



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 05:54 PM UTC

PDB ID : 7OLD / pdb_00007old
EMDB ID : EMD-12977
Title : Thermophilic eukaryotic 80S ribosome at pe/E (TI)-POST state
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2021-05-19
Resolution : 3.00 Å (reported)
Based on initial model : 4V88

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

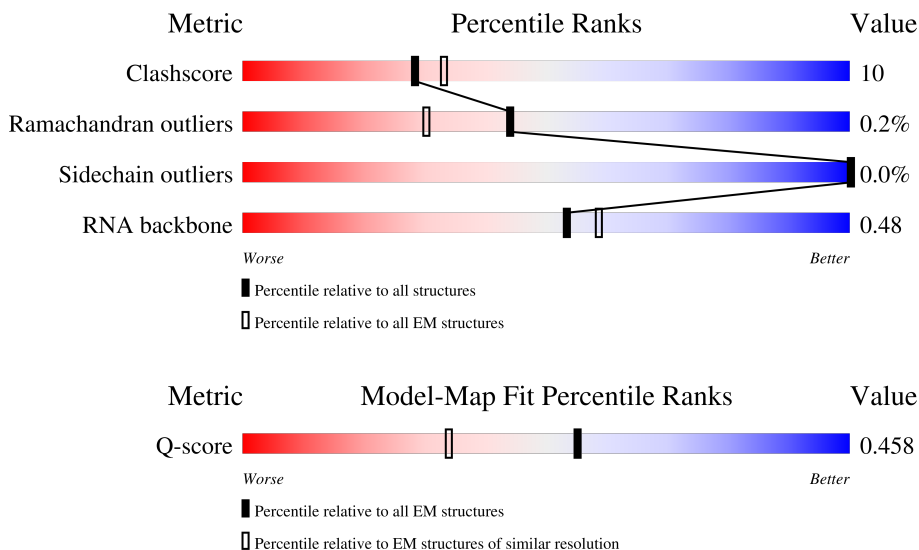
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	3337	62% (green), 27% (yellow), 6% (orange), 5% (grey)
2	2	1796	47% (green), 40% (yellow), 11% (orange), 2% (red), 2% (grey)
3	3	120	70% (green), 25% (yellow), 5% (orange), 0% (red), 0% (grey)

























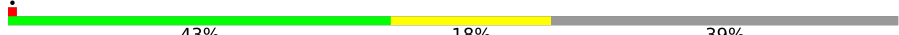
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Mol	Chain	Length	Quality of chain
4	4	156	65% 29% 6%
5	5	75	8% 9% 53% 37%
6	A	316	56% 43%
7	B	302	10% 30% 12% 57%
8	C	845	64% 32%
9	LA	254	80% 18%
10	LB	392	82% 17%
11	LC	365	82% 17%
12	LD	304	80% 19%
13	LE	200	79% 18%
14	LF	249	86% 14%
15	LG	262	75% 14% 11%
16	LH	229	62% 21% 17%
17	LI	219	83% 16%
18	LJ	173	79% 18%
19	LK	165	6% 43% 50% 5%
20	LL	213	80% 18%
21	LM	142	83% 16%
22	LN	203	77% 23%
23	LO	204	88% 11%
24	LP	187	81% 12% 7%
25	LQ	213	75% 11% 14%
26	LR	192	81% 15%
27	LS	174	81% 18%
28	LT	160	88% 11%



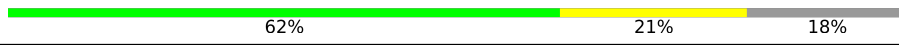









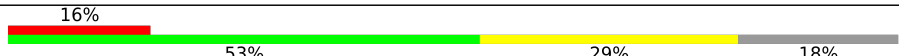
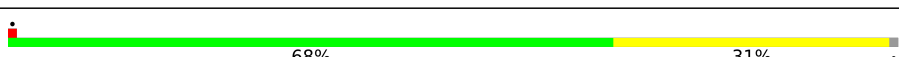
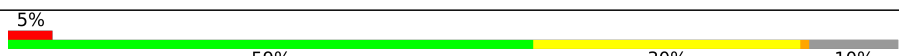

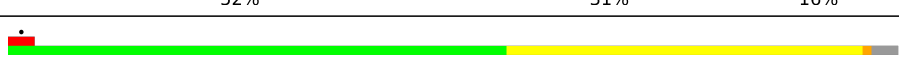



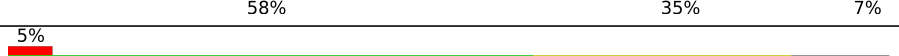
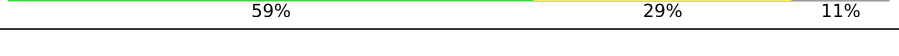

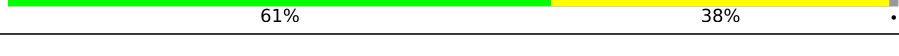

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Mol	Chain	Length	Quality of chain
29	LU	127	
30	LV	139	
31	LW	205	
32	LX	156	
33	LY	138	
34	LZ	135	
35	La	149	
36	Lb	65	
37	Lc	108	
38	Ld	120	
39	Le	131	
40	Lf	109	
41	Lg	119	
42	Lh	126	
43	Li	110	
44	Lj	95	
45	Lk	94	
46	Ll	51	
47	Lm	127	
48	Ln	25	
48	Lr	25	
49	Lo	106	
50	Lp	92	
51	Lq	147	
52	Ls	312	





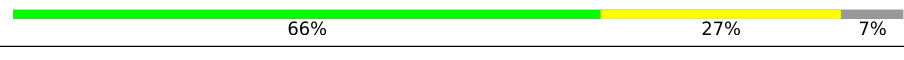


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Mol	Chain	Length	Quality of chain
53	SA	285	
54	SB	255	
55	SC	263	
56	SD	254	
57	SE	264	
58	SF	212	
59	SG	239	
60	SH	203	
61	SI	202	
62	SJ	190	
63	SK	159	
64	SL	161	
65	SM	144	
66	SN	151	
67	SO	150	
68	SP	153	
69	SQ	143	
70	SR	143	
71	SS	156	
72	ST	153	
73	SU	116	
74	SV	98	
75	SW	130	
76	SX	145	
77	SY	136	

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Mol	Chain	Length	Quality of chain
78	SZ	99	
79	Sa	119	
80	Sb	82	
81	Sc	68	
82	Sd	56	
83	Se	62	
84	Sf	154	

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 214209 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	3192	68264	30474	12339	22259	3192	0	0

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1765	37645	16822	6706	12352	1765	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	119	2535	1132	453	831	119	0	0

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	156	3319	1484	589	1090	156	0	0

- Molecule 5 is a RNA chain called pe/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	5	75	1589	710	279	525	75	0	0

- Molecule 6 is a protein called Putative guanine nucleotide-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A	312	2438	1534	424	468	12	0	0

- Molecule 7 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	B	129	982	584	198	200	0	0

- Molecule 8 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	C	813	6335	4024	1092	1192	27	0	0

- Molecule 9 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LA	248	1891	1182	378	328	3	0	0

- Molecule 10 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LB	387	3088	1964	576	535	13	0	0

- Molecule 11 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LC	363	2758	1741	527	481	9	0	0

- Molecule 12 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LD	300	2440	1545	431	461	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LE	194	1518	974	274	267	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	247	Total	C	N	O	S	0	0
			2017	1294	376	344	3		

- Molecule 15 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	234	Total	C	N	O	S	0	0
			1891	1212	349	325	5		

- Molecule 16 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	191	Total	C	N	O	S	0	0
			1505	955	269	275	6		

- Molecule 17 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	217	Total	C	N	O	S	0	0
			1760	1109	343	299	9		

- Molecule 18 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	167	Total	C	N	O	S	0	0
			1367	854	268	239	6		

- Molecule 19 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	156	Total	C	N	O	S	0	0
			1174	737	214	221	2		

- Molecule 20 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	209	Total	C	N	O	S	0	0
			1666	1037	340	287	2		

- Molecule 21 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LM	141	1125	714	216	194	1	0	0

- Molecule 22 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LN	202	1703	1062	360	277	4	0	0

- Molecule 23 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LO	203	1610	1034	305	266	5	0	0

- Molecule 24 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LP	174	1378	856	278	241	3	0	0

- Molecule 25 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LQ	183	1481	935	306	238	2	0	0

- Molecule 26 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LR	184	1506	928	324	249	5	0	0

- Molecule 27 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	LS	173	1425	917	266	238	4	0	0

- Molecule 28 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LT	158	1266	803	246	215	2	0	0

- Molecule 29 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LU	100	810	526	140	143	1	0	0

- Molecule 30 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LV	137	1012	644	189	172	7	0	0

- Molecule 31 is a protein called 60S ribosomal protein L24-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	LW	133	1075	667	221	185	2	0	0

- Molecule 32 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	LX	121	967	621	176	170	0	0

- Molecule 33 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	LY	133	1056	658	213	183	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	LZ	135	1111	713	207	187	4	0	0

- Molecule 35 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	La	148	1180	745	239	194	2	0	0

- Molecule 36 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Lb	63	515	314	113	88		0	0

- Molecule 37 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Lc	95	708	450	122	131	5	0	0

- Molecule 38 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ld	112	907	573	178	155	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Le	124	1001	629	205	161	6	0	0

- Molecule 40 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Lf	107	853	540	170	142	1	0	0

- Molecule 41 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Lg	112	891	554	181	152	4	0	0

- Molecule 42 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 43 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Li	101	Total	C	N	O	S	0	0
			826	509	181	135	1		

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lj	88	Total	C	N	O	S	0	0
			698	427	154	112	5		

- Molecule 45 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

- Molecule 46 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Ll	50	Total	C	N	O	0	0
			435	275	97	63		

- Molecule 47 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lm	52	Total	C	N	O	S	0	0
			418	261	86	65	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	2	MET	-	initiating methionine	UNP G0S8G4

- Molecule 48 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	25	Total	C	N	O	S	0	0
			233	142	63	27	1		
48	Lr	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

- Molecule 49 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lo	104	Total	C	N	O	S	0	0
			822	520	161	136	5		

- Molecule 50 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lp	91	Total	C	N	O	S	0	0
			697	430	138	123	6		

- Molecule 51 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	Lq	141	Total	C	N	O	0	0
			1083	678	215	190		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ls	189	Total	C	N	O	S	0	0
			1449	927	250	265	7		

- Molecule 53 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SA	208	Total	C	N	O	S	0	0
			1641	1051	289	295	6		

- Molecule 54 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SB	224	Total	C	N	O	S	0	0
			1810	1150	338	317	5		

- Molecule 55 is a protein called 40S ribosomal protein S2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SC	216	1672	1074	294	301	3	0	0

- Molecule 56 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	SD	214	1683	1063	307	305	8	0	0

- Molecule 57 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SE	261	2072	1314	389	362	7	0	0

- Molecule 58 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	SF	199	1557	971	294	285	7	0	0

- Molecule 59 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SG	232	1875	1171	376	323	5	0	0

- Molecule 60 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
60	SH	198	1584	997	303	284	0	0

- Molecule 61 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SI	201	1621	1009	330	281	1	0	0

- Molecule 62 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SJ	179	1466	933	290	241	2	0	0

- Molecule 63 is a protein called 40S ribosomal protein s10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SK	89	742	487	124	129	2	0	0

- Molecule 64 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SL	149	1214	775	235	199	5	0	0

- Molecule 65 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SM	118	923	577	167	171	8	0	0

- Molecule 66 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SN	150	1182	756	220	205	1	0	0

- Molecule 67 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SO	135	1005	615	199	186	5	0	0

- Molecule 68 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SP	128	1036	659	197	177	3	0	0

- Molecule 69 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	SQ	138	1081	693	202	184	2	0	0

- Molecule 70 is a protein called 40S ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	SR	128	1045	657	190	195	3	0	0

- Molecule 71 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	SS	137	1118	699	222	196	1	0	0

- Molecule 72 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	ST	142	1117	694	221	201	1	0	0

- Molecule 73 is a protein called 40S ribosomal protein S20-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SU	103	819	517	150	148	4	0	0

- Molecule 74 is a protein called 40S ribosomal protein S21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SV	86	664	408	124	128	4	0	0

- Molecule 75 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	SW	129	1037	659	195	178	5	0	0

- Molecule 76 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SX	142	Total	C	N	O	S	0	0
			1099	694	215	188	2		

- Molecule 77 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SY	121	Total	C	N	O	S	0	0
			977	614	192	169	2		

- Molecule 78 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SZ	69	Total	C	N	O	S	0	0
			546	345	101	98	2		

- Molecule 79 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sa	104	Total	C	N	O	S	0	0
			839	518	177	137	7		

- Molecule 80 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	81	Total	C	N	O	S	0	0
			611	386	111	107	7		

- Molecule 81 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sc	60	Total	C	N	O	S	0	0
			473	292	93	87	1		

- Molecule 82 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sd	52	Total	C	N	O	S	0	0
			419	261	84	70	4		

- Molecule 83 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
83	Se	43	347	217	73	57	0	0

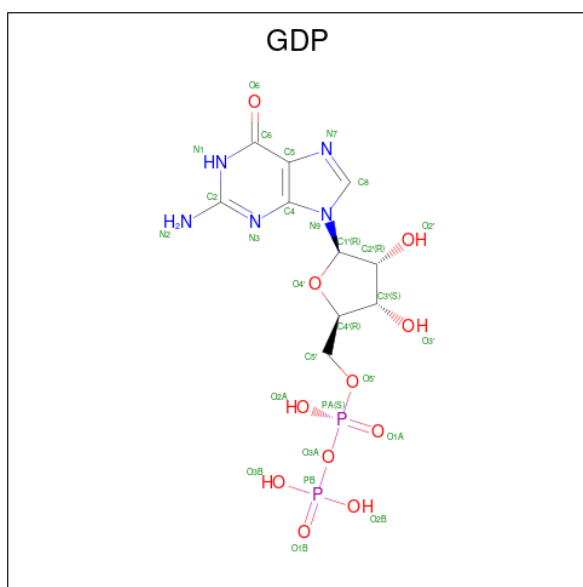
- Molecule 84 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	Sf	74	613	388	117	102	6	0	0

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
85	1	2	2	2	0
85	C	1	1	1	0

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
86	C	1	28	10	5	11	2	0

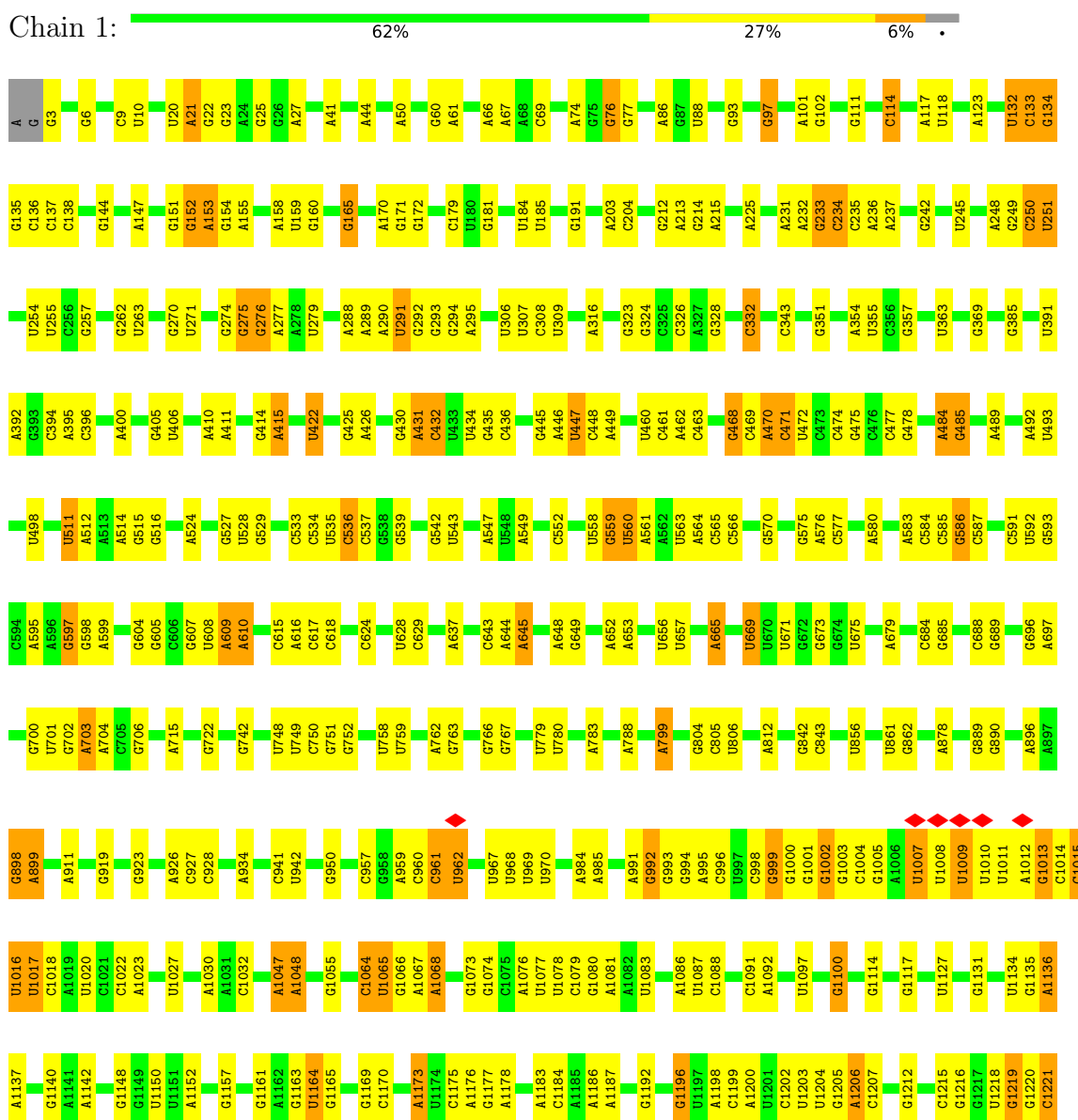
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	Lg	1	Total 1	Zn 1	0
87	Lj	1	Total 1	Zn 1	0
87	Lm	1	Total 1	Zn 1	0
87	Lo	1	Total 1	Zn 1	0
87	Lp	1	Total 1	Zn 1	0
87	Sa	1	Total 1	Zn 1	0
87	Sb	1	Total 1	Zn 1	0
87	Sd	1	Total 1	Zn 1	0

