



## wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 11:20 pm BST

PDB ID : 8BRM  
EMDB ID : EMD-16222  
Title : Giardia ribosome in POST-T state, no E-site tRNA (A6)  
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.  
Deposited on : 2022-11-23  
Resolution : 3.33 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

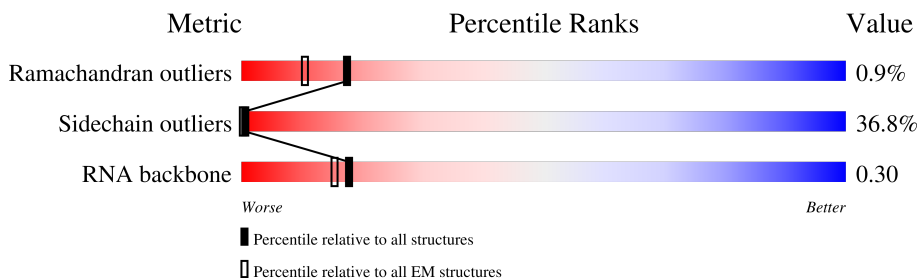
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.33 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	251	<div> <div>10%</div> <div>79%</div> <div>21%</div> </div>
2	LB	379	<div> <div>10%</div> <div>72%</div> <div>28%</div> </div>
3	LC	316	<div> <div>8%</div> <div>76%</div> <div>22%</div> <div>.</div> </div>
4	LD	143	<div> <div>58%</div> <div>41%</div> <div>..</div> </div>
5	LE	121	<div> <div>50%</div> <div>46%</div> <div>.</div> </div>
6	LF	297	<div> <div>43%</div> <div>70%</div> <div>28%</div> <div>.</div> </div>
7	LG	51	<div> <div>10%</div> <div>69%</div> <div>29%</div> <div>.</div> </div>
8	LH	235	<div> <div>22%</div> <div>69%</div> <div>22%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
9	LI	225	
10	LJ	185	
11	LK	210	
12	LL	173	
13	LM	234	
14	LN	131	
15	LO	204	
16	LP	197	
17	LQ	164	
18	LR	179	
19	LS	196	
20	LT	173	
21	LU	159	
22	LV	124	
23	LW	142	
24	LX	189	
25	LY	141	
26	LZ	135	
27	La	135	
28	Lb	149	
29	Lc	62	
30	Ld	109	
31	Le	106	
32	Lf	136	
33	Lg	123	

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Mol	Chain	Length	Quality of chain
34	Lh	120	
35	Li	124	
36	Lj	90	
37	Lk	89	
38	Ll	77	
39	Ln	217	
40	Lo	25	
41	Lp	106	
42	Lq	94	
43	Ls	127	
44	Lt	2697	
45	SA	245	
46	SB	242	
47	SC	217	
48	SD	248	
49	SE	268	
50	SF	190	
51	SG	248	
52	SH	190	
53	SI	174	
54	SJ	130	
55	SK	189	
56	SL	134	
57	SM	154	
58	SO	143	

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Mol	Chain	Length	Quality of chain
59	SP	154	
60	SQ	145	
61	SR	145	
62	ST	158	
63	SU	137	
64	SV	154	
65	SW	139	
66	SX	126	
67	SY	89	
68	Sb	132	
69	Sc	88	
70	Sd	109	
71	Se	81	
72	Sg	64	
73	Sh	51	
74	Sj	69	
75	St	1454	

## 2 Entry composition

There are 75 unique types of molecules in this entry. The entry contains 173978 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 Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	250	Total	C	N	O	S	0	0
			1886	1163	389	322	12		

- Molecule 2 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	378	Total	C	N	O	S	0	0
			2987	1886	566	514	21		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LC	309	Total	C	N	O	S	0	0
			2408	1514	468	418	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LD	142	Total	C	N	O	P	0	0
			3038	1350	563	983	142		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LE	117	Total	C	N	O	P	0	0
			2502	1116	457	812	117		

- Molecule 6 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LF	291	Total	C	N	O	S	0	0
			2337	1479	435	415	8		

- Molecule 7 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	LG	50	Total	C	N	O	0	0
			439	281	94	64		

- Molecule 8 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LH	213	Total	C	N	O	S	0	0
			1726	1097	314	310	5		

- Molecule 9 is a protein called Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	187	Total	C	N	O	S	0	0
			1494	952	274	263	5		

- Molecule 10 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LJ	184	Total	C	N	O	S	0	0
			1452	917	264	261	10		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LK	147	Total	C	N	O	S	0	0
			1207	762	231	210	4		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	165	Total	C	N	O	S	0	0
			1322	833	247	237	5		

- Molecule 13 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	201	Total	C	N	O	S	0	0
			1605	999	325	274	7		

- Molecule 14 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LN	130	Total	C	N	O	S	0	0
			1024	649	186	183	6		

- Molecule 15 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LO	203	Total	C	N	O	S	0	0
			1708	1080	357	265	6		

- Molecule 16 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LP	194	Total	C	N	O	S	0	0
			1578	994	306	266	12		

- Molecule 17 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LQ	153	Total	C	N	O	S	0	0
			1231	778	239	210	4		

- Molecule 18 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LR	178	Total	C	N	O	S	0	0
			1402	871	279	243	9		

- Molecule 19 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LS	192	Total	C	N	O	S	0	0
			1592	983	334	270	5		

- Molecule 20 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LT	170	Total	C	N	O	S	0	0
			1423	899	272	243	9		

- Molecule 21 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LU	156	Total	C	N	O	S	0	0
			1257	784	259	207	7		

- Molecule 22 is a protein called Ribosomal protein L22e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LV	103	Total	C	N	O	S	0	0
			845	540	145	158	2		

- Molecule 23 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LW	132	Total	C	N	O	S	0	0
			1015	641	193	176	5		

- Molecule 24 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LX	63	Total	C	N	O	S	0	0
			538	340	109	82	7		

- Molecule 25 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LY	119	Total	C	N	O	S	0	0
			962	619	174	166	3		

- Molecule 26 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LZ	133	Total	C	N	O	S	0	0
			1076	665	219	184	8		

- Molecule 27 is a protein called Ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	La	127	Total	C	N	O	S	0	0
			1013	638	190	179	6		

- Molecule 28 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Lb	148	Total	C	N	O	S	0	0
			1201	759	240	199	3		

- Molecule 29 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Lc	51	Total	C	N	O	S	0	0
			425	254	97	72	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	102	Total	C	N	O	S	0	0
			770	485	135	146	4		

- Molecule 31 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Le	100	Total	C	N	O		0	0
			818	518	158	142			

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lf	130	Total	C	N	O	S	0	0
			1077	683	215	173	6		

- Molecule 33 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lg	98	Total	C	N	O	S	0	0
			778	498	147	130	3		

- Molecule 34 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lh	96	Total	C	N	O	S	0	0
			774	478	161	131	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	120	Total	C	N	O	S	0	0
			969	613	190	161	5		

- Molecule 36 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lj	89	Total	C	N	O	S	0	0
			731	462	146	119	4		

- Molecule 37 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lk	88	Total	C	N	O	S	0	0
			711	435	152	117	7		

- Molecule 38 is a protein called Ribosomal protein L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ll	72	Total	C	N	O	S	0	0
			558	353	99	102	4		

- Molecule 39 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Ln	211	Total	C	N	O	S	0	0
			1678	1082	294	297	5		

- Molecule 40 is a protein called Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lo	25	Total	C	N	O	S	0	0
			227	140	57	27	3		

- Molecule 41 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lp	93	Total	C	N	O	S	0	0
			767	478	159	125	5		

- Molecule 42 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lq	91	Total	C	N	O	S	0	0
			708	437	144	120	7		

- Molecule 43 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ls	47	Total	C	N	O	S	0	0
			388	234	83	64	7		

- Molecule 44 is a RNA chain called Large Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lt	2594	Total	C	N	O	P	0	0
			55663	24736	10313	18020	2594		

- Molecule 45 is a protein called Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	196	Total	C	N	O	S	0	0
			1569	1013	274	274	8		

- Molecule 46 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	216	Total	C	N	O	S	0	0
			1667	1059	302	301	5		

- Molecule 47 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	209	Total	C	N	O	S	0	0
			1658	1045	305	292	16		

- Molecule 48 is a protein called Ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD	229	Total	C	N	O	S	0	0
			1855	1172	346	324	13		

- Molecule 49 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SE	260	Total	C	N	O	S	0	0
			2085	1333	384	356	12		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	186	Total	C	N	O	S	0	0
			1442	896	275	262	9		

- Molecule 51 is a protein called Ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SG	209	Total	C	N	O	S	0	0
			1646	1033	312	291	10		

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	184	Total	C	N	O	S	0	0
			1481	948	258	268	7		

- Molecule 53 is a protein called Ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	173	Total	C	N	O	S	0	0
			1357	850	260	244	3		

- Molecule 54 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SJ	129	Total	C	N	O	S	0	0
			1031	659	192	177	3		

- Molecule 55 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SK	176	Total	C	N	O	S	0	0
			1423	889	281	247	6		

- Molecule 56 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	100	Total	C	N	O	S	0	0
			819	530	138	148	3		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	151	Total	C	N	O	S	0	0
			1251	794	246	205	6		

- Molecule 58 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SO	139	Total	C	N	O	S	0	0
			1080	683	213	181	3		

- Molecule 59 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	150	Total	C	N	O	S	0	0
			1192	758	228	201	5		

- Molecule 60 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	125	Total	C	N	O	S	0	0
			916	564	189	160	3		

- Molecule 61 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	116	Total	C	N	O	S	0	0
			943	601	184	150	8		

- Molecule 62 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	151	Total	C	N	O	S	0	0
			1180	736	229	212	3		

- Molecule 63 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	108	Total	C	N	O	S	0	0
			872	542	167	158	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	104	THR	ALA	conflict	UNP A8BRG5

- Molecule 64 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	141	Total	C	N	O	S	0	0
			1117	687	227	197	6		

- Molecule 65 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	137	Total	C	N	O	S	0	0
			1071	680	202	186	3		

- Molecule 66 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	100	Total	C	N	O	S	0	0
			794	507	145	137	5		

- Molecule 67 is a protein called Ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SY	86	Total	C	N	O	S	0	0
			651	403	120	122	6		

- Molecule 68 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sb	118	Total	C	N	O	S	0	0
			941	598	177	160	6		

- Molecule 69 is a protein called Ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sc	73	Total	C	N	O	S	0	0
			578	366	104	102	6		

- Molecule 70 is a protein called Ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sd	101	Total	C	N	O	S	0	0
			821	504	171	139	7		

- Molecule 71 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Se	79	Total	C	N	O	S	0	0
			621	392	109	115	5		

- Molecule 72 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Sg	63	Total	C	N	O	S	0	0
			505	311	100	92	2		

- Molecule 73 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sh	50	Total	C	N	O	S	0	0
			417	264	80	67	6		

- Molecule 74 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sj	62	Total	C	N	O	S	0	0
			509	322	104	82	1		

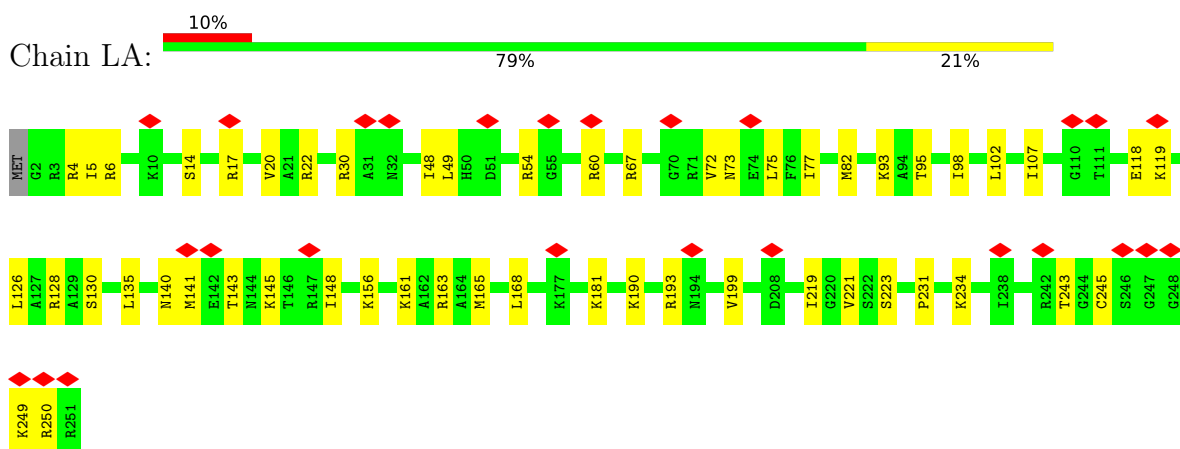
- Molecule 75 is a RNA chain called Small Subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	St	1454	Total	C	N	O	P	0	0
			31176	13861	5772	10090	1453		

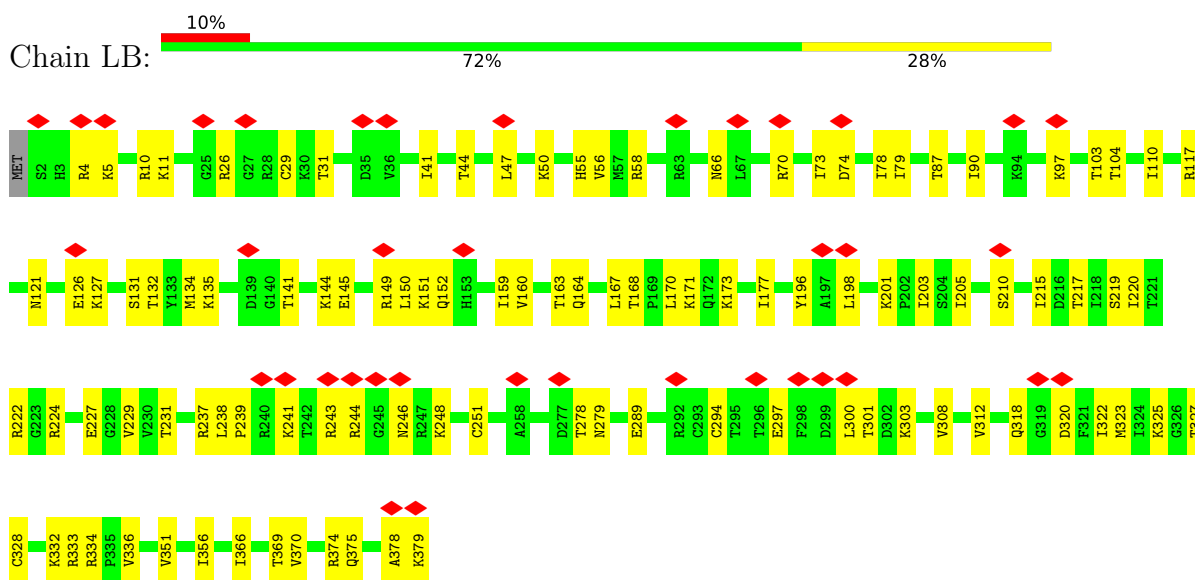
### 3 Residue-property plots

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.

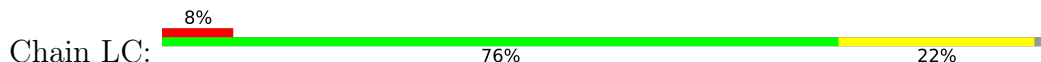
#### • Molecule 1: Ribosomal protein L2

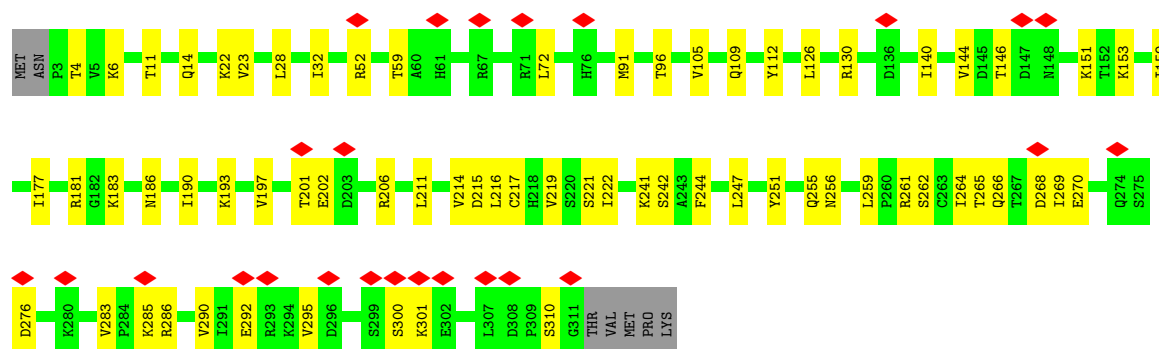


#### • Molecule 2: Ribosomal protein L3



#### • Molecule 3: Ribosomal protein L4

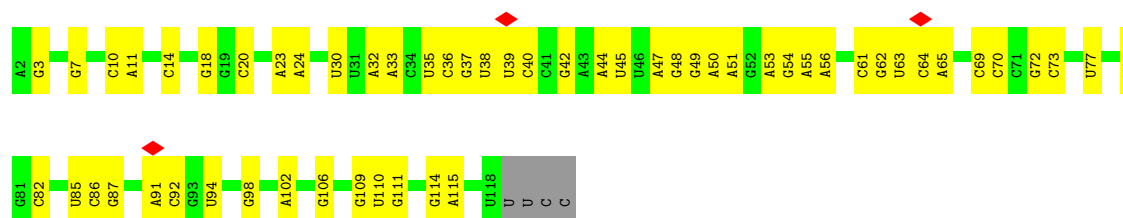




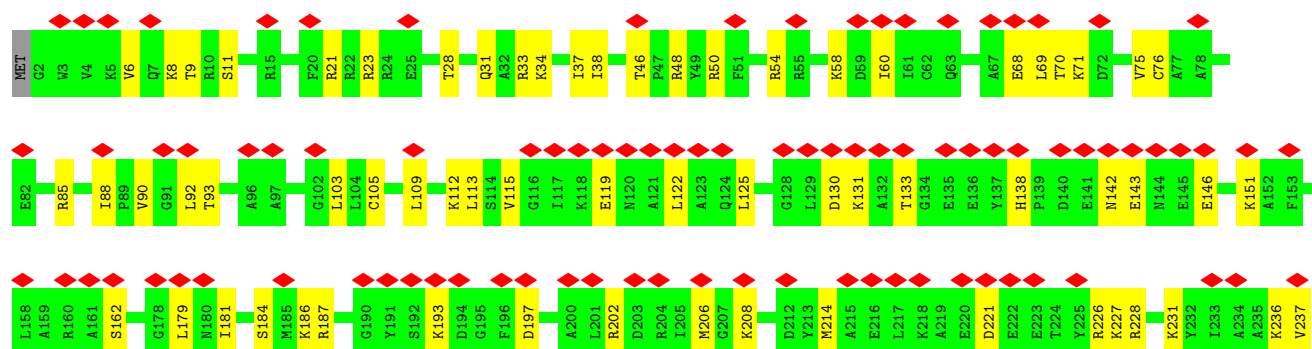
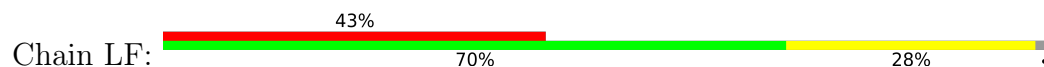
• Molecule 4: 5.8S rRNA



