



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2017 – 03:20 AM EDT

PDB ID : 4Y4P
Title : Crystal structure of the *Thermus thermophilus* 70S ribosome with rRNA modifications and bound to mRNA and A-, P- and E-site tRNAs at 2.5Å resolution
Authors : Polikanov, Y.S.; Melnikov, S.V.; Soll, D.; Steitz, T.A.
Deposited on : unknown
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

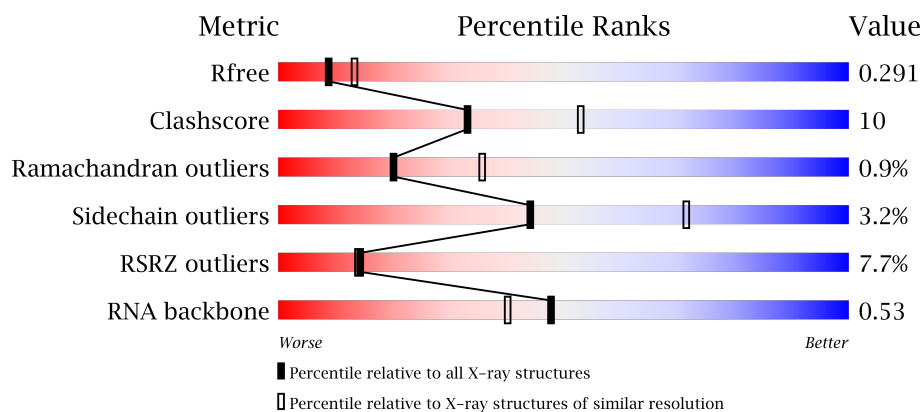
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.







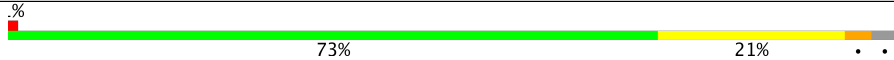
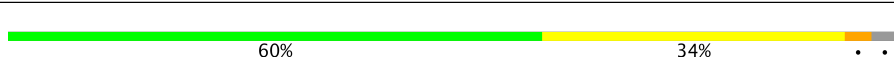
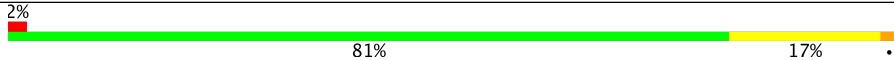
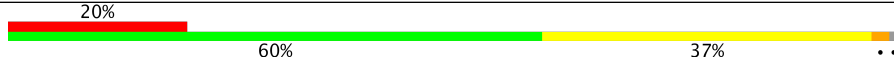
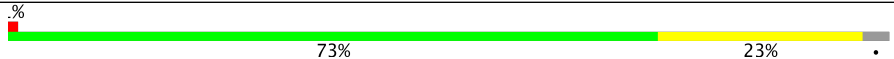
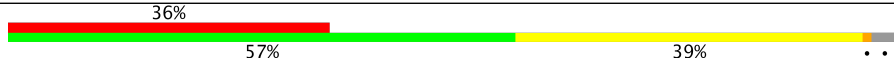
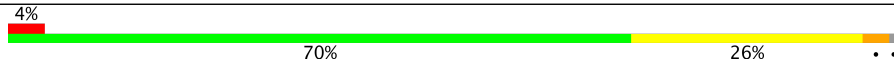
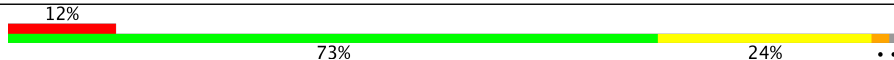


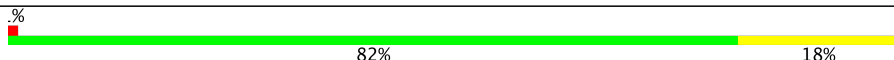
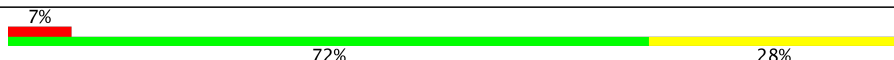
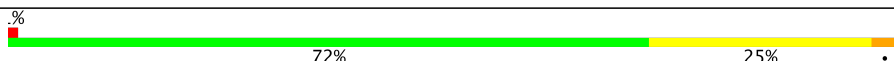
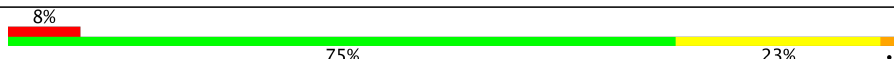
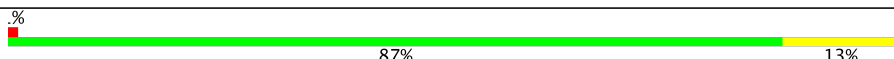

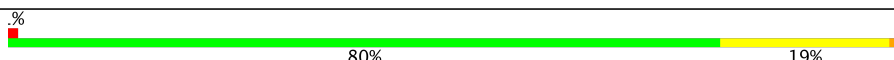
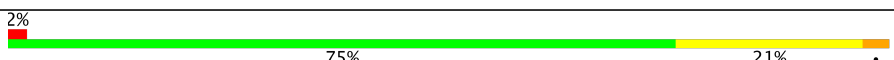
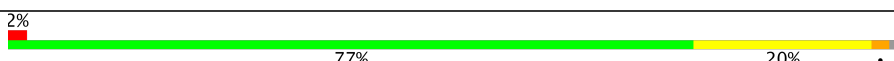
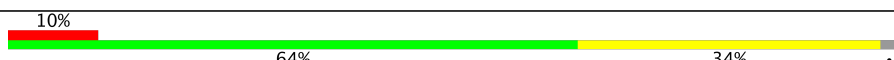
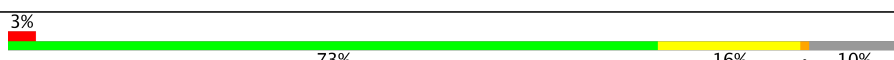
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)
RNA backbone	2435	1019 (2.90-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1A	2915	
1	2A	2915	
2	1B	121	
2	2B	121	

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

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

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

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

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	16	101	-	-	-	X
56	MG	1A	3013	-	-	-	X
56	MG	1A	3016	-	-	-	X
56	MG	1A	3055	-	-	-	X
56	MG	1A	3056	-	-	-	X
56	MG	1A	3063	-	-	-	X
56	MG	1A	3068	-	-	-	X
56	MG	1A	3095	-	-	-	X
56	MG	1A	3104	-	-	-	X
56	MG	1A	3125	-	-	-	X
56	MG	1A	3151	-	-	-	X
56	MG	1A	3162	-	-	-	X
56	MG	1A	3165	-	-	-	X
56	MG	1A	3171	-	-	-	X
56	MG	1A	3177	-	-	-	X
56	MG	1A	3185	-	-	-	X
56	MG	1A	3189	-	-	-	X
56	MG	1A	3194	-	-	-	X
56	MG	1A	3200	-	-	-	X
56	MG	1A	3248	-	-	-	X
56	MG	1A	3252	-	-	-	X
56	MG	1A	3280	-	-	-	X
56	MG	1A	3306	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1A	3307	-	-	-	X
56	MG	1A	3309	-	-	-	X
56	MG	1A	3311	-	-	-	X
56	MG	1A	3313	-	-	-	X
56	MG	1A	3338	-	-	-	X
56	MG	1A	3347	-	-	-	X
56	MG	1A	3351	-	-	-	X
56	MG	1A	3354	-	-	-	X
56	MG	1A	3458	-	-	-	X
56	MG	1A	3509	-	-	-	X
56	MG	1A	3552	-	-	-	X
56	MG	1A	3559	-	-	-	X
56	MG	1A	3576	-	-	-	X
56	MG	1A	3578	-	-	-	X
56	MG	1A	3603	-	-	-	X
56	MG	1A	3628	-	-	-	X
56	MG	1A	3658	-	-	-	X
56	MG	1A	3704	-	-	-	X
56	MG	1A	3744	-	-	-	X
56	MG	1A	3753	-	-	-	X
56	MG	1A	3803	-	-	-	X
56	MG	1A	3809	-	-	-	X
56	MG	1A	3842	-	-	-	X
56	MG	1A	3857	-	-	-	X
56	MG	1A	3865	-	-	-	X
56	MG	1A	3871	-	-	-	X
56	MG	1A	3971	-	-	-	X
56	MG	1A	4047	-	-	-	X
56	MG	1A	4072	-	-	-	X
56	MG	1A	4076	-	-	-	X
56	MG	1A	4078	-	-	-	X
56	MG	1A	4086	-	-	-	X
56	MG	1A	4090	-	-	-	X
56	MG	1A	4093	-	-	-	X
56	MG	1A	4115	-	-	-	X
56	MG	1A	4124	-	-	-	X
56	MG	1A	4141	-	-	-	X
56	MG	1B	3010	-	-	-	X
56	MG	1B	3019	-	-	-	X
56	MG	1D	301	-	-	-	X
56	MG	1D	302	-	-	-	X
56	MG	1D	310	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	1D	312	-	-	-	X
56	MG	1E	304	-	-	-	X
56	MG	1N	201	-	-	-	X
56	MG	1N	204	-	-	-	X
56	MG	1O	202	-	-	-	X
56	MG	1O	203	-	-	-	X
56	MG	1S	3001	-	-	-	X
56	MG	1U	202	-	-	-	X
56	MG	1Y	504	-	-	-	X
56	MG	1a	1657	-	-	-	X
56	MG	1a	1659	-	-	-	X
56	MG	1a	1699	-	-	-	X
56	MG	2A	3003	-	-	-	X
56	MG	2A	3014	-	-	-	X
56	MG	2A	3025	-	-	-	X
56	MG	2A	3070	-	-	-	X
56	MG	2A	3083	-	-	-	X
56	MG	2A	3092	-	-	-	X
56	MG	2A	3093	-	-	-	X
56	MG	2A	3096	-	-	-	X
56	MG	2A	3108	-	-	-	X
56	MG	2A	3160	-	-	-	X
56	MG	2A	3165	-	-	-	X
56	MG	2A	3167	-	-	-	X
56	MG	2A	3181	-	-	-	X
56	MG	2A	3191	-	-	-	X
56	MG	2A	3347	-	-	-	X
56	MG	2A	3364	-	-	-	X
56	MG	2A	3409	-	-	-	X
56	MG	2A	3444	-	-	-	X
56	MG	2A	3445	-	-	-	X
56	MG	2A	3448	-	-	-	X
56	MG	2A	3449	-	-	-	X
56	MG	2A	3455	-	-	-	X
56	MG	2A	3461	-	-	-	X
56	MG	2A	3468	-	-	-	X
56	MG	2A	3472	-	-	-	X
56	MG	2A	3486	-	-	-	X
56	MG	2A	3493	-	-	-	X
56	MG	2A	3579	-	-	-	X
56	MG	2A	3633	-	-	-	X
56	MG	2A	3673	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
56	MG	2A	3677	-	-	-	X
56	MG	2A	3687	-	-	-	X
56	MG	2A	3745	-	-	-	X
56	MG	2A	3814	-	-	-	X
56	MG	2A	3856	-	-	-	X
56	MG	2A	3876	-	-	-	X
56	MG	2A	3883	-	-	-	X
56	MG	2A	3886	-	-	-	X
56	MG	2A	3897	-	-	-	X
56	MG	2A	3900	-	-	-	X
56	MG	2A	3906	-	-	-	X
56	MG	2B	3008	-	-	-	X
56	MG	2D	304	-	-	-	X
56	MG	2F	304	-	-	-	X
56	MG	2U	201	-	-	-	X
56	MG	2a	3010	-	-	-	X
56	MG	2a	3041	-	-	-	X
56	MG	2a	3091	-	-	-	X
56	MG	2a	3165	-	-	-	X
56	MG	2a	3208	-	-	-	X
58	ZN	15	101	-	-	-	X
58	ZN	25	102	-	-	-	X

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 300910 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2871	Total	C	N	O	P	0	0	0
			61852	27531	11572	19878	2871			
1	2A	2800	Total	C	N	O	P	0	0	0
			60322	26848	11284	19390	2800			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
22	20	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 53 is a RNA chain called mRNA.

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

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

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

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

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

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2E	9	Total	Mg	0	0
			9	9		
56	17	1	Total	Mg	0	0
			1	1		
56	2d	1	Total	Mg	0	0
			1	1		
56	1T	2	Total	Mg	0	0
			2	2		
56	1N	6	Total	Mg	0	0
			6	6		
56	20	3	Total	Mg	0	0
			3	3		
56	18	3	Total	Mg	0	0
			3	3		
56	2W	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1Y	3	Total 3	Mg 3	0	0
56	13	3	Total 3	Mg 3	0	0
56	1f	2	Total 2	Mg 2	0	0
56	1P	4	Total 4	Mg 4	0	0
56	2B	21	Total 21	Mg 21	0	0
56	2a	244	Total 244	Mg 244	0	0
56	1E	11	Total 11	Mg 11	0	0
56	1b	2	Total 2	Mg 2	0	0
56	2l	2	Total 2	Mg 2	0	0
56	2F	4	Total 4	Mg 4	0	0
56	16	3	Total 3	Mg 3	0	0
56	28	2	Total 2	Mg 2	0	0
56	2e	1	Total 1	Mg 1	0	0
56	1W	5	Total 5	Mg 5	0	0
56	1A	1141	Total 1141	Mg 1141	0	0
56	1t	1	Total 1	Mg 1	0	0
56	1n	2	Total 2	Mg 2	0	0
56	2P	1	Total 1	Mg 1	0	0
56	1X	6	Total 6	Mg 6	0	0
56	12	1	Total 1	Mg 1	0	0
56	1y	4	Total 4	Mg 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2i	1	Total 1	Mg 1	0	0
56	1S	3	Total 3	Mg 3	0	0
56	25	4	Total 4	Mg 4	0	0
56	2T	3	Total 3	Mg 3	0	0
56	1D	12	Total 12	Mg 12	0	0
56	2N	1	Total 1	Mg 1	0	0
56	1e	1	Total 1	Mg 1	0	0
56	2G	1	Total 1	Mg 1	0	0
56	1I	1	Total 1	Mg 1	0	0
56	2f	1	Total 1	Mg 1	0	0
56	1V	3	Total 3	Mg 3	0	0
56	2X	3	Total 3	Mg 3	0	0
56	1w	11	Total 11	Mg 11	0	0
56	1a	229	Total 229	Mg 229	0	0
56	2Q	3	Total 3	Mg 3	0	0
56	15	2	Total 2	Mg 2	0	0
56	1x	16	Total 16	Mg 16	0	0
56	2j	2	Total 2	Mg 2	0	0
56	1R	3	Total 3	Mg 3	0	0
56	1s	1	Total 1	Mg 1	0	0
56	2v	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	2U	4	Total 4	Mg 4	0	0
56	1G	5	Total 5	Mg 5	0	0
56	2O	1	Total 1	Mg 1	0	0
56	11	3	Total 3	Mg 3	0	0
56	1d	1	Total 1	Mg 1	0	0
56	2n	1	Total 1	Mg 1	0	0
56	2g	1	Total 1	Mg 1	0	0
56	2Y	1	Total 1	Mg 1	0	0
56	1v	1	Total 1	Mg 1	0	0
56	2x	5	Total 5	Mg 5	0	0
56	2R	1	Total 1	Mg 1	0	0
56	1Z	3	Total 3	Mg 3	0	0
56	2D	5	Total 5	Mg 5	0	0
56	2q	2	Total 2	Mg 2	0	0
56	1U	8	Total 8	Mg 8	0	0
56	2r	2	Total 2	Mg 2	0	0
56	1O	7	Total 7	Mg 7	0	0
56	27	1	Total 1	Mg 1	0	0
56	19	2	Total 2	Mg 2	0	0
56	1l	3	Total 3	Mg 3	0	0
56	2V	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	1F	8	Total	Mg	0	0
			8	8		
56	10	6	Total	Mg	0	0
			6	6		
56	2t	1	Total	Mg	0	0
			1	1		
56	1Q	6	Total	Mg	0	0
			6	6		
56	2A	909	Total	Mg	0	0
			909	909		
56	23	2	Total	Mg	0	0
			2	2		
56	2Z	1	Total	Mg	0	0
			1	1		
56	1B	37	Total	Mg	0	0
			37	37		
56	2y	7	Total	Mg	0	0
			7	7		
56	2w	8	Total	Mg	0	0
			8	8		

- Molecule 57 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	1A	1	Total	K	0	0
			1	1		
57	2A	1	Total	K	0	0
			1	1		

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	1Y	1	Total	Zn	0	0
			1	1		
58	14	1	Total	Zn	0	0
			1	1		
58	1n	1	Total	Zn	0	0
			1	1		
58	15	1	Total	Zn	0	0
			1	1		
58	29	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	19	1	Total	Zn	0	0
			1	1		
58	26	1	Total	Zn	0	0
			1	1		
58	25	1	Total	Zn	0	0
			1	1		
58	24	1	Total	Zn	0	0
			1	1		
58	2n	1	Total	Zn	0	0
			1	1		
58	2Y	1	Total	Zn	0	0
			1	1		
58	16	1	Total	Zn	0	0
			1	1		

- Molecule 59 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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

- Molecule 60 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	1A	2238	Total O 2238 2238	0	0
60	1B	68	Total O 68 68	0	0
60	1D	28	Total O 28 28	0	0
60	1E	28	Total O 28 28	0	0
60	1F	13	Total O 13 13	0	0
60	1G	7	Total O 7 7	0	0
60	1H	2	Total O 2 2	0	0
60	1I	3	Total O 3 3	0	0
60	1N	7	Total O 7 7	0	0
60	1O	8	Total O 8 8	0	0
60	1P	23	Total O 23 23	0	0
60	1Q	14	Total O 14 14	0	0
60	1R	14	Total O 14 14	0	0
60	1S	5	Total O 5 5	0	0
60	1T	8	Total O 8 8	0	0
60	1U	11	Total O 11 11	0	0
60	1V	9	Total O 9 9	0	0
60	1W	6	Total O 6 6	0	0
60	1X	8	Total O 8 8	0	0
60	1Y	4	Total O 4 4	0	0
60	1Z	1	Total O 1 1	0	0
60	10	12	Total O 12 12	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	11	10	Total 10	O 10	0	0
60	12	4	Total 4	O 4	0	0
60	13	6	Total 6	O 6	0	0
60	14	1	Total 1	O 1	0	0
60	15	6	Total 6	O 6	0	0
60	16	3	Total 3	O 3	0	0
60	17	9	Total 9	O 9	0	0
60	18	13	Total 13	O 13	0	0
60	1a	438	Total 438	O 438	0	0
60	1b	1	Total 1	O 1	0	0
60	1d	1	Total 1	O 1	0	0
60	1e	1	Total 1	O 1	0	0
60	1f	1	Total 1	O 1	0	0
60	1g	1	Total 1	O 1	0	0
60	1i	1	Total 1	O 1	0	0
60	1l	8	Total 8	O 8	0	0
60	1m	2	Total 2	O 2	0	0
60	1o	1	Total 1	O 1	0	0
60	1p	1	Total 1	O 1	0	0
60	1q	4	Total 4	O 4	0	0
60	1u	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1v	5	Total 5	O 5	0	0
60	1w	21	Total 21	O 21	0	0
60	1x	15	Total 15	O 15	0	0
60	1y	1	Total 1	O 1	0	0
60	2A	1389	Total 1389	O 1389	0	0
60	2B	26	Total 26	O 26	0	0
60	2D	28	Total 28	O 28	0	0
60	2E	16	Total 16	O 16	0	0
60	2F	16	Total 16	O 16	0	0
60	2H	1	Total 1	O 1	0	0
60	2I	4	Total 4	O 4	0	0
60	2N	1	Total 1	O 1	0	0
60	2P	14	Total 14	O 14	0	0
60	2Q	2	Total 2	O 2	0	0
60	2R	2	Total 2	O 2	0	0
60	2T	6	Total 6	O 6	0	0
60	2U	2	Total 2	O 2	0	0
60	2V	2	Total 2	O 2	0	0
60	2W	2	Total 2	O 2	0	0
60	2X	5	Total 5	O 5	0	0
60	2Y	1	Total 1	O 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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60	20	7	Total 7	O 7	0	0
60	21	12	Total 12	O 12	0	0
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60	23	1	Total 1	O 1	0	0
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60	29	1	Total 1	O 1	0	0
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60	2e	2	Total 2	O 2	0	0
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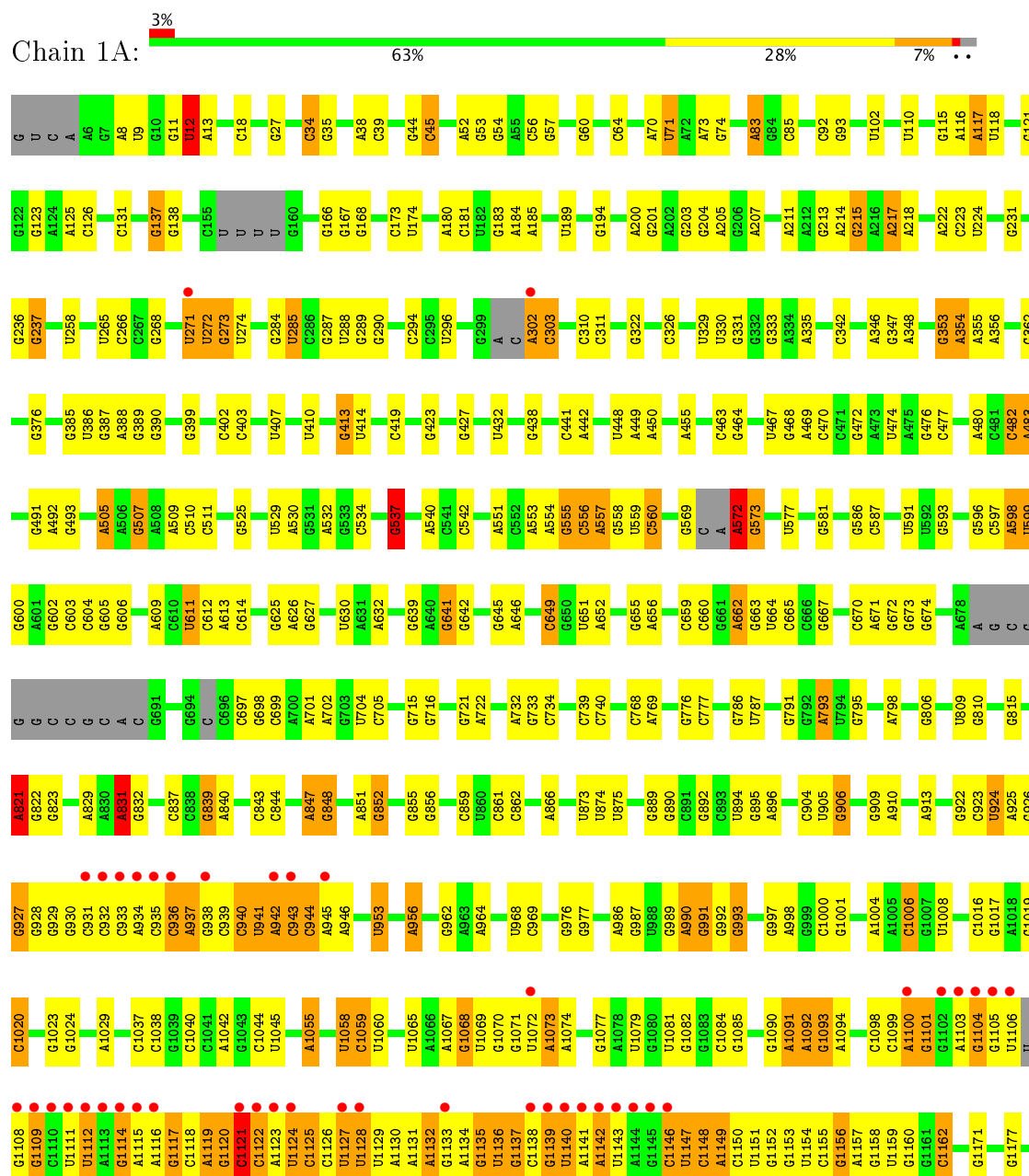
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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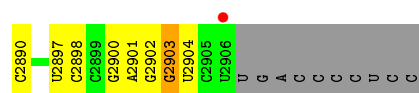
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

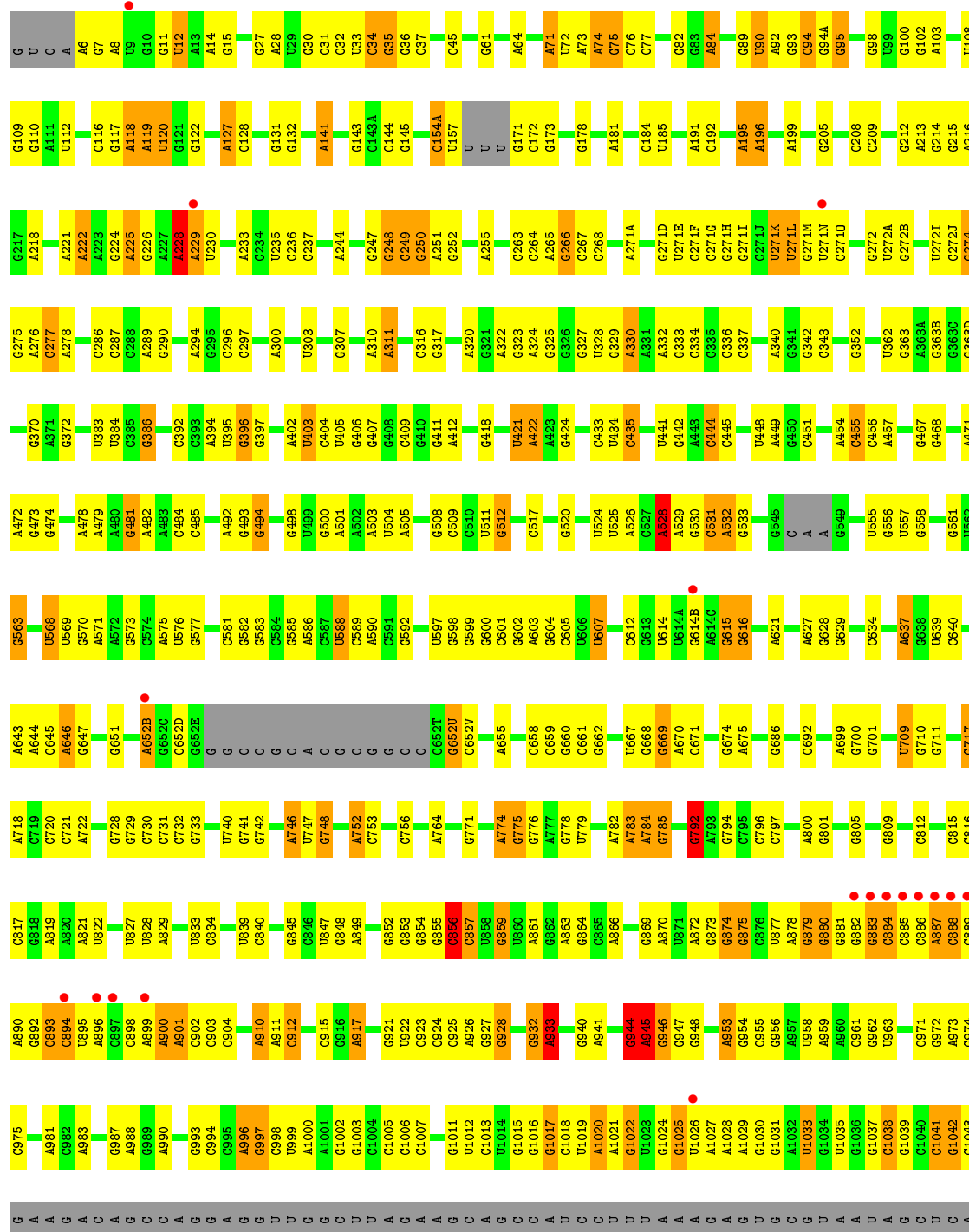
• Molecule 1: 23S Ribosomal RNA



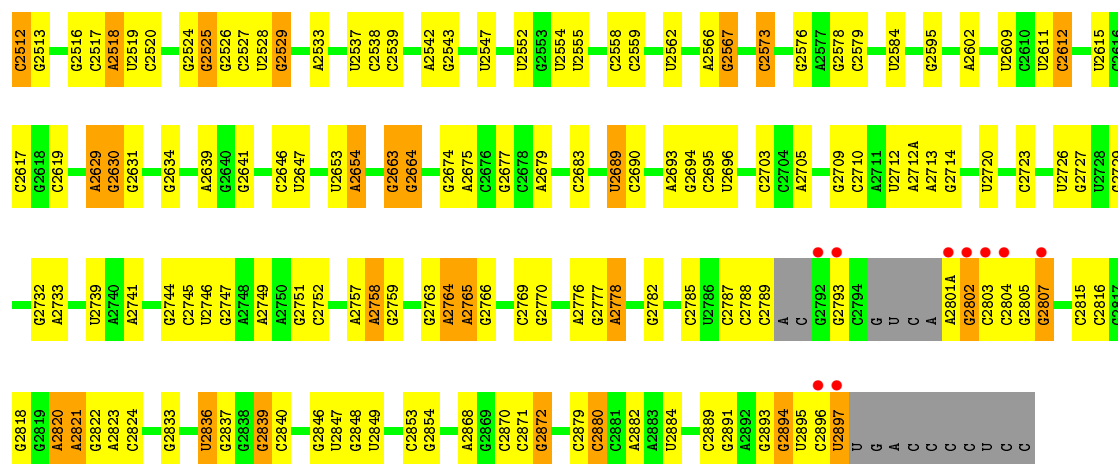
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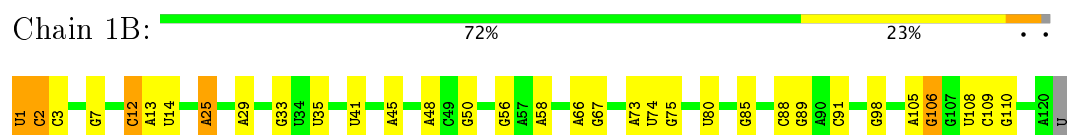
● Molecule 1: 23S Ribosomal RNA



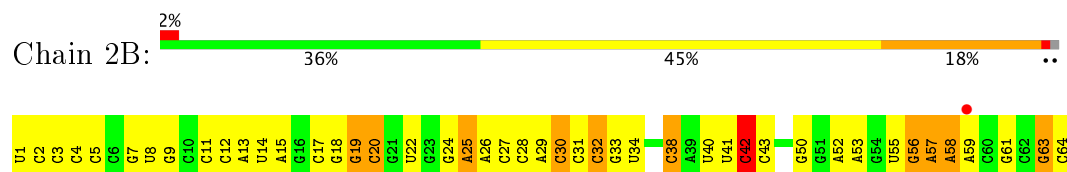
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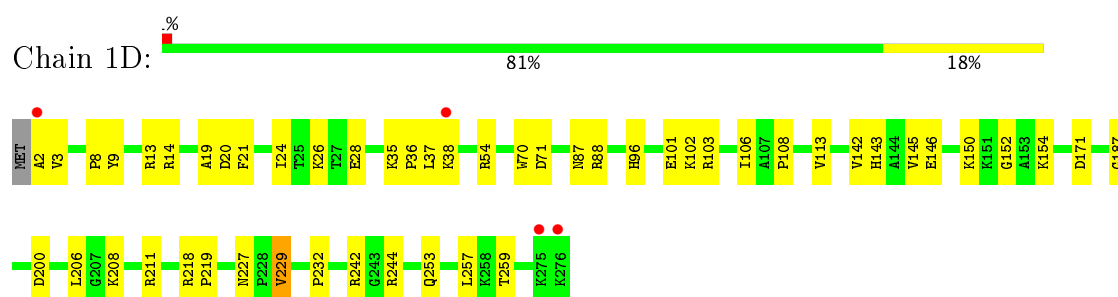
• Molecule 2: 5S Ribosomal RNA



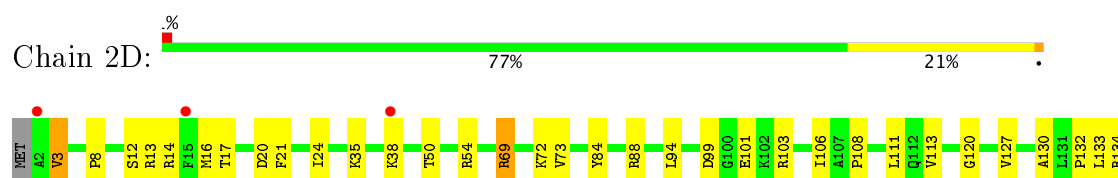
• Molecule 2: 5S Ribosomal RNA



• Molecule 3: 50S ribosomal protein L2

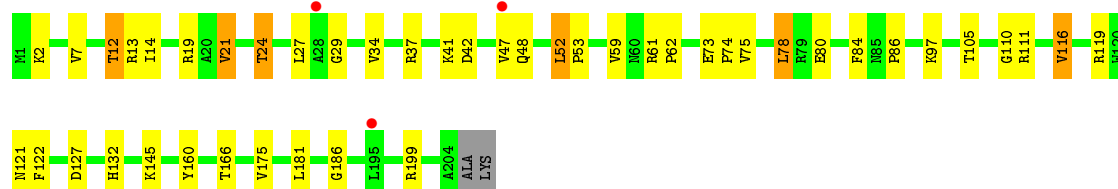
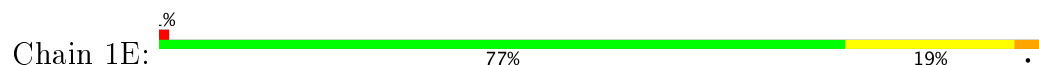


• Molecule 3: 50S ribosomal protein L2

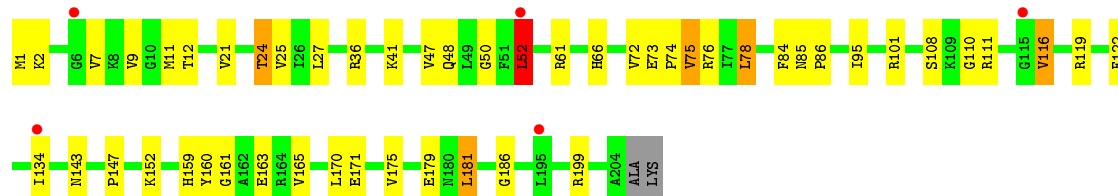
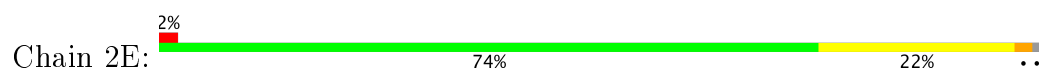




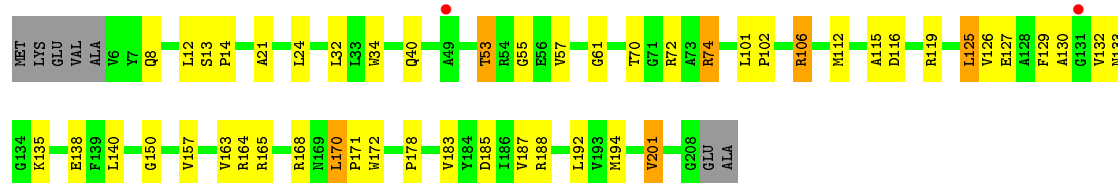
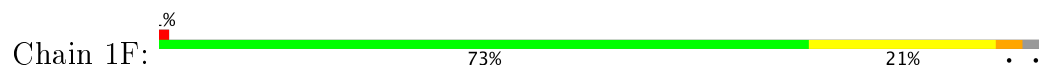
• Molecule 4: 50S ribosomal protein L3



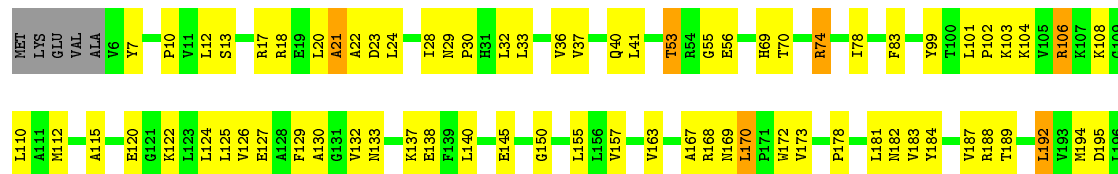
• Molecule 4: 50S ribosomal protein L3



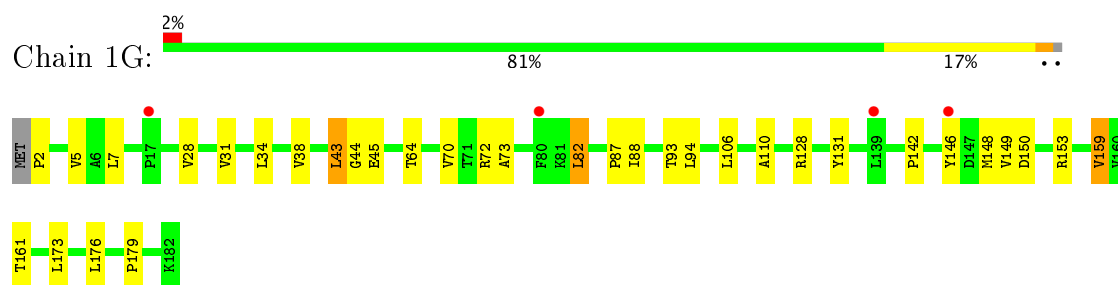
• Molecule 5: 50S ribosomal protein L4



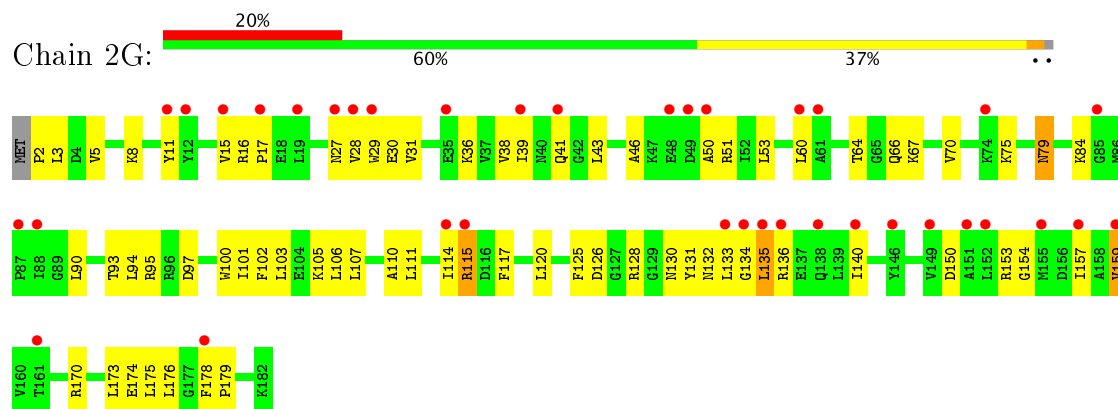
• Molecule 5: 50S ribosomal protein L4



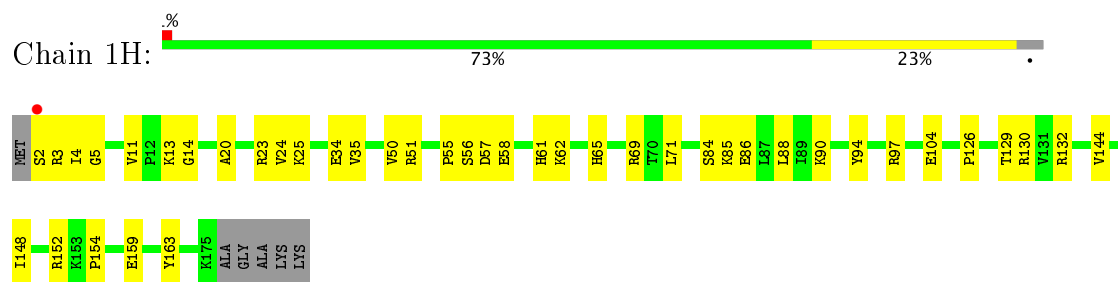
• Molecule 6: 50S ribosomal protein L5



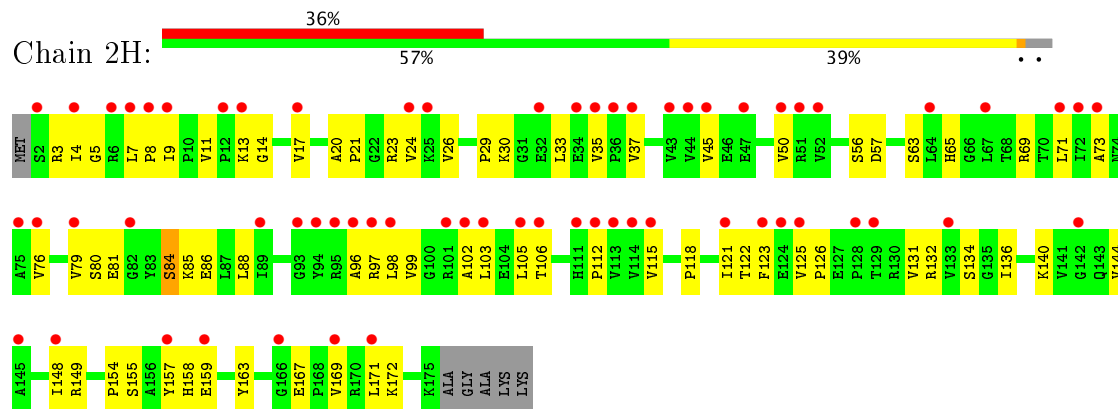
• Molecule 6: 50S ribosomal protein L5



• Molecule 7: 50S ribosomal protein L6



• Molecule 7: 50S ribosomal protein L6

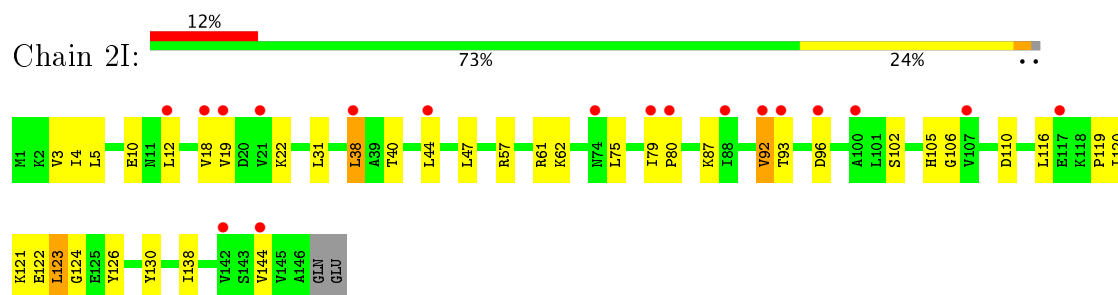


• Molecule 8: 50S ribosomal protein L9

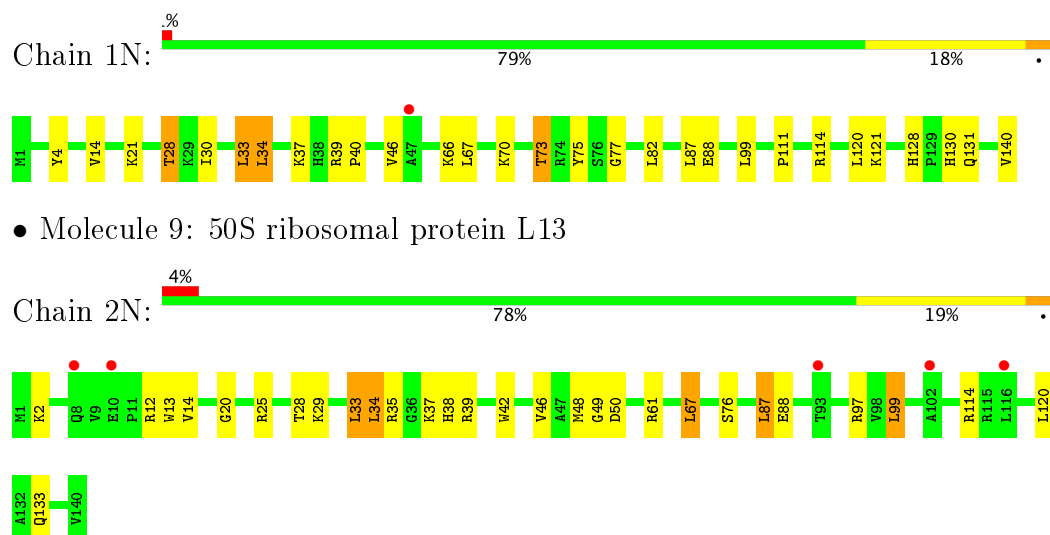




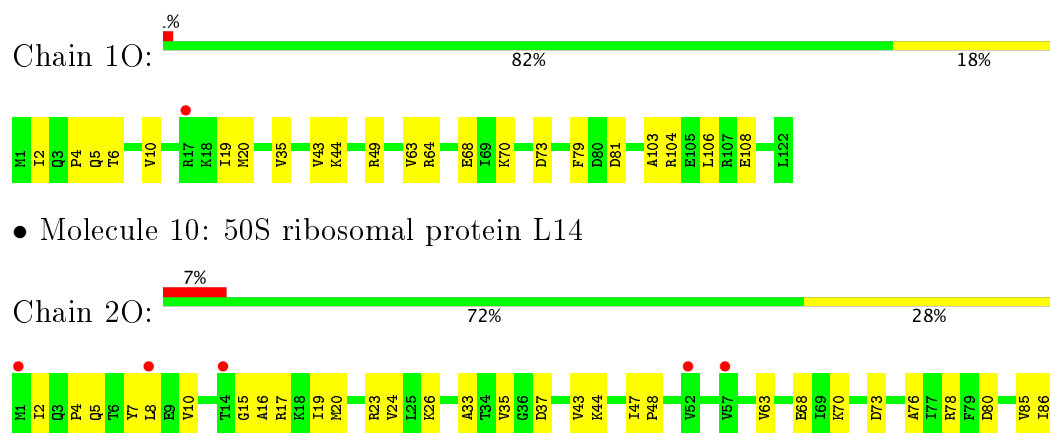
- Molecule 8: 50S ribosomal protein L9



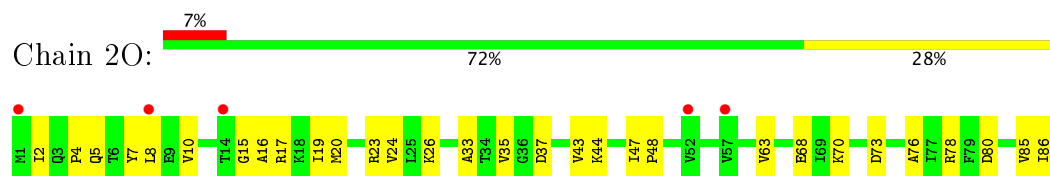
- Molecule 9: 50S ribosomal protein L13

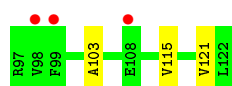


- Molecule 10: 50S ribosomal protein L14

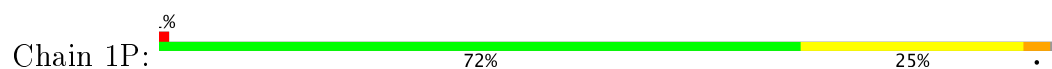


- Molecule 10: 50S ribosomal protein L14

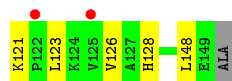
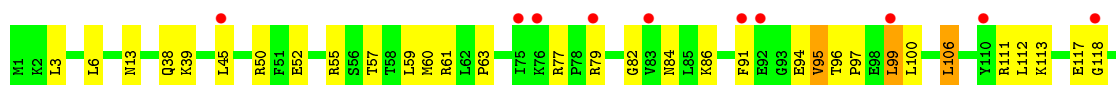
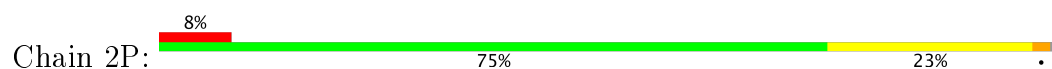




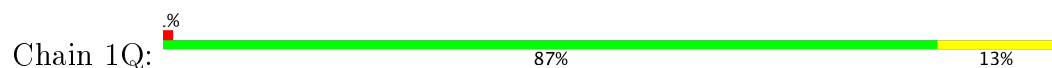
- Molecule 11: 50S ribosomal protein L15



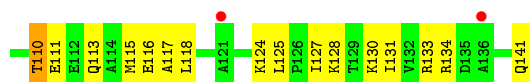
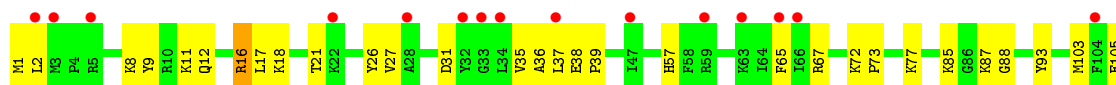
- Molecule 11: 50S ribosomal protein L15



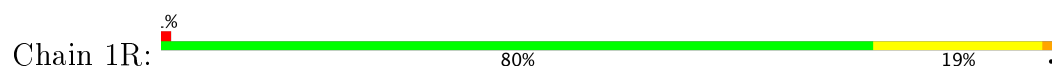
- Molecule 12: 50S ribosomal protein L16



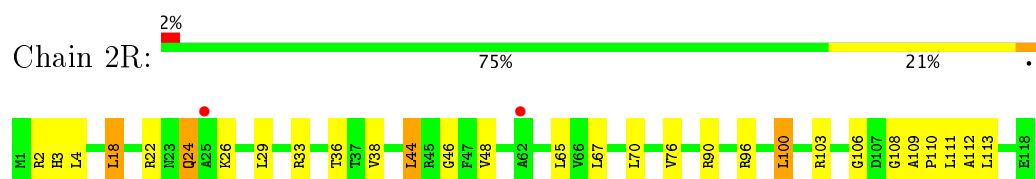
- Molecule 12: 50S ribosomal protein L16



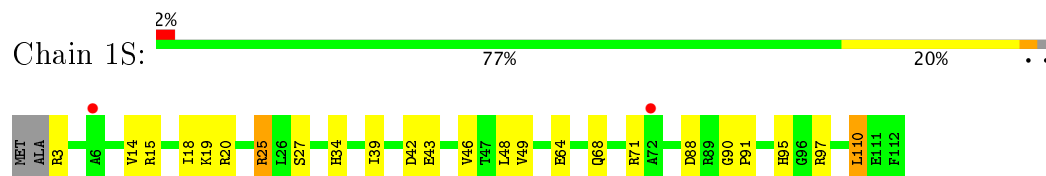
- Molecule 13: 50S ribosomal protein L17



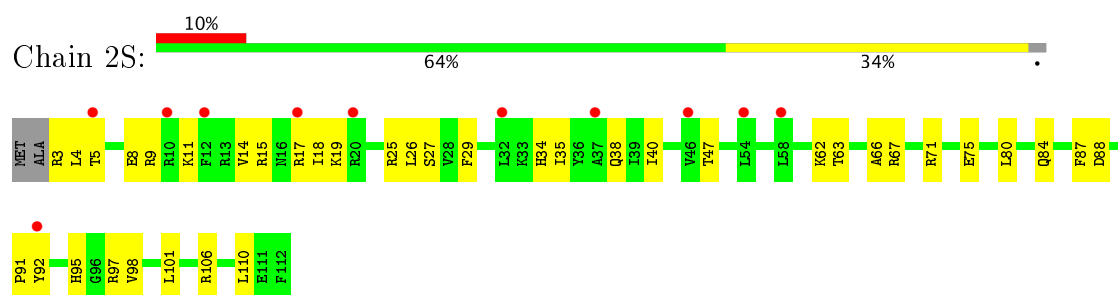
- Molecule 13: 50S ribosomal protein L17



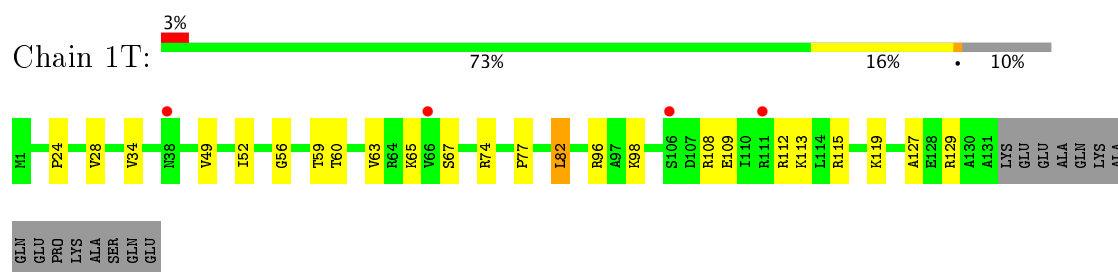
- Molecule 14: 50S ribosomal protein L18



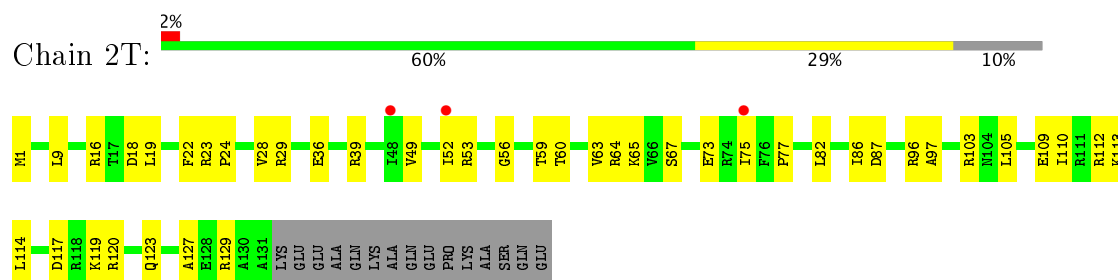
- Molecule 14: 50S ribosomal protein L18



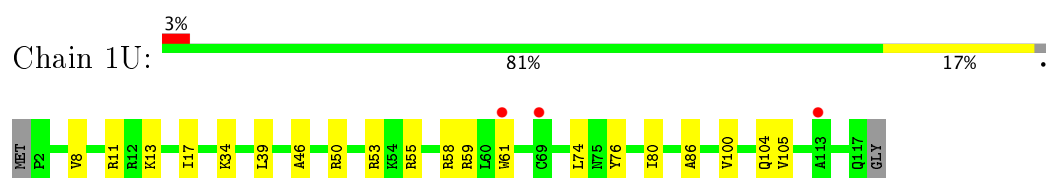
- Molecule 15: 50S ribosomal protein L19



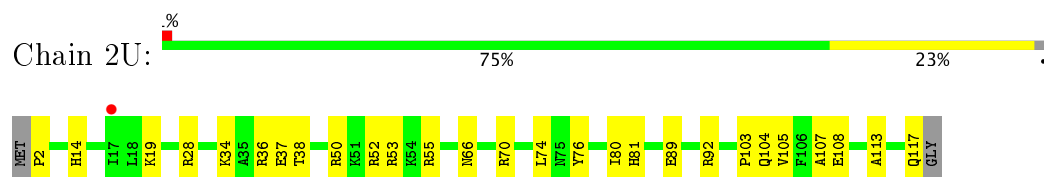
- Molecule 15: 50S ribosomal protein L19



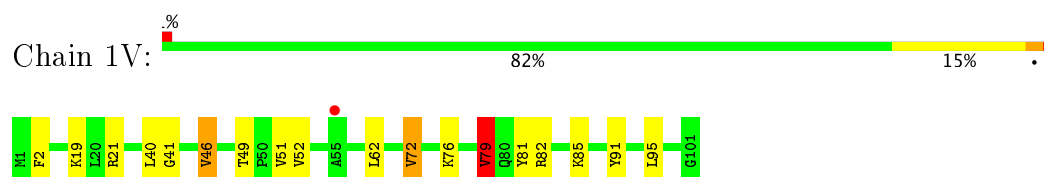
- Molecule 16: 50S ribosomal protein L20



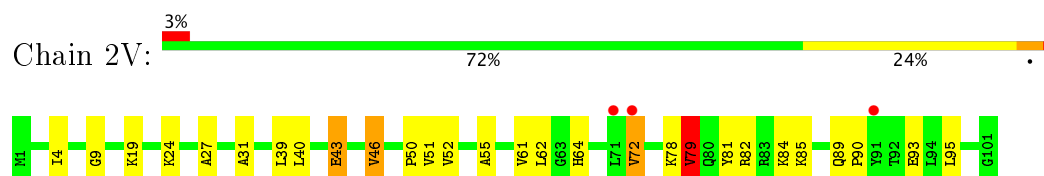
- Molecule 16: 50S ribosomal protein L20



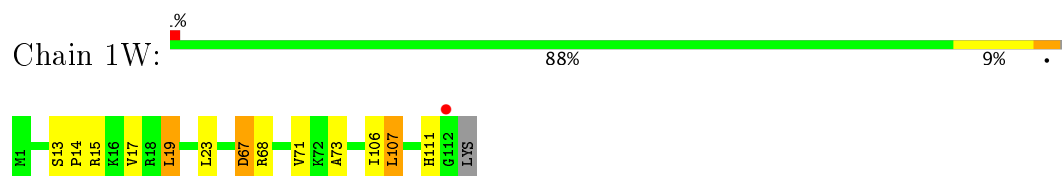
- Molecule 17: 50S ribosomal protein L21



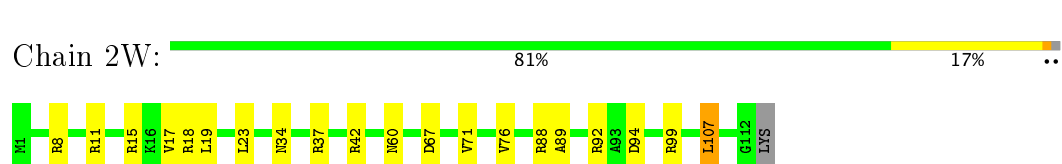
- Molecule 17: 50S ribosomal protein L21



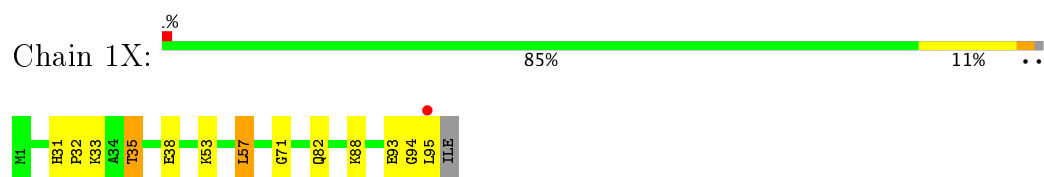
- Molecule 18: 50S ribosomal protein L22



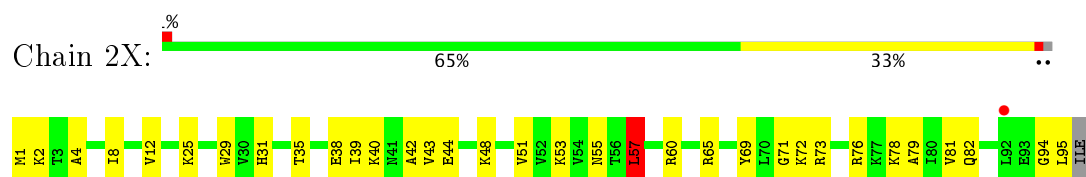
- Molecule 18: 50S ribosomal protein L22



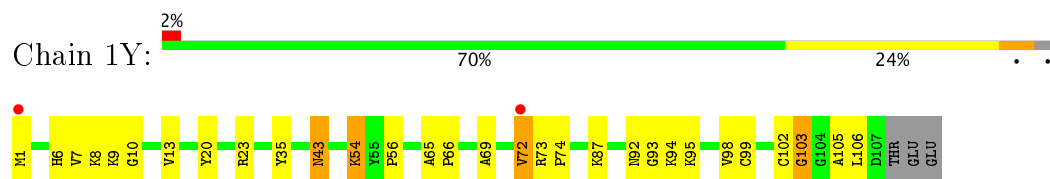
- Molecule 19: 50S ribosomal protein L23



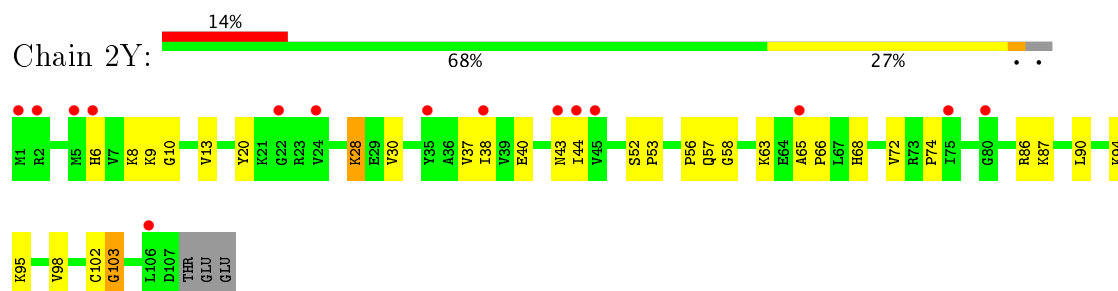
- Molecule 19: 50S ribosomal protein L23



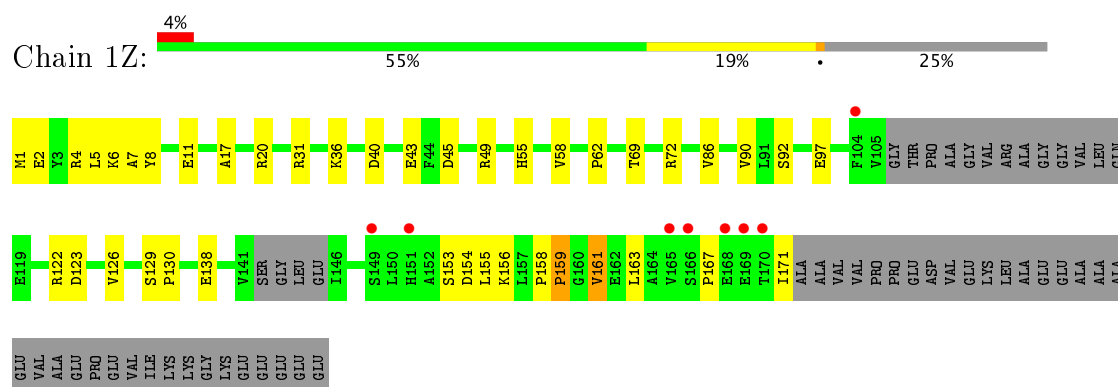
• Molecule 20: 50S ribosomal protein L24



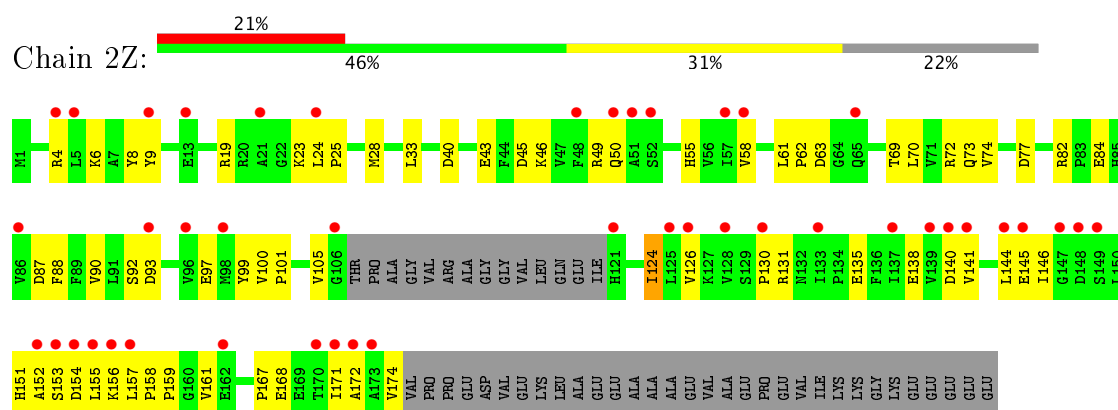
• Molecule 20: 50S ribosomal protein L24



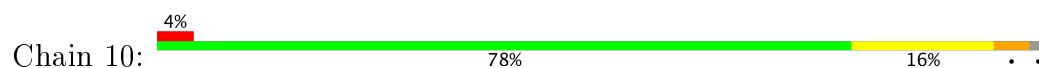
• Molecule 21: 50S ribosomal protein L25

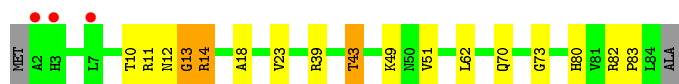


• Molecule 21: 50S ribosomal protein L25

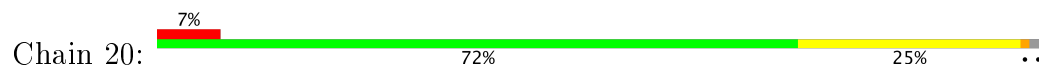


• Molecule 22: 50S ribosomal protein L27

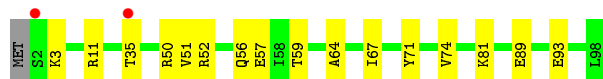
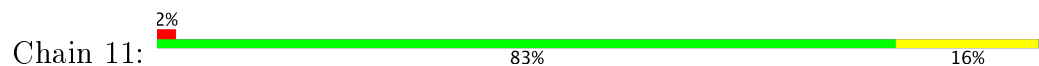




- Molecule 22: 50S ribosomal protein L27



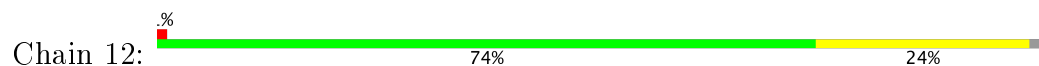
- Molecule 23: 50S ribosomal protein L28



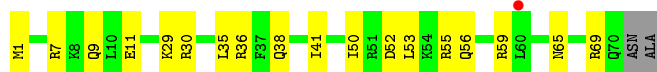
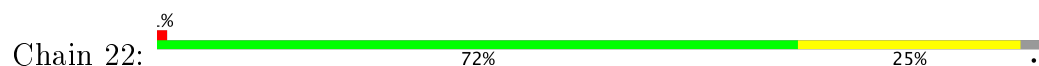
- Molecule 23: 50S ribosomal protein L28



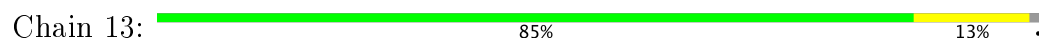
- Molecule 24: 50S ribosomal protein L29



- Molecule 24: 50S ribosomal protein L29

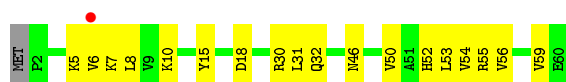


- Molecule 25: 50S ribosomal protein L30

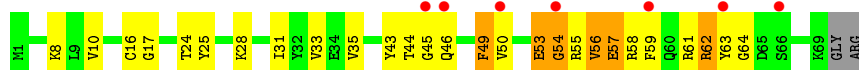


- Molecule 25: 50S ribosomal protein L30

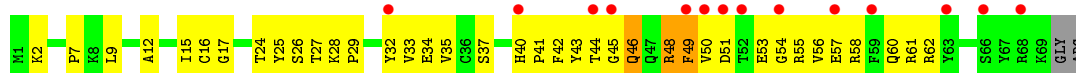
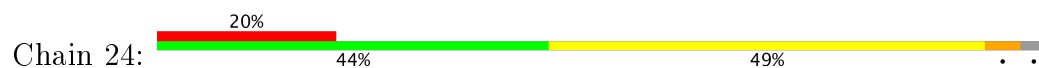




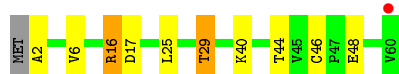
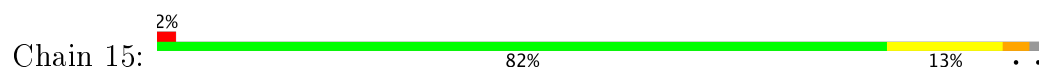
- Molecule 26: 50S ribosomal protein L31



- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



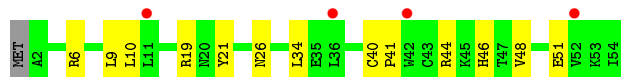
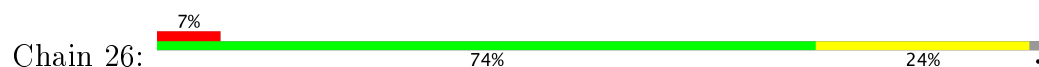
- Molecule 27: 50S ribosomal protein L32



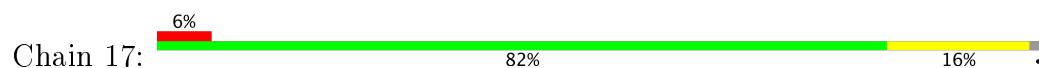
- Molecule 28: 50S ribosomal protein L33



- Molecule 28: 50S ribosomal protein L33

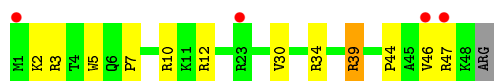
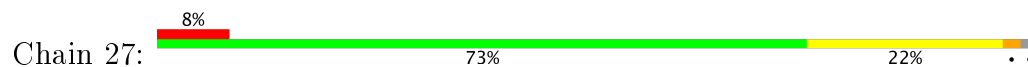


- Molecule 29: 50S ribosomal protein L34





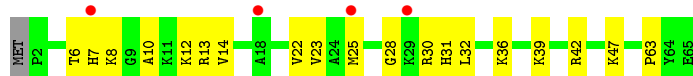
- Molecule 29: 50S ribosomal protein L34



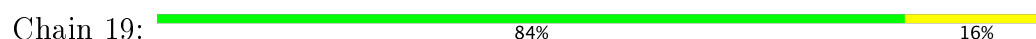
- Molecule 30: 50S ribosomal protein L35



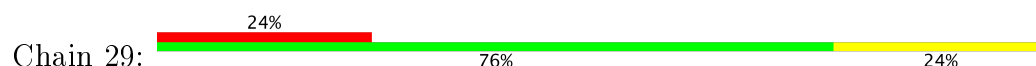
- Molecule 30: 50S ribosomal protein L35



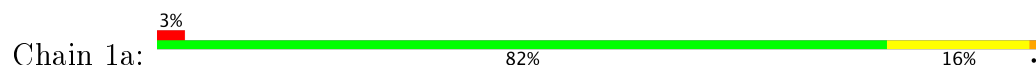
- Molecule 31: 50S ribosomal protein L36

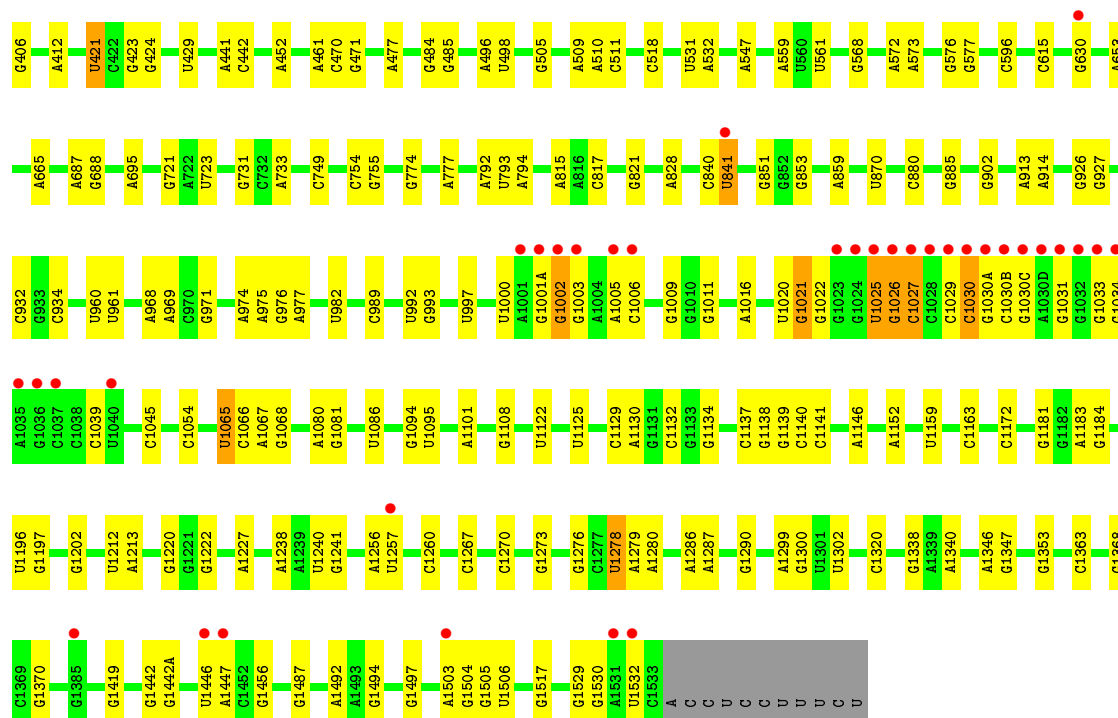


- Molecule 31: 50S ribosomal protein L36

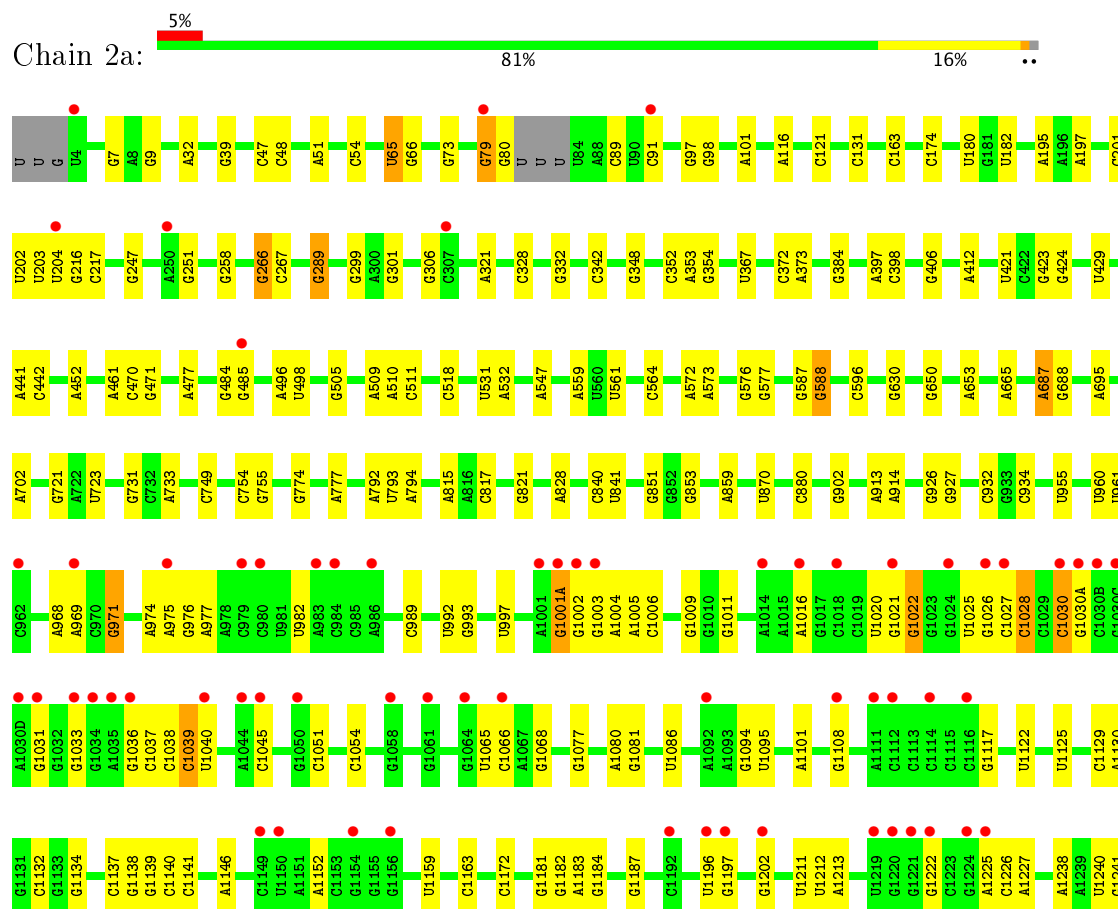


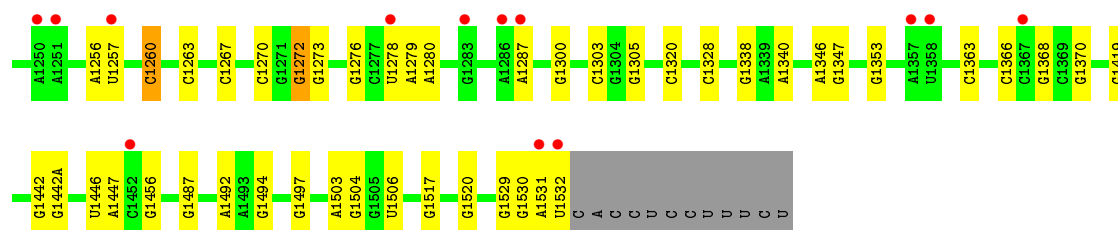
- Molecule 32: 16S Ribosomal RNA



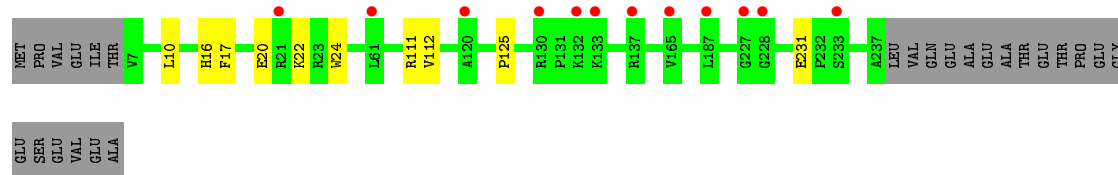
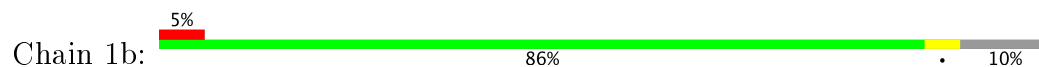


• Molecule 32: 16S Ribosomal RNA

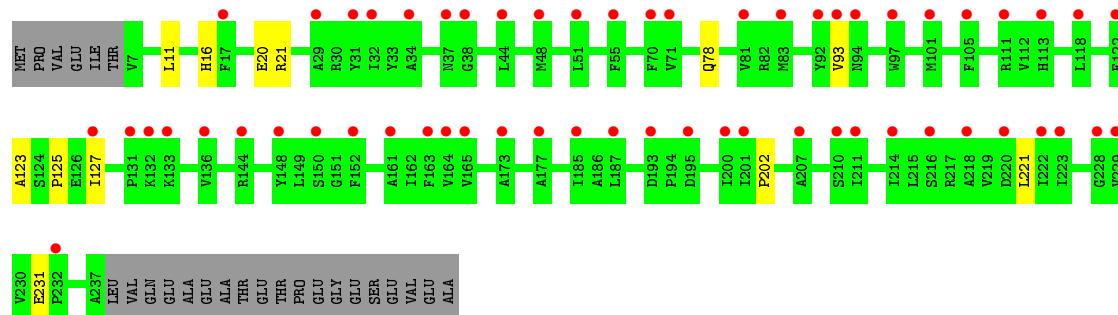
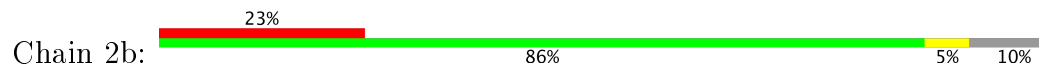




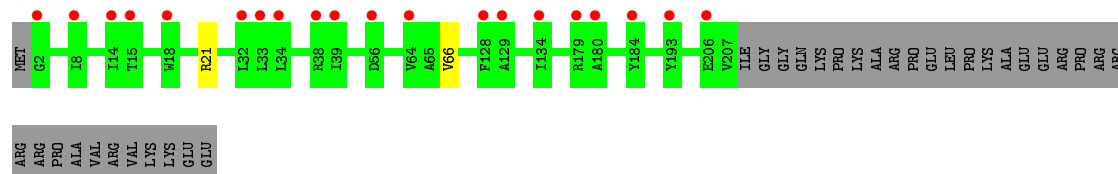
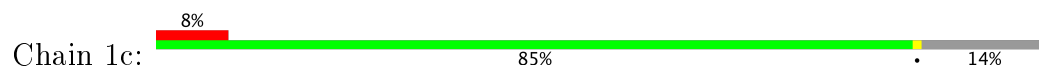
• Molecule 33: 30S ribosomal protein S2



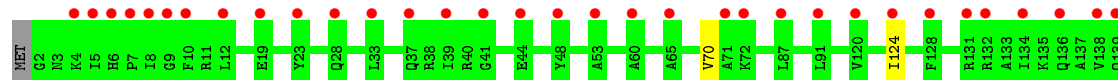
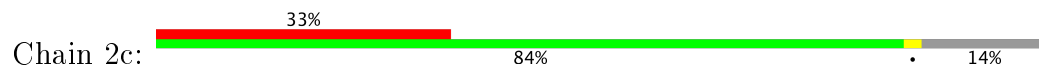
• Molecule 33: 30S ribosomal protein S2

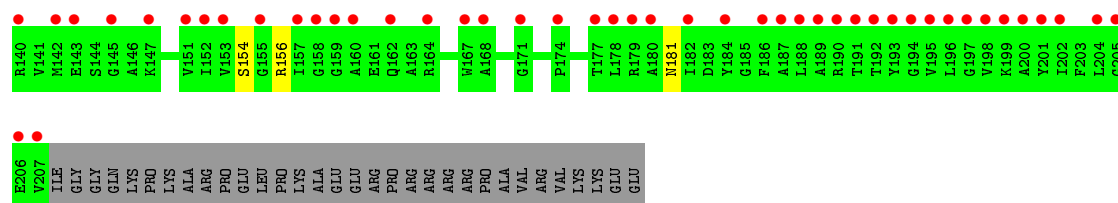


• Molecule 34: 30S ribosomal protein S3

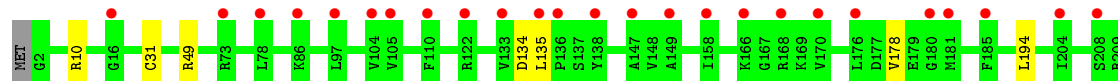


• Molecule 34: 30S ribosomal protein S3

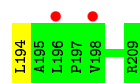
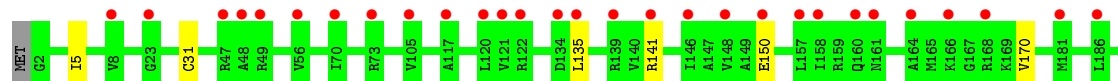




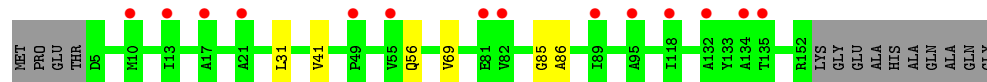
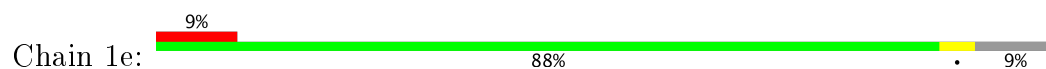
- Molecule 35: 30S ribosomal protein S4



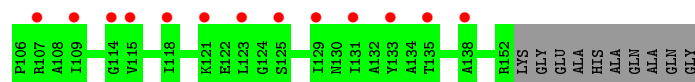
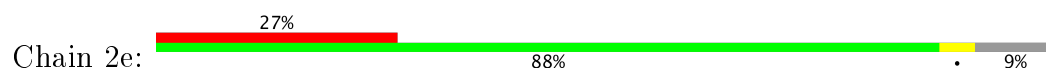
- Molecule 35: 30S ribosomal protein S4



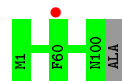
- Molecule 36: 30S ribosomal protein S5



- Molecule 36: 30S ribosomal protein S5



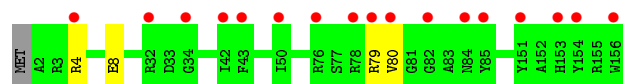
- Molecule 37: 30S ribosomal protein S6



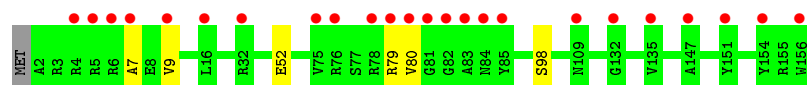
- Molecule 37: 30S ribosomal protein S6



- Molecule 38: 30S ribosomal protein S7



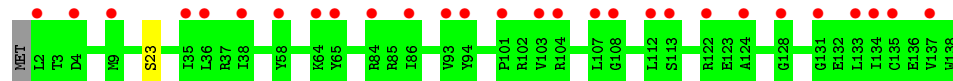
- Molecule 38: 30S ribosomal protein S7



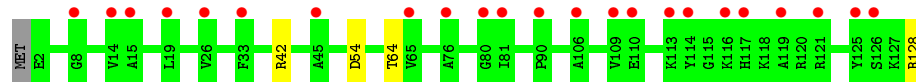
- Molecule 39: 30S ribosomal protein S8



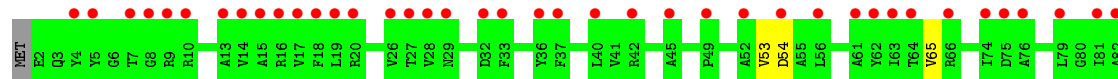
- Molecule 39: 30S ribosomal protein S8

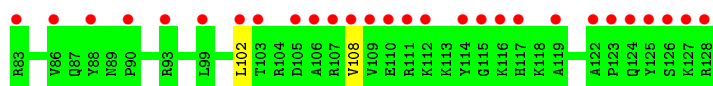


- Molecule 40: 30S ribosomal protein S9

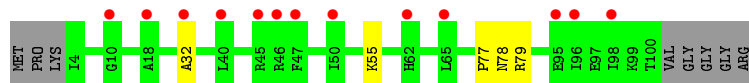
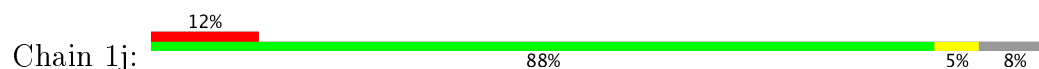


- Molecule 40: 30S ribosomal protein S9

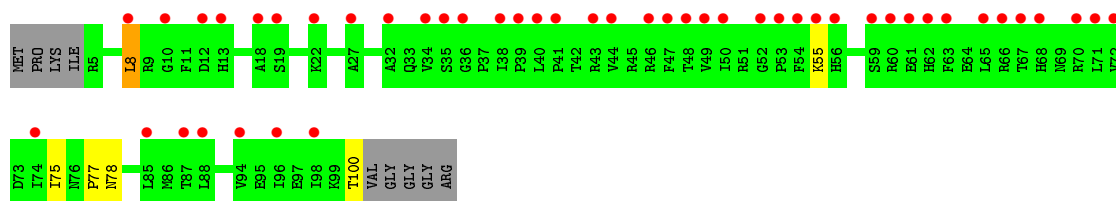
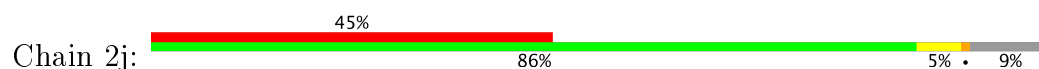




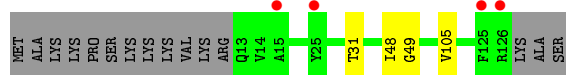
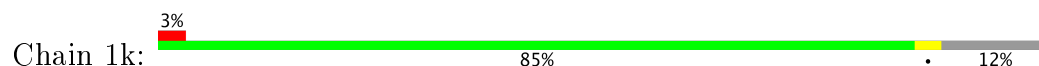
- Molecule 41: 30S ribosomal protein S10



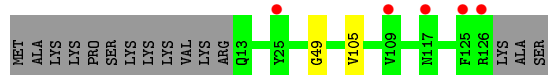
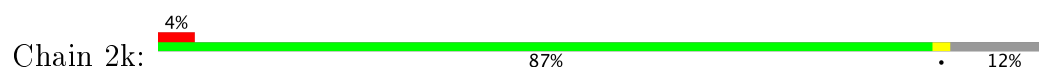
- Molecule 41: 30S ribosomal protein S10



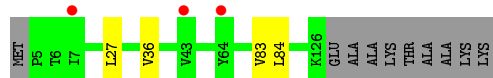
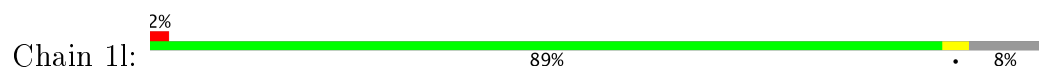
- Molecule 42: 30S ribosomal protein S11



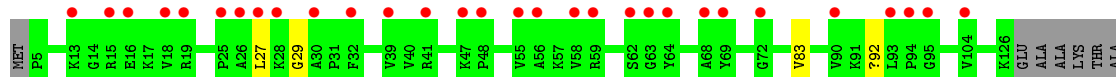
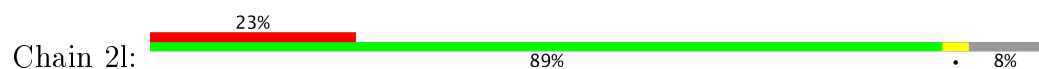
- Molecule 42: 30S ribosomal protein S11



- Molecule 43: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S12



ALA
LYS
LYS

- Molecule 44: 30S ribosomal protein S13



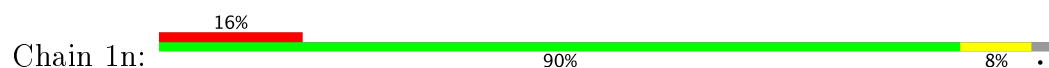
MET A2 G26 R102 T109 K121 K122 A123 P124 ARG LYS

- Molecule 44: 30S ribosomal protein S13



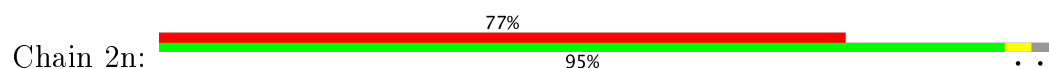
MET ALA I4 A5 G6 V7 Y23 A42 D47 V60 L66 E67 G68 E69 L70 R71 A72 E73 A76 I77 I78 M82 D83 I84 Y87 R88 G89 L90 R91 R92 R93 R94 G95 L96 P97 V98 R99 G100 Q101 R102 T103 R104 T105 N106 A118 G119 K120 K121 K122 A123 P124 ARG LYS

- Molecule 45: 30S ribosomal protein S14 type Z



MET A2 R3 L6 I7 R12 T13 F16 K17 T22 R23 Y24 V34 R41 R57 W61

- Molecule 45: 30S ribosomal protein S14 type Z



MET A2 R3 K4 A5 L6 I7 E8 K9 A10 K11 R12 T13 P14 K15 F16 K17 V18 Y21 T22 R23 C24 V25 R26 C27 G28 R29 A30 R31 S32 Y33 T34 R35 F36 F37 G38 L39 C40 R41 I42 C43 L44 R45 E46 L47 A48 H49 K50 G51 Q52 L53 P54 G55 V56 R57 K58 A59 S60 W61

- Molecule 46: 30S ribosomal protein S15



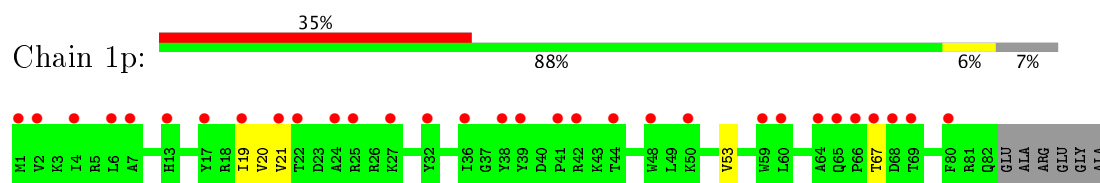
MET P2 E7 L39 L57 L66 Y69 I87 R88 G89

- Molecule 46: 30S ribosomal protein S15

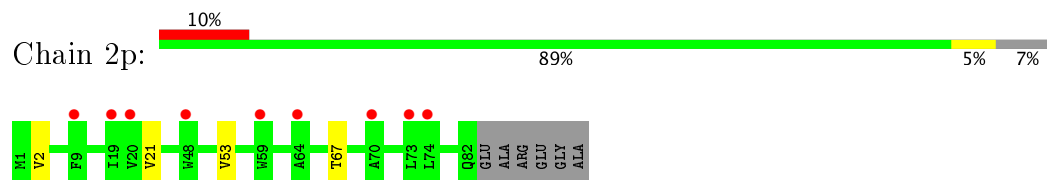


MET P2 F15 A16 Y27 L31 L39 G61 R88 G89

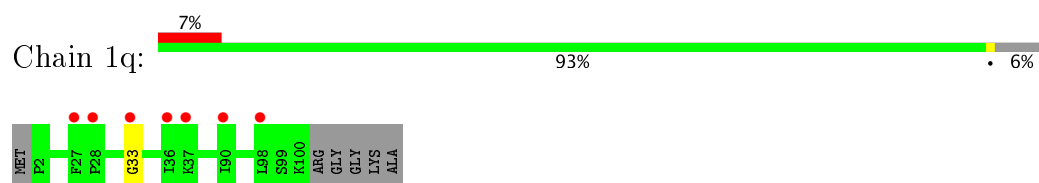
- Molecule 47: 30S ribosomal protein S16



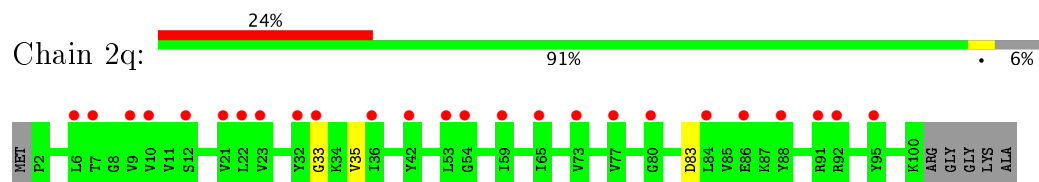
- Molecule 47: 30S ribosomal protein S16



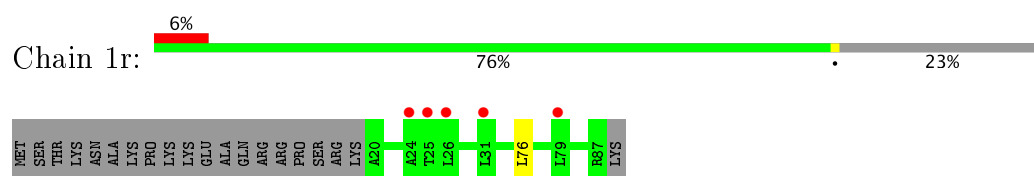
- Molecule 48: 30S ribosomal protein S17



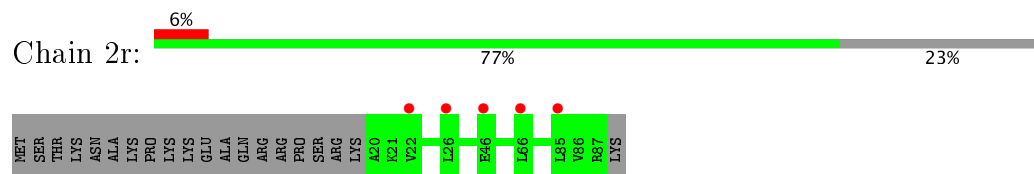
- Molecule 48: 30S ribosomal protein S17



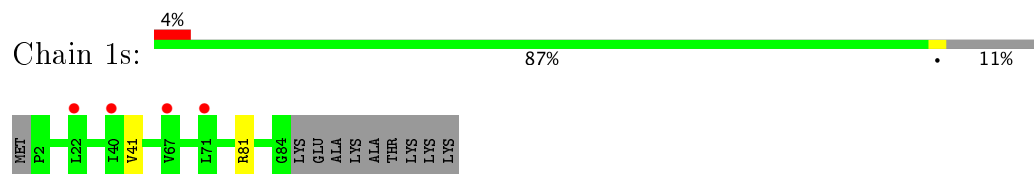
- Molecule 49: 30S ribosomal protein S18



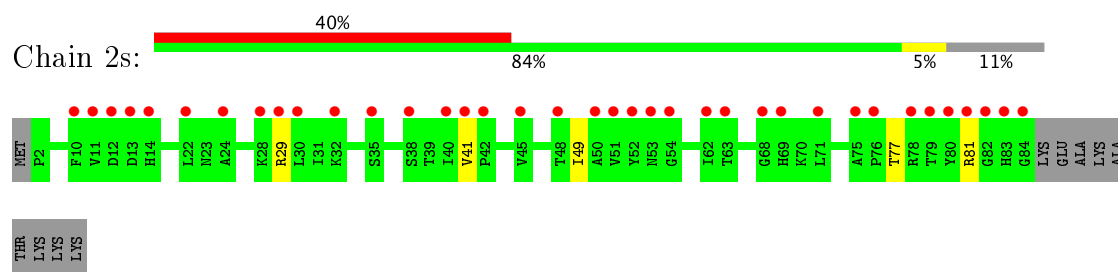
- Molecule 49: 30S ribosomal protein S18