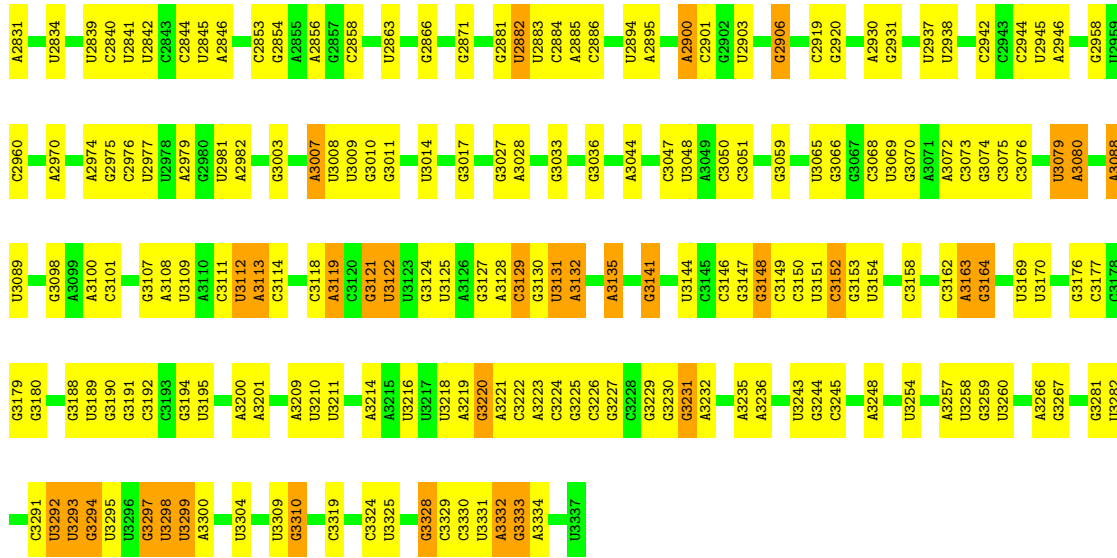
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

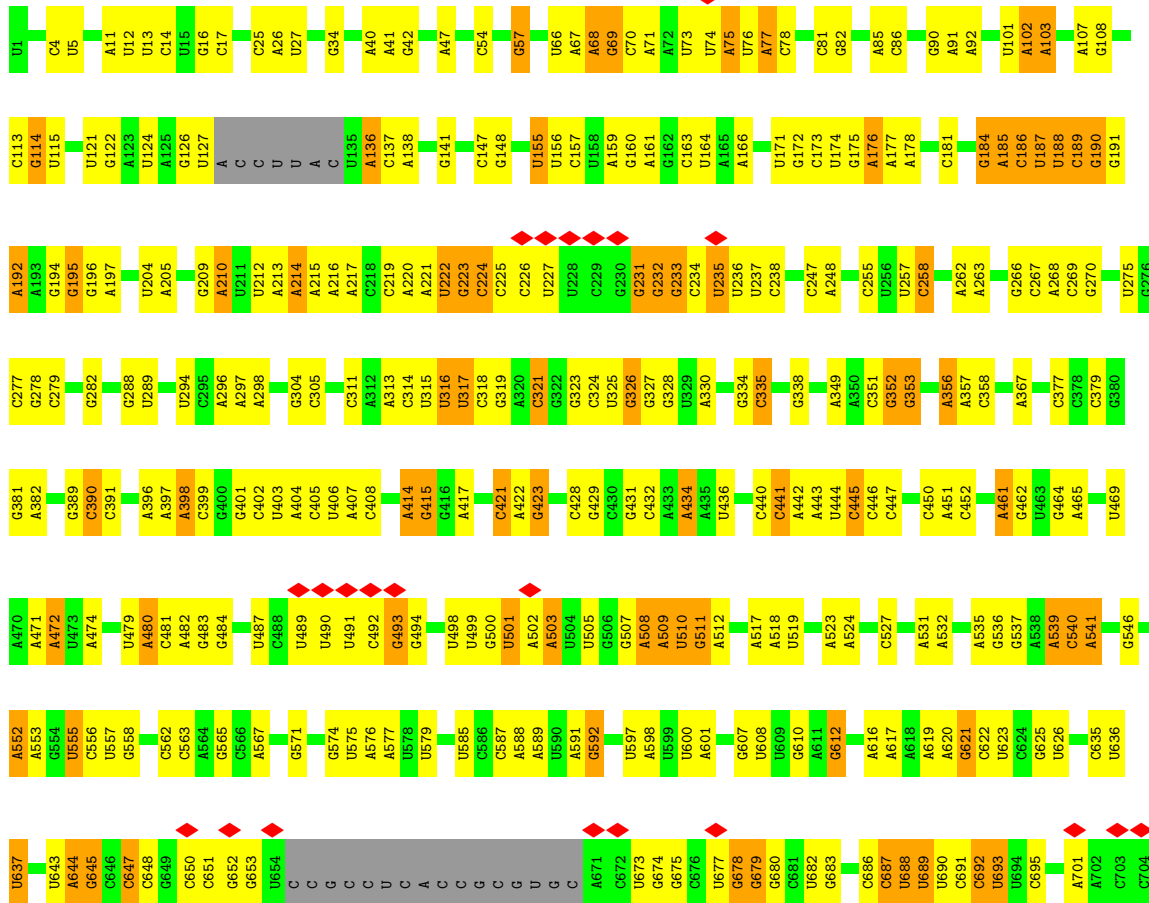
• Molecule 1: 26S rRNA

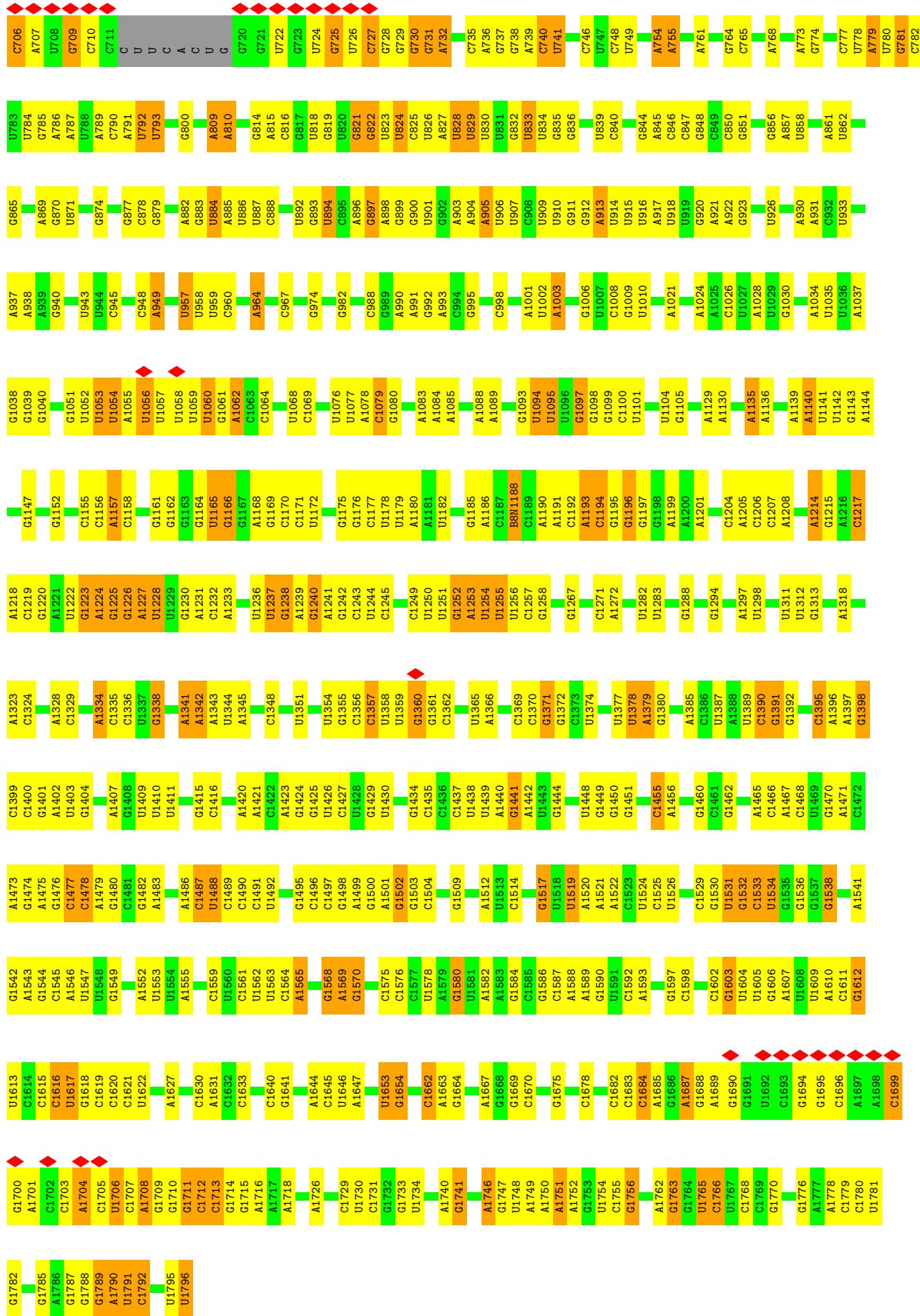


G2687	U2476	G2181	U2075	C1818	U1704	G1578	A1464	A1313	C1222
U2688	U2477	A2182	A2076	A1819	C1705	A1582	A1465	U1314	A1223
U2709	A2478	A2186	A2092	A1821	U1706	A1583	G1466	C1322	U1224
U2711	G2485	A2187	G2083	A1822	G1707	A1584	U1467	G1225	G1225
G2712	A2486	U2188	G2084	G1826	U1707	A1585	G1468	C1323	G1226
G2713	A2487	A2192	G2085	C1826	A1713	U1586	G1469	U1324	A1227
C2714	G2488	A2206	A2094	C1829	G1714	U1587	A1474	A1331	A1228
U2611	U2315	G2212	C2095	A1830	A1730	C1588	G1475	G1332	U1230
U2611	G2318	G2211	U2096	A1838	G1731	C1589	G1476	C1231	C1231
A2615	A2320	G2212	U2100	G1843	A1732	U1595	C1480	U1236	U1236
A2616	A2321	G2213	A2101	G1846	G1733	U1596	A1481	C1237	C1237
G2617	U2314	G2216	A2102	C1846	C1734	U1597	G1485	C1238	C1238
G2618	A2315	U2217	A2106	A1875	A1740	U1598	G1486	G1239	G1239
U2619	G2318	A2218	A2106	A1876	C1741	U1599	A1487	U1241	U1241
U2620	A2330	A2219	A2106	G1858	U1742	U1600	A1487	A1242	A1242
G2621	A2331	C2220	A2107	A1859	U1743	U1601	G1488	A1243	A1243
G2622	G2332	A2221	A2110	U1860	C1744	U1602	C1491	G1244	G1244
G2623	G2333	A2222	U2111	A1866	U1745	U1609	U1495	G1245	G1245
G2624	G2334	A2223	A2112	A1866	G1746	C1611	U1506	G1246	A1246
G2625	G2335	G2224	U2117	A1875	G1750	G1619	U1516	C1247	C1247
G2626	G2336	U2227	G2118	A1876	U1751	G1620	A1517	U1248	U1248
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C2643	G2366	G2236	G2148	G1907	A1767	A1635	G1544	C1266	C1266
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G2649	C2368	A2244	U2155	G1920	A1778	C1637	G1546	G1268	G1268
A2650	C2370	A2248	G2148	G1921	A1779	U1639	C1546	A1269	A1269
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A2657	U2389	G2276	U2168	A1936	G1792	U1660	G1554	G1289	G1289
A2663	U2390	C2271	G2169	G1937	A1793	U1661	G1555	A1291	A1291
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A2667	U2392	U2273	G2172	U1939	U1795	C1663	U1560	G1296	G1296
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U2669	G2398	G2278	G2173	G1942	U1798	A1677	U1563	C1299	C1299
U2670	C2407	G2278	G2173	G	U1799	U1685	A1567	A1300	A1300
U2671	A2408	U2281	A2176	C	U1800	U1685	A1568	A1301	A1301
U2672	U2409	U2297	A2177	C	C1801	A1695	A1569	G1457	G1457
U2673	A2410	G2298	A2177	C	U1813	A1696	U1570	G1458	G1458
U2674	G2414			C		C1697	G1571	G1459	G1459
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U2677				C				G1463	G1463
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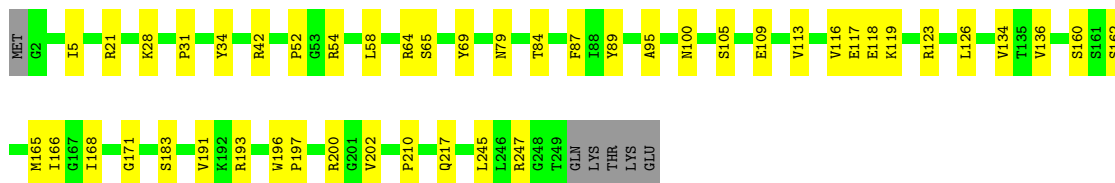


• Molecule 2: 18S rRNA

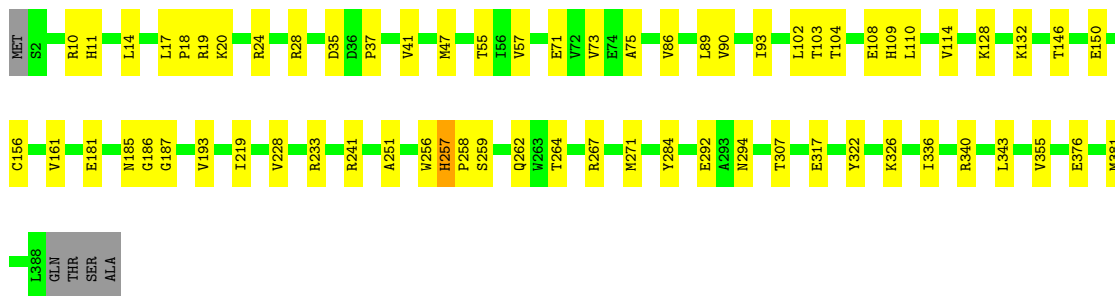
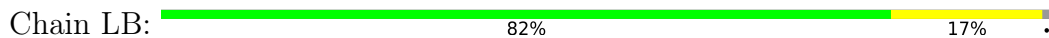




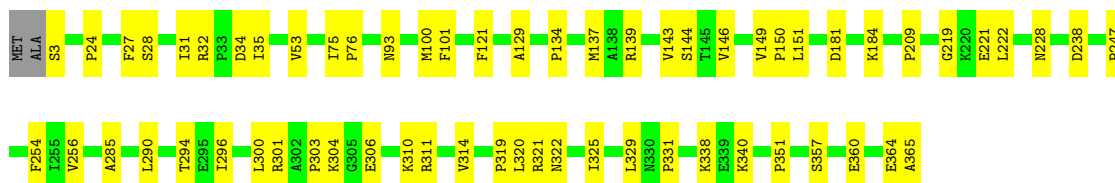
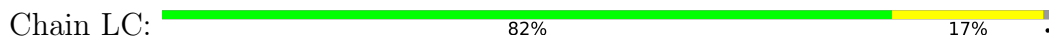
• Molecule 3: 5S rRNA



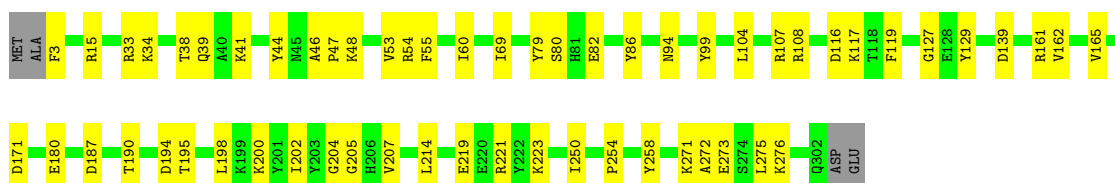
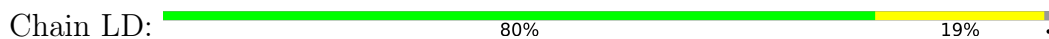
• Molecule 10: 60S ribosomal protein L3-like protein