• Molecule 5: 5S rRNA

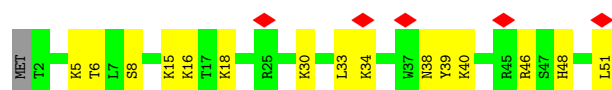


• Molecule 6: Ribosomal protein L5

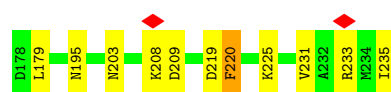




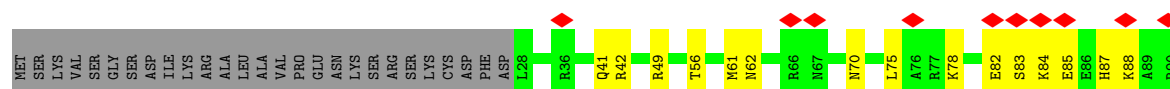
• Molecule 7: Ribosomal protein L39



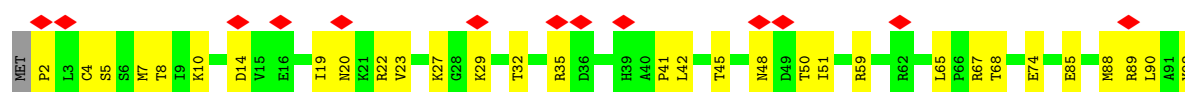
• Molecule 8: Ribosomal protein L7

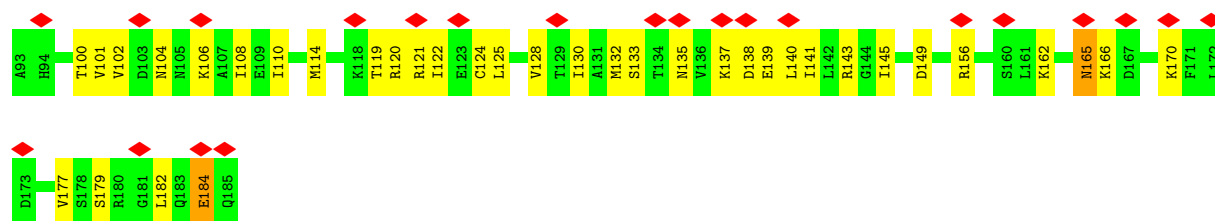


• Molecule 9: Ribosomal protein L7a

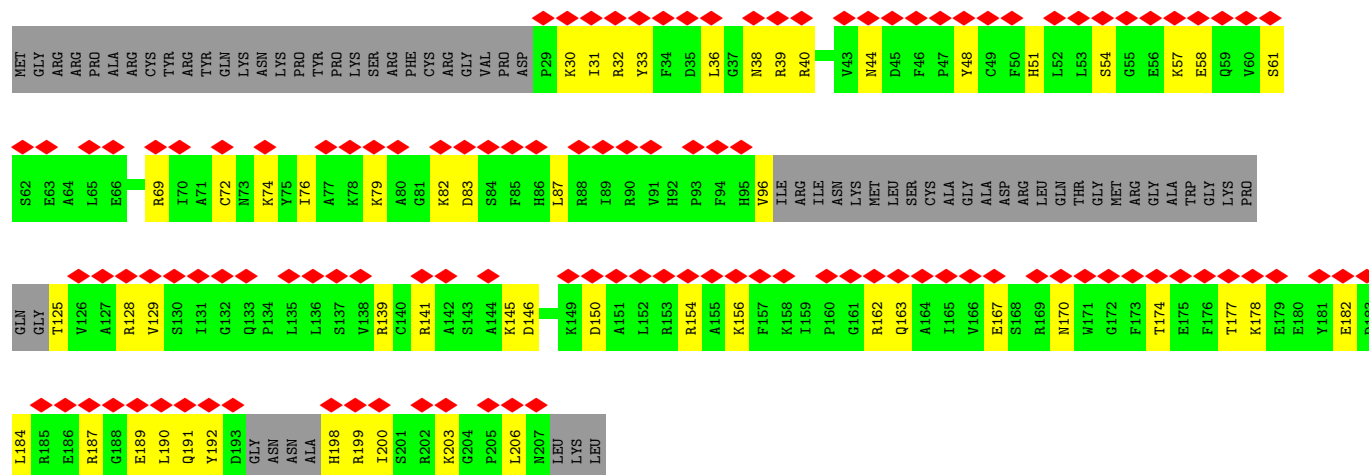


• Molecule 10: Ribosomal protein L6

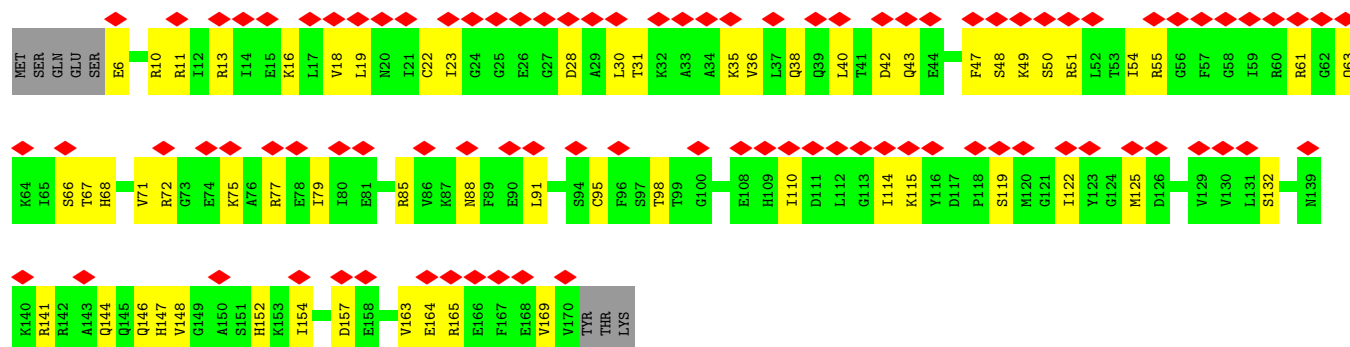




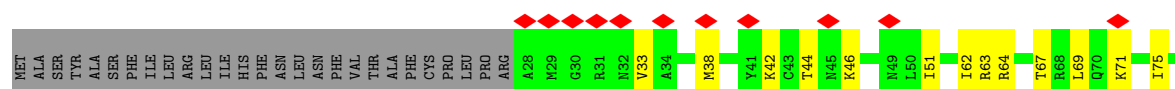
• Molecule 11: Ribosomal protein L10

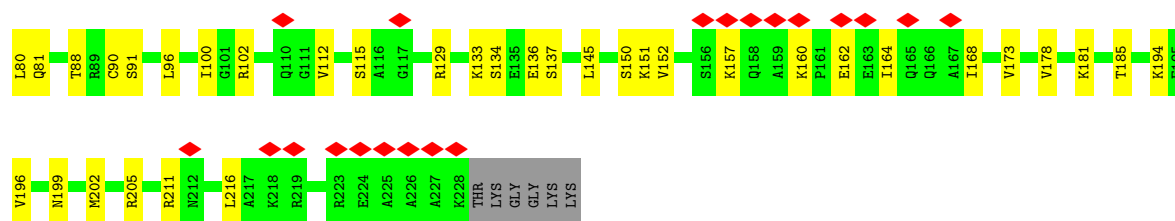


• Molecule 12: Ribosomal protein L11

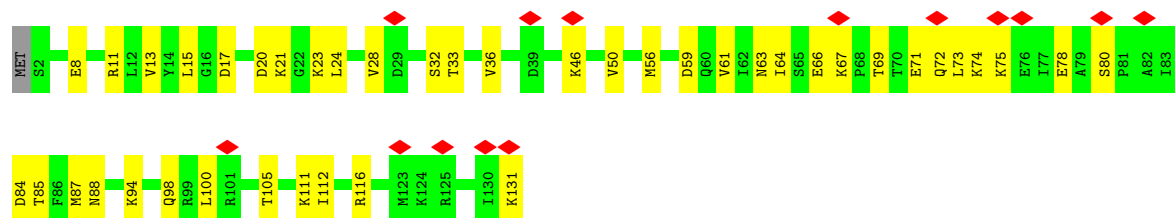


• Molecule 13: Ribosomal protein L13

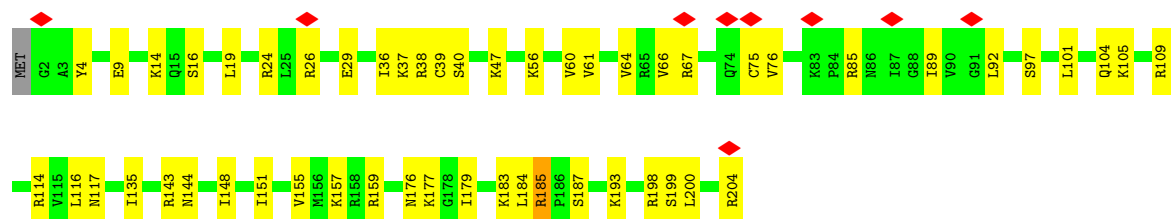
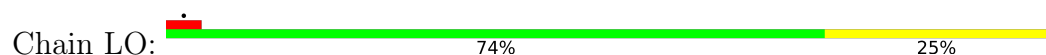




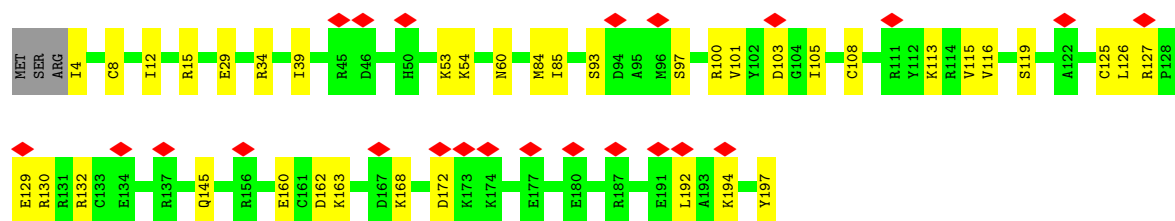
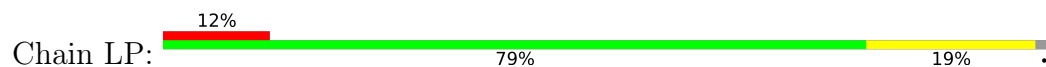
• Molecule 14: Ribosomal protein L14



• Molecule 15: Ribosomal protein L15

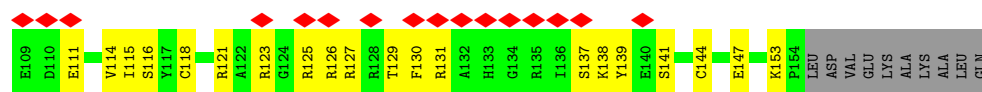


• Molecule 16: Ribosomal protein L13a

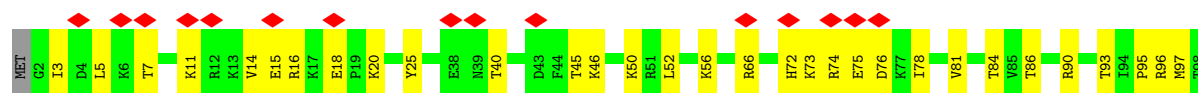
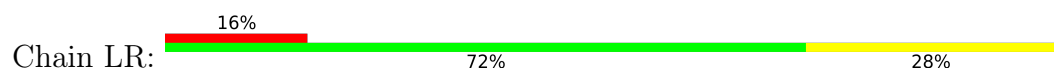


• Molecule 17: Ribosomal protein L17

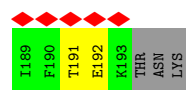
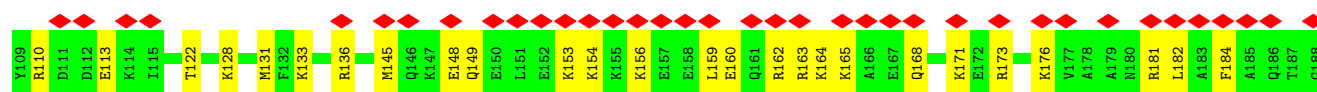
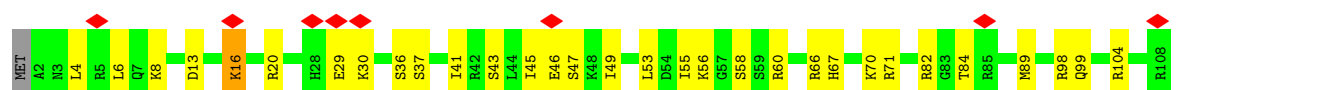




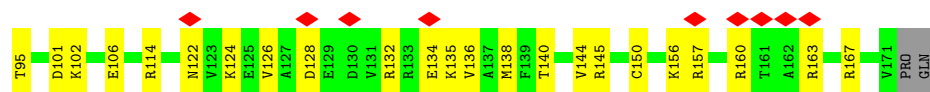
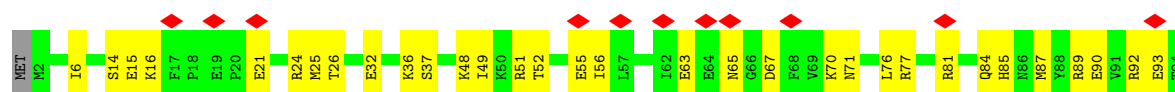
• Molecule 18: Ribosomal protein L18



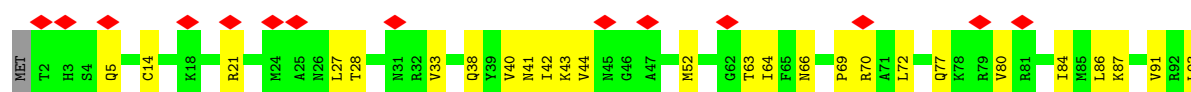
• Molecule 19: Ribosomal protein L19

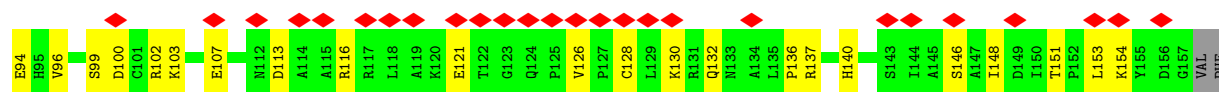


• Molecule 20: Ribosomal protein L18a

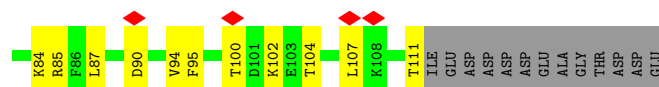
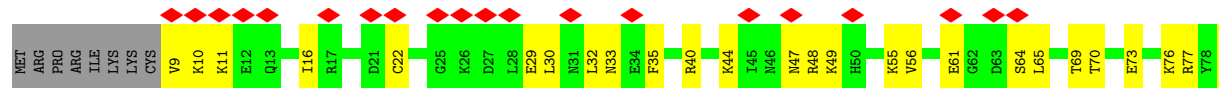


• Molecule 21: Ribosomal protein L21

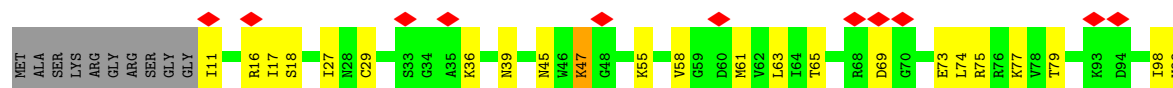
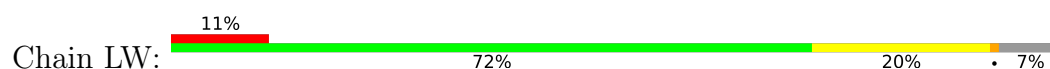




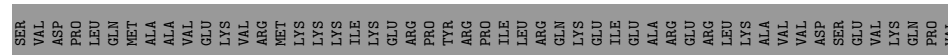
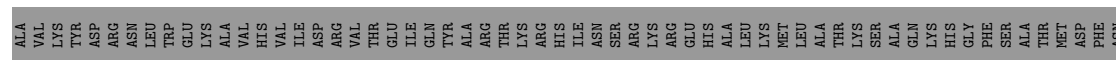
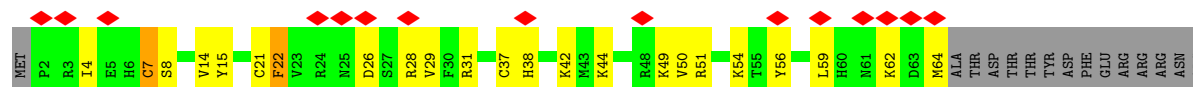
- Molecule 22: Ribosomal protein L22e



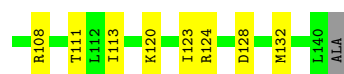
- Molecule 23: Ribosomal protein L23



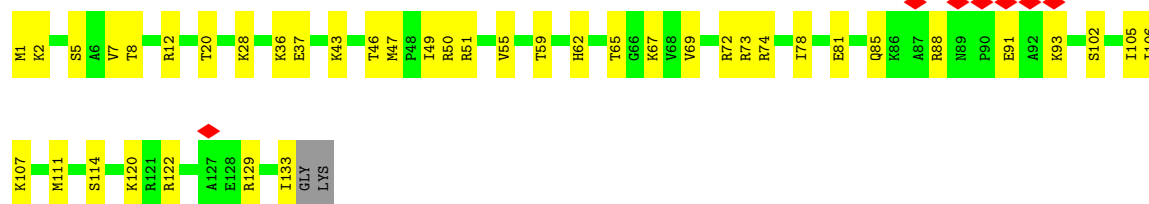
- Molecule 24: Ribosomal protein L24



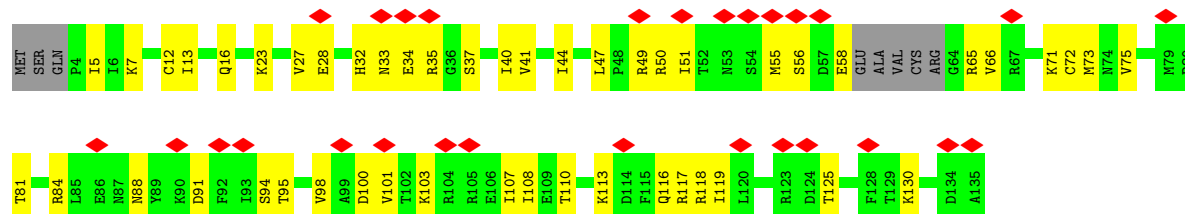
- Molecule 25: Ribosomal protein L23A



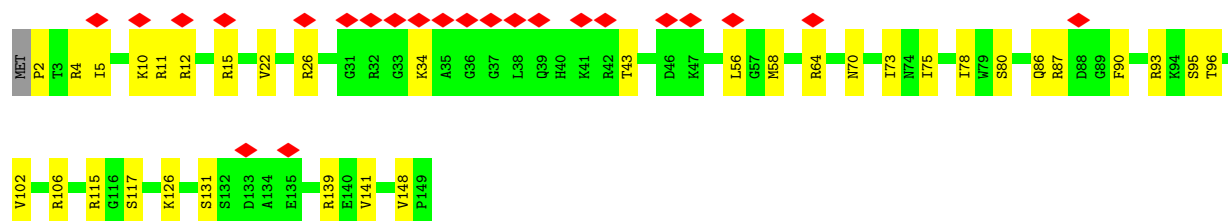
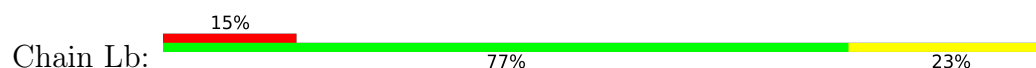
- Molecule 26: Ribosomal protein L26



