



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 10:27 PM GMT

PDB ID : 4WZO
Title : Complex of 70S ribosome with tRNA-fMet and mRNA
Authors : Rozov, A.; Demeshkina, N.; Yusupov, M.; Yusupova, G.
Deposited on : 2014-11-20
Resolution : 3.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

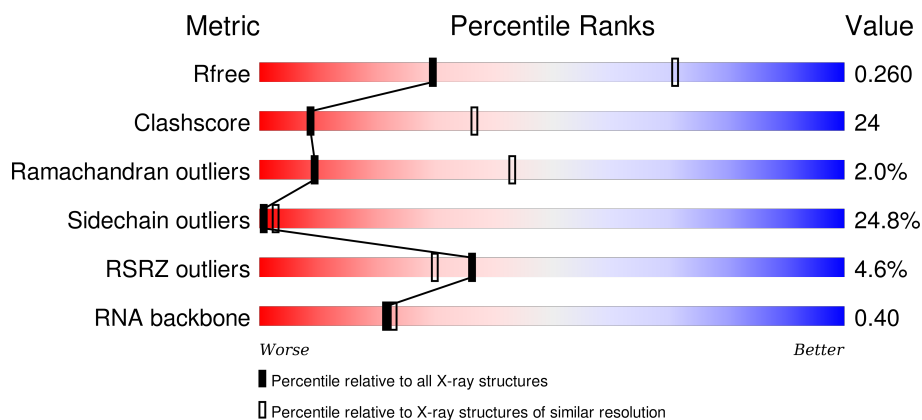
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)
RNA backbone	2183	1005 (3.82-2.78)

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

Mol	Chain	Length	Quality of chain
1	13	1522	<div> <div>24%</div> <div>45%</div> <div>24%</div> <div>5%</div> </div>
1	1G	1522	<div> <div>24%</div> <div>49%</div> <div>21%</div> <div>• •</div> </div>
2	12	256	<div> <div>17%</div> <div>32%</div> <div>42%</div> <div>17%</div> <div>• 7%</div> </div>
2	1E	256	<div> <div>5%</div> <div>38%</div> <div>40%</div> <div>15%</div> <div>7%</div> </div>

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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	
8	72	138	
8	7E	138	
9	82	128	
9	8E	128	
10	1A	105	
10	1I	105	
11	2A	129	
11	2I	129	
12	3A	132	
12	3I	132	
13	4A	126	
13	4I	126	
14	5A	61	
14	5I	61	
15	6A	89	




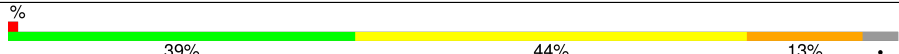
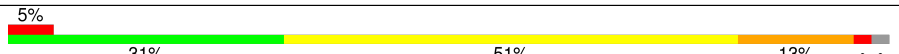
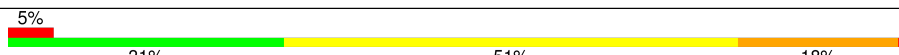
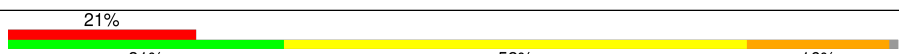
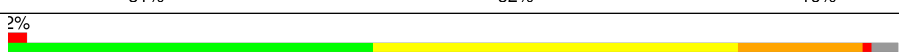
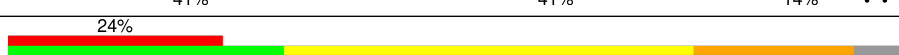
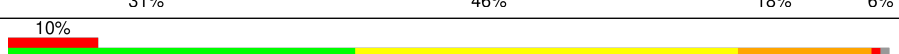
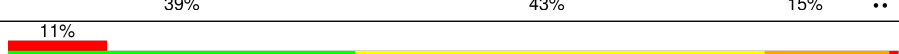
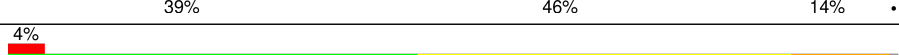
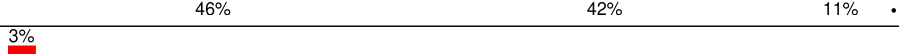



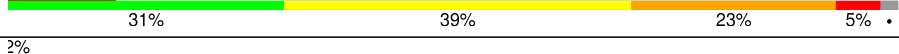
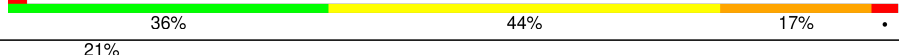
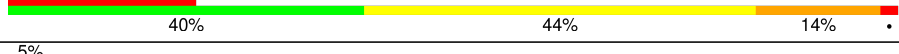

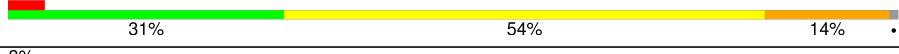
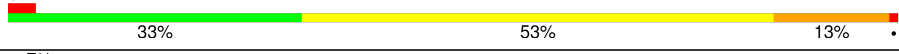

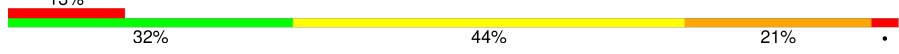

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Mol	Chain	Length	Quality of chain
15	6I	89	
16	7A	88	
16	7I	88	
17	8A	105	
17	8I	105	
18	9A	88	
18	9I	88	
19	AA	93	
19	AI	93	
20	BA	106	
20	BI	106	
21	1B	27	
21	1F	27	
22	1K	77	
23	2K	77	
24	3K	76	
24	3L	76	
25	4K	27	
25	4L	27	
26	14	2917	
26	1H	2917	
27	16	122	
27	1J	122	
28	7I	229	
29	11	276	

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Mol	Chain	Length	Quality of chain
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	61	148	
34	69	148	
35	15	140	
35	58	140	
36	25	122	
36	68	122	
37	35	150	
37	78	150	
38	45	141	
38	88	141	
39	55	118	
39	98	118	
40	65	112	
40	A8	112	
41	75	146	
41	B8	146	% 


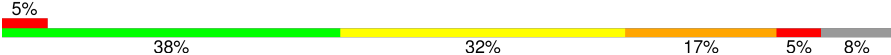

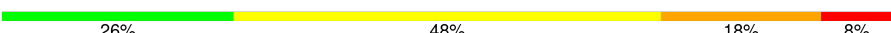
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Mol	Chain	Length	Quality of chain
42	85	118	
42	C8	118	
43	95	101	
43	D8	101	
44	A5	113	
44	E8	113	
45	B5	96	
45	F8	96	
46	C5	110	
46	G8	110	
47	D5	206	
47	H8	206	
48	E5	85	
48	I8	85	
49	F5	98	
49	J8	98	
50	G5	72	
50	K8	72	
51	H5	60	
51	L8	60	
52	I5	71	
52	M8	71	
53	J5	60	
53	N8	60	
54	L5	49	

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Mol	Chain	Length	Quality of chain
54	P8	49	
55	M5	65	
55	Q8	65	
56	2L	77	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	11	302	-	-	-	X
57	MG	13	1601	-	-	-	X
57	MG	13	1610	-	-	-	X
57	MG	13	1618	-	-	-	X
57	MG	13	1619	-	-	-	X
57	MG	13	1621	-	-	-	X
57	MG	13	1622	-	-	-	X
57	MG	13	1631	-	-	-	X
57	MG	13	1635	-	-	-	X
57	MG	13	1643	-	-	-	X
57	MG	13	1644	-	-	-	X
57	MG	13	1646	-	-	-	X
57	MG	13	1647	-	-	-	X
57	MG	13	1650	-	-	-	X
57	MG	13	1655	-	-	-	X
57	MG	13	1657	-	-	-	X
57	MG	13	1658	-	-	-	X
57	MG	13	1661	-	-	-	X
57	MG	14	3004	-	-	-	X
57	MG	14	3007	-	-	-	X
57	MG	14	3009	-	-	-	X
57	MG	14	3011	-	-	-	X
57	MG	14	3014	-	-	-	X
57	MG	14	3019	-	-	-	X
57	MG	14	3020	-	-	-	X
57	MG	14	3024	-	-	-	X
57	MG	14	3030	-	-	-	X
57	MG	14	3035	-	-	-	X
57	MG	14	3036	-	-	-	X
57	MG	14	3038	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	14	3039	-	-	-	X
57	MG	14	3041	-	-	-	X
57	MG	14	3045	-	-	-	X
57	MG	14	3047	-	-	-	X
57	MG	14	3048	-	-	-	X
57	MG	14	3049	-	-	-	X
57	MG	14	3052	-	-	-	X
57	MG	14	3054	-	-	-	X
57	MG	14	3058	-	-	-	X
57	MG	14	3059	-	-	-	X
57	MG	14	3060	-	-	-	X
57	MG	14	3062	-	-	-	X
57	MG	14	3063	-	-	-	X
57	MG	14	3065	-	-	-	X
57	MG	14	3076	-	-	-	X
57	MG	14	3081	-	-	-	X
57	MG	14	3082	-	-	-	X
57	MG	14	3091	-	-	-	X
57	MG	14	3093	-	-	-	X
57	MG	14	3094	-	-	-	X
57	MG	14	3100	-	-	-	X
57	MG	14	3101	-	-	-	X
57	MG	14	3103	-	-	-	X
57	MG	14	3105	-	-	-	X
57	MG	14	3113	-	-	-	X
57	MG	14	3119	-	-	-	X
57	MG	14	3124	-	-	-	X
57	MG	14	3126	-	-	-	X
57	MG	14	3127	-	-	-	X
57	MG	14	3133	-	-	-	X
57	MG	14	3141	-	-	-	X
57	MG	14	3142	-	-	-	X
57	MG	14	3155	-	-	-	X
57	MG	14	3159	-	-	-	X
57	MG	14	3160	-	-	-	X
57	MG	14	3166	-	-	-	X
57	MG	14	3168	-	-	-	X
57	MG	14	3173	-	-	-	X
57	MG	14	3179	-	-	-	X
57	MG	14	3186	-	-	-	X
57	MG	14	3188	-	-	-	X
57	MG	14	3192	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	14	3197	-	-	-	X
57	MG	14	3204	-	-	-	X
57	MG	14	3212	-	-	-	X
57	MG	14	3214	-	-	-	X
57	MG	14	3215	-	-	-	X
57	MG	14	3218	-	-	-	X
57	MG	14	3261	-	-	-	X
57	MG	1G	1601	-	-	-	X
57	MG	1G	1602	-	-	-	X
57	MG	1G	1603	-	-	-	X
57	MG	1G	1616	-	-	-	X
57	MG	1G	1617	-	-	-	X
57	MG	1G	1627	-	-	-	X
57	MG	1G	1630	-	-	-	X
57	MG	1G	1650	-	-	-	X
57	MG	1G	1660	-	-	-	X
57	MG	1G	1662	-	-	-	X
57	MG	1H	3002	-	-	-	X
57	MG	1H	3005	-	-	-	X
57	MG	1H	3007	-	-	-	X
57	MG	1H	3016	-	-	-	X
57	MG	1H	3019	-	-	-	X
57	MG	1H	3020	-	-	-	X
57	MG	1H	3022	-	-	-	X
57	MG	1H	3025	-	-	-	X
57	MG	1H	3027	-	-	-	X
57	MG	1H	3029	-	-	-	X
57	MG	1H	3032	-	-	-	X
57	MG	1H	3036	-	-	-	X
57	MG	1H	3037	-	-	-	X
57	MG	1H	3041	-	-	-	X
57	MG	1H	3042	-	-	-	X
57	MG	1H	3044	-	-	-	X
57	MG	1H	3046	-	-	-	X
57	MG	1H	3048	-	-	-	X
57	MG	1H	3051	-	-	-	X
57	MG	1H	3052	-	-	-	X
57	MG	1H	3060	-	-	-	X
57	MG	1H	3063	-	-	-	X
57	MG	1H	3064	-	-	-	X
57	MG	1H	3073	-	-	-	X
57	MG	1H	3082	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	1H	3089	-	-	-	X
57	MG	1H	3090	-	-	-	X
57	MG	1H	3091	-	-	-	X
57	MG	1H	3093	-	-	-	X
57	MG	1H	3098	-	-	-	X
57	MG	1H	3102	-	-	-	X
57	MG	1H	3106	-	-	-	X
57	MG	1H	3109	-	-	-	X
57	MG	1H	3111	-	-	-	X
57	MG	1H	3113	-	-	-	X
57	MG	1H	3116	-	-	-	X
57	MG	1H	3117	-	-	-	X
57	MG	1H	3120	-	-	-	X
57	MG	1H	3122	-	-	-	X
57	MG	1H	3134	-	-	-	X
57	MG	1H	3136	-	-	-	X
57	MG	1H	3140	-	-	-	X
57	MG	1H	3148	-	-	-	X
57	MG	1H	3150	-	-	-	X
57	MG	1H	3171	-	-	-	X
57	MG	1H	3181	-	-	-	X
57	MG	1H	3192	-	-	-	X
57	MG	1H	3200	-	-	-	X
57	MG	1H	3203	-	-	-	X
57	MG	1H	3218	-	-	-	X
57	MG	1H	3226	-	-	-	X
57	MG	1H	3241	-	-	-	X
57	MG	1H	3242	-	-	-	X
57	MG	1H	3246	-	-	-	X
57	MG	1H	3265	-	-	-	X
57	MG	1H	3269	-	-	-	X
57	MG	1H	3274	-	-	-	X
57	MG	1H	3275	-	-	-	X
57	MG	2K	101	-	-	-	X
57	MG	2L	101	-	-	-	X
57	MG	4E	201	-	-	-	X
57	MG	78	202	-	-	-	X
57	MG	88	201	-	-	-	X
57	MG	J8	101	-	-	-	X
57	MG	L8	101	-	-	-	X

2 Entry composition [i](#)

There are 59 unique types of molecules in this entry. The entry contains 295920 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	1497	Total	C	N	O	P	0	0	0
			32185	14324	5968	10396	1497			
1	1G	1497	Total	C	N	O	P	0	0	0
			32182	14324	5968	10394	1496			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1E	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	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	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3E	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	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	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	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	155	Total	C	N	O	S	0	0	0
			1256	781	252	217	6			
7	62	147	Total	C	N	O	S	0	0	0
			1194	744	237	207	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	127	Total	C	N	O		0	0	0
			1009	639	197	173				
9	82	127	Total	C	N	O		0	0	0
			1009	639	197	173				

- 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	66	Total	C	N	O	S	0	0	0
			522	327	99	95	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	2I	119	Total	C	N	O	S	0	0	0
			884	549	168	164	3			
11	2A	116	Total	C	N	O	S	0	0	0
			864	537	164	160	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	122	Total	C	N	O	S	0	0	0
			956	603	193	159	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	4I	117	Total	C	N	O	S	0	0	0
			933	577	192	162	2			
13	4A	117	Total	C	N	O	S	0	0	0
			933	577	192	162	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	5I	60	Total	C	N	O	S	0	0	0
			491	312	104	71	4			
14	5A	52	Total	C	N	O	S	0	0	0
			418	262	90	62	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	6I	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			
15	6A	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	7I	84	Total	C	N	O	S	0	0	0
			705	446	140	118	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	72	Total	C	N	O	0	0	0
			590	376	117	97			
18	9A	72	Total	C	N	O	0	0	0
			590	376	117	97			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AI	81	Total	C	N	O	S	0	0	0
			647	413	119	113	2			
19	AA	78	Total	C	N	O	S	0	0	0
			624	398	115	109	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	BI	99	Total	C	N	O	S	0	0	0
			762	470	162	128	2			
20	BA	99	Total	C	N	O	S	0	0	0
			762	470	162	128	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	1F	25	Total	C	N	O	0	0	0
			217	134	52	31			
21	1B	22	Total	C	N	O	0	0	0
			188	116	44	28			

- Molecule 22 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	1K	70	Total	C	N	O	P	0	0	0
			1497	669	274	485	69			

- Molecule 23 is a RNA chain called tRNA-fMet.

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			

- Molecule 24 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	3K	76	Total	C	N	O	P	S	0	0	0
			1627	730	290	530	75	2			
24	3L	76	Total	C	N	O	P	S	0	0	0
			1627	730	290	530	75	2			

- Molecule 25 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	4K	13	Total	C	N	O	P	0	0	0
			285	129	62	81	13			
25	4L	9	Total	C	N	O	P	0	0	0
			197	89	42	57	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	1H	2902	Total	C	N	O	P	0	0	0
			62497	27816	11684	20095	2902			
26	14	2877	Total	C	N	O	P	0	0	0
			61968	27579	11594	19918	2877			

- 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	93	Total	C	N	O	0	0	0
			737	465	139	133			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	11	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	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	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			
30	29	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	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	181	Total	C	N	O	S	0	0	0
			1473	942	268	259	4			
32	49	181	Total	C	N	O	S	0	0	0
			1473	942	268	259	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	51	174	Total	C	N	O	S	0	0	0
			1336	848	251	236	1			
33	59	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			

- Molecule 34 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	61	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			
34	69	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	58	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			
35	15	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	68	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			
36	25	122	Total	C	N	O	S	0	0	0
			932	588	171	169	4			

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	78	150	Total	C	N	O	S	0	0	0
			1144	712	232	197	3			
37	35	147	Total	C	N	O	S	0	0	0
			1122	698	229	192	3			

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	88	137	Total	C	N	O	S	0	0	0
			1077	688	206	177	6			
38	45	141	Total	C	N	O	S	0	0	0
			1121	715	212	187	7			

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	98	118	Total	C	N	O	S	0	0	0
			967	604	203	159	1			
39	55	117	Total	C	N	O		0	0	0
			959	599	202	158				

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	A8	111	Total	C	N	O	0	0	0
			881	556	176	149			
40	65	111	Total	C	N	O	0	0	0
			881	556	176	149			

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	B8	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			
41	75	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	C8	117	Total	C	N	O	S	0	0	0
			963	610	202	150	1			
42	85	117	Total	C	N	O	S	0	0	0
			963	610	202	150	1			

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	D8	101	Total	C	N	O	S	0	0	0
			778	501	142	134	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	95	101	Total	C	N	O	S	0	0	0
			778	501	142	134	1			

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	E8	113	Total	C	N	O	S	0	0	0
			899	566	177	154	2			
44	A5	111	Total	C	N	O	S	0	0	0
			886	558	174	152	2			

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	F8	94	Total	C	N	O	S	0	0	0
			742	482	134	125	1			
45	B5	92	Total	C	N	O		0	0	0
			725	471	131	123				

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	G8	104	Total	C	N	O	S	0	0	0
			791	510	149	127	5			
46	C5	104	Total	C	N	O	S	0	0	0
			794	510	152	127	5			

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	H8	135	Total	C	N	O	S	0	0	0
			1110	714	202	192	2			
47	D5	137	Total	C	N	O	S	0	0	0
			1126	725	202	197	2			

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	I8	80	Total	C	N	O	S	0	0	0
			626	388	132	105	1			
48	E5	77	Total	C	N	O	S	0	0	0
			612	379	129	103	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I8	6	ALA	GLY	conflict	UNP P60493
I8	8	ALA	GLY	conflict	UNP P60493
E5	6	ALA	GLY	conflict	UNP P60493
E5	8	ALA	GLY	conflict	UNP P60493

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	J8	97	Total	C	N	O	S	0	0	0
			762	481	150	130	1			
49	F5	94	Total	C	N	O	S	0	0	0
			737	463	146	127	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	K8	67	Total	C	N	O	S	0	0	0
			563	349	114	99	1			
50	G5	66	Total	C	N	O	S	0	0	0
			558	346	113	98	1			

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	L8	57	Total	C	N	O		0	0	0
			452	288	88	76				
51	H5	59	Total	C	N	O		0	0	0
			468	298	90	80				

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	M8	66	Total	C	N	O	S	0	0	0
			533	335	96	97	5			
52	I5	63	Total	C	N	O	S	0	0	0
			515	326	93	91	5			

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	N8	54	Total	C	N	O	S	0	0	0
			422	264	85	68	5			
53	J5	56	Total	C	N	O	S	0	0	0
			434	272	87	70	5			

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	P8	47	Total	C	N	O	S	0	0	0
			409	251	102	54	2			
54	L5	46	Total	C	N	O	S	0	0	0
			398	245	98	53	2			

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	Q8	60	Total	C	N	O	S	0	0	0
			480	306	98	74	2			
55	M5	60	Total	C	N	O	S	0	0	0
			477	303	98	74	2			

- Molecule 56 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	2L	77	Total	C	N	O	P	S	0	0
			1645	734	298	535	77	1		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	98	1	Total	Mg	0	0
			1	1		
57	45	1	Total	Mg	0	0
			1	1		
57	P8	1	Total	Mg	0	0
			1	1		
57	13	99	Total	Mg	0	0
			99	99		
57	1J	3	Total	Mg	0	0
			3	3		
57	35	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	16	11	Total 11	Mg 11	0	0
57	25	1	Total 1	Mg 1	0	0
57	M5	1	Total 1	Mg 1	0	0
57	2K	2	Total 2	Mg 2	0	0
57	L8	1	Total 1	Mg 1	0	0
57	4I	1	Total 1	Mg 1	0	0
57	I8	2	Total 2	Mg 2	0	0
57	68	2	Total 2	Mg 2	0	0
57	29	2	Total 2	Mg 2	0	0
57	78	2	Total 2	Mg 2	0	0
57	J8	2	Total 2	Mg 2	0	0
57	1G	72	Total 72	Mg 72	0	0
57	4E	1	Total 1	Mg 1	0	0
57	11	3	Total 3	Mg 3	0	0
57	1H	444	Total 444	Mg 444	0	0
57	88	1	Total 1	Mg 1	0	0
57	14	327	Total 327	Mg 327	0	0
57	3E	1	Total 1	Mg 1	0	0
57	55	1	Total 1	Mg 1	0	0
57	3L	2	Total 2	Mg 2	0	0
57	41	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	2L	2	Total	Mg	0	0
			2	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	32	1	Total	Zn	0	0
			1	1		
58	3E	1	Total	Zn	0	0
			1	1		
58	5I	1	Total	Zn	0	0
			1	1		
58	5A	1	Total	Zn	0	0
			1	1		
58	G8	1	Total	Zn	0	0
			1	1		
58	C5	1	Total	Zn	0	0
			1	1		

- Molecule 59 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	13	144	Total	O	0	0
			144	144		
59	3E	2	Total	O	0	0
			2	2		
59	1I	1	Total	O	0	0
			1	1		
59	3I	2	Total	O	0	0
			2	2		
59	5I	2	Total	O	0	0
			2	2		
59	2K	6	Total	O	0	0
			6	6		
59	4K	2	Total	O	0	0
			2	2		
59	1H	933	Total	O	0	0
			933	933		
59	16	22	Total	O	0	0
			22	22		
59	11	11	Total	O	0	0
			11	11		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	21	3	Total 3	O 3	0	0
59	31	9	Total 9	O 9	0	0
59	78	6	Total 6	O 6	0	0
59	D8	1	Total 1	O 1	0	0
59	F8	2	Total 2	O 2	0	0
59	G8	2	Total 2	O 2	0	0
59	I8	5	Total 5	O 5	0	0
59	J8	1	Total 1	O 1	0	0
59	L8	1	Total 1	O 1	0	0
59	P8	2	Total 2	O 2	0	0
59	Q8	1	Total 1	O 1	0	0
59	1G	48	Total 48	O 48	0	0
59	14	592	Total 592	O 592	0	0
59	19	8	Total 8	O 8	0	0
59	29	5	Total 5	O 5	0	0
59	39	4	Total 4	O 4	0	0
59	25	6	Total 6	O 6	0	0
59	35	2	Total 2	O 2	0	0
59	55	3	Total 3	O 3	0	0
59	75	1	Total 1	O 1	0	0
59	A5	1	Total 1	O 1	0	0

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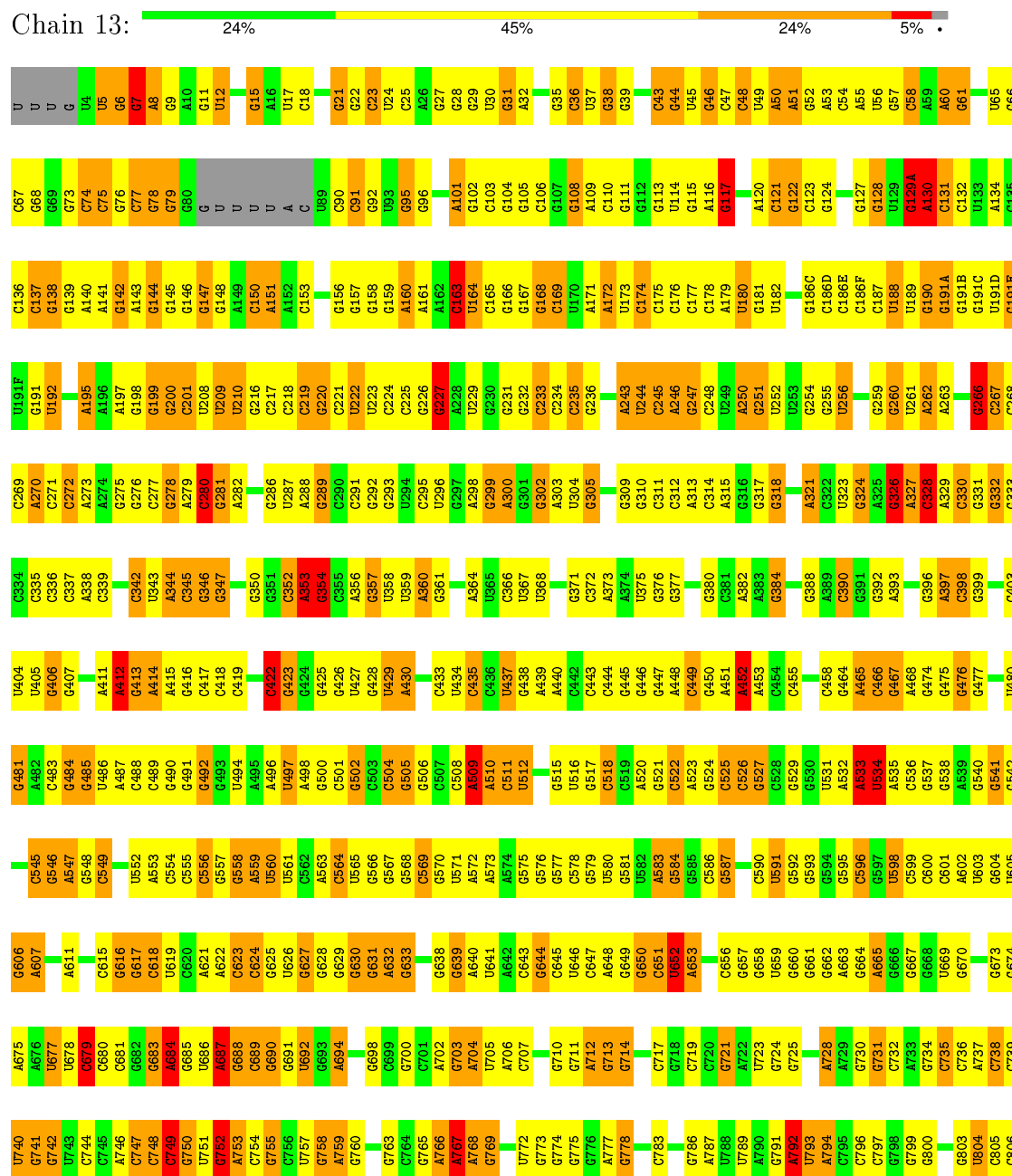
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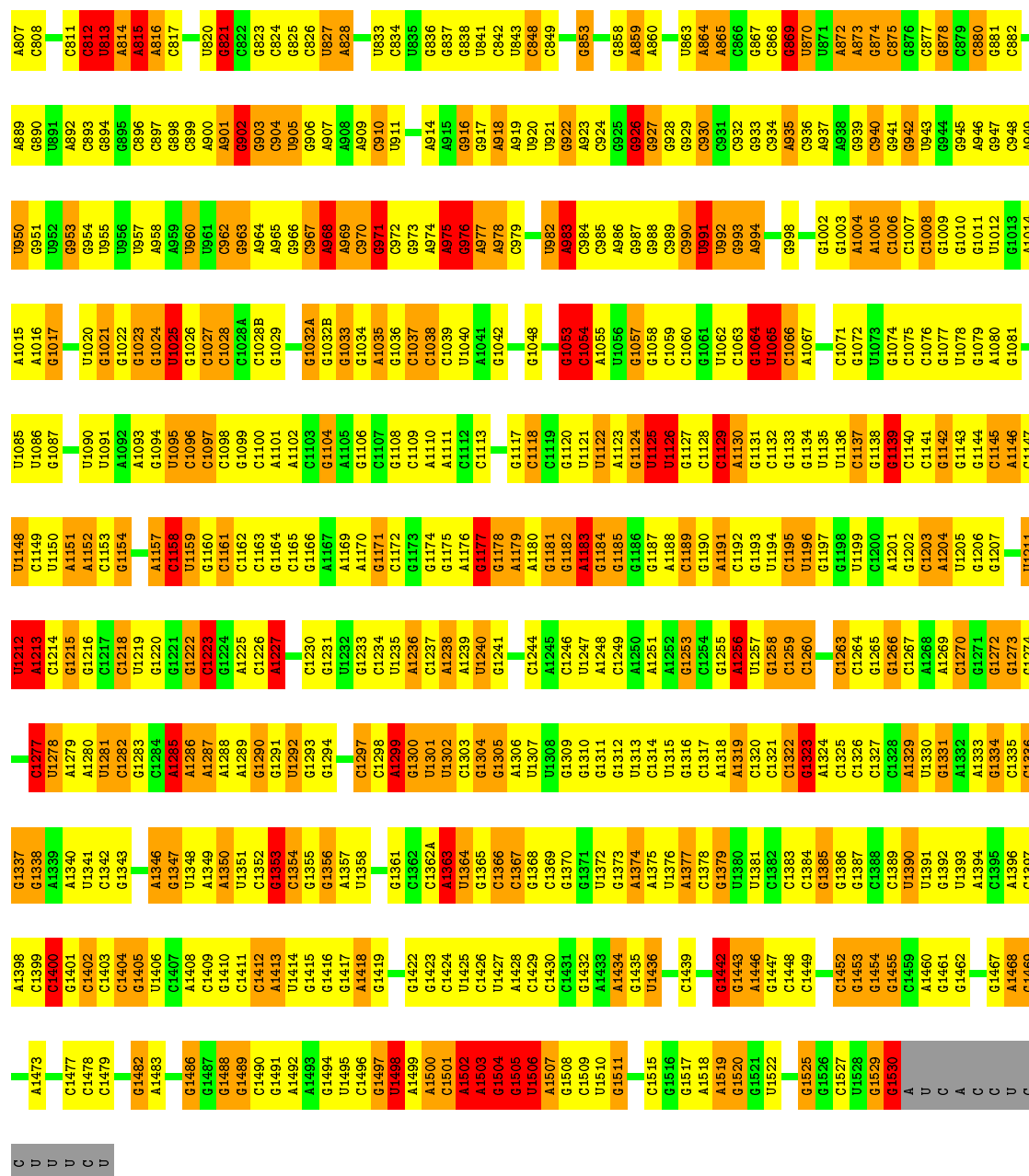
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	H5	2	Total	O	0	0
			2	2		
59	L5	1	Total	O	0	0
			1	1		
59	M5	1	Total	O	0	0
			1	1		

3 Residue-property plots

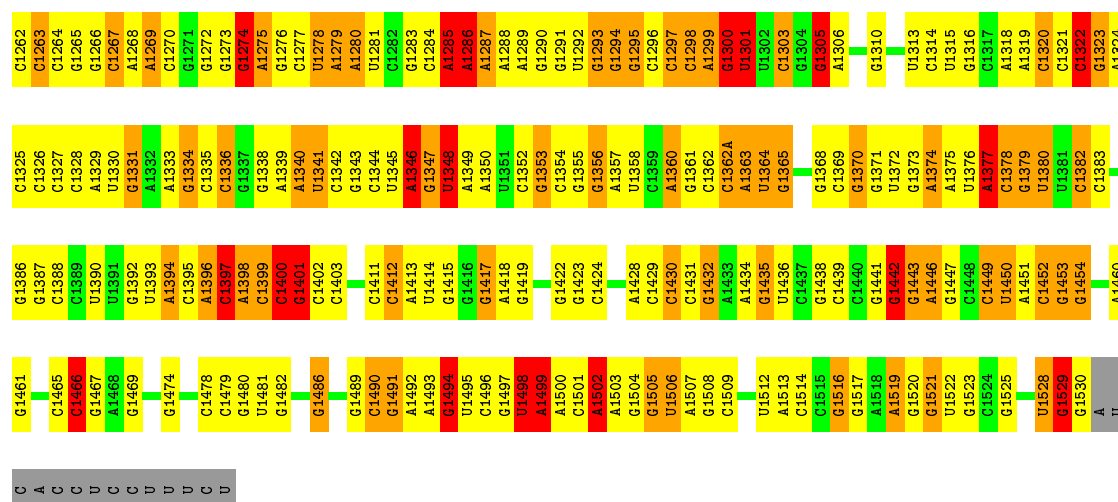
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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