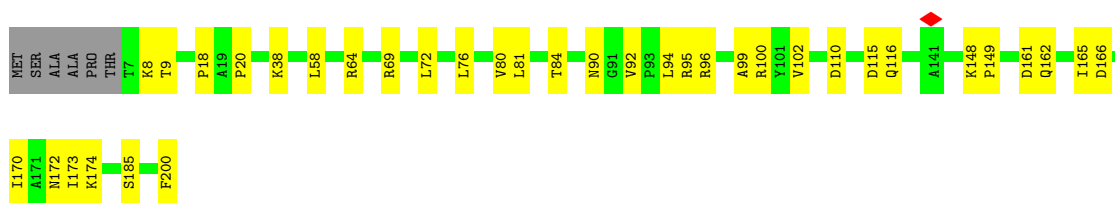
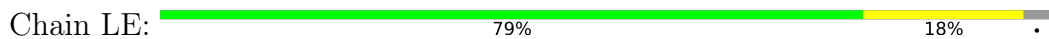
• Molecule 11: 60S ribosomal protein L4-like protein




• Molecule 12: 60S ribosomal protein l5-like protein

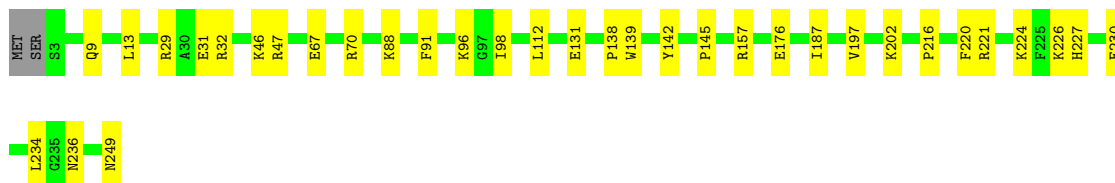


• Molecule 13: 60S ribosomal protein L6




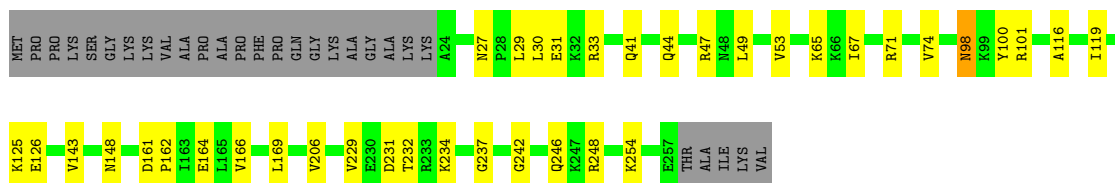
• Molecule 14: 60S ribosomal protein l7-like protein

Chain LF:  86% 14%



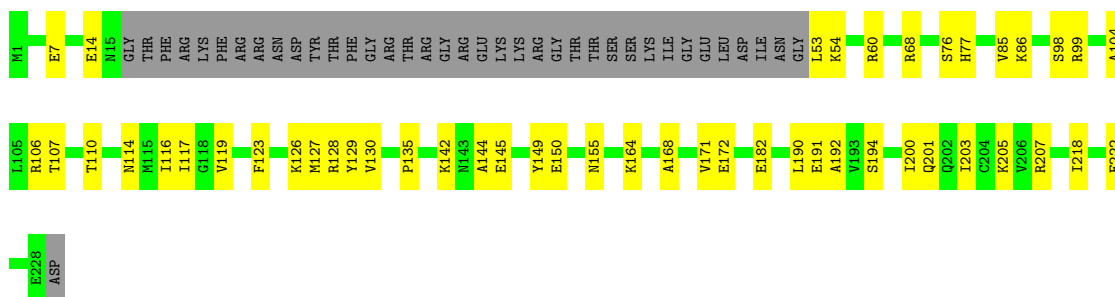
• Molecule 15: 60S ribosomal protein L8

Chain LG:  75% 14% 11%




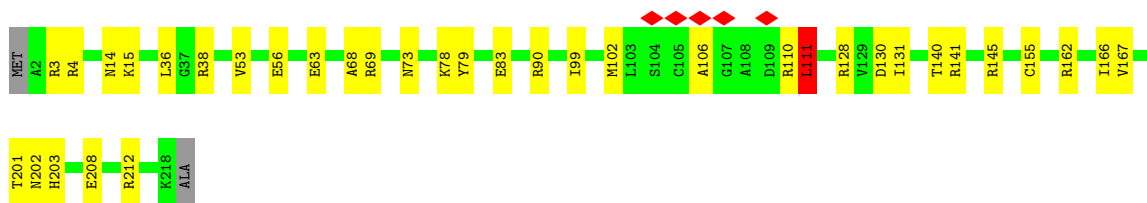
• Molecule 16: 60S ribosomal protein l9-like protein

Chain LH:  62% 21% 17%




• Molecule 17: 60S ribosomal protein L10-like protein

Chain LI:  83% 16%

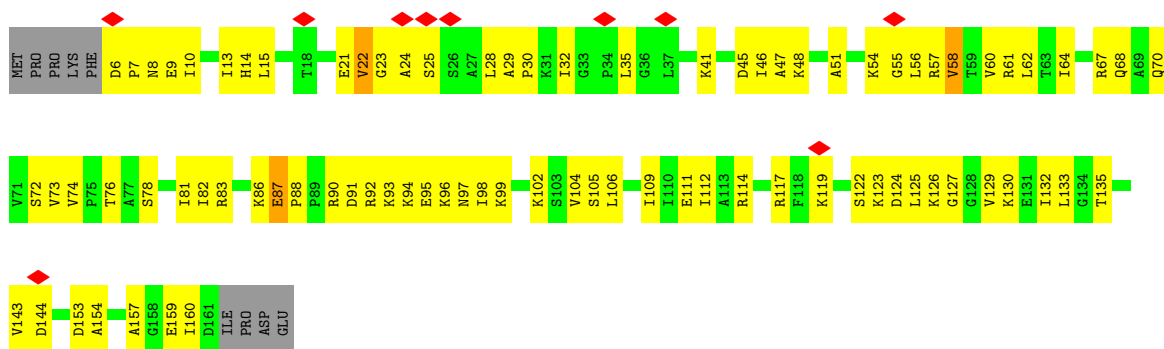


• Molecule 18: Putative ribosomal protein

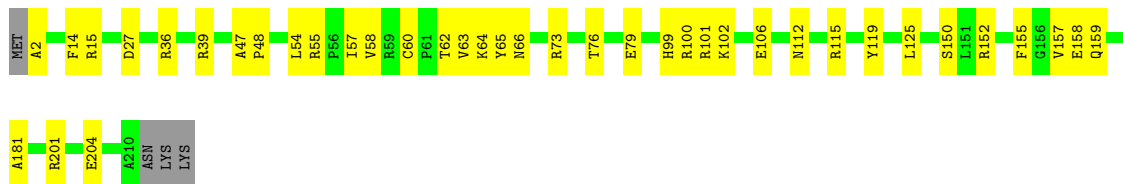
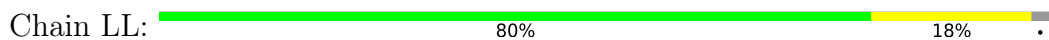
Chain LJ:  79% 18%



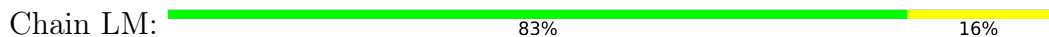
• Molecule 19: 60S ribosomal protein L12-like protein



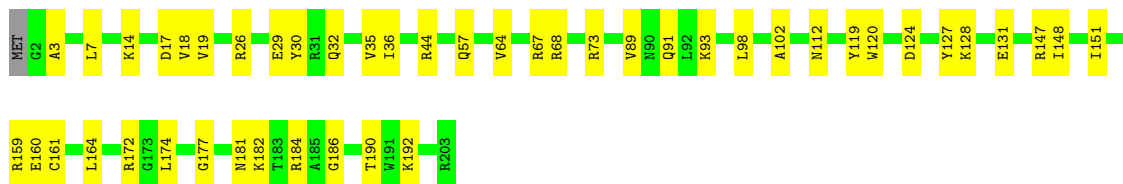
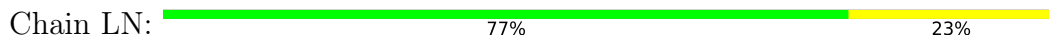
• Molecule 20: 60S ribosomal protein L13



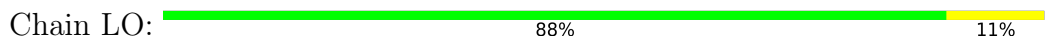
• Molecule 21: 60S ribosomal protein L14-like protein

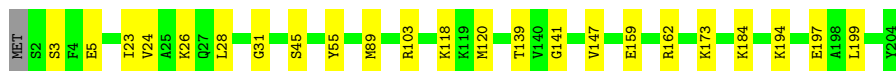


• Molecule 22: Ribosomal protein L15

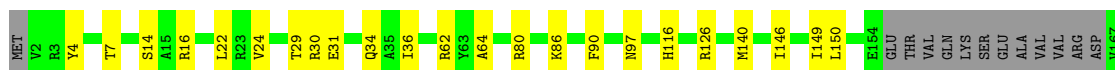
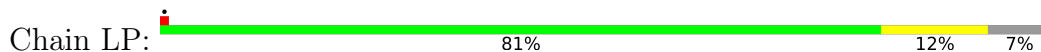


• Molecule 23: 60S ribosomal protein L16-like protein

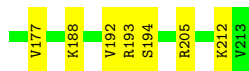
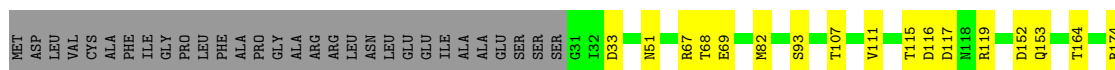
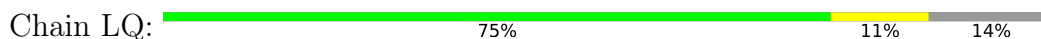




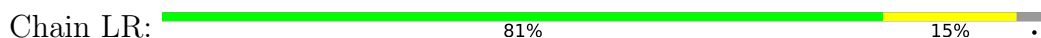
- Molecule 24: 60S ribosomal protein l17-like protein



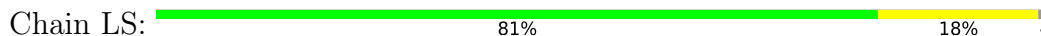
- Molecule 25: Ribosomal protein L18-like protein



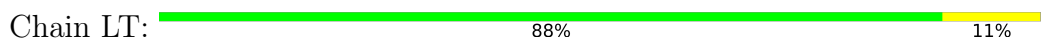
- Molecule 26: Ribosomal protein L19



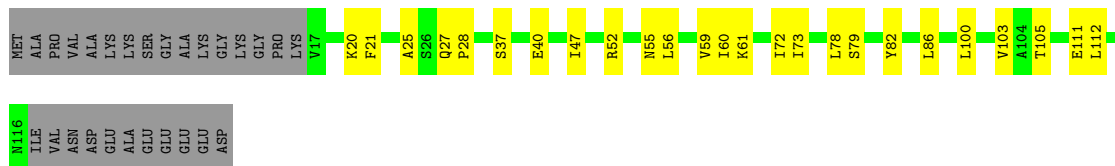
- Molecule 27: 60S ribosomal protein L20



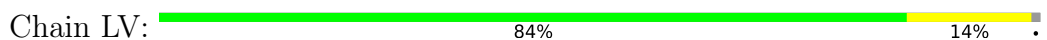
- Molecule 28: 60S ribosomal protein l21-like protein



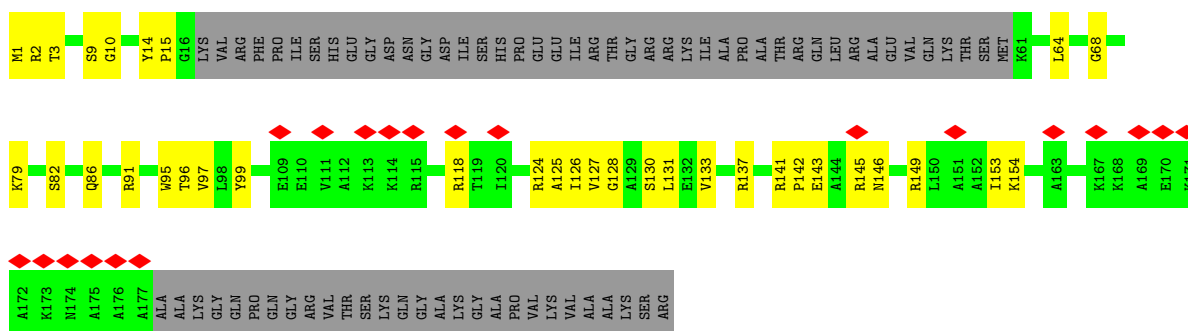
- Molecule 29: 60S ribosomal protein L22-like protein



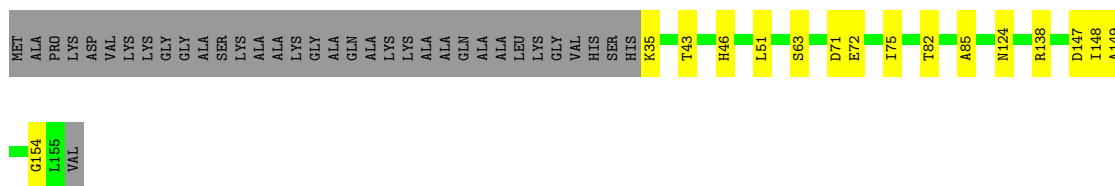
- Molecule 30: 60S ribosomal protein l23-like protein



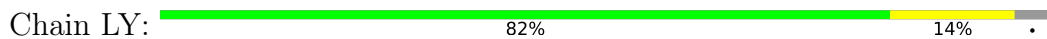
- Molecule 31: 60S ribosomal protein L24-like protein



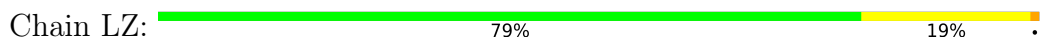
- Molecule 32: 60S ribosomal protein L25-like protein

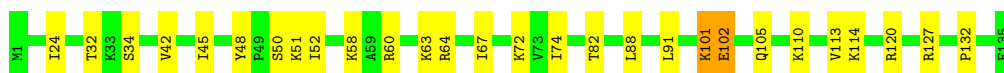


- Molecule 33: 60S ribosomal protein L26-like protein

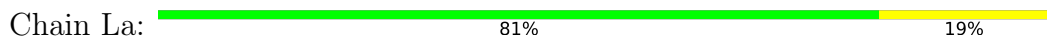


- Molecule 34: 60S ribosomal protein L27

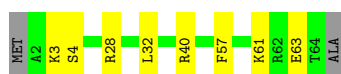
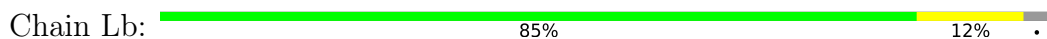




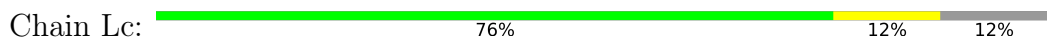
- Molecule 35: 60S ribosomal protein L28-like protein



- Molecule 36: 60S ribosomal protein L29



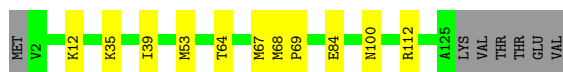
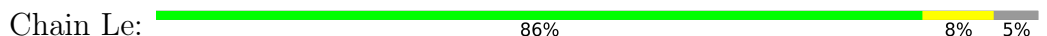
- Molecule 37: 60S ribosomal protein l30-like protein



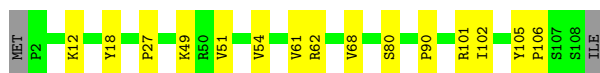
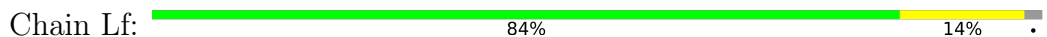
- Molecule 38: Putative 60S ribosomal protein



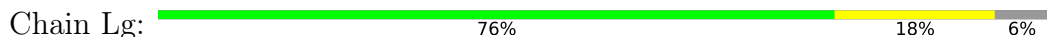
- Molecule 39: 60S ribosomal protein L32-like protein



- Molecule 40: 60S ribosomal protein l33-like protein

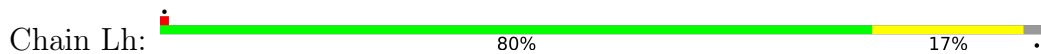


- Molecule 41: Ribosomal protein l34-like protein





- Molecule 42: Dolichyl-diphosphooligosaccharide--protein glycotransferase



- Molecule 43: 60S ribosomal protein L36



- Molecule 44: Ribosomal protein L37



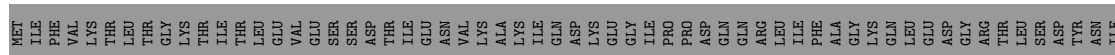
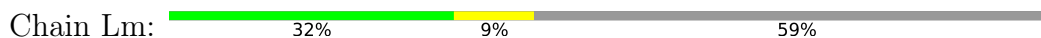
- Molecule 45: 60S ribosomal protein L38-like protein



