Full wwPDB X-ray Structure Validation Report

Apr 19, 2026 – 03:45 PM UTC

PDB ID	:	5DOX / pdb_00005dox
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with Hygromycin-A at 3.1A resolution
Authors	:	Polikanov, Y.S.; Starosta, A.L.; Juette, M.F.; Altman, R.B.; Terry, D.S.; Lu, W.; Burnett, B.J.; Dinos, G.; Reynolds, K.; Blanchard, S.C.; Steitz, T.A.; Wilson, D.N.
Deposited on	:	2015-09-11
Resolution	:	3.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

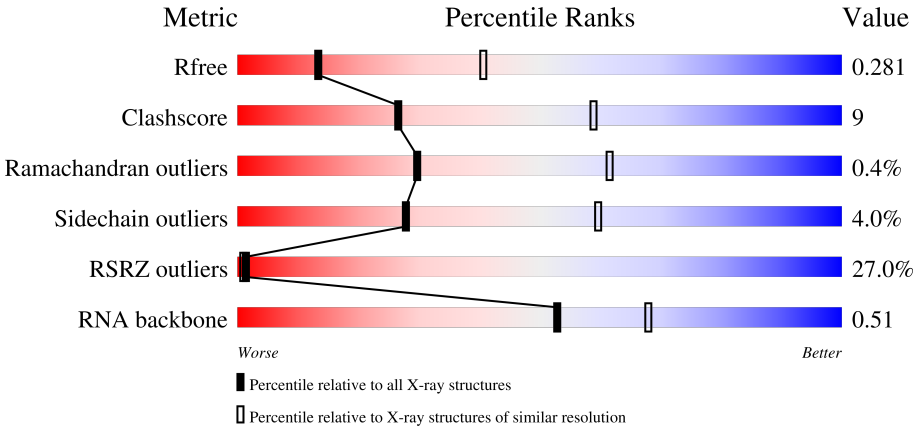
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)
RNA backbone	3983	1022 (3.32-2.88)

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	12% 61% 32% 6%
1	2A	2915	9% 55% 37% 7%
2	1B	121	12% 65% 32%
2	2B	121	12% 53% 40% 6%

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Mol	Chain	Length	Quality of chain
3	1D	276	26% 72% 26%
3	2D	276	20% 78% 18%
4	1E	206	28% 75% 21%
4	2E	206	11% 74% 22%
5	1F	210	19% 70% 25%
5	2F	210	13% 67% 28%
6	1G	182	37% 68% 30%
6	2G	182	60% 48% 48%
7	1H	180	49% 71% 25%
7	2H	180	26% 75% 20%
8	1I	148	28% 76% 21%
8	2I	148	23% 75% 22%
9	1N	140	13% 80% 19%
9	2N	140	28% 84% 15%
10	1O	122	12% 78% 22%
10	2O	122	19% 77% 23%
11	1P	150	21% 76% 22%
11	2P	150	23% 70% 27%
12	1Q	141	27% 79% 20%
12	2Q	141	18% 72% 28%
13	1R	118	10% 82% 14%
13	2R	118	8% 65% 31%
14	1S	112	32% 78% 19%
14	2S	112	37% 78% 20%
15	1T	146	23% 68% 21% 10%

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Mol	Chain	Length	Quality of chain
15	2T	146	15% 76% 13% 10%
16	1U	118	26% 83% 14%
16	2U	118	11% 81% 17%
17	1V	101	27% 76% 22%
17	2V	101	25% 74% 23%
18	1W	113	17% 78% 19%
18	2W	113	4% 70% 27%
19	1X	96	17% 78% 21%
19	2X	96	8% 79% 19%
20	1Y	110	29% 77% 18%
20	2Y	110	27% 72% 25%
21	1Z	206	14% 71% 24%
21	2Z	206	35% 73% 23%
22	10	85	22% 71% 19% 9%
22	20	85	26% 66% 25% 9%
23	11	98	29% 82% 16%
23	21	98	27% 70% 28%
24	12	72	24% 79% 18%
24	22	72	17% 74% 22%
25	13	60	32% 70% 27%
25	23	60	12% 77% 22%
26	14	71	46% 58% 37%
26	24	71	55% 55% 35% 7%
27	15	60	10% 67% 27% 5%
27	25	60	7% 73% 22%

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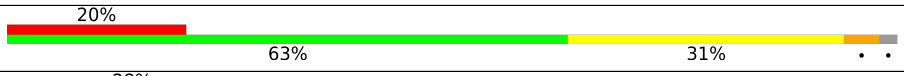
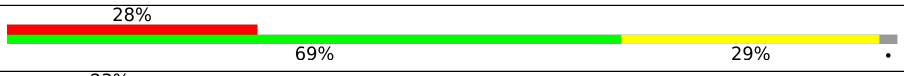
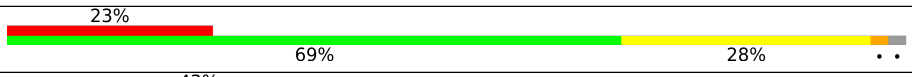
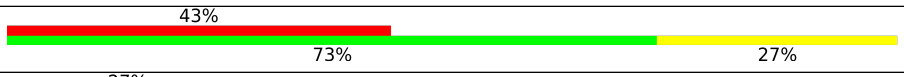
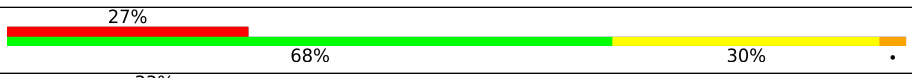
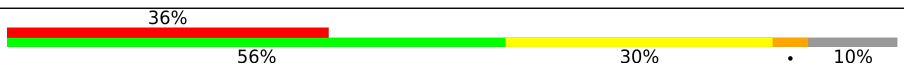
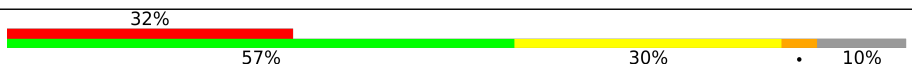
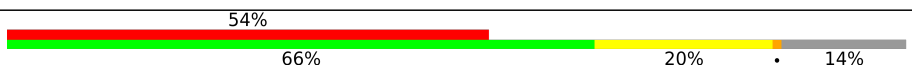
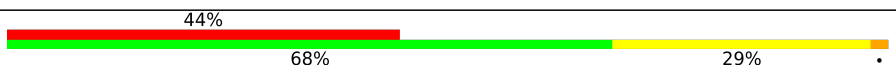
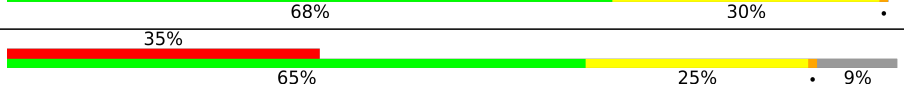
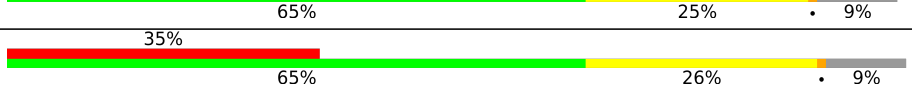
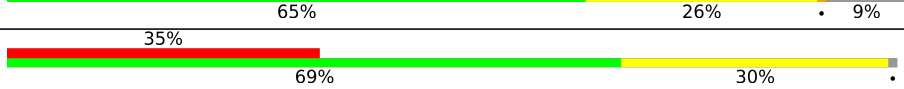
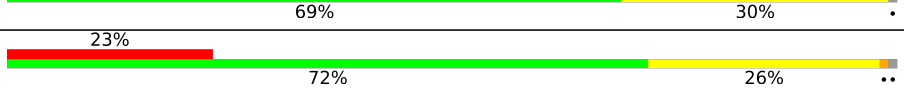
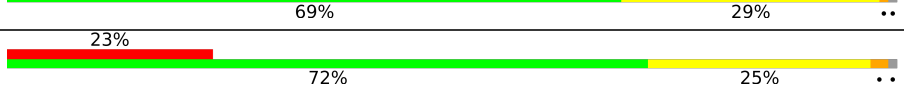
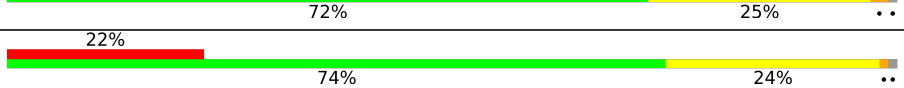
Mol	Chain	Length	Quality of chain
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	
40	1i	128	

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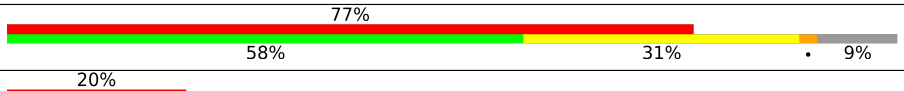
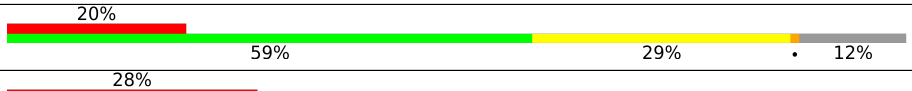
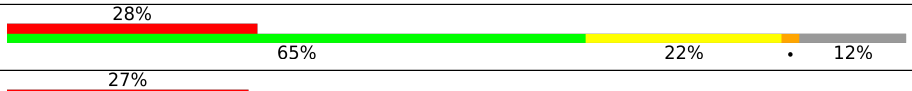
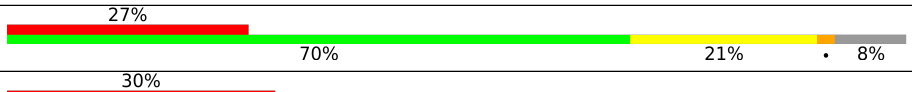
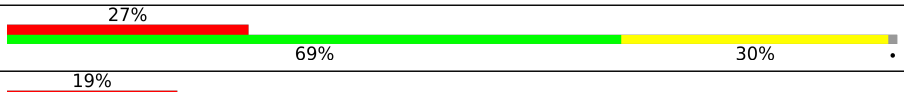
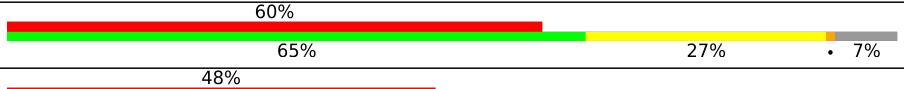
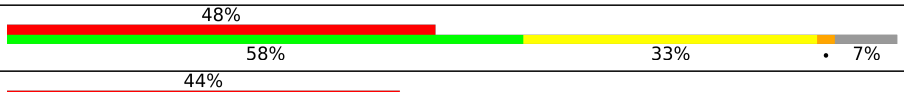
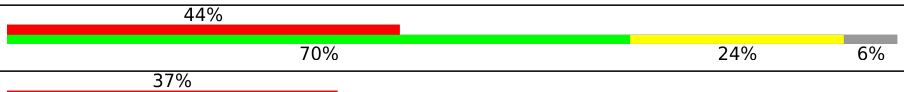
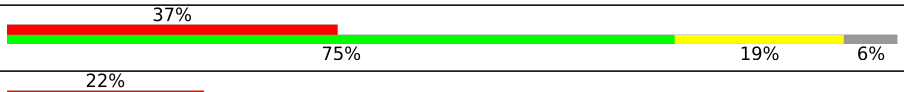
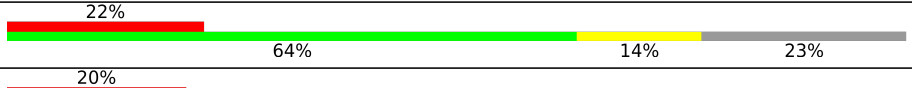
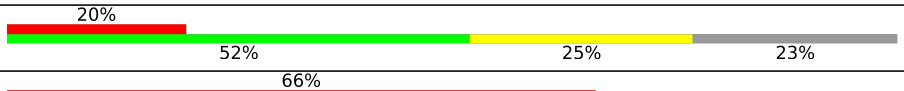
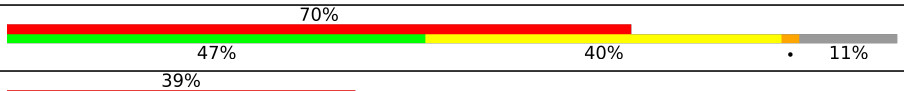
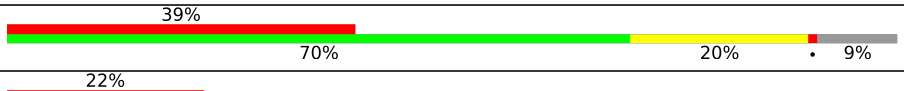
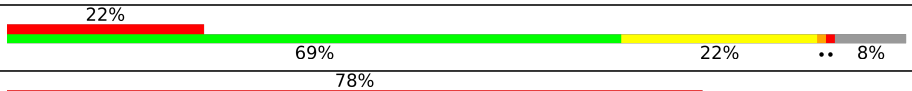
Mol	Chain	Length	Quality of chain
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	
52	2u	27	

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
53	MG	1A	3453	-	-	-	X
53	MG	1a	3057	-	-	-	X
53	MG	2a	1632	-	-	-	X
53	MG	2a	1643	-	-	-	X
53	MG	2a	1692	-	-	-	X
53	MG	2a	1705	-	-	-	X

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 289588 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2872	Total	C	N	O	P	0	0	0
			61869	27540	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61758	27491	11552	19850	2865			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total	C	N	O	0	0	0
			877	553	175	149			
14	2S	110	Total	C	N	O	0	0	0
			870	549	173	148			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	2Z	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			
23	21	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			986	625	193	168			
40	2i	126	Total	C	N	O	0	0	0
			966	613	186	167			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			719	446	142	131			
41	2j	96	Total	C	N	O	0	0	0
			710	442	137	131			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			
44	2m	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			
50	2s	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			
51	2t	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			

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

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

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
53	1A	761	Total Mg 761 761	0	0
53	1B	23	Total Mg 23 23	0	0
53	1D	8	Total Mg 8 8	0	0
53	1E	6	Total Mg 6 6	0	0
53	1F	6	Total Mg 6 6	0	0
53	1G	2	Total Mg 2 2	0	0
53	1H	2	Total Mg 2 2	0	0
53	1N	2	Total Mg 2 2	0	0
53	1P	3	Total Mg 3 3	0	0
53	1Q	4	Total Mg 4 4	0	0
53	1R	6	Total Mg 6 6	0	0
53	1T	4	Total Mg 4 4	0	0
53	1U	3	Total Mg 3 3	0	0
53	1V	2	Total Mg 2 2	0	0
53	1W	3	Total Mg 3 3	0	0
53	1Z	1	Total Mg 1 1	0	0
53	10	6	Total Mg 6 6	0	0
53	11	2	Total Mg 2 2	0	0
53	13	3	Total Mg 3 3	0	0
53	15	5	Total Mg 5 5	0	0
53	17	2	Total Mg 2 2	0	0
53	18	2	Total Mg 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
53	19	4	Total Mg 4 4	0	0
53	1a	143	Total Mg 143 143	0	0
53	1b	1	Total Mg 1 1	0	0
53	1d	2	Total Mg 2 2	0	0
53	1e	1	Total Mg 1 1	0	0
53	1f	1	Total Mg 1 1	0	0
53	1g	2	Total Mg 2 2	0	0
53	1h	1	Total Mg 1 1	0	0
53	1k	1	Total Mg 1 1	0	0
53	1l	2	Total Mg 2 2	0	0
53	1n	1	Total Mg 1 1	0	0
53	1o	2	Total Mg 2 2	0	0
53	1r	1	Total Mg 1 1	0	0
53	1t	1	Total Mg 1 1	0	0
53	2A	518	Total Mg 518 518	0	0
53	2B	19	Total Mg 19 19	0	0
53	2D	3	Total Mg 3 3	0	0
53	2E	6	Total Mg 6 6	0	0
53	2F	2	Total Mg 2 2	0	0
53	2I	1	Total Mg 1 1	0	0
53	2N	1	Total Mg 1 1	0	0

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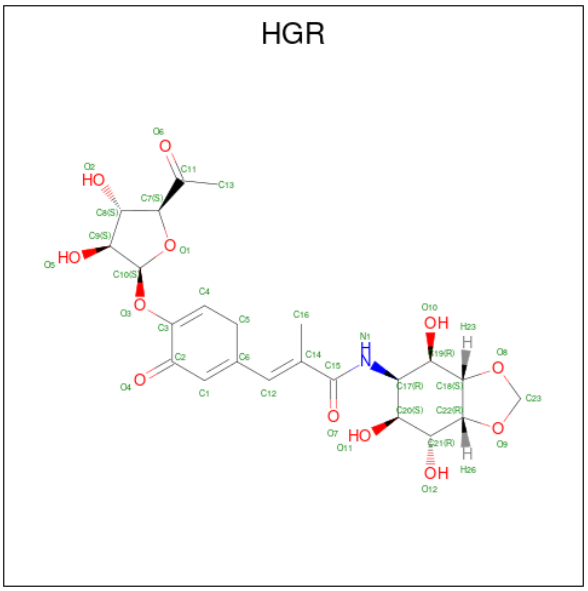
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
53	2O	2	Total Mg 2 2	0	0
53	2P	1	Total Mg 1 1	0	0
53	2Q	3	Total Mg 3 3	0	0
53	2R	1	Total Mg 1 1	0	0
53	2T	3	Total Mg 3 3	0	0
53	2V	1	Total Mg 1 1	0	0
53	2W	1	Total Mg 1 1	0	0
53	2Y	1	Total Mg 1 1	0	0
53	20	1	Total Mg 1 1	0	0
53	28	2	Total Mg 2 2	0	0
53	2a	129	Total Mg 129 129	0	0
53	2e	1	Total Mg 1 1	0	0
53	2k	1	Total Mg 1 1	0	0
53	2l	1	Total Mg 1 1	0	0
53	2t	1	Total Mg 1 1	0	0

- Molecule 54 is Hygromycin A (CCD ID: HGR) (formula: $C_{23}H_{29}NO_{12}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	1A	1	Total C N O 36 23 1 12	0	0
54	2A	1	Total C N O 36 23 1 12	0	0

- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
55	1Y	1	Total Zn 1 1	0	0
55	14	1	Total Zn 1 1	0	0
55	15	1	Total Zn 1 1	0	0
55	16	1	Total Zn 1 1	0	0
55	19	1	Total Zn 1 1	0	0
55	1n	1	Total Zn 1 1	0	0
55	2Y	1	Total Zn 1 1	0	0
55	24	1	Total Zn 1 1	0	0
55	25	1	Total Zn 1 1	0	0
55	26	1	Total Zn 1 1	0	0

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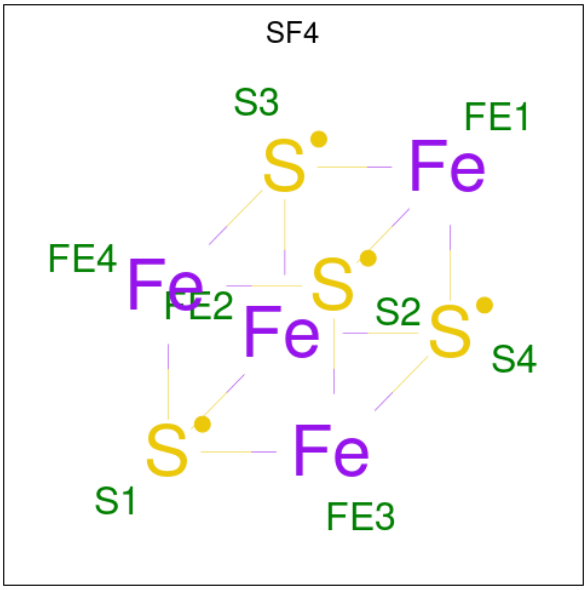
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
55	29	1	Total Zn 1 1	0	0
55	2n	1	Total Zn 1 1	0	0

- Molecule 56 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	1d	1	Total Fe S 8 4 4	0	0
56	2d	1	Total Fe S 8 4 4	0	0

- Molecule 57 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1A	1448	Total O 1448 1448	0	0
57	1B	37	Total O 37 37	0	0
57	1D	23	Total O 23 23	0	0
57	1E	20	Total O 20 20	0	0
57	1F	20	Total O 20 20	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	1G	6	Total O 6 6	0	0
57	1H	4	Total O 4 4	0	0
57	1I	2	Total O 2 2	0	0
57	1N	24	Total O 24 24	0	0
57	1O	4	Total O 4 4	0	0
57	1P	9	Total O 9 9	0	0
57	1Q	8	Total O 8 8	0	0
57	1R	6	Total O 6 6	0	0
57	1T	15	Total O 15 15	0	0
57	1U	16	Total O 16 16	0	0
57	1V	9	Total O 9 9	0	0
57	1W	9	Total O 9 9	0	0
57	1X	7	Total O 7 7	0	0
57	1Y	5	Total O 5 5	0	0
57	1Z	2	Total O 2 2	0	0
57	10	10	Total O 10 10	0	0
57	11	7	Total O 7 7	0	0
57	12	2	Total O 2 2	0	0
57	13	8	Total O 8 8	0	0
57	14	1	Total O 1 1	0	0
57	15	8	Total O 8 8	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	16	1	Total O 1 1	0	0
57	17	2	Total O 2 2	0	0
57	18	3	Total O 3 3	0	0
57	19	4	Total O 4 4	0	0
57	1a	226	Total O 226 226	0	0
57	1d	5	Total O 5 5	0	0
57	1e	2	Total O 2 2	0	0
57	1f	2	Total O 2 2	0	0
57	1g	1	Total O 1 1	0	0
57	1h	1	Total O 1 1	0	0
57	1k	1	Total O 1 1	0	0
57	1l	6	Total O 6 6	0	0
57	1m	1	Total O 1 1	0	0
57	1o	7	Total O 7 7	0	0
57	1p	3	Total O 3 3	0	0
57	1t	2	Total O 2 2	0	0
57	1u	1	Total O 1 1	0	0
57	2A	648	Total O 648 648	0	0
57	2B	24	Total O 24 24	0	0
57	2D	14	Total O 14 14	0	0
57	2E	4	Total O 4 4	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	2F	3	Total O 3 3	0	0
57	2H	1	Total O 1 1	0	0
57	2I	1	Total O 1 1	0	0
57	2N	3	Total O 3 3	0	0
57	2O	3	Total O 3 3	0	0
57	2P	4	Total O 4 4	0	0
57	2Q	4	Total O 4 4	0	0
57	2R	4	Total O 4 4	0	0
57	2S	1	Total O 1 1	0	0
57	2T	5	Total O 5 5	0	0
57	2U	3	Total O 3 3	0	0
57	2W	3	Total O 3 3	0	0
57	2X	2	Total O 2 2	0	0
57	2Y	2	Total O 2 2	0	0
57	2Z	3	Total O 3 3	0	0
57	20	2	Total O 2 2	0	0
57	21	2	Total O 2 2	0	0
57	22	1	Total O 1 1	0	0
57	23	1	Total O 1 1	0	0
57	24	1	Total O 1 1	0	0
57	25	1	Total O 1 1	0	0

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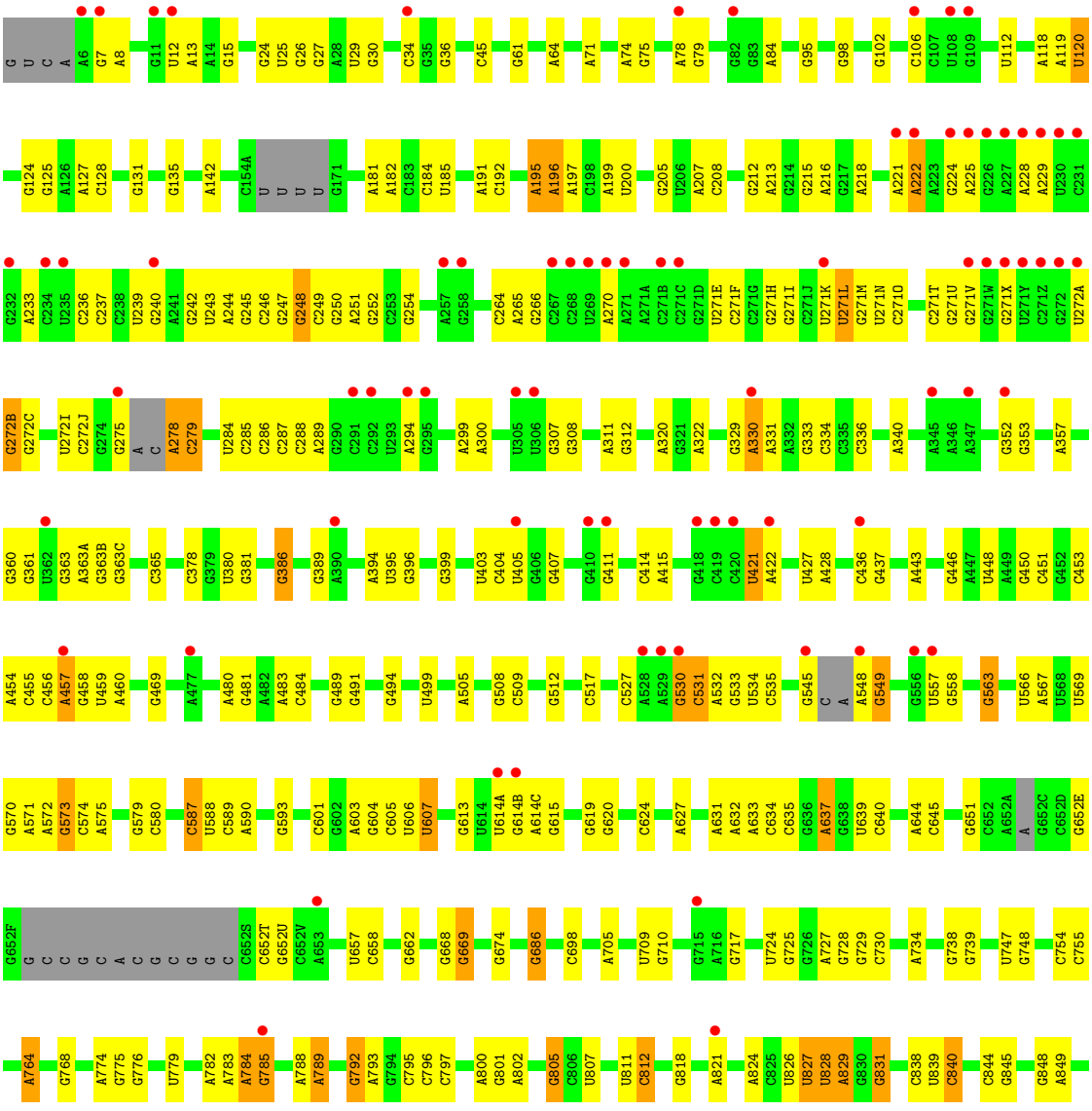
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	26	1	Total O 1 1	0	0
57	27	2	Total O 2 2	0	0
57	28	3	Total O 3 3	0	0
57	2a	179	Total O 179 179	0	0
57	2d	1	Total O 1 1	0	0
57	2e	2	Total O 2 2	0	0
57	2f	3	Total O 3 3	0	0
57	2l	3	Total O 3 3	0	0
57	2m	1	Total O 1 1	0	0
57	2o	1	Total O 1 1	0	0
57	2p	1	Total O 1 1	0	0
57	2q	1	Total O 1 1	0	0
57	2r	3	Total O 3 3	0	0
57	2t	3	Total O 3 3	0	0

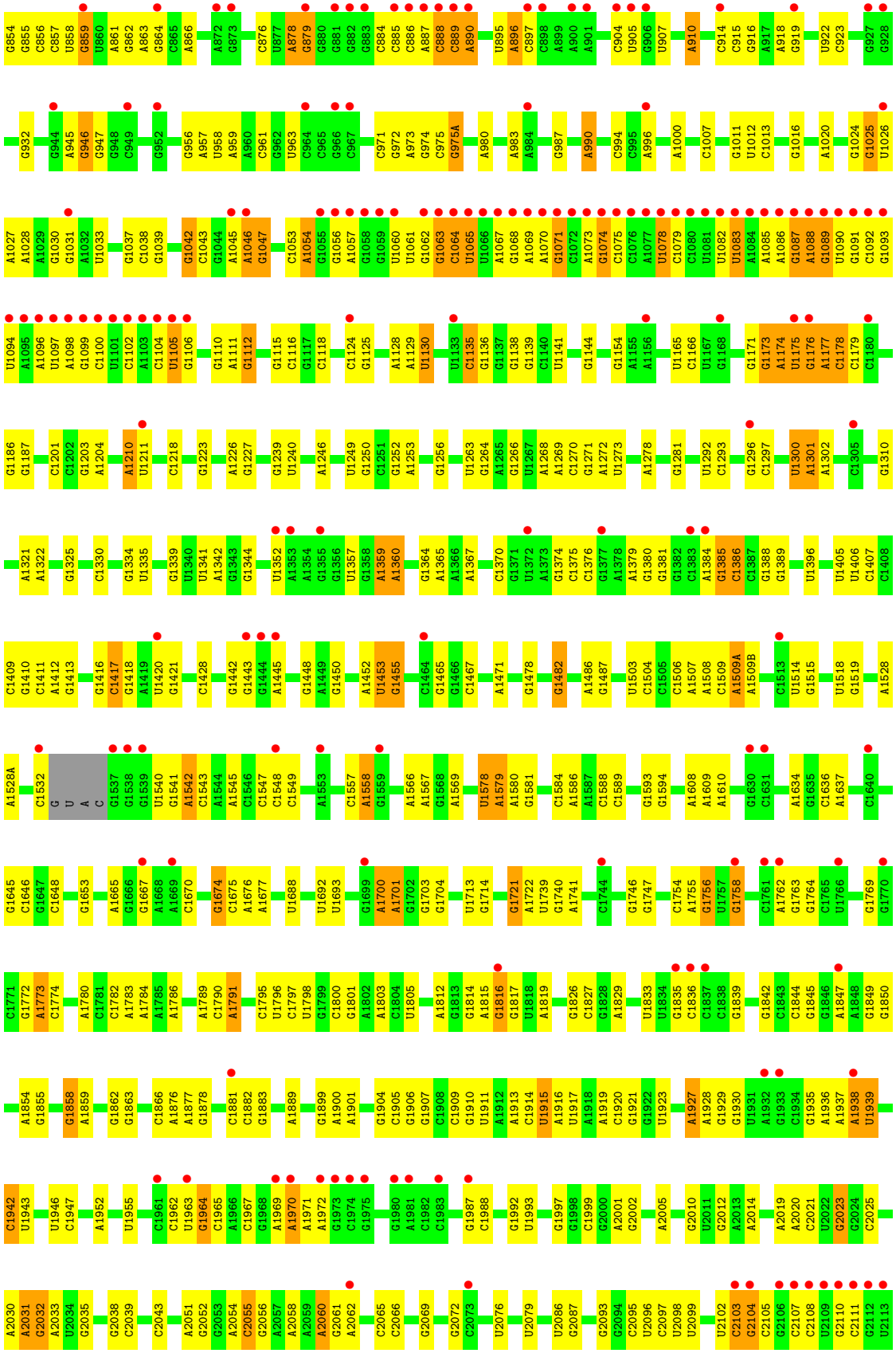
3 Residue-property plots (i)

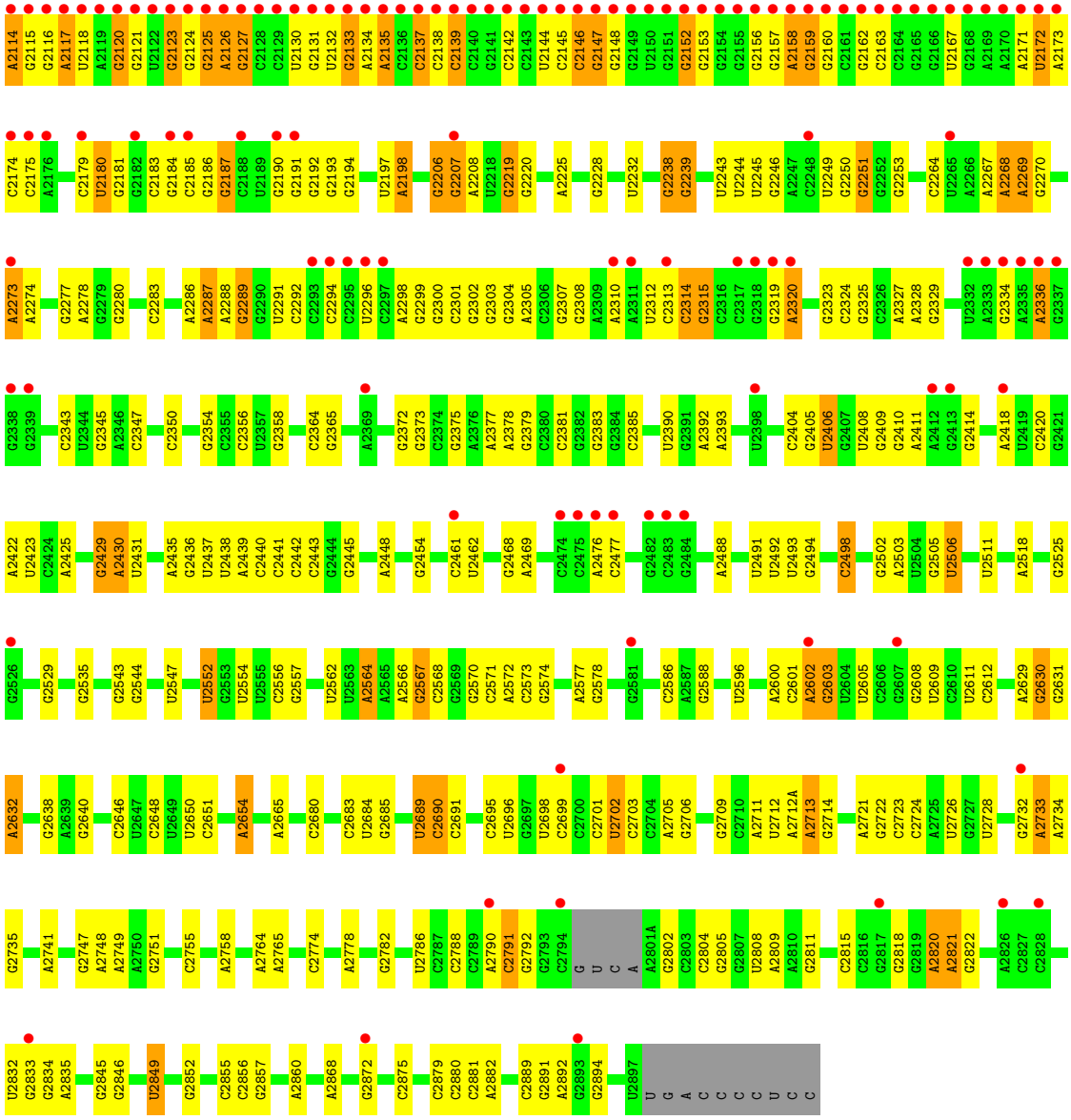
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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:

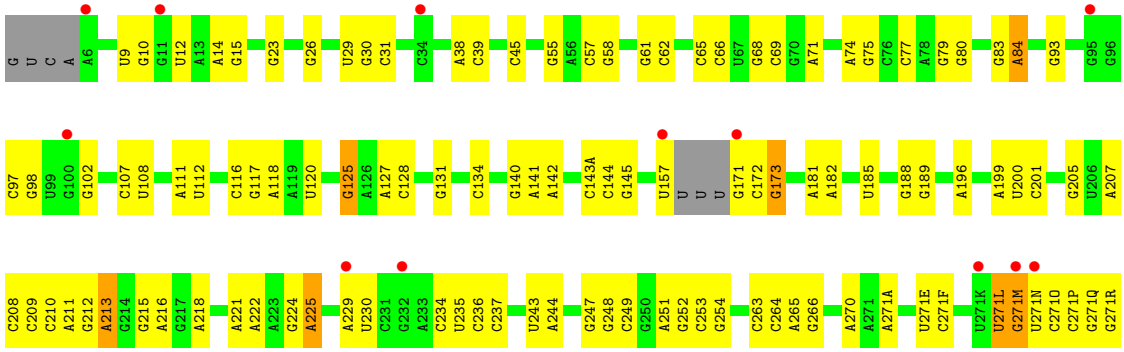


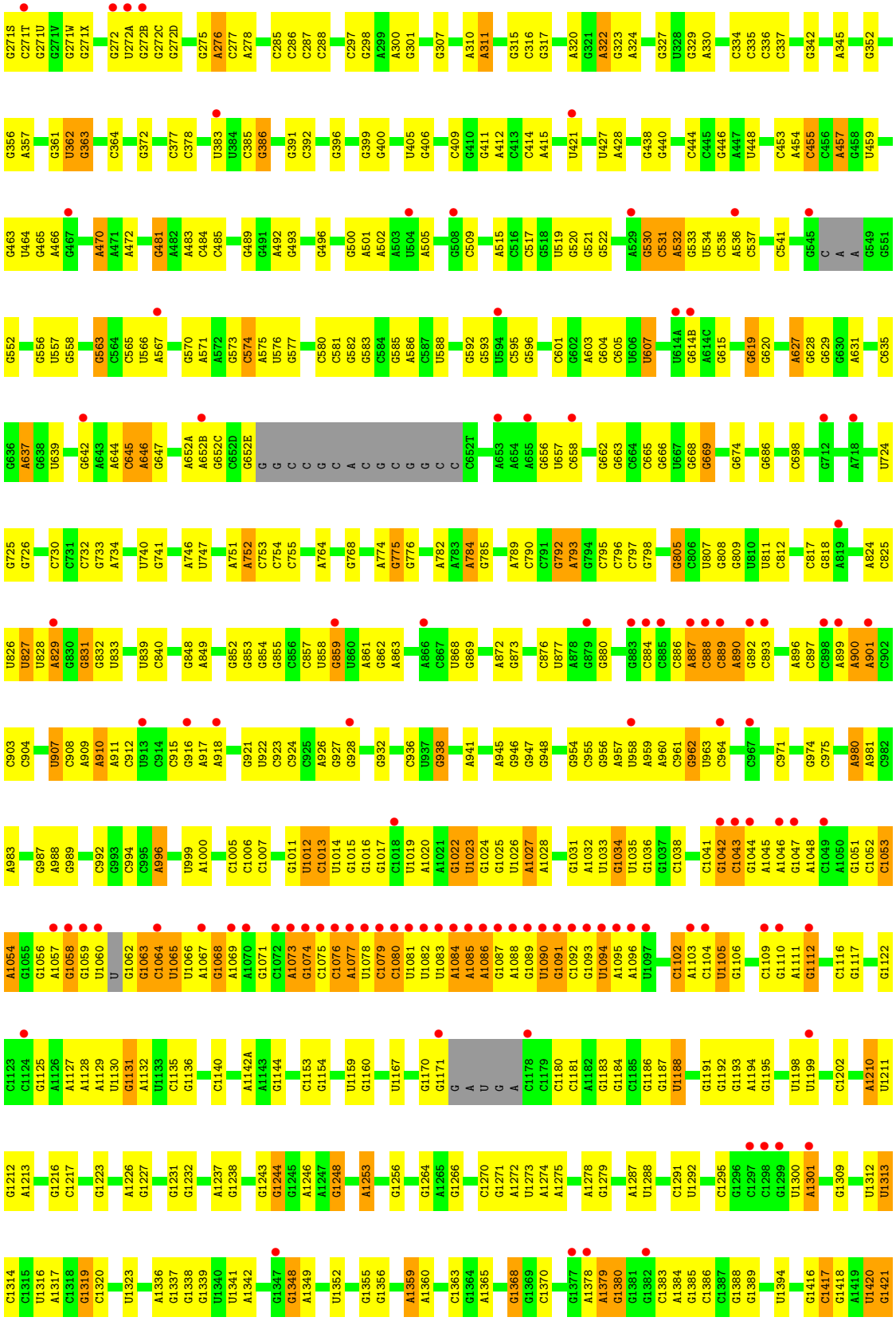




• Molecule 1: 23S Ribosomal RNA

Chain 2A:

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G356 A357 G361 U362 G363 C364 G372 C377 C378 U383 U384 C385 G386 G391 C392 G396 G399 G400 U405 G406 C409 G410 G411 A412 C413 C414 A415 U421 U427 A428 G438 G440 C444 C445 G446 A447 U448 C453 A454 C455 C456 A457 G458 U459
G463 U464 G465 A466 G467 A470 A471 A472 G481 A482 A483 C484 C485 G489 G491 A492 G493 G496 G500 A501 A502 A503 U504 A505 G508 C509 A515 C516 C517 G518 U519 G520 G521 G522 A529 G530 C531 A532 G533 U534 C535 A536 C537 C541 G545 C A A G549 G551
G552 G556 U557 G558 G563 C564 C565 U566 A567 G570 A571 A572 G573 C574 A575 U576 G577 C580 C581 G582 G583 C584 G585 A586 C587 U588 G592 G593 U594 C595 G596 C601 G602 A603 G604 C605 U606 U607 U614A G614B A614C G615 G619 G620 A627 G628 G629 G630 A631 C635
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G725 G726 C730 C731 C732 G733 A734 U740 G741 A746 U747 A751 A752 C753 C754 C755 A764 G768 A774 G775 G776 A782 A783 A784 G785 A789 C790 C791 G792 A793 G794 C795 C796 C797 G798 G805 C806 U807 G808 G809 U810 U811 C812 C817 G818 A819 A824 C825
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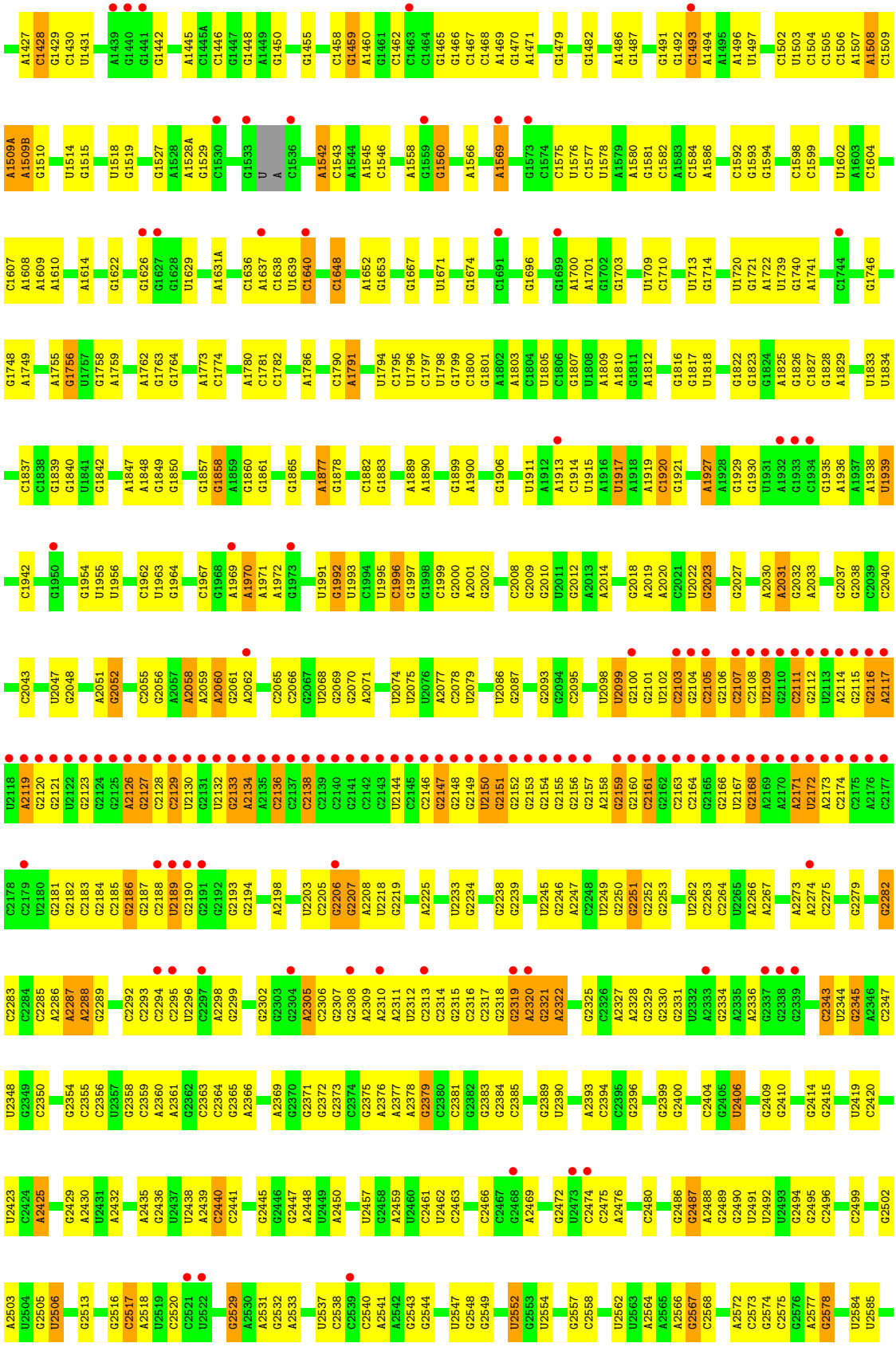
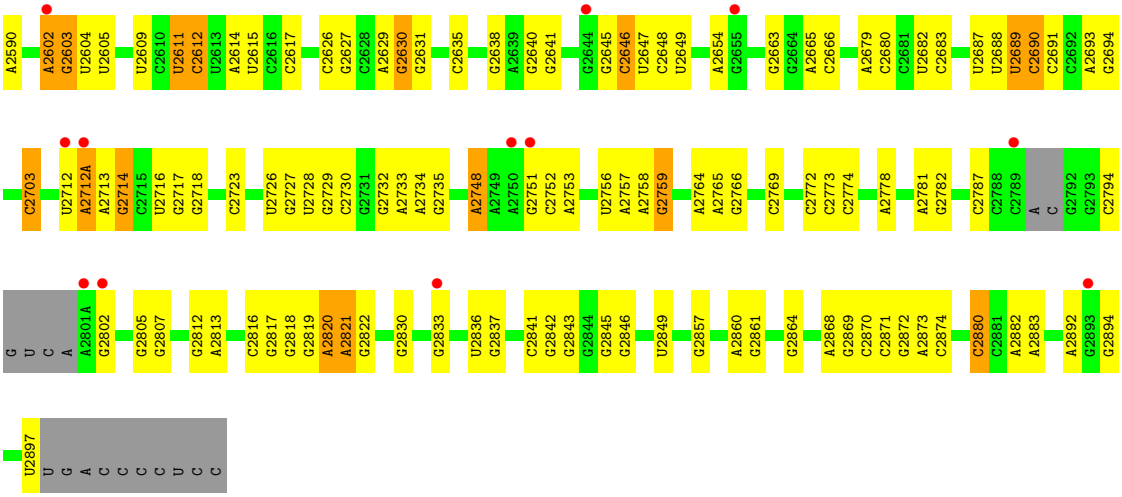
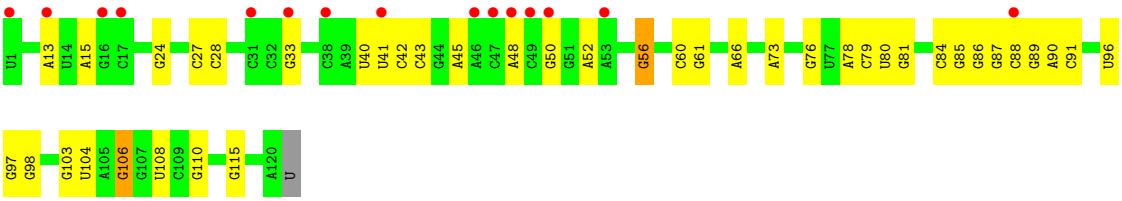
C903 C904 U907 C908 A909 A910 A911 C912 U913 C914 C915 G916 A917 A918 G921 U922 C923 C924 C925 A926 G927 G928 G932 C936 U937 G938 A941 A945 G946 G947 G948 G954 C955 G956 A957 U958 A959 A960 C961 G962 U963 C964 C967 C971 G974 C975 A980 A981 C982
A983 G987 A988 G989 C992 G993 C994 C995 A996 U999 A1000 C1005 C1006 C1007 G1011 U1012 C1013 U1014 G1015 G1016 G1017 C1018 U1019 A1020 A1021 G1022 U1023 G1024 G1025 U1026 A1027 A1028 G1031 A1032 U1033 G1034 U1035 G1036 G1037 C1038 C1041 G1042 C1043 G1044 A1045 A1046 G1047 A1048 C1049 A1050 G1051 C1052 C1053
A1054 G1055 G1056 A1057 G1058 G1059 U1060 U G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075 C1076 A1077 U1078 C1079 C1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 G1089 U1090 G1091 C1092 G1093 U1094 A1095 A1096 U1097 C1102 A1103 C1104 U1105 G1106 C1109 G1110 A1111 G1112 C1116 G1117 G1122
C1123 C1124 G1125 A1126 A1127 A1128 A1129 U1130 G1131 A1132 U1133 C1135 G1136 C1140 A1142A A1143 G1144 C1153 G1154 U1159 G1160 U1167 G1170 G1171 G A U G A C1178 C1179 C1180 C1181 A1182 G1183 G1184 C1185 G1186 G1187 U1188 G1191 G1192 G1193 A1194 G1195 U1198 U1199 C1202 A1210 U1211
G1212 A1213 G1216 C1217 G1223 A1226 G1227 G1231 G1232 A1237 G1238 G1243 G1244 G1245 A1246 A1247 G1248 A1253 G1256 G1264 A1265 G1266 C1270 G1271 A1272 U1273 A1274 A1275 A1278 G1279 A1287 U1288 C1291 U1292 C1295 G1296 C1297 G1298 G1299 U1300 A1301 G1309 U1312 U1313
C1314 C1315 U1316 A1317 C1318 G1319 C1320 U1323 A1336 G1337 G1338 G1339 U1340 U1341 A1342 G1347 G1348 A1349 U1352 G1355 G1356 A1359 A1360 C1363 G1364 A1365 G1368 G1369 C1370 G1377 A1378 A1379 G1380 G1381 G1382 C1383 A1384 G1385 C1386 C1387 G1388 G1389 U1394 G1416 C1417 G1418 A1419 U1420 G1421





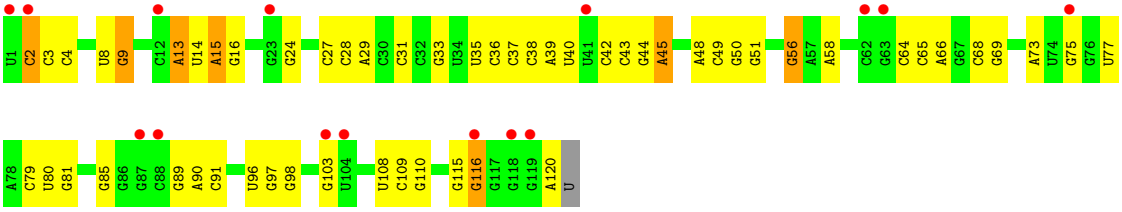
• Molecule 2: 5S Ribosomal RNA

Chain 1B:



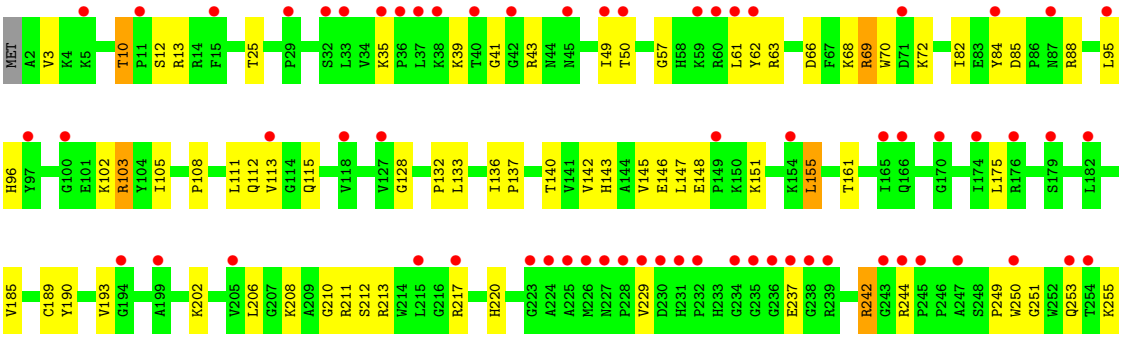
• Molecule 2: 5S Ribosomal RNA

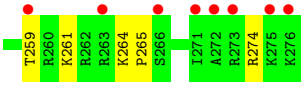
Chain 2B:



• Molecule 3: 50S ribosomal protein L2

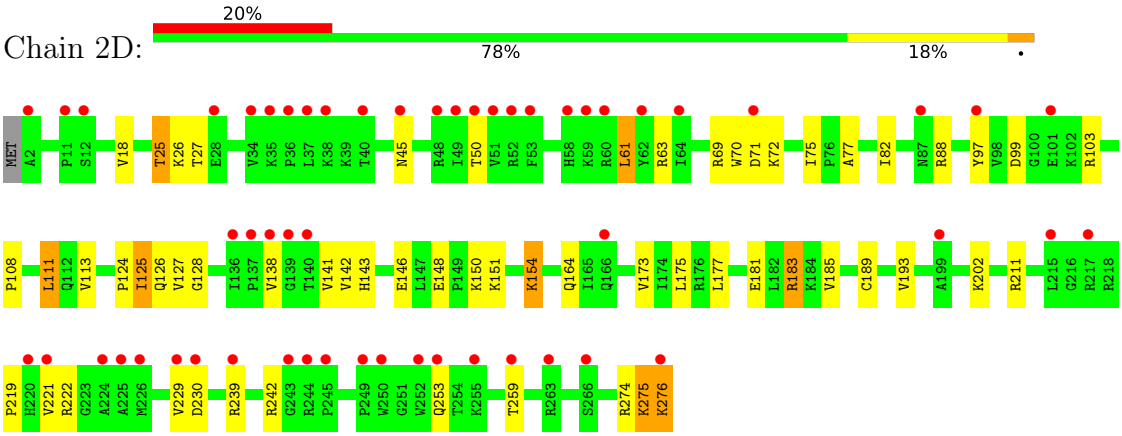
Chain 1D:





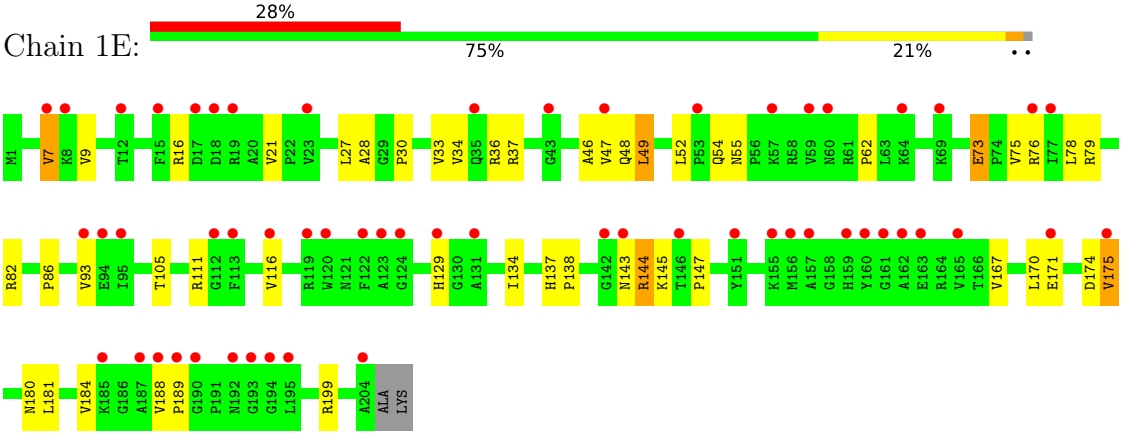
• Molecule 3: 50S ribosomal protein L2

Chain 2D:



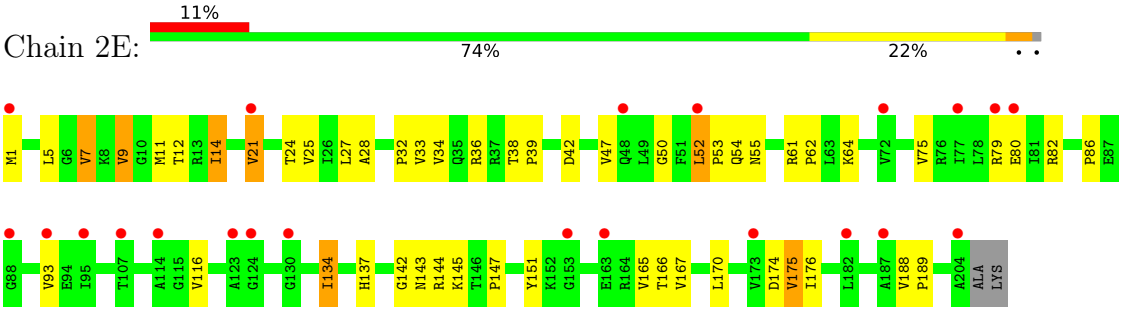
• Molecule 4: 50S ribosomal protein L3

Chain 1E:



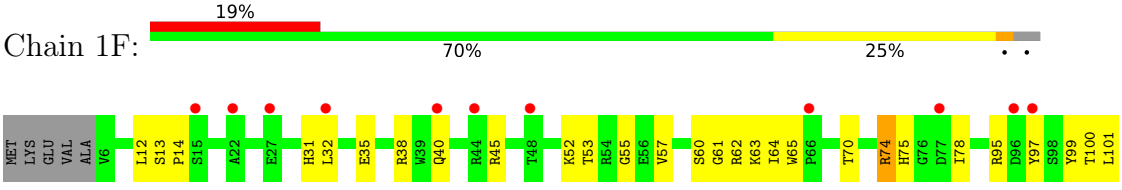
• Molecule 4: 50S ribosomal protein L3

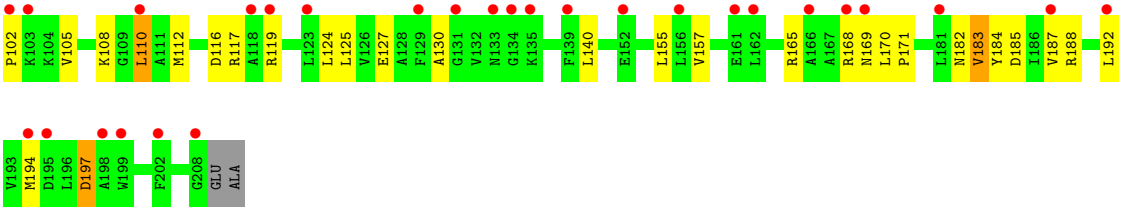
Chain 2E:



• Molecule 5: 50S ribosomal protein L4

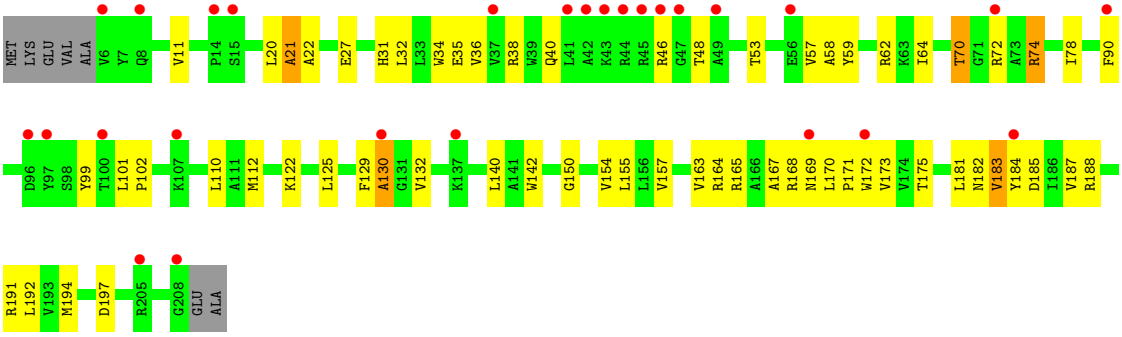
Chain 1F:





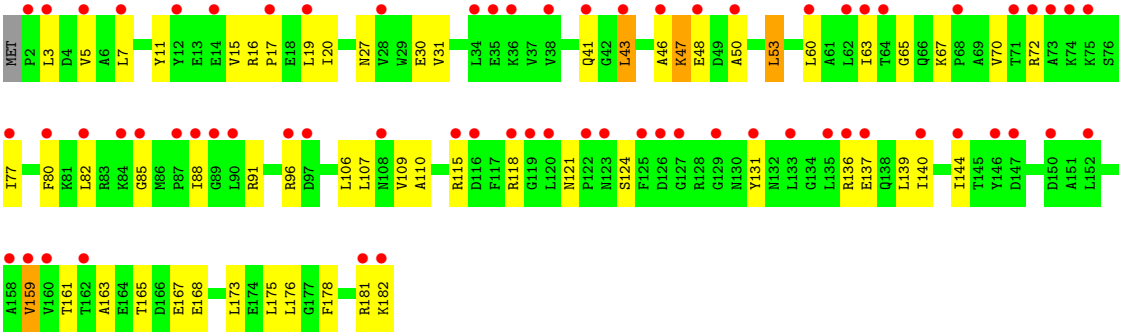
• Molecule 5: 50S ribosomal protein L4

Chain 2F:



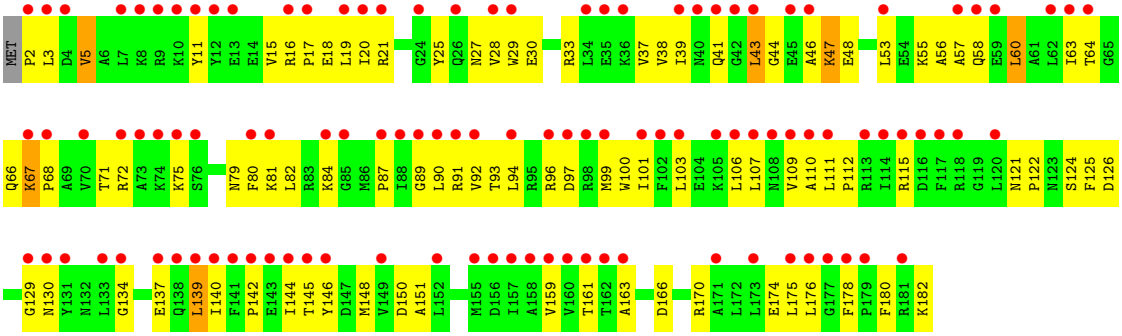
• Molecule 6: 50S ribosomal protein L5

Chain 1G:



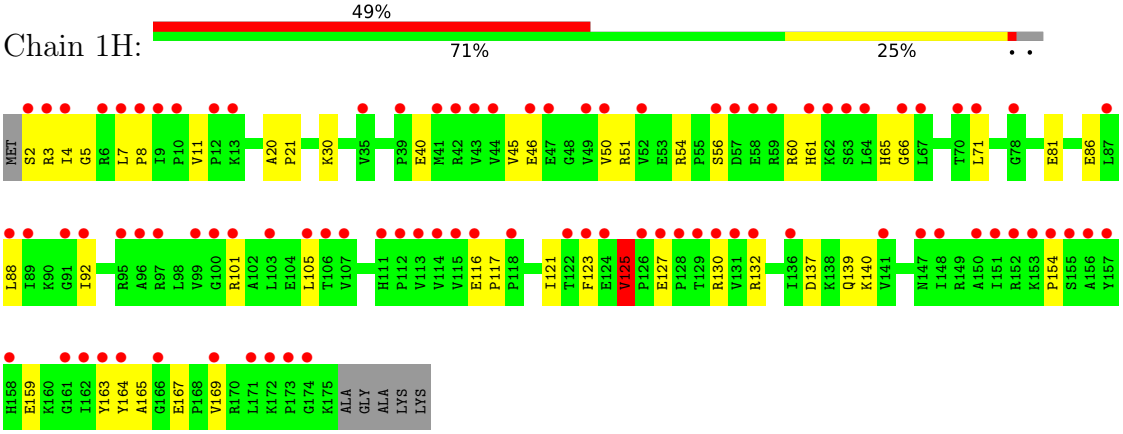
• Molecule 6: 50S ribosomal protein L5

Chain 2G:



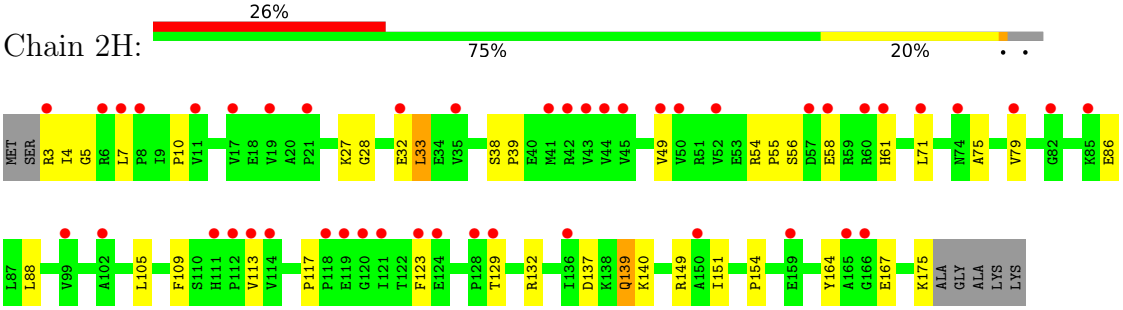
• Molecule 7: 50S ribosomal protein L6

Chain 1H:



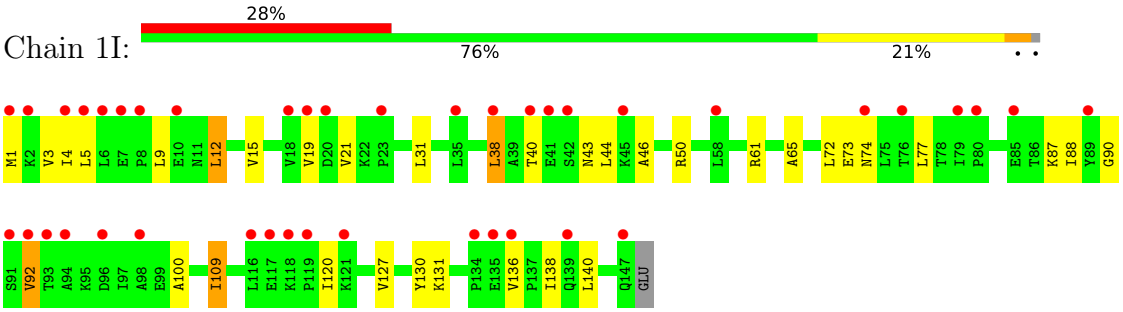
• Molecule 7: 50S ribosomal protein L6

Chain 2H:



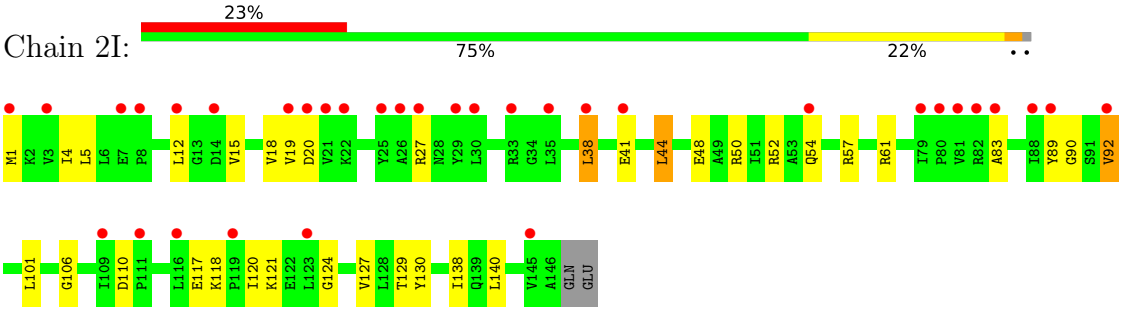
• Molecule 8: 50S ribosomal protein L9

Chain 1I:



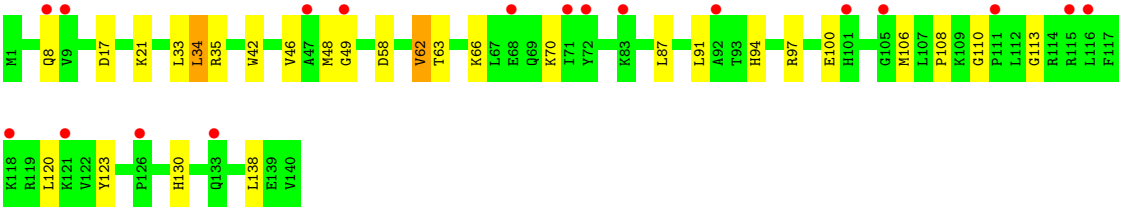
• Molecule 8: 50S ribosomal protein L9

Chain 2I:



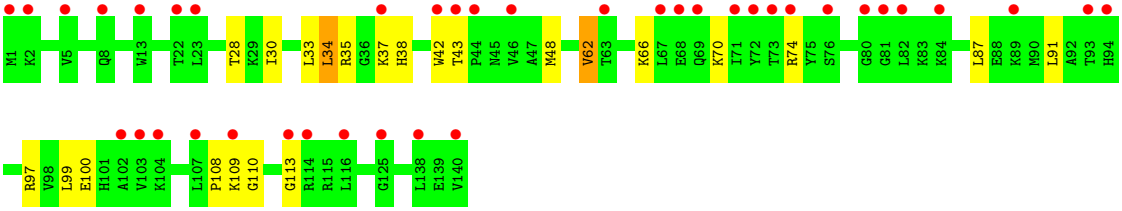
• Molecule 9: 50S ribosomal protein L13

Chain 1N:



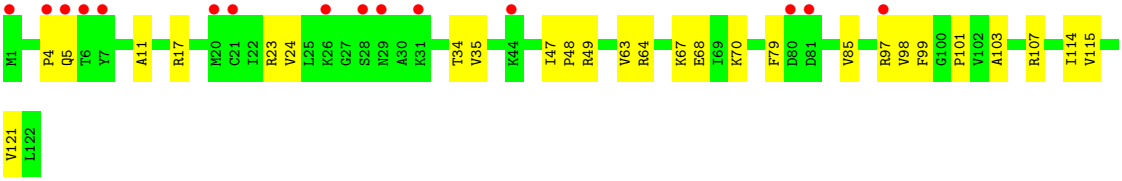
• Molecule 9: 50S ribosomal protein L13

Chain 2N:



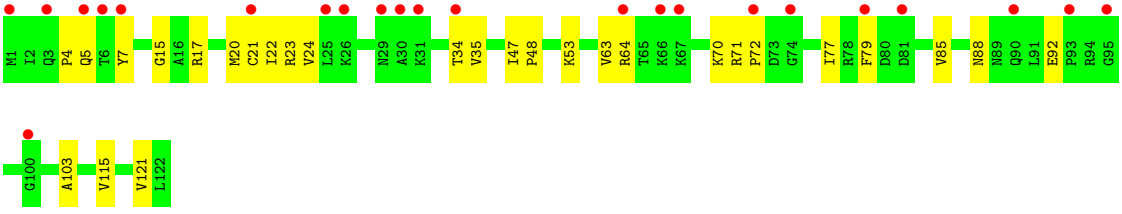
• Molecule 10: 50S ribosomal protein L14

Chain 1O:



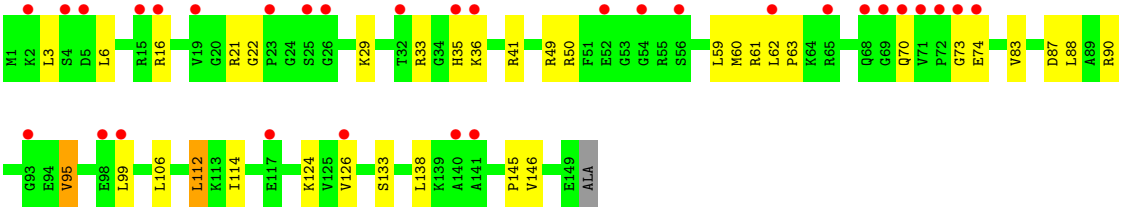
• Molecule 10: 50S ribosomal protein L14

Chain 2O:



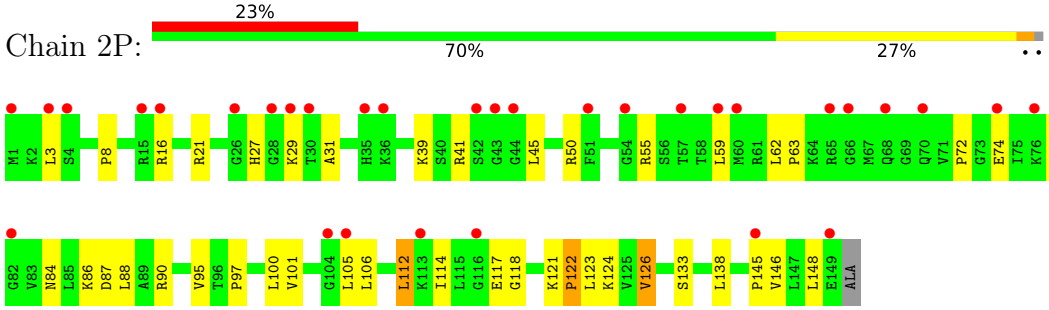
• Molecule 11: 50S ribosomal protein L15

Chain 1P:



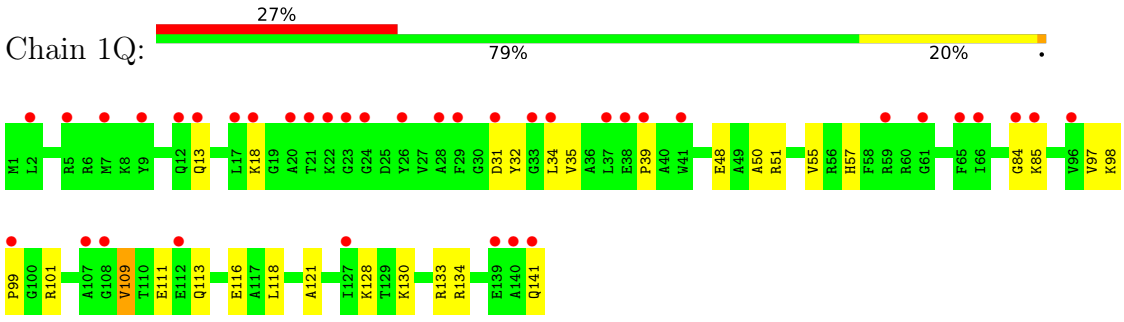
• Molecule 11: 50S ribosomal protein L15

Chain 2P:



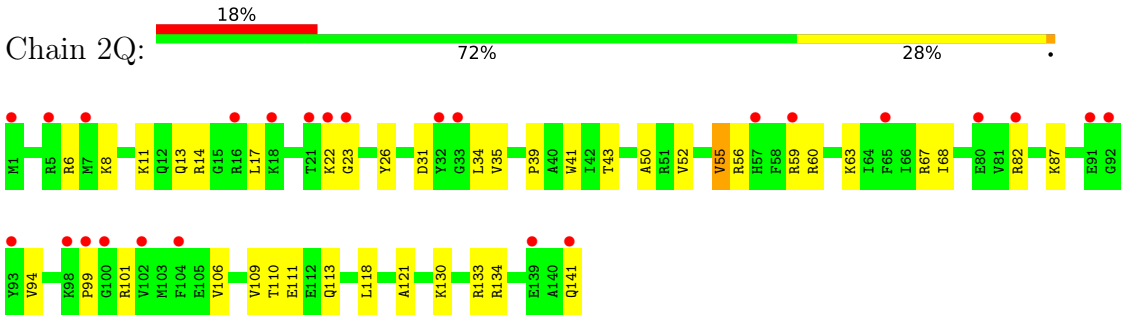
• Molecule 12: 50S ribosomal protein L16

Chain 1Q:



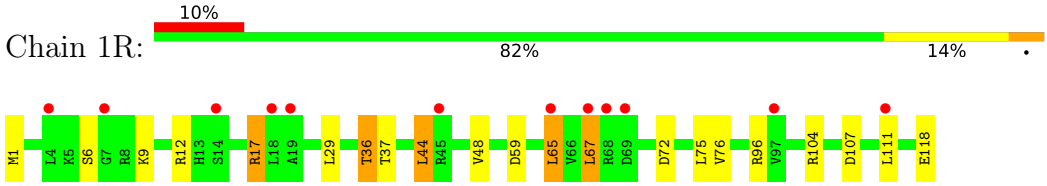
• Molecule 12: 50S ribosomal protein L16

Chain 2Q:



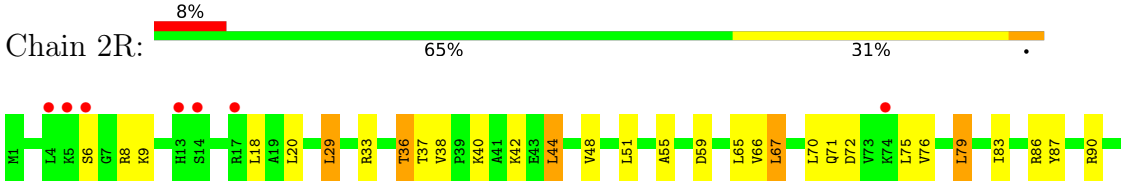
• Molecule 13: 50S ribosomal protein L17

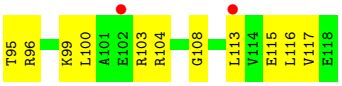
Chain 1R:



• Molecule 13: 50S ribosomal protein L17

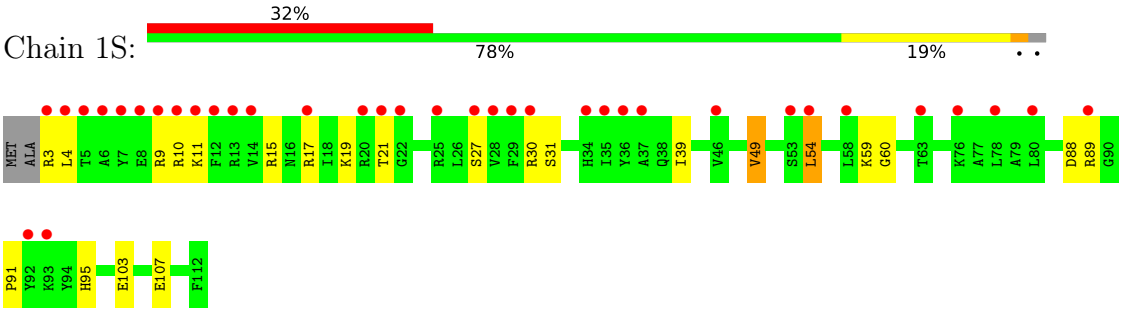
Chain 2R:





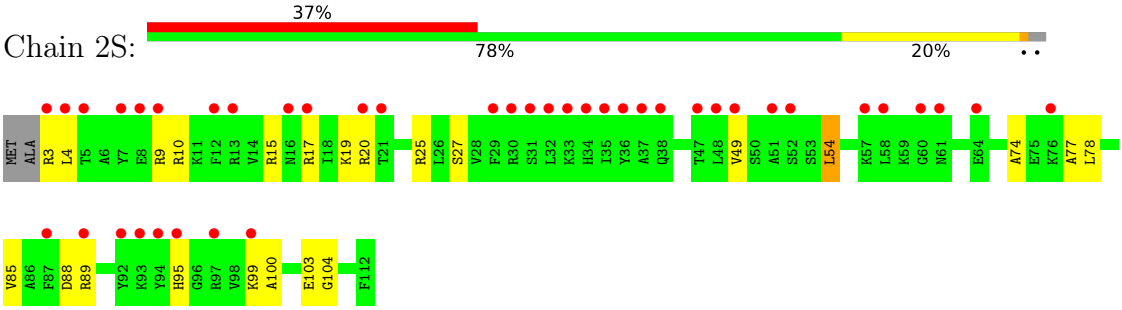
• Molecule 14: 50S ribosomal protein L18

Chain 1S:



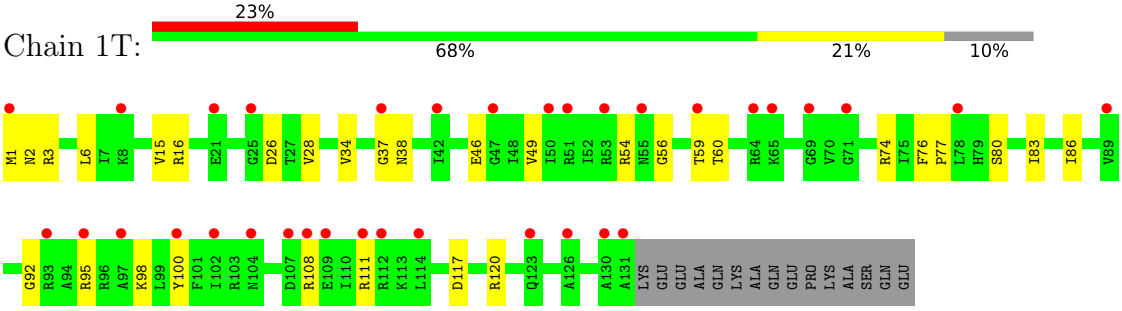
• Molecule 14: 50S ribosomal protein L18

Chain 2S:



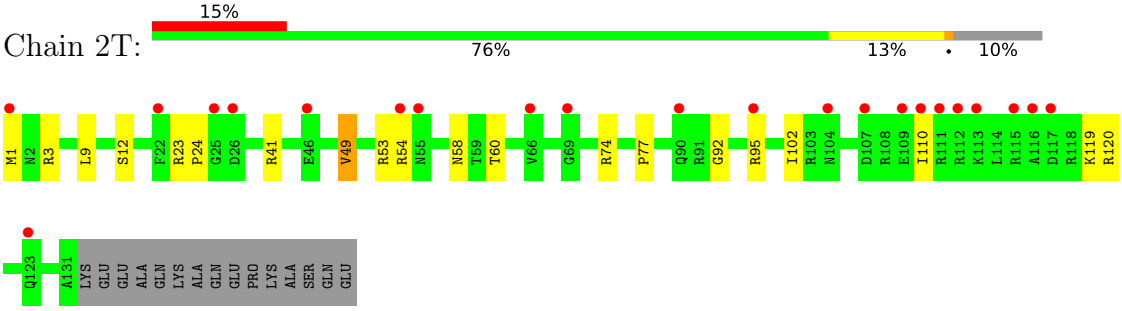
• Molecule 15: 50S ribosomal protein L19

Chain 1T:



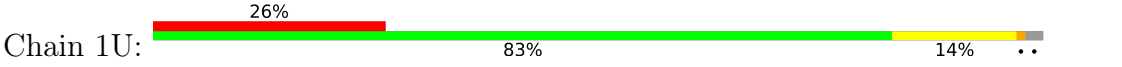
• Molecule 15: 50S ribosomal protein L19

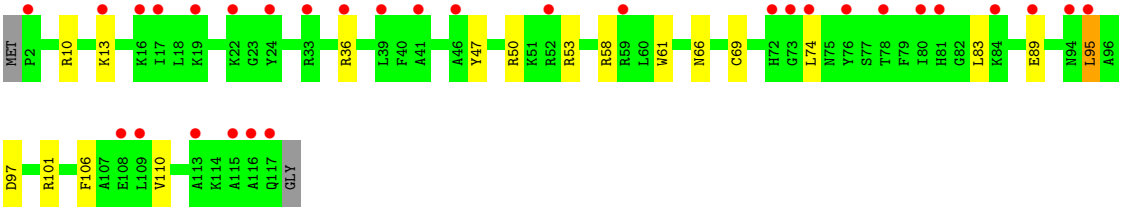
Chain 2T:



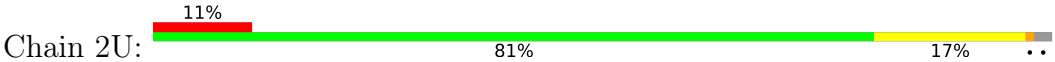
• Molecule 16: 50S ribosomal protein L20

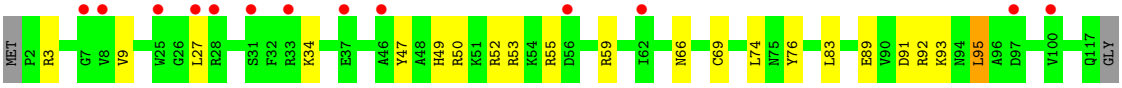
Chain 1U:



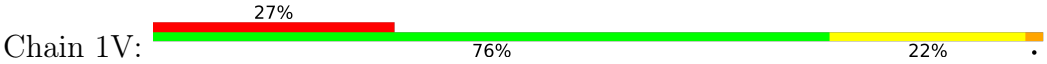


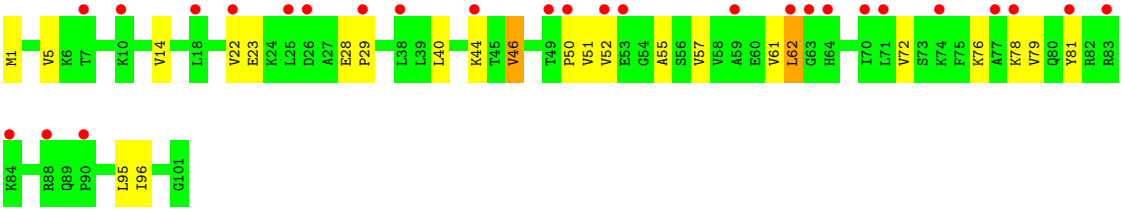
• Molecule 16: 50S ribosomal protein L20



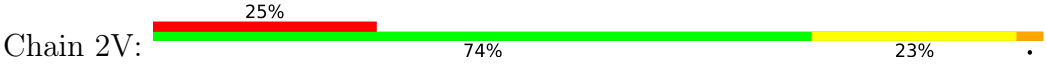


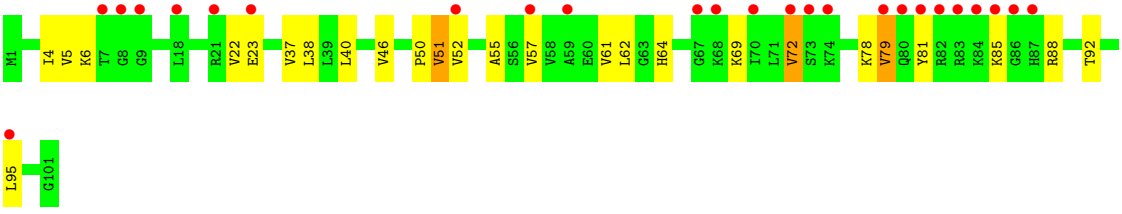
• Molecule 17: 50S ribosomal protein L21



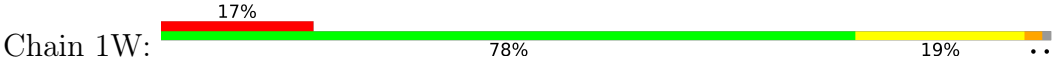


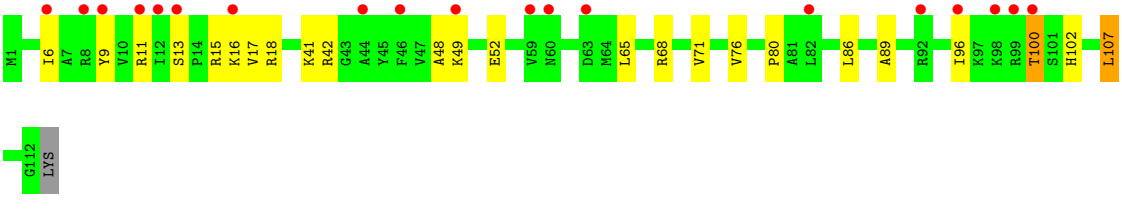
• Molecule 17: 50S ribosomal protein L21



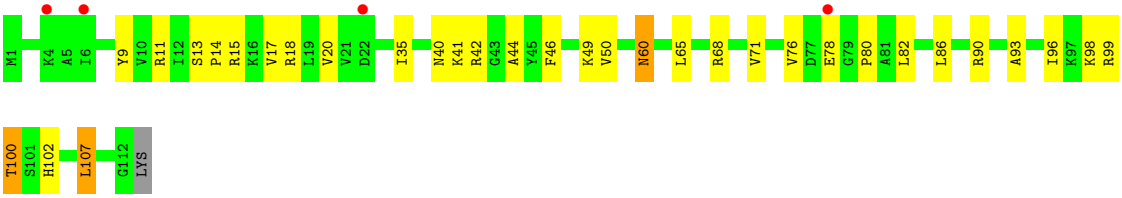


• Molecule 18: 50S ribosomal protein L22

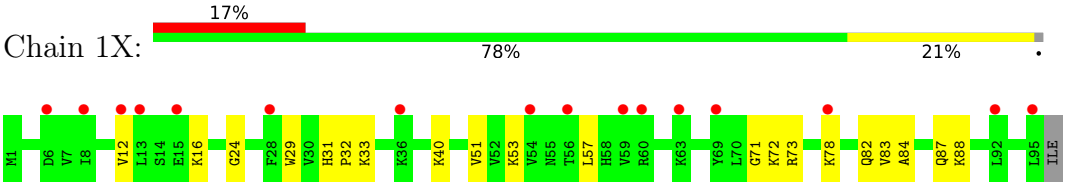




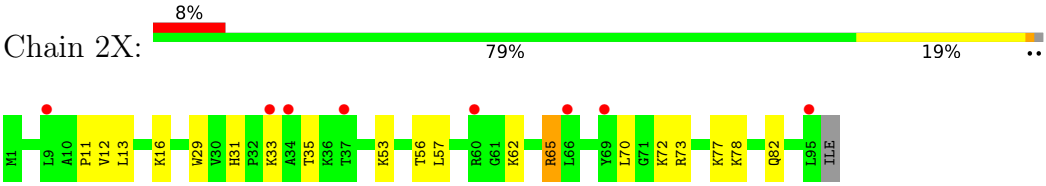
• Molecule 18: 50S ribosomal protein L22



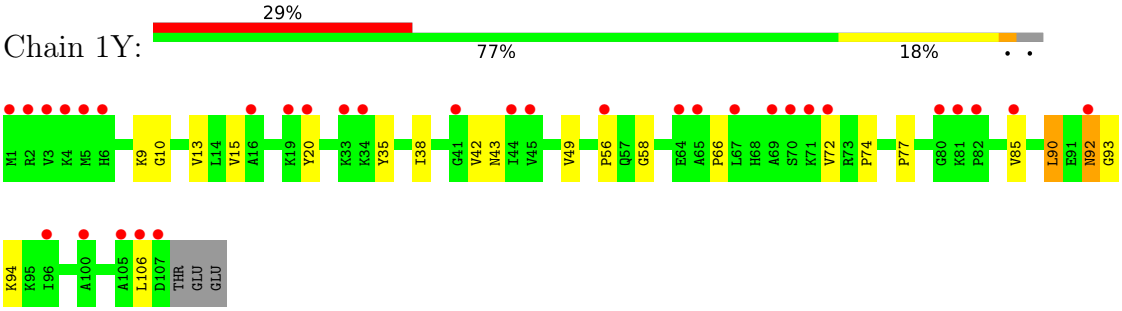
• Molecule 19: 50S ribosomal protein L23



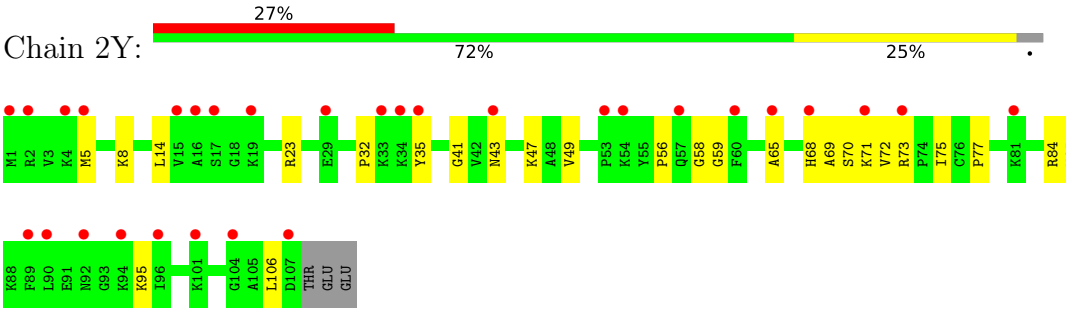
• Molecule 19: 50S ribosomal protein L23



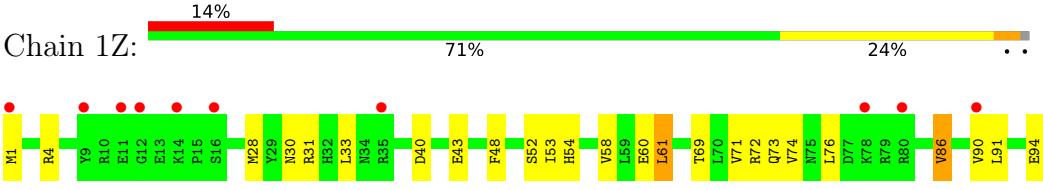
• Molecule 20: 50S ribosomal protein L24

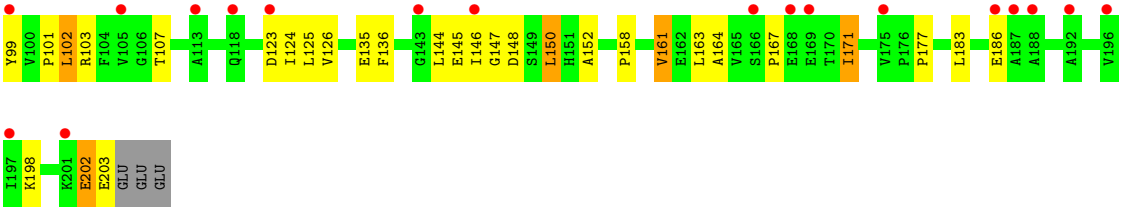


• Molecule 20: 50S ribosomal protein L24



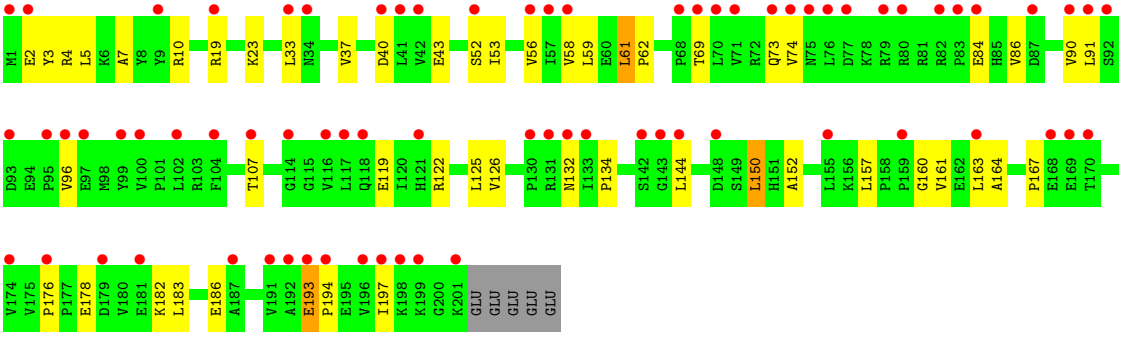
• Molecule 21: 50S ribosomal protein L25





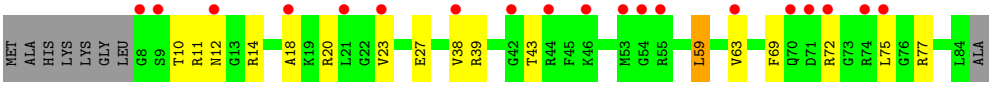
• Molecule 21: 50S ribosomal protein L25

Chain 2Z:



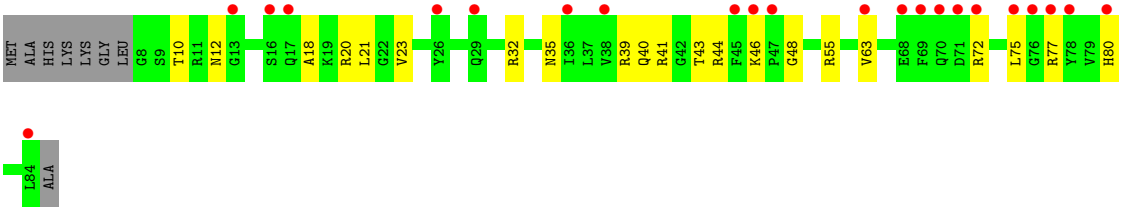
• Molecule 22: 50S ribosomal protein L27

Chain 10:



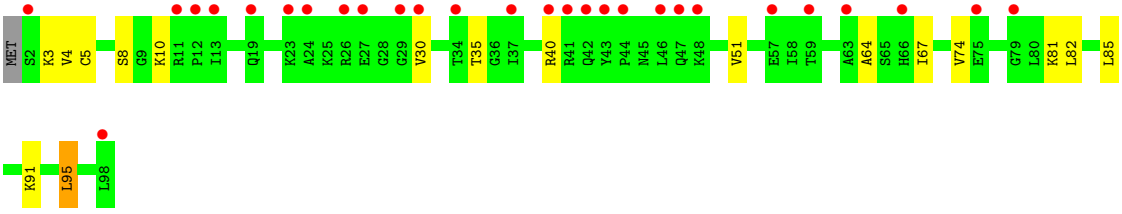
• Molecule 22: 50S ribosomal protein L27

Chain 20:



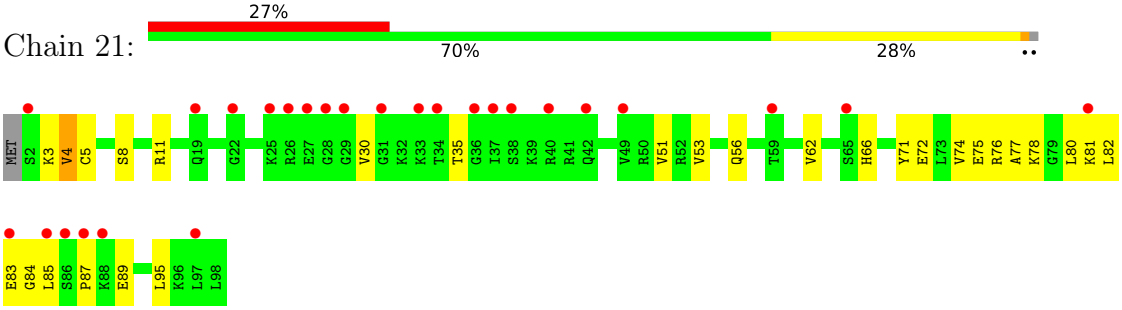
• Molecule 23: 50S ribosomal protein L28

Chain 11:



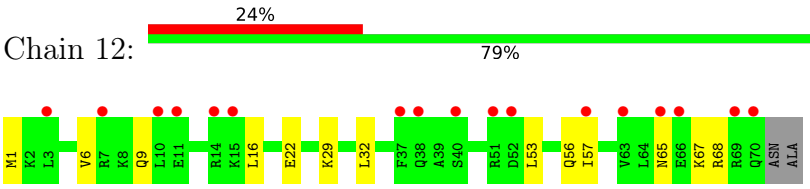
• Molecule 23: 50S ribosomal protein L28

Chain 21:



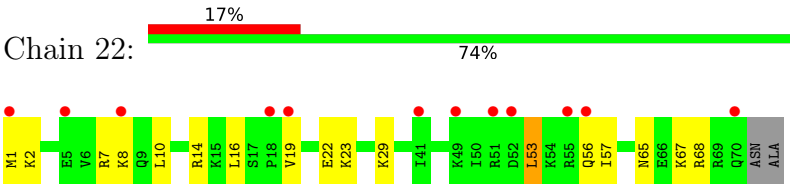
• Molecule 24: 50S ribosomal protein L29

Chain 12:



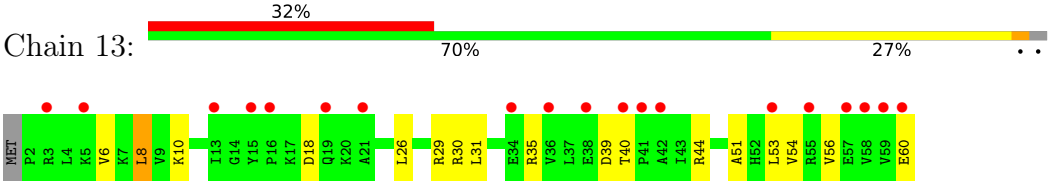
• Molecule 24: 50S ribosomal protein L29

Chain 22:



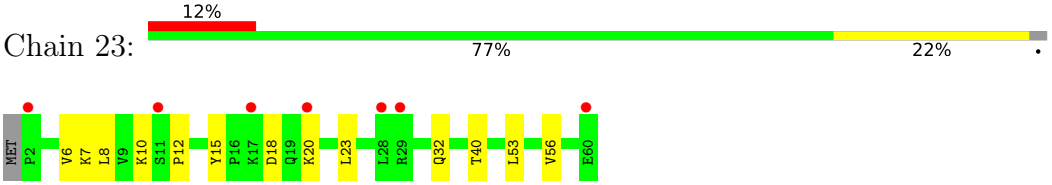
• Molecule 25: 50S ribosomal protein L30

Chain 13:



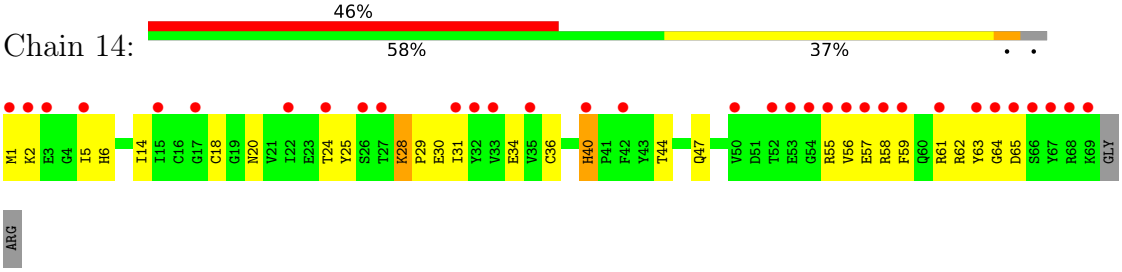
• Molecule 25: 50S ribosomal protein L30

Chain 23:



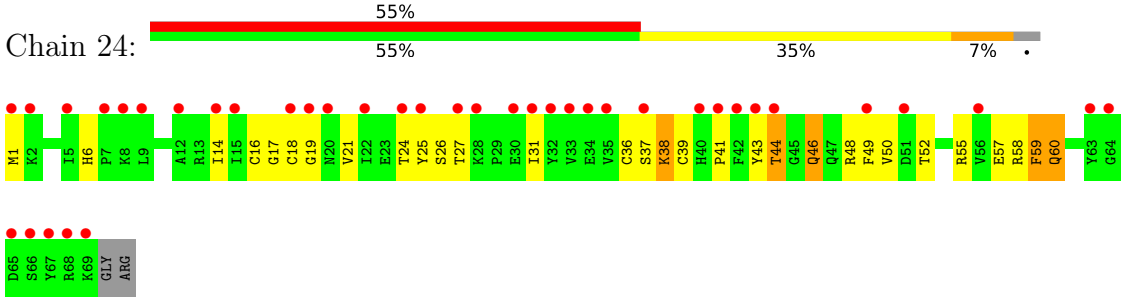
• Molecule 26: 50S ribosomal protein L31

Chain 14:



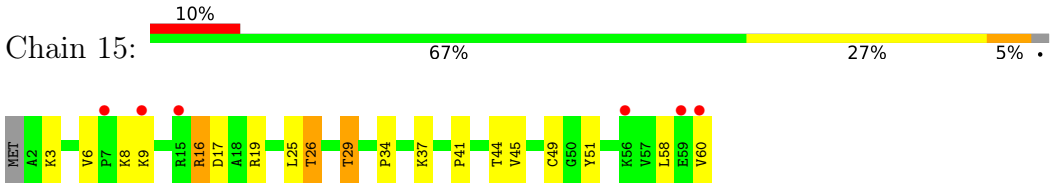
• Molecule 26: 50S ribosomal protein L31

Chain 24:



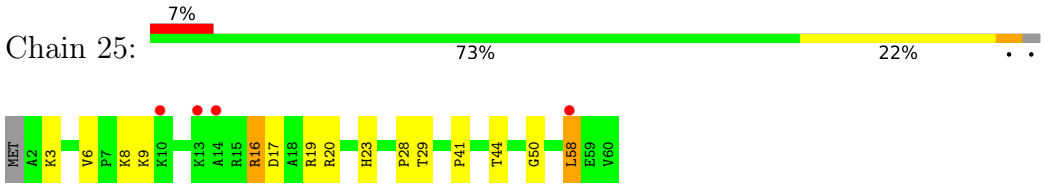
• Molecule 27: 50S ribosomal protein L32

Chain 15:



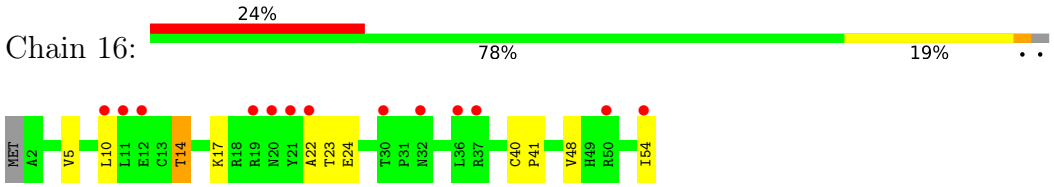
• Molecule 27: 50S ribosomal protein L32

Chain 25:



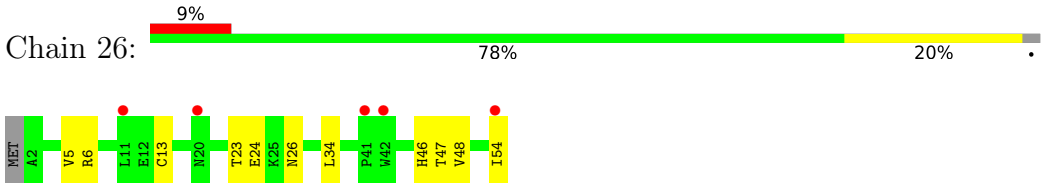
• Molecule 28: 50S ribosomal protein L33

Chain 16:



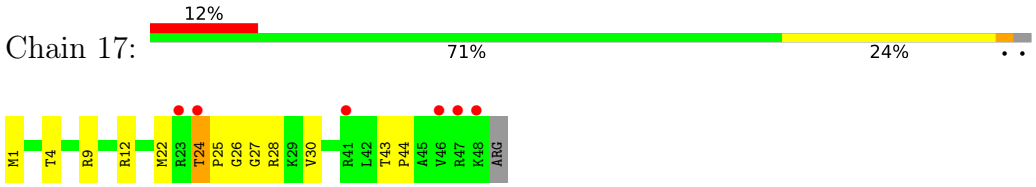
• Molecule 28: 50S ribosomal protein L33

Chain 26:



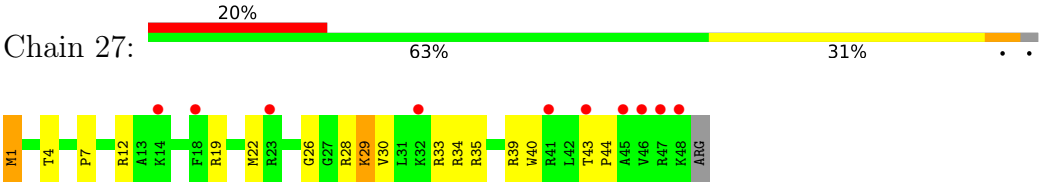
• Molecule 29: 50S ribosomal protein L34

Chain 17:



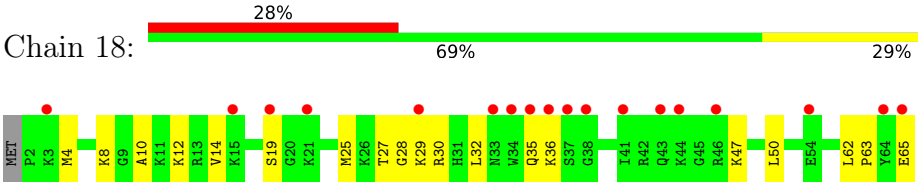
• Molecule 29: 50S ribosomal protein L34

Chain 27:



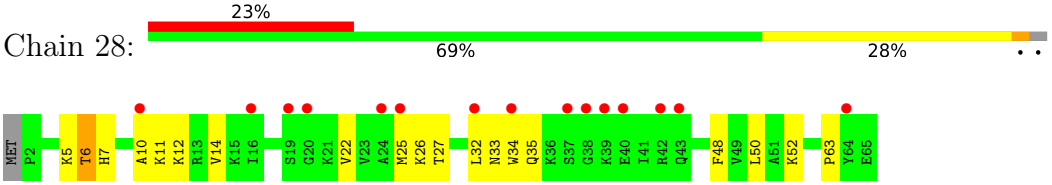
• Molecule 30: 50S ribosomal protein L35

Chain 18:



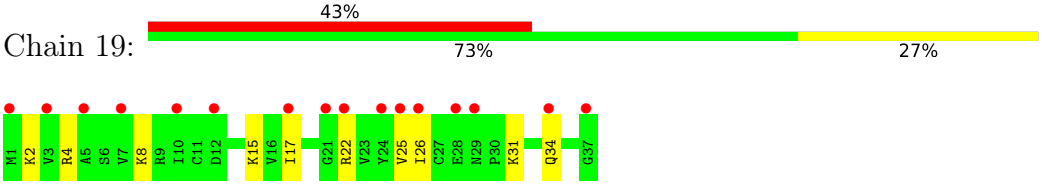
• Molecule 30: 50S ribosomal protein L35

Chain 28:



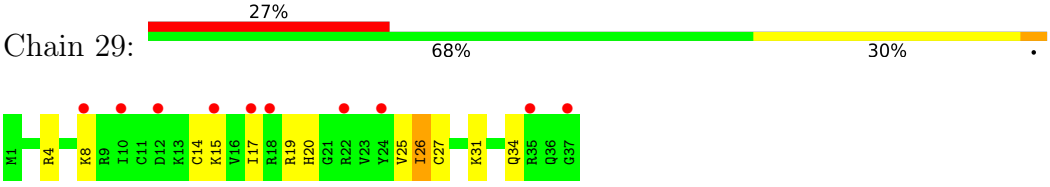
• Molecule 31: 50S ribosomal protein L36

Chain 19:



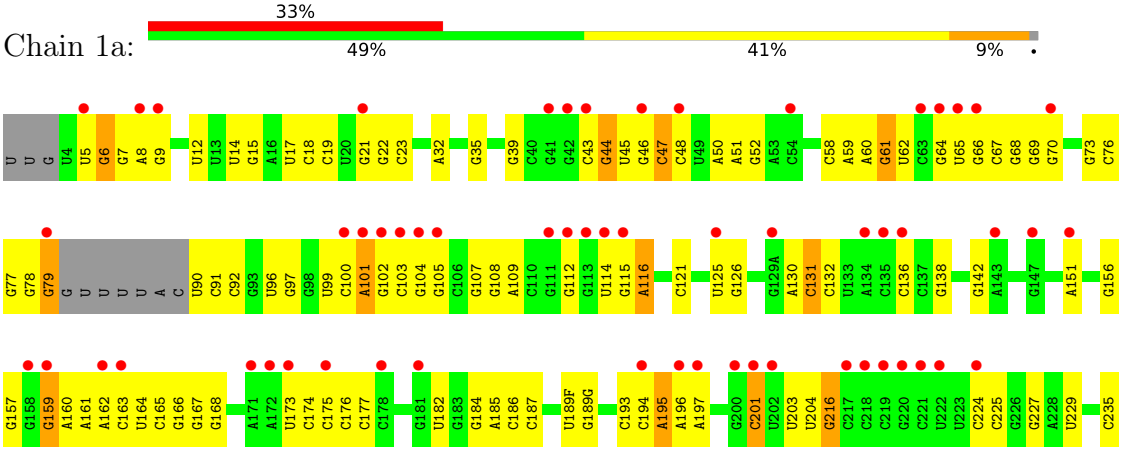
• Molecule 31: 50S ribosomal protein L36

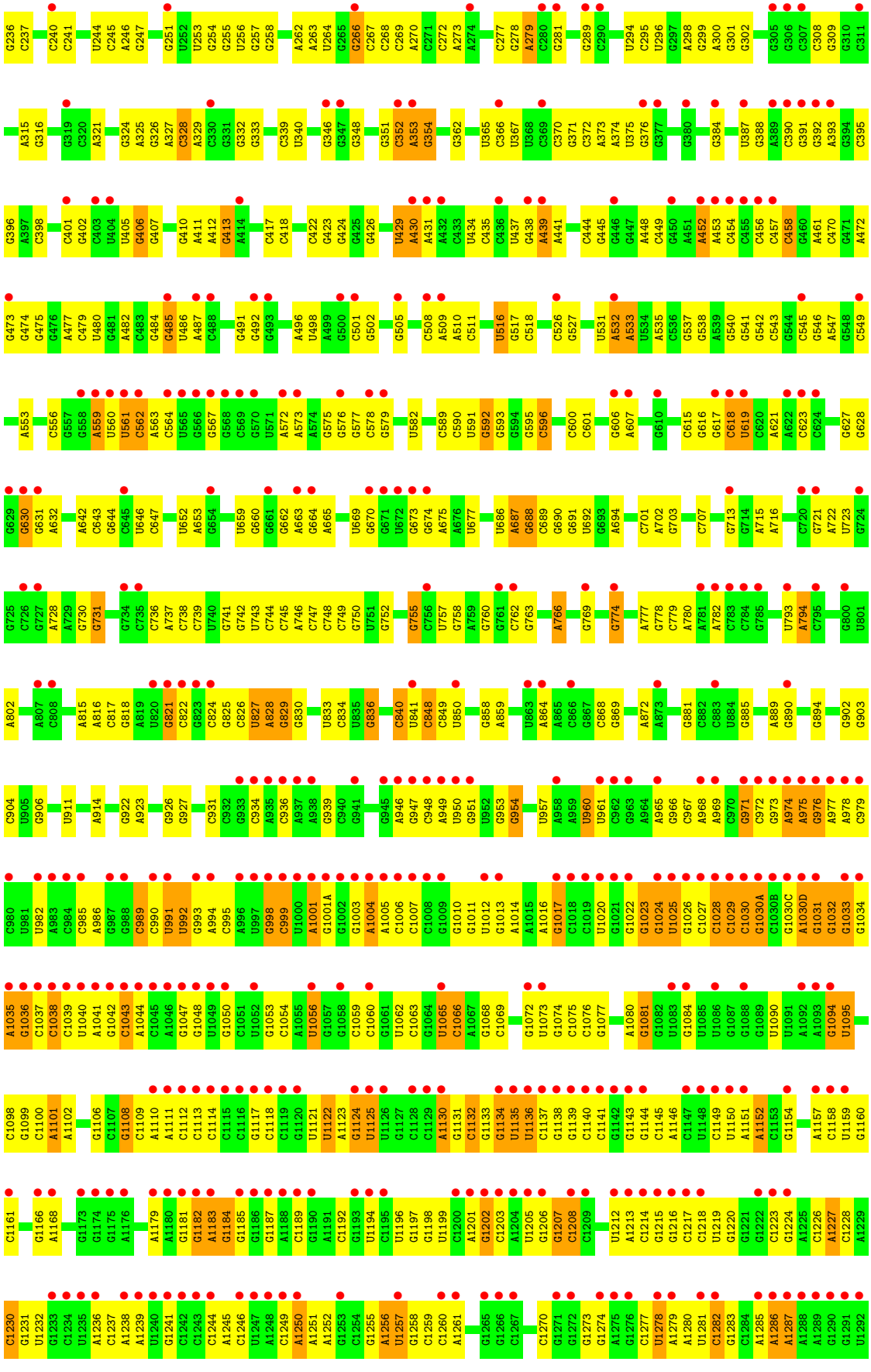
Chain 29:

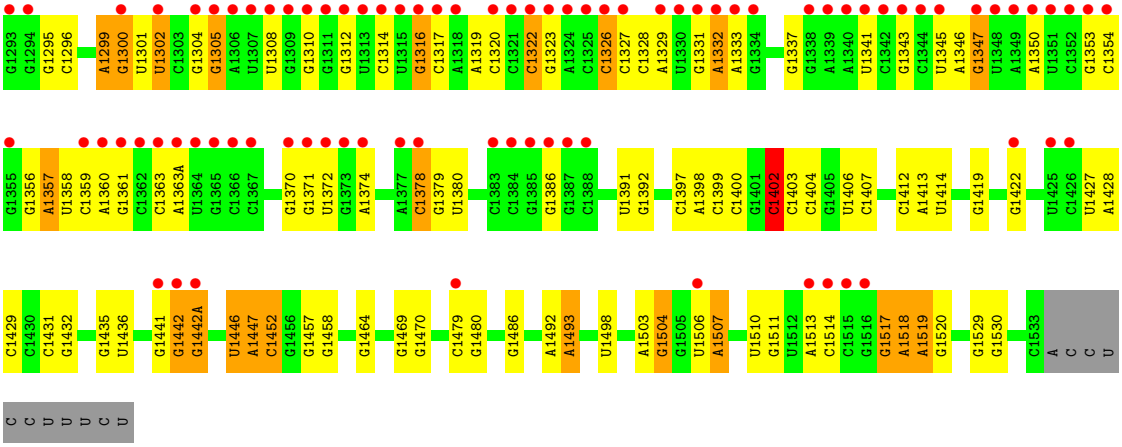


• Molecule 32: 16S Ribosomal RNA

Chain 1a:

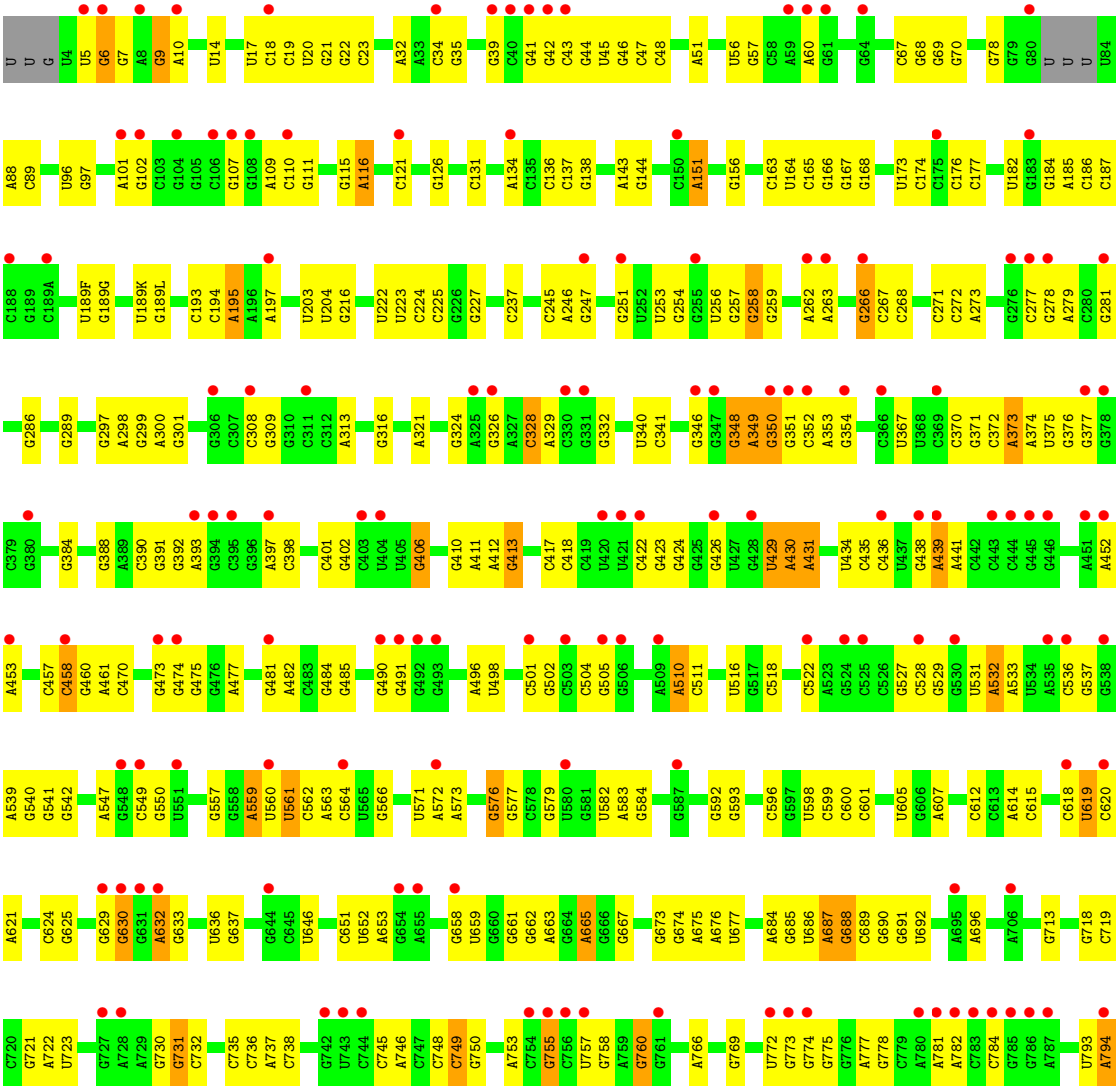


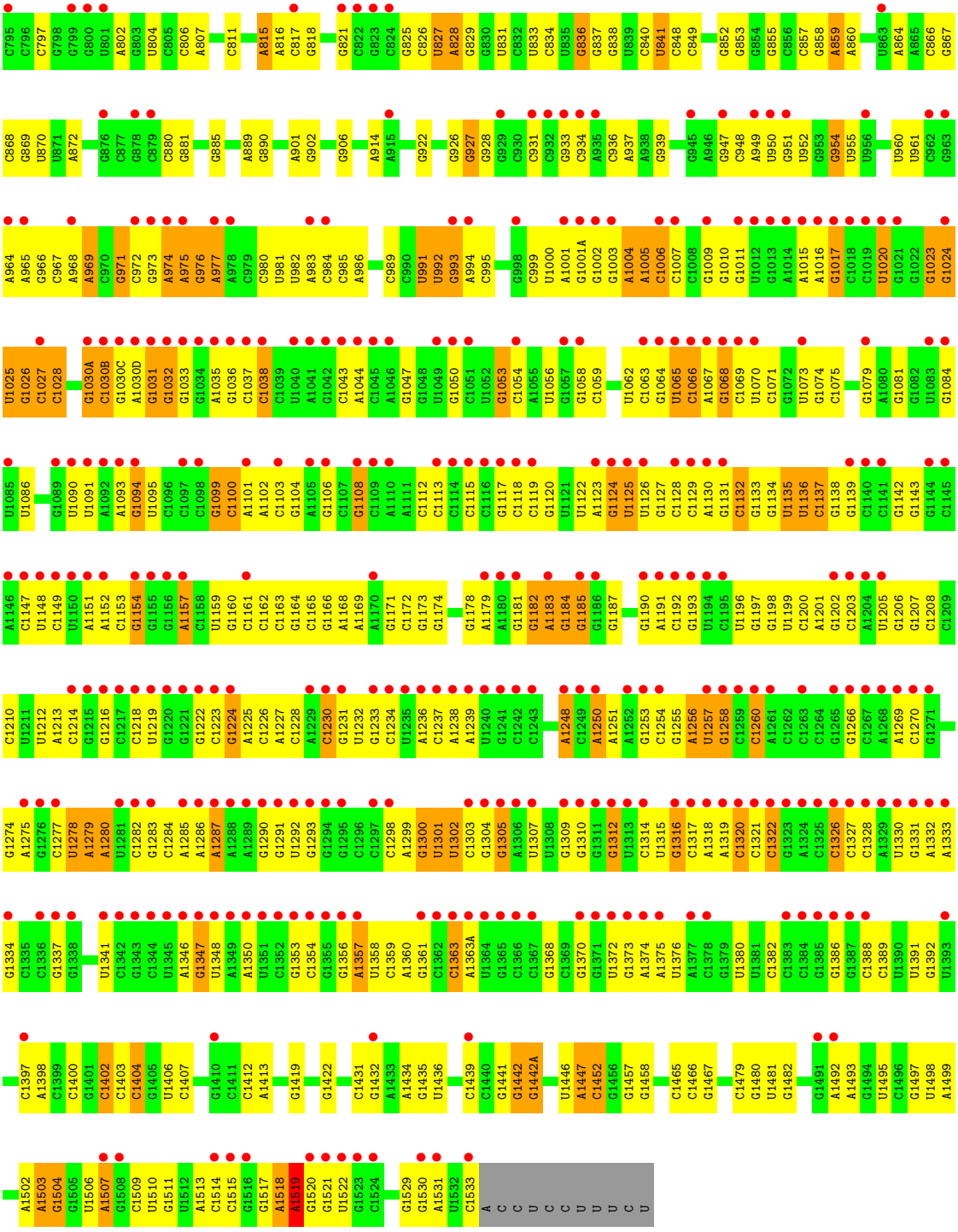




• Molecule 32: 16S Ribosomal RNA

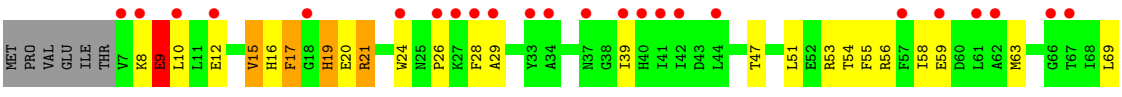
Chain 2a:

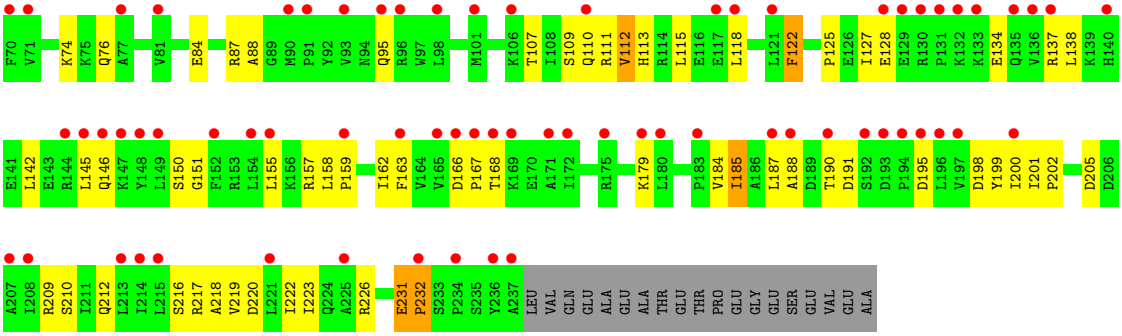




• Molecule 33: 30S ribosomal protein S2

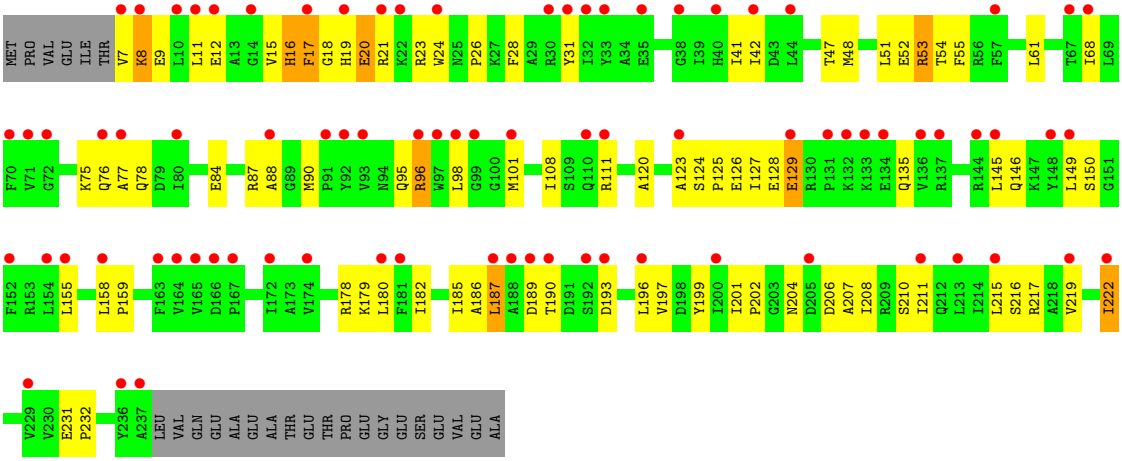
Chain 1b:





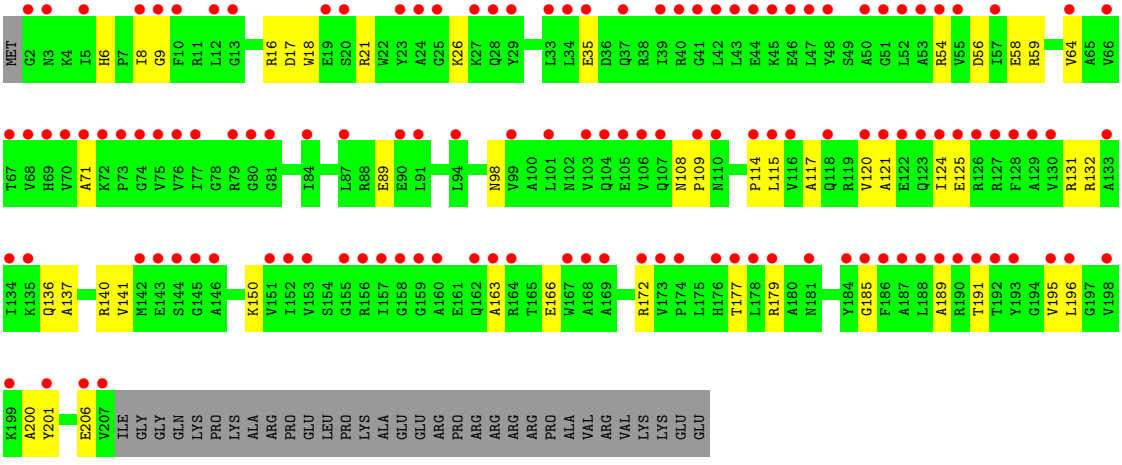
• Molecule 33: 30S ribosomal protein S2

Chain 2b:



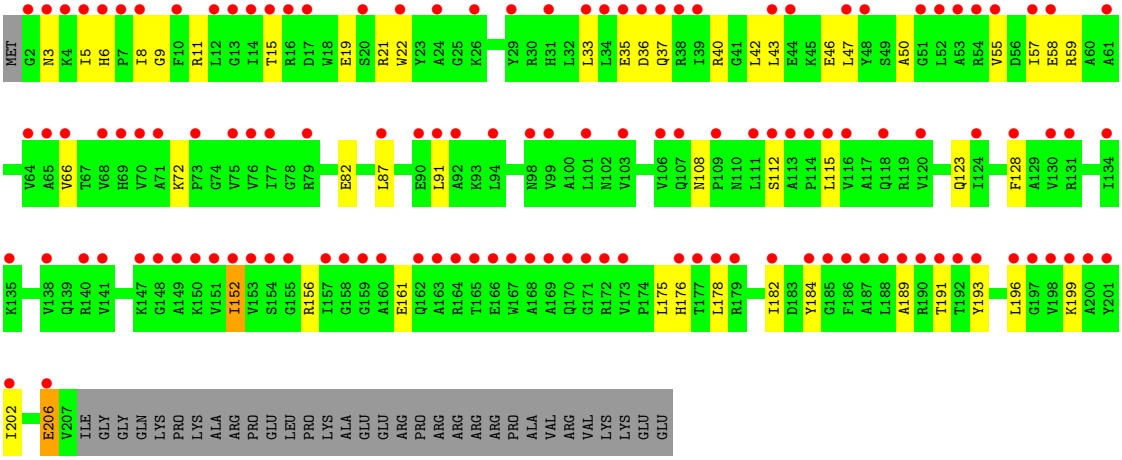
• Molecule 34: 30S ribosomal protein S3

Chain 1c:



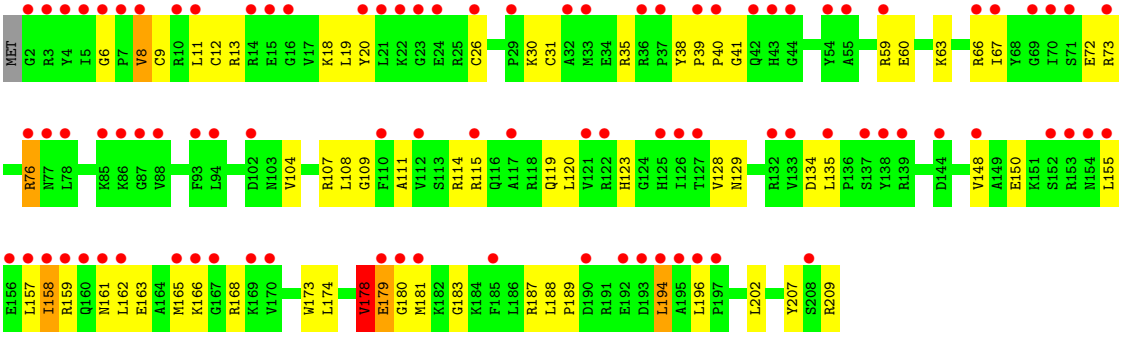
• Molecule 34: 30S ribosomal protein S3

Chain 2c:



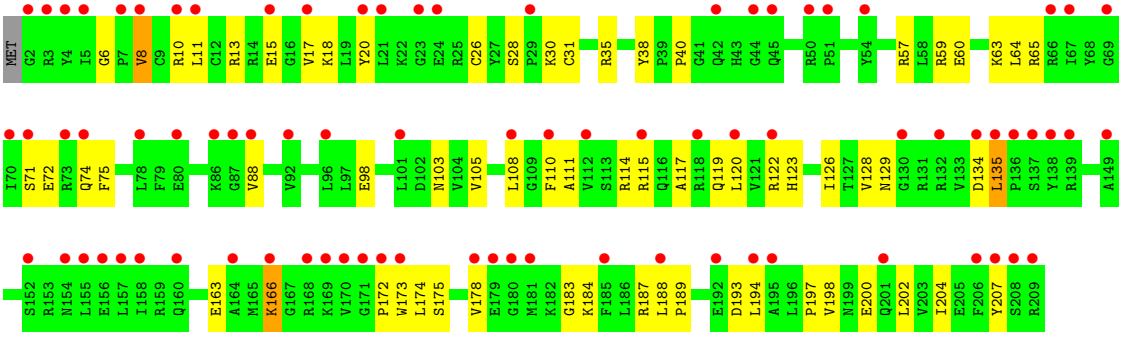
• Molecule 35: 30S ribosomal protein S4

Chain 1d:



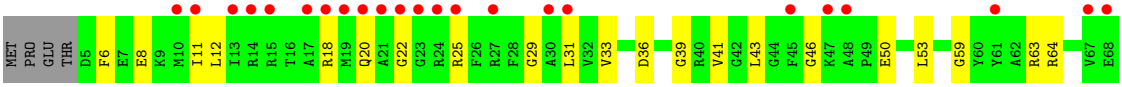
• Molecule 35: 30S ribosomal protein S4

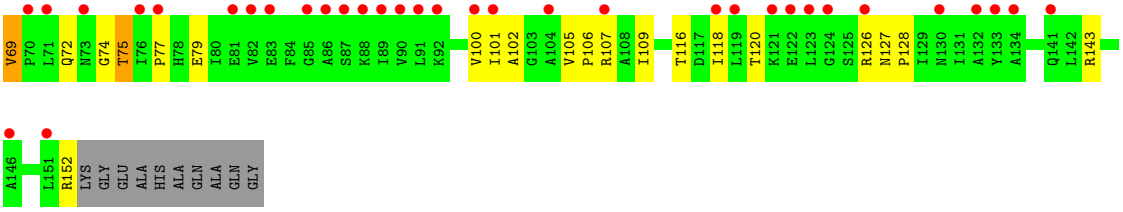
Chain 2d:



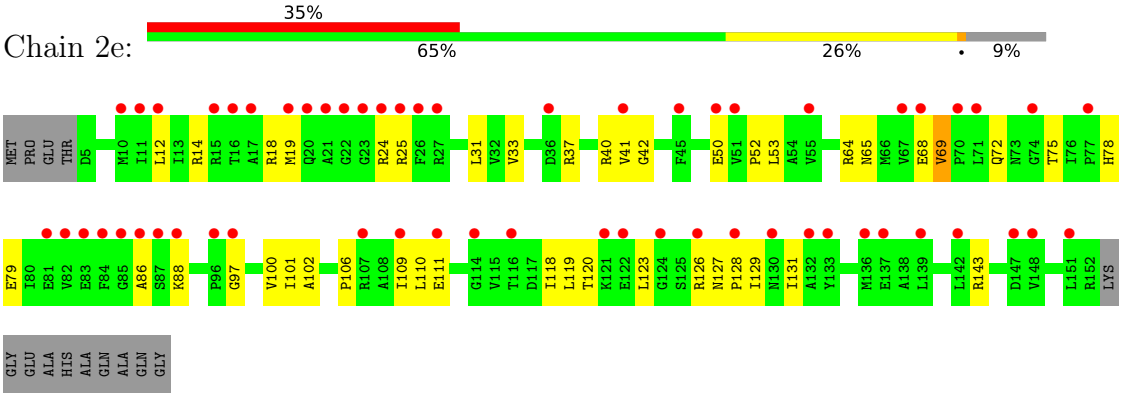
• Molecule 36: 30S ribosomal protein S5

Chain 1e:

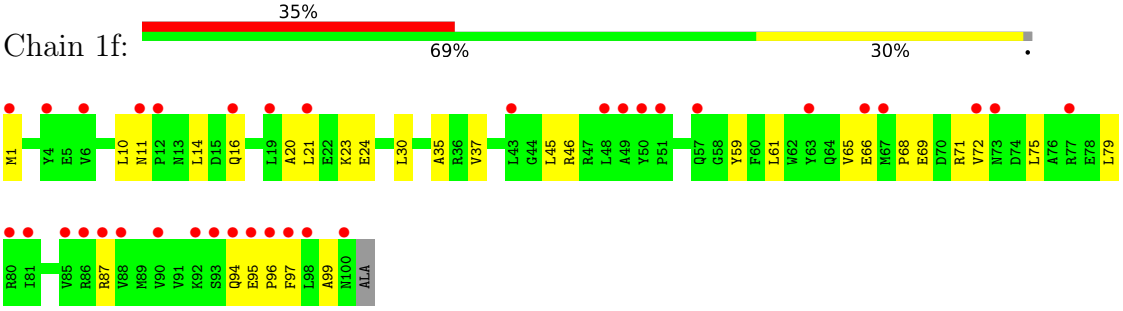




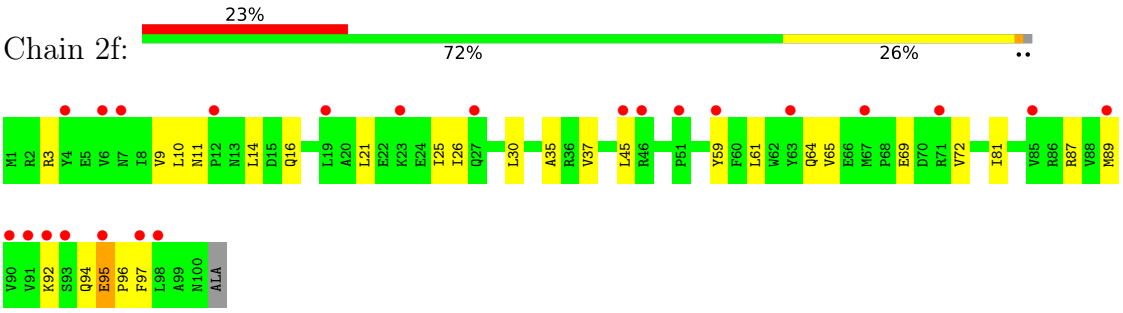
• Molecule 36: 30S ribosomal protein S5



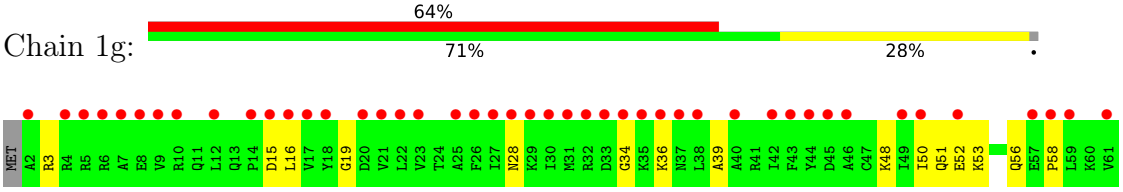
• Molecule 37: 30S ribosomal protein S6

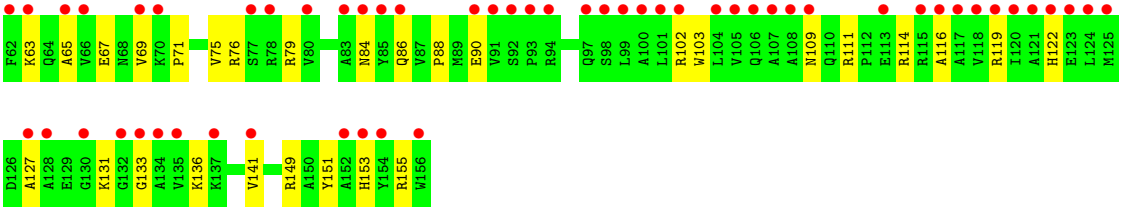


• Molecule 37: 30S ribosomal protein S6



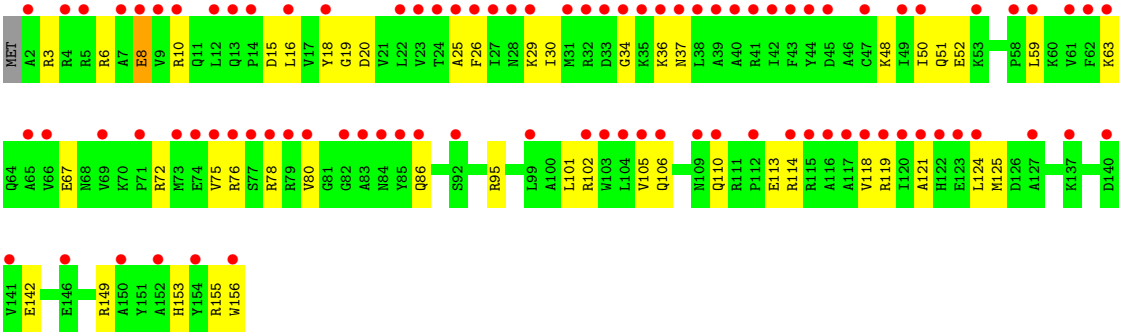
• Molecule 38: 30S ribosomal protein S7





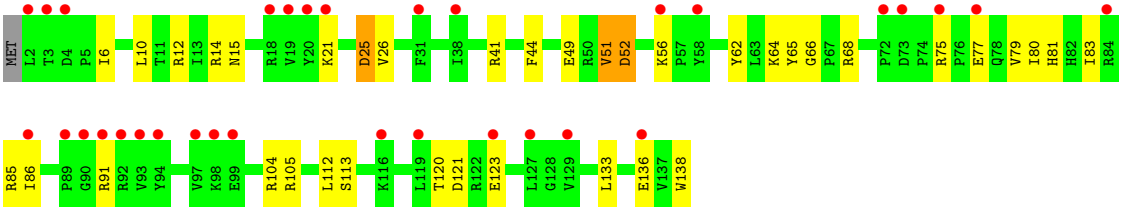
• Molecule 38: 30S ribosomal protein S7

Chain 2g:



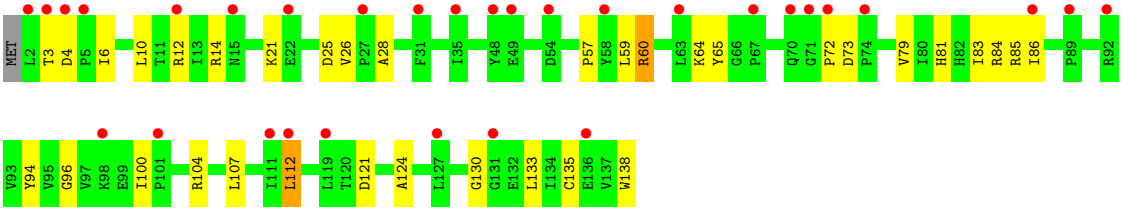
• Molecule 39: 30S ribosomal protein S8

Chain 1h:



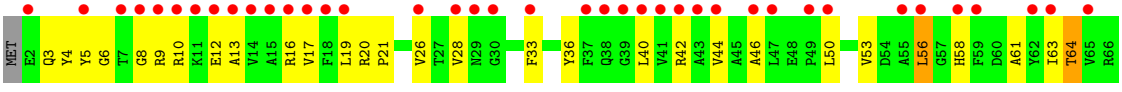
• Molecule 39: 30S ribosomal protein S8

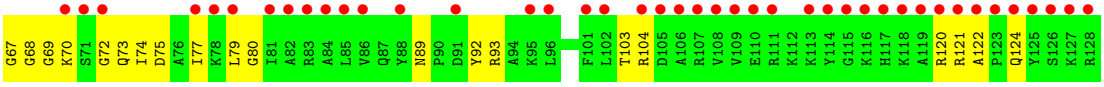
Chain 2h:



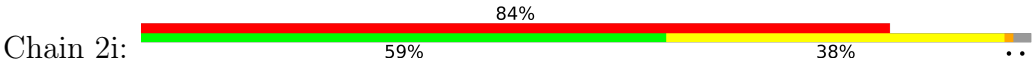
• Molecule 40: 30S ribosomal protein S9

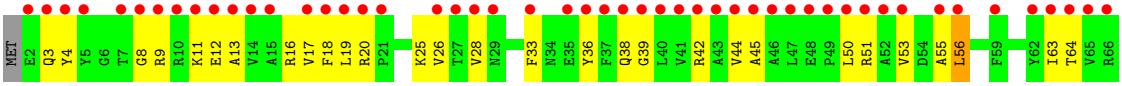
Chain 1i:

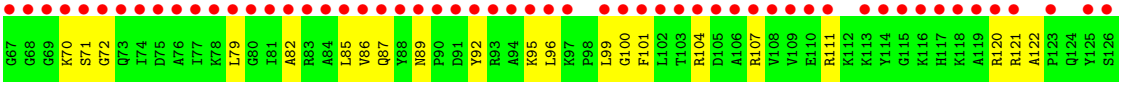




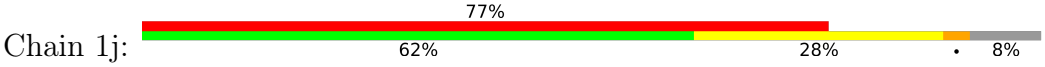
• Molecule 40: 30S ribosomal protein S9

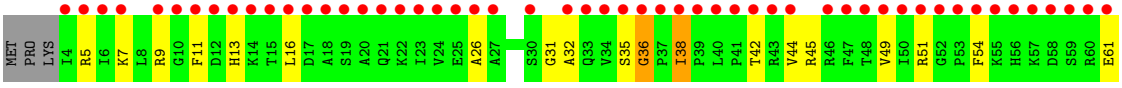


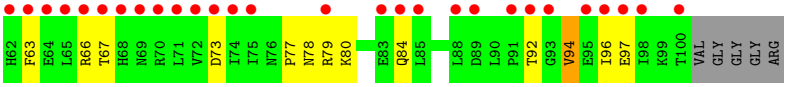




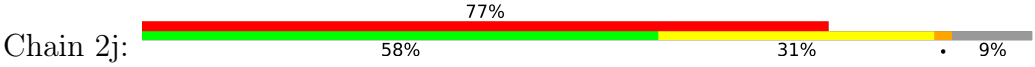
• Molecule 41: 30S ribosomal protein S10

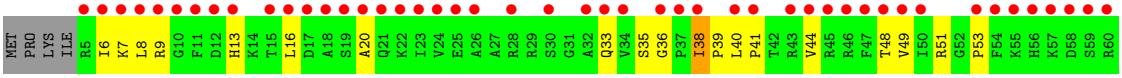


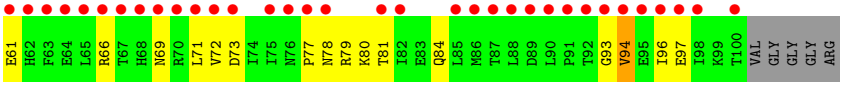




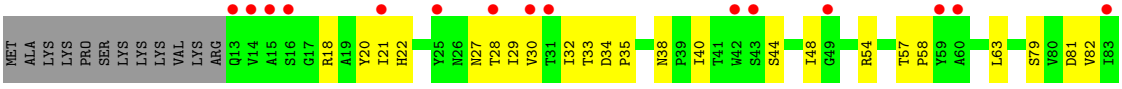
• Molecule 41: 30S ribosomal protein S10





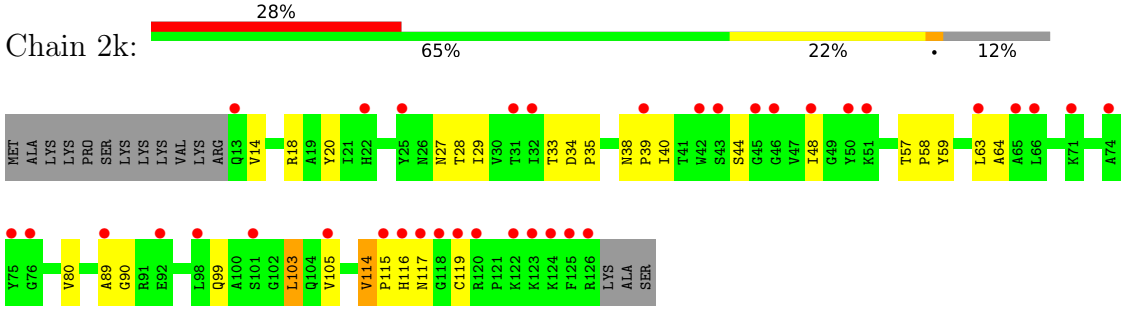


• Molecule 42: 30S ribosomal protein S11



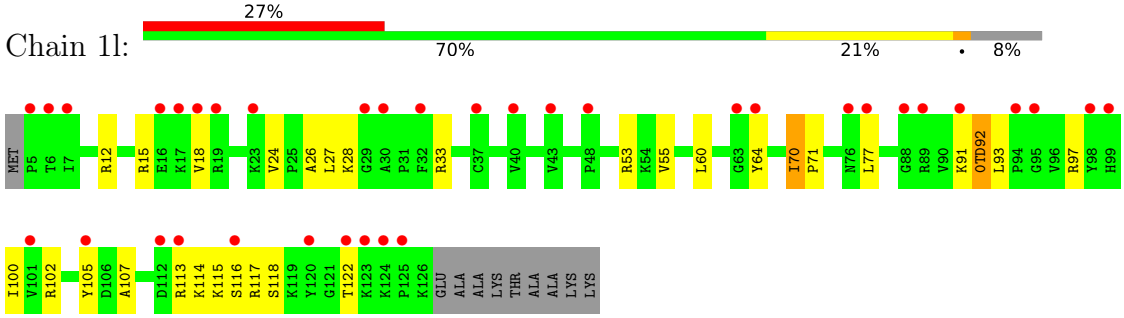
• Molecule 42: 30S ribosomal protein S11

Chain 2k:



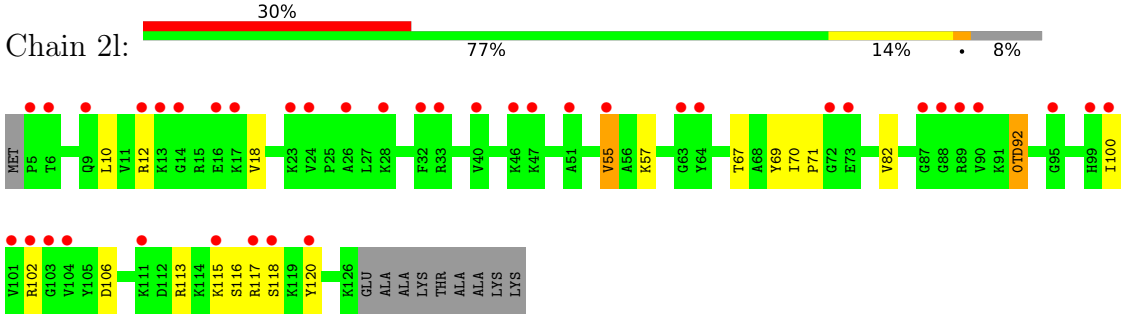
• Molecule 43: 30S ribosomal protein S12

Chain 1l:



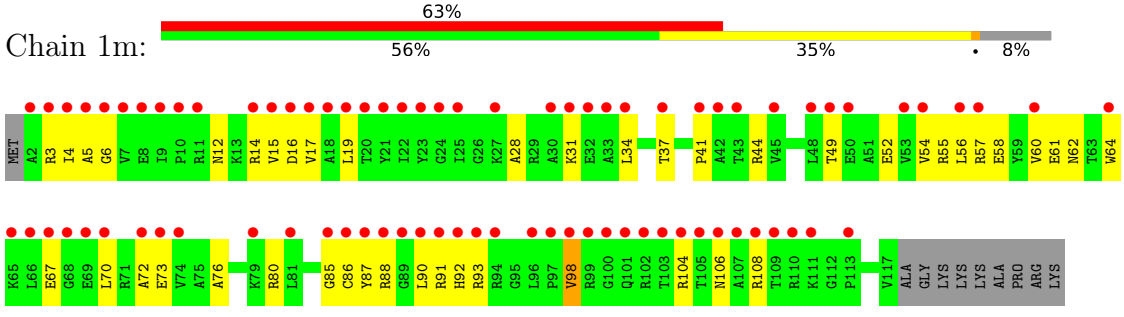
• Molecule 43: 30S ribosomal protein S12

Chain 2l:



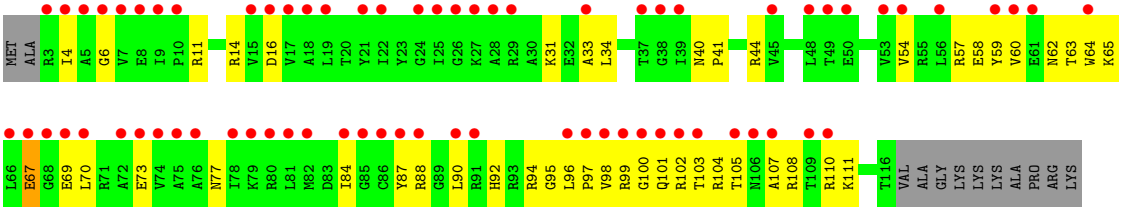
• Molecule 44: 30S ribosomal protein S13

Chain 1m:

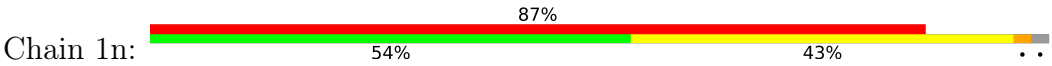


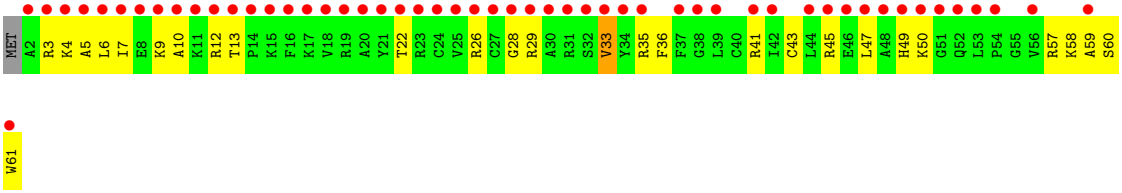
• Molecule 44: 30S ribosomal protein S13

Chain 2m:

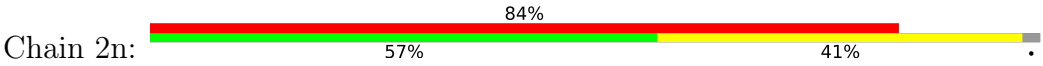


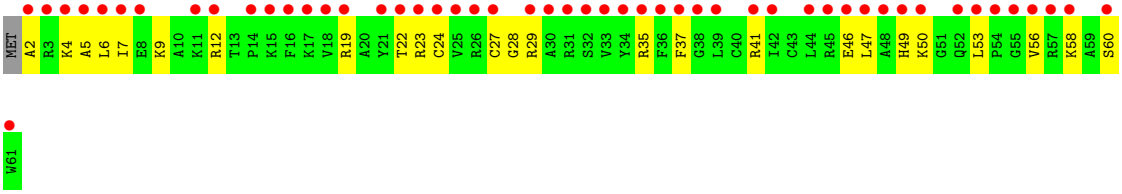
• Molecule 45: 30S ribosomal protein S14 type Z



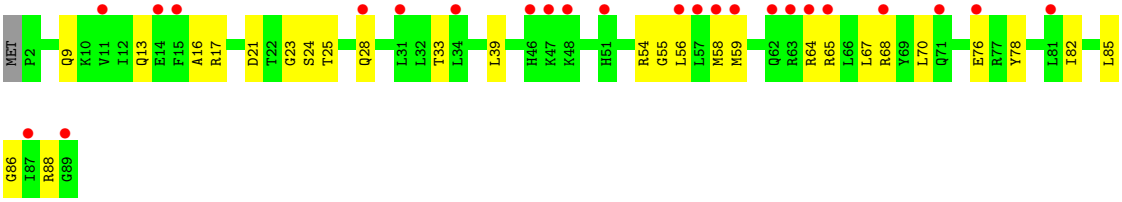


• Molecule 45: 30S ribosomal protein S14 type Z

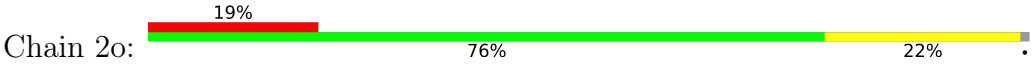


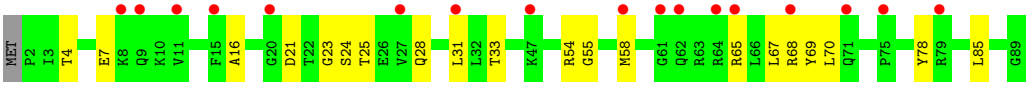


• Molecule 46: 30S ribosomal protein S15

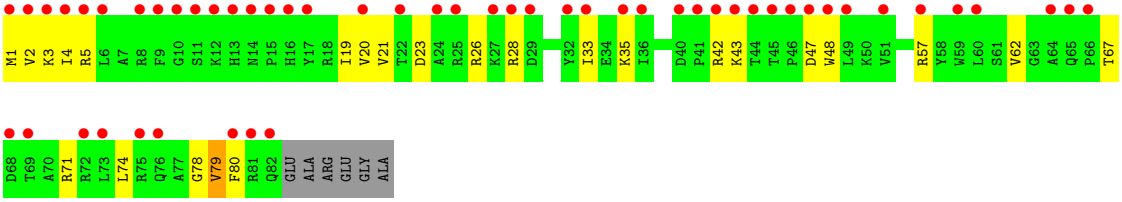


• Molecule 46: 30S ribosomal protein S15

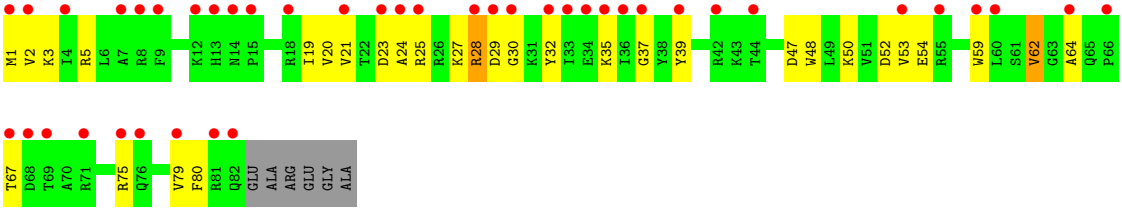




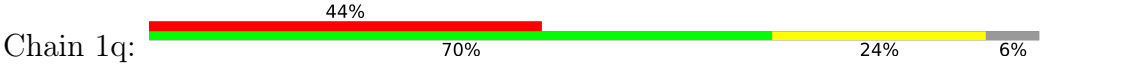
• Molecule 47: 30S ribosomal protein S16

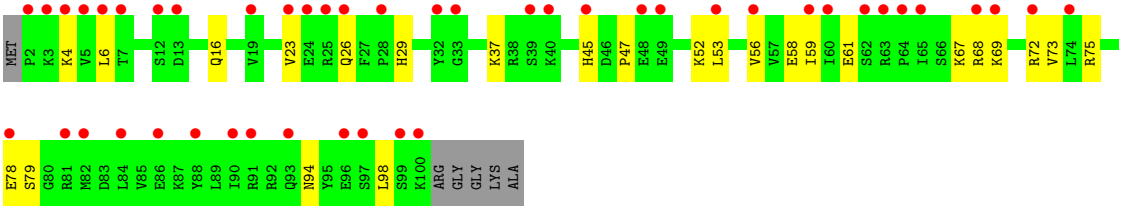


• Molecule 47: 30S ribosomal protein S16

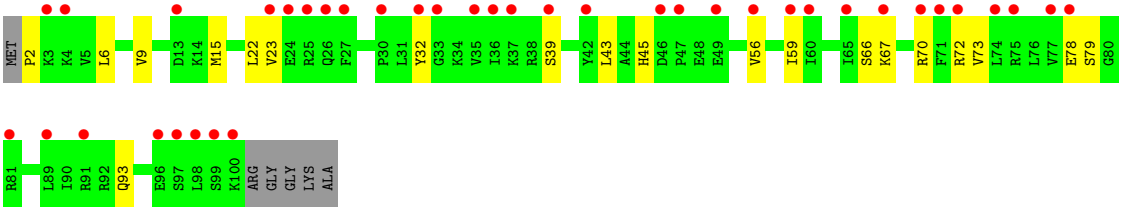


• Molecule 48: 30S ribosomal protein S17





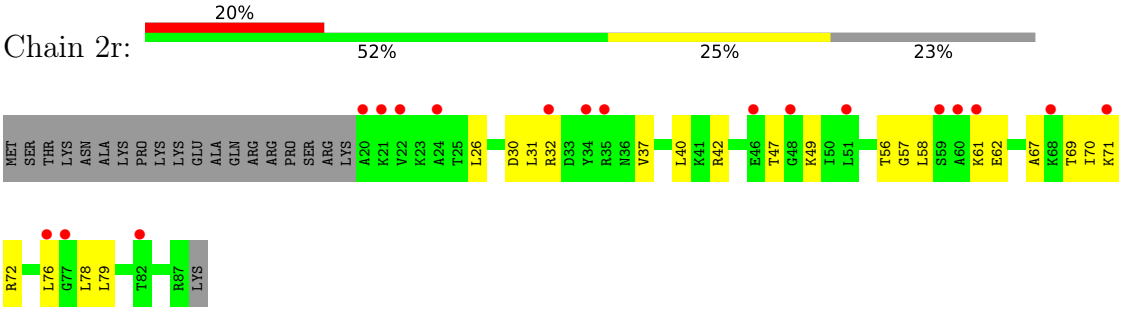
• Molecule 48: 30S ribosomal protein S17



• Molecule 49: 30S ribosomal protein S18

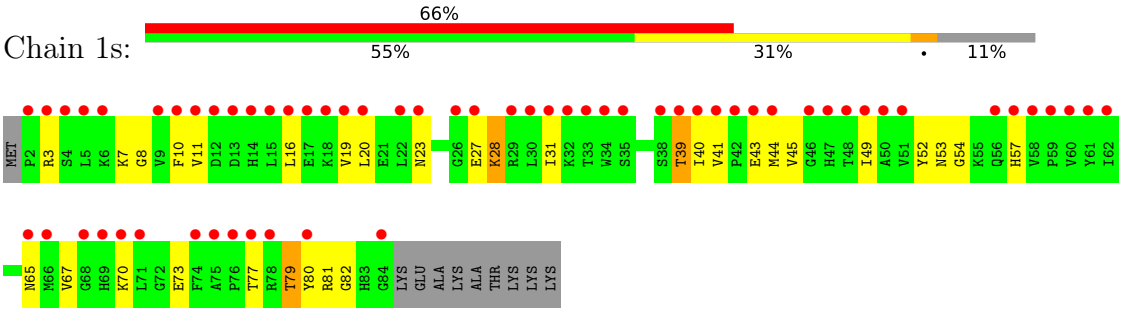
• Molecule 49: 30S ribosomal protein S18

Chain 2r:



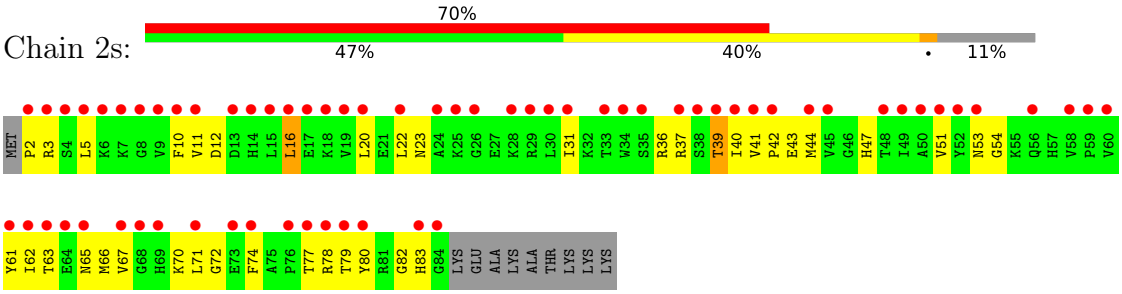
• Molecule 50: 30S ribosomal protein S19

Chain 1s:



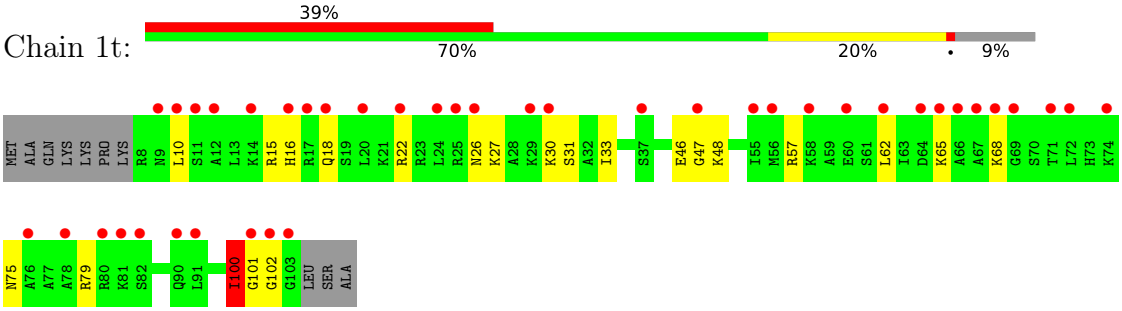
• Molecule 50: 30S ribosomal protein S19

Chain 2s:



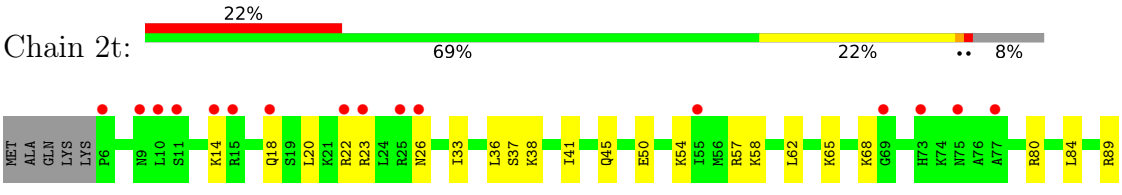
• Molecule 51: 30S ribosomal protein S20

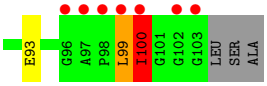
Chain 1t:



• Molecule 51: 30S ribosomal protein S20

Chain 2t:



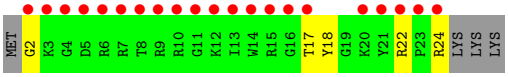


• Molecule 52: 30S ribosomal protein Thx

Chain 1u:

• Molecule 52: 30S ribosomal protein Thx

Chain 2u:



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 448.29Å 619.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	309.69 – 3.10 309.69 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (309.69-3.10) 99.8 (309.69-3.10)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 3.07Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.232 , 0.284 0.230 , 0.281	Depositor DCC
R_{free} test set	52205 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	81.2	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 999.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	289588	wwPDB-VP
Average B, all atoms (Å^2)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.62% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, MG, M2G, 4OC, 2MA, UR3, ZN, 0TD, PSU, 5MC, 2MU, OMG, HGR, MA6, 7MG, 5MU, 2MG

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	0.18	0/69029	0.32	2/107746 (0.0%)
1	2A	0.14	0/68901	0.31	0/107544
2	1B	0.15	0/2876	0.28	0/4486
2	2B	0.13	0/2878	0.26	0/4490
3	1D	0.35	0/2181	0.78	2/2940 (0.1%)
3	2D	0.31	0/2186	0.80	1/2944 (0.0%)
4	1E	0.40	0/1592	0.83	0/2149
4	2E	0.33	0/1592	0.86	4/2149 (0.2%)
5	1F	0.36	0/1619	0.80	0/2193
5	2F	0.31	0/1615	0.84	1/2188 (0.0%)
6	1G	0.31	0/1451	0.82	2/1961 (0.1%)
6	2G	0.32	0/1449	0.87	2/1957 (0.1%)
7	1H	0.35	0/1356	0.82	2/1834 (0.1%)
7	2H	0.29	0/1350	0.86	0/1826
8	1I	0.32	0/1109	0.79	0/1512
8	2I	0.30	0/1091	0.80	1/1490 (0.1%)
9	1N	0.36	0/1148	0.82	2/1547 (0.1%)
9	2N	0.28	0/1144	0.80	2/1543 (0.1%)
10	1O	0.36	0/943	0.75	0/1269
10	2O	0.31	0/943	0.75	0/1269
11	1P	0.35	0/1152	0.77	2/1533 (0.1%)
11	2P	0.29	0/1152	0.79	0/1533
12	1Q	0.35	0/1143	0.74	0/1527
12	2Q	0.30	0/1143	0.76	0/1527
13	1R	0.39	0/982	0.74	0/1312
13	2R	0.34	0/982	0.72	0/1312
14	1S	0.32	0/887	0.79	1/1180 (0.1%)
14	2S	0.32	0/880	0.81	0/1172
15	1T	0.33	0/1105	0.73	0/1477
15	2T	0.30	0/1097	0.76	0/1468
16	1U	0.41	0/977	0.73	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
16	2U	0.31	0/977	0.74	1/1301 (0.1%)
17	1V	0.38	0/786	0.74	0/1053
17	2V	0.29	0/782	0.73	0/1049
18	1W	0.42	0/897	0.78	0/1205
18	2W	0.34	0/897	0.77	0/1205
19	1X	0.35	0/764	0.69	0/1025
19	2X	0.29	0/764	0.72	0/1025
20	1Y	0.34	0/823	0.78	1/1099 (0.1%)
20	2Y	0.28	0/823	0.78	0/1100
21	1Z	0.32	0/1620	0.83	0/2200
21	2Z	0.32	0/1590	0.86	4/2162 (0.2%)
22	10	0.32	0/616	0.72	0/821
22	20	0.28	0/616	0.78	0/821
23	11	0.33	0/761	0.74	0/1013
23	21	0.30	0/766	0.75	0/1018
24	12	0.33	0/590	0.73	0/781
24	22	0.27	0/594	0.72	0/785
25	13	0.37	0/474	0.85	0/635
25	23	0.29	0/469	0.81	0/630
26	14	0.35	0/559	1.00	5/754 (0.7%)
26	24	0.36	0/549	0.94	3/741 (0.4%)
27	15	0.41	0/473	0.88	2/639 (0.3%)
27	25	0.37	0/469	0.77	0/635
28	16	0.34	0/460	0.67	0/613
28	26	0.30	0/456	0.67	0/608
29	17	0.37	0/426	0.81	0/561
29	27	0.33	0/426	0.82	0/561
30	18	0.35	0/525	0.76	0/691
30	28	0.30	0/525	0.71	0/691
31	19	0.37	0/310	0.74	0/407
31	29	0.28	0/310	0.80	0/407
32	1a	0.14	0/35795	0.31	0/55864
32	2a	0.13	1/35890 (0.0%)	0.30	0/56012
33	1b	0.32	0/1876	0.88	6/2533 (0.2%)
33	2b	0.35	0/1860	0.89	4/2518 (0.2%)
34	1c	0.31	0/1582	0.82	0/2137
34	2c	0.32	0/1566	0.81	2/2119 (0.1%)
35	1d	0.32	0/1695	0.81	0/2274
35	2d	0.29	0/1698	0.77	0/2277
36	1e	0.32	0/1149	0.81	0/1548
36	2e	0.32	0/1149	0.86	4/1548 (0.3%)
37	1f	0.29	0/827	0.76	2/1120 (0.2%)
37	2f	0.29	0/829	0.78	2/1123 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
38	1g	0.32	0/1254	0.81	0/1683
38	2g	0.30	0/1248	0.78	0/1676
39	1h	0.29	0/1118	0.84	4/1506 (0.3%)
39	2h	0.27	0/1108	0.80	2/1494 (0.1%)
40	1i	0.33	0/1005	0.85	2/1351 (0.1%)
40	2i	0.33	0/985	0.81	0/1329
41	1j	0.35	0/732	0.86	2/993 (0.2%)
41	2j	0.35	0/723	0.89	0/984
42	1k	0.32	0/849	0.81	0/1150
42	2k	0.32	0/848	0.82	1/1149 (0.1%)
43	1l	0.28	0/937	0.77	1/1260 (0.1%)
43	2l	0.28	0/937	0.78	0/1260
44	1m	0.34	0/924	0.83	1/1242 (0.1%)
44	2m	0.33	0/905	0.89	2/1217 (0.2%)
45	1n	0.34	0/501	0.75	0/664
45	2n	0.32	0/501	0.75	0/664
46	1o	0.29	0/739	0.77	0/985
46	2o	0.28	0/739	0.77	0/985
47	1p	0.31	0/697	0.79	0/939
47	2p	0.30	0/693	0.70	0/935
48	1q	0.29	0/836	0.75	2/1117 (0.2%)
48	2q	0.26	0/836	0.71	0/1117
49	1r	0.29	0/560	0.73	0/746
49	2r	0.27	0/560	0.70	0/746
50	1s	0.30	0/663	0.80	0/895
50	2s	0.35	0/660	0.81	0/893
51	1t	0.28	0/734	0.82	0/969
51	2t	0.30	0/736	0.75	0/976
52	1u	0.30	0/203	0.78	0/266
52	2u	0.29	0/203	0.82	0/266
All	All	0.22	1/308400 (0.0%)	0.49	77/461145 (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
3	2D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1498	UR3	O3'-P	5.05	1.61	1.56

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1042	G	OP1-P-O3'	-9.52	79.44	108.00
6	2G	67	LYS	CA-C-N	7.07	126.99	119.85
6	2G	67	LYS	C-N-CA	7.07	126.99	119.85
1	1A	1042	G	OP2-P-O3'	-6.91	87.28	108.00
33	1b	231	GLU	CA-C-N	6.82	128.36	119.84
33	1b	231	GLU	C-N-CA	6.82	128.36	119.84
33	2b	231	GLU	CA-C-N	6.59	128.08	119.84
33	2b	231	GLU	C-N-CA	6.59	128.08	119.84
16	2U	9	VAL	N-CA-C	6.48	116.52	110.42
39	1h	75	ARG	CA-C-N	6.35	126.32	119.78
39	1h	75	ARG	C-N-CA	6.35	126.32	119.78
27	15	26	THR	CA-C-N	6.12	124.13	119.66
27	15	26	THR	C-N-CA	6.12	124.13	119.66
20	1Y	92	ASN	N-CA-C	6.07	118.39	111.11
3	2D	275	LYS	N-CA-C	-6.00	100.47	109.96
33	1b	9	GLU	CB-CA-C	-5.97	108.69	115.79
9	2N	110	GLY	CA-C-N	5.93	125.14	118.97
9	2N	110	GLY	C-N-CA	5.93	125.14	118.97
37	2f	95	GLU	CA-C-N	5.92	125.93	119.89
37	2f	95	GLU	C-N-CA	5.92	125.93	119.89
26	24	19	GLY	N-CA-C	-5.89	107.12	115.43
34	2c	108	ASN	CA-C-N	5.87	125.55	119.56
34	2c	108	ASN	C-N-CA	5.87	125.55	119.56
44	1m	106	ASN	CB-CA-C	-5.77	109.91	116.54
9	1N	110	GLY	CA-C-N	5.76	124.97	118.97
9	1N	110	GLY	C-N-CA	5.76	124.97	118.97
8	2I	124	GLY	N-CA-C	5.74	117.73	110.38
44	2m	40	ASN	CA-C-N	5.74	125.59	119.28
44	2m	40	ASN	C-N-CA	5.74	125.59	119.28
33	1b	128	GLU	N-CA-C	-5.73	106.05	113.16
4	2E	52	LEU	CA-C-N	-5.68	114.12	119.85
4	2E	52	LEU	C-N-CA	-5.68	114.12	119.85
48	1q	29	HIS	CA-C-N	5.59	125.06	119.24
48	1q	29	HIS	C-N-CA	5.59	125.06	119.24
11	1P	22	GLY	CA-C-N	5.58	124.93	118.85
11	1P	22	GLY	C-N-CA	5.58	124.93	118.85
37	1f	95	GLU	CA-C-N	5.58	125.58	119.89
37	1f	95	GLU	C-N-CA	5.58	125.58	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
39	1h	56	LYS	CA-C-N	5.56	125.74	119.90
39	1h	56	LYS	C-N-CA	5.56	125.74	119.90
6	1G	65	GLY	N-CA-C	-5.52	107.62	115.30
41	1j	36	GLY	CA-C-N	5.51	126.73	119.84
41	1j	36	GLY	C-N-CA	5.51	126.73	119.84
33	2b	129	GLU	N-CA-C	-5.50	106.61	113.15
43	1l	105	TYR	CB-CA-C	-5.49	110.27	116.63
33	1b	166	ASP	CA-C-N	5.48	125.10	119.56
33	1b	166	ASP	C-N-CA	5.48	125.10	119.56
36	2e	127	ASN	CA-C-N	5.47	124.93	119.24
36	2e	127	ASN	C-N-CA	5.47	124.93	119.24
21	2Z	193	GLU	CA-C-N	5.45	126.30	119.98
21	2Z	193	GLU	C-N-CA	5.45	126.30	119.98
3	1D	244	ARG	CA-C-N	-5.38	114.83	120.38
3	1D	244	ARG	C-N-CA	-5.38	114.83	120.38
40	1i	89	ASN	CA-C-N	5.33	125.41	119.87
40	1i	89	ASN	C-N-CA	5.33	125.41	119.87
36	2e	69	VAL	CA-C-N	5.32	126.49	119.84
36	2e	69	VAL	C-N-CA	5.32	126.49	119.84
5	2F	58	ALA	N-CA-C	5.32	117.16	111.36
33	2b	23	ARG	N-CA-C	-5.16	106.57	112.92
7	1H	125	VAL	CA-C-N	5.15	124.60	119.24
7	1H	125	VAL	C-N-CA	5.15	124.60	119.24
4	2E	176	ILE	CA-C-N	5.14	125.44	119.47
4	2E	176	ILE	C-N-CA	5.14	125.44	119.47
26	14	65	ASP	N-CA-C	-5.14	106.25	112.88
26	24	59	PHE	CA-C-N	5.13	130.94	121.70
26	24	59	PHE	C-N-CA	5.13	130.94	121.70
26	14	40	HIS	CA-C-N	5.10	125.13	119.32
26	14	40	HIS	C-N-CA	5.10	125.13	119.32
21	2Z	176	PRO	CA-C-N	5.10	125.57	120.52
21	2Z	176	PRO	C-N-CA	5.10	125.57	120.52
6	1G	53	LEU	N-CA-C	-5.08	106.92	112.72
42	2k	116	HIS	N-CA-C	5.08	115.71	108.54
26	14	28	LYS	CA-C-N	5.05	124.65	119.05
26	14	28	LYS	C-N-CA	5.05	124.65	119.05
14	1S	60	GLY	N-CA-C	5.03	120.90	114.66
39	2h	73	ASP	CA-C-N	5.00	125.07	119.87
39	2h	73	ASP	C-N-CA	5.00	125.07	119.87

