



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:30 AM UTC

PDB ID : 7Z3N / pdb_00007z3n
EMDB ID : EMD-14479
Title : Cryo-EM structure of the ribosome-associated RAC complex on the 80S ribosome - RAC-1 conformation
Authors : Kisonaite, M.; Wild, K.; Sinning, I.
Deposited on : 2022-03-02
Resolution : 3.20 Å(reported)
Based on initial model : 7OLC

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:

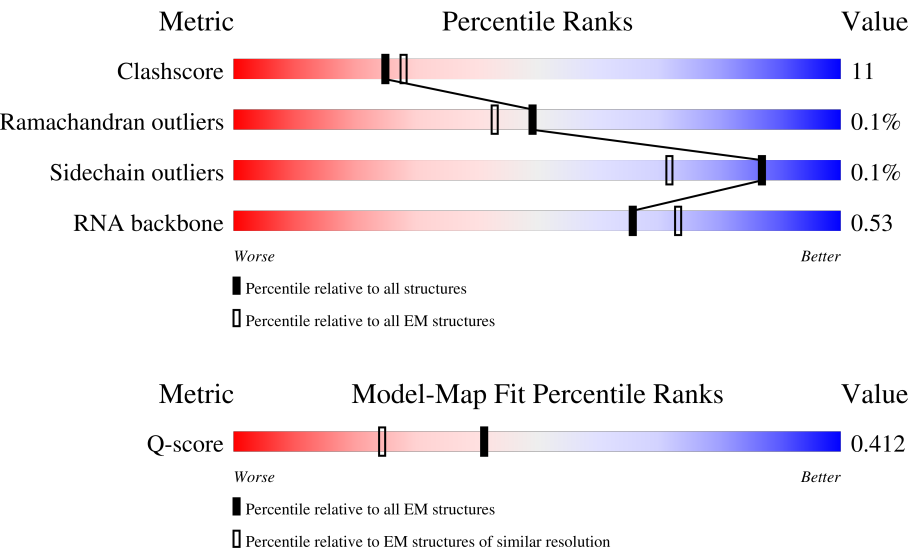
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.20 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	15020 (2.70 - 3.70)

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	
2	2	1796	
3	3	120	

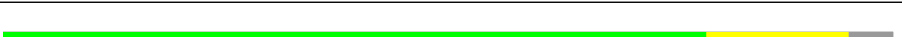
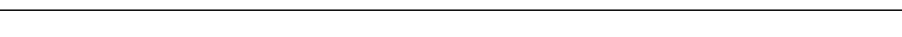
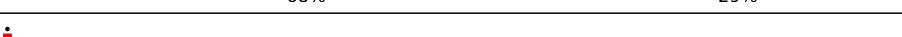
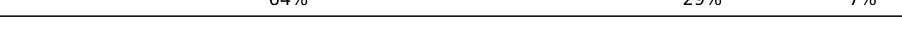
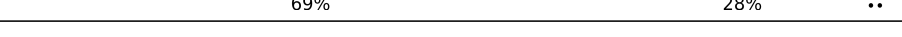
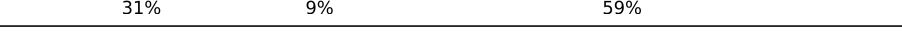
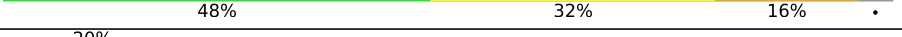
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Mol	Chain	Length	Quality of chain
4	4	156	
5	A	316	
6	B	302	
7	C	446	
8	D	578	
9	LA	254	
10	LB	392	
11	LC	365	
12	LD	304	
13	LE	200	
14	LF	249	
15	LG	262	
16	LH	192	
17	LI	219	
18	LJ	173	
19	LK	165	
20	LL	213	
21	LM	142	
22	LN	203	
23	LO	204	
24	LP	187	
25	LQ	213	
26	LR	192	
27	LS	174	
28	LT	160	

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Mol	Chain	Length	Quality of chain
29	LU	127	
30	LV	139	
31	LW	161	
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	81	
46	Ll	51	
47	Lm	128	
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	NC	27	
54	SA	285	
55	SB	255	
56	SC	263	
57	SD	254	
58	SE	264	
59	SF	212	
60	SG	239	
61	SH	203	
62	SI	202	
63	SJ	190	
64	SK	159	
65	SL	161	
66	SM	144	
67	SN	151	
68	SO	150	
69	SP	153	
70	SQ	143	
71	SR	143	
72	SS	156	
73	ST	153	
74	SU	116	
75	SV	98	
76	SW	130	
77	SX	145	

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Mol	Chain	Length	Quality of chain
78	SY	136	
79	SZ	99	
80	Sa	119	
81	Sb	82	
82	Sc	68	
83	Sd	56	
84	Se	62	
85	Sf	154	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 213543 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
1	1	3191	Total	C	N	O	P	0	0
			68242	30465	12334	22252	3191		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1772	Total	C	N	O	P	0	0
			37781	16882	6728	12399	1772		

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

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

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

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

- Molecule 5 is a protein called Putative guanine nucleotide-binding protein.

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

- Molecule 6 is a protein called HABP4_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	B	31	Total	C	N	O	0	0
			243	144	49	50		

- Molecule 7 is a protein called Putative ribosome associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	444	Total	C	N	O	S	0	0
			3548	2211	661	672	4		

- Molecule 8 is a protein called Putative heat shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	519	Total	C	N	O	S	0	0
			3942	2470	689	780	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LA	252	Total	C	N	O	S	0	0
			1925	1203	385	334	3		

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

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

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

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

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

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

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

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

- 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	235	Total	C	N	O	S	0	0
			1900	1218	351	326	5		

- Molecule 16 is a protein called uL6.

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	155	Total	C	N	O	S	0	0
			762	452	155	155			

- 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
21	LM	141	Total	C	N	O	S	0	0
			1125	714	216	194	1		

- Molecule 22 is a protein called Ribosomal protein L15.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	203	Total	C	N	O	S	0	0
			1613	1036	305	267	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	186	Total	C	N	O	S	0	0
			1472	912	295	262	3		

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

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

- Molecule 26 is a protein called Ribosomal protein L19.

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	102	Total	C	N	O	S	0	0
			827	538	143	145	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	135	Total	C	N	O	S	0	0
			994	633	185	169	7		

- Molecule 31 is a protein called eL24.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	LX	121	Total	C	N	O	0	0
			965	620	175	170		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LY	134	Total	C	N	O	S	0	0
			1065	664	215	184	2		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lb	62	Total	C	N	O		0	0
			508	310	112	86			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lc	97	Total	C	N	O	S	0	0
			722	458	125	134	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ld	119	Total	C	N	O	S	0	0
			965	607	188	168	2		

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

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

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

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

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

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

- 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	102	Total	C	N	O	S	0	0
			836	515	184	136	1		

- Molecule 44 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lj	86	Total	C	N	O	S	0	0
			684	418	152	109	5		

- Molecule 45 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lk	80	Total	C	N	O	S	0	0
			658	415	126	115	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 Putative ribosomal protein.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	1	MET	SER	conflict	UNP G0S8G4
Lm	2	GLN	ARG	conflict	UNP G0S8G4

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ln	24	Total	C	N	O	S	0	0
			224	136	61	26	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	S	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 Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	NC	27	Total	C	N	O	S	0	0
			135	81	27	27			

- Molecule 54 is a protein called 40S ribosomal protein S0.

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

- Molecule 55 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SB	232	Total	C	N	O	S	0	0
			1871	1190	351	325	5		

- Molecule 56 is a protein called 40S ribosomal protein S2-like protein.

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

- Molecule 57 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SD	214	Total	C	N	O	S	0	0
			1688	1068	307	305	8		

- Molecule 58 is a protein called 40S ribosomal protein S4.

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

- Molecule 59 is a protein called 40S ribosomal protein s5-like protein.

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

- Molecule 60 is a protein called 40S ribosomal protein S6.

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

- Molecule 61 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SH	195	Total	C	N	O		0	0
			1562	983	300	279			

- Molecule 62 is a protein called 40S ribosomal protein S8.

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

- Molecule 63 is a protein called 40S ribosomal protein s9-like protein.

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

- Molecule 64 is a protein called 40S ribosomal protein s10-like protein.

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

- Molecule 65 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SL	150	Total	C	N	O	S	0	0
			1222	780	236	201	5		

- Molecule 66 is a protein called 40S ribosomal protein S12.

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

- Molecule 67 is a protein called 40S ribosomal protein S13-like protein.

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

- Molecule 68 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SO	135	Total	C	N	O	S	0	0
			1002	614	199	184	5		

- Molecule 69 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	115	Total	C	N	O	S	0	0
			917	583	172	159	3		

- Molecule 70 is a protein called 40S ribosomal protein S16-like protein.

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

- Molecule 71 is a protein called 40S ribosomal protein S17-like protein.

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

- Molecule 72 is a protein called Putative ribosomal protein.

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

- Molecule 73 is a protein called 40S ribosomal protein S19-like protein.

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

- Molecule 74 is a protein called 40S ribosomal protein S20-like protein.

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

- Molecule 75 is a protein called 40S ribosomal protein S21-like protein.

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

- Molecule 76 is a protein called 40S ribosomal protein S22-like protein.

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

- Molecule 77 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	132	Total	C	N	O	S	0	0
			1061	668	209	182	2		

- Molecule 79 is a protein called 40S ribosomal protein S25.

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

- Molecule 80 is a protein called 40S ribosomal protein S26.

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

- Molecule 81 is a protein called Ribosomal protein s27-like protein.

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

- Molecule 82 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Sc	61	Total	C	N	O	S	0	0
			484	298	97	88	1		

- Molecule 83 is a protein called Ribosomal protein uS14.

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

- Molecule 84 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	Se	40	Total	C	N	O	0	0
			322	202	67	53		

- Molecule 85 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Sf	73	Total	C	N	O	S	0	0
			604	382	115	101	6		

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

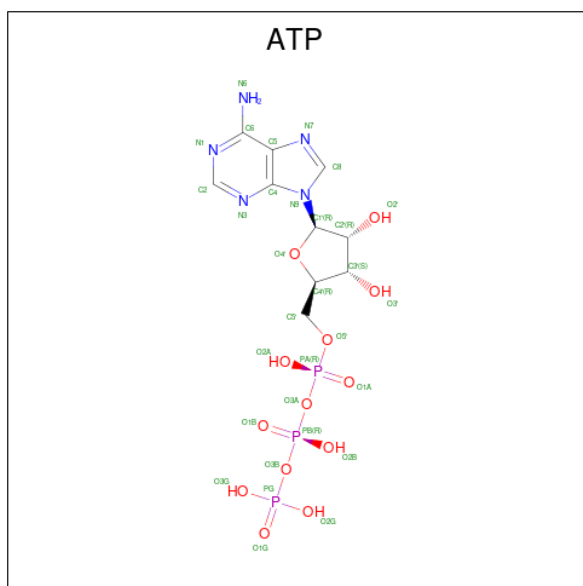
Mol	Chain	Residues	Atoms		AltConf
86	1	360	Total	Mg	0
			360	360	
86	2	66	Total	Mg	0
			66	66	
86	3	6	Total	Mg	0
			6	6	
86	4	10	Total	Mg	0
			10	10	
86	D	1	Total	Mg	0
			1	1	
86	LB	1	Total	Mg	0
			1	1	
86	LC	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LJ	1	Total	Mg	0
			1	1	
86	LN	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	
86	LV	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	LW	1	Total	Mg	0
			1	1	
86	Lb	1	Total	Mg	0
			1	1	
86	SN	1	Total	Mg	0
			1	1	
86	SO	1	Total	Mg	0
			1	1	
86	SQ	1	Total	Mg	0
			1	1	

- Molecule 87 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
87	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total	Zn	0
			1	1	
88	Lj	1	Total	Zn	0
			1	1	
88	Lm	1	Total	Zn	0
			1	1	

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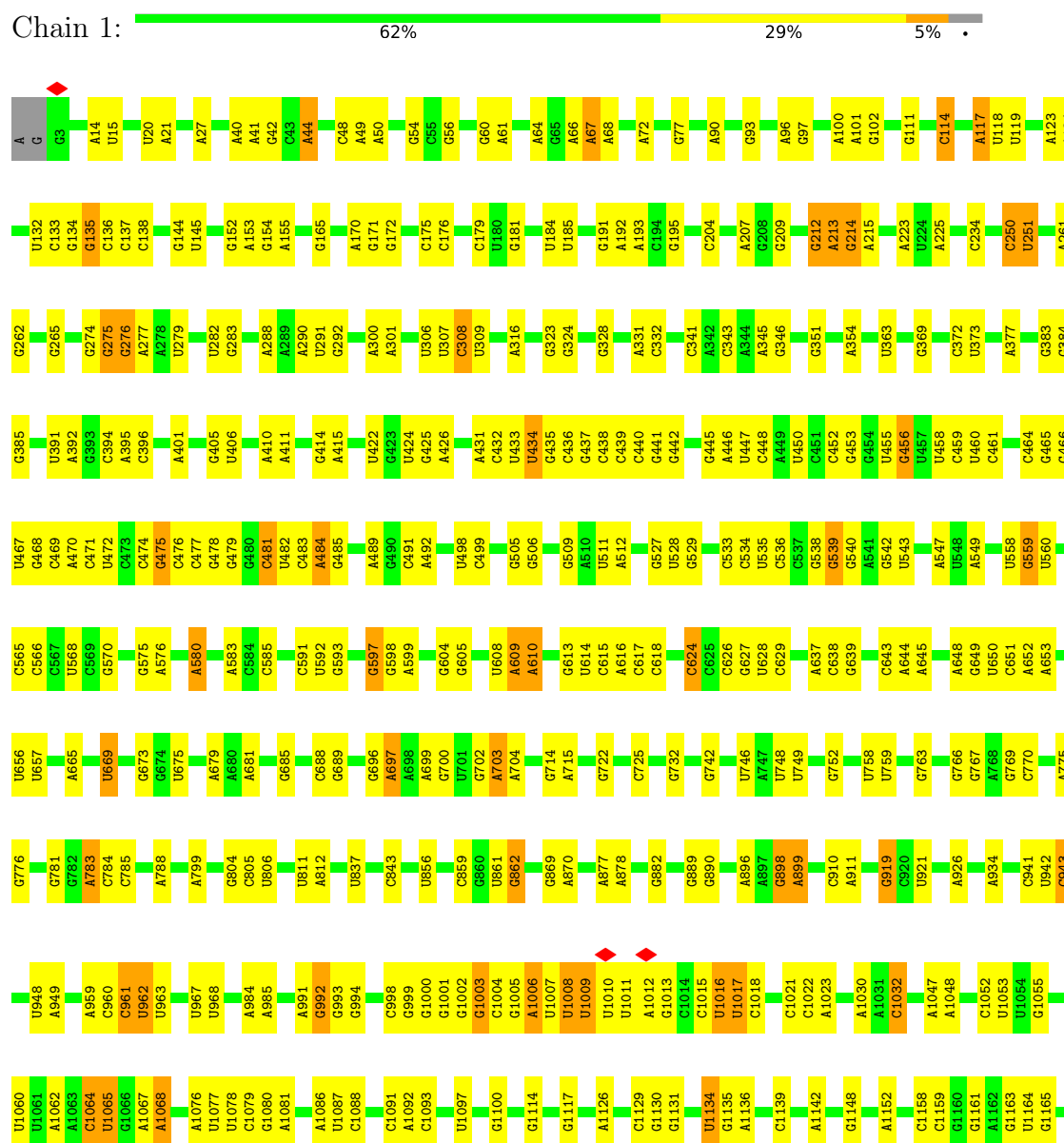
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Mol	Chain	Residues	Atoms		AltConf
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sb	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0

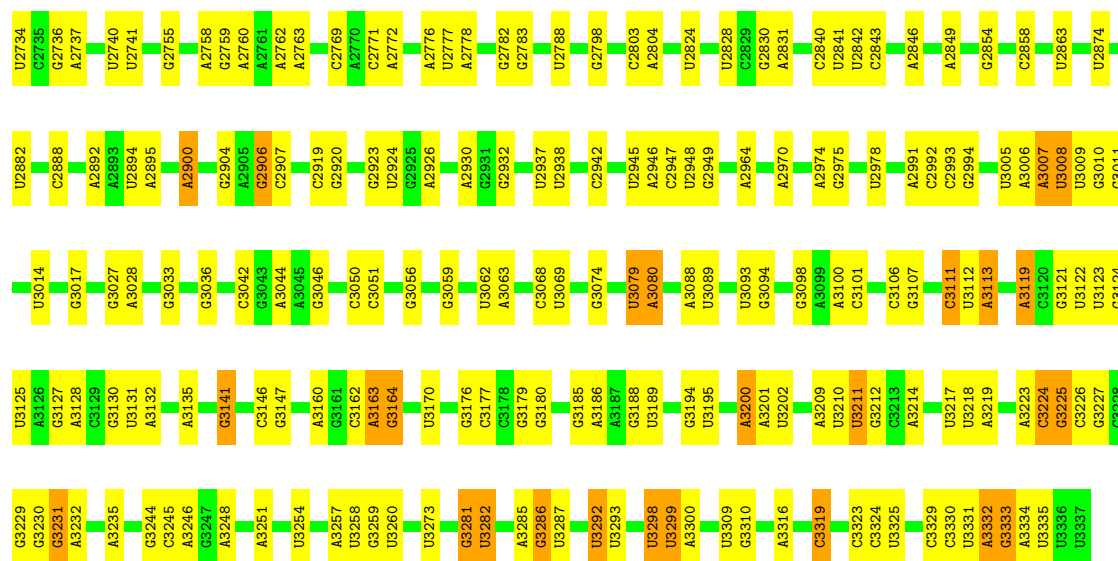
3 Residue-property plots

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.