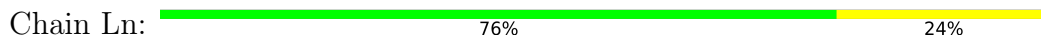
- Molecule 46: Ribosomal protein eL39



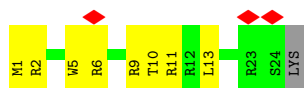
- Molecule 47: Ubiquitin



- Molecule 48: 60S ribosomal protein L41-A



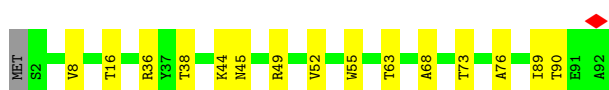
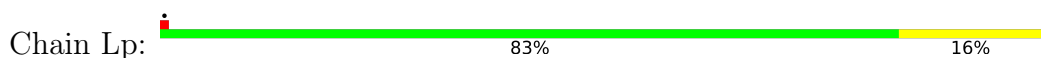
• Molecule 48: 60S ribosomal protein L41-A



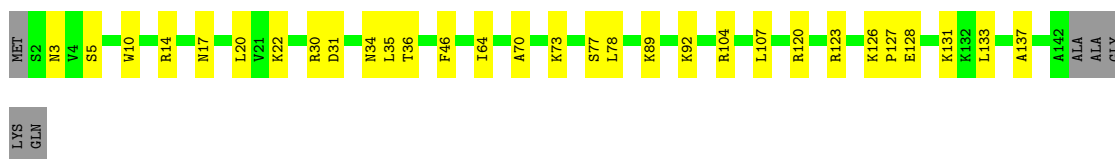
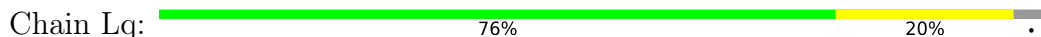
• Molecule 49: 60S ribosomal protein L44-like protein



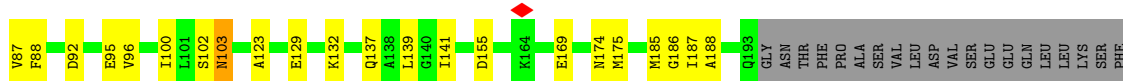
• Molecule 50: 60S ribosomal protein L43-like protein

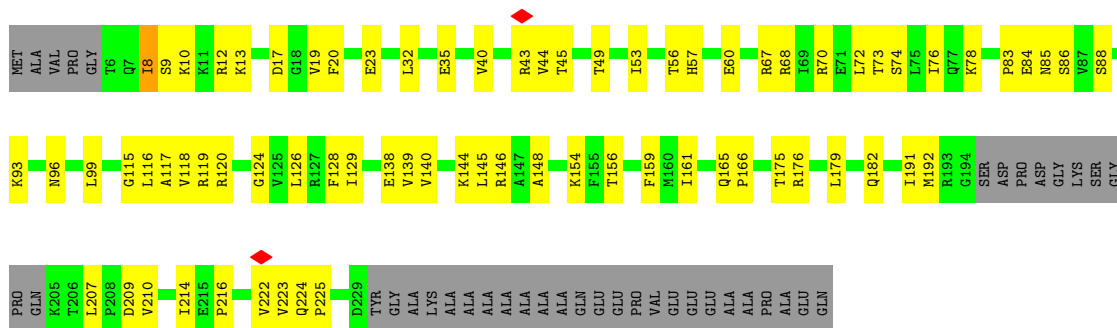


• Molecule 51: Putative 60S ribosomal protein

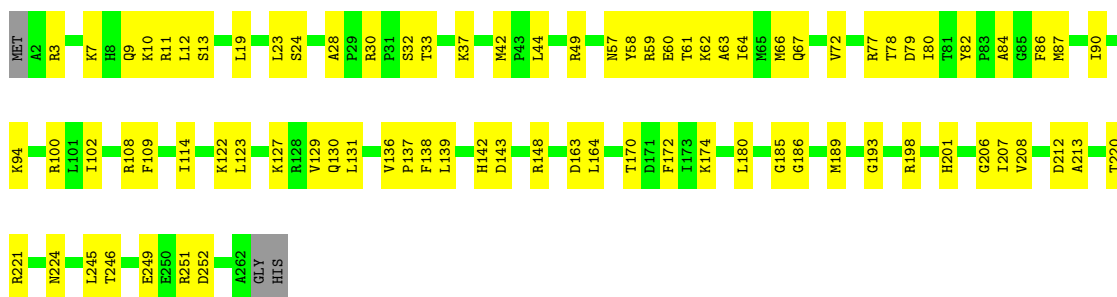


• Molecule 52: 60S acidic ribosomal protein P0

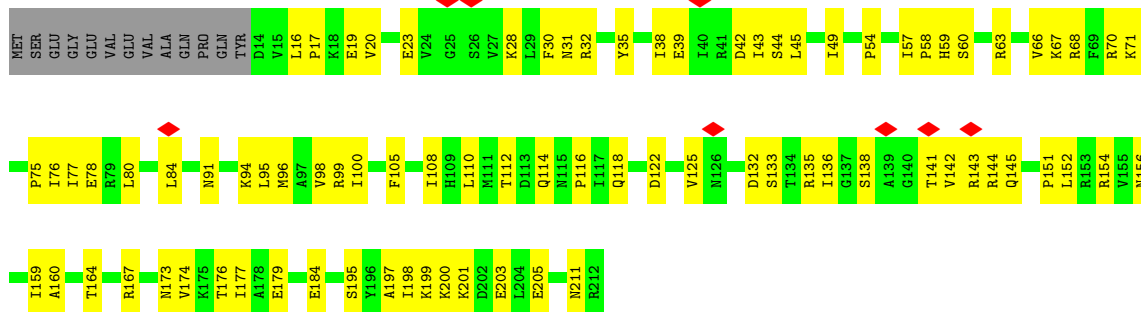




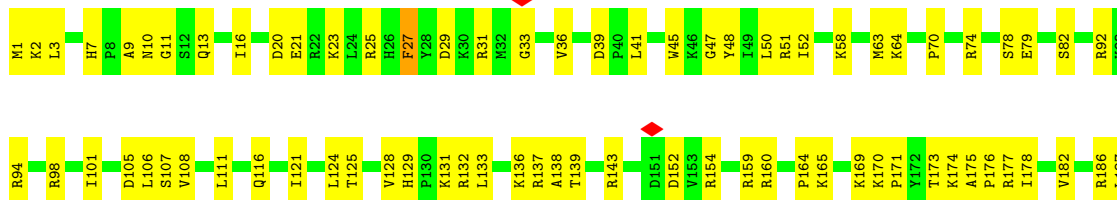
• Molecule 57: 40S ribosomal protein S4



• Molecule 58: 40S ribosomal protein s5-like protein

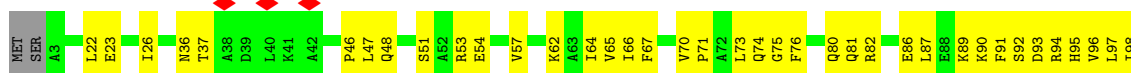


• Molecule 59: 40S ribosomal protein S6





• Molecule 60: 40S ribosomal protein S7



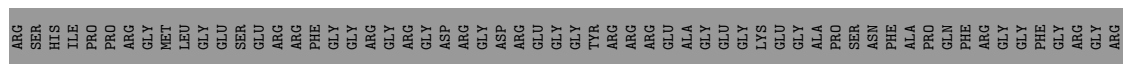
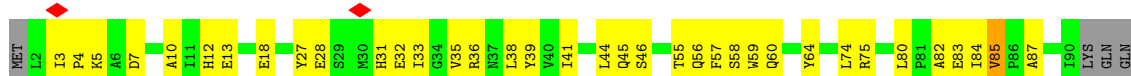
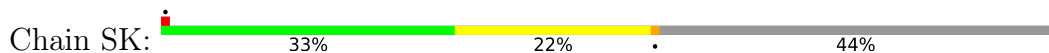
• Molecule 61: 40S ribosomal protein S8



• Molecule 62: 40S ribosomal protein s9-like protein

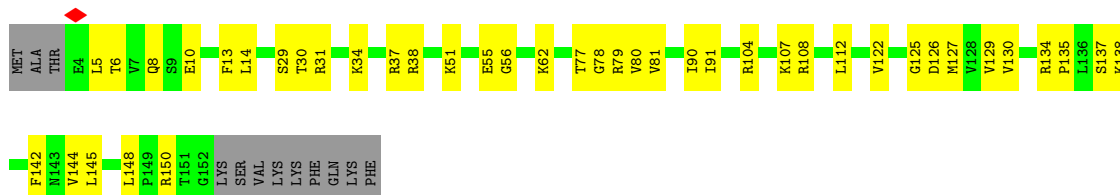


• Molecule 63: 40S ribosomal protein s10-like protein

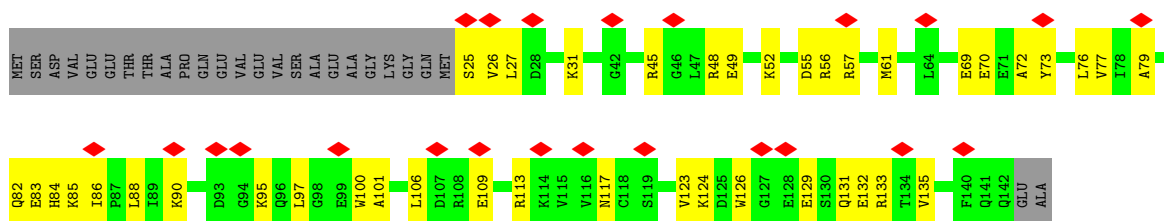


GLY
ASP
ALA
PRO
SER
SER

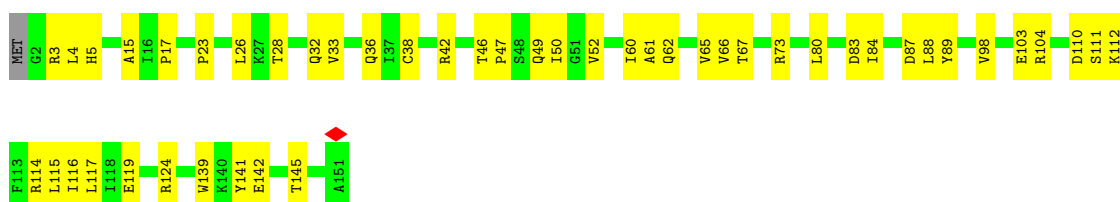
• Molecule 64: 40S ribosomal protein S11-like protein



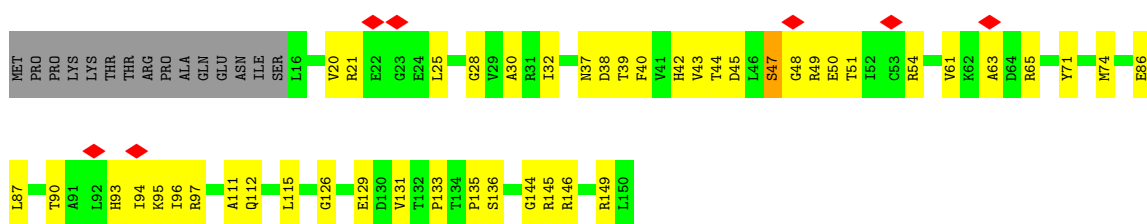
• Molecule 65: 40S ribosomal protein S12



• Molecule 66: 40S ribosomal protein S13-like protein

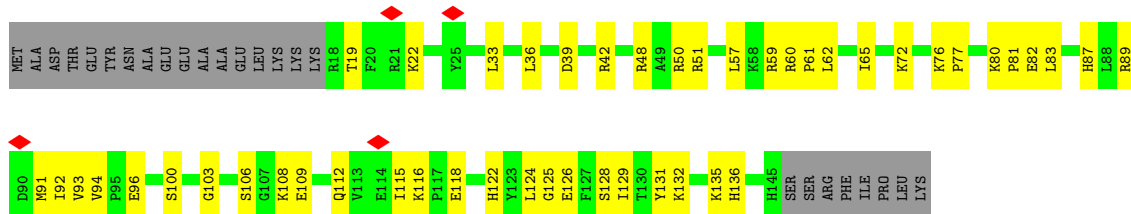


• Molecule 67: 40S ribosomal protein S14-like protein

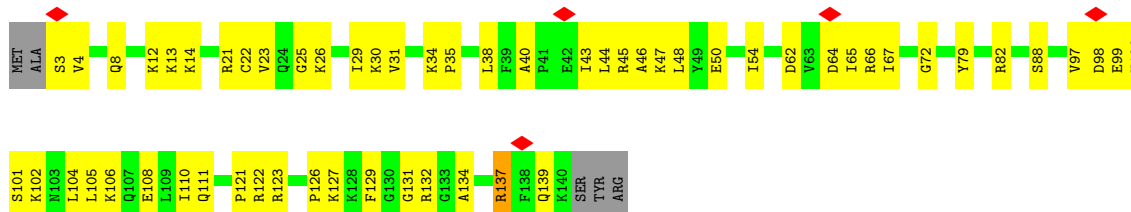


• Molecule 68: 40S ribosomal protein s15-like protein

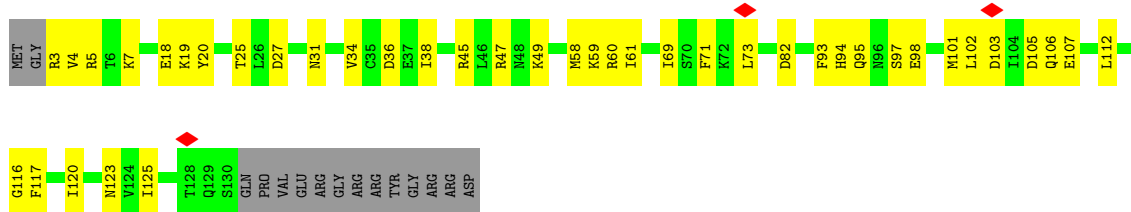




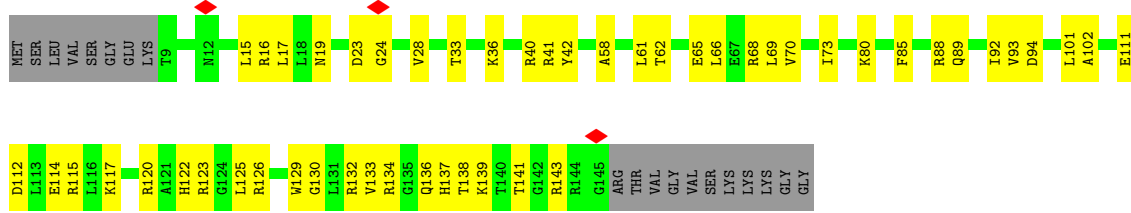
• Molecule 69: 40S ribosomal protein S16-like protein



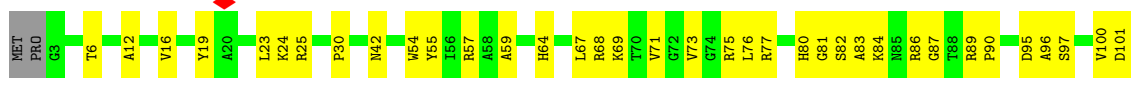
• Molecule 70: 40S ribosomal protein S17-like protein



• Molecule 71: Putative ribosomal protein

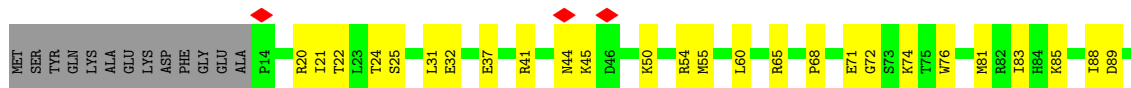


• Molecule 72: 40S ribosomal protein S19-like protein





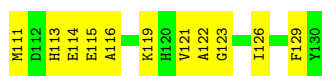
- Molecule 73: 40S ribosomal protein S20-like protein



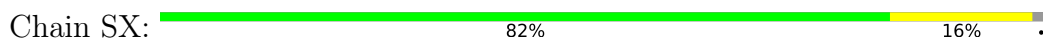
- Molecule 74: 40S ribosomal protein S21-like protein



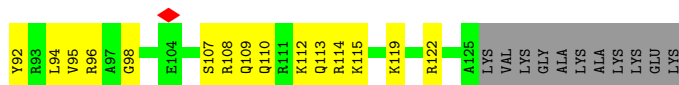
- Molecule 75: 40S ribosomal protein S22-like protein