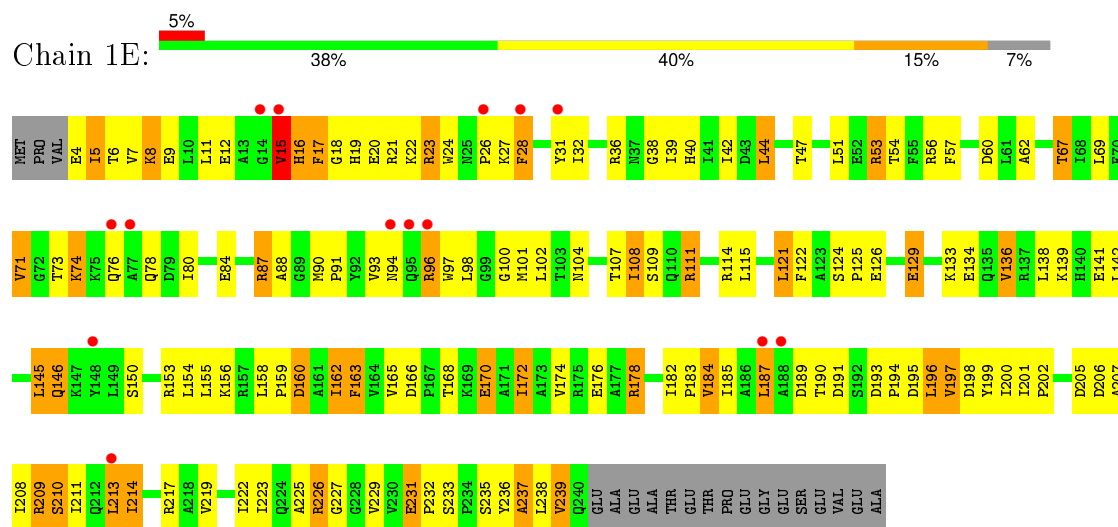




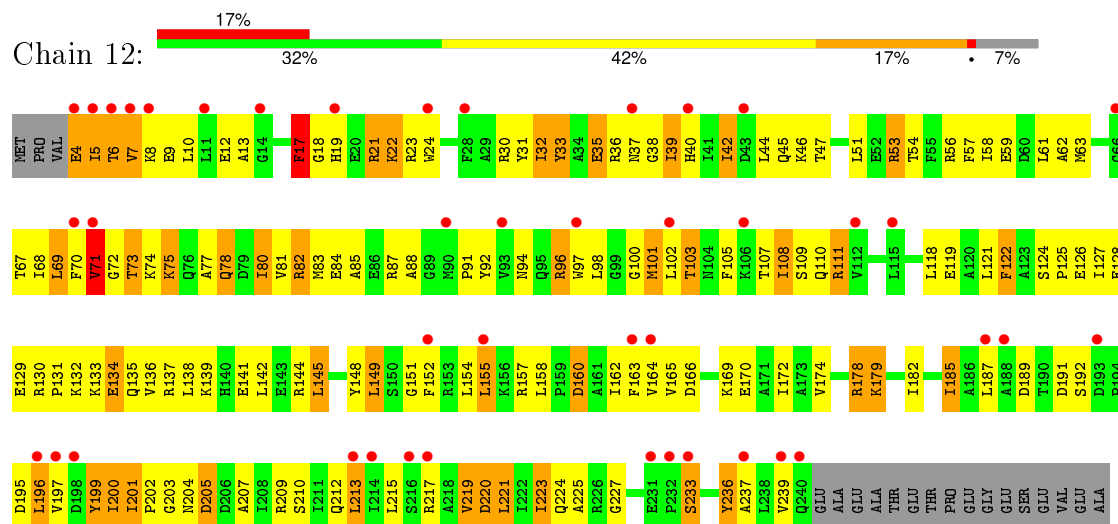
A1201	G1138	G1072	G1013	U952	G886	C912	G741	G674	G604	G541	A478	C330	A263	G191C
G1202	G1189	U1073	A1014	G953	G890	U913	G742	A675	U605	G542	C479	G331	U264	U191D
C1203	G1074	G1074	A1015	G954	U891	A814	U743	A676	G606	G406	U480	G332	G265	G191E
A1204	C1141	C1075	A1016	U955	G892	A815	G744	U677	A607	G407	G481	G333	G266	U191F
G1206	G1142	U1078	G1017	U956	A893	A816	G745	G746	A608	A408	A482	C334	G267	G191
G1207	G1143	G1079	C1018	U957	G894	C917	A746	G681	C612	A547	C483	C335	U192	U192
C1208	G1039	U1080	G1019	A958	G894	G818	G747	G682	G612	G548	G484	C336	C271	C193
C1209	A1146	G1081	U1020	A959	G895	A819	C748	G683	C615	G549	G485	C337	C272	C194
G1210	C1147	G1082	G1023	U960	C896	U820	C749	A684	C616	C550	U486	A338	C273	A195
C1211	U1083	U1083	G1024	U961	C897	G821	G750	G685	G616	U551	A487	C339	A274	A196
A1212	G1148	G1083	G1025	C962	C898	C322	G751	U686	G617	U552	G488	U340	G275	A197
A1213	G1084	U1025	U1025	G963	C899	G823	G752	A687	C618	A553	C489	C341	G276	G198
A1214	U1085	G1026	G1026	G964	A900	C824	A753	G688	U619	C554	G490	C342	G277	G199
C1214	A1151	C1027	C1027	A965	G900	G825	C754	C689	C620	C555	G491	C342	G278	G200
G1215	G1086	G1087	U1087	G966	G903	C826	G755	C690	A621	C556	G492	C345	A279	C201
C1216	C1152	C1087	C1028	C967	G904	C826	G756	G690	A622	C557	G492	C346	C280	U208
C1218	G1154	U1091	C1028A	G968	G904	U827	C756	G691	G623	C558	A495	A349	G281	U209
C1218	G1154	A1092	G1028B	A968	G905	A828	G757	G692	G624	A559	A496	A349	G282	U210
U1219	G1156	G1093	G1029	G969	G906	G829	U757	U692	G625	U560	U497	G350	C283	G216
G1220	A1157	G1094	C1030	C970	A907	G830	G758	A694	U626	U561	A498	G351	G284	C217
G1221	C1188	U1095	A1032	G971	A908	U831	G763	A696	U627	C562	G500	C352	G285	C218
G1222	U1159	G1096	G1032A	G973	C910	G832	G764	U697	G628	A563	C501	C353	G286	C219
C1223	G1160	C1097	G1032B	A974	U911	G698	A766	G698	G629	C564	G502	G354	U287	G220
G1224	C1161	G1098	G1033	A975	C912	U841	A767	C699	G630	U565	C503	G357	A288	C221
A1225	C1162	G1099	G1034	G976	A913	C842	A768	G700	G631	C566	C504	U358	G289	U222
C1226	G1163	C1100	A1035	A977	A914	U843	G768	C701	A632	C567	G505	U358	U294	U223
A1227	G1164	A1101	G1036	A978	A915	C948	C770	A704	G633	C568	G506	U359	C224	C224
C1228	C1102	C1037	C1037	G979	G916	C949	G771	U704	G634	C569	C507	A360	C225	C225
A1229	C1103	G1038	C1038	C980	G917	U772	U772	G707	G635	C570	C508	G361	G226	G226
C1230	A1169	G1039	G1039	U981	A918	G855	G773	G707	G636	U571	A509	G362	G227	G227
G1231	A1170	A1105	U1040	U982	A919	C856	G774	C708	G637	A572	A510	A363	A300	A228
U1232	G1171	G1108	A1041	A983	U920	C857	G775	G709	G638	A573	C511	A364	G301	U229
G1233	C1172	C984	G1042	C984	U921	G858	A777	G710	A642	C575	U512	A365	G302	G230
C1234	G1173	A1111	A1043	C985	G922	A859	C778	A712	G643	C576	C513	C366	A303	G231
U1235	C1174	C1111	G1044	A986	C924	G861	C779	G713	G644	C577	C514	U367	U304	G232
A1236	C1112	G1113	C1045	G987	C924	G862	A780	G713	G645	C578	U516	G371	G305	C233
C1237	C1113	G1114	A1046	U991	G925	C962	C783	G718	U646	C579	U517	C372	G306	C234
A1238	G1178	G1114	G1047	U992	G926	U863	G783	C719	C647	U580	C518	A373	G307	C235
A1239	A1179	C1115	G1048	U993	G927	A864	C784	C720	A648	C581	C519	A374	C308	G236
U1240	G1180	C1116	U1049	A994	C932	C866	G785	G721	G649	G584	A520	U375	G309	G237
G1241	G1181	G1117	G1050	A995	C932	G867	G786	A722	G650	G585	G521	U376	G310	C242
C1242	C1182	C1118	C1051	C995	C933	C868	A787	U723	C651	C586	C522	G377	C312	A243
G1243	A1183	U1053	U1053	A996	C934	C968	C788	G725	U652	C587	A523	A382	C313	U244
C1244	G1184	U1121	G1053	U997	A935	C969	U788	G726	A653	C588	C526	A383	C314	C245
A1245	G1185	U1122	A1054	G998	C936	U870	U789	G726	G658	C589	G527	A384	A246	G247
C1246	G1186	A1123	A1055	C998A	A937	U871	G790	G727	U659	C590	C528	C385	G317	A250
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A1248	A1188	U1125	G1057	A1000	C939	A873	U792	A728	G661	C592	G530	G388	C320	G254
C1249	C1189	U1126	G1058	G1001	C940	G874	A794	A729	G662	C593	U531	A389	A321	G255
A1250	G1190	G1127	C1059	G1002	G941	C875	C794	G730	G663	C594	A532	A390	C322	U256
A1251	A1191	C1128	U1062	G1003	G942	G876	C797	G731	G664	C596	A533	C391	U323	U257
C1252	C1192	C1129	C1063	A1004	U943	C877	C797	G732	A665	C597	A534	G392	G324	G258
G1255	G1193	A1130	G1064	C1005	G944	G878	A733	G733	G666	U598	C336	A393	A325	G259
A1256	U1194	G1132	U1065	C1006	G945	C880	U801	G734	G667	C599	A467	G394	G326	G260
U1257	G1196	G1133	C1066	C1007	A946	G881	A802	C735	G668	C600	G537	G396	A327	U261
G1258	G1197	G1134	A1067	G1008	G947	G882	G803	C736	U669	C601	G538	A397	C328	C262
C1259	G1198	U1135	G1068	G1009	C948	C883	U804	A737	G670	A602	G539	C398	G263	A262
A1261	U1199	U1136	C1071	G1010	A949	C884	C805	C738	G671	G603	G540			
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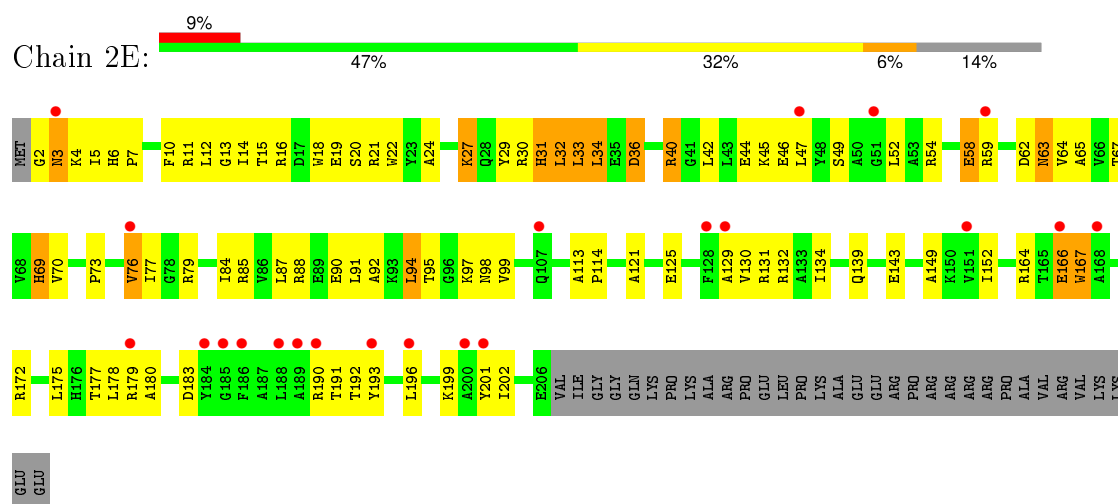
• Molecule 2: 30S ribosomal protein S2



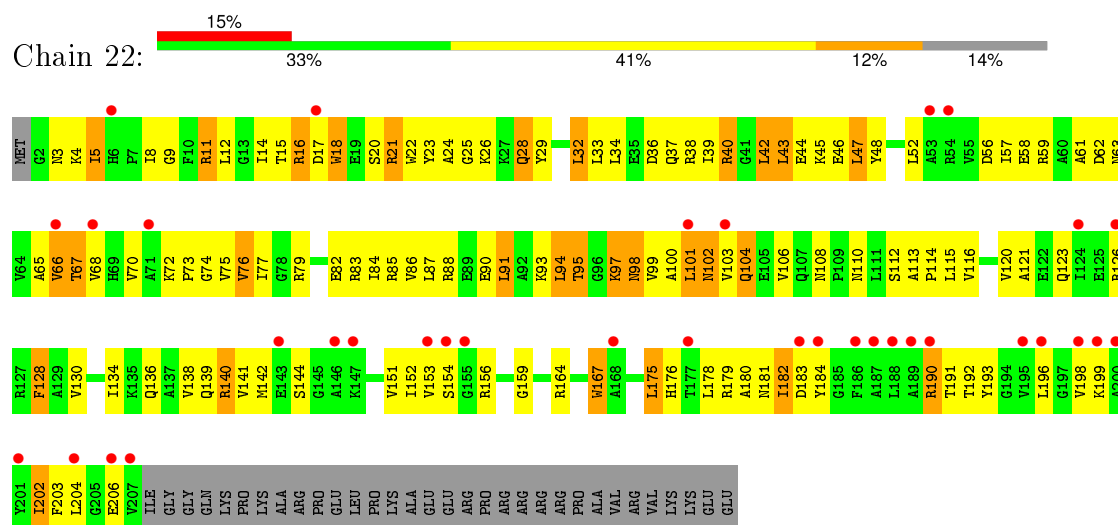
• Molecule 2: 30S ribosomal protein S2



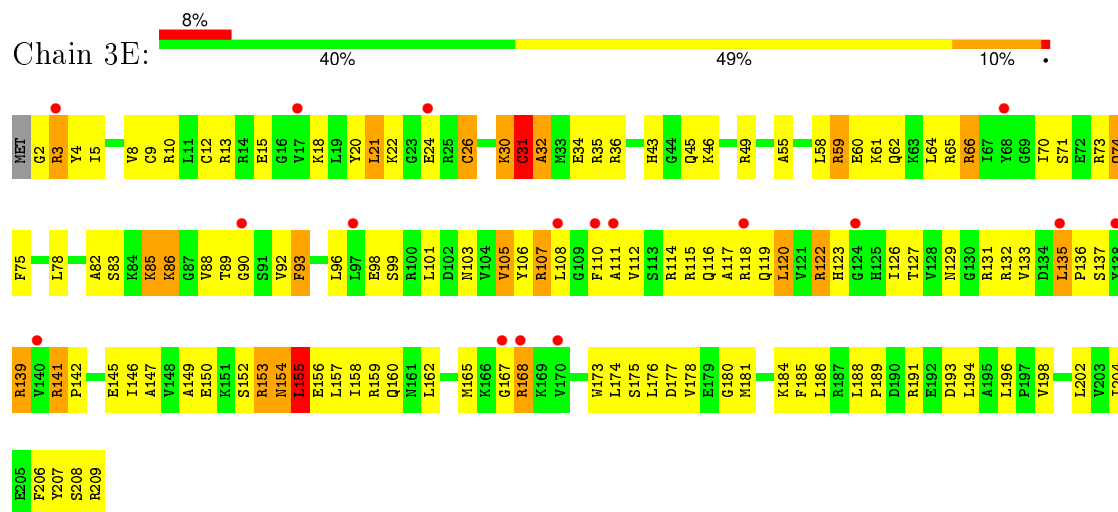
• Molecule 3: 30S ribosomal protein S3



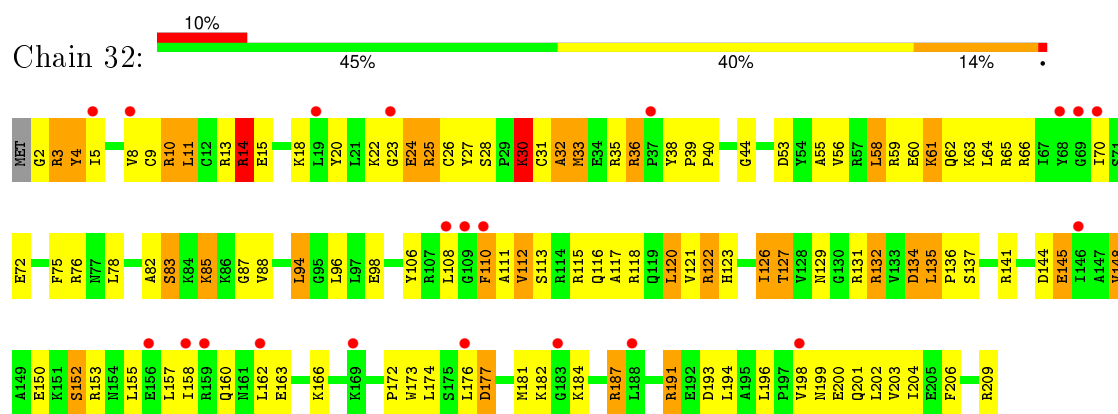
• Molecule 3: 30S ribosomal protein S3



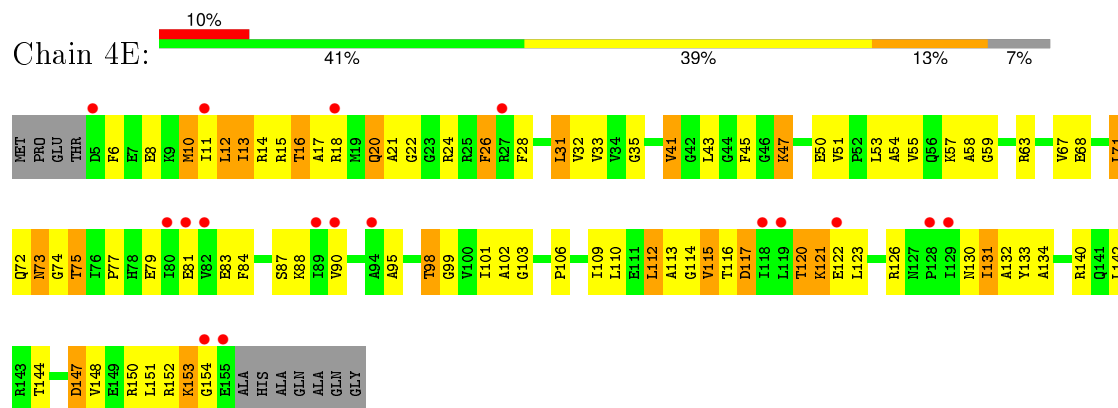
• Molecule 4: 30S ribosomal protein S4



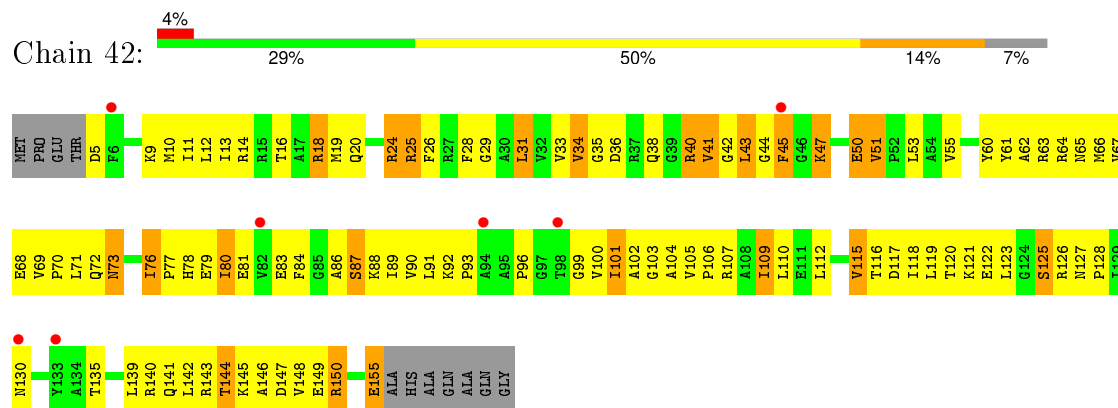
• Molecule 4: 30S ribosomal protein S4



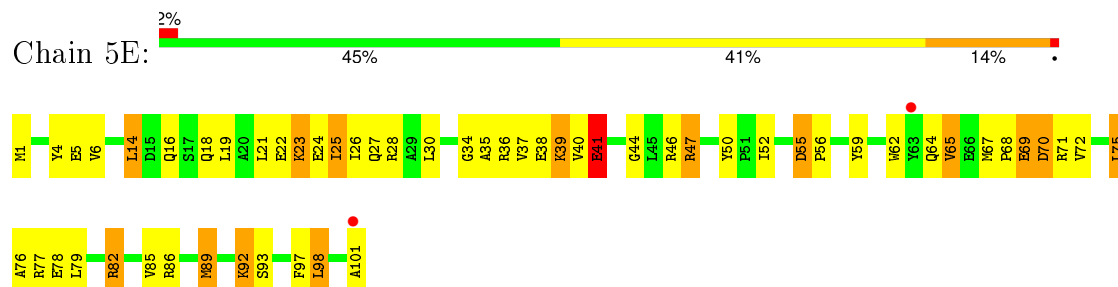
• Molecule 5: 30S ribosomal protein S5



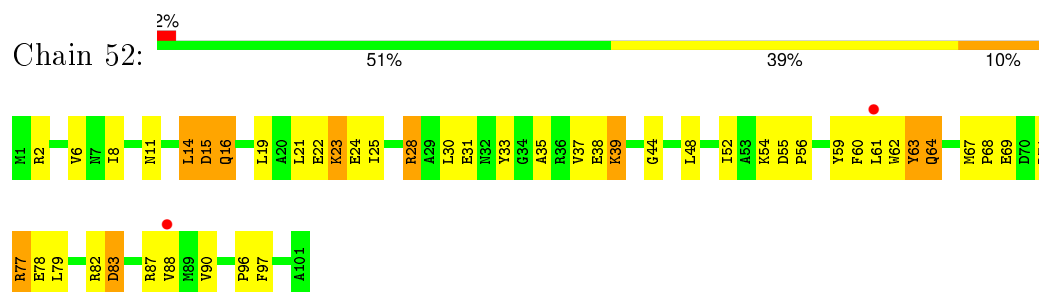
• Molecule 5: 30S ribosomal protein S5



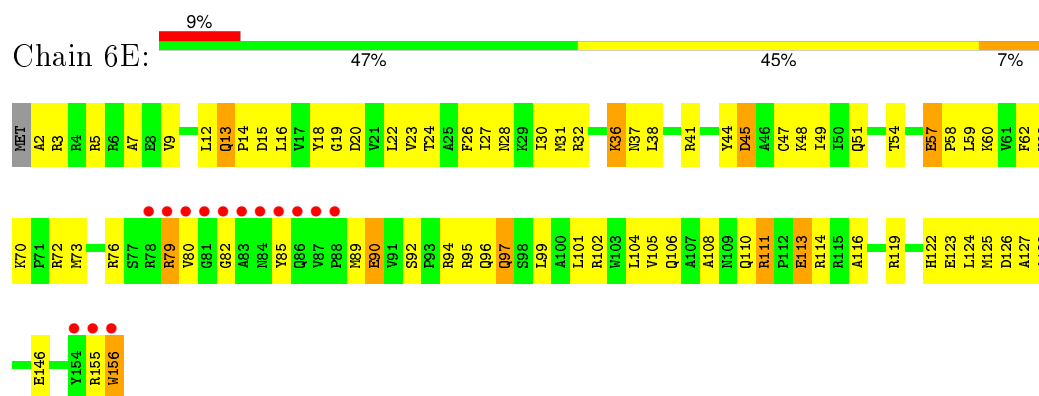
• Molecule 6: 30S ribosomal protein S6



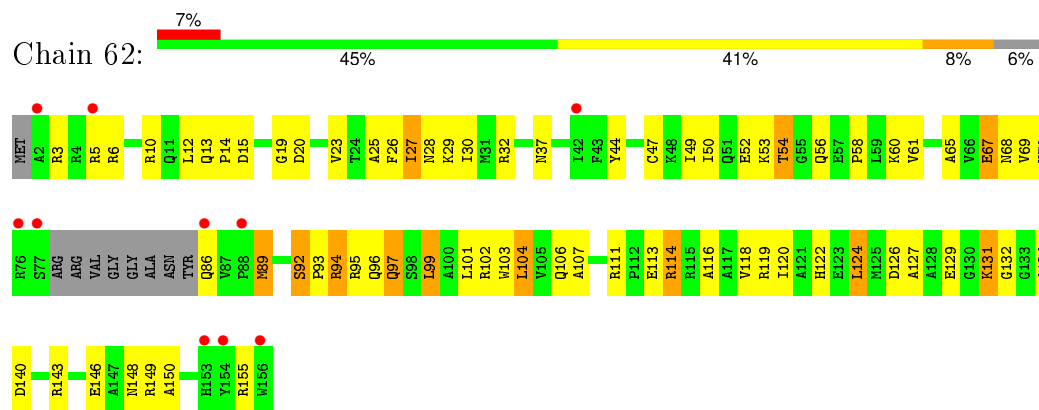
- Molecule 6: 30S ribosomal protein S6



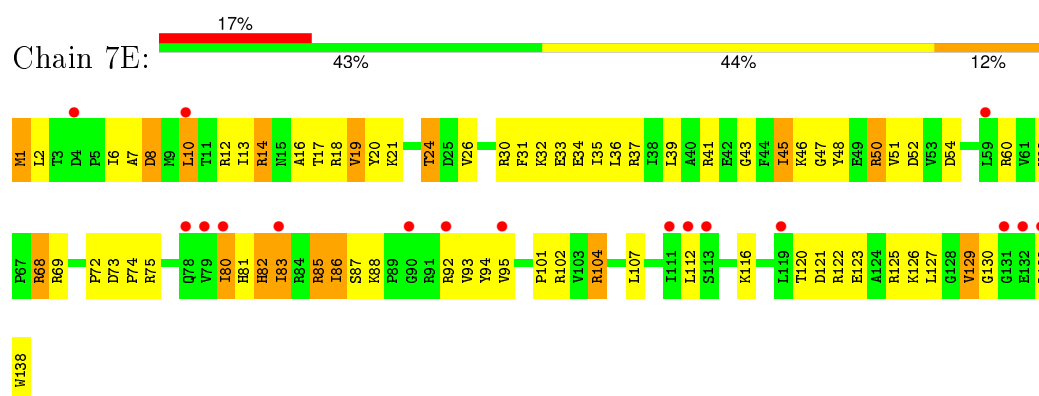
- Molecule 7: 30S ribosomal protein S7



- Molecule 7: 30S ribosomal protein S7



- Molecule 8: 30S ribosomal protein S8



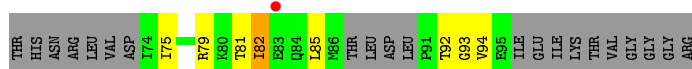
- Chain 72:
-
- | Category | Percentage |
|----------|------------|
| 4% | |
| 43% | |
| 45% | |
| 12% | |

- Chain 8E:
-
- 35% 47% 17%
- MET E2 Q3 Y4 Y5 G6 T7 G8 R9 R10 A13 V14 V17 F18 I19 R20 P21 N23 G24 K25 V26 N29 G30 Q31 D32 F33 N34 E35 Y36 F37 Q38 G39 L40 V41 R42 A43 V44 A45 A46 L47 E48 P49 L50 R51 A52 V53 D54 A55 F59 D60 A61 Y62 I63 T64 V65

- Chain 82:
-
- 4% 36% 52% 10% ..

- Chain 1I:
-
- Sequence logo for Chain 1I. The y-axis represents information content in bits. The x-axis shows positions 1 to 100. A bar chart at the top indicates the percentage of positions with conservation greater than 1.9 bits: 19% (red), 39% (green), 40% (yellow), 15% (orange), and 6% (grey).

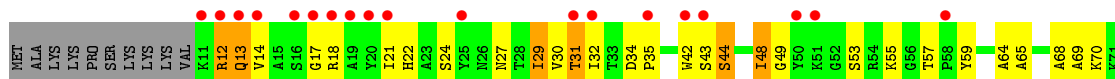
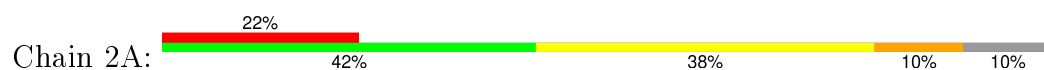
- Chain 1A:
-
- 5% 29% 26% 8% 37%
- MET PRO LYS ARG ILE LYS LEU ARG GLY F11 D12 H13 K14 T15 L16 D17 V24 E25 R28 R29 S30 G31 ALA GLN VAL S35 G36 P37 I38 P39 L40 P41 T42 R43 V44 ARG ARG ARG PHE PHE T48 V49 I50 R51 G52 P53 F54 R55 H56 K57 D58 S59 R60 E61 H62 F63 E64 LEU L67



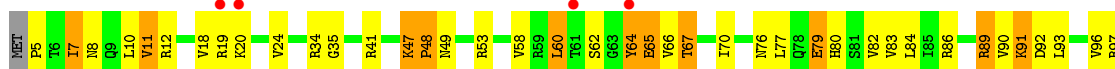
- Molecule 11: 30S ribosomal protein S11



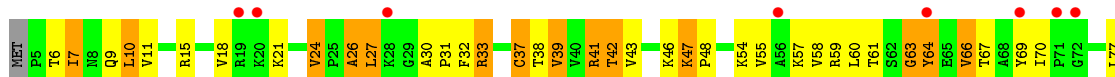
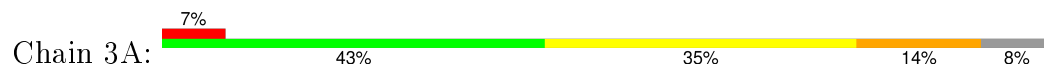
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



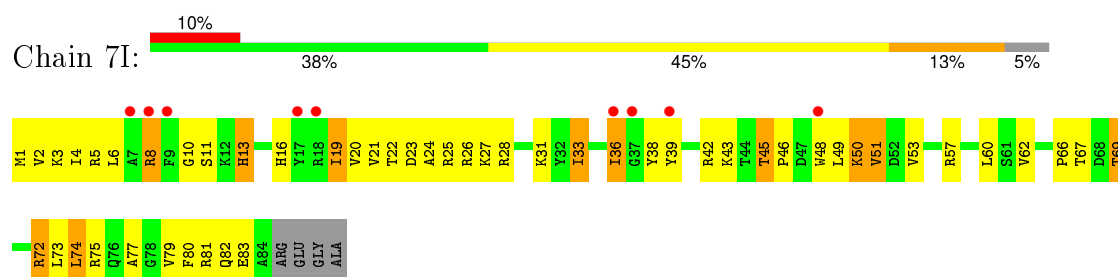
- Molecule 12: 30S ribosomal protein S12



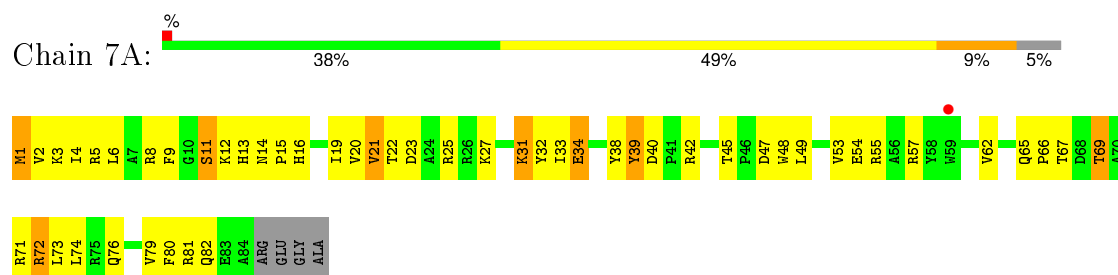
- Molecule 13: 30S ribosomal protein S13



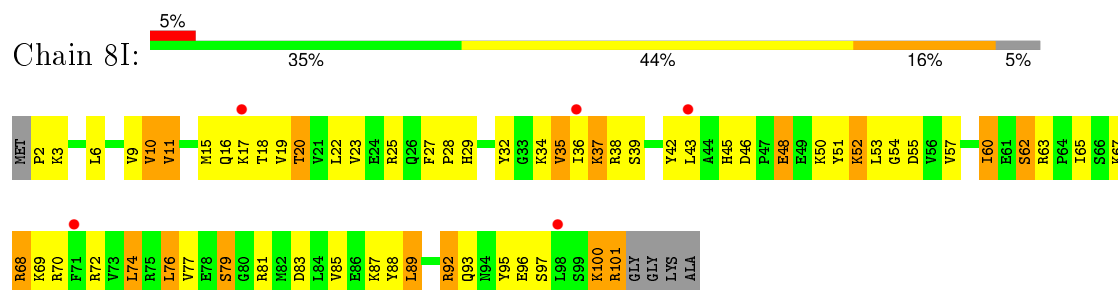
- Molecule 16: 30S ribosomal protein S16



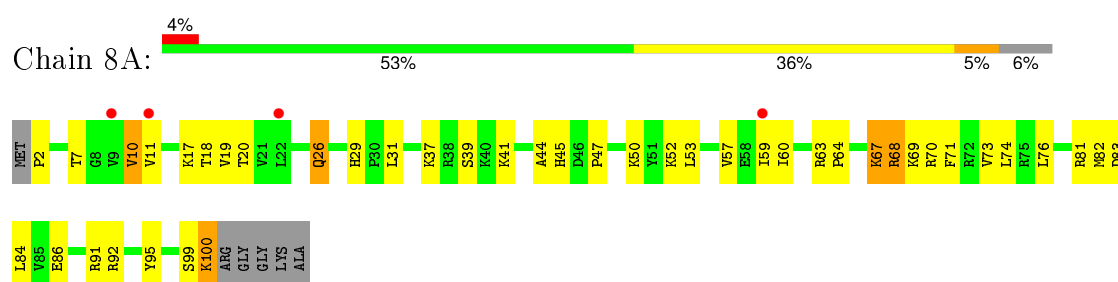
- Molecule 16: 30S ribosomal protein S16