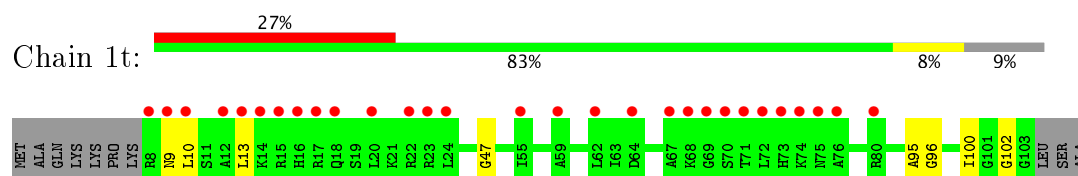
- Molecule 50: 30S ribosomal protein S19



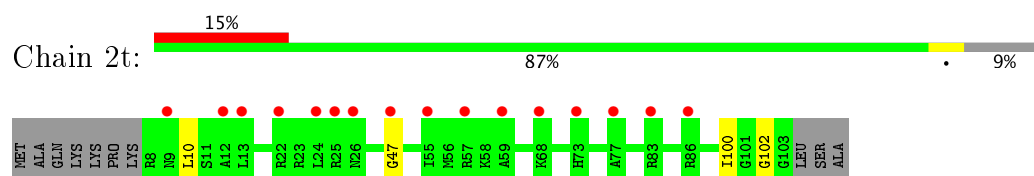
- Molecule 50: 30S ribosomal protein S19



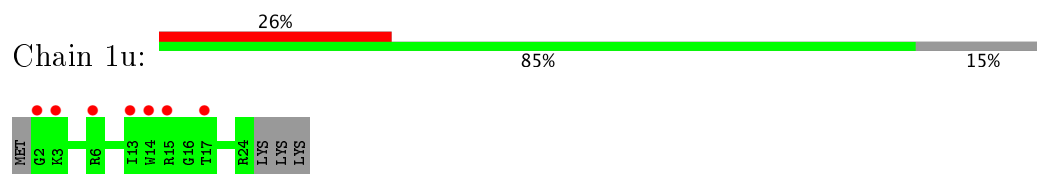
- Molecule 51: 30S ribosomal protein S20



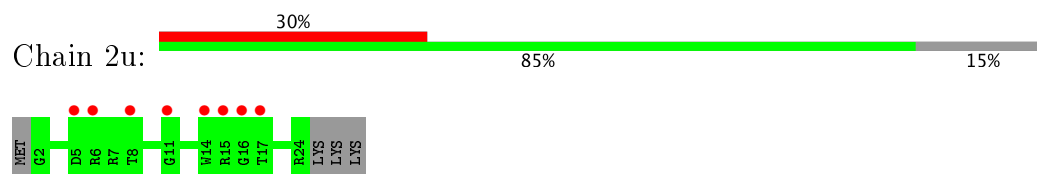
- Molecule 51: 30S ribosomal protein S20



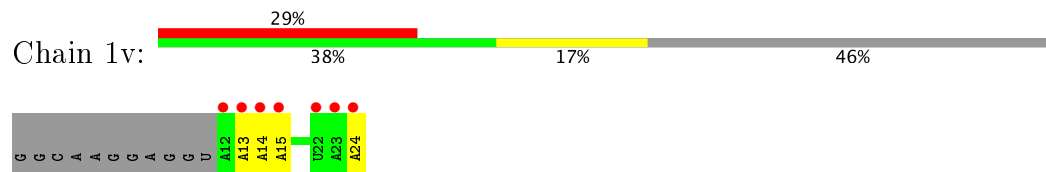
- Molecule 52: 30S ribosomal protein Thx



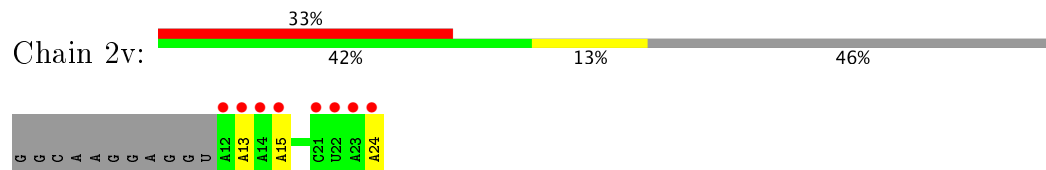
- Molecule 52: 30S ribosomal protein Thx



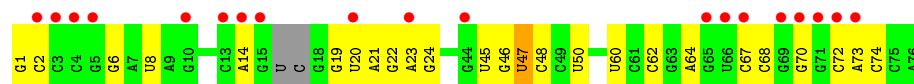
- Molecule 53: mRNA



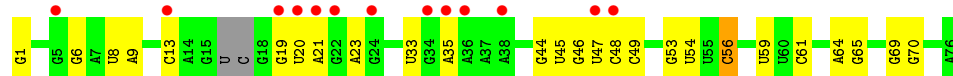
- Molecule 53: mRNA



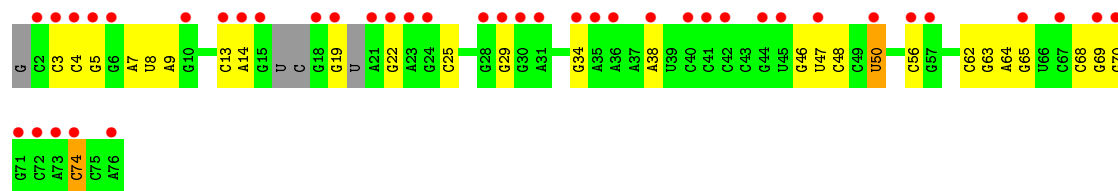
- Molecule 54: A-site and E-site tRNAs



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



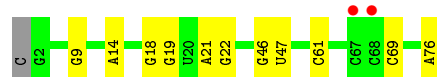
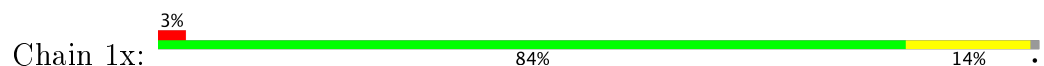
- Molecule 54: A-site and E-site tRNAs



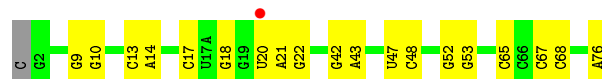
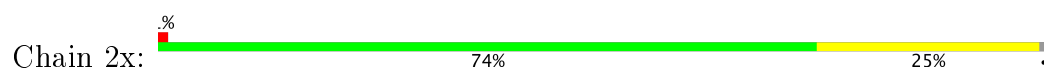
- Molecule 54: A-site and E-site tRNAs



- Molecule 55: P-site tRNA



- Molecule 55: P-site tRNA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.70Å 450.05Å 624.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	122.01 – 2.50 198.78 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.8 (122.01-2.50) 97.8 (198.78-2.50)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.52Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.231 , 0.281 0.244 , 0.291	Depositor DCC
R_{free} test set	98495 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	47.4	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	300910	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.61	0/69009	1.05	129/107712 (0.1%)
1	2A	0.52	1/67293 (0.0%)	1.03	84/105034 (0.1%)
2	1B	0.51	1/2882 (0.0%)	0.87	0/4494
2	2B	0.59	1/2879 (0.0%)	1.01	4/4487 (0.1%)
3	1D	0.44	0/2186	0.61	0/2944
3	2D	0.38	0/2186	0.61	0/2944
4	1E	0.43	0/1592	0.61	0/2149
4	2E	0.37	0/1592	0.59	0/2149
5	1F	0.40	0/1619	0.58	0/2193
5	2F	0.37	0/1615	0.58	0/2188
6	1G	0.34	0/1448	0.54	0/1957
6	2G	0.36	0/1453	0.58	0/1963
7	1H	0.36	0/1356	0.55	0/1834
7	2H	0.33	0/1356	0.55	0/1834
8	1I	0.31	0/1112	0.55	0/1514
8	2I	0.30	0/1079	0.54	0/1475
9	1N	0.39	0/1144	0.57	0/1543
9	2N	0.36	0/1144	0.58	0/1543
10	1O	0.42	0/943	0.58	0/1269
10	2O	0.35	0/943	0.54	0/1269
11	1P	0.39	0/1152	0.60	0/1533
11	2P	0.36	0/1152	0.62	0/1533
12	1Q	0.41	0/1143	0.57	0/1527
12	2Q	0.37	0/1143	0.60	0/1527
13	1R	0.43	0/982	0.63	0/1312
13	2R	0.38	0/982	0.60	0/1312
14	1S	0.34	0/883	0.56	0/1176
14	2S	0.38	0/880	0.59	0/1172
15	1T	0.39	0/1105	0.61	1/1477 (0.1%)
15	2T	0.36	0/1097	0.59	0/1468
16	1U	0.46	0/977	0.62	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.39	0/977	0.60	0/1301
17	1V	0.45	0/782	0.62	0/1049
17	2V	0.35	0/782	0.59	0/1049
18	1W	0.45	0/897	0.66	0/1205
18	2W	0.39	0/897	0.58	0/1205
19	1X	0.44	0/764	0.61	0/1025
19	2X	0.40	0/764	0.63	1/1025 (0.1%)
20	1Y	0.39	0/819	0.57	0/1095
20	2Y	0.35	0/819	0.56	0/1095
21	1Z	0.35	0/1267	0.59	0/1717
21	2Z	0.31	0/1299	0.53	0/1763
22	10	0.43	0/662	0.66	1/881 (0.1%)
22	20	0.33	0/662	0.56	0/881
23	11	0.39	0/762	0.58	0/1014
23	21	0.35	0/762	0.57	0/1014
24	12	0.35	0/590	0.56	0/781
24	22	0.33	0/590	0.51	0/781
25	13	0.41	0/474	0.60	0/635
25	23	0.33	0/469	0.57	0/630
26	14	0.35	0/565	0.69	1/761 (0.1%)
26	24	0.37	0/545	0.64	0/737
27	15	0.42	0/469	0.64	0/635
27	25	0.38	0/469	0.60	1/635 (0.2%)
28	16	0.44	0/460	0.56	0/613
28	26	0.35	0/456	0.51	0/608
29	17	0.44	0/426	0.70	0/561
29	27	0.42	0/426	0.66	0/561
30	18	0.41	0/525	0.59	0/691
30	28	0.39	0/525	0.60	0/691
31	19	0.42	0/310	0.60	0/407
31	29	0.38	0/310	0.60	0/407
32	1a	0.43	0/35795	0.92	40/55864 (0.1%)
32	2a	0.45	3/35886 (0.0%)	0.98	62/56005 (0.1%)
33	1b	0.31	0/1881	0.59	0/2542
33	2b	0.34	0/1860	0.57	0/2518
34	1c	0.28	0/1572	0.49	0/2126
34	2c	0.34	0/1566	0.55	0/2119
35	1d	0.31	0/1685	0.54	0/2262
35	2d	0.31	0/1704	0.52	0/2284
36	1e	0.31	0/1145	0.55	0/1543
36	2e	0.34	0/1149	0.61	0/1548
37	1f	0.32	0/823	0.53	0/1115
37	2f	0.32	0/829	0.51	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.29	0/1250	0.52	0/1679
38	2g	0.31	0/1254	0.54	0/1683
39	1h	0.30	0/1108	0.54	0/1494
39	2h	0.30	0/1108	0.55	0/1494
40	1i	0.31	0/1002	0.59	0/1346
40	2i	0.32	0/997	0.56	0/1343
41	1j	0.30	0/722	0.54	0/982
41	2j	0.34	0/727	0.59	1/988 (0.1%)
42	1k	0.30	0/844	0.55	0/1145
42	2k	0.31	0/848	0.52	0/1149
43	1l	0.34	0/937	0.54	0/1260
43	2l	0.32	0/937	0.59	1/1260 (0.1%)
44	1m	0.32	0/969	0.57	0/1302
44	2m	0.31	0/961	0.57	0/1291
45	1n	0.33	0/501	0.51	0/664
45	2n	0.31	0/501	0.53	0/664
46	1o	0.30	0/739	0.49	0/985
46	2o	0.30	0/739	0.51	0/985
47	1p	0.31	0/697	0.54	0/939
47	2p	0.31	0/693	0.53	0/935
48	1q	0.33	0/836	0.55	0/1117
48	2q	0.31	0/836	0.52	0/1117
49	1r	0.32	0/560	0.53	0/746
49	2r	0.30	0/560	0.51	0/746
50	1s	0.29	0/667	0.58	0/900
50	2s	0.38	0/661	0.66	0/893
51	1t	0.28	0/730	0.53	0/965
51	2t	0.30	0/729	0.54	0/965
52	1u	0.27	0/203	0.46	0/266
52	2u	0.34	0/203	0.50	0/266
53	1v	0.46	0/310	0.93	0/480
53	2v	0.60	0/310	0.91	0/480
54	1w	0.57	1/1606 (0.1%)	1.10	3/2497 (0.1%)
54	1y	0.56	1/1606 (0.1%)	1.13	9/2497 (0.4%)
54	2w	0.53	0/1556	1.12	2/2418 (0.1%)
54	2y	0.59	1/1583 (0.1%)	1.17	4/2459 (0.2%)
55	1x	0.57	3/1725 (0.2%)	1.16	16/2689 (0.6%)
55	2x	0.49	0/1725	1.06	8/2689 (0.3%)
All	All	0.49	12/316686 (0.0%)	0.92	368/474113 (0.1%)

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
43	2l	0	1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	2y	1	G	OP3-P	-10.21	1.48	1.61
2	1B	1	U	OP3-P	-10.20	1.49	1.61
54	1y	1	G	OP3-P	-10.20	1.49	1.61
2	2B	1	U	OP3-P	-9.87	1.49	1.61
54	1w	1	G	OP3-P	-9.63	1.49	1.61
32	2a	1272	G	N1-C2	-9.38	1.30	1.37
32	2a	1272	G	C6-N1	-8.82	1.33	1.39
55	1x	14	A	N7-C5	-5.80	1.35	1.39
55	1x	22	G	N7-C5	5.47	1.42	1.39
32	2a	1263	C	N3-C4	-5.32	1.30	1.33
1	2A	2287	A	N9-C4	-5.20	1.34	1.37
55	1x	14	A	C8-N7	-5.06	1.28	1.31

All (368) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1263	C	N1-C2-O2	22.29	132.27	118.90
32	2a	1272	G	N3-C2-N2	21.80	135.16	119.90
32	2a	1272	G	C5-C6-O6	20.59	140.96	128.60
32	2a	1272	G	N1-C2-N2	-18.95	99.14	116.20
32	2a	1263	C	C2-N3-C4	15.04	127.42	119.90
1	1A	1686	U	O5'-P-OP2	-14.11	93.01	105.70
32	2a	1263	C	N3-C2-O2	-12.82	112.93	121.90
1	1A	1121	C	N1-C2-O2	12.15	126.19	118.90
32	2a	1272	G	N1-C6-O6	-12.10	112.64	119.90
32	2a	1272	G	C6-N1-C2	12.00	132.30	125.10
32	2a	1263	C	C5-C6-N1	11.97	126.99	121.00
1	1A	1132	A	N1-C6-N6	-11.68	111.59	118.60
1	1A	1109	G	C5-C6-O6	10.74	135.04	128.60
32	2a	1272	G	C5-C6-N1	-10.27	106.37	111.50
1	1A	1121	C	C2-N3-C4	10.09	124.94	119.90
55	1x	14	A	C4-C5-C6	10.08	122.04	117.00
1	1A	599	U	O5'-P-OP1	-10.05	96.65	105.70
32	2a	1263	C	C6-N1-C2	-9.80	116.38	120.30
1	1A	1020	C	N1-C2-O2	-9.76	113.04	118.90
1	1A	1807	G	O5'-P-OP2	-9.76	96.92	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	14	A	C5-N7-C8	9.62	108.71	103.90
1	1A	611	U	O5'-P-OP2	-9.61	97.05	105.70
2	2B	80	U	O4'-C1'-N1	9.56	115.85	108.20
55	1x	46	G	C6-N1-C2	-9.00	119.70	125.10
32	1a	1034	G	N3-C2-N2	8.56	125.89	119.90
1	1A	2189	U	C2-N1-C1'	8.55	127.96	117.70
1	1A	1109	G	C6-N1-C2	8.53	130.22	125.10
1	1A	1398	U	O5'-P-OP1	-8.49	98.06	105.70
1	1A	537	G	O4'-C1'-N9	8.48	114.98	108.20
1	2A	2136	C	N1-C2-O2	8.47	123.98	118.90
1	2A	2473	U	C2-N1-C1'	8.45	127.84	117.70
32	2a	1001(A)	G	N3-C4-N9	8.41	131.04	126.00
1	1A	649	C	O5'-P-OP1	-8.39	98.15	105.70
32	1a	1030(B)	C	C2-N1-C1'	8.36	128.00	118.80
32	1a	1034	G	N9-C4-C5	-8.27	102.09	105.40
1	2A	1352	U	O5'-P-OP1	-8.26	98.27	105.70
54	1y	33	U	C2-N1-C1'	8.22	127.57	117.70
32	2a	1272	G	C2-N3-C4	-8.21	107.79	111.90
32	2a	1039	C	C5-C4-N4	-8.12	114.52	120.20
32	2a	79	G	C5-C6-O6	8.08	133.45	128.60
1	1A	1121	C	N3-C2-O2	-8.02	116.29	121.90
32	2a	1263	C	C4-C5-C6	-7.98	113.41	117.40
1	1A	848	G	O5'-P-OP2	-7.90	98.59	105.70
1	2A	2149	G	N3-C4-N9	7.89	130.74	126.00
32	2a	1263	C	C2-N1-C1'	7.83	127.42	118.80
32	1a	1030(B)	C	C6-N1-C2	-7.82	117.17	120.30
1	1A	798	A	O5'-P-OP1	-7.75	98.73	105.70
1	2A	2492	U	O5'-P-OP1	-7.74	98.74	105.70
19	2X	57	LEU	CA-CB-CG	7.70	133.00	115.30
32	2a	1263	C	C5-C4-N4	7.69	125.58	120.20
55	2x	14	A	C4-C5-C6	7.67	120.83	117.00
32	2a	1272	G	C4-N9-C1'	7.64	136.44	126.50
55	1x	22	G	C5-N7-C8	-7.57	100.52	104.30
32	2a	1272	G	C8-N9-C1'	-7.56	117.17	127.00
32	2a	1039	C	C2-N1-C1'	7.56	127.11	118.80
1	1A	2189	U	N1-C2-O2	7.55	128.09	122.80
1	1A	1232	G	N1-C6-O6	-7.54	115.37	119.90
1	1A	2504	U	O5'-P-OP1	-7.53	98.93	105.70
55	1x	14	A	C5-C6-N1	-7.51	113.95	117.70
55	1x	22	G	C4-C5-C6	-7.46	114.33	118.80
1	1A	2189	U	N3-C2-O2	-7.43	117.00	122.20
1	1A	2260	C	O5'-P-OP2	-7.39	99.05	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	254	G	O5'-P-OP1	-7.30	99.13	105.70
1	1A	821	A	C8-N9-C4	-7.29	102.88	105.80
55	2x	14	A	C5-N7-C8	7.28	107.54	103.90
54	1y	56	C	N1-C2-O2	7.24	123.24	118.90
1	2A	801	G	O5'-P-OP2	-7.23	99.19	105.70
1	1A	1045	U	O5'-P-OP2	-7.19	99.23	105.70
32	1a	1034	G	C4-C5-N7	7.18	113.67	110.80
32	1a	1030	C	N1-C2-O2	7.08	123.15	118.90
32	1a	1034	G	C6-N1-C2	7.04	129.33	125.10
1	1A	1132	A	C5-C6-N6	7.03	129.32	123.70
32	2a	754	C	C2-N1-C1'	7.03	126.53	118.80
32	1a	1027	C	N3-C2-O2	-6.99	117.00	121.90
54	1y	33	U	N1-C2-O2	6.97	127.68	122.80
1	2A	2139	C	C2-N1-C1'	6.92	126.41	118.80
1	1A	2077	C	OP1-P-O3'	6.91	120.41	105.20
32	1a	1027	C	N3-C4-C5	-6.87	119.15	121.90
32	1a	1002	G	N3-C4-N9	6.82	130.09	126.00
32	1a	1034	G	N3-C4-N9	6.80	130.08	126.00
32	1a	1034	G	C8-N9-C1'	-6.76	118.21	127.00
1	2A	512	G	O4'-C1'-N9	6.75	113.60	108.20
1	1A	1020	C	C2-N1-C1'	-6.75	111.38	118.80
1	1A	2014	G	P-O3'-C3'	6.74	127.79	119.70
1	1A	1121	C	C6-N1-C2	-6.72	117.61	120.30
32	2a	1039	C	C6-N1-C1'	-6.70	112.76	120.80
1	2A	2473	U	N1-C2-O2	6.69	127.49	122.80
1	1A	2015	U	O5'-P-OP1	-6.67	99.70	105.70
32	2a	1004	A	N7-C8-N9	6.67	117.14	113.80
32	2a	754	C	N1-C2-O2	6.65	122.89	118.90
32	1a	1002	G	C4-N9-C1'	6.64	135.14	126.50
32	2a	1263	C	N1-C2-N3	-6.64	114.55	119.20
1	1A	840	A	O5'-P-OP2	-6.64	99.72	105.70
32	1a	1025	U	N1-C2-O2	6.64	127.44	122.80
1	1A	993	G	O5'-P-OP1	-6.63	99.73	105.70
1	2A	2492	U	O5'-P-OP2	6.56	118.57	110.70
1	1A	2727	G	O5'-P-OP2	-6.56	99.80	105.70
1	1A	215	G	O4'-C1'-N9	6.52	113.42	108.20
32	1a	1027	C	C5-C4-N4	6.51	124.76	120.20
32	1a	1002	G	C8-N9-C1'	-6.50	118.55	127.00
1	2A	2136	C	N3-C2-O2	-6.48	117.36	121.90
1	2A	2149	G	C8-N9-C1'	-6.48	118.58	127.00
1	2A	2149	G	C4-N9-C1'	6.47	134.91	126.50
54	1w	47	U	C2-N1-C1'	6.47	125.46	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	892	G	O4'-C1'-N9	6.45	113.36	108.20
1	1A	2566	U	O5'-P-OP1	-6.41	99.93	105.70
1	1A	1128	U	N3-C4-C5	6.39	118.43	114.60
32	2a	1263	C	N3-C4-N4	-6.38	113.53	118.00
32	1a	1034	G	C4-N9-C1'	6.35	134.76	126.50
1	2A	2149	G	N9-C4-C5	-6.35	102.86	105.40
54	1y	64	A	C5-C6-N6	6.35	128.78	123.70
1	2A	1698	A	O4'-C1'-N9	6.33	113.27	108.20
1	1A	1221	G	OP1-P-O3'	6.33	119.12	105.20
1	2A	1131	G	O4'-C1'-N9	6.32	113.26	108.20
1	1A	1121	C	C5-C4-N4	6.32	124.62	120.20
1	2A	2897	U	C2-N1-C1'	6.32	125.28	117.70
32	2a	588	G	O5'-P-OP2	-6.27	100.06	105.70
1	1A	1109	G	N3-C2-N2	6.26	124.28	119.90
1	1A	2054	G	C5-N7-C8	6.22	107.41	104.30
32	2a	1037	C	C6-N1-C2	-6.21	117.81	120.30
1	1A	2694	U	O5'-P-OP2	-6.19	100.13	105.70
1	1A	806	G	C5-C6-O6	-6.19	124.89	128.60
1	2A	2473	U	N3-C2-O2	-6.17	117.88	122.20
32	1a	1030(B)	C	C5-C6-N1	6.17	124.09	121.00
1	1A	1958	A	O4'-C1'-N9	6.16	113.13	108.20
1	2A	2430	A	O4'-C1'-N9	6.16	113.13	108.20
1	1A	809	U	C5-C4-O4	-6.15	122.21	125.90
55	1x	46	G	C5-C6-N1	6.15	114.57	111.50
54	1y	64	A	N1-C6-N6	-6.14	114.92	118.60
1	1A	1859	G	O5'-P-OP2	-6.13	100.19	105.70
54	2y	58	A	OP1-P-O3'	6.12	118.66	105.20
55	1x	22	G	C8-N9-C1'	6.11	134.95	127.00
32	1a	841	U	C5-C6-N1	6.11	125.75	122.70
1	1A	2180	A	N1-C2-N3	6.10	132.35	129.30
1	1A	2641	A	P-O3'-C3'	6.10	127.02	119.70
32	2a	1001(A)	G	N9-C4-C5	-6.10	102.96	105.40
1	2A	576	U	O5'-P-OP1	-6.09	100.22	105.70
54	1w	22	G	N1-C6-O6	6.05	123.53	119.90
1	2A	2174	C	C2-N1-C1'	6.05	125.45	118.80
32	2a	1366	C	C2-N3-C4	6.03	122.92	119.90
54	2y	22	G	N1-C6-O6	6.03	123.52	119.90
55	2x	14	A	C5-C6-N1	-6.03	114.69	117.70
1	2A	614	U	N3-C2-O2	-6.03	117.98	122.20
1	1A	2803	A	C2-N3-C4	6.00	113.60	110.60
1	2A	928	G	C8-N9-C4	-5.99	104.00	106.40
1	1A	572	A	P-O3'-C3'	5.98	126.87	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1039	C	N1-C2-O2	5.98	122.49	118.90
32	1a	266	G	P-O3'-C3'	5.97	126.87	119.70
1	1A	2180	A	P-O3'-C3'	5.97	126.86	119.70
1	2A	1372	U	C5-C4-O4	-5.96	122.32	125.90
1	2A	1314	C	C5-C6-N1	5.96	123.98	121.00
1	2A	783	A	C2-N3-C4	5.94	113.57	110.60
1	2A	2140	C	C2-N1-C1'	5.93	125.33	118.80
32	1a	1030	C	C2-N3-C4	5.92	122.86	119.90
55	1x	22	G	N3-C4-N9	-5.92	122.45	126.00
1	1A	1109	G	N1-C6-O6	-5.91	116.36	119.90
1	1A	894	U	C2-N1-C1'	5.89	124.77	117.70
32	2a	1187	G	N3-C4-N9	-5.89	122.47	126.00
1	1A	476	G	N1-C6-O6	-5.88	116.37	119.90
1	1A	605	G	C5-C6-O6	5.88	132.13	128.60
1	1A	1020	C	C6-N1-C1'	5.87	127.84	120.80
1	2A	2363	C	C6-N1-C2	5.87	122.65	120.30
32	2a	1039	C	N3-C4-N4	5.87	122.11	118.00
32	1a	1278	U	C5-C6-N1	5.87	125.63	122.70
1	1A	852	G	N9-C4-C5	-5.87	103.05	105.40
1	2A	1313	U	C2-N1-C1'	5.86	124.73	117.70
32	1a	1030(B)	C	N1-C2-O2	5.85	122.41	118.90
1	1A	2826	C	C6-N1-C2	-5.83	117.97	120.30
1	2A	2149	G	C6-C5-N7	-5.83	126.90	130.40
54	2w	50	U	C5-C4-O4	-5.82	122.41	125.90
32	2a	1030	C	N1-C2-O2	5.82	122.39	118.90
1	1A	2627	U	O5'-P-OP1	-5.81	100.47	105.70
1	2A	2139	C	C6-N1-C1'	-5.80	113.83	120.80
1	1A	1109	G	C5-C6-N1	-5.80	108.60	111.50
1	1A	1121	C	N3-C4-C5	-5.79	119.58	121.90
15	1T	82	LEU	CA-CB-CG	-5.79	101.99	115.30
1	1A	2858	G	O4'-C1'-N9	5.78	112.83	108.20
1	1A	2431	U	N3-C4-O4	-5.77	115.36	119.40
1	2A	1993	U	O5'-P-OP1	-5.76	100.51	105.70
55	1x	14	A	C8-N9-C1'	-5.76	117.33	127.70
1	1A	1121	C	C2-N1-C1'	5.75	125.13	118.80
55	2x	20	U	N1-C2-O2	5.75	126.83	122.80
55	1x	22	G	C5-C6-N1	5.75	114.38	111.50
1	2A	944	G	C4-N9-C1'	5.75	133.97	126.50
32	2a	266	G	N3-C4-C5	-5.74	125.73	128.60
1	1A	1232	G	C5-C6-O6	5.74	132.04	128.60
1	2A	2473	U	C6-N1-C1'	-5.74	113.17	121.20
32	2a	1054	C	C2-N1-C1'	5.73	125.11	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2689	U	P-O3'-C3'	5.72	126.57	119.70
1	2A	1992	G	P-O3'-C3'	5.72	126.56	119.70
1	1A	1121	C	C5-C6-N1	5.71	123.86	121.00
55	1x	22	G	N3-C4-C5	5.71	131.45	128.60
1	2A	856	C	C6-N1-C2	-5.70	118.02	120.30
1	1A	12	U	C2-N1-C1'	5.69	124.53	117.70
54	1y	33	U	N3-C2-O2	-5.69	118.22	122.20
32	2a	1225	A	C5-C6-N6	5.69	128.25	123.70
1	1A	1720	U	C5-C6-N1	-5.66	119.87	122.70
32	1a	1034	G	C6-C5-N7	-5.66	127.00	130.40
32	2a	299	G	C5-C6-O6	-5.66	125.21	128.60
55	2x	20	U	N3-C2-O2	-5.65	118.24	122.20
1	2A	2152	G	N3-C4-N9	5.64	129.38	126.00
2	2B	30	C	C6-N1-C2	-5.64	118.05	120.30
1	1A	322	G	C5-N7-C8	5.63	107.12	104.30
55	1x	22	G	C4-N9-C1'	-5.63	119.17	126.50
1	1A	2697	G	N1-C6-O6	-5.63	116.52	119.90
1	2A	746	A	O4'-C1'-N9	5.62	112.70	108.20
43	2l	29	GLY	N-CA-C	-5.62	99.05	113.10
1	1A	472	G	N1-C6-O6	5.62	123.27	119.90
1	1A	793	A	O4'-C1'-N9	5.61	112.69	108.20
1	2A	2174	C	N1-C2-O2	5.61	122.26	118.90
55	1x	14	A	C4-N9-C1'	5.60	136.38	126.30
1	1A	1991	A	OP1-P-O3'	5.59	117.50	105.20
1	2A	933	A	O4'-C1'-N9	5.58	112.66	108.20
1	1A	2299	A	O4'-C1'-N9	5.57	112.66	108.20
1	2A	228	A	P-O3'-C3'	5.57	126.39	119.70
32	2a	1054	C	O4'-C1'-N1	5.57	112.66	108.20
2	2B	1	U	C2-N1-C1'	5.57	124.38	117.70
32	1a	754	C	C2-N1-C1'	5.56	124.92	118.80
32	2a	299	G	N1-C6-O6	5.56	123.23	119.90
1	1A	598	A	O5'-P-OP1	-5.55	100.70	105.70
1	2A	1791	A	O5'-P-OP1	-5.55	100.71	105.70
1	2A	2107	C	C2-N3-C4	5.53	122.66	119.90
1	1A	399	G	O4'-C1'-N9	5.53	112.62	108.20
54	2w	74	C	N1-C2-O2	5.53	122.22	118.90
1	2A	444	C	O5'-P-OP1	-5.50	100.75	105.70
1	1A	2078	G	O4'-C1'-N9	-5.50	103.80	108.20
1	1A	1694	G	O4'-C1'-N9	-5.49	103.81	108.20
32	2a	1028	C	C2-N3-C4	5.49	122.65	119.90
1	2A	747	U	O5'-P-OP1	-5.49	100.76	105.70
1	1A	2442	A	C2-N3-C4	5.49	113.34	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1028	C	C5-C6-N1	5.48	123.74	121.00
1	1A	1342	G	O5'-P-OP2	-5.47	100.77	105.70
1	1A	1700	G	C8-N9-C4	-5.47	104.21	106.40
55	2x	17	C	C2-N1-C1'	5.46	124.81	118.80
1	1A	587	C	N1-C2-O2	-5.46	115.63	118.90
1	2A	1313	U	O4'-C1'-N1	5.46	112.56	108.20
1	1A	472	G	C5-C6-O6	-5.45	125.33	128.60
1	1A	356	A	N1-C6-N6	-5.44	115.33	118.60
1	1A	1657	C	N1-C2-O2	5.44	122.17	118.90
26	14	54	GLY	N-CA-C	5.44	126.70	113.10
1	1A	184	A	P-O3'-C3'	5.44	126.22	119.70
1	2A	1372	U	N3-C4-O4	5.43	123.20	119.40
1	2A	2712	U	O4'-C1'-N1	5.43	112.54	108.20
32	1a	1026	G	O4'-C1'-N9	5.43	112.54	108.20
55	1x	22	G	N1-C6-O6	-5.41	116.65	119.90
1	1A	795	G	O4'-C1'-N9	5.41	112.53	108.20
54	1y	56	C	C2-N3-C4	5.40	122.60	119.90
32	2a	1001(A)	G	C4-C5-N7	5.40	112.96	110.80
54	1y	33	U	C6-N1-C1'	-5.40	113.64	121.20
1	1A	732	A	C8-N9-C4	-5.39	103.64	105.80
1	1A	2613	C	C6-N1-C2	-5.38	118.15	120.30
32	1a	1021	G	O4'-C1'-N9	5.38	112.50	108.20
32	2a	754	C	N3-C2-O2	-5.38	118.14	121.90
1	1A	1462	G	O4'-C1'-N9	5.37	112.50	108.20
32	1a	1002	G	N3-C4-C5	-5.37	125.92	128.60
1	2A	2149	G	C4-C5-N7	5.37	112.95	110.80
32	2a	79	G	N1-C6-O6	-5.37	116.68	119.90
1	2A	226	G	O4'-C1'-N9	5.36	112.49	108.20
1	1A	2701	U	P-O3'-C3'	5.35	126.12	119.70
32	2a	1001(A)	G	C8-N9-C1'	-5.34	120.06	127.00
54	2y	58	A	P-O3'-C3'	5.34	126.11	119.70
32	2a	1022	G	N3-C2-N2	5.33	123.63	119.90
1	2A	792	G	O4'-C1'-N9	-5.33	103.94	108.20
32	2a	289	G	O5'-P-OP2	-5.32	100.91	105.70
1	1A	605	G	N1-C6-O6	-5.32	116.71	119.90
32	2a	1004	A	C8-N9-C4	-5.32	103.67	105.80
1	1A	2431	U	N1-C2-O2	5.31	126.52	122.80
1	2A	1314	C	C6-N1-C2	-5.31	118.18	120.30
1	1A	1177	G	O4'-C1'-N9	5.31	112.45	108.20
1	2A	1279	G	O5'-P-OP2	-5.31	100.92	105.70
1	2A	1698	A	C6-C5-N7	-5.31	128.59	132.30
1	1A	2189	U	C6-N1-C1'	-5.30	113.77	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1x	46	G	C5-C6-O6	-5.30	125.42	128.60
32	1a	1065	U	P-O3'-C3'	5.30	126.06	119.70
1	1A	2697	G	C6-C5-N7	5.29	133.57	130.40
32	2a	1001(A)	G	C4-N9-C1'	5.29	133.38	126.50
1	1A	831	A	N9-C4-C5	5.29	107.92	105.80
1	1A	1874	C	N1-C2-O2	-5.29	115.73	118.90
32	1a	841	U	C6-N1-C2	-5.28	117.83	121.00
32	1a	1025	U	N3-C2-O2	-5.27	118.51	122.20
1	2A	912	C	C6-N1-C2	-5.27	118.19	120.30
32	2a	65	U	P-O3'-C3'	5.27	126.02	119.70
32	2a	1001(A)	G	N3-C4-C5	-5.26	125.97	128.60
32	1a	1030	C	N3-C2-O2	-5.26	118.22	121.90
1	2A	945	A	O4'-C1'-N9	5.26	112.41	108.20
1	1A	2074	G	N1-C6-O6	-5.26	116.75	119.90
1	1A	285	U	O4'-C1'-N1	5.26	112.40	108.20
1	2A	141	A	N7-C8-N9	5.25	116.43	113.80
32	2a	1260	C	C6-N1-C2	-5.25	118.20	120.30
1	2A	2142	C	C2-N1-C1'	5.25	124.58	118.80
1	2A	1530	C	P-O3'-C3'	5.25	126.00	119.70
1	2A	528	A	P-O3'-C3'	5.23	125.98	119.70
41	2j	8	LEU	CA-CB-CG	5.23	127.34	115.30
1	2A	646	A	O4'-C1'-N9	5.23	112.38	108.20
1	1A	2331	G	C5-N7-C8	-5.22	101.69	104.30
1	2A	383	U	O4'-C1'-N1	5.22	112.38	108.20
1	1A	2054	G	C4-C5-N7	-5.22	108.71	110.80
1	2A	2152	G	C5-C6-O6	-5.21	125.47	128.60
32	2a	754	C	C6-N1-C1'	-5.21	114.54	120.80
1	1A	1219	A	P-O3'-C3'	5.21	125.96	119.70
1	1A	2883	A	O4'-C1'-N9	5.20	112.36	108.20
1	2A	845	G	C4-N9-C1'	5.20	133.26	126.50
1	2A	528	A	OP1-P-O3'	5.20	116.64	105.20
1	1A	856	G	N1-C6-O6	-5.19	116.78	119.90
1	1A	1709	C	N3-C2-O2	-5.19	118.27	121.90
1	1A	855	G	O5'-P-OP2	-5.18	101.04	105.70
32	1a	421	U	C2-N1-C1'	5.18	123.92	117.70
32	2a	299	G	C6-C5-N7	-5.18	127.29	130.40
1	1A	815	G	C5-C6-O6	5.18	131.71	128.60
32	2a	687	A	P-O3'-C3'	5.17	125.91	119.70
1	1A	2074	G	C5-C6-O6	5.17	131.70	128.60
32	1a	1067	A	P-O3'-C3'	5.16	125.90	119.70
54	1w	60	U	N3-C2-O2	-5.16	118.59	122.20
1	2A	2427	C	O5'-P-OP1	-5.16	101.06	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	266	G	P-O3'-C3'	5.16	125.89	119.70
32	2a	955	U	C2-N3-C4	5.16	130.09	127.00
22	10	13	GLY	N-CA-C	5.15	125.98	113.10
1	2A	228	A	OP1-P-O3'	5.15	116.54	105.20
1	1A	734	C	C6-N1-C2	-5.14	118.24	120.30
1	1A	2258	G	C8-N9-C4	5.14	108.46	106.40
32	1a	204	U	N1-C2-O2	5.14	126.40	122.80
55	2x	17	C	C6-N1-C2	-5.14	118.24	120.30
32	1a	615	C	C6-N1-C2	-5.13	118.25	120.30
1	1A	2598	C	C6-N1-C2	-5.12	118.25	120.30
1	2A	1377	G	N1-C6-O6	-5.12	116.83	119.90
1	2A	1411	C	C2-N1-C1'	5.12	124.43	118.80
1	1A	991	G	O5'-P-OP1	-5.11	101.10	105.70
1	1A	1255	A	P-O3'-C3'	5.11	125.84	119.70
1	2A	748	G	C4-N9-C1'	-5.11	119.86	126.50
54	1y	56	C	N3-C2-O2	-5.10	118.33	121.90
2	2B	42	C	N1-C2-O2	5.10	121.96	118.90
1	1A	2204	G	N3-C4-N9	-5.09	122.94	126.00
1	1A	2701	U	C6-N1-C2	-5.09	117.94	121.00
1	1A	2228	G	C4-N9-C1'	5.09	133.12	126.50
1	2A	912	C	N1-C2-O2	5.09	121.95	118.90
1	2A	1597	A	N1-C6-N6	-5.09	115.55	118.60
54	2y	43	C	C2-N1-C1'	5.09	124.39	118.80
32	2a	971	G	C4-C5-N7	-5.08	108.77	110.80
1	2A	2512	C	N1-C2-O2	-5.08	115.85	118.90
32	1a	1034	G	N1-C2-N3	-5.07	120.86	123.90
1	1A	419	C	O5'-P-OP1	-5.07	101.14	105.70
1	1A	1810	U	O4'-C1'-N1	5.07	112.25	108.20
1	1A	815	G	N1-C6-O6	-5.06	116.86	119.90
1	2A	2046	G	C8-N9-C1'	-5.06	120.42	127.00
1	1A	740	C	N1-C2-O2	5.06	121.93	118.90
1	1A	1474	C	N3-C2-O2	-5.06	118.36	121.90
27	25	58	LEU	CA-CB-CG	5.06	126.93	115.30
32	1a	1030(B)	C	C6-N1-C1'	-5.05	114.73	120.80
1	1A	410	U	C2-N1-C1'	-5.05	111.64	117.70
1	1A	2838	C	N1-C2-O2	-5.05	115.87	118.90
1	1A	2250	G	N3-C4-N9	5.05	129.03	126.00
1	2A	2804	C	C6-N1-C2	-5.05	118.28	120.30
1	1A	2621	U	C5-C6-N1	-5.05	120.18	122.70
1	2A	1698	A	N1-C6-N6	5.04	121.63	118.60
1	2A	944	G	C8-N9-C1'	-5.04	120.45	127.00
1	2A	1298	C	O5'-P-OP2	-5.04	101.16	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	12	U	C5-C6-N1	5.04	125.22	122.70
32	2a	299	G	C4-C5-N7	5.04	112.81	110.80
1	2A	928	G	N7-C8-N9	5.03	115.62	113.10
55	2x	14	A	C8-N9-C1'	-5.02	118.66	127.70
1	1A	560	C	N3-C2-O2	-5.02	118.38	121.90
32	1a	913	A	P-O3'-C3'	5.02	125.72	119.70
1	2A	1653	G	P-O3'-C3'	5.02	125.72	119.70
1	2A	2321	G	C4-N9-C1'	5.01	133.01	126.50
1	2A	2139	C	N1-C2-O2	5.01	121.91	118.90
1	2A	2167	U	N1-C2-O2	5.01	126.31	122.80
32	2a	913	A	P-O3'-C3'	5.01	125.71	119.70
1	1A	1146	C	C2-N1-C1'	5.00	124.30	118.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	2l	92	0TD	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	61852	0	31193	648	0
1	2A	60322	0	30425	904	0
2	1B	2577	0	1305	21	0
2	2B	2575	0	1303	65	0
3	1D	2136	0	2218	45	0
3	2D	2136	0	2218	58	0
4	1E	1559	0	1618	31	0
4	2E	1559	0	1618	37	0
5	1F	1584	0	1625	34	0
5	2F	1580	0	1619	54	0
6	1G	1423	0	1436	22	0
6	2G	1428	0	1438	73	0
7	1H	1330	0	1407	26	0
7	2H	1330	0	1407	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	1I	1097	0	1140	31	0
8	2I	1064	0	1082	24	0
9	1N	1117	0	1184	21	0
9	2N	1117	0	1184	22	0
10	1O	933	0	996	17	0
10	2O	933	0	996	23	0
11	1P	1135	0	1212	36	0
11	2P	1135	0	1212	32	0
12	1Q	1122	0	1179	14	0
12	2Q	1122	0	1179	33	0
13	1R	968	0	1033	12	0
13	2R	968	0	1033	21	0
14	1S	873	0	927	19	0
14	2S	870	0	923	31	0
15	1T	1091	0	1151	17	0
15	2T	1083	0	1136	31	0
16	1U	959	0	1019	18	0
16	2U	959	0	1019	25	0
17	1V	771	0	830	10	0
17	2V	771	0	830	22	0
18	1W	886	0	940	8	0
18	2W	886	0	940	13	0
19	1X	750	0	814	10	0
19	2X	750	0	814	28	0
20	1Y	806	0	881	21	0
20	2Y	806	0	881	23	0
21	1Z	1240	0	1240	24	0
21	2Z	1271	0	1273	46	0
22	10	653	0	674	14	0
22	20	653	0	674	19	0
23	11	755	0	826	11	0
23	21	755	0	826	20	0
24	12	588	0	643	11	0
24	22	588	0	643	16	0
25	13	469	0	518	5	0
25	23	464	0	514	12	0
26	14	552	0	533	20	0
26	24	532	0	503	31	0
27	15	455	0	465	7	0
27	25	455	0	465	11	0
28	16	453	0	473	12	0
28	26	449	0	469	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	17	418	0	467	7	0
29	27	418	0	467	17	0
30	18	517	0	582	19	0
30	28	517	0	582	17	0
31	19	307	0	335	4	0
31	29	307	0	335	8	0
32	1a	32246	0	16295	0	0
32	2a	32327	0	16339	0	0
33	1b	1846	0	1867	0	0
33	2b	1825	0	1828	0	0
34	1c	1548	0	1535	0	0
34	2c	1542	0	1517	0	0
35	1d	1655	0	1672	0	0
35	2d	1674	0	1714	0	0
36	1e	1129	0	1185	0	0
36	2e	1133	0	1191	0	0
37	1f	810	0	804	0	0
37	2f	816	0	808	0	0
38	1g	1231	0	1238	0	0
38	2g	1235	0	1249	0	0
39	1h	1088	0	1126	0	0
39	2h	1088	0	1126	0	0
40	1i	983	0	986	0	0
40	2i	978	0	966	0	0
41	1j	709	0	650	0	0
41	2j	714	0	672	0	0
42	1k	829	0	825	0	0
42	2k	833	0	836	0	0
43	1l	932	0	981	0	0
43	2l	932	0	981	0	0
44	1m	958	0	1002	0	0
44	2m	950	0	988	0	0
45	1n	492	0	529	0	0
45	2n	492	0	529	0	0
46	1o	728	0	760	0	0
46	2o	728	0	760	0	0
47	1p	681	0	697	0	0
47	2p	677	0	686	0	0
48	1q	823	0	891	0	0
48	2q	823	0	891	0	0
49	1r	555	0	618	0	0
49	2r	555	0	618	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	1s	652	0	662	0	0
50	2s	646	0	644	0	0
51	1t	728	0	798	0	0
51	2t	727	0	796	0	0
52	1u	199	0	208	0	0
52	2u	199	0	208	0	0
53	1v	277	0	140	0	0
53	2v	277	0	140	0	0
54	1w	1592	0	819	0	0
54	1y	1585	0	804	0	0
54	2w	1544	0	788	0	0
54	2y	1565	0	795	0	0
55	1x	1625	0	828	0	0
55	2x	1625	0	828	0	0
56	10	6	0	0	0	0
56	11	3	0	0	0	0
56	12	1	0	0	0	0
56	13	3	0	0	0	0
56	15	2	0	0	0	0
56	16	3	0	0	0	0
56	17	1	0	0	0	0
56	18	3	0	0	0	0
56	19	2	0	0	0	0
56	1A	1141	0	0	0	0
56	1B	37	0	0	0	0
56	1D	12	0	0	0	0
56	1E	11	0	0	0	0
56	1F	8	0	0	0	0
56	1G	5	0	0	0	0
56	1I	1	0	0	0	0
56	1N	6	0	0	0	0
56	1O	7	0	0	0	0
56	1P	4	0	0	0	0
56	1Q	6	0	0	0	0
56	1R	3	0	0	0	0
56	1S	3	0	0	0	0
56	1T	2	0	0	0	0
56	1U	8	0	0	0	0
56	1V	3	0	0	0	0
56	1W	5	0	0	0	0
56	1X	6	0	0	0	0
56	1Y	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	1Z	3	0	0	0	0
56	1a	229	0	0	0	0
56	1b	2	0	0	0	0
56	1d	1	0	0	0	0
56	1e	1	0	0	0	0
56	1f	2	0	0	0	0
56	1l	3	0	0	0	0
56	1n	2	0	0	0	0
56	1s	1	0	0	0	0
56	1t	1	0	0	0	0
56	1v	1	0	0	0	0
56	1w	11	0	0	0	0
56	1x	16	0	0	0	0
56	1y	4	0	0	0	0
56	20	3	0	0	0	0
56	23	2	0	0	0	0
56	25	4	0	0	0	0
56	27	1	0	0	0	0
56	28	2	0	0	0	0
56	2A	909	0	0	0	0
56	2B	21	0	0	0	0
56	2D	5	0	0	0	0
56	2E	9	0	0	0	0
56	2F	4	0	0	0	0
56	2G	1	0	0	0	0
56	2N	1	0	0	0	0
56	2O	1	0	0	0	0
56	2P	1	0	0	0	0
56	2Q	3	0	0	0	0
56	2R	1	0	0	0	0
56	2T	3	0	0	0	0
56	2U	4	0	0	0	0
56	2V	1	0	0	0	0
56	2W	3	0	0	0	0
56	2X	3	0	0	0	0
56	2Y	1	0	0	0	0
56	2Z	1	0	0	0	0
56	2a	244	0	0	0	0
56	2d	1	0	0	0	0
56	2e	1	0	0	0	0
56	2f	1	0	0	0	0
56	2g	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	2i	1	0	0	0	0
56	2j	2	0	0	0	0
56	2l	2	0	0	0	0
56	2n	1	0	0	0	0
56	2q	2	0	0	0	0
56	2r	2	0	0	0	0
56	2t	1	0	0	0	0
56	2v	2	0	0	0	0
56	2w	8	0	0	0	0
56	2x	5	0	0	0	0
56	2y	7	0	0	0	0
57	1A	1	0	0	0	0
57	2A	1	0	0	0	0
58	14	1	0	0	0	0
58	15	1	0	0	0	0
58	16	1	0	0	0	0
58	19	1	0	0	0	0
58	1Y	1	0	0	0	0
58	1n	1	0	0	0	0
58	24	1	0	0	0	0
58	25	1	0	0	0	0
58	26	1	0	0	0	0
58	29	1	0	0	0	0
58	2Y	1	0	0	0	0
58	2n	1	0	0	0	0
59	1d	8	0	0	0	0
59	2d	8	0	0	0	0
60	10	12	0	0	0	0
60	11	10	0	0	0	0
60	12	4	0	0	0	0
60	13	6	0	0	0	0
60	14	1	0	0	0	0
60	15	6	0	0	0	0
60	16	3	0	0	0	0
60	17	9	0	0	0	0
60	18	13	0	0	1	0
60	1A	2238	0	0	95	0
60	1B	68	0	0	3	0
60	1D	28	0	0	1	0
60	1E	28	0	0	3	0
60	1F	13	0	0	1	0
60	1G	7	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	1H	2	0	0	0	0
60	1I	3	0	0	0	0
60	1N	7	0	0	1	0
60	1O	8	0	0	0	0
60	1P	23	0	0	3	0
60	1Q	14	0	0	0	0
60	1R	14	0	0	0	0
60	1S	5	0	0	0	0
60	1T	8	0	0	1	0
60	1U	11	0	0	1	0
60	1V	9	0	0	0	0
60	1W	6	0	0	0	0
60	1X	8	0	0	2	0
60	1Y	4	0	0	0	0
60	1Z	1	0	0	0	0
60	1a	438	0	0	0	0
60	1b	1	0	0	0	0
60	1d	1	0	0	0	0
60	1e	1	0	0	0	0
60	1f	1	0	0	0	0
60	1g	1	0	0	0	0
60	1i	1	0	0	0	0
60	1l	8	0	0	0	0
60	1m	2	0	0	0	0
60	1o	1	0	0	0	0
60	1p	1	0	0	0	0
60	1q	4	0	0	0	0
60	1u	1	0	0	0	0
60	1v	5	0	0	0	0
60	1w	21	0	0	0	0
60	1x	15	0	0	0	0
60	1y	1	0	0	0	0
60	20	7	0	0	0	0
60	21	12	0	0	0	0
60	22	1	0	0	0	0
60	23	1	0	0	0	0
60	25	4	0	0	1	0
60	26	1	0	0	0	0
60	27	4	0	0	1	0
60	28	6	0	0	2	0
60	29	1	0	0	0	0
60	2A	1389	0	0	90	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	2B	26	0	0	1	0
60	2D	28	0	0	2	0
60	2E	16	0	0	0	0
60	2F	16	0	0	0	0
60	2H	1	0	0	0	0
60	2I	4	0	0	0	0
60	2N	1	0	0	0	0
60	2P	14	0	0	1	0
60	2Q	2	0	0	0	0
60	2R	2	0	0	0	0
60	2T	6	0	0	0	0
60	2U	2	0	0	0	0
60	2V	2	0	0	0	0
60	2W	2	0	0	0	0
60	2X	5	0	0	0	0
60	2Y	1	0	0	1	0
60	2Z	2	0	0	0	0
60	2a	377	0	0	0	0
60	2d	1	0	0	0	0
60	2e	2	0	0	0	0
60	2g	1	0	0	0	0
60	2i	1	0	0	0	0
60	2j	4	0	0	0	0
60	2l	5	0	0	0	0
60	2o	1	0	0	0	0
60	2p	2	0	0	0	0
60	2q	1	0	0	0	0
60	2r	1	0	0	0	0
60	2t	4	0	0	0	0
60	2u	1	0	0	0	0
60	2v	1	0	0	0	0
60	2w	2	0	0	0	0
60	2x	7	0	0	0	0
60	2y	19	0	0	0	0
All	All	300910	0	196690	2580	0