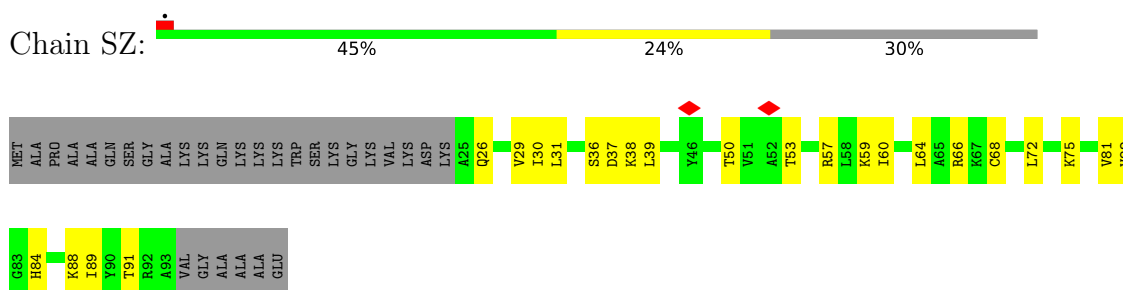
- Molecule 76: 40S ribosomal protein s23-like protein



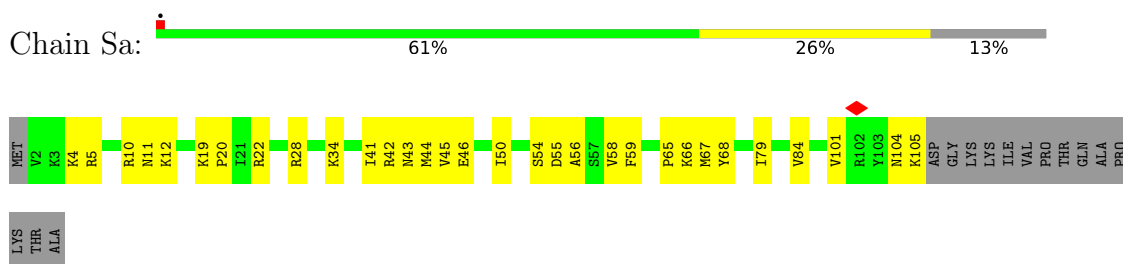
- Molecule 77: 40S ribosomal protein S24



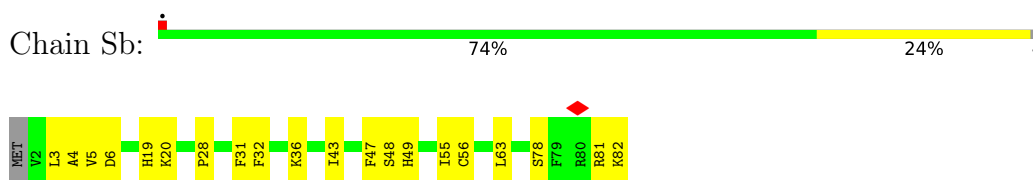
- Molecule 78: 40S ribosomal protein S25



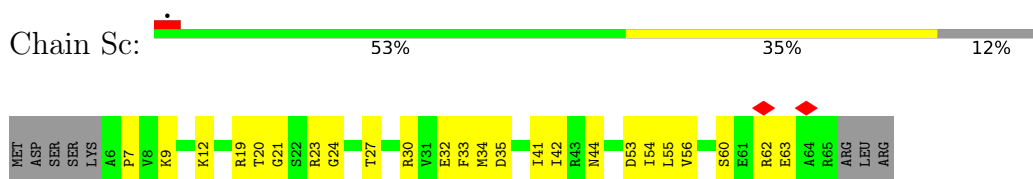
- Molecule 79: 40S ribosomal protein S26



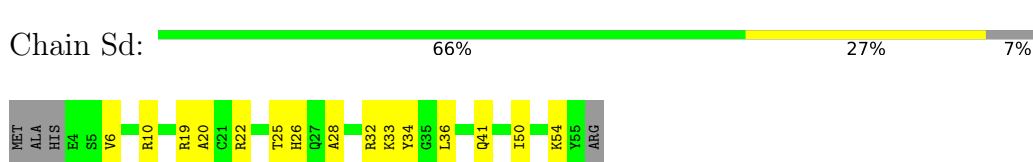
- Molecule 80: Ribosomal protein s27-like protein



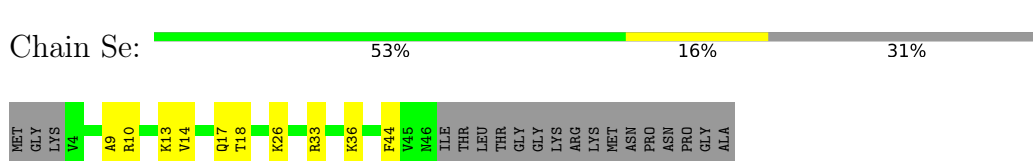
- Molecule 81: 40S ribosomal protein S28-like protein



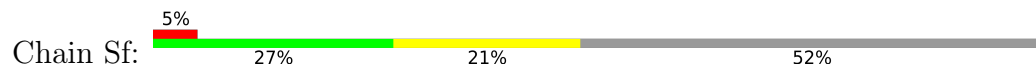
- Molecule 82: Ribosomal protein uS14



- Molecule 83: 40S ribosomal protein S30



• Molecule 84: 40S ribosomal protein S27a-like protein



MET GLN ILE PHE VAL LYS THR LEU THR LEU GLY LYS THR ILE THR LEU LEU VAL GLU PRO SER ASP THR ILE ASP THR VAL LYS SER LYS ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU ASP GLY THR SER ASP TYR ASN

ILE GLN LYS SER THR LEU HIS VAL LEU ARG LEU ARG GLY ALA K78 K79 K82 K83 V84 Y85 T86 T87 P88 H93 K94 R95 K96 K97 V98 Y105 Y106 K107 V108 D111 G112 K113 I114 E115 R116 L117 R118 R119 E120 C121 P122 N123 C126 G127 A128 G129 V130 F131

M132 A133 S134 D137 R138 Q139 R143 C144 H145 L146 F150 D151 LYS SER SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35338	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32.51	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	15.757	Depositor
Minimum map value	-8.328	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.575	Depositor
Recommended contour level	1.3	Depositor
Map size (Å)	534.60004, 534.60004, 534.60004	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, DDE, GDP, MG, B8N

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	1	0.19	0/76390	0.34	0/119106
2	2	0.16	0/42072	0.38	0/65562
3	3	0.16	0/2833	0.29	0/4413
4	4	0.17	0/3710	0.30	0/5778
5	5	0.29	0/1773	0.88	0/2759
6	A	0.14	0/2495	0.44	0/3390
7	B	0.15	0/991	0.43	0/1319
8	C	0.16	0/6434	0.50	6/8716 (0.1%)
9	LA	0.21	0/1930	0.42	0/2597
10	LB	0.19	0/3156	0.37	0/4238
11	LC	0.17	0/2815	0.34	0/3795
12	LD	0.16	0/2487	0.35	0/3341
13	LE	0.15	0/1547	0.38	0/2081
14	LF	0.18	0/2055	0.34	0/2758
15	LG	0.15	0/1920	0.38	0/2568
16	LH	0.18	0/1525	0.37	0/2050
17	LI	0.17	0/1797	0.37	1/2413 (0.0%)
18	LJ	0.18	0/1389	0.48	0/1856
19	LK	0.20	0/1188	0.65	0/1597
20	LL	0.17	0/1695	0.40	0/2276
21	LM	0.14	0/1144	0.29	0/1539
22	LN	0.19	0/1740	0.32	0/2332
23	LO	0.18	0/1644	0.32	0/2205
24	LP	0.17	0/1400	0.33	0/1884
25	LQ	0.18	0/1507	0.35	0/2017
26	LR	0.17	0/1525	0.37	0/2028
27	LS	0.19	0/1460	0.34	0/1965
28	LT	0.17	0/1292	0.30	0/1738
29	LU	0.15	0/823	0.40	0/1101
30	LV	0.21	0/1030	0.42	0/1384
31	LW	0.16	0/1088	0.40	0/1443
32	LX	0.15	0/983	0.34	0/1325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.15	0/1070	0.34	0/1432
34	LZ	0.16	0/1134	0.41	2/1519 (0.1%)
35	La	0.18	0/1212	0.36	0/1627
36	Lb	0.15	0/525	0.29	0/694
37	Lc	0.15	0/717	0.31	0/964
38	Ld	0.20	0/921	0.39	0/1233
39	Le	0.18	0/1019	0.30	0/1358
40	Lf	0.20	0/874	0.36	0/1176
41	Lg	0.18	0/904	0.34	0/1210
42	Lh	0.14	0/1014	0.33	0/1349
43	Li	0.19	0/833	0.42	0/1100
44	Lj	0.20	0/712	0.40	0/944
45	Lk	0.18	0/640	0.45	1/850 (0.1%)
46	Ll	0.19	0/445	0.47	0/593
47	Lm	0.18	0/424	0.37	0/561
48	Ln	0.22	0/234	0.41	0/300
48	Lr	0.12	0/225	0.34	0/289
49	Lo	0.16	0/835	0.33	0/1105
50	Lp	0.19	0/705	0.41	0/940
51	Lq	0.15	0/1101	0.33	0/1482
52	Ls	0.15	0/1477	0.48	2/1995 (0.1%)
53	SA	0.16	0/1683	0.41	0/2299
54	SB	0.17	0/1838	0.51	1/2472 (0.0%)
55	SC	0.16	0/1703	0.40	0/2303
56	SD	0.16	0/1706	0.47	0/2291
57	SE	0.15	0/2112	0.41	0/2842
58	SF	0.15	0/1578	0.42	0/2130
59	SG	0.16	0/1906	0.46	0/2547
60	SH	0.15	0/1609	0.43	0/2171
61	SI	0.16	0/1654	0.45	0/2213
62	SJ	0.15	0/1489	0.41	0/1993
63	SK	0.18	0/764	0.50	0/1038
64	SL	0.15	0/1241	0.45	0/1666
65	SM	0.15	0/934	0.49	0/1255
66	SN	0.16	0/1205	0.41	0/1627
67	SO	0.15	0/1017	0.48	0/1365
68	SP	0.14	0/1055	0.42	0/1411
69	SQ	0.16	0/1098	0.51	1/1472 (0.1%)
70	SR	0.15	0/1060	0.44	0/1424
71	SS	0.14	0/1133	0.42	0/1520
72	ST	0.14	0/1137	0.41	0/1533
73	SU	0.18	0/828	0.47	0/1112
74	SV	0.16	0/671	0.38	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SW	0.20	0/1055	0.54	0/1416
76	SX	0.18	0/1116	0.39	0/1489
77	SY	0.21	0/991	0.60	0/1324
78	SZ	0.12	0/550	0.40	0/736
79	Sa	0.16	0/852	0.43	0/1136
80	Sb	0.14	0/623	0.55	0/843
81	Sc	0.15	0/476	0.48	0/639
82	Sd	0.20	0/427	0.54	0/570
83	Se	0.19	0/351	0.47	0/463
84	Sf	0.14	0/623	0.46	0/824
All	All	0.18	0/229344	0.39	14/335319 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
10	LB	0	1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	SB	35	PRO	CA-N-CD	-8.11	100.64	112.00
69	SQ	137	ARG	CB-CG-CD	-6.95	95.32	111.30
8	C	373	ASP	CA-C-N	6.11	133.21	121.54
8	C	373	ASP	C-N-CA	6.11	133.21	121.54
52	Ls	102	SER	CA-C-N	5.71	132.45	121.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	LB	257	HIS	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68264	0	34387	627	0
2	2	37645	0	18955	733	0
3	3	2535	0	1284	23	0
4	4	3319	0	1678	40	0
5	5	1589	0	810	63	0
6	A	2438	0	2385	109	0
7	B	982	0	948	37	0
8	C	6335	0	6419	190	0
9	LA	1891	0	1958	36	0
10	LB	3088	0	3206	49	0
11	LC	2758	0	2883	49	0
12	LD	2440	0	2431	40	0
13	LE	1518	0	1619	24	0
14	LF	2017	0	2130	26	0
15	LG	1891	0	2053	30	0
16	LH	1505	0	1581	37	0
17	LI	1760	0	1798	24	0
18	LJ	1367	0	1405	21	0
19	LK	1174	0	1247	83	0
20	LL	1666	0	1756	29	0
21	LM	1125	0	1198	16	0
22	LN	1703	0	1767	33	0
23	LO	1610	0	1702	16	0
24	LP	1378	0	1423	17	0
25	LQ	1481	0	1596	23	0
26	LR	1506	0	1603	26	0
27	LS	1425	0	1484	23	0
28	LT	1266	0	1328	13	0
29	LU	810	0	851	21	0
30	LV	1012	0	1076	16	0
31	LW	1075	0	1146	26	0
32	LX	967	0	1054	13	0
33	LY	1056	0	1143	16	0
34	LZ	1111	0	1181	20	0
35	La	1180	0	1203	23	0
36	Lb	515	0	533	6	0
37	Lc	708	0	753	9	0
38	Ld	907	0	961	17	0
39	Le	1001	0	1070	7	0
40	Lf	853	0	880	11	0
41	Lg	891	0	958	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Lh	1003	0	1116	16	0
43	Li	826	0	908	27	0
44	Lj	698	0	726	15	0
45	Lk	632	0	693	8	0
46	Ll	435	0	473	23	0
47	Lm	418	0	459	8	0
48	Ln	233	0	284	8	0
48	Lr	224	0	271	7	0
49	Lo	822	0	891	5	0
50	Lp	697	0	737	11	0
51	Lq	1083	0	1140	24	0
52	Ls	1449	0	1488	41	0
53	SA	1641	0	1650	37	0
54	SB	1810	0	1906	71	0
55	SC	1672	0	1777	51	0
56	SD	1683	0	1748	64	0
57	SE	2072	0	2155	69	0
58	SF	1557	0	1608	79	0
59	SG	1875	0	1983	76	0
60	SH	1584	0	1666	50	0
61	SI	1621	0	1645	66	0
62	SJ	1466	0	1582	37	0
63	SK	742	0	738	35	0
64	SL	1214	0	1280	32	0
65	SM	923	0	946	36	0
66	SN	1182	0	1264	39	0
67	SO	1005	0	1036	40	0
68	SP	1036	0	1094	42	0
69	SQ	1081	0	1151	59	0
70	SR	1045	0	1083	35	0
71	SS	1118	0	1172	44	0
72	ST	1117	0	1133	43	0
73	SU	819	0	895	38	0
74	SV	664	0	662	15	0
75	SW	1037	0	1076	42	0
76	SX	1099	0	1169	19	0
77	SY	977	0	1044	54	0
78	SZ	546	0	591	18	0
79	Sa	839	0	891	35	0
80	Sb	611	0	634	17	0
81	Sc	473	0	500	25	0
82	Sd	419	0	419	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	Se	347	0	387	9	0
84	Sf	613	0	653	36	0
85	1	2	0	0	0	0
85	C	1	0	0	0	0
86	C	28	0	12	1	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
87	Sb	1	0	0	0	0
87	Sd	1	0	0	0	0
All	All	214209	0	162579	3550	0

