



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 16, 2026 – 08:00 am BST

PDB ID : 6GSL / pdb_00006gsl
Title : Structure of T. thermophilus 70S ribosome complex with mRNA, tRNA^{fMet} and cognate tRNA^{Arg} in the A-site
Authors : Rozov, A.; Yusupov, M.; Yusupova, G.
Deposited on : 2018-06-14
Resolution : 3.16 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

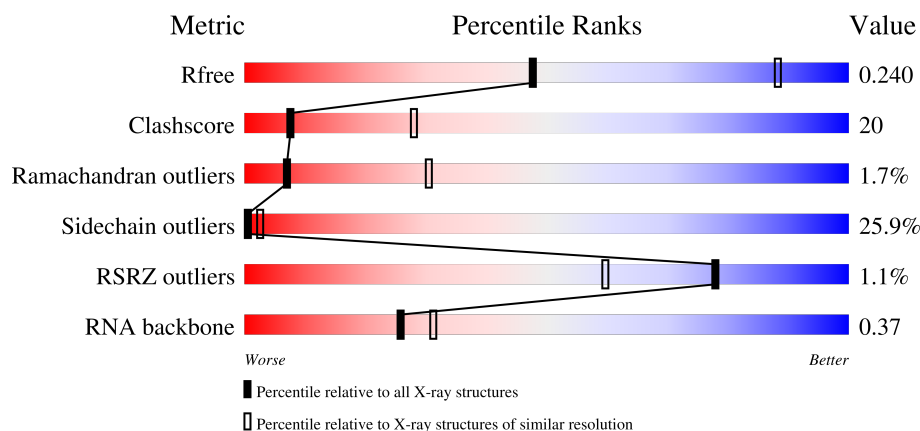
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.16 Å.

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



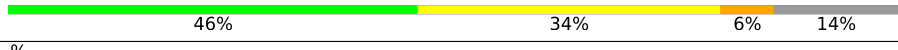
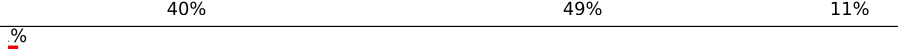
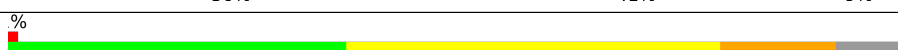
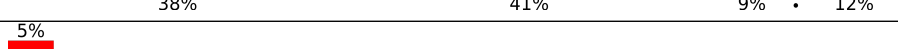
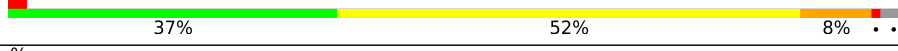
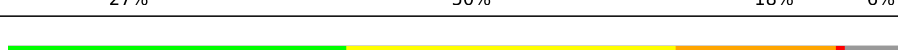
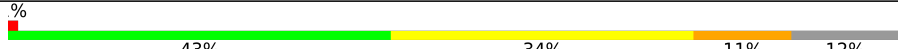
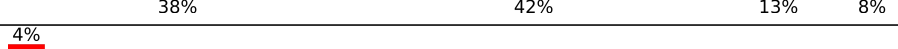
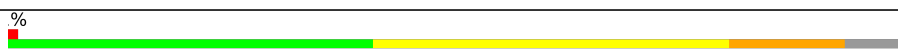
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)
RNA backbone	3983	1113 (3.42-2.90)

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

Mol	Chain	Length	Quality of chain
1	13	1522	35% 47% 17% •
1	1G	1522	36% 48% 16% •
2	12	256	29% 46% 16% • 7%
2	1E	256	27% 46% 16% • 10%

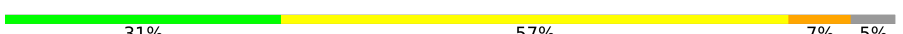
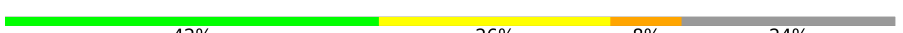
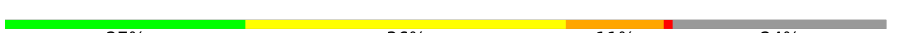
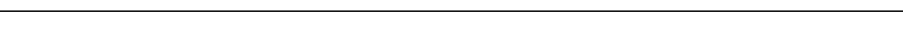
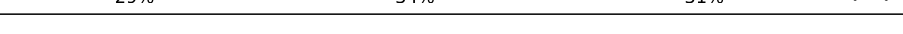
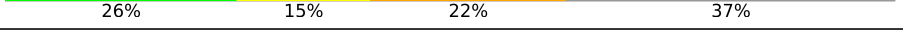
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Mol	Chain	Length	Quality of chain
3	22	239	% 
3	2E	239	
4	32	209	% 
4	3E	209	% 
5	42	162	% 
5	4E	162	% 
6	52	101	
6	5E	101	
7	62	156	% 
7	6E	156	5% 
8	72	138	2% 
8	7E	138	
9	82	128	2% 
9	8E	128	% 
10	1A	105	
10	1I	105	
11	2A	129	% 
11	2I	129	2% 
12	3A	132	8% 
12	3I	132	5% 
13	4A	126	4% 
13	4I	126	% 
14	5A	61	5% 
14	5I	61	
15	6A	89	

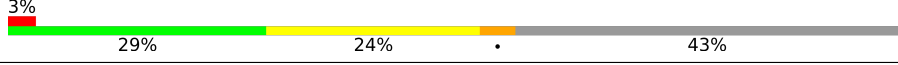
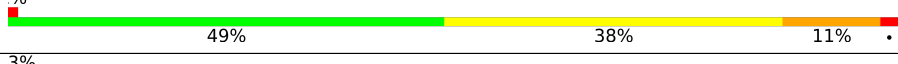
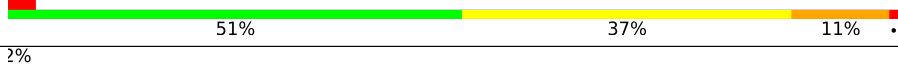
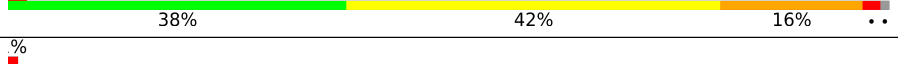
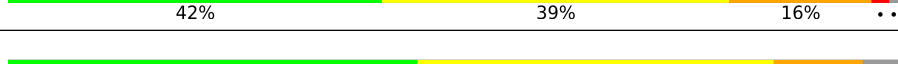
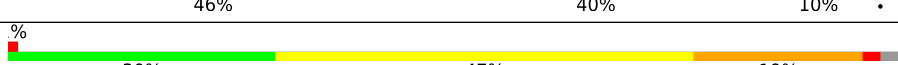
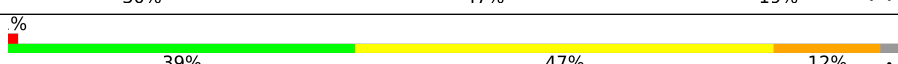
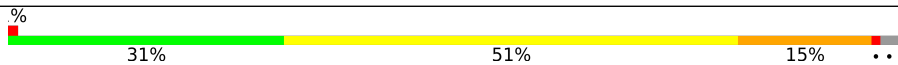
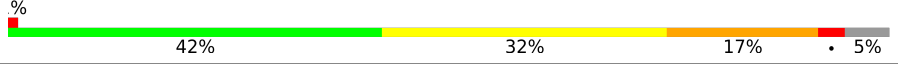
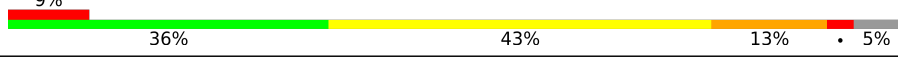
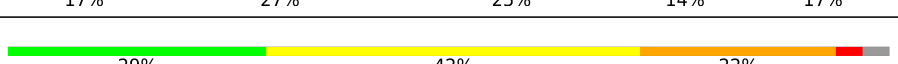
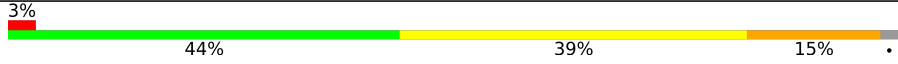
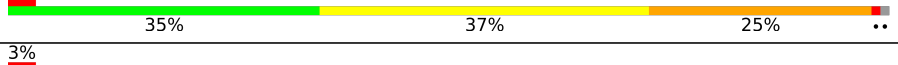
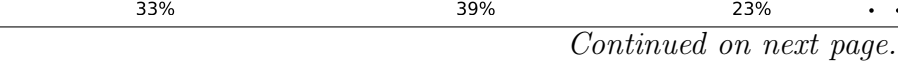
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Mol	Chain	Length	Quality of chain
15	6I	89	
16	7A	88	
16	7I	88	
17	8A	105	
17	8I	105	
18	9A	88	
18	9I	88	
19	AA	93	
19	AI	93	
20	BA	106	
20	BI	106	
21	1B	27	
21	1F	27	
22	1K	77	
22	1L	77	
23	2K	77	
23	2L	77	
24	3K	77	
24	3L	77	
25	4K	27	
25	4L	27	
26	14	2917	
26	1H	2917	
27	16	122	
27	1J	122	

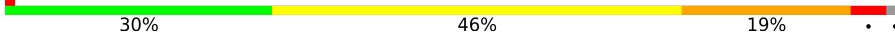
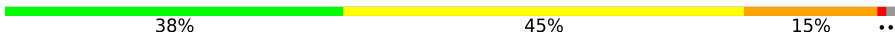
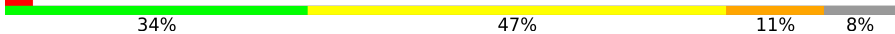
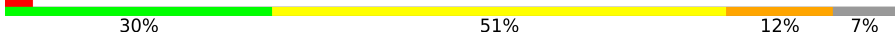
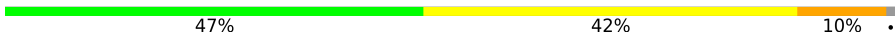
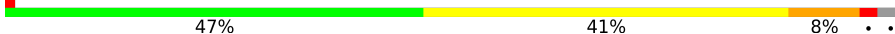
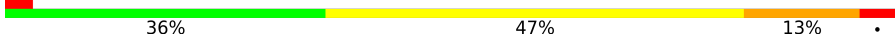
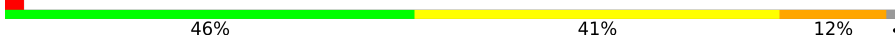
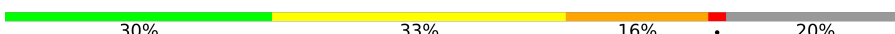
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Mol	Chain	Length	Quality of chain
28	71	229	
28	79	229	
29	11	276	
29	19	276	
30	21	206	
30	29	206	
31	31	210	
31	39	210	
32	41	182	
32	49	182	
33	51	180	
33	59	180	
34	18	125	
34	28	125	
35	61	148	
35	69	148	
36	38	173	
37	48	147	
38	15	140	
38	58	140	
39	25	122	
39	68	122	
40	35	150	
40	78	150	
41	45	141	

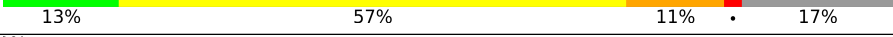
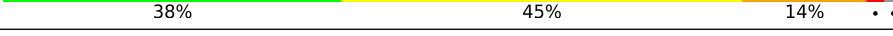
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Mol	Chain	Length	Quality of chain
41	88	141	
42	55	118	
42	98	118	
43	65	112	
43	A8	112	
44	75	146	
44	B8	146	
45	85	118	
45	C8	118	
46	95	101	
46	D8	101	
47	A5	113	
47	E8	113	
48	B5	96	
48	F8	96	
49	C5	110	
49	G8	110	
50	D5	206	
50	H8	206	
51	E5	85	
51	I8	85	
52	F5	98	
52	J8	98	
53	G5	72	
53	K8	72	

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Mol	Chain	Length	Quality of chain
54	H5	60	
54	L8	60	
55	M8	71	
56	J5	60	
56	N8	60	
57	O8	54	
58	L5	49	
58	P8	49	
59	M5	65	
59	Q8	65	

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
60	MG	13	1644	-	-	-	X
60	MG	1H	3219	-	-	-	X
60	MG	1H	3269	-	-	-	X
61	SF4	32	303	-	-	X	-
61	SF4	3E	303	-	-	X	-

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 306138 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	13	1512	Total	C	N	O	P	0	0	0
			32497	14464	6017	10504	1512			
1	1G	1509	Total	C	N	O	P	0	0	0
			32437	14437	6010	10481	1509			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1E	231	Total	C	N	O	S	0	0	0
			1874	1199	334	336	5			
2	12	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2E	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			
3	22	195	Total	C	N	O	S	0	0	0
			1533	969	297	266	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3E	207	Total	C	N	O	S	0	0	0
			1690	1058	336	289	7			
4	32	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4E	149	Total	C	N	O	S	0	0	0
			1142	722	216	200	4			
5	42	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	5E	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			
6	52	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	6E	154	Total	C	N	O	S	0	0	0
			1242	770	250	216	6			
7	62	138	Total	C	N	O	S	0	0	0
			1110	689	221	194	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	7E	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			
8	72	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	8E	126	Total	C	N	O		0	0	0
			1000	634	196	170				
9	82	124	Total	C	N	O		0	0	0
			983	624	190	169				

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1I	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1A	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	2I	111	Total	C	N	O	S	0	0	0
			823	512	154	154	3			
11	2A	113	Total	C	N	O	S	0	0	0
			835	520	156	156	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	3I	122	Total	C	N	O	S	0	0	0
			956	603	193	159	1			
12	3A	121	Total	C	N	O	S	0	0	0
			947	597	191	158	1			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	4I	119	Total	C	N	O	S	0	0	0
			936	579	191	164	2			
13	4A	111	Total	C	N	O	S	0	0	0
			887	549	180	156	2			

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	5I	61	Total	C	N	O	S	0	0	0
			499	317	105	72	5			
14	5A	57	Total	C	N	O	S	0	0	0
			466	297	97	68	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	6I	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			
15	6A	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	7I	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			
16	7A	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	8I	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			
17	8A	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	9I	67	Total	C	N	O	0	0	0
			544	349	104	91			
18	9A	67	Total	C	N	O	0	0	0
			544	349	104	91			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AI	80	Total	C	N	O	S	0	0	0
			643	411	118	112	2			
19	AA	62	Total	C	N	O	S	0	0	0
			481	306	85	88	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BI	98	Total	C	N	O	S	0	0	0
			751	464	158	127	2			
20	BA	98	Total	C	N	O	S	0	0	0
			757	467	161	127	2			

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	1F	24	Total	C	N	O	0	0	0
			208	128	50	30			
21	1B	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 22 is a RNA chain called tRNAArg.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
22	1K	72	Total	C	N	O	P	S	0	0	0
			1544	690	282	498	72	2			
22	1L	74	Total	C	N	O	P	S	0	0	0
			1584	708	287	513	74	2			

- Molecule 23 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	2K	77	Total	C	N	O	P	S	0	0	0
			1646	735	298	535	77	1			
23	2L	77	Total	C	N	O	P	S	0	0	0
			1646	735	298	535	77	1			

- Molecule 24 is a RNA chain called tRNAArg.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	3K	73	Total	C	N	O	P	0	0	0
			1561	696	285	507	73			
24	3L	74	Total	C	N	O	P	0	0	0
			1581	705	287	515	74			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3K	6	U	C	conflict	GB 1387059712
3L	6	U	C	conflict	GB 1387059712

- Molecule 25 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	4K	21	Total	C	N	O	P	0	0	0
			462	207	97	137	21			
25	4L	17	Total	C	N	O	P	0	0	0
			374	167	77	113	17			

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	1H	2895	Total	C	N	O	P	0	0	0
			62351	27751	11658	20047	2895			
26	14	2895	Total	C	N	O	P	0	0	0
			62347	27751	11660	20042	2894			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1H	161	U	UNK	conflict	GB 55771382
1H	654A	A	G	conflict	GB 55771382
1H	654E	C	G	conflict	GB 55771382
1H	654P	G	C	conflict	GB 55771382
1H	654T	A	C	conflict	GB 55771382
1H	1058	U	G	conflict	GB 55771382
1H	1080	A	C	conflict	GB 55771382
14	158	U	UNK	conflict	GB 55771382
14	654A	A	G	conflict	GB 55771382
14	654E	C	G	conflict	GB 55771382
14	654P	G	C	conflict	GB 55771382
14	654T	A	C	conflict	GB 55771382
14	1058	U	G	conflict	GB 55771382
14	1080	A	C	conflict	GB 55771382

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	16	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			
27	1J	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			

- Molecule 28 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	71	134	Total	C	N	O	S	0	0	0
			1043	659	196	187	1			
28	79	130	Total	C	N	O	S	0	0	0
			1010	637	188	184	1			

- Molecule 29 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	11	273	Total	C	N	O	S	0	0	0
			2120	1338	421	358	3			
29	19	273	Total	C	N	O	S	0	0	0
			2120	1338	421	358	3			

- Molecule 30 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	21	203	Total	C	N	O	S	0	0	0
			1558	985	298	269	6			
30	29	203	Total	C	N	O	S	0	0	0
			1558	985	298	269	6			

- Molecule 31 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	31	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			
31	39	206	Total	C	N	O	S	0	0	0
			1610	1026	301	281	2			

- Molecule 32 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	41	179	Total	C	N	O	S	0	0	0
			1457	931	265	257	4			
32	49	179	Total	C	N	O	S	0	0	0
			1457	931	265	257	4			

- Molecule 33 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	51	171	Total	C	N	O	S	0	0	0
			1312	832	246	233	1			
33	59	171	Total	C	N	O	S	0	0	0
			1312	832	246	233	1			

- Molecule 34 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	18	30	Total	C	N	O	S	0	0	0
			237	150	38	48	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	28	30	Total	C	N	O	S	0	0	0
			237	150	38	48	1			

- Molecule 35 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	61	145	Total	C	N	O	S	0	0	0
			1131	723	200	207	1			
35	69	145	Total	C	N	O	S	0	0	0
			1131	723	200	207	1			

- Molecule 36 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	38	143	Total	C	N	O	S	0	0	0
			1089	694	191	202	2			

- Molecule 37 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	48	142	Total	C	N	O	S	0	0	0
			1047	665	184	193	5			

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	58	137	Total	C	N	O	S	0	0	0
			1096	706	205	181	4			
38	15	137	Total	C	N	O	S	0	0	0
			1096	707	205	181	3			

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	68	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			
39	25	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	78	147	Total	C	N	O	S	0	0	0
			1122	698	229	192	3			
40	35	148	Total	C	N	O	S	0	0	0
			1130	704	230	193	3			

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	88	141	Total	C	N	O	S	0	0	0
			1113	709	210	187	7			
41	45	138	Total	C	N	O	S	0	0	0
			1099	702	208	183	6			

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	98	118	Total	C	N	O	S	0	0	0
			967	604	203	159	1			
42	55	118	Total	C	N	O	S	0	0	0
			967	604	203	159	1			

- Molecule 43 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	A8	111	Total	C	N	O		0	0	0
			881	556	176	149				
43	65	110	Total	C	N	O		0	0	0
			876	553	175	148				

- Molecule 44 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	B8	136	Total	C	N	O	S	0	0	0
			1132	704	232	195	1			
44	75	134	Total	C	N	O		0	0	0
			1115	694	229	192				

- Molecule 45 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	C8	115	Total	C	N	O	S	0	0	0
			950	603	199	147	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	85	117	Total	C	N	O	S	0	0	0
			963	610	202	150	1			

- Molecule 46 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	D8	101	Total	C	N	O	S	0	0	0
			778	501	142	134	1			
46	95	100	Total	C	N	O	S	0	0	0
			774	499	141	133	1			

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	E8	112	Total	C	N	O	S	0	0	0
			890	560	175	153	2			
47	A5	111	Total	C	N	O	S	0	0	0
			886	558	174	152	2			

- Molecule 48 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	F8	95	Total	C	N	O	S	0	0	0
			743	482	134	126	1			
48	B5	94	Total	C	N	O	S	0	0	0
			738	479	133	125	1			

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	G8	105	Total	C	N	O	S	0	0	0
			784	504	147	128	5			
49	C5	106	Total	C	N	O	S	0	0	0
			785	504	147	129	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	H8	165	Total	C	N	O	S	0	0	0
			1330	851	241	236	2			
50	D5	200	Total	C	N	O	S	0	0	0
			1582	1008	279	292	3			

- Molecule 51 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	I8	81	Total	C	N	O	S	0	0	0
			630	389	133	107	1			
51	E5	78	Total	C	N	O	S	0	0	0
			616	381	130	104	1			

- Molecule 52 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	J8	93	Total	C	N	O	S	0	0	0
			729	457	145	126	1			
52	F5	94	Total	C	N	O	S	0	0	0
			737	463	146	127	1			

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	K8	69	Total	C	N	O	S	0	0	0
			576	358	116	101	1			
53	G5	66	Total	C	N	O	S	0	0	0
			558	346	113	98	1			

- Molecule 54 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
54	L8	58	Total	C	N	O	0	0	0
			459	293	89	77			
54	H5	58	Total	C	N	O	0	0	0
			459	293	89	77			

- Molecule 55 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	M8	48	Total	C	N	O	S	0	0	0
			371	237	62	67	5			

- Molecule 56 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	N8	50	Total	C	N	O	S	0	0	0
			386	241	77	63	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	J5	56	Total	C	N	O	S	0	0	0
			434	272	87	70	5			

- Molecule 57 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	O8	45	Total	C	N	O	S	0	0	0
			389	241	79	65	4			

- Molecule 58 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	P8	47	Total	C	N	O	S	0	0	0
			401	246	99	54	2			
58	L5	47	Total	C	N	O	S	0	0	0
			409	251	102	54	2			

- Molecule 59 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	Q8	64	Total	C	N	O	S	0	0	0
			516	331	102	81	2			
59	M5	64	Total	C	N	O	S	0	0	0
			516	331	102	81	2			

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	13	227	Total	Mg	0	0
			227	227		
60	3E	2	Total	Mg	0	0
			2	2		
60	5E	2	Total	Mg	0	0
			2	2		
60	6I	1	Total	Mg	0	0
			1	1		
60	1K	2	Total	Mg	0	0
			2	2		
60	2K	7	Total	Mg	0	0
			7	7		
60	4K	1	Total	Mg	0	0
			1	1		

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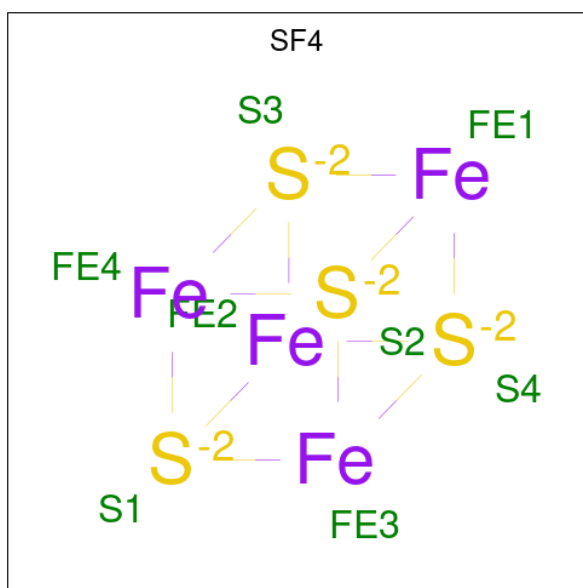
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1H	669	Total 669	Mg 669	0	0
60	16	20	Total 20	Mg 20	0	0
60	11	6	Total 6	Mg 6	0	0
60	21	2	Total 2	Mg 2	0	0
60	31	2	Total 2	Mg 2	0	0
60	41	1	Total 1	Mg 1	0	0
60	78	1	Total 1	Mg 1	0	0
60	88	4	Total 4	Mg 4	0	0
60	98	2	Total 2	Mg 2	0	0
60	I8	2	Total 2	Mg 2	0	0
60	N8	1	Total 1	Mg 1	0	0
60	P8	1	Total 1	Mg 1	0	0
60	Q8	1	Total 1	Mg 1	0	0
60	1G	167	Total 167	Mg 167	0	0
60	32	2	Total 2	Mg 2	0	0
60	52	1	Total 1	Mg 1	0	0
60	2A	1	Total 1	Mg 1	0	0
60	1L	1	Total 1	Mg 1	0	0
60	2L	2	Total 2	Mg 2	0	0
60	4L	2	Total 2	Mg 2	0	0
60	14	607	Total 607	Mg 607	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	1J	8	Total 8	Mg 8	0	0
60	29	5	Total 5	Mg 5	0	0
60	39	2	Total 2	Mg 2	0	0
60	25	2	Total 2	Mg 2	0	0
60	35	1	Total 1	Mg 1	0	0
60	45	2	Total 2	Mg 2	0	0
60	55	2	Total 2	Mg 2	0	0
60	75	1	Total 1	Mg 1	0	0
60	C5	1	Total 1	Mg 1	0	0
60	E5	1	Total 1	Mg 1	0	0
60	F5	1	Total 1	Mg 1	0	0
60	M5	1	Total 1	Mg 1	0	0

- Molecule 61 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
61	3E	1	Total	Fe	S	0	0
			8	4	4		
61	32	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	5I	1	Total	Zn	0	0
			1	1		
62	5A	1	Total	Zn	0	0
			1	1		

- Molecule 63 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	13	544	Total	O	0	0
			544	544		
63	1E	1	Total	O	0	0
			1	1		
63	3E	1	Total	O	0	0
			1	1		
63	4E	2	Total	O	0	0
			2	2		
63	8E	1	Total	O	0	0
			1	1		
63	1I	1	Total	O	0	0
			1	1		
63	3I	5	Total	O	0	0
			5	5		
63	5I	3	Total	O	0	0
			3	3		
63	6I	4	Total	O	0	0
			4	4		
63	BI	1	Total	O	0	0
			1	1		
63	1F	1	Total	O	0	0
			1	1		
63	1K	1	Total	O	0	0
			1	1		
63	2K	16	Total	O	0	0
			16	16		
63	4K	13	Total	O	0	0
			13	13		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	1H	1966	Total 1966	O 1966	0	0
63	16	42	Total 42	O 42	0	0
63	11	12	Total 12	O 12	0	0
63	21	9	Total 9	O 9	0	0
63	31	8	Total 8	O 8	0	0
63	58	3	Total 3	O 3	0	0
63	78	10	Total 10	O 10	0	0
63	88	7	Total 7	O 7	0	0
63	98	1	Total 1	O 1	0	0
63	A8	2	Total 2	O 2	0	0
63	B8	3	Total 3	O 3	0	0
63	C8	7	Total 7	O 7	0	0
63	D8	1	Total 1	O 1	0	0
63	F8	1	Total 1	O 1	0	0
63	G8	3	Total 3	O 3	0	0
63	I8	5	Total 5	O 5	0	0
63	J8	10	Total 10	O 10	0	0
63	L8	4	Total 4	O 4	0	0
63	P8	1	Total 1	O 1	0	0
63	Q8	7	Total 7	O 7	0	0
63	1G	397	Total 397	O 397	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	32	5	Total 5	O 5	0	0
63	42	1	Total 1	O 1	0	0
63	52	4	Total 4	O 4	0	0
63	3A	2	Total 2	O 2	0	0
63	5A	1	Total 1	O 1	0	0
63	6A	1	Total 1	O 1	0	0
63	7A	2	Total 2	O 2	0	0
63	9A	2	Total 2	O 2	0	0
63	BA	2	Total 2	O 2	0	0
63	2L	7	Total 7	O 7	0	0
63	4L	8	Total 8	O 8	0	0
63	14	1520	Total 1520	O 1520	0	0
63	1J	23	Total 23	O 23	0	0
63	19	12	Total 12	O 12	0	0
63	29	9	Total 9	O 9	0	0
63	39	8	Total 8	O 8	0	0
63	15	1	Total 1	O 1	0	0
63	25	13	Total 13	O 13	0	0
63	35	5	Total 5	O 5	0	0
63	45	4	Total 4	O 4	0	0
63	85	4	Total 4	O 4	0	0

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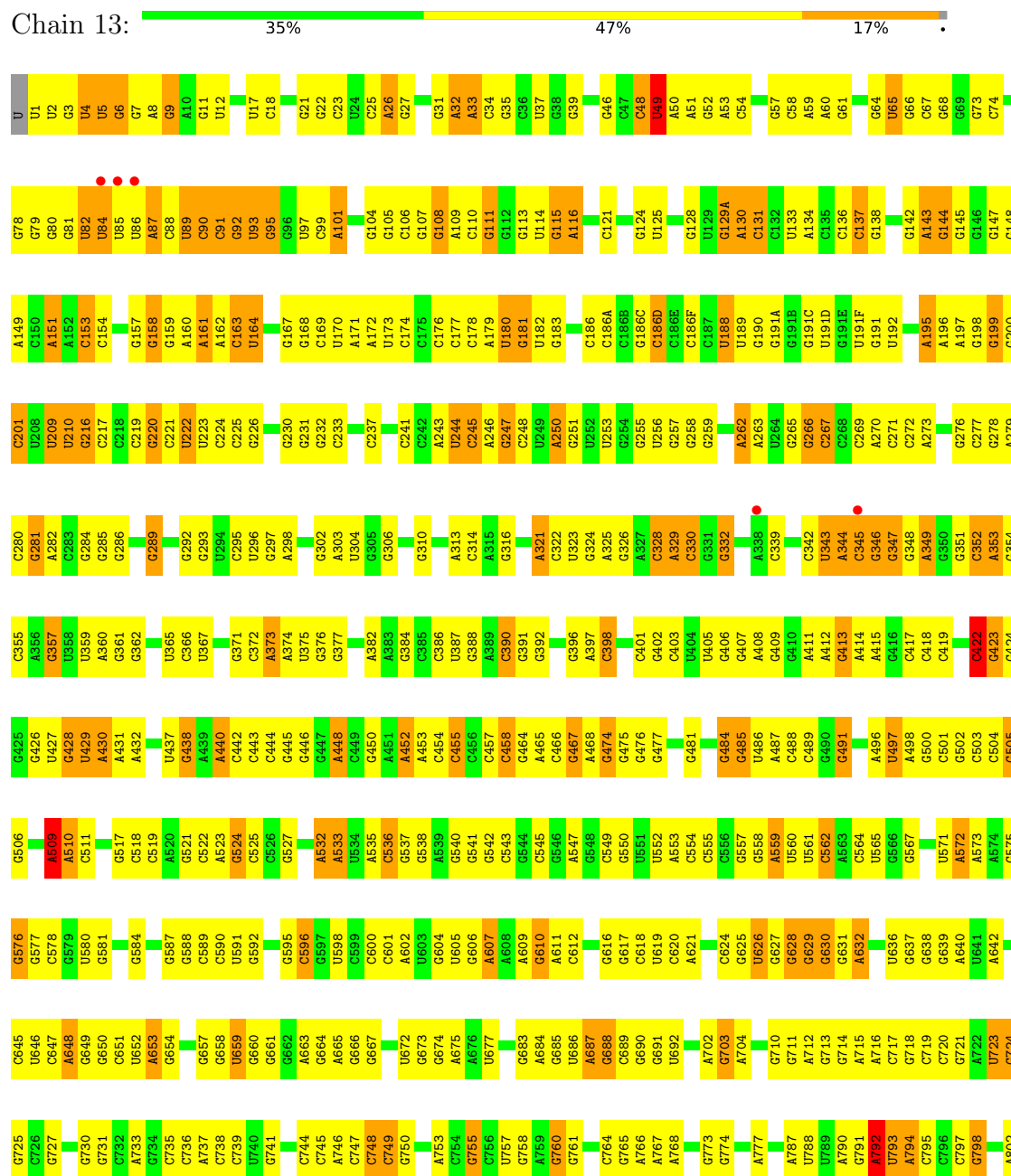
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
63	A5	1	Total	O	0	0
			1	1		
63	B5	1	Total	O	0	0
			1	1		
63	C5	1	Total	O	0	0
			1	1		
63	E5	3	Total	O	0	0
			3	3		
63	F5	6	Total	O	0	0
			6	6		
63	L5	2	Total	O	0	0
			2	2		
63	M5	9	Total	O	0	0
			9	9		

3 Residue-property plots

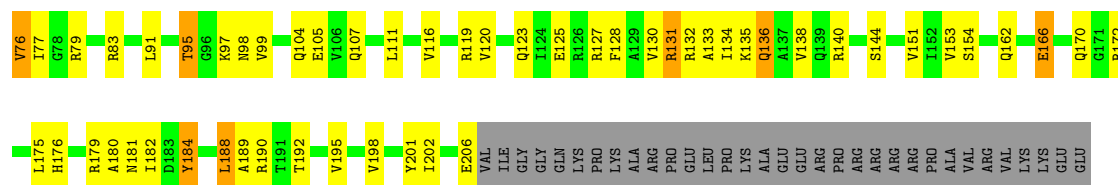
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: 16S ribosomal RNA

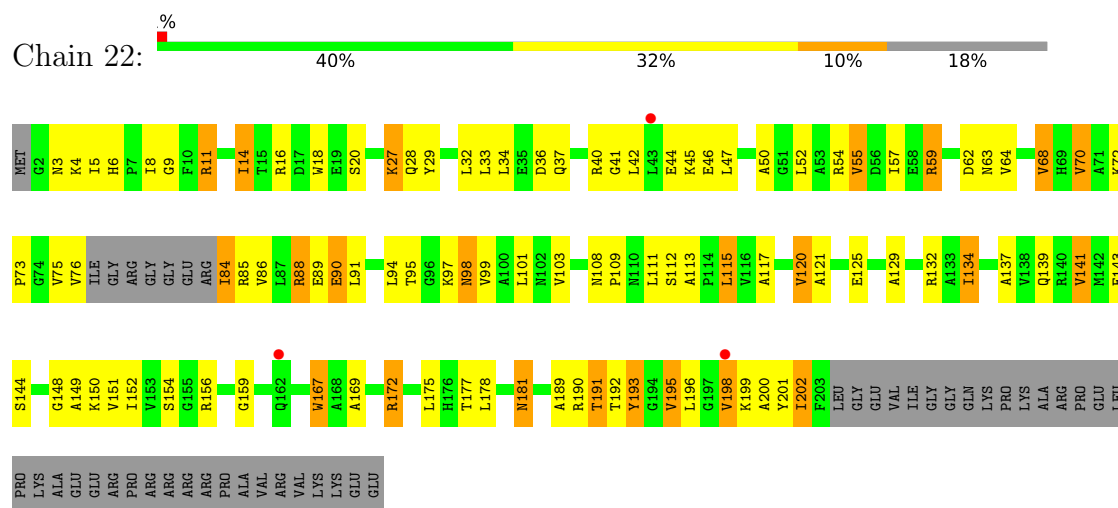


A1285	C1218	U1150	U1085	G1021	U957	A872	G791	C720	C647	U571	G502	G413	C328	C235
A1286	U1219	A1151	U1086	G1022	A958	A873	A792	G721		A572	C503	A414	A329	G236
A1287	G1203	A1152	G1087	G1023	A959	G874	U793	A722	G650	A573	C504	A415	C330	G237
A1288	G1221	C1153	G1088	G1024	U960	C875	A794	U723	C651	A574	G505	G416	G331	G238
A1289	G1222	G1154	U1089	U1025	U961			G724	G575	G576	G506	C419	G332	U239
U1292	C1223	G1155	U1090	G1026	G962	G878	G800	G725	A653	G577	C507	U420	G333	C240
U1293	G1224	G1156	U1091	C1027	G963	C879		G726			C508	U421		
G1293	A1225	A1157	A1092	C1028		C880	U804	G727	C656	C578	A509	U422	U340	A243
G1294	C1226	A1158	A1093	G1028A	G966	C881	C805	A728		C579	A510	C421	C341	U244
G1295	A1227	U1159	G1094	C1028B	C967	C882		A729	G660	U580	C511	G422		C245
C1296	C1228	U1160	U1095	G1029	A968	C883	C811	G730		G581	U512	G423	A344	C246
C1297		G1161	A0969	G1030	C969	U884		G731	A663	U582	C513	G424		G247
C1298	U1232	C1162	C1097	G1031	C970	G885	A815		A664	A583	C514	G425	G346	
A1299		C1163	C971	A1032	C972	G886	A816	G735	A665	G584	G515	U427	G347	A250
G1300	C1237		C973	G1032A	G973	C888	C817	G736	G666	U516	U516	U428		G251
U1301	A1238	A1170	C1100	G1032B	G974	C889	G818	A737		C517	C518	U429	G350	G254
C1302	U1239	G1171	G1033	G1033	A974	A889	A819	C738	U669	C589	C519	A430	G351	
C1303	U1240	C1172	A1102	G1034	A975	C890	U820	C739	G670	C590	C519	A431	C352	G257
G1304	G1241	G1173	C1103	A1035	G976	U891	C821	U740		U591	A520		A353	G258
G1305	C1242	G1174	G1104	G1036	A977	A892	C822	G741	G673	G592	G521	U434	G354	U261
A1306	C1243	G1175	A1105	C1037	A978		G823	G742	G674	C522	G522	U435	G362	A262
U1307		A1176	G1106	C1038	C979	G906	C824	G745	A675	C596	A523	U436	A363	G266
	C1244	G1177	C1107	C1039	C980	U910	G825	A746	A676	G597		U437	U359	G267
G1312	A1245	G1178	G1108	U1040	U981	C911	C826	G747	U677	C600	G526	U438	A360	
	C1246	A1179	C1109	A1041	U982	C912	C827	C748	G679	C601	G528	U439	G361	
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A1248	A1248	A1181	A1111	C1043	C984	C914		G750	G683	G603	G530	C442	U367	G269
C1249	C1249	G1182	C1112	A1044	C985	A915	U833	G751	A684	G604	U531	C443	A366	U261
G1250	A1251	G1183	C1113	C1045	A986	C916	U834	G752	G685	U605	A532	G447	G371	A272
A1252	C1114	G1184	G987	A1046	C987	G917	A753	A754	U686	G606	A533	C448	G372	A274
		G1185				A918	G837	G754	A687	A607	U534	C449	C373	G275
G1255	G1255	A1188	U991	G1050	U992	A919	G838	G755	A688	A535	A535	C450	A373	G276
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G1257	G1257	G1190	A994	U1052	G124	U921	C842	U757	G690	C612	G537	C452	U375	G278
A1324	C1258	A1191	C995	C1053	U922		C843	G758	G691	C613	G538	C453	G376	A279
C1325	U1259	C1192	A996	A1055	G926		C848	A759	U692	A614	A539		G377	C280
C1260	G1260		U997	U1056	G927		C849	G760	G693	C615	G540	C458	G377	
A1261	A1261	U1196	G998	G1057	G928	G928	U850		A694	G616	G541	C464	A382	G281
C1262	C1262	G1197	C998A	C1058	G929	G929	G851	G764	A695	C617	G542	C466	A383	G286
C1263		U1198	U999	C1059			C852	G765	A696	C618		C467	A386	G289
G1264	G1264	U1199	A1000	C1060	G933	G933	C853	A766	U619	A547		C468	C386	C290
C1265	C1265	G1131	G1001	G1061	A934	A935	C854	A767	C699	C620	G550	C474	C380	
G1266	G1266	C1132	G1002	C1062	C935	C936	G855	A768	A700	A621		C475	C395	C295
C1267	C1267	G1133	G1003	C1063	G936		C857	G769	G701	A622	C555	G481	G396	U296
A1268	A1268	G1134	G1004	G1064			C858		A702	G623	C556	C482	G397	G297
		U1135	A1005	C1069	G939	G939	G859	G774	A706	G624	C557	C483	A397	A298
G1271	G1271	C1137	C1006	U1070	C940	C941	A860	G775	C707	U625	G558	G484	G299	G299
G1272	G1272	G1138	C1007	U1071	G942	G942	C861	A777	C708	U626	A559	U486	C398	
C1273	C1273	G1139	C1008	C1071	U943	U943	C862	G778		G628	U560	U487	G402	A300
G1274	G1274	C1140	G1011	G1072	G944	G944	U863	G779	G711	U561	U561	A488		A315
A1275	A1275	G1141		U1073	G945	G945	A864	A780	A712	C562	C562	C489	U405	A321
C1276	C1276	G1142	A1014	G1077	G947	G947	A865		G713	A563	C564	C496	G406	G407
G1277	G1277	G1143	U1078	U1078	C948	C948	C866	G785	G714	C565	C565	A495	U323	U323
C1278	C1278	G1144	A1015	G1079			G867	G786	A715	U565	U565	U497	A408	A408
U1279	U1279	C1145	A1016	G1079			C868	A787	A716	G567	G567	U498	G409	G324
A1280	A1280	G1146	G1017	G1080	G953	G954	C869	U788		G637	G637	A498	G410	A325
U1281	U1281	A1147	C1018	G1081	G954	G954	U870	U789	G717	G638	G638	G500	A411	G326
C1282	C1282	G1148	C1019	G1081	U955	U955	U871	A790	C719	U646	G570	C501	A412	A327
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A1349	C1284													