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

All (2580) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1128:U:H3	1:1A:1132:A:N6	1.34	1.25
1:2A:2136:C:N4	1:2A:2155:G:H1	1.44	1.15
1:1A:1128:U:O4	1:1A:1132:A:N1	1.85	1.09
1:2A:2138:C:N4	1:2A:2153:G:H1	1.48	1.09
1:1A:1740:U:H1'	3:1D:14:ARG:HH22	1.22	1.01
1:1A:2122:G:H1	1:1A:2211:U:H3	1.14	0.96
1:2A:1693:U:H1'	3:2D:14:ARG:HH22	1.31	0.95
1:1A:1004:A:N6	1:1A:1037:C:N3	55.53	0.94
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.50	0.94
1:2A:2129:C:H42	1:2A:2159:G:H1	1.06	0.93
1:1A:1105:G:H1	1:1A:1125:C:H42	0.99	0.93
1:1A:2511:C:OP1	60:1A:5012:HOH:O	1.83	0.93
1:1A:2439:C:OP1	60:1A:5528:HOH:O	1.87	0.93
1:1A:2702:C:OP1	13:1R:17:ARG:NH2	2.01	0.93
1:2A:1002:G:H1	1:2A:1038:C:H42	42.63	0.93
20:1Y:92:ASN:HB3	20:1Y:94:LYS:H	1.33	0.92
1:1A:2143:G:H1	1:1A:2199:C:H42	1.07	0.92
1:2A:1011:G:H1	1:2A:1018:C:H42	18.07	0.92
1:2A:1171:G:N2	1:2A:1178:C:N3	2.18	0.92
1:2A:1422:G:H5''	10:2O:48:PRO:HB3	99.55	0.90
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.35	0.90
1:2A:2127:G:N2	1:2A:2161:C:C2	2.40	0.90
2:2B:7:G:H21	14:2S:38:GLN:HE22	1.21	0.89
1:2A:2136:C:N4	1:2A:2155:G:N1	2.19	0.89
1:1A:1099:C:H42	1:1A:1152:G:H1	1.17	0.88
1:1A:1105:G:H1	1:1A:1125:C:N4	1.71	0.88
22:10:10:THR:HG22	22:10:12:ASN:H	1.37	0.88
1:2A:2136:C:N3	1:2A:2155:G:N2	2.22	0.87
1:1A:2121:U:H3	1:1A:2212:G:H1	0.91	0.85
1:2A:2127:G:N1	1:2A:2161:C:C4	2.44	0.85
1:2A:854:G:H2'	1:2A:855:G:H8	1.38	0.85
1:2A:2014:A:H4'	18:2W:92:ARG:HH22	1.37	0.85
1:2A:1689:A:H62	1:2A:1698:A:H2	1.20	0.85
1:2A:2345:G:H4'	1:2A:2346:A:H5''	1.58	0.85
11:2P:52:GLU:OE1	11:2P:55:ARG:NH1	2.08	0.85
1:1A:1378:G:OP1	60:1A:4704:HOH:O	1.94	0.85
1:1A:303:C:H42	1:1A:385:G:H1	1.21	0.85
1:2A:2807:G:N1	1:2A:2893:G:O6	2.09	0.85
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.11	0.85
1:1A:1694:G:OP1	60:1A:5101:HOH:O	1.94	0.85
11:1P:52:GLU:OE1	11:1P:55:ARG:NH1	2.10	0.85
1:1A:1740:U:O2	3:1D:14:ARG:NH2	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1111:U:O2	1:1A:1119:A:N6	2.11	0.84
1:1A:929:G:H1	1:1A:940:C:H42	1.25	0.83
1:2A:1466:G:HO2'	1:2A:1546:C:HO2'	1.15	0.83
1:2A:2127:G:C2	1:2A:2161:C:N3	2.46	0.83
1:1A:2831:A:OP2	60:1A:5352:HOH:O	1.97	0.83
23:21:2:SER:HB3	23:21:46:LEU:HD12	1.60	0.83
1:2A:2099:U:H3	1:2A:2190:G:H1	1.22	0.83
1:1A:606:G:N2	1:1A:632:A:N7	49.87	0.83
1:1A:2158:C:N3	1:1A:2177:G:N2	2.26	0.83
17:2V:72:VAL:HG13	17:2V:85:LYS:HB2	1.61	0.83
1:2A:1204:A:H2	1:2A:1241:A:H62	1.28	0.82
11:2P:100:LEU:HD12	11:2P:112:LEU:HD11	1.60	0.82
1:2A:2138:C:N3	1:2A:2153:G:N2	2.24	0.82
1:1A:2143:G:H1	1:1A:2199:C:N4	1.78	0.82
1:2A:2129:C:N4	1:2A:2159:G:H1	1.77	0.82
11:2P:59:LEU:HD11	30:28:10:ALA:HB2	1.62	0.81
1:2A:2524:G:N7	60:2A:5109:HOH:O	2.13	0.81
1:1A:889:G:N7	60:1A:5371:HOH:O	2.14	0.81
10:2O:35:VAL:HG11	10:2O:103:ALA:HB3	1.62	0.81
3:2D:13:ARG:NH1	3:2D:16:MET:SD	2.54	0.81
1:1A:2152:U:H2'	1:1A:2180:A:H61	1.45	0.81
1:1A:1140:U:H1'	1:1A:1143:U:H5	1.46	0.81
1:2A:1021:A:H62	1:2A:1141:U:H3	1.28	0.80
1:1A:2832:G:OP2	60:1A:5352:HOH:O	1.98	0.80
7:2H:84:SER:HB3	7:2H:132:ARG:HH11	1.47	0.80
1:1A:2158:C:N4	1:1A:2177:G:N1	2.29	0.80
1:2A:1389:G:N7	60:2A:4894:HOH:O	2.14	0.80
1:1A:1108:G:H1	1:1A:1123:A:H61	1.30	0.80
1:1A:2156:A:C4	1:1A:2180:A:H2	1.99	0.80
1:2A:2822:G:OP2	60:2A:5369:HOH:O	1.99	0.80
1:2A:1647:G:OP1	60:2A:4350:HOH:O	2.00	0.79
1:2A:962:G:OP1	60:2A:4399:HOH:O	2.00	0.79
1:2A:1670:C:OP1	60:2A:4902:HOH:O	2.00	0.79
1:2A:1153:C:OP1	16:2U:92:ARG:NH2	2.15	0.79
3:1D:242:ARG:NH1	60:1D:412:HOH:O	2.16	0.79
1:2A:2127:G:C2	1:2A:2161:C:C4	2.71	0.79
6:2G:64:THR:HB	6:2G:94:LEU:HD21	1.63	0.79
5:1F:70:THR:HG23	5:1F:72:ARG:H	1.48	0.79
1:2A:711:G:N2	1:2A:720:C:O2	2.16	0.79
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.65	0.78
1:2A:1002:G:H1	1:2A:1038:C:N4	42.44	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:882:G:H2'	1:2A:883:G:H8	1.48	0.78
1:2A:1011:G:H1	1:2A:1018:C:N4	18.23	0.78
1:2A:1818:U:OP2	3:2D:157:ARG:NH1	2.16	0.78
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.16	0.78
1:1A:294:C:H42	1:1A:390:G:H1	1.29	0.78
1:1A:656:A:OP1	11:1P:65:ARG:NH1	2.16	0.78
1:1A:1151:U:H2'	1:1A:1152:G:C8	2.18	0.78
1:2A:1119:C:H2'	1:2A:1120:G:C8	3.10	0.78
1:1A:2146:G:H1	1:1A:2196:C:H42	1.31	0.78
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.65	0.78
1:1A:1085:G:H1	1:1A:1162:C:H42	1.31	0.78
1:2A:1634:A:OP1	60:2A:4877:HOH:O	2.01	0.78
1:1A:1044:C:OP1	60:1A:4714:HOH:O	2.02	0.77
1:1A:2460:A:OP1	60:1A:5012:HOH:O	2.01	0.77
1:2A:948:G:OP1	60:2A:4399:HOH:O	2.00	0.77
1:2A:2287:A:H62	1:2A:2344:U:H3	1.33	0.77
1:2A:987:G:H1	1:2A:1218:C:H42	46.31	0.77
1:2A:1530:C:O2'	1:2A:1531:C:O5'	2.01	0.77
2:2B:27:C:N4	2:2B:56:G:O6	2.18	0.77
2:2B:7:G:H1	2:2B:114:C:H42	1.33	0.77
1:2A:2127:G:C6	1:2A:2161:C:N4	2.53	0.77
1:1A:532:A:N6	1:1A:1206:G:O2'	79.90	0.77
1:2A:1826:G:H4'	3:2D:242:ARG:HE	1.47	0.77
1:1A:1711:A:OP1	60:1A:5025:HOH:O	2.02	0.77
60:1A:5352:HOH:O	4:1E:110:GLY:O	2.02	0.77
1:1A:925:A:N6	1:1A:945:A:O2'	2.17	0.76
1:2A:424:G:N7	60:2A:5062:HOH:O	2.18	0.76
23:21:50:ARG:HG2	23:21:59:THR:HG22	1.68	0.76
1:1A:2007:G:OP2	60:1A:5698:HOH:O	2.02	0.76
1:2A:2126:A:N6	1:2A:2162:G:O2'	2.18	0.76
8:2I:4:ILE:HG12	8:2I:18:VAL:HG22	1.68	0.76
2:2B:17:C:O2	2:2B:67:G:N2	2.17	0.76
1:1A:1055:A:OP2	9:1N:37:LYS:NZ	2.19	0.76
1:2A:532:A:N6	1:2A:1206:G:O2'	62.55	0.76
1:2A:1155:A:H5''	16:2U:55:ARG:HH11	1.50	0.75
1:2A:1783:A:OP2	60:2A:4560:HOH:O	2.03	0.75
1:1A:2227:G:H3'	1:1A:2228:G:C8	2.22	0.75
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.68	0.75
1:1A:1151:U:H2'	1:1A:1152:G:H8	1.51	0.75
5:2F:53:THR:HG23	5:2F:55:GLY:H	1.52	0.75
12:1Q:111:GLU:OE2	12:1Q:133:ARG:NH2	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2332:U:O4	60:2A:4436:HOH:O	2.04	0.75
1:2A:1693:U:O2	3:2D:14:ARG:NH2	2.18	0.75
1:1A:1099:C:N4	1:1A:1152:G:H1	1.85	0.75
1:2A:2308:G:O6	1:2A:2311:A:N6	2.19	0.75
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.69	0.74
1:2A:880:G:N2	1:2A:898:C:O2	2.19	0.74
22:20:10:THR:HG22	22:20:12:ASN:H	1.52	0.74
2:2B:22:U:H3	2:2B:61:G:H1	1.36	0.74
1:1A:1059:C:OP2	60:1A:5073:HOH:O	2.04	0.74
1:2A:1015:G:H2'	1:2A:1016:G:H8	1.50	0.74
21:2Z:153:SER:HB3	21:2Z:167:PRO:HB3	1.69	0.74
1:1A:786:G:OP1	60:1A:5040:HOH:O	2.06	0.74
1:2A:2884:U:OP2	60:2A:4309:HOH:O	2.06	0.74
1:2A:1119:C:H2'	1:2A:1120:G:H8	2.41	0.74
15:2T:65:LYS:HE3	15:2T:67:SER:HB2	1.68	0.74
1:1A:493:G:OP1	29:17:33:ARG:NH1	2.22	0.73
30:18:6:THR:HG22	30:18:63:PRO:HD2	1.70	0.73
1:2A:2310:A:N1	6:2G:79:ASN:ND2	2.36	0.73
9:2N:128:HIS:O	9:2N:131:GLN:NE2	2.21	0.73
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.69	0.73
1:1A:542:C:OP1	27:15:16:ARG:NH2	2.22	0.73
1:1A:2145:G:H1	1:1A:2197:C:H42	1.34	0.73
1:2A:1156:A:OP2	60:2A:4427:HOH:O	2.07	0.73
2:2B:117:G:N7	60:2B:3126:HOH:O	2.22	0.73
1:1A:1123:A:H2'	1:1A:1124:U:H4'	1.70	0.73
1:2A:792:G:O6	60:2A:4331:HOH:O	2.06	0.73
3:2D:152:GLY:O	60:2D:427:HOH:O	2.05	0.73
12:2Q:26:TYR:O	12:2Q:67:ARG:NH1	2.21	0.73
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.70	0.73
22:10:11:ARG:O	22:10:14:ARG:NH2	2.20	0.72
1:2A:794:G:OP1	60:2A:4747:HOH:O	2.07	0.72
1:1A:1848:G:OP1	3:1D:88:ARG:NH2	2.22	0.72
1:2A:1671:U:OP2	60:2A:4902:HOH:O	2.08	0.72
1:2A:822:U:OP2	60:2A:4800:HOH:O	2.07	0.72
1:1A:2421:G:O2'	60:1A:5384:HOH:O	2.06	0.72
1:2A:854:G:H2'	1:2A:855:G:C8	2.23	0.72
1:1A:1101:G:H1	1:1A:1150:C:H42	1.37	0.72
1:1A:2820:A:N6	1:1A:2900:G:O2'	2.22	0.72
1:1A:2695:C:O2	10:1O:70:LYS:NZ	2.18	0.72
14:1S:25:ARG:NH1	14:1S:42:ASP:OD1	2.23	0.72
23:21:21:ARG:HD3	23:21:35:THR:HG21	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2822:G:N7	60:2A:5368:HOH:O	2.23	0.72
1:2A:728:G:H5''	3:2D:13:ARG:HH21	1.55	0.72
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.72	0.72
1:1A:2180:A:O2'	1:1A:2181:G:OP2	2.07	0.72
1:1A:701:A:OP2	60:1A:4755:HOH:O	2.08	0.71
1:1A:1829:U:H5'	3:1D:259:THR:HG22	1.72	0.71
1:2A:1566:A:OP1	3:2D:211:ARG:NH1	2.22	0.71
1:2A:531:C:OP1	1:2A:561:G:N1	2.22	0.71
1:1A:2288:G:N7	60:1A:5504:HOH:O	2.23	0.71
14:2S:38:GLN:NE2	14:2S:47:THR:OG1	2.21	0.71
4:2E:119:ARG:HD2	4:2E:160:TYR:HB2	1.70	0.71
7:2H:7:LEU:HD12	7:2H:8:PRO:HD2	1.72	0.71
1:1A:1810:U:OP2	60:1A:5038:HOH:O	2.06	0.71
1:1A:873:U:OP1	60:1A:5528:HOH:O	2.08	0.71
1:2A:987:G:O2'	1:2A:1000:A:N3	2.23	0.71
1:1A:1939:PSU:O2	60:1A:5275:HOH:O	2.08	0.71
1:2A:467:G:OP2	29:27:34:ARG:HD3	1.90	0.71
1:2A:1271:G:OP2	60:2A:4350:HOH:O	2.08	0.71
1:2A:1031:G:H5''	31:29:8:LYS:HE3	1.73	0.71
1:2A:1693:U:H1'	3:2D:14:ARG:NH2	2.04	0.71
5:2F:140:LEU:HD11	5:2F:170:LEU:HD11	1.71	0.71
1:1A:1069:U:OP2	60:1A:4871:HOH:O	2.08	0.71
1:1A:1716:A:OP2	60:1A:4989:HOH:O	2.07	0.71
1:1A:2798:C:OP1	4:1E:41:LYS:NZ	2.18	0.71
1:1A:927:G:H2'	1:1A:928:G:H8	1.54	0.71
1:1A:943:C:N3	1:1A:944:C:N4	2.38	0.71
14:1S:68:GLN:HG3	14:1S:71:ARG:HH21	1.55	0.71
1:2A:692:C:O2'	3:2D:38:LYS:NZ	2.21	0.71
1:1A:2772:G:N7	60:1A:4321:HOH:O	2.24	0.71
1:1A:1924:C:OP1	3:1D:242:ARG:NH1	2.22	0.70
1:1A:331:G:N7	60:1A:4450:HOH:O	2.24	0.70
1:2A:568:U:O4	60:2A:4947:HOH:O	2.08	0.70
6:2G:79:ASN:OD1	6:2G:79:ASN:N	2.24	0.70
1:1A:2776:G:OP2	60:1A:4740:HOH:O	2.09	0.70
1:2A:2677:G:N3	60:2A:5258:HOH:O	2.24	0.70
20:1Y:54:LYS:HA	20:1Y:56:PRO:HD3	1.72	0.70
26:14:53:GLU:HG3	26:14:54:GLY:H	1.55	0.70
1:1A:1299:A:OP1	60:1A:5877:HOH:O	2.08	0.70
1:2A:131:G:OP1	60:2A:4066:HOH:O	2.08	0.70
1:2A:2490:G:O6	60:2A:4471:HOH:O	2.09	0.70
1:1A:2802:C:O2	1:1A:2903:G:N2	2.22	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2478:A:OP2	31:29:2:LYS:NZ	2.24	0.70
1:1A:928:G:N2	1:1A:943:C:O2	2.25	0.70
20:2Y:102:CYS:SG	20:2Y:103:GLY:N	2.63	0.70
1:1A:1740:U:H1'	3:1D:14:ARG:NH2	2.04	0.70
1:1A:2440:G:OP1	60:1A:5528:HOH:O	2.08	0.70
1:1A:1296:G:OP2	11:1P:21:ARG:NH1	2.25	0.70
2:1B:105:A:OP1	21:1Z:72:ARG:NH1	2.24	0.70
1:2A:882:G:H2'	1:2A:883:G:C8	2.26	0.70
1:2A:89:G:H3'	1:2A:90:U:H5''	1.72	0.70
3:2D:108:PRO:HG2	3:2D:111:LEU:HB2	1.73	0.70
1:1A:1361:C:OP2	60:1A:4704:HOH:O	2.09	0.70
1:2A:1019:U:H3	1:2A:1142(A):A:H62	1.38	0.70
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.25	0.70
1:1A:1060:U:OP2	60:1A:5073:HOH:O	2.10	0.70
10:1O:35:VAL:HG11	10:1O:103:ALA:HB3	1.72	0.70
1:2A:109:G:N7	60:2A:5070:HOH:O	2.25	0.70
2:2B:41:U:H5	6:2G:70:VAL:H	1.40	0.70
1:1A:2045:G:H5'	1:1A:2629:C:H4'	1.74	0.69
1:1A:2149:G:H1	1:1A:2183:C:H42	1.37	0.69
1:1A:2641:A:O2'	1:1A:2642:G:OP2	2.10	0.69
1:1A:1857:G:H4'	3:1D:242:ARG:HE	1.56	0.69
24:22:1:MET:N	24:22:52:ASP:OD1	2.23	0.69
1:2A:1973:G:OP1	60:2A:5051:HOH:O	2.10	0.69
1:2A:2710:C:N4	60:2A:4933:HOH:O	2.24	0.69
8:2I:92:VAL:HG13	8:2I:120:ILE:HB	1.75	0.69
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.65	0.69
1:2A:1360:A:OP2	9:2N:35:ARG:NH2	117.66	0.69
5:2F:20:LEU:HD13	5:2F:125:LEU:HD13	1.74	0.69
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.10	0.69
1:2A:963:U:OP2	60:2A:4399:HOH:O	2.09	0.69
6:2G:15:VAL:HG13	6:2G:175:LEU:HD23	1.74	0.69
1:1A:1312:G:O5'	18:1W:15:ARG:NH2	2.25	0.69
1:1A:1785:C:H5	15:1T:96:ARG:NH2	1.91	0.69
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.58	0.69
8:1I:129:THR:HG22	8:1I:139:GLN:HE22	1.58	0.69
5:2F:157:VAL:HB	5:2F:194:MET:HG2	1.74	0.69
1:1A:2362:C:OP2	60:1A:5166:HOH:O	2.09	0.69
5:2F:101:LEU:O	5:2F:106:ARG:NH1	2.26	0.69
1:2A:1016:G:O6	1:2A:1147:C:N4	2.26	0.69
11:2P:95:VAL:HA	11:2P:99:LEU:HD21	1.73	0.69
1:2A:775:G:O3'	60:2A:4370:HOH:O	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.75	0.68
1:1A:2384:G:O6	60:1A:4543:HOH:O	2.06	0.68
1:2A:2250:G:OP1	12:2Q:85:LYS:NZ	2.26	0.68
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.29	0.68
1:2A:1278:A:OP1	13:2R:36:THR:HG22	1.93	0.68
1:2A:307:G:N1	1:2A:310:A:OP2	2.27	0.68
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.29	0.68
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.27	0.68
1:2A:249:C:O2	30:28:12:LYS:NZ	2.25	0.68
1:2A:1817:G:OP1	3:2D:88:ARG:NH2	2.25	0.68
1:1A:1990:G:OP1	60:1A:4816:HOH:O	2.11	0.68
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.26	0.68
1:1A:1552:C:H2'	1:1A:1553:A:H8	1.59	0.68
1:2A:2305:A:H5''	6:2G:134:GLY:HA3	1.76	0.68
11:1P:59:LEU:HD11	30:18:10:ALA:HB2	1.74	0.68
4:1E:127:ASP:OD2	60:1E:411:HOH:O	2.10	0.68
1:1A:1100:A:H61	1:1A:1151:U:H3	1.42	0.68
4:2E:52:LEU:HB3	4:2E:76:ARG:HD3	1.76	0.68
5:1F:157:VAL:HB	5:1F:194:MET:HG2	1.77	0.67
1:1A:1431:G:O2'	1:1A:1442:U:O2	2.09	0.67
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.29	0.67
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.12	0.67
1:1A:2850:C:OP2	60:1A:5118:HOH:O	2.12	0.67
1:1A:2884:C:OP1	60:1A:5250:HOH:O	2.11	0.67
1:2A:2268:A:OP1	60:2A:4307:HOH:O	2.11	0.67
1:2A:481:G:N7	60:2A:5310:HOH:O	2.27	0.67
1:2A:922:U:O2'	22:20:29:GLN:NE2	2.27	0.67
7:1H:94:TYR:OH	7:1H:152:ARG:NH1	2.26	0.67
1:2A:266:G:H5''	1:2A:268:C:H41	11.17	0.67
1:1A:1202:A:OP1	16:1U:55:ARG:NH1	2.28	0.67
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.30	0.67
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.74	0.67
1:1A:1228:G:O2'	25:13:29:ARG:NH1	2.26	0.67
2:2B:55:U:H1'	6:2G:29:TRP:HD1	1.59	0.67
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.28	0.67
1:2A:1024:G:OP2	60:2A:4644:HOH:O	2.13	0.67
1:2A:2727:G:O2'	10:2O:70:LYS:NZ	2.28	0.67
1:2A:821:A:N1	60:2A:4282:HOH:O	2.27	0.67
1:2A:1803:A:O2'	3:2D:259:THR:HG21	1.95	0.67
4:2E:47:VAL:HG11	4:2E:86:PRO:HD2	1.75	0.67
1:1A:2286:A:OP2	60:1A:5505:HOH:O	2.13	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:45:GLU:OE2	60:1G:3104:HOH:O	2.12	0.67
60:1A:5352:HOH:O	13:1R:3:HIS:NE2	2.27	0.67
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	1.77	0.67
18:2W:34:ASN:OD1	18:2W:37:ARG:NH2	2.26	0.67
14:1S:15:ARG:O	14:1S:19:LYS:HG2	1.94	0.67
1:2A:1218:C:H42	1:2A:1231:G:H1	1.43	0.67
2:2B:55:U:O2'	6:2G:27:ASN:ND2	2.25	0.67
1:1A:290:G:N7	60:1A:5216:HOH:O	2.28	0.66
1:1A:787:U:OP2	60:1A:4742:HOH:O	2.12	0.66
1:2A:2143:C:H2'	1:2A:2144:U:O4'	1.95	0.66
1:2A:861:A:N3	2:2B:79:C:O2'	2.27	0.66
1:1A:1997:G:OP2	60:1A:4758:HOH:O	2.12	0.66
1:1A:593:G:O6	60:1A:5012:HOH:O	2.11	0.66
1:2A:2782:G:OP2	60:2A:4806:HOH:O	2.12	0.66
17:2V:40:LEU:HB2	17:2V:46:VAL:HG13	1.76	0.66
1:1A:2564:2MU:OP2	60:1A:5027:HOH:O	2.12	0.66
1:1A:715:G:N7	60:1A:5891:HOH:O	2.28	0.66
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.75	0.66
1:1A:2158:C:N4	1:1A:2177:G:C6	2.63	0.66
1:2A:1673:U:O2'	60:2A:4420:HOH:O	2.13	0.66
5:2F:40:GLN:HE22	5:2F:184:TYR:H	1.42	0.66
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.77	0.66
1:1A:1070:G:OP2	60:1A:4871:HOH:O	2.13	0.66
23:21:51:VAL:HG11	23:21:74:VAL:HG21	1.77	0.66
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.28	0.66
15:1T:98:LYS:NZ	60:1T:8106:HOH:O	2.17	0.66
1:2A:1648:C:OP1	60:2A:4350:HOH:O	2.12	0.66
1:2A:2518:A:OP2	60:2A:4219:HOH:O	2.13	0.66
1:2A:2547:U:O2	10:2O:23:ARG:NH2	2.28	0.66
24:12:52:ASP:O	24:12:56:GLN:HG3	1.96	0.66
1:1A:2055:A:OP1	60:1A:4436:HOH:O	2.12	0.66
26:24:24:THR:OG1	26:24:25:TYR:N	2.29	0.66
1:2A:2362:G:N3	60:2A:5180:HOH:O	2.29	0.66
1:2A:731:C:OP1	60:2A:4876:HOH:O	2.13	0.66
1:1A:1649:A:OP1	60:1A:5524:HOH:O	2.13	0.66
11:1P:100:LEU:HD12	11:1P:112:LEU:HD11	1.78	0.66
1:2A:1959:G:N7	60:2A:4532:HOH:O	2.29	0.66
7:2H:35:VAL:HG13	7:2H:71:LEU:HD22	1.78	0.66
1:1A:1077:G:H5''	31:19:8:LYS:HE3	1.77	0.65
1:1A:265:U:O4	60:1A:5675:HOH:O	2.10	0.65
1:1A:930:G:H22	1:1A:939:C:H42	1.42	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:1E:119:ARG:HD2	4:1E:160:TYR:HB2	1.77	0.65
1:2A:322:A:OP2	5:2F:169:ASN:HB2	1.96	0.65
1:1A:1159:U:H2'	1:1A:1160:G:H8	1.61	0.65
1:1A:2164:C:N3	1:1A:2171:G:O6	2.30	0.65
8:1I:4:ILE:HG12	8:1I:18:VAL:HG22	1.77	0.65
6:2G:120:LEU:N	6:2G:179:PRO:O	2.25	0.65
8:2I:4:ILE:HD11	8:2I:44:LEU:HD12	1.77	0.65
1:1A:2158:C:N3	1:1A:2177:G:C2	2.65	0.65
1:2A:1395:A:OP1	60:2A:4567:HOH:O	2.13	0.65
5:2F:103:LYS:HA	5:2F:106:ARG:HG3	1.78	0.65
13:2R:24:GLN:HE22	13:2R:36:THR:HG21	1.61	0.65
1:1A:1441:A:OP1	60:1A:5524:HOH:O	2.14	0.65
1:1A:625:G:O2'	1:1A:702:A:N6	2.29	0.65
5:1F:13:SER:OG	5:1F:127:GLU:OE1	2.12	0.65
1:1A:992:G:OP2	60:1A:5140:HOH:O	2.15	0.65
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.79	0.65
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.32	0.65
1:2A:2136:C:H42	1:2A:2155:G:H1	1.32	0.65
1:2A:271(H):G:H2'	1:2A:271(I):G:H8	1.62	0.65
21:1Z:11:GLU:O	21:1Z:36:LYS:NZ	2.27	0.64
1:2A:2058:A:OP1	60:2A:4924:HOH:O	2.13	0.64
1:2A:2141:G:O6	1:2A:2150:U:O2	2.15	0.64
2:2B:66:A:H61	2:2B:108:U:H2'	1.62	0.64
1:1A:1243:U:O4	60:1A:5606:HOH:O	2.08	0.64
1:1A:83:A:H5'	20:1Y:8:LYS:HG2	1.78	0.64
1:1A:1105:G:N2	1:1A:1125:C:N3	2.42	0.64
1:2A:1434:A:H61	1:2A:1558:A:H62	1.43	0.64
1:2A:2042:A:OP1	60:2A:4114:HOH:O	2.15	0.64
1:2A:2499:C:OP2	60:2A:4650:HOH:O	2.15	0.64
6:2G:135:LEU:HD21	6:2G:157:ILE:HD12	1.78	0.64
12:2Q:57:HIS:HD2	12:2Q:117:ALA:HB2	1.61	0.64
3:1D:108:PRO:HB3	3:1D:143:HIS:CE1	2.33	0.64
5:1F:133:ASN:N	5:1F:138:GLU:OE1	2.31	0.64
23:21:50:ARG:NH1	23:21:57:GLU:OE2	2.23	0.64
7:2H:96:ALA:HB1	7:2H:103:LEU:HD11	1.80	0.64
11:1P:63:PRO:HG2	30:18:25:MET:HB2	1.78	0.64
7:1H:3:ARG:NH1	7:1H:5:GLY:H	1.96	0.64
2:2B:14:U:OP2	2:2B:70:C:O2'	2.13	0.64
1:2A:1801:G:OP2	3:2D:154:LYS:NZ	2.30	0.64
5:2F:12:LEU:HB2	5:2F:124:LEU:HD11	1.79	0.64
3:1D:71:ASP:HB3	3:1D:103:ARG:HH12	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:27:34:ARG:HE	29:27:39:ARG:HG2	1.63	0.64
1:2A:1411:C:H42	1:2A:1591:G:H1	1.46	0.64
1:2A:2759:G:OP2	60:2A:4824:HOH:O	2.15	0.64
26:14:24:THR:OG1	26:14:25:TYR:N	2.30	0.64
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.12	0.64
1:2A:1033:U:OP1	31:29:9:ARG:NH2	2.22	0.64
1:2A:494:G:OP1	18:2W:8:ARG:NH1	2.31	0.64
1:1A:1452:U:H2'	1:1A:1453:C:C6	2.32	0.64
1:1A:2562:G:OP1	60:1A:4989:HOH:O	2.15	0.64
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.78	0.64
1:2A:132:G:O6	60:2A:4610:HOH:O	2.11	0.64
1:2A:449:A:OP2	60:2A:4655:HOH:O	2.15	0.64
26:14:56:VAL:HG23	26:14:57:GLU:H	1.61	0.64
10:1O:104:ARG:CZ	15:1T:34:VAL:HG11	2.28	0.64
1:2A:1355:G:O6	60:2A:5022:HOH:O	2.13	0.64
1:2A:322:A:OP1	5:2F:168:ARG:HD2	1.98	0.64
1:1A:2149:G:H1	1:1A:2183:C:N4	1.96	0.63
5:2F:145:GLU:OE1	5:2F:145:GLU:N	2.31	0.63
7:2H:125:VAL:HG12	7:2H:131:VAL:HG22	1.80	0.63
1:1A:2128:G:H1	1:1A:2205:C:H42	1.44	0.63
1:2A:1011:G:OP2	16:2U:70:ARG:NH2	2.31	0.63
12:2Q:11:LYS:HE3	12:2Q:88:GLY:O	1.97	0.63
1:1A:121:G:OP2	60:1A:4220:HOH:O	2.15	0.63
3:1D:8:PRO:HB3	3:1D:14:ARG:HD2	1.79	0.63
1:2A:1833:U:OP1	60:2A:5389:HOH:O	2.15	0.63
1:2A:370:G:N7	60:2A:4061:HOH:O	2.30	0.63
1:2A:1920:4OC:HM22	1:2A:1921:G:H5'	1.80	0.63
1:2A:2498:C:OP2	60:2A:4650:HOH:O	2.15	0.63
5:2F:110:LEU:HD21	5:2F:181:LEU:HD23	1.81	0.63
1:1A:1718:U:O4	60:1A:4989:HOH:O	2.13	0.63
19:1X:88:LYS:HE2	19:1X:93:GLU:HG3	1.81	0.63
11:1P:60:MET:HA	30:18:13:ARG:NH1	2.13	0.63
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.30	0.63
8:1I:77:LEU:HD12	8:1I:101:LEU:HD13	1.81	0.62
1:2A:2746:U:OP1	7:2H:85:LYS:NZ	2.28	0.62
3:2D:69:ARG:HE	3:2D:130:ALA:HB2	1.64	0.62
1:1A:1103:A:N6	1:1A:1133:G:OP2	2.31	0.62
1:1A:2205:C:H2'	1:1A:2206:G:H8	1.64	0.62
29:27:34:ARG:HG3	29:27:34:ARG:HH11	1.63	0.62
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.39	0.62
1:2A:875:G:O6	1:2A:902:C:N4	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1834:A:O2'	3:1D:259:THR:HG21	1.99	0.62
1:2A:1653:G:H3'	13:2R:2:ARG:HD3	1.81	0.62
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.33	0.62
1:1A:1103:A:H61	1:1A:1127:U:H3	1.46	0.62
1:1A:303:C:N3	1:1A:385:G:N2	2.43	0.62
1:1A:414:U:O4	60:1A:5867:HOH:O	2.10	0.62
1:2A:829:A:N7	1:2A:2248:C:H5'	2.13	0.62
1:2A:900:A:O2'	1:2A:901:A:OP1	2.15	0.62
1:1A:2328:C:O2'	6:1G:128:ARG:NH2	2.32	0.62
1:2A:2162:G:H4'	1:2A:2172:U:H2'	1.81	0.62
2:2B:31:C:H4'	6:2G:29:TRP:CZ2	2.35	0.62
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.81	0.62
1:1A:1104:G:H1	1:1A:1126:C:H42	1.46	0.62
26:24:33:VAL:HG12	26:24:35:VAL:H	1.64	0.62
1:2A:2136:C:O2'	1:2A:2137:C:O5'	2.18	0.62
6:2G:38:VAL:HG22	6:2G:93:THR:HG23	1.81	0.62
17:1V:72:VAL:HG13	17:1V:85:LYS:HB3	1.81	0.62
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.31	0.62
1:2A:2318:G:H21	14:2S:3:ARG:HD3	1.64	0.62
1:2A:271(G):C:H2'	1:2A:271(H):G:H8	1.65	0.62
7:1H:84:SER:OG	7:1H:132:ARG:NH1	2.33	0.62
1:1A:2130:C:H2'	1:1A:2131:U:H6	1.65	0.62
1:1A:1219:A:H4'	1:1A:1220:U:OP1	1.99	0.61
1:1A:2150:C:H42	1:1A:2182:G:H1	1.47	0.61
1:2A:2138:C:H42	1:2A:2153:G:H1	0.71	0.61
1:2A:2663:G:H3'	1:2A:2664:G:H8	1.64	0.61
1:2A:848:G:C2	1:2A:933:A:H1'	2.35	0.61
1:1A:1159:U:H2'	1:1A:1160:G:C8	2.35	0.61
21:2Z:4:ARG:HG2	21:2Z:58:VAL:HB	1.82	0.61
5:1F:140:LEU:HD11	5:1F:170:LEU:HD11	1.81	0.61
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.82	0.61
4:2E:36:ARG:HG2	4:2E:47:VAL:HG12	1.81	0.61
7:2H:144:VAL:O	7:2H:148:ILE:HG12	2.00	0.61
1:1A:131:C:O2	1:1A:231:G:N2	72.17	0.61
15:1T:65:LYS:HE3	15:1T:67:SER:HB2	1.83	0.61
24:22:1:MET:SD	24:22:56:GLN:NE2	2.73	0.61
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.28	0.61
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.81	0.61
8:1I:140:LEU:HD22	8:1I:142:VAL:HG13	1.82	0.61
12:1Q:18:LYS:O	12:1Q:98:LYS:NZ	2.27	0.61
1:1A:2784:C:H2'	1:1A:2785:C:C6	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:149:ARG:NH1	7:2H:167:GLU:OE1	2.34	0.61
21:1Z:138:GLU:H	21:1Z:156:LYS:HZ3	1.46	0.61
2:2B:43:C:O4'	6:2G:66:GLN:NE2	2.33	0.61
1:2A:1030:G:OP2	12:2Q:128:LYS:NZ	2.32	0.61
1:2A:2484:G:H1'	12:2Q:124:LYS:HD2	1.83	0.61
10:2O:80:ASP:OD2	15:2T:64:ARG:NH2	2.34	0.61
1:2A:1011:G:N2	1:2A:1018:C:N3	20.85	0.61
21:1Z:69:THR:HG22	21:1Z:90:VAL:HA	1.81	0.60
8:2I:93:THR:H	8:2I:96:ASP:HB2	1.66	0.60
1:1A:2340:A:H2'	1:1A:2341:G:C8	2.37	0.60
1:2A:1300:U:H4'	1:2A:1301:A:H5''	1.81	0.60
8:2I:124:GLY:H	8:2I:144:VAL:HG23	1.65	0.60
7:1H:56:SER:HB3	7:1H:61:HIS:ND1	2.17	0.60
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.35	0.60
1:2A:2324:C:H5''	1:2A:2325:G:H5'	1.84	0.60
1:2A:422:A:OP2	60:2A:4062:HOH:O	2.16	0.60
2:2B:24:G:H4'	2:2B:25:A:N7	2.17	0.60
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.01	0.60
1:1A:1451:U:H2'	1:1A:1452:U:C6	2.37	0.60
1:1A:555:G:N1	1:1A:2045:G:OP1	2.30	0.60
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.34	0.60
15:2T:109:GLU:HG2	15:2T:112:ARG:NH2	2.17	0.60
1:1A:1405:A:H2'	1:1A:1406:A:H5'	1.83	0.60
1:1A:2175:G:H2'	1:1A:2176:G:C8	2.36	0.60
1:1A:2624:C:OP2	27:15:2:ALA:N	2.34	0.60
1:2A:1812:A:OP2	60:2A:5276:HOH:O	2.16	0.60
2:2B:40:U:H2'	26:24:2:LYS:HE3	1.83	0.60
2:2B:83:G:H1	2:2B:94:C:H42	1.48	0.60
1:1A:181:C:OP1	60:1A:4235:HOH:O	2.17	0.60
16:2U:66:ASN:HD21	16:2U:70:ARG:HH21	1.50	0.60
1:1A:2348:A:H61	22:10:43:THR:HG22	1.67	0.60
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.36	0.60
1:2A:2144:U:H1'	1:2A:2148:G:N2	2.17	0.60
26:14:54:GLY:N	26:14:55:ARG:HA	2.17	0.60
1:1A:2349:G:OP1	60:1A:4319:HOH:O	2.17	0.60
1:2A:615:G:OP1	5:2F:40:GLN:HG2	2.02	0.60
1:1A:2776:G:N7	60:1A:4738:HOH:O	2.31	0.59
4:1E:29:GLY:HA3	60:1E:419:HOH:O	2.00	0.59
3:2D:164:GLN:HB3	3:2D:176:ARG:HG2	1.84	0.59
6:2G:173:LEU:HD23	6:2G:176:LEU:HD12	1.85	0.59
2:2B:42:C:O2'	6:2G:67:LYS:O	2.13	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2156:G:H2'	1:2A:2157:G:C2	2.37	0.59
1:2A:2815:C:H5'	27:25:29:THR:HG21	1.84	0.59
4:2E:179:GLU:HG3	15:2T:9:LEU:HD21	1.84	0.59
19:2X:29:TRP:CZ3	19:2X:76:ARG:HG3	2.36	0.59
7:1H:97:ARG:NE	7:1H:104:GLU:OE1	2.35	0.59
1:1A:2766:A:O2'	31:19:15:LYS:NZ	2.35	0.59
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.84	0.59
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.84	0.59
1:2A:1253:A:OP1	60:2A:4014:HOH:O	2.16	0.59
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.37	0.59
19:2X:48:LYS:NZ	24:22:30:ARG:HH22	2.00	0.59
1:1A:2430:A:OP2	30:18:29:LYS:NZ	2.36	0.59
1:1A:1140:U:H1'	1:1A:1143:U:C5	2.34	0.59
1:1A:2825:C:H5'	27:15:29:THR:HG21	1.84	0.59
8:1I:126:TYR:HB2	8:1I:142:VAL:HG23	1.84	0.59
1:2A:2096:U:H3	1:2A:2193:G:H1	1.49	0.59
16:2U:104:GLN:NE2	16:2U:105:VAL:HG23	2.17	0.59
21:2Z:45:ASP:O	21:2Z:49:ARG:HG2	2.01	0.59
1:1A:1100:A:N6	1:1A:1151:U:H3	2.01	0.59
1:2A:2376:A:H3'	1:2A:2377:A:H8	1.66	0.59
1:2A:2448:A:OP1	60:2A:4843:HOH:O	2.16	0.59
6:2G:15:VAL:HG22	6:2G:175:LEU:HB3	1.83	0.59
1:1A:2150:C:H2'	1:1A:2151:C:O4'	2.01	0.59
2:1B:66:A:H61	2:1B:109:C:H5'	1.67	0.59
1:2A:1220:A:OP2	16:2U:19:LYS:NZ	2.34	0.59
1:1A:1037:C:H2'	1:1A:1038:C:H6	2.26	0.59
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.85	0.59
1:2A:878:A:H61	1:2A:899:A:H1'	1.66	0.59
1:2A:848:G:N3	1:2A:933:A:H1'	2.17	0.59
22:10:70:GLN:OE1	22:10:80:HIS:NE2	2.31	0.59
1:1A:1410:G:P	23:11:3:LYS:HG3	2.43	0.59
8:1I:92:VAL:HG11	8:1I:144:VAL:HG11	1.85	0.59
1:2A:1507:A:O2'	1:2A:1508:A:O5'	2.20	0.59
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.03	0.59
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.85	0.59
9:2N:67:LEU:HD12	9:2N:87:LEU:HD13	1.85	0.59
1:1A:2297:C:OP2	28:16:6:ARG:NH1	2.35	0.58
30:28:30:ARG:O	60:28:201:HOH:O	2.16	0.58
1:2A:2364:C:OP1	22:20:55:ARG:NH1	2.33	0.58
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.02	0.58
1:1A:1305:G:N2	1:1A:1331:G:H1'	39.95	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2146:G:H1	1:1A:2196:C:N4	2.00	0.58
1:1A:83:A:H5''	20:1Y:8:LYS:HE3	1.85	0.58
1:1A:997:G:OP1	12:1Q:16:ARG:NH2	2.35	0.58
1:2A:855:G:H2'	1:2A:856:C:C6	2.38	0.58
31:19:2:LYS:HE2	31:19:31:LYS:O	2.03	0.58
1:1A:2879:G:H2'	1:1A:2880:C:O4'	2.03	0.58
1:2A:2394:C:OP2	30:28:30:ARG:NH1	2.35	0.58
1:2A:271(G):C:H2'	1:2A:271(H):G:C8	2.38	0.58
1:2A:307:G:H21	1:2A:330:A:H62	1.52	0.58
1:2A:1815:A:OP2	3:2D:54:ARG:NH2	2.35	0.58
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.86	0.58
8:2I:31:LEU:HD21	8:2I:38:LEU:HG	1.84	0.58
10:1O:2:ILE:HD12	10:1O:6:THR:HG21	1.85	0.58
1:1A:2130:C:H2'	1:1A:2131:U:C6	2.39	0.58
1:1A:2145:G:H1	1:1A:2197:C:N4	2.01	0.58
2:1B:89:G:OP1	60:1B:3145:HOH:O	2.17	0.58
26:24:16:CYS:SG	26:24:17:GLY:N	2.77	0.58
1:2A:1264:G:OP1	27:25:19:ARG:NH2	2.21	0.58
5:2F:187:VAL:HG12	11:2P:3:LEU:HD12	1.85	0.58
11:2P:97:PRO:HD3	11:2P:126:VAL:O	2.03	0.58
1:1A:1435:G:H2'	1:1A:1436:U:C6	3.27	0.58
1:1A:173:C:H2'	1:1A:174:U:C6	2.39	0.58
26:24:41:PRO:HG3	26:24:49:PHE:CE2	2.39	0.58
1:2A:903:C:H2'	1:2A:904:C:C6	2.39	0.58
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.86	0.58
11:2P:39:LYS:HB2	11:2P:45:LEU:HG	1.85	0.58
26:14:57:GLU:HB3	26:14:58:ARG:HA	1.85	0.58
1:1A:1071:G:C4	1:1A:1180:C:H1'	2.38	0.58
1:2A:2317:C:N4	1:2A:2318:G:O6	2.36	0.58
3:2D:101:GLU:OE2	3:2D:103:ARG:NH1	2.35	0.58
3:2D:3:VAL:HG13	3:2D:17:THR:HB	1.86	0.58
1:1A:810:G:OP1	60:1A:5161:HOH:O	2.17	0.58
1:2A:1007:C:N3	1:2A:1022:G:O6	17.01	0.58
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.39	0.58
1:1A:1834:A:H4'	3:1D:259:THR:HG23	1.85	0.58
24:22:9:GLN:HE22	24:22:56:GLN:HB3	1.69	0.58
11:2P:60:MET:HA	30:28:13:ARG:NH1	2.19	0.58
1:2A:2469:A:H3'	1:2A:2470:G:H8	1.69	0.58
14:2S:92:TYR:HB3	14:2S:98:VAL:HG21	1.85	0.58
5:1F:61:GLY:O	60:1F:407:HOH:O	2.17	0.58
1:2A:108:U:H2'	1:2A:109:G:H8	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2151:G:H2'	1:2A:2152:G:H8	1.68	0.58
1:2A:247:G:H4'	1:2A:386:G:C5	2.39	0.58
1:1A:1232:G:H5''	17:1V:81:TYR:CE1	2.38	0.57
11:1P:94:GLU:OE2	11:1P:124:LYS:NZ	2.37	0.57
19:2X:48:LYS:HZ3	24:22:30:ARG:HH22	1.50	0.57
1:2A:2183:C:H2'	1:2A:2184:G:H8	1.69	0.57
1:2A:76:C:H42	1:2A:93:G:H1	27.10	0.57
7:2H:17:VAL:HG13	7:2H:26:VAL:HG22	1.85	0.57
12:1Q:110:THR:HG23	12:1Q:113:GLN:HB2	1.86	0.57
1:2A:1448:G:N7	60:2A:4812:HOH:O	2.33	0.57
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.39	0.57
31:29:10:ILE:HD11	31:29:34:GLN:HE21	1.68	0.57
1:2A:2141:G:H2'	1:2A:2142:C:O4'	2.04	0.57
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.69	0.57
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.04	0.57
1:1A:701:A:N7	60:1A:4756:HOH:O	2.33	0.57
4:1E:7:VAL:HG12	4:1E:27:LEU:HB3	1.86	0.57
30:28:28:GLY:O	30:28:36:LYS:NZ	2.27	0.57
1:2A:2031:A:N3	1:2A:2455:G:O2'	2.32	0.57
2:2B:50:G:OP1	14:2S:63:THR:N	2.36	0.57
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.38	0.57
20:2Y:28:LYS:HG3	20:2Y:40:GLU:HG2	1.85	0.57
1:1A:1037:C:H2'	1:1A:1038:C:C6	2.90	0.57
1:1A:2457:G:OP1	5:1F:74:ARG:NH2	2.36	0.57
1:1A:1829:U:H5'	3:1D:259:THR:CG2	2.34	0.57
22:20:11:ARG:O	22:20:14:ARG:NH2	2.36	0.57
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.86	0.57
1:2A:1839:G:C8	1:2A:1927:A:H1'	2.40	0.57
1:2A:397:G:N7	60:2A:4631:HOH:O	2.32	0.57
1:2A:2318:G:H21	14:2S:3:ARG:CD	2.17	0.57
27:15:16:ARG:HG3	27:15:17:ASP:N	2.19	0.57
1:2A:2129:C:N3	1:2A:2159:G:N2	2.46	0.57
7:2H:159:GLU:HG2	7:2H:169:VAL:HG11	1.87	0.57
1:1A:1071:G:O2'	60:1A:4871:HOH:O	2.09	0.57
60:1A:6276:HOH:O	3:1D:14:ARG:HG3	2.04	0.57
17:1V:76:LYS:HB2	17:1V:81:TYR:HB3	1.86	0.57
1:2A:1021:A:N6	1:2A:1141:U:H3	2.00	0.57
1:2A:1857:G:O2'	1:2A:1885:A:N6	2.35	0.57
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.04	0.57
11:2P:79:ARG:O	11:2P:111:ARG:N	2.33	0.57
14:2S:67:ARG:HG2	14:2S:71:ARG:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:1A:6427:HOH:O	28:16:19:ARG:HD2	2.04	0.57
1:1A:1211:U:H2'	1:1A:1212:C:C6	2.39	0.57
1:1A:2699:U:OP2	60:1A:4849:HOH:O	2.17	0.57
1:2A:212:G:H2'	1:2A:213:A:O4'	2.05	0.57
1:2A:2269:A:OP1	60:2A:4307:HOH:O	2.18	0.57
1:2A:296:C:O3'	20:2Y:95:LYS:NZ	2.38	0.57
21:1Z:126:VAL:HG13	21:1Z:161:VAL:HG23	1.85	0.57
1:2A:1769:G:O2'	1:2A:1958:C:OP1	2.20	0.57
1:2A:276:A:H5''	1:2A:277:C:H5'	1.85	0.57
1:1A:2442:A:H2'	1:1A:2442:A:N3	2.20	0.56
9:1N:67:LEU:HD12	9:1N:87:LEU:HD22	1.86	0.56
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.87	0.56
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.31	0.56
1:2A:2376:A:N3	14:2S:106:ARG:NH2	2.51	0.56
9:1N:67:LEU:O	9:1N:88:GLU:HG3	2.06	0.56
11:2P:63:PRO:HG2	30:28:25:MET:HB2	1.87	0.56
1:1A:1346:U:H4'	1:1A:1347:A:H5''	1.87	0.56
1:2A:740:U:H2'	1:2A:741:G:C8	2.40	0.56
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.38	0.56
2:2B:57:A:N3	6:2G:29:TRP:HB3	2.20	0.56
16:2U:50:ARG:HH12	17:2V:72:VAL:HA	1.71	0.56
1:1A:2155:G:O2'	1:1A:2178:G:N2	2.38	0.56
1:1A:2897:U:H2'	1:1A:2898:C:C6	2.40	0.56
1:1A:673:G:H2'	1:1A:674:G:C8	2.96	0.56
1:1A:346:A:OP1	5:1F:168:ARG:HD2	2.05	0.56
1:1A:641:G:OP1	5:1F:40:GLN:HG2	2.05	0.56
11:1P:106:LEU:HD13	11:1P:112:LEU:HG	1.86	0.56
1:2A:577:G:O2'	1:2A:1254:A:OP1	2.23	0.56
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.40	0.56
1:2A:1530:C:HO2'	1:2A:1531:C:P	2.29	0.56
1:1A:1108:G:P	1:1A:1116:A:H1'	2.46	0.56
1:1A:2008:A:OP2	60:1A:5695:HOH:O	2.17	0.56
1:2A:1798:U:H5'	3:2D:259:THR:CG2	2.31	0.56
7:2H:99:VAL:N	7:2H:102:ALA:O	2.38	0.56
1:1A:1133:G:H2'	1:1A:1135:G:C8	2.41	0.56
1:1A:2647:C:O2'	4:1E:80:GLU:OE2	2.21	0.56
13:1R:67:LEU:HD13	13:1R:76:VAL:HG21	1.86	0.56
17:1V:40:LEU:HB2	17:1V:46:VAL:HG13	1.87	0.56
6:2G:102:PHE:HZ	6:2G:157:ILE:HD13	1.71	0.56
1:1A:1221:G:H1'	1:1A:1222:A:H5''	1.88	0.56
21:1Z:154:ASP:OD1	21:1Z:154:ASP:N	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.86	0.56
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.40	0.56
1:2A:2820:A:O2'	1:2A:2821:A:OP1	2.20	0.56
6:2G:75:LYS:HA	6:2G:84:LYS:HD2	1.88	0.56
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.38	0.56
24:12:23:LYS:O	24:12:27:GLU:HG3	2.06	0.56
1:1A:1699:A:OP1	13:1R:8:ARG:NH1	2.37	0.56
1:1A:1000:C:OP1	12:1Q:87:LYS:HE3	2.06	0.56
1:2A:2127:G:N1	1:2A:2161:C:N4	2.53	0.56
1:2A:271(H):G:H2'	1:2A:271(I):G:C8	2.40	0.56
1:2A:884:C:N3	1:2A:893:C:O2'	2.35	0.56
1:2A:887:A:H4'	1:2A:888:C:C5	2.40	0.56
26:24:9:LEU:HD23	26:24:27:THR:HG23	1.88	0.56
1:2A:987:G:H1	1:2A:1218:C:N4	45.90	0.56
12:2Q:141:GLN:NE2	21:2Z:74:VAL:O	2.37	0.56
20:2Y:94:LYS:NZ	60:2Y:601:HOH:O	2.38	0.56
29:27:34:ARG:NE	29:27:39:ARG:HG2	2.20	0.56
1:2A:2630:G:H2'	1:2A:2631:G:C8	2.40	0.56
1:2A:500:G:N1	1:2A:503:A:OP2	2.38	0.56
6:2G:41:GLN:HE21	6:2G:153:ARG:HB3	1.70	0.56
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.88	0.55
21:1Z:138:GLU:H	21:1Z:156:LYS:NZ	2.04	0.55
28:26:10:LEU:HD13	28:26:19:ARG:HD3	1.88	0.55
6:2G:36:LYS:HD3	6:2G:95:ARG:NH1	2.21	0.55
14:2S:67:ARG:O	14:2S:71:ARG:HG3	2.05	0.55
1:2A:2316:C:O2'	6:2G:128:ARG:NH2	2.38	0.55
1:2A:236:C:H2'	1:2A:237:C:H6	1.70	0.55
2:2B:75:G:H22	21:2Z:73:GLN:NE2	2.04	0.55
26:14:63:TYR:N	26:14:64:GLY:HA2	2.21	0.55
1:1A:611:U:H2'	1:1A:612:C:C6	2.41	0.55
3:1D:2:ALA:N	3:1D:200:ASP:OD2	2.39	0.55
3:2D:127:VAL:HA	3:2D:193:VAL:HG23	1.88	0.55
3:2D:232:PRO:O	60:2D:404:HOH:O	2.18	0.55
13:2R:100:LEU:HD11	13:2R:113:LEU:HD23	1.89	0.55
1:2A:2882:A:OP1	13:2R:96:ARG:NE	2.39	0.55
15:2T:16:ARG:NH2	15:2T:18:ASP:OD2	2.39	0.55
1:1A:1109:G:N2	1:1A:1122:C:O2'	2.39	0.55
1:1A:1233:U:H4'	17:1V:79:VAL:HG22	1.88	0.55
6:2G:131:TYR:HE2	6:2G:133:LEU:HD23	1.72	0.55
23:11:50:ARG:HD2	23:11:57:GLU:OE2	2.07	0.55
1:1A:2157:A:H5'	1:1A:2182:G:H4'	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:1F:125:LEU:HD12	5:1F:194:MET:HB2	1.87	0.55
6:1G:72:ARG:NH1	6:1G:87:PRO:HG3	2.21	0.55
10:2O:17:ARG:HH21	10:2O:47:ILE:HG21	1.71	0.55
21:2Z:72:ARG:NH2	21:2Z:97:GLU:O	2.38	0.55
28:16:6:ARG:NH1	28:16:26:ASN:HB2	2.22	0.55
1:1A:1111:U:H5''	1:1A:1112:U:OP2	2.06	0.55
7:1H:3:ARG:HH11	7:1H:4:ILE:H	1.54	0.55
1:2A:1865:G:N2	1:2A:1877:A:OP2	2.39	0.55
1:2A:403:U:H4'	1:2A:404:C:H5'	1.88	0.55
1:2A:482:A:H1'	1:2A:498:G:N2	2.22	0.55
9:2N:12:ARG:NH2	9:2N:50:ASP:OD2	2.39	0.55
1:1A:1108:G:OP1	1:1A:1116:A:O2'	2.23	0.55
1:1A:2227:G:H8	1:1A:2228:G:N7	2.04	0.55
1:2A:1412:A:H2'	1:2A:1413:G:C8	2.42	0.55
3:2D:171:ASP:O	3:2D:187:GLY:N	2.37	0.55
1:1A:1108:G:H1	1:1A:1123:A:N6	2.03	0.55
18:1W:68:ARG:HH11	18:1W:111:HIS:HA	1.71	0.55
1:2A:863:A:H2'	1:2A:864:G:C8	2.41	0.55
1:1A:1827:U:H2'	1:1A:1828:C:C6	2.41	0.55
14:1S:39:ILE:HB	14:1S:49:VAL:HG13	1.89	0.55
1:2A:93:G:H2'	1:2A:94:C:C6	2.42	0.55
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.36	0.55
10:2O:63:VAL:HG11	10:2O:85:VAL:HG23	1.89	0.55
1:1A:1633:A:H2'	1:1A:1634:C:C6	2.41	0.55
1:1A:843:C:H2'	1:1A:844:C:C6	2.42	0.55
1:2A:1041:C:H1'	1:2A:1115:G:N2	2.22	0.55
1:2A:1580:A:H3'	1:2A:1581:G:H8	1.72	0.55
1:2A:668:G:H5'	1:2A:669:G:OP2	2.07	0.55
8:1I:3:VAL:HG12	8:1I:38:LEU:HA	1.88	0.54
26:24:40:HIS:HB3	26:24:43:TYR:HB2	1.89	0.54
1:2A:34:C:H2'	1:2A:35:G:H8	4.32	0.54
1:2A:586:A:N1	1:2A:809:G:O2'	2.31	0.54
3:2D:103:ARG:HG3	3:2D:103:ARG:HH11	1.71	0.54
1:1A:85:C:H4'	1:1A:102:U:H1'	1.89	0.54
6:1G:38:VAL:HG22	6:1G:93:THR:HG23	1.87	0.54
9:2N:35:ARG:HD3	9:2N:37:LYS:HD2	1.88	0.54
1:1A:2784:C:H2'	1:1A:2785:C:H6	1.72	0.54
1:1A:294:C:N3	1:1A:390:G:N2	2.44	0.54
1:2A:1423:G:OP1	1:2A:1492:G:O2'	2.26	0.54
1:2A:1762:A:N1	60:2A:4405:HOH:O	2.34	0.54
5:2F:184:TYR:CZ	5:2F:188:ARG:HD2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:60:ARG:NH2	29:27:47:ARG:HH12	2.05	0.54
1:1A:602:G:H2'	1:1A:603:C:C6	2.43	0.54
8:1I:93:THR:H	8:1I:96:ASP:HB2	1.73	0.54
25:23:8:LEU:HG	25:23:31:LEU:HD23	1.90	0.54
27:25:56:LYS:NZ	27:25:58:LEU:O	2.39	0.54
1:2A:2785:C:OP1	4:2E:41:LYS:NZ	2.28	0.54
1:2A:2815:C:H2'	1:2A:2816:C:H6	1.72	0.54
1:2A:955:C:OP1	12:2Q:87:LYS:HE3	2.07	0.54
6:2G:11:TYR:O	6:2G:16:ARG:HG2	2.06	0.54
1:1A:2148:A:N3	1:1A:2149:G:H1'	2.23	0.54
1:2A:652(D):C:H42	1:2A:652(U):G:H1	1.54	0.54
2:2B:28:C:H2'	2:2B:29:A:O4'	2.07	0.54
7:2H:20:ALA:HB3	7:2H:23:ARG:HG3	1.90	0.54
1:1A:2603:C:H2'	1:1A:2604:G:C8	2.41	0.54
1:1A:2880:C:H2'	1:1A:2881:C:O4'	2.07	0.54
1:1A:525:G:N7	60:1A:5331:HOH:O	2.33	0.54
14:1S:64:GLU:HB3	26:14:59:PHE:CE2	85.87	0.54
22:20:32:ARG:H	22:20:35:ASN:ND2	2.06	0.54
1:1A:1091:A:OP1	1:1A:1091:A:H4'	2.07	0.54
1:1A:1466:U:O2'	1:1A:1467:G:OP1	2.21	0.54
1:1A:2801:C:OP1	4:1E:61:ARG:NH2	2.41	0.54
3:2D:8:PRO:HB3	3:2D:14:ARG:HD2	1.89	0.54
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.90	0.54
9:2N:20:GLY:HA2	9:2N:61:ARG:HG3	1.88	0.54
1:2A:637:A:H2'	11:2P:117:GLU:OE2	2.08	0.54
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.41	0.54
21:2Z:50:GLN:OE1	21:2Z:50:GLN:N	2.41	0.54
1:1A:2348:A:H61	22:10:43:THR:CG2	2.19	0.54
1:1A:1131:A:HO2'	1:1A:1150:C:HO2'	1.53	0.54
1:1A:123:G:H21	29:17:48:LYS:HG2	1.72	0.54
1:1A:1289:G:O3'	11:1P:7:ARG:NH2	2.41	0.54
1:1A:2159:C:H2'	1:1A:2160:C:C6	2.43	0.54
26:24:60:GLN:O	26:24:62:ARG:N	2.40	0.54
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.90	0.54
15:2T:49:VAL:HG12	15:2T:63:VAL:HG22	1.90	0.54
17:2V:62:LEU:CD1	17:2V:95:LEU:HB2	2.38	0.54
1:1A:1695:C:OP1	60:1A:5101:HOH:O	2.17	0.54
4:1E:59:VAL:HG21	4:1E:74:PRO:HB3	1.89	0.54
10:1O:64:ARG:HB2	10:1O:79:PHE:CG	2.43	0.54
11:1P:91:PHE:O	11:1P:121:LYS:NZ	2.36	0.54
1:2A:2142:C:H2'	1:2A:2143:C:O4'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2474:C:H5''	1:2A:2475:C:OP2	2.08	0.54
4:2E:72:VAL:HG12	4:2E:73:GLU:O	2.07	0.54
7:2H:3:ARG:HH22	7:2H:65:HIS:HB3	1.72	0.54
1:1A:231:G:C8	30:18:5:LYS:HG2	2.43	0.54
1:1A:1700:G:H3'	13:1R:2:ARG:HD3	1.89	0.54
1:2A:728:G:H4'	3:2D:13:ARG:HE	1.73	0.54
1:2A:72:U:OP1	60:2A:4855:HOH:O	2.19	0.54
1:1A:1137:G:C6	1:1A:1147:U:C2	2.96	0.53
1:1A:2367:C:H1'	22:10:39:ARG:HH21	1.73	0.53
6:1G:131:TYR:HB3	6:1G:159:VAL:HG13	1.90	0.53
15:1T:24:PRO:HA	15:1T:49:VAL:HG23	1.89	0.53
1:2A:1448:G:H4'	1:2A:1542:A:OP1	2.08	0.53
1:2A:2430:A:OP2	60:2A:4409:HOH:O	2.17	0.53
20:2Y:13:VAL:HG12	20:2Y:74:PRO:HA	1.88	0.53
1:1A:1462:G:O2'	1:1A:1463:C:OP2	2.24	0.53
1:1A:2071:G:N7	60:1A:5009:HOH:O	2.33	0.53
1:2A:2134:A:N3	1:2A:2134:A:H2'	2.23	0.53
2:2B:14:U:O2	2:2B:108:U:H4'	2.07	0.53
1:1A:1105:G:H2'	1:1A:1106:U:C5	2.43	0.53
1:1A:1552:C:H2'	1:1A:1553:A:C8	2.41	0.53
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.21	0.53
1:2A:1152:C:H2'	1:2A:1153:C:H6	1.72	0.53
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	1.89	0.53
1:1A:1775:C:H5'	1:1A:1776:G:OP2	2.08	0.53
1:1A:2642:G:H2'	1:1A:2643:G:C8	2.43	0.53
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.41	0.53
1:1A:551:A:O2'	1:1A:2065:C:O2	2.26	0.53
1:1A:302:A:H2'	1:1A:303:C:C6	2.43	0.53
1:1A:927:G:H2'	1:1A:928:G:C8	2.40	0.53
6:1G:150:ASP:OD1	6:1G:150:ASP:N	2.41	0.53
15:1T:49:VAL:HG12	15:1T:63:VAL:HG22	1.90	0.53
1:2A:320:A:OP2	5:2F:137:LYS:NZ	2.29	0.53
1:2A:568:U:H5'	1:2A:945:A:N1	2.23	0.53
4:2E:11:MET:HG2	4:2E:24:THR:HB	1.90	0.53
1:1A:2193:A:O2'	1:1A:2194:U:H5''	2.09	0.53
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.42	0.53
1:2A:1006:C:H2'	1:2A:1007:C:C6	2.81	0.53
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.07	0.53
20:2Y:30:VAL:HG22	20:2Y:37:VAL:HG12	1.90	0.53
1:1A:1961:5MU:OP1	1:1A:2616:U:O2'	2.27	0.53
1:1A:2011:G:O6	60:1A:5950:HOH:O	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:4:TYR:CE2	16:1U:100:VAL:HG11	2.43	0.53
21:1Z:163:LEU:HD23	21:1Z:167:PRO:HG3	1.91	0.53
23:21:56:GLN:HE21	23:21:87:PRO:HG3	1.74	0.53
1:2A:2148:G:H2'	1:2A:2149:G:C8	2.44	0.53
1:2A:2497:A:H5''	60:2A:4025:HOH:O	2.09	0.53
7:2H:24:VAL:HG22	7:2H:35:VAL:HB	1.91	0.53
14:2S:27:SER:HA	14:2S:88:ASP:HB3	1.91	0.53
1:1A:1101:G:H1	1:1A:1150:C:N4	2.04	0.53
1:1A:1898:A:H2'	1:1A:1899:A:C8	2.43	0.53
1:1A:2812:A:H1'	1:1A:2904:U:H1'	1.90	0.53
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.33	0.53
1:2A:796:C:H2'	1:2A:797:C:C6	2.44	0.53
1:2A:884:C:H3'	1:2A:885:C:C6	2.44	0.53
5:2F:13:SER:HB3	5:2F:127:GLU:HG3	1.90	0.53
12:2Q:38:GLU:HG3	12:2Q:127:ILE:HG22	1.90	0.53
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.89	0.53
1:2A:857:C:H4'	22:20:23:VAL:HG21	1.91	0.53
1:2A:2019:A:N7	27:25:9:LYS:HE2	2.24	0.53
1:2A:2184:G:H2'	1:2A:2185:C:C6	2.43	0.53
1:2A:2468:G:C2	1:2A:2481:G:N3	2.77	0.53
7:2H:98:LEU:HB2	7:2H:125:VAL:HG22	1.90	0.53
1:1A:904:C:H4'	22:10:23:VAL:HG21	1.89	0.53
26:14:33:VAL:HG12	26:14:35:VAL:H	1.74	0.53
20:1Y:87:LYS:HB3	20:1Y:95:LYS:HD2	1.90	0.53
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.09	0.53
6:2G:41:GLN:HG3	6:2G:154:GLY:O	2.09	0.53
2:2B:31:C:H4'	6:2G:29:TRP:HZ2	1.74	0.53
12:2Q:17:LEU:HB3	12:2Q:39:PRO:HB2	1.90	0.53
1:1A:1201:A:OP1	16:1U:55:ARG:HD2	2.10	0.52
1:1A:1338:U:H2'	1:1A:1339:C:C6	2.44	0.52
1:1A:167:G:H2'	1:1A:168:G:C8	3.11	0.52
1:1A:1915:C:OP1	60:1A:5837:HOH:O	2.19	0.52
1:1A:2250:G:H2'	1:1A:2250:G:N3	2.23	0.52
1:1A:2759:U:OP1	7:1H:85:LYS:NZ	2.32	0.52
1:1A:342:C:O2	1:1A:347:G:N2	7.86	0.52
1:1A:1040:C:OP1	16:1U:53:ARG:NH2	2.42	0.52
1:2A:11:G:C2'	1:2A:12:U:H5'	2.39	0.52
1:2A:144:C:H2'	1:2A:145:G:H8	1.74	0.52
3:2D:169:GLU:HG2	3:2D:174:ILE:HD11	1.90	0.52
6:2G:5:VAL:H	6:2G:8:LYS:HE2	1.74	0.52
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2175:G:H2'	1:1A:2176:G:H8	1.73	0.52
1:1A:2044:U:O2'	1:1A:2629:C:H5'	2.10	0.52
9:1N:70:LYS:HD3	9:1N:87:LEU:HD12	1.91	0.52
19:1X:35:THR:HG22	19:1X:38:GLU:HB2	1.91	0.52
25:23:52:HIS:CD2	25:23:53:LEU:HG	2.45	0.52
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.09	0.52
1:2A:236:C:H2'	1:2A:237:C:C6	2.44	0.52
1:2A:455:C:N3	1:2A:472:A:H2'	2.24	0.52
2:2B:4:C:H42	2:2B:117:G:H1	1.56	0.52
1:1A:2147:G:N1	1:1A:2194:U:OP1	2.20	0.52
1:1A:964:A:N3	2:1B:80:U:O2'	2.35	0.52
1:1A:831:A:N6	3:1D:229:VAL:HG11	2.24	0.52
1:2A:2151:G:H2'	1:2A:2152:G:C8	2.44	0.52
4:2E:9:VAL:HG22	4:2E:25:VAL:HB	1.91	0.52
1:1A:2661:U:H2'	1:1A:2662:U:C6	2.44	0.52
60:1A:4906:HOH:O	11:1P:39:LYS:HE3	2.09	0.52
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.25	0.52
1:2A:2303:G:O2'	6:2G:132:ASN:HB2	2.09	0.52
1:2A:817:C:N3	1:2A:1529:G:N1	115.23	0.52
7:2H:33:LEU:HD11	7:2H:136:ILE:HG22	1.90	0.52
2:2B:7:G:N2	14:2S:38:GLN:HE22	1.99	0.52
1:1A:1320:A:N3	1:1A:1343:C:H1'	2.24	0.52
1:1A:1425:A:H4'	1:1A:1426:G:OP2	2.09	0.52
1:1A:1823:G:O2'	1:1A:1861:C:OP1	2.25	0.52
1:1A:941:U:O2'	1:1A:942:A:OP1	2.23	0.52
1:2A:1345:C:OP2	60:2A:4866:HOH:O	2.19	0.52
1:2A:1899:G:N3	1:2A:1899:G:H2'	2.24	0.52
1:2A:2128:C:N3	1:2A:2160:G:O6	2.43	0.52
1:2A:928:G:H8	1:2A:928:G:O5'	1.92	0.52
11:2P:38:GLN:O	11:2P:39:LYS:HB3	2.08	0.52
21:2Z:73:GLN:O	21:2Z:87:ASP:N	2.34	0.52
26:14:61:ARG:HG3	26:14:62:ARG:N	2.24	0.52
1:1A:2429:C:OP1	11:1P:65:ARG:NH2	2.43	0.52
1:1A:1613:A:OP1	3:1D:211:ARG:NH1	2.43	0.52
19:2X:94:GLY:H	19:2X:95:LEU:HA	1.74	0.52
26:14:28:LYS:HE2	26:14:31:ILE:HD11	1.91	0.52
1:1A:123:G:N2	29:17:48:LYS:HG2	2.24	0.52
1:1A:1882:U:H2'	1:1A:1883:C:O4'	2.08	0.52
1:1A:18:C:O2'	1:1A:577:U:OP1	2.21	0.52
4:1E:111:ARG:HD2	4:1E:160:TYR:CD2	2.45	0.52
8:1I:5:LEU:HD11	8:1I:19:VAL:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:1Y:6:HIS:HE1	20:1Y:72:VAL:O	1.93	0.52
1:2A:1431:U:H2'	1:2A:1432:C:C6	2.44	0.52
1:2A:2144:U:O2'	1:2A:2147:G:O6	2.23	0.52
1:2A:674:G:H2'	1:2A:675:A:H8	5.04	0.52
4:2E:1:MET:HE3	4:2E:199:ARG:HD2	1.92	0.52
21:2Z:141:VAL:HG13	21:2Z:144:LEU:HB3	1.92	0.52
2:2B:75:G:N2	21:2Z:87:ASP:OD1	2.37	0.52
1:1A:2227:G:H3'	1:1A:2228:G:N7	2.24	0.52
1:2A:1231:G:H2'	1:2A:1232:G:C8	2.45	0.52
1:2A:1805:U:O2	3:2D:50:THR:HB	2.10	0.52
8:2I:110:ASP:N	8:2I:130:TYR:OH	2.35	0.52
14:2S:35:ILE:HG12	14:2S:101:LEU:HD12	1.90	0.52
1:1A:1115:A:H1'	1:1A:1142:A:H4'	1.90	0.52
10:1O:20:MET:HE3	10:1O:44:LYS:HE3	1.91	0.52
1:2A:2319:G:N2	14:2S:3:ARG:HD2	2.25	0.52
1:2A:728:G:C5'	3:2D:13:ARG:HH21	2.22	0.52
1:1A:2264:G:OP2	60:1A:5857:HOH:O	2.19	0.52
1:1A:2373:A:OP1	30:18:27:THR:OG1	2.19	0.52
1:1A:2699:U:H2'	1:1A:2700:U:O4'	2.09	0.52
1:2A:1489:U:HO2'	1:2A:1490:A:H8	1.58	0.52
1:2A:184:C:H2'	1:2A:185:U:C6	2.45	0.52
1:2A:859:G:N2	1:2A:917:A:OP2	2.44	0.52
2:2B:30:C:H2'	2:2B:31:C:H5'	1.91	0.52
6:2G:173:LEU:O	6:2G:178:PHE:N	2.37	0.52
1:1A:1239:A:H62	1:1A:1299:A:N6	21.01	0.51
1:1A:1246:C:H42	1:1A:1291:G:H1	3.65	0.51
1:1A:704:U:H2'	1:1A:705:C:C6	2.45	0.51
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.25	0.51
1:1A:1001:G:H5''	12:1Q:77:LYS:HD2	1.92	0.51
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.43	0.51
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.45	0.51
1:2A:2176:A:H2'	1:2A:2177:C:C6	2.45	0.51
1:2A:2314:C:H2'	1:2A:2315:G:C8	2.44	0.51
1:2A:2483:C:N3	12:2Q:124:LYS:NZ	2.55	0.51
2:2B:20:C:H42	2:2B:63:G:H1	1.59	0.51
2:2B:87:G:N2	2:2B:90:A:OP2	2.36	0.51
3:2D:20:ASP:N	3:2D:20:ASP:OD1	2.35	0.51
26:14:44:THR:O	26:14:46:GLN:N	2.43	0.51
1:1A:553:A:O2'	1:1A:554:A:H5'	2.10	0.51
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.92	0.51
1:2A:996:A:H1'	17:2V:9:GLY:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:12:7:ARG:O	24:12:11:GLU:HG3	2.11	0.51
1:1A:1141:A:C8	1:1A:1142:A:C8	2.98	0.51
2:1B:25:A:OP2	60:1B:3134:HOH:O	2.19	0.51
12:1Q:16:ARG:HG3	12:1Q:18:LYS:HG3	1.93	0.51
19:1X:57:LEU:HA	60:1X:3101:HOH:O	2.11	0.51
22:20:63:VAL:HG21	22:20:83:PRO:HG3	1.91	0.51
1:2A:2127:G:N2	1:2A:2161:C:N3	2.58	0.51
1:2A:77:C:OP1	24:22:59:ARG:HD3	2.10	0.51
1:2A:852:G:H2'	1:2A:853:G:H8	1.75	0.51
15:2T:36:GLU:O	15:2T:39:ARG:HG2	2.11	0.51
1:1A:2128:G:H1	1:1A:2205:C:N4	2.09	0.51
1:1A:776:G:C6	3:1D:208:LYS:HB2	2.46	0.51
1:1A:831:A:C6	3:1D:229:VAL:HG11	2.45	0.51
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.46	0.51
6:2G:106:LEU:O	6:2G:111:LEU:HD12	2.10	0.51
11:2P:84:ASN:OD1	11:2P:117:GLU:HB2	2.10	0.51
1:2A:1019:U:H3	1:2A:1142(A):A:N6	2.07	0.51
1:2A:1349:A:OP1	60:2A:4475:HOH:O	2.19	0.51
1:2A:1364:G:P	23:21:3:LYS:HG3	2.51	0.51
1:2A:1853:A:N1	1:2A:2087:G:H1'	2.25	0.51
1:2A:271(K):U:H4'	1:2A:271(L):U:OP2	2.09	0.51
2:2B:24:G:O4'	2:2B:26:A:N6	2.35	0.51
6:2G:3:LEU:HD12	6:2G:8:LYS:NZ	2.25	0.51
28:16:10:LEU:HD13	28:16:19:ARG:HD3	1.91	0.51
5:1F:187:VAL:HG12	11:1P:3:LEU:HD12	1.92	0.51
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.46	0.51
1:2A:265:A:C8	1:2A:266:G:H1'	2.45	0.51
2:2B:24:G:N7	2:2B:56:G:H2'	2.25	0.51
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.91	0.51
1:1A:1121:C:H2'	1:1A:1122:C:H5'	1.92	0.51
1:1A:1898:A:H2'	1:1A:1899:A:H8	1.76	0.51
1:1A:2801:C:O2'	1:1A:2819:A:N3	2.37	0.51
9:1N:21:LYS:NZ	9:1N:140:VAL:OXT	2.24	0.51
1:2A:643:A:N1	1:2A:2369:A:O2'	2.39	0.51
1:2A:646:A:H2'	1:2A:647:G:O4'	2.11	0.51
1:2A:892:G:H3'	1:2A:893:C:H5''	1.93	0.51
8:1I:27:ARG:HD3	23:11:71:TYR:CE2	2.45	0.51
1:1A:183:G:OP2	60:1A:4833:HOH:O	2.19	0.51
10:1O:4:PRO:O	10:1O:5:GLN:HB2	2.10	0.51
1:2A:1442:G:N3	1:2A:1442:G:H2'	2.87	0.51
1:2A:2815:C:H2'	1:2A:2816:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2G:103:LEU:HA	6:2G:106:LEU:HB3	1.93	0.51
6:2G:170:ARG:HH12	6:2G:174:GLU:CD	2.13	0.51
1:2A:208:C:H2'	1:2A:209:C:C6	2.46	0.51
1:1A:906:G:O2'	1:1A:962:G:O6	2.22	0.51
8:1I:76:THR:HG22	8:1I:141:LYS:HE2	1.93	0.51
20:1Y:7:VAL:HG21	20:1Y:72:VAL:HG12	1.92	0.51
1:2A:1477:A:H2'	1:2A:1478:G:O4'	2.11	0.51
1:2A:1264:G:H2'	1:2A:2014:A:N6	2.26	0.51
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.92	0.51
6:2G:173:LEU:HB3	6:2G:178:PHE:CG	2.46	0.51
1:1A:1004:A:H5''	1:1A:1024:G:H1	27.67	0.50
1:1A:1085:G:H1	1:1A:1162:C:N4	2.07	0.50
1:1A:2053:A:N3	1:1A:2467:G:O2'	2.40	0.50
1:1A:2153:G:H5'	1:1A:2155:G:C8	2.46	0.50
3:1D:9:TYR:CZ	3:1D:13:ARG:HG2	2.45	0.50
7:1H:20:ALA:HB3	7:1H:23:ARG:HB2	1.92	0.50
1:2A:2431:U:OP1	60:2A:4148:HOH:O	2.19	0.50
1:2A:2820:A:OP2	13:2R:2:ARG:NH2	2.44	0.50
1:2A:893:C:H2'	1:2A:894:C:C5	2.46	0.50
21:2Z:77:ASP:N	21:2Z:82:ARG:O	2.34	0.50
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.91	0.50
1:1A:1410:G:OP2	23:11:3:LYS:HG3	2.12	0.50
1:1A:2163:G:C6	1:1A:2164:C:C2	3.00	0.50
15:1T:112:ARG:HG3	15:1T:115:ARG:NH2	2.26	0.50
1:1A:2041:A:O4'	16:1U:34:LYS:HE3	2.11	0.50
29:27:34:ARG:HG3	29:27:34:ARG:NH1	2.27	0.50
1:2A:1607:C:H4'	1:2A:1608:A:O5'	2.11	0.50
1:2A:2185:C:H2'	1:2A:2186:G:O4'	2.11	0.50
1:2A:2318:G:H21	14:2S:3:ARG:NE	2.09	0.50
1:2A:637:A:H5''	11:2P:117:GLU:HG2	1.94	0.50
7:2H:24:VAL:HG13	7:2H:37:VAL:HG21	1.94	0.50
1:1A:964:A:H5''	2:1B:98:G:O2'	2.11	0.50
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.47	0.50
1:2A:1270:C:H5''	1:2A:1271:G:O5'	2.11	0.50
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.46	0.50
1:2A:2357:U:OP1	22:20:20:ARG:NE	2.35	0.50
1:2A:2705:A:OP2	60:2A:4355:HOH:O	2.19	0.50
1:2A:731:C:H5''	60:2A:4876:HOH:O	2.11	0.50
5:2F:150:GLY:HA2	5:2F:172:TRP:CE3	2.46	0.50
10:2O:10:VAL:HG21	10:2O:16:ALA:HB3	1.93	0.50
1:2A:1335:U:OP1	19:2X:65:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:236:G:H4'	1:1A:413:G:C5	2.47	0.50
1:2A:1116:C:H2'	1:2A:1117:G:H5''	4.86	0.50
3:2D:206:LEU:O	3:2D:211:ARG:HD3	2.12	0.50
4:2E:50:GLY:HA3	4:2E:75:VAL:HG11	1.94	0.50
6:2G:110:ALA:HB1	6:2G:140:ILE:HG22	1.93	0.50
10:2O:24:VAL:HG12	10:2O:33:ALA:HB2	1.93	0.50
1:1A:928:G:H3'	1:1A:929:G:H8	1.76	0.50
5:1F:150:GLY:HA2	5:1F:172:TRP:CE3	2.47	0.50
14:1S:19:LYS:HE2	14:1S:25:ARG:CZ	2.41	0.50
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.46	0.50
1:2A:1920:4OC:O5'	1:2A:1920:4OC:H6	2.11	0.50
1:2A:2145:C:O2'	1:2A:2147:G:N7	2.44	0.50
1:2A:2167:U:H3'	1:2A:2168:G:H21	1.77	0.50
1:2A:746:A:H2'	1:2A:2612:C:H5''	1.93	0.50
1:2A:557:U:H2'	1:2A:558:G:H8	1.75	0.50
1:2A:981:A:OP1	60:2A:4304:HOH:O	2.19	0.50
5:2F:53:THR:HG22	5:2F:56:GLU:HG3	1.93	0.50
1:2A:2749:A:H1'	7:2H:63:SER:HB3	1.93	0.50
8:2I:102:SER:O	8:2I:106:GLY:N	2.40	0.50
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.93	0.50
1:1A:2143:G:H2'	1:1A:2144:U:C6	2.47	0.50
1:1A:599:U:H2'	1:1A:600:G:C8	2.46	0.50
9:1N:30:ILE:HG22	9:1N:34:LEU:HD22	1.92	0.50
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.11	0.50
1:2A:120:U:H5''	1:2A:122:G:OP2	2.12	0.50
1:2A:2342:C:O2'	1:2A:2374:C:OP1	2.29	0.50
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.26	0.50
1:2A:947:G:H2'	1:2A:948:G:C8	2.47	0.50
11:2P:106:LEU:HD13	11:2P:112:LEU:HG	1.93	0.50
2:2B:7:G:H5'	14:2S:29:PHE:CE2	2.46	0.50
1:2A:2319:G:H22	14:2S:3:ARG:HD2	1.76	0.50
27:15:40:LYS:NZ	27:15:44:THR:O	2.38	0.50
1:1A:1874:C:H5'	3:1D:253:GLN:OE1	2.11	0.50
1:1A:1814:A:H5'	1:1A:2620:G:H4'	1.94	0.50
2:1B:41:U:H5	6:1G:70:VAL:H	1.59	0.50
4:1E:12:THR:HG22	4:1E:13:ARG:H	1.77	0.50
6:1G:28:VAL:O	6:1G:31:VAL:HG13	2.11	0.50
8:1I:101:LEU:HG	8:1I:107:VAL:HG13	1.93	0.50
15:1T:60:THR:HG22	15:1T:77:PRO:HA	1.93	0.50
19:1X:31:HIS:NE2	60:1X:3103:HOH:O	2.35	0.50
1:2A:1153:C:H2'	1:2A:1154:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1218:C:N4	1:2A:1231:G:H1	2.08	0.50
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.92	0.50
1:2A:2823:A:OP1	4:2E:159:HIS:NE2	2.45	0.50
1:2A:817:C:O2'	1:2A:839:U:H5''	2.11	0.50
1:2A:821:A:H2'	1:2A:946:G:H5''	1.93	0.50
4:2E:73:GLU:HG2	4:2E:74:PRO:HD2	1.94	0.50
1:2A:2315:G:H1'	6:2G:126:ASP:OD2	2.11	0.50
21:2Z:23:LYS:HD3	21:2Z:40:ASP:HA	1.93	0.50
1:1A:1452:U:H2'	1:1A:1453:C:H6	1.76	0.50
1:1A:2376:C:H2'	1:1A:2377:G:O4'	2.12	0.50
1:1A:2420:U:H2'	1:1A:2421:G:C8	2.47	0.50
1:1A:922:G:H2'	1:1A:923:C:O4'	2.11	0.50
27:25:52:TYR:HB3	27:25:57:VAL:HG21	1.94	0.50
1:2A:1459:G:OP2	60:2A:5251:HOH:O	2.19	0.50
1:2A:71:A:H5''	1:2A:73:A:C8	2.47	0.50
1:2A:863:A:H2'	1:2A:864:G:H8	1.77	0.50
3:2D:176:ARG:O	3:2D:176:ARG:HG3	2.11	0.50
6:2G:120:LEU:HD12	6:2G:178:PHE:HB3	1.93	0.50
1:1A:2141:A:O2'	1:1A:2142:G:H5''	2.12	0.50
1:1A:2251:G:OP2	60:1A:5809:HOH:O	2.20	0.50
1:1A:268:G:H4'	23:11:81:LYS:HG2	1.93	0.50
1:2A:833:U:H2'	1:2A:834:C:C6	2.91	0.50
2:2B:33:G:H5'	6:2G:2:PRO:HD3	1.94	0.50
12:2Q:65:PHE:HB2	12:2Q:105:GLU:HB2	1.93	0.50
1:1A:2661:U:H2'	1:1A:2662:U:H6	1.77	0.49
3:1D:206:LEU:O	3:1D:211:ARG:HD3	2.12	0.49
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	1.93	0.49
1:2A:1530:C:H1'	1:2A:1531:C:OP1	2.12	0.49
1:1A:1546:G:H2'	1:1A:1547:C:C6	2.47	0.49
26:24:40:HIS:CE1	26:24:42:PHE:HB3	2.48	0.49
26:24:48:ARG:HG3	26:24:51:ASP:O	2.12	0.49
1:2A:2025:C:H2'	1:2A:2026:C:C6	2.47	0.49
6:2G:106:LEU:O	6:2G:110:ALA:HB3	2.13	0.49
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.12	0.49
1:1A:2185:C:OP1	1:1A:2187:G:N2	2.45	0.49
1:1A:929:G:H1	1:1A:940:C:N4	2.01	0.49
20:1Y:98:VAL:HG12	20:1Y:105:ALA:HA	1.94	0.49
1:2A:1882:C:H5''	23:21:26:ARG:HH21	1.77	0.49
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.47	0.49
12:2Q:12:GLN:NE2	12:2Q:72:LYS:HG3	2.27	0.49
1:1A:1821:C:H5''	1:1A:1822:A:OP1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1847:G:O2'	1:1A:1848:G:OP2	2.29	0.49
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.93	0.49
14:1S:34:HIS:O	14:1S:97:ARG:NH2	2.45	0.49
18:1W:71:VAL:HA	18:1W:107:LEU:HD12	1.93	0.49
1:2A:2683:C:OP1	15:2T:53:ARG:NH2	2.42	0.49
1:2A:32:C:N4	1:2A:33:U:O4	2.46	0.49
1:2A:34:C:H2'	1:2A:35:G:C8	5.13	0.49
5:2F:133:ASN:N	5:2F:138:GLU:OE1	2.46	0.49
6:2G:103:LEU:HD23	6:2G:106:LEU:HD23	1.93	0.49
6:2G:3:LEU:HD22	26:24:25:TYR:CZ	2.46	0.49
7:2H:11:VAL:HG21	7:2H:50:VAL:HG23	1.94	0.49
8:2I:5:LEU:HD11	8:2I:19:VAL:HG22	1.93	0.49
12:2Q:37:LEU:HD21	12:2Q:130:LYS:HE2	1.94	0.49
19:2X:4:ALA:HB1	19:2X:42:ALA:HA	1.94	0.49
1:2A:2490:G:H8	1:2A:2490:G:OP2	1.96	0.49
1:2A:2641:G:H5''	9:2N:76:SER:HB3	1.94	0.49
10:2O:86:ILE:HG22	10:2O:94:ARG:HD2	1.95	0.49
12:2Q:12:GLN:HE21	12:2Q:72:LYS:HG3	1.76	0.49
1:1A:1466:U:HO2'	1:1A:1467:G:P	2.34	0.49
1:1A:1495:G:H4'	1:1A:1589:A:OP1	2.12	0.49
1:1A:2262:G:OP1	12:1Q:85:LYS:NZ	2.45	0.49
1:1A:2339:A:H2'	1:1A:2340:A:C8	2.47	0.49
1:1A:2476:C:H1'	60:1A:5819:HOH:O	2.11	0.49
1:1A:2576:A:C2	1:1A:2659:U:H4'	2.47	0.49
1:1A:64:C:H5'	19:1X:71:GLY:HA3	1.94	0.49
10:1O:64:ARG:HB2	10:1O:79:PHE:CD2	2.47	0.49
18:1W:67:ASP:N	18:1W:67:ASP:OD1	2.45	0.49
27:25:6:VAL:HG12	60:25:5001:HOH:O	2.13	0.49
1:2A:456:C:H4'	60:2A:5139:HOH:O	2.11	0.49
2:2B:32:C:H42	2:2B:50:G:H1	1.59	0.49
6:2G:136:ARG:HA	6:2G:154:GLY:HA3	1.93	0.49
1:1A:1639:G:H2'	1:1A:1640:G:C8	2.48	0.49
1:1A:1809:U:H2'	1:1A:1815:A:N6	2.27	0.49
1:1A:2255:U:H2'	1:1A:2256:U:C6	2.48	0.49
1:1A:2588:G:H1'	60:1A:4548:HOH:O	2.11	0.49
1:1A:2897:U:H2'	1:1A:2898:C:H6	1.78	0.49
1:1A:510:C:H2'	1:1A:511:C:C6	2.48	0.49
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.45	0.49
7:1H:88:LEU:HD23	7:1H:130:ARG:HG2	1.94	0.49
15:1T:127:ALA:C	15:1T:129:ARG:H	2.16	0.49
1:2A:1021:A:H3'	1:2A:1021:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:82:G:N1	1:2A:103:A:OP2	2.37	0.49
1:2A:1155:A:H5''	16:2U:55:ARG:NH1	2.25	0.49
1:2A:2121:G:H1	1:2A:2177:C:H42	1.59	0.49
1:2A:2893:G:H5''	1:2A:2894:G:O4'	2.12	0.49
4:2E:2:LYS:HB2	4:2E:95:ILE:HD12	1.95	0.49
1:1A:1106:U:N3	1:1A:1108:G:O2'	2.43	0.49
26:24:53:GLU:HG2	26:24:54:GLY:H	1.77	0.49
26:24:7:PRO:HB2	26:24:27:THR:HG21	1.95	0.49
1:2A:127:A:H5''	1:2A:128:C:C6	2.47	0.49
1:2A:1360:A:OP1	1:2A:1360:A:H8	4.96	0.49
1:2A:141:A:C8	1:2A:1408:C:O2'	2.65	0.49
1:2A:2785:C:O2'	4:2E:66:HIS:ND1	2.43	0.49
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.78	0.49
9:2N:38:HIS:CE1	9:2N:39:ARG:HG3	2.48	0.49
1:2A:1224:C:O2	17:2V:85:LYS:NZ	2.45	0.49
1:1A:1109:G:O2'	1:1A:1122:C:N4	2.46	0.49
1:1A:1128:U:C4	1:1A:1132:A:N1	2.74	0.49
1:1A:1676:G:H2'	1:1A:1677:C:C6	2.48	0.49
1:1A:2642:G:H2'	1:1A:2643:G:H8	1.78	0.49
6:1G:146:TYR:O	6:1G:149:VAL:HG12	2.13	0.49
21:1Z:153:SER:HB3	21:1Z:167:PRO:HB3	1.95	0.49
1:2A:1263:U:H2'	1:2A:1264:G:C8	2.47	0.49
1:2A:2171:A:N3	1:2A:2172:U:N3	2.61	0.49
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.48	0.49
1:2A:2882:A:H5'	13:2R:96:ARG:HG3	1.95	0.49
1:2A:588:U:H2'	1:2A:589:C:C6	2.48	0.49
3:2D:148:GLU:HB2	3:2D:151:LYS:HD2	1.94	0.49
4:2E:52:LEU:O	4:2E:76:ARG:N	2.28	0.49
4:2E:7:VAL:HG12	4:2E:27:LEU:HB3	1.95	0.49
10:2O:68:GLU:HB3	10:2O:78:ARG:HB2	1.95	0.49
1:1A:1288:A:N3	1:1A:1352:C:O2'	95.78	0.49
1:2A:1019:U:H2'	1:2A:1020:A:H8	1.77	0.49
8:2I:122:GLU:O	8:2I:126:TYR:OH	2.28	0.49
9:2N:67:LEU:O	9:2N:88:GLU:HG3	2.13	0.49
12:2Q:118:LEU:HD12	12:2Q:131:ILE:HG23	1.95	0.49
21:2Z:92:SER:O	21:2Z:130:PRO:HG3	2.12	0.49
1:2A:1235:G:C6	1:2A:1236:G:N1	2.81	0.48
1:2A:222:A:H5''	1:2A:421:U:OP1	2.13	0.48
1:2A:7:G:H4'	9:2N:13:TRP:CZ2	2.48	0.48
1:1A:1832:G:OP2	3:1D:154:LYS:NZ	2.39	0.48
8:1I:77:LEU:HD21	8:1I:100:ALA:HB1	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:114:ARG:HD3	60:1N:303:HOH:O	2.12	0.48
10:1O:64:ARG:HD2	10:1O:81:ASP:OD1	2.13	0.48
30:28:6:THR:HG22	30:28:63:PRO:HD2	1.94	0.48
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.48	0.48
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.13	0.48
1:2A:601:C:O2	1:2A:605:C:H4'	2.12	0.48
1:2A:816:C:H2'	1:2A:817:C:H6	1.78	0.48
1:2A:855:G:H1	1:2A:922:U:H3	1.59	0.48
6:2G:39:ILE:HG12	6:2G:157:ILE:HG12	1.95	0.48
9:2N:33:LEU:HA	9:2N:38:HIS:HD2	1.77	0.48
1:1A:1112:U:H2'	1:1A:1114:G:OP2	2.13	0.48
1:1A:2153:G:H5''	1:1A:2154:U:H3'	1.94	0.48
5:1F:24:LEU:HD23	5:1F:115:ALA:HA	1.95	0.48
12:1Q:111:GLU:O	12:1Q:115:MET:HG2	2.13	0.48
1:2A:1912:A:OP1	60:2A:4443:HOH:O	2.19	0.48
1:2A:531:C:OP1	1:2A:561:G:N2	2.47	0.48
5:2F:20:LEU:HD23	5:2F:22:ALA:HB2	1.95	0.48
21:2Z:33:LEU:HD11	21:2Z:90:VAL:HG21	1.96	0.48
1:1A:1817:A:H1'	1:1A:1960:A:N6	2.28	0.48
1:1A:2298:A:H4'	1:1A:2299:A:O4'	2.13	0.48
1:1A:2849:G:H5'	13:1R:46:GLY:HA2	1.94	0.48
4:1E:47:VAL:HG11	4:1E:86:PRO:HD2	1.94	0.48
1:2A:1021:A:H3'	1:2A:1021:A:C8	2.48	0.48
1:2A:1580:A:H3'	1:2A:1581:G:C8	2.48	0.48
1:2A:250:G:C6	1:2A:251:A:C6	3.02	0.48
1:1A:1688:A:H2'	1:1A:1689:G:O4'	2.12	0.48
1:1A:174:U:H4'	1:1A:207:A:H4'	1.96	0.48
1:1A:1921:G:H2'	1:1A:1921:G:N3	2.27	0.48
2:1B:48:A:H4'	14:1S:95:HIS:HD2	1.77	0.48
1:2A:1292:U:H2'	1:2A:1293:C:C6	2.48	0.48
1:2A:557:U:H2'	1:2A:558:G:C8	2.49	0.48
1:2A:855:G:C6	1:2A:856:C:N4	2.82	0.48
4:2E:111:ARG:HD2	4:2E:160:TYR:CD2	2.47	0.48
7:2H:118:PRO:HG2	7:2H:121:ILE:HG13	1.95	0.48
16:2U:76:TYR:CZ	16:2U:80:ILE:HG13	2.49	0.48
1:1A:1793:A:H2'	60:1A:5028:HOH:O	2.14	0.48
1:1A:1857:G:H4'	3:1D:242:ARG:NE	2.27	0.48
1:1A:310:C:H2'	1:1A:311:C:H6	1.79	0.48
16:1U:59:ARG:HD3	60:1U:305:HOH:O	2.13	0.48
1:2A:2117:A:O2'	1:2A:2118:U:H5''	2.14	0.48
1:2A:2137:C:N3	1:2A:2155:G:C6	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:58:A:H2'	2:2B:59:A:O4'	2.14	0.48
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.44	0.48
10:2O:73:ASP:HB2	15:2T:82:LEU:CD1	2.43	0.48
16:2U:113:ALA:O	16:2U:117:GLN:HG2	2.14	0.48
18:2W:71:VAL:HA	18:2W:107:LEU:HD12	1.95	0.48
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.47	0.48
19:2X:57:LEU:HD22	19:2X:78:LYS:HE2	1.95	0.48
20:2Y:38:ILE:HD13	20:2Y:66:PRO:HA	1.96	0.48
21:2Z:138:GLU:H	21:2Z:156:LYS:HE2	1.79	0.48
21:2Z:171:ILE:HD12	21:2Z:172:ALA:H	1.78	0.48
24:12:22:GLU:OE2	24:12:68:ARG:NH2	2.45	0.48
1:1A:976:G:H5'	1:1A:1358:U:O2'	103.21	0.48
1:1A:2255:U:OP1	60:1A:4235:HOH:O	2.20	0.48
1:1A:2304:C:H2'	1:1A:2305:C:H6	1.78	0.48
8:1I:86:THR:HG22	8:1I:122:GLU:OE1	2.13	0.48
1:1A:1785:C:OP1	15:1T:96:ARG:NH1	2.46	0.48
1:2A:2218:U:H1'	23:21:52:ARG:HH12	1.78	0.48
26:24:46:GLN:HE21	26:24:48:ARG:HD3	1.78	0.48
1:2A:1151:G:H4'	16:2U:81:HIS:ND1	2.29	0.48
1:2A:141:A:H8	1:2A:1408:C:HO2'	1.57	0.48
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.77	0.48
1:2A:471:A:H2'	1:2A:472:A:O4'	2.13	0.48
1:2A:652(U):G:H2'	1:2A:652(V):C:O4'	2.14	0.48
1:2A:670:A:H4'	1:2A:671:C:O5'	2.14	0.48
2:2B:11:C:H3'	2:2B:12:C:C6	2.49	0.48
2:2B:55:U:H1'	6:2G:29:TRP:CD1	2.44	0.48
14:2S:34:HIS:O	14:2S:97:ARG:NH2	2.44	0.48
1:1A:2545:A:H2'	1:1A:2546:A:O4'	2.14	0.48
29:27:12:ARG:NH2	29:27:44:PRO:HB3	2.28	0.48
1:2A:1899:G:O2'	1:2A:1900:A:OP2	2.28	0.48
1:2A:251:A:C5	1:2A:252:G:H1'	2.48	0.48
1:2A:2674:G:H2'	1:2A:2675:A:C8	2.49	0.48
1:2A:555:U:O2'	1:2A:556:G:N7	2.43	0.48
1:2A:848:G:C4	1:2A:933:A:H8	2.32	0.48
2:2B:75:G:H1	21:2Z:73:GLN:NE2	2.12	0.48
16:2U:28:ARG:NH1	16:2U:38:THR:OG1	2.41	0.48
2:2B:75:G:H1	21:2Z:73:GLN:HE22	1.60	0.48
1:1A:1099:C:C4	1:1A:1100:A:C8	3.02	0.48
1:1A:768:C:H2'	1:1A:769:A:C8	2.48	0.48
1:1A:890:G:O2'	1:1A:906:G:O6	46.32	0.48
21:1Z:45:ASP:O	21:1Z:49:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1567:A:OP2	3:2D:84:TYR:OH	2.20	0.48
1:2A:1721:G:H8	1:2A:1741:A:H62	1.61	0.48
1:2A:2095:C:H2'	1:2A:2096:U:O4'	2.14	0.48
1:2A:2193:G:H2'	1:2A:2194:G:H8	1.79	0.48
1:2A:2238:G:H5''	60:2A:5271:HOH:O	2.14	0.48
1:2A:392:C:H5''	1:2A:409:C:H5''	1.96	0.48
1:2A:90:U:H1'	1:2A:92:A:C8	2.49	0.48
7:2H:106:THR:HG22	7:2H:112:PRO:HB3	1.95	0.48
21:2Z:55:HIS:HE1	21:2Z:135:GLU:HB2	1.77	0.48
1:1A:1210:G:H2'	1:1A:1211:U:C6	2.49	0.48
1:1A:441:C:H2'	1:1A:442:A:C8	2.49	0.48
3:1D:218:ARG:HB3	3:1D:219:PRO:HD2	1.96	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.62	0.48
19:1X:94:GLY:CA	19:1X:95:LEU:HB2	2.44	0.48
23:21:50:ARG:HD2	23:21:57:GLU:OE2	2.14	0.48
1:2A:1794:U:H2'	1:2A:1795:C:H6	1.79	0.48
1:2A:2152:G:C2	1:2A:2153:G:H1'	2.49	0.48
1:2A:2889:C:H2'	1:2A:2891:G:O4'	2.14	0.48
1:2A:332:A:O2'	1:2A:334:C:OP2	2.26	0.48
1:2A:74:A:H5'	1:2A:75:G:O4'	2.14	0.48
4:2E:111:ARG:HD2	4:2E:160:TYR:CE2	2.49	0.48
10:2O:68:GLU:OE1	10:2O:78:ARG:NH1	2.43	0.48
14:2S:62:LYS:O	14:2S:66:ALA:N	2.44	0.48
1:2A:445:C:OP1	16:2U:2:PRO:HA	2.13	0.48
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.62	0.48
21:2Z:154:ASP:N	21:2Z:154:ASP:OD1	2.37	0.48
1:1A:2180:A:HO2'	1:1A:2181:G:P	2.37	0.47
1:1A:909:G:H2'	1:1A:910:A:O4'	2.14	0.47
2:1B:88:C:H2'	2:1B:89:G:O4'	2.14	0.47
3:1D:20:ASP:OD1	3:1D:20:ASP:N	2.40	0.47
6:1G:7:LEU:HD21	6:1G:176:LEU:HD22	1.96	0.47
1:2A:2165:G:H2'	1:2A:2166:G:O4'	2.13	0.47
1:2A:2192:G:H5'	1:2A:2193:G:OP2	2.14	0.47
2:2B:68:C:H2'	2:2B:69:G:H8	1.78	0.47
7:2H:73:ALA:O	7:2H:76:VAL:HG22	2.14	0.47
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.44	0.47
1:1A:1154:U:H2'	1:1A:1155:C:O4'	2.14	0.47
5:1F:150:GLY:HA2	5:1F:172:TRP:CD2	2.48	0.47
1:1A:721:G:O2'	5:1F:74:ARG:HD3	2.14	0.47
11:1P:43:GLY:HA3	60:1P:303:HOH:O	2.13	0.47
14:1S:43:GLU:OE2	22:10:49:LYS:NZ	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1X:94:GLY:H	19:1X:95:LEU:HB2	1.79	0.47
1:2A:2529:G:O6	31:29:31:LYS:NZ	2.47	0.47
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.14	0.47
1:2A:1968:G:OP1	60:2A:5052:HOH:O	2.20	0.47
1:2A:2498:C:H3'	60:2A:4650:HOH:O	2.13	0.47
1:2A:2769:C:H2'	1:2A:2770:G:O4'	2.13	0.47
1:2A:473:G:H2'	1:2A:474:G:H8	2.54	0.47
1:2A:75:G:H4'	24:22:55:ARG:NH1	2.29	0.47
5:2F:202:PHE:O	5:2F:206:ILE:HG12	2.13	0.47
1:1A:1305:G:H22	1:1A:1331:G:H1'	40.22	0.47
4:1E:24:THR:HG22	4:1E:186:GLY:O	2.13	0.47
1:2A:1005:C:C2	1:2A:1143:A:C6	3.02	0.47
1:2A:2115:G:H4'	1:2A:2167:U:C4	2.49	0.47
1:2A:492:A:H2'	1:2A:493:G:O4'	2.14	0.47
1:1A:1081:U:H2'	1:1A:1082:G:C8	2.49	0.47
1:1A:968:U:H2'	1:1A:969:C:C6	2.49	0.47
7:1H:4:ILE:O	7:1H:69:ARG:HD2	2.14	0.47
23:21:83:GLU:N	23:21:83:GLU:OE1	2.43	0.47
28:26:40:CYS:O	28:26:44:ARG:N	2.48	0.47
1:2A:1138:G:C6	1:2A:1140:C:H1'	6.36	0.47
1:2A:2144:U:H1'	1:2A:2148:G:H22	1.79	0.47
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.49	0.47
1:2A:602:G:O2'	1:2A:655:A:N6	2.47	0.47
1:2A:872:A:H2'	1:2A:873:G:H8	1.78	0.47
1:2A:921:G:C6	1:2A:922:U:C4	3.02	0.47
1:2A:993:G:H2'	1:2A:993:G:N3	3.20	0.47
1:1A:2159:C:H2'	1:1A:2160:C:H6	1.80	0.47
8:1I:12:LEU:HD23	8:1I:12:LEU:HA	1.72	0.47
1:2A:1152:C:H2'	1:2A:1153:C:C6	2.49	0.47
1:2A:910:A:N1	1:2A:2277:G:H1'	2.30	0.47
2:2B:118:G:C2	2:2B:119:G:H1'	2.50	0.47
5:2F:40:GLN:NE2	5:2F:182:ASN:HB2	2.30	0.47
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	1.97	0.47
12:2Q:12:GLN:HE21	12:2Q:73:PRO:HD2	1.80	0.47
21:2Z:151:HIS:ND1	21:2Z:168:GLU:O	2.47	0.47
1:1A:505:A:N3	1:1A:507:G:H5''	2.28	0.47
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.70	0.47
1:2A:2630:G:H2'	1:2A:2631:G:H8	1.78	0.47
9:2N:25:ARG:O	9:2N:29:LYS:HE2	2.15	0.47
17:2V:4:ILE:HD12	17:2V:39:LEU:HB3	1.97	0.47
1:1A:2126:G:H1	1:1A:2207:C:H42	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2614:A:OP1	60:1A:5843:HOH:O	2.20	0.47
1:1A:662:A:H4'	1:1A:663:G:O5'	2.15	0.47
11:1P:90:ARG:NH1	11:1P:105:LEU:HD11	2.30	0.47
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.96	0.47
1:2A:117:G:C6	1:2A:119:A:C6	3.03	0.47
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.30	0.47
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.49	0.47
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.80	0.47
1:2A:2191:G:H2'	1:2A:2192:G:O4'	2.15	0.47
1:2A:569:U:H5''	60:2A:4285:HOH:O	2.14	0.47
1:2A:528:A:H8	9:2N:114:ARG:NH2	2.12	0.47
1:2A:912:C:P	12:2Q:8:LYS:HZ3	2.37	0.47
20:2Y:87:LYS:HB3	20:2Y:95:LYS:HD3	1.95	0.47
1:1A:2023:A:OP1	13:1R:9:LYS:NZ	2.41	0.47
1:2A:118:A:C8	1:2A:119:A:C8	3.03	0.47
1:2A:1557:C:OP2	1:2A:1558:A:O2'	2.20	0.47
1:2A:1608:A:H1'	1:2A:1610:A:OP2	2.15	0.47
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.49	0.47
1:2A:2504:U:OP2	60:2A:4333:HOH:O	2.20	0.47
1:2A:839:U:H2'	1:2A:840:C:C6	2.50	0.47
2:2B:105:A:H5'	2:2B:106:G:OP2	2.14	0.47
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.14	0.47
5:2F:178:PRO:HB2	5:2F:201:VAL:HG21	1.97	0.47
5:2F:53:THR:HG23	5:2F:55:GLY:N	2.26	0.47
11:2P:60:MET:HA	30:28:13:ARG:HH12	1.80	0.47
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.32	0.47
15:2T:29:ARG:HB3	15:2T:87:ASP:HB2	1.96	0.47
26:14:16:CYS:SG	26:14:17:GLY:N	2.88	0.47
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.97	0.47
1:1A:180:A:H2'	1:1A:181:C:C6	2.50	0.47
1:1A:2569:G:H2'	1:1A:2570:C:C6	2.50	0.47
1:1A:704:U:H2'	1:1A:705:C:H6	1.80	0.47
2:1B:2:C:H2'	2:1B:3:C:C6	2.50	0.47
5:1F:135:LYS:HB2	5:1F:138:GLU:CD	2.35	0.47
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.49	0.47
16:1U:8:VAL:HG23	16:1U:11:ARG:HH21	1.79	0.47
1:2A:1033:U:P	31:29:9:ARG:HH22	2.34	0.47
1:2A:1002:G:C6	1:2A:1003:G:H8	4.21	0.47
1:2A:1300:U:H4'	1:2A:1301:A:C5'	2.45	0.47
12:2Q:16:ARG:HG2	12:2Q:18:LYS:HG3	1.97	0.47
1:2A:1288:U:O4	13:2R:106:GLY:HA3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.14	0.47
1:1A:347:G:C8	5:1F:171:PRO:HG3	2.50	0.47
4:1E:34:VAL:HG22	4:1E:48:GLN:HG2	1.97	0.47
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.50	0.47
1:2A:1371:G:H2'	1:2A:1372:U:H5	1.80	0.47
1:2A:2358:G:N2	60:28:203:HOH:O	2.40	0.47
1:2A:597:U:H2'	1:2A:598:G:C8	2.50	0.47
19:2X:72:LYS:HG2	19:2X:73:ARG:O	2.15	0.47
1:1A:1068:G:OP2	1:1A:1068:G:H8	6.90	0.47
1:1A:1091:A:OP1	1:1A:1092:A:H3'	2.14	0.47
1:1A:1120:G:C2	1:1A:1121:C:H1'	2.50	0.47
1:1A:2124:U:H3	1:1A:2209:G:H1	1.61	0.47
1:1A:2121:U:O4	1:1A:2212:G:O6	2.34	0.47
4:1E:105:THR:OG1	4:1E:199:ARG:NH2	2.48	0.47
8:1I:6:LEU:HD11	8:1I:37:VAL:HG23	1.97	0.47
10:1O:19:ILE:HG22	10:1O:43:VAL:HA	1.96	0.47
17:1V:62:LEU:HD11	17:1V:95:LEU:HB2	1.96	0.47
26:24:16:CYS:HA	26:24:33:VAL:HB	1.96	0.47
1:2A:1115:G:H2'	1:2A:1116:C:O4'	2.15	0.47
1:2A:1169:G:H1	1:2A:1180:C:H42	1.63	0.47
1:2A:2014:A:H4'	18:2W:92:ARG:NH2	2.17	0.47
1:2A:2619:C:OP1	4:2E:152:LYS:NZ	2.45	0.47
7:2H:84:SER:HB3	7:2H:132:ARG:NH1	2.23	0.47
1:2A:2094:G:P	8:2I:22:LYS:HD2	2.54	0.47
12:2Q:111:GLU:OE2	12:2Q:133:ARG:NH2	2.43	0.47
1:1A:1324:A:OP1	13:1R:36:THR:HG23	2.15	0.46
1:1A:1473:A:H4'	1:1A:1474:C:O4'	2.15	0.46
1:1A:2579:G:H2'	1:1A:2580:C:C6	2.51	0.46
1:2A:2298:A:N6	1:2A:2318:G:C8	2.84	0.46
1:2A:229:A:O5'	1:2A:230:U:H5'	2.15	0.46
1:2A:2764:A:H5''	1:2A:2765:A:OP2	2.14	0.46
1:2A:2639:A:C2	1:2A:2778:A:C8	3.03	0.46
1:2A:286:C:H2'	1:2A:287:C:C6	2.50	0.46
1:2A:856:C:O5'	1:2A:856:C:H6	1.98	0.46
2:2B:83:G:H1	2:2B:94:C:N4	2.13	0.46
4:2E:48:GLN:HE21	4:2E:78:LEU:HG	1.79	0.46
6:2G:126:ASP:HB2	6:2G:130:ASN:HB2	1.96	0.46
28:16:40:CYS:HA	28:16:41:PRO:HD3	1.80	0.46
1:1A:2045:G:H4'	1:1A:2629:C:O3'	2.15	0.46
1:1A:572:A:H1'	1:1A:573:G:OP1	2.14	0.46
3:1D:26:LYS:HE2	3:1D:28:GLU:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2432:A:N1	23:21:35:THR:HG22	2.31	0.46
1:2A:817:C:N4	1:2A:1529:G:O6	111.75	0.46
1:2A:882:G:H1	1:2A:894:C:H42	1.63	0.46
1:2A:993:G:O6	1:2A:994:C:N4	2.49	0.46
7:2H:169:VAL:HG12	7:2H:171:LEU:HD23	1.96	0.46
13:2R:18:LEU:HD21	13:2R:22:ARG:CZ	2.45	0.46
1:1A:273:G:O2'	1:1A:274:U:H5''	2.15	0.46
3:1D:8:PRO:HB3	3:1D:14:ARG:CD	2.45	0.46
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.51	0.46
8:1I:109:ILE:HD11	8:1I:130:TYR:CE2	2.51	0.46
8:1I:129:THR:HG22	8:1I:139:GLN:NE2	2.26	0.46
26:24:15:ILE:HB	26:24:32:TYR:HD1	1.80	0.46
1:2A:1035:U:H3	1:2A:1120:G:H1	1.64	0.46
1:2A:1171:G:OP2	1:2A:1171:G:H8	1.98	0.46
15:2T:64:ARG:HG3	15:2T:73:GLU:HG2	1.96	0.46
1:1A:1105:G:H2'	1:1A:1106:U:C6	2.51	0.46
1:1A:1103:A:N6	1:1A:1127:U:H3	2.12	0.46
1:1A:956:A:N1	1:1A:2289:G:H1'	2.31	0.46
1:1A:646:A:OP2	11:1P:108:LYS:NZ	2.43	0.46
1:1A:939:C:H2'	1:1A:940:C:C6	2.50	0.46
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	1.98	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.74	0.46
24:22:38:GLN:O	24:22:41:ILE:HG12	2.14	0.46
1:2A:94(A):G:H2'	1:2A:95:G:O4'	2.15	0.46
5:2F:10:PRO:HB3	5:2F:17:ARG:CZ	2.45	0.46
21:2Z:93:ASP:CB	21:2Z:131:ARG:HH22	2.29	0.46
1:1A:1139:G:H3'	1:1A:1140:U:H5''	1.98	0.46
1:1A:137:G:O2'	1:1A:138:G:H5'	2.16	0.46
1:1A:1995:G:OP2	60:1A:4765:HOH:O	2.21	0.46
1:1A:559:U:H2'	1:1A:560:C:C6	2.50	0.46
1:1A:581:G:OP1	9:1N:111:PRO:HD2	2.16	0.46
1:1A:953:U:O2'	12:1Q:101:ARG:NH2	2.46	0.46
6:1G:82:LEU:HD21	6:1G:88:ILE:HG21	1.98	0.46
8:1I:77:LEU:HB3	8:1I:142:VAL:HG12	1.97	0.46
26:24:53:GLU:HG3	26:24:56:VAL:HG13	1.98	0.46
1:2A:448:U:O4	1:2A:583:G:H1'	2.15	0.46
1:2A:647:G:O5'	1:2A:647:G:H8	1.97	0.46
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.97	0.46
10:2O:26:LYS:NZ	10:2O:37:ASP:OD2	2.40	0.46
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.15	0.46
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1132:A:N3	1:1A:1132:A:H5''	2.30	0.46
1:1A:265:U:H2'	1:1A:266:C:C6	2.50	0.46
1:1A:2859:U:H4'	1:1A:2878:A:C2	2.50	0.46
2:1B:29:A:O2'	2:1B:58:A:N1	2.43	0.46
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.98	0.46
11:1P:138:LEU:HD23	11:1P:145:PRO:HB3	1.98	0.46
20:1Y:13:VAL:HG12	20:1Y:74:PRO:HA	1.98	0.46
20:1Y:6:HIS:CD2	20:1Y:6:HIS:H	2.32	0.46
28:26:34:LEU:H	28:26:51:GLU:HG2	1.80	0.46
1:2A:2370:G:C6	1:2A:2371:G:C6	3.04	0.46
1:2A:395:U:O2'	1:2A:396:G:N7	2.42	0.46
19:2X:8:ILE:O	24:22:36:ARG:NH2	2.46	0.46
21:2Z:105:VAL:O	21:2Z:140:ASP:HA	2.16	0.46
26:14:55:ARG:N	26:14:56:VAL:HA	2.31	0.46
1:1A:166:G:H2'	1:1A:167:G:C8	3.79	0.46
1:1A:1897:C:H2'	1:1A:1898:A:O4'	2.16	0.46
1:1A:928:G:C2	1:1A:929:G:H1'	2.51	0.46
25:23:18:ASP:OD1	25:23:18:ASP:N	2.44	0.46
1:2A:1231:G:H2'	1:2A:1232:G:H8	1.80	0.46
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.51	0.46
1:2A:526:A:O2'	1:2A:2043:C:O2	2.30	0.46
1:2A:2360:A:H2'	1:2A:2361:A:O4'	2.16	0.46
1:2A:2396:G:O2'	60:2A:5236:HOH:O	2.16	0.46
1:2A:286:C:H2'	1:2A:287:C:H6	1.80	0.46
8:2I:123:LEU:HD12	8:2I:123:LEU:HA	1.76	0.46
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.16	0.46
15:2T:19:LEU:HD22	15:2T:86:ILE:HD12	1.96	0.46
1:1A:1464:G:N7	60:1A:4647:HOH:O	2.36	0.46
1:1A:2740:G:O2'	10:1O:70:LYS:NZ	2.45	0.46
12:1Q:30:GLY:HA2	12:1Q:107:ALA:HB2	1.98	0.46
1:2A:1027:A:C6	1:2A:1126:A:C4	3.04	0.46
1:2A:1240:U:OP2	6:2G:115:ARG:HA	150.02	0.46
2:2B:42:C:C4	2:2B:43:C:C4	3.04	0.46
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.81	0.46
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.42	0.46
21:2Z:155:LEU:HB3	21:2Z:157:LEU:HG	1.97	0.46
1:1A:11:G:H2'	1:1A:12:U:H5''	1.96	0.46
1:1A:1405:A:C2	1:1A:1418:U:O4	2.68	0.46
2:1B:91:C:H5'	12:1Q:18:LYS:HA	1.97	0.46
4:1E:97:LYS:HB3	4:1E:97:LYS:HE2	1.65	0.46
6:1G:43:LEU:HD11	6:1G:153:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:128:HIS:NE2	11:1P:148:LEU:HD11	2.30	0.46
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.51	0.46
1:2A:2156:G:H2'	1:2A:2157:G:C4	2.49	0.46
1:2A:2595:G:N7	60:2A:5057:HOH:O	2.35	0.46
1:2A:311:A:C6	1:2A:328:U:C4	3.04	0.46
1:2A:774:A:N3	1:2A:774:A:H2'	2.31	0.46
2:2B:19:G:H2'	2:2B:20:C:O4'	2.15	0.46
3:2D:21:PHE:HB3	3:2D:24:ILE:HD12	1.97	0.46
12:2Q:85:LYS:HG2	22:20:7:LEU:HB2	1.98	0.46
1:2A:2379:G:O2'	14:2S:17:ARG:NH2	2.48	0.46
19:2X:44:GLU:O	19:2X:48:LYS:N	2.49	0.46
20:2Y:20:TYR:CE2	20:2Y:43:ASN:HA	2.51	0.46
1:1A:655:G:OP2	30:18:15:LYS:NZ	2.31	0.46
1:1A:664:U:H2'	1:1A:665:C:C6	2.51	0.46
1:1A:649:C:O2'	1:1A:704:U:OP1	2.32	0.46
8:1I:48:GLU:HB3	8:1I:52:ARG:HH12	1.80	0.46
30:28:8:LYS:HB3	30:28:12:LYS:HE3	1.98	0.46
1:2A:940:G:N3	1:2A:1191:G:H4'	2.31	0.46
1:2A:1784:A:O2'	60:2A:4593:HOH:O	2.21	0.46
1:2A:600:G:O6	60:2A:4478:HOH:O	2.21	0.46
1:2A:628:G:H2'	1:2A:629:G:C8	2.51	0.46
1:2A:944:G:H5''	1:2A:945:A:O5'	2.15	0.46
1:2A:764:A:H5'	3:2D:210:GLY:HA2	1.98	0.46
5:2F:7:TYR:O	5:2F:22:ALA:N	2.49	0.46
12:2Q:36:ALA:HB2	12:2Q:103:MET:SD	2.55	0.46
20:2Y:43:ASN:CG	20:2Y:65:ALA:HB3	2.37	0.46
1:1A:1137:G:C6	1:1A:1138:C:C4	3.04	0.45
1:1A:2205:C:H2'	1:1A:2206:G:C8	2.47	0.45
1:1A:2303:U:H2'	1:1A:2304:C:C6	2.51	0.45
1:1A:2411:G:H1'	60:1A:6427:HOH:O	2.16	0.45
1:1A:2430:A:H2'	1:1A:2431:U:C6	2.50	0.45
1:1A:2473:C:H2'	1:1A:2474:U:C6	2.51	0.45
1:1A:2864:G:H2'	1:1A:2865:C:C6	2.51	0.45
1:1A:667:G:OP1	60:1A:5361:HOH:O	2.21	0.45
29:27:2:LYS:NZ	60:27:203:HOH:O	2.49	0.45
1:2A:1272:A:H3'	1:2A:1273:U:H5''	1.97	0.45
1:2A:1510:G:H2'	1:2A:1511:C:C6	2.52	0.45
1:2A:2315:G:H2'	1:2A:2316:C:H6	1.81	0.45
1:2A:27:G:N2	1:2A:512:G:H1'	2.31	0.45
5:2F:18:ARG:NH1	5:2F:127:GLU:OE2	2.43	0.45
6:2G:51:ARG:HA	6:2G:51:ARG:HD3	1.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:103:ARG:HD3	13:2R:108:GLY:O	2.15	0.45
15:2T:18:ASP:OD1	15:2T:18:ASP:N	2.42	0.45
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.51	0.45
1:1A:602:G:OP1	60:1A:5436:HOH:O	2.21	0.45
1:1A:92:C:H2'	1:1A:93:G:O4'	2.16	0.45
4:1E:105:THR:OG1	4:1E:166:THR:OG1	2.22	0.45
5:1F:165:ARG:HG3	5:1F:168:ARG:NH2	2.31	0.45
1:1A:2331:G:N2	14:1S:3:ARG:HA	2.31	0.45
23:21:23:LYS:HB3	23:21:29:GLY:HA3	1.97	0.45
30:28:23:VAL:CG1	30:28:47:LYS:HD3	2.46	0.45
1:2A:1017:G:O6	1:2A:1146:C:N4	2.49	0.45
1:2A:2135:A:H5'	1:2A:2159:G:O2'	2.16	0.45
1:2A:829:A:C5	1:2A:2248:C:H5'	2.51	0.45
1:2A:263:C:H2'	1:2A:264:C:O4'	2.17	0.45
1:2A:2723:C:OP1	13:2R:3:HIS:ND1	2.25	0.45
1:2A:320:A:H4'	1:2A:322:A:C8	2.51	0.45
1:2A:661:C:H2'	1:2A:662:G:C8	2.52	0.45
10:2O:19:ILE:HG22	10:2O:43:VAL:HA	1.98	0.45
14:2S:11:LYS:HG3	14:2S:91:PRO:HD3	1.97	0.45
19:2X:94:GLY:N	19:2X:95:LEU:HA	2.30	0.45
28:16:13:CYS:SG	28:16:47:THR:HG21	2.57	0.45
1:1A:1006:C:N3	1:1A:1023:G:N2	22.59	0.45
1:1A:1121:C:O2	1:1A:1122:C:H2'	2.16	0.45
1:1A:1935:A:H4'	1:1A:1936:C:H5"	1.98	0.45
1:1A:924:U:H3	1:1A:945:A:H2	1.65	0.45
4:1E:121:ASN:ND2	60:1E:408:HOH:O	2.39	0.45
1:2A:2357:U:P	22:20:20:ARG:HE	2.38	0.45
1:2A:1192:G:O6	60:2A:4615:HOH:O	2.20	0.45
1:2A:511:U:H4'	1:2A:1235:G:H4'	1.96	0.45
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.16	0.45
1:2A:1857:G:C6	1:2A:1858:G:N1	2.85	0.45
1:2A:2377:A:H2'	1:2A:2378:A:C8	2.51	0.45
1:2A:2516:G:C6	1:2A:2517:C:C4	3.05	0.45
1:2A:658:C:H2'	1:2A:659:C:C6	2.52	0.45
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.52	0.45
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.99	0.45
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.16	0.45
1:1A:1281:G:H5"	60:1A:5107:HOH:O	2.16	0.45
1:1A:1549:U:H2'	1:1A:1550:C:C6	2.51	0.45
1:1A:1683:C:H2'	1:1A:1684:A:C8	2.51	0.45
1:1A:1945:U:H2'	1:1A:1946:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2178:G:H8	1:1A:2178:G:OP2	1.99	0.45
1:1A:2143:G:N2	1:1A:2199:C:N3	2.48	0.45
1:1A:1539:C:N4	1:1A:2227:G:O2'	2.47	0.45
2:1B:33:G:C2	2:1B:50:G:C2	3.04	0.45
8:1I:79:ILE:HB	8:1I:144:VAL:HG12	1.99	0.45
25:23:10:LYS:NZ	25:23:15:TYR:OH	2.47	0.45
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.32	0.45
1:2A:2330:G:H21	22:20:42:GLY:N	2.15	0.45
1:2A:2473:U:H2'	1:2A:2473:U:O2	2.15	0.45
1:2A:709:U:H2'	1:2A:710:G:C8	2.52	0.45
1:1A:2796:G:N7	60:1A:5760:HOH:O	2.36	0.45
21:1Z:7:ALA:O	21:1Z:62:PRO:HD3	2.17	0.45
24:22:52:ASP:O	24:22:56:GLN:HG3	2.17	0.45
1:2A:1245:G:OP1	11:2P:13:ASN:ND2	2.36	0.45
1:2A:265:A:H1'	1:2A:266:G:O4'	2.17	0.45
1:2A:660:G:H5'	5:2F:99:TYR:CE1	2.52	0.45
5:2F:28:ILE:HG23	5:2F:112:MET:HE3	1.98	0.45
4:2E:27:LEU:HD22	15:2T:1:MET:HE1	1.99	0.45
1:2A:328:U:H4'	20:2Y:68:HIS:CG	2.51	0.45
1:1A:2108:U:H2'	1:1A:2109:G:H8	1.81	0.45
1:1A:2150:C:N4	1:1A:2182:G:H1	2.14	0.45
1:1A:348:A:N6	1:1A:362:G:O2'	2.50	0.45
5:1F:101:LEU:HD12	5:1F:102:PRO:HD2	1.98	0.45
1:2A:1912:A:C8	1:2A:1918:A:C2	3.05	0.45
2:2B:25:A:H2'	2:2B:26:A:H8	1.82	0.45
1:2A:2562:U:H1'	10:2O:23:ARG:HE	1.81	0.45
19:2X:25:LYS:HA	19:2X:81:VAL:O	2.16	0.45
1:1A:2157:A:H2	1:1A:2158:C:C2	2.35	0.45
1:1A:2880:C:OP1	13:1R:57:ARG:NH1	2.37	0.45
16:1U:58:ARG:HA	16:1U:61:TRP:CE3	2.51	0.45
25:23:10:LYS:HB3	25:23:53:LEU:HA	1.99	0.45
1:2A:1910:G:H2'	1:2A:1911:PSU:H6	1.82	0.45
1:2A:2065:C:H2'	1:2A:2066:C:H6	1.82	0.45
1:2A:2320:A:H2'	1:2A:2320:A:N3	2.32	0.45
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.40	0.45
1:2A:699:A:H2'	1:2A:700:G:O4'	2.17	0.45
1:2A:884:C:H3'	1:2A:885:C:H6	1.82	0.45
3:2D:12:SER:HB3	3:2D:208:LYS:HB3	1.97	0.45
4:2E:24:THR:HG22	4:2E:186:GLY:O	2.17	0.45
7:2H:80:SER:OG	7:2H:81:GLU:OE1	2.33	0.45
1:1A:1405:A:H2	1:1A:1418:U:O4	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1958:A:OP1	1:1A:1959:A:H5'	2.16	0.45
1:1A:2285:A:H2'	1:1A:2286:A:C8	2.51	0.45
1:1A:2803:A:H5'	1:1A:2902:G:H21	1.82	0.45
1:1A:34:C:H5''	1:1A:35:G:OP2	2.17	0.45
5:1F:188:ARG:HA	11:1P:3:LEU:HD11	1.99	0.45
1:1A:1202:A:P	16:1U:55:ARG:HH11	2.38	0.45
20:1Y:92:ASN:HB3	20:1Y:94:LYS:N	2.16	0.45
25:23:46:ASN:O	25:23:50:VAL:HG22	2.17	0.45
26:24:46:GLN:C	26:24:48:ARG:H	2.20	0.45
1:2A:839:U:H1'	1:2A:1191:G:H1'	1.98	0.45
1:2A:1509(B):A:H2'	1:2A:1510:G:C8	2.51	0.45
1:2A:2129:C:H5'	1:2A:2130:U:OP2	2.17	0.45
1:2A:741:G:H2'	1:2A:742:G:O4'	2.70	0.45
4:2E:181:LEU:HA	4:2E:181:LEU:HD12	1.83	0.45
13:2R:67:LEU:CD1	13:2R:76:VAL:HG21	2.47	0.45
19:2X:35:THR:HG22	19:2X:38:GLU:H	1.81	0.45
21:2Z:146:ILE:HG12	21:2Z:174:VAL:HG13	1.98	0.45
1:1A:1093:G:H2'	1:1A:1156:G:N2	2.32	0.45
1:1A:354:A:HO2'	1:1A:355:A:H8	1.63	0.45
3:1D:108:PRO:HB3	3:1D:143:HIS:HE1	1.82	0.45
3:1D:232:PRO:HB3	3:1D:244:ARG:CZ	2.47	0.45
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.52	0.45
9:1N:128:HIS:O	9:1N:131:GLN:NE2	2.50	0.45
1:2A:1374:G:H2'	1:2A:1375:C:C6	2.52	0.45
1:2A:195:A:H5''	1:2A:196:A:O5'	2.16	0.45
1:2A:322:A:C5	1:2A:340:A:C2	3.05	0.45
2:2B:7:G:H1	2:2B:114:C:N4	2.08	0.45
15:2T:16:ARG:HB3	15:2T:18:ASP:OD1	2.17	0.45
1:2A:2019:A:O4'	16:2U:34:LYS:HE3	2.17	0.45
16:2U:52:ARG:HA	16:2U:55:ARG:HE	1.82	0.45
14:1S:20:ARG:NH2	22:10:51:VAL:O	2.45	0.45
1:1A:213:G:H2'	1:1A:214:A:O4'	2.16	0.45
1:1A:597:C:N3	4:1E:145:LYS:NZ	2.65	0.45
15:1T:56:GLY:O	15:1T:59:THR:HG22	2.17	0.45
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.17	0.45
18:1W:68:ARG:NH1	18:1W:111:HIS:HA	2.32	0.45
1:2A:1147:C:H2'	1:2A:1148:A:H8	1.81	0.45
1:2A:1353:A:H2'	1:2A:1354:A:C8	2.52	0.45
1:2A:1449:A:HO2'	1:2A:1529:G:H21	1.64	0.45
1:2A:2162:G:H4'	1:2A:2172:U:C2'	2.45	0.45
1:2A:2261:C:O2'	1:2A:2262:U:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:570:G:H2'	1:2A:2030:A:C5	2.51	0.45
3:2D:218:ARG:HB3	3:2D:219:PRO:HD2	1.99	0.45
3:2D:73:VAL:HG13	3:2D:120:GLY:HA3	1.97	0.45
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.50	0.45
6:2G:131:TYR:CE2	6:2G:133:LEU:HD23	2.51	0.45
1:1A:1846:A:OP2	3:1D:54:ARG:NH2	2.37	0.44
1:1A:2304:C:H2'	1:1A:2305:C:C6	2.52	0.44
1:1A:329:U:H2'	1:1A:330:U:C6	2.53	0.44
1:2A:154(A):C:H42	1:2A:171:G:H1	1.65	0.44
1:2A:2070:G:H2'	1:2A:2071:A:C8	2.51	0.44
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.53	0.44
1:2A:2332:U:H5'	1:2A:2336:A:N6	2.33	0.44
1:2A:61:G:H5'	24:22:50:ILE:HG21	1.99	0.44
1:2A:639:U:H2'	1:2A:640:C:C6	2.52	0.44
1:2A:947:G:N2	1:2A:971:C:C2	2.85	0.44
30:18:42:ARG:HD2	60:18:212:HOH:O	2.17	0.44
1:1A:1550:C:H2'	1:1A:1551:C:H6	1.82	0.44
1:1A:1787:G:H4'	1:1A:1789:G:O4'	2.17	0.44
1:1A:2054:G:H1'	4:1E:145:LYS:HD3	1.99	0.44
1:1A:449:A:H2'	1:1A:450:A:C8	2.53	0.44
6:1G:43:LEU:HB3	6:1G:44:GLY:H	1.55	0.44
1:1A:2764:G:C4	7:1H:2:SER:HA	2.52	0.44
16:1U:104:GLN:NE2	16:1U:105:VAL:HG23	2.32	0.44
1:2A:1286:A:C8	1:2A:1287:A:H4'	8.10	0.44
1:2A:1462:C:H4'	1:2A:2703:C:H5'	2.00	0.44
1:2A:2184:G:O2'	1:2A:2185:C:H5'	2.17	0.44
1:2A:2350:C:H5''	30:28:42:ARG:HD3	1.99	0.44
1:2A:275:G:C2	1:2A:276:A:C4	3.05	0.44
7:2H:103:LEU:HB3	7:2H:115:VAL:HB	1.98	0.44
10:2O:20:MET:HE3	10:2O:44:LYS:HE3	1.99	0.44
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	1.99	0.44
1:1A:116:A:H8	1:1A:116:A:O5'	4.42	0.44
2:1B:12:C:H2'	22:10:73:GLY:HA3	1.99	0.44
21:1Z:1:MET:HA	21:1Z:2:GLU:HA	1.70	0.44
1:2A:1359:A:C2	1:2A:1372:U:O4	2.71	0.44
1:2A:1785:A:OP1	60:2A:4173:HOH:O	2.21	0.44
1:2A:2305:A:H1'	6:2G:136:ARG:HB3	1.98	0.44
1:2A:2853:C:H2'	1:2A:2854:G:H8	1.82	0.44
7:2H:122:THR:O	7:2H:134:SER:OG	2.35	0.44
16:2U:81:HIS:CG	16:2U:117:GLN:HE22	2.35	0.44
20:2Y:56:PRO:C	20:2Y:58:GLY:H	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:297:C:OP1	20:2Y:87:LYS:HG3	2.18	0.44
1:1A:2108:U:H2'	1:1A:2109:G:C8	2.53	0.44
1:1A:2619:G:H2'	1:1A:2620:G:O4'	2.17	0.44
1:1A:2665:U:H2'	1:1A:2666:A:C8	2.53	0.44
5:1F:32:LEU:HD13	5:1F:112:MET:HE1	2.00	0.44
22:20:45:PHE:HE1	22:20:77:ARG:NE	2.14	0.44
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.53	0.44
1:2A:1237:A:OP1	60:2A:4545:HOH:O	2.21	0.44
1:2A:1131:G:O6	1:2A:2040:C:H1'	2.18	0.44
1:2A:2133:G:C2	1:2A:2157:G:C5	3.06	0.44
1:2A:2184:G:H2'	1:2A:2185:C:H6	1.80	0.44
1:2A:911:A:O4'	1:2A:2264:C:H4'	2.17	0.44
1:2A:2470:G:O6	1:2A:2481:G:C2	2.70	0.44
1:2A:2059:A:C8	1:2A:2503:2MA:HM23	2.53	0.44
1:2A:2552:2MU:H6	1:2A:2552:2MU:O5'	2.17	0.44
1:2A:721:C:H2'	1:2A:722:A:C8	2.52	0.44
2:2B:29:A:H2'	2:2B:30:C:C6	2.53	0.44
11:2P:6:LEU:HD23	11:2P:6:LEU:HA	1.81	0.44
15:2T:127:ALA:C	15:2T:129:ARG:H	2.20	0.44
17:2V:31:ALA:O	17:2V:61:VAL:HG12	2.18	0.44
24:12:41:ILE:HG13	24:12:43:GLN:HG3	1.99	0.44
1:1A:1099:C:N3	1:1A:1152:G:N2	2.53	0.44
1:1A:2177:G:N3	1:1A:2177:G:H2'	2.33	0.44
23:21:67:ILE:N	23:21:68:PRO:HD2	2.32	0.44
26:24:57:GLU:CB	26:24:58:ARG:HA	2.48	0.44
1:2A:1037:G:C2	1:2A:1119:C:C2	3.06	0.44
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.81	0.44
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.18	0.44
1:2A:2168:G:C8	1:2A:2170:A:N7	2.85	0.44
1:2A:248:G:C2	1:2A:2431:U:H4'	2.53	0.44
1:2A:7:G:N2	1:2A:2896:C:O2	2.49	0.44
1:2A:336:C:H2'	1:2A:337:C:C6	2.91	0.44
1:2A:441:U:H2'	1:2A:442:G:C8	2.53	0.44
1:2A:973:A:H8	1:2A:973:A:OP1	2.01	0.44
4:2E:101:ARG:HD3	4:2E:170:LEU:C	2.37	0.44
6:2G:131:TYR:HB3	6:2G:159:VAL:HG13	2.00	0.44
6:2G:8:LYS:HE2	6:2G:8:LYS:HB3	1.81	0.44
13:2R:26:LYS:HE2	13:2R:70:LEU:O	2.17	0.44
15:2T:56:GLY:O	15:2T:59:THR:HG22	2.17	0.44
20:2Y:86:ARG:HB2	20:2Y:98:VAL:HG23	1.99	0.44
28:16:34:LEU:H	28:16:51:GLU:HG2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1201:A:P	16:1U:55:ARG:HD2	2.57	0.44
1:1A:1314:A:C2	1:1A:2035:A:C4	3.06	0.44
1:1A:1821:C:H2'	1:1A:1822:A:C5	2.52	0.44
1:1A:2177:G:H3'	1:1A:2178:G:C8	2.52	0.44
1:1A:2073:A:H5'	1:1A:2590:G:O4'	2.18	0.44
10:1O:64:ARG:HD3	10:1O:79:PHE:CD1	2.52	0.44
1:2A:112:U:H5'	24:22:65:ASN:ND2	2.32	0.44
1:2A:1507:A:O2'	1:2A:1508:A:H8	2.01	0.44
6:2G:173:LEU:HB3	6:2G:178:PHE:CD2	2.53	0.44
1:1A:1115:A:H2'	1:1A:1119:A:N7	2.32	0.44
1:1A:2291:G:O6	22:10:14:ARG:HG3	2.18	0.44
1:1A:556:C:H4'	1:1A:557:A:H5''	1.98	0.44
1:1A:895:G:H2'	1:1A:896:A:C8	2.53	0.44
1:1A:937:A:H2'	1:1A:938:G:O4'	2.17	0.44
6:1G:64:THR:HB	6:1G:94:LEU:HD21	1.98	0.44
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.83	0.44
1:1A:326:C:P	20:1Y:73:ARG:HH22	2.41	0.44
26:24:49:PHE:HB3	26:24:50:VAL:H	1.49	0.44
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.52	0.44
1:2A:674:G:H1'	5:2F:74:ARG:HD3	2.00	0.44
6:2G:11:TYR:HB2	6:2G:176:LEU:HD21	1.98	0.44
13:2R:24:GLN:NE2	13:2R:36:THR:HG21	2.32	0.44
1:1A:1411:A:O2'	23:11:11:ARG:NH1	2.51	0.44
1:1A:1513:G:H2'	1:1A:1594:C:H41	1.83	0.44
1:1A:1997:G:H2'	1:1A:1998:U:O4'	2.17	0.44
1:1A:2371:C:H2'	1:1A:2372:A:O4'	2.18	0.44
1:1A:8:A:H2'	1:1A:9:U:C6	2.53	0.44
7:1H:55:PRO:HG2	7:1H:61:HIS:ND1	2.32	0.44
13:1R:103:ARG:HD3	13:1R:108:GLY:O	2.18	0.44
1:2A:1137:G:H2'	1:2A:1138:G:O4'	2.17	0.44
1:2A:2542:A:H4'	1:2A:2543:G:C8	2.53	0.44
1:2A:2849:U:H4'	1:2A:2868:A:C2	2.53	0.44
1:2A:892:G:H3'	1:2A:893:C:C5'	2.47	0.44
2:2B:33:G:N3	2:2B:50:G:N2	2.66	0.44
3:2D:108:PRO:HB3	3:2D:143:HIS:HE1	1.82	0.44
3:2D:133:LEU:HB3	3:2D:173:VAL:HG11	1.99	0.44
4:2E:108:SER:HB3	4:2E:165:VAL:CG2	2.47	0.44
7:2H:45:VAL:HG12	7:2H:50:VAL:HG22	1.99	0.44
20:2Y:52:SER:HB2	20:2Y:53:PRO:HD2	2.00	0.44
18:1W:19:LEU:HB3	27:15:25:LEU:HD11	2.00	0.44
1:1A:1117:G:H1'	1:1A:1135:G:H2'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1634:C:H2'	1:1A:1635:C:H6	1.82	0.44
1:2A:11:G:H2'	1:2A:12:U:H5'	1.99	0.44
1:2A:1664:A:OP1	60:2A:5119:HOH:O	2.21	0.44
1:2A:76:C:N4	1:2A:93:G:H1	26.27	0.44
2:2B:18:G:O2'	2:2B:19:G:H5'	2.18	0.44
5:2F:155:LEU:HB2	5:2F:189:THR:HG21	2.00	0.44
7:2H:103:LEU:HD21	7:2H:105:LEU:HD21	2.00	0.44
7:2H:56:SER:OG	7:2H:57:ASP:N	2.50	0.44
21:2Z:126:VAL:HG13	21:2Z:161:VAL:HG23	2.00	0.44
24:12:32:LEU:HD22	24:12:36:ARG:HH11	1.82	0.43
1:1A:1149:A:H8	1:1A:1149:A:OP2	2.00	0.43
1:1A:2735:G:H2'	1:1A:2736:C:C6	2.53	0.43
1:1A:71:U:H5'	24:12:61:LEU:HD12	1.99	0.43
1:1A:791:G:OP1	4:1E:132:HIS:ND1	2.41	0.43
2:1B:66:A:N6	2:1B:109:C:H5'	2.30	0.43
14:1S:27:SER:HA	14:1S:88:ASP:HB3	2.00	0.43
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.18	0.43
1:2A:2131:G:N7	1:2A:2133:G:C2	2.86	0.43
1:2A:2168:G:H8	1:2A:2170:A:N7	2.16	0.43
1:2A:218:A:C2	1:2A:235:U:H4'	2.52	0.43
1:2A:601:C:O2'	5:2F:104:LYS:NZ	2.49	0.43
2:2B:17:C:H2'	2:2B:18:G:O4'	2.18	0.43
2:2B:24:G:N2	2:2B:27:C:N3	2.59	0.43
5:2F:32:LEU:O	5:2F:36:VAL:HG23	2.18	0.43
11:2P:128:HIS:NE2	11:2P:148:LEU:HD11	2.33	0.43
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.81	0.43
1:1A:166:G:H2'	1:1A:167:G:H8	3.46	0.43
1:1A:2051:G:H2'	1:1A:2053:A:OP1	2.17	0.43
3:1D:145:VAL:HG12	3:1D:146:GLU:O	2.17	0.43
21:1Z:92:SER:O	21:1Z:130:PRO:HG2	2.17	0.43
22:20:38:VAL:HG11	22:20:45:PHE:HD2	1.83	0.43
26:24:60:GLN:O	26:24:62:ARG:HG2	2.18	0.43
1:2A:2010:G:H5''	18:2W:42:ARG:HB2	2.00	0.43
1:2A:2018:G:H2'	1:2A:2019:A:O4'	2.18	0.43
1:2A:2311:A:O2'	1:2A:2312:U:O4'	2.32	0.43
1:2A:2343:C:O3'	1:2A:2373:G:H4'	2.18	0.43
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.52	0.43
1:2A:2745:C:C4	1:2A:2746:U:C4	3.06	0.43
1:2A:2787:C:H2'	1:2A:2788:C:H6	1.84	0.43
1:2A:652(B):A:H61	1:2A:655:A:H1'	1.82	0.43
1:2A:93:G:H2'	1:2A:94:C:H6	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2B:3:C:H2'	2:2B:4:C:C6	2.54	0.43
6:2G:41:GLN:NE2	6:2G:153:ARG:HB3	2.33	0.43
6:2G:70:VAL:HA	6:2G:90:LEU:HD23	1.99	0.43
10:2O:7:TYR:CZ	10:2O:44:LYS:HG3	2.54	0.43
15:2T:105:LEU:HB2	15:2T:110:ILE:HG13	2.00	0.43
15:2T:73:GLU:OE2	15:2T:103:ARG:NE	2.37	0.43
1:1A:1212:C:H2'	1:1A:1213:U:C6	2.54	0.43
1:1A:2190:G:O6	1:1A:2193:A:H5''	2.18	0.43
1:1A:2198:A:H2'	1:1A:2199:C:C6	2.53	0.43
11:1P:121:LYS:O	11:1P:123:LEU:N	2.51	0.43
21:1Z:158:PRO:HA	21:1Z:159:PRO:HD3	1.93	0.43
26:24:12:ALA:CB	26:24:26:SER:HB3	2.49	0.43
26:24:41:PRO:HG3	26:24:49:PHE:CZ	2.53	0.43
1:2A:1171:G:N2	1:2A:1178:C:C4	2.86	0.43
1:2A:118:A:N3	1:2A:178:G:H1'	2.33	0.43
1:2A:1529:G:O6	1:2A:1530:C:N4	2.51	0.43
1:2A:1800:C:OP2	3:2D:183:ARG:NH2	2.51	0.43
1:2A:1945:G:O6	1:2A:1960:A:N6	2.52	0.43
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.53	0.43
1:2A:2065:C:H4'	1:2A:2251:OMG:HM22	2.00	0.43
1:2A:2280:G:O2'	1:2A:2388:A:N1	2.41	0.43
1:2A:2752:C:O5'	1:2A:2752:C:H6	2.02	0.43
1:2A:848:G:C4	1:2A:933:A:C8	3.05	0.43
7:2H:3:ARG:HH12	7:2H:5:GLY:CA	2.30	0.43
7:2H:97:ARG:O	7:2H:103:LEU:HD12	2.18	0.43
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	2.01	0.43
1:1A:1104:G:H1	1:1A:1126:C:N4	2.13	0.43
1:1A:2874:G:OP1	15:1T:119:LYS:HD2	2.19	0.43
1:1A:44:G:H5''	1:1A:45:C:OP1	2.17	0.43
60:1A:5923:HOH:O	9:1N:73:THR:HG21	2.18	0.43
20:1Y:35:TYR:CE2	20:1Y:69:ALA:HB3	2.53	0.43
1:2A:171:G:H2'	1:2A:172:C:C6	2.53	0.43
1:2A:1913:A:H4'	1:2A:1914:C:C5'	2.49	0.43
1:2A:2193:G:H2'	1:2A:2194:G:C8	2.53	0.43
1:2A:990:A:N6	1:2A:1186:G:H1'	2.34	0.43
8:2I:124:GLY:N	8:2I:144:VAL:HG23	2.32	0.43
12:2Q:125:LEU:C	12:2Q:127:ILE:H	2.22	0.43
1:2A:1155:A:OP1	16:2U:55:ARG:HD2	2.19	0.43
16:2U:66:ASN:OD1	16:2U:70:ARG:NE	2.48	0.43
19:2X:55:ASN:O	19:2X:79:ALA:HA	2.18	0.43
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1098:C:H2'	1:1A:1099:C:H6	1.83	0.43
1:1A:1825:U:H2'	1:1A:1826:C:C6	2.54	0.43
1:1A:2137:G:C2	1:1A:2139:A:N7	2.87	0.43
1:1A:2164:C:O2	1:1A:2171:G:N1	2.35	0.43
1:1A:237:G:OP1	60:1A:6419:HOH:O	2.21	0.43
1:1A:2641:A:HO2'	1:1A:2642:G:P	2.40	0.43
11:1P:47:ASP:N	11:1P:47:ASP:OD1	4.18	0.43
23:21:52:ARG:HH21	23:21:57:GLU:HB2	1.83	0.43
1:2A:1002:G:N2	1:2A:1038:C:N3	41.75	0.43
1:2A:1324:G:C2	1:2A:1331:A:C2	3.07	0.43
1:2A:1746:G:C2	1:2A:1747:G:C8	3.06	0.43
1:2A:2489:G:O2'	1:2A:2490:G:H5'	2.19	0.43
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.17	0.43
1:2A:990:A:C6	1:2A:1186:G:H1'	2.54	0.43
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.54	0.43
5:2F:126:VAL:HG21	5:2F:129:PHE:CE1	2.53	0.43
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.99	0.43
7:2H:155:SER:HB3	7:2H:158:HIS:O	2.18	0.43
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.82	0.43
21:2Z:145:GLU:HG3	21:2Z:146:ILE:N	2.33	0.43
23:11:50:ARG:HG2	23:11:59:THR:HG22	2.01	0.43
1:1A:2402:U:P	30:18:35:GLN:HE22	2.42	0.43
6:1G:34:LEU:HD23	6:1G:161:THR:HG22	2.01	0.43
15:1T:109:GLU:O	15:1T:113:LYS:HG2	2.19	0.43
1:2A:108:U:H2'	1:2A:109:G:C8	2.51	0.43
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.17	0.43
1:2A:2059:A:O2'	5:2F:69:HIS:HD2	2.02	0.43
1:2A:208:C:H2'	1:2A:209:C:H6	1.82	0.43
1:2A:2110:G:H3'	1:2A:2111:C:H5'	2.00	0.43
1:2A:2149:G:C6	1:2A:2150:U:C2	3.07	0.43
1:2A:2061:G:H5''	1:2A:2503:2MA:C2	2.49	0.43
1:2A:589:C:H2'	1:2A:590:A:C8	2.54	0.43
1:2A:643:A:C8	28:26:44:ARG:NH1	2.87	0.43
5:2F:37:VAL:O	5:2F:41:LEU:HG	2.18	0.43
27:15:46:CYS:SG	27:15:48:GLU:HB2	2.59	0.43
31:19:32:HIS:O	31:19:34:GLN:HG3	2.18	0.43
1:1A:1566:U:H2'	1:1A:1567:G:O4'	2.18	0.43
1:1A:2314:G:C2	1:1A:2327:G:C2	3.07	0.43
1:1A:1537:G:O2'	3:1D:101:GLU:HB2	2.18	0.43
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.17	0.43
7:1H:24:VAL:HG22	7:1H:35:VAL:HB	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:1H:25:LYS:HG3	7:1H:34:GLU:HG2	2.00	0.43
7:1H:61:HIS:O	7:1H:65:HIS:HB2	2.19	0.43
10:1O:20:MET:CE	10:1O:44:LYS:HE3	2.49	0.43
1:2A:1636:C:H2'	1:2A:1637:A:C8	2.54	0.43
1:2A:2321:G:H2'	1:2A:2321:G:N3	2.34	0.43
1:2A:2629:A:H1'	1:2A:2630:G:H5''	2.01	0.43
1:2A:37:C:H4'	1:2A:451:C:OP1	2.18	0.43
1:2A:874:G:H5'	1:2A:875:G:OP2	2.19	0.43
12:2Q:73:PRO:HA	12:2Q:93:TYR:CD1	2.53	0.43
1:1A:2283:G:OP1	22:10:18:ALA:HB1	2.18	0.43
1:1A:1908:C:O5'	1:1A:1908:C:H6	2.01	0.43
1:1A:2158:C:C2	1:1A:2177:G:N2	2.86	0.43
1:1A:905:U:O2	1:1A:2280:A:H2'	2.18	0.43
5:1F:32:LEU:HD22	5:1F:112:MET:HE3	1.99	0.43
7:1H:58:GLU:O	7:1H:62:LYS:HG3	2.18	0.43
11:1P:55:ARG:NH1	60:1P:315:HOH:O	2.52	0.43
1:2A:923:C:C4'	22:20:29:GLN:HE21	2.31	0.43
1:2A:116:C:H2'	1:2A:117:G:O4'	2.19	0.43
1:2A:1204:A:N6	1:2A:1240:U:H2'	2.33	0.43
1:2A:1665:A:H2'	1:2A:1666:G:O4'	2.18	0.43
1:2A:1799:G:O2'	3:2D:183:ARG:NH1	2.49	0.43
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.19	0.43
1:2A:2516:G:O6	1:2A:2517:C:N4	2.51	0.43
1:2A:932:G:H4'	1:2A:933:A:O5'	2.18	0.43
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	2.01	0.43
1:2A:2094:G:OP1	8:2I:22:LYS:HD2	2.19	0.43
14:2S:5:THR:OG1	14:2S:8:GLU:HG2	2.18	0.43
20:2Y:9:LYS:HA	20:2Y:10:GLY:HA2	1.60	0.43
21:2Z:28:MET:HE1	21:2Z:61:LEU:HD21	2.00	0.43
21:2Z:6:LYS:HE3	21:2Z:8:TYR:HE2	1.83	0.43
29:17:20:ALA:HA	29:17:23:ARG:HH21	1.84	0.43
1:1A:1323:G:H2'	1:1A:1324:A:C8	3.10	0.43
1:1A:2162:C:O2	1:1A:2174:G:N2	2.52	0.43
1:1A:2160:C:C2	1:1A:2176:G:C2	3.06	0.43
1:1A:2315:G:O6	60:1A:5145:HOH:O	2.20	0.43
1:1A:936:C:H2'	1:1A:937:A:O4'	4.20	0.43
24:22:7:ARG:O	24:22:11:GLU:HG3	2.19	0.43
25:23:7:LYS:NZ	25:23:32:GLN:O	2.42	0.43
1:2A:1260:G:C6	1:2A:1261:C:C4	3.06	0.43
1:2A:1496:A:OP2	1:2A:1496:A:H8	2.02	0.43
1:2A:1589:C:H2'	1:2A:1590:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1411:C:N4	1:2A:1591:G:H1	2.14	0.43
1:2A:1776:G:O6	60:2A:4213:HOH:O	2.21	0.43
1:2A:2432:A:C6	1:2A:2433:A:C6	3.07	0.43
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.54	0.43
1:2A:783:A:O2'	1:2A:785:G:OP1	2.30	0.43
1:2A:839:U:H3'	1:2A:840:C:H6	3.16	0.43
7:2H:157:TYR:CE1	7:2H:172:LYS:HG3	2.54	0.43
15:2T:119:LYS:O	15:2T:123:GLN:HG3	2.19	0.43
21:2Z:40:ASP:OD2	21:2Z:43:GLU:HG3	2.18	0.43
1:1A:1132:A:H5'	1:1A:1133:G:OP1	2.19	0.43
1:1A:2802:C:O2'	1:1A:2803:A:H4'	2.18	0.43
1:1A:989:G:O3'	60:1A:4831:HOH:O	2.21	0.43
3:1D:96:HIS:CD2	3:1D:102:LYS:HE2	2.54	0.43
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.37	0.43
20:1Y:20:TYR:HB3	20:1Y:23:ARG:HG3	2.00	0.43
1:2A:752:A:P	29:27:3:ARG:HH22	2.42	0.43
30:28:14:VAL:HG13	30:28:22:VAL:HG13	2.01	0.43
1:2A:1857:G:C6	1:2A:1858:G:C6	3.07	0.43
1:2A:1923:U:H2'	1:2A:1924:C:C6	2.54	0.43
1:2A:2125:G:H1'	1:2A:2173:A:N6	2.34	0.43
1:2A:2447:G:N2	1:2A:2450:A:OP2	2.52	0.43
1:2A:800:A:OP1	1:2A:800:A:H8	2.01	0.43
1:2A:994:C:O2'	1:2A:996:A:OP1	2.23	0.43
2:2B:25:A:H2'	2:2B:26:A:C8	2.54	0.43
2:2B:64:C:H2'	2:2B:65:C:C6	2.54	0.43
6:2G:125:PHE:CE2	6:2G:170:ARG:HD3	2.53	0.43
7:2H:69:ARG:O	7:2H:73:ALA:N	2.30	0.43
8:2I:79:ILE:HA	8:2I:80:PRO:HD2	1.92	0.43
9:2N:35:ARG:HB2	9:2N:37:LYS:HG3	2.00	0.43
1:2A:563:G:H21	16:2U:37:GLU:CD	2.22	0.43
1:1A:1093:G:H2'	1:1A:1156:G:H22	1.84	0.42
1:1A:2121:U:O2	1:1A:2212:G:N2	2.34	0.42
1:1A:2800:C:H1'	4:1E:62:PRO:HG3	2.01	0.42
5:1F:178:PRO:HB2	5:1F:201:VAL:HG21	2.00	0.42
8:1I:116:LEU:HD21	8:1I:119:PRO:HA	1.99	0.42
19:2X:1:MET:H3	24:22:29:LYS:HE3	1.84	0.42
1:2A:999:U:O2'	1:2A:1000:A:H5'	2.19	0.42
1:2A:1278:A:H2'	1:2A:1279:G:C8	2.54	0.42
1:2A:2558:C:H2'	1:2A:2559:C:O4'	2.18	0.42
1:2A:729:G:OP1	3:2D:12:SER:HB2	2.19	0.42
13:2R:38:VAL:HG22	13:2R:112:ALA:HB2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.18	0.42
14:2S:25:ARG:HG2	14:2S:40:ILE:HB	2.01	0.42
10:2O:76:ALA:HB3	15:2T:75:ILE:HB	2.01	0.42
19:2X:60:ARG:HH22	29:27:47:ARG:NH1	2.17	0.42
1:2A:64:A:H2	19:2X:69:TYR:CD2	2.37	0.42
21:2Z:100:VAL:HA	21:2Z:101:PRO:HD3	1.86	0.42
1:1A:1475:G:H2'	1:1A:1476:C:C6	2.54	0.42
2:1B:7:G:N7	60:1B:3119:HOH:O	2.36	0.42
9:1N:67:LEU:HA	9:1N:87:LEU:HD22	2.01	0.42
16:1U:17:ILE:HG23	16:1U:39:LEU:HD12	2.00	0.42
25:23:5:LYS:O	25:23:56:VAL:HA	2.18	0.42
1:2A:1630:G:H2'	1:2A:1631:C:C6	2.54	0.42
1:2A:1131:G:H8	1:2A:2025:C:H4'	1.84	0.42
1:2A:2612:C:OP2	27:25:2:ALA:N	2.52	0.42
1:2A:433:C:O2'	1:2A:434:U:H5'	2.19	0.42
1:2A:878:A:N6	1:2A:899:A:O2'	2.52	0.42
6:2G:179:PRO:HG3	26:24:43:TYR:OH	2.18	0.42
11:2P:38:GLN:HG2	11:2P:45:LEU:H	1.85	0.42
1:2A:1754:C:H5	15:2T:96:ARG:NH2	2.17	0.42
24:12:61:LEU:HA	24:12:61:LEU:HD23	1.76	0.42
26:14:8:LYS:HE3	26:14:10:VAL:CG1	2.49	0.42
26:14:63:TYR:CD1	26:14:63:TYR:N	2.87	0.42
1:1A:1477:U:H2'	1:1A:1478:C:C6	2.55	0.42
1:1A:2145:G:H2'	1:1A:2146:G:C8	2.54	0.42
1:1A:651:U:O4	11:1P:107:LYS:HE2	2.19	0.42
4:1E:37:ARG:HA	4:1E:42:ASP:OD2	2.19	0.42
14:1S:90:GLY:HA3	14:1S:91:PRO:HD2	1.93	0.42
21:1Z:1:MET:HG3	21:1Z:55:HIS:ND1	2.33	0.42
1:2A:1253:A:H4'	60:2A:4847:HOH:O	2.19	0.42
1:2A:1406:U:O2	1:2A:1517:G:N2	33.48	0.42
1:2A:1473:G:C6	1:2A:1474:C:C4	3.07	0.42
9:2N:42:TRP:HA	9:2N:48:MET:HE1	2.00	0.42
14:2S:4:LEU:HA	14:2S:4:LEU:HD23	1.81	0.42
14:2S:80:LEU:HA	14:2S:80:LEU:HD12	1.77	0.42
21:2Z:153:SER:O	21:2Z:155:LEU:N	2.52	0.42
1:1A:125:A:H5''	1:1A:126:C:C6	2.55	0.42
1:1A:1756:U:H2'	1:1A:1757:C:C6	2.54	0.42
1:1A:2227:G:H5''	1:1A:2228:G:C5	2.55	0.42
1:1A:469:A:H1'	1:1A:1246:C:O4'	2.19	0.42
1:1A:722:A:C8	1:1A:851:A:C6	3.07	0.42
1:1A:776:G:OP2	3:1D:13:ARG:NH2	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.39	0.42
5:1F:106:ARG:HG2	5:1F:106:ARG:H	1.50	0.42
21:1Z:123:ASP:N	21:1Z:123:ASP:OD1	2.52	0.42
25:23:6:VAL:HA	25:23:56:VAL:HG22	2.00	0.42
26:24:12:ALA:HB3	26:24:26:SER:HB3	2.00	0.42
1:2A:1328:G:H2'	1:2A:1330:C:C5	2.54	0.42
1:2A:14:A:C6	1:2A:526:A:C2	3.07	0.42
6:2G:107:LEU:HD21	6:2G:178:PHE:CE1	2.54	0.42
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	2.01	0.42
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.53	0.42
21:2Z:9:TYR:OH	21:2Z:63:ASP:OD2	2.23	0.42
23:11:52:ARG:HD3	23:11:56:GLN:O	2.20	0.42
1:1A:1122:C:O2'	1:1A:1123:A:N7	2.52	0.42
1:1A:1124:U:H5'	1:1A:1125:C:OP1	2.20	0.42
1:1A:1633:A:H2'	1:1A:1634:C:H6	1.84	0.42
1:1A:2177:G:H3'	1:1A:2178:G:H8	1.85	0.42
1:1A:2658:C:H2'	1:1A:2659:U:O4'	2.19	0.42
1:1A:284:G:C2	1:1A:285:U:O4	2.72	0.42
1:1A:52:A:H2'	1:1A:53:G:O4'	2.19	0.42
4:1E:14:ILE:HG13	4:1E:21:VAL:HG13	2.01	0.42
11:1P:82:GLY:HA2	11:1P:113:LYS:O	2.19	0.42
1:2A:1371:G:C6	1:2A:1372:U:C4	6.73	0.42
1:2A:1506:C:H2'	1:2A:1507:A:H5'	2.01	0.42
1:2A:2291:U:O2'	1:2A:2374:C:H1'	2.19	0.42
1:2A:478:A:N1	1:2A:500:G:H4'	2.34	0.42
1:2A:732:C:H2'	1:2A:733:G:O4'	2.20	0.42
1:2A:1354:A:O3'	3:2D:38:LYS:HE2	2.20	0.42
4:2E:110:GLY:HA2	4:2E:161:GLY:HA3	2.01	0.42
6:2G:150:ASP:OD1	6:2G:150:ASP:N	2.47	0.42
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.20	0.42
1:1A:1223:C:O5'	1:1A:1223:C:H6	2.02	0.42
1:1A:1550:C:H2'	1:1A:1551:C:C6	2.54	0.42
1:1A:2018:C:H4'	1:1A:2019:G:OP1	2.19	0.42
1:1A:2295:C:H2'	1:1A:2296:C:O4'	2.20	0.42
5:1F:32:LEU:HD22	5:1F:112:MET:CE	2.50	0.42
5:1F:34:TRP:CH2	11:1P:8:PRO:HB3	2.54	0.42
1:1A:2331:G:H22	14:1S:3:ARG:HA	1.85	0.42
21:1Z:17:ALA:HA	21:1Z:20:ARG:NH1	2.34	0.42
23:21:94:LEU:O	23:21:97:LEU:HB2	2.18	0.42
28:26:40:CYS:HA	28:26:41:PRO:HD3	1.92	0.42
1:2A:1683:C:H2'	1:2A:1684:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1987:G:H2'	1:2A:1988:C:H6	1.84	0.42
1:2A:2107:C:H5''	1:2A:2108:C:OP2	2.20	0.42
1:2A:2364:C:H2'	1:2A:2365:G:O4'	2.18	0.42
1:2A:271(D):G:H2'	1:2A:271(E):U:C6	2.55	0.42
1:2A:2801(A):A:H5'	1:2A:2802:G:C8	2.54	0.42
1:2A:585:G:O6	1:2A:756:C:N4	57.29	0.42
1:2A:612:C:C2	1:2A:616:G:N2	2.88	0.42
1:2A:6:A:N3	9:2N:133:GLN:NE2	2.67	0.42
1:2A:778:G:C6	1:2A:779:U:N3	2.88	0.42
5:2F:120:GLU:HG3	5:2F:122:LYS:HG2	2.01	0.42
12:2Q:31:ASP:HA	12:2Q:134:ARG:HH11	1.85	0.42
21:2Z:171:ILE:HD12	21:2Z:172:ALA:N	2.35	0.42
6:1G:5:VAL:HG12	26:14:25:TYR:CE2	2.55	0.42
28:16:14:THR:HG21	28:16:48:VAL:HG13	2.02	0.42
1:1A:1525:G:N2	1:1A:1562:U:C2	2.87	0.42
1:1A:2324:U:OP1	6:1G:73:ALA:HA	2.20	0.42
1:1A:2760:G:O6	1:1A:2768:C:H5''	2.19	0.42
1:1A:27:G:C2	1:1A:537:G:N3	2.87	0.42
7:1H:144:VAL:O	7:1H:148:ILE:HG13	2.19	0.42
1:2A:988:A:H5''	25:23:31:LEU:HD11	2.02	0.42
1:2A:1002:G:C2	1:2A:1003:G:H1'	2.88	0.42
1:2A:1006:C:C2	1:2A:1138:G:N2	2.88	0.42
1:2A:1441:G:O5'	1:2A:1441:G:H8	2.86	0.42
1:2A:2404:C:O3'	11:2P:77:ARG:NH2	2.53	0.42
1:2A:2526:G:H2'	1:2A:2527:C:H6	1.83	0.42
1:2A:2639:A:O3'	9:2N:97:ARG:NH2	2.47	0.42
1:2A:569:U:H1'	1:2A:947:G:O4'	2.20	0.42
1:2A:597:U:H2'	1:2A:598:G:H8	1.85	0.42
1:2A:879:G:C6	1:2A:880:G:C2	3.08	0.42
2:2B:13:A:H4'	2:2B:15:A:C5	2.54	0.42
15:2T:22:PHE:CE1	15:2T:52:ILE:HD11	2.54	0.42
20:2Y:44:ILE:HA	20:2Y:63:LYS:O	2.19	0.42
1:1A:1478:C:H2'	1:1A:1479:U:O4'	2.20	0.42
1:1A:2132:G:OP2	1:1A:2132:G:H2'	2.19	0.42
1:1A:2541:G:H5''	1:1A:2542:A:H5''	2.02	0.42
1:1A:2623:U:H5'	1:1A:2623:U:H6	1.85	0.42
1:1A:342:C:N3	1:1A:347:G:N1	6.83	0.42
1:1A:482:C:O2'	1:1A:483:A:OP2	2.35	0.42
4:1E:48:GLN:NE2	4:1E:78:LEU:HG	2.35	0.42
14:1S:110:LEU:HA	14:1S:110:LEU:HD12	1.72	0.42
19:1X:31:HIS:HA	19:1X:32:PRO:HD3	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:20:48:GLY:HA3	22:20:80:HIS:CE1	2.55	0.42
1:2A:1124:C:H2'	1:2A:1125:G:O4'	2.20	0.42
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.19	0.42
1:2A:2428:G:H5''	1:2A:2429:G:OP1	2.20	0.42
1:2A:255:A:O2'	1:2A:384:U:OP1	2.21	0.42
1:2A:652(B):A:N6	1:2A:655:A:H1'	2.34	0.42
1:2A:854:G:N2	1:2A:924:C:N3	2.68	0.42
1:2A:881:G:H3'	1:2A:882:G:H8	1.84	0.42
1:2A:729:G:C6	3:2D:208:LYS:HB2	2.54	0.42
4:2E:1:MET:O	4:2E:84:PHE:HB2	2.20	0.42
12:2Q:57:HIS:NE2	12:2Q:116:GLU:HB3	2.35	0.42
1:1A:2209:G:C6	1:1A:2210:C:C4	3.07	0.42
1:1A:223:C:H2'	1:1A:224:U:C6	2.55	0.42
1:1A:606:G:N3	1:1A:632:A:N6	53.02	0.42
4:1E:7:VAL:CG1	4:1E:27:LEU:HB3	2.50	0.42
7:1H:3:ARG:HH22	7:1H:65:HIS:HB3	1.85	0.42
1:2A:1120:G:C2	1:2A:1154:G:C2	34.82	0.42
1:2A:1470:G:H5''	1:2A:1471:A:OP1	2.19	0.42
1:2A:1641:A:H2'	1:2A:1642:G:O4'	2.20	0.42
1:2A:2363:C:O2	22:20:39:ARG:NH2	2.53	0.42
1:2A:2709:G:O2'	1:2A:2710:C:H5'	2.19	0.42
1:2A:30:G:H2'	1:2A:31:C:O4'	2.19	0.42
1:2A:861:A:C2	1:2A:917:A:C4	3.07	0.42
2:2B:13:A:H2'	2:2B:70:C:O2'	2.20	0.42
4:2E:108:SER:HB3	4:2E:165:VAL:HG21	2.01	0.42
2:2B:38:C:O4'	14:2S:95:HIS:NE2	2.53	0.42
22:10:82:ARG:HA	22:10:83:PRO:HD3	1.88	0.42
29:17:24:THR:HG22	29:17:26:GLY:H	1.85	0.42
30:18:29:LYS:HE2	30:18:45:GLY:HA2	2.00	0.42
1:1A:1016:C:H2'	1:1A:1017:G:O4'	2.19	0.42
1:1A:1402:G:OP2	60:1A:4902:HOH:O	2.21	0.42
1:1A:207:A:C2	1:1A:224:U:H4'	2.55	0.42
1:1A:2142:G:O2'	1:1A:2143:G:H5'	2.20	0.42
1:1A:2672:A:H2'	1:1A:2673:G:O4'	2.20	0.42
1:1A:698:G:H2'	1:1A:699:C:C6	2.55	0.42
2:1B:74:U:H2'	2:1B:75:G:O4'	2.20	0.42
25:23:7:LYS:N	25:23:55:ARG:O	2.47	0.42
26:24:28:LYS:HA	26:24:29:PRO:HD3	1.79	0.42
1:2A:1042:G:H4'	1:2A:1042:G:OP1	2.19	0.42
1:2A:1579:A:H2'	1:2A:1580:A:C8	2.55	0.42
1:2A:2579:C:H4'	4:2E:134:ILE:HG12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:27:G:O2'	1:2A:28:A:OP2	2.36	0.42
1:2A:607:U:OP1	5:2F:102:PRO:HA	2.20	0.42
1:2A:652(D):C:N4	1:2A:652(U):G:H1	2.17	0.42
1:2A:717:G:H2'	1:2A:718:A:O4'	2.20	0.42
3:2D:275:LYS:HA	3:2D:275:LYS:HD2	1.92	0.42
1:2A:1490:A:O2'	3:2D:99:ASP:OD1	2.38	0.42
6:2G:36:LYS:HD3	6:2G:95:ARG:HH12	1.84	0.42
15:2T:28:VAL:HG13	15:2T:86:ILE:HG23	2.01	0.42
16:2U:103:PRO:O	16:2U:107:ALA:N	2.53	0.42
21:2Z:70:LEU:HA	21:2Z:70:LEU:HD23	1.76	0.42
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	2.02	0.42
28:16:34:LEU:N	28:16:51:GLU:HG2	2.36	0.41
11:1P:59:LEU:HD23	30:18:13:ARG:HH11	1.85	0.41
1:1A:1074:A:N6	1:1A:1171:G:H2'	2.35	0.41
1:1A:1263:C:O2	1:1A:1273:G:N2	18.26	0.41
1:1A:200:A:H2'	1:1A:201:G:O4'	2.20	0.41
1:1A:2116:G:P	8:1I:22:LYS:HD2	2.60	0.41
3:1D:19:ALA:HB3	3:1D:21:PHE:CE1	2.55	0.41
7:1H:90:LYS:HD3	7:1H:159:GLU:HG2	2.01	0.41
20:1Y:43:ASN:HD22	20:1Y:43:ASN:HA	1.60	0.41
23:21:89:GLU:O	23:21:93:GLU:HG2	2.20	0.41
1:2A:2347:C:O2'	28:26:21:TYR:OH	2.33	0.41
29:27:5:TRP:CD1	29:27:7:PRO:HD3	2.55	0.41
1:2A:1287:A:C5	1:2A:1288:U:C4	3.08	0.41
1:2A:1359:A:N1	1:2A:1372:U:C4	2.88	0.41
1:2A:1866:C:H2'	1:2A:1876:A:O4'	2.20	0.41
1:2A:2298:A:N3	1:2A:2321:G:C2	2.88	0.41
1:2A:2319:G:N2	14:2S:3:ARG:HA	2.35	0.41
1:2A:2525:G:N2	1:2A:2539:C:C2	2.88	0.41
1:2A:2507:C:H5''	1:2A:2573:C:C4	2.55	0.41
1:2A:2820:A:C5	13:2R:4:LEU:HD11	2.55	0.41
1:2A:853:G:C2	1:2A:854:G:C4	3.07	0.41
5:2F:29:ASN:O	5:2F:112:MET:HE1	2.20	0.41
8:2I:62:LYS:HE3	8:2I:62:LYS:HB2	1.85	0.41
11:2P:121:LYS:O	11:2P:123:LEU:N	2.53	0.41
17:2V:84:LYS:O	17:2V:85:LYS:HD2	2.19	0.41
25:13:59:VAL:O	25:13:60:GLU:HG2	2.20	0.41
28:16:33:LYS:HA	28:16:51:GLU:OE2	2.20	0.41
29:17:46:VAL:HG13	29:17:48:LYS:NZ	2.35	0.41
30:18:33:ASN:HA	30:18:36:LYS:HD2	2.03	0.41
1:1A:1073:A:C2	1:1A:2500:A:H5'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1091:A:O2'	1:1A:1093:G:C4	2.67	0.41
1:1A:116:A:C8	1:1A:117:A:C8	3.08	0.41
1:1A:1553:A:O2'	1:1A:1556:A:N6	2.53	0.41
1:1A:1827:U:H2'	1:1A:1828:C:H6	1.85	0.41
1:1A:2346:G:H4'	1:1A:2347:A:OP2	2.20	0.41
1:1A:2564:2MU:O5'	1:1A:2564:2MU:H6	2.20	0.41
1:1A:2641:A:H1'	1:1A:2642:G:O5'	2.20	0.41
1:1A:2666:A:N1	1:1A:2677:A:H5''	2.35	0.41
1:1A:2764:G:H4'	7:1H:4:ILE:HD11	2.02	0.41
17:1V:21:ARG:NH1	17:1V:91:TYR:CZ	2.89	0.41
18:1W:73:ALA:HB3	18:1W:106:ILE:HD12	2.02	0.41
26:24:53:GLU:H	26:24:53:GLU:CD	2.23	0.41
1:2A:1019:U:H2'	1:2A:1020:A:C8	2.54	0.41
1:2A:1113:U:H2'	1:2A:1114:G:C8	2.55	0.41
1:2A:1157:G:O2'	25:23:31:LEU:HD12	2.20	0.41
1:2A:1478:G:O2'	1:2A:1558:A:N1	2.48	0.41
1:2A:1628:G:H2'	1:2A:1629:U:C6	2.55	0.41
1:2A:2112:G:C2	1:2A:2113:U:H1'	2.55	0.41
1:2A:945:A:C4	1:2A:2448:A:C2	3.08	0.41
1:2A:2694:G:C6	1:2A:2695:C:C4	3.08	0.41
1:2A:322:A:H4'	1:2A:323:G:OP2	2.19	0.41
1:2A:84:A:N1	1:2A:98:G:O2'	2.36	0.41
1:2A:925:C:H2'	1:2A:926:A:H8	1.84	0.41
3:2D:101:GLU:CD	3:2D:103:ARG:HH12	2.22	0.41
16:2U:104:GLN:O	16:2U:107:ALA:HB3	2.21	0.41
23:11:51:VAL:HG11	23:11:74:VAL:HG21	2.02	0.41
1:1A:110:U:H5'	24:12:65:ASN:ND2	2.34	0.41
28:16:9:LEU:HD13	28:16:51:GLU:HB2	2.01	0.41
1:1A:467:U:H2'	1:1A:468:G:C8	2.56	0.41
1:1A:613:A:H2'	1:1A:614:C:O4'	2.20	0.41
1:1A:831:A:O4'	3:1D:227:ASN:ND2	2.53	0.41
1:1A:847:A:OP1	1:1A:847:A:H8	2.03	0.41
1:1A:904:C:N4	1:1A:905:U:O4	2.53	0.41
27:25:16:ARG:HG3	27:25:17:ASP:N	2.36	0.41
1:2A:144:C:H2'	1:2A:145:G:C8	2.54	0.41
1:2A:1913:A:H4'	1:2A:1914:C:O5'	2.18	0.41
1:2A:2164:C:C5	1:2A:2165:G:H1'	2.55	0.41
1:2A:2372:G:H1'	28:26:46:HIS:CE1	2.55	0.41
1:2A:274:G:H2'	1:2A:275:G:C8	2.56	0.41
1:2A:2776:A:H4'	1:2A:2777:G:H5''	2.01	0.41
1:2A:328:U:H4'	20:2Y:68:HIS:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:484:C:H2'	1:2A:485:C:C6	2.56	0.41
1:2A:524:U:H2'	1:2A:525:U:C6	2.55	0.41
1:2A:971:C:H2'	1:2A:972:G:O4'	2.21	0.41
5:2F:192:LEU:HD22	5:2F:194:MET:HG3	2.02	0.41
5:2F:29:ASN:HA	5:2F:30:PRO:HD3	1.92	0.41
11:2P:55:ARG:HA	60:2P:4007:HOH:O	2.20	0.41
17:2V:19:LYS:HE3	17:2V:62:LEU:HD21	2.02	0.41
1:2A:336:C:H4'	20:2Y:6:HIS:CD2	2.55	0.41
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.20	0.41
21:2Z:24:LEU:HA	21:2Z:25:PRO:HD3	1.90	0.41
1:1A:2854:G:O6	60:1A:5078:HOH:O	2.22	0.41
1:1A:2856:G:H2'	1:1A:2857:U:O4'	2.20	0.41
1:1A:287:G:N7	1:1A:448:U:H2'	2.35	0.41
1:1A:2881:C:N3	60:1A:5080:HOH:O	2.37	0.41
1:1A:491:G:C6	1:1A:492:A:N6	2.89	0.41
1:1A:672:G:O5'	1:1A:672:G:H8	2.04	0.41
4:1E:52:LEU:HA	4:1E:53:PRO:HD3	1.92	0.41
9:1N:73:THR:OG1	9:1N:82:LEU:HD11	2.21	0.41
16:1U:34:LYS:HD3	16:1U:34:LYS:HA	1.57	0.41
1:2A:1876:A:H2'	1:2A:1877:A:C8	2.56	0.41
1:2A:2653:U:H5''	1:2A:2654:A:OP2	2.21	0.41
1:2A:342:G:O2'	1:2A:343:C:H5'	2.20	0.41
1:2A:479:A:O2'	1:2A:481:G:H5'	2.21	0.41
1:2A:588:U:O5'	1:2A:588:U:H6	2.04	0.41
1:2A:881:G:H3'	1:2A:882:G:C8	2.55	0.41
3:2D:132:PRO:HD3	3:2D:190:TYR:CZ	2.55	0.41
3:2D:72:LYS:HD2	3:2D:103:ARG:NH1	2.36	0.41
7:2H:30:LYS:N	7:2H:79:VAL:O	2.50	0.41
1:1A:1273:G:OP1	16:1U:13:LYS:HG2	2.21	0.41
1:1A:1513:G:O2'	1:1A:1593:C:O2'	2.17	0.41
1:1A:215:G:H21	1:1A:217:A:H62	1.67	0.41
1:1A:402:C:H2'	1:1A:403:C:C6	2.55	0.41
2:1B:14:U:O2	2:1B:108:U:H4'	2.20	0.41
5:1F:164:ARG:O	5:1F:168:ARG:HB2	2.20	0.41
5:1F:8:GLN:HE22	5:1F:21:ALA:HA	1.85	0.41
6:1G:106:LEU:HA	6:1G:110:ALA:HB3	2.01	0.41
8:1I:75:LEU:HD22	8:1I:105:HIS:CD2	2.55	0.41
8:1I:47:LEU:HD23	8:1I:47:LEU:HA	1.79	0.41
11:1P:126:VAL:HG12	11:1P:148:LEU:HD23	2.03	0.41
11:1P:27:HIS:HB2	60:1P:321:HOH:O	2.19	0.41
12:1Q:134:ARG:CZ	21:1Z:122:ARG:HH21	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:1V:2:PHE:CE2	17:1V:41:GLY:HA3	2.55	0.41
26:24:40:HIS:O	26:24:44:THR:HG22	2.20	0.41
1:2A:1213:A:H2'	1:2A:1214:A:O4'	2.20	0.41
1:2A:1297:C:OP1	1:2A:2710:C:H4'	2.21	0.41
1:2A:191:A:H2'	1:2A:192:C:C6	2.54	0.41
1:2A:2365:G:O6	30:28:39:LYS:HE3	2.20	0.41
1:2A:927:G:H2'	1:2A:928:G:O4'	2.20	0.41
5:2F:195:ASP:HB3	5:2F:198:ALA:H	1.85	0.41
7:2H:4:ILE:O	7:2H:69:ARG:HD2	2.20	0.41
8:2I:116:LEU:HD11	8:2I:120:ILE:HG13	2.02	0.41
8:2I:61:ARG:HD3	8:2I:61:ARG:HA	1.75	0.41
19:2X:35:THR:O	19:2X:39:ILE:HG13	2.21	0.41
1:1A:493:G:P	29:17:33:ARG:HH12	2.43	0.41
1:1A:1277:G:H2'	1:1A:1278:G:C8	2.56	0.41
1:1A:1668:G:OP2	60:1A:5519:HOH:O	2.22	0.41
1:1A:2157:A:H2'	1:1A:2157:A:N3	2.35	0.41
1:1A:2418:U:C2	11:1P:72:PRO:HG2	2.55	0.41
1:1A:2638:C:H2'	1:1A:2639:G:O4'	2.20	0.41
1:1A:386:U:H6	1:1A:386:U:H2'	1.69	0.41
1:1A:821:A:H2'	1:1A:821:A:N3	2.36	0.41
3:1D:70:TRP:CE2	3:1D:150:LYS:HD3	2.56	0.41
60:1A:6391:HOH:O	9:1N:28:THR:HG23	2.20	0.41
9:1N:39:ARG:HA	9:1N:40:PRO:HD3	1.92	0.41
15:1T:108:ARG:HG3	15:1T:109:GLU:N	2.34	0.41
1:2A:1221(A):C:C2	1:2A:1229:G:C2	3.09	0.41
1:2A:1232:G:H2'	1:2A:1233:C:C6	2.56	0.41
1:2A:1359:A:H2'	1:2A:1360:A:H5'	2.03	0.41
1:2A:1431:U:H2'	1:2A:1432:C:H6	1.84	0.41
1:2A:2539:C:H4'	31:29:35:ARG:NH2	2.36	0.41
1:2A:996:A:C2	1:2A:997:G:C8	3.09	0.41
2:2B:41:U:O4	6:2G:70:VAL:HB	2.21	0.41
9:2N:34:LEU:O	9:2N:49:GLY:HA3	2.20	0.41
2:2B:91:C:H5'	12:2Q:18:LYS:HA	2.02	0.41
23:11:89:GLU:O	23:11:93:GLU:HG2	2.21	0.41
1:1A:1560:U:O2'	1:1A:1561:C:H5'	2.20	0.41
1:1A:2190:G:N1	1:1A:2193:A:C8	2.88	0.41
1:1A:2245:U:H2'	1:1A:2246:G:C8	2.55	0.41
1:1A:2327:G:H2'	1:1A:2328:C:C6	2.56	0.41
1:1A:333:G:N3	1:1A:353:G:O2'	2.46	0.41
1:1A:861:C:H2'	1:1A:862:C:C6	2.56	0.41
4:1E:47:VAL:O	4:1E:80:GLU:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:1N:33:LEU:HD12	9:1N:33:LEU:HA	1.80	0.41
11:1P:81:GLN:NE2	11:1P:105:LEU:O	2.54	0.41
29:27:30:VAL:O	29:27:34:ARG:HG2	2.21	0.41
1:2A:1288:U:C2	1:2A:1327:C:O2	2.74	0.41
1:2A:1848:A:C4	1:2A:1849:G:C8	3.09	0.41
1:2A:2135:A:H2'	1:2A:2136:C:C6	2.56	0.41
1:2A:2335:A:C8	1:2A:2337:G:C5	3.09	0.41
1:2A:2366:A:H2'	1:2A:2367:G:O4'	2.20	0.41
1:2A:2584:U:O5'	1:2A:2584:U:H6	2.04	0.41
1:2A:2747:G:H21	1:2A:2757:A:H62	1.67	0.41
1:2A:829:A:N7	1:2A:2247:A:O2'	2.45	0.41
1:2A:953:A:C2	1:2A:954:G:C8	3.09	0.41
1:2A:1826:G:H4'	3:2D:242:ARG:HH21	1.84	0.41
7:2H:121:ILE:HD11	7:2H:140:LYS:HG2	2.02	0.41
25:13:18:ASP:OD1	25:13:18:ASP:N	2.49	0.41
1:1A:54:G:O2'	1:1A:125:A:N1	2.38	0.41
1:1A:2023:A:H2'	1:1A:2024:G:C8	2.55	0.41
1:1A:739:C:O2'	3:1D:38:LYS:NZ	2.47	0.41
12:2Q:85:LYS:HG2	22:20:7:LEU:CB	2.50	0.41
26:24:62:ARG:HA	26:24:62:ARG:HD3	1.75	0.41
29:27:34:ARG:NH2	29:27:39:ARG:HG2	2.35	0.41
1:2A:2507:C:H2'	1:2A:2508:G:O4'	2.20	0.41
1:2A:2758:A:C2	1:2A:2759:G:H1'	2.56	0.41
1:2A:394:A:C6	1:2A:395:U:C4	3.09	0.41
1:2A:468:G:N7	29:27:39:ARG:NH2	2.69	0.41
1:2A:7:G:H4'	9:2N:13:TRP:CH2	2.55	0.41
2:2B:11:C:H3'	2:2B:12:C:H6	1.86	0.41
5:2F:23:ASP:O	5:2F:24:LEU:HD12	2.21	0.41
8:2I:87:LYS:NZ	8:2I:122:GLU:OE2	2.53	0.41
15:2T:24:PRO:HA	15:2T:49:VAL:HG23	2.02	0.41
16:2U:89:GLU:HB2	17:2V:50:PRO:HB3	2.01	0.41
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	2.03	0.41
1:1A:1118:C:H2'	1:1A:1139:G:O6	2.20	0.41
1:1A:1720:U:OP1	60:1A:5027:HOH:O	2.21	0.41
1:1A:2136:A:H2	1:1A:2190:G:H1'	1.85	0.41
1:1A:2158:C:C4	1:1A:2177:G:N1	2.88	0.41
1:1A:310:C:H2'	1:1A:311:C:C6	2.55	0.41
1:1A:463:C:H2'	1:1A:464:G:C8	2.56	0.41
3:1D:35:LYS:HB2	3:1D:36:PRO:HD2	2.02	0.41
7:1H:56:SER:OG	7:1H:57:ASP:N	2.54	0.41
21:1Z:126:VAL:CG1	21:1Z:161:VAL:HG23	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:109:G:H2'	1:2A:110:G:O4'	2.21	0.41
1:2A:228:A:O2'	1:2A:229:A:H4'	2.21	0.41
1:2A:2848:G:C8	15:2T:97:ALA:HB2	2.56	0.41
1:2A:484:C:H2'	1:2A:485:C:H6	1.86	0.41
1:2A:956:G:H5''	12:2Q:77:LYS:HD2	2.02	0.41
2:2B:94:C:H2'	2:2B:95:C:C6	2.56	0.41
4:2E:50:GLY:CA	4:2E:75:VAL:HG11	2.50	0.41
7:2H:9:ILE:HG12	7:2H:69:ARG:HG3	2.03	0.41
8:2I:75:LEU:HD22	8:2I:105:HIS:CD2	2.55	0.41
11:2P:57:THR:O	11:2P:61:ARG:HG3	2.21	0.41
14:2S:8:GLU:HG2	14:2S:8:GLU:H	1.54	0.41
17:2V:62:LEU:HD22	17:2V:93:GLU:HG2	2.01	0.41
1:2A:571:A:O2'	17:2V:78:LYS:HE2	2.21	0.41
21:2Z:158:PRO:HA	21:2Z:159:PRO:HD3	1.92	0.41
1:1A:1739:U:O2'	1:1A:1740:U:H2'	2.20	0.41
1:1A:1765:U:H2'	1:1A:1766:G:O4'	2.21	0.41
1:1A:2331:G:N1	14:1S:3:ARG:HA	2.36	0.41
1:1A:271:U:H4'	1:1A:272:U:OP2	2.18	0.41
3:1D:37:LEU:HD22	3:1D:87:ASN:ND2	2.36	0.41
4:1E:2:LYS:HA	4:1E:84:PHE:CE1	2.56	0.41
8:1I:118:LYS:HA	8:1I:119:PRO:HD3	1.95	0.41
11:1P:98:GLU:O	11:1P:101:VAL:HG12	2.21	0.41
20:1Y:65:ALA:HA	20:1Y:66:PRO:HD3	1.93	0.41
21:1Z:6:LYS:HD3	21:1Z:8:TYR:OH	2.20	0.41
1:2A:372:G:H8	23:21:65:SER:O	2.04	0.41
26:24:44:THR:O	26:24:46:GLN:N	2.54	0.41
28:26:9:LEU:HD13	28:26:51:GLU:HB2	2.03	0.41
1:2A:1567:A:H2'	3:2D:84:TYR:HE2	1.85	0.41
1:2A:1785:A:N6	60:2A:5150:HOH:O	2.54	0.41
1:2A:195:A:N7	60:2A:4402:HOH:O	2.37	0.41
1:2A:224:G:H2'	1:2A:225:A:O4'	2.21	0.41
1:2A:289:A:H2'	1:2A:290:G:O4'	2.21	0.41
7:2H:13:LYS:HA	7:2H:14:GLY:HA2	1.49	0.41
15:2T:23:ARG:NH1	15:2T:120:ARG:HD3	2.35	0.41
16:2U:104:GLN:O	16:2U:108:GLU:HG3	2.21	0.41
60:2A:4018:HOH:O	16:2U:14:HIS:HE1	2.04	0.41
21:2Z:138:GLU:H	21:2Z:156:LYS:CE	2.34	0.41
21:2Z:61:LEU:HA	21:2Z:62:PRO:HD3	1.94	0.41
26:14:49:PHE:HB3	26:14:50:VAL:H	1.39	0.41
1:1A:1116:A:N6	1:1A:1142:A:N3	2.68	0.41
1:1A:2196:C:H6	1:1A:2196:C:OP2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2679:C:H2'	1:1A:2680:G:O4'	2.20	0.41
1:1A:2804:C:H2'	1:1A:2805:G:C8	2.55	0.41
1:1A:38:A:H2'	1:1A:39:C:C6	2.56	0.41
3:1D:171:ASP:O	3:1D:187:GLY:N	2.45	0.41
1:1A:2801:C:P	4:1E:61:ARG:HH21	2.44	0.41
6:1G:173:LEU:HD23	6:1G:176:LEU:HD12	2.03	0.41
1:1A:1423:G:P	10:1O:49:ARG:HH12	96.08	0.41
1:1A:572:A:H61	17:1V:19:LYS:H	1.69	0.41
28:26:34:LEU:N	28:26:51:GLU:HG2	2.36	0.41
1:2A:815:C:C2	1:2A:1193:G:C2	3.08	0.41
1:2A:1464:C:H2'	1:2A:1465:G:C8	2.56	0.41
1:2A:1529:G:C6	1:2A:1530:C:C4	3.09	0.41
1:2A:1859:A:N6	1:2A:1883:G:O2'	2.53	0.41
1:2A:2055:C:H5'	1:2A:2056:G:O5'	2.21	0.41
1:2A:2140:C:O2	1:2A:2140:C:H2'	2.21	0.41
1:2A:2148:G:H2'	1:2A:2149:G:N7	2.35	0.41
1:2A:2336:A:H61	22:20:43:THR:HG22	1.85	0.41
1:2A:2510:C:C4	1:2A:2511:U:C4	3.09	0.41
1:2A:2512:C:H5''	1:2A:2513:G:OP2	2.21	0.41
1:2A:2519:U:H5'	1:2A:2567:G:H21	1.86	0.41
1:2A:2679:A:C2	1:2A:2729:G:C2	3.09	0.41
1:2A:2741:A:N6	1:2A:2763:G:O2'	2.54	0.41
1:2A:2839:G:C6	1:2A:2840:C:N3	2.89	0.41
1:2A:35:G:H2'	1:2A:36:G:O4'	2.20	0.41
1:2A:581:C:H2'	1:2A:582:G:C8	2.56	0.41
2:2B:71:C:H2'	2:2B:72:G:C8	2.56	0.41
11:2P:52:GLU:HB3	11:2P:55:ARG:CZ	2.50	0.41
11:2P:94:GLU:HG2	11:2P:96:THR:HG23	2.03	0.41
12:2Q:110:THR:HG23	12:2Q:113:GLN:OE1	2.21	0.41
12:2Q:31:ASP:HA	12:2Q:134:ARG:NH1	2.36	0.41
13:2R:109:ALA:HA	13:2R:110:PRO:HD2	1.91	0.41
17:2V:27:ALA:O	17:2V:64:HIS:HE1	2.04	0.41
23:11:64:ALA:HA	23:11:67:ILE:HG13	2.02	0.40
28:16:10:LEU:O	28:16:51:GLU:HA	2.20	0.40
1:1A:1759:C:H2'	1:1A:1760:U:O4'	2.22	0.40
1:1A:2156:A:C5	1:1A:2180:A:H2	2.35	0.40
1:1A:2742:G:H2'	1:1A:2743:C:O4'	2.21	0.40
1:1A:943:C:H2'	1:1A:944:C:C6	2.56	0.40
3:1D:21:PHE:HB3	3:1D:24:ILE:HD12	2.02	0.40
5:1F:12:LEU:HB3	5:1F:126:VAL:HG12	2.03	0.40
15:1T:127:ALA:C	15:1T:129:ARG:N	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1Z:4:ARG:HG2	21:1Z:58:VAL:HB	2.01	0.40
1:2A:1593:G:H2'	1:2A:1594:G:H8	1.87	0.40
1:2A:2528:U:O2'	1:2A:2529:G:H3'	2.21	0.40
6:2G:46:ALA:HB2	6:2G:53:LEU:HG	2.02	0.40
9:2N:99:LEU:HA	9:2N:99:LEU:HD23	1.89	0.40
15:2T:113:LYS:O	15:2T:114:LEU:HD23	2.21	0.40
1:2A:1188:U:C4'	17:2V:79:VAL:HG22	2.49	0.40
18:2W:60:ASN:N	18:2W:60:ASN:HD22	2.19	0.40
21:2Z:28:MET:HA	21:2Z:88:PHE:O	2.21	0.40
1:1A:1229:G:H5'	25:13:29:ARG:NH1	2.36	0.40
1:1A:1529:G:H4'	1:1A:1530:G:OP2	4.46	0.40
1:1A:1572:G:C6	1:1A:1573:G:C2	3.08	0.40
1:1A:2368:C:H2'	1:1A:2369:U:O4'	2.21	0.40
1:1A:1058:U:O4	9:1N:28:THR:HG21	2.21	0.40
12:1Q:43:THR:HA	12:1Q:94:VAL:HG12	2.03	0.40
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.57	0.40
1:2A:1021:A:C8	1:2A:1021:A:C3'	3.04	0.40
1:2A:1263:U:C4	1:2A:1264:G:C6	3.08	0.40
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.57	0.40
1:2A:2070:G:H2'	1:2A:2071:A:H8	1.85	0.40
1:2A:2369:A:C6	1:2A:2370:G:C5	3.09	0.40
1:2A:2419:U:H6	1:2A:2419:U:O5'	2.04	0.40
1:2A:2533:A:O2'	1:2A:2664:G:H5''	2.21	0.40
1:2A:244:A:C2	1:2A:255:A:C4	3.10	0.40
1:2A:272:G:H4'	1:2A:272(A):U:H5''	2.02	0.40
1:2A:582:G:H2'	1:2A:583:G:C8	2.56	0.40
1:2A:778:G:C5	1:2A:779:U:C4	3.09	0.40
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	2.02	0.40
6:2G:111:LEU:HD23	6:2G:117:PHE:CE1	2.56	0.40
6:2G:27:ASN:O	6:2G:30:GLU:HB3	2.20	0.40
7:2H:115:VAL:HG12	7:2H:123:PHE:CE2	2.56	0.40
10:2O:2:ILE:HB	10:2O:33:ALA:HB3	2.03	0.40
17:2V:89:GLN:HA	17:2V:90:PRO:HD3	1.88	0.40
18:2W:11:ARG:NH1	18:2W:99:ARG:O	2.54	0.40
1:2A:64:A:O3'	19:2X:71:GLY:HA3	2.20	0.40
1:2A:84:A:H5''	20:2Y:8:LYS:HE3	2.02	0.40
21:2Z:46:LYS:O	21:2Z:50:GLN:NE2	2.50	0.40
24:12:9:GLN:HE22	24:12:56:GLN:HB3	1.86	0.40
1:1A:1136:U:N3	1:1A:1148:C:H1'	2.37	0.40
1:1A:1494:G:HO2'	1:1A:1934:A:HO2'	126.04	0.40
1:1A:1891:G:N2	1:1A:1904:C:O2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2132:G:OP1	1:1A:2140:U:N3	2.54	0.40
2:1B:12:C:H4'	2:1B:13:A:OP1	2.22	0.40
8:1I:122:GLU:HB2	8:1I:126:TYR:OH	2.21	0.40
8:1I:9:LEU:HD21	8:1I:35:LEU:HD13	2.02	0.40
1:1A:1068:G:N7	9:1N:66:LYS:HE2	2.36	0.40
20:1Y:92:ASN:CG	20:1Y:94:LYS:HG2	2.41	0.40
29:27:34:ARG:HH21	29:27:39:ARG:HG2	1.85	0.40
1:2A:1015:G:H2'	1:2A:1016:G:C8	2.41	0.40
1:2A:1266:G:O4'	18:2W:15:ARG:NH2	2.54	0.40
1:2A:2048:G:OP1	60:2A:4976:HOH:O	2.22	0.40
1:2A:2064:C:H1'	1:2A:2450:A:C2	2.56	0.40
1:2A:2070:G:H2'	1:2A:2071:A:O4'	2.21	0.40
1:2A:2525:G:C2	1:2A:2539:C:C2	3.09	0.40
1:2A:30:G:C6	1:2A:31:C:C4	3.09	0.40
1:2A:434:U:H2'	1:2A:435:C:C6	6.11	0.40
1:2A:569:U:C4	1:2A:570:G:C6	3.10	0.40
1:2A:644:A:C2	1:2A:2369:A:H1'	2.56	0.40
1:2A:848:G:H2'	1:2A:849:A:C8	2.55	0.40
2:2B:80:U:O2'	2:2B:81:G:H8	2.05	0.40
5:2F:78:ILE:HA	5:2F:83:PHE:CD2	2.56	0.40
6:2G:111:LEU:HA	6:2G:114:ILE:HD12	2.01	0.40
6:2G:16:ARG:HH11	6:2G:16:ARG:HG3	1.85	0.40
11:2P:95:VAL:HG23	11:2P:100:LEU:HD21	2.03	0.40
11:2P:126:VAL:HG12	11:2P:148:LEU:CD2	2.51	0.40
1:2A:748:G:C8	18:2W:89:ALA:HB1	2.56	0.40
22:10:62:LEU:HA	22:10:62:LEU:HD23	1.89	0.40
26:14:62:ARG:HB3	26:14:63:TYR:H	1.65	0.40
1:1A:1371:G:OP1	60:1A:5441:HOH:O	2.22	0.40
1:1A:2863:C:H2'	1:1A:2864:G:C8	2.57	0.40
1:1A:56:C:H2'	1:1A:57:G:O4'	2.21	0.40
1:1A:540:A:H1'	1:1A:604:C:H1'	2.04	0.40
1:1A:831:A:C8	1:1A:839:G:C5	3.09	0.40
1:1A:986:A:H2'	1:1A:987:G:O4'	2.60	0.40
9:1N:121:LYS:HD3	9:1N:130:HIS:CE1	2.56	0.40
11:1P:21:ARG:HD3	11:1P:21:ARG:HA	1.95	0.40
14:1S:25:ARG:HB3	14:1S:25:ARG:HH11	1.87	0.40
16:1U:46:ALA:O	16:1U:50:ARG:HG2	2.22	0.40
18:1W:13:SER:HA	18:1W:14:PRO:HD3	1.92	0.40
21:1Z:40:ASP:OD2	21:1Z:43:GLU:HG3	2.21	0.40
21:1Z:72:ARG:NH2	21:1Z:97:GLU:O	2.53	0.40
1:2A:1007:C:OP1	9:2N:37:LYS:NZ	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1028:A:H2'	1:2A:1029:A:C8	2.56	0.40
1:2A:1515:G:C2	1:2A:1516:C:C2	3.10	0.40
1:2A:1688:U:H2'	1:2A:1698:A:N6	2.36	0.40
1:2A:2118:U:N3	1:2A:2149:G:H1'	2.36	0.40
1:2A:2128:C:O5'	1:2A:2128:C:H6	2.04	0.40
1:2A:2187:G:C6	1:2A:2188:C:C4	3.10	0.40
1:2A:185:U:H4'	1:2A:218:A:H4'	2.02	0.40
5:2F:108:LYS:HE2	5:2F:108:LYS:HB2	1.88	0.40
6:2G:107:LEU:HA	6:2G:111:LEU:HD13	2.04	0.40
1:1A:1111:U:H1'	1:1A:1120:G:C2	2.56	0.40
1:1A:1120:G:N1	1:1A:1121:C:H1'	2.37	0.40
1:1A:1140:U:H2'	1:1A:1141:A:C8	2.56	0.40
1:1A:1476:C:H2'	1:1A:1477:U:C6	2.56	0.40
1:1A:1992:A:H4'	1:1A:1993:A:OP1	2.21	0.40
1:1A:2180:A:H1'	1:1A:2181:G:O5'	2.22	0.40
1:1A:2388:A:H2'	1:1A:2389:A:O4'	2.21	0.40
1:1A:2697:G:H5'	10:1O:68:GLU:OE2	2.21	0.40
1:1A:2724:U:OP1	1:1A:2727:G:H4'	2.21	0.40
1:1A:510:C:H2'	1:1A:511:C:H6	1.87	0.40
1:1A:591:U:H5'	1:1A:990:A:N6	2.37	0.40
1:1A:645:G:N3	1:1A:645:G:H2'	2.35	0.40
1:1A:993:G:H2'	1:1A:993:G:N3	2.74	0.40
11:1P:18:ARG:NH2	11:1P:21:ARG:NH1	2.69	0.40
14:1S:46:VAL:HG12	14:1S:48:LEU:HD12	2.02	0.40
24:22:35:LEU:CD1	24:22:53:LEU:HD12	2.51	0.40
1:2A:2615:U:C2	27:25:7:PRO:HA	2.56	0.40
1:2A:993:G:C2	1:2A:1162:G:C2	3.09	0.40
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.56	0.40
1:2A:1858:G:O6	60:2A:4492:HOH:O	2.21	0.40
1:2A:2205:C:H1'	1:2A:2220:G:N2	2.37	0.40
1:2A:2299:G:H2'	1:2A:2300:G:H8	1.87	0.40
1:2A:2505:G:O6	1:2A:2576:G:H2'	2.22	0.40
1:2A:2720:U:C4	1:2A:2872:G:C6	3.10	0.40
1:2A:274:G:H2'	1:2A:275:G:H8	1.86	0.40
1:2A:2836:U:H2'	1:2A:2837:G:H8	1.81	0.40
1:2A:877:U:O2'	1:2A:900:A:N6	2.55	0.40
14:2S:26:LEU:HD22	14:2S:87:PHE:CD1	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1D	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
3	2D	273/276 (99%)	260 (95%)	11 (4%)	2 (1%)	25	43
4	1E	202/206 (98%)	193 (96%)	8 (4%)	1 (0%)	32	53
4	2E	202/206 (98%)	194 (96%)	7 (4%)	1 (0%)	32	53
5	1F	201/210 (96%)	198 (98%)	2 (1%)	1 (0%)	32	53
5	2F	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	18	32
6	1G	179/182 (98%)	170 (95%)	9 (5%)	0	100	100
6	2G	179/182 (98%)	168 (94%)	10 (6%)	1 (1%)	28	48
7	1H	172/180 (96%)	164 (95%)	7 (4%)	1 (1%)	28	48
7	2H	172/180 (96%)	158 (92%)	12 (7%)	2 (1%)	15	27
8	1I	144/148 (97%)	132 (92%)	12 (8%)	0	100	100
8	2I	144/148 (97%)	128 (89%)	14 (10%)	2 (1%)	13	23
9	1N	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
9	2N	138/140 (99%)	133 (96%)	4 (3%)	1 (1%)	25	43
10	1O	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
10	2O	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
11	1P	147/150 (98%)	139 (95%)	8 (5%)	0	100	100
11	2P	147/150 (98%)	137 (93%)	10 (7%)	0	100	100
12	1Q	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
12	2Q	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	25	43
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
13	2R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	1S	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
14	2S	108/112 (96%)	105 (97%)	2 (2%)	1 (1%)	20	36
15	1T	129/146 (88%)	123 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	2T	129/146 (88%)	125 (97%)	4 (3%)	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%)	97 (98%)	1 (1%)	1 (1%)	18	32
17	2V	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	18	32
18	1W	110/113 (97%)	110 (100%)	0	0	100	100
18	2W	110/113 (97%)	110 (100%)	0	0	100	100
19	1X	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
19	2X	93/96 (97%)	88 (95%)	4 (4%)	1 (1%)	17	29
20	1Y	105/110 (96%)	98 (93%)	5 (5%)	2 (2%)	9	15
20	2Y	105/110 (96%)	99 (94%)	4 (4%)	2 (2%)	9	15
21	1Z	148/206 (72%)	136 (92%)	11 (7%)	1 (1%)	25	43
21	2Z	156/206 (76%)	141 (90%)	15 (10%)	0	100	100
22	10	81/85 (95%)	80 (99%)	0	1 (1%)	15	27
22	20	81/85 (95%)	77 (95%)	3 (4%)	1 (1%)	15	27
23	11	95/98 (97%)	92 (97%)	3 (3%)	0	100	100
23	21	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
24	12	68/72 (94%)	68 (100%)	0	0	100	100
24	22	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
25	13	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
25	23	57/60 (95%)	53 (93%)	3 (5%)	1 (2%)	10	17
26	14	67/71 (94%)	58 (87%)	4 (6%)	5 (8%)	1	1
26	24	67/71 (94%)	53 (79%)	10 (15%)	4 (6%)	2	1
27	15	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
27	25	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	50 (98%)	1 (2%)	0	100	100
29	17	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
29	27	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	8	12
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	61 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	35 (100%)	0	0	100	100
33	1b	229/256 (90%)	200 (87%)	22 (10%)	7 (3%)	5	6
33	2b	229/256 (90%)	202 (88%)	19 (8%)	8 (4%)	4	5
34	1c	204/239 (85%)	188 (92%)	15 (7%)	1 (0%)	32	53
34	2c	204/239 (85%)	187 (92%)	15 (7%)	2 (1%)	18	32
35	1d	206/209 (99%)	196 (95%)	9 (4%)	1 (0%)	32	53
35	2d	206/209 (99%)	197 (96%)	8 (4%)	1 (0%)	32	53
36	1e	146/162 (90%)	137 (94%)	6 (4%)	3 (2%)	8	13
36	2e	146/162 (90%)	139 (95%)	5 (3%)	2 (1%)	13	23
37	1f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
37	2f	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
38	1g	153/156 (98%)	144 (94%)	6 (4%)	3 (2%)	9	14
38	2g	153/156 (98%)	143 (94%)	7 (5%)	3 (2%)	9	14
39	1h	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
39	2h	135/138 (98%)	131 (97%)	4 (3%)	0	100	100
40	1i	125/128 (98%)	115 (92%)	9 (7%)	1 (1%)	22	39
40	2i	125/128 (98%)	114 (91%)	10 (8%)	1 (1%)	22	39
41	1j	95/105 (90%)	86 (90%)	4 (4%)	5 (5%)	2	2
41	2j	94/105 (90%)	85 (90%)	5 (5%)	4 (4%)	3	3
42	1k	112/129 (87%)	106 (95%)	4 (4%)	2 (2%)	10	17
42	2k	112/129 (87%)	107 (96%)	3 (3%)	2 (2%)	10	17
43	1l	119/132 (90%)	115 (97%)	4 (3%)	0	100	100
43	2l	119/132 (90%)	112 (94%)	7 (6%)	0	100	100
44	1m	121/126 (96%)	114 (94%)	7 (6%)	0	100	100
44	2m	120/126 (95%)	110 (92%)	9 (8%)	1 (1%)	22	39
45	1n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
45	2n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
46	1o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
46	2o	86/89 (97%)	81 (94%)	4 (5%)	1 (1%)	15	27
47	1p	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	14	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	2p	80/88 (91%)	76 (95%)	3 (4%)	1 (1%)	14	25
48	1q	97/105 (92%)	93 (96%)	3 (3%)	1 (1%)	18	32
48	2q	97/105 (92%)	94 (97%)	2 (2%)	1 (1%)	18	32
49	1r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
49	2r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
50	1s	81/93 (87%)	75 (93%)	5 (6%)	1 (1%)	15	27
50	2s	81/93 (87%)	74 (91%)	5 (6%)	2 (2%)	6	10
51	1t	94/106 (89%)	87 (93%)	0	7 (7%)	1	1
51	2t	94/106 (89%)	86 (92%)	4 (4%)	4 (4%)	3	3
52	1u	21/27 (78%)	21 (100%)	0	0	100	100
52	2u	21/27 (78%)	21 (100%)	0	0	100	100
All	All	11370/12128 (94%)	10779 (95%)	488 (4%)	103 (1%)	20	36