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2D	274	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	61869	0	31203	652	0
1	2A	61758	0	31151	777	0
2	1B	2572	0	1305	30	0
2	2B	2573	0	1306	39	0
3	1D	2131	0	2207	52	0
3	2D	2136	0	2218	36	0
4	1E	1559	0	1618	32	0
4	2E	1559	0	1618	31	0
5	1F	1584	0	1625	43	0
5	2F	1580	0	1619	44	0
6	1G	1426	0	1445	44	0
6	2G	1424	0	1441	75	0
7	1H	1330	0	1407	30	0
7	2H	1324	0	1402	23	0
8	1I	1094	0	1127	26	0
8	2I	1076	0	1094	18	0
9	1N	1121	0	1195	20	0
9	2N	1117	0	1184	16	0
10	1O	933	0	996	23	0
10	2O	933	0	996	19	0
11	1P	1135	0	1212	33	0
11	2P	1135	0	1212	36	0
12	1Q	1122	0	1179	19	0
12	2Q	1122	0	1179	31	0
13	1R	968	0	1033	13	0
13	2R	968	0	1033	28	0
14	1S	877	0	938	18	0
14	2S	870	0	923	19	0
15	1T	1091	0	1151	21	0
15	2T	1083	0	1136	14	0
16	1U	959	0	1019	14	0
16	2U	959	0	1019	19	0
17	1V	775	0	841	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	2V	771	0	830	15	0
18	1W	886	0	940	17	0
18	2W	886	0	940	22	0
19	1X	750	0	814	12	0
19	2X	750	0	814	11	0
20	1Y	810	0	892	14	0
20	2Y	810	0	887	20	0
21	1Z	1587	0	1598	31	0
21	2Z	1557	0	1564	36	0
22	10	608	0	622	14	0
22	20	608	0	622	16	0
23	11	754	0	823	10	0
23	21	759	0	837	18	0
24	12	588	0	643	7	0
24	22	592	0	654	12	0
25	13	469	0	518	7	0
25	23	464	0	514	8	0
26	14	546	0	522	22	0
26	24	536	0	514	26	0
27	15	459	0	476	15	0
27	25	455	0	465	9	0
28	16	453	0	473	5	0
28	26	449	0	469	7	0
29	17	418	0	467	6	0
29	27	418	0	467	13	0
30	18	517	0	582	20	0
30	28	517	0	582	16	0
31	19	307	0	335	6	0
31	29	307	0	335	8	0
32	1a	32246	0	16296	532	0
32	2a	32331	0	16339	493	0
33	1b	1842	0	1862	58	0
33	2b	1825	0	1828	59	0
34	1c	1558	0	1557	34	0
34	2c	1542	0	1517	33	0
35	1d	1665	0	1687	51	0
35	2d	1668	0	1703	49	0
36	1e	1133	0	1191	30	0
36	2e	1133	0	1191	28	0
37	1f	814	0	808	18	0
37	2f	816	0	808	19	0
38	1g	1235	0	1249	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	2g	1229	0	1238	36	0
39	1h	1098	0	1143	29	0
39	2h	1088	0	1126	27	0
40	1i	986	0	990	40	0
40	2i	966	0	953	36	0
41	1j	719	0	672	26	0
41	2j	710	0	661	27	0
42	1k	834	0	838	26	0
42	2k	833	0	836	23	0
43	1l	932	0	981	26	0
43	2l	932	0	981	15	0
44	1m	914	0	954	34	0
44	2m	895	0	920	32	0
45	1n	492	0	529	27	0
45	2n	492	0	529	27	0
46	1o	728	0	760	22	0
46	2o	728	0	760	14	0
47	1p	681	0	697	17	0
47	2p	677	0	686	22	0
48	1q	823	0	891	16	0
48	2q	823	0	891	12	0
49	1r	555	0	618	10	0
49	2r	555	0	618	14	0
50	1s	648	0	658	25	0
50	2s	645	0	635	33	0
51	1t	732	0	809	15	0
51	2t	733	0	795	17	0
52	1u	199	0	208	6	0
52	2u	199	0	208	4	0
53	10	6	0	0	0	0
53	11	2	0	0	0	0
53	13	3	0	0	0	0
53	15	5	0	0	0	0
53	17	2	0	0	0	0
53	18	2	0	0	0	0
53	19	4	0	0	0	0
53	1A	761	0	0	0	0
53	1B	23	0	0	0	0
53	1D	8	0	0	0	0
53	1E	6	0	0	0	0
53	1F	6	0	0	0	0
53	1G	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	1H	2	0	0	0	0
53	1N	2	0	0	0	0
53	1P	3	0	0	0	0
53	1Q	4	0	0	0	0
53	1R	6	0	0	0	0
53	1T	4	0	0	0	0
53	1U	3	0	0	0	0
53	1V	2	0	0	0	0
53	1W	3	0	0	0	0
53	1Z	1	0	0	0	0
53	1a	143	0	0	0	0
53	1b	1	0	0	0	0
53	1d	2	0	0	0	0
53	1e	1	0	0	0	0
53	1f	1	0	0	0	0
53	1g	2	0	0	0	0
53	1h	1	0	0	0	0
53	1k	1	0	0	0	0
53	1l	2	0	0	0	0
53	1n	1	0	0	0	0
53	1o	2	0	0	0	0
53	1r	1	0	0	0	0
53	1t	1	0	0	0	0
53	20	1	0	0	0	0
53	28	2	0	0	0	0
53	2A	518	0	0	0	0
53	2B	19	0	0	0	0
53	2D	3	0	0	0	0
53	2E	6	0	0	0	0
53	2F	2	0	0	0	0
53	2I	1	0	0	0	0
53	2N	1	0	0	0	0
53	2O	2	0	0	0	0
53	2P	1	0	0	0	0
53	2Q	3	0	0	0	0
53	2R	1	0	0	0	0
53	2T	3	0	0	0	0
53	2V	1	0	0	0	0
53	2W	1	0	0	0	0
53	2Y	1	0	0	0	0
53	2a	129	0	0	0	0
53	2e	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	2k	1	0	0	0	0
53	2l	1	0	0	0	0
53	2t	1	0	0	0	0
54	1A	36	0	29	1	0
54	2A	36	0	29	2	0
55	14	1	0	0	0	0
55	15	1	0	0	0	0
55	16	1	0	0	0	0
55	19	1	0	0	0	0
55	1Y	1	0	0	0	0
55	1n	1	0	0	0	0
55	24	1	0	0	0	0
55	25	1	0	0	0	0
55	26	1	0	0	0	0
55	29	1	0	0	0	0
55	2Y	1	0	0	0	0
55	2n	1	0	0	0	0
56	1d	8	0	0	0	0
56	2d	8	0	0	0	0
57	10	10	0	0	1	0
57	11	7	0	0	0	0
57	12	2	0	0	0	0
57	13	8	0	0	0	0
57	14	1	0	0	0	0
57	15	8	0	0	0	0
57	16	1	0	0	0	0
57	17	2	0	0	0	0
57	18	3	0	0	0	0
57	19	4	0	0	0	0
57	1A	1448	0	0	74	0
57	1B	37	0	0	2	0
57	1D	23	0	0	0	0
57	1E	20	0	0	0	0
57	1F	20	0	0	1	0
57	1G	6	0	0	0	0
57	1H	4	0	0	0	0
57	1I	2	0	0	0	0
57	1N	24	0	0	0	0
57	1O	4	0	0	1	0
57	1P	9	0	0	1	0
57	1Q	8	0	0	0	0
57	1R	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	1T	15	0	0	0	0
57	1U	16	0	0	2	0
57	1V	9	0	0	0	0
57	1W	9	0	0	0	0
57	1X	7	0	0	0	0
57	1Y	5	0	0	0	0
57	1Z	2	0	0	0	0
57	1a	226	0	0	8	0
57	1d	5	0	0	0	0
57	1e	2	0	0	0	0
57	1f	2	0	0	0	0
57	1g	1	0	0	1	0
57	1h	1	0	0	0	0
57	1k	1	0	0	1	0
57	1l	6	0	0	1	0
57	1m	1	0	0	1	0
57	1o	7	0	0	1	0
57	1p	3	0	0	0	0
57	1t	2	0	0	0	0
57	1u	1	0	0	0	0
57	20	2	0	0	0	0
57	21	2	0	0	0	0
57	22	1	0	0	0	0
57	23	1	0	0	0	0
57	24	1	0	0	0	0
57	25	1	0	0	0	0
57	26	1	0	0	0	0
57	27	2	0	0	0	0
57	28	3	0	0	0	0
57	2A	648	0	0	30	0
57	2B	24	0	0	0	0
57	2D	14	0	0	0	0
57	2E	4	0	0	0	0
57	2F	3	0	0	0	0
57	2H	1	0	0	0	0
57	2I	1	0	0	0	0
57	2N	3	0	0	0	0
57	2O	3	0	0	0	0
57	2P	4	0	0	0	0
57	2Q	4	0	0	0	0
57	2R	4	0	0	1	0
57	2S	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	2T	5	0	0	0	0
57	2U	3	0	0	0	0
57	2W	3	0	0	0	0
57	2X	2	0	0	0	0
57	2Y	2	0	0	0	0
57	2Z	3	0	0	0	0
57	2a	179	0	0	8	0
57	2d	1	0	0	0	0
57	2e	2	0	0	0	0
57	2f	3	0	0	0	0
57	2l	3	0	0	0	0
57	2m	1	0	0	0	0
57	2o	1	0	0	0	0
57	2p	1	0	0	0	0
57	2q	1	0	0	0	0
57	2r	3	0	0	0	0
57	2t	3	0	0	0	0
All	All	289588	0	192910	4147	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (4147) 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	1.34	1.23
32:1a:1237:C:H42	32:1a:1337:G:H1	1.05	1.01
32:1a:1003:G:H2'	32:1a:1004:A:H4'	1.41	0.99
32:1a:78:G:H1	32:1a:91:C:N4	1.60	0.99
1:1A:2105:C:H42	1:1A:2184:G:H1	1.06	0.99
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.41	0.99
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.46	0.98
1:1A:1064:C:H42	1:1A:1074:G:H1	1.10	0.97
1:1A:1091:G:H1	1:1A:1100:C:H42	1.05	0.97
1:2A:1063:G:H1	1:2A:1075:C:N4	1.63	0.96
32:1a:73:G:H1	32:1a:96:U:H3	1.01	0.96
32:1a:1314:C:H42	32:1a:1323:G:H1	1.14	0.96
32:2a:1162:C:N4	32:2a:1174:G:H1	1.64	0.95
32:2a:1254:C:H42	32:2a:1283:G:H1	0.98	0.93
1:2A:1087:G:H1	1:2A:1102:C:N4	1.67	0.93
32:2a:1002:G:H1	32:2a:1038:C:H42	1.15	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1087:G:H1	1:2A:1102:C:H42	0.94	0.92
1:1A:1082:U:O4	1:1A:1086:A:N1	2.03	0.92
32:1a:78:G:H1	32:1a:91:C:H42	1.09	0.91
32:2a:1129:C:N4	32:2a:1143:G:H1	1.68	0.90
32:2a:1254:C:N4	32:2a:1283:G:H1	1.68	0.90
1:1A:1091:G:H1	1:1A:1100:C:N4	1.71	0.88
1:1A:2105:C:N4	1:1A:2184:G:H1	1.71	0.88
1:2A:2136:C:C2	1:2A:2155:G:N2	2.42	0.87
32:1a:78:G:N2	32:1a:91:C:N3	2.23	0.87
1:2A:1064:C:N4	1:2A:1074:G:H1	1.72	0.86
32:2a:1162:C:H42	32:2a:1174:G:H1	0.91	0.86
32:2a:1165:C:H42	32:2a:1171:G:H1	1.22	0.86
32:2a:1318:A:H5"	50:2s:3:ARG:HH22	1.41	0.86
32:1a:138:G:H1	32:1a:225:C:H42	1.22	0.85
32:2a:1129:C:H42	32:2a:1143:G:H1	1.21	0.85
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.39	0.85
34:1c:58:GLU:HB3	41:1j:92:THR:HG21	1.59	0.85
1:2A:1087:G:N2	1:2A:1102:C:N3	2.25	0.84
32:1a:77:G:H1	32:1a:92:C:H42	1.23	0.84
10:1O:48:PRO:HB3	32:1a:1422:G:H5"	1.60	0.83
10:2O:48:PRO:HB3	32:2a:1422:G:H5"	1.59	0.83
35:1d:6:GLY:H	35:1d:115:ARG:HH12	1.25	0.83
32:2a:1165:C:N4	32:2a:1171:G:H1	1.77	0.83
1:2A:1063:G:N2	1:2A:1075:C:N3	2.26	0.82
32:2a:532:A:H61	34:2c:193:TYR:HB3	1.44	0.82
32:1a:1237:C:N4	32:1a:1337:G:H1	1.76	0.82
32:2a:1441:G:H5"	32:2a:1442:G:H5'	1.63	0.81
1:1A:279:C:H42	1:1A:361:G:H1	1.28	0.81
32:1a:532:A:N6	32:1a:1206:G:O2'	2.13	0.81
4:2E:11:MET:HG2	4:2E:24:THR:HG22	1.61	0.81
1:1A:1064:C:N4	1:1A:1074:G:H1	1.79	0.81
1:1A:2849:U:OP2	15:1T:95:ARG:NH1	2.13	0.80
32:2a:501:C:OP1	43:2l:117:ARG:NH2	2.15	0.80
32:1a:1025:U:O2	32:1a:1036:G:O6	1.99	0.80
1:1A:2307:G:N1	6:1G:43:LEU:O	2.13	0.80
34:2c:11:ARG:HB3	34:2c:15:THR:HB	1.62	0.80
32:1a:1135:U:H5"	32:1a:1136:U:H5	1.47	0.80
50:1s:19:VAL:HG21	50:1s:44:MET:HG2	1.62	0.80
32:1a:1006:C:N3	32:1a:1023:G:O6	2.14	0.79
29:17:24:THR:HG22	29:17:27:GLY:H	1.47	0.79
32:1a:1314:C:N4	32:1a:1323:G:H1	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1063:G:N1	1:2A:1075:C:N4	2.30	0.79
26:14:55:ARG:O	26:14:57:GLU:N	2.16	0.79
34:1c:189:ALA:HB3	34:1c:196:LEU:HB2	1.65	0.79
2:2B:43:C:H5"	26:24:1:MET:HG2	1.64	0.79
1:2A:1064:C:N3	1:2A:1074:G:N2	2.31	0.78
32:1a:1216:G:H5"	45:1n:5:ALA:HB2	1.64	0.78
32:1a:559:A:H4'	32:1a:560:U:H3'	1.66	0.78
32:1a:999:C:H42	32:1a:1042:G:H1	1.28	0.78
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.49	0.78
1:1A:1250:G:OP1	57:1A:3801:HOH:O	2.01	0.78
35:1d:18:LYS:NZ	35:1d:31:CYS:SG	2.56	0.78
2:2B:27:C:H5"	14:2S:54:LEU:HD11	1.65	0.78
1:2A:1064:C:N4	1:2A:1074:G:N1	2.31	0.77
32:1a:1441:G:H5"	32:1a:1442:G:H5'	1.63	0.77
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.66	0.77
1:1A:517:C:OP1	27:15:16:ARG:NH2	2.17	0.77
15:1T:54:ARG:HA	15:1T:59:THR:HG22	1.66	0.77
1:1A:2706:G:N7	57:1A:3839:HOH:O	2.17	0.77
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.17	0.77
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.49	0.76
1:1A:2102:U:O2	1:1A:2187:G:O6	2.04	0.76
32:2a:1162:C:N3	32:2a:1174:G:N2	2.33	0.76
3:1D:69:ARG:NH2	3:1D:128:GLY:O	2.18	0.76
14:1S:3:ARG:NH1	14:1S:4:LEU:O	2.19	0.76
1:2A:2343:C:HO2'	1:2A:2373:G:HO2'	1.29	0.76
35:2d:60:GLU:HG3	35:2d:202:LEU:HD12	1.68	0.76
32:1a:1030:C:N3	32:1a:1031:G:N2	2.32	0.76
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.68	0.75
32:1a:664:G:H22	32:1a:741:G:H1	1.34	0.75
33:1b:187:LEU:HA	33:1b:201:ILE:HB	1.68	0.75
39:1h:12:ARG:HD2	39:1h:26:VAL:HG12	1.69	0.75
32:2a:1115:C:H42	32:2a:1185:G:H1	1.33	0.75
1:2A:1094:U:OP1	1:2A:1096:A:N6	2.19	0.75
32:2a:1360:A:OP2	45:2n:35:ARG:NH2	2.19	0.75
22:10:10:THR:HG22	22:10:12:ASN:H	1.52	0.75
1:2A:2318:G:H21	14:2S:3:ARG:HE	1.32	0.75
1:1A:2103:C:H42	1:1A:2186:G:H1	1.33	0.74
1:1A:2685:G:N2	1:1A:2724:C:O2	2.19	0.74
10:1O:97:ARG:NH1	32:1a:339:C:OP2	2.19	0.74
1:2A:2138:C:N3	1:2A:2153:G:O6	2.20	0.74
32:1a:1278:U:H5'	32:1a:1279:A:H5'	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1264:G:OP1	27:15:19:ARG:NH2	2.20	0.74
1:1A:2099:U:H3	1:1A:2190:G:H1	1.32	0.74
1:1A:249:C:O2	30:18:12:LYS:NZ	2.21	0.74
1:1A:446:G:OP2	57:1A:3802:HOH:O	2.05	0.74
32:1a:1001(A):G:O6	32:1a:1039:C:N3	2.21	0.74
1:2A:988:A:N7	57:2A:3614:HOH:O	2.20	0.74
32:2a:1047:G:H1	32:2a:1210:C:H42	1.33	0.73
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.21	0.73
1:2A:958:U:OP2	12:2Q:14:ARG:NH1	2.21	0.73
34:2c:50:ALA:HB1	34:2c:72:LYS:HB2	1.71	0.73
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.70	0.73
1:1A:567:A:OP2	11:1P:29:LYS:NZ	2.18	0.73
1:1A:2429:G:OP2	57:1A:3803:HOH:O	2.07	0.73
26:24:59:PHE:HA	26:24:60:GLN:C	2.12	0.73
1:1A:574:C:N3	4:1E:145:LYS:NZ	2.37	0.73
1:1A:2111:C:OP2	1:1A:2145:C:N4	2.22	0.73
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.70	0.73
32:2a:1002:G:H1	32:2a:1038:C:N4	1.87	0.73
44:2m:31:LYS:HA	44:2m:34:LEU:HD12	1.70	0.73
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.21	0.73
26:14:58:ARG:HG3	50:1s:65:ASN:HA	1.70	0.73
1:2A:2287:A:H61	1:2A:2344:U:H3	1.35	0.73
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.21	0.73
1:1A:2683:C:O2	10:1O:70:LYS:NZ	2.18	0.72
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.70	0.72
37:1f:1:MET:HE3	37:1f:66:GLU:HG2	1.69	0.72
1:2A:320:A:N3	5:2F:169:ASN:ND2	2.38	0.72
32:1a:1350:A:H61	32:1a:1372:U:H3	1.36	0.72
41:1j:7:LYS:HB3	41:1j:97:GLU:HB2	1.71	0.72
1:2A:1031:G:H5"	31:29:8:LYS:HE3	1.70	0.72
32:1a:136:C:H42	32:1a:227:G:H1	1.36	0.72
1:2A:489:G:N7	18:2W:49:LYS:NZ	2.37	0.72
16:2U:50:ARG:HG2	16:2U:53:ARG:HH22	1.55	0.72
3:2D:61:LEU:O	3:2D:63:ARG:NH1	2.23	0.72
1:1A:1453:U:O2'	1:1A:1455:G:N7	2.23	0.72
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.72	0.72
42:2k:99:GLN:HG2	42:2k:105:VAL:HG21	1.71	0.72
1:1A:1297:C:OP1	57:1A:3806:HOH:O	2.08	0.72
4:1E:28:ALA:HB3	4:1E:93:VAL:HG12	1.72	0.72
32:2a:981:U:OP1	45:2n:9:LYS:NZ	2.23	0.72
23:11:3:LYS:HG3	23:11:4:VAL:H	1.55	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.71	0.72
1:1A:563:G:OP2	57:1A:3804:HOH:O	2.08	0.71
1:1A:527:C:OP1	57:1A:3808:HOH:O	2.08	0.71
1:2A:1059:G:N1	1:2A:1079:C:N4	2.39	0.71
32:2a:1133:G:H2'	32:2a:1134:G:H8	1.54	0.71
21:1Z:198:LYS:HD2	21:1Z:202:GLU:HG2	1.71	0.71
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.55	0.71
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.23	0.71
3:2D:275:LYS:HB3	3:2D:276:LYS:HA	1.72	0.71
32:1a:1179:A:OP2	40:1i:93:ARG:NH2	2.23	0.71
1:2A:1062:G:HO2'	1:2A:1063:G:H8	1.37	0.71
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.73	0.71
21:1Z:74:VAL:HG22	21:1Z:86:VAL:HG13	1.73	0.71
39:1h:120:THR:H	39:1h:123:GLU:HB2	1.56	0.71
1:1A:2096:U:H3	1:1A:2193:G:H1	1.38	0.71
1:2A:2640:G:O3'	9:2N:74:ARG:NH2	2.21	0.71
1:2A:2154:G:H2'	1:2A:2155:G:H8	1.55	0.71
2:1B:43:C:H5"	26:14:1:MET:HG2	1.73	0.71
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.24	0.71
32:1a:1090:U:H3	32:1a:1095:U:H3	1.36	0.71
33:2b:15:VAL:HG23	33:2b:16:HIS:HD2	1.54	0.71
44:2m:102:ARG:NH1	44:2m:105:THR:OG1	2.24	0.71
14:1S:11:LYS:HG3	14:1S:91:PRO:HD3	1.73	0.71
32:1a:949:A:H61	32:1a:1232:U:H3	1.39	0.71
33:1b:157:ARG:NH1	33:1b:158:LEU:O	2.23	0.71
35:1d:107:ARG:HH12	35:1d:194:LEU:HD11	1.56	0.71
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.23	0.71
14:2S:49:VAL:HG21	14:2S:77:ALA:HA	1.71	0.71
1:1A:1124:C:OP1	57:1A:3809:HOH:O	2.09	0.71
9:1N:123:TYR:HH	9:1N:130:HIS:HE2	1.32	0.71
32:1a:501:C:OP1	43:1l:117:ARG:NH2	2.23	0.71
33:1b:134:GLU:HG3	33:1b:137:ARG:HH21	1.56	0.71
1:2A:1378:A:O2'	1:2A:1380:G:N7	2.21	0.71
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.73	0.71
36:2e:40:ARG:HE	36:2e:68:GLU:HG2	1.56	0.71
1:1A:563:G:OP2	57:1A:3807:HOH:O	2.08	0.70
32:1a:77:G:H1	32:1a:92:C:N4	1.88	0.70
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.73	0.70
34:1c:8:ILE:HD12	34:1c:16:ARG:HD2	1.73	0.70
37:2f:11:ASN:HB3	37:2f:14:LEU:HG	1.72	0.70
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:331:A:N1	57:1A:3867:HOH:O	2.23	0.70
1:1A:2445:G:OP1	5:1F:74:ARG:NH2	2.24	0.70
1:2A:789:A:N1	57:2A:3632:HOH:O	2.25	0.70
40:2i:9:ARG:HG3	40:2i:104:ARG:HE	1.56	0.70
1:1A:1859:A:N6	1:1A:1883:G:O2'	2.24	0.70
22:10:14:ARG:NH2	57:10:201:HOH:O	2.21	0.70
25:23:10:LYS:NZ	25:23:15:TYR:OH	2.25	0.70
1:1A:862:G:OP2	57:1A:3805:HOH:O	2.08	0.70
44:2m:65:LYS:NZ	44:2m:73:GLU:OE1	2.25	0.70
48:2q:66:SER:O	48:2q:70:ARG:NH1	2.25	0.70
46:1o:16:ALA:HB1	46:1o:21:ASP:HB3	1.72	0.70
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.22	0.70
38:2g:75:VAL:HB	38:2g:86:GLN:HG3	1.73	0.70
32:2a:834:C:O2	32:2a:852:G:N2	2.19	0.70
39:2h:12:ARG:HD2	39:2h:26:VAL:HG12	1.74	0.70
1:1A:1772:G:OP1	57:1A:3812:HOH:O	2.10	0.69
9:1N:70:LYS:HD3	9:1N:87:LEU:HD12	1.74	0.69
32:1a:559:A:OP1	36:1e:126:ARG:NH2	2.25	0.69
19:2X:57:LEU:HD11	19:2X:78:LYS:HE2	1.74	0.69
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.25	0.69
32:2a:1006:C:N3	32:2a:1023:G:O6	2.25	0.69
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.73	0.69
32:1a:1028:C:H42	32:1a:1033:G:H1	1.40	0.69
6:2G:60:LEU:HD21	6:2G:68:PRO:HG3	1.74	0.69
1:1A:1774:C:OP1	57:1A:3810:HOH:O	2.09	0.69
6:2G:115:ARG:NH1	44:2m:6:GLY:O	2.24	0.69
22:20:10:THR:HG22	22:20:12:ASN:H	1.57	0.69
32:2a:1218:C:OP1	45:2n:12:ARG:NH2	2.25	0.69
1:1A:1082:U:N3	1:1A:1086:A:N6	2.09	0.69
19:1X:57:LEU:HD11	19:1X:78:LYS:HE2	1.74	0.69
1:2A:1065:U:H3	1:2A:1073:A:H61	1.40	0.69
12:2Q:39:PRO:HD3	12:2Q:99:PRO:HG3	1.74	0.69
32:2a:975:A:H4'	32:2a:976:G:H5"	1.75	0.69
32:2a:1222:G:OP2	32:2a:1322:C:N4	2.26	0.69
12:2Q:8:LYS:HA	21:2Z:197:ILE:HB	1.75	0.69
4:1E:47:VAL:HG21	4:1E:86:PRO:HD2	1.75	0.69
2:2B:66:A:H61	2:2B:109:C:H5'	1.58	0.69
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.09	0.69
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.75	0.69
40:2i:51:ARG:HG2	40:2i:56:LEU:HD21	1.75	0.69
41:2j:35:SER:HB3	41:2j:73:ASP:H	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1054:A:H61	1:1A:1105:U:H3	1.41	0.68
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.23	0.68
3:2D:25:THR:OG1	3:2D:26:LYS:N	2.25	0.68
1:1A:530:G:N1	1:1A:2023:G:OP1	2.22	0.68
40:1i:9:ARG:HG3	40:1i:104:ARG:HE	1.57	0.68
21:2Z:10:ARG:NH1	21:2Z:37:VAL:O	2.26	0.68
1:1A:1795:C:O2	3:1D:255:LYS:NZ	2.27	0.68
32:1a:749:C:H2'	32:1a:750:G:H8	1.59	0.68
1:2A:1059:G:N2	1:2A:1079:C:N3	2.41	0.68
32:2a:1165:C:N3	32:2a:1171:G:N2	2.41	0.68
1:1A:252:G:OP1	11:1P:50:ARG:NH1	2.27	0.68
25:13:8:LEU:HD13	25:13:31:LEU:HD23	1.75	0.68
32:1a:1123:A:H4'	41:1j:36:GLY:HA3	1.76	0.68
1:2A:832:G:OP1	57:2A:3602:HOH:O	2.12	0.68
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.75	0.68
26:24:18:CYS:SG	26:24:39:CYS:HB3	2.34	0.68
32:2a:811:C:O2'	32:2a:901:A:N1	2.27	0.68
35:2d:175:SER:HB3	35:2d:184:LYS:HB3	1.75	0.68
32:2a:1503:A:OP1	32:2a:1531:A:O2'	2.12	0.68
32:1a:411:A:OP1	35:1d:30:LYS:NZ	2.27	0.67
37:1f:20:ALA:HA	37:1f:23:LYS:HD3	1.76	0.67
50:1s:3:ARG:NH1	50:1s:8:GLY:O	2.27	0.67
1:1A:947:G:OP1	57:1A:3820:HOH:O	2.13	0.67
1:1A:963:U:OP1	57:1A:3816:HOH:O	2.12	0.67
1:1A:1186:G:OP1	57:1A:3813:HOH:O	2.11	0.67
1:2A:1812:A:H1'	3:2D:45:ASN:HD22	1.59	0.67
32:2a:677:U:H3	32:2a:713:G:H22	1.41	0.67
1:1A:2144:U:O2	1:1A:2148:G:N1	2.27	0.67
7:1H:56:SER:OG	7:1H:61:HIS:ND1	2.26	0.67
32:1a:1047:G:H5"	45:1n:4:LYS:HD3	1.74	0.67
38:1g:75:VAL:HB	38:1g:86:GLN:HG3	1.75	0.67
1:2A:987:G:O2'	1:2A:1000:A:N3	2.27	0.67
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.76	0.67
32:2a:34:C:H42	32:2a:550:G:H1	1.42	0.67
1:1A:2343:C:O2'	1:1A:2373:G:O2'	2.09	0.67
1:2A:637:A:OP1	11:2P:133:SER:OG	2.10	0.67
3:1D:147:LEU:HD13	3:1D:155:LEU:HD21	1.75	0.67
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.28	0.67
1:1A:1992:G:OP1	57:1A:3815:HOH:O	2.12	0.67
2:1B:76:G:N7	57:1B:3102:HOH:O	2.28	0.67
1:1A:574:C:OP1	57:1A:3818:HOH:O	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:1O:11:ALA:O	10:1O:99:PHE:N	2.25	0.67
36:1e:33:VAL:HG21	36:1e:109:ILE:HA	1.76	0.67
1:2A:1059:G:C6	1:2A:1079:C:N4	2.63	0.67
1:2A:1223:G:N2	1:2A:1226:A:OP2	2.28	0.67
32:2a:1005:A:O2'	32:2a:1036:G:N2	2.28	0.67
1:1A:197:A:N6	1:1A:2430:A:O2'	2.27	0.67
1:2A:1087:G:N1	1:2A:1102:C:N4	2.32	0.67
1:2A:2138:C:O2	1:2A:2153:G:N1	2.27	0.67
6:1G:47:LYS:HG3	6:1G:48:GLU:H	1.59	0.67
31:19:15:LYS:HE2	31:19:17:ILE:HD11	1.76	0.67
32:1a:64:G:H4'	32:1a:65:U:H3'	1.76	0.67
32:1a:1030:C:N4	32:1a:1031:G:N1	2.39	0.67
1:1A:1310:G:O6	57:1A:3819:HOH:O	2.12	0.67
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.76	0.67
32:2a:750:G:N2	46:2o:23:GLY:O	2.20	0.67
1:1A:2879:C:OP2	57:1A:3823:HOH:O	2.13	0.66
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.77	0.66
35:2d:108:LEU:HD21	35:2d:183:GLY:HA3	1.76	0.66
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.27	0.66
32:1a:1059:C:H42	32:1a:1198:G:H1	1.42	0.66
1:2A:751:A:OP1	57:2A:3603:HOH:O	2.13	0.66
1:2A:2129:C:N3	1:2A:2159:G:O6	2.29	0.66
18:2W:65:LEU:HD12	18:2W:68:ARG:HE	1.60	0.66
50:2s:40:ILE:HG13	50:2s:71:LEU:HD12	1.78	0.66
1:1A:1773:A:OP2	57:1A:3817:HOH:O	2.12	0.66
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.12	0.66
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.78	0.66
1:1A:2611:U:C4	27:15:3:LYS:HG2	2.30	0.66
5:1F:197:ASP:N	5:1F:197:ASP:OD1	2.27	0.66
1:1A:120:U:OP2	57:1A:3822:HOH:O	2.13	0.66
1:1A:1091:G:N2	1:1A:1100:C:N3	2.42	0.66
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.77	0.66
32:1a:1076:C:H42	32:1a:1081:G:H1	1.42	0.66
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.78	0.66
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.78	0.66
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.29	0.66
32:1a:1402:4OC:HM22	32:1a:1403:C:H5'	1.77	0.66
15:1T:16:ARG:NH2	15:1T:83:ILE:O	2.25	0.66
35:1d:166:LYS:NZ	35:1d:179:GLU:OE2	2.28	0.66
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.31	0.66
1:1A:2689:U:H4'	1:1A:2690:C:H5'	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:137:GLU:HB2	6:1G:140:ILE:HG13	1.78	0.66
1:2A:1604:C:OP1	57:2A:3606:HOH:O	2.14	0.66
6:2G:27:ASN:HB3	6:2G:30:GLU:HG3	1.76	0.66
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.28	0.66
34:2c:21:ARG:NH2	34:2c:58:GLU:OE2	2.28	0.66
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.78	0.66
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	1.77	0.65
32:2a:1318:A:O2'	50:2s:37:ARG:HB2	1.96	0.65
1:1A:2051:A:OP2	57:1A:3821:HOH:O	2.13	0.65
32:1a:582:U:OP1	46:1o:68:ARG:NH2	2.29	0.65
38:1g:153:HIS:CE1	42:1k:58:PRO:HD2	2.32	0.65
1:2A:831:G:OP1	57:2A:3605:HOH:O	2.13	0.65
1:2A:1671:U:OP2	57:2A:3604:HOH:O	2.13	0.65
24:22:1:MET:SD	24:22:56:GLN:NE2	2.68	0.65
32:1a:142:G:O2'	32:1a:196:A:N1	2.26	0.65
32:1a:957:U:H4'	50:1s:79:THR:HB	1.78	0.65
44:1m:12:ASN:O	44:1m:44:ARG:NH1	2.30	0.65
1:2A:1842:G:O2'	3:2D:253:GLN:NE2	2.19	0.65
32:2a:1134:G:H2'	32:2a:1135:U:H5'	1.76	0.65
1:1A:1667:G:O6	57:1A:3814:HOH:O	2.11	0.65
32:1a:936:C:H42	32:1a:1379:G:H1	1.43	0.65
32:1a:998:G:O6	32:1a:1043:C:N3	2.29	0.65
44:1m:3:ARG:HD2	44:1m:4:ILE:HG12	1.78	0.65
44:1m:52:GLU:HG2	44:1m:55:ARG:HH21	1.61	0.65
48:1q:59:ILE:HG22	48:1q:73:VAL:HA	1.78	0.65
1:1A:1085:A:O2'	1:1A:1104:C:O2'	2.14	0.65
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.61	0.65
1:2A:2157:G:H5"	1:2A:2158:A:H5'	1.76	0.65
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.78	0.65
26:24:46:GLN:OE1	26:24:46:GLN:N	2.29	0.65
32:2a:376:G:N7	57:2a:1810:HOH:O	2.29	0.65
1:2A:2133:G:O2'	1:2A:2158:A:N6	2.27	0.65
1:2A:2682:U:OP2	57:2A:3607:HOH:O	2.14	0.65
32:2a:673:G:H2'	32:2a:674:G:C8	2.31	0.65
32:2a:1030(A):G:H21	32:2a:1030(C):G:H3'	1.62	0.65
1:1A:1443:G:N7	57:1A:3907:HOH:O	2.29	0.65
1:2A:566:U:H5"	11:2P:29:LYS:HE3	1.78	0.65
1:2A:2166:G:H22	1:2A:2172:U:H5	1.44	0.65
2:2B:42:C:O2	6:2G:93:THR:N	2.28	0.65
32:2a:134:A:N1	47:2p:25:ARG:NH2	2.40	0.65
1:1A:2055:C:O2	57:1A:3811:HOH:O	2.10	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.30	0.65
32:1a:1072:G:H21	33:1b:107:THR:HG21	1.62	0.65
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.79	0.65
37:1f:11:ASN:HB3	37:1f:14:LEU:HG	1.78	0.65
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.30	0.65
29:27:34:ARG:NH1	29:27:39:ARG:HG2	2.12	0.65
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.31	0.65
1:1A:1920:4OC:HM22	1:1A:1921:G:H5'	1.78	0.64
39:1h:25:ASP:N	39:1h:25:ASP:OD1	2.30	0.64
1:2A:1316:U:H2'	1:2A:1317:A:C8	2.32	0.64
1:1A:2270:G:OP2	57:1A:3827:HOH:O	2.15	0.64
1:1A:2638:G:P	4:1E:82:ARG:HH12	2.19	0.64
1:2A:1466:G:HO2'	1:2A:1546:C:HO2'	1.40	0.64
32:2a:977:A:N6	32:2a:1224:G:OP1	2.30	0.64
35:2d:187:ARG:NH2	35:2d:193:ASP:OD2	2.30	0.64
43:2l:71:PRO:O	43:2l:102:ARG:NH1	2.30	0.64
49:2r:32:ARG:HA	49:2r:69:THR:HG21	1.78	0.64
1:1A:1064:C:H3'	1:1A:1065:U:H5"	1.79	0.64
1:1A:2066:C:OP1	57:1A:3826:HOH:O	2.14	0.64
1:1A:2124:G:H1	1:1A:2174:C:H42	1.44	0.64
17:1V:40:LEU:HB2	17:1V:46:VAL:HG22	1.80	0.64
32:1a:1003:G:C2	32:1a:1004:A:H1'	2.33	0.64
36:1e:74:GLY:HA3	36:1e:116:THR:HG22	1.78	0.64
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.62	0.64
1:1A:1798:U:OP2	3:1D:274:ARG:NH2	2.29	0.64
10:1O:98:VAL:HG11	10:1O:114:ILE:HG23	1.79	0.64
45:1n:6:LEU:O	45:1n:10:ALA:N	2.31	0.64
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.30	0.64
6:2G:29:TRP:O	6:2G:33:ARG:NH1	2.27	0.64
27:25:41:PRO:O	27:25:44:THR:OG1	2.14	0.64
48:2q:45:HIS:HB3	48:2q:72:ARG:HG3	1.78	0.64
1:1A:1016:G:N7	57:1A:3908:HOH:O	2.29	0.64
1:2A:1075:C:H2'	1:2A:1076:C:H5'	1.78	0.64
4:2E:28:ALA:HB3	4:2E:93:VAL:HG12	1.80	0.64
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.79	0.64
1:1A:2105:C:N3	1:1A:2184:G:N2	2.40	0.64
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.97	0.64
1:2A:134:C:H42	1:2A:145:G:H1	1.45	0.64
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.31	0.64
8:1I:40:THR:OG1	8:1I:43:ASN:OD1	2.16	0.64
32:1a:825:G:O2'	39:1h:12:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:195:ASP:O	39:1h:68:ARG:NH2	2.31	0.64
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.79	0.64
1:2A:805:G:N2	1:2A:829:A:OP1	2.30	0.64
6:1G:41:GLN:HG2	6:1G:43:LEU:HD13	1.80	0.64
7:1H:86:GLU:HB2	7:1H:165:ALA:HB2	1.80	0.64
1:2A:2310:A:N1	6:2G:79:ASN:ND2	2.45	0.64
8:2I:41:GLU:HA	8:2I:44:LEU:HB2	1.80	0.64
32:2a:316:G:OP2	32:2a:351:G:O2'	2.15	0.64
32:2a:536:C:OP2	57:2a:1801:HOH:O	2.15	0.64
1:1A:2722:G:OP2	57:1A:3825:HOH:O	2.14	0.64
1:2A:84:A:N1	1:2A:98:G:O2'	2.28	0.64
1:2A:392:C:H5"	1:2A:409:C:H5"	1.80	0.64
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.98	0.64
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.78	0.64
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.31	0.64
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.14	0.64
11:2P:87:ASP:O	11:2P:90:ARG:NH1	2.31	0.64
32:2a:1164:G:H1	32:2a:1172:C:N4	1.95	0.64
3:1D:39:LYS:NZ	3:1D:57:GLY:O	2.30	0.63
32:1a:1006:C:O2	32:1a:1023:G:N1	2.27	0.63
32:1a:1255:G:H1	32:1a:1282:C:H42	1.46	0.63
34:1c:26:LYS:HG3	45:1n:36:PHE:HD1	1.62	0.63
39:1h:49:GLU:OE2	39:1h:62:TYR:OH	2.13	0.63
32:2a:324:G:N7	57:2a:1811:HOH:O	2.30	0.63
38:2g:20:ASP:OD2	38:2g:63:LYS:NZ	2.30	0.63
1:1A:859:G:O2'	1:1A:916:G:O6	2.13	0.63
1:1A:1907:G:H1	1:1A:1923:U:H3	1.47	0.63
48:1q:67:LYS:O	48:1q:69:LYS:N	2.31	0.63
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.62	0.63
32:2a:954:G:H21	32:2a:1227:A:H62	1.46	0.63
32:2a:1136:U:OP2	32:2a:1137:C:N4	2.32	0.63
32:2a:1254:C:N3	32:2a:1283:G:N2	2.42	0.63
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	1.80	0.63
1:1A:2404:C:OP2	57:1A:3828:HOH:O	2.15	0.63
44:2m:16:ASP:HB3	44:2m:34:LEU:HD11	1.80	0.63
1:1A:805:G:N2	1:1A:829:A:OP1	2.31	0.63
50:1s:20:LEU:HD23	50:1s:23:ASN:HD22	1.63	0.63
1:2A:270:A:OP2	1:2A:271(X):G:N1	2.24	0.63
1:2A:858:U:OP1	22:20:44:ARG:NH2	2.32	0.63
9:2N:42:TRP:HA	9:2N:48:MET:HE1	1.80	0.63
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:411:A:OP1	35:2d:30:LYS:NZ	2.32	0.63
1:1A:2418:A:OP2	30:18:29:LYS:NZ	2.32	0.63
6:1G:67:LYS:HD3	26:14:5:ILE:HD12	1.79	0.63
1:2A:1316:U:H2'	1:2A:1317:A:H8	1.62	0.63
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.80	0.63
39:2h:10:LEU:HD22	39:2h:83:ILE:HD11	1.81	0.63
50:2s:22:LEU:HD12	50:2s:31:ILE:HD11	1.80	0.63
7:1H:127:GLU:OE2	7:1H:130:ARG:NH1	2.31	0.63
1:2A:400:G:N7	57:2A:3644:HOH:O	2.30	0.63
1:2A:2000:G:N7	57:2A:3649:HOH:O	2.31	0.63
13:2R:67:LEU:HD12	13:2R:76:VAL:HG21	1.81	0.63
44:2m:58:GLU:O	44:2m:62:ASN:ND2	2.31	0.63
1:2A:2065:C:H4'	1:2A:2251:OMG:HM23	1.79	0.63
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.32	0.63
26:24:1:MET:HB3	26:24:6:HIS:CD2	2.34	0.63
1:1A:2646:C:OP2	1:1A:2732:G:O2'	2.16	0.63
7:1H:40:GLU:OE2	7:1H:60:ARG:NH1	2.30	0.63
32:1a:976:G:OP2	32:1a:1358:U:O2'	2.16	0.63
1:2A:833:U:O2	11:2P:55:ARG:NH1	2.31	0.63
1:2A:2318:G:N2	14:2S:3:ARG:HE	1.96	0.63
37:2f:37:VAL:HA	37:2f:65:VAL:HG12	1.78	0.63
1:1A:1056:G:H4'	1:1A:1086:A:H8	1.63	0.62
39:2h:21:LYS:O	39:2h:65:TYR:OH	2.17	0.62
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.64	0.62
32:1a:6:G:H4'	32:1a:298:A:H4'	1.79	0.62
32:2a:1100:C:N4	32:2a:1103:C:OP1	2.32	0.62
5:1F:188:ARG:HA	11:1P:3:LEU:HD11	1.80	0.62
12:1Q:35:VAL:HG13	12:1Q:130:LYS:HB3	1.80	0.62
32:1a:407:G:H5"	35:1d:115:ARG:HB3	1.80	0.62
32:1a:501:C:H1'	32:1a:549:C:H1'	1.81	0.62
13:2R:29:LEU:HB3	13:2R:75:LEU:HD21	1.80	0.62
32:2a:1086:U:H3	32:2a:1099:G:H22	1.47	0.62
33:2b:84:GLU:HG3	33:2b:215:LEU:HB3	1.80	0.62
32:1a:452:A:H62	32:1a:480:U:H3	1.46	0.62
1:2A:399:G:OP2	57:2A:3608:HOH:O	2.16	0.62
1:2A:857:C:OP1	22:20:77:ARG:NH2	2.31	0.62
32:2a:624:C:H2'	32:2a:625:G:H8	1.62	0.62
32:2a:1133:G:H2'	32:2a:1134:G:C8	2.34	0.62
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	1.99	0.62
32:2a:1314:C:N4	50:2s:2:PRO:O	2.32	0.62
40:2i:89:ASN:HB3	40:2i:92:TYR:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2638:G:OP2	4:1E:82:ARG:NH1	2.30	0.62
7:1H:3:ARG:HE	7:1H:54:ARG:HH12	1.48	0.62
32:1a:826:C:H4'	39:1h:12:ARG:HG3	1.80	0.62
1:2A:243:U:OP1	30:28:6:THR:OG1	2.14	0.62
7:2H:27:LYS:NZ	7:2H:32:GLU:OE1	2.33	0.62
32:2a:1319:A:H61	32:2a:1361:G:H21	1.47	0.62
47:2p:20:VAL:HG23	47:2p:35:LYS:HA	1.81	0.62
1:2A:1128:A:N7	1:2A:2489:G:O2'	2.31	0.62
1:2A:1496:A:N3	1:2A:1577:C:O2'	2.33	0.62
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.62	0.62
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.82	0.62
10:1O:23:ARG:NH1	57:1O:201:HOH:O	2.26	0.62
18:1W:86:LEU:HD22	18:1W:96:ILE:HD11	1.81	0.62
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.33	0.62
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.82	0.62
16:2U:49:HIS:HA	16:2U:52:ARG:HG2	1.82	0.62
32:2a:1388:C:O2'	57:2a:1802:HOH:O	2.16	0.62
32:1a:1130:A:O2'	40:1i:3:GLN:NE2	2.32	0.62
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.82	0.62
1:2A:2012:G:OP1	18:2W:11:ARG:NH2	2.30	0.62
7:2H:56:SER:OG	7:2H:61:HIS:ND1	2.29	0.62
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.29	0.62
1:1A:2547:U:O2	10:1O:23:ARG:NH2	2.32	0.62
24:12:16:LEU:O	24:12:67:LYS:NZ	2.33	0.62
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.81	0.62
35:2d:6:GLY:H	35:2d:115:ARG:HH12	1.48	0.62
1:1A:2123:G:O6	1:1A:2175:C:N3	2.33	0.62
28:16:23:THR:OG1	28:16:24:GLU:N	2.31	0.62
32:1a:448:A:OP2	32:1a:485:G:N2	2.27	0.62
32:1a:1112:C:H1'	34:1c:179:ARG:HD3	1.81	0.62
35:1d:107:ARG:HH21	35:1d:114:ARG:HH22	1.48	0.62
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	1.82	0.62
1:1A:2079:U:O3'	23:11:35:THR:OG1	2.18	0.61
32:1a:1252:A:H61	32:1a:1285:A:H61	1.47	0.61
32:2a:1016:A:C5	32:2a:1017:G:H1'	2.35	0.61
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.28	0.61
32:1a:673:G:H2'	32:1a:674:G:C8	2.35	0.61
1:2A:2577:A:H2'	1:2A:2614:A:N6	2.14	0.61
33:2b:76:GLN:HB2	33:2b:208:ILE:HG12	1.81	0.61
1:2A:1889:A:H2'	1:2A:1890:A:C8	2.34	0.61
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:150:ASP:OD1	6:2G:151:ALA:N	2.33	0.61
12:2Q:59:ARG:HD3	12:2Q:60:ARG:HG3	1.80	0.61
41:2j:44:VAL:HG13	41:2j:66:ARG:HG2	1.82	0.61
1:1A:2035:G:OP1	57:1A:3832:HOH:O	2.16	0.61
32:1a:593:G:H1	32:1a:646:U:H3	1.49	0.61
32:1a:677:U:H3	32:1a:713:G:H22	1.47	0.61
32:1a:975:A:H4'	32:1a:976:G:H5"	1.82	0.61
32:1a:1226:C:OP2	44:1m:91:ARG:NH2	2.31	0.61
44:2m:54:VAL:HA	44:2m:57:ARG:HB3	1.82	0.61
1:1A:637:A:OP1	11:1P:133:SER:OG	2.16	0.61
1:1A:973:A:OP2	57:1A:3831:HOH:O	2.16	0.61
1:2A:1428:C:O2'	1:2A:1569:A:OP2	2.14	0.61
6:2G:146:TYR:HB3	44:2m:11:ARG:HH22	1.65	0.61
51:2t:57:ARG:HH12	51:2t:100:ILE:HB	1.64	0.61
13:1R:67:LEU:HD22	13:1R:76:VAL:HG21	1.83	0.61
32:1a:564:C:O2'	39:1h:91:ARG:NH1	2.28	0.61
35:1d:20:TYR:HD1	35:1d:26:CYS:HB3	1.65	0.61
1:2A:247:G:H4'	1:2A:386:G:C5	2.35	0.61
1:2A:2103:C:H42	1:2A:2185:C:H42	1.46	0.61
1:2A:2575:C:H5'	4:2E:144:ARG:HG2	1.82	0.61
6:2G:60:LEU:HA	6:2G:63:ILE:HB	1.83	0.61
32:2a:1250:A:H61	32:2a:1354:C:H1'	1.66	0.61
37:1f:97:PHE:HB3	49:1r:31:LEU:HB2	1.83	0.61
40:1i:26:VAL:HA	40:1i:61:ALA:HB3	1.82	0.61
32:2a:1025:U:O2'	32:2a:1026:G:H8	1.82	0.61
1:1A:2115:G:O2'	1:1A:2167:U:O2	2.19	0.61
32:1a:107:G:OP1	32:1a:325:A:N6	2.34	0.61
1:2A:807:U:O2'	1:2A:2060:A:N1	2.29	0.61
3:1D:133:LEU:HD23	3:1D:136:ILE:HD12	1.83	0.61
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.81	0.61
32:1a:578:C:O2'	32:1a:728:A:N3	2.29	0.61
1:2A:1786:A:OP1	57:2A:3609:HOH:O	2.16	0.61
1:2A:2253:G:OP1	57:2A:3601:HOH:O	2.16	0.61
8:2I:1:MET:HE2	8:2I:38:LEU:HD21	1.83	0.61
11:2P:59:LEU:HD11	30:28:10:ALA:HA	1.81	0.61
13:2R:96:ARG:NE	13:2R:115:GLU:OE2	2.32	0.61
32:2a:736:C:H2'	32:2a:737:A:C8	2.35	0.61
32:1a:999:C:N4	32:1a:1042:G:H1	1.96	0.61
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.83	0.61
8:2I:90:GLY:O	8:2I:121:LYS:NZ	2.29	0.61
32:2a:1129:C:N3	32:2a:1143:G:N2	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1380:U:C4	38:2g:3:ARG:HG2	2.36	0.61
35:2d:8:VAL:HA	35:2d:11:LEU:HD13	1.82	0.61
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.17	0.60
36:1e:152:ARG:HD3	39:1h:79:VAL:HG13	1.81	0.60
1:2A:642:G:O2'	1:2A:644:A:N7	2.33	0.60
32:2a:134:A:H61	47:2p:25:ARG:HH12	1.48	0.60
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.36	0.60
32:2a:1380:U:O2	32:2a:1382:C:N4	2.30	0.60
7:1H:164:TYR:HB2	7:1H:167:GLU:HB2	1.83	0.60
11:1P:88:LEU:HD11	11:1P:114:ILE:HD12	1.82	0.60
37:1f:99:ALA:HB2	49:1r:31:LEU:HD11	1.83	0.60
46:1o:33:THR:HG21	46:1o:85:LEU:HD22	1.83	0.60
1:2A:2590:A:O3'	3:2D:239:ARG:NH2	2.34	0.60
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.82	0.60
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.83	0.60
1:1A:1418:G:OP2	57:1A:3833:HOH:O	2.16	0.60
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.81	0.60
33:1b:54:THR:HG21	33:1b:201:ILE:HD11	1.81	0.60
1:2A:1024:G:O2'	1:2A:1144:G:O2'	2.19	0.60
1:2A:1032:A:H2	1:2A:1122:G:H22	1.48	0.60
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.82	0.60
6:2G:68:PRO:HB3	6:2G:92:VAL:HB	1.84	0.60
32:2a:1149:C:O2'	32:2a:1280:A:N1	2.28	0.60
33:2b:15:VAL:HG23	33:2b:16:HIS:CD2	2.34	0.60
1:1A:2782:G:OP2	57:1A:3830:HOH:O	2.16	0.60
28:26:23:THR:OG1	28:26:24:GLU:N	2.31	0.60
32:2a:1126:U:H3	41:2j:40:LEU:HD21	1.67	0.60
1:1A:403:U:H4'	1:1A:404:C:H5'	1.83	0.60
33:2b:178:ARG:HB3	39:2h:72:PRO:HA	1.82	0.60
27:15:41:PRO:O	27:15:44:THR:OG1	2.18	0.60
32:1a:1183:A:H3'	32:1a:1184:G:H5"	1.82	0.60
1:2A:1090:U:H2'	1:2A:1091:G:H8	1.67	0.60
6:2G:71:THR:N	6:2G:89:GLY:O	2.24	0.60
35:2d:71:SER:OG	35:2d:74:GLN:OE1	2.18	0.60
35:2d:163:GLU:O	35:2d:166:LYS:HG2	2.02	0.60
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.34	0.60
4:2E:52:LEU:HB3	4:2E:53:PRO:HD2	1.84	0.60
25:23:8:LEU:O	25:23:32:GLN:N	2.29	0.60
26:24:58:ARG:HG3	50:2s:65:ASN:HA	1.84	0.60
34:2c:189:ALA:HB3	34:2c:196:LEU:HB2	1.82	0.60
32:1a:246:A:N1	32:1a:278:G:O2'	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2572:A:OP1	1:2A:2574:G:O2'	2.20	0.60
14:2S:3:ARG:NH1	14:2S:4:LEU:O	2.35	0.60
32:2a:636:U:H5'	48:2q:2:PRO:HG3	1.83	0.60
32:2a:1359:C:O2'	32:2a:1361:G:N7	2.35	0.60
1:1A:1020:A:N1	1:1A:1141:U:O2'	2.33	0.60
1:1A:1063:G:H1	1:1A:1075:C:H42	1.48	0.60
1:1A:1087:G:H1	1:1A:1102:C:H42	1.49	0.60
3:1D:202:LYS:NZ	32:1a:774:G:OP1	2.35	0.60
35:1d:178:VAL:O	35:1d:180:GLY:N	2.34	0.60
18:2W:86:LEU:HD22	18:2W:96:ILE:HD11	1.83	0.60
36:2e:88:LYS:HB3	36:2e:123:LEU:HB2	1.84	0.60
1:1A:2159:G:H2'	1:1A:2160:G:C8	2.37	0.60
16:1U:97:ASP:OD1	16:1U:101:ARG:NH1	2.35	0.60
22:10:11:ARG:O	22:10:14:ARG:NH2	2.35	0.60
30:18:28:GLY:O	30:18:36:LYS:NZ	2.33	0.60
32:1a:1132:C:H2'	32:1a:1133:G:H8	1.66	0.60
44:1m:87:TYR:HA	44:1m:90:LEU:HD12	1.83	0.60
45:1n:47:LEU:HD23	45:1n:50:LYS:HD3	1.84	0.60
47:1p:20:VAL:HG23	47:1p:35:LYS:HA	1.84	0.60
32:2a:1134:G:N2	32:2a:1136:U:O4	2.35	0.60
3:1D:112:GLN:HB2	3:1D:115:GLN:HB3	1.84	0.59
44:1m:86:CYS:HB2	50:1s:73:GLU:HB3	1.83	0.59
1:2A:889:C:O2'	1:2A:890:A:O5'	2.20	0.59
1:2A:2305:A:H5"	6:2G:134:GLY:HA3	1.82	0.59
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.34	0.59
51:2t:65:LYS:HA	51:2t:68:LYS:HD3	1.84	0.59
1:1A:106:C:HO2'	1:1A:294:A:HO2'	1.50	0.59
1:1A:2156:G:O6	1:1A:2157:G:N2	2.35	0.59
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.33	0.59
32:1a:370:C:H2'	32:1a:371:G:C8	2.37	0.59
32:1a:662:G:H2'	32:1a:663:A:C8	2.37	0.59
33:1b:24:TRP:HZ3	33:1b:29:ALA:HB2	1.67	0.59
35:1d:173:TRP:HA	35:1d:187:ARG:HG2	1.84	0.59
40:1i:16:ARG:HB2	40:1i:64:THR:HG23	1.84	0.59
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.83	0.59
7:2H:149:ARG:NH1	7:2H:167:GLU:OE2	2.34	0.59
32:2a:1439:C:OP1	51:2t:38:LYS:NZ	2.24	0.59
32:1a:826:C:O2	39:1h:15:ASN:ND2	2.35	0.59
39:1h:21:LYS:O	39:1h:65:TYR:OH	2.21	0.59
1:2A:1058:G:H1	1:2A:1079:C:H41	1.49	0.59
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1056:G:N1	1:1A:1102:C:OP2	2.30	0.59
8:1I:72:LEU:O	8:1I:74:ASN:N	2.32	0.59
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.02	0.59
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.84	0.59
21:2Z:119:GLU:OE1	21:2Z:122:ARG:NH1	2.34	0.59
32:2a:1178:G:N2	32:2a:1181:G:OP2	2.35	0.59
1:1A:2774:C:OP2	57:1A:3835:HOH:O	2.17	0.59
1:1A:1486:A:H2'	1:1A:1487:G:H8	1.67	0.59
40:1i:26:VAL:HB	40:1i:33:PHE:HB2	1.84	0.59
1:2A:1991:U:H2'	1:2A:1992:G:H5"	1.85	0.59
35:2d:98:GLU:HG3	35:2d:194:LEU:HD21	1.83	0.59
41:2j:61:GLU:OE2	45:2n:58:LYS:NZ	2.36	0.59
1:1A:2632:A:HO2'	1:1A:2811:G:HO2'	1.48	0.59
10:1O:64:ARG:NH1	10:1O:101:PRO:O	2.35	0.59
32:1a:1060:C:H4'	41:1j:51:ARG:HB3	1.85	0.59
1:2A:271(L):U:H4'	1:2A:271(M):G:H5'	1.84	0.59
1:2A:947:G:OP2	57:2A:3610:HOH:O	2.17	0.59
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.83	0.59
4:2E:167:VAL:HG22	4:2E:170:LEU:HD11	1.84	0.59
5:2F:188:ARG:HA	11:2P:3:LEU:HD11	1.85	0.59
42:2k:27:ASN:OD1	42:2k:28:THR:N	2.35	0.59
1:1A:1239:G:H2'	1:1A:1240:U:O4'	2.03	0.59
1:1A:2103:C:N4	1:1A:2186:G:H1	2.01	0.59
35:1d:6:GLY:O	35:1d:115:ARG:NH1	2.36	0.59
32:2a:116:A:H61	32:2a:313:A:H1'	1.68	0.59
32:2a:1376:U:O4	38:2g:10:ARG:NH2	2.36	0.59
1:1A:399:G:OP2	57:1A:3837:HOH:O	2.17	0.59
1:1A:1173:G:O2'	1:1A:1174:A:O4'	2.21	0.59
1:1A:2375:G:O2'	1:1A:2377:A:N7	2.31	0.59
32:1a:407:G:OP1	35:1d:115:ARG:NH2	2.34	0.59
1:2A:140:G:N3	1:2A:142:A:N6	2.49	0.59
1:2A:635:C:O2'	1:2A:639:U:OP1	2.20	0.59
1:2A:2495:G:H5"	12:2Q:82:ARG:HG2	1.85	0.59
6:2G:64:THR:HB	6:2G:94:LEU:HD11	1.85	0.59
1:1A:251:A:C5	1:1A:252:G:H1'	2.38	0.58
33:1b:223:ILE:HG22	33:1b:226:ARG:HH21	1.68	0.58
44:1m:31:LYS:HA	44:1m:34:LEU:HD12	1.84	0.58
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.68	0.58
34:2c:152:ILE:HG23	34:2c:199:LYS:HB2	1.84	0.58
1:1A:451:C:OP1	5:1F:52:LYS:NZ	2.36	0.58
32:1a:157:G:H1	32:1a:164:U:H3	1.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.84	0.58
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.20	0.58
25:23:15:TYR:O	25:23:20:LYS:NZ	2.36	0.58
32:2a:985:C:H2'	32:2a:986:A:C8	2.38	0.58
32:2a:1255:G:H2'	32:2a:1258:G:H21	1.68	0.58
1:1A:1339:G:H5"	19:1X:16:LYS:HD3	1.85	0.58
32:1a:300:A:O2'	32:1a:564:C:N3	2.33	0.58
32:1a:316:G:OP2	32:1a:351:G:O2'	2.22	0.58
32:1a:990:C:N4	32:1a:991:U:O4	2.35	0.58
35:1d:108:LEU:HD21	35:1d:183:GLY:HA3	1.85	0.58
32:2a:593:G:H1	32:2a:646:U:H3	1.50	0.58
35:2d:119:GLN:O	35:2d:123:HIS:ND1	2.37	0.58
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.85	0.58
35:1d:158:ILE:HG13	35:1d:159:ARG:N	2.18	0.58
37:1f:10:LEU:HD13	37:1f:61:LEU:HD13	1.86	0.58
48:1q:45:HIS:HB3	48:1q:72:ARG:HG3	1.83	0.58
51:1t:46:GLU:HG3	51:1t:48:LYS:HD2	1.84	0.58
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.85	0.58
32:2a:1047:G:H1	32:2a:1210:C:N4	2.01	0.58
1:1A:1970:A:OP1	57:1A:3834:HOH:O	2.16	0.58
32:1a:517:G:N1	32:1a:533:A:OP2	2.27	0.58
32:1a:946:A:O2'	32:1a:1333:A:N3	2.32	0.58
32:1a:1237:C:N3	32:1a:1337:G:N2	2.45	0.58
1:2A:1073:A:H2'	1:2A:1074:G:C8	2.38	0.58
1:2A:1491:G:H2'	1:2A:1492:G:H8	1.69	0.58
1:2A:2425:A:N7	57:2A:3653:HOH:O	2.32	0.58
32:2a:828:A:N6	32:2a:858:G:O2'	2.35	0.58
32:2a:928:G:O2'	32:2a:1533:C:OP1	2.21	0.58
32:2a:1278:U:H5"	32:2a:1279:A:H5'	1.86	0.58
32:1a:1001(A):G:N1	32:1a:1039:C:O2	2.30	0.58
32:1a:1069:C:O2'	32:1a:1192:C:O2	2.22	0.58
36:1e:12:LEU:HD12	36:1e:128:PRO:HB2	1.84	0.58
1:2A:1051:G:H4'	1:2A:2752:C:H1'	1.86	0.58
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.38	0.58
1:1A:288:C:H2'	1:1A:289:A:C8	2.38	0.58
1:1A:651:G:OP1	30:18:19:SER:OG	2.14	0.58
1:1A:1713:U:H2'	1:1A:1714:G:H8	1.69	0.58
32:1a:1414:U:H3	32:1a:1486:G:H1	1.52	0.58
33:1b:168:THR:OG1	33:1b:191:ASP:O	2.17	0.58
42:1k:34:ASP:HB3	42:1k:40:ILE:HD11	1.85	0.58
44:1m:72:ALA:O	44:1m:76:ALA:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.36	0.58
1:2A:2136:C:N4	1:2A:2155:G:H1	2.00	0.58
2:2B:96:U:H2'	2:2B:97:G:C8	2.39	0.58
12:1Q:34:LEU:HB2	12:1Q:118:LEU:HD22	1.86	0.58
36:1e:102:ALA:HB1	36:1e:106:PRO:HG2	1.86	0.58
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.39	0.58
32:2a:401:C:H2'	32:2a:402:G:C8	2.39	0.58
32:2a:1009:G:H1	32:2a:1020:U:H3	1.51	0.58
1:1A:1937:A:H1'	1:1A:1939:5MU:H72	1.86	0.58
1:1A:2857:G:N2	1:1A:2860:A:OP2	2.34	0.58
32:1a:17:U:H2'	32:1a:18:C:C6	2.39	0.58
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.84	0.58
32:2a:1050:G:H1	32:2a:1208:C:H42	1.50	0.58
37:2f:10:LEU:HD13	37:2f:61:LEU:HD13	1.85	0.58
40:2i:16:ARG:N	40:2i:64:THR:O	2.37	0.58
32:1a:401:C:H2'	32:1a:402:G:C8	2.39	0.58
32:1a:1255:G:OP1	34:1c:26:LYS:NZ	2.34	0.58
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.04	0.58
32:2a:1115:C:N4	32:2a:1185:G:H1	1.99	0.58
32:1a:96:U:H2'	32:1a:97:G:C8	2.38	0.57
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.85	0.57
1:2A:320:A:O2'	1:2A:322:A:OP2	2.20	0.57
1:2A:2105:C:H42	1:2A:2183:C:H42	1.52	0.57
32:2a:927:G:O2'	32:2a:1503:A:N6	2.37	0.57
32:2a:952:U:O4	44:2m:102:ARG:NH2	2.37	0.57
43:2l:113:ARG:NH2	43:2l:115:LYS:O	2.36	0.57
32:1a:546:G:OP1	35:1d:73:ARG:HG2	2.04	0.57
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.37	0.57
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.37	0.57
6:2G:137:GLU:HB2	6:2G:140:ILE:HG12	1.86	0.57
32:2a:691:G:H2'	32:2a:692:U:C6	2.39	0.57
1:1A:2012:G:OP1	18:1W:11:ARG:NH2	2.37	0.57
33:1b:109:SER:HA	33:1b:112:VAL:HG13	1.85	0.57
1:2A:1000:A:OP2	1:2A:1154:G:N1	2.33	0.57
1:2A:1090:U:H2'	1:2A:1091:G:C8	2.40	0.57
1:2A:2638:G:P	4:2E:82:ARG:HH12	2.26	0.57
48:2q:9:VAL:HG22	48:2q:56:VAL:HG22	1.85	0.57
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.37	0.57
11:1P:95:VAL:HA	11:1P:99:LEU:HD12	1.86	0.57
1:2A:249:C:O2	30:28:12:LYS:NZ	2.37	0.57
1:2A:1073:A:H2'	1:2A:1074:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:15:VAL:HG21	6:2G:176:LEU:HD23	1.86	0.57
7:2H:33:LEU:HD13	7:2H:75:ALA:HB1	1.85	0.57
1:1A:662:G:H5"	11:1P:16:ARG:HG2	1.87	0.57
16:1U:69:CYS:HB3	16:1U:74:LEU:HD12	1.87	0.57
32:1a:736:C:H2'	32:1a:737:A:C8	2.40	0.57
32:1a:1006:C:N3	32:1a:1023:G:C6	2.72	0.57
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.36	0.57
1:2A:1082:U:OP2	1:2A:1085:A:N6	2.38	0.57
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.35	0.57
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.37	0.57
1:1A:1721:G:H8	1:1A:1741:A:H62	1.53	0.57
35:1d:8:VAL:HA	35:1d:11:LEU:HD13	1.87	0.57
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.87	0.57
1:2A:1338:G:O6	19:2X:62:LYS:NZ	2.37	0.57
1:2A:1790:C:N3	57:2A:3654:HOH:O	2.32	0.57
1:2A:2136:C:C4	1:2A:2155:G:N1	2.63	0.57
13:2R:71:GLN:NE2	57:2R:8101:HOH:O	2.32	0.57
1:1A:530:G:H4'	1:1A:531:C:OP1	2.04	0.57
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.22	0.57
7:2H:56:SER:HG	7:2H:61:HIS:HD1	1.48	0.57
26:24:16:CYS:SG	26:24:17:GLY:N	2.77	0.57
32:2a:136:C:H42	32:2a:227:G:H1	1.51	0.57
1:1A:1815:A:N1	57:1A:3922:HOH:O	2.32	0.57
1:1A:2134:A:O2'	1:1A:2159:G:N3	2.37	0.57
21:1Z:152:ALA:HB1	21:1Z:163:LEU:HD21	1.86	0.57
32:1a:923:A:O2'	32:1a:1399:C:OP2	2.18	0.57
47:1p:57:ARG:NH2	47:1p:78:GLY:O	2.37	0.57
32:2a:23:C:OP2	32:2a:561:U:N3	2.36	0.57
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.87	0.57
1:1A:1849:G:H2'	1:1A:1850:G:H8	1.70	0.57
21:1Z:103:ARG:HD3	21:1Z:136:PHE:CG	2.39	0.57
32:1a:564:C:OP1	43:1l:15:ARG:NE	2.30	0.57
32:1a:1277:C:H1'	32:1a:1282:C:C2	2.40	0.57
35:2d:98:GLU:O	35:2d:103:ASN:ND2	2.37	0.57
1:1A:192:C:O2'	1:1A:802:A:N3	2.35	0.57
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.86	0.57
32:1a:21:G:OP1	57:1a:3201:HOH:O	2.18	0.57
32:1a:1308:U:H3	32:1a:1329:A:H61	1.52	0.57
37:1f:69:GLU:OE1	37:1f:69:GLU:N	2.31	0.57
1:2A:530:G:N1	1:2A:2023:G:OP1	2.35	0.57
1:2A:910:A:N3	1:2A:2264:C:O2'	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2773:C:OP1	4:2E:166:THR:OG1	2.22	0.57
32:2a:1226:C:O2'	44:2m:103:THR:O	2.19	0.57
32:2a:1372:U:OP1	40:2i:72:GLY:N	2.37	0.57
40:2i:51:ARG:HA	40:2i:56:LEU:HD11	1.87	0.57
46:2o:67:LEU:HB3	46:2o:78:TYR:HE1	1.70	0.57
1:1A:422:A:OP2	57:1A:3840:HOH:O	2.17	0.56
6:1G:181:ARG:HG3	6:1G:182:LYS:H	1.69	0.56
32:1a:21:G:H2'	32:1a:22:G:C8	2.40	0.56
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.05	0.56
50:1s:41:VAL:HG12	50:1s:43:GLU:H	1.70	0.56
1:2A:463:G:N2	1:2A:466:A:OP2	2.35	0.56
1:2A:2680:C:H5'	4:2E:189:PRO:HA	1.87	0.56
4:2E:134:ILE:HA	4:2E:137:HIS:HD2	1.69	0.56
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.70	0.56
6:1G:115:ARG:NH1	44:1m:6:GLY:O	2.36	0.56
1:2A:1062:G:O2'	1:2A:1063:G:H8	1.88	0.56
6:2G:18:GLU:OE2	6:2G:21:ARG:NH2	2.36	0.56
18:2W:9:TYR:H	18:2W:102:HIS:CE1	2.23	0.56
21:2Z:126:VAL:HG11	21:2Z:161:VAL:HG13	1.85	0.56
32:2a:662:G:H2'	32:2a:663:A:C8	2.39	0.56
40:2i:42:ARG:HH11	40:2i:71:SER:HB3	1.69	0.56
1:1A:7:G:H2'	1:1A:8:A:C8	2.40	0.56
1:1A:184:C:H2'	1:1A:185:U:C6	2.40	0.56
1:1A:207:A:H2'	1:1A:208:C:O4'	2.03	0.56
1:1A:330:A:HO2'	1:1A:331:A:H8	1.53	0.56
1:1A:631:A:OP2	30:18:47:LYS:NZ	2.27	0.56
1:1A:1092:C:N4	1:1A:1099:G:H1	2.04	0.56
6:1G:7:LEU:HD22	6:1G:176:LEU:HD22	1.86	0.56
21:1Z:52:SER:OG	21:1Z:53:ILE:N	2.38	0.56
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.21	0.56
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.87	0.56
50:1s:11:VAL:HG11	50:1s:16:LEU:HD13	1.86	0.56
1:2A:446:G:OP1	16:2U:3:ARG:NH1	2.38	0.56
1:2A:466:A:P	29:27:34:ARG:HH21	2.28	0.56
1:2A:2002:G:N7	57:2A:3651:HOH:O	2.32	0.56
1:2A:2154:G:H2'	1:2A:2155:G:C8	2.39	0.56
32:2a:976:G:N2	32:2a:1363:C:OP2	2.38	0.56
35:2d:72:GLU:OE2	35:2d:207:TYR:OH	2.20	0.56
1:1A:458:G:O2'	1:1A:469:G:O6	2.23	0.56
1:1A:789:A:N6	57:1A:3931:HOH:O	2.34	0.56
32:1a:1076:C:N4	32:1a:1081:G:H1	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:72:ARG:HG2	6:2G:87:PRO:HA	1.87	0.56
23:21:77:ALA:HA	23:21:80:LEU:HD13	1.88	0.56
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.21	0.56
45:2n:37:PHE:HZ	45:2n:56:VAL:HG21	1.70	0.56
1:1A:854:G:H2'	1:1A:855:G:C8	2.41	0.56
1:1A:2267:A:H5"	1:1A:2268:A:H5'	1.88	0.56
32:1a:1236:A:H4'	32:1a:1304:G:H4'	1.86	0.56
1:2A:244:A:H4'	11:2P:74:GLU:HB2	1.86	0.56
1:2A:581:C:H2'	1:2A:582:G:C8	2.41	0.56
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.86	0.56
14:1S:27:SER:HA	14:1S:88:ASP:HB3	1.87	0.56
32:1a:936:C:N4	32:1a:1379:G:H1	2.03	0.56
32:1a:998:G:N1	32:1a:1043:C:O2	2.37	0.56
1:2A:628:G:H2'	1:2A:629:G:C8	2.40	0.56
2:2B:15:A:H3'	2:2B:16:G:H8	1.71	0.56
32:2a:1163:C:N4	32:2a:1173:G:H1	2.03	0.56
1:1A:1330:C:OP1	57:1A:3836:HOH:O	2.17	0.56
6:1G:11:TYR:HA	6:1G:15:VAL:HB	1.88	0.56
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.30	0.56
32:1a:1202:G:H2'	32:1a:1203:C:O4'	2.05	0.56
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.41	0.56
1:2A:854:G:H2'	1:2A:855:G:H8	1.71	0.56
1:2A:2193:G:H2'	1:2A:2194:G:C8	2.41	0.56
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.87	0.56
32:2a:438:G:H5'	35:2d:123:HIS:HD2	1.71	0.56
32:2a:837:G:H2'	32:2a:838:G:C8	2.41	0.56
32:2a:1165:C:H3'	32:2a:1166:G:H8	1.71	0.56
32:2a:1412:C:H2'	32:2a:1413:A:C8	2.41	0.56
1:1A:1223:G:N2	1:1A:1226:A:OP2	2.30	0.56
1:1A:2058:A:N6	57:1A:3965:HOH:O	2.39	0.56
6:1G:46:ALA:HB3	6:1G:53:LEU:HD23	1.87	0.56
32:1a:1350:A:N6	32:1a:1372:U:H3	2.04	0.56
32:1a:1360:A:OP2	45:1n:35:ARG:NH2	2.39	0.56
34:1c:18:TRP:HZ2	45:1n:57:ARG:HB3	1.69	0.56
1:2A:271(T):C:H2'	1:2A:271(U):G:H8	1.71	0.56
1:2A:872:A:H2'	1:2A:873:G:C8	2.40	0.56
20:2Y:23:ARG:NH2	20:2Y:41:GLY:O	2.39	0.56
32:2a:413:G:H22	32:2a:429:U:H5"	1.69	0.56
32:2a:831:U:H3	32:2a:855:G:H1	1.53	0.56
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.40	0.56
1:1A:889:C:O2'	1:1A:890:A:O5'	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.41	0.56
32:1a:35:G:O2'	43:1l:118:SER:O	2.23	0.56
42:1k:18:ARG:NH2	42:1k:35:PRO:O	2.38	0.56
42:1k:85:ARG:HD3	42:1k:113:PRO:HD3	1.88	0.56
45:1n:3:ARG:NH2	45:1n:28:GLY:O	2.39	0.56
21:2Z:91:LEU:HD11	21:2Z:96:VAL:HG11	1.88	0.56
1:1A:27:G:N2	1:1A:512:G:H1'	2.21	0.56
1:1A:709:U:H2'	1:1A:710:G:C8	2.41	0.56
32:1a:946:A:H2'	32:1a:947:G:C8	2.41	0.56
32:1a:1372:U:OP1	40:1i:72:GLY:N	2.38	0.56
7:2H:3:ARG:HE	7:2H:54:ARG:HH12	1.53	0.56
18:2W:78:GLU:OE2	18:2W:99:ARG:NH1	2.31	0.56
32:2a:1318:A:H5"	50:2s:3:ARG:NH2	2.17	0.56
48:2q:6:LEU:HD23	48:2q:23:VAL:HG21	1.88	0.56
51:2t:50:GLU:HB2	51:2t:99:LEU:HD22	1.87	0.56
1:1A:36:G:N3	1:1A:450:G:O2'	2.39	0.55
3:1D:146:GLU:HB2	3:1D:189:CYS:HB3	1.88	0.55
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.39	0.55
32:1a:1187:G:N3	45:1n:60:SER:OG	2.40	0.55
33:1b:163:PHE:HD1	33:1b:185:ILE:HG13	1.71	0.55
1:2A:938:G:OP2	30:28:52:LYS:NZ	2.34	0.55
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.40	0.55
1:2A:2882:A:H5'	13:2R:96:ARG:HB2	1.87	0.55
1:1A:271(E):U:H2'	1:1A:271(F):C:C6	2.41	0.55
1:1A:827:U:OP1	57:1A:3803:HOH:O	2.18	0.55
32:1a:376:G:H1	32:1a:387:U:H3	1.52	0.55
33:1b:69:LEU:HB3	33:1b:162:ILE:HG22	1.88	0.55
34:1c:150:LYS:HB3	34:1c:201:TYR:HB2	1.86	0.55
1:2A:1038:C:H42	1:2A:1117:G:H1	1.54	0.55
1:2A:1486:A:H2'	1:2A:1487:G:H8	1.71	0.55
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.41	0.55
26:14:59:PHE:HE1	50:1s:45:VAL:HG21	1.72	0.55
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.22	0.55
32:1a:266:G:H5"	32:1a:268:C:H41	1.71	0.55
32:1a:362:G:N2	32:1a:365:U:OP2	2.39	0.55
32:1a:1518:MA6:N6	32:1a:1519:MA6:H103	2.22	0.55
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	1.88	0.55
1:1A:571:A:OP2	57:1A:3841:HOH:O	2.18	0.55
32:1a:1028:C:N4	32:1a:1033:G:H1	2.05	0.55
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.41	0.55
33:1b:231:GLU:HB3	33:1b:232:PRO:HD2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:1g:88:PRO:HG3	38:1g:149:ARG:HA	1.87	0.55
46:1o:68:ARG:NH1	57:1o:3102:HOH:O	2.39	0.55
1:2A:265:A:N1	1:2A:427:U:O2'	2.38	0.55
1:2A:1920:4OC:HM22	1:2A:1921:G:H5'	1.88	0.55
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.41	0.55
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.70	0.55
32:2a:1237:C:H42	32:2a:1337:G:H1	1.53	0.55
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.89	0.55
32:1a:750:G:N2	46:1o:23:GLY:O	2.23	0.55
32:1a:1033:G:H2'	32:1a:1034:G:C8	2.41	0.55
32:1a:1132:C:H2'	32:1a:1133:G:C8	2.42	0.55
34:1c:18:TRP:O	34:1c:21:ARG:NH1	2.40	0.55
1:2A:143(A):C:H2'	1:2A:144:C:C6	2.42	0.55
11:2P:88:LEU:HD11	11:2P:114:ILE:HD12	1.87	0.55
24:22:29:LYS:HG2	24:22:57:ILE:HD13	1.88	0.55
25:23:18:ASP:OD1	25:23:18:ASP:N	2.39	0.55
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.88	0.55
1:1A:286:C:H2'	1:1A:287:C:C6	2.41	0.55
1:1A:2126:A:C6	1:1A:2163:C:H4'	2.42	0.55
1:1A:2791:C:H2'	1:1A:2792:G:C8	2.41	0.55
1:2A:2805:G:H2'	1:2A:2807:G:H8	1.71	0.55
6:2G:142:PRO:HB2	26:24:31:ILE:HG21	1.89	0.55
32:2a:1298:C:OP2	38:2g:114:ARG:NH2	2.35	0.55
1:1A:1703:G:H2'	1:1A:1704:G:H8	1.71	0.55
1:1A:2126:A:N3	1:1A:2162:G:N2	2.53	0.55
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.21	0.55
32:1a:269:C:H2'	32:1a:270:A:C8	2.42	0.55
32:1a:567:G:N2	57:1a:3209:HOH:O	2.28	0.55
32:1a:1256:A:H5"	32:1a:1257:U:OP1	2.07	0.55
1:2A:2245:U:H5"	1:2A:2246:G:H5'	1.89	0.55
1:2A:2371:G:N3	28:26:46:HIS:HE1	2.04	0.55
6:2G:112:PRO:HG3	26:24:43:TYR:HE2	1.70	0.55
26:24:24:THR:OG1	26:24:25:TYR:N	2.36	0.55
32:2a:370:C:H2'	32:2a:371:G:C8	2.42	0.55
38:2g:155:ARG:NH1	38:2g:156:TRP:OXT	2.40	0.55
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.87	0.55
1:1A:336:C:O2'	20:1Y:35:TYR:OH	2.22	0.55
1:1A:807:U:OP2	11:1P:41:ARG:NH2	2.40	0.55
12:1Q:39:PRO:HD3	12:1Q:99:PRO:HG3	1.89	0.55
1:2A:627:A:H4'	1:2A:628:G:H5'	1.89	0.55
2:2B:3:C:H2'	2:2B:4:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:177:LEU:HD11	3:2D:183:ARG:HG3	1.89	0.55
32:2a:376:G:O3'	47:2p:5:ARG:NH1	2.33	0.55
32:2a:662:G:O2'	32:2a:836:G:OP1	2.24	0.55
32:2a:973:G:H3'	32:2a:974:A:H5"	1.88	0.55
38:2g:16:LEU:HD13	40:2i:45:ALA:HB2	1.88	0.55
41:2j:6:ILE:HB	41:2j:72:VAL:HG23	1.89	0.55
46:2o:4:THR:HG23	46:2o:7:GLU:H	1.71	0.55
1:1A:2296:U:OP2	14:1S:9:ARG:NH2	2.40	0.55
1:1A:2336:A:H61	22:10:43:THR:HG22	1.71	0.55
31:19:25:VAL:HB	31:19:34:GLN:HB2	1.88	0.55
32:1a:1025:U:O4	32:1a:1035:A:N6	2.40	0.55
32:1a:1343:G:H4'	40:1i:122:ALA:HB3	1.89	0.55
32:1a:1346:A:N1	32:1a:1374:A:H5"	2.22	0.55
7:2H:105:LEU:HB3	7:2H:113:VAL:HB	1.89	0.55
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.89	0.55
32:2a:410:G:OP1	35:2d:30:LYS:NZ	2.27	0.55
39:2h:81:HIS:ND1	39:2h:138:TRP:OXT	2.23	0.55
1:1A:668:G:H5'	1:1A:669:G:OP2	2.07	0.55
1:1A:1227:G:OP1	16:1U:13:LYS:NZ	2.38	0.55
6:1G:19:LEU:HG	6:1G:175:LEU:HD22	1.88	0.55
7:1H:88:LEU:HD23	7:1H:130:ARG:HG3	1.89	0.55
32:1a:1074:G:OP1	36:1e:64:ARG:NH1	2.40	0.55
1:2A:863:A:P	12:2Q:22:LYS:HG3	2.47	0.55
1:2A:2102:U:O2	1:2A:2187:G:O6	2.24	0.55
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.21	0.55
32:2a:539:A:OP2	43:2l:115:LYS:NZ	2.36	0.55
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.42	0.55
40:2i:53:VAL:HG23	40:2i:55:ALA:H	1.72	0.55
1:1A:1465:G:O2'	1:1A:1545:A:N1	2.37	0.54
2:1B:115:G:N2	57:1B:3105:HOH:O	2.31	0.54
18:1W:80:PRO:O	18:1W:100:THR:HB	2.06	0.54
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.39	0.54
34:1c:26:LYS:HD3	41:1j:45:ARG:HH22	1.72	0.54
1:2A:2371:G:O2'	28:26:46:HIS:ND1	2.33	0.54
32:2a:1346:A:N7	38:2g:10:ARG:NH2	2.55	0.54
34:2c:22:TRP:HB3	34:2c:59:ARG:H	1.72	0.54
39:2h:28:ALA:HB3	39:2h:57:PRO:HB2	1.89	0.54
32:1a:1030:C:N3	32:1a:1031:G:C2	2.75	0.54
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.41	0.54
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.72	0.54
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:2V:6:LYS:HB2	17:2V:38:LEU:HD11	1.89	0.54
32:2a:582:U:OP1	46:2o:68:ARG:NH2	2.40	0.54
32:2a:1001:A:H2'	32:2a:1001(A):G:H8	1.71	0.54
1:1A:271(T):C:H2'	1:1A:271(U):G:H8	1.72	0.54
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.21	0.54
33:1b:74:LYS:NZ	33:1b:205:ASP:OD2	2.38	0.54
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.89	0.54
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.40	0.54
10:2O:77:ILE:HG13	15:2T:74:ARG:HG2	1.88	0.54
35:2d:13:ARG:HB2	35:2d:40:PRO:HD3	1.89	0.54
44:2m:14:ARG:HA	44:2m:44:ARG:HA	1.88	0.54
50:2s:41:VAL:HG12	50:2s:44:MET:HG3	1.87	0.54
4:1E:54:GLN:OE1	4:1E:55:ASN:N	2.41	0.54
15:1T:111:ARG:NH2	32:1a:1464:G:OP2	2.40	0.54
26:14:59:PHE:CE1	50:1s:45:VAL:HG21	2.42	0.54
43:1l:70:ILE:HG12	43:1l:100:ILE:HD12	1.89	0.54
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.89	0.54
31:29:17:ILE:HB	31:29:26:ILE:HD11	1.89	0.54
32:2a:775:G:N2	32:2a:804:U:O4	2.40	0.54
9:1N:42:TRP:CD1	9:1N:48:MET:HE1	2.42	0.54
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.25	0.54
32:1a:747:C:OP2	32:1a:748:C:N4	2.37	0.54
32:1a:978:A:O2'	32:1a:1322:C:N3	2.30	0.54
33:1b:118:LEU:HD21	33:1b:138:LEU:HD22	1.90	0.54
38:1g:151:TYR:OH	42:1k:54:ARG:NH1	2.41	0.54
1:2A:644:A:H4'	1:2A:645:C:C5	2.41	0.54
1:2A:1153:C:H5'	16:2U:76:TYR:HE2	1.72	0.54
1:2A:2010:G:N7	57:2A:3657:HOH:O	2.34	0.54
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.42	0.54
32:2a:745:C:H2'	32:2a:746:A:C8	2.42	0.54
1:1A:84:A:N1	1:1A:98:G:O2'	2.35	0.54
1:1A:698:C:O2'	1:1A:734:A:N6	2.40	0.54
1:1A:919:G:N2	1:1A:2269:A:OP2	2.41	0.54
1:1A:2103:C:N3	1:1A:2186:G:N2	2.50	0.54
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.25	0.54
32:1a:1237:C:O2'	32:1a:1300:G:N2	2.40	0.54
1:2A:674:G:H1'	5:2F:74:ARG:HE	1.73	0.54
1:2A:1056:G:H21	1:2A:1104:C:H42	1.55	0.54
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.42	0.54
15:2T:9:LEU:O	15:2T:12:SER:OG	2.22	0.54
34:2c:40:ARG:NH1	34:2c:55:VAL:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:52:PRO:HG2	36:2e:53:LEU:HD12	1.89	0.54
40:2i:26:VAL:HB	40:2i:33:PHE:HB2	1.89	0.54
40:2i:121:ARG:NH1	40:2i:122:ALA:O	2.41	0.54
1:1A:1919:A:O2'	32:1a:1517:G:N3	2.38	0.54
1:2A:30:G:H2'	1:2A:31:C:C6	2.43	0.54
1:2A:2008:C:H2'	1:2A:2009:G:H8	1.72	0.54
32:2a:222:U:H2'	32:2a:223:U:C6	2.42	0.54
32:2a:1104:G:H5'	33:2b:111:ARG:HH21	1.72	0.54
1:1A:1833:U:O2'	1:1A:1969:A:N1	2.32	0.54
9:1N:62:VAL:HG11	9:1N:66:LYS:HB2	1.89	0.54
1:2A:588:U:H1'	5:2F:90:PHE:HB3	1.89	0.54
1:2A:628:G:H2'	1:2A:629:G:H8	1.73	0.54
1:2A:2812:G:H2'	1:2A:2813:A:C8	2.43	0.54
5:2F:165:ARG:HA	5:2F:168:ARG:HE	1.73	0.54
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.41	0.54
33:2b:90:MET:HE3	33:2b:222:ILE:HD13	1.88	0.54
1:2A:453:C:O2	1:2A:457:A:O2'	2.25	0.54
1:2A:1167:U:O2	1:2A:1183:G:N2	2.41	0.54
32:2a:390:C:O2'	47:2p:28:ARG:NH2	2.41	0.54
32:2a:1135:U:H5"	32:2a:1136:U:H5	1.72	0.54
32:2a:1373:G:H5"	38:2g:36:LYS:HE2	1.89	0.54
50:2s:12:ASP:O	50:2s:16:LEU:N	2.31	0.54
5:1F:108:LYS:HE2	5:1F:112:MET:HE3	1.88	0.54
32:1a:501:C:O2	32:1a:549:C:O2'	2.21	0.54
32:1a:1220:G:N2	50:1s:54:GLY:O	2.39	0.54
32:1a:1239:A:O2'	38:1g:114:ARG:O	2.22	0.54
2:2B:45:A:OP2	6:2G:96:ARG:NH2	2.41	0.54
33:2b:145:LEU:HD22	33:2b:149:LEU:HD12	1.90	0.54
1:1A:2005:A:OP1	57:1A:3838:HOH:O	2.17	0.53
12:1Q:32:TYR:OH	12:1Q:133:ARG:NH2	2.41	0.53
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.42	0.53
1:2A:2144:U:H1'	1:2A:2147:G:O6	2.09	0.53
3:2D:72:LYS:HB3	3:2D:75:ILE:HD12	1.90	0.53
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.90	0.53
6:2G:46:ALA:HB2	6:2G:53:LEU:HD12	1.88	0.53
40:2i:96:LEU:O	40:2i:100:GLY:N	2.41	0.53
1:1A:1364:G:N2	1:1A:1367:A:OP2	2.36	0.53
5:1F:40:GLN:NE2	5:1F:182:ASN:HB2	2.23	0.53
32:1a:186:C:H2'	32:1a:187:C:C6	2.43	0.53
32:1a:1358:U:H5"	45:1n:33:VAL:O	2.08	0.53
1:2A:189:G:O2'	1:2A:207:A:N6	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:66:A:N6	2:2B:109:C:OP2	2.41	0.53
32:2a:35:G:O2'	43:2l:118:SER:O	2.26	0.53
32:2a:401:C:H2'	32:2a:402:G:H8	1.73	0.53
1:1A:1805:U:O2	3:1D:50:THR:HB	2.08	0.53
7:1H:117:PRO:HG3	7:1H:123:PHE:CD2	2.44	0.53
38:1g:65:ALA:O	38:1g:69:VAL:HG23	2.08	0.53
1:2A:336:C:H2'	1:2A:337:C:H6	1.74	0.53
1:2A:1919:A:N1	32:2a:1495:U:O2'	2.36	0.53
6:2G:25:TYR:HB3	6:2G:30:GLU:HB2	1.90	0.53
13:2R:33:ARG:NH2	13:2R:115:GLU:OE1	2.30	0.53
40:2i:9:ARG:H	40:2i:79:LEU:HD23	1.74	0.53
1:1A:106:C:O2'	1:1A:294:A:O2'	2.23	0.53
5:1F:31:HIS:NE2	5:1F:35:GLU:OE2	2.39	0.53
32:1a:437:U:O2	35:1d:119:GLN:NE2	2.41	0.53
1:2A:271(R):G:H2'	1:2A:271(S):G:H8	1.73	0.53
1:2A:861:A:N3	2:2B:79:C:O2'	2.40	0.53
1:2A:1849:G:H2'	1:2A:1850:G:H8	1.73	0.53
32:2a:401:C:O2'	32:2a:621:A:N3	2.40	0.53
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.44	0.53
32:1a:1006:C:O5'	32:1a:1006:C:H6	1.92	0.53
36:1e:31:LEU:HD22	36:1e:43:LEU:HD11	1.91	0.53
1:2A:2406:U:C2	11:2P:72:PRO:HG2	2.44	0.53
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	1.90	0.53
6:2G:80:PHE:O	6:2G:82:LEU:N	2.41	0.53
12:2Q:52:VAL:HA	12:2Q:55:VAL:HG22	1.90	0.53
32:2a:17:U:H2'	32:2a:18:C:C6	2.43	0.53
33:2b:76:GLN:HG3	33:2b:206:ASP:O	2.08	0.53
34:2c:33:LEU:O	34:2c:37:GLN:HG2	2.08	0.53
1:1A:191:A:N1	57:1A:3933:HOH:O	2.34	0.53
1:1A:320:A:N3	5:1F:169:ASN:ND2	2.56	0.53
18:1W:86:LEU:HB2	18:1W:96:ILE:HG13	1.89	0.53
25:13:18:ASP:OD1	25:13:18:ASP:N	2.41	0.53
38:1g:51:GLN:O	38:1g:51:GLN:NE2	2.42	0.53
1:2A:271(A):A:N7	1:2A:271(W):G:N2	2.54	0.53
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.40	0.53
1:2A:541:C:O2	1:2A:552:G:N2	2.36	0.53
1:2A:910:A:C5	12:2Q:13:GLN:HG3	2.43	0.53
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.09	0.53
2:2B:37:C:O2	14:2S:95:HIS:NE2	2.41	0.53
10:2O:17:ARG:HE	10:2O:47:ILE:HG23	1.74	0.53
12:2Q:34:LEU:HB2	12:2Q:118:LEU:HD22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:684:A:H1'	42:2k:39:PRO:HD2	1.91	0.53
32:2a:1124:G:H4'	32:2a:1125:U:OP1	2.08	0.53
34:2c:156:ARG:NH2	34:2c:161:GLU:OE2	2.42	0.53
35:2d:59:ARG:HH11	35:2d:59:ARG:HA	1.73	0.53
36:2e:33:VAL:HG21	36:2e:109:ILE:HA	1.89	0.53
1:1A:2390:U:P	30:18:35:GLN:HE22	2.32	0.53
3:1D:175:LEU:HD12	3:1D:185:VAL:HG21	1.91	0.53
8:1I:72:LEU:C	8:1I:74:ASN:H	2.16	0.53
1:2A:586:A:N1	1:2A:809:G:O2'	2.36	0.53
1:2A:848:G:H2'	1:2A:849:A:C8	2.44	0.53
4:2E:14:ILE:HG13	4:2E:21:VAL:HG23	1.89	0.53
1:1A:1909:C:H2'	1:1A:1910:G:H8	1.73	0.53
6:1G:139:LEU:HD23	6:1G:144:ILE:HG22	1.90	0.53
32:1a:486:U:H2'	32:1a:487:A:H8	1.73	0.53
35:1d:11:LEU:HD23	35:1d:66:ARG:HB3	1.91	0.53
1:2A:775:G:N2	1:2A:793:A:O3'	2.41	0.53
1:2A:796:C:H2'	1:2A:797:C:C6	2.44	0.53
1:2A:1639:U:H2'	1:2A:1640:C:H5"	1.91	0.53
7:2H:3:ARG:NH1	7:2H:5:GLY:H	2.07	0.53
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.91	0.53
25:23:8:LEU:HD13	25:23:23:LEU:HD21	1.89	0.53
32:2a:890:G:O2'	32:2a:906:G:O6	2.25	0.53
32:2a:1131:G:H1	32:2a:1143:G:H21	1.56	0.53
32:2a:1347:G:C8	40:2i:107:ARG:HB3	2.44	0.53
35:2d:88:VAL:HG13	36:2e:97:GLY:HA2	1.91	0.53
40:2i:3:GLN:HE21	40:2i:18:PHE:HB3	1.73	0.53
40:2i:17:VAL:HG23	40:2i:63:ILE:HG12	1.91	0.53
47:2p:48:TRP:CD1	47:2p:48:TRP:H	2.27	0.53
48:2q:22:LEU:HD11	48:2q:39:SER:HB2	1.91	0.53
1:1A:587:C:OP1	11:1P:21:ARG:NH2	2.35	0.53
2:1B:41:U:H5	6:1G:70:VAL:H	1.57	0.53
25:13:10:LYS:HB3	25:13:53:LEU:HA	1.90	0.53
32:1a:60:A:N1	32:1a:107:G:O2'	2.32	0.53
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.91	0.53
32:2a:825:G:O2'	39:2h:12:ARG:NH2	2.42	0.53
1:1A:1412:A:H2'	1:1A:1413:G:C8	2.44	0.53
3:1D:72:LYS:HG3	3:1D:103:ARG:NH2	2.24	0.53
32:1a:606:G:N2	32:1a:631:G:N7	2.57	0.53
32:1a:971:G:H1	32:1a:1363(A):A:H5'	1.73	0.53
44:1m:54:VAL:HA	44:1m:57:ARG:HB3	1.89	0.53
1:2A:448:U:C4	1:2A:583:G:H1'	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:570:G:H2'	1:2A:2030:A:C6	2.44	0.53
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.91	0.53
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.25	0.53
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.91	0.53
30:28:6:THR:HG23	30:28:63:PRO:HD2	1.90	0.53
32:2a:501:C:H2'	32:2a:502:G:C8	2.43	0.53
32:2a:964:A:N3	32:2a:969:A:O2'	2.36	0.53
32:2a:1103:C:H4'	33:2b:98:LEU:HD13	1.90	0.53
40:2i:95:LYS:HA	40:2i:99:LEU:HD13	1.91	0.53
24:12:1:MET:SD	24:12:56:GLN:NE2	2.77	0.52
32:1a:994:A:N7	32:1a:1216:G:H4'	2.24	0.52
32:1a:1144:G:H21	32:1a:1146:A:H62	1.57	0.52
43:1l:71:PRO:O	43:1l:102:ARG:NH1	2.42	0.52
44:1m:49:THR:HB	44:1m:52:GLU:HG3	1.91	0.52
1:2A:335:C:H4'	20:2Y:73:ARG:HD2	1.89	0.52
1:2A:662:G:H5"	11:2P:16:ARG:HG2	1.91	0.52
1:2A:1592:C:H2'	1:2A:1593:G:C8	2.44	0.52
4:2E:134:ILE:HA	4:2E:137:HIS:CD2	2.44	0.52
34:2c:66:VAL:HG11	34:2c:91:LEU:HD21	1.90	0.52
1:1A:709:U:H2'	1:1A:710:G:H8	1.75	0.52
32:1a:70:G:H1	32:1a:99:U:H3	1.56	0.52
32:1a:279:A:C5	48:1q:98:LEU:HD23	2.45	0.52
1:2A:1105:U:H2'	1:2A:1106:G:H8	1.74	0.52
3:2D:70:TRP:CE2	3:2D:150:LYS:HD3	2.43	0.52
18:2W:80:PRO:O	18:2W:100:THR:HB	2.09	0.52
32:2a:537:G:OP2	57:2a:1803:HOH:O	2.18	0.52
32:2a:991:U:H4'	32:2a:992:U:O5'	2.10	0.52
32:2a:1050:G:H1	32:2a:1208:C:N4	2.07	0.52
32:2a:1237:C:O2'	32:2a:1300:G:N1	2.41	0.52
2:1B:27:C:H5"	14:1S:54:LEU:HD11	1.89	0.52
4:1E:78:LEU:O	4:1E:79:ARG:NH1	2.42	0.52
32:1a:244:U:O4'	32:1a:894:G:N2	2.42	0.52
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.44	0.52
1:2A:2635:C:O2'	4:2E:80:GLU:OE2	2.22	0.52
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.90	0.52
32:2a:933:G:O6	38:2g:3:ARG:NH2	2.42	0.52
1:1A:286:C:H2'	1:1A:287:C:H6	1.75	0.52
1:1A:378:C:N4	57:1A:3991:HOH:O	2.42	0.52
1:1A:1335:U:O4	57:1A:3829:HOH:O	2.15	0.52
1:1A:1789:A:H5"	3:1D:220:HIS:O	2.09	0.52
26:14:20:ASN:ND2	26:14:36:CYS:SG	2.82	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.91	0.52
32:1a:1347:G:N2	32:1a:1374:A:O5'	2.43	0.52
44:1m:73:GLU:HA	44:1m:76:ALA:HB3	1.91	0.52
1:2A:1016:G:H2'	1:2A:1017:G:H8	1.74	0.52
1:2A:1755:A:N6	1:2A:2694:G:O2'	2.42	0.52
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	1.90	0.52
19:2X:56:THR:HB	19:2X:77:LYS:HE2	1.92	0.52
23:21:77:ALA:HB1	23:21:82:LEU:HD11	1.91	0.52
32:2a:1124:G:N2	32:2a:1125:U:O4	2.43	0.52
1:1A:1862:G:H2'	1:1A:1863:G:H8	1.75	0.52
6:1G:121:ASN:ND2	6:1G:124:SER:OG	2.43	0.52
21:1Z:1:MET:N	21:1Z:135:GLU:OE2	2.42	0.52
32:1a:1047:G:H21	32:1a:1215:G:H5'	1.74	0.52
36:1e:59:GLY:O	36:1e:63:ARG:HG3	2.10	0.52
46:1o:64:ARG:NH1	46:1o:68:ARG:HH21	2.07	0.52
1:2A:827:U:O2'	1:2A:2068:U:C2	2.59	0.52
1:2A:1653:G:C6	13:2R:9:LYS:HB2	2.45	0.52
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.45	0.52
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.28	0.52
26:24:48:ARG:HG3	26:24:52:THR:HG23	1.90	0.52
36:2e:101:ILE:O	36:2e:120:THR:OG1	2.26	0.52
44:2m:87:TYR:HA	44:2m:90:LEU:HD12	1.91	0.52
1:1A:365:C:OP2	57:1A:3844:HOH:O	2.19	0.52
1:1A:1094:U:N3	1:1A:1097:U:OP2	2.35	0.52
4:1E:134:ILE:HA	4:1E:137:HIS:CD2	2.45	0.52
24:12:29:LYS:HG2	24:12:57:ILE:HD13	1.92	0.52
32:1a:749:C:H2'	32:1a:750:G:C8	2.42	0.52
38:1g:116:ALA:HA	38:1g:119:ARG:HB3	1.90	0.52
43:1l:117:ARG:NH1	57:1l:301:HOH:O	2.42	0.52
1:2A:2567:G:H2'	1:2A:2568:C:C6	2.45	0.52
11:2P:124:LYS:HE3	11:2P:146:VAL:HG21	1.90	0.52
17:2V:72:VAL:HG13	17:2V:85:LYS:HB3	1.91	0.52
32:2a:880:C:H5"	43:2l:12:ARG:HH12	1.74	0.52
1:1A:1385:G:O2'	1:1A:1396:U:O2	2.25	0.52
1:1A:1674:G:N2	1:1A:1677:A:N1	2.57	0.52
1:1A:2206:G:H5'	1:1A:2207:G:C5	2.44	0.52
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.21	0.52
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.45	0.52
42:1k:124:LYS:HE3	42:1k:125:PHE:CE2	2.45	0.52
1:2A:854:G:H2'	1:2A:855:G:C8	2.44	0.52
1:2A:1082:U:O4	1:2A:1086:A:N1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2115:G:H21	1:2A:2171:A:H61	1.57	0.52
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.90	0.52
32:2a:736:C:H2'	32:2a:737:A:H8	1.74	0.52
32:2a:985:C:H2'	32:2a:986:A:H8	1.74	0.52
50:2s:11:VAL:HB	50:2s:16:LEU:HD12	1.92	0.52
1:1A:2312:U:H5'	6:1G:88:ILE:HD11	1.91	0.52
1:1A:2364:C:H2'	1:1A:2365:G:O4'	2.09	0.52
4:1E:16:ARG:NH1	4:1E:171:GLU:OE2	2.42	0.52
4:1E:143:ASN:HB2	4:1E:147:PRO:HD2	1.92	0.52
26:14:24:THR:OG1	26:14:25:TYR:N	2.43	0.52
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.45	0.52
1:2A:2106:G:C5	1:2A:2107:C:H1'	2.43	0.52
1:2A:2330:G:O2'	22:20:41:ARG:O	2.24	0.52
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.91	0.52
32:2a:600:C:H2'	32:2a:601:C:C6	2.45	0.52
32:2a:1031:G:H2'	32:2a:1032:G:C8	2.45	0.52
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.24	0.52
49:2r:67:ALA:HA	49:2r:70:ILE:HD12	1.91	0.52
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.92	0.52
16:1U:10:ARG:NH1	57:1U:302:HOH:O	2.43	0.52
17:1V:14:VAL:HB	17:1V:96:ILE:HG13	1.91	0.52
18:1W:13:SER:HB3	18:1W:16:LYS:HD2	1.91	0.52
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.91	0.52
32:1a:395:C:H2'	32:1a:396:G:C8	2.45	0.52
38:1g:133:GLY:HA2	38:1g:136:LYS:HE2	1.91	0.52
41:1j:61:GLU:OE1	45:1n:45:ARG:NE	2.41	0.52
1:2A:1186:G:H2'	1:2A:1187:G:O4'	2.10	0.52
1:2A:1448:G:H5"	1:2A:1542:A:OP1	2.10	0.52
4:2E:38:THR:O	4:2E:42:ASP:N	2.40	0.52
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.42	0.52
15:2T:1:MET:HE2	15:2T:3:ARG:HG2	1.92	0.52
32:2a:35:G:H1	32:2a:549:C:H42	1.58	0.52
33:2b:193:ASP:HB3	33:2b:196:LEU:HB2	1.91	0.52
36:2e:31:LEU:HD11	36:2e:129:ILE:HA	1.92	0.52
50:2s:39:THR:HA	50:2s:70:LYS:HD3	1.91	0.52
1:1A:489:G:N7	18:1W:49:LYS:NZ	2.58	0.52
1:1A:635:C:O2'	1:1A:639:U:OP1	2.26	0.52
1:1A:639:U:H2'	1:1A:640:C:C6	2.45	0.52
1:1A:768:G:O2'	1:1A:1379:A:N1	2.39	0.52
1:1A:807:U:O2'	1:1A:2060:A:N1	2.42	0.52
3:1D:61:LEU:O	3:1D:63:ARG:NH1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:167:PRO:HG2	33:1b:188:ALA:HB2	1.92	0.52
1:2A:111:A:O3'	24:22:65:ASN:ND2	2.42	0.52
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.45	0.52
7:2H:137:ASP:HB3	7:2H:140:LYS:HB3	1.91	0.52
32:2a:501:C:H1'	32:2a:549:C:H1'	1.92	0.52
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.91	0.52
33:2b:187:LEU:HA	33:2b:201:ILE:HB	1.91	0.52
1:1A:200:U:O2	1:1A:386:G:N2	2.43	0.51
1:1A:279:C:N4	1:1A:361:G:H1	2.03	0.51
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.10	0.51
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.45	0.51
32:1a:575:G:O2'	32:1a:821:G:H5'	2.10	0.51
32:1a:659:U:H2'	32:1a:660:G:C8	2.45	0.51
32:1a:1095:U:P	32:1a:1108:G:H1	2.33	0.51
36:1e:11:ILE:HG21	36:1e:105:VAL:HG22	1.92	0.51
1:2A:300:A:H2'	1:2A:334:C:H1'	1.92	0.51
1:2A:455:C:N3	1:2A:472:A:H2'	2.25	0.51
1:2A:1491:G:H2'	1:2A:1492:G:C8	2.45	0.51
1:2A:1827:C:O2'	1:2A:1970:A:N3	2.38	0.51
24:22:7:ARG:HA	24:22:10:LEU:HD12	1.93	0.51
32:2a:1255:G:O2'	32:2a:1258:G:N3	2.32	0.51
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.45	0.51
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.25	0.51
33:2b:48:MET:O	33:2b:52:GLU:N	2.35	0.51
39:2h:64:LYS:HG2	39:2h:79:VAL:HG21	1.90	0.51
44:2m:97:PRO:HG3	44:2m:110:ARG:HG3	1.92	0.51
1:1A:271(T):C:H2'	1:1A:271(U):G:C8	2.45	0.51
1:1A:728:G:H5"	3:1D:13:ARG:HH21	1.76	0.51
1:1A:1176:G:H4'	1:1A:1177:A:OP1	2.09	0.51
1:1A:1296:G:OP1	1:1A:2709:G:O2'	2.15	0.51
4:1E:167:VAL:HG12	4:1E:170:LEU:HD11	1.93	0.51
34:1c:117:ALA:HB2	34:1c:200:ALA:HB2	1.92	0.51
39:1h:81:HIS:ND1	39:1h:138:TRP:OXT	2.42	0.51
1:2A:619:G:OP2	1:2A:620:G:N2	2.43	0.51
1:2A:2319:G:N2	14:2S:3:ARG:HD3	2.26	0.51
4:2E:54:GLN:OE1	4:2E:55:ASN:N	2.44	0.51
32:2a:781:A:O2'	32:2a:1522:U:O2	2.28	0.51
32:2a:1319:A:H61	32:2a:1361:G:N2	2.08	0.51
32:1a:778:G:H1'	42:1k:119:CYS:HB3	1.91	0.51
32:1a:991:U:H4'	32:1a:992:U:O5'	2.10	0.51
49:1r:76:LEU:HD23	49:1r:78:LEU:HD11	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:315:G:H2'	1:2A:316:C:C6	2.45	0.51
1:2A:2287:A:O2'	1:2A:2288:A:H3'	2.11	0.51
1:2A:2313:C:H5"	6:2G:91:ARG:HD3	1.93	0.51
8:2I:57:ARG:O	8:2I:61:ARG:HG2	2.11	0.51
34:2c:87:LEU:O	34:2c:91:LEU:N	2.42	0.51
36:2e:126:ARG:HA	36:2e:131:ILE:HD11	1.91	0.51
1:1A:459:U:H2'	1:1A:460:A:H8	1.74	0.51
1:1A:1292:U:H2'	1:1A:1293:C:C6	2.46	0.51
1:1A:1858:G:N2	1:1A:1883:G:H2'	2.25	0.51
1:1A:2054:A:C2	27:15:8:LYS:HG3	2.45	0.51
11:1P:49:ARG:NH1	30:18:4:MET:HE1	2.25	0.51
11:1P:49:ARG:HH12	30:18:4:MET:HE1	1.75	0.51
16:1U:47:TYR:HA	16:1U:50:ARG:HH11	1.75	0.51
16:1U:106:PHE:O	16:1U:110:VAL:HG23	2.11	0.51
32:1a:828:A:N6	32:1a:858:G:O2'	2.44	0.51
38:1g:36:LYS:HA	38:1g:39:ALA:HB3	1.93	0.51
39:1h:86:ILE:HG13	39:1h:133:LEU:HD22	1.93	0.51
45:1n:22:THR:O	45:1n:33:VAL:HG21	2.10	0.51
1:2A:900:A:H2'	1:2A:901:A:C8	2.46	0.51
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.09	0.51
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.20	0.51
1:2A:2821:A:H2'	1:2A:2822:G:C8	2.46	0.51
18:2W:11:ARG:HD3	18:2W:82:LEU:HD12	1.92	0.51
32:2a:1274:G:N2	32:2a:1275:A:H62	2.09	0.51
32:2a:1452:C:H4'	32:2a:1457:G:C8	2.46	0.51
33:2b:12:GLU:HA	33:2b:15:VAL:HG22	1.91	0.51
36:2e:12:LEU:HD12	36:2e:128:PRO:HB2	1.92	0.51
1:1A:2095:C:H42	1:1A:2194:G:H1	1.56	0.51
20:1Y:77:PRO:HD2	20:1Y:106:LEU:HD23	1.93	0.51
21:1Z:91:LEU:HD11	21:1Z:96:VAL:HG11	1.92	0.51
32:1a:652:U:O4	32:1a:752:G:O2'	2.23	0.51
32:1a:1001:A:H61	32:1a:1040:U:H3	1.58	0.51
32:1a:1279:A:N3	32:1a:1279:A:H2'	2.26	0.51
33:1b:24:TRP:CZ3	33:1b:26:PRO:HA	2.45	0.51
1:2A:361:G:O2'	1:2A:362:U:H5'	2.11	0.51
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.76	0.51
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.27	0.51
1:2A:2390:U:P	30:28:35:GLN:HE22	2.33	0.51
32:2a:1164:G:H1	32:2a:1172:C:H42	1.58	0.51
1:1A:271(H):G:H5'	23:11:81:LYS:HE2	1.92	0.51
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1842:G:O2'	3:1D:253:GLN:NE2	2.35	0.51
32:1a:736:C:H2'	32:1a:737:A:H8	1.75	0.51
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.46	0.51
34:1c:35:GLU:CD	34:1c:59:ARG:HH22	2.17	0.51
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.92	0.51
6:2G:122:PRO:HG3	6:2G:182:LYS:H	1.74	0.51
13:2R:79:LEU:HA	13:2R:83:ILE:HD12	1.92	0.51
32:2a:164:U:H2'	32:2a:165:C:C6	2.46	0.51
33:2b:16:HIS:CG	33:2b:17:PHE:N	2.78	0.51
33:2b:128:GLU:HG3	33:2b:135:GLN:NE2	2.26	0.51
36:2e:78:HIS:CE1	36:2e:143:ARG:H	2.28	0.51
45:2n:22:THR:HG21	45:2n:35:ARG:HG2	1.92	0.51
50:2s:23:ASN:HD21	50:2s:43:GLU:HB3	1.76	0.51
32:1a:600:C:H2'	32:1a:601:C:C6	2.45	0.51
32:1a:1030:C:N4	32:1a:1031:G:C6	2.71	0.51
32:1a:1125:U:H4'	41:1j:5:ARG:HH12	1.75	0.51
36:1e:101:ILE:O	36:1e:120:THR:OG1	2.26	0.51
42:1k:27:ASN:OD1	42:1k:28:THR:N	2.44	0.51
1:2A:1127:A:N7	1:2A:2488:A:O2'	2.43	0.51
1:2A:1999:C:O2	1:2A:2687:U:O2'	2.25	0.51
5:2F:46:ARG:HB3	5:2F:48:THR:HG23	1.92	0.51
6:2G:106:LEU:HD12	6:2G:110:ALA:HB3	1.92	0.51
21:2Z:152:ALA:HB1	21:2Z:163:LEU:HD21	1.93	0.51
32:2a:9:G:H2'	32:2a:10:A:C8	2.46	0.51
32:2a:1002:G:N2	32:2a:1038:C:N3	2.58	0.51
32:2a:1239:A:O2'	38:2g:114:ARG:O	2.25	0.51
1:1A:247:G:H4'	1:1A:386:G:C5	2.45	0.51
1:1A:1756:G:H4'	1:1A:1758:G:O4'	2.10	0.51
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.43	0.51
24:12:1:MET:HE3	24:12:6:VAL:HG22	1.93	0.51
27:15:8:LYS:O	27:15:9:LYS:HD2	2.11	0.51
32:1a:22:G:H2'	32:1a:23:C:C6	2.46	0.51
32:1a:235:C:H2'	32:1a:236:G:H8	1.75	0.51
32:1a:1131:G:H22	32:1a:1143:G:H21	1.58	0.51
48:1q:56:VAL:HB	48:1q:78:GLU:HB3	1.93	0.51
1:2A:557:U:H2'	1:2A:558:G:C8	2.46	0.51
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.46	0.51
1:2A:2293:C:H2'	1:2A:2294:C:C6	2.45	0.51
1:2A:2372:G:O2'	57:2A:3613:HOH:O	2.19	0.51
16:2U:89:GLU:HG3	17:2V:50:PRO:HB3	1.92	0.51
32:2a:619:U:N3	35:2d:134:ASP:OD1	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1123:A:H4'	41:2j:36:GLY:HA3	1.91	0.51
34:2c:19:GLU:O	34:2c:40:ARG:NH2	2.42	0.51
35:2d:163:GLU:HA	35:2d:166:LYS:HE2	1.92	0.51
37:2f:69:GLU:OE1	37:2f:69:GLU:N	2.33	0.51
1:1A:878:A:H2'	1:1A:879:G:H5'	1.93	0.51
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.46	0.51
32:1a:184:G:H2'	32:1a:185:A:C8	2.46	0.51
32:1a:1001:A:H2'	32:1a:1001(A):G:H8	1.74	0.51
1:2A:1159:U:H2'	1:2A:1160:G:H8	1.76	0.51
1:2A:2168:G:N1	1:2A:2171:A:OP2	2.44	0.51
1:2A:2640:G:H1	1:2A:2774:C:H42	1.59	0.51
32:2a:21:G:H2'	32:2a:22:G:C8	2.45	0.51
32:2a:297:G:H4'	32:2a:557:G:H4'	1.92	0.51
32:2a:689:C:OP1	42:2k:44:SER:OG	2.26	0.51
32:2a:718:G:H5'	42:2k:117:ASN:OD1	2.10	0.51
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.46	0.51
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.92	0.51
1:1A:64:A:O3'	19:1X:71:GLY:HA3	2.11	0.51
3:1D:108:PRO:HG3	3:1D:143:HIS:CE1	2.46	0.51
17:1V:5:VAL:HG11	17:1V:57:VAL:HG11	1.92	0.51
32:1a:833:U:H2'	32:1a:834:C:C6	2.46	0.51
38:1g:63:LYS:O	38:1g:67:GLU:HG2	2.10	0.51
39:1h:6:ILE:HB	39:1h:85:ARG:HH11	1.76	0.51
1:2A:83:G:H1	1:2A:102:G:HO2'	1.57	0.51
5:2F:185:ASP:OD1	5:2F:188:ARG:NH1	2.38	0.51
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.46	0.51
1:1A:242:G:O2'	1:1A:254:G:O6	2.23	0.50
1:1A:1092:C:H42	1:1A:1099:G:H1	1.58	0.50
1:1A:2139:C:N3	1:1A:2152:G:O6	2.44	0.50
13:1R:96:ARG:NH2	13:1R:118:GLU:OE2	2.44	0.50
35:1d:155:LEU:HD22	35:1d:158:ILE:HG23	1.93	0.50
1:2A:1339:G:H5"	19:2X:16:LYS:HD3	1.92	0.50
1:2A:1418:G:N7	57:2A:3661:HOH:O	2.34	0.50
1:2A:2114:A:H2'	1:2A:2115:G:H8	1.76	0.50
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.46	0.50
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.44	0.50
29:27:22:MET:HA	29:27:28:ARG:HG2	1.93	0.50
33:2b:189:ASP:HB3	33:2b:204:ASN:HA	1.93	0.50
1:1A:2303:G:O6	57:1A:3848:HOH:O	2.20	0.50
6:1G:16:ARG:NE	6:1G:31:VAL:HG21	2.26	0.50
10:1O:63:VAL:HG11	10:1O:85:VAL:HG23	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:701:C:OP1	32:1a:702:A:O2'	2.23	0.50
32:1a:939:G:H5'	38:1g:102:ARG:HH12	1.74	0.50
32:1a:998:G:H2'	32:1a:999:C:C6	2.46	0.50
42:1k:48:ILE:HG21	42:1k:63:LEU:HB3	1.93	0.50
47:1p:43:LYS:HG2	47:1p:48:TRP:CD2	2.47	0.50
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.11	0.50
1:2A:662:G:H2'	1:2A:663:G:H8	1.75	0.50
1:2A:774:A:H2'	1:2A:774:A:N3	2.26	0.50
1:2A:1065:U:H4'	1:2A:1066:U:H5'	1.92	0.50
32:2a:571:U:O4	32:2a:864:A:N6	2.43	0.50
32:2a:1226:C:H3'	44:2m:96:LEU:HD21	1.93	0.50
32:2a:1305:G:OP1	52:2u:2:GLY:N	2.44	0.50
32:2a:1442:G:O2'	32:2a:1442(A):G:O5'	2.28	0.50
34:2c:8:ILE:HG12	34:2c:184:TYR:HB3	1.91	0.50
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.92	0.50
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.47	0.50
1:1A:1937:A:N6	57:1A:3994:HOH:O	2.42	0.50
7:1H:40:GLU:CD	7:1H:60:ARG:HH12	2.19	0.50
32:1a:533:A:O2'	32:1a:535:A:OP2	2.26	0.50
32:1a:757:U:OP1	32:1a:822:C:O2'	2.26	0.50
32:1a:1138:G:C6	32:1a:1140:C:H1'	2.46	0.50
32:1a:1194:U:H5'	36:1e:22:GLY:O	2.11	0.50
32:1a:1205:U:H4'	34:1c:195:VAL:HG23	1.93	0.50
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.46	0.50
1:2A:234:C:H2'	1:2A:235:U:H6	1.76	0.50
1:2A:1063:G:O2'	1:2A:1064:C:H5'	2.11	0.50
2:2B:33:G:H5'	6:2G:2:PRO:HG3	1.93	0.50
9:2N:30:ILE:HG22	9:2N:34:LEU:HD22	1.93	0.50
17:2V:69:LYS:HA	17:2V:88:ARG:HG2	1.92	0.50
32:2a:167:G:H2'	32:2a:168:G:C8	2.47	0.50
32:2a:1202:G:O4'	45:2n:29:ARG:NH1	2.44	0.50
50:2s:36:ARG:HG2	50:2s:51:VAL:HG12	1.93	0.50
1:1A:910:A:C5	12:1Q:13:GLN:HG3	2.46	0.50
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.45	0.50
1:1A:1578:U:C2'	1:1A:1579:A:H5'	2.42	0.50
1:1A:2206:G:H5'	1:1A:2207:G:N7	2.27	0.50
23:11:5:CYS:SG	23:11:8:SER:OG	2.67	0.50
25:13:29:ARG:HG3	25:13:30:ARG:HG3	1.94	0.50
32:1a:69:G:H2'	32:1a:70:G:H8	1.77	0.50
32:1a:1014:A:N3	32:1a:1219:U:H1'	2.27	0.50
57:1a:3214:HOH:O	46:1o:17:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.77	0.50
1:2A:1709:U:H2'	1:2A:1710:C:C6	2.46	0.50
1:2A:2728:U:H2'	1:2A:2729:G:C8	2.47	0.50
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.92	0.50
1:1A:1278:A:OP1	13:1R:36:THR:HG23	2.12	0.50
1:1A:2294:C:P	14:1S:89:ARG:HH22	2.35	0.50
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.93	0.50
8:1I:38:LEU:HB3	8:1I:40:THR:HG23	1.93	0.50
32:1a:175:C:H2'	32:1a:176:C:C6	2.47	0.50
44:1m:85:GLY:HA2	44:1m:93:ARG:HH22	1.75	0.50
49:1r:47:THR:HG23	49:1r:49:LYS:HG3	1.94	0.50
1:2A:1075:C:H4'	12:2Q:59:ARG:NH1	2.26	0.50
1:2A:1076:C:H4'	1:2A:1077:A:OP1	2.12	0.50
1:2A:1420:U:HO2'	1:2A:1421:G:P	2.35	0.50
1:2A:2393:A:H5"	11:2P:63:PRO:HB3	1.94	0.50
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.58	0.50
6:2G:15:VAL:HG13	6:2G:175:LEU:HB3	1.92	0.50
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.94	0.50
1:1A:265:A:N1	1:1A:427:U:O2'	2.37	0.50
1:1A:2123:G:C2	1:1A:2124:G:H1'	2.47	0.50
1:1A:2815:C:H5'	27:15:29:THR:HG21	1.94	0.50
32:1a:444:C:H2'	32:1a:445:G:H8	1.77	0.50
32:1a:1244:C:H2'	32:1a:1245:A:C8	2.46	0.50
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.47	0.50
42:1k:34:ASP:OD1	42:1k:38:ASN:N	2.44	0.50
43:1l:113:ARG:NH2	43:1l:115:LYS:O	2.44	0.50
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.46	0.50
32:2a:794:A:O2'	32:2a:1521:G:O3'	2.30	0.50
32:2a:837:G:H1	32:2a:849:C:H42	1.57	0.50
1:1A:2751:G:C4	7:1H:2:SER:HA	2.47	0.50
27:15:34:PRO:O	27:15:37:LYS:NZ	2.41	0.50
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.47	0.50
32:1a:1250:A:H2'	32:1a:1251:A:O4'	2.11	0.50
32:1a:1302:U:C6	44:1m:17:VAL:HG11	2.47	0.50
1:2A:521:G:H2'	1:2A:522:G:H8	1.76	0.50
1:2A:574:C:N3	4:2E:145:LYS:NZ	2.41	0.50
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.09	0.50
32:2a:390:C:H2'	32:2a:391:G:C8	2.47	0.50
32:2a:826:C:H4'	39:2h:12:ARG:HG3	1.92	0.50
32:2a:1233:G:H2'	32:2a:1234:C:C6	2.47	0.50
51:2t:33:ILE:O	51:2t:37:SER:OG	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:143:ASN:HD22	4:1E:147:PRO:CD	2.25	0.50
9:1N:62:VAL:HG13	9:1N:66:LYS:HD2	1.92	0.50
14:1S:10:ARG:HH21	14:1S:91:PRO:HB2	1.77	0.50
16:1U:101:ARG:NH2	57:1U:301:HOH:O	2.33	0.50
29:17:26:GLY:O	29:17:30:VAL:HG23	2.12	0.50
32:1a:77:G:N2	32:1a:92:C:N3	2.55	0.50
33:1b:21:ARG:HB3	33:1b:39:ILE:HD13	1.94	0.50
33:1b:87:ARG:NH2	33:1b:220:ASP:OD1	2.34	0.50
36:1e:100:VAL:HA	36:1e:118:ILE:HG22	1.94	0.50
39:1h:44:PHE:HB3	39:1h:80:ILE:HD11	1.93	0.50
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.92	0.50
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.47	0.50
32:2a:1128:C:O2'	32:2a:1148:U:N3	2.44	0.50
1:1A:2135:A:H62	1:1A:2156:G:H21	1.60	0.50
1:1A:2741:A:OP1	31:19:22:ARG:NH1	2.42	0.50
6:1G:77:ILE:HB	6:1G:82:LEU:HD12	1.93	0.50
6:1G:106:LEU:HD12	6:1G:110:ALA:HB3	1.94	0.50
32:1a:112:G:H1	32:1a:315:A:H61	1.58	0.50
32:1a:840:C:H5'	32:1a:840:C:H6	1.77	0.50
32:1a:1048:G:H2'	32:1a:1050:G:H8	1.77	0.50
33:1b:19:HIS:CE1	33:1b:20:GLU:HG3	2.47	0.50
33:1b:155:LEU:HD11	33:1b:159:PRO:HG3	1.93	0.50
38:1g:109:ASN:HA	38:1g:119:ARG:HD3	1.92	0.50
50:1s:3:ARG:NH1	50:1s:10:PHE:HB2	2.27	0.50
1:2A:362:U:O2'	1:2A:363:G:H5'	2.12	0.50
1:2A:1246:A:OP1	5:2F:38:ARG:NH1	2.41	0.50
1:2A:2547:U:H2'	1:2A:2548:G:H8	1.77	0.50
2:2B:48:A:H2'	2:2B:49:C:C6	2.46	0.50
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.44	0.50
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.41	0.50
32:2a:559:A:OP1	36:2e:126:ARG:NH2	2.41	0.50
42:2k:80:VAL:HG22	42:2k:103:LEU:HB3	1.94	0.50
1:1A:272(B):G:H2'	1:1A:272(C):G:C8	2.47	0.49
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.46	0.49
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.46	0.49
1:1A:2144:U:H2'	1:1A:2147:G:H1	1.77	0.49
1:1A:2552:2MU:O5'	1:1A:2552:2MU:H6	2.12	0.49
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.46	0.49
32:1a:542:G:H5'	35:1d:41:GLY:HA3	1.94	0.49
33:1b:217:ARG:HA	33:1b:220:ASP:HB2	1.94	0.49
38:1g:119:ARG:NH2	57:1g:5001:HOH:O	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:84:A:H5'	20:2Y:8:LYS:HB3	1.93	0.49
1:2A:2184:G:N1	1:2A:2185:C:O2	2.44	0.49
1:2A:2189:U:H2'	1:2A:2190:G:H8	1.76	0.49
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.45	0.49
29:27:26:GLY:O	29:27:30:VAL:HG23	2.12	0.49
32:2a:1067:A:O2'	32:2a:1068:G:OP2	2.30	0.49
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.27	0.49
32:1a:410:G:OP1	35:1d:30:LYS:NZ	2.45	0.49
33:1b:55:PHE:HD1	33:1b:58:ILE:HD12	1.77	0.49
1:2A:747:U:O2	1:2A:2014:A:H1'	2.12	0.49
1:2A:795:C:H2'	1:2A:796:C:H6	1.77	0.49
1:2A:1791:A:N6	1:2A:1828:G:O2'	2.45	0.49
1:2A:2066:C:OP1	57:2A:3615:HOH:O	2.20	0.49
1:2A:2189:U:H2'	1:2A:2190:G:C8	2.47	0.49
1:2A:2375:G:O2'	1:2A:2377:A:N7	2.40	0.49
1:2A:2461:C:H2'	1:2A:2462:U:C6	2.46	0.49
1:2A:2552:2MU:OP2	57:2A:3612:HOH:O	2.19	0.49
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.94	0.49
10:2O:88:ASN:HD21	10:2O:92:GLU:HB2	1.76	0.49
30:28:26:LYS:HD2	30:28:48:PHE:CD2	2.47	0.49
44:2m:95:GLY:O	44:2m:110:ARG:HB3	2.12	0.49
48:2q:59:ILE:HG22	48:2q:73:VAL:HA	1.94	0.49
1:1A:1268:A:H2'	1:1A:1269:A:O4'	2.12	0.49
1:1A:1790:C:H5"	1:1A:1791:A:OP1	2.13	0.49
1:1A:2250:G:N7	57:1A:3927:HOH:O	2.33	0.49
1:1A:2882:A:H5'	13:1R:96:ARG:HB2	1.94	0.49
2:1B:41:U:O3'	26:14:2:LYS:NZ	2.45	0.49
4:1E:54:GLN:HB2	4:1E:76:ARG:HG2	1.94	0.49
7:1H:7:LEU:HD12	7:1H:8:PRO:HD2	1.94	0.49
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.94	0.49
32:1a:240:C:H2'	32:1a:241:C:C6	2.47	0.49
32:1a:1010:G:H2'	32:1a:1011:G:C8	2.47	0.49
37:1f:37:VAL:HA	37:1f:65:VAL:HG12	1.94	0.49
48:1q:45:HIS:CD2	48:1q:47:PRO:HG3	2.48	0.49
1:2A:55:G:O2'	1:2A:127:A:N1	2.43	0.49
1:2A:483:A:O2'	20:2Y:49:VAL:O	2.27	0.49
1:2A:1278:A:OP1	13:2R:36:THR:HG23	2.13	0.49
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.47	0.49
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.12	0.49
12:2Q:35:VAL:HG13	12:2Q:130:LYS:HB3	1.93	0.49
16:2U:50:ARG:HG2	16:2U:53:ARG:NH2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:14:LYS:O	51:2t:18:GLN:HG3	2.13	0.49
1:1A:764:A:H5'	3:1D:210:GLY:HA2	1.95	0.49
1:1A:795:C:H2'	1:1A:796:C:H6	1.77	0.49
32:1a:782:A:OP1	57:1a:3202:HOH:O	2.19	0.49
32:1a:949:A:N6	32:1a:1232:U:H3	2.08	0.49
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.47	0.49
34:1c:6:HIS:CD2	45:1n:49:HIS:HB3	2.47	0.49
38:1g:153:HIS:HE1	42:1k:57:THR:HB	1.77	0.49
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.28	0.49
41:1j:78:ASN:O	41:1j:80:LYS:N	2.45	0.49
42:1k:82:VAL:HB	42:1k:108:ILE:HG12	1.95	0.49
1:2A:271(L):U:H5"	8:2I:50:ARG:HH12	1.77	0.49
1:2A:1210:A:H5"	1:2A:1212:G:O4'	2.13	0.49
4:2E:143:ASN:HD22	4:2E:147:PRO:HD2	1.78	0.49
8:2I:27:ARG:HD2	23:21:71:TYR:CE2	2.48	0.49
32:2a:349:A:H2'	32:2a:350:G:H5"	1.95	0.49
32:2a:620:C:C2	35:2d:135:LEU:HG	2.47	0.49
32:2a:677:U:H3	32:2a:713:G:N2	2.08	0.49
32:2a:1030(A):G:H1'	32:2a:1030(C):G:C5	2.48	0.49
47:2p:52:ASP:OD1	47:2p:54:GLU:HG2	2.12	0.49
1:1A:389:G:O6	11:1P:70:GLN:HB3	2.12	0.49
1:1A:1352:U:OP1	57:1A:3845:HOH:O	2.19	0.49
1:1A:1448:G:O2'	1:1A:1528(A):A:N1	2.35	0.49
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.27	0.49
9:1N:17:ASP:O	9:1N:21:LYS:HE2	2.13	0.49
21:1Z:102:LEU:HD11	21:1Z:124:ILE:HB	1.94	0.49
32:1a:659:U:H2'	32:1a:660:G:H8	1.76	0.49
33:1b:88:ALA:HB2	33:1b:219:VAL:HG13	1.95	0.49
33:1b:212:GLN:O	33:1b:216:SER:OG	2.24	0.49
38:1g:48:LYS:O	38:1g:52:GLU:HG2	2.13	0.49
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.48	0.49
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.47	0.49
1:2A:2602:A:H4'	1:2A:2603:G:OP1	2.11	0.49
24:22:19:VAL:HG12	24:22:23:LYS:HE3	1.94	0.49
32:2a:167:G:H2'	32:2a:168:G:H8	1.77	0.49
34:2c:19:GLU:HB3	34:2c:40:ARG:HH12	1.77	0.49
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.85	0.49
1:1A:272(I):U:H2'	1:1A:272(J):C:H6	1.77	0.49
1:1A:2378:A:H2'	14:1S:21:THR:HG21	1.95	0.49
5:1F:40:GLN:HE22	5:1F:182:ASN:HB2	1.76	0.49
32:1a:545:C:H5'	35:1d:72:GLU:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:911:U:OP2	43:1l:97:ARG:NH2	2.27	0.49
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.44	0.49
51:1t:65:LYS:HA	51:1t:68:LYS:HD3	1.93	0.49
1:2A:26:G:H1'	1:2A:515:A:H61	1.77	0.49
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.43	0.49
6:2G:75:LYS:HA	6:2G:84:LYS:HG3	1.95	0.49
32:2a:328:C:H4'	32:2a:329:A:H5'	1.93	0.49
32:2a:1157:A:H61	32:2a:1178:G:H21	1.61	0.49
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	1.95	0.49
43:2l:57:LYS:HA	43:2l:67:THR:HA	1.94	0.49
1:1A:1028:A:N6	1:1A:1125:G:H2'	2.27	0.49
1:1A:1064:C:H3'	1:1A:1065:U:C5'	2.42	0.49
1:1A:1094:U:H1'	1:1A:1097:U:H5	1.77	0.49
32:1a:333:G:H4'	51:1t:16:HIS:CE1	2.47	0.49
32:1a:1016:A:C5	32:1a:1017:G:H1'	2.47	0.49
1:2A:900:A:H2'	1:2A:901:A:H8	1.76	0.49
1:2A:1266:G:O2'	1:2A:2012:G:O6	2.30	0.49
1:2A:1446:C:H42	1:2A:1465:G:H1	1.61	0.49
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.28	0.49
32:2a:6:G:C4	36:2e:119:LEU:HD11	2.48	0.49
32:2a:286:G:O6	57:2a:1804:HOH:O	2.20	0.49
32:2a:971:G:H1	32:2a:1363(A):A:H5'	1.77	0.49
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.12	0.49
32:2a:1090:U:H2'	32:2a:1091:U:H6	1.77	0.49
32:2a:1129:C:N4	32:2a:1143:G:N1	2.49	0.49
34:2c:6:HIS:CD2	45:2n:49:HIS:HB3	2.48	0.49
35:2d:173:TRP:CG	35:2d:189:PRO:HG3	2.48	0.49
36:2e:79:GLU:OE1	36:2e:79:GLU:N	2.39	0.49
1:1A:2001:A:H2'	1:1A:2002:G:C8	2.48	0.49
1:1A:2588:G:OP1	57:1A:3850:HOH:O	2.20	0.49
8:1I:65:ALA:HB1	8:1I:136:VAL:HG11	1.95	0.49
15:1T:26:ASP:OD1	15:1T:120:ARG:NH2	2.36	0.49
32:1a:664:G:N2	32:1a:741:G:H1	2.04	0.49
32:1a:1343:G:O2'	40:1i:121:ARG:HD2	2.13	0.49
32:1a:1347:G:H22	32:1a:1374:A:P	2.35	0.49
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.48	0.49
32:2a:262:A:H2'	32:2a:263:A:C8	2.47	0.49
32:2a:277:C:H2'	32:2a:278:G:H8	1.77	0.49
32:2a:636:U:H2'	32:2a:637:G:H8	1.78	0.49
32:2a:1073:U:H2'	32:2a:1074:G:C8	2.48	0.49
32:2a:1309:G:O2'	44:2m:77:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:857:C:H4'	22:10:23:VAL:HG21	1.95	0.49
1:1A:1297:C:O2'	1:1A:1302:A:N1	2.39	0.49
1:1A:1634:A:OP2	57:1A:3849:HOH:O	2.20	0.49
1:1A:2245:U:O2'	1:1A:2436:G:OP2	2.29	0.49
3:1D:41:GLY:O	3:1D:43:ARG:NH1	2.45	0.49
38:1g:79:ARG:HA	38:1g:84:ASN:HA	1.95	0.49
49:1r:56:THR:OG1	49:1r:57:GLY:N	2.45	0.49
1:2A:531:C:H4'	1:2A:532:A:H5"	1.94	0.49
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.42	0.49
8:2I:50:ARG:O	8:2I:54:GLN:HG2	2.13	0.49
12:2Q:17:LEU:HD21	12:2Q:41:TRP:HE1	1.78	0.49
21:2Z:132:ASN:HD22	21:2Z:160:GLY:HA3	1.77	0.49
32:2a:69:G:H2'	32:2a:70:G:H8	1.76	0.49
32:2a:1228:C:P	44:2m:108:ARG:HH12	2.36	0.49
33:2b:180:LEU:HB2	33:2b:182:ILE:HG13	1.95	0.49
45:2n:9:LYS:HA	45:2n:12:ARG:HG2	1.95	0.49
1:1A:1045:A:H5'	1:1A:1046:A:H5"	1.95	0.49
1:1A:1795:C:O2'	1:1A:1901:A:OP1	2.20	0.49
1:1A:1814:G:O6	57:1A:3847:HOH:O	2.19	0.49
1:1A:2159:G:H2'	1:1A:2160:G:H8	1.77	0.49
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.28	0.49
32:1a:741:G:H5"	46:1o:59:MET:HE1	1.95	0.49
32:1a:1117:G:H4'	40:1i:104:ARG:HH12	1.78	0.49
32:1a:1228:C:N4	44:1m:104:ARG:O	2.42	0.49
33:1b:150:SER:OG	33:1b:151:GLY:N	2.44	0.49
38:1g:90:GLU:CD	38:1g:90:GLU:H	2.21	0.49
42:1k:18:ARG:HA	42:1k:81:ASP:H	1.78	0.49
1:2A:79:G:H2'	1:2A:80:G:H8	1.77	0.49
1:2A:200:U:O2	1:2A:386:G:N2	2.46	0.49
1:2A:459:U:H5"	29:27:40:TRP:CD2	2.48	0.49
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.48	0.49
5:2F:31:HIS:NE2	5:2F:35:GLU:OE2	2.44	0.49
12:2Q:68:ILE:HG22	12:2Q:101:ARG:HE	1.78	0.49
21:2Z:40:ASP:HB3	21:2Z:43:GLU:HB2	1.95	0.49
32:2a:34:C:N3	32:2a:550:G:N2	2.41	0.49
32:2a:67:C:H2'	32:2a:68:G:C8	2.48	0.49
32:2a:614:A:H2'	32:2a:615:C:C6	2.48	0.49
32:2a:737:A:H2'	32:2a:738:C:C6	2.48	0.49
32:2a:753:A:OP1	46:2o:69:TYR:OH	2.24	0.49
32:2a:1151:A:H5"	41:2j:41:PRO:HA	1.94	0.49
32:2a:1187:G:N3	45:2n:60:SER:OG	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:45:LEU:HD12	37:2f:59:TYR:HD1	1.78	0.49
38:2g:113:GLU:HG2	38:2g:119:ARG:HG2	1.95	0.49
41:2j:9:ARG:HG2	41:2j:69:ASN:ND2	2.27	0.49
1:1A:330:A:H2	1:1A:1210:A:O2'	1.96	0.48
1:1A:674:G:O2'	5:1F:74:ARG:HD3	2.13	0.48
1:1A:854:G:H1	1:1A:923:C:H42	1.61	0.48
1:1A:1675:C:H2'	1:1A:1676:A:O4'	2.13	0.48
1:1A:2313:C:H4'	6:1G:91:ARG:HD3	1.95	0.48
3:1D:66:ASP:HB2	3:1D:103:ARG:HD2	1.95	0.48
8:1I:77:LEU:HD21	8:1I:100:ALA:HB3	1.95	0.48
10:1O:107:ARG:NH2	32:1a:346:G:OP2	2.46	0.48
11:1P:63:PRO:HB2	30:18:30:ARG:HH21	1.78	0.48
21:1Z:125:LEU:HG	21:1Z:164:ALA:HB3	1.95	0.48
32:1a:328:C:H4'	32:1a:329:A:H5'	1.94	0.48
32:1a:1380:U:C4	38:1g:3:ARG:HG2	2.48	0.48
38:1g:15:ASP:OD1	38:1g:19:GLY:N	2.46	0.48
44:1m:16:ASP:OD1	44:1m:16:ASP:N	2.46	0.48
1:2A:336:C:HO2'	20:2Y:35:TYR:HH	1.60	0.48
1:2A:807:U:OP2	11:2P:41:ARG:NH2	2.46	0.48
1:2A:2104:G:N2	1:2A:2105:C:C2	2.81	0.48
1:2A:2299:G:N1	1:2A:2318:G:N7	2.61	0.48
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.13	0.48
45:2n:24:CYS:HB3	45:2n:29:ARG:H	1.77	0.48
47:2p:75:ARG:HE	47:2p:80:PHE:HD2	1.61	0.48
1:1A:571:A:O2'	17:1V:78:LYS:HE2	2.13	0.48
1:1A:861:A:N3	2:1B:79:C:O2'	2.46	0.48
1:1A:2314:C:H2'	1:1A:2315:G:C8	2.48	0.48
1:1A:2734:A:H2'	1:1A:2735:G:O4'	2.13	0.48
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.12	0.48
32:1a:201:C:H42	32:1a:216:G:H1	1.60	0.48
32:1a:277:C:H2'	32:1a:278:G:H8	1.77	0.48
32:1a:401:C:H2'	32:1a:402:G:H8	1.77	0.48
32:1a:1028:C:N3	32:1a:1033:G:N2	2.58	0.48
43:1l:53:ARG:HG3	43:1l:93:LEU:HD21	1.94	0.48
52:1u:14:TRP:HE3	52:1u:15:ARG:HD3	1.77	0.48
1:2A:1105:U:H2'	1:2A:1106:G:C8	2.48	0.48
1:2A:1825:A:H2'	1:2A:1826:G:C8	2.49	0.48
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.78	0.48
1:2A:2266:A:H5'	1:2A:2267:A:C8	2.48	0.48
32:2a:60:A:N1	32:2a:107:G:O2'	2.36	0.48
32:2a:256:U:H2'	32:2a:257:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1404:5MC:O2	32:2a:1519:MA6:O2'	2.29	0.48
1:1A:322:A:OP2	5:1F:169:ASN:HB2	2.14	0.48
1:1A:1543:C:H5"	57:1A:4485:HOH:O	2.13	0.48
1:1A:2115:G:N3	1:1A:2117:A:N6	2.52	0.48
2:1B:45:A:OP2	6:1G:96:ARG:NH2	2.47	0.48
9:1N:46:VAL:HG23	9:1N:48:MET:HB2	1.95	0.48
32:1a:79:G:C6	32:1a:90:U:N3	2.81	0.48
32:1a:255:G:H1'	48:1q:16:GLN:HE21	1.78	0.48
32:1a:376:G:H5"	47:1p:5:ARG:HD2	1.95	0.48
32:1a:1030(C):G:H2'	32:1a:1030(D):A:C8	2.43	0.48
1:2A:107:C:H2'	1:2A:108:U:H6	1.77	0.48
1:2A:1059:G:N1	1:2A:1079:C:C4	2.81	0.48
32:2a:837:G:H2'	32:2a:838:G:H8	1.78	0.48
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.47	0.48
40:2i:16:ARG:HB2	40:2i:64:THR:HB	1.95	0.48
1:1A:1819:A:H5"	3:1D:161:THR:HG21	1.95	0.48
1:1A:2506:U:O2	54:1A:3749:HGR:H23	2.14	0.48
6:1G:80:PHE:HB2	6:1G:82:LEU:HG	1.96	0.48
21:1Z:40:ASP:HB3	21:1Z:43:GLU:HB2	1.94	0.48
32:1a:405:U:OP1	32:1a:406:G:O2'	2.25	0.48
32:1a:642:A:N3	39:1h:113:SER:OG	2.40	0.48
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.49	0.48
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.48	0.48
40:1i:13:ALA:HB2	40:1i:68:GLY:HA3	1.95	0.48
1:2A:1058:G:H1	1:2A:1079:C:N4	2.11	0.48
1:2A:1363:C:O2'	1:2A:1809:A:N3	2.41	0.48
1:2A:2127:G:O6	1:2A:2161:C:N3	2.47	0.48
1:2A:2641:G:P	9:2N:74:ARG:HH22	2.36	0.48
18:2W:46:PHE:O	18:2W:50:VAL:HG23	2.13	0.48
20:2Y:68:HIS:HB3	20:2Y:71:LYS:HG3	1.95	0.48
32:2a:557:G:OP2	57:2a:1806:HOH:O	2.20	0.48
33:2b:53:ARG:O	33:2b:55:PHE:N	2.46	0.48
1:1A:566:U:H5"	11:1P:29:LYS:HE3	1.94	0.48
1:1A:1411:C:H2'	1:1A:1412:A:C8	2.49	0.48
1:1A:1756:G:O6	57:1A:3842:HOH:O	2.18	0.48
32:1a:1201:A:H4'	32:1a:1202:G:O5'	2.13	0.48
32:1a:1304:G:N2	32:1a:1332:A:N7	2.61	0.48
32:1a:1326:C:H5"	52:1u:18:TYR:O	2.13	0.48
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.82	0.48
40:1i:8:GLY:HA2	40:1i:79:LEU:HD23	1.95	0.48
43:1l:24:VAL:HB	43:1l:27:LEU:HD22	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:49:C:H2'	2:2B:50:G:C8	2.48	0.48
14:2S:100:ALA:O	14:2S:104:GLY:N	2.42	0.48
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.49	0.48
32:2a:539:A:H2'	32:2a:540:G:C8	2.48	0.48
32:2a:950:U:H2'	32:2a:951:G:C8	2.48	0.48
41:2j:7:LYS:O	41:2j:97:GLU:HB2	2.14	0.48
1:1A:2138:C:N3	1:1A:2153:G:O6	2.46	0.48
10:1O:17:ARG:HE	10:1O:47:ILE:HG23	1.78	0.48
33:1b:115:LEU:HD13	33:1b:145:LEU:HB3	1.95	0.48
36:1e:143:ARG:NH1	39:1h:77:GLU:OE1	2.47	0.48
41:1j:49:VAL:HG23	45:1n:41:ARG:HB2	1.94	0.48
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.13	0.48
1:2A:2115:G:N2	1:2A:2171:A:H61	2.11	0.48
1:2A:2306:C:OP2	1:2A:2307:G:O2'	2.30	0.48
1:2A:2316:C:H2'	1:2A:2317:C:C6	2.49	0.48
1:2A:2787:C:H1'	4:2E:62:PRO:HG3	1.94	0.48
32:2a:165:C:H2'	32:2a:166:G:C8	2.48	0.48
32:2a:1356:G:H2'	32:2a:1357:A:C8	2.48	0.48
1:1A:2832:U:OP2	57:1A:3852:HOH:O	2.20	0.48
2:1B:90:A:C5	2:1B:91:C:H1'	2.48	0.48
4:1E:48:GLN:HE21	4:1E:78:LEU:HG	1.79	0.48
6:1G:46:ALA:HB1	6:1G:50:ALA:O	2.13	0.48
7:1H:30:LYS:NZ	7:1H:81:GLU:O	2.47	0.48
32:1a:721:G:H4'	32:1a:722:A:O4'	2.14	0.48
32:1a:1001:A:H2'	32:1a:1001(A):G:C8	2.49	0.48
33:1b:142:LEU:O	33:1b:146:GLN:HG3	2.14	0.48
33:1b:222:ILE:HG22	33:1b:226:ARG:HD3	1.96	0.48
35:1d:59:ARG:HA	35:1d:59:ARG:HH11	1.77	0.48
44:1m:88:ARG:NH2	57:1m:5001:HOH:O	2.46	0.48
1:2A:740:U:H2'	1:2A:741:G:C8	2.48	0.48
1:2A:2245:U:O2'	1:2A:2436:G:OP2	2.20	0.48
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.14	0.48
6:2G:43:LEU:HB3	6:2G:44:GLY:H	1.47	0.48
18:2W:60:ASN:HD22	18:2W:60:ASN:N	2.12	0.48
35:2d:15:GLU:HB3	35:2d:63:LYS:HE2	1.96	0.48
36:2e:78:HIS:HE1	36:2e:143:ARG:H	1.59	0.48
44:2m:107:ALA:HB3	44:2m:111:LYS:HE3	1.96	0.48
49:2r:47:THR:HG23	49:2r:49:LYS:HG3	1.96	0.48
1:1A:26:G:C6	1:1A:27:G:N1	2.82	0.48
1:1A:971:C:H2'	1:1A:972:G:O4'	2.12	0.48
32:1a:58:C:H2'	32:1a:59:A:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:473:G:H2'	32:1a:474:G:C8	2.49	0.48
32:1a:1277:C:H2'	32:1a:1279:A:H8	1.79	0.48
32:1a:1305:G:OP1	52:1u:2:GLY:N	2.47	0.48
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.48	0.48
6:2G:139:LEU:HA	6:2G:144:ILE:HB	1.96	0.48
21:2Z:7:ALA:O	21:2Z:62:PRO:HD3	2.14	0.48
22:20:32:ARG:H	22:20:35:ASN:ND2	2.12	0.48
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.14	0.48
50:2s:23:ASN:ND2	50:2s:43:GLU:HB3	2.28	0.48
4:1E:73:GLU:H	4:1E:73:GLU:CD	2.22	0.48
5:1F:65:TRP:CZ2	5:1F:75:HIS:HD2	2.31	0.48
6:1G:136:ARG:HG3	6:1G:137:GLU:HG3	1.96	0.48
32:1a:339:C:H2'	32:1a:340:U:C6	2.49	0.48
32:1a:1250:A:O3'	40:1i:67:GLY:HA2	2.13	0.48
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.95	0.48
39:1h:112:LEU:HD23	39:1h:133:LEU:HA	1.95	0.48
39:1h:121:ASP:OD1	39:1h:121:ASP:N	2.44	0.48
44:1m:91:ARG:HB2	44:1m:98:VAL:HG13	1.96	0.48
46:1o:25:THR:HG21	46:1o:70:LEU:HB2	1.96	0.48
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.54	0.48
1:2A:2845:G:H5"	15:2T:54:ARG:O	2.13	0.48
32:2a:193:C:H2'	32:2a:194:C:C6	2.48	0.48
49:2r:58:LEU:HB3	49:2r:62:GLU:HB2	1.96	0.48
1:1A:1045:A:H1'	1:1A:1047:G:N3	2.29	0.48
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.14	0.48
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.29	0.48
4:1E:143:ASN:HD22	4:1E:147:PRO:HD2	1.78	0.48
5:1F:13:SER:OG	5:1F:127:GLU:OE2	2.27	0.48
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.61	0.48
32:1a:235:C:H2'	32:1a:236:G:C8	2.48	0.48
32:1a:579:G:H4'	46:1o:54:ARG:HH21	1.78	0.48
35:1d:111:ALA:HB2	35:1d:120:LEU:HD12	1.96	0.48
1:2A:1336:A:H2'	1:2A:1337:G:C8	2.49	0.48
1:2A:1827:C:OP2	3:2D:222:ARG:NH1	2.47	0.48
1:2A:1833:U:H2'	1:2A:1834:U:H6	1.78	0.48
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.44	0.48
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.96	0.48
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.28	0.48
32:2a:1001:A:H2'	32:2a:1001(A):G:C8	2.49	0.48
32:2a:1307:U:H3	32:2a:1330:U:H3	1.62	0.48
1:1A:573:G:O2'	1:1A:574:C:H3'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:792:G:O2'	1:1A:2440:C:N3	2.41	0.47
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.96	0.47
32:1a:560:U:H4'	32:1a:561:U:O5'	2.13	0.47
32:1a:985:C:H2'	32:1a:986:A:H8	1.79	0.47
32:1a:1106:G:H5"	34:1c:172:ARG:HG2	1.96	0.47
32:1a:1111:A:N1	34:1c:177:THR:OG1	2.40	0.47
32:1a:1316:G:N7	50:1s:7:LYS:NZ	2.62	0.47
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.48	0.47
46:1o:67:LEU:HB3	46:1o:78:TYR:HE1	1.79	0.47
1:2A:484:C:H2'	1:2A:485:C:C6	2.49	0.47
1:2A:1024:G:HO2'	1:2A:1144:G:HO2'	1.49	0.47
1:2A:2184:G:C2	1:2A:2185:C:H1'	2.49	0.47
2:2B:2:C:H2'	2:2B:3:C:H6	1.79	0.47
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD2	1.95	0.47
32:2a:632:A:H3'	32:2a:633:G:H8	1.79	0.47
32:2a:662:G:H2'	32:2a:663:A:H8	1.79	0.47
32:2a:1069:C:O2'	32:2a:1192:C:O2	2.32	0.47
32:2a:1131:G:H2'	32:2a:1132:C:C6	2.49	0.47
32:2a:1326:C:H5"	52:2u:18:TYR:O	2.14	0.47
39:2h:26:VAL:O	39:2h:59:LEU:N	2.43	0.47
44:2m:65:LYS:HG3	44:2m:69:GLU:HG2	1.94	0.47
47:2p:21:VAL:HG11	47:2p:59:TRP:CE2	2.48	0.47
1:1A:7:G:H2'	1:1A:8:A:H8	1.78	0.47
1:1A:2103:C:H2'	1:1A:2104:G:H5'	1.96	0.47
1:1A:2511:U:O2'	4:1E:138:PRO:O	2.27	0.47
1:1A:2567:G:H2'	1:1A:2568:C:C6	2.49	0.47
1:1A:2728:U:H5'	10:1O:70:LYS:HZ3	1.80	0.47
3:1D:95:LEU:HD11	3:1D:105:ILE:HG12	1.96	0.47
3:1D:137:PRO:O	3:1D:140:THR:OG1	2.26	0.47
13:1R:59:ASP:OD1	13:1R:59:ASP:N	2.47	0.47
32:1a:434:U:H2'	32:1a:435:C:C6	2.49	0.47
32:1a:674:G:H2'	32:1a:675:A:H8	1.78	0.47
48:1q:67:LYS:C	48:1q:69:LYS:H	2.22	0.47
1:2A:310:A:H1'	1:2A:311:A:H2'	1.96	0.47
1:2A:817:C:H2'	1:2A:818:G:O4'	2.14	0.47
1:2A:1248:G:C5	16:2U:3:ARG:HB2	2.49	0.47
1:2A:1466:G:O2'	1:2A:1546:C:O2'	2.17	0.47
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.13	0.47
10:2O:15:GLY:O	10:2O:47:ILE:HG13	2.15	0.47
11:2P:62:LEU:HD11	30:28:50:LEU:HD11	1.96	0.47
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:457:C:H42	32:2a:474:G:H1	1.61	0.47
32:2a:1279:A:H2'	32:2a:1279:A:N3	2.28	0.47
32:2a:1434:A:H61	32:2a:1467:G:H1'	1.79	0.47
33:2b:48:MET:HA	33:2b:51:LEU:HB2	1.95	0.47
1:1A:1252:G:N7	16:1U:36:ARG:NH1	2.62	0.47
1:1A:1342:A:O2'	1:1A:1344:G:OP2	2.30	0.47
9:1N:97:ARG:HA	9:1N:100:GLU:HB2	1.96	0.47
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.95	0.47
21:1Z:28:MET:HE1	21:1Z:61:LEU:HD21	1.96	0.47
32:1a:829:G:H2'	32:1a:830:G:H8	1.79	0.47
1:2A:580:C:H2'	1:2A:581:C:C6	2.50	0.47
1:2A:852:G:H2'	1:2A:853:G:C8	2.49	0.47
1:2A:2247:A:H3'	57:2A:3743:HOH:O	2.13	0.47
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.50	0.47
1:2A:2816:C:O2	1:2A:2883:A:O2'	2.29	0.47
2:2B:66:A:N6	2:2B:109:C:H5'	2.29	0.47
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.14	0.47
32:2a:109:A:C6	32:2a:326:G:C6	3.02	0.47
32:2a:189(K):U:H2'	32:2a:189(L):G:C8	2.50	0.47
32:2a:749:C:H2'	32:2a:750:G:H8	1.80	0.47
32:2a:1058:G:N2	41:2j:53:PRO:HG3	2.29	0.47
32:2a:1153:C:H2'	32:2a:1154:G:O4'	2.15	0.47
35:2d:30:LYS:HG2	35:2d:35:ARG:NH2	2.30	0.47
35:2d:111:ALA:HB2	35:2d:120:LEU:HD12	1.95	0.47
42:2k:48:ILE:HD11	42:2k:64:ALA:HA	1.96	0.47
1:1A:414:C:H2'	1:1A:415:A:C8	2.49	0.47
1:1A:839:U:H2'	1:1A:840:C:C6	2.50	0.47
6:1G:72:ARG:HB3	6:1G:85:GLY:HA2	1.96	0.47
6:1G:109:VAL:HG21	26:14:14:ILE:HD13	1.96	0.47
11:1P:62:LEU:HD11	30:18:50:LEU:HD11	1.96	0.47
21:1Z:99:TYR:HB3	21:1Z:123:ASP:OD2	2.13	0.47
23:11:91:LYS:HG2	23:11:95:LEU:HD22	1.97	0.47
32:1a:67:C:H2'	32:1a:68:G:C8	2.50	0.47
32:1a:794:A:OP2	57:1a:3203:HOH:O	2.20	0.47
32:1a:1072:G:N2	33:1b:107:THR:HG21	2.28	0.47
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.49	0.47
32:1a:1319:A:H61	32:1a:1361:G:N2	2.12	0.47
47:1p:43:LYS:HA	47:1p:48:TRP:HB3	1.95	0.47
18:2W:20:VAL:HG11	18:2W:44:ALA:HA	1.96	0.47
32:2a:67:C:H2'	32:2a:68:G:H8	1.79	0.47
32:2a:579:G:O3'	46:2o:54:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:757:U:H2'	32:2a:758:G:O4'	2.14	0.47
32:2a:947:G:H2'	32:2a:948:C:O4'	2.15	0.47
32:2a:1236:A:H4'	32:2a:1304:G:H4'	1.95	0.47
33:2b:185:ILE:HA	33:2b:199:TYR:HB2	1.95	0.47
1:1A:748:G:C8	18:1W:89:ALA:HB1	2.50	0.47
1:1A:2123:G:N1	1:1A:2175:C:O2	2.43	0.47
1:1A:2158:A:O2'	1:1A:2159:G:O4'	2.31	0.47
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.14	0.47
2:1B:87:G:N2	2:1B:89:G:H3'	2.29	0.47
5:1F:14:PRO:HD2	5:1F:127:GLU:OE2	2.14	0.47
20:1Y:90:LEU:HD23	20:1Y:94:LYS:HB2	1.96	0.47
27:15:49:CYS:SG	27:15:51:TYR:HB2	2.55	0.47
32:1a:737:A:H2'	32:1a:738:C:C6	2.49	0.47
32:1a:1041:A:H2'	32:1a:1042:G:C8	2.50	0.47
32:1a:1114:C:H1'	45:1n:60:SER:HB3	1.96	0.47
32:1a:1236:A:H2'	32:1a:1237:C:C6	2.49	0.47
1:2A:272:G:N7	1:2A:421:U:H2'	2.29	0.47
1:2A:947:G:H2'	1:2A:948:G:C8	2.49	0.47
1:2A:2626:C:H2'	1:2A:2627:G:O4'	2.14	0.47
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.50	0.47
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.47	0.47
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.97	0.47
6:2G:19:LEU:HG	6:2G:175:LEU:HD22	1.95	0.47
11:2P:138:LEU:HD23	11:2P:145:PRO:HB3	1.96	0.47
17:2V:64:HIS:HD2	17:2V:92:THR:OG1	1.98	0.47
32:2a:841:U:H6	32:2a:841:U:P	2.38	0.47
32:2a:1028:C:H1'	32:2a:1033:G:H22	1.79	0.47
32:2a:1102:A:O3'	33:2b:96:ARG:NH2	2.48	0.47
32:2a:1182:G:H5'	32:2a:1184:G:H5"	1.95	0.47
32:2a:1431:C:H2'	32:2a:1432:G:O4'	2.15	0.47
33:2b:18:GLY:HA2	33:2b:42:ILE:HG13	1.96	0.47
1:1A:221:A:N1	1:1A:265:A:O2'	2.46	0.47
1:1A:494:G:H4'	18:1W:6:ILE:HB	1.96	0.47
1:1A:1031:G:H5"	31:19:8:LYS:HE3	1.96	0.47
1:1A:1803:A:O2'	3:1D:259:THR:HG21	2.14	0.47
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.45	0.47
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.95	0.47
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	1.97	0.47
32:1a:994:A:N3	45:1n:5:ALA:HA	2.29	0.47
32:1a:1135:U:H5"	32:1a:1136:U:C5	2.38	0.47
33:1b:59:GLU:HG2	33:1b:63:MET:HE3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.80	0.47
48:1q:78:GLU:HG2	48:1q:79:SER:H	1.78	0.47
1:2A:576:U:H2'	1:2A:577:G:C8	2.50	0.47
1:2A:595:C:H2'	1:2A:596:G:C8	2.49	0.47
1:2A:1462:C:H4'	1:2A:2703:C:H5'	1.96	0.47
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.50	0.47
2:2B:42:C:H4'	6:2G:67:LYS:O	2.15	0.47
3:2D:124:PRO:O	3:2D:126:GLN:N	2.48	0.47
6:2G:129:GLY:O	6:2G:161:THR:HB	2.15	0.47
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.95	0.47
13:2R:95:THR:HG22	13:2R:116:LEU:HD23	1.97	0.47
23:21:85:LEU:HD23	23:21:89:GLU:HB3	1.96	0.47
26:24:36:CYS:SG	26:24:38:LYS:HB2	2.55	0.47
32:2a:184:G:H2'	32:2a:185:A:C8	2.49	0.47
32:2a:624:C:H2'	32:2a:625:G:C8	2.46	0.47
32:2a:675:A:O2'	42:2k:114:VAL:O	2.29	0.47
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.49	0.47
32:2a:1256:A:H5'	32:2a:1258:G:O4'	2.14	0.47
42:2k:48:ILE:HG21	42:2k:63:LEU:HB3	1.96	0.47
44:2m:88:ARG:O	44:2m:92:HIS:ND1	2.46	0.47
1:1A:607:U:OP1	5:1F:102:PRO:HA	2.15	0.47
