



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 01:57 AM UTC

PDB ID : 7CPV / pdb_00007cpv
EMDB ID : EMD-30433
Title : Cryo-EM structure of 80S ribosome from mouse testis
Authors : Huo, Y.G.; He, X.; Jiang, T.; Qin, Y.; Guo, X.J.; Sha, J.H.
Deposited on : 2020-08-08
Resolution : 3.03 Å(reported)

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:

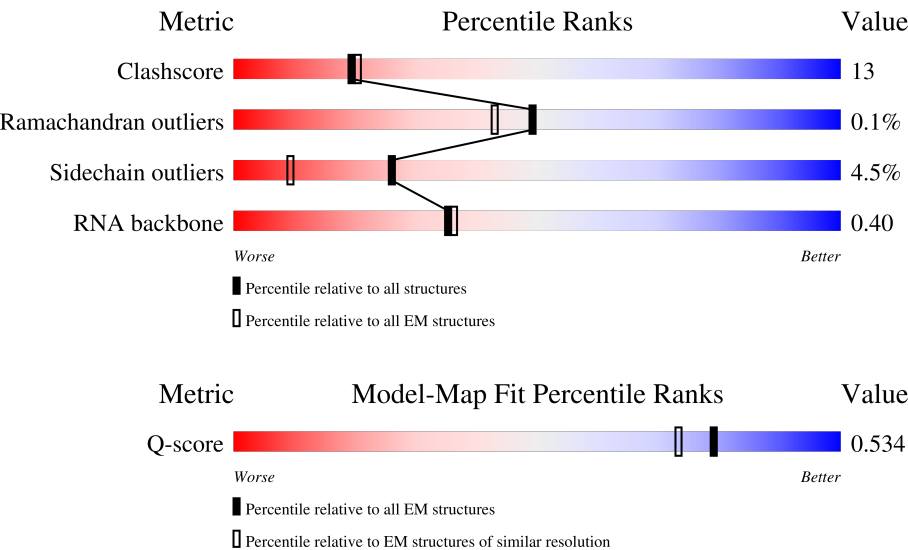
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.03 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.



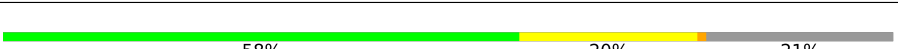
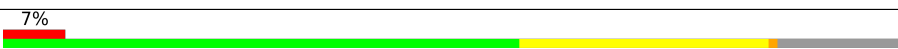
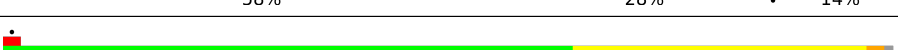
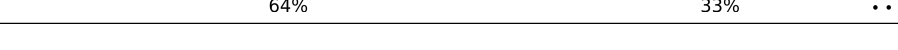
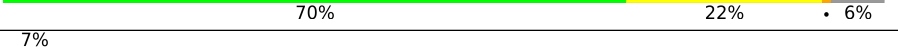
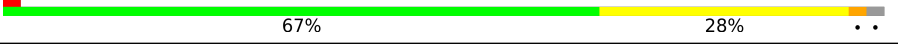
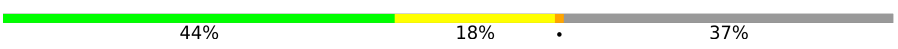
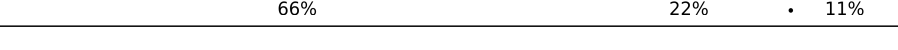
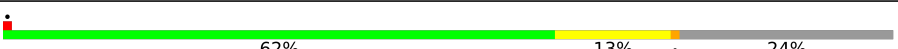
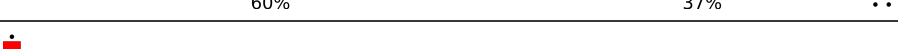
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13929 (2.53 - 3.53)

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	LA	257	72%23%••
2	LB	403	65%32%••
3	LC	419	65%21%•14%

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Mol	Chain	Length	Quality of chain
4	LD	297	
5	LE	296	
6	LF	270	
7	LG	266	
8	LH	192	
9	LI	214	
10	LJ	178	
11	LL	211	
12	LM	217	
13	LN	204	
14	LO	203	
15	LP	184	
16	LQ	188	
17	LR	196	
18	LS	176	
19	LT	160	
20	LU	128	
21	LV	140	
22	LW	157	
23	LX	156	
24	LY	145	
25	LZ	136	
26	La	148	
27	Lb	160	
28	Lc	115	

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Mol	Chain	Length	Quality of chain
29	Ld	125	
30	Le	135	
31	Lf	110	
32	Lg	117	
33	Lh	123	
34	Li	105	
35	Lj	97	
36	Lk	70	
37	Ll	51	
38	Lm	128	
39	Ln	25	
40	Lo	106	
41	Lp	92	
42	Lr	137	
43	L5	4731	
44	L7	120	
45	L8	158	
46	S2	1870	
47	SA	295	
48	SB	264	
49	SD	243	
50	SE	263	
51	SF	204	
52	SH	194	
53	SI	208	

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Mol	Chain	Length	Quality of chain
54	SK	165	
55	SL	158	
56	SP	145	
57	SQ	146	
58	SR	135	
59	SS	152	
60	ST	145	
61	SU	119	
62	SV	83	
63	SX	143	
64	Sa	115	
65	Sc	69	
66	Sd	56	
67	Sg	317	
68	SC	293	
69	SG	249	
70	SJ	194	
71	SN	151	
72	SO	151	
73	SW	130	
74	SY	133	
75	SZ	125	
76	Sb	84	
77	Se	133	
78	S6	75	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 206030 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 protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	397	Total	C	N	O	S	0	0
			3202	2039	603	546	14		

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	362	Total	C	N	O	S	0	0
			2891	1819	577	480	15		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	293	Total	C	N	O	S	0	0
			2385	1506	440	425	14		

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	231	Total	C	N	O	S	0	0
			1874	1195	358	317	4		

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	214	Total	C	N	O	S	0	0
			1771	1139	337	287	8		

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LG	229	Total	C	N	O	S	0	0
			1848	1179	354	311	4		

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	190	Total	C	N	O	S	0	0
			1519	956	284	273	6		

- Molecule 9 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	201	Total	C	N	O	S	0	0
			1631	1037	316	267	11		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	171	Total	C	N	O	S	0	0
			1371	866	255	244	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LL	206	Total	C	N	O	S	0	0
			1667	1043	343	277	4		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LM	136	Total	C	N	O	S	0	0
			1125	721	218	179	7		

- Molecule 13 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LO	201	Total	C	N	O	S	0	0
			1640	1055	320	259	6		

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LP	154	Total	C	N	O	S	0	0
			1251	782	243	217	9		

- Molecule 16 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LQ	187	Total	C	N	O	S	0	0
			1515	948	314	249	4		

- Molecule 17 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LR	174	Total	C	N	O	S	0	0
			1457	901	316	231	9		

- Molecule 18 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LS	175	Total	C	N	O	S	0	0
			1451	924	283	234	10		

- Molecule 19 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LT	160	Total	C	N	O	S	0	0
			1307	829	253	218	7		

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LU	100	Total	C	N	O	S	0	0
			817	523	143	149	2		

- Molecule 21 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 22 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LW	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 23 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LY	132	Total	C	N	O	S	0	0
			1102	692	223	184	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	La	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 27 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Lb	99	Total	C	N	O	S	0	0
			807	505	174	124	4		

- Molecule 28 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lc	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ld	108	Total	C	N	O	S	0	0
			896	566	172	156	2		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lf	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lg	110	Total	C	N	O	S	0	0
			873	546	180	141	6		

- Molecule 33 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lh	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 35 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lk	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 37 is a protein called Ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ll	50	Total	C	N	O	S	0	0
			438	279	93	64	2		

- Molecule 38 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 39 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lr	124	Total	C	N	O	S	0	0
			994	616	206	167	5		

- Molecule 43 is a RNA chain called Mus musculus 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	L5	3541	Total	C	N	O	P	0	0
			75913	33809	13873	24691	3540		

- Molecule 44 is a RNA chain called Mus musculus 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a RNA chain called Mus musculus 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 46 is a RNA chain called Mus musculus 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1637	Total	C	N	O	P	0	0
			34941	15601	6275	11429	1636		

- Molecule 47 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	207	Total	C	N	O	S	0	0
			1636	1042	288	298	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD	224	Total	C	N	O	S	0	0
			1744	1111	314	312	7		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SF	179	Total	C	N	O	S	0	0
			1416	888	262	259	7		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	180	Total	C	N	O	S	0	0
			1449	924	266	258	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	183	Total	C	N	O	S	0	0
			1499	943	293	258	5		

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SK	90	Total	C	N	O	S	0	0
			760	495	135	124	6		

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SL	135	Total	C	N	O	S	0	0
			1110	708	207	189	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SP	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SQ	139	Total	C	N	O	S	0	0
			1109	704	210	192	3		

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SR	131	Total	C	N	O	S	0	0
			1064	668	198	194	4		

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SS	140	Total	C	N	O	S	0	0
			1157	728	231	197	1		

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	ST	140	Total	C	N	O	S	0	0
			1090	681	212	195	2		

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SU	95	Total	C	N	O	S	0	0
			753	471	142	136	4		

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SV	81	Total	C	N	O	S	0	0
			619	379	116	119	5		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SX	139	Total	C	N	O	S	0	0
			1080	682	214	181	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Sa	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Sc	54	Total	C	N	O	S	0	0
			416	257	80	77	2		

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sd	54	Total	C	N	O	S	0	0
			455	284	93	73	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sg	276	Total	C	N	O	S	0	0
			2148	1357	378	401	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SC	215	Total	C	N	O	S	1	0
			1673	1085	288	291	9		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SG	204	Total	C	N	O	S	0	0
			1645	1029	330	280	6		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SJ	138	Total	C	N	O	S	0	0
			1162	743	230	187	2		

- Molecule 71 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 72 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 73 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	110	Total	C	N	O	S	0	0
			891	565	173	149	4		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ	72	Total	C	N	O	S	0	0
			574	368	104	101	1		

- Molecule 76 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	48	Total	C	N	O	S	0	0
			384	234	86	63	1		

- Molecule 78 is a RNA chain called Met-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	LN	1	Total	Mg	0
			1	1	
79	LP	1	Total	Mg	0
			1	1	
79	LT	1	Total	Mg	0
			1	1	
79	LV	1	Total	Mg	0
			1	1	
79	Le	1	Total	Mg	0
			1	1	
79	Lf	1	Total	Mg	0
			1	1	
79	L5	173	Total	Mg	0
			173	173	
79	L7	3	Total	Mg	0
			3	3	
79	L8	5	Total	Mg	0
			5	5	
79	S2	59	Total	Mg	0
			59	59	
79	SF	1	Total	Mg	0
			1	1	

- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	Lg	1	Total	Zn	0
			1	1	
80	Lj	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
80	Lm	1	Total 1	Zn 1	0
80	Lo	1	Total 1	Zn 1	0
80	Lp	1	Total 1	Zn 1	0
80	Sa	1	Total 1	Zn 1	0
80	Sd	1	Total 1	Zn 1	0

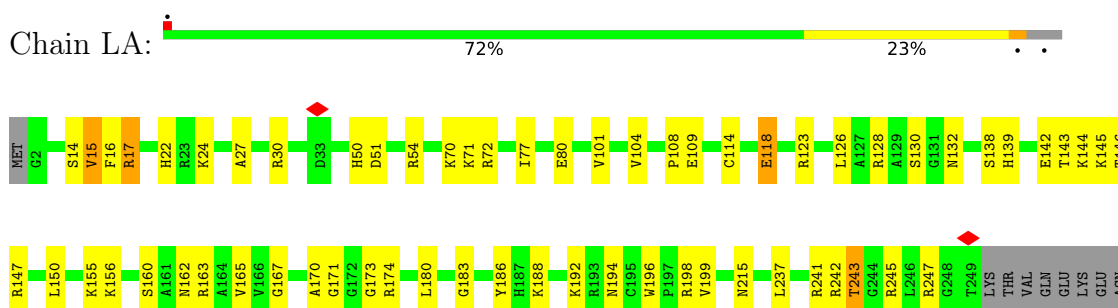
- Molecule 81 is water.

Mol	Chain	Residues	Atoms		AltConf
81	LB	1	Total 1	O 1	0
81	LH	1	Total 1	O 1	0
81	LI	2	Total 2	O 2	0
81	LN	1	Total 1	O 1	0
81	La	1	Total 1	O 1	0
81	L5	7	Total 7	O 7	0
81	S2	2	Total 2	O 2	0

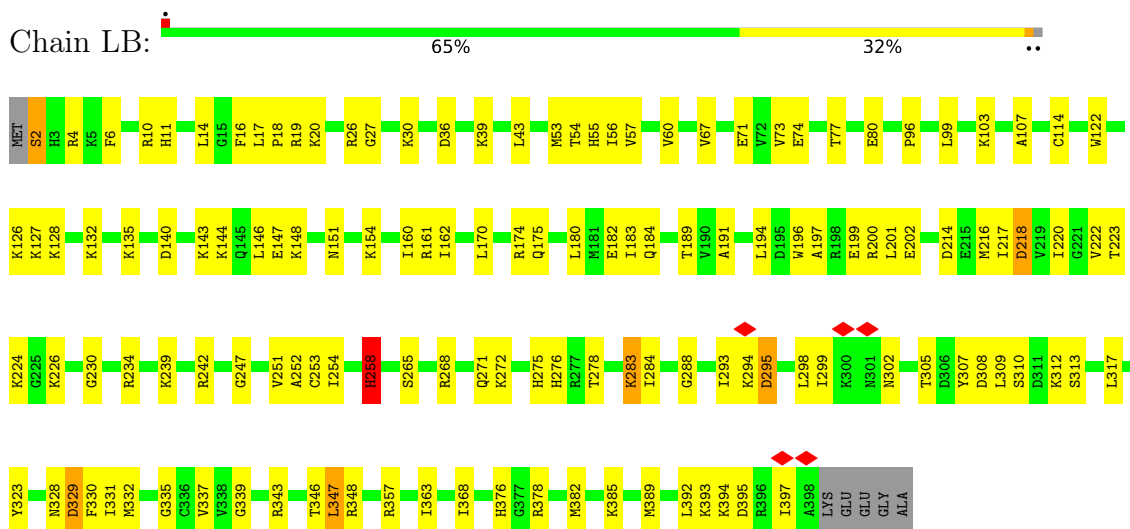
3 Residue-property plots

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.