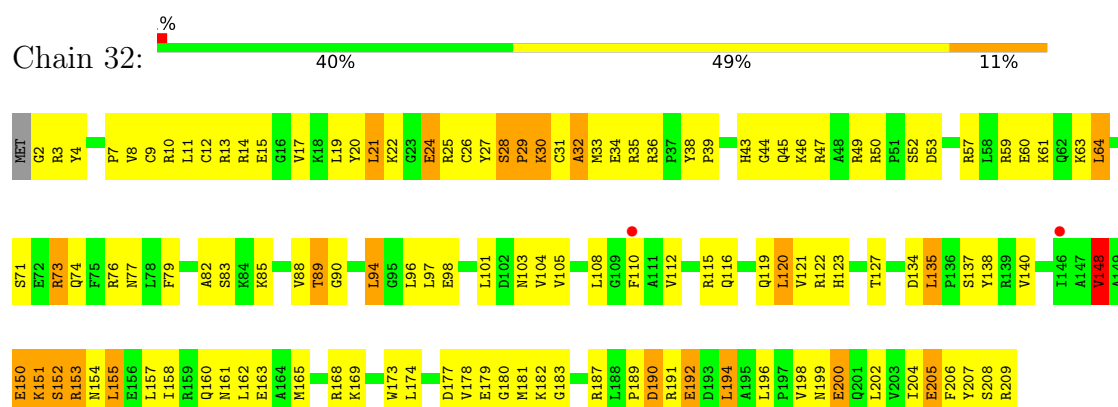
• Molecule 3: 30S ribosomal protein S3



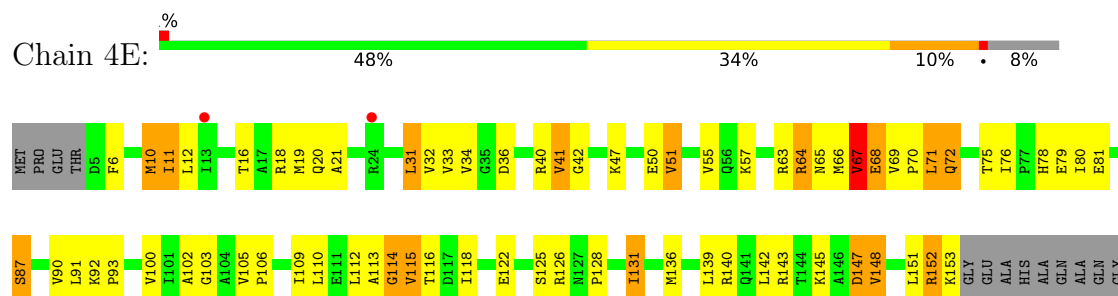
• Molecule 4: 30S ribosomal protein S4



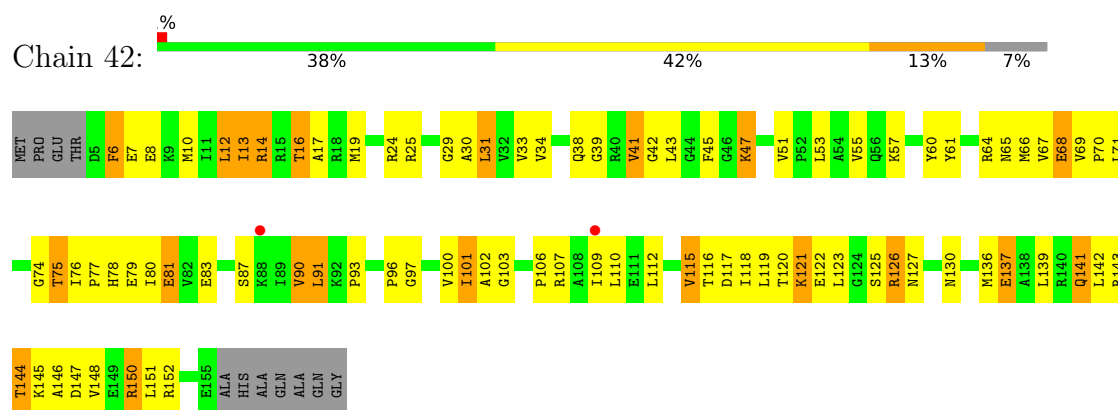
• Molecule 4: 30S ribosomal protein S4



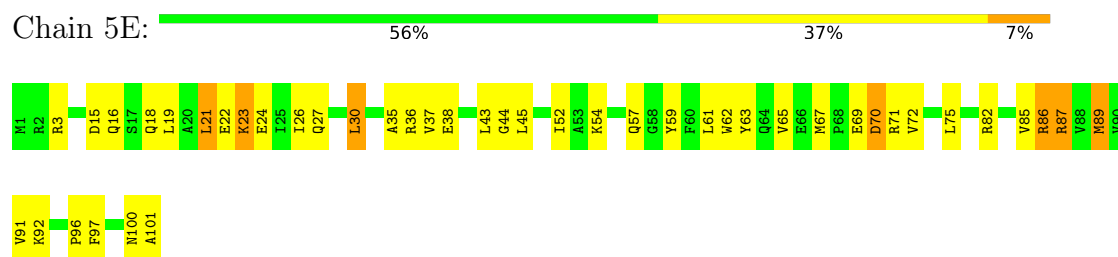
- Molecule 5: 30S ribosomal protein S5



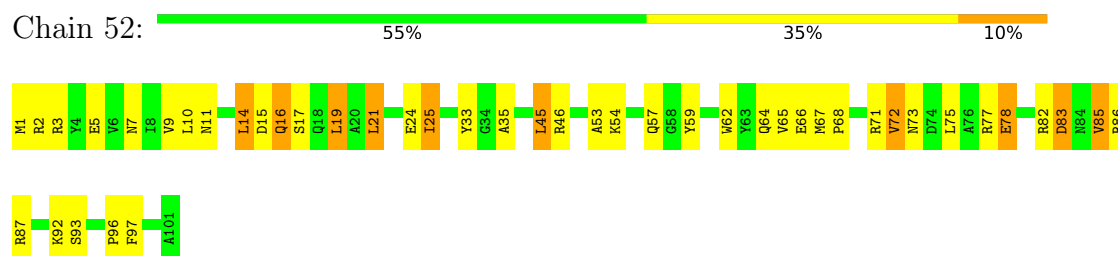
- Molecule 5: 30S ribosomal protein S5



- Molecule 6: 30S ribosomal protein S6

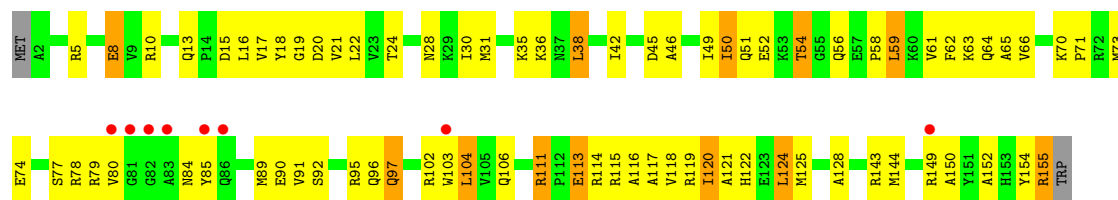


- Molecule 6: 30S ribosomal protein S6



- Molecule 7: 30S ribosomal protein S7

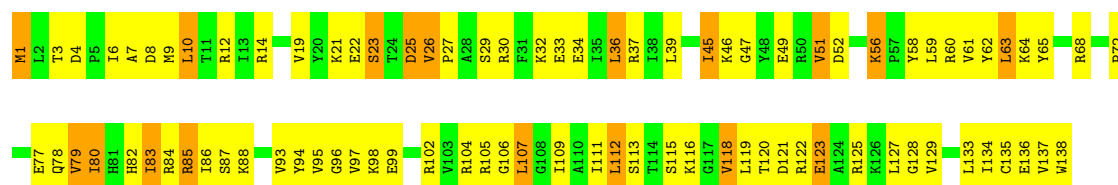
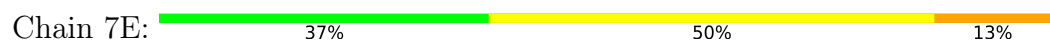




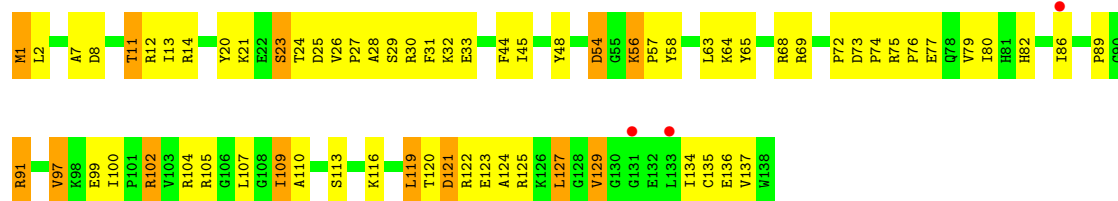
• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8



• Molecule 8: 30S ribosomal protein S8

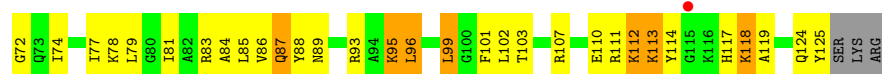


• Molecule 9: 30S ribosomal protein S9

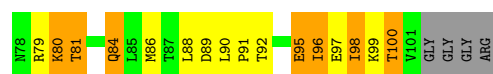




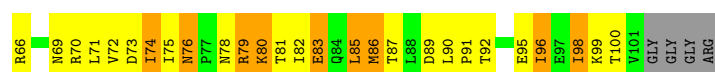
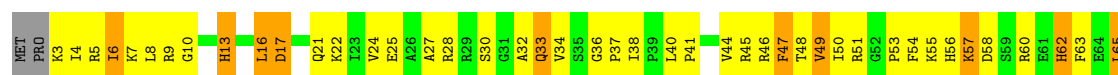
• Molecule 9: 30S ribosomal protein S9



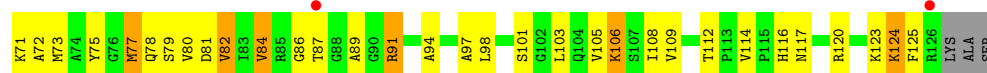
• Molecule 10: 30S ribosomal protein S10



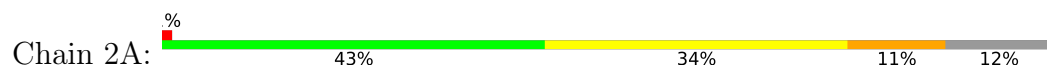
• Molecule 10: 30S ribosomal protein S10



• Molecule 11: 30S ribosomal protein S11

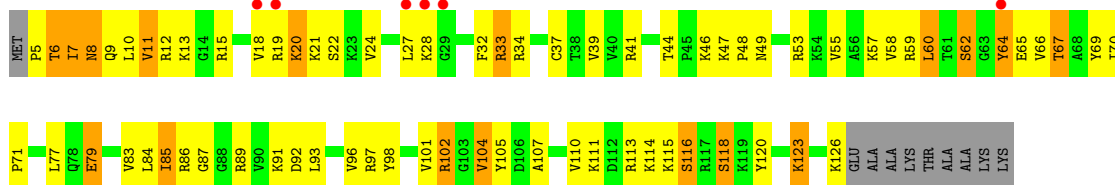


• Molecule 11: 30S ribosomal protein S11

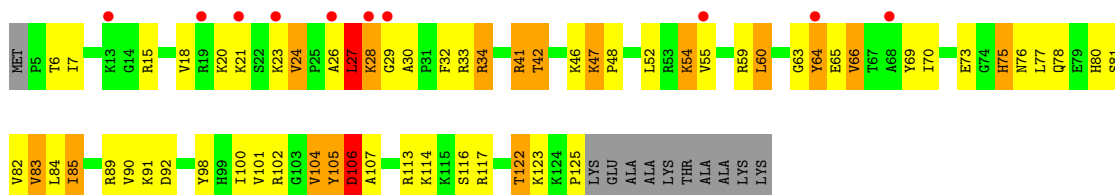




Chain 3I:



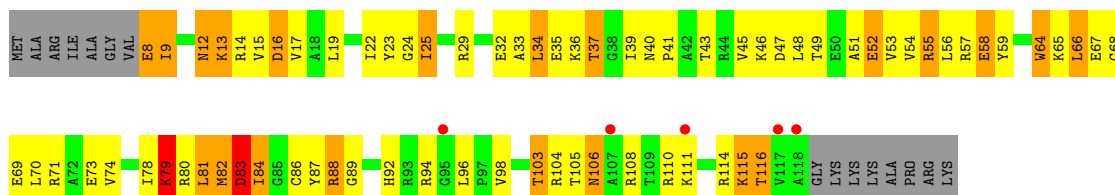
Chain 3A:

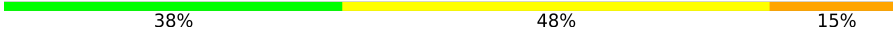


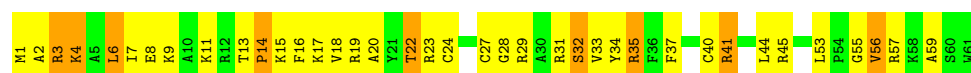
Chain 4I:



Chain 4A: 4% 30% 40% 17% 9%

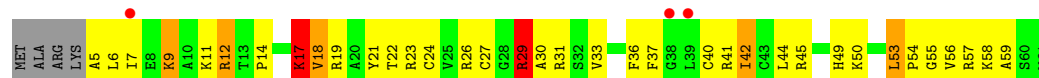


Chain 5I: 



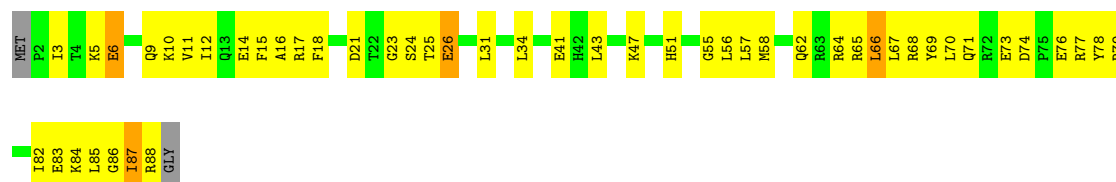
- Molecule 14: 30S ribosomal protein S14 type Z

Chain 5A: 



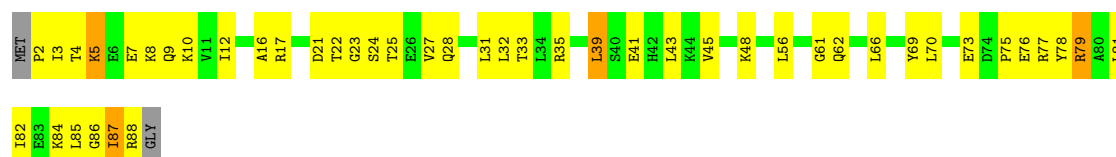
- Molecule 15: 30S ribosomal protein S15

Chain 6I: 



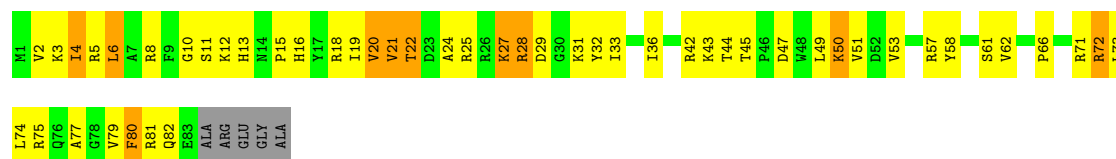
- Molecule 15: 30S ribosomal protein S15

Chain 6A: 



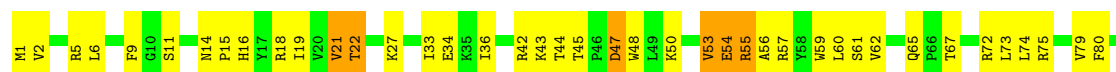
- Molecule 16: 30S ribosomal protein S16

Chain 7I: 



- Molecule 16: 30S ribosomal protein S16

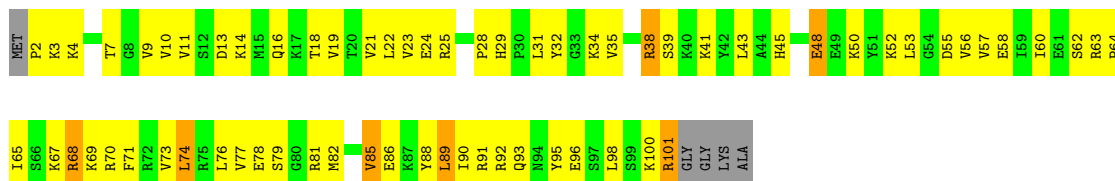
Chain 7A: 



ARG
GLU
GLY
ALA

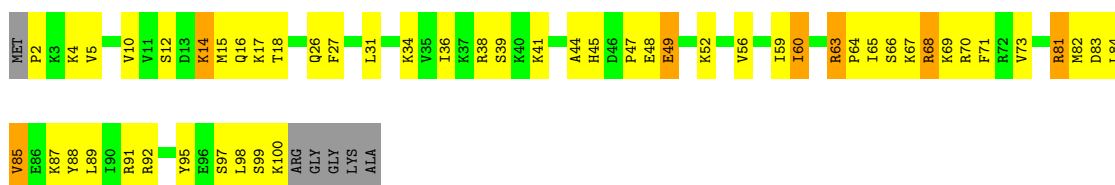
• Molecule 17: 30S ribosomal protein S17

Chain 8I: 31% 57% 7% 5%



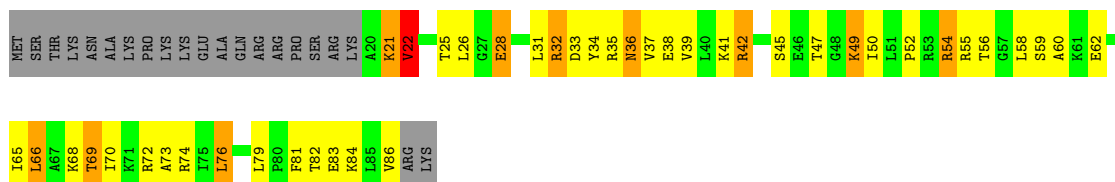
• Molecule 17: 30S ribosomal protein S17

Chain 8A: 45% 43% 7% 6%



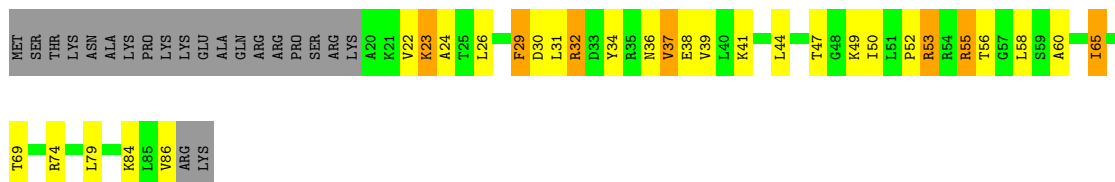
• Molecule 18: 30S ribosomal protein S18

Chain 9I: 27% 36% 11% 24%



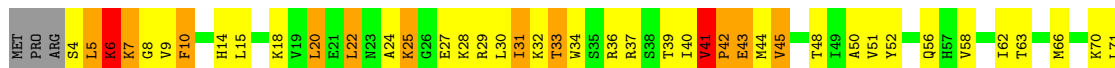
• Molecule 18: 30S ribosomal protein S18

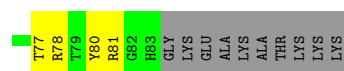
Chain 9A: 42% 26% 8% 24%



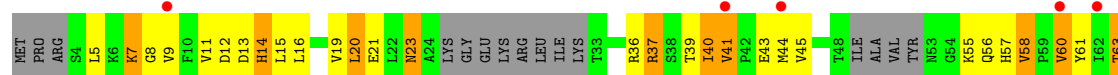
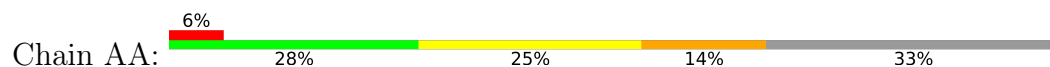
• Molecule 19: 30S ribosomal protein S19

Chain AI: 37% 35% 12% 14%

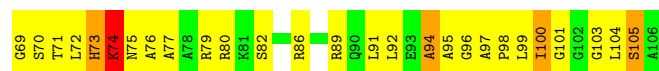
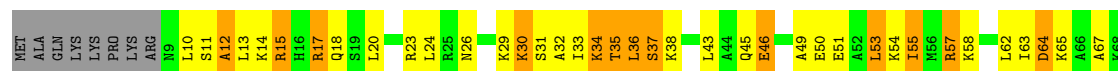
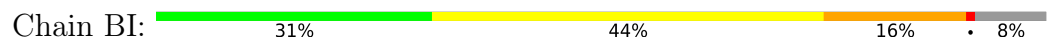




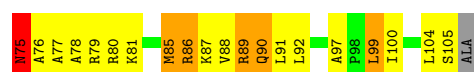
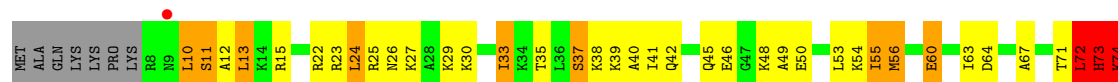
- Molecule 19: 30S ribosomal protein S19



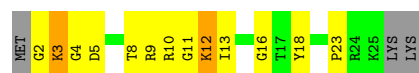
- Molecule 20: 30S ribosomal protein S20



- Molecule 20: 30S ribosomal protein S20



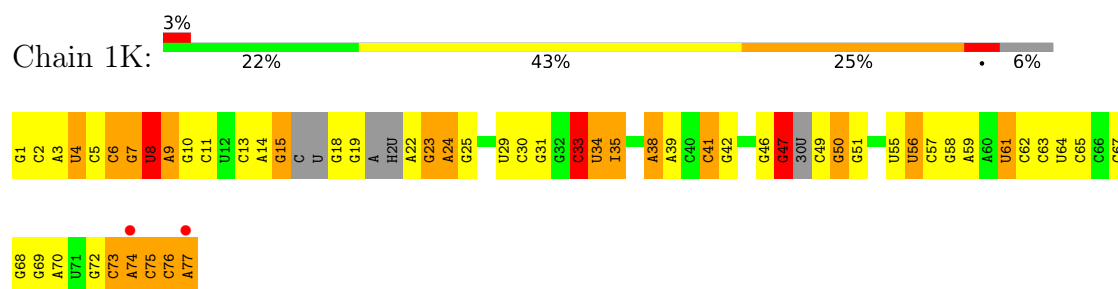
- Molecule 21: 30S ribosomal protein Thx



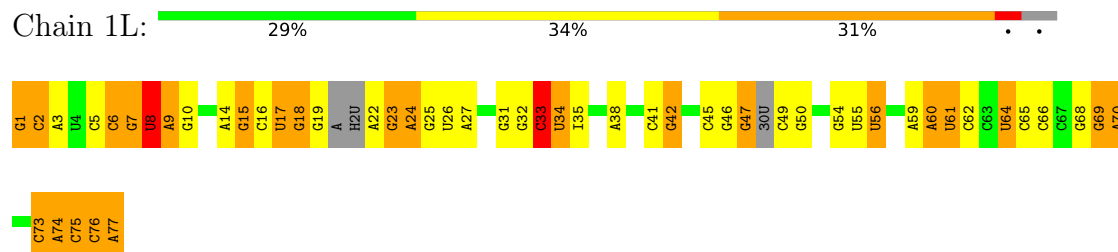
- Molecule 21: 30S ribosomal protein Thx



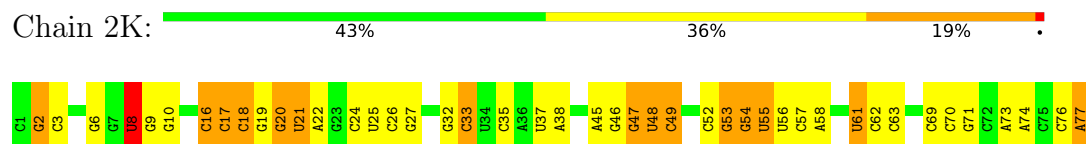
- Molecule 22: tRNAArg



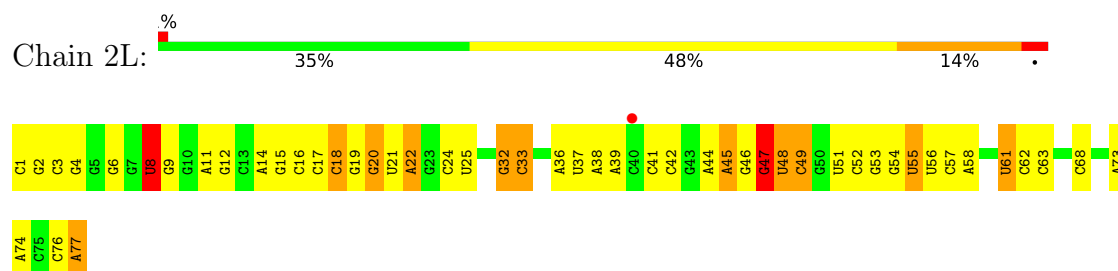
• Molecule 22: tRNAArg



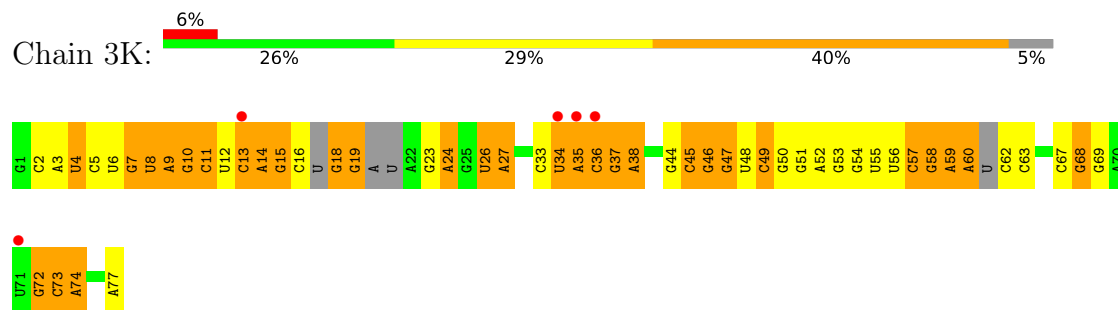
• Molecule 23: tRNAfMet



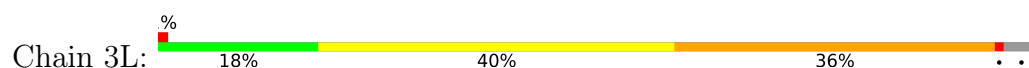
• Molecule 23: tRNAfMet

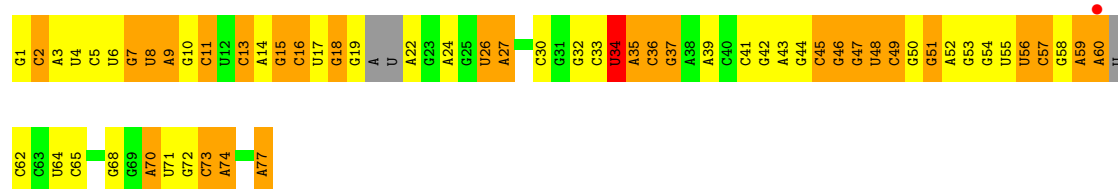


• Molecule 24: tRNAArg



• Molecule 24: tRNAArg

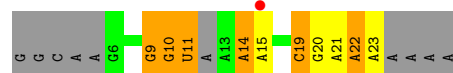




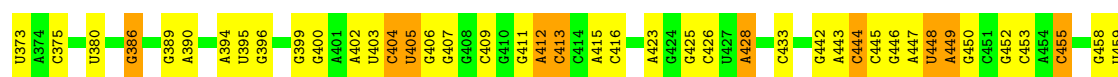
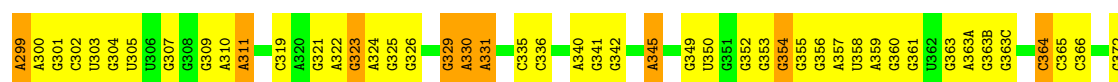
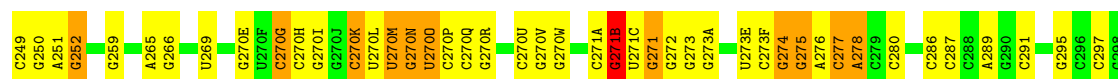
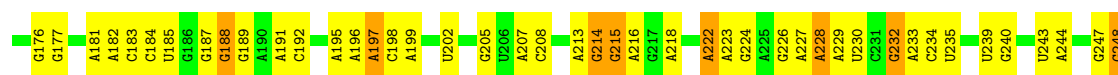
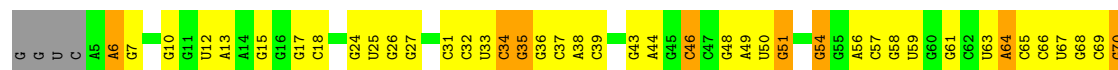
- Molecule 25: mRNA



- Molecule 25: mRNA

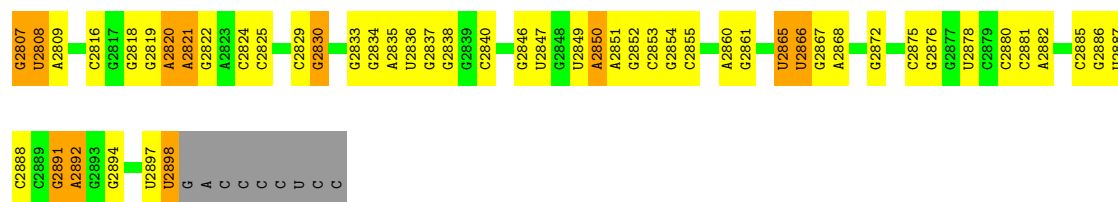


- Molecule 26: 23S ribosomal RNA

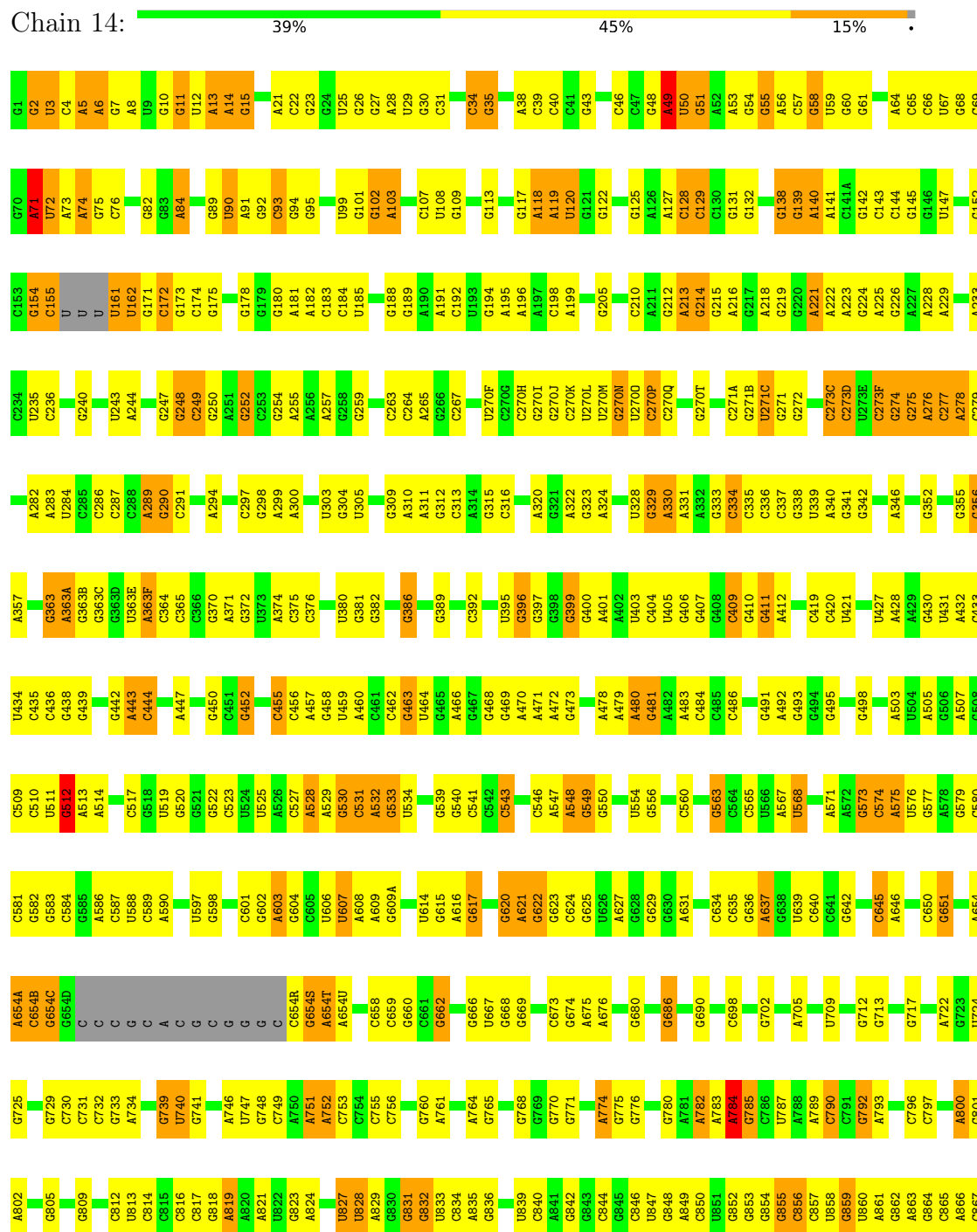




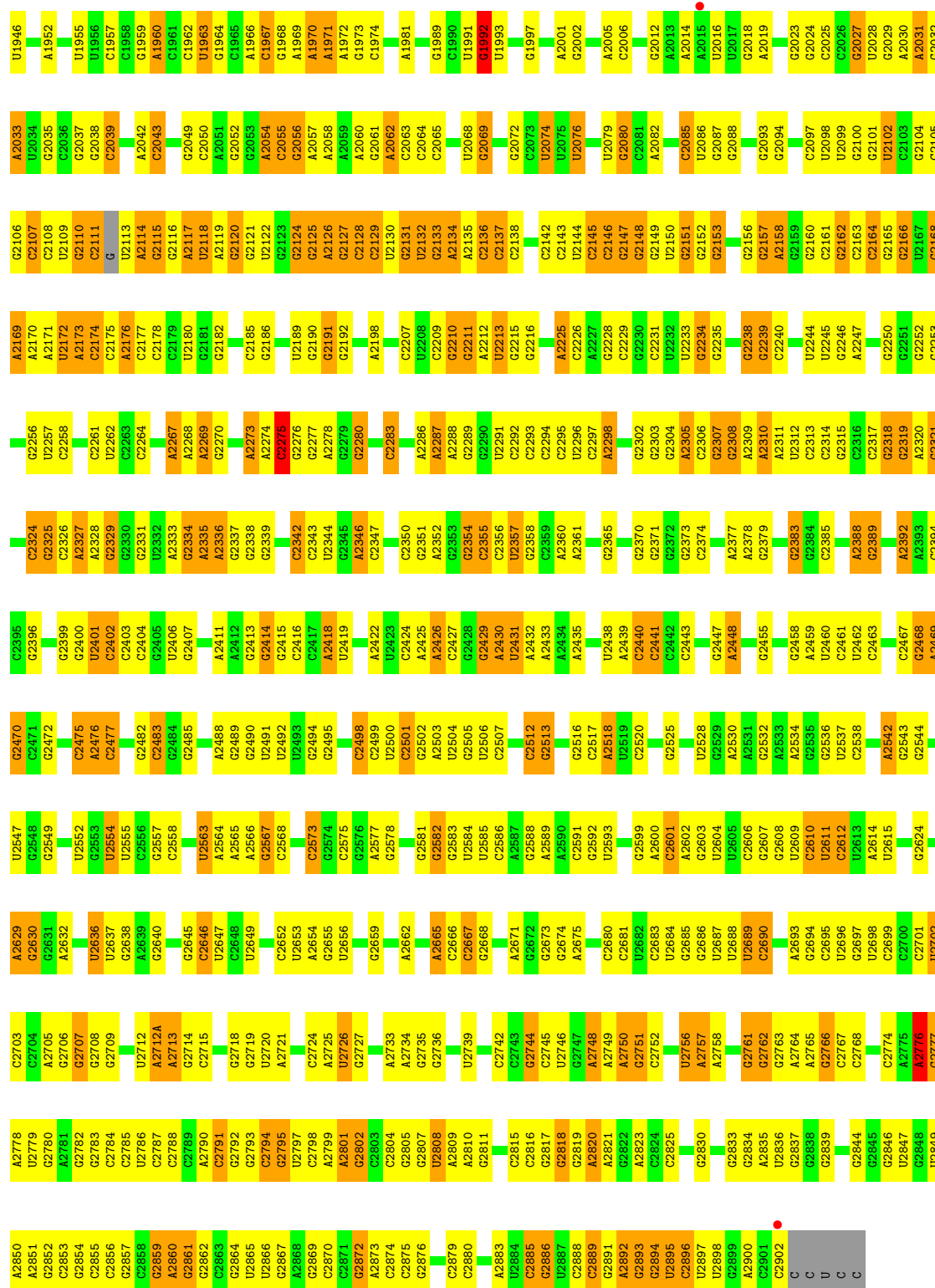
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G2735	C2666	A2589	A2505	C2346	A2274	C2188	A2126	A2051	A1969	C1879	U1794	G1695	G1627
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A2740	G2668	G2591	G2508	C2350	G2276	G2190	G2128	G2053	A1971	G1883	U1796	G1697	U1629
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C2743	A2675	G2597	C2515	C2356	G2282	C2196	G2132	A2057	G1980	A1889	G1795	U1706	A1632
G2744	C2676	A2598	G2516	U2357	C2283	U2197	G2133	A2058	A1981	A1890	G1800	G1801	G1633
A2747	A2679	G2599	C2517	U2358	C2284	A2198	A2134	A2059	C1982	A1891	G1802		
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A2750	G2681	C2601	U2519	A2360	A2286	C2205	G2136	A2061	G1984	A1900			
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	U2684	G2603	G2525	G2372	G2288	C2209	C2138	C2065	A1986	C1902			
	G2685			G2373	G2289	G2210	C2140	G2066					
	G2686			G2374	U2291	G2211		G2067					
	U2756	C2606	G2529	G2375	U2449	A2212	C2143	U2068	G1989	G1906			
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	C2690	C2610	G2533	G2379	A2453	G2216	C2147	U2074	U1993				
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A2765	G2692	C2612		C2381	A2305	G2224	G2149	U2079	G1997	C1914			
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A2775	U2698			A2388	U2322	U2232	G2155	G2094	G2004	G1921			
A2776	G2777	U2621	U2547	A2389	U2311	G2233	G2156	U2096	A2005	U1922			
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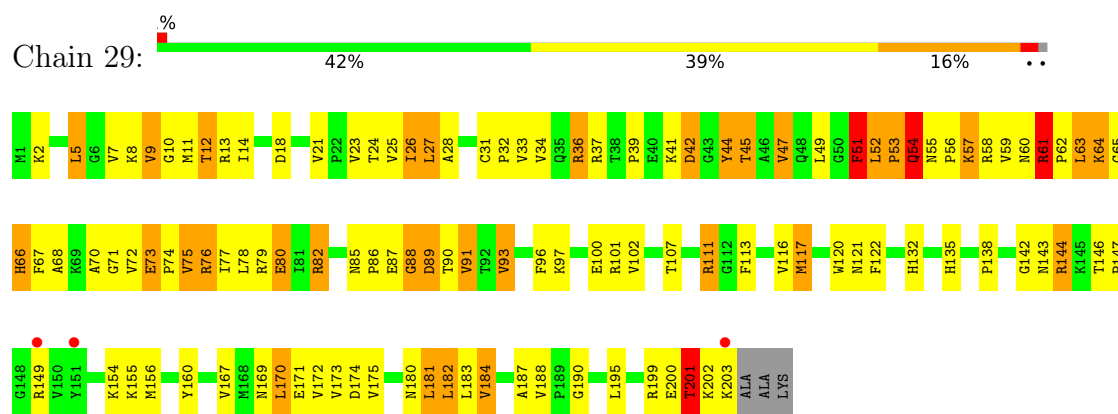