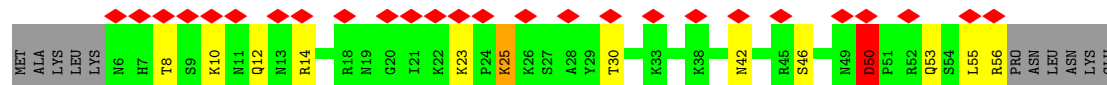
• Molecule 27: Ribosomal protein L27



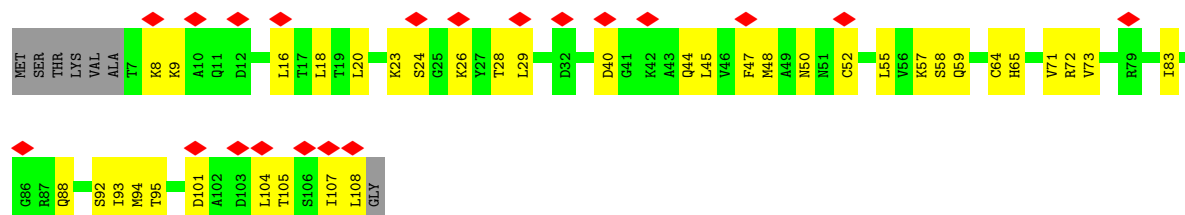
• Molecule 28: Ribosomal protein L27a



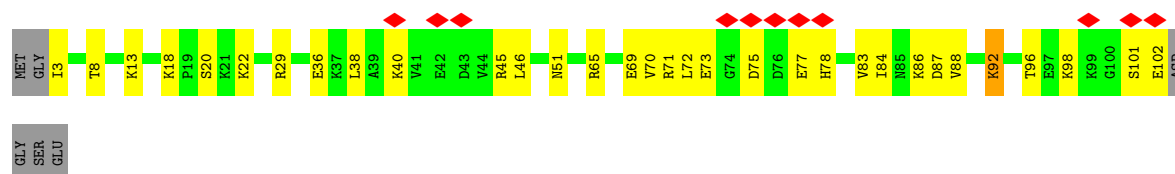
• Molecule 29: Ribosomal protein L29



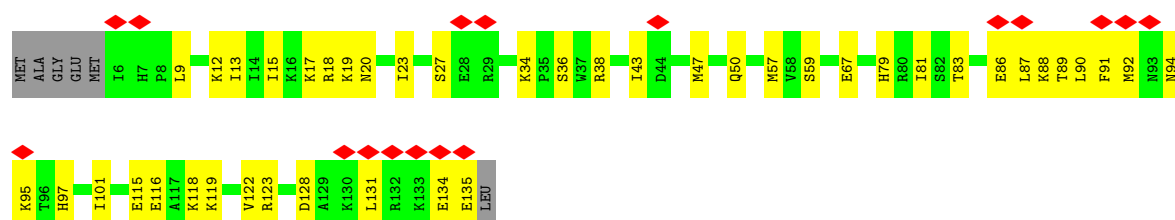
• Molecule 30: Ribosomal protein L30



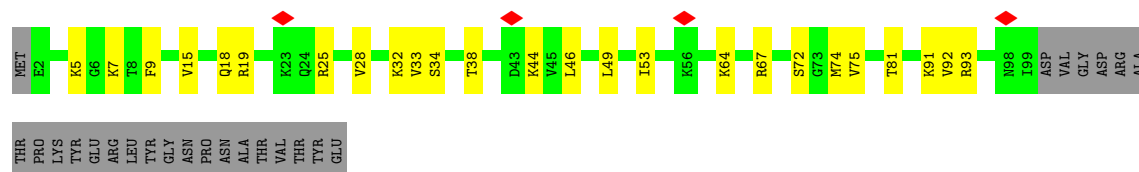
- Molecule 31: Ribosomal protein L31B



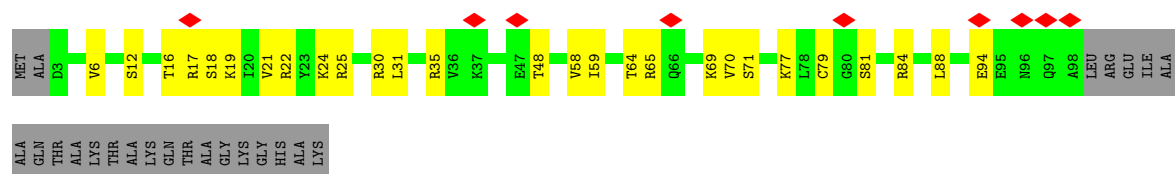
- Molecule 32: Ribosomal protein L32



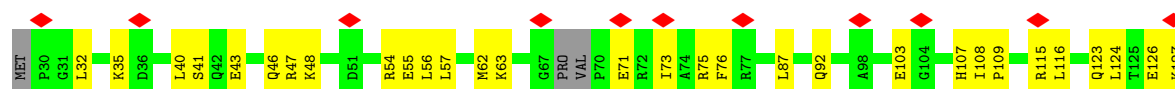
- Molecule 33: Ribosomal protein L35a

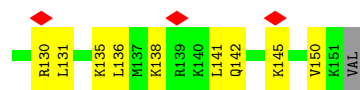


- Molecule 34: Ribosomal protein L34

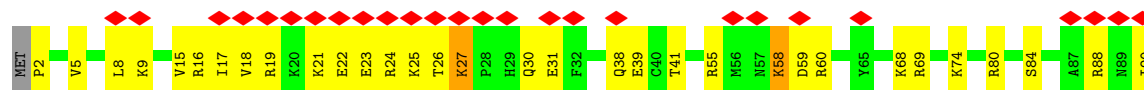


- Molecule 35: Ribosomal protein L29

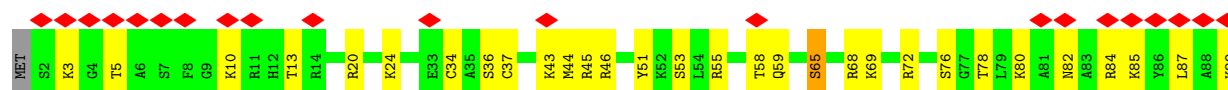




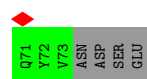
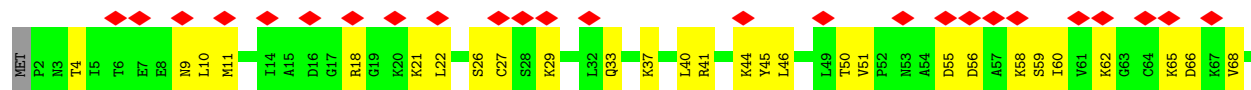
- Molecule 36: Ribosomal protein L36-1



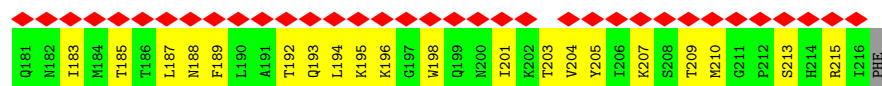
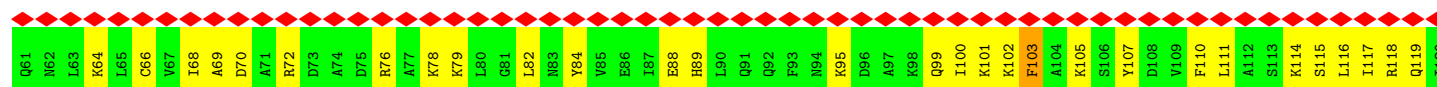
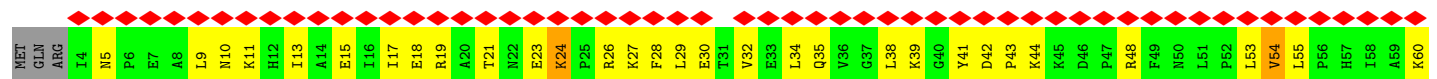
- Molecule 37: Ribosomal protein L37



- Molecule 38: Ribosomal protein L38e



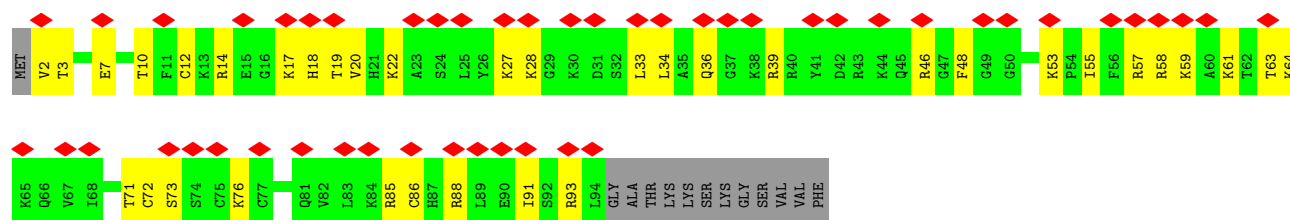
- Molecule 39: Ribosomal protein L10a



- Molecule 40: Ribosomal protein L41



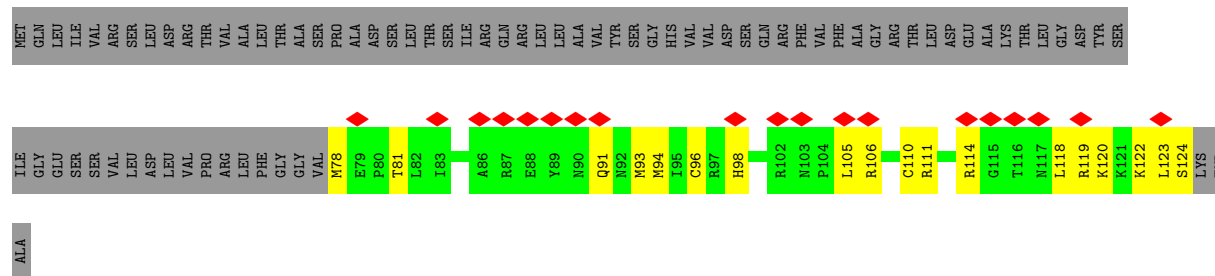
• Molecule 41: Ribosomal protein L44



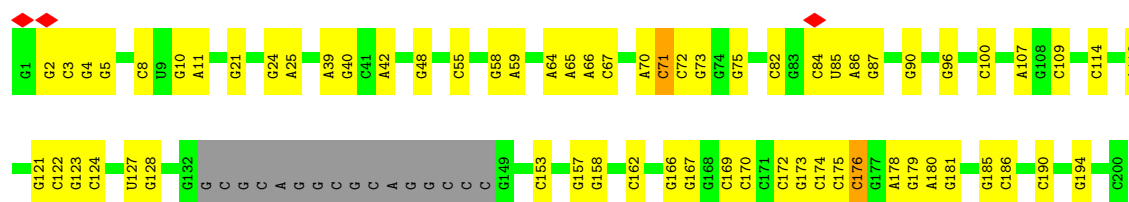
• Molecule 42: Ribosomal protein L37a



• Molecule 43: Ubiquitin/Ribosomal protein L40e

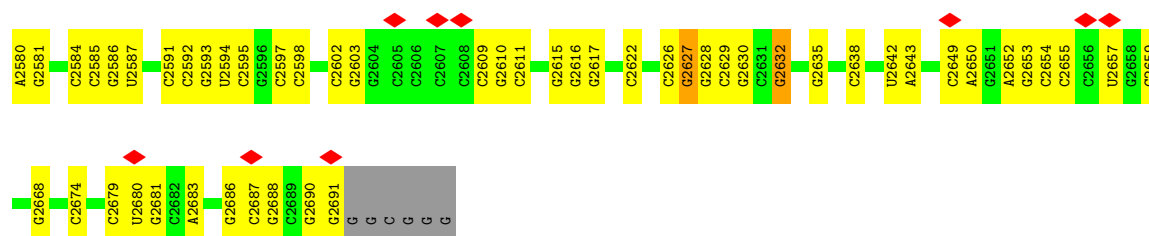


• Molecule 44: Large Subunit rRNA

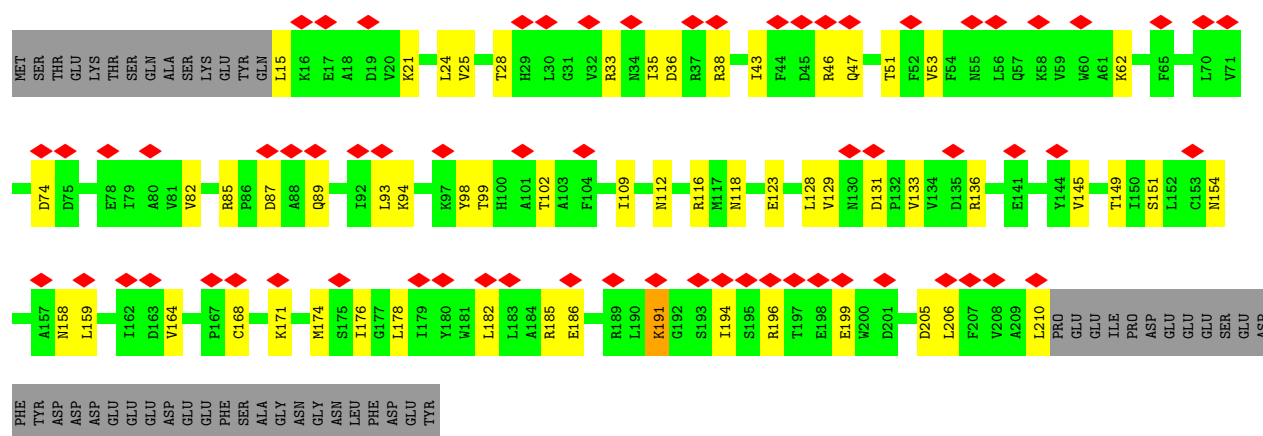




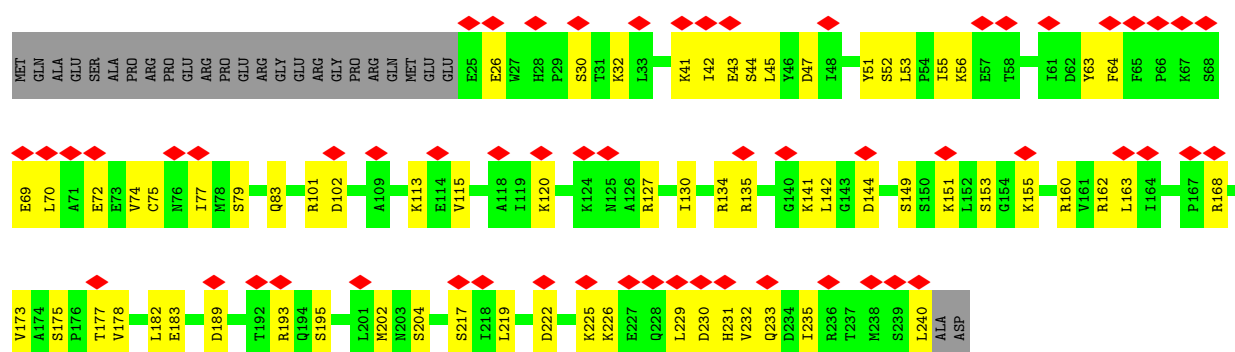
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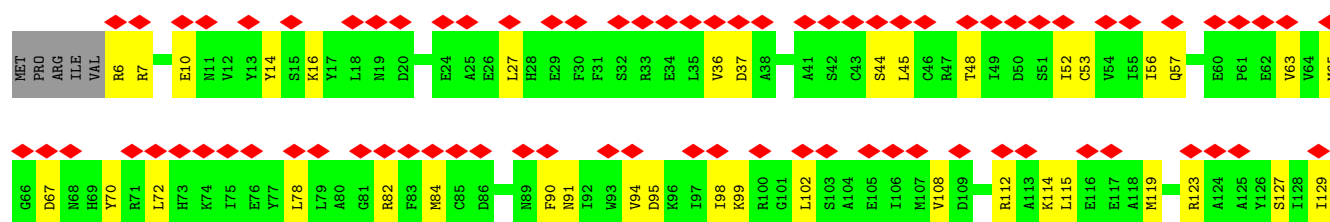
• Molecule 45: Ribosomal protein SA