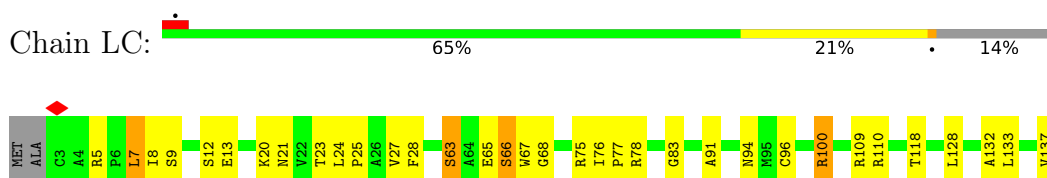
- Molecule 1: 60S ribosomal protein L8

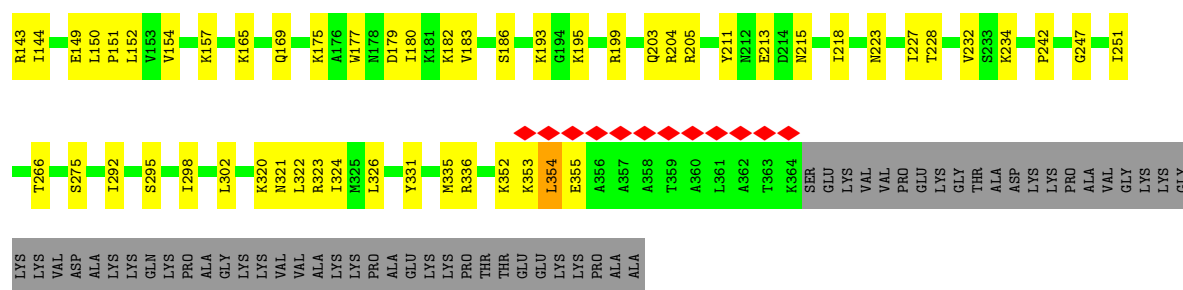


- Molecule 2: 60S ribosomal protein L3



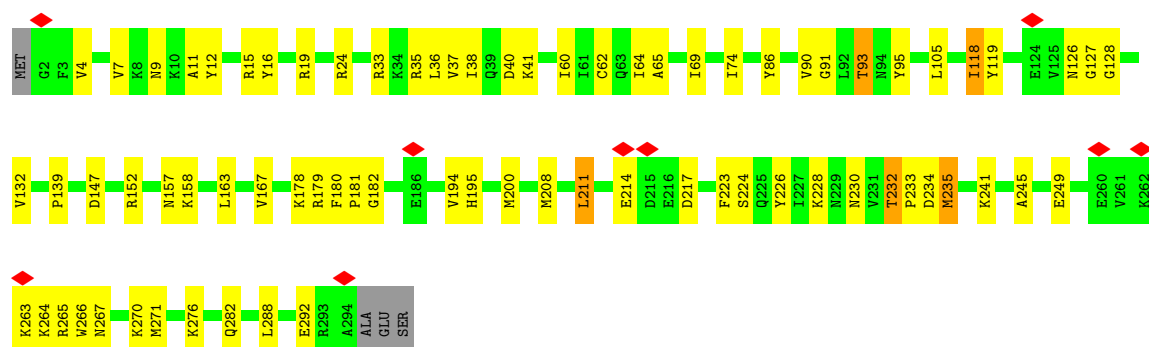
- Molecule 3: 60S ribosomal protein L4





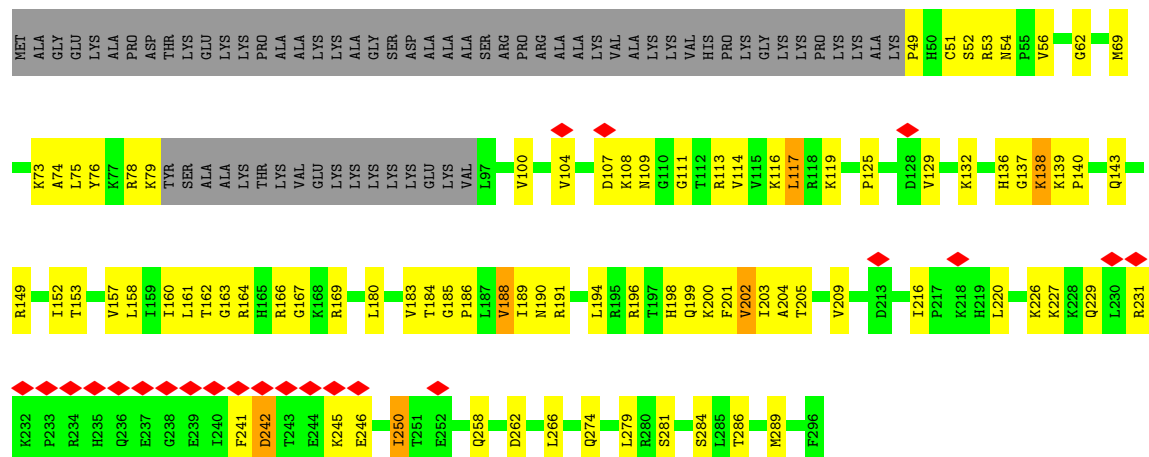
• Molecule 4: 60S ribosomal protein L5

Chain LD: 73% 24%



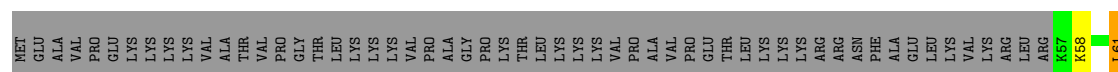
• Molecule 5: 60S ribosomal protein L6

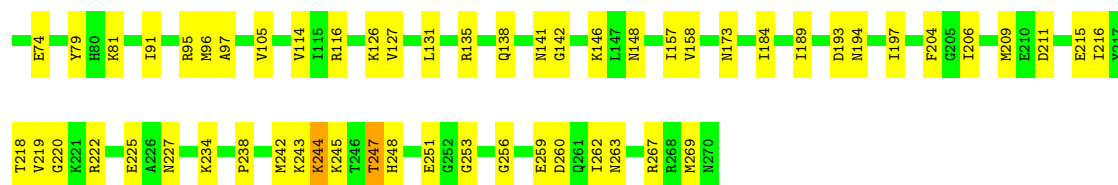
Chain LE: 49% 27% 22%



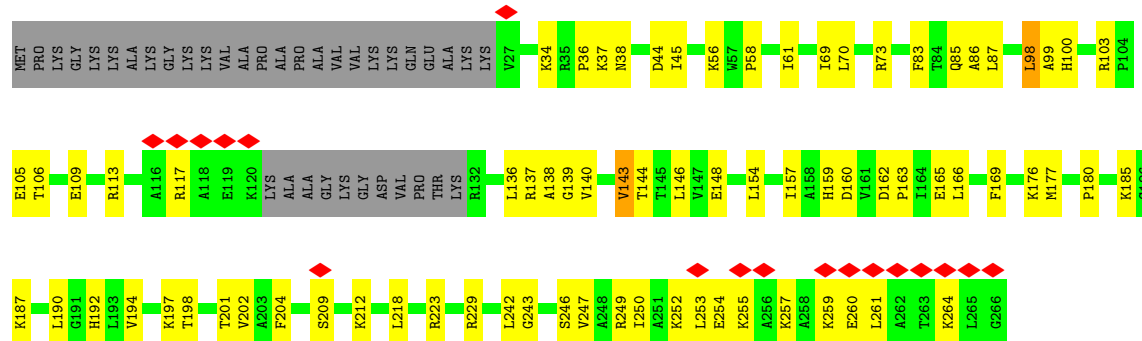
• Molecule 6: 60S ribosomal protein L7

Chain LF: 58% 20% 21%

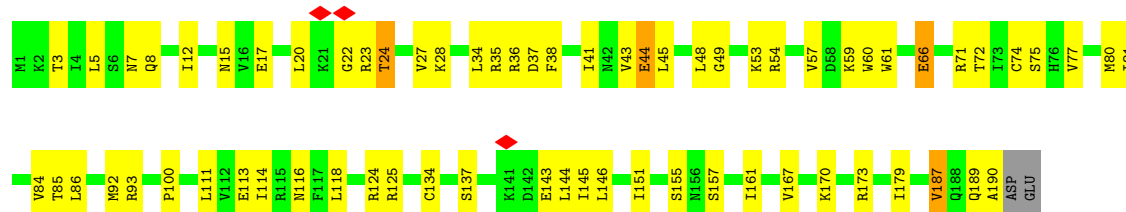




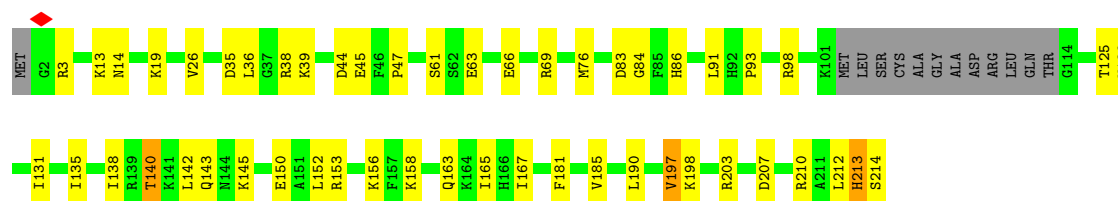
• Molecule 7: 60S ribosomal protein L7a



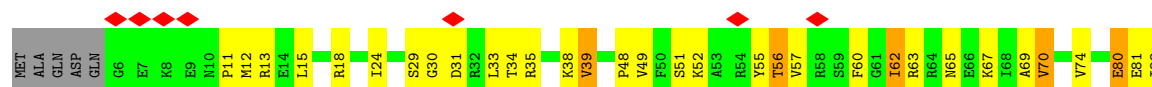
• Molecule 8: 60S ribosomal protein L9

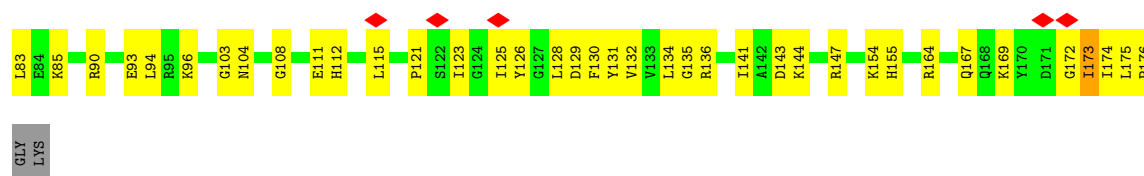


• Molecule 9: 60S ribosomal protein L10-like

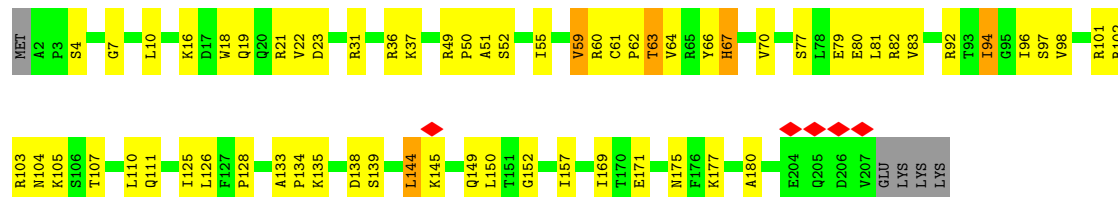


• Molecule 10: 60S ribosomal protein L11

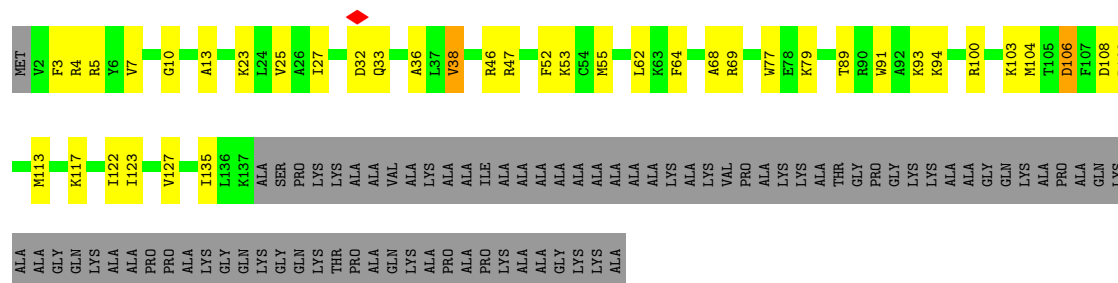




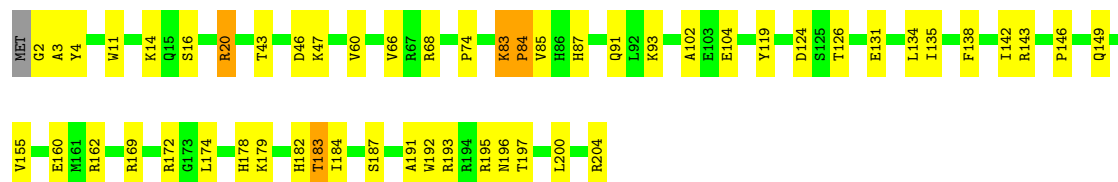
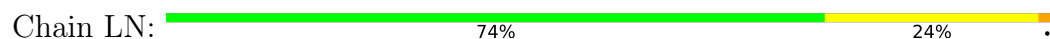
- Molecule 11: 60S ribosomal protein L13



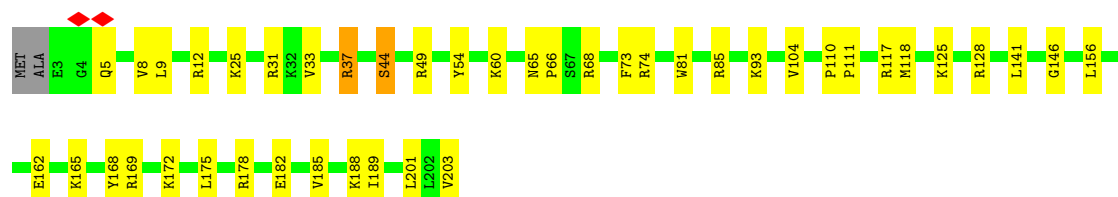
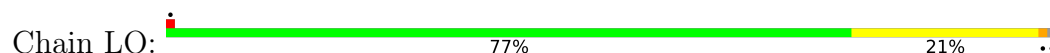
- Molecule 12: 60S ribosomal protein L14

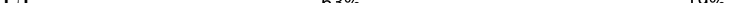


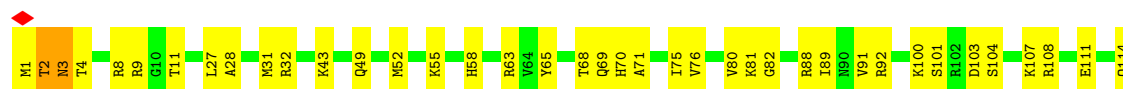
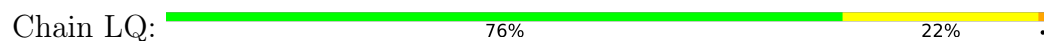
- Molecule 13: 60S ribosomal protein L15

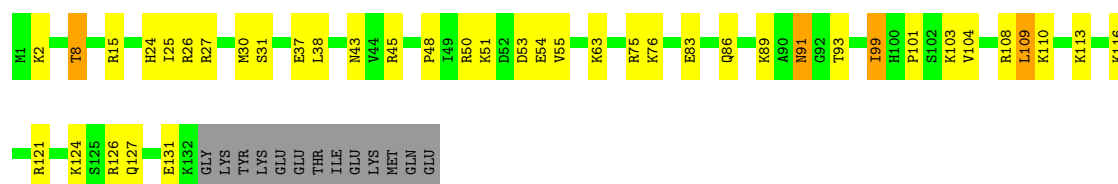


- Molecule 14: 60S ribosomal protein L13a

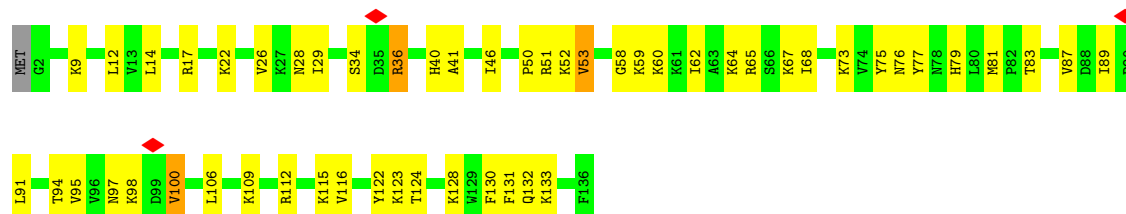


- Chain LP:  63% 19% 16%

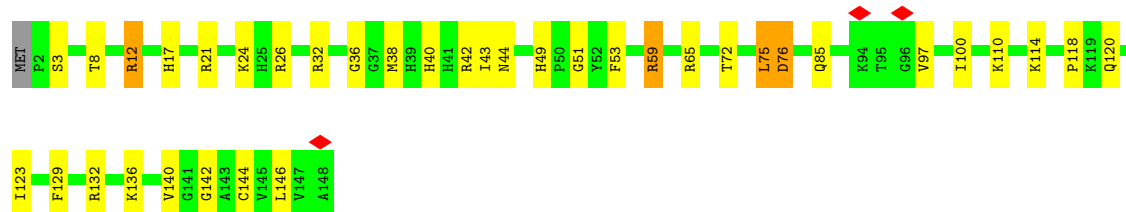
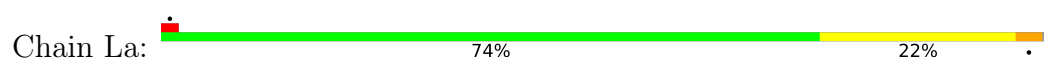




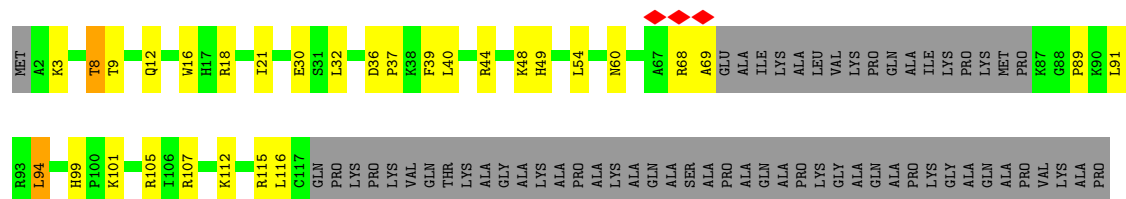
- Molecule 25: 60S ribosomal protein L27



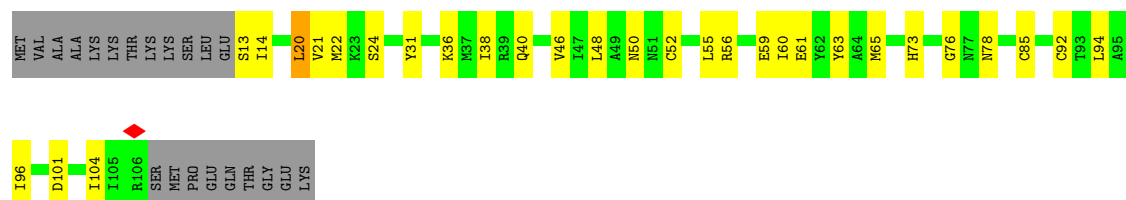
- Molecule 26: 60S ribosomal protein L27a



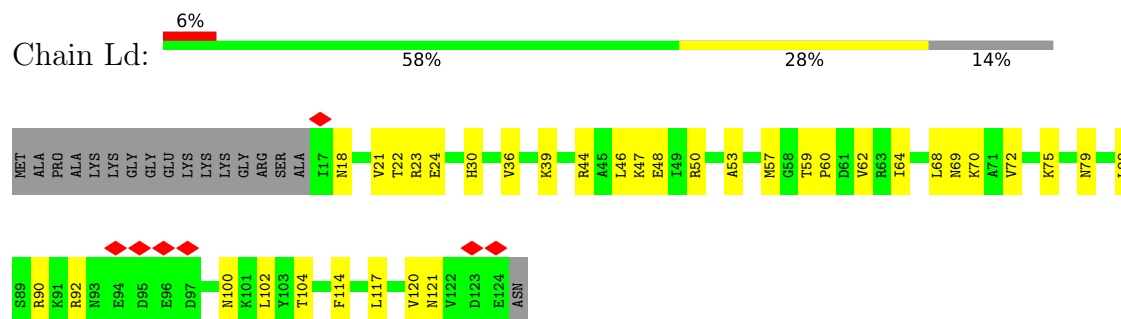
- Molecule 27: 60S ribosomal protein L29



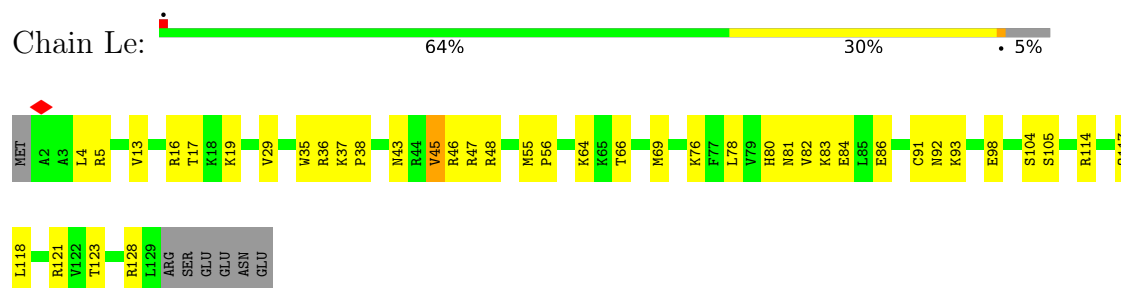
- Molecule 28: 60S ribosomal protein L30



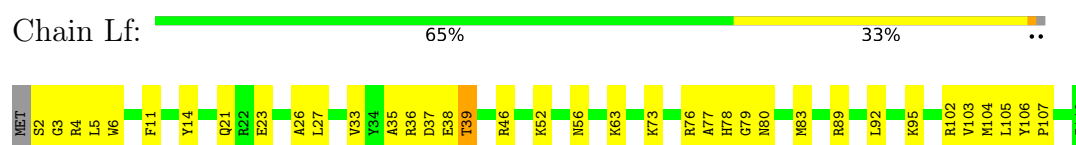
- Molecule 29: 60S ribosomal protein L31



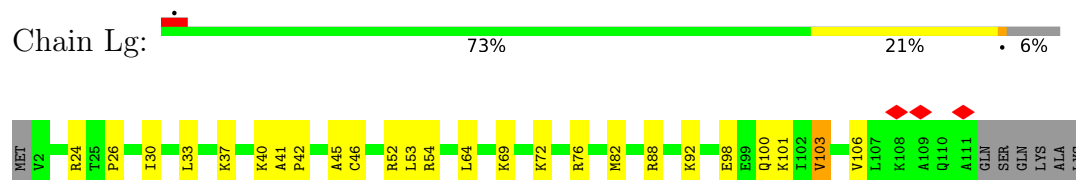
- Molecule 30: 60S ribosomal protein L32



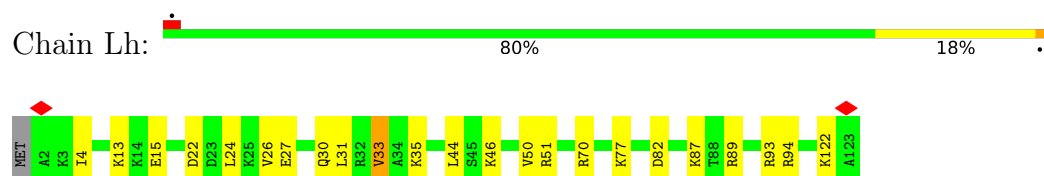
- Molecule 31: 60S ribosomal protein L35a