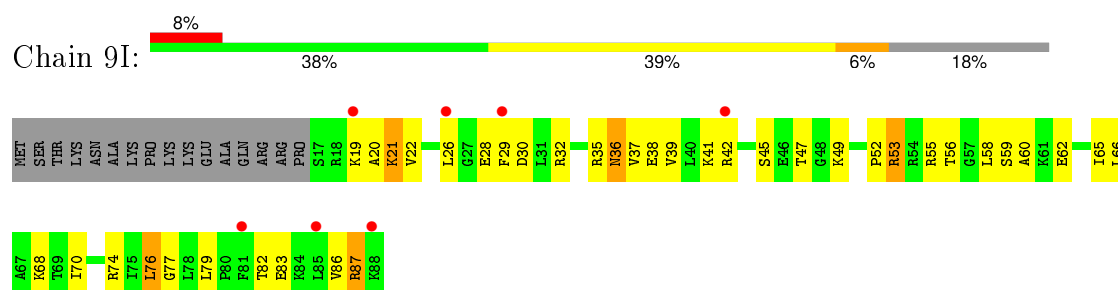
- Molecule 17: 30S ribosomal protein S17



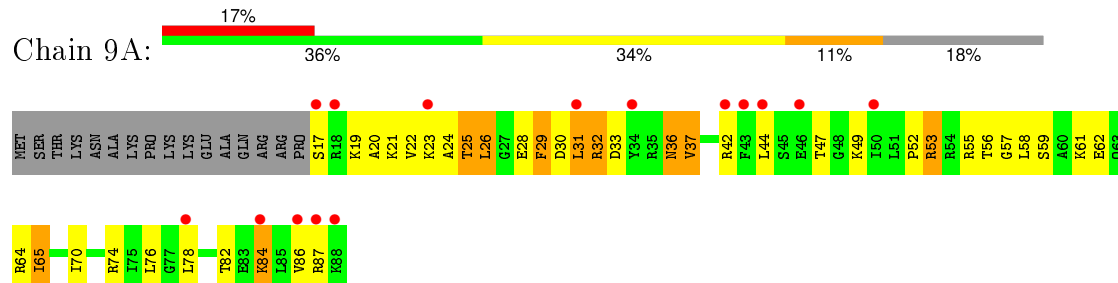
- Molecule 17: 30S ribosomal protein S17



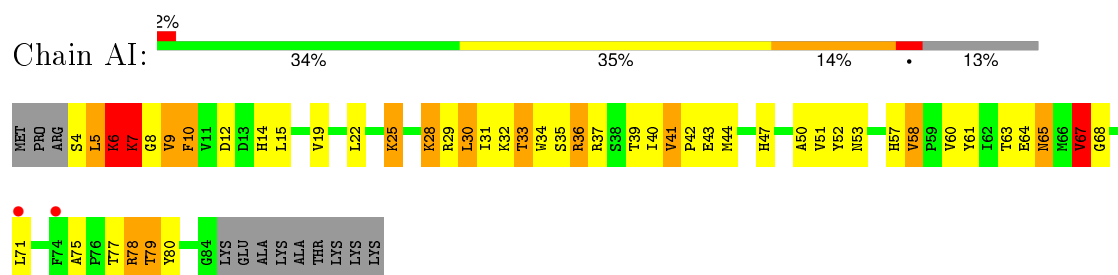
- Molecule 18: 30S ribosomal protein S18



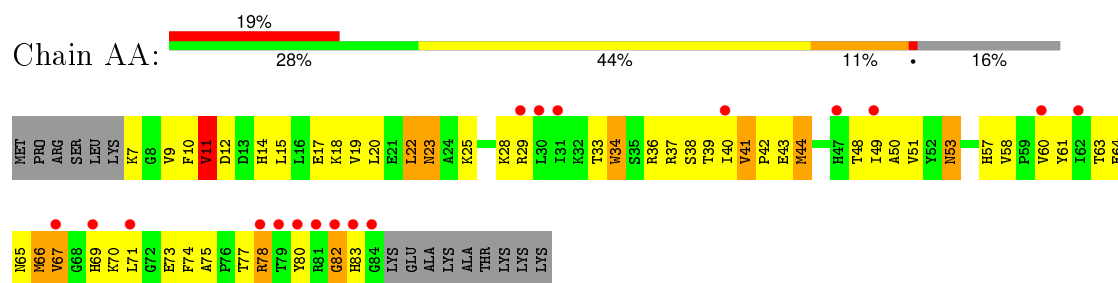
- Molecule 18: 30S ribosomal protein S18



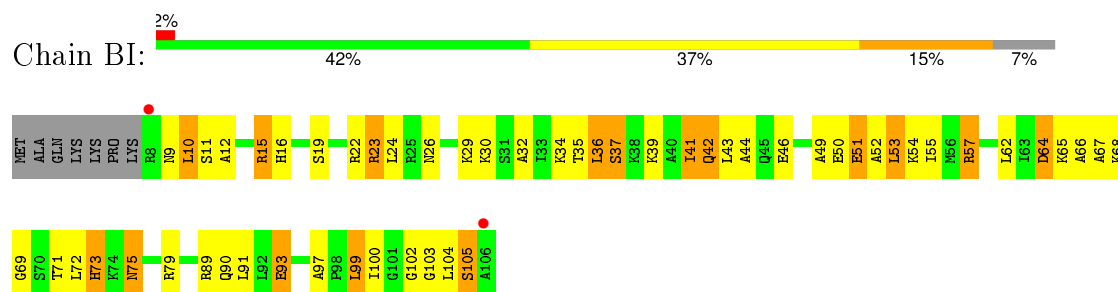
- Molecule 19: 30S ribosomal protein S19



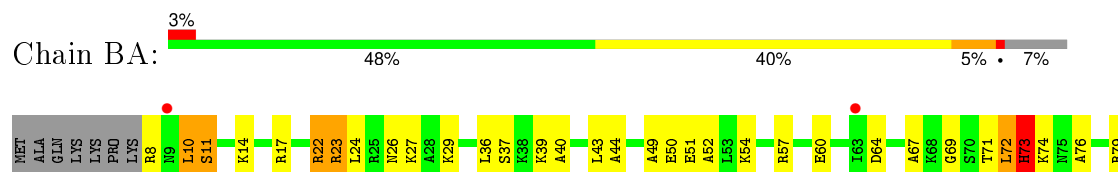
- Molecule 19: 30S ribosomal protein S19

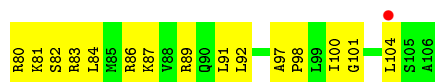


- Molecule 20: 30S ribosomal protein S20

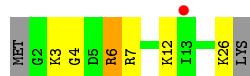


- Molecule 20: 30S ribosomal protein S20

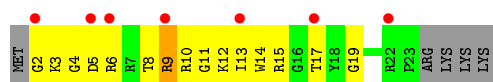




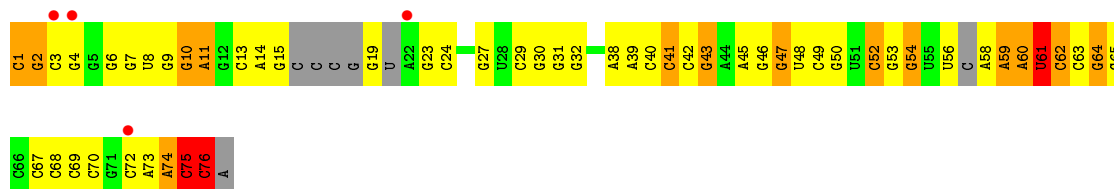
- Molecule 21: 30S ribosomal protein Thx



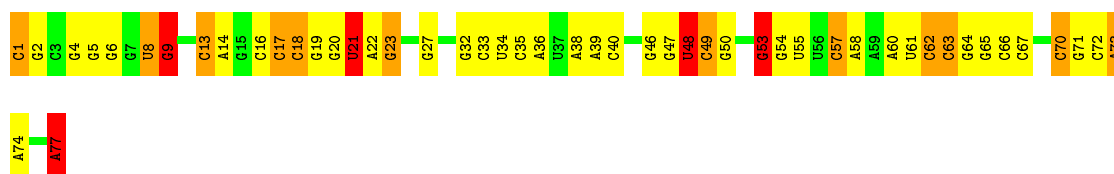
- Molecule 21: 30S ribosomal protein Thx



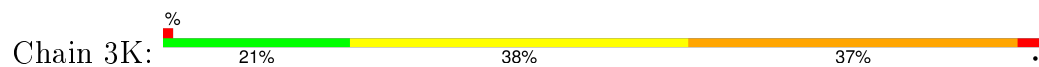
- Molecule 22: tRNA-fMet



- Molecule 23: tRNA-fMet

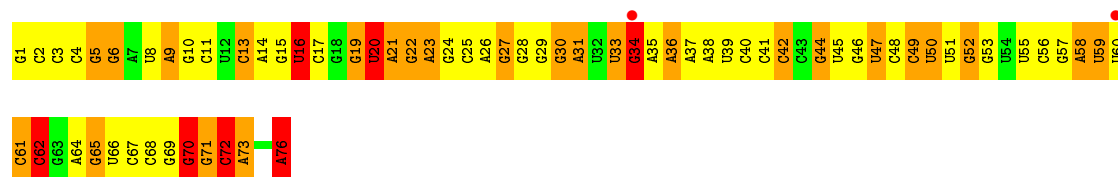


- Molecule 24: tRNA-Phe

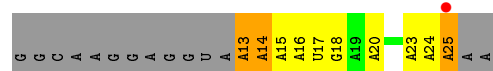
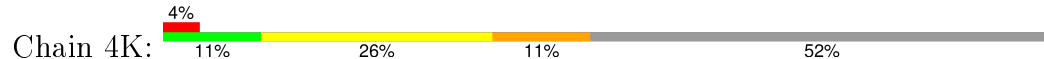


- Molecule 24: tRNA-Phe





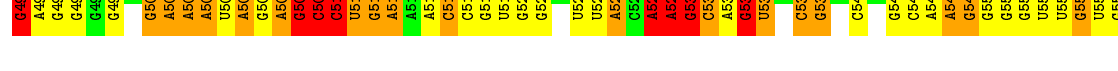
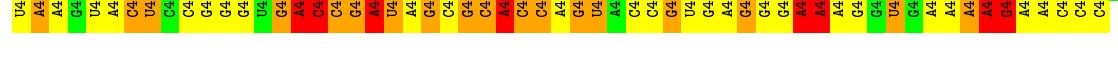
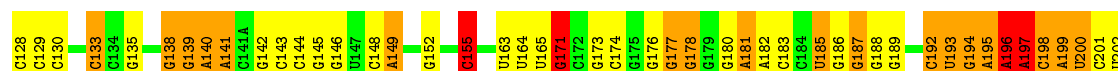
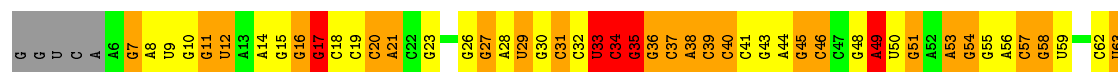
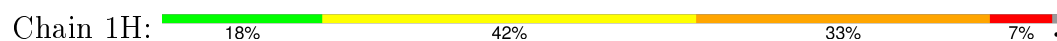
- Molecule 25: mRNA



- Molecule 25: mRNA

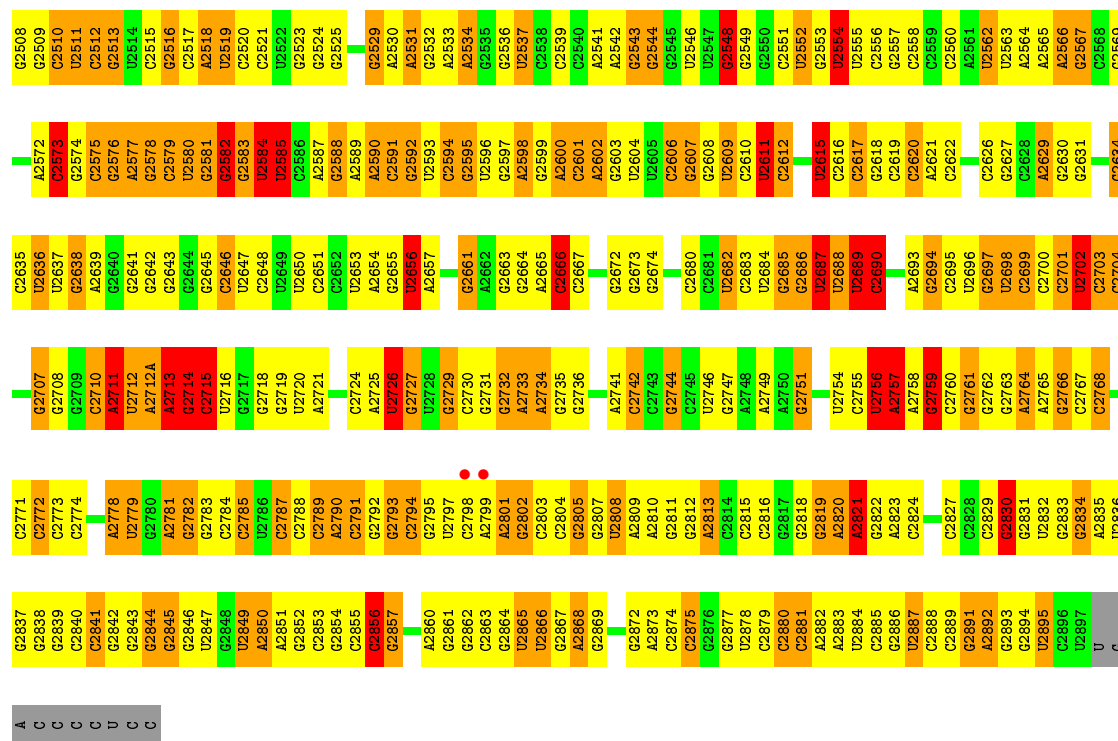


- Molecule 26: 23S ribosomal RNA



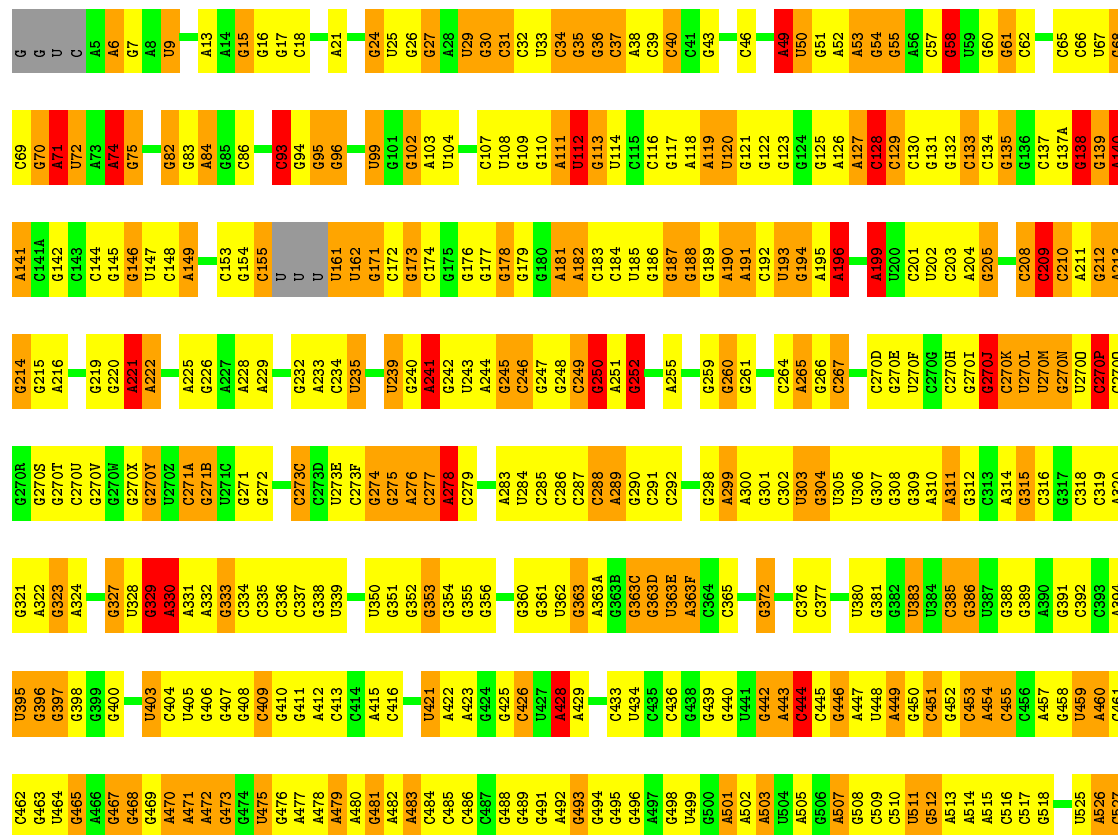






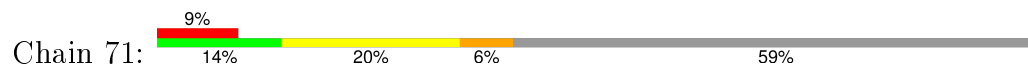
• Molecule 26: 23S ribosomal RNA

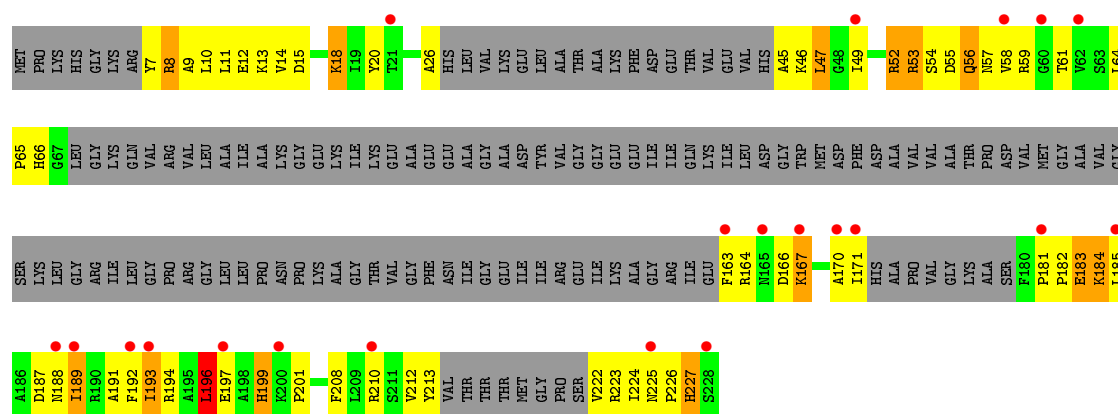
Chain 14: 21% 42% 29% 7%.



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G1388	U1326	A1265	U1205	C1140	A1073	U1012	A953	A890	U827	C766	G699	G654D	G598	A529
G1389	C1327	G1266	G1206	U1141	C1074	C1013	G954	G892	U828	U767	A699	C654E	G599	A530
U1390	G1328	U1267	C1207	U1142	C1075	U1014	C955	C893	G829	G768	G700	C654F	G600	C531
U1391	A1329	A1268	G1208	A1143	C1076	G1015	G956	G894	G830	G769	G701	G654G	G601	A532
A1392	C1330	A1269	G1209	A1144	A	G1016	A957	U895	G831	G770	G702	G654H	G602	G533
A1393	A1331	A1270	A1210	G1144	U	G1017	U958	A896	G832	G771	U703	C654I	G603	U534
U1394	C1332	G1271	U1211	C1145	C	G1018	A959	C897	U833	C772	G704	A654J	A604	C535
C1333	C1333	A1272	G1212	C1146	U	U1019	A960	C898	C834	U773	A705	C654K	G605	A536
A1336	A1336	A1273	A1213	C1147	U	A1020	C961	A899	A835	A774	A706	C654L	U606	C537
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G1400	G1339	G1277	G1218	G1151	A	G1024	C965	C903	U839	G778	G710	G654P	G609A	G545
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C1403	A1342	G1280	C1221	G1154	A	A1027	G968	G906	G843	A781	G713	G654S	G612	A548
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G1410	A1349	A1287	G1228	G1162	A1095	G1034	C974A	U913	C850	A788	C720	C658	G618A	A566
G1411	C1350	U1288	G1229	G1163	A1096	U1035	G975	C914	U851	A789	C721	C659	G619	U557
A1412	C1351	C1289	G1230	G1164	U1097	G1036	C976	C915	G852	C790	A722	G660	G620	G558
G1413	U1352	C1290	G1231	U1165	A1098		G977	G916	G853	C791		C661	A621	G559
C1414	A1353	G1291	C1232	C1166	G1099	G1037	G978	A917	G854	G792	G728	G662	A622	C560
U1415	A1354	U1292	G1233	G1167	C1100	C1040	G979	A918	G855	A793	G729	G663	G623	G561
G1416	G1355	A1293	G1234	G1168	U1101	G1041	A980	G919	C856	G794	C730	C664	C624	U562
C1417	G1356	G1294	C1235	G1169	C1102	G1042	A981	G920	C857	G795	C731	C665		G563
G1418	U1357	G1295	G1235	G1170	A1103	G1043	C982	G921	U858	C796	G732	G666	A627	C564
A1419	C1358	G1296	G1236	G1171	C1104	A1044	A983	U922	G859	C797	G733	U667	G628	C565
U1420	A1359	A1237	G1237	G1173	U1050	A1045	C984	C923	U860	G798	A734	G668	G630	U566
G1421	C1360	G1238	A1174	A1174		A1046	A985	C924	A861	G799	A735	A667	A567	
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G1423	C1363	U1240	G1176	A1176	G1110	A1048	G987	A926	A863	G802	C737	C671	A632	U569
G1424	G1364	A1241	A1177	A1177	A1111	C1049	A988	G928	C864	A802	C738	C672	A633	G570
G1425	A1365	A1242	C1178		G1112	A1050	G989	G929	C865		G739	C673	C634	A571
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A1427	C1367	G1244	C1180	C1180	G1114	C1052	C991	G932	C867	C907	G741	A675	G636	G573
C1428	G1368	C1304	C1181	C1181	G1115	C1053	C992	A933	U868	U807	A676	A637	A637	C574
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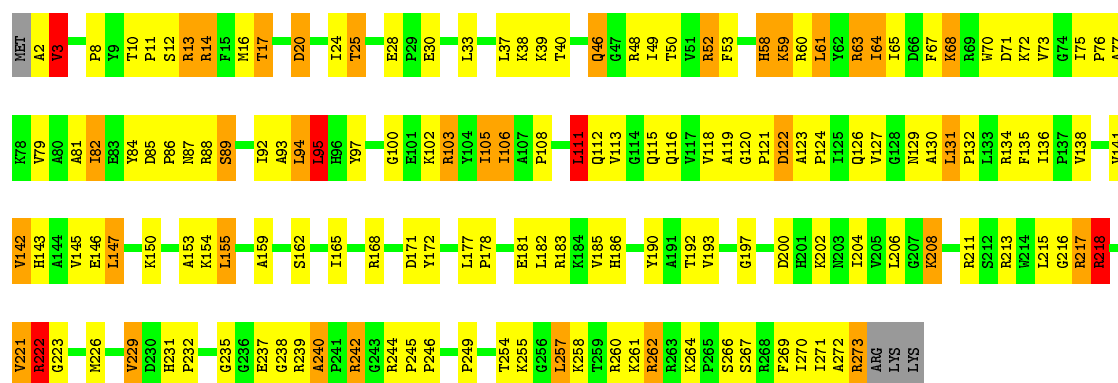
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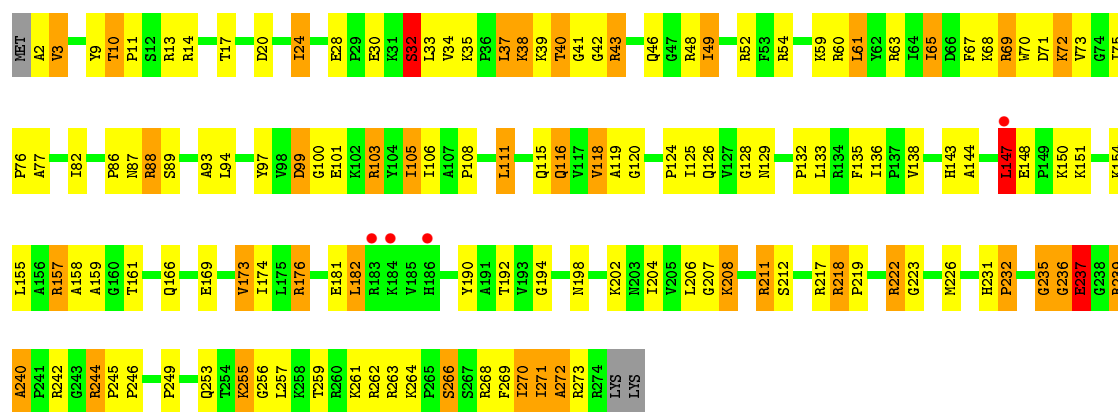
• Molecule 29: 50S ribosomal protein L2

Chain 11: 43% 42% 12% ..



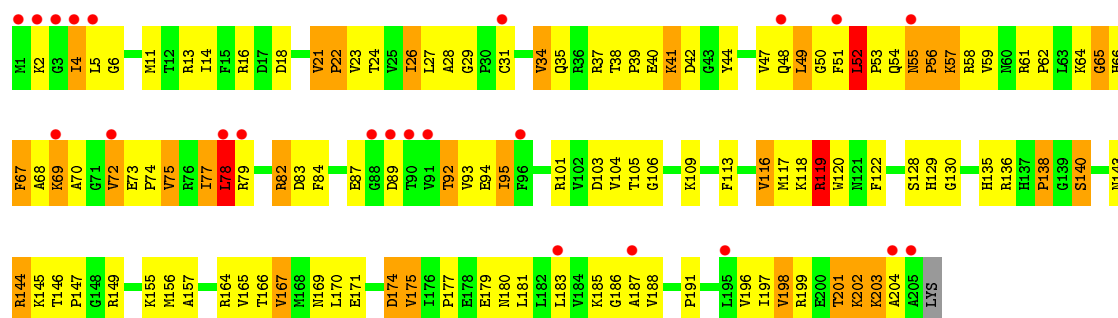
• Molecule 29: 50S ribosomal protein L2

Chain 19: 49% 35% 14% ..

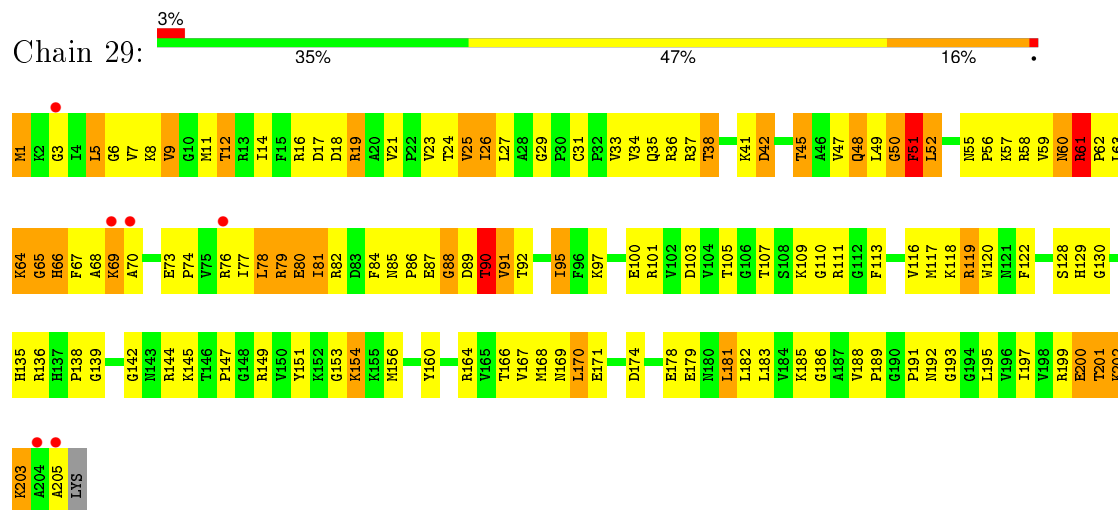


• Molecule 30: 50S ribosomal protein L3

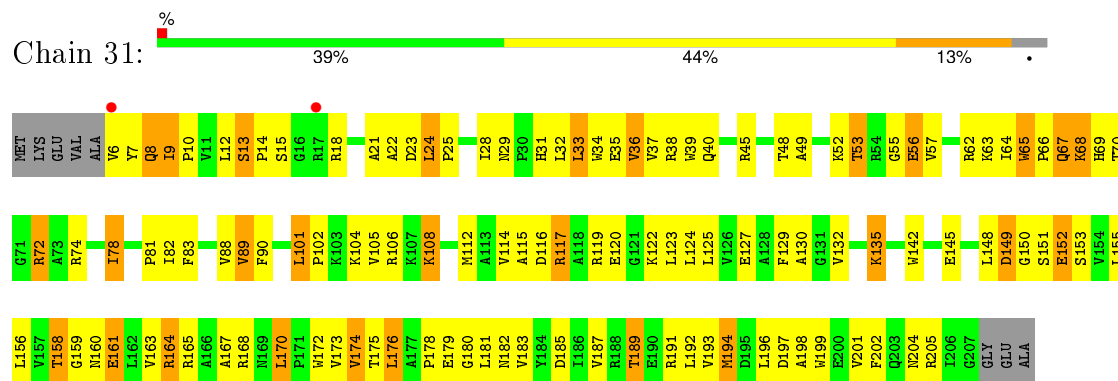
Chain 21: 11% 41% 43% 15% .