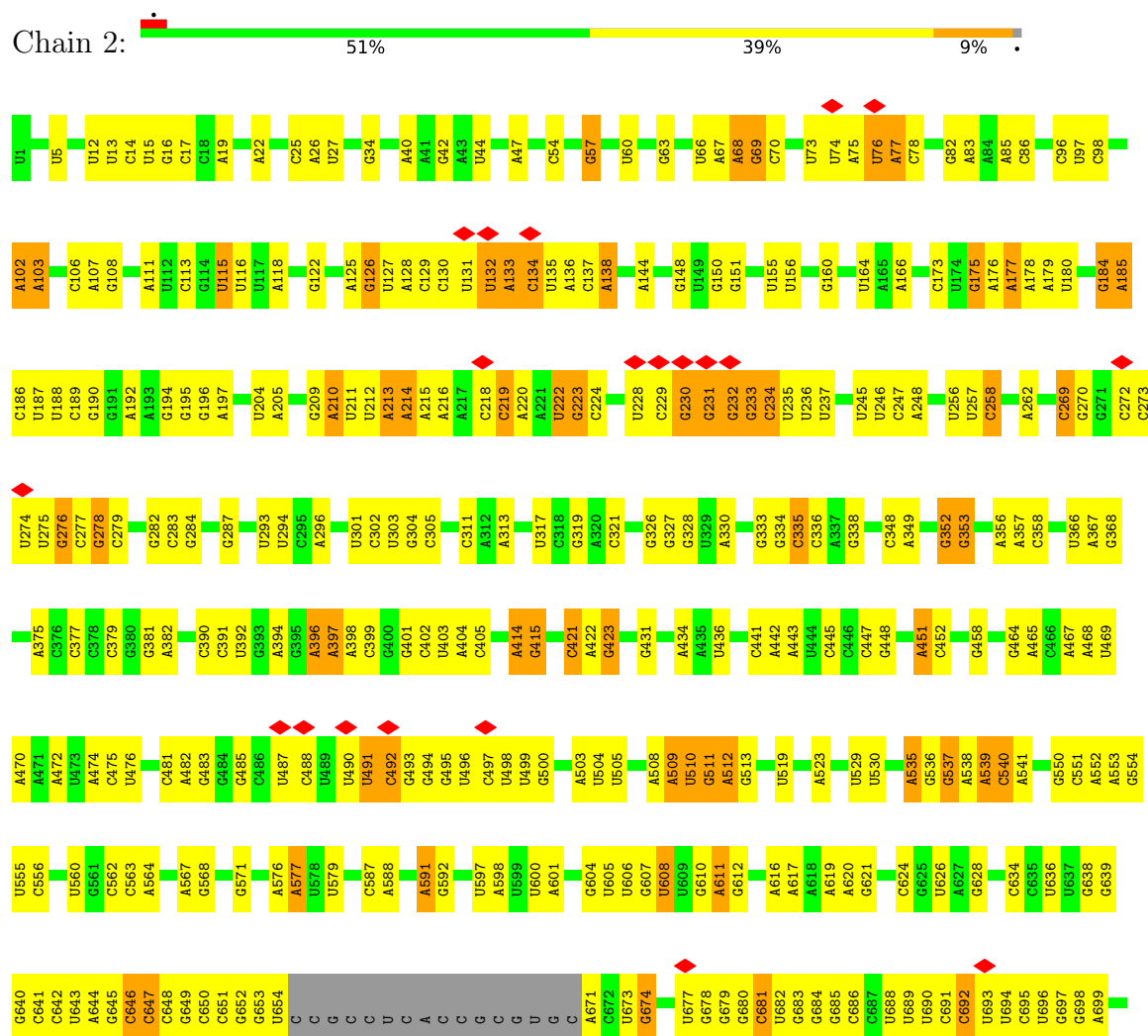
• Molecule 1: 26S rRNA

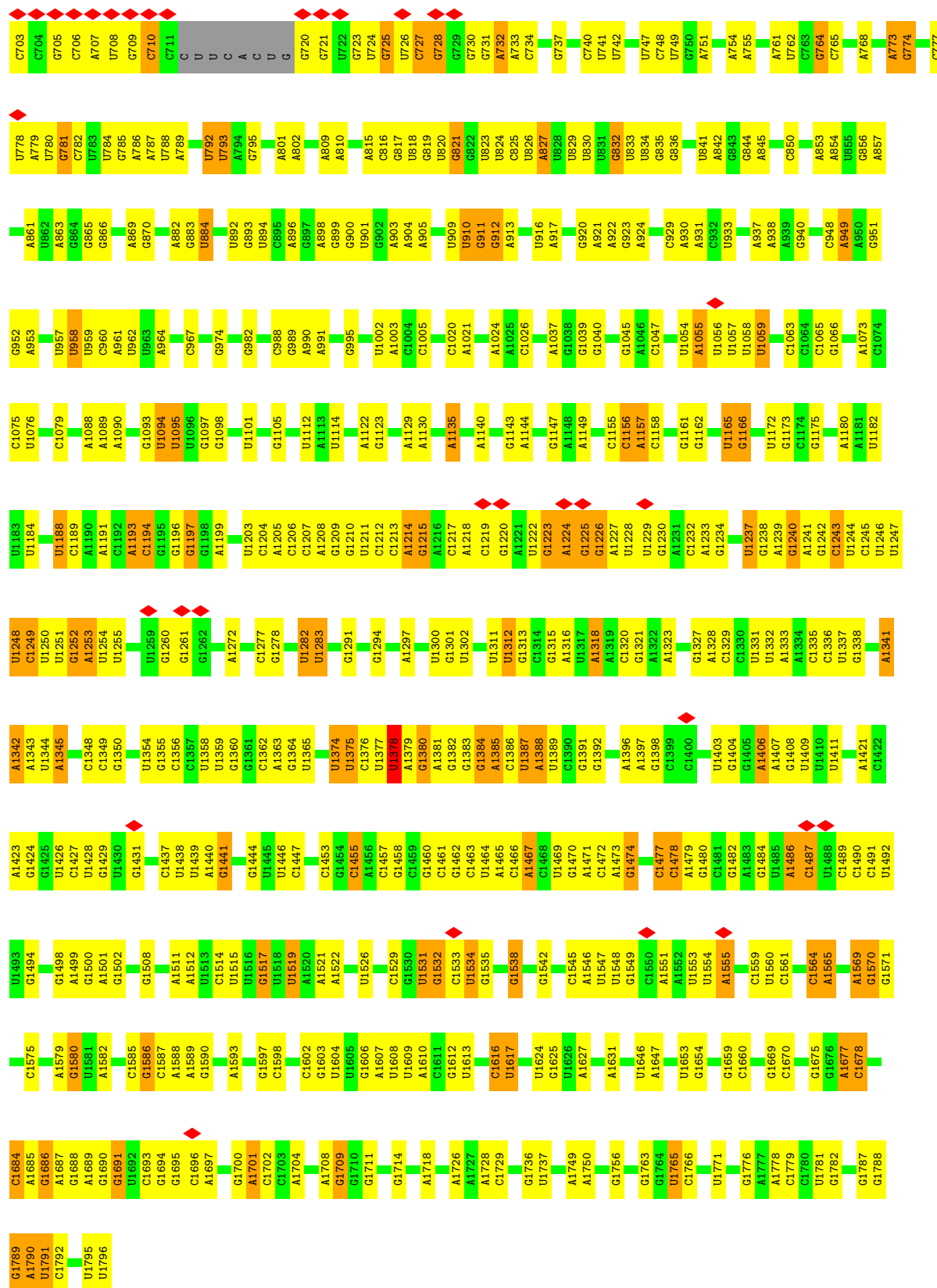




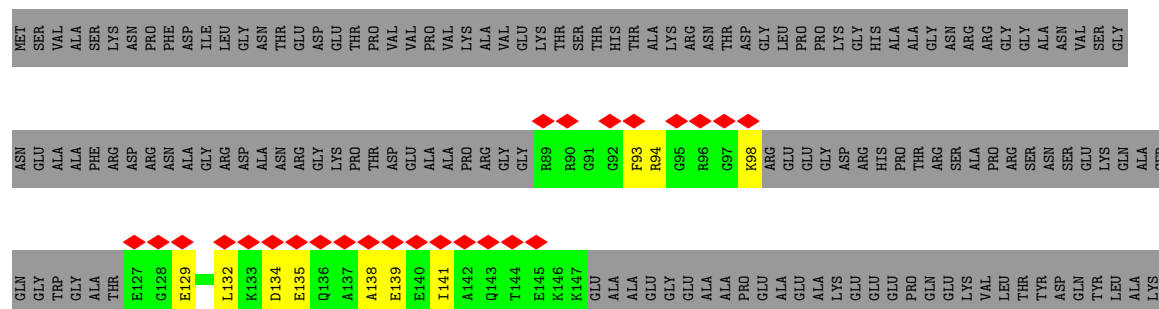


• Molecule 2: 18S rRNA



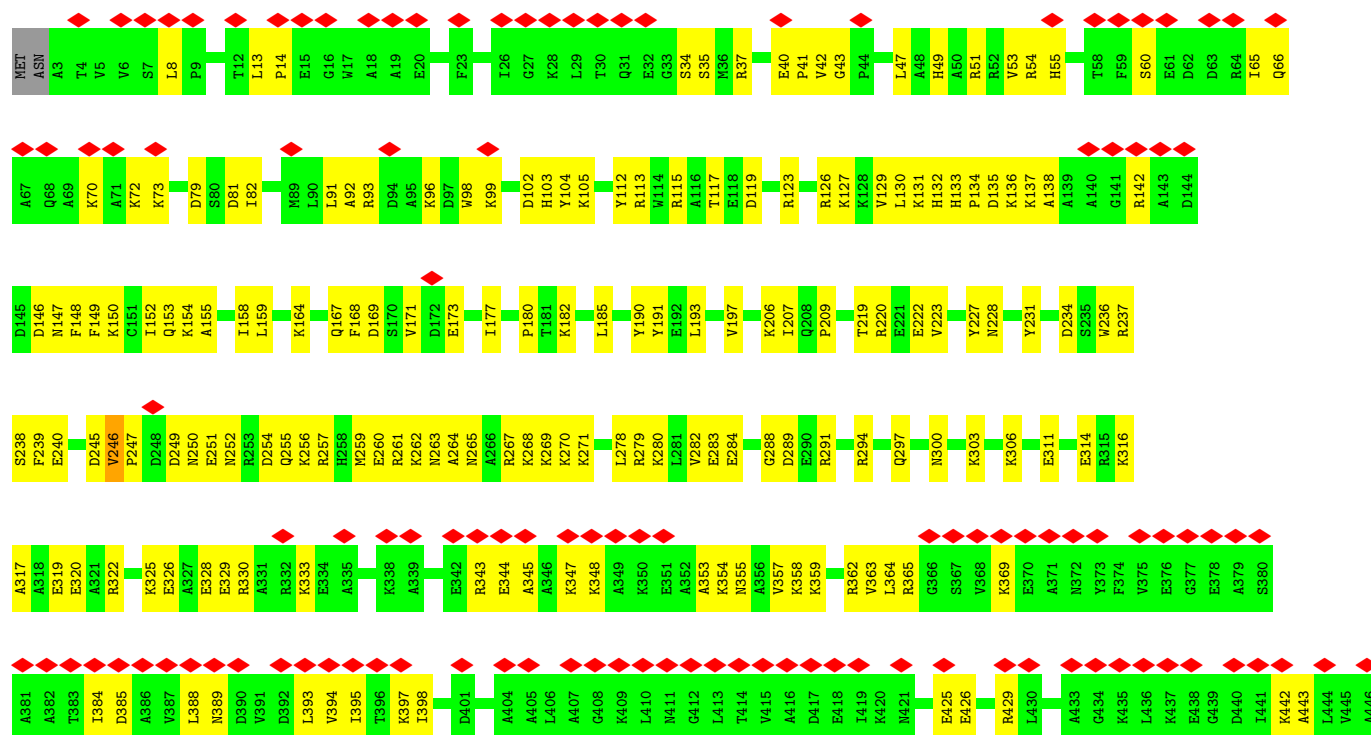


• Molecule 3: 5S rRNA

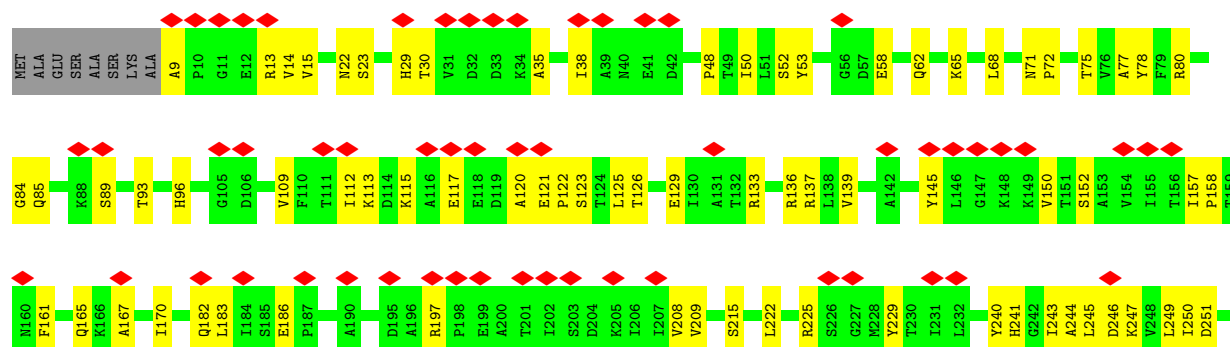


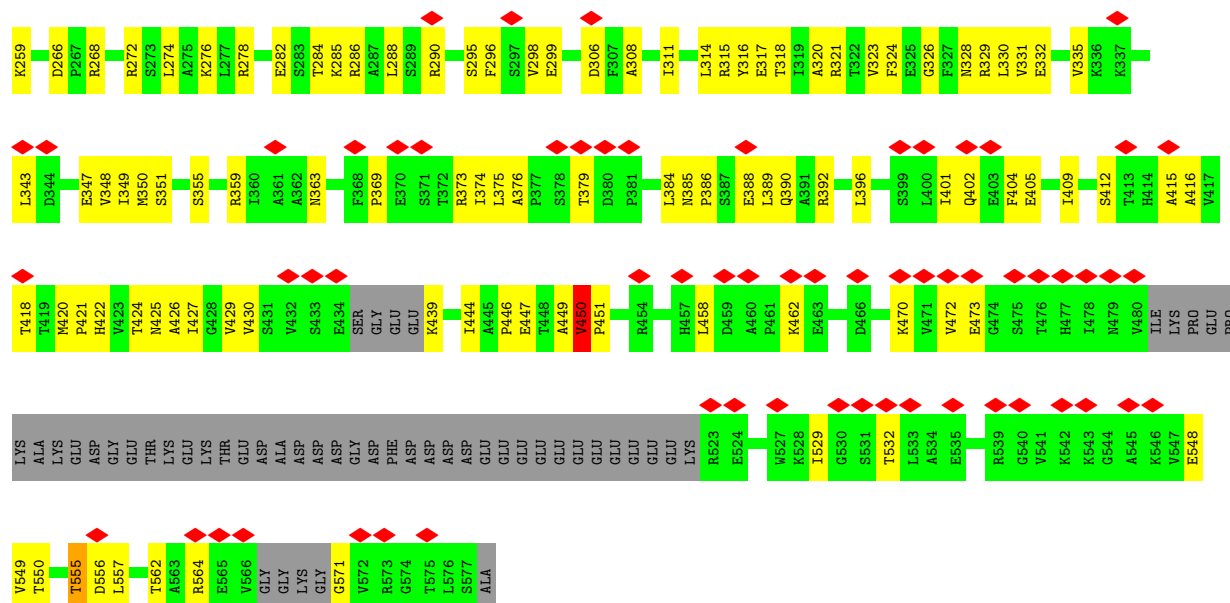
ARG

Chain C: 27% 60% 39%



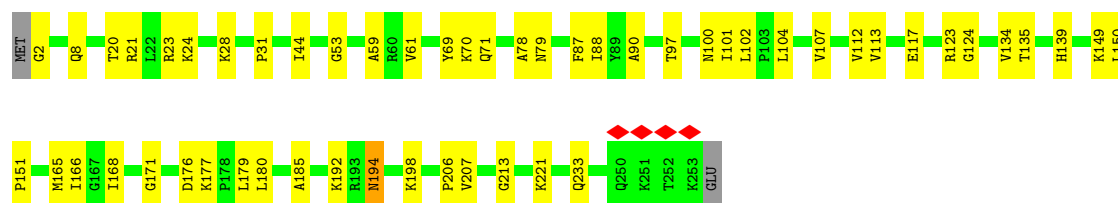
Chain D:





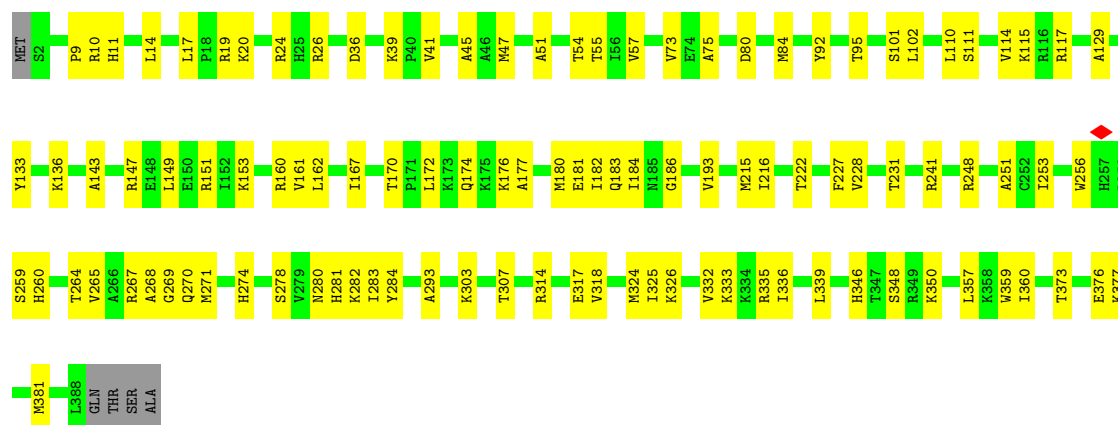
• Molecule 9: 60S ribosomal protein L2-like protein

Chain LA: 78% 21%



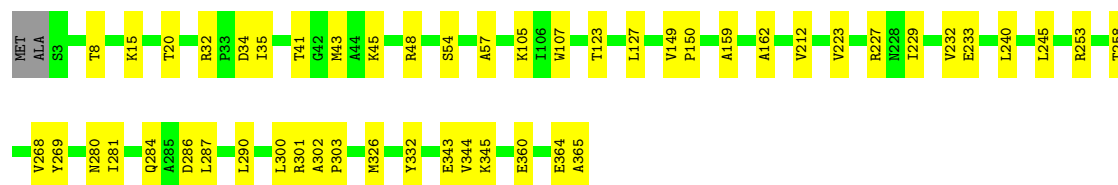
• Molecule 10: 60S ribosomal protein L3-like protein

Chain LB: 72% 27%



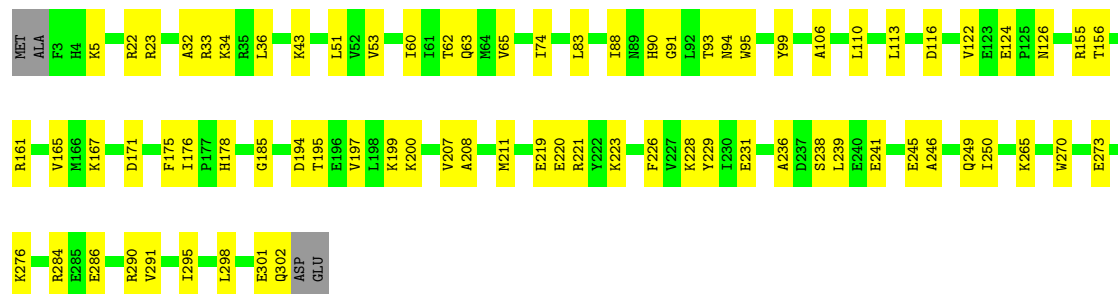
• Molecule 11: 60S ribosomal protein L4-like protein

Chain LC: 86% 14%



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

Chain LD: 74% 25% .



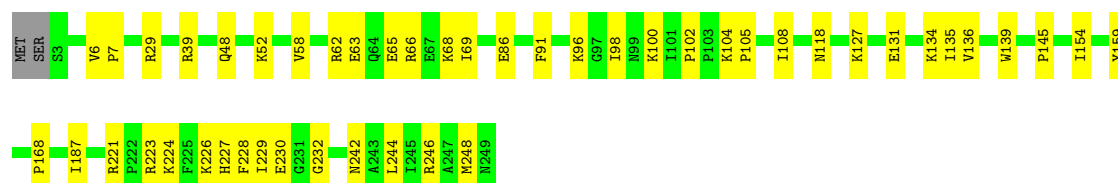
- Molecule 13: 60S ribosomal protein L6

Chain LE: 73% 24% .