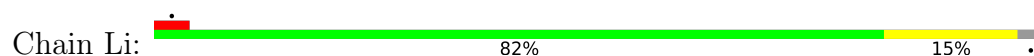
- Molecule 32: 60S ribosomal protein L34



- Molecule 33: 60S ribosomal protein L35



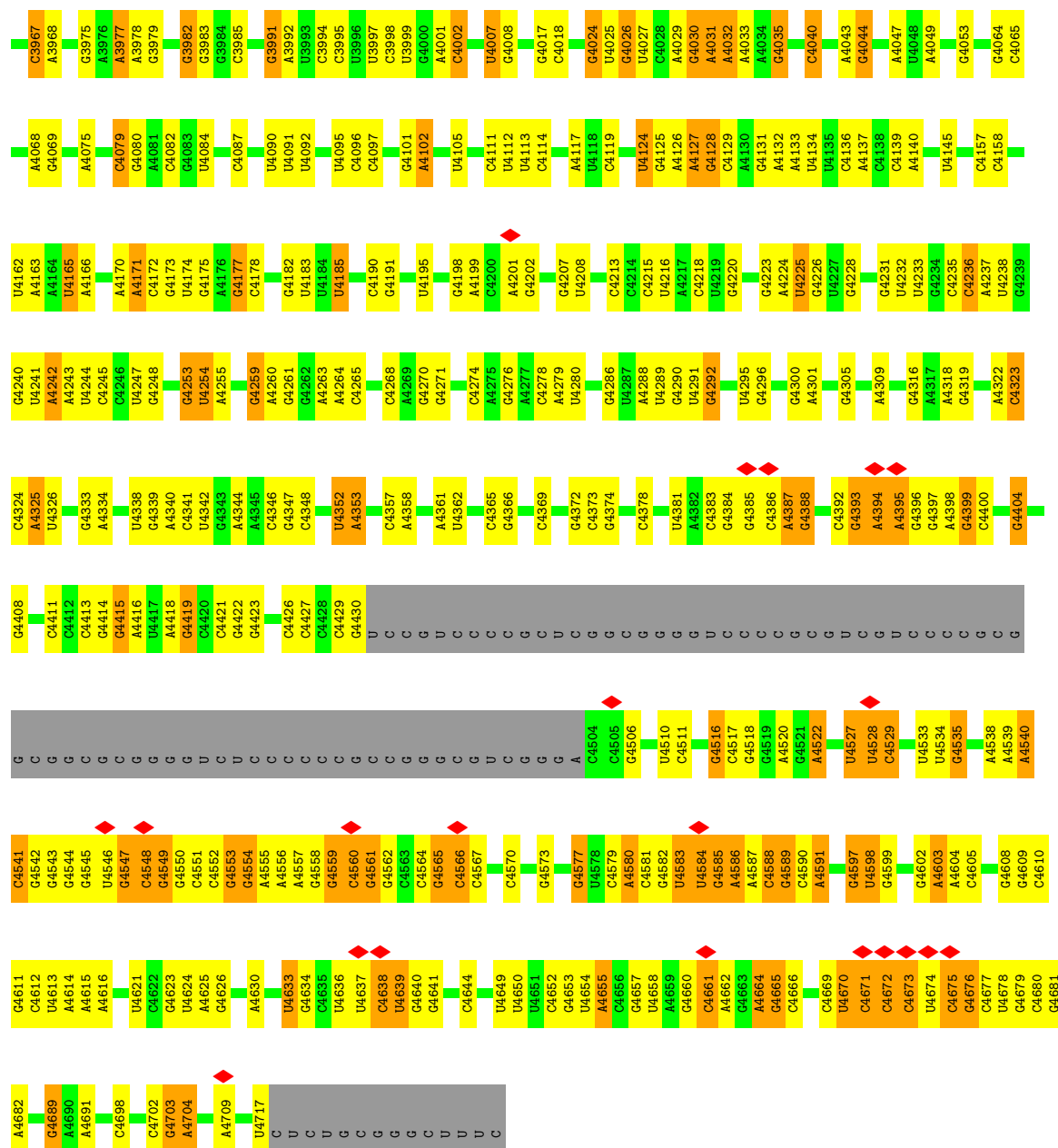
- Molecule 34: 60S ribosomal protein L36



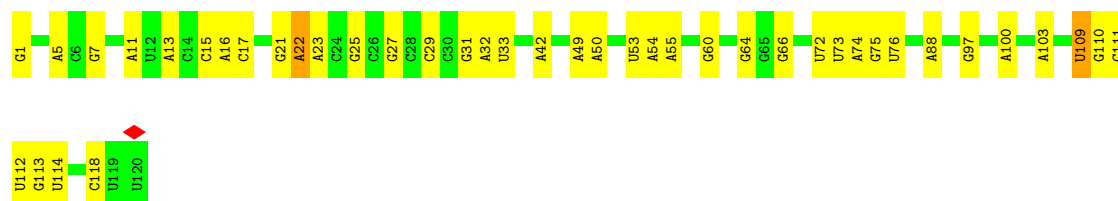


WORLDWIDE
PDB
PROTEIN DATA BANK





• Molecule 44: Mus musculus 5S ribosomal RNA

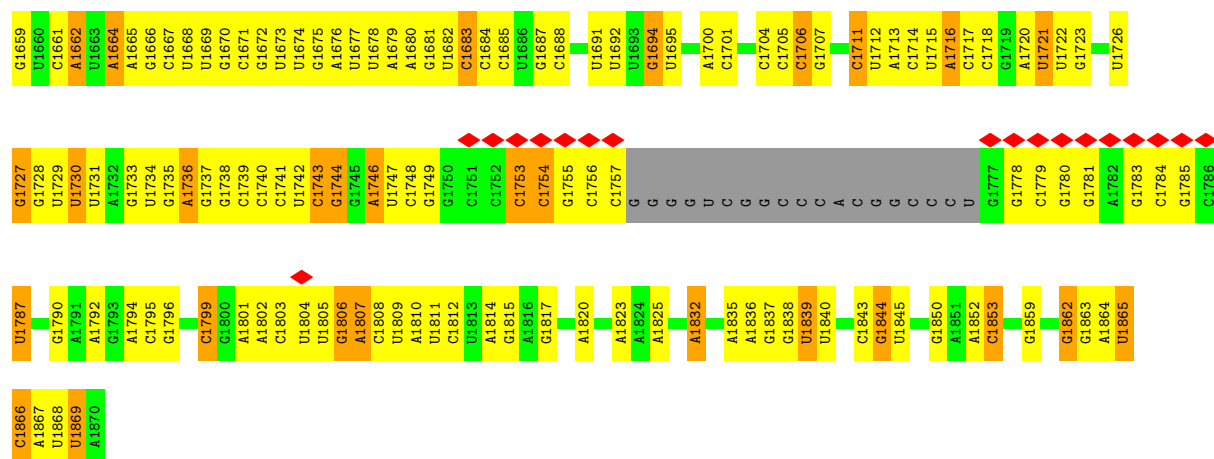


• Molecule 45: Mus musculus 5.8S ribosomal RNA

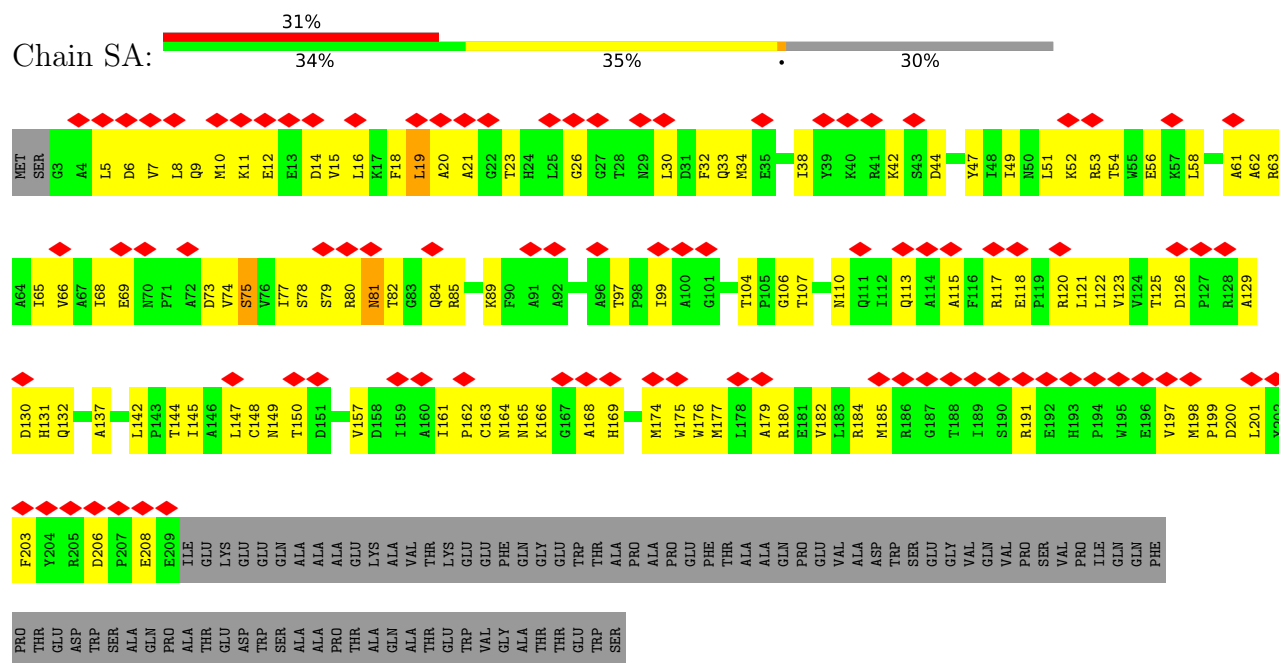




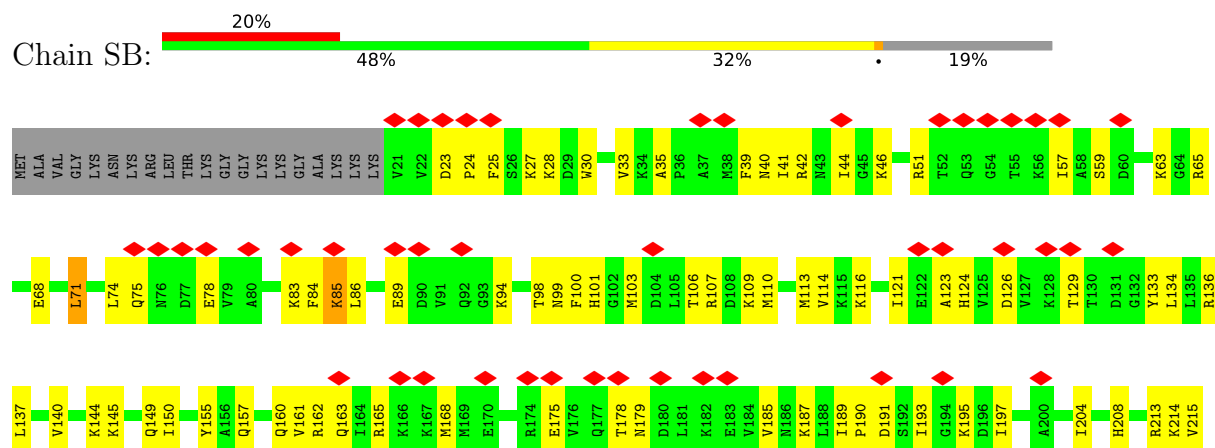
U1587	C1513	U1442	A1370	G1236	U1157	A1088	A1010	G934	A870	C798	G
G1588	C1514	U1445	A1371	G1237	G1158	U1089	G1011	G935	A871	G799	C
A1589	G1515	U1446	U1301	C1238	G1159	G1090	A1012	G943	U872	U800	C
G1590	G1516	U1447	A1302	U1239	U1160	U1091	A1013	U944	A873	U801	C
C1591	C1517	A1448	G1303	U1240	U1161	G1092	U1014	U945	G874	U802	U
G1592	C1518	A1449	C1304	A1241	U1162	G1093	U1015	U946	G875	U806	U
C1593	U1520	G1448	C1305	A1242	G1165	U1094	U1016	U947	A876	U805	G
A1594	G1521	A1449	U1306	U1243	G1166	G1095	U1017	C952	C877	U806	C
U1595	G1522	G1452	C1307	U1244	G1167	G1096	U1018	G953	C878	A810	C
C1596	A1523	U1453	U1308	U1245	U1172	G1097	U1019	G954	G879	A811	U748
G1597	G1524	C1454	U1309	U1246	U1173	U1098	C1020	U955	C879	A812	C749
C1598	G1525	A1455	C1310	C1247	U1174	C1103	A1021	A956	G881	C880	U750
G1599	A1456	A1456	U1311	U1248	U1175	C1104	U1022	G957	G882	A813	C751
U1600	G1457	G1457	C1312	U1249	U1176	U1102	A1023	A958	U883	A814	G
G1601	U1463	U1463	G1313	A1251	C1181	G1103	U1024	U961	U884	A817	G
A1602	U1464	C1465	C1314	A1252	C1182	C1104	U1025	U962	G885	G818	C
C1603	A1466	A1466	G1315	C1253	A1183	C1107	U1026	G963	U886	A819	C
G1604	C1467	C1467	U1316	A1254	G1188	C1110	A1028	A964	U887	G820	G
U1607	U1537	C1472	C1317	C1255	U1189	U1112	G1030	A965	U888	U821	C
C1610	G1538	G1473	G1318	G1256	A1190	U1113	A1031	U969	U889	G822	C
G1614	C1542	C1474	C1319	A1259	U1191	U1114	U1032	U970	U890	U823	U
A1615	G1543	A1475	G1320	U1260	A1192	U1115	A1033	G971	U891	C825	C
U1616	C1544	G1476	U1321	C1261	U1193	U1116	G1034	A973	U892	U824	C
C1617	U1545	C1477	G1322	G1262	A1194	C1117	A1035	U974	G893	A826	G
G1618	A1546	U1478	G1323	U1263	U1195	U1118	U1036	G975	U894	A827	A
C1619	G1547	U1479	U1324	U1264	A1196	C1119	A1037	A976	U895	G828	U
A1620	U1548	A1481	G1325	U1265	U1197	U1120	U1040	G977	C896	C830	C
U1621	G1549	C1482	U1326	A1266	A1198	U1121	U1041	C978	A831	A831	U
G1622	U1550	G1483	U1327	C1267	U1199	C1122	U1042	U979	G832	G832	C
C1623	G1551	C1484	U1328	U1272	A1200	G1125	U1043	A982	G833	G833	U
A1624	U1552	A1485	A1333	C1273	A1201	C1126	G1044	G983	C834	C834	U
G1625	G1553	U1486	U1334	G1274	U1202	G1127	U1045	A984	C835	C835	A
C1626	C1554	A1487	G1335	U1275	G1203	U1130	G1058	G985	C836	C836	G
G1627	U1555	C1488	G1336	G1276	U1204	G1133	A1059	G986	G837	G837	U
C1628	U1556	A1489	C1337	A1277	G1205	C1134	G1060	G987	A838	A838	G
U1629	A1557	C1490	G1338	U1278	A1215	G1135	A1061	U988	G839	G839	A
G1632	G1558	G1491	U1339	C1279	C1216	U1136	U1062	C989	C840	C840	U
C1633	U1561	U1492	U1340	U1280	A1217	G1137	A1063	A991	G841	G841	G
A1634	G1562	C1493	U1341	G1281	U1218	C1139	C1064	G992	C904	C904	U
C1635	U1563	G1494	C1342	U1282	C1219	U1140	U1065	G993	A905	A905	U
G1636	C1564	U1495	U1343	A1283	A1220	G1141	C1076	G994	C906	C906	C
C1637	G1565	U1496	U1344	G1284	G1222	G1142	U1066	C995	U907	U907	C
A1638	U1566	C1497	U1345	C1285	U1223	G1143	G1077	G996	G908	G908	C
G1639	C1567	G1498	G1346	U1286	G1224	A1144	C1078	A997	U909	U909	C
U1640	U1568	A1499	G1347	A1287	A1225	A1145	U1079	A998	G846	G846	C
C1641	G1569	U1500	G1348	G1288	G1226	C1146	C1079	G999	G847	G847	G
G1649	A1570	C1501	U1349	U1289	U1227	U1147	C1080	A1002	U849	U849	G
A1651	G1571	G1502	G1350	A1290	G1228	A1148	U1083	U1005	C852	C852	C
C1652	U1572	C1503	G1351	U1291	U1229	U1149	A1084	U1006	G853	G853	C
G1653	G1573	U1504	U1352	G1292	C1231	A1150	A1085	C1007	C854	C854	U
C1654	U1574	U1505	U1353	U1293	C1232	G1151	U1086	U1008	U858	U858	C
U1655	C1575	A1506	U1354	A1294	U1233	U1152	C1087	C1009	C860	C860	C
G1656	U1576	U1507	U1355	U1295	G1234	U1153	U1088	A1009	A863	A863	U
A1657	A1580	C1508	U1356	G1296	C1235	U1154	U1089	U1010	G869	G869	C
C1658	U1581	U1509	G1357	A1297	U1236	U1155	G1087	U1011			
G1659	G1582	U1510	U1358	U1298	U1237	U1156		U1012			
U1660	U1583	U1511	U1359	U1299	U1238	U1157		U1013			
G1661	G1584	U1512	U1360	U1300	U1299	U1158		U1014			
A1662	U1585	U1513	U1361	U1301	U1300	U1159		U1015			
C1663	U1586	U1514	U1362	U1302	U1301	U1160		U1016			
U1664	G1587	U1515	U1363	U1303	U1302	U1161		U1017			
G1665	A1588	U1516	U1364	U1304	U1303	U1162		U1018			
C1666	U1589	U1517	U1365	U1305	U1304	U1163		U1019			
U1667	G1590	U1518	U1366	U1306	U1305	U1164		U1020			
G1668	U1591	U1519	U1367	U1307	U1306	U1165		U1021			
U1669	G1592	U1520	U1368	U1308	U1307	U1166		U1022			
C1670	U1593	U1521	U1369	U1309	U1308	U1167		U1023			
A1671	G1594	U1522	U1370	U1310	U1309	U1168		U1024			
G1672	U1595	U1523	U1371	U1311	U1310	U1169		U1025			
C1673	C1596	U1524	U1372	U1312	U1311	U1170		U1026			
U1674	U1597	A1525	U1373	U1313	U1312	U1171		U1027			
G1675	G1598	U1526	U1374	U1314	U1313	U1172		U1028			
C1676	U1599	U1527	U1375	U1315	U1314	U1173		U1029			
U1677	G1600	U1528	U1376	U1316	U1315	U1174		U1030			
G1678	A1601	U1529	U1377	U1317	U1316	U1175		U1031			
C1679	C1602	U1530	U1378	U1318	U1317	U1176		U1032			
U1680	U1603	U1531	U1379	U1319	U1318	U1177		U1033			
A1681	G1604	U1532	U1380	U1320	U1319	U1178		U1034			
C1682	U1607	U1533	U1381	U1321	U1320	U1179		U1035			
G1683	G1608	U1534	U1382	U1322	U1321	U1180		U1036			
U1684	A1609	U1535	U1383	U1323	U1322	U1181		U1037			
C1685	C1610	U1536	U1384	U1324	U1323	U1182		U1038			
G1686	U1611	U1537	U1385	U1325	U1324	U1183		U1039			
A1687	G1612	U1538	U1386	U1326	U1325	U1184		U1040			
C1688	C1613	U1539	U1387	U1327	U1326	U1185		U1041			
U1689	U1614	U1540	U1388	U1328	U1327	U1186		U1042			
G1690	A1615	U1541	U1389	U1329	U1328	U1187		U1043			
C1691	G1616	U1542	U1390	U1330	U1329	U1188		U1044			
U1692	U1617	U1543	U1391	U1331	U1330	U1189		U1045			
A1693	C1618	U1544	U1392	U1332	U1331	U1190		U1046			
C1694	G1619	U1545	U1393	U1333	U1332	U1191		U1047			
U1695	U1620	U1546	U1394	U1334	U1333	U1192		U1048			
G1696	A1621	U1547	U1395	U1335	U1334	U1193		U1049			
C1697	C1622	U1548	U1396	U1336	U1335	U1194		U1050			
U1698	U1623	U1549	U1397	U1337	U1336	U1195		U1051			
A1699	G1624	U1550	U1398	U1338	U1337	U1196		U1052			
C1700	U1625	U1551	U1399	U1339	U1338	U1197		U1053			
U1701	C1626	U1552	U1400	U1340	U1339	U1198		U1054			
G1702	U1627	U1553	U1401	U1341	U1340	U1199		U1055			
C1703	A1628	U1554	U1402	U1342	U1341	U1200		U1056			
U1704	G1629	U1555	U1403	U1343	U1342	U1201		U1057			
A1705	U1630	U1556	U1404	U1344	U1343	U1202		U1058			
C1706	C1631	U1557	U1405	U1345	U1344	U1203		U1059			
U1707	U1632	U1558	U1406	U1346	U1345	U1204		U1060			
A1708	G1633	U1559	U1407	U1347	U1346	U1205		U1061			
C1709	U1634	U1560	U1408	U1348	U1347	U1206		U1062			
U1710	A1635	U1561	U1409	U1349	U1348	U1207		U1063			
G1711	C1636	U1562	U1410	U1350	U1349	U1208		U1064			
C1712	U1637	U1563	U1411	U1351	U1350	U1209		U1065			
U1713	A1638	U1564	U1412	U1352	U1351	U1210		U1066			
G1714	G1639	U1565	U1413	U1353	U1352	U1211		U1067			
A1715	U1640	U1566	U1414	U1354	U1353	U1212		U1068			
C1716	C1641	U1567	U1415	U1355	U1354	U1213		U1069			
U1717	U1642	U1568	U1416	U1356	U1355	U1214		U1070			
G1718	A1643	U1569	U1417	U1357	U1356	U1215		U1071			
C1719	C1644	U1570	U1418	U1358	U1357	U1216		U1072			
U1720	U1645	U1571	U1419	U1359	U1358	U1217		U1073			
A1721	G1646	U1572	U1420	U1360	U1359	U1218		U1074			
C1722	A1647	U									