1:1A:1054:A:N6	1:1A:1105:U:H3	2.09	0.47
1:1A:1341:U:O4'	19:1X:57:LEU:HD23	2.15	0.47
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.47	0.47
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.50	0.47
2:1B:96:U:H2'	2:1B:97:G:C8	2.50	0.47
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.96	0.47
5:1F:183:VAL:O	5:1F:187:VAL:HG23	2.15	0.47
8:1I:46:ALA:O	8:1I:50:ARG:HG2	2.14	0.47
32:1a:45:U:H2'	32:1a:46:G:C8	2.49	0.47
32:1a:272:C:H2'	32:1a:273:A:C8	2.50	0.47
32:1a:508:C:OP1	35:1d:209:ARG:NH2	2.47	0.47
32:1a:617:G:H1	32:1a:623:C:H42	1.63	0.47
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.49	0.47
32:1a:1124:G:N2	32:1a:1125:U:O4	2.47	0.47
32:1a:1149:C:H2'	32:1a:1150:U:O4'	2.15	0.47
32:1a:1250:A:H61	32:1a:1354:C:H1'	1.80	0.47
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.15	0.47
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.97	0.47
34:1c:18:TRP:CZ2	45:1n:57:ARG:HB3	2.48	0.47
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.80	0.47
43:1l:27:LEU:O	43:1l:33:ARG:NH2	2.43	0.47
46:1o:64:ARG:HH12	46:1o:68:ARG:HH21	1.63	0.47
52:1u:14:TRP:CE3	52:1u:15:ARG:HD3	2.49	0.47
1:2A:253:C:OP2	30:28:5:LYS:NZ	2.44	0.47
1:2A:377:C:H2'	1:2A:378:C:C6	2.50	0.47
1:2A:852:G:H2'	1:2A:853:G:H8	1.79	0.47
1:2A:872:A:H2'	1:2A:873:G:H8	1.80	0.47
1:2A:1035:U:H2'	1:2A:1036:G:C8	2.49	0.47
1:2A:1995:U:H5"	1:2A:1996:C:H2'	1.95	0.47
1:2A:2058:A:H5"	1:2A:2059:A:OP2	2.15	0.47
1:2A:2206:G:H5"	1:2A:2207:G:C8	2.50	0.47
1:2A:2781:A:H5"	1:2A:2782:G:H5'	1.96	0.47
3:2D:77:ALA:HA	3:2D:97:TYR:HA	1.96	0.47
13:2R:55:ALA:HB2	13:2R:79:LEU:HD13	1.96	0.47
24:22:8:LYS:HA	24:22:8:LYS:HD2	1.78	0.47
27:25:20:ARG:HG2	27:25:23:HIS:ND1	2.30	0.47
32:2a:186:C:H2'	32:2a:187:C:C6	2.49	0.47
32:2a:439:A:C5	32:2a:441:A:H1'	2.49	0.47
32:2a:868:C:H2'	32:2a:869:G:O4'	2.14	0.47
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.50	0.47
38:2g:48:LYS:O	38:2g:52:GLU:HG2	2.14	0.47
48:2q:78:GLU:HG2	48:2q:79:SER:H	1.80	0.47
50:2s:36:ARG:HD2	50:2s:53:ASN:HA	1.96	0.47
1:1A:2125:G:H1	1:1A:2172:U:P	2.38	0.47
1:1A:2180:U:H2'	1:1A:2181:G:C8	2.49	0.47
1:1A:2323:G:H2'	1:1A:2324:C:O4'	2.15	0.47
2:1B:103:G:H21	21:1Z:73:GLN:NE2	2.12	0.47
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.97	0.47
32:1a:73:G:H2'	32:1a:76:C:C6	2.49	0.47
32:1a:559:A:H5"	32:1a:560:U:H3'	1.96	0.47
35:1d:166:LYS:HA	35:1d:178:VAL:HG21	1.96	0.47
37:1f:21:LEU:O	37:1f:24:GLU:HB3	2.15	0.47
40:1i:40:LEU:HD11	40:1i:70:LYS:HB3	1.97	0.47
1:2A:903:C:H2'	1:2A:904:C:C6	2.49	0.47
1:2A:992:C:OP1	16:2U:47:TYR:OH	2.23	0.47
1:2A:1721:G:N1	1:2A:1739:U:OP2	2.47	0.47
1:2A:2008:C:H2'	1:2A:2009:G:C8	2.49	0.47
1:2A:2298:A:H2'	1:2A:2299:G:O4'	2.15	0.47
1:2A:2378:A:C8	1:2A:2379:G:H1'	2.49	0.47
1:2A:2543:G:H2'	1:2A:2544:G:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2864:G:OP1	15:2T:119:LYS:HE3	2.15	0.47
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.48	0.47
7:2H:28:GLY:HA3	7:2H:79:VAL:HB	1.95	0.47
32:2a:1318:A:H4'	50:2s:10:PHE:CD2	2.49	0.47
39:2h:96:GLY:O	39:2h:100:ILE:HG13	2.14	0.47
46:2o:28:GLN:HA	46:2o:31:LEU:HD12	1.97	0.47
1:1A:288:C:H2'	1:1A:289:A:H8	1.76	0.47
1:1A:796:C:H2'	1:1A:797:C:C6	2.50	0.47
1:1A:1904:G:O2'	1:1A:1928:A:N1	2.44	0.47
1:1A:2145:C:H5"	1:1A:2146:C:C5	2.49	0.47
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.50	0.47
1:1A:2577:A:O4'	27:15:3:LYS:HB2	2.14	0.47
6:1G:118:ARG:O	6:1G:181:ARG:HB3	2.15	0.47
32:1a:131:C:H2'	32:1a:132:C:C6	2.50	0.47
32:1a:454:C:H41	32:1a:477:A:H61	1.63	0.47
35:1d:108:LEU:HD13	35:1d:174:LEU:HD22	1.97	0.47
1:2A:1312:U:H4'	1:2A:1313:U:O5'	2.15	0.47
1:2A:1468:C:H2'	1:2A:1469:A:C8	2.50	0.47
1:2A:1748:G:H2'	1:2A:1749:A:C8	2.50	0.47
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.29	0.47
2:2B:24:G:O2'	2:2B:56:G:N7	2.42	0.47
5:2F:34:TRP:CZ3	11:2P:8:PRO:HB3	2.50	0.47
7:2H:117:PRO:HG3	7:2H:123:PHE:CD2	2.50	0.47
32:2a:674:G:H2'	32:2a:675:A:H8	1.80	0.47
32:2a:689:C:H2'	32:2a:690:G:O4'	2.15	0.47
32:2a:1216:G:H5"	45:2n:5:ALA:HB2	1.95	0.47
32:2a:1375:A:O2'	38:2g:29:LYS:NZ	2.48	0.47
33:2b:16:HIS:HB3	33:2b:210:SER:OG	2.15	0.47
35:2d:20:TYR:CD1	35:2d:26:CYS:HB3	2.50	0.47
37:2f:26:ILE:O	37:2f:30:LEU:HG	2.14	0.47
41:2j:38:ILE:HG12	41:2j:71:LEU:HB3	1.96	0.47
50:2s:62:ILE:HG23	50:2s:66:MET:HG3	1.95	0.47
1:1A:534:U:H2'	1:1A:535:C:C6	2.50	0.47
1:1A:747:U:O2	1:1A:2014:A:H1'	2.15	0.47
1:1A:1027:A:C2	1:1A:2488:A:H5'	2.49	0.47
1:1A:1557:C:H5"	1:1A:1558:A:OP2	2.15	0.47
1:1A:2680:C:H5'	4:1E:189:PRO:HA	1.97	0.47
3:1D:85:ASP:OD2	3:1D:88:ARG:NH1	2.42	0.47
5:1F:63:LYS:NZ	5:1F:75:HIS:O	2.44	0.47
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.11	0.47
11:1P:87:ASP:O	11:1P:90:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.13	0.47
32:1a:108:G:H1	51:1t:15:ARG:HG2	1.80	0.47
32:1a:824:C:H2'	32:1a:825:G:C8	2.50	0.47
32:1a:985:C:H2'	32:1a:986:A:C8	2.49	0.47
32:1a:1059:C:N4	32:1a:1198:G:H1	2.10	0.47
32:1a:1069:C:OP2	57:1a:3204:HOH:O	2.20	0.47
41:1j:26:ALA:HB1	41:1j:84:GLN:HE21	1.80	0.47
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.97	0.47
1:2A:208:C:H2'	1:2A:209:C:H6	1.79	0.47
1:2A:956:G:H2'	1:2A:957:A:H2'	1.97	0.47
1:2A:1202:C:H42	1:2A:1243:G:H1	1.60	0.47
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.15	0.47
5:2F:130:ALA:H	5:2F:142:TRP:CD1	2.33	0.47
14:2S:74:ALA:O	14:2S:78:LEU:HG	2.14	0.47
32:2a:815:A:N7	32:2a:1509:C:O2'	2.38	0.47
32:2a:1058:G:H22	41:2j:53:PRO:HG3	1.80	0.47
32:2a:1074:G:OP1	36:2e:64:ARG:NH1	2.48	0.47
32:2a:1163:C:H42	32:2a:1173:G:H1	1.63	0.47
37:2f:89:MET:HE1	49:2r:72:ARG:HB3	1.96	0.47
40:2i:16:ARG:O	40:2i:64:THR:N	2.44	0.47
40:2i:28:VAL:HG22	40:2i:63:ILE:HB	1.97	0.47
1:1A:299:A:N1	1:1A:322:A:O2'	2.46	0.46
1:1A:1064:C:N3	1:1A:1074:G:N2	2.53	0.46
1:1A:1541:G:H3'	1:1A:1542:A:H2'	1.97	0.46
1:1A:1942:5MC:OP2	1:1A:1943:U:O2'	2.27	0.46
1:1A:2849:U:P	15:1T:95:ARG:HH12	2.37	0.46
2:1B:66:A:H61	2:1B:108:U:H2'	1.80	0.46
5:1F:60:SER:OG	5:1F:61:GLY:N	2.48	0.46
6:1G:107:LEU:HD21	6:1G:178:PHE:CE1	2.50	0.46
17:1V:28:GLU:HG3	17:1V:29:PRO:HD2	1.97	0.46
19:1X:72:LYS:HG2	19:1X:73:ARG:O	2.15	0.46
20:1Y:56:PRO:C	20:1Y:58:GLY:H	2.23	0.46
22:10:10:THR:HG22	22:10:12:ASN:N	2.24	0.46
32:1a:473:G:H2'	32:1a:474:G:H8	1.78	0.46
32:1a:991:U:H1'	32:1a:992:U:OP2	2.16	0.46
32:1a:1003:G:N2	32:1a:1038:C:N3	2.63	0.46
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.50	0.46
33:1b:158:LEU:HA	33:1b:159:PRO:HD3	1.84	0.46
34:1c:71:ALA:HB2	34:1c:115:LEU:HD21	1.96	0.46
1:2A:263:C:H2'	1:2A:264:C:O4'	2.15	0.46
1:2A:1822:G:H2'	1:2A:1823:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.47	0.46
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.96	0.46
32:2a:612:C:O2	32:2a:629:G:N2	2.48	0.46
32:2a:826:C:H2'	32:2a:827:U:C6	2.51	0.46
33:2b:24:TRP:CZ3	33:2b:26:PRO:HA	2.50	0.46
33:2b:125:PRO:O	33:2b:127:ILE:N	2.44	0.46
39:2h:112:LEU:HD11	39:2h:124:ALA:HB2	1.96	0.46
43:2l:113:ARG:NH2	43:2l:116:SER:HB2	2.30	0.46
48:2q:15:MET:HE1	48:2q:43:LEU:HD22	1.97	0.46
1:1A:222:A:H5"	1:1A:421:U:OP1	2.15	0.46
1:1A:535:C:O3'	16:1U:53:ARG:NH1	2.48	0.46
1:1A:1866:C:H2'	1:1A:1876:A:O4'	2.15	0.46
1:1A:1992:G:OP2	57:1A:3854:HOH:O	2.21	0.46
2:1B:88:C:H2'	2:1B:89:G:O4'	2.15	0.46
27:15:45:VAL:HG11	27:15:58:LEU:HD13	1.96	0.46
32:1a:401:C:OP2	35:1d:73:ARG:NH2	2.48	0.46
32:1a:957:U:H5"	50:1s:81:ARG:HH12	1.80	0.46
32:1a:960:U:H1'	32:1a:1223:C:H5'	1.98	0.46
32:1a:1025:U:C2	32:1a:1036:G:O6	2.68	0.46
32:1a:1359:C:O2'	32:1a:1361:G:N7	2.47	0.46
35:1d:12:CYS:SG	35:1d:19:LEU:HB2	2.56	0.46
40:1i:42:ARG:O	40:1i:74:ILE:HG21	2.15	0.46
1:2A:899:A:H2'	1:2A:899:A:N3	2.30	0.46
1:2A:1082:U:O4	1:2A:1086:A:C6	2.68	0.46
1:2A:1278:A:H2'	1:2A:1279:G:C8	2.51	0.46
1:2A:2251:OMG:HM22	1:2A:2252:G:H5'	1.98	0.46
54:2A:3515:HGR:C16	54:2A:3515:HGR:H3	2.45	0.46
23:21:85:LEU:H	23:21:85:LEU:HD12	1.81	0.46
32:2a:1108:G:OP1	34:2c:175:LEU:N	2.48	0.46
32:2a:1250:A:H2'	32:2a:1251:A:O4'	2.15	0.46
38:2g:149:ARG:NE	42:2k:59:TYR:OH	2.49	0.46
38:2g:153:HIS:NE2	42:2k:58:PRO:HD2	2.30	0.46
39:2h:86:ILE:HG12	39:2h:135:CYS:HA	1.97	0.46
44:2m:33:ALA:HB2	44:2m:64:TRP:CZ3	2.49	0.46
1:1A:1567:A:OP2	3:1D:84:TYR:OH	2.28	0.46
1:1A:1703:G:H2'	1:1A:1704:G:C8	2.49	0.46
19:1X:40:LYS:HG3	19:1X:51:VAL:HB	1.97	0.46
22:10:27:GLU:HB2	22:10:69:PHE:HD1	1.80	0.46
32:1a:12:U:H4'	32:1a:526:C:H4'	1.97	0.46
32:1a:262:A:H2'	32:1a:263:A:C8	2.50	0.46
32:1a:324:G:N1	32:1a:327:A:OP2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:669:U:H2'	32:1a:670:G:C8	2.50	0.46
32:1a:741:G:H2'	32:1a:742:G:H8	1.80	0.46
32:1a:881:G:OP2	43:1l:12:ARG:NH2	2.49	0.46
32:1a:1201:A:H1'	32:1a:1202:G:OP2	2.15	0.46
37:1f:30:LEU:HB3	37:1f:35:ALA:HB3	1.97	0.46
44:1m:19:LEU:HD21	44:1m:56:LEU:HD21	1.98	0.46
1:2A:125:G:H5"	29:27:19:ARG:HD3	1.96	0.46
1:2A:1180:C:H2'	1:2A:1181:C:H6	1.80	0.46
1:2A:1506:C:H2'	1:2A:1507:A:H5'	1.97	0.46
1:2A:1999:C:H5"	1:2A:2723:C:O2'	2.15	0.46
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.97	0.46
32:2a:629:G:H2'	32:2a:630:G:O4'	2.15	0.46
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.96	0.46
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	1.96	0.46
50:2s:36:ARG:NH2	50:2s:72:GLY:O	2.48	0.46
1:1A:459:U:H2'	1:1A:460:A:C8	2.50	0.46
1:1A:956:G:H2'	1:1A:957:A:H2'	1.96	0.46
1:1A:1588:C:H2'	1:1A:1589:C:H6	1.80	0.46
1:1A:2650:U:H2'	1:1A:2651:C:C6	2.51	0.46
5:1F:110:LEU:HA	5:1F:183:VAL:HG12	1.97	0.46
29:17:22:MET:HA	29:17:28:ARG:HG2	1.98	0.46
32:1a:1121:U:H2'	32:1a:1122:U:C6	2.50	0.46
42:1k:29:ILE:HG12	42:1k:44:SER:HB2	1.98	0.46
47:1p:74:LEU:HD23	47:1p:79:VAL:HG21	1.97	0.46
1:2A:2262:U:H2'	1:2A:2263:C:C6	2.51	0.46
1:2A:2712:U:H1'	1:2A:2712(A):A:C8	2.51	0.46
1:2A:2716:U:H2'	1:2A:2717:G:H8	1.80	0.46
5:2F:155:LEU:HD23	5:2F:192:LEU:HD12	1.96	0.46
32:2a:19:C:H5"	36:2e:86:ALA:HB3	1.97	0.46
32:2a:473:G:H2'	32:2a:474:G:H8	1.81	0.46
39:2h:28:ALA:HA	39:2h:59:LEU:HG	1.97	0.46
40:2i:36:TYR:CZ	40:2i:70:LYS:HE2	2.50	0.46
1:1A:244:A:H4'	11:1P:74:GLU:HB2	1.97	0.46
1:1A:601:C:O2'	1:1A:605:C:OP1	2.29	0.46
1:1A:907:U:H4'	12:1Q:101:ARG:HH22	1.80	0.46
1:1A:2437:U:H2'	1:1A:2438:U:C6	2.50	0.46
8:1I:72:LEU:HD12	8:1I:138:ILE:HG21	1.98	0.46
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.96	0.46
19:1X:12:VAL:HG22	19:1X:29:TRP:CE2	2.51	0.46
32:1a:193:C:H2'	32:1a:194:C:C6	2.50	0.46
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1345:U:OP1	40:1i:120:ARG:NH1	2.47	0.46
41:1j:7:LYS:N	41:1j:97:GLU:O	2.40	0.46
42:1k:79:SER:HA	42:1k:104:GLN:HB3	1.96	0.46
1:2A:323:G:C8	5:2F:171:PRO:HG3	2.50	0.46
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.50	0.46
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	1.98	0.46
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.15	0.46
32:2a:721:G:H4'	32:2a:722:A:O4'	2.16	0.46
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	1.97	0.46
50:2s:3:ARG:NH2	50:2s:10:PHE:HB2	2.30	0.46
1:1A:142:A:O2'	1:1A:1407:C:O2'	2.27	0.46
1:1A:858:U:O2	1:1A:2268:A:H2'	2.16	0.46
1:1A:918:A:N3	2:1B:80:U:O2'	2.44	0.46
1:1A:1130:U:N3	1:1A:2025:C:OP1	2.28	0.46
1:1A:2076:U:OP2	1:1A:2238:G:N2	2.38	0.46
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.51	0.46
1:1A:2695:C:H2'	1:1A:2696:U:C6	2.51	0.46
2:1B:80:U:H2'	2:1B:81:G:C8	2.51	0.46
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.31	0.46
22:10:38:VAL:HB	22:10:59:LEU:HD23	1.98	0.46
28:16:14:THR:O	28:16:17:LYS:NZ	2.48	0.46
32:1a:73:G:N2	32:1a:96:U:O2	2.38	0.46
32:1a:352:C:O2'	32:1a:354:G:OP1	2.24	0.46
32:1a:1073:U:H2'	32:1a:1074:G:H8	1.80	0.46
32:1a:1479:C:H2'	32:1a:1480:G:H8	1.81	0.46
35:1d:76:ARG:HD3	35:1d:207:TYR:CZ	2.51	0.46
1:2A:1799:G:O2'	3:2D:181:GLU:OE2	2.28	0.46
1:2A:2359:C:H2'	1:2A:2360:A:O4'	2.15	0.46
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.97	0.46
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.31	0.46
2:2B:14:U:O3'	2:2B:108:U:O2'	2.30	0.46
5:2F:110:LEU:HA	5:2F:183:VAL:HG12	1.98	0.46
26:24:44:THR:O	26:24:44:THR:OG1	2.28	0.46
32:2a:392:G:H2'	32:2a:393:A:H8	1.81	0.46
32:2a:665:A:H2'	32:2a:732:C:O2	2.16	0.46
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.16	0.46
1:1A:480:A:N3	1:1A:499:U:O2'	2.44	0.46
1:1A:889:C:O2'	1:1A:890:A:O4'	2.33	0.46
1:1A:1721:G:H2'	1:1A:1740:G:O6	2.15	0.46
4:1E:174:ASP:OD1	4:1E:175:VAL:N	2.49	0.46
28:16:10:LEU:HD23	28:16:22:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:392:G:H2'	32:1a:393:A:H8	1.80	0.46
32:1a:592:G:H1	32:1a:647:C:H42	1.64	0.46
32:1a:1251:A:H4'	40:1i:12:GLU:HG3	1.97	0.46
32:1a:1457:G:H2'	32:1a:1458:G:C8	2.50	0.46
33:1b:223:ILE:HA	33:1b:226:ARG:HB2	1.98	0.46
35:1d:109:GLY:HA3	35:1d:165:MET:HE2	1.98	0.46
40:1i:53:VAL:HB	40:1i:92:TYR:CZ	2.50	0.46
43:1l:113:ARG:NH2	43:1l:116:SER:HB2	2.31	0.46
1:2A:271(T):C:H2'	1:2A:271(U):G:C8	2.51	0.46
1:2A:764:A:H2	3:2D:219:PRO:HG3	1.81	0.46
1:2A:1954:G:O2'	1:2A:1956:U:O4	2.30	0.46
1:2A:2233:U:H2'	1:2A:2234:G:C8	2.51	0.46
1:2A:2513:G:N2	4:2E:151:TYR:OH	2.41	0.46
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.50	0.46
15:2T:102:ILE:HB	15:2T:110:ILE:HG12	1.98	0.46
19:2X:11:PRO:HG2	19:2X:13:LEU:HD21	1.98	0.46
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.30	0.46
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.34	0.46
49:2r:56:THR:OG1	49:2r:57:GLY:N	2.47	0.46
1:1A:774:A:N3	1:1A:774:A:H2'	2.31	0.46
1:1A:844:C:H2'	1:1A:845:G:H5'	1.97	0.46
1:1A:1111:A:N3	1:1A:1112:G:H1'	2.31	0.46
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.51	0.46
5:1F:32:LEU:HD11	5:1F:105:VAL:HG13	1.98	0.46
12:1Q:50:ALA:HB1	12:1Q:121:ALA:HB1	1.98	0.46
26:14:62:ARG:C	26:14:64:GLY:HA2	2.40	0.46
32:1a:15:G:H21	36:1e:18:ARG:HA	1.81	0.46
32:1a:526:C:OP2	43:1l:91:LYS:HE3	2.16	0.46
32:1a:1198:G:H2'	32:1a:1199:U:C6	2.50	0.46
48:1q:4:LYS:O	48:1q:61:GLU:N	2.42	0.46
1:2A:817:C:O2'	1:2A:839:U:H5"	2.16	0.46
1:2A:2104:G:O6	1:2A:2185:C:N3	2.49	0.46
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.51	0.46
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.50	0.46
6:2G:103:LEU:HD23	6:2G:106:LEU:HD23	1.98	0.46
21:2Z:7:ALA:HB3	21:2Z:61:LEU:HD12	1.98	0.46
26:24:57:GLU:CB	26:24:58:ARG:HA	2.45	0.46
32:2a:96:U:H2'	32:2a:97:G:C8	2.51	0.46
38:2g:6:ARG:C	38:2g:8:GLU:H	2.23	0.46
1:1A:436:C:H2'	1:1A:437:G:H8	1.81	0.46
1:1A:818:G:OP2	57:1A:3858:HOH:O	2.21	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:958:U:O2	2:1B:90:A:O2'	2.27	0.46
1:1A:1301:A:O2'	1:1A:1302:A:H3'	2.15	0.46
1:1A:1783:A:H5'	1:1A:2608:G:H4'	1.98	0.46
1:1A:2072:G:N2	57:1A:4041:HOH:O	2.48	0.46
1:1A:2562:U:H1'	10:1O:23:ARG:HH21	1.81	0.46
1:1A:2712:U:O2'	1:1A:2713:A:H5'	2.16	0.46
32:1a:60:A:H4'	32:1a:61:G:H5'	1.98	0.46
32:1a:553:A:H5"	43:1l:24:VAL:HG21	1.97	0.46
32:1a:716:A:H1'	42:1k:117:ASN:O	2.16	0.46
32:1a:1033:G:H2'	32:1a:1034:G:H8	1.79	0.46
43:1l:53:ARG:CB	43:1l:93:LEU:HD11	2.46	0.46
1:2A:127:A:H5"	1:2A:128:C:O4'	2.16	0.46
1:2A:571:A:N6	1:2A:2499:C:O3'	2.48	0.46
1:2A:859:G:O2'	1:2A:916:G:O6	2.33	0.46
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.51	0.46
1:2A:1652:A:OP1	13:2R:8:ARG:NH1	2.48	0.46
1:2A:2128:C:N3	1:2A:2160:G:O6	2.48	0.46
18:2W:35:ILE:HG23	27:25:28:PRO:HD2	1.98	0.46
35:2d:173:TRP:HA	35:2d:187:ARG:HG2	1.98	0.46
40:2i:25:LYS:HA	40:2i:25:LYS:HD3	1.83	0.46
1:1A:307:G:H21	1:1A:330:A:H62	1.63	0.46
1:1A:1357:U:OP2	57:1A:3853:HOH:O	2.20	0.46
1:1A:1448:G:H1'	1:1A:1528:A:N1	2.31	0.46
22:10:18:ALA:O	22:10:20:ARG:NH1	2.49	0.46
32:1a:418:C:H1'	32:1a:540:G:O2'	2.16	0.46
32:1a:1004:A:H5'	32:1a:1024:G:H22	1.81	0.46
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.49	0.46
35:1d:148:VAL:HG11	35:1d:158:ILE:HD13	1.97	0.46
46:1o:82:ILE:HD12	46:1o:88:ARG:HB2	1.97	0.46
1:2A:887:A:O2'	1:2A:889:C:H5	1.99	0.46
1:2A:1028:A:N3	1:2A:2486:G:O2'	2.45	0.46
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.47	0.46
1:2A:2206:G:H8	1:2A:2207:G:N7	2.14	0.46
5:2F:70:THR:HG23	5:2F:72:ARG:H	1.81	0.46
9:2N:108:PRO:O	9:2N:113:GLY:HA3	2.16	0.46
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.16	0.46
32:2a:1075:C:OP1	33:2b:179:LYS:HE2	2.16	0.46
32:2a:1256:A:H5"	32:2a:1257:U:OP1	2.15	0.46
35:2d:103:ASN:OD1	35:2d:114:ARG:NH2	2.31	0.46
50:2s:23:ASN:OD1	50:2s:47:HIS:HE1	1.99	0.46
50:2s:66:MET:HB2	50:2s:74:PHE:HZ	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:548:A:O2'	1:1A:549:G:OP1	2.31	0.45
1:1A:795:C:H2'	1:1A:796:C:C6	2.51	0.45
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.51	0.45
1:1A:2197:U:H1'	1:1A:2198:A:C8	2.51	0.45
1:1A:2249:U:N3	1:1A:2253:G:OP2	2.47	0.45
1:1A:2310:A:H2	6:1G:77:ILE:HG21	1.81	0.45
1:1A:2572:A:OP1	1:1A:2574:G:O2'	2.31	0.45
6:1G:60:LEU:HA	6:1G:63:ILE:HB	1.98	0.45
32:1a:1122:U:O4	32:1a:1123:A:N6	2.49	0.45
32:1a:1151:A:O2'	32:1a:1152:A:O5'	2.30	0.45
32:1a:1255:G:H1	32:1a:1282:C:N4	2.12	0.45
32:1a:1431:C:H2'	32:1a:1432:G:O4'	2.16	0.45
43:1l:28:LYS:HE2	43:1l:64:TYR:CE2	2.51	0.45
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.48	0.45
47:1p:48:TRP:CD1	47:1p:48:TRP:H	2.34	0.45
1:2A:483:A:O2'	20:2Y:59:GLY:N	2.48	0.45
1:2A:519:U:H2'	1:2A:520:G:H8	1.81	0.45
1:2A:1713:U:H2'	1:2A:1714:G:C8	2.51	0.45
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.16	0.45
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.51	0.45
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.51	0.45
23:21:72:GLU:O	23:21:76:ARG:HG3	2.16	0.45
32:2a:583:A:H2'	32:2a:584:G:O4'	2.16	0.45
32:2a:1457:G:H2'	32:2a:1458:G:H8	1.81	0.45
36:2e:18:ARG:HG2	36:2e:25:ARG:O	2.17	0.45
47:2p:59:TRP:HA	47:2p:62:VAL:HG12	1.98	0.45
1:1A:224:G:H2'	1:1A:225:A:O4'	2.16	0.45
1:1A:828:U:H4'	1:1A:831:G:N1	2.32	0.45
1:1A:1540:U:OP1	57:1A:3855:HOH:O	2.21	0.45
4:1E:37:ARG:HB2	4:1E:46:ALA:H	1.81	0.45
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	1.98	0.45
22:10:23:VAL:HG13	22:10:38:VAL:HG22	1.97	0.45
32:1a:78:G:N2	32:1a:91:C:C2	2.82	0.45
32:1a:374:A:C6	32:1a:375:U:C4	3.05	0.45
46:1o:76:GLU:OE1	46:1o:76:GLU:N	2.49	0.45
50:1s:53:ASN:HB2	50:1s:77:THR:HG22	1.98	0.45
1:2A:383:U:H2'	1:2A:385:C:H5	1.82	0.45
1:2A:656:G:H2'	1:2A:657:U:O4'	2.15	0.45
1:2A:2252:G:H2'	1:2A:2253:G:O4'	2.16	0.45
1:2A:2356:C:O3'	22:20:20:ARG:HD3	2.16	0.45
6:2G:107:LEU:HD21	6:2G:178:PHE:HE1	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:43:THR:HG22	12:2Q:94:VAL:HG12	1.99	0.45
32:2a:9:G:H2'	32:2a:10:A:H8	1.81	0.45
32:2a:983:A:H5'	32:2a:984:C:OP2	2.17	0.45
32:2a:1151:A:C5'	41:2j:41:PRO:HA	2.46	0.45
33:2b:17:PHE:O	33:2b:41:ILE:HG23	2.16	0.45
33:2b:19:HIS:CG	33:2b:20:GLU:H	2.34	0.45
34:2c:123:GLN:O	34:2c:128:PHE:HB2	2.16	0.45
37:2f:45:LEU:HD12	37:2f:59:TYR:CD1	2.52	0.45
1:1A:624:C:O2'	1:1A:657:U:OP1	2.32	0.45
1:1A:896:A:H2	21:1Z:177:PRO:HD2	1.82	0.45
1:1A:1798:U:H5'	3:1D:259:THR:CG2	2.47	0.45
1:1A:2310:A:C2	6:1G:77:ILE:HG21	2.50	0.45
9:1N:94:HIS:HB3	9:1N:97:ARG:HD3	1.97	0.45
21:1Z:145:GLU:O	21:1Z:148:ASP:N	2.48	0.45
27:15:16:ARG:NH1	27:15:17:ASP:OD1	2.48	0.45
32:1a:176:C:H2'	32:1a:177:C:H6	1.81	0.45
32:1a:255:G:H1'	48:1q:16:GLN:NE2	2.31	0.45
32:1a:827:U:H5"	32:1a:828:A:OP2	2.16	0.45
1:2A:2133:G:N3	1:2A:2157:G:H2'	2.31	0.45
1:2A:2399:G:H2'	1:2A:2400:G:O4'	2.17	0.45
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.98	0.45
6:2G:11:TYR:O	6:2G:16:ARG:HG2	2.16	0.45
9:2N:62:VAL:HG11	9:2N:66:LYS:HB2	1.99	0.45
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.98	0.45
32:2a:667:G:OP1	32:2a:732:C:O2'	2.28	0.45
32:2a:1346:A:N1	32:2a:1374:A:H5"	2.32	0.45
38:2g:153:HIS:CE1	42:2k:57:THR:HB	2.51	0.45
43:2l:55:VAL:HG22	43:2l:69:TYR:HA	1.98	0.45
1:1A:453:C:O2	1:1A:457:A:O2'	2.35	0.45
1:1A:588:U:H2'	1:1A:589:C:C6	2.51	0.45
1:1A:728:G:H4'	3:1D:13:ARG:HE	1.82	0.45
1:1A:779:U:OP1	3:1D:49:ILE:HG13	2.16	0.45
1:1A:2162:G:H2'	1:1A:2163:C:O4'	2.17	0.45
1:1A:2821:A:H2'	1:1A:2822:G:C8	2.51	0.45
4:1E:181:LEU:HD11	15:1T:6:LEU:HD23	1.99	0.45
6:1G:124:SER:HB2	6:1G:131:TYR:CE1	2.51	0.45
32:1a:828:A:H2'	32:1a:829:G:O4'	2.17	0.45
32:1a:890:G:O2'	32:1a:906:G:O6	2.25	0.45
32:1a:1207:2MG:O2'	32:1a:1208:C:OP1	2.32	0.45
35:1d:157:LEU:O	35:1d:161:ASN:ND2	2.50	0.45
46:1o:24:SER:O	46:1o:28:GLN:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:1s:52:TYR:HB2	50:1s:57:HIS:CE1	2.51	0.45
1:2A:62:C:H42	1:2A:93:G:H1	1.63	0.45
1:2A:272(C):G:H2'	1:2A:272(D):G:H8	1.81	0.45
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.34	0.45
1:2A:2645:G:H4'	1:2A:2732:G:O3'	2.17	0.45
1:2A:2830:G:O2'	1:2A:2883:A:N1	2.42	0.45
9:2N:35:ARG:HH21	9:2N:42:TRP:HZ2	1.64	0.45
11:2P:81:GLN:NE2	11:2P:105:LEU:O	2.44	0.45
21:2Z:2:GLU:HG2	21:2Z:56:VAL:HB	1.98	0.45
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.72	0.45
23:21:83:GLU:OE1	23:21:83:GLU:N	2.47	0.45
27:25:8:LYS:O	27:25:9:LYS:HD2	2.16	0.45
32:2a:1070:U:H2'	32:2a:1071:C:C6	2.52	0.45
32:2a:1094:G:O2'	32:2a:1108:G:N1	2.49	0.45
32:2a:1225:A:H2'	32:2a:1226:C:C5	2.52	0.45
35:2d:108:LEU:HD12	35:2d:108:LEU:HA	1.86	0.45
44:2m:16:ASP:OD1	44:2m:16:ASP:N	2.45	0.45
47:2p:47:ASP:OD1	47:2p:47:ASP:N	2.48	0.45
1:1A:212:G:H2'	1:1A:213:A:O4'	2.16	0.45
6:1G:173:LEU:HB3	6:1G:178:PHE:CD2	2.52	0.45
10:1O:115:VAL:HG13	10:1O:121:VAL:HG21	1.98	0.45
12:1Q:31:ASP:HA	12:1Q:134:ARG:NH1	2.31	0.45
32:1a:741:G:H2'	32:1a:742:G:C8	2.51	0.45
32:1a:1447:A:H5"	32:1a:1452:C:OP2	2.16	0.45
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.49	0.45
47:1p:5:ARG:HH12	47:1p:28:ARG:HA	1.81	0.45
1:2A:570:G:H2'	1:2A:2030:A:C5	2.52	0.45
1:2A:582:G:H2'	1:2A:583:G:C8	2.51	0.45
1:2A:1849:G:H2'	1:2A:1850:G:C8	2.51	0.45
1:2A:2185:C:N4	1:2A:2186:G:C6	2.85	0.45
1:2A:2376:A:H8	1:2A:2376:A:OP1	2.00	0.45
2:2B:64:C:H2'	2:2B:65:C:C6	2.52	0.45
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.98	0.45
12:2Q:31:ASP:N	12:2Q:106:VAL:O	2.46	0.45
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.16	0.45
32:2a:737:A:H5"	37:2f:92:LYS:HG3	1.99	0.45
32:2a:1502:A:H5'	32:2a:1504:G:N7	2.32	0.45
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.99	0.45
33:2b:88:ALA:HB2	33:2b:219:VAL:HG22	1.99	0.45
1:1A:593:G:H4'	30:18:63:PRO:HB3	1.99	0.45
1:1A:2556:C:H2'	1:1A:2557:G:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:96:HIS:CD2	3:1D:102:LYS:HG2	2.52	0.45
3:1D:206:LEU:O	3:1D:211:ARG:HD3	2.17	0.45
15:1T:28:VAL:O	15:1T:46:GLU:HA	2.17	0.45
16:1U:89:GLU:HG3	17:1V:50:PRO:HB3	1.99	0.45
25:13:26:LEU:O	25:13:35:ARG:NE	2.49	0.45
32:1a:47:C:OP2	32:1a:366:C:N4	2.43	0.45
32:1a:707:C:H4'	42:1k:20:TYR:CG	2.51	0.45
32:1a:1245:A:H2'	32:1a:1246:C:O4'	2.17	0.45
34:1c:114:PRO:HG3	34:1c:185:GLY:HA3	1.99	0.45
37:1f:96:PRO:HB3	49:1r:30:ASP:CG	2.42	0.45
39:1h:64:LYS:HG2	39:1h:79:VAL:HG21	1.99	0.45
41:1j:44:VAL:HG22	41:1j:66:ARG:HE	1.82	0.45
1:2A:207:A:H2'	1:2A:208:C:O4'	2.17	0.45
1:2A:212:G:H2'	1:2A:213:A:O4'	2.16	0.45
1:2A:492:A:H2'	1:2A:493:G:O4'	2.16	0.45
1:2A:567:A:P	11:2P:29:LYS:HZ1	2.38	0.45
1:2A:580:C:H2'	1:2A:581:C:H6	1.81	0.45
1:2A:665:C:H2'	1:2A:666:G:C8	2.51	0.45
1:2A:888:C:H2'	1:2A:889:C:C4	2.51	0.45
1:2A:2250:G:C8	1:2A:2496:C:H5"	2.51	0.45
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.51	0.45
1:2A:2841:C:H2'	1:2A:2842:G:C8	2.52	0.45
10:2O:64:ARG:HD2	10:2O:79:PHE:CD1	2.52	0.45
32:2a:115:G:H4'	32:2a:116:A:O5'	2.16	0.45
32:2a:473:G:H2'	32:2a:474:G:C8	2.51	0.45
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.99	0.45
34:2c:206:GLU:H	34:2c:206:GLU:HG2	1.52	0.45
38:2g:78:ARG:HG2	38:2g:80:VAL:HG23	1.97	0.45
45:2n:4:LYS:O	45:2n:7:ILE:HG12	2.17	0.45
1:1A:1028:A:H61	1:1A:1125:G:H2'	1.80	0.45
2:1B:104:U:O2'	21:1Z:72:ARG:HG2	2.17	0.45
5:1F:12:LEU:HD13	5:1F:124:LEU:HD11	1.98	0.45
7:1H:3:ARG:HH22	7:1H:66:GLY:N	2.15	0.45
23:11:51:VAL:HG11	23:11:74:VAL:HG21	1.98	0.45
32:1a:263:A:OP1	51:1t:79:ARG:HD3	2.16	0.45
32:1a:308:C:H2'	32:1a:309:G:C8	2.52	0.45
32:1a:1075:C:OP1	33:1b:179:LYS:HE2	2.17	0.45
32:1a:1252:A:H61	32:1a:1285:A:N6	2.14	0.45
32:1a:1285:A:H1'	32:1a:1286:A:OP2	2.17	0.45
40:1i:3:GLN:HG3	40:1i:20:ARG:HE	1.81	0.45
42:1k:29:ILE:HG23	42:1k:44:SER:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:1m:92:HIS:CE1	44:1m:98:VAL:HG21	2.52	0.45
47:1p:47:ASP:OD1	47:1p:47:ASP:N	2.49	0.45
48:1q:26:GLN:HE21	48:1q:37:LYS:HE3	1.81	0.45
1:2A:515:A:H1'	1:2A:581:C:H1'	1.99	0.45
1:2A:724:U:H2'	1:2A:725:G:O4'	2.17	0.45
1:2A:1043:C:H42	1:2A:1112:G:H1	1.64	0.45
1:2A:1065:U:O2	1:2A:1066:U:N3	2.50	0.45
1:2A:1636:C:H2'	1:2A:1637:A:H8	1.82	0.45
1:2A:1638:C:H2'	1:2A:1639:U:O4'	2.16	0.45
3:2D:25:THR:HG23	3:2D:82:ILE:H	1.80	0.45
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.17	0.45
21:2Z:3:TYR:O	21:2Z:58:VAL:N	2.42	0.45
25:23:7:LYS:NZ	25:23:32:GLN:O	2.49	0.45
32:2a:676:A:H1'	42:2k:115:PRO:HB3	1.99	0.45
33:2b:87:ARG:NH2	33:2b:216:SER:O	2.50	0.45
38:2g:76:ARG:HH22	38:2g:95:ARG:CZ	2.30	0.45
39:2h:86:ILE:HG21	39:2h:133:LEU:HD13	1.99	0.45
40:2i:11:LYS:C	40:2i:13:ALA:H	2.25	0.45
51:2t:36:LEU:HD13	51:2t:58:LYS:HG3	1.99	0.45
1:1A:1334:G:OP2	57:1A:3856:HOH:O	2.21	0.45
1:1A:2124:G:H1	1:1A:2174:C:N4	2.12	0.45
17:1V:52:VAL:HG23	17:1V:55:ALA:HB3	1.99	0.45
18:1W:9:TYR:H	18:1W:102:HIS:CE1	2.35	0.45
32:1a:69:G:H2'	32:1a:70:G:C8	2.51	0.45
32:1a:509:A:N3	32:1a:543:C:O2'	2.42	0.45
32:1a:738:C:H2'	32:1a:739:C:C6	2.52	0.45
32:1a:762:C:H2'	32:1a:763:G:H8	1.82	0.45
32:1a:1192:C:O2	36:1e:25:ARG:NH2	2.26	0.45
34:1c:9:GLY:HA3	45:1n:49:HIS:HA	1.99	0.45
37:1f:46:ARG:HD2	37:1f:46:ARG:HA	1.73	0.45
40:1i:3:GLN:HA	40:1i:20:ARG:HG2	1.98	0.45
40:1i:5:TYR:HE1	40:1i:16:ARG:HB3	1.82	0.45
41:1j:38:ILE:O	41:1j:38:ILE:HG13	2.17	0.45
41:1j:63:PHE:HE2	45:1n:45:ARG:HG3	1.81	0.45
42:1k:32:ILE:O	42:1k:40:ILE:N	2.36	0.45
43:1l:26:ALA:HB1	43:1l:60:LEU:HD22	1.99	0.45
1:2A:662:G:H2'	1:2A:663:G:C8	2.52	0.45
1:2A:1016:G:H2'	1:2A:1017:G:C8	2.51	0.45
2:2B:96:U:H2'	2:2B:97:G:H8	1.80	0.45
5:2F:164:ARG:O	5:2F:168:ARG:HG3	2.16	0.45
6:2G:53:LEU:HD23	6:2G:53:LEU:HA	1.76	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.82	0.45
11:2P:50:ARG:HH21	30:28:7:HIS:HD2	1.64	0.45
12:2Q:31:ASP:HA	12:2Q:134:ARG:NH1	2.31	0.45
21:2Z:152:ALA:HB3	21:2Z:167:PRO:HA	1.98	0.45
29:27:30:VAL:HG22	29:27:33:ARG:HH22	1.81	0.45
32:2a:348:G:H2'	32:2a:349:A:C8	2.51	0.45
32:2a:1058:G:H2'	32:2a:1059:C:O4'	2.17	0.45
39:2h:14:ARG:HH11	39:2h:83:ILE:HG23	1.82	0.45
45:2n:9:LYS:HE2	45:2n:9:LYS:HB3	1.73	0.45
47:2p:19:ILE:HD11	47:2p:39:TYR:HB2	1.98	0.45
1:1A:24:G:H2'	1:1A:25:U:O4'	2.17	0.45
1:1A:246:C:N4	30:18:8:LYS:HG3	2.32	0.45
1:1A:2698:U:H2'	1:1A:2699:C:C6	2.52	0.45
4:1E:7:VAL:HG13	4:1E:27:LEU:HB3	1.97	0.45
8:1I:1:MET:N	8:1I:21:VAL:O	2.42	0.45
13:1R:72:ASP:OD2	13:1R:75:LEU:HB2	2.17	0.45
15:1T:28:VAL:HG13	15:1T:86:ILE:HG23	1.98	0.45
20:1Y:92:ASN:H	20:1Y:92:ASN:HD22	1.65	0.45
26:14:63:TYR:N	26:14:64:GLY:HA2	2.32	0.45
32:1a:256:U:H2'	32:1a:257:G:H8	1.82	0.45
32:1a:688:G:H2'	32:1a:689:C:C6	2.52	0.45
32:1a:715:A:H2'	32:1a:716:A:C8	2.52	0.45
32:1a:950:U:H2'	32:1a:951:G:C8	2.52	0.45
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.14	0.45
1:2A:1812:A:H1'	3:2D:45:ASN:ND2	2.30	0.45
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.47	0.45
1:2A:2155:G:C2	1:2A:2156:G:H1'	2.52	0.45
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.81	0.45
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.16	0.45
3:2D:18:VAL:HG12	3:2D:211:ARG:NH2	2.31	0.45
3:2D:146:GLU:HB2	3:2D:189:CYS:HB3	1.99	0.45
10:2O:20:MET:HE2	10:2O:22:ILE:HG22	1.98	0.45
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.98	0.45
32:2a:258:G:H2'	32:2a:259:G:H8	1.82	0.45
32:2a:991:U:H1'	32:2a:992:U:OP2	2.17	0.45
32:2a:1202:G:H2'	32:2a:1203:C:O4'	2.16	0.45
33:2b:124:SER:HB2	33:2b:125:PRO:HD3	1.97	0.45
34:2c:182:ILE:HA	34:2c:202:ILE:O	2.17	0.45
37:2f:3:ARG:HD3	37:2f:64:GLN:NE2	2.32	0.45
39:2h:104:ARG:HD3	39:2h:104:ARG:HA	1.70	0.45
1:1A:443:A:N7	5:1F:45:ARG:HG2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:443:A:H1'	1:1A:1201:C:O4'	2.17	0.45
1:1A:1670:C:O2	4:1E:129:HIS:NE2	2.44	0.45
1:1A:1910:G:H22	1:1A:1920:4OC:C2	2.29	0.45
2:1B:40:U:H2'	26:14:2:LYS:HE3	1.99	0.45
8:1I:87:LYS:HB2	8:1I:87:LYS:HE3	1.72	0.45
11:1P:35:HIS:HA	57:1P:301:HOH:O	2.17	0.45
32:1a:5:U:H5'	32:1a:6:G:C5	2.52	0.45
32:1a:479:C:H2'	32:1a:480:U:O4'	2.17	0.45
32:1a:686:U:O4	32:1a:703:G:O2'	2.31	0.45
32:1a:1314:C:N3	32:1a:1323:G:N2	2.52	0.45
33:1b:109:SER:O	33:1b:112:VAL:HG22	2.16	0.45
38:1g:153:HIS:HA	38:1g:155:ARG:NH1	2.32	0.45
45:1n:59:ALA:HB1	45:1n:61:TRP:HZ3	1.82	0.45
1:2A:188:G:H1	1:2A:208:C:H42	1.65	0.45
1:2A:581:C:H2'	1:2A:582:G:H8	1.82	0.45
1:2A:754:C:H2'	1:2A:755:C:C6	2.52	0.45
1:2A:824:A:H1'	1:2A:2358:G:N7	2.32	0.45
1:2A:854:G:H1	1:2A:923:C:H42	1.64	0.45
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.52	0.45
1:2A:1005:C:H2'	1:2A:1006:C:H6	1.82	0.45
1:2A:1713:U:H2'	1:2A:1714:G:H8	1.82	0.45
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.99	0.45
1:2A:2820:A:HO2'	1:2A:2821:A:P	2.39	0.45
22:20:18:ALA:O	22:20:20:ARG:NH1	2.47	0.45
32:2a:143:A:O3'	32:2a:144:G:H8	2.00	0.45
32:2a:392:G:H2'	32:2a:393:A:C8	2.52	0.45
32:2a:426:G:OP1	35:2d:38:TYR:OH	2.26	0.45
33:2b:101:MET:HA	33:2b:108:ILE:HG13	1.99	0.45
37:2f:94:GLN:N	37:2f:94:GLN:OE1	2.50	0.45
45:2n:24:CYS:HB3	45:2n:29:ARG:N	2.31	0.45
1:1A:270:A:OP2	1:1A:271(X):G:N2	2.48	0.44
1:1A:1000:A:H62	1:1A:1154:G:H2'	1.82	0.44
1:1A:2137:C:O2	1:1A:2137:C:H2'	2.18	0.44
1:1A:2314:C:H2'	1:1A:2315:G:H8	1.82	0.44
9:1N:91:LEU:HD23	9:1N:91:LEU:HA	1.84	0.44
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.32	0.44
32:1a:308:C:H2'	32:1a:309:G:H8	1.82	0.44
32:1a:950:U:H2'	32:1a:951:G:H8	1.82	0.44
32:1a:1239:A:H62	32:1a:1299:A:N6	2.15	0.44
32:1a:1249:C:O4'	40:1i:70:LYS:HE3	2.17	0.44
32:1a:1249:C:O3'	40:1i:73:GLN:NE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:185:U:H4'	1:2A:218:A:H4'	1.99	0.44
1:2A:751:A:H5'	18:2W:90:ARG:HA	1.99	0.44
1:2A:1131:G:C2	1:2A:1132:A:C4	3.05	0.44
1:2A:1592:C:H2'	1:2A:1593:G:H8	1.81	0.44
1:2A:2287:A:N6	1:2A:2344:U:H3	2.08	0.44
23:21:75:GLU:HA	23:21:78:LYS:HE2	1.99	0.44
32:2a:246:A:N1	32:2a:278:G:O2'	2.40	0.44
32:2a:300:A:O2'	32:2a:564:C:N3	2.49	0.44
32:2a:748:C:H1'	32:2a:749:C:OP2	2.17	0.44
32:2a:1119:C:H2'	32:2a:1120:G:H8	1.81	0.44
33:2b:47:THR:O	33:2b:51:LEU:N	2.42	0.44
37:2f:30:LEU:HB3	37:2f:35:ALA:HB3	2.00	0.44
41:2j:78:ASN:O	41:2j:80:LYS:N	2.50	0.44
45:2n:47:LEU:HA	45:2n:50:LYS:HB2	1.98	0.44
1:1A:862:G:O2'	2:1B:78:A:N3	2.50	0.44
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.99	0.44
32:1a:662:G:H2'	32:1a:663:A:H8	1.80	0.44
32:1a:731:G:OP1	32:1a:766:A:H1'	2.17	0.44
42:1k:18:ARG:HG3	42:1k:33:THR:OG1	2.17	0.44
43:1l:113:ARG:C	43:1l:114:LYS:HD2	2.43	0.44
45:1n:26:ARG:HD3	45:1n:43:CYS:SG	2.57	0.44
1:2A:285:C:H2'	1:2A:286:C:C6	2.52	0.44
1:2A:981:A:N1	1:2A:2027:G:O2'	2.48	0.44
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.32	0.44
1:2A:1191:G:H2'	1:2A:1192:G:H8	1.83	0.44
1:2A:2103:C:N4	1:2A:2185:C:H42	2.14	0.44
1:2A:2345:G:N3	1:2A:2381:C:H2'	2.33	0.44
1:2A:2562:U:H1'	10:2O:23:ARG:HE	1.82	0.44
2:2B:80:U:H2'	2:2B:81:G:C8	2.52	0.44
7:2H:149:ARG:NH1	7:2H:154:PRO:HG2	2.33	0.44
21:2Z:193:GLU:HA	21:2Z:194:PRO:HD3	1.83	0.44
23:21:4:VAL:HB	23:21:11:ARG:HG2	1.99	0.44
32:2a:502:G:H4'	32:2a:550:G:H4'	1.99	0.44
32:2a:993:G:H2'	32:2a:995:C:H41	1.82	0.44
33:2b:47:THR:HA	33:2b:202:PRO:HG2	2.00	0.44
1:1A:307:G:H21	1:1A:330:A:N6	2.15	0.44
1:1A:1381:G:N7	57:1A:3946:HOH:O	2.35	0.44
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.98	0.44
20:1Y:15:VAL:HG21	20:1Y:42:VAL:HG11	1.99	0.44
26:14:44:THR:OG1	26:14:47:GLN:HB2	2.18	0.44
32:1a:947:G:H2'	32:1a:948:C:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1007:C:N3	32:1a:1022:G:O6	2.50	0.44
32:1a:1012:U:H2'	32:1a:1013:G:C8	2.52	0.44
32:1a:1023:G:H2'	32:1a:1024:G:C8	2.53	0.44
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.39	0.44
37:1f:94:GLN:HG3	49:1r:32:ARG:HD3	1.98	0.44
40:1i:21:PRO:HA	40:1i:58:HIS:O	2.17	0.44
41:1j:11:PHE:CE1	41:1j:67:THR:HG22	2.52	0.44
1:2A:1720:U:H2'	1:2A:1721:G:O4'	2.17	0.44
1:2A:1755:A:H2	1:2A:2716:U:H1'	1.82	0.44
1:2A:1837:C:OP1	32:2a:784:C:H4'	2.17	0.44
5:2F:74:ARG:H	5:2F:74:ARG:HG3	1.45	0.44
5:2F:122:LYS:HB3	5:2F:191:ARG:HD2	1.99	0.44
13:2R:36:THR:HG22	13:2R:37:THR:H	1.83	0.44
17:2V:40:LEU:HB2	17:2V:46:VAL:HG12	2.00	0.44
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.52	0.44
32:2a:373:A:H1'	32:2a:481:G:N3	2.33	0.44
32:2a:673:G:H2'	32:2a:674:G:H8	1.79	0.44
32:2a:928:G:H1	32:2a:1389:C:H42	1.64	0.44
32:2a:939:G:OP1	38:2g:102:ARG:NH1	2.46	0.44
32:2a:1069:C:H42	32:2a:1106:G:H1	1.66	0.44
1:1A:854:G:H2'	1:1A:855:G:H8	1.80	0.44
1:1A:904:C:H2'	1:1A:905:U:C6	2.52	0.44
1:1A:2408:U:OP2	57:1A:3857:HOH:O	2.21	0.44
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.99	0.44
32:1a:689:C:OP1	42:1k:27:ASN:ND2	2.50	0.44
32:1a:757:U:H2'	32:1a:758:G:O4'	2.18	0.44
35:1d:13:ARG:HB2	35:1d:40:PRO:HD3	1.99	0.44
48:1q:52:LYS:HG2	48:1q:53:LEU:H	1.82	0.44
50:1s:16:LEU:HD12	50:1s:16:LEU:HA	1.87	0.44
1:2A:107:C:H2'	1:2A:108:U:C6	2.52	0.44
1:2A:585:G:OP1	57:2A:3617:HOH:O	2.21	0.44
1:2A:795:C:H2'	1:2A:796:C:C6	2.52	0.44
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.99	0.44
1:2A:1013:C:H2'	1:2A:1014:U:C6	2.53	0.44
1:2A:1287:A:O4'	13:2R:104:ARG:HD3	2.17	0.44
1:2A:1468:C:H2'	1:2A:1469:A:H8	1.83	0.44
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.52	0.44
2:2B:13:A:O2'	2:2B:14:U:H3'	2.17	0.44
3:2D:108:PRO:HD2	3:2D:111:LEU:HG	1.99	0.44
6:2G:41:GLN:NE2	6:2G:56:ALA:HB1	2.32	0.44
32:2a:110:C:H2'	32:2a:111:G:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1280:A:H5'	41:2j:40:LEU:HD22	1.97	0.44
33:2b:204:ASN:ND2	33:2b:207:ALA:H	2.16	0.44
36:2e:78:HIS:HB3	39:2h:107:LEU:HD12	1.99	0.44
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	1.99	0.44
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.82	0.44
1:1A:2301:C:H2'	1:1A:2302:G:C8	2.52	0.44
14:1S:103:GLU:O	14:1S:107:GLU:HG3	2.18	0.44
32:1a:66:G:C2	32:1a:104:G:H1'	2.52	0.44
50:1s:40:ILE:HG22	50:1s:67:VAL:HA	1.99	0.44
1:2A:1721:G:H8	1:2A:1741:A:H62	1.65	0.44
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.53	0.44
6:2G:145:THR:HG22	6:2G:148:MET:HE3	1.98	0.44
7:2H:56:SER:OG	7:2H:58:GLU:HG2	2.18	0.44
32:2a:272:C:H2'	32:2a:273:A:C8	2.52	0.44
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	2.00	0.44
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	2.00	0.44
33:2b:187:LEU:HD21	33:2b:204:ASN:O	2.16	0.44
34:2c:6:HIS:NE2	34:2c:8:ILE:HB	2.32	0.44
44:2m:6:GLY:O	44:2m:67:GLU:HG2	2.18	0.44
1:1A:264:C:O2'	1:1A:265:A:H2'	2.18	0.44
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.52	0.44
1:1A:1321:A:H2'	1:1A:1322:A:O4'	2.18	0.44
1:1A:1409:C:H2'	1:1A:1410:G:C8	2.52	0.44
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.50	0.44
1:1A:2032:G:OP2	1:1A:2454:G:O2'	2.32	0.44
1:1A:2299:G:H2'	1:1A:2300:G:C8	2.52	0.44
1:1A:2336:A:H61	22:10:43:THR:CG2	2.30	0.44
1:1A:2393:A:O2'	11:1P:60:MET:O	2.28	0.44
2:1B:48:A:OP2	14:1S:30:ARG:NH2	2.51	0.44
4:1E:36:ARG:HG2	4:1E:47:VAL:HG22	2.00	0.44
7:1H:46:GLU:OE2	7:1H:51:ARG:NH2	2.34	0.44
32:1a:266:G:N3	32:1a:266:G:H2'	2.33	0.44
32:1a:491:G:H2'	32:1a:492:G:H8	1.83	0.44
32:1a:1084:G:H5'	32:1a:1102:A:OP2	2.16	0.44
32:1a:1098:C:H4'	32:1a:1168:A:H2	1.81	0.44
32:1a:1259:C:O2'	32:1a:1283:G:N2	2.49	0.44
35:1d:104:VAL:O	35:1d:108:LEU:HB2	2.18	0.44
38:1g:103:TRP:HH2	38:1g:141:VAL:HG21	1.82	0.44
51:1t:27:LYS:O	51:1t:31:SER:OG	2.32	0.44
1:2A:208:C:H2'	1:2A:209:C:C6	2.52	0.44
1:2A:247:G:H4'	1:2A:386:G:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(A):A:N1	1:2A:272(D):G:O2'	2.48	0.44
1:2A:1069:A:C6	1:2A:1095:A:H4'	2.52	0.44
1:2A:1833:U:H2'	1:2A:1834:U:C6	2.52	0.44
1:2A:2010:G:OP1	18:2W:41:LYS:HD3	2.18	0.44
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.52	0.44
3:2D:125:ILE:HB	37:2f:81:ILE:HD11	1.99	0.44
6:2G:11:TYR:HA	6:2G:15:VAL:HB	2.00	0.44
9:2N:70:LYS:HD3	9:2N:87:LEU:HD12	1.99	0.44
12:2Q:17:LEU:HD21	12:2Q:41:TRP:NE1	2.32	0.44
13:2R:59:ASP:OD1	13:2R:59:ASP:N	2.49	0.44
32:2a:857:C:H2'	32:2a:858:G:O4'	2.17	0.44
32:2a:1063:C:H3'	32:2a:1064:G:H2'	1.99	0.44
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.52	0.44
32:2a:1291:G:H4'	40:2i:38:GLN:O	2.17	0.44
40:2i:4:TYR:O	40:2i:19:LEU:N	2.36	0.44
43:2l:92:0TD:H4	43:2l:92:0TD:H8	1.73	0.44
47:2p:28:ARG:HG3	47:2p:29:ASP:N	2.31	0.44
51:2t:37:SER:O	51:2t:41:ILE:HG12	2.17	0.44
1:1A:783:A:O2'	1:1A:785:G:OP1	2.29	0.44
1:1A:1071:G:H1'	1:1A:1089:G:C8	2.52	0.44
1:1A:1141:U:OP2	9:1N:63:THR:OG1	2.30	0.44
1:1A:1999:C:H5"	1:1A:2723:C:O2'	2.17	0.44
1:1A:2405:G:O2'	1:1A:2411:A:N6	2.48	0.44
1:1A:2438:U:O2'	1:1A:2440:C:OP1	2.25	0.44
3:1D:25:THR:HG1	3:1D:82:ILE:H	1.66	0.44
9:1N:58:ASP:OD1	9:1N:58:ASP:N	2.48	0.44
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.18	0.44
25:13:51:ALA:HA	25:13:54:VAL:HG12	2.00	0.44
32:1a:165:C:H2'	32:1a:166:G:C8	2.53	0.44
32:1a:1134:G:H2'	32:1a:1135:U:H5'	2.00	0.44
32:1a:1158:C:H5	32:1a:1181:G:H1	1.66	0.44
32:1a:1371:G:O3'	40:1i:69:GLY:HA3	2.17	0.44
40:1i:42:ARG:NH2	40:1i:75:ASP:OD1	2.50	0.44
42:1k:22:HIS:O	57:1k:5001:HOH:O	2.21	0.44
47:1p:71:ARG:HG3	47:1p:80:PHE:CZ	2.52	0.44
50:1s:28:LYS:HB2	50:1s:28:LYS:HE2	1.73	0.44
1:2A:320:A:H4'	1:2A:322:A:N7	2.33	0.44
1:2A:1319:G:C6	1:2A:1320:C:N4	2.86	0.44
1:2A:1487:G:H1	1:2A:1502:C:H42	1.66	0.44
2:2B:90:A:N7	2:2B:91:C:H1'	2.33	0.44
3:2D:276:LYS:H	3:2D:276:LYS:HG3	1.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:124:SER:O	6:2G:124:SER:OG	2.36	0.44
11:2P:106:LEU:HD22	11:2P:112:LEU:HG	2.00	0.44
12:2Q:50:ALA:HB1	12:2Q:121:ALA:HB1	1.99	0.44
32:2a:373:A:H61	32:2a:391:G:H1'	1.83	0.44
32:2a:1002:G:H2'	32:2a:1003:G:C8	2.53	0.44
33:2b:127:ILE:C	33:2b:129:GLU:H	2.25	0.44
37:2f:97:PHE:CZ	49:2r:61:LYS:HE3	2.52	0.44
41:2j:80:LYS:O	41:2j:84:GLN:HB2	2.17	0.44
47:2p:20:VAL:HG21	47:2p:32:TYR:CG	2.52	0.44
1:1A:570:G:H2'	1:1A:2030:A:C5	2.53	0.44
1:1A:724:U:H2'	1:1A:725:G:O4'	2.17	0.44
1:1A:800:A:H8	1:1A:800:A:OP1	2.00	0.44
1:1A:918:A:H5"	2:1B:98:G:O2'	2.17	0.44
1:1A:1098:A:H3'	1:1A:1099:G:H8	1.83	0.44
32:1a:167:G:H2'	32:1a:168:G:C8	2.53	0.44
32:1a:184:G:H2'	32:1a:185:A:H8	1.83	0.44
32:1a:562:C:H1'	43:1l:15:ARG:HB3	1.99	0.44
32:1a:691:G:H2'	32:1a:692:U:C6	2.53	0.44
32:1a:979:C:OP1	32:1a:1223:C:N4	2.51	0.44
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.51	0.44
32:1a:1457:G:H2'	32:1a:1458:G:H8	1.81	0.44
34:1c:121:ALA:O	34:1c:125:GLU:HG3	2.17	0.44
34:1c:131:ARG:HH22	36:1e:50:GLU:CD	2.26	0.44
41:1j:13:HIS:HA	41:1j:16:LEU:HB3	2.00	0.44
1:2A:377:C:H2'	1:2A:378:C:H6	1.82	0.44
1:2A:438:G:H2'	1:2A:440:G:C8	2.53	0.44
1:2A:519:U:H2'	1:2A:520:G:C8	2.52	0.44
1:2A:595:C:H2'	1:2A:596:G:H8	1.83	0.44
1:2A:980:A:N3	1:2A:2037:G:O2'	2.50	0.44
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.17	0.44
1:2A:1629:U:O4	57:2A:3611:HOH:O	2.19	0.44
1:2A:2098:U:H2'	1:2A:2099:U:O4'	2.17	0.44
1:2A:2294:C:P	14:2S:89:ARG:HH22	2.41	0.44
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	1.99	0.44
12:2Q:55:VAL:HG23	21:2Z:183:LEU:HD11	1.99	0.44
21:2Z:157:LEU:HD11	21:2Z:163:LEU:HB2	2.00	0.44
32:2a:41:G:H2'	32:2a:42:G:C8	2.52	0.44
32:2a:1253:G:H5'	41:2j:44:VAL:O	2.17	0.44
35:2d:8:VAL:O	35:2d:11:LEU:HB2	2.18	0.44
1:1A:1063:G:H1	1:1A:1075:C:N4	2.14	0.44
1:1A:1087:G:H1	1:1A:1102:C:N4	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.48	0.44
1:1A:2135:A:H62	1:1A:2156:G:N2	2.16	0.44
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.53	0.44
9:1N:108:PRO:O	9:1N:113:GLY:HA3	2.17	0.44
32:1a:224:C:H2'	32:1a:225:C:C6	2.53	0.44
33:1b:15:VAL:HG12	33:1b:16:HIS:HD2	1.83	0.44
34:1c:6:HIS:NE2	34:1c:8:ILE:HB	2.33	0.44
36:1e:72:GLN:O	36:1e:75:THR:HG22	2.18	0.44
41:1j:42:THR:HG21	41:1j:66:ARG:HB3	2.00	0.44
43:1l:28:LYS:HE2	43:1l:64:TYR:HE2	1.83	0.44
1:2A:210:C:OP2	29:27:29:LYS:HE3	2.18	0.44
1:2A:286:C:H2'	1:2A:287:C:C6	2.53	0.44
1:2A:1275:A:N1	1:2A:1295:C:O2'	2.49	0.44
1:2A:1458:C:H4'	1:2A:1459:G:O4'	2.18	0.44
1:2A:2487:G:H2'	1:2A:2488:A:C8	2.53	0.44
1:2A:2641:G:OP1	9:2N:74:ARG:NH1	2.49	0.44
1:2A:2869:G:H2'	1:2A:2870:C:O4'	2.18	0.44
2:2B:16:G:H1	2:2B:68:C:H42	1.65	0.44
4:2E:7:VAL:HG13	4:2E:27:LEU:HB3	2.00	0.44
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	2.00	0.44
22:20:21:LEU:HD21	22:20:41:ARG:CZ	2.48	0.44
24:22:16:LEU:O	24:22:67:LYS:NZ	2.50	0.44
32:2a:258:G:H1	32:2a:268:C:H42	1.65	0.44
32:2a:1255:G:H1	32:2a:1282:C:H42	1.66	0.44
32:2a:1481:U:H2'	32:2a:1482:G:C8	2.53	0.44
38:2g:72:ARG:NH2	38:2g:142:GLU:OE1	2.51	0.44
1:1A:587:C:O2	11:1P:33:ARG:NH2	2.35	0.43
1:1A:2120:G:C2	1:1A:2121:G:C4	3.06	0.43
4:1E:30:PRO:HD3	4:1E:180:ASN:ND2	2.32	0.43
26:14:55:ARG:O	26:14:57:GLU:HG2	2.17	0.43
32:1a:692:U:O2'	32:1a:694:A:N7	2.32	0.43
32:1a:778:G:H2'	32:1a:779:C:O4'	2.18	0.43
32:1a:1378:C:N4	32:1a:1379:G:N3	2.66	0.43
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.83	0.43
44:1m:5:ALA:HB1	44:1m:61:GLU:HG2	1.99	0.43
1:2A:1598:C:H2'	1:2A:1599:C:C6	2.53	0.43
1:2A:2384:G:OP2	22:20:55:ARG:NH2	2.45	0.43
1:2A:2394:C:H1'	57:2A:3764:HOH:O	2.18	0.43
1:2A:2506:U:O2	54:2A:3515:HGR:H23	2.17	0.43
32:2a:22:G:H2'	32:2a:23:C:C6	2.52	0.43
32:2a:126:G:OP1	32:2a:605:U:O2'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:165:C:H2'	32:2a:166:G:H8	1.82	0.43
32:2a:522:C:H5"	43:2l:120:TYR:OH	2.17	0.43
32:2a:772:U:H2'	32:2a:773:G:O4'	2.18	0.43
32:2a:1067:A:H2'	32:2a:1093:A:H4'	2.00	0.43
38:2g:37:ASN:ND2	40:2i:39:GLY:O	2.46	0.43
38:2g:101:LEU:O	38:2g:105:VAL:HG23	2.17	0.43
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	2.00	0.43
1:1A:380:U:H2'	1:1A:381:G:C8	2.53	0.43
1:1A:2379:G:O2'	14:1S:17:ARG:NH1	2.42	0.43
6:1G:11:TYR:O	6:1G:16:ARG:HG2	2.18	0.43
15:1T:60:THR:HG22	15:1T:77:PRO:HA	2.00	0.43
30:18:4:MET:HE2	30:18:4:MET:HB3	1.75	0.43
32:1a:194:C:H2'	32:1a:195:A:H5"	1.99	0.43
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.33	0.43
32:1a:1378:C:H1'	38:1g:76:ARG:HH22	1.82	0.43
39:1h:51:VAL:HG12	39:1h:52:ASP:H	1.82	0.43
52:1u:12:LYS:HE3	52:1u:19:GLY:HA3	1.99	0.43
1:2A:251:A:C5	1:2A:252:G:H1'	2.53	0.43
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.83	0.43
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.53	0.43
1:2A:2114:A:H8	1:2A:2114:A:O5'	2.01	0.43
1:2A:2494:G:C4	1:2A:2495:G:C8	3.06	0.43
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.46	0.43
20:2Y:14:LEU:HB2	20:2Y:75:ILE:HD11	2.00	0.43
25:23:12:PRO:HB2	25:23:20:LYS:HG2	1.99	0.43
32:2a:1053:G:N7	32:2a:1200:C:H5"	2.32	0.43
35:2d:120:LEU:HB3	35:2d:126:ILE:HD11	1.99	0.43
50:2s:61:TYR:CE2	50:2s:63:THR:HG22	2.53	0.43
1:1A:705:A:C2	1:1A:727:A:H1'	2.54	0.43
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.82	0.43
1:1A:1246:A:OP1	5:1F:38:ARG:NH1	2.46	0.43
1:1A:1578:U:H2'	1:1A:1579:A:H5'	1.99	0.43
1:1A:2564:A:OP1	1:1A:2648:C:O2'	2.30	0.43
1:1A:2846:G:P	15:1T:54:ARG:HB2	2.58	0.43
1:1A:2881:C:H2'	1:1A:2882:A:O4'	2.18	0.43
8:1I:9:LEU:HD23	8:1I:12:LEU:HD13	2.00	0.43
19:1X:31:HIS:HA	19:1X:32:PRO:HD3	1.87	0.43
32:1a:263:A:H2'	32:1a:264:U:C6	2.54	0.43
32:1a:833:U:H2'	32:1a:834:C:H6	1.82	0.43
32:1a:992:U:H2'	32:1a:1043:C:H41	1.82	0.43
34:1c:17:ASP:O	34:1c:54:ARG:NH2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:6:LEU:HD23	48:1q:23:VAL:HG21	1.99	0.43
1:2A:79:G:H2'	1:2A:80:G:C8	2.54	0.43
1:2A:307:G:N1	1:2A:310:A:OP2	2.50	0.43
1:2A:665:C:H2'	1:2A:666:G:H8	1.83	0.43
1:2A:909:A:C6	1:2A:912:C:C2	3.06	0.43
1:2A:1199:U:OP1	57:2A:3618:HOH:O	2.21	0.43
1:2A:2363:C:O2	22:20:39:ARG:NH2	2.48	0.43
2:2B:38:C:O2	2:2B:48:A:H1'	2.18	0.43
22:20:48:GLY:HA3	22:20:80:HIS:ND1	2.33	0.43
26:24:41:PRO:HG3	26:24:49:PHE:CD2	2.53	0.43
32:2a:636:U:H2'	32:2a:637:G:C8	2.53	0.43
32:2a:658:G:C6	32:2a:659:U:C4	3.06	0.43
32:2a:1031:G:O2'	32:2a:1032:G:H5'	2.18	0.43
32:2a:1190:G:O2'	34:2c:3:ASN:HB3	2.18	0.43
33:2b:8:LYS:HG3	33:2b:9:GLU:H	1.83	0.43
39:2h:3:THR:OG1	39:2h:4:ASP:N	2.51	0.43
39:2h:121:ASP:OD1	39:2h:121:ASP:N	2.50	0.43
41:2j:38:ILE:HA	41:2j:39:PRO:HD3	1.88	0.43
42:2k:29:ILE:HG23	42:2k:44:SER:HB3	2.00	0.43
50:2s:16:LEU:HD23	50:2s:20:LEU:HD12	2.00	0.43
1:1A:863:A:H2'	1:1A:864:G:C8	2.54	0.43
1:1A:1097:U:H2'	1:1A:1098:A:O4'	2.18	0.43
1:1A:1300:U:H4'	1:1A:1301:A:H5"	2.00	0.43
1:1A:1310:G:OP2	29:17:9:ARG:NE	2.40	0.43
2:1B:40:U:O2'	2:1B:43:C:OP2	2.32	0.43
3:1D:12:SER:HB2	3:1D:208:LYS:HB3	2.00	0.43
5:1F:170:LEU:HA	5:1F:171:PRO:HD3	1.84	0.43
8:1I:88:ILE:HG22	8:1I:90:GLY:H	1.83	0.43
16:1U:95:LEU:HD12	16:1U:95:LEU:HA	1.84	0.43
17:1V:22:VAL:HG23	17:1V:23:GLU:O	2.17	0.43
32:1a:79:G:C2	32:1a:90:U:O2	2.70	0.43
32:1a:114:U:H1'	32:1a:353:A:H1'	1.99	0.43
32:1a:448:A:H2'	32:1a:449:C:C6	2.53	0.43
32:1a:675:A:H1'	42:1k:116:HIS:CD2	2.54	0.43
32:1a:826:C:H2'	32:1a:827:U:C6	2.53	0.43
33:1b:53:ARG:HH22	33:1b:200:ILE:HD12	1.83	0.43
47:1p:43:LYS:HG2	47:1p:48:TRP:CG	2.53	0.43
1:2A:38:A:H2'	1:2A:39:C:C6	2.53	0.43
1:2A:57:C:H2'	1:2A:58:G:O4'	2.18	0.43
1:2A:1270:C:O2'	1:2A:1648:C:OP2	2.30	0.43
1:2A:1805:U:O2	3:2D:50:THR:HB	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2052:G:O4'	4:2E:142:GLY:HA3	2.19	0.43
1:2A:2117:A:N6	1:2A:2172:U:O4	2.51	0.43
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.53	0.43
11:2P:27:HIS:O	11:2P:31:ALA:HA	2.18	0.43
15:2T:23:ARG:HD3	15:2T:120:ARG:NH1	2.33	0.43
17:2V:62:LEU:HD21	17:2V:95:LEU:HB2	1.99	0.43
26:24:1:MET:HE2	26:24:6:HIS:CD2	2.52	0.43
32:2a:417:C:H2'	32:2a:418:C:C6	2.53	0.43
32:2a:735:C:H5'	49:2r:71:LYS:HD3	1.99	0.43
33:2b:7:VAL:HG12	33:2b:8:LYS:HG2	2.00	0.43
40:2i:50:LEU:HB3	40:2i:56:LEU:HG	1.99	0.43
41:2j:16:LEU:HD23	41:2j:94:VAL:HG22	2.01	0.43
42:2k:38:ASN:HA	42:2k:39:PRO:HD3	1.90	0.43
1:1A:569:U:C4	1:1A:570:G:C6	3.06	0.43
1:1A:824:A:H1'	1:1A:2358:G:N7	2.33	0.43
1:1A:910:A:N1	1:1A:2277:G:H1'	2.32	0.43
1:1A:1011:G:OP2	16:1U:66:ASN:ND2	2.51	0.43
1:1A:1406:U:H2'	1:1A:1407:C:C6	2.54	0.43
1:1A:1816:G:H8	3:1D:62:TYR:CZ	2.37	0.43
1:1A:2031:A:O2'	1:1A:2454:G:N2	2.50	0.43
1:1A:2319:G:H22	14:1S:3:ARG:CD	2.23	0.43
1:1A:2654:A:N1	1:1A:2665:A:H5"	2.33	0.43
1:1A:2788:C:O2'	1:1A:2809:A:N3	2.44	0.43
6:1G:16:ARG:O	6:1G:20:ILE:HG13	2.18	0.43
9:1N:34:LEU:O	9:1N:49:GLY:HA3	2.18	0.43
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.64	0.43
32:1a:59:A:H5"	32:1a:387:U:H5"	2.01	0.43
32:1a:96:U:H2'	32:1a:97:G:H8	1.84	0.43
32:1a:99:U:H2'	32:1a:100:C:C6	2.53	0.43
32:1a:848:C:H2'	32:1a:849:C:C6	2.53	0.43
32:1a:957:U:H5"	50:1s:81:ARG:NH1	2.34	0.43
33:1b:53:ARG:HA	33:1b:56:ARG:HH11	1.83	0.43
39:1h:104:ARG:HA	39:1h:104:ARG:HD3	1.79	0.43
48:1q:94:ASN:O	48:1q:98:LEU:HD13	2.18	0.43
49:1r:34:TYR:CD1	49:1r:35:ARG:HG3	2.54	0.43
49:1r:76:LEU:HB3	49:1r:78:LEU:HG	2.00	0.43
1:2A:534:U:H2'	1:2A:535:C:C6	2.53	0.43
1:2A:768:G:O2'	1:2A:1379:A:N1	2.46	0.43
1:2A:862:G:H2'	1:2A:863:A:O4'	2.19	0.43
1:2A:907:U:O2'	12:2Q:101:ARG:NH2	2.51	0.43
1:2A:1034:G:O5'	1:2A:1034:G:H8	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1080:C:H2'	1:2A:1081:U:C6	2.53	0.43
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.18	0.43
1:2A:2540:C:H2'	1:2A:2541:A:O4'	2.18	0.43
1:2A:2794:C:N4	1:2A:2802:G:O6	2.51	0.43
1:2A:2819:G:H2'	1:2A:2821:A:N7	2.34	0.43
1:2A:2846:G:P	15:2T:54:ARG:HB2	2.59	0.43
21:2Z:182:LYS:HD3	21:2Z:186:GLU:OE2	2.18	0.43
26:24:1:MET:HE2	26:24:6:HIS:CG	2.53	0.43
32:2a:56:U:H2'	32:2a:57:G:C8	2.54	0.43
32:2a:194:C:H2'	32:2a:195:A:H5"	2.01	0.43
32:2a:632:A:H3'	32:2a:633:G:C8	2.54	0.43
32:2a:696:A:N1	32:2a:797:C:O2'	2.46	0.43
32:2a:853:G:O6	57:2a:1807:HOH:O	2.20	0.43
32:2a:1185:G:H8	32:2a:1185:G:O5'	2.02	0.43
32:2a:1227:A:OP1	50:2s:80:TYR:OH	2.28	0.43
33:2b:120:ALA:O	33:2b:125:PRO:HG2	2.18	0.43
40:2i:50:LEU:HD23	40:2i:85:LEU:HD11	2.00	0.43
1:1A:248:G:C2	1:1A:2431:U:H4'	2.52	0.43
1:1A:1548:C:H2'	1:1A:1549:C:C6	2.53	0.43
1:1A:1882:C:H2'	1:1A:1883:G:O4'	2.19	0.43
1:1A:2442:C:H2'	1:1A:2443:C:H6	1.82	0.43
1:1A:2820:A:O2'	1:1A:2821:A:OP1	2.32	0.43
3:1D:68:LYS:HE3	3:1D:70:TRP:CH2	2.53	0.43
6:1G:3:LEU:HD23	6:1G:3:LEU:HA	1.77	0.43
6:1G:47:LYS:NZ	6:1G:80:PHE:O	2.38	0.43
6:1G:115:ARG:HB3	6:1G:136:ARG:HH21	1.84	0.43
8:1I:40:THR:O	8:1I:44:LEU:HB2	2.19	0.43
8:1I:109:ILE:HD12	8:1I:130:TYR:CZ	2.53	0.43
9:1N:34:LEU:HD21	9:1N:120:LEU:HB2	2.01	0.43
11:1P:63:PRO:HB2	30:18:30:ARG:NH2	2.33	0.43
15:1T:1:MET:HE2	15:1T:3:ARG:HG2	1.99	0.43
26:14:18:CYS:SG	26:14:20:ASN:HB2	2.58	0.43
31:19:2:LYS:NZ	31:19:31:LYS:O	2.51	0.43
32:1a:430:A:OP1	35:1d:9:CYS:HB2	2.18	0.43
32:1a:1065:U:H1'	32:1a:1066:C:OP2	2.18	0.43
43:1l:53:ARG:HB3	43:1l:93:LEU:HD11	2.00	0.43
45:1n:9:LYS:O	45:1n:12:ARG:HG2	2.19	0.43
1:2A:631:A:N3	1:2A:2415:G:O2'	2.48	0.43
1:2A:868:U:C4	1:2A:869:G:N7	2.87	0.43
1:2A:899:A:O2'	1:2A:900:A:H5'	2.19	0.43
3:2D:111:LEU:HD23	3:2D:127:VAL:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2P:121:LYS:HG3	11:2P:122:PRO:HD2	2.00	0.43
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.54	0.43
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.36	0.43
19:2X:65:ARG:HD2	19:2X:70:LEU:HD22	2.00	0.43
32:2a:376:G:H5"	47:2p:5:ARG:HD2	2.00	0.43
32:2a:490:G:H2'	32:2a:491:G:C8	2.54	0.43
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.54	0.43
32:2a:1184:G:H2'	32:2a:1185:G:C8	2.54	0.43
39:2h:4:ASP:OD2	39:2h:85:ARG:NH1	2.51	0.43
41:2j:13:HIS:HA	41:2j:16:LEU:HB2	2.01	0.43
1:1A:239:U:H2'	1:1A:240:G:O4'	2.18	0.43
1:1A:1359:A:N3	1:1A:1359:A:H5'	2.33	0.43
1:1A:2602:A:H4'	1:1A:2603:G:OP1	2.18	0.43
8:1I:31:LEU:HD21	8:1I:38:LEU:HD13	2.01	0.43
11:1P:124:LYS:HE3	11:1P:146:VAL:HG21	2.00	0.43
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.83	0.43
32:1a:109:A:C6	32:1a:326:G:C6	3.07	0.43
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.59	0.43
33:1b:15:VAL:HG12	33:1b:16:HIS:CD2	2.54	0.43
33:1b:19:HIS:NE2	33:1b:20:GLU:HG3	2.34	0.43
36:1e:102:ALA:HB3	36:1e:107:ARG:HB2	2.01	0.43
38:1g:50:ILE:HD11	38:1g:58:PRO:HB3	2.01	0.43
50:1s:39:THR:HA	50:1s:70:LYS:HD3	2.00	0.43
51:1t:30:LYS:HA	51:1t:33:ILE:HD12	2.01	0.43
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.43
1:2A:1195:G:O2'	1:2A:1226:A:N1	2.40	0.43
1:2A:2843:G:H1	1:2A:2874:C:H42	1.66	0.43
7:2H:10:PRO:HA	7:2H:49:VAL:HG22	2.01	0.43
8:2I:129:THR:HA	8:2I:138:ILE:O	2.19	0.43
9:2N:109:LYS:HD2	9:2N:109:LYS:N	2.34	0.43
11:2P:100:LEU:HD22	11:2P:105:LEU:HD12	2.01	0.43
32:2a:576:G:N2	32:2a:760:G:OP2	2.52	0.43
32:2a:651:C:H2'	32:2a:652:U:C6	2.54	0.43
32:2a:1027:C:H5"	32:2a:1028:C:C5	2.54	0.43
32:2a:1168:A:H2'	32:2a:1169:A:O4'	2.19	0.43
32:2a:1248:A:N3	40:2i:70:LYS:NZ	2.60	0.43
32:2a:1347:G:N2	32:2a:1374:A:O5'	2.49	0.43
34:2c:22:TRP:HB2	34:2c:59:ARG:HB2	1.99	0.43
37:2f:97:PHE:HD2	49:2r:31:LEU:HD12	1.83	0.43
1:1A:300:A:H2'	1:1A:334:C:H1'	2.01	0.43
1:1A:312:G:H4'	1:1A:331:A:C2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:579:G:H2'	1:1A:580:C:C6	2.54	0.43
1:1A:1078:U:N3	1:1A:1088:A:H5"	2.34	0.43
1:1A:2012:G:P	18:1W:11:ARG:HH22	2.41	0.43
1:1A:2392:A:N3	11:1P:61:ARG:HG2	2.33	0.43
3:1D:264:LYS:HA	3:1D:265:PRO:HD3	1.92	0.43
4:1E:134:ILE:HA	4:1E:137:HIS:HD2	1.84	0.43
6:1G:165:THR:OG1	6:1G:168:GLU:HG3	2.19	0.43
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	2.01	0.43
14:1S:15:ARG:O	14:1S:19:LYS:HG2	2.19	0.43
26:14:28:LYS:HB2	26:14:31:ILE:HD11	1.99	0.43
26:14:34:GLU:HG2	44:1m:3:ARG:HA	2.01	0.43
27:15:16:ARG:HG3	27:15:17:ASP:N	2.33	0.43
32:1a:299:G:C6	32:1a:300:A:C6	3.06	0.43
41:1j:9:ARG:HH12	41:1j:97:GLU:HG3	1.83	0.43
44:1m:34:LEU:HD13	44:1m:41:PRO:HB3	2.01	0.43
1:2A:271(Q):G:H2'	1:2A:271(R):G:H8	1.84	0.43
1:2A:336:C:H2'	1:2A:337:C:C6	2.54	0.43
1:2A:657:U:H2'	1:2A:658:C:C6	2.54	0.43
1:2A:1022:G:C5	1:2A:1140:C:C4	3.07	0.43
1:2A:2109:U:N3	1:2A:2181:G:O6	2.52	0.43
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.19	0.43
10:2O:34:THR:OG1	10:2O:35:VAL:N	2.51	0.43
11:2P:84:ASN:HB3	11:2P:117:GLU:O	2.19	0.43
17:2V:22:VAL:HG23	17:2V:23:GLU:O	2.18	0.43
21:2Z:5:LEU:O	21:2Z:59:LEU:HA	2.19	0.43
21:2Z:183:LEU:HA	21:2Z:186:GLU:HB2	2.01	0.43
23:21:81:LYS:HB3	23:21:81:LYS:HE2	1.73	0.43
32:2a:858:G:H1	32:2a:870:U:P	2.42	0.43
32:2a:965:A:H5'	32:2a:969:A:O4'	2.18	0.43
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.51	0.43
32:2a:1068:G:N2	32:2a:1191:A:N3	2.53	0.43
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.84	0.43
39:2h:25:ASP:CG	39:2h:60:ARG:HG2	2.44	0.43
43:2l:10:LEU:HB3	48:2q:32:TYR:CE2	2.54	0.43
1:1A:112:U:H5'	24:12:65:ASN:ND2	2.33	0.43
1:1A:191:A:H2'	1:1A:192:C:C6	2.54	0.43
1:1A:272(I):U:H2'	1:1A:272(J):C:C6	2.53	0.43
1:1A:729:G:OP1	3:1D:10:THR:OG1	2.27	0.43
1:1A:1063:G:H2'	1:1A:1064:C:H5	1.84	0.43
1:1A:1754:C:H2'	1:1A:1755:A:O4'	2.19	0.43
1:1A:2010:G:H5"	18:1W:42:ARG:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2747:G:O6	1:1A:2755:C:H5”	2.19	0.43
9:1N:138:LEU:HD23	9:1N:138:LEU:HA	1.75	0.43
32:1a:44:G:C2	32:1a:45:U:H1’	2.54	0.43
32:1a:618:C:N4	32:1a:621:A:N7	2.67	0.43
32:1a:1226:C:H4’	50:1s:80:TYR:CZ	2.54	0.43
32:1a:1308:U:H3	32:1a:1329:A:N6	2.16	0.43
35:1d:178:VAL:HG12	35:1d:179:GLU:H	1.83	0.43
43:1l:92:0TD:H4	43:1l:92:0TD:H8	1.86	0.43
43:1l:117:ARG:HG2	43:1l:122:THR:HB	2.01	0.43
44:1m:76:ALA:O	44:1m:80:ARG:HG2	2.18	0.43
46:1o:82:ILE:O	46:1o:86:GLY:N	2.51	0.43
1:2A:876:C:H2’	1:2A:877:U:O4’	2.19	0.43
1:2A:1027:A:C2	1:2A:2488:A:H5’	2.54	0.43
1:2A:1223:G:C2	1:2A:1227:G:C5	3.07	0.43
1:2A:1528(A):A:H2’	1:2A:1529:G:O4’	2.19	0.43
1:2A:2845:G:H2’	1:2A:2846:G:C8	2.54	0.43
1:2A:2880:C:O2’	13:2R:90:ARG:NH1	2.51	0.43
2:2B:9:G:OP1	14:2S:25:ARG:NH2	2.50	0.43
6:2G:37:VAL:HG23	6:2G:99:MET:HG3	2.01	0.43
6:2G:101:ILE:HG21	26:24:25:TYR:HB2	2.01	0.43
13:2R:100:LEU:HD11	13:2R:113:LEU:HD23	1.99	0.43
20:2Y:77:PRO:HD2	20:2Y:106:LEU:HD23	2.00	0.43
21:2Z:4:ARG:HD3	21:2Z:58:VAL:HB	2.00	0.43
27:25:16:ARG:HD2	27:25:17:ASP:OD1	2.18	0.43
31:29:14:CYS:HA	31:29:27:CYS:HB2	2.00	0.43
32:2a:137:C:H2’	32:2a:138:G:H8	1.84	0.43
32:2a:277:C:H2’	32:2a:278:G:C8	2.54	0.43
32:2a:806:C:H2’	32:2a:807:A:H8	1.84	0.43
32:2a:1193:G:O2’	36:2e:25:ARG:NH2	2.51	0.43
32:2a:1266:G:N2	32:2a:1269:A:OP2	2.49	0.43
33:2b:219:VAL:O	33:2b:222:ILE:HG13	2.18	0.43
38:2g:18:TYR:CD1	38:2g:59:LEU:HD13	2.54	0.43
1:1A:739:G:OP1	57:1A:3860:HOH:O	2.21	0.43
1:1A:857:C:OP1	22:10:77:ARG:NH2	2.46	0.43
1:1A:910:A:N3	1:1A:2264:C:O2’	2.51	0.43
1:1A:947:G:OP2	57:1A:3862:HOH:O	2.21	0.43
1:1A:2171:A:H1’	1:1A:2172:U:C6	2.54	0.43
1:1A:2570:G:H2’	1:1A:2571:C:O4’	2.18	0.43
5:1F:95:ARG:HB3	5:1F:97:TYR:CE2	2.54	0.43
12:1Q:84:GLY:O	12:1Q:85:LYS:HB2	2.18	0.43
15:1T:98:LYS:HB3	15:1T:100:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:30:ASN:OD1	21:1Z:33:LEU:N	2.51	0.43
30:18:62:LEU:HB3	30:18:65:GLU:HG2	2.00	0.43
32:1a:67:C:H42	32:1a:102:G:H1	1.66	0.43
32:1a:100:C:H2'	32:1a:101:A:C8	2.53	0.43
32:1a:688:G:H2'	32:1a:689:C:H6	1.84	0.43
32:1a:1184:G:OP1	32:1a:1184:G:H3'	2.19	0.43
34:1c:108:ASN:HA	34:1c:109:PRO:HD2	1.90	0.43
1:2A:77:C:O3'	24:22:14:ARG:NH2	2.52	0.43
1:2A:271(Q):G:H2'	1:2A:271(R):G:C8	2.54	0.43
1:2A:960:A:H5'	1:2A:2457:U:H4'	2.01	0.43
1:2A:1065:U:H3	1:2A:1073:A:N6	2.12	0.43
1:2A:1193:G:H2'	1:2A:1194:A:C8	2.54	0.43
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.18	0.43
1:2A:2282:G:H4'	1:2A:2389:G:O2'	2.19	0.43
1:2A:2641:G:P	9:2N:74:ARG:HH12	2.42	0.43
32:2a:560:U:H5'	32:2a:566:G:N2	2.34	0.43
32:2a:735:C:H2'	32:2a:736:C:C6	2.54	0.43
32:2a:833:U:H2'	32:2a:834:C:C6	2.54	0.43
32:2a:1004:A:H5'	32:2a:1025:U:C5	2.53	0.43
33:2b:146:GLN:O	33:2b:150:SER:HB2	2.19	0.43
35:2d:128:VAL:HG12	35:2d:129:ASN:HD22	1.84	0.43
44:2m:84:ILE:HB	50:2s:66:MET:HE2	2.01	0.43
47:2p:21:VAL:HG11	47:2p:59:TRP:NE1	2.34	0.43
1:1A:1186:G:H2'	1:1A:1187:G:O4'	2.19	0.42
1:1A:1547:C:H2'	1:1A:1548:C:C6	2.54	0.42
1:1A:2405:G:O2'	1:1A:2406:U:OP1	2.31	0.42
1:1A:2845:G:H5"	15:1T:54:ARG:O	2.19	0.42
2:1B:24:G:N7	2:1B:56:G:H2'	2.34	0.42
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	2.01	0.42
21:1Z:48:PHE:HE1	21:1Z:71:VAL:HG11	1.83	0.42
32:1a:1295:G:O2'	44:1m:14:ARG:NH1	2.52	0.42
33:1b:110:GLN:HA	33:1b:113:HIS:CD2	2.54	0.42
1:2A:271(R):G:H2'	1:2A:271(S):G:C8	2.54	0.42
1:2A:754:C:H2'	1:2A:755:C:H6	1.84	0.42
1:2A:910:A:C6	1:2A:911:A:C6	3.07	0.42
1:2A:1053:C:O2'	1:2A:1054:A:OP1	2.30	0.42
1:2A:1183:G:H2'	1:2A:1184:G:H8	1.84	0.42
1:2A:2305:A:H2'	1:2A:2306:C:C6	2.54	0.42
1:2A:2419:U:H2'	1:2A:2420:C:C6	2.54	0.42
3:2D:71:ASP:HB3	3:2D:103:ARG:HH12	1.84	0.42
4:2E:5:LEU:HD11	4:2E:79:ARG:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:19:ARG:HG2	31:29:20:HIS:ND1	2.33	0.42
32:2a:950:U:H2'	32:2a:951:G:H8	1.83	0.42
32:2a:1230:C:H2'	32:2a:1231:G:H8	1.83	0.42
35:2d:17:VAL:HG11	35:2d:197:PRO:HB2	2.01	0.42
44:2m:99:ARG:HB2	44:2m:101:GLN:NE2	2.34	0.42
45:2n:46:GLU:O	45:2n:50:LYS:HG2	2.19	0.42
51:2t:38:LYS:HB3	51:2t:38:LYS:HE2	1.83	0.42
1:1A:29:U:H2'	1:1A:30:G:C8	2.54	0.42
1:1A:563:G:H5'	1:1A:572:A:H4'	2.01	0.42
1:1A:975(A):G:H1'	1:1A:990:A:C2	2.54	0.42
1:1A:1359:A:H2'	1:1A:1360:A:H5'	2.00	0.42
1:1A:1482:G:N2	1:1A:1507:A:H1'	2.34	0.42
7:1H:137:ASP:HB3	7:1H:140:LYS:HB3	2.01	0.42
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.52	0.42
32:1a:201:C:H42	32:1a:216:G:H22	1.65	0.42
32:1a:253:U:H2'	32:1a:254:G:C8	2.55	0.42
32:1a:954:G:H21	32:1a:1227:A:H61	1.66	0.42
38:1g:28:ASN:HD21	38:1g:36:LYS:NZ	2.16	0.42
39:1h:86:ILE:HG21	39:1h:133:LEU:HD13	2.02	0.42
47:1p:1:MET:HG3	47:1p:3:LYS:HG3	2.00	0.42
1:2A:918:A:H5"	2:2B:98:G:O2'	2.19	0.42
1:2A:923:C:H2'	1:2A:924:C:C6	2.54	0.42
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.48	0.42
1:2A:2104:G:O6	1:2A:2185:C:C4	2.72	0.42
2:2B:40:U:O2'	2:2B:43:C:OP2	2.25	0.42
6:2G:41:GLN:HG2	6:2G:43:LEU:HD13	2.01	0.42
6:2G:66:GLN:HE21	6:2G:92:VAL:HG23	1.85	0.42
9:2N:97:ARG:HA	9:2N:100:GLU:HB2	2.00	0.42
11:2P:121:LYS:O	11:2P:123:LEU:N	2.50	0.42
32:2a:266:G:H3'	48:2q:67:LYS:HB2	2.01	0.42
32:2a:374:A:C6	32:2a:375:U:C4	3.07	0.42
32:2a:1112:C:C4	34:2c:178:LEU:HD12	2.53	0.42
32:2a:1258:G:H8	32:2a:1258:G:OP2	2.01	0.42
32:2a:1322:C:H5"	44:2m:100:GLY:HA3	2.01	0.42
42:2k:58:PRO:HA	42:2k:90:GLY:HA2	2.00	0.42
1:1A:124:G:OP1	1:1A:1376:C:O2'	2.28	0.42
1:1A:185:U:H4'	1:1A:218:A:H4'	2.00	0.42
1:1A:848:G:H2'	1:1A:849:A:C8	2.54	0.42
1:1A:1007:C:H5"	9:1N:35:ARG:NH1	2.35	0.42
1:1A:1082:U:C4	1:1A:1086:A:N1	2.84	0.42
1:1A:2105:C:N4	1:1A:2184:G:N1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2705:A:O2'	1:1A:2852:G:OP1	2.30	0.42
7:1H:116:GLU:HA	7:1H:117:PRO:HD3	1.93	0.42
8:1I:5:LEU:HD11	8:1I:19:VAL:HG22	2.02	0.42
9:1N:48:MET:HE2	9:1N:48:MET:HB3	1.43	0.42
19:1X:84:ALA:HB3	19:1X:87:GLN:CD	2.44	0.42
32:1a:295:C:H2'	32:1a:296:U:O4'	2.19	0.42
32:1a:390:C:H2'	32:1a:391:G:C8	2.55	0.42
32:1a:953:G:H5'	32:1a:965:A:H61	1.85	0.42
33:1b:74:LYS:HD3	33:1b:76:GLN:NE2	2.34	0.42
33:1b:184:VAL:H	33:1b:198:ASP:HB2	1.83	0.42
38:1g:127:ALA:HA	38:1g:131:LYS:O	2.19	0.42
40:1i:10:ARG:HG2	40:1i:75:ASP:HB2	2.01	0.42
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.55	0.42
1:2A:414:C:H2'	1:2A:415:A:C8	2.54	0.42
1:2A:563:G:C4	1:2A:2018:G:C2	3.06	0.42
1:2A:571:A:O2'	17:2V:78:LYS:HE2	2.20	0.42
1:2A:698:C:O2'	1:2A:734:A:N6	2.53	0.42
1:2A:751:A:C6	1:2A:789:A:C5	3.07	0.42
1:2A:947:G:N2	1:2A:971:C:C2	2.87	0.42
1:2A:1748:G:H2'	1:2A:1749:A:H8	1.84	0.42
6:2G:96:ARG:O	6:2G:99:MET:HB3	2.20	0.42
8:2I:117:GLU:HG3	8:2I:118:LYS:H	1.85	0.42
13:2R:20:LEU:HD21	13:2R:40:LYS:HD3	2.02	0.42
18:2W:40:ASN:O	18:2W:41:LYS:HG2	2.19	0.42
32:2a:390:C:H2'	32:2a:391:G:H8	1.84	0.42
32:2a:1216:G:OP1	45:2n:2:ALA:HA	2.19	0.42
33:2b:28:PHE:CE2	33:2b:190:THR:HA	2.54	0.42
34:2c:156:ARG:NH1	34:2c:193:TYR:O	2.52	0.42
35:2d:173:TRP:CD1	35:2d:174:LEU:HG	2.53	0.42
35:2d:200:GLU:O	35:2d:204:ILE:HG12	2.19	0.42
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.59	0.42
50:2s:80:TYR:CZ	50:2s:82:GLY:HA2	2.54	0.42
1:1A:587:C:P	11:1P:21:ARG:HH22	2.41	0.42
1:1A:634:C:H2'	1:1A:635:C:C6	2.54	0.42
1:1A:686:G:N2	1:1A:788:A:H61	2.17	0.42
1:1A:1024:G:O2'	1:1A:1144:G:O2'	2.37	0.42
1:1A:1263:U:C4	1:1A:1264:G:C6	3.08	0.42
1:1A:2097:C:H2'	1:1A:2098:U:C6	2.54	0.42
1:1A:2711:A:H5"	1:1A:2712:U:H5"	2.01	0.42
1:1A:2732:G:H3'	1:1A:2733:A:O4'	2.20	0.42
1:1A:2786:U:O2'	4:1E:62:PRO:O	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:96:HIS:HD2	3:1D:102:LYS:HG2	1.84	0.42
5:1F:102:PRO:HB2	5:1F:105:VAL:HG23	2.01	0.42
5:1F:117:ARG:HA	5:1F:117:ARG:HD3	1.91	0.42
6:1G:15:VAL:HG21	6:1G:176:LEU:HD23	2.01	0.42
7:1H:86:GLU:HB2	7:1H:165:ALA:CB	2.47	0.42
18:1W:65:LEU:HD12	18:1W:68:ARG:HE	1.84	0.42
32:1a:115:G:H4'	32:1a:116:A:O5'	2.19	0.42
32:1a:454:C:H41	32:1a:477:A:N6	2.17	0.42
32:1a:1028:C:N4	32:1a:1033:G:N1	2.66	0.42
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.84	0.42
36:1e:29:GLY:HA2	36:1e:46:GLY:O	2.19	0.42
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	2.00	0.42
1:2A:668:G:H5'	1:2A:669:G:OP2	2.19	0.42
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.35	0.42
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.53	0.42
1:2A:1939:5MU:OP1	1:2A:2604:U:O2'	2.38	0.42
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.55	0.42
17:2V:4:ILE:HG22	17:2V:38:LEU:HD12	2.01	0.42
32:2a:730:G:C5	32:2a:731:G:H1'	2.54	0.42
32:2a:1005:A:H8	32:2a:1024:G:N2	2.17	0.42
32:2a:1479:C:H2'	32:2a:1480:G:H8	1.83	0.42
1:1A:222:A:H3'	1:1A:421:U:H5'	2.02	0.42
1:1A:271(U):G:H2'	1:1A:271(V):G:H8	1.83	0.42
1:1A:579:G:O2'	1:1A:2019:A:OP1	2.34	0.42
1:1A:855:G:H2'	1:1A:856:C:C6	2.55	0.42
1:1A:884:C:H3'	1:1A:885:C:C6	2.55	0.42
1:1A:1881:C:H2'	1:1A:1882:C:C6	2.55	0.42
1:1A:2138:C:O2	1:1A:2153:G:N1	2.51	0.42
1:1A:2232:U:P	23:11:40:ARG:HH12	2.42	0.42
1:1A:2701:C:H2'	1:1A:2702:U:H2'	2.00	0.42
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.89	0.42
32:1a:491:G:H2'	32:1a:492:G:C8	2.55	0.42
32:1a:590:C:H2'	32:1a:591:U:C6	2.54	0.42
32:1a:595:G:H1'	32:1a:596:C:H5	1.84	0.42
32:1a:1094:G:O5'	32:1a:1095:U:H5	2.03	0.42
32:1a:1144:G:N2	32:1a:1146:A:H62	2.16	0.42
32:1a:1446:U:H4'	32:1a:1447:A:N7	2.34	0.42
33:1b:8:LYS:H	33:1b:8:LYS:HG3	1.54	0.42
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	2.01	0.42
38:1g:53:LYS:HE3	38:1g:122:HIS:NE2	2.34	0.42
44:1m:91:ARG:HB2	44:1m:98:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:1q:58:GLU:OE1	48:1q:75:ARG:NE	2.52	0.42
1:2A:1527:G:N2	1:2A:1545:A:OP2	2.50	0.42
1:2A:1739:U:O2'	1:2A:1740:G:H8	2.01	0.42
1:2A:2047:U:H2'	1:2A:2048:G:C8	2.55	0.42
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.20	0.42
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.52	0.42
2:2B:29:A:O2'	2:2B:58:A:N1	2.53	0.42
4:2E:38:THR:HA	4:2E:39:PRO:HD3	1.94	0.42
5:2F:38:ARG:HG2	5:2F:99:TYR:OH	2.20	0.42
7:2H:139:GLN:HG2	7:2H:140:LYS:N	2.35	0.42
15:2T:92:GLY:O	15:2T:120:ARG:NH2	2.52	0.42
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.54	0.42
32:2a:1127:G:H2'	32:2a:1128:C:O4'	2.19	0.42
32:2a:1165:C:H2'	32:2a:1166:G:O4'	2.20	0.42
32:2a:1301:U:O2'	32:2a:1302:U:H5'	2.19	0.42
42:2k:18:ARG:HD2	42:2k:20:TYR:CE2	2.54	0.42
42:2k:18:ARG:NH2	42:2k:35:PRO:O	2.51	0.42
47:2p:59:TRP:HB3	47:2p:64:ALA:HB2	2.01	0.42
1:1A:797:C:OP2	5:1F:62:ARG:HB2	2.20	0.42
1:1A:888:C:H2'	1:1A:889:C:C5	2.55	0.42
1:1A:1270:C:H4'	1:1A:1325:G:N7	2.34	0.42
1:1A:1653:G:C6	13:1R:9:LYS:HB2	2.55	0.42
1:1A:1849:G:H2'	1:1A:1850:G:C8	2.52	0.42
1:1A:1987:G:H2'	1:1A:1988:C:H6	1.84	0.42
1:1A:2120:G:N2	1:1A:2179:C:H1'	2.34	0.42
1:1A:2721:A:OP1	57:1A:3864:HOH:O	2.22	0.42
32:1a:472:A:H5"	47:1p:80:PHE:HB3	2.01	0.42
32:1a:994:A:N1	32:1a:1047:G:H4'	2.34	0.42
32:1a:1230:C:H2'	32:1a:1231:G:H8	1.85	0.42
1:2A:211:A:H2'	1:2A:212:G:O4'	2.19	0.42
1:2A:481:G:O5'	20:2Y:47:LYS:NZ	2.41	0.42
1:2A:644:A:C2	1:2A:2369:A:H1'	2.55	0.42
1:2A:963:U:H1'	1:2A:2250:G:O6	2.19	0.42
1:2A:1069:A:H2'	1:2A:1073:A:N7	2.34	0.42
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.54	0.42
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.19	0.42
1:2A:2129:C:O2	1:2A:2159:G:N1	2.36	0.42
1:2A:2181:G:H2'	1:2A:2182:G:O4'	2.19	0.42
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.19	0.42
6:2G:109:VAL:C	6:2G:112:PRO:HD2	2.44	0.42
10:2O:71:ARG:HA	10:2O:72:PRO:HD3	1.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2Q:11:LYS:HD3	12:2Q:87:LYS:HD3	2.01	0.42
16:2U:92:ARG:HA	16:2U:95:LEU:HB2	2.00	0.42
32:2a:17:U:H2'	32:2a:18:C:H6	1.84	0.42
32:2a:193:C:H2'	32:2a:194:C:H6	1.84	0.42
32:2a:253:U:H2'	32:2a:254:G:C8	2.55	0.42
32:2a:1004:A:C5	32:2a:1037:C:C4	3.08	0.42
44:2m:94:ARG:HA	44:2m:94:ARG:HD3	1.83	0.42
52:2u:18:TYR:CE1	52:2u:24:ARG:HG2	2.54	0.42
1:1A:1514:U:H2'	1:1A:1515:G:H8	1.85	0.42
1:1A:2328:A:H2'	1:1A:2329:G:H8	1.84	0.42
1:1A:2640:G:N7	57:1A:3923:HOH:O	2.37	0.42
3:1D:70:TRP:HB3	3:1D:190:TYR:CE2	2.55	0.42
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	2.01	0.42
32:1a:302:G:N3	32:1a:556:C:H4'	2.34	0.42
32:1a:836:G:H1	32:1a:850:U:H3	1.68	0.42
32:1a:1131:G:H2'	32:1a:1132:C:C6	2.54	0.42
32:1a:1428:A:H2'	32:1a:1429:C:C6	2.54	0.42
38:1g:56:GLN:O	38:1g:58:PRO:HD3	2.20	0.42
41:1j:16:LEU:HA	41:1j:94:VAL:HG21	2.00	0.42
1:2A:784:A:C8	1:2A:792:G:C5	3.08	0.42
1:2A:1059:G:C2	1:2A:1079:C:N3	2.87	0.42
1:2A:1062:G:O2'	1:2A:1063:G:H5'	2.19	0.42
1:2A:1180:C:H2'	1:2A:1181:C:C6	2.55	0.42
1:2A:1653:G:C4	13:2R:9:LYS:HD2	2.55	0.42
4:2E:61:ARG:HA	4:2E:64:LYS:HB2	2.01	0.42
5:2F:27:GLU:O	5:2F:112:MET:HE2	2.19	0.42
6:2G:5:VAL:HG12	26:24:25:TYR:HE2	1.83	0.42
6:2G:18:GLU:HB3	6:2G:175:LEU:HD21	2.02	0.42
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	2.02	0.42
12:2Q:63:LYS:HA	21:2Z:178:GLU:HG2	2.02	0.42
17:2V:37:VAL:O	17:2V:51:VAL:HG23	2.20	0.42
23:21:3:LYS:HB3	23:21:4:VAL:H	1.64	0.42
32:2a:541:G:H2'	32:2a:542:G:C8	2.54	0.42
32:2a:859:A:H2'	32:2a:860:A:O4'	2.20	0.42
32:2a:936:C:H2'	32:2a:937:A:O4'	2.20	0.42
34:2c:9:GLY:HA3	45:2n:49:HIS:HA	2.02	0.42
38:2g:25:ALA:O	38:2g:29:LYS:HG2	2.19	0.42
43:2l:82:VAL:O	43:2l:106:ASP:HB2	2.18	0.42
1:1A:78:A:H2'	1:1A:79:G:H8	1.84	0.42
1:1A:236:C:H2'	1:1A:237:C:C6	2.55	0.42
1:1A:245:G:O6	30:18:8:LYS:HE3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1385:G:H1'	1:1A:1386:C:C6	2.55	0.42
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	2.19	0.42
1:1A:1514:U:H2'	1:1A:1515:G:C8	2.55	0.42
1:1A:2543:G:H2'	1:1A:2544:G:C8	2.55	0.42
15:1T:37:GLY:HA2	15:1T:38:ASN:HA	1.60	0.42
26:14:40:HIS:O	26:14:44:THR:HG23	2.19	0.42
32:1a:457:C:H2'	32:1a:458:C:H6	1.83	0.42
32:1a:457:C:H2'	32:1a:458:C:C6	2.55	0.42
32:1a:516:PSU:C2	32:1a:517:G:C6	3.08	0.42
32:1a:589:C:H2'	32:1a:590:C:C6	2.53	0.42
32:1a:627:G:H2'	32:1a:628:G:H8	1.83	0.42
32:1a:762:C:H2'	32:1a:763:G:C8	2.54	0.42
32:1a:973:G:N3	41:1j:54:PHE:HE1	2.18	0.42
32:1a:1016:A:O2'	32:1a:1217:C:O2'	2.33	0.42
32:1a:1118:C:H1'	32:1a:1179:A:N3	2.35	0.42
32:1a:1241:G:H1	32:1a:1296:C:H42	1.67	0.42
34:1c:21:ARG:HH22	34:1c:56:ASP:CG	2.28	0.42
37:1f:75:LEU:O	37:1f:79:LEU:HG	2.20	0.42
40:1i:36:TYR:CE1	40:1i:70:LYS:HE2	2.55	0.42
40:1i:73:GLN:O	40:1i:77:ILE:HG13	2.18	0.42
42:1k:21:ILE:HG12	42:1k:30:VAL:HG22	2.01	0.42
1:2A:29:U:H2'	1:2A:30:G:C8	2.55	0.42
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.20	0.42
1:2A:807:U:H2'	1:2A:808:G:H8	1.85	0.42
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.50	0.42
1:2A:1084:A:H8	1:2A:1085:A:H4'	1.84	0.42
1:2A:2019:A:O4'	16:2U:34:LYS:HE3	2.19	0.42
1:2A:2136:C:H42	1:2A:2156:G:N2	2.18	0.42
1:2A:2302:G:O2'	6:2G:126:ASP:O	2.35	0.42
1:2A:2638:G:OP2	4:2E:82:ARG:NH1	2.44	0.42
2:2B:15:A:OP2	2:2B:69:G:N2	2.53	0.42
6:2G:96:ARG:N	6:2G:99:MET:HE2	2.34	0.42
22:20:40:GLN:NE2	22:20:43:THR:HA	2.35	0.42
32:2a:504:C:H1'	32:2a:510:A:C4	2.55	0.42
32:2a:992:U:H1'	32:2a:993:G:OP2	2.19	0.42
32:2a:1079:G:O3'	36:2e:14:ARG:NH2	2.47	0.42
32:2a:1255:G:O3'	32:2a:1258:G:H1'	2.20	0.42
33:2b:28:PHE:CE1	33:2b:31:TYR:HD2	2.38	0.42
34:2c:43:LEU:HD22	34:2c:47:LEU:HD12	2.02	0.42
35:2d:172:PRO:HB2	35:2d:187:ARG:HH21	1.85	0.42
49:2r:76:LEU:HD23	49:2r:78:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:54:LYS:HA	51:2t:57:ARG:CZ	2.49	0.42
1:1A:78:A:H2'	1:1A:79:G:C8	2.55	0.42
1:1A:243:U:OP2	30:18:8:LYS:NZ	2.33	0.42
1:1A:606:U:H4'	1:1A:658:C:H4'	2.01	0.42
1:1A:812:C:H5"	1:1A:1250:G:O2'	2.20	0.42
1:1A:922:U:H2'	1:1A:923:C:C6	2.55	0.42
1:1A:1037:G:H1	1:1A:1118:C:H42	1.68	0.42
15:1T:74:ARG:HG2	15:1T:76:PHE:CZ	2.55	0.42
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.55	0.42
21:1Z:4:ARG:HD2	21:1Z:60:GLU:OE2	2.20	0.42
21:1Z:158:PRO:O	21:1Z:161:VAL:HG13	2.20	0.42
23:11:82:LEU:HA	23:11:85:LEU:HD12	2.02	0.42
32:1a:689:C:H2'	32:1a:690:G:O4'	2.20	0.42
32:1a:743:U:H2'	32:1a:744:C:C6	2.55	0.42
32:1a:973:G:H3'	32:1a:974:A:H5"	2.01	0.42
32:1a:1010:G:H2'	32:1a:1011:G:H8	1.85	0.42
32:1a:1109:C:H2'	32:1a:1110:A:O4'	2.19	0.42
32:1a:1273:G:H2'	32:1a:1274:G:O4'	2.20	0.42
33:1b:122:PHE:HD1	33:1b:122:PHE:HA	1.63	0.42
34:1c:136:GLN:HB3	34:1c:140:ARG:NH2	2.35	0.42
1:2A:619:G:H5"	1:2A:620:G:OP2	2.20	0.42
1:2A:1042:G:H2'	1:2A:1043:C:C6	2.55	0.42
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.35	0.42
1:2A:1368:G:OP1	29:27:28:ARG:NH2	2.49	0.42
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.55	0.42
1:2A:2466:C:OP1	31:29:4:ARG:HB2	2.20	0.42
3:2D:202:LYS:NZ	32:2a:773:G:O2'	2.47	0.42
5:2F:170:LEU:HA	5:2F:171:PRO:HD3	1.82	0.42
6:2G:170:ARG:NH2	6:2G:182:LYS:O	2.31	0.42
9:2N:33:LEU:HD12	9:2N:38:HIS:CE1	2.55	0.42
32:2a:69:G:H2'	32:2a:70:G:C8	2.54	0.42
32:2a:176:C:H2'	32:2a:177:C:H6	1.84	0.42
32:2a:457:C:H2'	32:2a:458:C:H6	1.84	0.42
32:2a:955:U:O2'	50:2s:83:HIS:HD2	2.03	0.42
32:2a:994:A:H61	32:2a:1047:G:H4'	1.85	0.42
32:2a:1277:C:O2'	32:2a:1279:A:H8	2.03	0.42
32:2a:1292:U:H2'	32:2a:1293:G:H8	1.85	0.42
32:2a:1447:A:H5"	32:2a:1452:C:OP2	2.19	0.42
34:2c:5:ILE:HD13	41:2j:51:ARG:HH22	1.84	0.42
34:2c:36:ASP:OD1	34:2c:57:ILE:HD13	2.20	0.42
47:2p:37:GLY:HA3	47:2p:50:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:271(L):U:OP1	8:1I:50:ARG:NH1	2.53	0.42
1:1A:1827:C:O2'	1:1A:1970:A:N3	2.39	0.42
1:1A:1946:U:H2'	1:1A:1947:C:C6	2.55	0.42
1:1A:2544:G:H1'	1:1A:2646:C:H4'	2.01	0.42
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.19	0.42
3:1D:249:PRO:HD2	3:1D:250:TRP:CZ3	2.54	0.42
4:1E:47:VAL:HG12	4:1E:49:LEU:HD22	2.01	0.42
8:1I:4:ILE:HD11	8:1I:44:LEU:HD12	2.02	0.42
8:1I:88:ILE:HG22	8:1I:90:GLY:N	2.35	0.42
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.55	0.42
12:1Q:31:ASP:HA	12:1Q:134:ARG:HH12	1.84	0.42
15:1T:92:GLY:C	15:1T:117:ASP:HB2	2.44	0.42
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	2.01	0.42
23:11:5:CYS:HB3	23:11:10:LYS:H	1.85	0.42
29:17:24:THR:HA	29:17:25:PRO:HD3	1.92	0.42
32:1a:413:G:H22	32:1a:429:U:H5"	1.84	0.42
47:1p:23:ASP:HB3	47:1p:26:ARG:HB2	2.02	0.42
51:1t:101:GLY:HA3	51:1t:102:GLY:HA2	1.89	0.42
1:2A:484:C:H2'	1:2A:485:C:H6	1.85	0.42
1:2A:963:U:H2'	1:2A:964:C:H6	1.85	0.42
1:2A:1012:U:O4	9:2N:28:THR:HG21	2.20	0.42
1:2A:1102:C:H2'	1:2A:1103:A:C8	2.55	0.42
1:2A:1575:C:H2'	1:2A:1576:U:H6	1.85	0.42
1:2A:1807:G:N2	1:2A:1810:A:OP2	2.49	0.42
1:2A:2010:G:H5"	18:2W:42:ARG:HB2	2.02	0.42
1:2A:2058:A:N6	57:2A:3712:HOH:O	2.51	0.42
2:2B:115:G:H2'	2:2B:116:G:C8	2.55	0.42
5:2F:165:ARG:HA	5:2F:168:ARG:NE	2.35	0.42
6:2G:111:LEU:HB2	6:2G:112:PRO:HD3	2.01	0.42
26:24:37:SER:HA	26:24:43:TYR:CD2	2.55	0.42
32:2a:272:C:H2'	32:2a:273:A:H8	1.85	0.42
32:2a:1003:G:C8	32:2a:1004:A:H1'	2.55	0.42
32:2a:1138:G:H3'	32:2a:1138:G:N3	2.35	0.42
32:2a:1316:G:N2	32:2a:1319:A:OP2	2.53	0.42
32:2a:1320:C:OP1	50:2s:70:LYS:HG3	2.20	0.42
33:2b:158:LEU:HA	33:2b:159:PRO:HD3	1.87	0.42
36:2e:42:GLY:HA3	36:2e:65:ASN:O	2.20	0.42
39:2h:86:ILE:HG13	39:2h:133:LEU:HD22	2.01	0.42
46:2o:24:SER:O	46:2o:28:GLN:HG3	2.20	0.42
1:1A:308:G:O2'	1:1A:329:G:N2	2.53	0.41
1:1A:613:G:O2'	1:1A:614(C):A:N1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:987:G:O2'	1:1A:1000:A:N3	2.48	0.41
1:1A:1056:G:H5"	1:1A:1057:A:O4'	2.20	0.41
1:1A:1083:U:N3	1:1A:1086:A:OP2	2.51	0.41
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.55	0.41
1:1A:2114:A:H3'	1:1A:2115:G:C8	2.55	0.41
1:1A:2133:G:C2	1:1A:2157:G:H2'	2.55	0.41
5:1F:165:ARG:HA	5:1F:168:ARG:HD3	2.02	0.41
17:1V:1:MET:HE1	17:1V:44:LYS:HG2	2.01	0.41
26:14:28:LYS:HA	26:14:29:PRO:HD3	1.82	0.41
31:19:2:LYS:HD3	31:19:4:ARG:NH2	2.35	0.41
32:1a:253:U:H2'	32:1a:254:G:H8	1.84	0.41
32:1a:374:A:N1	32:1a:390:C:O2'	2.47	0.41
32:1a:1305:G:H1	32:1a:1331:G:H1'	1.85	0.41
32:1a:1327:C:H2'	32:1a:1328:C:C6	2.55	0.41
33:1b:9:GLU:OE2	33:1b:217:ARG:NH2	2.53	0.41
34:1c:26:LYS:HA	45:1n:36:PHE:CE1	2.56	0.41
1:2A:112:U:H5'	24:22:65:ASN:ND2	2.35	0.41
1:2A:171:G:H2'	1:2A:172:C:C6	2.55	0.41
1:2A:646:A:H2'	1:2A:647:G:C8	2.55	0.41
1:2A:1216:G:C6	1:2A:1217:C:C4	3.08	0.41
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.20	0.41
1:2A:2420:C:P	30:28:33:ASN:H	2.43	0.41
2:2B:75:G:O2'	21:2Z:10:ARG:NH2	2.52	0.41
6:2G:112:PRO:HG3	26:24:43:TYR:CE2	2.53	0.41
6:2G:121:ASN:HA	6:2G:122:PRO:HD2	1.95	0.41
19:2X:72:LYS:HG2	19:2X:73:ARG:O	2.20	0.41
32:2a:102:G:O2'	32:2a:151:A:N3	2.44	0.41
32:2a:528:C:H3'	32:2a:529:G:H8	1.84	0.41
32:2a:778:G:H1'	42:2k:119:CYS:HB3	2.02	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.20	0.41
32:2a:1201:A:H4'	32:2a:1202:G:H5"	2.02	0.41
32:2a:1205:U:H2'	32:2a:1206:G:C8	2.55	0.41
33:2b:61:LEU:HD23	33:2b:68:ILE:HD11	2.01	0.41
33:2b:87:ARG:NH2	33:2b:219:VAL:HB	2.35	0.41
1:1A:135:G:O6	57:1A:3859:HOH:O	2.21	0.41
1:1A:632:A:H2'	1:1A:633:A:C8	2.55	0.41
1:1A:1374:G:H2'	1:1A:1375:C:O4'	2.20	0.41
1:1A:1915:5MU:H2'	1:1A:1916:A:O4'	2.20	0.41
1:1A:2684:U:H1'	10:1O:70:LYS:HD2	2.01	0.41
2:1B:86:G:H1	2:1B:91:C:H42	1.67	0.41
3:1D:13:ARG:HA	3:1D:13:ARG:HD3	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:74:ARG:NH1	57:1F:402:HOH:O	2.52	0.41
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	2.01	0.41
19:1X:24:GLY:O	19:1X:83:VAL:HG22	2.20	0.41
32:1a:630:G:N2	57:1a:3231:HOH:O	2.52	0.41
32:1a:673:G:O3'	37:1f:87:ARG:NH2	2.53	0.41
33:1b:179:LYS:HB3	33:1b:179:LYS:HE3	1.84	0.41
47:1p:4:ILE:HG12	47:1p:21:VAL:HB	2.01	0.41
1:2A:1022:G:O2'	1:2A:1024:G:O6	2.30	0.41
1:2A:1348:G:O6	1:2A:1349:A:N6	2.53	0.41
1:2A:1379:A:O5'	1:2A:1379:A:H8	2.03	0.41
1:2A:2206:G:H5"	1:2A:2207:G:N7	2.34	0.41
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.52	0.41
6:2G:46:ALA:HB2	6:2G:53:LEU:HB2	2.01	0.41
9:2N:91:LEU:HD23	9:2N:91:LEU:HA	1.84	0.41
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.53	0.41
21:2Z:91:LEU:HD12	21:2Z:91:LEU:HA	1.88	0.41
21:2Z:132:ASN:O	21:2Z:134:PRO:HD3	2.20	0.41
24:22:53:LEU:O	24:22:57:ILE:HG13	2.20	0.41
27:25:50:GLY:HA2	27:25:58:LEU:HD23	2.03	0.41
32:2a:176:C:H2'	32:2a:177:C:C6	2.56	0.41
32:2a:866:C:C4	32:2a:867:G:H1'	2.55	0.41
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.85	0.41
35:2d:65:ARG:HG3	35:2d:75:PHE:CD1	2.54	0.41
44:2m:4:ILE:HD11	44:2m:60:VAL:HG11	2.01	0.41
1:1A:127:A:H5"	1:1A:128:C:O4'	2.20	0.41
1:1A:1385:G:H4'	1:1A:1386:C:OP1	2.20	0.41
5:1F:38:ARG:HG2	5:1F:99:TYR:OH	2.20	0.41
7:1H:125:VAL:HG12	7:1H:127:GLU:O	2.20	0.41
8:1I:9:LEU:HD12	8:1I:9:LEU:HA	1.77	0.41
10:1O:63:VAL:HG23	10:1O:64:ARG:HG2	2.01	0.41
13:1R:36:THR:HG22	13:1R:37:THR:H	1.85	0.41
21:1Z:152:ALA:HB3	21:1Z:167:PRO:HA	2.03	0.41
32:1a:7:G:O2'	36:1e:120:THR:O	2.38	0.41
32:1a:294:U:H2'	32:1a:295:C:C6	2.55	0.41
32:1a:439:A:C5	32:1a:441:A:H1'	2.55	0.41
32:1a:615:C:H2'	32:1a:616:G:O4'	2.20	0.41
32:1a:779:C:H2'	32:1a:780:A:O4'	2.20	0.41
32:1a:1029:C:C4	32:1a:1032:G:O6	2.73	0.41
32:1a:1047:G:H1'	32:1a:1215:G:O2'	2.21	0.41
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.21	0.41
34:1c:16:ARG:HE	34:1c:54:ARG:HH21	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:1i:16:ARG:HH11	40:1i:64:THR:HG21	1.85	0.41
50:1s:31:ILE:HB	50:1s:49:ILE:HG12	2.01	0.41
1:2A:172:C:H2'	1:2A:173:G:H8	1.85	0.41
1:2A:438:G:H2'	1:2A:440:G:H8	1.86	0.41
1:2A:752:A:H3'	29:27:1:MET:SD	2.60	0.41
1:2A:996:A:OP2	16:2U:93:LYS:NZ	2.42	0.41
1:2A:1479:G:H5"	1:2A:1560:G:H4'	2.02	0.41
1:2A:1486:A:H2'	1:2A:1487:G:C8	2.52	0.41
1:2A:1935:G:H1'	1:2A:1964:G:N2	2.36	0.41
1:2A:2516:G:C5	1:2A:2517:C:C4	3.09	0.41
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.55	0.41
10:2O:4:PRO:HA	10:2O:21:CYS:O	2.20	0.41
26:24:26:SER:OG	26:24:27:THR:N	2.54	0.41
32:2a:975:A:N1	41:2j:48:THR:HB	2.35	0.41
32:2a:1148:U:H2'	32:2a:1149:C:O4'	2.19	0.41
37:2f:21:LEU:O	37:2f:25:ILE:HG12	2.21	0.41
1:1A:380:U:H2'	1:1A:381:G:H8	1.85	0.41
1:1A:1047:G:H2'	1:1A:1110:G:H1	1.85	0.41
1:1A:1388:G:H2'	1:1A:1389:G:H8	1.84	0.41
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.20	0.41
1:1A:2461:C:H2'	1:1A:2462:U:C6	2.56	0.41
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.20	0.41
5:1F:155:LEU:HD23	5:1F:192:LEU:HD12	2.02	0.41
7:1H:40:GLU:OE1	7:1H:61:HIS:NE2	2.42	0.41
10:1O:34:THR:OG1	10:1O:35:VAL:N	2.53	0.41
12:1Q:109:VAL:HG22	12:1Q:113:GLN:OE1	2.19	0.41
32:1a:8:A:H5'	36:1e:101:ILE:HG22	2.02	0.41
32:1a:125:U:H2'	32:1a:126:G:C8	2.56	0.41
32:1a:456:C:H2'	32:1a:457:C:C6	2.55	0.41
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	2.02	0.41
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.55	0.41
1:2A:557:U:H2'	1:2A:558:G:H8	1.85	0.41
1:2A:959:A:C6	1:2A:960:A:C6	3.08	0.41
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.42	0.41
1:2A:2188:C:H3'	1:2A:2189:U:H5"	2.02	0.41
1:2A:2354:G:H2'	1:2A:2355:C:C6	2.56	0.41
2:2B:40:U:N3	2:2B:44:G:OP2	2.31	0.41
6:2G:125:PHE:HB3	6:2G:166:ASP:CG	2.45	0.41
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	2.03	0.41
13:2R:86:ARG:H	13:2R:86:ARG:HG2	1.64	0.41
22:20:43:THR:OG1	22:20:46:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:20:72:ARG:HB2	22:20:75:LEU:HB2	2.02	0.41
32:2a:949:A:H61	32:2a:1232:U:H3	1.68	0.41
32:2a:952:U:H4'	32:2a:964:A:N1	2.35	0.41
32:2a:1010:G:N1	32:2a:1020:U:H1'	2.36	0.41
32:2a:1312:G:H5'	50:2s:5:LEU:HD21	2.02	0.41
32:2a:1346:A:OP1	40:2i:120:ARG:NH1	2.47	0.41
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.21	0.41
33:2b:12:GLU:CA	33:2b:15:VAL:HG22	2.51	0.41
35:2d:28:SER:C	35:2d:30:LYS:H	2.29	0.41
47:2p:1:MET:HG3	47:2p:3:LYS:HG3	2.01	0.41
51:2t:80:ARG:O	51:2t:84:LEU:HB2	2.20	0.41
1:1A:826:U:H2'	1:1A:828:U:O4'	2.20	0.41
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.20	0.41
1:1A:1839:G:C8	1:1A:1927:A:H1'	2.55	0.41
1:1A:1844:C:H2'	1:1A:1845:G:H8	1.86	0.41
1:1A:2420:C:H5'	28:16:54:ILE:HD11	2.03	0.41
10:1O:49:ARG:NH1	32:1a:1422:G:O3'	2.52	0.41
32:1a:541:G:H2'	32:1a:542:G:H8	1.85	0.41
32:1a:643:C:H2'	32:1a:644:G:H8	1.83	0.41
32:1a:868:C:H2'	32:1a:869:G:O4'	2.20	0.41
32:1a:1179:A:O3'	40:1i:103:THR:OG1	2.38	0.41
38:1g:16:LEU:HD13	40:1i:44:VAL:N	2.36	0.41
40:1i:6:GLY:HA3	40:1i:80:GLY:O	2.20	0.41
1:2A:236:C:H2'	1:2A:237:C:C6	2.55	0.41
1:2A:275:G:H2'	1:2A:276:A:O4'	2.20	0.41
1:2A:286:C:H2'	1:2A:287:C:H6	1.86	0.41
1:2A:356:G:H2'	1:2A:357:A:C8	2.55	0.41
1:2A:797:C:OP2	5:2F:62:ARG:HB2	2.20	0.41
1:2A:927:G:H2'	1:2A:928:G:O4'	2.20	0.41
1:2A:1309:G:H4'	29:27:7:PRO:HG2	2.01	0.41
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.51	0.41
1:2A:1860:G:N2	1:2A:1883:G:H1'	2.34	0.41
1:2A:2105:C:H42	1:2A:2183:C:N4	2.16	0.41
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.20	0.41
8:2I:101:LEU:O	8:2I:106:GLY:N	2.53	0.41
14:2S:99:LYS:HE2	14:2S:103:GLU:OE2	2.20	0.41
16:2U:69:CYS:HB3	16:2U:74:LEU:HD12	2.02	0.41
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.29	0.41
32:2a:7:G:H5'	32:2a:298:A:O4'	2.20	0.41
32:2a:20:U:H2'	32:2a:21:G:O4'	2.21	0.41
32:2a:308:C:H2'	32:2a:309:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1320:C:O2	50:2s:36:ARG:NH2	2.46	0.41
32:2a:1327:C:H2'	32:2a:1328:C:C6	2.55	0.41
38:2g:50:ILE:HG22	38:2g:125:MET:HG3	2.02	0.41
40:2i:82:ALA:O	40:2i:86:VAL:HG23	2.20	0.41
51:2t:89:ARG:O	51:2t:93:GLU:N	2.44	0.41
1:1A:394:A:C6	1:1A:395:U:C4	3.09	0.41
1:1A:557:U:H2'	1:1A:558:G:H8	1.85	0.41
1:1A:818:G:H4'	1:1A:838:C:O3'	2.21	0.41
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.55	0.41
1:1A:1417:C:H2'	1:1A:1418:G:O4'	2.21	0.41
1:1A:1645:G:H5"	1:1A:1646:C:O4'	2.20	0.41
1:1A:2239:G:H5'	3:1D:251:GLY:HA3	2.02	0.41
1:1A:2748:A:H5'	7:1H:4:ILE:HD12	2.01	0.41
2:1B:60:C:H2'	2:1B:61:G:H8	1.85	0.41
11:1P:59:LEU:HD11	30:18:10:ALA:HA	2.01	0.41
32:1a:537:G:H5"	43:1l:113:ARG:HH11	1.86	0.41
32:1a:1056:U:O5'	34:1c:163:ALA:HB2	2.20	0.41
32:1a:1232:U:H5"	40:1i:124:GLN:O	2.21	0.41
34:1c:131:ARG:NH1	34:1c:166:GLU:OE2	2.53	0.41
36:1e:77:PRO:O	39:1h:105:ARG:HG2	2.20	0.41
44:1m:60:VAL:HG22	44:1m:64:TRP:HZ3	1.85	0.41
47:1p:71:ARG:HG3	47:1p:80:PHE:HZ	1.86	0.41
1:2A:65:C:H2'	1:2A:66:C:C6	2.56	0.41
1:2A:68:G:H2'	1:2A:69:C:O4'	2.21	0.41
1:2A:327:G:N2	20:2Y:70:SER:OG	2.53	0.41
1:2A:500:G:N2	1:2A:502:A:H3'	2.35	0.41
1:2A:797:C:H2'	1:2A:798:G:H8	1.86	0.41
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.55	0.41
1:2A:1287:A:C5	1:2A:1288:U:C4	3.09	0.41
1:2A:2111:C:N4	1:2A:2147:G:H22	2.19	0.41
1:2A:2817:G:OP1	13:2R:99:LYS:NZ	2.48	0.41
4:2E:9:VAL:HG22	4:2E:25:VAL:O	2.20	0.41
8:2I:48:GLU:HG3	8:2I:52:ARG:NH1	2.36	0.41
32:2a:184:G:H2'	32:2a:185:A:H8	1.85	0.41
32:2a:224:C:H2'	32:2a:225:C:C6	2.56	0.41
32:2a:340:U:H2'	32:2a:341:C:C6	2.56	0.41
37:2f:96:PRO:HB3	49:2r:30:ASP:CG	2.45	0.41
45:2n:23:ARG:HD2	45:2n:28:GLY:O	2.21	0.41
49:2r:26:LEU:HD11	49:2r:42:ARG:HD2	2.02	0.41
1:1A:1030:G:OP2	12:1Q:128:LYS:NZ	2.54	0.41
1:1A:1862:G:H2'	1:1A:1863:G:C8	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:111:ARG:HA	13:1R:1:MET:SD	2.61	0.41
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.52	0.41
8:1I:61:ARG:HA	8:1I:61:ARG:HD3	1.81	0.41
13:1R:65:LEU:HD12	13:1R:65:LEU:HA	1.84	0.41
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.66	0.41
32:1a:903:G:H2'	32:1a:904:C:C6	2.56	0.41
33:1b:28:PHE:CD2	33:1b:190:THR:HA	2.56	0.41
39:1h:66:GLY:N	39:1h:77:GLU:O	2.53	0.41
1:2A:234:C:H2'	1:2A:235:U:C6	2.56	0.41
1:2A:746:A:H2'	1:2A:2612:C:H5"	2.02	0.41
1:2A:1756:G:H4'	1:2A:1758:G:O4'	2.21	0.41
1:2A:2186:G:C2	1:2A:2187:G:C5	3.08	0.41
1:2A:2306:C:H3'	1:2A:2307:G:H2'	2.03	0.41
1:2A:2420:C:H5'	28:26:54:ILE:HD11	2.02	0.41
1:2A:2462:U:H2'	1:2A:2463:C:C6	2.55	0.41
1:2A:2728:U:H5'	10:2O:70:LYS:NZ	2.35	0.41
1:2A:2812:G:H2'	1:2A:2813:A:H8	1.86	0.41
8:2I:83:ALA:HA	8:2I:89:TYR:CD2	2.55	0.41
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.55	0.41
20:2Y:35:TYR:CE2	20:2Y:69:ALA:HB3	2.56	0.41
32:2a:299:G:H2'	32:2a:300:A:C8	2.56	0.41
32:2a:435:C:H2'	32:2a:436:C:C6	2.56	0.41
32:2a:598:U:H4'	39:2h:94:TYR:CD2	2.56	0.41
32:2a:1015:A:H2'	32:2a:1016:A:C8	2.56	0.41
32:2a:1223:C:P	50:2s:78:ARG:HH21	2.43	0.41
32:2a:1402:4OC:H6	32:2a:1402:4OC:O5'	2.21	0.41
33:2b:84:GLU:OE1	33:2b:216:SER:HA	2.21	0.41
36:2e:19:MET:SD	36:2e:24:ARG:HB3	2.59	0.41
37:2f:9:VAL:HB	37:2f:87:ARG:HB2	2.02	0.41
46:2o:33:THR:HG21	46:2o:85:LEU:HD22	2.02	0.41
49:2r:40:LEU:HB3	49:2r:79:LEU:HD11	2.02	0.41
1:1A:245:G:O5'	11:1P:73:GLY:HA2	2.20	0.41
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.56	0.41
1:1A:2147:G:H2'	1:1A:2148:G:H4'	2.02	0.41
1:1A:2219:G:H2'	1:1A:2220:G:H8	1.85	0.41
1:1A:2356:C:O3'	22:10:20:ARG:HD3	2.21	0.41
3:1D:132:PRO:HD3	3:1D:190:TYR:CZ	2.56	0.41
32:1a:62:U:H3	32:1a:105:G:H1	1.69	0.41
32:1a:730:G:C5	32:1a:731:G:H1'	2.55	0.41
32:1a:1095:U:OP1	32:1a:1108:G:N2	2.47	0.41
32:1a:1205:U:H2'	32:1a:1206:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:1c:120:VAL:O	34:1c:124:ILE:HG12	2.20	0.41
43:1l:77:LEU:HD21	43:1l:107:ALA:HA	2.03	0.41
46:1o:78:TYR:CZ	46:1o:82:ILE:HD13	2.55	0.41
1:2A:908:C:OP1	12:2Q:22:LYS:HE2	2.20	0.41
1:2A:960:A:H2'	1:2A:962:G:H5'	2.02	0.41
1:2A:1007:C:OP1	9:2N:37:LYS:NZ	2.50	0.41
1:2A:1188:U:C4'	17:2V:79:VAL:HG22	2.51	0.41
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.56	0.41
1:2A:1759:A:C4'	1:2A:2714:G:H21	2.34	0.41
1:2A:2149:G:N1	1:2A:2150:U:O2	2.54	0.41
1:2A:2666:C:H42	7:2H:109:PHE:HA	1.86	0.41
6:2G:33:ARG:O	6:2G:161:THR:HG23	2.20	0.41
6:2G:174:GLU:HB2	6:2G:180:PHE:HE2	1.85	0.41
12:2Q:26:TYR:O	12:2Q:67:ARG:NH1	2.51	0.41
20:2Y:5:MET:HE2	20:2Y:32:PRO:HA	2.03	0.41
21:2Z:125:LEU:HG	21:2Z:164:ALA:HB3	2.02	0.41
32:2a:430:A:H2'	32:2a:431:A:O4'	2.20	0.41
32:2a:501:C:H2'	32:2a:502:G:H8	1.83	0.41
32:2a:833:U:H2'	32:2a:834:C:H6	1.86	0.41
32:2a:983:A:OP1	45:2n:6:LEU:HD21	2.20	0.41
34:2c:112:SER:HB3	34:2c:115:LEU:HD22	2.03	0.41
36:2e:37:ARG:HH12	36:2e:111:GLU:HG2	1.86	0.41
37:2f:95:GLU:HA	37:2f:96:PRO:HD3	1.90	0.41
40:2i:99:LEU:HD23	40:2i:101:PHE:CE2	2.56	0.41
44:2m:60:VAL:HG23	44:2m:64:TRP:HE3	1.86	0.41
47:2p:27:LYS:HG3	47:2p:30:GLY:HA3	2.02	0.41
1:1A:278:A:O2'	1:1A:279:C:OP1	2.37	0.41
1:1A:340:A:O2'	5:1F:168:ARG:NH2	2.54	0.41
1:1A:489:G:H2'	1:1A:491:G:O4'	2.21	0.41
1:1A:784:A:OP1	57:1A:3850:HOH:O	2.22	0.41
1:1A:827:U:O2	1:1A:2246:G:H4'	2.21	0.41
1:1A:1138:G:N3	9:1N:106:MET:HE2	2.36	0.41
1:1A:2051:A:H5'	1:1A:2578:G:O4'	2.20	0.41
1:1A:2065:C:H4'	1:1A:2251:OMG:HM22	2.03	0.41
1:1A:2134:A:N7	1:1A:2157:G:O2'	2.49	0.41
1:1A:2287:A:C8	1:1A:2289:G:C8	3.09	0.41
1:1A:2320:A:H2'	1:1A:2320:A:N3	2.36	0.41
4:1E:144:ARG:HB3	4:1E:145:LYS:H	1.56	0.41
20:1Y:20:TYR:CE2	20:1Y:43:ASN:HA	2.56	0.41
21:1Z:54:HIS:ND1	21:1Z:101:PRO:HG3	2.35	0.41
32:1a:176:C:H2'	32:1a:177:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:193:C:H2'	32:1a:194:C:H6	1.85	0.41
32:1a:438:G:H5'	35:1d:123:HIS:HD2	1.85	0.41
32:1a:674:G:H2'	32:1a:675:A:C8	2.56	0.41
32:1a:1030(A):G:H2'	32:1a:1030(C):G:OP2	2.21	0.41
32:1a:1047:G:O2'	32:1a:1215:G:O3'	2.34	0.41
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.56	0.41
32:1a:1350:A:C2	38:1g:34:GLY:HA3	2.56	0.41
34:1c:16:ARG:NE	34:1c:54:ARG:HH21	2.18	0.41
35:1d:38:TYR:HA	35:1d:39:PRO:HD3	1.93	0.41
36:1e:6:PHE:CD1	36:1e:36:ASP:HB3	2.56	0.41
36:1e:127:ASN:HA	36:1e:128:PRO:HD3	1.90	0.41
37:1f:45:LEU:HD12	37:1f:59:TYR:HD1	1.85	0.41
1:2A:224:G:H2'	1:2A:225:A:O4'	2.21	0.41
1:2A:470:A:OP1	5:2F:59:TYR:HE1	2.04	0.41
1:2A:601:C:O2'	1:2A:605:C:H5"	2.21	0.41
1:2A:732:C:H2'	1:2A:733:G:O4'	2.21	0.41
1:2A:954:G:H5"	12:2Q:13:GLN:HB3	2.03	0.41
1:2A:1192:G:C2	1:2A:1193:G:C8	3.09	0.41
1:2A:1388:G:H2'	1:2A:1389:G:H8	1.86	0.41
1:2A:1598:C:H2'	1:2A:1599:C:H6	1.86	0.41
1:2A:1840:G:OP2	57:2A:3616:HOH:O	2.20	0.41
1:2A:2295:C:OP1	14:2S:10:ARG:NH1	2.54	0.41
1:2A:2432:A:OP2	57:2A:3619:HOH:O	2.21	0.41
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	2.03	0.41
6:2G:27:ASN:OD1	6:2G:28:VAL:N	2.54	0.41
13:2R:51:LEU:HD22	13:2R:66:VAL:HG13	2.03	0.41
16:2U:52:ARG:HA	16:2U:55:ARG:HG3	2.02	0.41
18:2W:13:SER:HA	18:2W:14:PRO:HD3	1.92	0.41
19:2X:65:ARG:HB2	19:2X:65:ARG:NH2	2.35	0.41
28:26:13:CYS:SG	28:26:47:THR:HG21	2.60	0.41
32:2a:685:G:C2	32:2a:686:U:C4	3.09	0.41
32:2a:687:A:N3	32:2a:688:G:H1'	2.35	0.41
32:2a:981:U:P	45:2n:9:LYS:HZ2	2.43	0.41
32:2a:986:A:H1'	50:2s:54:GLY:O	2.20	0.41
32:2a:1165:C:H3'	32:2a:1166:G:C8	2.53	0.41
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.21	0.41
32:2a:1350:A:C2	38:2g:34:GLY:HA3	2.56	0.41
33:2b:16:HIS:CB	33:2b:204:ASN:HB2	2.50	0.41
33:2b:28:PHE:CD2	33:2b:190:THR:HA	2.56	0.41
33:2b:76:GLN:OE1	33:2b:76:GLN:N	2.46	0.41
35:2d:20:TYR:HD1	35:2d:26:CYS:HB3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:100:VAL:HA	36:2e:118:ILE:HG22	2.03	0.41
38:2g:26:PHE:CE2	38:2g:30:ILE:HD11	2.56	0.41
38:2g:153:HIS:CE1	42:2k:58:PRO:HD2	2.56	0.41
40:2i:4:TYR:HD1	40:2i:87:GLN:HE21	1.69	0.41
41:2j:8:LEU:HD12	41:2j:20:ALA:HB2	2.02	0.41
42:2k:33:THR:HG22	42:2k:39:PRO:HA	2.03	0.41
51:2t:20:LEU:O	51:2t:23:ARG:HG2	2.21	0.41
51:2t:57:ARG:NH1	51:2t:100:ILE:HB	2.34	0.41
1:1A:195:A:H5"	1:1A:196:A:O5'	2.21	0.41
1:1A:754:C:H2'	1:1A:755:C:C6	2.56	0.41
12:1Q:18:LYS:O	12:1Q:98:LYS:HE3	2.21	0.41
12:1Q:57:HIS:NE2	12:1Q:116:GLU:HB3	2.36	0.41
18:1W:41:LYS:HD3	27:15:25:LEU:HD11	2.01	0.41
22:10:72:ARG:HB2	22:10:75:LEU:HB2	2.03	0.41
32:1a:1442:G:O2'	32:1a:1442(A):G:O5'	2.34	0.41
35:1d:159:ARG:O	35:1d:163:GLU:HG3	2.21	0.41
41:1j:63:PHE:CE2	45:1n:45:ARG:HG3	2.56	0.41
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.77	0.41
50:1s:27:GLU:HA	50:1s:28:LYS:HA	1.87	0.41
1:2A:97:C:OP1	24:22:2:LYS:NZ	2.50	0.41
1:2A:287:C:H2'	1:2A:288:C:C6	2.57	0.41
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.44	0.41
1:2A:826:U:H2'	1:2A:828:U:O4'	2.21	0.41
1:2A:1469:A:H2'	1:2A:1470:G:O4'	2.21	0.41
1:2A:1882:C:H3'	1:2A:1883:G:H8	1.85	0.41
1:2A:2729:G:H2'	1:2A:2730:C:C6	2.56	0.41
1:2A:2734:A:H2'	1:2A:2735:G:O4'	2.21	0.41
1:2A:2751:G:H3'	1:2A:2752:C:C6	2.56	0.41
4:2E:32:PRO:HD2	4:2E:50:GLY:O	2.21	0.41
4:2E:188:VAL:HA	4:2E:189:PRO:HD3	1.93	0.41
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.56	0.41
11:2P:39:LYS:HD2	11:2P:45:LEU:HD11	2.02	0.41
16:2U:34:LYS:HD3	16:2U:34:LYS:HA	1.61	0.41
23:21:5:CYS:SG	23:21:62:VAL:HG23	2.61	0.41
32:2a:541:G:H2'	32:2a:542:G:H8	1.86	0.41
32:2a:1030(A):G:H2'	32:2a:1030(B):C:H5"	2.02	0.41
32:2a:1047:G:H5"	45:2n:4:LYS:HD3	2.02	0.41
32:2a:1065:U:H1'	32:2a:1066:C:OP2	2.21	0.41
33:2b:155:LEU:HD21	33:2b:159:PRO:HD3	2.03	0.41
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.21	0.41
42:2k:34:ASP:HB3	42:2k:40:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.21	0.41
1:1A:589:C:P	11:1P:16:ARG:HH12	2.44	0.40
1:1A:1636:C:H2'	1:1A:1637:A:C8	2.56	0.40
1:1A:1665:A:H4'	10:1O:67:LYS:HB2	2.02	0.40
1:1A:1692:U:O2'	1:1A:1693:U:H2'	2.21	0.40
1:1A:1854:A:H2'	1:1A:1855:G:O4'	2.21	0.40
1:1A:2304:G:H22	1:1A:2312:U:H3	1.69	0.40
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	2.03	0.40
7:1H:101:ARG:NH2	7:1H:121:ILE:O	2.54	0.40
21:1Z:72:ARG:HA	21:1Z:72:ARG:HD3	1.96	0.40
21:1Z:150:LEU:HB3	21:1Z:171:ILE:HD11	2.03	0.40
32:1a:262:A:H4'	51:1t:75:ASN:HB2	2.03	0.40
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.56	0.40
33:1b:12:GLU:HB2	33:1b:16:HIS:CD2	2.56	0.40
44:1m:15:VAL:O	44:1m:19:LEU:HD13	2.21	0.40
1:2A:921:G:C6	1:2A:922:U:C4	3.09	0.40
1:2A:1023:U:O2'	1:2A:1122:G:H5'	2.20	0.40
1:2A:1198:U:H2'	1:2A:1199:U:C6	2.56	0.40
1:2A:1865:G:N2	1:2A:1877:A:OP2	2.52	0.40
1:2A:2077:A:H2'	1:2A:2078:C:H6	1.86	0.40
1:2A:2116:G:H2'	1:2A:2117:A:C2	2.57	0.40
1:2A:2772:C:H2'	1:2A:2773:C:C6	2.56	0.40
6:2G:38:VAL:HA	6:2G:93:THR:HA	2.03	0.40
7:2H:38:SER:HA	7:2H:39:PRO:HD3	1.98	0.40
21:2Z:132:ASN:ND2	21:2Z:160:GLY:HA3	2.35	0.40
32:2a:254:G:OP1	48:2q:66:SER:OG	2.18	0.40
32:2a:271:C:H2'	32:2a:272:C:C6	2.56	0.40
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.21	0.40
34:2c:42:LEU:O	34:2c:46:GLU:HG2	2.20	0.40
35:2d:57:ARG:HG2	35:2d:202:LEU:HB3	2.02	0.40
39:2h:6:ILE:HB	39:2h:85:ARG:NH1	2.36	0.40
42:2k:58:PRO:HG3	42:2k:89:ALA:O	2.21	0.40
1:1A:284:U:H2'	1:1A:285:C:C6	2.56	0.40
1:1A:483:A:O2'	20:1Y:49:VAL:O	2.37	0.40
1:1A:764:A:O4'	3:1D:213:ARG:HG3	2.22	0.40
1:1A:1082:U:O4	1:1A:1086:A:C6	2.72	0.40
1:1A:1263:U:H2'	1:1A:1264:G:C8	2.56	0.40
1:1A:1266:G:O2'	1:1A:2012:G:O6	2.38	0.40
1:1A:1688:U:H1'	1:1A:1701:A:C6	2.57	0.40
5:1F:140:LEU:HD11	5:1F:170:LEU:HD11	2.02	0.40
14:1S:11:LYS:HD3	14:1S:15:ARG:NH1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:1W:48:ALA:O	18:1W:52:GLU:HG2	2.20	0.40
21:1Z:183:LEU:HA	21:1Z:186:GLU:HB2	2.03	0.40
32:1a:130:A:O2'	32:1a:131:C:O5'	2.35	0.40
32:1a:159:G:N2	32:1a:162:A:OP2	2.34	0.40
32:1a:229:U:H5"	47:1p:33:ILE:HD13	2.03	0.40
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.56	0.40
33:1b:47:THR:HA	33:1b:202:PRO:HG2	2.02	0.40
35:1d:63:LYS:O	35:1d:67:ILE:HG13	2.21	0.40
46:1o:9:GLN:O	46:1o:13:GLN:HG3	2.21	0.40
1:2A:297:C:H2'	1:2A:298:G:O4'	2.21	0.40
1:2A:372:G:O2'	1:2A:400:G:O6	2.37	0.40
1:2A:962:G:H2'	1:2A:963:U:O4'	2.22	0.40
1:2A:1243:G:H2'	1:2A:1244:G:O4'	2.21	0.40
1:2A:1417:C:H2'	1:2A:1418:G:O4'	2.22	0.40
1:2A:1857:G:C6	1:2A:1858:G:C6	3.09	0.40
1:2A:2531:A:C8	7:2H:175:LYS:HB3	2.56	0.40
6:2G:126:ASP:HB3	6:2G:130:ASN:H	1.86	0.40
10:2O:7:TYR:CE1	10:2O:20:MET:HB2	2.56	0.40
14:2S:20:ARG:HA	14:2S:20:ARG:HD2	1.86	0.40
26:24:14:ILE:O	26:24:21:VAL:HA	2.21	0.40
32:2a:434:U:H2'	32:2a:435:C:C6	2.57	0.40
32:2a:1000:U:C4	32:2a:1001:A:N7	2.90	0.40
32:2a:1315:U:H2'	32:2a:1316:G:O4'	2.21	0.40
33:2b:186:ALA:HB3	33:2b:197:VAL:HG11	2.04	0.40
38:2g:106:GLN:O	38:2g:110:GLN:HG2	2.21	0.40
45:2n:37:PHE:CE1	45:2n:53:LEU:HD13	2.56	0.40
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	2.03	0.40
1:1A:251:A:C4	1:1A:252:G:H1'	2.56	0.40
1:1A:590:A:P	5:1F:95:ARG:HH21	2.44	0.40
1:1A:1548:C:H2'	1:1A:1549:C:H6	1.86	0.40
1:1A:1588:C:H2'	1:1A:1589:C:C6	2.56	0.40
1:1A:1935:G:H1'	1:1A:1964:G:N2	2.36	0.40
1:1A:2287:A:O2'	1:1A:2288:A:H3'	2.21	0.40
1:1A:2437:U:H2'	1:1A:2438:U:H6	1.86	0.40
1:1A:2492:U:H2'	1:1A:2493:U:C6	2.57	0.40
1:1A:2630:G:H2'	1:1A:2631:G:C8	2.56	0.40
2:1B:28:C:OP1	14:1S:31:SER:OG	2.38	0.40
8:1I:131:LYS:HB2	8:1I:131:LYS:HE3	1.80	0.40
11:1P:106:LEU:HD22	11:1P:112:LEU:HG	2.04	0.40
12:1Q:39:PRO:HA	12:1Q:97:VAL:O	2.21	0.40
12:1Q:48:GLU:CD	12:1Q:51:ARG:HH21	2.28	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:19:C:H4’	32:1a:864:A:O4’	2.22	0.40
32:1a:50:A:H1’	32:1a:52:G:C8	2.56	0.40
32:1a:102:G:H2’	32:1a:103:C:C6	2.55	0.40
32:1a:160:A:H2’	32:1a:161:A:O4’	2.21	0.40
32:1a:417:C:H42	32:1a:426:G:H1	1.68	0.40
32:1a:745:C:H2’	32:1a:746:A:C8	2.57	0.40
32:1a:989:C:C2	32:1a:1216:G:N2	2.89	0.40
35:1d:20:TYR:CD1	35:1d:26:CYS:HB3	2.52	0.40
37:1f:97:PHE:HD2	49:1r:31:LEU:HD13	1.87	0.40
45:1n:4:LYS:O	45:1n:7:ILE:HG12	2.20	0.40
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.56	0.40
51:1t:22:ARG:O	51:1t:26:ASN:ND2	2.55	0.40
1:2A:996:A:H4’	16:2U:91:ASP:OD2	2.21	0.40
1:2A:1301:A:H2	1:2A:1626:G:N3	2.18	0.40
1:2A:1798:U:H5’	3:2D:259:THR:CG2	2.50	0.40
1:2A:2023:G:H5’	1:2A:2617:C:H4’	2.03	0.40
1:2A:2689:U:H4’	1:2A:2690:C:O5’	2.22	0.40
1:2A:2716:U:H2’	1:2A:2717:G:C8	2.56	0.40
5:2F:165:ARG:HG2	5:2F:168:ARG:HH21	1.85	0.40
6:2G:11:TYR:CE2	6:2G:16:ARG:HD3	2.56	0.40
13:2R:38:VAL:HG12	13:2R:42:LYS:HE3	2.03	0.40
13:2R:70:LEU:O	13:2R:72:ASP:N	2.53	0.40
15:2T:24:PRO:HA	15:2T:49:VAL:HG22	2.03	0.40
26:24:37:SER:O	26:24:43:TYR:HB3	2.21	0.40
32:2a:308:C:H2’	32:2a:309:G:H8	1.86	0.40
32:2a:376:G:H2’	32:2a:377:G:H8	1.87	0.40
32:2a:406:G:H21	35:2d:119:GLN:NE2	2.19	0.40
32:2a:599:C:H4’	39:2h:130:GLY:C	2.46	0.40
32:2a:922:G:H1’	36:2e:19:MET:HB2	2.02	0.40
32:2a:980:C:O2	45:2n:19:ARG:HA	2.21	0.40
35:2d:10:ARG:HB2	35:2d:40:PRO:HG3	2.03	0.40
38:2g:15:ASP:OD1	38:2g:19:GLY:N	2.55	0.40
1:1A:801:G:O6	5:1F:53:THR:OG1	2.39	0.40
1:1A:821:A:H2’	1:1A:946:G:H5”	2.03	0.40
1:1A:1835:G:H2’	1:1A:1836:C:C6	2.56	0.40
1:1A:1909:C:H2’	1:1A:1910:G:C8	2.54	0.40
1:1A:2019:A:N7	27:15:9:LYS:HE2	2.36	0.40
1:1A:2298:A:H2’	1:1A:2299:G:O4’	2.20	0.40
1:1A:2875:C:O2’	15:1T:2:ASN:OD1	2.38	0.40
4:1E:188:VAL:HA	4:1E:189:PRO:HD3	1.91	0.40
8:1I:72:LEU:C	8:1I:74:ASN:N	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:6:LEU:HA	11:1P:6:LEU:HD23	1.80	0.40
12:1Q:141:GLN:NE2	21:1Z:74:VAL:O	2.31	0.40
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.21	0.40
21:1Z:54:HIS:CG	21:1Z:101:PRO:HG3	2.56	0.40
32:1a:19:C:P	36:1e:127:ASN:HD22	2.44	0.40
32:1a:501:C:H2'	32:1a:502:G:C8	2.57	0.40
32:1a:939:G:O6	57:1a:3205:HOH:O	2.22	0.40
32:1a:994:A:H2'	32:1a:995:C:O4'	2.21	0.40
34:1c:137:ALA:O	34:1c:141:VAL:HG23	2.21	0.40
36:1e:39:GLY:HA2	36:1e:69:VAL:HG13	2.04	0.40
1:2A:84:A:H5'	20:2Y:8:LYS:CB	2.51	0.40
1:2A:253:C:H2'	1:2A:254:G:O4'	2.21	0.40
1:2A:356:G:H2'	1:2A:357:A:H8	1.87	0.40
1:2A:521:G:H2'	1:2A:522:G:C8	2.56	0.40
1:2A:536:A:H2'	1:2A:537:C:C6	2.57	0.40
1:2A:1213:A:N3	1:2A:1238:G:O2'	2.52	0.40
1:2A:1291:C:H2'	1:2A:1292:U:C6	2.56	0.40
1:2A:1323:U:OP1	18:2W:98:LYS:NZ	2.40	0.40
1:2A:1355:G:H2'	1:2A:1356:G:O4'	2.21	0.40
1:2A:2728:U:H2'	1:2A:2729:G:H8	1.87	0.40
5:2F:183:VAL:O	5:2F:187:VAL:HG23	2.22	0.40
6:2G:39:ILE:HB	6:2G:92:VAL:HG13	2.03	0.40
16:2U:27:LEU:HD23	16:2U:27:LEU:HA	1.86	0.40
23:21:56:GLN:HE21	23:21:87:PRO:HG3	1.85	0.40
32:2a:457:C:N3	32:2a:474:G:N2	2.56	0.40
32:2a:1005:A:H8	32:2a:1024:G:H21	1.68	0.40
32:2a:1504:G:OP1	32:2a:1507:A:H4'	2.20	0.40
33:2b:75:LYS:HA	33:2b:78:GLN:HB2	2.03	0.40
38:2g:63:LYS:O	38:2g:67:GLU:HG2	2.21	0.40
38:2g:118:VAL:HA	38:2g:121:ALA:HB3	2.03	0.40
44:2m:59:TYR:CZ	44:2m:63:THR:HG21	2.57	0.40
47:2p:23:ASP:OD1	47:2p:24:ALA:N	2.55	0.40
1:1A:1904:G:H2'	1:1A:1905:C:O4'	2.22	0.40
1:1A:2600:A:O2'	1:1A:2601:C:H5'	2.21	0.40
1:1A:2804:C:H2'	1:1A:2805:G:H8	1.87	0.40
1:1A:2855:C:H2'	1:1A:2856:C:H6	1.85	0.40
15:1T:77:PRO:HB2	15:1T:80:SER:HB2	2.03	0.40
17:1V:52:VAL:CG2	17:1V:55:ALA:HB3	2.52	0.40
17:1V:62:LEU:HD21	17:1V:95:LEU:HB2	2.03	0.40
32:1a:537:G:H2'	32:1a:538:G:H8	1.86	0.40
32:1a:687:A:N3	32:1a:688:G:H1'	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:111:ARG:NH2	33:1b:145:LEU:HD21	2.37	0.40
35:1d:30:LYS:HG2	35:1d:35:ARG:NH2	2.35	0.40
38:1g:69:VAL:O	38:1g:71:PRO:HD3	2.22	0.40
39:1h:83:ILE:HA	39:1h:136:GLU:O	2.21	0.40
42:1k:84:VAL:HG11	42:1k:91:ARG:HD2	2.03	0.40
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.21	0.40
1:2A:464:U:H2'	1:2A:465:G:O4'	2.21	0.40
1:2A:565:C:H4'	1:2A:1253:A:N6	2.37	0.40
1:2A:1341:U:OP2	1:2A:1394:U:O2'	2.33	0.40
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.56	0.40
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.21	0.40
1:2A:2557:G:H2'	1:2A:2558:C:C6	2.57	0.40
1:2A:2679:A:H4'	4:2E:165:VAL:HG11	2.04	0.40
2:2B:38:C:O4'	14:2S:95:HIS:NE2	2.54	0.40
2:2B:38:C:H2'	2:2B:39:A:C8	2.56	0.40
12:2Q:23:GLY:O	12:2Q:101:ARG:NH1	2.54	0.40
20:2Y:43:ASN:ND2	20:2Y:65:ALA:HB3	2.36	0.40
29:27:34:ARG:HH12	29:27:39:ARG:HG2	1.85	0.40
30:28:11:LYS:HA	30:28:11:LYS:HD2	1.84	0.40
30:28:34:TRP:CG	30:28:35:GLN:N	2.88	0.40
32:2a:45:U:H2'	32:2a:46:G:C8	2.56	0.40
32:2a:458:C:H2'	32:2a:460:G:O4'	2.21	0.40
32:2a:1103:C:H2'	32:2a:1104:G:O4'	2.21	0.40
32:2a:1125:U:HO2'	32:2a:1126:U:H2'	1.86	0.40
32:2a:1198:G:H2'	32:2a:1199:U:C6	2.56	0.40
33:2b:11:LEU:HD12	33:2b:217:ARG:HH22	1.87	0.40
35:2d:122:ARG:HA	35:2d:122:ARG:HD2	1.93	0.40
38:2g:124:LEU:HD23	38:2g:124:LEU:HA	1.91	0.40
39:2h:26:VAL:HG22	39:2h:59:LEU:HB2	2.04	0.40
44:2m:102:ARG:HH21	44:2m:104:ARG:HD3	1.87	0.40
51:2t:22:ARG:O	51:2t:26:ASN:ND2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	258 (94%)	15 (6%)	0	100	100
3	2D	273/276 (99%)	254 (93%)	18 (7%)	1 (0%)	30	61
4	1E	202/206 (98%)	195 (96%)	6 (3%)	1 (0%)	24	57
4	2E	202/206 (98%)	195 (96%)	7 (4%)	0	100	100
5	1F	201/210 (96%)	198 (98%)	2 (1%)	1 (0%)	24	57
5	2F	201/210 (96%)	198 (98%)	1 (0%)	2 (1%)	12	41
6	1G	179/182 (98%)	167 (93%)	11 (6%)	1 (1%)	21	52
6	2G	179/182 (98%)	168 (94%)	9 (5%)	2 (1%)	11	39
7	1H	172/180 (96%)	166 (96%)	5 (3%)	1 (1%)	21	52
7	2H	171/180 (95%)	168 (98%)	3 (2%)	0	100	100
8	1I	145/148 (98%)	134 (92%)	10 (7%)	1 (1%)	18	49
8	2I	144/148 (97%)	135 (94%)	9 (6%)	0	100	100
9	1N	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
9	2N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
10	1O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	1P	147/150 (98%)	138 (94%)	8 (5%)	1 (1%)	18	49
11	2P	147/150 (98%)	137 (93%)	9 (6%)	1 (1%)	18	49
12	1Q	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
12	2Q	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
13	1R	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
13	2R	116/118 (98%)	115 (99%)	1 (1%)	0	100	100
14	1S	108/112 (96%)	103 (95%)	4 (4%)	1 (1%)	14	44
14	2S	108/112 (96%)	105 (97%)	3 (3%)	0	100	100
15	1T	129/146 (88%)	125 (97%)	4 (3%)	0	100	100
15	2T	129/146 (88%)	127 (98%)	2 (2%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	114 (100%)	0	0	100	100
17	1V	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
17	2V	99/101 (98%)	95 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	1W	110/113 (97%)	110 (100%)	0	0	100	100
18	2W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
19	1X	93/96 (97%)	88 (95%)	5 (5%)	0	100	100
19	2X	93/96 (97%)	87 (94%)	6 (6%)	0	100	100
20	1Y	105/110 (96%)	98 (93%)	7 (7%)	0	100	100
20	2Y	105/110 (96%)	100 (95%)	5 (5%)	0	100	100
21	1Z	201/206 (98%)	194 (96%)	7 (4%)	0	100	100
21	2Z	199/206 (97%)	191 (96%)	8 (4%)	0	100	100
22	10	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
22	20	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	11	95/98 (97%)	94 (99%)	1 (1%)	0	100	100
23	21	95/98 (97%)	93 (98%)	2 (2%)	0	100	100
24	12	68/72 (94%)	68 (100%)	0	0	100	100
24	22	68/72 (94%)	68 (100%)	0	0	100	100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	23	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
26	14	67/71 (94%)	57 (85%)	9 (13%)	1 (2%)	8	32
26	24	67/71 (94%)	55 (82%)	10 (15%)	2 (3%)	3	19
27	15	57/60 (95%)	54 (95%)	3 (5%)	0	100	100
27	25	57/60 (95%)	53 (93%)	4 (7%)	0	100	100
28	16	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
28	26	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
29	17	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
29	27	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
30	18	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100	100
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	203 (89%)	20 (9%)	6 (3%)	4	21
33	2b	229/256 (90%)	205 (90%)	13 (6%)	11 (5%)	2	11
34	1c	204/239 (85%)	198 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	2c	204/239 (85%)	194 (95%)	10 (5%)	0	100	100
35	1d	206/209 (99%)	197 (96%)	7 (3%)	2 (1%)	12	41
35	2d	206/209 (99%)	199 (97%)	6 (3%)	1 (0%)	24	57
36	1e	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
36	2e	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
37	1f	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
37	2f	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
38	1g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
38	2g	153/156 (98%)	144 (94%)	8 (5%)	1 (1%)	18	49
39	1h	135/138 (98%)	132 (98%)	3 (2%)	0	100	100
39	2h	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
40	1i	125/128 (98%)	114 (91%)	10 (8%)	1 (1%)	16	47
40	2i	124/128 (97%)	114 (92%)	8 (6%)	2 (2%)	7	30
41	1j	95/105 (90%)	84 (88%)	9 (10%)	2 (2%)	5	25
41	2j	94/105 (90%)	87 (93%)	6 (6%)	1 (1%)	11	39
42	1k	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	6	28
42	2k	112/129 (87%)	107 (96%)	5 (4%)	0	100	100
43	1l	119/132 (90%)	112 (94%)	7 (6%)	0	100	100
43	2l	119/132 (90%)	111 (93%)	8 (7%)	0	100	100
44	1m	114/126 (90%)	109 (96%)	4 (4%)	1 (1%)	14	44
44	2m	112/126 (89%)	109 (97%)	2 (2%)	1 (1%)	14	44
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
46	1o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	2o	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
47	1p	80/88 (91%)	76 (95%)	4 (5%)	0	100	100
47	2p	80/88 (91%)	77 (96%)	3 (4%)	0	100	100
48	1q	97/105 (92%)	93 (96%)	3 (3%)	1 (1%)	12	41
48	2q	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
49	1r	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
49	2r	66/88 (75%)	63 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
50	1s	81/93 (87%)	74 (91%)	7 (9%)	0	100 100
50	2s	81/93 (87%)	75 (93%)	6 (7%)	0	100 100
51	1t	94/106 (89%)	91 (97%)	2 (2%)	1 (1%)	11 39
51	2t	96/106 (91%)	91 (95%)	4 (4%)	1 (1%)	12 41
52	1u	21/27 (78%)	21 (100%)	0	0	100 100
52	2u	21/27 (78%)	21 (100%)	0	0	100 100
All	All	11440/12128 (94%)	10932 (96%)	458 (4%)	50 (0%)	30 61