All (103) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
7	1H	126	PRO
21	1Z	159	PRO
26	14	62	ARG
33	1b	10	LEU
38	1g	79	ARG
40	1i	54	ASP
41	1j	55	LYS
50	1s	81	ARG
51	1t	10	LEU
51	1t	100	ILE
5	2F	21	ALA
5	2F	130	ALA
7	2H	126	PRO
8	2I	10	GLU
17	2V	79	VAL
26	24	55	ARG
26	24	61	ARG
29	27	46	VAL
33	2b	16	HIS
33	2b	123	ALA
34	2c	181	ASN

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Mol	Chain	Res	Type
38	2g	79	ARG
44	2m	4	ILE
50	2s	81	ARG
51	2t	10	LEU
17	1V	79	VAL
26	14	45	GLY
26	14	56	VAL
42	1k	49	GLY
3	2D	69	ARG
6	2G	50	ALA
8	2I	40	THR
14	2S	84	GLN
26	24	45	GLY
40	2i	54	ASP
51	2t	47	GLY
4	1E	52	LEU
22	10	13	GLY
33	1b	17	PHE
38	1g	80	VAL
41	1j	32	ALA
41	1j	77	PRO
41	1j	78	ASN
51	1t	47	GLY
51	1t	96	GLY
51	1t	102	GLY
4	2E	52	LEU
9	2N	2	LYS
19	2X	2	LYS
26	24	46	GLN
33	2b	125	PRO
36	2e	37	ARG
41	2j	77	PRO
48	2q	33	GLY
50	2s	29	ARG
26	14	57	GLU
33	1b	16	HIS
33	1b	20	GLU
33	1b	22	LYS
34	1c	66	VAL
35	1d	178	VAL
36	1e	86	ALA
51	1t	95	ALA

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Mol	Chain	Res	Type
3	2D	3	VAL
20	2Y	103	GLY
33	2b	20	GLU
33	2b	78	GLN
34	2c	156	ARG
38	2g	7	ALA
38	2g	80	VAL
41	2j	78	ASN
51	2t	100	ILE
20	1Y	54	LYS
26	14	53	GLU
33	1b	231	GLU
41	1j	79	ARG
42	1k	105	VAL
20	2Y	57	GLN
22	20	4	LYS
33	2b	21	ARG
33	2b	231	GLU
41	2j	55	LYS
42	2k	49	GLY
46	2o	88	ARG
38	1g	4	ARG
51	1t	9	ASN
7	2H	29	PRO
36	2e	69	VAL
42	2k	105	VAL
47	2p	53	VAL
48	1q	33	GLY
25	23	59	VAL
51	2t	102	GLY
20	1Y	103	GLY
36	1e	69	VAL
36	1e	85	GLY
47	1p	53	VAL
33	2b	202	PRO
41	2j	75	ILE
12	2Q	27	VAL
35	2d	5	ILE
33	1b	125	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1D	215/218 (99%)	209 (97%)	6 (3%)	49	76
3	2D	215/218 (99%)	208 (97%)	7 (3%)	43	70
4	1E	164/166 (99%)	154 (94%)	10 (6%)	22	40
4	2E	164/166 (99%)	154 (94%)	10 (6%)	22	40
5	1F	160/166 (96%)	150 (94%)	10 (6%)	21	38
5	2F	159/166 (96%)	150 (94%)	9 (6%)	24	44
6	1G	143/156 (92%)	139 (97%)	4 (3%)	49	76
6	2G	143/156 (92%)	135 (94%)	8 (6%)	25	45
7	1H	144/148 (97%)	141 (98%)	3 (2%)	59	83
7	2H	144/148 (97%)	142 (99%)	2 (1%)	71	90
8	1I	113/124 (91%)	108 (96%)	5 (4%)	33	57
8	2I	105/124 (85%)	99 (94%)	6 (6%)	24	44
9	1N	118/119 (99%)	110 (93%)	8 (7%)	18	34
9	2N	118/119 (99%)	109 (92%)	9 (8%)	15	29
10	1O	100/100 (100%)	98 (98%)	2 (2%)	60	84
10	2O	100/100 (100%)	99 (99%)	1 (1%)	80	93
11	1P	115/116 (99%)	109 (95%)	6 (5%)	27	49
11	2P	115/116 (99%)	112 (97%)	3 (3%)	51	78
12	1Q	111/111 (100%)	108 (97%)	3 (3%)	50	77
12	2Q	111/111 (100%)	105 (95%)	6 (5%)	26	47
13	1R	101/101 (100%)	90 (89%)	11 (11%)	7	14
13	2R	101/101 (100%)	94 (93%)	7 (7%)	18	34
14	1S	86/88 (98%)	84 (98%)	2 (2%)	56	81
14	2S	85/88 (97%)	83 (98%)	2 (2%)	54	80
15	1T	115/127 (91%)	113 (98%)	2 (2%)	66	87
15	2T	113/127 (89%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	1U	93/94 (99%)	92 (99%)	1 (1%)	78	92
16	2U	93/94 (99%)	91 (98%)	2 (2%)	57	82
17	1V	80/82 (98%)	74 (92%)	6 (8%)	16	29
17	2V	80/82 (98%)	74 (92%)	6 (8%)	16	29
18	1W	90/92 (98%)	85 (94%)	5 (6%)	25	45
18	2W	90/92 (98%)	85 (94%)	5 (6%)	25	45
19	1X	77/78 (99%)	75 (97%)	2 (3%)	51	78
19	2X	77/78 (99%)	76 (99%)	1 (1%)	73	90
20	1Y	85/91 (93%)	82 (96%)	3 (4%)	41	68
20	2Y	85/91 (93%)	82 (96%)	3 (4%)	41	68
21	1Z	135/179 (75%)	129 (96%)	6 (4%)	33	57
21	2Z	137/179 (76%)	136 (99%)	1 (1%)	87	96
22	10	65/67 (97%)	63 (97%)	2 (3%)	45	73
22	20	65/67 (97%)	64 (98%)	1 (2%)	70	89
23	11	80/83 (96%)	79 (99%)	1 (1%)	73	90
23	21	80/83 (96%)	78 (98%)	2 (2%)	53	79
24	12	65/67 (97%)	64 (98%)	1 (2%)	70	89
24	22	65/67 (97%)	65 (100%)	0	100	100
25	13	51/52 (98%)	49 (96%)	2 (4%)	37	63
25	23	50/52 (96%)	48 (96%)	2 (4%)	36	62
26	14	59/63 (94%)	58 (98%)	1 (2%)	66	87
26	24	53/63 (84%)	49 (92%)	4 (8%)	16	29
27	15	50/52 (96%)	47 (94%)	3 (6%)	22	41
27	25	50/52 (96%)	47 (94%)	3 (6%)	22	41
28	16	51/52 (98%)	49 (96%)	2 (4%)	37	63
28	26	50/52 (96%)	49 (98%)	1 (2%)	60	84
29	17	41/42 (98%)	40 (98%)	1 (2%)	54	80
29	27	41/42 (98%)	40 (98%)	1 (2%)	54	80
30	18	54/55 (98%)	52 (96%)	2 (4%)	39	66
30	28	54/55 (98%)	52 (96%)	2 (4%)	39	66
31	19	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	29	34/34 (100%)	33 (97%)	1 (3%)	48	75
33	1b	192/220 (87%)	189 (98%)	3 (2%)	68	88
33	2b	187/220 (85%)	183 (98%)	4 (2%)	59	83
34	1c	142/188 (76%)	141 (99%)	1 (1%)	87	96
34	2c	140/188 (74%)	137 (98%)	3 (2%)	59	83
35	1d	169/181 (93%)	163 (96%)	6 (4%)	40	67
35	2d	173/181 (96%)	167 (96%)	6 (4%)	41	68
36	1e	113/123 (92%)	110 (97%)	3 (3%)	50	77
36	2e	114/123 (93%)	110 (96%)	4 (4%)	41	68
37	1f	84/90 (93%)	84 (100%)	0	100	100
37	2f	85/90 (94%)	83 (98%)	2 (2%)	54	80
38	1g	119/127 (94%)	118 (99%)	1 (1%)	85	95
38	2g	120/127 (94%)	117 (98%)	3 (2%)	53	79
39	1h	114/119 (96%)	112 (98%)	2 (2%)	64	86
39	2h	114/119 (96%)	113 (99%)	1 (1%)	82	94
40	1i	90/99 (91%)	87 (97%)	3 (3%)	43	70
40	2i	89/99 (90%)	85 (96%)	4 (4%)	32	56
41	1j	66/92 (72%)	66 (100%)	0	100	100
41	2j	69/92 (75%)	67 (97%)	2 (3%)	48	75
42	1k	82/99 (83%)	80 (98%)	2 (2%)	54	80
42	2k	83/99 (84%)	83 (100%)	0	100	100
43	1l	96/108 (89%)	92 (96%)	4 (4%)	34	59
43	2l	96/108 (89%)	94 (98%)	2 (2%)	59	83
44	1m	93/101 (92%)	92 (99%)	1 (1%)	78	92
44	2m	92/101 (91%)	91 (99%)	1 (1%)	78	92
45	1n	49/50 (98%)	44 (90%)	5 (10%)	8	16
45	2n	49/50 (98%)	47 (96%)	2 (4%)	35	61
46	1o	78/80 (98%)	76 (97%)	2 (3%)	51	78
46	2o	78/80 (98%)	77 (99%)	1 (1%)	73	90
47	1p	69/74 (93%)	65 (94%)	4 (6%)	23	43
47	2p	68/74 (92%)	65 (96%)	3 (4%)	33	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	1q	94/97 (97%)	94 (100%)	0	100	100
48	2q	94/97 (97%)	92 (98%)	2 (2%)	59	83
49	1r	59/77 (77%)	58 (98%)	1 (2%)	66	87
49	2r	59/77 (77%)	59 (100%)	0	100	100
50	1s	69/80 (86%)	68 (99%)	1 (1%)	71	90
50	2s	67/80 (84%)	64 (96%)	3 (4%)	32	56
51	1t	70/82 (85%)	69 (99%)	1 (1%)	71	90
51	2t	70/82 (85%)	70 (100%)	0	100	100
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	18 (100%)	0	100	100
All	All	9303/10064 (92%)	9005 (97%)	298 (3%)	44	71

All (298) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	3	VAL
3	1D	106	ILE
3	1D	113	VAL
3	1D	142	VAL
3	1D	229	VAL
3	1D	257	LEU
4	1E	12	THR
4	1E	19	ARG
4	1E	21	VAL
4	1E	24	THR
4	1E	73	GLU
4	1E	75	VAL
4	1E	78	LEU
4	1E	116	VAL
4	1E	175	VAL
4	1E	181	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	74	ARG
5	1F	106	ARG
5	1F	125	LEU
5	1F	132	VAL
5	1F	170	LEU

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Mol	Chain	Res	Type
5	1F	183	VAL
5	1F	192	LEU
5	1F	201	VAL
6	1G	43	LEU
6	1G	82	LEU
6	1G	148	MET
6	1G	159	VAL
7	1H	51	ARG
7	1H	71	LEU
7	1H	129	THR
8	1I	38	LEU
8	1I	47	LEU
8	1I	92	VAL
8	1I	107	VAL
8	1I	142	VAL
9	1N	14	VAL
9	1N	28	THR
9	1N	33	LEU
9	1N	34	LEU
9	1N	46	VAL
9	1N	73	THR
9	1N	99	LEU
9	1N	120	LEU
10	1O	10	VAL
10	1O	108	GLU
11	1P	65	ARG
11	1P	95	VAL
11	1P	98	GLU
11	1P	106	LEU
11	1P	112	LEU
11	1P	125	VAL
12	1Q	35	VAL
12	1Q	109	VAL
12	1Q	110	THR
13	1R	6	SER
13	1R	24	GLN
13	1R	29	LEU
13	1R	36	THR
13	1R	44	LEU
13	1R	54	LEU
13	1R	65	LEU
13	1R	79	LEU

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Mol	Chain	Res	Type
13	1R	100	LEU
13	1R	111	LEU
13	1R	114	VAL
14	1S	25	ARG
14	1S	110	LEU
15	1T	28	VAL
15	1T	74	ARG
16	1U	74	LEU
17	1V	46	VAL
17	1V	51	VAL
17	1V	52	VAL
17	1V	72	VAL
17	1V	79	VAL
17	1V	82	ARG
18	1W	17	VAL
18	1W	19	LEU
18	1W	23	LEU
18	1W	67	ASP
18	1W	107	LEU
19	1X	35	THR
19	1X	57	LEU
20	1Y	1	MET
20	1Y	43	ASN
20	1Y	72	VAL
21	1Z	5	LEU
21	1Z	86	VAL
21	1Z	129	SER
21	1Z	155	LEU
21	1Z	161	VAL
21	1Z	171	ILE
22	10	14	ARG
22	10	43	THR
23	11	35	THR
24	12	40	SER
25	13	23	LEU
25	13	54	VAL
26	14	49	PHE
27	15	6	VAL
27	15	16	ARG
27	15	29	THR
28	16	37	ARG
28	16	48	VAL

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Mol	Chain	Res	Type
29	17	43	THR
30	18	31	HIS
30	18	32	LEU
33	1b	24	TRP
33	1b	111	ARG
33	1b	112	VAL
34	1c	21	ARG
35	1d	10	ARG
35	1d	31	CYS
35	1d	49	ARG
35	1d	134	ASP
35	1d	135	LEU
35	1d	194	LEU
36	1e	31	LEU
36	1e	41	VAL
36	1e	56	GLN
38	1g	8	GLU
39	1h	69	ARG
39	1h	112	LEU
40	1i	42	ARG
40	1i	64	THR
40	1i	128	ARG
42	1k	31	THR
42	1k	48	ILE
43	1l	27	LEU
43	1l	36	VAL
43	1l	83	VAL
43	1l	84	LEU
44	1m	102	ARG
45	1n	3	ARG
45	1n	6	LEU
45	1n	22	THR
45	1n	23	ARG
45	1n	33	VAL
46	1o	7	GLU
46	1o	39	LEU
47	1p	19	ILE
47	1p	20	VAL
47	1p	21	VAL
47	1p	67	THR
49	1r	76	LEU
50	1s	41	VAL

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Mol	Chain	Res	Type
51	1t	13	LEU
3	2D	94	LEU
3	2D	106	ILE
3	2D	113	VAL
3	2D	134	ARG
3	2D	142	VAL
3	2D	259	THR
3	2D	276	LYS
4	2E	12	THR
4	2E	21	VAL
4	2E	24	THR
4	2E	52	LEU
4	2E	75	VAL
4	2E	78	LEU
4	2E	116	VAL
4	2E	163	GLU
4	2E	175	VAL
4	2E	181	LEU
5	2F	53	THR
5	2F	70	THR
5	2F	74	ARG
5	2F	106	ARG
5	2F	170	LEU
5	2F	183	VAL
5	2F	192	LEU
5	2F	197	ASP
5	2F	201	VAL
6	2G	28	VAL
6	2G	31	VAL
6	2G	43	LEU
6	2G	60	LEU
6	2G	79	ASN
6	2G	115	ARG
6	2G	135	LEU
6	2G	159	VAL
7	2H	84	SER
7	2H	88	LEU
8	2I	38	LEU
8	2I	47	LEU
8	2I	57	ARG
8	2I	92	VAL
8	2I	121	LYS

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Mol	Chain	Res	Type
8	2I	123	LEU
9	2N	14	VAL
9	2N	28	THR
9	2N	33	LEU
9	2N	34	LEU
9	2N	46	VAL
9	2N	67	LEU
9	2N	87	LEU
9	2N	99	LEU
9	2N	120	LEU
10	2O	8	LEU
11	2P	95	VAL
11	2P	99	LEU
11	2P	106	LEU
12	2Q	1	MET
12	2Q	2	LEU
12	2Q	16	ARG
12	2Q	21	THR
12	2Q	35	VAL
12	2Q	110	THR
13	2R	18	LEU
13	2R	24	GLN
13	2R	29	LEU
13	2R	44	LEU
13	2R	65	LEU
13	2R	100	LEU
13	2R	111	LEU
14	2S	75	GLU
14	2S	110	LEU
16	2U	36	ARG
16	2U	74	LEU
17	2V	43	GLU
17	2V	46	VAL
17	2V	51	VAL
17	2V	72	VAL
17	2V	79	VAL
17	2V	82	ARG
18	2W	17	VAL
18	2W	19	LEU
18	2W	23	LEU
18	2W	67	ASP
18	2W	107	LEU

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Mol	Chain	Res	Type
19	2X	57	LEU
20	2Y	28	LYS
20	2Y	72	VAL
20	2Y	90	LEU
21	2Z	124	ILE
22	20	14	ARG
23	21	4	VAL
23	21	95	LEU
25	23	30	ARG
25	23	54	VAL
26	24	34	GLU
26	24	37	SER
26	24	48	ARG
26	24	49	PHE
27	25	6	VAL
27	25	16	ARG
27	25	29	THR
28	26	48	VAL
29	27	39	ARG
30	28	31	HIS
30	28	32	LEU
31	29	17	ILE
33	2b	11	LEU
33	2b	93	VAL
33	2b	127	ILE
33	2b	221	LEU
34	2c	70	VAL
34	2c	124	ILE
34	2c	154	SER
35	2d	31	CYS
35	2d	135	LEU
35	2d	141	ARG
35	2d	150	GLU
35	2d	170	VAL
35	2d	194	LEU
36	2e	13	ILE
36	2e	31	LEU
36	2e	41	VAL
36	2e	64	ARG
37	2f	21	LEU
37	2f	72	VAL
38	2g	9	VAL

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Mol	Chain	Res	Type
38	2g	52	GLU
38	2g	98	SER
39	2h	23	SER
40	2i	53	VAL
40	2i	65	VAL
40	2i	102	LEU
40	2i	108	VAL
41	2j	8	LEU
41	2j	100	THR
43	2l	27	LEU
43	2l	83	VAL
44	2m	47	ASP
45	2n	22	THR
45	2n	33	VAL
46	2o	39	LEU
47	2p	2	VAL
47	2p	21	VAL
47	2p	67	THR
48	2q	35	VAL
48	2q	83	ASP
50	2s	41	VAL
50	2s	49	ILE
50	2s	77	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
4	1E	48	GLN
5	1F	8	GLN
8	1I	105	HIS
13	1R	71	GLN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	43	ASN
23	1I	56	GLN
24	12	9	GLN
25	13	32	GLN
34	1c	6	HIS
34	1c	162	GLN
34	1c	181	ASN
35	1d	116	GLN

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Mol	Chain	Res	Type
35	1d	119	GLN
35	1d	123	HIS
35	1d	125	HIS
36	1e	78	HIS
37	1f	100	ASN
38	1g	28	ASN
38	1g	86	GLN
40	1i	3	GLN
40	1i	31	GLN
40	1i	34	ASN
40	1i	58	HIS
40	1i	89	ASN
40	1i	124	GLN
41	1j	56	HIS
42	1k	99	GLN
43	1l	99	HIS
47	1p	16	HIS
48	1q	26	GLN
50	1s	23	ASN
50	1s	69	HIS
50	1s	83	HIS
3	2D	87	ASN
4	2E	48	GLN
5	2F	69	HIS
6	2G	41	GLN
9	2N	38	HIS
10	2O	3	GLN
12	2Q	12	GLN
12	2Q	13	GLN
12	2Q	57	HIS
12	2Q	123	HIS
13	2R	13	HIS
14	2S	38	GLN
15	2T	79	HIS
16	2U	81	HIS
16	2U	117	GLN
18	2W	60	ASN
19	2X	31	HIS
19	2X	82	GLN
20	2Y	6	HIS
21	2Z	55	HIS
21	2Z	73	GLN

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Mol	Chain	Res	Type
22	20	35	ASN
23	21	56	GLN
24	22	9	GLN
24	22	65	ASN
26	24	46	GLN
33	2b	40	HIS
33	2b	94	ASN
33	2b	140	HIS
34	2c	6	HIS
34	2c	37	GLN
34	2c	98	ASN
34	2c	104	GLN
35	2d	119	GLN
35	2d	123	HIS
35	2d	125	HIS
35	2d	161	ASN
36	2e	73	ASN
36	2e	78	HIS
36	2e	130	ASN
37	2f	64	GLN
37	2f	73	ASN
38	2g	28	ASN
38	2g	86	GLN
38	2g	109	ASN
39	2h	78	GLN
40	2i	3	GLN
40	2i	58	HIS
40	2i	89	ASN
40	2i	124	GLN
42	2k	22	HIS
42	2k	78	GLN
43	2l	49	ASN
43	2l	99	HIS
44	2m	12	ASN
44	2m	77	ASN
46	2o	28	GLN
50	2s	47	HIS
51	2t	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2861/2915 (98%)	414 (14%)	43 (1%)
1	2A	2788/2915 (95%)	510 (18%)	28 (1%)
2	1B	120/121 (99%)	11 (9%)	1 (0%)
2	2B	118/121 (97%)	35 (29%)	0
32	1a	1494/1521 (98%)	241 (16%)	0
32	2a	1498/1521 (98%)	253 (16%)	0
53	1v	12/24 (50%)	4 (33%)	0
53	2v	12/24 (50%)	3 (25%)	0
54	1w	71/76 (93%)	22 (30%)	0
54	1y	71/76 (93%)	23 (32%)	0
54	2w	68/76 (89%)	27 (39%)	0
54	2y	69/76 (90%)	23 (33%)	0
55	1x	75/77 (97%)	8 (10%)	0
55	2x	75/77 (97%)	16 (21%)	0
All	All	9332/9620 (97%)	1590 (17%)	72 (0%)

All (1590) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	13	A
1	1A	34	C
1	1A	45	C
1	1A	60	G
1	1A	70	A
1	1A	71	U
1	1A	73	A
1	1A	74	G
1	1A	83	A
1	1A	117	A
1	1A	118	U
1	1A	137	G
1	1A	185	A
1	1A	189	U
1	1A	194	G
1	1A	203	G
1	1A	204	G
1	1A	205	A
1	1A	211	A
1	1A	217	A
1	1A	218	A
1	1A	222	A
1	1A	237	G

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Mol	Chain	Res	Type
1	1A	258	U
1	1A	271	U
1	1A	272	U
1	1A	273	G
1	1A	288	U
1	1A	289	G
1	1A	296	U
1	1A	303	C
1	1A	335	A
1	1A	353	G
1	1A	354	A
1	1A	376	G
1	1A	387	G
1	1A	388	A
1	1A	389	G
1	1A	407	U
1	1A	413	G
1	1A	423	G
1	1A	427	G
1	1A	432	U
1	1A	438	G
1	1A	455	A
1	1A	470	C
1	1A	474	U
1	1A	477	C
1	1A	480	A
1	1A	482	C
1	1A	483	A
1	1A	505	A
1	1A	507	G
1	1A	529	U
1	1A	530	A
1	1A	534	C
1	1A	537	G
1	1A	555	G
1	1A	556	C
1	1A	557	A
1	1A	558	G
1	1A	569	G
1	1A	573	G
1	1A	586	G
1	1A	596	G

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Mol	Chain	Res	Type
1	1A	598	A
1	1A	609	A
1	1A	626	A
1	1A	627	G
1	1A	630	U
1	1A	639	G
1	1A	641	G
1	1A	642	G
1	1A	652	A
1	1A	659	C
1	1A	660	C
1	1A	662	A
1	1A	670	C
1	1A	671	A
1	1A	697	C
1	1A	716	G
1	1A	733	G
1	1A	777	C
1	1A	822	G
1	1A	823	G
1	1A	829	A
1	1A	831	A
1	1A	832	G
1	1A	837	C
1	1A	839	G
1	1A	848	G
1	1A	852	G
1	1A	859	C
1	1A	866	A
1	1A	874	U
1	1A	875	U
1	1A	906	G
1	1A	913	A
1	1A	924	U
1	1A	926	G
1	1A	927	G
1	1A	931	C
1	1A	932	C
1	1A	933	C
1	1A	934	A
1	1A	935	C
1	1A	936	C

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Mol	Chain	Res	Type
1	1A	937	A
1	1A	940	C
1	1A	941	U
1	1A	942	A
1	1A	943	C
1	1A	944	C
1	1A	946	A
1	1A	953	U
1	1A	956	A
1	1A	977	G
1	1A	990	A
1	1A	991	G
1	1A	998	A
1	1A	1006	C
1	1A	1008	U
1	1A	1019	G
1	1A	1020	C
1	1A	1029	A
1	1A	1042	A
1	1A	1055	A
1	1A	1058	U
1	1A	1059	C
1	1A	1068	G
1	1A	1072	U
1	1A	1073	A
1	1A	1079	U
1	1A	1084	C
1	1A	1090	G
1	1A	1091	A
1	1A	1092	A
1	1A	1093	G
1	1A	1094	A
1	1A	1100	A
1	1A	1101	G
1	1A	1104	G
1	1A	1112	U
1	1A	1114	G
1	1A	1117	G
1	1A	1119	A
1	1A	1120	G
1	1A	1121	C
1	1A	1122	C

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Mol	Chain	Res	Type
1	1A	1124	U
1	1A	1125	C
1	1A	1127	U
1	1A	1129	U
1	1A	1130	A
1	1A	1134	A
1	1A	1135	G
1	1A	1136	U
1	1A	1137	G
1	1A	1139	G
1	1A	1140	U
1	1A	1142	A
1	1A	1146	C
1	1A	1147	U
1	1A	1148	C
1	1A	1149	A
1	1A	1153	G
1	1A	1156	G
1	1A	1157	A
1	1A	1158	G
1	1A	1162	C
1	1A	1180	C
1	1A	1181	G
1	1A	1195	G
1	1A	1201	A
1	1A	1217	G
1	1A	1218	G
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1222	A
1	1A	1223	C
1	1A	1256	U
1	1A	1299	A
1	1A	1302	G
1	1A	1317	G
1	1A	1318	A
1	1A	1322	A
1	1A	1346	U
1	1A	1347	A
1	1A	1349	G
1	1A	1366	C

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Mol	Chain	Res	Type
1	1A	1391	C
1	1A	1398	U
1	1A	1405	A
1	1A	1406	A
1	1A	1411	A
1	1A	1426	G
1	1A	1430	A
1	1A	1431	G
1	1A	1441	A
1	1A	1442	U
1	1A	1462	G
1	1A	1463	C
1	1A	1466	U
1	1A	1467	G
1	1A	1474	C
1	1A	1491	A
1	1A	1497	G
1	1A	1502	G
1	1A	1514	C
1	1A	1529	G
1	1A	1539	C
1	1A	1540	A
1	1A	1554	A
1	1A	1555	C
1	1A	1556	A
1	1A	1569	U
1	1A	1586	G
1	1A	1587	U
1	1A	1605	A
1	1A	1613	A
1	1A	1616	A
1	1A	1625	U
1	1A	1627	A
1	1A	1628	G
1	1A	1631	C
1	1A	1632	A
1	1A	1654	A
1	1A	1686	U
1	1A	1694	G
1	1A	1695	C
1	1A	1701	A
1	1A	1721	G

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Mol	Chain	Res	Type
1	1A	1741	C
1	1A	1743	G
1	1A	1747	A
1	1A	1750	G
1	1A	1767	A
1	1A	1768	U
1	1A	1776	G
1	1A	1787	G
1	1A	1794	G
1	1A	1795	G
1	1A	1804	A
1	1A	1811	A
1	1A	1813	C
1	1A	1817	A
1	1A	1822	A
1	1A	1831	C
1	1A	1847	G
1	1A	1848	G
1	1A	1859	G
1	1A	1860	A
1	1A	1878	A
1	1A	1889	G
1	1A	1892	G
1	1A	1899	A
1	1A	1911	A
1	1A	1922	A
1	1A	1928	G
1	1A	1951	G
1	1A	1952	G
1	1A	1959	A
1	1A	1960	A
1	1A	1977	U
1	1A	1985	U
1	1A	1989	C
1	1A	1992	A
1	1A	1993	A
1	1A	1994	A
1	1A	2014	G
1	1A	2015	U
1	1A	2019	G
1	1A	2042	A
1	1A	2045	G

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Mol	Chain	Res	Type
1	1A	2053	A
1	1A	2054	G
1	1A	2055	A
1	1A	2057	G
1	1A	2061	C
1	1A	2065	C
1	1A	2077	C
1	1A	2078	G
1	1A	2082	A
1	1A	2083	G
1	1A	2084	A
1	1A	2091	G
1	1A	2115	G
1	1A	2132	G
1	1A	2135	U
1	1A	2136	A
1	1A	2137	G
1	1A	2138	G
1	1A	2143	G
1	1A	2149	G
1	1A	2151	C
1	1A	2152	U
1	1A	2153	G
1	1A	2154	U
1	1A	2155	G
1	1A	2156	A
1	1A	2157	A
1	1A	2162	C
1	1A	2163	G
1	1A	2164	C
1	1A	2166	U
1	1A	2168	C
1	1A	2172	U
1	1A	2173	G
1	1A	2178	G
1	1A	2179	G
1	1A	2180	A
1	1A	2181	G
1	1A	2182	G
1	1A	2184	G
1	1A	2187	G
1	1A	2188	G