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

The worst 5 of 3550 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)
46:L1:48:ARG:HH21	46:L1:49:LEU:HG	1.21	1.05
5:5:52:G:N2	5:5:61:C:C2	2.27	1.01
2:2:709:G:H1	2:2:722:U:H3	1.05	1.00
2:2:974:G:H1	2:2:1021:A:HO2'	1.13	0.95
19:LK:64:ILE:H	19:LK:70:GLN:HE21	1.14	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
6	A	310/316 (98%)	298 (96%)	12 (4%)	0	100	100
7	B	121/302 (40%)	110 (91%)	9 (7%)	2 (2%)	7	32
8	C	808/845 (96%)	756 (94%)	47 (6%)	5 (1%)	21	56
9	LA	246/254 (97%)	222 (90%)	24 (10%)	0	100	100
10	LB	385/392 (98%)	363 (94%)	22 (6%)	0	100	100
11	LC	361/365 (99%)	331 (92%)	30 (8%)	0	100	100
12	LD	298/304 (98%)	289 (97%)	8 (3%)	1 (0%)	36	70
13	LE	192/200 (96%)	172 (90%)	20 (10%)	0	100	100
14	LF	245/249 (98%)	232 (95%)	13 (5%)	0	100	100
15	LG	232/262 (88%)	218 (94%)	14 (6%)	0	100	100
16	LH	189/229 (82%)	183 (97%)	6 (3%)	0	100	100
17	LI	215/219 (98%)	201 (94%)	13 (6%)	1 (0%)	24	60
18	LJ	165/173 (95%)	154 (93%)	11 (7%)	0	100	100
19	LK	154/165 (93%)	129 (84%)	21 (14%)	4 (3%)	4	23
20	LL	207/213 (97%)	193 (93%)	14 (7%)	0	100	100
21	LM	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
22	LN	200/203 (98%)	188 (94%)	12 (6%)	0	100	100
23	LO	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
24	LP	170/187 (91%)	163 (96%)	7 (4%)	0	100	100
25	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
26	LR	182/192 (95%)	180 (99%)	2 (1%)	0	100	100
27	LS	171/174 (98%)	160 (94%)	11 (6%)	0	100	100
28	LT	156/160 (98%)	152 (97%)	4 (3%)	0	100	100
29	LU	98/127 (77%)	90 (92%)	8 (8%)	0	100	100
30	LV	135/139 (97%)	129 (96%)	6 (4%)	0	100	100
31	LW	131/205 (64%)	123 (94%)	8 (6%)	0	100	100
32	LX	119/156 (76%)	116 (98%)	3 (2%)	0	100	100
33	LY	131/138 (95%)	128 (98%)	3 (2%)	0	100	100
34	LZ	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	50
35	La	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
36	Lb	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
37	Lc	93/108 (86%)	90 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	Ld	110/120 (92%)	105 (96%)	5 (4%)	0	100	100
39	Le	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
40	Lf	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
41	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
42	Lh	120/126 (95%)	115 (96%)	5 (4%)	0	100	100
43	Li	99/110 (90%)	96 (97%)	3 (3%)	0	100	100
44	Lj	86/95 (90%)	79 (92%)	7 (8%)	0	100	100
45	Lk	74/94 (79%)	69 (93%)	5 (7%)	0	100	100
46	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
47	Lm	50/127 (39%)	48 (96%)	2 (4%)	0	100	100
48	Ln	23/25 (92%)	23 (100%)	0	0	100	100
48	Lr	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
50	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
51	Lq	139/147 (95%)	130 (94%)	9 (6%)	0	100	100
52	Ls	187/312 (60%)	180 (96%)	6 (3%)	1 (0%)	24	60
53	SA	206/285 (72%)	188 (91%)	17 (8%)	1 (0%)	24	60
54	SB	220/255 (86%)	196 (89%)	24 (11%)	0	100	100
55	SC	214/263 (81%)	201 (94%)	13 (6%)	0	100	100
56	SD	210/254 (83%)	196 (93%)	13 (6%)	1 (0%)	24	60
57	SE	259/264 (98%)	243 (94%)	16 (6%)	0	100	100
58	SF	197/212 (93%)	178 (90%)	18 (9%)	1 (0%)	24	60
59	SG	230/239 (96%)	221 (96%)	7 (3%)	2 (1%)	14	48
60	SH	196/203 (97%)	185 (94%)	11 (6%)	0	100	100
61	SI	199/202 (98%)	189 (95%)	10 (5%)	0	100	100
62	SJ	177/190 (93%)	169 (96%)	8 (4%)	0	100	100
63	SK	87/159 (55%)	81 (93%)	5 (6%)	1 (1%)	11	43
64	SL	147/161 (91%)	138 (94%)	9 (6%)	0	100	100
65	SM	116/144 (81%)	101 (87%)	15 (13%)	0	100	100
66	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
67	SO	133/150 (89%)	118 (89%)	14 (10%)	1 (1%)	16	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	SP	126/153 (82%)	114 (90%)	12 (10%)	0	100	100
69	SQ	136/143 (95%)	124 (91%)	12 (9%)	0	100	100
70	SR	126/143 (88%)	119 (94%)	7 (6%)	0	100	100
71	SS	135/156 (86%)	125 (93%)	10 (7%)	0	100	100
72	ST	140/153 (92%)	130 (93%)	10 (7%)	0	100	100
73	SU	101/116 (87%)	89 (88%)	12 (12%)	0	100	100
74	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
75	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
76	SX	140/145 (97%)	127 (91%)	13 (9%)	0	100	100
77	SY	119/136 (88%)	112 (94%)	6 (5%)	1 (1%)	16	50
78	SZ	67/99 (68%)	64 (96%)	3 (4%)	0	100	100
79	Sa	102/119 (86%)	98 (96%)	4 (4%)	0	100	100
80	Sb	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
81	Sc	58/68 (85%)	55 (95%)	3 (5%)	0	100	100
82	Sd	50/56 (89%)	45 (90%)	5 (10%)	0	100	100
83	Se	41/62 (66%)	38 (93%)	3 (7%)	0	100	100
84	Sf	72/154 (47%)	61 (85%)	11 (15%)	0	100	100
All	All	12503/14119 (89%)	11723 (94%)	757 (6%)	23 (0%)	44	76

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	C	487	VAL
7	B	104	ARG
8	C	374	CYS
52	Ls	103	ASN
58	SF	31	ASN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
6	A	271/274 (99%)	271 (100%)	0	100	100
7	B	93/224 (42%)	93 (100%)	0	100	100
8	C	693/719 (96%)	693 (100%)	0	100	100
9	LA	192/198 (97%)	192 (100%)	0	100	100
10	LB	327/331 (99%)	327 (100%)	0	100	100
11	LC	284/285 (100%)	284 (100%)	0	100	100
12	LD	250/253 (99%)	250 (100%)	0	100	100
13	LE	162/166 (98%)	162 (100%)	0	100	100
14	LF	213/215 (99%)	213 (100%)	0	100	100
15	LG	202/222 (91%)	201 (100%)	1 (0%)	81	89
16	LH	168/200 (84%)	168 (100%)	0	100	100
17	LI	182/183 (100%)	182 (100%)	0	100	100
18	LJ	145/150 (97%)	145 (100%)	0	100	100
19	LK	127/136 (93%)	127 (100%)	0	100	100
20	LL	172/176 (98%)	172 (100%)	0	100	100
21	LM	116/117 (99%)	116 (100%)	0	100	100
22	LN	179/180 (99%)	179 (100%)	0	100	100
23	LO	162/163 (99%)	162 (100%)	0	100	100
24	LP	140/152 (92%)	140 (100%)	0	100	100
25	LQ	155/178 (87%)	155 (100%)	0	100	100
26	LR	153/160 (96%)	153 (100%)	0	100	100
27	LS	153/154 (99%)	153 (100%)	0	100	100
28	LT	134/135 (99%)	134 (100%)	0	100	100
29	LU	88/108 (82%)	88 (100%)	0	100	100
30	LV	101/102 (99%)	101 (100%)	0	100	100
31	LW	107/163 (66%)	107 (100%)	0	100	100
32	LX	108/129 (84%)	108 (100%)	0	100	100
33	LY	116/119 (98%)	116 (100%)	0	100	100
34	LZ	121/121 (100%)	121 (100%)	0	100	100
35	La	121/122 (99%)	121 (100%)	0	100	100
36	Lb	54/55 (98%)	54 (100%)	0	100	100
37	Lc	77/88 (88%)	77 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Ld	96/105 (91%)	96 (100%)	0	100	100
39	Le	107/114 (94%)	107 (100%)	0	100	100
40	Lf	88/90 (98%)	88 (100%)	0	100	100
41	Lg	97/102 (95%)	97 (100%)	0	100	100
42	Lh	109/112 (97%)	109 (100%)	0	100	100
43	Li	85/93 (91%)	85 (100%)	0	100	100
44	Lj	72/78 (92%)	72 (100%)	0	100	100
45	Lk	73/88 (83%)	73 (100%)	0	100	100
46	Ll	45/46 (98%)	45 (100%)	0	100	100
47	Lm	47/114 (41%)	47 (100%)	0	100	100
48	Ln	23/23 (100%)	23 (100%)	0	100	100
48	Lr	22/23 (96%)	22 (100%)	0	100	100
49	Lo	88/90 (98%)	88 (100%)	0	100	100
50	Lp	73/74 (99%)	73 (100%)	0	100	100
51	Lq	109/112 (97%)	109 (100%)	0	100	100
52	Ls	155/255 (61%)	155 (100%)	0	100	100
53	SA	178/225 (79%)	178 (100%)	0	100	100
54	SB	197/223 (88%)	197 (100%)	0	100	100
55	SC	181/206 (88%)	181 (100%)	0	100	100
56	SD	182/206 (88%)	182 (100%)	0	100	100
57	SE	219/221 (99%)	219 (100%)	0	100	100
58	SF	167/178 (94%)	167 (100%)	0	100	100
59	SG	198/204 (97%)	198 (100%)	0	100	100
60	SH	172/177 (97%)	172 (100%)	0	100	100
61	SI	163/164 (99%)	163 (100%)	0	100	100
62	SJ	154/162 (95%)	154 (100%)	0	100	100
63	SK	77/126 (61%)	77 (100%)	0	100	100
64	SL	132/143 (92%)	132 (100%)	0	100	100
65	SM	101/121 (84%)	101 (100%)	0	100	100
66	SN	129/130 (99%)	129 (100%)	0	100	100
67	SO	103/117 (88%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SP	111/132 (84%)	111 (100%)	0	100	100
69	SQ	111/115 (96%)	111 (100%)	0	100	100
70	SR	119/131 (91%)	119 (100%)	0	100	100
71	SS	120/135 (89%)	120 (100%)	0	100	100
72	ST	114/124 (92%)	114 (100%)	0	100	100
73	SU	93/103 (90%)	93 (100%)	0	100	100
74	SV	69/80 (86%)	69 (100%)	0	100	100
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SX	113/116 (97%)	113 (100%)	0	100	100
77	SY	104/115 (90%)	104 (100%)	0	100	100
78	SZ	60/80 (75%)	60 (100%)	0	100	100
79	Sa	91/103 (88%)	91 (100%)	0	100	100
80	Sb	70/71 (99%)	70 (100%)	0	100	100
81	Sc	53/61 (87%)	53 (100%)	0	100	100
82	Sd	43/46 (94%)	43 (100%)	0	100	100
83	Se	37/51 (72%)	37 (100%)	0	100	100
84	Sf	67/139 (48%)	67 (100%)	0	100	100
All	All	10695/11815 (90%)	10694 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	LG	98	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
52	Ls	103	ASN
61	SI	52	ASN
53	SA	99	GLN
56	SD	182	GLN
64	SL	109	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3189/3337 (95%)	591 (18%)	75 (2%)
2	2	1761/1796 (98%)	391 (22%)	65 (3%)
3	3	118/120 (98%)	10 (8%)	1 (0%)
4	4	155/156 (99%)	23 (14%)	1 (0%)
5	5	74/75 (98%)	45 (60%)	9 (12%)
All	All	5297/5484 (96%)	1060 (20%)	151 (2%)

5 of 1060 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	21	A
1	1	23	G
1	1	27	A
1	1	41	A
1	1	44	A

5 of 151 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1055	A
5	5	9	A
2	2	1094	U
2	2	1378	U
5	5	73	C

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

2 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
8	DDE	C	701	8	18,20,21	1.01	1 (5%)	17,28,30	0.92	1 (5%)
2	B8N	2	1188	2	25,29,30	2.57	5 (20%)	28,42,45	1.33	3 (10%)

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
8	DDE	C	701	8	-	6/20/21/23	0/1/1/1
2	B8N	2	1188	2	-	3/16/34/35	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1188	B8N	O4-C4	9.49	1.42	1.23
2	2	1188	B8N	C2-N3	-3.89	1.32	1.38
2	2	1188	B8N	C4-N3	-3.86	1.33	1.40
2	2	1188	B8N	C4-C5	-3.57	1.39	1.47
2	2	1188	B8N	C6-C5	3.05	1.39	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1188	B8N	N3-C2-N1	3.41	120.88	116.72
2	2	1188	B8N	C4-N3-C2	-3.15	121.74	125.62
8	C	701	DDE	CA-CB-CG	-2.79	106.87	113.77
2	2	1188	B8N	O4'-C1'-C2'	2.12	108.09	105.15

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	701	DDE	NAD-CBI-CBW-NCB
8	C	701	DDE	CBI-CBW-NCB-CAC
8	C	701	DDE	CBI-CBW-NCB-CAA
8	C	701	DDE	CAU-CBW-NCB-CAC
8	C	701	DDE	CAU-CBW-NCB-CAA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	701	DDE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 11 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	GDP	C	901	85	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)

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
86	GDP	C	901	85	-	5/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	C	901	GDP	C5-C4	3.08	1.47	1.38
86	C	901	GDP	C6-N1	-2.50	1.34	1.38
86	C	901	GDP	C5-N7	-2.08	1.34	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	C	901	GDP	C5-C4-N3	-6.21	118.51	128.39
86	C	901	GDP	C2-N3-C4	5.11	121.10	112.30
86	C	901	GDP	N9-C4-N3	4.58	135.11	125.95
86	C	901	GDP	C6-C5-N7	3.28	136.26	130.29
86	C	901	GDP	C4-C5-N7	-2.62	106.53	110.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

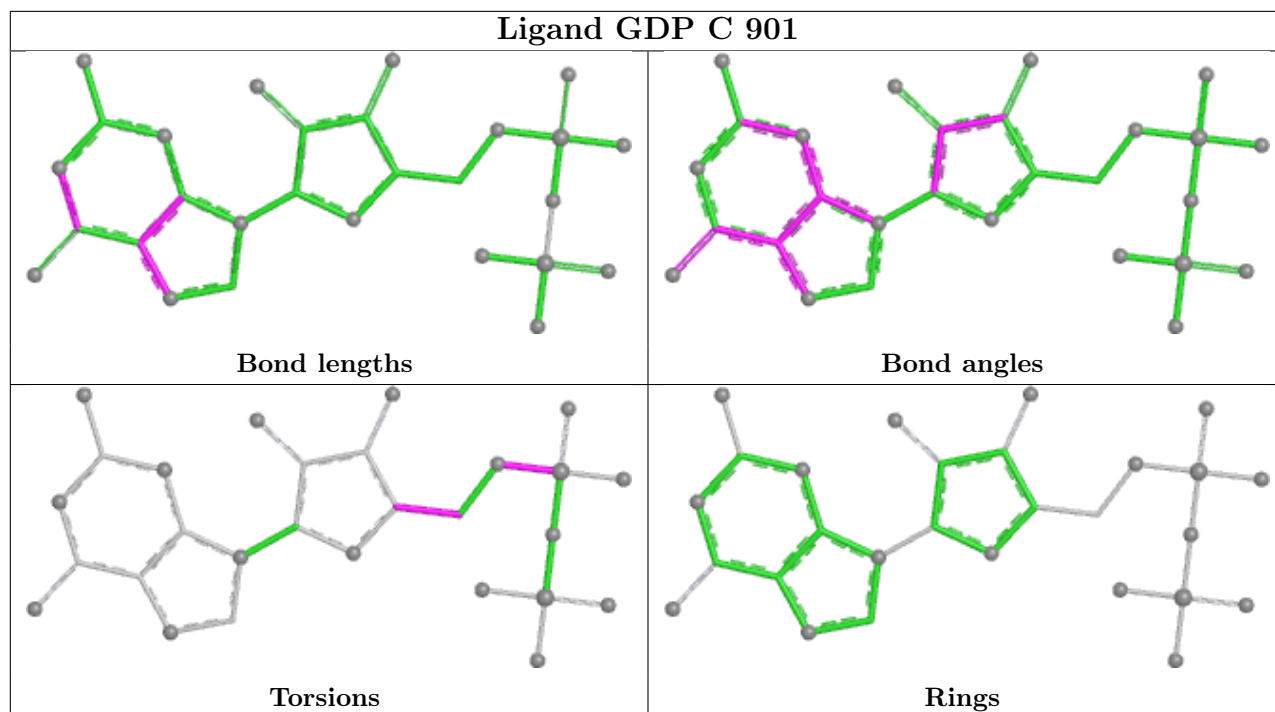
Mol	Chain	Res	Type	Atoms
86	C	901	GDP	C5'-O5'-PA-O3A
86	C	901	GDP	C5'-O5'-PA-O1A
86	C	901	GDP	C5'-O5'-PA-O2A
86	C	901	GDP	O4'-C4'-C5'-O5'
86	C	901	GDP	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	C	901	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	1937:C	O3'	1938:G	P	5.81

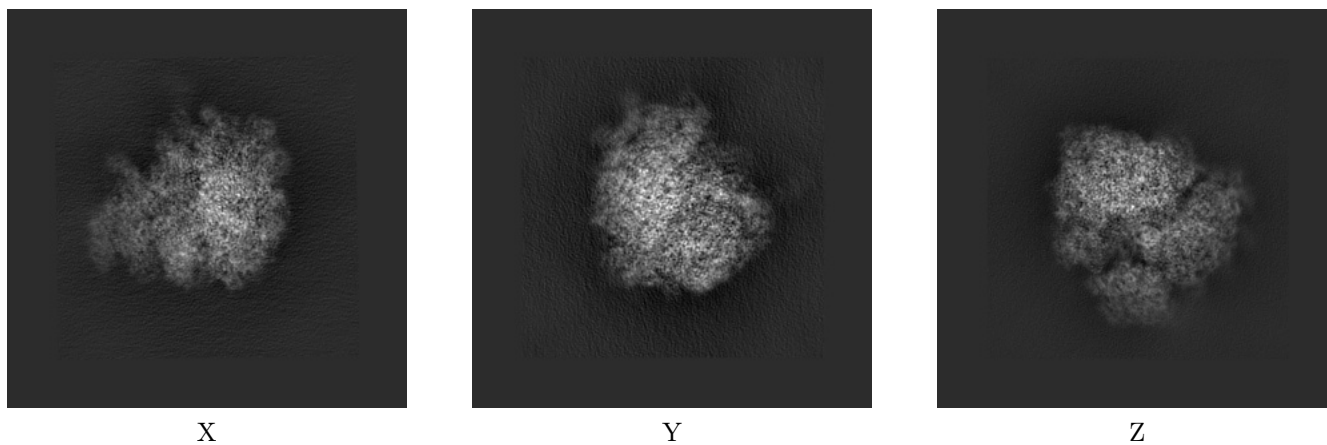
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12977. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