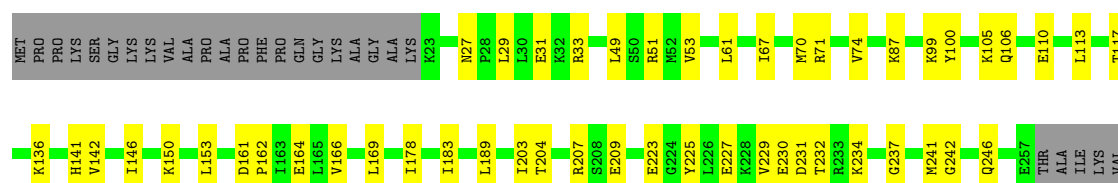
- Molecule 14: 60S ribosomal protein l7-like protein

Chain LF: 80% 19% .



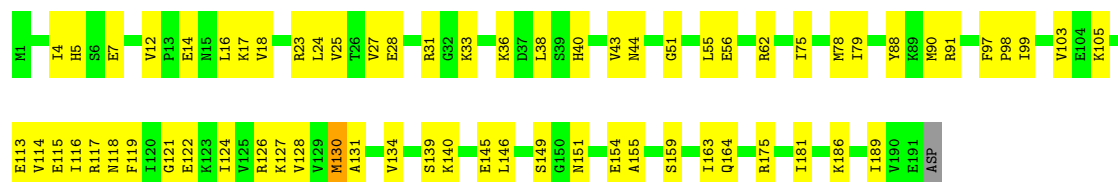
- Molecule 15: 60S ribosomal protein L8

Chain LG: 71% 19% 10%



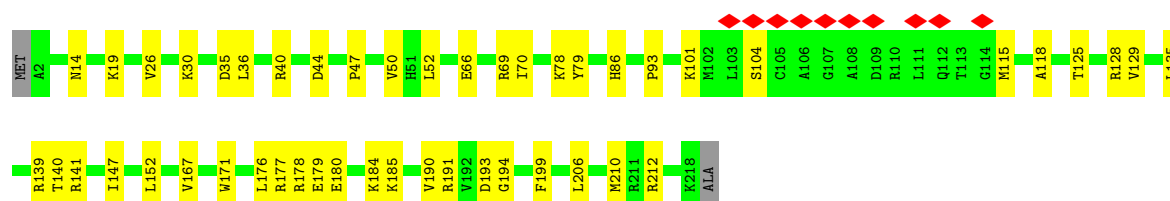
- Molecule 16: uL6

Chain LH: 



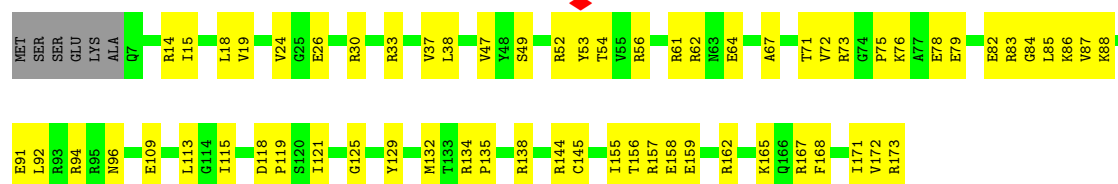
- Molecule 17: 60S ribosomal protein L10-like protein

Chain LI: 



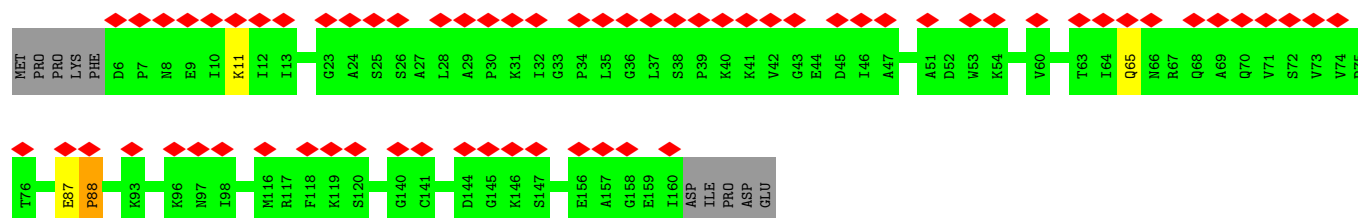
- Molecule 18: Putative ribosomal protein

Chain LJ: 



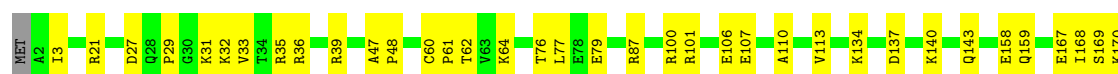
- Molecule 19: 60S ribosomal protein L12-like protein

Chain LK: 



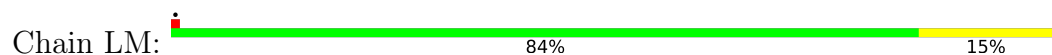
- Molecule 20: 60S ribosomal protein L13

Chain LL: 





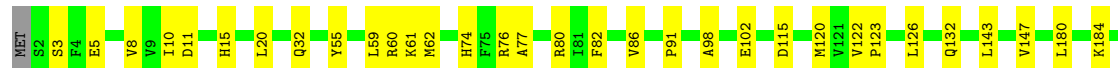
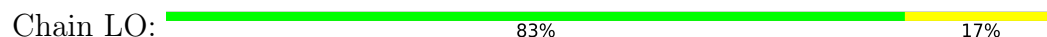
- Molecule 21: 60S ribosomal protein L14-like protein



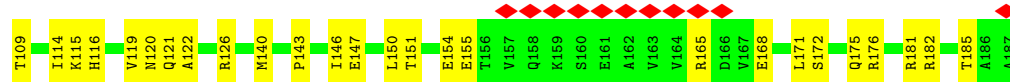
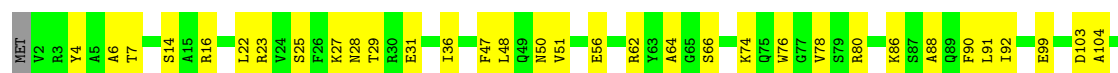
- Molecule 22: Ribosomal protein L15



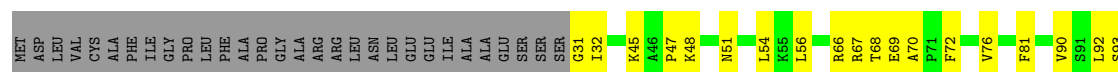
- Molecule 23: 60S ribosomal protein L16-like protein



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



- Molecule 25: Ribosomal protein L18-like protein





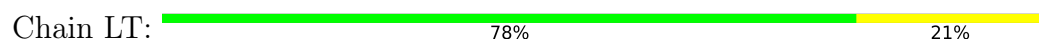
- Molecule 26: Ribosomal protein L19



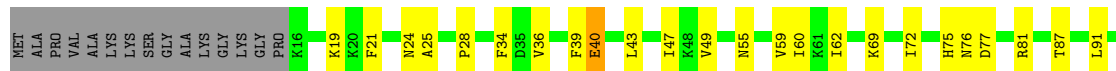
- Molecule 27: 60S ribosomal protein L20



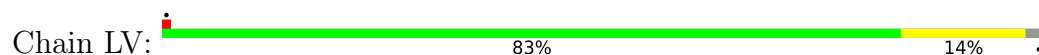
- Molecule 28: 60S ribosomal protein l21-like protein



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

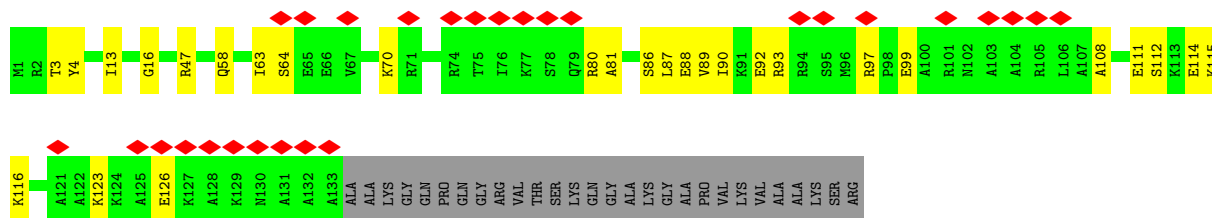


- Molecule 30: 60S ribosomal protein l23-like protein

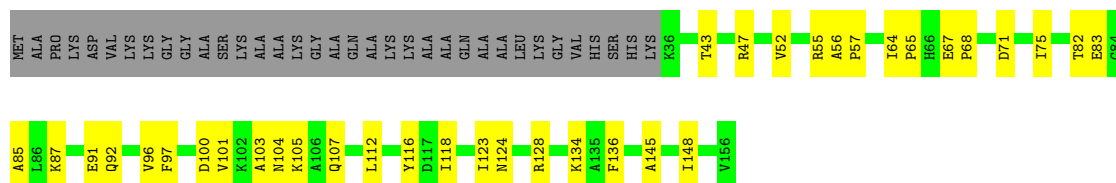




• Molecule 31: eL24



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



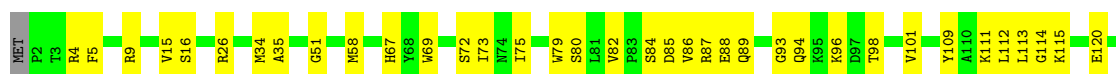
• Molecule 33: 60S ribosomal protein L26-like protein



• Molecule 34: 60S ribosomal protein L27



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





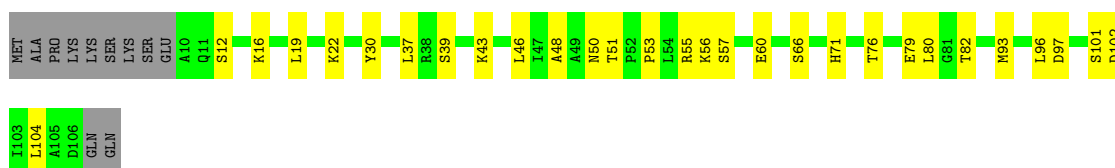
- Molecule 36: 60S ribosomal protein L29

Chain Lb: 78% 17% 5%



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

Chain Lc: 63% 27% 10%



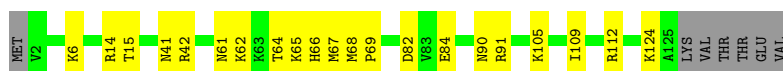
- Molecule 38: Putative 60S ribosomal protein

Chain Ld: 71% 28% .



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

Chain Le: 79% 16% 5%



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

Chain Lf: 78% 20% .



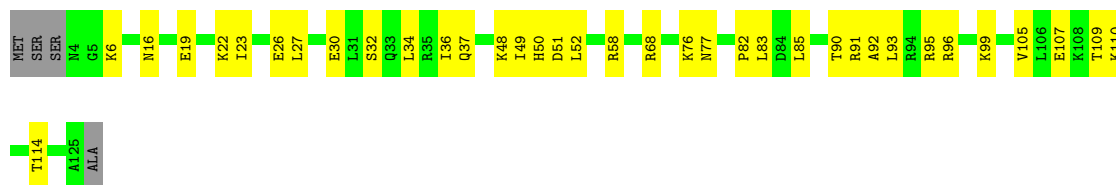
- Molecule 41: Ribosomal protein l34-like protein

Chain Lg: 66% 28% 6%



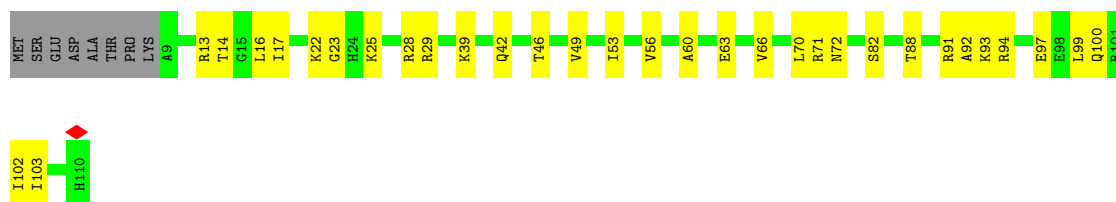
- Molecule 42: Dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh:  68% 29% .



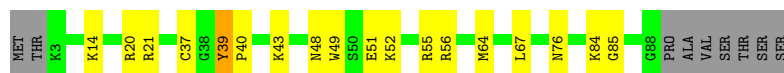
- Molecule 43: 60S ribosomal protein L36

Chain Li:  64% 29% 7%



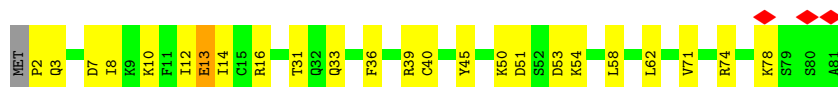
- Molecule 44: Ribosomal protein L37

Chain Lj:  72% 18% 9%



- Molecule 45: eL38

Chain Lk:  69% 28% ..



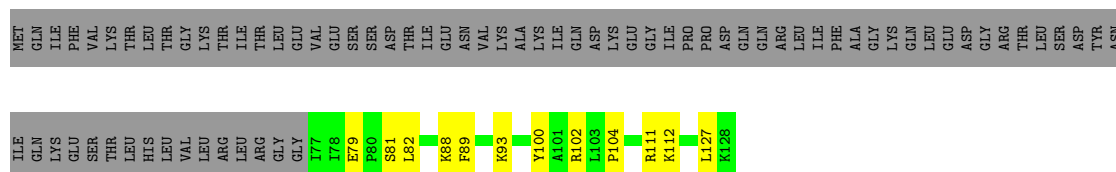
- Molecule 46: Ribosomal protein eL39

Chain Ll:  82% 16% .



- Molecule 47: Putative ribosomal protein

Chain Lm:  31% 9% 59%



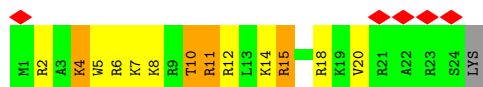
- Molecule 48: 60S ribosomal protein L41-A

Chain Ln: 



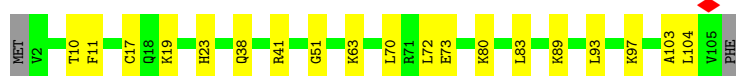
- Molecule 48: 60S ribosomal protein L41-A

Chain Lr: 



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

Chain Lo: 



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

Chain Lp: 

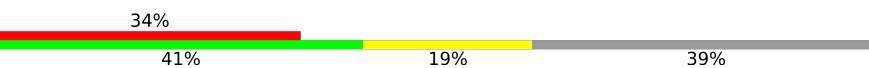


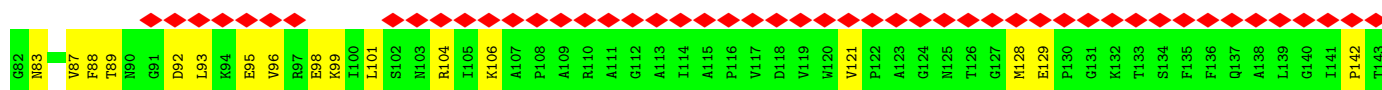
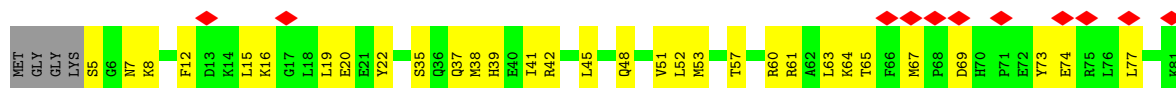
- Molecule 51: Putative 60S ribosomal protein

Chain Lq: 

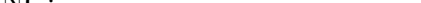


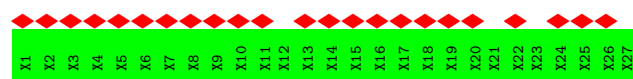
- Molecule 52: 60S acidic ribosomal protein P0

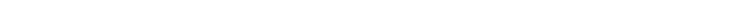
Chain Ls: 

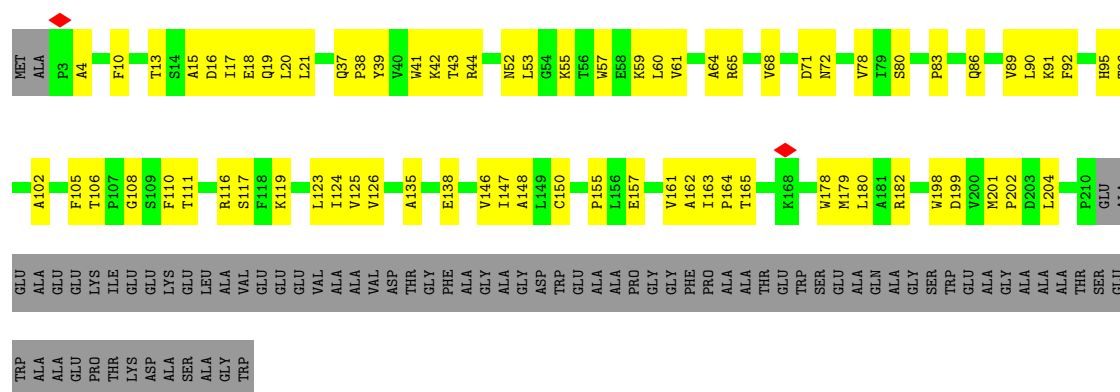


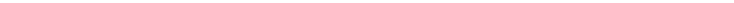


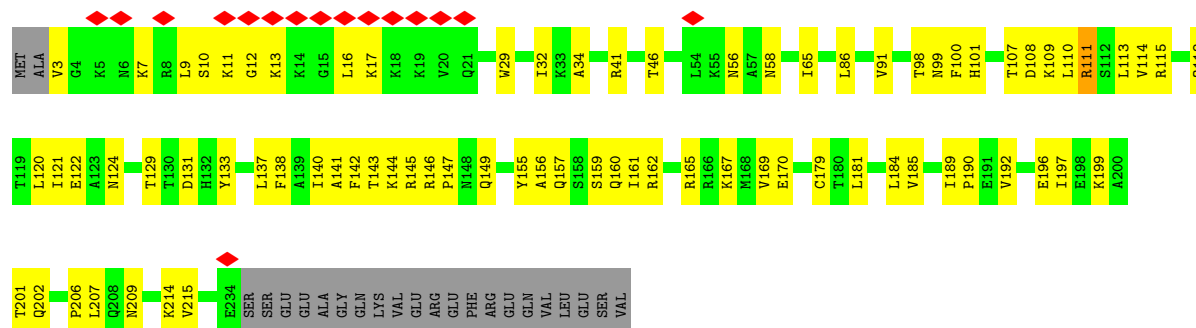
Chain NC:  85% 100%



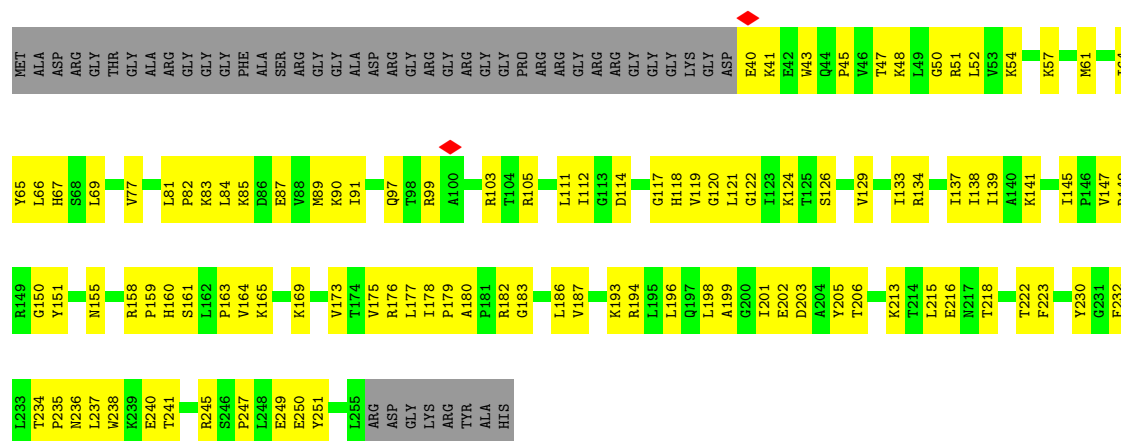
Chain SA: 