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
26	14	56	VAL
33	1b	17	PHE
33	1b	21	ARG
33	1b	125	PRO
33	1b	232	PRO
42	1k	118	GLY
48	1q	68	ARG
33	2b	16	HIS
33	2b	53	ARG
33	2b	54	THR
33	2b	232	PRO
44	2m	67	GLU
8	1I	73	GLU
14	1S	59	LYS
35	1d	178	VAL
35	1d	179	GLU
41	1j	79	ARG
26	24	55	ARG
26	24	60	GLN
33	2b	17	PHE
33	2b	21	ARG
33	2b	123	ALA
33	2b	126	GLU
40	2i	12	GLU
41	2j	79	ARG
4	1E	52	LEU
3	2D	125	ILE
5	2F	130	ALA

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Mol	Chain	Res	Type
6	2G	47	LYS
6	2G	81	LYS
38	2g	8	GLU
6	1G	47	LYS
33	1b	95	GLN
44	1m	67	GLU
5	2F	21	ALA
33	2b	8	LYS
33	2b	95	GLN
7	1H	92	ILE
11	1P	36	LYS
51	1t	100	ILE
33	2b	20	GLU
51	2t	100	ILE
33	1b	127	ILE
40	1i	56	LEU
35	2d	166	LYS
40	2i	44	VAL
41	1j	77	PRO
11	2P	122	PRO
42	1k	105	VAL

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	214/218 (98%)	201 (94%)	13 (6%)	17 46
3	2D	215/218 (99%)	197 (92%)	18 (8%)	10 35
4	1E	164/166 (99%)	152 (93%)	12 (7%)	13 40
4	2E	164/166 (99%)	152 (93%)	12 (7%)	13 40
5	1F	160/166 (96%)	152 (95%)	8 (5%)	22 53
5	2F	159/166 (96%)	151 (95%)	8 (5%)	22 53
6	1G	144/156 (92%)	140 (97%)	4 (3%)	38 66
6	2G	142/156 (91%)	136 (96%)	6 (4%)	26 58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	1H	144/148 (97%)	139 (96%)	5 (4%)	32	62
7	2H	143/148 (97%)	137 (96%)	6 (4%)	26	58
8	1I	111/124 (90%)	104 (94%)	7 (6%)	16	45
8	2I	108/124 (87%)	101 (94%)	7 (6%)	15	44
9	1N	119/119 (100%)	115 (97%)	4 (3%)	32	63
9	2N	118/119 (99%)	114 (97%)	4 (3%)	32	63
10	1O	100/100 (100%)	99 (99%)	1 (1%)	68	79
10	2O	100/100 (100%)	98 (98%)	2 (2%)	48	72
11	1P	115/116 (99%)	111 (96%)	4 (4%)	32	62
11	2P	115/116 (99%)	111 (96%)	4 (4%)	32	62
12	1Q	111/111 (100%)	109 (98%)	2 (2%)	51	73
12	2Q	111/111 (100%)	108 (97%)	3 (3%)	39	67
13	1R	101/101 (100%)	93 (92%)	8 (8%)	11	37
13	2R	101/101 (100%)	93 (92%)	8 (8%)	11	37
14	1S	87/88 (99%)	85 (98%)	2 (2%)	44	70
14	2S	85/88 (97%)	83 (98%)	2 (2%)	43	69
15	1T	115/127 (91%)	112 (97%)	3 (3%)	40	68
15	2T	113/127 (89%)	111 (98%)	2 (2%)	51	73
16	1U	93/94 (99%)	91 (98%)	2 (2%)	45	71
16	2U	93/94 (99%)	90 (97%)	3 (3%)	34	64
17	1V	81/82 (99%)	75 (93%)	6 (7%)	13	40
17	2V	80/82 (98%)	76 (95%)	4 (5%)	22	53
18	1W	90/92 (98%)	87 (97%)	3 (3%)	33	63
18	2W	90/92 (98%)	86 (96%)	4 (4%)	25	56
19	1X	77/78 (99%)	76 (99%)	1 (1%)	61	77
19	2X	77/78 (99%)	75 (97%)	2 (3%)	40	68
20	1Y	86/91 (94%)	83 (96%)	3 (4%)	32	62
20	2Y	86/91 (94%)	84 (98%)	2 (2%)	44	70
21	1Z	169/179 (94%)	156 (92%)	13 (8%)	12	38
21	2Z	165/179 (92%)	161 (98%)	4 (2%)	43	69
22	10	61/67 (91%)	58 (95%)	3 (5%)	22	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
22	20	61/67 (91%)	60 (98%)	1 (2%)	55 75
23	11	79/83 (95%)	77 (98%)	2 (2%)	42 69
23	21	81/83 (98%)	78 (96%)	3 (4%)	30 61
24	12	65/67 (97%)	63 (97%)	2 (3%)	35 64
24	22	66/67 (98%)	65 (98%)	1 (2%)	57 75
25	13	51/52 (98%)	46 (90%)	5 (10%)	7 29
25	23	50/52 (96%)	47 (94%)	3 (6%)	17 47
26	14	58/63 (92%)	56 (97%)	2 (3%)	32 63
26	24	54/63 (86%)	50 (93%)	4 (7%)	13 40
27	15	51/52 (98%)	46 (90%)	5 (10%)	7 29
27	25	50/52 (96%)	46 (92%)	4 (8%)	11 37
28	16	51/52 (98%)	48 (94%)	3 (6%)	18 48
28	26	50/52 (96%)	47 (94%)	3 (6%)	17 47
29	17	41/42 (98%)	37 (90%)	4 (10%)	7 29
29	27	41/42 (98%)	36 (88%)	5 (12%)	5 20
30	18	54/55 (98%)	52 (96%)	2 (4%)	30 61
30	28	54/55 (98%)	50 (93%)	4 (7%)	13 40
31	19	34/34 (100%)	33 (97%)	1 (3%)	37 66
31	29	34/34 (100%)	33 (97%)	1 (3%)	37 66
33	1b	191/220 (87%)	183 (96%)	8 (4%)	26 58
33	2b	187/220 (85%)	184 (98%)	3 (2%)	55 75
34	1c	144/188 (77%)	138 (96%)	6 (4%)	26 58
34	2c	140/188 (74%)	135 (96%)	5 (4%)	31 62
35	1d	171/181 (94%)	161 (94%)	10 (6%)	18 48
35	2d	172/181 (95%)	168 (98%)	4 (2%)	44 70
36	1e	114/123 (93%)	110 (96%)	4 (4%)	32 62
36	2e	114/123 (93%)	110 (96%)	4 (4%)	32 62
37	1f	85/90 (94%)	83 (98%)	2 (2%)	43 69
37	2f	85/90 (94%)	83 (98%)	2 (2%)	43 69
38	1g	120/127 (94%)	119 (99%)	1 (1%)	73 81
38	2g	119/127 (94%)	118 (99%)	1 (1%)	73 81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	1h	116/119 (98%)	112 (97%)	4 (3%)	32 63
39	2h	114/119 (96%)	111 (97%)	3 (3%)	40 68
40	1i	91/99 (92%)	89 (98%)	2 (2%)	45 71
40	2i	88/99 (89%)	86 (98%)	2 (2%)	44 70
41	1j	68/92 (74%)	65 (96%)	3 (4%)	25 56
41	2j	68/92 (74%)	64 (94%)	4 (6%)	18 48
42	1k	83/99 (84%)	82 (99%)	1 (1%)	63 78
42	2k	83/99 (84%)	80 (96%)	3 (4%)	31 62
43	1l	96/108 (89%)	93 (97%)	3 (3%)	35 64
43	2l	96/108 (89%)	94 (98%)	2 (2%)	47 71
44	1m	90/101 (89%)	88 (98%)	2 (2%)	45 71
44	2m	87/101 (86%)	85 (98%)	2 (2%)	44 70
45	1n	49/50 (98%)	47 (96%)	2 (4%)	27 59
45	2n	49/50 (98%)	49 (100%)	0	100 100
46	1o	78/80 (98%)	78 (100%)	0	100 100
46	2o	78/80 (98%)	78 (100%)	0	100 100
47	1p	69/74 (93%)	63 (91%)	6 (9%)	9 34
47	2p	68/74 (92%)	64 (94%)	4 (6%)	18 48
48	1q	94/97 (97%)	94 (100%)	0	100 100
48	2q	94/97 (97%)	93 (99%)	1 (1%)	65 78
49	1r	59/77 (77%)	58 (98%)	1 (2%)	53 74
49	2r	59/77 (77%)	58 (98%)	1 (2%)	53 74
50	1s	68/80 (85%)	65 (96%)	3 (4%)	25 56
50	2s	67/80 (84%)	62 (92%)	5 (8%)	12 39
51	1t	71/82 (87%)	68 (96%)	3 (4%)	26 58
51	2t	70/82 (85%)	66 (94%)	4 (6%)	18 49
52	1u	18/22 (82%)	18 (100%)	0	100 100
52	2u	18/22 (82%)	18 (100%)	0	100 100
All	All	9363/10064 (93%)	8992 (96%)	371 (4%)	28 60

All (371) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	10	THR
3	1D	69	ARG
3	1D	103	ARG
3	1D	113	VAL
3	1D	142	VAL
3	1D	155	LEU
3	1D	193	VAL
3	1D	212	SER
3	1D	217	ARG
3	1D	229	VAL
3	1D	237	GLU
3	1D	242	ARG
4	1E	7	VAL
4	1E	9	VAL
4	1E	21	VAL
4	1E	33	VAL
4	1E	34	VAL
4	1E	49	LEU
4	1E	73	GLU
4	1E	75	VAL
4	1E	116	VAL
4	1E	144	ARG
4	1E	175	VAL
4	1E	184	VAL
5	1F	57	VAL
5	1F	70	THR
5	1F	74	ARG
5	1F	100	THR
5	1F	110	LEU
5	1F	125	LEU
5	1F	183	VAL
5	1F	197	ASP
6	1G	5	VAL
6	1G	43	LEU
6	1G	159	VAL
6	1G	167	GLU
7	1H	45	VAL
7	1H	71	LEU
7	1H	105	LEU
7	1H	125	VAL
7	1H	139	GLN
8	1I	12	LEU

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Mol	Chain	Res	Type
8	1I	15	VAL
8	1I	38	LEU
8	1I	92	VAL
8	1I	109	ILE
8	1I	127	VAL
8	1I	140	LEU
9	1N	8	GLN
9	1N	33	LEU
9	1N	34	LEU
9	1N	62	VAL
10	1O	24	VAL
11	1P	83	VAL
11	1P	95	VAL
11	1P	112	LEU
11	1P	126	VAL
12	1Q	55	VAL
12	1Q	109	VAL
13	1R	6	SER
13	1R	17	ARG
13	1R	29	LEU
13	1R	36	THR
13	1R	44	LEU
13	1R	65	LEU
13	1R	67	LEU
13	1R	111	LEU
14	1S	49	VAL
14	1S	54	LEU
15	1T	15	VAL
15	1T	34	VAL
15	1T	49	VAL
16	1U	83	LEU
16	1U	95	LEU
17	1V	46	VAL
17	1V	51	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	72	VAL
17	1V	79	VAL
18	1W	17	VAL
18	1W	100	THR
18	1W	107	LEU
19	1X	88	LYS

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Mol	Chain	Res	Type
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	90	LEU
21	1Z	58	VAL
21	1Z	61	LEU
21	1Z	76	LEU
21	1Z	86	VAL
21	1Z	94	GLU
21	1Z	102	LEU
21	1Z	107	THR
21	1Z	126	VAL
21	1Z	150	LEU
21	1Z	161	VAL
21	1Z	171	ILE
21	1Z	202	GLU
21	1Z	203	GLU
22	10	39	ARG
22	10	59	LEU
22	10	63	VAL
23	11	30	VAL
23	11	95	LEU
24	12	32	LEU
24	12	53	LEU
25	13	6	VAL
25	13	8	LEU
25	13	40	THR
25	13	56	VAL
25	13	60	GLU
26	14	30	GLU
26	14	61	ARG
27	15	6	VAL
27	15	16	ARG
27	15	26	THR
27	15	29	THR
27	15	60	VAL
28	16	5	VAL
28	16	14	THR
28	16	48	VAL
29	17	1	MET
29	17	4	THR
29	17	24	THR
29	17	43	THR

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Mol	Chain	Res	Type
30	18	14	VAL
30	18	32	LEU
31	19	26	ILE
33	1b	9	GLU
33	1b	10	LEU
33	1b	15	VAL
33	1b	19	HIS
33	1b	51	LEU
33	1b	112	VAL
33	1b	122	PHE
33	1b	185	ILE
34	1c	64	VAL
34	1c	89	GLU
34	1c	98	ASN
34	1c	132	ARG
34	1c	191	THR
34	1c	206	GLU
35	1d	8	VAL
35	1d	76	ARG
35	1d	135	LEU
35	1d	150	GLU
35	1d	158	ILE
35	1d	168	ARG
35	1d	178	VAL
35	1d	188	LEU
35	1d	194	LEU
35	1d	196	LEU
36	1e	41	VAL
36	1e	69	VAL
36	1e	75	THR
36	1e	79	GLU
37	1f	16	GLN
37	1f	72	VAL
38	1g	111	ARG
39	1h	14	ARG
39	1h	25	ASP
39	1h	51	VAL
39	1h	52	ASP
40	1i	28	VAL
40	1i	64	THR
41	1j	38	ILE
41	1j	94	VAL

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Mol	Chain	Res	Type
41	1j	96	ILE
42	1k	114	VAL
43	1l	18	VAL
43	1l	55	VAL
43	1l	70	ILE
44	1m	70	LEU
44	1m	98	VAL
45	1n	13	THR
45	1n	33	VAL
47	1p	2	VAL
47	1p	19	ILE
47	1p	42	ARG
47	1p	62	VAL
47	1p	67	THR
47	1p	79	VAL
49	1r	37	VAL
50	1s	28	LYS
50	1s	39	THR
50	1s	79	THR
51	1t	10	LEU
51	1t	62	LEU
51	1t	100	ILE
3	2D	25	THR
3	2D	27	THR
3	2D	61	LEU
3	2D	99	ASP
3	2D	111	LEU
3	2D	113	VAL
3	2D	138	VAL
3	2D	141	VAL
3	2D	142	VAL
3	2D	154	LYS
3	2D	164	GLN
3	2D	173	VAL
3	2D	183	ARG
3	2D	193	VAL
3	2D	221	VAL
3	2D	229	VAL
3	2D	230	ASP
3	2D	276	LYS
4	2E	1	MET
4	2E	7	VAL

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Mol	Chain	Res	Type
4	2E	9	VAL
4	2E	12	THR
4	2E	14	ILE
4	2E	21	VAL
4	2E	33	VAL
4	2E	34	VAL
4	2E	75	VAL
4	2E	116	VAL
4	2E	134	ILE
4	2E	175	VAL
5	2F	20	LEU
5	2F	53	THR
5	2F	57	VAL
5	2F	70	THR
5	2F	74	ARG
5	2F	175	THR
5	2F	183	VAL
5	2F	197	ASP
6	2G	3	LEU
6	2G	5	VAL
6	2G	43	LEU
6	2G	60	LEU
6	2G	139	LEU
6	2G	159	VAL
7	2H	7	LEU
7	2H	33	LEU
7	2H	71	LEU
7	2H	88	LEU
7	2H	129	THR
7	2H	139	GLN
8	2I	15	VAL
8	2I	20	ASP
8	2I	38	LEU
8	2I	44	LEU
8	2I	92	VAL
8	2I	127	VAL
8	2I	140	LEU
9	2N	34	LEU
9	2N	43	THR
9	2N	62	VAL
9	2N	99	LEU
10	2O	24	VAL

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Mol	Chain	Res	Type
10	2O	53	LYS
11	2P	95	VAL
11	2P	112	LEU
11	2P	126	VAL
11	2P	148	LEU
12	2Q	6	ARG
12	2Q	55	VAL
12	2Q	109	VAL
13	2R	6	SER
13	2R	18	LEU
13	2R	29	LEU
13	2R	36	THR
13	2R	44	LEU
13	2R	65	LEU
13	2R	67	LEU
13	2R	79	LEU
14	2S	54	LEU
14	2S	85	VAL
15	2T	49	VAL
15	2T	95	ARG
16	2U	59	ARG
16	2U	83	LEU
16	2U	95	LEU
17	2V	51	VAL
17	2V	61	VAL
17	2V	72	VAL
17	2V	79	VAL
18	2W	17	VAL
18	2W	60	ASN
18	2W	100	THR
18	2W	107	LEU
19	2X	35	THR
19	2X	65	ARG
20	2Y	72	VAL
20	2Y	85	VAL
21	2Z	61	LEU
21	2Z	86	VAL
21	2Z	107	THR
21	2Z	150	LEU
22	20	63	VAL
23	21	4	VAL
23	21	30	VAL

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Mol	Chain	Res	Type
23	21	95	LEU
24	22	53	LEU
25	23	6	VAL
25	23	40	THR
25	23	56	VAL
26	24	38	LYS
26	24	44	THR
26	24	46	GLN
26	24	50	VAL
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
27	25	58	LEU
28	26	5	VAL
28	26	34	LEU
28	26	48	VAL
29	27	1	MET
29	27	4	THR
29	27	29	LYS
29	27	35	ARG
29	27	43	THR
30	28	6	THR
30	28	14	VAL
30	28	22	VAL
30	28	32	LEU
31	29	26	ILE
33	2b	96	ARG
33	2b	187	LEU
33	2b	222	ILE
34	2c	35	GLU
34	2c	82	GLU
34	2c	152	ILE
34	2c	191	THR
34	2c	206	GLU
35	2d	8	VAL
35	2d	135	LEU
35	2d	178	VAL
35	2d	188	LEU
36	2e	41	VAL
36	2e	69	VAL
36	2e	72	GLN
36	2e	75	THR

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Mol	Chain	Res	Type
37	2f	16	GLN
37	2f	72	VAL
38	2g	51	GLN
39	2h	60	ARG
39	2h	84	ARG
39	2h	112	LEU
40	2i	20	ARG
40	2i	56	LEU
41	2j	33	GLN
41	2j	38	ILE
41	2j	94	VAL
41	2j	96	ILE
42	2k	14	VAL
42	2k	103	LEU
42	2k	114	VAL
43	2l	18	VAL
43	2l	55	VAL
44	2m	70	LEU
44	2m	98	VAL
47	2p	2	VAL
47	2p	28	ARG
47	2p	62	VAL
47	2p	67	THR
48	2q	93	GLN
49	2r	37	VAL
50	2s	16	LEU
50	2s	39	THR
50	2s	67	VAL
50	2s	77	THR
50	2s	79	THR
51	2t	45	GLN
51	2t	62	LEU
51	2t	99	LEU
51	2t	100	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (131) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	166	GLN
3	1D	201	HIS
4	1E	48	GLN
4	1E	137	HIS

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Mol	Chain	Res	Type
4	1E	180	ASN
5	1F	8	GLN
5	1F	75	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	121	ASN
9	1N	94	HIS
9	1N	133	GLN
13	1R	13	HIS
13	1R	24	GLN
13	1R	71	GLN
15	1T	58	ASN
18	1W	40	ASN
18	1W	60	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	92	ASN
21	1Z	73	GLN
21	1Z	132	ASN
21	1Z	151	HIS
23	11	16	ASN
23	11	56	GLN
24	12	65	ASN
25	13	32	GLN
30	18	35	GLN
33	1b	113	HIS
33	1b	212	GLN
34	1c	102	ASN
34	1c	104	GLN
34	1c	118	GLN
34	1c	176	HIS
35	1d	129	ASN
35	1d	160	GLN
35	1d	199	ASN
36	1e	20	GLN
38	1g	28	ASN
38	1g	148	ASN
38	1g	153	HIS
40	1i	3	GLN
40	1i	34	ASN
40	1i	73	GLN
41	1j	13	HIS

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Mol	Chain	Res	Type
41	1j	62	HIS
41	1j	68	HIS
42	1k	93	GLN
44	1m	77	ASN
46	1o	62	GLN
47	1p	13	HIS
47	1p	16	HIS
48	1q	16	GLN
48	1q	26	GLN
49	1r	63	GLN
50	1s	23	ASN
3	2D	45	ASN
3	2D	87	ASN
3	2D	126	GLN
3	2D	166	GLN
3	2D	253	GLN
4	2E	48	GLN
4	2E	143	ASN
4	2E	180	ASN
5	2F	69	HIS
5	2F	75	HIS
6	2G	40	ASN
6	2G	132	ASN
9	2N	94	HIS
10	2O	5	GLN
11	2P	35	HIS
12	2Q	123	HIS
13	2R	13	HIS
13	2R	24	GLN
13	2R	31	HIS
13	2R	50	HIS
13	2R	61	HIS
13	2R	71	GLN
15	2T	58	ASN
16	2U	94	ASN
17	2V	64	HIS
19	2X	31	HIS
19	2X	82	GLN
20	2Y	57	GLN
21	2Z	54	HIS
21	2Z	55	HIS
21	2Z	73	GLN

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Mol	Chain	Res	Type
21	2Z	132	ASN
21	2Z	151	HIS
23	21	16	ASN
23	21	56	GLN
24	22	65	ASN
30	28	35	GLN
30	28	43	GLN
33	2b	40	HIS
33	2b	45	GLN
33	2b	135	GLN
34	2c	6	HIS
34	2c	69	HIS
34	2c	98	ASN
34	2c	136	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	129	ASN
36	2e	20	GLN
36	2e	72	GLN
36	2e	78	HIS
37	2f	73	ASN
38	2g	13	GLN
38	2g	28	ASN
38	2g	64	GLN
38	2g	106	GLN
40	2i	3	GLN
40	2i	73	GLN
40	2i	117	HIS
41	2j	62	HIS
41	2j	69	ASN
43	2l	75	HIS
43	2l	99	HIS
44	2m	77	ASN
47	2p	16	HIS
48	2q	93	GLN
49	2r	63	GLN
50	2s	23	ASN
50	2s	47	HIS
50	2s	57	HIS
50	2s	65	ASN
50	2s	83	HIS
51	2t	18	GLN

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Mol	Chain	Res	Type
51	2t	26	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	442 (15%)	15 (0%)
1	2A	2858/2915 (98%)	498 (17%)	24 (0%)
2	1B	119/121 (98%)	12 (10%)	0
2	2B	119/121 (98%)	18 (15%)	0
32	1a	1497/1521 (98%)	276 (18%)	0
32	2a	1501/1521 (98%)	276 (18%)	0
All	All	8959/9114 (98%)	1522 (16%)	39 (0%)

All (1522) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	15	G
1	1A	34	C
1	1A	45	C
1	1A	61	G
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	95	G
1	1A	102	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	125	G
1	1A	131	G
1	1A	181	A
1	1A	182	A
1	1A	196	A
1	1A	199	A
1	1A	205	G
1	1A	215	G
1	1A	216	A
1	1A	222	A
1	1A	228	A

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Mol	Chain	Res	Type
1	1A	229	A
1	1A	233	A
1	1A	248	G
1	1A	250	G
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	275	G
1	1A	279	C
1	1A	311	A
1	1A	330	A
1	1A	333	G
1	1A	352	G
1	1A	353	G
1	1A	357	A
1	1A	360	G
1	1A	363	G
1	1A	363(A)	A
1	1A	363(B)	G
1	1A	363(C)	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	407	G
1	1A	411	G
1	1A	421	U
1	1A	428	A
1	1A	448	U
1	1A	454	A
1	1A	455	C
1	1A	456	C
1	1A	457	A
1	1A	481	G
1	1A	484	C
1	1A	505	A
1	1A	508	G
1	1A	509	C

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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	575	A
1	1A	587	C
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(A)	U
1	1A	614(B)	G
1	1A	615	G
1	1A	619	G
1	1A	620	G
1	1A	627	A
1	1A	637	A
1	1A	644	A
1	1A	645	C
1	1A	652(E)	G
1	1A	652(T)	C
1	1A	652(U)	G
1	1A	669	G
1	1A	686	G
1	1A	717	G
1	1A	730	C
1	1A	738	G
1	1A	764	A
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	789	A
1	1A	792	G
1	1A	793	A
1	1A	805	G
1	1A	812	C
1	1A	827	U

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Mol	Chain	Res	Type
1	1A	828	U
1	1A	829	A
1	1A	831	G
1	1A	859	G
1	1A	866	A
1	1A	876	C
1	1A	878	A
1	1A	879	G
1	1A	886	C
1	1A	887	A
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	910	A
1	1A	914	C
1	1A	915	C
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	959	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	975(A)	G
1	1A	980	A
1	1A	983	A
1	1A	990	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1025	G
1	1A	1026	U
1	1A	1033	U
1	1A	1038	C
1	1A	1039	G
1	1A	1042	G
1	1A	1043	C
1	1A	1046	A
1	1A	1047	G
1	1A	1053	C

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Mol	Chain	Res	Type
1	1A	1054	A
1	1A	1060	U
1	1A	1061	U
1	1A	1062	G
1	1A	1063	G
1	1A	1064	C
1	1A	1065	U
1	1A	1068	G
1	1A	1069	A
1	1A	1070	A
1	1A	1071	G
1	1A	1073	A
1	1A	1074	G
1	1A	1078	U
1	1A	1079	C
1	1A	1083	U
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1093	G
1	1A	1096	A
1	1A	1105	U
1	1A	1112	G
1	1A	1115	G
1	1A	1116	C
1	1A	1128	A
1	1A	1129	A
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1139	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	1203	G
1	1A	1204	A
1	1A	1211	U

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Mol	Chain	Res	Type
1	1A	1218	C
1	1A	1249	U
1	1A	1253	A
1	1A	1256	G
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	1359	A
1	1A	1360	A
1	1A	1365	A
1	1A	1370	C
1	1A	1384	A
1	1A	1385	G
1	1A	1386	C
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	1452	A
1	1A	1453	U
1	1A	1455	G
1	1A	1467	C
1	1A	1471	A
1	1A	1478	G
1	1A	1482	G
1	1A	1506	C
1	1A	1508	A
1	1A	1509	C
1	1A	1509(A)	A
1	1A	1532	C
1	1A	1542	A
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A

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Mol	Chain	Res	Type
1	1A	1580	A
1	1A	1581	G
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A
1	1A	1610	A
1	1A	1648	C
1	1A	1674	G
1	1A	1700	A
1	1A	1701	A
1	1A	1721	G
1	1A	1722	A
1	1A	1739	U
1	1A	1746	G
1	1A	1747	G
1	1A	1756	G
1	1A	1758	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1769	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1784	A
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1812	A
1	1A	1816	G
1	1A	1829	A
1	1A	1847	A
1	1A	1858	G
1	1A	1877	A
1	1A	1878	G
1	1A	1889	A
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1914	C
1	1A	1927	A

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Mol	Chain	Res	Type
1	1A	1929	G
1	1A	1930	G
1	1A	1936	A
1	1A	1938	A
1	1A	1952	A
1	1A	1955	U
1	1A	1963	U
1	1A	1964	G
1	1A	1965	C
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A
1	1A	1972	A
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2021	C
1	1A	2023	G
1	1A	2031	A
1	1A	2032	G
1	1A	2033	A
1	1A	2043	C
1	1A	2052	G
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2062	A
1	1A	2069	G
1	1A	2093	G
1	1A	2103	C
1	1A	2104	G
1	1A	2107	C
1	1A	2108	C
1	1A	2110	G
1	1A	2114	A
1	1A	2116	G
1	1A	2117	A
1	1A	2118	U
1	1A	2120	G
1	1A	2123	G
1	1A	2125	G

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Mol	Chain	Res	Type
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2135	A
1	1A	2137	C
1	1A	2139	C
1	1A	2142	C
1	1A	2146	C
1	1A	2147	G
1	1A	2152	G
1	1A	2158	A
1	1A	2159	G
1	1A	2172	U
1	1A	2173	A
1	1A	2180	U
1	1A	2183	C
1	1A	2185	C
1	1A	2187	G
1	1A	2191	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2219	G
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2273	A
1	1A	2278	A
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2308	G
1	1A	2314	C
1	1A	2315	G

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Mol	Chain	Res	Type
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2354	G
1	1A	2372	G
1	1A	2383	G
1	1A	2385	C
1	1A	2406	U
1	1A	2409	G
1	1A	2410	G
1	1A	2414	G
1	1A	2422	A
1	1A	2423	U
1	1A	2425	A
1	1A	2429	G
1	1A	2430	A
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2448	A
1	1A	2468	G
1	1A	2469	A
1	1A	2476	A
1	1A	2477	C
1	1A	2491	U
1	1A	2494	G
1	1A	2498	C
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2525	G
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2564	A
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C

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Mol	Chain	Res	Type
1	1A	2586	C
1	1A	2596	U
1	1A	2602	A
1	1A	2603	G
1	1A	2609	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2632	A
1	1A	2654	A
1	1A	2689	U
1	1A	2690	C
1	1A	2691	C
1	1A	2702	U
1	1A	2703	C
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2758	A
1	1A	2764	A
1	1A	2765	A
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2808	U
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2834	G
1	1A	2835	A
1	1A	2849	U
1	1A	2872	G
1	1A	2880	C
1	1A	2892	A
1	1A	2894	G
2	1B	13	A
2	1B	15	A
2	1B	33	G

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Mol	Chain	Res	Type
2	1B	42	C
2	1B	50	G
2	1B	52	A
2	1B	56	G
2	1B	73	A
2	1B	84	C
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	6	G
32	1a	9	G
32	1a	14	U
32	1a	32	A
32	1a	39	G
32	1a	43	C
32	1a	44	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	79	G
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	151	A
32	1a	156	G
32	1a	159	G
32	1a	163	C
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(F)	U
32	1a	189(G)	G
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	237	C
32	1a	245	C

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Mol	Chain	Res	Type
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	279	A
32	1a	281	G
32	1a	289	G
32	1a	301	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	348	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	388	G
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	430	A
32	1a	431	A
32	1a	439	A
32	1a	452	A
32	1a	453	A
32	1a	458	C
32	1a	461	A
32	1a	470	C
32	1a	475	G
32	1a	482	A
32	1a	484	G
32	1a	485	G
32	1a	496	A

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Mol	Chain	Res	Type
32	1a	498	U
32	1a	505	G
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	531	U
32	1a	532	A
32	1a	533	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	562	C
32	1a	563	A
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	592	G
32	1a	596	C
32	1a	607	A
32	1a	618	C
32	1a	619	U
32	1a	630	G
32	1a	632	A
32	1a	653	A
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	731	G
32	1a	755	G
32	1a	760	G
32	1a	766	A
32	1a	774	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	802	A
32	1a	815	A
32	1a	816	A
32	1a	817	C
32	1a	818	G

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Mol	Chain	Res	Type
32	1a	821	G
32	1a	827	U
32	1a	828	A
32	1a	829	G
32	1a	836	G
32	1a	840	C
32	1a	841	U
32	1a	848	C
32	1a	859	A
32	1a	872	A
32	1a	885	G
32	1a	889	A
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	931	C
32	1a	934	C
32	1a	954	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	989	C
32	1a	991	U
32	1a	992	U
32	1a	993	G
32	1a	998	G
32	1a	999	C
32	1a	1001	A
32	1a	1004	A
32	1a	1005	A
32	1a	1017	G
32	1a	1020	U
32	1a	1023	G

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Mol	Chain	Res	Type
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(D)	A
32	1a	1031	G
32	1a	1032	G
32	1a	1033	G
32	1a	1035	A
32	1a	1036	G
32	1a	1037	C
32	1a	1038	C
32	1a	1043	C
32	1a	1044	A
32	1a	1053	G
32	1a	1054	C
32	1a	1056	U
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1081	G
32	1a	1094	G
32	1a	1095	U
32	1a	1099	G
32	1a	1100	C
32	1a	1101	A
32	1a	1108	G
32	1a	1113	C
32	1a	1122	U
32	1a	1124	G
32	1a	1125	U
32	1a	1130	A
32	1a	1132	C
32	1a	1134	G
32	1a	1135	U
32	1a	1136	U
32	1a	1137	C
32	1a	1139	G

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Mol	Chain	Res	Type
32	1a	1152	A
32	1a	1154	G
32	1a	1157	A
32	1a	1159	U
32	1a	1160	G
32	1a	1161	C
32	1a	1166	G
32	1a	1182	G
32	1a	1183	A
32	1a	1184	G
32	1a	1185	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1214	C
32	1a	1224	G
32	1a	1227	A
32	1a	1230	C
32	1a	1238	A
32	1a	1250	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1261	A
32	1a	1270	C
32	1a	1278	U
32	1a	1280	A
32	1a	1281	U
32	1a	1282	C
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1301	U
32	1a	1302	U
32	1a	1305	G
32	1a	1310	G
32	1a	1312	G

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Mol	Chain	Res	Type
32	1a	1316	G
32	1a	1317	C
32	1a	1320	C
32	1a	1322	C
32	1a	1326	C
32	1a	1332	A
32	1a	1341	U
32	1a	1347	G
32	1a	1353	G
32	1a	1357	A
32	1a	1363	C
32	1a	1370	G
32	1a	1378	C
32	1a	1386	G
32	1a	1397	C
32	1a	1398	A
32	1a	1402	4OC
32	1a	1406	U
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1452	C
32	1a	1493	A
32	1a	1503	A
32	1a	1504	G
32	1a	1506	U
32	1a	1507	A
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
1	2A	9	U
1	2A	10	G
1	2A	12	U
1	2A	14	A
1	2A	15	G
1	2A	23	G
1	2A	45	C
1	2A	61	G
1	2A	71	A

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Mol	Chain	Res	Type
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	118	A
1	2A	120	U
1	2A	125	G
1	2A	131	G
1	2A	141	A
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	199	A
1	2A	201	C
1	2A	205	G
1	2A	213	A
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	271(P)	C
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	276	A
1	2A	277	C
1	2A	278	A
1	2A	311	A
1	2A	317	G
1	2A	322	A
1	2A	324	A
1	2A	329	G
1	2A	330	A
1	2A	342	G

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Mol	Chain	Res	Type
1	2A	345	A
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	364	C
1	2A	386	G
1	2A	391	G
1	2A	396	G
1	2A	405	U
1	2A	406	G
1	2A	411	G
1	2A	412	A
1	2A	428	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	496	G
1	2A	501	A
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	556	G
1	2A	563	G
1	2A	573	G
1	2A	574	C
1	2A	575	A
1	2A	592	G
1	2A	593	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	619	G
1	2A	627	A
1	2A	637	A

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Mol	Chain	Res	Type
1	2A	645	C
1	2A	646	A
1	2A	652(A)	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(E)	G
1	2A	669	G
1	2A	686	G
1	2A	726	G
1	2A	730	C
1	2A	753	C
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	793	A
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	829	A
1	2A	831	G
1	2A	859	G
1	2A	880	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	892	G
1	2A	893	C
1	2A	896	A
1	2A	897	C
1	2A	900	A
1	2A	901	A
1	2A	907	U
1	2A	910	A
1	2A	915	C
1	2A	917	A

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Mol	Chain	Res	Type
1	2A	926	A
1	2A	932	G
1	2A	936	C
1	2A	938	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	961	C
1	2A	962	G
1	2A	974	G
1	2A	975	C
1	2A	980	A
1	2A	983	A
1	2A	989	G
1	2A	996	A
1	2A	999	U
1	2A	1012	U
1	2A	1013	C
1	2A	1022	G
1	2A	1023	U
1	2A	1025	G
1	2A	1026	U
1	2A	1027	A
1	2A	1033	U
1	2A	1034	G
1	2A	1041	C
1	2A	1042	G
1	2A	1043	C
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1058	G
1	2A	1060	U
1	2A	1063	G
1	2A	1064	C
1	2A	1065	U
1	2A	1067	A

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Mol	Chain	Res	Type
1	2A	1068	G
1	2A	1071	G
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1080	C
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1088	A
1	2A	1089	G
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G
1	2A	1094	U
1	2A	1102	C
1	2A	1105	U
1	2A	1109	C
1	2A	1110	G
1	2A	1111	A
1	2A	1112	G
1	2A	1116	C
1	2A	1129	A
1	2A	1130	U
1	2A	1131	G
1	2A	1135	C
1	2A	1136	G
1	2A	1142(A)	A
1	2A	1170	G
1	2A	1171	G
1	2A	1188	U
1	2A	1211	U
1	2A	1237	A
1	2A	1244	G
1	2A	1248	G
1	2A	1253	A
1	2A	1256	G

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Mol	Chain	Res	Type
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1274	A
1	2A	1300	U
1	2A	1301	A
1	2A	1313	U
1	2A	1314	C
1	2A	1319	G
1	2A	1342	A
1	2A	1348	G
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	1383	C
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1459	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1494	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A

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Mol	Chain	Res	Type
1	2A	1509(B)	A
1	2A	1542	A
1	2A	1543	C
1	2A	1558	A
1	2A	1560	G
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1584	C
1	2A	1586	A
1	2A	1602	U
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1631(A)	A
1	2A	1640	C
1	2A	1648	C
1	2A	1667	G
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1701	A
1	2A	1703	G
1	2A	1722	A
1	2A	1746	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A
1	2A	1774	C
1	2A	1780	A
1	2A	1781	C
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1829	A
1	2A	1847	A
1	2A	1848	A

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Mol	Chain	Res	Type
1	2A	1858	G
1	2A	1861	G
1	2A	1877	A
1	2A	1878	G
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1917	PSU
1	2A	1927	A
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	1993	U
1	2A	1996	C
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2032	G
1	2A	2033	A
1	2A	2043	C
1	2A	2052	G
1	2A	2055	C
1	2A	2056	G
1	2A	2058	A
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A
1	2A	2069	G
1	2A	2093	G
1	2A	2095	C
1	2A	2099	U
1	2A	2100	G
1	2A	2101	G

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Mol	Chain	Res	Type
1	2A	2103	C
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2117	A
1	2A	2119	A
1	2A	2120	G
1	2A	2121	G
1	2A	2123	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2130	U
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2136	C
1	2A	2138	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2150	U
1	2A	2151	G
1	2A	2159	G
1	2A	2161	C
1	2A	2163	C
1	2A	2164	C
1	2A	2167	U
1	2A	2168	G
1	2A	2172	U
1	2A	2173	A
1	2A	2174	C
1	2A	2186	G
1	2A	2189	U
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A

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Mol	Chain	Res	Type
1	2A	2218	U
1	2A	2219	G
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2249	U
1	2A	2275	C
1	2A	2279	G
1	2A	2282	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2292	C
1	2A	2305	A
1	2A	2308	G
1	2A	2309	A
1	2A	2311	A
1	2A	2312	U
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2336	A
1	2A	2343	C
1	2A	2345	G
1	2A	2347	C
1	2A	2348	U
1	2A	2350	C
1	2A	2366	A
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2396	G
1	2A	2406	U
1	2A	2409	G
1	2A	2410	G
1	2A	2414	G
1	2A	2423	U
1	2A	2425	A
1	2A	2429	G

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Mol	Chain	Res	Type
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2459	A
1	2A	2474	C
1	2A	2476	A
1	2A	2480	C
1	2A	2487	G
1	2A	2490	G
1	2A	2491	U
1	2A	2492	U
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2517	C
1	2A	2518	A
1	2A	2520	C
1	2A	2529	G
1	2A	2532	G
1	2A	2549	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2602	A
1	2A	2603	G
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2615	U
1	2A	2629	A
1	2A	2630	G
1	2A	2646	C
1	2A	2654	A
1	2A	2663	G
1	2A	2689	U
1	2A	2690	C

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Mol	Chain	Res	Type
1	2A	2691	C
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2718	G
1	2A	2726	U
1	2A	2733	A
1	2A	2748	A
1	2A	2757	A
1	2A	2759	G
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2769	C
1	2A	2778	A
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2861	G
1	2A	2872	G
1	2A	2873	A
1	2A	2880	C
1	2A	2892	A
1	2A	2894	G
1	2A	2897	U
2	2B	2	C
2	2B	8	U
2	2B	9	G
2	2B	13	A
2	2B	15	A
2	2B	28	C
2	2B	31	C
2	2B	35	U
2	2B	36	C
2	2B	45	A
2	2B	51	G
2	2B	56	G
2	2B	73	A
2	2B	85	G
2	2B	89	G

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Mol	Chain	Res	Type
2	2B	110	G
2	2B	116	G
2	2B	120	A
32	2a	5	U
32	2a	6	G
32	2a	9	G
32	2a	14	U
32	2a	32	A
32	2a	39	G
32	2a	43	C
32	2a	44	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	78	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	151	A
32	2a	156	G
32	2a	163	C
32	2a	173	U
32	2a	174	C
32	2a	182	U
32	2a	189(F)	U
32	2a	189(G)	G
32	2a	195	A
32	2a	197	A
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	237	C
32	2a	245	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	279	A

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Mol	Chain	Res	Type
32	2a	281	G
32	2a	289	G
32	2a	301	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	348	G
32	2a	349	A
32	2a	350	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	413	G
32	2a	422	C
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	431	A
32	2a	439	A
32	2a	452	A
32	2a	453	A
32	2a	458	C
32	2a	461	A
32	2a	470	C
32	2a	475	G
32	2a	477	A
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G

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Mol	Chain	Res	Type
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	559	A
32	2a	561	U
32	2a	562	C
32	2a	563	A
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	592	G
32	2a	596	C
32	2a	607	A
32	2a	618	C
32	2a	619	U
32	2a	630	G
32	2a	632	A
32	2a	653	A
32	2a	661	G
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	723	U
32	2a	731	G
32	2a	749	C
32	2a	755	G
32	2a	760	G
32	2a	766	A
32	2a	774	G
32	2a	777	A
32	2a	793	U
32	2a	794	A
32	2a	802	A
32	2a	815	A
32	2a	816	A
32	2a	817	C
32	2a	818	G

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Mol	Chain	Res	Type
32	2a	821	G
32	2a	827	U
32	2a	828	A
32	2a	829	G
32	2a	836	G
32	2a	840	C
32	2a	841	U
32	2a	848	C
32	2a	859	A
32	2a	872	A
32	2a	885	G
32	2a	889	A
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	931	C
32	2a	934	C
32	2a	954	G
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	989	C
32	2a	991	U
32	2a	992	U
32	2a	993	G
32	2a	999	C
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1017	G
32	2a	1020	U
32	2a	1023	G
32	2a	1024	G

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Mol	Chain	Res	Type
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1030(D)	A
32	2a	1031	G
32	2a	1032	G
32	2a	1035	A
32	2a	1038	C
32	2a	1043	C
32	2a	1044	A
32	2a	1053	G
32	2a	1054	C
32	2a	1056	U
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1081	G
32	2a	1094	G
32	2a	1095	U
32	2a	1099	G
32	2a	1100	C
32	2a	1101	A
32	2a	1108	G
32	2a	1113	C
32	2a	1117	G
32	2a	1122	U
32	2a	1124	G
32	2a	1125	U
32	2a	1130	A
32	2a	1132	C
32	2a	1135	U
32	2a	1136	U
32	2a	1137	C
32	2a	1139	G
32	2a	1147	C
32	2a	1152	A
32	2a	1154	G
32	2a	1157	A
32	2a	1159	U

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Mol	Chain	Res	Type
32	2a	1160	G
32	2a	1161	C
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1185	G
32	2a	1196	U
32	2a	1197	G
32	2a	1212	U
32	2a	1213	A
32	2a	1214	C
32	2a	1224	G
32	2a	1230	C
32	2a	1238	A
32	2a	1248	A
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1260	C
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1287	A
32	2a	1290	G
32	2a	1299	A
32	2a	1300	G
32	2a	1301	U
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1310	G
32	2a	1312	G
32	2a	1316	G
32	2a	1317	C
32	2a	1320	C
32	2a	1322	C
32	2a	1326	C
32	2a	1332	A
32	2a	1341	U
32	2a	1347	G

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Mol	Chain	Res	Type
32	2a	1353	G
32	2a	1357	A
32	2a	1363	C
32	2a	1370	G
32	2a	1386	G
32	2a	1397	C
32	2a	1398	A
32	2a	1406	U
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1492	A
32	2a	1493	A
32	2a	1497	G
32	2a	1499	A
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

All (39) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	195	A
1	1A	266	G
1	1A	278	A
1	1A	827	U
1	1A	840	C
1	1A	888	C
1	1A	895	U
1	1A	1065	U
1	1A	1067	A
1	1A	1176	G
1	1A	1210	A

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Mol	Chain	Res	Type
1	1A	1442	G
1	1A	2126	A
1	1A	2430	A
1	1A	2689	U
1	2A	266	G
1	2A	271(M)	G
1	2A	752	A
1	2A	827	U
1	2A	840	C
1	2A	900	A
1	2A	1053	C
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1210	A
1	2A	1273	U
1	2A	1379	A
1	2A	1420	U
1	2A	1442	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2288	A
1	2A	2321	G
1	2A	2602	A
1	2A	2689	U
1	2A	2756	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MC	1A	1942	1	19,22,23	1.62	3 (15%)	26,32,35	1.15	3 (11%)
1	2MU	2A	2552	1,53	19,22,24	1.28	3 (15%)	25,31,36	1.92	5 (20%)
32	PSU	2a	516	53,32	18,21,22	1.37	2 (11%)	21,30,33	2.07	5 (23%)
32	5MC	1a	1407	32	19,22,23	1.66	2 (10%)	26,32,35	1.11	2 (7%)
1	5MU	2A	1915	1	19,22,23	1.42	5 (26%)	27,32,35	2.20	9 (33%)
1	2MA	1A	2503	1,53	22,25,26	1.46	5 (22%)	32,37,40	2.32	8 (25%)
32	5MC	1a	1400	32	19,22,23	1.71	3 (15%)	26,32,35	1.12	2 (7%)
32	5MC	1a	1404	32	19,22,23	1.69	3 (15%)	26,32,35	1.15	2 (7%)
32	MA6	1a	1518	32	23,26,27	1.54	4 (17%)	33,38,41	2.32	13 (39%)
1	4OC	2A	1920	1	19,22,24	0.82	0	25,31,35	1.05	1 (4%)
1	OMG	1A	2251	1	23,26,27	1.21	3 (13%)	32,38,41	2.00	6 (18%)
1	5MU	1A	1939	1	19,22,23	1.45	5 (26%)	27,32,35	2.30	6 (22%)
43	0TD	1l	92	43	8,9,10	4.52	2 (25%)	6,11,13	4.67	2 (33%)
32	5MC	2a	1404	32	19,22,23	1.71	3 (15%)	26,32,35	1.14	3 (11%)
1	PSU	1A	1911	1	18,21,22	1.36	2 (11%)	21,30,33	2.00	3 (14%)
1	OMG	2A	2251	1,53	23,26,27	1.19	3 (13%)	32,38,41	1.95	6 (18%)
43	0TD	2l	92	43	8,9,10	4.54	2 (25%)	6,11,13	4.31	2 (33%)
32	MA6	2a	1519	32	23,26,27	1.51	4 (17%)	33,38,41	2.44	13 (39%)
32	2MG	1a	1207	32	23,26,27	1.25	3 (13%)	33,38,41	2.25	8 (24%)
32	7MG	2a	527	32	23,26,27	1.29	3 (13%)	27,39,42	2.65	7 (25%)
32	2MG	2a	1207	32	23,26,27	1.25	3 (13%)	33,38,41	2.11	6 (18%)
32	5MC	2a	1400	32	19,22,23	1.70	3 (15%)	26,32,35	1.14	2 (7%)
32	UR3	1a	1498	32	19,22,23	1.02	2 (10%)	26,32,35	1.72	2 (7%)
1	PSU	2A	1917	1	18,21,22	1.38	2 (11%)	21,30,33	2.01	4 (19%)
1	5MU	2A	1939	1	19,22,23	1.38	5 (26%)	27,32,35	2.18	6 (22%)
32	5MC	1a	967	32	19,22,23	1.64	2 (10%)	26,32,35	1.06	2 (7%)
1	PSU	2A	1911	1	18,21,22	1.37	2 (11%)	21,30,33	2.07	4 (19%)
1	5MC	2A	1942	1	19,22,23	1.64	3 (15%)	26,32,35	1.13	2 (7%)
32	5MC	2a	967	32	19,22,23	1.75	3 (15%)	26,32,35	1.13	3 (11%)
1	PSU	2A	2605	1	18,21,22	1.37	2 (11%)	21,30,33	2.02	4 (19%)
32	7MG	1a	527	32	23,26,27	1.31	3 (13%)	27,39,42	2.62	7 (25%)
1	PSU	1A	1917	1,53	18,21,22	1.36	2 (11%)	21,30,33	1.99	3 (14%)
32	MA6	1a	1519	32	23,26,27	1.54	4 (17%)	33,38,41	2.35	12 (36%)
1	2MA	2A	2503	1,53	22,25,26	1.52	4 (18%)	32,37,40	2.37	7 (21%)
1	5MC	1A	1962	1	19,22,23	1.66	3 (15%)	26,32,35	1.11	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
32	4OC	2a	1402	32	20,23,24	0.76	0	25,32,35	0.92	1 (4%)
32	M2G	1a	966	32	24,27,28	1.29	3 (12%)	33,40,43	1.88	6 (18%)
1	2MU	1A	2552	1,53	19,22,24	1.21	2 (10%)	25,31,36	1.87	6 (24%)
32	5MC	2a	1407	32	19,22,23	1.59	3 (15%)	26,32,35	1.14	3 (11%)
1	5MC	2A	1962	1	19,22,23	1.54	3 (15%)	26,32,35	1.12	2 (7%)
32	MA6	2a	1518	32	23,26,27	1.62	4 (17%)	33,38,41	2.30	12 (36%)
1	5MU	1A	1915	1,53	19,22,23	1.43	6 (31%)	27,32,35	2.21	9 (33%)
32	PSU	1a	516	53,32	18,21,22	1.37	2 (11%)	21,30,33	2.01	4 (19%)
1	4OC	1A	1920	1	19,22,24	0.78	0	25,31,35	0.80	0
1	PSU	1A	2605	1	18,21,22	1.41	3 (16%)	21,30,33	1.95	4 (19%)
32	M2G	2a	966	32	24,27,28	1.30	3 (12%)	33,40,43	1.87	5 (15%)
32	4OC	1a	1402	32	20,23,24	0.75	0	25,32,35	0.96	1 (4%)
32	UR3	2a	1498	32	19,22,23	1.03	1 (5%)	26,32,35	1.73	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
1	5MC	1A	1942	1	-	0/7/25/26	0/2/2/2
1	2MU	2A	2552	1,53	-	1/9/27/28	0/2/2/2
32	PSU	2a	516	53,32	-	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	-	2/7/25/26	0/2/2/2
1	2MA	1A	2503	1,53	-	1/7/25/26	0/3/3/3
32	5MC	1a	1400	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	2/11/29/30	0/3/3/3
1	4OC	2A	1920	1	-	1/9/27/30	0/2/2/2
1	OMG	1A	2251	1	-	0/9/27/28	0/3/3/3
1	5MU	1A	1939	1	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	3/7/12/14	-
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	2A	2251	1,53	-	0/9/27/28	0/3/3/3
43	0TD	2l	92	43	-	1/7/12/14	-
32	MA6	2a	1519	32	-	7/11/29/30	0/3/3/3
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	7MG	2a	527	32	-	1/7/37/38	0/3/3/3
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
32	5MC	2a	1400	32	-	4/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	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	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/7/25/26	0/2/2/2
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	7MG	1a	527	32	-	3/7/37/38	0/3/3/3
1	PSU	1A	1917	1,53	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
1	2MA	2A	2503	1,53	-	3/7/25/26	0/3/3/3
1	5MC	1A	1962	1	-	2/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	2/9/29/30	0/2/2/2
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
1	2MU	1A	2552	1,53	-	0/9/27/28	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1962	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	3/11/29/30	0/3/3/3
1	5MU	1A	1915	1,53	-	2/7/25/26	0/2/2/2
32	PSU	1a	516	53,32	-	0/7/25/26	0/2/2/2
1	4OC	1A	1920	1	-	1/9/27/30	0/2/2/2
1	PSU	1A	2605	1	-	0/7/25/26	0/2/2/2
32	M2G	2a	966	32	-	0/11/29/30	0/3/3/3
32	4OC	1a	1402	32	-	2/9/29/30	0/2/2/2
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2

All (133) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-12.34	1.69	1.82
43	1l	92	0TD	CB-SB	-12.20	1.70	1.82
32	2a	967	5MC	C5-C4	6.48	1.49	1.44
32	2a	1404	5MC	C5-C4	6.36	1.48	1.44
32	1a	1400	5MC	C5-C4	6.23	1.48	1.44
32	2a	1400	5MC	C5-C4	6.21	1.48	1.44
32	1a	1404	5MC	C5-C4	6.11	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	1407	5MC	C5-C4	6.06	1.48	1.44
1	1A	1962	5MC	C5-C4	6.02	1.48	1.44
1	2A	1942	5MC	C5-C4	5.86	1.48	1.44
1	1A	1942	5MC	C5-C4	5.84	1.48	1.44
32	1a	967	5MC	C5-C4	5.84	1.48	1.44
32	2a	1407	5MC	C5-C4	5.65	1.48	1.44
1	2A	1962	5MC	C5-C4	5.41	1.48	1.44
32	2a	1518	MA6	C5-C4	5.10	1.48	1.39
32	1a	1518	MA6	C5-C4	4.85	1.47	1.39
32	1a	1519	MA6	C5-C4	4.84	1.47	1.39
1	2A	2503	2MA	C5-C4	4.80	1.47	1.39
32	2a	1519	MA6	C5-C4	4.68	1.47	1.39
1	1A	2503	2MA	C5-C4	4.27	1.46	1.39
1	2A	1911	PSU	C6-C5	3.63	1.39	1.35
1	2A	1917	PSU	C6-C5	3.51	1.39	1.35
32	2a	516	PSU	C6-C5	3.47	1.39	1.35
1	1A	1911	PSU	C6-C5	3.46	1.39	1.35
1	1A	1917	PSU	C6-C5	3.45	1.39	1.35
32	1a	516	PSU	C6-C5	3.44	1.39	1.35
1	2A	2605	PSU	C6-C5	3.42	1.39	1.35
32	2a	1518	MA6	C5-C6	3.37	1.50	1.41
32	1a	966	M2G	C5-C4	3.27	1.47	1.38
32	2a	527	7MG	C5-C4	3.26	1.47	1.37
32	1a	527	7MG	C5-C4	3.25	1.47	1.37
32	2a	966	M2G	C5-C4	3.21	1.47	1.38
1	1A	2605	PSU	C6-C5	3.20	1.38	1.35
32	1a	1207	2MG	C5-C4	3.18	1.47	1.38
1	2A	2251	OMG	C5-C4	3.18	1.47	1.38
32	2a	1207	2MG	C5-C4	3.17	1.47	1.38
1	1A	2251	OMG	C5-C4	3.14	1.47	1.38
32	1a	527	7MG	C4-N9	-3.10	1.34	1.37
32	1a	1518	MA6	C5-C6	3.07	1.49	1.41
1	1A	1939	5MU	C6-C5	3.03	1.39	1.34
32	1a	967	5MC	C6-C5	3.00	1.39	1.34
32	1a	966	M2G	C2-N2	2.98	1.40	1.35
32	2a	966	M2G	C2-N2	2.93	1.40	1.35
32	2a	1519	MA6	C5-C6	2.91	1.48	1.41
1	1A	1939	5MU	C4-N3	-2.91	1.33	1.38
32	2a	1400	5MC	C6-C5	2.89	1.39	1.34
32	1a	1404	5MC	C6-C5	2.88	1.39	1.34
1	1A	2605	PSU	C4-N3	-2.88	1.33	1.38
32	1a	1400	5MC	C6-C5	2.87	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1A	1915	5MU	C2-N1	2.86	1.42	1.38
32	1a	1519	MA6	C5-C6	2.83	1.48	1.41
32	2a	967	5MC	C6-C5	2.81	1.39	1.34
1	2A	1939	5MU	C6-C5	2.80	1.39	1.34
32	2a	527	7MG	C4-N9	-2.79	1.34	1.37
1	2A	1915	5MU	C2-N1	2.79	1.42	1.38
1	1A	1942	5MC	C6-C5	2.77	1.39	1.34
32	1a	1407	5MC	C6-C5	2.75	1.39	1.34
1	2A	1915	5MU	C6-C5	2.75	1.39	1.34
1	1A	1962	5MC	C6-C5	2.75	1.39	1.34
1	2A	1942	5MC	C6-C5	2.73	1.39	1.34
1	2A	1962	5MC	C6-C5	2.73	1.39	1.34
32	2a	1407	5MC	C6-C5	2.72	1.39	1.34
1	2A	2503	2MA	C5-C6	2.71	1.48	1.41
1	1A	2552	2MU	C4-N3	-2.67	1.34	1.38
1	2A	2552	2MU	C4-N3	-2.66	1.34	1.38
1	2A	2605	PSU	C4-N3	-2.64	1.33	1.38
1	1A	1915	5MU	C4-N3	-2.63	1.33	1.38
32	2a	1404	5MC	C6-C5	2.62	1.38	1.34
32	1a	516	PSU	C4-N3	-2.60	1.34	1.38
1	1A	1915	5MU	C6-C5	2.59	1.38	1.34
1	2A	1917	PSU	C4-N3	-2.58	1.34	1.38
1	1A	1911	PSU	C4-N3	-2.57	1.34	1.38
1	2A	1939	5MU	C4-C5	2.55	1.49	1.44
1	2A	1939	5MU	C4-N3	-2.54	1.34	1.38
1	2A	1911	PSU	C4-N3	-2.53	1.34	1.38
1	2A	1915	5MU	C4-N3	-2.53	1.34	1.38
43	1l	92	0TD	CB-CA	-2.53	1.53	1.54
32	2a	516	PSU	C4-N3	-2.53	1.34	1.38
1	1A	2251	OMG	C6-N1	-2.52	1.34	1.38
1	1A	2503	2MA	C5-C6	2.52	1.48	1.41
1	1A	1917	PSU	C4-N3	-2.51	1.34	1.38
1	1A	2503	2MA	C5-N7	-2.50	1.34	1.39
1	2A	2251	OMG	C6-N1	-2.48	1.34	1.38
1	1A	1939	5MU	C4-C5	2.47	1.48	1.44
32	2a	1207	2MG	C6-N1	-2.44	1.34	1.38
32	2a	1519	MA6	C8-N7	2.39	1.36	1.31
1	2A	2503	2MA	C8-N7	2.39	1.36	1.31
1	1A	1939	5MU	C2-N3	-2.37	1.33	1.38
32	1a	1519	MA6	C5-N7	-2.35	1.34	1.39
1	1A	1942	5MC	C6-N1	-2.34	1.34	1.38
1	1A	2605	PSU	C2-N3	-2.33	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1518	MA6	C8-N7	2.33	1.36	1.31
1	1A	1962	5MC	C6-N1	-2.33	1.34	1.38
1	1A	2503	2MA	C8-N7	2.31	1.36	1.31
1	1A	2251	OMG	C5-N7	-2.31	1.34	1.39
32	2a	966	M2G	C6-N1	-2.30	1.34	1.38
32	1a	1207	2MG	C6-N1	-2.30	1.34	1.38
32	2a	527	7MG	C6-N1	-2.30	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.29	1.34	1.38
1	2A	1915	5MU	C4-C5	2.29	1.48	1.44
1	2A	1942	5MC	C6-N1	-2.28	1.34	1.38
1	2A	2503	2MA	C5-N7	-2.28	1.34	1.39
32	1a	1498	UR3	C2-N1	2.27	1.41	1.38
32	1a	1400	5MC	C6-N1	-2.26	1.34	1.38
32	1a	1518	MA6	C8-N7	2.26	1.36	1.31
32	2a	1404	5MC	C6-N1	-2.25	1.34	1.38
32	1a	1207	2MG	C2-N3	2.24	1.36	1.32
1	1A	1915	5MU	C4-C5	2.22	1.48	1.44
32	1a	1404	5MC	C6-N1	-2.22	1.34	1.38
1	2A	1939	5MU	C6-N1	-2.21	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.21	1.34	1.38
1	2A	2552	2MU	C5-C4	2.20	1.48	1.43
32	2a	1519	MA6	C5-N7	-2.20	1.35	1.39
32	1a	966	M2G	C6-N1	-2.19	1.34	1.38
32	1a	1519	MA6	C8-N7	2.19	1.35	1.31
32	2a	1400	5MC	C6-N1	-2.18	1.34	1.38
32	2a	1498	UR3	C2-N1	2.17	1.41	1.38
1	1A	1915	5MU	C6-N1	-2.17	1.34	1.38
1	2A	2251	OMG	C5-N7	-2.16	1.34	1.39
43	2l	92	0TD	CB-CA	-2.15	1.54	1.54
1	1A	2552	2MU	C5-C4	2.15	1.48	1.43
1	2A	2552	2MU	C2-N1	2.12	1.41	1.38
32	1a	527	7MG	C6-N1	-2.12	1.34	1.38
32	2a	1207	2MG	C2-N3	2.10	1.36	1.32
32	2a	1407	5MC	C6-N1	-2.08	1.34	1.38
1	1A	1915	5MU	C2-N3	-2.08	1.34	1.38
32	2a	967	5MC	C6-N1	-2.08	1.34	1.38
1	2A	1939	5MU	C2-N3	-2.06	1.34	1.38
1	1A	2503	2MA	C4-N9	-2.06	1.33	1.37
32	1a	1518	MA6	C5-N7	-2.05	1.35	1.39
1	2A	1915	5MU	C6-N1	-2.04	1.34	1.38
32	1a	1498	UR3	C6-C5	2.03	1.39	1.35
32	2a	1518	MA6	C5-N7	-2.02	1.35	1.39

All (228) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	1l	92	0TD	CSB-SB-CB	-10.82	82.91	102.36
43	2l	92	0TD	CSB-SB-CB	-9.83	84.69	102.36
32	2a	527	7MG	N9-C4-N3	9.01	138.66	125.46
32	1a	527	7MG	N9-C4-N3	8.81	138.38	125.46
1	2A	2503	2MA	C5-C4-N3	-8.79	117.92	127.18
1	1A	2503	2MA	C5-C4-N3	-8.50	118.22	127.18
32	1a	1207	2MG	C2-N3-C4	7.17	120.96	112.00
32	2a	1207	2MG	C2-N3-C4	7.01	120.78	112.00
32	1a	1498	UR3	C4-N3-C2	-6.93	119.00	124.58
32	2a	1498	UR3	C4-N3-C2	-6.90	119.03	124.58
1	2A	2503	2MA	N3-C4-N9	6.84	135.68	126.99
1	2A	1911	PSU	N1-C2-N3	6.45	121.97	115.17
32	2a	516	PSU	N1-C2-N3	6.42	121.94	115.17
1	1A	2251	OMG	C5-C4-N3	-6.40	118.20	128.39
1	1A	2503	2MA	N3-C4-N9	6.37	135.07	126.99
1	2A	1917	PSU	N1-C2-N3	6.36	121.88	115.17
1	2A	2605	PSU	N1-C2-N3	6.26	121.77	115.17
1	1A	1917	PSU	N1-C2-N3	6.25	121.76	115.17
1	1A	1911	PSU	N1-C2-N3	6.24	121.75	115.17
32	1a	966	M2G	C5-C4-N3	-6.17	118.57	128.39
32	1a	516	PSU	N1-C2-N3	6.16	121.67	115.17
1	2A	2251	OMG	C5-C4-N3	-6.15	118.61	128.39
32	2a	966	M2G	C5-C4-N3	-6.11	118.67	128.39
32	1a	1207	2MG	C5-C4-N3	-6.03	118.79	128.39
32	1a	1519	MA6	C5-C4-N3	-6.01	118.44	126.72
1	1A	2605	PSU	N1-C2-N3	5.88	121.37	115.17
32	2a	1207	2MG	C5-C4-N3	-5.80	119.15	128.39
32	2a	1519	MA6	C5-C4-N3	-5.74	118.81	126.72
1	1A	1939	5MU	N3-C2-N1	5.74	122.36	114.89
1	1A	1939	5MU	C4-N3-C2	-5.68	119.90	127.34
32	2a	1518	MA6	C5-C4-N3	-5.63	118.97	126.72
32	1a	1518	MA6	C5-C4-N3	-5.52	119.12	126.72
32	1a	527	7MG	N9-C8-N7	-5.48	95.62	103.37
32	2a	527	7MG	N9-C8-N7	-5.46	95.65	103.37
32	2a	527	7MG	C5-C4-N3	-5.36	118.06	128.13
1	2A	1939	5MU	C4-N3-C2	-5.35	120.33	127.34
32	1a	527	7MG	C5-C4-N3	-5.21	118.34	128.13
1	2A	2552	2MU	N3-C2-N1	5.09	121.52	114.89
1	2A	1939	5MU	N3-C2-N1	5.09	121.51	114.89
1	1A	2552	2MU	N3-C2-N1	5.07	121.49	114.89
1	1A	2251	OMG	C2-N3-C4	5.05	120.99	112.30
1	2A	2251	OMG	C2-N3-C4	4.92	120.78	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2A	1915	5MU	N3-C2-N1	4.92	121.29	114.89
1	2A	2552	2MU	C4-N3-C2	-4.91	120.52	126.61
1	1A	2251	OMG	N9-C4-N3	4.89	135.72	125.95
1	1A	1939	5MU	C5-C6-N1	-4.74	118.17	123.31
32	1a	1519	MA6	N3-C4-N9	4.72	135.19	127.17
32	1a	966	M2G	C2-N3-C4	4.71	121.22	112.51
32	2a	1519	MA6	C9-N6-C6	-4.67	108.63	120.52
1	1A	1915	5MU	C4-N3-C2	-4.65	121.25	127.34
32	2a	1518	MA6	C4-C5-N7	-4.64	105.27	110.58
1	1A	1915	5MU	N3-C2-N1	4.62	120.91	114.89
32	2a	966	M2G	C2-N3-C4	4.60	121.01	112.51
32	2a	527	7MG	C2-N3-C4	4.52	120.08	112.30
1	2A	2251	OMG	N9-C4-N3	4.51	134.98	125.95
1	1A	2552	2MU	C4-N3-C2	-4.49	121.04	126.61
32	1a	966	M2G	N9-C4-N3	4.48	134.91	125.95
1	1A	1939	5MU	C5-C4-N3	4.47	119.21	115.32
1	2A	1939	5MU	C5-C4-N3	4.44	119.19	115.32
1	1A	1915	5MU	C5-C4-N3	4.43	119.18	115.32
32	1a	527	7MG	C2-N3-C4	4.43	119.92	112.30
1	2A	1915	5MU	C4-N3-C2	-4.42	121.54	127.34
32	2a	1518	MA6	C9-N6-C6	-4.42	109.29	120.52
32	2a	1518	MA6	C2-N1-C6	4.40	122.57	111.83
32	2a	966	M2G	N9-C4-N3	4.36	134.68	125.95
32	1a	1518	MA6	C2-N1-C6	4.36	122.49	111.83
1	2A	1915	5MU	C1'-N1-C2	4.34	125.38	117.59
32	2a	1207	2MG	N9-C4-N3	4.32	134.59	125.95
32	2a	1519	MA6	C10-N6-C6	-4.31	109.55	120.52
32	2a	1519	MA6	N3-C4-N9	4.29	134.46	127.17
32	1a	1207	2MG	N9-C4-N3	4.29	134.53	125.95
32	1a	1518	MA6	C9-N6-C6	-4.28	109.63	120.52
32	1a	1518	MA6	C4-C5-N7	-4.20	105.78	110.58
1	2A	1911	PSU	C4-N3-C2	-4.18	120.61	126.37
1	1A	2605	PSU	C4-N3-C2	-4.15	120.65	126.37
32	1a	1519	MA6	C2-N1-C6	4.14	121.94	111.83
32	2a	1519	MA6	C2-N1-C6	4.14	121.93	111.83
32	1a	1518	MA6	N3-C4-N9	4.11	134.16	127.17
32	1a	1519	MA6	C9-N6-C6	-4.11	110.07	120.52
32	2a	516	PSU	C4-N3-C2	-4.10	120.72	126.37
1	2A	1939	5MU	C5-C6-N1	-4.09	118.87	123.31
1	2A	1917	PSU	C4-N3-C2	-4.07	120.76	126.37
1	1A	1917	PSU	C4-N3-C2	-4.03	120.83	126.37
32	1a	516	PSU	C4-N3-C2	-4.00	120.86	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1A	1911	PSU	C4-N3-C2	-3.98	120.89	126.37
1	2A	2605	PSU	C4-N3-C2	-3.96	120.91	126.37
1	1A	1915	5MU	C1'-N1-C2	3.93	124.65	117.59
32	2a	516	PSU	O2-C2-N1	-3.90	118.77	122.79
1	1A	1915	5MU	O4-C4-C5	-3.88	120.48	124.92
1	2A	1939	5MU	O4-C4-C5	-3.88	120.48	124.92
32	2a	1518	MA6	N3-C4-N9	3.87	133.75	127.17
32	2a	1519	MA6	C4-C5-N7	-3.82	106.22	110.58
1	1A	1962	5MC	C5-C6-N1	-3.75	119.25	123.31
1	2A	1915	5MU	O4-C4-C5	-3.67	120.71	124.92
32	1a	1519	MA6	C4-C5-N7	-3.67	106.39	110.58
1	2A	1915	5MU	C5-C4-N3	3.66	118.51	115.32
32	2a	1519	MA6	C2-N3-C4	3.65	120.76	111.83
32	1a	1519	MA6	C2-N3-C4	3.65	120.74	111.83
1	2A	1939	5MU	O2-C2-N1	-3.62	118.08	122.80
32	1a	1518	MA6	C2-N3-C4	3.61	120.66	111.83
32	2a	1518	MA6	C2-N3-C4	3.61	120.65	111.83
1	1A	1911	PSU	O2-C2-N1	-3.60	119.08	122.79
1	1A	1939	5MU	O4-C4-C5	-3.59	120.81	124.92
1	2A	2605	PSU	O2-C2-N1	-3.59	119.09	122.79
1	2A	1915	5MU	C1'-N1-C6	-3.58	115.25	121.15
1	2A	1911	PSU	O2-C2-N1	-3.57	119.11	122.79
1	1A	1915	5MU	C1'-N1-C6	-3.57	115.28	121.15
32	1a	516	PSU	O2-C2-N1	-3.57	119.11	122.79
32	1a	1400	5MC	C5-C6-N1	-3.55	119.46	123.31
32	2a	1400	5MC	C5-C6-N1	-3.51	119.50	123.31
1	1A	1939	5MU	O2-C2-N1	-3.50	118.25	122.80
32	1a	1404	5MC	C5-C6-N1	-3.46	119.56	123.31
32	1a	1207	2MG	C6-C5-N7	3.44	136.54	130.29
1	1A	2503	2MA	C4-C5-N7	-3.43	106.66	110.58
1	2A	2503	2MA	C4-C5-N7	-3.40	106.70	110.58
1	2A	1917	PSU	O2-C2-N1	-3.37	119.31	122.79
32	2a	1207	2MG	C6-C5-N7	3.37	136.43	130.29
1	1A	1917	PSU	O2-C2-N1	-3.37	119.31	122.79
32	2a	967	5MC	C5-C6-N1	-3.36	119.67	123.31
32	1a	1519	MA6	N1-C6-N6	3.36	120.94	116.86
32	2a	966	M2G	C6-C5-N7	3.34	136.37	130.29
32	1a	1498	UR3	C5-C4-N3	3.33	119.42	115.04
1	1A	1942	5MC	C5-C6-N1	-3.30	119.73	123.31
1	2A	1942	5MC	C5-C6-N1	-3.30	119.73	123.31
32	1a	1518	MA6	N1-C2-N3	-3.28	123.62	128.58
1	2A	1962	5MC	C5-C6-N1	-3.27	119.76	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	1a	966	M2G	C6-C5-N7	3.25	136.20	130.29
32	2a	1404	5MC	C5-C6-N1	-3.24	119.79	123.31
32	2a	1498	UR3	C5-C4-N3	3.20	119.26	115.04
32	2a	1519	MA6	N1-C2-N3	-3.19	123.75	128.58
1	2A	2251	OMG	C6-C5-N7	3.11	135.96	130.29
32	2a	1519	MA6	C10-N6-C9	-3.09	106.24	116.18
32	1a	1519	MA6	N1-C2-N3	-3.08	123.92	128.58
32	2a	1518	MA6	N1-C2-N3	-3.07	123.94	128.58
1	2A	2552	2MU	C5-C4-N3	3.06	119.09	114.80
32	2a	1518	MA6	C5-N7-C8	3.03	108.22	103.45
32	1a	1518	MA6	C10-N6-C6	-3.03	112.81	120.52
1	2A	2552	2MU	O4-C4-C5	-3.03	119.94	125.16
32	2a	1407	5MC	C5-C6-N1	-3.02	120.03	123.31
32	2a	1519	MA6	N1-C6-N6	2.96	120.46	116.86
1	1A	2552	2MU	O2-C2-N1	-2.95	118.95	122.80
32	1a	1518	MA6	C5-N7-C8	2.92	108.04	103.45
32	1a	967	5MC	C5-C4-N3	-2.92	118.76	121.75
1	1A	2503	2MA	N6-C6-N1	2.90	120.95	117.03
32	1a	1407	5MC	C5-C4-N3	-2.88	118.80	121.75
43	2l	92	0TD	OD2-CG-CB	2.87	119.36	113.15
1	2A	2503	2MA	N6-C6-N1	2.86	120.88	117.03
32	1a	1404	5MC	C5-C4-N3	-2.85	118.83	121.75
32	1a	1519	MA6	C10-N6-C6	-2.84	113.29	120.52
32	2a	527	7MG	C5-C6-N1	2.83	115.92	110.94
1	1A	2251	OMG	C6-C5-N7	2.83	135.44	130.29
32	2a	1404	5MC	C5-C4-N3	-2.78	118.90	121.75
1	1A	2552	2MU	O4-C4-C5	-2.77	120.38	125.16
1	1A	1942	5MC	C5-C4-N3	-2.77	118.91	121.75
1	2A	2552	2MU	O2-C2-N1	-2.76	119.21	122.80
1	2A	1942	5MC	C5-C4-N3	-2.75	118.93	121.75
32	1a	527	7MG	C5-C6-N1	2.75	115.77	110.94
32	2a	1407	5MC	C5-C4-N3	-2.74	118.94	121.75
32	1a	1207	2MG	C4-C5-N7	-2.74	106.33	110.67
43	1l	92	0TD	OD2-CG-CB	2.73	119.06	113.15
32	2a	966	M2G	C4-C5-N7	-2.72	106.36	110.67
32	2a	1400	5MC	C5-C4-N3	-2.70	118.98	121.75
32	1a	967	5MC	C5-C6-N1	-2.70	120.38	123.31
1	1A	2552	2MU	C2'-C1'-N1	-2.70	109.12	114.24
32	1a	1518	MA6	C4-N9-C8	2.70	108.57	105.74
32	1a	1519	MA6	C5-N7-C8	2.69	107.67	103.45
1	1A	2552	2MU	C5-C4-N3	2.67	118.54	114.80
1	2A	1920	4OC	O2-C2-N3	-2.67	118.12	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	967	5MC	C5-C4-N3	-2.67	119.02	121.75
32	2a	1519	MA6	C5-N7-C8	2.63	107.59	103.45
1	1A	1915	5MU	C5-C6-N1	-2.61	120.48	123.31
32	1a	1407	5MC	C5-C6-N1	-2.60	120.49	123.31
32	1a	1518	MA6	C10-N6-C9	-2.59	107.86	116.18
32	1a	966	M2G	C4-C5-N7	-2.58	106.57	110.67
1	2A	2251	OMG	C4-C5-N7	-2.58	106.58	110.67
32	1a	1400	5MC	C5-C4-N3	-2.58	119.11	121.75
32	2a	1518	MA6	C10-N6-C9	-2.57	107.92	116.18
1	1A	2605	PSU	O2-C2-N1	-2.56	120.14	122.79
32	2a	1518	MA6	C6-C5-N7	2.52	137.46	133.43
32	2a	1207	2MG	C4-C5-N7	-2.52	106.68	110.67
32	2a	1518	MA6	C10-N6-C6	-2.51	114.13	120.52
1	1A	1962	5MC	C5-C4-N3	-2.50	119.20	121.75
1	1A	2503	2MA	C2-N1-C6	2.47	121.89	118.10
1	2A	2503	2MA	C5-N7-C8	2.47	107.33	103.45
32	2a	1519	MA6	C4-N9-C8	2.45	108.31	105.74
1	2A	1962	5MC	C5-C4-N3	-2.44	119.26	121.75
1	2A	2503	2MA	C2-N1-C6	2.43	121.83	118.10
1	1A	2503	2MA	C5-N7-C8	2.42	107.25	103.45
32	1a	1207	2MG	N1-C2-N2	2.41	119.03	116.56
32	1a	1519	MA6	C4-N9-C8	2.41	108.26	105.74
32	2a	527	7MG	C5-C4-N9	-2.40	103.26	106.33
32	1a	527	7MG	C5-C4-N9	-2.40	103.26	106.33
1	2A	1915	5MU	O2-C2-N3	-2.37	117.12	121.49
1	1A	1915	5MU	O2-C2-N3	-2.36	117.14	121.49
1	1A	2251	OMG	C4-C5-N7	-2.35	106.95	110.67
32	1a	1518	MA6	C6-C5-N7	2.35	137.18	133.43
1	1A	2251	OMG	O6-C6-C5	-2.31	120.43	126.53
1	1A	2605	PSU	C5-C6-N1	-2.31	118.94	122.14
32	1a	1402	4OC	C6-C5-C4	2.31	119.78	117.00
1	1A	2503	2MA	C4-N9-C8	2.27	108.13	105.74
32	1a	516	PSU	O4'-C1'-C2'	2.24	108.25	105.15
1	2A	1915	5MU	C5-C6-N1	-2.24	120.89	123.31
32	2a	1407	5MC	O2-C2-N3	-2.23	118.81	122.33
32	2a	1402	4OC	C6-C5-C4	2.21	119.67	117.00
32	1a	1519	MA6	C5-C6-N6	-2.20	121.84	125.33
32	2a	527	7MG	O6-C6-C5	-2.20	122.22	127.62
1	1A	1915	5MU	C5M-C5-C4	2.19	121.12	118.78
32	1a	527	7MG	O6-C6-C5	-2.18	122.26	127.62
1	2A	2503	2MA	C4-N9-C8	2.18	108.03	105.74
32	2a	516	PSU	O4'-C1'-C2'	2.16	108.14	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	2a	1518	MA6	C4-N9-C8	2.14	107.99	105.74
32	1a	1518	MA6	N9-C8-N7	-2.14	110.90	113.94
1	1A	2503	2MA	C6-C5-N7	2.12	136.19	132.09
1	2A	2605	PSU	C5-C6-N1	-2.11	119.21	122.14
1	2A	1917	PSU	C5-C6-N1	-2.11	119.22	122.14
32	1a	966	M2G	O6-C6-C5	-2.11	120.98	126.53
32	2a	1498	UR3	C3U-N3-C4	2.10	120.78	117.87
32	2a	516	PSU	C5-C6-N1	-2.09	119.24	122.14
32	2a	1404	5MC	CM5-C5-C6	-2.08	120.03	122.85
1	2A	1915	5MU	C5M-C5-C4	2.08	121.00	118.78
32	2a	1519	MA6	C5-C6-N6	-2.08	122.04	125.33
1	1A	1942	5MC	O2-C2-N3	-2.05	119.09	122.33
32	1a	1207	2MG	O3'-C3'-C2'	2.05	118.39	111.82
32	1a	1207	2MG	O6-C6-C5	-2.04	121.16	126.53
32	2a	1207	2MG	N1-C2-N2	2.03	118.63	116.56
1	2A	1911	PSU	C5-C6-N1	-2.03	119.32	122.14
32	2a	967	5MC	O2-C2-N3	-2.03	119.14	122.33
1	2A	2251	OMG	O6-C6-C5	-2.01	121.23	126.53

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1915	5MU	O4'-C1'-N1-C2
1	1A	1915	5MU	O4'-C1'-N1-C6
32	1a	1402	4OC	O4'-C4'-C5'-O5'
43	1l	92	0TD	O-C-CA-CB
43	1l	92	0TD	CG-CB-SB-CSB
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
32	2a	1518	MA6	C5-C6-N6-C9
32	2a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C5-C6-N6-C9
32	2a	1519	MA6	C5-C6-N6-C10
32	2a	1519	MA6	N1-C6-N6-C9
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1518	MA6	N1-C6-N6-C9
32	1a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	7MG	C3'-C4'-C5'-O5'
1	1A	1962	5MC	O4'-C4'-C5'-O5'
32	1a	1518	MA6	C5-C6-N6-C9

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Mol	Chain	Res	Type	Atoms
32	1a	1518	MA6	C5-C6-N6-C10
32	2a	1402	4OC	C3'-C4'-C5'-O5'
32	2a	1400	5MC	C2'-C1'-N1-C6
1	2A	2552	2MU	O4'-C4'-C5'-O5'
43	2l	92	0TD	CG-CB-SB-CSB
1	2A	2503	2MA	O4'-C4'-C5'-O5'
32	1a	527	7MG	O4'-C4'-C5'-O5'
32	2a	1400	5MC	O4'-C1'-N1-C6
32	2a	1519	MA6	C4'-C5'-O5'-P
1	1A	1962	5MC	C3'-C4'-C5'-O5'
32	2a	527	7MG	C4'-C5'-O5'-P
32	1a	1519	MA6	C5-C6-N6-C10
32	2a	1519	MA6	N1-C6-N6-C10
32	1a	527	7MG	C4'-C5'-O5'-P
43	1l	92	0TD	CA-CB-SB-CSB
1	2A	2503	2MA	C4'-C5'-O5'-P
1	1A	1920	4OC	C3'-C2'-O2'-CM2
32	2a	1400	5MC	O4'-C1'-N1-C2
32	2a	1400	5MC	C2'-C1'-N1-C2
32	2a	1518	MA6	C5-C6-N6-C10
32	1a	1519	MA6	O4'-C4'-C5'-O5'
1	2A	2503	2MA	C3'-C4'-C5'-O5'
1	2A	1920	4OC	C2'-C1'-N1-C2
1	1A	2503	2MA	O4'-C4'-C5'-O5'

There are no ring outliers.