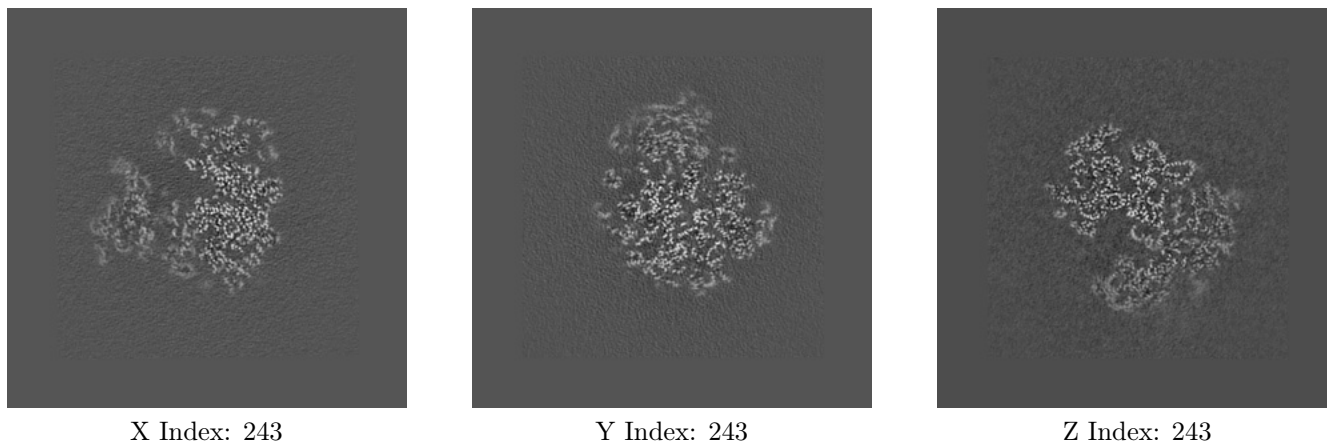
6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

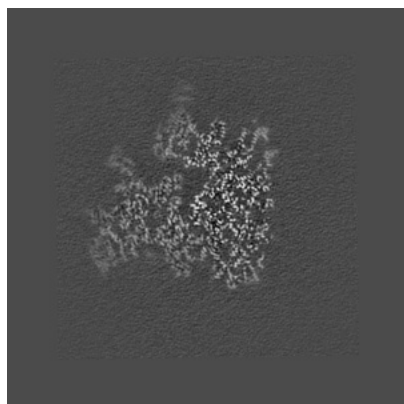
6.2.1 Primary map



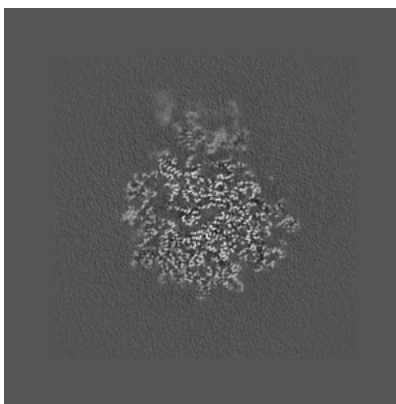
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

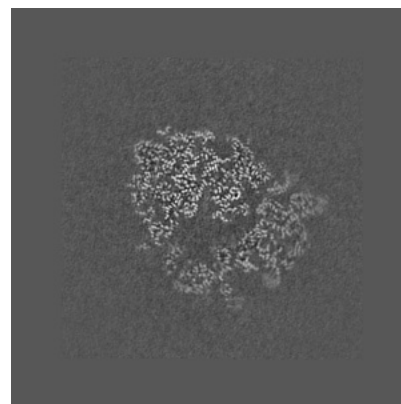
6.3.1 Primary map



X Index: 254



Y Index: 267

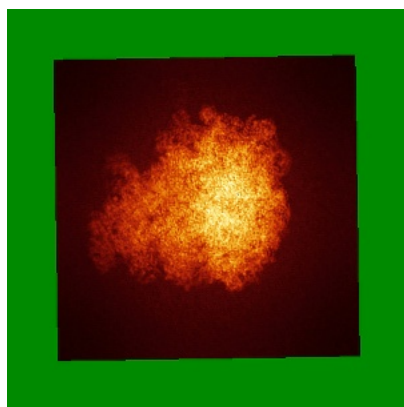


Z Index: 258

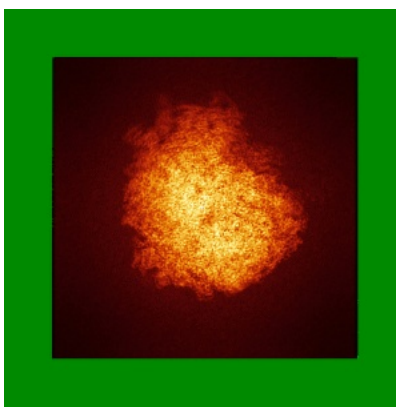
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [\(i\)](#)

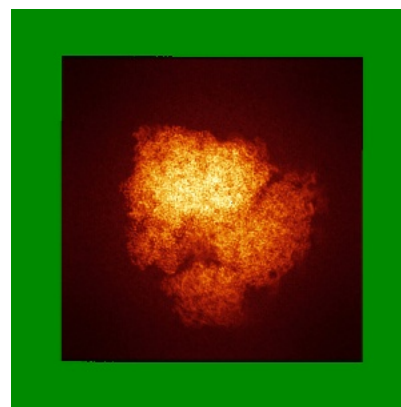
6.4.1 Primary map



X



Y

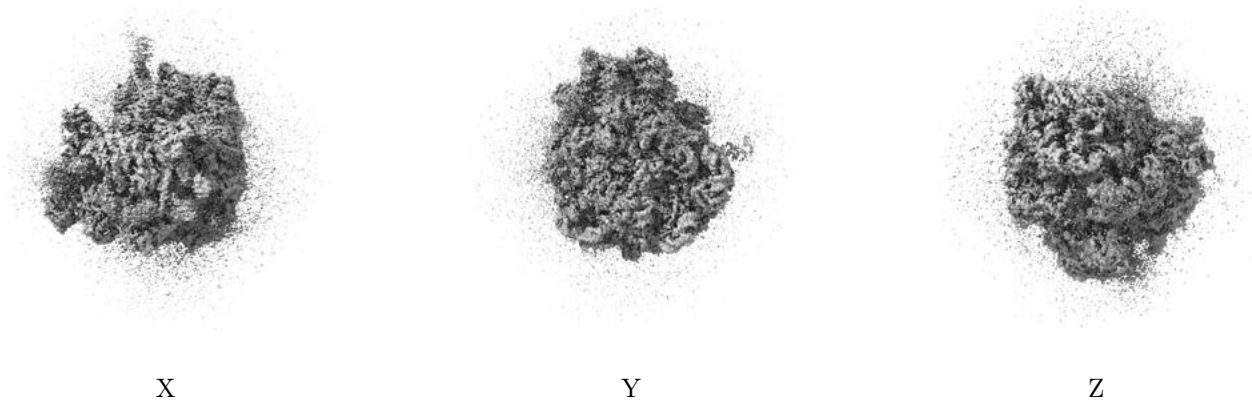


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

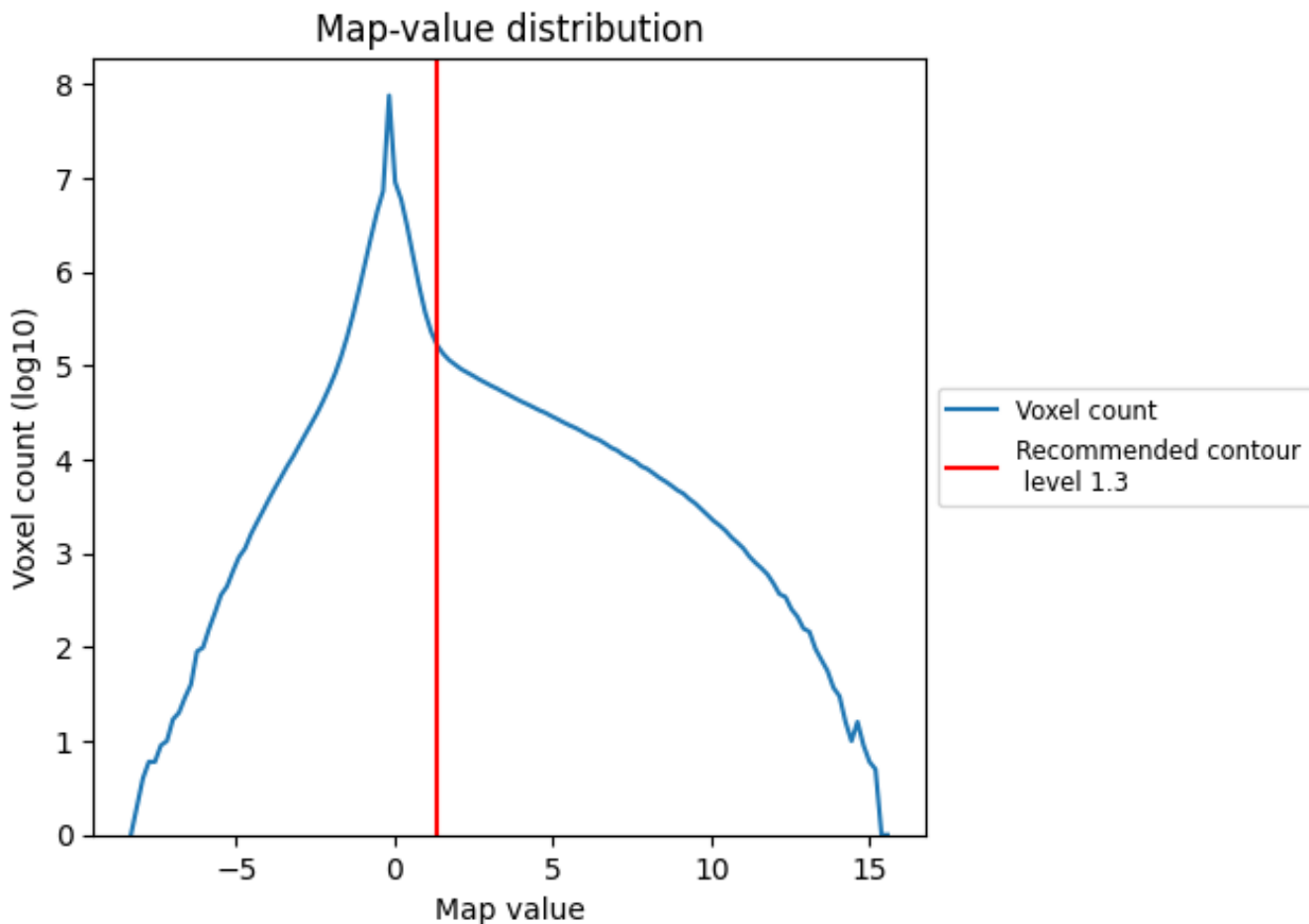
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

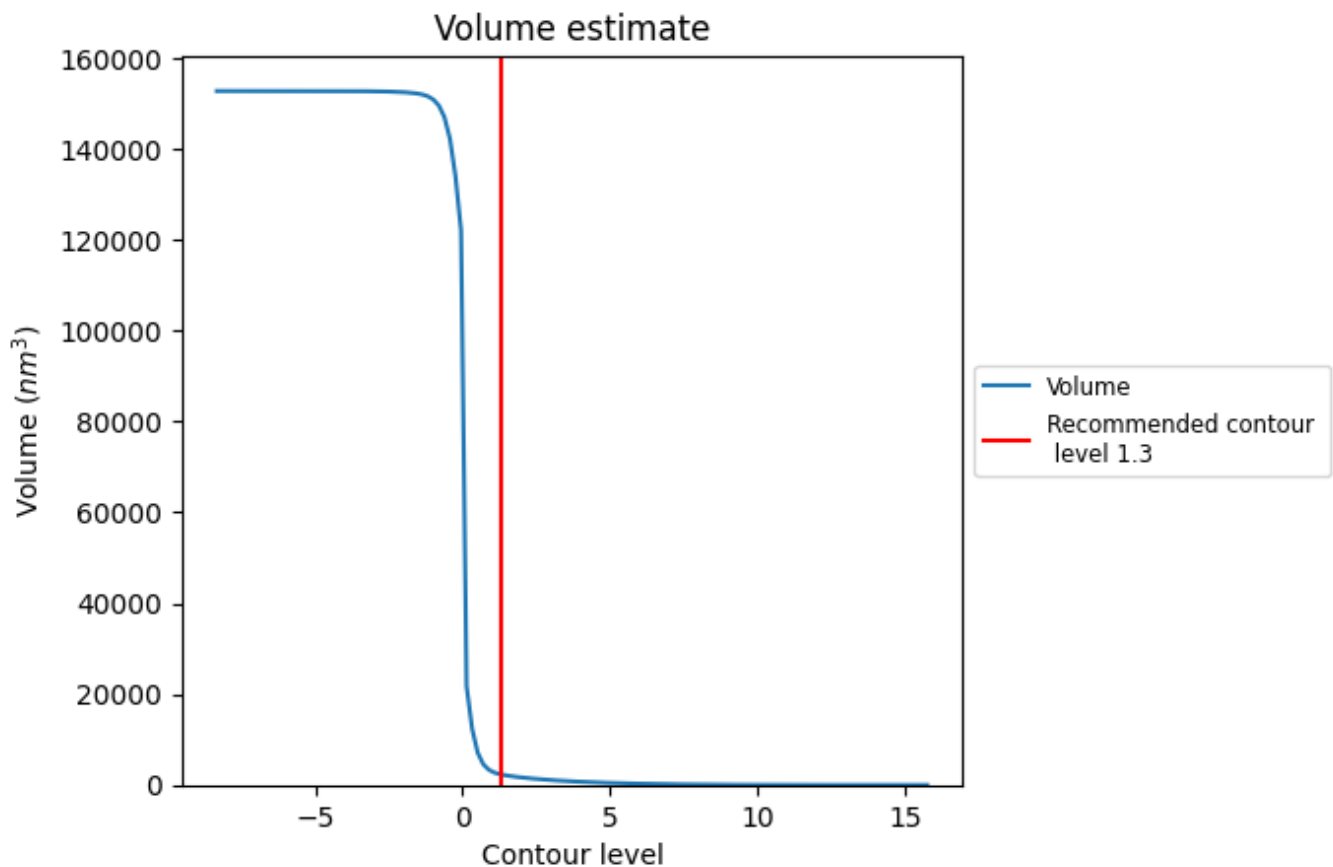
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

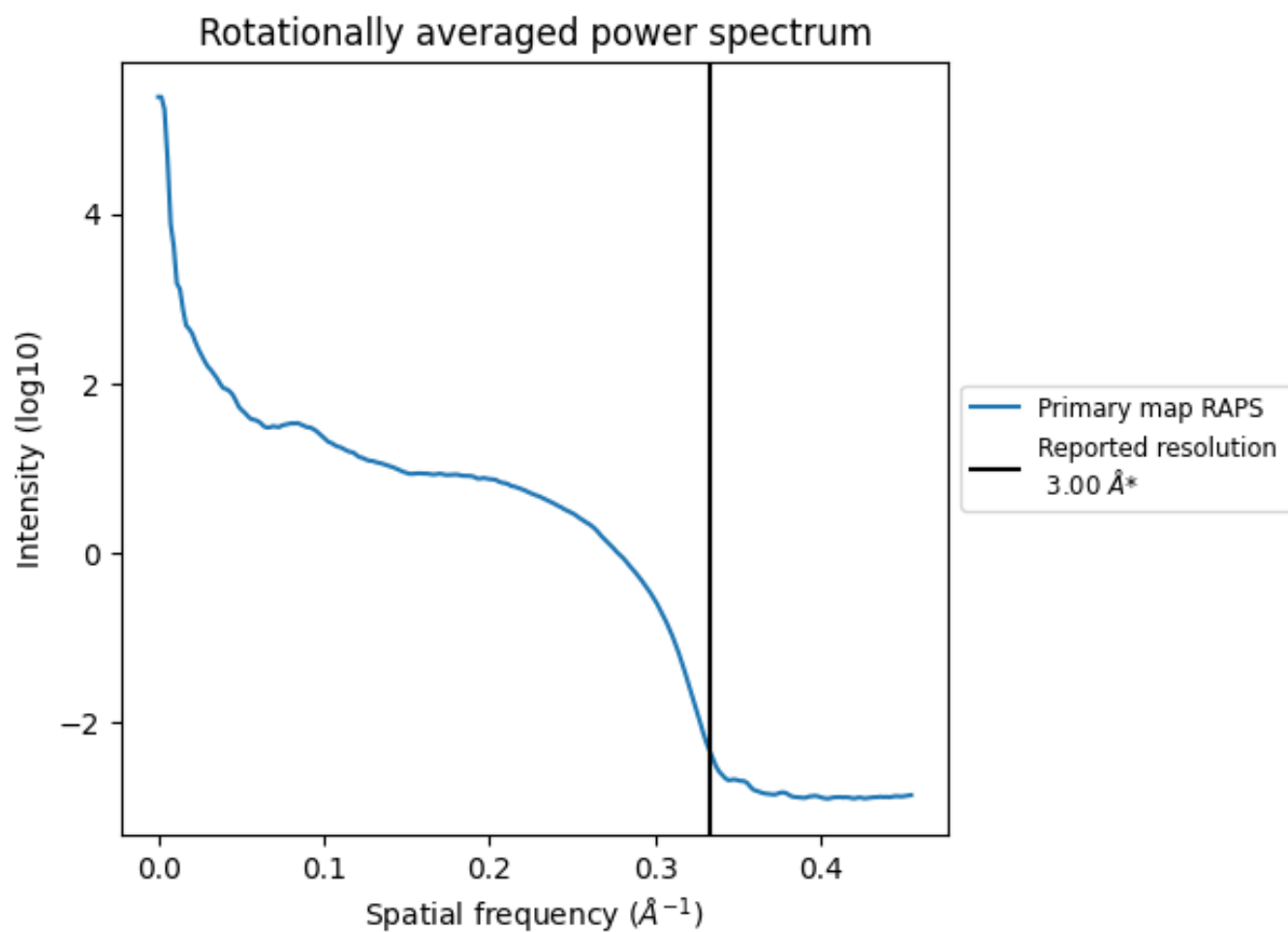
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2327 nm³; this corresponds to an approximate mass of 2102 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