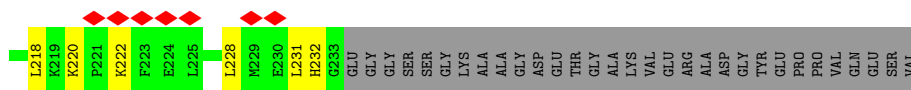


• Molecule 47: 40S ribosomal protein SA

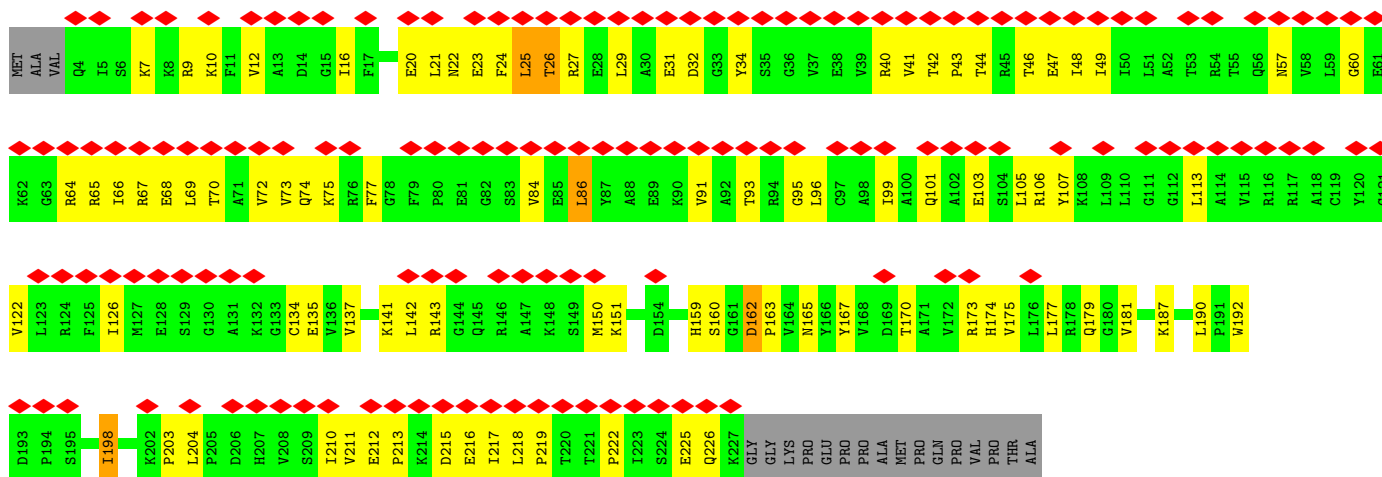


• Molecule 48: 40S ribosomal protein S3a

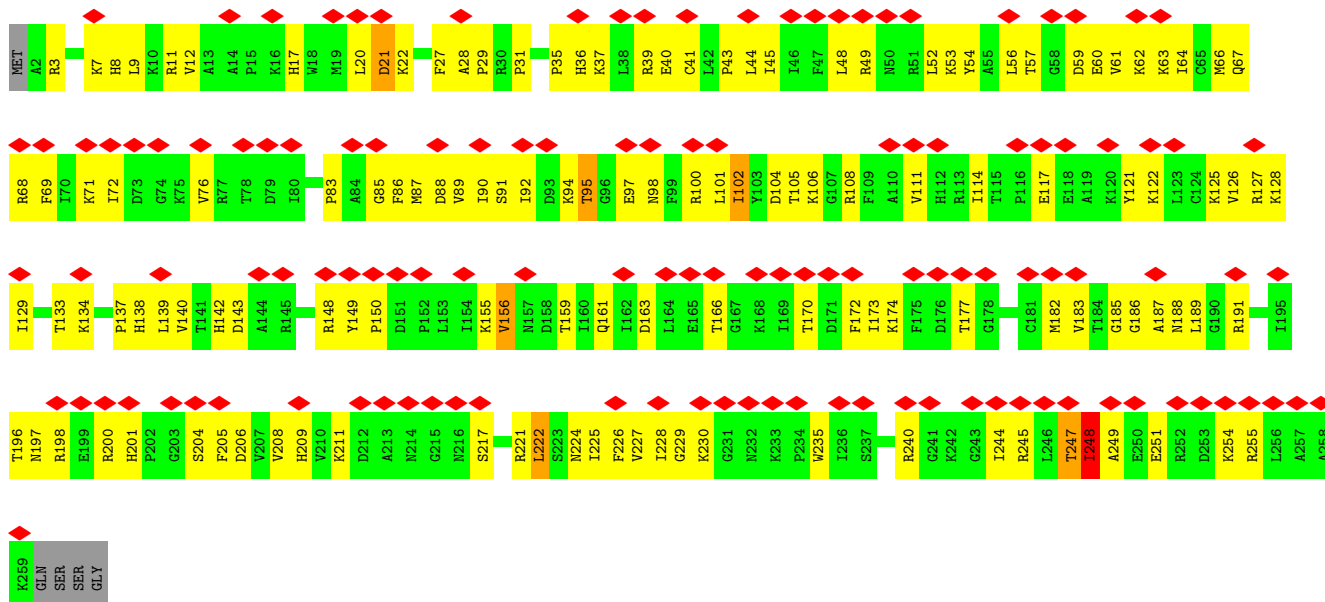




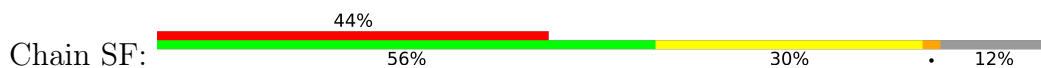
• Molecule 49: 40S ribosomal protein S3

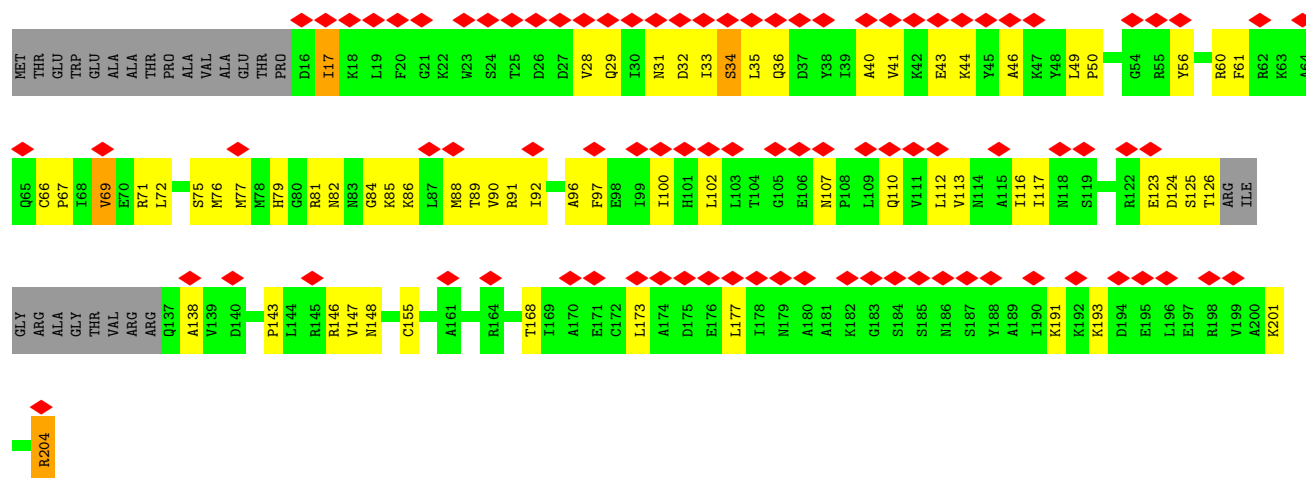


• Molecule 50: 40S ribosomal protein S4, X isoform

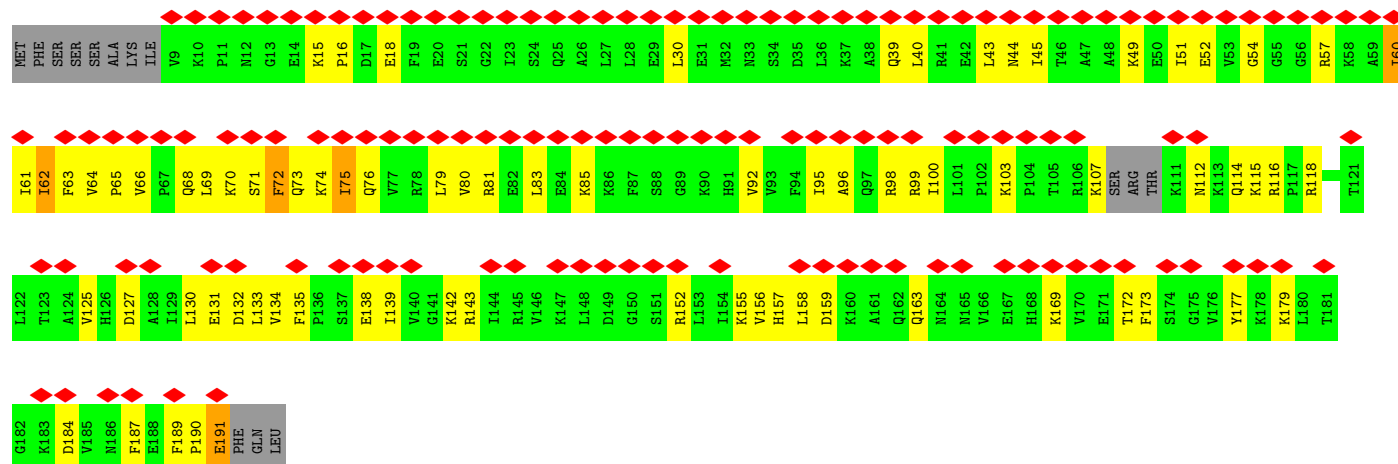
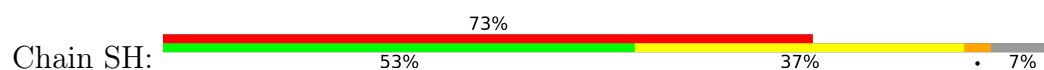


• Molecule 51: 40S ribosomal protein S5

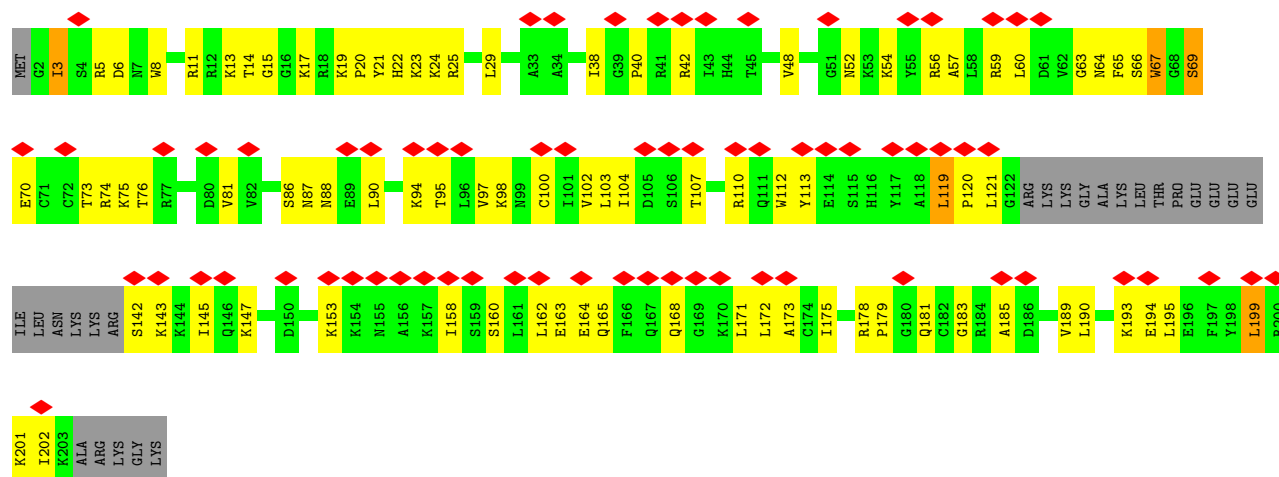




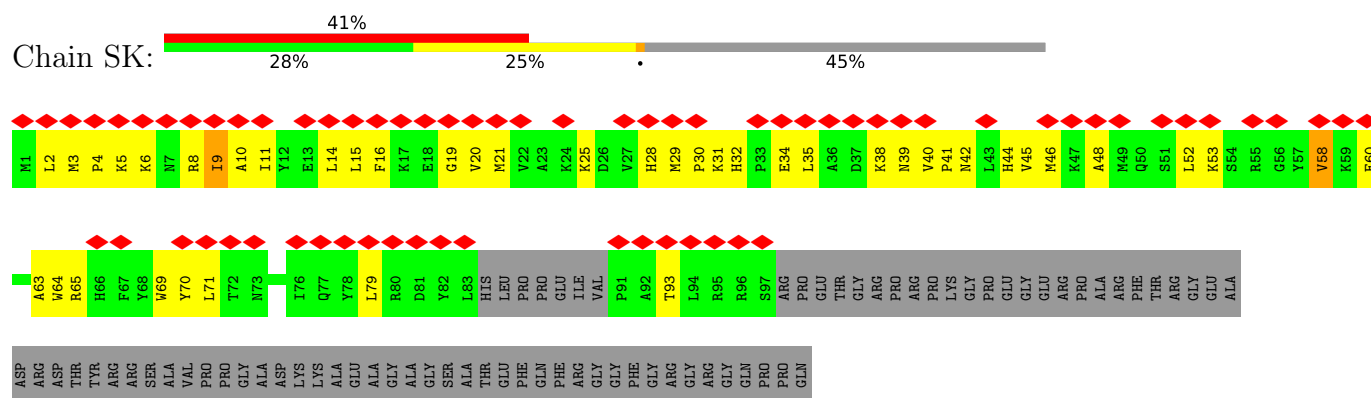
- Molecule 52: 40S ribosomal protein S7



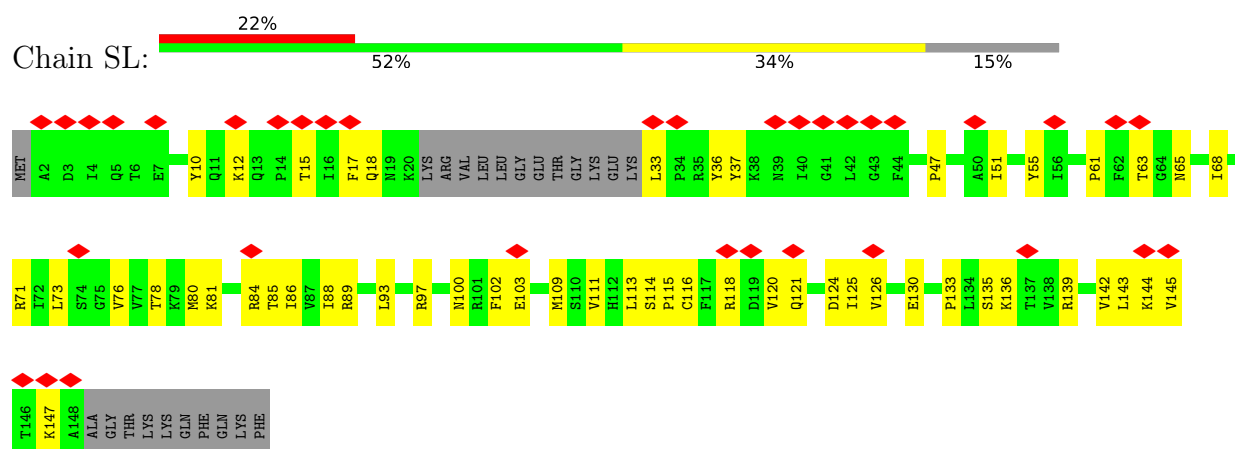
- Molecule 53: 40S ribosomal protein S8



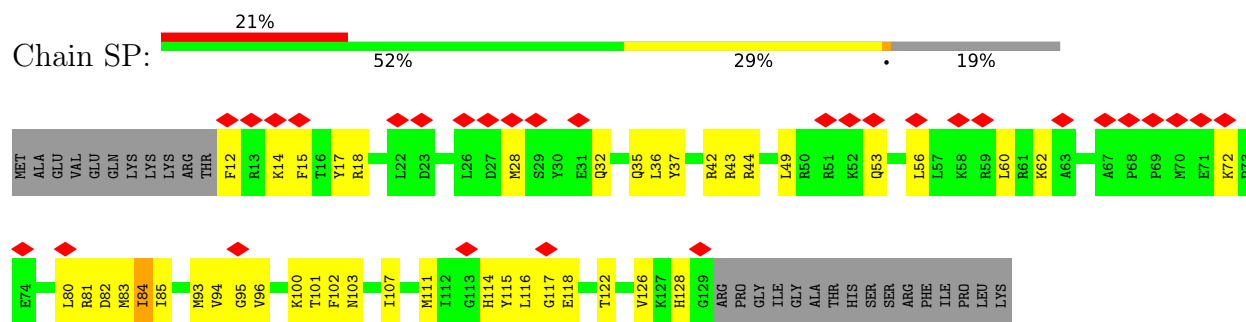
- Molecule 54: 40S ribosomal protein S10