21 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1A	1942	5MC	1	0
1	2A	2552	2MU	1	0
32	1a	1518	MA6	1	0
1	2A	1920	4OC	1	0
1	1A	2251	OMG	1	0
1	1A	1939	5MU	1	0
43	1l	92	0TD	1	0
32	2a	1404	5MC	1	0
1	2A	2251	OMG	2	0
43	2l	92	0TD	1	0
32	2a	1519	MA6	2	0
32	1a	1207	2MG	1	0
1	2A	1939	5MU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	1a	1519	MA6	1	0
32	2a	1402	4OC	2	0
1	1A	2552	2MU	1	0
32	2a	1518	MA6	1	0
1	1A	1915	5MU	1	0
32	1a	516	PSU	1	0
1	1A	1920	4OC	2	0
32	1a	1402	4OC	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1734 ligands modelled in this entry, 1730 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	$\#\|Z\| > 2$
54	HGR	1A	3749	-	39,39,39	2.41	9 (23%)	48,58,58	1.68	12 (25%)
56	SF4	2d	501	35	0,12,12	-	-	-		
56	SF4	1d	501	35	0,12,12	-	-	-		
54	HGR	2A	3515	-	39,39,39	2.41	8 (20%)	48,58,58	1.74	11 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	HGR	1A	3749	-	-	6/20/79/79	0/4/4/4
56	SF4	2d	501	35	-	-	0/6/5/5
56	SF4	1d	501	35	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	HGR	2A	3515	-	-	7/20/79/79	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2A	3515	HGR	C12-C14	9.17	1.55	1.33
54	1A	3749	HGR	C12-C14	9.13	1.55	1.33
54	2A	3515	HGR	C5-C4	-5.57	1.39	1.49
54	1A	3749	HGR	C5-C4	-5.55	1.39	1.49
54	1A	3749	HGR	C5-C6	-5.40	1.39	1.50
54	2A	3515	HGR	C5-C6	-5.29	1.39	1.50
54	2A	3515	HGR	C3-C2	-4.77	1.39	1.48
54	1A	3749	HGR	C3-C2	-4.73	1.39	1.48
54	1A	3749	HGR	O4-C2	4.53	1.36	1.24
54	2A	3515	HGR	O4-C2	4.51	1.36	1.24
54	1A	3749	HGR	O8-C23	2.50	1.45	1.41
54	2A	3515	HGR	O8-C23	2.48	1.45	1.41
54	2A	3515	HGR	O9-C23	2.28	1.45	1.41
54	1A	3749	HGR	O9-C23	2.22	1.45	1.41
54	1A	3749	HGR	C1-C2	-2.10	1.39	1.44
54	2A	3515	HGR	C1-C2	-2.10	1.39	1.44
54	1A	3749	HGR	C1-C6	2.01	1.39	1.36

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	2A	3515	HGR	C10-C9-C8	-5.20	95.82	102.29
54	1A	3749	HGR	C4-C5-C6	4.26	121.43	112.35
54	2A	3515	HGR	C4-C5-C6	4.19	121.29	112.35
54	1A	3749	HGR	C10-C9-C8	-3.71	97.66	102.29
54	2A	3515	HGR	O1-C10-C9	-3.61	100.39	104.98
54	1A	3749	HGR	O8-C18-C22	-3.44	98.75	106.03
54	2A	3515	HGR	O8-C18-C22	-3.34	98.97	106.03
54	1A	3749	HGR	O9-C22-C18	-3.32	99.01	106.03
54	2A	3515	HGR	O9-C22-C18	-3.31	99.04	106.03
54	2A	3515	HGR	O4-C2-C3	-3.07	116.67	121.28
54	1A	3749	HGR	O4-C2-C3	-3.05	116.70	121.28
54	1A	3749	HGR	C12-C6-C1	-3.01	116.00	119.35
54	2A	3515	HGR	C12-C6-C1	-2.86	116.16	119.35
54	1A	3749	HGR	O1-C10-C9	-2.82	101.39	104.98
54	2A	3515	HGR	C23-O9-C22	-2.67	102.25	106.31
54	1A	3749	HGR	C23-O9-C22	-2.65	102.27	106.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	1A	3749	HGR	C4-C3-C2	-2.49	119.66	121.81
54	2A	3515	HGR	C1-C2-C3	2.31	120.41	116.06
54	1A	3749	HGR	C1-C2-C3	2.28	120.35	116.06
54	1A	3749	HGR	O3-C3-C2	2.27	116.63	112.51
54	2A	3515	HGR	C4-C3-C2	-2.21	119.91	121.81
54	1A	3749	HGR	C9-C8-C7	-2.15	99.15	101.69
54	2A	3515	HGR	O3-C3-C2	2.07	116.26	112.51

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	2A	3515	HGR	C14-C12-C6-C1
54	1A	3749	HGR	C12-C14-C15-O7
54	1A	3749	HGR	C12-C14-C15-N1
54	2A	3515	HGR	C12-C14-C15-O7
54	2A	3515	HGR	C12-C14-C15-N1
54	1A	3749	HGR	C2-C3-O3-C10
54	2A	3515	HGR	C2-C3-O3-C10
54	2A	3515	HGR	C16-C14-C15-N1
54	1A	3749	HGR	C16-C14-C15-O7
54	2A	3515	HGR	C16-C14-C15-O7
54	1A	3749	HGR	C16-C14-C15-N1
54	2A	3515	HGR	C19-C17-N1-C15
54	1A	3749	HGR	C19-C17-N1-C15

There are no ring outliers.

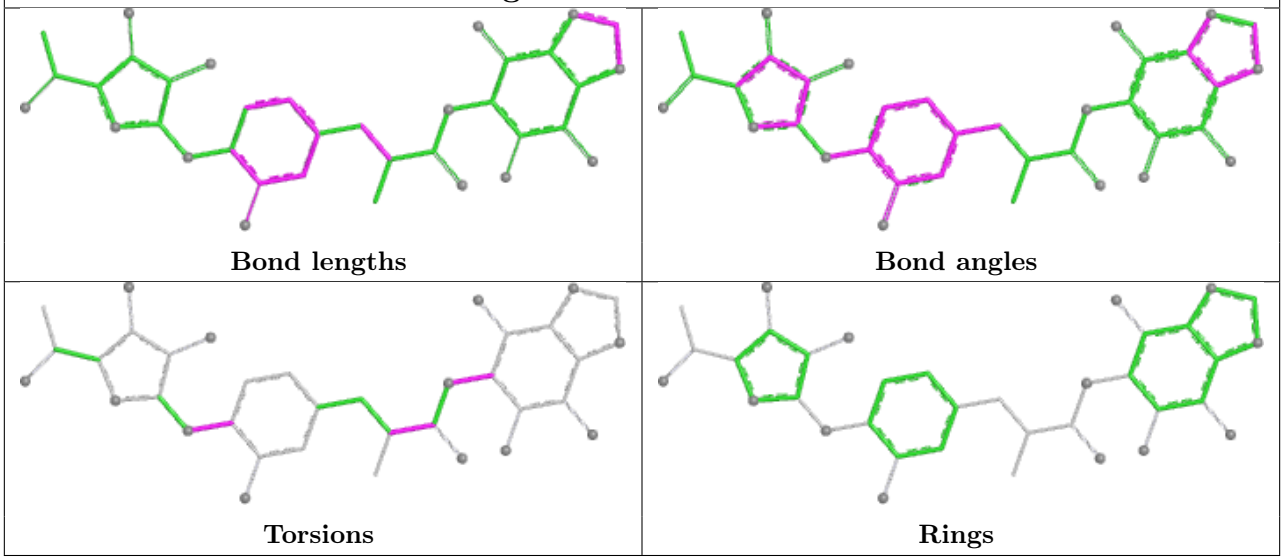
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	1A	3749	HGR	1	0
54	2A	3515	HGR	2	0

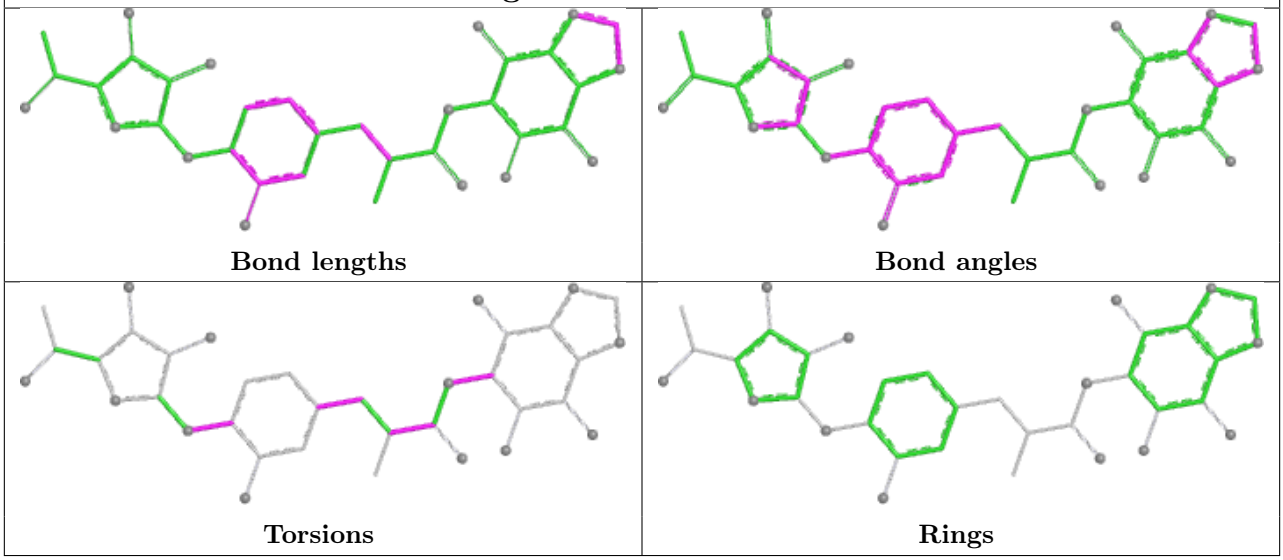
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 HGR 1A 3749



Ligand HGR 2A 3515



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	2861/2915 (98%)	1.19	361 (12%)	8	4	28, 61, 116, 129	0
1	2A	2856/2915 (97%)	0.76	254 (8%)	15	8	34, 66, 117, 137	0
2	1B	120/121 (99%)	1.11	15 (12%)	8	5	44, 84, 99, 108	0
2	2B	120/121 (99%)	1.20	15 (12%)	8	5	51, 90, 104, 111	0
3	1D	275/276 (99%)	1.64	73 (26%)	1	1	39, 63, 82, 98	0
3	2D	275/276 (99%)	1.29	55 (20%)	3	1	40, 66, 83, 99	0
4	1E	204/206 (99%)	1.52	57 (27%)	1	1	37, 64, 84, 99	0
4	2E	204/206 (99%)	0.93	22 (10%)	11	6	38, 68, 86, 102	0
5	1F	203/210 (96%)	1.38	39 (19%)	3	1	35, 71, 95, 116	0
5	2F	203/210 (96%)	1.18	27 (13%)	7	4	38, 75, 96, 118	0
6	1G	181/182 (99%)	1.94	68 (37%)	1	0	85, 105, 113, 120	0
6	2G	181/182 (99%)	2.51	110 (60%)	0	0	85, 107, 115, 123	0
7	1H	174/180 (96%)	2.12	89 (51%)	0	0	63, 84, 97, 104	0
7	2H	173/180 (96%)	1.53	46 (26%)	1	1	69, 89, 100, 106	0
8	1I	147/148 (99%)	1.61	41 (27%)	1	1	70, 97, 107, 111	0
8	2I	146/148 (98%)	1.37	34 (23%)	2	1	67, 98, 108, 111	0
9	1N	140/140 (100%)	1.03	18 (12%)	7	4	32, 49, 75, 93	0
9	2N	140/140 (100%)	1.61	39 (27%)	1	1	67, 86, 100, 108	0
10	1O	122/122 (100%)	0.95	15 (12%)	8	5	39, 61, 81, 88	0
10	2O	122/122 (100%)	1.41	23 (18%)	3	1	59, 80, 94, 101	0
11	1P	149/150 (99%)	1.52	31 (20%)	2	1	37, 75, 96, 103	0
11	2P	149/150 (99%)	1.42	34 (22%)	2	1	41, 79, 99, 107	0
12	1Q	141/141 (100%)	1.59	38 (26%)	1	1	45, 69, 85, 93	0
12	2Q	141/141 (100%)	1.27	25 (17%)	4	2	52, 75, 90, 95	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	1R	118/118 (100%)	0.97	12 (10%) 12 6	38, 55, 71, 89	0
13	2R	118/118 (100%)	0.73	9 (7%) 20 11	41, 59, 73, 91	0
14	1S	110/112 (98%)	1.89	36 (32%) 1 0	62, 83, 97, 99	0
14	2S	110/112 (98%)	1.72	41 (37%) 1 0	67, 87, 100, 103	0
15	1T	131/146 (89%)	1.51	34 (25%) 1 1	53, 74, 95, 104	0
15	2T	131/146 (89%)	1.16	22 (16%) 4 2	59, 77, 96, 106	0
16	1U	116/118 (98%)	1.54	31 (26%) 1 1	34, 58, 80, 86	0
16	2U	116/118 (98%)	1.11	13 (11%) 10 5	43, 63, 85, 90	0
17	1V	101/101 (100%)	1.63	27 (26%) 1 1	39, 68, 86, 99	0
17	2V	101/101 (100%)	1.50	25 (24%) 2 1	45, 74, 91, 102	0
18	1W	112/113 (99%)	1.21	19 (16%) 4 2	34, 48, 75, 102	0
18	2W	112/113 (99%)	0.68	4 (3%) 46 26	39, 52, 80, 102	0
19	1X	95/96 (98%)	1.30	16 (16%) 4 2	40, 61, 84, 98	0
19	2X	95/96 (98%)	1.00	8 (8%) 17 9	45, 65, 87, 98	0
20	1Y	107/110 (97%)	1.85	32 (29%) 1 1	55, 75, 93, 103	0
20	2Y	107/110 (97%)	1.60	30 (28%) 1 1	63, 79, 96, 106	0
21	1Z	203/206 (98%)	1.19	29 (14%) 6 3	46, 76, 99, 114	0
21	2Z	201/206 (97%)	1.71	73 (36%) 1 0	71, 100, 110, 118	0
22	10	77/85 (90%)	1.51	19 (24%) 2 1	51, 65, 84, 88	0
22	20	77/85 (90%)	1.58	22 (28%) 1 1	57, 70, 87, 90	0
23	11	97/98 (98%)	1.68	28 (28%) 1 1	42, 70, 92, 99	0
23	21	97/98 (98%)	1.50	26 (26%) 1 1	45, 72, 94, 101	0
24	12	70/72 (97%)	1.53	17 (24%) 2 1	51, 74, 89, 103	0
24	22	70/72 (97%)	1.23	12 (17%) 4 2	56, 78, 91, 100	0
25	13	59/60 (98%)	1.60	19 (32%) 1 0	45, 64, 90, 106	0
25	23	59/60 (98%)	1.22	7 (11%) 9 5	53, 70, 92, 105	0
26	14	69/71 (97%)	1.96	33 (47%) 0 0	103, 112, 118, 122	0
26	24	69/71 (97%)	2.36	39 (56%) 0 0	102, 113, 119, 122	0
27	15	59/60 (98%)	0.98	6 (10%) 12 6	33, 53, 75, 91	0
27	25	59/60 (98%)	0.96	4 (6%) 23 12	38, 57, 76, 91	0
28	16	53/54 (98%)	1.49	13 (24%) 2 1	57, 69, 85, 88	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
28	26	53/54 (98%)	1.04	5 (9%) 14 8	61, 73, 89, 90	0
29	17	48/49 (97%)	1.12	6 (12%) 8 5	35, 44, 81, 96	0
29	27	48/49 (97%)	1.00	10 (20%) 2 1	37, 47, 81, 98	0
30	18	64/65 (98%)	1.51	18 (28%) 1 1	48, 63, 76, 86	0
30	28	64/65 (98%)	1.30	15 (23%) 2 1	54, 67, 79, 88	0
31	19	37/37 (100%)	2.04	16 (43%) 0 0	57, 70, 86, 91	0
31	29	37/37 (100%)	1.72	10 (27%) 1 1	65, 77, 90, 94	0
32	1a	1488/1521 (97%)	1.86	506 (34%) 1 0	69, 105, 124, 132	0
32	2a	1492/1521 (98%)	1.72	462 (30%) 1 1	70, 105, 124, 132	0
33	1b	231/256 (90%)	1.92	93 (40%) 0 0	98, 108, 115, 117	0
33	2b	231/256 (90%)	1.80	82 (35%) 1 0	98, 109, 115, 119	0
34	1c	206/239 (86%)	2.69	130 (63%) 0 0	102, 112, 118, 122	0
34	2c	206/239 (86%)	2.61	128 (62%) 0 0	102, 112, 117, 122	0
35	1d	208/209 (99%)	2.17	92 (44%) 0 0	89, 102, 111, 119	0
35	2d	208/209 (99%)	2.03	81 (38%) 1 0	88, 101, 111, 119	0
36	1e	148/162 (91%)	1.92	57 (38%) 1 0	80, 100, 107, 113	0
36	2e	148/162 (91%)	2.05	57 (38%) 1 0	82, 101, 108, 114	0
37	1f	100/101 (99%)	1.73	35 (35%) 1 0	82, 97, 106, 111	0
37	2f	100/101 (99%)	1.42	23 (23%) 2 1	84, 98, 107, 110	0
38	1g	155/156 (99%)	2.67	100 (64%) 0 0	103, 112, 118, 120	0
38	2g	155/156 (99%)	2.51	91 (58%) 0 0	103, 113, 118, 121	0
39	1h	137/138 (99%)	1.43	32 (23%) 2 1	88, 101, 108, 114	0
39	2h	137/138 (99%)	1.46	31 (22%) 2 1	88, 101, 108, 115	0
40	1i	127/128 (99%)	2.79	81 (63%) 0 0	100, 114, 120, 121	0
40	2i	126/128 (98%)	3.64	107 (84%) 0 0	100, 114, 120, 124	0
41	1j	97/105 (92%)	3.24	81 (83%) 0 0	102, 113, 120, 122	0
41	2j	96/105 (91%)	3.28	81 (84%) 0 0	105, 114, 120, 121	0
42	1k	114/129 (88%)	1.31	26 (22%) 2 1	79, 100, 112, 120	0
42	2k	114/129 (88%)	1.80	36 (31%) 1 1	84, 101, 109, 112	0
43	1l	121/132 (91%)	1.69	36 (29%) 1 1	78, 94, 102, 113	0
43	2l	121/132 (91%)	1.78	39 (32%) 1 0	79, 93, 102, 106	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
44	1m	116/126 (92%)	2.96	80 (68%)	0	0	102, 114, 119, 121	0
44	2m	114/126 (90%)	2.63	71 (62%)	0	0	105, 113, 118, 121	0
45	1n	60/61 (98%)	3.89	53 (88%)	0	0	103, 113, 119, 120	0
45	2n	60/61 (98%)	3.38	51 (85%)	0	0	104, 113, 119, 122	0
46	1o	88/89 (98%)	1.56	24 (27%)	1	1	78, 96, 106, 111	0
46	2o	88/89 (98%)	1.38	17 (19%)	3	1	81, 98, 107, 111	0
47	1p	82/88 (93%)	2.64	53 (64%)	0	0	93, 102, 111, 113	0
47	2p	82/88 (93%)	2.15	42 (51%)	0	0	92, 100, 108, 114	0
48	1q	99/105 (94%)	2.13	46 (46%)	0	0	88, 100, 108, 110	0
48	2q	99/105 (94%)	1.90	39 (39%)	1	0	87, 99, 107, 110	0
49	1r	68/88 (77%)	1.59	19 (27%)	1	1	85, 98, 107, 115	0
49	2r	68/88 (77%)	1.61	18 (26%)	1	1	91, 101, 109, 118	0
50	1s	83/93 (89%)	2.92	61 (73%)	0	0	105, 114, 119, 126	0
50	2s	83/93 (89%)	3.09	65 (78%)	0	0	100, 114, 121, 124	0
51	1t	96/106 (90%)	2.04	41 (42%)	0	0	90, 102, 110, 114	0
51	2t	98/106 (92%)	1.50	23 (23%)	2	1	77, 94, 105, 109	0
52	1u	23/27 (85%)	4.37	21 (91%)	0	0	109, 113, 117, 119	0
52	2u	23/27 (85%)	4.12	21 (91%)	0	0	108, 113, 119, 119	0
All	All	20573/21242 (96%)	1.54	5547 (26%)	1	1	28, 87, 118, 137	0

All (5547) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1A	1091	G	19.5
1	1A	1093	G	18.4
1	1A	1087	G	17.5
1	1A	1072	C	17.0
1	1A	1089	G	15.5
32	1a	1349	A	14.6
1	1A	1092	C	13.8
1	1A	1090	U	13.7
35	2d	2	GLY	13.6
20	1Y	1	MET	13.0
34	2c	3	ASN	11.9
1	1A	1075	C	11.6
1	1A	1088	A	11.6

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Mol	Chain	Res	Type	RSRZ
1	1A	1071	G	11.5
1	1A	1081	U	11.3
32	1a	1286	A	10.9
1	1A	1080	C	10.5
52	2u	6	ARG	10.5
1	1A	1063	G	10.2
32	2a	1116	C	10.1
36	2e	20	GLN	10.0
35	2d	69	GLY	9.9
41	1j	53	PRO	9.6
35	1d	4	TYR	9.5
32	1a	1036	G	9.5
1	1A	1076	C	9.3
45	1n	2	ALA	9.3
47	1p	14	ASN	9.2
32	2a	1312	G	9.2
40	2i	105	ASP	9.2
1	1A	1082	U	9.1
44	1m	107	ALA	9.1
34	2c	160	ALA	8.9
32	1a	1350	A	8.9
36	2e	22	GLY	8.9
1	2A	2162	G	8.9
36	2e	21	ALA	8.9
21	2Z	192	ALA	8.8
42	2k	123	LYS	8.8
8	1I	117	GLU	8.8
32	1a	1353	G	8.8
45	1n	16	PHE	8.8
34	2c	4	LYS	8.7
35	1d	2	GLY	8.7
38	1g	42	ILE	8.7
32	1a	1352	C	8.7
1	1A	1074	G	8.7
1	1A	888	C	8.6
1	1A	2174	C	8.5
32	1a	1348	U	8.3
23	21	2	SER	8.3
1	1A	1079	C	8.2
41	2j	20	ALA	8.2
3	1D	276	LYS	8.2
32	1a	1137	C	8.2

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Mol	Chain	Res	Type	RSRZ
48	1q	7	THR	8.1
1	1A	1070	A	8.1
32	2a	1349	A	8.1
50	2s	8	GLY	8.0
32	2a	1348	U	8.0
40	2i	47	LEU	8.0
52	2u	5	ASP	7.9
36	2e	86	ALA	7.9
44	1m	102	ARG	7.8
45	1n	15	LYS	7.8
40	2i	102	LEU	7.8
1	1A	2173	A	7.8
1	1A	2166	G	7.7
6	1G	35	GLU	7.7
23	11	26	ARG	7.7
47	1p	11	SER	7.6
40	2i	81	ILE	7.6
32	2a	1373	G	7.6
1	1A	1094	U	7.5
1	1A	2116	G	7.5
1	1A	2168	G	7.5
32	1a	1138	G	7.5
50	2s	5	LEU	7.4
6	2G	73	ALA	7.4
1	2A	2174	C	7.4
44	1m	87	TYR	7.4
5	2F	44	ARG	7.4
1	1A	2113	U	7.4
14	1S	13	ARG	7.4
26	24	63	TYR	7.3
7	1H	2	SER	7.3
1	1A	1073	A	7.3
40	2i	74	ILE	7.3
42	2k	117	ASN	7.3
1	2A	2127	G	7.3
1	1A	2320	A	7.2
32	2a	1353	G	7.2
1	1A	2167	U	7.2
1	1A	1097	U	7.2
3	2D	50	THR	7.2
32	1a	1092	A	7.2
44	2m	100	GLY	7.2

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Mol	Chain	Res	Type	RSRZ
20	1Y	2	ARG	7.1
45	1n	23	ARG	7.1
1	1A	2165	G	7.1
1	1A	1064	C	7.1
3	1D	36	PRO	7.1
34	1c	52	LEU	7.1
45	1n	30	ALA	7.1
1	1A	1083	U	7.1
32	1a	1308	U	7.1
32	2a	1287	A	7.1
32	2a	1372	U	7.0
1	1A	1057	A	7.0
38	1g	117	ALA	7.0
44	1m	90	LEU	7.0
1	1A	1068	G	7.0
52	1u	4	GLY	7.0
41	2j	62	HIS	7.0
1	1A	2296	U	7.0
1	1A	887	A	7.0
45	2n	2	ALA	6.9
1	1A	1102	C	6.9
40	2i	13	ALA	6.9
1	1A	2160	G	6.9
1	2A	2118	U	6.9
32	2a	1149	C	6.9
1	2A	2119	A	6.9
35	1d	5	ILE	6.9
1	1A	2161	C	6.8
1	1A	2164	C	6.8
52	1u	6	ARG	6.8
1	1A	2319	G	6.8
1	1A	1077	A	6.8
1	1A	2139	C	6.8
38	2g	25	ALA	6.8
20	2Y	1	MET	6.8
1	1A	2171	A	6.8
51	2t	6	PRO	6.8
52	2u	14	TRP	6.8
35	2d	4	TYR	6.8
1	1A	2117	A	6.7
34	1c	160	ALA	6.7
45	2n	15	LYS	6.7

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Mol	Chain	Res	Type	RSRZ
47	1p	12	LYS	6.7
40	1i	121	ARG	6.7
34	2c	33	LEU	6.7
1	1A	2172	U	6.7
32	1a	974	A	6.7
21	2Z	193	GLU	6.7
32	2a	1286	A	6.7
36	2e	85	GLY	6.7
6	2G	72	ARG	6.7
1	1A	2141	G	6.6
37	1f	94	GLN	6.6
33	2b	101	MET	6.6
1	1A	2108	C	6.6
32	1a	1287	A	6.6
1	1A	2163	C	6.6
32	1a	1288	A	6.6
32	2a	1248	A	6.6
1	2A	2125	G	6.6
6	2G	41	GLN	6.6
10	1O	5	GLN	6.6
35	2d	122	ARG	6.6
34	1c	39	ILE	6.5
40	2i	66	ARG	6.5
1	2A	2168	G	6.5
3	1D	227	ASN	6.5
42	2k	126	ARG	6.5
32	2a	1092	A	6.5
34	1c	192	THR	6.5
52	1u	3	LYS	6.5
6	2G	3	LEU	6.5
32	2a	1150	U	6.5
40	2i	42	ARG	6.5
14	2S	5	THR	6.5
34	1c	50	ALA	6.5
21	1Z	197	ILE	6.5
44	2m	6	GLY	6.5
1	2A	1076	C	6.5
1	2A	2170	A	6.5
34	1c	55	VAL	6.5
8	1I	118	LYS	6.5
1	1A	1104	C	6.4
32	2a	1249	C	6.4

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Mol	Chain	Res	Type	RSRZ
40	1i	46	ALA	6.4
40	2i	14	VAL	6.4
1	1A	1062	G	6.4
1	1A	1176	G	6.4
1	1A	2142	C	6.4
40	2i	10	ARG	6.4
1	1A	226	G	6.4
3	2D	38	LYS	6.4
45	2n	16	PHE	6.4
45	1n	14	PRO	6.4
40	2i	106	ALA	6.3
32	1a	1317	C	6.3
1	1A	2147	G	6.3
32	1a	1111	A	6.3
32	1a	1248	A	6.3
40	2i	108	VAL	6.3
6	1G	82	LEU	6.3
48	1q	26	GLN	6.3
6	2G	2	PRO	6.3
33	1b	196	LEU	6.3
34	2c	154	SER	6.3
34	1c	47	LEU	6.3
46	1o	65	ARG	6.3
52	1u	23	PRO	6.2
34	1c	68	VAL	6.2
50	1s	71	LEU	6.2
34	1c	71	ALA	6.2
36	2e	25	ARG	6.2
1	1A	2151	G	6.2
32	1a	1139	G	6.2
32	2a	1193	G	6.2
34	1c	70	VAL	6.2
1	1A	1086	A	6.2
36	1e	21	ALA	6.2
9	2N	84	LYS	6.2
44	1m	27	LYS	6.2
32	1a	1247	U	6.2
41	2j	34	VAL	6.2
1	1A	2114	A	6.1
32	2a	1374	A	6.1
6	1G	80	PHE	6.1
11	1P	71	VAL	6.1

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Mol	Chain	Res	Type	RSRZ
1	2A	2147	G	6.1
41	2j	50	ILE	6.1
35	1d	6	GLY	6.1
11	2P	68	GLN	6.1
40	1i	122	ALA	6.1
41	1j	55	LYS	6.1
26	24	35	VAL	6.1
38	1g	31	MET	6.1
41	2j	23	ILE	6.1
37	1f	98	LEU	6.1
50	2s	9	VAL	6.1
1	1A	2132	U	6.1
1	1A	2338	G	6.1
40	2i	89	ASN	6.1
40	2i	109	VAL	6.0
34	1c	159	GLY	6.0
5	2F	41	LEU	6.0
35	2d	11	LEU	6.0
14	1S	93	LYS	6.0
32	2a	1066	C	6.0
38	1g	116	ALA	6.0
44	2m	19	LEU	6.0
34	2c	158	GLY	6.0
34	1c	53	ALA	6.0
40	2i	46	ALA	6.0
32	1a	1037	C	6.0
22	10	74	ARG	6.0
24	12	69	ARG	6.0
41	1j	48	THR	6.0
1	1A	1101	U	6.0
32	1a	570	G	6.0
17	2V	81	TYR	6.0
34	2c	53	ALA	6.0
38	2g	33	ASP	5.9
32	1a	1183	A	5.9
23	11	2	SER	5.9
43	1l	94	PRO	5.9
34	2c	151	VAL	5.9
36	1e	25	ARG	5.9
32	1a	1307	U	5.9
51	2t	10	LEU	5.9
38	1g	25	ALA	5.9

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Mol	Chain	Res	Type	RSRZ
35	1d	3	ARG	5.9
32	1a	1327	C	5.9
14	1S	4	LEU	5.9
32	1a	1188	A	5.9
32	2a	1288	A	5.9
32	2a	1319	A	5.9
40	1i	106	ALA	5.9
1	1A	2149	G	5.9
32	1a	1343	G	5.9
50	1s	9	VAL	5.9
9	1N	115	ARG	5.9
1	1A	1078	U	5.8
6	2G	90	LEU	5.8
38	1g	120	ILE	5.8
40	1i	40	LEU	5.8
34	1c	130	VAL	5.8
40	1i	108	VAL	5.8
1	2A	614(B)	G	5.8
32	2a	1064	G	5.8
52	1u	21	TYR	5.8
40	2i	7	THR	5.8
52	1u	14	TRP	5.8
1	2A	2173	A	5.8
32	1a	1136	U	5.8
40	1i	107	ARG	5.8
10	2O	34	THR	5.8
1	2A	2148	G	5.8
35	1d	148	VAL	5.8
1	1A	2129	C	5.8
32	1a	1354	C	5.8
32	1a	1289	A	5.8
32	2a	1191	A	5.8
9	2N	44	PRO	5.8
32	2a	1017	G	5.7
39	2h	2	LEU	5.7
50	1s	16	LEU	5.7
7	1H	161	GLY	5.7
1	2A	2153	G	5.7
41	2j	55	LYS	5.7
1	2A	2136	C	5.7
32	1a	1235	U	5.7
50	2s	15	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
35	2d	5	ILE	5.7
40	2i	71	SER	5.7
3	2D	35	LYS	5.7
35	1d	157	LEU	5.7
40	1i	105	ASP	5.7
1	2A	2165	G	5.7
32	1a	1371	G	5.7
32	1a	1342	C	5.7
52	2u	9	ARG	5.7
16	1U	89	GLU	5.7
32	2a	1354	C	5.6
44	2m	4	ILE	5.6
8	1I	119	PRO	5.6
44	1m	45	VAL	5.6
44	1m	103	THR	5.6
47	2p	69	THR	5.6
32	2a	1148	U	5.6
38	1g	124	LEU	5.6
44	2m	102	ARG	5.6
32	1a	1344	C	5.6
1	1A	1067	A	5.6
1	1A	1103	A	5.6
1	1A	2162	G	5.6
1	1A	2337	G	5.6
1	2A	2166	G	5.6
29	27	48	LYS	5.6
32	2a	1202	G	5.6
45	1n	17	LYS	5.6
44	1m	100	GLY	5.6
34	2c	68	VAL	5.6
34	2c	76	VAL	5.6
1	2A	2171	A	5.6
32	1a	1318	A	5.6
45	2n	25	VAL	5.6
1	1A	2153	G	5.6
32	2a	1094	G	5.6
32	2a	1371	G	5.6
34	2c	52	LEU	5.6
36	1e	18	ARG	5.6
10	2O	31	LYS	5.6
20	2Y	4	LYS	5.6
8	1I	41	GLU	5.6

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Mol	Chain	Res	Type	RSRZ
42	1k	60	ALA	5.6
34	1c	193	TYR	5.6
1	1A	2136	C	5.6
1	1A	2137	C	5.6
34	1c	124	ILE	5.6
1	1A	1058	G	5.5
32	2a	1036	G	5.5
34	1c	206	GLU	5.5
40	2i	104	ARG	5.5
45	1n	3	ARG	5.5
50	1s	4	SER	5.5
1	1A	2107	C	5.5
1	1A	2125	G	5.5
38	1g	26	PHE	5.5
1	2A	2167	U	5.5
48	1q	78	GLU	5.5
40	2i	63	ILE	5.5
50	2s	31	ILE	5.5
38	1g	118	VAL	5.5
40	1i	119	ALA	5.5
43	2l	13	LYS	5.5
6	1G	88	ILE	5.5
32	2a	824	C	5.5
6	2G	137	GLU	5.5
1	1A	2130	U	5.5
32	1a	1148	U	5.5
32	1a	1364	U	5.5
32	1a	933	G	5.5
32	1a	1202	G	5.5
17	1V	49	THR	5.4
33	1b	101	MET	5.4
45	2n	30	ALA	5.4
26	24	64	GLY	5.4
43	2l	32	PHE	5.4
51	1t	11	SER	5.4
45	2n	34	TYR	5.4
24	22	52	ASP	5.4
1	2A	1536	C	5.4
41	2j	19	SER	5.4
1	2A	2126	A	5.4
32	1a	782	A	5.4
38	2g	124	LEU	5.4

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Mol	Chain	Res	Type	RSRZ
41	2j	64	GLU	5.4
32	1a	1174	G	5.4
32	2a	1310	G	5.4
38	2g	82	GLY	5.4
40	1i	30	GLY	5.4
39	2h	4	ASP	5.4
3	1D	59	LYS	5.4
38	1g	101	LEU	5.4
40	2i	44	VAL	5.4
1	2A	2116	G	5.4
1	2A	2160	G	5.4
7	1H	156	ALA	5.4
32	1a	1046	A	5.4
38	1g	35	LYS	5.4
34	2c	169	ALA	5.3
40	1i	128	ARG	5.3
45	1n	26	ARG	5.3
33	2b	99	GLY	5.3
40	2i	11	LYS	5.3
41	1j	47	PHE	5.3
41	1j	54	PHE	5.3
41	1j	93	GLY	5.3
44	2m	9	ILE	5.3
1	1A	2115	G	5.3
1	1A	2152	G	5.3
32	1a	1186	G	5.3
1	1A	2143	C	5.3
6	2G	116	ASP	5.3
12	1Q	28	ALA	5.3
3	1D	234	GLY	5.3
52	2u	23	PRO	5.3
38	2g	32	ARG	5.3
44	1m	86	CYS	5.3
32	2a	1224	G	5.3
43	1l	124	LYS	5.3
50	2s	35	SER	5.3
23	21	36	GLY	5.3
40	2i	75	ASP	5.3
44	2m	87	TYR	5.3
38	2g	2	ALA	5.3
1	1A	2119	A	5.3
32	1a	1290	G	5.3

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Mol	Chain	Res	Type	RSRZ
32	1a	1351	U	5.3
32	1a	1373	G	5.3
6	1G	73	ALA	5.3
41	1j	58	ASP	5.3
44	1m	2	ALA	5.3
34	1c	2	GLY	5.2
43	2l	16	GLU	5.2
38	1g	36	LYS	5.2
1	1A	529	A	5.2
1	1A	1066	U	5.2
1	1A	1762	A	5.2
1	2A	229	A	5.2
3	1D	37	LEU	5.2
44	1m	85	GLY	5.2
40	2i	49	PRO	5.2
44	2m	60	VAL	5.2
44	1m	56	LEU	5.2
32	1a	1363	C	5.2
42	2k	118	GLY	5.2
47	2p	29	ASP	5.2
50	1s	13	ASP	5.2
19	2X	33	LYS	5.2
34	1c	153	VAL	5.2
33	1b	29	ALA	5.2
40	2i	40	LEU	5.2
1	2A	2169	A	5.2
48	1q	24	GLU	5.2
45	1n	39	LEU	5.2
41	1j	49	VAL	5.2
26	24	66	SER	5.2
41	1j	35	SER	5.2
45	1n	52	GLN	5.2
1	1A	2135	A	5.1
32	1a	1157	A	5.1
15	1T	37	GLY	5.1
34	2c	155	GLY	5.1
1	2A	2154	G	5.1
38	2g	27	ILE	5.1
12	1Q	5	ARG	5.1
45	1n	31	ARG	5.1
34	2c	167	TRP	5.1
38	1g	59	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
44	1m	33	ALA	5.1
35	2d	137	SER	5.1
40	2i	37	PHE	5.1
32	2a	1205	U	5.1
32	2a	1235	U	5.1
50	1s	51	VAL	5.1
51	1t	9	ASN	5.1
41	2j	53	PRO	5.1
32	2a	1326	C	5.1
41	1j	40	LEU	5.1
35	2d	23	GLY	5.1
4	1E	155	LYS	5.1
41	2j	40	LEU	5.1
34	1c	186	PHE	5.1
47	2p	82	GLN	5.1
3	1D	228	PRO	5.1
38	1g	7	ALA	5.0
38	2g	34	GLY	5.0
41	2j	49	VAL	5.0
34	1c	144	SER	5.0
40	2i	107	ARG	5.0
38	2g	38	LEU	5.0
48	2q	24	GLU	5.0
41	1j	72	VAL	5.0
1	2A	2172	U	5.0
2	2B	1	U	5.0
32	1a	1240	U	5.0
6	1G	75	LYS	5.0
1	1A	1099	G	5.0
32	1a	1271	G	5.0
6	2G	88	ILE	5.0
40	2i	77	ILE	5.0
4	1E	163	GLU	5.0
45	1n	50	LYS	5.0
38	2g	59	LEU	5.0
50	2s	71	LEU	5.0
1	2A	171	G	5.0
9	2N	74	ARG	5.0
29	17	47	ARG	5.0
7	1H	88	LEU	5.0
44	1m	34	LEU	5.0
45	1n	6	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
40	2i	78	LYS	5.0
41	2j	24	VAL	5.0
41	2j	69	ASN	5.0
24	22	1	MET	5.0
40	2i	12	GLU	5.0
51	1t	18	GLN	5.0
31	19	37	GLY	5.0
36	1e	23	GLY	5.0
38	1g	22	LEU	5.0
1	2A	2124	G	4.9
1	1A	1095	A	4.9
14	2S	92	TYR	4.9
32	1a	1149	C	4.9
38	1g	134	ALA	4.9
23	21	26	ARG	4.9
52	1u	15	ARG	4.9
1	1A	2109	U	4.9
34	2c	116	VAL	4.9
1	1A	548	A	4.9
1	1A	2138	C	4.9
32	1a	1260	C	4.9
32	2a	1192	C	4.9
41	2j	65	LEU	4.9
44	1m	101	GLN	4.9
45	1n	61	TRP	4.9
32	2a	1194	U	4.9
32	2a	1313	U	4.9
40	1i	109	VAL	4.9
32	2a	1118	C	4.9
33	1b	175	ARG	4.9
34	1c	176	HIS	4.9
36	1e	82	VAL	4.9
38	2g	9	VAL	4.9
44	1m	98	VAL	4.9
7	1H	105	LEU	4.9
34	2c	43	LEU	4.9
33	1b	133	LYS	4.9
52	1u	17	THR	4.9
38	2g	28	ASN	4.9
45	2n	19	ARG	4.9
32	1a	500	G	4.9
32	1a	1361	G	4.9

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Mol	Chain	Res	Type	RSRZ
52	1u	5	ASP	4.9
47	1p	10	GLY	4.8
38	2g	36	LYS	4.8
40	1i	118	LYS	4.8
38	2g	5	ARG	4.8
15	1T	104	ASN	4.8
50	1s	2	PRO	4.8
6	2G	62	LEU	4.8
6	1G	84	LYS	4.8
7	2H	120	GLY	4.8
32	2a	60	A	4.8
44	1m	65	LYS	4.8
20	2Y	2	ARG	4.8
36	1e	118	ILE	4.8
50	2s	3	ARG	4.8
34	2c	37	GLN	4.8
33	2b	190	THR	4.8
1	1A	2127	G	4.8
32	2a	933	G	4.8
50	1s	57	HIS	4.8
8	2I	25	TYR	4.8
9	1N	118	LYS	4.8
24	12	15	LYS	4.8
40	2i	120	ARG	4.8
1	2A	2111	C	4.8
32	1a	623	C	4.8
32	1a	949	A	4.8
45	1n	22	THR	4.8
45	1n	48	ALA	4.8
32	1a	1115	C	4.8
40	2i	21	PRO	4.8
1	1A	1065	U	4.8
6	1G	74	LYS	4.8
47	1p	42	ARG	4.8
1	1A	2124	G	4.8
32	1a	1182	G	4.8
35	1d	93	PHE	4.8
6	2G	142	PRO	4.8
27	25	10	LYS	4.8
45	2n	50	LYS	4.8
32	1a	935	A	4.8
32	1a	1360	A	4.8

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Mol	Chain	Res	Type	RSRZ
34	1c	10	PHE	4.8
31	19	12	ASP	4.8
34	2c	47	LEU	4.8
40	1i	102	LEU	4.8
41	2j	59	SER	4.8
10	1O	29	ASN	4.7
28	26	54	ILE	4.7
1	1A	2126	A	4.7
32	2a	1352	C	4.7
27	15	59	GLU	4.7
38	2g	42	ILE	4.7
44	2m	106	ASN	4.7
1	2A	2319	G	4.7
32	2a	1523	G	4.7
11	2P	66	GLY	4.7
34	2c	2	GLY	4.7
35	1d	69	GLY	4.7
51	1t	103	GLY	4.7
1	1A	1026	U	4.7
32	2a	1522	U	4.7
34	1c	66	VAL	4.7
34	1c	179	ARG	4.7
36	1e	24	ARG	4.7
43	1l	89	ARG	4.7
50	1s	11	VAL	4.7
32	2a	1317	C	4.7
50	2s	4	SER	4.7
34	2c	159	GLY	4.7
44	1m	99	ARG	4.7
52	1u	9	ARG	4.7
41	1j	61	GLU	4.7
32	2a	1347	G	4.7
6	2G	140	ILE	4.7
32	2a	325	A	4.7
33	2b	72	GLY	4.7
42	2k	71	LYS	4.7
38	2g	16	LEU	4.7
33	2b	96	ARG	4.7
44	2m	7	VAL	4.7
40	2i	2	GLU	4.7
41	2j	67	THR	4.7
26	14	65	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
32	1a	1341	U	4.7
18	1W	11	ARG	4.7
35	1d	14	ARG	4.7
50	1s	15	LEU	4.7
41	2j	47	PHE	4.7
32	1a	218	C	4.7
3	1D	253	GLN	4.6
10	2O	5	GLN	4.6
38	2g	103	TRP	4.6
14	2S	33	LYS	4.6
33	2b	40	HIS	4.6
6	2G	139	LEU	4.6
26	24	9	LEU	4.6
36	1e	85	GLY	4.6
40	1i	47	LEU	4.6
14	1S	12	PHE	4.6
1	2A	1087	G	4.6
32	2a	1068	G	4.6
50	2s	2	PRO	4.6
1	1A	1069	A	4.6
1	1A	1096	A	4.6
1	1A	2602	A	4.6
32	1a	1306	A	4.6
34	2c	152	ILE	4.6
1	1A	2140	C	4.6
1	2A	1075	C	4.6
41	1j	57	LYS	4.6
45	1n	9	LYS	4.6
13	1R	68	ARG	4.6
33	1b	98	LEU	4.6
44	2m	68	GLY	4.6
38	2g	112	PRO	4.6
32	2a	1065	U	4.6
41	2j	38	ILE	4.6
6	1G	72	ARG	4.6
7	1H	6	ARG	4.6
34	1c	33	LEU	4.6
38	1g	38	LEU	4.6
32	1a	1385	G	4.6
32	2a	1117	G	4.6
32	2a	1190	G	4.6
34	1c	158	GLY	4.6

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Mol	Chain	Res	Type	RSRZ
44	2m	24	GLY	4.6
32	1a	1246	C	4.6
41	1j	63	PHE	4.6
47	2p	1	MET	4.6
38	1g	109	ASN	4.6
40	2i	110	GLU	4.6
50	2s	53	ASN	4.6
34	1c	156	ARG	4.6
33	1b	67	THR	4.6
26	14	64	GLY	4.6
50	1s	18	LYS	4.6
1	1A	2295	C	4.6
32	1a	1187	G	4.6
32	1a	1367	C	4.6
32	2a	1370	G	4.6
36	2e	130	ASN	4.6
48	2q	98	LEU	4.6
40	2i	103	THR	4.6
27	15	60	VAL	4.6
44	2m	98	VAL	4.6
14	1S	3	ARG	4.5
14	1S	9	ARG	4.5
34	1c	157	ILE	4.5
38	1g	32	ARG	4.5
42	2k	120	ARG	4.5
38	2g	74	GLU	4.5
11	1P	70	GLN	4.5
40	2i	41	VAL	4.5
41	1j	38	ILE	4.5
7	1H	166	GLY	4.5
7	1H	153	LYS	4.5
20	1Y	16	ALA	4.5
47	1p	69	THR	4.5
32	2a	1324	A	4.5
38	1g	27	ILE	4.5
45	1n	34	TYR	4.5
32	2a	378	G	4.5
34	1c	43	LEU	4.5
51	1t	62	LEU	4.5
36	1e	81	GLU	4.5
3	1D	230	ASP	4.5
9	2N	104	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
48	2q	37	LYS	4.5
38	1g	115	ARG	4.5
33	1b	118	LEU	4.5
39	1h	2	LEU	4.5
1	2A	2117	A	4.5
32	2a	1318	A	4.5
33	1b	131	PRO	4.5
43	1l	18	VAL	4.5
26	14	66	SER	4.5
32	2a	755	G	4.5
34	2c	185	GLY	4.5
40	2i	33	PHE	4.5
32	1a	220	G	4.5
32	1a	1020	U	4.5
52	1u	8	THR	4.5
21	2Z	169	GLU	4.5
34	1c	44	GLU	4.5
35	1d	24	GLU	4.5
41	1j	25	GLU	4.5
32	1a	1332	A	4.5
32	2a	1236	A	4.5
44	2m	101	GLN	4.5
45	1n	41	ARG	4.5
46	1o	62	GLN	4.5
32	2a	879	C	4.4
32	2a	1119	C	4.4
8	1I	91	SER	4.4
44	1m	22	ILE	4.4
1	1A	2154	G	4.4
32	1a	1034	G	4.4
51	1t	68	LYS	4.4
33	1b	7	VAL	4.4
41	1j	44	VAL	4.4
41	2j	44	VAL	4.4
45	1n	33	VAL	4.4
21	1Z	118	GLN	4.4
40	2i	45	ALA	4.4
18	1W	13	SER	4.4
34	2c	134	ILE	4.4
44	1m	4	ILE	4.4
32	2a	1067	A	4.4
52	2u	8	THR	4.4

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Mol	Chain	Res	Type	RSRZ
40	2i	62	TYR	4.4
29	17	41	ARG	4.4
38	2g	79	ARG	4.4
45	2n	41	ARG	4.4
45	2n	36	PHE	4.4
3	1D	243	GLY	4.4
34	2c	24	ALA	4.4
40	2i	68	GLY	4.4
45	2n	52	GLN	4.4
52	2u	16	GLY	4.4
32	1a	1224	G	4.4
33	2b	44	LEU	4.4
45	2n	32	SER	4.4
9	2N	73	THR	4.4
44	1m	109	THR	4.4
14	1S	17	ARG	4.4
34	2c	172	ARG	4.4
44	2m	99	ARG	4.4
32	2a	978	A	4.4
34	2c	64	VAL	4.4
1	1A	886	C	4.4
1	2A	2137	C	4.4
32	2a	1195	C	4.4
47	1p	1	MET	4.4
36	1e	86	ALA	4.4
33	2b	110	GLN	4.4
47	1p	82	GLN	4.4
42	1k	123	LYS	4.4
41	2j	48	THR	4.4
34	2c	55	VAL	4.4
44	1m	53	VAL	4.4
14	1S	6	ALA	4.4
40	2i	82	ALA	4.4
40	1i	39	GLY	4.4
52	1u	16	GLY	4.4
52	2u	2	GLY	4.4
19	1X	95	LEU	4.4
32	1a	1333	A	4.4
41	1j	65	LEU	4.4
45	1n	47	LEU	4.4
50	1s	5	LEU	4.4
1	1A	2477	C	4.4

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Mol	Chain	Res	Type	RSRZ
8	2I	22	LYS	4.4
32	1a	1366	C	4.4
32	2a	1314	C	4.4
20	2Y	5	MET	4.3
1	2A	2152	G	4.3
33	2b	172	ILE	4.3
45	1n	7	ILE	4.3
41	2j	70	ARG	4.3
48	2q	70	ARG	4.3
1	1A	2169	A	4.3
32	1a	975	A	4.3
40	1i	86	VAL	4.3
45	1n	56	VAL	4.3
1	1A	271(Y)	U	4.3
40	2i	90	PRO	4.3
3	2D	37	LEU	4.3
3	2D	59	LYS	4.3
5	1F	27	GLU	4.3
6	1G	89	GLY	4.3
35	2d	66	ARG	4.3
52	2u	10	ARG	4.3
50	1s	14	HIS	4.3
32	2a	1155	G	4.3
50	2s	33	THR	4.3
44	1m	97	PRO	4.3
22	20	78	TYR	4.3
34	1c	48	TYR	4.3
40	2i	97	LYS	4.3
50	2s	6	LYS	4.3
44	2m	56	LEU	4.3
1	1A	231	C	4.3
32	1a	1112	C	4.3
52	1u	13	ILE	4.3
35	1d	66	ARG	4.3
44	1m	110	ARG	4.3
42	2k	42	TRP	4.3
40	1i	117	HIS	4.3
34	1c	73	PRO	4.3
36	2e	26	PHE	4.3
43	1l	32	PHE	4.3
22	20	84	LEU	4.3
28	16	10	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
35	2d	54	TYR	4.3
38	1g	12	LEU	4.3
7	1H	57	ASP	4.3
38	2g	40	ALA	4.3
40	2i	43	ALA	4.3
34	2c	39	ILE	4.3
41	1j	52	GLY	4.3
51	2t	25	ARG	4.3
32	2a	823	G	4.3
32	2a	782	A	4.3
41	1j	33	GLN	4.3
20	2Y	94	LYS	4.3
6	1G	87	PRO	4.3
40	2i	50	LEU	4.3
4	2E	204	ALA	4.3
40	1i	42	ARG	4.3
40	1i	120	ARG	4.3
51	2t	15	ARG	4.3
43	2l	118	SER	4.3
50	1s	56	GLN	4.3
1	1A	2123	G	4.2
1	2A	2141	G	4.2
1	2A	2190	G	4.2
26	24	40	HIS	4.2
32	1a	1312	G	4.2
32	1a	219	C	4.2
41	2j	8	LEU	4.2
40	2i	121	ARG	4.2
45	1n	29	ARG	4.2
6	2G	134	GLY	4.2
31	29	37	GLY	4.2
34	1c	155	GLY	4.2
45	2n	38	GLY	4.2
48	2q	33	GLY	4.2
52	1u	11	GLY	4.2
36	1e	88	LYS	4.2
50	2s	51	VAL	4.2
6	2G	34	LEU	4.2
6	2G	111	LEU	4.2
14	1S	20	ARG	4.2
14	2S	4	LEU	4.2
47	1p	44	THR	4.2

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Mol	Chain	Res	Type	RSRZ
1	2A	2320	A	4.2
32	1a	977	A	4.2
32	1a	1285	A	4.2
1	2A	2112	G	4.2
1	2A	2161	C	4.2
1	2A	2163	C	4.2
32	1a	630	G	4.2
32	1a	1234	C	4.2
32	1a	1347	G	4.2
34	2c	206	GLU	4.2
45	2n	46	GLU	4.2
40	1i	127	LYS	4.2
8	2I	3	VAL	4.2
34	2c	153	VAL	4.2
40	1i	17	VAL	4.2
41	2j	46	ARG	4.2
46	1o	63	ARG	4.2
40	2i	101	PHE	4.2
15	1T	131	ALA	4.2
41	1j	68	HIS	4.2
28	16	54	ILE	4.2
45	1n	10	ALA	4.2
36	1e	22	GLY	4.2
40	1i	125	TYR	4.2
3	1D	275	LYS	4.2
49	2r	68	LYS	4.2
7	1H	58	GLU	4.2
36	2e	81	GLU	4.2
1	1A	227	A	4.2
8	2I	20	ASP	4.2
41	2j	43	ARG	4.2
32	1a	63	C	4.2
35	1d	155	LEU	4.2
45	2n	53	LEU	4.2
1	1A	1059	G	4.2
32	1a	1048	G	4.2
32	2a	1311	G	4.2
32	2a	1323	G	4.2
38	2g	83	ALA	4.2
34	1c	51	GLY	4.2
52	2u	4	GLY	4.2
43	2l	101	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
45	2n	35	ARG	4.2
50	2s	30	LEU	4.2
6	2G	76	SER	4.2
48	1q	13	ASP	4.2
32	2a	1269	A	4.2
11	2P	36	LYS	4.2
40	1i	11	LYS	4.2
41	2j	22	LYS	4.2
44	1m	43	THR	4.2
50	2s	41	VAL	4.1
40	2i	96	LEU	4.1
45	2n	39	LEU	4.1
51	1t	10	LEU	4.1
40	1i	15	ALA	4.1
11	1P	54	GLY	4.1
52	2u	11	GLY	4.1
1	1A	1847	A	4.1
1	2A	1046	A	4.1
8	1I	40	THR	4.1
15	2T	112	ARG	4.1
32	1a	1035	A	4.1
35	2d	3	ARG	4.1
21	2Z	191	VAL	4.1
45	2n	18	VAL	4.1
32	1a	979	C	4.1
32	1a	1060	C	4.1
50	2s	74	PHE	4.1
1	1A	2318	G	4.1
9	2N	8	GLN	4.1
24	12	70	GLN	4.1
3	1D	38	LYS	4.1
28	26	20	ASN	4.1
8	1I	80	PRO	4.1
48	2q	99	SER	4.1
12	1Q	59	ARG	4.1
14	2S	3	ARG	4.1
8	2I	145	VAL	4.1
17	2V	72	VAL	4.1
38	2g	80	VAL	4.1
40	2i	88	TYR	4.1
35	1d	192	GLU	4.1
50	2s	44	MET	4.1

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Mol	Chain	Res	Type	RSRZ
1	2A	1072	C	4.1
38	2g	106	GLN	4.1
21	2Z	68	PRO	4.1
30	28	19	SER	4.1
43	1l	113	ARG	4.1
43	2l	33	ARG	4.1
1	1A	2110	G	4.1
32	2a	108	G	4.1
40	1i	41	VAL	4.1
33	1b	148	TYR	4.1
32	2a	1240	U	4.1
45	1n	4	LYS	4.1
52	2u	12	LYS	4.1
7	2H	136	ILE	4.1
38	1g	30	ILE	4.1
34	2c	71	ALA	4.1
14	1S	30	ARG	4.1
44	2m	10	PRO	4.1
1	1A	477	A	4.1
5	2F	169	ASN	4.1
32	1a	1110	A	4.1
12	2Q	33	GLY	4.1
14	1S	22	GLY	4.1
41	2j	68	HIS	4.1
44	1m	106	ASN	4.1
32	1a	1141	C	4.1
40	1i	126	SER	4.1
6	2G	106	LEU	4.1
34	2c	106	VAL	4.1
14	2S	93	LYS	4.1
26	24	67	TYR	4.1
50	2s	63	THR	4.1
41	1j	64	GLU	4.1
50	2s	10	PHE	4.1
1	1A	2133	G	4.1
1	1A	2156	G	4.1
32	2a	800	G	4.1
47	2p	7	ALA	4.1
35	1d	73	ARG	4.1
48	1q	68	ARG	4.1
4	1E	193	GLY	4.1
36	2e	97	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
34	2c	115	LEU	4.0
35	2d	170	VAL	4.0
38	2g	23	VAL	4.0
50	1s	20	LEU	4.0
38	1g	77	SER	4.0
1	1A	1085	A	4.0
42	2k	75	TYR	4.0
2	1B	47	C	4.0
32	1a	1030	C	4.0
32	2a	1030(B)	C	4.0
32	2a	1321	C	4.0
41	1j	23	ILE	4.0
50	2s	62	ILE	4.0
38	1g	8	GLU	4.0
3	2D	48	ARG	4.0
34	1c	40	ARG	4.0
35	2d	118	ARG	4.0
38	1g	99	LEU	4.0
1	1A	2148	G	4.0
1	2A	1347	G	4.0
5	1F	133	ASN	4.0
20	1Y	4	LYS	4.0
32	1a	1021	G	4.0
32	1a	1026	G	4.0
32	2a	1031	G	4.0
40	1i	78	LYS	4.0
43	1l	112	ASP	4.0
52	2u	13	ILE	4.0
32	1a	163	C	4.0
32	1a	822	C	4.0
6	2G	68	PRO	4.0
6	2G	85	GLY	4.0
17	2V	74	LYS	4.0
36	2e	67	VAL	4.0
45	1n	18	VAL	4.0
47	2p	13	HIS	4.0
49	2r	61	LYS	4.0
10	2O	29	ASN	4.0
8	2I	27	ARG	4.0
35	2d	115	ARG	4.0
40	2i	126	SER	4.0
41	1j	96	ILE	4.0

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Mol	Chain	Res	Type	RSRZ
45	1n	42	ILE	4.0
50	1s	49	ILE	4.0
1	2A	2110	G	4.0
32	2a	631	G	4.0
6	1G	62	LEU	4.0
34	1c	91	LEU	4.0
42	2k	13	GLN	4.0
3	1D	235	GLY	4.0
1	1A	257	A	4.0
1	1A	2335	A	4.0
32	1a	937	A	4.0
1	2A	2164	C	4.0
3	1D	239	ARG	4.0
7	1H	3	ARG	4.0
24	12	14	ARG	4.0
48	1q	63	ARG	4.0
6	2G	63	ILE	4.0
40	1i	37	PHE	4.0
41	1j	98	ILE	4.0
43	2l	64	TYR	4.0
8	1I	85	GLU	4.0
50	1s	27	GLU	4.0
1	1A	2122	U	4.0
40	1i	19	LEU	4.0
46	1o	57	LEU	4.0
47	1p	3	LYS	4.0
38	1g	9	VAL	4.0
22	20	13	GLY	4.0
46	2o	9	GLN	4.0
32	2a	377	G	4.0
32	2a	1521	G	4.0
36	2e	15	ARG	4.0
40	1i	77	ILE	4.0
44	2m	25	ILE	4.0
1	1A	1098	A	4.0
9	2N	102	ALA	4.0
51	2t	97	ALA	4.0
32	2a	1140	C	4.0
32	2a	1259	C	4.0
33	1b	117	GLU	4.0
40	2i	91	ASP	4.0
33	1b	187	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
48	1q	100	LYS	4.0
41	2j	10	GLY	3.9
19	1X	60	ARG	3.9
40	1i	83	ARG	3.9
45	1n	19	ARG	3.9
50	1s	44	MET	3.9
3	1D	231	HIS	3.9
42	2k	74	ALA	3.9
3	2D	276	LYS	3.9
36	1e	130	ASN	3.9
5	1F	162	LEU	3.9
2	2B	119	G	3.9
32	1a	1185	G	3.9
32	2a	1001(A)	G	3.9
50	2s	77	THR	3.9
16	2U	97	ASP	3.9
6	2G	28	VAL	3.9
14	1S	14	VAL	3.9
3	2D	52	ARG	3.9
34	1c	109	PRO	3.9
32	1a	1249	C	3.9
32	2a	308	C	3.9
32	2a	1320	C	3.9
41	1j	51	ARG	3.9
9	1N	8	GLN	3.9
40	2i	73	GLN	3.9
5	2F	42	ALA	3.9
38	1g	29	LYS	3.9
49	1r	84	LYS	3.9
7	1H	67	LEU	3.9
34	2c	101	LEU	3.9
35	2d	192	GLU	3.9
44	1m	15	VAL	3.9
14	2S	52	SER	3.9
15	1T	107	ASP	3.9
17	2V	83	ARG	3.9
25	23	29	ARG	3.9
50	1s	35	SER	3.9
48	1q	28	PRO	3.9
47	1p	65	GLN	3.9
1	1A	2120	G	3.9
1	1A	2155	G	3.9

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Mol	Chain	Res	Type	RSRZ
1	1A	2334	G	3.9
1	1A	2476	A	3.9
32	2a	975	A	3.9
32	2a	1250	A	3.9
1	1A	1744	C	3.9
20	2Y	34	LYS	3.9
20	2Y	71	LYS	3.9
32	1a	1515	C	3.9
32	2a	444	C	3.9
32	2a	783	C	3.9
32	2a	972	C	3.9
40	1i	82	ALA	3.9
41	2j	71	LEU	3.9
32	2a	1364	U	3.9
9	2N	43	THR	3.9
35	1d	139	ARG	3.9
51	1t	80	ARG	3.9
41	2j	37	PRO	3.9
9	2N	71	ILE	3.9
38	1g	106	GLN	3.9
9	1N	47	ALA	3.9
34	1c	42	LEU	3.9
34	1c	187	ALA	3.9
40	1i	43	ALA	3.9
1	1A	225	A	3.9
5	1F	168	ARG	3.9
21	1Z	80	ARG	3.9
38	2g	78	ARG	3.9
48	2q	25	ARG	3.9
1	1A	1973	G	3.9
1	2A	1091	G	3.9
1	2A	2179	C	3.9
32	1a	1029	C	3.9
32	2a	1186	G	3.9
41	1j	34	VAL	3.9
12	1Q	112	GLU	3.9
1	1A	1211	U	3.9
6	1G	123	ASN	3.9
6	2G	42	GLY	3.9
11	2P	104	GLY	3.9
25	13	16	PRO	3.9
38	2g	84	ASN	3.9

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Mol	Chain	Res	Type	RSRZ
34	1c	199	LYS	3.9
35	2d	70	ILE	3.9
43	2l	100	ILE	3.9
44	1m	111	LYS	3.9
36	2e	84	PHE	3.9
46	2o	62	GLN	3.9
47	2p	9	PHE	3.9
34	1c	115	LEU	3.9
35	1d	162	LEU	3.9
44	2m	90	LEU	3.9
34	2c	168	ALA	3.9
47	1p	24	ALA	3.9
11	2P	65	ARG	3.8
50	1s	78	ARG	3.8
38	1g	66	VAL	3.8
34	1c	23	TYR	3.8
1	1A	2170	A	3.8
1	2A	1301	A	3.8
2	1B	48	A	3.8
34	1c	145	GLY	3.8
40	1i	123	PRO	3.8
35	1d	161	ASN	3.8
41	1j	22	LYS	3.8
43	1l	91	LYS	3.8
32	2a	950	U	3.8
32	2a	1154	G	3.8
34	2c	118	GLN	3.8
50	1s	12	ASP	3.8
6	2G	53	LEU	3.8
11	2P	105	LEU	3.8
45	1n	53	LEU	3.8
15	1T	130	ALA	3.8
36	1e	104	ALA	3.8
41	1j	60	ARG	3.8
42	2k	89	ALA	3.8
47	1p	13	HIS	3.8
51	2t	73	HIS	3.8
38	1g	5	ARG	3.8
41	2j	72	VAL	3.8
45	2n	56	VAL	3.8
45	2n	27	CYS	3.8
36	2e	88	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
47	2p	12	LYS	3.8
51	1t	74	LYS	3.8
34	1c	188	LEU	3.8
32	1a	452	A	3.8
32	1a	1180	A	3.8
32	2a	1179	A	3.8
32	2a	1289	A	3.8
45	2n	31	ARG	3.8
47	2p	23	ASP	3.8
49	1r	59	SER	3.8
44	2m	5	ALA	3.8
32	1a	136	C	3.8
32	1a	1314	C	3.8
38	1g	156	TRP	3.8
33	2b	7	VAL	3.8
50	1s	41	VAL	3.8
1	1A	232	G	3.8
1	1A	614(B)	G	3.8
1	1A	2106	G	3.8
1	1A	2121	G	3.8
32	1a	1181	G	3.8
32	2a	1516	G	3.8
35	1d	169	LYS	3.8
11	1P	74	GLU	3.8
14	1S	8	GLU	3.8
14	1S	92	TYR	3.8
3	1D	50	THR	3.8
7	2H	112	PRO	3.8
50	1s	31	ILE	3.8
33	2b	152	PHE	3.8
41	2j	63	PHE	3.8
22	10	75	LEU	3.8
35	2d	132	ARG	3.8
41	1j	20	ALA	3.8
44	1m	30	ALA	3.8
32	1a	453	A	3.8
1	1A	2150	U	3.8
1	2A	2130	U	3.8
32	1a	1203	C	3.8
6	2G	35	GLU	3.8
7	2H	128	PRO	3.8
12	2Q	80	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
15	2T	69	GLY	3.8
25	23	60	GLU	3.8
45	1n	28	GLY	3.8
48	2q	42	TYR	3.8
50	2s	49	ILE	3.8
36	1e	70	PRO	3.8
7	1H	152	ARG	3.8
52	2u	17	THR	3.8
1	1A	1630	G	3.8
1	1A	2131	G	3.8
32	1a	102	G	3.8
32	1a	392	G	3.8
32	1a	951	G	3.8
32	1a	1017	G	3.8
32	1a	1291	G	3.8
33	1b	192	SER	3.8
33	1b	197	VAL	3.8
35	2d	152	SER	3.8
51	2t	11	SER	3.8
38	1g	20	ASP	3.8
41	2j	96	ILE	3.8
33	2b	187	LEU	3.8
35	2d	136	PRO	3.8
52	1u	7	ARG	3.8
12	2Q	104	PHE	3.8
44	2m	70	LEU	3.8
1	2A	1085	A	3.8
32	1a	134	A	3.8
32	1a	968	A	3.8
32	1a	1049	U	3.8
32	1a	1261	A	3.8
1	2A	2139	C	3.7
7	2H	165	ALA	3.7
32	1a	962	C	3.7
35	1d	195	ALA	3.7
7	1H	172	LYS	3.7
20	1Y	3	VAL	3.7
37	2f	90	VAL	3.7
40	2i	86	VAL	3.7
44	2m	27	LYS	3.7
1	1A	224	G	3.7
1	1A	966	G	3.7

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Mol	Chain	Res	Type	RSRZ
1	1A	2159	G	3.7
1	2A	2151	G	3.7
32	2a	654	G	3.7
32	2a	1034	G	3.7
44	1m	9	ILE	3.7
34	1c	172	ARG	3.7
11	1P	98	GLU	3.7
34	1c	174	PRO	3.7
41	1j	37	PRO	3.7
41	2j	7	LYS	3.7
44	1m	5	ALA	3.7
1	2A	1090	U	3.7
6	1G	38	VAL	3.7
35	2d	74	GLN	3.7
38	2g	13	GLN	3.7
1	1A	1084	A	3.7
1	2A	1067	A	3.7
20	1Y	6	HIS	3.7
41	1j	56	HIS	3.7
32	1a	1326	C	3.7
32	2a	1141	C	3.7
3	1D	176	ARG	3.7
6	2G	39	ILE	3.7
41	1j	5	ARG	3.7
51	2t	22	ARG	3.7
35	1d	194	LEU	3.7
7	1H	47	GLU	3.7
39	2h	27	PRO	3.7
6	2G	8	LYS	3.7
33	2b	22	LYS	3.7
33	2b	133	LYS	3.7
1	2A	2115	G	3.7
32	2a	278	G	3.7
32	2a	1258	G	3.7
36	2e	116	THR	3.7
38	1g	127	ALA	3.7
40	2i	52	ALA	3.7
38	1g	23	VAL	3.7
40	1i	38	GLN	3.7
34	1c	69	HIS	3.7
50	2s	65	ASN	3.7
1	2A	1083	U	3.7

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Mol	Chain	Res	Type	RSRZ
28	26	42	TRP	3.7
33	2b	97	TRP	3.7
34	2c	57	ILE	3.7
7	1H	171	LEU	3.7
15	1T	114	LEU	3.7
4	1E	142	GLY	3.7
14	2S	29	PHE	3.7
34	2c	171	GLY	3.7
50	1s	74	PHE	3.7
51	1t	102	GLY	3.7
1	2A	2789	C	3.7
7	1H	126	PRO	3.7
6	2G	74	LYS	3.7
32	1a	135	C	3.7
32	1a	999	C	3.7
32	1a	1195	C	3.7
21	2Z	2	GLU	3.7
45	2n	21	TYR	3.7
20	2Y	16	ALA	3.7
34	2c	191	THR	3.7
36	1e	17	ALA	3.7
7	1H	113	VAL	3.7
41	1j	62	HIS	3.7
50	2s	69	HIS	3.7
34	2c	157	ILE	3.7
1	2A	2131	G	3.7
1	2A	2149	G	3.7
32	1a	823	G	3.7
39	2h	112	LEU	3.7
21	1Z	143	GLY	3.7
23	21	29	GLY	3.7
34	1c	128	PHE	3.7
47	1p	80	PHE	3.7
50	1s	68	GLY	3.7
3	2D	230	ASP	3.7
12	1Q	38	GLU	3.7
21	1Z	99	TYR	3.7
26	14	67	TYR	3.7
35	1d	179	GLU	3.7
38	2g	44	TYR	3.7
8	1I	19	VAL	3.7
34	2c	138	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
47	1p	2	VAL	3.7
1	2A	2142	C	3.7
12	1Q	37	LEU	3.7
42	2k	63	LEU	3.7
26	24	49	PHE	3.7
1	2A	2121	G	3.6
5	2F	97	TYR	3.6
20	1Y	45	VAL	3.6
32	2a	1222	G	3.6
32	2a	1305	G	3.6
38	2g	150	ALA	3.6
41	2j	58	ASP	3.6
45	1n	25	VAL	3.6
50	1s	50	ALA	3.6
6	2G	118	ARG	3.6
26	24	27	THR	3.6
32	1a	978	A	3.6
32	2a	1151	A	3.6
34	1c	37	GLN	3.6
42	2k	48	ILE	3.6
20	2Y	68	HIS	3.6
48	1q	4	LYS	3.6
1	1A	967	C	3.6
7	1H	128	PRO	3.6
7	1H	173	PRO	3.6
33	1b	194	PRO	3.6
44	2m	97	PRO	3.6
45	2n	54	PRO	3.6
50	2s	76	PRO	3.6
20	2Y	73	ARG	3.6
21	2Z	56	VAL	3.6
33	1b	188	ALA	3.6
38	1g	141	VAL	3.6
47	2p	32	TYR	3.6
51	1t	22	ARG	3.6
4	1E	17	ASP	3.6
5	2F	100	THR	3.6
7	1H	7	LEU	3.6
34	1c	134	ILE	3.6
50	2s	16	LEU	3.6
1	2A	2150	U	3.6
10	2O	26	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
17	1V	44	LYS	3.6
32	2a	1351	U	3.6
11	2P	35	HIS	3.6
32	1a	1370	G	3.6
3	2D	53	PHE	3.6
36	2e	74	GLY	3.6
43	2l	88	GLY	3.6
32	2a	1035	A	3.6
39	2h	101	PRO	3.6
41	1j	43	ARG	3.6
41	2j	78	ASN	3.6
44	1m	91	ARG	3.6
1	1A	271(Z)	C	3.6
7	2H	58	GLU	3.6
8	1I	10	GLU	3.6
32	1a	1039	C	3.6
32	1a	1129	C	3.6
34	1c	169	ALA	3.6
35	1d	8	VAL	3.6
38	1g	105	VAL	3.6
40	1i	14	VAL	3.6
51	1t	67	ALA	3.6
49	2r	34	TYR	3.6
30	18	3	LYS	3.6
40	2i	70	LYS	3.6
32	1a	560	U	3.6
43	2l	72	GLY	3.6
11	1P	15	ARG	3.6
26	14	56	VAL	3.6
18	1W	60	ASN	3.6
1	1A	1559	G	3.6
21	2Z	168	GLU	3.6
32	1a	159	G	3.6
32	1a	1233	G	3.6
32	1a	1293	G	3.6
32	2a	1058	G	3.6
36	1e	122	GLU	3.6
44	2m	8	GLU	3.6
1	1A	2062	A	3.6
6	2G	84	LYS	3.6
12	2Q	22	LYS	3.6
20	1Y	5	MET	3.6

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Mol	Chain	Res	Type	RSRZ
6	2G	152	LEU	3.6
24	22	49	LYS	3.6
35	1d	138	TYR	3.6
35	2d	188	LEU	3.6
38	2g	12	LEU	3.6
44	1m	48	LEU	3.6
16	2U	31	SER	3.6
41	1j	59	SER	3.6
1	1A	34	C	3.6
1	1A	268	C	3.6
21	2Z	93	ASP	3.6
52	1u	24	ARG	3.6
6	2G	87	PRO	3.6
6	2G	92	VAL	3.6
33	1b	71	VAL	3.6
35	1d	121	VAL	3.6
41	1j	18	ALA	3.6
41	2j	77	PRO	3.6
44	2m	54	VAL	3.6
44	2m	107	ALA	3.6
50	1s	60	VAL	3.6
3	1D	87	ASN	3.6
29	17	48	LYS	3.6
32	1a	65	U	3.6
34	1c	3	ASN	3.6
40	2i	29	ASN	3.6
47	1p	35	LYS	3.6
34	2c	48	TYR	3.6
40	1i	79	LEU	3.6
45	2n	6	LEU	3.6
39	2h	3	THR	3.6
45	1n	32	SER	3.6
41	2j	17	ASP	3.6
1	1A	347	A	3.5
1	1A	2134	A	3.5
1	2A	232	G	3.5
1	2A	1171	G	3.5
1	2A	2176	A	3.5
18	1W	8	ARG	3.5
32	1a	266	G	3.5
32	1a	1215	G	3.5
32	1a	1365	G	3.5

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Mol	Chain	Res	Type	RSRZ
32	1a	1374	A	3.5
33	1b	95	GLN	3.5
33	1b	40	HIS	3.5
35	1d	153	ARG	3.5
40	1i	9	ARG	3.5
40	2i	59	PHE	3.5
41	2j	66	ARG	3.5
45	2n	37	PHE	3.5
48	1q	93	GLN	3.5
4	1E	159	HIS	3.5
40	1i	72	GLY	3.5
32	2a	1328	C	3.5
39	2h	5	PRO	3.5
33	2b	8	LYS	3.5
6	2G	20	ILE	3.5
36	1e	13	ILE	3.5
32	1a	1135	U	3.5
32	1a	1212	U	3.5
32	2a	1345	U	3.5
6	2G	115	ARG	3.5
26	24	68	ARG	3.5
33	2b	67	THR	3.5
50	1s	39	THR	3.5
11	1P	69	GLY	3.5
51	1t	101	GLY	3.5
8	2I	21	VAL	3.5
48	1q	23	VAL	3.5
45	2n	5	ALA	3.5
48	2q	100	LYS	3.5
50	2s	11	VAL	3.5
33	1b	225	ALA	3.5
34	2c	109	PRO	3.5
28	26	11	LEU	3.5
32	1a	976	G	3.5
32	2a	998	G	3.5
32	2a	1003	G	3.5
1	2A	2128	C	3.5
32	1a	290	C	3.5
32	1a	1027	C	3.5
32	1a	1359	C	3.5
32	2a	1514	C	3.5
34	2c	182	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
47	2p	33	ILE	3.5
38	2g	77	SER	3.5
5	1F	96	ASP	3.5
5	1F	208	GLY	3.5
9	2N	113	GLY	3.5
35	1d	180	GLY	3.5
38	1g	34	GLY	3.5
40	2i	117	HIS	3.5
43	2l	95	GLY	3.5
40	2i	17	VAL	3.5
35	1d	55	ALA	3.5
36	1e	119	LEU	3.5
41	1j	85	LEU	3.5
44	2m	48	LEU	3.5
38	2g	120	ILE	3.5
7	2H	6	ARG	3.5
38	1g	119	ARG	3.5
40	2i	83	ARG	3.5
45	2n	23	ARG	3.5
52	2u	15	ARG	3.5
32	1a	389	A	3.5
1	1A	292	C	3.5
1	1A	1100	C	3.5
46	1o	15	PHE	3.5
1	1A	272	G	3.5
1	1A	1835	G	3.5
1	2A	1058	G	3.5
11	2P	29	LYS	3.5
11	2P	30	THR	3.5
31	29	8	LYS	3.5
36	1e	47	LYS	3.5
33	1b	165	VAL	3.5
8	2I	14	ASP	3.5
36	2e	17	ALA	3.5
33	2b	213	LEU	3.5
35	1d	7	PRO	3.5
37	1f	67	MET	3.5
45	1n	54	PRO	3.5
41	1j	50	ILE	3.5
51	1t	55	ILE	3.5
34	2c	164	ARG	3.5
40	2i	95	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
49	2r	71	LYS	3.5
32	1a	1239	A	3.5
32	1a	1324	A	3.5
32	2a	1375	A	3.5
34	2c	120	VAL	3.5
38	2g	110	GLN	3.5
44	1m	89	GLY	3.5
50	2s	19	VAL	3.5
51	1t	69	GLY	3.5
6	1G	90	LEU	3.5
7	1H	63	SER	3.5
34	1c	87	LEU	3.5
1	2A	2175	C	3.5
3	1D	226	MET	3.5
10	1O	1	MET	3.5
32	1a	934	C	3.5
32	2a	962	C	3.5
37	1f	1	MET	3.5
1	1A	882	G	3.5
1	2A	1933	G	3.5
2	2B	118	G	3.5
32	1a	112	G	3.5
33	2b	21	ARG	3.5
44	2m	88	ARG	3.5
1	1A	362	U	3.5
2	1B	1	U	3.5
37	1f	95	GLU	3.4
43	2l	73	GLU	3.4
4	1E	69	LYS	3.4
6	2G	11	TYR	3.4
26	14	59	PHE	3.4
44	1m	21	TYR	3.4
35	2d	92	VAL	3.4
37	1f	90	VAL	3.4
11	2P	43	GLY	3.4
39	1h	90	GLY	3.4
42	2k	31	THR	3.4
44	1m	68	GLY	3.4
6	1G	152	LEU	3.4
11	2P	59	LEU	3.4
13	2R	13	HIS	3.4
23	11	42	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
34	1c	189	ALA	3.4
20	1Y	44	ILE	3.4
33	1b	137	ARG	3.4
33	2b	137	ARG	3.4
43	2l	89	ARG	3.4
32	2a	1285	A	3.4
41	1j	17	ASP	3.4
47	1p	59	TRP	3.4
2	1B	49	C	3.4
22	10	46	LYS	3.4
32	2a	1243	C	3.4
35	1d	185	PHE	3.4
1	1A	906	G	3.4
1	1A	952	G	3.4
1	2A	859	G	3.4
1	2A	2189	U	3.4
32	1a	1050	G	3.4
32	1a	1309	G	3.4
32	2a	757	U	3.4
5	1F	134	GLY	3.4
11	2P	82	GLY	3.4
33	1b	149	LEU	3.4
33	2b	11	LEU	3.4
38	2g	109	ASN	3.4
34	2c	149	ALA	3.4
41	1j	26	ALA	3.4
51	1t	71	THR	3.4
15	2T	1	MET	3.4
33	1b	200	ILE	3.4
50	2s	38	SER	3.4
30	28	39	LYS	3.4
38	2g	35	LYS	3.4
38	2g	156	TRP	3.4
42	2k	122	LYS	3.4
52	1u	12	LYS	3.4
8	1I	20	ASP	3.4
44	2m	67	GLU	3.4
32	2a	1204	A	3.4
32	2a	1350	A	3.4
37	2f	63	TYR	3.4
40	1i	62	TYR	3.4
34	1c	76	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
34	2c	198	VAL	3.4
40	2i	26	VAL	3.4
50	2s	60	VAL	3.4
3	1D	170	GLY	3.4
15	2T	111	ARG	3.4
32	1a	1140	C	3.4
32	1a	1158	C	3.4
34	1c	190	ARG	3.4
41	2j	93	GLY	3.4
35	2d	195	ALA	3.4
43	1l	19	ARG	3.4
1	1A	405	U	3.4
4	1E	146	THR	3.4
21	2Z	133	ILE	3.4
32	1a	202	U	3.4
32	1a	950	U	3.4
32	1a	1372	U	3.4
34	2c	170	GLN	3.4
38	2g	86	GLN	3.4
41	1j	100	THR	3.4
43	2l	99	HIS	3.4
35	1d	37	PRO	3.4
17	1V	74	LYS	3.4
32	1a	1310	G	3.4
32	2a	41	G	3.4
32	2a	973	G	3.4
32	2a	1221	G	3.4
47	2p	59	TRP	3.4
48	1q	99	SER	3.4
41	2j	11	PHE	3.4
44	1m	16	ASP	3.4
25	13	38	GLU	3.4
33	1b	221	LEU	3.4
34	1c	101	LEU	3.4
36	1e	91	LEU	3.4
5	2F	47	GLY	3.4
6	2G	89	GLY	3.4
36	2e	23	GLY	3.4
43	1l	95	GLY	3.4
1	1A	2333	A	3.4
11	2P	81	GLN	3.4
23	11	59	THR	3.4

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Mol	Chain	Res	Type	RSRZ
32	1a	873	A	3.4
32	2a	1001	A	3.4
34	2c	192	THR	3.4
10	2O	66	LYS	3.4
11	1P	72	PRO	3.4
30	18	33	ASN	3.4
35	1d	154	ASN	3.4
41	1j	21	GLN	3.4
41	2j	57	LYS	3.4
45	2n	17	LYS	3.4
32	1a	1128	C	3.4
32	2a	277	C	3.4
1	1A	12	U	3.4
32	1a	1125	U	3.4
39	2h	31	PHE	3.4
3	2D	34	VAL	3.4
7	1H	64	LEU	3.4
34	2c	44	GLU	3.4
34	1c	126	ARG	3.4
34	1c	198	VAL	3.4
38	1g	6	ARG	3.4
38	1g	104	LEU	3.4
39	2h	49	GLU	3.4
44	1m	70	LEU	3.4
45	2n	44	LEU	3.4
46	2o	65	ARG	3.4
1	2A	2337	G	3.4
32	1a	1316	G	3.4
40	2i	36	TYR	3.4
45	1n	21	TYR	3.4
3	1D	236	GLY	3.4
35	2d	181	MET	3.4
6	1G	77	ILE	3.4
48	2q	67	LYS	3.4
14	1S	5	THR	3.4
24	22	70	GLN	3.4
36	2e	70	PRO	3.4
40	2i	64	THR	3.4
45	1n	13	THR	3.4
32	2a	262	A	3.3
32	2a	1239	A	3.3
33	1b	163	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
48	2q	71	PHE	3.3
1	1A	2128	C	3.3
1	2A	2132	U	3.3
2	1B	38	C	3.3
4	2E	163	GLU	3.3
17	2V	73	SER	3.3
32	1a	1362	C	3.3
32	2a	932	C	3.3
32	2a	1242	C	3.3
32	2a	1282	C	3.3
35	1d	115	ARG	3.3
38	2g	115	ARG	3.3
42	2k	43	SER	3.3
43	2l	12	ARG	3.3
45	2n	57	ARG	3.3
50	1s	38	SER	3.3
51	1t	17	ARG	3.3
42	2k	119	CYS	3.3
26	24	51	ASP	3.3
4	2E	153	GLY	3.3
16	2U	46	ALA	3.3
20	1Y	19	LYS	3.3
21	2Z	1	MET	3.3
46	1o	48	LYS	3.3
49	1r	20	ALA	3.3
26	24	14	ILE	3.3
34	1c	84	ILE	3.3
47	1p	36	ILE	3.3
37	1f	96	PRO	3.3
1	2A	1627	G	3.3
3	2D	87	ASN	3.3
32	1a	46	G	3.3
32	1a	973	G	3.3
32	2a	326	G	3.3
3	2D	217	ARG	3.3
37	2f	46	ARG	3.3
6	2G	149	VAL	3.3
34	2c	188	LEU	3.3
1	1A	6	A	3.3
1	1A	2336	A	3.3
32	1a	1179	A	3.3
32	1a	1201	A	3.3

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Mol	Chain	Res	Type	RSRZ
40	2i	92	TYR	3.3
44	2m	72	ALA	3.3
46	1o	59	MET	3.3
10	2O	81	ASP	3.3
11	1P	5	ASP	3.3
47	1p	17	TYR	3.3
1	1A	2175	C	3.3
1	1A	2294	C	3.3
32	1a	224	C	3.3
32	1a	578	C	3.3
32	2a	618	C	3.3
32	2a	1037	C	3.3
32	2a	1270	C	3.3
32	2a	1524	C	3.3
17	2V	87	HIS	3.3
36	2e	96	PRO	3.3
38	1g	97	GLN	3.3
41	1j	39	PRO	3.3
33	2b	196	LEU	3.3
38	2g	43	PHE	3.3
3	2D	250	TRP	3.3
34	1c	195	VAL	3.3
44	1m	74	VAL	3.3
15	1T	65	LYS	3.3
18	1W	98	LYS	3.3
1	1A	410	G	3.3
1	2A	2155	G	3.3
32	1a	347	G	3.3
32	1a	1311	G	3.3
10	2O	100	GLY	3.3
34	1c	152	ILE	3.3
34	2c	163	ALA	3.3
35	2d	71	SER	3.3
38	2g	92	SER	3.3
43	2l	63	GLY	3.3
45	2n	7	ILE	3.3
8	2I	29	TYR	3.3
33	2b	148	TYR	3.3
40	2i	125	TYR	3.3
1	2A	1084	A	3.3
33	2b	131	PRO	3.3
35	1d	39	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	1A	272(A)	U	3.3
1	1A	2265	U	3.3
3	2D	140	THR	3.3
18	1W	99	ARG	3.3
32	1a	1313	U	3.3
41	1j	70	ARG	3.3
1	2A	2145	C	3.3
1	2A	2313	C	3.3
32	1a	783	C	3.3
32	1a	972	C	3.3
32	2a	784	C	3.3
32	2a	1045	C	3.3
38	2g	62	PHE	3.3
45	2n	47	LEU	3.3
40	2i	53	VAL	3.3
35	2d	154	ASN	3.3
39	2h	15	ASN	3.3
43	1l	17	LYS	3.3
15	1T	109	GLU	3.3
36	2e	132	ALA	3.3
44	2m	18	ALA	3.3
12	1Q	23	GLY	3.3
12	1Q	33	GLY	3.3
24	12	40	SER	3.3
36	1e	133	TYR	3.3
38	1g	98	SER	3.3
44	2m	21	TYR	3.3
42	1k	126	ARG	3.3
1	2A	883	G	3.3
6	1G	71	THR	3.3
6	2G	107	LEU	3.3
32	1a	1142	G	3.3
32	2a	587	G	3.3
32	2a	1024	G	3.3
32	2a	1057	G	3.3
32	2a	1387	G	3.3
26	24	42	PHE	3.3
33	1b	44	LEU	3.3
33	2b	10	LEU	3.3
16	1U	22	LYS	3.3
34	2c	173	VAL	3.3
50	1s	58	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
51	2t	14	LYS	3.3
1	1A	1352	U	3.3
1	2A	2122	U	3.3
32	2a	1268	A	3.3
42	1k	42	TRP	3.3
6	2G	114	ILE	3.3
13	2R	102	GLU	3.3
32	1a	1189	C	3.3
32	2a	1115	C	3.3
32	2a	1129	C	3.3
32	2a	1223	C	3.3
32	2a	1515	C	3.3
36	1e	11	ILE	3.3
38	2g	50	ILE	3.3
40	2i	94	ALA	3.3
45	2n	48	ALA	3.3
20	1Y	80	GLY	3.3
33	1b	130	ARG	3.2
39	1h	58	TYR	3.2
45	2n	26	ARG	3.2
41	2j	91	PRO	3.2
45	2n	14	PRO	3.2
49	1r	31	LEU	3.2
6	2G	58	GLN	3.2
35	1d	42	GLN	3.2
33	1b	190	THR	3.2
50	1s	33	THR	3.2
31	19	1	MET	3.2
14	2S	51	ALA	3.2
20	1Y	92	ASN	3.2
34	2c	14	ILE	3.2
41	2j	75	ILE	3.2
1	2A	1973	G	3.2
1	2A	2338	G	3.2
11	1P	93	GLY	3.2
20	2Y	29	GLU	3.2
21	1Z	12	GLY	3.2
32	1a	70	G	3.2
32	1a	1216	G	3.2
32	1a	1276	G	3.2
32	1a	1330	U	3.2
32	2a	247	G	3.2

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Mol	Chain	Res	Type	RSRZ
32	2a	630	G	3.2
32	2a	1139	G	3.2
34	2c	166	GLU	3.2
1	1A	345	A	3.2
32	1a	171	A	3.2
32	2a	1531	A	3.2
46	2o	68	ARG	3.2
38	2g	154	TYR	3.2
48	2q	32	TYR	3.2
50	2s	61	TYR	3.2
6	1G	2	PRO	3.2
8	1I	2	LYS	3.2
21	2Z	92	SER	3.2
32	1a	564	C	3.2
32	2a	1260	C	3.2
41	2j	85	LEU	3.2
44	1m	19	LEU	3.2
44	1m	96	LEU	3.2
47	1p	43	LYS	3.2
50	2s	7	LYS	3.2
52	1u	20	LYS	3.2
5	2F	96	ASP	3.2
6	2G	156	ASP	3.2
26	24	33	VAL	3.2
35	2d	42	GLN	3.2
6	1G	140	ILE	3.2
21	1Z	1	MET	3.2
31	19	17	ILE	3.2
35	1d	70	ILE	3.2
4	1E	123	ALA	3.2
4	2E	130	GLY	3.2
11	2P	54	GLY	3.2
24	12	66	GLU	3.2
30	18	46	ARG	3.2
38	2g	37	ASN	3.2
51	1t	25	ARG	3.2
51	2t	9	ASN	3.2
6	2G	7	LEU	3.2
11	2P	3	LEU	3.2
34	1c	201	TYR	3.2
37	2f	98	LEU	3.2
38	1g	154	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
32	2a	1126	U	3.2
1	1A	1056	G	3.2
1	2A	1699	G	3.2
7	2H	50	VAL	3.2
21	2Z	74	VAL	3.2
22	20	63	VAL	3.2
32	1a	281	G	3.2
32	1a	438	G	3.2
32	1a	998	G	3.2
32	1a	1340	A	3.2
32	2a	452	A	3.2
1	2A	34	C	3.2
1	2A	2108	C	3.2
6	2G	161	THR	3.2
14	1S	21	THR	3.2
32	2a	40	C	3.2
32	2a	1344	C	3.2
21	1Z	146	ILE	3.2
5	2F	45	ARG	3.2
34	2c	200	ALA	3.2
47	2p	24	ALA	3.2
50	2s	78	ARG	3.2
50	1s	43	GLU	3.2
10	1O	26	LYS	3.2
9	2N	107	LEU	3.2
20	2Y	90	LEU	3.2
46	1o	31	LEU	3.2
37	1f	4	TYR	3.2
39	1h	20	TYR	3.2
33	1b	183	PRO	3.2
34	2c	114	PRO	3.2
6	2G	109	VAL	3.2
7	2H	17	VAL	3.2
40	1i	28	VAL	3.2
44	1m	7	VAL	3.2
45	1n	37	PHE	3.2
21	2Z	52	SER	3.2
24	22	56	GLN	3.2
32	1a	1257	U	3.2
24	22	51	ARG	3.2
36	2e	24	ARG	3.2
38	2g	102	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
40	2i	93	ARG	3.2
41	1j	67	THR	3.2
44	1m	25	ILE	3.2
44	1m	49	THR	3.2
44	2m	39	ILE	3.2
1	2A	2062	A	3.2
1	2A	2135	A	3.2
44	2m	33	ALA	3.2
7	1H	62	LYS	3.2
32	2a	491	G	3.2
32	2a	1365	G	3.2
33	1b	169	LYS	3.2
35	2d	130	GLY	3.2
1	2A	1049	C	3.2
6	2G	59	GLU	3.2
32	1a	1113	C	3.2
32	1a	1200	C	3.2
32	1a	1384	C	3.2
37	2f	45	LEU	3.2
40	2i	56	LEU	3.2
31	29	24	TYR	3.2
21	1Z	175	VAL	3.2
35	2d	88	VAL	3.2
40	1i	18	PHE	3.2
47	1p	51	VAL	3.2
50	1s	59	PRO	3.2
5	2F	72	ARG	3.2
9	2N	1	MET	3.2
21	2Z	197	ILE	3.2
22	10	72	ARG	3.2
36	2e	107	ARG	3.2
37	1f	86	ARG	3.2
38	1g	125	MET	3.2
40	2i	15	ALA	3.2
44	1m	20	THR	3.2
21	2Z	77	ASP	3.1
35	2d	166	LYS	3.1
36	2e	124	GLY	3.1
21	2Z	91	LEU	3.1
40	2i	85	LEU	3.1
7	1H	124	GLU	3.1
18	2W	78	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
3	2D	45	ASN	3.1
4	1E	60	ASN	3.1
4	1E	160	TYR	3.1
14	1S	28	VAL	3.1
40	2i	18	PHE	3.1
1	1A	258	G	3.1
1	1A	1537	G	3.1
1	2A	1080	C	3.1
32	1a	280	C	3.1
32	1a	671	G	3.1
32	1a	866	C	3.1
32	1a	947	G	3.1
32	1a	1030(A)	G	3.1
32	2a	102	G	3.1
32	2a	351	G	3.1
32	2a	1128	C	3.1
32	2a	1322	C	3.1
32	2a	1325	C	3.1
41	1j	46	ARG	3.1
47	2p	42	ARG	3.1
50	1s	29	ARG	3.1
3	1D	271	ILE	3.1
41	1j	13	HIS	3.1
12	1Q	141	GLN	3.1
3	1D	259	THR	3.1
4	1E	157	ALA	3.1
30	18	29	LYS	3.1
30	28	10	ALA	3.1
33	1b	147	LYS	3.1
35	2d	149	ALA	3.1
39	1h	98	LYS	3.1
41	1j	42	THR	3.1
17	2V	95	LEU	3.1
35	2d	108	LEU	3.1
47	1p	49	LEU	3.1
5	1F	161	GLU	3.1
37	2f	95	GLU	3.1
32	2a	1393	U	3.1
33	2b	57	PHE	3.1
39	1h	31	PHE	3.1
41	1j	24	VAL	3.1
43	1l	40	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
3	1D	60	ARG	3.1
5	1F	102	PRO	3.1
6	2G	98	ARG	3.1
12	2Q	16	ARG	3.1
17	1V	81	TYR	3.1
21	2Z	194	PRO	3.1
22	20	77	ARG	3.1
40	2i	9	ARG	3.1
52	1u	18	TYR	3.1
52	2u	21	TYR	3.1
6	2G	157	ILE	3.1
32	1a	1093	A	3.1
32	1a	1151	A	3.1
32	2a	1016	A	3.1
20	2Y	19	LYS	3.1
38	1g	50	ILE	3.1
21	1Z	192	ALA	3.1
38	1g	40	ALA	3.1
1	1A	234	C	3.1
1	1A	1761	C	3.1
1	1A	2313	C	3.1
1	2A	1691	C	3.1
3	2D	40	THR	3.1
15	1T	59	THR	3.1
32	1a	1217	C	3.1
40	2i	27	THR	3.1
1	1A	109	G	3.1
1	1A	1933	G	3.1
6	2G	129	GLY	3.1
12	2Q	100	GLY	3.1
32	1a	558	G	3.1
32	2a	1033	G	3.1
34	2c	51	GLY	3.1
43	2l	14	GLY	3.1
22	20	71	ASP	3.1
35	1d	144	ASP	3.1
39	2h	54	ASP	3.1
4	1E	171	GLU	3.1
25	13	34	GLU	3.1
7	2H	45	VAL	3.1
7	1H	59	ARG	3.1
15	1T	51	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
37	1f	97	PHE	3.1
49	1r	29	PHE	3.1
20	2Y	53	PRO	3.1
36	1e	77	PRO	3.1
41	1j	91	PRO	3.1
15	1T	55	ASN	3.1
34	1c	72	LYS	3.1
35	1d	181	MET	3.1
40	2i	113	LYS	3.1
15	2T	90	GLN	3.1
33	2b	237	ALA	3.1
34	1c	123	GLN	3.1
35	1d	32	ALA	3.1
41	2j	32	ALA	3.1
44	2m	75	ALA	3.1
9	1N	116	LEU	3.1
34	1c	196	LEU	3.1
46	1o	34	LEU	3.1
51	1t	24	LEU	3.1
1	1A	229	A	3.1
2	1B	13	A	3.1
9	2N	81	GLY	3.1
15	1T	69	GLY	3.1
26	14	52	THR	3.1
29	17	24	THR	3.1
32	1a	938	A	3.1
32	1a	946	A	3.1
32	2a	935	A	3.1
50	2s	39	THR	3.1
7	1H	155	SER	3.1
1	2A	2177	C	3.1
9	2N	103	VAL	3.1
32	1a	784	C	3.1
32	2a	395	C	3.1
32	2a	1362	C	3.1
32	2a	1397	C	3.1
33	1b	70	PHE	3.1
37	1f	6	VAL	3.1
38	1g	78	ARG	3.1
40	1i	65	VAL	3.1
41	2j	61	GLU	3.1
43	1l	16	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
44	2m	17	VAL	3.1
47	1p	5	ARG	3.1
50	2s	73	GLU	3.1
3	2D	36	PRO	3.1
6	1G	36	LYS	3.1
23	21	33	LYS	3.1
25	23	2	PRO	3.1
33	1b	91	PRO	3.1
50	1s	32	LYS	3.1
1	1A	240	G	3.1
1	1A	881	G	3.1
4	1E	151	TYR	3.1
5	2F	184	TYR	3.1
7	1H	41	MET	3.1
14	2S	7	TYR	3.1
32	1a	945	G	3.1
32	1a	1094	G	3.1
32	1a	1386	G	3.1
32	2a	350	G	3.1
32	2a	492	G	3.1
32	2a	548	G	3.1
38	1g	18	TYR	3.1
40	1i	81	ILE	3.1
42	1k	25	TYR	3.1
33	2b	188	ALA	3.1
6	2G	19	LEU	3.1
6	2G	133	LEU	3.1
8	2I	38	LEU	3.1
16	1U	78	THR	3.1
25	13	55	ARG	3.1
35	2d	209	ARG	3.1
3	1D	266	SER	3.1
6	1G	5	VAL	3.1
26	24	56	VAL	3.1
34	2c	130	VAL	3.1
38	1g	17	VAL	3.1
1	1A	653	A	3.1
1	2A	2114	A	3.1
6	2G	75	LYS	3.1
7	1H	127	GLU	3.1
32	1a	197	A	3.1
32	1a	393	A	3.1

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Mol	Chain	Res	Type	RSRZ
48	2q	4	LYS	3.1
50	2s	18	LYS	3.1
34	2c	36	ASP	3.1
40	1i	91	ASP	3.1
12	1Q	39	PRO	3.1
42	2k	115	PRO	3.1
14	2S	36	TYR	3.1
39	1h	94	TYR	3.1
1	1A	889	C	3.0
1	1A	2185	C	3.0
1	2A	1092	C	3.0
32	2a	175	C	3.0
15	2T	55	ASN	3.0
28	16	22	ALA	3.0
31	19	29	ASN	3.0
33	1b	145	LEU	3.0
34	1c	178	LEU	3.0
44	2m	66	LEU	3.0
48	1q	53	LEU	3.0
40	1i	58	HIS	3.0
6	2G	138	GLN	3.0
8	1I	147	GLN	3.0
23	11	47	GLN	3.0
36	1e	141	GLN	3.0
1	1A	2112	G	3.0
1	2A	1044	G	3.0
1	2A	1382	G	3.0
5	2F	46	ARG	3.0
10	2O	95	GLY	3.0
32	1a	66	G	3.0
32	1a	380	G	3.0
32	2a	42	G	3.0
32	2a	773	G	3.0
32	2a	1108	G	3.0
32	2a	1144	G	3.0
32	2a	1295	G	3.0
40	1i	115	GLY	3.0
44	1m	24	GLY	3.0
3	2D	259	THR	3.0
1	1A	306	U	3.0
3	1D	229	VAL	3.0
8	2I	19	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
20	1Y	85	VAL	3.0
8	1I	121	LYS	3.0
26	14	2	LYS	3.0
21	2Z	142	SER	3.0
50	1s	40	ILE	3.0
26	24	65	ASP	3.0
34	2c	29	TYR	3.0
38	1g	44	TYR	3.0
1	1A	270	A	3.0
1	2A	2333	A	3.0
1	2A	2801(A)	A	3.0
16	1U	116	ALA	3.0
32	2a	787	A	3.0
38	2g	65	ALA	3.0
41	1j	88	LEU	3.0
41	2j	18	ALA	3.0
42	2k	65	ALA	3.0
42	2k	66	LEU	3.0
48	1q	6	LEU	3.0
32	1a	1044	A	3.0
17	2V	21	ARG	3.0
38	1g	84	ASN	3.0
32	2a	744	C	3.0
32	2a	1363	C	3.0
33	1b	18	GLY	3.0
51	2t	18	GLN	3.0
1	1A	2111	C	3.0
1	2A	2107	C	3.0
1	2A	2138	C	3.0
32	1a	1119	C	3.0
6	2G	64	THR	3.0
9	2N	22	THR	3.0
38	1g	135	VAL	3.0
43	2l	28	LYS	3.0
45	2n	58	LYS	3.0
23	21	27	GLU	3.0
26	14	3	GLU	3.0
30	18	65	GLU	3.0
41	1j	74	ILE	3.0
1	2A	614(A)	U	3.0
1	1A	1377	G	3.0
1	1A	2184	G	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	1093	G	3.0
32	1a	79	G	3.0
32	1a	1190	G	3.0
32	1a	1222	G	3.0
32	2a	1355	G	3.0
17	1V	38	LEU	3.0
40	2i	79	LEU	3.0
46	1o	56	LEU	3.0
18	1W	44	ALA	3.0
33	2b	77	ALA	3.0
38	2g	18	TYR	3.0
3	1D	244	ARG	3.0
14	2S	17	ARG	3.0
26	14	61	ARG	3.0
44	1m	108	ARG	3.0
51	2t	23	ARG	3.0
4	2E	124	GLY	3.0
7	2H	74	ASN	3.0
34	1c	135	LYS	3.0
36	1e	20	GLN	3.0
38	2g	137	LYS	3.0
43	2l	9	GLN	3.0
51	2t	75	ASN	3.0
1	2A	2602	A	3.0
31	19	3	VAL	3.0
32	1a	622	A	3.0
32	2a	1306	A	3.0
32	2a	1363(A)	A	3.0
34	2c	141	VAL	3.0
36	1e	100	VAL	3.0
44	2m	15	VAL	3.0
6	2G	117	PHE	3.0
2	2B	88	C	3.0
7	1H	148	ILE	3.0
9	2N	42	TRP	3.0
26	14	22	ILE	3.0
32	1a	1242	C	3.0
32	2a	1327	C	3.0
50	2s	34	TRP	3.0
47	1p	15	PRO	3.0
5	1F	32	LEU	3.0
17	1V	83	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
21	2Z	82	ARG	3.0
23	11	41	ARG	3.0
34	1c	127	ARG	3.0
49	2r	32	ARG	3.0
32	1a	1194	U	3.0
32	2a	1125	U	3.0
11	1P	36	LYS	3.0
1	1A	530	G	3.0
1	2A	916	G	3.0
1	2A	2157	G	3.0
7	2H	79	VAL	3.0
26	24	18	CYS	3.0
32	2a	266	G	3.0
32	2a	947	G	3.0
32	2a	1241	G	3.0
32	2a	1309	G	3.0
37	2f	27	GLN	3.0
47	2p	30	GLY	3.0
32	1a	492	G	3.0
32	1a	568	G	3.0
32	1a	890	G	3.0
32	1a	1154	G	3.0
38	1g	80	VAL	3.0
51	1t	26	ASN	3.0
33	1b	57	PHE	3.0
36	1e	45	PHE	3.0
7	2H	129	THR	3.0
40	1i	7	THR	3.0
41	2j	15	THR	3.0
22	10	53	MET	3.0
36	2e	109	ILE	3.0
50	2s	40	ILE	3.0
6	1G	137	GLU	3.0
7	2H	71	LEU	3.0
26	14	53	GLU	3.0
34	1c	122	GLU	3.0
25	13	41	PRO	3.0
32	1a	965	A	3.0
32	2a	1252	A	3.0
38	2g	104	LEU	3.0
44	1m	10	PRO	3.0
50	2s	42	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
50	2s	59	PRO	3.0
44	2m	3	ARG	3.0
3	2D	225	ALA	3.0
25	23	11	SER	3.0
33	1b	207	ALA	3.0
36	2e	87	SER	3.0
44	1m	42	ALA	3.0
1	1A	291	C	3.0
1	1A	898	C	3.0
32	1a	217	C	3.0
32	1a	1030(B)	C	3.0
32	2a	1533	C	3.0
35	1d	170	VAL	3.0
36	2e	51	VAL	3.0
41	2j	13	HIS	3.0
32	1a	1150	U	3.0
3	1D	45	ASN	3.0
41	1j	69	ASN	3.0
44	2m	78	ILE	3.0
44	2m	82	MET	3.0
50	1s	66	MET	3.0
8	2I	123	LEU	2.9
39	2h	63	LEU	2.9
6	2G	181	ARG	2.9
11	2P	15	ARG	2.9
40	1i	104	ARG	2.9
1	1A	2104	G	2.9
1	2A	545	G	2.9
1	2A	2133	G	2.9
1	2A	2655	G	2.9
32	1a	800	G	2.9
32	2a	80	G	2.9
32	2a	821	G	2.9
32	2a	1021	G	2.9
32	2a	1508	G	2.9
6	2G	81	LYS	2.9
41	1j	27	ALA	2.9
42	1k	124	LYS	2.9
8	2I	89	TYR	2.9
9	2N	76	SER	2.9
38	1g	85	TYR	2.9
32	1a	414	A	2.9

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Mol	Chain	Res	Type	RSRZ
32	2a	781	A	2.9
7	1H	158	HIS	2.9
7	2H	43	VAL	2.9
34	1c	120	VAL	2.9
37	2f	6	VAL	2.9
38	2g	118	VAL	2.9
13	1R	69	ASP	2.9
20	1Y	107	ASP	2.9
42	2k	116	HIS	2.9
44	1m	92	HIS	2.9
49	1r	30	ASP	2.9
4	1E	113	PHE	2.9
16	1U	117	GLN	2.9
22	10	70	GLN	2.9
39	2h	70	GLN	2.9
4	1E	77	ILE	2.9
12	2Q	1	MET	2.9
15	2T	104	ASN	2.9
12	2Q	21	THR	2.9
15	1T	112	ARG	2.9
15	2T	95	ARG	2.9
26	24	24	THR	2.9
30	28	32	LEU	2.9
32	2a	5	U	2.9
38	1g	4	ARG	2.9
50	2s	37	ARG	2.9
5	2F	56	GLU	2.9
12	1Q	139	GLU	2.9
33	2b	91	PRO	2.9
39	1h	136	GLU	2.9
38	1g	152	ALA	2.9
5	1F	97	TYR	2.9
19	1X	69	TYR	2.9
37	1f	63	TYR	2.9
43	1l	120	TYR	2.9
18	1W	59	VAL	2.9
5	1F	131	GLY	2.9
34	2c	197	GLY	2.9
46	1o	89	GLY	2.9
1	2A	1377	G	2.9
1	2A	2159	G	2.9
1	2A	2893	G	2.9

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Mol	Chain	Res	Type	RSRZ
32	1a	115	G	2.9
32	1a	1088	G	2.9
32	2a	1290	G	2.9
32	2a	1385	G	2.9
34	2c	10	PHE	2.9
11	2P	70	GLN	2.9
33	1b	41	ILE	2.9
38	1g	49	ILE	2.9
41	1j	4	ILE	2.9
1	1A	2176	A	2.9
1	2A	1096	A	2.9
14	2S	32	LEU	2.9
27	15	15	ARG	2.9
32	1a	994	A	2.9
32	1a	1004	A	2.9
34	2c	91	LEU	2.9
34	2c	179	ARG	2.9
35	2d	168	ARG	2.9
37	2f	71	ARG	2.9
39	2h	92	ARG	2.9
44	1m	81	LEU	2.9
45	1n	12	ARG	2.9
47	1p	72	ARG	2.9
10	1O	21	CYS	2.9
20	1Y	71	LYS	2.9
1	1A	1961	C	2.9
1	1A	2188	C	2.9
1	2A	2140	C	2.9
17	1V	29	PRO	2.9
8	2I	83	ALA	2.9
32	2a	34	C	2.9
32	2a	1018	C	2.9
38	1g	100	ALA	2.9
40	1i	12	GLU	2.9
44	1m	8	GLU	2.9
48	1q	96	GLU	2.9
1	1A	614(A)	U	2.9
1	2A	2109	U	2.9
32	2a	1020	U	2.9
34	1c	106	VAL	2.9
50	2s	58	VAL	2.9
3	1D	223	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
11	1P	26	GLY	2.9
17	1V	63	GLY	2.9
20	1Y	41	GLY	2.9
36	1e	87	SER	2.9
37	2f	97	PHE	2.9
41	2j	30	SER	2.9
48	2q	97	SER	2.9
38	1g	122	HIS	2.9
36	1e	89	ILE	2.9
5	1F	40	GLN	2.9
35	2d	21	LEU	2.9
38	1g	10	ARG	2.9
41	1j	66	ARG	2.9
43	1l	77	LEU	2.9
47	1p	73	LEU	2.9
8	1I	96	ASP	2.9
34	1c	45	LYS	2.9
1	1A	944	G	2.9
1	1A	1539	G	2.9
1	2A	272(B)	G	2.9
1	2A	2156	G	2.9
3	1D	237	GLU	2.9
6	2G	13	GLU	2.9
23	11	24	ALA	2.9
32	1a	181	G	2.9
32	1a	579	G	2.9
32	1a	1001(A)	G	2.9
32	1a	1294	G	2.9
32	2a	331	G	2.9
32	2a	493	G	2.9
32	2a	963	G	2.9
32	2a	1002	G	2.9
32	2a	1253	G	2.9
38	1g	128	ALA	2.9
40	1i	55	ALA	2.9
41	1j	95	GLU	2.9
47	1p	64	ALA	2.9
1	1A	1045	A	2.9
1	2A	901	A	2.9
32	1a	983	A	2.9
35	2d	178	VAL	2.9
6	1G	131	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
31	19	24	TYR	2.9
32	1a	454	C	2.9
32	1a	488	C	2.9
32	1a	624	C	2.9
32	1a	1114	C	2.9
32	1a	1208	C	2.9
32	2a	1027	C	2.9
32	2a	1090	U	2.9
42	2k	45	GLY	2.9
23	11	11	ARG	2.9
4	1E	129	HIS	2.9
5	2F	43	LYS	2.9
6	1G	135	LEU	2.9
12	1Q	17	LEU	2.9
22	20	36	ILE	2.9
37	2f	93	SER	2.9
33	1b	132	LYS	2.9
37	2f	92	LYS	2.9
38	2g	99	LEU	2.9
41	1j	16	LEU	2.9
45	2n	42	ILE	2.9
3	2D	166	GLN	2.9
34	1c	162	GLN	2.9
48	2q	26	GLN	2.9
38	2g	45	ASP	2.9
34	2c	189	ALA	2.9
41	1j	41	PRO	2.9
41	2j	41	PRO	2.9
41	2j	87	THR	2.9
49	2r	20	ALA	2.9
49	2r	60	ALA	2.9
22	10	12	ASN	2.9
23	11	27	GLU	2.9
25	13	60	GLU	2.9
48	1q	86	GLU	2.9
38	1g	21	VAL	2.9
17	2V	8	GLY	2.9
18	1W	46	PHE	2.9
20	2Y	35	TYR	2.9
22	20	69	PHE	2.9
26	14	17	GLY	2.9
39	1h	84	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
40	1i	16	ARG	2.9
47	1p	75	ARG	2.9
49	1r	32	ARG	2.9
51	2t	69	GLY	2.9
52	2u	24	ARG	2.9
1	1A	228	A	2.9
1	1A	1975	G	2.9
1	1A	2607	G	2.9
1	1A	2790	A	2.9
1	2A	1089	G	2.9
31	29	17	ILE	2.9
32	1a	42	G	2.9
32	1a	289	G	2.9
32	1a	572	A	2.9
6	1G	34	LEU	2.9
11	2P	1	MET	2.9
17	1V	25	LEU	2.9
32	1a	941	G	2.9
32	1a	971	G	2.9
32	1a	1266	G	2.9
32	1a	1331	G	2.9
32	2a	134	A	2.9
32	2a	438	G	2.9
32	2a	1042	G	2.9
32	2a	1156	G	2.9
32	2a	1357	A	2.9
34	2c	5	ILE	2.9
38	2g	73	MET	2.9
41	2j	16	LEU	2.9
43	1l	123	LYS	2.9
46	2o	58	MET	2.9
49	1r	58	LEU	2.9
50	1s	22	LEU	2.9
7	1H	111	HIS	2.8
41	2j	56	HIS	2.8
1	1A	269	U	2.8
11	1P	4	SER	2.8
1	1A	1974	C	2.8
1	1A	2118	U	2.8
1	2A	2144	U	2.8
32	1a	1281	U	2.8
32	2a	1097	C	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	1113	C	2.8
3	1D	247	ALA	2.8
12	1Q	31	ASP	2.8
20	1Y	69	ALA	2.8
33	1b	171	ALA	2.8
40	2i	55	ALA	2.8
10	2O	6	THR	2.8
41	2j	81	THR	2.8
50	1s	77	THR	2.8
41	2j	25	GLU	2.8
44	1m	67	GLU	2.8
4	1E	143	ASN	2.8
24	12	63	VAL	2.8
33	1b	136	VAL	2.8
38	1g	69	VAL	2.8
44	2m	64	TRP	2.8
3	1D	217	ARG	2.8
23	21	40	ARG	2.8
26	14	68	ARG	2.8
6	2G	105	LYS	2.8
6	1G	3	LEU	2.8
17	2V	70	ILE	2.8
18	1W	6	ILE	2.8
21	2Z	117	LEU	2.8
23	11	46	LEU	2.8
23	11	98	LEU	2.8
26	14	54	GLY	2.8
41	1j	11	PHE	2.8
41	1j	36	GLY	2.8
50	1s	84	GLY	2.8
50	2s	28	LYS	2.8
33	1b	42	ILE	2.8
33	2b	31	TYR	2.8
34	2c	178	LEU	2.8
35	1d	158	ILE	2.8
35	1d	196	LEU	2.8
36	2e	71	LEU	2.8
51	2t	96	GLY	2.8
7	1H	4	ILE	2.8
7	1H	92	ILE	2.8
47	1p	32	TYR	2.8
48	1q	88	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
50	2s	14	HIS	2.8
10	2O	3	GLN	2.8
34	1c	118	GLN	2.8
1	2A	536	A	2.8
1	2A	1069	A	2.8
32	2a	780	A	2.8
35	1d	71	SER	2.8
35	1d	208	SER	2.8
27	25	14	ALA	2.8
1	1A	271(X)	G	2.8
1	1A	418	G	2.8
1	1A	1538	G	2.8
1	2A	2304	G	2.8
32	1a	1272	G	2.8
32	1a	1323	G	2.8
32	2a	551	U	2.8
32	2a	1030(C)	G	2.8
32	2a	1216	G	2.8
35	1d	40	PRO	2.8
38	2g	14	PRO	2.8
50	1s	76	PRO	2.8
7	2H	57	ASP	2.8
1	1A	2475	C	2.8
1	2A	2295	C	2.8
2	1B	17	C	2.8
15	1T	21	GLU	2.8
26	24	30	GLU	2.8
40	1i	110	GLU	2.8
45	2n	22	THR	2.8
32	1a	194	C	2.8
32	1a	1147	C	2.8
32	1a	1383	C	2.8
32	2a	1298	C	2.8
33	2b	93	VAL	2.8
35	1d	159	ARG	2.8
38	1g	94	ARG	2.8
47	2p	34	GLU	2.8
52	1u	22	ARG	2.8
16	1U	13	LYS	2.8
33	1b	37	ASN	2.8
34	2c	199	LYS	2.8
17	1V	70	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
23	11	13	ILE	2.8
39	2h	35	ILE	2.8
23	11	43	TYR	2.8
48	1q	45	HIS	2.8
6	2G	26	GLN	2.8
35	1d	137	SER	2.8
40	1i	71	SER	2.8
51	1t	12	ALA	2.8
42	2k	39	PRO	2.8
48	1q	64	PRO	2.8
5	2F	6	VAL	2.8
33	1b	168	THR	2.8
33	2b	219	VAL	2.8
38	2g	75	VAL	2.8
44	2m	74	VAL	2.8
10	1O	44	LYS	2.8
39	1h	99	GLU	2.8
40	2i	127	LYS	2.8
41	1j	14	LYS	2.8
1	2A	6	A	2.8
32	1a	1130	A	2.8
5	2F	172	TRP	2.8
14	2S	58	LEU	2.8
32	2a	1257	U	2.8
33	1b	152	PHE	2.8
34	2c	94	LEU	2.8
38	1g	16	LEU	2.8
23	21	22	GLY	2.8
34	2c	124	ILE	2.8
43	1l	88	GLY	2.8
45	2n	55	GLY	2.8
50	1s	26	GLY	2.8
1	1A	1836	C	2.8
9	1N	72	TYR	2.8
14	1S	36	TYR	2.8
32	1a	113	G	2.8
32	1a	390	C	2.8
32	1a	391	G	2.8
32	1a	993	G	2.8
32	1a	1243	C	2.8
32	1a	1514	C	2.8
32	2a	276	G	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	490	G	2.8
32	2a	1032	G	2.8
35	2d	207	TYR	2.8
34	2c	69	HIS	2.8
6	2G	110	ALA	2.8
34	2c	187	ALA	2.8
50	2s	50	ALA	2.8
24	12	7	ARG	2.8
28	16	50	ARG	2.8
29	17	23	ARG	2.8
48	2q	81	ARG	2.8
52	2u	22	ARG	2.8
6	2G	10	LYS	2.8
8	2I	119	PRO	2.8
10	1O	4	PRO	2.8
11	1P	2	LYS	2.8
11	2P	145	PRO	2.8
21	2Z	116	VAL	2.8
26	24	7	PRO	2.8
29	27	14	LYS	2.8
34	2c	20	SER	2.8
34	2c	147	LYS	2.8
38	2g	105	VAL	2.8
40	2i	118	LYS	2.8
44	2m	45	VAL	2.8
17	2V	7	THR	2.8
36	2e	83	GLU	2.8
41	1j	83	GLU	2.8
44	1m	37	THR	2.8
48	2q	78	GLU	2.8
6	2G	101	ILE	2.8
12	1Q	29	PHE	2.8
33	2b	163	PHE	2.8
34	1c	57	ILE	2.8
34	1c	167	TRP	2.8
36	1e	124	GLY	2.8
14	2S	61	ASN	2.8
1	2A	1081	U	2.8
6	2G	12	TYR	2.8
32	1a	1001	A	2.8
32	1a	1040	U	2.8
32	2a	949	A	2.8