• Molecule 26: 23S ribosomal RNA

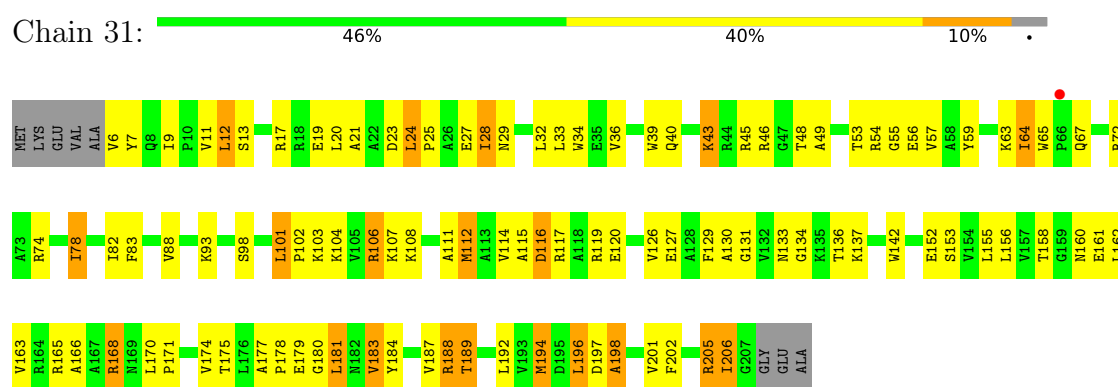


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C1782	U1690	U1602	G1522	A1453	G1382	A1302	G1225	C1150	A1077	U1014	G947	G879
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C1901	G1717		G1542	G1473	U1399		G1252	G1168		U1035	U969	A899
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C1914	A1729	A1637	A1558	U1482	C1408		G1259	G1176	U1108	G1042	G975	A899
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A1936	G1752	C1657	C1577	A1493	G1421	G1348	G1271	U1188	G1117	G1051	C986	A918
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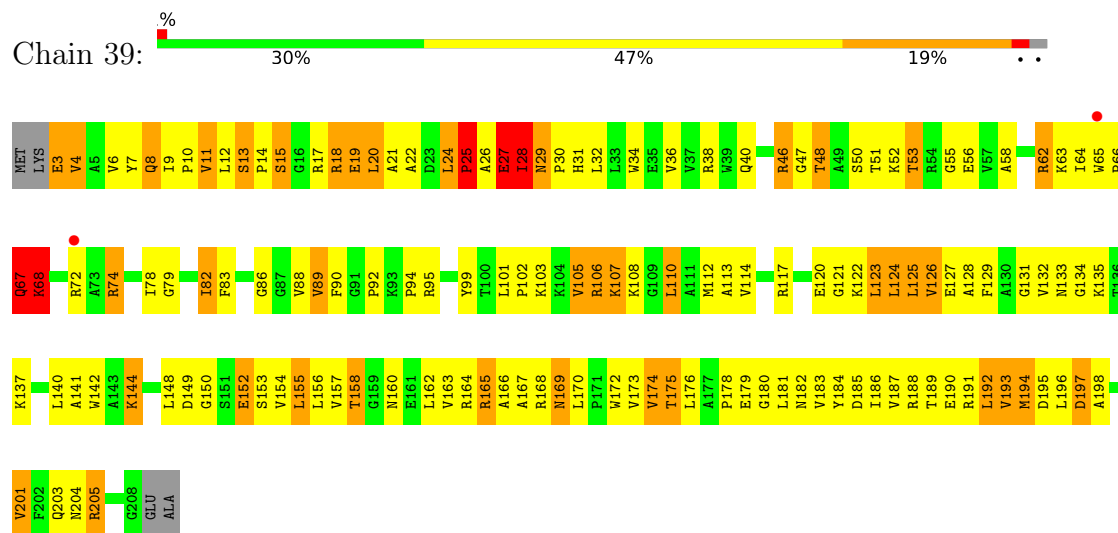




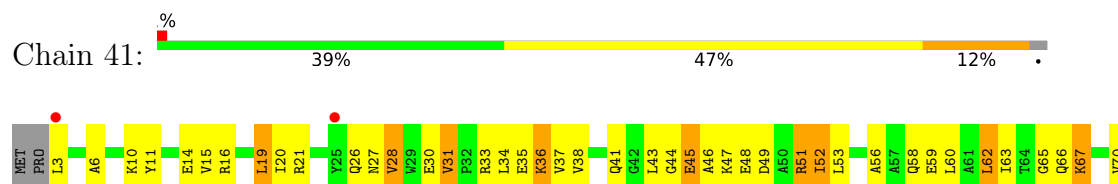
• Molecule 31: 50S ribosomal protein L4

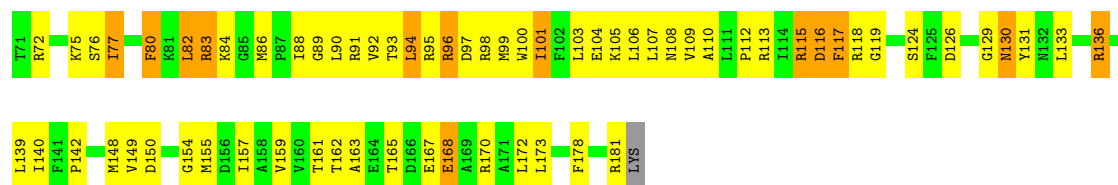


• Molecule 31: 50S ribosomal protein L4

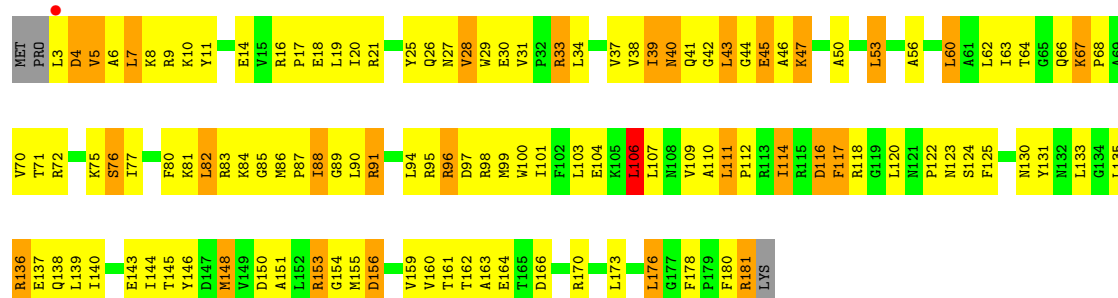


• Molecule 32: 50S ribosomal protein L5

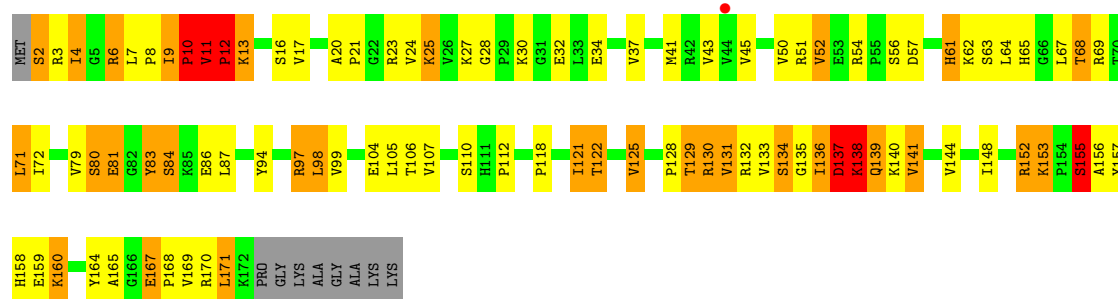
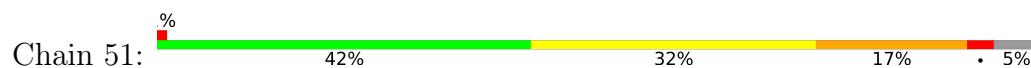




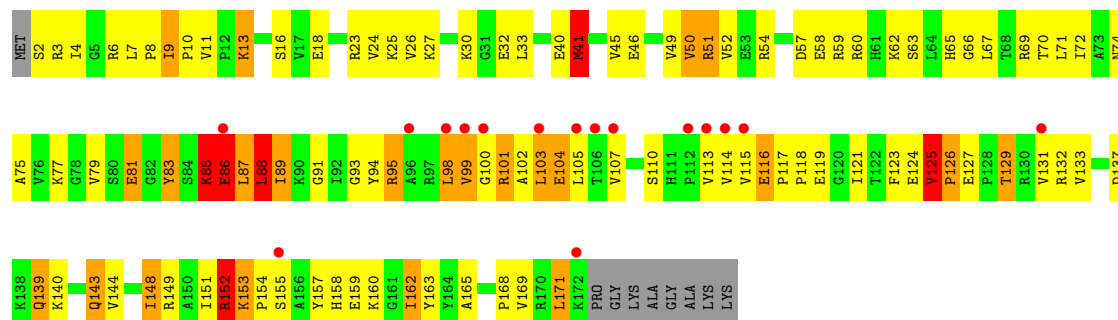
• Molecule 32: 50S ribosomal protein L5



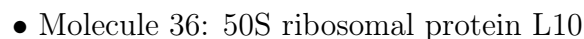
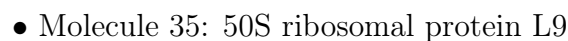
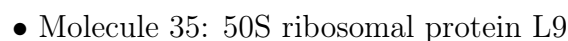
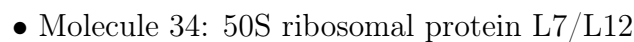
• Molecule 33: 50S ribosomal protein L6

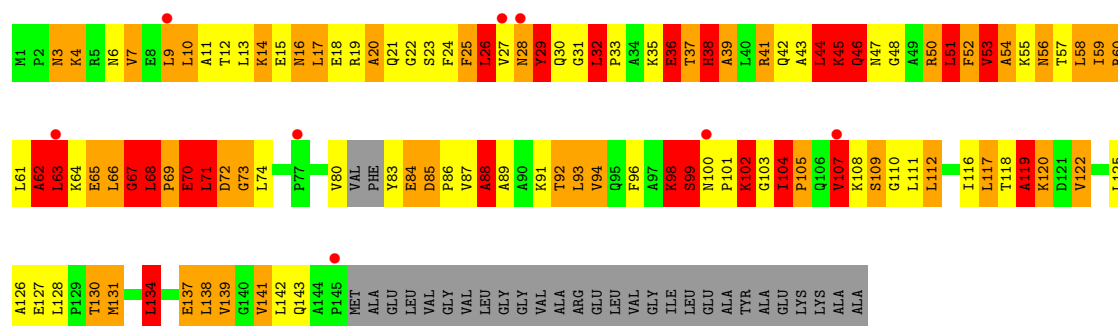


• Molecule 33: 50S ribosomal protein L6



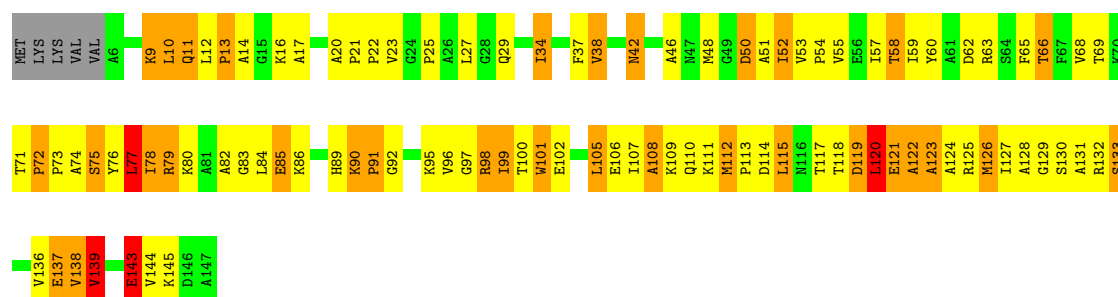
• Molecule 34: 50S ribosomal protein L7/L12





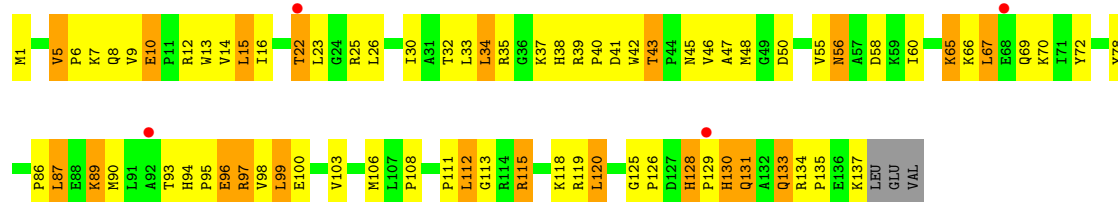
• Molecule 37: 50S ribosomal protein L11

Chain 48: 29% 42% 22%



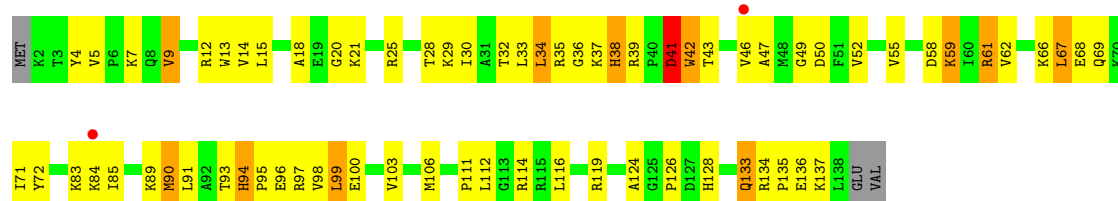
• Molecule 38: 50S ribosomal protein L13

Chain 58: 3% 44% 39% 15%



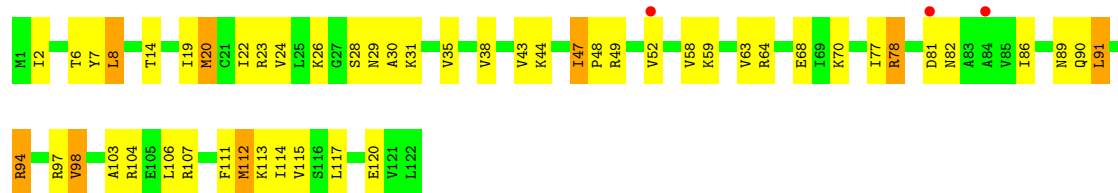
• Molecule 38: 50S ribosomal protein L13

Chain 15: % 47% 42% 8%

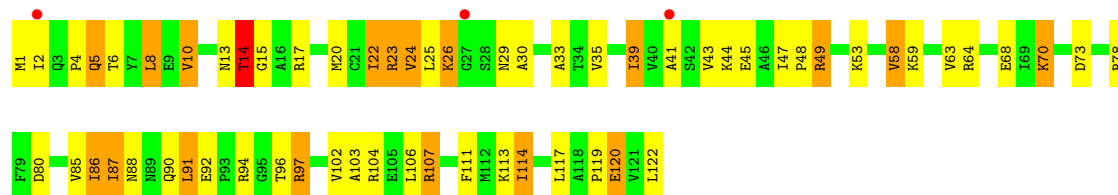


• Molecule 39: 50S ribosomal protein L14

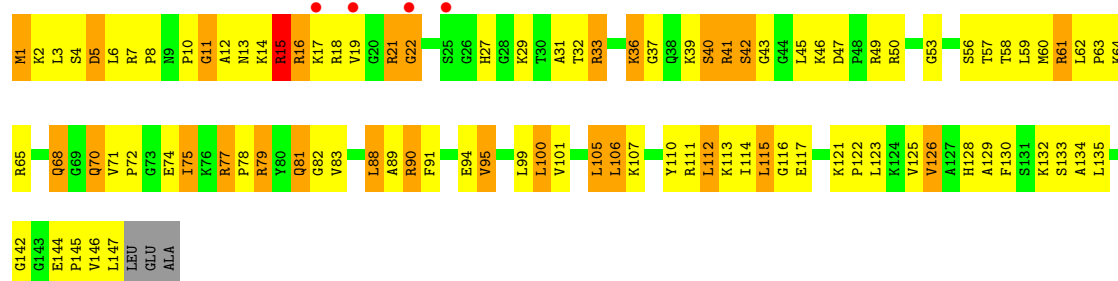
Chain 68: 2% 58% 35% 7%



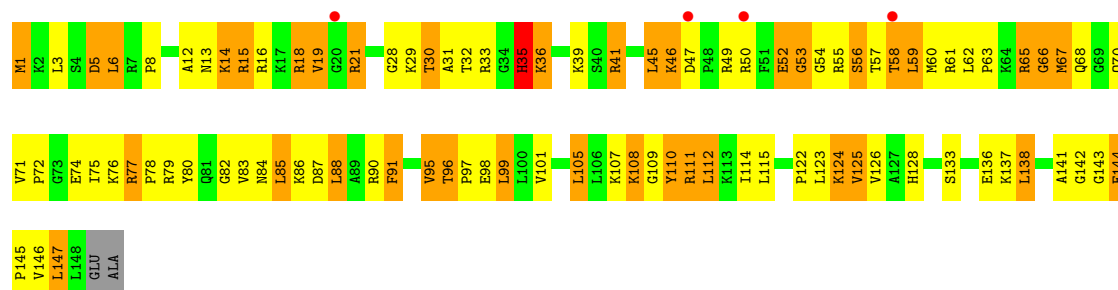
• Molecule 39: 50S ribosomal protein L14



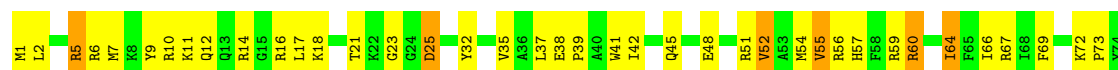
• Molecule 40: 50S ribosomal protein L15



• Molecule 40: 50S ribosomal protein L15

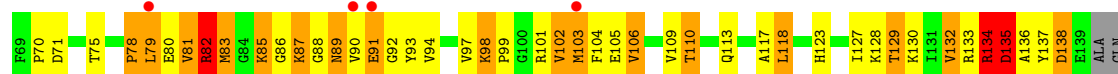
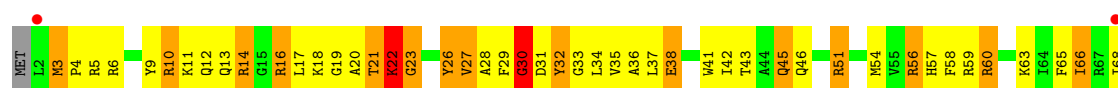


• Molecule 41: 50S ribosomal protein L16

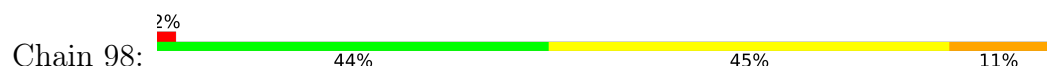




• Molecule 41: 50S ribosomal protein L16



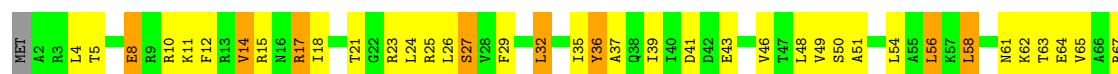
• Molecule 42: 50S ribosomal protein L17



• Molecule 42: 50S ribosomal protein L17



• Molecule 43: 50S ribosomal protein L18

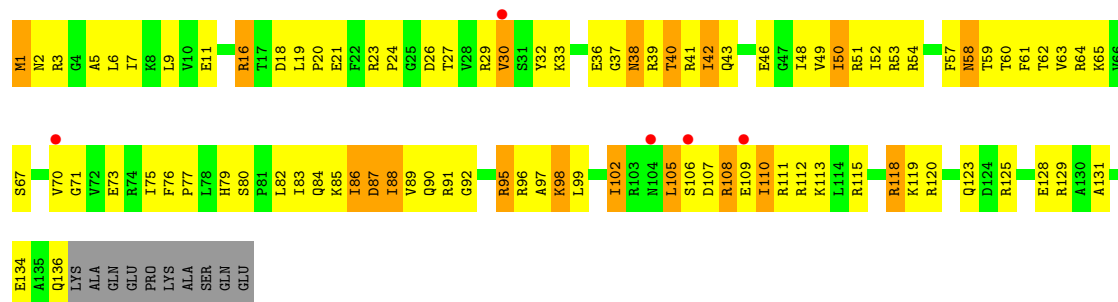


• Molecule 43: 50S ribosomal protein L18

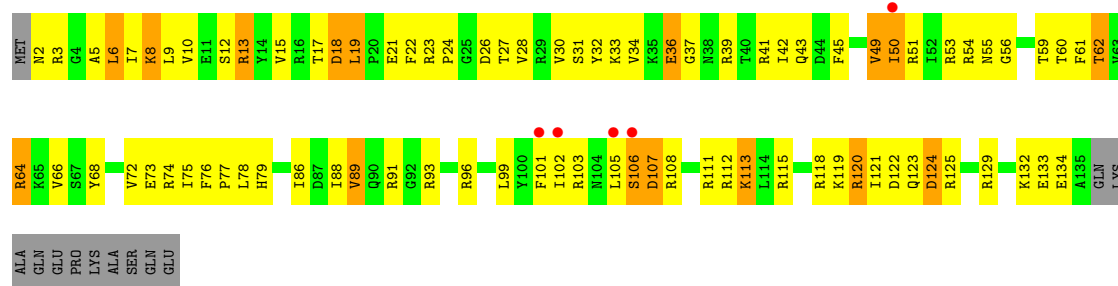




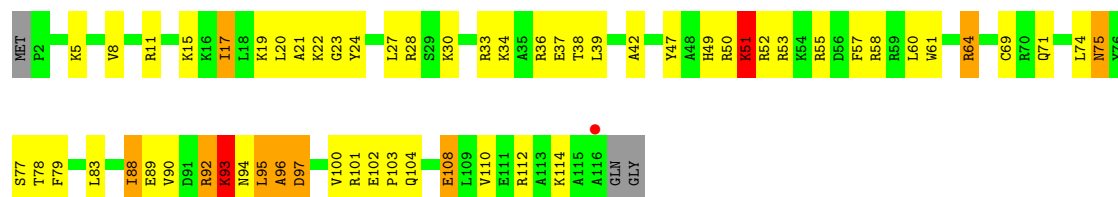
• Molecule 44: 50S ribosomal protein L19



• Molecule 44: 50S ribosomal protein L19



• Molecule 45: 50S ribosomal protein L20

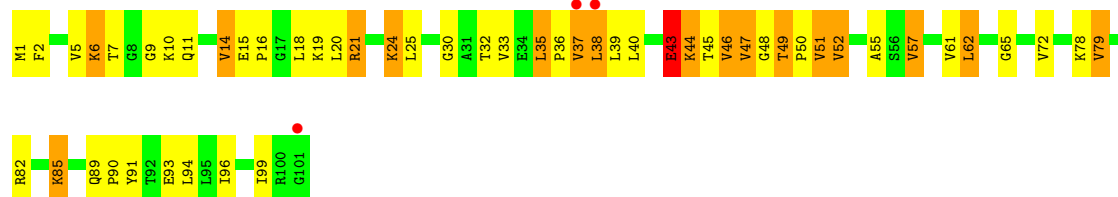


• Molecule 45: 50S ribosomal protein L20

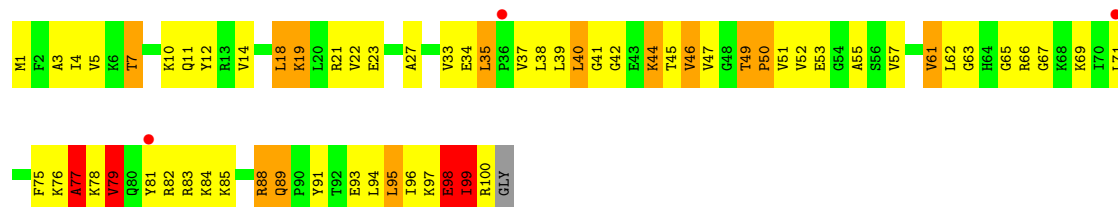




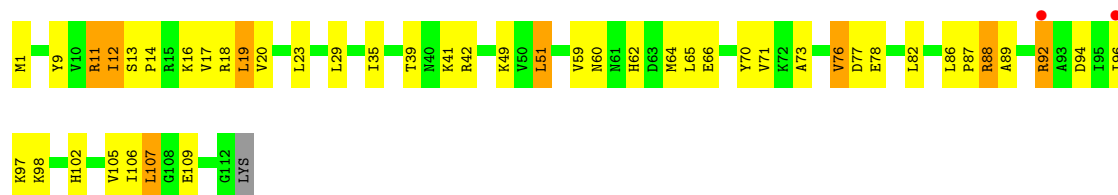
- Molecule 46: 50S ribosomal protein L21



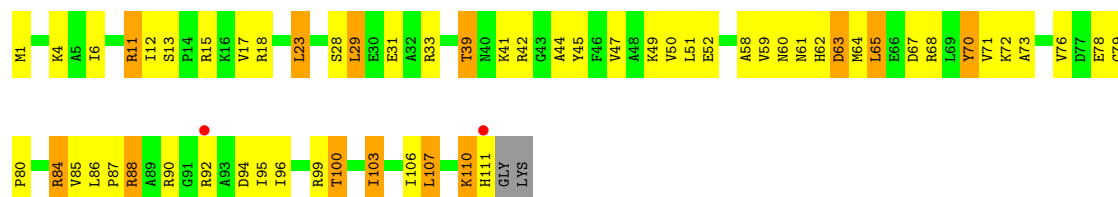
- Molecule 46: 50S ribosomal protein L21



- Molecule 47: 50S ribosomal protein L22

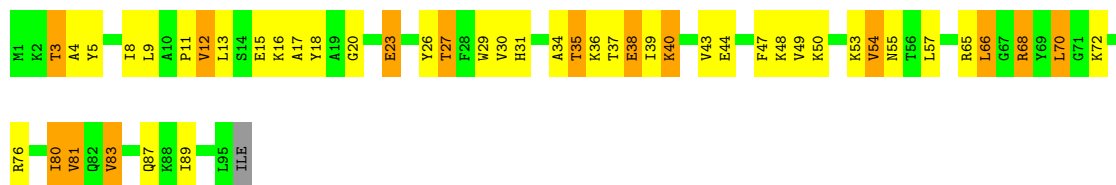


- Molecule 47: 50S ribosomal protein L22



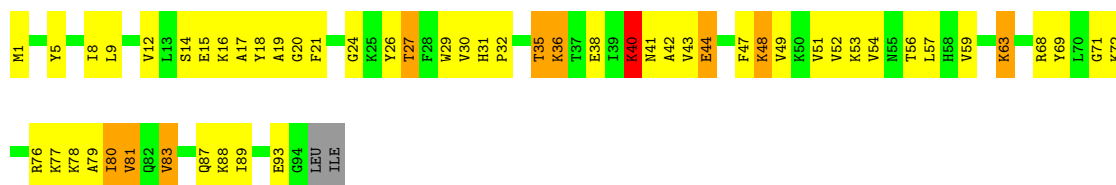
- Molecule 48: 50S ribosomal protein L23

Chain F8:  50% 34% 15% .



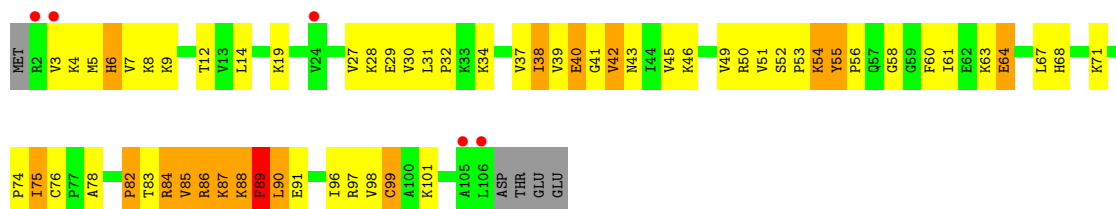
- Molecule 48: 50S ribosomal protein L23

Chain B5:  42% 46% 9% ..

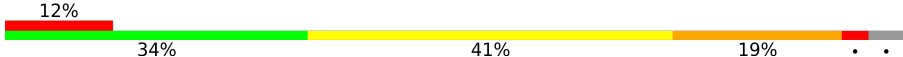


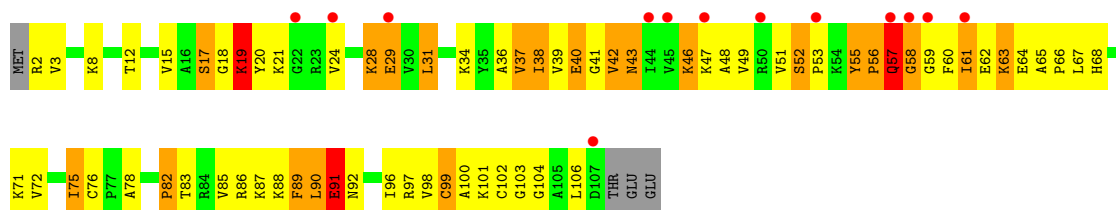
- Molecule 49: 50S ribosomal protein L24

Chain G8:  5% 40% 40% 15% . 5%

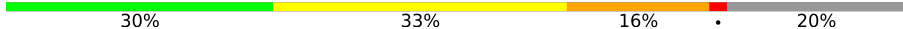


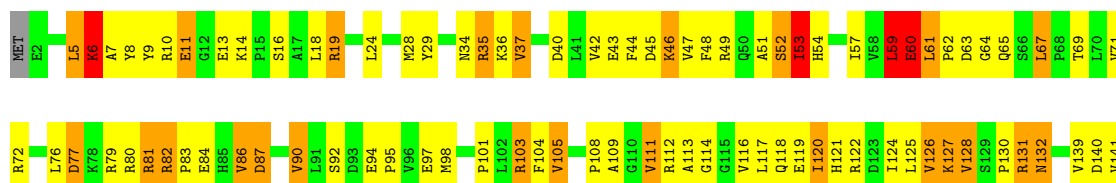
- Molecule 49: 50S ribosomal protein L24

Chain C5:  12% 34% 41% 19% . .

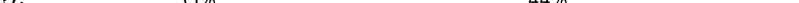


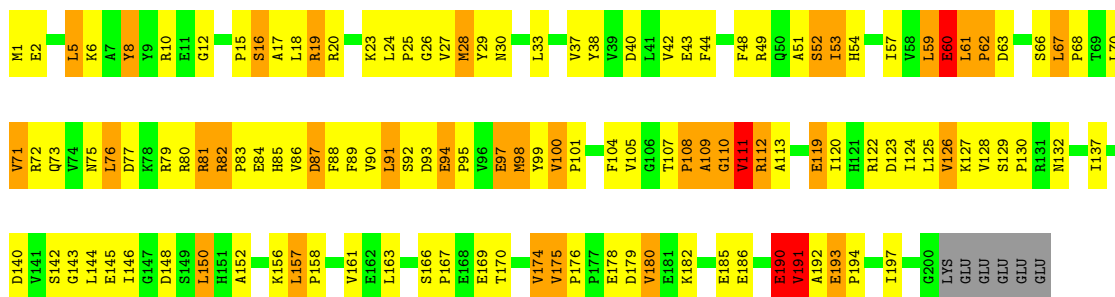
- Molecule 50: 50S ribosomal protein L25

Chain H8:  30% 33% 16% . 20%

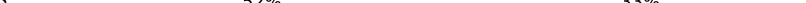


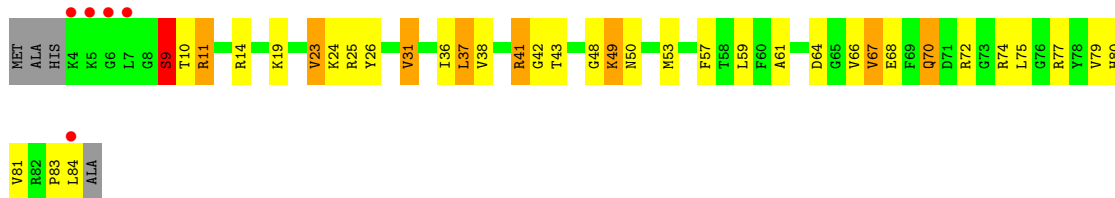
- Molecule 50: 50S ribosomal protein L25

Chain D5:  35% 44% 16% . .