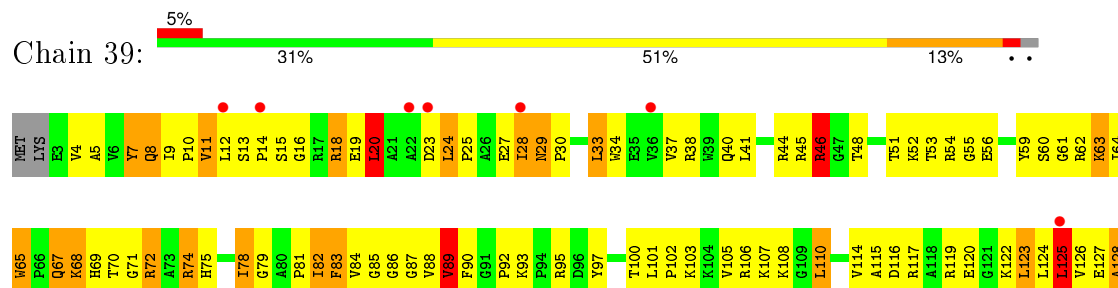
- Molecule 30: 50S ribosomal protein L3

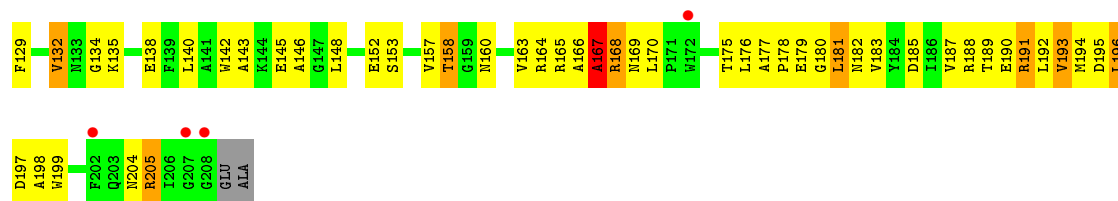


- Molecule 31: 50S ribosomal protein L4

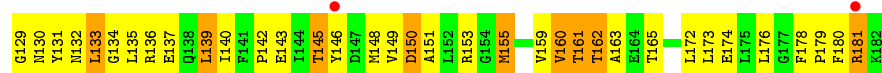
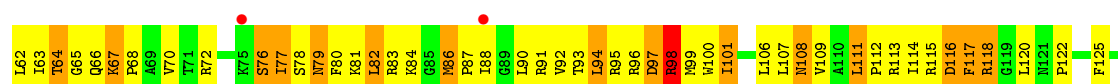


- Molecule 31: 50S ribosomal protein L4

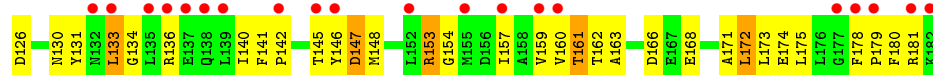
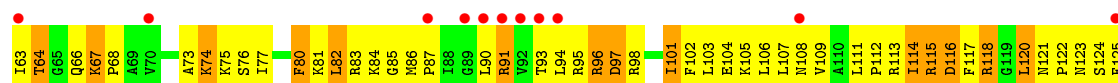




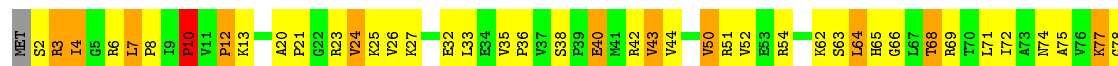
• Molecule 32: 50S ribosomal protein L5



• Molecule 32: 50S ribosomal protein L5

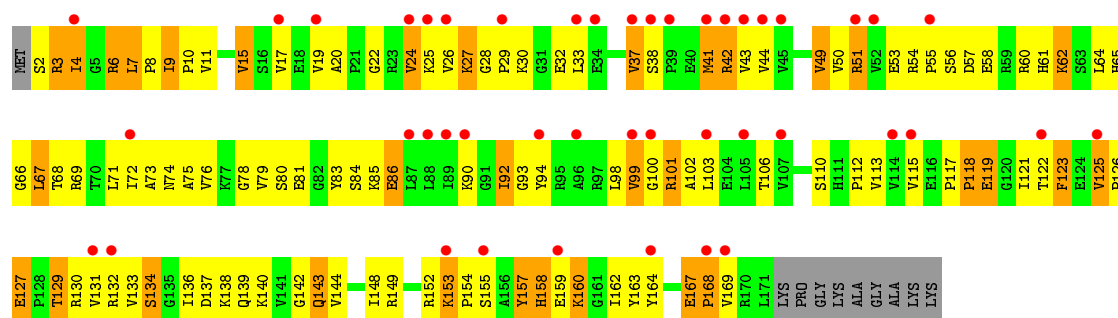


• Molecule 33: 50S ribosomal protein L6

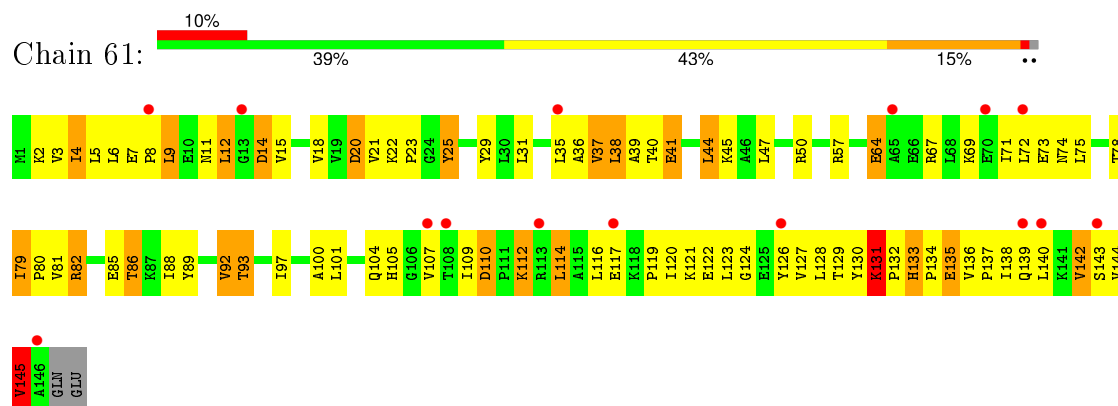


• Molecule 33: 50S ribosomal protein L6

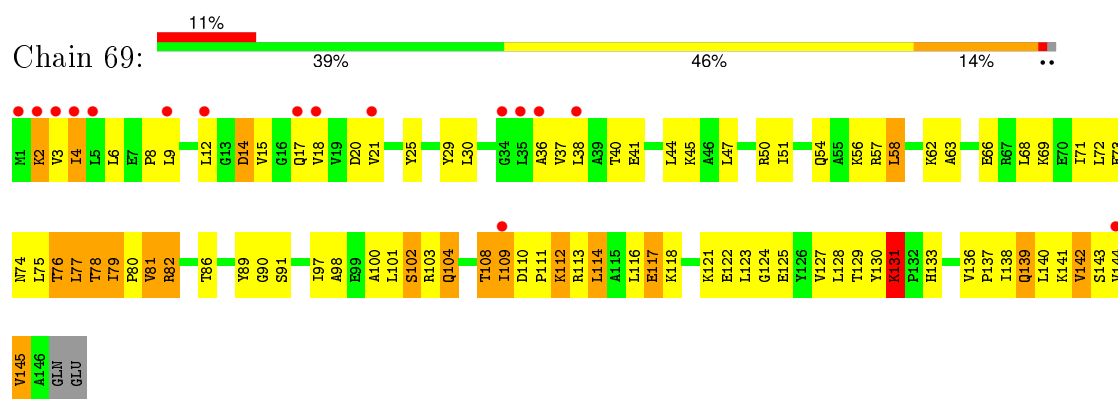




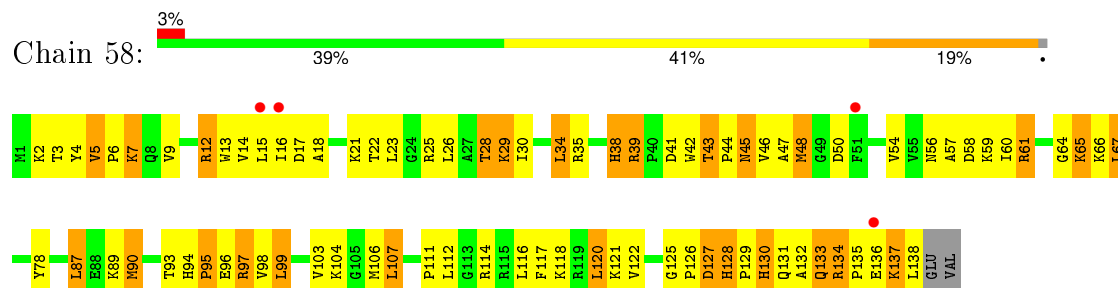
- Molecule 34: 50S ribosomal protein L9



- Molecule 34: 50S ribosomal protein L9

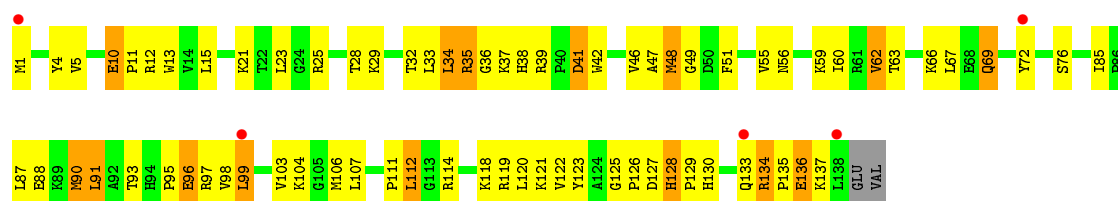


- Molecule 35: 50S ribosomal protein L13

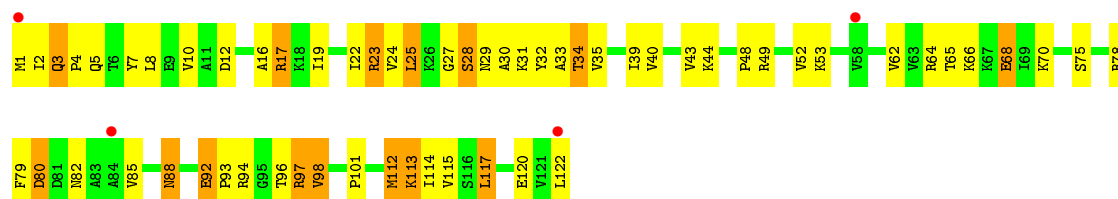


- Molecule 35: 50S ribosomal protein L13

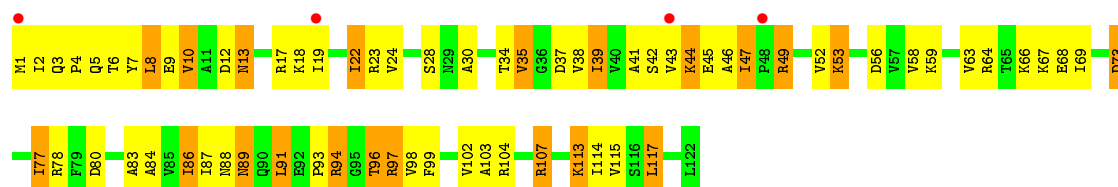
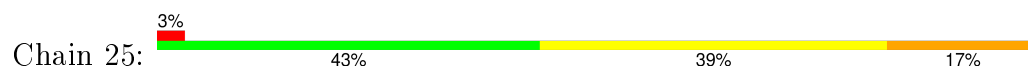




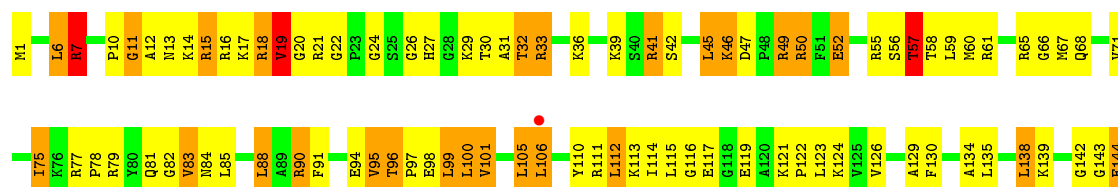
• Molecule 36: 50S ribosomal protein L14



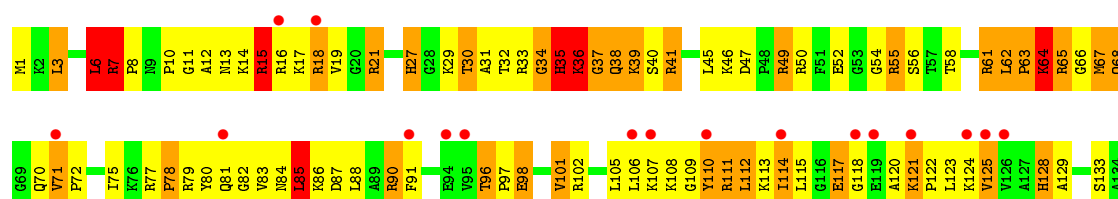
• Molecule 36: 50S ribosomal protein L14

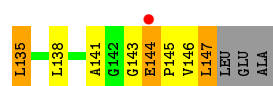


• Molecule 37: 50S ribosomal protein L15

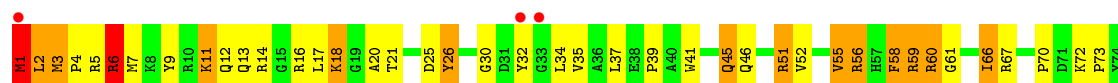


• Molecule 37: 50S ribosomal protein L15

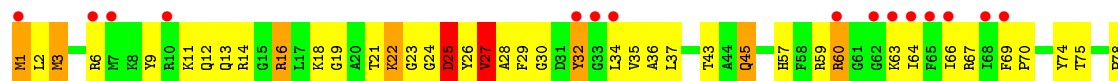




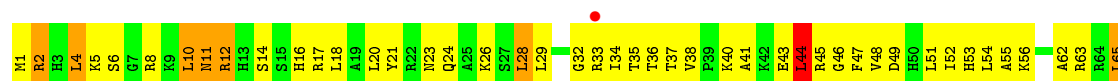
- Molecule 38: 50S ribosomal protein L16



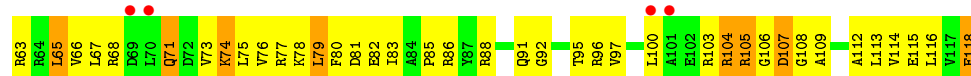
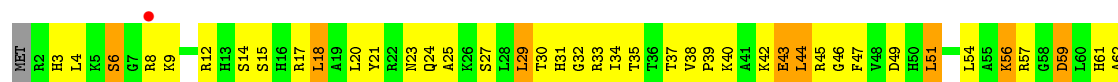
- Molecule 38: 50S ribosomal protein L16



- Molecule 39: 50S ribosomal protein L17

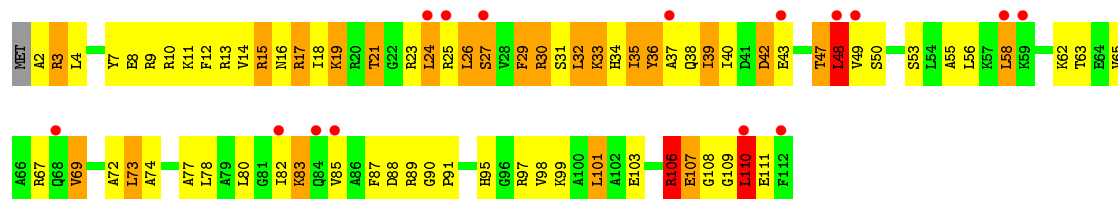


- Molecule 39: 50S ribosomal protein L17



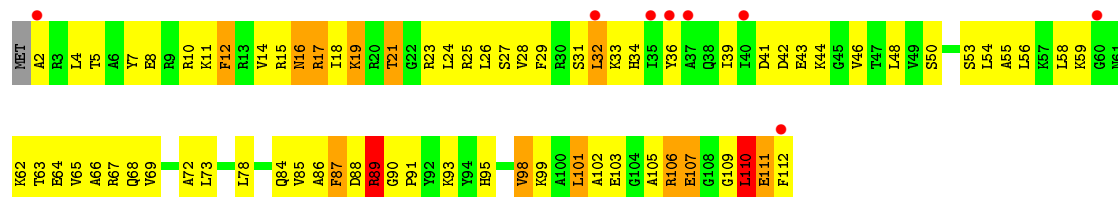
- Molecule 40: 50S ribosomal protein L18





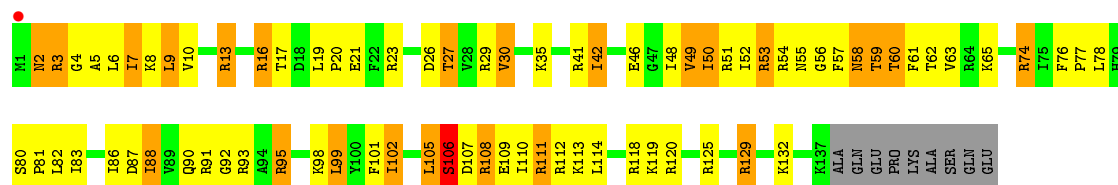
• Molecule 40: 50S ribosomal protein L18

Chain 65: ..



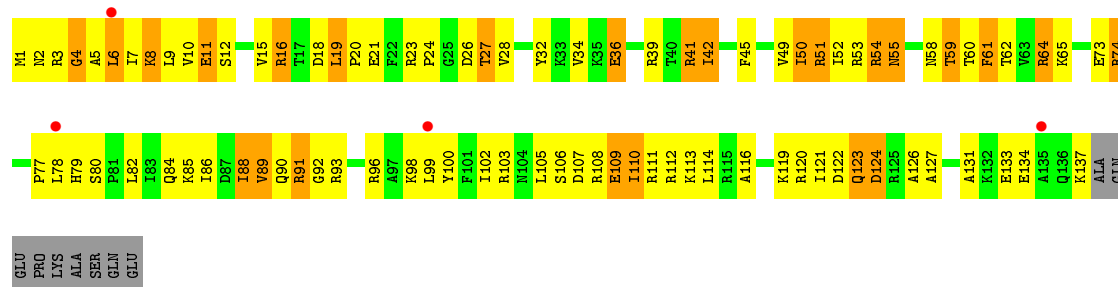
• Molecule 41: 50S ribosomal protein L19

Chain B8: ..



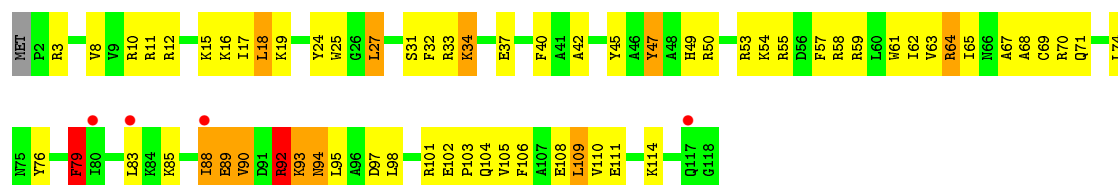
• Molecule 41: 50S ribosomal protein L19

Chain 75: ..

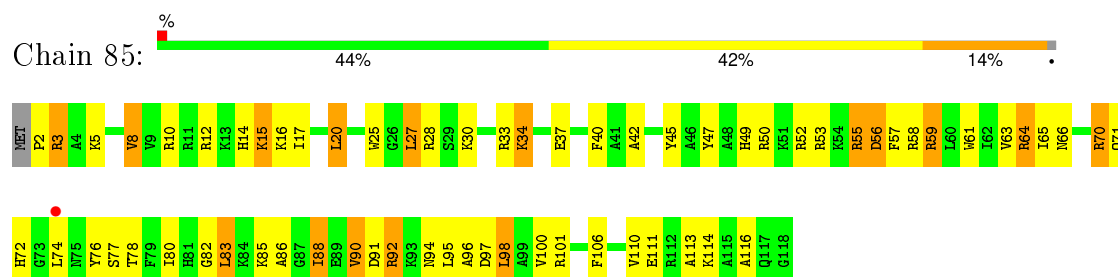


• Molecule 42: 50S ribosomal protein L20

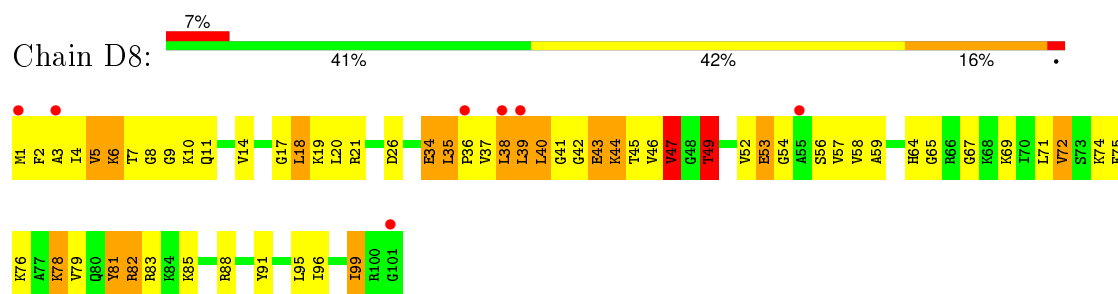
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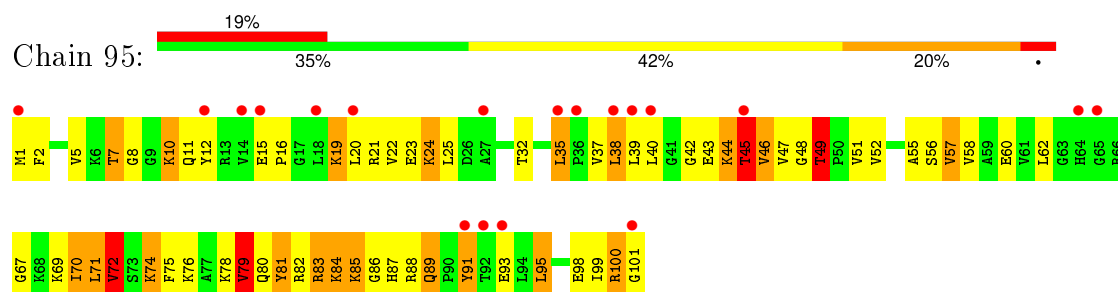
- Molecule 42: 50S ribosomal protein L20



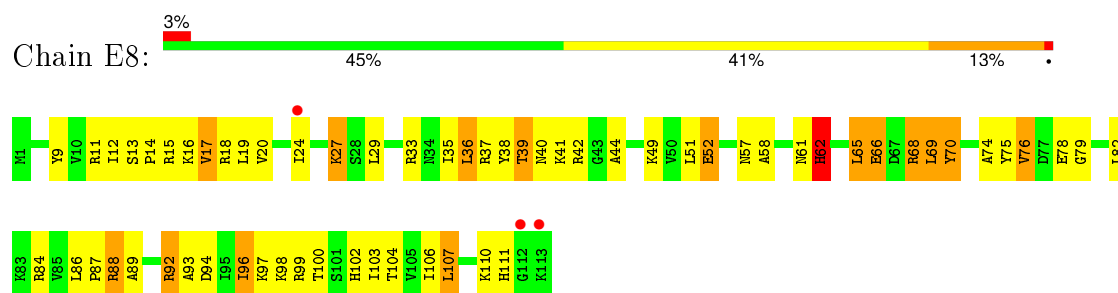
- Molecule 43: 50S ribosomal protein L21



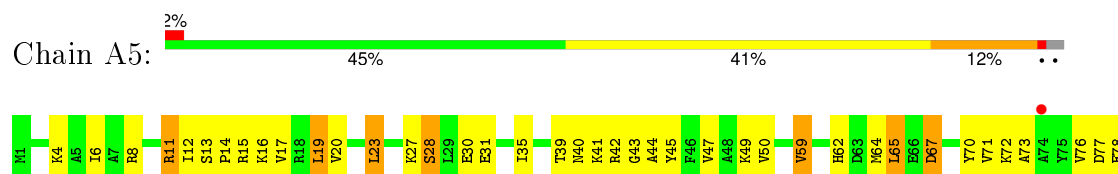
- Molecule 43: 50S ribosomal protein L21

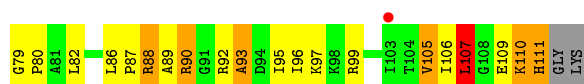


- Molecule 44: 50S ribosomal protein L22

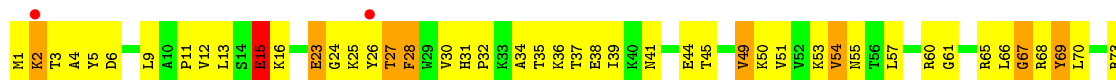


- Molecule 44: 50S ribosomal protein L22

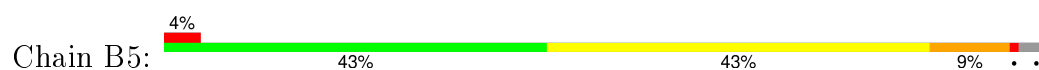




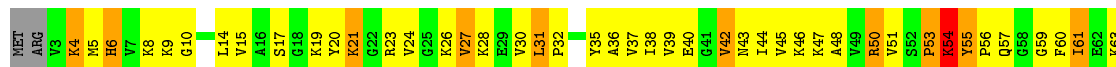
- Molecule 45: 50S ribosomal protein L23



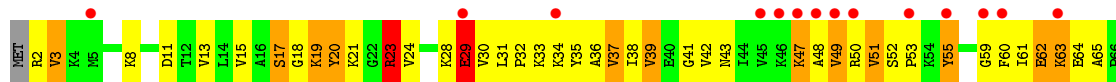
- Molecule 45: 50S ribosomal protein L23



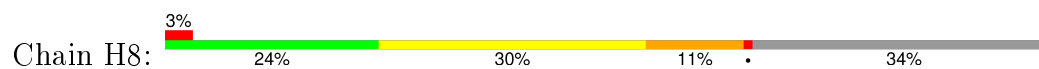
- Molecule 46: 50S ribosomal protein L24

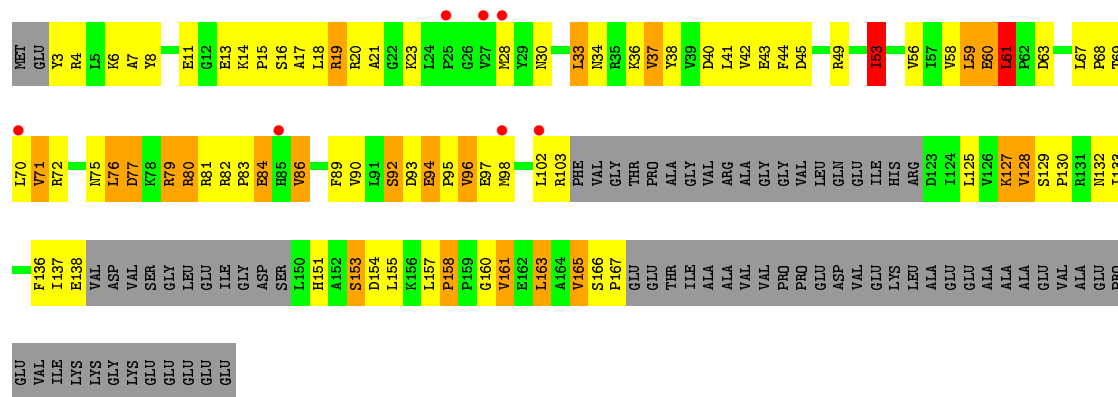


- Molecule 46: 50S ribosomal protein L24

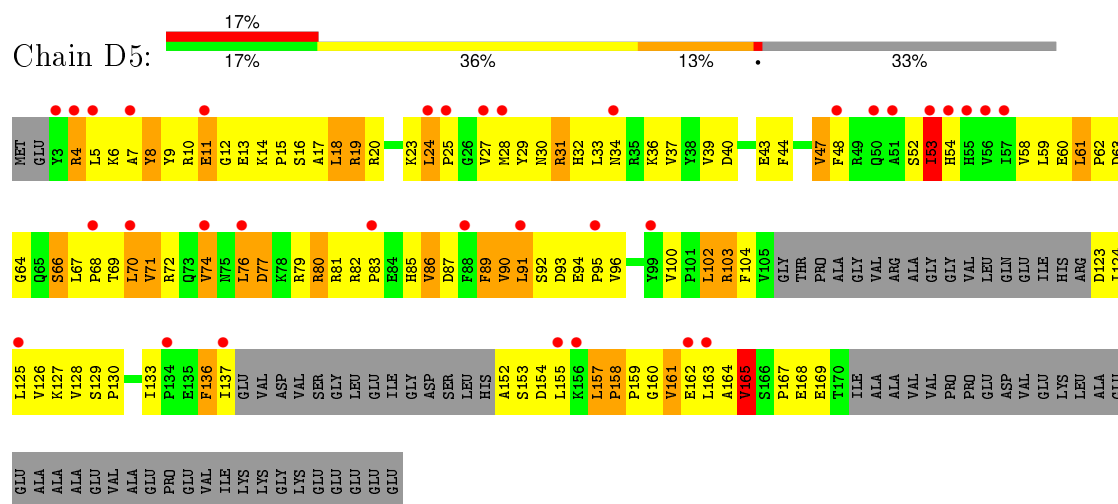


- Molecule 47: 50S ribosomal protein L25

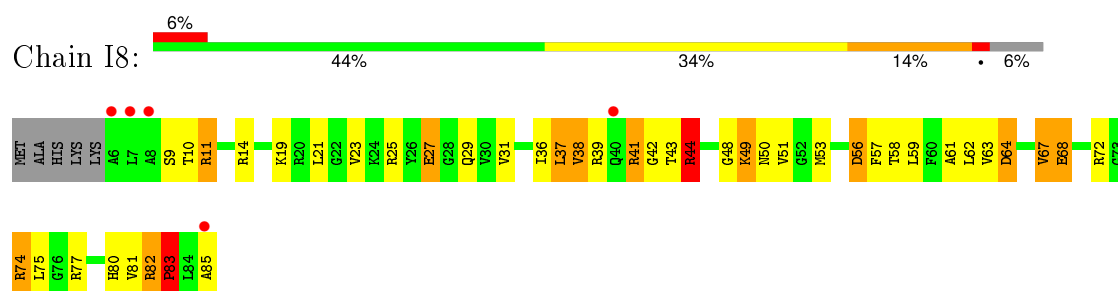




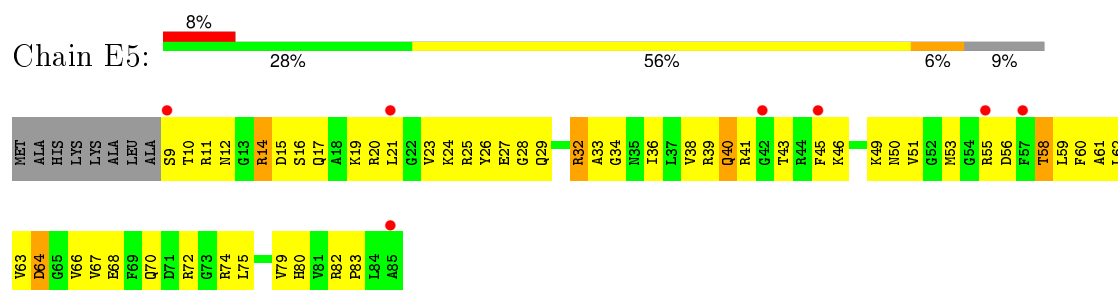
• Molecule 47: 50S ribosomal protein L25



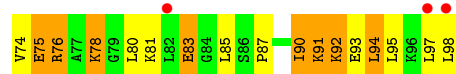
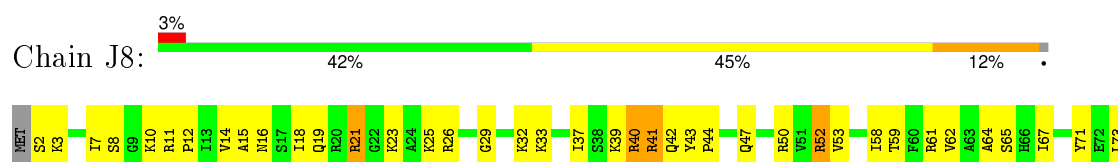
• Molecule 48: 50S ribosomal protein L27



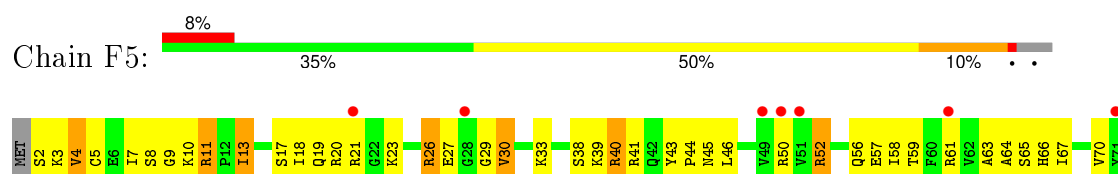
• Molecule 48: 50S ribosomal protein L27



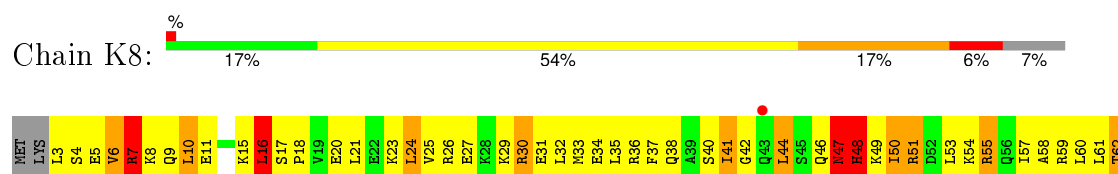
• Molecule 49: 50S ribosomal protein L28



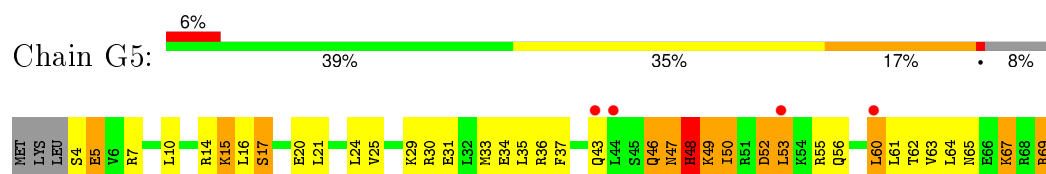
- Molecule 49: 50S ribosomal protein L28



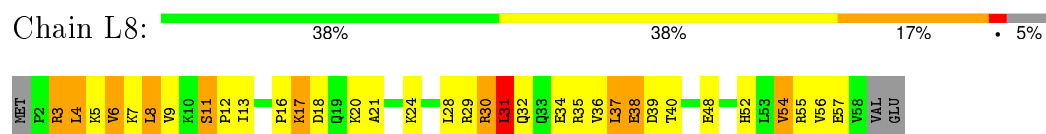
- Molecule 50: 50S ribosomal protein L29



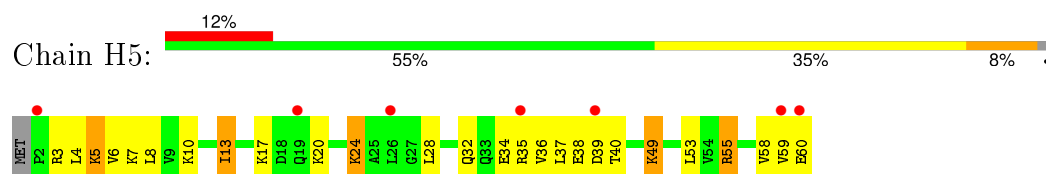
- Molecule 50: 50S ribosomal protein L29



- Molecule 51: 50S ribosomal protein L30

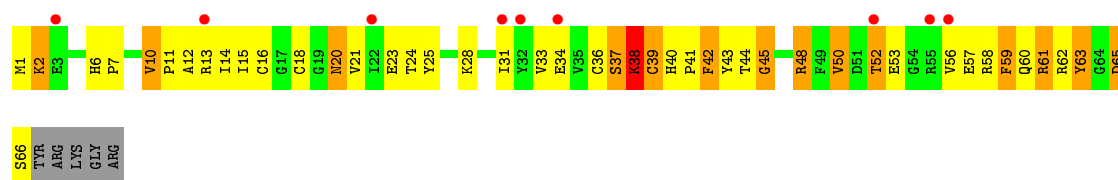


- Molecule 51: 50S ribosomal protein L30




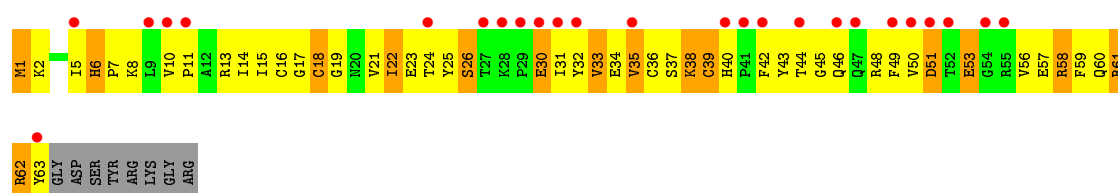
- Molecule 52: 50S ribosomal protein L31

Chain M8: 



- Molecule 52: 50S ribosomal protein L31

Chain I5: 



- Molecule 53: 50S ribosomal protein L32

Chain N8: 



- Molecule 53: 50S ribosomal protein L32

Chain J5: 

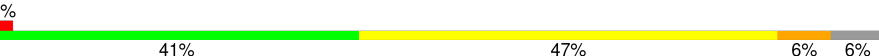


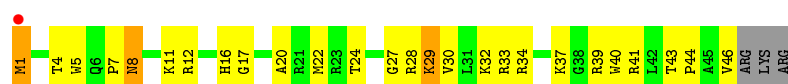
- Molecule 54: 50S ribosomal protein L34

Chain P8: 



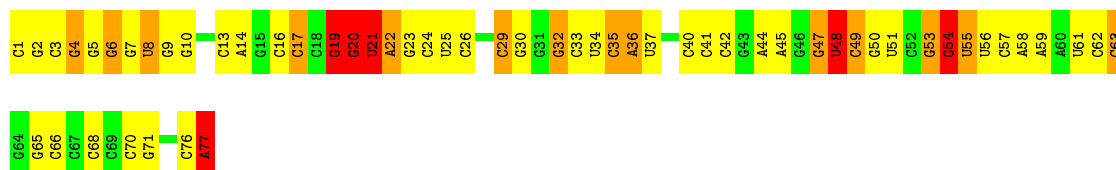
- Molecule 54: 50S ribosomal protein L34

Chain L5: 