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Mol	Chain	Res	Type	RSRZ
32	2a	1044	A	2.8
32	2a	1085	U	2.8
32	2a	1130	A	2.8
32	2a	1180	A	2.8
35	1d	20	TYR	2.8
33	1b	140	HIS	2.8
16	1U	33	ARG	2.8
17	1V	88	ARG	2.8
30	28	42	ARG	2.8
31	29	18	ARG	2.8
31	29	22	ARG	2.8
32	2a	1109	C	2.8
32	2a	1218	C	2.8
33	1b	77	ALA	2.8
34	1c	168	ALA	2.8
35	2d	73	ARG	2.8
43	1l	30	ALA	2.8
44	2m	110	ARG	2.8
47	2p	28	ARG	2.8
32	1a	201	C	2.8
32	1a	1028	C	2.8
7	1H	10	PRO	2.8
7	1H	154	PRO	2.8
7	2H	11	VAL	2.8
32	1a	774	G	2.8
32	1a	1274	G	2.8
32	2a	993	G	2.8
32	2a	1131	G	2.8
32	2a	1233	G	2.8
38	2g	66	VAL	2.8
38	2g	71	PRO	2.8
48	1q	56	VAL	2.8
48	2q	35	VAL	2.8
30	28	37	SER	2.8
40	1i	50	LEU	2.8
47	2p	60	LEU	2.8
49	1r	78	LEU	2.8
28	16	12	GLU	2.8
36	2e	137	GLU	2.8
26	14	15	ILE	2.8
46	2o	15	PHE	2.7
47	1p	45	THR	2.8

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Mol	Chain	Res	Type	RSRZ
48	1q	90	ILE	2.8
4	1E	194	GLY	2.7
6	1G	116	ASP	2.7
14	2S	30	ARG	2.7
15	2T	54	ARG	2.7
34	2c	176	HIS	2.7
50	1s	47	HIS	2.7
16	1U	16	LYS	2.7
29	27	45	ALA	2.7
41	2j	26	ALA	2.7
43	1l	23	LYS	2.7
17	1V	52	VAL	2.7
21	2Z	73	GLN	2.7
32	1a	1073	U	2.7
32	2a	994	A	2.7
32	2a	1091	U	2.7
32	2a	1123	A	2.7
32	2a	1183	A	2.7
34	2c	66	VAL	2.7
7	1H	71	LEU	2.7
33	1b	155	LEU	2.7
33	2b	98	LEU	2.7
35	2d	135	LEU	2.7
35	2d	157	LEU	2.7
1	2A	888	C	2.7
7	1H	70	THR	2.7
8	2I	41	GLU	2.7
15	1T	1	MET	2.7
23	21	38	SER	2.7
26	14	26	SER	2.7
26	14	24	THR	2.7
32	1a	100	C	2.7
32	1a	1209	C	2.7
32	1a	1214	C	2.7
32	2a	1043	C	2.7
45	1n	8	GLU	2.7
4	1E	161	GLY	2.7
34	1c	13	GLY	2.7
41	2j	36	GLY	2.7
47	2p	37	GLY	2.7
17	1V	26	ASP	2.7
32	1a	104	G	2.7

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Mol	Chain	Res	Type	RSRZ
32	1a	251	G	2.7
32	1a	1304	G	2.7
32	2a	1030(A)	G	2.7
32	2a	1271	G	2.7
35	2d	134	ASP	2.7
44	1m	3	ARG	2.7
45	2n	12	ARG	2.7
46	1o	64	ARG	2.7
28	16	20	ASN	2.7
40	1i	114	TYR	2.7
33	1b	237	ALA	2.7
33	2b	123	ALA	2.7
40	1i	84	ALA	2.7
51	1t	66	ALA	2.7
7	1H	44	VAL	2.7
38	1g	86	GLN	2.7
38	2g	61	VAL	2.7
40	2i	3	GLN	2.7
6	1G	120	LEU	2.7
7	2H	8	PRO	2.7
8	2I	30	LEU	2.7
14	1S	80	LEU	2.7
40	1i	56	LEU	2.7
1	2A	1082	U	2.7
3	1D	15	PHE	2.7
3	1D	49	ILE	2.7
6	1G	63	ILE	2.7
7	1H	162	ILE	2.7
8	1I	4	ILE	2.7
8	1I	79	ILE	2.7
32	1a	125	U	2.7
32	2a	1219	U	2.7
32	2a	1281	U	2.7
33	2b	68	ILE	2.7
36	2e	11	ILE	2.7
38	2g	49	ILE	2.7
39	1h	86	ILE	2.7
48	1q	60	ILE	2.7
50	1s	62	ILE	2.7
1	2A	899	A	2.7
1	2A	1932	A	2.7
3	1D	32	SER	2.7

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Mol	Chain	Res	Type	RSRZ
20	2Y	104	GLY	2.7
32	1a	431	A	2.7
32	1a	1213	A	2.7
32	2a	974	A	2.7
32	2a	977	A	2.7
32	2a	1332	A	2.7
32	2a	1377	A	2.7
35	1d	44	GLY	2.7
43	1l	29	GLY	2.7
41	2j	45	ARG	2.7
48	2q	72	ARG	2.7
43	2l	17	LYS	2.7
45	2n	11	LYS	2.7
1	1A	2317	C	2.7
1	2A	2129	C	2.7
1	2A	2297	C	2.7
2	2B	2	C	2.7
15	2T	26	ASP	2.7
32	1a	178	C	2.7
32	1a	1325	C	2.7
34	2c	201	TYR	2.7
3	1D	224	ALA	2.7
20	2Y	65	ALA	2.7
22	10	18	ALA	2.7
34	1c	163	ALA	2.7
37	1f	100	ASN	2.7
38	2g	7	ALA	2.7
20	1Y	72	VAL	2.7
38	1g	91	VAL	2.7
40	2i	65	VAL	2.7
6	2G	43	LEU	2.7
9	2N	138	LEU	2.7
35	2d	78	LEU	2.7
39	1h	127	LEU	2.7
47	1p	60	LEU	2.7
1	2A	272	G	2.7
1	2A	2120	G	2.7
15	1T	123	GLN	2.7
32	1a	505	G	2.7
32	2a	107	G	2.7
32	2a	742	G	2.7
32	2a	761	G	2.7

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Mol	Chain	Res	Type	RSRZ
48	1q	2	PRO	2.7
35	2d	67	ILE	2.7
36	2e	10	MET	2.7
47	1p	9	PHE	2.7
3	2D	60	ARG	2.7
6	2G	9	ARG	2.7
7	1H	101	ARG	2.7
7	2H	82	GLY	2.7
15	1T	47	GLY	2.7
21	2Z	84	GLU	2.7
44	2m	69	GLU	2.7
48	2q	96	GLU	2.7
22	10	44	ARG	2.7
11	1P	25	SER	2.7
12	2Q	98	LYS	2.7
16	1U	19	LYS	2.7
23	21	34	THR	2.7
34	2c	131	ARG	2.7
44	1m	11	ARG	2.7
44	1m	57	ARG	2.7
47	2p	25	ARG	2.7
30	18	19	SER	2.7
33	2b	132	LYS	2.7
45	2n	61	TRP	2.7
49	1r	68	LYS	2.7
51	1t	82	SER	2.7
1	1A	305	U	2.7
1	1A	1963	U	2.7
2	1B	41	U	2.7
32	1a	114	U	2.7
32	1a	561	U	2.7
32	1a	841	U	2.7
1	2A	1070	A	2.7
32	1a	162	A	2.7
32	2a	263	A	2.7
32	2a	439	A	2.7
32	2a	655	A	2.7
32	2a	1170	A	2.7
6	2G	146	TYR	2.7
16	1U	41	ALA	2.7
16	1U	76	TYR	2.7
38	1g	108	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
7	2H	7	LEU	2.7
17	2V	79	VAL	2.7
23	11	30	VAL	2.7
26	14	35	VAL	2.7
33	1b	121	LEU	2.7
34	1c	116	VAL	2.7
35	2d	194	LEU	2.7
36	2e	139	LEU	2.7
41	2j	94	VAL	2.7
47	2p	2	VAL	2.7
49	1r	76	LEU	2.7
1	1A	2461	C	2.7
6	1G	41	GLN	2.7
8	2I	80	PRO	2.7
32	1a	948	C	2.7
32	1a	1282	C	2.7
32	2a	1051	C	2.7
35	1d	33	MET	2.7
37	2f	89	MET	2.7
3	2D	239	ARG	2.7
15	1T	93	ARG	2.7
16	1U	59	ARG	2.7
44	1m	104	ARG	2.7
6	2G	67	LYS	2.7
15	2T	109	GLU	2.7
33	1b	128	GLU	2.7
40	2i	39	GLY	2.7
44	2m	61	GLU	2.7
44	2m	86	CYS	2.7
45	1n	11	LYS	2.7
45	1n	38	GLY	2.7
50	2s	84	GLY	2.7
52	1u	2	GLY	2.7
6	2G	145	THR	2.7
41	1j	92	THR	2.7
1	1A	352	G	2.7
1	2A	2100	G	2.7
1	2A	2751	G	2.7
32	1a	1166	G	2.7
32	1a	1265	G	2.7
32	2a	1009	G	2.7
32	2a	1220	G	2.7

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Mol	Chain	Res	Type	RSRZ
32	2a	1304	G	2.7
32	2a	1331	G	2.7
8	1I	42	SER	2.7
15	1T	126	ALA	2.7
16	1U	115	ALA	2.7
19	2X	34	ALA	2.7
34	1c	133	ALA	2.7
38	1g	46	ALA	2.7
1	1A	2332	U	2.7
5	1F	181	LEU	2.7
6	1G	160	VAL	2.7
7	1H	114	VAL	2.7
8	2I	35	LEU	2.7
19	1X	59	VAL	2.7
21	2Z	58	VAL	2.7
25	13	53	LEU	2.7
32	1a	672	U	2.7
32	1a	997	U	2.7
32	1a	1012	U	2.7
32	2a	1070	U	2.7
34	2c	34	LEU	2.7
34	2c	111	LEU	2.7
36	1e	61	TYR	2.7
37	2f	91	VAL	2.7
44	1m	66	LEU	2.7
10	1O	81	ASP	2.7
18	1W	63	ASP	2.7
21	1Z	123	ASP	2.7
1	1A	996	A	2.6
1	2A	655	A	2.6
18	2W	6	ILE	2.6
14	1S	29	PHE	2.6
32	1a	1329	A	2.6
32	2a	453	A	2.6
32	2a	1229	A	2.6
33	2b	42	ILE	2.6
36	1e	101	ILE	2.6
43	1l	48	PRO	2.6
33	1b	90	MET	2.6
4	1E	76	ARG	2.6
19	2X	60	ARG	2.6
39	1h	91	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
40	1i	111	ARG	2.6
47	1p	57	ARG	2.6
47	2p	71	ARG	2.6
49	2r	35	ARG	2.6
14	1S	11	LYS	2.6
21	2Z	198	LYS	2.6
35	1d	166	LYS	2.6
1	1A	1383	C	2.6
1	1A	2103	C	2.6
1	2A	893	C	2.6
1	2A	1124	C	2.6
23	1l	75	GLU	2.6
32	1a	618	C	2.6
32	2a	756	C	2.6
32	2a	1230	C	2.6
34	1c	35	GLU	2.6
34	1c	90	GLU	2.6
35	1d	15	GLU	2.6
6	2G	162	THR	2.6
7	1H	129	THR	2.6
7	1H	150	ALA	2.6
8	2I	92	VAL	2.6
11	1P	99	LEU	2.6
14	1S	53	SER	2.6
14	1S	54	LEU	2.6
20	1Y	67	LEU	2.6
21	2Z	163	LEU	2.6
24	22	19	VAL	2.6
33	1b	62	ALA	2.6
33	2b	71	VAL	2.6
37	1f	19	LEU	2.6
38	2g	22	LEU	2.6
38	2g	141	VAL	2.6
42	2k	105	VAL	2.6
44	2m	96	LEU	2.6
46	2o	27	VAL	2.6
50	1s	30	LEU	2.6
21	1Z	9	TYR	2.6
38	2g	85	TYR	2.6
43	1l	98	TYR	2.6
51	1t	16	HIS	2.6
1	2A	1110	G	2.6

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Mol	Chain	Res	Type	RSRZ
3	2D	64	ILE	2.6
18	1W	96	ILE	2.6
30	28	16	ILE	2.6
6	1G	136	ARG	2.6
1	1A	271(K)	U	2.6
6	2G	108	ASN	2.6
7	2H	21	PRO	2.6
8	2I	8	PRO	2.6
32	1a	305	G	2.6
32	1a	769	G	2.6
32	1a	1422	G	2.6
32	2a	473	G	2.6
32	2a	1530	G	2.6
34	2c	202	ILE	2.6
42	1k	83	ILE	2.6
44	2m	16	ASP	2.6
12	2Q	141	GLN	2.6
14	2S	12	PHE	2.6
22	20	70	GLN	2.6
26	24	69	LYS	2.6
33	1b	96	ARG	2.6
34	2c	7	PRO	2.6
38	2g	4	ARG	2.6
35	2d	160	GLN	2.6
7	1H	66	GLY	2.6
34	1c	41	GLY	2.6
40	2i	80	GLY	2.6
42	2k	76	GLY	2.6
1	1A	294	A	2.6
1	1A	528	A	2.6
1	1A	1970	A	2.6
1	2A	718	A	2.6
1	2A	1088	A	2.6
2	1B	53	A	2.6
11	2P	74	GLU	2.6
21	2Z	181	GLU	2.6
32	1a	1168	A	2.6
32	2a	1238	A	2.6
44	1m	50	GLU	2.6
44	2m	73	GLU	2.6
14	2S	21	THR	2.6
21	2Z	107	THR	2.6

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Mol	Chain	Res	Type	RSRZ
26	14	27	THR	2.6
34	2c	177	THR	2.6
9	2N	23	LEU	2.6
21	2Z	90	VAL	2.6
47	1p	6	LEU	2.6
48	2q	89	LEU	2.6
51	1t	72	LEU	2.6
1	1A	419	C	2.6
1	1A	885	C	2.6
1	1A	1881	C	2.6
1	2A	1297	C	2.6
1	2A	2143	C	2.6
32	1a	1038	C	2.6
32	1a	1388	C	2.6
38	1g	92	SER	2.6
42	1k	59	TYR	2.6
23	11	23	LYS	2.6
29	27	47	ARG	2.6
36	2e	121	LYS	2.6
38	2g	10	ARG	2.6
41	1j	7	LYS	2.6
42	1k	91	ARG	2.6
44	2m	80	ARG	2.6
3	2D	249	PRO	2.6
5	1F	202	PHE	2.6
10	2O	1	MET	2.6
12	1Q	99	PRO	2.6
21	2Z	83	PRO	2.6
26	24	41	PRO	2.6
36	2e	45	PHE	2.6
40	1i	33	PHE	2.6
6	1G	150	ASP	2.6
8	2I	54	GLN	2.6
15	2T	107	ASP	2.6
41	2j	76	ASN	2.6
11	2P	116	GLY	2.6
33	2b	38	GLY	2.6
40	2i	69	GLY	2.6
48	1q	33	GLY	2.6
1	1A	557	U	2.6
1	2A	2522	U	2.6
7	2H	119	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
22	20	68	GLU	2.6
35	1d	156	GLU	2.6
38	1g	57	GLU	2.6
1	1A	879	G	2.6
1	1A	1443	G	2.6
32	1a	377	G	2.6
32	1a	1047	G	2.6
32	1a	1173	G	2.6
32	2a	774	G	2.6
3	1D	95	LEU	2.6
8	1I	5	LEU	2.6
22	20	75	LEU	2.6
40	1i	96	LEU	2.6
6	2G	70	VAL	2.6
8	1I	94	ALA	2.6
20	1Y	100	ALA	2.6
26	14	50	VAL	2.6
35	1d	88	VAL	2.6
35	2d	112	VAL	2.6
45	1n	20	ALA	2.6
48	2q	23	VAL	2.6
1	1A	422	A	2.6
2	1B	46	A	2.6
5	1F	135	LYS	2.6
5	2F	107	LYS	2.6
6	2G	36	LYS	2.6
19	1X	8	ILE	2.6
20	1Y	34	LYS	2.6
32	1a	1005	A	2.6
35	1d	132	ARG	2.6
41	2j	5	ARG	2.6
48	2q	75	ARG	2.6
30	18	37	SER	2.6
34	2c	77	ILE	2.6
3	2D	226	MET	2.6
35	1d	43	HIS	2.6
33	1b	28	PHE	2.6
35	2d	29	PRO	2.6
1	1A	1983	C	2.6
1	1A	2146	C	2.6
1	2A	1064	C	2.6
1	2A	2146	C	2.6

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Mol	Chain	Res	Type	RSRZ
30	28	43	GLN	2.6
32	1a	221	C	2.6
32	1a	1322	C	2.6
24	12	52	ASP	2.6
33	1b	135	GLN	2.6
38	1g	45	ASP	2.6
40	1i	124	GLN	2.6
12	1Q	24	GLY	2.6
35	2d	87	GLY	2.6
35	2d	180	GLY	2.6
37	1f	11	ASN	2.6
15	1T	78	LEU	2.6
17	1V	53	GLU	2.6
25	13	57	GLU	2.6
33	1b	154	LEU	2.6
35	1d	135	LEU	2.6
36	1e	123	LEU	2.6
40	2i	99	LEU	2.6
41	2j	97	GLU	2.6
44	2m	81	LEU	2.6
6	2G	163	ALA	2.6
22	10	23	VAL	2.6
36	1e	90	VAL	2.6
39	1h	93	VAL	2.6
50	1s	19	VAL	2.6
4	1E	19	ARG	2.6
13	1R	45	ARG	2.6
18	1W	100	THR	2.6
32	1a	173	U	2.6
32	1a	1065	U	2.6
36	1e	15	ARG	2.6
43	1l	6	THR	2.6
46	1o	47	LYS	2.6
1	1A	271(W)	G	2.6
1	1A	1055	G	2.6
1	1A	2893	G	2.6
1	2A	1112	G	2.6
32	1a	105	G	2.6
32	1a	629	G	2.6
32	1a	1072	G	2.6
32	1a	1117	G	2.6
32	2a	945	G	2.6

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Mol	Chain	Res	Type	RSRZ
32	2a	1293	G	2.6
32	2a	1386	G	2.6
39	2h	58	TYR	2.6
42	2k	22	HIS	2.6
7	2H	118	PRO	2.6
1	2A	819	A	2.6
12	1Q	12	GLN	2.6
30	18	35	GLN	2.6
6	2G	24	GLY	2.6
11	2P	28	GLY	2.6
35	1d	87	GLY	2.6
39	2h	71	GLY	2.6
6	2G	130	ASN	2.6
14	2S	48	LEU	2.6
1	1A	2179	C	2.6
8	1I	7	GLU	2.6
3	2D	221	VAL	2.6
32	1a	1223	C	2.6
32	2a	369	C	2.6
32	2a	1019	C	2.6
32	2a	1203	C	2.6
32	2a	1303	C	2.6
34	1c	19	GLU	2.6
6	1G	115	ARG	2.6
15	1T	53	ARG	2.6
23	21	49	VAL	2.6
33	1b	144	ARG	2.6
34	1c	75	VAL	2.6
33	1b	179	LYS	2.6
34	1c	121	ALA	2.6
36	2e	55	VAL	2.6
40	2i	28	VAL	2.6
40	2i	84	ALA	2.6
48	1q	5	VAL	2.6
18	1W	49	LYS	2.6
21	2Z	199	LYS	2.6
21	2Z	201	LYS	2.6
22	20	46	LYS	2.6
37	1f	92	LYS	2.6
48	1q	3	LYS	2.6
9	2N	63	THR	2.6
11	1P	32	THR	2.6

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Mol	Chain	Res	Type	RSRZ
44	2m	105	THR	2.6
47	2p	67	THR	2.6
11	2P	60	MET	2.5
1	2A	1097	U	2.5
3	1D	84	TYR	2.5
16	1U	72	HIS	2.5
8	1I	8	PRO	2.5
24	22	18	PRO	2.5
33	1b	26	PRO	2.5
33	2b	167	PRO	2.5
47	1p	41	PRO	2.5
20	2Y	17	SER	2.5
22	20	16	SER	2.5
9	2N	69	GLN	2.5
14	2S	38	GLN	2.5
5	1F	192	LEU	2.5
6	1G	43	LEU	2.5
19	2X	9	LEU	2.5
33	1b	61	LEU	2.5
35	1d	94	LEU	2.5
36	1e	71	LEU	2.5
39	2h	119	LEU	2.5
1	1A	2482	G	2.5
1	1A	2833	G	2.5
1	2A	100	G	2.5
2	1B	16	G	2.5
4	1E	57	LYS	2.5
7	1H	52	VAL	2.5
7	2H	3	ARG	2.5
21	2Z	79	ARG	2.5
22	10	71	ASP	2.5
12	2Q	139	GLU	2.5
23	11	48	LYS	2.5
31	19	25	VAL	2.5
32	1a	1143	G	2.5
32	2a	104	G	2.5
32	2a	505	G	2.5
32	2a	644	G	2.5
32	2a	786	G	2.5
34	1c	64	VAL	2.5
36	1e	92	LYS	2.5
36	2e	126	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
37	2f	7	ASN	2.5
38	1g	28	ASN	2.5
41	1j	89	ASP	2.5
41	2j	12	ASP	2.5
41	2j	28	ARG	2.5
43	2l	104	VAL	2.5
46	2o	47	LYS	2.5
47	1p	40	ASP	2.5
47	2p	81	ARG	2.5
48	2q	56	VAL	2.5
50	2s	13	ASP	2.5
52	2u	7	ARG	2.5
32	2a	1093	A	2.5
34	1c	24	ALA	2.5
37	1f	66	GLU	2.5
51	1t	60	GLU	2.5
52	2u	20	LYS	2.5
1	1A	890	A	2.5
1	1A	2412	A	2.5
1	2A	653	A	2.5
32	1a	172	A	2.5
32	1a	432	A	2.5
32	1a	1041	A	2.5
32	1a	1339	A	2.5
7	1H	122	THR	2.5
28	16	30	THR	2.5
41	1j	15	THR	2.5
41	2j	82	ILE	2.5
1	1A	964	C	2.5
1	1A	1532	C	2.5
32	1a	508	C	2.5
32	2a	443	C	2.5
32	2a	549	C	2.5
32	2a	1145	C	2.5
32	2a	1378	C	2.5
34	2c	128	PHE	2.5
48	2q	27	PHE	2.5
50	1s	10	PHE	2.5
6	1G	17	PRO	2.5
7	1H	164	TYR	2.5
16	1U	24	TYR	2.5
48	2q	30	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
5	2F	15	SER	2.5
1	2A	272(A)	U	2.5
1	2A	2113	U	2.5
7	2H	166	GLY	2.5
17	2V	67	GLY	2.5
22	10	9	SER	2.5
11	1P	68	GLN	2.5
26	24	19	GLY	2.5
32	1a	991	U	2.5
32	2a	1049	U	2.5
33	1b	180	LEU	2.5
41	2j	90	LEU	2.5
11	1P	16	ARG	2.5
14	2S	76	LYS	2.5
26	14	58	ARG	2.5
46	2o	79	ARG	2.5
47	1p	8	ARG	2.5
48	1q	40	LYS	2.5
7	1H	99	VAL	2.5
22	10	38	VAL	2.5
33	2b	229	VAL	2.5
34	2c	103	VAL	2.5
36	2e	82	VAL	2.5
37	2f	85	VAL	2.5
50	2s	45	VAL	2.5
5	1F	195	ASP	2.5
34	2c	65	ALA	2.5
38	1g	33	ASP	2.5
40	1i	29	ASN	2.5
44	1m	69	GLU	2.5
45	1n	46	GLU	2.5
47	1p	68	ASP	2.5
33	2b	32	ILE	2.5
35	1d	165	MET	2.5
36	2e	16	THR	2.5
47	1p	48	TRP	2.5
48	1q	82	MET	2.5
6	1G	125	PHE	2.5
38	1g	62	PHE	2.5
42	2k	125	PHE	2.5
1	1A	872	A	2.5
1	1A	2311	A	2.5

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Mol	Chain	Res	Type	RSRZ
1	2A	652(B)	A	2.5
32	1a	101	A	2.5
32	1a	607	A	2.5
32	1a	1513	A	2.5
32	2a	695	A	2.5
32	2a	1046	A	2.5
1	1A	295	G	2.5
1	1A	873	G	2.5
1	2A	1299	G	2.5
32	1a	147	G	2.5
32	1a	673	G	2.5
32	1a	1009	G	2.5
32	1a	1253	G	2.5
32	2a	61	G	2.5
32	2a	394	G	2.5
32	2a	428	G	2.5
32	2a	951	G	2.5
32	2a	1013	G	2.5
32	2a	1291	G	2.5
3	1D	11	PRO	2.5
6	2G	17	PRO	2.5
30	18	64	TYR	2.5
34	2c	31	HIS	2.5
37	1f	12	PRO	2.5
40	2i	4	TYR	2.5
50	1s	42	PRO	2.5
6	2G	175	LEU	2.5
1	1A	1124	C	2.5
1	1A	1548	C	2.5
1	1A	2297	C	2.5
4	1E	43	GLY	2.5
6	2G	177	GLY	2.5
7	1H	100	GLY	2.5
9	2N	80	GLY	2.5
10	2O	74	GLY	2.5
14	2S	13	ARG	2.5
14	2S	97	ARG	2.5
15	2T	115	ARG	2.5
17	2V	68	LYS	2.5
18	1W	92	ARG	2.5
32	1a	352	C	2.5
32	2a	817	C	2.5

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Mol	Chain	Res	Type	RSRZ
32	2a	1006	C	2.5
32	2a	1103	C	2.5
32	2a	1161	C	2.5
32	2a	1277	C	2.5
33	1b	66	GLY	2.5
36	1e	27	ARG	2.5
37	1f	87	ARG	2.5
39	2h	131	GLY	2.5
52	2u	3	LYS	2.5
10	1O	28	SER	2.5
34	1c	28	GLN	2.5
17	2V	52	VAL	2.5
33	2b	165	VAL	2.5
35	1d	112	VAL	2.5
38	1g	61	VAL	2.5
43	2l	90	VAL	2.5
45	2n	33	VAL	2.5
47	2p	21	VAL	2.5
51	1t	76	ALA	2.5
1	2A	421	U	2.5
24	22	5	GLU	2.5
32	2a	1341	U	2.5
41	1j	97	GLU	2.5
21	2Z	34	ASN	2.5
41	2j	73	ASP	2.5
48	1q	65	ILE	2.5
6	2G	155	MET	2.5
26	14	1	MET	2.5
3	1D	254	THR	2.5
11	2P	57	THR	2.5
21	2Z	170	THR	2.5
4	1E	189	PRO	2.5
4	1E	119	ARG	2.5
6	2G	176	LEU	2.5
7	1H	157	TYR	2.5
7	2H	61	HIS	2.5
9	1N	101	HIS	2.5
11	2P	16	ARG	2.5
14	1S	7	TYR	2.5
39	2h	72	PRO	2.5
14	2S	20	ARG	2.5
21	2Z	155	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
23	21	81	LYS	2.5
30	18	21	LYS	2.5
33	2b	155	LEU	2.5
34	2c	79	ARG	2.5
34	2c	190	ARG	2.5
35	2d	96	LEU	2.5
41	1j	9	ARG	2.5
43	2l	111	LYS	2.5
44	1m	31	LYS	2.5
47	1p	16	HIS	2.5
47	2p	35	LYS	2.5
49	2r	21	LYS	2.5
6	1G	85	GLY	2.5
15	1T	25	GLY	2.5
32	2a	101	A	2.5
9	2N	140	VAL	2.5
12	1Q	13	GLN	2.5
21	2Z	118	GLN	2.5
25	13	36	VAL	2.5
29	17	46	VAL	2.5
33	2b	76	GLN	2.5
33	2b	174	VAL	2.5
34	1c	151	VAL	2.5
34	2c	99	VAL	2.5
40	1i	44	VAL	2.5
1	1A	275	G	2.5
1	2A	271(M)	G	2.5
3	1D	272	ALA	2.5
12	1Q	20	ALA	2.5
14	1S	27	SER	2.5
32	1a	158	G	2.5
32	1a	493	G	2.5
32	1a	610	G	2.5
32	1a	724	G	2.5
32	1a	1013	G	2.5
32	1a	1024	G	2.5
32	2a	251	G	2.5
32	2a	306	G	2.5
32	2a	1089	G	2.5
32	2a	1215	G	2.5
32	2a	1356	G	2.5
33	1b	34	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	112	SER	2.5
38	1g	121	ALA	2.5
41	1j	30	SER	2.5
42	1k	43	SER	2.5
48	2q	39	SER	2.5
12	1Q	66	ILE	2.5
12	2Q	91	GLU	2.5
14	1S	35	ILE	2.5
21	1Z	169	GLU	2.5
24	12	11	GLU	2.5
31	19	26	ILE	2.5
33	2b	129	GLU	2.5
34	1c	46	GLU	2.5
42	1k	21	ILE	2.5
1	1A	1640	C	2.5
1	2A	2105	C	2.5
32	1a	48	C	2.5
38	2g	31	MET	2.5
7	2H	123	PHE	2.5
21	2Z	75	ASN	2.5
21	2Z	148	ASP	2.5
38	1g	43	PHE	2.5
47	1p	29	ASP	2.5
1	2A	1060	U	2.5
3	1D	250	TRP	2.5
4	1E	12	THR	2.5
32	2a	956	U	2.5
32	2a	1083	U	2.5
50	1s	48	THR	2.5
7	1H	130	ARG	2.5
10	2O	64	ARG	2.5
12	2Q	82	ARG	2.5
26	14	55	ARG	2.5
26	14	69	LYS	2.5
29	27	41	ARG	2.5
31	29	15	LYS	2.5
33	1b	27	LYS	2.5
35	1d	59	ARG	2.5
36	2e	27	ARG	2.5
44	2m	91	ARG	2.5
47	1p	25	ARG	2.5
50	1s	70	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
3	1D	232	PRO	2.5
21	2Z	144	LEU	2.5
35	1d	197	PRO	2.5
37	1f	43	LEU	2.5
47	1p	46	PRO	2.5
7	1H	61	HIS	2.5
40	1i	88	TYR	2.5
7	1H	174	GLY	2.5
12	1Q	108	GLY	2.5
35	1d	23	GLY	2.5
35	1d	167	GLY	2.5
40	2i	67	GLY	2.5
40	2i	115	GLY	2.5
43	1l	63	GLY	2.5
6	1G	28	VAL	2.5
7	2H	114	VAL	2.5
33	1b	81	VAL	2.5
34	1c	207	VAL	2.5
39	1h	19	VAL	2.5
43	2l	40	VAL	2.5
44	2m	53	VAL	2.5
34	1c	104	GLN	2.5
40	2i	87	GLN	2.5
46	1o	28	GLN	2.5
12	1Q	140	ALA	2.4
15	2T	116	ALA	2.4
34	2c	92	ALA	2.4
50	1s	75	ALA	2.4
3	2D	49	ILE	2.4
7	2H	121	ILE	2.4
11	1P	56	SER	2.4
26	14	31	ILE	2.4
38	2g	47	CYS	2.4
41	2j	6	ILE	2.4
43	1l	37	CYS	2.4
45	1n	24	CYS	2.4
45	1n	27	CYS	2.4
47	1p	4	ILE	2.4
1	1A	1932	A	2.4
1	1A	1969	A	2.4
1	2A	1913	A	2.4
6	1G	14	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
32	1a	487	A	2.4
32	2a	968	A	2.4
32	2a	1146	A	2.4
33	1b	12	GLU	2.4
33	2b	12	GLU	2.4
40	2i	35	GLU	2.4
40	1i	59	PHE	2.4
3	2D	263	ARG	2.4
5	2F	137	LYS	2.4
6	2G	40	ASN	2.4
24	12	51	ARG	2.4
35	1d	77	ASN	2.4
36	1e	126	ARG	2.4
39	1h	18	ARG	2.4
40	1i	116	LYS	2.4
43	2l	47	LYS	2.4
1	1A	928	G	2.4
1	1A	1770	G	2.4
1	1A	1980	G	2.4
1	1A	2483	C	2.4
1	2A	2308	G	2.4
2	1B	50	G	2.4
2	2B	23	G	2.4
17	1V	7	THR	2.4
19	1X	56	THR	2.4
19	2X	95	LEU	2.4
32	1a	376	G	2.4
32	1a	455	C	2.4
32	1a	567	G	2.4
32	1a	674	G	2.4
32	1a	1002	G	2.4
32	1a	1030(C)	G	2.4
32	2a	39	G	2.4
32	2a	110	C	2.4
32	2a	785	G	2.4
32	2a	878	G	2.4
32	2a	931	C	2.4
32	2a	1147	C	2.4
32	2a	1214	C	2.4
6	1G	122	PRO	2.4
42	1k	121	PRO	2.4
1	1A	1105	U	2.4

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Mol	Chain	Res	Type	RSRZ
1	2A	504	U	2.4
32	1a	619	U	2.4
32	1a	850	U	2.4
32	1a	1000	U	2.4
32	2a	404	U	2.4
33	2b	236	TYR	2.4
6	2G	159	VAL	2.4
14	2S	49	VAL	2.4
21	1Z	196	VAL	2.4
23	11	79	GLY	2.4
23	21	28	GLY	2.4
31	19	7	VAL	2.4
34	1c	173	VAL	2.4
35	1d	16	GLY	2.4
35	2d	8	VAL	2.4
37	1f	88	VAL	2.4
3	1D	225	ALA	2.4
3	2D	253	GLN	2.4
11	1P	141	ALA	2.4
36	1e	134	ALA	2.4
38	1g	65	ALA	2.4
6	2G	144	ILE	2.4
16	1U	17	ILE	2.4
39	2h	111	ILE	2.4
30	28	25	MET	2.4
14	2S	31	SER	2.4
21	1Z	97	GLU	2.4
38	1g	113	GLU	2.4
42	1k	16	SER	2.4
6	1G	181	ARG	2.4
9	2N	89	LYS	2.4
15	1T	108	ARG	2.4
17	1V	10	LYS	2.4
24	12	37	PHE	2.4
27	25	13	LYS	2.4
40	2i	111	ARG	2.4
41	2j	60	ARG	2.4
47	2p	8	ARG	2.4
47	2p	55	ARG	2.4
50	1s	3	ARG	2.4
51	1t	29	LYS	2.4
51	1t	58	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
34	1c	12	LEU	2.4
35	2d	101	LEU	2.4
48	1q	74	LEU	2.4
1	1A	1046	A	2.4
23	1l	34	THR	2.4
41	1j	12	ASP	2.4
43	1l	122	THR	2.4
44	1m	105	THR	2.4
44	2m	103	THR	2.4
49	1r	82	THR	2.4
51	2t	26	ASN	2.4
32	1a	8	A	2.4
32	1a	958	A	2.4
32	1a	1238	A	2.4
32	2a	572	A	2.4
32	2a	965	A	2.4
32	2a	1507	A	2.4
33	2b	189	ASP	2.4
34	1c	114	PRO	2.4
3	2D	138	VAL	2.4
3	2D	243	GLY	2.4
4	1E	190	GLY	2.4
5	2F	208	GLY	2.4
7	2H	99	VAL	2.4
21	2Z	99	TYR	2.4
21	2Z	143	GLY	2.4
33	2b	19	HIS	2.4
36	2e	133	TYR	2.4
45	1n	51	GLY	2.4
46	2o	11	VAL	2.4
50	2s	80	TYR	2.4
1	2A	964	C	2.4
17	2V	59	ALA	2.4
32	1a	43	C	2.4
32	1a	175	C	2.4
32	2a	43	C	2.4
32	2a	863	U	2.4
32	2a	1124	G	2.4
32	2a	1265	G	2.4
32	2a	1307	U	2.4
33	1b	39	ILE	2.4
33	1b	208	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
44	2m	28	ALA	2.4
1	1A	11	G	2.4
1	1A	556	G	2.4
1	1A	1060	U	2.4
1	2A	271(K)	U	2.4
1	2A	879	G	2.4
1	2A	1533	G	2.4
1	2A	2339	G	2.4
1	2A	2644	G	2.4
32	1a	9	G	2.4
32	1a	734	G	2.4
32	1a	1083	U	2.4
35	1d	160	GLN	2.4
41	1j	84	GLN	2.4
44	2m	84	ILE	2.4
46	2o	71	GLN	2.4
36	1e	10	MET	2.4
41	2j	86	MET	2.4
5	1F	44	ARG	2.4
6	1G	182	LYS	2.4
6	2G	113	ARG	2.4
10	1O	97	ARG	2.4
14	2S	57	LYS	2.4
20	1Y	33	LYS	2.4
24	22	8	LYS	2.4
27	15	9	LYS	2.4
35	1d	85	LYS	2.4
42	1k	125	PHE	2.4
44	2m	29	ARG	2.4
48	2q	3	LYS	2.4
35	2d	156	GLU	2.4
8	1I	38	LEU	2.4
10	2O	21	CYS	2.4
13	1R	65	LEU	2.4
7	1H	118	PRO	2.4
12	1Q	21	THR	2.4
50	1s	34	TRP	2.4
39	1h	72	PRO	2.4
40	2i	123	PRO	2.4
44	1m	113	PRO	2.4
3	1D	118	VAL	2.4
7	1H	35	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
36	2e	148	VAL	2.4
50	2s	67	VAL	2.4
3	2D	58	HIS	2.4
3	2D	62	TYR	2.4
12	2Q	57	HIS	2.4
15	1T	71	GLY	2.4
23	21	31	GLY	2.4
26	14	32	TYR	2.4
41	1j	10	GLY	2.4
48	1q	32	TYR	2.4
51	2t	103	GLY	2.4
1	2A	918	A	2.4
1	2A	1073	A	2.4
4	2E	77	ILE	2.4
7	1H	151	ILE	2.4
9	1N	71	ILE	2.4
12	1Q	107	ALA	2.4
24	22	41	ILE	2.4
35	2d	164	ALA	2.4
32	1a	1176	A	2.4
32	2a	451	A	2.4
48	2q	59	ILE	2.4
3	1D	166	GLN	2.4
7	1H	13	LYS	2.4
12	2Q	18	LYS	2.4
21	1Z	14	LYS	2.4
23	11	19	GLN	2.4
36	2e	136	MET	2.4
37	1f	16	GLN	2.4
46	1o	58	MET	2.4
46	1o	71	GLN	2.4
7	1H	132	ARG	2.4
15	1T	111	ARG	2.4
16	2U	33	ARG	2.4
5	1F	129	PHE	2.4
14	2S	87	PHE	2.4
1	1A	108	U	2.4
1	1A	420	C	2.4
1	1A	2398	U	2.4
1	2A	2294	C	2.4
3	1D	61	LEU	2.4
3	1D	215	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
6	2G	103	LEU	2.4
9	2N	82	LEU	2.4
11	1P	52	GLU	2.4
16	1U	109	LEU	2.4
17	1V	18	LEU	2.4
19	2X	66	LEU	2.4
20	1Y	106	LEU	2.4
21	2Z	76	LEU	2.4
31	19	28	GLU	2.4
32	1a	330	C	2.4
32	1a	366	C	2.4
32	1a	526	C	2.4
32	1a	545	C	2.4
32	1a	1425	U	2.4
32	2a	188	C	2.4
32	2a	1038	C	2.4
32	2a	1098	C	2.4
36	1e	83	GLU	2.4
39	2h	22	GLU	2.4
49	2r	59	SER	2.4
1	1A	1106	G	2.4
1	1A	1355	G	2.4
1	2A	928	G	2.4
1	2A	1626	G	2.4
1	2A	2206	G	2.4
2	2B	103	G	2.4
32	1a	346	G	2.4
32	1a	661	G	2.4
32	1a	785	G	2.4
32	2a	1181	G	2.4
32	2a	1185	G	2.4
7	1H	39	PRO	2.4
7	1H	141	VAL	2.4
8	1I	18	VAL	2.4
8	1I	134	PRO	2.4
8	2I	111	PRO	2.4
23	11	44	PRO	2.4
25	13	59	VAL	2.4
34	2c	70	VAL	2.4
35	2d	172	PRO	2.4
41	2j	100	THR	2.4
43	1l	43	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
43	1l	101	VAL	2.4
44	1m	60	VAL	2.4
47	1p	22	THR	2.4
50	2s	48	THR	2.4
51	2t	98	PRO	2.4
11	1P	35	HIS	2.4
12	2Q	23	GLY	2.4
16	1U	81	HIS	2.4
21	2Z	179	ASP	2.4
30	18	38	GLY	2.4
30	28	38	GLY	2.4
47	2p	14	ASN	2.4
33	2b	193	ASP	2.4
34	1c	77	ILE	2.4
34	2c	184	TYR	2.4
37	2f	4	TYR	2.4
47	1p	47	ASP	2.4
48	2q	13	ASP	2.4
4	1E	187	ALA	2.4
15	1T	50	ILE	2.4
21	2Z	57	ILE	2.4
26	24	15	ILE	2.4
41	2j	98	ILE	2.4
3	2D	255	LYS	2.4
4	1E	8	LYS	2.4
14	2S	99	LYS	2.4
12	1Q	7	MET	2.4
12	2Q	7	MET	2.4
16	2U	28	ARG	2.4
38	2g	76	ARG	2.4
38	2g	114	ARG	2.4
40	1i	10	ARG	2.4
48	1q	91	ARG	2.4
49	1r	54	ARG	2.4
31	19	34	GLN	2.4
40	2i	38	GLN	2.4
8	1I	35	LEU	2.4
24	12	10	LEU	2.4
33	2b	145	LEU	2.4
34	2c	12	LEU	2.4
36	2e	151	LEU	2.4
39	2h	127	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
40	1i	85	LEU	2.4
46	2o	31	LEU	2.4
1	1A	1981	A	2.4
1	2A	1086	A	2.4
1	2A	1378	A	2.4
1	2A	1439	A	2.4
1	2A	2310	A	2.4
1	2A	2712(A)	A	2.4
6	1G	48	GLU	2.4
11	2P	149	GLU	2.4
17	2V	23	GLU	2.4
32	1a	151	A	2.4
32	1a	1204	A	2.4
32	1a	1236	A	2.4
32	1a	1377	A	2.4
33	2b	134	GLU	2.4
34	2c	58	GLU	2.4
44	1m	73	GLU	2.4
49	2r	46	GLU	2.4
11	2P	42	SER	2.4
35	1d	152	SER	2.4
42	2k	101	SER	2.4
1	1A	235	U	2.4
1	1A	1175	U	2.4
1	1A	1766	U	2.4
1	2A	913	U	2.4
30	28	34	TRP	2.4
32	2a	743	U	2.4
35	2d	7	PRO	2.4
44	1m	54	VAL	2.4
1	1A	271(B)	C	2.3
1	1A	436	C	2.3
1	1A	914	C	2.3
1	1A	1513	C	2.3
1	1A	1837	C	2.3
1	1A	2828	C	2.3
1	2A	967	C	2.3
1	2A	1043	C	2.3
1	2A	1298	C	2.3
2	2B	62	C	2.3
32	1a	401	C	2.3
32	1a	824	C	2.3

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Mol	Chain	Res	Type	RSRZ
32	1a	990	C	2.3
32	1a	1019	C	2.3
32	1a	1161	C	2.3
32	2a	754	C	2.3
32	2a	1063	C	2.3
32	2a	1366	C	2.3
3	1D	194	GLY	2.3
21	2Z	114	GLY	2.3
22	10	42	GLY	2.3
35	1d	127	THR	2.3
38	2g	24	THR	2.3
40	2i	72	GLY	2.3
51	1t	47	GLY	2.3
4	1E	64	LYS	2.3
4	1E	95	ILE	2.3
7	1H	89	ILE	2.3
8	1I	74	ASN	2.3
13	2R	17	ARG	2.3
21	2Z	187	ALA	2.3
26	24	31	ILE	2.3
28	16	32	ASN	2.3
34	1c	110	ASN	2.3
34	1c	129	ALA	2.3
35	2d	86	LYS	2.3
33	1b	193	ASP	2.3
34	2c	38	ARG	2.3
34	2c	113	ALA	2.3
34	2c	193	TYR	2.3
36	1e	30	ALA	2.3
36	1e	132	ALA	2.3
38	2g	53	LYS	2.3
44	2m	22	ILE	2.3
44	2m	79	LYS	2.3
45	2n	45	ARG	2.3
47	2p	36	ILE	2.3
49	2r	24	ALA	2.3
50	1s	6	LYS	2.3
5	1F	119	ARG	2.3
6	1G	12	TYR	2.3
6	1G	118	ARG	2.3
8	1I	89	TYR	2.3
10	1O	7	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
16	2U	56	ASP	2.3
47	2p	68	ASP	2.3
1	2A	2123	G	2.3
1	2A	2802	G	2.3
32	1a	576	G	2.3
32	1a	1031	G	2.3
32	1a	1042	G	2.3
32	1a	1241	G	2.3
32	1a	1300	G	2.3
32	1a	1338	G	2.3
4	1E	195	LEU	2.3
9	2N	116	LEU	2.3
13	1R	4	LEU	2.3
16	2U	27	LEU	2.3
21	2Z	41	LEU	2.3
33	2b	154	LEU	2.3
34	2c	162	GLN	2.3
34	2c	196	LEU	2.3
36	1e	151	LEU	2.3
41	2j	54	PHE	2.3
42	1k	13	GLN	2.3
4	2E	80	GLU	2.3
16	1U	108	GLU	2.3
21	1Z	186	GLU	2.3
36	2e	68	GLU	2.3
46	1o	14	GLU	2.3
48	2q	49	GLU	2.3
4	1E	59	VAL	2.3
7	1H	50	VAL	2.3
7	1H	107	VAL	2.3
9	2N	5	VAL	2.3
9	2N	46	VAL	2.3
17	2V	57	VAL	2.3
33	2b	164	VAL	2.3
9	1N	126	PRO	2.3
23	21	65	SER	2.3
23	21	86	SER	2.3
32	2a	197	A	2.3
32	2a	1030(D)	A	2.3
32	2a	1346	A	2.3
35	2d	208	SER	2.3
45	2n	60	SER	2.3

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Mol	Chain	Res	Type	RSRZ
48	1q	62	SER	2.3
48	2q	47	PRO	2.3
3	1D	40	THR	2.3
3	1D	42	GLY	2.3
4	2E	107	THR	2.3
7	1H	91	GLY	2.3
17	1V	84	LYS	2.3
17	2V	86	GLY	2.3
21	1Z	201	LYS	2.3
32	1a	1250	A	2.3
8	1I	76	THR	2.3
34	1c	185	GLY	2.3
35	2d	169	LYS	2.3
44	1m	94	ARG	2.3
44	2m	37	THR	2.3
45	2n	4	LYS	2.3
50	2s	25	LYS	2.3
15	2T	110	ILE	2.3
21	1Z	35	ARG	2.3
7	1H	96	ALA	2.3
16	1U	46	ALA	2.3
23	21	37	ILE	2.3
26	24	22	ILE	2.3
31	29	10	ILE	2.3
33	1b	214	ILE	2.3
35	2d	158	ILE	2.3
36	1e	76	ILE	2.3
43	1l	99	HIS	2.3
1	1A	2144	U	2.3
4	1E	192	ASN	2.3
12	2Q	93	TYR	2.3
15	1T	100	TYR	2.3
18	1W	9	TYR	2.3
32	1a	387	U	2.3
32	1a	820	U	2.3
32	1a	1345	U	2.3
37	2f	59	TYR	2.3
38	1g	37	ASN	2.3
1	1A	271(C)	C	2.3
1	1A	2145	C	2.3
1	1A	2474	C	2.3
1	2A	2103	C	2.3

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Mol	Chain	Res	Type	RSRZ
6	1G	147	ASP	2.3
32	1a	457	C	2.3
32	1a	726	C	2.3
32	1a	795	C	2.3
32	1a	1267	C	2.3
32	2a	121	C	2.3
32	2a	503	C	2.3
32	2a	1254	C	2.3
11	2P	51	PHE	2.3
33	2b	158	LEU	2.3
35	1d	110	PHE	2.3
40	1i	101	PHE	2.3
50	2s	20	LEU	2.3
17	2V	80	GLN	2.3
22	20	17	GLN	2.3
42	1k	99	GLN	2.3
26	14	57	GLU	2.3
34	1c	105	GLU	2.3
34	1c	125	GLU	2.3
36	2e	111	GLU	2.3
39	1h	77	GLU	2.3
1	1A	715	G	2.3
1	1A	1987	G	2.3
1	1A	2190	G	2.3
1	1A	2526	G	2.3
1	2A	642	G	2.3
1	2A	1059	G	2.3
4	1E	165	VAL	2.3
7	1H	49	VAL	2.3
7	1H	169	VAL	2.3
12	1Q	96	VAL	2.3
32	1a	111	G	2.3
32	1a	473	G	2.3
32	1a	1003	G	2.3
32	1a	1022	G	2.3
32	1a	1033	G	2.3
32	1a	1334	G	2.3
32	2a	524	G	2.3
32	2a	1079	G	2.3
32	2a	1266	G	2.3
42	1k	14	VAL	2.3
43	2l	55	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
3	1D	154	LYS	2.3
13	2R	74	LYS	2.3
16	1U	84	LYS	2.3
35	1d	22	LYS	2.3
37	2f	23	LYS	2.3
43	2l	115	LYS	2.3
51	1t	65	LYS	2.3
3	2D	245	PRO	2.3
6	1G	96	ARG	2.3
28	16	37	ARG	2.3
33	1b	159	PRO	2.3
33	1b	167	PRO	2.3
33	1b	234	PRO	2.3
33	2b	111	ARG	2.3
38	2g	58	PRO	2.3
43	1l	5	PRO	2.3
3	1D	238	GLY	2.3
4	1E	112	GLY	2.3
12	1Q	41	TRP	2.3
12	1Q	127	ILE	2.3
25	13	13	ILE	2.3
34	2c	22	TRP	2.3
46	2o	20	GLY	2.3
21	1Z	113	ALA	2.3
35	1d	117	ALA	2.3
38	2g	116	ALA	2.3
45	1n	5	ALA	2.3
48	1q	97	SER	2.3
49	1r	60	ALA	2.3
50	2s	24	ALA	2.3
4	1E	156	MET	2.3
4	2E	1	MET	2.3
10	1O	20	MET	2.3
26	24	25	TYR	2.3
34	1c	29	TYR	2.3
8	1I	6	LEU	2.3
14	2S	16	ASN	2.3
16	1U	94	ASN	2.3
20	2Y	92	ASN	2.3
28	16	11	LEU	2.3
35	1d	11	LEU	2.3
1	1A	330	A	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	1353	A	2.3
1	1A	2310	A	2.3
1	2A	1095	A	2.3
1	2A	2134	A	2.3
12	1Q	65	PHE	2.3
19	1X	28	PHE	2.3
32	1a	864	A	2.3
32	2a	1101	A	2.3
6	1G	97	ASP	2.3
18	2W	22	ASP	2.3
33	1b	195	ASP	2.3
32	1a	222	U	2.3
32	1a	1025	U	2.3
32	1a	1302	U	2.3
32	1a	1315	U	2.3
19	1X	15	GLU	2.3
35	2d	179	GLU	2.3
50	2s	64	GLU	2.3
2	1B	88	C	2.3
4	1E	185	LYS	2.3
8	1I	45	LYS	2.3
8	1I	136	VAL	2.3
8	2I	81	VAL	2.3
11	2P	113	LYS	2.3
30	18	44	LYS	2.3
32	1a	307	C	2.3
32	1a	883	C	2.3
32	2a	536	C	2.3
32	2a	1069	C	2.3
35	2d	17	VAL	2.3
37	1f	85	VAL	2.3
43	2l	23	LYS	2.3
47	2p	79	VAL	2.3
21	2Z	131	ARG	2.3
36	1e	14	ARG	2.3
36	1e	107	ARG	2.3
38	2g	119	ARG	2.3
39	1h	75	ARG	2.3
44	1m	88	ARG	2.3
44	1m	93	ARG	2.3
45	1n	35	ARG	2.3
46	1o	68	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
47	1p	81	ARG	2.3
48	1q	81	ARG	2.3
49	1r	87	ARG	2.3
20	1Y	56	PRO	2.3
34	2c	73	PRO	2.3
40	1i	63	ILE	2.3
43	1l	125	PRO	2.3
11	2P	44	GLY	2.3
13	1R	7	GLY	2.3
4	1E	131	ALA	2.3
5	1F	198	ALA	2.3
30	18	34	TRP	2.3
50	2s	68	GLY	2.3
38	1g	2	ALA	2.3
38	1g	107	ALA	2.3
42	1k	15	ALA	2.3
44	2m	76	ALA	2.3
10	1O	6	THR	2.3
43	2l	6	THR	2.3
5	1F	156	LEU	2.3
7	2H	111	HIS	2.3
8	1I	116	LEU	2.3
10	2O	25	LEU	2.3
19	1X	92	LEU	2.3
22	10	21	LEU	2.3
33	1b	213	LEU	2.3
37	2f	19	LEU	2.3
40	2i	19	LEU	2.3
49	2r	76	LEU	2.3
1	1A	271(V)	G	2.3
1	1A	1296	G	2.3
1	1A	2484	G	2.3
1	2A	1074	G	2.3
2	2B	116	G	2.3
6	2G	141	PHE	2.3
32	1a	64	G	2.3
32	1a	963	G	2.3
32	1a	1058	G	2.3
32	1a	1516	G	2.3
32	2a	1106	G	2.3
33	1b	33	TYR	2.3
35	1d	54	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
42	2k	50	TYR	2.3
50	1s	61	TYR	2.3
36	1e	73	ASN	2.3
37	1f	73	ASN	2.3
50	1s	23	ASN	2.3
21	2Z	40	ASP	2.3
33	1b	110	GLN	2.3
36	2e	36	ASP	2.3
7	2H	42	ARG	2.3
7	2H	49	VAL	2.3
7	2H	113	VAL	2.3
7	2H	124	GLU	2.3
9	2N	68	GLU	2.3
15	1T	89	VAL	2.3
21	2Z	174	VAL	2.3
28	16	19	ARG	2.3
30	28	40	GLU	2.3
31	29	35	ARG	2.3
32	1a	274	A	2.3
32	1a	573	A	2.3
32	2a	632	A	2.3
32	2a	1492	A	2.3
34	1c	143	GLU	2.3
35	1d	36	ARG	2.3
35	1d	133	VAL	2.3
38	2g	146	GLU	2.3
40	1i	2	GLU	2.3
40	2i	48	GLU	2.3
40	2i	51	ARG	2.3
44	1m	14	ARG	2.3
49	1r	28	GLU	2.3
1	2A	157	U	2.3
32	1a	5	U	2.3
32	1a	1056	U	2.3
32	2a	1012	U	2.3
7	1H	112	PRO	2.3
9	1N	111	PRO	2.3
15	1T	102	ILE	2.3
37	1f	81	ILE	2.3
51	2t	100	ILE	2.3
4	1E	204	ALA	2.3
13	1R	19	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
31	19	5	ALA	2.3
38	2g	117	ALA	2.3
40	2i	100	GLY	2.3
49	2r	77	GLY	2.3
1	1A	904	C	2.3
1	1A	2073	C	2.3
32	1a	549	C	2.3
32	1a	720	C	2.3
32	2a	422	C	2.3
32	2a	1237	C	2.3
3	1D	182	LEU	2.3
5	1F	123	LEU	2.3
6	1G	60	LEU	2.3
6	1G	162	THR	2.3
7	1H	87	LEU	2.3
14	1S	63	THR	2.3
21	2Z	69	THR	2.3
28	16	36	LEU	2.3
36	2e	12	LEU	2.3
51	1t	20	LEU	2.3
23	11	66	HIS	2.3
34	2c	6	HIS	2.3
45	1n	49	HIS	2.3
13	2R	14	SER	2.3
21	1Z	16	SER	2.3
6	2G	131	TYR	2.3
21	2Z	104	PHE	2.3
22	20	26	TYR	2.3
38	2g	26	PHE	2.3
39	2h	48	TYR	2.3
40	2i	5	TYR	2.3
40	2i	114	TYR	2.3
43	2l	120	TYR	2.3
3	1D	35	LYS	2.3
6	1G	108	ASN	2.3
9	2N	109	LYS	2.3
13	2R	5	LYS	2.3
19	1X	78	LYS	2.3
38	2g	41	ARG	2.3
40	2i	20	ARG	2.3
48	2q	91	ARG	2.3
50	2s	56	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
4	1E	116	VAL	2.3
8	1I	92	VAL	2.3
20	2Y	107	ASP	2.3
33	2b	166	ASP	2.3
39	1h	4	ASP	2.3
39	1h	97	VAL	2.3
6	2G	45	GLU	2.2
38	1g	123	GLU	2.2
39	2h	136	GLU	2.2
50	2s	17	GLU	2.2
1	1A	82	G	2.2
1	1A	411	G	2.2
1	1A	883	G	2.2
1	1A	2157	G	2.2
1	1A	2182	G	2.2
1	1A	2191	G	2.2
1	2A	467	G	2.2
1	2A	508	G	2.2
1	2A	1950	G	2.2
32	1a	129(A)	G	2.2
32	1a	306	G	2.2
32	1a	670	G	2.2
32	1a	713	G	2.2
32	1a	1193	G	2.2
32	1a	1441	G	2.2
32	1a	1442	G	2.2
32	2a	446	G	2.2
32	2a	474	G	2.2
16	1U	80	ILE	2.2
33	1b	172	ILE	2.2
48	2q	60	ILE	2.2
4	1E	53	PRO	2.2
6	1G	119	GLY	2.2
21	2Z	176	PRO	2.2
35	2d	44	GLY	2.2
36	2e	77	PRO	2.2
38	1g	93	PRO	2.2
40	1i	49	PRO	2.2
40	2i	8	GLY	2.2
43	2l	5	PRO	2.2
6	2G	46	ALA	2.2
6	2G	57	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
7	2H	41	MET	2.2
10	2O	30	ALA	2.2
20	1Y	65	ALA	2.2
44	2m	26	GLY	2.2
51	2t	102	GLY	2.2
1	1A	1372	U	2.2
1	1A	1384	A	2.2
1	1A	1420	U	2.2
1	1A	1553	A	2.2
1	1A	1669	A	2.2
1	1A	1972	A	2.2
1	2A	887	A	2.2
1	2A	1969	A	2.2
3	2D	215	LEU	2.2
13	1R	18	LEU	2.2
19	1X	13	LEU	2.2
32	1a	404	U	2.2
32	1a	1030(D)	A	2.2
32	1a	1052	U	2.2
32	2a	706	A	2.2
32	2a	964	A	2.2
32	2a	1329	A	2.2
34	1c	94	LEU	2.2
37	1f	48	LEU	2.2
49	1r	85	LEU	2.2
6	2G	80	PHE	2.2
9	2N	94	HIS	2.2
10	2O	79	PHE	2.2
23	21	59	THR	2.2
35	2d	185	PHE	2.2
45	2n	49	HIS	2.2
49	2r	82	THR	2.2
50	2s	79	THR	2.2
3	2D	266	SER	2.2
9	1N	121	LYS	2.2
9	2N	72	TYR	2.2
12	1Q	9	TYR	2.2
17	1V	78	LYS	2.2
18	1W	16	LYS	2.2
20	1Y	70	SER	2.2
21	1Z	166	SER	2.2
26	24	2	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
26	24	32	TYR	2.2
42	1k	122	LYS	2.2
46	2o	8	LYS	2.2
1	1A	106	C	2.2
1	1A	1180	C	2.2
1	1A	2293	C	2.2
14	1S	10	ARG	2.2
14	1S	89	ARG	2.2
31	19	22	ARG	2.2
32	1a	501	C	2.2
32	1a	984	C	2.2
32	1a	1116	C	2.2
32	2a	501	C	2.2
45	2n	29	ARG	2.2
47	2p	18	ARG	2.2
4	1E	35	GLN	2.2
8	1I	139	GLN	2.2
21	2Z	196	VAL	2.2
33	1b	146	GLN	2.2
34	2c	75	VAL	2.2
41	2j	33	GLN	2.2
5	1F	152	GLU	2.2
6	2G	4	ASP	2.2
33	1b	129	GLU	2.2
35	2d	15	GLU	2.2
36	2e	50	GLU	2.2
38	1g	52	GLU	2.2
41	1j	73	ASP	2.2
8	2I	88	ILE	2.2
34	2c	8	ILE	2.2
35	1d	67	ILE	2.2
51	2t	55	ILE	2.2
3	1D	149	PRO	2.2
3	2D	11	PRO	2.2
3	2D	137	PRO	2.2
3	1D	33	LEU	2.2
3	2D	199	ALA	2.2
4	1E	124	GLY	2.2
5	1F	110	LEU	2.2
6	1G	19	LEU	2.2
8	1I	1	MET	2.2
12	1Q	2	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
13	2R	4	LEU	2.2
14	2S	37	ALA	2.2
15	1T	97	ALA	2.2
17	1V	59	ALA	2.2
17	2V	9	GLY	2.2
21	2Z	130	PRO	2.2
25	13	21	ALA	2.2
34	1c	9	GLY	2.2
36	1e	31	LEU	2.2
36	1e	48	ALA	2.2
38	2g	121	ALA	2.2
39	1h	89	PRO	2.2
44	1m	72	ALA	2.2
51	1t	56	MET	2.2
3	2D	252	TRP	2.2
33	2b	24	TRP	2.2
26	14	42	PHE	2.2
1	1A	919	G	2.2
1	2A	892	G	2.2
1	2A	1441	G	2.2
5	1F	48	THR	2.2
9	2N	93	THR	2.2
14	2S	34	HIS	2.2
25	13	40	THR	2.2
26	24	8	LYS	2.2
27	15	56	LYS	2.2
32	1a	450	G	2.2
32	1a	654	G	2.2
32	1a	1084	G	2.2
32	1a	1175	G	2.2
32	2a	481	G	2.2
32	2a	727	G	2.2
32	2a	1334	G	2.2
38	1g	70	LYS	2.2
39	1h	3	THR	2.2
6	2G	91	ARG	2.2
32	2a	772	U	2.2
32	2a	1292	U	2.2
33	1b	236	TYR	2.2
35	2d	138	TYR	2.2
38	1g	102	ARG	2.2
42	1k	120	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
42	2k	25	TYR	2.2
44	2m	59	TYR	2.2
1	1A	900	A	2.2
1	1A	901	A	2.2
1	2A	529	A	2.2
1	2A	2274	A	2.2
32	1a	969	A	2.2
32	2a	794	A	2.2
32	2a	983	A	2.2
32	2a	1157	A	2.2
33	2b	192	SER	2.2
7	1H	43	VAL	2.2
21	2Z	42	VAL	2.2
34	1c	99	VAL	2.2
38	2g	69	VAL	2.2
39	1h	129	VAL	2.2
5	2F	8	GLN	2.2
30	18	43	GLN	2.2
34	1c	107	GLN	2.2
47	1p	76	GLN	2.2
7	2H	32	GLU	2.2
8	2I	7	GLU	2.2
16	2U	37	GLU	2.2
24	12	57	ILE	2.2
26	24	34	GLU	2.2
35	1d	26	CYS	2.2
36	2e	122	GLU	2.2
1	1A	267	C	2.2
1	1A	2699	C	2.2
1	2A	1079	C	2.2
2	1B	31	C	2.2
32	1a	936	C	2.2
32	1a	1378	C	2.2
32	2a	822	C	2.2
32	2a	1054	C	2.2
4	2E	52	LEU	2.2
6	1G	129	GLY	2.2
7	1H	8	PRO	2.2
7	1H	103	LEU	2.2
8	1I	23	PRO	2.2
8	1I	98	ALA	2.2
11	1P	62	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
21	2Z	33	LEU	2.2
22	10	54	GLY	2.2
27	25	58	LEU	2.2
33	1b	232	PRO	2.2
34	1c	74	GLY	2.2
34	1c	80	GLY	2.2
34	1c	142	MET	2.2
34	2c	17	ASP	2.2
35	1d	190	ASP	2.2
34	1c	146	ALA	2.2
34	2c	61	ALA	2.2
36	2e	19	MET	2.2
36	2e	147	ASP	2.2
38	1g	14	PRO	2.2
38	1g	83	ALA	2.2
41	1j	71	LEU	2.2
42	1k	98	LEU	2.2
46	2o	75	PRO	2.2
7	2H	85	LYS	2.2
18	2W	4	LYS	2.2
30	18	15	LYS	2.2
33	1b	106	LYS	2.2
38	1g	137	LYS	2.2
4	1E	15	PHE	2.2
3	1D	263	ARG	2.2
4	1E	120	TRP	2.2
4	1E	122	PHE	2.2
7	1H	123	PHE	2.2
15	2T	22	PHE	2.2
22	20	45	PHE	2.2
33	2b	181	PHE	2.2
16	1U	52	ARG	2.2
17	2V	82	ARG	2.2
43	2l	117	ARG	2.2
47	1p	28	ARG	2.2
7	1H	106	THR	2.2
26	14	40	HIS	2.2
38	2g	122	HIS	2.2
12	2Q	32	TYR	2.2
33	2b	33	TYR	2.2
3	1D	127	VAL	2.2
9	1N	9	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
25	13	58	VAL	2.2
5	1F	15	SER	2.2
43	1l	116	SER	2.2
1	2A	958	U	2.2
1	2A	1094	U	2.2
1	2A	2712	U	2.2
2	2B	41	U	2.2
32	1a	565	U	2.2
32	1a	793	U	2.2
32	1a	1159	U	2.2
32	1a	1205	U	2.2
32	2a	560	U	2.2
35	2d	45	GLN	2.2
7	1H	136	ILE	2.2
33	2b	200	ILE	2.2
43	1l	7	ILE	2.2
5	1F	169	ASN	2.2
1	1A	271	A	2.2
1	1A	859	G	2.2
1	1A	2413	G	2.2
1	1A	2732	G	2.2
1	1A	2872	G	2.2
1	2A	2833	G	2.2
4	2E	182	LEU	2.2
6	2G	143	GLU	2.2
7	2H	159	GLU	2.2
32	1a	21	G	2.2
32	1a	196	A	2.2
32	1a	446	G	2.2
32	1a	566	G	2.2
32	1a	664	G	2.2
32	1a	1387	G	2.2
32	2a	64	G	2.2
32	2a	426	G	2.2
32	2a	1084	G	2.2
34	1c	181	ASN	2.2
34	2c	98	ASN	2.2
32	2a	1105	A	2.2
32	2a	1338	G	2.2
32	2a	1491	G	2.2
43	1l	76	ASN	2.2
6	2G	99	MET	2.2

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Mol	Chain	Res	Type	RSRZ
13	1R	67	LEU	2.2
14	1S	58	LEU	2.2
49	2r	51	LEU	2.2
6	2G	158	ALA	2.2
12	2Q	92	GLY	2.2
21	1Z	188	ALA	2.2
22	10	8	GLY	2.2
23	11	29	GLY	2.2
31	19	21	GLY	2.2
34	2c	148	GLY	2.2
36	2e	114	GLY	2.2
38	1g	133	GLY	2.2
45	1n	59	ALA	2.2
47	2p	64	ALA	2.2
50	1s	46	GLY	2.2
15	2T	113	LYS	2.2
20	2Y	54	LYS	2.2
34	2c	26	LYS	2.2
48	1q	69	LYS	2.2
29	27	23	ARG	2.2
35	2d	206	PHE	2.2
39	2h	12	ARG	2.2
45	2n	3	ARG	2.2
1	1A	1305	C	2.2
1	2A	889	C	2.2
1	2A	898	C	2.2
1	2A	1104	C	2.2
1	2A	1934	C	2.2
32	1a	54	C	2.2
32	1a	562	C	2.2
32	1a	1007	C	2.2
32	2a	620	C	2.2
32	2a	934	C	2.2
32	2a	1007	C	2.2
32	2a	1388	C	2.2
3	2D	220	HIS	2.2
14	2S	95	HIS	2.2
22	20	80	HIS	2.2
29	27	43	THR	2.2
34	2c	15	THR	2.2
42	1k	28	THR	2.2
44	2m	49	THR	2.2

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Mol	Chain	Res	Type	RSRZ
11	2P	80	TYR	2.2
28	16	21	TYR	2.2
33	1b	93	VAL	2.2
34	1c	184	TYR	2.2
37	1f	50	TYR	2.2
44	1m	17	VAL	2.2
44	1m	23	TYR	2.2
47	2p	39	TYR	2.2
50	2s	52	TYR	2.2
9	1N	133	GLN	2.2
13	2R	6	SER	2.2
20	2Y	57	GLN	2.2
24	12	38	GLN	2.2
31	19	10	ILE	2.2
46	1o	87	ILE	2.2
6	1G	7	LEU	2.2
48	2q	74	LEU	2.2
8	2I	1	MET	2.2
4	2E	114	ALA	2.2
6	1G	50	ALA	2.2
8	2I	26	ALA	2.2
9	1N	68	GLU	2.2
21	2Z	132	ASN	2.2
33	2b	35	GLU	2.2
41	2j	95	GLU	2.2
39	1h	116	LYS	2.2
39	2h	98	LYS	2.2
40	1i	70	LYS	2.2
40	2i	116	LYS	2.2
43	2l	26	ALA	2.2
44	2m	50	GLU	2.2
45	2n	8	GLU	2.2
42	2k	46	GLY	2.2
42	2k	51	LYS	2.2
51	1t	78	ALA	2.2
1	1A	230	U	2.2
1	2A	271(N)	U	2.2
1	2A	594	U	2.2
2	2B	104	U	2.2
3	2D	139	GLY	2.2
4	2E	88	GLY	2.2
32	2a	420	U	2.2

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Mol	Chain	Res	Type	RSRZ
32	2a	580	U	2.2
32	2a	1073	U	2.2
36	2e	128	PRO	2.2
38	1g	130	GLY	2.2
50	2s	26	GLY	2.2
51	1t	81	LYS	2.2
8	2I	33	ARG	2.2
21	2Z	80	ARG	2.2
35	1d	76	ARG	2.2
20	2Y	60	PHE	2.2
21	2Z	87	ASP	2.2
31	29	12	ASP	2.2
35	2d	110	PHE	2.2
38	1g	15	ASP	2.2
38	2g	140	ASP	2.2
39	1h	73	ASP	2.2
45	2n	24	CYS	2.2
1	1A	221	A	2.2
1	1A	821	A	2.2
1	1A	2158	A	2.2
1	1A	2418	A	2.2
1	1A	2826	A	2.2
1	2A	1103	A	2.2
32	1a	430	A	2.2
32	1a	439	A	2.2
32	2a	509	A	2.2
32	2a	728	A	2.2
32	2a	1333	A	2.2
1	1A	1667	G	2.2
1	1A	1758	G	2.2
1	2A	1042	G	2.2
2	2B	63	G	2.2
2	2B	75	G	2.2
32	1a	821	G	2.2
32	1a	1120	G	2.2
32	1a	1206	G	2.2
32	2a	799	G	2.2
32	2a	1276	G	2.2
17	1V	64	HIS	2.2
4	1E	23	VAL	2.1
4	2E	72	VAL	2.1
7	1H	115	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
8	1I	93	THR	2.1
14	2S	47	THR	2.1
19	2X	37	THR	2.1
21	2Z	71	VAL	2.1
34	1c	177	THR	2.1
46	1o	11	VAL	2.1
14	2S	94	TYR	2.1
43	1l	64	TYR	2.1
1	2A	885	C	2.1
1	2A	2521	C	2.1
2	2B	12	C	2.1
3	1D	174	ILE	2.1
26	24	5	ILE	2.1
32	1a	240	C	2.1
32	1a	1045	C	2.1
32	1a	1218	C	2.1
32	1a	1244	C	2.1
32	1a	1320	C	2.1
32	2a	106	C	2.1
32	2a	330	C	2.1
32	2a	366	C	2.1
32	2a	403	C	2.1
32	2a	522	C	2.1
32	2a	564	C	2.1
32	2a	1114	C	2.1
32	2a	1263	C	2.1
39	1h	38	ILE	2.1
41	1j	6	ILE	2.1
14	1S	78	LEU	2.1
16	1U	39	LEU	2.1
17	2V	18	LEU	2.1
23	21	42	GLN	2.1
23	21	85	LEU	2.1
33	2b	215	LEU	2.1
47	2p	76	GLN	2.1
15	1T	8	LYS	2.1
26	24	1	MET	2.1
26	24	28	LYS	2.1
36	1e	19	MET	2.1
37	1f	93	SER	2.1
38	2g	29	LYS	2.1
5	1F	22	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	16	ARG	2.1
8	1I	135	GLU	2.1
11	1P	117	GLU	2.1
14	2S	64	GLU	2.1
23	11	40	ARG	2.1
23	11	57	GLU	2.1
26	24	12	ALA	2.1
38	2g	39	ALA	2.1
41	1j	19	SER	2.1
44	1m	18	ALA	2.1
51	2t	77	ALA	2.1
10	2O	72	PRO	2.1
16	1U	73	GLY	2.1
17	1V	90	PRO	2.1
25	13	3	ARG	2.1
35	2d	171	GLY	2.1
37	2f	12	PRO	2.1
40	1i	8	GLY	2.1
44	1m	41	PRO	2.1
44	2m	85	GLY	2.1
47	2p	15	PRO	2.1
48	1q	72	ARG	2.1
24	12	65	ASN	2.1
50	1s	65	ASN	2.1
1	1A	1133	U	2.1
3	2D	71	ASP	2.1
32	1a	982	U	2.1
32	1a	1126	U	2.1
35	1d	193	ASP	2.1
41	2j	89	ASP	2.1
3	1D	205	VAL	2.1
5	1F	187	VAL	2.1
12	2Q	102	VAL	2.1
15	2T	66	VAL	2.1
21	1Z	105	VAL	2.1
22	10	63	VAL	2.1
34	1c	103	VAL	2.1
43	2l	24	VAL	2.1
44	1m	64	TRP	2.1
38	1g	153	HIS	2.1
48	1q	19	VAL	2.1
50	1s	69	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
34	2c	165	THR	2.1
41	2j	92	THR	2.1
10	2O	7	TYR	2.1
26	14	5	ILE	2.1
26	14	63	TYR	2.1
32	1a	509	A	2.1
32	1a	996	A	2.1
32	1a	1275	A	2.1
32	2a	10	A	2.1
32	2a	59	A	2.1
32	2a	1014	A	2.1
41	1j	75	ILE	2.1
13	1R	111	LEU	2.1
21	2Z	70	LEU	2.1
23	21	88	LYS	2.1
23	21	97	LEU	2.1
44	1m	79	LYS	2.1
47	1p	27	LYS	2.1
48	1q	84	LEU	2.1
51	1t	30	LYS	2.1
1	1A	927	G	2.1
1	1A	1444	G	2.1
1	1A	1699	G	2.1
1	1A	1816	G	2.1
1	1A	2339	G	2.1
1	2A	11	G	2.1
1	2A	712	G	2.1
2	1B	33	G	2.1
4	2E	79	ARG	2.1
5	1F	166	ALA	2.1
5	2F	49	ALA	2.1
5	2F	130	ALA	2.1
5	2F	205	ARG	2.1
11	1P	65	ARG	2.1
14	2S	9	ARG	2.1
15	1T	64	ARG	2.1
32	1a	200	G	2.1
32	1a	384	G	2.1
32	1a	721	G	2.1
32	1a	987	G	2.1
32	1a	988	G	2.1
32	1a	1442(A)	G	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	281	G	2.1
32	2a	346	G	2.1
32	2a	347	G	2.1
32	2a	530	G	2.1
32	2a	538	G	2.1
32	2a	1316	G	2.1
32	2a	1343	G	2.1
32	2a	1361	G	2.1
32	2a	1410	G	2.1
32	2a	1520	G	2.1
34	1c	79	ARG	2.1
35	1d	122	ARG	2.1
37	1f	77	ARG	2.1
48	1q	25	ARG	2.1
51	1t	90	GLN	2.1
7	2H	150	ALA	2.1
9	1N	92	ALA	2.1
16	1U	113	ALA	2.1
23	11	63	ALA	2.1
4	1E	94	GLU	2.1
7	1H	56	SER	2.1
7	1H	78	GLY	2.1
1	1A	2794	C	2.1
1	2A	1109	C	2.1
1	2A	1493	C	2.1
1	2A	1640	C	2.1
1	2A	2474	C	2.1
1	2A	2539	C	2.1
3	1D	29	PRO	2.1
3	1D	100	GLY	2.1
11	1P	23	PRO	2.1
11	1P	73	GLY	2.1
20	1Y	64	GLU	2.1
21	1Z	11	GLU	2.1
26	24	37	SER	2.1
34	2c	13	GLY	2.1
35	2d	80	GLU	2.1
48	1q	49	GLU	2.1
32	1a	103	C	2.1
32	1a	1006	C	2.1
32	1a	1018	C	2.1
32	2a	150	C	2.1

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Mol	Chain	Res	Type	RSRZ
32	2a	189(A)	C	2.1
32	2a	528	C	2.1
32	2a	795	C	2.1
32	2a	1234	C	2.1
32	2a	1297	C	2.1
32	2a	1384	C	2.1
6	2G	178	PHE	2.1
4	1E	18	ASP	2.1
4	2E	173	VAL	2.1
5	1F	77	ASP	2.1
9	2N	13	TRP	2.1
15	2T	117	ASP	2.1
16	2U	8	VAL	2.1
21	2Z	100	VAL	2.1
33	2b	136	VAL	2.1
50	2s	83	HIS	2.1
1	2A	1078	U	2.1
1	2A	1199	U	2.1
3	1D	62	TYR	2.1
6	1G	146	TYR	2.1
6	2G	173	LEU	2.1
9	2N	67	LEU	2.1
13	2R	113	LEU	2.1
14	2S	35	ILE	2.1
16	1U	74	LEU	2.1
19	1X	36	LYS	2.1
25	23	17	LYS	2.1
29	27	32	LYS	2.1
32	1a	1086	U	2.1
32	1a	1278	U	2.1
33	1b	215	LEU	2.1
34	2c	87	LEU	2.1
34	2c	150	LYS	2.1
35	1d	126	ILE	2.1
42	2k	124	LYS	2.1
48	2q	36	ILE	2.1
35	2d	20	TYR	2.1
43	1l	105	TYR	2.1
50	1s	80	TYR	2.1
50	2s	22	LEU	2.1
7	1H	42	ARG	2.1
9	2N	114	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
15	1T	95	ARG	2.1
21	2Z	19	ARG	2.1
33	2b	144	ARG	2.1
35	2d	10	ARG	2.1
45	1n	45	ARG	2.1
47	2p	75	ARG	2.1
50	2s	29	ARG	2.1
3	1D	199	ALA	2.1
3	2D	2	ALA	2.1
4	2E	187	ALA	2.1
5	1F	118	ALA	2.1
6	1G	46	ALA	2.1
6	2G	171	ALA	2.1
20	1Y	105	ALA	2.1
25	13	19	GLN	2.1
25	13	42	ALA	2.1
33	2b	88	ALA	2.1
34	2c	107	GLN	2.1
38	2g	152	ALA	2.1
40	2i	76	ALA	2.1
43	2l	51	ALA	2.1
1	1A	222	A	2.1
1	1A	390	A	2.1
1	1A	984	A	2.1
1	2A	1077	A	2.1
7	1H	12	PRO	2.1
7	1H	46	GLU	2.1
9	2N	125	GLY	2.1
14	2S	60	GLY	2.1
21	1Z	168	GLU	2.1
32	1a	663	A	2.1
32	1a	1363(A)	A	2.1
32	2a	393	A	2.1
32	2a	397	A	2.1
34	1c	25	GLY	2.1
35	2d	24	GLU	2.1
36	1e	68	GLU	2.1
37	2f	51	PRO	2.1
39	2h	89	PRO	2.1
44	1m	6	GLY	2.1
3	1D	179	SER	2.1
29	27	18	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
7	1H	147	ASN	2.1
1	1A	7	G	2.1
1	1A	545	G	2.1
1	1A	1031	G	2.1
1	1A	2817	G	2.1
1	2A	1047	G	2.1
1	2A	1440	G	2.1
1	2A	1559	G	2.1
2	2B	87	G	2.1
3	1D	113	VAL	2.1
7	2H	19	VAL	2.1
7	2H	35	VAL	2.1
7	2H	52	VAL	2.1
32	1a	41	G	2.1
32	1a	631	G	2.1
32	1a	761	G	2.1
32	1a	1124	G	2.1
32	1a	1134	G	2.1
32	2a	629	G	2.1
32	2a	876	G	2.1
32	2a	1011	G	2.1
32	2a	1050	G	2.1
47	1p	20	VAL	2.1
49	2r	22	VAL	2.1
1	2A	884	C	2.1
1	2A	1018	C	2.1
1	2A	1530	C	2.1
1	2A	2188	C	2.1
32	1a	569	C	2.1
32	1a	735	C	2.1
32	1a	980	C	2.1
32	1a	1118	C	2.1
32	1a	1321	C	2.1
32	2a	311	C	2.1
32	2a	1217	C	2.1
32	2a	1342	C	2.1
32	2a	1439	C	2.1
3	1D	71	ASP	2.1
6	1G	126	ASP	2.1
9	1N	83	LYS	2.1
9	2N	2	LYS	2.1
9	2N	37	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
12	1Q	85	LYS	2.1
14	1S	34	HIS	2.1
14	1S	76	LYS	2.1
19	1X	63	LYS	2.1
20	2Y	101	LYS	2.1
21	1Z	78	LYS	2.1
45	1n	44	LEU	2.1
46	1o	46	HIS	2.1
46	1o	51	HIS	2.1
49	1r	61	LYS	2.1
7	1H	9	ILE	2.1
12	1Q	34	LEU	2.1
20	1Y	96	ILE	2.1
20	2Y	96	ILE	2.1
33	1b	10	LEU	2.1
33	2b	80	ILE	2.1
33	2b	149	LEU	2.1
33	2b	222	ILE	2.1
35	1d	21	LEU	2.1
41	2j	88	LEU	2.1
48	2q	65	ILE	2.1
51	1t	64	ASP	2.1
3	1D	273	ARG	2.1
3	2D	244	ARG	2.1
7	1H	95	ARG	2.1
7	1H	97	ARG	2.1
12	2Q	5	ARG	2.1
12	2Q	59	ARG	2.1
14	1S	25	ARG	2.1
3	1D	97	TYR	2.1
3	2D	97	TYR	2.1
7	1H	163	TYR	2.1
26	24	44	THR	2.1
33	2b	30	ARG	2.1
34	1c	67	THR	2.1
35	1d	10	ARG	2.1
30	28	64	TYR	2.1
44	2m	109	THR	2.1
4	1E	162	ALA	2.1
40	1i	13	ALA	2.1
4	2E	48	GLN	2.1
23	21	19	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
32	1a	863	U	2.1
32	1a	1292	U	2.1
32	2a	421	U	2.1
32	2a	801	U	2.1
9	1N	49	GLY	2.1
9	1N	105	GLY	2.1
22	20	76	GLY	2.1
33	2b	14	GLY	2.1
34	1c	81	GLY	2.1
44	2m	38	GLY	2.1
3	1D	245	PRO	2.1
5	2F	14	PRO	2.1
15	2T	46	GLU	2.1
23	21	83	GLU	2.1
23	21	87	PRO	2.1
28	26	41	PRO	2.1
33	1b	59	GLU	2.1
33	2b	70	PHE	2.1
34	2c	35	GLU	2.1
34	2c	90	GLU	2.1
37	1f	51	PRO	2.1
38	1g	90	GLU	2.1
44	1m	32	GLU	2.1
48	1q	48	GLU	2.1
4	1E	188	VAL	2.1
4	2E	93	VAL	2.1
6	1G	159	VAL	2.1
7	2H	44	VAL	2.1
21	2Z	96	VAL	2.1
22	20	38	VAL	2.1
26	14	33	VAL	2.1
29	27	46	VAL	2.1
36	1e	67	VAL	2.1
36	2e	41	VAL	2.1
42	1k	30	VAL	2.1
48	2q	77	VAL	2.1
1	1A	457	A	2.1
1	2A	1057	A	2.1
3	1D	5	LYS	2.1
12	1Q	22	LYS	2.1
26	24	20	ASN	2.1
30	18	36	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
32	1a	143	A	2.1
32	1a	559	A	2.1
32	1a	781	A	2.1
32	1a	807	A	2.1
32	2a	1041	A	2.1
33	1b	8	LYS	2.1
35	1d	86	LYS	2.1
38	2g	63	LYS	2.1
39	1h	21	LYS	2.1
40	1i	95	LYS	2.1
6	1G	144	ILE	2.1
6	2G	21	ARG	2.1
6	2G	94	LEU	2.1
6	2G	96	ARG	2.1
7	2H	60	ARG	2.1
8	2I	79	ILE	2.1
16	2U	62	ILE	2.1
22	10	55	ARG	2.1
23	11	37	ILE	2.1
33	2b	180	LEU	2.1
34	1c	8	ILE	2.1
34	1c	34	LEU	2.1
34	1c	54	ARG	2.1
35	2d	139	ARG	2.1
36	2e	142	LEU	2.1
42	2k	98	LEU	2.1
6	1G	64	THR	2.1
20	1Y	20	TYR	2.1
21	2Z	9	TYR	2.1
34	1c	191	THR	2.1
40	1i	5	TYR	2.1
1	1A	949	C	2.1
1	2A	271(T)	C	2.1
1	2A	658	C	2.1
1	2A	95	G	2.1
1	2A	2104	G	2.1
1	2A	2191	G	2.1
1	2A	2468	G	2.1
3	2D	224	ALA	2.1
4	2E	123	ALA	2.1
6	1G	158	ALA	2.1
7	2H	102	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
11	1P	140	ALA	2.1
14	1S	37	ALA	2.1
17	1V	77	ALA	2.1
30	28	24	ALA	2.1
32	1a	311	C	2.1
32	1a	1043	C	2.1
32	2a	352	C	2.1
32	2a	525	C	2.1
32	1a	727	G	2.1
32	1a	1305	G	2.1
32	1a	1355	G	2.1
32	2a	183	G	2.1
32	2a	255	G	2.1
32	2a	354	G	2.1
32	2a	445	G	2.1
32	2a	506	G	2.1
32	2a	658	G	2.1
32	2a	929	G	2.1
32	2a	1283	G	2.1
32	2a	1337	G	2.1
37	1f	49	ALA	2.1
40	2i	119	ALA	2.1
11	2P	26	GLY	2.1
12	1Q	84	GLY	2.1
16	2U	7	GLY	2.1
30	28	20	GLY	2.1
35	2d	201	GLN	2.1
43	2l	87	GLY	2.1
43	2l	103	GLY	2.1
5	2F	90	PHE	2.1
6	1G	68	PRO	2.1
12	2Q	99	PRO	2.1
20	1Y	82	PRO	2.1
21	2Z	95	PRO	2.1
34	2c	186	PHE	2.1
38	1g	58	PRO	2.1
38	2g	8	GLU	2.1
38	2g	123	GLU	2.1
39	2h	67	PRO	2.1
39	2h	74	PRO	2.1
42	2k	92	GLU	2.1
49	1r	62	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	2A	383	U	2.0
1	2A	2473	U	2.0
3	2D	51	VAL	2.0
4	1E	47	VAL	2.0
4	1E	175	VAL	2.0
4	2E	21	VAL	2.0
5	1F	103	LYS	2.0
17	1V	22	VAL	2.0
20	2Y	15	VAL	2.0
23	21	25	LYS	2.0
32	2a	1040	U	2.0
32	2a	1330	U	2.0
36	1e	121	LYS	2.0
39	1h	56	LYS	2.0
40	1i	113	LYS	2.0
42	1k	105	VAL	2.0
11	2P	4	SER	2.0
13	1R	14	SER	2.0
48	1q	12	SER	2.0
48	1q	39	SER	2.0
51	1t	37	SER	2.0
15	1T	42	ILE	2.0
17	1V	62	LEU	2.0
17	1V	71	LEU	2.0
24	12	3	LEU	2.0
25	23	28	LEU	2.0
33	2b	211	ILE	2.0
35	1d	78	LEU	2.0
35	2d	50	ARG	2.0
35	2d	120	LEU	2.0
37	1f	80	ARG	2.0
46	1o	81	LEU	2.0
48	1q	59	ILE	2.0
51	2t	99	LEU	2.0
6	2G	29	TRP	2.0
33	1b	24	TRP	2.0
35	1d	125	HIS	2.0
35	2d	173	TRP	2.0
5	1F	194	MET	2.0
1	1A	78	A	2.0
1	1A	2273	A	2.0
1	1A	2369	A	2.0

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Mol	Chain	Res	Type	RSRZ
1	2A	567	A	2.0
1	2A	2750	A	2.0
6	2G	97	ASP	2.0
10	1O	80	ASP	2.0
19	2X	69	TYR	2.0
25	13	15	TYR	2.0
32	1a	353	A	2.0
32	1a	532	A	2.0
32	1a	1279	A	2.0
32	2a	535	A	2.0
32	2a	915	A	2.0
32	2a	1015	A	2.0
32	2a	1110	A	2.0
32	2a	1261	A	2.0
32	2a	1275	A	2.0
33	2b	92	TYR	2.0
36	1e	146	ALA	2.0
38	2g	127	ALA	2.0
42	1k	31	THR	2.0
6	1G	127	GLY	2.0
10	2O	90	GLN	2.0
12	1Q	61	GLY	2.0
5	1F	66	PRO	2.0
10	2O	93	PRO	2.0
12	2Q	65	PHE	2.0
37	1f	57	GLN	2.0
42	1k	49	GLY	2.0
49	2r	48	GLY	2.0
23	11	12	PRO	2.0
27	15	7	PRO	2.0
35	1d	29	PRO	2.0
47	2p	66	PRO	2.0
3	2D	101	GLU	2.0
7	1H	116	GLU	2.0
1	1A	897	C	2.0
1	1A	1631	C	2.0
1	2A	1744	C	2.0
10	2O	67	LYS	2.0
20	2Y	33	LYS	2.0
20	2Y	81	LYS	2.0
21	2Z	97	GLU	2.0
25	13	5	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
25	23	20	LYS	2.0
30	18	54	GLU	2.0
32	2a	436	C	2.0
32	2a	1267	C	2.0
32	2a	1336	C	2.0
32	2a	1367	C	2.0
32	2a	1383	C	2.0
34	2c	135	LYS	2.0
38	1g	63	LYS	2.0
46	1o	76	GLU	2.0
6	2G	160	VAL	2.0
7	1H	131	VAL	2.0
11	1P	19	VAL	2.0
16	2U	100	VAL	2.0
19	1X	54	VAL	2.0
32	1a	436	C	2.0
32	1a	456	C	2.0
32	1a	808	C	2.0
32	1a	1008	C	2.0
32	1a	1479	C	2.0
51	1t	14	LYS	2.0
37	1f	72	VAL	2.0
40	1i	26	VAL	2.0
47	2p	53	VAL	2.0
1	1A	785	G	2.0
1	1A	864	G	2.0
1	1A	1168	G	2.0
1	1A	2207	G	2.0
1	1A	2581	G	2.0
1	2A	1573	G	2.0
6	1G	133	LEU	2.0
6	2G	120	LEU	2.0
8	2I	12	LEU	2.0
8	2I	82	ARG	2.0
14	2S	89	ARG	2.0
16	1U	36	ARG	2.0
16	1U	95	LEU	2.0
21	2Z	102	LEU	2.0
32	1a	319	G	2.0
32	1a	485	G	2.0
32	1a	606	G	2.0
32	1a	617	G	2.0

