



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 04:54 pm BST

PDB ID : 8BTR
EMDB ID : EMD-16235
Title : Giardia Ribosome in PRE-T Hybrid State (D2)
Authors : Majumdar, S.; Emmerich, A.G.; Sanyal, S.
Deposited on : 2022-11-29
Resolution : 3.25 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.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

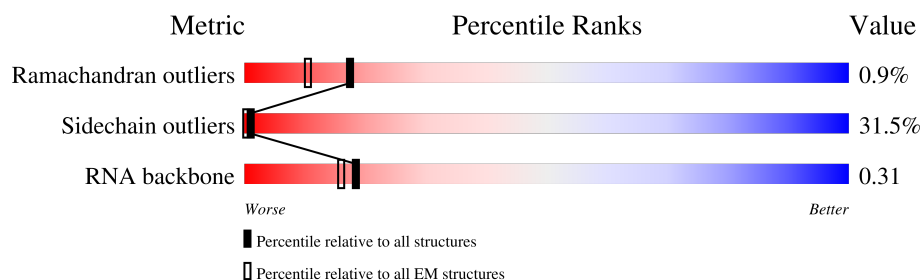
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.25 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 ≥ 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	
2	LB	379	
3	LC	316	
4	LD	142	
5	LE	121	
6	LF	297	
7	LG	51	
8	LH	235	

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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	144	

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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	
76	u	75	
77	v	75	
78	y	11	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 177509 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	247	Total	C	N	O	S	0	0
			1855	1145	379	319	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	310	Total	C	N	O	S	0	0
			2415	1518	469	420	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	293	Total	C	N	O	S	0	0
			2355	1490	439	418	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	212	Total	C	N	O	S	0	0
			1717	1092	313	307	5		

- Molecule 9 is a protein called Ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LI	186	Total	C	N	O	S	0	0
			1487	947	273	262	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	195	Total	C	N	O	S	0	0
			1594	1001	315	270	8		

- Molecule 12 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LL	166	Total	C	N	O	S	0	0
			1334	842	248	239	5		

- Molecule 13 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LM	200	Total	C	N	O	S	0	0
			1600	996	324	273	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	155	Total	C	N	O	S	0	0
			1247	788	241	214	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	161	Total	C	N	O	S	0	0
			1342	829	283	226	4		

- 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	133	Total	C	N	O	S	0	0
			1019	643	194	177	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	115	Total	C	N	O	S	0	0
			931	598	168	162	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	126	Total	C	N	O	S	0	0
			1004	633	189	176	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	55	Total	C	N	O	S	0	0
			456	275	103	76	2		

- Molecule 30 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ld	100	Total	C	N	O	S	0	0
			753	473	131	145	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	101	Total	C	N	O	S	0	0
			815	504	169	138	4		

- Molecule 35 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Li	122	Total	C	N	O	S	0	0
			983	623	192	163	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	200	Total	C	N	O	S	0	0
			1592	1025	278	284	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	2593	Total	C	N	O	P	0	0
			55643	24727	10311	18012	2593		

- Molecule 45 is a protein called Ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	197	Total	C	N	O	S	0	0
			1578	1018	276	276	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	206	Total	C	N	O	S	0	0
			1636	1030	302	288	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	257	Total	C	N	O	S	0	0
			2055	1312	378	353	12		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SF	179	Total	C	N	O	S	0	0
			1400	871	266	254	9		

- Molecule 51 is a protein called Ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SG	238	Total	C	N	O	S	0	0
			1889	1188	360	331	10		

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SH	177	Total	C	N	O	S	0	0
			1430	918	248	258	6		

- Molecule 53 is a protein called Ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SI	168	Total	C	N	O	S	0	0
			1316	826	252	235	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	97	Total	C	N	O	S	0	0
			798	515	135	144	4		

- Molecule 57 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	152	Total	C	N	O	S	0	0
			1260	799	247	208	6		

- Molecule 58 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SO	140	Total	C	N	O	S	0	0
			1089	688	216	182	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
			1193	762	225	202	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SP	6	ALA	SER	conflict	UNP A8BE02
SP	7	PRO	LYS	conflict	UNP A8BE02
SP	38	TYR	CYS	conflict	UNP A8BE02
SP	49	GLN	ARG	conflict	UNP A8BE02

