.90	0.09	51,51,51,51	0
55	MG	2A	3317	1/1	0.90	0.18	59,59,59,59	0
55	MG	1a	1601	1/1	0.90	0.23	69,69,69,69	0
55	MG	1A	4035	1/1	0.90	0.10	51,51,51,51	0
55	MG	2A	3128	1/1	0.90	0.25	65,65,65,65	0
55	MG	1a	1605	1/1	0.90	0.20	63,63,63,63	0
55	MG	1A	3423	1/1	0.90	0.22	39,39,39,39	0
55	MG	1A	3313	1/1	0.90	0.10	57,57,57,57	0
55	MG	1a	1749	1/1	0.90	0.24	63,63,63,63	0
55	MG	2A	3330	1/1	0.90	0.23	73,73,73,73	0
55	MG	2A	3590	1/1	0.90	0.14	45,45,45,45	0
55	MG	2A	3333	1/1	0.90	0.14	45,45,45,45	0
55	MG	2A	3139	1/1	0.90	0.11	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2a	1643	1/1	0.90	0.12	58,58,58,58	0
55	MG	1A	4043	1/1	0.90	0.10	55,55,55,55	0
55	MG	2A	3143	1/1	0.90	0.21	61,61,61,61	0
55	MG	1a	1616	1/1	0.90	0.14	50,50,50,50	0
55	MG	1a	1620	1/1	0.90	0.23	59,59,59,59	0
55	MG	1a	1624	1/1	0.90	0.26	65,65,65,65	0
55	MG	1A	3932	1/1	0.90	0.19	42,42,42,42	0
55	MG	2A	3156	1/1	0.90	0.17	49,49,49,49	0
55	MG	1a	1765	1/1	0.90	0.09	74,74,74,74	0
55	MG	1A	3786	1/1	0.90	0.21	61,61,61,61	0
55	MG	2A	3615	1/1	0.90	0.13	46,46,46,46	0
55	MG	1a	1767	1/1	0.90	0.10	55,55,55,55	0
55	MG	2A	3387	1/1	0.90	0.10	32,32,32,32	0
55	MG	2A	3628	1/1	0.90	0.10	44,44,44,44	0
55	MG	1B	212	1/1	0.90	0.15	59,59,59,59	0
55	MG	2A	3393	1/1	0.90	0.10	64,64,64,64	0
55	MG	1A	3281	1/1	0.90	0.10	41,41,41,41	0
55	MG	2A	3640	1/1	0.90	0.13	38,38,38,38	0
55	MG	2A	3644	1/1	0.90	0.10	35,35,35,35	0
55	MG	2a	1679	1/1	0.90	0.34	59,59,59,59	0
55	MG	2A	3171	1/1	0.90	0.17	39,39,39,39	0
55	MG	1a	1630	1/1	0.90	0.28	72,72,72,72	0
55	MG	1a	1631	1/1	0.90	0.14	72,72,72,72	0
55	MG	1B	219	1/1	0.90	0.14	45,45,45,45	0
55	MG	1a	1781	1/1	0.90	0.14	65,65,65,65	0
55	MG	1B	222	1/1	0.90	0.13	63,63,63,63	0
55	MG	2A	3417	1/1	0.90	0.12	51,51,51,51	0
55	MG	2A	3671	1/1	0.90	0.13	58,58,58,58	0
55	MG	1A	3948	1/1	0.90	0.13	40,40,40,40	0
55	MG	1A	3483	1/1	0.90	0.13	45,45,45,45	0
55	MG	2a	1694	1/1	0.90	0.41	66,66,66,66	0
55	MG	1a	1787	1/1	0.90	0.09	76,76,76,76	0
55	MG	1A	3798	1/1	0.90	0.19	66,66,66,66	0
55	MG	2a	1698	1/1	0.90	0.40	53,53,53,53	0
55	MG	2a	1700	1/1	0.90	0.33	61,61,61,61	0
55	MG	2A	3679	1/1	0.90	0.09	69,69,69,69	0
55	MG	1A	3802	1/1	0.90	0.15	31,31,31,31	0
55	MG	2A	3189	1/1	0.90	0.15	46,46,46,46	0
55	MG	2A	3434	1/1	0.90	0.12	56,56,56,56	0
55	MG	2a	1709	1/1	0.90	0.27	66,66,66,66	0
55	MG	1a	1644	1/1	0.90	0.17	61,61,61,61	0
55	MG	1A	3171	1/1	0.90	0.12	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3708	1/1	0.90	0.09	65,65,65,65	0
55	MG	1A	3494	1/1	0.90	0.10	53,53,53,53	0
55	MG	1A	3962	1/1	0.90	0.08	43,43,43,43	0
55	MG	1A	3262	1/1	0.90	0.18	55,55,55,55	0
55	MG	1l	201	1/1	0.90	0.07	76,76,76,76	0
55	MG	1A	3820	1/1	0.90	0.10	27,27,27,27	0
55	MG	1A	3731	1/1	0.90	0.11	44,44,44,44	0
55	MG	1A	3502	1/1	0.90	0.14	44,44,44,44	0
55	MG	2A	3461	1/1	0.90	0.12	43,43,43,43	0
55	MG	1A	3588	1/1	0.90	0.14	35,35,35,35	0
55	MG	2A	3463	1/1	0.90	0.20	65,65,65,65	0
55	MG	1F	308	1/1	0.90	0.09	51,51,51,51	0
55	MG	2a	1741	1/1	0.90	0.29	62,62,62,62	0
55	MG	2a	1743	1/1	0.90	0.13	63,63,63,63	0
55	MG	1A	3831	1/1	0.90	0.17	28,28,28,28	0
55	MG	1G	203	1/1	0.90	0.13	72,72,72,72	0
55	MG	1A	3284	1/1	0.90	0.23	50,50,50,50	0
55	MG	1A	3172	1/1	0.90	0.09	39,39,39,39	0
55	MG	2A	3226	1/1	0.90	0.13	35,35,35,35	0
55	MG	1A	3509	1/1	0.90	0.30	66,66,66,66	0
55	MG	1A	3511	1/1	0.90	0.20	49,49,49,49	0
55	MG	2a	1757	1/1	0.90	0.14	57,57,57,57	0
55	MG	1A	3988	1/1	0.90	0.18	42,42,42,42	0
55	MG	2A	3718	1/1	0.90	0.18	59,59,59,59	0
55	MG	1a	1674	1/1	0.90	0.28	61,61,61,61	0
55	MG	2A	3012	1/1	0.90	0.23	43,43,43,43	0
55	MG	1A	3268	1/1	0.90	0.27	62,62,62,62	0
55	MG	1A	3990	1/1	0.90	0.13	47,47,47,47	0
55	MG	2A	3495	1/1	0.90	0.07	53,53,53,53	0
55	MG	1O	204	1/1	0.90	0.10	47,47,47,47	0
55	MG	1A	3621	1/1	0.90	0.11	35,35,35,35	0
55	MG	2A	3043	1/1	0.90	0.10	54,54,54,54	0
55	MG	1R	204	1/1	0.90	0.09	29,29,29,29	0
55	MG	2B	215	1/1	0.90	0.09	69,69,69,69	0
55	MG	2A	3247	1/1	0.90	0.20	68,68,68,68	0
55	MG	1A	3996	1/1	0.90	0.13	56,56,56,56	0
55	MG	2A	3250	1/1	0.90	0.24	43,43,43,43	0
55	MG	2E	302	1/1	0.90	0.23	57,57,57,57	0
55	MG	2A	3256	1/1	0.90	0.12	57,57,57,57	0
55	MG	2A	3050	1/1	0.90	0.23	51,51,51,51	0
55	MG	2A	3051	1/1	0.90	0.07	43,43,43,43	0
55	MG	1A	3225	1/1	0.90	0.24	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3075	1/1	0.90	0.18	57,57,57,57	0
55	MG	1A	3869	1/1	0.90	0.10	39,39,39,39	0
55	MG	1U	211	1/1	0.90	0.27	43,43,43,43	0
55	MG	1a	1701	1/1	0.90	0.08	51,51,51,51	0
55	MG	1V	202	1/1	0.90	0.34	48,48,48,48	0
55	MG	1A	3405	1/1	0.90	0.17	64,64,64,64	0
55	MG	1a	1708	1/1	0.90	0.22	58,58,58,58	0
55	MG	21	101	1/1	0.90	0.16	51,51,51,51	0
55	MG	1A	3188	1/1	0.90	0.25	58,58,58,58	0
55	MG	1A	3336	1/1	0.90	0.12	48,48,48,48	0
55	MG	2A	3277	1/1	0.90	0.14	62,62,62,62	0
55	MG	1a	1712	1/1	0.90	0.42	57,57,57,57	0
55	MG	2A	3283	1/1	0.90	0.23	62,62,62,62	0
55	MG	1A	3456	1/1	0.90	0.25	42,42,42,42	0
55	MG	1A	3768	1/1	0.90	0.10	39,39,39,39	0
55	MG	2A	3101	1/1	0.90	0.18	63,63,63,63	0
55	MG	1A	3418	1/1	0.90	0.17	64,64,64,64	0
55	MG	1A	3167	1/1	0.90	0.15	54,54,54,54	0
58	ZN	24	501	1/1	0.90	0.19	140,140,140,140	0
55	MG	1A	3555	1/1	0.91	0.14	40,40,40,40	0
55	MG	2A	3006	1/1	0.91	0.18	60,60,60,60	0
55	MG	2A	3011	1/1	0.91	0.09	45,45,45,45	0
55	MG	2A	3255	1/1	0.91	0.24	49,49,49,49	0
55	MG	1A	3399	1/1	0.91	0.17	43,43,43,43	0
55	MG	2a	1603	1/1	0.91	0.22	58,58,58,58	0
55	MG	1A	3461	1/1	0.91	0.28	48,48,48,48	0
55	MG	2a	1605	1/1	0.91	0.20	63,63,63,63	0
55	MG	2A	3025	1/1	0.91	0.14	47,47,47,47	0
55	MG	2A	3261	1/1	0.91	0.10	46,46,46,46	0
55	MG	2A	3032	1/1	0.91	0.33	60,60,60,60	0
55	MG	2A	3538	1/1	0.91	0.11	56,56,56,56	0
55	MG	2a	1613	1/1	0.91	0.11	64,64,64,64	0
55	MG	2A	3034	1/1	0.91	0.14	51,51,51,51	0
55	MG	1A	3567	1/1	0.91	0.12	24,24,24,24	0
55	MG	1A	3740	1/1	0.91	0.56	29,29,29,29	0
55	MG	1B	229	1/1	0.91	0.09	36,36,36,36	0
55	MG	1A	3912	1/1	0.91	0.12	65,65,65,65	0
55	MG	2A	3552	1/1	0.91	0.14	45,45,45,45	0
55	MG	2A	3044	1/1	0.91	0.08	61,61,61,61	0
55	MG	1A	3400	1/1	0.91	0.23	39,39,39,39	0
55	MG	1A	3570	1/1	0.91	0.08	37,37,37,37	0
55	MG	2a	1629	1/1	0.91	0.13	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1B	233	1/1	0.91	0.12	60,60,60,60	0
55	MG	1A	3109	1/1	0.91	0.27	28,28,28,28	0
55	MG	1A	3402	1/1	0.91	0.14	58,58,58,58	0
55	MG	1A	3355	1/1	0.91	0.11	57,57,57,57	0
55	MG	1D	310	1/1	0.91	0.20	65,65,65,65	0
55	MG	1A	3250	1/1	0.91	0.23	56,56,56,56	0
55	MG	2A	3069	1/1	0.91	0.15	43,43,43,43	0
55	MG	1A	3929	1/1	0.91	0.10	49,49,49,49	0
55	MG	1A	3930	1/1	0.91	0.13	23,23,23,23	0
55	MG	2A	3075	1/1	0.91	0.10	44,44,44,44	0
55	MG	2A	3079	1/1	0.91	0.14	46,46,46,46	0
55	MG	1A	3408	1/1	0.91	0.22	58,58,58,58	0
55	MG	1A	3585	1/1	0.91	0.10	35,35,35,35	0
55	MG	1A	3762	1/1	0.91	0.23	49,49,49,49	0
55	MG	1a	1688	1/1	0.91	0.21	43,43,43,43	0
55	MG	1A	3763	1/1	0.91	0.21	60,60,60,60	0
55	MG	2a	1654	1/1	0.91	0.21	62,62,62,62	0
55	MG	1a	1695	1/1	0.91	0.38	57,57,57,57	0
55	MG	2a	1656	1/1	0.91	0.16	68,68,68,68	0
55	MG	1A	3480	1/1	0.91	0.37	61,61,61,61	0
55	MG	1N	201	1/1	0.91	0.15	61,61,61,61	0
55	MG	1A	3590	1/1	0.91	0.09	35,35,35,35	0
55	MG	1A	3481	1/1	0.91	0.24	49,49,49,49	0
55	MG	2a	1662	1/1	0.91	0.26	58,58,58,58	0
55	MG	1A	3325	1/1	0.91	0.22	60,60,60,60	0
55	MG	1a	1705	1/1	0.91	0.19	53,53,53,53	0
55	MG	1a	1707	1/1	0.91	0.21	64,64,64,64	0
55	MG	1A	3771	1/1	0.91	0.15	60,60,60,60	0
55	MG	2a	1669	1/1	0.91	0.10	62,62,62,62	0
55	MG	1A	3111	1/1	0.91	0.13	39,39,39,39	0
55	MG	2A	3332	1/1	0.91	0.26	57,57,57,57	0
55	MG	1A	3081	1/1	0.91	0.06	26,26,26,26	0
55	MG	1A	3497	1/1	0.91	0.20	65,65,65,65	0
55	MG	1A	3498	1/1	0.91	0.13	60,60,60,60	0
55	MG	2A	3339	1/1	0.91	0.20	62,62,62,62	0
55	MG	2a	1680	1/1	0.91	0.26	51,51,51,51	0
55	MG	1A	3211	1/1	0.91	0.06	40,40,40,40	0
55	MG	1A	3330	1/1	0.91	0.07	45,45,45,45	0
55	MG	2A	3351	1/1	0.91	0.13	54,54,54,54	0
55	MG	2A	3134	1/1	0.91	0.17	55,55,55,55	0
55	MG	2A	3637	1/1	0.91	0.10	49,49,49,49	0
55	MG	1A	3787	1/1	0.91	0.07	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1U	202	1/1	0.91	0.20	52,52,52,52	0
55	MG	2A	3643	1/1	0.91	0.11	59,59,59,59	0
55	MG	2A	3137	1/1	0.91	0.15	66,66,66,66	0
55	MG	1a	1720	1/1	0.91	0.16	66,66,66,66	0
55	MG	1A	3972	1/1	0.91	0.10	39,39,39,39	0
55	MG	1A	3370	1/1	0.91	0.14	42,42,42,42	0
55	MG	1A	3331	1/1	0.91	0.17	43,43,43,43	0
55	MG	1A	3212	1/1	0.91	0.14	32,32,32,32	0
55	MG	2a	1699	1/1	0.91	0.22	48,48,48,48	0
55	MG	1a	1740	1/1	0.91	0.07	62,62,62,62	0
55	MG	2a	1701	1/1	0.91	0.37	58,58,58,58	0
55	MG	1A	3641	1/1	0.91	0.13	45,45,45,45	0
55	MG	2A	3670	1/1	0.91	0.09	55,55,55,55	0
55	MG	2a	1705	1/1	0.91	0.40	71,71,71,71	0
55	MG	1W	202	1/1	0.91	0.07	47,47,47,47	0
55	MG	2a	1707	1/1	0.91	0.38	57,57,57,57	0
55	MG	1A	3642	1/1	0.91	0.12	65,65,65,65	0
55	MG	1A	3806	1/1	0.91	0.13	31,31,31,31	0
55	MG	2a	1710	1/1	0.91	0.30	51,51,51,51	0
55	MG	1A	3017	1/1	0.91	0.20	47,47,47,47	0
55	MG	2A	3162	1/1	0.91	0.13	55,55,55,55	0
55	MG	1A	3811	1/1	0.91	0.18	28,28,28,28	0
55	MG	2a	1714	1/1	0.91	0.26	65,65,65,65	0
55	MG	2a	1715	1/1	0.91	0.12	62,62,62,62	0
55	MG	1a	1751	1/1	0.91	0.09	91,91,91,91	0
55	MG	2a	1717	1/1	0.91	0.28	66,66,66,66	0
55	MG	2a	1718	1/1	0.91	0.08	58,58,58,58	0
55	MG	1A	3814	1/1	0.91	0.09	31,31,31,31	0
55	MG	2A	3419	1/1	0.91	0.09	69,69,69,69	0
55	MG	11	104	1/1	0.91	0.11	40,40,40,40	0
55	MG	2A	3685	1/1	0.91	0.21	64,64,64,64	0
55	MG	1A	3131	1/1	0.91	0.11	43,43,43,43	0
55	MG	2a	1731	1/1	0.91	0.14	49,49,49,49	0