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Mol	Chain	Res	Type	RSRZ
32	1a	1144	G	2.0
32	2a	6	G	2.0
32	2a	380	G	2.0
32	2a	1231	G	2.0
32	2a	1294	G	2.0
32	2a	1432	G	2.0
34	2c	16	ARG	2.0
34	2c	140	ARG	2.0
35	2d	155	LEU	2.0
39	1h	92	ARG	2.0
51	1t	91	LEU	2.0
3	2D	12	SER	2.0
4	2E	95	ILE	2.0
18	1W	12	ILE	2.0
30	18	41	ILE	2.0
34	1c	20	SER	2.0
39	2h	86	ILE	2.0
47	1p	33	ILE	2.0
1	1A	905	U	2.0
20	2Y	43	ASN	2.0
32	1a	961	U	2.0
32	1a	1506	U	2.0
5	1F	199	TRP	2.0
16	2U	25	TRP	2.0
21	2Z	121	HIS	2.0
37	2f	67	MET	2.0
21	1Z	187	ALA	2.0
41	1j	32	ALA	2.0
12	1Q	26	TYR	2.0
26	24	43	TYR	2.0
47	2p	44	THR	2.0
19	1X	6	ASP	2.0
33	1b	166	ASP	2.0
33	2b	205	ASP	2.0
35	1d	102	ASP	2.0
48	2q	46	ASP	2.0
5	1F	139	PHE	2.0
6	2G	102	PHE	2.0
15	2T	25	GLY	2.0
20	2Y	89	PHE	2.0
33	2b	17	PHE	2.0
38	1g	132	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
46	2o	61	GLY	2.0
6	2G	179	PRO	2.0
10	1O	31	LYS	2.0
11	2P	76	LYS	2.0
12	1Q	18	LYS	2.0
15	2T	123	GLN	2.0
16	1U	2	PRO	2.0
17	1V	50	PRO	2.0
17	2V	84	LYS	2.0
17	2V	85	LYS	2.0
20	1Y	81	LYS	2.0
21	2Z	159	PRO	2.0
22	20	29	GLN	2.0
22	20	47	PRO	2.0
34	1c	27	LYS	2.0
35	2d	51	PRO	2.0
41	2j	21	GLN	2.0
43	2l	46	LYS	2.0
47	1p	66	PRO	2.0
1	1A	1156	A	2.0
1	1A	1445	A	2.0
1	1A	1938	A	2.0
1	2A	829	A	2.0
1	2A	866	A	2.0
1	2A	1569	A	2.0
1	2A	1637	A	2.0
3	2D	28	GLU	2.0
3	2D	229	VAL	2.0
4	1E	7	VAL	2.0
4	1E	93	VAL	2.0
5	2F	37	VAL	2.0
11	1P	126	VAL	2.0
13	1R	97	VAL	2.0
14	1S	46	VAL	2.0
14	2S	8	GLU	2.0
19	1X	12	VAL	2.0
21	1Z	90	VAL	2.0
32	2a	8	A	2.0
32	2a	1152	A	2.0
39	1h	123	GLU	2.0
50	1s	17	GLU	2.0
22	20	72	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
24	22	55	ARG	2.0
34	1c	164	ARG	2.0
34	2c	54	ARG	2.0
41	1j	79	ARG	2.0
41	2j	9	ARG	2.0
43	2l	102	ARG	2.0
46	2o	64	ARG	2.0
8	1I	58	LEU	2.0
8	2I	116	LEU	2.0
18	1W	82	LEU	2.0
37	1f	21	LEU	2.0
39	1h	119	LEU	2.0
3	1D	165	ILE	2.0
3	2D	136	ILE	2.0
8	2I	109	ILE	2.0
34	1c	5	ILE	2.0
42	2k	32	ILE	2.0
47	2p	4	ILE	2.0
1	1A	1464	C	2.0
1	1A	2248	C	2.0
1	2A	1178	C	2.0
1	2A	1463	C	2.0
32	1a	369	C	2.0
32	1a	403	C	2.0
32	1a	645	C	2.0
32	1a	756	C	2.0
32	1a	762	C	2.0
32	1a	985	C	2.0
32	1a	1426	C	2.0
32	2a	18	C	2.0
32	2a	458	C	2.0
32	2a	984	C	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, 95^{th} 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	5MC	1a	967	21/22	0.53	0.20	101,111,125,127	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
32	M2G	1a	966	25/26	0.68	0.18	96,110,117,129	0
32	5MC	2a	967	21/22	0.70	0.16	100,110,124,141	0
32	2MG	2a	1207	24/25	0.73	0.17	101,114,128,130	0
32	2MG	1a	1207	24/25	0.79	0.20	97,115,130,140	0
43	0TD	1l	92	10/11	0.80	0.19	76,97,100,136	0
1	5MU	2A	1915	21/22	0.81	0.13	89,104,108,127	0
32	M2G	2a	966	25/26	0.81	0.16	95,107,118,128	0
32	4OC	1a	1402	22/23	0.82	0.16	77,90,106,109	0
32	PSU	1a	516	20/21	0.83	0.11	92,103,110,110	0
1	PSU	2A	1917	20/21	0.84	0.11	83,98,115,116	0
32	5MC	2a	1400	21/22	0.84	0.17	87,100,110,117	0
1	PSU	1A	1917	20/21	0.85	0.12	83,98,110,113	0
32	5MC	1a	1400	21/22	0.86	0.14	72,98,109,116	0
32	7MG	2a	527	24/25	0.86	0.16	83,97,107,118	0
32	UR3	2a	1498	21/22	0.86	0.12	81,91,99,114	0
43	0TD	2l	92	10/11	0.86	0.16	79,94,103,117	0
1	PSU	2A	1911	20/21	0.87	0.10	80,92,102,104	0
1	4OC	2A	1920	21/23	0.87	0.11	86,93,100,101	0
1	5MU	1A	1915	21/22	0.87	0.12	91,100,109,124	0
1	PSU	1A	1911	20/21	0.88	0.11	82,93,98,102	0
32	PSU	2a	516	20/21	0.88	0.11	88,104,112,114	0
32	5MC	1a	1404	21/22	0.88	0.15	72,90,104,107	0
32	5MC	1a	1407	21/22	0.89	0.16	71,88,94,103	0
32	4OC	2a	1402	22/23	0.89	0.12	94,102,113,115	0
1	2MA	2A	2503	23/24	0.90	0.15	35,40,53,57	0
1	4OC	1A	1920	21/23	0.90	0.13	82,92,98,101	0
32	5MC	2a	1407	21/22	0.91	0.12	83,89,96,99	0
32	7MG	1a	527	24/25	0.91	0.13	85,94,100,105	0
32	5MC	2a	1404	21/22	0.91	0.12	70,87,106,107	0
32	UR3	1a	1498	21/22	0.92	0.11	80,88,95,99	0
1	2MA	1A	2503	23/24	0.93	0.18	31,36,45,65	0
1	5MU	1A	1939	21/22	0.93	0.13	42,55,63,65	0
32	MA6	1a	1519	24/25	0.93	0.17	61,84,94,101	0
1	5MC	1A	1962	21/22	0.93	0.17	49,70,83,86	0
1	5MU	2A	1939	21/22	0.93	0.15	45,59,65,67	0
32	MA6	2a	1518	24/25	0.93	0.12	56,95,102,108	0
32	MA6	2a	1519	24/25	0.93	0.17	78,91,99,106	0
1	5MC	2A	1962	21/22	0.93	0.14	51,71,84,90	0
1	2MU	2A	2552	21/23	0.94	0.12	38,47,60,60	0
1	PSU	2A	2605	20/21	0.94	0.13	36,51,56,56	0
32	MA6	1a	1518	24/25	0.94	0.13	58,81,89,95	0
1	OMG	2A	2251	24/25	0.94	0.13	43,54,59,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	5MC	1A	1942	21/22	0.94	0.11	50,71,80,88	0
1	2MU	1A	2552	21/23	0.95	0.14	37,44,57,60	0
1	PSU	1A	2605	20/21	0.95	0.12	33,49,55,60	0
1	5MC	2A	1942	21/22	0.95	0.09	57,73,79,89	0
1	OMG	1A	2251	24/25	0.96	0.12	34,50,55,60	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
53	MG	1a	3021	1/1	0.47	0.28	86,86,86,86	0
53	MG	2B	216	1/1	0.50	0.33	81,81,81,81	0
53	MG	2a	1705	1/1	0.50	0.69	91,91,91,91	0
53	MG	1A	3545	1/1	0.53	0.29	89,89,89,89	0
53	MG	1A	3556	1/1	0.57	0.23	77,77,77,77	0
53	MG	1A	3446	1/1	0.59	0.28	76,76,76,76	0
53	MG	1a	3109	1/1	0.59	0.28	100,100,100,100	0
53	MG	1A	3094	1/1	0.61	0.27	73,73,73,73	0
53	MG	2a	1640	1/1	0.61	0.15	84,84,84,84	0
53	MG	1h	8001	1/1	0.61	0.18	88,88,88,88	0
53	MG	2a	1706	1/1	0.61	0.23	98,98,98,98	0
53	MG	1a	3092	1/1	0.62	0.23	104,104,104,104	0
53	MG	1D	308	1/1	0.62	0.22	63,63,63,63	0
53	MG	2a	1612	1/1	0.62	0.30	93,93,93,93	0
53	MG	2A	3433	1/1	0.63	0.23	65,65,65,65	0
53	MG	1A	3727	1/1	0.64	0.39	80,80,80,80	0
53	MG	1A	3445	1/1	0.64	0.21	90,90,90,90	0
53	MG	2A	3018	1/1	0.65	0.15	74,74,74,74	0
53	MG	2A	3387	1/1	0.65	0.18	69,69,69,69	0
53	MG	1A	3453	1/1	0.66	0.42	87,87,87,87	0
53	MG	1a	3089	1/1	0.66	0.30	72,72,72,72	0
53	MG	2a	1701	1/1	0.66	0.26	93,93,93,93	0
53	MG	1A	3526	1/1	0.66	0.32	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2D	301	1/1	0.66	0.30	76,76,76,76	0
53	MG	1a	3125	1/1	0.67	0.23	95,95,95,95	0
53	MG	1f	8001	1/1	0.67	0.26	86,86,86,86	0
53	MG	1A	3574	1/1	0.67	0.27	82,82,82,82	0
53	MG	2a	1617	1/1	0.67	0.22	71,71,71,71	0
53	MG	1A	3374	1/1	0.67	0.13	68,68,68,68	0
53	MG	2a	1689	1/1	0.67	0.28	88,88,88,88	0
53	MG	2A	3103	1/1	0.67	0.30	76,76,76,76	0
53	MG	1A	3399	1/1	0.67	0.16	64,64,64,64	0
53	MG	1a	3002	1/1	0.67	0.14	96,96,96,96	0
53	MG	2A	3164	1/1	0.68	0.23	57,57,57,57	0
53	MG	2A	3075	1/1	0.68	0.16	73,73,73,73	0
53	MG	2A	3378	1/1	0.69	0.17	69,69,69,69	0
53	MG	2A	3067	1/1	0.69	0.28	56,56,56,56	0
53	MG	1A	3621	1/1	0.69	0.32	67,67,67,67	0
53	MG	2A	3427	1/1	0.70	0.14	84,84,84,84	0
53	MG	2A	3118	1/1	0.70	0.27	78,78,78,78	0
53	MG	2A	3444	1/1	0.70	0.15	59,59,59,59	0
53	MG	1a	3047	1/1	0.70	0.26	80,80,80,80	0
53	MG	1a	3086	1/1	0.70	0.18	77,77,77,77	0
53	MG	1A	3030	1/1	0.70	0.22	61,61,61,61	0
53	MG	2A	3425	1/1	0.71	0.13	68,68,68,68	0
53	MG	2A	3323	1/1	0.71	0.35	74,74,74,74	0
53	MG	2a	1694	1/1	0.71	0.13	74,74,74,74	0
53	MG	1A	3062	1/1	0.71	0.18	71,71,71,71	0
53	MG	1a	3136	1/1	0.71	0.28	83,83,83,83	0
53	MG	2a	1620	1/1	0.71	0.20	89,89,89,89	0
53	MG	1A	3598	1/1	0.72	0.17	109,109,109,109	0
53	MG	2A	3033	1/1	0.72	0.19	50,50,50,50	0
53	MG	1a	3116	1/1	0.72	0.12	137,137,137,137	0
53	MG	1A	3718	1/1	0.72	0.20	76,76,76,76	0
53	MG	1r	3001	1/1	0.72	0.12	87,87,87,87	0
53	MG	2B	205	1/1	0.73	0.20	73,73,73,73	0
53	MG	2a	1646	1/1	0.73	0.34	74,74,74,74	0
53	MG	1A	3614	1/1	0.73	0.25	64,64,64,64	0
53	MG	1a	3023	1/1	0.73	0.17	51,51,51,51	0
53	MG	2a	1695	1/1	0.73	0.21	88,88,88,88	0
53	MG	1e	201	1/1	0.73	0.37	73,73,73,73	0
53	MG	1G	8002	1/1	0.73	0.15	88,88,88,88	0
53	MG	1A	3510	1/1	0.73	0.26	41,41,41,41	0
53	MG	2a	1716	1/1	0.73	0.25	85,85,85,85	0
53	MG	2A	3227	1/1	0.74	0.25	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3133	1/1	0.74	0.19	69,69,69,69	0
53	MG	1A	3542	1/1	0.74	0.20	78,78,78,78	0
53	MG	2A	3023	1/1	0.74	0.30	63,63,63,63	0
53	MG	1A	3732	1/1	0.74	0.28	76,76,76,76	0
53	MG	1B	3010	1/1	0.74	0.14	51,51,51,51	0
53	MG	2a	1659	1/1	0.74	0.35	101,101,101,101	0
53	MG	1a	3056	1/1	0.74	0.22	74,74,74,74	0
53	MG	1a	3076	1/1	0.74	0.17	87,87,87,87	0
53	MG	2A	3479	1/1	0.74	0.18	56,56,56,56	0
53	MG	2A	3502	1/1	0.74	0.26	94,94,94,94	0
53	MG	1A	3139	1/1	0.74	0.17	57,57,57,57	0
53	MG	2B	214	1/1	0.74	0.16	53,53,53,53	0
53	MG	1A	3283	1/1	0.74	0.28	71,71,71,71	0
53	MG	2a	1725	1/1	0.74	0.22	97,97,97,97	0
53	MG	28	8002	1/1	0.75	0.21	51,51,51,51	0
53	MG	1a	3059	1/1	0.75	0.24	92,92,92,92	0
53	MG	1g	3001	1/1	0.75	0.21	78,78,78,78	0
53	MG	2a	1671	1/1	0.76	0.27	70,70,70,70	0
53	MG	1Q	201	1/1	0.76	0.22	54,54,54,54	0
53	MG	2A	3240	1/1	0.76	0.14	60,60,60,60	0
53	MG	1A	3013	1/1	0.76	0.32	69,69,69,69	0
53	MG	2a	1633	1/1	0.76	0.40	103,103,103,103	0
53	MG	2A	3337	1/1	0.76	0.28	53,53,53,53	0
53	MG	2a	1641	1/1	0.76	0.35	67,67,67,67	0
53	MG	2A	3368	1/1	0.76	0.17	77,77,77,77	0
53	MG	2A	3192	1/1	0.76	0.22	62,62,62,62	0
53	MG	2a	1643	1/1	0.77	0.41	102,102,102,102	0
53	MG	1A	3708	1/1	0.77	0.24	44,44,44,44	0
53	MG	2a	1650	1/1	0.77	0.13	80,80,80,80	0
53	MG	1l	202	1/1	0.77	0.12	81,81,81,81	0
53	MG	1A	3396	1/1	0.77	0.32	59,59,59,59	0
53	MG	1a	3065	1/1	0.77	0.30	82,82,82,82	0
53	MG	1a	3099	1/1	0.77	0.27	67,67,67,67	0
53	MG	2A	3223	1/1	0.77	0.24	61,61,61,61	0
53	MG	1A	3413	1/1	0.77	0.18	57,57,57,57	0
53	MG	2A	3055	1/1	0.77	0.14	59,59,59,59	0
53	MG	2A	3478	1/1	0.77	0.15	81,81,81,81	0
53	MG	2A	3269	1/1	0.77	0.28	75,75,75,75	0
53	MG	1a	3113	1/1	0.77	0.15	97,97,97,97	0
53	MG	2A	3242	1/1	0.78	0.13	62,62,62,62	0
53	MG	1A	3250	1/1	0.78	0.13	80,80,80,80	0
53	MG	1A	3469	1/1	0.78	0.15	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3508	1/1	0.78	0.34	65,65,65,65	0
53	MG	2A	3123	1/1	0.78	0.18	68,68,68,68	0
53	MG	2A	3135	1/1	0.78	0.26	65,65,65,65	0
53	MG	1a	3068	1/1	0.78	0.16	90,90,90,90	0
53	MG	2A	3168	1/1	0.78	0.15	57,57,57,57	0
53	MG	2A	3064	1/1	0.78	0.18	69,69,69,69	0
53	MG	2a	1611	1/1	0.78	0.16	97,97,97,97	0
53	MG	2a	1700	1/1	0.78	0.17	80,80,80,80	0
53	MG	1A	3659	1/1	0.78	0.17	85,85,85,85	0
53	MG	2A	3071	1/1	0.78	0.15	68,68,68,68	0
53	MG	1A	3164	1/1	0.78	0.33	53,53,53,53	0
53	MG	2a	1632	1/1	0.78	0.42	89,89,89,89	0
53	MG	2A	3476	1/1	0.78	0.18	75,75,75,75	0
53	MG	1A	3197	1/1	0.79	0.16	74,74,74,74	0
53	MG	1a	3049	1/1	0.79	0.34	80,80,80,80	0
53	MG	1A	3535	1/1	0.79	0.16	68,68,68,68	0
53	MG	1A	3541	1/1	0.79	0.19	72,72,72,72	0
53	MG	1a	3133	1/1	0.79	0.27	81,81,81,81	0
53	MG	1A	3623	1/1	0.79	0.17	94,94,94,94	0
53	MG	1A	3465	1/1	0.79	0.14	62,62,62,62	0
53	MG	1A	3104	1/1	0.79	0.17	58,58,58,58	0
53	MG	2a	1688	1/1	0.79	0.19	82,82,82,82	0
53	MG	2A	3082	1/1	0.79	0.34	69,69,69,69	0
53	MG	1a	3018	1/1	0.79	0.19	86,86,86,86	0
53	MG	2A	3111	1/1	0.79	0.17	63,63,63,63	0
53	MG	2a	1607	1/1	0.79	0.15	85,85,85,85	0
53	MG	1A	3026	1/1	0.79	0.15	48,48,48,48	0
53	MG	2A	3413	1/1	0.79	0.30	71,71,71,71	0
53	MG	1A	3516	1/1	0.79	0.20	53,53,53,53	0
53	MG	1a	3036	1/1	0.79	0.22	88,88,88,88	0
53	MG	2a	1720	1/1	0.79	0.18	75,75,75,75	0
53	MG	1t	201	1/1	0.79	0.21	77,77,77,77	0
53	MG	2k	3001	1/1	0.79	0.16	86,86,86,86	0
53	MG	2A	3248	1/1	0.80	0.27	63,63,63,63	0
53	MG	2A	3267	1/1	0.80	0.15	70,70,70,70	0
53	MG	1A	3466	1/1	0.80	0.14	87,87,87,87	0
53	MG	1A	3257	1/1	0.80	0.24	53,53,53,53	0
53	MG	2A	3332	1/1	0.80	0.32	66,66,66,66	0
53	MG	1A	3275	1/1	0.80	0.14	38,38,38,38	0
53	MG	1a	3045	1/1	0.80	0.16	76,76,76,76	0
53	MG	1A	3591	1/1	0.80	0.23	61,61,61,61	0
53	MG	1a	3131	1/1	0.80	0.23	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3058	1/1	0.80	0.17	49,49,49,49	0
53	MG	1a	3052	1/1	0.80	0.31	75,75,75,75	0
53	MG	2A	3109	1/1	0.80	0.12	67,67,67,67	0
53	MG	1A	3295	1/1	0.80	0.20	57,57,57,57	0
53	MG	1a	3057	1/1	0.80	0.73	88,88,88,88	0
53	MG	1A	3323	1/1	0.80	0.30	52,52,52,52	0
53	MG	1A	3102	1/1	0.80	0.13	85,85,85,85	0
53	MG	2a	1692	1/1	0.80	0.40	82,82,82,82	0
53	MG	2A	3147	1/1	0.80	0.23	53,53,53,53	0
53	MG	2A	3493	1/1	0.80	0.20	52,52,52,52	0
53	MG	1T	204	1/1	0.80	0.17	83,83,83,83	0
53	MG	1n	101	1/1	0.80	0.63	106,106,106,106	0
53	MG	1Z	8001	1/1	0.80	0.16	58,58,58,58	0
53	MG	2B	208	1/1	0.80	0.17	79,79,79,79	0
53	MG	2a	1715	1/1	0.80	0.24	84,84,84,84	0
53	MG	1A	3630	1/1	0.80	0.21	70,70,70,70	0
53	MG	2A	3010	1/1	0.80	0.29	67,67,67,67	0
53	MG	2a	1723	1/1	0.80	0.20	77,77,77,77	0
53	MG	1a	3008	1/1	0.80	0.16	95,95,95,95	0
53	MG	1A	3394	1/1	0.80	0.18	61,61,61,61	0
53	MG	2A	3104	1/1	0.81	0.39	79,79,79,79	0
53	MG	1A	3538	1/1	0.81	0.15	65,65,65,65	0
53	MG	1A	3069	1/1	0.81	0.31	63,63,63,63	0
53	MG	2A	3385	1/1	0.81	0.20	71,71,71,71	0
53	MG	1A	3387	1/1	0.81	0.17	46,46,46,46	0
53	MG	1A	3084	1/1	0.81	0.09	73,73,73,73	0
53	MG	2A	3422	1/1	0.81	0.16	72,72,72,72	0
53	MG	1A	3184	1/1	0.81	0.12	55,55,55,55	0
53	MG	1A	3130	1/1	0.81	0.13	63,63,63,63	0
53	MG	1a	3103	1/1	0.81	0.15	81,81,81,81	0
53	MG	1a	3107	1/1	0.81	0.17	92,92,92,92	0
53	MG	2A	3182	1/1	0.81	0.19	58,58,58,58	0
53	MG	2a	1683	1/1	0.81	0.28	89,89,89,89	0
53	MG	1a	3040	1/1	0.81	0.10	76,76,76,76	0
53	MG	2A	3216	1/1	0.81	0.33	65,65,65,65	0
53	MG	1A	3739	1/1	0.81	0.15	36,36,36,36	0
53	MG	2A	3050	1/1	0.81	0.14	45,45,45,45	0
53	MG	1B	3002	1/1	0.81	0.11	76,76,76,76	0
53	MG	2a	1699	1/1	0.81	0.19	85,85,85,85	0
53	MG	1A	3060	1/1	0.81	0.16	53,53,53,53	0
53	MG	1A	3525	1/1	0.81	0.24	73,73,73,73	0
53	MG	2B	209	1/1	0.81	0.16	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3253	1/1	0.81	0.14	54,54,54,54	0
53	MG	2a	1713	1/1	0.81	0.11	100,100,100,100	0
53	MG	1A	3609	1/1	0.81	0.22	56,56,56,56	0
53	MG	1A	3360	1/1	0.81	0.27	77,77,77,77	0
53	MG	2O	201	1/1	0.81	0.15	48,48,48,48	0
53	MG	2A	3313	1/1	0.81	0.10	63,63,63,63	0
53	MG	1A	3531	1/1	0.81	0.31	78,78,78,78	0
53	MG	1A	3362	1/1	0.81	0.13	63,63,63,63	0
53	MG	2A	3027	1/1	0.82	0.12	63,63,63,63	0
53	MG	2A	3030	1/1	0.82	0.17	73,73,73,73	0
53	MG	1A	3128	1/1	0.82	0.26	60,60,60,60	0
53	MG	2A	3184	1/1	0.82	0.12	52,52,52,52	0
53	MG	2A	3045	1/1	0.82	0.20	61,61,61,61	0
53	MG	1A	3589	1/1	0.82	0.18	91,91,91,91	0
53	MG	1A	3719	1/1	0.82	0.15	71,71,71,71	0
53	MG	1A	3095	1/1	0.82	0.13	67,67,67,67	0
53	MG	1A	3010	1/1	0.82	0.11	67,67,67,67	0
53	MG	2A	3494	1/1	0.82	0.10	66,66,66,66	0
53	MG	1A	3319	1/1	0.82	0.19	70,70,70,70	0
53	MG	1A	3761	1/1	0.82	0.14	64,64,64,64	0
53	MG	2B	204	1/1	0.82	0.21	63,63,63,63	0
53	MG	2A	3249	1/1	0.82	0.19	64,64,64,64	0
53	MG	2A	3078	1/1	0.82	0.14	62,62,62,62	0
53	MG	1a	3033	1/1	0.82	0.15	83,83,83,83	0
53	MG	1A	3206	1/1	0.82	0.21	67,67,67,67	0
53	MG	1a	3039	1/1	0.82	0.40	62,62,62,62	0
53	MG	1A	3136	1/1	0.82	0.21	63,63,63,63	0
53	MG	1B	3015	1/1	0.82	0.18	64,64,64,64	0
53	MG	2a	1712	1/1	0.82	0.15	103,103,103,103	0
53	MG	2A	3008	1/1	0.82	0.23	60,60,60,60	0
53	MG	2A	3120	1/1	0.82	0.26	64,64,64,64	0
53	MG	1A	3429	1/1	0.82	0.12	63,63,63,63	0
53	MG	1A	3038	1/1	0.82	0.20	35,35,35,35	0
53	MG	1A	3561	1/1	0.82	0.59	70,70,70,70	0
53	MG	2A	3161	1/1	0.82	0.18	54,54,54,54	0
53	MG	2e	3001	1/1	0.82	0.34	74,74,74,74	0
53	MG	2a	1623	1/1	0.82	0.11	66,66,66,66	0
53	MG	2t	201	1/1	0.82	0.48	80,80,80,80	0
53	MG	1a	3066	1/1	0.83	0.17	74,74,74,74	0
53	MG	1a	3003	1/1	0.83	0.17	77,77,77,77	0
53	MG	2A	3117	1/1	0.83	0.29	73,73,73,73	0
53	MG	1A	3363	1/1	0.83	0.20	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3382	1/1	0.83	0.13	51,51,51,51	0
53	MG	1a	3081	1/1	0.83	0.29	63,63,63,63	0
53	MG	1A	3745	1/1	0.83	0.26	81,81,81,81	0
53	MG	2A	3409	1/1	0.83	0.12	53,53,53,53	0
53	MG	1a	3087	1/1	0.83	0.10	87,87,87,87	0
53	MG	1A	3748	1/1	0.83	0.13	62,62,62,62	0
53	MG	2A	3016	1/1	0.83	0.14	70,70,70,70	0
53	MG	1A	3370	1/1	0.83	0.10	57,57,57,57	0
53	MG	1a	3026	1/1	0.83	0.26	65,65,65,65	0
53	MG	2a	1658	1/1	0.83	0.29	74,74,74,74	0
53	MG	2A	3434	1/1	0.83	0.26	57,57,57,57	0
53	MG	2A	3437	1/1	0.83	0.19	83,83,83,83	0
53	MG	1A	3042	1/1	0.83	0.16	53,53,53,53	0
53	MG	1A	3378	1/1	0.83	0.15	72,72,72,72	0
53	MG	1A	3287	1/1	0.83	0.15	49,49,49,49	0
53	MG	1A	3050	1/1	0.83	0.19	78,78,78,78	0
53	MG	1A	3074	1/1	0.83	0.10	64,64,64,64	0
53	MG	1A	3255	1/1	0.83	0.15	57,57,57,57	0
53	MG	2A	3229	1/1	0.83	0.22	72,72,72,72	0
53	MG	1A	3014	1/1	0.83	0.34	52,52,52,52	0
53	MG	2B	202	1/1	0.83	0.35	85,85,85,85	0
53	MG	1U	201	1/1	0.83	0.43	45,45,45,45	0
53	MG	1a	3135	1/1	0.83	0.19	105,105,105,105	0
53	MG	1A	3027	1/1	0.83	0.08	66,66,66,66	0
53	MG	11	3002	1/1	0.83	0.19	51,51,51,51	0
53	MG	2B	211	1/1	0.83	0.14	62,62,62,62	0
53	MG	2B	212	1/1	0.83	0.22	71,71,71,71	0
53	MG	2B	213	1/1	0.83	0.26	70,70,70,70	0
53	MG	15	102	1/1	0.83	0.15	47,47,47,47	0
53	MG	2A	3088	1/1	0.83	0.19	67,67,67,67	0
53	MG	2A	3304	1/1	0.83	0.11	57,57,57,57	0
53	MG	1A	3436	1/1	0.83	0.18	49,49,49,49	0
53	MG	1g	3002	1/1	0.83	0.09	83,83,83,83	0
53	MG	1A	3210	1/1	0.84	0.12	60,60,60,60	0
53	MG	1A	3548	1/1	0.84	0.55	69,69,69,69	0
53	MG	1A	3464	1/1	0.84	0.17	36,36,36,36	0
53	MG	1A	3126	1/1	0.84	0.14	55,55,55,55	0
53	MG	2a	1634	1/1	0.84	0.35	78,78,78,78	0
53	MG	1A	3303	1/1	0.84	0.19	52,52,52,52	0
53	MG	2A	3234	1/1	0.84	0.11	73,73,73,73	0
53	MG	2A	3235	1/1	0.84	0.18	53,53,53,53	0
53	MG	2A	3081	1/1	0.84	0.29	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3251	1/1	0.84	0.14	59,59,59,59	0
53	MG	1A	3099	1/1	0.84	0.12	64,64,64,64	0
53	MG	1A	3330	1/1	0.84	0.14	66,66,66,66	0
53	MG	1A	3031	1/1	0.84	0.17	56,56,56,56	0
53	MG	2a	1682	1/1	0.84	0.13	76,76,76,76	0
53	MG	1a	3029	1/1	0.84	0.18	72,72,72,72	0
53	MG	1A	3426	1/1	0.84	0.16	56,56,56,56	0
53	MG	2A	3287	1/1	0.84	0.18	63,63,63,63	0
53	MG	2A	3115	1/1	0.84	0.17	47,47,47,47	0
53	MG	1B	3012	1/1	0.84	0.12	64,64,64,64	0
53	MG	1A	3264	1/1	0.84	0.22	68,68,68,68	0
53	MG	1A	3431	1/1	0.84	0.26	62,62,62,62	0
53	MG	1a	3044	1/1	0.84	0.14	61,61,61,61	0
53	MG	1A	3096	1/1	0.84	0.14	62,62,62,62	0
53	MG	2A	3376	1/1	0.84	0.18	77,77,77,77	0
53	MG	1A	3364	1/1	0.84	0.16	82,82,82,82	0
53	MG	2A	3152	1/1	0.84	0.17	48,48,48,48	0
53	MG	2I	3001	1/1	0.84	0.11	81,81,81,81	0
53	MG	2a	1714	1/1	0.84	0.18	101,101,101,101	0
53	MG	1A	3112	1/1	0.84	0.14	70,70,70,70	0
53	MG	2A	3039	1/1	0.84	0.15	51,51,51,51	0
53	MG	2A	3398	1/1	0.84	0.08	61,61,61,61	0
53	MG	1A	3713	1/1	0.84	0.29	54,54,54,54	0
53	MG	1a	3055	1/1	0.84	0.17	74,74,74,74	0
53	MG	2a	1614	1/1	0.84	0.13	84,84,84,84	0
53	MG	2a	1615	1/1	0.84	0.12	79,79,79,79	0
53	MG	2l	3001	1/1	0.84	0.19	53,53,53,53	0
53	MG	1A	3715	1/1	0.84	0.13	84,84,84,84	0
53	MG	1A	3549	1/1	0.85	0.25	63,63,63,63	0
53	MG	2A	3151	1/1	0.85	0.17	64,64,64,64	0
53	MG	1a	3062	1/1	0.85	0.13	69,69,69,69	0
53	MG	1A	3551	1/1	0.85	0.12	58,58,58,58	0
53	MG	2A	3396	1/1	0.85	0.23	68,68,68,68	0
53	MG	1P	203	1/1	0.85	0.08	72,72,72,72	0
53	MG	2a	1629	1/1	0.85	0.14	61,61,61,61	0
53	MG	1A	3496	1/1	0.85	0.15	73,73,73,73	0
53	MG	2A	3047	1/1	0.85	0.11	59,59,59,59	0
53	MG	1a	3069	1/1	0.85	0.17	75,75,75,75	0
53	MG	2a	1638	1/1	0.85	0.33	74,74,74,74	0
53	MG	2A	3189	1/1	0.85	0.12	55,55,55,55	0
53	MG	1a	3141	1/1	0.85	0.17	70,70,70,70	0
53	MG	2A	3430	1/1	0.85	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
53	MG	1a	3072	1/1	0.85	0.23	83,83,83,83	0
53	MG	1A	3560	1/1	0.85	0.26	66,66,66,66	0
53	MG	2a	1652	1/1	0.85	0.33	80,80,80,80	0
53	MG	2a	1653	1/1	0.85	0.21	67,67,67,67	0
53	MG	1A	3228	1/1	0.85	0.14	65,65,65,65	0
53	MG	2A	3443	1/1	0.85	0.23	88,88,88,88	0
53	MG	1A	3633	1/1	0.85	0.20	57,57,57,57	0
53	MG	2a	1675	1/1	0.85	0.15	83,83,83,83	0
53	MG	1A	3650	1/1	0.85	0.14	42,42,42,42	0
53	MG	1A	3314	1/1	0.85	0.21	57,57,57,57	0
53	MG	2A	3236	1/1	0.85	0.22	42,42,42,42	0
53	MG	1A	3707	1/1	0.85	0.59	38,38,38,38	0
53	MG	1B	3007	1/1	0.85	0.16	43,43,43,43	0
53	MG	2a	1693	1/1	0.85	0.22	82,82,82,82	0
53	MG	1A	3447	1/1	0.85	0.22	59,59,59,59	0
53	MG	2A	3004	1/1	0.85	0.13	53,53,53,53	0
53	MG	2A	3105	1/1	0.85	0.43	74,74,74,74	0
53	MG	2A	3006	1/1	0.85	0.09	51,51,51,51	0
53	MG	1a	3106	1/1	0.85	0.14	74,74,74,74	0
53	MG	2A	3286	1/1	0.85	0.26	56,56,56,56	0
53	MG	1a	3015	1/1	0.85	0.17	73,73,73,73	0
53	MG	2A	3015	1/1	0.85	0.23	45,45,45,45	0
53	MG	1A	3116	1/1	0.85	0.09	48,48,48,48	0
53	MG	1a	3110	1/1	0.85	0.12	82,82,82,82	0
53	MG	2A	3020	1/1	0.85	0.12	54,54,54,54	0
53	MG	1A	3490	1/1	0.85	0.25	48,48,48,48	0
53	MG	2A	3344	1/1	0.85	0.42	54,54,54,54	0
53	MG	2A	3350	1/1	0.85	0.39	72,72,72,72	0
53	MG	2A	3363	1/1	0.85	0.09	52,52,52,52	0
53	MG	2Q	3001	1/1	0.85	0.20	66,66,66,66	0
53	MG	2A	3364	1/1	0.85	0.13	68,68,68,68	0
53	MG	2A	3138	1/1	0.85	0.28	55,55,55,55	0
53	MG	2A	3144	1/1	0.85	0.34	49,49,49,49	0
53	MG	1A	3717	1/1	0.86	0.19	79,79,79,79	0
53	MG	1A	3332	1/1	0.86	0.16	61,61,61,61	0
53	MG	2A	3346	1/1	0.86	0.24	68,68,68,68	0
53	MG	2a	1602	1/1	0.86	0.10	88,88,88,88	0
53	MG	2a	1605	1/1	0.86	0.14	82,82,82,82	0
53	MG	2a	1606	1/1	0.86	0.12	55,55,55,55	0
53	MG	15	106	1/1	0.86	0.15	86,86,86,86	0
53	MG	1A	3081	1/1	0.86	0.36	46,46,46,46	0
53	MG	1A	3720	1/1	0.86	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3078	1/1	0.86	0.12	65,65,65,65	0
53	MG	2A	3369	1/1	0.86	0.11	56,56,56,56	0
53	MG	2a	1616	1/1	0.86	0.17	92,92,92,92	0
53	MG	1A	3721	1/1	0.86	0.13	69,69,69,69	0
53	MG	1a	3009	1/1	0.86	0.24	70,70,70,70	0
53	MG	2A	3381	1/1	0.86	0.09	69,69,69,69	0
53	MG	1A	3599	1/1	0.86	0.28	54,54,54,54	0
53	MG	2A	3019	1/1	0.86	0.09	60,60,60,60	0
53	MG	2A	3163	1/1	0.86	0.16	55,55,55,55	0
53	MG	1A	3728	1/1	0.86	0.12	77,77,77,77	0
53	MG	1A	3144	1/1	0.86	0.33	48,48,48,48	0
53	MG	2A	3180	1/1	0.86	0.15	59,59,59,59	0
53	MG	1A	3004	1/1	0.86	0.09	42,42,42,42	0
53	MG	2A	3420	1/1	0.86	0.20	54,54,54,54	0
53	MG	1a	3025	1/1	0.86	0.23	84,84,84,84	0
53	MG	2A	3188	1/1	0.86	0.28	66,66,66,66	0
53	MG	1A	3546	1/1	0.86	0.21	77,77,77,77	0
53	MG	2A	3036	1/1	0.86	0.19	55,55,55,55	0
53	MG	2A	3213	1/1	0.86	0.21	64,64,64,64	0
53	MG	1A	3221	1/1	0.86	0.11	70,70,70,70	0
53	MG	2a	1667	1/1	0.86	0.38	74,74,74,74	0
53	MG	1a	3031	1/1	0.86	0.21	75,75,75,75	0
53	MG	2A	3226	1/1	0.86	0.16	49,49,49,49	0
53	MG	1A	3629	1/1	0.86	0.17	59,59,59,59	0
53	MG	2A	3449	1/1	0.86	0.13	59,59,59,59	0
53	MG	1a	3111	1/1	0.86	0.13	78,78,78,78	0
53	MG	1A	3306	1/1	0.86	0.10	56,56,56,56	0
53	MG	1A	3076	1/1	0.86	0.17	60,60,60,60	0
53	MG	2A	3489	1/1	0.86	0.14	55,55,55,55	0
53	MG	2A	3491	1/1	0.86	0.20	71,71,71,71	0
53	MG	1A	3648	1/1	0.86	0.69	73,73,73,73	0
53	MG	1B	3011	1/1	0.86	0.13	58,58,58,58	0
53	MG	1A	3519	1/1	0.86	0.24	75,75,75,75	0
53	MG	1a	3134	1/1	0.86	0.16	94,94,94,94	0
53	MG	1A	3315	1/1	0.86	0.12	53,53,53,53	0
53	MG	2B	203	1/1	0.86	0.10	76,76,76,76	0
53	MG	1a	3048	1/1	0.86	0.21	66,66,66,66	0
53	MG	1A	3674	1/1	0.86	0.19	82,82,82,82	0
53	MG	1A	3681	1/1	0.86	0.23	63,63,63,63	0
53	MG	2A	3271	1/1	0.86	0.23	49,49,49,49	0
53	MG	1A	3270	1/1	0.86	0.16	62,62,62,62	0
53	MG	1A	3569	1/1	0.86	0.26	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2a	1722	1/1	0.86	0.15	78,78,78,78	0
53	MG	1T	202	1/1	0.86	0.14	83,83,83,83	0
53	MG	2a	1724	1/1	0.86	0.32	91,91,91,91	0
53	MG	1A	3273	1/1	0.86	0.20	50,50,50,50	0
53	MG	2B	215	1/1	0.86	0.11	69,69,69,69	0
53	MG	2A	3316	1/1	0.86	0.11	46,46,46,46	0
53	MG	1A	3714	1/1	0.86	0.19	74,74,74,74	0
53	MG	1A	3239	1/1	0.86	0.14	56,56,56,56	0
53	MG	2F	301	1/1	0.87	0.38	62,62,62,62	0
53	MG	1A	3747	1/1	0.87	0.13	58,58,58,58	0
53	MG	2A	3295	1/1	0.87	0.11	54,54,54,54	0
53	MG	2A	3094	1/1	0.87	0.13	76,76,76,76	0
53	MG	2A	3095	1/1	0.87	0.17	71,71,71,71	0
53	MG	1A	3521	1/1	0.87	0.13	64,64,64,64	0
53	MG	1A	3310	1/1	0.87	0.71	49,49,49,49	0
53	MG	1A	3175	1/1	0.87	0.27	54,54,54,54	0
53	MG	1A	3008	1/1	0.87	0.15	57,57,57,57	0
53	MG	2a	1608	1/1	0.87	0.10	94,94,94,94	0
53	MG	1B	3008	1/1	0.87	0.27	69,69,69,69	0
53	MG	1A	3316	1/1	0.87	0.39	68,68,68,68	0
53	MG	1A	3258	1/1	0.87	0.14	40,40,40,40	0
53	MG	1A	3642	1/1	0.87	0.18	88,88,88,88	0
53	MG	1A	3262	1/1	0.87	0.29	55,55,55,55	0
53	MG	1A	3442	1/1	0.87	0.26	68,68,68,68	0
53	MG	2A	3132	1/1	0.87	0.27	56,56,56,56	0
53	MG	1E	305	1/1	0.87	0.18	79,79,79,79	0
53	MG	2a	1627	1/1	0.87	0.13	78,78,78,78	0
53	MG	1A	3544	1/1	0.87	0.38	64,64,64,64	0
53	MG	2A	3143	1/1	0.87	0.27	47,47,47,47	0
53	MG	1N	3001	1/1	0.87	0.36	77,77,77,77	0
53	MG	1a	3060	1/1	0.87	0.19	81,81,81,81	0
53	MG	2A	3148	1/1	0.87	0.28	60,60,60,60	0
53	MG	2a	1639	1/1	0.87	0.23	69,69,69,69	0
53	MG	1A	3052	1/1	0.87	0.18	61,61,61,61	0
53	MG	1A	3676	1/1	0.87	0.14	89,89,89,89	0
53	MG	2A	3153	1/1	0.87	0.17	59,59,59,59	0
53	MG	2A	3160	1/1	0.87	0.24	53,53,53,53	0
53	MG	1A	3680	1/1	0.87	0.14	41,41,41,41	0
53	MG	1A	3200	1/1	0.87	0.24	55,55,55,55	0
53	MG	1A	3703	1/1	0.87	0.17	62,62,62,62	0
53	MG	2A	3165	1/1	0.87	0.11	54,54,54,54	0
53	MG	1a	3070	1/1	0.87	0.26	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2a	1661	1/1	0.87	0.19	87,87,87,87	0
53	MG	2A	3170	1/1	0.87	0.15	61,61,61,61	0
53	MG	1A	3057	1/1	0.87	0.31	47,47,47,47	0
53	MG	1A	3361	1/1	0.87	0.28	69,69,69,69	0
53	MG	1A	3463	1/1	0.87	0.27	48,48,48,48	0
53	MG	1A	3555	1/1	0.87	0.25	35,35,35,35	0
53	MG	2a	1686	1/1	0.87	0.12	88,88,88,88	0
53	MG	2A	3447	1/1	0.87	0.12	72,72,72,72	0
53	MG	18	101	1/1	0.87	0.38	68,68,68,68	0
53	MG	2A	3025	1/1	0.87	0.17	58,58,58,58	0
53	MG	2A	3201	1/1	0.87	0.32	62,62,62,62	0
53	MG	1A	3274	1/1	0.87	0.16	61,61,61,61	0
53	MG	2A	3029	1/1	0.87	0.13	59,59,59,59	0
53	MG	1A	3098	1/1	0.87	0.12	64,64,64,64	0
53	MG	1A	3279	1/1	0.87	0.27	53,53,53,53	0
53	MG	1A	3078	1/1	0.87	0.13	67,67,67,67	0
53	MG	1A	3476	1/1	0.87	0.15	39,39,39,39	0
53	MG	2A	3503	1/1	0.87	0.15	67,67,67,67	0
53	MG	2a	1709	1/1	0.87	0.11	105,105,105,105	0
53	MG	1a	3104	1/1	0.87	0.10	92,92,92,92	0
53	MG	1A	3100	1/1	0.87	0.59	36,36,36,36	0
53	MG	1A	3063	1/1	0.87	0.23	36,36,36,36	0
53	MG	2A	3239	1/1	0.87	0.17	73,73,73,73	0
53	MG	1A	3065	1/1	0.87	0.17	52,52,52,52	0
53	MG	2A	3063	1/1	0.87	0.24	41,41,41,41	0
53	MG	1A	3731	1/1	0.87	0.20	71,71,71,71	0
53	MG	1A	3091	1/1	0.87	0.07	76,76,76,76	0
53	MG	1A	3606	1/1	0.87	0.17	58,58,58,58	0
53	MG	2A	3257	1/1	0.87	0.13	60,60,60,60	0
53	MG	1a	3115	1/1	0.87	0.13	82,82,82,82	0
53	MG	1A	3308	1/1	0.87	0.24	68,68,68,68	0
53	MG	1a	3117	1/1	0.87	0.09	78,78,78,78	0
53	MG	1a	3123	1/1	0.87	0.10	81,81,81,81	0
53	MG	2A	3042	1/1	0.88	0.25	62,62,62,62	0
53	MG	1A	3662	1/1	0.88	0.15	82,82,82,82	0
53	MG	1a	3120	1/1	0.88	0.09	92,92,92,92	0
53	MG	2A	3048	1/1	0.88	0.10	64,64,64,64	0
53	MG	1A	3533	1/1	0.88	0.11	90,90,90,90	0
53	MG	1A	3290	1/1	0.88	0.11	51,51,51,51	0
53	MG	1A	3328	1/1	0.88	0.42	61,61,61,61	0
53	MG	1A	3113	1/1	0.88	0.31	63,63,63,63	0
53	MG	2A	3383	1/1	0.88	0.14	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3006	1/1	0.88	0.10	85,85,85,85	0
53	MG	1a	3063	1/1	0.88	0.09	73,73,73,73	0
53	MG	2A	3392	1/1	0.88	0.24	51,51,51,51	0
53	MG	2a	1626	1/1	0.88	0.10	72,72,72,72	0
53	MG	2A	3072	1/1	0.88	0.19	71,71,71,71	0
53	MG	1A	3059	1/1	0.88	0.12	76,76,76,76	0
53	MG	2a	1631	1/1	0.88	0.09	59,59,59,59	0
53	MG	2A	3403	1/1	0.88	0.17	69,69,69,69	0
53	MG	1A	3706	1/1	0.88	0.10	71,71,71,71	0
53	MG	1a	3014	1/1	0.88	0.08	88,88,88,88	0
53	MG	1A	3602	1/1	0.88	0.11	50,50,50,50	0
53	MG	1a	3016	1/1	0.88	0.27	77,77,77,77	0
53	MG	1A	3402	1/1	0.88	0.10	50,50,50,50	0
53	MG	1A	3346	1/1	0.88	0.26	71,71,71,71	0
53	MG	1A	3359	1/1	0.88	0.17	66,66,66,66	0
53	MG	1a	3080	1/1	0.88	0.23	66,66,66,66	0
53	MG	1A	3615	1/1	0.88	0.21	73,73,73,73	0
53	MG	1a	3082	1/1	0.88	0.09	70,70,70,70	0
53	MG	2A	3441	1/1	0.88	0.13	57,57,57,57	0
53	MG	1a	3083	1/1	0.88	0.09	59,59,59,59	0
53	MG	1A	3236	1/1	0.88	0.14	64,64,64,64	0
53	MG	2A	3245	1/1	0.88	0.17	46,46,46,46	0
53	MG	2a	1662	1/1	0.88	0.24	74,74,74,74	0
53	MG	1a	3027	1/1	0.88	0.20	65,65,65,65	0
53	MG	2a	1670	1/1	0.88	0.20	67,67,67,67	0
53	MG	1a	3088	1/1	0.88	0.20	107,107,107,107	0
53	MG	1A	3002	1/1	0.88	0.10	51,51,51,51	0
53	MG	1A	3628	1/1	0.88	0.20	58,58,58,58	0
53	MG	2A	3131	1/1	0.88	0.33	34,34,34,34	0
53	MG	1A	3105	1/1	0.88	0.10	66,66,66,66	0
53	MG	1A	3153	1/1	0.88	0.21	52,52,52,52	0
53	MG	2A	3274	1/1	0.88	0.14	71,71,71,71	0
53	MG	2A	3282	1/1	0.88	0.49	59,59,59,59	0
53	MG	2A	3136	1/1	0.88	0.24	62,62,62,62	0
53	MG	1A	3208	1/1	0.88	0.20	47,47,47,47	0
53	MG	2A	3290	1/1	0.88	0.22	49,49,49,49	0
53	MG	1A	3557	1/1	0.88	0.21	55,55,55,55	0
53	MG	1a	3042	1/1	0.88	0.39	64,64,64,64	0
53	MG	2A	3145	1/1	0.88	0.14	55,55,55,55	0
53	MG	2A	3314	1/1	0.88	0.17	55,55,55,55	0
53	MG	2A	3315	1/1	0.88	0.30	59,59,59,59	0
53	MG	1A	3025	1/1	0.88	0.26	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3319	1/1	0.88	0.19	50,50,50,50	0
53	MG	2A	3320	1/1	0.88	0.32	73,73,73,73	0
53	MG	1A	3215	1/1	0.88	0.28	59,59,59,59	0
53	MG	10	104	1/1	0.88	0.11	57,57,57,57	0
53	MG	10	106	1/1	0.88	0.18	78,78,78,78	0
53	MG	2A	3338	1/1	0.88	0.08	49,49,49,49	0
53	MG	2E	301	1/1	0.88	0.27	45,45,45,45	0
53	MG	2A	3341	1/1	0.88	0.17	45,45,45,45	0
53	MG	2A	3342	1/1	0.88	0.12	61,61,61,61	0
53	MG	11	3001	1/1	0.88	0.19	73,73,73,73	0
53	MG	2A	3038	1/1	0.88	0.07	56,56,56,56	0
53	MG	2Y	502	1/1	0.88	0.14	57,57,57,57	0
53	MG	1A	3320	1/1	0.88	0.18	46,46,46,46	0
53	MG	2A	3353	1/1	0.88	0.11	64,64,64,64	0
53	MG	1A	3649	1/1	0.89	0.14	72,72,72,72	0
53	MG	1Q	202	1/1	0.89	0.12	50,50,50,50	0
53	MG	1A	3163	1/1	0.89	0.27	54,54,54,54	0
53	MG	1A	3651	1/1	0.89	0.14	78,78,78,78	0
53	MG	1a	3079	1/1	0.89	0.19	73,73,73,73	0
53	MG	2A	3504	1/1	0.89	0.11	74,74,74,74	0
53	MG	1A	3657	1/1	0.89	0.11	44,44,44,44	0
53	MG	2A	3509	1/1	0.89	0.12	61,61,61,61	0
53	MG	2A	3514	1/1	0.89	0.26	50,50,50,50	0
53	MG	1W	201	1/1	0.89	0.19	47,47,47,47	0
53	MG	1A	3403	1/1	0.89	0.11	68,68,68,68	0
53	MG	1A	3125	1/1	0.89	0.12	49,49,49,49	0
53	MG	1A	3067	1/1	0.89	0.08	66,66,66,66	0
53	MG	2B	206	1/1	0.89	0.12	74,74,74,74	0
53	MG	2B	207	1/1	0.89	0.12	62,62,62,62	0
53	MG	1A	3428	1/1	0.89	0.24	39,39,39,39	0
53	MG	2A	3049	1/1	0.89	0.10	57,57,57,57	0
53	MG	1A	3083	1/1	0.89	0.32	61,61,61,61	0
53	MG	2A	3053	1/1	0.89	0.14	64,64,64,64	0
53	MG	1A	3191	1/1	0.89	0.32	31,31,31,31	0
53	MG	2A	3058	1/1	0.89	0.28	52,52,52,52	0
53	MG	2A	3252	1/1	0.89	0.29	42,42,42,42	0
53	MG	2A	3061	1/1	0.89	0.14	65,65,65,65	0
53	MG	1A	3433	1/1	0.89	0.23	47,47,47,47	0
53	MG	1a	3095	1/1	0.89	0.11	66,66,66,66	0
53	MG	1A	3129	1/1	0.89	0.17	54,54,54,54	0
53	MG	2A	3069	1/1	0.89	0.17	60,60,60,60	0
53	MG	2N	8001	1/1	0.89	0.08	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3272	1/1	0.89	0.10	41,41,41,41	0
53	MG	2O	202	1/1	0.89	0.17	47,47,47,47	0
53	MG	1A	3036	1/1	0.89	0.20	76,76,76,76	0
53	MG	1A	3345	1/1	0.89	0.32	56,56,56,56	0
53	MG	1A	3710	1/1	0.89	0.10	52,52,52,52	0
53	MG	1A	3131	1/1	0.89	0.20	68,68,68,68	0
53	MG	2A	3080	1/1	0.89	0.16	66,66,66,66	0
53	MG	1a	3108	1/1	0.89	0.11	61,61,61,61	0
53	MG	1A	3356	1/1	0.89	0.24	41,41,41,41	0
53	MG	1A	3207	1/1	0.89	0.27	49,49,49,49	0
53	MG	2A	3089	1/1	0.89	0.09	71,71,71,71	0
53	MG	1A	3132	1/1	0.89	0.08	49,49,49,49	0
53	MG	1A	3070	1/1	0.89	0.20	74,74,74,74	0
53	MG	2A	3098	1/1	0.89	0.15	54,54,54,54	0
53	MG	2A	3099	1/1	0.89	0.13	46,46,46,46	0
53	MG	2A	3321	1/1	0.89	0.15	47,47,47,47	0
53	MG	2a	1619	1/1	0.89	0.12	81,81,81,81	0
53	MG	2A	3322	1/1	0.89	0.22	53,53,53,53	0
53	MG	2a	1621	1/1	0.89	0.08	88,88,88,88	0
53	MG	1A	3573	1/1	0.89	0.16	92,92,92,92	0
53	MG	2a	1625	1/1	0.89	0.17	69,69,69,69	0
53	MG	2A	3325	1/1	0.89	0.20	53,53,53,53	0
53	MG	2A	3327	1/1	0.89	0.23	51,51,51,51	0
53	MG	1A	3213	1/1	0.89	0.20	64,64,64,64	0
53	MG	1A	3586	1/1	0.89	0.24	41,41,41,41	0
53	MG	1A	3072	1/1	0.89	0.29	58,58,58,58	0
53	MG	1A	3216	1/1	0.89	0.40	55,55,55,55	0
53	MG	2A	3112	1/1	0.89	0.13	37,37,37,37	0
53	MG	1A	3592	1/1	0.89	0.15	49,49,49,49	0
53	MG	1A	3595	1/1	0.89	0.19	68,68,68,68	0
53	MG	2A	3349	1/1	0.89	0.15	62,62,62,62	0
53	MG	1a	3132	1/1	0.89	0.11	65,65,65,65	0
53	MG	2A	3119	1/1	0.89	0.13	72,72,72,72	0
53	MG	2A	3358	1/1	0.89	0.12	49,49,49,49	0
53	MG	1A	3048	1/1	0.89	0.18	48,48,48,48	0
53	MG	2A	3122	1/1	0.89	0.11	47,47,47,47	0
53	MG	1A	3485	1/1	0.89	0.13	72,72,72,72	0
53	MG	2a	1655	1/1	0.89	0.23	78,78,78,78	0
53	MG	2a	1657	1/1	0.89	0.18	68,68,68,68	0
53	MG	2A	3127	1/1	0.89	0.33	66,66,66,66	0
53	MG	1A	3487	1/1	0.89	0.14	45,45,45,45	0
53	MG	2a	1660	1/1	0.89	0.08	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3377	1/1	0.89	0.11	50,50,50,50	0
53	MG	1A	3372	1/1	0.89	0.21	59,59,59,59	0
53	MG	2a	1663	1/1	0.89	0.17	62,62,62,62	0
53	MG	2a	1665	1/1	0.89	0.15	76,76,76,76	0
53	MG	2a	1666	1/1	0.89	0.16	66,66,66,66	0
53	MG	2A	3133	1/1	0.89	0.15	63,63,63,63	0
53	MG	1A	3760	1/1	0.89	0.27	42,42,42,42	0
53	MG	1a	3143	1/1	0.89	0.19	79,79,79,79	0
53	MG	1a	3041	1/1	0.89	0.12	96,96,96,96	0
53	MG	2a	1680	1/1	0.89	0.39	56,56,56,56	0
53	MG	1A	3223	1/1	0.89	0.19	71,71,71,71	0
53	MG	1A	3509	1/1	0.89	0.13	77,77,77,77	0
53	MG	1B	3005	1/1	0.89	0.18	52,52,52,52	0
53	MG	1B	3006	1/1	0.89	0.08	47,47,47,47	0
53	MG	1A	3227	1/1	0.89	0.40	61,61,61,61	0
53	MG	2A	3406	1/1	0.89	0.20	49,49,49,49	0
53	MG	1A	3515	1/1	0.89	0.20	75,75,75,75	0
53	MG	1A	3384	1/1	0.89	0.12	30,30,30,30	0
53	MG	2A	3414	1/1	0.89	0.09	70,70,70,70	0
53	MG	1a	3053	1/1	0.89	0.08	60,60,60,60	0
53	MG	2A	3157	1/1	0.89	0.13	55,55,55,55	0
53	MG	1A	3625	1/1	0.89	0.23	49,49,49,49	0
53	MG	1A	3034	1/1	0.89	0.24	50,50,50,50	0
53	MG	1A	3388	1/1	0.89	0.39	53,53,53,53	0
53	MG	1B	3018	1/1	0.89	0.13	69,69,69,69	0
53	MG	2A	3014	1/1	0.89	0.26	53,53,53,53	0
53	MG	2A	3435	1/1	0.89	0.21	88,88,88,88	0
53	MG	1A	3145	1/1	0.89	0.32	26,26,26,26	0
53	MG	1A	3051	1/1	0.89	0.12	60,60,60,60	0
53	MG	2A	3171	1/1	0.89	0.15	62,62,62,62	0
53	MG	1F	302	1/1	0.89	0.18	43,43,43,43	0
53	MG	2A	3446	1/1	0.89	0.12	59,59,59,59	0
53	MG	1A	3397	1/1	0.89	0.16	35,35,35,35	0
53	MG	1H	202	1/1	0.89	0.09	50,50,50,50	0
53	MG	2A	3453	1/1	0.89	0.18	66,66,66,66	0
53	MG	2a	1729	1/1	0.89	0.16	65,65,65,65	0
53	MG	2A	3022	1/1	0.89	0.12	67,67,67,67	0
53	MG	1A	3647	1/1	0.89	0.10	66,66,66,66	0
53	MG	1A	3158	1/1	0.89	0.13	55,55,55,55	0
53	MG	2A	3198	1/1	0.89	0.21	40,40,40,40	0
53	MG	2A	3090	1/1	0.90	0.22	77,77,77,77	0
53	MG	2A	3093	1/1	0.90	0.48	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3019	1/1	0.90	0.18	81,81,81,81	0
53	MG	2A	3276	1/1	0.90	0.11	57,57,57,57	0
53	MG	1A	3254	1/1	0.90	0.21	48,48,48,48	0
53	MG	1A	3736	1/1	0.90	0.16	68,68,68,68	0
53	MG	1A	3007	1/1	0.90	0.17	56,56,56,56	0
53	MG	1A	3744	1/1	0.90	0.11	74,74,74,74	0
53	MG	2A	3291	1/1	0.90	0.15	45,45,45,45	0
53	MG	1A	3088	1/1	0.90	0.12	71,71,71,71	0
53	MG	1a	3028	1/1	0.90	0.11	59,59,59,59	0
53	MG	2A	3306	1/1	0.90	0.15	68,68,68,68	0
53	MG	2B	217	1/1	0.90	0.09	98,98,98,98	0
53	MG	2A	3307	1/1	0.90	0.20	69,69,69,69	0
53	MG	2A	3309	1/1	0.90	0.17	50,50,50,50	0
53	MG	2A	3312	1/1	0.90	0.21	70,70,70,70	0
53	MG	1A	3616	1/1	0.90	0.17	87,87,87,87	0
53	MG	1a	3030	1/1	0.90	0.10	59,59,59,59	0
53	MG	1A	3618	1/1	0.90	0.16	81,81,81,81	0
53	MG	1A	3757	1/1	0.90	0.34	51,51,51,51	0
53	MG	2P	201	1/1	0.90	0.19	49,49,49,49	0
53	MG	1A	3103	1/1	0.90	0.07	81,81,81,81	0
53	MG	2T	203	1/1	0.90	0.12	52,52,52,52	0
53	MG	1d	502	1/1	0.90	0.09	58,58,58,58	0
53	MG	1A	3622	1/1	0.90	0.11	55,55,55,55	0
53	MG	2a	1601	1/1	0.90	0.10	71,71,71,71	0
53	MG	1A	3211	1/1	0.90	0.12	50,50,50,50	0
53	MG	1A	3011	1/1	0.90	0.32	49,49,49,49	0
53	MG	2A	3324	1/1	0.90	0.21	51,51,51,51	0
53	MG	1A	3321	1/1	0.90	0.10	54,54,54,54	0
53	MG	1a	3043	1/1	0.90	0.16	90,90,90,90	0
53	MG	2A	3330	1/1	0.90	0.28	47,47,47,47	0
53	MG	1A	3266	1/1	0.90	0.13	65,65,65,65	0
53	MG	2A	3336	1/1	0.90	0.27	66,66,66,66	0
53	MG	1A	3417	1/1	0.90	0.17	59,59,59,59	0
53	MG	1A	3422	1/1	0.90	0.17	22,22,22,22	0
53	MG	1A	3017	1/1	0.90	0.10	56,56,56,56	0
53	MG	1A	3644	1/1	0.90	0.14	78,78,78,78	0
53	MG	1A	3329	1/1	0.90	0.23	37,37,37,37	0
53	MG	2A	3345	1/1	0.90	0.15	55,55,55,55	0
53	MG	1A	3271	1/1	0.90	0.10	44,44,44,44	0
53	MG	2a	1624	1/1	0.90	0.11	55,55,55,55	0
53	MG	2A	3348	1/1	0.90	0.15	58,58,58,58	0
53	MG	1a	3054	1/1	0.90	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
53	MG	1D	303	1/1	0.90	0.10	58,58,58,58	0
53	MG	1A	3543	1/1	0.90	0.11	60,60,60,60	0
53	MG	1A	3064	1/1	0.90	0.15	57,57,57,57	0
53	MG	2A	3149	1/1	0.90	0.10	52,52,52,52	0
53	MG	2A	3150	1/1	0.90	0.12	46,46,46,46	0
53	MG	2A	3366	1/1	0.90	0.10	37,37,37,37	0
53	MG	1A	3180	1/1	0.90	0.22	57,57,57,57	0
53	MG	1A	3655	1/1	0.90	0.20	77,77,77,77	0
53	MG	1A	3181	1/1	0.90	0.27	65,65,65,65	0
53	MG	1A	3350	1/1	0.90	0.25	59,59,59,59	0
53	MG	2a	1642	1/1	0.90	0.07	70,70,70,70	0
53	MG	1A	3041	1/1	0.90	0.46	59,59,59,59	0
53	MG	1A	3281	1/1	0.90	0.12	56,56,56,56	0
53	MG	2a	1647	1/1	0.90	0.11	64,64,64,64	0
53	MG	1A	3675	1/1	0.90	0.11	63,63,63,63	0
53	MG	1R	205	1/1	0.90	0.10	25,25,25,25	0
53	MG	2A	3384	1/1	0.90	0.10	45,45,45,45	0
53	MG	1A	3282	1/1	0.90	0.34	61,61,61,61	0
53	MG	1A	3021	1/1	0.90	0.22	27,27,27,27	0
53	MG	2A	3034	1/1	0.90	0.07	60,60,60,60	0
53	MG	1A	3461	1/1	0.90	0.15	86,86,86,86	0
53	MG	1U	202	1/1	0.90	0.12	49,49,49,49	0
53	MG	1A	3694	1/1	0.90	0.20	76,76,76,76	0
53	MG	1W	202	1/1	0.90	0.23	52,52,52,52	0
53	MG	2A	3187	1/1	0.90	0.18	45,45,45,45	0
53	MG	1A	3558	1/1	0.90	0.08	53,53,53,53	0
53	MG	10	103	1/1	0.90	0.16	39,39,39,39	0
53	MG	1A	3704	1/1	0.90	0.11	53,53,53,53	0
53	MG	10	105	1/1	0.90	0.19	62,62,62,62	0
53	MG	2A	3199	1/1	0.90	0.21	26,26,26,26	0
53	MG	1A	3232	1/1	0.90	0.15	60,60,60,60	0
53	MG	2a	1679	1/1	0.90	0.10	74,74,74,74	0
53	MG	2A	3428	1/1	0.90	0.15	83,83,83,83	0
53	MG	2A	3211	1/1	0.90	0.26	50,50,50,50	0
53	MG	2A	3432	1/1	0.90	0.08	62,62,62,62	0
53	MG	2A	3052	1/1	0.90	0.20	66,66,66,66	0
53	MG	1A	3118	1/1	0.90	0.19	53,53,53,53	0
53	MG	2A	3218	1/1	0.90	0.20	44,44,44,44	0
53	MG	2A	3220	1/1	0.90	0.10	37,37,37,37	0
53	MG	1A	3141	1/1	0.90	0.16	62,62,62,62	0
53	MG	1a	3090	1/1	0.90	0.11	88,88,88,88	0
53	MG	1A	3367	1/1	0.90	0.21	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3445	1/1	0.90	0.12	46,46,46,46	0
53	MG	1A	3302	1/1	0.90	0.39	63,63,63,63	0
53	MG	2A	3230	1/1	0.90	0.10	46,46,46,46	0
53	MG	2A	3232	1/1	0.90	0.19	47,47,47,47	0
53	MG	1A	3470	1/1	0.90	0.18	71,71,71,71	0
53	MG	19	103	1/1	0.90	0.24	47,47,47,47	0
53	MG	2A	3068	1/1	0.90	0.12	59,59,59,59	0
53	MG	1A	3245	1/1	0.90	0.12	48,48,48,48	0
53	MG	1A	3479	1/1	0.90	0.16	58,58,58,58	0
53	MG	1a	3004	1/1	0.90	0.10	65,65,65,65	0
53	MG	2A	3492	1/1	0.90	0.19	83,83,83,83	0
53	MG	2A	3244	1/1	0.90	0.09	48,48,48,48	0
53	MG	2A	3073	1/1	0.90	0.13	61,61,61,61	0
53	MG	1A	3205	1/1	0.90	0.12	40,40,40,40	0
53	MG	1A	3307	1/1	0.90	0.21	34,34,34,34	0
53	MG	1A	3383	1/1	0.90	0.24	71,71,71,71	0
53	MG	1A	3491	1/1	0.90	0.13	65,65,65,65	0
53	MG	2A	3256	1/1	0.90	0.17	58,58,58,58	0
53	MG	1A	3024	1/1	0.90	0.52	62,62,62,62	0
53	MG	1A	3309	1/1	0.90	0.30	46,46,46,46	0
53	MG	1A	3607	1/1	0.90	0.12	86,86,86,86	0
53	MG	1A	3248	1/1	0.91	0.11	55,55,55,55	0
53	MG	1A	3204	1/1	0.91	0.19	57,57,57,57	0
53	MG	1A	3023	1/1	0.91	0.22	60,60,60,60	0
53	MG	1A	3687	1/1	0.91	0.17	74,74,74,74	0
53	MG	1A	3692	1/1	0.91	0.11	36,36,36,36	0
53	MG	1A	3305	1/1	0.91	0.11	60,60,60,60	0
53	MG	1A	3562	1/1	0.91	0.28	70,70,70,70	0
53	MG	2A	3011	1/1	0.91	0.22	52,52,52,52	0
53	MG	2A	3137	1/1	0.91	0.13	56,56,56,56	0
53	MG	1A	3368	1/1	0.91	0.13	62,62,62,62	0
53	MG	1A	3369	1/1	0.91	0.22	47,47,47,47	0
53	MG	1a	3061	1/1	0.91	0.12	78,78,78,78	0
53	MG	1A	3161	1/1	0.91	0.20	51,51,51,51	0
53	MG	2A	3326	1/1	0.91	0.12	55,55,55,55	0
53	MG	1V	3002	1/1	0.91	0.09	62,62,62,62	0
53	MG	1A	3583	1/1	0.91	0.12	53,53,53,53	0
53	MG	2A	3331	1/1	0.91	0.18	65,65,65,65	0
53	MG	1A	3162	1/1	0.91	0.30	51,51,51,51	0
53	MG	1A	3712	1/1	0.91	0.12	53,53,53,53	0
53	MG	10	101	1/1	0.91	0.15	67,67,67,67	0
53	MG	1A	3028	1/1	0.91	0.17	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3340	1/1	0.91	0.11	53,53,53,53	0
53	MG	2A	3028	1/1	0.91	0.07	57,57,57,57	0
53	MG	2A	3156	1/1	0.91	0.12	50,50,50,50	0
53	MG	2A	3343	1/1	0.91	0.31	50,50,50,50	0
53	MG	2a	1603	1/1	0.91	0.22	79,79,79,79	0
53	MG	1A	3377	1/1	0.91	0.19	60,60,60,60	0
53	MG	2A	3158	1/1	0.91	0.26	54,54,54,54	0
53	MG	1A	3482	1/1	0.91	0.07	55,55,55,55	0
53	MG	1A	3117	1/1	0.91	0.14	63,63,63,63	0
53	MG	2a	1609	1/1	0.91	0.11	60,60,60,60	0
53	MG	2A	3162	1/1	0.91	0.31	52,52,52,52	0
53	MG	1A	3171	1/1	0.91	0.12	46,46,46,46	0
53	MG	2A	3035	1/1	0.91	0.15	65,65,65,65	0
53	MG	2A	3354	1/1	0.91	0.13	68,68,68,68	0
53	MG	1A	3312	1/1	0.91	0.23	44,44,44,44	0
53	MG	2A	3361	1/1	0.91	0.10	64,64,64,64	0
53	MG	2A	3362	1/1	0.91	0.20	51,51,51,51	0
53	MG	2A	3167	1/1	0.91	0.16	56,56,56,56	0
53	MG	1A	3601	1/1	0.91	0.11	43,43,43,43	0
53	MG	1A	3173	1/1	0.91	0.25	48,48,48,48	0
53	MG	17	101	1/1	0.91	0.11	38,38,38,38	0
53	MG	1A	3723	1/1	0.91	0.09	62,62,62,62	0
53	MG	2A	3374	1/1	0.91	0.09	48,48,48,48	0
53	MG	1A	3726	1/1	0.91	0.13	56,56,56,56	0
53	MG	1A	3492	1/1	0.91	0.09	80,80,80,80	0
53	MG	1A	3174	1/1	0.91	0.35	44,44,44,44	0
53	MG	1A	3267	1/1	0.91	0.11	42,42,42,42	0
53	MG	2A	3051	1/1	0.91	0.42	69,69,69,69	0
53	MG	1a	3091	1/1	0.91	0.14	62,62,62,62	0
53	MG	2a	1635	1/1	0.91	0.18	59,59,59,59	0
53	MG	1A	3317	1/1	0.91	0.21	52,52,52,52	0
53	MG	1A	3512	1/1	0.91	0.10	64,64,64,64	0
53	MG	2A	3386	1/1	0.91	0.08	55,55,55,55	0
53	MG	1A	3514	1/1	0.91	0.14	83,83,83,83	0
53	MG	2A	3391	1/1	0.91	0.11	51,51,51,51	0
53	MG	2A	3060	1/1	0.91	0.08	52,52,52,52	0
53	MG	1a	3010	1/1	0.91	0.09	83,83,83,83	0
53	MG	1A	3743	1/1	0.91	0.16	65,65,65,65	0
53	MG	2a	1648	1/1	0.91	0.22	52,52,52,52	0
53	MG	2A	3217	1/1	0.91	0.20	64,64,64,64	0
53	MG	2a	1651	1/1	0.91	0.18	76,76,76,76	0
53	MG	1A	3005	1/1	0.91	0.35	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3073	1/1	0.91	0.12	62,62,62,62	0
53	MG	2a	1654	1/1	0.91	0.07	67,67,67,67	0
53	MG	1A	3019	1/1	0.91	0.09	53,53,53,53	0
53	MG	1A	3047	1/1	0.91	0.22	59,59,59,59	0
53	MG	1A	3409	1/1	0.91	0.12	30,30,30,30	0
53	MG	2A	3421	1/1	0.91	0.08	56,56,56,56	0
53	MG	1A	3185	1/1	0.91	0.21	51,51,51,51	0
53	MG	1A	3276	1/1	0.91	0.24	43,43,43,43	0
53	MG	2A	3426	1/1	0.91	0.13	56,56,56,56	0
53	MG	2A	3231	1/1	0.91	0.20	49,49,49,49	0
53	MG	1A	3421	1/1	0.91	0.28	40,40,40,40	0
53	MG	1A	3277	1/1	0.91	0.24	39,39,39,39	0
53	MG	1A	3537	1/1	0.91	0.20	59,59,59,59	0
53	MG	1A	3423	1/1	0.91	0.12	63,63,63,63	0
53	MG	1A	3077	1/1	0.91	0.19	51,51,51,51	0
53	MG	1A	3194	1/1	0.91	0.15	51,51,51,51	0
53	MG	2A	3436	1/1	0.91	0.11	61,61,61,61	0
53	MG	1a	3032	1/1	0.91	0.23	56,56,56,56	0
53	MG	1A	3149	1/1	0.91	0.24	31,31,31,31	0
53	MG	2A	3091	1/1	0.91	0.28	68,68,68,68	0
53	MG	2a	1684	1/1	0.91	0.11	75,75,75,75	0
53	MG	2A	3092	1/1	0.91	0.25	68,68,68,68	0
53	MG	1a	3034	1/1	0.91	0.11	61,61,61,61	0
53	MG	1A	3347	1/1	0.91	0.12	52,52,52,52	0
53	MG	2a	1691	1/1	0.91	0.46	76,76,76,76	0
53	MG	1a	3037	1/1	0.91	0.07	84,84,84,84	0
53	MG	2A	3448	1/1	0.91	0.21	80,80,80,80	0
53	MG	2A	3097	1/1	0.91	0.18	67,67,67,67	0
53	MG	2A	3452	1/1	0.91	0.17	67,67,67,67	0
53	MG	1A	3243	1/1	0.91	0.12	50,50,50,50	0
53	MG	1a	3137	1/1	0.91	0.20	86,86,86,86	0
53	MG	1a	3138	1/1	0.91	0.17	115,115,115,115	0
53	MG	2a	1702	1/1	0.91	0.09	62,62,62,62	0
53	MG	2a	1703	1/1	0.91	0.12	91,91,91,91	0
53	MG	2a	1704	1/1	0.91	0.08	110,110,110,110	0
53	MG	1A	3351	1/1	0.91	0.15	40,40,40,40	0
53	MG	1a	3142	1/1	0.91	0.21	57,57,57,57	0
53	MG	2A	3106	1/1	0.91	0.18	54,54,54,54	0
53	MG	2A	3108	1/1	0.91	0.25	54,54,54,54	0
53	MG	1D	301	1/1	0.91	0.10	59,59,59,59	0
53	MG	2A	3284	1/1	0.91	0.26	56,56,56,56	0
53	MG	1A	3285	1/1	0.91	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1D	307	1/1	0.91	0.21	87,87,87,87	0
53	MG	2A	3114	1/1	0.91	0.13	78,78,78,78	0
53	MG	2A	3507	1/1	0.91	0.30	93,93,93,93	0
53	MG	1A	3012	1/1	0.91	0.38	47,47,47,47	0
53	MG	1A	3289	1/1	0.91	0.14	39,39,39,39	0
53	MG	2A	3300	1/1	0.91	0.07	41,41,41,41	0
53	MG	2A	3519	1/1	0.91	0.12	70,70,70,70	0
53	MG	2A	3301	1/1	0.91	0.11	45,45,45,45	0
53	MG	1a	3046	1/1	0.91	0.09	65,65,65,65	0
53	MG	1A	3246	1/1	0.91	0.08	40,40,40,40	0
53	MG	1A	3448	1/1	0.91	0.11	64,64,64,64	0
54	HGR	2A	3515	36/36	0.91	0.17	36,61,70,76	0
55	ZN	2n	501	1/1	0.91	0.16	160,160,160,160	0
53	MG	1A	3481	1/1	0.92	0.16	55,55,55,55	0
53	MG	1F	301	1/1	0.92	0.12	28,28,28,28	0
53	MG	2A	3121	1/1	0.92	0.13	62,62,62,62	0
53	MG	2A	3001	1/1	0.92	0.07	48,48,48,48	0
53	MG	2A	3310	1/1	0.92	0.13	52,52,52,52	0
53	MG	1A	3400	1/1	0.92	0.10	58,58,58,58	0
53	MG	1F	303	1/1	0.92	0.16	40,40,40,40	0
53	MG	1A	3256	1/1	0.92	0.07	52,52,52,52	0
53	MG	2A	3009	1/1	0.92	0.16	57,57,57,57	0
53	MG	2B	218	1/1	0.92	0.11	62,62,62,62	0
53	MG	1A	3486	1/1	0.92	0.19	52,52,52,52	0
53	MG	1A	3688	1/1	0.92	0.09	76,76,76,76	0
53	MG	1A	3568	1/1	0.92	0.30	51,51,51,51	0
53	MG	2F	302	1/1	0.92	0.08	64,64,64,64	0
53	MG	1A	3294	1/1	0.92	0.27	39,39,39,39	0
53	MG	1A	3695	1/1	0.92	0.10	57,57,57,57	0
53	MG	2A	3141	1/1	0.92	0.19	68,68,68,68	0
53	MG	1Q	203	1/1	0.92	0.10	35,35,35,35	0
53	MG	1A	3348	1/1	0.92	0.19	51,51,51,51	0
53	MG	1A	3411	1/1	0.92	0.12	32,32,32,32	0
53	MG	1A	3049	1/1	0.92	0.06	51,51,51,51	0
53	MG	1A	3585	1/1	0.92	0.12	55,55,55,55	0
53	MG	2A	3024	1/1	0.92	0.10	57,57,57,57	0
53	MG	1A	3122	1/1	0.92	0.12	61,61,61,61	0
53	MG	1A	3497	1/1	0.92	0.12	35,35,35,35	0
53	MG	1A	3590	1/1	0.92	0.19	54,54,54,54	0
53	MG	1a	3071	1/1	0.92	0.08	68,68,68,68	0
53	MG	1A	3499	1/1	0.92	0.12	63,63,63,63	0
53	MG	2A	3031	1/1	0.92	0.11	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3501	1/1	0.92	0.11	59,59,59,59	0
53	MG	1a	3077	1/1	0.92	0.26	69,69,69,69	0
53	MG	2a	1610	1/1	0.92	0.14	74,74,74,74	0
53	MG	1A	3503	1/1	0.92	0.17	43,43,43,43	0
53	MG	1A	3508	1/1	0.92	0.20	77,77,77,77	0
53	MG	1A	3354	1/1	0.92	0.15	63,63,63,63	0
53	MG	1A	3080	1/1	0.92	0.10	67,67,67,67	0
53	MG	2A	3040	1/1	0.92	0.41	66,66,66,66	0
53	MG	1A	3263	1/1	0.92	0.13	61,61,61,61	0
53	MG	2A	3351	1/1	0.92	0.09	59,59,59,59	0
53	MG	2A	3044	1/1	0.92	0.07	57,57,57,57	0
53	MG	2A	3169	1/1	0.92	0.22	48,48,48,48	0
53	MG	2a	1622	1/1	0.92	0.14	83,83,83,83	0
53	MG	1A	3604	1/1	0.92	0.11	64,64,64,64	0
53	MG	1a	3085	1/1	0.92	0.09	45,45,45,45	0
53	MG	1A	3189	1/1	0.92	0.22	26,26,26,26	0
53	MG	1A	3724	1/1	0.92	0.08	38,38,38,38	0
53	MG	1A	3020	1/1	0.92	0.14	35,35,35,35	0
53	MG	1A	3018	1/1	0.92	0.18	64,64,64,64	0
53	MG	1A	3518	1/1	0.92	0.08	37,37,37,37	0
53	MG	1A	3730	1/1	0.92	0.13	52,52,52,52	0
53	MG	1A	3107	1/1	0.92	0.17	63,63,63,63	0
53	MG	2A	3194	1/1	0.92	0.27	33,33,33,33	0
53	MG	2A	3196	1/1	0.92	0.34	27,27,27,27	0
53	MG	2a	1637	1/1	0.92	0.17	65,65,65,65	0
53	MG	2A	3057	1/1	0.92	0.13	65,65,65,65	0
53	MG	1a	3094	1/1	0.92	0.12	88,88,88,88	0
53	MG	2A	3059	1/1	0.92	0.14	42,42,42,42	0
53	MG	2A	3203	1/1	0.92	0.19	28,28,28,28	0
53	MG	2A	3204	1/1	0.92	0.32	64,64,64,64	0
53	MG	2A	3206	1/1	0.92	0.08	48,48,48,48	0
53	MG	2a	1644	1/1	0.92	0.09	91,91,91,91	0
53	MG	2a	1645	1/1	0.92	0.08	64,64,64,64	0
53	MG	1A	3233	1/1	0.92	0.12	58,58,58,58	0
53	MG	2A	3212	1/1	0.92	0.23	37,37,37,37	0
53	MG	1a	3097	1/1	0.92	0.13	82,82,82,82	0
53	MG	2a	1649	1/1	0.92	0.10	55,55,55,55	0
53	MG	1A	3734	1/1	0.92	0.26	69,69,69,69	0
53	MG	1A	3522	1/1	0.92	0.12	70,70,70,70	0
53	MG	2A	3065	1/1	0.92	0.15	37,37,37,37	0
53	MG	1a	3007	1/1	0.92	0.08	64,64,64,64	0
53	MG	2A	3221	1/1	0.92	0.12	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3105	1/1	0.92	0.10	60,60,60,60	0
53	MG	1A	3108	1/1	0.92	0.15	45,45,45,45	0
53	MG	2A	3070	1/1	0.92	0.27	57,57,57,57	0
53	MG	2A	3415	1/1	0.92	0.10	61,61,61,61	0
53	MG	2A	3416	1/1	0.92	0.25	45,45,45,45	0
53	MG	1A	3740	1/1	0.92	0.24	48,48,48,48	0
53	MG	1A	3742	1/1	0.92	0.14	36,36,36,36	0
53	MG	1A	3202	1/1	0.92	0.40	33,33,33,33	0
53	MG	2a	1664	1/1	0.92	0.10	68,68,68,68	0
53	MG	1A	3527	1/1	0.92	0.13	56,56,56,56	0
53	MG	1A	3528	1/1	0.92	0.14	72,72,72,72	0
53	MG	1A	3241	1/1	0.92	0.14	50,50,50,50	0
53	MG	1A	3109	1/1	0.92	0.10	69,69,69,69	0
53	MG	1a	3020	1/1	0.92	0.09	86,86,86,86	0
53	MG	2A	3084	1/1	0.92	0.13	49,49,49,49	0
53	MG	2A	3241	1/1	0.92	0.11	53,53,53,53	0
53	MG	1A	3756	1/1	0.92	0.10	47,47,47,47	0
53	MG	1A	3022	1/1	0.92	0.20	58,58,58,58	0
53	MG	1A	3758	1/1	0.92	0.17	66,66,66,66	0
53	MG	1A	3632	1/1	0.92	0.10	68,68,68,68	0
53	MG	1A	3278	1/1	0.92	0.13	51,51,51,51	0
53	MG	2a	1687	1/1	0.92	0.12	76,76,76,76	0
53	MG	2A	3250	1/1	0.92	0.09	51,51,51,51	0
53	MG	1A	3452	1/1	0.92	0.12	63,63,63,63	0
53	MG	1B	3003	1/1	0.92	0.18	60,60,60,60	0
53	MG	1A	3085	1/1	0.92	0.16	58,58,58,58	0
53	MG	2A	3096	1/1	0.92	0.13	67,67,67,67	0
53	MG	2A	3258	1/1	0.92	0.15	53,53,53,53	0
53	MG	2A	3259	1/1	0.92	0.28	45,45,45,45	0
53	MG	2A	3265	1/1	0.92	0.13	60,60,60,60	0
53	MG	1A	3455	1/1	0.92	0.18	65,65,65,65	0
53	MG	2A	3459	1/1	0.92	0.13	53,53,53,53	0
53	MG	2A	3268	1/1	0.92	0.23	60,60,60,60	0
53	MG	1A	3114	1/1	0.92	0.15	66,66,66,66	0
53	MG	1A	3322	1/1	0.92	0.26	47,47,47,47	0
53	MG	2A	3482	1/1	0.92	0.23	72,72,72,72	0
53	MG	1A	3137	1/1	0.92	0.10	40,40,40,40	0
53	MG	1A	3086	1/1	0.92	0.17	58,58,58,58	0
53	MG	2A	3275	1/1	0.92	0.09	37,37,37,37	0
53	MG	1A	3652	1/1	0.92	0.14	59,59,59,59	0
53	MG	2A	3277	1/1	0.92	0.21	61,61,61,61	0
53	MG	1B	3014	1/1	0.92	0.24	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3252	1/1	0.92	0.10	60,60,60,60	0
53	MG	2a	1718	1/1	0.92	0.15	93,93,93,93	0
53	MG	1B	3017	1/1	0.92	0.11	54,54,54,54	0
53	MG	1A	3177	1/1	0.92	0.25	35,35,35,35	0
53	MG	2A	3289	1/1	0.92	0.34	50,50,50,50	0
53	MG	1A	3288	1/1	0.92	0.24	47,47,47,47	0
53	MG	1A	3342	1/1	0.92	0.26	72,72,72,72	0
53	MG	2a	1727	1/1	0.92	0.16	76,76,76,76	0
53	MG	2A	3293	1/1	0.92	0.11	37,37,37,37	0
53	MG	2A	3294	1/1	0.92	0.12	53,53,53,53	0
53	MG	1A	3478	1/1	0.92	0.12	56,56,56,56	0
53	MG	2A	3299	1/1	0.92	0.14	56,56,56,56	0
53	MG	1A	3087	1/1	0.92	0.46	61,61,61,61	0
54	HGR	1A	3749	36/36	0.92	0.15	24,38,52,65	0
53	MG	1E	304	1/1	0.92	0.12	43,43,43,43	0
53	MG	2A	3303	1/1	0.92	0.16	39,39,39,39	0
53	MG	1A	3229	1/1	0.93	0.17	57,57,57,57	0
53	MG	1A	3138	1/1	0.93	0.12	56,56,56,56	0
53	MG	2A	3113	1/1	0.93	0.24	62,62,62,62	0
53	MG	1A	3259	1/1	0.93	0.25	39,39,39,39	0
53	MG	1A	3410	1/1	0.93	0.15	43,43,43,43	0
53	MG	2a	1604	1/1	0.93	0.26	59,59,59,59	0
53	MG	1A	3182	1/1	0.93	0.11	39,39,39,39	0
53	MG	2A	3243	1/1	0.93	0.20	35,35,35,35	0
53	MG	1D	302	1/1	0.93	0.29	49,49,49,49	0
53	MG	1A	3119	1/1	0.93	0.16	31,31,31,31	0
53	MG	1A	3480	1/1	0.93	0.13	61,61,61,61	0
53	MG	1a	3024	1/1	0.93	0.13	68,68,68,68	0
53	MG	1a	3093	1/1	0.93	0.11	71,71,71,71	0
53	MG	1A	3415	1/1	0.93	0.10	31,31,31,31	0
53	MG	2a	1613	1/1	0.93	0.11	83,83,83,83	0
53	MG	1A	3040	1/1	0.93	0.20	57,57,57,57	0
53	MG	2A	3254	1/1	0.93	0.20	47,47,47,47	0
53	MG	2A	3255	1/1	0.93	0.07	71,71,71,71	0
53	MG	2A	3397	1/1	0.93	0.07	54,54,54,54	0
53	MG	1A	3484	1/1	0.93	0.09	54,54,54,54	0
53	MG	1A	3619	1/1	0.93	0.09	55,55,55,55	0
53	MG	2A	3405	1/1	0.93	0.14	49,49,49,49	0
53	MG	1A	3418	1/1	0.93	0.07	65,65,65,65	0
53	MG	2A	3408	1/1	0.93	0.13	43,43,43,43	0
53	MG	2A	3037	1/1	0.93	0.27	67,67,67,67	0
53	MG	2A	3410	1/1	0.93	0.10	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3032	1/1	0.93	0.12	30,30,30,30	0
53	MG	1F	304	1/1	0.93	0.07	39,39,39,39	0
53	MG	1A	3212	1/1	0.93	0.09	48,48,48,48	0
53	MG	1A	3166	1/1	0.93	0.11	42,42,42,42	0
53	MG	2A	3417	1/1	0.93	0.12	60,60,60,60	0
53	MG	1A	3325	1/1	0.93	0.11	50,50,50,50	0
53	MG	1A	3299	1/1	0.93	0.14	37,37,37,37	0
53	MG	1A	3552	1/1	0.93	0.10	72,72,72,72	0
53	MG	1a	3038	1/1	0.93	0.15	52,52,52,52	0
53	MG	1A	3554	1/1	0.93	0.18	66,66,66,66	0
53	MG	1A	3015	1/1	0.93	0.21	48,48,48,48	0
53	MG	1Q	204	1/1	0.93	0.17	53,53,53,53	0
53	MG	2A	3283	1/1	0.93	0.19	46,46,46,46	0
53	MG	1R	204	1/1	0.93	0.45	47,47,47,47	0
53	MG	1A	3637	1/1	0.93	0.17	42,42,42,42	0
53	MG	1T	201	1/1	0.93	0.15	68,68,68,68	0
53	MG	1A	3134	1/1	0.93	0.09	63,63,63,63	0
53	MG	1a	3127	1/1	0.93	0.13	73,73,73,73	0
53	MG	1a	3130	1/1	0.93	0.14	63,63,63,63	0
53	MG	1A	3733	1/1	0.93	0.13	42,42,42,42	0
53	MG	1A	3331	1/1	0.93	0.06	56,56,56,56	0
53	MG	1A	3500	1/1	0.93	0.14	68,68,68,68	0
53	MG	2A	3298	1/1	0.93	0.07	47,47,47,47	0
53	MG	1A	3435	1/1	0.93	0.13	46,46,46,46	0
53	MG	1a	3050	1/1	0.93	0.07	67,67,67,67	0
53	MG	2A	3066	1/1	0.93	0.16	51,51,51,51	0
53	MG	2A	3166	1/1	0.93	0.08	53,53,53,53	0
53	MG	2A	3450	1/1	0.93	0.25	84,84,84,84	0
53	MG	1A	3220	1/1	0.93	0.12	38,38,38,38	0
53	MG	1A	3336	1/1	0.93	0.35	34,34,34,34	0
53	MG	1A	3565	1/1	0.93	0.10	69,69,69,69	0
53	MG	1A	3566	1/1	0.93	0.09	58,58,58,58	0
53	MG	2A	3477	1/1	0.93	0.12	64,64,64,64	0
53	MG	1A	3379	1/1	0.93	0.10	71,71,71,71	0
53	MG	2A	3173	1/1	0.93	0.13	32,32,32,32	0
53	MG	2A	3175	1/1	0.93	0.21	48,48,48,48	0
53	MG	2A	3487	1/1	0.93	0.13	59,59,59,59	0
53	MG	1A	3746	1/1	0.93	0.31	55,55,55,55	0
53	MG	1a	3058	1/1	0.93	0.10	68,68,68,68	0
53	MG	1A	3151	1/1	0.93	0.15	62,62,62,62	0
53	MG	2A	3318	1/1	0.93	0.09	63,63,63,63	0
53	MG	2a	1676	1/1	0.93	0.09	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3186	1/1	0.93	0.19	31,31,31,31	0
53	MG	2A	3077	1/1	0.93	0.14	53,53,53,53	0
53	MG	2a	1681	1/1	0.93	0.15	64,64,64,64	0
53	MG	1A	3511	1/1	0.93	0.11	67,67,67,67	0
53	MG	1A	3344	1/1	0.93	0.14	60,60,60,60	0
53	MG	2A	3505	1/1	0.93	0.16	77,77,77,77	0
53	MG	1A	3663	1/1	0.93	0.20	47,47,47,47	0
53	MG	1A	3667	1/1	0.93	0.14	36,36,36,36	0
53	MG	1k	3001	1/1	0.93	0.13	66,66,66,66	0
53	MG	2A	3086	1/1	0.93	0.17	70,70,70,70	0
53	MG	1A	3110	1/1	0.93	0.15	51,51,51,51	0
53	MG	2A	3200	1/1	0.93	0.11	54,54,54,54	0
53	MG	1A	3253	1/1	0.93	0.14	65,65,65,65	0
53	MG	2A	3202	1/1	0.93	0.09	48,48,48,48	0
53	MG	2A	3335	1/1	0.93	0.18	48,48,48,48	0
53	MG	2a	1698	1/1	0.93	0.08	79,79,79,79	0
53	MG	1o	102	1/1	0.93	0.11	67,67,67,67	0
53	MG	1a	3067	1/1	0.93	0.19	80,80,80,80	0
53	MG	1A	3224	1/1	0.93	0.22	30,30,30,30	0
53	MG	2A	3339	1/1	0.93	0.15	40,40,40,40	0
53	MG	1A	3154	1/1	0.93	0.09	50,50,50,50	0
53	MG	19	104	1/1	0.93	0.51	49,49,49,49	0
53	MG	1A	3456	1/1	0.93	0.08	43,43,43,43	0
53	MG	2A	3214	1/1	0.93	0.20	35,35,35,35	0
53	MG	1A	3520	1/1	0.93	0.11	74,74,74,74	0
53	MG	1A	3311	1/1	0.93	0.18	53,53,53,53	0
53	MG	1A	3056	1/1	0.93	0.10	40,40,40,40	0
53	MG	1B	3009	1/1	0.93	0.08	41,41,41,41	0
53	MG	2A	3100	1/1	0.93	0.11	59,59,59,59	0
53	MG	2D	303	1/1	0.93	0.08	60,60,60,60	0
53	MG	2A	3222	1/1	0.93	0.34	58,58,58,58	0
53	MG	2E	303	1/1	0.93	0.08	57,57,57,57	0
53	MG	2E	305	1/1	0.93	0.18	52,52,52,52	0
53	MG	2E	306	1/1	0.93	0.23	68,68,68,68	0
53	MG	2A	3012	1/1	0.93	0.07	51,51,51,51	0
53	MG	2A	3224	1/1	0.93	0.26	64,64,64,64	0
53	MG	2A	3013	1/1	0.93	0.13	80,80,80,80	0
53	MG	1A	3596	1/1	0.93	0.09	58,58,58,58	0
53	MG	1A	3353	1/1	0.93	0.08	60,60,60,60	0
53	MG	2A	3107	1/1	0.93	0.23	62,62,62,62	0
53	MG	1A	3401	1/1	0.93	0.19	71,71,71,71	0
53	MG	1a	3013	1/1	0.93	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
53	MG	2T	201	1/1	0.93	0.10	56,56,56,56	0
53	MG	2T	202	1/1	0.93	0.07	58,58,58,58	0
55	ZN	24	501	1/1	0.93	0.12	173,173,173,173	0
53	MG	2A	3110	1/1	0.93	0.07	45,45,45,45	0
53	MG	2A	3317	1/1	0.94	0.21	59,59,59,59	0
53	MG	1a	3084	1/1	0.94	0.10	60,60,60,60	0
53	MG	1A	3608	1/1	0.94	0.06	55,55,55,55	0
53	MG	2A	3041	1/1	0.94	0.09	65,65,65,65	0
53	MG	13	101	1/1	0.94	0.25	41,41,41,41	0
53	MG	15	101	1/1	0.94	0.29	54,54,54,54	0
53	MG	1A	3440	1/1	0.94	0.15	65,65,65,65	0
53	MG	2A	3046	1/1	0.94	0.05	45,45,45,45	0
53	MG	1A	3611	1/1	0.94	0.22	51,51,51,51	0
53	MG	1A	3612	1/1	0.94	0.21	51,51,51,51	0
53	MG	2A	3172	1/1	0.94	0.19	52,52,52,52	0
53	MG	2A	3328	1/1	0.94	0.07	45,45,45,45	0
53	MG	1A	3165	1/1	0.94	0.25	29,29,29,29	0
53	MG	18	102	1/1	0.94	0.23	51,51,51,51	0
53	MG	2A	3179	1/1	0.94	0.06	39,39,39,39	0
53	MG	2A	3334	1/1	0.94	0.10	55,55,55,55	0
53	MG	1A	3443	1/1	0.94	0.10	69,69,69,69	0
53	MG	2A	3181	1/1	0.94	0.20	58,58,58,58	0
53	MG	1A	3444	1/1	0.94	0.17	54,54,54,54	0
53	MG	1a	3001	1/1	0.94	0.07	60,60,60,60	0
53	MG	1A	3524	1/1	0.94	0.24	91,91,91,91	0
53	MG	1A	3142	1/1	0.94	0.09	45,45,45,45	0
53	MG	1a	3100	1/1	0.94	0.13	92,92,92,92	0
53	MG	1A	3244	1/1	0.94	0.11	53,53,53,53	0
53	MG	1A	3280	1/1	0.94	0.27	55,55,55,55	0
53	MG	2W	3001	1/1	0.94	0.08	58,58,58,58	0
53	MG	1A	3167	1/1	0.94	0.05	20,20,20,20	0
53	MG	2A	3195	1/1	0.94	0.14	57,57,57,57	0
53	MG	2A	3062	1/1	0.94	0.08	58,58,58,58	0
53	MG	2A	3347	1/1	0.94	0.19	56,56,56,56	0
53	MG	1A	3530	1/1	0.94	0.13	37,37,37,37	0
53	MG	1A	3750	1/1	0.94	0.07	73,73,73,73	0
53	MG	1A	3451	1/1	0.94	0.19	51,51,51,51	0
53	MG	1a	3011	1/1	0.94	0.06	64,64,64,64	0
53	MG	1A	3532	1/1	0.94	0.14	73,73,73,73	0
53	MG	1A	3375	1/1	0.94	0.09	69,69,69,69	0
53	MG	1A	3101	1/1	0.94	0.11	73,73,73,73	0
53	MG	1a	3114	1/1	0.94	0.10	100,100,100,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3207	1/1	0.94	0.17	54,54,54,54	0
53	MG	2A	3209	1/1	0.94	0.09	50,50,50,50	0
53	MG	1A	3326	1/1	0.94	0.18	44,44,44,44	0
53	MG	1A	3327	1/1	0.94	0.15	62,62,62,62	0
53	MG	1A	3539	1/1	0.94	0.11	69,69,69,69	0
53	MG	2A	3074	1/1	0.94	0.10	64,64,64,64	0
53	MG	2A	3370	1/1	0.94	0.10	59,59,59,59	0
53	MG	2a	1618	1/1	0.94	0.12	63,63,63,63	0
53	MG	1a	3118	1/1	0.94	0.13	92,92,92,92	0
53	MG	1a	3119	1/1	0.94	0.49	79,79,79,79	0
53	MG	1A	3382	1/1	0.94	0.12	56,56,56,56	0
53	MG	1a	3122	1/1	0.94	0.09	60,60,60,60	0
53	MG	2A	3380	1/1	0.94	0.09	52,52,52,52	0
53	MG	1A	3090	1/1	0.94	0.07	64,64,64,64	0
53	MG	1a	3124	1/1	0.94	0.13	100,100,100,100	0
53	MG	1A	3148	1/1	0.94	0.27	35,35,35,35	0
53	MG	2A	3085	1/1	0.94	0.15	70,70,70,70	0
53	MG	2A	3225	1/1	0.94	0.29	57,57,57,57	0
53	MG	2a	1630	1/1	0.94	0.21	66,66,66,66	0
53	MG	1A	3037	1/1	0.94	0.07	57,57,57,57	0
53	MG	1a	3129	1/1	0.94	0.09	61,61,61,61	0
53	MG	2A	3388	1/1	0.94	0.12	61,61,61,61	0
53	MG	1A	3150	1/1	0.94	0.12	38,38,38,38	0
53	MG	1A	3075	1/1	0.94	0.45	57,57,57,57	0
53	MG	2a	1636	1/1	0.94	0.13	60,60,60,60	0
53	MG	1A	3043	1/1	0.94	0.12	54,54,54,54	0
53	MG	1A	3474	1/1	0.94	0.08	57,57,57,57	0
53	MG	1A	3475	1/1	0.94	0.23	65,65,65,65	0
53	MG	2A	3400	1/1	0.94	0.07	65,65,65,65	0
53	MG	1A	3337	1/1	0.94	0.29	26,26,26,26	0
53	MG	1B	3016	1/1	0.94	0.14	38,38,38,38	0
53	MG	2A	3238	1/1	0.94	0.10	57,57,57,57	0
53	MG	1A	3339	1/1	0.94	0.19	46,46,46,46	0
53	MG	1A	3340	1/1	0.94	0.20	50,50,50,50	0
53	MG	1B	3020	1/1	0.94	0.11	42,42,42,42	0
53	MG	1A	3341	1/1	0.94	0.13	61,61,61,61	0
53	MG	1A	3291	1/1	0.94	0.12	49,49,49,49	0
53	MG	2A	3101	1/1	0.94	0.14	50,50,50,50	0
53	MG	1A	3071	1/1	0.94	0.46	37,37,37,37	0
53	MG	2A	3247	1/1	0.94	0.12	58,58,58,58	0
53	MG	1D	306	1/1	0.94	0.08	52,52,52,52	0
53	MG	1A	3407	1/1	0.94	0.17	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3677	1/1	0.94	0.10	46,46,46,46	0
53	MG	2A	3423	1/1	0.94	0.21	67,67,67,67	0
53	MG	2a	1656	1/1	0.94	0.09	52,52,52,52	0
53	MG	2A	3251	1/1	0.94	0.08	41,41,41,41	0
53	MG	1A	3183	1/1	0.94	0.15	29,29,29,29	0
53	MG	1A	3218	1/1	0.94	0.22	57,57,57,57	0
53	MG	1E	306	1/1	0.94	0.09	46,46,46,46	0
53	MG	1A	3097	1/1	0.94	0.21	50,50,50,50	0
53	MG	1A	3412	1/1	0.94	0.12	56,56,56,56	0
53	MG	1A	3159	1/1	0.94	0.10	49,49,49,49	0
53	MG	1A	3693	1/1	0.94	0.18	41,41,41,41	0
53	MG	1G	8001	1/1	0.94	0.09	77,77,77,77	0
53	MG	2A	3260	1/1	0.94	0.20	41,41,41,41	0
53	MG	2A	3262	1/1	0.94	0.25	30,30,30,30	0
53	MG	2a	1668	1/1	0.94	0.08	76,76,76,76	0
53	MG	2A	3439	1/1	0.94	0.11	49,49,49,49	0
53	MG	1A	3349	1/1	0.94	0.10	32,32,32,32	0
53	MG	2a	1673	1/1	0.94	0.17	55,55,55,55	0
53	MG	2A	3442	1/1	0.94	0.13	37,37,37,37	0
53	MG	1A	3495	1/1	0.94	0.16	49,49,49,49	0
53	MG	2a	1677	1/1	0.94	0.07	82,82,82,82	0
53	MG	1A	3700	1/1	0.94	0.10	39,39,39,39	0
53	MG	2A	3007	1/1	0.94	0.10	56,56,56,56	0
53	MG	1N	3002	1/1	0.94	0.11	92,92,92,92	0
53	MG	1A	3416	1/1	0.94	0.12	41,41,41,41	0
53	MG	1A	3576	1/1	0.94	0.16	19,19,19,19	0
53	MG	1A	3580	1/1	0.94	0.17	38,38,38,38	0
53	MG	2A	3126	1/1	0.94	0.33	51,51,51,51	0
53	MG	1A	3581	1/1	0.94	0.27	64,64,64,64	0
53	MG	2A	3278	1/1	0.94	0.16	56,56,56,56	0
53	MG	2A	3281	1/1	0.94	0.17	48,48,48,48	0
53	MG	2A	3460	1/1	0.94	0.16	69,69,69,69	0
53	MG	2A	3461	1/1	0.94	0.07	65,65,65,65	0
53	MG	2A	3469	1/1	0.94	0.10	56,56,56,56	0
53	MG	2A	3470	1/1	0.94	0.10	71,71,71,71	0
53	MG	1A	3222	1/1	0.94	0.30	47,47,47,47	0
53	MG	2a	1696	1/1	0.94	0.17	67,67,67,67	0
53	MG	1A	3188	1/1	0.94	0.35	39,39,39,39	0
53	MG	1A	3160	1/1	0.94	0.12	51,51,51,51	0
53	MG	2A	3134	1/1	0.94	0.14	67,67,67,67	0
53	MG	1A	3123	1/1	0.94	0.15	56,56,56,56	0
53	MG	2A	3288	1/1	0.94	0.08	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3017	1/1	0.94	0.11	58,58,58,58	0
53	MG	1A	3192	1/1	0.94	0.27	26,26,26,26	0
53	MG	1a	3064	1/1	0.94	0.07	75,75,75,75	0
53	MG	2A	3140	1/1	0.94	0.14	68,68,68,68	0
53	MG	1T	203	1/1	0.94	0.10	58,58,58,58	0
53	MG	2A	3496	1/1	0.94	0.08	68,68,68,68	0
53	MG	2A	3499	1/1	0.94	0.08	54,54,54,54	0
53	MG	1A	3504	1/1	0.94	0.09	53,53,53,53	0
53	MG	2A	3296	1/1	0.94	0.26	39,39,39,39	0
53	MG	1A	3507	1/1	0.94	0.09	43,43,43,43	0
53	MG	1A	3269	1/1	0.94	0.10	55,55,55,55	0
53	MG	1U	203	1/1	0.94	0.31	73,73,73,73	0
53	MG	2a	1721	1/1	0.94	0.17	80,80,80,80	0
53	MG	2A	3026	1/1	0.94	0.23	57,57,57,57	0
53	MG	1V	3001	1/1	0.94	0.10	40,40,40,40	0
53	MG	2A	3510	1/1	0.94	0.13	38,38,38,38	0
53	MG	1A	3193	1/1	0.94	0.22	43,43,43,43	0
53	MG	1A	3066	1/1	0.94	0.18	54,54,54,54	0
53	MG	2B	201	1/1	0.94	0.08	75,75,75,75	0
53	MG	1A	3196	1/1	0.94	0.10	31,31,31,31	0
53	MG	1A	3600	1/1	0.94	0.42	46,46,46,46	0
53	MG	1A	3432	1/1	0.94	0.15	58,58,58,58	0
53	MG	1A	3079	1/1	0.94	0.10	74,74,74,74	0
53	MG	1A	3237	1/1	0.94	0.30	41,41,41,41	0
53	MG	1A	3605	1/1	0.94	0.21	63,63,63,63	0
53	MG	1A	3039	1/1	0.94	0.19	67,67,67,67	0
53	MG	1A	3437	1/1	0.94	0.09	36,36,36,36	0
53	MG	2V	3001	1/1	0.95	0.14	46,46,46,46	0
53	MG	2A	3395	1/1	0.95	0.13	72,72,72,72	0
53	MG	2A	3054	1/1	0.95	0.06	63,63,63,63	0
53	MG	28	8001	1/1	0.95	0.12	64,64,64,64	0
53	MG	1a	3035	1/1	0.95	0.09	84,84,84,84	0
53	MG	2A	3056	1/1	0.95	0.07	60,60,60,60	0
53	MG	1P	201	1/1	0.95	0.16	57,57,57,57	0
53	MG	2A	3401	1/1	0.95	0.08	52,52,52,52	0
53	MG	1A	3152	1/1	0.95	0.07	30,30,30,30	0
53	MG	1A	3725	1/1	0.95	0.23	71,71,71,71	0
53	MG	1A	3381	1/1	0.95	0.25	48,48,48,48	0
53	MG	1a	3126	1/1	0.95	0.07	104,104,104,104	0
53	MG	1A	3498	1/1	0.95	0.21	65,65,65,65	0
53	MG	1A	3061	1/1	0.95	0.23	46,46,46,46	0
53	MG	2A	3412	1/1	0.95	0.13	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3626	1/1	0.95	0.08	26,26,26,26	0
53	MG	1A	3029	1/1	0.95	0.14	52,52,52,52	0
53	MG	1A	3201	1/1	0.95	0.27	22,22,22,22	0
53	MG	1A	3386	1/1	0.95	0.08	70,70,70,70	0
53	MG	1A	3313	1/1	0.95	0.24	52,52,52,52	0
53	MG	2A	3418	1/1	0.95	0.11	63,63,63,63	0
53	MG	2A	3419	1/1	0.95	0.06	36,36,36,36	0
53	MG	1A	3505	1/1	0.95	0.13	51,51,51,51	0
53	MG	1A	3738	1/1	0.95	0.12	43,43,43,43	0
53	MG	1A	3506	1/1	0.95	0.15	50,50,50,50	0
53	MG	2A	3177	1/1	0.95	0.16	54,54,54,54	0
53	MG	2A	3424	1/1	0.95	0.06	63,63,63,63	0
53	MG	1A	3641	1/1	0.95	0.10	78,78,78,78	0
53	MG	1a	3139	1/1	0.95	0.08	70,70,70,70	0
53	MG	1a	3051	1/1	0.95	0.20	54,54,54,54	0
53	MG	2A	3297	1/1	0.95	0.13	48,48,48,48	0
53	MG	1A	3155	1/1	0.95	0.16	53,53,53,53	0
53	MG	2A	3431	1/1	0.95	0.16	63,63,63,63	0
53	MG	2A	3076	1/1	0.95	0.15	59,59,59,59	0
53	MG	2A	3185	1/1	0.95	0.10	35,35,35,35	0
53	MG	1A	3389	1/1	0.95	0.07	47,47,47,47	0
53	MG	2A	3302	1/1	0.95	0.08	38,38,38,38	0
53	MG	1A	3390	1/1	0.95	0.08	27,27,27,27	0
53	MG	1A	3391	1/1	0.95	0.10	42,42,42,42	0
53	MG	2A	3305	1/1	0.95	0.13	40,40,40,40	0
53	MG	1W	203	1/1	0.95	0.10	51,51,51,51	0
53	MG	2A	3191	1/1	0.95	0.23	54,54,54,54	0
53	MG	1A	3226	1/1	0.95	0.06	40,40,40,40	0
53	MG	2A	3083	1/1	0.95	0.10	50,50,50,50	0
53	MG	2A	3311	1/1	0.95	0.09	50,50,50,50	0
53	MG	1A	3570	1/1	0.95	0.22	62,62,62,62	0
53	MG	10	102	1/1	0.95	0.30	37,37,37,37	0
53	MG	1A	3449	1/1	0.95	0.07	57,57,57,57	0
53	MG	1l	201	1/1	0.95	0.08	73,73,73,73	0
53	MG	1A	3395	1/1	0.95	0.09	54,54,54,54	0
53	MG	1A	3753	1/1	0.95	0.11	63,63,63,63	0
53	MG	1A	3156	1/1	0.95	0.29	43,43,43,43	0
53	MG	2A	3458	1/1	0.95	0.13	44,44,44,44	0
53	MG	1A	3656	1/1	0.95	0.07	56,56,56,56	0
53	MG	1A	3127	1/1	0.95	0.06	60,60,60,60	0
53	MG	1A	3398	1/1	0.95	0.07	55,55,55,55	0
53	MG	2A	3464	1/1	0.95	0.08	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3466	1/1	0.95	0.13	63,63,63,63	0
53	MG	2A	3003	1/1	0.95	0.11	68,68,68,68	0
53	MG	1A	3318	1/1	0.95	0.17	51,51,51,51	0
53	MG	2A	3471	1/1	0.95	0.10	52,52,52,52	0
53	MG	2A	3473	1/1	0.95	0.11	57,57,57,57	0
53	MG	2A	3475	1/1	0.95	0.08	57,57,57,57	0
53	MG	1A	3584	1/1	0.95	0.17	61,61,61,61	0
53	MG	15	105	1/1	0.95	0.07	47,47,47,47	0
53	MG	1A	3352	1/1	0.95	0.18	68,68,68,68	0
53	MG	1B	3004	1/1	0.95	0.06	66,66,66,66	0
53	MG	2A	3215	1/1	0.95	0.17	32,32,32,32	0
53	MG	2A	3486	1/1	0.95	0.17	63,63,63,63	0
53	MG	17	102	1/1	0.95	0.14	50,50,50,50	0
53	MG	1a	3075	1/1	0.95	0.11	43,43,43,43	0
53	MG	2A	3490	1/1	0.95	0.10	51,51,51,51	0
53	MG	1A	3284	1/1	0.95	0.23	28,28,28,28	0
53	MG	1A	3140	1/1	0.95	0.10	53,53,53,53	0
53	MG	2a	1672	1/1	0.95	0.18	61,61,61,61	0
53	MG	19	101	1/1	0.95	0.08	40,40,40,40	0
53	MG	2a	1674	1/1	0.95	0.09	68,68,68,68	0
53	MG	1A	3523	1/1	0.95	0.14	73,73,73,73	0
53	MG	1A	3046	1/1	0.95	0.18	51,51,51,51	0
53	MG	1A	3358	1/1	0.95	0.16	58,58,58,58	0
53	MG	2A	3501	1/1	0.95	0.08	56,56,56,56	0
53	MG	1A	3593	1/1	0.95	0.09	34,34,34,34	0
53	MG	1A	3684	1/1	0.95	0.10	76,76,76,76	0
53	MG	1A	3685	1/1	0.95	0.10	56,56,56,56	0
53	MG	2A	3228	1/1	0.95	0.23	49,49,49,49	0
53	MG	2A	3021	1/1	0.95	0.06	46,46,46,46	0
53	MG	1a	3005	1/1	0.95	0.12	53,53,53,53	0
53	MG	1A	3594	1/1	0.95	0.07	48,48,48,48	0
53	MG	1A	3106	1/1	0.95	0.09	55,55,55,55	0
53	MG	2A	3513	1/1	0.95	0.29	60,60,60,60	0
53	MG	1A	3691	1/1	0.95	0.17	84,84,84,84	0
53	MG	1A	3209	1/1	0.95	0.07	35,35,35,35	0
53	MG	1A	3003	1/1	0.95	0.16	59,59,59,59	0
53	MG	2A	3237	1/1	0.95	0.13	56,56,56,56	0
53	MG	1A	3265	1/1	0.95	0.43	66,66,66,66	0
53	MG	1a	3012	1/1	0.95	0.06	75,75,75,75	0
53	MG	1A	3092	1/1	0.95	0.12	74,74,74,74	0
53	MG	1A	3240	1/1	0.95	0.27	28,28,28,28	0
53	MG	2A	3360	1/1	0.95	0.09	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	2A	3032	1/1	0.95	0.31	42,42,42,42	0
53	MG	1A	3365	1/1	0.95	0.10	38,38,38,38	0
53	MG	2B	210	1/1	0.95	0.38	55,55,55,55	0
53	MG	1D	305	1/1	0.95	0.15	66,66,66,66	0
53	MG	1a	3017	1/1	0.95	0.08	71,71,71,71	0
53	MG	2A	3365	1/1	0.95	0.08	75,75,75,75	0
53	MG	2a	1708	1/1	0.95	0.09	73,73,73,73	0
53	MG	1A	3603	1/1	0.95	0.25	44,44,44,44	0
53	MG	1A	3366	1/1	0.95	0.06	37,37,37,37	0
53	MG	1A	3296	1/1	0.95	0.14	24,24,24,24	0
53	MG	1E	301	1/1	0.95	0.09	38,38,38,38	0
53	MG	2A	3372	1/1	0.95	0.12	34,34,34,34	0
53	MG	1a	3022	1/1	0.95	0.07	77,77,77,77	0
53	MG	2a	1717	1/1	0.95	0.25	94,94,94,94	0
53	MG	1A	3146	1/1	0.95	0.33	47,47,47,47	0
53	MG	2a	1719	1/1	0.95	0.10	93,93,93,93	0
53	MG	1A	3016	1/1	0.95	0.25	66,66,66,66	0
53	MG	2A	3142	1/1	0.95	0.14	49,49,49,49	0
53	MG	2E	304	1/1	0.95	0.20	36,36,36,36	0
53	MG	2A	3379	1/1	0.95	0.12	47,47,47,47	0
53	MG	1A	3540	1/1	0.95	0.12	48,48,48,48	0
53	MG	1A	3054	1/1	0.95	0.18	64,64,64,64	0
53	MG	1A	3334	1/1	0.95	0.15	37,37,37,37	0
53	MG	2a	1728	1/1	0.95	0.15	85,85,85,85	0
53	MG	1A	3272	1/1	0.95	0.08	53,53,53,53	0
53	MG	1A	3111	1/1	0.95	0.17	66,66,66,66	0
53	MG	1A	3430	1/1	0.95	0.07	49,49,49,49	0
53	MG	2A	3261	1/1	0.95	0.12	43,43,43,43	0
53	MG	1A	3217	1/1	0.95	0.32	57,57,57,57	0
53	MG	1A	3617	1/1	0.95	0.08	93,93,93,93	0
53	MG	2A	3389	1/1	0.95	0.11	64,64,64,64	0
53	MG	1A	3547	1/1	0.95	0.09	62,62,62,62	0
53	MG	1A	3124	1/1	0.95	0.10	40,40,40,40	0
53	MG	1A	3089	1/1	0.96	0.07	61,61,61,61	0
53	MG	2A	3333	1/1	0.96	0.13	30,30,30,30	0
53	MG	1A	3190	1/1	0.96	0.13	31,31,31,31	0
53	MG	1D	304	1/1	0.96	0.10	25,25,25,25	0
53	MG	1A	3172	1/1	0.96	0.16	23,23,23,23	0
53	MG	1d	503	1/1	0.96	0.07	99,99,99,99	0
53	MG	1A	3579	1/1	0.96	0.07	68,68,68,68	0
53	MG	1A	3483	1/1	0.96	0.07	32,32,32,32	0
53	MG	1A	3636	1/1	0.96	0.06	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3073	1/1	0.96	0.05	72,72,72,72	0
53	MG	1a	3074	1/1	0.96	0.07	67,67,67,67	0
53	MG	1A	3055	1/1	0.96	0.07	58,58,58,58	0
53	MG	1E	303	1/1	0.96	0.15	45,45,45,45	0
53	MG	2A	3155	1/1	0.96	0.04	50,50,50,50	0
53	MG	2A	3462	1/1	0.96	0.08	73,73,73,73	0
53	MG	1A	3638	1/1	0.96	0.08	56,56,56,56	0
53	MG	1A	3722	1/1	0.96	0.22	62,62,62,62	0
53	MG	1o	101	1/1	0.96	0.07	82,82,82,82	0
53	MG	1A	3324	1/1	0.96	0.15	34,34,34,34	0
53	MG	1A	3292	1/1	0.96	0.10	42,42,42,42	0
53	MG	2A	3472	1/1	0.96	0.07	57,57,57,57	0
53	MG	1A	3643	1/1	0.96	0.08	31,31,31,31	0
53	MG	2A	3474	1/1	0.96	0.06	65,65,65,65	0
53	MG	2A	3352	1/1	0.96	0.08	49,49,49,49	0
53	MG	1A	3238	1/1	0.96	0.20	39,39,39,39	0
53	MG	2A	3002	1/1	0.96	0.06	55,55,55,55	0
53	MG	2A	3355	1/1	0.96	0.07	62,62,62,62	0
53	MG	2A	3356	1/1	0.96	0.14	56,56,56,56	0
53	MG	2A	3481	1/1	0.96	0.18	66,66,66,66	0
53	MG	1A	3120	1/1	0.96	0.21	53,53,53,53	0
53	MG	1A	3082	1/1	0.96	0.35	42,42,42,42	0
53	MG	2A	3005	1/1	0.96	0.11	51,51,51,51	0
53	MG	2A	3488	1/1	0.96	0.10	66,66,66,66	0
53	MG	1A	3534	1/1	0.96	0.13	35,35,35,35	0
53	MG	1A	3441	1/1	0.96	0.09	52,52,52,52	0
53	MG	1A	3536	1/1	0.96	0.09	52,52,52,52	0
53	MG	2A	3263	1/1	0.96	0.16	50,50,50,50	0
53	MG	1A	3494	1/1	0.96	0.10	63,63,63,63	0
53	MG	2A	3367	1/1	0.96	0.10	56,56,56,56	0
53	MG	2A	3266	1/1	0.96	0.17	55,55,55,55	0
53	MG	2A	3497	1/1	0.96	0.07	86,86,86,86	0
53	MG	1A	3214	1/1	0.96	0.14	41,41,41,41	0
53	MG	2A	3500	1/1	0.96	0.07	64,64,64,64	0
53	MG	1A	3195	1/1	0.96	0.13	54,54,54,54	0
53	MG	2A	3371	1/1	0.96	0.07	36,36,36,36	0
53	MG	1A	3737	1/1	0.96	0.26	23,23,23,23	0
53	MG	1A	3147	1/1	0.96	0.07	32,32,32,32	0
53	MG	2A	3375	1/1	0.96	0.10	51,51,51,51	0
53	MG	1A	3597	1/1	0.96	0.10	40,40,40,40	0
53	MG	1A	3661	1/1	0.96	0.07	21,21,21,21	0
53	MG	1R	203	1/1	0.96	0.09	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3741	1/1	0.96	0.14	36,36,36,36	0
53	MG	2A	3511	1/1	0.96	0.07	39,39,39,39	0
53	MG	2A	3512	1/1	0.96	0.09	46,46,46,46	0
53	MG	2A	3183	1/1	0.96	0.25	32,32,32,32	0
53	MG	1A	3179	1/1	0.96	0.08	37,37,37,37	0
53	MG	2A	3517	1/1	0.96	0.08	47,47,47,47	0
53	MG	2A	3279	1/1	0.96	0.18	32,32,32,32	0
53	MG	1R	206	1/1	0.96	0.10	52,52,52,52	0
53	MG	1A	3198	1/1	0.96	0.07	38,38,38,38	0
53	MG	1A	3665	1/1	0.96	0.12	61,61,61,61	0
53	MG	1A	3335	1/1	0.96	0.33	42,42,42,42	0
53	MG	1A	3404	1/1	0.96	0.09	63,63,63,63	0
53	MG	2a	1678	1/1	0.96	0.07	69,69,69,69	0
53	MG	2A	3190	1/1	0.96	0.16	34,34,34,34	0
53	MG	1A	3405	1/1	0.96	0.09	45,45,45,45	0
53	MG	1A	3219	1/1	0.96	0.23	60,60,60,60	0
53	MG	2A	3102	1/1	0.96	0.06	40,40,40,40	0
53	MG	1A	3199	1/1	0.96	0.08	45,45,45,45	0
53	MG	2A	3292	1/1	0.96	0.13	49,49,49,49	0
53	MG	1A	3678	1/1	0.96	0.08	33,33,33,33	0
53	MG	2A	3197	1/1	0.96	0.17	41,41,41,41	0
53	MG	2A	3399	1/1	0.96	0.09	63,63,63,63	0
53	MG	1A	3755	1/1	0.96	0.07	75,75,75,75	0
53	MG	1a	3112	1/1	0.96	0.08	91,91,91,91	0
53	MG	2A	3402	1/1	0.96	0.06	53,53,53,53	0
53	MG	1A	3679	1/1	0.96	0.07	38,38,38,38	0
53	MG	2B	219	1/1	0.96	0.07	79,79,79,79	0
53	MG	1A	3338	1/1	0.96	0.29	62,62,62,62	0
53	MG	1A	3068	1/1	0.96	0.09	67,67,67,67	0
53	MG	1A	3035	1/1	0.96	0.10	52,52,52,52	0
53	MG	2E	302	1/1	0.96	0.26	49,49,49,49	0
53	MG	1A	3033	1/1	0.96	0.20	37,37,37,37	0
53	MG	1A	3414	1/1	0.96	0.13	57,57,57,57	0
53	MG	2A	3411	1/1	0.96	0.06	44,44,44,44	0
53	MG	1A	3203	1/1	0.96	0.19	25,25,25,25	0
53	MG	2A	3208	1/1	0.96	0.14	27,27,27,27	0
53	MG	1A	3689	1/1	0.96	0.10	75,75,75,75	0
53	MG	1A	3225	1/1	0.96	0.17	52,52,52,52	0
53	MG	1A	3513	1/1	0.96	0.11	56,56,56,56	0
53	MG	1A	3001	1/1	0.96	0.05	41,41,41,41	0
53	MG	2a	1711	1/1	0.96	0.09	105,105,105,105	0
53	MG	1A	3115	1/1	0.96	0.07	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3053	1/1	0.96	0.12	49,49,49,49	0
53	MG	2A	3043	1/1	0.96	0.09	43,43,43,43	0
53	MG	2Q	3002	1/1	0.96	0.15	51,51,51,51	0
53	MG	2Q	3003	1/1	0.96	0.14	45,45,45,45	0
53	MG	13	103	1/1	0.96	0.13	50,50,50,50	0
53	MG	1a	3128	1/1	0.96	0.11	93,93,93,93	0
53	MG	2A	3219	1/1	0.96	0.26	54,54,54,54	0
53	MG	2A	3124	1/1	0.96	0.17	44,44,44,44	0
53	MG	1A	3697	1/1	0.96	0.11	37,37,37,37	0
53	MG	1A	3517	1/1	0.96	0.07	69,69,69,69	0
53	MG	2A	3129	1/1	0.96	0.08	55,55,55,55	0
53	MG	2A	3130	1/1	0.96	0.14	57,57,57,57	0
53	MG	1A	3701	1/1	0.96	0.17	58,58,58,58	0
53	MG	2a	1726	1/1	0.96	0.14	62,62,62,62	0
53	MG	1A	3044	1/1	0.96	0.06	55,55,55,55	0
53	MG	1A	3286	1/1	0.96	0.16	44,44,44,44	0
53	MG	1A	3567	1/1	0.96	0.09	97,97,97,97	0
53	MG	1A	3425	1/1	0.96	0.08	39,39,39,39	0
53	MG	1A	3385	1/1	0.96	0.11	58,58,58,58	0
53	MG	1A	3261	1/1	0.96	0.13	59,59,59,59	0
53	MG	1B	3023	1/1	0.96	0.06	68,68,68,68	0
53	MG	2A	3329	1/1	0.96	0.06	58,58,58,58	0
53	MG	2A	3440	1/1	0.96	0.06	43,43,43,43	0
53	MG	2A	3233	1/1	0.96	0.11	60,60,60,60	0
53	MG	1A	3627	1/1	0.96	0.10	52,52,52,52	0
56	SF4	1d	501	8/8	0.96	0.06	85,105,119,125	0
56	SF4	2d	501	8/8	0.96	0.06	87,107,123,125	0
53	MG	1A	3242	1/1	0.97	0.19	35,35,35,35	0
53	MG	1A	3587	1/1	0.97	0.11	51,51,51,51	0
53	MG	2A	3205	1/1	0.97	0.15	33,33,33,33	0
53	MG	2A	3498	1/1	0.97	0.08	82,82,82,82	0
53	MG	1A	3588	1/1	0.97	0.06	61,61,61,61	0
53	MG	15	104	1/1	0.97	0.20	63,63,63,63	0
53	MG	1B	3019	1/1	0.97	0.08	40,40,40,40	0
53	MG	1A	3343	1/1	0.97	0.06	53,53,53,53	0
53	MG	2A	3394	1/1	0.97	0.10	54,54,54,54	0
53	MG	2A	3125	1/1	0.97	0.16	33,33,33,33	0
53	MG	1B	3021	1/1	0.97	0.08	64,64,64,64	0
53	MG	1B	3022	1/1	0.97	0.09	32,32,32,32	0
53	MG	2A	3128	1/1	0.97	0.07	59,59,59,59	0
53	MG	1A	3419	1/1	0.97	0.18	40,40,40,40	0
53	MG	1A	3169	1/1	0.97	0.14	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1A	3170	1/1	0.97	0.13	56,56,56,56	0
53	MG	1A	3458	1/1	0.97	0.06	27,27,27,27	0
53	MG	1A	3502	1/1	0.97	0.13	52,52,52,52	0
53	MG	1b	3001	1/1	0.97	0.05	90,90,90,90	0
53	MG	19	105	1/1	0.97	0.16	74,74,74,74	0
53	MG	2A	3518	1/1	0.97	0.08	47,47,47,47	0
53	MG	1A	3459	1/1	0.97	0.06	45,45,45,45	0
53	MG	1A	3460	1/1	0.97	0.14	50,50,50,50	0
53	MG	1A	3231	1/1	0.97	0.09	46,46,46,46	0
53	MG	2A	3139	1/1	0.97	0.23	35,35,35,35	0
53	MG	1A	3653	1/1	0.97	0.06	54,54,54,54	0
53	MG	1A	3009	1/1	0.97	0.05	45,45,45,45	0
53	MG	1A	3093	1/1	0.97	0.11	67,67,67,67	0
53	MG	1A	3427	1/1	0.97	0.11	39,39,39,39	0
53	MG	1A	3729	1/1	0.97	0.06	57,57,57,57	0
53	MG	1A	3658	1/1	0.97	0.07	35,35,35,35	0
53	MG	2A	3146	1/1	0.97	0.14	49,49,49,49	0
53	MG	1A	3249	1/1	0.97	0.22	54,54,54,54	0
53	MG	1A	3467	1/1	0.97	0.10	57,57,57,57	0
53	MG	1A	3468	1/1	0.97	0.10	73,73,73,73	0
53	MG	2a	1669	1/1	0.97	0.10	71,71,71,71	0
53	MG	1A	3371	1/1	0.97	0.07	43,43,43,43	0
53	MG	1F	305	1/1	0.97	0.06	41,41,41,41	0
53	MG	1F	306	1/1	0.97	0.20	48,48,48,48	0
53	MG	1A	3234	1/1	0.97	0.16	44,44,44,44	0
53	MG	2A	3154	1/1	0.97	0.17	36,36,36,36	0
53	MG	1A	3666	1/1	0.97	0.45	41,41,41,41	0
53	MG	1A	3473	1/1	0.97	0.08	48,48,48,48	0
53	MG	2A	3429	1/1	0.97	0.09	71,71,71,71	0
53	MG	1A	3373	1/1	0.97	0.26	63,63,63,63	0
53	MG	1A	3045	1/1	0.97	0.10	32,32,32,32	0
53	MG	2A	3079	1/1	0.97	0.10	54,54,54,54	0
53	MG	2A	3246	1/1	0.97	0.08	38,38,38,38	0
53	MG	1A	3333	1/1	0.97	0.13	39,39,39,39	0
53	MG	1P	202	1/1	0.97	0.11	50,50,50,50	0
53	MG	1A	3477	1/1	0.97	0.09	49,49,49,49	0
53	MG	1A	3434	1/1	0.97	0.09	24,24,24,24	0
53	MG	2A	3438	1/1	0.97	0.07	47,47,47,47	0
53	MG	1A	3613	1/1	0.97	0.34	48,48,48,48	0
53	MG	1A	3564	1/1	0.97	0.06	46,46,46,46	0
53	MG	2a	1690	1/1	0.97	0.09	82,82,82,82	0
53	MG	1A	3376	1/1	0.97	0.07	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3098	1/1	0.97	0.05	75,75,75,75	0
53	MG	1R	202	1/1	0.97	0.11	66,66,66,66	0
53	MG	1A	3297	1/1	0.97	0.31	40,40,40,40	0
53	MG	1a	3102	1/1	0.97	0.05	58,58,58,58	0
53	MG	1A	3135	1/1	0.97	0.11	49,49,49,49	0
53	MG	2a	1697	1/1	0.97	0.06	48,48,48,48	0
53	MG	1A	3439	1/1	0.97	0.10	54,54,54,54	0
53	MG	1A	3752	1/1	0.97	0.07	47,47,47,47	0
53	MG	2A	3176	1/1	0.97	0.09	32,32,32,32	0
53	MG	1A	3355	1/1	0.97	0.16	39,39,39,39	0
53	MG	2A	3451	1/1	0.97	0.08	71,71,71,71	0
53	MG	2A	3178	1/1	0.97	0.18	36,36,36,36	0
53	MG	2A	3264	1/1	0.97	0.14	30,30,30,30	0
53	MG	2A	3456	1/1	0.97	0.07	63,63,63,63	0
53	MG	1A	3620	1/1	0.97	0.08	58,58,58,58	0
53	MG	1A	3690	1/1	0.97	0.16	46,46,46,46	0
53	MG	2A	3357	1/1	0.97	0.12	73,73,73,73	0
53	MG	2a	1710	1/1	0.97	0.06	76,76,76,76	0
53	MG	1A	3408	1/1	0.97	0.11	51,51,51,51	0
53	MG	1A	3571	1/1	0.97	0.09	69,69,69,69	0
53	MG	2A	3463	1/1	0.97	0.06	70,70,70,70	0
53	MG	1A	3380	1/1	0.97	0.08	47,47,47,47	0
53	MG	2A	3270	1/1	0.97	0.21	65,65,65,65	0
53	MG	2A	3468	1/1	0.97	0.06	58,58,58,58	0
53	MG	1A	3624	1/1	0.97	0.07	19,19,19,19	0
53	MG	1B	3001	1/1	0.97	0.05	70,70,70,70	0
53	MG	2A	3273	1/1	0.97	0.06	55,55,55,55	0
53	MG	1A	3301	1/1	0.97	0.22	38,38,38,38	0
53	MG	1A	3696	1/1	0.97	0.08	57,57,57,57	0
53	MG	1A	3357	1/1	0.97	0.17	41,41,41,41	0
53	MG	1A	3577	1/1	0.97	0.10	42,42,42,42	0
53	MG	1A	3489	1/1	0.97	0.08	69,69,69,69	0
53	MG	1A	3702	1/1	0.97	0.10	76,76,76,76	0
53	MG	1A	3157	1/1	0.97	0.09	38,38,38,38	0
53	MG	2A	3193	1/1	0.97	0.10	27,27,27,27	0
53	MG	1A	3176	1/1	0.97	0.10	24,24,24,24	0
53	MG	1A	3705	1/1	0.97	0.08	42,42,42,42	0
53	MG	2A	3485	1/1	0.97	0.13	58,58,58,58	0
53	MG	2A	3285	1/1	0.97	0.14	46,46,46,46	0
53	MG	1A	3304	1/1	0.97	0.11	38,38,38,38	0
53	MG	1A	3186	1/1	0.97	0.18	21,21,21,21	0
53	MG	2a	1628	1/1	0.97	0.16	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1B	3013	1/1	0.97	0.13	41,41,41,41	0
55	ZN	14	501	1/1	0.97	0.06	168,168,168,168	0
55	ZN	1n	102	1/1	0.97	0.11	159,159,159,159	0
53	MG	1A	3635	1/1	0.97	0.07	56,56,56,56	0
53	MG	2A	3116	1/1	0.97	0.08	51,51,51,51	0
53	MG	1A	3187	1/1	0.97	0.16	31,31,31,31	0
53	MG	13	102	1/1	0.97	0.08	35,35,35,35	0
53	MG	1A	3682	1/1	0.98	0.14	63,63,63,63	0
53	MG	1A	3121	1/1	0.98	0.04	50,50,50,50	0
53	MG	1a	3121	1/1	0.98	0.06	94,94,94,94	0
53	MG	1A	3645	1/1	0.98	0.09	39,39,39,39	0
53	MG	2A	3516	1/1	0.98	0.04	34,34,34,34	0
53	MG	1A	3686	1/1	0.98	0.11	59,59,59,59	0
53	MG	1A	3646	1/1	0.98	0.04	64,64,64,64	0
53	MG	1A	3006	1/1	0.98	0.12	31,31,31,31	0
53	MG	2A	3454	1/1	0.98	0.07	61,61,61,61	0
53	MG	2A	3455	1/1	0.98	0.07	66,66,66,66	0
53	MG	2a	1685	1/1	0.98	0.17	55,55,55,55	0
53	MG	1A	3406	1/1	0.98	0.08	50,50,50,50	0
53	MG	2A	3457	1/1	0.98	0.08	78,78,78,78	0
53	MG	1A	3392	1/1	0.98	0.09	34,34,34,34	0
53	MG	1A	3424	1/1	0.98	0.07	48,48,48,48	0
53	MG	1A	3393	1/1	0.98	0.08	35,35,35,35	0
53	MG	2A	3404	1/1	0.98	0.09	44,44,44,44	0
53	MG	1A	3268	1/1	0.98	0.10	23,23,23,23	0
53	MG	1A	3260	1/1	0.98	0.14	29,29,29,29	0
53	MG	2A	3407	1/1	0.98	0.10	49,49,49,49	0
53	MG	1A	3298	1/1	0.98	0.18	22,22,22,22	0
53	MG	2A	3467	1/1	0.98	0.05	60,60,60,60	0
53	MG	1A	3735	1/1	0.98	0.06	54,54,54,54	0
53	MG	1A	3143	1/1	0.98	0.07	20,20,20,20	0
53	MG	1A	3300	1/1	0.98	0.19	47,47,47,47	0
53	MG	2A	3159	1/1	0.98	0.07	44,44,44,44	0
53	MG	1A	3699	1/1	0.98	0.09	78,78,78,78	0
53	MG	2A	3308	1/1	0.98	0.09	36,36,36,36	0
53	MG	2A	3359	1/1	0.98	0.05	54,54,54,54	0
53	MG	2D	302	1/1	0.98	0.07	49,49,49,49	0
53	MG	1A	3488	1/1	0.98	0.20	69,69,69,69	0
53	MG	2A	3210	1/1	0.98	0.07	37,37,37,37	0
53	MG	2a	1707	1/1	0.98	0.10	82,82,82,82	0
53	MG	1A	3529	1/1	0.98	0.13	55,55,55,55	0
53	MG	1A	3247	1/1	0.98	0.08	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1a	3140	1/1	0.98	0.12	101,101,101,101	0
53	MG	1A	3553	1/1	0.98	0.05	36,36,36,36	0
53	MG	1A	3235	1/1	0.98	0.08	36,36,36,36	0
53	MG	2A	3483	1/1	0.98	0.06	50,50,50,50	0
53	MG	1A	3664	1/1	0.98	0.09	49,49,49,49	0
53	MG	1A	3582	1/1	0.98	0.05	61,61,61,61	0
53	MG	1A	3450	1/1	0.98	0.06	40,40,40,40	0
53	MG	1a	3101	1/1	0.98	0.04	65,65,65,65	0
53	MG	1A	3634	1/1	0.98	0.05	58,58,58,58	0
53	MG	1A	3669	1/1	0.98	0.04	61,61,61,61	0
53	MG	2A	3373	1/1	0.98	0.14	38,38,38,38	0
53	MG	1A	3711	1/1	0.98	0.12	57,57,57,57	0
53	MG	2A	3174	1/1	0.98	0.07	23,23,23,23	0
53	MG	2R	8001	1/1	0.98	0.07	30,30,30,30	0
53	MG	1A	3751	1/1	0.98	0.04	37,37,37,37	0
53	MG	2A	3495	1/1	0.98	0.10	64,64,64,64	0
53	MG	1A	3671	1/1	0.98	0.05	60,60,60,60	0
53	MG	1A	3230	1/1	0.98	0.10	23,23,23,23	0
53	MG	1A	3754	1/1	0.98	0.09	32,32,32,32	0
53	MG	1A	3493	1/1	0.98	0.08	49,49,49,49	0
53	MG	20	8001	1/1	0.98	0.04	49,49,49,49	0
53	MG	1A	3610	1/1	0.98	0.06	40,40,40,40	0
53	MG	2A	3087	1/1	0.98	0.09	64,64,64,64	0
53	MG	1A	3716	1/1	0.98	0.08	57,57,57,57	0
53	MG	1A	3178	1/1	0.98	0.04	30,30,30,30	0
53	MG	1A	3759	1/1	0.98	0.04	23,23,23,23	0
53	MG	1A	3640	1/1	0.98	0.05	43,43,43,43	0
53	MG	2A	3506	1/1	0.98	0.07	62,62,62,62	0
55	ZN	2Y	501	1/1	0.98	0.06	92,92,92,92	0
53	MG	1A	3559	1/1	0.98	0.07	58,58,58,58	0
55	ZN	26	501	1/1	0.98	0.05	84,84,84,84	0
55	ZN	29	501	1/1	0.98	0.04	89,89,89,89	0
53	MG	1A	3762	1/1	0.98	0.15	26,26,26,26	0
53	MG	1A	3293	1/1	0.98	0.19	43,43,43,43	0
53	MG	1A	3454	1/1	0.98	0.05	57,57,57,57	0
53	MG	2A	3390	1/1	0.99	0.06	45,45,45,45	0
53	MG	1A	3575	1/1	0.99	0.09	83,83,83,83	0
53	MG	1A	3420	1/1	0.99	0.16	28,28,28,28	0
53	MG	1A	3698	1/1	0.99	0.04	27,27,27,27	0
53	MG	1E	302	1/1	0.99	0.09	43,43,43,43	0
53	MG	1A	3462	1/1	0.99	0.04	53,53,53,53	0
53	MG	1A	3639	1/1	0.99	0.04	26,26,26,26	0

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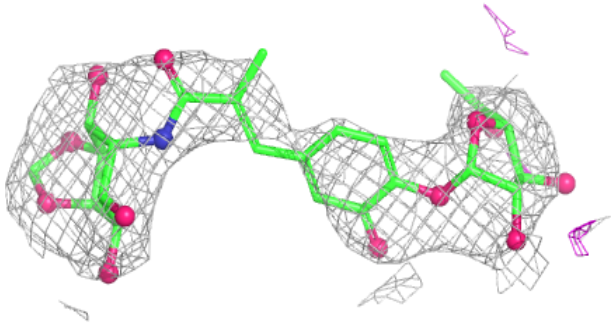
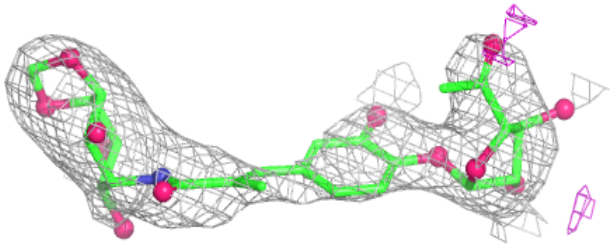
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
53	MG	1R	201	1/1	0.99	0.12	41,41,41,41	0
53	MG	1A	3683	1/1	0.99	0.04	61,61,61,61	0
53	MG	1A	3578	1/1	0.99	0.06	30,30,30,30	0
53	MG	1A	3471	1/1	0.99	0.04	54,54,54,54	0
53	MG	2A	3280	1/1	0.99	0.06	43,43,43,43	0
53	MG	1A	3563	1/1	0.99	0.03	25,25,25,25	0
53	MG	1A	3670	1/1	0.99	0.05	48,48,48,48	0
53	MG	1a	3096	1/1	0.99	0.04	63,63,63,63	0
53	MG	1A	3631	1/1	0.99	0.06	53,53,53,53	0
53	MG	2A	3484	1/1	0.99	0.05	45,45,45,45	0
53	MG	1A	3672	1/1	0.99	0.03	33,33,33,33	0
55	ZN	1Y	201	1/1	0.99	0.12	80,80,80,80	0
53	MG	1A	3673	1/1	0.99	0.05	32,32,32,32	0
55	ZN	15	103	1/1	0.99	0.04	43,43,43,43	0
55	ZN	16	501	1/1	0.99	0.08	65,65,65,65	0
53	MG	1A	3709	1/1	0.99	0.05	75,75,75,75	0
53	MG	1A	3472	1/1	0.99	0.12	46,46,46,46	0
53	MG	1H	201	1/1	0.99	0.05	50,50,50,50	0
55	ZN	25	501	1/1	0.99	0.10	66,66,66,66	0
53	MG	1A	3572	1/1	0.99	0.04	74,74,74,74	0
53	MG	1A	3168	1/1	0.99	0.18	26,26,26,26	0
53	MG	1A	3660	1/1	0.99	0.04	50,50,50,50	0
53	MG	2A	3465	1/1	0.99	0.13	41,41,41,41	0
53	MG	1A	3438	1/1	0.99	0.06	33,33,33,33	0
53	MG	2A	3480	1/1	1.00	0.11	72,72,72,72	0
53	MG	1A	3457	1/1	1.00	0.04	30,30,30,30	0
53	MG	1A	3654	1/1	1.00	0.04	31,31,31,31	0
53	MG	1A	3550	1/1	1.00	0.03	23,23,23,23	0
55	ZN	19	102	1/1	1.00	0.04	51,51,51,51	0
53	MG	2A	3393	1/1	1.00	0.02	29,29,29,29	0
53	MG	1A	3668	1/1	1.00	0.02	26,26,26,26	0

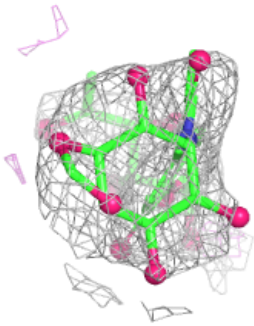
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around HGR 2A 3515:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

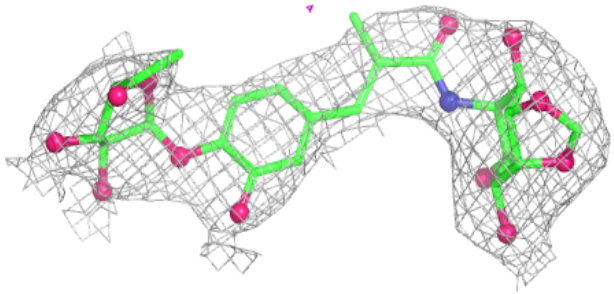


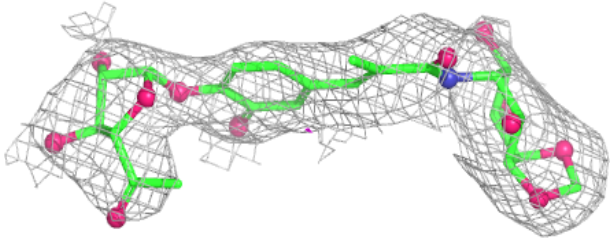


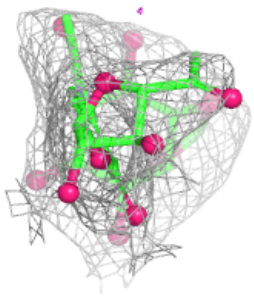


Electron density around HGR 1A 3749:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.