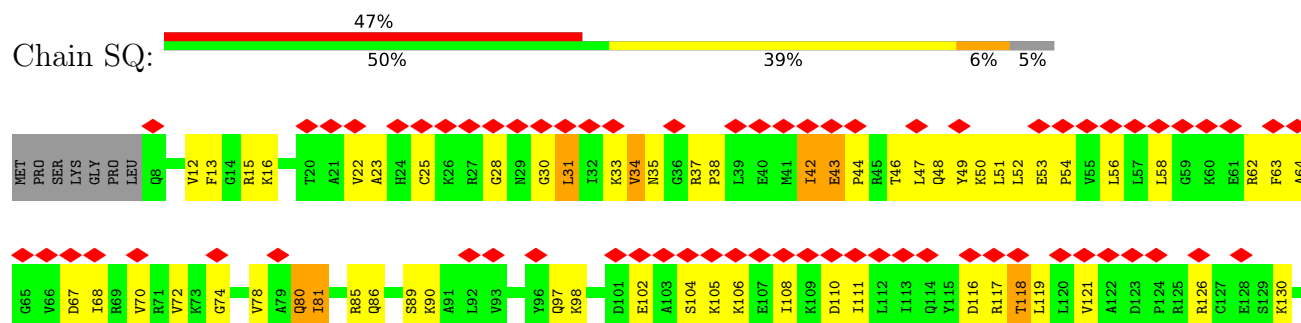
- Molecule 55: 40S ribosomal protein S11

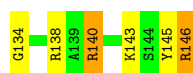


- Molecule 56: 40S ribosomal protein S15

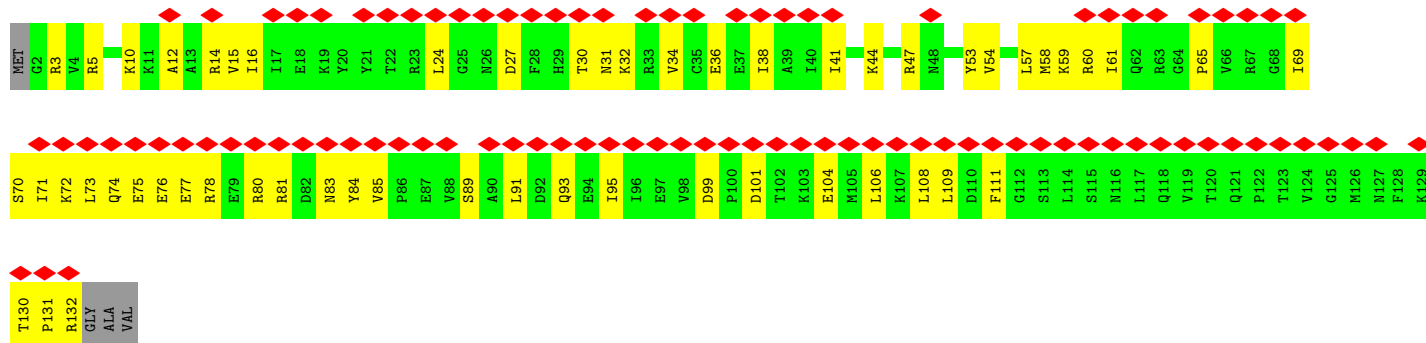


- Molecule 57: 40S ribosomal protein S16

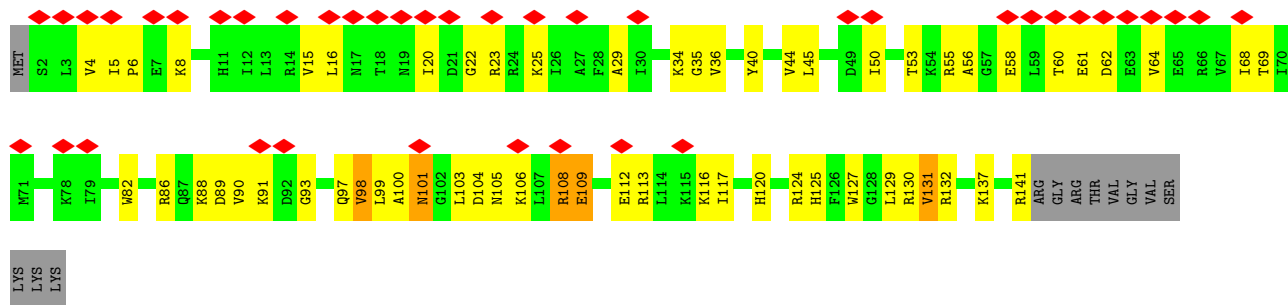




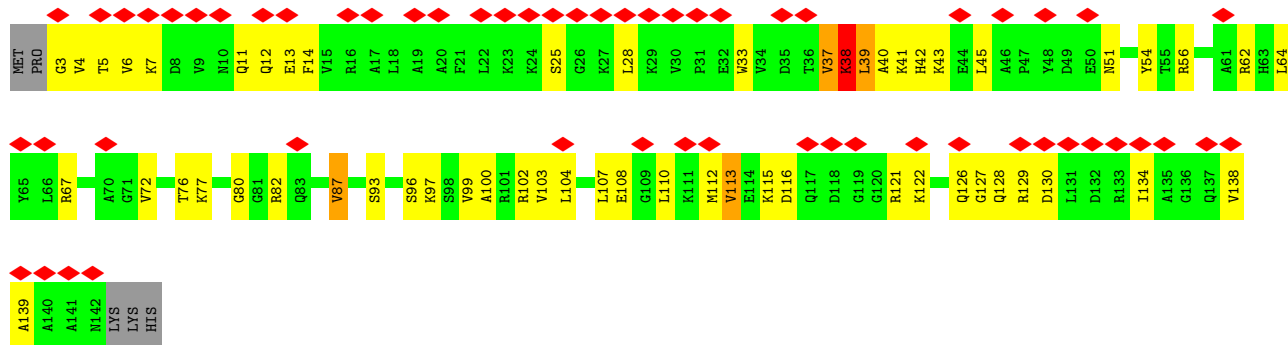
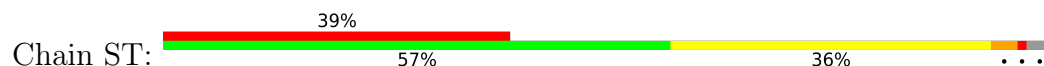
- Molecule 58: 40S ribosomal protein S17



- Molecule 59: 40S ribosomal protein S18

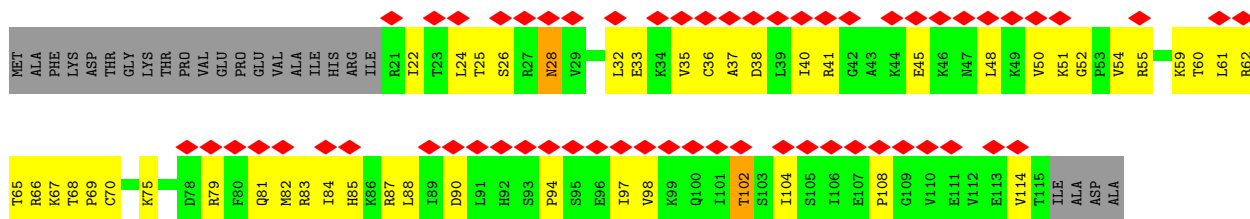


- Molecule 60: 40S ribosomal protein S19

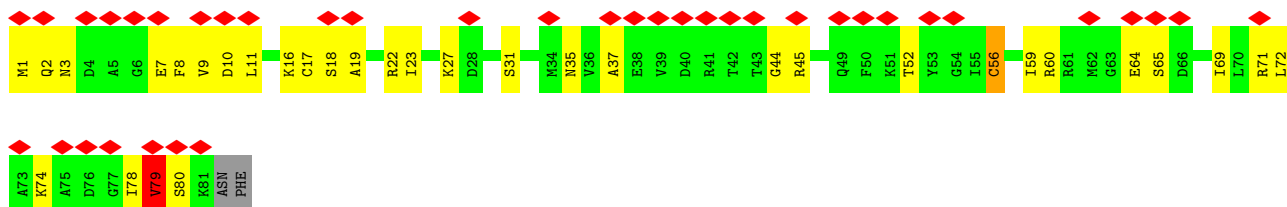


- Molecule 61: 40S ribosomal protein S20

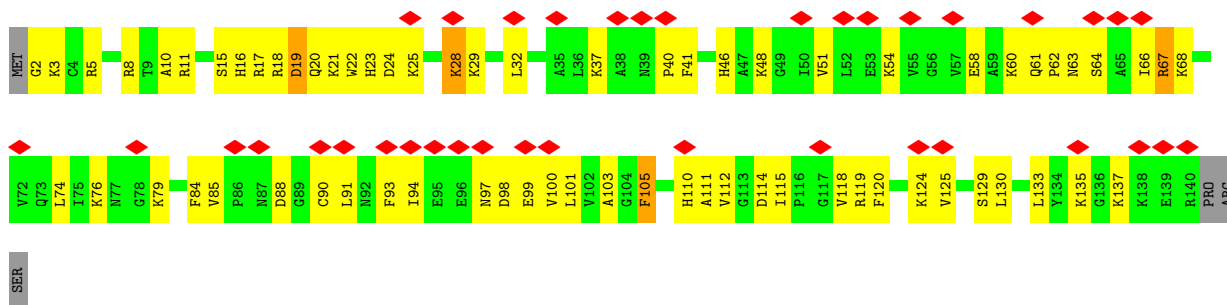




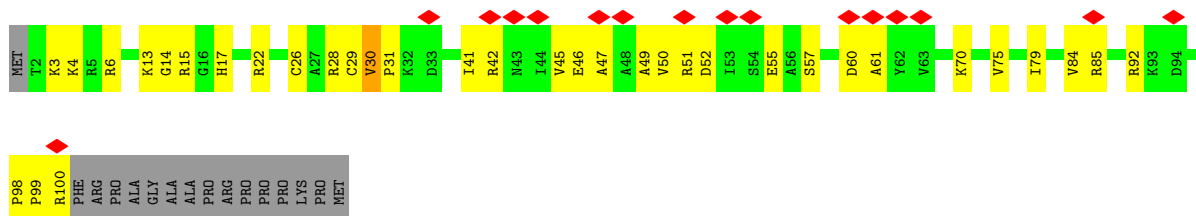
• Molecule 62: 40S ribosomal protein S21



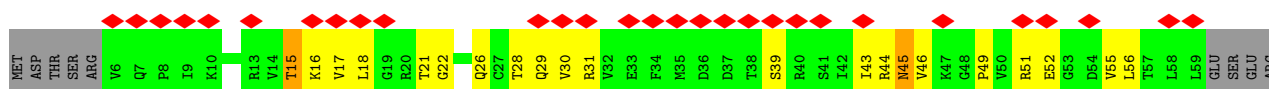
• Molecule 63: 40S ribosomal protein S23



• Molecule 64: 40S ribosomal protein S26

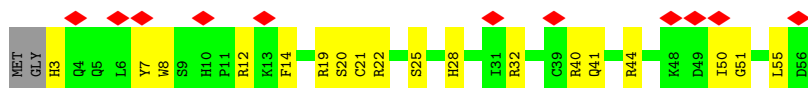


• Molecule 65: 40S ribosomal protein S28

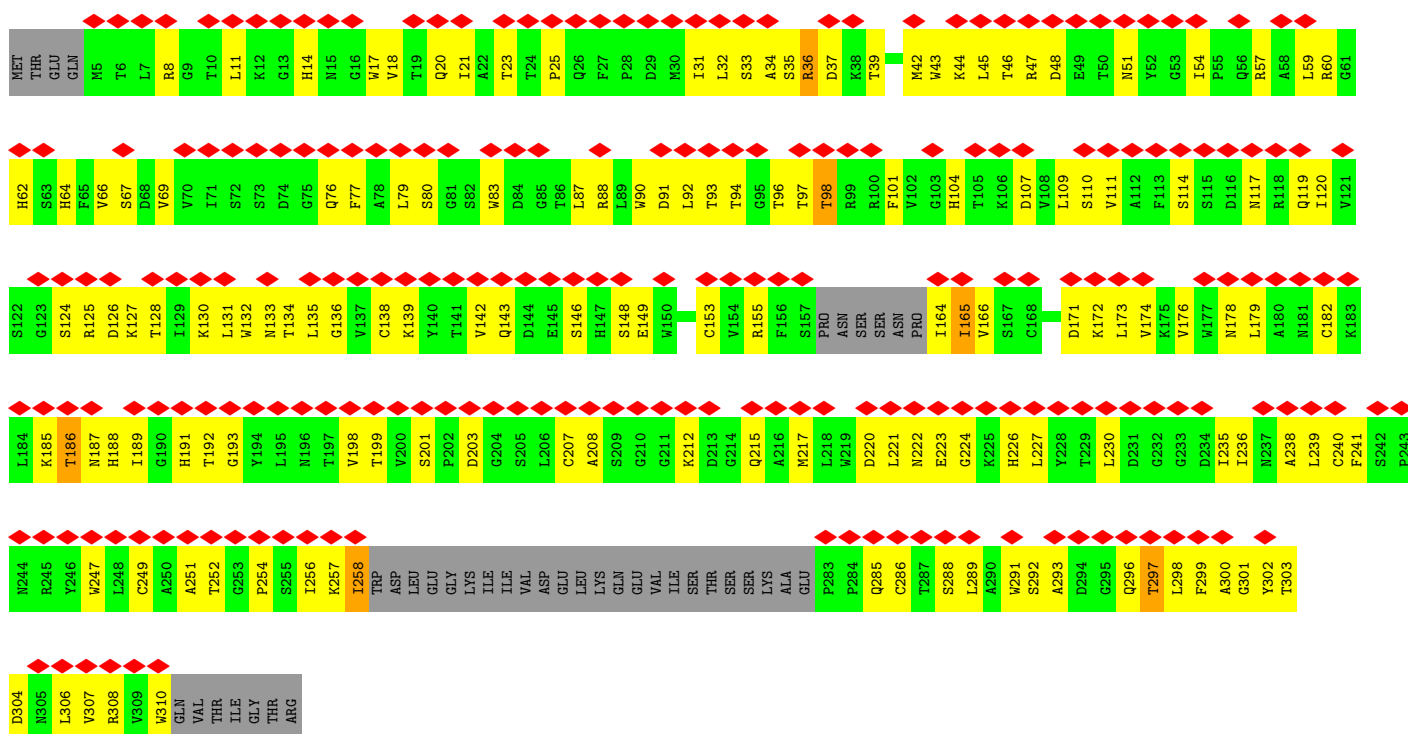


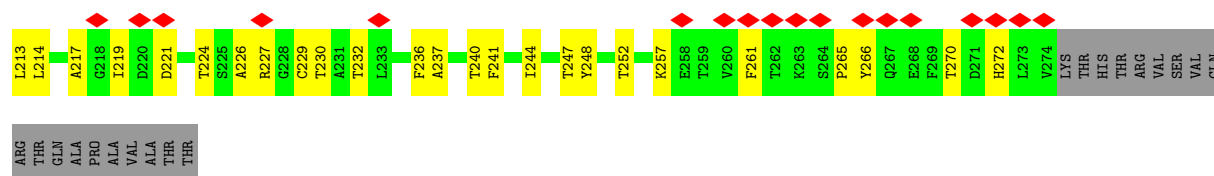
GLU
ALA
ARG
ARG
LEU
ARG

• Molecule 66: 40S ribosomal protein S29

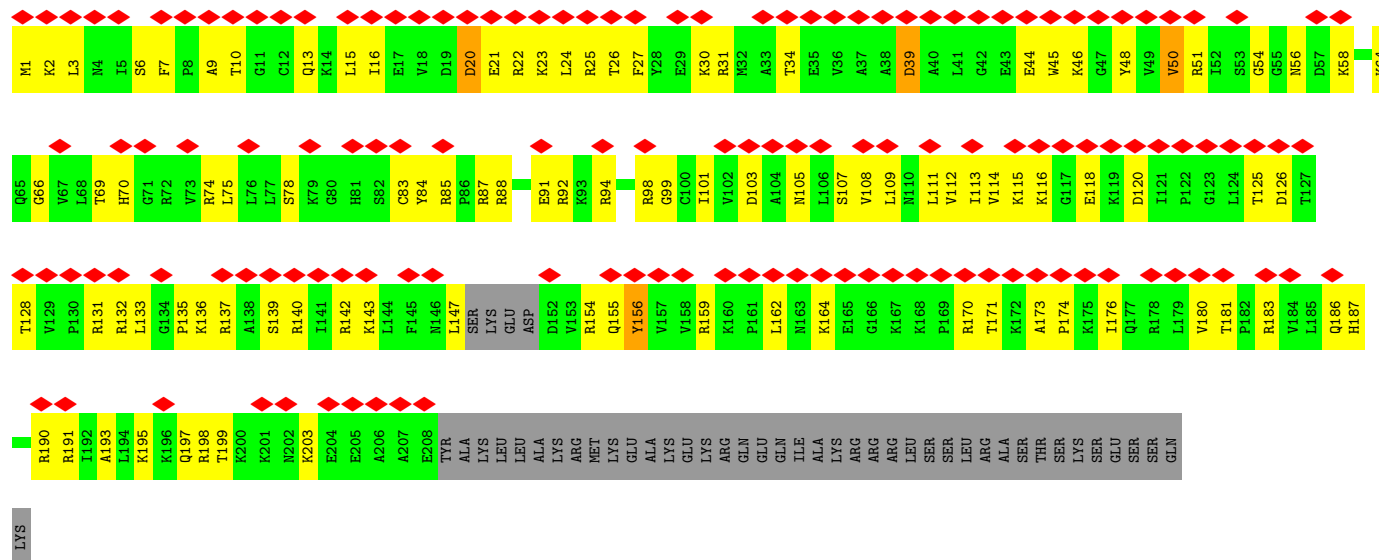


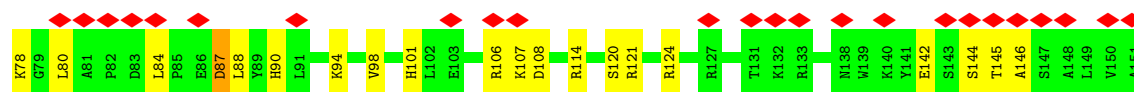
• Molecule 67: Receptor of activated protein C kinase 1