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Mol	Chain	Res	Type
1	1A	2189	U
1	1A	2193	A
1	1A	2194	U
1	1A	2197	C
1	1A	2200	C
1	1A	2203	G
1	1A	2204	G
1	1A	2206	G
1	1A	2207	C
1	1A	2214	G
1	1A	2220	A
1	1A	2227	G
1	1A	2228	G
1	1A	2229	A
1	1A	2231	G
1	1A	2237	A
1	1A	2250	G
1	1A	2251	G
1	1A	2280	A
1	1A	2281	A
1	1A	2292	G
1	1A	2295	C
1	1A	2299	A
1	1A	2317	A
1	1A	2320	G
1	1A	2321	A
1	1A	2332	A
1	1A	2337	G
1	1A	2346	G
1	1A	2359	C
1	1A	2362	C
1	1A	2373	A
1	1A	2384	G
1	1A	2395	G
1	1A	2397	C
1	1A	2418	U
1	1A	2422	G
1	1A	2436	C
1	1A	2437	A
1	1A	2441	G
1	1A	2442	A
1	1A	2443	U

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Mol	Chain	Res	Type
1	1A	2447	A
1	1A	2451	A
1	1A	2453	C
1	1A	2460	A
1	1A	2486	C
1	1A	2488	A
1	1A	2514	G
1	1A	2517	G
1	1A	2518	U
1	1A	2530	A
1	1A	2541	G
1	1A	2561	G
1	1A	2566	U
1	1A	2578	A
1	1A	2579	G
1	1A	2585	C
1	1A	2586	G
1	1A	2590	G
1	1A	2614	A
1	1A	2621	U
1	1A	2623	U
1	1A	2624	C
1	1A	2641	A
1	1A	2642	G
1	1A	2653	G
1	1A	2666	A
1	1A	2701	U
1	1A	2702	C
1	1A	2703	C
1	1A	2714	U
1	1A	2725	A
1	1A	2726	A
1	1A	2727	G
1	1A	2739	U
1	1A	2746	A
1	1A	2770	A
1	1A	2771	A
1	1A	2778	A
1	1A	2782	C
1	1A	2791	A
1	1A	2803	A
1	1A	2804	C

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Mol	Chain	Res	Type
1	1A	2806	G
1	1A	2813	G
1	1A	2828	G
1	1A	2830	A
1	1A	2831	A
1	1A	2845	A
1	1A	2846	U
1	1A	2879	G
1	1A	2882	G
1	1A	2890	C
1	1A	2901	A
1	1A	2903	G
2	1B	2	C
2	1B	12	C
2	1B	25	A
2	1B	35	U
2	1B	45	A
2	1B	56	G
2	1B	67	G
2	1B	73	A
2	1B	85	G
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	47	C
32	1a	48	C
32	1a	51	A
32	1a	54	C
32	1a	61	G
32	1a	65	U
32	1a	79	G
32	1a	91	C
32	1a	97	G
32	1a	98	G
32	1a	101	A
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	163	C

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Mol	Chain	Res	Type
32	1a	174	C
32	1a	180	U
32	1a	182	U
32	1a	195	A
32	1a	197	A
32	1a	201	C
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	217	C
32	1a	247	G
32	1a	251	G
32	1a	258	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	301	G
32	1a	306	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	342	C
32	1a	348	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	384	G
32	1a	397	A
32	1a	398	C
32	1a	406	G
32	1a	412	A
32	1a	421	U
32	1a	423	G
32	1a	424	G
32	1a	429	U
32	1a	441	A
32	1a	442	C
32	1a	452	A

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Mol	Chain	Res	Type
32	1a	461	A
32	1a	470	C
32	1a	471	G
32	1a	477	A
32	1a	484	G
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	531	U
32	1a	532	A
32	1a	547	A
32	1a	559	A
32	1a	561	U
32	1a	568	G
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	630	G
32	1a	653	A
32	1a	665	A
32	1a	687	A
32	1a	688	G
32	1a	695	A
32	1a	721	G
32	1a	723	U
32	1a	731	G
32	1a	733	A
32	1a	749	C
32	1a	755	G
32	1a	774	G
32	1a	777	A
32	1a	792	A
32	1a	793	U
32	1a	794	A
32	1a	815	A

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Mol	Chain	Res	Type
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	853	G
32	1a	859	A
32	1a	870	U
32	1a	880	C
32	1a	885	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	932	C
32	1a	934	C
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	982	U
32	1a	989	C
32	1a	992	U
32	1a	993	G
32	1a	997	U
32	1a	1000	U
32	1a	1001(A)	G
32	1a	1002	G
32	1a	1003	G
32	1a	1005	A
32	1a	1006	C
32	1a	1009	G
32	1a	1011	G
32	1a	1016	A
32	1a	1020	U
32	1a	1021	G

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Mol	Chain	Res	Type
32	1a	1022	G
32	1a	1025	U
32	1a	1026	G
32	1a	1027	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(C)	G
32	1a	1031	G
32	1a	1033	G
32	1a	1039	C
32	1a	1045	C
32	1a	1054	C
32	1a	1065	U
32	1a	1066	C
32	1a	1068	G
32	1a	1080	A
32	1a	1081	G
32	1a	1086	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1108	G
32	1a	1122	U
32	1a	1125	U
32	1a	1129	C
32	1a	1130	A
32	1a	1132	C
32	1a	1134	G
32	1a	1137	C
32	1a	1138	G
32	1a	1139	G
32	1a	1140	C
32	1a	1141	C
32	1a	1146	A
32	1a	1152	A
32	1a	1159	U
32	1a	1163	C
32	1a	1172	C
32	1a	1181	G
32	1a	1183	A
32	1a	1184	G

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Mol	Chain	Res	Type
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1212	U
32	1a	1213	A
32	1a	1220	G
32	1a	1222	G
32	1a	1227	A
32	1a	1238	A
32	1a	1240	U
32	1a	1241	G
32	1a	1256	A
32	1a	1257	U
32	1a	1260	C
32	1a	1267	C
32	1a	1270	C
32	1a	1273	G
32	1a	1276	G
32	1a	1278	U
32	1a	1279	A
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1290	G
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1338	G
32	1a	1340	A
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1368	G
32	1a	1370	G
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1446	U
32	1a	1447	A
32	1a	1456	G

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Mol	Chain	Res	Type
32	1a	1487	G
32	1a	1492	A
32	1a	1494	G
32	1a	1497	G
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1517	G
32	1a	1529	G
32	1a	1530	G
32	1a	1532	U
53	1v	13	A
53	1v	14	A
53	1v	15	A
53	1v	24	A
54	1w	2	C
54	1w	6	G
54	1w	8	4SU
54	1w	14	A
54	1w	19	G
54	1w	20	U
54	1w	21	A
54	1w	23	A
54	1w	24	G
54	1w	45	U
54	1w	46	7MG
54	1w	47	U
54	1w	48	C
54	1w	50	U
54	1w	62	C
54	1w	64	A
54	1w	67	C
54	1w	68	C
54	1w	70	G
54	1w	72	C
54	1w	73	A
54	1w	74	C
55	1x	9	G
55	1x	18	G
55	1x	19	G
55	1x	21	A

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Mol	Chain	Res	Type
55	1x	47	U
55	1x	61	C
55	1x	69	C
55	1x	76	A
54	1y	6	G
54	1y	8	4SU
54	1y	9	A
54	1y	13	C
54	1y	19	G
54	1y	20	U
54	1y	21	A
54	1y	23	A
54	1y	35	A
54	1y	44	G
54	1y	45	U
54	1y	46	7MG
54	1y	47	U
54	1y	48	C
54	1y	49	C
54	1y	53	G
54	1y	54	5MU
54	1y	56	C
54	1y	59	U
54	1y	61	C
54	1y	65	G
54	1y	69	G
54	1y	70	G
1	2A	8	A
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	35	G
1	2A	45	C
1	2A	71	A
1	2A	74	A
1	2A	75	G
1	2A	84	A
1	2A	90	U
1	2A	94	C
1	2A	95	G
1	2A	100	G
1	2A	102	G

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Mol	Chain	Res	Type
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	127	A
1	2A	154(A)	C
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	196	A
1	2A	199	A
1	2A	205	G
1	2A	214	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	225	A
1	2A	228	A
1	2A	229	A
1	2A	233	A
1	2A	248	G
1	2A	249	C
1	2A	250	G
1	2A	267	C
1	2A	271(A)	A
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	271(O)	C
1	2A	272(B)	G
1	2A	272(I)	U
1	2A	272(J)	C
1	2A	274	G
1	2A	277	C
1	2A	278	A
1	2A	294	A
1	2A	303	U
1	2A	311	A
1	2A	316	C
1	2A	317	G
1	2A	324	A

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Mol	Chain	Res	Type
1	2A	325	G
1	2A	327	G
1	2A	329	G
1	2A	330	A
1	2A	333	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	363(B)	G
1	2A	363(D)	G
1	2A	386	G
1	2A	396	G
1	2A	402	A
1	2A	403	U
1	2A	405	U
1	2A	406	G
1	2A	407	G
1	2A	411	G
1	2A	412	A
1	2A	418	G
1	2A	421	U
1	2A	422	A
1	2A	435	C
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	481	G
1	2A	494	G
1	2A	501	A
1	2A	504	U
1	2A	505	A
1	2A	508	G
1	2A	509	C
1	2A	517	C
1	2A	520	G
1	2A	529	A
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	563	G

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Mol	Chain	Res	Type
1	2A	568	U
1	2A	573	G
1	2A	575	A
1	2A	588	U
1	2A	592	G
1	2A	599	G
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	621	A
1	2A	627	A
1	2A	634	C
1	2A	637	A
1	2A	645	C
1	2A	651	G
1	2A	652(B)	A
1	2A	652(U)	G
1	2A	667	U
1	2A	669	G
1	2A	686	G
1	2A	701	G
1	2A	709	U
1	2A	717	G
1	2A	730	C
1	2A	752	A
1	2A	753	C
1	2A	771	G
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	819	A
1	2A	827	U
1	2A	828	U
1	2A	847	U

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Mol	Chain	Res	Type
1	2A	857	C
1	2A	859	G
1	2A	866	A
1	2A	869	G
1	2A	870	A
1	2A	874	G
1	2A	875	G
1	2A	879	G
1	2A	880	G
1	2A	884	C
1	2A	886	C
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	894	C
1	2A	895	U
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	915	C
1	2A	917	A
1	2A	932	G
1	2A	933	A
1	2A	941	A
1	2A	944	G
1	2A	945	A
1	2A	946	G
1	2A	953	A
1	2A	958	U
1	2A	959	A
1	2A	961	C
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	997	G
1	2A	998	C
1	2A	1012	U
1	2A	1013	C

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Mol	Chain	Res	Type
1	2A	1017	G
1	2A	1020	A
1	2A	1022	G
1	2A	1025	G
1	2A	1026	U
1	2A	1033	U
1	2A	1038	C
1	2A	1039	G
1	2A	1041	C
1	2A	1042	G
1	2A	1043	C
1	2A	1114	G
1	2A	1116	C
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1139	G
1	2A	1142	U
1	2A	1144	G
1	2A	1166	C
1	2A	1169	G
1	2A	1171	G
1	2A	1180	C
1	2A	1188	U
1	2A	1205	U
1	2A	1206	G
1	2A	1210	A
1	2A	1211	U
1	2A	1218	C
1	2A	1220	A
1	2A	1224	C
1	2A	1237	A
1	2A	1248	G
1	2A	1250	G
1	2A	1252	G
1	2A	1253	A
1	2A	1256	G
1	2A	1268	A
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1287	A

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Mol	Chain	Res	Type
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A
1	2A	1345	C
1	2A	1352	U
1	2A	1359	A
1	2A	1360	A
1	2A	1365	A
1	2A	1368	G
1	2A	1370	C
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1411	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1427	A
1	2A	1428	C
1	2A	1435	G
1	2A	1437	C
1	2A	1445	A
1	2A	1449	A
1	2A	1450	G
1	2A	1460	A
1	2A	1467	C
1	2A	1471	A
1	2A	1482	G
1	2A	1490	A
1	2A	1493	C
1	2A	1494	A
1	2A	1495	A
1	2A	1496	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1514	U
1	2A	1531	C

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Mol	Chain	Res	Type
1	2A	1532	C
1	2A	1533	G
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1616	A
1	2A	1629	U
1	2A	1647	G
1	2A	1648	C
1	2A	1654	A
1	2A	1674	G
1	2A	1696	G
1	2A	1700	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1739	U
1	2A	1740	G
1	2A	1746	G
1	2A	1747(A)	G
1	2A	1756	G
1	2A	1758	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1769	G
1	2A	1773	A
1	2A	1780	A
1	2A	1782	C
1	2A	1786	A
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G

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Mol	Chain	Res	Type
1	2A	1811	G
1	2A	1812	A
1	2A	1816	G
1	2A	1828	G
1	2A	1835	G
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1857	G
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1913	A
1	2A	1914	C
1	2A	1929	G
1	2A	1930	G
1	2A	1931	U
1	2A	1936	A
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2027	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2062	A

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Mol	Chain	Res	Type
1	2A	2069	G
1	2A	2093	G
1	2A	2099	U
1	2A	2105	C
1	2A	2108	C
1	2A	2110	G
1	2A	2111	C
1	2A	2112	G
1	2A	2116	G
1	2A	2119	A
1	2A	2120	G
1	2A	2122	U
1	2A	2125	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2131	G
1	2A	2132	U
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2137	C
1	2A	2138	C
1	2A	2140	C
1	2A	2142	C
1	2A	2146	C
1	2A	2150	U
1	2A	2151	G
1	2A	2154	G
1	2A	2155	G
1	2A	2156	G
1	2A	2157	G
1	2A	2158	A
1	2A	2161	C
1	2A	2165	G
1	2A	2166	G
1	2A	2167	U
1	2A	2168	G
1	2A	2169	A
1	2A	2172	U
1	2A	2174	C
1	2A	2178	C

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Mol	Chain	Res	Type
1	2A	2185	C
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2225	A
1	2A	2232	U
1	2A	2235	G
1	2A	2239	G
1	2A	2275	C
1	2A	2279	G
1	2A	2283	C
1	2A	2287	A
1	2A	2302	G
1	2A	2305	A
1	2A	2308	G
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2324	C
1	2A	2325	G
1	2A	2327	A
1	2A	2328	A
1	2A	2329	G
1	2A	2334	G
1	2A	2336	A
1	2A	2341	G
1	2A	2346	A
1	2A	2347	C
1	2A	2350	C
1	2A	2354	G
1	2A	2376	A
1	2A	2383	G
1	2A	2385	C
1	2A	2403	C
1	2A	2406	U
1	2A	2410	G
1	2A	2419	U
1	2A	2425	A

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Mol	Chain	Res	Type
1	2A	2426	A
1	2A	2429	G
1	2A	2430	A
1	2A	2434	A
1	2A	2435	A
1	2A	2439	A
1	2A	2441	C
1	2A	2445	G
1	2A	2448	A
1	2A	2458	G
1	2A	2465	C
1	2A	2468	G
1	2A	2469	A
1	2A	2474	C
1	2A	2476	A
1	2A	2477	C
1	2A	2478	A
1	2A	2490	G
1	2A	2491	U
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2520	C
1	2A	2525	G
1	2A	2529	G
1	2A	2554	U
1	2A	2555	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2602	A
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2629	A
1	2A	2630	G
1	2A	2634	G
1	2A	2654	A
1	2A	2663	G
1	2A	2664	G

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Mol	Chain	Res	Type
1	2A	2689	U
1	2A	2690	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2739	U
1	2A	2744	G
1	2A	2751	G
1	2A	2758	A
1	2A	2764	A
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2789	C
1	2A	2793	G
1	2A	2802	G
1	2A	2803	C
1	2A	2807	G
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2824	C
1	2A	2833	G
1	2A	2836	U
1	2A	2839	G
1	2A	2872	G
1	2A	2879	C
1	2A	2880	C
1	2A	2894	G
1	2A	2895	U
1	2A	2897	U
2	2B	2	C
2	2B	5	C
2	2B	8	U
2	2B	9	G
2	2B	19	G
2	2B	20	C
2	2B	25	A
2	2B	32	C
2	2B	34	U

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Mol	Chain	Res	Type
2	2B	38	C
2	2B	42	C
2	2B	52	A
2	2B	53	A
2	2B	56	G
2	2B	57	A
2	2B	58	A
2	2B	63	G
2	2B	65	C
2	2B	66	A
2	2B	67	G
2	2B	72	G
2	2B	73	A
2	2B	74	U
2	2B	75	G
2	2B	85	G
2	2B	88	C
2	2B	90	A
2	2B	91	C
2	2B	106	G
2	2B	108	U
2	2B	110	G
2	2B	114	C
2	2B	116	G
2	2B	119	G
2	2B	120	A
32	2a	7	G
32	2a	9	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	51	A
32	2a	54	C
32	2a	65	U
32	2a	66	G
32	2a	73	G
32	2a	79	G
32	2a	80	G
32	2a	89	C
32	2a	91	C
32	2a	97	G

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Mol	Chain	Res	Type
32	2a	98	G
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	131	C
32	2a	163	C
32	2a	174	C
32	2a	180	U
32	2a	182	U
32	2a	195	A
32	2a	197	A
32	2a	201	C
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	217	C
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	289	G
32	2a	301	G
32	2a	306	G
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	342	C
32	2a	348	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	397	A
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	421	U

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Mol	Chain	Res	Type
32	2a	423	G
32	2a	424	G
32	2a	429	U
32	2a	441	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	471	G
32	2a	477	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	531	U
32	2a	532	A
32	2a	547	A
32	2a	559	A
32	2a	561	U
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	587	G
32	2a	588	G
32	2a	596	C
32	2a	630	G
32	2a	650	G
32	2a	653	A
32	2a	665	A
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	702	A
32	2a	721	G
32	2a	723	U

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Mol	Chain	Res	Type
32	2a	731	G
32	2a	733	A
32	2a	749	C
32	2a	755	G
32	2a	774	G
32	2a	777	A
32	2a	792	A
32	2a	793	U
32	2a	794	A
32	2a	815	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	853	G
32	2a	859	A
32	2a	870	U
32	2a	880	C
32	2a	902	G
32	2a	914	A
32	2a	926	G
32	2a	927	G
32	2a	932	C
32	2a	934	C
32	2a	960	U
32	2a	961	U
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	974	A
32	2a	975	A
32	2a	976	G
32	2a	977	A
32	2a	982	U
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	997	U
32	2a	1001(A)	G
32	2a	1002	G

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Mol	Chain	Res	Type
32	2a	1003	G
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1011	G
32	2a	1016	A
32	2a	1020	U
32	2a	1021	G
32	2a	1022	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1030	C
32	2a	1030(A)	G
32	2a	1031	G
32	2a	1033	G
32	2a	1036	G
32	2a	1038	C
32	2a	1039	C
32	2a	1040	U
32	2a	1045	C
32	2a	1051	C
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1077	G
32	2a	1080	A
32	2a	1081	G
32	2a	1086	U
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1108	G
32	2a	1117	G
32	2a	1122	U
32	2a	1125	U
32	2a	1129	C
32	2a	1130	A
32	2a	1132	C
32	2a	1134	G
32	2a	1137	C

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Mol	Chain	Res	Type
32	2a	1138	G
32	2a	1139	G
32	2a	1140	C
32	2a	1141	C
32	2a	1146	A
32	2a	1152	A
32	2a	1159	U
32	2a	1163	C
32	2a	1172	C
32	2a	1181	G
32	2a	1182	G
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1202	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1222	G
32	2a	1226	C
32	2a	1227	A
32	2a	1238	A
32	2a	1240	U
32	2a	1241	G
32	2a	1256	A
32	2a	1257	U
32	2a	1260	C
32	2a	1267	C
32	2a	1270	C
32	2a	1272	G
32	2a	1273	G
32	2a	1276	G
32	2a	1278	U
32	2a	1279	A
32	2a	1280	A
32	2a	1287	A
32	2a	1300	G
32	2a	1303	C
32	2a	1305	G
32	2a	1320	C
32	2a	1328	C

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Mol	Chain	Res	Type
32	2a	1338	G
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1363	C
32	2a	1368	G
32	2a	1370	G
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1456	G
32	2a	1487	G
32	2a	1492	A
32	2a	1494	G
32	2a	1497	G
32	2a	1503	A
32	2a	1504	G
32	2a	1506	U
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G
32	2a	1531	A
32	2a	1532	U
53	2v	13	A
53	2v	15	A
53	2v	24	A
54	2w	3	C
54	2w	4	C
54	2w	5	G
54	2w	7	A
54	2w	8	4SU
54	2w	9	A
54	2w	13	C
54	2w	14	A
54	2w	19	G
54	2w	22	G
54	2w	25	C
54	2w	29	G

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Mol	Chain	Res	Type
54	2w	34	G
54	2w	38	A
54	2w	46	7MG
54	2w	47	U
54	2w	48	C
54	2w	50	U
54	2w	56	C
54	2w	62	C
54	2w	63	G
54	2w	64	A
54	2w	65	G
54	2w	68	C
54	2w	69	G
54	2w	70	G
54	2w	74	C
55	2x	9	G
55	2x	10	G
55	2x	13	C
55	2x	18	G
55	2x	21	A
55	2x	22	G
55	2x	42	G
55	2x	43	A
55	2x	47	U
55	2x	48	C
55	2x	52	G
55	2x	53	G
55	2x	65	C
55	2x	67	C
55	2x	68	C
55	2x	76	A
54	2y	15	G
54	2y	19	G
54	2y	23	A
54	2y	24	G
54	2y	25	C
54	2y	27	G
54	2y	34	G
54	2y	45	U
54	2y	49	C
54	2y	52	G
54	2y	53	G

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Mol	Chain	Res	Type
54	2y	55	PSU
54	2y	56	C
54	2y	57	G
54	2y	58	A
54	2y	59	U
54	2y	61	C
54	2y	62	C
54	2y	63	G
54	2y	65	G
54	2y	69	G
54	2y	70	G
54	2y	73	A

All (72) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	115	G
1	1A	185	A
1	1A	271	U
1	1A	302	A
1	1A	509	A
1	1A	572	A
1	1A	596	G
1	1A	793	A
1	1A	821	A
1	1A	847	A
1	1A	913	A
1	1A	941	U
1	1A	1019	G
1	1A	1065	U
1	1A	1067	A
1	1A	1093	G
1	1A	1119	A
1	1A	1188	A
1	1A	1201	A
1	1A	1219	A
1	1A	1220	U
1	1A	1221	G
1	1A	1255	A
1	1A	1321	A
1	1A	1347	A

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Mol	Chain	Res	Type
1	1A	1425	A
1	1A	1466	U
1	1A	1554	A
1	1A	1654	A
1	1A	1700	G
1	1A	2014	G
1	1A	2156	A
1	1A	2180	A
1	1A	2192	A
1	1A	2203	G
1	1A	2205	C
1	1A	2418	U
1	1A	2442	A
1	1A	2451	A
1	1A	2641	A
1	1A	2701	U
1	1A	2769	U
2	1B	1	U
1	2A	34	C
1	2A	195	A
1	2A	196	A
1	2A	228	A
1	2A	266	G
1	2A	271(K)	U
1	2A	271(M)	G
1	2A	277	C
1	2A	528	A
1	2A	752	A
1	2A	774	A
1	2A	827	U
1	2A	856	C
1	2A	883	G
1	2A	900	A
1	2A	1210	A
1	2A	1420	U
1	2A	1442	G
1	2A	1530	C
1	2A	1608	A
1	2A	1653	G
1	2A	1913	A
1	2A	1992	G
1	2A	2119	A

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Mol	Chain	Res	Type
1	2A	2126	A
1	2A	2406	U
1	2A	2439	A
1	2A	2689	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	PSU	1A	1933	1	16,21,22	1.35	3 (18%)	20,30,33	3.38	6 (30%)
1	5MU	1A	1937	1	14,22,23	0.70	0	16,32,35	2.12	3 (18%)
1	PSU	1A	1939	1	16,21,22	1.59	3 (18%)	20,30,33	3.57	7 (35%)
1	4OC	1A	1942	1	15,22,24	0.74	0	19,31,35	0.79	0
1	5MU	1A	1961	1,56	14,22,23	0.79	1 (7%)	16,32,35	1.92	3 (18%)
1	5MC	1A	1964	1,56	15,22,23	1.40	1 (6%)	17,32,35	1.31	2 (11%)
1	5MC	1A	1984	1,56	15,22,23	1.34	1 (6%)	17,32,35	0.90	1 (5%)
1	OMG	1A	2263	1,55,56	18,26,27	1.24	2 (11%)	22,38,41	2.20	6 (27%)
1	2MA	1A	2515	1,56	18,25,26	1.69	4 (22%)	17,37,40	1.89	2 (11%)
1	2MU	1A	2564	1,56	14,22,24	0.86	1 (7%)	18,31,36	1.80	1 (5%)
1	PSU	1A	2617	1,56	16,21,22	1.84	3 (18%)	20,30,33	3.52	6 (30%)
32	2MG	1a	1207	32	19,26,27	1.34	2 (10%)	20,38,41	2.30	7 (35%)
32	5MC	1a	1400	32	15,22,23	1.39	1 (6%)	17,32,35	1.27	2 (11%)
32	4OC	1a	1402	32	16,23,24	0.81	0	19,32,35	1.52	1 (5%)
32	5MC	1a	1404	32	15,22,23	1.43	1 (6%)	17,32,35	1.13	2 (11%)
32	5MC	1a	1407	32	15,22,23	1.45	1 (6%)	17,32,35	1.16	2 (11%)
32	UR3	1a	1498	32	14,22,23	0.84	1 (7%)	16,32,35	0.77	1 (6%)
32	MA6	1a	1518	32	16,26,27	0.92	1 (6%)	18,38,41	2.44	7 (38%)
32	MA6	1a	1519	32	16,26,27	1.09	1 (6%)	18,38,41	2.10	5 (27%)
32	PSU	1a	516	32	16,21,22	1.28	2 (12%)	20,30,33	3.58	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	7MG	1a	527	32,56	20,26,27	1.59	3 (15%)	22,39,42	2.62	5 (22%)
32	M2G	1a	966	32	20,27,28	1.47	3 (15%)	21,40,43	2.24	7 (33%)
32	5MC	1a	967	32	15,22,23	1.42	1 (6%)	17,32,35	1.15	2 (11%)
43	0TD	1l	92	43	5,9,10	5.20	4 (80%)	3,11,13	4.30	2 (66%)
54	PSU	1w	32	54,56	16,21,22	1.31	1 (6%)	20,30,33	3.59	6 (30%)
54	MIA	1w	37	54	23,31,32	1.73	2 (8%)	25,44,47	1.62	5 (20%)
54	PSU	1w	39	54	16,21,22	1.37	1 (6%)	20,30,33	3.60	7 (35%)
54	7MG	1w	46	54	20,26,27	1.55	2 (10%)	22,39,42	2.97	5 (22%)
54	5MU	1w	54	54	14,22,23	0.78	0	16,32,35	2.26	3 (18%)
54	PSU	1w	55	54	16,21,22	1.19	1 (6%)	20,30,33	3.85	6 (30%)
54	4SU	1w	8	54	14,21,22	1.23	1 (7%)	15,30,33	1.56	2 (13%)
55	5MC	1x	32	55	15,22,23	1.42	1 (6%)	17,32,35	1.24	2 (11%)
55	5MU	1x	54	55,56	14,22,23	0.82	0	16,32,35	2.48	3 (18%)
55	PSU	1x	55	55,56	16,21,22	1.53	2 (12%)	20,30,33	3.61	7 (35%)
55	4SU	1x	8	55	14,21,22	1.34	2 (14%)	15,30,33	3.02	2 (13%)
54	PSU	1y	32	54	16,21,22	1.14	1 (6%)	20,30,33	3.69	6 (30%)
54	MIA	1y	37	54	18,24,32	1.23	2 (11%)	17,35,47	1.92	2 (11%)
54	PSU	1y	39	54	16,21,22	1.28	1 (6%)	20,30,33	3.63	6 (30%)
54	7MG	1y	46	54	20,26,27	1.71	2 (10%)	22,39,42	2.98	6 (27%)
54	5MU	1y	54	54	14,22,23	0.82	1 (7%)	16,32,35	2.37	3 (18%)
54	PSU	1y	55	54	16,21,22	1.47	1 (6%)	20,30,33	3.61	7 (35%)
54	4SU	1y	8	54	14,21,22	1.22	1 (7%)	15,30,33	1.73	2 (13%)
1	PSU	2A	1911	1	16,21,22	1.32	1 (6%)	20,30,33	3.75	6 (30%)
1	5MU	2A	1915	1	14,22,23	0.71	0	16,32,35	2.07	3 (18%)
1	PSU	2A	1917	1	16,21,22	1.43	1 (6%)	20,30,33	3.68	6 (30%)
1	4OC	2A	1920	1	15,22,24	0.75	0	19,31,35	0.86	0
1	5MU	2A	1939	1,56	14,22,23	0.80	1 (7%)	16,32,35	2.00	3 (18%)
1	5MC	2A	1942	1	15,22,23	1.30	1 (6%)	17,32,35	1.33	3 (17%)
1	5MC	2A	1962	1,56	15,22,23	1.35	1 (6%)	17,32,35	1.33	2 (11%)
1	OMG	2A	2251	1,55,56	18,26,27	1.28	2 (11%)	22,38,41	2.05	6 (27%)
1	2MA	2A	2503	1,56	18,25,26	1.47	4 (22%)	17,37,40	1.60	2 (11%)
1	2MU	2A	2552	1,56	14,22,24	1.12	1 (7%)	18,31,36	2.09	1 (5%)
1	PSU	2A	2605	1	16,21,22	1.19	1 (6%)	20,30,33	3.20	6 (30%)
32	2MG	2a	1207	32	19,26,27	1.29	2 (10%)	20,38,41	2.29	7 (35%)
32	5MC	2a	1400	32	15,22,23	1.44	1 (6%)	17,32,35	1.12	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	4OC	2a	1402	32,56	16,23,24	0.70	0	19,32,35	1.39	2 (10%)
32	5MC	2a	1404	32	15,22,23	1.43	1 (6%)	17,32,35	1.12	2 (11%)
32	5MC	2a	1407	32	15,22,23	1.40	1 (6%)	17,32,35	0.98	1 (5%)
32	UR3	2a	1498	32	14,22,23	0.81	0	16,32,35	0.75	0
32	MA6	2a	1518	32	16,26,27	1.01	1 (6%)	18,38,41	2.41	6 (33%)
32	MA6	2a	1519	32	16,26,27	1.06	1 (6%)	18,38,41	2.43	5 (27%)
32	PSU	2a	516	32	16,21,22	1.19	1 (6%)	20,30,33	3.68	7 (35%)
32	7MG	2a	527	32,56	20,26,27	1.81	2 (10%)	22,39,42	2.62	5 (22%)
32	M2G	2a	966	32	20,27,28	1.42	3 (15%)	21,40,43	2.24	6 (28%)
32	5MC	2a	967	32	15,22,23	1.61	2 (13%)	17,32,35	0.92	1 (5%)
43	0TD	2l	92	43	5,9,10	3.42	2 (40%)	3,11,13	3.20	1 (33%)
54	PSU	2w	32	54	16,21,22	1.39	1 (6%)	20,30,33	3.55	6 (30%)
54	MIA	2w	37	54	20,27,32	1.80	3 (15%)	21,39,47	1.63	6 (28%)
54	PSU	2w	39	54	16,21,22	1.29	1 (6%)	20,30,33	3.71	7 (35%)
54	7MG	2w	46	54	20,26,27	1.71	2 (10%)	22,39,42	2.51	4 (18%)
54	5MU	2w	54	54	14,22,23	0.71	0	16,32,35	2.54	2 (12%)
54	PSU	2w	55	54,56	16,21,22	1.14	1 (6%)	20,30,33	3.79	6 (30%)
54	4SU	2w	8	54	14,21,22	1.27	1 (7%)	15,30,33	1.22	2 (13%)
55	5MC	2x	32	55	15,22,23	1.33	1 (6%)	17,32,35	1.13	1 (5%)
55	5MU	2x	54	55	14,22,23	0.75	0	16,32,35	2.20	3 (18%)
55	PSU	2x	55	55	16,21,22	1.35	1 (6%)	20,30,33	3.63	7 (35%)
55	4SU	2x	8	55	14,21,22	1.27	2 (14%)	15,30,33	2.45	2 (13%)
54	PSU	2y	32	54	16,21,22	1.19	1 (6%)	20,30,33	3.57	6 (30%)
54	MIA	2y	37	54	18,24,32	1.19	2 (11%)	17,35,47	1.92	2 (11%)
54	PSU	2y	39	54	16,21,22	1.42	1 (6%)	20,30,33	3.79	6 (30%)
54	7MG	2y	46	54	20,26,27	1.88	3 (15%)	22,39,42	3.37	8 (36%)
54	5MU	2y	54	54	14,22,23	0.73	0	16,32,35	2.39	2 (12%)
54	PSU	2y	55	54	16,21,22	1.30	2 (12%)	20,30,33	3.77	7 (35%)
54	4SU	2y	8	54	14,21,22	1.33	1 (7%)	15,30,33	1.49	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1A	1933	1	-	0/7/25/26	0/2/2/2
1	5MU	1A	1937	1	-	0/3/25/26	0/2/2/2
1	PSU	1A	1939	1	-	0/7/25/26	0/2/2/2
1	4OC	1A	1942	1	-	0/5/27/30	0/2/2/2
1	5MU	1A	1961	1,56	-	0/3/25/26	0/2/2/2
1	5MC	1A	1964	1,56	-	0/3/25/26	0/2/2/2
1	5MC	1A	1984	1,56	-	0/3/25/26	0/2/2/2
1	OMG	1A	2263	1,55,56	-	0/5/27/28	0/3/3/3
1	2MA	1A	2515	1,56	-	0/3/25/26	0/3/3/3
1	2MU	1A	2564	1,56	-	0/5/27/28	0/2/2/2
1	PSU	1A	2617	1,56	-	0/7/25/26	0/2/2/2
32	2MG	1a	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	1a	1400	32	-	0/3/25/26	0/2/2/2
32	4OC	1a	1402	32	-	0/7/29/30	0/2/2/2
32	5MC	1a	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/3/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	1a	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	1a	516	32	-	0/7/25/26	0/2/2/2
32	7MG	1a	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	1a	966	32	-	0/7/29/30	0/3/3/3
32	5MC	1a	967	32	-	0/3/25/26	0/2/2/2
43	0TD	1l	92	43	-	0/2/12/14	0/0/0/0
54	PSU	1w	32	54,56	-	0/7/25/26	0/2/2/2
54	MIA	1w	37	54	-	0/11/33/34	0/3/3/3
54	PSU	1w	39	54	-	0/7/25/26	0/2/2/2
54	7MG	1w	46	54	-	0/7/37/38	0/3/3/3
54	5MU	1w	54	54	-	0/3/25/26	0/2/2/2
54	PSU	1w	55	54	-	0/7/25/26	0/2/2/2
54	4SU	1w	8	54	-	0/3/25/26	0/2/2/2
55	5MC	1x	32	55	-	0/3/25/26	0/2/2/2
55	5MU	1x	54	55,56	-	0/3/25/26	0/2/2/2
55	PSU	1x	55	55,56	-	0/7/25/26	0/2/2/2
55	4SU	1x	8	55	-	0/3/25/26	0/2/2/2
54	PSU	1y	32	54	-	0/7/25/26	0/2/2/2
54	MIA	1y	37	54	-	0/3/25/34	0/3/3/3
54	PSU	1y	39	54	-	0/7/25/26	0/2/2/2
54	7MG	1y	46	54	-	0/7/37/38	0/3/3/3
54	5MU	1y	54	54	-	0/3/25/26	0/2/2/2
54	PSU	1y	55	54	-	0/7/25/26	0/2/2/2
54	4SU	1y	8	54	-	0/3/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	2A	1915	1	-	0/3/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
1	4OC	2A	1920	1	-	0/5/27/30	0/2/2/2
1	5MU	2A	1939	1,56	-	0/3/25/26	0/2/2/2
1	5MC	2A	1942	1	-	0/3/25/26	0/2/2/2
1	5MC	2A	1962	1,56	-	0/3/25/26	0/2/2/2
1	OMG	2A	2251	1,55,56	-	0/5/27/28	0/3/3/3
1	2MA	2A	2503	1,56	-	0/3/25/26	0/3/3/3
1	2MU	2A	2552	1,56	-	0/5/27/28	0/2/2/2
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/5/27/28	0/3/3/3
32	5MC	2a	1400	32	-	0/3/25/26	0/2/2/2
32	4OC	2a	1402	32,56	-	0/7/29/30	0/2/2/2
32	5MC	2a	1404	32	-	0/3/25/26	0/2/2/2
32	5MC	2a	1407	32	-	0/3/25/26	0/2/2/2
32	UR3	2a	1498	32	-	0/3/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/7/29/30	0/3/3/3
32	MA6	2a	1519	32	-	0/7/29/30	0/3/3/3
32	PSU	2a	516	32	-	0/7/25/26	0/2/2/2
32	7MG	2a	527	32,56	-	0/7/37/38	0/3/3/3
32	M2G	2a	966	32	-	0/7/29/30	0/3/3/3
32	5MC	2a	967	32	-	0/3/25/26	0/2/2/2
43	0TD	2l	92	43	-	0/2/12/14	0/0/0/0
54	PSU	2w	32	54	-	0/7/25/26	0/2/2/2
54	MIA	2w	37	54	-	0/7/29/34	0/3/3/3
54	PSU	2w	39	54	-	0/7/25/26	0/2/2/2
54	7MG	2w	46	54	-	0/7/37/38	0/3/3/3
54	5MU	2w	54	54	-	0/3/25/26	0/2/2/2
54	PSU	2w	55	54,56	-	0/7/25/26	0/2/2/2
54	4SU	2w	8	54	-	0/3/25/26	0/2/2/2
55	5MC	2x	32	55	-	0/3/25/26	0/2/2/2
55	5MU	2x	54	55	-	0/3/25/26	0/2/2/2
55	PSU	2x	55	55	-	0/7/25/26	0/2/2/2
55	4SU	2x	8	55	-	0/3/25/26	0/2/2/2
54	PSU	2y	32	54	-	0/7/25/26	0/2/2/2
54	MIA	2y	37	54	-	0/3/25/34	0/3/3/3
54	PSU	2y	39	54	-	0/7/25/26	0/2/2/2
54	7MG	2y	46	54	-	0/7/37/38	0/3/3/3
54	5MU	2y	54	54	-	0/3/25/26	0/2/2/2
54	PSU	2y	55	54	-	0/7/25/26	0/2/2/2
54	4SU	2y	8	54	-	0/3/25/26	0/2/2/2

All (115) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	2l	92	0TD	CB-SB	-6.86	1.67	1.84
54	1w	37	MIA	C2-S10	-6.85	1.70	1.75
43	1l	92	0TD	CB-SB	-6.82	1.67	1.84
54	2w	37	MIA	C2-S10	-6.08	1.70	1.75
1	1A	2617	PSU	C5-C1'	-5.47	1.47	1.52
1	1A	1939	PSU	C5-C1'	-4.91	1.48	1.52
54	1y	55	PSU	C5-C1'	-4.79	1.48	1.52
55	1x	55	PSU	C5-C1'	-4.57	1.48	1.52
54	2y	39	PSU	C5-C1'	-4.54	1.48	1.52
1	2A	1917	PSU	C5-C1'	-4.30	1.48	1.52
54	2w	32	PSU	C5-C1'	-4.22	1.48	1.52
54	1w	39	PSU	C5-C1'	-4.11	1.48	1.52
55	2x	55	PSU	C5-C1'	-4.08	1.48	1.52
54	2y	8	4SU	C4-S4	-4.05	1.59	1.67
54	2w	8	4SU	C4-S4	-3.97	1.59	1.67
54	1w	32	PSU	C5-C1'	-3.85	1.48	1.52
54	1w	8	4SU	C4-S4	-3.78	1.60	1.67
54	2w	39	PSU	C5-C1'	-3.73	1.49	1.52
1	1A	1933	PSU	C5-C1'	-3.72	1.49	1.52
54	2y	55	PSU	C5-C1'	-3.72	1.49	1.52
54	1y	39	PSU	C5-C1'	-3.62	1.49	1.52
1	2A	1911	PSU	C5-C1'	-3.59	1.49	1.52
55	1x	8	4SU	C2-N3	-3.44	1.31	1.38
55	2x	8	4SU	C4-S4	-3.44	1.60	1.67
54	1w	55	PSU	C5-C1'	-3.40	1.49	1.52
54	1y	8	4SU	C4-S4	-3.40	1.61	1.67
54	2y	32	PSU	C5-C1'	-3.26	1.49	1.52
32	2a	516	PSU	C5-C1'	-3.25	1.49	1.52
32	1a	516	PSU	C5-C1'	-3.19	1.49	1.52
43	1l	92	0TD	CSB-SB	-3.18	1.73	1.79
1	2A	2605	PSU	C5-C1'	-3.16	1.49	1.52
55	1x	8	4SU	C4-S4	-3.16	1.61	1.67
54	2w	55	PSU	C5-C1'	-3.11	1.49	1.52
54	1y	32	PSU	C5-C1'	-2.82	1.49	1.52
55	2x	8	4SU	C2-N3	-2.67	1.32	1.38
1	2A	2552	2MU	O5'-C5'	-2.65	1.41	1.44
1	1A	2617	PSU	C2-N1	-2.63	1.32	1.38
1	1A	2617	PSU	C2-N3	-2.57	1.33	1.38
43	1l	92	0TD	CA-N	-2.43	1.39	1.47
1	1A	2515	2MA	O5'-C5'	-2.40	1.41	1.44
32	1a	527	7MG	O5'-C5'	-2.27	1.41	1.44
1	1A	1939	PSU	C2-N1	-2.20	1.33	1.38
54	2y	55	PSU	C2-N1	-2.18	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	516	PSU	C2-N3	-2.14	1.33	1.38
1	2A	2503	2MA	O5'-C5'	-2.11	1.41	1.44
1	2A	1939	5MU	C2-N3	-2.11	1.34	1.38
1	1A	1939	PSU	C2-N3	-2.07	1.34	1.38
32	2a	967	5MC	O5'-C5'	-2.06	1.41	1.44
1	1A	2564	2MU	C2-N3	-2.05	1.34	1.38
1	1A	1933	PSU	O5'-C5'	-2.03	1.41	1.44
1	1A	1961	5MU	C2-N3	-2.03	1.34	1.38
55	1x	55	PSU	O5'-C5'	-2.02	1.41	1.44
54	1y	54	5MU	C2-N3	-2.02	1.34	1.38
1	1A	1933	PSU	C2-N3	-2.00	1.34	1.38
32	1a	1498	UR3	C4-N3	2.24	1.41	1.38
54	2w	37	MIA	C6-N1	2.27	1.36	1.33
54	1y	37	MIA	C2-N3	2.35	1.36	1.32
54	2y	37	MIA	C2-N3	2.44	1.36	1.32
1	2A	2503	2MA	C5-C4	2.64	1.46	1.40
54	2y	46	7MG	C4-N3	2.73	1.37	1.34
1	1A	2515	2MA	C5-C4	2.77	1.46	1.40
32	1a	1518	MA6	C5-C4	2.91	1.47	1.40
43	2l	92	0TD	CA-C	2.91	1.54	1.50
1	2A	2251	OMG	C5-C4	2.97	1.47	1.40
1	1A	2263	OMG	C5-C4	2.99	1.47	1.40
32	2a	1519	MA6	C5-C4	3.10	1.47	1.40
32	1a	966	M2G	C5-C4	3.13	1.47	1.40
32	1a	1519	MA6	C5-C4	3.14	1.47	1.40
32	1a	1207	2MG	C5-C4	3.15	1.47	1.40
1	2A	2503	2MA	C6-N6	3.15	1.34	1.27
32	2a	527	7MG	C5-C4	3.16	1.47	1.39
32	2a	1207	2MG	C5-C4	3.16	1.47	1.40
54	1w	37	MIA	C5-C4	3.20	1.47	1.40
32	2a	1518	MA6	C5-C4	3.22	1.47	1.40
54	2w	46	7MG	C5-C4	3.23	1.47	1.39
32	2a	966	M2G	C5-C4	3.24	1.47	1.40
32	2a	966	M2G	C2-N2	3.26	1.40	1.34
32	1a	527	7MG	C5-C4	3.29	1.48	1.39
54	2y	37	MIA	C5-C4	3.31	1.48	1.40
54	2w	37	MIA	C5-C4	3.34	1.48	1.40
54	1y	46	7MG	C5-C4	3.38	1.48	1.39
54	1y	37	MIA	C5-C4	3.39	1.48	1.40
1	1A	2263	OMG	C6-C5	3.41	1.47	1.41
54	1w	46	7MG	C5-C4	3.43	1.48	1.39
1	2A	2503	2MA	C6-C5	3.57	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	966	M2G	C2-N2	3.67	1.40	1.34
32	1a	966	M2G	C6-C5	3.69	1.48	1.41
54	2y	46	7MG	C5-C4	3.69	1.49	1.39
1	1A	2515	2MA	C6-N6	3.72	1.36	1.27
1	2A	2251	OMG	C6-C5	3.73	1.48	1.41
32	2a	966	M2G	C6-C5	3.84	1.48	1.41
32	1a	1207	2MG	C6-C5	3.94	1.48	1.41
32	2a	1207	2MG	C6-C5	3.99	1.48	1.41
1	1A	2515	2MA	C6-C5	4.47	1.48	1.41
1	2A	1942	5MC	C5-C4	4.51	1.48	1.41
1	2A	1962	5MC	C5-C4	4.56	1.48	1.41
32	2a	1407	5MC	C5-C4	4.62	1.48	1.41
55	2x	32	5MC	C5-C4	4.65	1.48	1.41
1	1A	1964	5MC	C5-C4	4.67	1.48	1.41
1	1A	1984	5MC	C5-C4	4.71	1.48	1.41
54	1w	46	7MG	C6-C5	4.81	1.47	1.41
32	1a	1404	5MC	C5-C4	4.83	1.48	1.41
32	1a	1400	5MC	C5-C4	4.85	1.48	1.41
55	1x	32	5MC	C5-C4	4.90	1.48	1.41
32	1a	1407	5MC	C5-C4	4.93	1.48	1.41
32	2a	1404	5MC	C5-C4	5.01	1.48	1.41
32	1a	967	5MC	C5-C4	5.01	1.48	1.41
32	2a	1400	5MC	C5-C4	5.02	1.48	1.41
32	1a	527	7MG	C6-C5	5.22	1.47	1.41
32	2a	967	5MC	C5-C4	5.63	1.49	1.41
54	1y	46	7MG	C6-C5	5.77	1.48	1.41
54	2y	46	7MG	C6-C5	5.90	1.48	1.41
54	2w	46	7MG	C6-C5	5.98	1.48	1.41
32	2a	527	7MG	C6-C5	6.62	1.49	1.41
43	1l	92	0TD	CA-C	8.52	1.61	1.50

All (328) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2y	55	PSU	N1-C2-N3	-10.53	120.82	128.40
54	2w	39	PSU	N1-C2-N3	-10.29	121.00	128.40
32	2a	516	PSU	N1-C2-N3	-10.08	121.15	128.40
32	1a	516	PSU	N1-C2-N3	-10.02	121.19	128.40
1	2A	1911	PSU	N1-C2-N3	-9.95	121.24	128.40
54	1w	55	PSU	N1-C2-N3	-9.91	121.27	128.40
54	1y	32	PSU	N1-C2-N3	-9.84	121.32	128.40
54	1y	39	PSU	N1-C2-N3	-9.77	121.37	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2w	55	PSU	N1-C2-N3	-9.75	121.39	128.40
54	1y	55	PSU	C5-C4-N3	-9.74	117.44	125.43
54	2y	39	PSU	N1-C2-N3	-9.68	121.43	128.40
54	2y	32	PSU	N1-C2-N3	-9.65	121.45	128.40
1	2A	2605	PSU	N1-C2-N3	-9.52	121.55	128.40
54	1w	39	PSU	N1-C2-N3	-9.48	121.58	128.40
1	2A	1917	PSU	N1-C2-N3	-9.45	121.60	128.40
54	1w	32	PSU	N1-C2-N3	-9.43	121.62	128.40
55	1x	55	PSU	N1-C2-N3	-9.42	121.62	128.40
1	1A	1933	PSU	N1-C2-N3	-9.40	121.64	128.40
54	2w	32	PSU	N1-C2-N3	-9.13	121.83	128.40
1	2A	1917	PSU	C5-C4-N3	-9.12	117.95	125.43
55	2x	55	PSU	C5-C4-N3	-9.08	117.98	125.43
55	2x	55	PSU	N1-C2-N3	-9.07	121.87	128.40
1	1A	2617	PSU	N1-C2-N3	-8.98	121.94	128.40
54	1w	39	PSU	C5-C4-N3	-8.87	118.15	125.43
54	1w	55	PSU	C5-C4-N3	-8.79	118.22	125.43
54	2y	39	PSU	C5-C4-N3	-8.78	118.22	125.43
55	1x	55	PSU	C5-C4-N3	-8.78	118.23	125.43
1	1A	1939	PSU	N1-C2-N3	-8.76	122.10	128.40
54	1y	32	PSU	C5-C4-N3	-8.75	118.25	125.43
54	2w	32	PSU	C5-C4-N3	-8.72	118.28	125.43
54	1y	55	PSU	N1-C2-N3	-8.66	122.17	128.40
1	2A	1911	PSU	C5-C4-N3	-8.66	118.33	125.43
54	2y	32	PSU	C5-C4-N3	-8.58	118.39	125.43
54	1y	39	PSU	C5-C4-N3	-8.57	118.40	125.43
32	2a	516	PSU	C5-C4-N3	-8.53	118.43	125.43
1	1A	1939	PSU	C5-C4-N3	-8.52	118.44	125.43
1	1A	2617	PSU	C5-C4-N3	-8.46	118.49	125.43
54	1w	32	PSU	C5-C4-N3	-8.38	118.56	125.43
54	2w	55	PSU	C5-C4-N3	-8.33	118.59	125.43
54	2y	55	PSU	C5-C4-N3	-8.29	118.63	125.43
54	2w	39	PSU	C5-C4-N3	-8.20	118.70	125.43
32	1a	516	PSU	C5-C4-N3	-8.02	118.85	125.43
1	1A	1933	PSU	C5-C4-N3	-7.42	119.34	125.43
54	2y	37	MIA	N3-C2-N1	-6.74	122.98	128.86
54	1y	37	MIA	N3-C2-N1	-6.60	123.11	128.86
32	2a	1518	MA6	N3-C2-N1	-6.36	123.32	128.86
32	1a	1518	MA6	N3-C2-N1	-6.36	123.32	128.86
32	2a	1519	MA6	N3-C2-N1	-6.35	123.33	128.86
1	2A	2605	PSU	C5-C4-N3	-6.04	120.47	125.43
55	1x	54	5MU	C5-C4-N3	-5.98	118.64	125.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1402	4OC	CM4-N4-C4	-5.95	117.80	122.94
54	1w	46	7MG	C5-C6-N1	-5.90	114.11	123.37
54	2w	54	5MU	C5-C4-N3	-5.89	118.75	125.24
54	2w	55	PSU	C5-C1'-C2'	-5.66	105.78	115.55
55	2x	54	5MU	C5-C4-N3	-5.64	119.02	125.24
54	1y	54	5MU	C5-C4-N3	-5.61	119.05	125.24
54	1w	54	5MU	C5-C4-N3	-5.57	119.10	125.24
54	1w	55	PSU	C5-C1'-C2'	-5.56	105.96	115.55
54	2y	46	7MG	C5-C6-N1	-5.53	114.69	123.37
54	2y	46	7MG	C5-C4-N3	-5.49	117.31	126.47
55	1x	8	4SU	C5-C4-N3	-5.48	116.80	123.73
54	2y	54	5MU	C5-C4-N3	-5.45	119.23	125.24
54	1y	46	7MG	C5-C6-N1	-5.38	114.93	123.37
1	1A	1937	5MU	C5-C4-N3	-5.18	119.53	125.24
54	2y	39	PSU	C5-C1'-C2'	-5.16	106.65	115.55
54	2w	46	7MG	C5-C6-N1	-5.02	115.49	123.37
32	1a	527	7MG	C5-C6-N1	-5.01	115.50	123.37
32	1a	1519	MA6	N3-C2-N1	-4.92	124.57	128.86
1	1A	1939	PSU	C5-C1'-C2'	-4.89	107.11	115.55
32	2a	527	7MG	C5-C4-N3	-4.89	118.30	126.47
1	2A	1915	5MU	C5-C4-N3	-4.77	119.98	125.24
54	1y	46	7MG	C5-C4-N3	-4.75	118.54	126.47
55	2x	8	4SU	C5-C4-N3	-4.74	117.74	123.73
54	1w	37	MIA	C12-N6-C6	-4.72	117.18	123.26
32	2a	1402	4OC	CM4-N4-C4	-4.70	118.89	122.94
32	2a	527	7MG	C5-C6-N1	-4.58	116.19	123.37
32	1a	527	7MG	C5-C4-N3	-4.52	118.92	126.47
1	1A	2617	PSU	C5-C6-N1	-4.46	118.61	124.39
1	1A	2263	OMG	C6-C5-C4	-4.43	116.44	120.84
1	2A	1939	5MU	C5-C4-N3	-4.40	120.38	125.24
54	2w	46	7MG	C5-C4-N3	-4.29	119.30	126.47
32	1a	1207	2MG	C5-C6-N1	-4.26	117.42	123.48
54	1y	8	4SU	C5-C4-N3	-4.21	118.41	123.73
32	2a	966	M2G	C5-C6-N1	-4.20	117.51	123.48
1	2A	1939	5MU	C5-C6-N1	-4.19	117.61	122.15
32	2a	1207	2MG	C5-C6-N1	-4.18	117.53	123.48
54	1w	46	7MG	C5-C4-N3	-4.09	119.64	126.47
1	1A	1933	PSU	C5-C6-N1	-4.06	119.13	124.39
1	2A	1911	PSU	C5-C1'-C2'	-4.04	108.57	115.55
32	1a	966	M2G	C5-C6-N1	-4.00	117.79	123.48
55	2x	55	PSU	C5-C6-N1	-4.00	119.21	124.39
55	1x	55	PSU	C5-C6-N1	-3.97	119.25	124.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2w	32	PSU	C5-C6-N1	-3.94	119.28	124.39
1	1A	1961	5MU	C5-C4-N3	-3.94	120.89	125.24
1	2A	2605	PSU	C5-C6-N1	-3.93	119.30	124.39
1	1A	1939	PSU	C5-C6-N1	-3.91	119.32	124.39
54	2w	39	PSU	C5-C6-N1	-3.89	119.34	124.39
54	1y	55	PSU	C5-C6-N1	-3.87	119.38	124.39
1	2A	1917	PSU	C5-C6-N1	-3.86	119.39	124.39
32	1a	1518	MA6	C4-C5-N7	-3.85	105.69	109.41
1	1A	2263	OMG	N3-C2-N1	-3.82	121.88	127.46
1	2A	2251	OMG	C5-C6-N1	-3.76	118.13	123.48
54	1w	32	PSU	C5-C1'-C2'	-3.74	109.10	115.55
54	2y	39	PSU	C5-C6-N1	-3.73	119.56	124.39
54	2y	32	PSU	C5-C6-N1	-3.68	119.62	124.39
54	2y	55	PSU	C5-C6-N1	-3.66	119.64	124.39
32	2a	1207	2MG	C6-C5-C4	-3.65	117.21	120.84
54	2w	55	PSU	C5-C6-N1	-3.64	119.67	124.39
32	1a	1207	2MG	C6-C5-C4	-3.63	117.23	120.84
32	2a	516	PSU	C5-C6-N1	-3.62	119.69	124.39
54	1w	32	PSU	C5-C6-N1	-3.62	119.69	124.39
54	1w	39	PSU	C5-C6-N1	-3.62	119.69	124.39
32	2a	1207	2MG	C4-C5-N7	-3.61	105.92	109.41
1	1A	1961	5MU	C5-C6-N1	-3.55	118.30	122.15
32	1a	966	M2G	C6-C5-C4	-3.54	117.33	120.84
1	1A	2263	OMG	C5-C6-N1	-3.51	118.49	123.48
32	1a	516	PSU	C5-C6-N1	-3.48	119.87	124.39
32	2a	1518	MA6	C9-N6-C6	-3.46	109.05	119.51
32	1a	1207	2MG	C4-C5-N7	-3.43	106.10	109.41
54	1y	39	PSU	C5-C6-N1	-3.42	119.95	124.39
32	2a	1518	MA6	C4-C5-N7	-3.39	106.14	109.41
54	1y	32	PSU	C5-C6-N1	-3.33	120.07	124.39
32	2a	966	M2G	C6-C5-C4	-3.31	117.56	120.84
1	2A	1917	PSU	C5-C1'-C2'	-3.29	109.87	115.55
54	2w	37	MIA	C4-C5-N7	-3.29	106.23	109.41
1	2A	2251	OMG	N3-C2-N1	-3.27	122.69	127.46
55	2x	55	PSU	C5-C1'-C2'	-3.26	109.92	115.55
54	1w	8	4SU	C5-C4-N3	-3.21	119.68	123.73
32	1a	1519	MA6	C9-N6-C6	-3.19	109.85	119.51
54	2w	37	MIA	C12-N6-C6	-3.19	120.12	122.85
1	1A	2515	2MA	C4-C5-N7	-3.18	106.34	109.41
32	1a	1519	MA6	C4-C5-N7	-3.17	106.34	109.41
54	1w	37	MIA	C5-C6-N1	-3.16	117.48	120.64
1	2A	1911	PSU	C5-C6-N1	-3.15	120.30	124.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2251	OMG	C6-C5-C4	-3.15	117.71	120.84
54	2y	55	PSU	C5-C1'-C2'	-3.15	110.12	115.55
54	2w	37	MIA	C5-C6-N1	-3.15	117.50	120.64
54	1y	37	MIA	C4-C5-N7	-3.08	106.43	109.41
32	1a	1518	MA6	C9-N6-C6	-3.07	110.23	119.51
54	1w	55	PSU	C5-C6-N1	-3.06	120.43	124.39
32	1a	1400	5MC	C5-C6-N1	-3.05	118.84	122.15
32	2a	1519	MA6	C9-N6-C6	-3.00	110.44	119.51
54	1w	46	7MG	C5-C4-N9	-2.96	102.00	106.31
1	1A	1964	5MC	C5-C6-N1	-2.85	119.06	122.15
32	2a	1519	MA6	C4-C5-N7	-2.82	106.68	109.41
32	2a	966	M2G	C4-C5-N7	-2.81	106.69	109.41
54	2w	39	PSU	C5-C1'-C2'	-2.79	110.74	115.55
54	1w	37	MIA	C4-C5-N7	-2.77	106.73	109.41
32	1a	966	M2G	C4-C5-N7	-2.76	106.74	109.41
1	2A	1915	5MU	C5-C6-N1	-2.76	119.16	122.15
1	2A	2251	OMG	C4-C5-N7	-2.75	106.75	109.41
55	1x	55	PSU	C5-C1'-C2'	-2.75	110.80	115.55
32	1a	967	5MC	C5-C6-N1	-2.73	119.19	122.15
54	2w	32	PSU	C5-C1'-C2'	-2.70	110.89	115.55
54	2y	8	4SU	C5-C4-N3	-2.69	120.34	123.73
1	2A	1962	5MC	C5-C6-N1	-2.67	119.25	122.15
54	1y	32	PSU	C5-C1'-C2'	-2.66	110.97	115.55
54	2y	46	7MG	C5-C4-N9	-2.65	102.46	106.31
1	2A	1942	5MC	CM5-C5-C4	-2.58	119.00	121.65
1	1A	2617	PSU	C5-C1'-C2'	-2.57	111.12	115.55
32	2a	1400	5MC	C5-C6-N1	-2.57	119.37	122.15
54	1w	37	MIA	N3-C2-N1	-2.55	122.27	126.85
54	1y	54	5MU	C5-C6-N1	-2.54	119.40	122.15
32	1a	966	M2G	CM2-N2-C2	-2.53	118.93	121.34
54	1y	46	7MG	C5-C4-N9	-2.52	102.65	106.31
32	2a	516	PSU	C5-C1'-C2'	-2.51	111.22	115.55
32	2a	966	M2G	CM1-N2-C2	-2.51	118.95	121.34
54	2y	37	MIA	C4-C5-N7	-2.50	106.99	109.41
54	2y	46	7MG	N1-C2-N3	-2.49	121.42	125.45
32	2a	1518	MA6	C10-N6-C9	-2.49	107.98	116.03
32	1a	1404	5MC	C5-C6-N1	-2.47	119.47	122.15
54	2w	8	4SU	C5-C4-N3	-2.43	120.67	123.73
55	1x	54	5MU	C5-C6-N1	-2.42	119.53	122.15
32	2a	967	5MC	C5-C6-N1	-2.40	119.55	122.15
43	1l	92	0TD	O-C-CA	-2.40	119.56	125.15
54	2w	37	MIA	N3-C2-N1	-2.38	122.57	126.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1407	5MC	C5-C6-N1	-2.37	119.59	122.15
32	1a	1518	MA6	C10-N6-C9	-2.36	108.38	116.03
55	2x	54	5MU	C5-C6-N1	-2.35	119.61	122.15
1	2A	2605	PSU	C5-C1'-C2'	-2.33	111.52	115.55
1	2A	1942	5MC	C5-C6-N1	-2.32	119.64	122.15
54	1y	55	PSU	C5-C1'-C2'	-2.28	111.61	115.55
1	2A	2503	2MA	C4-C5-N7	-2.26	107.22	109.41
32	2a	1207	2MG	CM2-N2-C2	-2.26	120.88	123.63
1	1A	2263	OMG	C4-C5-N7	-2.26	107.23	109.41
54	1w	54	5MU	C5-C6-N1	-2.25	119.72	122.15
32	2a	1207	2MG	C1'-N9-C4	-2.24	122.77	126.64
1	1A	1937	5MU	C5-C6-N1	-2.22	119.75	122.15
32	1a	1207	2MG	N3-C2-N1	-2.18	122.93	126.23
32	1a	1518	MA6	C1'-N9-C4	-2.10	123.01	126.64
55	1x	32	5MC	C5-C6-N1	-2.09	119.89	122.15
32	2a	1404	5MC	C5-C6-N1	-2.08	119.90	122.15
54	1w	39	PSU	C5-C1'-C2'	-2.08	111.96	115.55
32	1a	527	7MG	C5-C4-N9	-2.05	103.33	106.31
32	2a	1402	4OC	C5-C4-N3	-2.04	119.80	123.21
32	2a	1518	MA6	C1'-N9-C4	-2.04	123.11	126.64
1	1A	1933	PSU	C5-C1'-C2'	-2.03	112.05	115.55
32	1a	1518	MA6	C10-N6-C6	-2.01	113.43	119.51
55	1x	55	PSU	O4'-C1'-C2'	2.01	107.69	104.45
54	2w	37	MIA	N6-C6-N1	2.02	121.13	118.55
54	1y	39	PSU	O4'-C1'-C2'	2.04	107.72	104.45
1	1A	1939	PSU	O4'-C1'-C2'	2.05	107.75	104.45
54	1w	39	PSU	O4'-C1'-C2'	2.06	107.76	104.45
54	1y	46	7MG	C2-N3-C4	2.08	119.78	113.95
54	2w	39	PSU	O4'-C1'-C2'	2.10	107.83	104.45
1	1A	1984	5MC	N4-C4-N3	2.10	120.11	117.00
32	2a	1407	5MC	N4-C4-N3	2.11	120.12	117.00
55	2x	55	PSU	O4'-C1'-C2'	2.12	107.85	104.45
32	2a	527	7MG	C2-N3-C4	2.17	120.04	113.95
32	1a	516	PSU	O4'-C1'-C2'	2.20	107.98	104.45
32	1a	967	5MC	N4-C4-N3	2.20	120.26	117.00
32	1a	1404	5MC	N4-C4-N3	2.20	120.26	117.00
32	2a	516	PSU	O4'-C1'-C2'	2.22	108.02	104.45
54	2y	55	PSU	O4'-C1'-C2'	2.24	108.05	104.45
54	2y	32	PSU	O4'-C1'-C2'	2.25	108.06	104.45
54	1y	55	PSU	O4'-C1'-C2'	2.25	108.07	104.45
32	1a	1498	UR3	C3U-N3-C4	2.31	121.21	118.15
54	2y	46	7MG	C2-N3-C4	2.36	120.58	113.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1400	5MC	N4-C4-N3	2.38	120.53	117.00
32	1a	966	M2G	N3-C2-N2	2.51	119.74	117.15
32	2a	1404	5MC	N4-C4-N3	2.53	120.74	117.00
32	1a	1407	5MC	N4-C4-N3	2.53	120.74	117.00
32	1a	1400	5MC	N4-C4-N3	2.54	120.76	117.00
32	1a	1207	2MG	N2-C2-N3	2.69	119.56	116.95
1	2A	1942	5MC	N4-C4-N3	2.92	121.32	117.00
1	1A	1964	5MC	N4-C4-N3	2.93	121.33	117.00
55	2x	32	5MC	N4-C4-N3	2.94	121.34	117.00
54	2w	37	MIA	C2-N1-C6	2.97	122.21	113.47
54	2y	46	7MG	N2-C2-N3	2.98	122.00	117.24
55	1x	32	5MC	N4-C4-N3	3.00	121.44	117.00
54	1w	37	MIA	C2-N1-C6	3.19	122.86	113.47
54	2w	8	4SU	C2-N3-C4	3.37	120.08	115.11
1	2A	1962	5MC	N4-C4-N3	3.63	122.36	117.00
32	1a	1519	MA6	N1-C6-N6	3.68	120.91	117.00
54	1y	55	PSU	C6-N1-C2	3.77	121.40	115.36
54	1y	39	PSU	C6-N1-C2	3.93	121.64	115.36
1	2A	1911	PSU	C6-N1-C2	3.93	121.65	115.36
32	1a	1519	MA6	C2-N1-C6	3.93	121.47	111.82
54	1w	39	PSU	C6-N1-C2	3.98	121.73	115.36
54	1w	55	PSU	C6-N1-C2	4.01	121.78	115.36
32	2a	1207	2MG	C6-N1-C2	4.03	122.40	115.18
55	2x	55	PSU	C6-N1-C2	4.07	121.87	115.36
55	1x	55	PSU	C6-N1-C2	4.07	121.87	115.36
1	1A	1939	PSU	C6-N1-C2	4.11	121.94	115.36
54	1y	32	PSU	C6-N1-C2	4.16	122.02	115.36
54	2y	32	PSU	C6-N1-C2	4.17	122.03	115.36
54	2y	39	PSU	C6-N1-C2	4.18	122.05	115.36
1	2A	1917	PSU	C6-N1-C2	4.19	122.07	115.36
54	2w	32	PSU	C6-N1-C2	4.21	122.10	115.36
54	2w	55	PSU	C6-N1-C2	4.23	122.12	115.36
1	2A	2251	OMG	C6-N1-C2	4.23	122.14	116.06
32	2a	1519	MA6	C2-N1-C6	4.24	122.23	111.82
54	2y	8	4SU	C2-N3-C4	4.28	121.42	115.11
32	1a	516	PSU	C6-N1-C2	4.29	122.22	115.36
54	1w	32	PSU	C6-N1-C2	4.34	122.31	115.36
32	1a	1207	2MG	C6-N1-C2	4.36	122.98	115.18
54	2w	39	PSU	C6-N1-C2	4.39	122.39	115.36
32	2a	516	PSU	C6-N1-C2	4.40	122.41	115.36
1	1A	1933	PSU	C6-N1-C2	4.43	122.45	115.36
32	2a	1518	MA6	C2-N1-C6	4.44	122.71	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2A	2605	PSU	C6-N1-C2	4.44	122.47	115.36
32	1a	1207	2MG	C2-N3-C4	4.56	120.31	115.11
32	2a	527	7MG	C6-N1-C2	4.56	122.62	116.06
32	2a	1519	MA6	N1-C6-N6	4.60	121.88	117.00
32	1a	1518	MA6	C2-N1-C6	4.60	123.12	111.82
1	2A	1939	5MU	C4-N3-C2	4.65	119.23	115.16
54	1w	8	4SU	C2-N3-C4	4.66	121.99	115.11
54	1y	8	4SU	C2-N3-C4	4.67	122.00	115.11
32	2a	1207	2MG	C2-N3-C4	4.67	120.44	115.11
1	1A	2617	PSU	C6-N1-C2	4.68	122.85	115.36
1	1A	1961	5MU	C4-N3-C2	4.73	119.29	115.16
54	2w	46	7MG	C6-N1-C2	4.84	123.02	116.06
32	2a	966	M2G	C2-N3-C4	4.85	120.65	115.11
1	1A	2263	OMG	C6-N1-C2	4.86	123.05	116.06
54	2y	55	PSU	C6-N1-C2	4.87	123.15	115.36
32	1a	527	7MG	C6-N1-C2	4.89	123.09	116.06
32	1a	966	M2G	C2-N3-C4	4.96	120.77	115.11
1	1A	2263	OMG	C2-N3-C4	5.01	121.01	115.16
1	2A	2251	OMG	C2-N3-C4	5.12	121.13	115.16
1	2A	2605	PSU	C4-N3-C2	5.20	119.70	115.16
32	2a	966	M2G	C6-N1-C2	5.21	122.39	116.18
32	1a	966	M2G	C6-N1-C2	5.34	122.54	116.18
43	2l	92	0TD	CSB-SB-CB	5.37	111.61	101.60
1	2A	2503	2MA	C2-N3-C4	5.74	120.37	115.41
1	2A	1915	5MU	C4-N3-C2	5.83	120.26	115.16
55	2x	54	5MU	C4-N3-C2	5.85	120.28	115.16
1	1A	1933	PSU	C4-N3-C2	5.90	120.32	115.16
1	1A	2617	PSU	C4-N3-C2	5.91	120.33	115.16
1	1A	1937	5MU	C4-N3-C2	5.92	120.34	115.16
54	1y	46	7MG	C6-N1-C2	6.14	124.89	116.06
1	1A	1939	PSU	C4-N3-C2	6.28	120.66	115.16
54	1w	54	5MU	C4-N3-C2	6.37	120.73	115.16
1	1A	2515	2MA	C2-N3-C4	6.46	120.99	115.41
54	1w	32	PSU	C4-N3-C2	6.46	120.81	115.16
54	2w	32	PSU	C4-N3-C2	6.47	120.82	115.16
54	1w	46	7MG	C6-N1-C2	6.53	125.46	116.06
55	1x	55	PSU	C4-N3-C2	6.60	120.93	115.16
54	1y	55	PSU	C4-N3-C2	6.64	120.97	115.16
54	2y	55	PSU	C4-N3-C2	6.67	120.99	115.16
54	1y	54	5MU	C4-N3-C2	6.72	121.04	115.16
55	2x	55	PSU	C4-N3-C2	6.77	121.08	115.16
1	2A	1917	PSU	C4-N3-C2	6.81	121.12	115.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	2y	32	PSU	C4-N3-C2	6.82	121.13	115.16
54	2w	55	PSU	C4-N3-C2	6.84	121.14	115.16
54	2y	39	PSU	C4-N3-C2	6.87	121.17	115.16
43	1l	92	0TD	CSB-SB-CB	6.88	114.44	101.60
32	2a	516	PSU	C4-N3-C2	6.88	121.18	115.16
54	2y	46	7MG	C6-N1-C2	6.92	126.02	116.06
54	2w	39	PSU	C4-N3-C2	6.97	121.26	115.16
54	1w	39	PSU	C4-N3-C2	7.00	121.28	115.16
32	1a	516	PSU	C4-N3-C2	7.10	121.36	115.16
54	1w	55	PSU	C4-N3-C2	7.19	121.45	115.16
54	1y	32	PSU	C4-N3-C2	7.24	121.49	115.16
55	1x	54	5MU	C4-N3-C2	7.25	121.50	115.16
1	1A	2564	2MU	C4-N3-C2	7.25	120.36	114.13
54	2y	54	5MU	C4-N3-C2	7.31	121.55	115.16
54	1y	39	PSU	C4-N3-C2	7.48	121.70	115.16
1	2A	1911	PSU	C4-N3-C2	7.53	121.75	115.16
54	2w	46	7MG	N3-C4-N9	7.65	136.76	126.98
54	2w	54	5MU	C4-N3-C2	7.70	121.90	115.16
55	2x	8	4SU	C2-N3-C4	7.95	126.84	115.11
1	2A	2552	2MU	C4-N3-C2	8.02	121.02	114.13
32	1a	527	7MG	N3-C4-N9	8.41	137.72	126.98
32	2a	527	7MG	N3-C4-N9	8.56	137.91	126.98
54	1w	46	7MG	N3-C4-N9	8.88	138.32	126.98
54	1y	46	7MG	N3-C4-N9	9.26	138.80	126.98
55	1x	8	4SU	C2-N3-C4	9.95	129.79	115.11
54	2y	46	7MG	N3-C4-N9	10.36	140.22	126.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1A	1939	PSU	1	0
1	1A	1961	5MU	1	0
1	1A	2564	2MU	2	0
1	2A	1911	PSU	1	0
1	2A	1915	5MU	1	0
1	2A	1917	PSU	1	0
1	2A	1920	4OC	2	0
1	2A	2251	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2A	2503	2MA	2	0
1	2A	2552	2MU	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2853 ligands modelled in this entry, 2851 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
59	SF4	1d	501	35	0,12,12	0.00	-	0,24,24	0.00	-
59	SF4	2d	501	35	0,12,12	0.00	-	0,24,24	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	SF4	1d	501	35	-	0/0/48/48	0/6/5/5
59	SF4	2d	501	35	-	0/0/48/48	0/6/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1A	2860/2915 (98%)	0.70	77 (2%) 55 58	24, 43, 91, 103	0
1	2A	2789/2915 (95%)	0.09	81 (2%) 52 55	28, 48, 89, 106	0
2	1B	120/121 (99%)	0.63	0 100 100	39, 61, 72, 90	0
2	2B	120/121 (99%)	-0.04	2 (1%) 70 72	45, 68, 77, 91	0
3	1D	275/276 (99%)	0.64	4 (1%) 74 75	25, 42, 58, 80	0
3	2D	275/276 (99%)	0.45	4 (1%) 74 75	28, 45, 61, 78	0
4	1E	204/206 (99%)	0.68	3 (1%) 74 75	23, 46, 66, 80	0
4	2E	204/206 (99%)	0.60	5 (2%) 58 60	26, 50, 67, 80	0
5	1F	203/210 (96%)	0.84	2 (0%) 82 83	22, 51, 76, 91	0
5	2F	203/210 (96%)	0.28	1 (0%) 90 91	27, 56, 76, 91	0
6	1G	181/182 (99%)	0.65	4 (2%) 62 64	48, 69, 80, 92	0
6	2G	181/182 (99%)	1.21	37 (20%) 1 1	54, 73, 81, 93	0
7	1H	174/180 (96%)	0.65	1 (0%) 89 89	47, 64, 74, 83	0
7	2H	174/180 (96%)	1.85	64 (36%) 0 0	54, 70, 78, 83	0
8	1I	146/148 (98%)	0.50	6 (4%) 38 40	49, 73, 82, 85	0
8	2I	146/148 (98%)	0.86	18 (12%) 5 4	50, 73, 82, 86	0
9	1N	140/140 (100%)	0.92	1 (0%) 87 88	31, 48, 67, 77	0
9	2N	140/140 (100%)	0.61	5 (3%) 43 45	37, 53, 71, 80	0
10	1O	122/122 (100%)	0.46	1 (0%) 86 86	23, 40, 60, 74	0
10	2O	122/122 (100%)	0.90	9 (7%) 15 15	45, 59, 72, 81	0
11	1P	149/150 (99%)	0.85	1 (0%) 87 88	24, 53, 75, 81	0
11	2P	149/150 (99%)	0.59	12 (8%) 13 12	29, 58, 76, 85	0
12	1Q	141/141 (100%)	0.79	2 (1%) 75 76	33, 51, 68, 77	0
12	2Q	141/141 (100%)	1.02	17 (12%) 5 4	37, 56, 73, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	0.67	1 (0%) 86 86	29, 40, 55, 62	0
13	2R	118/118 (100%)	0.37	2 (1%) 70 72	31, 43, 58, 65	0
14	1S	110/112 (98%)	0.76	2 (1%) 69 70	49, 62, 72, 77	0
14	2S	110/112 (98%)	0.88	11 (10%) 8 7	55, 66, 75, 79	0
15	1T	131/146 (89%)	0.59	4 (3%) 49 52	38, 51, 72, 77	0
15	2T	131/146 (89%)	0.52	3 (2%) 61 63	43, 53, 74, 78	0
16	1U	116/118 (98%)	1.04	3 (2%) 56 59	26, 39, 55, 73	0
16	2U	116/118 (98%)	0.27	1 (0%) 84 85	33, 46, 61, 73	0
17	1V	101/101 (100%)	0.94	1 (0%) 82 83	28, 51, 67, 76	0
17	2V	101/101 (100%)	0.29	3 (2%) 51 53	33, 57, 70, 76	0
18	1W	112/113 (99%)	0.92	1 (0%) 84 85	26, 37, 55, 88	0
18	2W	112/113 (99%)	0.34	0 100 100	30, 41, 57, 88	0
19	1X	95/96 (98%)	0.81	1 (1%) 80 81	30, 44, 63, 75	0
19	2X	95/96 (98%)	0.28	1 (1%) 80 81	34, 49, 65, 76	0
20	1Y	107/110 (97%)	0.79	2 (1%) 67 69	45, 57, 74, 83	0
20	2Y	107/110 (97%)	0.94	15 (14%) 3 3	48, 61, 76, 86	0
21	1Z	154/206 (74%)	0.63	8 (5%) 28 29	38, 64, 86, 96	0
21	2Z	160/206 (77%)	1.53	44 (27%) 1 0	72, 83, 93, 99	0
22	10	83/85 (97%)	0.77	3 (3%) 43 45	25, 38, 59, 71	0
22	20	83/85 (97%)	0.91	6 (7%) 16 16	41, 66, 78, 82	0
23	11	97/98 (98%)	0.53	2 (2%) 64 66	23, 44, 71, 77	0
23	21	97/98 (98%)	0.79	6 (6%) 21 22	38, 58, 74, 82	0
24	12	70/72 (97%)	0.82	1 (1%) 75 76	40, 57, 66, 79	0
24	22	70/72 (97%)	0.19	1 (1%) 75 76	46, 61, 69, 78	0
25	13	59/60 (98%)	0.89	0 100 100	29, 45, 69, 83	0
25	23	59/60 (98%)	0.52	1 (1%) 70 72	36, 51, 72, 87	0
26	14	69/71 (97%)	0.69	7 (10%) 8 7	64, 79, 89, 97	0
26	24	69/71 (97%)	1.17	14 (20%) 1 1	70, 80, 89, 97	0
27	15	59/60 (98%)	0.97	1 (1%) 70 72	25, 36, 57, 72	0
27	25	59/60 (98%)	0.21	0 100 100	30, 40, 60, 71	0
28	16	53/54 (98%)	0.71	0 100 100	38, 51, 64, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.67	4 (7%)	15 15	42, 54, 65, 71	0
29	17	48/49 (97%)	0.92	3 (6%)	21 21	24, 31, 58, 69	0
29	27	48/49 (97%)	0.70	4 (8%)	12 12	28, 35, 58, 70	0
30	18	64/65 (98%)	0.84	2 (3%)	49 52	33, 42, 50, 66	0
30	28	64/65 (98%)	0.85	4 (6%)	21 21	38, 46, 53, 67	0
31	19	37/37 (100%)	0.88	0	100 100	37, 50, 67, 68	0
31	29	37/37 (100%)	1.58	9 (24%)	1 0	46, 54, 71, 72	0
32	1a	1488/1521 (97%)	0.38	48 (3%)	48 51	42, 72, 92, 103	0
32	2a	1491/1521 (98%)	0.43	77 (5%)	28 29	44, 74, 93, 103	0
33	1b	231/256 (90%)	0.50	12 (5%)	28 29	69, 82, 89, 94	0
33	2b	231/256 (90%)	1.27	58 (25%)	1 0	72, 83, 89, 94	0
34	1c	206/239 (86%)	0.83	20 (9%)	8 8	67, 80, 86, 92	0
34	2c	206/239 (86%)	1.81	79 (38%)	0 0	69, 82, 88, 93	0
35	1d	208/209 (99%)	0.93	25 (12%)	5 4	56, 72, 80, 87	0
35	2d	208/209 (99%)	1.13	31 (14%)	3 2	58, 71, 80, 88	0
36	1e	148/162 (91%)	0.88	14 (9%)	9 8	56, 72, 80, 86	0
36	2e	148/162 (91%)	1.66	43 (29%)	1 0	59, 74, 83, 87	0
37	1f	100/101 (99%)	0.31	1 (1%)	82 83	50, 66, 76, 78	0
37	2f	100/101 (99%)	0.21	1 (1%)	82 83	60, 72, 80, 86	0
38	1g	155/156 (99%)	0.88	17 (10%)	6 5	62, 74, 83, 100	0
38	2g	155/156 (99%)	1.02	24 (15%)	2 2	65, 76, 84, 102	0
39	1h	137/138 (99%)	0.65	7 (5%)	29 30	60, 72, 78, 83	0
39	2h	137/138 (99%)	1.15	28 (20%)	1 1	64, 74, 80, 84	0
40	1i	127/128 (99%)	1.09	23 (18%)	1 1	51, 75, 83, 87	0
40	2i	127/128 (99%)	2.38	68 (53%)	0 0	71, 85, 91, 92	0
41	1j	97/105 (92%)	0.89	13 (13%)	4 3	59, 78, 90, 95	0
41	2j	96/105 (91%)	2.16	47 (48%)	0 0	74, 87, 94, 98	0
42	1k	114/129 (88%)	0.65	4 (3%)	44 47	52, 69, 80, 83	0
42	2k	114/129 (88%)	0.57	5 (4%)	35 37	55, 71, 81, 87	0
43	1l	121/132 (91%)	0.62	3 (2%)	58 60	53, 64, 74, 77	0
43	2l	121/132 (91%)	1.34	30 (24%)	1 0	55, 67, 75, 80	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	123/126 (97%)	0.60	7 (5%) 24 25	54, 69, 78, 82	0
44	2m	122/126 (96%)	1.65	39 (31%) 0 0	73, 84, 90, 94	0
45	1n	60/61 (98%)	1.14	10 (16%) 2 1	57, 69, 78, 82	0
45	2n	60/61 (98%)	3.36	47 (78%) 0 0	78, 85, 93, 95	0
46	1o	88/89 (98%)	0.61	5 (5%) 24 25	56, 69, 78, 83	0
46	2o	88/89 (98%)	0.59	5 (5%) 24 25	57, 70, 80, 83	0
47	1p	82/88 (93%)	1.76	31 (37%) 0 0	58, 70, 80, 83	0
47	2p	82/88 (93%)	1.01	9 (10%) 6 5	59, 69, 81, 82	0
48	1q	99/105 (94%)	0.79	7 (7%) 17 17	57, 70, 79, 82	0
48	2q	99/105 (94%)	1.22	25 (25%) 1 0	60, 70, 79, 82	0
49	1r	68/88 (77%)	0.56	5 (7%) 15 15	60, 68, 79, 82	0
49	2r	68/88 (77%)	0.50	5 (7%) 15 15	60, 70, 80, 82	0
50	1s	83/93 (89%)	0.74	4 (4%) 31 32	70, 79, 86, 91	0
50	2s	83/93 (89%)	2.16	37 (44%) 0 0	74, 81, 88, 94	0
51	1t	96/106 (90%)	1.38	29 (30%) 1 0	58, 71, 80, 86	0
51	2t	96/106 (90%)	1.04	16 (16%) 2 1	59, 71, 81, 85	0
52	1u	23/27 (85%)	1.43	7 (30%) 0 0	65, 74, 78, 80	0
52	2u	23/27 (85%)	1.99	8 (34%) 0 0	68, 75, 80, 83	0
53	1v	13/24 (54%)	2.66	7 (53%) 0 0	60, 74, 92, 98	0
53	2v	13/24 (54%)	3.36	8 (61%) 0 0	65, 78, 95, 98	0
54	1w	67/76 (88%)	1.86	19 (28%) 1 0	44, 89, 97, 101	0
54	1y	67/76 (88%)	0.99	13 (19%) 1 1	37, 91, 97, 101	0
54	2w	65/76 (85%)	2.68	41 (63%) 0 0	56, 96, 101, 104	0
54	2y	66/76 (86%)	1.20	14 (21%) 1 1	51, 95, 99, 100	0
55	1x	72/77 (93%)	0.31	2 (2%) 53 56	33, 66, 84, 87	0
55	2x	72/77 (93%)	0.23	1 (1%) 75 76	52, 81, 90, 95	0
All	All	20875/21748 (95%)	0.69	1607 (7%) 14 14	22, 63, 89, 106	0

All (1607) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	25	VAL	12.7
38	2g	82	GLY	10.8

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Mol	Chain	Res	Type	RSRZ
44	1m	124	PRO	10.1
44	2m	124	PRO	10.0
54	2w	71	G	9.6
54	1w	70	G	9.2
36	2e	12	LEU	8.9
50	2s	80	TYR	8.6
45	2n	39	LEU	8.4
54	2y	36	A	8.4
45	2n	34	TYR	8.4
40	2i	115	GLY	8.3
5	2F	208	GLY	8.3
32	2a	1030(B)	C	8.2
54	2w	70	G	8.0
50	2s	79	THR	7.9
44	2m	123	ALA	7.8
21	2Z	144	LEU	7.8
54	1w	71	G	7.7
21	2Z	149	SER	7.6
34	2c	198	VAL	7.5
40	2i	7	THR	7.3
45	2n	38	GLY	7.3
34	2c	182	ILE	7.3
41	2j	47	PHE	7.2
6	2G	29	TRP	7.2
33	2b	165	VAL	7.1
1	2A	229	A	7.1
34	2c	157	ILE	7.0
54	2w	72	C	7.0
44	2m	119	GLY	7.0
34	2c	8	ILE	6.9
53	2v	14	A	6.7
34	2c	155	GLY	6.6
1	2A	883	G	6.6
50	2s	82	GLY	6.6
33	2b	118	LEU	6.5
26	24	49	PHE	6.5
53	2v	24	A	6.5
34	2c	124	ILE	6.5
36	2e	90	VAL	6.4
1	2A	2154	G	6.3
7	2H	45	VAL	6.2
44	2m	120	LYS	6.2

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Mol	Chain	Res	Type	RSRZ
21	2Z	155	LEU	6.1
41	2j	85	LEU	6.1
50	2s	41	VAL	6.1
38	2g	83	ALA	6.1
41	2j	72	VAL	6.0
21	2Z	141	VAL	6.0
54	1w	44	G	6.0
43	2l	39	VAL	6.0
51	1t	9	ASN	6.0
45	2n	13	THR	6.0
44	2m	90	LEU	6.0
54	2w	4	C	5.9
51	1t	13	LEU	5.9
7	2H	72	ILE	5.9
50	2s	50	ALA	5.9
1	2A	2155	G	5.9
44	1m	2	ALA	5.9
32	1a	1001(A)	G	5.8
32	2a	1030(A)	G	5.8
32	1a	1030(B)	C	5.8
54	2w	31	A	5.8
40	2i	17	VAL	5.8
36	2e	94	ALA	5.7
54	1y	35	A	5.6
40	2i	36	TYR	5.6
40	1i	14	VAL	5.6
44	2m	60	VAL	5.6
40	2i	76	ALA	5.6
53	2v	12	A	5.6
1	1A	2162	C	5.6
34	2c	53	ALA	5.5
44	2m	87	TYR	5.5
54	2w	3	C	5.5
38	1g	79	ARG	5.5
1	1A	1141	A	5.5
41	2j	50	ILE	5.5
52	2u	6	ARG	5.5
38	2g	81	GLY	5.5
38	2g	80	VAL	5.4
40	2i	114	TYR	5.4
36	2e	29	GLY	5.4
45	2n	42	ILE	5.3

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Mol	Chain	Res	Type	RSRZ
38	2g	16	LEU	5.3
34	2c	194	GLY	5.3
7	2H	52	VAL	5.3
54	2w	13	C	5.3
7	2H	128	PRO	5.3
53	2v	23	A	5.3
7	2H	35	VAL	5.2
33	2b	92	TYR	5.2
1	2A	2802	G	5.2
7	2H	102	ALA	5.2
41	2j	48	THR	5.2
40	2i	61	ALA	5.2
26	24	63	TYR	5.2
45	2n	50	LYS	5.2
41	2j	55	LYS	5.2
12	2Q	33	GLY	5.2
45	2n	36	PHE	5.2
53	1v	14	A	5.2
1	2A	2145	C	5.2
6	2G	28	VAL	5.2
34	2c	145	GLY	5.1
41	2j	71	LEU	5.1
21	2Z	139	VAL	5.1
1	2A	2139	C	5.1
38	2g	4	ARG	5.1
20	2Y	45	VAL	5.1
54	1w	69	G	5.1
33	2b	81	VAL	5.1
40	2i	52	ALA	5.1
38	2g	156	TRP	5.1
40	2i	14	VAL	5.1
54	2y	34	G	5.1
50	2s	13	ASP	5.1
32	2a	1035	A	5.0
54	1w	72	C	5.0
44	2m	118	ALA	5.0
26	14	66	SER	5.0
32	1a	163	C	5.0
45	2n	6	LEU	5.0
54	2y	35	A	5.0
45	2n	58	LYS	5.0
39	1h	93	VAL	5.0

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Mol	Chain	Res	Type	RSRZ
53	1v	24	A	5.0
26	24	50	VAL	4.9
34	2c	6	HIS	4.9
40	2i	125	TYR	4.9
43	2l	95	GLY	4.9
44	1m	123	ALA	4.9
45	2n	53	LEU	4.9
40	2i	9	ARG	4.9
51	1t	12	ALA	4.9
1	2A	888	C	4.9
53	1v	12	A	4.9
23	2l	2	SER	4.9
41	2j	74	ILE	4.9
38	1g	80	VAL	4.8
1	2A	885	C	4.8
40	2i	79	LEU	4.8
38	2g	7	ALA	4.8
20	2Y	5	MET	4.8
33	2b	136	VAL	4.8
43	2l	55	VAL	4.8
1	1A	936	C	4.8
44	2m	122	LYS	4.8
40	2i	15	ALA	4.8
44	2m	82	MET	4.8
41	2j	54	PHE	4.8
41	2j	65	LEU	4.8
32	1a	1036	G	4.7
32	2a	1034	G	4.7
32	2a	1036	G	4.7
26	24	51	ASP	4.7
33	2b	152	PHE	4.7
1	2A	896	A	4.7
21	2Z	57	ILE	4.7
1	2A	884	C	4.7
7	2H	105	LEU	4.7
41	2j	10	GLY	4.7
41	2j	39	PRO	4.7
6	1G	139	LEU	4.7
33	2b	101	MET	4.7
40	1i	106	ALA	4.7
22	20	45	PHE	4.7
48	1q	27	PHE	4.7

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Mol	Chain	Res	Type	RSRZ
1	2A	887	A	4.7
38	2g	6	ARG	4.7
1	1A	1142	A	4.6
53	2v	13	A	4.6
18	1W	112	GLY	4.6
40	2i	103	THR	4.6
50	2s	63	THR	4.6
1	1A	2163	G	4.6
51	1t	14	LYS	4.6
34	2c	180	ALA	4.6
40	2i	109	VAL	4.6
35	1d	180	GLY	4.6
40	2i	127	LYS	4.6
1	1A	1140	U	4.6
54	1w	20	U	4.6
38	1g	82	GLY	4.6
45	2n	24	CYS	4.5
44	2m	102	ARG	4.5
1	2A	2133	G	4.5
34	2c	188	LEU	4.5
50	2s	14	HIS	4.5
1	2A	2153	G	4.5
53	1v	23	A	4.5
21	2Z	173	ALA	4.5
7	2H	98	LEU	4.5
53	2v	22	U	4.5
32	2a	1033	G	4.5
44	2m	96	LEU	4.5
45	2n	44	LEU	4.5
33	2b	214	ILE	4.5
36	2e	86	ALA	4.5
34	1c	15	THR	4.4
1	2A	2149	G	4.4
54	1w	4	C	4.4
40	2i	81	ILE	4.4
38	1g	156	TRP	4.4
45	2n	47	LEU	4.4
1	2A	2160	G	4.4
34	2c	167	TRP	4.4
36	2e	109	ILE	4.4
45	1n	2	ALA	4.4
39	2h	2	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
40	2i	106	ALA	4.4
45	2n	61	TRP	4.4
40	2i	128	ARG	4.4
7	2H	115	VAL	4.4
40	2i	126	SER	4.4
1	1A	2153	G	4.4
7	2H	37	VAL	4.3
14	2S	32	LEU	4.3
7	2H	123	PHE	4.3
1	2A	2141	G	4.3
44	2m	100	GLY	4.3
40	2i	116	LYS	4.3
36	2e	31	LEU	4.3
1	2A	2146	C	4.3
35	2d	168	ARG	4.3
1	1A	1115	A	4.3
48	2q	80	GLY	4.3
20	2Y	65	ALA	4.3
6	2G	11	TYR	4.3
33	2b	34	ALA	4.3
44	2m	97	PRO	4.3
51	1t	70	SER	4.3
33	2b	187	LEU	4.3
32	1a	1002	G	4.3
32	2a	1001(A)	G	4.3
45	2n	10	ALA	4.3
40	2i	86	VAL	4.3
48	2q	92	ARG	4.3
50	2s	75	ALA	4.3
34	1c	39	ILE	4.2
36	2e	80	ILE	4.2
1	1A	1110	C	4.2
54	2w	2	C	4.2
45	2n	37	PHE	4.2
51	2t	9	ASN	4.2
21	1Z	169	GLU	4.2
45	2n	12	ARG	4.2
33	2b	200	ILE	4.2
1	1A	1138	C	4.2
54	1y	34	G	4.2
54	2w	5	G	4.2
47	1p	1	MET	4.2

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Mol	Chain	Res	Type	RSRZ
32	1a	1257	U	4.2
1	1A	1144	A	4.2
32	1a	162	A	4.2
42	1k	25	TYR	4.2
41	2j	98	ILE	4.2
36	2e	81	GLU	4.2
31	29	16	VAL	4.2
36	2e	10	MET	4.2
36	2e	115	VAL	4.2
21	2Z	125	LEU	4.2
40	2i	27	THR	4.2
34	2c	160	ALA	4.2
54	1w	73	A	4.2
54	1y	13	C	4.2
54	1y	36	A	4.2
22	20	3	HIS	4.1
52	2u	15	ARG	4.1
54	1w	2	C	4.1
50	2s	52	TYR	4.1
44	2m	78	ILE	4.1
45	2n	29	ARG	4.1
1	2A	2127	G	4.1
44	2m	6	GLY	4.1
44	2m	68	GLY	4.1
21	2Z	170	THR	4.1
1	1A	932	C	4.1
4	2E	52	LEU	4.1
32	1a	204	U	4.1
33	2b	37	ASN	4.1
32	1a	1023	G	4.1
40	2i	124	GLN	4.1
34	2c	60	ALA	4.1
1	1A	933	C	4.1
45	2n	51	GLY	4.1
53	1v	22	U	4.1
39	2h	93	VAL	4.1
54	2w	69	G	4.1
7	2H	6	ARG	4.1
41	2j	40	LEU	4.1
54	2w	56	C	4.1
40	2i	49	PRO	4.1
1	1A	2173	G	4.1

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Mol	Chain	Res	Type	RSRZ
34	2c	197	GLY	4.1
29	17	48	LYS	4.0
32	2a	1150	U	4.0
35	2d	164	ALA	4.0
32	1a	1026	G	4.0
32	2a	1220	G	4.0
47	1p	2	VAL	4.0
50	1s	40	ILE	4.0
21	2Z	96	VAL	4.0
48	2q	23	VAL	4.0
54	1w	3	C	4.0
32	1a	160	A	4.0
32	1a	161	A	4.0
40	2i	123	PRO	4.0
50	2s	81	ARG	4.0
12	2Q	22	LYS	4.0
26	24	54	GLY	4.0
1	1A	931	C	4.0
38	2g	32	ARG	4.0
40	2i	83	ARG	4.0
45	2n	7	ILE	4.0
1	1A	1112	U	4.0
34	2c	189	ALA	4.0
38	2g	85	TYR	4.0
51	1t	69	GLY	4.0
32	2a	1532	U	4.0
40	1i	117	HIS	4.0
36	2e	22	GLY	4.0
1	1A	2167	C	3.9
41	1j	98	ILE	3.9
51	1t	71	THR	3.9
1	1A	934	A	3.9
1	2A	2116	G	3.9
54	2w	28	G	3.9
21	2Z	148	ASP	3.9
50	2s	71	LEU	3.9
54	2w	73	A	3.9
1	1A	1105	G	3.9
34	2c	206	GLU	3.9
35	2d	158	ILE	3.9
36	2e	11	ILE	3.9
41	2j	13	HIS	3.9