- Molecule 55: 50S ribosomal protein L35

Chain Q8: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	210.20 Å 448.80 Å 621.00 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	153.41 – 3.30 153.41 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (153.41-3.30) 92.6 (153.41-3.30)	Depositor EDS
R_{merge}	0.46	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 3.33 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.191 , 0.258 0.195 , 0.260	Depositor DCC
R_{free} test set	2000 reflections (0.25%)	DCC
Wilson B-factor (Å ²)	94.6	Xtriage
Anisotropy	0.246	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 89.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 871092 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	295920	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: OMC, 5MU, ZN, MIA, MG, 4SU, 7MG, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	13	0.84	15/36028 (0.0%)	1.50	521/56231 (0.9%)
1	1G	0.74	0/36025	1.40	370/56227 (0.7%)
2	12	0.43	0/1959	0.71	3/2642 (0.1%)
2	1E	0.46	0/1959	0.74	1/2642 (0.0%)
3	22	0.43	0/1636	0.67	1/2205 (0.0%)
3	2E	0.54	0/1629	0.72	0/2195
4	32	0.50	0/1732	0.76	0/2318
4	3E	0.58	0/1732	0.77	2/2318 (0.1%)
5	42	0.54	0/1171	0.75	0/1576
5	4E	0.57	0/1171	0.74	0/1576
6	52	0.55	0/855	0.70	0/1154
6	5E	0.59	0/855	0.72	0/1154
7	62	0.47	0/1211	0.64	0/1622
7	6E	0.53	0/1275	0.64	0/1709
8	72	0.48	0/1135	0.69	0/1527
8	7E	0.56	0/1135	0.79	0/1527
9	82	0.44	0/1028	0.69	0/1379
9	8E	0.49	0/1028	0.72	0/1379
10	1A	0.48	0/529	0.70	0/706
10	1I	0.46	0/814	0.71	0/1095
11	2A	0.49	0/879	0.72	0/1187
11	2I	0.61	0/899	0.83	1/1213 (0.1%)
12	3A	0.60	0/972	0.81	0/1301
12	3I	0.67	0/972	0.87	0/1301
13	4A	0.41	0/943	0.66	0/1265
13	4I	0.55	0/943	0.76	0/1265
14	5A	0.52	0/423	0.75	0/560
14	5I	0.75	1/500 (0.2%)	0.74	0/664
15	6A	0.53	0/744	0.70	0/992
15	6I	0.63	0/744	0.81	0/992
16	7A	0.49	0/721	0.73	0/970
16	7I	0.48	0/721	0.74	1/970 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	8A	0.54	0/836	0.70	0/1117
17	8I	0.62	0/847	0.76	0/1131
18	9A	0.51	0/595	0.71	0/790
18	9I	0.57	0/595	0.79	0/790
19	AA	0.42	0/638	0.70	1/860 (0.1%)
19	AI	0.55	0/661	0.88	1/890 (0.1%)
20	BA	0.47	0/764	0.77	0/1007
20	BI	0.44	0/764	0.70	0/1007
21	1B	0.55	0/192	0.71	0/252
21	1F	0.51	0/221	0.76	0/288
22	1K	0.73	1/1623 (0.1%)	1.34	22/2521 (0.9%)
23	2K	1.17	6/1721 (0.3%)	1.62	36/2682 (1.3%)
24	3K	0.98	11/1669 (0.7%)	1.28	13/2599 (0.5%)
24	3L	1.00	11/1669 (0.7%)	1.37	33/2599 (1.3%)
25	4K	0.96	0/322	1.53	8/500 (1.6%)
25	4L	0.85	0/222	1.36	2/344 (0.6%)
26	14	1.00	78/69405 (0.1%)	1.72	1985/108348 (1.8%)
26	1H	1.21	256/69998 (0.4%)	1.93	3118/109276 (2.9%)
27	16	0.93	2/2928 (0.1%)	1.75	90/4568 (2.0%)
27	1J	0.75	0/2928	1.52	41/4568 (0.9%)
28	71	0.82	0/749	0.80	0/1004
29	11	0.89	3/2165 (0.1%)	1.04	7/2919 (0.2%)
29	19	0.76	0/2170	0.95	3/2926 (0.1%)
30	21	0.73	0/1601	0.98	5/2160 (0.2%)
30	29	0.70	0/1601	0.99	5/2160 (0.2%)
31	31	0.81	1/1620 (0.1%)	0.93	3/2194 (0.1%)
31	39	0.67	1/1645 (0.1%)	0.94	2/2228 (0.1%)
32	41	0.62	0/1498	0.82	2/2016 (0.1%)
32	49	0.45	0/1498	0.73	0/2016
33	51	0.66	0/1362	0.89	3/1841 (0.2%)
33	59	0.48	0/1332	0.84	1/1802 (0.1%)
34	61	0.59	0/1151	0.86	0/1558
34	69	0.53	0/1151	0.77	2/1558 (0.1%)
35	15	0.56	0/1131	0.80	0/1525
35	58	0.69	0/1131	0.94	0/1525
36	25	0.68	0/942	0.82	0/1269
36	68	0.76	0/942	0.82	0/1269
37	35	0.66	0/1139	1.01	6/1514 (0.4%)
37	78	0.75	0/1161	1.05	1/1544 (0.1%)
38	45	0.69	0/1142	0.94	3/1527 (0.2%)
38	88	0.86	0/1097	1.10	3/1466 (0.2%)
39	55	0.69	0/973	0.93	1/1302 (0.1%)
39	98	0.65	0/981	0.96	2/1312 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
40	65	0.57	0/891	0.96	2/1187 (0.2%)
40	A8	0.78	0/891	1.02	4/1187 (0.3%)
41	75	0.65	0/1155	0.82	1/1542 (0.1%)
41	B8	0.73	0/1155	0.94	1/1542 (0.1%)
42	85	0.60	0/981	0.79	1/1306 (0.1%)
42	C8	0.80	0/981	0.98	3/1306 (0.2%)
43	95	0.65	0/789	0.90	1/1057 (0.1%)
43	D8	0.73	0/789	0.94	2/1057 (0.2%)
44	A5	0.74	0/897	0.88	1/1204 (0.1%)
44	E8	0.77	0/910	0.92	1/1220 (0.1%)
45	B5	0.78	0/739	0.86	0/993
45	F8	0.92	2/756 (0.3%)	1.00	1/1014 (0.1%)
46	C5	0.73	0/807	1.03	3/1076 (0.3%)
46	G8	0.79	0/804	1.09	5/1073 (0.5%)
47	D5	0.46	0/1151	0.74	0/1557
47	H8	0.60	0/1135	0.88	0/1535
48	E5	0.67	0/620	0.87	0/827
48	I8	0.80	0/634	1.00	0/847
49	F5	0.63	0/744	0.92	1/989 (0.1%)
49	J8	0.83	0/769	1.00	0/1022
50	G5	0.61	0/560	0.82	0/741
50	K8	0.82	0/565	1.01	1/748 (0.1%)
51	H5	0.59	0/473	0.74	0/635
51	L8	0.74	0/457	1.04	1/613 (0.2%)
52	I5	0.52	0/527	0.92	0/709
52	M8	0.58	0/545	0.96	1/733 (0.1%)
53	J5	0.73	0/448	0.93	0/606
53	N8	0.65	0/436	0.87	0/589
54	L5	0.75	0/406	0.95	0/536
54	P8	0.88	0/417	0.99	0/550
55	M5	0.96	1/483 (0.2%)	1.14	3/634 (0.5%)
55	Q8	1.27	3/486 (0.6%)	1.65	9/638 (1.4%)
56	2L	1.26	13/1742 (0.7%)	1.51	30/2712 (1.1%)
All	All	0.92	405/318291 (0.1%)	1.52	6371/476619 (1.3%)

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	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	1E	0	2
4	32	0	3
4	3E	0	1
6	5E	0	1
9	82	0	1
10	1A	0	1
11	2A	0	1
12	3A	0	1
13	4A	0	1
13	4I	0	1
14	5A	0	1
19	AI	0	2
20	BA	0	3
29	11	0	2
29	19	0	5
30	21	0	4
30	29	0	5
31	31	0	1
31	39	0	4
32	41	0	1
32	49	0	1
33	59	0	1
34	61	0	4
34	69	0	1
35	15	0	1
36	25	0	1
37	35	0	3
37	78	0	2
38	45	0	5
38	88	0	3
39	98	0	1
40	65	0	1
40	A8	0	2
41	75	0	2
41	B8	0	2
42	85	0	3
42	C8	0	2
43	95	0	1
44	A5	0	2
45	B5	0	2
46	C5	0	3
46	G8	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
47	D5	0	2
47	H8	0	3
48	E5	0	1
48	I8	0	2
49	J8	0	1
50	G5	0	2
50	K8	0	3
52	I5	0	2
52	M8	0	1
53	N8	0	1
55	M5	0	2
55	Q8	0	7
All	All	0	116

The worst 5 of 405 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2L	55	U	N1-C2	22.39	1.58	1.38
23	2K	21	U	C5-C6	18.80	1.51	1.34
56	2L	21	U	C5-C6	18.33	1.50	1.34
24	3L	20	U	C5-C6	17.50	1.49	1.34
24	3K	16	U	C5-C6	17.45	1.49	1.34

The worst 5 of 6371 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	1H	1899	G	N3-C4-N9	-22.03	112.78	126.00
26	1H	2430	A	C2-N3-C4	-19.32	100.94	110.60
26	1H	783	A	C5-N7-C8	-17.81	94.99	103.90
26	1H	774	A	C2-N3-C4	-17.32	101.94	110.60
26	1H	2430	A	N1-C6-N6	16.97	128.78	118.60

There are no chirality outliers.

5 of 116 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1E	15	VAL	Peptide
2	1E	237	ALA	Peptide
4	3E	31	CYS	Peptide
13	4I	107	ALA	Peptide
6	5E	41	GLU	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	32185	0	16244	1069	0
1	1G	32182	0	16244	1090	0
2	12	1924	0	1975	113	0
2	1E	1924	0	1975	127	0
3	22	1612	0	1677	111	0
3	2E	1605	0	1668	60	0
4	32	1702	0	1763	110	0
4	3E	1702	0	1762	110	0
5	42	1155	0	1213	83	0
5	4E	1155	0	1213	68	0
6	52	842	0	857	35	0
6	5E	842	0	857	47	0
7	62	1194	0	1234	58	0
7	6E	1256	0	1296	61	0
8	72	1115	0	1177	59	0
8	7E	1115	0	1177	68	0
9	82	1009	0	1037	81	0
9	8E	1009	0	1037	78	0
10	1A	522	0	530	31	0
10	1I	801	0	849	54	0
11	2A	864	0	881	52	0
11	2I	884	0	904	44	0
12	3A	956	0	1046	56	0
12	3I	956	0	1046	48	0
13	4A	933	0	992	62	0
13	4I	933	0	992	60	0
14	5A	418	0	456	36	0
14	5I	491	0	529	38	0
15	6A	733	0	771	40	0
15	6I	733	0	771	43	0
16	7A	705	0	725	36	0
16	7I	705	0	725	57	0
17	8A	823	0	891	27	0
17	8I	834	0	904	63	0
18	9A	590	0	662	27	0
18	9I	590	0	662	31	0
19	AA	624	0	636	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	AI	647	0	665	46	0
20	BA	762	0	861	41	0
20	BI	762	0	861	51	0
21	1B	188	0	195	16	0
21	1F	217	0	234	7	0
22	1K	1497	0	770	36	0
23	2K	1646	0	845	38	0
24	3K	1627	0	838	64	0
24	3L	1627	0	838	78	0
25	4K	285	0	143	16	0
25	4L	197	0	99	6	0
26	14	61968	0	31239	1915	0
26	1H	62497	0	31504	1930	2
27	16	2617	0	1328	93	0
27	1J	2617	0	1328	122	0
28	71	737	0	743	64	0
29	11	2115	0	2195	124	0
29	19	2120	0	2197	121	0
30	21	1568	0	1634	105	0
30	29	1568	0	1634	131	0
31	31	1585	0	1632	108	0
31	39	1610	0	1655	144	0
32	41	1473	0	1535	107	0
32	49	1473	0	1535	101	0
33	51	1336	0	1418	96	0
33	59	1307	0	1382	93	0
34	61	1136	0	1223	70	0
34	69	1136	0	1223	59	0
35	15	1104	0	1180	54	0
35	58	1104	0	1180	74	0
36	25	932	0	996	59	0
36	68	932	0	996	45	0
37	35	1122	0	1206	121	0
37	78	1144	0	1228	111	0
38	45	1121	0	1179	91	0
38	88	1077	0	1121	77	0
39	55	959	0	1021	70	0
39	98	967	0	1033	76	0
40	65	881	0	943	73	0
40	A8	881	0	943	70	0
41	75	1141	0	1202	71	0
41	B8	1141	0	1202	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	85	963	0	1022	69	0
42	C8	963	0	1022	63	0
43	95	778	0	852	81	0
43	D8	778	0	852	56	0
44	A5	886	0	948	40	0
44	E8	899	0	964	50	0
45	B5	725	0	778	33	0
45	F8	742	0	803	47	0
46	C5	794	0	884	67	0
46	G8	791	0	881	66	0
47	D5	1126	0	1154	92	0
47	H8	1110	0	1141	75	0
48	E5	612	0	633	42	0
48	I8	626	0	642	41	0
49	F5	737	0	813	35	0
49	J8	762	0	848	41	0
50	G5	558	0	610	26	1
50	K8	563	0	612	52	0
51	H5	468	0	518	15	1
51	L8	452	0	503	29	0
52	I5	515	0	514	60	0
52	M8	533	0	526	54	0
53	J5	434	0	454	33	0
53	N8	422	0	440	27	0
54	L5	398	0	441	25	0
54	P8	409	0	454	14	0
55	M5	477	0	540	47	0
55	Q8	480	0	549	104	0
56	2L	1645	0	843	40	0
57	11	3	0	0	0	0
57	13	99	0	0	0	0
57	14	327	0	0	0	0
57	16	11	0	0	0	0
57	1G	72	0	0	0	0
57	1H	444	0	0	0	0
57	1J	3	0	0	0	0
57	25	1	0	0	0	0
57	29	2	0	0	0	0
57	2K	2	0	0	0	0
57	2L	2	0	0	0	0
57	35	1	0	0	0	0
57	3E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	3L	2	0	0	0	0
57	4I	2	0	0	0	0
57	45	1	0	0	0	0
57	4E	1	0	0	0	0
57	4I	1	0	0	0	0
57	55	1	0	0	0	0
57	68	2	0	0	0	0
57	78	2	0	0	0	0
57	88	1	0	0	0	0
57	98	1	0	0	0	0
57	I8	2	0	0	0	0
57	J8	2	0	0	0	0
57	L8	1	0	0	0	0
57	M5	1	0	0	0	0
57	P8	1	0	0	0	0
58	32	1	0	0	0	0
58	3E	1	0	0	0	0
58	5A	1	0	0	0	0
58	5I	1	0	0	0	0
58	C5	1	0	0	0	0
58	G8	1	0	0	0	0
59	11	11	0	0	1	0
59	13	144	0	0	30	0
59	14	592	0	0	151	0
59	16	22	0	0	0	0
59	19	8	0	0	1	0
59	1G	48	0	0	9	0
59	1H	933	0	0	316	0
59	1I	1	0	0	0	0
59	21	3	0	0	1	0
59	25	6	0	0	1	0
59	29	5	0	0	2	0
59	2K	6	0	0	0	0
59	31	9	0	0	0	0
59	35	2	0	0	0	0
59	39	4	0	0	0	0
59	3E	2	0	0	1	0
59	3I	2	0	0	0	0
59	4K	2	0	0	0	0
59	55	3	0	0	2	0
59	5I	2	0	0	0	0
59	75	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	78	6	0	0	2	0
59	A5	1	0	0	0	0
59	D8	1	0	0	0	0
59	F8	2	0	0	0	0
59	G8	2	0	0	0	0
59	H5	2	0	0	1	0
59	I8	5	0	0	2	0
59	J8	1	0	0	0	0
59	L5	1	0	0	0	0
59	L8	1	0	0	1	0
59	M5	1	0	0	0	0
59	P8	2	0	0	0	0
59	Q8	1	0	0	0	0
All	All	295920	0	197803	11212	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 24.

The worst 5 of 11212 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:270(L):U:H3	34:61:50:ARG:HG2	1.19	1.06
26:1H:2714:G:OP2	59:1H:3574:HOH:O	1.71	1.06
26:1H:2781:A:H5'	26:1H:2782:G:H5'	1.35	1.06
26:1H:741:G:OP1	59:1H:3910:HOH:O	1.74	1.05
26:1H:1614:A:OP1	59:1H:3862:HOH:O	1.75	1.04

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)
26:1H:654(H):G:O2'	51:H5:55:ARG:NH2[2_464]	2.11	0.09
26:1H:277:C:O2'	50:G5:49:LYS:NZ[2_564]	2.16	0.04

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	12	235/256 (92%)	192 (82%)	37 (16%)	6 (3%)	7	36
2	1E	235/256 (92%)	193 (82%)	39 (17%)	3 (1%)	15	52
3	22	204/239 (85%)	182 (89%)	22 (11%)	0	100	100
3	2E	203/239 (85%)	185 (91%)	18 (9%)	0	100	100
4	32	206/209 (99%)	180 (87%)	22 (11%)	4 (2%)	10	45
4	3E	206/209 (99%)	190 (92%)	13 (6%)	3 (2%)	13	49
5	42	149/162 (92%)	135 (91%)	13 (9%)	1 (1%)	26	66
5	4E	149/162 (92%)	139 (93%)	9 (6%)	1 (1%)	26	66
6	52	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
6	5E	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
7	62	143/156 (92%)	135 (94%)	7 (5%)	1 (1%)	26	66
7	6E	153/156 (98%)	143 (94%)	10 (6%)	0	100	100
8	72	136/138 (99%)	124 (91%)	10 (7%)	2 (2%)	13	49
8	7E	136/138 (99%)	124 (91%)	11 (8%)	1 (1%)	26	66
9	82	125/128 (98%)	112 (90%)	12 (10%)	1 (1%)	24	62
9	8E	125/128 (98%)	106 (85%)	18 (14%)	1 (1%)	24	62
10	1A	56/105 (53%)	48 (86%)	8 (14%)	0	100	100
10	1I	97/105 (92%)	88 (91%)	8 (8%)	1 (1%)	19	58
11	2A	114/129 (88%)	101 (89%)	10 (9%)	3 (3%)	7	36
11	2I	117/129 (91%)	100 (86%)	16 (14%)	1 (1%)	21	60
12	3A	120/132 (91%)	101 (84%)	14 (12%)	5 (4%)	3	23
12	3I	120/132 (91%)	103 (86%)	17 (14%)	0	100	100
13	4A	115/126 (91%)	97 (84%)	16 (14%)	2 (2%)	11	47
13	4I	115/126 (91%)	95 (83%)	19 (16%)	1 (1%)	21	60
14	5A	48/61 (79%)	38 (79%)	9 (19%)	1 (2%)	9	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	5I	58/61 (95%)	45 (78%)	11 (19%)	2 (3%)	5	29
15	6A	86/89 (97%)	74 (86%)	12 (14%)	0	100	100
15	6I	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
16	7A	82/88 (93%)	76 (93%)	6 (7%)	0	100	100
16	7I	82/88 (93%)	76 (93%)	5 (6%)	1 (1%)	16	54
17	8A	97/105 (92%)	92 (95%)	5 (5%)	0	100	100
17	8I	98/105 (93%)	93 (95%)	5 (5%)	0	100	100
18	9A	70/88 (80%)	61 (87%)	9 (13%)	0	100	100
18	9I	70/88 (80%)	62 (89%)	7 (10%)	1 (1%)	14	50
19	AA	76/93 (82%)	59 (78%)	14 (18%)	3 (4%)	4	25
19	AI	79/93 (85%)	65 (82%)	10 (13%)	4 (5%)	2	19
20	BA	97/106 (92%)	85 (88%)	11 (11%)	1 (1%)	19	58
20	BI	97/106 (92%)	83 (86%)	14 (14%)	0	100	100
21	1B	20/27 (74%)	19 (95%)	1 (5%)	0	100	100
21	1F	23/27 (85%)	21 (91%)	2 (9%)	0	100	100
28	7I	83/229 (36%)	79 (95%)	2 (2%)	2 (2%)	7	38
29	11	270/276 (98%)	253 (94%)	13 (5%)	4 (2%)	13	49
29	19	271/276 (98%)	248 (92%)	18 (7%)	5 (2%)	11	46
30	21	203/206 (98%)	160 (79%)	33 (16%)	10 (5%)	3	19
30	29	203/206 (98%)	149 (73%)	45 (22%)	9 (4%)	3	22
31	31	200/210 (95%)	180 (90%)	19 (10%)	1 (0%)	34	71
31	39	204/210 (97%)	163 (80%)	34 (17%)	7 (3%)	5	29
32	41	179/182 (98%)	155 (87%)	20 (11%)	4 (2%)	8	41
32	49	179/182 (98%)	150 (84%)	28 (16%)	1 (1%)	30	68
33	51	172/180 (96%)	146 (85%)	19 (11%)	7 (4%)	3	24
33	59	168/180 (93%)	125 (74%)	35 (21%)	8 (5%)	3	20
34	61	144/148 (97%)	119 (83%)	21 (15%)	4 (3%)	6	34
34	69	144/148 (97%)	115 (80%)	26 (18%)	3 (2%)	9	42
35	15	136/140 (97%)	119 (88%)	15 (11%)	2 (2%)	13	49
35	58	136/140 (97%)	114 (84%)	18 (13%)	4 (3%)	6	34
36	25	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	24	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	68	120/122 (98%)	114 (95%)	5 (4%)	1 (1%)	24	62
37	35	145/150 (97%)	110 (76%)	26 (18%)	9 (6%)	2	14
37	78	148/150 (99%)	117 (79%)	26 (18%)	5 (3%)	5	29
38	45	139/141 (99%)	109 (78%)	27 (19%)	3 (2%)	8	41
38	88	133/141 (94%)	110 (83%)	19 (14%)	4 (3%)	5	33
39	55	115/118 (98%)	107 (93%)	7 (6%)	1 (1%)	21	60
39	98	116/118 (98%)	99 (85%)	16 (14%)	1 (1%)	21	60
40	65	109/112 (97%)	85 (78%)	20 (18%)	4 (4%)	4	27
40	A8	109/112 (97%)	87 (80%)	20 (18%)	2 (2%)	11	46
41	75	135/146 (92%)	117 (87%)	17 (13%)	1 (1%)	26	66
41	B8	135/146 (92%)	114 (84%)	20 (15%)	1 (1%)	26	66
42	85	115/118 (98%)	99 (86%)	16 (14%)	0	100	100
42	C8	115/118 (98%)	102 (89%)	11 (10%)	2 (2%)	11	47
43	95	99/101 (98%)	79 (80%)	16 (16%)	4 (4%)	4	24
43	D8	99/101 (98%)	91 (92%)	6 (6%)	2 (2%)	9	43
44	A5	109/113 (96%)	97 (89%)	9 (8%)	3 (3%)	6	34
44	E8	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
45	B5	90/96 (94%)	80 (89%)	8 (9%)	2 (2%)	8	41
45	F8	92/96 (96%)	83 (90%)	8 (9%)	1 (1%)	17	57
46	C5	102/110 (93%)	75 (74%)	20 (20%)	7 (7%)	1	11
46	G8	102/110 (93%)	80 (78%)	15 (15%)	7 (7%)	1	11
47	D5	131/206 (64%)	101 (77%)	24 (18%)	6 (5%)	3	21
47	H8	129/206 (63%)	104 (81%)	19 (15%)	6 (5%)	3	20
48	E5	75/85 (88%)	65 (87%)	9 (12%)	1 (1%)	15	52
48	I8	78/85 (92%)	67 (86%)	9 (12%)	2 (3%)	7	36
49	F5	92/98 (94%)	84 (91%)	7 (8%)	1 (1%)	17	57
49	J8	95/98 (97%)	85 (90%)	8 (8%)	2 (2%)	9	42
50	G5	64/72 (89%)	58 (91%)	4 (6%)	2 (3%)	5	32
50	K8	65/72 (90%)	56 (86%)	5 (8%)	4 (6%)	2	14
51	H5	57/60 (95%)	50 (88%)	7 (12%)	0	100	100
51	L8	55/60 (92%)	50 (91%)	4 (7%)	1 (2%)	11	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	I5	61/71 (86%)	33 (54%)	25 (41%)	3 (5%)	3	19
52	M8	64/71 (90%)	39 (61%)	22 (34%)	3 (5%)	3	20
53	J5	54/60 (90%)	49 (91%)	5 (9%)	0	100	100
53	N8	52/60 (87%)	43 (83%)	7 (14%)	2 (4%)	4	26
54	L5	44/49 (90%)	43 (98%)	1 (2%)	0	100	100
54	P8	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
55	M5	58/65 (89%)	46 (79%)	9 (16%)	3 (5%)	2	18
55	Q8	58/65 (89%)	36 (62%)	15 (26%)	7 (12%)	0	3
All	All	11153/12175 (92%)	9578 (86%)	1350 (12%)	225 (2%)	9	43

5 of 225 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	9I	22	VAL
30	21	78	LEU
30	21	83	ASP
33	51	169	VAL
37	78	57	THR

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%)	148 (72%)	57 (28%)	0	2
2	1E	205/220 (93%)	158 (77%)	47 (23%)	1	4
3	22	160/188 (85%)	121 (76%)	39 (24%)	1	3
3	2E	159/188 (85%)	128 (80%)	31 (20%)	2	7
4	32	180/181 (99%)	140 (78%)	40 (22%)	1	4
4	3E	180/181 (99%)	146 (81%)	34 (19%)	2	8
5	42	116/123 (94%)	80 (69%)	36 (31%)	0	1
5	4E	116/123 (94%)	86 (74%)	30 (26%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	52	90/90 (100%)	73 (81%)	17 (19%)	2	8
6	5E	90/90 (100%)	70 (78%)	20 (22%)	1	4
7	62	121/127 (95%)	97 (80%)	24 (20%)	1	7
7	6E	126/127 (99%)	98 (78%)	28 (22%)	1	4
8	72	119/119 (100%)	91 (76%)	28 (24%)	1	4
8	7E	119/119 (100%)	93 (78%)	26 (22%)	1	5
9	82	98/99 (99%)	77 (79%)	21 (21%)	1	5
9	8E	98/99 (99%)	71 (72%)	27 (28%)	0	2
10	1A	58/92 (63%)	43 (74%)	15 (26%)	0	2
10	1I	89/92 (97%)	68 (76%)	21 (24%)	1	3
11	2A	88/99 (89%)	72 (82%)	16 (18%)	2	9
11	2I	90/99 (91%)	73 (81%)	17 (19%)	2	8
12	3A	103/109 (94%)	81 (79%)	22 (21%)	1	5
12	3I	103/109 (94%)	80 (78%)	23 (22%)	1	4
13	4A	94/101 (93%)	60 (64%)	34 (36%)	0	1
13	4I	94/101 (93%)	71 (76%)	23 (24%)	1	3
14	5A	43/50 (86%)	33 (77%)	10 (23%)	1	4
14	5I	49/50 (98%)	42 (86%)	7 (14%)	4	19
15	6A	79/80 (99%)	64 (81%)	15 (19%)	2	8
15	6I	79/80 (99%)	68 (86%)	11 (14%)	4	20
16	7A	72/74 (97%)	53 (74%)	19 (26%)	0	2
16	7I	72/74 (97%)	56 (78%)	16 (22%)	1	4
17	8A	94/97 (97%)	80 (85%)	14 (15%)	4	17
17	8I	95/97 (98%)	73 (77%)	22 (23%)	1	4
18	9A	63/77 (82%)	44 (70%)	19 (30%)	0	1
18	9I	63/77 (82%)	53 (84%)	10 (16%)	3	14
19	AA	67/80 (84%)	54 (81%)	13 (19%)	2	7
19	AI	70/80 (88%)	45 (64%)	25 (36%)	0	1
20	BA	76/82 (93%)	66 (87%)	10 (13%)	5	22
20	BI	76/82 (93%)	55 (72%)	21 (28%)	0	2
21	1B	17/22 (77%)	16 (94%)	1 (6%)	24	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	1F	20/22 (91%)	19 (95%)	1 (5%)	30	68
28	71	77/181 (42%)	58 (75%)	19 (25%)	1	3
29	11	214/218 (98%)	162 (76%)	52 (24%)	1	3
29	19	214/218 (98%)	162 (76%)	52 (24%)	1	3
30	21	165/166 (99%)	130 (79%)	35 (21%)	1	5
30	29	165/166 (99%)	128 (78%)	37 (22%)	1	4
31	31	161/166 (97%)	123 (76%)	38 (24%)	1	3
31	39	163/166 (98%)	125 (77%)	38 (23%)	1	4
32	41	155/156 (99%)	109 (70%)	46 (30%)	0	1
32	49	155/156 (99%)	112 (72%)	43 (28%)	0	2
33	51	145/148 (98%)	112 (77%)	33 (23%)	1	4
33	59	142/148 (96%)	108 (76%)	34 (24%)	1	3
34	61	122/124 (98%)	89 (73%)	33 (27%)	0	2
34	69	122/124 (98%)	87 (71%)	35 (29%)	0	1
35	15	117/119 (98%)	93 (80%)	24 (20%)	1	6
35	58	117/119 (98%)	85 (73%)	32 (27%)	0	2
36	25	100/100 (100%)	72 (72%)	28 (28%)	0	2
36	68	100/100 (100%)	78 (78%)	22 (22%)	1	5
37	35	114/116 (98%)	70 (61%)	44 (39%)	0	0
37	78	116/116 (100%)	79 (68%)	37 (32%)	0	1
38	45	111/111 (100%)	85 (77%)	26 (23%)	1	4
38	88	103/111 (93%)	73 (71%)	30 (29%)	0	1
39	55	100/101 (99%)	78 (78%)	22 (22%)	1	5
39	98	101/101 (100%)	80 (79%)	21 (21%)	1	6
40	65	87/88 (99%)	68 (78%)	19 (22%)	1	5
40	A8	87/88 (99%)	58 (67%)	29 (33%)	0	1
41	75	120/127 (94%)	83 (69%)	37 (31%)	0	1
41	B8	120/127 (94%)	85 (71%)	35 (29%)	0	1
42	85	93/94 (99%)	71 (76%)	22 (24%)	1	3
42	C8	93/94 (99%)	73 (78%)	20 (22%)	1	5
43	95	82/82 (100%)	53 (65%)	29 (35%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	D8	82/82 (100%)	56 (68%)	26 (32%)	0	1
44	A5	91/92 (99%)	65 (71%)	26 (29%)	0	1
44	E8	92/92 (100%)	68 (74%)	24 (26%)	0	2
45	B5	74/78 (95%)	57 (77%)	17 (23%)	1	4
45	F8	76/78 (97%)	56 (74%)	20 (26%)	0	2
46	C5	85/91 (93%)	60 (71%)	25 (29%)	0	1
46	G8	85/91 (93%)	57 (67%)	28 (33%)	0	1
47	D5	126/179 (70%)	95 (75%)	31 (25%)	1	3
47	H8	124/179 (69%)	96 (77%)	28 (23%)	1	4
48	E5	62/67 (92%)	48 (77%)	14 (23%)	1	4
48	I8	61/67 (91%)	44 (72%)	17 (28%)	0	2
49	F5	79/83 (95%)	56 (71%)	23 (29%)	0	1
49	J8	82/83 (99%)	61 (74%)	21 (26%)	0	2
50	G5	62/67 (92%)	41 (66%)	21 (34%)	0	1
50	K8	62/67 (92%)	44 (71%)	18 (29%)	0	1
51	H5	51/52 (98%)	38 (74%)	13 (26%)	1	2
51	L8	49/52 (94%)	33 (67%)	16 (33%)	0	1
52	I5	57/63 (90%)	40 (70%)	17 (30%)	0	1
52	M8	59/63 (94%)	43 (73%)	16 (27%)	0	2
53	J5	48/52 (92%)	34 (71%)	14 (29%)	0	1
53	N8	47/52 (90%)	35 (74%)	12 (26%)	1	2
54	L5	39/42 (93%)	31 (80%)	8 (20%)	1	6
54	P8	40/42 (95%)	31 (78%)	9 (22%)	1	4
55	M5	49/55 (89%)	36 (74%)	13 (26%)	0	2
55	Q8	50/55 (91%)	33 (66%)	17 (34%)	0	1
All	All	9429/10075 (94%)	7093 (75%)	2336 (25%)	1	3

5 of 2336 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	I8	44	ARG
4	32	191	ARG
46	C5	19	LYS

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Mol	Chain	Res	Type
50	K8	9	GLN
2	12	56	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
48	I8	29	GLN
5	42	127	ASN
40	65	34	HIS
2	12	19	HIS
5	42	130	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	13	1495/1522 (98%)	395 (26%)	38 (2%)
1	1G	1495/1522 (98%)	396 (26%)	36 (2%)
22	1K	65/77 (84%)	28 (43%)	3 (4%)
23	2K	76/77 (98%)	16 (21%)	1 (1%)
24	3K	75/76 (98%)	35 (46%)	6 (8%)
24	3L	74/76 (97%)	38 (51%)	2 (2%)
25	4K	12/27 (44%)	2 (16%)	0
25	4L	9/27 (33%)	4 (44%)	1 (11%)
26	14	2874/2917 (98%)	803 (27%)	48 (1%)
26	1H	2901/2917 (99%)	734 (25%)	52 (1%)
27	16	121/122 (99%)	25 (20%)	0
27	1J	121/122 (99%)	39 (32%)	1 (0%)
56	2L	75/77 (97%)	22 (29%)	3 (4%)
All	All	9393/9559 (98%)	2537 (27%)	191 (2%)

5 of 2537 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	13	5	U
1	13	6	G
1	13	7	G
1	13	8	A
1	13	9	G

5 of 191 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	1H	2062	A
1	1G	274	A
26	14	2157	G
26	1H	2167	U
26	1H	2611	U