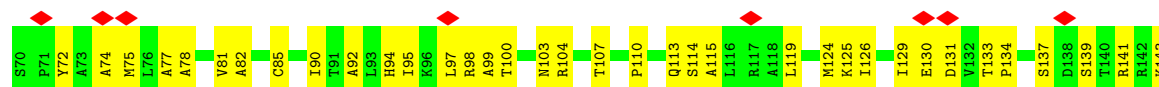
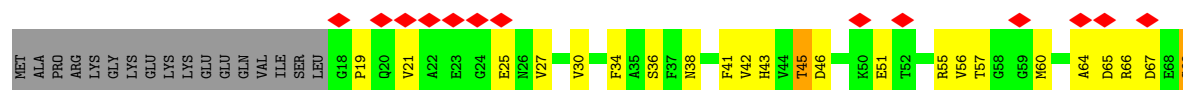


• Molecule 69: 40S ribosomal protein S6

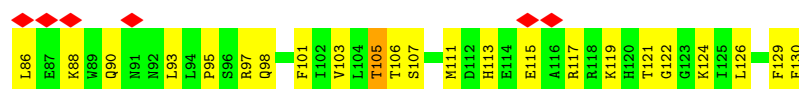




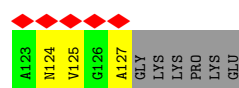
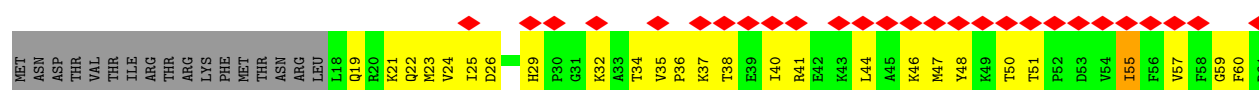
- Molecule 72: 40S ribosomal protein S14



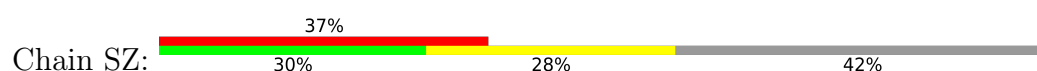
- Molecule 73: 40S ribosomal protein S15a



- Molecule 74: 40S ribosomal protein S24



- Molecule 75: 40S ribosomal protein S25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100403	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.102	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.026	Depositor
Map size ($\text{\AA}$)	416.0, 416.0, 416.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LA	0.57	0/1936	0.56	0/2596
2	LB	0.54	0/3269	0.54	0/4375
3	LC	0.57	0/2945	0.57	0/3953
4	LD	0.46	0/2431	0.48	0/3256
5	LE	0.46	0/1910	0.52	0/2562
6	LF	0.59	0/1805	0.54	0/2408
7	LG	0.46	0/1880	0.53	0/2531
8	LH	0.47	0/1537	0.55	0/2065
9	LI	0.49	0/1669	0.47	0/2227
10	LJ	0.38	0/1394	0.54	0/1864
11	LL	0.52	0/1698	0.54	0/2274
12	LM	0.52	0/1146	0.54	1/1531 (0.1%)
13	LN	0.63	0/1746	0.55	0/2338
14	LO	0.56	0/1670	0.50	0/2232
15	LP	0.57	0/1277	0.50	0/1712
16	LQ	0.60	0/1539	0.57	0/2053
17	LR	0.49	0/1473	0.51	0/1947
18	LS	0.58	0/1491	0.54	0/2000
19	LT	0.53	0/1335	0.46	0/1781
20	LU	0.39	0/831	0.50	0/1115
21	LV	0.53	0/987	0.51	0/1324
22	LW	0.51	0/532	0.51	0/708
23	LX	0.49	0/984	0.44	0/1323
24	LY	0.52	0/1119	0.52	0/1488
25	LZ	0.47	0/1130	0.51	0/1507
26	La	0.59	0/1193	0.50	0/1593
27	Lb	0.47	0/821	0.52	0/1082
28	Lc	0.47	0/742	0.50	0/996
29	Ld	0.52	0/911	0.50	0/1227
30	Le	0.62	0/1071	0.53	0/1429
31	Lf	0.59	0/895	0.57	0/1198
32	Lg	0.53	0/883	0.54	0/1178

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lh	0.48	0/1023	0.50	0/1350
34	Li	0.44	0/843	0.49	0/1115
35	Lj	0.58	0/720	0.58	0/952
36	Lk	0.41	0/574	0.44	0/760
37	Ll	0.55	0/448	0.60	0/592
38	Lm	0.58	0/425	0.57	0/564
39	Ln	0.36	0/240	0.56	0/305
40	Lo	0.49	0/855	0.52	0/1128
41	Lp	0.51	0/718	0.47	0/953
42	Lr	0.56	0/1009	0.53	0/1353
43	L5	0.58	0/84917	0.43	1/132450 (0.0%)
44	L7	0.56	0/2858	0.39	0/4455
45	L8	0.59	0/3701	0.41	0/5766
46	S2	0.31	0/39073	0.40	0/60890
47	SA	0.28	0/1673	0.51	0/2275
48	SB	0.28	0/1756	0.48	0/2350
49	SD	0.28	0/1772	0.53	0/2385
50	SE	0.27	0/2092	0.54	0/2816
51	SF	0.27	0/1436	0.50	0/1930
52	SH	0.26	0/1470	0.55	0/1968
53	SI	0.29	0/1526	0.52	0/2038
54	SK	0.27	0/780	0.50	0/1046
55	SL	0.31	0/1130	0.48	0/1514
56	SP	0.28	0/1000	0.45	0/1335
57	SQ	0.29	0/1126	0.60	1/1506 (0.1%)
58	SR	0.25	0/1078	0.51	0/1447
59	SS	0.29	0/1175	0.52	0/1575
60	ST	0.29	0/1108	0.47	0/1486
61	SU	0.24	0/762	0.52	0/1023
62	SV	0.43	0/625	0.56	0/836
63	SX	0.30	0/1097	0.55	0/1464
64	Sa	0.36	0/805	0.54	0/1079
65	Sc	0.26	0/418	0.65	0/562
66	Sd	0.30	0/466	0.50	0/618
67	Sg	0.25	0/2199	0.56	0/2989
68	SC	0.33	0/1712	0.51	0/2314
69	SG	0.24	0/1666	0.50	0/2222
70	SJ	0.25	0/1178	0.54	0/1574
71	SN	0.31	0/1232	0.47	0/1656
72	SO	0.32	0/1015	0.56	0/1361
73	SW	0.34	0/1051	0.53	0/1406
74	SY	0.23	0/907	0.53	0/1204
75	SZ	0.26	0/580	0.53	0/780

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	Sb	0.26	0/665	0.50	0/891
77	Se	0.24	0/386	0.54	0/504
78	S6	0.27	0/1795	0.47	0/2798
All	All	0.48	0/221335	0.46	3/325458 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	LB	0	2
3	LC	0	2
10	LJ	0	1
12	LM	0	1
31	Lf	0	1
50	SE	0	1
52	SH	0	1
60	ST	0	1
70	SJ	0	1
All	All	0	11

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
12	LM	135	ILE	N-CA-C	-5.84	106.80	112.29
57	SQ	80	GLN	N-CA-C	-5.57	107.13	114.04
43	L5	416	G	O4'-C1'-N9	5.19	115.99	108.20

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	LB	16	PHE	Peptide
2	LB	258	HIS	Peptide
3	LC	354	LEU	Peptide
3	LC	66	SER	Peptide
10	LJ	173	ILE	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	1898	0	1993	44	0
2	LB	3202	0	3347	98	0
3	LC	2891	0	3071	69	0
4	LD	2385	0	2409	48	0
5	LE	1874	0	2007	68	0
6	LF	1771	0	1886	44	0
7	LG	1848	0	1981	62	0
8	LH	1519	0	1603	44	0
9	LI	1631	0	1682	30	0
10	LJ	1371	0	1405	45	0
11	LL	1667	0	1771	43	0
12	LM	1125	0	1202	30	0
13	LN	1701	0	1749	37	0
14	LO	1640	0	1792	33	0
15	LP	1251	0	1282	29	0
16	LQ	1515	0	1639	34	0
17	LR	1457	0	1601	37	0
18	LS	1451	0	1488	43	0
19	LT	1307	0	1380	37	0
20	LU	817	0	839	22	0
21	LV	973	0	1034	19	0
22	LW	519	0	533	10	0
23	LX	967	0	1040	17	0
24	LY	1102	0	1189	29	0
25	LZ	1107	0	1182	39	0
26	La	1164	0	1213	35	0
27	Lb	807	0	875	28	0
28	Lc	732	0	769	20	0
29	Ld	896	0	941	25	0
30	Le	1053	0	1147	28	0
31	Lf	876	0	912	25	0
32	Lg	873	0	961	21	0
33	Lh	1015	0	1156	17	0
34	Li	832	0	917	10	0
35	Lj	705	0	739	10	0
36	Lk	568	0	635	15	0
37	Ll	438	0	474	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lm	419	0	452	12	0
39	Ln	239	0	289	6	0
40	Lo	842	0	914	30	0
41	Lp	708	0	756	11	0
42	Lr	994	0	1057	21	0
43	L5	75913	0	38337	1211	0
44	L7	2558	0	1296	29	0
45	L8	3314	0	1683	51	0
46	S2	34941	0	17646	898	0
47	SA	1636	0	1641	96	0
48	SB	1729	0	1803	69	0
49	SD	1744	0	1837	88	0
50	SE	2050	0	2156	101	0
51	SF	1416	0	1458	48	0
52	SH	1449	0	1539	63	0
53	SI	1499	0	1561	75	0
54	SK	760	0	783	46	0
55	SL	1110	0	1165	44	0
56	SP	981	0	1026	37	0
57	SQ	1109	0	1174	53	0
58	SR	1064	0	1118	50	0
59	SS	1157	0	1213	43	0
60	ST	1090	0	1116	48	0
61	SU	753	0	815	33	0
62	SV	619	0	620	36	0
63	SX	1080	0	1147	62	0
64	Sa	792	0	841	27	0
65	Sc	416	0	445	15	0
66	Sd	455	0	446	22	0
67	Sg	2148	0	2108	115	0
68	SC	1673	0	1766	75	0
69	SG	1645	0	1780	103	0
70	SJ	1162	0	1252	64	0
71	SN	1208	0	1294	35	0
72	SO	1002	0	1023	46	0
73	SW	1034	0	1080	54	0
74	SY	891	0	948	55	0
75	SZ	574	0	627	30	0
76	Sb	651	0	672	26	0
77	Se	384	0	422	13	0
78	S6	1604	0	816	42	0
79	L5	173	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	L7	3	0	0	0	0
79	L8	5	0	0	0	0
79	LN	1	0	0	0	0
79	LP	1	0	0	0	0
79	LT	1	0	0	0	0
79	LV	1	0	0	0	0
79	Le	1	0	0	0	0
79	Lf	1	0	0	0	0
79	S2	59	0	0	0	0
79	SF	1	0	0	0	0
80	Lg	1	0	0	0	0
80	Lj	1	0	0	0	0
80	Lm	1	0	0	0	0
80	Lo	1	0	0	0	0
80	Lp	1	0	0	0	0
80	Sa	1	0	0	0	0
80	Sd	1	0	0	0	0
81	L5	7	0	0	0	0
81	LB	1	0	0	0	0
81	LH	1	0	0	0	0
81	LI	2	0	0	1	0
81	LN	1	0	0	0	0
81	La	1	0	0	0	0
81	S2	2	0	0	1	0
All	All	206030	0	151966	4449	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 13.

The worst 5 of 4449 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)
37:L1:36:MET:HE3	37:L1:37:TYR:CD1	1.63	1.32
46:S2:1744:G:N2	46:S2:1792:A:H62	1.34	1.23
46:S2:1744:G:H21	46:S2:1792:A:N6	1.45	1.11
43:L5:741:A:H62	43:L5:829:G:N2	1.54	1.03
43:L5:950:G:C2	43:L5:1037:G:C2	2.52	0.98

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	
1	LA	246/257 (96%)	218 (89%)	28 (11%)	0	100	100
2	LB	395/403 (98%)	367 (93%)	28 (7%)	0	100	100
3	LC	360/419 (86%)	326 (91%)	33 (9%)	1 (0%)	36	67
4	LD	291/297 (98%)	270 (93%)	21 (7%)	0	100	100
5	LE	227/296 (77%)	207 (91%)	20 (9%)	0	100	100
6	LF	212/270 (78%)	200 (94%)	12 (6%)	0	100	100
7	LG	225/266 (85%)	209 (93%)	16 (7%)	0	100	100
8	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
9	LI	197/214 (92%)	187 (95%)	10 (5%)	0	100	100
10	LJ	169/178 (95%)	147 (87%)	22 (13%)	0	100	100
11	LL	204/211 (97%)	186 (91%)	17 (8%)	1 (0%)	24	57
12	LM	134/217 (62%)	121 (90%)	13 (10%)	0	100	100
13	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	41
14	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
15	LP	152/184 (83%)	140 (92%)	12 (8%)	0	100	100
16	LQ	185/188 (98%)	173 (94%)	12 (6%)	0	100	100
17	LR	172/196 (88%)	166 (96%)	6 (4%)	0	100	100
18	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
19	LT	158/160 (99%)	150 (95%)	8 (5%)	0	100	100
20	LU	98/128 (77%)	85 (87%)	13 (13%)	0	100	100
21	LV	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
22	LW	60/157 (38%)	55 (92%)	5 (8%)	0	100	100
23	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
24	LY	130/145 (90%)	124 (95%)	6 (5%)	0	100	100
25	LZ	133/136 (98%)	116 (87%)	17 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	La	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
27	Lb	95/160 (59%)	88 (93%)	7 (7%)	0	100	100
28	Lc	92/115 (80%)	85 (92%)	7 (8%)	0	100	100
29	Ld	106/125 (85%)	93 (88%)	13 (12%)	0	100	100
30	Le	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	16	46
31	Lf	107/110 (97%)	102 (95%)	5 (5%)	0	100	100
32	Lg	108/117 (92%)	104 (96%)	4 (4%)	0	100	100
33	Lh	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	Li	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
35	Lj	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
36	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	Lm	49/128 (38%)	46 (94%)	1 (2%)	2 (4%)	2	11
39	Ln	23/25 (92%)	23 (100%)	0	0	100	100
40	Lo	101/106 (95%)	93 (92%)	8 (8%)	0	100	100
41	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	Lr	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
47	SA	205/295 (70%)	179 (87%)	25 (12%)	1 (0%)	24	57
48	SB	211/264 (80%)	193 (92%)	18 (8%)	0	100	100
49	SD	222/243 (91%)	193 (87%)	29 (13%)	0	100	100
50	SE	256/263 (97%)	229 (90%)	26 (10%)	1 (0%)	30	61
51	SF	175/204 (86%)	156 (89%)	19 (11%)	0	100	100
52	SH	176/194 (91%)	155 (88%)	21 (12%)	0	100	100
53	SI	179/208 (86%)	168 (94%)	11 (6%)	0	100	100
54	SK	86/165 (52%)	73 (85%)	13 (15%)	0	100	100
55	SL	131/158 (83%)	124 (95%)	7 (5%)	0	100	100
56	SP	116/145 (80%)	110 (95%)	6 (5%)	0	100	100
57	SQ	137/146 (94%)	118 (86%)	18 (13%)	1 (1%)	18	49
58	SR	129/135 (96%)	116 (90%)	13 (10%)	0	100	100
59	SS	138/152 (91%)	125 (91%)	12 (9%)	1 (1%)	18	49
60	ST	138/145 (95%)	131 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SU	93/119 (78%)	86 (92%)	7 (8%)	0	100	100
62	SV	79/83 (95%)	71 (90%)	7 (9%)	1 (1%)	9	35
63	SX	137/143 (96%)	123 (90%)	14 (10%)	0	100	100
64	Sa	97/115 (84%)	87 (90%)	9 (9%)	1 (1%)	12	41
65	Sc	52/69 (75%)	42 (81%)	10 (19%)	0	100	100
66	Sd	52/56 (93%)	47 (90%)	5 (10%)	0	100	100
67	Sg	270/317 (85%)	218 (81%)	52 (19%)	0	100	100
68	SC	214/293 (73%)	199 (93%)	15 (7%)	0	100	100
69	SG	200/249 (80%)	184 (92%)	16 (8%)	0	100	100
70	SJ	130/194 (67%)	118 (91%)	12 (9%)	0	100	100
71	SN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
72	SO	132/151 (87%)	116 (88%)	15 (11%)	1 (1%)	16	46
73	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
74	SY	108/133 (81%)	93 (86%)	15 (14%)	0	100	100
75	SZ	70/125 (56%)	62 (89%)	8 (11%)	0	100	100
76	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
77	Se	44/133 (33%)	38 (86%)	6 (14%)	0	100	100
All	All	10668/12499 (85%)	9753 (91%)	901 (8%)	14 (0%)	49	78