55	MG	1a	1761	1/1	0.91	0.10	46,46,46,46	0
55	MG	1A	3998	1/1	0.91	0.10	54,54,54,54	0
55	MG	1A	3379	1/1	0.91	0.19	61,61,61,61	0
55	MG	18	107	1/1	0.91	0.12	38,38,38,38	0
55	MG	2A	3437	1/1	0.91	0.11	48,48,48,48	0
55	MG	1A	4013	1/1	0.91	0.14	53,53,53,53	0
55	MG	1A	3153	1/1	0.91	0.27	32,32,32,32	0
55	MG	2a	1744	1/1	0.91	0.14	69,69,69,69	0
55	MG	1a	1603	1/1	0.91	0.14	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3698	1/1	0.91	0.18	58,58,58,58	0
55	MG	1A	3523	1/1	0.91	0.18	48,48,48,48	0
55	MG	2a	1750	1/1	0.91	0.18	68,68,68,68	0
55	MG	1A	3670	1/1	0.91	0.08	58,58,58,58	0
55	MG	1A	3048	1/1	0.91	0.08	43,43,43,43	0
55	MG	2a	1754	1/1	0.91	0.23	60,60,60,60	0
55	MG	2A	3456	1/1	0.91	0.09	36,36,36,36	0
55	MG	2A	3190	1/1	0.91	0.11	61,61,61,61	0
55	MG	1A	3234	1/1	0.91	0.20	47,47,47,47	0
55	MG	1A	3834	1/1	0.91	0.08	59,59,59,59	0
55	MG	1A	3444	1/1	0.91	0.07	58,58,58,58	0
55	MG	1A	3694	1/1	0.91	0.10	19,19,19,19	0
55	MG	1a	1622	1/1	0.91	0.29	57,57,57,57	0
55	MG	1A	3236	1/1	0.91	0.23	50,50,50,50	0
55	MG	2A	3465	1/1	0.91	0.17	64,64,64,64	0
55	MG	1A	4031	1/1	0.91	0.11	70,70,70,70	0
55	MG	2A	3469	1/1	0.91	0.20	71,71,71,71	0
55	MG	1A	3531	1/1	0.91	0.34	65,65,65,65	0
55	MG	2A	3473	1/1	0.91	0.12	68,68,68,68	0
55	MG	1A	3850	1/1	0.91	0.12	41,41,41,41	0
55	MG	2A	3206	1/1	0.91	0.15	60,60,60,60	0
55	MG	2B	208	1/1	0.91	0.29	70,70,70,70	0
55	MG	1A	3447	1/1	0.91	0.12	44,44,44,44	0
55	MG	2A	3478	1/1	0.91	0.16	59,59,59,59	0
55	MG	2A	3215	1/1	0.91	0.19	71,71,71,71	0
55	MG	1A	3344	1/1	0.91	0.06	28,28,28,28	0
55	MG	1A	4036	1/1	0.91	0.14	53,53,53,53	0
55	MG	1A	3853	1/1	0.91	0.08	33,33,33,33	0
55	MG	1A	3858	1/1	0.91	0.10	49,49,49,49	0
55	MG	1l	202	1/1	0.91	0.14	66,66,66,66	0
55	MG	2a	1790	1/1	0.91	0.20	51,51,51,51	0
55	MG	1A	3723	1/1	0.91	0.14	64,64,64,64	0
55	MG	1A	3729	1/1	0.91	0.12	21,21,21,21	0
55	MG	2a	1796	1/1	0.91	0.15	65,65,65,65	0
55	MG	1A	4051	1/1	0.91	0.16	48,48,48,48	0
55	MG	1A	3862	1/1	0.91	0.10	50,50,50,50	0
55	MG	1a	1643	1/1	0.91	0.16	52,52,52,52	0
55	MG	1B	208	1/1	0.91	0.16	81,81,81,81	0
55	MG	2O	201	1/1	0.91	0.18	54,54,54,54	0
55	MG	1B	211	1/1	0.91	0.15	56,56,56,56	0
55	MG	2R	201	1/1	0.91	0.15	57,57,57,57	0
55	MG	1A	3065	1/1	0.91	0.27	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3234	1/1	0.91	0.19	45,45,45,45	0
55	MG	2t	201	1/1	0.91	0.10	61,61,61,61	0
55	MG	1A	3274	1/1	0.91	0.12	61,61,61,61	0
55	MG	2Y	201	1/1	0.91	0.17	53,53,53,53	0
55	MG	2A	3240	1/1	0.91	0.21	70,70,70,70	0
55	MG	1a	1651	1/1	0.91	0.26	64,64,64,64	0
55	MG	1B	216	1/1	0.91	0.11	54,54,54,54	0
55	MG	1A	3876	1/1	0.91	0.10	27,27,27,27	0
55	MG	1x	114	1/1	0.91	0.19	53,53,53,53	0
55	MG	2A	3238	1/1	0.92	0.09	58,58,58,58	0
55	MG	1A	3629	1/1	0.92	0.14	24,24,24,24	0
55	MG	2A	3029	1/1	0.92	0.12	53,53,53,53	0
55	MG	2A	3505	1/1	0.92	0.07	66,66,66,66	0
55	MG	2A	3243	1/1	0.92	0.12	62,62,62,62	0
55	MG	2A	3030	1/1	0.92	0.11	45,45,45,45	0
55	MG	1A	3774	1/1	0.92	0.24	58,58,58,58	0
55	MG	1a	1669	1/1	0.92	0.20	58,58,58,58	0
55	MG	1E	304	1/1	0.92	0.15	38,38,38,38	0
55	MG	2A	3516	1/1	0.92	0.09	22,22,22,22	0
55	MG	1A	3631	1/1	0.92	0.11	23,23,23,23	0
55	MG	1A	3380	1/1	0.92	0.20	65,65,65,65	0
55	MG	2A	3254	1/1	0.92	0.21	34,34,34,34	0
55	MG	2A	3520	1/1	0.92	0.17	59,59,59,59	0
55	MG	1E	312	1/1	0.92	0.26	39,39,39,39	0
55	MG	2A	3525	1/1	0.92	0.09	49,49,49,49	0
55	MG	1A	3634	1/1	0.92	0.07	17,17,17,17	0
55	MG	1A	3162	1/1	0.92	0.22	31,31,31,31	0
55	MG	2A	3529	1/1	0.92	0.15	60,60,60,60	0
55	MG	2a	1624	1/1	0.92	0.26	57,57,57,57	0
55	MG	1A	3339	1/1	0.92	0.09	53,53,53,53	0
55	MG	2a	1626	1/1	0.92	0.25	46,46,46,46	0
55	MG	1A	3097	1/1	0.92	0.20	38,38,38,38	0
55	MG	1A	3387	1/1	0.92	0.26	59,59,59,59	0
55	MG	1A	3521	1/1	0.92	0.12	47,47,47,47	0
55	MG	1A	3341	1/1	0.92	0.53	65,65,65,65	0
55	MG	2A	3542	1/1	0.92	0.08	49,49,49,49	0
55	MG	1a	1689	1/1	0.92	0.24	44,44,44,44	0
55	MG	1A	3795	1/1	0.92	0.10	57,57,57,57	0
55	MG	2A	3268	1/1	0.92	0.16	48,48,48,48	0
55	MG	2A	3061	1/1	0.92	0.23	45,45,45,45	0
55	MG	2A	3067	1/1	0.92	0.15	62,62,62,62	0
55	MG	1a	1694	1/1	0.92	0.24	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3389	1/1	0.92	0.17	56,56,56,56	0
55	MG	1A	3800	1/1	0.92	0.10	42,42,42,42	0
55	MG	1A	3312	1/1	0.92	0.07	60,60,60,60	0
55	MG	1A	3238	1/1	0.92	0.24	49,49,49,49	0
55	MG	1A	3805	1/1	0.92	0.07	25,25,25,25	0
55	MG	1A	3659	1/1	0.92	0.15	49,49,49,49	0
55	MG	2A	3287	1/1	0.92	0.14	45,45,45,45	0
55	MG	2A	3293	1/1	0.92	0.25	54,54,54,54	0
55	MG	2a	1652	1/1	0.92	0.18	48,48,48,48	0
55	MG	2A	3567	1/1	0.92	0.14	55,55,55,55	0
55	MG	1A	3975	1/1	0.92	0.11	35,35,35,35	0
55	MG	2A	3295	1/1	0.92	0.12	55,55,55,55	0
55	MG	1A	3397	1/1	0.92	0.06	37,37,37,37	0
55	MG	1A	3114	1/1	0.92	0.11	42,42,42,42	0
55	MG	2A	3090	1/1	0.92	0.15	43,43,43,43	0
55	MG	1A	3121	1/1	0.92	0.15	36,36,36,36	0
55	MG	2A	3302	1/1	0.92	0.25	63,63,63,63	0
55	MG	1A	3672	1/1	0.92	0.12	58,58,58,58	0
55	MG	1A	3674	1/1	0.92	0.08	17,17,17,17	0
55	MG	1A	3678	1/1	0.92	0.24	59,59,59,59	0
55	MG	1A	3821	1/1	0.92	0.09	45,45,45,45	0
55	MG	1A	3824	1/1	0.92	0.12	24,24,24,24	0
55	MG	2a	1670	1/1	0.92	0.27	57,57,57,57	0
55	MG	1A	3537	1/1	0.92	0.13	47,47,47,47	0
55	MG	1A	4000	1/1	0.92	0.09	38,38,38,38	0
55	MG	1A	4002	1/1	0.92	0.12	51,51,51,51	0
55	MG	1X	105	1/1	0.92	0.11	40,40,40,40	0
55	MG	2A	3601	1/1	0.92	0.13	57,57,57,57	0
55	MG	2A	3320	1/1	0.92	0.32	49,49,49,49	0
55	MG	2A	3116	1/1	0.92	0.29	69,69,69,69	0
55	MG	1A	3540	1/1	0.92	0.09	23,23,23,23	0
55	MG	2A	3607	1/1	0.92	0.06	43,43,43,43	0
55	MG	2A	3119	1/1	0.92	0.24	41,41,41,41	0
55	MG	2A	3121	1/1	0.92	0.17	63,63,63,63	0
55	MG	1A	4009	1/1	0.92	0.09	55,55,55,55	0
55	MG	1A	3688	1/1	0.92	0.10	54,54,54,54	0
55	MG	1A	3276	1/1	0.92	0.13	60,60,60,60	0
55	MG	1A	3247	1/1	0.92	0.09	37,37,37,37	0
55	MG	2A	3133	1/1	0.92	0.10	35,35,35,35	0
55	MG	1A	3545	1/1	0.92	0.13	41,41,41,41	0
55	MG	1A	3838	1/1	0.92	0.16	38,38,38,38	0
55	MG	18	101	1/1	0.92	0.16	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3551	1/1	0.92	0.09	39,39,39,39	0
55	MG	1A	3001	1/1	0.92	0.09	39,39,39,39	0
55	MG	1A	3845	1/1	0.92	0.22	37,37,37,37	0
55	MG	2A	3352	1/1	0.92	0.08	50,50,50,50	0
55	MG	2A	3354	1/1	0.92	0.15	51,51,51,51	0
55	MG	1a	1754	1/1	0.92	0.14	72,72,72,72	0
55	MG	1A	3465	1/1	0.92	0.08	56,56,56,56	0
55	MG	2A	3654	1/1	0.92	0.11	55,55,55,55	0
55	MG	2A	3657	1/1	0.92	0.08	50,50,50,50	0
55	MG	2A	3660	1/1	0.92	0.09	60,60,60,60	0
55	MG	2A	3145	1/1	0.92	0.13	41,41,41,41	0
55	MG	2A	3146	1/1	0.92	0.23	59,59,59,59	0
55	MG	1a	1757	1/1	0.92	0.07	60,60,60,60	0
55	MG	1A	3468	1/1	0.92	0.16	58,58,58,58	0
55	MG	1A	4030	1/1	0.92	0.26	52,52,52,52	0
55	MG	2A	3151	1/1	0.92	0.07	44,44,44,44	0
55	MG	2A	3389	1/1	0.92	0.10	32,32,32,32	0
55	MG	1A	3327	1/1	0.92	0.13	65,65,65,65	0
55	MG	1A	3177	1/1	0.92	0.14	48,48,48,48	0
55	MG	2A	3674	1/1	0.92	0.19	52,52,52,52	0
55	MG	2A	3394	1/1	0.92	0.13	41,41,41,41	0
55	MG	1a	1608	1/1	0.92	0.25	52,52,52,52	0
55	MG	2a	1720	1/1	0.92	0.23	62,62,62,62	0
55	MG	1a	1610	1/1	0.92	0.10	68,68,68,68	0
55	MG	1A	3364	1/1	0.92	0.20	34,34,34,34	0
55	MG	1A	3472	1/1	0.92	0.27	35,35,35,35	0
55	MG	1A	3478	1/1	0.92	0.20	36,36,36,36	0
55	MG	2A	3166	1/1	0.92	0.13	40,40,40,40	0
55	MG	2a	1733	1/1	0.92	0.20	56,56,56,56	0
55	MG	2A	3411	1/1	0.92	0.07	62,62,62,62	0
55	MG	1A	3077	1/1	0.92	0.06	29,29,29,29	0
55	MG	1a	1621	1/1	0.92	0.25	64,64,64,64	0
55	MG	1A	4038	1/1	0.92	0.17	67,67,67,67	0
55	MG	1A	4039	1/1	0.92	0.18	52,52,52,52	0
55	MG	2A	3420	1/1	0.92	0.15	38,38,38,38	0
55	MG	2a	1742	1/1	0.92	0.17	62,62,62,62	0
55	MG	1A	3367	1/1	0.92	0.18	50,50,50,50	0
55	MG	1a	1626	1/1	0.92	0.13	47,47,47,47	0
55	MG	1A	3094	1/1	0.92	0.11	48,48,48,48	0
55	MG	2A	3180	1/1	0.92	0.19	61,61,61,61	0
55	MG	1A	3577	1/1	0.92	0.11	29,29,29,29	0
55	MG	2A	3182	1/1	0.92	0.12	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3435	1/1	0.92	0.16	39,39,39,39	0
55	MG	1a	1788	1/1	0.92	0.18	59,59,59,59	0
55	MG	2A	3703	1/1	0.92	0.30	52,52,52,52	0
55	MG	1A	3221	1/1	0.92	0.13	36,36,36,36	0
55	MG	2A	3439	1/1	0.92	0.11	47,47,47,47	0
55	MG	2A	3441	1/1	0.92	0.09	36,36,36,36	0
55	MG	1a	1793	1/1	0.92	0.07	59,59,59,59	0
55	MG	1A	4045	1/1	0.92	0.09	51,51,51,51	0
55	MG	2a	1760	1/1	0.92	0.22	60,60,60,60	0
55	MG	1A	3879	1/1	0.92	0.11	60,60,60,60	0
55	MG	1A	3885	1/1	0.92	0.09	61,61,61,61	0
55	MG	1B	204	1/1	0.92	0.07	36,36,36,36	0
55	MG	2A	3453	1/1	0.92	0.12	45,45,45,45	0
55	MG	2A	3454	1/1	0.92	0.09	39,39,39,39	0
55	MG	1B	205	1/1	0.92	0.24	63,63,63,63	0
55	MG	1A	3486	1/1	0.92	0.27	33,33,33,33	0
55	MG	1A	3421	1/1	0.92	0.10	61,61,61,61	0
55	MG	1a	1640	1/1	0.92	0.07	64,64,64,64	0
55	MG	1A	3287	1/1	0.92	0.09	42,42,42,42	0
55	MG	2B	207	1/1	0.92	0.29	69,69,69,69	0
55	MG	2a	1774	1/1	0.92	0.12	61,61,61,61	0
55	MG	1a	1642	1/1	0.92	0.13	50,50,50,50	0
55	MG	1A	3592	1/1	0.92	0.09	21,21,21,21	0
55	MG	1A	3750	1/1	0.92	0.61	30,30,30,30	0
55	MG	1A	3911	1/1	0.92	0.09	65,65,65,65	0
55	MG	2A	3467	1/1	0.92	0.08	37,37,37,37	0
55	MG	1A	3752	1/1	0.92	0.07	37,37,37,37	0
55	MG	2A	3211	1/1	0.92	0.21	54,54,54,54	0
55	MG	1A	3913	1/1	0.92	0.10	61,61,61,61	0
55	MG	2a	1788	1/1	0.92	0.12	77,77,77,77	0
55	MG	1A	3758	1/1	0.92	0.12	37,37,37,37	0
55	MG	2D	306	1/1	0.92	0.17	43,43,43,43	0
55	MG	2a	1794	1/1	0.92	0.23	67,67,67,67	0
55	MG	1A	3595	1/1	0.92	0.11	60,60,60,60	0
55	MG	2A	3219	1/1	0.92	0.22	41,41,41,41	0
55	MG	1A	3145	1/1	0.92	0.16	47,47,47,47	0
55	MG	1A	3258	1/1	0.92	0.32	50,50,50,50	0