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

23 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	OMC	1K	33	22	15,22,23	2.16	4 (26%)	20,31,34	1.58	3 (15%)
22	5MU	1K	55	22	13,22,23	1.64	2 (15%)	16,32,35	1.30	1 (6%)
23	OMC	2K	33	23	15,22,23	2.24	4 (26%)	20,31,34	1.85	2 (10%)
23	7MG	2K	47	23	20,26,27	3.28	5 (25%)	23,39,42	2.27	5 (21%)
23	5MU	2K	55	23	13,22,23	1.63	2 (15%)	16,32,35	1.64	3 (18%)
23	PSU	2K	56	23	15,21,22	1.03	2 (13%)	16,30,33	1.74	3 (18%)
23	4SU	2K	8	23	12,21,22	2.96	2 (16%)	15,30,33	0.55	0
56	OMC	2L	33	56	15,22,23	2.14	4 (26%)	20,31,34	1.76	3 (15%)
56	7MG	2L	47	56	20,26,27	3.27	5 (25%)	23,39,42	2.26	5 (21%)
56	PSU	2L	56	56	15,21,22	1.15	1 (6%)	16,30,33	2.08	4 (25%)
56	4SU	2L	8	56	12,21,22	3.39	2 (16%)	15,30,33	0.64	0
24	PSU	3K	32	24	15,21,22	1.03	1 (6%)	16,30,33	1.96	4 (25%)
24	MIA	3K	37	24	22,31,32	1.05	2 (9%)	26,44,47	2.69	4 (15%)
24	PSU	3K	39	24	15,21,22	1.06	1 (6%)	16,30,33	2.08	4 (25%)
24	7MG	3K	46	24	20,26,27	3.28	5 (25%)	23,39,42	2.31	7 (30%)
24	PSU	3K	55	24	15,21,22	1.13	3 (20%)	16,30,33	2.03	4 (25%)
24	4SU	3K	8	24	12,21,22	3.29	2 (16%)	15,30,33	0.97	1 (6%)
24	PSU	3L	32	24	15,21,22	1.22	1 (6%)	16,30,33	2.03	3 (18%)
24	MIA	3L	37	24	22,31,32	1.51	2 (9%)	26,44,47	2.13	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PSU	3L	39	24	15,21,22	1.03	1 (6%)	16,30,33	1.90	3 (18%)
24	7MG	3L	46	24	20,26,27	3.36	5 (25%)	23,39,42	2.05	5 (21%)
24	PSU	3L	55	24	15,21,22	0.98	1 (6%)	16,30,33	1.88	4 (25%)
24	4SU	3L	8	24	12,21,22	3.28	2 (16%)	15,30,33	1.33	1 (6%)

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	OMC	1K	33	22	-	0/5/27/28	0/2/2/2
22	5MU	1K	55	22	-	0/3/25/26	0/2/2/2
23	OMC	2K	33	23	-	0/5/27/28	0/2/2/2
23	7MG	2K	47	23	-	0/7/37/38	0/3/3/3
23	5MU	2K	55	23	-	0/3/25/26	0/2/2/2
23	PSU	2K	56	23	-	0/7/25/26	0/2/2/2
23	4SU	2K	8	23	-	0/3/25/26	0/2/2/2
56	OMC	2L	33	56	-	0/5/27/28	0/2/2/2
56	7MG	2L	47	56	-	0/7/37/38	0/3/3/3
56	PSU	2L	56	56	-	0/7/25/26	0/2/2/2
56	4SU	2L	8	56	-	0/3/25/26	0/2/2/2
24	PSU	3K	32	24	-	0/7/25/26	0/2/2/2
24	MIA	3K	37	24	-	0/11/33/34	0/3/3/3
24	PSU	3K	39	24	-	0/7/25/26	0/2/2/2
24	7MG	3K	46	24	-	0/7/37/38	0/3/3/3
24	PSU	3K	55	24	-	0/7/25/26	0/2/2/2
24	4SU	3K	8	24	-	0/3/25/26	0/2/2/2
24	PSU	3L	32	24	-	0/7/25/26	0/2/2/2
24	MIA	3L	37	24	-	0/11/33/34	0/3/3/3
24	PSU	3L	39	24	-	0/7/25/26	0/2/2/2
24	7MG	3L	46	24	-	0/7/37/38	0/3/3/3
24	PSU	3L	55	24	-	0/7/25/26	0/2/2/2
24	4SU	3L	8	24	-	0/3/25/26	0/2/2/2

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	3L	46	7MG	C5-C4	-5.80	1.23	1.39
24	3K	46	7MG	C5-C4	-5.60	1.24	1.39
56	2L	47	7MG	C5-C4	-5.32	1.25	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	2K	47	7MG	C5-C4	-5.26	1.25	1.39
22	1K	55	5MU	C4-N3	-3.03	1.27	1.33

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	2K	47	7MG	C5-C4-N3	-7.92	118.67	126.74
56	2L	47	7MG	C5-C4-N3	-7.51	119.09	126.74
24	3K	46	7MG	C5-C4-N3	-7.43	119.17	126.74
24	3L	46	7MG	C5-C4-N3	-5.96	120.67	126.74
24	3L	8	4SU	C5-C4-N3	-4.59	118.70	123.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	2K	33	OMC	2	0
23	2K	47	7MG	3	0
23	2K	55	5MU	1	0
23	2K	8	4SU	1	0
56	2L	33	OMC	1	0
56	2L	47	7MG	2	0
56	2L	56	PSU	2	0
56	2L	8	4SU	1	0
24	3K	37	MIA	1	0
24	3K	39	PSU	2	0
24	3K	46	7MG	2	0
24	3K	55	PSU	2	0
24	3K	8	4SU	1	0
24	3L	37	MIA	2	0
24	3L	55	PSU	1	0
24	3L	8	4SU	5	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 995 ligands modelled in this entry, 995 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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
56	2L	1
22	1K	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1K	69:C	O3'	70:C	P	5.53
1	2L	54:G	O3'	55:U	P	2.94

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	1497/1522 (98%)	-0.58	0 100 100	70, 114, 187, 287	0
1	1G	1497/1522 (98%)	-0.66	0 100 100	79, 129, 197, 297	0
2	12	237/256 (92%)	0.88	43 (18%) 2 1	143, 175, 203, 210	0
2	1E	237/256 (92%)	0.26	14 (5%) 26 20	124, 155, 178, 191	0
3	22	206/239 (86%)	1.02	35 (16%) 2 2	132, 155, 182, 195	0
3	2E	205/239 (85%)	0.72	22 (10%) 8 6	101, 124, 154, 164	0
4	32	208/209 (99%)	0.73	21 (10%) 9 8	118, 137, 157, 163	0
4	3E	208/209 (99%)	0.60	17 (8%) 14 11	100, 127, 145, 153	0
5	42	151/162 (93%)	0.37	7 (4%) 36 30	115, 132, 153, 171	0
5	4E	151/162 (93%)	0.75	17 (11%) 7 5	93, 117, 136, 166	0
6	52	101/101 (100%)	0.49	2 (1%) 68 62	102, 116, 134, 144	0
6	5E	101/101 (100%)	0.33	2 (1%) 68 62	89, 112, 132, 144	0
7	62	147/156 (94%)	0.28	11 (7%) 17 14	122, 138, 151, 165	0
7	6E	155/156 (99%)	0.35	14 (9%) 12 9	108, 123, 152, 169	0
8	72	138/138 (100%)	0.36	6 (4%) 39 32	111, 137, 150, 157	0
8	7E	138/138 (100%)	0.71	23 (16%) 2 2	107, 122, 136, 144	0
9	82	127/128 (99%)	0.42	5 (3%) 43 36	125, 161, 179, 186	0
9	8E	127/128 (99%)	0.30	1 (0%) 87 84	98, 142, 161, 174	0
10	1A	66/105 (62%)	0.47	5 (7%) 17 14	130, 158, 176, 188	0
10	1I	99/105 (94%)	0.91	20 (20%) 1 1	98, 147, 178, 183	0
11	2A	116/129 (89%)	1.32	29 (25%) 1 1	103, 124, 142, 169	0
11	2I	119/129 (92%)	0.66	8 (6%) 21 17	85, 112, 156, 180	0
12	3A	122/132 (92%)	0.50	9 (7%) 17 14	97, 113, 129, 145	0
12	3I	122/132 (92%)	0.24	4 (3%) 50 43	83, 93, 119, 143	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	4A	117/126 (92%)	0.66	21 (17%) 2 1	125, 155, 178, 192	0
13	4I	117/126 (92%)	0.15	4 (3%) 49 42	95, 131, 145, 162	0
14	5A	52/61 (85%)	0.83	5 (9%) 10 9	138, 151, 163, 167	0
14	5I	60/61 (98%)	0.45	2 (3%) 50 43	101, 113, 127, 134	0
15	6A	88/89 (98%)	-0.04	0 100 100	99, 120, 141, 148	0
15	6I	88/89 (98%)	0.17	5 (5%) 27 22	87, 110, 128, 134	0
16	7A	84/88 (95%)	0.23	1 (1%) 81 76	108, 123, 139, 168	0
16	7I	84/88 (95%)	0.67	9 (10%) 8 6	113, 127, 155, 174	0
17	8A	99/105 (94%)	0.35	4 (4%) 42 34	101, 116, 131, 136	0
17	8I	100/105 (95%)	0.34	5 (5%) 32 26	100, 117, 127, 131	0
18	9A	72/88 (81%)	1.34	15 (20%) 1 1	109, 130, 167, 194	0
18	9I	72/88 (81%)	0.81	7 (9%) 10 9	96, 115, 152, 185	0
19	AA	78/93 (83%)	1.07	18 (23%) 1 1	137, 178, 195, 198	0
19	AI	81/93 (87%)	0.21	2 (2%) 61 54	107, 129, 146, 157	0
20	BA	99/106 (93%)	0.38	3 (3%) 54 47	104, 122, 141, 156	0
20	BI	99/106 (93%)	0.29	2 (2%) 68 62	120, 135, 156, 164	0
21	1B	22/27 (81%)	1.42	7 (31%) 1 1	122, 142, 149, 152	0
21	1F	25/27 (92%)	0.42	1 (4%) 42 34	106, 118, 135, 147	0
22	1K	68/77 (88%)	0.51	4 (5%) 26 20	117, 196, 214, 216	0
23	2K	72/77 (93%)	-0.42	0 100 100	80, 108, 138, 146	0
24	3K	70/76 (92%)	-0.25	1 (1%) 78 73	83, 231, 262, 266	0
24	3L	70/76 (92%)	-0.09	2 (2%) 55 49	96, 239, 268, 279	0
25	4K	13/27 (48%)	0.29	1 (7%) 16 13	83, 115, 170, 170	0
25	4L	9/27 (33%)	-0.04	0 100 100	100, 136, 151, 157	0
26	14	2877/2917 (98%)	-0.38	17 (0%) 90 88	62, 96, 237, 329	0
26	1H	2902/2917 (99%)	-0.37	12 (0%) 93 92	50, 81, 226, 314	0
27	16	122/122 (100%)	-0.65	1 (0%) 87 84	76, 99, 116, 199	0
27	1J	122/122 (100%)	-0.75	0 100 100	98, 136, 162, 199	0
28	7I	93/229 (40%)	1.10	21 (22%) 1 1	109, 115, 131, 143	0
29	11	272/276 (98%)	0.12	0 100 100	52, 71, 87, 95	0
29	19	273/276 (98%)	0.28	4 (1%) 76 71	60, 83, 100, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
30	21	205/206 (99%)	0.60	23 (11%) 7 5	59, 95, 137, 152	0
30	29	205/206 (99%)	0.23	6 (2%) 55 49	70, 104, 144, 178	0
31	31	202/210 (96%)	0.10	2 (0%) 84 80	55, 84, 120, 142	0
31	39	206/210 (98%)	0.55	11 (5%) 30 24	70, 110, 163, 190	0
32	41	181/182 (99%)	0.42	9 (4%) 32 26	85, 110, 141, 149	0
32	49	181/182 (99%)	0.98	38 (20%) 1 1	133, 152, 174, 187	0
33	51	174/180 (96%)	0.19	3 (1%) 73 67	88, 108, 123, 136	0
33	59	170/180 (94%)	1.27	44 (25%) 1 1	131, 193, 221, 241	0
34	61	146/148 (98%)	0.58	15 (10%) 9 7	81, 135, 151, 154	0
34	69	146/148 (98%)	0.46	16 (10%) 7 6	97, 138, 155, 163	0
35	15	138/140 (98%)	0.44	5 (3%) 46 39	87, 114, 146, 168	0
35	58	138/140 (98%)	0.33	4 (2%) 55 49	73, 95, 129, 147	0
36	25	122/122 (100%)	0.38	4 (3%) 50 43	75, 96, 112, 124	0
36	68	122/122 (100%)	0.52	4 (3%) 50 43	65, 85, 103, 115	0
37	35	147/150 (98%)	0.82	18 (12%) 5 4	70, 114, 145, 159	0
37	78	150/150 (100%)	0.01	3 (2%) 68 62	57, 85, 111, 159	0
38	45	141/141 (100%)	1.17	30 (21%) 1 1	80, 111, 139, 153	0
38	88	137/141 (97%)	0.39	7 (5%) 32 25	63, 84, 103, 146	0
39	55	117/118 (99%)	0.32	5 (4%) 39 32	69, 88, 105, 121	0
39	98	118/118 (100%)	0.53	4 (3%) 49 42	70, 91, 111, 121	0
40	65	111/112 (99%)	0.51	8 (7%) 18 15	104, 128, 140, 146	0
40	A8	111/112 (99%)	0.80	15 (13%) 4 3	81, 95, 120, 129	0
41	75	137/146 (93%)	0.12	4 (2%) 55 49	86, 104, 164, 200	0
41	B8	137/146 (93%)	0.11	1 (0%) 89 86	80, 99, 151, 186	0
42	85	117/118 (99%)	0.24	1 (0%) 85 82	76, 103, 142, 163	0
42	C8	117/118 (99%)	0.22	4 (3%) 49 42	63, 83, 117, 136	0
43	95	101/101 (100%)	0.98	19 (18%) 2 1	72, 129, 143, 161	0
43	D8	101/101 (100%)	0.45	7 (6%) 20 16	63, 108, 131, 145	0
44	A5	111/113 (98%)	0.29	2 (1%) 71 65	69, 83, 117, 151	0
44	E8	113/113 (100%)	0.25	3 (2%) 58 51	66, 80, 116, 158	0
45	B5	92/96 (95%)	0.60	4 (4%) 39 32	78, 94, 113, 133	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
45	F8	94/96 (97%)	0.60	5 (5%) 30 24	65, 77, 101, 118	0
46	C5	104/110 (94%)	0.84	19 (18%) 2 1	98, 120, 152, 163	0
46	G8	104/110 (94%)	0.17	3 (2%) 55 49	76, 98, 132, 143	0
47	D5	137/206 (66%)	1.18	34 (24%) 1 1	118, 147, 190, 205	0
47	H8	135/206 (65%)	0.51	7 (5%) 31 25	89, 115, 161, 183	0
48	E5	77/85 (90%)	0.84	7 (9%) 11 9	81, 97, 115, 148	0
48	I8	80/85 (94%)	0.42	5 (6%) 23 19	66, 78, 106, 122	0
49	F5	94/98 (95%)	0.66	8 (8%) 13 10	72, 94, 135, 145	0
49	J8	97/98 (98%)	0.28	3 (3%) 52 46	60, 79, 122, 155	0
50	G5	66/72 (91%)	0.61	4 (6%) 25 20	95, 113, 128, 155	0
50	K8	67/72 (93%)	0.35	1 (1%) 76 71	70, 89, 107, 139	0
51	H5	59/60 (98%)	0.76	7 (11%) 6 5	87, 104, 146, 161	0
51	L8	57/60 (95%)	0.09	0 100 100	70, 86, 105, 121	0
52	I5	63/71 (88%)	1.50	25 (39%) 0 1	163, 192, 207, 213	0
52	M8	66/71 (92%)	0.77	9 (13%) 4 3	120, 156, 195, 205	0
53	J5	56/60 (93%)	0.13	2 (3%) 46 39	69, 94, 139, 149	0
53	N8	54/60 (90%)	0.19	2 (3%) 45 38	62, 100, 155, 165	0
54	L5	46/49 (93%)	0.09	1 (2%) 65 59	61, 71, 82, 95	0
54	P8	47/49 (95%)	-0.19	0 100 100	53, 60, 76, 85	0
55	M5	60/65 (92%)	0.56	3 (5%) 32 26	78, 90, 114, 129	0
55	Q8	60/65 (92%)	0.13	0 100 100	64, 77, 102, 113	0
56	2L	73/77 (94%)	-0.34	0 100 100	91, 123, 156, 173	0
All	All	20765/21734 (95%)	0.08	953 (4%) 36 30	50, 110, 186, 329	0

The worst 5 of 953 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	4A	6	GLY	10.5
31	39	208	GLY	9.4
30	21	204	ALA	8.0
18	9A	88	LYS	8.0
38	45	65	PHE	7.8

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
24	PSU	3K	55	20/21	0.78	0.16	-	233,248,253,253	0
24	4SU	3K	8	20/21	0.44	0.22	-	240,248,252,254	0
24	MIA	3L	37	29/30	0.78	0.28	-	158,185,200,208	0
23	7MG	2K	47	24/25	0.94	0.13	-	113,121,127,130	0
23	PSU	2K	56	20/21	0.93	0.12	-	95,103,113,113	0
22	OMC	1K	33	21/22	0.93	0.18	-	114,132,138,141	0
22	5MU	1K	55	21/22	0.87	0.19	-	147,158,168,170	0
24	4SU	3L	8	20/21	0.70	0.12	-	239,245,250,250	0
24	PSU	3L	55	20/21	0.71	0.18	-	244,253,256,256	0
23	5MU	2K	55	21/22	0.95	0.13	-	96,109,114,116	0
24	7MG	3K	46	24/25	0.69	0.19	-	234,242,250,254	0
24	7MG	3L	46	24/25	0.75	0.16	-	242,245,250,252	0
56	OMC	2L	33	21/22	0.96	0.15	-	105,114,117,119	0
56	PSU	2L	56	20/21	0.92	0.10	-	116,124,129,135	0
24	PSU	3L	32	20/21	0.80	0.18	-	165,176,183,185	0
24	PSU	3K	39	20/21	0.94	0.12	-	126,143,151,159	0
24	PSU	3K	32	20/21	0.88	0.19	-	149,154,157,159	0
23	OMC	2K	33	21/22	0.95	0.16	-	84,91,99,106	0
56	4SU	2L	8	20/21	0.91	0.16	-	127,132,138,139	0
56	7MG	2L	47	24/25	0.94	0.13	-	137,143,153,157	0
24	MIA	3K	37	29/30	0.90	0.19	-	139,155,160,161	0
23	4SU	2K	8	20/21	0.92	0.15	-	101,110,114,119	0
24	PSU	3L	39	20/21	0.89	0.15	-	156,173,181,188	0