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
64	Sa	47	ALA
30	Le	92	ASN
47	SA	12	GLU
11	LL	51	ALA
13	LN	84	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
1	LA	190/199 (96%)	184 (97%)	6 (3%)	34	64
2	LB	344/348 (99%)	328 (95%)	16 (5%)	23	55
3	LC	304/348 (87%)	293 (96%)	11 (4%)	31	62
4	LD	245/249 (98%)	232 (95%)	13 (5%)	20	51
5	LE	208/256 (81%)	194 (93%)	14 (7%)	15	43
6	LF	185/234 (79%)	181 (98%)	4 (2%)	45	71
7	LG	197/223 (88%)	193 (98%)	4 (2%)	48	73
8	LH	169/171 (99%)	160 (95%)	9 (5%)	20	51
9	LI	170/180 (94%)	163 (96%)	7 (4%)	27	58
10	LJ	144/149 (97%)	132 (92%)	12 (8%)	10	34
11	LL	173/178 (97%)	163 (94%)	10 (6%)	18	48
12	LM	116/157 (74%)	114 (98%)	2 (2%)	53	75
13	LN	171/172 (99%)	166 (97%)	5 (3%)	37	67
14	LO	172/173 (99%)	168 (98%)	4 (2%)	44	70
15	LP	135/163 (83%)	127 (94%)	8 (6%)	18	47
16	LQ	164/165 (99%)	159 (97%)	5 (3%)	36	66
17	LR	154/175 (88%)	150 (97%)	4 (3%)	40	69
18	LS	155/156 (99%)	146 (94%)	9 (6%)	18	48
19	LT	140/140 (100%)	132 (94%)	8 (6%)	18	49
20	LU	90/114 (79%)	82 (91%)	8 (9%)	9	32
21	LV	100/107 (94%)	97 (97%)	3 (3%)	36	66
22	LW	54/126 (43%)	51 (94%)	3 (6%)	19	49
23	LX	106/133 (80%)	104 (98%)	2 (2%)	50	73
24	LY	123/135 (91%)	117 (95%)	6 (5%)	22	53
25	LZ	117/118 (99%)	113 (97%)	4 (3%)	32	63
26	La	120/121 (99%)	113 (94%)	7 (6%)	18	48
27	Lb	83/124 (67%)	79 (95%)	4 (5%)	23	54
28	Lc	79/97 (81%)	76 (96%)	3 (4%)	29	60
29	Ld	99/110 (90%)	99 (100%)	0	100	100
30	Le	114/121 (94%)	108 (95%)	6 (5%)	20	51
31	Lf	88/89 (99%)	84 (96%)	4 (4%)	24	56
32	Lg	94/100 (94%)	93 (99%)	1 (1%)	65	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	82
34	Li	86/89 (97%)	83 (96%)	3 (4%)	32	62
35	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	78
36	Lk	64/65 (98%)	62 (97%)	2 (3%)	35	65
37	Ll	46/47 (98%)	41 (89%)	5 (11%)	6	23
38	Lm	47/116 (40%)	44 (94%)	3 (6%)	16	44
39	Ln	24/24 (100%)	24 (100%)	0	100	100
40	Lo	91/94 (97%)	83 (91%)	8 (9%)	9	32
41	Lp	74/75 (99%)	70 (95%)	4 (5%)	20	50
42	Lr	108/121 (89%)	103 (95%)	5 (5%)	24	55
47	SA	173/242 (72%)	165 (95%)	8 (5%)	24	55
48	SB	194/229 (85%)	191 (98%)	3 (2%)	57	77
49	SD	188/202 (93%)	179 (95%)	9 (5%)	23	54
50	SE	221/225 (98%)	205 (93%)	16 (7%)	13	40
51	SF	152/170 (89%)	144 (95%)	8 (5%)	20	51
52	SH	161/174 (92%)	154 (96%)	7 (4%)	26	57
53	SI	159/180 (88%)	151 (95%)	8 (5%)	22	53
54	SK	81/136 (60%)	78 (96%)	3 (4%)	30	61
55	SL	123/142 (87%)	118 (96%)	5 (4%)	27	58
56	SP	107/130 (82%)	103 (96%)	4 (4%)	30	61
57	SQ	115/121 (95%)	106 (92%)	9 (8%)	11	37
58	SR	119/121 (98%)	115 (97%)	4 (3%)	32	63
59	SS	122/132 (92%)	112 (92%)	10 (8%)	10	35
60	ST	110/115 (96%)	104 (94%)	6 (6%)	19	50
61	SU	88/107 (82%)	80 (91%)	8 (9%)	9	31
62	SV	65/67 (97%)	62 (95%)	3 (5%)	24	55
63	SX	111/115 (96%)	105 (95%)	6 (5%)	20	50
64	Sa	86/98 (88%)	84 (98%)	2 (2%)	44	70
65	Sc	48/62 (77%)	45 (94%)	3 (6%)	16	45
66	Sd	48/49 (98%)	48 (100%)	0	100	100
67	Sg	237/275 (86%)	222 (94%)	15 (6%)	16	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SC	182/224 (81%)	180 (99%)	2 (1%)	65	80
69	SG	178/218 (82%)	171 (96%)	7 (4%)	28	59
70	SJ	126/168 (75%)	116 (92%)	10 (8%)	11	36
71	SN	130/131 (99%)	128 (98%)	2 (2%)	57	77
72	SO	104/119 (87%)	99 (95%)	5 (5%)	23	54
73	SW	112/113 (99%)	104 (93%)	8 (7%)	13	40
74	SY	93/115 (81%)	89 (96%)	4 (4%)	26	57
75	SZ	64/103 (62%)	63 (98%)	1 (2%)	55	76
76	Sb	75/76 (99%)	69 (92%)	6 (8%)	11	36
77	Se	39/106 (37%)	36 (92%)	3 (8%)	12	37
All	All	9336/10617 (88%)	8917 (96%)	419 (4%)	26	56

5 of 419 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	Lr	28	GLU
53	SI	52	ASN
73	SW	55	ASP
47	SA	75	SER
50	SE	102	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 190 such sidechains are listed below:

Mol	Chain	Res	Type
49	SD	165	ASN
58	SR	31	ASN
50	SE	138	HIS
52	SH	91	HIS
62	SV	29	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	L5	3523/4731 (74%)	905 (25%)	22 (0%)
44	L7	119/120 (99%)	12 (10%)	0
45	L8	155/158 (98%)	35 (22%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	S2	1627/1870 (87%)	448 (27%)	7 (0%)
78	S6	74/75 (98%)	35 (47%)	2 (2%)
All	All	5498/6954 (79%)	1435 (26%)	31 (0%)

5 of 1435 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	L5	17	A
43	L5	20	U
43	L5	21	G
43	L5	25	A
43	L5	30	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
43	L5	2540	C
46	S2	1343	U
43	L5	3417	A
78	S6	53	G
46	S2	547	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 254 ligands modelled in this entry, 254 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

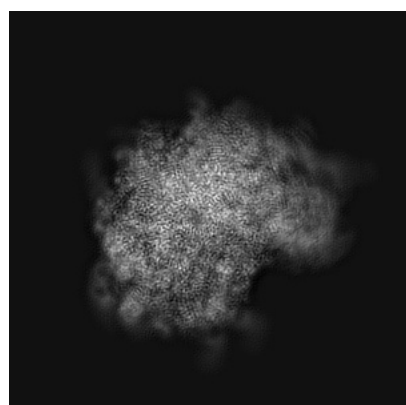
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30433. These allow visual inspection of the internal detail of the map and identification of artifacts.

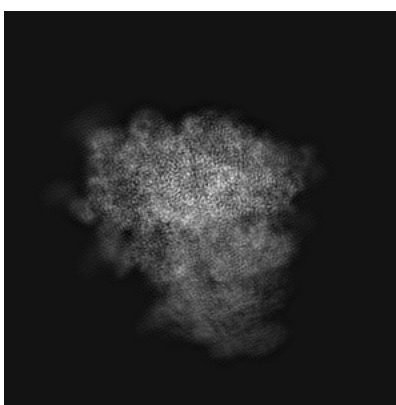
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

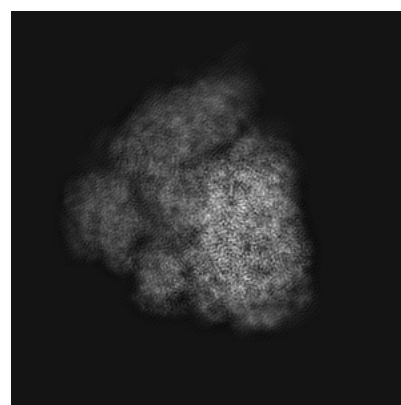
6.1.1 Primary map



X



Y

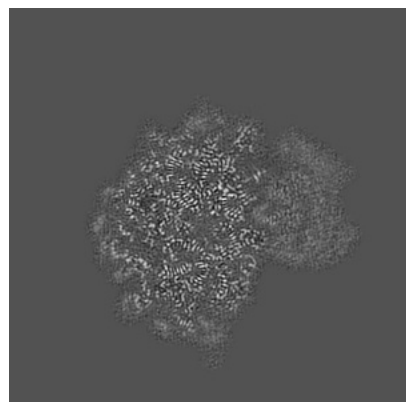


Z

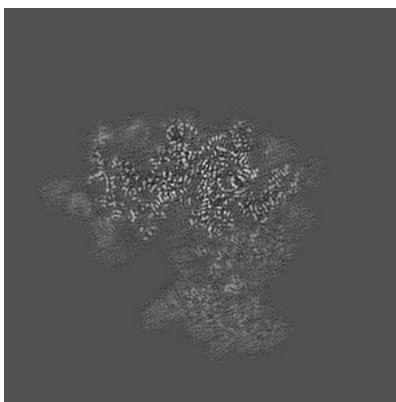
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

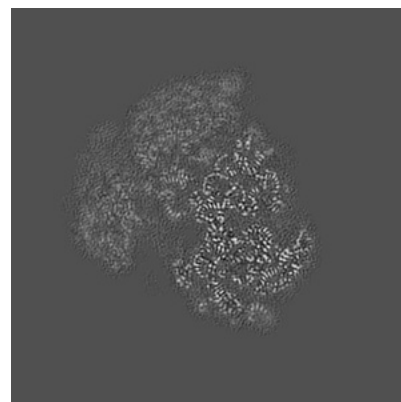
6.2.1 Primary map



X Index: 200



Y Index: 200

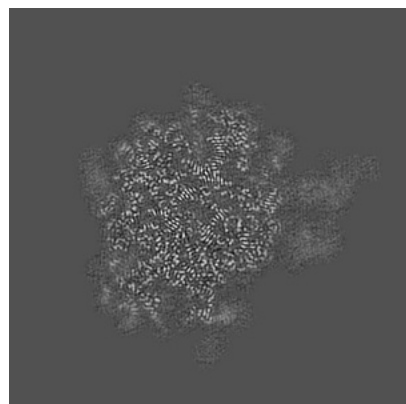


Z Index: 200

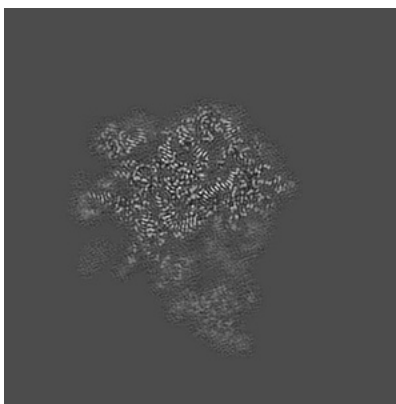
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

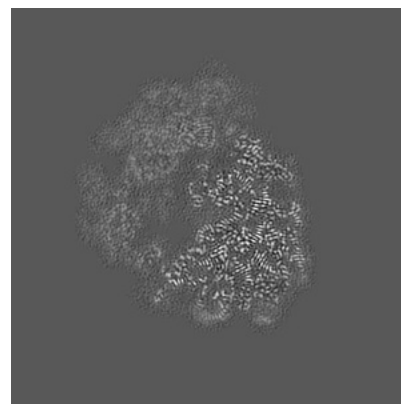
6.3.1 Primary map



X Index: 229



Y Index: 158

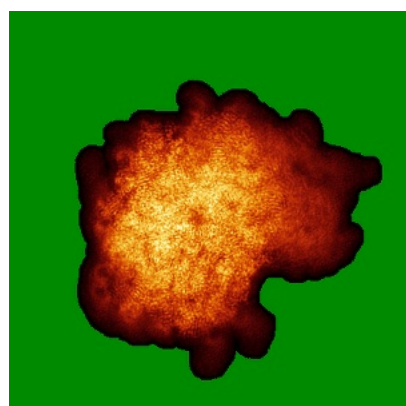


Z Index: 183

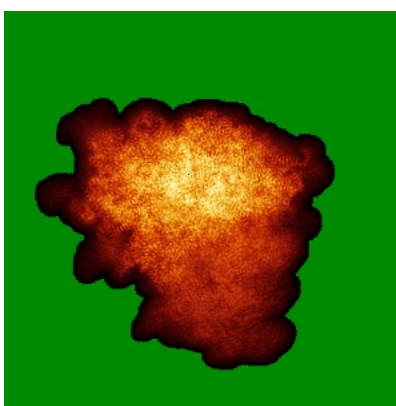
The images above show the largest variance slices of the map in three orthogonal directions.

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

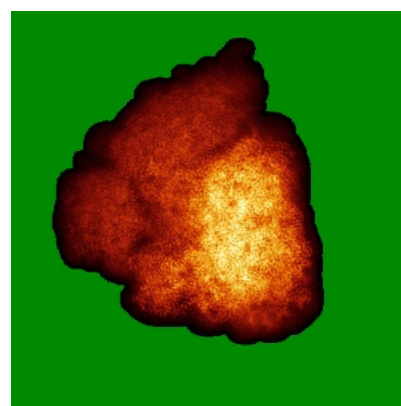
6.4.1 Primary map



X



Y

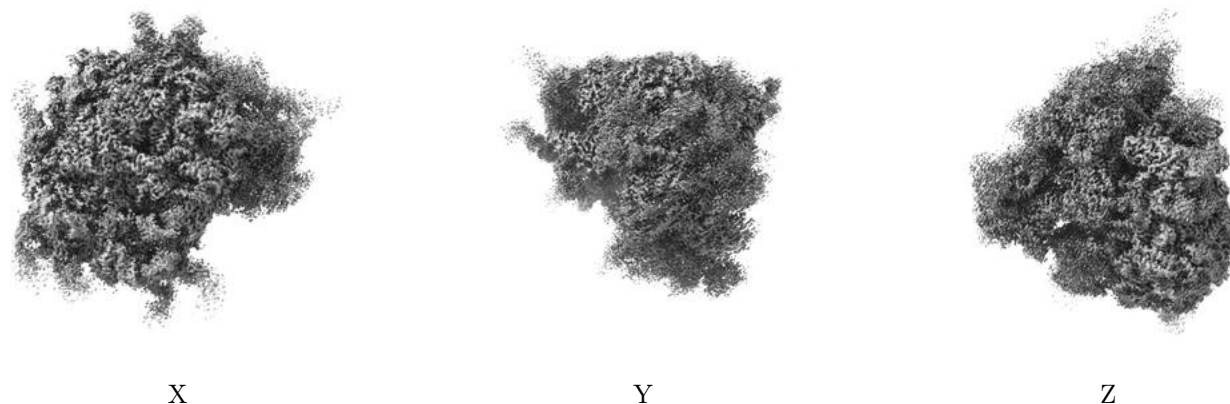


Z

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 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

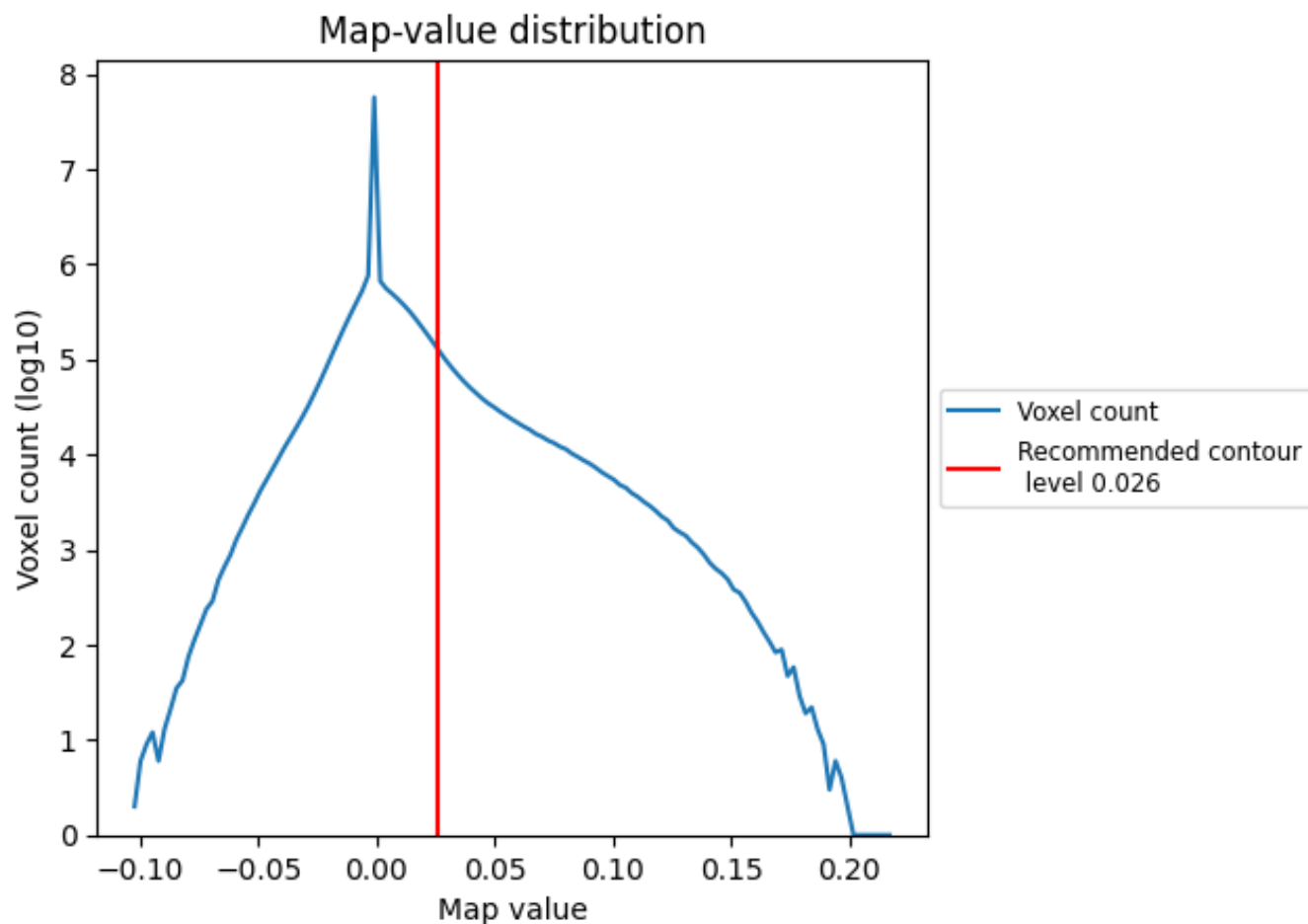
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