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Mol	Chain	Res	Type	RSRZ
43	2l	68	ALA	3.9
1	2A	2804	C	3.9
7	2H	76	VAL	3.9
34	1c	193	TYR	3.9
33	2b	122	PHE	3.9
1	2A	886	C	3.9
52	2u	16	GLY	3.8
50	2s	24	ALA	3.8
6	2G	19	LEU	3.8
34	2c	158	GLY	3.8
20	2Y	44	ILE	3.8
32	1a	1447	A	3.8
21	2Z	52	SER	3.8
32	1a	1033	G	3.8
19	2X	92	LEU	3.8
12	2Q	65	PHE	3.8
47	2p	9	PHE	3.8
47	1p	19	ILE	3.8
51	1t	67	ALA	3.8
21	2Z	50	GLN	3.8
39	2h	128	GLY	3.8
52	2u	11	GLY	3.8
32	1a	1028	C	3.8
34	2c	134	ILE	3.8
36	1e	10	MET	3.8
32	1a	1001	A	3.8
33	2b	228	GLY	3.8
38	2g	76	ARG	3.8
31	29	13	LYS	3.8
34	2c	202	ILE	3.8
35	2d	146	ILE	3.8
54	2w	6	G	3.8
41	1j	46	ARG	3.8
7	2H	113	VAL	3.8
12	2Q	37	LEU	3.8
33	1b	165	VAL	3.8
34	2c	33	LEU	3.8
32	2a	1061	G	3.8
54	1y	24	G	3.8
54	2w	29	G	3.8
35	1d	208	SER	3.8
41	2j	67	THR	3.8

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Mol	Chain	Res	Type	RSRZ
34	2c	4	LYS	3.7
40	2i	37	PHE	3.7
47	1p	80	PHE	3.7
1	2A	2174	C	3.7
34	2c	87	LEU	3.7
21	2Z	152	ALA	3.7
43	2l	56	ALA	3.7
38	1g	84	ASN	3.7
35	2d	48	ALA	3.7
3	1D	276	LYS	3.7
1	2A	882	G	3.7
47	1p	38	TYR	3.7
1	2A	2128	C	3.7
7	2H	142	GLY	3.7
7	2H	166	GLY	3.7
34	2c	205	GLY	3.7
6	2G	39	ILE	3.7
50	2s	12	ASP	3.7
32	1a	1030(C)	G	3.7
32	1a	1031	G	3.7
54	1y	47	U	3.7
7	2H	157	TYR	3.7
38	1g	153	HIS	3.7
48	2q	9	VAL	3.7
54	2w	30	G	3.6
40	2i	18	PHE	3.6
51	1t	24	LEU	3.6
38	2g	79	ARG	3.6
41	1j	47	PHE	3.6
44	2m	94	ARG	3.6
1	1A	1555	C	3.6
1	2A	2140	C	3.6
36	2e	13	ILE	3.6
21	2Z	140	ASP	3.6
51	1t	16	HIS	3.6
6	2G	41	GLN	3.6
47	1p	21	VAL	3.6
32	2a	1531	A	3.6
54	1w	14	A	3.6
1	1A	1145	G	3.6
21	2Z	137	ILE	3.6
41	2j	96	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
50	2s	35	SER	3.6
33	2b	51	LEU	3.6
50	2s	51	VAL	3.6
40	2i	45	ALA	3.6
42	2k	25	TYR	3.6
47	1p	39	TYR	3.6
33	2b	32	ILE	3.6
45	2n	40	CYS	3.6
51	1t	72	LEU	3.6
1	2A	2159	G	3.6
7	2H	47	GLU	3.6
6	1G	146	TYR	3.6
11	2P	91	PHE	3.5
32	1a	344	A	3.5
40	2i	99	LEU	3.5
3	2D	2	ALA	3.5
7	2H	145	ALA	3.5
8	2I	100	ALA	3.5
34	2c	153	VAL	3.5
40	2i	62	TYR	3.5
45	2n	35	ARG	3.5
32	1a	1446	U	3.5
51	1t	20	LEU	3.5
44	2m	5	ALA	3.5
1	1A	2151	C	3.5
38	2g	154	TYR	3.5
1	2A	1026	U	3.5
35	1d	147	ALA	3.5
40	2i	82	ALA	3.5
7	2H	24	VAL	3.5
6	2G	146	TYR	3.5
36	2e	133	TYR	3.5
8	2I	88	ILE	3.5
32	2a	1002	G	3.5
36	1e	95	ALA	3.5
36	2e	33	VAL	3.5
40	2i	90	PRO	3.5
51	1t	8	ARG	3.5
53	2v	21	C	3.5
36	2e	131	ILE	3.5
21	2Z	172	ALA	3.5
38	2g	147	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
47	1p	66	PRO	3.5
53	1v	13	A	3.5
48	2q	22	LEU	3.5
7	2H	106	THR	3.5
12	2Q	136	ALA	3.5
52	2u	14	TRP	3.5
1	1A	1109	G	3.5
47	2p	20	VAL	3.5
38	2g	84	ASN	3.5
32	2a	1018	C	3.4
11	2P	92	GLU	3.4
34	2c	178	LEU	3.4
14	2S	5	THR	3.4
41	2j	56	HIS	3.4
43	2l	28	LYS	3.4
36	2e	8	GLU	3.4
32	1a	1531	A	3.4
39	2h	122	ARG	3.4
1	2A	2113	U	3.4
1	1A	943	C	3.4
50	2s	30	LEU	3.4
52	2u	5	ASP	3.4
6	2G	149	VAL	3.4
33	2b	201	ILE	3.4
36	2e	84	PHE	3.4
32	2a	1219	U	3.4
32	1a	1029	C	3.4
26	14	59	PHE	3.4
34	2c	41	GLY	3.4
30	28	29	LYS	3.4
33	2b	71	VAL	3.4
3	2D	38	LYS	3.4
32	1a	1024	G	3.4
23	21	62	VAL	3.4
6	2G	157	ILE	3.4
14	2S	54	LEU	3.4
48	2q	36	ILE	3.4
34	2c	191	THR	3.4
35	2d	117	ALA	3.4
40	2i	4	TYR	3.4
1	2A	2138	C	3.4
46	2o	27	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
54	1w	67	C	3.4
47	1p	7	ALA	3.3
51	1t	76	ALA	3.3
36	2e	105	VAL	3.3
26	14	54	GLY	3.3
36	2e	20	GLN	3.3
34	2c	5	ILE	3.3
34	2c	196	LEU	3.3
41	2j	63	PHE	3.3
40	2i	88	TYR	3.3
34	2c	190	ARG	3.3
39	2h	104	ARG	3.3
43	2l	41	ARG	3.3
44	2m	104	ARG	3.3
40	2i	28	VAL	3.3
21	2Z	156	LYS	3.3
41	2j	62	HIS	3.3
8	2l	19	VAL	3.3
40	1i	116	LYS	3.3
32	1a	1037	C	3.3
41	2j	88	LEU	3.3
47	1p	42	ARG	3.3
1	2A	2144	U	3.3
54	2w	45	U	3.3
1	2A	2157	G	3.3
40	1i	8	GLY	3.3
7	2H	171	LEU	3.3
49	2r	85	LEU	3.3
1	2A	2136	C	3.3
33	2b	161	ALA	3.3
51	1t	68	LYS	3.3
27	15	60	VAL	3.3
35	1d	133	VAL	3.3
6	2G	178	PHE	3.3
7	2H	73	ALA	3.3
33	2b	38	GLY	3.3
1	1A	1878	A	3.3
23	11	2	SER	3.3
34	2c	199	LYS	3.3
43	2l	62	SER	3.3
47	1p	27	LYS	3.3
29	17	46	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
40	1i	26	VAL	3.3
43	2l	25	PRO	3.2
7	2H	93	GLY	3.2
34	2c	186	PHE	3.2
36	1e	132	ALA	3.2
47	1p	4	ILE	3.2
47	1p	22	THR	3.2
1	1A	942	A	3.2
40	2i	5	TYR	3.2
7	2H	44	VAL	3.2
34	2c	174	PRO	3.2
44	1m	26	GLY	3.2
45	2n	49	HIS	3.2
13	2R	62	ALA	3.2
45	2n	2	ALA	3.2
1	1A	1143	U	3.2
35	1d	138	TYR	3.2
7	2H	133	VAL	3.2
28	26	52	VAL	3.2
31	29	25	VAL	3.2
38	2g	5	ARG	3.2
41	2j	49	VAL	3.2
50	1s	67	VAL	3.2
44	2m	103	THR	3.2
47	1p	59	TRP	3.2
1	1A	271	U	3.2
1	1A	1128	U	3.2
31	29	20	HIS	3.2
45	2n	30	ALA	3.2
12	2Q	104	PHE	3.2
32	2a	1257	U	3.2
41	2j	59	SER	3.2
45	2n	18	VAL	3.2
1	2A	2173	A	3.2
42	2k	126	ARG	3.2
26	24	40	HIS	3.2
1	1A	2174	G	3.2
1	1A	935	C	3.2
12	2Q	32	TYR	3.2
34	2c	48	TYR	3.2
35	1d	135	LEU	3.2
32	2a	1286	A	3.2

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Mol	Chain	Res	Type	RSRZ
4	2E	134	ILE	3.2
6	2G	88	ILE	3.2
32	2a	1040	U	3.2
45	2n	27	CYS	3.2
52	1u	14	TRP	3.2
34	2c	147	LYS	3.2
7	2H	103	LEU	3.2
26	24	32	TYR	3.1
35	2d	135	LEU	3.2
36	2e	135	THR	3.1
7	2H	159	GLU	3.1
1	2A	2132	U	3.1
48	1q	90	ILE	3.1
36	2e	125	SER	3.1
40	2i	93	ARG	3.1
34	2c	192	THR	3.1
39	2h	112	LEU	3.1
52	1u	17	THR	3.1
34	1c	184	TYR	3.1
48	2q	95	TYR	3.1
34	2c	187	ALA	3.1
36	2e	138	ALA	3.1
39	2h	64	LYS	3.1
1	1A	1111	U	3.1
22	10	3	HIS	3.1
1	1A	1139	G	3.1
32	2a	1202	G	3.1
54	2w	65	G	3.1
21	1Z	170	THR	3.1
21	2Z	51	ALA	3.1
41	1j	32	ALA	3.1
45	2n	46	GLU	3.1
43	2l	48	PRO	3.1
47	1p	41	PRO	3.1
54	2y	61	C	3.1
1	2A	2123	G	3.1
6	2G	152	LEU	3.1
7	2H	101	ARG	3.1
40	2i	66	ARG	3.1
1	1A	1122	C	3.1
1	1A	1146	C	3.1
32	1a	345	C	3.1

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Mol	Chain	Res	Type	RSRZ
34	2c	179	ARG	3.1
7	2H	64	LEU	3.1
1	1A	1104	G	3.1
1	1A	2184	G	3.1
50	2s	69	HIS	3.1
1	1A	2154	U	3.1
20	2Y	1	MET	3.1
54	1y	20	U	3.1
44	2m	88	ARG	3.1
44	2m	93	ARG	3.1
32	1a	1027	C	3.1
44	1m	122	LYS	3.1
50	2s	84	GLY	3.1
50	2s	22	LEU	3.1
7	2H	43	VAL	3.1
26	24	59	PHE	3.0
36	2e	89	ILE	3.0
44	2m	91	ARG	3.0
45	2n	41	ARG	3.0
51	1t	80	ARG	3.0
54	2w	22	G	3.0
45	2n	11	LYS	3.0
26	24	45	GLY	3.0
50	2s	68	GLY	3.0
1	2A	2803	C	3.0
6	2G	35	GLU	3.0
32	2a	1149	C	3.0
35	2d	120	LEU	3.0
40	2i	122	ALA	3.0
40	1i	65	VAL	3.0
43	2l	94	PRO	3.0
53	2v	15	A	3.0
1	1A	1106	U	3.0
38	1g	85	TYR	3.0
47	2p	48	TRP	3.0
50	2s	83	HIS	3.0
33	2b	207	ALA	3.0
34	2c	164	ARG	3.0
44	2m	76	ALA	3.0
17	2V	72	VAL	3.0
40	2i	108	VAL	3.0
34	1c	206	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	2162	G	3.0
7	2H	71	LEU	3.0
32	1a	1003	G	3.0
32	1a	1030(A)	G	3.0
32	2a	1030	C	3.0
34	2c	128	PHE	3.0
34	2c	171	GLY	3.0
32	2a	983	A	3.0
53	1v	15	A	3.0
54	2w	38	A	3.0
43	2l	64	TYR	3.0
12	2Q	121	ALA	3.0
21	2Z	157	LEU	3.0
47	1p	24	ALA	3.0
6	2G	159	VAL	3.0
7	2H	125	VAL	3.0
38	1g	34	GLY	3.0
35	2d	134	ASP	3.0
36	2e	78	HIS	3.0
40	1i	126	SER	3.0
47	1p	17	TYR	3.0
7	2H	7	LEU	3.0
34	1c	32	LEU	3.0
6	2G	85	GLY	3.0
7	2H	79	VAL	3.0
11	2P	79	ARG	3.0
20	2Y	43	ASN	3.0
54	2w	34	G	3.0
33	2b	55	PHE	3.0
41	2j	87	THR	3.0
41	2j	60	ARG	3.0
38	2g	75	VAL	2.9
50	2s	45	VAL	2.9
36	2e	50	GLU	2.9
34	1c	134	ILE	2.9
1	2A	2793	G	2.9
44	2m	121	LYS	2.9
12	2Q	28	ALA	2.9
7	2H	50	VAL	2.9
48	2q	21	VAL	2.9
32	1a	1532	U	2.9
36	1e	89	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
33	1b	233	SER	2.9
6	2G	151	ALA	2.9
9	2N	10	GLU	2.9
54	2y	56	C	2.9
55	1x	67	C	2.9
9	2N	102	ALA	2.9
40	2i	13	ALA	2.9
39	2h	65	TYR	2.9
43	2l	27	LEU	2.9
32	2a	1251	A	2.9
45	1n	61	TRP	2.9
7	2H	32	GLU	2.9
33	2b	70	PHE	2.9
35	1d	110	PHE	2.9
1	2A	2896	C	2.9
54	2y	15	G	2.9
33	2b	127	ILE	2.9
50	2s	40	ILE	2.9
8	2l	74	ASN	2.9
7	2H	36	PRO	2.9
49	1r	26	LEU	2.9
39	2h	135	CYS	2.9
48	2q	32	TYR	2.9
7	2H	114	VAL	2.9
51	1t	74	LYS	2.9
40	2i	33	PHE	2.9
48	1q	36	ILE	2.9
54	1y	38	A	2.9
6	2G	135	LEU	2.9
6	2G	161	THR	2.9
19	1X	95	LEU	2.9
35	2d	47	ARG	2.9
41	2j	70	ARG	2.9
47	1p	44	THR	2.9
1	2A	2161	C	2.9
34	2c	23	TYR	2.9
40	1i	113	LYS	2.9
11	2P	125	VAL	2.9
39	2h	4	ASP	2.9
51	1t	75	ASN	2.9
1	1A	1114	G	2.9
1	1A	2176	G	2.9

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Mol	Chain	Res	Type	RSRZ
7	2H	34	GLU	2.9
43	2l	32	PHE	2.9
45	1n	7	ILE	2.9
54	1w	5	G	2.9
54	1w	15	G	2.9
34	2c	132	ARG	2.9
41	2j	32	ALA	2.9
7	2H	111	HIS	2.9
46	1o	69	TYR	2.9
1	1A	2164	C	2.8
32	2a	1114	C	2.8
40	2i	75	ASP	2.8
51	2t	47	GLY	2.8
6	2G	87	PRO	2.8
21	2Z	133	ILE	2.8
45	2n	4	LYS	2.8
33	2b	173	ALA	2.8
8	2I	38	LEU	2.8
32	1a	1035	A	2.8
8	1I	117	GLU	2.8
40	2i	105	ASP	2.8
45	2n	8	GLU	2.8
6	2G	136	ARG	2.8
8	2I	144	VAL	2.8
30	28	25	MET	2.8
51	2t	55	ILE	2.8
34	2c	200	ALA	2.8
21	2Z	5	LEU	2.8
1	1A	2181	G	2.8
45	2n	56	VAL	2.8
23	2I	68	PRO	2.8
32	2a	307	C	2.8
40	2i	110	GLU	2.8
7	2H	96	ALA	2.8
36	2e	21	ALA	2.8
7	2H	13	LYS	2.8
33	1b	228	GLY	2.8
8	1I	19	VAL	2.8
21	2Z	126	VAL	2.8
54	2w	19	G	2.8
39	2h	58	TYR	2.8
32	2a	204	U	2.8

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Mol	Chain	Res	Type	RSRZ
51	2t	73	HIS	2.8
44	2m	84	ILE	2.8
29	17	47	ARG	2.8
32	2a	1092	A	2.8
7	2H	8	PRO	2.8
43	2l	18	VAL	2.8
32	2a	1030(C)	G	2.8
32	2a	1196	U	2.8
11	2P	118	GLY	2.8
21	2Z	145	GLU	2.8
35	2d	196	LEU	2.8
39	2h	133	LEU	2.8
22	20	5	LYS	2.8
1	2A	652(B)	A	2.8
1	2A	2801(A)	A	2.8
6	2G	27	ASN	2.8
33	1b	120	ALA	2.8
33	2b	29	ALA	2.8
32	2a	1108	G	2.8
1	1A	2807	C	2.8
35	2d	49	ARG	2.8
51	1t	17	ARG	2.8
21	2Z	58	VAL	2.7
43	1l	43	VAL	2.7
51	1t	18	GLN	2.7
1	1A	1116	A	2.7
34	2c	9	GLY	2.7
39	2h	131	GLY	2.7
8	2l	79	ILE	2.7
40	2i	63	ILE	2.7
43	1l	7	ILE	2.7
20	2Y	106	LEU	2.7
35	1d	78	LEU	2.7
41	2j	46	ARG	2.7
21	1Z	168	GLU	2.7
35	2d	161	ASN	2.7
1	1A	1124	U	2.7
23	2l	63	ALA	2.7
33	2b	31	TYR	2.7
51	1t	55	ILE	2.7
1	2A	2119	A	2.7
49	2r	26	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
26	24	57	GLU	2.7
1	2A	2112	G	2.7
1	2A	2151	G	2.7
1	2A	2807	G	2.7
36	2e	107	ARG	2.7
14	2S	37	ALA	2.7
46	1o	87	ILE	2.7
50	2s	48	THR	2.7
54	2y	33	U	2.7
38	1g	154	TYR	2.7
32	2a	975	A	2.7
7	2H	112	PRO	2.7
36	2e	114	GLY	2.7
32	2a	980	C	2.7
36	1e	81	GLU	2.7
32	2a	1224	G	2.7
54	2w	44	G	2.7
6	2G	138	GLN	2.7
6	2G	140	ILE	2.7
12	2Q	2	LEU	2.7
34	1c	14	ILE	2.7
39	2h	134	ILE	2.7
44	2m	4	ILE	2.7
47	1p	32	TYR	2.7
1	2A	1847	A	2.7
6	2G	48	GLU	2.7
34	1c	179	ARG	2.7
45	2n	14	PRO	2.7
8	2I	142	VAL	2.7
34	2c	120	VAL	2.7
54	1w	13	C	2.7
1	2A	2118	U	2.7
7	1H	2	SER	2.7
21	1Z	149	SER	2.7
35	1d	176	LEU	2.7
48	2q	59	ILE	2.7
38	1g	78	ARG	2.7
7	2H	82	GLY	2.7
33	1b	132	LYS	2.7
47	2p	59	TRP	2.7
1	1A	1100	A	2.7
41	2j	61	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
54	2w	42	C	2.7
10	2O	8	LEU	2.7
35	2d	186	LEU	2.7
41	2j	68	HIS	2.7
42	1k	125	PHE	2.7
45	1n	16	PHE	2.7
1	2A	2148	G	2.7
7	2H	94	TYR	2.7
6	2G	17	PRO	2.7
32	1a	1034	G	2.7
1	1A	1103	A	2.6
32	2a	1016	A	2.6
32	2a	1250	A	2.6
34	2c	44	GLU	2.6
29	27	47	ARG	2.6
35	1d	149	ALA	2.6
45	2n	45	ARG	2.6
41	2j	22	LYS	2.6
50	2s	62	ILE	2.6
51	1t	62	LEU	2.6
45	2n	55	GLY	2.6
50	2s	54	GLY	2.6
38	1g	32	ARG	2.6
12	1Q	81	VAL	2.6
7	2H	75	ALA	2.6
32	2a	1001	A	2.6
1	1A	1127	U	2.6
34	1c	33	LEU	2.6
41	2j	36	GLY	2.6
47	2p	19	ILE	2.6
32	2a	962	C	2.6
32	1a	1032	G	2.6
35	2d	148	VAL	2.6
54	1w	10	G	2.6
54	2w	18	G	2.6
9	2N	93	THR	2.6
42	2k	117	ASN	2.6
50	2s	53	ASN	2.6
24	22	60	LEU	2.6
35	1d	105	VAL	2.6
36	1e	134	ALA	2.6
36	2e	16	THR	2.6

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Mol	Chain	Res	Type	RSRZ
38	2g	9	VAL	2.6
41	1j	18	ALA	2.6
43	2l	72	GLY	2.6
48	2q	73	VAL	2.6
32	2a	1358	U	2.6
35	2d	157	LEU	2.6
45	2n	16	PHE	2.6
48	1q	28	PRO	2.6
51	2t	22	ARG	2.6
2	2B	59	A	2.6
40	1i	33	PHE	2.6
34	2c	19	GLU	2.6
50	2s	38	SER	2.6
33	2b	220	ASP	2.6
34	2c	131	ARG	2.6
34	2c	10	PHE	2.6
50	2s	10	PHE	2.6
1	2A	2156	G	2.6
32	2a	79	G	2.6
54	2w	35	A	2.6
1	1A	1121	C	2.6
20	2Y	80	GLY	2.6
40	1i	125	TYR	2.6
43	2l	69	TYR	2.6
21	2Z	154	ASP	2.6
47	1p	68	ASP	2.6
41	2j	27	ALA	2.6
33	2b	229	VAL	2.6
34	1c	64	VAL	2.6
14	2S	58	LEU	2.6
7	2H	4	ILE	2.6
33	2b	185	ILE	2.6
21	2Z	153	SER	2.6
32	2a	250	A	2.6
32	2a	1154	G	2.6
37	2f	55	ASP	2.6
1	1A	2196	C	2.6
40	2i	19	LEU	2.5
47	1p	60	LEU	2.5
54	2w	47	U	2.5
15	2T	52	ILE	2.5
42	2k	125	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
40	2i	20	ARG	2.5
34	1c	18	TRP	2.5
41	2j	52	GLY	2.5
6	2G	12	TYR	2.5
45	1n	34	TYR	2.5
54	2w	23	A	2.5
47	1p	67	THR	2.5
21	1Z	165	VAL	2.5
36	2e	123	LEU	2.5
40	1i	109	VAL	2.5
54	2y	62	C	2.5
34	2c	37	GLN	2.5
46	1o	57	LEU	2.5
48	1q	98	LEU	2.5
48	2q	6	LEU	2.5
51	1t	23	ARG	2.5
40	2i	74	ILE	2.5
40	2i	32	ASP	2.5
47	1p	13	HIS	2.5
12	2Q	3	MET	2.5
33	2b	83	MET	2.5
33	2b	210	SER	2.5
1	2A	2170	A	2.5
26	24	52	THR	2.5
33	2b	218	ALA	2.5
35	2d	160	GLN	2.5
1	1A	1133	G	2.5
7	2H	67	LEU	2.5
12	2Q	59	ARG	2.5
32	2a	1197	G	2.5
39	1h	2	LEU	2.5
1	1A	1072	U	2.5
1	1A	2906	U	2.5
35	1d	86	LYS	2.5
31	29	19	ARG	2.5
47	1p	48	TRP	2.5
44	2m	23	TYR	2.5
1	2A	2126	A	2.5
4	1E	195	LEU	2.5
22	10	7	LEU	2.5
34	1c	34	LEU	2.5
34	2c	72	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
48	2q	77	VAL	2.5
4	2E	115	GLY	2.5
26	14	45	GLY	2.5
38	2g	109	ASN	2.5
54	2w	74	C	2.5
1	1A	1108	G	2.5
7	2H	89	ILE	2.5
32	2a	1021	G	2.5
32	2a	1050	G	2.5
32	2a	1156	G	2.5
34	1c	128	PHE	2.5
54	2y	53	G	2.5
48	2q	91	ARG	2.5
52	1u	15	ARG	2.5
6	2G	60	LEU	2.5
39	2h	94	TYR	2.5
50	1s	71	LEU	2.5
32	2a	1066	C	2.5
39	2h	38	ILE	2.5
52	1u	13	ILE	2.5
50	2s	78	ARG	2.5
1	2A	2110	G	2.5
54	2y	5	G	2.5
42	1k	15	ALA	2.5
51	2t	59	ALA	2.5
11	2P	99	LEU	2.5
39	2h	84	ARG	2.5
1	2A	2117	A	2.5
3	1D	275	LYS	2.5
32	2a	1357	A	2.5
33	2b	211	ILE	2.5
37	1f	60	PHE	2.5
41	1j	96	ILE	2.5
45	1n	17	LYS	2.5
54	2w	21	A	2.5
1	2A	894	C	2.5
32	2a	91	C	2.5
33	2b	48	MET	2.5
6	2G	49	ASP	2.5
1	2A	2100	G	2.5
32	2a	1003	G	2.5
32	2a	1064	G	2.5

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Mol	Chain	Res	Type	RSRZ
34	2c	159	GLY	2.5
36	2e	17	ALA	2.5
40	1i	76	ALA	2.5
40	2i	8	GLY	2.5
48	2q	33	GLY	2.5
33	1b	61	LEU	2.4
6	2G	74	LYS	2.4
8	2I	92	VAL	2.4
48	2q	10	VAL	2.4
48	2q	12	SER	2.4
39	2h	35	ILE	2.4
1	1A	945	A	2.4
1	1A	1113	A	2.4
32	1a	1005	A	2.4
1	2A	2137	C	2.4
50	2s	76	PRO	2.4
54	2w	67	C	2.4
31	29	37	GLY	2.4
46	1o	89	GLY	2.4
20	2Y	6	HIS	2.4
34	2c	162	GLN	2.4
40	2i	111	ARG	2.4
47	2p	64	ALA	2.4
32	2a	1222	G	2.4
35	1d	97	LEU	2.4
36	2e	43	LEU	2.4
6	2G	15	VAL	2.4
32	1a	1025	U	2.4
7	2H	124	GLU	2.4
34	1c	8	ILE	2.4
36	1e	13	ILE	2.4
36	2e	14	ARG	2.4
36	2e	93	PRO	2.4
1	2A	889	C	2.4
40	1i	15	ALA	2.4
43	2l	16	GLU	2.4
54	2y	19	G	2.4
45	2n	43	CYS	2.4
33	1b	130	ARG	2.4
33	2b	113	HIS	2.4
44	2m	92	HIS	2.4
1	1A	2186	C	2.4