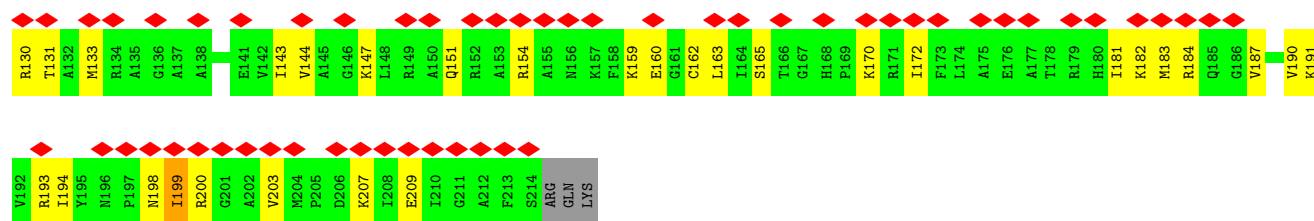


• Molecule 46: Ribosomal protein S2

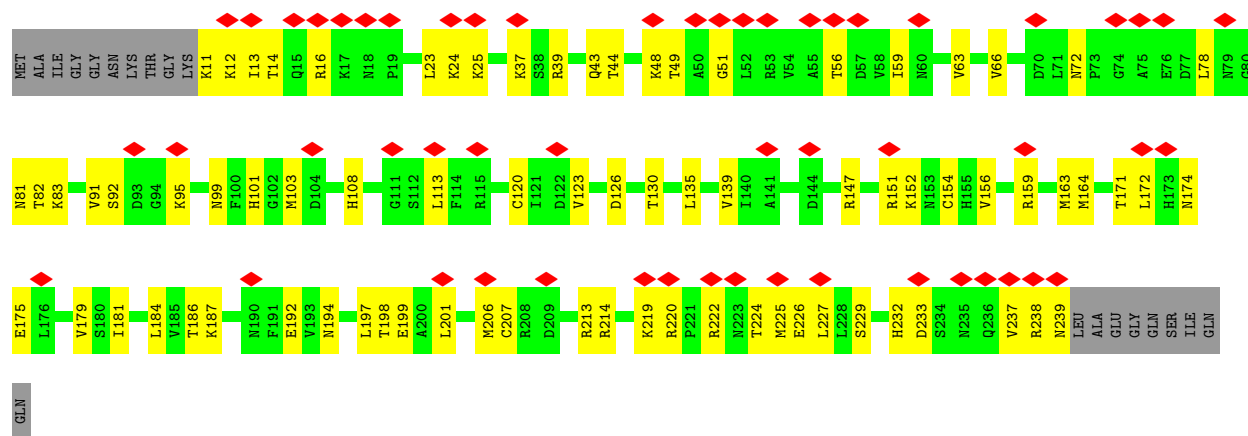


• Molecule 47: Ribosomal protein S3

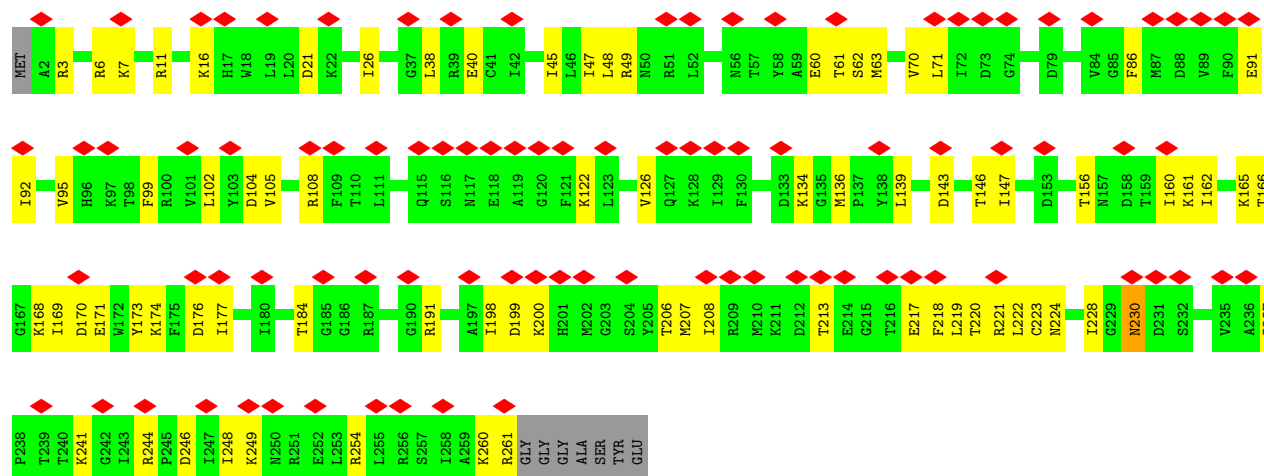




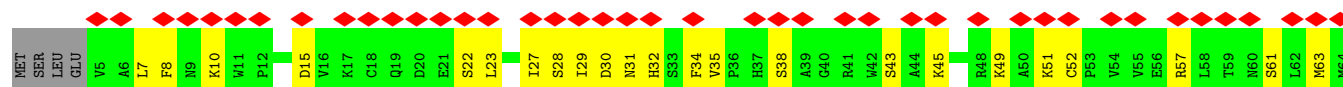
• Molecule 48: Ribosomal protein S3a

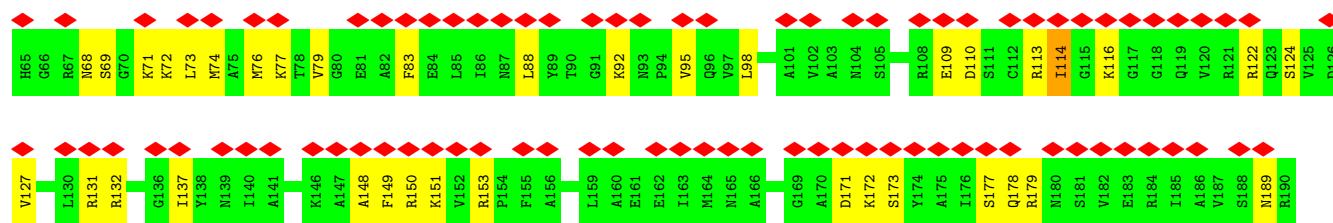


• Molecule 49: Ribosomal protein S4

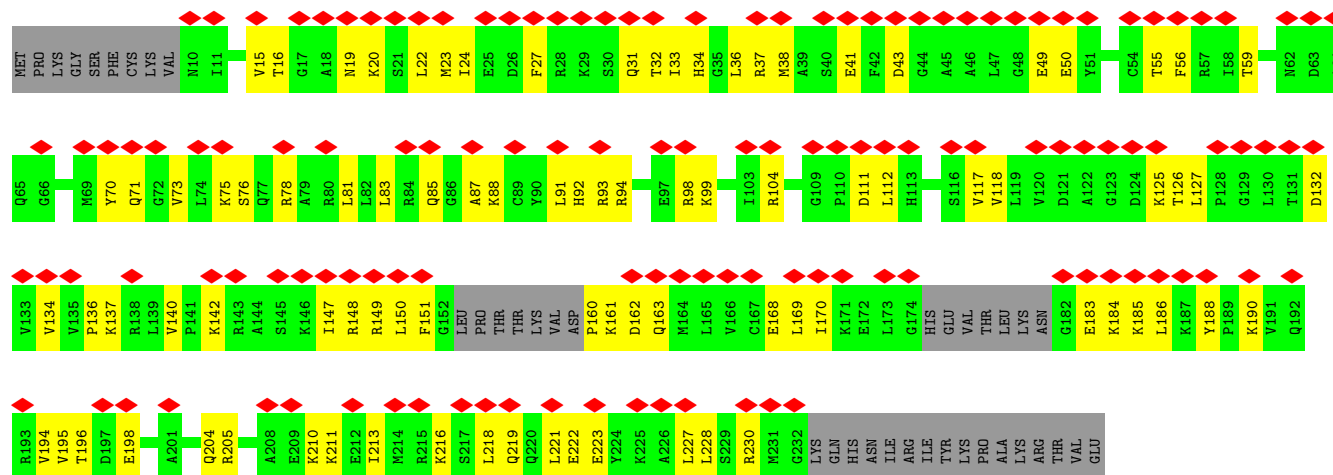


• Molecule 50: Ribosomal protein S5

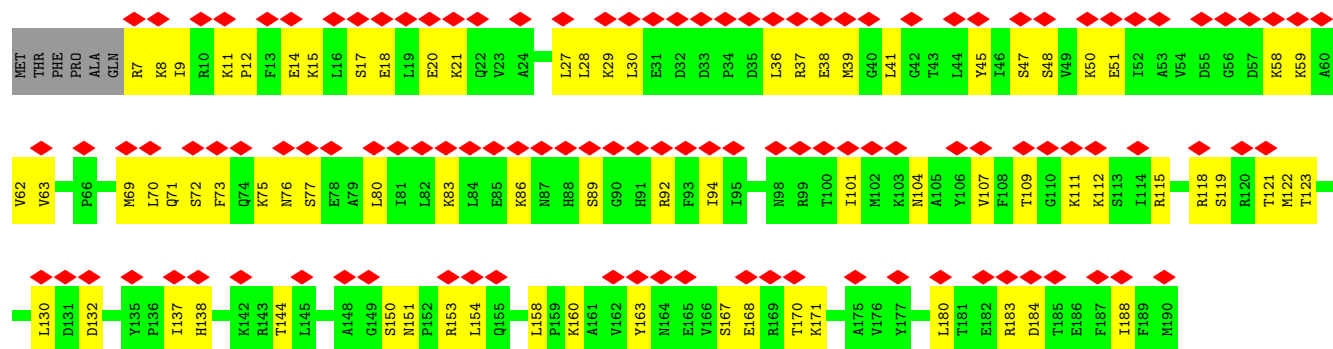




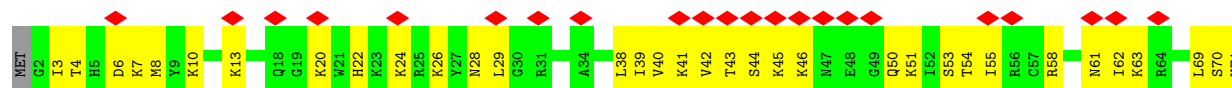
• Molecule 51: Ribosomal protein S6



• Molecule 52: Ribosomal protein S7

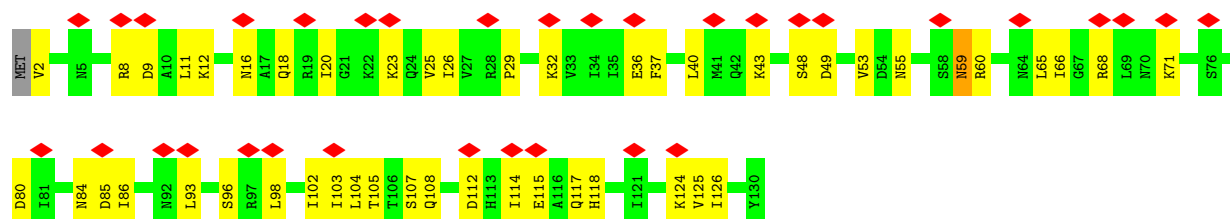


• Molecule 53: Ribosomal protein S8

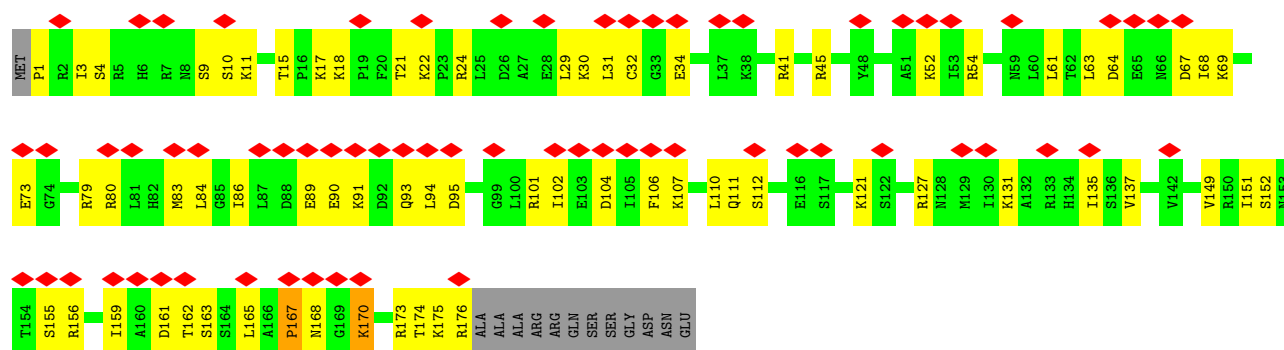




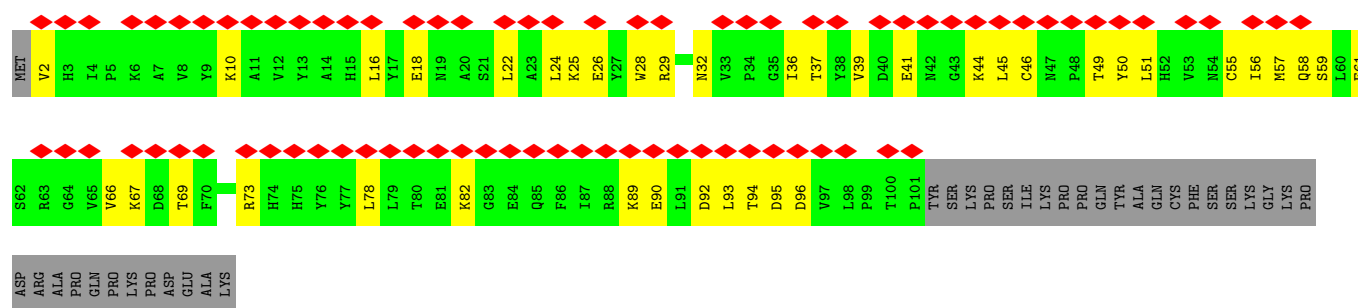
• Molecule 54: Ribosomal protein S15A



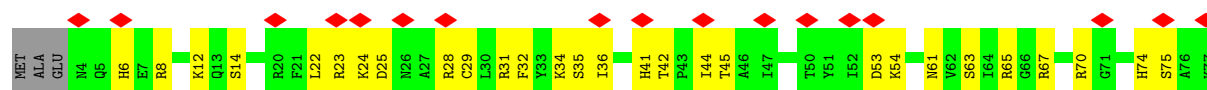
• Molecule 55: Ribosomal protein S9

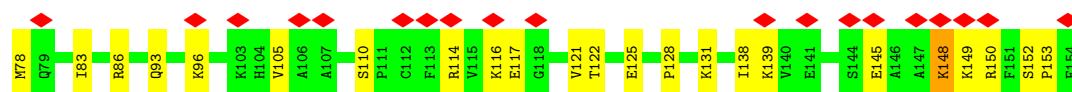


• Molecule 56: Ribosomal protein S10B

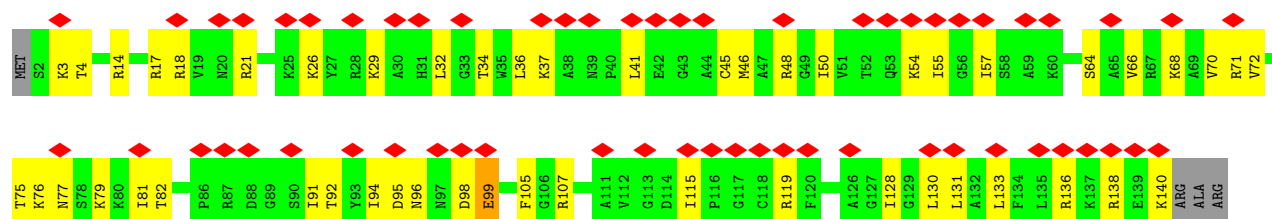
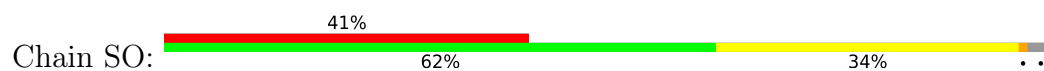


• Molecule 57: Ribosomal protein S11

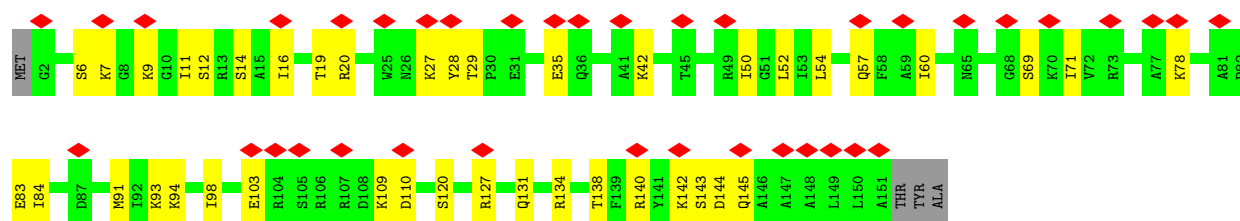
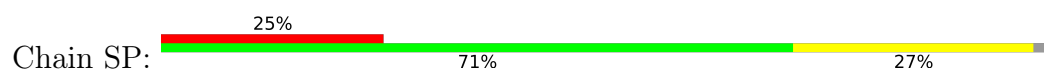




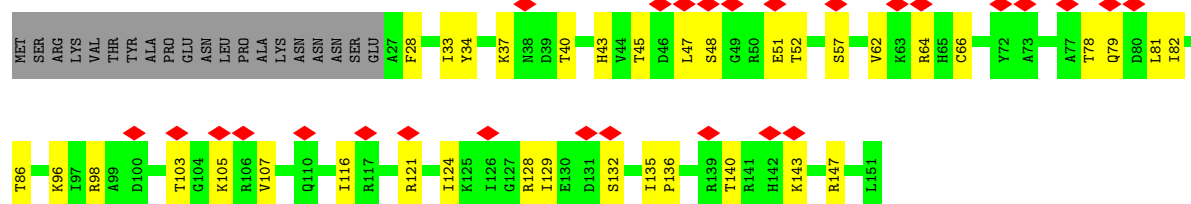
• Molecule 58: Ribosomal protein S23



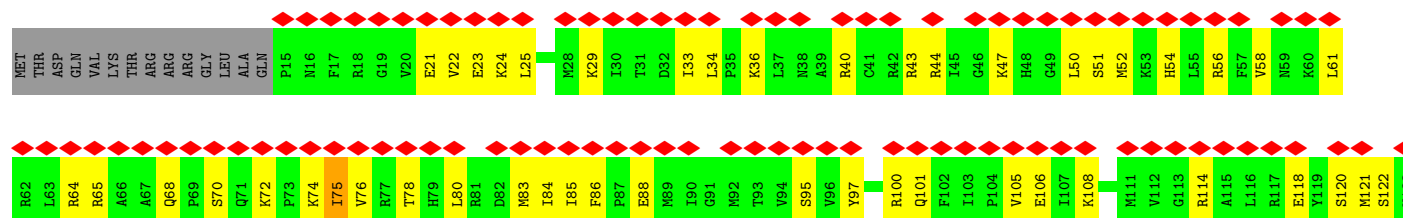
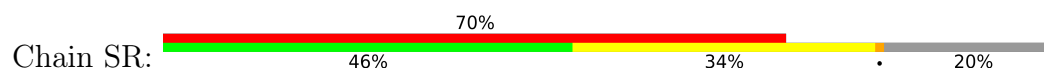
• Molecule 59: Ribosomal protein S13

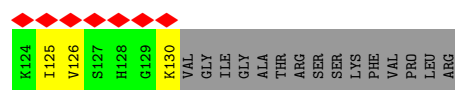


• Molecule 60: Ribosomal protein S14

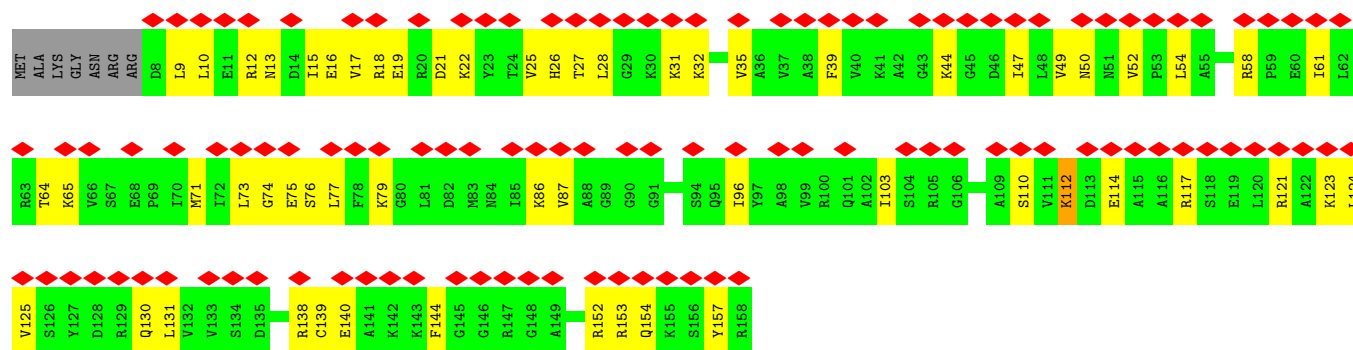
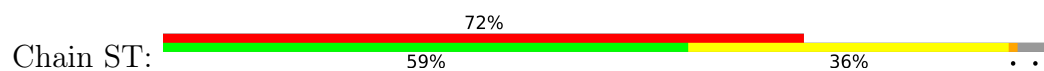


• Molecule 61: Ribosomal protein S15

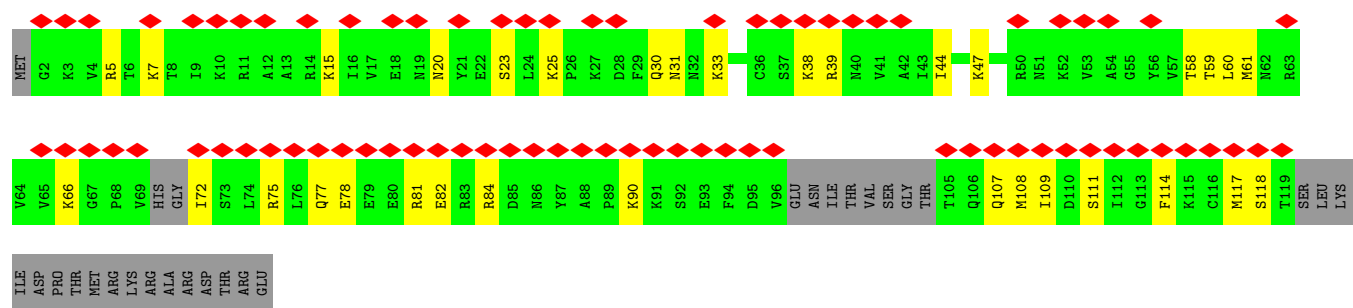




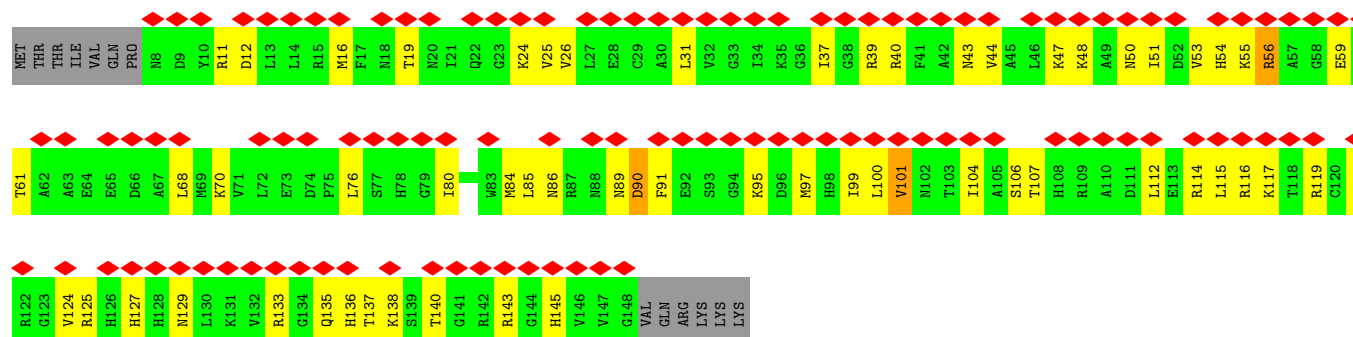
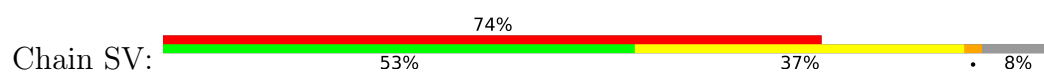
• Molecule 62: Ribosomal protein S16