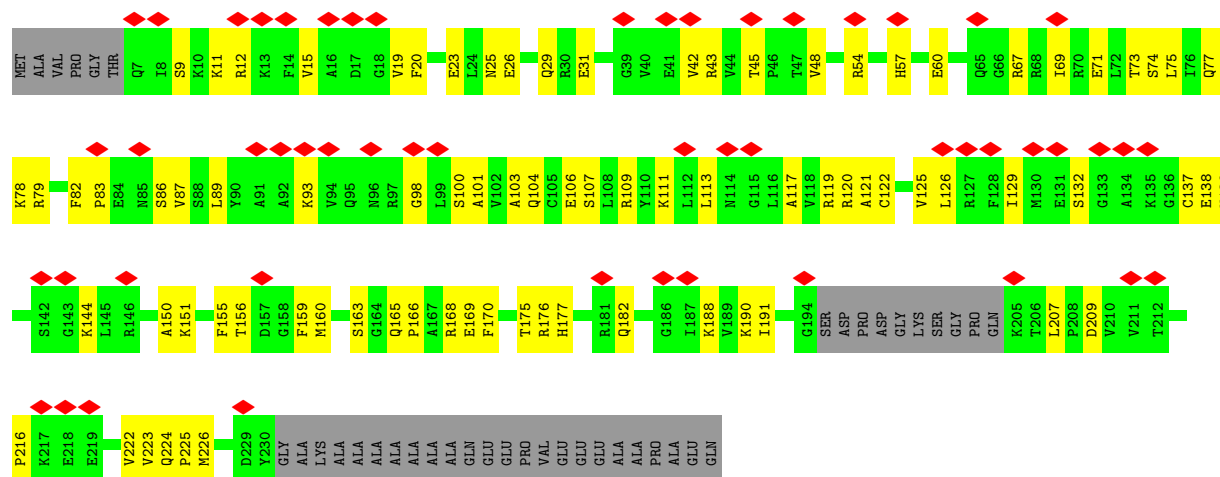
Chain SB: 



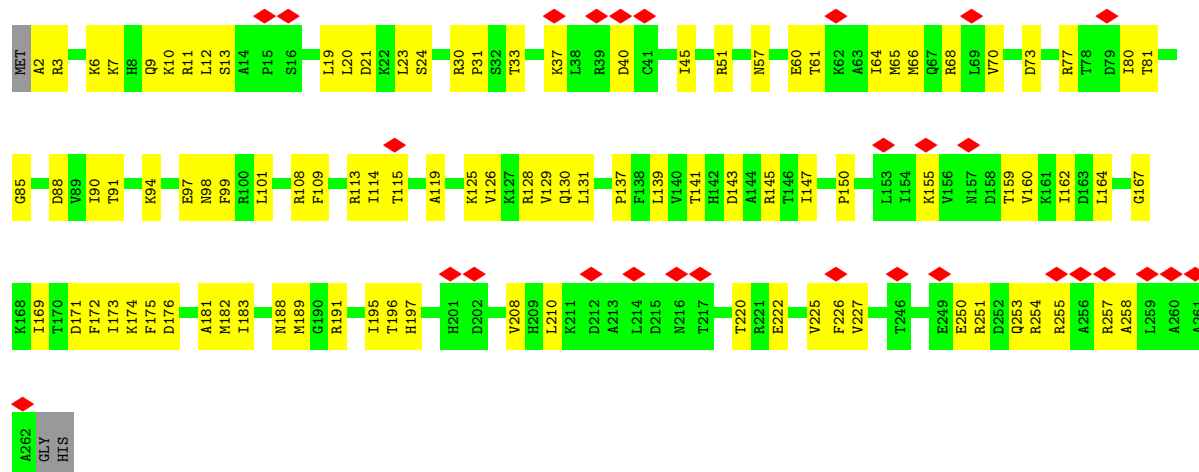
Chain SC:



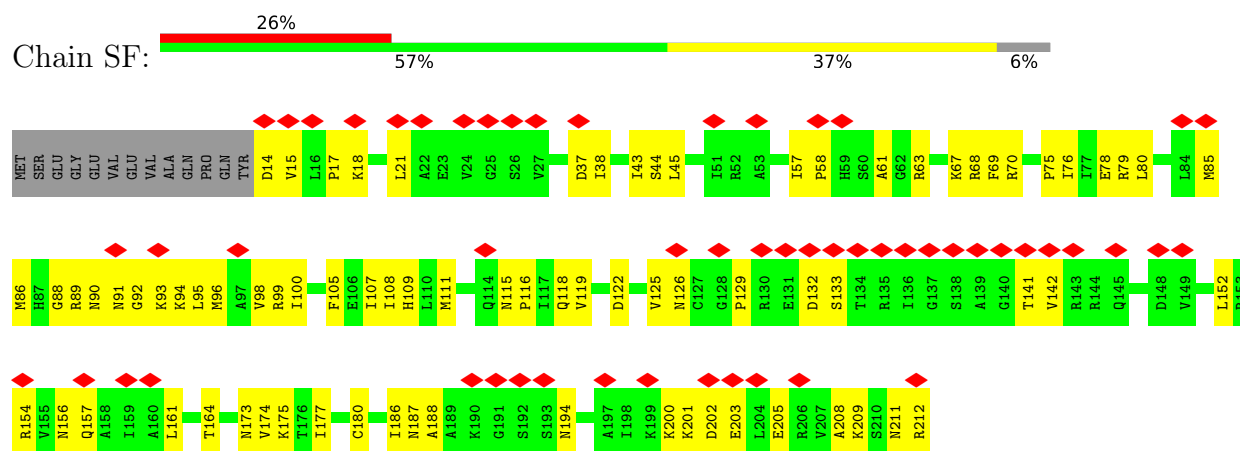
• Molecule 57: 40S ribosomal protein S3-like protein



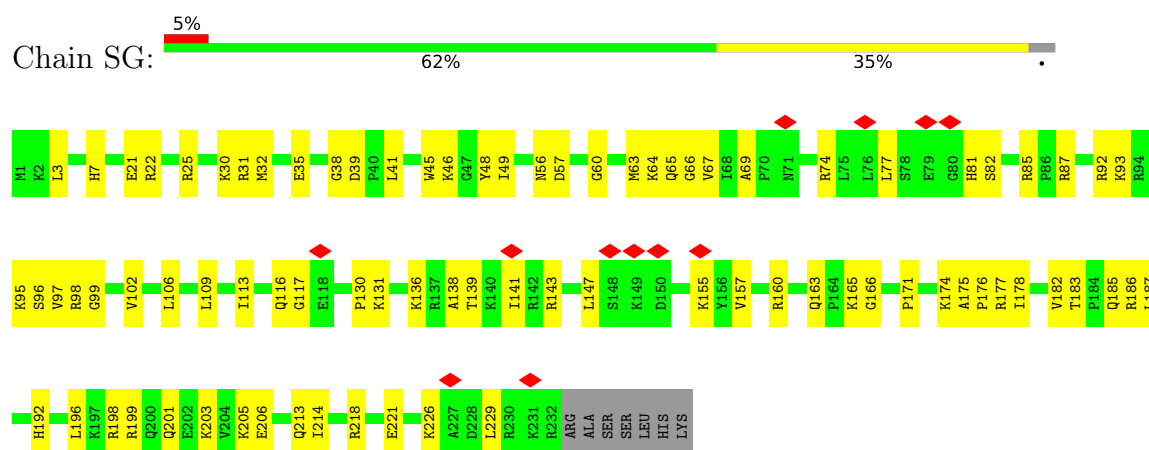
• Molecule 58: 40S ribosomal protein S4



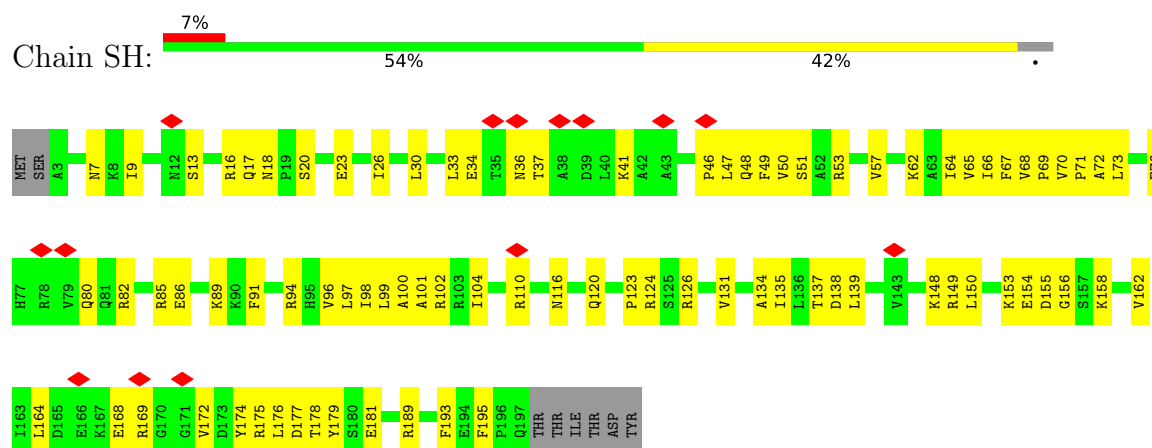
- Molecule 59: 40S ribosomal protein s5-like protein



- Molecule 60: 40S ribosomal protein S6

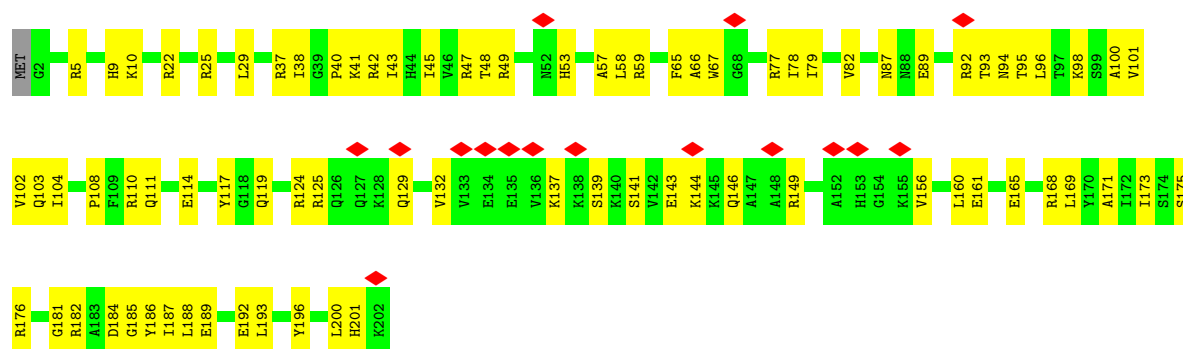


- Molecule 61: 40S ribosomal protein S7

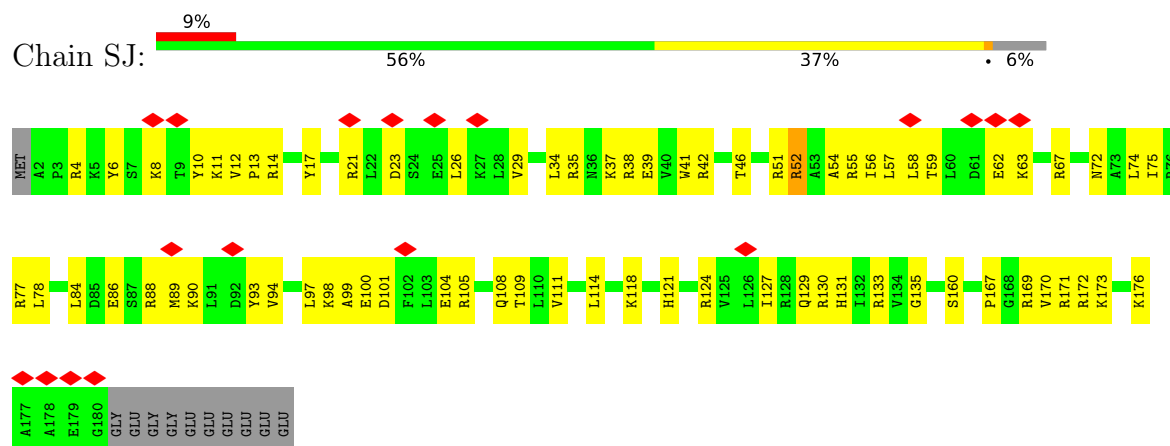


- Molecule 62: 40S ribosomal protein S8

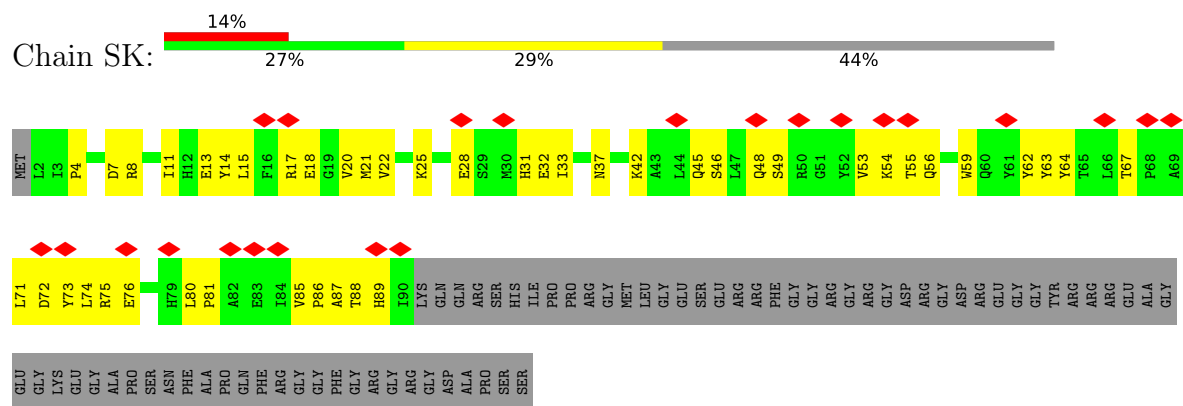




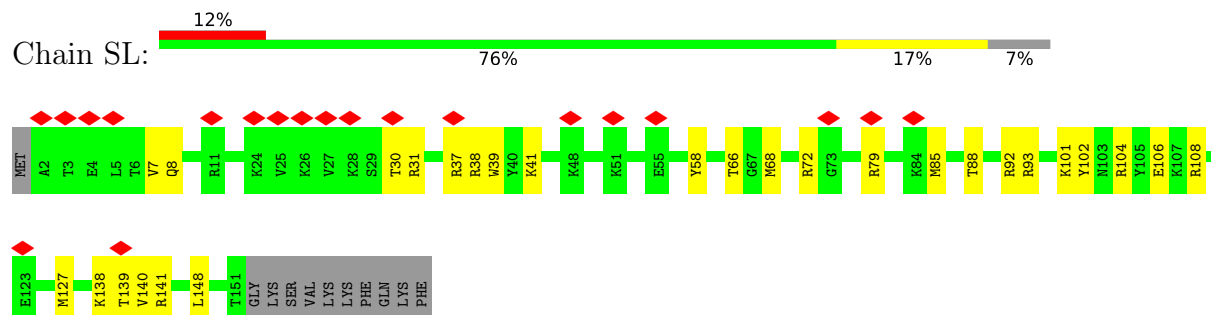
- Molecule 63: 40S ribosomal protein s9-like protein



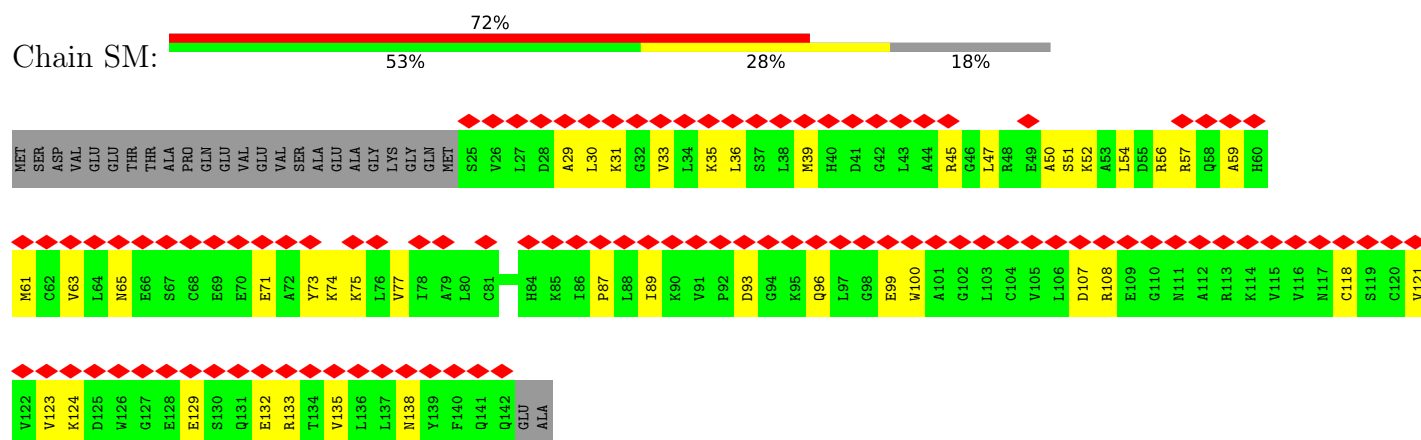
- Molecule 64: 40S ribosomal protein s10-like protein



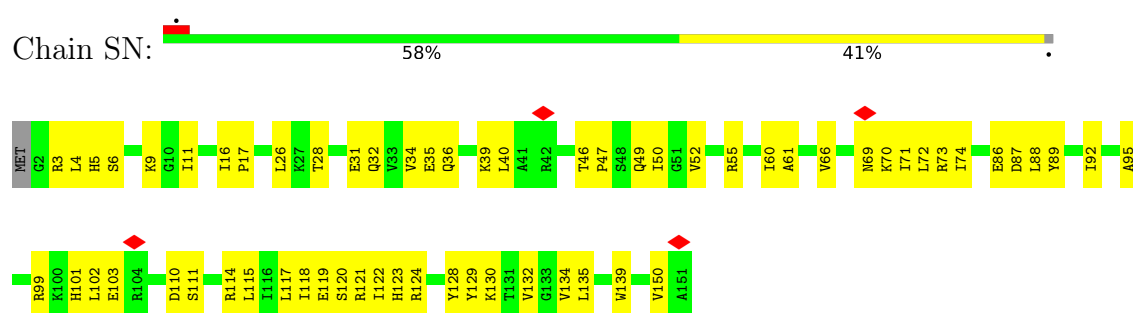
- Molecule 65: 40S ribosomal protein S11-like protein