55	MG	1a	1657	1/1	0.92	0.10	47,47,47,47	0
55	MG	2F	301	1/1	0.92	0.12	47,47,47,47	0
55	MG	1x	112	1/1	0.92	0.17	68,68,68,68	0
55	MG	2k	201	1/1	0.92	0.16	63,63,63,63	0
55	MG	1A	3191	1/1	0.92	0.14	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3429	1/1	0.92	0.19	57,57,57,57	0
55	MG	2A	3488	1/1	0.92	0.30	39,39,39,39	0
55	MG	1A	3095	1/1	0.92	0.13	35,35,35,35	0
55	MG	2A	3005	1/1	0.92	0.10	62,62,62,62	0
55	MG	1A	3435	1/1	0.92	0.18	40,40,40,40	0
55	MG	1A	3931	1/1	0.92	0.08	13,13,13,13	0
55	MG	1A	3628	1/1	0.92	0.10	34,34,34,34	0
55	MG	1B	237	1/1	0.92	0.08	38,38,38,38	0
55	MG	2A	3235	1/1	0.92	0.24	64,64,64,64	0
57	T8B	2A	3717	44/44	0.92	0.10	58,66,71,76	0
55	MG	2A	3236	1/1	0.92	0.22	52,52,52,52	0
55	MG	2A	3024	1/1	0.92	0.12	56,56,56,56	0
55	MG	1a	1710	1/1	0.93	0.12	56,56,56,56	0
55	MG	2A	3531	1/1	0.93	0.09	60,60,60,60	0
55	MG	1W	201	1/1	0.93	0.21	45,45,45,45	0
55	MG	2A	3095	1/1	0.93	0.12	35,35,35,35	0
55	MG	2a	1610	1/1	0.93	0.17	63,63,63,63	0
55	MG	2A	3534	1/1	0.93	0.10	41,41,41,41	0
55	MG	2a	1614	1/1	0.93	0.16	64,64,64,64	0
55	MG	2a	1615	1/1	0.93	0.26	67,67,67,67	0
55	MG	2A	3099	1/1	0.93	0.11	57,57,57,57	0
55	MG	2A	3289	1/1	0.93	0.16	38,38,38,38	0
55	MG	1A	3301	1/1	0.93	0.06	38,38,38,38	0
55	MG	1A	3303	1/1	0.93	0.16	48,48,48,48	0
55	MG	2A	3104	1/1	0.93	0.19	52,52,52,52	0
55	MG	1X	102	1/1	0.93	0.36	36,36,36,36	0
55	MG	2A	3549	1/1	0.93	0.10	43,43,43,43	0
55	MG	1A	3516	1/1	0.93	0.11	40,40,40,40	0
55	MG	1A	3019	1/1	0.93	0.12	32,32,32,32	0
55	MG	2A	3109	1/1	0.93	0.14	46,46,46,46	0
55	MG	1A	3133	1/1	0.93	0.08	31,31,31,31	0
55	MG	1A	3873	1/1	0.93	0.14	54,54,54,54	0
55	MG	1A	3875	1/1	0.93	0.10	18,18,18,18	0
55	MG	11	103	1/1	0.93	0.07	64,64,64,64	0
55	MG	1A	3345	1/1	0.93	0.25	47,47,47,47	0
55	MG	1A	3143	1/1	0.93	0.10	38,38,38,38	0
55	MG	2a	1634	1/1	0.93	0.12	62,62,62,62	0
55	MG	2A	3309	1/1	0.93	0.11	61,61,61,61	0
55	MG	2A	3312	1/1	0.93	0.17	47,47,47,47	0
55	MG	1A	3884	1/1	0.93	0.10	43,43,43,43	0
55	MG	1A	3767	1/1	0.93	0.14	37,37,37,37	0
55	MG	18	103	1/1	0.93	0.13	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3318	1/1	0.93	0.33	49,49,49,49	0
55	MG	2a	1641	1/1	0.93	0.35	56,56,56,56	0
55	MG	1A	3453	1/1	0.93	0.25	41,41,41,41	0
55	MG	1A	3889	1/1	0.93	0.07	47,47,47,47	0
55	MG	1A	3892	1/1	0.93	0.08	38,38,38,38	0
55	MG	1A	4037	1/1	0.93	0.10	47,47,47,47	0
55	MG	1A	3769	1/1	0.93	0.10	50,50,50,50	0
55	MG	2A	3325	1/1	0.93	0.14	60,60,60,60	0
55	MG	1A	3348	1/1	0.93	0.08	62,62,62,62	0
55	MG	1A	4040	1/1	0.93	0.15	32,32,32,32	0
55	MG	2A	3328	1/1	0.93	0.19	46,46,46,46	0
55	MG	1A	3902	1/1	0.93	0.12	55,55,55,55	0
55	MG	2A	3592	1/1	0.93	0.21	77,77,77,77	0
55	MG	1A	3310	1/1	0.93	0.40	42,42,42,42	0
55	MG	1a	1759	1/1	0.93	0.09	63,63,63,63	0
55	MG	2A	3142	1/1	0.93	0.17	65,65,65,65	0
55	MG	2a	1661	1/1	0.93	0.13	62,62,62,62	0
55	MG	1A	3909	1/1	0.93	0.09	31,31,31,31	0
55	MG	1A	3350	1/1	0.93	0.12	33,33,33,33	0
55	MG	1A	3311	1/1	0.93	0.44	36,36,36,36	0
55	MG	1a	1614	1/1	0.93	0.10	47,47,47,47	0
55	MG	2A	3342	1/1	0.93	0.21	54,54,54,54	0
55	MG	1A	4046	1/1	0.93	0.13	41,41,41,41	0
55	MG	1a	1618	1/1	0.93	0.26	64,64,64,64	0
55	MG	1A	4047	1/1	0.93	0.14	54,54,54,54	0
55	MG	2a	1672	1/1	0.93	0.10	64,64,64,64	0
55	MG	1A	3648	1/1	0.93	0.18	57,57,57,57	0
55	MG	1A	4054	1/1	0.93	0.13	59,59,59,59	0
55	MG	2A	3613	1/1	0.93	0.08	62,62,62,62	0
55	MG	1a	1778	1/1	0.93	0.20	57,57,57,57	0
55	MG	1A	3231	1/1	0.93	0.17	43,43,43,43	0
55	MG	2A	3620	1/1	0.93	0.10	53,53,53,53	0
55	MG	2A	3623	1/1	0.93	0.06	35,35,35,35	0
55	MG	2A	3367	1/1	0.93	0.08	41,41,41,41	0
55	MG	1A	3005	1/1	0.93	0.08	46,46,46,46	0
55	MG	1A	3782	1/1	0.93	0.12	58,58,58,58	0
55	MG	2A	3375	1/1	0.93	0.08	34,34,34,34	0
55	MG	1A	3917	1/1	0.93	0.12	51,51,51,51	0
55	MG	2a	1688	1/1	0.93	0.31	50,50,50,50	0
55	MG	1A	3406	1/1	0.93	0.09	47,47,47,47	0
55	MG	1A	3921	1/1	0.93	0.09	18,18,18,18	0
55	MG	1A	3542	1/1	0.93	0.16	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3466	1/1	0.93	0.27	52,52,52,52	0
55	MG	2A	3647	1/1	0.93	0.09	64,64,64,64	0
55	MG	2a	1695	1/1	0.93	0.25	50,50,50,50	0
55	MG	2A	3649	1/1	0.93	0.07	55,55,55,55	0
55	MG	1A	3791	1/1	0.93	0.07	53,53,53,53	0
55	MG	1A	3671	1/1	0.93	0.11	49,49,49,49	0
55	MG	1A	3544	1/1	0.93	0.14	40,40,40,40	0
55	MG	1a	1795	1/1	0.93	0.10	56,56,56,56	0
55	MG	2A	3179	1/1	0.93	0.18	59,59,59,59	0
55	MG	1B	224	1/1	0.93	0.12	59,59,59,59	0
55	MG	1A	3193	1/1	0.93	0.21	47,47,47,47	0
55	MG	2A	3404	1/1	0.93	0.10	53,53,53,53	0
55	MG	1A	3796	1/1	0.93	0.11	47,47,47,47	0
55	MG	1A	3935	1/1	0.93	0.09	63,63,63,63	0
55	MG	1A	3546	1/1	0.93	0.13	44,44,44,44	0
55	MG	1A	3150	1/1	0.93	0.09	41,41,41,41	0
55	MG	1A	3938	1/1	0.93	0.16	49,49,49,49	0
55	MG	1A	3412	1/1	0.93	0.08	47,47,47,47	0
55	MG	1A	3051	1/1	0.93	0.23	50,50,50,50	0
55	MG	1a	1648	1/1	0.93	0.21	68,68,68,68	0
55	MG	2A	3423	1/1	0.93	0.26	60,60,60,60	0
55	MG	2A	3192	1/1	0.93	0.24	62,62,62,62	0
55	MG	2A	3193	1/1	0.93	0.23	61,61,61,61	0
55	MG	2A	3430	1/1	0.93	0.21	58,58,58,58	0
55	MG	1a	1649	1/1	0.93	0.14	59,59,59,59	0
55	MG	2A	3683	1/1	0.93	0.08	46,46,46,46	0
55	MG	1A	3416	1/1	0.93	0.11	56,56,56,56	0
55	MG	2a	1724	1/1	0.93	0.14	49,49,49,49	0
55	MG	1A	3417	1/1	0.93	0.14	36,36,36,36	0
55	MG	1A	3955	1/1	0.93	0.07	53,53,53,53	0
55	MG	2A	3687	1/1	0.93	0.17	61,61,61,61	0
55	MG	1x	103	1/1	0.93	0.26	68,68,68,68	0
55	MG	1a	1653	1/1	0.93	0.19	60,60,60,60	0
55	MG	1A	3807	1/1	0.93	0.22	39,39,39,39	0
55	MG	2A	3203	1/1	0.93	0.22	64,64,64,64	0
55	MG	2a	1735	1/1	0.93	0.15	61,61,61,61	0
55	MG	1A	3698	1/1	0.93	0.07	21,21,21,21	0
55	MG	2A	3205	1/1	0.93	0.14	52,52,52,52	0
55	MG	1A	3159	1/1	0.93	0.07	40,40,40,40	0
55	MG	2A	3207	1/1	0.93	0.17	58,58,58,58	0
55	MG	1x	110	1/1	0.93	0.07	36,36,36,36	0
55	MG	1E	305	1/1	0.93	0.19	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3201	1/1	0.93	0.16	49,49,49,49	0
55	MG	1A	3705	1/1	0.93	0.07	20,20,20,20	0
55	MG	1A	3280	1/1	0.93	0.17	60,60,60,60	0
55	MG	1A	3062	1/1	0.93	0.10	61,61,61,61	0
55	MG	1A	3082	1/1	0.93	0.20	29,29,29,29	0
55	MG	2A	3222	1/1	0.93	0.09	72,72,72,72	0
55	MG	2a	1751	1/1	0.93	0.13	64,64,64,64	0
55	MG	1F	309	1/1	0.93	0.21	33,33,33,33	0
55	MG	2A	3010	1/1	0.93	0.06	34,34,34,34	0
55	MG	1A	3491	1/1	0.93	0.06	32,32,32,32	0
55	MG	1A	3090	1/1	0.93	0.07	42,42,42,42	0
55	MG	2A	3466	1/1	0.93	0.33	46,46,46,46	0
55	MG	2A	3013	1/1	0.93	0.12	37,37,37,37	0
55	MG	1A	3827	1/1	0.93	0.06	24,24,24,24	0
55	MG	1A	3828	1/1	0.93	0.13	24,24,24,24	0
55	MG	1A	3493	1/1	0.93	0.17	38,38,38,38	0
55	MG	1A	3029	1/1	0.93	0.26	30,30,30,30	0
55	MG	1A	3495	1/1	0.93	0.18	52,52,52,52	0
55	MG	1A	3069	1/1	0.93	0.18	28,28,28,28	0
55	MG	1a	1678	1/1	0.93	0.09	52,52,52,52	0
55	MG	1a	1679	1/1	0.93	0.21	56,56,56,56	0
55	MG	1a	1680	1/1	0.93	0.17	67,67,67,67	0
55	MG	1a	1681	1/1	0.93	0.14	46,46,46,46	0
55	MG	2A	3482	1/1	0.93	0.09	50,50,50,50	0
55	MG	1A	3333	1/1	0.93	0.22	45,45,45,45	0
55	MG	2A	3485	1/1	0.93	0.12	61,61,61,61	0
55	MG	1A	3836	1/1	0.93	0.12	46,46,46,46	0
55	MG	1A	3290	1/1	0.93	0.14	45,45,45,45	0
55	MG	2a	1775	1/1	0.93	0.26	59,59,59,59	0
55	MG	2A	3048	1/1	0.93	0.17	58,58,58,58	0
55	MG	2D	305	1/1	0.93	0.22	43,43,43,43	0
55	MG	1O	205	1/1	0.93	0.11	65,65,65,65	0
55	MG	1a	1686	1/1	0.93	0.37	71,71,71,71	0
55	MG	1P	206	1/1	0.93	0.38	40,40,40,40	0
55	MG	2a	1784	1/1	0.93	0.29	52,52,52,52	0
55	MG	1A	3432	1/1	0.93	0.17	32,32,32,32	0
55	MG	1R	201	1/1	0.93	0.11	33,33,33,33	0
55	MG	2A	3253	1/1	0.93	0.38	59,59,59,59	0
55	MG	1A	3256	1/1	0.93	0.25	57,57,57,57	0
55	MG	2F	303	1/1	0.93	0.16	71,71,71,71	0
55	MG	2a	1792	1/1	0.93	0.05	70,70,70,70	0
55	MG	2A	3499	1/1	0.93	0.21	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1693	1/1	0.93	0.21	48,48,48,48	0
55	MG	1A	3843	1/1	0.93	0.07	47,47,47,47	0
55	MG	2A	3065	1/1	0.93	0.12	51,51,51,51	0
55	MG	2T	201	1/1	0.93	0.11	62,62,62,62	0
55	MG	2V	201	1/1	0.93	0.14	48,48,48,48	0
55	MG	2A	3258	1/1	0.93	0.18	67,67,67,67	0
55	MG	1A	3506	1/1	0.93	0.23	51,51,51,51	0
55	MG	1a	1697	1/1	0.93	0.29	48,48,48,48	0
55	MG	1A	3507	1/1	0.93	0.11	35,35,35,35	0
55	MG	1A	3747	1/1	0.93	0.16	55,55,55,55	0
55	MG	1a	1700	1/1	0.93	0.40	44,44,44,44	0
55	MG	2A	3078	1/1	0.93	0.13	59,59,59,59	0
55	MG	2A	3515	1/1	0.93	0.08	63,63,63,63	0
55	MG	1A	4008	1/1	0.93	0.08	38,38,38,38	0
55	MG	1U	206	1/1	0.93	0.12	42,42,42,42	0
55	MG	1A	3010	1/1	0.93	0.16	42,42,42,42	0
55	MG	1U	212	1/1	0.93	0.13	49,49,49,49	0
55	MG	1A	3294	1/1	0.93	0.11	42,42,42,42	0
55	MG	2A	3273	1/1	0.93	0.17	56,56,56,56	0
56	K	2A	3278	1/1	0.93	0.16	73,73,73,73	0
57	T8B	1A	4052	44/44	0.93	0.10	48,53,59,65	0
55	MG	1A	3180	1/1	0.93	0.08	50,50,50,50	0
55	MG	2A	3086	1/1	0.93	0.16	58,58,58,58	0
55	MG	1A	3512	1/1	0.93	0.12	52,52,52,52	0
55	MG	1A	3458	1/1	0.94	0.30	63,63,63,63	0
55	MG	1a	1634	1/1	0.94	0.20	46,46,46,46	0
55	MG	2A	3546	1/1	0.94	0.08	58,58,58,58	0
55	MG	1A	3459	1/1	0.94	0.33	44,44,44,44	0
55	MG	2A	3311	1/1	0.94	0.17	67,67,67,67	0
55	MG	1A	3981	1/1	0.94	0.05	33,33,33,33	0
55	MG	2a	1621	1/1	0.94	0.30	47,47,47,47	0
55	MG	1A	3305	1/1	0.94	0.18	54,54,54,54	0
55	MG	1A	3263	1/1	0.94	0.07	48,48,48,48	0
55	MG	2A	3316	1/1	0.94	0.12	51,51,51,51	0
55	MG	1A	3753	1/1	0.94	0.05	24,24,24,24	0
55	MG	1A	3757	1/1	0.94	0.07	34,34,34,34	0
55	MG	1A	3264	1/1	0.94	0.12	44,44,44,44	0
55	MG	2A	3144	1/1	0.94	0.10	49,49,49,49	0
55	MG	2A	3562	1/1	0.94	0.09	52,52,52,52	0
55	MG	1G	202	1/1	0.94	0.14	48,48,48,48	0
55	MG	1A	3854	1/1	0.94	0.09	65,65,65,65	0