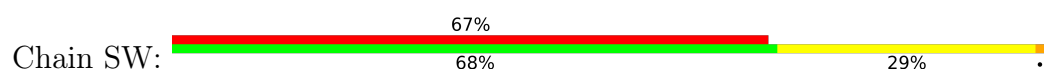
• Molecule 63: Ribosomal protein S17

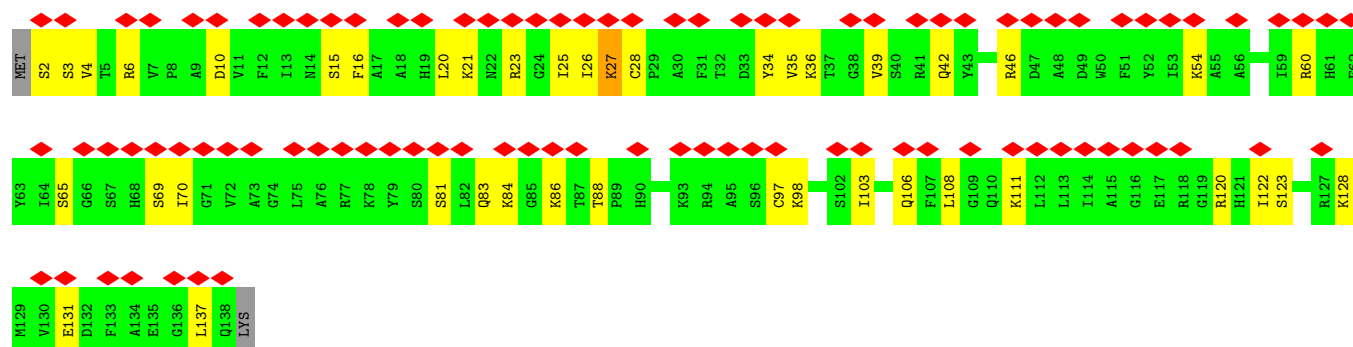


• Molecule 64: Ribosomal protein S18

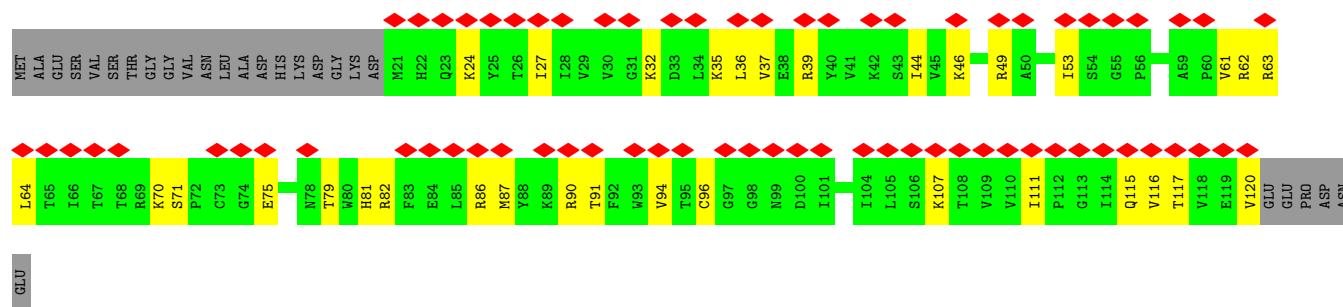


• Molecule 65: Ribosomal protein S19e

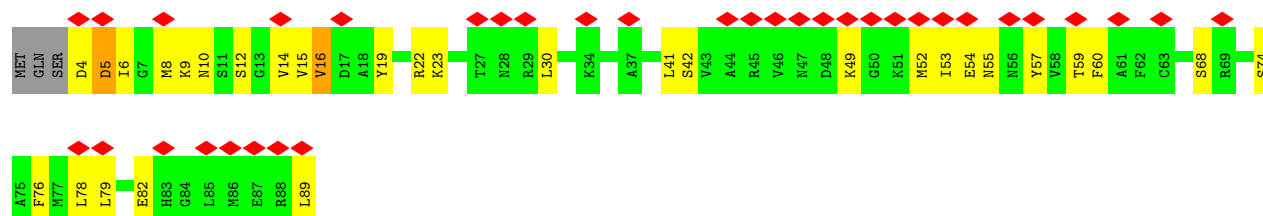
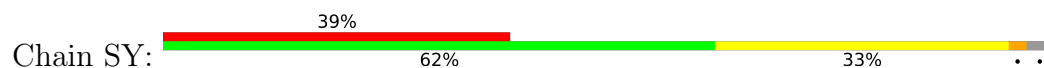




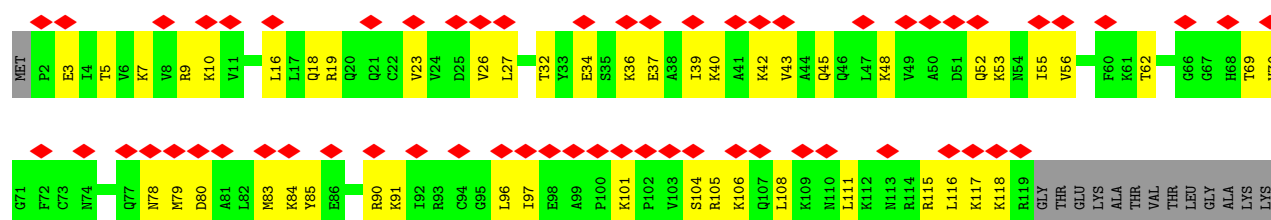
• Molecule 66: Ribosomal protein S20



• Molecule 67: Ribosomal protein S21

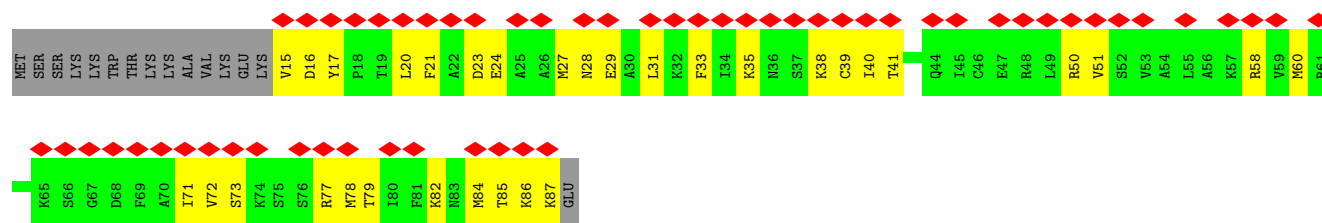


• Molecule 68: Ribosomal protein S24

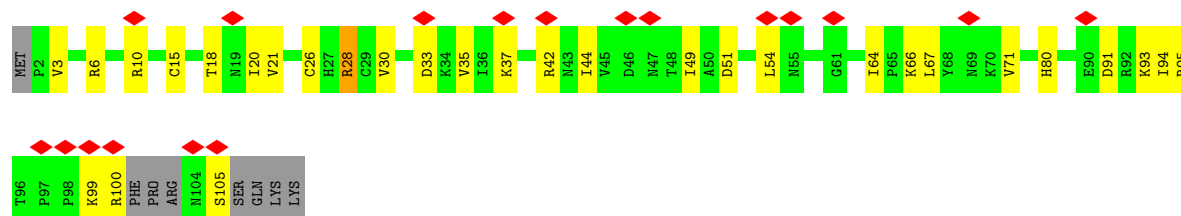


• Molecule 69: Ribosomal protein S25

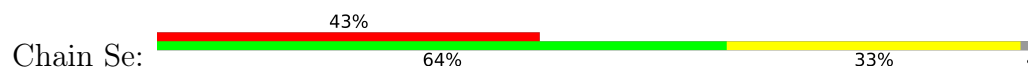




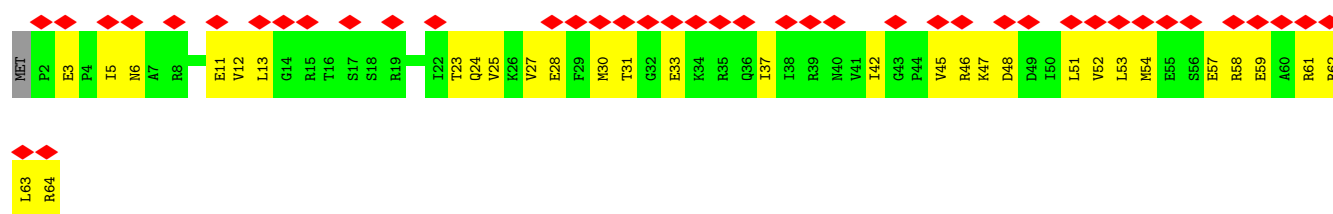
• Molecule 70: Ribosomal protein S26



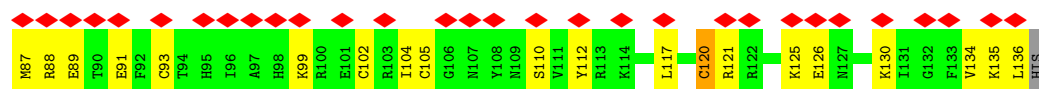
• Molecule 71: Ribosomal protein S27



• Molecule 72: Ribosomal protein S28

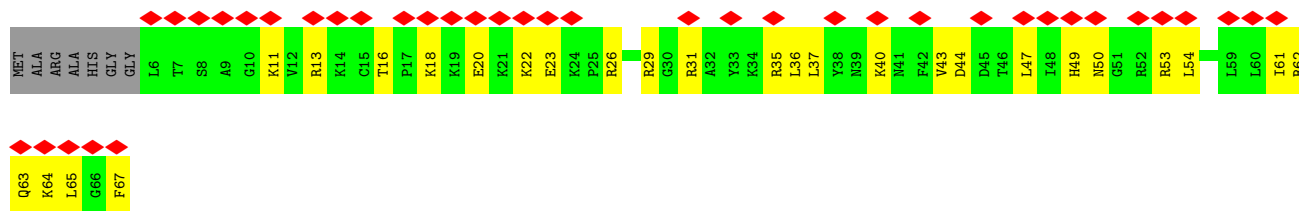


• Molecule 73: Ribosomal protein S29A

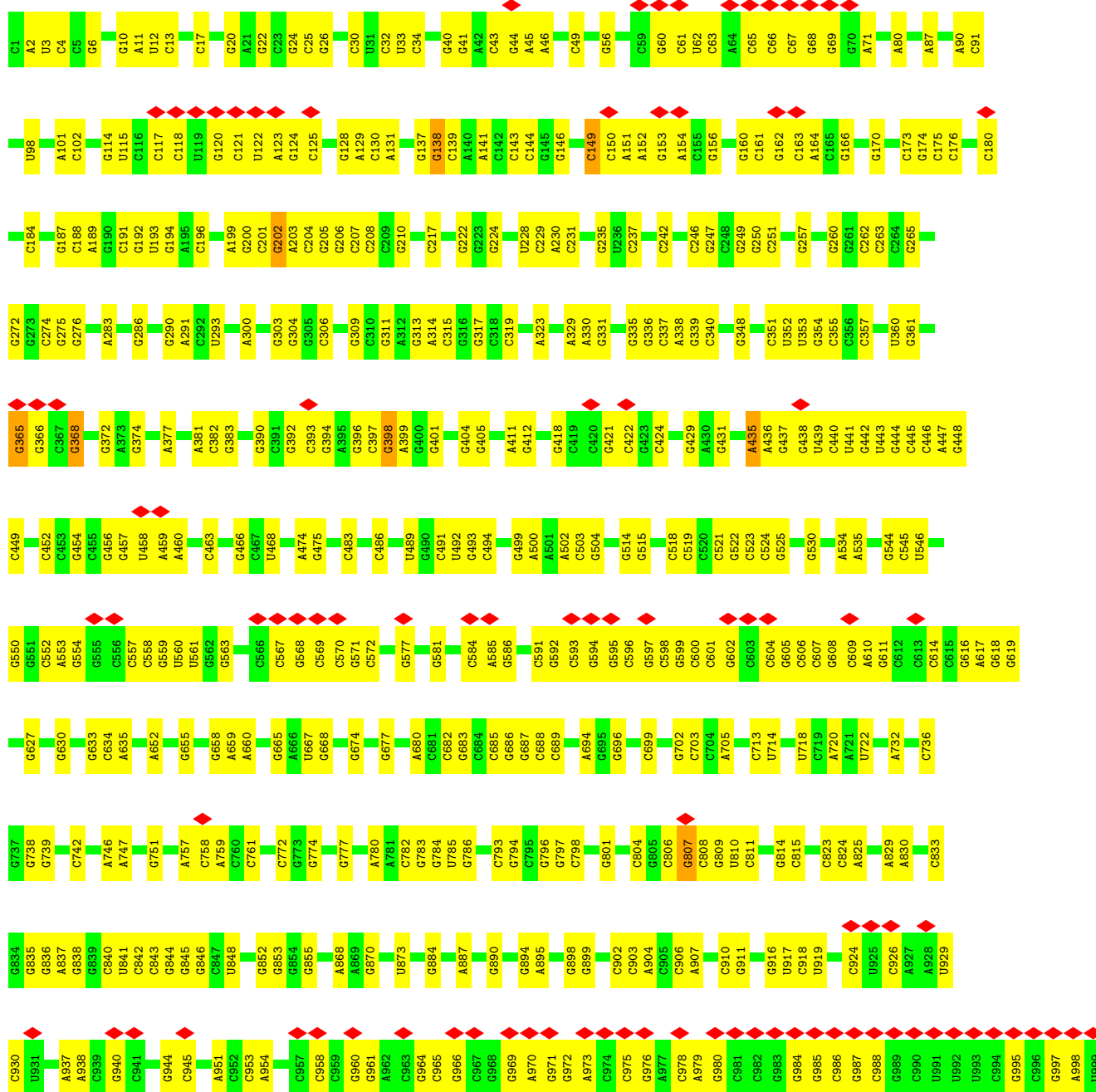


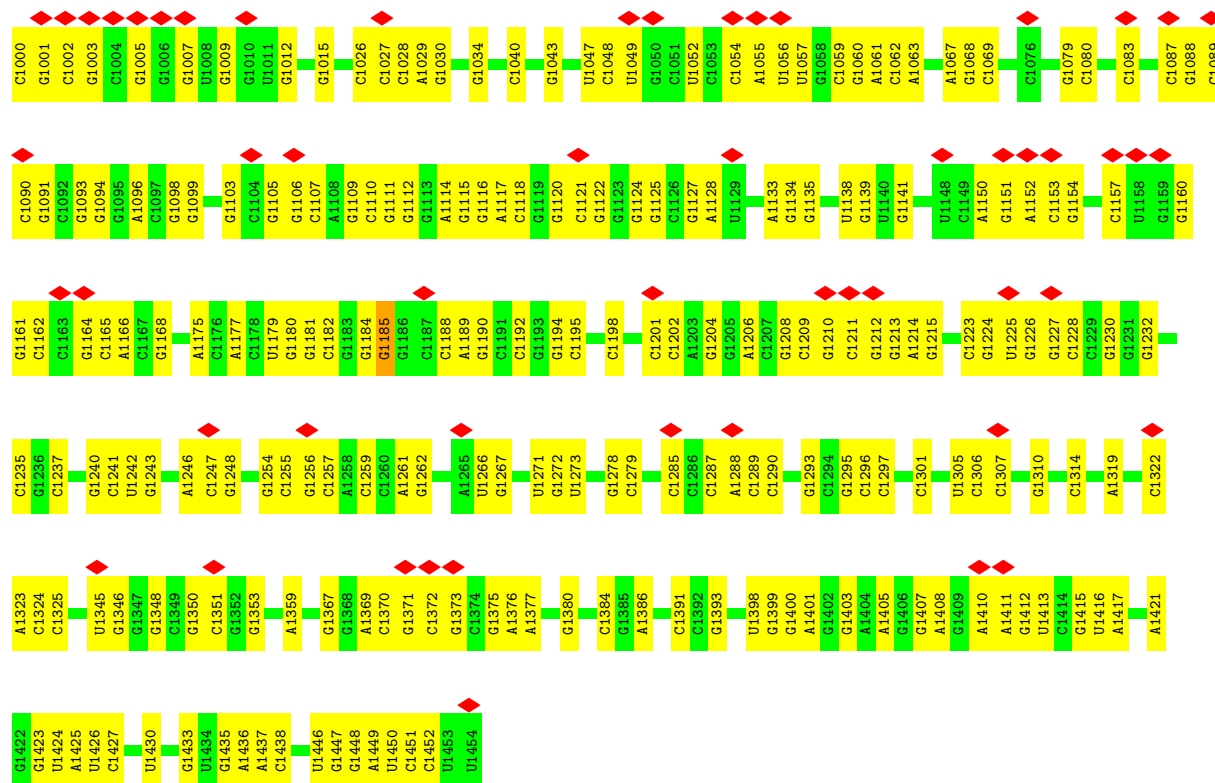
• Molecule 74: Ribosomal protein S30





# Molecule 75: Small Subunit rRNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17963	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 ( $e^-/\text{\AA}^2$ )	30.0	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	15.203	Depositor
Minimum map value	-7.156	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.84	Depositor
Map size ( $\text{\AA}$ )	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.82, 0.82, 0.82	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	0.58	0/1919	0.81	0/2577
2	LB	0.57	0/3058	0.82	0/4129
3	LC	0.58	0/2459	0.78	0/3335
4	LD	0.59	0/3393	0.85	1/5292 (0.0%)
5	LE	0.59	0/2798	0.83	0/4361
6	LF	0.58	0/2380	0.77	0/3193
7	LG	0.52	0/450	0.82	0/601
8	LH	0.56	0/1756	0.80	1/2367 (0.0%)
9	LI	0.57	0/1520	0.76	0/2052
10	LJ	0.58	0/1479	0.82	1/1997 (0.1%)
11	LK	0.58	0/1231	0.76	0/1646
12	LL	0.60	0/1346	0.78	0/1807
13	LM	0.58	0/1628	0.79	0/2180
14	LN	0.55	0/1037	0.79	0/1390
15	LO	0.56	0/1751	0.80	1/2346 (0.0%)
16	LP	0.55	0/1610	0.78	0/2160
17	LQ	0.60	0/1257	0.80	1/1681 (0.1%)
18	LR	0.60	0/1425	0.84	0/1907
19	LS	0.55	0/1609	0.77	0/2129
20	LT	0.56	0/1457	0.80	0/1957
21	LU	0.55	0/1283	0.79	0/1725
22	LV	0.56	0/861	0.85	0/1158
23	LW	0.58	0/1035	0.80	1/1396 (0.1%)
24	LX	0.54	0/553	0.93	2/736 (0.3%)
25	LY	0.56	0/982	0.84	1/1326 (0.1%)
26	LZ	0.59	0/1091	0.80	0/1454
27	La	0.58	0/1030	0.80	0/1388
28	Lb	0.59	0/1231	0.80	0/1647
29	Lc	0.59	0/432	0.89	1/572 (0.2%)
30	Ld	0.60	0/778	0.77	0/1051
31	Le	0.56	0/832	0.79	0/1118
32	Lf	0.59	0/1101	0.77	0/1467
33	Lg	0.58	0/793	0.83	0/1062
34	Lh	0.59	0/789	0.83	0/1060