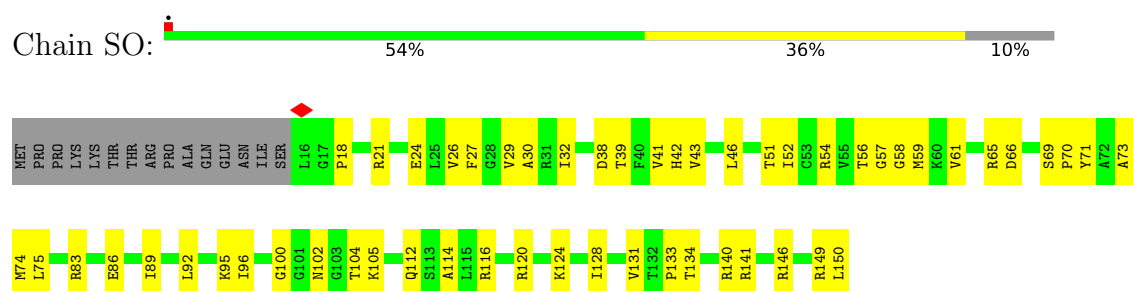
- Molecule 66: 40S ribosomal protein S12



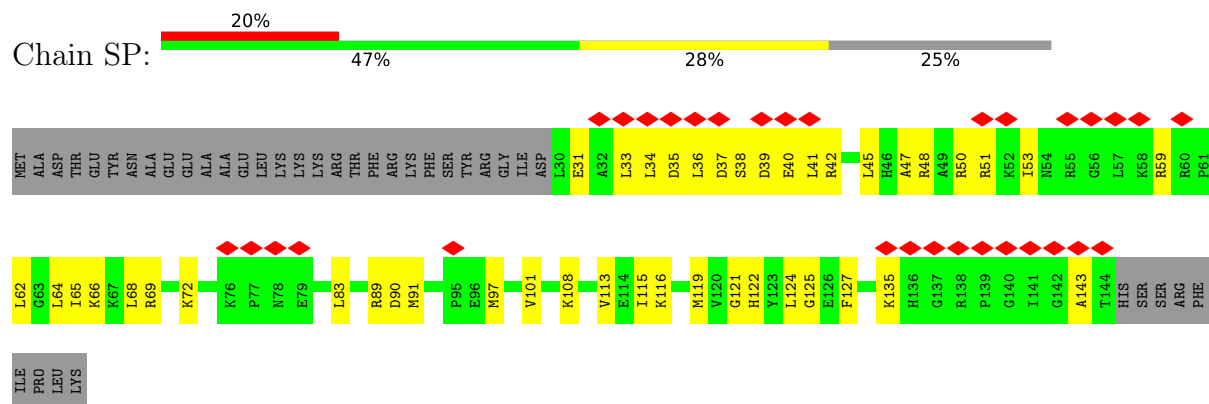
- Molecule 67: 40S ribosomal protein S13-like protein



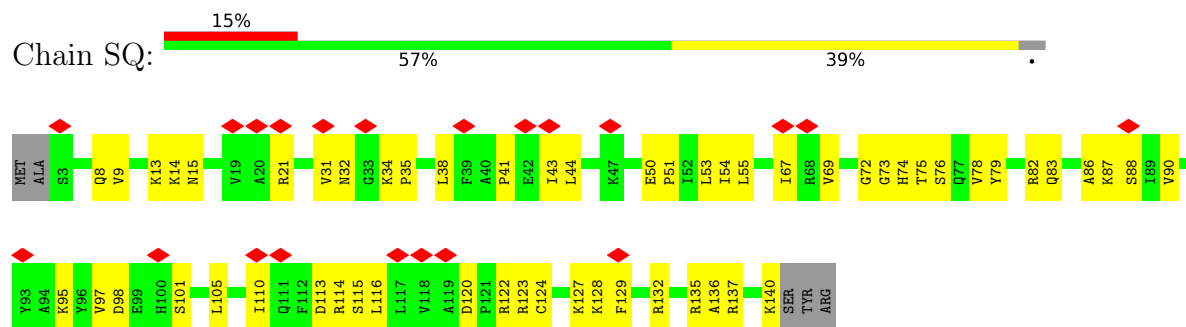
- Molecule 68: 40S ribosomal protein S14-like protein



- Molecule 69: 40S ribosomal protein s15-like protein



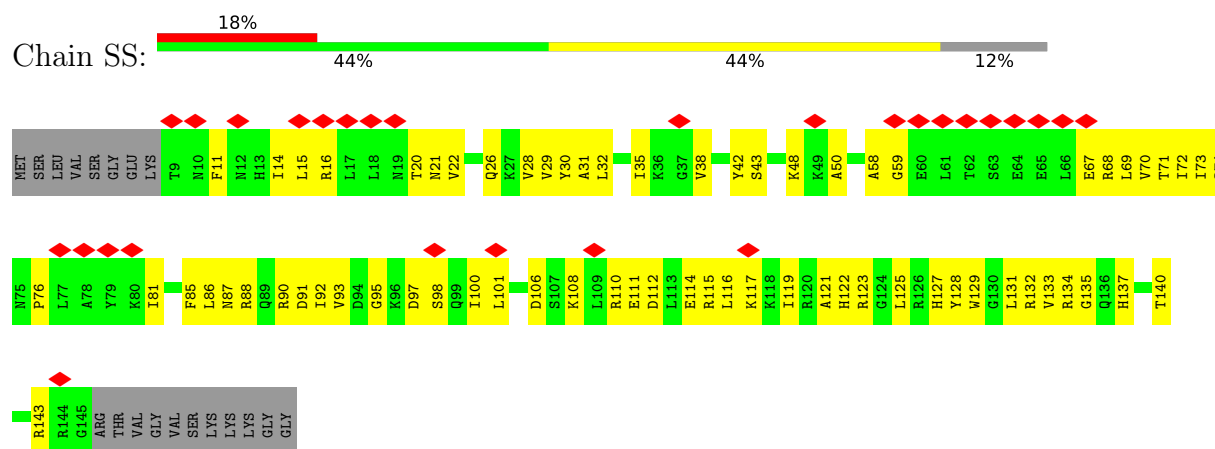
- Molecule 70: 40S ribosomal protein S16-like protein



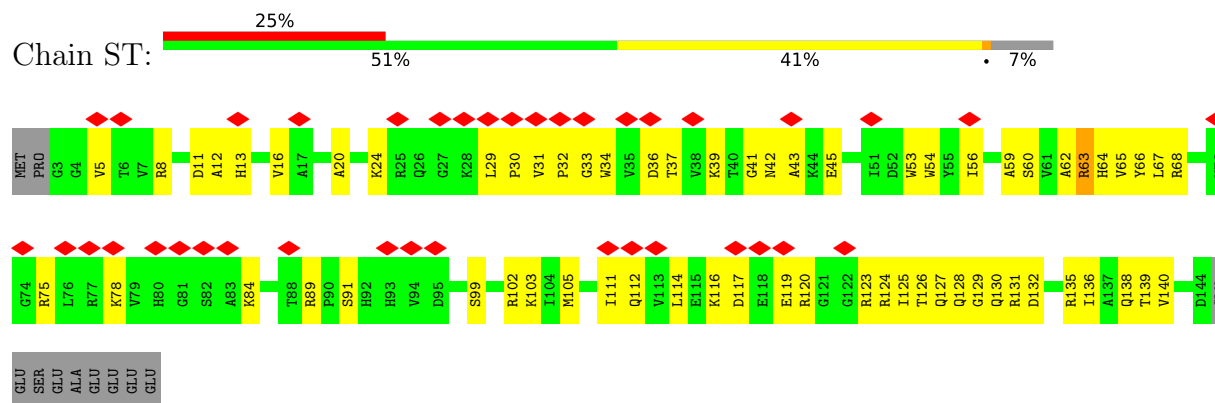
- Molecule 71: 40S ribosomal protein S17-like protein



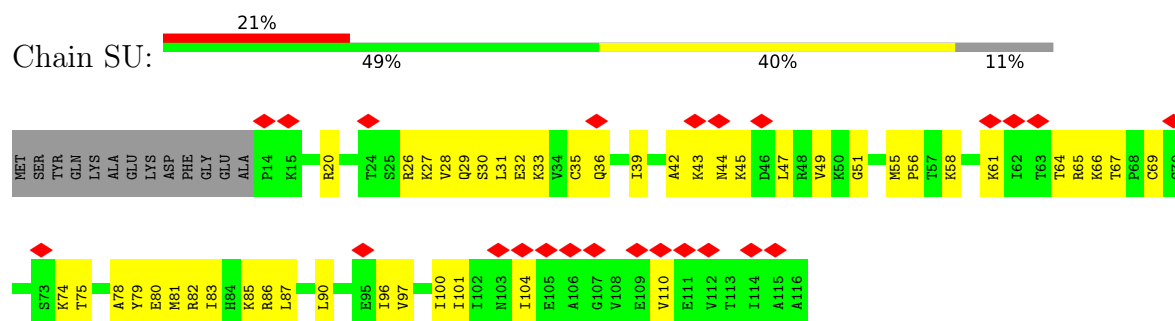
- Molecule 72: Putative ribosomal protein



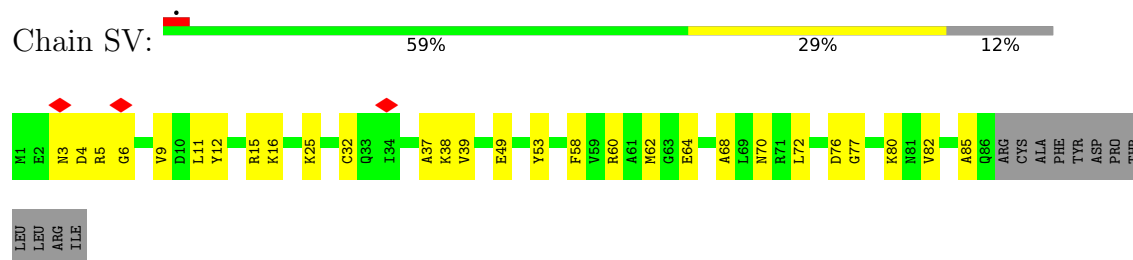
- Molecule 73: 40S ribosomal protein S19-like protein



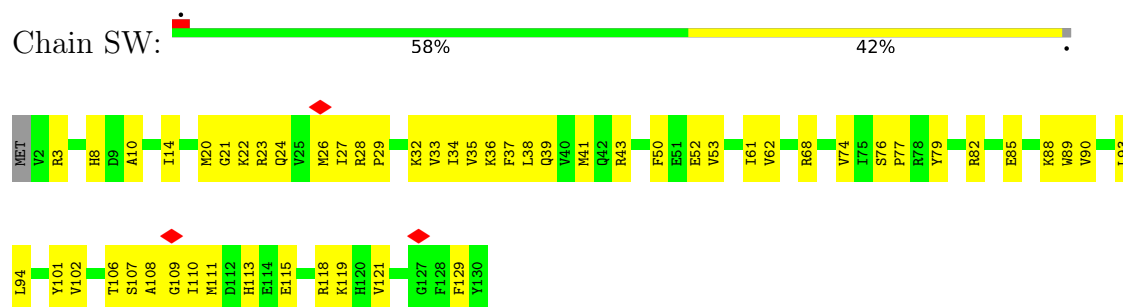
- Molecule 74: 40S ribosomal protein S20-like protein



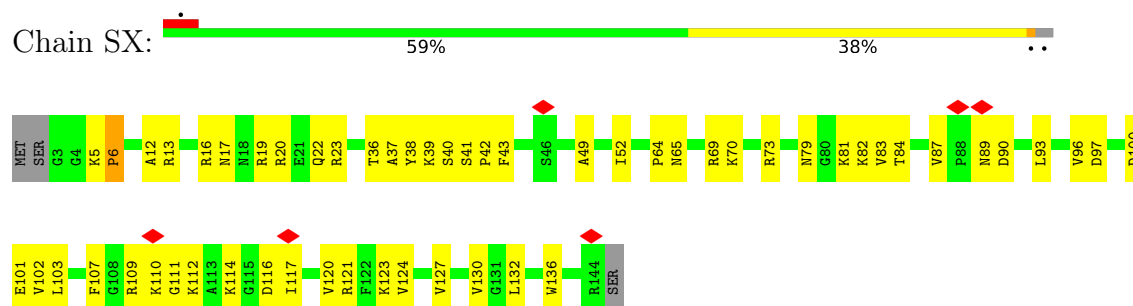
- Molecule 75: 40S ribosomal protein S21-like protein



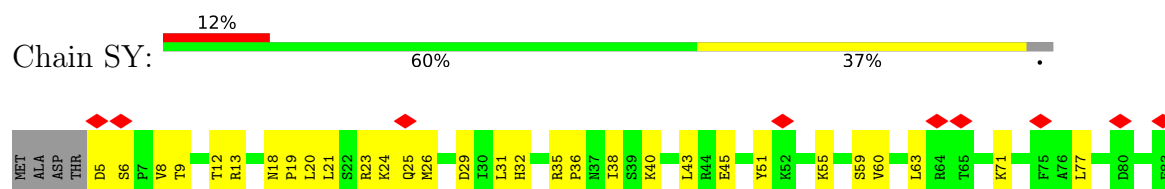
- Molecule 76: 40S ribosomal protein S22-like protein

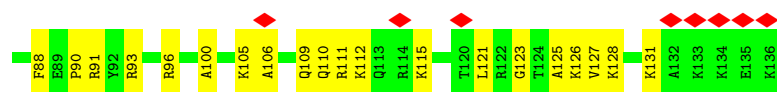


- Molecule 77: 40S ribosomal protein s23-like protein

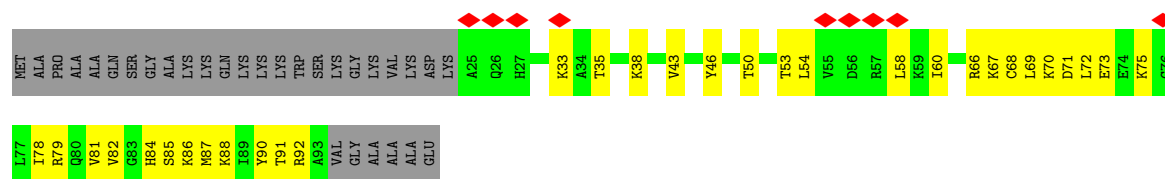


- Molecule 78: 40S ribosomal protein S24

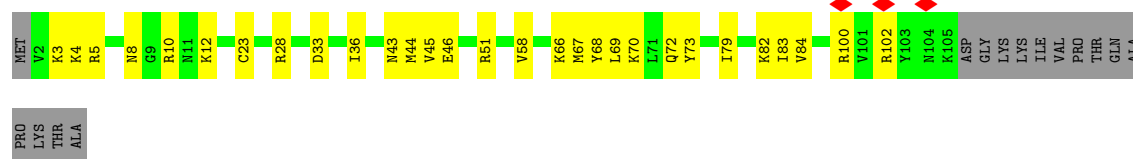




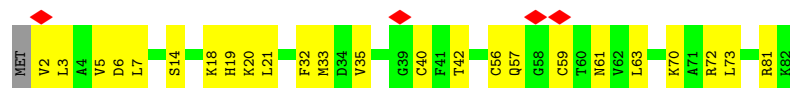
- Molecule 79: 40S ribosomal protein S25



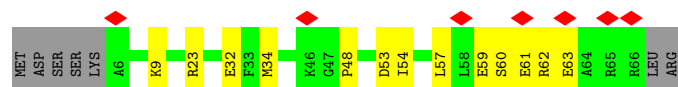
- Molecule 80: 40S ribosomal protein S26



- Molecule 81: Ribosomal protein s27-like protein



- Molecule 82: 40S ribosomal protein S28-like protein

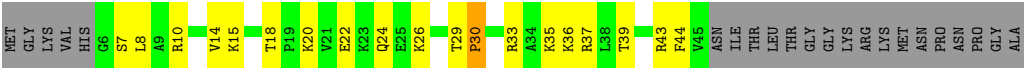


- Molecule 83: Ribosomal protein uS14

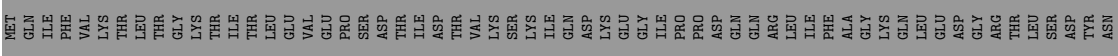
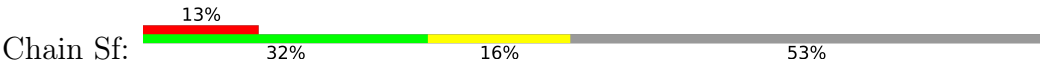


- Molecule 84: 40S ribosomal protein S30





● Molecule 85: 40S ribosomal protein S27a-like protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	305951	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 ($e^-/\text{\AA}^2$)	39.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	25.266	Depositor
Minimum map value	-11.982	Depositor
Average map value	-0.007	Depositor
Map value standard deviation	0.913	Depositor
Recommended contour level	1.8	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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SAC, MG, ZN, OMG, ATP