55	MG	1a	1789	1/1	0.94	0.12	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1646	1/1	0.94	0.10	64,64,64,64	0
55	MG	1A	3060	1/1	0.94	0.15	35,35,35,35	0
55	MG	1A	3533	1/1	0.94	0.09	50,50,50,50	0
55	MG	1A	3012	1/1	0.94	0.33	26,26,26,26	0
55	MG	1A	3467	1/1	0.94	0.12	52,52,52,52	0
55	MG	2A	3158	1/1	0.94	0.16	54,54,54,54	0
55	MG	1A	3865	1/1	0.94	0.11	57,57,57,57	0
55	MG	2A	3578	1/1	0.94	0.12	60,60,60,60	0
55	MG	1A	3271	1/1	0.94	0.19	43,43,43,43	0
55	MG	1N	206	1/1	0.94	0.08	43,43,43,43	0
55	MG	2A	3163	1/1	0.94	0.30	43,43,43,43	0
55	MG	1d	3201	1/1	0.94	0.25	56,56,56,56	0
55	MG	1A	3078	1/1	0.94	0.13	50,50,50,50	0
55	MG	1A	3043	1/1	0.94	0.24	42,42,42,42	0
55	MG	2A	3348	1/1	0.94	0.09	49,49,49,49	0
55	MG	1A	3652	1/1	0.94	0.10	45,45,45,45	0
55	MG	2A	3169	1/1	0.94	0.25	39,39,39,39	0
55	MG	1A	3655	1/1	0.94	0.10	62,62,62,62	0
55	MG	1n	101	1/1	0.94	0.42	67,67,67,67	0
55	MG	2A	3174	1/1	0.94	0.10	55,55,55,55	0
55	MG	1P	202	1/1	0.94	0.20	45,45,45,45	0
55	MG	1P	203	1/1	0.94	0.23	36,36,36,36	0
55	MG	2A	3361	1/1	0.94	0.10	39,39,39,39	0
55	MG	2A	3605	1/1	0.94	0.10	41,41,41,41	0
55	MG	2A	3364	1/1	0.94	0.09	37,37,37,37	0
55	MG	2A	3366	1/1	0.94	0.09	42,42,42,42	0
55	MG	1A	3657	1/1	0.94	0.09	51,51,51,51	0
55	MG	1A	3883	1/1	0.94	0.11	58,58,58,58	0
55	MG	2A	3373	1/1	0.94	0.12	44,44,44,44	0
55	MG	2a	1667	1/1	0.94	0.14	36,36,36,36	0
55	MG	1A	3237	1/1	0.94	0.26	54,54,54,54	0
55	MG	1R	203	1/1	0.94	0.47	41,41,41,41	0
55	MG	1A	3175	1/1	0.94	0.12	42,42,42,42	0
55	MG	2A	3617	1/1	0.94	0.13	63,63,63,63	0
55	MG	2A	3378	1/1	0.94	0.07	46,46,46,46	0
55	MG	2a	1674	1/1	0.94	0.21	66,66,66,66	0
55	MG	1A	3776	1/1	0.94	0.06	49,49,49,49	0
55	MG	2A	3382	1/1	0.94	0.12	59,59,59,59	0
55	MG	1x	105	1/1	0.94	0.11	67,67,67,67	0
55	MG	2A	3184	1/1	0.94	0.20	66,66,66,66	0
55	MG	1a	1668	1/1	0.94	0.28	52,52,52,52	0
55	MG	2A	3392	1/1	0.94	0.07	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1S	201	1/1	0.94	0.18	49,49,49,49	0
55	MG	1A	3477	1/1	0.94	0.17	36,36,36,36	0
55	MG	2A	3188	1/1	0.94	0.09	48,48,48,48	0
55	MG	1T	201	1/1	0.94	0.12	52,52,52,52	0
55	MG	2A	3646	1/1	0.94	0.08	64,64,64,64	0
55	MG	2a	1687	1/1	0.94	0.20	52,52,52,52	0
55	MG	1A	3890	1/1	0.94	0.08	53,53,53,53	0
55	MG	2A	3648	1/1	0.94	0.14	56,56,56,56	0
55	MG	1a	1675	1/1	0.94	0.24	63,63,63,63	0
55	MG	1A	3324	1/1	0.94	0.28	61,61,61,61	0
55	MG	1U	204	1/1	0.94	0.15	61,61,61,61	0
55	MG	2A	3407	1/1	0.94	0.11	40,40,40,40	0
55	MG	2A	3656	1/1	0.94	0.06	41,41,41,41	0
55	MG	1A	3550	1/1	0.94	0.12	35,35,35,35	0
55	MG	1A	3895	1/1	0.94	0.10	54,54,54,54	0
55	MG	1A	3898	1/1	0.94	0.08	20,20,20,20	0
55	MG	1A	3277	1/1	0.94	0.10	46,46,46,46	0
55	MG	1A	3205	1/1	0.94	0.23	60,60,60,60	0
55	MG	1A	3100	1/1	0.94	0.18	30,30,30,30	0
55	MG	1A	3785	1/1	0.94	0.16	39,39,39,39	0
55	MG	2A	3421	1/1	0.94	0.20	63,63,63,63	0
55	MG	2A	3202	1/1	0.94	0.15	54,54,54,54	0
55	MG	1A	3676	1/1	0.94	0.07	37,37,37,37	0
55	MG	2A	3016	1/1	0.94	0.28	60,60,60,60	0
55	MG	2A	3020	1/1	0.94	0.18	46,46,46,46	0
55	MG	2A	3676	1/1	0.94	0.06	65,65,65,65	0
55	MG	2A	3426	1/1	0.94	0.06	54,54,54,54	0
55	MG	1A	3243	1/1	0.94	0.15	45,45,45,45	0
55	MG	1W	204	1/1	0.94	0.14	31,31,31,31	0
55	MG	1W	206	1/1	0.94	0.12	24,24,24,24	0
55	MG	2A	3209	1/1	0.94	0.13	58,58,58,58	0
55	MG	1A	3790	1/1	0.94	0.14	40,40,40,40	0
55	MG	2A	3214	1/1	0.94	0.12	49,49,49,49	0
55	MG	2A	3031	1/1	0.94	0.10	28,28,28,28	0
55	MG	1a	1691	1/1	0.94	0.14	49,49,49,49	0
55	MG	1A	3244	1/1	0.94	0.25	51,51,51,51	0
55	MG	1A	3490	1/1	0.94	0.25	35,35,35,35	0
55	MG	1A	3685	1/1	0.94	0.11	46,46,46,46	0
55	MG	1A	3568	1/1	0.94	0.10	54,54,54,54	0
55	MG	10	101	1/1	0.94	0.15	46,46,46,46	0
55	MG	2A	3451	1/1	0.94	0.08	36,36,36,36	0
55	MG	2a	1728	1/1	0.94	0.07	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	10	102	1/1	0.94	0.20	52,52,52,52	0
55	MG	2A	3045	1/1	0.94	0.12	55,55,55,55	0
55	MG	10	104	1/1	0.94	0.07	41,41,41,41	0
55	MG	2A	3696	1/1	0.94	0.21	48,48,48,48	0
55	MG	1A	3689	1/1	0.94	0.10	47,47,47,47	0
55	MG	1A	3797	1/1	0.94	0.13	42,42,42,42	0
55	MG	11	102	1/1	0.94	0.09	41,41,41,41	0
55	MG	1A	3245	1/1	0.94	0.19	35,35,35,35	0
55	MG	1A	3179	1/1	0.94	0.17	31,31,31,31	0
55	MG	2A	3054	1/1	0.94	0.23	53,53,53,53	0
55	MG	12	101	1/1	0.94	0.10	49,49,49,49	0
55	MG	2A	3056	1/1	0.94	0.09	48,48,48,48	0
55	MG	13	103	1/1	0.94	0.11	45,45,45,45	0
55	MG	1A	4048	1/1	0.94	0.13	47,47,47,47	0
55	MG	2a	1746	1/1	0.94	0.12	57,57,57,57	0
55	MG	2A	3709	1/1	0.94	0.16	55,55,55,55	0
55	MG	15	107	1/1	0.94	0.10	66,66,66,66	0
55	MG	2A	3239	1/1	0.94	0.14	57,57,57,57	0
55	MG	2A	3063	1/1	0.94	0.09	44,44,44,44	0
55	MG	16	101	1/1	0.94	0.07	47,47,47,47	0
55	MG	1A	3375	1/1	0.94	0.14	45,45,45,45	0
55	MG	1A	3002	1/1	0.94	0.09	54,54,54,54	0
55	MG	2A	3070	1/1	0.94	0.09	48,48,48,48	0
55	MG	2A	3071	1/1	0.94	0.09	52,52,52,52	0
55	MG	1B	201	1/1	0.94	0.08	47,47,47,47	0
55	MG	2A	3073	1/1	0.94	0.08	42,42,42,42	0
55	MG	1A	3285	1/1	0.94	0.25	49,49,49,49	0
55	MG	2A	3251	1/1	0.94	0.32	57,57,57,57	0
55	MG	1A	3071	1/1	0.94	0.25	45,45,45,45	0
55	MG	1A	3216	1/1	0.94	0.22	25,25,25,25	0
55	MG	2A	3486	1/1	0.94	0.09	46,46,46,46	0
55	MG	2a	1764	1/1	0.94	0.08	62,62,62,62	0
55	MG	1A	3709	1/1	0.94	0.06	41,41,41,41	0
55	MG	1B	210	1/1	0.94	0.08	48,48,48,48	0
55	MG	1A	3715	1/1	0.94	0.13	19,19,19,19	0
55	MG	2A	3490	1/1	0.94	0.12	63,63,63,63	0
55	MG	1a	1728	1/1	0.94	0.16	54,54,54,54	0
55	MG	2D	301	1/1	0.94	0.14	39,39,39,39	0
55	MG	2A	3259	1/1	0.94	0.26	49,49,49,49	0
55	MG	1a	1729	1/1	0.94	0.21	54,54,54,54	0
55	MG	1a	1732	1/1	0.94	0.13	61,61,61,61	0
55	MG	1A	3438	1/1	0.94	0.14	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2a	1776	1/1	0.94	0.18	67,67,67,67	0
55	MG	1A	3721	1/1	0.94	0.09	39,39,39,39	0
55	MG	2A	3092	1/1	0.94	0.14	49,49,49,49	0
55	MG	1a	1738	1/1	0.94	0.08	45,45,45,45	0
55	MG	1a	1739	1/1	0.94	0.17	57,57,57,57	0
55	MG	1A	3942	1/1	0.94	0.09	26,26,26,26	0
55	MG	1A	3945	1/1	0.94	0.06	36,36,36,36	0
55	MG	2A	3100	1/1	0.94	0.09	53,53,53,53	0
55	MG	2N	201	1/1	0.94	0.11	57,57,57,57	0
55	MG	1a	1611	1/1	0.94	0.09	70,70,70,70	0
55	MG	2A	3506	1/1	0.94	0.07	59,59,59,59	0
55	MG	2a	1789	1/1	0.94	0.07	46,46,46,46	0
55	MG	2A	3507	1/1	0.94	0.15	58,58,58,58	0
55	MG	1A	3083	1/1	0.94	0.09	30,30,30,30	0
55	MG	2T	202	1/1	0.94	0.13	38,38,38,38	0
55	MG	2A	3274	1/1	0.94	0.08	63,63,63,63	0
55	MG	1A	3725	1/1	0.94	0.07	48,48,48,48	0
55	MG	1A	3951	1/1	0.94	0.11	55,55,55,55	0
55	MG	2A	3106	1/1	0.94	0.10	49,49,49,49	0
55	MG	1A	3084	1/1	0.94	0.09	26,26,26,26	0
55	MG	2A	3282	1/1	0.94	0.12	58,58,58,58	0
55	MG	1A	3293	1/1	0.94	0.15	45,45,45,45	0
55	MG	1a	1752	1/1	0.94	0.13	59,59,59,59	0
55	MG	2A	3285	1/1	0.94	0.20	55,55,55,55	0
55	MG	1A	3223	1/1	0.94	0.12	47,47,47,47	0
55	MG	2A	3521	1/1	0.94	0.08	44,44,44,44	0
55	MG	1A	3224	1/1	0.94	0.10	37,37,37,37	0
55	MG	2A	3292	1/1	0.94	0.23	65,65,65,65	0
55	MG	1A	3602	1/1	0.94	0.11	37,37,37,37	0
55	MG	2x	101	1/1	0.94	0.15	65,65,65,65	0
55	MG	1A	3021	1/1	0.94	0.27	55,55,55,55	0
55	MG	1A	3343	1/1	0.94	0.10	39,39,39,39	0
55	MG	1A	3737	1/1	0.94	0.08	25,25,25,25	0
55	MG	1A	3394	1/1	0.94	0.10	49,49,49,49	0
55	MG	1A	3395	1/1	0.94	0.21	50,50,50,50	0
55	MG	1A	3396	1/1	0.94	0.10	55,55,55,55	0
55	MG	2A	3126	1/1	0.94	0.09	40,40,40,40	0
55	MG	1A	3120	1/1	0.94	0.25	30,30,30,30	0
55	MG	1A	3228	1/1	0.94	0.12	48,48,48,48	0
55	MG	1A	3346	1/1	0.94	0.11	50,50,50,50	0
55	MG	1A	3154	1/1	0.95	0.25	48,48,48,48	0
55	MG	1A	3647	1/1	0.95	0.04	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1X	103	1/1	0.95	0.15	38,38,38,38	0
55	MG	1A	3155	1/1	0.95	0.06	36,36,36,36	0
55	MG	1A	3651	1/1	0.95	0.10	45,45,45,45	0
55	MG	1Z	301	1/1	0.95	0.17	60,60,60,60	0
55	MG	2D	303	1/1	0.95	0.18	48,48,48,48	0
55	MG	2D	304	1/1	0.95	0.07	34,34,34,34	0
55	MG	1a	1773	1/1	0.95	0.07	83,83,83,83	0
55	MG	1A	3801	1/1	0.95	0.10	37,37,37,37	0
55	MG	2E	301	1/1	0.95	0.11	39,39,39,39	0
55	MG	1A	3424	1/1	0.95	0.37	65,65,65,65	0
55	MG	1A	3653	1/1	0.95	0.12	45,45,45,45	0
55	MG	10	103	1/1	0.95	0.06	48,48,48,48	0
55	MG	1A	3804	1/1	0.95	0.16	34,34,34,34	0
55	MG	1A	3361	1/1	0.95	0.15	35,35,35,35	0
55	MG	1A	3656	1/1	0.95	0.21	54,54,54,54	0
55	MG	1a	1784	1/1	0.95	0.08	65,65,65,65	0
55	MG	1A	3992	1/1	0.95	0.05	35,35,35,35	0
55	MG	1A	3993	1/1	0.95	0.04	29,29,29,29	0
55	MG	2A	3464	1/1	0.95	0.06	45,45,45,45	0
55	MG	2P	201	1/1	0.95	0.12	59,59,59,59	0
55	MG	2Q	202	1/1	0.95	0.20	45,45,45,45	0
55	MG	1A	3510	1/1	0.95	0.20	53,53,53,53	0
55	MG	1A	3809	1/1	0.95	0.21	34,34,34,34	0
55	MG	2R	202	1/1	0.95	0.09	47,47,47,47	0
55	MG	13	102	1/1	0.95	0.14	47,47,47,47	0
55	MG	1a	1790	1/1	0.95	0.06	57,57,57,57	0
55	MG	1A	3426	1/1	0.95	0.20	45,45,45,45	0
55	MG	2A	3471	1/1	0.95	0.09	64,64,64,64	0
55	MG	1A	3362	1/1	0.95	0.33	45,45,45,45	0
55	MG	15	103	1/1	0.95	0.18	41,41,41,41	0
55	MG	15	106	1/1	0.95	0.20	43,43,43,43	0
55	MG	1A	3812	1/1	0.95	0.18	39,39,39,39	0
55	MG	1A	4007	1/1	0.95	0.06	57,57,57,57	0
55	MG	17	104	1/1	0.95	0.14	34,34,34,34	0
55	MG	27	101	1/1	0.95	0.19	50,50,50,50	0
55	MG	2A	3479	1/1	0.95	0.08	29,29,29,29	0
55	MG	17	105	1/1	0.95	0.07	41,41,41,41	0
55	MG	1A	3662	1/1	0.95	0.10	47,47,47,47	0
55	MG	2A	3212	1/1	0.95	0.41	67,67,67,67	0
55	MG	1A	3106	1/1	0.95	0.06	38,38,38,38	0
55	MG	1A	4010	1/1	0.95	0.08	39,39,39,39	0
55	MG	1A	3667	1/1	0.95	0.06	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3818	1/1	0.95	0.06	20,20,20,20	0
55	MG	1A	3161	1/1	0.95	0.05	30,30,30,30	0
55	MG	2A	3220	1/1	0.95	0.27	57,57,57,57	0