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	Li	0.55	0/980	0.77	0/1302
36	Lj	0.58	0/741	0.80	0/982
37	Lk	0.61	0/727	0.86	0/963
38	Ll	0.58	0/562	0.83	1/749 (0.1%)
39	Ln	0.64	0/1710	0.86	0/2305
40	Lo	0.51	0/229	0.68	0/291
41	Lp	0.57	0/778	0.75	0/1029
42	Lq	0.55	0/717	0.81	0/955
43	Ls	0.58	0/392	0.90	0/522
44	Lt	0.61	0/62235	0.86	33/97128 (0.0%)
45	SA	0.59	0/1603	0.82	1/2178 (0.0%)
46	SB	0.61	0/1700	0.84	2/2293 (0.1%)
47	SC	0.60	0/1685	0.81	0/2262
48	SD	0.58	0/1890	0.80	0/2546
49	SE	0.58	0/2131	0.77	0/2874
50	SF	0.62	0/1465	0.79	0/1970
51	SG	0.58	0/1665	0.83	1/2219 (0.0%)
52	SH	0.58	0/1508	0.84	0/2032
53	SI	0.58	0/1378	0.80	0/1848
54	SJ	0.59	0/1048	0.80	1/1412 (0.1%)
55	SK	0.58	0/1443	0.84	1/1930 (0.1%)
56	SL	0.60	0/842	0.81	0/1147
57	SM	0.57	0/1280	0.83	0/1712
58	SO	0.57	0/1095	0.80	0/1467
59	SP	0.57	0/1215	0.74	0/1632
60	SQ	0.60	0/928	0.88	0/1246
61	SR	0.61	0/961	0.82	0/1284
62	ST	0.62	0/1192	0.83	0/1594
63	SU	0.59	0/879	0.82	0/1170
64	SV	0.60	0/1133	0.87	0/1519
65	SW	0.63	0/1095	0.79	0/1473
66	SX	0.59	0/809	0.77	0/1092
67	SY	0.61	0/659	0.83	0/883
68	Sb	0.57	0/956	0.81	0/1279
69	Sc	0.62	0/584	0.78	0/779
70	Sd	0.57	0/833	0.79	1/1118 (0.1%)
71	Se	0.61	0/635	0.79	0/861
72	Sg	0.61	0/508	0.83	0/677
73	Sh	0.58	0/425	0.92	2/563 (0.4%)
74	Sj	0.57	0/518	0.87	0/690
75	St	0.60	1/34858 (0.0%)	0.87	17/54401 (0.0%)
All	All	0.60	1/186346 (0.0%)	0.84	70/272644 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	St	149	C	O3'-P	5.11	1.67	1.61

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Lt	1356	C	C2'-C3'-O3'	8.06	127.24	109.50
44	Lt	1506	A	C2'-C3'-O3'	8.01	127.12	109.50
55	SK	167	PRO	N-CA-CB	-7.99	93.71	103.30
44	Lt	1349	G	C2'-C3'-O3'	7.98	127.06	109.50
29	Lc	50	ASP	CB-CA-C	7.86	126.13	110.40

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	248/251 (99%)	237 (96%)	11 (4%)	0	100	100
2	LB	376/379 (99%)	357 (95%)	17 (4%)	2 (0%)	25	56
3	LC	307/316 (97%)	293 (95%)	12 (4%)	2 (1%)	19	50
6	LF	289/297 (97%)	271 (94%)	17 (6%)	1 (0%)	37	66
7	LG	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
8	LH	211/235 (90%)	205 (97%)	6 (3%)	0	100	100
9	LI	183/225 (81%)	177 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	LJ	182/185 (98%)	168 (92%)	11 (6%)	3 (2%)	8	33
11	LK	141/210 (67%)	133 (94%)	8 (6%)	0	100	100
12	LL	163/173 (94%)	159 (98%)	3 (2%)	1 (1%)	22	53
13	LM	199/234 (85%)	190 (96%)	7 (4%)	2 (1%)	13	43
14	LN	128/131 (98%)	120 (94%)	7 (6%)	1 (1%)	16	47
15	LO	201/204 (98%)	194 (96%)	6 (3%)	1 (0%)	25	56
16	LP	192/197 (98%)	187 (97%)	4 (2%)	1 (0%)	25	56
17	LQ	151/164 (92%)	144 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	166 (94%)	8 (4%)	2 (1%)	12	41
19	LS	190/196 (97%)	183 (96%)	5 (3%)	2 (1%)	12	41
20	LT	168/173 (97%)	160 (95%)	8 (5%)	0	100	100
21	LU	154/159 (97%)	142 (92%)	9 (6%)	3 (2%)	6	30
22	LV	101/124 (82%)	87 (86%)	12 (12%)	2 (2%)	6	29
23	LW	130/142 (92%)	128 (98%)	2 (2%)	0	100	100
24	LX	61/189 (32%)	58 (95%)	3 (5%)	0	100	100
25	LY	117/141 (83%)	110 (94%)	6 (5%)	1 (1%)	14	44
26	LZ	131/135 (97%)	124 (95%)	6 (5%)	1 (1%)	16	47
27	La	123/135 (91%)	112 (91%)	10 (8%)	1 (1%)	16	47
28	Lb	146/149 (98%)	140 (96%)	4 (3%)	2 (1%)	9	35
29	Lc	49/62 (79%)	44 (90%)	3 (6%)	2 (4%)	2	16
30	Ld	100/109 (92%)	96 (96%)	4 (4%)	0	100	100
31	Le	98/106 (92%)	94 (96%)	3 (3%)	1 (1%)	13	43
32	Lf	128/136 (94%)	121 (94%)	6 (5%)	1 (1%)	16	47
33	Lg	96/123 (78%)	93 (97%)	3 (3%)	0	100	100
34	Lh	94/120 (78%)	89 (95%)	4 (4%)	1 (1%)	12	41
35	Li	116/124 (94%)	109 (94%)	6 (5%)	1 (1%)	14	44
36	Lj	87/90 (97%)	79 (91%)	6 (7%)	2 (2%)	5	26
37	Lk	86/89 (97%)	79 (92%)	5 (6%)	2 (2%)	5	26
38	Ll	70/77 (91%)	67 (96%)	3 (4%)	0	100	100
39	Ln	207/217 (95%)	169 (82%)	30 (14%)	8 (4%)	2	17
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	Lp	91/106 (86%)	91 (100%)	0	0	100	100
42	Lq	89/94 (95%)	82 (92%)	6 (7%)	1 (1%)	12	41
43	Ls	45/127 (35%)	42 (93%)	2 (4%)	1 (2%)	5	27
45	SA	194/245 (79%)	183 (94%)	10 (5%)	1 (0%)	25	56
46	SB	214/242 (88%)	199 (93%)	15 (7%)	0	100	100
47	SC	207/217 (95%)	191 (92%)	14 (7%)	2 (1%)	13	43
48	SD	227/248 (92%)	213 (94%)	13 (6%)	1 (0%)	30	61
49	SE	258/268 (96%)	244 (95%)	13 (5%)	1 (0%)	30	61
50	SF	184/190 (97%)	173 (94%)	8 (4%)	3 (2%)	8	33
51	SG	203/248 (82%)	192 (95%)	9 (4%)	2 (1%)	13	43
52	SH	182/190 (96%)	166 (91%)	15 (8%)	1 (0%)	25	56
53	SI	171/174 (98%)	161 (94%)	9 (5%)	1 (1%)	22	53
54	SJ	127/130 (98%)	117 (92%)	8 (6%)	2 (2%)	8	33
55	SK	174/189 (92%)	164 (94%)	7 (4%)	3 (2%)	7	32
56	SL	98/134 (73%)	92 (94%)	5 (5%)	1 (1%)	13	43
57	SM	149/154 (97%)	135 (91%)	9 (6%)	5 (3%)	3	19
58	SO	137/143 (96%)	132 (96%)	4 (3%)	1 (1%)	19	50
59	SP	148/154 (96%)	144 (97%)	4 (3%)	0	100	100
60	SQ	123/145 (85%)	111 (90%)	11 (9%)	1 (1%)	16	47
61	SR	114/145 (79%)	103 (90%)	8 (7%)	3 (3%)	4	24
62	ST	149/158 (94%)	141 (95%)	6 (4%)	2 (1%)	10	37
63	SU	102/137 (74%)	99 (97%)	3 (3%)	0	100	100
64	SV	139/154 (90%)	123 (88%)	12 (9%)	4 (3%)	3	22
65	SW	135/139 (97%)	126 (93%)	7 (5%)	2 (2%)	8	34
66	SX	98/126 (78%)	97 (99%)	1 (1%)	0	100	100
67	SY	84/89 (94%)	79 (94%)	2 (2%)	3 (4%)	3	18
68	Sb	116/132 (88%)	108 (93%)	8 (7%)	0	100	100
69	Sc	71/88 (81%)	67 (94%)	4 (6%)	0	100	100
70	Sd	97/109 (89%)	91 (94%)	6 (6%)	0	100	100
71	Se	77/81 (95%)	74 (96%)	3 (4%)	0	100	100
72	Sg	61/64 (95%)	53 (87%)	7 (12%)	1 (2%)	8	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	Sh	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
74	Sj	60/69 (87%)	55 (92%)	4 (7%)	1 (2%)	7	32
All	All	10042/11192 (90%)	9447 (94%)	506 (5%)	89 (1%)	17	44

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	LC	255	GLN
27	La	98	VAL
29	Lc	25	LYS
29	Lc	50	ASP
36	Lj	58	LYS

### 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	191/192 (100%)	139 (73%)	52 (27%)	0	1
2	LB	312/313 (100%)	209 (67%)	103 (33%)	0	1
3	LC	256/263 (97%)	190 (74%)	66 (26%)	0	1
6	LF	236/242 (98%)	155 (66%)	81 (34%)	0	1
7	LG	47/48 (98%)	32 (68%)	15 (32%)	0	1
8	LH	184/204 (90%)	132 (72%)	52 (28%)	0	1
9	LI	165/198 (83%)	113 (68%)	52 (32%)	0	1
10	LJ	163/164 (99%)	98 (60%)	65 (40%)	0	0
11	LK	127/177 (72%)	74 (58%)	53 (42%)	0	0
12	LL	141/149 (95%)	83 (59%)	58 (41%)	0	0
13	LM	169/197 (86%)	123 (73%)	46 (27%)	0	1
14	LN	110/111 (99%)	69 (63%)	41 (37%)	0	0
15	LO	174/175 (99%)	122 (70%)	52 (30%)	0	1
16	LP	162/165 (98%)	125 (77%)	37 (23%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LQ	130/139 (94%)	81 (62%)	49 (38%)	0	0
18	LR	154/155 (99%)	106 (69%)	48 (31%)	0	1
19	LS	163/167 (98%)	105 (64%)	58 (36%)	0	0
20	LT	151/154 (98%)	96 (64%)	55 (36%)	0	0
21	LU	130/133 (98%)	85 (65%)	45 (35%)	0	1
22	LV	91/110 (83%)	56 (62%)	35 (38%)	0	0
23	LW	108/114 (95%)	78 (72%)	30 (28%)	0	1
24	LX	61/174 (35%)	38 (62%)	23 (38%)	0	0
25	LY	107/123 (87%)	79 (74%)	28 (26%)	0	1
26	LZ	114/115 (99%)	74 (65%)	40 (35%)	0	1
27	La	112/119 (94%)	64 (57%)	48 (43%)	0	0
28	Lb	126/127 (99%)	94 (75%)	32 (25%)	0	2
29	Lc	47/57 (82%)	34 (72%)	13 (28%)	0	1
30	Ld	87/92 (95%)	50 (58%)	37 (42%)	0	0
31	Le	88/92 (96%)	56 (64%)	32 (36%)	0	0
32	Lf	116/120 (97%)	74 (64%)	42 (36%)	0	0
33	Lg	82/103 (80%)	57 (70%)	25 (30%)	0	1
34	Lh	85/100 (85%)	59 (69%)	26 (31%)	0	1
35	Li	103/107 (96%)	65 (63%)	38 (37%)	0	0
36	Lj	77/78 (99%)	45 (58%)	32 (42%)	0	0
37	Lk	73/74 (99%)	44 (60%)	29 (40%)	0	0
38	Ll	63/68 (93%)	36 (57%)	27 (43%)	0	0
39	Ln	183/189 (97%)	83 (45%)	100 (55%)	0	0
40	Lo	22/22 (100%)	14 (64%)	8 (36%)	0	0
41	Lp	83/93 (89%)	47 (57%)	36 (43%)	0	0
42	Lq	71/73 (97%)	44 (62%)	27 (38%)	0	0
43	Ls	43/110 (39%)	26 (60%)	17 (40%)	0	0
45	SA	171/217 (79%)	115 (67%)	56 (33%)	0	1
46	SB	179/201 (89%)	114 (64%)	65 (36%)	0	0
47	SC	174/182 (96%)	107 (62%)	67 (38%)	0	0
48	SD	207/220 (94%)	130 (63%)	77 (37%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	SE	228/232 (98%)	150 (66%)	78 (34%)	0	1
50	SF	153/157 (98%)	95 (62%)	58 (38%)	0	0
51	SG	176/213 (83%)	90 (51%)	86 (49%)	0	0
52	SH	165/170 (97%)	91 (55%)	74 (45%)	0	0
53	SI	147/148 (99%)	92 (63%)	55 (37%)	0	0
54	SJ	114/115 (99%)	68 (60%)	46 (40%)	0	0
55	SK	155/164 (94%)	88 (57%)	67 (43%)	0	0
56	SL	89/119 (75%)	50 (56%)	39 (44%)	0	0
57	SM	134/136 (98%)	87 (65%)	47 (35%)	0	1
58	SO	111/114 (97%)	61 (55%)	50 (45%)	0	0
59	SP	125/130 (96%)	84 (67%)	41 (33%)	0	1
60	SQ	86/113 (76%)	51 (59%)	35 (41%)	0	0
61	SR	104/128 (81%)	56 (54%)	48 (46%)	0	0
62	ST	125/130 (96%)	68 (54%)	57 (46%)	0	0
63	SU	98/124 (79%)	65 (66%)	33 (34%)	0	1
64	SV	118/131 (90%)	59 (50%)	59 (50%)	0	0
65	SW	113/115 (98%)	72 (64%)	41 (36%)	0	0
66	SX	89/110 (81%)	56 (63%)	33 (37%)	0	0
67	SY	69/72 (96%)	39 (56%)	30 (44%)	0	0
68	Sb	103/113 (91%)	55 (53%)	48 (47%)	0	0
69	Sc	65/79 (82%)	33 (51%)	32 (49%)	0	0
70	Sd	95/103 (92%)	65 (68%)	30 (32%)	0	1
71	Se	71/73 (97%)	44 (62%)	27 (38%)	0	0
72	Sg	56/57 (98%)	26 (46%)	30 (54%)	0	0
73	Sh	44/45 (98%)	24 (54%)	20 (46%)	0	0
74	Sj	55/58 (95%)	29 (53%)	26 (47%)	0	0
All	All	8726/9575 (91%)	5518 (63%)	3208 (37%)	0	0

5 of 3208 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	SB	175	SER
52	SH	122	MET

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Mol	Chain	Res	Type
74	Sj	50	ASN
47	SC	115	LEU
46	SB	168	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 126 such sidechains are listed below:

Mol	Chain	Res	Type
39	Ln	5	ASN
64	SV	135	GLN
47	SC	57	GLN
64	SV	129	ASN
69	Sc	36	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	141/143 (98%)	57 (40%)	10 (7%)
44	Lt	2588/2697 (95%)	1103 (42%)	0
5	LE	116/121 (95%)	55 (47%)	4 (3%)
75	St	1453/1454 (99%)	649 (44%)	0
All	All	4298/4415 (97%)	1864 (43%)	14 (0%)

5 of 1864 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	2	C
4	LD	7	C
4	LD	8	C
4	LD	10	G
4	LD	12	C

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	LD	111	C
4	LD	117	C
5	LE	114	G
5	LE	50	A
5	LE	110	U

## 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](#)

There are no ligands in this entry.

## 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.

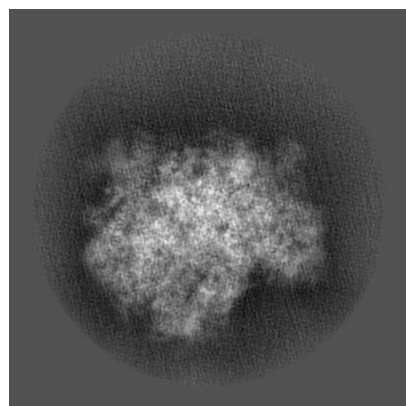
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16222. These allow visual inspection of the internal detail of the map and identification of artifacts.

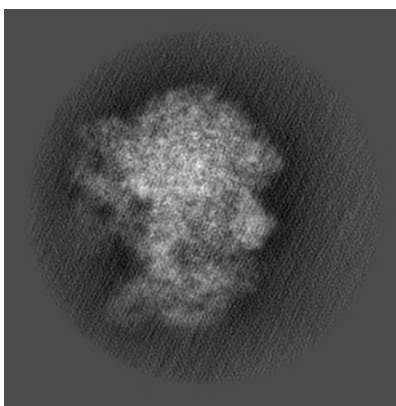
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

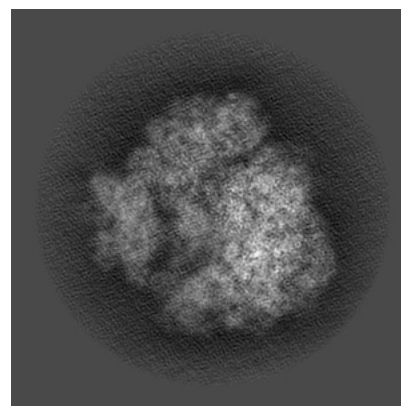
#### 6.1.1 Primary map



X

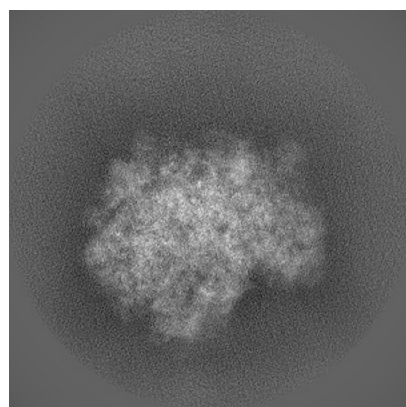


Y

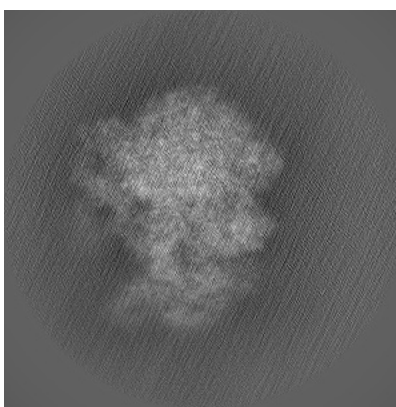


Z

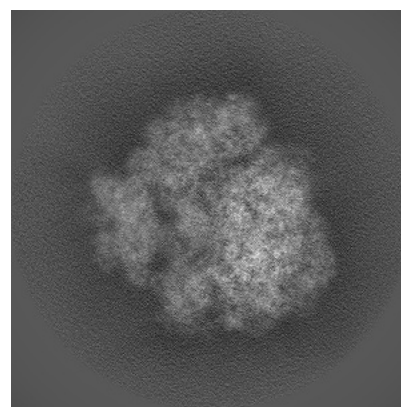
#### 6.1.2 Raw map



X



Y

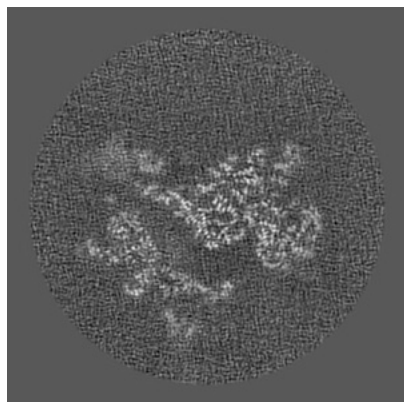


Z

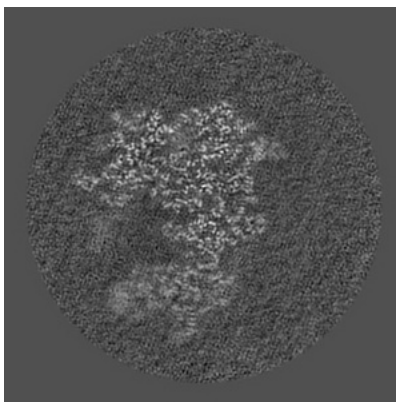
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