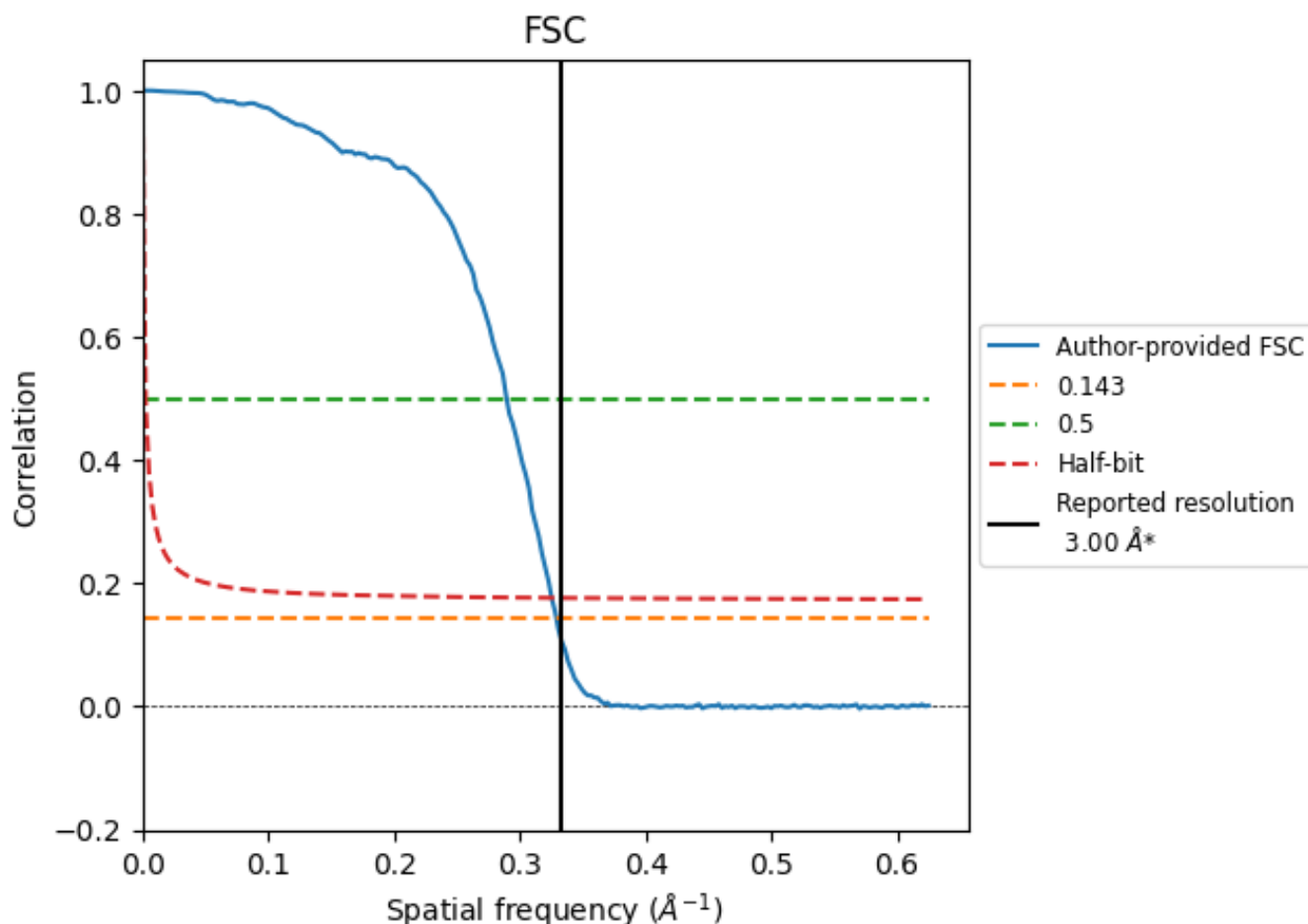


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

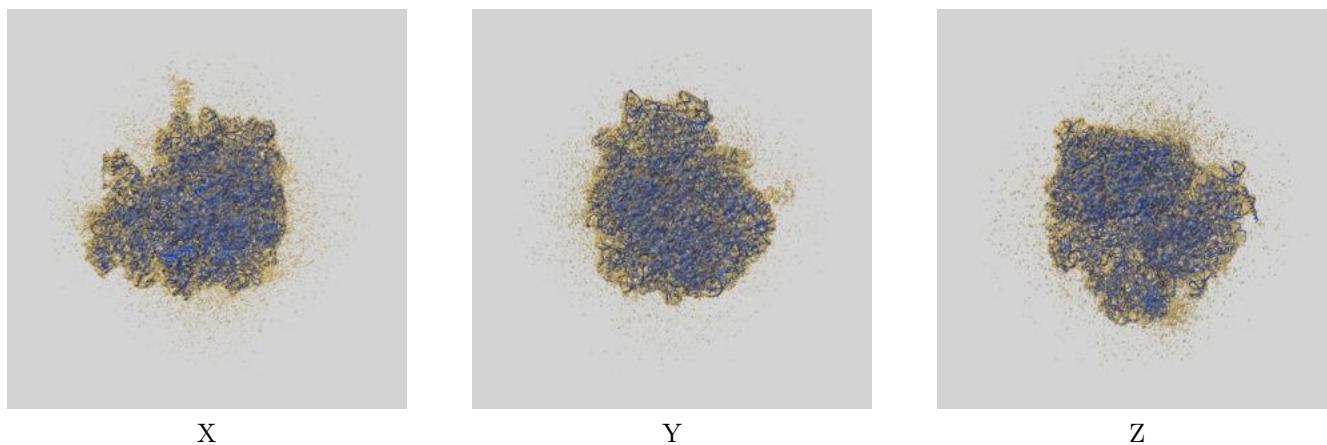
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.45	3.07
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

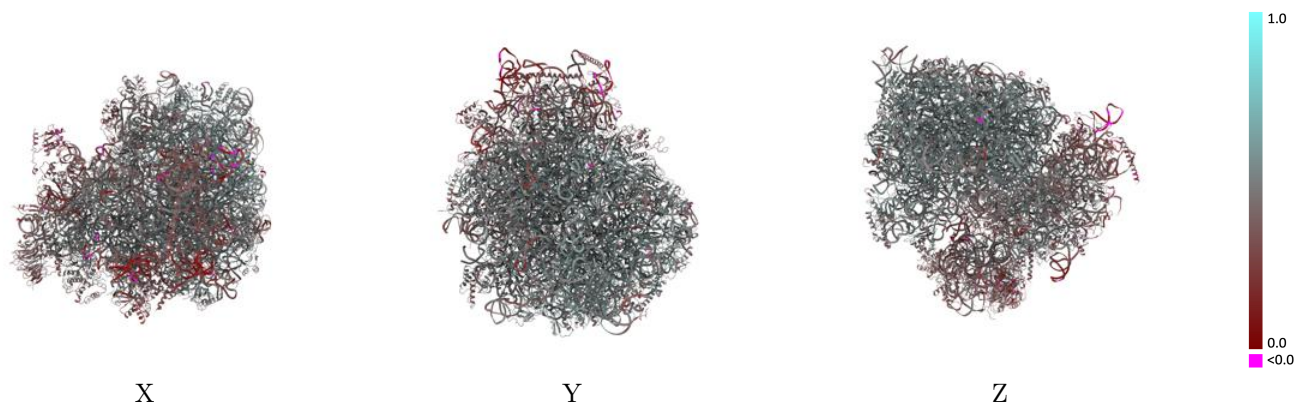
This section contains information regarding the fit between EMDB map EMD-12977 and PDB model 7OLD. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



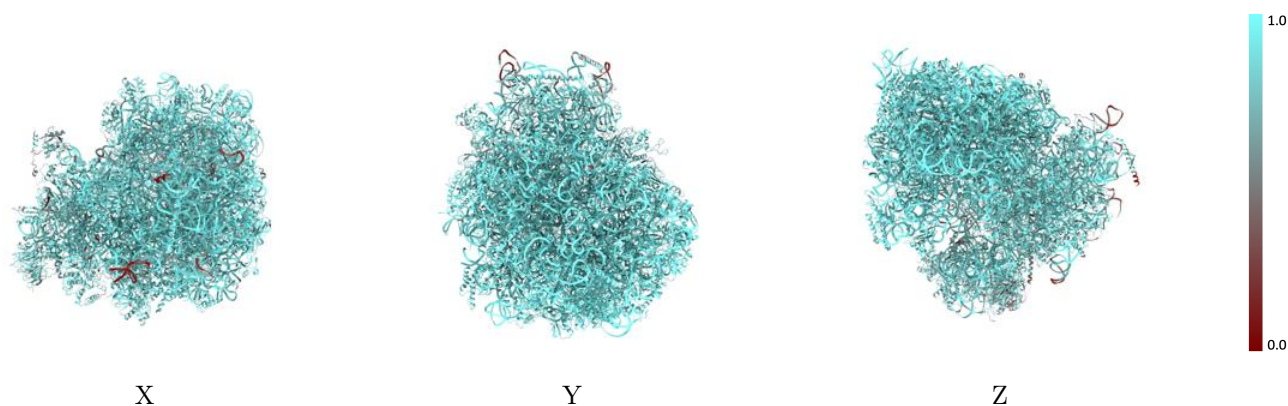
The images above show the 3D surface view of the map at the recommended contour level 1.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



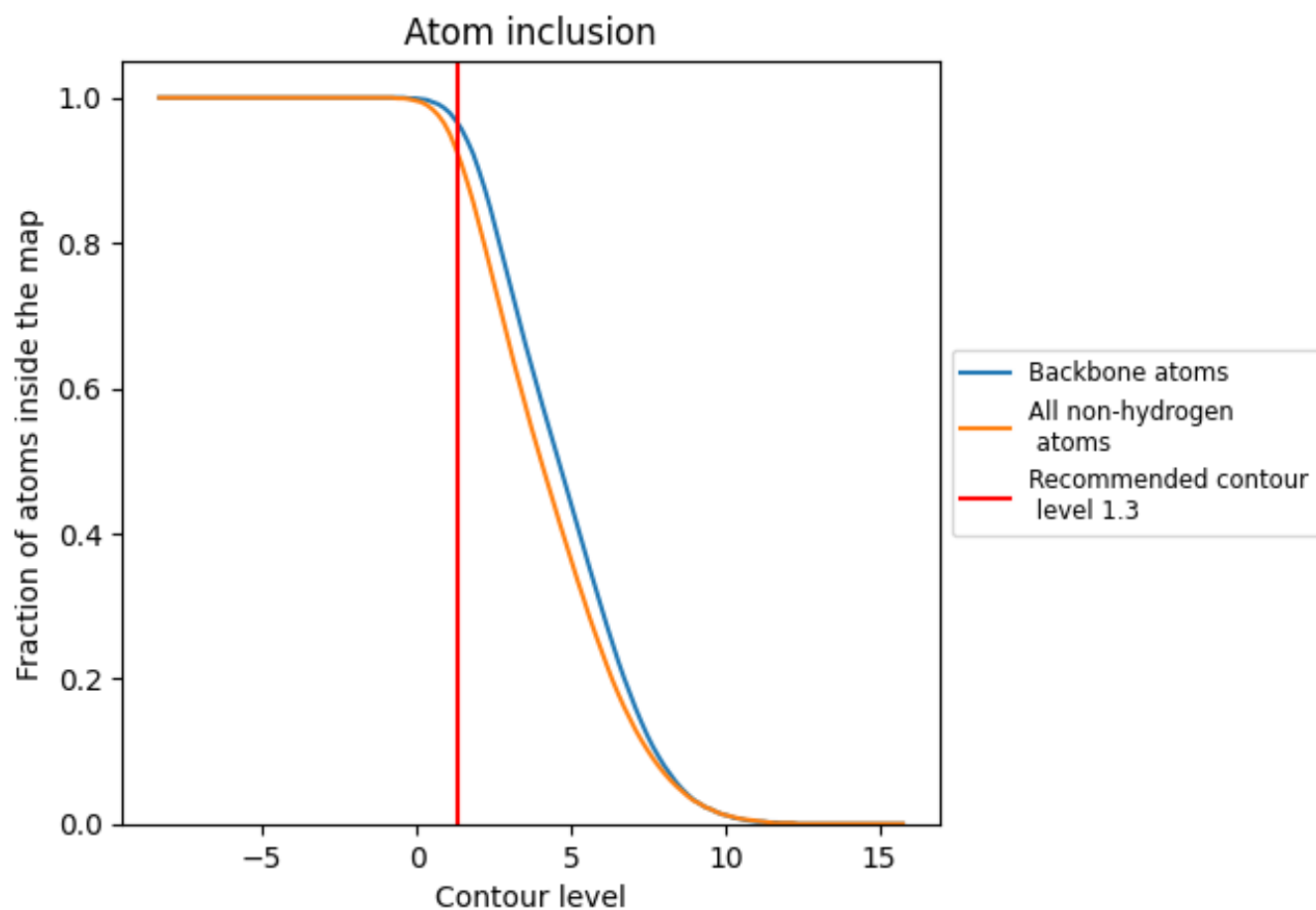
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (1.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.4580
1	 0.9780	 0.4930
2	 0.9300	 0.4030
3	 0.9910	 0.5110
4	 0.9830	 0.4840
5	 0.6780	 0.3570
A	 0.8020	 0.3700
B	 0.6150	 0.3830
C	 0.8720	 0.4370
LA	 0.9650	 0.5360
LB	 0.9590	 0.5330
LC	 0.9570	 0.5250
LD	 0.9260	 0.4780
LE	 0.9150	 0.4860
LF	 0.9470	 0.5210
LG	 0.9210	 0.4720
LH	 0.9300	 0.5120
LI	 0.9530	 0.5240
LJ	 0.9290	 0.4680
LK	 0.7890	 0.3150
LL	 0.9550	 0.5100
LM	 0.9360	 0.5080
LN	 0.9610	 0.5380
LO	 0.9610	 0.5320
LP	 0.9590	 0.5320
LQ	 0.9560	 0.5340
LR	 0.9410	 0.4900
LS	 0.9620	 0.5310
LT	 0.9570	 0.5280
LU	 0.9080	 0.4290
LV	 0.9580	 0.5320
LW	 0.7670	 0.4030
LX	 0.9440	 0.5030
LY	 0.9320	 0.5070
LZ	 0.9310	 0.4930





















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Chain	Atom inclusion	Q-score
La	 0.9600	 0.5370
Lb	 0.9520	 0.4880
Lc	 0.9430	 0.4950
Ld	 0.9080	 0.4940
Le	 0.9740	 0.5480
Lf	 0.9590	 0.5440
Lg	 0.9550	 0.5140
Lh	 0.9070	 0.4760
Li	 0.9360	 0.4850
Lj	 0.9790	 0.5450
Lk	 0.9320	 0.4590
Ll	 0.9420	 0.4950
Lm	 0.9480	 0.5260
Ln	 0.9150	 0.5020
Lo	 0.9540	 0.5290
Lp	 0.9510	 0.5150
Lq	 0.9570	 0.5190
Lr	 0.7830	 0.4190
Ls	 0.8330	 0.4150
SA	 0.8880	 0.4490
SB	 0.7660	 0.2910
SC	 0.9100	 0.4910
SD	 0.8480	 0.4250
SE	 0.8910	 0.4490
SF	 0.7960	 0.3450
SG	 0.8230	 0.3420
SH	 0.8380	 0.3630
SI	 0.8570	 0.4040
SJ	 0.8970	 0.4560
SK	 0.8590	 0.3730
SL	 0.9080	 0.4630
SM	 0.6290	 0.2470
SN	 0.8850	 0.4120
SO	 0.8060	 0.3310
SP	 0.8330	 0.3510
SQ	 0.8040	 0.3680
SR	 0.8260	 0.4010
SS	 0.8160	 0.3510
ST	 0.8020	 0.3520
SU	 0.7740	 0.3670
SV	 0.9060	 0.4560
SW	 0.8950	 0.4760

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Chain	Atom inclusion	Q-score
SX	 0.9180	 0.5100
SY	 0.8600	 0.3990
SZ	 0.7860	 0.3200
Sa	 0.8810	 0.4260
Sb	 0.8320	 0.3420
Sc	 0.8510	 0.3760
Sd	 0.9050	 0.4180
Se	 0.8660	 0.4530
Sf	 0.6850	 0.2450