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Mol	Chain	Res	Type	RSRZ
54	1y	48	C	2.4
54	2w	14	A	2.4
44	2m	66	LEU	2.4
12	2Q	63	LYS	2.4
33	2b	93	VAL	2.4
43	2l	13	LYS	2.4
45	2n	15	LYS	2.4
45	2n	23	ARG	2.4
52	1u	6	ARG	2.4
14	2S	92	TYR	2.4
34	2c	142	MET	2.4
40	1i	81	ILE	2.4
43	2l	63	GLY	2.4
7	2H	12	PRO	2.4
32	1a	102	G	2.4
32	2a	1024	G	2.4
41	2j	41	PRO	2.4
54	2w	15	G	2.4
54	2y	65	G	2.4
7	2H	129	THR	2.4
31	29	12	ASP	2.4
12	2Q	34	LEU	2.4
10	1O	17	ARG	2.4
32	1a	1030	C	2.4
10	2O	52	VAL	2.4
29	27	46	VAL	2.4
34	2c	195	VAL	2.4
35	1d	104	VAL	2.4
12	2Q	47	ILE	2.4
34	2c	39	ILE	2.4
39	1h	6	ILE	2.4
40	1i	110	GLU	2.4
43	2l	47	LYS	2.4
49	1r	24	ALA	2.4
51	2t	12	ALA	2.4
1	2A	2115	G	2.4
54	2w	57	G	2.4
35	1d	168	ARG	2.4
35	2d	141	ARG	2.4
40	2i	16	ARG	2.4
39	2h	36	LEU	2.4
21	2Z	147	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
39	2h	137	VAL	2.4
54	1y	21	A	2.4
1	1A	1985	U	2.4
20	1Y	1	MET	2.4
34	2c	152	ILE	2.4
50	2s	42	PRO	2.4
21	2Z	93	ASP	2.4
33	2b	111	ARG	2.4
45	1n	57	ARG	2.4
48	2q	7	THR	2.4
39	1h	112	LEU	2.4
1	2A	2319	G	2.3
32	2a	1283	G	2.3
40	1i	80	GLY	2.3
48	1q	33	GLY	2.3
25	23	6	VAL	2.3
7	2H	9	ILE	2.3
21	1Z	104	PHE	2.3
22	20	44	ARG	2.3
33	1b	21	ARG	2.3
35	2d	122	ARG	2.3
41	2j	43	ARG	2.3
14	1S	72	ALA	2.3
49	2r	46	GLU	2.3
52	2u	17	THR	2.3
33	1b	133	LYS	2.3
21	2Z	24	LEU	2.3
48	2q	53	LEU	2.3
49	1r	79	LEU	2.3
51	2t	24	LEU	2.3
1	2A	2165	G	2.3
21	2Z	86	VAL	2.3
35	1d	170	VAL	2.3
42	2k	109	VAL	2.3
11	2P	122	PRO	2.3
12	1Q	59	ARG	2.3
40	2i	10	ARG	2.3
51	2t	83	ARG	2.3
54	1w	65	G	2.3
54	2w	24	G	2.3
54	2y	57	G	2.3
1	1A	2168	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	1A	2814	C	2.3
1	2A	2143	C	2.3
21	2Z	13	GLU	2.3
54	2w	40	C	2.3
22	10	2	ALA	2.3
40	1i	45	ALA	2.3
40	1i	119	ALA	2.3
44	2m	42	ALA	2.3
21	2Z	4	ARG	2.3
34	1c	38	ARG	2.3
40	2i	107	ARG	2.3
21	1Z	151	HIS	2.3
7	2H	169	VAL	2.3
40	2i	26	VAL	2.3
41	2j	34	VAL	2.3
43	2l	58	VAL	2.3
1	1A	2130	C	2.3
1	2A	897	C	2.3
51	1t	59	ALA	2.3
26	24	44	THR	2.3
47	1p	69	THR	2.3
9	2N	116	LEU	2.3
40	1i	19	LEU	2.3
33	2b	164	VAL	2.3
35	2d	181	MET	2.3
15	2T	48	ILE	2.3
33	2b	223	ILE	2.3
35	1d	185	PHE	2.3
6	2G	50	ALA	2.3
15	1T	111	ARG	2.3
20	2Y	2	ARG	2.3
24	12	13	ALA	2.3
34	1c	180	ALA	2.3
38	2g	151	TYR	2.3
41	1j	45	ARG	2.3
45	2n	59	ALA	2.3
32	2a	1026	G	2.3
34	2c	193	TYR	2.3
45	1n	13	THR	2.3
51	2t	57	ARG	2.3
33	2b	232	PRO	2.3
36	1e	55	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
54	2w	50	U	2.3
7	2H	97	ARG	2.3
20	2Y	75	ILE	2.3
23	2I	67	ILE	2.3
33	1b	227	GLY	2.3
34	2c	140	ARG	2.3
35	2d	70	ILE	2.3
36	2e	129	ILE	2.3
41	1j	10	GLY	2.3
41	1j	50	ILE	2.3
48	2q	54	GLY	2.3
11	2P	76	LYS	2.3
16	1U	69	CYS	2.3
21	2Z	9	TYR	2.3
31	29	24	TYR	2.3
11	2P	45	LEU	2.3
47	2p	73	LEU	2.3
47	2p	74	LEU	2.3
49	1r	31	LEU	2.3
1	2A	614(B)	G	2.3
54	2w	76	A	2.3
1	1A	1220	U	2.3
45	2n	31	ARG	2.3
6	2G	155	MET	2.3
36	1e	118	ILE	2.3
36	2e	30	ALA	2.3
47	1p	64	ALA	2.3
10	2O	96	THR	2.3
34	2c	201	TYR	2.3
46	1o	66	LEU	2.3
51	2t	13	LEU	2.3
1	2A	2310	A	2.2
33	2b	131	PRO	2.2
36	2e	121	LYS	2.2
47	1p	25	ARG	2.2
1	2A	2166	G	2.2
44	2m	106	ASN	2.2
54	1y	5	G	2.2
8	1I	106	GLY	2.2
8	2I	21	VAL	2.2
10	2O	98	VAL	2.2
33	2b	193	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
33	2b	216	SER	2.2
41	2j	35	SER	2.2
33	2b	222	ILE	2.2
39	1h	38	ILE	2.2
33	2b	163	PHE	2.2
21	2Z	121	HIS	2.2
6	2G	133	LEU	2.2
8	2I	12	LEU	2.2
11	2P	110	TYR	2.2
14	2S	10	ARG	2.2
26	24	68	ARG	2.2
29	27	23	ARG	2.2
33	2b	144	ARG	2.2
39	2h	107	LEU	2.2
48	1q	37	LYS	2.2
50	2s	29	ARG	2.2
51	1t	10	LEU	2.2
1	1A	2161	C	2.2
32	2a	1112	C	2.2
55	1x	68	C	2.2
1	2A	2169	A	2.2
21	2Z	106	GLY	2.2
21	2Z	128	VAL	2.2
32	2a	986	A	2.2
35	2d	8	VAL	2.2
35	2d	105	VAL	2.2
1	2A	9	U	2.2
26	24	66	SER	2.2
41	2j	19	SER	2.2
32	2a	485	G	2.2
35	1d	158	ILE	2.2
43	2l	26	ALA	2.2
8	2I	93	THR	2.2
35	1d	122	ARG	2.2
17	2V	71	LEU	2.2
48	2q	84	LEU	2.2
50	1s	22	LEU	2.2
34	2c	184	TYR	2.2
36	1e	49	PRO	2.2
41	2j	53	PRO	2.2
5	1F	131	GLY	2.2
34	1c	2	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
21	1Z	166	SER	2.2
34	2c	138	VAL	2.2
35	1d	181	MET	2.2
35	2d	56	VAL	2.2
39	2h	9	MET	2.2
41	2j	94	VAL	2.2
32	2a	1014	A	2.2
12	2Q	5	ARG	2.2
22	20	74	ARG	2.2
35	2d	73	ARG	2.2
36	1e	21	ALA	2.2
36	2e	118	ILE	2.2
38	1g	76	ARG	2.2
45	1n	41	ARG	2.2
51	1t	15	ARG	2.2
3	2D	15	PHE	2.2
33	2b	17	PHE	2.2
38	1g	43	PHE	2.2
44	1m	109	THR	2.2
1	1A	1221	G	2.2
32	2a	1031	G	2.2
54	2w	10	G	2.2
54	2y	1	G	2.2
34	2c	12	LEU	2.2
34	2c	28	GLN	2.2
34	2c	136	GLN	2.2
41	2j	8	LEU	2.2
47	1p	65	GLN	2.2
51	1t	64	ASP	2.2
40	2i	112	LYS	2.2
7	2H	2	SER	2.2
42	1k	126	ARG	2.2
43	2l	15	ARG	2.2
51	1t	22	ARG	2.2
30	28	7	HIS	2.2
7	2H	121	ILE	2.2
13	2R	25	ALA	2.2
21	2Z	21	ALA	2.2
49	1r	25	THR	2.2
54	1w	23	A	2.2
8	2I	117	GLU	2.2
10	2O	99	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
21	2Z	162	GLU	2.2
48	2q	86	GLU	2.2
4	2E	195	LEU	2.2
34	2c	91	LEU	2.2
43	2l	93	LEU	2.2
51	2t	26	ASN	2.2
1	1A	938	G	2.2
1	1A	2137	G	2.2
7	2H	51	ARG	2.2
14	2S	20	ARG	2.2
40	1i	114	TYR	2.2
40	1i	121	ARG	2.2
8	2l	18	VAL	2.2
32	2a	4	U	2.2
1	2A	2164	C	2.2
14	1S	6	ALA	2.2
35	2d	150	GLU	2.2
7	2H	25	LYS	2.2
39	1h	86	ILE	2.2
1	1A	302	A	2.2
1	2A	899	A	2.2
32	1a	1030(D)	A	2.2
32	2a	1287	A	2.2
34	2c	204	LEU	2.2
44	2m	70	LEU	2.2
49	2r	66	LEU	2.2
35	1d	73	ARG	2.2
38	1g	4	ARG	2.2
38	2g	78	ARG	2.2
1	1A	2843	G	2.2
1	2A	2125	G	2.2
33	2b	150	SER	2.2
45	2n	21	TYR	2.2
9	2N	8	GLN	2.2
11	2P	83	VAL	2.2
32	1a	841	U	2.2
34	2c	151	VAL	2.2
34	2c	168	ALA	2.2
43	2l	30	ALA	2.2
46	2o	16	ALA	2.2
1	1A	2183	C	2.2
6	2G	114	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
15	2T	75	ILE	2.2
21	2Z	171	ILE	2.2
39	1h	134	ILE	2.2
40	2i	29	ASN	2.2
6	1G	80	PHE	2.2
21	2Z	48	PHE	2.2
32	1a	101	A	2.2
32	2a	1044	A	2.2
32	2a	1225	A	2.2
44	2m	73	GLU	2.2
26	14	46	GLN	2.1
33	2b	133	LYS	2.1
50	2s	32	LYS	2.1
17	2V	91	TYR	2.1
28	26	42	TRP	2.1
1	2A	2897	U	2.1
22	20	2	ALA	2.1
32	1a	1040	U	2.1
36	2e	55	VAL	2.1
43	2l	104	VAL	2.1
34	2c	71	ALA	2.1
6	2G	115	ARG	2.1
7	2H	95	ARG	2.1
11	2P	75	ILE	2.1
16	2U	17	ILE	2.1
30	18	6	THR	2.1
38	1g	42	ILE	2.1
38	2g	132	GLY	2.1
40	2i	64	THR	2.1
21	2Z	130	PRO	2.1
32	1a	1006	C	2.1
32	2a	979	C	2.1
28	26	36	LEU	2.1
33	2b	44	LEU	2.1
41	1j	40	LEU	2.1
33	2b	132	LYS	2.1
44	1m	121	LYS	2.1
15	1T	106	SER	2.1
33	2b	195	ASP	2.1
8	1I	103	ARG	2.1
10	2O	1	MET	2.1
20	2Y	35	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
40	2i	54	ASP	2.1
48	2q	88	TYR	2.1
1	2A	2167	U	2.1
5	1F	49	ALA	2.1
14	2S	46	VAL	2.1
35	2d	121	VAL	2.1
36	1e	135	THR	2.1
1	1A	2175	G	2.1
1	2A	2131	G	2.1
1	2A	2792	G	2.1
8	1I	109	ILE	2.1
32	1a	630	G	2.1
47	1p	50	LYS	2.1
33	2b	105	PHE	2.1
32	2a	984	C	2.1
51	1t	73	HIS	2.1
23	2l	61	ARG	2.1
32	1a	1503	A	2.1
41	2j	66	ARG	2.1
45	2n	57	ARG	2.1
31	29	29	ASN	2.1
3	1D	2	ALA	2.1
6	2G	61	ALA	2.1
7	2H	17	VAL	2.1
13	1R	109	ALA	2.1
20	1Y	72	VAL	2.1
26	14	50	VAL	2.1
36	1e	17	ALA	2.1
54	1w	66	U	2.1
34	2c	177	THR	2.1
48	2q	65	ILE	2.1
8	1I	35	LEU	2.1
8	2I	44	LEU	2.1
40	2i	40	LEU	2.1
32	1a	104	G	2.1
1	1A	2160	C	2.1
1	2A	2175	C	2.1
8	2I	96	ASP	2.1
10	2O	108	GLU	2.1
32	1a	100	C	2.1
33	1b	137	ARG	2.1
39	2h	108	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
4	1E	28	ALA	2.1
9	1N	47	ALA	2.1
16	1U	113	ALA	2.1
34	2c	207	VAL	2.1
36	1e	82	VAL	2.1
43	2l	90	VAL	2.1
6	1G	17	PRO	2.1
14	2S	12	PHE	2.1
14	2S	17	ARG	2.1
34	2c	143	GLU	2.1
40	2i	56	LEU	2.1
40	2i	102	LEU	2.1
41	1j	95	GLU	2.1
35	1d	166	LYS	2.1
32	2a	1367	C	2.1
52	1u	2	GLY	2.1
54	1y	22	G	2.1
29	27	1	MET	2.1
34	2c	139	GLN	2.1
11	1P	125	VAL	2.1
34	2c	65	ALA	2.1
39	2h	124	ALA	2.1
38	1g	151	TYR	2.1
40	1i	90	PRO	2.1
52	2u	8	THR	2.1
20	2Y	38	ILE	2.1
34	1c	56	ASP	2.1
41	1j	62	HIS	2.1
41	2j	12	ASP	2.1
50	2s	28	LYS	2.1
28	26	11	LEU	2.1
47	1p	6	LEU	2.1
15	1T	38	ASN	2.1
21	2Z	65	GLN	2.1
1	2A	2182	G	2.1
2	2B	119	G	2.1
30	28	18	ALA	2.1
32	1a	292	G	2.1
32	2a	1221	G	2.1
10	2O	57	VAL	2.1
23	11	35	THR	2.1
34	2c	7	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
51	2t	68	LYS	2.1
52	1u	3	LYS	2.1
39	2h	103	VAL	2.1
44	2m	7	VAL	2.1
45	2n	22	THR	2.1
50	2s	11	VAL	2.1
30	18	7	HIS	2.1
32	2a	1111	A	2.1
48	2q	42	TYR	2.1
39	2h	86	ILE	2.1
40	2i	117	HIS	2.1
47	1p	36	ILE	2.1
39	2h	113	SER	2.1
41	1j	65	LEU	2.1
33	2b	94	ASN	2.1
4	2E	6	GLY	2.1
6	2G	134	GLY	2.1
44	2m	95	GLY	2.1
46	2o	61	GLY	2.1
3	1D	38	LYS	2.1
35	2d	166	LYS	2.1
40	2i	42	ARG	2.1
43	2l	59	ARG	2.1
45	1n	12	ARG	2.1
17	1V	55	ALA	2.0
32	2a	1116	C	2.0
34	1c	129	ALA	2.0
35	1d	136	PRO	2.0
40	2i	119	ALA	2.0
47	2p	70	ALA	2.0
54	2w	41	C	2.0
10	2O	14	THR	2.0
38	2g	135	VAL	2.0
26	14	63	TYR	2.0
32	1a	1385	G	2.0
33	2b	148	TYR	2.0
54	1y	19	G	2.0
35	1d	204	ILE	2.0
38	1g	50	ILE	2.0
32	2a	1030(D)	A	2.0
35	2d	139	ARG	2.0
44	2m	99	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
33	2b	97	TRP	2.0
33	2b	177	ALA	2.0
51	2t	77	ALA	2.0
1	1A	2131	U	2.0
1	2A	2109	U	2.0
1	2A	2142	C	2.0
3	2D	205	VAL	2.0
4	1E	47	VAL	2.0
8	2I	107	VAL	2.0
32	1a	150	C	2.0
32	2a	1027	C	2.0
32	2a	1278	U	2.0
32	2a	1452	C	2.0
35	2d	198	VAL	2.0
41	2j	44	VAL	2.0
49	2r	22	VAL	2.0
36	2e	45	PHE	2.0
43	2l	19	ARG	2.0
44	2m	71	ARG	2.0
51	2t	25	ARG	2.0
51	2t	86	ARG	2.0
1	1A	2813	G	2.0
32	2a	1058	G	2.0
1	1A	1123	A	2.0
32	2a	969	A	2.0
8	2I	80	PRO	2.0
21	2Z	98	MET	2.0
16	1U	61	TRP	2.0
39	2h	101	PRO	2.0
41	2j	18	ALA	2.0
1	2A	271(N)	U	2.0
15	1T	66	VAL	2.0
20	2Y	24	VAL	2.0
36	2e	34	VAL	2.0
55	2x	20	U	2.0
1	1A	2210	C	2.0
20	2Y	22	GLY	2.0
7	2H	148	ILE	2.0
12	2Q	66	ILE	2.0
32	2a	1045	C	2.0
32	2a	1192	C	2.0
35	1d	16	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
35	2d	23	GLY	2.0
33	1b	187	LEU	2.0
41	2j	38	ILE	2.0
46	2o	31	LEU	2.0
43	1l	64	TYR	2.0
46	2o	15	PHE	2.0
1	1A	1102	G	2.0
45	2n	9	LYS	2.0
54	2w	36	A	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
54	7MG	1w	46	24/25	0.78	0.20	-	76,90,101,124	0
32	5MC	2a	1404	21/22	0.92	0.21	-	47,59,74,77	0
1	2MU	2A	2552	21/23	0.97	0.20	-	28,38,46,52	0
1	4OC	1A	1942	21/23	0.96	0.20	-	42,55,61,65	0
1	2MA	1A	2515	23/24	0.98	0.24	-	20,26,31,34	0
1	5MU	2A	1915	21/22	0.91	0.18	-	64,72,79,93	0
43	0TD	1l	92	10/11	0.87	0.23	-	61,64,70,74	0
32	2MG	2a	1207	24/25	0.85	0.17	-	74,85,90,98	0
54	PSU	2w	32	20/21	0.90	0.32	-	69,85,94,103	0
1	2MA	2A	2503	23/24	0.98	0.20	-	25,30,35,37	0
54	PSU	1w	39	20/21	0.93	0.23	-	50,70,80,83	0
1	PSU	2A	2605	20/21	0.97	0.18	-	25,33,40,42	0
32	PSU	2a	516	20/21	0.92	0.15	-	65,72,79,83	0
54	PSU	2w	39	20/21	0.91	0.33	-	80,88,96,102	0
1	PSU	1A	2617	20/21	0.98	0.20	-	24,31,37,39	0
32	MA6	1a	1519	24/25	0.97	0.21	-	39,48,57,71	0
54	MIA	1y	37	22/30	0.87	0.23	-	76,83,93,94	0
32	5MC	1a	1404	21/22	0.97	0.19	-	32,43,50,53	0
1	5MC	1A	1964	21/22	0.97	0.21	-	38,47,52,60	0
32	7MG	1a	527	24/25	0.96	0.19	-	40,50,60,67	0
1	5MU	1A	1937	21/22	0.95	0.18	-	56,67,75,82	0
32	4OC	1a	1402	22/23	0.97	0.18	-	37,47,55,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	OMG	1A	2263	24/25	0.97	0.22	-	22,32,39,44	0
54	5MU	1w	54	21/22	0.94	0.16	-	55,67,78,79	0
1	2MU	1A	2564	21/23	0.98	0.22	-	26,36,40,46	0
54	MIA	2y	37	22/30	0.76	0.27	-	72,86,94,120	0
54	PSU	2w	55	20/21	0.76	0.29	-	80,94,98,113	0
54	5MU	2y	54	21/22	0.71	0.31	-	79,93,108,123	0
32	7MG	2a	527	24/25	0.94	0.19	-	61,70,77,88	0
54	4SU	2w	8	20/21	0.75	0.30	-	81,98,120,128	0
1	5MC	1A	1984	21/22	0.98	0.18	-	31,38,48,57	0
32	5MC	1a	1400	21/22	0.98	0.19	-	39,53,61,67	0
1	5MC	2A	1962	21/22	0.96	0.18	-	28,43,52,59	0
54	5MU	2w	54	21/22	0.86	0.21	-	66,85,93,101	0
1	5MU	1A	1961	21/22	0.98	0.19	-	21,33,38,44	0
54	PSU	2y	39	20/21	0.85	0.23	-	78,84,100,112	0
54	PSU	1y	55	20/21	0.72	0.20	-	72,89,99,120	0
32	MA6	2a	1519	24/25	0.95	0.26	-	47,65,74,81	0
54	PSU	1y	39	20/21	0.91	0.18	-	71,81,89,95	0
1	5MU	2A	1939	21/22	0.97	0.17	-	24,34,41,46	0
32	5MC	2a	967	21/22	0.90	0.19	-	62,71,79,86	0
32	UR3	1a	1498	21/22	0.98	0.18	-	38,43,50,54	0
55	5MU	1x	54	21/22	0.95	0.14	-	57,71,79,83	0
32	5MC	2a	1400	21/22	0.96	0.23	-	70,74,80,93	0
32	5MC	1a	967	21/22	0.96	0.21	-	51,58,67,70	0
32	5MC	1a	1407	21/22	0.97	0.19	-	34,42,56,62	0
1	5MC	2A	1942	21/22	0.97	0.16	-	45,50,58,61	0
54	4SU	1y	8	20/21	0.79	0.23	-	80,98,105,114	0
54	PSU	1w	32	20/21	0.93	0.20	-	59,72,79,83	0
55	5MC	1x	32	21/22	0.96	0.21	-	44,54,67,73	0
54	7MG	2y	46	24/25	0.65	0.20	-	68,95,99,128	0
54	7MG	1y	46	24/25	0.83	0.24	-	76,95,106,115	0
32	2MG	1a	1207	24/25	0.93	0.14	-	62,72,76,80	0
54	MIA	2w	37	25/30	0.88	0.29	-	70,82,91,110	0
1	PSU	2A	1917	20/21	0.94	0.21	-	56,65,75,76	0
54	5MU	1y	54	21/22	0.79	0.20	-	76,87,95,116	0
54	4SU	1w	8	20/21	0.83	0.20	-	75,86,105,114	0
54	PSU	2y	55	20/21	0.77	0.28	-	80,96,115,118	0
32	PSU	1a	516	20/21	0.94	0.16	-	63,70,78,78	0
32	MA6	1a	1518	24/25	0.97	0.21	-	31,47,51,57	0
55	PSU	2x	55	20/21	0.88	0.18	-	69,84,106,107	0
54	PSU	1y	32	20/21	0.84	0.23	-	69,87,94,95	0
1	PSU	1A	1933	20/21	0.97	0.21	-	49,59,62,66	0
1	OMG	2A	2251	24/25	0.97	0.17	-	27,36,44,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	PSU	2A	1911	20/21	0.93	0.17	-	56,60,66,70	0
32	M2G	2a	966	25/26	0.87	0.22	-	52,69,95,99	0
54	4SU	2y	8	20/21	0.83	0.12	-	87,94,106,113	0
55	4SU	2x	8	20/21	0.84	0.16	-	74,85,90,96	0
32	4OC	2a	1402	22/23	0.92	0.17	-	45,63,71,90	0
54	7MG	2w	46	24/25	0.77	0.24	-	83,96,107,134	0
32	UR3	2a	1498	21/22	0.95	0.20	-	48,58,62,68	0
43	0TD	2l	92	10/11	0.93	0.23	-	65,68,73,79	0
54	PSU	2y	32	20/21	0.77	0.21	-	73,89,97,108	0
55	PSU	1x	55	20/21	0.94	0.16	-	56,67,81,87	0
55	5MC	2x	32	21/22	0.92	0.19	-	65,78,87,88	0
54	PSU	1w	55	20/21	0.80	0.22	-	72,81,90,98	0
55	4SU	1x	8	20/21	0.96	0.17	-	46,60,69,73	0
32	MA6	2a	1518	24/25	0.95	0.20	-	41,63,74,82	0
1	PSU	1A	1939	20/21	0.95	0.23	-	53,60,71,72	0
54	MIA	1w	37	29/30	0.93	0.22	-	43,62,74,78	0
55	5MU	2x	54	21/22	0.86	0.24	-	71,87,95,100	0
32	5MC	2a	1407	21/22	0.95	0.20	-	48,57,69,76	0
32	M2G	1a	966	25/26	0.96	0.20	-	41,55,61,77	0
1	4OC	2A	1920	21/23	0.95	0.23	-	46,57,62,72	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1B	3010	1/1	0.88	0.82	35.83	73,73,73,73	0
56	MG	1A	3016	1/1	0.86	0.33	26.20	51,51,51,51	0
56	MG	2A	3165	1/1	0.93	0.35	22.86	49,49,49,49	0
56	MG	2F	304	1/1	0.97	0.50	22.20	53,53,53,53	0
56	MG	1A	3162	1/1	0.96	0.43	21.27	44,44,44,44	0
56	MG	1A	3354	1/1	0.96	0.38	20.12	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3906	1/1	0.87	0.66	18.72	62,62,62,62	0
56	MG	1A	3306	1/1	0.97	0.47	18.44	38,38,38,38	0
56	MG	1A	3189	1/1	0.88	0.41	18.38	43,43,43,43	0
56	MG	1A	3857	1/1	0.91	0.36	16.91	48,48,48,48	0
56	MG	2A	3468	1/1	0.88	0.30	16.35	59,59,59,59	0
56	MG	1A	4141	1/1	0.98	0.36	16.01	50,50,50,50	0
56	MG	2A	3687	1/1	0.90	0.37	15.51	63,63,63,63	0
56	MG	2A	3493	1/1	0.86	0.38	14.78	53,53,53,53	0
56	MG	1N	201	1/1	0.87	0.61	12.72	59,59,59,59	0
56	MG	2a	3091	1/1	0.93	0.42	12.65	76,76,76,76	0
56	MG	1a	1699	1/1	0.95	0.28	11.93	40,40,40,40	0
56	MG	2A	3167	1/1	0.90	0.27	11.53	52,52,52,52	0
56	MG	2A	3444	1/1	0.95	0.29	11.26	49,49,49,49	0
56	MG	2A	3886	1/1	0.92	0.29	11.20	45,45,45,45	0
56	MG	1A	3803	1/1	0.97	0.39	11.14	44,44,44,44	0
56	MG	1A	3309	1/1	0.97	0.29	10.80	33,33,33,33	0
56	MG	2A	3677	1/1	0.98	0.32	10.71	35,35,35,35	0
56	MG	2a	3208	1/1	0.96	0.30	10.69	75,75,75,75	0
56	MG	1N	204	1/1	0.96	0.51	10.49	64,64,64,64	0
56	MG	2A	3486	1/1	0.98	0.36	10.10	55,55,55,55	0
56	MG	1U	202	1/1	0.73	0.49	9.97	73,73,73,73	0
56	MG	1A	4078	1/1	0.97	0.33	9.70	41,41,41,41	0
56	MG	1A	3865	1/1	0.96	0.36	9.57	43,43,43,43	0
56	MG	2A	3449	1/1	0.95	0.38	9.47	47,47,47,47	0
56	MG	2A	3096	1/1	0.84	0.26	9.43	59,59,59,59	0
56	MG	1A	3809	1/1	0.98	0.31	9.16	51,51,51,51	0
56	MG	2A	3455	1/1	0.91	0.30	8.94	54,54,54,54	0
56	MG	1A	3509	1/1	0.96	0.30	8.86	45,45,45,45	0
56	MG	1A	3307	1/1	0.89	0.32	8.86	45,45,45,45	0
56	MG	1Y	504	1/1	0.97	0.41	8.84	48,48,48,48	0
56	MG	1A	4124	1/1	0.95	0.36	8.55	46,46,46,46	0
56	MG	1A	4076	1/1	0.61	0.29	8.47	75,75,75,75	0
56	MG	2A	3003	1/1	0.95	0.28	8.38	43,43,43,43	0
56	MG	1A	3578	1/1	0.97	0.28	8.32	33,33,33,33	0
56	MG	2A	3092	1/1	0.98	0.27	8.24	43,43,43,43	0
56	MG	2A	3191	1/1	0.92	0.21	8.14	50,50,50,50	0
56	MG	1A	3013	1/1	0.95	0.33	7.84	35,35,35,35	0
56	MG	2A	3856	1/1	0.93	0.32	7.82	41,41,41,41	0
56	MG	2A	3083	1/1	0.98	0.43	7.77	49,49,49,49	0
56	MG	1A	3311	1/1	0.97	0.25	7.41	48,48,48,48	0
56	MG	1A	3603	1/1	0.95	0.28	7.35	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3200	1/1	0.98	0.27	6.91	23,23,23,23	0
56	MG	2A	3409	1/1	0.98	0.23	6.78	47,47,47,47	0
56	MG	1A	3842	1/1	0.97	0.27	6.75	26,26,26,26	0
56	MG	2D	304	1/1	0.87	0.36	6.71	45,45,45,45	0
58	ZN	25	102	1/1	0.97	0.31	6.63	68,68,68,68	0
56	MG	1A	3194	1/1	0.97	0.27	6.57	43,43,43,43	0
56	MG	2A	3900	1/1	0.96	0.34	6.52	44,44,44,44	0
56	MG	1A	3056	1/1	0.99	0.27	6.51	28,28,28,28	0
56	MG	2A	3445	1/1	0.90	0.24	6.50	55,55,55,55	0
56	MG	2A	3160	1/1	0.93	0.25	6.49	44,44,44,44	0
56	MG	1A	3458	1/1	0.75	0.29	6.40	54,54,54,54	0
56	MG	1A	3177	1/1	0.97	0.27	6.38	38,38,38,38	0
56	MG	1A	3628	1/1	0.98	0.27	6.19	28,28,28,28	0
56	MG	2A	3461	1/1	0.98	0.26	5.92	52,52,52,52	0
56	MG	1A	3338	1/1	0.98	0.20	5.87	49,49,49,49	0
56	MG	1A	3351	1/1	0.94	0.29	5.49	49,49,49,49	0
56	MG	1a	1659	1/1	0.97	0.26	5.27	62,62,62,62	0
56	MG	1A	3559	1/1	0.97	0.27	5.08	34,34,34,34	0
56	MG	1D	302	1/1	0.94	0.44	5.01	55,55,55,55	0
56	MG	1A	3055	1/1	0.95	0.27	5.01	43,43,43,43	0
56	MG	2A	3633	1/1	0.97	0.24	4.98	55,55,55,55	0
56	MG	2A	3070	1/1	0.98	0.24	4.86	42,42,42,42	0
56	MG	2A	3897	1/1	0.94	0.32	4.80	57,57,57,57	0
56	MG	1A	3280	1/1	0.93	0.26	4.77	50,50,50,50	0
56	MG	2U	201	1/1	0.97	0.24	4.73	40,40,40,40	0
56	MG	1A	4086	1/1	0.98	0.33	4.71	43,43,43,43	0
56	MG	2A	3347	1/1	0.94	0.24	4.69	51,51,51,51	0
56	MG	2A	3814	1/1	0.88	0.29	4.51	55,55,55,55	0
56	MG	1O	203	1/1	0.93	0.31	4.50	63,63,63,63	0
56	MG	1A	3104	1/1	0.91	0.27	4.49	40,40,40,40	0
56	MG	1A	3753	1/1	0.93	0.27	4.49	34,34,34,34	0
56	MG	2a	3041	1/1	0.97	0.26	4.49	50,50,50,50	0
56	MG	1a	1657	1/1	0.95	0.24	4.32	57,57,57,57	0
56	MG	1A	4115	1/1	0.96	0.35	4.30	51,51,51,51	0
56	MG	1O	202	1/1	0.89	0.50	4.30	67,67,67,67	0
56	MG	1A	4072	1/1	0.70	0.37	4.22	62,62,62,62	0
56	MG	2A	3108	1/1	0.97	0.23	4.11	44,44,44,44	0
56	MG	1A	3744	1/1	0.90	0.28	4.07	74,74,74,74	0
56	MG	1A	4090	1/1	0.98	0.29	4.06	37,37,37,37	0
56	MG	1A	3068	1/1	0.98	0.24	4.04	38,38,38,38	0
56	MG	2A	3364	1/1	0.58	0.17	3.98	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1D	310	1/1	0.95	0.34	3.97	39,39,39,39	0
56	MG	1A	3171	1/1	0.94	0.33	3.86	53,53,53,53	0
56	MG	2A	3883	1/1	0.87	0.34	3.84	56,56,56,56	0
56	MG	2B	3008	1/1	0.81	0.18	3.82	58,58,58,58	0
56	MG	1A	3576	1/1	0.84	0.25	3.71	57,57,57,57	0
56	MG	1A	4047	1/1	0.95	0.27	3.70	50,50,50,50	0
58	ZN	15	101	1/1	1.00	0.27	3.60	37,37,37,37	0
56	MG	2A	3025	1/1	0.98	0.27	3.51	42,42,42,42	0
56	MG	1A	3971	1/1	0.79	0.24	3.51	44,44,44,44	0
56	MG	1D	301	1/1	0.97	0.27	3.51	46,46,46,46	0
56	MG	2A	3448	1/1	0.99	0.20	3.47	49,49,49,49	0
56	MG	2A	3093	1/1	0.88	0.25	3.43	54,54,54,54	0
56	MG	2A	3673	1/1	0.92	0.24	3.43	64,64,64,64	0
56	MG	1A	3185	1/1	0.90	0.24	3.43	47,47,47,47	0
56	MG	16	101	1/1	0.90	0.25	3.42	45,45,45,45	0
56	MG	1E	304	1/1	0.82	0.24	3.41	55,55,55,55	0
56	MG	2A	3745	1/1	0.71	0.20	3.39	56,56,56,56	0
56	MG	2a	3010	1/1	0.74	0.18	3.38	76,76,76,76	0
56	MG	2A	3876	1/1	0.72	0.30	3.14	66,66,66,66	0
56	MG	1A	3347	1/1	0.97	0.24	3.13	44,44,44,44	0
56	MG	1A	3063	1/1	0.92	0.20	3.07	38,38,38,38	0
56	MG	1A	3313	1/1	0.90	0.25	3.03	49,49,49,49	0
56	MG	1A	3165	1/1	0.92	0.24	2.97	48,48,48,48	0
56	MG	1S	3001	1/1	0.85	0.30	2.94	51,51,51,51	0
56	MG	1D	312	1/1	0.96	0.27	2.80	42,42,42,42	0
56	MG	1A	3658	1/1	0.96	0.24	2.75	37,37,37,37	0
56	MG	2A	3014	1/1	0.92	0.26	2.73	43,43,43,43	0
56	MG	1A	3552	1/1	0.88	0.22	2.64	60,60,60,60	0
56	MG	1A	4093	1/1	0.95	0.27	2.62	35,35,35,35	0
56	MG	2A	3579	1/1	0.87	0.18	2.59	60,60,60,60	0
56	MG	1A	3248	1/1	0.83	0.26	2.51	47,47,47,47	0
56	MG	1A	3704	1/1	0.88	0.24	2.50	49,49,49,49	0
56	MG	2A	3181	1/1	0.98	0.22	2.44	40,40,40,40	0
56	MG	1A	3095	1/1	0.85	0.20	2.43	55,55,55,55	0
56	MG	1A	3252	1/1	0.89	0.23	2.36	52,52,52,52	0
56	MG	1A	3125	1/1	0.95	0.26	2.29	41,41,41,41	0
56	MG	1A	3151	1/1	0.87	0.23	2.29	47,47,47,47	0
56	MG	1B	3019	1/1	0.93	0.23	2.22	56,56,56,56	0
56	MG	1A	3871	1/1	0.90	0.26	2.18	49,49,49,49	0
56	MG	2A	3472	1/1	0.94	0.18	2.13	60,60,60,60	0
56	MG	2a	3165	1/1	0.93	0.26	2.10	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3192	1/1	0.96	0.19	1.97	44,44,44,44	0
56	MG	2A	3714	1/1	0.98	0.23	1.91	39,39,39,39	0
56	MG	2A	3899	1/1	0.94	0.21	1.84	45,45,45,45	0
56	MG	1A	3751	1/1	0.87	0.27	1.82	48,48,48,48	0
56	MG	1A	3728	1/1	0.86	0.24	1.82	26,26,26,26	0
56	MG	19	101	1/1	0.88	0.26	1.81	49,49,49,49	0
56	MG	1A	3644	1/1	0.99	0.22	1.77	33,33,33,33	0
56	MG	1A	3748	1/1	0.97	0.23	1.75	25,25,25,25	0
56	MG	2A	3013	1/1	0.99	0.19	1.73	44,44,44,44	0
56	MG	1A	4107	1/1	0.96	0.26	1.73	42,42,42,42	0
56	MG	2A	3635	1/1	0.92	0.18	1.72	43,43,43,43	0
56	MG	1A	3605	1/1	0.98	0.20	1.58	32,32,32,32	0
56	MG	2A	3552	1/1	0.93	0.18	1.56	59,59,59,59	0
56	MG	2A	3112	1/1	0.83	0.17	1.51	42,42,42,42	0
56	MG	1A	3887	1/1	0.97	0.23	1.51	31,31,31,31	0
56	MG	1n	103	1/1	0.99	0.23	1.49	48,48,48,48	0
56	MG	2A	3538	1/1	0.97	0.19	1.48	35,35,35,35	0
56	MG	1A	3745	1/1	0.88	0.23	1.42	19,19,19,19	0
56	MG	1a	1701	1/1	0.92	0.22	1.38	51,51,51,51	0
56	MG	1A	3729	1/1	0.93	0.26	1.35	42,42,42,42	0
56	MG	2A	3910	1/1	0.95	0.27	1.27	57,57,57,57	0
56	MG	1A	4079	1/1	0.88	0.25	1.25	46,46,46,46	0
56	MG	1a	1607	1/1	0.90	0.20	1.23	67,67,67,67	0
56	MG	1P	203	1/1	0.99	0.27	1.21	30,30,30,30	0
56	MG	2F	303	1/1	0.97	0.21	1.20	48,48,48,48	0
56	MG	1a	1652	1/1	0.94	0.20	1.20	63,63,63,63	0
56	MG	2A	3484	1/1	0.88	0.21	1.19	53,53,53,53	0
56	MG	1X	103	1/1	0.98	0.25	1.19	40,40,40,40	0
56	MG	1A	3035	1/1	0.98	0.23	1.18	20,20,20,20	0
56	MG	2U	204	1/1	0.81	0.21	1.10	45,45,45,45	0
56	MG	2a	3192	1/1	0.72	0.20	1.08	63,63,63,63	0
56	MG	2B	3009	1/1	0.87	0.16	1.08	61,61,61,61	0
56	MG	1A	3757	1/1	0.91	0.23	1.07	27,27,27,27	0
56	MG	2A	3095	1/1	0.93	0.19	1.05	39,39,39,39	0
56	MG	1A	3811	1/1	0.98	0.22	1.04	45,45,45,45	0
56	MG	1W	203	1/1	0.99	0.24	1.04	30,30,30,30	0
56	MG	2A	3761	1/1	0.97	0.23	1.01	46,46,46,46	0
56	MG	1A	3355	1/1	0.97	0.26	0.94	47,47,47,47	0
56	MG	1A	4080	1/1	0.96	0.24	0.93	23,23,23,23	0
56	MG	1A	3041	1/1	0.96	0.23	0.87	38,38,38,38	0
58	ZN	16	102	1/1	1.00	0.22	0.84	44,44,44,44	0
56	MG	1B	3027	1/1	0.96	0.22	0.82	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1n	102	1/1	0.88	0.24	0.81	66,66,66,66	0
56	MG	2A	3756	1/1	0.88	0.18	0.78	42,42,42,42	0
56	MG	2A	3697	1/1	0.95	0.18	0.73	34,34,34,34	0
56	MG	1A	3793	1/1	0.99	0.24	0.72	37,37,37,37	0
56	MG	2A	3098	1/1	0.91	0.17	0.71	49,49,49,49	0
56	MG	2w	105	1/1	0.95	0.31	0.64	70,70,70,70	0
56	MG	2A	3026	1/1	0.97	0.19	0.61	36,36,36,36	0
56	MG	2a	3244	1/1	0.96	0.18	0.60	43,43,43,43	0
56	MG	1A	4118	1/1	0.98	0.25	0.60	36,36,36,36	0
56	MG	2A	3235	1/1	0.94	0.18	0.58	50,50,50,50	0
56	MG	2A	3144	1/1	0.94	0.19	0.55	45,45,45,45	0
56	MG	18	101	1/1	0.84	0.24	0.54	47,47,47,47	0
56	MG	2A	3905	1/1	0.96	0.23	0.54	38,38,38,38	0
56	MG	1E	302	1/1	0.82	0.24	0.53	58,58,58,58	0
56	MG	1A	3285	1/1	0.96	0.22	0.50	39,39,39,39	0
58	ZN	1Y	501	1/1	0.99	0.19	0.47	60,60,60,60	0
56	MG	2A	3040	1/1	0.89	0.18	0.46	52,52,52,52	0
56	MG	1A	3054	1/1	0.97	0.23	0.46	39,39,39,39	0
56	MG	1A	3855	1/1	0.93	0.22	0.46	53,53,53,53	0
56	MG	1A	3654	1/1	0.88	0.24	0.44	36,36,36,36	0
56	MG	1F	304	1/1	0.98	0.25	0.42	40,40,40,40	0
56	MG	1A	4108	1/1	0.95	0.23	0.42	48,48,48,48	0
56	MG	1A	3606	1/1	0.98	0.23	0.39	36,36,36,36	0
56	MG	1D	306	1/1	0.98	0.21	0.39	32,32,32,32	0
56	MG	1A	3532	1/1	0.95	0.23	0.39	36,36,36,36	0
56	MG	1A	3376	1/1	0.92	0.21	0.38	51,51,51,51	0
56	MG	2r	101	1/1	0.92	0.15	0.33	68,68,68,68	0
56	MG	1a	1603	1/1	0.89	0.18	0.32	59,59,59,59	0
56	MG	1A	3608	1/1	0.95	0.20	0.31	51,51,51,51	0
56	MG	1a	1823	1/1	0.78	0.21	0.31	68,68,68,68	0
56	MG	1A	3963	1/1	0.90	0.23	0.30	60,60,60,60	0
56	MG	1A	4081	1/1	0.95	0.22	0.30	44,44,44,44	0
56	MG	2U	203	1/1	0.94	0.25	0.29	46,46,46,46	0
56	MG	1A	4051	1/1	0.92	0.23	0.27	38,38,38,38	0
56	MG	1A	3229	1/1	0.91	0.23	0.26	33,33,33,33	0
56	MG	2A	3001	1/1	0.91	0.19	0.24	47,47,47,47	0
56	MG	2A	3151	1/1	0.97	0.18	0.23	40,40,40,40	0
56	MG	1A	3526	1/1	0.95	0.24	0.21	53,53,53,53	0
56	MG	1U	204	1/1	0.95	0.22	0.20	38,38,38,38	0
56	MG	1a	1829	1/1	0.77	0.20	0.20	73,73,73,73	0
56	MG	1A	4098	1/1	0.92	0.21	0.16	45,45,45,45	0
56	MG	2A	3534	1/1	0.93	0.19	0.12	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3130	1/1	0.92	0.23	0.12	41,41,41,41	0
56	MG	2B	3006	1/1	0.92	0.23	0.11	59,59,59,59	0
56	MG	2A	3884	1/1	0.74	0.19	0.08	42,42,42,42	0
56	MG	2f	3001	1/1	0.98	0.19	0.08	41,41,41,41	0
56	MG	1A	3193	1/1	0.95	0.21	0.03	34,34,34,34	0
56	MG	2A	3888	1/1	0.88	0.20	-0.01	57,57,57,57	0
56	MG	1a	1614	1/1	0.96	0.17	-0.03	45,45,45,45	0
56	MG	2A	3187	1/1	0.91	0.17	-0.07	50,50,50,50	0
56	MG	2A	3626	1/1	0.92	0.19	-0.08	53,53,53,53	0
56	MG	1A	4101	1/1	0.96	0.20	-0.11	39,39,39,39	0
56	MG	1x	103	1/1	0.58	0.16	-0.11	71,71,71,71	0
56	MG	1A	4117	1/1	0.98	0.22	-0.13	39,39,39,39	0
56	MG	1A	3078	1/1	0.97	0.22	-0.13	31,31,31,31	0
56	MG	2a	3238	1/1	0.81	0.17	-0.14	62,62,62,62	0
56	MG	1A	3358	1/1	0.94	0.23	-0.15	33,33,33,33	0
56	MG	2a	3161	1/1	0.93	0.21	-0.18	91,91,91,91	0
56	MG	1A	3172	1/1	0.94	0.22	-0.20	43,43,43,43	0
56	MG	2A	3904	1/1	0.98	0.19	-0.23	41,41,41,41	0
56	MG	2A	3560	1/1	0.92	0.19	-0.24	63,63,63,63	0
56	MG	2A	3162	1/1	0.95	0.17	-0.25	53,53,53,53	0
56	MG	1A	3135	1/1	0.97	0.23	-0.26	32,32,32,32	0
56	MG	1D	304	1/1	0.93	0.19	-0.27	30,30,30,30	0
56	MG	2A	3832	1/1	0.81	0.16	-0.27	54,54,54,54	0
56	MG	1A	4059	1/1	0.98	0.20	-0.28	21,21,21,21	0
56	MG	1A	3562	1/1	0.95	0.21	-0.28	24,24,24,24	0
56	MG	2A	3542	1/1	0.97	0.16	-0.28	39,39,39,39	0
56	MG	1A	4099	1/1	0.95	0.21	-0.28	41,41,41,41	0
56	MG	1Q	201	1/1	0.96	0.20	-0.29	36,36,36,36	0
56	MG	2A	3121	1/1	0.87	0.18	-0.29	42,42,42,42	0
56	MG	1A	4132	1/1	0.99	0.23	-0.29	39,39,39,39	0
56	MG	1A	3707	1/1	0.94	0.21	-0.31	29,29,29,29	0
56	MG	2A	3126	1/1	0.87	0.18	-0.32	58,58,58,58	0
56	MG	2a	3232	1/1	0.87	0.23	-0.36	77,77,77,77	0
56	MG	1A	3379	1/1	0.97	0.21	-0.39	37,37,37,37	0
56	MG	1A	3650	1/1	0.98	0.20	-0.39	35,35,35,35	0
56	MG	1A	3863	1/1	0.82	0.23	-0.42	50,50,50,50	0
56	MG	1B	3022	1/1	0.97	0.19	-0.44	60,60,60,60	0
56	MG	2A	3849	1/1	0.87	0.18	-0.44	44,44,44,44	0
56	MG	2A	3410	1/1	0.88	0.16	-0.45	55,55,55,55	0
56	MG	2A	3692	1/1	0.97	0.17	-0.47	56,56,56,56	0
56	MG	1A	4129	1/1	0.93	0.23	-0.49	42,42,42,42	0
56	MG	2A	3452	1/1	0.86	0.19	-0.50	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3643	1/1	0.86	0.15	-0.52	34,34,34,34	0
56	MG	1b	3001	1/1	0.89	0.15	-0.53	83,83,83,83	0
56	MG	1A	3686	1/1	0.92	0.20	-0.54	35,35,35,35	0
56	MG	1A	3781	1/1	0.74	0.21	-0.55	32,32,32,32	0
56	MG	1A	3205	1/1	0.97	0.20	-0.57	42,42,42,42	0
56	MG	1A	3668	1/1	0.85	0.20	-0.59	28,28,28,28	0
56	MG	1B	3023	1/1	0.95	0.18	-0.60	54,54,54,54	0
56	MG	1A	4114	1/1	0.97	0.21	-0.63	34,34,34,34	0
56	MG	2A	3877	1/1	0.97	0.19	-0.64	28,28,28,28	0
56	MG	1A	3693	1/1	0.88	0.19	-0.64	40,40,40,40	0
56	MG	1A	3010	1/1	0.97	0.20	-0.64	39,39,39,39	0
56	MG	2A	3694	1/1	0.92	0.15	-0.65	51,51,51,51	0
56	MG	2w	107	1/1	0.66	0.22	-0.66	75,75,75,75	0
56	MG	2A	3638	1/1	0.94	0.18	-0.66	43,43,43,43	0
56	MG	1a	1617	1/1	0.72	0.18	-0.66	63,63,63,63	0
56	MG	2a	3103	1/1	0.64	0.16	-0.69	76,76,76,76	0
56	MG	2A	3127	1/1	0.93	0.13	-0.71	50,50,50,50	0
56	MG	1A	3414	1/1	0.96	0.19	-0.71	39,39,39,39	0
56	MG	1A	4012	1/1	0.86	0.20	-0.72	34,34,34,34	0
56	MG	1A	4109	1/1	0.94	0.21	-0.74	49,49,49,49	0
56	MG	1D	305	1/1	0.88	0.18	-0.74	42,42,42,42	0
56	MG	1a	1825	1/1	0.98	0.18	-0.75	37,37,37,37	0
56	MG	1A	3921	1/1	0.91	0.17	-0.77	50,50,50,50	0
56	MG	2A	3441	1/1	0.90	0.15	-0.78	51,51,51,51	0
56	MG	1a	1730	1/1	0.93	0.16	-0.80	80,80,80,80	0
56	MG	1A	4097	1/1	0.97	0.15	-0.80	47,47,47,47	0
56	MG	1A	3700	1/1	0.98	0.20	-0.80	16,16,16,16	0
56	MG	16	104	1/1	0.97	0.21	-0.81	53,53,53,53	0
58	ZN	19	103	1/1	0.99	0.19	-0.82	44,44,44,44	0
56	MG	2a	3076	1/1	0.79	0.15	-0.82	73,73,73,73	0
56	MG	2A	3080	1/1	0.80	0.16	-0.83	58,58,58,58	0
58	ZN	26	501	1/1	0.96	0.14	-0.83	60,60,60,60	0
56	MG	2A	3634	1/1	0.95	0.17	-0.83	34,34,34,34	0
56	MG	1A	3652	1/1	0.96	0.20	-0.87	31,31,31,31	0
56	MG	1E	311	1/1	0.85	0.20	-0.87	42,42,42,42	0
56	MG	2a	3145	1/1	0.86	0.20	-0.87	76,76,76,76	0
56	MG	1D	309	1/1	0.94	0.18	-0.88	46,46,46,46	0
56	MG	1A	3691	1/1	0.90	0.20	-0.89	41,41,41,41	0
56	MG	2a	3096	1/1	0.78	0.14	-0.91	65,65,65,65	0
56	MG	1A	3619	1/1	0.98	0.20	-0.93	31,31,31,31	0
56	MG	1l	201	1/1	0.98	0.16	-0.95	43,43,43,43	0
56	MG	2Q	3003	1/1	0.98	0.17	-0.95	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1745	1/1	0.87	0.16	-0.95	55,55,55,55	0
56	MG	1N	202	1/1	0.85	0.22	-0.95	48,48,48,48	0
56	MG	1A	3074	1/1	0.93	0.21	-0.97	27,27,27,27	0
56	MG	1A	3122	1/1	0.96	0.22	-0.97	44,44,44,44	0
56	MG	2A	3840	1/1	0.98	0.18	-0.97	43,43,43,43	0
56	MG	1A	4116	1/1	0.90	0.22	-1.00	41,41,41,41	0
56	MG	2A	3142	1/1	0.96	0.17	-1.00	41,41,41,41	0
56	MG	2A	3903	1/1	0.93	0.14	-1.01	58,58,58,58	0
56	MG	1U	207	1/1	0.96	0.20	-1.01	31,31,31,31	0
56	MG	1F	308	1/1	0.93	0.20	-1.01	53,53,53,53	0
56	MG	2A	3907	1/1	0.93	0.16	-1.01	57,57,57,57	0
56	MG	2a	3046	1/1	0.72	0.17	-1.02	64,64,64,64	0
56	MG	2T	3002	1/1	0.85	0.15	-1.02	58,58,58,58	0
56	MG	2A	3548	1/1	0.97	0.17	-1.04	38,38,38,38	0
56	MG	2A	3619	1/1	0.95	0.16	-1.04	37,37,37,37	0
56	MG	2A	3513	1/1	0.98	0.15	-1.06	34,34,34,34	0
56	MG	2A	3615	1/1	0.79	0.13	-1.06	51,51,51,51	0
56	MG	1A	3460	1/1	0.93	0.22	-1.07	48,48,48,48	0
56	MG	2A	3841	1/1	0.97	0.16	-1.08	30,30,30,30	0
56	MG	2a	3229	1/1	0.90	0.15	-1.11	69,69,69,69	0
56	MG	2a	3105	1/1	0.82	0.17	-1.14	45,45,45,45	0
56	MG	1A	3680	1/1	0.92	0.19	-1.16	44,44,44,44	0
56	MG	1A	3741	1/1	0.80	0.18	-1.18	45,45,45,45	0
56	MG	1U	203	1/1	0.91	0.23	-1.19	42,42,42,42	0
56	MG	2a	3128	1/1	0.87	0.12	-1.19	87,87,87,87	0
56	MG	2a	3189	1/1	0.94	0.16	-1.20	48,48,48,48	0
58	ZN	24	501	1/1	0.72	0.10	-1.21	128,128,128,128	0
56	MG	2A	3890	1/1	0.86	0.16	-1.21	61,61,61,61	0
56	MG	1A	3843	1/1	0.99	0.21	-1.22	31,31,31,31	0
56	MG	2D	301	1/1	0.95	0.15	-1.22	57,57,57,57	0
56	MG	2a	3157	1/1	0.93	0.12	-1.23	64,64,64,64	0
56	MG	2j	8002	1/1	0.90	0.16	-1.25	66,66,66,66	0
56	MG	2A	3140	1/1	0.93	0.18	-1.27	50,50,50,50	0
56	MG	2a	3047	1/1	0.83	0.12	-1.31	52,52,52,52	0
56	MG	1G	3003	1/1	0.88	0.11	-1.31	66,66,66,66	0
58	ZN	14	501	1/1	0.92	0.11	-1.32	99,99,99,99	0
58	ZN	2Y	501	1/1	0.96	0.13	-1.36	81,81,81,81	0
56	MG	1A	4119	1/1	0.98	0.23	-1.37	34,34,34,34	0
56	MG	1x	107	1/1	0.76	0.12	-1.38	61,61,61,61	0
56	MG	2t	3001	1/1	0.52	0.15	-1.39	60,60,60,60	0
59	SF4	1d	501	8/8	0.98	0.13	-1.39	59,71,76,86	0
56	MG	2A	3737	1/1	0.94	0.13	-1.40	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3105	1/1	0.98	0.17	-1.40	40,40,40,40	0
56	MG	2D	303	1/1	0.95	0.15	-1.40	35,35,35,35	0
56	MG	1a	1654	1/1	0.80	0.17	-1.42	49,49,49,49	0
56	MG	2U	202	1/1	0.89	0.13	-1.43	54,54,54,54	0
56	MG	1A	3166	1/1	0.87	0.22	-1.44	38,38,38,38	0
56	MG	1a	1740	1/1	0.99	0.17	-1.45	35,35,35,35	0
56	MG	1A	3666	1/1	0.87	0.16	-1.46	34,34,34,34	0
56	MG	2A	3645	1/1	0.93	0.16	-1.48	40,40,40,40	0
56	MG	2A	3034	1/1	0.90	0.15	-1.49	45,45,45,45	0
56	MG	2A	3674	1/1	0.96	0.17	-1.50	55,55,55,55	0
56	MG	1A	3195	1/1	0.93	0.21	-1.51	40,40,40,40	0
56	MG	1A	3800	1/1	0.88	0.15	-1.51	65,65,65,65	0
56	MG	1A	3042	1/1	0.98	0.18	-1.52	40,40,40,40	0
56	MG	1R	202	1/1	0.92	0.18	-1.54	38,38,38,38	0
56	MG	2A	3726	1/1	0.84	0.13	-1.55	56,56,56,56	0
56	MG	2T	3001	1/1	0.91	0.13	-1.55	53,53,53,53	0
56	MG	1A	3764	1/1	0.89	0.18	-1.57	31,31,31,31	0
56	MG	1A	3514	1/1	0.96	0.20	-1.57	53,53,53,53	0
56	MG	1A	3873	1/1	0.98	0.21	-1.58	35,35,35,35	0
56	MG	1A	3961	1/1	0.98	0.18	-1.59	38,38,38,38	0
56	MG	1A	3919	1/1	0.95	0.18	-1.59	38,38,38,38	0
56	MG	1Q	202	1/1	0.96	0.20	-1.61	46,46,46,46	0
56	MG	1A	3730	1/1	0.75	0.18	-1.62	43,43,43,43	0
56	MG	1A	3405	1/1	0.91	0.21	-1.63	42,42,42,42	0
58	ZN	29	101	1/1	0.97	0.08	-1.64	73,73,73,73	0
56	MG	1A	3909	1/1	0.97	0.20	-1.64	40,40,40,40	0
56	MG	2A	3475	1/1	0.86	0.16	-1.66	44,44,44,44	0
56	MG	1A	3752	1/1	0.82	0.19	-1.66	41,41,41,41	0
56	MG	1A	3040	1/1	0.95	0.20	-1.66	36,36,36,36	0
58	ZN	1n	101	1/1	0.98	0.12	-1.68	71,71,71,71	0
56	MG	1A	3775	1/1	0.98	0.21	-1.68	27,27,27,27	0
56	MG	1A	3535	1/1	0.93	0.20	-1.70	45,45,45,45	0
56	MG	2A	3037	1/1	0.97	0.14	-1.70	35,35,35,35	0
56	MG	2X	101	1/1	0.96	0.10	-1.71	37,37,37,37	0
56	MG	1A	3190	1/1	0.90	0.21	-1.72	39,39,39,39	0
56	MG	2a	3173	1/1	0.87	0.12	-1.72	62,62,62,62	0
56	MG	1A	3187	1/1	0.91	0.21	-1.74	47,47,47,47	0
56	MG	1A	3641	1/1	0.82	0.17	-1.75	65,65,65,65	0
56	MG	1A	3595	1/1	0.92	0.21	-1.76	59,59,59,59	0
56	MG	1A	4104	1/1	0.94	0.15	-1.77	30,30,30,30	0
56	MG	1a	1608	1/1	0.95	0.18	-1.77	60,60,60,60	0
56	MG	2A	3163	1/1	0.94	0.13	-1.78	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2e	3001	1/1	0.95	0.08	-1.79	79,79,79,79	0
56	MG	2Q	3001	1/1	0.97	0.15	-1.80	50,50,50,50	0
56	MG	2l	201	1/1	0.96	0.14	-1.81	66,66,66,66	0
56	MG	1a	1747	1/1	0.94	0.14	-1.82	49,49,49,49	0
56	MG	2A	3158	1/1	0.98	0.17	-1.84	41,41,41,41	0
56	MG	2n	502	1/1	0.95	0.06	-1.84	86,86,86,86	0
56	MG	1A	3750	1/1	0.97	0.21	-1.85	29,29,29,29	0
56	MG	1A	3066	1/1	0.93	0.17	-1.89	35,35,35,35	0
56	MG	1a	1634	1/1	0.95	0.17	-1.91	27,27,27,27	0
56	MG	2a	3097	1/1	0.83	0.13	-1.91	72,72,72,72	0
56	MG	2a	3241	1/1	0.94	0.10	-1.92	41,41,41,41	0
56	MG	1A	4140	1/1	0.96	0.18	-1.92	31,31,31,31	0
56	MG	2A	3889	1/1	0.97	0.11	-1.94	49,49,49,49	0
56	MG	13	101	1/1	0.88	0.22	-1.95	55,55,55,55	0
56	MG	1a	1827	1/1	0.86	0.14	-1.95	58,58,58,58	0
56	MG	1A	3790	1/1	0.96	0.18	-1.99	25,25,25,25	0
56	MG	2A	3530	1/1	0.97	0.15	-1.99	37,37,37,37	0
56	MG	2A	3565	1/1	0.94	0.16	-2.00	36,36,36,36	0
56	MG	2W	201	1/1	0.96	0.14	-2.00	57,57,57,57	0
56	MG	1D	303	1/1	0.94	0.14	-2.00	37,37,37,37	0
56	MG	1A	3653	1/1	0.94	0.19	-2.00	27,27,27,27	0
56	MG	1A	3109	1/1	0.99	0.20	-2.00	35,35,35,35	0
56	MG	1A	3902	1/1	0.95	0.21	-2.01	33,33,33,33	0
56	MG	2A	3690	1/1	0.96	0.12	-2.02	61,61,61,61	0
56	MG	1A	4077	1/1	0.98	0.19	-2.04	11,11,11,11	0
56	MG	1a	1618	1/1	0.96	0.17	-2.04	48,48,48,48	0
56	MG	2A	3581	1/1	0.98	0.17	-2.05	25,25,25,25	0
56	MG	2A	3516	1/1	0.97	0.14	-2.05	56,56,56,56	0
56	MG	2A	3103	1/1	0.96	0.15	-2.06	42,42,42,42	0
56	MG	2a	3113	1/1	0.97	0.14	-2.08	46,46,46,46	0
56	MG	1A	4002	1/1	0.94	0.20	-2.08	33,33,33,33	0
56	MG	2A	3812	1/1	0.79	0.13	-2.09	47,47,47,47	0
56	MG	1E	309	1/1	0.94	0.15	-2.10	50,50,50,50	0
56	MG	2a	3200	1/1	0.96	0.14	-2.12	76,76,76,76	0
56	MG	2A	3207	1/1	0.92	0.14	-2.13	44,44,44,44	0
56	MG	1A	3657	1/1	0.95	0.18	-2.15	27,27,27,27	0
56	MG	28	102	1/1	0.76	0.18	-2.17	52,52,52,52	0
56	MG	1A	3184	1/1	0.84	0.15	-2.17	62,62,62,62	0
56	MG	1a	1806	1/1	0.90	0.13	-2.19	66,66,66,66	0
56	MG	2A	3570	1/1	0.95	0.13	-2.19	53,53,53,53	0
56	MG	2G	3001	1/1	0.83	0.16	-2.19	51,51,51,51	0
56	MG	1A	3241	1/1	0.96	0.18	-2.19	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3514	1/1	0.96	0.13	-2.20	32,32,32,32	0
56	MG	2X	103	1/1	0.95	0.11	-2.20	46,46,46,46	0
56	MG	1A	3663	1/1	0.98	0.18	-2.21	28,28,28,28	0
56	MG	1A	4130	1/1	0.97	0.18	-2.21	38,38,38,38	0
56	MG	2a	3195	1/1	0.93	0.13	-2.22	41,41,41,41	0
56	MG	2a	3149	1/1	0.86	0.12	-2.22	56,56,56,56	0
56	MG	1X	101	1/1	0.84	0.17	-2.23	40,40,40,40	0
56	MG	1A	3735	1/1	0.97	0.18	-2.24	41,41,41,41	0
56	MG	1a	1751	1/1	0.84	0.14	-2.25	70,70,70,70	0
56	MG	2A	3564	1/1	0.94	0.15	-2.25	31,31,31,31	0
56	MG	1A	3746	1/1	0.87	0.20	-2.26	55,55,55,55	0
56	MG	2A	3122	1/1	0.94	0.13	-2.27	39,39,39,39	0
56	MG	2a	3098	1/1	0.97	0.14	-2.27	46,46,46,46	0
56	MG	2A	3016	1/1	0.91	0.14	-2.28	61,61,61,61	0
56	MG	1A	3596	1/1	0.93	0.20	-2.31	51,51,51,51	0
56	MG	1A	3228	1/1	0.96	0.20	-2.33	41,41,41,41	0
56	MG	2A	3650	1/1	0.97	0.14	-2.34	41,41,41,41	0
56	MG	1A	4096	1/1	0.94	0.14	-2.35	30,30,30,30	0
56	MG	1a	1737	1/1	0.94	0.11	-2.35	66,66,66,66	0
56	MG	2A	3577	1/1	0.77	0.12	-2.37	56,56,56,56	0
56	MG	1A	3880	1/1	0.95	0.17	-2.39	30,30,30,30	0
59	SF4	2d	501	8/8	0.97	0.11	-2.41	61,71,85,99	0
56	MG	1A	3626	1/1	0.94	0.14	-2.42	44,44,44,44	0
56	MG	2a	3082	1/1	0.94	0.14	-2.43	54,54,54,54	0
56	MG	2a	3175	1/1	0.95	0.13	-2.45	46,46,46,46	0
58	ZN	2n	501	1/1	0.96	0.09	-2.46	107,107,107,107	0
56	MG	1A	3756	1/1	0.92	0.20	-2.46	39,39,39,39	0
56	MG	1a	1629	1/1	0.81	0.16	-2.46	57,57,57,57	0
56	MG	2A	3601	1/1	0.97	0.15	-2.48	39,39,39,39	0
56	MG	2A	3606	1/1	0.92	0.15	-2.49	61,61,61,61	0
56	MG	2A	3902	1/1	0.97	0.14	-2.51	43,43,43,43	0
56	MG	1a	1826	1/1	0.89	0.06	-2.54	58,58,58,58	0
56	MG	1A	3328	1/1	0.88	0.17	-2.57	64,64,64,64	0
56	MG	2A	3881	1/1	0.89	0.14	-2.57	48,48,48,48	0
56	MG	2a	3154	1/1	0.96	0.11	-2.58	68,68,68,68	0
56	MG	2a	3217	1/1	0.96	0.07	-2.59	61,61,61,61	0
56	MG	1A	3237	1/1	0.96	0.19	-2.60	38,38,38,38	0
56	MG	1E	308	1/1	0.95	0.11	-2.60	34,34,34,34	0
56	MG	1A	3120	1/1	0.94	0.18	-2.61	42,42,42,42	0
56	MG	2A	3145	1/1	0.97	0.15	-2.63	36,36,36,36	0
56	MG	1A	3859	1/1	0.90	0.19	-2.64	44,44,44,44	0
56	MG	1A	3034	1/1	0.87	0.16	-2.65	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1822	1/1	0.96	0.11	-2.66	54,54,54,54	0
56	MG	1a	1667	1/1	0.91	0.12	-2.66	65,65,65,65	0
56	MG	2a	3092	1/1	0.93	0.13	-2.67	51,51,51,51	0
56	MG	1A	3210	1/1	0.90	0.16	-2.67	42,42,42,42	0
56	MG	2E	304	1/1	0.89	0.12	-2.68	46,46,46,46	0
56	MG	2a	3070	1/1	0.80	0.15	-2.69	61,61,61,61	0
56	MG	1A	3144	1/1	0.81	0.19	-2.69	52,52,52,52	0
56	MG	1A	3861	1/1	0.94	0.17	-2.70	33,33,33,33	0
56	MG	2A	3709	1/1	0.97	0.14	-2.72	33,33,33,33	0
56	MG	1A	3904	1/1	0.93	0.17	-2.72	36,36,36,36	0
56	MG	1A	3984	1/1	0.98	0.16	-2.74	34,34,34,34	0
56	MG	2A	3613	1/1	0.91	0.16	-2.75	33,33,33,33	0
56	MG	2A	3576	1/1	0.96	0.15	-2.79	39,39,39,39	0
56	MG	2A	3562	1/1	0.89	0.11	-2.81	37,37,37,37	0
56	MG	1a	1778	1/1	0.94	0.17	-2.82	64,64,64,64	0
56	MG	1Q	205	1/1	0.96	0.17	-2.84	39,39,39,39	0
56	MG	2d	502	1/1	0.91	0.09	-2.84	68,68,68,68	0
56	MG	2A	3879	1/1	0.86	0.10	-2.84	37,37,37,37	0
56	MG	2A	3515	1/1	0.81	0.11	-2.84	55,55,55,55	0
56	MG	1A	3607	1/1	0.86	0.17	-2.85	35,35,35,35	0
56	MG	1A	3021	1/1	0.94	0.17	-2.85	45,45,45,45	0
56	MG	1U	205	1/1	0.95	0.16	-2.85	35,35,35,35	0
56	MG	2A	3550	1/1	0.95	0.15	-2.86	44,44,44,44	0
56	MG	1A	3046	1/1	0.99	0.17	-2.87	32,32,32,32	0
56	MG	1a	1776	1/1	0.91	0.12	-2.88	91,91,91,91	0
56	MG	1A	4142	1/1	0.97	0.17	-2.90	42,42,42,42	0
56	MG	1w	105	1/1	0.75	0.10	-2.94	87,87,87,87	0
56	MG	2A	3019	1/1	0.95	0.15	-2.96	38,38,38,38	0
56	MG	2A	3616	1/1	0.95	0.15	-2.98	46,46,46,46	0
56	MG	2A	3748	1/1	0.77	0.10	-2.99	57,57,57,57	0
56	MG	2A	3242	1/1	0.96	0.16	-3.00	52,52,52,52	0
56	MG	1a	1670	1/1	0.94	0.11	-3.01	59,59,59,59	0
56	MG	2a	3199	1/1	0.93	0.11	-3.02	72,72,72,72	0
56	MG	2A	3819	1/1	0.89	0.13	-3.02	64,64,64,64	0
56	MG	2A	3233	1/1	0.94	0.14	-3.04	32,32,32,32	0
56	MG	2A	3067	1/1	0.82	0.11	-3.07	57,57,57,57	0
56	MG	1A	4106	1/1	0.96	0.17	-3.08	29,29,29,29	0
56	MG	2A	3882	1/1	0.99	0.13	-3.08	44,44,44,44	0
56	MG	1N	203	1/1	0.96	0.19	-3.10	48,48,48,48	0
56	MG	1A	3481	1/1	0.96	0.14	-3.10	39,39,39,39	0
56	MG	2a	3090	1/1	0.66	0.11	-3.12	68,68,68,68	0
56	MG	1F	303	1/1	0.93	0.17	-3.12	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3211	1/1	0.92	0.10	-3.13	43,43,43,43	0
56	MG	2A	3568	1/1	0.71	0.14	-3.14	46,46,46,46	0
56	MG	1A	4111	1/1	0.94	0.17	-3.15	34,34,34,34	0
56	MG	1A	3772	1/1	0.92	0.16	-3.16	36,36,36,36	0
56	MG	2A	3895	1/1	0.90	0.15	-3.20	46,46,46,46	0
56	MG	1a	1724	1/1	0.97	0.10	-3.20	36,36,36,36	0
56	MG	1A	3574	1/1	0.94	0.18	-3.21	43,43,43,43	0
56	MG	1A	3243	1/1	0.95	0.15	-3.21	53,53,53,53	0
56	MG	1A	3731	1/1	0.99	0.18	-3.21	17,17,17,17	0
56	MG	1a	1620	1/1	0.81	0.15	-3.22	66,66,66,66	0
56	MG	1t	3001	1/1	0.93	0.13	-3.24	58,58,58,58	0
56	MG	1A	4127	1/1	0.97	0.18	-3.26	34,34,34,34	0
56	MG	1B	3005	1/1	0.94	0.16	-3.29	55,55,55,55	0
56	MG	2a	3203	1/1	0.95	0.14	-3.30	62,62,62,62	0
56	MG	2A	3898	1/1	0.99	0.13	-3.32	28,28,28,28	0
56	MG	1A	3221	1/1	0.83	0.17	-3.32	55,55,55,55	0
56	MG	1A	3008	1/1	0.99	0.18	-3.33	26,26,26,26	0
56	MG	1A	3533	1/1	0.92	0.18	-3.34	36,36,36,36	0
56	MG	2A	3722	1/1	0.87	0.10	-3.34	58,58,58,58	0
56	MG	1A	3038	1/1	0.98	0.13	-3.37	50,50,50,50	0
56	MG	2A	3051	1/1	0.80	0.15	-3.38	43,43,43,43	0
56	MG	1a	1653	1/1	0.99	0.13	-3.38	54,54,54,54	0
56	MG	1A	4137	1/1	0.97	0.18	-3.41	44,44,44,44	0
56	MG	2A	3776	1/1	0.95	0.13	-3.42	44,44,44,44	0
56	MG	2A	3046	1/1	0.96	0.11	-3.42	48,48,48,48	0
56	MG	1A	3893	1/1	0.98	0.18	-3.42	17,17,17,17	0
56	MG	1a	1752	1/1	0.90	0.13	-3.43	68,68,68,68	0
56	MG	2a	3151	1/1	0.88	0.09	-3.43	78,78,78,78	0
56	MG	2a	3114	1/1	0.92	0.13	-3.44	51,51,51,51	0
56	MG	2q	202	1/1	0.93	0.06	-3.45	78,78,78,78	0
56	MG	2A	3742	1/1	0.97	0.09	-3.46	49,49,49,49	0
56	MG	1a	1800	1/1	0.95	0.12	-3.46	70,70,70,70	0
56	MG	2A	3908	1/1	0.97	0.14	-3.49	44,44,44,44	0
56	MG	2A	3299	1/1	0.91	0.12	-3.51	51,51,51,51	0
56	MG	2A	3668	1/1	0.99	0.12	-3.52	45,45,45,45	0
56	MG	1A	3780	1/1	0.95	0.16	-3.53	21,21,21,21	0
56	MG	1X	104	1/1	0.91	0.18	-3.54	52,52,52,52	0
56	MG	2A	3735	1/1	0.96	0.10	-3.55	55,55,55,55	0
56	MG	1A	4112	1/1	0.94	0.17	-3.56	42,42,42,42	0
56	MG	1A	3508	1/1	0.95	0.14	-3.56	36,36,36,36	0
56	MG	1a	1611	1/1	0.96	0.16	-3.56	22,22,22,22	0
56	MG	1B	3006	1/1	0.91	0.15	-3.57	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3837	1/1	0.81	0.14	-3.61	37,37,37,37	0
56	MG	1F	302	1/1	0.85	0.16	-3.62	47,47,47,47	0
56	MG	1A	3482	1/1	0.92	0.16	-3.65	50,50,50,50	0
56	MG	1A	4010	1/1	0.80	0.20	-3.66	26,26,26,26	0
56	MG	2A	3476	1/1	0.94	0.13	-3.67	41,41,41,41	0
56	MG	1E	303	1/1	0.99	0.16	-3.68	26,26,26,26	0
56	MG	2A	3685	1/1	0.94	0.09	-3.69	53,53,53,53	0
56	MG	1A	3524	1/1	0.96	0.16	-3.70	47,47,47,47	0
56	MG	2a	3094	1/1	0.97	0.12	-3.73	68,68,68,68	0
56	MG	1A	3905	1/1	0.97	0.16	-3.74	46,46,46,46	0
56	MG	2A	3131	1/1	0.96	0.11	-3.74	42,42,42,42	0
56	MG	1A	3649	1/1	0.70	0.16	-3.75	54,54,54,54	0
56	MG	2A	3614	1/1	0.94	0.14	-3.78	36,36,36,36	0
56	MG	1a	1649	1/1	0.97	0.12	-3.79	45,45,45,45	0
56	MG	1A	3303	1/1	0.94	0.17	-3.81	33,33,33,33	0
56	MG	1a	1615	1/1	0.90	0.11	-3.81	67,67,67,67	0
56	MG	1A	3001	1/1	0.95	0.17	-3.83	42,42,42,42	0
56	MG	1A	3620	1/1	0.99	0.19	-3.85	25,25,25,25	0
56	MG	1B	3031	1/1	0.87	0.12	-3.89	67,67,67,67	0
56	MG	1x	116	1/1	0.95	0.12	-3.90	59,59,59,59	0
56	MG	2A	3057	1/1	0.88	0.07	-3.94	46,46,46,46	0
56	MG	1A	3646	1/1	0.96	0.18	-3.94	32,32,32,32	0
56	MG	2A	3857	1/1	0.84	0.13	-3.95	47,47,47,47	0
56	MG	1A	3903	1/1	0.92	0.17	-3.95	40,40,40,40	0
56	MG	2A	3011	1/1	0.88	0.07	-4.00	48,48,48,48	0
56	MG	1A	4091	1/1	0.95	0.16	-4.02	49,49,49,49	0
56	MG	1A	3923	1/1	0.96	0.14	-4.03	47,47,47,47	0
56	MG	1A	3960	1/1	0.96	0.18	-4.03	23,23,23,23	0
56	MG	1A	3806	1/1	0.97	0.17	-4.05	34,34,34,34	0
56	MG	2A	3099	1/1	0.89	0.13	-4.05	42,42,42,42	0
56	MG	2A	3620	1/1	0.95	0.10	-4.05	65,65,65,65	0
56	MG	2a	3119	1/1	0.85	0.15	-4.05	71,71,71,71	0
56	MG	1A	3240	1/1	0.91	0.15	-4.08	35,35,35,35	0
56	MG	2A	3545	1/1	0.95	0.14	-4.11	52,52,52,52	0
56	MG	2A	3637	1/1	0.95	0.11	-4.11	42,42,42,42	0
56	MG	1A	4133	1/1	0.92	0.15	-4.14	45,45,45,45	0
56	MG	1A	4068	1/1	0.70	0.18	-4.15	48,48,48,48	0
56	MG	1A	3076	1/1	0.92	0.15	-4.16	53,53,53,53	0
56	MG	1a	1819	1/1	0.84	0.10	-4.17	48,48,48,48	0
56	MG	2A	3499	1/1	0.93	0.11	-4.17	46,46,46,46	0
56	MG	1A	3634	1/1	0.92	0.18	-4.19	44,44,44,44	0
56	MG	1A	3640	1/1	0.94	0.17	-4.22	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	3187	1/1	0.92	0.13	-4.29	72,72,72,72	0
56	MG	1A	3360	1/1	0.96	0.16	-4.29	31,31,31,31	0
56	MG	2A	3541	1/1	0.94	0.14	-4.30	30,30,30,30	0
56	MG	1a	1795	1/1	0.81	0.12	-4.31	70,70,70,70	0
56	MG	1A	3449	1/1	0.97	0.12	-4.33	41,41,41,41	0
56	MG	1A	3015	1/1	0.94	0.16	-4.33	40,40,40,40	0
56	MG	1T	8002	1/1	0.97	0.14	-4.34	58,58,58,58	0
56	MG	2a	3118	1/1	0.91	0.12	-4.35	65,65,65,65	0
56	MG	1N	205	1/1	0.92	0.14	-4.35	57,57,57,57	0
56	MG	1A	4024	1/1	0.72	0.12	-4.35	71,71,71,71	0
56	MG	1A	3359	1/1	0.98	0.14	-4.36	38,38,38,38	0
56	MG	2A	3551	1/1	0.97	0.14	-4.37	39,39,39,39	0
56	MG	1A	3012	1/1	0.95	0.16	-4.37	30,30,30,30	0
56	MG	1A	3845	1/1	0.97	0.17	-4.39	38,38,38,38	0
56	MG	1A	4120	1/1	0.96	0.16	-4.42	44,44,44,44	0
56	MG	1A	3673	1/1	0.98	0.15	-4.45	29,29,29,29	0
56	MG	2a	3084	1/1	0.96	0.10	-4.49	44,44,44,44	0
56	MG	1A	3774	1/1	0.74	0.17	-4.56	55,55,55,55	0
56	MG	1A	3203	1/1	0.83	0.16	-4.59	50,50,50,50	0
56	MG	1A	3128	1/1	0.90	0.17	-4.62	41,41,41,41	0
56	MG	1A	3624	1/1	0.97	0.17	-4.64	28,28,28,28	0
56	MG	1A	3765	1/1	0.95	0.13	-4.66	25,25,25,25	0
56	MG	1A	4139	1/1	0.98	0.15	-4.68	35,35,35,35	0
56	MG	2a	3159	1/1	0.95	0.09	-4.70	71,71,71,71	0
56	MG	16	103	1/1	0.94	0.12	-4.70	54,54,54,54	0
56	MG	1A	3812	1/1	0.95	0.17	-4.74	45,45,45,45	0
56	MG	1a	1789	1/1	0.81	0.15	-4.74	72,72,72,72	0
56	MG	1A	4085	1/1	0.98	0.22	-4.75	21,21,21,21	0
56	MG	2A	3407	1/1	0.89	0.12	-4.76	61,61,61,61	0
56	MG	2A	3869	1/1	0.88	0.07	-4.77	56,56,56,56	0
56	MG	1A	3575	1/1	0.93	0.14	-4.80	33,33,33,33	0
56	MG	1U	206	1/1	0.94	0.12	-4.83	32,32,32,32	0
56	MG	2A	3007	1/1	0.95	0.10	-4.93	43,43,43,43	0
56	MG	2A	3061	1/1	0.94	0.12	-4.96	49,49,49,49	0
56	MG	1A	3043	1/1	0.94	0.19	-4.97	39,39,39,39	0
56	MG	1A	3208	1/1	0.85	0.16	-4.99	55,55,55,55	0
56	MG	1A	3885	1/1	0.96	0.15	-4.99	37,37,37,37	0
56	MG	2A	3660	1/1	0.95	0.08	-5.01	45,45,45,45	0
56	MG	1A	3675	1/1	0.95	0.16	-5.04	32,32,32,32	0
56	MG	2A	3715	1/1	0.87	0.13	-5.06	46,46,46,46	0
56	MG	1A	4074	1/1	0.70	0.15	-5.07	64,64,64,64	0
56	MG	2A	3248	1/1	0.93	0.13	-5.08	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1P	202	1/1	0.94	0.11	-5.16	31,31,31,31	0
56	MG	1A	3852	1/1	0.94	0.14	-5.16	33,33,33,33	0
56	MG	2A	3094	1/1	0.95	0.17	-5.17	44,44,44,44	0
56	MG	20	3003	1/1	0.92	0.09	-5.22	58,58,58,58	0
56	MG	2A	3693	1/1	0.92	0.11	-5.25	35,35,35,35	0
56	MG	2a	3071	1/1	0.89	0.08	-5.27	75,75,75,75	0
56	MG	1A	3310	1/1	0.92	0.18	-5.28	40,40,40,40	0
56	MG	2A	3808	1/1	0.83	0.12	-5.29	60,60,60,60	0
56	MG	1D	308	1/1	0.95	0.11	-5.29	48,48,48,48	0
56	MG	1A	3196	1/1	0.93	0.10	-5.30	59,59,59,59	0
56	MG	1A	3356	1/1	0.96	0.14	-5.32	39,39,39,39	0
56	MG	1A	4039	1/1	0.98	0.15	-5.33	21,21,21,21	0
56	MG	1A	3115	1/1	0.92	0.14	-5.34	57,57,57,57	0
56	MG	1a	1742	1/1	0.94	0.08	-5.35	51,51,51,51	0
56	MG	1a	1626	1/1	0.96	0.13	-5.38	61,61,61,61	0
56	MG	1l	102	1/1	0.98	0.10	-5.43	36,36,36,36	0
56	MG	2A	3404	1/1	0.96	0.10	-5.44	53,53,53,53	0
56	MG	1a	1791	1/1	0.94	0.09	-5.44	54,54,54,54	0
56	MG	1a	1613	1/1	0.92	0.08	-5.47	74,74,74,74	0
56	MG	1A	4121	1/1	0.98	0.17	-5.50	34,34,34,34	0
56	MG	1A	3439	1/1	0.98	0.14	-5.53	40,40,40,40	0
56	MG	1A	3670	1/1	0.96	0.16	-5.53	32,32,32,32	0
56	MG	1G	3001	1/1	0.95	0.15	-5.55	41,41,41,41	0
56	MG	1A	3612	1/1	0.96	0.12	-5.58	41,41,41,41	0
56	MG	1A	3230	1/1	0.89	0.18	-5.63	60,60,60,60	0
56	MG	2a	3080	1/1	0.86	0.11	-5.63	50,50,50,50	0
56	MG	1A	3892	1/1	0.95	0.13	-5.66	39,39,39,39	0
56	MG	1A	3810	1/1	0.92	0.15	-5.66	45,45,45,45	0
56	MG	2A	3020	1/1	0.96	0.08	-5.68	49,49,49,49	0
56	MG	1A	3366	1/1	0.98	0.17	-5.73	38,38,38,38	0
56	MG	1A	3174	1/1	0.98	0.14	-5.73	38,38,38,38	0
56	MG	1a	1668	1/1	0.92	0.13	-5.76	67,67,67,67	0
56	MG	1a	1754	1/1	0.94	0.09	-5.77	51,51,51,51	0
56	MG	2A	3768	1/1	0.93	0.10	-5.79	62,62,62,62	0
56	MG	1W	205	1/1	0.97	0.15	-5.82	39,39,39,39	0
56	MG	1A	3022	1/1	0.99	0.14	-5.83	21,21,21,21	0
56	MG	2A	3021	1/1	0.98	0.11	-5.85	28,28,28,28	0
56	MG	1A	3998	1/1	0.80	0.16	-5.99	65,65,65,65	0
56	MG	1A	3314	1/1	0.98	0.16	-6.03	33,33,33,33	0
56	MG	1A	3112	1/1	0.84	0.17	-6.04	49,49,49,49	0
56	MG	2A	3786	1/1	0.95	0.09	-6.07	48,48,48,48	0
56	MG	1A	3717	1/1	0.95	0.17	-6.08	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3555	1/1	0.92	0.10	-6.09	43,43,43,43	0
56	MG	1A	4071	1/1	0.85	0.15	-6.13	26,26,26,26	0
56	MG	1A	3688	1/1	0.99	0.15	-6.16	15,15,15,15	0
56	MG	1A	3070	1/1	0.90	0.15	-6.17	41,41,41,41	0
56	MG	1B	3018	1/1	0.94	0.15	-6.18	37,37,37,37	0
56	MG	1A	4001	1/1	0.98	0.19	-6.20	17,17,17,17	0
56	MG	2A	3524	1/1	0.97	0.11	-6.30	48,48,48,48	0
56	MG	2A	3846	1/1	0.87	0.09	-6.33	47,47,47,47	0
56	MG	2A	3631	1/1	0.95	0.11	-6.36	39,39,39,39	0
56	MG	1a	1638	1/1	0.95	0.14	-6.39	58,58,58,58	0
56	MG	1A	3097	1/1	0.99	0.11	-6.41	35,35,35,35	0
56	MG	2A	3666	1/1	0.93	0.10	-6.43	34,34,34,34	0
56	MG	2A	3834	1/1	0.97	0.10	-6.43	40,40,40,40	0
56	MG	1A	3159	1/1	0.95	0.15	-6.43	39,39,39,39	0
56	MG	1A	3047	1/1	0.96	0.15	-6.46	21,21,21,21	0
56	MG	1A	3020	1/1	0.97	0.15	-6.49	25,25,25,25	0
56	MG	2A	3032	1/1	0.92	0.10	-6.49	38,38,38,38	0
56	MG	1A	3767	1/1	0.96	0.14	-6.50	41,41,41,41	0
56	MG	1R	201	1/1	0.99	0.13	-6.51	30,30,30,30	0
56	MG	1A	3103	1/1	0.93	0.15	-6.55	38,38,38,38	0
56	MG	1A	4016	1/1	0.92	0.13	-6.56	46,46,46,46	0
56	MG	10	101	1/1	0.92	0.12	-6.57	63,63,63,63	0
56	MG	1A	3866	1/1	0.93	0.17	-6.63	46,46,46,46	0
56	MG	1A	3616	1/1	0.73	0.17	-6.64	40,40,40,40	0
56	MG	2A	3152	1/1	0.81	0.11	-6.64	62,62,62,62	0
56	MG	1A	3032	1/1	0.97	0.18	-6.65	31,31,31,31	0
56	MG	1A	4136	1/1	0.98	0.16	-6.65	40,40,40,40	0
56	MG	1A	4003	1/1	0.93	0.18	-6.67	20,20,20,20	0
56	MG	1E	310	1/1	0.82	0.09	-6.70	42,42,42,42	0
56	MG	1A	4062	1/1	0.97	0.12	-6.72	14,14,14,14	0
56	MG	1A	3598	1/1	0.93	0.13	-6.77	51,51,51,51	0
56	MG	2A	3618	1/1	0.98	0.08	-6.78	39,39,39,39	0
56	MG	2A	3848	1/1	0.93	0.10	-6.82	36,36,36,36	0
56	MG	2A	3624	1/1	0.97	0.10	-6.91	32,32,32,32	0
56	MG	1A	3395	1/1	0.83	0.16	-6.93	42,42,42,42	0
56	MG	2A	3855	1/1	0.85	0.11	-7.00	69,69,69,69	0
56	MG	2A	3547	1/1	0.94	0.09	-7.04	37,37,37,37	0
56	MG	1A	4122	1/1	0.95	0.13	-7.11	41,41,41,41	0
56	MG	1A	3033	1/1	0.96	0.17	-7.14	36,36,36,36	0
56	MG	2A	3594	1/1	0.91	0.09	-7.14	38,38,38,38	0
56	MG	1A	3659	1/1	0.96	0.15	-7.23	23,23,23,23	0
56	MG	1a	1771	1/1	0.93	0.08	-7.27	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3926	1/1	0.62	0.10	-7.27	53,53,53,53	0
56	MG	2A	3629	1/1	0.87	0.13	-7.32	43,43,43,43	0
56	MG	1a	1817	1/1	0.88	0.04	-7.39	79,79,79,79	0
56	MG	2A	3557	1/1	0.87	0.08	-7.47	45,45,45,45	0
56	MG	1a	1805	1/1	0.95	0.08	-7.48	47,47,47,47	0
56	MG	1A	3630	1/1	0.88	0.17	-7.52	32,32,32,32	0
56	MG	1a	1779	1/1	0.81	0.08	-7.54	65,65,65,65	0
56	MG	1A	3881	1/1	0.94	0.19	-7.55	37,37,37,37	0
56	MG	1A	3403	1/1	0.96	0.17	-7.61	27,27,27,27	0
56	MG	1A	3176	1/1	0.96	0.16	-7.63	37,37,37,37	0
56	MG	1A	3202	1/1	0.92	0.15	-7.72	32,32,32,32	0
56	MG	2A	3623	1/1	0.97	0.10	-7.91	48,48,48,48	0
56	MG	1A	4032	1/1	0.94	0.07	-8.00	68,68,68,68	0
56	MG	1a	1655	1/1	0.97	0.07	-8.19	43,43,43,43	0
56	MG	2A	3023	1/1	0.94	0.05	-8.23	48,48,48,48	0
56	MG	1A	4110	1/1	0.93	0.13	-8.24	56,56,56,56	0
56	MG	2a	3182	1/1	0.82	0.09	-8.26	71,71,71,71	0
56	MG	1A	3807	1/1	0.97	0.15	-8.26	38,38,38,38	0
56	MG	1A	3275	1/1	0.96	0.13	-8.31	44,44,44,44	0
56	MG	2A	3188	1/1	0.94	0.07	-8.42	36,36,36,36	0
56	MG	2A	3561	1/1	0.95	0.09	-8.51	62,62,62,62	0
56	MG	2A	3035	1/1	0.96	0.10	-8.61	31,31,31,31	0
56	MG	2A	3844	1/1	0.78	0.08	-8.65	50,50,50,50	0
56	MG	2A	3720	1/1	0.97	0.11	-8.66	41,41,41,41	0
56	MG	1A	3820	1/1	0.96	0.11	-8.67	41,41,41,41	0
56	MG	2A	3648	1/1	0.80	0.08	-8.88	51,51,51,51	0
56	MG	1A	3213	1/1	0.92	0.12	-9.01	42,42,42,42	0
56	MG	2A	3571	1/1	0.90	0.08	-9.04	35,35,35,35	0
56	MG	1A	3930	1/1	0.96	0.15	-9.08	30,30,30,30	0
56	MG	2A	3529	1/1	0.90	0.07	-9.24	43,43,43,43	0
56	MG	2A	3522	1/1	0.95	0.08	-9.26	59,59,59,59	0
56	MG	1A	3784	1/1	0.91	0.10	-9.28	39,39,39,39	0
56	MG	2A	3587	1/1	0.95	0.11	-9.32	37,37,37,37	0
56	MG	1A	3948	1/1	0.84	0.12	-9.56	60,60,60,60	0
56	MG	1a	1818	1/1	0.90	0.08	-9.74	54,54,54,54	0
56	MG	1A	3738	1/1	0.94	0.12	-9.98	43,43,43,43	0
56	MG	1a	1619	1/1	0.98	0.13	-10.01	62,62,62,62	0
56	MG	1A	3661	1/1	0.91	0.13	-10.15	32,32,32,32	0
56	MG	1A	4055	1/1	0.94	0.09	-10.28	33,33,33,33	0
56	MG	2A	3500	1/1	0.87	0.10	-10.53	55,55,55,55	0
56	MG	1A	3789	1/1	0.98	0.11	-10.67	29,29,29,29	0
56	MG	1A	3597	1/1	0.94	0.18	-10.91	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1709	1/1	0.80	0.07	-10.94	59,59,59,59	0
56	MG	2a	3222	1/1	0.92	0.09	-11.11	63,63,63,63	0
56	MG	1a	1741	1/1	0.95	0.08	-11.27	34,34,34,34	0
56	MG	2A	3504	1/1	0.95	0.09	-11.50	36,36,36,36	0
56	MG	1A	3906	1/1	0.89	0.12	-11.74	51,51,51,51	0
56	MG	1A	3594	1/1	0.93	0.13	-11.80	31,31,31,31	0
56	MG	1A	3669	1/1	0.93	0.10	-11.94	34,34,34,34	0
56	MG	1A	3007	1/1	0.92	0.14	-12.00	38,38,38,38	0
56	MG	1A	3947	1/1	0.81	0.12	-12.26	44,44,44,44	0
56	MG	1A	3914	1/1	0.98	0.10	-12.46	53,53,53,53	0
56	MG	1a	1758	1/1	0.97	0.06	-12.51	56,56,56,56	0
56	MG	2A	3521	1/1	0.93	0.11	-12.58	51,51,51,51	0
56	MG	1A	3577	1/1	0.99	0.17	-13.30	27,27,27,27	0
56	MG	1A	4013	1/1	0.96	0.13	-15.40	33,33,33,33	0
56	MG	1A	3882	1/1	0.96	0.17	-15.40	36,36,36,36	0
56	MG	1A	3938	1/1	0.94	0.08	-16.03	55,55,55,55	0
56	MG	1A	4063	1/1	0.95	0.08	-17.29	57,57,57,57	0
56	MG	1A	3939	1/1	0.91	0.14	-17.95	53,53,53,53	0
56	MG	1A	4011	1/1	0.93	0.10	-18.74	43,43,43,43	0
56	MG	1A	3621	1/1	0.97	0.11	-19.16	48,48,48,48	0
56	MG	1A	3635	1/1	0.98	0.11	-19.87	32,32,32,32	0
56	MG	2A	3792	1/1	0.86	0.10	-	51,51,51,51	0
56	MG	1A	3318	1/1	0.90	0.12	-	46,46,46,46	0
56	MG	1A	3315	1/1	0.90	0.35	-	61,61,61,61	0
56	MG	1A	3002	1/1	0.82	0.24	-	59,59,59,59	0
56	MG	2A	3312	1/1	0.93	0.12	-	51,51,51,51	0
56	MG	1A	4042	1/1	0.90	0.10	-	46,46,46,46	0
56	MG	2a	3155	1/1	0.64	0.12	-	81,81,81,81	0
56	MG	1A	3545	1/1	0.88	0.16	-	67,67,67,67	0
56	MG	1A	3636	1/1	0.96	0.07	-	38,38,38,38	0
56	MG	1A	3722	1/1	0.85	0.12	-	39,39,39,39	0
56	MG	1A	3821	1/1	0.91	0.16	-	47,47,47,47	0
56	MG	2A	3711	1/1	0.95	0.17	-	56,56,56,56	0
56	MG	1A	3273	1/1	0.92	0.28	-	53,53,53,53	0
56	MG	2A	3370	1/1	0.90	0.23	-	50,50,50,50	0
56	MG	2A	3465	1/1	0.88	0.22	-	55,55,55,55	0
56	MG	1A	3014	1/1	0.97	0.20	-	31,31,31,31	0
56	MG	2A	3443	1/1	0.98	0.28	-	50,50,50,50	0
56	MG	2A	3251	1/1	0.95	0.10	-	42,42,42,42	0
56	MG	1a	1660	1/1	0.91	0.12	-	74,74,74,74	0
56	MG	2A	3657	1/1	0.95	0.13	-	39,39,39,39	0
56	MG	2A	3760	1/1	0.97	0.56	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1672	1/1	0.65	0.17	-	73,73,73,73	0
56	MG	1A	3695	1/1	0.94	0.09	-	57,57,57,57	0
56	MG	2A	3492	1/1	0.90	0.17	-	54,54,54,54	0
56	MG	2A	3746	1/1	0.86	0.08	-	68,68,68,68	0
56	MG	1V	202	1/1	0.92	0.15	-	53,53,53,53	0
56	MG	2a	3153	1/1	0.79	0.17	-	74,74,74,74	0
56	MG	1A	3036	1/1	0.94	0.19	-	31,31,31,31	0
56	MG	2A	3428	1/1	0.94	0.15	-	52,52,52,52	0
56	MG	1A	3955	1/1	0.95	0.14	-	30,30,30,30	0
56	MG	2A	3419	1/1	0.88	0.14	-	51,51,51,51	0
56	MG	2a	3017	1/1	0.86	0.09	-	66,66,66,66	0
56	MG	2a	3234	1/1	0.82	0.13	-	66,66,66,66	0
56	MG	1A	3877	1/1	0.93	0.15	-	39,39,39,39	0
56	MG	1a	1744	1/1	0.80	0.25	-	73,73,73,73	0
56	MG	1G	3002	1/1	0.89	0.17	-	56,56,56,56	0
56	MG	2D	302	1/1	0.90	0.16	-	51,51,51,51	0
56	MG	1A	3263	1/1	0.96	0.18	-	52,52,52,52	0
56	MG	2a	3049	1/1	0.90	0.12	-	55,55,55,55	0
56	MG	1A	3797	1/1	0.95	0.14	-	53,53,53,53	0
56	MG	2a	3028	1/1	0.38	0.23	-	84,84,84,84	0
56	MG	1A	3805	1/1	0.93	0.23	-	54,54,54,54	0
56	MG	2A	3214	1/1	0.96	0.11	-	56,56,56,56	0
56	MG	2A	3420	1/1	0.95	0.37	-	43,43,43,43	0
56	MG	1a	1774	1/1	0.95	0.11	-	60,60,60,60	0
56	MG	1A	3415	1/1	0.94	0.30	-	59,59,59,59	0
56	MG	2A	3206	1/1	0.97	0.17	-	56,56,56,56	0
56	MG	2A	3089	1/1	0.90	0.12	-	46,46,46,46	0
56	MG	2A	3153	1/1	0.89	0.20	-	52,52,52,52	0
56	MG	1A	3107	1/1	0.97	0.18	-	35,35,35,35	0
56	MG	2B	3014	1/1	0.79	0.17	-	77,77,77,77	0
56	MG	2A	3185	1/1	0.94	0.08	-	45,45,45,45	0
56	MG	1a	1807	1/1	0.90	0.06	-	67,67,67,67	0
56	MG	2A	3437	1/1	0.93	0.13	-	67,67,67,67	0
56	MG	1A	3101	1/1	0.92	0.12	-	44,44,44,44	0
56	MG	1a	1761	1/1	0.91	0.11	-	64,64,64,64	0
56	MG	2A	3481	1/1	0.91	0.20	-	56,56,56,56	0
56	MG	2q	201	1/1	0.85	0.17	-	76,76,76,76	0
56	MG	2A	3520	1/1	0.77	0.11	-	65,65,65,65	0
56	MG	2a	3131	1/1	0.69	0.11	-	80,80,80,80	0
56	MG	1A	3412	1/1	0.96	0.21	-	52,52,52,52	0
56	MG	1A	3437	1/1	0.87	0.15	-	52,52,52,52	0
56	MG	2A	3325	1/1	0.91	0.10	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3350	1/1	0.88	0.25	-	59,59,59,59	0
56	MG	1A	3242	1/1	0.85	0.24	-	43,43,43,43	0
56	MG	1a	1632	1/1	0.95	0.18	-	52,52,52,52	0
56	MG	2A	3721	1/1	0.95	0.18	-	46,46,46,46	0
56	MG	2A	3688	1/1	0.93	0.09	-	38,38,38,38	0
56	MG	2a	3147	1/1	0.97	0.13	-	49,49,49,49	0
56	MG	1a	1765	1/1	0.93	0.11	-	49,49,49,49	0
56	MG	1A	3916	1/1	0.91	0.14	-	53,53,53,53	0
56	MG	2A	3183	1/1	0.93	0.17	-	56,56,56,56	0
56	MG	1A	3991	1/1	0.91	0.10	-	48,48,48,48	0
56	MG	2a	3202	1/1	0.90	0.17	-	64,64,64,64	0
56	MG	1A	3147	1/1	0.82	0.28	-	54,54,54,54	0
56	MG	2A	3172	1/1	0.94	0.09	-	47,47,47,47	0
56	MG	2B	3013	1/1	0.89	0.20	-	61,61,61,61	0
56	MG	1A	3459	1/1	0.86	0.23	-	47,47,47,47	0
56	MG	2A	3389	1/1	0.94	0.11	-	58,58,58,58	0
56	MG	2A	3362	1/1	0.85	0.12	-	68,68,68,68	0
56	MG	1A	3637	1/1	0.89	0.19	-	50,50,50,50	0
56	MG	2A	3580	1/1	0.94	0.23	-	49,49,49,49	0
56	MG	2A	3079	1/1	0.88	0.11	-	41,41,41,41	0
56	MG	1A	3874	1/1	0.89	0.12	-	40,40,40,40	0
56	MG	2w	102	1/1	0.88	0.17	-	62,62,62,62	0
56	MG	2A	3590	1/1	0.89	0.08	-	64,64,64,64	0
56	MG	1A	3030	1/1	0.98	0.18	-	34,34,34,34	0
56	MG	1a	1673	1/1	0.94	0.13	-	67,67,67,67	0
56	MG	1A	3849	1/1	0.96	0.26	-	44,44,44,44	0
56	MG	1A	4089	1/1	0.97	0.15	-	36,36,36,36	0
56	MG	1B	3001	1/1	0.98	0.30	-	48,48,48,48	0
56	MG	1A	3436	1/1	0.90	0.14	-	45,45,45,45	0
56	MG	2A	3044	1/1	0.92	0.10	-	48,48,48,48	0
56	MG	1B	3003	1/1	0.92	0.23	-	56,56,56,56	0
56	MG	1a	1728	1/1	0.91	0.24	-	48,48,48,48	0
56	MG	1A	3952	1/1	0.96	0.18	-	46,46,46,46	0
56	MG	1A	3501	1/1	0.90	0.25	-	51,51,51,51	0
56	MG	2A	3377	1/1	0.98	0.15	-	57,57,57,57	0
56	MG	2a	3050	1/1	0.89	0.20	-	61,61,61,61	0
56	MG	2A	3723	1/1	0.88	0.10	-	50,50,50,50	0
56	MG	1A	3672	1/1	0.91	0.16	-	31,31,31,31	0
56	MG	2B	3011	1/1	0.96	0.31	-	67,67,67,67	0
56	MG	1A	3733	1/1	0.92	0.12	-	52,52,52,52	0
56	MG	25	101	1/1	0.94	0.15	-	55,55,55,55	0
56	MG	2a	3107	1/1	0.94	0.14	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3927	1/1	0.94	0.10	-	47,47,47,47	0
56	MG	1A	3727	1/1	0.91	0.15	-	36,36,36,36	0
56	MG	2a	3139	1/1	0.94	0.11	-	73,73,73,73	0
56	MG	2A	3533	1/1	0.99	0.12	-	48,48,48,48	0
56	MG	1O	207	1/1	0.77	0.12	-	65,65,65,65	0
56	MG	1A	3418	1/1	0.86	0.11	-	54,54,54,54	0
56	MG	2A	3532	1/1	0.94	0.14	-	65,65,65,65	0
56	MG	2a	3193	1/1	0.93	0.12	-	73,73,73,73	0
56	MG	1A	3610	1/1	0.95	0.23	-	54,54,54,54	0
56	MG	1A	3541	1/1	0.85	0.13	-	73,73,73,73	0
56	MG	1x	110	1/1	0.87	0.14	-	52,52,52,52	0
56	MG	1A	3681	1/1	0.96	0.07	-	34,34,34,34	0
56	MG	1a	1658	1/1	0.96	0.13	-	57,57,57,57	0
56	MG	1A	3933	1/1	0.78	0.10	-	47,47,47,47	0
56	MG	2A	3339	1/1	0.94	0.20	-	51,51,51,51	0
56	MG	1A	3602	1/1	0.97	0.25	-	25,25,25,25	0
56	MG	1A	4075	1/1	0.92	0.13	-	42,42,42,42	0
56	MG	2B	3004	1/1	0.89	0.13	-	69,69,69,69	0
56	MG	2A	3416	1/1	0.92	0.15	-	59,59,59,59	0
56	MG	1a	1628	1/1	0.87	0.11	-	58,58,58,58	0
56	MG	1A	3152	1/1	0.84	0.21	-	55,55,55,55	0
56	MG	1A	3126	1/1	0.97	0.20	-	41,41,41,41	0
56	MG	1A	3287	1/1	0.95	0.18	-	30,30,30,30	0
56	MG	2A	3287	1/1	0.91	0.09	-	55,55,55,55	0
56	MG	1A	3139	1/1	0.96	0.14	-	48,48,48,48	0
56	MG	1a	1639	1/1	0.89	0.10	-	62,62,62,62	0
56	MG	1A	3519	1/1	0.90	0.16	-	49,49,49,49	0
56	MG	2A	3036	1/1	0.94	0.14	-	54,54,54,54	0
56	MG	1A	3276	1/1	0.98	0.14	-	49,49,49,49	0
56	MG	1A	3264	1/1	0.66	0.18	-	63,63,63,63	0
56	MG	2P	201	1/1	0.94	0.13	-	45,45,45,45	0
56	MG	1A	3326	1/1	0.86	0.18	-	41,41,41,41	0
56	MG	1A	3265	1/1	0.97	0.10	-	63,63,63,63	0
56	MG	2A	3332	1/1	0.77	0.34	-	62,62,62,62	0
56	MG	1E	305	1/1	0.93	0.22	-	57,57,57,57	0
56	MG	2a	3079	1/1	0.96	0.11	-	59,59,59,59	0
56	MG	1a	1625	1/1	0.81	0.26	-	63,63,63,63	0
56	MG	1A	4083	1/1	0.94	0.15	-	44,44,44,44	0
56	MG	1A	3831	1/1	0.95	0.15	-	70,70,70,70	0
56	MG	1a	1756	1/1	0.97	0.14	-	72,72,72,72	0
56	MG	2A	3279	1/1	0.96	0.28	-	53,53,53,53	0
56	MG	1A	3999	1/1	0.86	0.20	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3290	1/1	0.90	0.19	-	50,50,50,50	0
56	MG	1A	3951	1/1	0.89	0.20	-	72,72,72,72	0
56	MG	1A	3051	1/1	0.93	0.28	-	50,50,50,50	0
56	MG	2A	3038	1/1	0.97	0.16	-	31,31,31,31	0
56	MG	1A	3225	1/1	0.94	0.22	-	52,52,52,52	0
56	MG	1A	3170	1/1	0.94	0.15	-	39,39,39,39	0
56	MG	2a	3146	1/1	0.73	0.32	-	84,84,84,84	0
56	MG	2A	3062	1/1	0.95	0.20	-	61,61,61,61	0
56	MG	1A	3698	1/1	0.61	0.11	-	73,73,73,73	0
56	MG	1A	3890	1/1	0.90	0.16	-	57,57,57,57	0
56	MG	2A	3880	1/1	0.80	0.13	-	65,65,65,65	0
56	MG	1A	3278	1/1	0.93	0.20	-	51,51,51,51	0
56	MG	2A	3652	1/1	0.94	0.12	-	41,41,41,41	0
56	MG	1A	3037	1/1	0.95	0.42	-	40,40,40,40	0
56	MG	2A	3359	1/1	0.95	0.05	-	56,56,56,56	0
56	MG	2A	3769	1/1	0.76	0.10	-	62,62,62,62	0
56	MG	2A	3559	1/1	0.95	0.14	-	39,39,39,39	0
56	MG	2A	3508	1/1	0.95	0.10	-	60,60,60,60	0
56	MG	2A	3433	1/1	0.87	0.13	-	64,64,64,64	0
56	MG	2a	3212	1/1	0.99	0.12	-	51,51,51,51	0
56	MG	1A	3941	1/1	0.92	0.15	-	46,46,46,46	0
56	MG	1A	3083	1/1	0.85	0.26	-	44,44,44,44	0
56	MG	1a	1769	1/1	0.93	0.11	-	55,55,55,55	0
56	MG	1A	3791	1/1	0.93	0.17	-	43,43,43,43	0
56	MG	2A	3193	1/1	0.95	0.06	-	55,55,55,55	0
56	MG	2A	3892	1/1	0.48	0.31	-	78,78,78,78	0
56	MG	1w	101	1/1	0.88	0.14	-	64,64,64,64	0
56	MG	1A	3900	1/1	0.84	0.19	-	44,44,44,44	0
56	MG	2A	3213	1/1	0.95	0.23	-	45,45,45,45	0
56	MG	1a	1707	1/1	0.91	0.14	-	63,63,63,63	0
56	MG	1y	3001	1/1	0.88	0.09	-	64,64,64,64	0
56	MG	1e	201	1/1	0.80	0.12	-	79,79,79,79	0
56	MG	1A	3888	1/1	0.86	0.24	-	70,70,70,70	0
56	MG	2A	3874	1/1	0.88	0.17	-	53,53,53,53	0
56	MG	2w	101	1/1	0.86	0.20	-	73,73,73,73	0
56	MG	1A	3471	1/1	0.96	0.18	-	57,57,57,57	0
56	MG	1A	3965	1/1	0.98	0.14	-	67,67,67,67	0
56	MG	1A	3931	1/1	0.90	0.17	-	55,55,55,55	0
56	MG	2A	3426	1/1	0.88	0.23	-	63,63,63,63	0
56	MG	2a	3130	1/1	0.89	0.08	-	72,72,72,72	0
56	MG	1l	103	1/1	0.93	0.09	-	65,65,65,65	0
56	MG	1A	3754	1/1	0.88	0.20	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3029	1/1	0.95	0.24	-	38,38,38,38	0
56	MG	1A	3966	1/1	0.91	0.20	-	59,59,59,59	0
56	MG	1A	4084	1/1	0.75	0.12	-	50,50,50,50	0
56	MG	1A	4123	1/1	0.95	0.22	-	35,35,35,35	0
56	MG	2A	3136	1/1	0.93	0.18	-	45,45,45,45	0
56	MG	2A	3180	1/1	0.79	0.19	-	51,51,51,51	0
56	MG	1A	3981	1/1	0.91	0.09	-	52,52,52,52	0
56	MG	1A	3281	1/1	0.85	0.26	-	50,50,50,50	0
56	MG	2a	3204	1/1	0.67	0.44	-	86,86,86,86	0
56	MG	1a	1767	1/1	0.93	0.12	-	66,66,66,66	0
56	MG	2A	3458	1/1	0.87	0.11	-	65,65,65,65	0
56	MG	1A	3516	1/1	0.96	0.11	-	25,25,25,25	0
56	MG	1A	3292	1/1	0.96	0.17	-	56,56,56,56	0
56	MG	2A	3804	1/1	0.96	0.06	-	31,31,31,31	0
56	MG	2A	3479	1/1	0.89	0.17	-	54,54,54,54	0
56	MG	1A	4037	1/1	0.68	0.12	-	62,62,62,62	0
56	MG	1A	3896	1/1	0.94	0.22	-	47,47,47,47	0
56	MG	2A	3607	1/1	0.72	0.18	-	55,55,55,55	0
56	MG	1A	3956	1/1	0.83	0.17	-	61,61,61,61	0
56	MG	1A	3488	1/1	0.88	0.30	-	59,59,59,59	0
56	MG	2A	3585	1/1	0.96	0.10	-	43,43,43,43	0
56	MG	1A	3525	1/1	0.90	0.18	-	58,58,58,58	0
56	MG	2A	3005	1/1	0.91	0.22	-	48,48,48,48	0
56	MG	2A	3055	1/1	0.92	0.15	-	46,46,46,46	0
56	MG	1A	3011	1/1	0.98	0.13	-	46,46,46,46	0
56	MG	2A	3518	1/1	0.86	0.09	-	52,52,52,52	0
56	MG	1A	3494	1/1	0.96	0.21	-	39,39,39,39	0
56	MG	2A	3490	1/1	0.83	0.14	-	61,61,61,61	0
56	MG	1A	3555	1/1	0.66	0.26	-	60,60,60,60	0
56	MG	1A	3915	1/1	0.91	0.14	-	39,39,39,39	0
56	MG	1x	115	1/1	0.92	0.15	-	75,75,75,75	0
56	MG	1A	3496	1/1	0.95	0.16	-	38,38,38,38	0
56	MG	2A	3381	1/1	0.88	0.13	-	53,53,53,53	0
56	MG	2A	3265	1/1	0.81	0.17	-	59,59,59,59	0
56	MG	2A	3699	1/1	0.84	0.09	-	76,76,76,76	0
56	MG	1a	1692	1/1	0.91	0.09	-	69,69,69,69	0
56	MG	1a	1662	1/1	0.94	0.12	-	67,67,67,67	0
56	MG	1a	1650	1/1	0.90	0.12	-	53,53,53,53	0
56	MG	2A	3597	1/1	0.92	0.16	-	61,61,61,61	0
56	MG	2A	3762	1/1	0.93	0.09	-	52,52,52,52	0
56	MG	1a	1717	1/1	0.95	0.16	-	64,64,64,64	0
56	MG	2a	3032	1/1	0.96	0.10	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3527	1/1	0.93	0.12	-	31,31,31,31	0
56	MG	1A	3343	1/1	0.86	0.34	-	59,59,59,59	0
56	MG	1A	3836	1/1	0.91	0.23	-	54,54,54,54	0
56	MG	1A	3891	1/1	0.93	0.18	-	41,41,41,41	0
56	MG	1A	4105	1/1	0.87	0.13	-	44,44,44,44	0
56	MG	2A	3117	1/1	0.88	0.28	-	63,63,63,63	0
56	MG	2a	3177	1/1	0.93	0.07	-	67,67,67,67	0
56	MG	2A	3743	1/1	0.96	0.16	-	75,75,75,75	0
56	MG	1A	3817	1/1	0.96	0.19	-	45,45,45,45	0
56	MG	1a	1651	1/1	0.82	0.11	-	56,56,56,56	0
56	MG	1A	3913	1/1	0.78	0.24	-	80,80,80,80	0
56	MG	2A	3203	1/1	0.92	0.22	-	46,46,46,46	0
56	MG	2E	306	1/1	0.84	0.09	-	67,67,67,67	0
56	MG	2a	3044	1/1	0.96	0.19	-	57,57,57,57	0
56	MG	2A	3610	1/1	0.51	0.14	-	67,67,67,67	0
56	MG	1A	3158	1/1	0.93	0.19	-	56,56,56,56	0
56	MG	1A	3167	1/1	0.94	0.15	-	41,41,41,41	0
56	MG	1A	3699	1/1	0.85	0.25	-	64,64,64,64	0
56	MG	1A	3288	1/1	0.92	0.12	-	43,43,43,43	0
56	MG	2A	3408	1/1	0.90	0.10	-	51,51,51,51	0
56	MG	2A	3128	1/1	0.94	0.19	-	48,48,48,48	0
56	MG	1a	1612	1/1	0.76	0.09	-	74,74,74,74	0
56	MG	2A	3173	1/1	0.95	0.09	-	51,51,51,51	0
56	MG	1A	3627	1/1	0.84	0.13	-	62,62,62,62	0
56	MG	2a	3210	1/1	0.83	0.10	-	70,70,70,70	0
56	MG	1A	4043	1/1	0.85	0.10	-	50,50,50,50	0
56	MG	2a	3136	1/1	0.91	0.28	-	73,73,73,73	0
56	MG	1B	3034	1/1	0.91	0.19	-	58,58,58,58	0
56	MG	1A	3997	1/1	0.89	0.14	-	39,39,39,39	0
56	MG	1y	3002	1/1	0.91	0.16	-	75,75,75,75	0
56	MG	1W	202	1/1	0.96	0.24	-	50,50,50,50	0
56	MG	1A	4033	1/1	0.83	0.10	-	76,76,76,76	0
56	MG	1a	1691	1/1	0.90	0.21	-	69,69,69,69	0
56	MG	1T	8001	1/1	0.88	0.10	-	63,63,63,63	0
56	MG	2A	3707	1/1	0.87	0.06	-	61,61,61,61	0
56	MG	1a	1792	1/1	0.95	0.05	-	59,59,59,59	0
56	MG	1a	1777	1/1	0.90	0.16	-	55,55,55,55	0
56	MG	2A	3210	1/1	0.91	0.14	-	47,47,47,47	0
57	K	2A	3496	1/1	0.93	0.09	-	73,73,73,73	0
56	MG	1A	3638	1/1	0.95	0.06	-	53,53,53,53	0
56	MG	2A	3253	1/1	0.89	0.12	-	47,47,47,47	0
56	MG	1A	3236	1/1	0.93	0.35	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3466	1/1	0.83	0.15	-	64,64,64,64	0
56	MG	1A	3053	1/1	0.94	0.17	-	52,52,52,52	0
56	MG	1A	3065	1/1	0.94	0.22	-	33,33,33,33	0
56	MG	2A	3090	1/1	0.93	0.07	-	60,60,60,60	0
56	MG	1A	3062	1/1	0.95	0.23	-	59,59,59,59	0
56	MG	2A	3853	1/1	0.94	0.12	-	50,50,50,50	0
56	MG	1a	1790	1/1	0.65	0.20	-	73,73,73,73	0
56	MG	2A	3554	1/1	0.97	0.10	-	39,39,39,39	0
56	MG	2A	3823	1/1	0.84	0.15	-	73,73,73,73	0
56	MG	1A	3378	1/1	0.78	0.14	-	53,53,53,53	0
56	MG	2A	3651	1/1	0.92	0.14	-	44,44,44,44	0
56	MG	2a	3216	1/1	0.98	0.12	-	65,65,65,65	0
56	MG	1A	3703	1/1	0.89	0.11	-	56,56,56,56	0
56	MG	2a	3099	1/1	0.76	0.14	-	74,74,74,74	0
56	MG	1A	3647	1/1	0.92	0.22	-	29,29,29,29	0
56	MG	1A	3912	1/1	0.49	0.30	-	80,80,80,80	0
56	MG	2r	102	1/1	0.88	0.10	-	73,73,73,73	0
56	MG	1A	3548	1/1	0.87	0.12	-	49,49,49,49	0
56	MG	2A	3280	1/1	0.92	0.17	-	54,54,54,54	0
56	MG	2A	3401	1/1	0.96	0.16	-	52,52,52,52	0
56	MG	1A	3121	1/1	0.97	0.20	-	43,43,43,43	0
56	MG	1A	4015	1/1	0.97	0.14	-	37,37,37,37	0
56	MG	1a	1718	1/1	0.85	0.11	-	70,70,70,70	0
56	MG	2A	3868	1/1	0.63	0.16	-	69,69,69,69	0
56	MG	1W	204	1/1	0.92	0.14	-	40,40,40,40	0
56	MG	1A	3934	1/1	0.74	0.11	-	44,44,44,44	0
56	MG	1a	1799	1/1	0.95	0.08	-	49,49,49,49	0
56	MG	2a	3027	1/1	0.87	0.18	-	61,61,61,61	0
56	MG	1x	109	1/1	0.93	0.10	-	82,82,82,82	0
56	MG	1A	3082	1/1	0.95	0.27	-	49,49,49,49	0
56	MG	1A	3150	1/1	0.96	0.22	-	50,50,50,50	0
56	MG	1A	4028	1/1	0.92	0.12	-	69,69,69,69	0
56	MG	1A	3801	1/1	0.94	0.17	-	28,28,28,28	0
56	MG	2A	3772	1/1	0.93	0.14	-	53,53,53,53	0
56	MG	1A	3593	1/1	0.97	0.18	-	56,56,56,56	0
56	MG	2A	3166	1/1	0.96	0.29	-	47,47,47,47	0
56	MG	2A	3578	1/1	0.98	0.09	-	39,39,39,39	0
56	MG	1a	1816	1/1	0.98	0.13	-	48,48,48,48	0
56	MG	2A	3861	1/1	0.91	0.13	-	36,36,36,36	0
56	MG	1N	206	1/1	0.97	0.29	-	42,42,42,42	0
56	MG	2a	3143	1/1	0.82	0.07	-	73,73,73,73	0
56	MG	2a	3167	1/1	0.96	0.09	-	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1746	1/1	0.85	0.08	-	84,84,84,84	0
56	MG	1a	1768	1/1	0.97	0.06	-	53,53,53,53	0
56	MG	2F	302	1/1	0.89	0.16	-	53,53,53,53	0
56	MG	1A	3851	1/1	0.86	0.14	-	62,62,62,62	0
56	MG	1A	3829	1/1	0.85	0.13	-	59,59,59,59	0
56	MG	1A	4060	1/1	0.87	0.10	-	37,37,37,37	0
56	MG	1a	1645	1/1	0.83	0.22	-	80,80,80,80	0
56	MG	1a	1794	1/1	0.87	0.14	-	52,52,52,52	0
56	MG	2A	3031	1/1	0.96	0.06	-	45,45,45,45	0
56	MG	2A	3818	1/1	0.75	0.31	-	66,66,66,66	0
56	MG	1A	4066	1/1	0.88	0.11	-	71,71,71,71	0
56	MG	1A	3692	1/1	0.83	0.29	-	64,64,64,64	0
56	MG	1A	3413	1/1	0.98	0.21	-	36,36,36,36	0
56	MG	1x	108	1/1	0.92	0.15	-	63,63,63,63	0
56	MG	2A	3134	1/1	0.78	0.26	-	72,72,72,72	0
56	MG	1A	3026	1/1	0.84	0.10	-	60,60,60,60	0
56	MG	2A	3110	1/1	0.85	0.16	-	58,58,58,58	0
56	MG	2A	3159	1/1	0.96	0.16	-	53,53,53,53	0
56	MG	1A	3417	1/1	0.81	0.17	-	51,51,51,51	0
56	MG	1A	3994	1/1	0.56	0.33	-	76,76,76,76	0
56	MG	2a	3170	1/1	0.86	0.10	-	80,80,80,80	0
56	MG	2A	3771	1/1	0.92	0.13	-	39,39,39,39	0
56	MG	2A	3186	1/1	0.91	0.14	-	54,54,54,54	0
56	MG	1x	101	1/1	0.59	0.09	-	56,56,56,56	0
56	MG	1A	3507	1/1	0.83	0.21	-	51,51,51,51	0
56	MG	2a	3069	1/1	0.85	0.10	-	62,62,62,62	0
56	MG	1a	1803	1/1	0.76	0.22	-	73,73,73,73	0
56	MG	1a	1780	1/1	0.90	0.11	-	74,74,74,74	0
56	MG	1V	201	1/1	0.96	0.25	-	49,49,49,49	0
56	MG	1A	4006	1/1	0.83	0.11	-	76,76,76,76	0
56	MG	1a	1804	1/1	0.89	0.17	-	77,77,77,77	0
56	MG	2A	3511	1/1	0.97	0.17	-	24,24,24,24	0
56	MG	1A	4126	1/1	0.98	0.18	-	45,45,45,45	0
56	MG	1A	3089	1/1	0.90	0.26	-	48,48,48,48	0
56	MG	10	102	1/1	0.94	0.12	-	44,44,44,44	0
56	MG	2A	3738	1/1	0.86	0.19	-	59,59,59,59	0
56	MG	2a	3191	1/1	0.93	0.15	-	63,63,63,63	0
56	MG	1A	3908	1/1	0.96	0.09	-	65,65,65,65	0
56	MG	2A	3535	1/1	0.70	0.17	-	59,59,59,59	0
56	MG	2A	3789	1/1	0.88	0.10	-	49,49,49,49	0
56	MG	1A	3451	1/1	0.87	0.16	-	47,47,47,47	0
56	MG	1A	4053	1/1	0.91	0.37	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3066	1/1	0.92	0.10	-	41,41,41,41	0
56	MG	1a	1684	1/1	0.90	0.14	-	60,60,60,60	0
56	MG	1a	1802	1/1	0.97	0.07	-	52,52,52,52	0
56	MG	1A	3419	1/1	0.90	0.15	-	60,60,60,60	0
56	MG	2A	3807	1/1	0.92	0.07	-	61,61,61,61	0
56	MG	1A	3059	1/1	0.95	0.15	-	48,48,48,48	0
56	MG	1A	4138	1/1	0.97	0.26	-	43,43,43,43	0
56	MG	1A	3705	1/1	0.91	0.09	-	42,42,42,42	0
56	MG	2A	3575	1/1	0.94	0.11	-	39,39,39,39	0
56	MG	1A	3388	1/1	0.96	0.20	-	42,42,42,42	0
56	MG	1A	3254	1/1	0.96	0.22	-	53,53,53,53	0
56	MG	1A	3725	1/1	0.95	0.14	-	52,52,52,52	0
56	MG	2A	3675	1/1	0.92	0.17	-	55,55,55,55	0
56	MG	2a	3031	1/1	0.94	0.19	-	49,49,49,49	0
56	MG	1U	208	1/1	0.94	0.23	-	38,38,38,38	0
56	MG	2A	3706	1/1	0.98	0.12	-	47,47,47,47	0
56	MG	1A	3060	1/1	0.92	0.10	-	45,45,45,45	0
56	MG	1A	4041	1/1	0.93	0.14	-	36,36,36,36	0
56	MG	2A	3179	1/1	0.97	0.17	-	59,59,59,59	0
56	MG	2A	3608	1/1	0.80	0.09	-	61,61,61,61	0
56	MG	2A	3334	1/1	0.95	0.08	-	64,64,64,64	0
56	MG	1w	110	1/1	0.90	0.11	-	66,66,66,66	0
56	MG	2A	3348	1/1	0.94	0.20	-	48,48,48,48	0
56	MG	1A	3539	1/1	0.89	0.16	-	49,49,49,49	0
56	MG	2x	105	1/1	0.97	0.15	-	57,57,57,57	0
56	MG	1A	3530	1/1	0.86	0.21	-	63,63,63,63	0
56	MG	1A	3145	1/1	0.92	0.23	-	32,32,32,32	0
56	MG	1A	3678	1/1	0.94	0.12	-	61,61,61,61	0
56	MG	1B	3024	1/1	0.77	0.10	-	50,50,50,50	0
56	MG	2A	3716	1/1	0.72	0.63	-	55,55,55,55	0
56	MG	2a	3168	1/1	0.51	0.10	-	78,78,78,78	0
56	MG	1x	105	1/1	0.91	0.11	-	62,62,62,62	0
56	MG	2a	3169	1/1	0.97	0.08	-	51,51,51,51	0
56	MG	2A	3730	1/1	0.91	0.18	-	43,43,43,43	0
56	MG	1a	1687	1/1	0.91	0.18	-	50,50,50,50	0
56	MG	2a	3043	1/1	0.97	0.08	-	64,64,64,64	0
56	MG	2A	3526	1/1	0.86	0.09	-	41,41,41,41	0
56	MG	1O	204	1/1	0.75	0.12	-	58,58,58,58	0
56	MG	1O	205	1/1	0.96	0.08	-	44,44,44,44	0
56	MG	2A	3111	1/1	0.88	0.16	-	54,54,54,54	0
56	MG	2A	3540	1/1	0.61	0.13	-	47,47,47,47	0
56	MG	19	102	1/1	0.76	0.21	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3219	1/1	0.93	0.16	-	37,37,37,37	0
56	MG	1B	3028	1/1	0.94	0.08	-	61,61,61,61	0
56	MG	2A	3295	1/1	0.81	0.14	-	63,63,63,63	0
56	MG	2a	3095	1/1	0.94	0.11	-	71,71,71,71	0
56	MG	1A	3039	1/1	0.98	0.17	-	36,36,36,36	0
56	MG	2A	3584	1/1	0.96	0.24	-	37,37,37,37	0
56	MG	1A	4004	1/1	0.96	0.15	-	29,29,29,29	0
56	MG	2A	3054	1/1	0.93	0.19	-	54,54,54,54	0
56	MG	1A	3498	1/1	0.94	0.14	-	46,46,46,46	0
56	MG	1A	3950	1/1	0.92	0.09	-	41,41,41,41	0
56	MG	2O	8001	1/1	0.75	0.10	-	65,65,65,65	0
56	MG	1A	3075	1/1	0.90	0.11	-	28,28,28,28	0
56	MG	2A	3627	1/1	0.85	0.17	-	50,50,50,50	0
56	MG	2A	3843	1/1	0.81	0.17	-	58,58,58,58	0
56	MG	2W	202	1/1	0.78	0.22	-	58,58,58,58	0
56	MG	1l	202	1/1	0.86	0.13	-	69,69,69,69	0
56	MG	2a	3040	1/1	0.79	0.09	-	57,57,57,57	0
56	MG	1A	3173	1/1	0.97	0.17	-	42,42,42,42	0
56	MG	2A	3817	1/1	0.92	0.08	-	56,56,56,56	0
56	MG	1A	3478	1/1	0.88	0.23	-	65,65,65,65	0
56	MG	2a	3144	1/1	0.79	0.08	-	83,83,83,83	0
56	MG	1A	3808	1/1	0.89	0.16	-	36,36,36,36	0
56	MG	1A	3411	1/1	0.99	0.18	-	43,43,43,43	0
56	MG	2A	3800	1/1	0.95	0.08	-	67,67,67,67	0
56	MG	1O	206	1/1	0.87	0.24	-	84,84,84,84	0
56	MG	1a	1810	1/1	0.97	0.07	-	51,51,51,51	0
56	MG	1A	3269	1/1	0.95	0.12	-	52,52,52,52	0
56	MG	1A	3925	1/1	0.97	0.17	-	14,14,14,14	0
56	MG	1A	3426	1/1	0.96	0.14	-	50,50,50,50	0
56	MG	1A	3476	1/1	0.93	0.16	-	52,52,52,52	0
56	MG	2A	3281	1/1	0.93	0.16	-	63,63,63,63	0
56	MG	1A	3833	1/1	0.89	0.09	-	60,60,60,60	0
56	MG	1A	4027	1/1	0.87	0.09	-	50,50,50,50	0
56	MG	2a	3230	1/1	0.75	0.12	-	63,63,63,63	0
56	MG	1A	3274	1/1	0.91	0.17	-	36,36,36,36	0
56	MG	1A	4061	1/1	0.76	0.17	-	72,72,72,72	0
56	MG	2a	3106	1/1	0.87	0.16	-	62,62,62,62	0
56	MG	1A	3234	1/1	0.90	0.42	-	54,54,54,54	0
56	MG	2A	3434	1/1	0.82	0.14	-	59,59,59,59	0
56	MG	1A	4029	1/1	0.81	0.08	-	53,53,53,53	0
56	MG	2A	3736	1/1	0.98	0.13	-	67,67,67,67	0
56	MG	1A	3968	1/1	0.89	0.09	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3323	1/1	0.90	0.17	-	50,50,50,50	0
56	MG	2E	309	1/1	0.95	0.09	-	60,60,60,60	0
56	MG	2A	3268	1/1	0.90	0.18	-	63,63,63,63	0
56	MG	1Q	203	1/1	0.90	0.19	-	64,64,64,64	0
56	MG	1A	3181	1/1	0.96	0.14	-	54,54,54,54	0
56	MG	2A	3391	1/1	0.90	0.18	-	58,58,58,58	0
56	MG	1A	3495	1/1	0.93	0.26	-	42,42,42,42	0
56	MG	1a	1697	1/1	0.81	0.22	-	63,63,63,63	0
56	MG	1A	3475	1/1	0.95	0.11	-	42,42,42,42	0
56	MG	1A	3453	1/1	0.96	0.17	-	57,57,57,57	0
56	MG	2a	3150	1/1	0.91	0.05	-	78,78,78,78	0
56	MG	1A	3935	1/1	0.97	0.08	-	50,50,50,50	0
56	MG	1A	3123	1/1	0.88	0.24	-	54,54,54,54	0
56	MG	2A	3397	1/1	0.92	0.17	-	54,54,54,54	0
56	MG	2a	3006	1/1	0.89	0.17	-	74,74,74,74	0
56	MG	1Z	301	1/1	0.91	0.27	-	56,56,56,56	0
56	MG	1a	1734	1/1	0.98	0.08	-	67,67,67,67	0
56	MG	1A	3188	1/1	0.96	0.17	-	49,49,49,49	0
56	MG	1A	3322	1/1	0.72	0.17	-	59,59,59,59	0
56	MG	2A	3572	1/1	0.90	0.11	-	44,44,44,44	0
56	MG	1A	3381	1/1	0.92	0.14	-	43,43,43,43	0
56	MG	2A	3851	1/1	0.96	0.08	-	46,46,46,46	0
56	MG	1A	3206	1/1	0.88	0.14	-	55,55,55,55	0
56	MG	2A	3765	1/1	0.94	0.13	-	53,53,53,53	0