55	MG	1A	3366	1/1	0.95	0.17	27,27,27,27	0
55	MG	1A	3059	1/1	0.95	0.13	30,30,30,30	0
55	MG	1A	3518	1/1	0.95	0.08	39,39,39,39	0
55	MG	1A	3085	1/1	0.95	0.19	32,32,32,32	0
55	MG	2A	3494	1/1	0.95	0.06	46,46,46,46	0
55	MG	2a	1612	1/1	0.95	0.17	54,54,54,54	0
55	MG	1A	3675	1/1	0.95	0.16	32,32,32,32	0
55	MG	1a	1607	1/1	0.95	0.14	54,54,54,54	0
55	MG	1A	3436	1/1	0.95	0.22	31,31,31,31	0
55	MG	1A	4026	1/1	0.95	0.10	51,51,51,51	0
55	MG	1A	4027	1/1	0.95	0.12	46,46,46,46	0
55	MG	2a	1618	1/1	0.95	0.11	61,61,61,61	0
55	MG	1A	3369	1/1	0.95	0.18	39,39,39,39	0
55	MG	1A	4029	1/1	0.95	0.25	49,49,49,49	0
55	MG	1A	3164	1/1	0.95	0.07	34,34,34,34	0
55	MG	1A	3832	1/1	0.95	0.08	59,59,59,59	0
55	MG	1A	3086	1/1	0.95	0.26	38,38,38,38	0
55	MG	1a	1619	1/1	0.95	0.15	64,64,64,64	0
55	MG	1A	3683	1/1	0.95	0.09	54,54,54,54	0
55	MG	1A	3529	1/1	0.95	0.08	52,52,52,52	0
55	MG	2A	3001	1/1	0.95	0.28	57,57,57,57	0
55	MG	1A	3837	1/1	0.95	0.07	31,31,31,31	0
55	MG	1a	1623	1/1	0.95	0.17	51,51,51,51	0
55	MG	1A	3687	1/1	0.95	0.12	52,52,52,52	0
55	MG	2A	3008	1/1	0.95	0.13	65,65,65,65	0
55	MG	1A	3319	1/1	0.95	0.11	39,39,39,39	0
55	MG	1A	3322	1/1	0.95	0.07	43,43,43,43	0
55	MG	1A	3690	1/1	0.95	0.10	53,53,53,53	0
55	MG	2A	3248	1/1	0.95	0.18	36,36,36,36	0
55	MG	1A	3374	1/1	0.95	0.10	49,49,49,49	0
55	MG	1A	3269	1/1	0.95	0.31	33,33,33,33	0
55	MG	1A	3697	1/1	0.95	0.08	39,39,39,39	0
55	MG	2A	3018	1/1	0.95	0.07	58,58,58,58	0
55	MG	1A	3535	1/1	0.95	0.08	22,22,22,22	0
55	MG	1A	3377	1/1	0.95	0.29	40,40,40,40	0
55	MG	1A	3538	1/1	0.95	0.11	25,25,25,25	0
55	MG	2A	3026	1/1	0.95	0.16	45,45,45,45	0
55	MG	1A	3446	1/1	0.95	0.09	53,53,53,53	0
55	MG	1A	3116	1/1	0.95	0.10	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3448	1/1	0.95	0.14	41,41,41,41	0
55	MG	1A	4049	1/1	0.95	0.14	21,21,21,21	0
55	MG	2A	3536	1/1	0.95	0.08	36,36,36,36	0
55	MG	2a	1653	1/1	0.95	0.12	58,58,58,58	0
55	MG	2A	3537	1/1	0.95	0.08	47,47,47,47	0
55	MG	1A	4050	1/1	0.95	0.11	46,46,46,46	0
55	MG	1A	3860	1/1	0.95	0.08	31,31,31,31	0
55	MG	1A	3712	1/1	0.95	0.08	41,41,41,41	0
55	MG	2A	3543	1/1	0.95	0.08	64,64,64,64	0
55	MG	1A	3119	1/1	0.95	0.27	24,24,24,24	0
55	MG	1B	202	1/1	0.95	0.18	44,44,44,44	0
55	MG	2A	3267	1/1	0.95	0.17	43,43,43,43	0
55	MG	2A	3548	1/1	0.95	0.07	52,52,52,52	0
55	MG	1A	3863	1/1	0.95	0.06	38,38,38,38	0
55	MG	1A	3452	1/1	0.95	0.26	39,39,39,39	0
55	MG	1A	3087	1/1	0.95	0.08	39,39,39,39	0
55	MG	2A	3047	1/1	0.95	0.27	60,60,60,60	0
55	MG	1B	207	1/1	0.95	0.26	45,45,45,45	0
55	MG	2A	3555	1/1	0.95	0.07	52,52,52,52	0
55	MG	1A	3381	1/1	0.95	0.14	33,33,33,33	0
55	MG	1A	3455	1/1	0.95	0.15	34,34,34,34	0
55	MG	1A	3727	1/1	0.95	0.09	24,24,24,24	0
55	MG	1A	3176	1/1	0.95	0.17	38,38,38,38	0
55	MG	1A	3878	1/1	0.95	0.09	59,59,59,59	0
55	MG	1B	215	1/1	0.95	0.11	56,56,56,56	0
55	MG	1A	3383	1/1	0.95	0.40	41,41,41,41	0
55	MG	1a	1656	1/1	0.95	0.18	49,49,49,49	0
55	MG	1A	3882	1/1	0.95	0.06	72,72,72,72	0
55	MG	2A	3286	1/1	0.95	0.13	52,52,52,52	0
55	MG	2A	3060	1/1	0.95	0.08	44,44,44,44	0
55	MG	2A	3569	1/1	0.95	0.11	50,50,50,50	0
55	MG	2A	3288	1/1	0.95	0.16	63,63,63,63	0
55	MG	1A	3032	1/1	0.95	0.41	36,36,36,36	0
55	MG	2A	3572	1/1	0.95	0.08	53,53,53,53	0
55	MG	2A	3573	1/1	0.95	0.05	52,52,52,52	0
55	MG	2A	3290	1/1	0.95	0.36	57,57,57,57	0
55	MG	2A	3291	1/1	0.95	0.07	42,42,42,42	0
55	MG	1A	3044	1/1	0.95	0.11	44,44,44,44	0
55	MG	2a	1690	1/1	0.95	0.11	64,64,64,64	0
55	MG	1A	3561	1/1	0.95	0.06	29,29,29,29	0
55	MG	2A	3066	1/1	0.95	0.13	52,52,52,52	0
55	MG	1A	3886	1/1	0.95	0.07	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3297	1/1	0.95	0.15	29,29,29,29	0
55	MG	2A	3583	1/1	0.95	0.06	46,46,46,46	0
55	MG	2A	3068	1/1	0.95	0.23	59,59,59,59	0
55	MG	1A	3460	1/1	0.95	0.08	24,24,24,24	0
55	MG	2A	3589	1/1	0.95	0.04	49,49,49,49	0
55	MG	1A	3064	1/1	0.95	0.11	45,45,45,45	0
55	MG	1A	3183	1/1	0.95	0.20	27,27,27,27	0
55	MG	1A	3096	1/1	0.95	0.33	40,40,40,40	0
55	MG	1A	3893	1/1	0.95	0.07	62,62,62,62	0
55	MG	2A	3595	1/1	0.95	0.06	62,62,62,62	0
55	MG	1A	3464	1/1	0.95	0.24	54,54,54,54	0
55	MG	2A	3599	1/1	0.95	0.07	66,66,66,66	0
55	MG	1A	3027	1/1	0.95	0.11	29,29,29,29	0
55	MG	2A	3076	1/1	0.95	0.07	47,47,47,47	0
55	MG	2A	3077	1/1	0.95	0.06	35,35,35,35	0
55	MG	1a	1670	1/1	0.95	0.20	49,49,49,49	0
55	MG	2A	3310	1/1	0.95	0.09	44,44,44,44	0
55	MG	1B	234	1/1	0.95	0.08	60,60,60,60	0
55	MG	1A	3743	1/1	0.95	0.05	31,31,31,31	0
55	MG	1a	1673	1/1	0.95	0.27	56,56,56,56	0
55	MG	1A	3239	1/1	0.95	0.08	46,46,46,46	0
55	MG	2A	3083	1/1	0.95	0.07	28,28,28,28	0
55	MG	1A	3745	1/1	0.95	0.10	48,48,48,48	0
55	MG	1B	238	1/1	0.95	0.07	31,31,31,31	0
55	MG	1A	3904	1/1	0.95	0.14	50,50,50,50	0
55	MG	2A	3089	1/1	0.95	0.25	59,59,59,59	0
55	MG	2a	1721	1/1	0.95	0.07	45,45,45,45	0
55	MG	2a	1722	1/1	0.95	0.10	49,49,49,49	0
55	MG	2a	1723	1/1	0.95	0.06	64,64,64,64	0
55	MG	1D	304	1/1	0.95	0.08	28,28,28,28	0
55	MG	2A	3618	1/1	0.95	0.05	41,41,41,41	0
55	MG	1D	308	1/1	0.95	0.07	45,45,45,45	0
55	MG	2A	3621	1/1	0.95	0.13	74,74,74,74	0
55	MG	1D	309	1/1	0.95	0.24	26,26,26,26	0
55	MG	1A	3136	1/1	0.95	0.07	36,36,36,36	0
55	MG	2a	1730	1/1	0.95	0.28	64,64,64,64	0
55	MG	2A	3626	1/1	0.95	0.08	33,33,33,33	0
55	MG	1E	301	1/1	0.95	0.16	35,35,35,35	0
55	MG	2A	3630	1/1	0.95	0.16	57,57,57,57	0
55	MG	2A	3098	1/1	0.95	0.23	57,57,57,57	0
55	MG	1A	3141	1/1	0.95	0.14	21,21,21,21	0
55	MG	1A	3192	1/1	0.95	0.14	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1E	307	1/1	0.95	0.14	51,51,51,51	0
55	MG	2A	3331	1/1	0.95	0.12	48,48,48,48	0
55	MG	1A	3578	1/1	0.95	0.09	31,31,31,31	0
55	MG	2A	3103	1/1	0.95	0.07	45,45,45,45	0
55	MG	1A	3581	1/1	0.95	0.06	52,52,52,52	0
55	MG	1A	3751	1/1	0.95	0.09	35,35,35,35	0
55	MG	1F	303	1/1	0.95	0.06	31,31,31,31	0
55	MG	2A	3340	1/1	0.95	0.07	48,48,48,48	0
55	MG	1A	3142	1/1	0.95	0.09	34,34,34,34	0
55	MG	1A	3584	1/1	0.95	0.11	42,42,42,42	0
55	MG	2A	3653	1/1	0.95	0.11	39,39,39,39	0
55	MG	1A	3754	1/1	0.95	0.08	29,29,29,29	0
55	MG	1A	3756	1/1	0.95	0.07	24,24,24,24	0
55	MG	1A	3920	1/1	0.95	0.08	32,32,32,32	0
55	MG	1A	3288	1/1	0.95	0.09	42,42,42,42	0
55	MG	2A	3353	1/1	0.95	0.10	34,34,34,34	0
55	MG	1A	3587	1/1	0.95	0.07	36,36,36,36	0
55	MG	2A	3355	1/1	0.95	0.10	47,47,47,47	0
55	MG	1G	205	1/1	0.95	0.13	56,56,56,56	0
55	MG	2A	3118	1/1	0.95	0.33	61,61,61,61	0
55	MG	1A	3080	1/1	0.95	0.14	36,36,36,36	0
55	MG	1A	3926	1/1	0.95	0.16	52,52,52,52	0
55	MG	1A	3760	1/1	0.95	0.14	55,55,55,55	0
55	MG	1A	3246	1/1	0.95	0.23	37,37,37,37	0
55	MG	2A	3124	1/1	0.95	0.10	54,54,54,54	0
55	MG	1A	3195	1/1	0.95	0.24	58,58,58,58	0
55	MG	2a	1766	1/1	0.95	0.18	63,63,63,63	0
55	MG	2A	3370	1/1	0.95	0.05	41,41,41,41	0
55	MG	1A	3594	1/1	0.95	0.07	14,14,14,14	0
55	MG	1A	3248	1/1	0.95	0.12	36,36,36,36	0
55	MG	1A	3933	1/1	0.95	0.10	16,16,16,16	0
55	MG	1A	3596	1/1	0.95	0.07	35,35,35,35	0
55	MG	1A	3403	1/1	0.95	0.10	59,59,59,59	0
55	MG	1A	3404	1/1	0.95	0.25	40,40,40,40	0
55	MG	1A	3144	1/1	0.95	0.18	60,60,60,60	0
55	MG	2A	3383	1/1	0.95	0.08	32,32,32,32	0
55	MG	1P	204	1/1	0.95	0.18	25,25,25,25	0
55	MG	1P	205	1/1	0.95	0.18	31,31,31,31	0
55	MG	2A	3390	1/1	0.95	0.18	54,54,54,54	0
55	MG	2A	3140	1/1	0.95	0.10	33,33,33,33	0
55	MG	2a	1781	1/1	0.95	0.07	73,73,73,73	0
55	MG	1A	3940	1/1	0.95	0.06	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1718	1/1	0.95	0.10	60,60,60,60	0
55	MG	1Q	201	1/1	0.95	0.29	40,40,40,40	0
55	MG	1Q	203	1/1	0.95	0.06	41,41,41,41	0
55	MG	1A	3484	1/1	0.95	0.22	32,32,32,32	0
55	MG	1A	3943	1/1	0.95	0.07	28,28,28,28	0
55	MG	1A	3067	1/1	0.95	0.15	30,30,30,30	0
55	MG	1A	3489	1/1	0.95	0.49	33,33,33,33	0
55	MG	1A	3298	1/1	0.95	0.06	43,43,43,43	0
55	MG	2a	1791	1/1	0.95	0.12	56,56,56,56	0
55	MG	1A	3622	1/1	0.95	0.12	18,18,18,18	0
55	MG	1A	3952	1/1	0.95	0.07	59,59,59,59	0
55	MG	1A	3626	1/1	0.95	0.09	25,25,25,25	0
55	MG	1A	3300	1/1	0.95	0.19	45,45,45,45	0
55	MG	1A	3410	1/1	0.95	0.22	49,49,49,49	0
55	MG	1a	1741	1/1	0.95	0.21	75,75,75,75	0
55	MG	2A	3707	1/1	0.95	0.14	59,59,59,59	0
55	MG	1A	3411	1/1	0.95	0.13	45,45,45,45	0
55	MG	1a	1744	1/1	0.95	0.07	47,47,47,47	0
55	MG	1A	3004	1/1	0.95	0.06	25,25,25,25	0
55	MG	1A	3351	1/1	0.95	0.07	51,51,51,51	0
55	MG	2l	201	1/1	0.95	0.10	59,59,59,59	0
55	MG	1U	208	1/1	0.95	0.18	37,37,37,37	0
55	MG	2l	204	1/1	0.95	0.15	64,64,64,64	0
55	MG	1A	3202	1/1	0.95	0.09	58,58,58,58	0
55	MG	2A	3715	1/1	0.95	0.16	64,64,64,64	0
55	MG	1A	3354	1/1	0.95	0.15	52,52,52,52	0
55	MG	2A	3170	1/1	0.95	0.10	43,43,43,43	0
55	MG	2B	201	1/1	0.95	0.33	75,75,75,75	0
55	MG	2A	3428	1/1	0.95	0.10	56,56,56,56	0
55	MG	1A	3788	1/1	0.95	0.06	22,22,22,22	0
55	MG	1V	203	1/1	0.95	0.13	35,35,35,35	0
55	MG	1A	3499	1/1	0.95	0.06	40,40,40,40	0
55	MG	1A	3254	1/1	0.95	0.10	37,37,37,37	0
55	MG	1A	3152	1/1	0.95	0.19	21,21,21,21	0
55	MG	2A	3436	1/1	0.95	0.09	36,36,36,36	0
55	MG	1A	3971	1/1	0.95	0.06	30,30,30,30	0
55	MG	1A	3058	1/1	0.95	0.20	55,55,55,55	0
58	ZN	2Y	202	1/1	0.95	0.07	97,97,97,97	0
55	MG	1A	3504	1/1	0.95	0.08	43,43,43,43	0
55	MG	2A	3514	1/1	0.96	0.12	57,57,57,57	0
55	MG	1a	1714	1/1	0.96	0.28	47,47,47,47	0
55	MG	1A	3139	1/1	0.96	0.13	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	2A	3091	1/1	0.96	0.10	56,56,56,56	0
55	MG	23	101	1/1	0.96	0.09	52,52,52,52	0
55	MG	25	101	1/1	0.96	0.24	55,55,55,55	0
55	MG	1A	3877	1/1	0.96	0.14	53,53,53,53	0
55	MG	1X	101	1/1	0.96	0.07	28,28,28,28	0
55	MG	1A	3213	1/1	0.96	0.19	19,19,19,19	0
55	MG	1A	3214	1/1	0.96	0.14	35,35,35,35	0