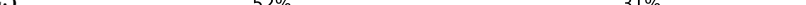


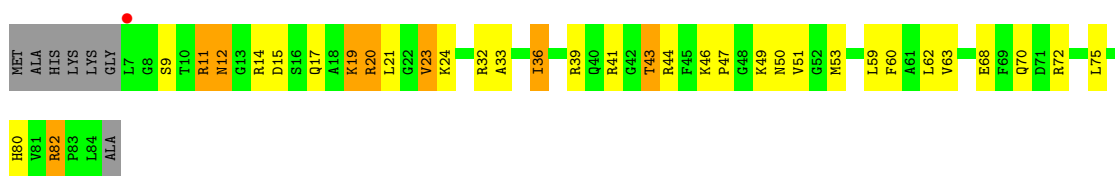
- Molecule 51: 50S ribosomal protein L27

Chain I8: 

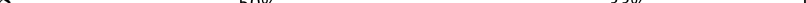


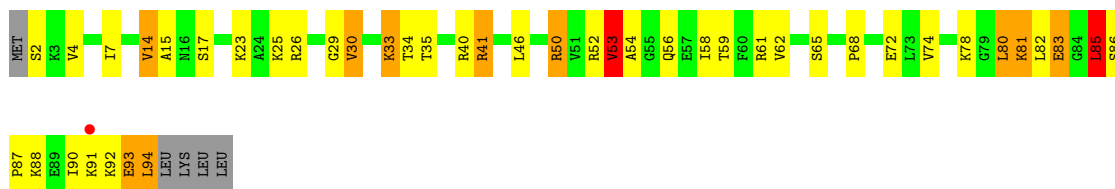
- Molecule 51: 50S ribosomal protein L27

Chain E5: 

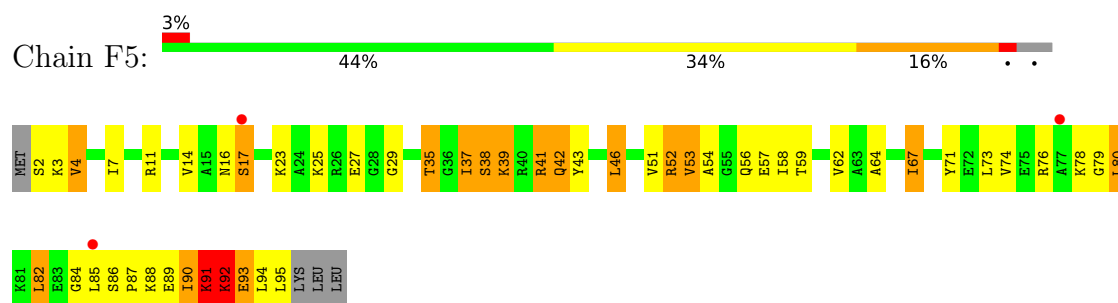


- Molecule 52: 50S ribosomal protein L28

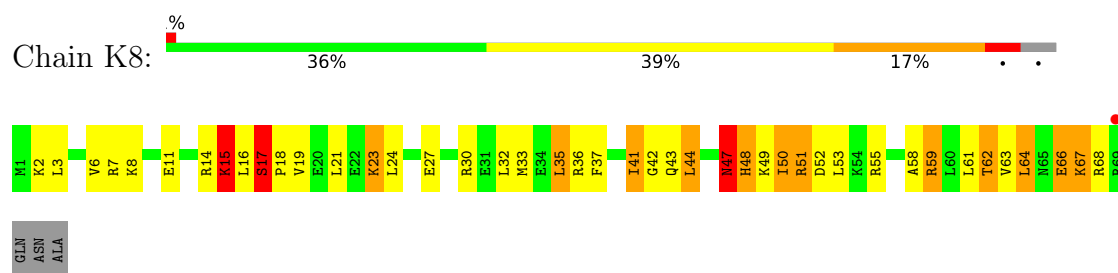
Chain J8: 



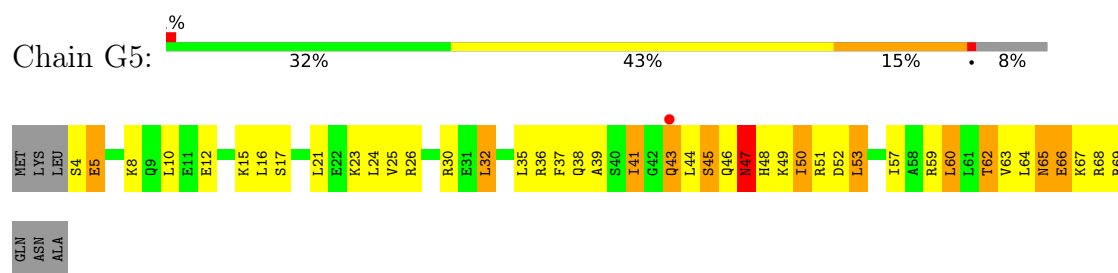
- Molecule 52: 50S ribosomal protein L28



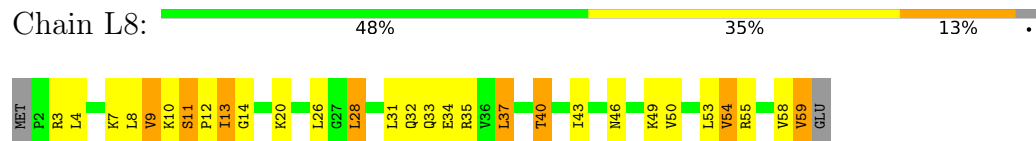
- Molecule 53: 50S ribosomal protein L29



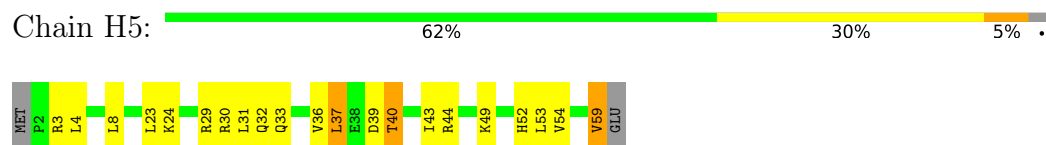
- Molecule 53: 50S ribosomal protein L29



- Molecule 54: 50S ribosomal protein L30

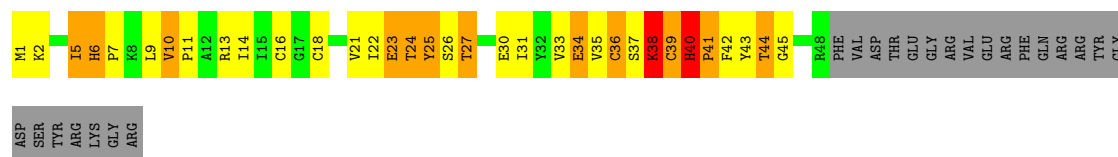


- Molecule 54: 50S ribosomal protein L30

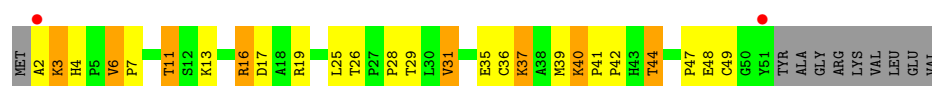
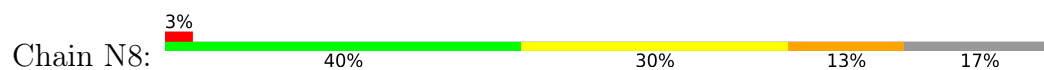


- Molecule 55: 50S ribosomal protein L31

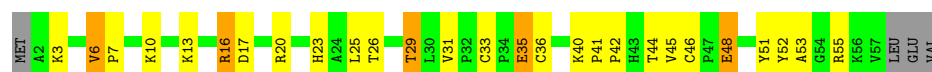




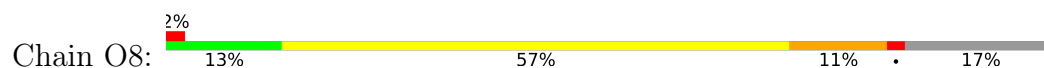
- Molecule 56: 50S ribosomal protein L32



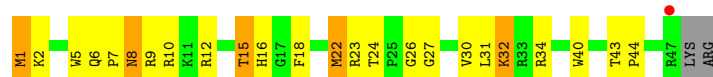
- Molecule 56: 50S ribosomal protein L32



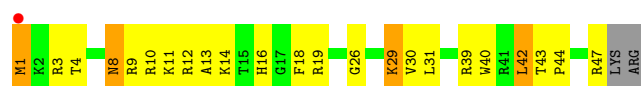
- Molecule 57: 50S ribosomal protein L33



- Molecule 58: 50S ribosomal protein L34



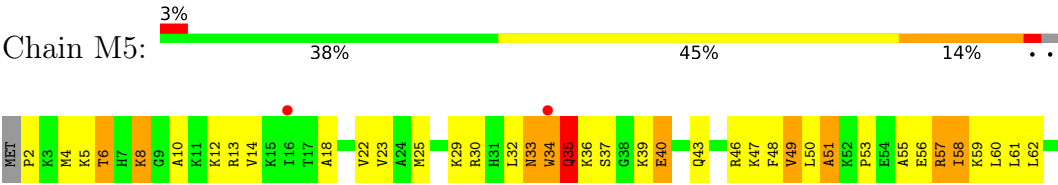
- Molecule 58: 50S ribosomal protein L34



- Molecule 59: 50S ribosomal protein L35



- Molecule 59: 50S ribosomal protein L35



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.05Å 449.39Å 618.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	153.44 – 3.16 153.44 – 3.16	Depositor EDS
% Data completeness (in resolution range)	100.0 (153.44-3.16) 88.4 (153.44-3.16)	Depositor EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.57 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	(Not available) , (Not available) 0.195 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (0.20%)	wwPDB-VP
Wilson B-factor (Å ²)	90.7	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 25.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	306138	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.45% 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: 7MG, OMC, RSP, 5MU, SF4, ZN, 2MA, PSU, 4SU, MG

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	13	0.45	0/36375	0.70	15/56770 (0.0%)
1	1G	0.40	0/36309	0.63	3/56668 (0.0%)
2	12	0.45	0/1959	0.72	0/2642
2	1E	0.43	0/1908	0.74	1/2573 (0.0%)
3	22	0.39	0/1556	0.69	0/2098
3	2E	0.43	0/1629	0.72	0/2195
4	32	0.41	0/1732	0.72	2/2318 (0.1%)
4	3E	0.45	0/1720	0.72	0/2305
5	42	0.42	0/1171	0.68	0/1576
5	4E	0.43	0/1158	0.72	1/1559 (0.1%)
6	52	0.44	0/855	0.62	0/1154
6	5E	0.47	0/855	0.64	0/1154
7	62	0.41	0/1122	0.71	2/1500 (0.1%)
7	6E	0.38	0/1259	0.62	0/1686
8	72	0.34	0/1135	0.61	0/1527
8	7E	0.43	0/1135	0.69	0/1527
9	82	0.33	0/1002	0.62	0/1346
9	8E	0.38	0/1019	0.70	0/1367
10	1A	0.42	0/814	0.69	0/1095
10	1I	0.54	1/814 (0.1%)	0.84	3/1095 (0.3%)
11	2A	0.39	0/850	0.60	0/1150
11	2I	0.48	0/838	0.72	0/1133
12	3A	0.49	0/963	0.77	0/1290
12	3I	0.57	0/972	0.88	0/1301
13	4A	0.38	0/897	0.74	0/1204
13	4I	0.42	0/946	0.72	0/1270
14	5A	0.46	0/475	0.94	3/632 (0.5%)
14	5I	0.48	0/508	0.86	0/674
15	6A	0.39	0/740	0.62	0/987
15	6I	0.46	0/740	0.65	0/987
16	7A	0.40	0/721	0.69	0/970
16	7I	0.44	0/716	0.70	0/963

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	8A	0.42	0/836	0.64	0/1117
17	8I	0.47	0/847	0.70	0/1131
18	9A	0.47	0/549	0.78	0/732
18	9I	0.47	0/549	0.78	0/732
19	AA	0.40	0/490	0.78	2/662 (0.3%)
19	AI	0.52	0/657	0.92	0/885
20	BA	0.45	0/759	0.75	2/1000 (0.2%)
20	BI	0.45	1/753 (0.1%)	0.73	0/993
21	1B	0.38	0/212	0.71	0/277
21	1F	0.43	0/212	0.70	0/277
22	1K	0.53	3/1578 (0.2%)	0.67	2/2445 (0.1%)
22	1L	0.55	3/1623 (0.2%)	0.67	2/2517 (0.1%)
23	2K	0.50	1/1721 (0.1%)	0.70	0/2682
23	2L	0.43	0/1721	0.64	0/2682
24	3K	0.46	0/1741	0.66	0/2703
24	3L	0.45	0/1764	0.67	1/2741 (0.0%)
25	4K	0.50	0/521	0.75	0/812
25	4L	0.41	0/420	0.62	0/652
26	14	0.51	0/69830	0.74	14/109010 (0.0%)
26	1H	0.57	0/69835	0.80	27/109020 (0.0%)
27	16	0.46	0/2928	0.75	0/4568
27	1J	0.43	0/2928	0.70	0/4568
28	71	0.37	0/1066	0.60	0/1439
28	79	0.29	0/1031	0.59	0/1394
29	11	0.70	0/2170	1.05	12/2926 (0.4%)
29	19	0.61	0/2170	0.97	5/2926 (0.2%)
30	21	0.70	1/1591 (0.1%)	0.92	2/2146 (0.1%)
30	29	0.53	0/1591	0.92	4/2146 (0.2%)
31	31	0.59	0/1620	0.83	0/2194
31	39	0.50	0/1645	0.89	7/2228 (0.3%)
32	41	0.46	0/1481	0.75	0/1994
32	49	0.39	0/1481	0.67	0/1994
33	51	0.52	0/1337	1.00	7/1809 (0.4%)
33	59	0.47	0/1337	0.95	7/1809 (0.4%)
34	18	0.58	0/236	0.93	0/315
34	28	0.53	0/236	0.91	0/315
35	61	0.44	0/1146	0.83	5/1551 (0.3%)
35	69	0.45	0/1146	0.81	4/1551 (0.3%)
36	38	0.76	1/1104 (0.1%)	1.45	23/1494 (1.5%)
37	48	0.43	0/1067	0.99	5/1448 (0.3%)
38	15	0.57	1/1123 (0.1%)	0.72	1/1515 (0.1%)
38	58	0.51	0/1123	0.80	0/1514
39	25	0.50	0/942	0.79	0/1269

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	68	0.53	0/942	0.75	0/1269
40	35	0.59	0/1147	1.06	4/1525 (0.3%)
40	78	0.61	0/1139	1.03	3/1514 (0.2%)
41	45	0.58	1/1120 (0.1%)	0.95	4/1498 (0.3%)
41	88	0.63	0/1134	0.93	2/1519 (0.1%)
42	55	0.51	0/981	0.80	0/1312
42	98	0.51	0/981	0.82	0/1312
43	65	0.69	1/886 (0.1%)	0.90	4/1180 (0.3%)
43	A8	0.55	0/891	0.97	2/1187 (0.2%)
44	75	0.55	1/1129 (0.1%)	0.76	0/1509
44	B8	0.55	0/1146	0.83	0/1531
45	85	0.50	0/981	0.77	0/1306
45	C8	0.58	0/968	0.87	1/1289 (0.1%)
46	95	0.51	0/785	0.88	0/1052
46	D8	0.56	0/789	0.90	2/1057 (0.2%)
47	A5	0.54	0/897	0.77	0/1204
47	E8	0.57	0/901	0.75	0/1209
48	B5	0.55	0/752	0.84	2/1010 (0.2%)
48	F8	0.62	0/757	0.85	0/1017
49	C5	0.51	0/798	0.95	0/1071
49	G8	0.62	0/797	0.92	3/1068 (0.3%)
50	D5	0.46	0/1615	0.91	5/2191 (0.2%)
50	H8	0.61	1/1359 (0.1%)	0.84	1/1841 (0.1%)
51	E5	0.51	0/624	0.79	0/832
51	I8	0.68	0/638	0.97	0/851
52	F5	0.53	0/744	0.80	0/989
52	J8	0.57	0/736	0.86	2/978 (0.2%)
53	G5	0.52	0/560	0.85	0/741
53	K8	0.59	0/578	0.91	2/766 (0.3%)
54	H5	0.50	0/464	0.77	0/623
54	L8	0.51	0/464	0.74	0/623
55	M8	0.70	1/380 (0.3%)	0.97	3/514 (0.6%)
56	J5	0.58	0/448	0.77	0/606
56	N8	0.74	1/399 (0.3%)	0.87	0/541
57	O8	0.66	0/396	1.14	0/529
58	L5	0.63	0/417	0.87	0/550
58	P8	0.72	0/409	0.95	0/540
59	M5	0.76	1/524 (0.2%)	1.03	0/691
59	Q8	0.62	0/524	1.05	3/691 (0.4%)
All	All	0.51	19/325210 (0.0%)	0.76	205/486635 (0.0%)

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

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	12	0	3
2	1E	0	5
3	22	0	1
3	2E	0	1
4	32	0	4
4	3E	0	1
5	4E	0	1
9	8E	0	1
10	1I	0	1
12	3A	0	2
12	3I	0	3
13	4A	0	4
14	5I	0	1
18	9I	0	2
19	AA	0	2
19	AI	0	4
20	BA	0	4
20	BI	0	2
29	11	0	7
29	19	0	6
30	21	0	6
30	29	0	7
31	31	0	2
31	39	0	5
32	41	0	2
32	49	0	3
33	51	0	5
33	59	0	5
34	18	0	2
34	28	0	2
35	61	0	3
35	69	0	1
36	38	0	21
37	48	0	11
38	15	0	2
38	58	0	1
40	35	0	7
40	78	0	4
41	45	0	9
43	A8	0	1
44	75	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
45	85	0	2
45	C8	0	4
46	95	0	4
46	D8	0	2
48	F8	0	1
49	C5	0	8
49	G8	0	3
50	D5	0	10
50	H8	0	2
52	F5	0	2
52	J8	0	1
53	G5	0	3
53	K8	0	1
55	M8	0	3
57	O8	0	2
59	M5	0	4
59	Q8	0	1
All	All	0	208

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	21	109	LYS	C-N	16.35	1.41	1.33
50	H8	157	LEU	C-O	-15.96	1.16	1.23
43	65	88	ASP	CA-C	13.99	1.61	1.53
38	15	94	HIS	C-O	12.81	1.30	1.23
36	38	85	ASP	C-N	10.13	1.44	1.34

The worst 5 of 205 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	11	40	THR	N-CA-C	11.86	125.66	110.24
33	51	153	LYS	CA-C-N	9.02	148.64	127.00
33	51	153	LYS	C-N-CA	9.02	148.64	127.00
41	45	82	ARG	N-CA-C	8.97	125.77	113.21
29	11	39	LYS	N-CA-C	8.68	129.29	110.80

There are no chirality outliers.

5 of 208 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1E	11	LEU	Peptide
2	1E	19	HIS	Peptide
2	1E	230	VAL	Peptide
2	1E	234	PRO	Peptide
2	1E	236	TYR	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	13	32497	0	16403	886	0
1	1G	32437	0	16372	865	0
2	12	1924	0	1975	134	0
2	1E	1874	0	1926	121	0
3	22	1533	0	1595	80	0
3	2E	1605	0	1668	57	0
4	32	1702	0	1765	100	0
4	3E	1690	0	1737	84	0
5	42	1155	0	1213	58	0
5	4E	1142	0	1204	51	0
6	52	842	0	857	35	0
6	5E	842	0	857	34	0
7	62	1110	0	1163	68	0
7	6E	1242	0	1286	54	0
8	72	1115	0	1177	55	0
8	7E	1115	0	1177	69	0
9	82	983	0	1006	71	0
9	8E	1000	0	1031	65	0
10	1A	801	0	849	87	0
10	1I	801	0	848	56	0
11	2A	835	0	847	40	0
11	2I	823	0	833	44	0
12	3A	947	0	1033	65	0
12	3I	956	0	1046	58	0
13	4A	887	0	935	67	0
13	4I	936	0	986	53	0
14	5A	466	0	499	32	0
14	5I	499	0	542	36	0
15	6A	729	0	768	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	6I	729	0	768	27	0
16	7A	705	0	725	29	0
16	7I	700	0	720	54	0
17	8A	823	0	891	37	0
17	8I	834	0	904	65	0
18	9A	544	0	605	21	0
18	9I	544	0	605	39	0
19	AA	481	0	468	28	0
19	AI	643	0	662	34	0
20	BA	757	0	856	50	0
20	BI	751	0	848	55	0
21	1B	208	0	221	21	0
21	1F	208	0	221	9	0
22	1K	1544	0	791	49	0
22	1L	1584	0	811	49	0
23	2K	1646	0	845	40	0
23	2L	1646	0	845	39	0
24	3K	1561	0	796	51	0
24	3L	1581	0	805	63	0
25	4K	462	0	229	12	0
25	4L	374	0	187	10	0
26	14	62347	0	31431	1550	0
26	1H	62351	0	31424	1627	0
27	16	2617	0	1328	74	0
27	1J	2617	0	1328	90	0
28	71	1043	0	1066	45	0
28	79	1010	0	1025	52	0
29	11	2120	0	2196	120	0
29	19	2120	0	2197	106	0
30	21	1558	0	1624	98	0
30	29	1558	0	1624	100	0
31	31	1585	0	1632	92	0
31	39	1610	0	1655	132	0
32	41	1457	0	1514	92	0
32	49	1457	0	1514	89	0
33	51	1312	0	1384	77	0
33	59	1312	0	1384	107	0
34	18	237	0	257	23	0
34	28	237	0	257	21	0
35	61	1131	0	1218	46	0
35	69	1131	0	1218	69	0
36	38	1089	0	1149	110	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	48	1047	0	1082	93	0
38	15	1096	0	1168	40	0
38	58	1096	0	1169	62	0
39	25	932	0	996	53	0
39	68	932	0	996	32	0
40	35	1130	0	1217	113	0
40	78	1122	0	1206	97	0
41	45	1099	0	1152	92	0
41	88	1113	0	1157	61	0
42	55	967	0	1033	38	0
42	98	967	0	1033	47	0
43	65	876	0	938	88	0
43	A8	881	0	943	46	0
44	75	1115	0	1169	67	0
44	B8	1132	0	1189	72	0
45	85	963	0	1022	70	0
45	C8	950	0	1011	53	0
46	95	774	0	849	63	0
46	D8	778	0	852	40	1
47	A5	886	0	948	34	0
47	E8	890	0	951	25	0
48	B5	738	0	792	47	0
48	F8	743	0	794	40	0
49	C5	785	0	844	64	0
49	G8	784	0	853	46	0
50	D5	1582	0	1613	86	0
50	H8	1330	0	1360	77	0
51	E5	616	0	633	38	0
51	I8	630	0	640	28	0
52	F5	737	0	813	50	0
52	J8	729	0	802	31	0
53	G5	558	0	610	32	0
53	K8	576	0	628	46	0
54	H5	459	0	512	13	0
54	L8	459	0	512	20	0
55	M8	371	0	372	36	0
56	J5	434	0	454	18	0
56	N8	386	0	402	31	0
57	O8	389	0	404	33	0
58	L5	409	0	454	19	0
58	P8	401	0	436	22	0
59	M5	516	0	582	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	Q8	516	0	582	38	0
60	11	6	0	0	0	0
60	13	227	0	0	0	0
60	14	607	0	0	0	0
60	16	20	0	0	0	0
60	1G	167	0	0	0	0
60	1H	669	0	0	0	0
60	1J	8	0	0	0	0
60	1K	2	0	0	0	0
60	1L	1	0	0	0	0
60	21	2	0	0	0	0
60	25	2	0	0	0	0
60	29	5	0	0	0	0
60	2A	1	0	0	0	0
60	2K	7	0	0	0	0
60	2L	2	0	0	0	0
60	31	2	0	0	0	0
60	32	2	0	0	0	0
60	35	1	0	0	0	0
60	39	2	0	0	0	0
60	3E	2	0	0	0	0
60	41	1	0	0	0	0
60	45	2	0	0	0	0
60	4K	1	0	0	0	0
60	4L	2	0	0	0	0
60	52	1	0	0	0	0
60	55	2	0	0	0	0
60	5E	2	0	0	0	0
60	6I	1	0	0	0	0
60	75	1	0	0	0	0
60	78	1	0	0	0	0
60	88	4	0	0	0	0
60	98	2	0	0	0	0
60	C5	1	0	0	0	0
60	E5	1	0	0	0	0
60	F5	1	0	0	0	0
60	I8	2	0	0	0	0
60	M5	1	0	0	0	0
60	N8	1	0	0	0	0
60	P8	1	0	0	0	0
60	Q8	1	0	0	0	0
61	32	8	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	3E	8	0	0	2	0
62	5A	1	0	0	0	0
62	5I	1	0	0	0	0
63	11	12	0	0	3	0
63	13	544	0	0	91	0
63	14	1520	0	0	275	0
63	15	1	0	0	0	0
63	16	42	0	0	7	0
63	19	12	0	0	4	0
63	1E	1	0	0	0	0
63	1F	1	0	0	0	0
63	1G	397	0	0	60	0
63	1H	1966	0	0	358	2
63	1I	1	0	0	0	0
63	1J	23	0	0	3	0
63	1K	1	0	0	0	0
63	21	9	0	0	2	0
63	25	13	0	0	1	0
63	29	9	0	0	2	0
63	2K	16	0	0	5	0
63	2L	7	0	0	0	0
63	31	8	0	0	0	0
63	32	5	0	0	0	0
63	35	5	0	0	1	0
63	39	8	0	0	1	0
63	3A	2	0	0	0	0
63	3E	1	0	0	0	0
63	3I	5	0	0	0	0
63	42	1	0	0	0	0
63	45	4	0	0	0	0
63	4E	2	0	0	0	0
63	4K	13	0	0	0	0
63	4L	8	0	0	1	0
63	52	4	0	0	1	0
63	58	3	0	0	0	0
63	5A	1	0	0	0	0
63	5I	3	0	0	2	0
63	6A	1	0	0	0	0
63	6I	4	0	0	0	0
63	78	10	0	0	4	0
63	7A	2	0	0	0	0
63	85	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	88	7	0	0	0	0
63	8E	1	0	0	0	0
63	98	1	0	0	0	0
63	9A	2	0	0	0	0
63	A5	1	0	0	0	0
63	A8	2	0	0	0	0
63	B5	1	0	0	0	0
63	B8	3	0	0	0	0
63	BA	2	0	0	0	0
63	BI	1	0	0	0	0
63	C5	1	0	0	0	0
63	C8	7	0	0	0	1
63	D8	1	0	0	0	0
63	E5	3	0	0	0	0
63	F5	6	0	0	1	0
63	F8	1	0	0	0	0
63	G8	3	0	0	0	0
63	I8	5	0	0	1	0
63	J8	10	0	0	2	0
63	L5	2	0	0	0	0
63	L8	4	0	0	2	0
63	M5	9	0	0	0	0
63	P8	1	0	0	0	0
63	Q8	7	0	0	0	0
All	All	306138	0	202999	9914	2

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 20.

The worst 5 of 9914 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)
26:1H:1268:A:OP1	63:1H:3723:HOH:O	1.66	1.12
26:14:1604:C:OP2	63:14:3715:HOH:O	1.65	1.11
26:1H:2032:G:H21	30:21:146:THR:HG23	1.17	1.07
26:1H:2711:A:OP2	63:1H:3724:HOH:O	1.71	1.06
26:14:1603:A:OP1	63:14:3715:HOH:O	1.74	1.05

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:D8:45:THR:CG2	63:1H:4620:HOH:O[4_465]	1.38	0.82
63:1H:4955:HOH:O	63:C8:206:HOH:O[4_565]	2.19	0.01

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	12	235/256 (92%)	183 (78%)	47 (20%)	5 (2%)	5	26
2	1E	227/256 (89%)	171 (75%)	54 (24%)	2 (1%)	14	43
3	22	191/239 (80%)	149 (78%)	41 (22%)	1 (0%)	24	55
3	2E	203/239 (85%)	169 (83%)	33 (16%)	1 (0%)	24	55
4	32	206/209 (99%)	168 (82%)	34 (16%)	4 (2%)	6	28
4	3E	205/209 (98%)	172 (84%)	31 (15%)	2 (1%)	12	41
5	42	149/162 (92%)	132 (89%)	17 (11%)	0	100	100
5	4E	147/162 (91%)	128 (87%)	18 (12%)	1 (1%)	18	49
6	52	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
6	5E	99/101 (98%)	88 (89%)	11 (11%)	0	100	100
7	62	134/156 (86%)	108 (81%)	24 (18%)	2 (2%)	8	33
7	6E	152/156 (97%)	139 (91%)	13 (9%)	0	100	100
8	72	136/138 (99%)	120 (88%)	16 (12%)	0	100	100
8	7E	136/138 (99%)	116 (85%)	20 (15%)	0	100	100
9	82	122/128 (95%)	104 (85%)	17 (14%)	1 (1%)	16	46
9	8E	124/128 (97%)	100 (81%)	22 (18%)	2 (2%)	7	32
10	1A	97/105 (92%)	79 (81%)	18 (19%)	0	100	100
10	1I	97/105 (92%)	83 (86%)	13 (13%)	1 (1%)	12	41
11	2A	111/129 (86%)	94 (85%)	16 (14%)	1 (1%)	14	43
11	2I	109/129 (84%)	94 (86%)	15 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	3A	119/132 (90%)	91 (76%)	23 (19%)	5 (4%)	2	13
12	3I	120/132 (91%)	101 (84%)	19 (16%)	0	100	100
13	4A	109/126 (86%)	84 (77%)	24 (22%)	1 (1%)	14	43
13	4I	117/126 (93%)	91 (78%)	25 (21%)	1 (1%)	14	43
14	5A	55/61 (90%)	38 (69%)	15 (27%)	2 (4%)	2	16
14	5I	59/61 (97%)	48 (81%)	9 (15%)	2 (3%)	3	16
15	6A	85/89 (96%)	77 (91%)	8 (9%)	0	100	100
15	6I	85/89 (96%)	72 (85%)	13 (15%)	0	100	100
16	7A	82/88 (93%)	71 (87%)	11 (13%)	0	100	100
16	7I	81/88 (92%)	73 (90%)	8 (10%)	0	100	100
17	8A	97/105 (92%)	87 (90%)	10 (10%)	0	100	100
17	8I	98/105 (93%)	88 (90%)	10 (10%)	0	100	100
18	9A	65/88 (74%)	56 (86%)	9 (14%)	0	100	100
18	9I	65/88 (74%)	57 (88%)	6 (9%)	2 (3%)	3	18
19	AA	56/93 (60%)	44 (79%)	12 (21%)	0	100	100
19	AI	78/93 (84%)	57 (73%)	15 (19%)	6 (8%)	1	4
20	BA	96/106 (91%)	79 (82%)	14 (15%)	3 (3%)	3	18
20	BI	96/106 (91%)	75 (78%)	17 (18%)	4 (4%)	2	13
21	1B	22/27 (82%)	16 (73%)	5 (23%)	1 (4%)	2	12
21	1F	22/27 (82%)	19 (86%)	2 (9%)	1 (4%)	2	12
28	7I	130/229 (57%)	114 (88%)	16 (12%)	0	100	100
28	79	126/229 (55%)	107 (85%)	19 (15%)	0	100	100
29	11	271/276 (98%)	231 (85%)	37 (14%)	3 (1%)	11	39
29	19	271/276 (98%)	234 (86%)	37 (14%)	0	100	100
30	21	201/206 (98%)	149 (74%)	44 (22%)	8 (4%)	2	14
30	29	201/206 (98%)	145 (72%)	50 (25%)	6 (3%)	3	19
31	31	200/210 (95%)	169 (84%)	28 (14%)	3 (2%)	8	33
31	39	204/210 (97%)	152 (74%)	46 (22%)	6 (3%)	3	20
32	41	177/182 (97%)	150 (85%)	26 (15%)	1 (1%)	21	52
32	49	177/182 (97%)	142 (80%)	32 (18%)	3 (2%)	7	30
33	51	169/180 (94%)	125 (74%)	35 (21%)	9 (5%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	59	169/180 (94%)	108 (64%)	54 (32%)	7 (4%)	2	14
34	18	28/125 (22%)	20 (71%)	7 (25%)	1 (4%)	2	16
34	28	28/125 (22%)	23 (82%)	4 (14%)	1 (4%)	2	16
35	61	143/148 (97%)	104 (73%)	35 (24%)	4 (3%)	4	20
35	69	143/148 (97%)	109 (76%)	30 (21%)	4 (3%)	4	20
36	38	141/173 (82%)	65 (46%)	54 (38%)	22 (16%)	0	0
37	48	140/147 (95%)	75 (54%)	57 (41%)	8 (6%)	1	9
38	15	135/140 (96%)	115 (85%)	20 (15%)	0	100	100
38	58	135/140 (96%)	108 (80%)	25 (18%)	2 (2%)	8	33
39	25	120/122 (98%)	108 (90%)	11 (9%)	1 (1%)	16	46
39	68	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
40	35	146/150 (97%)	95 (65%)	43 (30%)	8 (6%)	1	9
40	78	145/150 (97%)	112 (77%)	32 (22%)	1 (1%)	18	49
41	45	136/141 (96%)	98 (72%)	33 (24%)	5 (4%)	2	15
41	88	139/141 (99%)	116 (84%)	21 (15%)	2 (1%)	9	34
42	55	116/118 (98%)	103 (89%)	13 (11%)	0	100	100
42	98	116/118 (98%)	100 (86%)	16 (14%)	0	100	100
43	65	108/112 (96%)	82 (76%)	22 (20%)	4 (4%)	2	15
43	A8	109/112 (97%)	87 (80%)	22 (20%)	0	100	100
44	75	132/146 (90%)	110 (83%)	22 (17%)	0	100	100
44	B8	134/146 (92%)	105 (78%)	29 (22%)	0	100	100
45	85	115/118 (98%)	96 (84%)	19 (16%)	0	100	100
45	C8	113/118 (96%)	93 (82%)	18 (16%)	2 (2%)	6	29
46	95	98/101 (97%)	71 (72%)	21 (21%)	6 (6%)	1	7
46	D8	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
47	A5	109/113 (96%)	97 (89%)	12 (11%)	0	100	100
47	E8	110/113 (97%)	95 (86%)	15 (14%)	0	100	100
48	B5	92/96 (96%)	79 (86%)	13 (14%)	0	100	100
48	F8	93/96 (97%)	81 (87%)	11 (12%)	1 (1%)	11	39
49	C5	104/110 (94%)	66 (64%)	31 (30%)	7 (7%)	1	6
49	G8	103/110 (94%)	73 (71%)	30 (29%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	D5	198/206 (96%)	136 (69%)	54 (27%)	8 (4%)	2	14
50	H8	161/206 (78%)	123 (76%)	32 (20%)	6 (4%)	2	15
51	E5	76/85 (89%)	65 (86%)	11 (14%)	0	100	100
51	I8	79/85 (93%)	63 (80%)	15 (19%)	1 (1%)	9	36
52	F5	92/98 (94%)	81 (88%)	9 (10%)	2 (2%)	5	25
52	J8	91/98 (93%)	79 (87%)	12 (13%)	0	100	100
53	G5	64/72 (89%)	58 (91%)	5 (8%)	1 (2%)	7	32
53	K8	67/72 (93%)	57 (85%)	8 (12%)	2 (3%)	3	19
54	H5	56/60 (93%)	52 (93%)	4 (7%)	0	100	100
54	L8	56/60 (93%)	54 (96%)	2 (4%)	0	100	100
55	M8	46/71 (65%)	24 (52%)	20 (44%)	2 (4%)	2	13
56	J5	54/60 (90%)	47 (87%)	7 (13%)	0	100	100
56	N8	48/60 (80%)	42 (88%)	6 (12%)	0	100	100
57	O8	43/54 (80%)	26 (60%)	16 (37%)	1 (2%)	5	24
58	L5	45/49 (92%)	42 (93%)	3 (7%)	0	100	100
58	P8	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
59	M5	62/65 (95%)	49 (79%)	12 (19%)	1 (2%)	7	32
59	Q8	62/65 (95%)	47 (76%)	13 (21%)	2 (3%)	3	17
All	All	11677/12957 (90%)	9408 (81%)	2067 (18%)	202 (2%)	7	30

5 of 202 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	4I	12	ASN
30	21	78	LEU
30	21	83	ASP
33	51	10	PRO
34	18	25	ASP

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	
2	12	205/220 (93%)	153 (75%)	52 (25%)	0	3
2	1E	200/220 (91%)	140 (70%)	60 (30%)	0	1
3	22	153/188 (81%)	117 (76%)	36 (24%)	1	4
3	2E	159/188 (85%)	120 (76%)	39 (24%)	1	3
4	32	180/181 (99%)	146 (81%)	34 (19%)	1	8
4	3E	178/181 (98%)	147 (83%)	31 (17%)	2	9
5	42	116/123 (94%)	80 (69%)	36 (31%)	0	1
5	4E	115/123 (94%)	88 (76%)	27 (24%)	1	4
6	52	90/90 (100%)	74 (82%)	16 (18%)	2	8
6	5E	90/90 (100%)	73 (81%)	17 (19%)	1	8
7	62	114/127 (90%)	87 (76%)	27 (24%)	1	4
7	6E	125/127 (98%)	97 (78%)	28 (22%)	1	4
8	72	119/119 (100%)	100 (84%)	19 (16%)	2	11
8	7E	119/119 (100%)	92 (77%)	27 (23%)	1	4
9	82	95/99 (96%)	71 (75%)	24 (25%)	0	3
9	8E	97/99 (98%)	74 (76%)	23 (24%)	1	4
10	1A	89/92 (97%)	66 (74%)	23 (26%)	0	2
10	1I	89/92 (97%)	68 (76%)	21 (24%)	1	4
11	2A	85/99 (86%)	62 (73%)	23 (27%)	0	2
11	2I	84/99 (85%)	57 (68%)	27 (32%)	0	1
12	3A	102/109 (94%)	82 (80%)	20 (20%)	1	7
12	3I	103/109 (94%)	75 (73%)	28 (27%)	0	2
13	4A	90/101 (89%)	58 (64%)	32 (36%)	0	0
13	4I	93/101 (92%)	67 (72%)	26 (28%)	0	2
14	5A	47/50 (94%)	32 (68%)	15 (32%)	0	1
14	5I	50/50 (100%)	41 (82%)	9 (18%)	2	8
15	6A	79/80 (99%)	62 (78%)	17 (22%)	1	5
15	6I	79/80 (99%)	65 (82%)	14 (18%)	2	8
16	7A	72/74 (97%)	57 (79%)	15 (21%)	1	6
16	7I	72/74 (97%)	55 (76%)	17 (24%)	1	4
17	8A	94/97 (97%)	75 (80%)	19 (20%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	8I	95/97 (98%)	76 (80%)	19 (20%)	1	6
18	9A	58/77 (75%)	45 (78%)	13 (22%)	1	4
18	9I	58/77 (75%)	45 (78%)	13 (22%)	1	4
19	AA	52/80 (65%)	37 (71%)	15 (29%)	0	1
19	AI	70/80 (88%)	50 (71%)	20 (29%)	0	1
20	BA	76/82 (93%)	55 (72%)	21 (28%)	0	2
20	BI	75/82 (92%)	53 (71%)	22 (29%)	0	1
21	1B	19/22 (86%)	18 (95%)	1 (5%)	20	49
21	1F	19/22 (86%)	16 (84%)	3 (16%)	2	11
28	7I	110/181 (61%)	83 (76%)	27 (24%)	1	3
28	79	107/181 (59%)	94 (88%)	13 (12%)	5	20
29	11	214/218 (98%)	162 (76%)	52 (24%)	1	3
29	19	214/218 (98%)	164 (77%)	50 (23%)	1	4
30	21	165/166 (99%)	118 (72%)	47 (28%)	0	1
30	29	165/166 (99%)	126 (76%)	39 (24%)	1	4
31	31	161/166 (97%)	119 (74%)	42 (26%)	0	2
31	39	163/166 (98%)	113 (69%)	50 (31%)	0	1
32	41	153/156 (98%)	113 (74%)	40 (26%)	0	2
32	49	153/156 (98%)	109 (71%)	44 (29%)	0	1
33	51	142/148 (96%)	93 (66%)	49 (34%)	0	0
33	59	142/148 (96%)	108 (76%)	34 (24%)	1	3
34	18	26/90 (29%)	16 (62%)	10 (38%)	0	0
34	28	26/90 (29%)	11 (42%)	15 (58%)	0	0
35	61	122/124 (98%)	88 (72%)	34 (28%)	0	2
35	69	122/124 (98%)	79 (65%)	43 (35%)	0	0
36	38	115/135 (85%)	61 (53%)	54 (47%)	0	0
37	48	106/111 (96%)	66 (62%)	40 (38%)	0	0
38	15	116/119 (98%)	85 (73%)	31 (27%)	0	2
38	58	116/119 (98%)	88 (76%)	28 (24%)	1	3
39	25	100/100 (100%)	75 (75%)	25 (25%)	0	3
39	68	100/100 (100%)	84 (84%)	16 (16%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	35	115/116 (99%)	80 (70%)	35 (30%)	0	1
40	78	114/116 (98%)	72 (63%)	42 (37%)	0	0
41	45	109/111 (98%)	74 (68%)	35 (32%)	0	1
41	88	109/111 (98%)	92 (84%)	17 (16%)	2	12
42	55	101/101 (100%)	80 (79%)	21 (21%)	1	6
42	98	101/101 (100%)	75 (74%)	26 (26%)	0	3
43	65	87/88 (99%)	59 (68%)	28 (32%)	0	1
43	A8	87/88 (99%)	55 (63%)	32 (37%)	0	0
44	75	117/127 (92%)	85 (73%)	32 (27%)	0	2
44	B8	119/127 (94%)	88 (74%)	31 (26%)	0	2
45	85	93/94 (99%)	76 (82%)	17 (18%)	2	8
45	C8	92/94 (98%)	74 (80%)	18 (20%)	1	7
46	95	82/82 (100%)	62 (76%)	20 (24%)	1	3
46	D8	82/82 (100%)	54 (66%)	28 (34%)	0	0
47	A5	91/92 (99%)	64 (70%)	27 (30%)	0	1
47	E8	91/92 (99%)	71 (78%)	20 (22%)	1	5
48	B5	75/78 (96%)	57 (76%)	18 (24%)	1	3
48	F8	75/78 (96%)	56 (75%)	19 (25%)	0	3
49	C5	81/91 (89%)	57 (70%)	24 (30%)	0	1
49	G8	82/91 (90%)	61 (74%)	21 (26%)	0	3
50	D5	173/179 (97%)	128 (74%)	45 (26%)	0	2
50	H8	147/179 (82%)	102 (69%)	45 (31%)	0	1
51	E5	62/67 (92%)	49 (79%)	13 (21%)	1	6
51	I8	62/67 (92%)	47 (76%)	15 (24%)	1	3
52	F5	79/83 (95%)	52 (66%)	27 (34%)	0	0
52	J8	78/83 (94%)	52 (67%)	26 (33%)	0	1
53	G5	62/67 (92%)	41 (66%)	21 (34%)	0	0
53	K8	63/67 (94%)	41 (65%)	22 (35%)	0	0
54	H5	50/52 (96%)	42 (84%)	8 (16%)	2	11
54	L8	50/52 (96%)	37 (74%)	13 (26%)	0	2
55	M8	42/63 (67%)	29 (69%)	13 (31%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	J5	48/52 (92%)	39 (81%)	9 (19%)	1	8
56	N8	44/52 (85%)	33 (75%)	11 (25%)	0	3
57	O8	44/52 (85%)	30 (68%)	14 (32%)	0	1
58	L5	40/42 (95%)	33 (82%)	7 (18%)	2	9
58	P8	38/42 (90%)	32 (84%)	6 (16%)	2	11
59	M5	54/55 (98%)	40 (74%)	14 (26%)	0	2
59	Q8	54/55 (98%)	40 (74%)	14 (26%)	0	2
All	All	9836/10671 (92%)	7290 (74%)	2546 (26%)	0	2

5 of 2546 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	19	138	VAL
44	75	124	ASP
30	29	154	LYS
29	19	105	ILE
35	69	125	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68 such sidechains are listed below:

Mol	Chain	Res	Type
39	25	5	GLN
41	45	113	GLN
47	A5	111	HIS
42	98	71	GLN
40	78	84	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	13	1511/1522 (99%)	383 (25%)	36 (2%)
1	1G	1508/1522 (99%)	381 (25%)	37 (2%)
22	1K	67/77 (87%)	32 (47%)	5 (7%)
22	1L	70/77 (90%)	29 (41%)	6 (8%)
23	2K	76/77 (98%)	19 (25%)	2 (2%)
23	2L	76/77 (98%)	18 (23%)	1 (1%)
24	3K	69/77 (89%)	37 (53%)	4 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	3L	70/77 (90%)	37 (52%)	3 (4%)
25	4K	20/27 (74%)	14 (70%)	1 (5%)
25	4L	15/27 (55%)	9 (60%)	0
26	14	2892/2917 (99%)	723 (25%)	51 (1%)
26	1H	2893/2917 (99%)	707 (24%)	67 (2%)
27	16	121/122 (99%)	28 (23%)	2 (1%)
27	1J	121/122 (99%)	32 (26%)	1 (0%)
All	All	9509/9638 (98%)	2449 (25%)	216 (2%)

5 of 2449 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	13	2	U
1	13	3	G
1	13	4	U
1	13	5	U
1	13	6	G

5 of 216 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	16	44	G
1	1G	1126	U
26	14	1819	A
1	1G	80	G
1	1G	485	G

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

22 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	$\# Z > 2$
22	PSU	1K	56	22	18,21,22	1.26	1 (5%)	22,30,33	1.56	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	5MU	1K	55	22	19,22,23	3.97	5 (26%)	28,32,35	3.10	8 (28%)
22	4SU	1K	8	22	18,21,22	1.79	5 (27%)	26,30,33	2.70	8 (30%)
22	2MA	1L	38	22	22,25,26	3.67	8 (36%)	33,37,40	2.18	10 (30%)
22	RSP	1L	33	22	17,21,22	4.02	7 (41%)	22,30,33	0.97	1 (4%)
22	PSU	1L	56	41,22	18,21,22	1.13	1 (5%)	22,30,33	1.83	3 (13%)
23	PSU	2L	56	23	18,21,22	1.35	2 (11%)	22,30,33	1.46	2 (9%)
23	7MG	2K	47	23	22,26,27	3.01	7 (31%)	29,39,42	2.75	10 (34%)
23	OMC	2K	33	23	19,22,23	1.73	4 (21%)	26,31,34	0.92	0
22	RSP	1K	33	22	17,21,22	3.97	7 (41%)	22,30,33	0.92	1 (4%)
23	4SU	2K	8	23	18,21,22	1.91	5 (27%)	26,30,33	2.71	8 (30%)
22	2MA	1K	38	22	22,25,26	3.17	8 (36%)	33,37,40	2.13	10 (30%)
23	5MU	2K	55	23	19,22,23	3.88	5 (26%)	28,32,35	3.68	8 (28%)
23	7MG	2L	47	23	22,26,27	3.02	5 (22%)	29,39,42	2.84	10 (34%)
23	OMC	2L	33	23	19,22,23	1.85	3 (15%)	26,31,34	1.06	2 (7%)
22	5MU	1L	55	22	19,22,23	3.82	5 (26%)	28,32,35	3.13	9 (32%)
23	4SU	2L	8	23	18,21,22	1.72	3 (16%)	26,30,33	2.46	4 (15%)
22	4SU	1L	8	22	18,21,22	1.86	3 (16%)	26,30,33	2.23	6 (23%)
23	5MU	2L	55	23	19,22,23	3.79	5 (26%)	28,32,35	3.33	9 (32%)
22	7MG	1L	47	22	22,26,27	3.09	6 (27%)	29,39,42	2.81	10 (34%)
23	PSU	2K	56	23	18,21,22	1.23	2 (11%)	22,30,33	2.04	4 (18%)
22	7MG	1K	47	22	22,26,27	3.08	6 (27%)	29,39,42	2.81	10 (34%)

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
22	PSU	1K	56	22	-	0/7/25/26	0/2/2/2
22	5MU	1K	55	22	-	0/7/25/26	0/2/2/2
22	4SU	1K	8	22	-	2/7/25/26	0/2/2/2
22	2MA	1L	38	22	-	0/7/25/26	0/3/3/3
22	RSP	1L	33	22	-	3/7/25/26	0/2/2/2
22	PSU	1L	56	41,22	-	0/7/25/26	0/2/2/2
23	PSU	2L	56	23	-	0/7/25/26	0/2/2/2
23	7MG	2K	47	23	-	2/7/37/38	0/3/3/3
23	OMC	2K	33	23	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	RSP	1K	33	22	-	3/7/25/26	0/2/2/2
23	4SU	2K	8	23	-	0/7/25/26	0/2/2/2
22	2MA	1K	38	22	-	0/7/25/26	0/3/3/3
23	5MU	2K	55	23	-	0/7/25/26	0/2/2/2
23	7MG	2L	47	23	-	2/7/37/38	0/3/3/3
23	OMC	2L	33	23	-	0/9/27/28	0/2/2/2
22	5MU	1L	55	22	-	0/7/25/26	0/2/2/2
23	4SU	2L	8	23	-	0/7/25/26	0/2/2/2
22	4SU	1L	8	22	-	3/7/25/26	0/2/2/2
23	5MU	2L	55	23	-	0/7/25/26	0/2/2/2
22	7MG	1L	47	22	-	2/7/37/38	0/3/3/3
23	PSU	2K	56	23	-	0/7/25/26	0/2/2/2
22	7MG	1K	47	22	-	2/7/37/38	0/3/3/3

The worst 5 of 103 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	1K	55	5MU	C2-N1	12.82	1.59	1.38
23	2K	55	5MU	C2-N1	12.76	1.58	1.38
22	1L	33	RSP	C2-N3	12.50	1.49	1.36
22	1L	38	2MA	C4-N3	12.21	1.49	1.34
22	1L	55	5MU	C2-N1	12.12	1.57	1.38

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	2K	55	5MU	C5-C4-N3	12.77	126.21	115.31
23	2L	55	5MU	C5-C4-N3	10.91	124.63	115.31
22	1K	55	5MU	C5-C4-N3	9.76	123.64	115.31
22	1L	55	5MU	C5-C4-N3	9.67	123.57	115.31
23	2K	8	4SU	C4-N3-C2	-8.50	119.08	127.34

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	1K	33	RSP	C3'-C4'-C5'-O5'
23	2K	33	OMC	C1'-C2'-O2'-CM2
23	2K	47	7MG	C2'-C1'-N9-C8
22	1L	33	RSP	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
22	1K	8	4SU	O4'-C4'-C5'-O5'

There are no ring outliers.

16 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	1K	56	PSU	1	0
22	1K	8	4SU	4	0
22	1L	33	RSP	4	0
22	1L	56	PSU	1	0
23	2K	47	7MG	1	0
23	2K	33	OMC	1	0
22	1K	33	RSP	3	0
23	2K	8	4SU	1	0
22	1K	38	2MA	2	0
23	2K	55	5MU	3	0
23	2L	47	7MG	4	0
23	2L	33	OMC	1	0
23	2L	8	4SU	1	0
22	1L	8	4SU	1	0
23	2L	55	5MU	2	0
22	1K	47	7MG	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1768 ligands modelled in this entry, 1766 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	$\# Z > 2$
61	SF4	3E	303	4	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
61	SF4	32	303	4	0,12,12	-	-	-		

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	SF4	3E	303	4	-	-	0/6/5/5
61	SF4	32	303	4	-	-	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.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	3E	303	SF4	2	0
61	32	303	SF4	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
24	3L	1
24	3K	1
32	41	1
29	11	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	3L	49:C	O3'	50:G	P	6.50
1	3K	49:C	O3'	50:G	P	5.32
1	41	140:ILE	C	141:PHE	N	1.19
1	11	239:ARG	C	240:ALA	N	1.09

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	13	1512/1522 (99%)	-0.86	7 (0%) 87 75	68, 110, 180, 220	0
1	1G	1509/1522 (99%)	-0.82	7 (0%) 87 75	79, 125, 182, 224	0
2	12	237/256 (92%)	-0.36	1 (0%) 88 78	110, 137, 164, 180	0
2	1E	231/256 (90%)	-0.34	0 100 100	117, 151, 171, 180	0
3	22	195/239 (81%)	-0.28	3 (1%) 72 52	131, 151, 166, 176	0
3	2E	205/239 (85%)	-0.51	0 100 100	93, 117, 147, 162	0
4	32	208/209 (99%)	-0.26	2 (0%) 79 62	100, 122, 143, 147	0
4	3E	207/209 (99%)	-0.19	2 (0%) 79 62	92, 115, 134, 144	0
5	42	151/162 (93%)	-0.16	2 (1%) 75 55	107, 128, 149, 167	0
5	4E	149/162 (91%)	-0.26	2 (1%) 75 55	88, 109, 128, 132	0
6	52	101/101 (100%)	-0.57	0 100 100	92, 111, 129, 141	0
6	5E	101/101 (100%)	-0.43	0 100 100	91, 114, 128, 142	0
7	62	138/156 (88%)	-0.31	2 (1%) 73 53	121, 135, 148, 154	0
7	6E	154/156 (98%)	0.13	8 (5%) 33 19	111, 129, 154, 163	0
8	72	138/138 (100%)	-0.27	3 (2%) 62 41	112, 131, 143, 149	0
8	7E	138/138 (100%)	-0.31	0 100 100	98, 117, 128, 140	0
9	82	124/128 (96%)	-0.13	2 (1%) 70 50	122, 161, 175, 190	0
9	8E	126/128 (98%)	-0.17	1 (0%) 82 66	95, 145, 164, 171	0
10	1A	99/105 (94%)	-0.26	0 100 100	118, 138, 151, 153	0
10	1I	99/105 (94%)	-0.04	0 100 100	92, 124, 144, 148	0
11	2A	113/129 (87%)	-0.17	1 (0%) 81 64	92, 116, 131, 143	0
11	2I	111/129 (86%)	0.37	3 (2%) 56 35	86, 114, 135, 142	0
12	3A	121/132 (91%)	0.43	10 (8%) 17 10	91, 113, 134, 148	0
12	3I	122/132 (92%)	0.06	6 (4%) 35 20	77, 88, 113, 138	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	4A	111/126 (88%)	-0.16	5 (4%) 38 22	129, 155, 169, 174	0
13	4I	119/126 (94%)	-0.40	1 (0%) 82 66	86, 130, 147, 152	0
14	5A	57/61 (93%)	0.20	3 (5%) 32 18	138, 150, 162, 166	0
14	5I	61/61 (100%)	-0.54	0 100 100	94, 106, 121, 134	0
15	6A	87/89 (97%)	-0.43	0 100 100	96, 120, 138, 142	0
15	6I	87/89 (97%)	-0.44	0 100 100	91, 107, 128, 137	0
16	7A	84/88 (95%)	-0.45	0 100 100	99, 112, 133, 156	0
16	7I	83/88 (94%)	-0.28	0 100 100	104, 118, 149, 162	0
17	8A	99/105 (94%)	-0.27	0 100 100	101, 118, 129, 136	0
17	8I	100/105 (95%)	-0.24	0 100 100	97, 113, 127, 139	0
18	9A	67/88 (76%)	-0.62	0 100 100	100, 119, 136, 138	0
18	9I	67/88 (76%)	-0.41	0 100 100	97, 115, 138, 144	0
19	AA	62/93 (66%)	0.35	6 (9%) 13 8	146, 161, 169, 172	0
19	AI	80/93 (86%)	-0.22	0 100 100	106, 125, 148, 154	0
20	BA	98/106 (92%)	-0.45	1 (1%) 79 62	97, 119, 146, 163	0
20	BI	98/106 (92%)	-0.07	0 100 100	114, 127, 156, 162	0
21	1B	24/27 (88%)	-0.16	0 100 100	128, 147, 157, 166	0
21	1F	24/27 (88%)	-0.62	0 100 100	106, 116, 128, 142	0
22	1K	65/77 (84%)	-0.38	2 (3%) 51 31	89, 150, 178, 186	0
22	1L	67/77 (87%)	-0.51	0 100 100	112, 160, 182, 187	0
23	2K	72/77 (93%)	-0.65	0 100 100	78, 109, 139, 149	0
23	2L	72/77 (93%)	-0.49	1 (1%) 73 53	86, 125, 159, 170	0
24	3K	73/77 (94%)	0.44	5 (6%) 23 13	85, 166, 185, 189	0
24	3L	74/77 (96%)	0.22	1 (1%) 73 53	92, 168, 183, 186	0
25	4K	21/27 (77%)	0.65	4 (19%) 3 2	82, 143, 200, 201	0
25	4L	17/27 (62%)	0.59	1 (5%) 28 16	104, 151, 206, 207	0
26	14	2895/2917 (99%)	-0.97	5 (0%) 91 84	61, 95, 202, 230	0
26	1H	2895/2917 (99%)	-1.05	2 (0%) 92 88	54, 83, 192, 225	0
27	16	122/122 (100%)	-1.28	0 100 100	79, 104, 129, 209	0
27	1J	122/122 (100%)	-0.91	1 (0%) 82 66	101, 133, 153, 192	0
28	7I	134/229 (58%)	-0.08	3 (2%) 62 41	146, 186, 200, 206	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	79	130/229 (56%)	0.40	6 (4%) 37 21	156, 231, 253, 258	0
29	11	273/276 (98%)	-0.29	2 (0%) 84 69	50, 76, 93, 102	0
29	19	273/276 (98%)	-0.10	7 (2%) 57 36	60, 83, 99, 121	0
30	21	203/206 (98%)	0.11	5 (2%) 58 37	60, 94, 134, 148	0
30	29	203/206 (98%)	-0.31	3 (1%) 72 52	68, 100, 138, 150	0
31	31	202/210 (96%)	-0.31	1 (0%) 87 75	57, 88, 123, 137	0
31	39	206/210 (98%)	-0.40	2 (0%) 79 62	68, 110, 156, 176	0
32	41	179/182 (98%)	-0.48	2 (1%) 78 60	94, 115, 147, 155	0
32	49	179/182 (98%)	-0.04	1 (0%) 85 72	123, 143, 167, 181	0
33	51	171/180 (95%)	-0.01	1 (0%) 85 72	88, 113, 128, 137	0
33	59	171/180 (95%)	0.44	16 (9%) 14 8	107, 169, 188, 196	0
34	18	30/125 (24%)	-0.16	0 100 100	150, 157, 161, 162	0
34	28	30/125 (24%)	-0.09	0 100 100	151, 160, 165, 168	0
35	61	145/148 (97%)	-0.31	1 (0%) 84 69	88, 137, 156, 159	0
35	69	145/148 (97%)	-0.22	0 100 100	91, 129, 147, 155	0
36	38	143/173 (82%)	0.42	8 (5%) 30 17	154, 174, 183, 187	0
37	48	142/147 (96%)	-0.19	0 100 100	197, 208, 212, 214	0
38	15	137/140 (97%)	-0.09	2 (1%) 72 52	89, 114, 144, 154	0
38	58	137/140 (97%)	0.04	4 (2%) 53 34	77, 98, 134, 147	0
39	25	122/122 (100%)	0.13	3 (2%) 58 37	78, 96, 115, 129	0
39	68	122/122 (100%)	0.15	3 (2%) 58 37	70, 87, 104, 111	0
40	35	148/150 (98%)	-0.08	4 (2%) 56 35	71, 113, 146, 164	0
40	78	147/150 (98%)	-0.13	4 (2%) 56 35	62, 91, 113, 122	0
41	45	138/141 (97%)	-0.04	6 (4%) 40 23	82, 113, 133, 154	0
41	88	141/141 (100%)	-0.36	0 100 100	68, 89, 110, 140	0
42	55	118/118 (100%)	-0.54	0 100 100	69, 90, 109, 126	0
42	98	118/118 (100%)	-0.16	2 (1%) 69 48	74, 91, 111, 125	0
43	65	110/112 (98%)	-0.42	1 (0%) 81 64	97, 125, 144, 149	0
43	A8	111/112 (99%)	-0.63	0 100 100	82, 100, 120, 131	0
44	75	134/146 (91%)	-0.03	5 (3%) 45 26	89, 104, 145, 170	0
44	B8	136/146 (93%)	-0.08	5 (3%) 45 26	82, 98, 151, 167	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
45	85	117/118 (99%)	-0.12	0 100 100	76, 103, 136, 146	0
45	C8	115/118 (97%)	-0.17	1 (0%) 81 64	63, 87, 118, 127	0
46	95	100/101 (99%)	0.21	3 (3%) 52 32	79, 128, 146, 159	0
46	D8	101/101 (100%)	0.13	3 (2%) 52 32	65, 108, 129, 137	0
47	A5	111/113 (98%)	0.03	2 (1%) 67 47	72, 86, 115, 139	0
47	E8	112/113 (99%)	-0.49	2 (1%) 67 47	66, 80, 115, 146	0
48	B5	94/96 (97%)	-0.24	0 100 100	78, 94, 116, 128	0
48	F8	95/96 (98%)	-0.25	0 100 100	64, 80, 103, 116	0
49	C5	106/110 (96%)	0.73	13 (12%) 8 5	96, 119, 155, 170	0
49	G8	105/110 (95%)	0.24	5 (4%) 35 20	81, 101, 128, 143	0
50	D5	200/206 (97%)	-0.39	0 100 100	108, 141, 189, 200	0
50	H8	165/206 (80%)	-0.51	0 100 100	95, 126, 172, 180	0
51	E5	78/85 (91%)	-0.17	1 (1%) 75 55	82, 100, 115, 125	0
51	I8	81/85 (95%)	-0.08	5 (6%) 26 15	66, 85, 109, 130	0
52	F5	94/98 (95%)	0.26	3 (3%) 50 30	72, 93, 125, 131	0
52	J8	93/98 (94%)	-0.26	1 (1%) 78 60	66, 83, 126, 132	0
53	G5	66/72 (91%)	-0.19	1 (1%) 72 52	90, 114, 135, 157	0
53	K8	69/72 (95%)	-0.15	1 (1%) 73 53	71, 91, 108, 129	0
54	H5	58/60 (96%)	-0.20	0 100 100	88, 108, 134, 144	0
54	L8	58/60 (96%)	-0.46	0 100 100	73, 89, 119, 129	0
55	M8	48/71 (67%)	-0.39	0 100 100	118, 153, 165, 170	0
56	J5	56/60 (93%)	-0.27	0 100 100	67, 93, 142, 145	0
56	N8	50/60 (83%)	-0.20	2 (4%) 42 24	61, 92, 140, 144	0
57	O8	45/54 (83%)	0.27	1 (2%) 62 41	121, 140, 153, 158	0
58	L5	47/49 (95%)	-0.30	1 (2%) 63 42	64, 71, 95, 101	0
58	P8	47/49 (95%)	-0.51	1 (2%) 63 42	56, 64, 86, 99	0
59	M5	64/65 (98%)	-0.05	2 (3%) 51 31	79, 90, 104, 135	0
59	Q8	64/65 (98%)	-0.28	0 100 100	65, 81, 97, 110	0
All	All	21409/22595 (94%)	-0.50	245 (1%) 78 60	50, 110, 180, 258	0

The worst 5 of 245 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
56	N8	2	ALA	9.6
44	75	106	SER	6.5
7	6E	81	GLY	6.5
29	19	274	ARG	6.1
49	C5	53	PRO	5.9