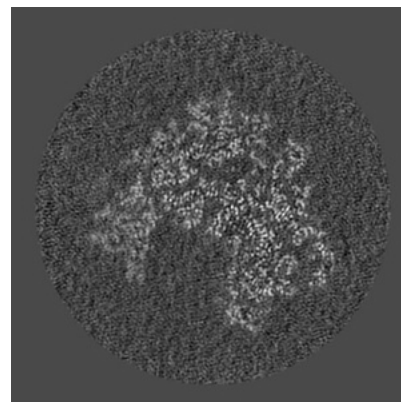
### 6.2.1 Primary map



X Index: 250

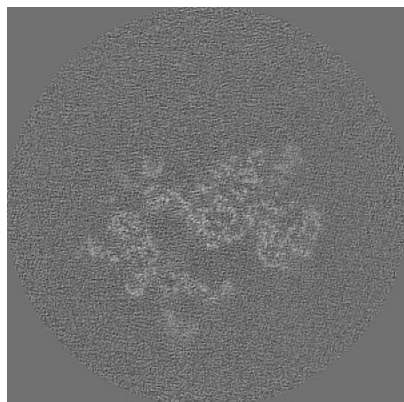


Y Index: 250

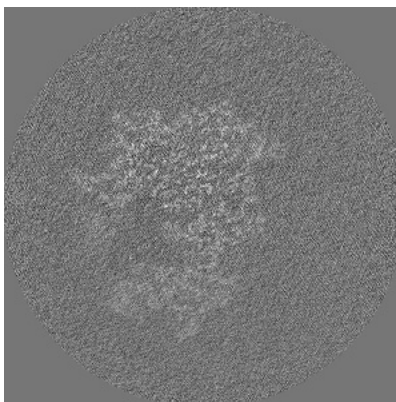


Z Index: 250

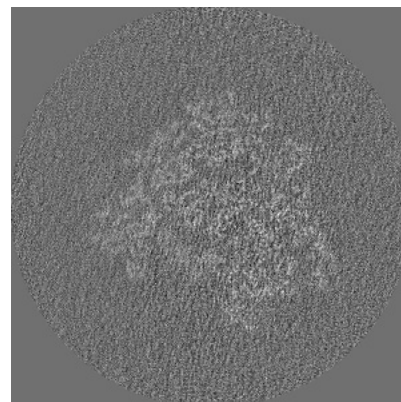
### 6.2.2 Raw map



X Index: 250



Y Index: 250

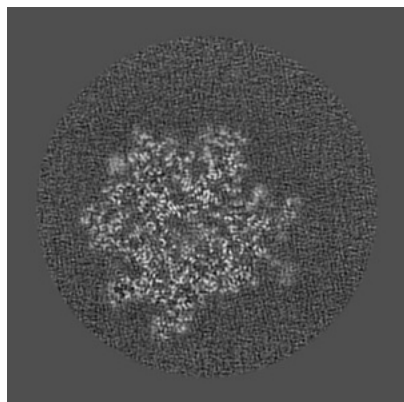


Z Index: 250

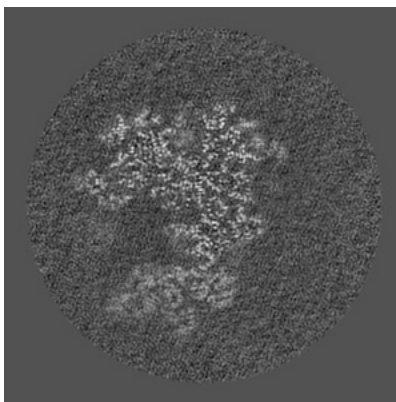
The images above show central slices of the map in three orthogonal directions.

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

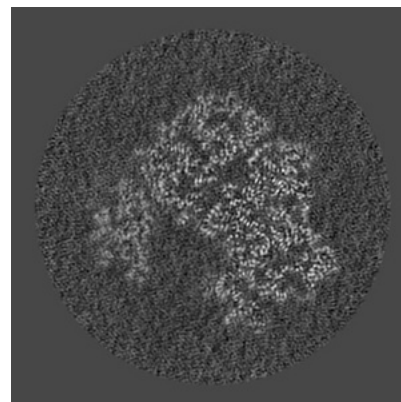
### 6.3.1 Primary map



X Index: 314

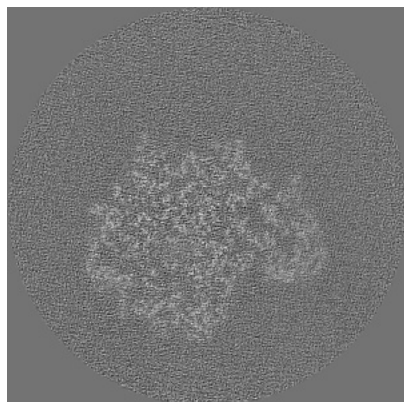


Y Index: 255

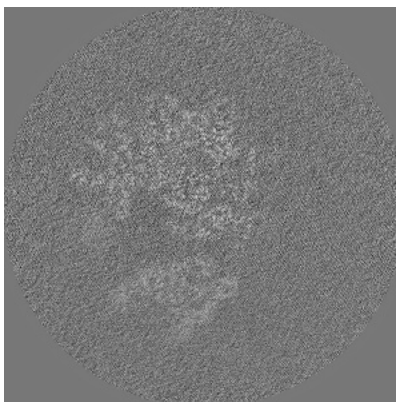


Z Index: 240

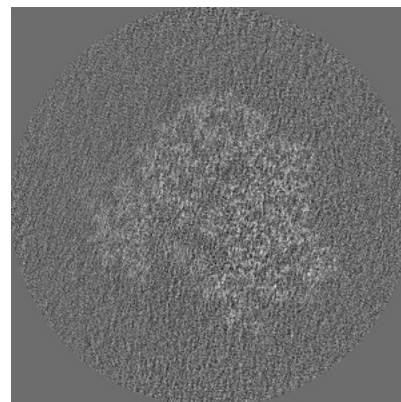
### 6.3.2 Raw map



X Index: 285



Y Index: 241

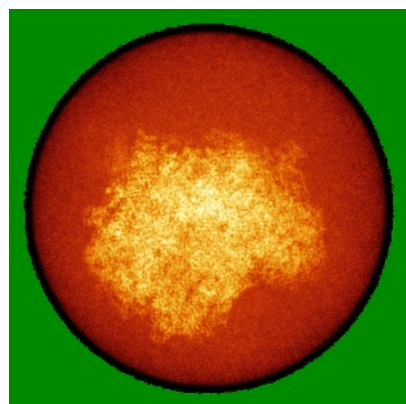


Z Index: 240

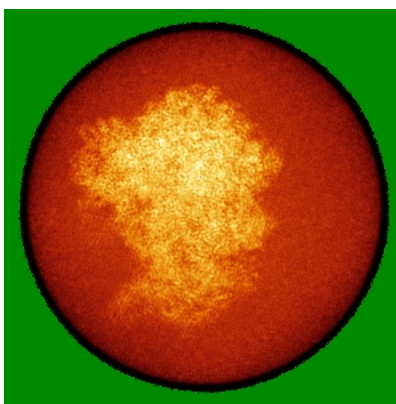
The images above show the largest variance slices of the map in three orthogonal directions.

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

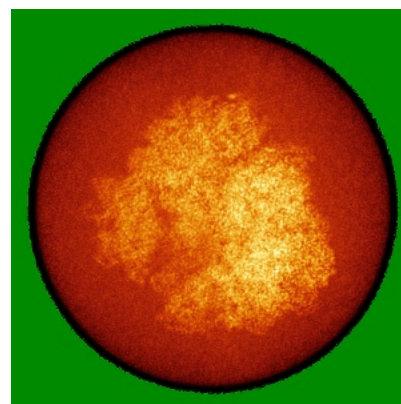
### 6.4.1 Primary map



X

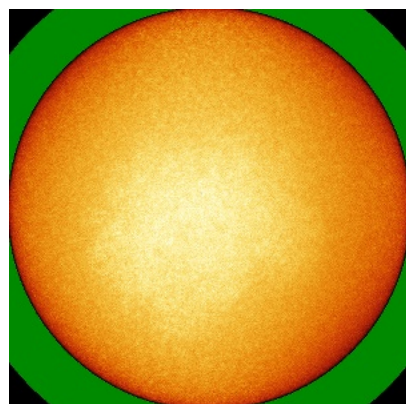


Y

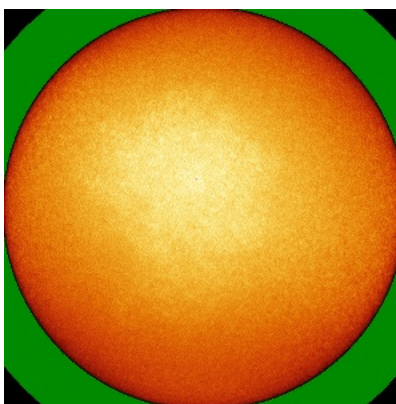


Z

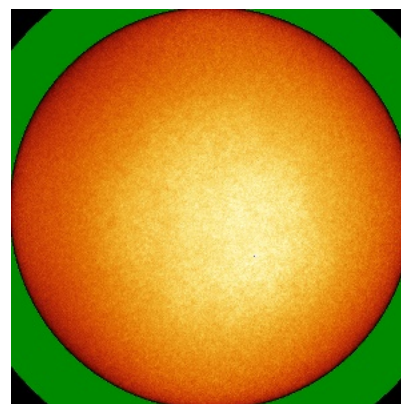
### 6.4.2 Raw map



X



Y

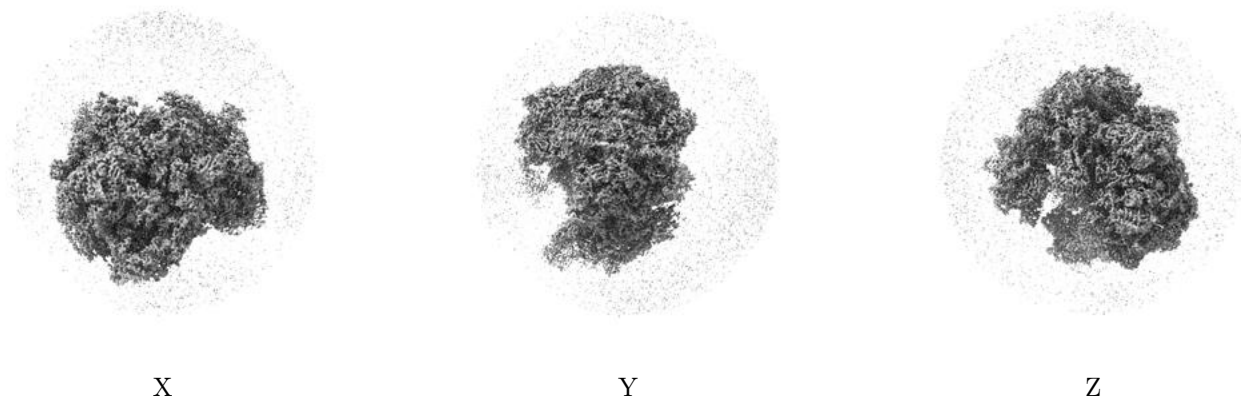


Z

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.

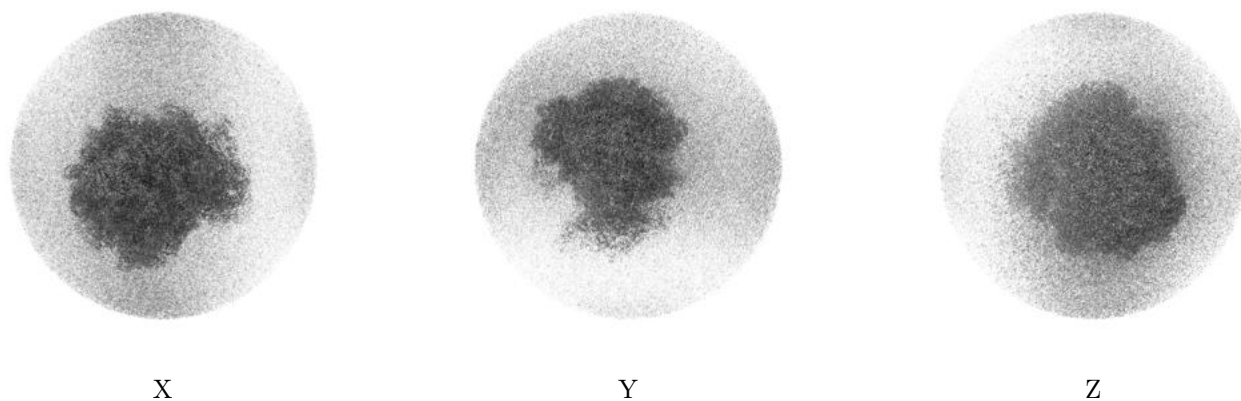
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.84. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

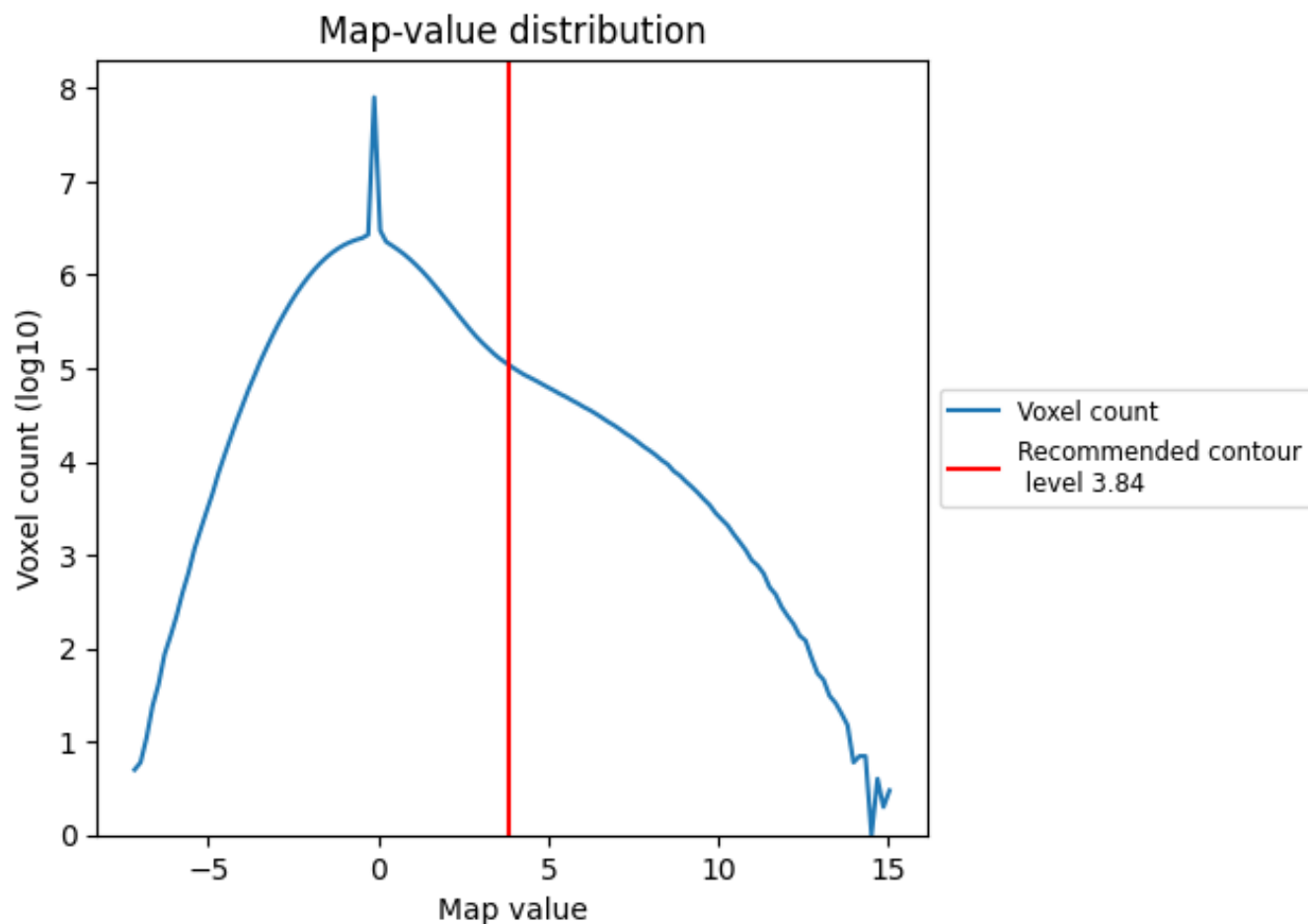
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

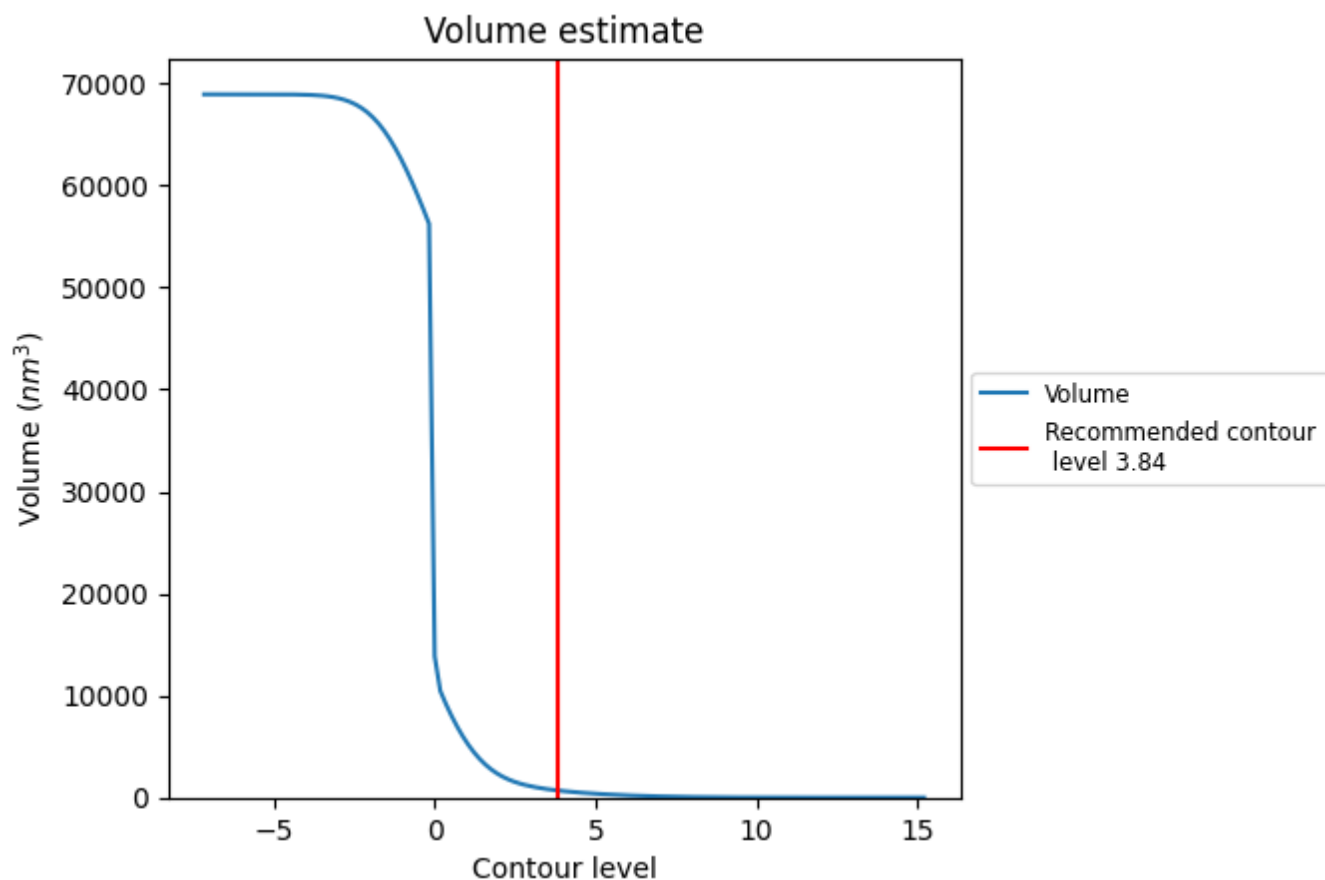
This section contains the results of statistical analysis of the map.