55	MG	2A	3096	1/1	0.96	0.15	43,43,43,43	0
55	MG	1A	3881	1/1	0.96	0.09	54,54,54,54	0
55	MG	1a	1722	1/1	0.96	0.08	57,57,57,57	0
55	MG	1A	3527	1/1	0.96	0.13	32,32,32,32	0
55	MG	2A	3528	1/1	0.96	0.17	61,61,61,61	0
55	MG	1Y	202	1/1	0.96	0.18	46,46,46,46	0
55	MG	1A	3110	1/1	0.96	0.04	43,43,43,43	0
55	MG	1A	3218	1/1	0.96	0.10	39,39,39,39	0
55	MG	1A	3070	1/1	0.96	0.20	42,42,42,42	0
55	MG	1a	1734	1/1	0.96	0.07	55,55,55,55	0
55	MG	1A	3644	1/1	0.96	0.10	43,43,43,43	0
55	MG	1A	3645	1/1	0.96	0.05	58,58,58,58	0
55	MG	1A	3308	1/1	0.96	0.30	25,25,25,25	0
55	MG	1A	3766	1/1	0.96	0.08	64,64,64,64	0
55	MG	2A	3540	1/1	0.96	0.09	58,58,58,58	0
55	MG	1A	3891	1/1	0.96	0.05	32,32,32,32	0
55	MG	1A	3358	1/1	0.96	0.21	31,31,31,31	0
55	MG	1A	3261	1/1	0.96	0.10	46,46,46,46	0
55	MG	1A	3650	1/1	0.96	0.09	59,59,59,59	0
55	MG	2A	3307	1/1	0.96	0.13	62,62,62,62	0
55	MG	1A	3220	1/1	0.96	0.07	29,29,29,29	0
55	MG	1A	3897	1/1	0.96	0.14	45,45,45,45	0
55	MG	1A	3042	1/1	0.96	0.11	19,19,19,19	0
55	MG	1A	3773	1/1	0.96	0.04	37,37,37,37	0
55	MG	15	101	1/1	0.96	0.27	27,27,27,27	0
55	MG	15	102	1/1	0.96	0.09	40,40,40,40	0
55	MG	2A	3314	1/1	0.96	0.12	64,64,64,64	0
55	MG	1A	3115	1/1	0.96	0.07	49,49,49,49	0
55	MG	15	105	1/1	0.96	0.17	31,31,31,31	0
55	MG	2A	3127	1/1	0.96	0.19	56,56,56,56	0
55	MG	1A	3265	1/1	0.96	0.22	42,42,42,42	0
55	MG	2A	3129	1/1	0.96	0.25	54,54,54,54	0
55	MG	1A	3907	1/1	0.96	0.06	58,58,58,58	0
55	MG	2A	3321	1/1	0.96	0.30	49,49,49,49	0
55	MG	2A	3131	1/1	0.96	0.15	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3181	1/1	0.96	0.15	31,31,31,31	0
55	MG	17	102	1/1	0.96	0.07	33,33,33,33	0
55	MG	1A	4053	1/1	0.96	0.13	57,57,57,57	0
55	MG	1A	3063	1/1	0.96	0.15	33,33,33,33	0
55	MG	1a	1762	1/1	0.96	0.15	62,62,62,62	0
55	MG	1a	1763	1/1	0.96	0.10	59,59,59,59	0
55	MG	1A	3185	1/1	0.96	0.16	32,32,32,32	0
55	MG	1A	3227	1/1	0.96	0.16	55,55,55,55	0
55	MG	18	102	1/1	0.96	0.31	38,38,38,38	0
55	MG	1A	3146	1/1	0.96	0.12	47,47,47,47	0
55	MG	2a	1645	1/1	0.96	0.08	51,51,51,51	0
55	MG	1a	1768	1/1	0.96	0.05	73,73,73,73	0
55	MG	2a	1647	1/1	0.96	0.05	51,51,51,51	0
55	MG	2A	3334	1/1	0.96	0.09	34,34,34,34	0
55	MG	2a	1649	1/1	0.96	0.17	58,58,58,58	0
55	MG	1A	3665	1/1	0.96	0.09	64,64,64,64	0
55	MG	2a	1651	1/1	0.96	0.19	51,51,51,51	0
55	MG	1A	3474	1/1	0.96	0.19	37,37,37,37	0
55	MG	1B	206	1/1	0.96	0.06	42,42,42,42	0
55	MG	2A	3147	1/1	0.96	0.15	52,52,52,52	0
55	MG	1A	3475	1/1	0.96	0.19	35,35,35,35	0
55	MG	1a	1602	1/1	0.96	0.12	63,63,63,63	0
55	MG	2A	3343	1/1	0.96	0.08	30,30,30,30	0
55	MG	2A	3587	1/1	0.96	0.06	67,67,67,67	0
55	MG	2A	3344	1/1	0.96	0.08	22,22,22,22	0
55	MG	2A	3345	1/1	0.96	0.16	39,39,39,39	0
55	MG	1A	3118	1/1	0.96	0.07	37,37,37,37	0
55	MG	2A	3349	1/1	0.96	0.09	34,34,34,34	0
55	MG	1B	209	1/1	0.96	0.07	48,48,48,48	0
55	MG	2A	3152	1/1	0.96	0.15	57,57,57,57	0
55	MG	1A	3918	1/1	0.96	0.09	17,17,17,17	0
55	MG	2A	3154	1/1	0.96	0.05	38,38,38,38	0
55	MG	2A	3155	1/1	0.96	0.10	55,55,55,55	0
55	MG	1A	3189	1/1	0.96	0.15	35,35,35,35	0
55	MG	2A	3357	1/1	0.96	0.05	29,29,29,29	0
55	MG	2A	3157	1/1	0.96	0.20	49,49,49,49	0
55	MG	1a	1783	1/1	0.96	0.06	42,42,42,42	0
55	MG	1A	3789	1/1	0.96	0.09	22,22,22,22	0
55	MG	2A	3160	1/1	0.96	0.33	59,59,59,59	0
55	MG	2A	3363	1/1	0.96	0.05	39,39,39,39	0
55	MG	2a	1676	1/1	0.96	0.12	52,52,52,52	0
55	MG	1A	3422	1/1	0.96	0.09	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1609	1/1	0.96	0.09	31,31,31,31	0
55	MG	1A	3275	1/1	0.96	0.08	32,32,32,32	0
55	MG	1A	3924	1/1	0.96	0.10	51,51,51,51	0
55	MG	2A	3369	1/1	0.96	0.06	31,31,31,31	0
55	MG	1B	217	1/1	0.96	0.06	45,45,45,45	0
55	MG	2A	3372	1/1	0.96	0.09	40,40,40,40	0
55	MG	1A	3233	1/1	0.96	0.11	20,20,20,20	0
55	MG	2A	3619	1/1	0.96	0.06	55,55,55,55	0
55	MG	2A	3167	1/1	0.96	0.12	49,49,49,49	0
55	MG	1a	1791	1/1	0.96	0.09	49,49,49,49	0
55	MG	2A	3622	1/1	0.96	0.11	49,49,49,49	0
55	MG	1B	220	1/1	0.96	0.09	42,42,42,42	0
55	MG	1A	3563	1/1	0.96	0.06	25,25,25,25	0
55	MG	2A	3379	1/1	0.96	0.09	28,28,28,28	0
55	MG	2A	3627	1/1	0.96	0.05	44,44,44,44	0
55	MG	1a	1617	1/1	0.96	0.06	51,51,51,51	0
55	MG	2A	3629	1/1	0.96	0.08	27,27,27,27	0
55	MG	2A	3381	1/1	0.96	0.14	59,59,59,59	0
55	MG	1A	3794	1/1	0.96	0.12	43,43,43,43	0
55	MG	2A	3632	1/1	0.96	0.06	35,35,35,35	0
55	MG	1A	3928	1/1	0.96	0.06	51,51,51,51	0
55	MG	1A	3053	1/1	0.96	0.08	27,27,27,27	0
55	MG	2A	3638	1/1	0.96	0.08	63,63,63,63	0
55	MG	1A	3677	1/1	0.96	0.09	18,18,18,18	0
55	MG	1A	3099	1/1	0.96	0.20	31,31,31,31	0
55	MG	2A	3641	1/1	0.96	0.10	43,43,43,43	0
55	MG	2a	1704	1/1	0.96	0.21	54,54,54,54	0
55	MG	2A	3642	1/1	0.96	0.06	37,37,37,37	0
55	MG	1A	3076	1/1	0.96	0.13	38,38,38,38	0
55	MG	1A	3799	1/1	0.96	0.07	21,21,21,21	0
55	MG	1A	3488	1/1	0.96	0.12	39,39,39,39	0
55	MG	1A	3046	1/1	0.96	0.17	48,48,48,48	0
55	MG	1A	3126	1/1	0.96	0.14	35,35,35,35	0
55	MG	2A	3396	1/1	0.96	0.06	32,32,32,32	0
55	MG	1A	3160	1/1	0.96	0.10	19,19,19,19	0
55	MG	1A	3431	1/1	0.96	0.20	27,27,27,27	0
55	MG	1A	3127	1/1	0.96	0.17	16,16,16,16	0
55	MG	1A	3433	1/1	0.96	0.25	47,47,47,47	0
55	MG	2A	3655	1/1	0.96	0.13	57,57,57,57	0
55	MG	1A	3434	1/1	0.96	0.25	35,35,35,35	0
55	MG	1A	3580	1/1	0.96	0.06	29,29,29,29	0
55	MG	2A	3658	1/1	0.96	0.07	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1D	303	1/1	0.96	0.04	19,19,19,19	0
55	MG	2A	3410	1/1	0.96	0.16	67,67,67,67	0
55	MG	1A	3695	1/1	0.96	0.07	34,34,34,34	0
55	MG	2A	3664	1/1	0.96	0.07	56,56,56,56	0
55	MG	2A	3412	1/1	0.96	0.13	47,47,47,47	0
55	MG	1A	3496	1/1	0.96	0.11	42,42,42,42	0
55	MG	1A	3242	1/1	0.96	0.15	51,51,51,51	0
55	MG	1A	3813	1/1	0.96	0.09	50,50,50,50	0
55	MG	1A	3699	1/1	0.96	0.11	26,26,26,26	0
55	MG	1E	303	1/1	0.96	0.22	32,32,32,32	0
55	MG	1A	3583	1/1	0.96	0.08	31,31,31,31	0
55	MG	1A	3701	1/1	0.96	0.10	25,25,25,25	0
55	MG	1E	306	1/1	0.96	0.10	31,31,31,31	0
55	MG	1A	3103	1/1	0.96	0.07	27,27,27,27	0
55	MG	1E	308	1/1	0.96	0.07	48,48,48,48	0
55	MG	1A	3959	1/1	0.96	0.15	34,34,34,34	0
55	MG	2a	1737	1/1	0.96	0.13	60,60,60,60	0
55	MG	2A	3427	1/1	0.96	0.06	32,32,32,32	0
55	MG	2A	3003	1/1	0.96	0.39	67,67,67,67	0
55	MG	1A	3437	1/1	0.96	0.10	43,43,43,43	0
55	MG	1A	3500	1/1	0.96	0.08	45,45,45,45	0
55	MG	1F	301	1/1	0.96	0.13	38,38,38,38	0
55	MG	1F	302	1/1	0.96	0.21	35,35,35,35	0
55	MG	2A	3009	1/1	0.96	0.13	50,50,50,50	0
55	MG	1A	3384	1/1	0.96	0.12	41,41,41,41	0
55	MG	1F	305	1/1	0.96	0.17	25,25,25,25	0
55	MG	1A	3966	1/1	0.96	0.09	47,47,47,47	0
55	MG	1A	3589	1/1	0.96	0.10	39,39,39,39	0
55	MG	2A	3440	1/1	0.96	0.07	27,27,27,27	0
55	MG	1A	3713	1/1	0.96	0.06	41,41,41,41	0
55	MG	1F	310	1/1	0.96	0.08	50,50,50,50	0
55	MG	2A	3017	1/1	0.96	0.05	33,33,33,33	0
55	MG	1A	3714	1/1	0.96	0.06	44,44,44,44	0
55	MG	2A	3446	1/1	0.96	0.19	38,38,38,38	0
55	MG	2A	3448	1/1	0.96	0.10	33,33,33,33	0
55	MG	1G	201	1/1	0.96	0.12	39,39,39,39	0
55	MG	2A	3450	1/1	0.96	0.16	53,53,53,53	0
55	MG	1A	3286	1/1	0.96	0.26	39,39,39,39	0
55	MG	1A	3066	1/1	0.96	0.09	35,35,35,35	0
55	MG	1A	3593	1/1	0.96	0.05	14,14,14,14	0
55	MG	1A	3013	1/1	0.96	0.08	29,29,29,29	0
55	MG	1A	3833	1/1	0.96	0.10	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1666	1/1	0.96	0.21	55,55,55,55	0
55	MG	1A	3505	1/1	0.96	0.23	30,30,30,30	0
55	MG	1A	3977	1/1	0.96	0.09	25,25,25,25	0
55	MG	2A	3035	1/1	0.96	0.08	44,44,44,44	0
55	MG	2A	3711	1/1	0.96	0.09	40,40,40,40	0
55	MG	1A	3979	1/1	0.96	0.06	38,38,38,38	0
55	MG	1A	3289	1/1	0.96	0.08	56,56,56,56	0
55	MG	1A	3600	1/1	0.96	0.04	19,19,19,19	0
55	MG	1A	3203	1/1	0.96	0.13	40,40,40,40	0
55	MG	1A	3985	1/1	0.96	0.06	14,14,14,14	0
55	MG	1A	3606	1/1	0.96	0.06	17,17,17,17	0
55	MG	1A	3987	1/1	0.96	0.15	63,63,63,63	0
55	MG	1A	3732	1/1	0.96	0.10	45,45,45,45	0
55	MG	1A	3166	1/1	0.96	0.29	34,34,34,34	0
55	MG	1A	3609	1/1	0.96	0.05	21,21,21,21	0
55	MG	2A	3241	1/1	0.96	0.07	55,55,55,55	0
55	MG	1A	3844	1/1	0.96	0.14	44,44,44,44	0
55	MG	1A	3610	1/1	0.96	0.05	24,24,24,24	0
55	MG	2A	3052	1/1	0.96	0.11	54,54,54,54	0
55	MG	2A	3476	1/1	0.96	0.09	61,61,61,61	0
55	MG	1A	3391	1/1	0.96	0.12	49,49,49,49	0
55	MG	1Q	202	1/1	0.96	0.14	33,33,33,33	0
55	MG	1A	3849	1/1	0.96	0.09	20,20,20,20	0
55	MG	1A	3134	1/1	0.96	0.15	39,39,39,39	0
55	MG	1A	3999	1/1	0.96	0.15	12,12,12,12	0
55	MG	1A	3393	1/1	0.96	0.22	47,47,47,47	0
55	MG	1A	3050	1/1	0.96	0.32	59,59,59,59	0
55	MG	2A	3252	1/1	0.96	0.30	48,48,48,48	0
55	MG	1A	4003	1/1	0.96	0.10	19,19,19,19	0
55	MG	1A	3619	1/1	0.96	0.08	28,28,28,28	0
55	MG	1S	202	1/1	0.96	0.06	45,45,45,45	0
55	MG	1A	4005	1/1	0.96	0.06	30,30,30,30	0
55	MG	2D	307	1/1	0.96	0.09	57,57,57,57	0
55	MG	1A	3449	1/1	0.96	0.35	32,32,32,32	0
55	MG	1A	3856	1/1	0.96	0.07	45,45,45,45	0
55	MG	1A	3450	1/1	0.96	0.28	44,44,44,44	0
55	MG	1A	3623	1/1	0.96	0.10	14,14,14,14	0
55	MG	1A	3624	1/1	0.96	0.06	21,21,21,21	0
55	MG	1A	4014	1/1	0.96	0.20	54,54,54,54	0
55	MG	1A	3625	1/1	0.96	0.08	63,63,63,63	0
55	MG	1U	209	1/1	0.96	0.14	30,30,30,30	0
55	MG	1a	1702	1/1	0.96	0.16	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3515	1/1	0.96	0.06	39,39,39,39	0
55	MG	1A	3207	1/1	0.96	0.11	44,44,44,44	0
55	MG	1A	3296	1/1	0.96	0.13	44,44,44,44	0
55	MG	2A	3269	1/1	0.96	0.27	39,39,39,39	0
55	MG	1a	1706	1/1	0.96	0.15	37,37,37,37	0
55	MG	2Q	204	1/1	0.96	0.15	59,59,59,59	0
55	MG	1A	3137	1/1	0.96	0.17	35,35,35,35	0
55	MG	1A	3520	1/1	0.96	0.12	28,28,28,28	0
55	MG	1A	4023	1/1	0.96	0.18	40,40,40,40	0
55	MG	1A	3872	1/1	0.96	0.05	54,54,54,54	0
55	MG	2U	201	1/1	0.96	0.10	49,49,49,49	0