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	0.11	0/76339	0.29	0/119028
2	2	0.12	0/42256	0.32	1/65852 (0.0%)
3	3	0.10	0/2833	0.28	0/4413
4	4	0.10	0/3710	0.31	0/5778
5	A	0.17	0/2495	0.51	0/3390
6	B	0.13	0/242	0.36	0/314
7	C	0.20	0/3606	0.52	0/4836
8	D	0.17	0/4002	0.48	1/5437 (0.0%)
9	LA	0.11	0/1964	0.39	0/2641
10	LB	0.12	0/3156	0.40	0/4238
11	LC	0.13	0/2815	0.37	0/3795
12	LD	0.15	0/2487	0.44	0/3341
13	LE	0.16	0/1547	0.44	0/2081
14	LF	0.16	0/2055	0.43	0/2758
15	LG	0.14	0/1929	0.43	0/2579
16	LH	0.15	0/1525	0.45	1/2050 (0.0%)
17	LI	0.13	0/1797	0.39	0/2413
18	LJ	0.19	0/1389	0.56	1/1856 (0.1%)
19	LK	0.12	0/761	0.40	0/1056
20	LL	0.14	0/1695	0.41	0/2276
21	LM	0.13	0/1144	0.39	0/1539
22	LN	0.13	0/1740	0.39	0/2332
23	LO	0.15	0/1638	0.46	0/2197
24	LP	0.16	0/1495	0.45	0/2014
25	LQ	0.11	0/1507	0.37	0/2017
26	LR	0.18	0/1525	0.48	0/2028
27	LS	0.13	0/1460	0.37	0/1965
28	LT	0.14	0/1292	0.38	0/1738
29	LU	0.21	0/840	0.55	1/1123 (0.1%)
30	LV	0.13	0/1012	0.40	0/1361
31	LW	0.17	0/1088	0.47	0/1443
32	LX	0.17	0/981	0.50	0/1324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LY	0.16	0/1079	0.43	0/1443
34	LZ	0.14	0/1134	0.44	0/1519
35	La	0.13	0/1212	0.40	0/1627
36	Lb	0.16	0/518	0.53	0/684
37	Lc	0.17	0/731	0.45	0/983
38	Ld	0.17	0/979	0.47	0/1308
39	Le	0.12	0/1019	0.37	0/1358
40	Lf	0.15	0/874	0.40	0/1176
41	Lg	0.16	0/904	0.43	0/1210
42	Lh	0.19	0/1014	0.51	0/1349
43	Li	0.19	0/844	0.51	0/1115
44	Lj	0.17	0/697	0.47	0/922
45	Lk	0.18	0/666	0.56	1/884 (0.1%)
46	Ll	0.11	0/445	0.34	0/593
47	Lm	0.16	0/424	0.53	0/561
48	Ln	0.38	0/225	0.90	0/289
48	Lr	0.39	0/225	0.90	0/289
49	Lo	0.12	0/835	0.37	0/1105
50	Lp	0.13	0/705	0.43	0/940
51	Lq	0.13	0/1101	0.40	0/1482
52	Ls	0.15	0/1477	0.47	0/1995
54	SA	0.21	0/1683	0.57	0/2299
55	SB	0.20	0/1900	0.55	1/2551 (0.0%)
56	SC	0.20	0/1703	0.55	0/2303
57	SD	0.20	0/1712	0.57	0/2299
58	SE	0.17	0/2112	0.51	0/2842
59	SF	0.20	0/1578	0.53	0/2130
60	SG	0.19	0/1906	0.47	0/2547
61	SH	0.19	0/1587	0.53	0/2140
62	SI	0.16	0/1654	0.48	0/2213
63	SJ	0.20	0/1489	0.59	1/1993 (0.1%)
64	SK	0.19	0/764	0.55	0/1038
65	SL	0.14	0/1249	0.41	0/1678
66	SM	0.20	0/934	0.57	0/1255
67	SN	0.20	0/1205	0.57	0/1627
68	SO	0.17	0/1014	0.52	0/1361
69	SP	0.19	0/932	0.55	0/1248
70	SQ	0.17	0/1098	0.52	0/1472
71	SR	0.24	0/1060	0.71	0/1424
72	SS	0.18	0/1133	0.53	0/1520
73	ST	0.23	0/1137	0.60	1/1533 (0.1%)
74	SU	0.17	0/828	0.55	0/1112
75	SV	0.15	0/671	0.47	0/900

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.20	0/1055	0.57	0/1416
77	SX	0.45	1/1116 (0.1%)	0.80	3/1489 (0.2%)
78	SY	0.17	0/1075	0.51	0/1431
79	SZ	0.16	0/550	0.52	0/736
80	Sa	0.13	0/852	0.39	0/1136
81	Sb	0.15	0/623	0.47	0/843
82	Sc	0.16	0/487	0.44	0/653
83	Sd	0.15	0/427	0.54	0/570
84	Se	0.60	1/325 (0.3%)	1.04	3/427 (0.7%)
85	Sf	0.11	0/614	0.34	0/813
All	All	0.14	2/227906 (0.0%)	0.39	15/333044 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
77	SX	6	PRO	CG-CD	-12.56	1.08	1.50
84	Se	30	PRO	CG-CD	-8.85	1.20	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	SX	6	PRO	N-CD-CG	-15.07	80.59	103.20
84	Se	30	PRO	CA-N-CD	-10.75	96.95	112.00
84	Se	30	PRO	N-CD-CG	-10.19	87.91	103.20
77	SX	6	PRO	CA-CB-CG	-8.70	87.97	104.50
73	ST	63	ARG	CB-CG-CD	7.46	128.45	111.30

There are no chirality outliers.

There are no planarity outliers.

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	1	68242	0	34371	600	0
2	2	37781	0	19038	612	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	2535	0	1284	28	0
4	4	3319	0	1678	39	0
5	A	2438	0	2385	102	0
6	B	243	0	237	9	0
7	C	3548	0	3547	151	0
8	D	3942	0	3967	135	0
9	LA	1925	0	1999	38	0
10	LB	3088	0	3206	77	0
11	LC	2758	0	2883	41	0
12	LD	2440	0	2431	59	0
13	LE	1518	0	1619	40	0
14	LF	2017	0	2130	40	0
15	LG	1900	0	2066	34	0
16	LH	1505	0	1581	47	0
17	LI	1760	0	1798	32	0
18	LJ	1367	0	1405	51	0
19	LK	762	0	362	2	0
20	LL	1666	0	1756	33	0
21	LM	1125	0	1198	19	0
22	LN	1703	0	1767	52	0
23	LO	1613	0	1706	23	0
24	LP	1472	0	1518	43	0
25	LQ	1481	0	1596	37	0
26	LR	1506	0	1603	36	0
27	LS	1425	0	1484	38	0
28	LT	1266	0	1328	27	0
29	LU	827	0	875	23	0
30	LV	994	0	1055	14	0
31	LW	1075	0	1146	21	0
32	LX	965	0	1050	23	0
33	LY	1065	0	1156	25	0
34	LZ	1111	0	1181	28	0
35	La	1180	0	1203	44	0
36	Lb	508	0	526	10	0
37	Lc	722	0	766	23	0
38	Ld	965	0	1028	26	0
39	Le	1001	0	1070	16	0
40	Lf	853	0	880	14	0
41	Lg	891	0	958	27	0
42	Lh	1003	0	1116	26	0
43	Li	836	0	915	25	0
44	Lj	684	0	712	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	Lk	658	0	721	19	0
46	Ll	435	0	473	7	0
47	Lm	418	0	459	12	0
48	Ln	224	0	271	12	0
48	Lr	224	0	271	17	0
49	Lo	822	0	891	16	0
50	Lp	697	0	737	18	0
51	Lq	1083	0	1140	29	0
52	Ls	1449	0	1488	57	0
53	NC	135	0	33	0	0
54	SA	1641	0	1650	67	0
55	SB	1871	0	1989	60	0
56	SC	1672	0	1777	89	0
57	SD	1688	0	1750	73	0
58	SE	2072	0	2155	84	0
59	SF	1557	0	1608	63	0
60	SG	1875	0	1983	69	0
61	SH	1562	0	1641	69	0
62	SI	1621	0	1645	66	0
63	SJ	1466	0	1582	70	0
64	SK	742	0	738	46	0
65	SL	1222	0	1289	25	0
66	SM	923	0	946	37	0
67	SN	1182	0	1264	59	0
68	SO	1002	0	1034	47	0
69	SP	917	0	978	37	0
70	SQ	1081	0	1151	50	0
71	SR	1045	0	1083	67	0
72	SS	1118	0	1172	58	0
73	ST	1117	0	1133	62	0
74	SU	819	0	895	48	0
75	SV	664	0	662	26	0
76	SW	1037	0	1076	47	0
77	SX	1099	0	1169	54	0
78	SY	1061	0	1150	45	0
79	SZ	546	0	591	28	0
80	Sa	839	0	891	27	0
81	Sb	611	0	633	24	0
82	Sc	484	0	513	14	0
83	Sd	419	0	418	28	0
84	Se	322	0	365	23	0
85	Sf	604	0	640	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	1	360	0	0	0	0
86	2	66	0	0	0	0
86	3	6	0	0	0	0
86	4	10	0	0	0	0
86	D	1	0	0	0	0
86	LB	1	0	0	0	0
86	LC	1	0	0	0	0
86	LI	1	0	0	0	0
86	LJ	1	0	0	0	0
86	LN	1	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	LW	1	0	0	0	0
86	Lb	1	0	0	0	0
86	SN	1	0	0	0	0
86	SO	1	0	0	0	0
86	SQ	1	0	0	0	0
87	D	31	0	12	1	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sb	1	0	0	0	0
88	Sd	1	0	0	0	0
All	All	213543	0	161647	3930	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 11.

The worst 5 of 3930 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)
7:C:246:VAL:CG2	7:C:259:MET:HE3	1.56	1.32
7:C:246:VAL:HG22	7:C:247:PRO:HD2	1.15	1.12
7:C:246:VAL:HG21	7:C:259:MET:CE	1.83	1.09
7:C:249:ASP:CG	8:D:259:LYS:HE2	1.79	1.08
7:C:246:VAL:HG21	7:C:259:MET:HE3	1.31	1.05

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
5	A	310/316 (98%)	287 (93%)	23 (7%)	0	100	100
6	B	27/302 (9%)	19 (70%)	8 (30%)	0	100	100
7	C	442/446 (99%)	423 (96%)	18 (4%)	1 (0%)	43	73
8	D	511/578 (88%)	496 (97%)	11 (2%)	4 (1%)	16	50
9	LA	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
10	LB	385/392 (98%)	365 (95%)	20 (5%)	0	100	100
11	LC	361/365 (99%)	346 (96%)	15 (4%)	0	100	100
12	LD	298/304 (98%)	290 (97%)	8 (3%)	0	100	100
13	LE	192/200 (96%)	178 (93%)	14 (7%)	0	100	100
14	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
15	LG	233/262 (89%)	229 (98%)	4 (2%)	0	100	100
16	LH	189/192 (98%)	184 (97%)	5 (3%)	0	100	100
17	LI	215/219 (98%)	202 (94%)	13 (6%)	0	100	100
18	LJ	165/173 (95%)	160 (97%)	5 (3%)	0	100	100
19	LK	153/165 (93%)	135 (88%)	17 (11%)	1 (1%)	18	52
20	LL	207/213 (97%)	201 (97%)	6 (3%)	0	100	100
21	LM	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
22	LN	200/203 (98%)	192 (96%)	8 (4%)	0	100	100
23	LO	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
24	LP	184/187 (98%)	177 (96%)	7 (4%)	0	100	100
25	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
26	LR	182/192 (95%)	176 (97%)	6 (3%)	0	100	100
27	LS	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
28	LT	156/160 (98%)	154 (99%)	2 (1%)	0	100	100
29	LU	100/127 (79%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	LV	133/139 (96%)	130 (98%)	3 (2%)	0	100	100
31	LW	131/161 (81%)	129 (98%)	2 (2%)	0	100	100
32	LX	119/156 (76%)	112 (94%)	7 (6%)	0	100	100
33	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
34	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
35	La	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
36	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
37	Lc	95/108 (88%)	95 (100%)	0	0	100	100
38	Ld	117/120 (98%)	115 (98%)	2 (2%)	0	100	100
39	Le	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
40	Lf	105/109 (96%)	100 (95%)	5 (5%)	0	100	100
41	Lg	110/119 (92%)	105 (96%)	5 (4%)	0	100	100
42	Lh	120/126 (95%)	116 (97%)	4 (3%)	0	100	100
43	Li	100/110 (91%)	95 (95%)	5 (5%)	0	100	100
44	Lj	84/95 (88%)	78 (93%)	5 (6%)	1 (1%)	10	42
45	Lk	78/81 (96%)	77 (99%)	1 (1%)	0	100	100
46	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
47	Lm	50/128 (39%)	50 (100%)	0	0	100	100
48	Ln	22/25 (88%)	22 (100%)	0	0	100	100
48	Lr	22/25 (88%)	22 (100%)	0	0	100	100
49	Lo	102/106 (96%)	99 (97%)	3 (3%)	0	100	100
50	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
51	Lq	139/147 (95%)	135 (97%)	4 (3%)	0	100	100
52	Ls	187/312 (60%)	182 (97%)	5 (3%)	0	100	100
54	SA	206/285 (72%)	195 (95%)	11 (5%)	0	100	100
55	SB	230/255 (90%)	214 (93%)	16 (7%)	0	100	100
56	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100
57	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
58	SE	259/264 (98%)	245 (95%)	14 (5%)	0	100	100
59	SF	197/212 (93%)	187 (95%)	10 (5%)	0	100	100
60	SG	230/239 (96%)	223 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SH	193/203 (95%)	187 (97%)	6 (3%)	0	100	100
62	SI	199/202 (98%)	196 (98%)	3 (2%)	0	100	100
63	SJ	177/190 (93%)	172 (97%)	5 (3%)	0	100	100
64	SK	87/159 (55%)	84 (97%)	3 (3%)	0	100	100
65	SL	148/161 (92%)	145 (98%)	3 (2%)	0	100	100
66	SM	116/144 (81%)	105 (90%)	11 (10%)	0	100	100
67	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
68	SO	133/150 (89%)	124 (93%)	9 (7%)	0	100	100
69	SP	113/153 (74%)	109 (96%)	4 (4%)	0	100	100
70	SQ	136/143 (95%)	128 (94%)	8 (6%)	0	100	100
71	SR	126/143 (88%)	121 (96%)	5 (4%)	0	100	100
72	SS	135/156 (86%)	125 (93%)	10 (7%)	0	100	100
73	ST	140/153 (92%)	135 (96%)	5 (4%)	0	100	100
74	SU	101/116 (87%)	95 (94%)	6 (6%)	0	100	100
75	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
76	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
77	SX	140/145 (97%)	130 (93%)	10 (7%)	0	100	100
78	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
79	SZ	67/99 (68%)	67 (100%)	0	0	100	100
80	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
81	Sb	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
82	Sc	59/68 (87%)	57 (97%)	2 (3%)	0	100	100
83	Sd	50/56 (89%)	47 (94%)	3 (6%)	0	100	100
84	Se	38/62 (61%)	38 (100%)	0	0	100	100
85	Sf	71/154 (46%)	64 (90%)	7 (10%)	0	100	100
All	All	12586/14205 (89%)	12071 (96%)	508 (4%)	7 (0%)	49	79

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	C	251	GLU
8	D	450	VAL
8	D	556	ASP

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Mol	Chain	Res	Type
19	LK	88	PRO
44	Lj	39	TYR

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 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	
5	A	271/274 (99%)	271 (100%)	0	100	100
6	B	22/224 (10%)	22 (100%)	0	100	100
7	C	358/367 (98%)	357 (100%)	1 (0%)	86	88
8	D	427/474 (90%)	427 (100%)	0	100	100
9	LA	196/198 (99%)	194 (99%)	2 (1%)	68	80
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	203/222 (91%)	203 (100%)	0	100	100
16	LH	168/169 (99%)	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
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	161/162 (99%)	161 (100%)	0	100	100
24	LP	151/152 (99%)	151 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	LT	134/135 (99%)	134 (100%)	0	100	100
29	LU	90/108 (83%)	90 (100%)	0	100	100
30	LV	99/102 (97%)	99 (100%)	0	100	100
31	LW	107/125 (86%)	107 (100%)	0	100	100
32	LX	108/129 (84%)	108 (100%)	0	100	100
33	LY	117/119 (98%)	117 (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	53/55 (96%)	53 (100%)	0	100	100
37	Lc	78/88 (89%)	78 (100%)	0	100	100
38	Ld	104/105 (99%)	104 (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	86/93 (92%)	86 (100%)	0	100	100
44	Lj	70/78 (90%)	70 (100%)	0	100	100
45	Lk	76/77 (99%)	76 (100%)	0	100	100
46	Ll	45/46 (98%)	45 (100%)	0	100	100
47	Lm	47/115 (41%)	47 (100%)	0	100	100
48	Ln	22/23 (96%)	17 (77%)	5 (23%)	1	5
48	Lr	22/23 (96%)	17 (77%)	5 (23%)	1	5
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
54	SA	178/225 (79%)	178 (100%)	0	100	100
55	SB	203/223 (91%)	203 (100%)	0	100	100
56	SC	181/206 (88%)	181 (100%)	0	100	100
57	SD	182/206 (88%)	182 (100%)	0	100	100
58	SE	219/221 (99%)	219 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	SF	167/178 (94%)	166 (99%)	1 (1%)	78	84
60	SG	198/204 (97%)	198 (100%)	0	100	100
61	SH	169/177 (96%)	169 (100%)	0	100	100
62	SI	163/164 (99%)	163 (100%)	0	100	100
63	SJ	154/162 (95%)	154 (100%)	0	100	100
64	SK	77/126 (61%)	77 (100%)	0	100	100
65	SL	133/143 (93%)	133 (100%)	0	100	100
66	SM	101/121 (84%)	101 (100%)	0	100	100
67	SN	129/130 (99%)	129 (100%)	0	100	100
68	SO	102/117 (87%)	102 (100%)	0	100	100
69	SP	99/132 (75%)	99 (100%)	0	100	100
70	SQ	111/115 (96%)	111 (100%)	0	100	100
71	SR	119/131 (91%)	119 (100%)	0	100	100
72	SS	120/135 (89%)	120 (100%)	0	100	100
73	ST	114/124 (92%)	114 (100%)	0	100	100
74	SU	93/103 (90%)	93 (100%)	0	100	100
75	SV	69/80 (86%)	69 (100%)	0	100	100
76	SW	112/113 (99%)	112 (100%)	0	100	100
77	SX	113/116 (97%)	113 (100%)	0	100	100
78	SY	112/115 (97%)	112 (100%)	0	100	100
79	SZ	60/80 (75%)	60 (100%)	0	100	100
80	Sa	91/103 (88%)	91 (100%)	0	100	100
81	Sb	70/71 (99%)	70 (100%)	0	100	100
82	Sc	54/61 (88%)	54 (100%)	0	100	100
83	Sd	43/46 (94%)	43 (100%)	0	100	100
84	Se	34/51 (67%)	34 (100%)	0	100	100
85	Sf	66/139 (48%)	66 (100%)	0	100	100
All	All	10610/11721 (90%)	10596 (100%)	14 (0%)	87	91

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	Ln	20	VAL

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Mol	Chain	Res	Type
48	Lr	4	LYS
59	SF	211	ASN
48	Lr	15	ARG
48	Lr	20	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
35	La	25	HIS
81	Sb	61	ASN
54	SA	52	ASN
80	Sa	80	HIS
71	SR	123	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	526 (16%)	51 (1%)
2	2	1770/1796 (98%)	377 (21%)	48 (2%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	26 (16%)	3 (1%)
All	All	5231/5409 (96%)	938 (17%)	103 (1%)

5 of 938 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A
1	1	41	A
1	1	44	A
1	1	50	A
1	1	60	G

5 of 103 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	211	U
2	2	555	U
3	3	72	G
2	2	228	U
2	2	275	U

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

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	$\# Z > 2$
23	SAC	LO	2	23	7,8,9	1.03	0	7,9,11	0.99	0
1	OMG	1	2578	1	23,26,27	0.43	0	32,38,41	0.50	0

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
23	SAC	LO	2	23	-	2/7/8/10	-
1	OMG	1	2578	1	-	2/9/27/28	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	LO	2	SAC	N-CA-CB-OG
23	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 464 ligands modelled in this entry, 463 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	$\# Z > 2$
87	ATP	D	601	86	32,33,33	0.26	0	48,52,52	0.28	0

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
87	ATP	D	601	86	-	9/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