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
22	7MG	1K	47	24/25	0.69	0.12	142,157,163,168	0
22	7MG	1L	47	24/25	0.74	0.08	159,163,169,177	0
22	4SU	1L	8	20/21	0.75	0.09	157,161,167,167	0
22	4SU	1K	8	20/21	0.83	0.09	142,150,156,156	0
23	PSU	2L	56	20/21	0.83	0.08	129,138,140,146	0
22	PSU	1L	56	20/21	0.85	0.06	140,148,154,154	0
23	5MU	2L	55	21/22	0.86	0.08	132,143,146,149	0
22	PSU	1K	56	20/21	0.86	0.07	116,128,139,144	0
22	RSP	1K	33	20/21	0.88	0.10	110,117,134,144	0
22	5MU	1L	55	21/22	0.88	0.06	137,142,147,154	0
23	4SU	2K	8	20/21	0.89	0.11	95,103,109,110	0
22	RSP	1L	33	20/21	0.90	0.08	126,132,145,149	0
23	PSU	2K	56	20/21	0.90	0.05	106,112,123,129	0
22	5MU	1K	55	21/22	0.90	0.06	119,130,139,146	0
23	7MG	2L	47	24/25	0.91	0.07	132,141,148,149	0
22	2MA	1L	38	23/24	0.92	0.08	104,116,119,122	0
23	7MG	2K	47	24/25	0.92	0.07	107,113,121,124	0
23	5MU	2K	55	21/22	0.93	0.06	109,116,123,133	0
23	4SU	2L	8	20/21	0.93	0.07	122,130,137,140	0
22	2MA	1K	38	23/24	0.95	0.06	83,88,93,97	0
23	OMC	2L	33	21/22	0.96	0.08	102,111,118,124	0
23	OMC	2K	33	21/22	0.97	0.08	83,88,93,95	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
60	MG	13	1722	1/1	0.23	0.33	124,124,124,124	0
60	MG	1K	102	1/1	0.32	0.24	134,134,134,134	0
60	MG	1H	3239	1/1	0.42	0.24	114,114,114,114	0
60	MG	1H	3259	1/1	0.42	0.21	174,174,174,174	0
60	MG	1H	3221	1/1	0.44	0.19	107,107,107,107	0
60	MG	1G	1647	1/1	0.44	0.31	104,104,104,104	0
60	MG	1G	1690	1/1	0.44	0.26	109,109,109,109	0
60	MG	14	3212	1/1	0.44	0.28	89,89,89,89	0
60	MG	14	3203	1/1	0.46	0.23	97,97,97,97	0
60	MG	1G	1672	1/1	0.48	0.26	110,110,110,110	0
60	MG	1J	203	1/1	0.49	0.21	128,128,128,128	0
60	MG	14	3236	1/1	0.50	0.35	103,103,103,103	0
60	MG	13	1724	1/1	0.52	0.26	107,107,107,107	0
60	MG	1G	1668	1/1	0.52	0.21	107,107,107,107	0
60	MG	14	3250	1/1	0.53	0.27	110,110,110,110	0
60	MG	45	201	1/1	0.53	0.19	111,111,111,111	0
60	MG	14	3256	1/1	0.54	0.29	108,108,108,108	0
60	MG	1H	3219	1/1	0.54	0.40	100,100,100,100	0
60	MG	13	1634	1/1	0.54	0.26	113,113,113,113	0
60	MG	14	3132	1/1	0.55	0.21	138,138,138,138	0
60	MG	14	3262	1/1	0.55	0.23	96,96,96,96	0
60	MG	1H	3267	1/1	0.56	0.26	90,90,90,90	0
60	MG	1H	3230	1/1	0.56	0.22	112,112,112,112	0
60	MG	14	3221	1/1	0.58	0.20	98,98,98,98	0
60	MG	14	3069	1/1	0.59	0.20	100,100,100,100	0
60	MG	1G	1667	1/1	0.59	0.21	121,121,121,121	0
60	MG	1H	3264	1/1	0.59	0.24	93,93,93,93	0
60	MG	14	3211	1/1	0.59	0.20	116,116,116,116	0
60	MG	14	3268	1/1	0.59	0.23	105,105,105,105	0
60	MG	13	1662	1/1	0.59	0.23	98,98,98,98	0
60	MG	13	1702	1/1	0.59	0.28	105,105,105,105	0
60	MG	1G	1670	1/1	0.60	0.18	105,105,105,105	0
60	MG	13	1700	1/1	0.61	0.18	108,108,108,108	0
60	MG	14	3209	1/1	0.61	0.28	95,95,95,95	0
60	MG	13	1696	1/1	0.61	0.24	104,104,104,104	0
60	MG	N8	101	1/1	0.62	0.15	92,92,92,92	0
60	MG	13	1725	1/1	0.62	0.31	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3012	1/1	0.62	0.25	107,107,107,107	0
60	MG	14	3241	1/1	0.62	0.19	103,103,103,103	0
60	MG	1G	1648	1/1	0.62	0.35	99,99,99,99	0
60	MG	14	3157	1/1	0.63	0.28	93,93,93,93	0
60	MG	1H	3165	1/1	0.63	0.22	99,99,99,99	0
60	MG	14	3246	1/1	0.63	0.27	110,110,110,110	0
60	MG	1H	3164	1/1	0.64	0.18	106,106,106,106	0
60	MG	1H	3139	1/1	0.64	0.16	85,85,85,85	0
60	MG	1H	3187	1/1	0.64	0.11	88,88,88,88	0
60	MG	1H	3285	1/1	0.64	0.23	96,96,96,96	0
60	MG	14	3226	1/1	0.64	0.18	100,100,100,100	0
60	MG	16	212	1/1	0.64	0.22	102,102,102,102	0
60	MG	1H	3213	1/1	0.64	0.30	112,112,112,112	0
60	MG	1H	3103	1/1	0.65	0.19	98,98,98,98	0
60	MG	13	1674	1/1	0.65	0.24	102,102,102,102	0
60	MG	1H	3224	1/1	0.65	0.22	80,80,80,80	0
60	MG	1H	3229	1/1	0.65	0.21	117,117,117,117	0
60	MG	13	1664	1/1	0.65	0.29	94,94,94,94	0
60	MG	1H	3315	1/1	0.65	0.23	92,92,92,92	0
60	MG	14	3270	1/1	0.65	0.31	103,103,103,103	0
60	MG	14	3337	1/1	0.65	0.23	105,105,105,105	0
60	MG	14	3140	1/1	0.65	0.39	97,97,97,97	0
60	MG	14	3147	1/1	0.65	0.16	74,74,74,74	0
60	MG	14	3302	1/1	0.66	0.14	99,99,99,99	0
60	MG	14	3023	1/1	0.66	0.20	64,64,64,64	0
60	MG	13	1686	1/1	0.66	0.19	113,113,113,113	0
60	MG	14	3107	1/1	0.66	0.22	75,75,75,75	0
60	MG	13	1677	1/1	0.67	0.16	94,94,94,94	0
60	MG	1G	1680	1/1	0.67	0.16	124,124,124,124	0
60	MG	1G	1637	1/1	0.67	0.18	146,146,146,146	0
60	MG	14	3182	1/1	0.67	0.18	101,101,101,101	0
60	MG	1H	3098	1/1	0.67	0.22	74,74,74,74	0
60	MG	1H	3227	1/1	0.67	0.21	108,108,108,108	0
60	MG	14	3030	1/1	0.67	0.14	104,104,104,104	0
60	MG	14	3298	1/1	0.67	0.21	117,117,117,117	0
60	MG	1H	3635	1/1	0.67	0.28	115,115,115,115	0
60	MG	14	3074	1/1	0.67	0.23	105,105,105,105	0
60	MG	1H	3646	1/1	0.67	0.17	99,99,99,99	0
60	MG	13	1701	1/1	0.67	0.39	102,102,102,102	0
60	MG	1H	3192	1/1	0.68	0.21	99,99,99,99	0
60	MG	14	3100	1/1	0.68	0.12	88,88,88,88	0
60	MG	13	1698	1/1	0.68	0.25	98,98,98,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	13	1668	1/1	0.68	0.39	91,91,91,91	0
60	MG	14	3231	1/1	0.68	0.25	94,94,94,94	0
60	MG	1G	1696	1/1	0.68	0.23	118,118,118,118	0
60	MG	1H	3320	1/1	0.69	0.28	92,92,92,92	0
60	MG	1G	1689	1/1	0.69	0.29	104,104,104,104	0
60	MG	14	3055	1/1	0.69	0.16	84,84,84,84	0
60	MG	1H	3193	1/1	0.69	0.34	93,93,93,93	0
60	MG	1H	3290	1/1	0.69	0.13	85,85,85,85	0
60	MG	1L	101	1/1	0.69	0.16	124,124,124,124	0
60	MG	14	3009	1/1	0.69	0.24	84,84,84,84	0
60	MG	13	1655	1/1	0.69	0.19	91,91,91,91	0
60	MG	13	1658	1/1	0.70	0.26	96,96,96,96	0
60	MG	1G	1643	1/1	0.70	0.33	96,96,96,96	0
60	MG	13	1704	1/1	0.70	0.26	91,91,91,91	0
60	MG	1H	3237	1/1	0.70	0.23	79,79,79,79	0
60	MG	1G	1693	1/1	0.70	0.21	103,103,103,103	0
60	MG	14	3240	1/1	0.70	0.22	93,93,93,93	0
60	MG	16	211	1/1	0.70	0.11	97,97,97,97	0
60	MG	14	3344	1/1	0.70	0.21	97,97,97,97	0
60	MG	14	3549	1/1	0.70	0.24	119,119,119,119	0
60	MG	13	1721	1/1	0.70	0.13	94,94,94,94	0
60	MG	1H	3183	1/1	0.70	0.18	80,80,80,80	0
60	MG	14	3146	1/1	0.71	0.26	91,91,91,91	0
60	MG	1H	3246	1/1	0.71	0.19	98,98,98,98	0
60	MG	14	3148	1/1	0.71	0.31	87,87,87,87	0
60	MG	1H	3317	1/1	0.71	0.23	95,95,95,95	0
60	MG	14	3257	1/1	0.71	0.22	111,111,111,111	0
60	MG	14	3259	1/1	0.71	0.28	100,100,100,100	0
60	MG	1H	3189	1/1	0.71	0.22	97,97,97,97	0
60	MG	1G	1681	1/1	0.71	0.29	104,104,104,104	0
60	MG	2K	102	1/1	0.71	0.20	106,106,106,106	0
60	MG	2K	104	1/1	0.71	0.20	88,88,88,88	0
60	MG	1G	1652	1/1	0.71	0.23	98,98,98,98	0
60	MG	1G	1663	1/1	0.71	0.27	101,101,101,101	0
60	MG	14	3124	1/1	0.71	0.30	89,89,89,89	0
60	MG	1H	3238	1/1	0.71	0.26	99,99,99,99	0
60	MG	13	1676	1/1	0.71	0.13	99,99,99,99	0
60	MG	14	3142	1/1	0.71	0.20	93,93,93,93	0
60	MG	5E	201	1/1	0.72	0.14	114,114,114,114	0
60	MG	13	1687	1/1	0.72	0.33	114,114,114,114	0
60	MG	1G	1632	1/1	0.72	0.21	93,93,93,93	0
60	MG	14	3077	1/1	0.72	0.35	103,103,103,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3250	1/1	0.72	0.17	102,102,102,102	0
60	MG	14	3181	1/1	0.72	0.23	88,88,88,88	0
60	MG	1H	3194	1/1	0.72	0.37	98,98,98,98	0
60	MG	14	3191	1/1	0.72	0.32	99,99,99,99	0
60	MG	13	1732	1/1	0.72	0.26	97,97,97,97	0
60	MG	2K	103	1/1	0.72	0.15	110,110,110,110	0
60	MG	35	201	1/1	0.72	0.15	87,87,87,87	0
60	MG	1H	3160	1/1	0.72	0.19	87,87,87,87	0
60	MG	13	1675	1/1	0.73	0.29	81,81,81,81	0
60	MG	1H	3286	1/1	0.73	0.25	89,89,89,89	0
60	MG	14	3079	1/1	0.73	0.22	112,112,112,112	0
60	MG	14	3249	1/1	0.73	0.26	99,99,99,99	0
60	MG	14	3327	1/1	0.73	0.18	100,100,100,100	0
60	MG	1G	1687	1/1	0.73	0.14	110,110,110,110	0
60	MG	14	3251	1/1	0.73	0.18	88,88,88,88	0
60	MG	1H	3176	1/1	0.73	0.19	106,106,106,106	0
60	MG	16	202	1/1	0.73	0.22	101,101,101,101	0
60	MG	13	1747	1/1	0.73	0.20	107,107,107,107	0
60	MG	1H	3185	1/1	0.73	0.20	86,86,86,86	0
60	MG	3E	301	1/1	0.74	0.21	127,127,127,127	0
60	MG	1G	1610	1/1	0.74	0.17	122,122,122,122	0
60	MG	14	3112	1/1	0.74	0.20	91,91,91,91	0
60	MG	14	3006	1/1	0.74	0.20	86,86,86,86	0
60	MG	1H	3094	1/1	0.74	0.23	87,87,87,87	0
60	MG	14	3133	1/1	0.74	0.12	107,107,107,107	0
60	MG	1H	3196	1/1	0.74	0.23	83,83,83,83	0
60	MG	1G	1673	1/1	0.74	0.25	97,97,97,97	0
60	MG	1H	3197	1/1	0.74	0.14	91,91,91,91	0
60	MG	1G	1646	1/1	0.74	0.21	103,103,103,103	0
60	MG	1H	3231	1/1	0.74	0.17	90,90,90,90	0
60	MG	3E	302	1/1	0.74	0.33	95,95,95,95	0
60	MG	13	1717	1/1	0.74	0.19	121,121,121,121	0
60	MG	1H	3114	1/1	0.74	0.14	57,57,57,57	0
60	MG	14	3188	1/1	0.74	0.25	82,82,82,82	0
60	MG	13	1667	1/1	0.75	0.21	84,84,84,84	0
60	MG	1H	3095	1/1	0.75	0.14	94,94,94,94	0
60	MG	13	1688	1/1	0.75	0.22	89,89,89,89	0
60	MG	31	302	1/1	0.75	0.26	90,90,90,90	0
60	MG	1H	3014	1/1	0.75	0.18	92,92,92,92	0
60	MG	1H	3112	1/1	0.75	0.25	104,104,104,104	0
60	MG	1H	3249	1/1	0.75	0.21	96,96,96,96	0
60	MG	1H	3113	1/1	0.75	0.17	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3318	1/1	0.75	0.14	114,114,114,114	0
60	MG	1H	3251	1/1	0.75	0.37	88,88,88,88	0
60	MG	14	3338	1/1	0.75	0.16	111,111,111,111	0
60	MG	14	3165	1/1	0.75	0.25	92,92,92,92	0
60	MG	1H	3328	1/1	0.75	0.14	96,96,96,96	0
60	MG	1H	3048	1/1	0.75	0.17	67,67,67,67	0
60	MG	14	3184	1/1	0.75	0.26	93,93,93,93	0
60	MG	1H	3262	1/1	0.75	0.30	94,94,94,94	0
60	MG	13	1652	1/1	0.76	0.22	94,94,94,94	0
60	MG	14	3073	1/1	0.76	0.24	110,110,110,110	0
60	MG	1H	3163	1/1	0.76	0.21	101,101,101,101	0
60	MG	1H	3597	1/1	0.76	0.20	103,103,103,103	0
60	MG	1H	3210	1/1	0.76	0.33	76,76,76,76	0
60	MG	5E	202	1/1	0.76	0.18	104,104,104,104	0
60	MG	14	3315	1/1	0.76	0.18	87,87,87,87	0
60	MG	13	1728	1/1	0.76	0.23	94,94,94,94	0
60	MG	16	208	1/1	0.76	0.18	104,104,104,104	0
60	MG	14	3248	1/1	0.76	0.26	95,95,95,95	0
60	MG	16	209	1/1	0.76	0.16	108,108,108,108	0
60	MG	13	1644	1/1	0.76	0.46	102,102,102,102	0
60	MG	14	3035	1/1	0.76	0.20	85,85,85,85	0
60	MG	29	302	1/1	0.76	0.15	85,85,85,85	0
60	MG	1H	3156	1/1	0.76	0.17	101,101,101,101	0
60	MG	14	3063	1/1	0.76	0.29	104,104,104,104	0
60	MG	14	3121	1/1	0.77	0.26	96,96,96,96	0
60	MG	14	3294	1/1	0.77	0.19	100,100,100,100	0
60	MG	1H	3083	1/1	0.77	0.16	80,80,80,80	0
60	MG	14	3245	1/1	0.77	0.16	101,101,101,101	0
60	MG	14	3309	1/1	0.77	0.17	77,77,77,77	0
60	MG	13	1642	1/1	0.77	0.14	100,100,100,100	0
60	MG	13	1692	1/1	0.77	0.21	99,99,99,99	0
60	MG	14	3334	1/1	0.77	0.16	117,117,117,117	0
60	MG	1H	3244	1/1	0.77	0.19	97,97,97,97	0
60	MG	1G	1671	1/1	0.77	0.20	96,96,96,96	0
60	MG	1H	3256	1/1	0.77	0.30	102,102,102,102	0
60	MG	14	3081	1/1	0.77	0.31	77,77,77,77	0
60	MG	14	3086	1/1	0.77	0.20	63,63,63,63	0
60	MG	1J	204	1/1	0.77	0.17	116,116,116,116	0
60	MG	14	3034	1/1	0.77	0.20	80,80,80,80	0
60	MG	1H	3258	1/1	0.77	0.34	88,88,88,88	0
60	MG	32	301	1/1	0.77	0.18	102,102,102,102	0
60	MG	1H	3111	1/1	0.78	0.14	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3084	1/1	0.78	0.17	102,102,102,102	0
60	MG	13	1679	1/1	0.78	0.22	90,90,90,90	0
60	MG	14	3333	1/1	0.78	0.13	110,110,110,110	0
60	MG	1H	3236	1/1	0.78	0.21	92,92,92,92	0
60	MG	1G	1649	1/1	0.78	0.23	108,108,108,108	0
60	MG	1H	3263	1/1	0.78	0.21	83,83,83,83	0
60	MG	14	3343	1/1	0.78	0.16	94,94,94,94	0
60	MG	1G	1653	1/1	0.78	0.24	108,108,108,108	0
60	MG	1G	1655	1/1	0.78	0.16	114,114,114,114	0
60	MG	14	3238	1/1	0.78	0.24	101,101,101,101	0
60	MG	1H	3296	1/1	0.78	0.12	92,92,92,92	0
60	MG	1H	3092	1/1	0.78	0.17	80,80,80,80	0
60	MG	14	3028	1/1	0.78	0.17	89,89,89,89	0
60	MG	14	3201	1/1	0.78	0.17	113,113,113,113	0
60	MG	1H	3060	1/1	0.79	0.17	90,90,90,90	0
60	MG	1H	3065	1/1	0.79	0.18	66,66,66,66	0
60	MG	13	1718	1/1	0.79	0.14	127,127,127,127	0
60	MG	14	3218	1/1	0.79	0.16	74,74,74,74	0
60	MG	14	3219	1/1	0.79	0.29	102,102,102,102	0
60	MG	1G	1640	1/1	0.79	0.15	95,95,95,95	0
60	MG	1H	3261	1/1	0.79	0.30	102,102,102,102	0
60	MG	1H	3091	1/1	0.79	0.23	91,91,91,91	0
60	MG	14	3323	1/1	0.79	0.11	91,91,91,91	0
60	MG	14	3326	1/1	0.79	0.15	91,91,91,91	0
60	MG	13	1620	1/1	0.79	0.12	72,72,72,72	0
60	MG	1H	3240	1/1	0.79	0.11	75,75,75,75	0
60	MG	1H	3242	1/1	0.79	0.23	88,88,88,88	0
60	MG	1H	3269	1/1	0.79	0.42	102,102,102,102	0
60	MG	13	1645	1/1	0.79	0.30	98,98,98,98	0
60	MG	14	3341	1/1	0.79	0.26	91,91,91,91	0
60	MG	1H	3190	1/1	0.79	0.14	92,92,92,92	0
60	MG	1G	1661	1/1	0.79	0.21	104,104,104,104	0
60	MG	4L	102	1/1	0.79	0.25	108,108,108,108	0
60	MG	13	1650	1/1	0.79	0.24	96,96,96,96	0
60	MG	14	3094	1/1	0.79	0.15	96,96,96,96	0
60	MG	13	1683	1/1	0.79	0.28	81,81,81,81	0
60	MG	13	1643	1/1	0.79	0.18	82,82,82,82	0
60	MG	14	3108	1/1	0.79	0.15	66,66,66,66	0
60	MG	1H	3154	1/1	0.80	0.26	100,100,100,100	0
60	MG	13	1697	1/1	0.80	0.24	97,97,97,97	0
60	MG	14	3058	1/1	0.80	0.20	88,88,88,88	0
60	MG	14	3061	1/1	0.80	0.18	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3158	1/1	0.80	0.21	72,72,72,72	0
60	MG	14	3068	1/1	0.80	0.22	70,70,70,70	0
60	MG	14	3260	1/1	0.80	0.22	91,91,91,91	0
60	MG	1H	3270	1/1	0.80	0.30	100,100,100,100	0
60	MG	1H	3280	1/1	0.80	0.34	78,78,78,78	0
60	MG	13	1606	1/1	0.80	0.21	131,131,131,131	0
60	MG	14	3190	1/1	0.80	0.19	81,81,81,81	0
60	MG	1G	1621	1/1	0.80	0.20	108,108,108,108	0
60	MG	1H	3199	1/1	0.80	0.20	94,94,94,94	0
60	MG	13	1654	1/1	0.80	0.14	96,96,96,96	0
60	MG	14	3208	1/1	0.80	0.21	89,89,89,89	0
60	MG	13	1681	1/1	0.80	0.19	97,97,97,97	0
60	MG	1G	1641	1/1	0.80	0.16	103,103,103,103	0
60	MG	1H	3084	1/1	0.80	0.19	102,102,102,102	0
60	MG	13	1669	1/1	0.80	0.18	97,97,97,97	0
60	MG	14	3102	1/1	0.80	0.24	82,82,82,82	0
60	MG	14	3220	1/1	0.80	0.12	92,92,92,92	0
60	MG	13	1685	1/1	0.80	0.21	85,85,85,85	0
60	MG	1H	3121	1/1	0.80	0.14	88,88,88,88	0
60	MG	1H	3037	1/1	0.80	0.14	87,87,87,87	0
60	MG	1H	3142	1/1	0.80	0.16	72,72,72,72	0
60	MG	1H	3260	1/1	0.80	0.19	178,178,178,178	0
60	MG	14	3130	1/1	0.80	0.15	80,80,80,80	0
60	MG	1H	3143	1/1	0.80	0.20	72,72,72,72	0
60	MG	1H	3655	1/1	0.80	0.18	107,107,107,107	0
60	MG	1H	3234	1/1	0.80	0.31	82,82,82,82	0
60	MG	1H	3147	1/1	0.80	0.21	86,86,86,86	0
60	MG	14	3093	1/1	0.81	0.15	98,98,98,98	0
60	MG	1H	3253	1/1	0.81	0.31	100,100,100,100	0
60	MG	1G	1634	1/1	0.81	0.18	106,106,106,106	0
60	MG	14	3029	1/1	0.81	0.18	85,85,85,85	0
60	MG	1H	3136	1/1	0.81	0.23	80,80,80,80	0
60	MG	14	3269	1/1	0.81	0.15	104,104,104,104	0
60	MG	13	1619	1/1	0.81	0.29	66,66,66,66	0
60	MG	14	3288	1/1	0.81	0.19	106,106,106,106	0
60	MG	1H	3106	1/1	0.81	0.19	89,89,89,89	0
60	MG	14	3295	1/1	0.81	0.16	101,101,101,101	0
60	MG	14	3210	1/1	0.81	0.40	84,84,84,84	0
60	MG	13	1632	1/1	0.81	0.22	88,88,88,88	0
60	MG	14	3122	1/1	0.81	0.20	79,79,79,79	0
60	MG	13	1689	1/1	0.81	0.16	97,97,97,97	0
60	MG	14	3060	1/1	0.81	0.28	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3245	1/1	0.81	0.21	94,94,94,94	0
60	MG	13	1670	1/1	0.81	0.19	102,102,102,102	0
60	MG	13	1659	1/1	0.81	0.15	121,121,121,121	0
60	MG	1G	1650	1/1	0.81	0.17	94,94,94,94	0
60	MG	14	3336	1/1	0.81	0.16	104,104,104,104	0
60	MG	14	3144	1/1	0.81	0.18	72,72,72,72	0
60	MG	1H	3120	1/1	0.81	0.15	101,101,101,101	0
60	MG	14	3339	1/1	0.81	0.12	112,112,112,112	0
60	MG	88	201	1/1	0.81	0.16	84,84,84,84	0
60	MG	1H	3326	1/1	0.81	0.12	98,98,98,98	0
60	MG	1G	1659	1/1	0.81	0.17	97,97,97,97	0
60	MG	14	3161	1/1	0.81	0.24	73,73,73,73	0
60	MG	14	3080	1/1	0.81	0.15	77,77,77,77	0
60	MG	1H	3101	1/1	0.81	0.26	76,76,76,76	0
60	MG	1G	1617	1/1	0.81	0.12	98,98,98,98	0
60	MG	39	302	1/1	0.81	0.21	90,90,90,90	0
60	MG	14	3183	1/1	0.81	0.22	94,94,94,94	0
60	MG	1H	3353	1/1	0.81	0.15	89,89,89,89	0
60	MG	55	202	1/1	0.81	0.23	91,91,91,91	0
60	MG	1G	1618	1/1	0.82	0.19	97,97,97,97	0
60	MG	1H	3066	1/1	0.82	0.25	87,87,87,87	0
60	MG	1H	3323	1/1	0.82	0.08	110,110,110,110	0
60	MG	1H	3135	1/1	0.82	0.27	77,77,77,77	0
60	MG	13	1671	1/1	0.82	0.14	98,98,98,98	0
60	MG	1H	3105	1/1	0.82	0.25	80,80,80,80	0
60	MG	1H	3169	1/1	0.82	0.24	82,82,82,82	0
60	MG	1H	3206	1/1	0.82	0.17	105,105,105,105	0
60	MG	14	3279	1/1	0.82	0.19	90,90,90,90	0
60	MG	1G	1692	1/1	0.82	0.11	88,88,88,88	0
60	MG	1G	1645	1/1	0.82	0.19	105,105,105,105	0
60	MG	14	3197	1/1	0.82	0.12	85,85,85,85	0
60	MG	1H	3209	1/1	0.82	0.19	82,82,82,82	0
60	MG	1G	1750	1/1	0.82	0.11	136,136,136,136	0
60	MG	14	3308	1/1	0.82	0.16	92,92,92,92	0
60	MG	1G	1754	1/1	0.82	0.11	135,135,135,135	0
60	MG	14	3095	1/1	0.82	0.28	70,70,70,70	0
60	MG	1H	3172	1/1	0.82	0.12	74,74,74,74	0
60	MG	13	1605	1/1	0.82	0.17	95,95,95,95	0
60	MG	1H	3274	1/1	0.82	0.21	90,90,90,90	0
60	MG	1H	3217	1/1	0.82	0.10	84,84,84,84	0
60	MG	1H	3034	1/1	0.82	0.16	77,77,77,77	0
60	MG	1H	3220	1/1	0.82	0.16	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1G	1654	1/1	0.82	0.18	109,109,109,109	0
60	MG	14	3027	1/1	0.82	0.26	89,89,89,89	0
60	MG	14	3128	1/1	0.82	0.16	101,101,101,101	0
60	MG	13	1665	1/1	0.82	0.28	106,106,106,106	0
60	MG	1H	3148	1/1	0.82	0.13	83,83,83,83	0
60	MG	1G	1660	1/1	0.82	0.21	93,93,93,93	0
60	MG	14	3547	1/1	0.82	0.19	96,96,96,96	0
60	MG	88	202	1/1	0.82	0.12	107,107,107,107	0
60	MG	14	3243	1/1	0.82	0.24	82,82,82,82	0
60	MG	13	1707	1/1	0.82	0.14	103,103,103,103	0
60	MG	1G	1666	1/1	0.82	0.17	96,96,96,96	0
60	MG	13	1806	1/1	0.82	0.18	107,107,107,107	0
60	MG	1G	1613	1/1	0.82	0.14	100,100,100,100	0
60	MG	13	1716	1/1	0.82	0.13	111,111,111,111	0
60	MG	14	3155	1/1	0.82	0.23	97,97,97,97	0
60	MG	1H	3191	1/1	0.83	0.30	79,79,79,79	0
60	MG	14	3185	1/1	0.83	0.13	78,78,78,78	0
60	MG	13	1657	1/1	0.83	0.16	129,129,129,129	0
60	MG	13	1627	1/1	0.83	0.18	83,83,83,83	0
60	MG	1H	3079	1/1	0.83	0.21	87,87,87,87	0
60	MG	14	3192	1/1	0.83	0.14	100,100,100,100	0
60	MG	1H	3282	1/1	0.83	0.16	83,83,83,83	0
60	MG	14	3150	1/1	0.83	0.21	94,94,94,94	0
60	MG	13	1646	1/1	0.83	0.20	87,87,87,87	0
60	MG	14	3156	1/1	0.83	0.17	74,74,74,74	0
60	MG	13	1617	1/1	0.83	0.39	82,82,82,82	0
60	MG	14	3598	1/1	0.83	0.17	129,129,129,129	0
60	MG	14	3305	1/1	0.83	0.09	97,97,97,97	0
60	MG	1H	3255	1/1	0.83	0.12	97,97,97,97	0
60	MG	13	1680	1/1	0.83	0.30	89,89,89,89	0
60	MG	14	3180	1/1	0.83	0.08	97,97,97,97	0
60	MG	1G	1638	1/1	0.83	0.16	92,92,92,92	0
60	MG	14	3134	1/1	0.83	0.25	93,93,93,93	0
60	MG	55	201	1/1	0.83	0.10	74,74,74,74	0
60	MG	1H	3309	1/1	0.83	0.15	117,117,117,117	0
60	MG	14	3167	1/1	0.84	0.08	84,84,84,84	0
60	MG	14	3304	1/1	0.84	0.16	94,94,94,94	0
60	MG	14	3169	1/1	0.84	0.26	87,87,87,87	0
60	MG	14	3235	1/1	0.84	0.30	101,101,101,101	0
60	MG	14	3172	1/1	0.84	0.20	89,89,89,89	0
60	MG	13	1636	1/1	0.84	0.35	99,99,99,99	0
60	MG	1H	3278	1/1	0.84	0.20	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3204	1/1	0.84	0.16	93,93,93,93	0
60	MG	1G	1624	1/1	0.84	0.15	97,97,97,97	0
60	MG	14	3330	1/1	0.84	0.09	105,105,105,105	0
60	MG	13	1653	1/1	0.84	0.14	99,99,99,99	0
60	MG	1H	3186	1/1	0.84	0.23	92,92,92,92	0
60	MG	14	3247	1/1	0.84	0.21	95,95,95,95	0
60	MG	14	3186	1/1	0.84	0.19	87,87,87,87	0
60	MG	13	1678	1/1	0.84	0.10	86,86,86,86	0
60	MG	13	1638	1/1	0.84	0.16	86,86,86,86	0
60	MG	13	1647	1/1	0.84	0.17	97,97,97,97	0
60	MG	1G	1669	1/1	0.84	0.35	90,90,90,90	0
60	MG	13	1705	1/1	0.84	0.14	89,89,89,89	0
60	MG	14	3538	1/1	0.84	0.18	101,101,101,101	0
60	MG	14	3145	1/1	0.84	0.20	92,92,92,92	0
60	MG	13	1656	1/1	0.84	0.18	110,110,110,110	0
60	MG	1H	3316	1/1	0.84	0.37	95,95,95,95	0
60	MG	1J	202	1/1	0.84	0.20	102,102,102,102	0
60	MG	1H	3140	1/1	0.84	0.11	74,74,74,74	0
60	MG	1H	3222	1/1	0.84	0.30	83,83,83,83	0
60	MG	13	1641	1/1	0.84	0.26	82,82,82,82	0
60	MG	1H	3321	1/1	0.84	0.18	90,90,90,90	0
60	MG	1G	1606	1/1	0.84	0.23	101,101,101,101	0
60	MG	14	3160	1/1	0.84	0.18	92,92,92,92	0
60	MG	13	1684	1/1	0.84	0.32	90,90,90,90	0
60	MG	1H	3031	1/1	0.84	0.20	73,73,73,73	0
60	MG	14	3170	1/1	0.85	0.21	82,82,82,82	0
60	MG	14	3228	1/1	0.85	0.33	92,92,92,92	0
60	MG	13	1616	1/1	0.85	0.17	116,116,116,116	0
60	MG	14	3125	1/1	0.85	0.49	93,93,93,93	0
60	MG	4L	101	1/1	0.85	0.20	104,104,104,104	0
60	MG	1H	3303	1/1	0.85	0.27	88,88,88,88	0
60	MG	14	3320	1/1	0.85	0.22	83,83,83,83	0
60	MG	1G	1601	1/1	0.85	0.26	98,98,98,98	0
60	MG	1H	3058	1/1	0.85	0.18	78,78,78,78	0
60	MG	14	3010	1/1	0.85	0.33	76,76,76,76	0
60	MG	1H	3313	1/1	0.85	0.11	87,87,87,87	0
60	MG	13	1666	1/1	0.85	0.31	84,84,84,84	0
60	MG	14	3024	1/1	0.85	0.23	62,62,62,62	0
60	MG	14	3335	1/1	0.85	0.15	82,82,82,82	0
60	MG	1G	1615	1/1	0.85	0.15	89,89,89,89	0
60	MG	13	1618	1/1	0.85	0.20	93,93,93,93	0
60	MG	13	1719	1/1	0.85	0.11	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	16	207	1/1	0.85	0.14	95,95,95,95	0
60	MG	14	3252	1/1	0.85	0.22	90,90,90,90	0
60	MG	14	3096	1/1	0.85	0.27	73,73,73,73	0
60	MG	1H	3167	1/1	0.85	0.23	77,77,77,77	0
60	MG	1H	3071	1/1	0.85	0.15	68,68,68,68	0
60	MG	1H	3100	1/1	0.85	0.20	76,76,76,76	0
60	MG	1H	3322	1/1	0.85	0.19	88,88,88,88	0
60	MG	14	3263	1/1	0.85	0.16	69,69,69,69	0
60	MG	11	304	1/1	0.85	0.19	97,97,97,97	0
60	MG	14	3215	1/1	0.85	0.34	95,95,95,95	0
60	MG	14	3117	1/1	0.85	0.18	85,85,85,85	0
60	MG	13	1633	1/1	0.85	0.15	90,90,90,90	0
60	MG	14	3168	1/1	0.85	0.12	102,102,102,102	0
60	MG	14	3293	1/1	0.85	0.15	95,95,95,95	0
60	MG	13	1708	1/1	0.85	0.15	119,119,119,119	0
60	MG	14	3222	1/1	0.85	0.07	90,90,90,90	0
60	MG	14	3223	1/1	0.85	0.11	97,97,97,97	0
60	MG	14	3284	1/1	0.86	0.24	86,86,86,86	0
60	MG	1H	3257	1/1	0.86	0.14	97,97,97,97	0
60	MG	14	3056	1/1	0.86	0.24	75,75,75,75	0
60	MG	14	3138	1/1	0.86	0.10	66,66,66,66	0
60	MG	14	3139	1/1	0.86	0.17	77,77,77,77	0
60	MG	14	3213	1/1	0.86	0.28	90,90,90,90	0
60	MG	16	203	1/1	0.86	0.13	94,94,94,94	0
60	MG	14	3303	1/1	0.86	0.16	97,97,97,97	0
60	MG	16	204	1/1	0.86	0.11	85,85,85,85	0
60	MG	1H	3232	1/1	0.86	0.34	88,88,88,88	0
60	MG	1H	3144	1/1	0.86	0.28	80,80,80,80	0
60	MG	1H	3024	1/1	0.86	0.14	89,89,89,89	0
60	MG	16	210	1/1	0.86	0.10	96,96,96,96	0
60	MG	1H	3211	1/1	0.86	0.15	90,90,90,90	0
60	MG	14	3321	1/1	0.86	0.28	76,76,76,76	0
60	MG	1H	3122	1/1	0.86	0.17	73,73,73,73	0
60	MG	1H	3216	1/1	0.86	0.05	100,100,100,100	0
60	MG	21	301	1/1	0.86	0.15	68,68,68,68	0
60	MG	1G	1745	1/1	0.86	0.23	108,108,108,108	0
60	MG	14	3332	1/1	0.86	0.11	90,90,90,90	0
60	MG	1H	3108	1/1	0.86	0.21	78,78,78,78	0
60	MG	1H	3218	1/1	0.86	0.17	89,89,89,89	0
60	MG	13	1621	1/1	0.86	0.20	63,63,63,63	0
60	MG	98	201	1/1	0.86	0.22	69,69,69,69	0
60	MG	1H	3181	1/1	0.86	0.21	85,85,85,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3195	1/1	0.86	0.18	86,86,86,86	0
60	MG	1G	1656	1/1	0.86	0.17	96,96,96,96	0
60	MG	14	3098	1/1	0.86	0.17	93,93,93,93	0
60	MG	1G	1657	1/1	0.86	0.15	113,113,113,113	0
60	MG	1H	3182	1/1	0.86	0.17	102,102,102,102	0
60	MG	14	3533	1/1	0.86	0.16	99,99,99,99	0
60	MG	13	1814	1/1	0.86	0.08	111,111,111,111	0
60	MG	14	3020	1/1	0.86	0.11	68,68,68,68	0
60	MG	13	1818	1/1	0.86	0.12	116,116,116,116	0
60	MG	1G	1662	1/1	0.86	0.14	118,118,118,118	0
60	MG	1J	201	1/1	0.86	0.10	117,117,117,117	0
60	MG	14	3119	1/1	0.86	0.14	83,83,83,83	0
60	MG	1H	3283	1/1	0.86	0.22	99,99,99,99	0
60	MG	1H	3203	1/1	0.86	0.23	74,74,74,74	0
60	MG	1H	3070	1/1	0.86	0.23	66,66,66,66	0
60	MG	1H	3020	1/1	0.86	0.19	62,62,62,62	0
60	MG	1H	3669	1/1	0.86	0.21	104,104,104,104	0
60	MG	14	3129	1/1	0.86	0.20	82,82,82,82	0
60	MG	1G	1631	1/1	0.86	0.18	104,104,104,104	0
60	MG	14	3052	1/1	0.86	0.14	82,82,82,82	0
60	MG	1G	1636	1/1	0.87	0.17	129,129,129,129	0
60	MG	14	3011	1/1	0.87	0.15	91,91,91,91	0
60	MG	14	3216	1/1	0.87	0.28	82,82,82,82	0
60	MG	14	3092	1/1	0.87	0.25	81,81,81,81	0
60	MG	1H	3145	1/1	0.87	0.20	80,80,80,80	0
60	MG	13	1651	1/1	0.87	0.17	98,98,98,98	0
60	MG	13	1699	1/1	0.87	0.18	96,96,96,96	0
60	MG	1H	3150	1/1	0.87	0.10	70,70,70,70	0
60	MG	1H	3096	1/1	0.87	0.17	84,84,84,84	0
60	MG	13	1604	1/1	0.87	0.18	80,80,80,80	0
60	MG	1G	1679	1/1	0.87	0.07	119,119,119,119	0
60	MG	14	3163	1/1	0.87	0.19	80,80,80,80	0
60	MG	14	3104	1/1	0.87	0.10	66,66,66,66	0
60	MG	14	3105	1/1	0.87	0.23	64,64,64,64	0
60	MG	14	3106	1/1	0.87	0.18	54,54,54,54	0
60	MG	14	3239	1/1	0.87	0.11	89,89,89,89	0
60	MG	1H	3075	1/1	0.87	0.12	59,59,59,59	0
60	MG	1H	3076	1/1	0.87	0.31	70,70,70,70	0
60	MG	14	3110	1/1	0.87	0.10	81,81,81,81	0
60	MG	1G	1686	1/1	0.87	0.10	101,101,101,101	0
60	MG	14	3045	1/1	0.87	0.15	63,63,63,63	0
60	MG	1H	3514	1/1	0.87	0.13	109,109,109,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3053	1/1	0.87	0.21	71,71,71,71	0
60	MG	1H	3102	1/1	0.87	0.10	86,86,86,86	0
60	MG	1H	3047	1/1	0.87	0.11	63,63,63,63	0
60	MG	1H	3138	1/1	0.87	0.10	66,66,66,66	0
60	MG	1H	3013	1/1	0.87	0.12	67,67,67,67	0
60	MG	14	3189	1/1	0.87	0.21	76,76,76,76	0
60	MG	13	1630	1/1	0.87	0.10	108,108,108,108	0
60	MG	1H	3171	1/1	0.87	0.10	67,67,67,67	0
60	MG	14	3131	1/1	0.87	0.11	97,97,97,97	0
60	MG	14	3589	1/1	0.87	0.09	120,120,120,120	0
60	MG	14	3261	1/1	0.87	0.17	96,96,96,96	0
60	MG	1H	3141	1/1	0.87	0.13	92,92,92,92	0
60	MG	14	3198	1/1	0.87	0.10	85,85,85,85	0
60	MG	1H	3312	1/1	0.87	0.19	76,76,76,76	0
60	MG	1G	1622	1/1	0.87	0.12	101,101,101,101	0
60	MG	13	1715	1/1	0.87	0.15	100,100,100,100	0
60	MG	1G	1626	1/1	0.87	0.15	99,99,99,99	0
60	MG	1H	3180	1/1	0.87	0.20	76,76,76,76	0
60	MG	14	3286	1/1	0.87	0.19	79,79,79,79	0
60	MG	1H	3110	1/1	0.87	0.12	92,92,92,92	0
60	MG	13	1613	1/1	0.87	0.15	92,92,92,92	0
60	MG	1H	3327	1/1	0.88	0.19	81,81,81,81	0
60	MG	13	1637	1/1	0.88	0.13	93,93,93,93	0
60	MG	14	3200	1/1	0.88	0.17	117,117,117,117	0
60	MG	1H	3168	1/1	0.88	0.10	72,72,72,72	0
60	MG	1G	1620	1/1	0.88	0.15	105,105,105,105	0
60	MG	14	3115	1/1	0.88	0.15	102,102,102,102	0
60	MG	14	3116	1/1	0.88	0.35	75,75,75,75	0
60	MG	1H	3272	1/1	0.88	0.24	68,68,68,68	0
60	MG	14	3118	1/1	0.88	0.18	81,81,81,81	0
60	MG	1H	3061	1/1	0.88	0.21	72,72,72,72	0
60	MG	1H	3243	1/1	0.88	0.23	81,81,81,81	0
60	MG	14	3078	1/1	0.88	0.10	90,90,90,90	0
60	MG	1G	1625	1/1	0.88	0.25	86,86,86,86	0
60	MG	1G	1682	1/1	0.88	0.13	107,107,107,107	0
60	MG	1H	3640	1/1	0.88	0.09	127,127,127,127	0
60	MG	14	3340	1/1	0.88	0.29	88,88,88,88	0
60	MG	13	1649	1/1	0.88	0.20	84,84,84,84	0
60	MG	14	3178	1/1	0.88	0.29	70,70,70,70	0
60	MG	14	3273	1/1	0.88	0.13	71,71,71,71	0
60	MG	14	3275	1/1	0.88	0.16	89,89,89,89	0
60	MG	1H	3109	1/1	0.88	0.20	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1G	1658	1/1	0.88	0.15	118,118,118,118	0
60	MG	14	3225	1/1	0.88	0.23	92,92,92,92	0
60	MG	14	3550	1/1	0.88	0.12	114,114,114,114	0
60	MG	1H	3202	1/1	0.88	0.06	82,82,82,82	0
60	MG	13	1729	1/1	0.88	0.28	90,90,90,90	0
60	MG	1G	1694	1/1	0.88	0.16	106,106,106,106	0
60	MG	13	1628	1/1	0.88	0.24	86,86,86,86	0
60	MG	1G	1728	1/1	0.88	0.15	120,120,120,120	0
60	MG	1G	1602	1/1	0.88	0.16	82,82,82,82	0
60	MG	1G	1604	1/1	0.88	0.17	90,90,90,90	0
60	MG	29	303	1/1	0.88	0.14	100,100,100,100	0
60	MG	29	305	1/1	0.88	0.13	110,110,110,110	0
60	MG	13	1713	1/1	0.88	0.15	92,92,92,92	0
60	MG	1H	3029	1/1	0.88	0.20	91,91,91,91	0
60	MG	1H	3298	1/1	0.88	0.13	82,82,82,82	0
60	MG	14	3194	1/1	0.88	0.13	89,89,89,89	0
60	MG	14	3313	1/1	0.88	0.23	81,81,81,81	0
60	MG	14	3206	1/1	0.89	0.28	80,80,80,80	0
60	MG	1H	3306	1/1	0.89	0.16	90,90,90,90	0
60	MG	1H	3308	1/1	0.89	0.13	94,94,94,94	0
60	MG	1H	3007	1/1	0.89	0.13	79,79,79,79	0
60	MG	1H	3310	1/1	0.89	0.15	84,84,84,84	0
60	MG	1H	3311	1/1	0.89	0.23	89,89,89,89	0
60	MG	1H	3085	1/1	0.89	0.15	79,79,79,79	0
60	MG	14	3214	1/1	0.89	0.15	84,84,84,84	0
60	MG	11	302	1/1	0.89	0.27	80,80,80,80	0
60	MG	1H	3087	1/1	0.89	0.21	86,86,86,86	0
60	MG	1G	1697	1/1	0.89	0.11	109,109,109,109	0
60	MG	1G	1710	1/1	0.89	0.11	106,106,106,106	0
60	MG	1H	3090	1/1	0.89	0.22	75,75,75,75	0
60	MG	14	3083	1/1	0.89	0.13	68,68,68,68	0
60	MG	1H	3009	1/1	0.89	0.15	86,86,86,86	0