55	MG	1A	3173	1/1	0.96	0.07	50,50,50,50	0
55	MG	1A	3635	1/1	0.96	0.05	14,14,14,14	0
55	MG	1W	205	1/1	0.96	0.19	43,43,43,43	0
55	MG	2A	3088	1/1	0.96	0.19	65,65,65,65	0
55	MG	2A	3588	1/1	0.97	0.04	50,50,50,50	0
55	MG	2A	3388	1/1	0.97	0.07	42,42,42,42	0
55	MG	2A	3210	1/1	0.97	0.13	50,50,50,50	0
55	MG	2A	3591	1/1	0.97	0.07	49,49,49,49	0
55	MG	1A	3157	1/1	0.97	0.06	35,35,35,35	0
55	MG	1A	3573	1/1	0.97	0.06	17,17,17,17	0
55	MG	2A	3213	1/1	0.97	0.13	47,47,47,47	0
55	MG	1A	3196	1/1	0.97	0.08	31,31,31,31	0
55	MG	2A	3596	1/1	0.97	0.13	69,69,69,69	0
55	MG	1A	3122	1/1	0.97	0.12	44,44,44,44	0
55	MG	2A	3598	1/1	0.97	0.06	42,42,42,42	0
55	MG	1A	3198	1/1	0.97	0.05	30,30,30,30	0
55	MG	2A	3217	1/1	0.97	0.10	49,49,49,49	0
55	MG	2A	3398	1/1	0.97	0.10	43,43,43,43	0
55	MG	1A	3030	1/1	0.97	0.04	37,37,37,37	0
55	MG	15	104	1/1	0.97	0.42	27,27,27,27	0
55	MG	2A	3401	1/1	0.97	0.10	22,22,22,22	0
55	MG	1A	3669	1/1	0.97	0.19	54,54,54,54	0
55	MG	2A	3606	1/1	0.97	0.07	41,41,41,41	0
55	MG	2A	3057	1/1	0.97	0.08	35,35,35,35	0
55	MG	1A	3022	1/1	0.97	0.10	33,33,33,33	0
55	MG	1A	3982	1/1	0.97	0.06	16,16,16,16	0
55	MG	1A	3101	1/1	0.97	0.29	35,35,35,35	0
55	MG	2A	3611	1/1	0.97	0.08	61,61,61,61	0
55	MG	17	101	1/1	0.97	0.06	30,30,30,30	0
55	MG	2A	3062	1/1	0.97	0.21	40,40,40,40	0
55	MG	2A	3614	1/1	0.97	0.14	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1721	1/1	0.97	0.08	47,47,47,47	0
55	MG	1A	3008	1/1	0.97	0.04	21,21,21,21	0
55	MG	17	103	1/1	0.97	0.10	30,30,30,30	0
55	MG	1a	1724	1/1	0.97	0.04	40,40,40,40	0
55	MG	1D	306	1/1	0.97	0.20	27,27,27,27	0
55	MG	2A	3232	1/1	0.97	0.07	35,35,35,35	0
55	MG	1D	307	1/1	0.97	0.14	39,39,39,39	0
55	MG	1A	3035	1/1	0.97	0.04	23,23,23,23	0
55	MG	1A	3775	1/1	0.97	0.09	43,43,43,43	0
55	MG	1A	3132	1/1	0.97	0.10	40,40,40,40	0
55	MG	2A	3625	1/1	0.97	0.10	37,37,37,37	0
55	MG	1D	311	1/1	0.97	0.13	38,38,38,38	0
55	MG	18	104	1/1	0.97	0.14	32,32,32,32	0
55	MG	1a	1737	1/1	0.97	0.17	48,48,48,48	0
55	MG	1A	3777	1/1	0.97	0.04	55,55,55,55	0
55	MG	1A	3249	1/1	0.97	0.09	51,51,51,51	0
55	MG	2A	3431	1/1	0.97	0.08	26,26,26,26	0
55	MG	1A	3586	1/1	0.97	0.09	33,33,33,33	0
55	MG	1A	3295	1/1	0.97	0.13	36,36,36,36	0
55	MG	1A	3679	1/1	0.97	0.06	45,45,45,45	0
55	MG	1A	3054	1/1	0.97	0.07	14,14,14,14	0
55	MG	1A	3681	1/1	0.97	0.07	30,30,30,30	0
55	MG	1A	3168	1/1	0.97	0.06	40,40,40,40	0
55	MG	2a	1668	1/1	0.97	0.32	57,57,57,57	0
55	MG	1A	3169	1/1	0.97	0.18	38,38,38,38	0
55	MG	1a	1748	1/1	0.97	0.07	52,52,52,52	0
55	MG	1A	3888	1/1	0.97	0.05	50,50,50,50	0
55	MG	2A	3087	1/1	0.97	0.05	40,40,40,40	0
55	MG	1E	313	1/1	0.97	0.12	52,52,52,52	0
55	MG	1A	3591	1/1	0.97	0.05	28,28,28,28	0
55	MG	1A	3299	1/1	0.97	0.06	20,20,20,20	0
55	MG	1A	3210	1/1	0.97	0.17	45,45,45,45	0
55	MG	2A	3447	1/1	0.97	0.15	52,52,52,52	0
55	MG	1A	3170	1/1	0.97	0.16	43,43,43,43	0
55	MG	1A	3519	1/1	0.97	0.09	24,24,24,24	0
55	MG	1A	3105	1/1	0.97	0.13	41,41,41,41	0
55	MG	1a	1615	1/1	0.97	0.06	56,56,56,56	0
55	MG	1A	3598	1/1	0.97	0.07	20,20,20,20	0
55	MG	2A	3097	1/1	0.97	0.11	52,52,52,52	0
55	MG	1A	3896	1/1	0.97	0.07	56,56,56,56	0
55	MG	1A	4012	1/1	0.97	0.10	35,35,35,35	0
55	MG	1A	3073	1/1	0.97	0.09	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3107	1/1	0.97	0.06	49,49,49,49	0
55	MG	1A	3899	1/1	0.97	0.12	43,43,43,43	0
55	MG	2A	3666	1/1	0.97	0.06	47,47,47,47	0
55	MG	1A	3604	1/1	0.97	0.04	14,14,14,14	0
55	MG	1A	3901	1/1	0.97	0.09	45,45,45,45	0
55	MG	1A	3605	1/1	0.97	0.09	26,26,26,26	0
55	MG	1a	1769	1/1	0.97	0.05	56,56,56,56	0
55	MG	1A	3903	1/1	0.97	0.10	57,57,57,57	0
55	MG	1A	3524	1/1	0.97	0.07	31,31,31,31	0
55	MG	1A	4022	1/1	0.97	0.05	47,47,47,47	0
55	MG	1a	1775	1/1	0.97	0.06	50,50,50,50	0
55	MG	2A	3675	1/1	0.97	0.10	36,36,36,36	0
55	MG	2A	3111	1/1	0.97	0.13	29,29,29,29	0
55	MG	1N	204	1/1	0.97	0.10	49,49,49,49	0
55	MG	2A	3470	1/1	0.97	0.15	49,49,49,49	0
55	MG	2A	3113	1/1	0.97	0.16	41,41,41,41	0
55	MG	2A	3114	1/1	0.97	0.16	39,39,39,39	0
55	MG	2A	3281	1/1	0.97	0.22	57,57,57,57	0
55	MG	1A	3906	1/1	0.97	0.06	56,56,56,56	0
55	MG	1A	3414	1/1	0.97	0.11	30,30,30,30	0
55	MG	1A	3608	1/1	0.97	0.03	18,18,18,18	0
55	MG	1A	3215	1/1	0.97	0.28	39,39,39,39	0
55	MG	1O	203	1/1	0.97	0.16	48,48,48,48	0
55	MG	1A	3706	1/1	0.97	0.07	13,13,13,13	0
55	MG	1A	3259	1/1	0.97	0.28	40,40,40,40	0
55	MG	1A	3108	1/1	0.97	0.12	27,27,27,27	0
55	MG	1A	3710	1/1	0.97	0.06	25,25,25,25	0
55	MG	2A	3125	1/1	0.97	0.07	50,50,50,50	0
55	MG	2A	3484	1/1	0.97	0.07	42,42,42,42	0
55	MG	1a	1638	1/1	0.97	0.07	48,48,48,48	0
55	MG	1a	1639	1/1	0.97	0.16	47,47,47,47	0
55	MG	1A	3613	1/1	0.97	0.04	26,26,26,26	0
55	MG	1A	3217	1/1	0.97	0.27	29,29,29,29	0
55	MG	2A	3296	1/1	0.97	0.11	38,38,38,38	0
55	MG	1A	3140	1/1	0.97	0.17	35,35,35,35	0
55	MG	2A	3700	1/1	0.97	0.09	45,45,45,45	0
55	MG	1A	3036	1/1	0.97	0.34	36,36,36,36	0
55	MG	2A	3132	1/1	0.97	0.10	45,45,45,45	0
55	MG	1A	3716	1/1	0.97	0.06	60,60,60,60	0
55	MG	1A	3532	1/1	0.97	0.13	51,51,51,51	0
55	MG	1A	3473	1/1	0.97	0.14	48,48,48,48	0
55	MG	1Q	206	1/1	0.97	0.08	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1Q	207	1/1	0.97	0.10	34,34,34,34	0
55	MG	1A	3922	1/1	0.97	0.07	27,27,27,27	0
55	MG	1R	202	1/1	0.97	0.15	50,50,50,50	0
55	MG	2a	1732	1/1	0.97	0.13	42,42,42,42	0
55	MG	1A	3178	1/1	0.97	0.29	29,29,29,29	0
55	MG	1A	3815	1/1	0.97	0.05	37,37,37,37	0
55	MG	1A	3088	1/1	0.97	0.14	30,30,30,30	0
55	MG	1A	3536	1/1	0.97	0.06	33,33,33,33	0
55	MG	1A	3222	1/1	0.97	0.11	44,44,44,44	0
55	MG	1m	3001	1/1	0.97	0.07	59,59,59,59	0
55	MG	1m	3002	1/1	0.97	0.05	65,65,65,65	0
55	MG	1A	3267	1/1	0.97	0.23	40,40,40,40	0
55	MG	1A	3539	1/1	0.97	0.05	32,32,32,32	0
55	MG	1A	3823	1/1	0.97	0.05	35,35,35,35	0
55	MG	1A	3318	1/1	0.97	0.32	30,30,30,30	0
55	MG	1U	203	1/1	0.97	0.20	40,40,40,40	0
55	MG	1A	3630	1/1	0.97	0.07	30,30,30,30	0
55	MG	1A	3038	1/1	0.97	0.05	34,34,34,34	0
55	MG	2a	1747	1/1	0.97	0.10	53,53,53,53	0
55	MG	1A	3320	1/1	0.97	0.09	51,51,51,51	0
55	MG	1U	207	1/1	0.97	0.10	33,33,33,33	0
55	MG	2B	209	1/1	0.97	0.11	60,60,60,60	0
55	MG	1A	3633	1/1	0.97	0.08	24,24,24,24	0
55	MG	1x	106	1/1	0.97	0.07	53,53,53,53	0
55	MG	2B	212	1/1	0.97	0.17	69,69,69,69	0
55	MG	1A	3321	1/1	0.97	0.07	47,47,47,47	0
55	MG	1A	3091	1/1	0.97	0.10	38,38,38,38	0
55	MG	1A	3939	1/1	0.97	0.08	27,27,27,27	0
55	MG	2A	3524	1/1	0.97	0.08	34,34,34,34	0
55	MG	1U	213	1/1	0.97	0.09	47,47,47,47	0
55	MG	1V	201	1/1	0.97	0.20	19,19,19,19	0
55	MG	1A	3485	1/1	0.97	0.10	20,20,20,20	0
55	MG	1A	3637	1/1	0.97	0.07	27,27,27,27	0
55	MG	1V	204	1/1	0.97	0.19	31,31,31,31	0
55	MG	1x	115	1/1	0.97	0.22	54,54,54,54	0
55	MG	1V	205	1/1	0.97	0.16	49,49,49,49	0
55	MG	1A	3270	1/1	0.97	0.14	40,40,40,40	0
55	MG	1A	3548	1/1	0.97	0.11	10,10,10,10	0
55	MG	1A	3946	1/1	0.97	0.05	27,27,27,27	0
55	MG	1A	3182	1/1	0.97	0.09	34,34,34,34	0
55	MG	1A	3949	1/1	0.97	0.08	51,51,51,51	0
55	MG	1A	3093	1/1	0.97	0.09	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3025	1/1	0.97	0.08	35,35,35,35	0
55	MG	1A	3553	1/1	0.97	0.10	27,27,27,27	0
55	MG	2F	302	1/1	0.97	0.08	57,57,57,57	0
55	MG	1A	3840	1/1	0.97	0.16	52,52,52,52	0
55	MG	2A	3347	1/1	0.97	0.09	56,56,56,56	0
55	MG	1B	213	1/1	0.97	0.19	55,55,55,55	0
55	MG	1A	3147	1/1	0.97	0.15	38,38,38,38	0
55	MG	2A	3015	1/1	0.97	0.07	32,32,32,32	0
55	MG	2A	3547	1/1	0.97	0.10	54,54,54,54	0
55	MG	2a	1780	1/1	0.97	0.06	69,69,69,69	0
55	MG	1X	104	1/1	0.97	0.07	39,39,39,39	0
55	MG	1A	3556	1/1	0.97	0.15	61,61,61,61	0
55	MG	1X	106	1/1	0.97	0.07	49,49,49,49	0
55	MG	1A	3148	1/1	0.97	0.12	33,33,33,33	0
55	MG	2A	3021	1/1	0.97	0.10	47,47,47,47	0
55	MG	2A	3553	1/1	0.97	0.06	77,77,77,77	0
55	MG	1A	3560	1/1	0.97	0.05	28,28,28,28	0
55	MG	1B	218	1/1	0.97	0.08	42,42,42,42	0
55	MG	1A	3117	1/1	0.97	0.21	24,24,24,24	0
55	MG	2A	3557	1/1	0.97	0.11	52,52,52,52	0
55	MG	2W	202	1/1	0.97	0.16	38,38,38,38	0
55	MG	2A	3027	1/1	0.97	0.09	46,46,46,46	0
55	MG	2A	3028	1/1	0.97	0.14	37,37,37,37	0
55	MG	2A	3362	1/1	0.97	0.22	58,58,58,58	0
55	MG	1Z	303	1/1	0.97	0.09	53,53,53,53	0
55	MG	1A	3960	1/1	0.97	0.06	35,35,35,35	0
55	MG	2A	3563	1/1	0.97	0.07	39,39,39,39	0
55	MG	1a	1696	1/1	0.97	0.07	40,40,40,40	0
55	MG	1A	3232	1/1	0.97	0.15	31,31,31,31	0
55	MG	2A	3033	1/1	0.97	0.20	54,54,54,54	0
55	MG	1A	3564	1/1	0.97	0.06	18,18,18,18	0
55	MG	1A	3026	1/1	0.97	0.30	34,34,34,34	0
55	MG	2A	3371	1/1	0.97	0.10	30,30,30,30	0
55	MG	1A	3020	1/1	0.97	0.05	16,16,16,16	0
55	MG	2l	203	1/1	0.97	0.10	64,64,64,64	0
55	MG	2A	3037	1/1	0.97	0.07	54,54,54,54	0
55	MG	2A	3200	1/1	0.97	0.11	51,51,51,51	0
55	MG	2A	3039	1/1	0.97	0.07	45,45,45,45	0
55	MG	2A	3376	1/1	0.97	0.09	38,38,38,38	0
55	MG	10	106	1/1	0.97	0.12	53,53,53,53	0
55	MG	2A	3576	1/1	0.97	0.08	27,27,27,27	0
55	MG	1A	3235	1/1	0.97	0.30	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3028	1/1	0.97	0.30	28,28,28,28	0
55	MG	2A	3579	1/1	0.97	0.09	67,67,67,67	0
55	MG	1B	228	1/1	0.97	0.07	35,35,35,35	0
55	MG	2a	1611	1/1	0.97	0.23	58,58,58,58	0
55	MG	1A	3018	1/1	0.97	0.05	20,20,20,20	0
55	MG	1A	3156	1/1	0.97	0.06	33,33,33,33	0
55	MG	12	102	1/1	0.97	0.15	43,43,43,43	0
55	MG	2A	3384	1/1	0.97	0.07	49,49,49,49	0
55	MG	2A	3385	1/1	0.97	0.06	29,29,29,29	0
55	MG	13	101	1/1	0.97	0.08	30,30,30,30	0
55	MG	2A	3429	1/1	0.98	0.10	52,52,52,52	0
55	MG	1A	3363	1/1	0.98	0.17	33,33,33,33	0
55	MG	1A	3031	1/1	0.98	0.15	24,24,24,24	0
55	MG	2A	3172	1/1	0.98	0.27	42,42,42,42	0
55	MG	1U	210	1/1	0.98	0.38	36,36,36,36	0
55	MG	1A	3123	1/1	0.98	0.11	36,36,36,36	0