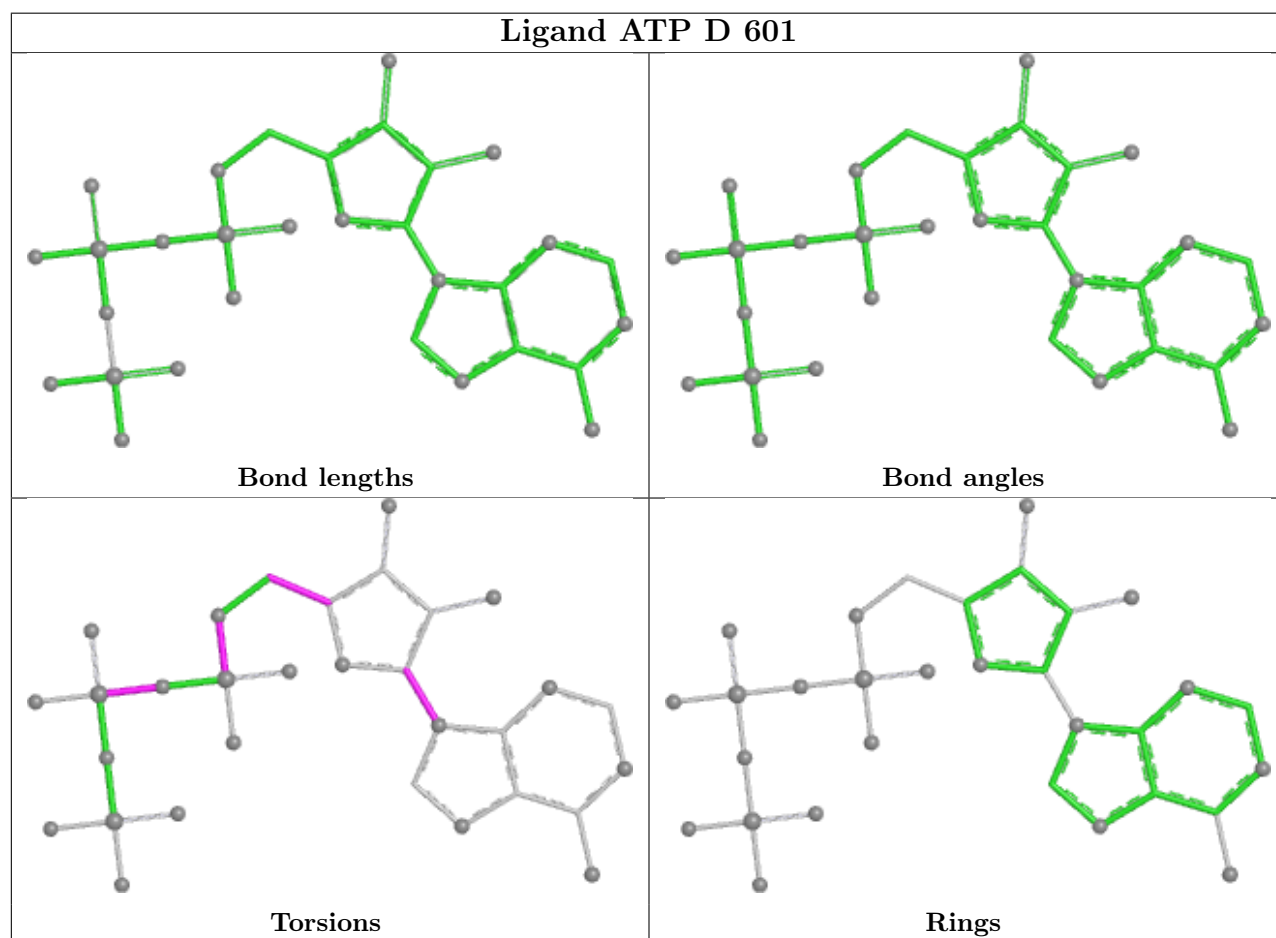
Mol	Chain	Res	Type	Atoms
87	D	601	ATP	C5'-O5'-PA-O3A
87	D	601	ATP	C3'-C4'-C5'-O5'
87	D	601	ATP	O4'-C4'-C5'-O5'
87	D	601	ATP	C2'-C1'-N9-C8
87	D	601	ATP	C2'-C1'-N9-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	D	601	ATP	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 ⓘ

There are no chain breaks in this entry.

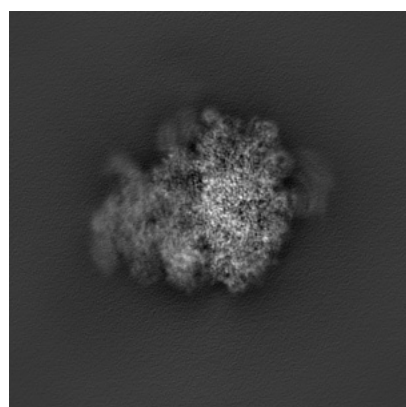
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14479. These allow visual inspection of the internal detail of the map and identification of artifacts.

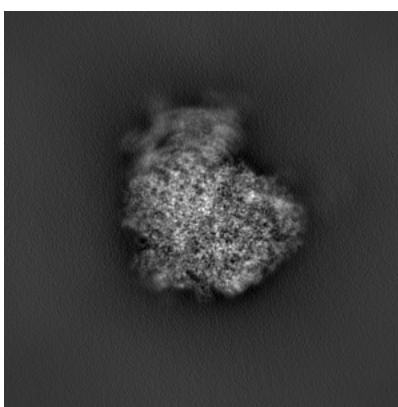
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

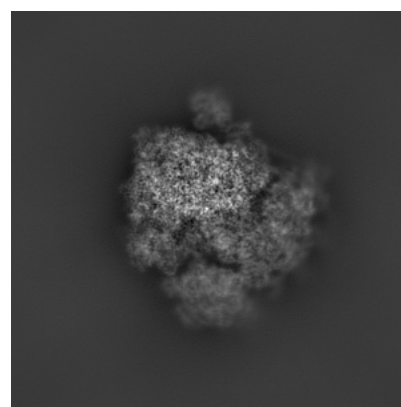
6.1.1 Primary map



X



Y

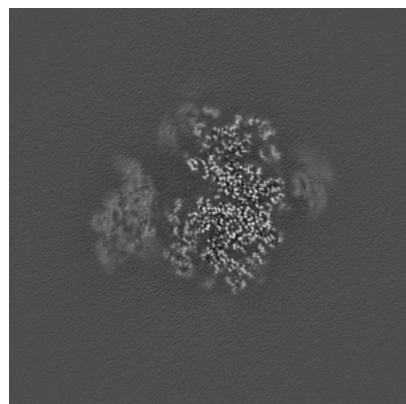


Z

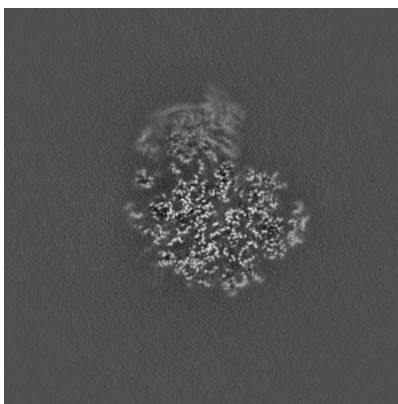
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

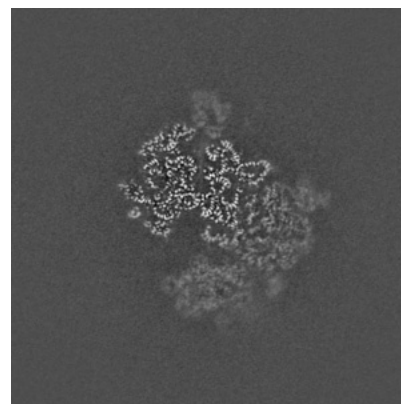
6.2.1 Primary map



X Index: 243



Y Index: 243

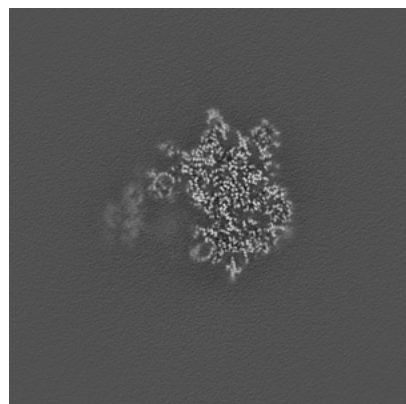


Z Index: 243

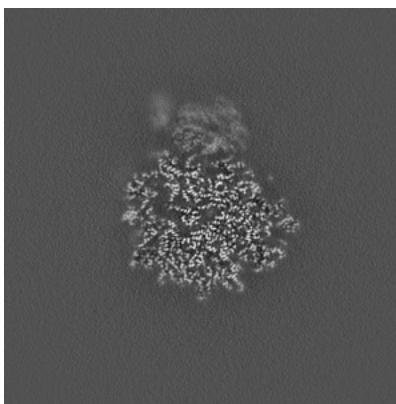
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

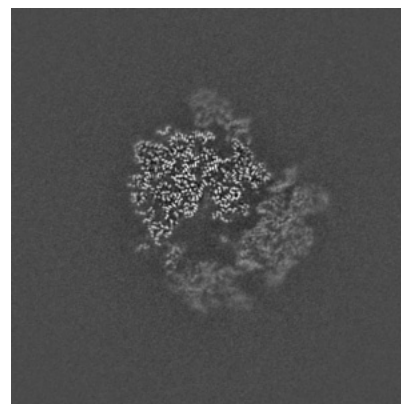
6.3.1 Primary map



X Index: 201



Y Index: 267

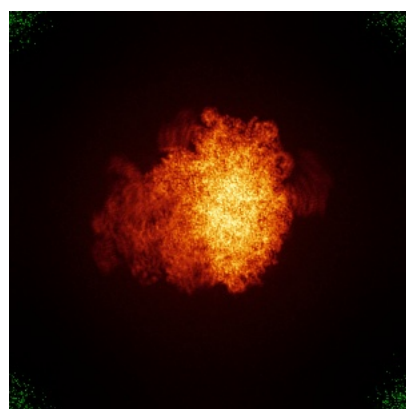


Z Index: 258

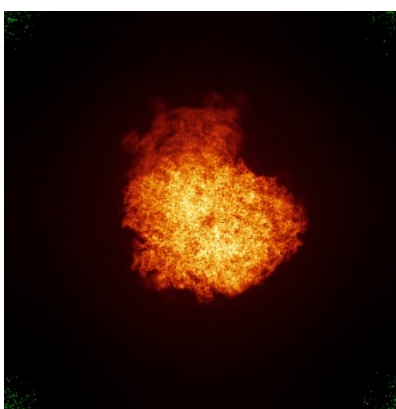
The images above show the largest variance slices of the map in three orthogonal directions.

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

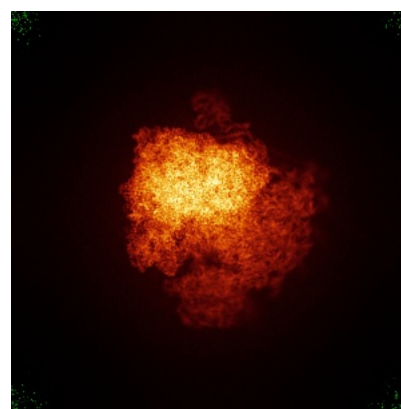
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

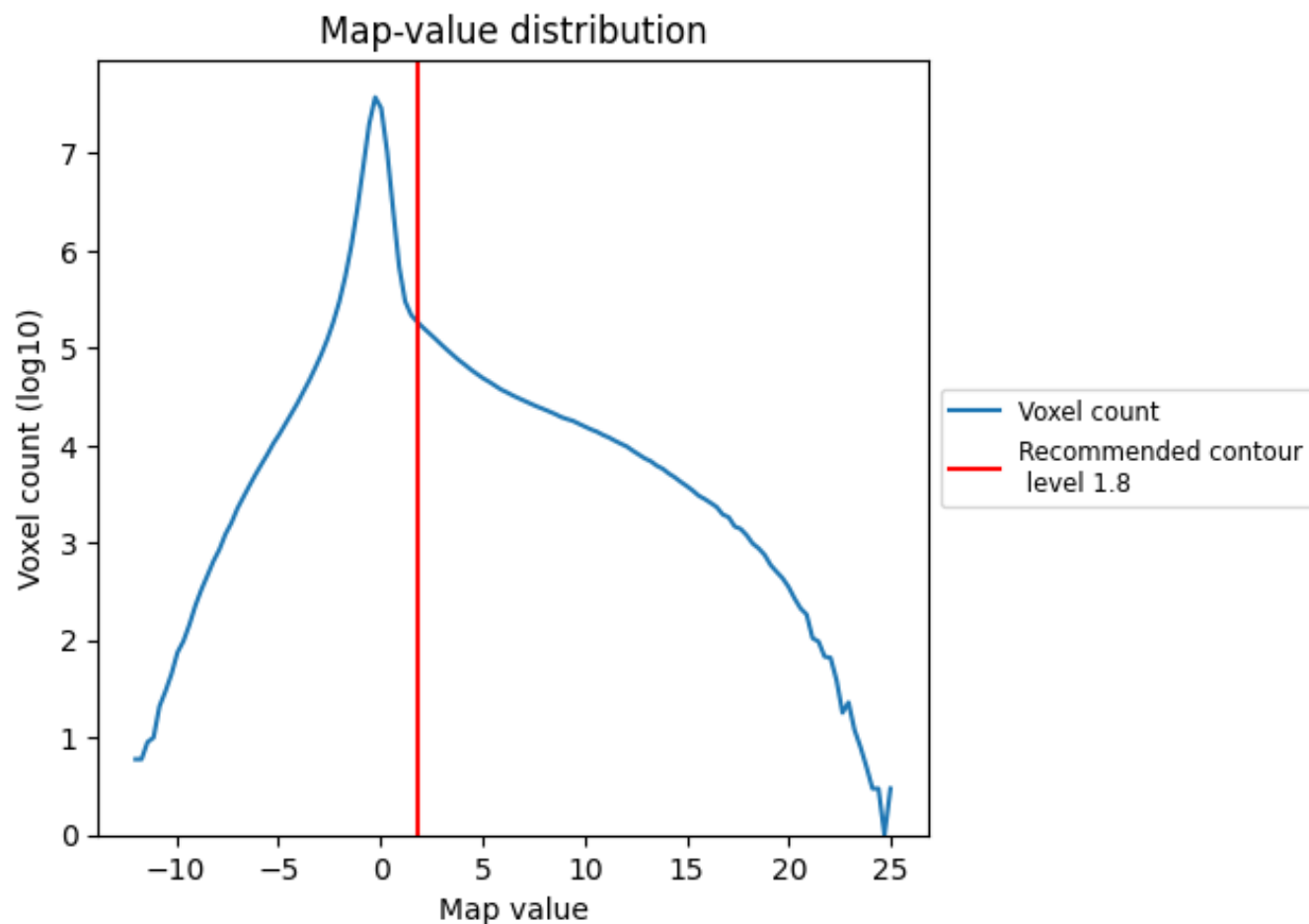
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

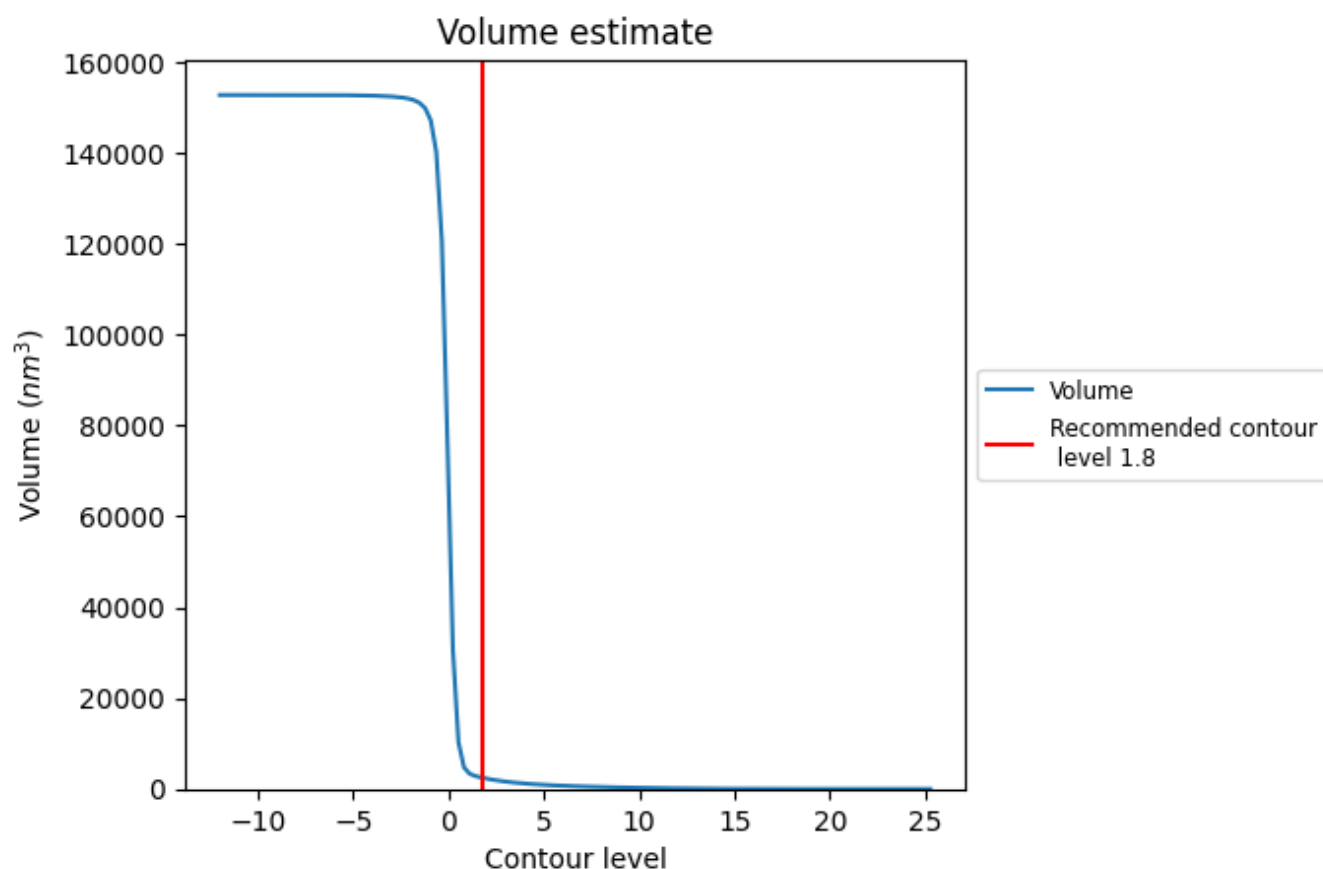
This section contains the results of statistical analysis of the map.

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.