60	MG	1H	3049	1/1	0.89	0.23	79,79,79,79	0
60	MG	14	3224	1/1	0.89	0.28	86,86,86,86	0
60	MG	1H	3166	1/1	0.89	0.08	99,99,99,99	0
60	MG	14	3158	1/1	0.89	0.19	80,80,80,80	0
60	MG	1H	3134	1/1	0.89	0.14	53,53,53,53	0
60	MG	1H	3266	1/1	0.89	0.16	75,75,75,75	0
60	MG	1H	3053	1/1	0.89	0.18	56,56,56,56	0
60	MG	1H	3011	1/1	0.89	0.13	86,86,86,86	0
60	MG	14	3166	1/1	0.89	0.08	92,92,92,92	0
60	MG	13	1731	1/1	0.89	0.42	95,95,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3008	1/1	0.89	0.15	96,96,96,96	0
60	MG	13	1723	1/1	0.89	0.23	80,80,80,80	0
60	MG	1G	1609	1/1	0.89	0.18	99,99,99,99	0
60	MG	1H	3174	1/1	0.89	0.12	75,75,75,75	0
60	MG	1G	1611	1/1	0.89	0.17	111,111,111,111	0
60	MG	1G	1612	1/1	0.89	0.12	131,131,131,131	0
60	MG	13	1635	1/1	0.89	0.15	81,81,81,81	0
60	MG	1H	3023	1/1	0.89	0.18	75,75,75,75	0
60	MG	1G	1665	1/1	0.89	0.14	74,74,74,74	0
60	MG	14	3543	1/1	0.89	0.20	93,93,93,93	0
60	MG	1H	3524	1/1	0.89	0.13	96,96,96,96	0
60	MG	1H	3281	1/1	0.89	0.29	93,93,93,93	0
60	MG	1G	1619	1/1	0.89	0.12	103,103,103,103	0
60	MG	14	3032	1/1	0.89	0.18	63,63,63,63	0
60	MG	1H	3068	1/1	0.89	0.16	73,73,73,73	0
60	MG	13	1755	1/1	0.89	0.20	105,105,105,105	0
60	MG	14	3044	1/1	0.89	0.29	80,80,80,80	0
60	MG	13	1672	1/1	0.89	0.14	83,83,83,83	0
60	MG	14	3193	1/1	0.89	0.13	100,100,100,100	0
60	MG	14	3267	1/1	0.89	0.17	89,89,89,89	0
60	MG	1H	3073	1/1	0.89	0.21	91,91,91,91	0
60	MG	13	1673	1/1	0.89	0.18	78,78,78,78	0
60	MG	13	1691	1/1	0.89	0.21	107,107,107,107	0
60	MG	14	3199	1/1	0.89	0.09	100,100,100,100	0
60	MG	1H	3035	1/1	0.89	0.15	85,85,85,85	0
60	MG	13	1820	1/1	0.89	0.22	101,101,101,101	0
60	MG	16	206	1/1	0.89	0.07	86,86,86,86	0
60	MG	1H	3124	1/1	0.90	0.08	88,88,88,88	0
60	MG	1H	3223	1/1	0.90	0.18	69,69,69,69	0
60	MG	13	1625	1/1	0.90	0.18	77,77,77,77	0
60	MG	13	1682	1/1	0.90	0.20	89,89,89,89	0
60	MG	1H	3228	1/1	0.90	0.21	82,82,82,82	0
60	MG	14	3290	1/1	0.90	0.10	103,103,103,103	0
60	MG	14	3143	1/1	0.90	0.10	78,78,78,78	0
60	MG	13	1690	1/1	0.90	0.17	86,86,86,86	0
60	MG	1H	3010	1/1	0.90	0.16	80,80,80,80	0
60	MG	1H	3036	1/1	0.90	0.12	94,94,94,94	0
60	MG	13	1626	1/1	0.90	0.14	104,104,104,104	0
60	MG	1H	3170	1/1	0.90	0.07	67,67,67,67	0
60	MG	1H	3201	1/1	0.90	0.18	85,85,85,85	0
60	MG	14	3152	1/1	0.90	0.15	104,104,104,104	0
60	MG	13	1601	1/1	0.90	0.17	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	88	203	1/1	0.90	0.12	73,73,73,73	0
60	MG	1H	3082	1/1	0.90	0.15	96,96,96,96	0
60	MG	13	1693	1/1	0.90	0.09	86,86,86,86	0
60	MG	14	3319	1/1	0.90	0.24	78,78,78,78	0
60	MG	1H	3018	1/1	0.90	0.18	56,56,56,56	0
60	MG	1H	3208	1/1	0.90	0.18	80,80,80,80	0
60	MG	14	3322	1/1	0.90	0.12	92,92,92,92	0
60	MG	13	1648	1/1	0.90	0.14	101,101,101,101	0
60	MG	1H	3379	1/1	0.90	0.14	94,94,94,94	0
60	MG	14	3229	1/1	0.90	0.35	91,91,91,91	0
60	MG	14	3230	1/1	0.90	0.21	94,94,94,94	0
60	MG	1G	1607	1/1	0.90	0.07	96,96,96,96	0
60	MG	14	3234	1/1	0.90	0.13	85,85,85,85	0
60	MG	1H	3057	1/1	0.90	0.15	81,81,81,81	0
60	MG	1H	3022	1/1	0.90	0.16	60,60,60,60	0
60	MG	14	3022	1/1	0.90	0.17	103,103,103,103	0
60	MG	1H	3527	1/1	0.90	0.09	111,111,111,111	0
60	MG	1H	3590	1/1	0.90	0.19	88,88,88,88	0
60	MG	14	3177	1/1	0.90	0.24	74,74,74,74	0
60	MG	1H	3595	1/1	0.90	0.14	108,108,108,108	0
60	MG	14	3244	1/1	0.90	0.14	85,85,85,85	0
60	MG	14	3109	1/1	0.90	0.17	77,77,77,77	0
60	MG	13	1639	1/1	0.90	0.08	83,83,83,83	0
60	MG	14	3345	1/1	0.90	0.33	87,87,87,87	0
60	MG	14	3403	1/1	0.90	0.08	115,115,115,115	0
60	MG	1H	3601	1/1	0.90	0.16	95,95,95,95	0
60	MG	1H	3605	1/1	0.90	0.11	112,112,112,112	0
60	MG	1H	3627	1/1	0.90	0.14	105,105,105,105	0
60	MG	13	1661	1/1	0.90	0.11	78,78,78,78	0
60	MG	1H	3093	1/1	0.90	0.18	80,80,80,80	0
60	MG	14	3036	1/1	0.90	0.18	71,71,71,71	0
60	MG	14	3566	1/1	0.90	0.15	117,117,117,117	0
60	MG	14	3255	1/1	0.90	0.25	103,103,103,103	0
60	MG	14	3597	1/1	0.90	0.16	107,107,107,107	0
60	MG	14	3039	1/1	0.90	0.20	70,70,70,70	0
60	MG	1H	3292	1/1	0.90	0.08	96,96,96,96	0
60	MG	1H	3650	1/1	0.90	0.17	99,99,99,99	0
60	MG	1H	3027	1/1	0.90	0.19	66,66,66,66	0
60	MG	14	3126	1/1	0.90	0.30	82,82,82,82	0
60	MG	1H	3252	1/1	0.90	0.20	68,68,68,68	0
60	MG	14	3195	1/1	0.90	0.18	85,85,85,85	0
60	MG	14	3264	1/1	0.90	0.12	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3188	1/1	0.90	0.09	84,84,84,84	0
60	MG	25	202	1/1	0.90	0.18	120,120,120,120	0
60	MG	1H	3028	1/1	0.90	0.12	98,98,98,98	0
60	MG	1H	3307	1/1	0.90	0.16	83,83,83,83	0
60	MG	1G	1688	1/1	0.90	0.27	102,102,102,102	0
60	MG	1H	3162	1/1	0.90	0.24	85,85,85,85	0
60	MG	M5	101	1/1	0.90	0.13	98,98,98,98	0
60	MG	13	1750	1/1	0.91	0.14	101,101,101,101	0
60	MG	14	3037	1/1	0.91	0.31	71,71,71,71	0
60	MG	13	1663	1/1	0.91	0.07	95,95,95,95	0
60	MG	13	1766	1/1	0.91	0.08	113,113,113,113	0
60	MG	1G	1674	1/1	0.91	0.12	95,95,95,95	0
60	MG	1H	3043	1/1	0.91	0.18	88,88,88,88	0
60	MG	1H	3088	1/1	0.91	0.08	71,71,71,71	0
60	MG	1H	3026	1/1	0.91	0.17	74,74,74,74	0
60	MG	1G	1629	1/1	0.91	0.19	97,97,97,97	0
60	MG	1H	3233	1/1	0.91	0.10	84,84,84,84	0
60	MG	1H	3069	1/1	0.91	0.15	65,65,65,65	0
60	MG	14	3310	1/1	0.91	0.14	92,92,92,92	0
60	MG	1G	1633	1/1	0.91	0.09	100,100,100,100	0
60	MG	13	1794	1/1	0.91	0.05	137,137,137,137	0
60	MG	14	3065	1/1	0.91	0.13	72,72,72,72	0
60	MG	1H	3268	1/1	0.91	0.05	81,81,81,81	0
60	MG	13	1730	1/1	0.91	0.24	94,94,94,94	0
60	MG	14	3071	1/1	0.91	0.11	63,63,63,63	0
60	MG	14	3072	1/1	0.91	0.12	93,93,93,93	0
60	MG	14	3153	1/1	0.91	0.30	81,81,81,81	0
60	MG	1H	3179	1/1	0.91	0.07	92,92,92,92	0
60	MG	1H	3052	1/1	0.91	0.30	82,82,82,82	0
60	MG	13	1612	1/1	0.91	0.12	85,85,85,85	0
60	MG	1G	1642	1/1	0.91	0.10	100,100,100,100	0
60	MG	1G	1707	1/1	0.91	0.10	117,117,117,117	0
60	MG	1H	3324	1/1	0.91	0.09	109,109,109,109	0
60	MG	14	3237	1/1	0.91	0.17	96,96,96,96	0
60	MG	1G	1717	1/1	0.91	0.08	100,100,100,100	0
60	MG	1G	1719	1/1	0.91	0.07	118,118,118,118	0
60	MG	1H	3241	1/1	0.91	0.29	87,87,87,87	0
60	MG	1G	1738	1/1	0.91	0.08	99,99,99,99	0
60	MG	14	3087	1/1	0.91	0.15	79,79,79,79	0
60	MG	14	3342	1/1	0.91	0.11	106,106,106,106	0
60	MG	11	305	1/1	0.91	0.17	48,48,48,48	0
60	MG	1H	3056	1/1	0.91	0.12	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1G	1751	1/1	0.91	0.05	164,164,164,164	0
60	MG	3I	301	1/1	0.91	0.09	81,81,81,81	0
60	MG	14	3415	1/1	0.91	0.09	81,81,81,81	0
60	MG	14	3521	1/1	0.91	0.07	111,111,111,111	0
60	MG	1H	3097	1/1	0.91	0.16	84,84,84,84	0
60	MG	1H	3184	1/1	0.91	0.13	92,92,92,92	0
60	MG	2L	101	1/1	0.91	0.18	84,84,84,84	0
60	MG	14	3546	1/1	0.91	0.15	83,83,83,83	0
60	MG	1G	1651	1/1	0.91	0.18	89,89,89,89	0
60	MG	1H	3155	1/1	0.91	0.11	87,87,87,87	0
60	MG	14	3005	1/1	0.91	0.14	83,83,83,83	0
60	MG	14	3554	1/1	0.91	0.12	108,108,108,108	0
60	MG	1H	3078	1/1	0.91	0.14	57,57,57,57	0
60	MG	14	3570	1/1	0.91	0.10	108,108,108,108	0
60	MG	1H	3099	1/1	0.91	0.16	79,79,79,79	0
60	MG	1H	3159	1/1	0.91	0.17	77,77,77,77	0
60	MG	1H	3125	1/1	0.91	0.12	91,91,91,91	0
60	MG	14	3606	1/1	0.91	0.20	102,102,102,102	0
60	MG	1H	3591	1/1	0.91	0.06	119,119,119,119	0
60	MG	1H	3594	1/1	0.91	0.08	122,122,122,122	0
60	MG	1H	3129	1/1	0.91	0.22	79,79,79,79	0
60	MG	1H	3131	1/1	0.91	0.15	83,83,83,83	0
60	MG	29	301	1/1	0.91	0.21	55,55,55,55	0
60	MG	1H	3302	1/1	0.91	0.20	88,88,88,88	0
60	MG	1H	3604	1/1	0.91	0.10	115,115,115,115	0
60	MG	13	1727	1/1	0.91	0.16	90,90,90,90	0
60	MG	1H	3618	1/1	0.91	0.12	110,110,110,110	0
60	MG	1H	3304	1/1	0.91	0.08	79,79,79,79	0
60	MG	13	1608	1/1	0.91	0.13	78,78,78,78	0
60	MG	1H	3637	1/1	0.91	0.10	112,112,112,112	0
60	MG	1H	3225	1/1	0.91	0.09	89,89,89,89	0
60	MG	14	3204	1/1	0.91	0.12	76,76,76,76	0
60	MG	75	201	1/1	0.91	0.14	91,91,91,91	0
60	MG	1H	3644	1/1	0.91	0.17	106,106,106,106	0
60	MG	1H	3544	1/1	0.92	0.08	108,108,108,108	0
60	MG	1G	1698	1/1	0.92	0.12	101,101,101,101	0
60	MG	1H	3577	1/1	0.92	0.06	123,123,123,123	0
60	MG	1H	3133	1/1	0.92	0.14	71,71,71,71	0
60	MG	1H	3175	1/1	0.92	0.08	82,82,82,82	0
60	MG	13	1640	1/1	0.92	0.11	84,84,84,84	0
60	MG	1H	3177	1/1	0.92	0.37	82,82,82,82	0
60	MG	14	3312	1/1	0.92	0.11	99,99,99,99	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3008	1/1	0.92	0.16	72,72,72,72	0
60	MG	1H	3598	1/1	0.92	0.07	123,123,123,123	0
60	MG	14	3318	1/1	0.92	0.10	102,102,102,102	0
60	MG	1H	3080	1/1	0.92	0.13	80,80,80,80	0
60	MG	13	1805	1/1	0.92	0.07	171,171,171,171	0
60	MG	1H	3161	1/1	0.92	0.20	71,71,71,71	0
60	MG	1G	1766	1/1	0.92	0.12	107,107,107,107	0
60	MG	1H	3609	1/1	0.92	0.20	80,80,80,80	0
60	MG	14	3082	1/1	0.92	0.10	67,67,67,67	0
60	MG	1H	3314	1/1	0.92	0.12	91,91,91,91	0
60	MG	14	3329	1/1	0.92	0.11	103,103,103,103	0
60	MG	1H	3621	1/1	0.92	0.07	100,100,100,100	0
60	MG	13	1603	1/1	0.92	0.11	79,79,79,79	0
60	MG	14	3233	1/1	0.92	0.12	103,103,103,103	0
60	MG	1G	1608	1/1	0.92	0.13	106,106,106,106	0
60	MG	14	3090	1/1	0.92	0.12	64,64,64,64	0
60	MG	14	3164	1/1	0.92	0.09	78,78,78,78	0
60	MG	1K	101	1/1	0.92	0.11	91,91,91,91	0
60	MG	1H	3115	1/1	0.92	0.12	59,59,59,59	0
60	MG	1H	3639	1/1	0.92	0.08	105,105,105,105	0
60	MG	13	1615	1/1	0.92	0.15	75,75,75,75	0
60	MG	1H	3319	1/1	0.92	0.12	93,93,93,93	0
60	MG	1G	1664	1/1	0.92	0.09	101,101,101,101	0
60	MG	14	3171	1/1	0.92	0.13	91,91,91,91	0
60	MG	13	1624	1/1	0.92	0.14	103,103,103,103	0
60	MG	14	3017	1/1	0.92	0.14	73,73,73,73	0
60	MG	1H	3649	1/1	0.92	0.20	92,92,92,92	0
60	MG	13	1607	1/1	0.92	0.08	83,83,83,83	0
60	MG	14	3417	1/1	0.92	0.06	143,143,143,143	0
60	MG	14	3422	1/1	0.92	0.10	93,93,93,93	0
60	MG	14	3493	1/1	0.92	0.10	98,98,98,98	0
60	MG	14	3502	1/1	0.92	0.07	103,103,103,103	0
60	MG	1H	3287	1/1	0.92	0.15	81,81,81,81	0
60	MG	1H	3658	1/1	0.92	0.14	107,107,107,107	0
60	MG	1H	3212	1/1	0.92	0.31	78,78,78,78	0
60	MG	16	201	1/1	0.92	0.13	89,89,89,89	0
60	MG	14	3545	1/1	0.92	0.18	96,96,96,96	0
60	MG	13	1775	1/1	0.92	0.07	119,119,119,119	0
60	MG	14	3111	1/1	0.92	0.17	84,84,84,84	0
60	MG	1H	3325	1/1	0.92	0.23	87,87,87,87	0
60	MG	14	3258	1/1	0.92	0.17	76,76,76,76	0
60	MG	1H	3293	1/1	0.92	0.11	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1G	1628	1/1	0.92	0.13	90,90,90,90	0
60	MG	2K	107	1/1	0.92	0.09	106,106,106,106	0
60	MG	14	3577	1/1	0.92	0.13	111,111,111,111	0
60	MG	14	3578	1/1	0.92	0.12	105,105,105,105	0
60	MG	14	3585	1/1	0.92	0.11	114,114,114,114	0
60	MG	1G	1630	1/1	0.92	0.06	100,100,100,100	0
60	MG	1H	3059	1/1	0.92	0.28	77,77,77,77	0
60	MG	14	3120	1/1	0.92	0.23	70,70,70,70	0
60	MG	1H	3299	1/1	0.92	0.12	83,83,83,83	0
60	MG	14	3040	1/1	0.92	0.11	68,68,68,68	0
60	MG	14	3041	1/1	0.92	0.16	64,64,64,64	0
60	MG	1H	3300	1/1	0.92	0.13	86,86,86,86	0
60	MG	1H	3437	1/1	0.92	0.06	128,128,128,128	0
60	MG	1J	208	1/1	0.92	0.05	121,121,121,121	0
60	MG	14	3049	1/1	0.92	0.12	89,89,89,89	0
60	MG	1H	3130	1/1	0.92	0.13	87,87,87,87	0
60	MG	1H	3077	1/1	0.92	0.10	51,51,51,51	0
60	MG	14	3205	1/1	0.92	0.24	85,85,85,85	0
60	MG	16	216	1/1	0.92	0.06	113,113,113,113	0
60	MG	14	3207	1/1	0.92	0.14	92,92,92,92	0
60	MG	1G	1639	1/1	0.92	0.05	142,142,142,142	0
60	MG	16	220	1/1	0.92	0.14	111,111,111,111	0
60	MG	1H	3265	1/1	0.92	0.10	63,63,63,63	0
60	MG	14	3297	1/1	0.92	0.08	86,86,86,86	0
60	MG	14	3135	1/1	0.92	0.12	81,81,81,81	0
60	MG	C5	201	1/1	0.92	0.19	92,92,92,92	0
60	MG	14	3299	1/1	0.92	0.09	94,94,94,94	0
60	MG	1H	3041	1/1	0.93	0.12	53,53,53,53	0
60	MG	14	3046	1/1	0.93	0.17	80,80,80,80	0
60	MG	14	3306	1/1	0.93	0.19	89,89,89,89	0
60	MG	1H	3146	1/1	0.93	0.21	67,67,67,67	0
60	MG	1H	3123	1/1	0.93	0.14	77,77,77,77	0
60	MG	13	1816	1/1	0.93	0.09	126,126,126,126	0
60	MG	1H	3198	1/1	0.93	0.13	92,92,92,92	0
60	MG	1H	3149	1/1	0.93	0.18	92,92,92,92	0
60	MG	14	3136	1/1	0.93	0.14	75,75,75,75	0
60	MG	13	1817	1/1	0.93	0.09	121,121,121,121	0
60	MG	1H	3634	1/1	0.93	0.09	109,109,109,109	0
60	MG	1G	1724	1/1	0.93	0.05	143,143,143,143	0
60	MG	14	3062	1/1	0.93	0.17	70,70,70,70	0
60	MG	1G	1727	1/1	0.93	0.08	125,125,125,125	0
60	MG	1H	3151	1/1	0.93	0.24	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3325	1/1	0.93	0.07	97,97,97,97	0
60	MG	14	3067	1/1	0.93	0.16	59,59,59,59	0
60	MG	1G	1730	1/1	0.93	0.08	109,109,109,109	0
60	MG	14	3328	1/1	0.93	0.07	105,105,105,105	0
60	MG	1G	1737	1/1	0.93	0.06	112,112,112,112	0
60	MG	13	1712	1/1	0.93	0.09	113,113,113,113	0
60	MG	14	3331	1/1	0.93	0.06	94,94,94,94	0
60	MG	14	3227	1/1	0.93	0.13	86,86,86,86	0
60	MG	13	1787	1/1	0.93	0.08	99,99,99,99	0
60	MG	1H	3205	1/1	0.93	0.17	78,78,78,78	0
60	MG	1H	3641	1/1	0.93	0.08	111,111,111,111	0
60	MG	1G	1753	1/1	0.93	0.05	127,127,127,127	0
60	MG	1H	3301	1/1	0.93	0.10	99,99,99,99	0
60	MG	1G	1761	1/1	0.93	0.05	143,143,143,143	0
60	MG	1G	1762	1/1	0.93	0.07	123,123,123,123	0
60	MG	13	1706	1/1	0.93	0.12	87,87,87,87	0
60	MG	1H	3207	1/1	0.93	0.07	62,62,62,62	0
60	MG	1H	3132	1/1	0.93	0.08	79,79,79,79	0
60	MG	1H	3485	1/1	0.93	0.19	89,89,89,89	0
60	MG	2L	102	1/1	0.93	0.06	127,127,127,127	0
60	MG	1G	1616	1/1	0.93	0.17	87,87,87,87	0
60	MG	14	3088	1/1	0.93	0.23	60,60,60,60	0
60	MG	14	3408	1/1	0.93	0.08	107,107,107,107	0
60	MG	14	3411	1/1	0.93	0.07	81,81,81,81	0
60	MG	1H	3495	1/1	0.93	0.07	94,94,94,94	0
60	MG	1H	3667	1/1	0.93	0.12	98,98,98,98	0
60	MG	1H	3504	1/1	0.93	0.07	109,109,109,109	0
60	MG	14	3479	1/1	0.93	0.10	113,113,113,113	0
60	MG	1H	3017	1/1	0.93	0.11	53,53,53,53	0
60	MG	14	3495	1/1	0.93	0.11	110,110,110,110	0
60	MG	1H	3516	1/1	0.93	0.06	126,126,126,126	0
60	MG	14	3515	1/1	0.93	0.12	100,100,100,100	0
60	MG	14	3174	1/1	0.93	0.30	84,84,84,84	0
60	MG	14	3175	1/1	0.93	0.11	78,78,78,78	0
60	MG	14	3176	1/1	0.93	0.16	78,78,78,78	0
60	MG	14	3541	1/1	0.93	0.09	113,113,113,113	0
60	MG	1H	3517	1/1	0.93	0.07	61,61,61,61	0
60	MG	14	3253	1/1	0.93	0.14	86,86,86,86	0
60	MG	14	3097	1/1	0.93	0.11	69,69,69,69	0
60	MG	14	3179	1/1	0.93	0.12	92,92,92,92	0
60	MG	1G	1623	1/1	0.93	0.25	86,86,86,86	0
60	MG	1H	3055	1/1	0.93	0.16	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3552	1/1	0.93	0.07	132,132,132,132	0
60	MG	14	3013	1/1	0.93	0.14	64,64,64,64	0
60	MG	14	3555	1/1	0.93	0.06	120,120,120,120	0
60	MG	14	3016	1/1	0.93	0.10	67,67,67,67	0
60	MG	1H	3032	1/1	0.93	0.11	67,67,67,67	0
60	MG	14	3572	1/1	0.93	0.10	119,119,119,119	0
60	MG	14	3018	1/1	0.93	0.14	77,77,77,77	0
60	MG	1H	3532	1/1	0.93	0.08	117,117,117,117	0
60	MG	14	3187	1/1	0.93	0.10	93,93,93,93	0
60	MG	1H	3537	1/1	0.93	0.08	93,93,93,93	0
60	MG	14	3593	1/1	0.93	0.19	100,100,100,100	0
60	MG	14	3594	1/1	0.93	0.10	106,106,106,106	0
60	MG	13	1710	1/1	0.93	0.07	94,94,94,94	0
60	MG	1H	3568	1/1	0.93	0.18	66,66,66,66	0
60	MG	14	3599	1/1	0.93	0.11	96,96,96,96	0
60	MG	1G	1676	1/1	0.93	0.06	91,91,91,91	0
60	MG	1H	3573	1/1	0.93	0.12	122,122,122,122	0
60	MG	1H	3004	1/1	0.93	0.13	71,71,71,71	0
60	MG	14	3276	1/1	0.93	0.17	77,77,77,77	0
60	MG	1H	3582	1/1	0.93	0.09	99,99,99,99	0
60	MG	14	3031	1/1	0.93	0.07	89,89,89,89	0
60	MG	14	3196	1/1	0.93	0.16	108,108,108,108	0
60	MG	13	1757	1/1	0.93	0.06	120,120,120,120	0
60	MG	1G	1683	1/1	0.93	0.12	101,101,101,101	0
60	MG	1G	1635	1/1	0.93	0.17	81,81,81,81	0
60	MG	11	301	1/1	0.93	0.21	62,62,62,62	0
60	MG	13	1742	1/1	0.93	0.15	103,103,103,103	0
60	MG	14	3296	1/1	0.93	0.08	93,93,93,93	0
60	MG	1H	3118	1/1	0.93	0.08	73,73,73,73	0
60	MG	1H	3119	1/1	0.93	0.06	56,56,56,56	0
60	MG	1H	3039	1/1	0.93	0.11	66,66,66,66	0
60	MG	14	3301	1/1	0.93	0.07	85,85,85,85	0
60	MG	14	3127	1/1	0.93	0.10	76,76,76,76	0
60	MG	1H	3063	1/1	0.93	0.09	51,51,51,51	0
60	MG	1H	3295	1/1	0.94	0.06	85,85,85,85	0
60	MG	14	3324	1/1	0.94	0.17	85,85,85,85	0
60	MG	1H	3030	1/1	0.94	0.14	74,74,74,74	0
60	MG	1H	3617	1/1	0.94	0.16	91,91,91,91	0
60	MG	1H	3116	1/1	0.94	0.20	74,74,74,74	0
60	MG	14	3085	1/1	0.94	0.18	90,90,90,90	0
60	MG	1H	3016	1/1	0.94	0.16	70,70,70,70	0
60	MG	1H	3378	1/1	0.94	0.06	95,95,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3074	1/1	0.94	0.08	77,77,77,77	0
60	MG	1H	3404	1/1	0.94	0.07	63,63,63,63	0
60	MG	1H	3417	1/1	0.94	0.09	95,95,95,95	0
60	MG	1H	3422	1/1	0.94	0.11	96,96,96,96	0
60	MG	1H	3200	1/1	0.94	0.06	69,69,69,69	0
60	MG	14	3173	1/1	0.94	0.13	65,65,65,65	0
60	MG	1H	3439	1/1	0.94	0.10	96,96,96,96	0
60	MG	14	3014	1/1	0.94	0.17	73,73,73,73	0
60	MG	1H	3462	1/1	0.94	0.09	74,74,74,74	0
60	MG	1H	3645	1/1	0.94	0.15	94,94,94,94	0
60	MG	1H	3468	1/1	0.94	0.16	73,73,73,73	0
60	MG	14	3101	1/1	0.94	0.06	112,112,112,112	0
60	MG	1H	3469	1/1	0.94	0.11	85,85,85,85	0
60	MG	1H	3473	1/1	0.94	0.10	95,95,95,95	0
60	MG	1H	3653	1/1	0.94	0.05	122,122,122,122	0
60	MG	14	3379	1/1	0.94	0.07	72,72,72,72	0
60	MG	14	3254	1/1	0.94	0.05	110,110,110,110	0
60	MG	14	3404	1/1	0.94	0.05	111,111,111,111	0
60	MG	1H	3482	1/1	0.94	0.07	90,90,90,90	0
60	MG	14	3026	1/1	0.94	0.17	52,52,52,52	0
60	MG	14	3413	1/1	0.94	0.08	68,68,68,68	0
60	MG	6I	101	1/1	0.94	0.07	110,110,110,110	0
60	MG	1H	3660	1/1	0.94	0.06	124,124,124,124	0
60	MG	1H	3005	1/1	0.94	0.18	64,64,64,64	0
60	MG	1H	3668	1/1	0.94	0.14	97,97,97,97	0
60	MG	1H	3500	1/1	0.94	0.07	100,100,100,100	0
60	MG	13	1695	1/1	0.94	0.11	88,88,88,88	0
60	MG	1H	3506	1/1	0.94	0.07	119,119,119,119	0
60	MG	14	3509	1/1	0.94	0.20	90,90,90,90	0
60	MG	14	3513	1/1	0.94	0.08	111,111,111,111	0
60	MG	1G	1691	1/1	0.94	0.10	101,101,101,101	0
60	MG	13	1807	1/1	0.94	0.05	110,110,110,110	0
60	MG	1H	3178	1/1	0.94	0.12	122,122,122,122	0
60	MG	13	1810	1/1	0.94	0.05	114,114,114,114	0
60	MG	1H	3038	1/1	0.94	0.34	84,84,84,84	0
60	MG	14	3272	1/1	0.94	0.16	79,79,79,79	0
60	MG	1H	3126	1/1	0.94	0.24	80,80,80,80	0
60	MG	14	3274	1/1	0.94	0.09	70,70,70,70	0
60	MG	1H	3127	1/1	0.94	0.09	57,57,57,57	0
60	MG	1H	3533	1/1	0.94	0.06	117,117,117,117	0
60	MG	14	3277	1/1	0.94	0.09	84,84,84,84	0
60	MG	1G	1709	1/1	0.94	0.06	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3081	1/1	0.94	0.14	78,78,78,78	0
60	MG	14	3202	1/1	0.94	0.04	90,90,90,90	0
60	MG	14	3565	1/1	0.94	0.08	125,125,125,125	0
60	MG	14	3287	1/1	0.94	0.18	83,83,83,83	0
60	MG	14	3567	1/1	0.94	0.07	104,104,104,104	0
60	MG	14	3569	1/1	0.94	0.21	97,97,97,97	0
60	MG	14	3051	1/1	0.94	0.12	55,55,55,55	0
60	MG	1H	3157	1/1	0.94	0.13	68,68,68,68	0
60	MG	1H	3552	1/1	0.94	0.12	98,98,98,98	0
60	MG	13	1631	1/1	0.94	0.12	77,77,77,77	0
60	MG	1H	3571	1/1	0.94	0.07	106,106,106,106	0
60	MG	14	3057	1/1	0.94	0.12	69,69,69,69	0
60	MG	14	3591	1/1	0.94	0.05	120,120,120,120	0
60	MG	1H	3104	1/1	0.94	0.28	75,75,75,75	0
60	MG	14	3059	1/1	0.94	0.09	79,79,79,79	0
60	MG	11	303	1/1	0.94	0.22	89,89,89,89	0
60	MG	14	3300	1/1	0.94	0.09	98,98,98,98	0
60	MG	1G	1731	1/1	0.94	0.24	93,93,93,93	0
60	MG	1H	3025	1/1	0.94	0.06	68,68,68,68	0
60	MG	1H	3579	1/1	0.94	0.09	112,112,112,112	0
60	MG	1G	1741	1/1	0.94	0.15	106,106,106,106	0
60	MG	14	3066	1/1	0.94	0.11	73,73,73,73	0
60	MG	1H	3064	1/1	0.94	0.11	64,64,64,64	0
60	MG	14	3307	1/1	0.94	0.10	90,90,90,90	0
60	MG	1H	3587	1/1	0.94	0.06	79,79,79,79	0
60	MG	13	1802	1/1	0.94	0.17	103,103,103,103	0
60	MG	14	3070	1/1	0.94	0.11	57,57,57,57	0
60	MG	1H	3086	1/1	0.94	0.17	79,79,79,79	0
60	MG	1H	3046	1/1	0.94	0.07	59,59,59,59	0
60	MG	1H	3067	1/1	0.94	0.11	75,75,75,75	0
60	MG	14	3316	1/1	0.94	0.12	150,150,150,150	0
60	MG	14	3317	1/1	0.94	0.09	102,102,102,102	0
60	MG	1H	3012	1/1	0.94	0.12	90,90,90,90	0
60	MG	1H	3291	1/1	0.94	0.04	88,88,88,88	0
60	MG	13	1609	1/1	0.94	0.15	73,73,73,73	0
60	MG	2A	201	1/1	0.94	0.09	95,95,95,95	0
60	MG	1H	3002	1/1	0.94	0.17	49,49,49,49	0
60	MG	13	1611	1/1	0.95	0.04	96,96,96,96	0
60	MG	13	1823	1/1	0.95	0.05	124,124,124,124	0
60	MG	1H	3666	1/1	0.95	0.14	108,108,108,108	0
60	MG	1H	3294	1/1	0.95	0.14	73,73,73,73	0
60	MG	13	1797	1/1	0.95	0.06	113,113,113,113	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3128	1/1	0.95	0.05	75,75,75,75	0
60	MG	13	1799	1/1	0.95	0.06	104,104,104,104	0
60	MG	14	3149	1/1	0.95	0.06	91,91,91,91	0
60	MG	1G	1729	1/1	0.95	0.08	112,112,112,112	0
60	MG	1H	3538	1/1	0.95	0.07	101,101,101,101	0
60	MG	1H	3539	1/1	0.95	0.12	97,97,97,97	0
60	MG	1G	1735	1/1	0.95	0.09	113,113,113,113	0
60	MG	1G	1736	1/1	0.95	0.05	136,136,136,136	0
60	MG	1H	3214	1/1	0.95	0.10	63,63,63,63	0
60	MG	16	205	1/1	0.95	0.12	81,81,81,81	0
60	MG	14	3159	1/1	0.95	0.13	84,84,84,84	0
60	MG	1H	3215	1/1	0.95	0.05	71,71,71,71	0
60	MG	1H	3558	1/1	0.95	0.05	110,110,110,110	0
60	MG	14	3162	1/1	0.95	0.29	79,79,79,79	0
60	MG	1H	3561	1/1	0.95	0.14	88,88,88,88	0
60	MG	14	3075	1/1	0.95	0.13	65,65,65,65	0
60	MG	1H	3333	1/1	0.95	0.12	60,60,60,60	0
60	MG	1H	3342	1/1	0.95	0.09	54,54,54,54	0
60	MG	14	3346	1/1	0.95	0.26	81,81,81,81	0
60	MG	14	3370	1/1	0.95	0.07	107,107,107,107	0
60	MG	1H	3572	1/1	0.95	0.09	95,95,95,95	0
60	MG	14	3381	1/1	0.95	0.06	118,118,118,118	0
60	MG	1G	1757	1/1	0.95	0.05	134,134,134,134	0
60	MG	1H	3349	1/1	0.95	0.11	62,62,62,62	0
60	MG	16	215	1/1	0.95	0.06	101,101,101,101	0
60	MG	1H	3050	1/1	0.95	0.19	63,63,63,63	0
60	MG	14	3412	1/1	0.95	0.08	59,59,59,59	0
60	MG	16	219	1/1	0.95	0.14	104,104,104,104	0
60	MG	1H	3355	1/1	0.95	0.06	91,91,91,91	0
60	MG	14	3416	1/1	0.95	0.12	61,61,61,61	0
60	MG	1H	3580	1/1	0.95	0.08	105,105,105,105	0
60	MG	1H	3366	1/1	0.95	0.07	99,99,99,99	0
60	MG	14	3444	1/1	0.95	0.11	72,72,72,72	0
60	MG	14	3445	1/1	0.95	0.05	98,98,98,98	0
60	MG	14	3446	1/1	0.95	0.06	95,95,95,95	0
60	MG	14	3456	1/1	0.95	0.06	87,87,87,87	0
60	MG	14	3473	1/1	0.95	0.06	97,97,97,97	0
60	MG	1H	3369	1/1	0.95	0.06	88,88,88,88	0
60	MG	14	3487	1/1	0.95	0.06	123,123,123,123	0
60	MG	13	1744	1/1	0.95	0.05	116,116,116,116	0
60	MG	14	3091	1/1	0.95	0.11	84,84,84,84	0
60	MG	14	3499	1/1	0.95	0.07	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3152	1/1	0.95	0.07	83,83,83,83	0
60	MG	1H	3592	1/1	0.95	0.18	84,84,84,84	0
60	MG	14	3266	1/1	0.95	0.14	102,102,102,102	0
60	MG	1H	3388	1/1	0.95	0.06	104,104,104,104	0
60	MG	1H	3402	1/1	0.95	0.08	77,77,77,77	0
60	MG	14	3526	1/1	0.95	0.05	97,97,97,97	0
60	MG	14	3528	1/1	0.95	0.25	85,85,85,85	0
60	MG	14	3529	1/1	0.95	0.07	97,97,97,97	0
60	MG	41	201	1/1	0.95	0.11	86,86,86,86	0
60	MG	1H	3153	1/1	0.95	0.30	81,81,81,81	0
60	MG	14	3271	1/1	0.95	0.07	79,79,79,79	0
60	MG	1H	3305	1/1	0.95	0.07	85,85,85,85	0
60	MG	1H	3271	1/1	0.95	0.04	74,74,74,74	0
60	MG	13	1694	1/1	0.95	0.10	79,79,79,79	0
60	MG	13	1771	1/1	0.95	0.11	110,110,110,110	0
60	MG	P8	101	1/1	0.95	0.18	75,75,75,75	0
60	MG	Q8	401	1/1	0.95	0.17	87,87,87,87	0
60	MG	14	3278	1/1	0.95	0.13	85,85,85,85	0
60	MG	1H	3440	1/1	0.95	0.06	97,97,97,97	0
60	MG	14	3280	1/1	0.95	0.10	74,74,74,74	0
60	MG	14	3563	1/1	0.95	0.07	112,112,112,112	0
60	MG	14	3282	1/1	0.95	0.13	87,87,87,87	0
60	MG	14	3283	1/1	0.95	0.13	75,75,75,75	0
60	MG	14	3019	1/1	0.95	0.13	83,83,83,83	0
60	MG	1H	3611	1/1	0.95	0.06	120,120,120,120	0
60	MG	1H	3612	1/1	0.95	0.07	124,124,124,124	0
60	MG	1H	3616	1/1	0.95	0.10	97,97,97,97	0
60	MG	14	3573	1/1	0.95	0.13	93,93,93,93	0
60	MG	14	3576	1/1	0.95	0.16	101,101,101,101	0
60	MG	1H	3443	1/1	0.95	0.09	117,117,117,117	0
60	MG	1H	3276	1/1	0.95	0.11	64,64,64,64	0
60	MG	14	3580	1/1	0.95	0.07	103,103,103,103	0
60	MG	14	3113	1/1	0.95	0.06	64,64,64,64	0
60	MG	14	3114	1/1	0.95	0.10	85,85,85,85	0
60	MG	13	1741	1/1	0.95	0.06	104,104,104,104	0
60	MG	13	1808	1/1	0.95	0.11	104,104,104,104	0
60	MG	1H	3631	1/1	0.95	0.10	113,113,113,113	0
60	MG	1H	3471	1/1	0.95	0.13	73,73,73,73	0
60	MG	2K	101	1/1	0.95	0.11	89,89,89,89	0
60	MG	1H	3476	1/1	0.95	0.07	61,61,61,61	0
60	MG	14	3603	1/1	0.95	0.06	116,116,116,116	0
60	MG	1G	1685	1/1	0.95	0.08	121,121,121,121	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3015	1/1	0.95	0.18	56,56,56,56	0
60	MG	14	3123	1/1	0.95	0.08	92,92,92,92	0
60	MG	13	1779	1/1	0.95	0.04	105,105,105,105	0
60	MG	13	1782	1/1	0.95	0.16	101,101,101,101	0
60	MG	1H	3642	1/1	0.95	0.15	99,99,99,99	0
60	MG	1H	3499	1/1	0.95	0.14	82,82,82,82	0
60	MG	13	1751	1/1	0.95	0.07	88,88,88,88	0
60	MG	14	3042	1/1	0.95	0.12	84,84,84,84	0
60	MG	1H	3503	1/1	0.95	0.06	91,91,91,91	0
60	MG	39	301	1/1	0.95	0.10	103,103,103,103	0
60	MG	13	1789	1/1	0.95	0.06	109,109,109,109	0
60	MG	1H	3289	1/1	0.95	0.14	102,102,102,102	0
60	MG	14	3048	1/1	0.95	0.10	79,79,79,79	0
60	MG	1G	1695	1/1	0.95	0.15	108,108,108,108	0
60	MG	1H	3651	1/1	0.95	0.06	107,107,107,107	0
60	MG	13	1793	1/1	0.95	0.14	118,118,118,118	0
60	MG	1H	3003	1/1	0.95	0.12	68,68,68,68	0
60	MG	1H	3656	1/1	0.95	0.16	79,79,79,79	0
60	MG	1G	1708	1/1	0.95	0.05	121,121,121,121	0
60	MG	13	1804	1/1	0.96	0.04	114,114,114,114	0
60	MG	14	3141	1/1	0.96	0.08	72,72,72,72	0
60	MG	1H	3409	1/1	0.96	0.06	93,93,93,93	0
60	MG	1H	3647	1/1	0.96	0.13	96,96,96,96	0
60	MG	1H	3412	1/1	0.96	0.07	61,61,61,61	0
60	MG	14	3050	1/1	0.96	0.10	68,68,68,68	0
60	MG	1H	3006	1/1	0.96	0.08	59,59,59,59	0
60	MG	1G	1702	1/1	0.96	0.04	123,123,123,123	0
60	MG	1H	3542	1/1	0.96	0.04	127,127,127,127	0
60	MG	13	1602	1/1	0.96	0.17	68,68,68,68	0
60	MG	1G	1627	1/1	0.96	0.11	117,117,117,117	0
60	MG	14	3353	1/1	0.96	0.06	83,83,83,83	0
60	MG	14	3363	1/1	0.96	0.07	79,79,79,79	0
60	MG	1H	3545	1/1	0.96	0.08	84,84,84,84	0
60	MG	1G	1716	1/1	0.96	0.07	98,98,98,98	0
60	MG	14	3154	1/1	0.96	0.09	77,77,77,77	0
60	MG	14	3385	1/1	0.96	0.08	101,101,101,101	0
60	MG	14	3398	1/1	0.96	0.12	90,90,90,90	0
60	MG	1H	3424	1/1	0.96	0.04	110,110,110,110	0
60	MG	1H	3555	1/1	0.96	0.15	93,93,93,93	0
60	MG	1G	1720	1/1	0.96	0.06	127,127,127,127	0
60	MG	1H	3427	1/1	0.96	0.05	104,104,104,104	0
60	MG	1G	1726	1/1	0.96	0.06	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3064	1/1	0.96	0.12	65,65,65,65	0
60	MG	1H	3662	1/1	0.96	0.17	93,93,93,93	0
60	MG	1H	3664	1/1	0.96	0.14	97,97,97,97	0
60	MG	1H	3042	1/1	0.96	0.10	78,78,78,78	0
60	MG	14	3419	1/1	0.96	0.04	126,126,126,126	0
60	MG	1H	3567	1/1	0.96	0.10	70,70,70,70	0
60	MG	14	3425	1/1	0.96	0.12	100,100,100,100	0
60	MG	14	3441	1/1	0.96	0.06	92,92,92,92	0
60	MG	13	1709	1/1	0.96	0.06	89,89,89,89	0
60	MG	1G	1732	1/1	0.96	0.05	100,100,100,100	0
60	MG	13	1788	1/1	0.96	0.10	92,92,92,92	0
60	MG	14	3448	1/1	0.96	0.09	77,77,77,77	0
60	MG	14	3449	1/1	0.96	0.05	73,73,73,73	0
60	MG	1H	3442	1/1	0.96	0.12	92,92,92,92	0
60	MG	14	3459	1/1	0.96	0.06	97,97,97,97	0
60	MG	14	3463	1/1	0.96	0.07	92,92,92,92	0
60	MG	14	3468	1/1	0.96	0.06	117,117,117,117	0
60	MG	14	3472	1/1	0.96	0.04	88,88,88,88	0
60	MG	1H	3226	1/1	0.96	0.06	74,74,74,74	0
60	MG	14	3475	1/1	0.96	0.06	104,104,104,104	0
60	MG	1H	3574	1/1	0.96	0.05	91,91,91,91	0
60	MG	14	3483	1/1	0.96	0.06	108,108,108,108	0
60	MG	1H	3449	1/1	0.96	0.06	58,58,58,58	0
60	MG	1G	1742	1/1	0.96	0.04	100,100,100,100	0
60	MG	1H	3452	1/1	0.96	0.07	80,80,80,80	0
60	MG	1G	1747	1/1	0.96	0.15	96,96,96,96	0
60	MG	1G	1748	1/1	0.96	0.05	123,123,123,123	0
60	MG	14	3503	1/1	0.96	0.05	101,101,101,101	0
60	MG	14	3508	1/1	0.96	0.06	99,99,99,99	0
60	MG	1H	3458	1/1	0.96	0.12	96,96,96,96	0
60	MG	14	3510	1/1	0.96	0.07	92,92,92,92	0
60	MG	14	3512	1/1	0.96	0.07	98,98,98,98	0
60	MG	1H	3581	1/1	0.96	0.08	96,96,96,96	0
60	MG	1H	3459	1/1	0.96	0.09	92,92,92,92	0
60	MG	14	3520	1/1	0.96	0.12	91,91,91,91	0
60	MG	1H	3584	1/1	0.96	0.08	94,94,94,94	0
60	MG	14	3523	1/1	0.96	0.03	140,140,140,140	0
60	MG	1G	1755	1/1	0.96	0.04	135,135,135,135	0
60	MG	1H	3586	1/1	0.96	0.05	122,122,122,122	0
60	MG	1G	1758	1/1	0.96	0.06	137,137,137,137	0
60	MG	1G	1759	1/1	0.96	0.07	106,106,106,106	0