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3212	1/1	0.70	1.00	72.24	86,86,86,86	0
57	MG	1H	3274	1/1	0.81	0.87	71.11	86,86,86,86	0
57	MG	14	3060	1/1	0.81	0.55	60.52	83,83,83,83	0
57	MG	1H	3218	1/1	0.84	0.55	43.50	91,91,91,91	0
57	MG	1H	3226	1/1	0.89	0.42	39.78	70,70,70,70	0
57	MG	14	3020	1/1	0.81	0.59	36.59	76,76,76,76	0
57	MG	1H	3140	1/1	0.76	0.33	35.61	74,74,74,74	0
57	MG	14	3054	1/1	0.98	0.63	34.33	53,53,53,53	0
57	MG	1H	3242	1/1	0.72	0.54	32.03	79,79,79,79	0
57	MG	1H	3134	1/1	0.95	0.46	29.57	62,62,62,62	0
57	MG	14	3094	1/1	0.64	0.56	29.39	94,94,94,94	0
57	MG	14	3124	1/1	0.67	0.49	28.65	97,97,97,97	0
57	MG	1H	3269	1/1	0.81	0.69	28.43	74,74,74,74	0
57	MG	1H	3120	1/1	0.94	0.42	27.61	56,56,56,56	0
57	MG	1H	3073	1/1	0.78	0.36	26.13	55,55,55,55	0
57	MG	1H	3171	1/1	0.92	0.47	24.78	84,84,84,84	0
57	MG	13	1655	1/1	0.83	0.40	21.69	81,81,81,81	0
57	MG	1H	3041	1/1	0.97	0.30	20.65	68,68,68,68	0
57	MG	14	3179	1/1	0.57	0.56	19.28	100,100,100,100	0
57	MG	1H	3106	1/1	0.87	0.40	18.65	69,69,69,69	0
57	MG	14	3166	1/1	0.66	0.48	18.48	82,82,82,82	0
57	MG	14	3039	1/1	0.93	0.59	18.16	75,75,75,75	0
57	MG	14	3091	1/1	0.95	0.54	17.65	69,69,69,69	0
57	MG	1H	3122	1/1	0.93	0.39	16.96	81,81,81,81	0
57	MG	1H	3109	1/1	0.82	0.27	16.48	76,76,76,76	0
57	MG	13	1610	1/1	0.93	0.24	16.09	72,72,72,72	0
57	MG	1H	3111	1/1	0.82	0.39	15.65	71,71,71,71	0
57	MG	14	3049	1/1	0.98	0.38	15.53	63,63,63,63	0
57	MG	14	3047	1/1	0.90	0.43	15.21	56,56,56,56	0
57	MG	14	3100	1/1	0.86	0.32	15.19	82,82,82,82	0
57	MG	14	3101	1/1	0.95	0.42	14.88	84,84,84,84	0
57	MG	14	3036	1/1	0.90	0.38	14.37	64,64,64,64	0
57	MG	14	3197	1/1	0.91	0.32	14.34	78,78,78,78	0
57	MG	1H	3005	1/1	0.98	0.40	13.68	51,51,51,51	0
57	MG	14	3168	1/1	0.97	0.48	13.57	51,51,51,51	0
57	MG	1H	3181	1/1	0.73	0.25	13.45	75,75,75,75	0
57	MG	1G	1603	1/1	0.95	0.34	13.26	77,77,77,77	0
57	MG	1H	3048	1/1	0.96	0.30	13.22	69,69,69,69	0
57	MG	1H	3090	1/1	0.89	0.33	12.71	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3192	1/1	0.98	0.32	12.65	66,66,66,66	0
57	MG	1H	3027	1/1	0.98	0.34	12.57	35,35,35,35	0
57	MG	14	3019	1/1	0.97	0.41	12.55	77,77,77,77	0
57	MG	13	1658	1/1	0.99	0.25	12.52	91,91,91,91	0
57	MG	14	3035	1/1	0.95	0.38	12.40	59,59,59,59	0
57	MG	14	3045	1/1	0.95	0.30	12.39	66,66,66,66	0
57	MG	1H	3037	1/1	0.91	0.36	12.27	55,55,55,55	0
57	MG	1H	3042	1/1	0.86	0.27	12.22	77,77,77,77	0
57	MG	14	3063	1/1	0.93	0.25	12.03	80,80,80,80	0
57	MG	14	3103	1/1	0.67	0.38	11.42	74,74,74,74	0
57	MG	1H	3246	1/1	0.98	0.43	11.40	78,78,78,78	0
57	MG	14	3011	1/1	0.98	0.42	11.31	60,60,60,60	0
57	MG	14	3009	1/1	0.99	0.36	11.09	59,59,59,59	0
57	MG	1H	3002	1/1	0.98	0.38	10.99	47,47,47,47	0
57	MG	14	3188	1/1	0.98	0.41	10.77	87,87,87,87	0
57	MG	14	3218	1/1	0.61	0.42	10.70	74,74,74,74	0
57	MG	13	1644	1/1	0.96	0.40	10.68	78,78,78,78	0
57	MG	13	1622	1/1	0.97	0.34	10.38	65,65,65,65	0
57	MG	14	3062	1/1	0.96	0.29	10.24	70,70,70,70	0
57	MG	13	1650	1/1	0.84	0.34	10.19	88,88,88,88	0
57	MG	1G	1650	1/1	0.94	0.31	10.07	86,86,86,86	0
57	MG	13	1618	1/1	0.87	0.39	9.99	63,63,63,63	0
57	MG	14	3126	1/1	0.96	0.37	9.66	66,66,66,66	0
57	MG	1H	3032	1/1	0.97	0.30	9.63	75,75,75,75	0
57	MG	1G	1602	1/1	0.97	0.41	8.91	79,79,79,79	0
57	MG	14	3160	1/1	0.79	0.21	8.65	83,83,83,83	0
57	MG	1G	1662	1/1	0.98	0.37	8.64	91,91,91,91	0
57	MG	1H	3241	1/1	0.93	0.36	8.62	73,73,73,73	0
57	MG	14	3159	1/1	0.98	0.32	8.52	73,73,73,73	0
57	MG	1H	3098	1/1	0.76	0.27	8.36	83,83,83,83	0
57	MG	14	3105	1/1	0.92	0.23	8.35	89,89,89,89	0
57	MG	14	3204	1/1	0.96	0.30	8.23	71,71,71,71	0
57	MG	13	1619	1/1	0.90	0.28	8.15	72,72,72,72	0
57	MG	14	3141	1/1	0.91	0.29	8.11	67,67,67,67	0
57	MG	1H	3044	1/1	0.96	0.24	7.95	60,60,60,60	0
57	MG	1H	3051	1/1	0.99	0.32	7.88	50,50,50,50	0
57	MG	1H	3082	1/1	0.88	0.29	7.84	60,60,60,60	0
57	MG	1H	3052	1/1	0.99	0.36	7.64	42,42,42,42	0
57	MG	1H	3089	1/1	0.91	0.29	7.55	74,74,74,74	0
57	MG	14	3133	1/1	0.96	0.21	7.52	77,77,77,77	0
57	MG	14	3059	1/1	0.98	0.31	7.24	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3022	1/1	0.93	0.23	7.24	64,64,64,64	0
57	MG	13	1657	1/1	0.90	0.24	7.04	129,129,129,129	0
57	MG	1G	1617	1/1	0.98	0.25	6.89	88,88,88,88	0
57	MG	14	3014	1/1	0.96	0.31	6.89	72,72,72,72	0
57	MG	1H	3117	1/1	0.94	0.23	6.82	74,74,74,74	0
57	MG	1G	1660	1/1	0.92	0.23	6.65	124,124,124,124	0
57	MG	1H	3093	1/1	0.95	0.25	6.60	69,69,69,69	0
57	MG	14	3173	1/1	0.98	0.28	6.60	44,44,44,44	0
57	MG	13	1601	1/1	0.96	0.25	6.36	82,82,82,82	0
57	MG	14	3004	1/1	0.99	0.30	6.33	60,60,60,60	0
57	MG	1H	3007	1/1	0.98	0.38	6.33	47,47,47,47	0
57	MG	14	3214	1/1	0.85	0.25	6.30	84,84,84,84	0
57	MG	1H	3020	1/1	0.98	0.26	6.28	70,70,70,70	0
57	MG	1H	3203	1/1	0.91	0.28	6.10	62,62,62,62	0
57	MG	1H	3036	1/1	0.96	0.27	6.08	57,57,57,57	0
57	MG	1H	3113	1/1	0.96	0.28	6.08	81,81,81,81	0
57	MG	14	3058	1/1	0.93	0.32	5.98	77,77,77,77	0
57	MG	14	3065	1/1	0.95	0.33	5.97	58,58,58,58	0
57	MG	1H	3060	1/1	0.88	0.29	5.89	63,63,63,63	0
57	MG	14	3048	1/1	0.92	0.27	5.87	59,59,59,59	0
57	MG	14	3215	1/1	0.93	0.28	5.85	97,97,97,97	0
57	MG	2K	101	1/1	0.98	0.37	5.76	77,77,77,77	0
57	MG	14	3052	1/1	0.98	0.28	5.76	63,63,63,63	0
57	MG	1H	3063	1/1	0.97	0.29	5.73	56,56,56,56	0
57	MG	1H	3200	1/1	0.96	0.22	5.73	73,73,73,73	0
57	MG	13	1647	1/1	0.91	0.31	5.69	81,81,81,81	0
57	MG	1G	1627	1/1	0.96	0.30	5.63	103,103,103,103	0
57	MG	1H	3019	1/1	0.95	0.30	5.46	72,72,72,72	0
57	MG	1G	1616	1/1	0.93	0.20	5.32	105,105,105,105	0
57	MG	14	3038	1/1	0.99	0.39	5.32	55,55,55,55	0
57	MG	13	1661	1/1	0.72	0.40	5.26	89,89,89,89	0
57	MG	1H	3046	1/1	0.96	0.46	5.26	75,75,75,75	0
57	MG	13	1646	1/1	0.89	0.18	5.26	102,102,102,102	0
57	MG	13	1631	1/1	0.99	0.27	5.25	83,83,83,83	0
57	MG	13	1621	1/1	0.93	0.22	5.25	88,88,88,88	0
57	MG	14	3127	1/1	0.93	0.22	5.15	77,77,77,77	0
57	MG	1H	3016	1/1	0.94	0.24	4.87	71,71,71,71	0
57	MG	14	3155	1/1	0.99	0.31	4.75	70,70,70,70	0
57	MG	2L	101	1/1	0.98	0.31	4.61	80,80,80,80	0
57	MG	1H	3029	1/1	0.99	0.25	4.46	55,55,55,55	0
57	MG	14	3030	1/1	0.98	0.24	4.41	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3148	1/1	0.61	0.16	4.40	64,64,64,64	0
57	MG	14	3007	1/1	0.98	0.27	4.32	76,76,76,76	0
57	MG	13	1643	1/1	0.90	0.23	4.09	91,91,91,91	0
57	MG	13	1635	1/1	0.93	0.20	4.03	92,92,92,92	0
57	MG	L8	101	1/1	0.88	0.35	4.02	70,70,70,70	0
57	MG	14	3192	1/1	0.95	0.37	3.84	74,74,74,74	0
57	MG	1H	3064	1/1	0.79	0.26	3.80	52,52,52,52	0
57	MG	1H	3116	1/1	0.86	0.18	3.71	80,80,80,80	0
57	MG	14	3076	1/1	0.95	0.20	3.69	80,80,80,80	0
57	MG	1G	1601	1/1	0.98	0.27	3.63	90,90,90,90	0
57	MG	4E	201	1/1	0.93	0.46	3.62	88,88,88,88	0
57	MG	1H	3102	1/1	0.71	0.28	3.56	82,82,82,82	0
57	MG	14	3082	1/1	0.95	0.23	3.37	63,63,63,63	0
57	MG	J8	101	1/1	0.97	0.37	3.30	62,62,62,62	0
57	MG	1H	3265	1/1	0.93	0.20	3.29	83,83,83,83	0
57	MG	14	3024	1/1	0.97	0.22	3.23	78,78,78,78	0
57	MG	14	3081	1/1	0.96	0.20	3.14	94,94,94,94	0
57	MG	1H	3150	1/1	0.87	0.28	3.13	65,65,65,65	0
57	MG	14	3041	1/1	0.89	0.24	3.12	60,60,60,60	0
57	MG	14	3119	1/1	0.91	0.24	3.10	67,67,67,67	0
57	MG	14	3142	1/1	0.70	0.21	2.89	86,86,86,86	0
57	MG	1H	3136	1/1	0.81	0.22	2.85	55,55,55,55	0
57	MG	1H	3275	1/1	0.91	0.21	2.84	63,63,63,63	0
57	MG	11	302	1/1	0.90	0.35	2.79	48,48,48,48	0
57	MG	1G	1630	1/1	0.95	0.17	2.77	102,102,102,102	0
57	MG	14	3186	1/1	0.92	0.35	2.77	75,75,75,75	0
57	MG	14	3261	1/1	0.99	0.23	2.75	56,56,56,56	0
57	MG	1H	3091	1/1	0.87	0.21	2.56	71,71,71,71	0
57	MG	14	3113	1/1	0.94	0.22	2.48	76,76,76,76	0
57	MG	78	202	1/1	0.95	0.33	2.32	84,84,84,84	0
57	MG	1H	3025	1/1	0.89	0.18	2.24	66,66,66,66	0
57	MG	14	3093	1/1	0.85	0.20	2.20	62,62,62,62	0
57	MG	88	201	1/1	0.98	0.39	2.06	76,76,76,76	0
57	MG	13	1624	1/1	0.92	0.16	1.94	84,84,84,84	0
57	MG	14	3029	1/1	0.98	0.21	1.88	78,78,78,78	0
57	MG	14	3262	1/1	0.96	0.21	1.82	55,55,55,55	0
57	MG	1G	1638	1/1	0.98	0.21	1.73	83,83,83,83	0
57	MG	13	1606	1/1	0.96	0.17	1.72	83,83,83,83	0
57	MG	1H	3026	1/1	0.99	0.21	1.69	62,62,62,62	0
57	MG	1H	3156	1/1	0.93	0.31	1.66	81,81,81,81	0
57	MG	1H	3176	1/1	0.99	0.23	1.61	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3122	1/1	0.80	0.18	1.47	76,76,76,76	0
57	MG	14	3175	1/1	0.91	0.31	1.30	75,75,75,75	0
57	MG	1H	3085	1/1	0.91	0.16	1.24	58,58,58,58	0
57	MG	13	1609	1/1	0.95	0.17	1.24	82,82,82,82	0
57	MG	16	201	1/1	0.92	0.17	1.18	90,90,90,90	0
57	MG	1G	1642	1/1	0.89	0.26	1.15	93,93,93,93	0
58	ZN	C5	201	1/1	0.85	0.22	1.14	187,187,187,187	0
57	MG	1H	3144	1/1	0.97	0.21	1.10	95,95,95,95	0
57	MG	1G	1641	1/1	0.86	0.22	1.03	113,113,113,113	0
57	MG	1H	3212	1/1	0.97	0.24	1.01	62,62,62,62	0
57	MG	13	1652	1/1	0.83	0.16	0.94	104,104,104,104	0
57	MG	14	3111	1/1	0.80	0.34	0.86	89,89,89,89	0
57	MG	1H	3210	1/1	0.94	0.15	0.81	70,70,70,70	0
57	MG	13	1656	1/1	0.91	0.18	0.75	96,96,96,96	0
58	ZN	G8	201	1/1	0.81	0.26	0.74	176,176,176,176	0
57	MG	1H	3147	1/1	0.91	0.16	0.67	74,74,74,74	0
57	MG	1H	3435	1/1	0.96	0.20	0.66	90,90,90,90	0
57	MG	1H	3023	1/1	0.92	0.18	0.64	68,68,68,68	0
58	ZN	32	301	1/1	0.98	0.30	0.62	117,117,117,117	0
57	MG	1H	3074	1/1	0.71	0.21	0.62	63,63,63,63	0
57	MG	14	3136	1/1	0.98	0.20	0.60	66,66,66,66	0
57	MG	1H	3392	1/1	0.84	0.16	0.49	96,96,96,96	0
57	MG	1H	3354	1/1	0.90	0.20	0.48	66,66,66,66	0
57	MG	14	3037	1/1	0.98	0.26	0.40	61,61,61,61	0
58	ZN	3E	302	1/1	0.96	0.32	0.38	95,95,95,95	0
57	MG	1H	3133	1/1	0.95	0.21	0.38	54,54,54,54	0
57	MG	14	3130	1/1	0.96	0.19	0.38	84,84,84,84	0
57	MG	13	1654	1/1	0.98	0.12	0.30	133,133,133,133	0
57	MG	41	202	1/1	0.94	0.17	0.28	93,93,93,93	0
57	MG	1H	3079	1/1	0.99	0.23	0.26	66,66,66,66	0
57	MG	13	1611	1/1	0.93	0.18	0.25	107,107,107,107	0
57	MG	1G	1646	1/1	0.93	0.16	0.19	117,117,117,117	0
57	MG	14	3202	1/1	0.99	0.21	0.11	88,88,88,88	0
57	MG	1G	1613	1/1	0.93	0.17	0.05	89,89,89,89	0
57	MG	13	1605	1/1	0.96	0.19	-0.02	75,75,75,75	0
57	MG	13	1604	1/1	0.98	0.19	-0.04	79,79,79,79	0
57	MG	1G	1628	1/1	0.94	0.17	-0.06	108,108,108,108	0
57	MG	1H	3050	1/1	0.94	0.19	-0.11	68,68,68,68	0
57	MG	1H	3065	1/1	0.98	0.18	-0.16	58,58,58,58	0
57	MG	14	3140	1/1	0.93	0.20	-0.23	54,54,54,54	0
57	MG	J8	102	1/1	0.94	0.19	-0.23	68,68,68,68	0
57	MG	14	3272	1/1	0.98	0.21	-0.32	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	29	302	1/1	0.77	0.17	-0.33	68,68,68,68	0
57	MG	13	1628	1/1	0.89	0.19	-0.38	90,90,90,90	0
57	MG	1H	3342	1/1	0.94	0.17	-0.52	63,63,63,63	0
57	MG	55	201	1/1	0.95	0.18	-0.53	57,57,57,57	0
57	MG	1G	1632	1/1	0.98	0.12	-0.66	131,131,131,131	0
57	MG	1H	3375	1/1	0.98	0.16	-0.68	60,60,60,60	0
57	MG	14	3134	1/1	0.94	0.14	-0.69	72,72,72,72	0
57	MG	14	3231	1/1	0.95	0.18	-0.73	66,66,66,66	0
57	MG	13	1685	1/1	0.94	0.13	-0.75	93,93,93,93	0
57	MG	35	201	1/1	0.92	0.13	-0.76	77,77,77,77	0
57	MG	1H	3043	1/1	0.92	0.15	-0.86	75,75,75,75	0
57	MG	16	204	1/1	0.89	0.10	-0.89	78,78,78,78	0
57	MG	14	3283	1/1	0.89	0.14	-0.90	74,74,74,74	0
57	MG	14	3222	1/1	0.96	0.16	-0.91	62,62,62,62	0
57	MG	1H	3049	1/1	0.96	0.16	-0.91	58,58,58,58	0
58	ZN	5I	101	1/1	0.98	0.13	-0.92	100,100,100,100	0
57	MG	1H	3057	1/1	0.97	0.18	-0.92	60,60,60,60	0
57	MG	45	201	1/1	0.69	0.16	-0.93	98,98,98,98	0
57	MG	1G	1643	1/1	0.98	0.10	-0.97	97,97,97,97	0
57	MG	1H	3056	1/1	0.96	0.18	-1.03	46,46,46,46	0
57	MG	14	3256	1/1	0.97	0.15	-1.03	57,57,57,57	0
57	MG	13	1695	1/1	0.98	0.09	-1.07	87,87,87,87	0
57	MG	1H	3018	1/1	0.78	0.12	-1.11	80,80,80,80	0
57	MG	13	1699	1/1	0.90	0.07	-1.12	119,119,119,119	0
57	MG	13	1691	1/1	0.98	0.12	-1.16	78,78,78,78	0
58	ZN	5A	101	1/1	0.96	0.10	-1.16	139,139,139,139	0
57	MG	1G	1640	1/1	0.96	0.04	-1.19	107,107,107,107	0
57	MG	14	3221	1/1	0.97	0.18	-1.25	67,67,67,67	0
57	MG	1H	3033	1/1	0.97	0.18	-1.33	54,54,54,54	0
57	MG	14	3254	1/1	0.93	0.17	-1.35	69,69,69,69	0
57	MG	1H	3388	1/1	0.92	0.09	-1.37	75,75,75,75	0
57	MG	14	3241	1/1	0.96	0.12	-1.39	69,69,69,69	0
57	MG	1G	1667	1/1	0.97	0.10	-1.41	98,98,98,98	0
57	MG	1H	3157	1/1	0.87	0.13	-1.45	89,89,89,89	0
57	MG	1G	1607	1/1	0.94	0.12	-1.51	98,98,98,98	0
57	MG	3E	301	1/1	0.89	0.13	-1.51	127,127,127,127	0
57	MG	1G	1670	1/1	0.84	0.11	-1.52	129,129,129,129	0
57	MG	1H	3389	1/1	0.96	0.09	-1.57	87,87,87,87	0
57	MG	1H	3330	1/1	0.98	0.16	-1.59	49,49,49,49	0
57	MG	41	201	1/1	0.92	0.09	-1.59	82,82,82,82	0
57	MG	14	3121	1/1	0.98	0.15	-1.59	65,65,65,65	0
57	MG	1H	3078	1/1	0.79	0.14	-1.62	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3258	1/1	0.95	0.15	-1.69	80,80,80,80	0
57	MG	1H	3339	1/1	0.98	0.13	-1.69	50,50,50,50	0
57	MG	14	3322	1/1	0.96	0.14	-1.70	79,79,79,79	0
57	MG	13	1682	1/1	0.96	0.16	-1.70	84,84,84,84	0
57	MG	1H	3068	1/1	0.89	0.10	-1.71	63,63,63,63	0
57	MG	16	203	1/1	0.89	0.10	-1.73	98,98,98,98	0
57	MG	14	3242	1/1	0.97	0.13	-1.75	65,65,65,65	0
57	MG	1H	3105	1/1	0.95	0.13	-1.81	81,81,81,81	0
57	MG	13	1678	1/1	0.95	0.05	-1.82	106,106,106,106	0
57	MG	1H	3393	1/1	0.96	0.10	-1.83	58,58,58,58	0
57	MG	14	3285	1/1	0.98	0.11	-1.85	87,87,87,87	0
57	MG	1H	3138	1/1	0.84	0.11	-1.85	67,67,67,67	0
57	MG	14	3224	1/1	0.97	0.13	-1.86	55,55,55,55	0
57	MG	1H	3058	1/1	0.96	0.11	-1.87	71,71,71,71	0
57	MG	4I	201	1/1	0.96	0.06	-1.92	97,97,97,97	0
57	MG	14	3238	1/1	0.94	0.13	-1.92	76,76,76,76	0
57	MG	14	3236	1/1	0.96	0.12	-1.94	63,63,63,63	0
57	MG	1H	3345	1/1	0.98	0.15	-2.09	53,53,53,53	0
57	MG	1H	3441	1/1	0.93	0.13	-2.10	70,70,70,70	0
57	MG	13	1653	1/1	0.98	0.12	-2.11	92,92,92,92	0
57	MG	14	3223	1/1	0.93	0.13	-2.15	79,79,79,79	0
57	MG	14	3247	1/1	0.99	0.12	-2.20	65,65,65,65	0
57	MG	14	3017	1/1	0.94	0.15	-2.20	75,75,75,75	0
57	MG	14	3118	1/1	0.96	0.16	-2.23	58,58,58,58	0
57	MG	14	3280	1/1	0.97	0.14	-2.25	75,75,75,75	0
57	MG	1H	3297	1/1	0.99	0.12	-2.29	47,47,47,47	0
57	MG	1H	3302	1/1	0.98	0.15	-2.33	60,60,60,60	0
57	MG	1H	3402	1/1	0.92	0.10	-2.47	88,88,88,88	0
57	MG	14	3022	1/1	0.80	0.08	-2.49	89,89,89,89	0
57	MG	1G	1609	1/1	0.97	0.11	-2.52	106,106,106,106	0
57	MG	1G	1671	1/1	0.96	0.12	-2.52	117,117,117,117	0
57	MG	13	1687	1/1	0.89	0.07	-2.55	103,103,103,103	0
57	MG	1H	3432	1/1	0.96	0.11	-2.59	56,56,56,56	0
57	MG	1H	3340	1/1	0.96	0.14	-2.62	64,64,64,64	0
57	MG	13	1674	1/1	0.92	0.13	-2.74	83,83,83,83	0
57	MG	1H	3338	1/1	0.98	0.12	-2.75	60,60,60,60	0
57	MG	13	1694	1/1	0.98	0.09	-2.80	111,111,111,111	0
57	MG	14	3317	1/1	0.96	0.07	-2.80	76,76,76,76	0
57	MG	14	3078	1/1	0.99	0.10	-2.82	70,70,70,70	0
57	MG	1H	3317	1/1	0.94	0.12	-2.91	76,76,76,76	0
57	MG	1H	3298	1/1	0.96	0.14	-2.93	65,65,65,65	0
57	MG	13	1697	1/1	0.97	0.10	-2.94	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3429	1/1	0.97	0.08	-2.97	60,60,60,60	0
57	MG	1H	3316	1/1	0.90	0.08	-3.01	75,75,75,75	0
57	MG	14	3097	1/1	0.92	0.10	-3.04	62,62,62,62	0
57	MG	1H	3306	1/1	0.99	0.09	-3.07	70,70,70,70	0
57	MG	14	3274	1/1	0.98	0.10	-3.19	74,74,74,74	0
57	MG	14	3271	1/1	0.81	0.13	-3.19	92,92,92,92	0
57	MG	14	3268	1/1	0.94	0.11	-3.22	84,84,84,84	0
57	MG	1H	3420	1/1	0.95	0.12	-3.24	60,60,60,60	0
57	MG	1H	3290	1/1	0.98	0.11	-3.26	49,49,49,49	0
57	MG	1H	3362	1/1	0.97	0.15	-3.29	60,60,60,60	0
57	MG	14	3305	1/1	0.98	0.11	-3.38	74,74,74,74	0
57	MG	1H	3403	1/1	0.94	0.11	-3.45	76,76,76,76	0
57	MG	1H	3344	1/1	0.95	0.12	-3.49	57,57,57,57	0
57	MG	14	3304	1/1	0.76	0.12	-3.52	103,103,103,103	0
57	MG	1H	3124	1/1	0.92	0.12	-3.54	61,61,61,61	0
57	MG	14	3225	1/1	0.98	0.11	-3.55	55,55,55,55	0
57	MG	1H	3281	1/1	0.95	0.11	-3.62	55,55,55,55	0
57	MG	1H	3395	1/1	0.97	0.09	-3.65	73,73,73,73	0
57	MG	14	3299	1/1	0.87	0.05	-3.69	114,114,114,114	0
57	MG	14	3282	1/1	0.95	0.05	-3.89	92,92,92,92	0
57	MG	1H	3296	1/1	0.95	0.13	-3.93	51,51,51,51	0
57	MG	14	3323	1/1	0.93	0.11	-3.94	73,73,73,73	0
57	MG	14	3260	1/1	0.89	0.09	-3.94	86,86,86,86	0
57	MG	1H	3360	1/1	0.97	0.10	-3.95	67,67,67,67	0
57	MG	1H	3288	1/1	0.98	0.07	-4.05	55,55,55,55	0
57	MG	1H	3299	1/1	0.96	0.13	-4.14	49,49,49,49	0
57	MG	1H	3319	1/1	0.98	0.11	-4.23	60,60,60,60	0
57	MG	14	3250	1/1	0.93	0.12	-4.24	56,56,56,56	0
57	MG	1H	3333	1/1	0.99	0.10	-4.25	54,54,54,54	0
57	MG	14	3253	1/1	0.98	0.13	-4.27	66,66,66,66	0
57	MG	1H	3294	1/1	0.95	0.07	-4.29	65,65,65,65	0
57	MG	14	3249	1/1	0.98	0.12	-4.49	62,62,62,62	0
57	MG	1H	3311	1/1	0.95	0.08	-4.49	70,70,70,70	0
57	MG	1H	3282	1/1	0.94	0.09	-4.53	65,65,65,65	0
57	MG	14	3026	1/1	0.94	0.07	-4.55	83,83,83,83	0
57	MG	14	3306	1/1	0.93	0.07	-4.64	82,82,82,82	0
57	MG	1H	3346	1/1	0.91	0.09	-4.71	58,58,58,58	0
57	MG	14	3243	1/1	0.92	0.11	-4.80	74,74,74,74	0
57	MG	1H	3284	1/1	0.95	0.12	-4.86	51,51,51,51	0
57	MG	1H	3318	1/1	0.93	0.11	-4.93	55,55,55,55	0
57	MG	1H	3384	1/1	0.94	0.08	-4.93	68,68,68,68	0
57	MG	14	3234	1/1	0.90	0.12	-5.08	86,86,86,86	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3316	1/1	0.96	0.06	-5.10	88,88,88,88	0
57	MG	1H	3378	1/1	0.98	0.13	-5.16	59,59,59,59	0
57	MG	14	3259	1/1	0.98	0.10	-5.29	71,71,71,71	0
57	MG	14	3266	1/1	0.96	0.11	-5.58	73,73,73,73	0
57	MG	1H	3353	1/1	0.99	0.09	-6.28	62,62,62,62	0
57	MG	13	1649	1/1	0.91	0.07	-6.48	97,97,97,97	0
57	MG	1H	3314	1/1	0.71	0.10	-6.68	86,86,86,86	0
57	MG	1H	3334	1/1	0.97	0.08	-6.74	54,54,54,54	0
57	MG	1H	3373	1/1	0.97	0.05	-6.83	55,55,55,55	0
57	MG	1H	3304	1/1	0.96	0.07	-7.92	76,76,76,76	0
57	MG	1H	3426	1/1	0.96	0.07	-8.01	97,97,97,97	0
57	MG	1H	3413	1/1	0.98	0.08	-8.52	57,57,57,57	0
57	MG	14	3230	1/1	0.94	0.10	-8.86	65,65,65,65	0
57	MG	1H	3391	1/1	0.92	0.07	-9.27	91,91,91,91	0
57	MG	14	3292	1/1	0.89	0.08	-10.29	91,91,91,91	0
57	MG	1H	3285	1/1	0.98	0.12	-10.56	53,53,53,53	0
57	MG	1H	3383	1/1	0.98	0.07	-10.91	82,82,82,82	0
57	MG	1H	3434	1/1	0.93	0.14	-10.97	68,68,68,68	0
57	MG	1H	3347	1/1	0.98	0.07	-12.56	64,64,64,64	0
57	MG	14	3265	1/1	0.97	0.08	-13.37	72,72,72,72	0
57	MG	1H	3331	1/1	0.88	0.08	-16.34	74,74,74,74	0
57	MG	1H	3286	1/1	0.98	0.10	-18.34	62,62,62,62	0
57	MG	1H	3343	1/1	0.95	0.09	-19.11	57,57,57,57	0
57	MG	1H	3336	1/1	0.94	0.10	-	67,67,67,67	0
57	MG	14	3170	1/1	0.70	0.80	-	83,83,83,83	0
57	MG	1G	1648	1/1	0.70	0.25	-	99,99,99,99	0
57	MG	1H	3225	1/1	0.45	0.78	-	95,95,95,95	0
57	MG	16	208	1/1	0.73	0.09	-	102,102,102,102	0
57	MG	11	301	1/1	0.86	0.31	-	62,62,62,62	0
57	MG	14	3043	1/1	0.92	0.29	-	71,71,71,71	0
57	MG	1G	1610	1/1	0.93	0.20	-	111,111,111,111	0
57	MG	14	3313	1/1	0.94	0.06	-	101,101,101,101	0
57	MG	14	3015	1/1	0.97	0.32	-	69,69,69,69	0
57	MG	14	3157	1/1	0.86	0.76	-	79,79,79,79	0
57	MG	1H	3366	1/1	0.97	0.13	-	75,75,75,75	0
57	MG	13	1632	1/1	0.82	0.49	-	74,74,74,74	0
57	MG	1H	3153	1/1	0.96	0.63	-	83,83,83,83	0
57	MG	14	3295	1/1	0.97	0.09	-	78,78,78,78	0
57	MG	1H	3419	1/1	0.94	0.10	-	83,83,83,83	0
57	MG	1G	1651	1/1	0.72	0.59	-	94,94,94,94	0
57	MG	1H	3287	1/1	0.92	0.10	-	71,71,71,71	0
57	MG	16	205	1/1	0.58	0.40	-	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3326	1/1	0.93	0.09	-	104,104,104,104	0
57	MG	1H	3418	1/1	0.88	0.06	-	82,82,82,82	0
57	MG	14	3278	1/1	0.90	0.04	-	109,109,109,109	0
57	MG	1H	3015	1/1	0.95	0.23	-	52,52,52,52	0
57	MG	14	3012	1/1	0.95	0.59	-	60,60,60,60	0
57	MG	14	3187	1/1	0.95	0.35	-	81,81,81,81	0
57	MG	1H	3409	1/1	0.97	0.04	-	99,99,99,99	0
57	MG	13	1676	1/1	0.94	0.11	-	110,110,110,110	0
57	MG	1H	3400	1/1	0.87	0.08	-	85,85,85,85	0
57	MG	1H	3272	1/1	0.94	0.35	-	71,71,71,71	0
57	MG	14	3290	1/1	0.94	0.03	-	114,114,114,114	0
57	MG	13	1626	1/1	0.45	0.46	-	73,73,73,73	0
57	MG	1H	3433	1/1	0.97	0.12	-	56,56,56,56	0
57	MG	14	3206	1/1	0.86	0.29	-	78,78,78,78	0
57	MG	1H	3187	1/1	0.95	0.87	-	81,81,81,81	0
57	MG	1H	3173	1/1	0.90	0.57	-	99,99,99,99	0
57	MG	14	3165	1/1	0.98	0.45	-	86,86,86,86	0
57	MG	1H	3259	1/1	0.46	0.27	-	73,73,73,73	0
57	MG	1H	3292	1/1	0.97	0.18	-	58,58,58,58	0
57	MG	1H	3024	1/1	0.78	0.23	-	72,72,72,72	0
57	MG	14	3321	1/1	0.97	0.10	-	78,78,78,78	0
57	MG	14	3181	1/1	0.94	0.44	-	85,85,85,85	0
57	MG	14	3125	1/1	0.84	0.58	-	68,68,68,68	0
57	MG	14	3298	1/1	0.96	0.08	-	78,78,78,78	0
57	MG	29	301	1/1	0.94	0.34	-	67,67,67,67	0
57	MG	1H	3368	1/1	0.95	0.08	-	65,65,65,65	0
57	MG	1H	3099	1/1	0.84	0.09	-	88,88,88,88	0
57	MG	1H	3276	1/1	0.92	0.37	-	67,67,67,67	0
57	MG	14	3286	1/1	0.97	0.06	-	91,91,91,91	0
57	MG	1G	1633	1/1	0.93	0.09	-	141,141,141,141	0
57	MG	1H	3444	1/1	0.86	0.08	-	96,96,96,96	0
57	MG	16	206	1/1	0.92	0.32	-	83,83,83,83	0
57	MG	14	3003	1/1	0.99	0.27	-	54,54,54,54	0
57	MG	1H	3438	1/1	0.99	0.10	-	55,55,55,55	0
57	MG	1G	1622	1/1	0.90	0.41	-	80,80,80,80	0
57	MG	1G	1658	1/1	0.82	0.13	-	132,132,132,132	0
57	MG	1H	3038	1/1	0.98	0.26	-	55,55,55,55	0
57	MG	1H	3118	1/1	0.97	0.21	-	76,76,76,76	0
57	MG	14	3066	1/1	0.98	0.50	-	63,63,63,63	0
57	MG	1H	3168	1/1	0.85	0.43	-	100,100,100,100	0
57	MG	14	3180	1/1	0.74	0.39	-	112,112,112,112	0
57	MG	14	3153	1/1	0.88	0.49	-	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3275	1/1	0.99	0.10	-	90,90,90,90	0
57	MG	1H	3186	1/1	0.75	0.34	-	72,72,72,72	0
57	MG	1H	3220	1/1	0.92	0.40	-	62,62,62,62	0
57	MG	1H	3390	1/1	0.88	0.08	-	99,99,99,99	0
57	MG	14	3147	1/1	0.98	0.42	-	79,79,79,79	0
57	MG	1H	3211	1/1	0.96	0.32	-	78,78,78,78	0
57	MG	1G	1620	1/1	0.83	0.50	-	71,71,71,71	0
57	MG	98	201	1/1	0.94	0.43	-	70,70,70,70	0
57	MG	1H	3010	1/1	0.97	0.33	-	51,51,51,51	0
57	MG	14	3240	1/1	0.99	0.07	-	71,71,71,71	0
57	MG	14	3183	1/1	0.93	0.40	-	77,77,77,77	0
57	MG	13	1690	1/1	0.96	0.10	-	83,83,83,83	0
57	MG	14	3033	1/1	0.95	0.19	-	74,74,74,74	0
57	MG	1H	3301	1/1	0.98	0.12	-	61,61,61,61	0
57	MG	14	3227	1/1	0.94	0.13	-	64,64,64,64	0
57	MG	1G	1634	1/1	0.88	0.21	-	93,93,93,93	0
57	MG	14	3098	1/1	0.77	0.36	-	78,78,78,78	0
57	MG	1H	3321	1/1	0.97	0.12	-	74,74,74,74	0
57	MG	1H	3132	1/1	0.99	0.14	-	49,49,49,49	0
57	MG	1H	3370	1/1	0.98	0.17	-	60,60,60,60	0
57	MG	1H	3155	1/1	0.98	0.34	-	68,68,68,68	0
57	MG	1H	3231	1/1	0.93	0.43	-	79,79,79,79	0
57	MG	14	3161	1/1	0.87	0.47	-	88,88,88,88	0
57	MG	1G	1614	1/1	0.83	0.49	-	72,72,72,72	0
57	MG	1H	3170	1/1	0.76	0.49	-	88,88,88,88	0
57	MG	1H	3028	1/1	0.98	0.33	-	71,71,71,71	0
57	MG	1H	3260	1/1	0.96	0.48	-	71,71,71,71	0
57	MG	1G	1623	1/1	0.88	0.52	-	66,66,66,66	0
57	MG	14	3115	1/1	0.95	0.38	-	71,71,71,71	0
57	MG	1H	3034	1/1	0.92	0.18	-	62,62,62,62	0
57	MG	1H	3096	1/1	0.52	0.27	-	65,65,65,65	0
57	MG	14	3109	1/1	0.87	0.31	-	84,84,84,84	0
57	MG	13	1603	1/1	0.97	0.22	-	78,78,78,78	0
57	MG	1H	3255	1/1	0.71	0.33	-	81,81,81,81	0
57	MG	14	3068	1/1	0.97	0.33	-	81,81,81,81	0
57	MG	14	3273	1/1	0.95	0.10	-	69,69,69,69	0
57	MG	1H	3387	1/1	0.97	0.11	-	82,82,82,82	0
57	MG	1H	3367	1/1	0.95	0.12	-	90,90,90,90	0
57	MG	1H	3374	1/1	0.95	0.07	-	83,83,83,83	0
57	MG	1H	3061	1/1	0.98	0.32	-	52,52,52,52	0
57	MG	1G	1668	1/1	0.85	0.07	-	120,120,120,120	0
57	MG	1H	3369	1/1	0.96	0.16	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3238	1/1	0.96	0.39	-	101,101,101,101	0
57	MG	1H	3315	1/1	0.92	0.21	-	81,81,81,81	0
57	MG	1H	3021	1/1	0.92	0.36	-	62,62,62,62	0
57	MG	14	3002	1/1	0.98	0.33	-	64,64,64,64	0
57	MG	1H	3151	1/1	0.87	0.39	-	75,75,75,75	0
57	MG	14	3092	1/1	0.89	0.77	-	79,79,79,79	0
57	MG	1H	3327	1/1	0.96	0.11	-	81,81,81,81	0
57	MG	1H	3381	1/1	0.98	0.11	-	58,58,58,58	0
57	MG	14	3177	1/1	0.97	0.29	-	65,65,65,65	0
57	MG	14	3129	1/1	0.97	0.33	-	90,90,90,90	0
57	MG	13	1651	1/1	0.96	0.09	-	110,110,110,110	0
57	MG	1G	1629	1/1	0.96	0.18	-	96,96,96,96	0
57	MG	13	1637	1/1	0.94	0.17	-	105,105,105,105	0
57	MG	1H	3320	1/1	0.90	0.14	-	76,76,76,76	0
57	MG	1H	3277	1/1	0.77	0.46	-	89,89,89,89	0
57	MG	1H	3159	1/1	0.94	0.46	-	67,67,67,67	0
57	MG	1G	1647	1/1	0.94	0.56	-	101,101,101,101	0
57	MG	14	3209	1/1	0.95	0.26	-	84,84,84,84	0
57	MG	14	3269	1/1	0.99	0.08	-	108,108,108,108	0
57	MG	1H	3397	1/1	0.93	0.15	-	76,76,76,76	0
57	MG	14	3302	1/1	0.80	0.10	-	106,106,106,106	0
57	MG	14	3208	1/1	0.98	0.33	-	77,77,77,77	0
57	MG	14	3191	1/1	0.88	0.22	-	72,72,72,72	0
57	MG	14	3158	1/1	0.95	0.10	-	94,94,94,94	0
57	MG	14	3074	1/1	0.89	0.27	-	82,82,82,82	0
57	MG	1H	3280	1/1	0.94	0.44	-	72,72,72,72	0
57	MG	14	3138	1/1	0.96	0.45	-	74,74,74,74	0
57	MG	1H	3237	1/1	0.93	0.51	-	64,64,64,64	0