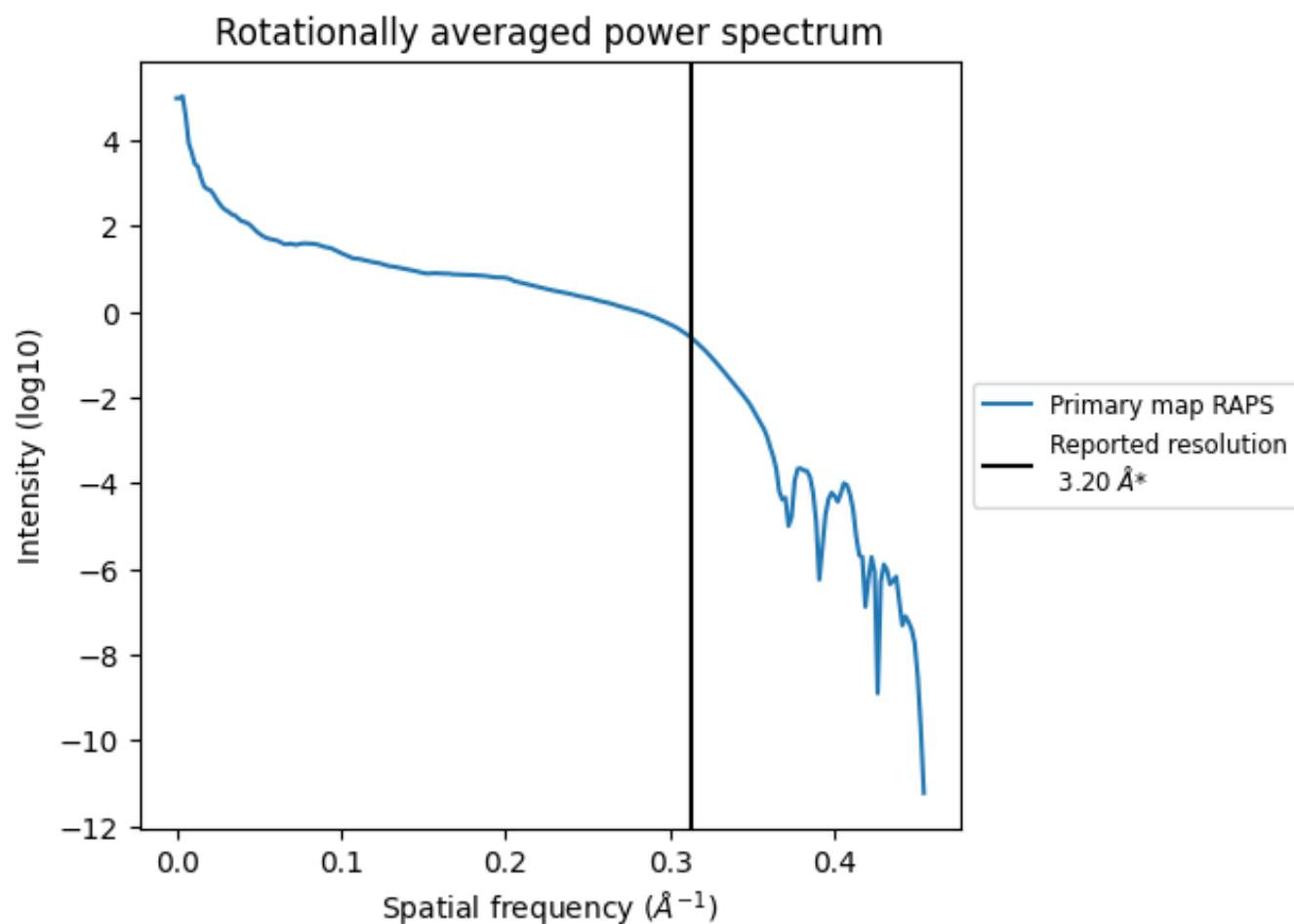
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2455 nm³; this corresponds to an approximate mass of 2218 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 ⓘ

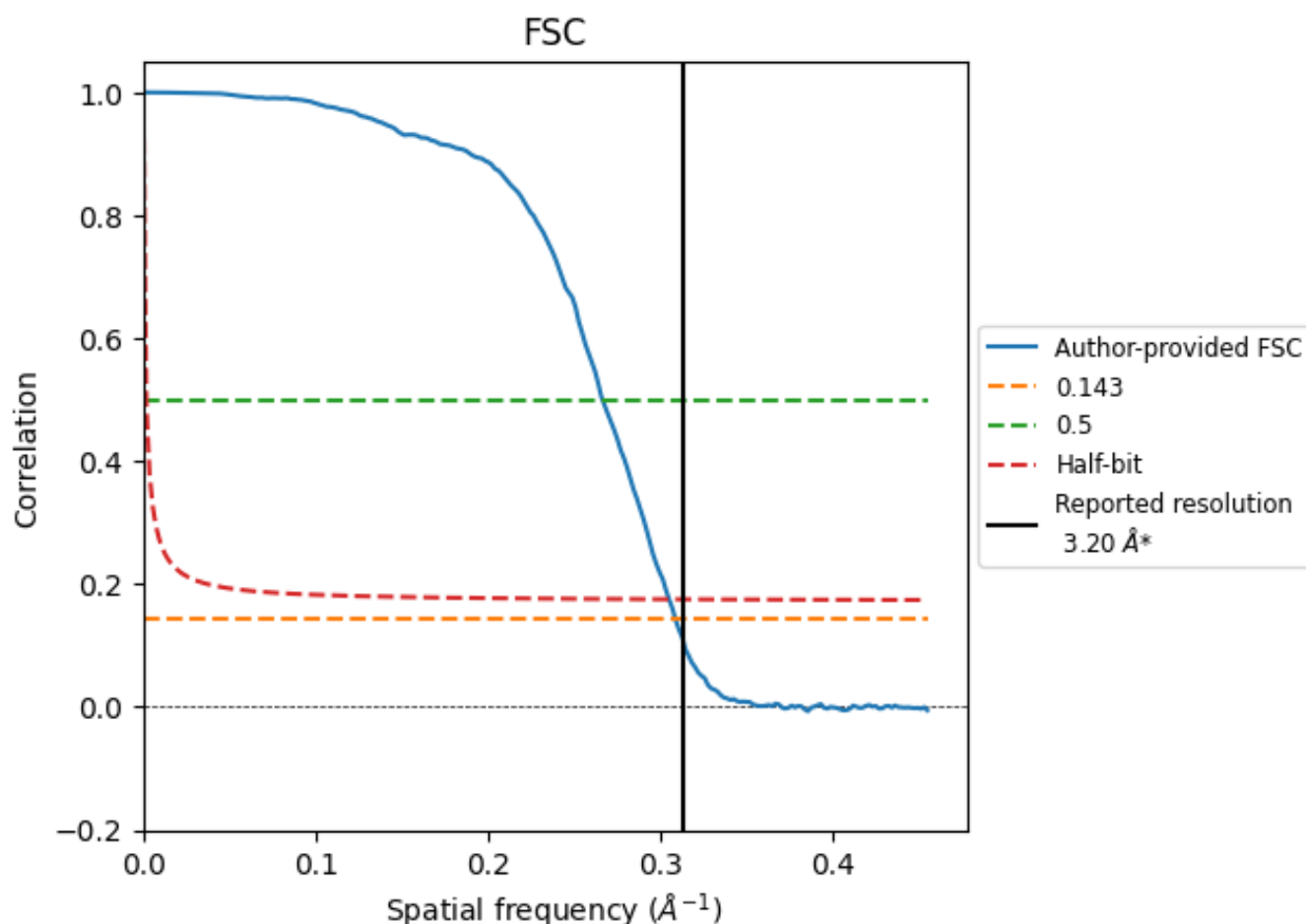


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

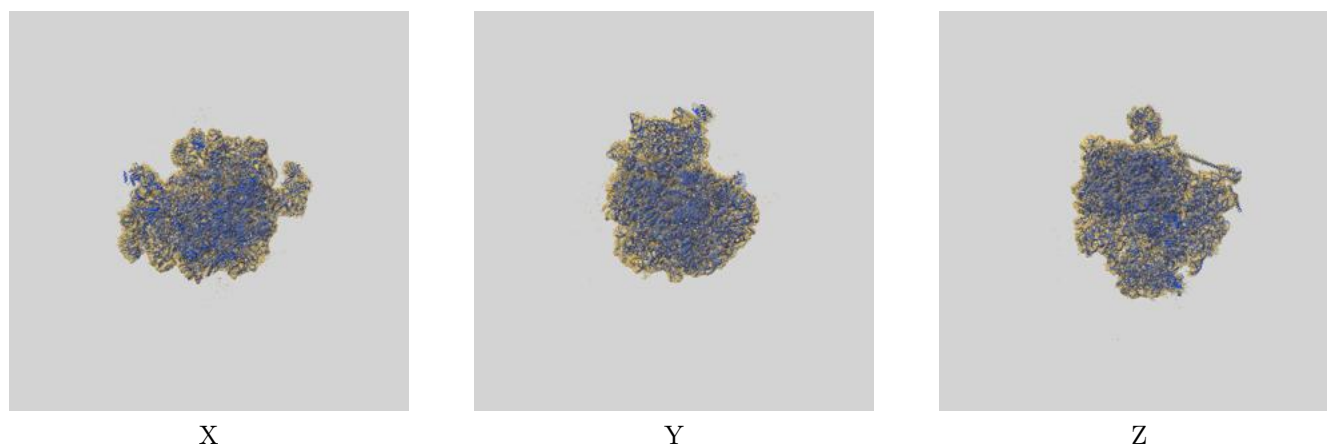
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.24	3.76	3.28
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

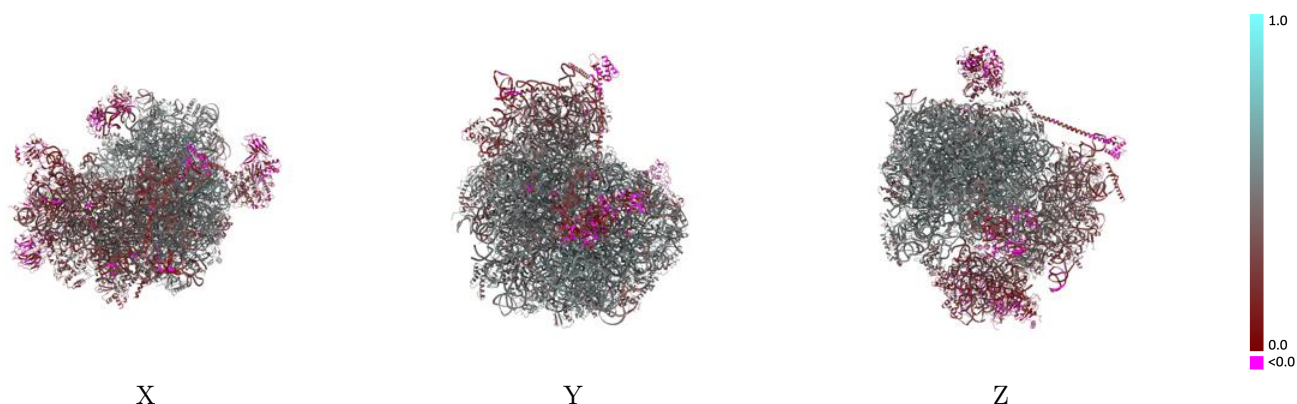
This section contains information regarding the fit between EMDB map EMD-14479 and PDB model 7Z3N. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



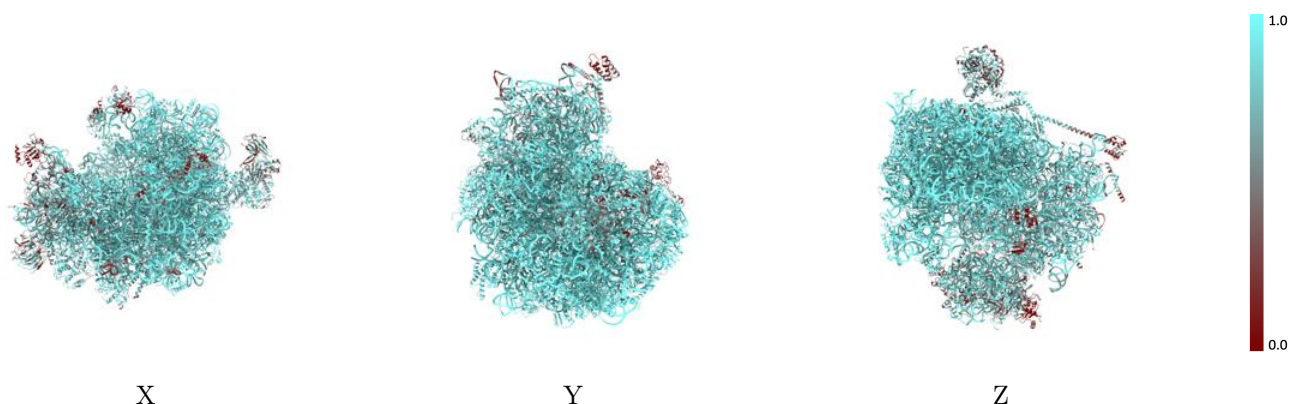
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



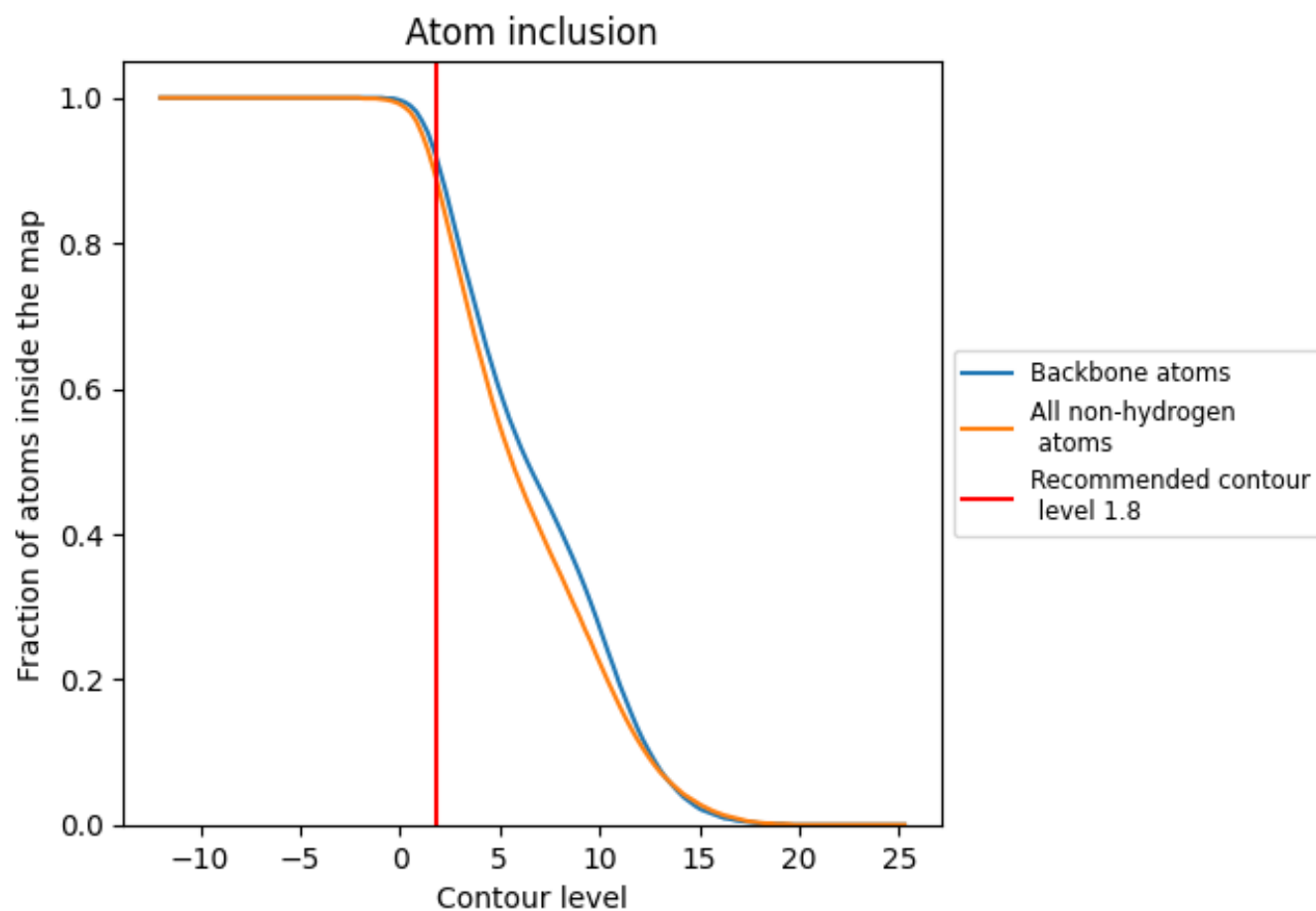
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 89% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.4120
1	 0.9880	 0.4980
2	 0.8990	 0.3370
3	 0.9980	 0.5030
4	 0.9910	 0.5000
A	 0.4790	 0.0780
B	 0.2210	 0.2020
C	 0.6150	 0.1840
D	 0.6300	 0.1330
LA	 0.9210	 0.5190
LB	 0.9500	 0.5120
LC	 0.9510	 0.5120
LD	 0.9420	 0.4510
LE	 0.9410	 0.4580
LF	 0.9420	 0.5010
LG	 0.9370	 0.4780
LH	 0.9400	 0.4780
LI	 0.9170	 0.4930
LJ	 0.9280	 0.4250
LK	 0.5540	 0.0750
LL	 0.9560	 0.4950
LM	 0.9410	 0.4810
LN	 0.9520	 0.5280
LO	 0.9520	 0.5010
LP	 0.8870	 0.4810
LQ	 0.9520	 0.5230
LR	 0.8990	 0.4550
LS	 0.9580	 0.5150
LT	 0.9530	 0.5120
LU	 0.9300	 0.4270
LV	 0.9370	 0.5110
LW	 0.7230	 0.3370
LX	 0.9310	 0.4820
LY	 0.9590	 0.5010
LZ	 0.9470	 0.4850



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Chain	Atom inclusion	Q-score
La	 0.9600	 0.5320
Lb	 0.9250	 0.4680
Lc	 0.9270	 0.4700
Ld	 0.8700	 0.4710
Le	 0.9490	 0.5300
Lf	 0.9540	 0.5330
Lg	 0.9350	 0.5080
Lh	 0.9310	 0.4610
Li	 0.9160	 0.4590
Lj	 0.9540	 0.5340
Lk	 0.8970	 0.4310
Ll	 0.9300	 0.4980
Lm	 0.9560	 0.5050
Ln	 0.7980	 0.4250
Lo	 0.9390	 0.5050
Lp	 0.9030	 0.4970
Lq	 0.9500	 0.5070
Lr	 0.6110	 0.2540
Ls	 0.4020	 0.1260
NC	 0.1630	 0.3150
SA	 0.8330	 0.3400
SB	 0.8310	 0.3800
SC	 0.8080	 0.3360
SD	 0.6140	 0.2280
SE	 0.7390	 0.3350
SF	 0.6190	 0.2630
SG	 0.8100	 0.3030
SH	 0.7880	 0.3120
SI	 0.7820	 0.3660
SJ	 0.7260	 0.3100
SK	 0.6310	 0.1850
SL	 0.7050	 0.3840
SM	 0.1260	 0.1360
SN	 0.8100	 0.3910
SO	 0.8760	 0.4160
SP	 0.6340	 0.1810
SQ	 0.6910	 0.2270
SR	 0.7400	 0.2330
SS	 0.6790	 0.1810
ST	 0.6450	 0.2010
SU	 0.6450	 0.2100
SV	 0.8390	 0.3370

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Chain	Atom inclusion	Q-score
SW	 0.8200	 0.3750
SX	 0.7890	 0.3600
SY	 0.7750	 0.2890
SZ	 0.7070	 0.1960
Sa	 0.8710	 0.4350
Sb	 0.8140	 0.3790
Sc	 0.7630	 0.3220
Sd	 0.6670	 0.2440
Se	 0.8520	 0.3280
Sf	 0.6220	 0.1060