60	MG	14	3534	1/1	0.96	0.09	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3461	1/1	0.96	0.08	68,68,68,68	0
60	MG	14	3281	1/1	0.96	0.11	64,64,64,64	0
60	MG	14	3542	1/1	0.96	0.07	97,97,97,97	0
60	MG	13	1763	1/1	0.96	0.05	112,112,112,112	0
60	MG	1G	1765	1/1	0.96	0.05	117,117,117,117	0
60	MG	1H	3275	1/1	0.96	0.05	79,79,79,79	0
60	MG	13	1720	1/1	0.96	0.06	108,108,108,108	0
60	MG	16	217	1/1	0.96	0.11	105,105,105,105	0
60	MG	1H	3277	1/1	0.96	0.10	78,78,78,78	0
60	MG	14	3551	1/1	0.96	0.08	125,125,125,125	0
60	MG	1H	3107	1/1	0.96	0.07	77,77,77,77	0
60	MG	14	3291	1/1	0.96	0.15	68,68,68,68	0
60	MG	13	1768	1/1	0.96	0.07	100,100,100,100	0
60	MG	14	3556	1/1	0.96	0.13	112,112,112,112	0
60	MG	14	3557	1/1	0.96	0.06	93,93,93,93	0
60	MG	14	3099	1/1	0.96	0.12	90,90,90,90	0
60	MG	1H	3478	1/1	0.96	0.11	87,87,87,87	0
60	MG	1H	3599	1/1	0.96	0.09	105,105,105,105	0
60	MG	14	3002	1/1	0.96	0.10	72,72,72,72	0
60	MG	14	3103	1/1	0.96	0.21	81,81,81,81	0
60	MG	1H	3600	1/1	0.96	0.04	122,122,122,122	0
60	MG	1H	3480	1/1	0.96	0.09	95,95,95,95	0
60	MG	14	3007	1/1	0.96	0.11	78,78,78,78	0
60	MG	14	3574	1/1	0.96	0.10	87,87,87,87	0
60	MG	11	306	1/1	0.96	0.05	95,95,95,95	0
60	MG	1H	3603	1/1	0.96	0.19	85,85,85,85	0
60	MG	13	1796	1/1	0.96	0.06	97,97,97,97	0
60	MG	14	3579	1/1	0.96	0.13	100,100,100,100	0
60	MG	13	1749	1/1	0.96	0.07	112,112,112,112	0
60	MG	14	3582	1/1	0.96	0.06	118,118,118,118	0
60	MG	1H	3606	1/1	0.96	0.04	112,112,112,112	0
60	MG	14	3587	1/1	0.96	0.08	113,113,113,113	0
60	MG	14	3588	1/1	0.96	0.07	124,124,124,124	0
60	MG	1H	3607	1/1	0.96	0.04	156,156,156,156	0
60	MG	1H	3491	1/1	0.96	0.09	79,79,79,79	0
60	MG	13	1660	1/1	0.96	0.07	94,94,94,94	0
60	MG	1H	3054	1/1	0.96	0.11	45,45,45,45	0
60	MG	14	3595	1/1	0.96	0.15	96,96,96,96	0
60	MG	14	3311	1/1	0.96	0.23	87,87,87,87	0
60	MG	1H	3615	1/1	0.96	0.06	103,103,103,103	0
60	MG	1H	3362	1/1	0.96	0.06	75,75,75,75	0
60	MG	14	3600	1/1	0.96	0.06	122,122,122,122	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3033	1/1	0.96	0.07	79,79,79,79	0
60	MG	13	1819	1/1	0.96	0.11	103,103,103,103	0
60	MG	1H	3373	1/1	0.96	0.08	68,68,68,68	0
60	MG	1G	1603	1/1	0.96	0.07	95,95,95,95	0
60	MG	14	3025	1/1	0.96	0.04	89,89,89,89	0
60	MG	1G	1677	1/1	0.96	0.12	79,79,79,79	0
60	MG	1G	1678	1/1	0.96	0.04	87,87,87,87	0
60	MG	1H	3510	1/1	0.96	0.07	106,106,106,106	0
60	MG	1H	3629	1/1	0.96	0.12	103,103,103,103	0
60	MG	1H	3630	1/1	0.96	0.04	141,141,141,141	0
60	MG	13	1800	1/1	0.96	0.15	103,103,103,103	0
60	MG	1H	3633	1/1	0.96	0.17	96,96,96,96	0
60	MG	13	1610	1/1	0.96	0.09	88,88,88,88	0
60	MG	1H	3382	1/1	0.96	0.07	72,72,72,72	0
60	MG	1H	3518	1/1	0.96	0.08	102,102,102,102	0
60	MG	1H	3137	1/1	0.96	0.08	82,82,82,82	0
60	MG	1H	3526	1/1	0.96	0.05	102,102,102,102	0
60	MG	1H	3391	1/1	0.96	0.15	92,92,92,92	0
60	MG	1H	3528	1/1	0.96	0.12	112,112,112,112	0
60	MG	1H	3643	1/1	0.96	0.10	111,111,111,111	0
60	MG	13	1803	1/1	0.96	0.04	143,143,143,143	0
60	MG	13	1795	1/1	0.97	0.08	108,108,108,108	0
60	MG	14	3399	1/1	0.97	0.04	133,133,133,133	0
60	MG	14	3400	1/1	0.97	0.04	109,109,109,109	0
60	MG	1H	3654	1/1	0.97	0.10	91,91,91,91	0
60	MG	13	1822	1/1	0.97	0.09	110,110,110,110	0
60	MG	14	3407	1/1	0.97	0.05	95,95,95,95	0
60	MG	1H	3445	1/1	0.97	0.07	72,72,72,72	0
60	MG	1H	3569	1/1	0.97	0.06	85,85,85,85	0
60	MG	13	1622	1/1	0.97	0.09	68,68,68,68	0
60	MG	1H	3450	1/1	0.97	0.05	94,94,94,94	0
60	MG	13	1826	1/1	0.97	0.12	98,98,98,98	0
60	MG	1H	3089	1/1	0.97	0.12	76,76,76,76	0
60	MG	1G	1733	1/1	0.97	0.04	106,106,106,106	0
60	MG	1H	3576	1/1	0.97	0.06	93,93,93,93	0
60	MG	14	3421	1/1	0.97	0.09	96,96,96,96	0
60	MG	1H	3297	1/1	0.97	0.05	89,89,89,89	0
60	MG	1H	3578	1/1	0.97	0.08	97,97,97,97	0
60	MG	14	3431	1/1	0.97	0.10	75,75,75,75	0
60	MG	14	3432	1/1	0.97	0.05	71,71,71,71	0
60	MG	14	3436	1/1	0.97	0.09	86,86,86,86	0
60	MG	1H	3330	1/1	0.97	0.08	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1G	1740	1/1	0.97	0.13	100,100,100,100	0
60	MG	1H	3332	1/1	0.97	0.06	67,67,67,67	0
60	MG	1H	3464	1/1	0.97	0.07	69,69,69,69	0
60	MG	14	3447	1/1	0.97	0.07	64,64,64,64	0
60	MG	1H	3467	1/1	0.97	0.06	92,92,92,92	0
60	MG	13	1827	1/1	0.97	0.08	112,112,112,112	0
60	MG	14	3451	1/1	0.97	0.07	87,87,87,87	0
60	MG	14	3452	1/1	0.97	0.04	108,108,108,108	0
60	MG	14	3455	1/1	0.97	0.05	78,78,78,78	0
60	MG	13	1754	1/1	0.97	0.08	83,83,83,83	0
60	MG	1G	1749	1/1	0.97	0.19	84,84,84,84	0
60	MG	14	3076	1/1	0.97	0.07	71,71,71,71	0
60	MG	14	3467	1/1	0.97	0.04	105,105,105,105	0
60	MG	1H	3470	1/1	0.97	0.11	98,98,98,98	0
60	MG	1H	3588	1/1	0.97	0.05	97,97,97,97	0
60	MG	1H	3589	1/1	0.97	0.15	83,83,83,83	0
60	MG	1H	3343	1/1	0.97	0.06	71,71,71,71	0
60	MG	14	3477	1/1	0.97	0.06	110,110,110,110	0
60	MG	13	1614	1/1	0.97	0.09	97,97,97,97	0
60	MG	14	3480	1/1	0.97	0.06	111,111,111,111	0
60	MG	14	3481	1/1	0.97	0.08	88,88,88,88	0
60	MG	13	1748	1/1	0.97	0.07	134,134,134,134	0
60	MG	14	3484	1/1	0.97	0.14	83,83,83,83	0
60	MG	14	3485	1/1	0.97	0.05	108,108,108,108	0
60	MG	14	3486	1/1	0.97	0.08	107,107,107,107	0
60	MG	16	214	1/1	0.97	0.07	102,102,102,102	0
60	MG	14	3489	1/1	0.97	0.04	104,104,104,104	0
60	MG	14	3490	1/1	0.97	0.12	92,92,92,92	0
60	MG	14	3492	1/1	0.97	0.05	73,73,73,73	0
60	MG	13	1780	1/1	0.97	0.04	109,109,109,109	0
60	MG	14	3494	1/1	0.97	0.09	103,103,103,103	0
60	MG	13	1758	1/1	0.97	0.05	109,109,109,109	0
60	MG	1H	3596	1/1	0.97	0.04	109,109,109,109	0
60	MG	14	3501	1/1	0.97	0.04	103,103,103,103	0
60	MG	1G	1763	1/1	0.97	0.04	123,123,123,123	0
60	MG	14	3285	1/1	0.97	0.09	81,81,81,81	0
60	MG	14	3504	1/1	0.97	0.04	89,89,89,89	0
60	MG	14	3505	1/1	0.97	0.05	98,98,98,98	0
60	MG	1G	1764	1/1	0.97	0.04	121,121,121,121	0
60	MG	14	3089	1/1	0.97	0.13	75,75,75,75	0
60	MG	13	1783	1/1	0.97	0.08	104,104,104,104	0
60	MG	14	3511	1/1	0.97	0.08	113,113,113,113	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3289	1/1	0.97	0.09	84,84,84,84	0
60	MG	13	1784	1/1	0.97	0.03	131,131,131,131	0
60	MG	13	1786	1/1	0.97	0.07	100,100,100,100	0
60	MG	14	3518	1/1	0.97	0.06	124,124,124,124	0
60	MG	14	3292	1/1	0.97	0.14	72,72,72,72	0
60	MG	52	201	1/1	0.97	0.10	125,125,125,125	0
60	MG	1H	3044	1/1	0.97	0.07	68,68,68,68	0
60	MG	14	3525	1/1	0.97	0.04	92,92,92,92	0
60	MG	1H	3072	1/1	0.97	0.09	60,60,60,60	0
60	MG	1H	3045	1/1	0.97	0.11	63,63,63,63	0
60	MG	1H	3383	1/1	0.97	0.12	77,77,77,77	0
60	MG	14	3531	1/1	0.97	0.17	68,68,68,68	0
60	MG	14	3532	1/1	0.97	0.06	80,80,80,80	0
60	MG	1H	3384	1/1	0.97	0.10	53,53,53,53	0
60	MG	1H	3019	1/1	0.97	0.09	50,50,50,50	0
60	MG	14	3535	1/1	0.97	0.05	100,100,100,100	0
60	MG	21	302	1/1	0.97	0.08	75,75,75,75	0
60	MG	14	3539	1/1	0.97	0.09	82,82,82,82	0
60	MG	14	3003	1/1	0.97	0.10	83,83,83,83	0
60	MG	14	3004	1/1	0.97	0.13	82,82,82,82	0
60	MG	13	1762	1/1	0.97	0.04	115,115,115,115	0
60	MG	14	3544	1/1	0.97	0.10	96,96,96,96	0
60	MG	1H	3512	1/1	0.97	0.18	93,93,93,93	0
60	MG	1H	3394	1/1	0.97	0.05	72,72,72,72	0
60	MG	78	201	1/1	0.97	0.17	80,80,80,80	0
60	MG	14	3548	1/1	0.97	0.05	104,104,104,104	0
60	MG	1H	3515	1/1	0.97	0.13	94,94,94,94	0
60	MG	1H	3614	1/1	0.97	0.10	96,96,96,96	0
60	MG	1H	3395	1/1	0.97	0.05	76,76,76,76	0
60	MG	88	204	1/1	0.97	0.27	83,83,83,83	0
60	MG	1H	3279	1/1	0.97	0.07	68,68,68,68	0
60	MG	1G	1675	1/1	0.97	0.03	130,130,130,130	0
60	MG	14	3015	1/1	0.97	0.04	68,68,68,68	0
60	MG	14	3314	1/1	0.97	0.13	90,90,90,90	0
60	MG	14	3558	1/1	0.97	0.14	103,103,103,103	0
60	MG	14	3560	1/1	0.97	0.08	104,104,104,104	0
60	MG	98	202	1/1	0.97	0.14	110,110,110,110	0
60	MG	14	3564	1/1	0.97	0.08	94,94,94,94	0
60	MG	I8	101	1/1	0.97	0.07	94,94,94,94	0
60	MG	13	1629	1/1	0.97	0.10	74,74,74,74	0
60	MG	1H	3521	1/1	0.97	0.08	88,88,88,88	0
60	MG	1H	3522	1/1	0.97	0.12	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3622	1/1	0.97	0.05	111,111,111,111	0
60	MG	14	3571	1/1	0.97	0.04	108,108,108,108	0
60	MG	1H	3626	1/1	0.97	0.18	78,78,78,78	0
60	MG	13	1764	1/1	0.97	0.06	80,80,80,80	0
60	MG	1H	3411	1/1	0.97	0.06	76,76,76,76	0
60	MG	13	1790	1/1	0.97	0.13	89,89,89,89	0
60	MG	1H	3415	1/1	0.97	0.05	80,80,80,80	0
60	MG	1H	3051	1/1	0.97	0.10	71,71,71,71	0
60	MG	1H	3001	1/1	0.97	0.07	57,57,57,57	0
60	MG	1H	3534	1/1	0.97	0.05	105,105,105,105	0
60	MG	1H	3254	1/1	0.97	0.23	71,71,71,71	0
60	MG	13	1791	1/1	0.97	0.04	127,127,127,127	0
60	MG	14	3586	1/1	0.97	0.15	91,91,91,91	0
60	MG	14	3033	1/1	0.97	0.11	80,80,80,80	0
60	MG	1H	3432	1/1	0.97	0.06	109,109,109,109	0
60	MG	1G	1614	1/1	0.97	0.04	81,81,81,81	0
60	MG	1H	3541	1/1	0.97	0.06	94,94,94,94	0
60	MG	1H	3433	1/1	0.97	0.07	109,109,109,109	0
60	MG	14	3038	1/1	0.97	0.12	47,47,47,47	0
60	MG	1H	3434	1/1	0.97	0.06	117,117,117,117	0
60	MG	14	3596	1/1	0.97	0.14	95,95,95,95	0
60	MG	14	3137	1/1	0.97	0.14	69,69,69,69	0
60	MG	13	1792	1/1	0.97	0.05	102,102,102,102	0
60	MG	1H	3547	1/1	0.97	0.05	110,110,110,110	0
60	MG	1G	1706	1/1	0.97	0.12	120,120,120,120	0
60	MG	14	3601	1/1	0.97	0.10	102,102,102,102	0
60	MG	14	3602	1/1	0.97	0.04	111,111,111,111	0
60	MG	14	3043	1/1	0.97	0.33	67,67,67,67	0
60	MG	13	1726	1/1	0.97	0.10	96,96,96,96	0
60	MG	14	3607	1/1	0.97	0.14	98,98,98,98	0
60	MG	14	3242	1/1	0.97	0.10	67,67,67,67	0
60	MG	13	1767	1/1	0.97	0.06	94,94,94,94	0
60	MG	1H	3648	1/1	0.97	0.07	109,109,109,109	0
60	MG	14	3352	1/1	0.97	0.06	64,64,64,64	0
60	MG	1J	205	1/1	0.97	0.04	113,113,113,113	0
60	MG	1J	206	1/1	0.97	0.04	109,109,109,109	0
60	MG	1H	3557	1/1	0.97	0.09	104,104,104,104	0
60	MG	14	3356	1/1	0.97	0.05	106,106,106,106	0
60	MG	1G	1712	1/1	0.97	0.04	107,107,107,107	0
60	MG	14	3369	1/1	0.97	0.05	66,66,66,66	0
60	MG	29	304	1/1	0.97	0.07	71,71,71,71	0
60	MG	1H	3441	1/1	0.97	0.05	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3372	1/1	0.97	0.08	90,90,90,90	0
60	MG	14	3374	1/1	0.97	0.06	74,74,74,74	0
60	MG	14	3377	1/1	0.97	0.05	65,65,65,65	0
60	MG	1H	3560	1/1	0.97	0.05	110,110,110,110	0
60	MG	1G	1718	1/1	0.97	0.05	102,102,102,102	0
60	MG	14	3383	1/1	0.97	0.05	84,84,84,84	0
60	MG	14	3384	1/1	0.97	0.06	73,73,73,73	0
60	MG	1H	3652	1/1	0.97	0.11	95,95,95,95	0
60	MG	14	3387	1/1	0.97	0.08	70,70,70,70	0
60	MG	F5	101	1/1	0.97	0.17	92,92,92,92	0
60	MG	14	3393	1/1	0.97	0.16	74,74,74,74	0
60	MG	14	3430	1/1	0.98	0.11	102,102,102,102	0
60	MG	13	1776	1/1	0.98	0.04	71,71,71,71	0
60	MG	13	1759	1/1	0.98	0.07	83,83,83,83	0
60	MG	1H	3284	1/1	0.98	0.03	93,93,93,93	0
60	MG	14	3438	1/1	0.98	0.04	96,96,96,96	0
60	MG	14	3439	1/1	0.98	0.04	74,74,74,74	0
60	MG	14	3440	1/1	0.98	0.05	89,89,89,89	0
60	MG	13	1737	1/1	0.98	0.09	90,90,90,90	0
60	MG	14	3265	1/1	0.98	0.04	81,81,81,81	0
60	MG	1H	3481	1/1	0.98	0.04	81,81,81,81	0
60	MG	1H	3392	1/1	0.98	0.06	63,63,63,63	0
60	MG	13	1811	1/1	0.98	0.04	95,95,95,95	0
60	MG	1G	1684	1/1	0.98	0.07	134,134,134,134	0
60	MG	14	3151	1/1	0.98	0.05	98,98,98,98	0
60	MG	14	3450	1/1	0.98	0.05	51,51,51,51	0
60	MG	1H	3486	1/1	0.98	0.08	71,71,71,71	0
60	MG	1H	3489	1/1	0.98	0.12	87,87,87,87	0
60	MG	14	3453	1/1	0.98	0.04	78,78,78,78	0
60	MG	14	3454	1/1	0.98	0.03	69,69,69,69	0
60	MG	13	1812	1/1	0.98	0.04	117,117,117,117	0
60	MG	1H	3593	1/1	0.98	0.03	104,104,104,104	0
60	MG	14	3458	1/1	0.98	0.04	98,98,98,98	0
60	MG	1H	3494	1/1	0.98	0.08	92,92,92,92	0
60	MG	14	3461	1/1	0.98	0.07	76,76,76,76	0
60	MG	14	3462	1/1	0.98	0.08	63,63,63,63	0
60	MG	1H	3398	1/1	0.98	0.04	55,55,55,55	0
60	MG	14	3465	1/1	0.98	0.04	84,84,84,84	0
60	MG	1H	3496	1/1	0.98	0.04	104,104,104,104	0
60	MG	1H	3497	1/1	0.98	0.06	86,86,86,86	0
60	MG	14	3469	1/1	0.98	0.08	91,91,91,91	0
60	MG	1H	3498	1/1	0.98	0.07	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3288	1/1	0.98	0.05	84,84,84,84	0
60	MG	1H	3403	1/1	0.98	0.05	74,74,74,74	0
60	MG	14	3476	1/1	0.98	0.04	93,93,93,93	0
60	MG	1H	3501	1/1	0.98	0.03	98,98,98,98	0
60	MG	14	3478	1/1	0.98	0.09	55,55,55,55	0
60	MG	14	3047	1/1	0.98	0.18	85,85,85,85	0
60	MG	1H	3502	1/1	0.98	0.04	74,74,74,74	0
60	MG	13	1813	1/1	0.98	0.04	113,113,113,113	0
60	MG	14	3482	1/1	0.98	0.06	67,67,67,67	0
60	MG	1G	1700	1/1	0.98	0.03	78,78,78,78	0
60	MG	1H	3406	1/1	0.98	0.04	55,55,55,55	0
60	MG	1H	3062	1/1	0.98	0.07	71,71,71,71	0
60	MG	1H	3509	1/1	0.98	0.04	96,96,96,96	0
60	MG	13	1781	1/1	0.98	0.08	100,100,100,100	0
60	MG	14	3488	1/1	0.98	0.05	100,100,100,100	0
60	MG	1H	3511	1/1	0.98	0.05	84,84,84,84	0
60	MG	13	1815	1/1	0.98	0.05	103,103,103,103	0
60	MG	1G	1711	1/1	0.98	0.05	95,95,95,95	0
60	MG	1G	1605	1/1	0.98	0.09	111,111,111,111	0
60	MG	1G	1714	1/1	0.98	0.05	94,94,94,94	0
60	MG	1G	1715	1/1	0.98	0.09	102,102,102,102	0
60	MG	14	3497	1/1	0.98	0.04	105,105,105,105	0
60	MG	14	3498	1/1	0.98	0.04	118,118,118,118	0
60	MG	1H	3513	1/1	0.98	0.04	93,93,93,93	0
60	MG	14	3500	1/1	0.98	0.06	114,114,114,114	0
60	MG	1H	3414	1/1	0.98	0.07	84,84,84,84	0
60	MG	13	1740	1/1	0.98	0.03	108,108,108,108	0
60	MG	1H	3235	1/1	0.98	0.06	58,58,58,58	0
60	MG	1H	3419	1/1	0.98	0.05	87,87,87,87	0
60	MG	1G	1723	1/1	0.98	0.04	125,125,125,125	0
60	MG	1H	3619	1/1	0.98	0.03	127,127,127,127	0
60	MG	1G	1725	1/1	0.98	0.04	110,110,110,110	0
60	MG	1H	3620	1/1	0.98	0.16	84,84,84,84	0
60	MG	13	1711	1/1	0.98	0.07	71,71,71,71	0
60	MG	1H	3519	1/1	0.98	0.04	88,88,88,88	0
60	MG	1H	3624	1/1	0.98	0.09	96,96,96,96	0
60	MG	1H	3625	1/1	0.98	0.12	93,93,93,93	0
60	MG	14	3517	1/1	0.98	0.10	80,80,80,80	0
60	MG	2K	106	1/1	0.98	0.08	100,100,100,100	0
60	MG	14	3519	1/1	0.98	0.04	98,98,98,98	0
60	MG	1H	3426	1/1	0.98	0.04	101,101,101,101	0
60	MG	1H	3628	1/1	0.98	0.16	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3522	1/1	0.98	0.03	108,108,108,108	0
60	MG	1G	1734	1/1	0.98	0.05	90,90,90,90	0
60	MG	1H	3523	1/1	0.98	0.05	104,104,104,104	0
60	MG	13	1798	1/1	0.98	0.04	91,91,91,91	0
60	MG	14	3527	1/1	0.98	0.06	74,74,74,74	0
60	MG	1H	3525	1/1	0.98	0.09	97,97,97,97	0
60	MG	1H	3632	1/1	0.98	0.03	119,119,119,119	0
60	MG	1G	1739	1/1	0.98	0.07	119,119,119,119	0
60	MG	1H	3428	1/1	0.98	0.08	76,76,76,76	0
60	MG	1H	3431	1/1	0.98	0.07	96,96,96,96	0
60	MG	1H	3329	1/1	0.98	0.06	74,74,74,74	0
60	MG	1G	1743	1/1	0.98	0.08	100,100,100,100	0
60	MG	14	3536	1/1	0.98	0.12	82,82,82,82	0
60	MG	14	3537	1/1	0.98	0.09	88,88,88,88	0
60	MG	1G	1744	1/1	0.98	0.05	143,143,143,143	0
60	MG	1H	3529	1/1	0.98	0.07	88,88,88,88	0
60	MG	1G	1746	1/1	0.98	0.08	96,96,96,96	0
60	MG	1H	3531	1/1	0.98	0.04	101,101,101,101	0
60	MG	4K	101	1/1	0.98	0.04	101,101,101,101	0
60	MG	13	1753	1/1	0.98	0.09	91,91,91,91	0
60	MG	1H	3117	1/1	0.98	0.06	63,63,63,63	0
60	MG	1H	3535	1/1	0.98	0.12	78,78,78,78	0
60	MG	1G	1752	1/1	0.98	0.11	147,147,147,147	0
60	MG	1H	3334	1/1	0.98	0.05	57,57,57,57	0
60	MG	1H	3335	1/1	0.98	0.04	57,57,57,57	0
60	MG	13	1703	1/1	0.98	0.08	74,74,74,74	0
60	MG	1G	1756	1/1	0.98	0.03	128,128,128,128	0
60	MG	14	3217	1/1	0.98	0.13	72,72,72,72	0
60	MG	14	3553	1/1	0.98	0.12	94,94,94,94	0
60	MG	1H	3540	1/1	0.98	0.16	77,77,77,77	0
60	MG	13	1821	1/1	0.98	0.06	102,102,102,102	0
60	MG	13	1623	1/1	0.98	0.05	91,91,91,91	0
60	MG	1H	3543	1/1	0.98	0.08	116,116,116,116	0
60	MG	1H	3350	1/1	0.98	0.06	66,66,66,66	0
60	MG	14	3559	1/1	0.98	0.04	120,120,120,120	0
60	MG	1H	3446	1/1	0.98	0.04	63,63,63,63	0
60	MG	14	3562	1/1	0.98	0.10	99,99,99,99	0
60	MG	1H	3546	1/1	0.98	0.07	103,103,103,103	0
60	MG	1H	3448	1/1	0.98	0.06	65,65,65,65	0
60	MG	1G	1644	1/1	0.98	0.06	95,95,95,95	0
60	MG	1H	3548	1/1	0.98	0.05	100,100,100,100	0
60	MG	32	302	1/1	0.98	0.03	126,126,126,126	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3568	1/1	0.98	0.04	78,78,78,78	0
60	MG	1H	3549	1/1	0.98	0.05	106,106,106,106	0
60	MG	14	3355	1/1	0.98	0.04	67,67,67,67	0
60	MG	1H	3657	1/1	0.98	0.12	105,105,105,105	0
60	MG	14	3359	1/1	0.98	0.05	79,79,79,79	0
60	MG	1H	3273	1/1	0.98	0.04	71,71,71,71	0
60	MG	14	3368	1/1	0.98	0.05	76,76,76,76	0
60	MG	14	3232	1/1	0.98	0.03	108,108,108,108	0
60	MG	1H	3659	1/1	0.98	0.07	97,97,97,97	0
60	MG	1H	3554	1/1	0.98	0.03	113,113,113,113	0
60	MG	1H	3661	1/1	0.98	0.05	97,97,97,97	0
60	MG	14	3376	1/1	0.98	0.04	63,63,63,63	0
60	MG	14	3581	1/1	0.98	0.04	124,124,124,124	0
60	MG	13	1769	1/1	0.98	0.04	81,81,81,81	0
60	MG	14	3583	1/1	0.98	0.03	116,116,116,116	0
60	MG	14	3584	1/1	0.98	0.04	108,108,108,108	0
60	MG	1H	3451	1/1	0.98	0.06	59,59,59,59	0
60	MG	14	3380	1/1	0.98	0.04	82,82,82,82	0
60	MG	1H	3665	1/1	0.98	0.11	83,83,83,83	0
60	MG	14	3382	1/1	0.98	0.04	94,94,94,94	0
60	MG	1H	3356	1/1	0.98	0.05	104,104,104,104	0
60	MG	14	3590	1/1	0.98	0.05	108,108,108,108	0
60	MG	1H	3559	1/1	0.98	0.11	91,91,91,91	0
60	MG	14	3592	1/1	0.98	0.07	106,106,106,106	0
60	MG	1H	3454	1/1	0.98	0.03	86,86,86,86	0
60	MG	14	3386	1/1	0.98	0.04	87,87,87,87	0
60	MG	1H	3457	1/1	0.98	0.03	97,97,97,97	0
60	MG	14	3388	1/1	0.98	0.05	90,90,90,90	0
60	MG	14	3389	1/1	0.98	0.09	88,88,88,88	0
60	MG	14	3392	1/1	0.98	0.04	82,82,82,82	0
60	MG	1H	3562	1/1	0.98	0.07	85,85,85,85	0
60	MG	14	3395	1/1	0.98	0.03	105,105,105,105	0
60	MG	14	3396	1/1	0.98	0.03	106,106,106,106	0
60	MG	14	3397	1/1	0.98	0.04	100,100,100,100	0
60	MG	1H	3563	1/1	0.98	0.03	105,105,105,105	0
60	MG	1H	3564	1/1	0.98	0.07	71,71,71,71	0
60	MG	1H	3565	1/1	0.98	0.05	94,94,94,94	0
60	MG	14	3401	1/1	0.98	0.04	93,93,93,93	0
60	MG	1H	3360	1/1	0.98	0.04	68,68,68,68	0
60	MG	13	1824	1/1	0.98	0.06	96,96,96,96	0
60	MG	14	3406	1/1	0.98	0.15	88,88,88,88	0
60	MG	1H	3364	1/1	0.98	0.07	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3570	1/1	0.98	0.12	71,71,71,71	0
60	MG	1J	207	1/1	0.98	0.04	116,116,116,116	0
60	MG	14	3409	1/1	0.98	0.04	119,119,119,119	0
60	MG	14	3410	1/1	0.98	0.04	115,115,115,115	0
60	MG	1H	3247	1/1	0.98	0.06	75,75,75,75	0
60	MG	1H	3248	1/1	0.98	0.05	83,83,83,83	0
60	MG	1H	3465	1/1	0.98	0.04	87,87,87,87	0
60	MG	14	3414	1/1	0.98	0.05	69,69,69,69	0
60	MG	1H	3466	1/1	0.98	0.09	80,80,80,80	0
60	MG	16	213	1/1	0.98	0.03	84,84,84,84	0
60	MG	25	201	1/1	0.98	0.03	121,121,121,121	0
60	MG	13	1734	1/1	0.98	0.04	87,87,87,87	0
60	MG	1H	3377	1/1	0.98	0.04	102,102,102,102	0
60	MG	14	3420	1/1	0.98	0.11	100,100,100,100	0
60	MG	13	1773	1/1	0.98	0.07	99,99,99,99	0
60	MG	1H	3173	1/1	0.98	0.03	74,74,74,74	0
60	MG	14	3423	1/1	0.98	0.04	87,87,87,87	0
60	MG	13	1736	1/1	0.98	0.03	87,87,87,87	0
60	MG	E5	101	1/1	0.98	0.14	95,95,95,95	0
60	MG	14	3427	1/1	0.98	0.05	60,60,60,60	0
60	MG	14	3428	1/1	0.98	0.09	96,96,96,96	0
60	MG	1H	3385	1/1	0.99	0.04	63,63,63,63	0
60	MG	1H	3386	1/1	0.99	0.04	56,56,56,56	0
60	MG	14	3460	1/1	0.99	0.05	62,62,62,62	0
60	MG	16	218	1/1	0.99	0.04	92,92,92,92	0
60	MG	13	1765	1/1	0.99	0.04	73,73,73,73	0
60	MG	1H	3575	1/1	0.99	0.03	100,100,100,100	0
60	MG	14	3464	1/1	0.99	0.03	59,59,59,59	0
60	MG	1H	3472	1/1	0.99	0.03	70,70,70,70	0
60	MG	14	3466	1/1	0.99	0.03	91,91,91,91	0
60	MG	1H	3389	1/1	0.99	0.03	79,79,79,79	0
60	MG	1H	3475	1/1	0.99	0.10	78,78,78,78	0
60	MG	1H	3390	1/1	0.99	0.03	91,91,91,91	0
60	MG	14	3470	1/1	0.99	0.04	65,65,65,65	0
60	MG	14	3471	1/1	0.99	0.03	81,81,81,81	0
60	MG	1H	3477	1/1	0.99	0.03	57,57,57,57	0
60	MG	13	1825	1/1	0.99	0.17	88,88,88,88	0
60	MG	14	3474	1/1	0.99	0.03	111,111,111,111	0
60	MG	1G	1699	1/1	0.99	0.03	95,95,95,95	0
60	MG	1H	3479	1/1	0.99	0.03	69,69,69,69	0
60	MG	1G	1701	1/1	0.99	0.03	81,81,81,81	0
60	MG	1H	3583	1/1	0.99	0.02	98,98,98,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3054	1/1	0.99	0.10	85,85,85,85	0
60	MG	1G	1703	1/1	0.99	0.03	100,100,100,100	0
60	MG	1G	1704	1/1	0.99	0.05	113,113,113,113	0
60	MG	1G	1705	1/1	0.99	0.07	108,108,108,108	0
60	MG	13	1738	1/1	0.99	0.05	79,79,79,79	0
60	MG	1H	3585	1/1	0.99	0.03	110,110,110,110	0
60	MG	13	1785	1/1	0.99	0.02	126,126,126,126	0
60	MG	13	1745	1/1	0.99	0.03	75,75,75,75	0
60	MG	1H	3483	1/1	0.99	0.03	61,61,61,61	0
60	MG	1H	3484	1/1	0.99	0.05	49,49,49,49	0
60	MG	1H	3396	1/1	0.99	0.04	82,82,82,82	0
60	MG	1G	1713	1/1	0.99	0.02	127,127,127,127	0
60	MG	14	3491	1/1	0.99	0.04	89,89,89,89	0
60	MG	1H	3397	1/1	0.99	0.04	68,68,68,68	0
60	MG	1H	3487	1/1	0.99	0.04	56,56,56,56	0
60	MG	1H	3488	1/1	0.99	0.03	81,81,81,81	0
60	MG	13	1746	1/1	0.99	0.03	86,86,86,86	0
60	MG	14	3496	1/1	0.99	0.04	89,89,89,89	0
60	MG	I8	102	1/1	0.99	0.09	70,70,70,70	0
60	MG	1H	3490	1/1	0.99	0.05	91,91,91,91	0
60	MG	1H	3399	1/1	0.99	0.03	75,75,75,75	0
60	MG	1G	1721	1/1	0.99	0.06	127,127,127,127	0
60	MG	1G	1722	1/1	0.99	0.11	97,97,97,97	0
60	MG	1H	3492	1/1	0.99	0.03	69,69,69,69	0
60	MG	1H	3493	1/1	0.99	0.02	98,98,98,98	0
60	MG	1H	3401	1/1	0.99	0.03	88,88,88,88	0
60	MG	1H	3336	1/1	0.99	0.03	64,64,64,64	0
60	MG	14	3506	1/1	0.99	0.02	84,84,84,84	0
60	MG	14	3507	1/1	0.99	0.05	90,90,90,90	0
60	MG	1H	3337	1/1	0.99	0.04	67,67,67,67	0
60	MG	1H	3602	1/1	0.99	0.03	105,105,105,105	0
60	MG	1H	3338	1/1	0.99	0.06	52,52,52,52	0
60	MG	1H	3405	1/1	0.99	0.02	67,67,67,67	0
60	MG	1H	3339	1/1	0.99	0.04	52,52,52,52	0
60	MG	1H	3407	1/1	0.99	0.04	78,78,78,78	0
60	MG	14	3514	1/1	0.99	0.04	104,104,104,104	0
60	MG	1H	3408	1/1	0.99	0.04	70,70,70,70	0
60	MG	14	3516	1/1	0.99	0.02	119,119,119,119	0
60	MG	1H	3608	1/1	0.99	0.04	102,102,102,102	0
60	MG	1H	3340	1/1	0.99	0.03	57,57,57,57	0
60	MG	1H	3610	1/1	0.99	0.03	107,107,107,107	0
60	MG	1H	3410	1/1	0.99	0.04	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3341	1/1	0.99	0.04	64,64,64,64	0
60	MG	14	3347	1/1	0.99	0.07	67,67,67,67	0
60	MG	14	3348	1/1	0.99	0.03	69,69,69,69	0
60	MG	14	3524	1/1	0.99	0.03	107,107,107,107	0
60	MG	14	3349	1/1	0.99	0.03	61,61,61,61	0
60	MG	14	3350	1/1	0.99	0.03	84,84,84,84	0
60	MG	14	3351	1/1	0.99	0.04	66,66,66,66	0
60	MG	1H	3613	1/1	0.99	0.10	79,79,79,79	0
60	MG	1H	3505	1/1	0.99	0.03	96,96,96,96	0
60	MG	14	3530	1/1	0.99	0.06	81,81,81,81	0
60	MG	14	3354	1/1	0.99	0.04	107,107,107,107	0
60	MG	13	1756	1/1	0.99	0.04	86,86,86,86	0
60	MG	1H	3507	1/1	0.99	0.07	70,70,70,70	0
60	MG	14	3357	1/1	0.99	0.04	61,61,61,61	0
60	MG	14	3358	1/1	0.99	0.03	72,72,72,72	0
60	MG	1H	3508	1/1	0.99	0.05	92,92,92,92	0
60	MG	14	3361	1/1	0.99	0.03	62,62,62,62	0
60	MG	14	3362	1/1	0.99	0.04	73,73,73,73	0
60	MG	1H	3413	1/1	0.99	0.06	59,59,59,59	0
60	MG	14	3540	1/1	0.99	0.05	91,91,91,91	0
60	MG	14	3364	1/1	0.99	0.03	80,80,80,80	0
60	MG	14	3365	1/1	0.99	0.03	57,57,57,57	0
60	MG	14	3367	1/1	0.99	0.04	63,63,63,63	0
60	MG	13	1809	1/1	0.99	0.07	94,94,94,94	0
60	MG	1H	3344	1/1	0.99	0.04	55,55,55,55	0
60	MG	1H	3416	1/1	0.99	0.05	98,98,98,98	0
60	MG	1H	3346	1/1	0.99	0.03	59,59,59,59	0
60	MG	14	3373	1/1	0.99	0.04	65,65,65,65	0
60	MG	1H	3623	1/1	0.99	0.13	83,83,83,83	0
60	MG	14	3375	1/1	0.99	0.04	66,66,66,66	0
60	MG	1H	3418	1/1	0.99	0.06	109,109,109,109	0
60	MG	1H	3348	1/1	0.99	0.03	60,60,60,60	0
60	MG	1H	3420	1/1	0.99	0.03	94,94,94,94	0
60	MG	1H	3421	1/1	0.99	0.03	66,66,66,66	0
60	MG	13	1770	1/1	0.99	0.06	78,78,78,78	0
60	MG	13	1739	1/1	0.99	0.03	93,93,93,93	0
60	MG	1H	3520	1/1	0.99	0.05	87,87,87,87	0
60	MG	1H	3425	1/1	0.99	0.02	78,78,78,78	0
60	MG	1H	3351	1/1	0.99	0.04	57,57,57,57	0
60	MG	1H	3352	1/1	0.99	0.05	64,64,64,64	0
60	MG	14	3561	1/1	0.99	0.06	89,89,89,89	0
60	MG	1G	1760	1/1	0.99	0.05	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	13	1772	1/1	0.99	0.03	109,109,109,109	0
60	MG	1H	3429	1/1	0.99	0.03	80,80,80,80	0
60	MG	14	3390	1/1	0.99	0.05	106,106,106,106	0
60	MG	14	3391	1/1	0.99	0.03	76,76,76,76	0
60	MG	1H	3636	1/1	0.99	0.03	121,121,121,121	0
60	MG	1H	3430	1/1	0.99	0.04	109,109,109,109	0
60	MG	14	3394	1/1	0.99	0.03	105,105,105,105	0
60	MG	1H	3638	1/1	0.99	0.02	101,101,101,101	0
60	MG	1H	3040	1/1	0.99	0.03	66,66,66,66	0
60	MG	1G	1767	1/1	0.99	0.02	107,107,107,107	0
60	MG	13	1735	1/1	0.99	0.06	87,87,87,87	0
60	MG	1H	3358	1/1	0.99	0.03	72,72,72,72	0
60	MG	14	3575	1/1	0.99	0.06	101,101,101,101	0
60	MG	1H	3530	1/1	0.99	0.05	83,83,83,83	0
60	MG	1H	3359	1/1	0.99	0.03	84,84,84,84	0
60	MG	1H	3435	1/1	0.99	0.04	103,103,103,103	0
60	MG	1H	3436	1/1	0.99	0.07	75,75,75,75	0
60	MG	14	3405	1/1	0.99	0.09	95,95,95,95	0
60	MG	13	1774	1/1	0.99	0.08	71,71,71,71	0
60	MG	1H	3438	1/1	0.99	0.04	59,59,59,59	0
60	MG	1H	3536	1/1	0.99	0.04	70,70,70,70	0
60	MG	14	3001	1/1	0.99	0.03	54,54,54,54	0
60	MG	1H	3361	1/1	0.99	0.04	63,63,63,63	0
60	MG	13	1733	1/1	0.99	0.04	69,69,69,69	0
60	MG	1H	3363	1/1	0.99	0.05	78,78,78,78	0
60	MG	13	1760	1/1	0.99	0.03	73,73,73,73	0
60	MG	1H	3365	1/1	0.99	0.05	85,85,85,85	0
60	MG	1H	3444	1/1	0.99	0.03	71,71,71,71	0
60	MG	2K	105	1/1	0.99	0.04	78,78,78,78	0
60	MG	1H	3367	1/1	0.99	0.09	70,70,70,70	0
60	MG	14	3418	1/1	0.99	0.09	91,91,91,91	0
60	MG	1H	3447	1/1	0.99	0.06	62,62,62,62	0
60	MG	1H	3368	1/1	0.99	0.04	49,49,49,49	0
60	MG	1H	3021	1/1	0.99	0.05	66,66,66,66	0
60	MG	1H	3370	1/1	0.99	0.05	59,59,59,59	0
60	MG	1H	3371	1/1	0.99	0.05	60,60,60,60	0
60	MG	14	3424	1/1	0.99	0.02	77,77,77,77	0
60	MG	1H	3550	1/1	0.99	0.14	83,83,83,83	0
60	MG	14	3426	1/1	0.99	0.03	91,91,91,91	0
60	MG	1H	3663	1/1	0.99	0.06	91,91,91,91	0
60	MG	1H	3551	1/1	0.99	0.02	110,110,110,110	0
60	MG	14	3604	1/1	0.99	0.07	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	14	3605	1/1	0.99	0.12	97,97,97,97	0
60	MG	14	3429	1/1	0.99	0.04	90,90,90,90	0
60	MG	1H	3372	1/1	0.99	0.03	59,59,59,59	0
60	MG	1H	3553	1/1	0.99	0.03	62,62,62,62	0
60	MG	1H	3453	1/1	0.99	0.07	57,57,57,57	0
60	MG	14	3433	1/1	0.99	0.03	83,83,83,83	0
60	MG	14	3434	1/1	0.99	0.05	77,77,77,77	0
60	MG	14	3435	1/1	0.99	0.05	96,96,96,96	0
60	MG	14	3021	1/1	0.99	0.06	78,78,78,78	0
60	MG	14	3437	1/1	0.99	0.02	83,83,83,83	0
60	MG	13	1777	1/1	0.99	0.04	90,90,90,90	0
60	MG	1H	3556	1/1	0.99	0.10	78,78,78,78	0
60	MG	1H	3455	1/1	0.99	0.02	61,61,61,61	0
60	MG	1H	3456	1/1	0.99	0.15	70,70,70,70	0
60	MG	14	3442	1/1	0.99	0.03	64,64,64,64	0
60	MG	14	3443	1/1	0.99	0.05	71,71,71,71	0
60	MG	1H	3374	1/1	0.99	0.06	64,64,64,64	0
60	MG	1H	3375	1/1	0.99	0.05	73,73,73,73	0
60	MG	1H	3376	1/1	0.99	0.03	59,59,59,59	0
60	MG	1H	3460	1/1	0.99	0.03	54,54,54,54	0
60	MG	13	1778	1/1	0.99	0.04	82,82,82,82	0
60	MG	13	1761	1/1	0.99	0.03	97,97,97,97	0
60	MG	45	202	1/1	0.99	0.15	97,97,97,97	0
60	MG	1H	3463	1/1	0.99	0.11	75,75,75,75	0
60	MG	1H	3566	1/1	0.99	0.12	71,71,71,71	0
60	MG	13	1714	1/1	0.99	0.03	103,103,103,103	0
60	MG	1H	3381	1/1	0.99	0.03	63,63,63,63	0
60	MG	13	1743	1/1	0.99	0.03	82,82,82,82	0
60	MG	13	1801	1/1	0.99	0.14	97,97,97,97	0
60	MG	13	1752	1/1	0.99	0.05	99,99,99,99	0
61	SF4	3E	303	8/8	0.99	0.03	84,96,103,108	0
61	SF4	32	303	8/8	0.99	0.03	102,118,124,127	0
62	ZN	5A	101	1/1	0.99	0.03	135,135,135,135	0
60	MG	1H	3331	1/1	1.00	0.03	64,64,64,64	0
60	MG	1H	3357	1/1	1.00	0.09	78,78,78,78	0
60	MG	14	3360	1/1	1.00	0.03	65,65,65,65	0
60	MG	1H	3347	1/1	1.00	0.06	60,60,60,60	0
60	MG	1H	3400	1/1	1.00	0.03	83,83,83,83	0
60	MG	1H	3354	1/1	1.00	0.04	66,66,66,66	0
60	MG	14	3457	1/1	1.00	0.02	92,92,92,92	0
60	MG	14	3378	1/1	1.00	0.10	59,59,59,59	0
60	MG	1H	3393	1/1	1.00	0.05	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
60	MG	1H	3380	1/1	1.00	0.02	63,63,63,63	0
60	MG	14	3366	1/1	1.00	0.01	55,55,55,55	0
60	MG	1H	3387	1/1	1.00	0.02	52,52,52,52	0
60	MG	1H	3423	1/1	1.00	0.02	74,74,74,74	0
60	MG	1H	3474	1/1	1.00	0.05	59,59,59,59	0
60	MG	1H	3345	1/1	1.00	0.03	52,52,52,52	0
60	MG	14	3371	1/1	1.00	0.03	75,75,75,75	0
62	ZN	5I	101	1/1	1.00	0.03	98,98,98,98	0
60	MG	14	3402	1/1	1.00	0.01	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.