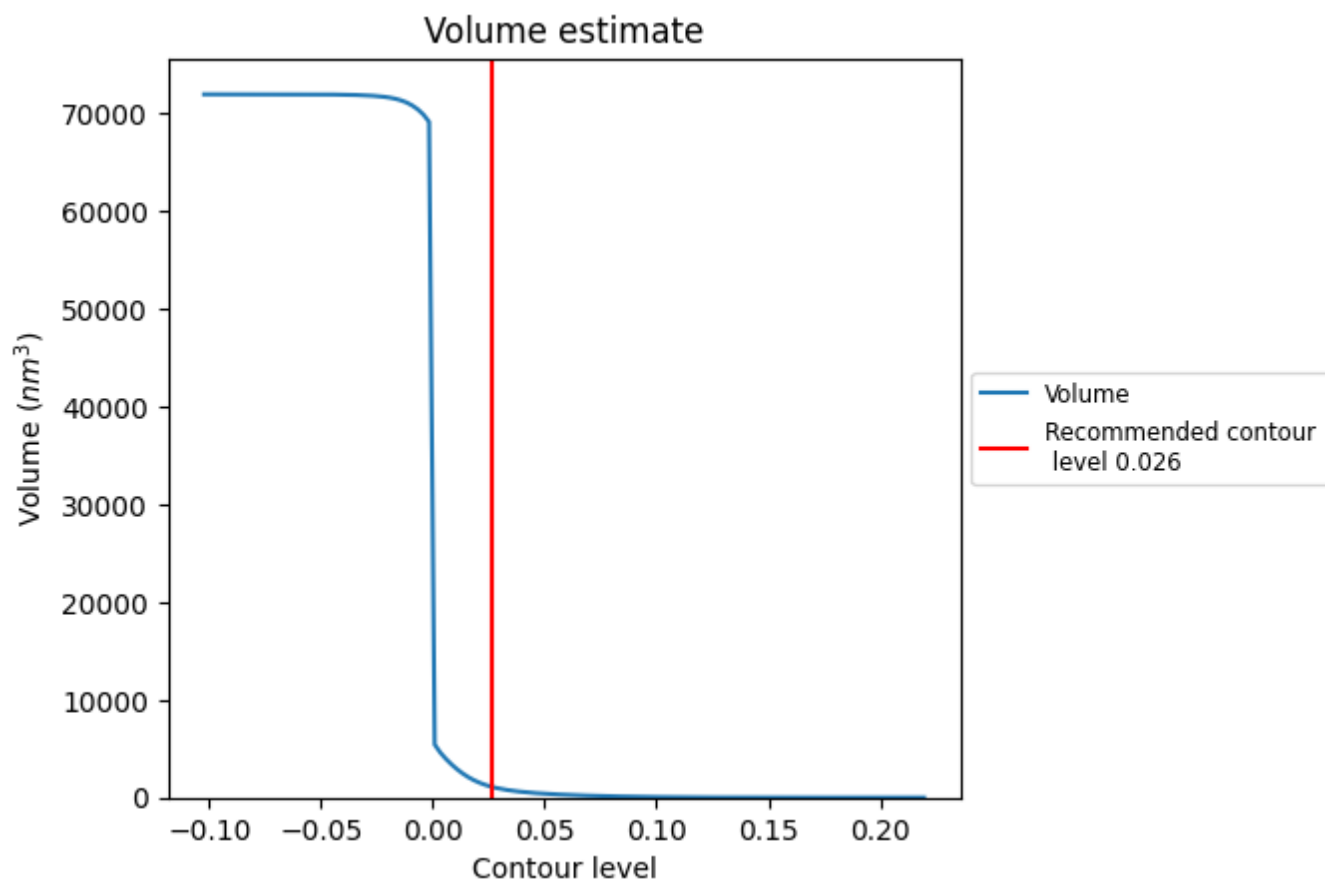
This section contains the results of statistical analysis of the map.

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.

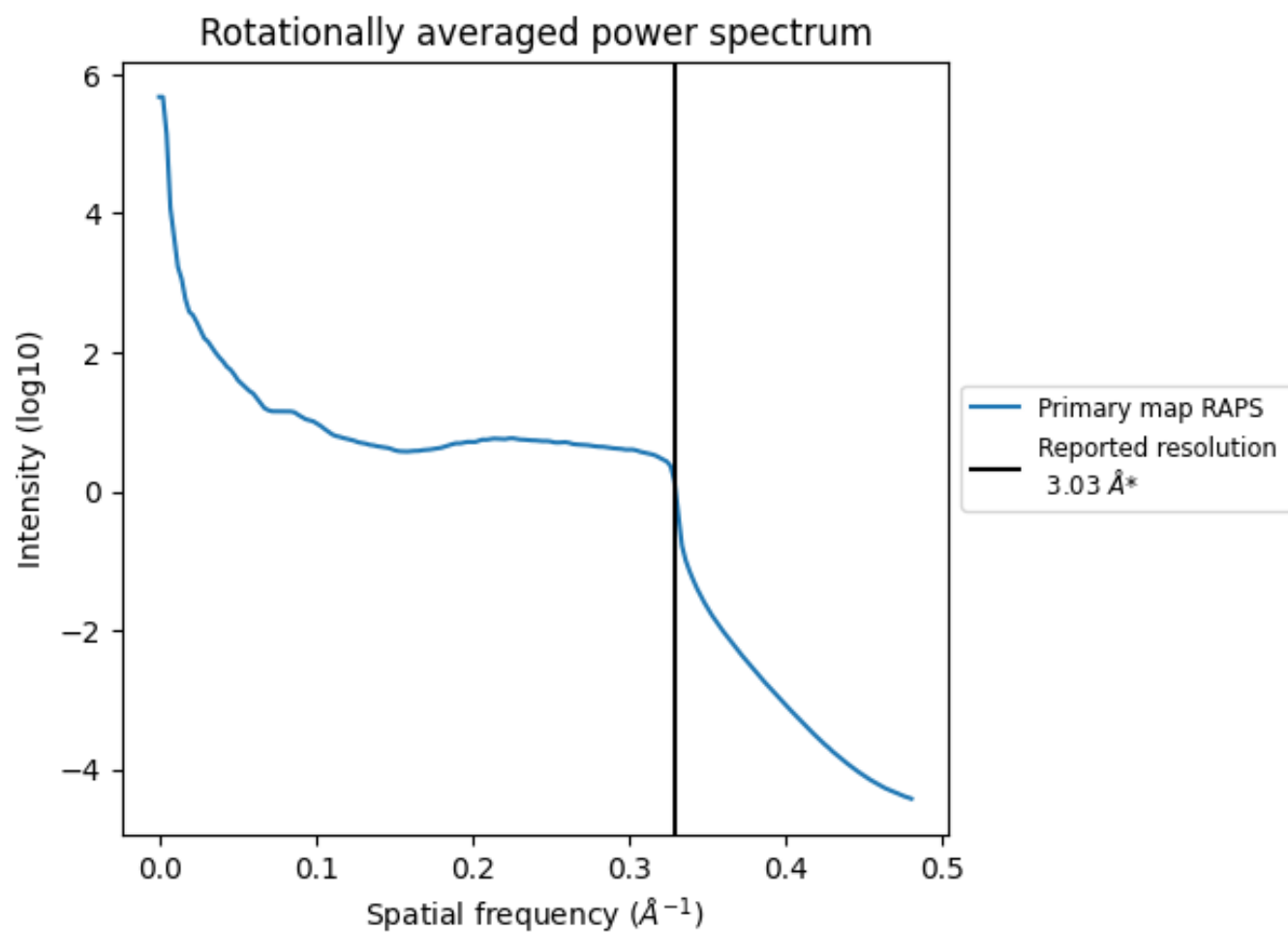
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1121 nm³; this corresponds to an approximate mass of 1013 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 0.330 Å⁻¹

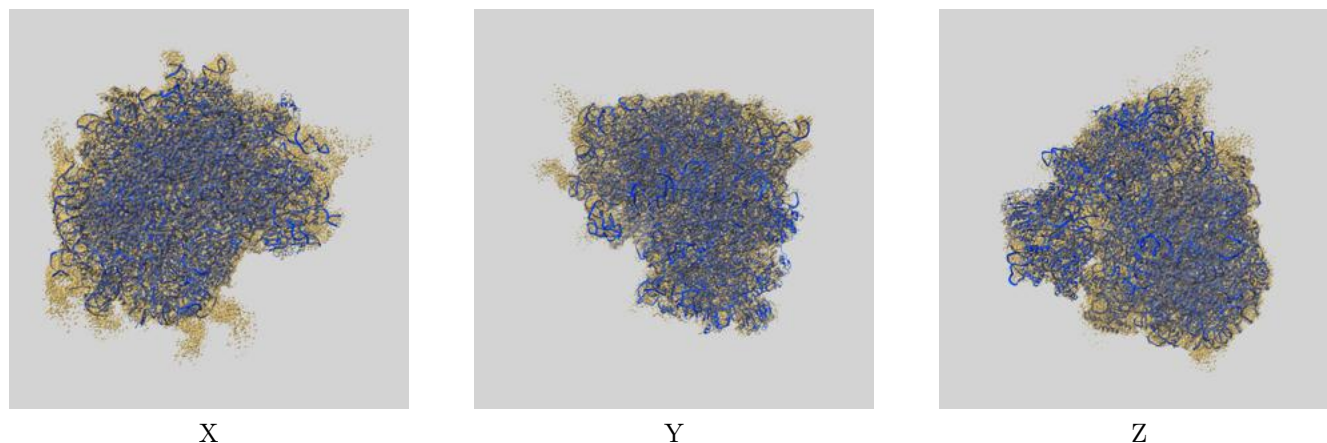
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

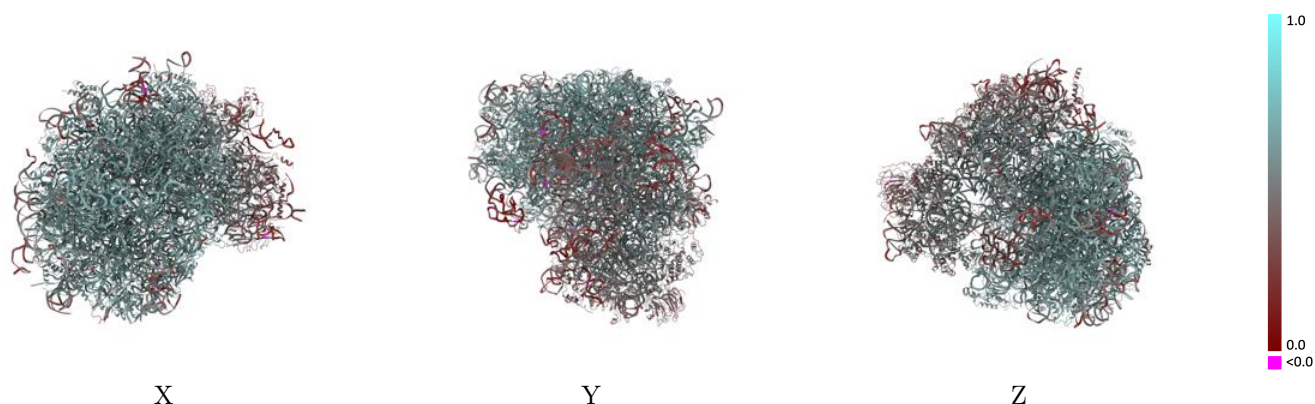
This section contains information regarding the fit between EMDB map EMD-30433 and PDB model 7CPV. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



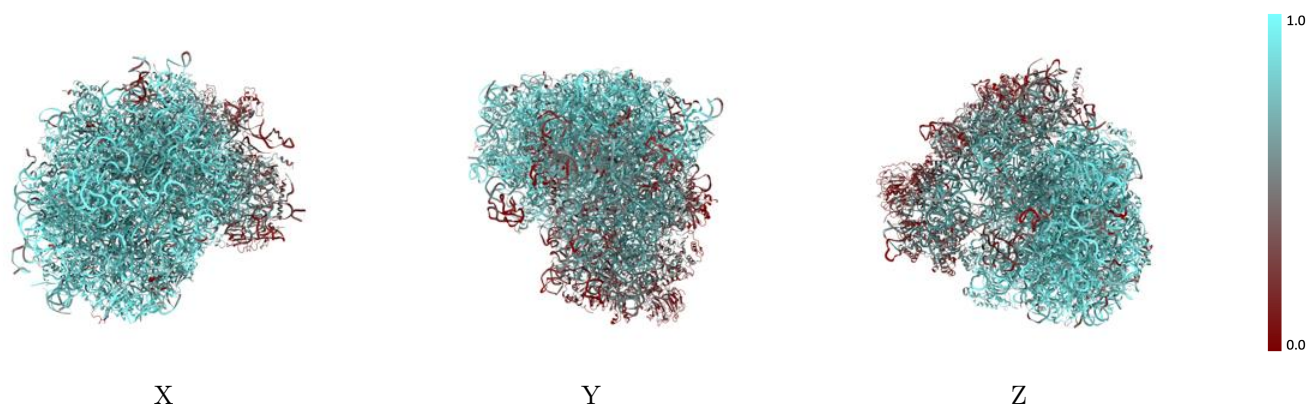
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



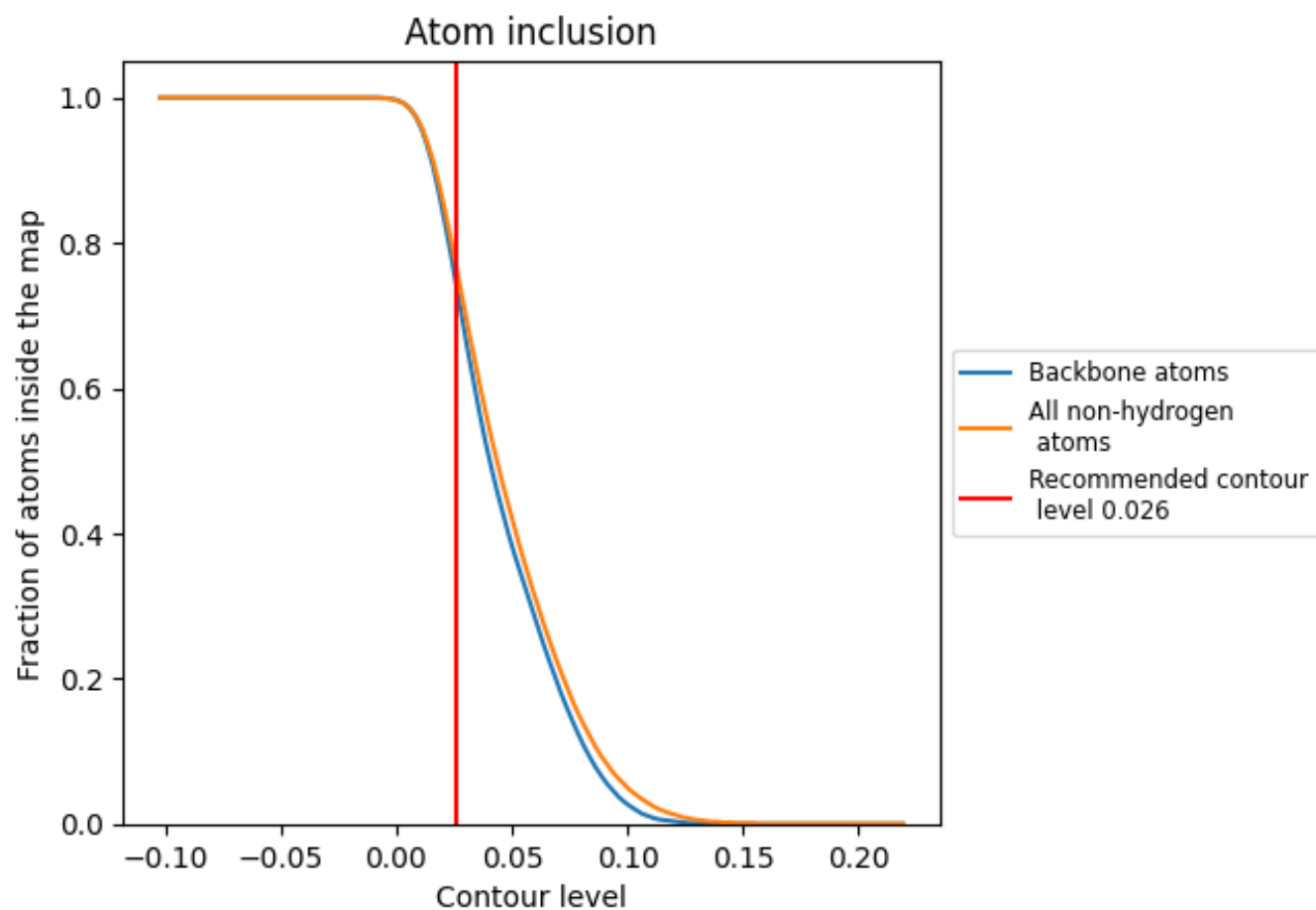
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 77% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7670	 0.5340
L5	 0.8900	 0.5640
L7	 0.9650	 0.6030
L8	 0.9130	 0.5840
LA	 0.8920	 0.6090
LB	 0.8740	 0.6030
LC	 0.8800	 0.5980
LD	 0.8430	 0.5780
LE	 0.7930	 0.5590
LF	 0.9000	 0.6140
LG	 0.7880	 0.5620
LH	 0.8490	 0.5800
LI	 0.8500	 0.5940
LJ	 0.7540	 0.5370
LL	 0.8490	 0.5880
LM	 0.8920	 0.5970
LN	 0.9330	 0.6220
LO	 0.8870	 0.6070
LP	 0.8860	 0.6100
LQ	 0.8970	 0.6160
LR	 0.7950	 0.5690
LS	 0.9110	 0.6180
LT	 0.8540	 0.5890
LU	 0.7580	 0.5440
LV	 0.8500	 0.5990
LW	 0.8660	 0.5990
LX	 0.8510	 0.5980
LY	 0.8700	 0.5980
LZ	 0.8350	 0.5760
La	 0.9150	 0.6210
Lb	 0.8260	 0.5870
Lc	 0.8290	 0.5700
Ld	 0.8250	 0.5880
Le	 0.8870	 0.6100
Lf	 0.9250	 0.6250



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Chain	Atom inclusion	Q-score
Lg	 0.8720	 0.5960
Lh	 0.8390	 0.5850
Li	 0.8250	 0.5760
Lj	 0.9200	 0.6130
Lk	 0.7270	 0.5590
Ll	 0.8690	 0.5980
Lm	 0.8920	 0.5950
Ln	 0.7290	 0.5580
Lo	 0.8400	 0.5970
Lp	 0.8230	 0.5980
Lr	 0.9030	 0.6060
S2	 0.6850	 0.4640
S6	 0.4330	 0.3540
SA	 0.4490	 0.4730
SB	 0.5820	 0.5100
SC	 0.5770	 0.4920
SD	 0.3150	 0.4170
SE	 0.4280	 0.4080
SF	 0.4180	 0.4670
SG	 0.3030	 0.4010
SH	 0.2560	 0.4030
SI	 0.5010	 0.4340
SJ	 0.4790	 0.3900
SK	 0.2770	 0.3950
SL	 0.6020	 0.4990
SN	 0.5330	 0.5020
SO	 0.6280	 0.5060
SP	 0.5700	 0.4750
SQ	 0.4200	 0.4580
SR	 0.2780	 0.4180
SS	 0.5480	 0.4830
ST	 0.4700	 0.4660
SU	 0.3200	 0.4240
SV	 0.4430	 0.4620
SW	 0.6370	 0.5280
SX	 0.5610	 0.4960
SY	 0.2950	 0.3490
SZ	 0.3480	 0.4350
Sa	 0.6500	 0.5190
Sb	 0.4570	 0.4450
Sc	 0.3690	 0.4500
Sd	 0.6390	 0.4780

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Chain	Atom inclusion	Q-score
Se	 0.3500	 0.4080
Sg	 0.2380	 0.3800