### 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.

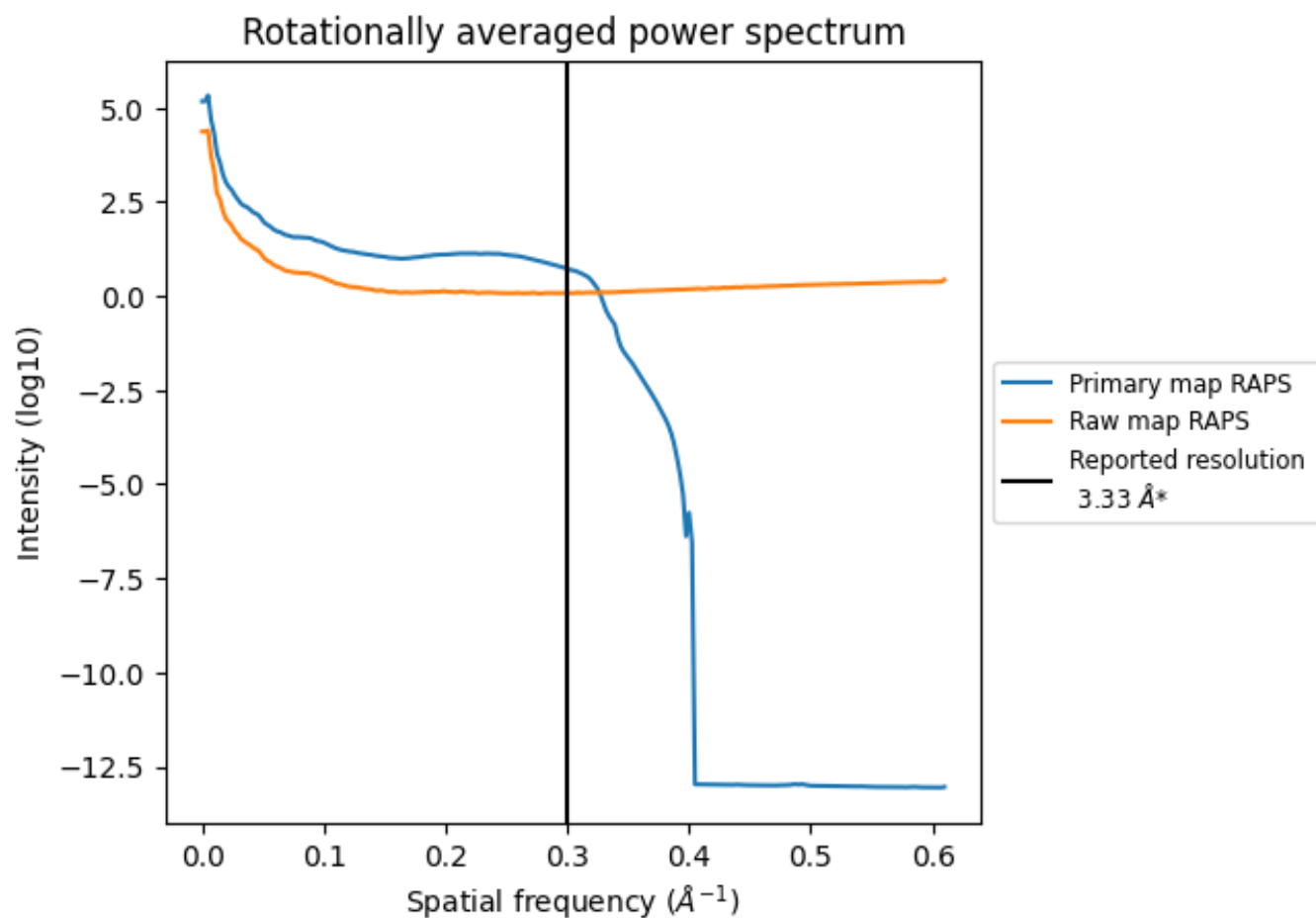
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690  $\text{nm}^3$ ; this corresponds to an approximate mass of 623 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 ⓘ

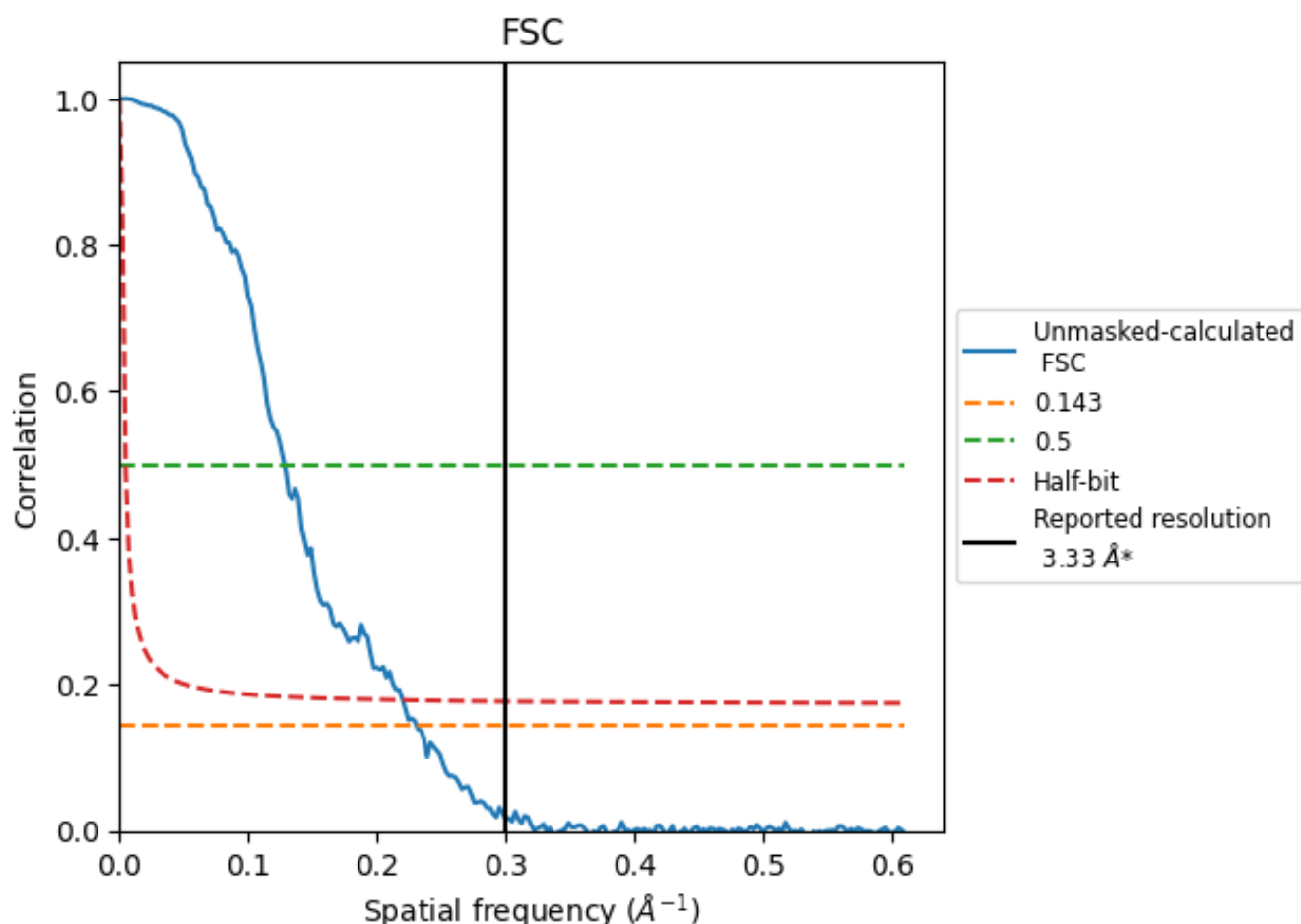


\*Reported resolution corresponds to spatial frequency of 0.300 Å<sup>-1</sup>

## 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 0.300 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

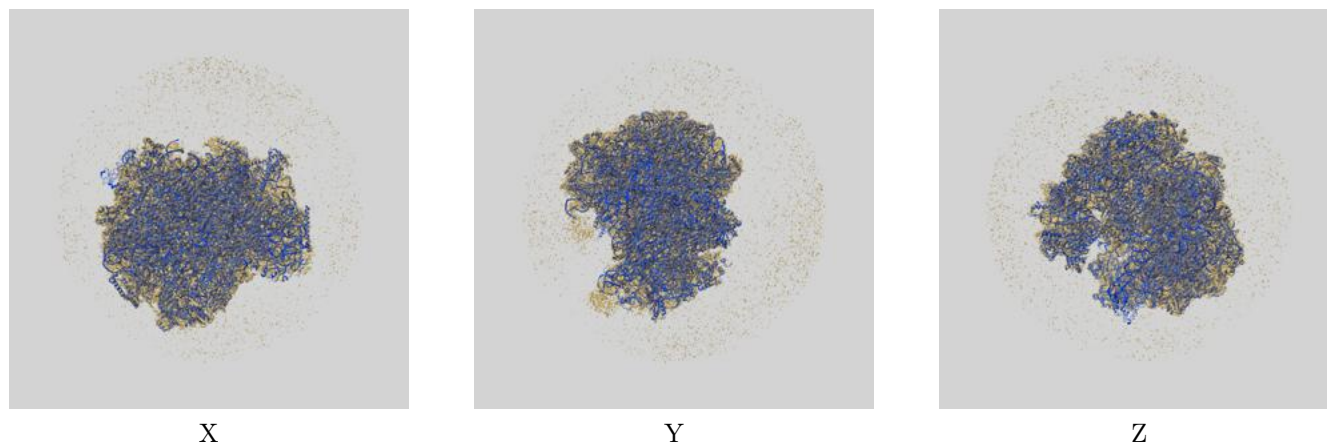
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.33	7.81	4.55

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.33 differs from the reported value 3.33 by more than 10 %

## 9 Map-model fit [i](#)

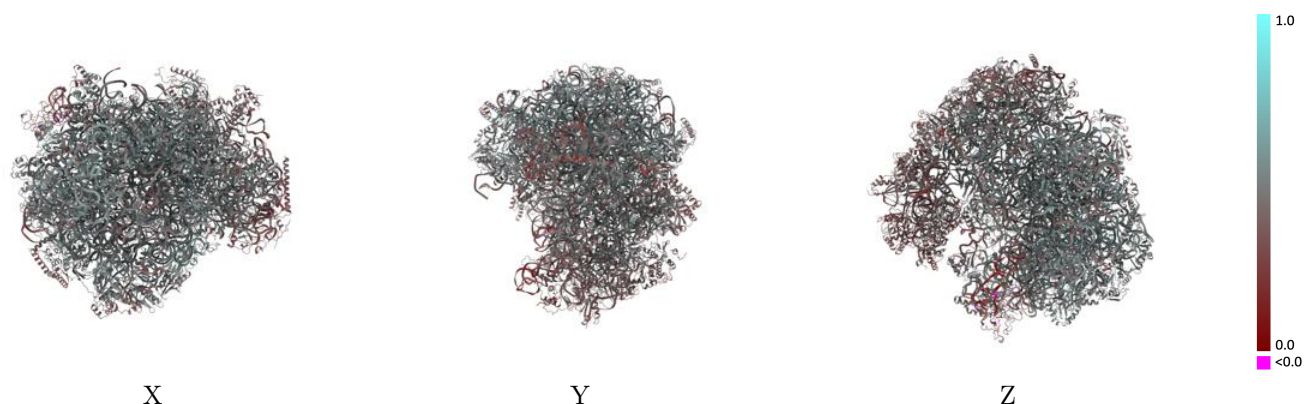
This section contains information regarding the fit between EMDB map EMD-16222 and PDB model 8BRM. Per-residue inclusion information can be found in section [3](#) on page [17](#).

### 9.1 Map-model overlay [i](#)



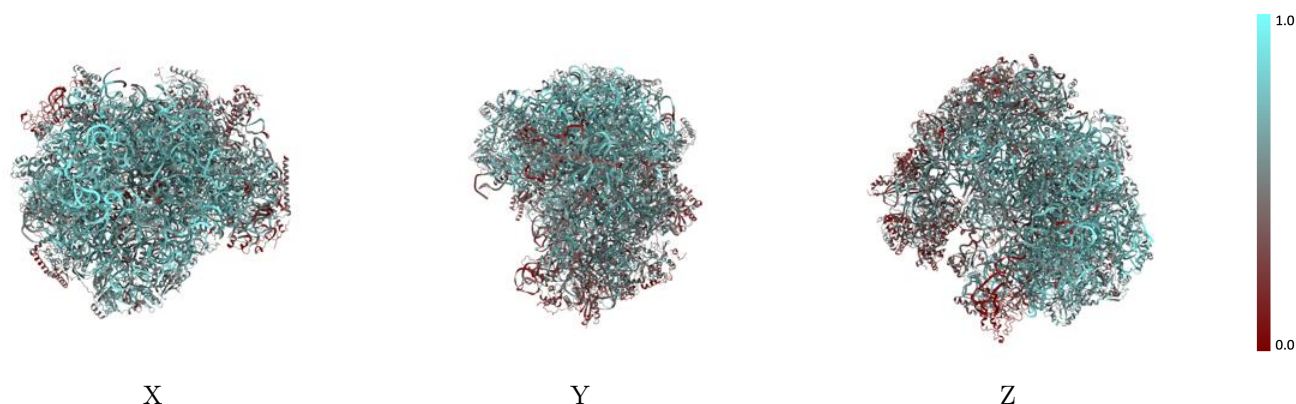
The images above show the 3D surface view of the map at the recommended contour level 3.84 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



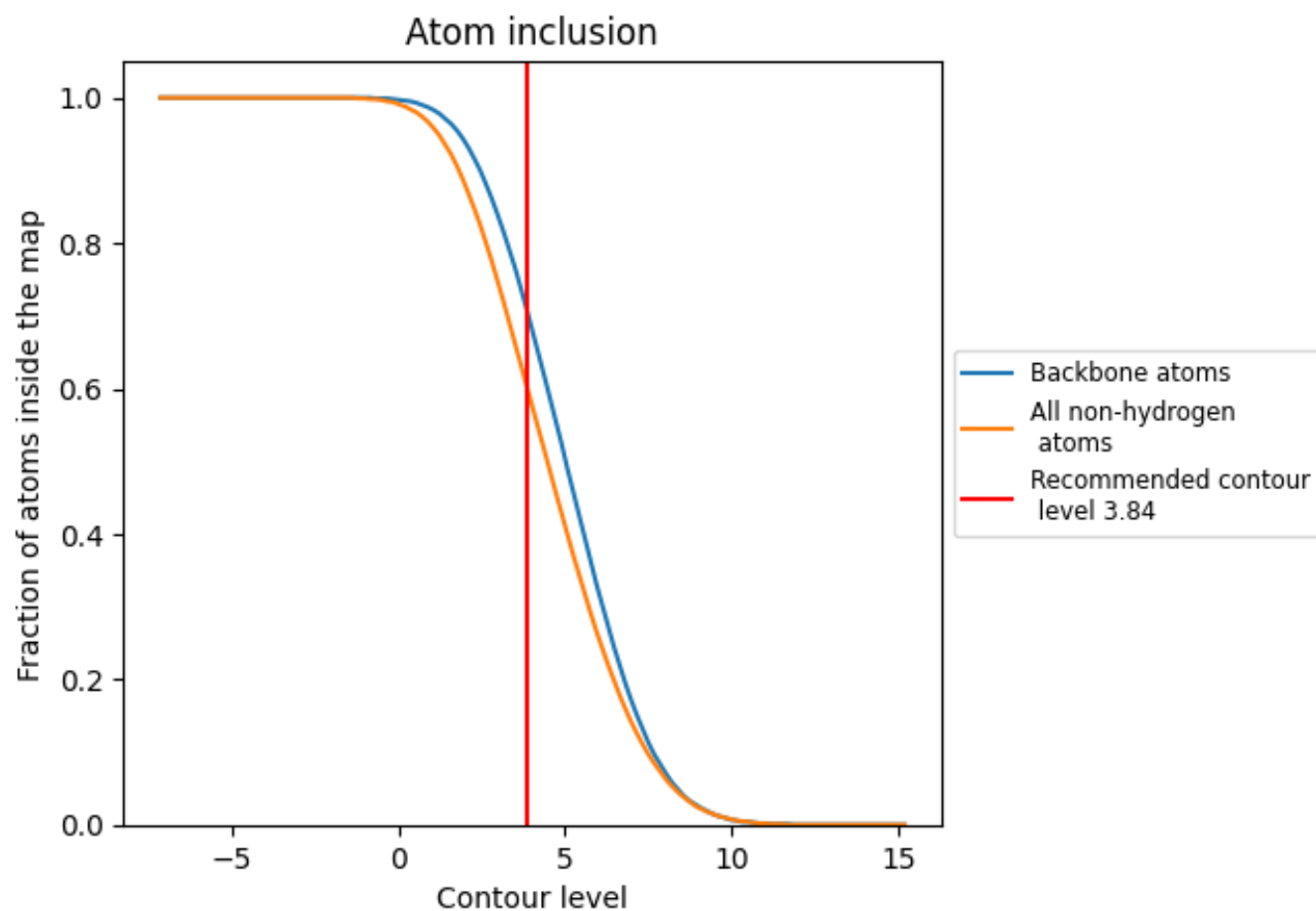
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.84).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 61% 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 (3.84) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6060	 0.4620
LA	 0.6240	 0.5340
LB	 0.6190	 0.5110
LC	 0.6410	 0.5090
LD	 0.8070	 0.5040
LE	 0.7330	 0.4610
LF	 0.4280	 0.4410
LG	 0.6480	 0.5170
LH	 0.5490	 0.4740
LI	 0.5590	 0.4750
LJ	 0.5570	 0.4720
LK	 0.2640	 0.3980
LL	 0.3910	 0.4250
LM	 0.5840	 0.4930
LN	 0.5890	 0.4600
LO	 0.6810	 0.5340
LP	 0.6170	 0.4810
LQ	 0.5950	 0.4910
LR	 0.5800	 0.5070
LS	 0.5650	 0.4830
LT	 0.6180	 0.4970
LU	 0.5400	 0.4850
LV	 0.5320	 0.4370
LW	 0.6000	 0.4970
LX	 0.5760	 0.4630
LY	 0.6300	 0.5090
LZ	 0.6690	 0.5010
La	 0.5180	 0.4570
Lb	 0.5600	 0.5150
Lc	 0.4200	 0.4750
Ld	 0.5420	 0.4720
Le	 0.6190	 0.5120
Lf	 0.5960	 0.5020
Lg	 0.6560	 0.5220
Lh	 0.6420	 0.5160



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Chain	Atom inclusion	Q-score
Li	 0.5970	 0.4830
Lj	 0.5140	 0.4700
Lk	 0.6340	 0.5170
Ll	 0.4920	 0.4250
Ln	 0.0400	 0.2830
Lo	 0.4430	 0.5050
Lp	 0.3860	 0.4610
Lq	 0.6190	 0.5110
Ls	 0.4570	 0.4570
Lt	 0.7260	 0.4880
SA	 0.4740	 0.4160
SB	 0.5130	 0.4580
SC	 0.3390	 0.3970
SD	 0.5300	 0.4600
SE	 0.4700	 0.4490
SF	 0.3170	 0.3810
SG	 0.3300	 0.3950
SH	 0.3470	 0.3910
SI	 0.5330	 0.4730
SJ	 0.5160	 0.4680
SK	 0.4670	 0.4250
SL	 0.2720	 0.3460
SM	 0.5330	 0.4920
SO	 0.4520	 0.4750
SP	 0.5320	 0.4670
SQ	 0.5540	 0.4650
SR	 0.2040	 0.3380
ST	 0.3000	 0.3600
SU	 0.2750	 0.3520
SV	 0.2610	 0.3570
SW	 0.3030	 0.3480
SX	 0.2930	 0.3810
SY	 0.4600	 0.4340
Sb	 0.3870	 0.4080
Sc	 0.2650	 0.3470
Sd	 0.5470	 0.4780
Se	 0.4300	 0.4350
Sg	 0.3340	 0.3990
Sh	 0.3730	 0.3760
Sj	 0.3420	 0.3940
St	 0.6570	 0.4310