55	MG	1A	3009	1/1	0.98	0.04	34,34,34,34	0
55	MG	1B	221	1/1	0.98	0.03	30,30,30,30	0
55	MG	1A	3976	1/1	0.98	0.10	25,25,25,25	0
55	MG	1A	3717	1/1	0.98	0.05	35,35,35,35	0
55	MG	1A	3061	1/1	0.98	0.12	26,26,26,26	0
55	MG	1A	3980	1/1	0.98	0.05	39,39,39,39	0
55	MG	1A	3719	1/1	0.98	0.07	39,39,39,39	0
55	MG	1V	206	1/1	0.98	0.14	40,40,40,40	0
55	MG	1A	3720	1/1	0.98	0.05	40,40,40,40	0
55	MG	2A	3444	1/1	0.98	0.06	30,30,30,30	0
55	MG	1A	3033	1/1	0.98	0.34	28,28,28,28	0
55	MG	1A	3158	1/1	0.98	0.06	32,32,32,32	0
55	MG	2A	3586	1/1	0.98	0.04	61,61,61,61	0
55	MG	2A	3064	1/1	0.98	0.06	29,29,29,29	0
55	MG	1A	3724	1/1	0.98	0.05	46,46,46,46	0
55	MG	1W	203	1/1	0.98	0.11	35,35,35,35	0
55	MG	1a	1771	1/1	0.98	0.04	70,70,70,70	0
55	MG	1A	3649	1/1	0.98	0.05	40,40,40,40	0
55	MG	1A	3726	1/1	0.98	0.05	45,45,45,45	0
55	MG	1A	3129	1/1	0.98	0.11	44,44,44,44	0
55	MG	1A	3045	1/1	0.98	0.04	30,30,30,30	0
55	MG	2A	3455	1/1	0.98	0.06	32,32,32,32	0
55	MG	1A	3014	1/1	0.98	0.10	32,32,32,32	0
55	MG	1A	3047	1/1	0.98	0.05	27,27,27,27	0
55	MG	1A	3415	1/1	0.98	0.16	30,30,30,30	0
55	MG	1A	3808	1/1	0.98	0.17	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3994	1/1	0.98	0.04	44,44,44,44	0
55	MG	1D	302	1/1	0.98	0.09	28,28,28,28	0
55	MG	1A	3995	1/1	0.98	0.04	36,36,36,36	0
55	MG	1A	3006	1/1	0.98	0.07	29,29,29,29	0
55	MG	1A	3997	1/1	0.98	0.09	43,43,43,43	0
55	MG	1A	3597	1/1	0.98	0.07	32,32,32,32	0
55	MG	1A	3049	1/1	0.98	0.05	34,34,34,34	0
55	MG	1A	3599	1/1	0.98	0.05	24,24,24,24	0
55	MG	2Q	201	1/1	0.98	0.13	46,46,46,46	0
55	MG	1A	3660	1/1	0.98	0.12	49,49,49,49	0
55	MG	1A	3739	1/1	0.98	0.06	24,24,24,24	0
55	MG	1A	3905	1/1	0.98	0.10	54,54,54,54	0
55	MG	1E	302	1/1	0.98	0.25	34,34,34,34	0
55	MG	1A	3661	1/1	0.98	0.09	42,42,42,42	0
55	MG	1A	3376	1/1	0.98	0.15	47,47,47,47	0
55	MG	2A	3336	1/1	0.98	0.04	62,62,62,62	0
55	MG	11	101	1/1	0.98	0.40	33,33,33,33	0
55	MG	2A	3338	1/1	0.98	0.10	60,60,60,60	0
55	MG	1A	3601	1/1	0.98	0.08	19,19,19,19	0
55	MG	1A	3547	1/1	0.98	0.06	14,14,14,14	0
55	MG	1A	3819	1/1	0.98	0.05	26,26,26,26	0
55	MG	1A	3199	1/1	0.98	0.10	44,44,44,44	0
55	MG	1A	3165	1/1	0.98	0.20	36,36,36,36	0
55	MG	1A	3822	1/1	0.98	0.06	49,49,49,49	0
55	MG	1A	3302	1/1	0.98	0.13	50,50,50,50	0
55	MG	2A	3346	1/1	0.98	0.06	34,34,34,34	0
55	MG	1A	4016	1/1	0.98	0.14	42,42,42,42	0
55	MG	1A	3915	1/1	0.98	0.09	60,60,60,60	0
55	MG	1A	3135	1/1	0.98	0.20	33,33,33,33	0
55	MG	1A	3068	1/1	0.98	0.22	26,26,26,26	0
55	MG	1F	304	1/1	0.98	0.03	31,31,31,31	0
55	MG	1A	3826	1/1	0.98	0.06	22,22,22,22	0
55	MG	1a	1690	1/1	0.98	0.13	46,46,46,46	0
55	MG	1F	306	1/1	0.98	0.14	31,31,31,31	0
55	MG	1A	3554	1/1	0.98	0.09	22,22,22,22	0
55	MG	2A	3635	1/1	0.98	0.06	43,43,43,43	0
55	MG	2A	3356	1/1	0.98	0.05	44,44,44,44	0
55	MG	1A	3673	1/1	0.98	0.07	42,42,42,42	0
55	MG	1A	3342	1/1	0.98	0.21	44,44,44,44	0
55	MG	1A	3011	1/1	0.98	0.07	24,24,24,24	0
55	MG	1A	3612	1/1	0.98	0.05	53,53,53,53	0
55	MG	1A	3306	1/1	0.98	0.38	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3755	1/1	0.98	0.12	31,31,31,31	0
55	MG	1A	3558	1/1	0.98	0.04	14,14,14,14	0
55	MG	1A	3615	1/1	0.98	0.08	21,21,21,21	0
55	MG	2A	3365	1/1	0.98	0.06	44,44,44,44	0
55	MG	2A	3504	1/1	0.98	0.07	35,35,35,35	0
55	MG	1A	3138	1/1	0.98	0.20	25,25,25,25	0
55	MG	1A	3617	1/1	0.98	0.04	30,30,30,30	0
55	MG	1A	3089	1/1	0.98	0.08	35,35,35,35	0
55	MG	2A	3508	1/1	0.98	0.06	46,46,46,46	0
55	MG	1A	3562	1/1	0.98	0.04	16,16,16,16	0
55	MG	18	105	1/1	0.98	0.24	43,43,43,43	0
55	MG	2A	3120	1/1	0.98	0.05	33,33,33,33	0
55	MG	1A	3037	1/1	0.98	0.17	33,33,33,33	0
55	MG	1A	3112	1/1	0.98	0.13	39,39,39,39	0
55	MG	2A	3659	1/1	0.98	0.11	36,36,36,36	0
55	MG	1A	3934	1/1	0.98	0.04	39,39,39,39	0
55	MG	2A	3002	1/1	0.98	0.17	42,42,42,42	0
55	MG	2A	3662	1/1	0.98	0.09	47,47,47,47	0
55	MG	1A	3113	1/1	0.98	0.06	14,14,14,14	0
55	MG	1A	3052	1/1	0.98	0.12	33,33,33,33	0
55	MG	2A	3665	1/1	0.98	0.04	54,54,54,54	0
55	MG	1A	3092	1/1	0.98	0.16	31,31,31,31	0
55	MG	1A	3691	1/1	0.98	0.07	9,9,9,9	0
55	MG	2A	3007	1/1	0.98	0.07	37,37,37,37	0
55	MG	1A	3352	1/1	0.98	0.29	30,30,30,30	0
55	MG	1A	3476	1/1	0.98	0.10	32,32,32,32	0
55	MG	1P	201	1/1	0.98	0.18	30,30,30,30	0
55	MG	1A	3941	1/1	0.98	0.06	23,23,23,23	0
55	MG	1A	3072	1/1	0.98	0.14	51,51,51,51	0
55	MG	2A	3386	1/1	0.98	0.07	37,37,37,37	0
55	MG	1A	3696	1/1	0.98	0.06	21,21,21,21	0
55	MG	1A	3772	1/1	0.98	0.04	37,37,37,37	0
55	MG	2A	3530	1/1	0.98	0.06	49,49,49,49	0
55	MG	1A	3522	1/1	0.98	0.30	44,44,44,44	0
55	MG	1A	3855	1/1	0.98	0.12	42,42,42,42	0
55	MG	1A	3003	1/1	0.98	0.03	20,20,20,20	0
55	MG	1A	3857	1/1	0.98	0.04	53,53,53,53	0
55	MG	1A	3024	1/1	0.98	0.14	21,21,21,21	0
55	MG	1a	1725	1/1	0.98	0.11	34,34,34,34	0
55	MG	2A	3022	1/1	0.98	0.03	41,41,41,41	0
55	MG	2A	3023	1/1	0.98	0.09	42,42,42,42	0
55	MG	2A	3397	1/1	0.98	0.10	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1a	1726	1/1	0.98	0.06	40,40,40,40	0
55	MG	1Q	205	1/1	0.98	0.07	45,45,45,45	0
55	MG	1A	3055	1/1	0.98	0.16	27,27,27,27	0
55	MG	1A	3576	1/1	0.98	0.11	20,20,20,20	0
55	MG	1a	1730	1/1	0.98	0.06	36,36,36,36	0
55	MG	1A	3702	1/1	0.98	0.07	29,29,29,29	0
55	MG	1a	1733	1/1	0.98	0.05	48,48,48,48	0
55	MG	2A	3694	1/1	0.98	0.04	51,51,51,51	0
55	MG	2A	3405	1/1	0.98	0.16	53,53,53,53	0
55	MG	1A	3149	1/1	0.98	0.26	35,35,35,35	0
55	MG	1A	3956	1/1	0.98	0.06	47,47,47,47	0
55	MG	1A	3704	1/1	0.98	0.05	63,63,63,63	0
55	MG	1A	3864	1/1	0.98	0.06	10,10,10,10	0
55	MG	1A	3056	1/1	0.98	0.29	28,28,28,28	0
55	MG	1A	3868	1/1	0.98	0.04	27,27,27,27	0
55	MG	2A	3416	1/1	0.98	0.05	40,40,40,40	0
55	MG	1A	3579	1/1	0.98	0.05	25,25,25,25	0
55	MG	2A	3038	1/1	0.98	0.12	45,45,45,45	0
55	MG	1A	3707	1/1	0.98	0.04	38,38,38,38	0
55	MG	2A	3040	1/1	0.98	0.08	32,32,32,32	0
55	MG	1A	3871	1/1	0.98	0.05	40,40,40,40	0
55	MG	1U	201	1/1	0.98	0.22	33,33,33,33	0
55	MG	1A	3784	1/1	0.98	0.07	13,13,13,13	0
55	MG	1A	3151	1/1	0.98	0.16	32,32,32,32	0
55	MG	1A	3040	1/1	0.98	0.08	39,39,39,39	0
55	MG	1A	3323	1/1	0.98	0.19	48,48,48,48	0
58	ZN	1n	102	1/1	0.98	0.04	71,71,71,71	0
55	MG	1A	3711	1/1	0.98	0.07	19,19,19,19	0
55	MG	1A	3186	1/1	0.98	0.07	45,45,45,45	0
58	ZN	2n	501	1/1	0.98	0.04	90,90,90,90	0
59	SF4	1d	3202	8/8	0.98	0.04	58,70,78,85	0
59	SF4	2d	501	8/8	0.98	0.04	68,75,83,84	0
55	MG	1D	305	1/1	0.99	0.10	26,26,26,26	0
55	MG	1A	3603	1/1	0.99	0.05	36,36,36,36	0
55	MG	1A	3722	1/1	0.99	0.07	15,15,15,15	0
55	MG	1A	3620	1/1	0.99	0.06	20,20,20,20	0
55	MG	1A	3866	1/1	0.99	0.04	52,52,52,52	0
55	MG	1A	3184	1/1	0.99	0.13	27,27,27,27	0
55	MG	1A	3559	1/1	0.99	0.05	38,38,38,38	0
55	MG	2A	3636	1/1	0.99	0.04	44,44,44,44	0
55	MG	1A	3842	1/1	0.99	0.05	38,38,38,38	0
55	MG	1A	3128	1/1	0.99	0.17	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3229	1/1	0.99	0.04	28,28,28,28	0
55	MG	1a	1770	1/1	0.99	0.02	48,48,48,48	0
55	MG	1A	3409	1/1	0.99	0.21	37,37,37,37	0
55	MG	1A	3963	1/1	0.99	0.03	19,19,19,19	0
55	MG	2A	3539	1/1	0.99	0.04	36,36,36,36	0
55	MG	1A	3964	1/1	0.99	0.05	38,38,38,38	0
55	MG	2A	3645	1/1	0.99	0.04	22,22,22,22	0
55	MG	1a	1731	1/1	0.99	0.09	32,32,32,32	0
55	MG	1A	3874	1/1	0.99	0.04	44,44,44,44	0
55	MG	1A	3684	1/1	0.99	0.03	35,35,35,35	0
55	MG	1A	4001	1/1	0.99	0.04	22,22,22,22	0
55	MG	2A	3650	1/1	0.99	0.06	26,26,26,26	0
55	MG	1E	310	1/1	0.99	0.07	14,14,14,14	0
55	MG	1A	3847	1/1	0.99	0.04	30,30,30,30	0
55	MG	1A	3848	1/1	0.99	0.03	22,22,22,22	0
55	MG	1A	3663	1/1	0.99	0.04	26,26,26,26	0
55	MG	1A	3016	1/1	0.99	0.19	49,49,49,49	0
55	MG	1A	3880	1/1	0.99	0.03	40,40,40,40	0
55	MG	1A	3627	1/1	0.99	0.06	37,37,37,37	0
55	MG	1A	3124	1/1	0.99	0.12	32,32,32,32	0
55	MG	1a	1743	1/1	0.99	0.08	56,56,56,56	0
55	MG	1A	3041	1/1	0.99	0.10	30,30,30,30	0
55	MG	2A	3406	1/1	0.99	0.06	50,50,50,50	0
55	MG	1A	4011	1/1	0.99	0.04	39,39,39,39	0
55	MG	1A	3566	1/1	0.99	0.12	22,22,22,22	0
55	MG	2A	3409	1/1	0.99	0.04	56,56,56,56	0
55	MG	1A	3174	1/1	0.99	0.11	37,37,37,37	0
55	MG	1A	3944	1/1	0.99	0.02	21,21,21,21	0
55	MG	1A	3978	1/1	0.99	0.04	36,36,36,36	0
55	MG	2A	3413	1/1	0.99	0.05	34,34,34,34	0
55	MG	2A	3414	1/1	0.99	0.03	33,33,33,33	0
55	MG	1A	3738	1/1	0.99	0.04	38,38,38,38	0
55	MG	1A	3487	1/1	0.99	0.21	41,41,41,41	0
55	MG	1A	3947	1/1	0.99	0.05	27,27,27,27	0
55	MG	2A	3279	1/1	0.99	0.11	15,15,15,15	0
55	MG	1a	1753	1/1	0.99	0.06	74,74,74,74	0
55	MG	1A	3057	1/1	0.99	0.03	9,9,9,9	0
58	ZN	1Y	203	1/1	0.99	0.04	85,85,85,85	0
55	MG	1a	1755	1/1	0.99	0.06	47,47,47,47	0
58	ZN	16	102	1/1	0.99	0.05	39,39,39,39	0
58	ZN	19	501	1/1	0.99	0.04	43,43,43,43	0
55	MG	1A	3007	1/1	0.99	0.12	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
55	MG	1A	3208	1/1	0.99	0.12	33,33,33,33	0
55	MG	2A	3522	1/1	0.99	0.04	33,33,33,33	0
58	ZN	25	102	1/1	0.99	0.03	66,66,66,66	0
58	ZN	26	501	1/1	0.99	0.05	66,66,66,66	0
58	ZN	29	501	1/1	0.99	0.04	69,69,69,69	0
55	MG	2A	3019	1/1	0.99	0.04	28,28,28,28	0
55	MG	1A	3654	1/1	0.99	0.05	27,27,27,27	0
55	MG	1A	3317	1/1	0.99	0.04	31,31,31,31	0
55	MG	1A	3728	1/1	1.00	0.06	18,18,18,18	0
55	MG	1A	3686	1/1	1.00	0.03	23,23,23,23	0
55	MG	1A	3693	1/1	1.00	0.08	37,37,37,37	0
55	MG	1A	3664	1/1	1.00	0.06	18,18,18,18	0
55	MG	1A	3867	1/1	1.00	0.04	17,17,17,17	0
55	MG	1A	4006	1/1	1.00	0.04	20,20,20,20	0
55	MG	1A	3549	1/1	1.00	0.05	34,34,34,34	0
55	MG	1a	1777	1/1	1.00	0.02	46,46,46,46	0
58	ZN	15	108	1/1	1.00	0.01	43,43,43,43	0
55	MG	2A	3633	1/1	1.00	0.06	31,31,31,31	0

6.5 Other polymers (i)

There are no such residues in this entry.