56	MG	1A	3694	1/1	0.89	0.17	-	61,61,61,61	0
56	MG	2A	3372	1/1	0.96	0.24	-	41,41,41,41	0
56	MG	1A	3942	1/1	0.83	0.10	-	56,56,56,56	0
56	MG	2A	3249	1/1	0.88	0.13	-	57,57,57,57	0
56	MG	1a	1689	1/1	0.85	0.12	-	73,73,73,73	0
56	MG	1A	4056	1/1	0.91	0.12	-	47,47,47,47	0
56	MG	1A	3483	1/1	0.92	0.17	-	46,46,46,46	0
56	MG	1a	1783	1/1	0.86	0.23	-	83,83,83,83	0
56	MG	1A	3277	1/1	0.95	0.20	-	38,38,38,38	0
56	MG	2A	3454	1/1	0.96	0.21	-	58,58,58,58	0
56	MG	2a	3014	1/1	0.86	0.11	-	64,64,64,64	0
56	MG	1A	3794	1/1	0.83	0.28	-	61,61,61,61	0
56	MG	2a	3152	1/1	0.89	0.17	-	67,67,67,67	0
56	MG	1A	3983	1/1	0.86	0.13	-	48,48,48,48	0
56	MG	1x	112	1/1	0.93	0.14	-	71,71,71,71	0
56	MG	1A	3467	1/1	0.98	0.16	-	45,45,45,45	0
56	MG	2a	3184	1/1	0.97	0.16	-	54,54,54,54	0
56	MG	1A	3796	1/1	0.96	0.18	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3501	1/1	0.85	0.12	-	59,59,59,59	0
56	MG	1A	3631	1/1	0.94	0.20	-	32,32,32,32	0
56	MG	1A	3696	1/1	0.84	0.21	-	61,61,61,61	0
56	MG	1A	3284	1/1	0.89	0.39	-	56,56,56,56	0
56	MG	1A	3689	1/1	0.97	0.23	-	51,51,51,51	0
56	MG	2a	3033	1/1	0.89	0.14	-	63,63,63,63	0
56	MG	1A	3153	1/1	0.92	0.14	-	37,37,37,37	0
56	MG	1w	103	1/1	0.85	0.14	-	57,57,57,57	0
56	MG	1A	3091	1/1	0.96	0.22	-	43,43,43,43	0
56	MG	1a	1775	1/1	0.67	0.19	-	76,76,76,76	0
56	MG	1A	3677	1/1	0.96	0.15	-	29,29,29,29	0
56	MG	2A	3747	1/1	0.83	0.11	-	51,51,51,51	0
56	MG	2A	3825	1/1	0.94	0.12	-	58,58,58,58	0
56	MG	2a	3016	1/1	0.87	0.14	-	66,66,66,66	0
56	MG	1A	3771	1/1	0.96	0.18	-	49,49,49,49	0
56	MG	1a	1723	1/1	0.91	0.10	-	61,61,61,61	0
56	MG	2l	202	1/1	0.84	0.09	-	70,70,70,70	0
56	MG	2B	3017	1/1	0.90	0.11	-	65,65,65,65	0
56	MG	1A	3683	1/1	0.93	0.19	-	40,40,40,40	0
56	MG	2A	3774	1/1	0.91	0.11	-	51,51,51,51	0
56	MG	1A	3100	1/1	0.94	0.18	-	60,60,60,60	0
56	MG	1A	3268	1/1	0.91	0.18	-	59,59,59,59	0
56	MG	2A	3718	1/1	0.90	0.36	-	64,64,64,64	0
56	MG	2A	3320	1/1	0.83	0.15	-	54,54,54,54	0
56	MG	1A	3614	1/1	0.80	0.13	-	39,39,39,39	0
56	MG	1A	3622	1/1	0.96	0.16	-	36,36,36,36	0
56	MG	1A	3400	1/1	0.96	0.16	-	54,54,54,54	0
56	MG	2A	3078	1/1	0.95	0.20	-	25,25,25,25	0
56	MG	1A	3506	1/1	0.97	0.19	-	42,42,42,42	0
56	MG	1P	204	1/1	0.95	0.21	-	47,47,47,47	0
56	MG	2A	3470	1/1	0.74	0.15	-	56,56,56,56	0
56	MG	1A	3140	1/1	0.95	0.14	-	43,43,43,43	0
56	MG	1A	3017	1/1	0.93	0.14	-	54,54,54,54	0
56	MG	2A	3778	1/1	0.94	0.18	-	52,52,52,52	0
56	MG	2A	3732	1/1	0.91	0.13	-	42,42,42,42	0
56	MG	1A	3198	1/1	0.97	0.20	-	41,41,41,41	0
56	MG	1a	1764	1/1	0.94	0.06	-	59,59,59,59	0
56	MG	2A	3862	1/1	0.91	0.11	-	71,71,71,71	0
56	MG	2a	3171	1/1	0.77	0.09	-	73,73,73,73	0
56	MG	2A	3231	1/1	0.99	0.15	-	49,49,49,49	0
56	MG	1A	3404	1/1	0.85	0.23	-	59,59,59,59	0
56	MG	1A	3832	1/1	0.86	0.10	-	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1738	1/1	0.58	0.21	-	66,66,66,66	0
56	MG	1A	3247	1/1	0.90	0.26	-	58,58,58,58	0
56	MG	2A	3277	1/1	0.96	0.17	-	50,50,50,50	0
56	MG	1A	3816	1/1	0.92	0.22	-	49,49,49,49	0
56	MG	1F	306	1/1	0.91	0.28	-	53,53,53,53	0
56	MG	1A	3398	1/1	0.94	0.31	-	58,58,58,58	0
56	MG	2B	3001	1/1	0.93	0.16	-	62,62,62,62	0
56	MG	2A	3058	1/1	0.73	0.18	-	66,66,66,66	0
56	MG	2A	3815	1/1	0.90	0.14	-	48,48,48,48	0
56	MG	1l	203	1/1	0.94	0.14	-	63,63,63,63	0
56	MG	2a	3163	1/1	0.96	0.10	-	72,72,72,72	0
56	MG	2A	3698	1/1	0.84	0.12	-	51,51,51,51	0
56	MG	1w	108	1/1	0.95	0.07	-	63,63,63,63	0
56	MG	1A	3632	1/1	0.93	0.12	-	34,34,34,34	0
56	MG	1A	3377	1/1	0.84	0.21	-	54,54,54,54	0
56	MG	1A	3260	1/1	0.93	0.12	-	39,39,39,39	0
56	MG	1A	3389	1/1	0.98	0.20	-	53,53,53,53	0
56	MG	1Q	204	1/1	0.88	0.15	-	51,51,51,51	0
56	MG	1A	3839	1/1	0.90	0.08	-	66,66,66,66	0
56	MG	2A	3415	1/1	0.94	0.10	-	50,50,50,50	0
56	MG	2a	3142	1/1	0.69	0.15	-	74,74,74,74	0
56	MG	1A	3116	1/1	0.91	0.22	-	47,47,47,47	0
56	MG	1A	3569	1/1	0.89	0.25	-	54,54,54,54	0
56	MG	1A	3346	1/1	0.96	0.19	-	48,48,48,48	0
56	MG	1A	3443	1/1	0.94	0.27	-	54,54,54,54	0
56	MG	1A	3824	1/1	0.72	0.16	-	70,70,70,70	0
56	MG	2a	3062	1/1	0.85	0.20	-	70,70,70,70	0
56	MG	1A	3550	1/1	0.92	0.19	-	38,38,38,38	0
56	MG	1A	3472	1/1	0.97	0.24	-	56,56,56,56	0
56	MG	2A	3194	1/1	0.89	0.24	-	67,67,67,67	0
56	MG	2A	3105	1/1	0.85	0.09	-	51,51,51,51	0
56	MG	1A	3878	1/1	0.89	0.23	-	33,33,33,33	0
56	MG	1a	1759	1/1	0.92	0.13	-	64,64,64,64	0
56	MG	2A	3354	1/1	0.83	0.15	-	68,68,68,68	0
56	MG	1A	3365	1/1	0.91	0.31	-	53,53,53,53	0
56	MG	2A	3053	1/1	0.73	0.21	-	54,54,54,54	0
56	MG	2A	3573	1/1	0.89	0.11	-	42,42,42,42	0
56	MG	1A	3216	1/1	0.94	0.42	-	50,50,50,50	0
56	MG	2A	3639	1/1	0.99	0.17	-	34,34,34,34	0
56	MG	1a	1665	1/1	0.92	0.10	-	78,78,78,78	0
56	MG	2A	3266	1/1	0.84	0.12	-	59,59,59,59	0
56	MG	2a	3060	1/1	0.87	0.11	-	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3295	1/1	0.94	0.14	-	48,48,48,48	0
56	MG	2B	3010	1/1	0.95	0.22	-	73,73,73,73	0
56	MG	2A	3676	1/1	0.92	0.09	-	48,48,48,48	0
56	MG	1A	3737	1/1	0.79	0.21	-	57,57,57,57	0
56	MG	2A	3425	1/1	0.93	0.16	-	58,58,58,58	0
56	MG	1a	1753	1/1	0.75	0.10	-	59,59,59,59	0
56	MG	1A	3357	1/1	0.87	0.23	-	56,56,56,56	0
56	MG	2A	3065	1/1	0.91	0.20	-	57,57,57,57	0
56	MG	2A	3803	1/1	0.89	0.10	-	42,42,42,42	0
56	MG	2A	3169	1/1	0.84	0.22	-	73,73,73,73	0
56	MG	2A	3678	1/1	0.90	0.09	-	49,49,49,49	0
56	MG	1A	3160	1/1	0.93	0.23	-	41,41,41,41	0
56	MG	1B	3030	1/1	0.96	0.15	-	59,59,59,59	0
56	MG	1A	3922	1/1	0.89	0.10	-	57,57,57,57	0
56	MG	2A	3267	1/1	0.91	0.11	-	58,58,58,58	0
56	MG	2a	3088	1/1	0.76	0.20	-	62,62,62,62	0
56	MG	2A	3891	1/1	0.68	0.15	-	71,71,71,71	0
56	MG	1A	3161	1/1	0.98	0.27	-	38,38,38,38	0
56	MG	1A	3024	1/1	0.88	0.17	-	43,43,43,43	0
56	MG	1A	3776	1/1	0.86	0.20	-	75,75,75,75	0
56	MG	1A	3073	1/1	0.77	0.35	-	69,69,69,69	0
56	MG	2A	3852	1/1	0.91	0.12	-	49,49,49,49	0
56	MG	1A	3294	1/1	0.96	0.19	-	52,52,52,52	0
56	MG	2A	3328	1/1	0.94	0.20	-	39,39,39,39	0
56	MG	1A	3546	1/1	0.87	0.19	-	45,45,45,45	0
56	MG	1A	3613	1/1	0.91	0.13	-	33,33,33,33	0
56	MG	1A	4064	1/1	0.82	0.13	-	66,66,66,66	0
56	MG	1A	3570	1/1	0.94	0.22	-	54,54,54,54	0
56	MG	1a	1731	1/1	0.95	0.16	-	50,50,50,50	0
56	MG	2A	3863	1/1	0.92	0.05	-	58,58,58,58	0
56	MG	2a	3009	1/1	0.98	0.07	-	60,60,60,60	0
56	MG	2A	3680	1/1	0.95	0.05	-	62,62,62,62	0
56	MG	2A	3870	1/1	0.98	0.18	-	33,33,33,33	0
56	MG	2A	3865	1/1	0.59	0.17	-	71,71,71,71	0
56	MG	2A	3071	1/1	0.93	0.06	-	52,52,52,52	0
56	MG	2A	3418	1/1	0.92	0.09	-	61,61,61,61	0
56	MG	2A	3893	1/1	0.81	0.08	-	66,66,66,66	0
56	MG	1A	3656	1/1	0.93	0.10	-	46,46,46,46	0
56	MG	2a	3039	1/1	0.91	0.21	-	73,73,73,73	0
56	MG	1A	3538	1/1	0.97	0.13	-	54,54,54,54	0
56	MG	2A	3082	1/1	0.84	0.12	-	50,50,50,50	0
56	MG	1A	3573	1/1	0.90	0.09	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3018	1/1	0.94	0.14	-	33,33,33,33	0
56	MG	2A	3873	1/1	0.98	0.12	-	40,40,40,40	0
56	MG	1A	3995	1/1	0.91	0.21	-	73,73,73,73	0
56	MG	2A	3322	1/1	0.88	0.11	-	60,60,60,60	0
56	MG	2A	3039	1/1	0.76	0.16	-	55,55,55,55	0
56	MG	2A	3556	1/1	0.82	0.16	-	43,43,43,43	0
56	MG	1a	1814	1/1	0.96	0.26	-	55,55,55,55	0
56	MG	2A	3184	1/1	0.98	0.25	-	48,48,48,48	0
56	MG	2v	3002	1/1	0.94	0.09	-	77,77,77,77	0
56	MG	2A	3440	1/1	0.95	0.20	-	43,43,43,43	0
56	MG	2a	3115	1/1	0.92	0.09	-	57,57,57,57	0
56	MG	2A	3024	1/1	0.93	0.13	-	49,49,49,49	0
56	MG	2A	3335	1/1	0.76	0.17	-	59,59,59,59	0
56	MG	1A	3813	1/1	0.95	0.21	-	56,56,56,56	0
56	MG	1A	3058	1/1	0.71	0.19	-	54,54,54,54	0
56	MG	2y	3005	1/1	0.75	0.30	-	82,82,82,82	0
56	MG	1a	1784	1/1	0.78	0.25	-	74,74,74,74	0
56	MG	1A	3421	1/1	0.79	0.15	-	46,46,46,46	0
56	MG	2A	3775	1/1	0.96	0.12	-	38,38,38,38	0
56	MG	1A	3245	1/1	0.90	0.26	-	64,64,64,64	0
56	MG	1a	1624	1/1	0.93	0.15	-	50,50,50,50	0
56	MG	2A	3665	1/1	0.97	0.09	-	52,52,52,52	0
56	MG	2A	3246	1/1	0.93	0.12	-	65,65,65,65	0
56	MG	1A	3072	1/1	0.98	0.26	-	19,19,19,19	0
56	MG	1A	3489	1/1	0.88	0.19	-	44,44,44,44	0
56	MG	1A	3929	1/1	0.88	0.15	-	42,42,42,42	0
56	MG	1A	3579	1/1	0.90	0.17	-	44,44,44,44	0
56	MG	1A	3231	1/1	0.89	0.23	-	51,51,51,51	0
56	MG	2A	3148	1/1	0.92	0.16	-	52,52,52,52	0
56	MG	1A	3718	1/1	0.66	0.13	-	67,67,67,67	0
56	MG	2A	3218	1/1	0.95	0.19	-	61,61,61,61	0
56	MG	2a	3059	1/1	0.95	0.13	-	74,74,74,74	0
56	MG	1A	4000	1/1	0.95	0.18	-	34,34,34,34	0
56	MG	2a	3074	1/1	0.82	0.09	-	63,63,63,63	0
56	MG	2a	3007	1/1	0.88	0.11	-	71,71,71,71	0
56	MG	1F	301	1/1	0.92	0.16	-	40,40,40,40	0
56	MG	1A	3937	1/1	0.89	0.24	-	31,31,31,31	0
56	MG	2A	3672	1/1	0.94	0.23	-	45,45,45,45	0
56	MG	1A	3515	1/1	0.95	0.10	-	29,29,29,29	0
56	MG	1A	3837	1/1	0.97	0.23	-	21,21,21,21	0
56	MG	1A	3769	1/1	0.94	0.24	-	29,29,29,29	0
56	MG	1A	3979	1/1	0.94	0.09	-	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2y	3007	1/1	0.94	0.15	-	68,68,68,68	0
56	MG	2A	3827	1/1	0.88	0.12	-	58,58,58,58	0
56	MG	1A	3448	1/1	0.90	0.16	-	59,59,59,59	0
56	MG	15	102	1/1	0.93	0.19	-	39,39,39,39	0
56	MG	2a	3042	1/1	0.84	0.24	-	58,58,58,58	0
56	MG	1a	1666	1/1	0.92	0.14	-	59,59,59,59	0
56	MG	1a	1664	1/1	0.90	0.25	-	62,62,62,62	0
56	MG	1A	3455	1/1	0.98	0.12	-	47,47,47,47	0
56	MG	2A	3909	1/1	0.96	0.15	-	43,43,43,43	0
56	MG	1A	3642	1/1	0.93	0.10	-	40,40,40,40	0
56	MG	1A	3136	1/1	0.93	0.08	-	52,52,52,52	0
56	MG	1a	1763	1/1	0.96	0.10	-	55,55,55,55	0
56	MG	2a	3220	1/1	0.91	0.12	-	66,66,66,66	0
56	MG	1A	3114	1/1	0.94	0.17	-	57,57,57,57	0
56	MG	1A	3599	1/1	0.97	0.16	-	21,21,21,21	0
56	MG	1B	3014	1/1	0.90	0.13	-	63,63,63,63	0
56	MG	1a	1633	1/1	0.93	0.21	-	60,60,60,60	0
56	MG	1A	4054	1/1	0.58	0.13	-	81,81,81,81	0
56	MG	1A	3587	1/1	0.90	0.21	-	38,38,38,38	0
56	MG	1a	1696	1/1	0.88	0.14	-	71,71,71,71	0
56	MG	2A	3321	1/1	0.93	0.13	-	54,54,54,54	0
56	MG	2A	3345	1/1	0.82	0.19	-	59,59,59,59	0
56	MG	1y	3003	1/1	0.92	0.23	-	71,71,71,71	0
56	MG	1A	3057	1/1	0.85	0.22	-	54,54,54,54	0
56	MG	1A	3710	1/1	0.91	0.12	-	68,68,68,68	0
56	MG	1A	3222	1/1	0.94	0.16	-	56,56,56,56	0
56	MG	1A	3325	1/1	0.88	0.21	-	64,64,64,64	0
56	MG	2A	3829	1/1	0.75	0.12	-	59,59,59,59	0
56	MG	1A	3894	1/1	0.83	0.10	-	73,73,73,73	0
56	MG	1A	3327	1/1	0.89	0.16	-	28,28,28,28	0
56	MG	2A	3256	1/1	0.94	0.31	-	53,53,53,53	0
56	MG	2A	3754	1/1	0.76	0.13	-	45,45,45,45	0
56	MG	25	103	1/1	0.94	0.21	-	52,52,52,52	0
56	MG	2A	3305	1/1	0.86	0.13	-	56,56,56,56	0
56	MG	1A	3452	1/1	0.94	0.23	-	58,58,58,58	0
56	MG	2A	3901	1/1	0.93	0.31	-	59,59,59,59	0
56	MG	2V	201	1/1	0.98	0.16	-	53,53,53,53	0
56	MG	2A	3788	1/1	0.91	0.10	-	53,53,53,53	0
56	MG	1A	3701	1/1	0.95	0.09	-	48,48,48,48	0
56	MG	1A	3087	1/1	0.84	0.22	-	32,32,32,32	0
56	MG	2A	3734	1/1	0.85	0.14	-	57,57,57,57	0
56	MG	2A	3512	1/1	0.89	0.12	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1B	3036	1/1	0.99	0.10	-	36,36,36,36	0
56	MG	2A	3361	1/1	0.93	0.15	-	51,51,51,51	0
56	MG	2a	3135	1/1	0.82	0.19	-	62,62,62,62	0
56	MG	2B	3005	1/1	0.79	0.13	-	53,53,53,53	0
56	MG	2A	3701	1/1	0.93	0.19	-	64,64,64,64	0
56	MG	2A	3417	1/1	0.89	0.10	-	41,41,41,41	0
56	MG	2A	3740	1/1	0.81	0.17	-	53,53,53,53	0
56	MG	2y	3002	1/1	0.80	0.13	-	64,64,64,64	0
56	MG	2A	3753	1/1	0.91	0.13	-	45,45,45,45	0
56	MG	2A	3138	1/1	0.91	0.15	-	59,59,59,59	0
56	MG	2A	3289	1/1	0.87	0.13	-	47,47,47,47	0
56	MG	1a	1760	1/1	0.86	0.17	-	74,74,74,74	0
56	MG	2A	3027	1/1	0.98	0.32	-	48,48,48,48	0
56	MG	2a	3183	1/1	0.81	0.10	-	76,76,76,76	0
56	MG	1a	1606	1/1	0.94	0.17	-	65,65,65,65	0
56	MG	2A	3866	1/1	0.95	0.11	-	42,42,42,42	0
56	MG	1A	3080	1/1	0.89	0.26	-	42,42,42,42	0
56	MG	1A	3954	1/1	0.58	0.16	-	58,58,58,58	0
56	MG	1A	3702	1/1	0.99	0.15	-	34,34,34,34	0
56	MG	1A	3209	1/1	0.89	0.26	-	68,68,68,68	0
56	MG	1a	1766	1/1	0.67	0.17	-	76,76,76,76	0
56	MG	2A	3269	1/1	0.89	0.17	-	53,53,53,53	0
56	MG	2E	308	1/1	0.76	0.14	-	38,38,38,38	0
56	MG	2a	3226	1/1	0.97	0.07	-	64,64,64,64	0
56	MG	2a	3117	1/1	0.89	0.85	-	81,81,81,81	0
56	MG	2A	3682	1/1	0.93	0.15	-	70,70,70,70	0
56	MG	2x	101	1/1	0.93	0.10	-	42,42,42,42	0
56	MG	1f	3001	1/1	0.95	0.20	-	34,34,34,34	0
56	MG	2A	3398	1/1	0.94	0.30	-	55,55,55,55	0
56	MG	2a	3111	1/1	0.95	0.14	-	76,76,76,76	0
56	MG	1a	1781	1/1	0.83	0.11	-	71,71,71,71	0
56	MG	1x	113	1/1	0.93	0.19	-	62,62,62,62	0
56	MG	1a	1671	1/1	0.79	0.15	-	66,66,66,66	0
56	MG	2a	3225	1/1	0.88	0.10	-	57,57,57,57	0
56	MG	1A	3585	1/1	0.94	0.08	-	66,66,66,66	0
56	MG	2A	3549	1/1	0.86	0.15	-	58,58,58,58	0
56	MG	2A	3796	1/1	0.87	0.10	-	49,49,49,49	0
56	MG	1A	3108	1/1	0.87	0.45	-	43,43,43,43	0
56	MG	2a	3156	1/1	0.89	0.13	-	69,69,69,69	0
56	MG	1A	3432	1/1	0.75	0.14	-	54,54,54,54	0
56	MG	1A	3565	1/1	0.93	0.32	-	71,71,71,71	0
56	MG	1a	1801	1/1	0.95	0.07	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3272	1/1	0.58	0.30	-	60,60,60,60	0
56	MG	2A	3196	1/1	0.90	0.14	-	56,56,56,56	0
56	MG	27	101	1/1	0.92	0.20	-	51,51,51,51	0
56	MG	1A	4005	1/1	0.95	0.11	-	50,50,50,50	0
56	MG	2A	3298	1/1	0.96	0.12	-	41,41,41,41	0
56	MG	1A	3407	1/1	0.87	0.36	-	65,65,65,65	0
56	MG	2A	3402	1/1	0.86	0.17	-	50,50,50,50	0
56	MG	1A	3782	1/1	0.96	0.19	-	25,25,25,25	0
56	MG	1A	3527	1/1	0.88	0.30	-	40,40,40,40	0
56	MG	1a	1787	1/1	0.92	0.07	-	72,72,72,72	0
56	MG	1a	1798	1/1	0.94	0.14	-	56,56,56,56	0
56	MG	2A	3363	1/1	0.92	0.22	-	65,65,65,65	0
56	MG	2A	3779	1/1	0.95	0.08	-	56,56,56,56	0
56	MG	2A	3358	1/1	0.76	0.12	-	65,65,65,65	0
56	MG	2A	3451	1/1	0.93	0.19	-	56,56,56,56	0
56	MG	1a	1704	1/1	0.78	0.20	-	63,63,63,63	0
56	MG	1a	1715	1/1	0.98	0.11	-	49,49,49,49	0
56	MG	1A	3023	1/1	0.91	0.17	-	59,59,59,59	0
56	MG	2A	3283	1/1	0.94	0.24	-	61,61,61,61	0
56	MG	2A	3097	1/1	0.97	0.13	-	56,56,56,56	0
56	MG	2A	3824	1/1	0.57	0.14	-	78,78,78,78	0
56	MG	2A	3600	1/1	0.97	0.15	-	40,40,40,40	0
56	MG	2A	3878	1/1	0.88	0.10	-	49,49,49,49	0
56	MG	2A	3860	1/1	0.87	0.12	-	59,59,59,59	0
56	MG	1A	3560	1/1	0.86	0.22	-	55,55,55,55	0
56	MG	1A	3917	1/1	0.84	0.17	-	80,80,80,80	0
56	MG	1A	3499	1/1	0.90	0.11	-	49,49,49,49	0
56	MG	2A	3385	1/1	0.96	0.24	-	52,52,52,52	0
56	MG	2A	3724	1/1	0.95	0.06	-	57,57,57,57	0
56	MG	2A	3797	1/1	0.95	0.15	-	52,52,52,52	0
56	MG	2A	3388	1/1	0.93	0.18	-	56,56,56,56	0
56	MG	25	105	1/1	0.90	0.09	-	58,58,58,58	0
56	MG	2A	3376	1/1	0.94	0.13	-	58,58,58,58	0
56	MG	1A	3623	1/1	0.82	0.21	-	59,59,59,59	0
56	MG	1A	3009	1/1	0.95	0.12	-	24,24,24,24	0
56	MG	2A	3896	1/1	0.89	0.18	-	39,39,39,39	0
56	MG	1X	102	1/1	0.91	0.22	-	46,46,46,46	0
56	MG	1A	3768	1/1	0.87	0.17	-	61,61,61,61	0
56	MG	1A	3492	1/1	0.80	0.29	-	52,52,52,52	0
56	MG	2A	3307	1/1	0.73	0.16	-	68,68,68,68	0
56	MG	1A	4094	1/1	0.90	0.09	-	37,37,37,37	0
56	MG	2A	3292	1/1	0.91	0.11	-	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3741	1/1	0.77	0.12	-	61,61,61,61	0
56	MG	1A	3651	1/1	0.94	0.22	-	32,32,32,32	0
56	MG	1A	3267	1/1	0.94	0.15	-	57,57,57,57	0
56	MG	2B	3020	1/1	0.91	0.20	-	78,78,78,78	0
56	MG	1A	3920	1/1	0.96	0.14	-	44,44,44,44	0
56	MG	1B	3011	1/1	0.85	0.16	-	55,55,55,55	0
56	MG	2a	3024	1/1	0.86	0.11	-	72,72,72,72	0
56	MG	2a	3021	1/1	0.98	0.14	-	65,65,65,65	0
56	MG	2A	3679	1/1	0.98	0.11	-	41,41,41,41	0
56	MG	1A	3709	1/1	0.88	0.31	-	52,52,52,52	0
56	MG	1A	3218	1/1	0.78	0.22	-	62,62,62,62	0
56	MG	1A	3178	1/1	0.97	0.26	-	21,21,21,21	0
56	MG	1A	3823	1/1	0.90	0.18	-	65,65,65,65	0
56	MG	2a	3081	1/1	0.83	0.18	-	49,49,49,49	0
56	MG	1A	3779	1/1	0.94	0.10	-	56,56,56,56	0
56	MG	2A	3205	1/1	0.89	0.22	-	52,52,52,52	0
56	MG	2A	3583	1/1	0.93	0.16	-	69,69,69,69	0
56	MG	1A	3868	1/1	0.96	0.15	-	47,47,47,47	0
56	MG	1A	3052	1/1	0.93	0.15	-	56,56,56,56	0
56	MG	1a	1773	1/1	0.78	0.14	-	90,90,90,90	0
56	MG	1A	3049	1/1	0.97	0.23	-	26,26,26,26	0
56	MG	2a	3214	1/1	0.69	0.16	-	91,91,91,91	0
56	MG	2A	3847	1/1	0.98	0.06	-	42,42,42,42	0
56	MG	2A	3161	1/1	0.93	0.18	-	44,44,44,44	0
56	MG	2A	3830	1/1	0.81	0.19	-	48,48,48,48	0
56	MG	1A	3940	1/1	0.63	0.12	-	48,48,48,48	0
56	MG	2A	3805	1/1	0.84	0.26	-	77,77,77,77	0
56	MG	1A	3886	1/1	0.91	0.13	-	57,57,57,57	0
56	MG	2A	3177	1/1	0.94	0.15	-	63,63,63,63	0
56	MG	2a	3224	1/1	0.88	0.20	-	74,74,74,74	0
56	MG	2A	3149	1/1	0.89	0.22	-	54,54,54,54	0
56	MG	2A	3085	1/1	0.87	0.12	-	44,44,44,44	0
56	MG	1A	3349	1/1	0.81	0.20	-	44,44,44,44	0
56	MG	2A	3244	1/1	0.88	0.09	-	54,54,54,54	0
56	MG	25	104	1/1	0.94	0.11	-	43,43,43,43	0
56	MG	1A	3304	1/1	0.94	0.29	-	55,55,55,55	0
56	MG	1A	3301	1/1	0.97	0.05	-	54,54,54,54	0
56	MG	1A	3957	1/1	0.97	0.11	-	55,55,55,55	0
56	MG	2A	3073	1/1	0.88	0.11	-	36,36,36,36	0
56	MG	2A	3602	1/1	0.95	0.14	-	42,42,42,42	0
56	MG	1a	1674	1/1	0.85	0.17	-	72,72,72,72	0
56	MG	1B	3013	1/1	0.95	0.09	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3391	1/1	0.92	0.20	-	41,41,41,41	0
56	MG	2A	3135	1/1	0.93	0.20	-	43,43,43,43	0
56	MG	1A	3830	1/1	0.24	0.16	-	66,66,66,66	0
56	MG	1d	502	1/1	0.90	0.23	-	67,67,67,67	0
56	MG	2Y	502	1/1	0.93	0.25	-	54,54,54,54	0
56	MG	2A	3238	1/1	0.90	0.39	-	56,56,56,56	0
56	MG	2B	3016	1/1	0.83	0.13	-	81,81,81,81	0
56	MG	1a	1811	1/1	0.75	0.08	-	77,77,77,77	0
56	MG	2a	3121	1/1	0.80	0.24	-	75,75,75,75	0
56	MG	1A	3257	1/1	0.74	0.24	-	68,68,68,68	0
56	MG	1w	104	1/1	0.95	0.13	-	69,69,69,69	0
56	MG	2A	3240	1/1	0.95	0.13	-	40,40,40,40	0
56	MG	2A	3075	1/1	0.92	0.19	-	37,37,37,37	0
56	MG	2a	3002	1/1	0.87	0.10	-	50,50,50,50	0
56	MG	2w	104	1/1	0.86	0.14	-	69,69,69,69	0
56	MG	1A	3402	1/1	0.95	0.23	-	54,54,54,54	0
56	MG	1a	1601	1/1	0.85	0.11	-	53,53,53,53	0
56	MG	2A	3845	1/1	0.95	0.13	-	42,42,42,42	0
56	MG	2A	3293	1/1	0.93	0.13	-	50,50,50,50	0
56	MG	1A	3169	1/1	0.79	0.23	-	55,55,55,55	0
56	MG	2a	3086	1/1	0.93	0.11	-	57,57,57,57	0
56	MG	2A	3605	1/1	0.90	0.15	-	51,51,51,51	0
56	MG	2A	3429	1/1	0.92	0.11	-	65,65,65,65	0
56	MG	1A	3980	1/1	0.64	0.11	-	74,74,74,74	0
56	MG	1a	1729	1/1	0.93	0.20	-	61,61,61,61	0
56	MG	2A	3399	1/1	0.90	0.15	-	60,60,60,60	0
56	MG	1A	3643	1/1	0.86	0.17	-	34,34,34,34	0
56	MG	2A	3382	1/1	0.93	0.07	-	50,50,50,50	0
56	MG	1A	3815	1/1	0.93	0.27	-	44,44,44,44	0
56	MG	2A	3489	1/1	0.94	0.17	-	41,41,41,41	0
56	MG	2A	3182	1/1	0.89	0.13	-	42,42,42,42	0
56	MG	2A	3310	1/1	0.95	0.15	-	62,62,62,62	0
56	MG	2A	3731	1/1	0.87	0.14	-	57,57,57,57	0
56	MG	1a	1714	1/1	0.88	0.14	-	66,66,66,66	0
56	MG	2A	3641	1/1	0.91	0.25	-	57,57,57,57	0
56	MG	1A	3580	1/1	0.91	0.27	-	39,39,39,39	0
56	MG	1A	3456	1/1	0.97	0.22	-	48,48,48,48	0
56	MG	2A	3130	1/1	0.91	0.19	-	53,53,53,53	0
56	MG	2A	3603	1/1	0.91	0.14	-	50,50,50,50	0
56	MG	1A	3742	1/1	0.94	0.13	-	64,64,64,64	0
56	MG	1A	3785	1/1	0.85	0.14	-	47,47,47,47	0
56	MG	1A	3766	1/1	0.90	0.08	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3478	1/1	0.90	0.15	-	50,50,50,50	0
56	MG	1A	4102	1/1	0.93	0.10	-	45,45,45,45	0
56	MG	2a	3122	1/1	0.79	0.16	-	73,73,73,73	0
56	MG	2A	3671	1/1	0.92	0.10	-	46,46,46,46	0
56	MG	2N	8001	1/1	0.92	0.17	-	47,47,47,47	0
56	MG	2A	3393	1/1	0.95	0.09	-	48,48,48,48	0
56	MG	2a	3019	1/1	0.93	0.11	-	57,57,57,57	0
56	MG	1a	1726	1/1	0.84	0.18	-	67,67,67,67	0
56	MG	1A	3799	1/1	0.93	0.18	-	57,57,57,57	0
56	MG	1A	3755	1/1	0.94	0.20	-	36,36,36,36	0
56	MG	1A	3463	1/1	0.96	0.16	-	53,53,53,53	0
56	MG	1A	3464	1/1	0.79	0.21	-	45,45,45,45	0
56	MG	2a	3196	1/1	0.93	0.11	-	64,64,64,64	0
56	MG	1A	4058	1/1	0.82	0.07	-	47,47,47,47	0
56	MG	1A	3235	1/1	0.90	0.25	-	66,66,66,66	0
56	MG	1A	3484	1/1	0.93	0.13	-	54,54,54,54	0
56	MG	2A	3859	1/1	0.87	0.10	-	53,53,53,53	0
57	K	1A	3584	1/1	0.95	0.13	-	58,58,58,58	0
56	MG	1A	3079	1/1	0.95	0.17	-	57,57,57,57	0
56	MG	2A	3052	1/1	0.83	0.16	-	58,58,58,58	0
56	MG	2A	3713	1/1	0.97	0.45	-	67,67,67,67	0
56	MG	1A	3371	1/1	0.91	0.14	-	45,45,45,45	0
56	MG	1A	3770	1/1	0.72	0.09	-	74,74,74,74	0
56	MG	1A	3217	1/1	0.93	0.29	-	47,47,47,47	0
56	MG	2a	3015	1/1	0.91	0.11	-	62,62,62,62	0
56	MG	2A	3421	1/1	0.93	0.16	-	61,61,61,61	0
56	MG	1A	3856	1/1	0.85	0.20	-	47,47,47,47	0
56	MG	1A	3440	1/1	0.82	0.17	-	50,50,50,50	0
56	MG	1A	3380	1/1	0.96	0.27	-	48,48,48,48	0
56	MG	1A	3528	1/1	0.95	0.17	-	45,45,45,45	0
56	MG	2A	3704	1/1	0.92	0.07	-	56,56,56,56	0
56	MG	1A	3331	1/1	0.93	0.23	-	54,54,54,54	0
56	MG	1A	3183	1/1	0.83	0.17	-	54,54,54,54	0
56	MG	1a	1815	1/1	0.85	0.07	-	64,64,64,64	0
56	MG	2A	3459	1/1	0.91	0.13	-	62,62,62,62	0
56	MG	1A	3758	1/1	0.88	0.10	-	71,71,71,71	0
56	MG	2B	3021	1/1	0.71	0.09	-	75,75,75,75	0
56	MG	2A	3810	1/1	0.71	0.20	-	51,51,51,51	0
56	MG	2A	3423	1/1	0.90	0.18	-	58,58,58,58	0
56	MG	1A	4128	1/1	0.92	0.32	-	43,43,43,43	0
56	MG	2a	3038	1/1	0.89	0.13	-	68,68,68,68	0
56	MG	2A	3291	1/1	0.72	0.15	-	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3438	1/1	0.89	0.19	-	68,68,68,68	0
56	MG	1A	3373	1/1	0.93	0.24	-	52,52,52,52	0
56	MG	2A	3488	1/1	0.74	0.21	-	65,65,65,65	0
56	MG	1A	3090	1/1	0.90	0.16	-	54,54,54,54	0
56	MG	1A	3521	1/1	0.76	0.18	-	65,65,65,65	0
56	MG	2A	3116	1/1	0.93	0.23	-	68,68,68,68	0
56	MG	1A	3872	1/1	0.96	0.23	-	33,33,33,33	0
56	MG	2A	3088	1/1	0.85	0.11	-	49,49,49,49	0
56	MG	2A	3539	1/1	0.91	0.16	-	62,62,62,62	0
56	MG	1a	1681	1/1	0.89	0.25	-	54,54,54,54	0
56	MG	1A	3883	1/1	0.95	0.16	-	68,68,68,68	0
56	MG	1A	3975	1/1	0.75	0.25	-	93,93,93,93	0
56	MG	1A	4045	1/1	0.79	0.10	-	38,38,38,38	0
56	MG	2A	3274	1/1	0.87	0.11	-	53,53,53,53	0
56	MG	2A	3712	1/1	0.82	0.15	-	63,63,63,63	0
56	MG	1A	3086	1/1	0.94	0.42	-	50,50,50,50	0
56	MG	2a	3219	1/1	0.91	0.07	-	65,65,65,65	0
56	MG	2A	3261	1/1	0.88	0.20	-	59,59,59,59	0
56	MG	1A	3715	1/1	0.97	0.09	-	54,54,54,54	0
56	MG	1A	3239	1/1	0.97	0.18	-	30,30,30,30	0
56	MG	2a	3045	1/1	0.94	0.06	-	65,65,65,65	0
56	MG	2A	3378	1/1	0.92	0.15	-	62,62,62,62	0
56	MG	2A	3230	1/1	0.90	0.13	-	48,48,48,48	0
56	MG	2A	3864	1/1	0.77	0.17	-	63,63,63,63	0
56	MG	1A	3422	1/1	0.96	0.24	-	38,38,38,38	0
56	MG	2A	3241	1/1	0.89	0.38	-	56,56,56,56	0
56	MG	2A	3510	1/1	0.86	0.18	-	46,46,46,46	0
56	MG	1A	3522	1/1	0.97	0.16	-	49,49,49,49	0
56	MG	1a	1622	1/1	0.93	0.28	-	62,62,62,62	0
56	MG	2a	3211	1/1	0.95	0.13	-	61,61,61,61	0
56	MG	1A	3542	1/1	0.89	0.21	-	75,75,75,75	0
56	MG	2a	3198	1/1	0.78	0.18	-	83,83,83,83	0
56	MG	1A	3232	1/1	0.92	0.10	-	47,47,47,47	0
56	MG	28	101	1/1	0.89	0.12	-	53,53,53,53	0
56	MG	2A	3894	1/1	0.95	0.15	-	55,55,55,55	0
56	MG	2A	3473	1/1	0.91	0.13	-	57,57,57,57	0
56	MG	2A	3684	1/1	0.82	0.10	-	44,44,44,44	0
56	MG	1A	3910	1/1	0.91	0.07	-	76,76,76,76	0
56	MG	2a	3186	1/1	0.94	0.12	-	53,53,53,53	0
56	MG	2A	3471	1/1	0.86	0.21	-	54,54,54,54	0
56	MG	1A	3457	1/1	0.95	0.16	-	59,59,59,59	0
56	MG	1A	3394	1/1	0.96	0.16	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1683	1/1	0.94	0.14	-	61,61,61,61	0
56	MG	2A	3254	1/1	0.93	0.51	-	53,53,53,53	0
56	MG	2A	3197	1/1	0.93	0.12	-	57,57,57,57	0
56	MG	1A	3468	1/1	0.80	0.32	-	68,68,68,68	0
56	MG	1A	3518	1/1	0.85	0.17	-	48,48,48,48	0
56	MG	2A	3226	1/1	0.97	0.11	-	58,58,58,58	0
56	MG	1A	3298	1/1	0.92	0.15	-	43,43,43,43	0
56	MG	1a	1713	1/1	0.90	0.08	-	68,68,68,68	0
56	MG	1A	3996	1/1	0.78	0.12	-	43,43,43,43	0
56	MG	2A	3356	1/1	0.88	0.30	-	55,55,55,55	0
56	MG	2A	3346	1/1	0.89	0.20	-	54,54,54,54	0
56	MG	1A	3352	1/1	0.89	0.22	-	64,64,64,64	0
56	MG	1A	3433	1/1	0.97	0.16	-	47,47,47,47	0
56	MG	1A	3155	1/1	0.93	0.20	-	47,47,47,47	0
56	MG	2x	103	1/1	0.93	0.13	-	64,64,64,64	0
56	MG	1a	1677	1/1	0.82	0.12	-	68,68,68,68	0
56	MG	2A	3681	1/1	0.94	0.08	-	50,50,50,50	0
56	MG	1A	3435	1/1	0.94	0.11	-	53,53,53,53	0
56	MG	2A	3858	1/1	0.96	0.13	-	43,43,43,43	0
56	MG	1A	4052	1/1	0.94	0.18	-	31,31,31,31	0
56	MG	2A	3119	1/1	0.90	0.19	-	47,47,47,47	0
56	MG	2A	3204	1/1	0.98	0.17	-	48,48,48,48	0
56	MG	1A	4007	1/1	0.69	0.09	-	86,86,86,86	0
56	MG	2A	3004	1/1	0.94	0.24	-	48,48,48,48	0
56	MG	2a	3227	1/1	0.90	0.12	-	59,59,59,59	0
56	MG	1A	3713	1/1	0.96	0.18	-	62,62,62,62	0
56	MG	1A	3664	1/1	0.92	0.14	-	48,48,48,48	0
56	MG	2A	3816	1/1	0.96	0.25	-	57,57,57,57	0
56	MG	10	103	1/1	0.94	0.18	-	45,45,45,45	0
56	MG	2A	3727	1/1	0.93	0.15	-	51,51,51,51	0
56	MG	2E	305	1/1	0.95	0.11	-	40,40,40,40	0
56	MG	1A	3840	1/1	0.93	0.11	-	63,63,63,63	0
56	MG	2a	3066	1/1	0.92	0.14	-	54,54,54,54	0
56	MG	2A	3636	1/1	0.98	0.15	-	59,59,59,59	0
56	MG	1A	3031	1/1	0.98	0.17	-	31,31,31,31	0
56	MG	1a	1716	1/1	0.91	0.22	-	53,53,53,53	0
56	MG	1A	3988	1/1	0.98	0.07	-	68,68,68,68	0
56	MG	2A	3485	1/1	0.93	0.23	-	63,63,63,63	0
56	MG	2A	3798	1/1	0.92	0.28	-	52,52,52,52	0
56	MG	2a	3180	1/1	0.94	0.11	-	73,73,73,73	0
56	MG	2A	3656	1/1	0.75	0.17	-	77,77,77,77	0
56	MG	2A	3450	1/1	0.89	0.20	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3382	1/1	0.84	0.17	-	54,54,54,54	0
56	MG	1a	1679	1/1	0.98	0.10	-	73,73,73,73	0
56	MG	1R	203	1/1	0.90	0.31	-	47,47,47,47	0
56	MG	1A	3582	1/1	0.97	0.20	-	54,54,54,54	0
56	MG	1G	3004	1/1	0.73	0.34	-	92,92,92,92	0
56	MG	1V	203	1/1	0.84	0.26	-	67,67,67,67	0
56	MG	1B	3008	1/1	0.95	0.15	-	57,57,57,57	0
56	MG	1A	3629	1/1	0.97	0.21	-	32,32,32,32	0
56	MG	2A	3854	1/1	0.50	0.09	-	77,77,77,77	0
56	MG	1A	3982	1/1	0.91	0.26	-	29,29,29,29	0
56	MG	1A	3655	1/1	0.91	0.12	-	39,39,39,39	0
56	MG	1A	3132	1/1	0.92	0.26	-	40,40,40,40	0
56	MG	2A	3821	1/1	0.84	0.18	-	79,79,79,79	0
56	MG	1a	1757	1/1	0.93	0.10	-	48,48,48,48	0
56	MG	1A	3362	1/1	0.89	0.24	-	54,54,54,54	0
56	MG	1A	3763	1/1	0.95	0.15	-	52,52,52,52	0
56	MG	1A	3581	1/1	0.83	0.16	-	58,58,58,58	0
56	MG	2A	3340	1/1	0.95	0.26	-	51,51,51,51	0
56	MG	1A	3255	1/1	0.95	0.24	-	47,47,47,47	0
56	MG	1A	3500	1/1	0.97	0.18	-	38,38,38,38	0
56	MG	2A	3329	1/1	0.91	0.41	-	56,56,56,56	0
56	MG	1A	3271	1/1	0.96	0.12	-	50,50,50,50	0
56	MG	2a	3190	1/1	0.98	0.07	-	66,66,66,66	0
56	MG	1A	3557	1/1	0.90	0.32	-	60,60,60,60	0
56	MG	2A	3324	1/1	0.94	0.09	-	41,41,41,41	0
56	MG	2A	3836	1/1	0.82	0.23	-	42,42,42,42	0
56	MG	1a	1725	1/1	0.96	0.20	-	55,55,55,55	0
56	MG	1A	3447	1/1	0.87	0.15	-	46,46,46,46	0
56	MG	2a	3205	1/1	0.99	0.22	-	70,70,70,70	0
56	MG	2A	3284	1/1	0.89	0.16	-	59,59,59,59	0
56	MG	2a	3243	1/1	0.95	0.13	-	64,64,64,64	0
56	MG	2A	3702	1/1	0.94	0.07	-	49,49,49,49	0
56	MG	1A	3441	1/1	0.87	0.10	-	56,56,56,56	0
56	MG	2A	3353	1/1	0.83	0.19	-	65,65,65,65	0
56	MG	2A	3221	1/1	0.98	0.10	-	48,48,48,48	0
56	MG	1A	3862	1/1	0.90	0.22	-	43,43,43,43	0
56	MG	2A	3195	1/1	0.86	0.21	-	56,56,56,56	0
56	MG	2A	3630	1/1	0.93	0.16	-	69,69,69,69	0
56	MG	1A	3901	1/1	0.90	0.21	-	43,43,43,43	0
56	MG	2a	3160	1/1	0.91	0.09	-	49,49,49,49	0
56	MG	2x	104	1/1	0.92	0.24	-	60,60,60,60	0
56	MG	2A	3806	1/1	0.93	0.11	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	3197	1/1	0.82	0.09	-	69,69,69,69	0
56	MG	1A	3847	1/1	0.93	0.09	-	48,48,48,48	0
56	MG	10	105	1/1	0.90	0.17	-	70,70,70,70	0
56	MG	2a	3058	1/1	0.83	0.20	-	73,73,73,73	0
56	MG	1f	3002	1/1	0.86	0.28	-	80,80,80,80	0
56	MG	2A	3286	1/1	0.88	0.20	-	55,55,55,55	0
56	MG	2A	3077	1/1	0.86	0.15	-	45,45,45,45	0
56	MG	1A	3110	1/1	0.90	0.12	-	42,42,42,42	0
56	MG	2R	201	1/1	0.91	0.11	-	48,48,48,48	0
56	MG	1A	3554	1/1	0.92	0.28	-	47,47,47,47	0
56	MG	1a	1678	1/1	0.91	0.18	-	63,63,63,63	0
56	MG	1A	3543	1/1	0.97	0.17	-	73,73,73,73	0
56	MG	2A	3793	1/1	0.87	0.16	-	56,56,56,56	0
56	MG	2A	3250	1/1	0.96	0.11	-	41,41,41,41	0
56	MG	1w	111	1/1	0.93	0.17	-	41,41,41,41	0
56	MG	2A	3783	1/1	0.90	0.25	-	58,58,58,58	0
56	MG	2A	3384	1/1	0.90	0.17	-	62,62,62,62	0
56	MG	2A	3041	1/1	0.93	0.20	-	49,49,49,49	0
56	MG	1A	3401	1/1	0.92	0.21	-	35,35,35,35	0
56	MG	1A	3479	1/1	0.94	0.17	-	38,38,38,38	0
56	MG	1A	3461	1/1	0.89	0.31	-	44,44,44,44	0
56	MG	23	101	1/1	0.94	0.32	-	61,61,61,61	0
56	MG	1A	3300	1/1	0.94	0.18	-	61,61,61,61	0
56	MG	2A	3068	1/1	0.95	0.14	-	56,56,56,56	0
56	MG	1A	3353	1/1	0.83	0.32	-	64,64,64,64	0
56	MG	1A	3788	1/1	0.92	0.10	-	59,59,59,59	0
56	MG	2A	3045	1/1	0.92	0.15	-	58,58,58,58	0
56	MG	2A	3048	1/1	0.97	0.12	-	41,41,41,41	0
56	MG	2A	3412	1/1	0.91	0.30	-	59,59,59,59	0
56	MG	2A	3239	1/1	0.88	0.40	-	52,52,52,52	0
56	MG	2A	3076	1/1	0.96	0.27	-	35,35,35,35	0
56	MG	1a	1685	1/1	0.91	0.14	-	51,51,51,51	0
56	MG	1w	102	1/1	0.97	0.17	-	61,61,61,61	0
56	MG	2A	3757	1/1	0.90	0.12	-	52,52,52,52	0
56	MG	1A	3854	1/1	0.92	0.12	-	51,51,51,51	0
56	MG	1A	3536	1/1	0.96	0.17	-	37,37,37,37	0
56	MG	2A	3338	1/1	0.84	0.22	-	62,62,62,62	0
56	MG	2a	3108	1/1	0.81	0.21	-	78,78,78,78	0
56	MG	2A	3457	1/1	0.97	0.34	-	57,57,57,57	0
56	MG	2A	3033	1/1	0.85	0.18	-	42,42,42,42	0
56	MG	2A	3257	1/1	0.94	0.19	-	65,65,65,65	0
56	MG	2A	3799	1/1	0.92	0.41	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1D	307	1/1	0.87	0.16	-	45,45,45,45	0
56	MG	2A	3227	1/1	0.88	0.18	-	57,57,57,57	0
56	MG	1A	4070	1/1	0.95	0.13	-	56,56,56,56	0
56	MG	2g	8001	1/1	0.85	0.12	-	75,75,75,75	0
56	MG	1A	3098	1/1	0.97	0.18	-	25,25,25,25	0
56	MG	1A	4095	1/1	0.70	0.17	-	67,67,67,67	0
56	MG	1A	3985	1/1	0.94	0.17	-	23,23,23,23	0
56	MG	1A	3976	1/1	0.72	0.14	-	72,72,72,72	0
56	MG	2A	3220	1/1	0.82	0.27	-	68,68,68,68	0
56	MG	2A	3234	1/1	0.88	0.14	-	52,52,52,52	0
56	MG	2A	3217	1/1	0.97	0.22	-	64,64,64,64	0
56	MG	2a	3223	1/1	0.97	0.16	-	52,52,52,52	0
56	MG	1a	1647	1/1	0.91	0.16	-	65,65,65,65	0
56	MG	2A	3744	1/1	0.93	0.15	-	55,55,55,55	0
56	MG	2A	3294	1/1	0.86	0.12	-	52,52,52,52	0
56	MG	1A	3586	1/1	0.91	0.22	-	49,49,49,49	0
56	MG	2a	3057	1/1	0.88	0.14	-	71,71,71,71	0
56	MG	1A	3679	1/1	0.86	0.25	-	39,39,39,39	0
56	MG	2a	3233	1/1	0.95	0.44	-	68,68,68,68	0
56	MG	2a	3055	1/1	0.92	0.07	-	51,51,51,51	0
56	MG	2A	3422	1/1	0.88	0.15	-	58,58,58,58	0
56	MG	1D	311	1/1	0.87	0.20	-	56,56,56,56	0
56	MG	2A	3306	1/1	0.94	0.12	-	58,58,58,58	0
56	MG	1A	3249	1/1	0.95	0.30	-	56,56,56,56	0
56	MG	1A	3712	1/1	0.97	0.08	-	40,40,40,40	0
56	MG	1A	3387	1/1	0.94	0.25	-	54,54,54,54	0
56	MG	1a	1770	1/1	0.96	0.10	-	60,60,60,60	0
56	MG	1x	111	1/1	0.96	0.12	-	66,66,66,66	0
56	MG	1A	3719	1/1	0.91	0.11	-	50,50,50,50	0
56	MG	1A	3335	1/1	0.88	0.36	-	62,62,62,62	0
56	MG	1A	3071	1/1	0.93	0.31	-	38,38,38,38	0
56	MG	1A	3568	1/1	0.92	0.26	-	50,50,50,50	0
56	MG	1A	3363	1/1	0.80	0.28	-	60,60,60,60	0
56	MG	2A	3155	1/1	0.91	0.12	-	59,59,59,59	0
56	MG	2A	3190	1/1	0.89	0.19	-	45,45,45,45	0
56	MG	2A	3106	1/1	0.97	0.09	-	59,59,59,59	0
56	MG	2a	3207	1/1	0.89	0.14	-	74,74,74,74	0
56	MG	2A	3006	1/1	0.90	0.23	-	56,56,56,56	0
56	MG	2A	3175	1/1	0.94	0.06	-	65,65,65,65	0
56	MG	1B	3004	1/1	0.91	0.29	-	50,50,50,50	0
56	MG	2A	3780	1/1	0.81	0.22	-	80,80,80,80	0
56	MG	1A	3409	1/1	0.96	0.23	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3102	1/1	0.99	0.04	-	56,56,56,56	0
56	MG	1A	3283	1/1	0.95	0.17	-	40,40,40,40	0
56	MG	1A	4009	1/1	0.97	0.21	-	27,27,27,27	0
56	MG	1a	1642	1/1	0.81	0.10	-	67,67,67,67	0
56	MG	1A	3454	1/1	0.93	0.20	-	59,59,59,59	0
56	MG	1A	3962	1/1	0.78	0.17	-	62,62,62,62	0
56	MG	2A	3228	1/1	0.96	0.18	-	65,65,65,65	0
56	MG	1A	3211	1/1	0.95	0.14	-	49,49,49,49	0
56	MG	1a	1782	1/1	0.71	0.17	-	79,79,79,79	0
56	MG	2a	3089	1/1	0.95	0.06	-	65,65,65,65	0
56	MG	2A	3212	1/1	0.87	0.13	-	52,52,52,52	0
56	MG	1A	4103	1/1	0.78	0.22	-	67,67,67,67	0
56	MG	1A	3490	1/1	0.93	0.11	-	50,50,50,50	0
56	MG	1a	1646	1/1	0.87	0.19	-	51,51,51,51	0
56	MG	2X	102	1/1	0.96	0.16	-	56,56,56,56	0
56	MG	1A	3611	1/1	0.98	0.23	-	25,25,25,25	0
56	MG	2A	3258	1/1	0.92	0.16	-	58,58,58,58	0
56	MG	1a	1705	1/1	0.92	0.18	-	63,63,63,63	0
56	MG	1A	3289	1/1	0.95	0.09	-	52,52,52,52	0
56	MG	1A	3736	1/1	0.96	0.15	-	46,46,46,46	0
56	MG	2a	3075	1/1	0.91	0.15	-	49,49,49,49	0
56	MG	2a	3162	1/1	0.96	0.08	-	62,62,62,62	0
56	MG	2A	3371	1/1	0.97	0.11	-	48,48,48,48	0
56	MG	2a	3134	1/1	0.96	0.15	-	64,64,64,64	0
56	MG	2a	3030	1/1	0.70	0.19	-	61,61,61,61	0
56	MG	2a	3026	1/1	0.66	0.17	-	64,64,64,64	0
56	MG	2A	3120	1/1	0.93	0.09	-	51,51,51,51	0
56	MG	2a	3166	1/1	0.58	0.13	-	84,84,84,84	0
56	MG	2A	3464	1/1	0.98	0.40	-	54,54,54,54	0
56	MG	1a	1694	1/1	0.88	0.11	-	58,58,58,58	0
56	MG	1A	3312	1/1	0.89	0.18	-	59,59,59,59	0
56	MG	1A	3827	1/1	0.95	0.25	-	50,50,50,50	0
56	MG	2A	3784	1/1	0.90	0.10	-	47,47,47,47	0
56	MG	1A	3786	1/1	0.18	0.32	-	81,81,81,81	0
56	MG	1A	3462	1/1	0.98	0.13	-	32,32,32,32	0
56	MG	1A	3502	1/1	0.94	0.26	-	49,49,49,49	0
56	MG	2a	3148	1/1	0.76	0.16	-	77,77,77,77	0
56	MG	2a	3126	1/1	0.90	0.09	-	69,69,69,69	0
56	MG	2A	3885	1/1	0.88	0.33	-	54,54,54,54	0
56	MG	2A	3875	1/1	0.88	0.50	-	76,76,76,76	0
56	MG	2A	3104	1/1	0.91	0.11	-	53,53,53,53	0
56	MG	2A	3275	1/1	0.83	0.19	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3408	1/1	0.88	0.19	-	60,60,60,60	0
56	MG	2a	3093	1/1	0.82	0.15	-	64,64,64,64	0
56	MG	2a	3054	1/1	0.91	0.14	-	65,65,65,65	0
56	MG	1A	3258	1/1	0.90	0.17	-	33,33,33,33	0
56	MG	2E	307	1/1	0.78	0.13	-	54,54,54,54	0
56	MG	1A	3777	1/1	0.95	0.13	-	55,55,55,55	0
56	MG	1A	3337	1/1	0.89	0.30	-	48,48,48,48	0
56	MG	20	3002	1/1	0.98	0.07	-	63,63,63,63	0
56	MG	1A	4046	1/1	0.95	0.13	-	30,30,30,30	0
56	MG	1S	3003	1/1	0.94	0.13	-	59,59,59,59	0
56	MG	2A	3357	1/1	0.98	0.10	-	39,39,39,39	0
56	MG	1A	3879	1/1	0.77	0.16	-	51,51,51,51	0
56	MG	2A	3751	1/1	0.94	0.12	-	61,61,61,61	0
56	MG	2A	3543	1/1	0.85	0.14	-	34,34,34,34	0
56	MG	2A	3337	1/1	0.90	0.09	-	47,47,47,47	0
56	MG	2A	3264	1/1	0.95	0.10	-	62,62,62,62	0
56	MG	2A	3318	1/1	0.93	0.15	-	48,48,48,48	0
56	MG	2A	3770	1/1	0.86	0.13	-	57,57,57,57	0
56	MG	2A	3247	1/1	0.84	0.12	-	51,51,51,51	0
56	MG	1a	1755	1/1	0.79	0.12	-	74,74,74,74	0
56	MG	1a	1750	1/1	0.94	0.10	-	85,85,85,85	0
56	MG	1A	3430	1/1	0.95	0.10	-	47,47,47,47	0
56	MG	1a	1640	1/1	0.95	0.05	-	58,58,58,58	0
56	MG	1A	3645	1/1	0.87	0.21	-	37,37,37,37	0
56	MG	1F	305	1/1	0.91	0.22	-	48,48,48,48	0
56	MG	2a	3109	1/1	0.92	0.20	-	67,67,67,67	0
56	MG	2A	3342	1/1	0.62	0.21	-	59,59,59,59	0
56	MG	2a	3242	1/1	0.95	0.20	-	55,55,55,55	0
56	MG	2A	3655	1/1	0.96	0.12	-	65,65,65,65	0
56	MG	2A	3272	1/1	0.89	0.18	-	51,51,51,51	0
56	MG	2A	3278	1/1	0.93	0.18	-	57,57,57,57	0
56	MG	2A	3431	1/1	0.92	0.14	-	62,62,62,62	0
56	MG	2A	3658	1/1	0.96	0.13	-	55,55,55,55	0
56	MG	2w	103	1/1	0.97	0.10	-	56,56,56,56	0
56	MG	1A	3520	1/1	0.97	0.25	-	41,41,41,41	0
56	MG	2a	3188	1/1	0.91	0.12	-	68,68,68,68	0
56	MG	1A	4030	1/1	0.93	0.12	-	44,44,44,44	0
56	MG	1A	4034	1/1	0.93	0.08	-	51,51,51,51	0
56	MG	2a	3078	1/1	0.91	0.27	-	74,74,74,74	0
56	MG	1a	1812	1/1	0.88	0.07	-	70,70,70,70	0
56	MG	1a	1748	1/1	0.97	0.11	-	43,43,43,43	0
56	MG	1A	3723	1/1	0.82	0.11	-	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3330	1/1	0.88	0.28	-	50,50,50,50	0
56	MG	2w	106	1/1	0.93	0.12	-	60,60,60,60	0
56	MG	1A	3474	1/1	0.86	0.30	-	60,60,60,60	0
56	MG	2y	3004	1/1	0.93	0.19	-	59,59,59,59	0
56	MG	1A	3932	1/1	0.95	0.19	-	45,45,45,45	0
56	MG	2A	3394	1/1	0.89	0.32	-	50,50,50,50	0
56	MG	1A	3192	1/1	0.90	0.19	-	52,52,52,52	0
56	MG	2A	3763	1/1	0.94	0.12	-	52,52,52,52	0
56	MG	2A	3794	1/1	0.93	0.09	-	67,67,67,67	0
56	MG	1A	3749	1/1	0.94	0.15	-	41,41,41,41	0
56	MG	2A	3018	1/1	0.90	0.24	-	44,44,44,44	0
56	MG	1A	3618	1/1	0.96	0.07	-	56,56,56,56	0
56	MG	1A	3798	1/1	0.86	0.09	-	63,63,63,63	0
56	MG	1A	3410	1/1	0.92	0.07	-	57,57,57,57	0
56	MG	1A	3368	1/1	0.93	0.29	-	47,47,47,47	0
56	MG	1A	3497	1/1	0.90	0.20	-	33,33,33,33	0
56	MG	2A	3400	1/1	0.92	0.25	-	56,56,56,56	0
56	MG	2A	3424	1/1	0.90	0.19	-	50,50,50,50	0
56	MG	1A	3324	1/1	0.89	0.25	-	55,55,55,55	0
56	MG	1A	3662	1/1	0.96	0.14	-	30,30,30,30	0
56	MG	1A	3297	1/1	0.98	0.29	-	32,32,32,32	0
56	MG	2A	3625	1/1	0.92	0.14	-	69,69,69,69	0
56	MG	1a	1686	1/1	0.88	0.09	-	54,54,54,54	0
56	MG	2A	3072	1/1	0.93	0.10	-	46,46,46,46	0
56	MG	2a	3138	1/1	0.76	0.24	-	79,79,79,79	0
56	MG	2A	3729	1/1	0.95	0.12	-	41,41,41,41	0
56	MG	1A	3344	1/1	0.81	0.27	-	64,64,64,64	0
56	MG	2a	3068	1/1	0.91	0.16	-	72,72,72,72	0
56	MG	2a	3178	1/1	0.84	0.22	-	75,75,75,75	0
56	MG	2A	3566	1/1	0.98	0.14	-	33,33,33,33	0
56	MG	10	106	1/1	0.87	0.16	-	65,65,65,65	0
56	MG	2A	3010	1/1	0.89	0.19	-	51,51,51,51	0
56	MG	1A	3556	1/1	0.97	0.33	-	42,42,42,42	0
56	MG	1A	3084	1/1	0.96	0.15	-	34,34,34,34	0
56	MG	1A	3227	1/1	0.88	0.29	-	42,42,42,42	0
56	MG	1a	1809	1/1	0.90	0.08	-	56,56,56,56	0
56	MG	1A	3392	1/1	0.87	0.27	-	56,56,56,56	0
56	MG	2A	3725	1/1	0.97	0.11	-	49,49,49,49	0
56	MG	1A	3092	1/1	0.94	0.21	-	50,50,50,50	0
56	MG	1A	3987	1/1	0.90	0.17	-	32,32,32,32	0
56	MG	2a	3064	1/1	0.90	0.10	-	81,81,81,81	0
56	MG	1A	3117	1/1	0.96	0.38	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	3206	1/1	0.92	0.17	-	69,69,69,69	0
56	MG	1A	3317	1/1	0.94	0.17	-	47,47,47,47	0
56	MG	2A	3311	1/1	0.92	0.12	-	63,63,63,63	0
56	MG	1A	4082	1/1	0.95	0.25	-	38,38,38,38	0
56	MG	2A	3124	1/1	0.94	0.10	-	48,48,48,48	0
56	MG	1A	3348	1/1	0.81	0.19	-	62,62,62,62	0
56	MG	2A	3189	1/1	0.89	0.11	-	52,52,52,52	0
56	MG	1A	3372	1/1	0.87	0.24	-	58,58,58,58	0
56	MG	2A	3495	1/1	0.94	0.15	-	51,51,51,51	0
56	MG	1A	3734	1/1	0.85	0.13	-	59,59,59,59	0
56	MG	2A	3387	1/1	0.87	0.20	-	59,59,59,59	0
56	MG	2A	3069	1/1	0.93	0.15	-	40,40,40,40	0
56	MG	2A	3509	1/1	0.96	0.16	-	38,38,38,38	0
56	MG	2A	3750	1/1	0.96	0.26	-	47,47,47,47	0
56	MG	1A	3238	1/1	0.79	0.17	-	57,57,57,57	0
56	MG	2A	3667	1/1	0.81	0.12	-	49,49,49,49	0
56	MG	1a	1693	1/1	0.93	0.08	-	58,58,58,58	0
56	MG	2A	3208	1/1	0.83	0.14	-	57,57,57,57	0
56	MG	2A	3008	1/1	0.86	0.14	-	49,49,49,49	0
56	MG	2A	3413	1/1	0.80	0.17	-	56,56,56,56	0
56	MG	1A	3814	1/1	0.98	0.17	-	45,45,45,45	0
56	MG	1A	3511	1/1	0.86	0.16	-	45,45,45,45	0
56	MG	1A	3826	1/1	0.95	0.14	-	42,42,42,42	0
56	MG	1A	3027	1/1	0.99	0.20	-	33,33,33,33	0
56	MG	1A	3660	1/1	0.89	0.25	-	31,31,31,31	0
56	MG	2w	108	1/1	0.76	0.15	-	66,66,66,66	0
56	MG	1A	3424	1/1	0.92	0.33	-	70,70,70,70	0
56	MG	1A	3510	1/1	0.94	0.11	-	45,45,45,45	0
56	MG	1a	1702	1/1	0.67	0.28	-	73,73,73,73	0
56	MG	1A	3609	1/1	0.89	0.14	-	50,50,50,50	0
56	MG	1w	109	1/1	0.91	0.10	-	67,67,67,67	0
56	MG	1A	3600	1/1	0.90	0.13	-	46,46,46,46	0
56	MG	2B	3007	1/1	0.94	0.25	-	55,55,55,55	0
56	MG	1B	3009	1/1	0.91	0.16	-	43,43,43,43	0
56	MG	2A	3872	1/1	0.62	0.07	-	44,44,44,44	0
56	MG	2A	3612	1/1	0.93	0.07	-	39,39,39,39	0
56	MG	2a	3008	1/1	0.92	0.26	-	68,68,68,68	0
56	MG	1A	3445	1/1	0.77	0.18	-	62,62,62,62	0
56	MG	1A	3296	1/1	0.98	0.25	-	58,58,58,58	0
56	MG	1A	4049	1/1	0.80	0.13	-	55,55,55,55	0
56	MG	2a	3176	1/1	0.88	0.11	-	62,62,62,62	0
56	MG	2A	3700	1/1	0.83	0.19	-	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1739	1/1	0.97	0.05	-	36,36,36,36	0
56	MG	1A	3732	1/1	0.94	0.23	-	64,64,64,64	0
56	MG	1A	3795	1/1	0.73	0.23	-	51,51,51,51	0
56	MG	13	102	1/1	0.90	0.24	-	53,53,53,53	0
56	MG	1A	3204	1/1	0.95	0.27	-	26,26,26,26	0
56	MG	1a	1676	1/1	0.74	0.18	-	67,67,67,67	0
56	MG	18	102	1/1	0.95	0.30	-	50,50,50,50	0
56	MG	2B	3018	1/1	0.94	0.18	-	65,65,65,65	0
56	MG	1A	3835	1/1	0.91	0.18	-	59,59,59,59	0
56	MG	1A	4134	1/1	0.92	0.32	-	46,46,46,46	0
56	MG	1A	4021	1/1	0.79	0.23	-	66,66,66,66	0
56	MG	1A	4131	1/1	0.93	0.19	-	58,58,58,58	0
56	MG	1A	3503	1/1	0.94	0.17	-	32,32,32,32	0
56	MG	1A	3293	1/1	0.96	0.25	-	50,50,50,50	0
56	MG	1A	3928	1/1	0.95	0.20	-	31,31,31,31	0
56	MG	2y	3003	1/1	0.95	0.11	-	70,70,70,70	0
56	MG	1A	3220	1/1	0.97	0.23	-	41,41,41,41	0
56	MG	2A	3494	1/1	0.96	0.27	-	50,50,50,50	0
56	MG	2A	3352	1/1	0.99	0.14	-	53,53,53,53	0
56	MG	2A	3137	1/1	0.95	0.09	-	42,42,42,42	0
56	MG	1A	3369	1/1	0.98	0.19	-	57,57,57,57	0
56	MG	1A	3050	1/1	0.98	0.28	-	32,32,32,32	0
56	MG	2A	3453	1/1	0.65	0.15	-	45,45,45,45	0
56	MG	1A	3875	1/1	0.27	0.24	-	60,60,60,60	0
56	MG	1A	3282	1/1	0.94	0.17	-	30,30,30,30	0
56	MG	1A	3003	1/1	0.98	0.15	-	27,27,27,27	0
56	MG	1A	3048	1/1	0.96	0.20	-	48,48,48,48	0
56	MG	2A	3820	1/1	0.98	0.07	-	49,49,49,49	0
56	MG	2A	3133	1/1	0.95	0.11	-	49,49,49,49	0
56	MG	1a	1602	1/1	0.95	0.10	-	72,72,72,72	0
56	MG	1A	3431	1/1	0.91	0.13	-	52,52,52,52	0
56	MG	1a	1621	1/1	0.94	0.15	-	42,42,42,42	0
56	MG	2A	3491	1/1	0.95	0.30	-	55,55,55,55	0
56	MG	1A	3633	1/1	0.98	0.16	-	58,58,58,58	0
56	MG	2A	3537	1/1	0.96	0.12	-	35,35,35,35	0
56	MG	1A	3958	1/1	0.94	0.10	-	44,44,44,44	0
56	MG	1A	3513	1/1	0.73	0.16	-	62,62,62,62	0
56	MG	1A	3316	1/1	0.91	0.19	-	58,58,58,58	0
56	MG	1a	1663	1/1	0.81	0.15	-	76,76,76,76	0
56	MG	1x	114	1/1	0.87	0.10	-	82,82,82,82	0
56	MG	1A	3341	1/1	0.93	0.30	-	55,55,55,55	0
56	MG	1A	3802	1/1	0.90	0.13	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3747	1/1	0.84	0.21	-	53,53,53,53	0
56	MG	1A	4125	1/1	0.92	0.34	-	54,54,54,54	0
56	MG	2a	3123	1/1	0.96	0.10	-	54,54,54,54	0
56	MG	2a	3239	1/1	0.92	0.14	-	65,65,65,65	0
56	MG	2a	3065	1/1	0.85	0.24	-	57,57,57,57	0
56	MG	2a	3104	1/1	0.74	0.19	-	75,75,75,75	0
56	MG	1A	4017	1/1	0.97	0.20	-	36,36,36,36	0
56	MG	2A	3285	1/1	0.93	0.12	-	49,49,49,49	0
56	MG	1A	3540	1/1	0.85	0.29	-	52,52,52,52	0
56	MG	2a	3235	1/1	0.93	0.06	-	71,71,71,71	0
56	MG	1A	4018	1/1	0.89	0.15	-	67,67,67,67	0
56	MG	1A	3197	1/1	0.98	0.19	-	52,52,52,52	0
56	MG	2A	3544	1/1	0.85	0.12	-	42,42,42,42	0
56	MG	1a	1636	1/1	0.81	0.21	-	67,67,67,67	0
56	MG	1A	3099	1/1	0.91	0.13	-	44,44,44,44	0
56	MG	1A	3259	1/1	0.90	0.16	-	40,40,40,40	0
56	MG	1P	201	1/1	0.96	0.13	-	26,26,26,26	0
56	MG	2A	3536	1/1	0.88	0.14	-	51,51,51,51	0
56	MG	1A	3674	1/1	0.90	0.16	-	39,39,39,39	0
56	MG	2a	3174	1/1	0.88	0.35	-	69,69,69,69	0
56	MG	1A	4135	1/1	0.90	0.23	-	44,44,44,44	0
56	MG	1A	3305	1/1	0.91	0.33	-	55,55,55,55	0
56	MG	2A	3317	1/1	0.88	0.13	-	55,55,55,55	0
56	MG	1I	3001	1/1	0.89	0.11	-	70,70,70,70	0
56	MG	1a	1623	1/1	0.92	0.14	-	60,60,60,60	0
56	MG	2a	3158	1/1	0.90	0.12	-	52,52,52,52	0
56	MG	1a	1732	1/1	0.96	0.16	-	48,48,48,48	0
56	MG	2A	3598	1/1	0.96	0.15	-	48,48,48,48	0
56	MG	1a	1610	1/1	0.84	0.46	-	79,79,79,79	0
56	MG	1A	3936	1/1	0.94	0.11	-	31,31,31,31	0
56	MG	1A	3067	1/1	0.98	0.18	-	51,51,51,51	0
56	MG	1A	3434	1/1	0.94	0.14	-	48,48,48,48	0
56	MG	1a	1695	1/1	0.95	0.15	-	68,68,68,68	0
56	MG	1A	3191	1/1	0.93	0.20	-	42,42,42,42	0
56	MG	1A	4036	1/1	0.91	0.08	-	43,43,43,43	0
56	MG	1A	4057	1/1	0.96	0.19	-	40,40,40,40	0
56	MG	1A	3853	1/1	0.79	0.10	-	52,52,52,52	0
56	MG	1A	3156	1/1	0.96	0.22	-	40,40,40,40	0
56	MG	1A	3564	1/1	0.90	0.19	-	40,40,40,40	0
56	MG	1A	3019	1/1	0.91	0.22	-	37,37,37,37	0
56	MG	2B	3012	1/1	0.96	0.23	-	55,55,55,55	0
56	MG	1A	3374	1/1	0.94	0.15	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3773	1/1	0.93	0.05	-	63,63,63,63	0
56	MG	2A	3313	1/1	0.88	0.22	-	64,64,64,64	0
56	MG	2A	3101	1/1	0.79	0.15	-	59,59,59,59	0
56	MG	2A	3379	1/1	0.95	0.21	-	53,53,53,53	0
56	MG	2A	3589	1/1	0.91	0.09	-	45,45,45,45	0
56	MG	1A	3332	1/1	0.83	0.32	-	56,56,56,56	0
56	MG	1A	3375	1/1	0.97	0.18	-	43,43,43,43	0
56	MG	1A	3085	1/1	0.99	0.26	-	30,30,30,30	0
56	MG	1a	1749	1/1	0.93	0.15	-	45,45,45,45	0
56	MG	1A	3993	1/1	0.95	0.14	-	37,37,37,37	0
56	MG	1Z	302	1/1	0.78	0.16	-	67,67,67,67	0
56	MG	2a	3036	1/1	0.85	0.18	-	83,83,83,83	0
56	MG	2A	3314	1/1	0.87	0.18	-	47,47,47,47	0
56	MG	1W	201	1/1	0.77	0.38	-	57,57,57,57	0
56	MG	2A	3323	1/1	0.90	0.13	-	56,56,56,56	0
56	MG	2A	3611	1/1	0.97	0.16	-	62,62,62,62	0
56	MG	1A	3973	1/1	0.90	0.10	-	85,85,85,85	0
56	MG	1A	3157	1/1	0.90	0.19	-	53,53,53,53	0
56	MG	1A	4092	1/1	0.94	0.22	-	37,37,37,37	0
56	MG	2A	3663	1/1	0.95	0.05	-	64,64,64,64	0
56	MG	2a	3127	1/1	0.66	0.15	-	85,85,85,85	0
56	MG	1A	3214	1/1	0.94	0.09	-	42,42,42,42	0
56	MG	2A	3154	1/1	0.98	0.14	-	48,48,48,48	0
56	MG	2A	3237	1/1	0.98	0.15	-	39,39,39,39	0
56	MG	1A	3625	1/1	0.97	0.17	-	19,19,19,19	0
56	MG	1A	3665	1/1	0.91	0.10	-	60,60,60,60	0
56	MG	1A	3138	1/1	0.96	0.23	-	36,36,36,36	0
56	MG	1A	4020	1/1	0.91	0.11	-	53,53,53,53	0
56	MG	2A	3531	1/1	0.86	0.23	-	51,51,51,51	0
56	MG	1A	3004	1/1	0.94	0.19	-	34,34,34,34	0
56	MG	2A	3644	1/1	0.86	0.21	-	64,64,64,64	0
56	MG	1A	4014	1/1	0.95	0.08	-	34,34,34,34	0
56	MG	2A	3336	1/1	0.97	0.18	-	53,53,53,53	0
56	MG	1a	1808	1/1	0.91	0.09	-	53,53,53,53	0
56	MG	2A	3270	1/1	0.94	0.10	-	53,53,53,53	0
56	MG	1Y	502	1/1	0.85	0.22	-	59,59,59,59	0
56	MG	2a	3137	1/1	0.71	0.18	-	79,79,79,79	0
56	MG	1A	3250	1/1	0.86	0.21	-	49,49,49,49	0
56	MG	2a	3085	1/1	0.94	0.11	-	65,65,65,65	0
56	MG	2a	3129	1/1	0.89	0.10	-	59,59,59,59	0
56	MG	1A	3491	1/1	0.88	0.15	-	59,59,59,59	0
56	MG	2A	3553	1/1	0.90	0.14	-	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3102	1/1	0.94	0.17	-	54,54,54,54	0
56	MG	2F	301	1/1	0.88	0.18	-	58,58,58,58	0
56	MG	1a	1698	1/1	0.91	0.07	-	52,52,52,52	0
56	MG	2A	3777	1/1	0.89	0.15	-	41,41,41,41	0
56	MG	1A	3783	1/1	0.87	0.22	-	34,34,34,34	0
56	MG	1A	3291	1/1	0.92	0.13	-	59,59,59,59	0
56	MG	1a	1680	1/1	0.88	0.09	-	64,64,64,64	0
56	MG	2A	3132	1/1	0.94	0.22	-	56,56,56,56	0
56	MG	1a	1661	1/1	0.81	0.14	-	70,70,70,70	0
56	MG	2A	3107	1/1	0.94	0.10	-	46,46,46,46	0
56	MG	1a	1635	1/1	0.62	0.13	-	75,75,75,75	0
56	MG	1A	3262	1/1	0.91	0.14	-	49,49,49,49	0
56	MG	1A	3064	1/1	0.97	0.20	-	53,53,53,53	0
56	MG	2A	3586	1/1	0.97	0.09	-	53,53,53,53	0
56	MG	2A	3365	1/1	0.88	0.11	-	56,56,56,56	0
56	MG	2A	3466	1/1	0.71	0.37	-	65,65,65,65	0
56	MG	1A	3844	1/1	0.95	0.17	-	54,54,54,54	0
56	MG	1A	4073	1/1	0.86	0.10	-	42,42,42,42	0
56	MG	2E	302	1/1	0.96	0.09	-	52,52,52,52	0
56	MG	2A	3315	1/1	0.89	0.22	-	54,54,54,54	0
56	MG	2A	3115	1/1	0.97	0.10	-	51,51,51,51	0
56	MG	2A	3406	1/1	0.74	0.27	-	55,55,55,55	0
56	MG	2A	3050	1/1	0.84	0.10	-	51,51,51,51	0
56	MG	2A	3296	1/1	0.97	0.20	-	45,45,45,45	0
56	MG	2A	3150	1/1	0.98	0.35	-	39,39,39,39	0
56	MG	2a	3063	1/1	0.66	0.15	-	74,74,74,74	0
56	MG	1A	3270	1/1	0.93	0.25	-	59,59,59,59	0
56	MG	1A	3340	1/1	0.92	0.27	-	58,58,58,58	0
56	MG	2A	3582	1/1	0.97	0.11	-	51,51,51,51	0
56	MG	2a	3056	1/1	0.84	0.14	-	63,63,63,63	0
56	MG	2A	3330	1/1	0.82	0.14	-	63,63,63,63	0
56	MG	1A	4069	1/1	0.92	0.12	-	42,42,42,42	0
56	MG	2a	3215	1/1	0.77	0.19	-	71,71,71,71	0
56	MG	1a	1793	1/1	0.95	0.25	-	82,82,82,82	0
56	MG	2A	3081	1/1	0.91	0.22	-	45,45,45,45	0
56	MG	1A	3256	1/1	0.95	0.10	-	57,57,57,57	0
56	MG	2A	3223	1/1	0.96	0.19	-	44,44,44,44	0
56	MG	1A	3244	1/1	0.93	0.21	-	49,49,49,49	0
56	MG	1a	1637	1/1	0.93	0.19	-	68,68,68,68	0
56	MG	1A	3261	1/1	0.79	0.25	-	55,55,55,55	0
56	MG	1A	3180	1/1	0.92	0.21	-	36,36,36,36	0
56	MG	2A	3719	1/1	0.93	0.20	-	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3567	1/1	0.85	0.08	-	54,54,54,54	0
56	MG	1F	307	1/1	0.95	0.13	-	50,50,50,50	0
56	MG	1A	3899	1/1	0.96	0.16	-	52,52,52,52	0
56	MG	1a	1735	1/1	0.91	0.18	-	57,57,57,57	0
56	MG	1A	3949	1/1	0.63	0.13	-	63,63,63,63	0
56	MG	1A	3523	1/1	0.92	0.26	-	44,44,44,44	0
56	MG	2A	3781	1/1	0.87	0.10	-	55,55,55,55	0
56	MG	1A	3081	1/1	0.95	0.18	-	34,34,34,34	0
56	MG	1A	3869	1/1	0.77	0.20	-	56,56,56,56	0
56	MG	2A	3017	1/1	0.92	0.24	-	52,52,52,52	0
56	MG	1A	3320	1/1	0.91	0.23	-	60,60,60,60	0
56	MG	1A	3438	1/1	0.84	0.21	-	50,50,50,50	0
56	MG	1B	3029	1/1	0.70	0.28	-	66,66,66,66	0
56	MG	1a	1788	1/1	0.65	0.10	-	69,69,69,69	0
56	MG	2i	8001	1/1	0.97	0.12	-	51,51,51,51	0
56	MG	1A	3425	1/1	0.88	0.17	-	55,55,55,55	0
56	MG	1A	3590	1/1	0.88	0.21	-	37,37,37,37	0
56	MG	1A	3175	1/1	0.96	0.21	-	40,40,40,40	0
56	MG	1A	3804	1/1	0.97	0.10	-	40,40,40,40	0
56	MG	2A	3243	1/1	0.87	0.10	-	52,52,52,52	0
56	MG	2A	3375	1/1	0.74	0.25	-	52,52,52,52	0
56	MG	1A	3531	1/1	0.82	0.16	-	67,67,67,67	0
56	MG	2a	3218	1/1	0.92	0.20	-	61,61,61,61	0
56	MG	2A	3403	1/1	0.84	0.18	-	60,60,60,60	0
56	MG	2a	3011	1/1	0.80	0.11	-	64,64,64,64	0
56	MG	1A	3671	1/1	0.62	0.27	-	67,67,67,67	0
56	MG	2A	3304	1/1	0.89	0.17	-	60,60,60,60	0
56	MG	2T	3003	1/1	0.92	0.13	-	63,63,63,63	0
56	MG	1A	3077	1/1	0.94	0.09	-	35,35,35,35	0
56	MG	1A	3299	1/1	0.90	0.20	-	61,61,61,61	0
56	MG	2A	3042	1/1	0.93	0.22	-	42,42,42,42	0
56	MG	1A	4050	1/1	0.98	0.23	-	32,32,32,32	0
56	MG	1i	101	1/1	0.93	0.13	-	38,38,38,38	0
56	MG	1a	1706	1/1	0.85	0.20	-	60,60,60,60	0
56	MG	2A	3255	1/1	0.88	0.15	-	59,59,59,59	0
56	MG	1a	1828	1/1	0.88	0.08	-	59,59,59,59	0
56	MG	1A	3889	1/1	0.91	0.25	-	60,60,60,60	0
56	MG	1G	3005	1/1	0.96	0.10	-	66,66,66,66	0
56	MG	1B	3020	1/1	0.91	0.22	-	82,82,82,82	0
56	MG	2A	3593	1/1	0.94	0.16	-	30,30,30,30	0
56	MG	1A	3990	1/1	0.78	0.16	-	52,52,52,52	0
56	MG	1a	1727	1/1	0.95	0.16	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3871	1/1	-0.25	0.20	-	70,70,70,70	0
56	MG	2a	3100	1/1	0.93	0.06	-	69,69,69,69	0
56	MG	1A	3119	1/1	0.95	0.25	-	51,51,51,51	0
56	MG	2A	3867	1/1	0.69	0.11	-	64,64,64,64	0
56	MG	1a	1630	1/1	0.89	0.13	-	60,60,60,60	0
56	MG	1A	3133	1/1	0.94	0.19	-	44,44,44,44	0
56	MG	2A	3833	1/1	0.92	0.14	-	55,55,55,55	0
56	MG	2A	3835	1/1	0.96	0.09	-	43,43,43,43	0
56	MG	1A	3773	1/1	0.96	0.07	-	41,41,41,41	0
56	MG	2a	3213	1/1	0.92	0.18	-	69,69,69,69	0
56	MG	1a	1675	1/1	0.82	0.13	-	60,60,60,60	0
56	MG	2a	3018	1/1	0.93	0.18	-	65,65,65,65	0
56	MG	2A	3661	1/1	0.87	0.20	-	56,56,56,56	0
56	MG	1A	3473	1/1	0.92	0.26	-	50,50,50,50	0
56	MG	2A	3649	1/1	0.95	0.09	-	69,69,69,69	0
56	MG	1A	3399	1/1	0.90	0.22	-	52,52,52,52	0
56	MG	1A	3858	1/1	0.89	0.13	-	30,30,30,30	0
56	MG	1A	3697	1/1	0.91	0.14	-	51,51,51,51	0
56	MG	2A	3123	1/1	0.92	0.10	-	56,56,56,56	0
56	MG	1O	201	1/1	0.96	0.11	-	63,63,63,63	0
56	MG	2A	3367	1/1	0.87	0.18	-	61,61,61,61	0
56	MG	2a	3110	1/1	0.88	0.08	-	73,73,73,73	0
56	MG	2A	3752	1/1	0.90	0.14	-	61,61,61,61	0
56	MG	2A	3850	1/1	0.60	0.10	-	59,59,59,59	0
56	MG	2A	3170	1/1	0.98	0.14	-	54,54,54,54	0
56	MG	2A	3288	1/1	0.94	0.11	-	49,49,49,49	0
56	MG	1A	3726	1/1	0.95	0.06	-	48,48,48,48	0
56	MG	2A	3043	1/1	0.94	0.12	-	53,53,53,53	0
56	MG	1A	3025	1/1	0.98	0.17	-	41,41,41,41	0
56	MG	1A	3442	1/1	0.94	0.27	-	56,56,56,56	0
56	MG	1a	1643	1/1	0.82	0.17	-	61,61,61,61	0
56	MG	1A	3342	1/1	0.90	0.25	-	57,57,57,57	0
56	MG	1A	3199	1/1	0.93	0.19	-	45,45,45,45	0
56	MG	2A	3199	1/1	0.98	0.18	-	50,50,50,50	0
56	MG	1A	3427	1/1	0.95	0.14	-	44,44,44,44	0
56	MG	1a	1616	1/1	0.96	0.12	-	55,55,55,55	0
56	MG	2a	3201	1/1	0.72	0.13	-	79,79,79,79	0
56	MG	1a	1824	1/1	0.89	0.13	-	73,73,73,73	0
56	MG	2A	3831	1/1	0.95	0.10	-	45,45,45,45	0
56	MG	1A	3864	1/1	0.97	0.15	-	35,35,35,35	0
56	MG	2A	3143	1/1	0.94	0.12	-	56,56,56,56	0
56	MG	2A	3411	1/1	0.93	0.17	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3574	1/1	0.87	0.12	-	44,44,44,44	0
56	MG	1A	3759	1/1	0.94	0.18	-	24,24,24,24	0
56	MG	1a	1669	1/1	0.88	0.23	-	73,73,73,73	0
56	MG	2A	3091	1/1	0.63	0.14	-	60,60,60,60	0
56	MG	1x	104	1/1	0.78	0.18	-	72,72,72,72	0
56	MG	2A	3028	1/1	0.87	0.14	-	54,54,54,54	0
56	MG	1A	3561	1/1	0.91	0.31	-	48,48,48,48	0
56	MG	1A	3825	1/1	0.90	0.12	-	57,57,57,57	0
56	MG	2A	3436	1/1	0.96	0.17	-	49,49,49,49	0
56	MG	1A	3841	1/1	0.98	0.15	-	27,27,27,27	0
56	MG	2a	3048	1/1	0.85	0.13	-	67,67,67,67	0
56	MG	1y	3004	1/1	0.58	0.15	-	86,86,86,86	0
56	MG	1A	3386	1/1	0.87	0.21	-	54,54,54,54	0
56	MG	1A	3420	1/1	0.90	0.26	-	55,55,55,55	0
56	MG	2A	3139	1/1	0.93	0.14	-	32,32,32,32	0
56	MG	1A	3486	1/1	0.94	0.19	-	42,42,42,42	0
56	MG	1S	3002	1/1	0.93	0.17	-	49,49,49,49	0
56	MG	2A	3236	1/1	0.94	0.07	-	53,53,53,53	0
56	MG	1A	3450	1/1	0.90	0.19	-	57,57,57,57	0
56	MG	2A	3828	1/1	0.81	0.13	-	80,80,80,80	0
56	MG	2a	3053	1/1	0.90	0.09	-	66,66,66,66	0
56	MG	1A	3505	1/1	0.89	0.14	-	47,47,47,47	0
56	MG	1A	3708	1/1	0.79	0.16	-	76,76,76,76	0
56	MG	2a	3035	1/1	0.84	0.12	-	63,63,63,63	0
56	MG	1A	3549	1/1	0.97	0.13	-	38,38,38,38	0
56	MG	1Y	503	1/1	0.92	0.15	-	78,78,78,78	0
56	MG	2A	3609	1/1	0.98	0.16	-	42,42,42,42	0
56	MG	1A	3212	1/1	0.98	0.37	-	32,32,32,32	0
56	MG	2A	3390	1/1	0.93	0.14	-	57,57,57,57	0
56	MG	2A	3503	1/1	0.85	0.13	-	58,58,58,58	0
56	MG	2A	3308	1/1	0.85	0.11	-	49,49,49,49	0
56	MG	1A	3714	1/1	0.94	0.18	-	46,46,46,46	0
56	MG	1A	3164	1/1	0.85	0.18	-	73,73,73,73	0
56	MG	2B	3015	1/1	0.98	0.19	-	50,50,50,50	0
56	MG	2A	3405	1/1	0.96	0.24	-	33,33,33,33	0
56	MG	2A	3813	1/1	0.78	0.11	-	48,48,48,48	0
56	MG	1a	1711	1/1	0.95	0.17	-	65,65,65,65	0
56	MG	1A	3850	1/1	0.94	0.18	-	53,53,53,53	0
56	MG	1E	307	1/1	0.85	0.19	-	70,70,70,70	0
56	MG	2A	3456	1/1	0.96	0.36	-	60,60,60,60	0
56	MG	1A	3818	1/1	0.92	0.18	-	57,57,57,57	0
56	MG	1a	1688	1/1	0.60	0.16	-	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3245	1/1	0.85	0.37	-	59,59,59,59	0
56	MG	2A	3059	1/1	0.98	0.17	-	46,46,46,46	0
56	MG	1A	3429	1/1	0.89	0.15	-	48,48,48,48	0
56	MG	1w	106	1/1	0.81	0.18	-	74,74,74,74	0
56	MG	1A	3867	1/1	0.89	0.13	-	69,69,69,69	0
56	MG	2A	3383	1/1	0.91	0.16	-	60,60,60,60	0
56	MG	1A	3168	1/1	0.97	0.14	-	42,42,42,42	0
56	MG	2v	3001	1/1	0.95	0.09	-	69,69,69,69	0
56	MG	1A	3860	1/1	0.98	0.18	-	47,47,47,47	0
56	MG	2A	3480	1/1	0.90	0.21	-	65,65,65,65	0
56	MG	1A	3572	1/1	0.90	0.12	-	55,55,55,55	0
56	MG	1A	4113	1/1	0.83	0.24	-	56,56,56,56	0
56	MG	2A	3599	1/1	0.93	0.18	-	51,51,51,51	0
56	MG	2A	3487	1/1	0.93	0.23	-	62,62,62,62	0
56	MG	1A	3321	1/1	0.94	0.34	-	51,51,51,51	0
56	MG	1A	3591	1/1	0.88	0.13	-	52,52,52,52	0
56	MG	2A	3507	1/1	0.89	0.14	-	64,64,64,64	0
56	MG	2A	3467	1/1	0.97	0.09	-	60,60,60,60	0
56	MG	2y	3006	1/1	0.88	0.07	-	86,86,86,86	0
56	MG	2A	3303	1/1	0.89	0.16	-	60,60,60,60	0
56	MG	2A	3114	1/1	0.97	0.18	-	55,55,55,55	0
56	MG	2a	3001	1/1	0.91	0.22	-	57,57,57,57	0
56	MG	1a	1682	1/1	0.92	0.27	-	66,66,66,66	0
56	MG	2A	3301	1/1	0.88	0.11	-	60,60,60,60	0
56	MG	1A	3154	1/1	0.87	0.55	-	51,51,51,51	0
56	MG	1A	3897	1/1	0.79	0.24	-	62,62,62,62	0
56	MG	2A	3086	1/1	0.95	0.21	-	44,44,44,44	0
56	MG	1A	3141	1/1	0.94	0.16	-	35,35,35,35	0
56	MG	1A	3604	1/1	0.92	0.14	-	65,65,65,65	0
56	MG	2a	3020	1/1	0.84	0.13	-	71,71,71,71	0
56	MG	2A	3225	1/1	0.88	0.13	-	62,62,62,62	0
56	MG	1A	3838	1/1	0.95	0.25	-	45,45,45,45	0
56	MG	2A	3074	1/1	0.74	0.11	-	73,73,73,73	0
56	MG	1a	1821	1/1	0.86	0.09	-	62,62,62,62	0
56	MG	2A	3164	1/1	0.97	0.25	-	53,53,53,53	0
56	MG	1a	1700	1/1	0.99	0.26	-	50,50,50,50	0
56	MG	1A	3687	1/1	0.95	0.18	-	31,31,31,31	0
56	MG	1A	3308	1/1	0.90	0.26	-	51,51,51,51	0
56	MG	1A	3106	1/1	0.96	0.19	-	25,25,25,25	0
56	MG	2A	3705	1/1	0.97	0.32	-	57,57,57,57	0
56	MG	1A	3477	1/1	0.98	0.25	-	48,48,48,48	0
56	MG	1A	3512	1/1	0.91	0.17	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	15	103	1/1	0.87	0.10	-	61,61,61,61	0
56	MG	1A	3667	1/1	0.94	0.20	-	61,61,61,61	0
56	MG	2A	3326	1/1	0.86	0.10	-	64,64,64,64	0
56	MG	1A	3974	1/1	0.88	0.06	-	45,45,45,45	0
56	MG	2A	3683	1/1	0.95	0.12	-	62,62,62,62	0
56	MG	1A	3504	1/1	0.92	0.19	-	44,44,44,44	0
56	MG	1Q	206	1/1	0.91	0.12	-	54,54,54,54	0
56	MG	1A	3367	1/1	0.93	0.23	-	57,57,57,57	0
56	MG	1A	3828	1/1	0.99	0.21	-	34,34,34,34	0
56	MG	1A	3302	1/1	0.85	0.21	-	56,56,56,56	0
56	MG	1A	4040	1/1	0.68	0.14	-	60,60,60,60	0
56	MG	1A	3319	1/1	0.94	0.14	-	63,63,63,63	0
56	MG	1a	1785	1/1	0.98	0.09	-	55,55,55,55	0
56	MG	2A	3622	1/1	0.97	0.25	-	63,63,63,63	0
56	MG	2a	3221	1/1	0.86	0.13	-	60,60,60,60	0
56	MG	2A	3588	1/1	0.92	0.10	-	47,47,47,47	0
56	MG	2A	3591	1/1	0.88	0.06	-	50,50,50,50	0
56	MG	1A	3953	1/1	0.91	0.10	-	46,46,46,46	0
56	MG	2A	3360	1/1	0.84	0.12	-	63,63,63,63	0
56	MG	2A	3156	1/1	0.96	0.15	-	48,48,48,48	0
56	MG	1B	3037	1/1	0.96	0.15	-	40,40,40,40	0
56	MG	1A	3972	1/1	0.96	0.16	-	60,60,60,60	0
56	MG	1A	3761	1/1	0.86	0.09	-	51,51,51,51	0
56	MG	1a	1743	1/1	0.85	0.12	-	73,73,73,73	0
56	MG	1A	3822	1/1	0.97	0.16	-	48,48,48,48	0
56	MG	1A	4008	1/1	0.83	0.14	-	56,56,56,56	0
56	MG	2a	3051	1/1	0.78	0.18	-	69,69,69,69	0
56	MG	2A	3647	1/1	0.85	0.22	-	51,51,51,51	0
56	MG	1A	3223	1/1	0.98	0.14	-	32,32,32,32	0
56	MG	2A	3344	1/1	0.88	0.19	-	55,55,55,55	0
56	MG	1A	3720	1/1	0.92	0.17	-	53,53,53,53	0
56	MG	2a	3240	1/1	0.77	0.36	-	63,63,63,63	0
56	MG	1A	3329	1/1	0.93	0.15	-	43,43,43,43	0
56	MG	2a	3034	1/1	0.76	0.17	-	72,72,72,72	0
56	MG	1B	3012	1/1	0.91	0.18	-	55,55,55,55	0
56	MG	2A	3670	1/1	0.89	0.12	-	70,70,70,70	0
56	MG	1A	3334	1/1	0.93	0.26	-	56,56,56,56	0
56	MG	2A	3030	1/1	0.94	0.13	-	51,51,51,51	0
56	MG	2A	3839	1/1	0.72	0.12	-	45,45,45,45	0
56	MG	2a	3237	1/1	0.96	0.07	-	66,66,66,66	0
56	MG	1A	3396	1/1	0.88	0.14	-	47,47,47,47	0
56	MG	2D	305	1/1	0.84	0.20	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1w	107	1/1	0.93	0.18	-	67,67,67,67	0
56	MG	1a	1712	1/1	0.92	0.19	-	67,67,67,67	0
56	MG	2A	3100	1/1	0.76	0.14	-	57,57,57,57	0
56	MG	2a	3077	1/1	0.90	0.21	-	61,61,61,61	0
56	MG	1A	3364	1/1	0.91	0.19	-	64,64,64,64	0
56	MG	2A	3252	1/1	0.96	0.30	-	52,52,52,52	0
56	MG	1A	4025	1/1	0.58	0.13	-	77,77,77,77	0
56	MG	2A	3446	1/1	0.96	0.27	-	45,45,45,45	0
56	MG	1A	3615	1/1	0.94	0.16	-	25,25,25,25	0
56	MG	2A	3200	1/1	0.93	0.15	-	42,42,42,42	0
56	MG	1A	4038	1/1	0.95	0.07	-	45,45,45,45	0
56	MG	1B	3021	1/1	0.92	0.26	-	46,46,46,46	0
56	MG	2A	3209	1/1	0.85	0.14	-	61,61,61,61	0
56	MG	1A	3465	1/1	0.90	0.18	-	60,60,60,60	0
56	MG	1a	1813	1/1	0.94	0.12	-	58,58,58,58	0
56	MG	2A	3759	1/1	0.89	0.12	-	46,46,46,46	0
56	MG	1A	3898	1/1	0.92	0.19	-	50,50,50,50	0
56	MG	2A	3271	1/1	0.84	0.13	-	49,49,49,49	0
56	MG	2A	3414	1/1	0.89	0.20	-	59,59,59,59	0
56	MG	2A	3567	1/1	0.97	0.08	-	50,50,50,50	0
56	MG	1A	3977	1/1	0.94	0.34	-	56,56,56,56	0
56	MG	1A	3944	1/1	0.90	0.15	-	60,60,60,60	0
56	MG	1A	3142	1/1	0.97	0.24	-	23,23,23,23	0
56	MG	2A	3659	1/1	0.94	0.07	-	59,59,59,59	0
56	MG	1a	1720	1/1	0.94	0.12	-	67,67,67,67	0
56	MG	2A	3282	1/1	0.89	0.24	-	63,63,63,63	0
56	MG	1A	3740	1/1	0.96	0.17	-	28,28,28,28	0
56	MG	2A	3669	1/1	0.95	0.12	-	42,42,42,42	0
56	MG	1A	3870	1/1	0.94	0.12	-	39,39,39,39	0
56	MG	2A	3276	1/1	0.95	0.18	-	55,55,55,55	0
56	MG	1B	3017	1/1	0.96	0.31	-	50,50,50,50	0
56	MG	2A	3056	1/1	0.78	0.17	-	60,60,60,60	0
56	MG	2A	3811	1/1	0.81	0.10	-	47,47,47,47	0
56	MG	1A	3907	1/1	0.95	0.23	-	54,54,54,54	0
56	MG	1A	3706	1/1	0.97	0.23	-	40,40,40,40	0
56	MG	2A	3063	1/1	0.90	0.12	-	67,67,67,67	0
56	MG	2A	3717	1/1	0.84	0.15	-	39,39,39,39	0
56	MG	2A	3569	1/1	0.93	0.09	-	49,49,49,49	0
56	MG	1B	3015	1/1	0.96	0.18	-	58,58,58,58	0
56	MG	1a	1721	1/1	0.88	0.11	-	58,58,58,58	0
56	MG	1A	3148	1/1	0.95	0.63	-	48,48,48,48	0
56	MG	2A	3432	1/1	0.86	0.19	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3384	1/1	0.86	0.22	-	57,57,57,57	0
56	MG	1A	4026	1/1	0.62	0.15	-	51,51,51,51	0
56	MG	1A	3834	1/1	0.63	0.34	-	69,69,69,69	0
56	MG	2A	3733	1/1	0.88	0.13	-	50,50,50,50	0
56	MG	2A	3157	1/1	0.97	0.14	-	58,58,58,58	0
56	MG	2A	3708	1/1	0.94	0.11	-	53,53,53,53	0
56	MG	2a	3025	1/1	0.97	0.18	-	57,57,57,57	0
56	MG	2A	3260	1/1	0.89	0.17	-	53,53,53,53	0
56	MG	2A	3386	1/1	0.92	0.13	-	63,63,63,63	0
56	MG	2A	3168	1/1	0.87	0.20	-	52,52,52,52	0
56	MG	2A	3621	1/1	0.96	0.09	-	51,51,51,51	0
56	MG	2A	3460	1/1	0.95	0.36	-	64,64,64,64	0
56	MG	2a	3083	1/1	0.75	0.21	-	72,72,72,72	0
56	MG	2A	3366	1/1	0.92	0.10	-	54,54,54,54	0
56	MG	1A	3648	1/1	0.86	0.12	-	55,55,55,55	0
56	MG	2a	3101	1/1	0.96	0.15	-	56,56,56,56	0
56	MG	17	101	1/1	0.93	0.22	-	54,54,54,54	0
56	MG	2A	3297	1/1	0.95	0.20	-	51,51,51,51	0
56	MG	2A	3198	1/1	0.94	0.14	-	61,61,61,61	0
56	MG	2A	3505	1/1	0.90	0.11	-	59,59,59,59	0
56	MG	2A	3506	1/1	0.95	0.25	-	31,31,31,31	0
56	MG	1a	1656	1/1	0.81	0.22	-	75,75,75,75	0
56	MG	1a	1772	1/1	0.93	0.13	-	39,39,39,39	0
56	MG	1x	106	1/1	0.91	0.22	-	63,63,63,63	0
56	MG	2A	3060	1/1	0.98	0.10	-	53,53,53,53	0
56	MG	2A	3755	1/1	0.96	0.14	-	50,50,50,50	0
56	MG	1a	1708	1/1	0.85	0.16	-	68,68,68,68	0
56	MG	2Q	3002	1/1	0.95	0.16	-	44,44,44,44	0
56	MG	2a	3140	1/1	0.81	0.06	-	57,57,57,57	0
56	MG	2E	303	1/1	0.92	0.12	-	49,49,49,49	0
56	MG	1A	4035	1/1	0.96	0.11	-	46,46,46,46	0
56	MG	1A	3339	1/1	0.97	0.14	-	51,51,51,51	0
56	MG	1B	3026	1/1	0.87	0.21	-	42,42,42,42	0
56	MG	2a	3112	1/1	0.91	0.10	-	54,54,54,54	0
56	MG	1A	3226	1/1	0.97	0.31	-	47,47,47,47	0
56	MG	1A	3537	1/1	0.83	0.24	-	49,49,49,49	0
56	MG	1A	3716	1/1	0.94	0.20	-	28,28,28,28	0
56	MG	2A	3497	1/1	0.94	0.12	-	63,63,63,63	0
56	MG	1A	3967	1/1	0.93	0.15	-	65,65,65,65	0
56	MG	2A	3109	1/1	0.96	0.15	-	37,37,37,37	0
56	MG	1a	1719	1/1	0.92	0.22	-	63,63,63,63	0
56	MG	23	102	1/1	0.95	0.21	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3946	1/1	0.87	0.13	-	49,49,49,49	0
56	MG	2a	3005	1/1	0.70	0.12	-	75,75,75,75	0
56	MG	1A	3778	1/1	0.90	0.08	-	57,57,57,57	0
56	MG	1A	4100	1/1	0.96	0.16	-	47,47,47,47	0
56	MG	1A	3945	1/1	0.85	0.21	-	41,41,41,41	0
56	MG	2A	3146	1/1	0.95	0.15	-	43,43,43,43	0
56	MG	1A	4022	1/1	0.93	0.11	-	72,72,72,72	0
56	MG	1x	102	1/1	0.80	0.21	-	63,63,63,63	0
56	MG	2A	3262	1/1	0.93	0.16	-	57,57,57,57	0
56	MG	2A	3316	1/1	0.91	0.17	-	54,54,54,54	0
56	MG	1A	3266	1/1	0.93	0.22	-	52,52,52,52	0
56	MG	1B	3025	1/1	0.84	0.16	-	77,77,77,77	0
56	MG	1a	1736	1/1	0.96	0.12	-	57,57,57,57	0
56	MG	1A	3787	1/1	0.76	0.14	-	55,55,55,55	0
56	MG	1A	3583	1/1	0.95	0.37	-	42,42,42,42	0
56	MG	1A	4019	1/1	0.92	0.20	-	42,42,42,42	0
56	MG	1A	3639	1/1	0.89	0.23	-	41,41,41,41	0
56	MG	2A	3015	1/1	0.94	0.20	-	43,43,43,43	0
56	MG	2A	3482	1/1	0.86	0.16	-	63,63,63,63	0
56	MG	1A	3846	1/1	0.91	0.12	-	53,53,53,53	0
56	MG	2A	3202	1/1	0.85	0.26	-	56,56,56,56	0
56	MG	2A	3474	1/1	0.81	0.19	-	55,55,55,55	0
56	MG	20	3001	1/1	0.93	0.17	-	59,59,59,59	0
56	MG	1A	3163	1/1	0.94	0.29	-	52,52,52,52	0
56	MG	2A	3604	1/1	0.94	0.20	-	64,64,64,64	0
56	MG	1A	3964	1/1	0.97	0.15	-	45,45,45,45	0
56	MG	2A	3392	1/1	0.97	0.11	-	55,55,55,55	0
56	MG	1v	3001	1/1	0.82	0.13	-	77,77,77,77	0
56	MG	2A	3689	1/1	0.97	0.08	-	71,71,71,71	0
56	MG	18	103	1/1	0.23	0.17	-	72,72,72,72	0
56	MG	1s	101	1/1	0.90	0.17	-	65,65,65,65	0
56	MG	1A	3094	1/1	0.95	0.10	-	52,52,52,52	0
56	MG	1A	4088	1/1	0.47	0.07	-	57,57,57,57	0
56	MG	1A	3685	1/1	0.96	0.23	-	60,60,60,60	0
56	MG	1A	3911	1/1	0.89	0.10	-	65,65,65,65	0
56	MG	1A	3096	1/1	0.76	0.27	-	49,49,49,49	0
56	MG	2A	3369	1/1	0.94	0.07	-	47,47,47,47	0
56	MG	2A	3686	1/1	0.83	0.14	-	57,57,57,57	0
56	MG	2A	3469	1/1	0.94	0.11	-	55,55,55,55	0
56	MG	1A	3137	1/1	0.97	0.20	-	33,33,33,33	0
56	MG	1A	3146	1/1	0.97	0.16	-	36,36,36,36	0
56	MG	2A	3728	1/1	0.94	0.09	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3617	1/1	0.88	0.12	-	38,38,38,38	0
56	MG	2A	3350	1/1	0.93	0.21	-	61,61,61,61	0
56	MG	2A	3749	1/1	0.92	0.11	-	48,48,48,48	0
56	MG	2A	3232	1/1	0.81	0.12	-	64,64,64,64	0
56	MG	2a	3164	1/1	0.94	0.21	-	73,73,73,73	0
56	MG	1A	3182	1/1	0.80	0.12	-	55,55,55,55	0
56	MG	2A	3640	1/1	0.95	0.26	-	45,45,45,45	0
56	MG	1A	3253	1/1	0.76	0.21	-	61,61,61,61	0
56	MG	2A	3302	1/1	0.96	0.19	-	66,66,66,66	0
56	MG	2A	3118	1/1	0.89	0.13	-	50,50,50,50	0
56	MG	1A	3088	1/1	0.95	0.11	-	47,47,47,47	0
56	MG	1A	3124	1/1	0.90	0.22	-	44,44,44,44	0
56	MG	1A	3676	1/1	0.97	0.21	-	24,24,24,24	0
56	MG	2A	3229	1/1	0.89	0.10	-	41,41,41,41	0
56	MG	2A	3395	1/1	0.93	0.21	-	50,50,50,50	0
56	MG	1A	3201	1/1	0.92	0.24	-	45,45,45,45	0
56	MG	2a	3003	1/1	0.84	0.16	-	64,64,64,64	0
56	MG	2A	3462	1/1	0.90	0.27	-	59,59,59,59	0
56	MG	2A	3463	1/1	0.72	0.14	-	57,57,57,57	0
56	MG	1A	3819	1/1	0.94	0.11	-	48,48,48,48	0
56	MG	1A	3617	1/1	0.93	0.16	-	33,33,33,33	0
56	MG	2B	3019	1/1	0.79	0.12	-	76,76,76,76	0
56	MG	1A	3876	1/1	0.94	0.18	-	49,49,49,49	0
56	MG	1A	3224	1/1	0.97	0.19	-	50,50,50,50	0
56	MG	1A	3127	1/1	0.85	0.44	-	51,51,51,51	0
56	MG	2A	3632	1/1	0.92	0.13	-	41,41,41,41	0
56	MG	2B	3003	1/1	0.82	0.20	-	74,74,74,74	0
56	MG	2A	3435	1/1	0.98	0.07	-	49,49,49,49	0
56	MG	1A	3571	1/1	0.91	0.21	-	57,57,57,57	0
56	MG	2a	3029	1/1	0.84	0.15	-	67,67,67,67	0
56	MG	2A	3442	1/1	0.94	0.14	-	50,50,50,50	0
56	MG	2A	3801	1/1	0.92	0.27	-	64,64,64,64	0
56	MG	2A	3343	1/1	0.89	0.11	-	57,57,57,57	0
56	MG	2A	3595	1/1	0.97	0.11	-	49,49,49,49	0
56	MG	2A	3215	1/1	0.95	0.17	-	37,37,37,37	0
56	MG	2a	3037	1/1	0.91	0.38	-	77,77,77,77	0
56	MG	2A	3703	1/1	0.89	0.13	-	47,47,47,47	0
56	MG	2A	3331	1/1	0.95	0.18	-	56,56,56,56	0
56	MG	1A	4067	1/1	0.92	0.14	-	56,56,56,56	0
56	MG	2A	3528	1/1	0.96	0.34	-	57,57,57,57	0
56	MG	1A	3721	1/1	0.90	0.19	-	57,57,57,57	0
56	MG	2A	3300	1/1	0.93	0.14	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2A	3523	1/1	0.92	0.13	-	27,27,27,27	0
56	MG	2A	3477	1/1	0.92	0.34	-	56,56,56,56	0
56	MG	2A	3739	1/1	0.96	0.10	-	59,59,59,59	0
56	MG	2y	3001	1/1	0.90	0.18	-	59,59,59,59	0
56	MG	2A	3790	1/1	0.74	0.21	-	65,65,65,65	0
56	MG	1A	3690	1/1	0.97	0.14	-	28,28,28,28	0
56	MG	1a	1641	1/1	0.91	0.18	-	58,58,58,58	0
56	MG	2a	3228	1/1	0.69	0.11	-	86,86,86,86	0
56	MG	2A	3439	1/1	0.90	0.21	-	60,60,60,60	0
56	MG	2a	3087	1/1	0.91	0.08	-	63,63,63,63	0
56	MG	1A	3290	1/1	0.98	0.24	-	46,46,46,46	0
56	MG	1A	3792	1/1	0.88	0.14	-	35,35,35,35	0
56	MG	1A	3179	1/1	0.95	0.21	-	36,36,36,36	0
56	MG	2A	3309	1/1	0.83	0.13	-	53,53,53,53	0
56	MG	1A	3588	1/1	0.80	0.19	-	46,46,46,46	0
56	MG	1B	3016	1/1	0.86	0.16	-	54,54,54,54	0
56	MG	1A	3336	1/1	0.97	0.27	-	41,41,41,41	0
56	MG	2a	3179	1/1	0.47	0.50	-	100,100,100,100	0
56	MG	2A	3141	1/1	0.96	0.09	-	51,51,51,51	0
56	MG	2A	3767	1/1	0.95	0.09	-	56,56,56,56	0
56	MG	1A	3345	1/1	0.97	0.28	-	47,47,47,47	0
56	MG	1A	3428	1/1	0.88	0.16	-	51,51,51,51	0
56	MG	1A	3028	1/1	0.98	0.24	-	34,34,34,34	0
56	MG	2A	3782	1/1	0.94	0.08	-	51,51,51,51	0
56	MG	2A	3764	1/1	0.95	0.11	-	66,66,66,66	0
56	MG	2a	3022	1/1	0.85	0.09	-	72,72,72,72	0
56	MG	1Z	303	1/1	0.97	0.17	-	56,56,56,56	0
56	MG	1b	3002	1/1	0.85	0.17	-	61,61,61,61	0
56	MG	1A	3446	1/1	0.60	0.18	-	61,61,61,61	0
56	MG	1A	3134	1/1	0.90	0.32	-	54,54,54,54	0
56	MG	1A	3918	1/1	0.88	0.13	-	56,56,56,56	0
56	MG	1a	1762	1/1	0.89	0.13	-	78,78,78,78	0
56	MG	1B	3032	1/1	0.69	0.23	-	80,80,80,80	0
56	MG	2A	3791	1/1	0.91	0.21	-	46,46,46,46	0
56	MG	2Z	8001	1/1	0.89	0.07	-	78,78,78,78	0
56	MG	2a	3141	1/1	0.89	0.18	-	94,94,94,94	0
56	MG	2A	3368	1/1	0.94	0.06	-	47,47,47,47	0
56	MG	1A	3131	1/1	0.89	0.17	-	72,72,72,72	0
56	MG	1A	3416	1/1	0.93	0.17	-	47,47,47,47	0
56	MG	2a	3012	1/1	0.76	0.14	-	71,71,71,71	0
56	MG	1A	3739	1/1	0.93	0.18	-	39,39,39,39	0
56	MG	2A	3113	1/1	0.80	0.13	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	3116	1/1	0.87	0.08	-	67,67,67,67	0
56	MG	2a	3052	1/1	0.93	0.15	-	62,62,62,62	0
56	MG	1A	3529	1/1	0.96	0.19	-	43,43,43,43	0
56	MG	1A	3370	1/1	0.74	0.27	-	57,57,57,57	0
56	MG	1A	3959	1/1	0.94	0.14	-	56,56,56,56	0
56	MG	2A	3374	1/1	0.64	0.26	-	65,65,65,65	0
56	MG	2A	3084	1/1	0.93	0.10	-	45,45,45,45	0
56	MG	2A	3517	1/1	0.97	0.12	-	42,42,42,42	0
56	MG	2A	3525	1/1	0.98	0.13	-	34,34,34,34	0
56	MG	1A	3143	1/1	0.91	0.18	-	55,55,55,55	0
56	MG	1A	3406	1/1	0.93	0.29	-	47,47,47,47	0
56	MG	2A	3758	1/1	0.95	0.23	-	58,58,58,58	0
56	MG	1a	1627	1/1	0.89	0.14	-	55,55,55,55	0
56	MG	2A	3519	1/1	0.92	0.17	-	33,33,33,33	0
56	MG	1A	3743	1/1	0.90	0.22	-	60,60,60,60	0
56	MG	1A	3558	1/1	0.91	0.12	-	52,52,52,52	0
56	MG	1A	3233	1/1	0.95	0.13	-	49,49,49,49	0
56	MG	2A	3327	1/1	0.95	0.12	-	50,50,50,50	0
56	MG	1A	3895	1/1	0.96	0.14	-	61,61,61,61	0
56	MG	2A	3201	1/1	0.95	0.10	-	51,51,51,51	0
56	MG	1A	3566	1/1	0.86	0.31	-	72,72,72,72	0
56	MG	1A	3487	1/1	0.82	0.23	-	70,70,70,70	0
56	MG	2W	203	1/1	0.84	0.25	-	59,59,59,59	0
56	MG	2A	3558	1/1	0.93	0.17	-	31,31,31,31	0
56	MG	1a	1648	1/1	0.89	0.16	-	59,59,59,59	0
56	MG	2B	3002	1/1	0.88	0.11	-	49,49,49,49	0
56	MG	2a	3194	1/1	0.94	0.11	-	68,68,68,68	0
56	MG	2a	3067	1/1	0.93	0.15	-	65,65,65,65	0
56	MG	1A	3186	1/1	0.96	0.32	-	39,39,39,39	0
56	MG	1A	4044	1/1	0.64	0.25	-	79,79,79,79	0
56	MG	2A	3049	1/1	0.99	0.16	-	23,23,23,23	0
56	MG	1A	3093	1/1	0.91	0.22	-	33,33,33,33	0
56	MG	2A	3171	1/1	0.90	0.12	-	38,38,38,38	0
56	MG	1A	3469	1/1	0.92	0.23	-	53,53,53,53	0
56	MG	2a	3004	1/1	0.82	0.16	-	57,57,57,57	0
56	MG	2A	3787	1/1	0.90	0.04	-	64,64,64,64	0
56	MG	1A	3551	1/1	0.96	0.16	-	37,37,37,37	0
56	MG	2a	3133	1/1	0.96	0.13	-	54,54,54,54	0
56	MG	1A	3884	1/1	0.92	0.09	-	48,48,48,48	0
56	MG	2A	3351	1/1	0.92	0.11	-	54,54,54,54	0
56	MG	1A	3724	1/1	0.90	0.21	-	58,58,58,58	0
56	MG	1A	3989	1/1	0.57	0.08	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	2a	3181	1/1	0.56	0.10	-	69,69,69,69	0
56	MG	1A	4023	1/1	0.98	0.14	-	47,47,47,47	0
56	MG	2a	3209	1/1	0.97	0.14	-	77,77,77,77	0
56	MG	1A	3601	1/1	0.99	0.18	-	11,11,11,11	0
56	MG	2A	3809	1/1	0.91	0.08	-	59,59,59,59	0
56	MG	1a	1631	1/1	0.89	0.24	-	54,54,54,54	0
56	MG	2a	3132	1/1	0.95	0.21	-	63,63,63,63	0
56	MG	2a	3231	1/1	0.83	0.11	-	68,68,68,68	0
56	MG	1A	3006	1/1	0.80	0.33	-	57,57,57,57	0
56	MG	2A	3664	1/1	0.96	0.15	-	54,54,54,54	0
56	MG	2A	3691	1/1	0.73	0.31	-	68,68,68,68	0
56	MG	1B	3007	1/1	0.51	0.25	-	85,85,85,85	0
56	MG	2A	3009	1/1	0.98	0.13	-	31,31,31,31	0
56	MG	2a	3073	1/1	0.92	0.12	-	66,66,66,66	0
56	MG	2A	3654	1/1	0.96	0.09	-	62,62,62,62	0
56	MG	2A	3012	1/1	0.96	0.13	-	39,39,39,39	0
56	MG	1A	4031	1/1	0.82	0.15	-	54,54,54,54	0
56	MG	1E	301	1/1	0.94	0.19	-	37,37,37,37	0
56	MG	13	103	1/1	0.92	0.21	-	47,47,47,47	0
56	MG	2A	3662	1/1	0.91	0.12	-	48,48,48,48	0
56	MG	2A	3842	1/1	0.95	0.14	-	59,59,59,59	0
56	MG	1A	3061	1/1	0.94	0.35	-	62,62,62,62	0
56	MG	2A	3219	1/1	0.93	0.20	-	51,51,51,51	0
56	MG	1a	1722	1/1	0.84	0.08	-	65,65,65,65	0
56	MG	1a	1609	1/1	0.97	0.11	-	54,54,54,54	0
56	MG	1a	1710	1/1	0.84	0.13	-	77,77,77,77	0
56	MG	1A	3682	1/1	0.92	0.21	-	35,35,35,35	0
56	MG	2a	3172	1/1	0.94	0.09	-	66,66,66,66	0
56	MG	2A	3341	1/1	0.79	0.11	-	52,52,52,52	0
56	MG	2A	3838	1/1	0.96	0.16	-	47,47,47,47	0
56	MG	2A	3373	1/1	0.92	0.06	-	52,52,52,52	0
56	MG	2a	3124	1/1	0.98	0.13	-	61,61,61,61	0
56	MG	1A	3286	1/1	0.99	0.41	-	49,49,49,49	0
56	MG	2A	3087	1/1	0.81	0.20	-	53,53,53,53	0
56	MG	1A	3943	1/1	0.94	0.19	-	81,81,81,81	0
56	MG	1A	3005	1/1	0.95	0.16	-	41,41,41,41	0
56	MG	2A	3646	1/1	0.88	0.15	-	55,55,55,55	0
56	MG	2a	3236	1/1	0.82	0.13	-	75,75,75,75	0
56	MG	2A	3263	1/1	0.95	0.13	-	55,55,55,55	0
56	MG	1A	3383	1/1	0.91	0.16	-	55,55,55,55	0
56	MG	1A	3485	1/1	0.93	0.18	-	48,48,48,48	0
56	MG	1a	1690	1/1	0.94	0.14	-	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1X	105	1/1	0.89	0.13	-	47,47,47,47	0
56	MG	2a	3013	1/1	0.75	0.11	-	78,78,78,78	0
56	MG	1A	3129	1/1	0.86	0.23	-	51,51,51,51	0
56	MG	2a	3185	1/1	0.96	0.15	-	47,47,47,47	0
56	MG	2A	3222	1/1	0.95	0.16	-	38,38,38,38	0
56	MG	1A	3118	1/1	0.93	0.22	-	38,38,38,38	0
56	MG	1A	3385	1/1	0.93	0.15	-	58,58,58,58	0
56	MG	2A	3592	1/1	0.97	0.20	-	57,57,57,57	0
56	MG	2A	3696	1/1	0.78	0.13	-	58,58,58,58	0
56	MG	1X	106	1/1	0.96	0.19	-	29,29,29,29	0
56	MG	2A	3125	1/1	0.96	0.16	-	44,44,44,44	0
56	MG	1A	3149	1/1	0.91	0.15	-	33,33,33,33	0
56	MG	1A	3069	1/1	0.98	0.25	-	20,20,20,20	0
56	MG	1A	3544	1/1	0.91	0.17	-	47,47,47,47	0
56	MG	2A	3224	1/1	0.88	0.22	-	52,52,52,52	0
56	MG	2A	3785	1/1	0.97	0.26	-	45,45,45,45	0
56	MG	1A	3207	1/1	0.81	0.28	-	54,54,54,54	0
56	MG	2A	3380	1/1	0.83	0.12	-	55,55,55,55	0
56	MG	2A	3355	1/1	0.93	0.10	-	51,51,51,51	0
56	MG	1a	1703	1/1	0.92	0.27	-	55,55,55,55	0
56	MG	2A	3795	1/1	0.76	0.11	-	37,37,37,37	0
56	MG	1A	3361	1/1	0.84	0.11	-	49,49,49,49	0
56	MG	2A	3498	1/1	0.90	0.11	-	55,55,55,55	0
56	MG	1A	3970	1/1	0.42	0.13	-	70,70,70,70	0
56	MG	2x	102	1/1	0.52	0.17	-	77,77,77,77	0
56	MG	2A	3002	1/1	0.97	0.30	-	57,57,57,57	0
56	MG	2j	8001	1/1	0.86	0.09	-	75,75,75,75	0
56	MG	1B	3002	1/1	0.80	0.33	-	58,58,58,58	0
56	MG	1A	3978	1/1	0.83	0.08	-	65,65,65,65	0
56	MG	1a	1820	1/1	0.93	0.08	-	57,57,57,57	0
56	MG	2A	3022	1/1	0.94	0.27	-	47,47,47,47	0
56	MG	2A	3802	1/1	0.84	0.13	-	56,56,56,56	0
56	MG	2A	3273	1/1	0.95	0.14	-	51,51,51,51	0
56	MG	10	104	1/1	0.83	0.30	-	64,64,64,64	0
56	MG	1a	1604	1/1	0.91	0.11	-	58,58,58,58	0
56	MG	1A	3045	1/1	0.96	0.20	-	36,36,36,36	0
56	MG	2A	3064	1/1	0.92	0.13	-	51,51,51,51	0
56	MG	1A	4048	1/1	0.85	0.08	-	48,48,48,48	0
56	MG	2A	3653	1/1	0.96	0.18	-	58,58,58,58	0
56	MG	2A	3766	1/1	0.80	0.11	-	52,52,52,52	0
56	MG	1A	3711	1/1	0.78	0.15	-	61,61,61,61	0
56	MG	1A	3589	1/1	0.95	0.23	-	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1a	1733	1/1	0.93	0.14	-	58,58,58,58	0
56	MG	2A	3546	1/1	0.78	0.12	-	44,44,44,44	0
56	MG	1A	3111	1/1	0.98	0.15	-	40,40,40,40	0
56	MG	1A	4087	1/1	0.90	0.21	-	54,54,54,54	0
56	MG	2a	3120	1/1	0.70	0.19	-	72,72,72,72	0
56	MG	1A	3333	1/1	0.85	0.11	-	52,52,52,52	0
56	MG	1A	3563	1/1	0.96	0.26	-	43,43,43,43	0
56	MG	1A	3397	1/1	0.90	0.23	-	47,47,47,47	0
56	MG	1A	3848	1/1	0.92	0.14	-	56,56,56,56	0
56	MG	1U	201	1/1	0.88	0.18	-	52,52,52,52	0
56	MG	1A	4065	1/1	0.91	0.18	-	51,51,51,51	0
56	MG	1A	3553	1/1	0.91	0.26	-	49,49,49,49	0
56	MG	2A	3178	1/1	0.93	0.24	-	57,57,57,57	0
56	MG	1A	3762	1/1	0.91	0.12	-	60,60,60,60	0
56	MG	2A	3483	1/1	0.95	0.16	-	55,55,55,55	0
56	MG	1A	3592	1/1	0.96	0.20	-	21,21,21,21	0
56	MG	2A	3695	1/1	0.98	0.09	-	38,38,38,38	0
56	MG	2A	3047	1/1	0.91	0.16	-	46,46,46,46	0
56	MG	1B	3035	1/1	0.95	0.11	-	59,59,59,59	0
56	MG	2A	3319	1/1	0.99	0.07	-	49,49,49,49	0
56	MG	2A	3596	1/1	0.87	0.11	-	47,47,47,47	0
56	MG	1a	1796	1/1	0.96	0.06	-	59,59,59,59	0
56	MG	1A	3393	1/1	0.98	0.18	-	50,50,50,50	0
56	MG	2A	3447	1/1	0.92	0.28	-	46,46,46,46	0
56	MG	1A	3215	1/1	0.95	0.06	-	65,65,65,65	0
56	MG	2A	3147	1/1	0.85	0.29	-	58,58,58,58	0
56	MG	2A	3259	1/1	0.78	0.15	-	61,61,61,61	0
56	MG	2A	3628	1/1	0.87	0.07	-	52,52,52,52	0
56	MG	2E	301	1/1	0.94	0.17	-	50,50,50,50	0
56	MG	1A	3044	1/1	0.93	0.20	-	37,37,37,37	0
56	MG	2A	3349	1/1	0.95	0.87	-	58,58,58,58	0
56	MG	2a	3102	1/1	0.98	0.14	-	58,58,58,58	0
56	MG	2A	3822	1/1	0.83	0.11	-	66,66,66,66	0
56	MG	1A	3547	1/1	0.98	0.14	-	53,53,53,53	0
56	MG	1B	3033	1/1	0.93	0.17	-	56,56,56,56	0
56	MG	2A	3174	1/1	0.94	0.15	-	53,53,53,53	0
56	MG	1A	3924	1/1	0.95	0.09	-	50,50,50,50	0
56	MG	2A	3710	1/1	0.85	0.14	-	63,63,63,63	0
56	MG	2a	3061	1/1	0.94	0.20	-	54,54,54,54	0
56	MG	2A	3430	1/1	0.89	0.10	-	51,51,51,51	0
56	MG	2A	3563	1/1	0.93	0.14	-	49,49,49,49	0
56	MG	1A	3517	1/1	0.98	0.14	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
56	MG	1A	3992	1/1	0.79	0.24	-	75,75,75,75	0
56	MG	1A	3444	1/1	0.96	0.22	-	63,63,63,63	0
56	MG	2A	3887	1/1	0.94	0.08	-	48,48,48,48	0
56	MG	1a	1797	1/1	0.93	0.13	-	64,64,64,64	0
56	MG	2A	3502	1/1	0.91	0.09	-	43,43,43,43	0
56	MG	12	101	1/1	0.88	0.21	-	60,60,60,60	0
56	MG	1A	3246	1/1	0.90	0.31	-	58,58,58,58	0
56	MG	1A	3390	1/1	0.87	0.18	-	35,35,35,35	0
56	MG	1A	3986	1/1	0.93	0.24	-	22,22,22,22	0
56	MG	1A	3969	1/1	0.69	0.14	-	66,66,66,66	0
56	MG	2A	3396	1/1	0.93	0.09	-	56,56,56,56	0
56	MG	2A	3642	1/1	0.80	0.18	-	47,47,47,47	0
56	MG	1a	1605	1/1	0.75	0.17	-	65,65,65,65	0
56	MG	1A	3760	1/1	0.95	0.22	-	35,35,35,35	0
56	MG	2A	3029	1/1	0.81	0.22	-	44,44,44,44	0
56	MG	1A	3470	1/1	0.92	0.17	-	47,47,47,47	0
56	MG	1E	306	1/1	0.88	0.15	-	31,31,31,31	0
56	MG	1A	3684	1/1	0.97	0.27	-	32,32,32,32	0
56	MG	1A	3534	1/1	0.97	0.18	-	33,33,33,33	0
56	MG	2A	3129	1/1	0.91	0.14	-	50,50,50,50	0
56	MG	2a	3125	1/1	0.95	0.10	-	65,65,65,65	0
56	MG	1A	3251	1/1	0.79	0.10	-	58,58,58,58	0
56	MG	2a	3023	1/1	0.95	0.08	-	47,47,47,47	0
56	MG	2A	3427	1/1	0.98	0.13	-	45,45,45,45	0
56	MG	1A	3493	1/1	0.95	0.20	-	36,36,36,36	0
56	MG	1a	1644	1/1	0.92	0.15	-	66,66,66,66	0
56	MG	1A	3279	1/1	0.91	0.17	-	38,38,38,38	0
56	MG	1A	3423	1/1	0.79	0.30	-	67,67,67,67	0
56	MG	2A	3826	1/1	0.86	0.11	-	54,54,54,54	0
56	MG	1A	3113	1/1	0.96	0.14	-	35,35,35,35	0
56	MG	2A	3176	1/1	0.95	0.13	-	46,46,46,46	0
56	MG	2A	3333	1/1	0.92	0.13	-	55,55,55,55	0
56	MG	2A	3216	1/1	0.89	0.13	-	56,56,56,56	0
56	MG	2a	3072	1/1	0.94	0.14	-	53,53,53,53	0
56	MG	1a	1786	1/1	0.86	0.09	-	64,64,64,64	0
56	MG	1A	3480	1/1	0.92	0.10	-	52,52,52,52	0

6.5 Other polymers

There are no such residues in this entry.