57	MG	1H	3303	1/1	0.97	0.10	-	61,61,61,61	0
57	MG	1H	3014	1/1	0.98	0.37	-	67,67,67,67	0
57	MG	1H	3209	1/1	0.96	0.26	-	76,76,76,76	0
57	MG	1H	3086	1/1	0.94	0.46	-	48,48,48,48	0
57	MG	1H	3095	1/1	0.82	0.36	-	74,74,74,74	0
57	MG	1H	3230	1/1	0.78	0.72	-	97,97,97,97	0
57	MG	1H	3216	1/1	0.86	0.38	-	75,75,75,75	0
57	MG	1H	3337	1/1	0.94	0.10	-	65,65,65,65	0
57	MG	1G	1626	1/1	0.90	0.28	-	81,81,81,81	0
57	MG	1H	3071	1/1	0.93	0.27	-	66,66,66,66	0
57	MG	1H	3154	1/1	0.86	0.37	-	101,101,101,101	0
57	MG	1H	3123	1/1	0.90	0.28	-	58,58,58,58	0
57	MG	1H	3428	1/1	0.71	0.07	-	103,103,103,103	0
57	MG	1G	1656	1/1	0.71	0.40	-	97,97,97,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3018	1/1	0.99	0.39	-	66,66,66,66	0
57	MG	1H	3195	1/1	0.92	0.89	-	70,70,70,70	0
57	MG	1H	3084	1/1	0.95	0.15	-	53,53,53,53	0
57	MG	1H	3076	1/1	0.89	0.27	-	77,77,77,77	0
57	MG	14	3089	1/1	0.85	0.20	-	56,56,56,56	0
57	MG	1H	3323	1/1	0.97	0.05	-	83,83,83,83	0
57	MG	14	3080	1/1	0.95	0.41	-	89,89,89,89	0
57	MG	1G	1649	1/1	0.96	0.42	-	70,70,70,70	0
57	MG	1H	3325	1/1	0.97	0.10	-	75,75,75,75	0
57	MG	14	3016	1/1	0.97	0.19	-	86,86,86,86	0
57	MG	1H	3104	1/1	0.94	0.30	-	69,69,69,69	0
57	MG	1H	3127	1/1	0.97	0.36	-	63,63,63,63	0
57	MG	1H	3406	1/1	0.94	0.12	-	106,106,106,106	0
57	MG	1H	3047	1/1	0.98	0.30	-	61,61,61,61	0
57	MG	1H	3341	1/1	0.98	0.08	-	47,47,47,47	0
57	MG	13	1633	1/1	0.89	0.39	-	90,90,90,90	0
57	MG	1H	3247	1/1	0.76	0.18	-	97,97,97,97	0
57	MG	1H	3310	1/1	0.95	0.09	-	91,91,91,91	0
57	MG	14	3296	1/1	0.90	0.12	-	110,110,110,110	0
57	MG	14	3324	1/1	0.96	0.11	-	77,77,77,77	0
57	MG	1H	3252	1/1	0.18	0.65	-	92,92,92,92	0
57	MG	1H	3175	1/1	0.88	0.48	-	64,64,64,64	0
57	MG	14	3008	1/1	0.98	0.32	-	59,59,59,59	0
57	MG	1H	3228	1/1	0.74	0.40	-	83,83,83,83	0
57	MG	1H	3174	1/1	0.55	0.29	-	88,88,88,88	0
57	MG	1H	3162	1/1	0.70	0.44	-	83,83,83,83	0
57	MG	1H	3271	1/1	0.79	0.59	-	90,90,90,90	0
57	MG	1H	3396	1/1	0.90	0.07	-	80,80,80,80	0
57	MG	14	3219	1/1	0.89	0.56	-	81,81,81,81	0
57	MG	1H	3386	1/1	0.91	0.06	-	96,96,96,96	0
57	MG	13	1636	1/1	0.96	0.08	-	103,103,103,103	0
57	MG	14	3050	1/1	0.98	0.35	-	63,63,63,63	0
57	MG	1H	3103	1/1	0.94	0.23	-	80,80,80,80	0
57	MG	14	3145	1/1	0.95	0.59	-	64,64,64,64	0
57	MG	14	3156	1/1	0.76	0.43	-	107,107,107,107	0
57	MG	1H	3191	1/1	0.81	0.61	-	102,102,102,102	0
57	MG	1H	3308	1/1	0.92	0.05	-	91,91,91,91	0
57	MG	1H	3350	1/1	0.98	0.10	-	74,74,74,74	0
57	MG	1H	3349	1/1	0.97	0.11	-	68,68,68,68	0
57	MG	1H	3070	1/1	0.82	0.31	-	64,64,64,64	0
57	MG	13	1641	1/1	0.96	0.37	-	74,74,74,74	0
57	MG	1G	1664	1/1	0.88	0.65	-	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3188	1/1	0.72	0.51	-	82,82,82,82	0
57	MG	1H	3240	1/1	0.64	0.30	-	73,73,73,73	0
57	MG	14	3217	1/1	0.88	0.11	-	83,83,83,83	0
57	MG	1G	1659	1/1	0.83	0.30	-	101,101,101,101	0
57	MG	1H	3196	1/1	0.85	0.29	-	84,84,84,84	0
57	MG	14	3277	1/1	0.91	0.07	-	98,98,98,98	0
57	MG	1G	1615	1/1	0.88	0.49	-	90,90,90,90	0
57	MG	1H	3312	1/1	0.97	0.17	-	93,93,93,93	0
57	MG	1H	3197	1/1	0.86	0.36	-	53,53,53,53	0
57	MG	1H	3135	1/1	0.90	0.28	-	74,74,74,74	0
57	MG	14	3149	1/1	0.96	0.31	-	96,96,96,96	0
57	MG	13	1668	1/1	0.94	0.17	-	119,119,119,119	0
57	MG	1H	3006	1/1	0.97	0.43	-	58,58,58,58	0
57	MG	14	3201	1/1	0.80	0.61	-	78,78,78,78	0
57	MG	14	3150	1/1	0.91	0.23	-	79,79,79,79	0
57	MG	1H	3003	1/1	0.97	0.24	-	53,53,53,53	0
57	MG	1H	3077	1/1	0.92	0.50	-	65,65,65,65	0
57	MG	14	3203	1/1	0.88	0.42	-	83,83,83,83	0
57	MG	14	3246	1/1	0.93	0.09	-	96,96,96,96	0
57	MG	1G	1618	1/1	0.96	0.27	-	100,100,100,100	0
57	MG	1H	3054	1/1	0.95	0.49	-	41,41,41,41	0
57	MG	1H	3436	1/1	0.98	0.16	-	50,50,50,50	0
57	MG	14	3327	1/1	0.82	0.08	-	108,108,108,108	0
57	MG	1H	3385	1/1	0.91	0.08	-	112,112,112,112	0
57	MG	1G	1652	1/1	0.82	0.31	-	82,82,82,82	0
57	MG	14	3171	1/1	0.87	0.56	-	71,71,71,71	0
57	MG	14	3189	1/1	0.80	0.28	-	69,69,69,69	0
57	MG	1H	3055	1/1	0.97	0.53	-	64,64,64,64	0
57	MG	1H	3408	1/1	0.94	0.07	-	67,67,67,67	0
57	MG	68	201	1/1	0.79	0.37	-	80,80,80,80	0
57	MG	14	3176	1/1	0.49	0.58	-	85,85,85,85	0
57	MG	1H	3250	1/1	0.91	0.29	-	71,71,71,71	0
57	MG	1H	3439	1/1	0.93	0.15	-	65,65,65,65	0
57	MG	1H	3278	1/1	0.84	0.66	-	68,68,68,68	0
57	MG	1G	1635	1/1	0.60	0.57	-	79,79,79,79	0
57	MG	13	1665	1/1	0.85	0.40	-	86,86,86,86	0
57	MG	14	3069	1/1	0.56	0.46	-	97,97,97,97	0
57	MG	13	1645	1/1	0.75	0.23	-	89,89,89,89	0
57	MG	1H	3189	1/1	0.94	0.26	-	70,70,70,70	0
57	MG	3L	102	1/1	0.97	0.28	-	165,165,165,165	0
57	MG	1H	3416	1/1	0.92	0.09	-	81,81,81,81	0
57	MG	14	3310	1/1	0.80	0.10	-	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3165	1/1	0.98	0.22	-	96,96,96,96	0
57	MG	13	1663	1/1	0.81	0.76	-	77,77,77,77	0
57	MG	1H	3262	1/1	0.60	0.50	-	75,75,75,75	0
57	MG	13	1607	1/1	0.95	0.22	-	88,88,88,88	0
57	MG	1H	3283	1/1	0.99	0.15	-	65,65,65,65	0
57	MG	1H	3214	1/1	0.95	0.45	-	55,55,55,55	0
57	MG	1H	3257	1/1	0.81	0.59	-	90,90,90,90	0
57	MG	13	1640	1/1	0.90	0.08	-	141,141,141,141	0
57	MG	1G	1631	1/1	0.37	0.24	-	97,97,97,97	0
57	MG	14	3139	1/1	0.72	0.14	-	93,93,93,93	0
57	MG	68	202	1/1	0.81	0.45	-	91,91,91,91	0
57	MG	1H	3356	1/1	0.95	0.07	-	81,81,81,81	0
57	MG	1H	3062	1/1	0.89	0.61	-	78,78,78,78	0
57	MG	13	1648	1/1	0.96	0.32	-	84,84,84,84	0
57	MG	14	3190	1/1	0.93	0.45	-	72,72,72,72	0
57	MG	14	3245	1/1	0.94	0.04	-	99,99,99,99	0
57	MG	14	3056	1/1	0.96	0.22	-	65,65,65,65	0
57	MG	14	3279	1/1	0.95	0.10	-	69,69,69,69	0
57	MG	1H	3423	1/1	0.79	0.09	-	65,65,65,65	0
57	MG	1H	3372	1/1	0.95	0.10	-	62,62,62,62	0
57	MG	1H	3163	1/1	0.78	0.28	-	65,65,65,65	0
57	MG	1H	3183	1/1	0.90	0.59	-	87,87,87,87	0
57	MG	1H	3177	1/1	0.78	0.24	-	57,57,57,57	0
57	MG	1H	3011	1/1	0.93	0.55	-	63,63,63,63	0
57	MG	1H	3198	1/1	0.78	0.62	-	77,77,77,77	0
57	MG	1G	1669	1/1	0.96	0.10	-	129,129,129,129	0
57	MG	1H	3258	1/1	0.93	0.41	-	86,86,86,86	0
57	MG	14	3226	1/1	0.97	0.13	-	67,67,67,67	0
57	MG	1H	3185	1/1	0.95	0.08	-	121,121,121,121	0
57	MG	1H	3245	1/1	0.93	0.49	-	96,96,96,96	0
57	MG	1H	3083	1/1	0.92	0.31	-	61,61,61,61	0
57	MG	1H	3125	1/1	0.94	0.46	-	77,77,77,77	0
57	MG	13	1693	1/1	0.71	0.07	-	118,118,118,118	0
57	MG	14	3005	1/1	0.98	0.31	-	61,61,61,61	0
57	MG	1H	3248	1/1	0.77	0.34	-	76,76,76,76	0
57	MG	1H	3059	1/1	0.81	0.28	-	75,75,75,75	0
57	MG	14	3061	1/1	0.93	0.55	-	67,67,67,67	0
57	MG	13	1638	1/1	0.90	0.56	-	84,84,84,84	0
57	MG	14	3123	1/1	0.98	0.31	-	73,73,73,73	0
57	MG	14	3207	1/1	0.90	0.33	-	70,70,70,70	0
57	MG	1H	3108	1/1	0.94	0.99	-	73,73,73,73	0
57	MG	13	1669	1/1	0.94	0.40	-	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3335	1/1	0.95	0.17	-	74,74,74,74	0
57	MG	14	3255	1/1	0.96	0.11	-	72,72,72,72	0
57	MG	14	3196	1/1	0.89	0.37	-	86,86,86,86	0
57	MG	1H	3081	1/1	0.97	0.21	-	47,47,47,47	0
57	MG	14	3006	1/1	0.98	0.41	-	53,53,53,53	0
57	MG	1H	3309	1/1	0.97	0.11	-	66,66,66,66	0
57	MG	14	3102	1/1	0.60	0.62	-	81,81,81,81	0
57	MG	1G	1608	1/1	0.92	0.31	-	88,88,88,88	0
57	MG	14	3211	1/1	0.68	0.47	-	101,101,101,101	0
57	MG	14	3232	1/1	0.96	0.09	-	67,67,67,67	0
57	MG	1H	3361	1/1	0.94	0.05	-	95,95,95,95	0
57	MG	1G	1672	1/1	0.64	0.09	-	117,117,117,117	0
57	MG	1H	3194	1/1	0.92	0.13	-	83,83,83,83	0
57	MG	14	3235	1/1	0.95	0.18	-	66,66,66,66	0
57	MG	14	3237	1/1	0.95	0.10	-	69,69,69,69	0
57	MG	1H	3201	1/1	0.83	0.55	-	68,68,68,68	0
57	MG	14	3044	1/1	0.91	0.29	-	82,82,82,82	0
57	MG	1H	3256	1/1	0.89	0.52	-	72,72,72,72	0
57	MG	1H	3399	1/1	0.98	0.04	-	111,111,111,111	0
57	MG	18	102	1/1	0.97	0.06	-	69,69,69,69	0
57	MG	1H	3088	1/1	0.87	0.25	-	65,65,65,65	0
57	MG	14	3312	1/1	0.91	0.09	-	115,115,115,115	0
57	MG	1G	1606	1/1	0.93	0.22	-	92,92,92,92	0
57	MG	14	3120	1/1	0.96	0.34	-	49,49,49,49	0
57	MG	78	201	1/1	0.93	0.26	-	60,60,60,60	0
57	MG	14	3032	1/1	0.93	0.37	-	98,98,98,98	0
57	MG	13	1620	1/1	0.96	0.20	-	61,61,61,61	0
57	MG	14	3178	1/1	0.82	0.28	-	76,76,76,76	0
57	MG	14	3163	1/1	0.95	0.49	-	72,72,72,72	0
57	MG	1H	3295	1/1	0.96	0.09	-	76,76,76,76	0
57	MG	13	1677	1/1	0.89	0.14	-	98,98,98,98	0
57	MG	1G	1624	1/1	0.84	0.37	-	71,71,71,71	0
57	MG	1G	1612	1/1	0.84	0.14	-	99,99,99,99	0
57	MG	1H	3182	1/1	0.84	0.25	-	78,78,78,78	0
57	MG	14	3293	1/1	0.93	0.08	-	84,84,84,84	0
57	MG	1H	3243	1/1	0.85	0.52	-	65,65,65,65	0
57	MG	1H	3017	1/1	0.92	0.19	-	81,81,81,81	0
57	MG	1H	3164	1/1	0.79	0.31	-	66,66,66,66	0
57	MG	1H	3328	1/1	0.94	0.05	-	91,91,91,91	0
57	MG	13	1684	1/1	0.97	0.11	-	95,95,95,95	0
57	MG	1H	3263	1/1	0.88	0.70	-	75,75,75,75	0
57	MG	1H	3130	1/1	0.82	0.40	-	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3149	1/1	0.97	0.23	-	61,61,61,61	0
57	MG	14	3314	1/1	0.97	0.06	-	91,91,91,91	0
57	MG	1H	3371	1/1	0.90	0.13	-	66,66,66,66	0
57	MG	14	3154	1/1	0.95	0.43	-	59,59,59,59	0
57	MG	1H	3179	1/1	0.89	0.41	-	81,81,81,81	0
57	MG	14	3288	1/1	0.87	0.09	-	108,108,108,108	0
57	MG	1H	3279	1/1	0.91	0.26	-	78,78,78,78	0
57	MG	1H	3405	1/1	0.97	0.10	-	72,72,72,72	0
57	MG	1H	3251	1/1	0.81	0.58	-	84,84,84,84	0
57	MG	1J	203	1/1	0.93	0.36	-	90,90,90,90	0
57	MG	1H	3415	1/1	0.94	0.09	-	105,105,105,105	0
57	MG	25	201	1/1	0.98	0.05	-	111,111,111,111	0
57	MG	1H	3348	1/1	0.91	0.12	-	90,90,90,90	0
57	MG	1H	3161	1/1	0.96	0.26	-	71,71,71,71	0
57	MG	1H	3030	1/1	0.97	0.28	-	79,79,79,79	0
57	MG	1G	1604	1/1	0.97	0.21	-	91,91,91,91	0
57	MG	13	1616	1/1	0.90	0.38	-	93,93,93,93	0
57	MG	1H	3180	1/1	0.88	0.16	-	80,80,80,80	0
57	MG	1H	3208	1/1	0.98	0.37	-	48,48,48,48	0
57	MG	14	3264	1/1	0.88	0.19	-	57,57,57,57	0
57	MG	14	3010	1/1	0.96	0.33	-	58,58,58,58	0
57	MG	13	1683	1/1	0.92	0.11	-	96,96,96,96	0
57	MG	1H	3352	1/1	0.97	0.05	-	68,68,68,68	0
57	MG	13	1689	1/1	0.91	0.10	-	115,115,115,115	0
57	MG	13	1696	1/1	0.87	0.05	-	101,101,101,101	0
57	MG	14	3148	1/1	0.90	0.31	-	93,93,93,93	0
57	MG	1H	3364	1/1	0.96	0.10	-	93,93,93,93	0
57	MG	1H	3101	1/1	0.91	0.41	-	70,70,70,70	0
57	MG	14	3182	1/1	0.89	0.24	-	84,84,84,84	0
57	MG	1J	201	1/1	0.70	0.32	-	88,88,88,88	0
57	MG	14	3195	1/1	0.82	0.51	-	88,88,88,88	0
57	MG	1H	3394	1/1	0.95	0.07	-	83,83,83,83	0
57	MG	14	3104	1/1	0.94	0.48	-	68,68,68,68	0
57	MG	1H	3094	1/1	0.94	0.35	-	60,60,60,60	0
57	MG	14	3318	1/1	0.84	0.14	-	84,84,84,84	0
57	MG	1H	3440	1/1	0.95	0.15	-	64,64,64,64	0
57	MG	14	3112	1/1	0.81	0.38	-	78,78,78,78	0
57	MG	14	3055	1/1	0.99	0.26	-	62,62,62,62	0
57	MG	14	3251	1/1	0.98	0.07	-	77,77,77,77	0
57	MG	1H	3001	1/1	0.96	0.61	-	83,83,83,83	0
57	MG	1H	3224	1/1	0.76	0.52	-	66,66,66,66	0
57	MG	14	3300	1/1	0.98	0.08	-	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	14	3164	1/1	0.52	0.76	-	94,94,94,94	0
57	MG	14	3137	1/1	0.91	0.12	-	76,76,76,76	0
57	MG	1H	3110	1/1	0.82	0.52	-	84,84,84,84	0
57	MG	14	3116	1/1	0.83	0.35	-	60,60,60,60	0
57	MG	1H	3363	1/1	0.96	0.10	-	69,69,69,69	0
57	MG	14	3325	1/1	0.89	0.10	-	104,104,104,104	0
57	MG	14	3169	1/1	0.86	0.32	-	59,59,59,59	0
57	MG	M5	101	1/1	0.68	0.36	-	85,85,85,85	0
57	MG	1G	1636	1/1	0.86	0.24	-	96,96,96,96	0
57	MG	1H	3305	1/1	0.99	0.13	-	49,49,49,49	0
57	MG	1H	3184	1/1	0.89	0.33	-	86,86,86,86	0
57	MG	1H	3075	1/1	0.86	0.46	-	59,59,59,59	0
57	MG	1G	1644	1/1	0.83	0.37	-	90,90,90,90	0
57	MG	14	3311	1/1	0.94	0.11	-	78,78,78,78	0
57	MG	1H	3206	1/1	0.95	0.65	-	73,73,73,73	0
57	MG	13	1662	1/1	0.49	0.56	-	88,88,88,88	0
57	MG	13	1698	1/1	0.91	0.11	-	105,105,105,105	0
57	MG	1H	3072	1/1	0.98	0.36	-	66,66,66,66	0
57	MG	14	3071	1/1	0.98	0.23	-	68,68,68,68	0
57	MG	14	3303	1/1	0.94	0.06	-	85,85,85,85	0
57	MG	1H	3167	1/1	0.60	0.36	-	79,79,79,79	0
57	MG	14	3162	1/1	0.93	0.19	-	102,102,102,102	0
57	MG	14	3110	1/1	0.96	0.24	-	82,82,82,82	0
57	MG	16	207	1/1	0.54	0.27	-	88,88,88,88	0
57	MG	1H	3178	1/1	0.83	0.19	-	91,91,91,91	0
57	MG	13	1613	1/1	0.95	0.47	-	74,74,74,74	0
57	MG	1H	3443	1/1	0.81	0.08	-	100,100,100,100	0
57	MG	14	3077	1/1	0.99	0.12	-	61,61,61,61	0
57	MG	14	3307	1/1	0.77	0.15	-	91,91,91,91	0
57	MG	1H	3293	1/1	0.98	0.17	-	62,62,62,62	0
57	MG	13	1686	1/1	0.95	0.13	-	89,89,89,89	0
57	MG	I8	101	1/1	0.92	0.08	-	91,91,91,91	0
57	MG	P8	101	1/1	0.94	0.40	-	65,65,65,65	0
57	MG	14	3220	1/1	0.93	0.26	-	84,84,84,84	0
57	MG	14	3233	1/1	0.96	0.15	-	82,82,82,82	0
57	MG	1H	3222	1/1	0.93	0.63	-	81,81,81,81	0
57	MG	1H	3382	1/1	0.89	0.07	-	74,74,74,74	0
57	MG	14	3075	1/1	0.95	0.26	-	103,103,103,103	0
57	MG	14	3087	1/1	0.96	0.38	-	76,76,76,76	0
57	MG	13	1664	1/1	0.66	0.58	-	95,95,95,95	0
57	MG	13	1667	1/1	0.18	0.38	-	119,119,119,119	0
57	MG	14	3135	1/1	0.80	0.37	-	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3411	1/1	0.94	0.09	-	133,133,133,133	0
57	MG	1H	3172	1/1	0.80	0.39	-	73,73,73,73	0
57	MG	14	3021	1/1	0.94	0.40	-	65,65,65,65	0
57	MG	13	1608	1/1	0.94	0.15	-	88,88,88,88	0
57	MG	14	3294	1/1	0.87	0.09	-	107,107,107,107	0
57	MG	1H	3234	1/1	0.94	0.56	-	86,86,86,86	0
57	MG	14	3073	1/1	0.98	0.31	-	81,81,81,81	0
57	MG	2K	102	1/1	0.79	0.11	-	111,111,111,111	0
57	MG	1H	3358	1/1	0.98	0.08	-	73,73,73,73	0
57	MG	1H	3239	1/1	0.91	0.52	-	71,71,71,71	0
57	MG	14	3090	1/1	0.89	0.20	-	77,77,77,77	0
57	MG	1H	3202	1/1	0.86	0.36	-	84,84,84,84	0
57	MG	1H	3322	1/1	0.95	0.12	-	74,74,74,74	0
57	MG	1H	3268	1/1	0.92	0.17	-	96,96,96,96	0
57	MG	16	210	1/1	0.94	0.05	-	88,88,88,88	0
57	MG	1H	3080	1/1	0.95	0.25	-	81,81,81,81	0
57	MG	13	1629	1/1	0.99	0.42	-	74,74,74,74	0
57	MG	11	303	1/1	0.85	0.64	-	48,48,48,48	0
57	MG	1H	3205	1/1	0.92	0.64	-	73,73,73,73	0
57	MG	1H	3430	1/1	0.97	0.16	-	50,50,50,50	0
57	MG	1H	3035	1/1	0.94	0.18	-	64,64,64,64	0
57	MG	14	3131	1/1	0.99	0.17	-	76,76,76,76	0
57	MG	14	3281	1/1	0.94	0.09	-	95,95,95,95	0
57	MG	1H	3215	1/1	0.86	0.34	-	79,79,79,79	0
57	MG	1H	3107	1/1	0.84	0.29	-	81,81,81,81	0
57	MG	1H	3100	1/1	0.67	0.39	-	84,84,84,84	0
57	MG	14	3151	1/1	0.72	0.35	-	71,71,71,71	0
57	MG	1G	1663	1/1	0.70	0.25	-	89,89,89,89	0
57	MG	14	3252	1/1	0.99	0.08	-	71,71,71,71	0
57	MG	1H	3414	1/1	0.87	0.09	-	87,87,87,87	0
57	MG	1H	3410	1/1	0.97	0.11	-	102,102,102,102	0
57	MG	1G	1611	1/1	0.86	0.11	-	98,98,98,98	0
57	MG	1H	3004	1/1	0.97	0.21	-	56,56,56,56	0
57	MG	14	3216	1/1	0.71	0.66	-	84,84,84,84	0
57	MG	14	3096	1/1	0.89	0.35	-	70,70,70,70	0
57	MG	14	3064	1/1	0.97	0.19	-	84,84,84,84	0
57	MG	1H	3379	1/1	0.92	0.12	-	83,83,83,83	0
57	MG	14	3046	1/1	0.93	0.43	-	61,61,61,61	0
57	MG	1H	3380	1/1	0.95	0.07	-	57,57,57,57	0
57	MG	14	3172	1/1	0.86	0.37	-	68,68,68,68	0
57	MG	14	3193	1/1	0.95	0.84	-	78,78,78,78	0
57	MG	14	3023	1/1	0.94	0.33	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3357	1/1	0.94	0.05	-	77,77,77,77	0
57	MG	1H	3067	1/1	0.95	0.33	-	70,70,70,70	0
57	MG	1H	3137	1/1	0.96	0.32	-	62,62,62,62	0
57	MG	14	3244	1/1	0.89	0.10	-	93,93,93,93	0
57	MG	14	3042	1/1	0.98	0.40	-	75,75,75,75	0
57	MG	1H	3227	1/1	0.87	0.66	-	66,66,66,66	0
57	MG	14	3210	1/1	0.88	0.20	-	78,78,78,78	0
57	MG	13	1692	1/1	0.95	0.06	-	100,100,100,100	0
57	MG	14	3263	1/1	0.90	0.06	-	99,99,99,99	0
57	MG	3L	101	1/1	0.97	0.43	-	156,156,156,156	0
57	MG	1H	3128	1/1	0.97	0.18	-	52,52,52,52	0
57	MG	14	3194	1/1	0.78	0.28	-	79,79,79,79	0
57	MG	1H	3437	1/1	0.96	0.13	-	64,64,64,64	0
57	MG	1H	3326	1/1	0.93	0.11	-	105,105,105,105	0
57	MG	14	3086	1/1	0.64	0.43	-	82,82,82,82	0
57	MG	14	3117	1/1	0.90	0.37	-	80,80,80,80	0
57	MG	14	3031	1/1	0.88	0.42	-	73,73,73,73	0
57	MG	1H	3244	1/1	0.79	0.53	-	88,88,88,88	0
57	MG	14	3289	1/1	0.97	0.06	-	106,106,106,106	0
57	MG	1H	3291	1/1	0.96	0.14	-	56,56,56,56	0
57	MG	1H	3235	1/1	0.91	0.52	-	69,69,69,69	0
57	MG	14	3319	1/1	0.98	0.10	-	63,63,63,63	0
57	MG	1H	3145	1/1	0.93	0.66	-	66,66,66,66	0
57	MG	1G	1619	1/1	0.98	0.30	-	103,103,103,103	0
57	MG	13	1688	1/1	0.97	0.10	-	74,74,74,74	0
57	MG	1G	1639	1/1	0.93	0.15	-	90,90,90,90	0
57	MG	1H	3121	1/1	0.87	0.54	-	73,73,73,73	0
57	MG	1H	3142	1/1	0.87	0.36	-	55,55,55,55	0
57	MG	13	1670	1/1	0.86	0.12	-	101,101,101,101	0
57	MG	14	3144	1/1	0.95	0.41	-	72,72,72,72	0
57	MG	1H	3421	1/1	0.97	0.08	-	104,104,104,104	0
57	MG	14	3107	1/1	0.69	0.32	-	76,76,76,76	0
57	MG	14	3184	1/1	0.92	0.65	-	75,75,75,75	0
57	MG	14	3308	1/1	0.93	0.07	-	106,106,106,106	0
57	MG	1H	3324	1/1	0.93	0.05	-	76,76,76,76	0
57	MG	1H	3013	1/1	0.98	0.21	-	63,63,63,63	0
57	MG	14	3106	1/1	0.96	0.64	-	86,86,86,86	0
57	MG	13	1681	1/1	0.99	0.09	-	71,71,71,71	0
57	MG	14	3301	1/1	0.98	0.06	-	92,92,92,92	0
57	MG	1H	3377	1/1	0.82	0.07	-	103,103,103,103	0
57	MG	14	3270	1/1	0.96	0.08	-	97,97,97,97	0
57	MG	1H	3169	1/1	0.71	0.70	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3254	1/1	0.90	0.44	-	94,94,94,94	0
57	MG	1G	1657	1/1	0.84	0.75	-	91,91,91,91	0
57	MG	14	3284	1/1	0.97	0.05	-	84,84,84,84	0
57	MG	13	1671	1/1	0.59	0.46	-	97,97,97,97	0
57	MG	1H	3146	1/1	0.89	0.51	-	80,80,80,80	0
57	MG	1H	3045	1/1	0.97	0.31	-	70,70,70,70	0
57	MG	14	3185	1/1	0.86	0.69	-	71,71,71,71	0
57	MG	1G	1637	1/1	0.94	0.47	-	85,85,85,85	0
57	MG	1G	1666	1/1	0.98	0.14	-	89,89,89,89	0
57	MG	14	3315	1/1	0.92	0.10	-	80,80,80,80	0
57	MG	1H	3404	1/1	0.72	0.06	-	110,110,110,110	0
57	MG	13	1614	1/1	0.86	0.61	-	70,70,70,70	0
57	MG	1H	3119	1/1	0.83	0.67	-	62,62,62,62	0
57	MG	13	1630	1/1	0.86	0.27	-	83,83,83,83	0
57	MG	1H	3115	1/1	0.87	0.20	-	63,63,63,63	0
57	MG	14	3174	1/1	0.80	0.86	-	87,87,87,87	0
57	MG	14	3099	1/1	0.71	0.18	-	108,108,108,108	0
57	MG	1H	3008	1/1	0.98	0.34	-	53,53,53,53	0
57	MG	1H	3425	1/1	0.96	0.09	-	110,110,110,110	0
57	MG	1H	3040	1/1	0.99	0.25	-	67,67,67,67	0
57	MG	1H	3401	1/1	0.96	0.05	-	80,80,80,80	0
57	MG	1H	3097	1/1	0.93	0.41	-	93,93,93,93	0
57	MG	14	3114	1/1	0.93	0.46	-	88,88,88,88	0
57	MG	1H	3261	1/1	0.79	0.68	-	80,80,80,80	0
57	MG	14	3167	1/1	0.71	0.31	-	91,91,91,91	0
57	MG	14	3085	1/1	0.95	0.23	-	64,64,64,64	0
57	MG	1H	3431	1/1	0.96	0.12	-	66,66,66,66	0
57	MG	1H	3365	1/1	0.98	0.12	-	68,68,68,68	0
57	MG	1H	3221	1/1	0.85	0.42	-	79,79,79,79	0
57	MG	14	3205	1/1	0.94	0.62	-	80,80,80,80	0
57	MG	1H	3217	1/1	0.93	0.36	-	97,97,97,97	0
57	MG	13	1617	1/1	0.94	0.62	-	70,70,70,70	0
57	MG	14	3070	1/1	0.96	0.30	-	74,74,74,74	0
57	MG	1H	3332	1/1	0.98	0.08	-	49,49,49,49	0
57	MG	1G	1605	1/1	0.92	0.10	-	104,104,104,104	0
57	MG	2L	102	1/1	0.66	0.28	-	96,96,96,96	0
57	MG	1G	1645	1/1	0.92	0.20	-	107,107,107,107	0
57	MG	14	3053	1/1	0.95	0.39	-	64,64,64,64	0
57	MG	14	3051	1/1	0.97	0.39	-	74,74,74,74	0
57	MG	1H	3219	1/1	0.72	0.30	-	77,77,77,77	0
57	MG	13	1666	1/1	0.93	0.23	-	116,116,116,116	0
57	MG	14	3297	1/1	0.96	0.07	-	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	1H	3160	1/1	0.88	0.39	-	67,67,67,67	0
57	MG	1H	3039	1/1	0.97	0.29	-	69,69,69,69	0
57	MG	1H	3223	1/1	0.91	0.31	-	63,63,63,63	0
57	MG	13	1612	1/1	0.77	0.24	-	84,84,84,84	0
57	MG	1H	3207	1/1	0.93	0.37	-	80,80,80,80	0
57	MG	13	1623	1/1	0.92	0.21	-	77,77,77,77	0
57	MG	14	3001	1/1	0.98	0.39	-	58,58,58,58	0
57	MG	14	3132	1/1	0.90	0.29	-	81,81,81,81	0
57	MG	13	1627	1/1	0.84	0.52	-	84,84,84,84	0
57	MG	1H	3139	1/1	0.95	0.55	-	62,62,62,62	0
57	MG	13	1660	1/1	0.92	0.28	-	61,61,61,61	0
57	MG	14	3079	1/1	0.99	0.31	-	56,56,56,56	0
57	MG	1H	3249	1/1	0.93	0.24	-	79,79,79,79	0
57	MG	1H	3351	1/1	0.96	0.06	-	79,79,79,79	0
57	MG	1H	3376	1/1	0.97	0.11	-	90,90,90,90	0
57	MG	14	3291	1/1	0.72	0.11	-	126,126,126,126	0
57	MG	14	3095	1/1	0.88	0.42	-	83,83,83,83	0
57	MG	1H	3087	1/1	0.84	0.31	-	80,80,80,80	0
57	MG	14	3028	1/1	0.96	0.39	-	67,67,67,67	0
57	MG	1H	3232	1/1	0.50	0.31	-	102,102,102,102	0
57	MG	13	1672	1/1	0.89	0.88	-	84,84,84,84	0
57	MG	13	1639	1/1	0.92	0.61	-	83,83,83,83	0
57	MG	14	3276	1/1	0.98	0.10	-	83,83,83,83	0
57	MG	1H	3417	1/1	0.94	0.07	-	73,73,73,73	0
57	MG	14	3128	1/1	0.94	0.16	-	98,98,98,98	0
57	MG	13	1679	1/1	0.98	0.07	-	100,100,100,100	0
57	MG	1H	3264	1/1	0.96	0.32	-	65,65,65,65	0
57	MG	1J	202	1/1	0.83	0.36	-	74,74,74,74	0
57	MG	14	3143	1/1	0.82	0.16	-	92,92,92,92	0
57	MG	1G	1654	1/1	0.90	0.38	-	92,92,92,92	0
57	MG	1H	3112	1/1	0.96	0.42	-	76,76,76,76	0
57	MG	1H	3166	1/1	0.90	0.40	-	75,75,75,75	0
57	MG	1G	1653	1/1	0.90	0.26	-	91,91,91,91	0
57	MG	1H	3092	1/1	0.86	0.30	-	67,67,67,67	0
57	MG	13	1680	1/1	0.95	0.09	-	91,91,91,91	0
57	MG	1H	3307	1/1	0.95	0.05	-	114,114,114,114	0
57	MG	1H	3273	1/1	0.94	0.61	-	85,85,85,85	0
57	MG	13	1634	1/1	0.77	0.19	-	110,110,110,110	0
57	MG	1H	3009	1/1	0.97	0.20	-	47,47,47,47	0
57	MG	1H	3193	1/1	0.95	0.34	-	65,65,65,65	0
57	MG	14	3257	1/1	0.90	0.12	-	89,89,89,89	0
57	MG	1H	3131	1/1	0.94	0.31	-	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	13	1659	1/1	0.50	0.41	-	100,100,100,100	0
57	MG	1G	1655	1/1	0.57	0.37	-	82,82,82,82	0
57	MG	14	3229	1/1	0.89	0.09	-	82,82,82,82	0
57	MG	1H	3442	1/1	0.98	0.06	-	73,73,73,73	0
57	MG	1H	3267	1/1	0.90	0.34	-	106,106,106,106	0
57	MG	1H	3313	1/1	0.95	0.06	-	84,84,84,84	0
57	MG	14	3198	1/1	0.89	0.65	-	86,86,86,86	0
57	MG	1H	3233	1/1	0.88	0.80	-	86,86,86,86	0
57	MG	1H	3152	1/1	0.76	0.38	-	92,92,92,92	0
57	MG	1H	3300	1/1	0.92	0.08	-	68,68,68,68	0
57	MG	1H	3158	1/1	0.92	0.35	-	59,59,59,59	0
57	MG	1H	3066	1/1	0.98	0.39	-	59,59,59,59	0
57	MG	1H	3253	1/1	0.85	0.41	-	67,67,67,67	0
57	MG	1G	1661	1/1	0.79	0.16	-	109,109,109,109	0
57	MG	13	1615	1/1	0.89	0.34	-	85,85,85,85	0
57	MG	14	3248	1/1	0.97	0.09	-	103,103,103,103	0
57	MG	1H	3190	1/1	0.61	0.29	-	94,94,94,94	0
57	MG	14	3309	1/1	0.96	0.11	-	86,86,86,86	0
57	MG	14	3027	1/1	0.83	0.14	-	94,94,94,94	0
57	MG	14	3199	1/1	0.87	0.53	-	95,95,95,95	0
57	MG	13	1642	1/1	0.80	0.46	-	80,80,80,80	0
57	MG	14	3200	1/1	0.57	0.38	-	90,90,90,90	0
57	MG	14	3088	1/1	0.94	0.30	-	76,76,76,76	0
57	MG	14	3067	1/1	0.97	0.45	-	71,71,71,71	0
57	MG	14	3152	1/1	0.98	0.38	-	93,93,93,93	0
57	MG	1G	1625	1/1	0.94	0.42	-	81,81,81,81	0
57	MG	1H	3427	1/1	0.82	0.07	-	122,122,122,122	0
57	MG	16	202	1/1	0.97	0.28	-	62,62,62,62	0
57	MG	14	3228	1/1	0.89	0.08	-	69,69,69,69	0
57	MG	14	3239	1/1	0.94	0.08	-	92,92,92,92	0
57	MG	14	3057	1/1	0.99	0.47	-	78,78,78,78	0
57	MG	1H	3359	1/1	0.97	0.07	-	79,79,79,79	0
57	MG	1H	3422	1/1	0.98	0.08	-	86,86,86,86	0
57	MG	14	3025	1/1	0.92	0.23	-	95,95,95,95	0
57	MG	14	3320	1/1	0.98	0.15	-	73,73,73,73	0
57	MG	13	1602	1/1	0.99	0.27	-	80,80,80,80	0
57	MG	1G	1665	1/1	0.91	0.07	-	117,117,117,117	0
57	MG	1H	3199	1/1	0.44	0.29	-	98,98,98,98	0
57	MG	13	1673	1/1	0.90	0.32	-	87,87,87,87	0
57	MG	13	1625	1/1	0.96	0.37	-	80,80,80,80	0
57	MG	14	3213	1/1	0.53	0.41	-	102,102,102,102	0
57	MG	1H	3412	1/1	0.99	0.05	-	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	16	211	1/1	0.89	0.07	-	99,99,99,99	0
57	MG	1H	3236	1/1	0.81	0.37	-	80,80,80,80	0
57	MG	1H	3204	1/1	0.78	0.93	-	77,77,77,77	0
57	MG	13	1675	1/1	0.96	0.14	-	70,70,70,70	0
57	MG	14	3108	1/1	0.51	0.35	-	77,77,77,77	0
57	MG	1H	3141	1/1	0.86	0.32	-	81,81,81,81	0
57	MG	14	3084	1/1	0.85	0.17	-	82,82,82,82	0
57	MG	1H	3012	1/1	0.89	0.39	-	69,69,69,69	0
57	MG	1H	3031	1/1	0.96	0.29	-	87,87,87,87	0
57	MG	1H	3069	1/1	0.89	0.15	-	69,69,69,69	0
57	MG	14	3146	1/1	0.98	0.39	-	71,71,71,71	0
57	MG	1H	3114	1/1	0.89	0.40	-	77,77,77,77	0
57	MG	1H	3126	1/1	0.85	0.30	-	67,67,67,67	0
57	MG	14	3083	1/1	0.81	0.41	-	57,57,57,57	0
57	MG	16	209	1/1	0.97	0.07	-	76,76,76,76	0
57	MG	14	3072	1/1	0.98	0.23	-	62,62,62,62	0
57	MG	1H	3398	1/1	0.92	0.07	-	98,98,98,98	0
57	MG	1H	3355	1/1	0.99	0.17	-	56,56,56,56	0
57	MG	14	3040	1/1	0.96	0.42	-	62,62,62,62	0
57	MG	1H	3407	1/1	0.95	0.09	-	77,77,77,77	0
57	MG	1H	3229	1/1	0.85	0.12	-	72,72,72,72	0
57	MG	1H	3143	1/1	0.82	0.37	-	64,64,64,64	0
57	MG	1H	3270	1/1	0.69	0.35	-	102,102,102,102	0
57	MG	14	3267	1/1	0.98	0.15	-	48,48,48,48	0
57	MG	1H	3266	1/1	0.96	0.35	-	85,85,85,85	0
57	MG	1G	1621	1/1	0.78	0.75	-	92,92,92,92	0
57	MG	14	3013	1/1	0.93	0.37	-	55,55,55,55	0
57	MG	1H	3424	1/1	0.98	0.08	-	94,94,94,94	0
57	MG	14	3034	1/1	0.95	0.18	-	82,82,82,82	0
57	MG	1H	3289	1/1	0.93	0.09	-	48,48,48,48	0
57	MG	1H	3129	1/1	0.72	0.29	-	93,93,93,93	0
57	MG	1H	3213	1/1	0.96	0.57	-	77,77,77,77	0
57	MG	1H	3053	1/1	0.66	0.66	-	76,76,76,76	0
57	MG	1H	3329	1/1	0.96	0.08	-	80,80,80,80	0
57	MG	14	3287	1/1	0.95	0.14	-	101,101,101,101	0

6.5 Other polymers

There are no such residues in this entry.