- Molecule 60 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SQ	126	Total	C	N	O	S	0	0
			920	566	189	162	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SQ	110	GLY	GLN	conflict	UNP E2RU83
SQ	112	SER	GLY	conflict	UNP E2RU83
SQ	113	ALA	SER	conflict	UNP E2RU83
SQ	115	GLY	ALA	conflict	UNP E2RU83

- Molecule 61 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SR	113	Total	C	N	O	S	0	0
			921	588	179	146	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	121	Total	C	N	O	S	0	0
			965	598	184	178	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	129	Total	C	N	O	S	0	0
			1027	627	210	184	6		

- Molecule 65 is a protein called Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SW	138	Total	C	N	O	S	0	0
			1080	686	204	187	3		

- Molecule 66 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SX	98	Total	C	N	O	S	0	0
			776	496	141	135	4		

- 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	116	Total	C	N	O	S	0	0
			923	587	172	158	6		

- Molecule 69 is a protein called Ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sc	74	Total	C	N	O	S	0	0
			588	371	105	106	6		

- Molecule 70 is a protein called Ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sd	97	Total	C	N	O	S	0	0
			787	485	162	133	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	62	Total	C	N	O	S	0	0
			498	306	99	91	2		

- Molecule 73 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sh	49	Total	C	N	O	S	0	0
			409	259	79	66	5		

- Molecule 74 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sj	67	Total	C	N	O	S	0	0
			543	341	114	87	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		

- Molecule 76 is a RNA chain called tRNA.

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

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	v	75	Total	C	N	O	P	0	0
			1602	716	296	516	74		

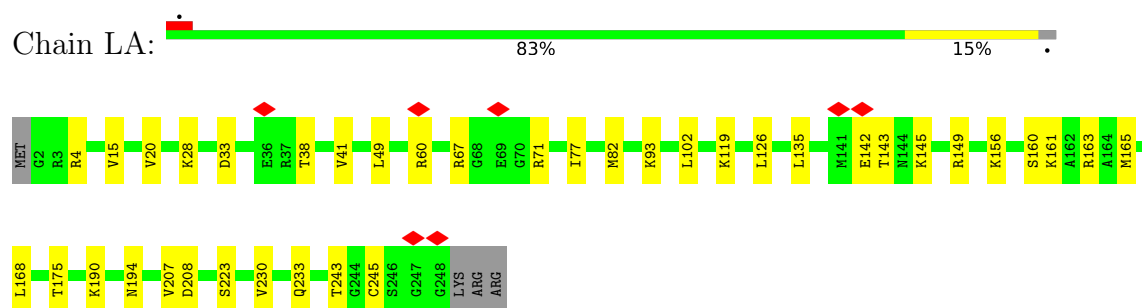
- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	y	11	Total	C	N	O	P	0	0
			243	109	52	71	11		

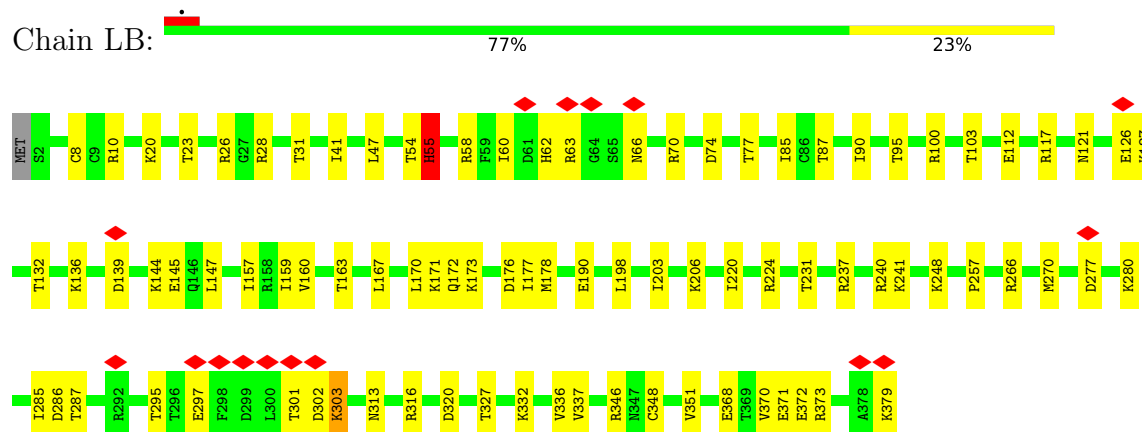
3 Residue-property plots [i](#)

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.

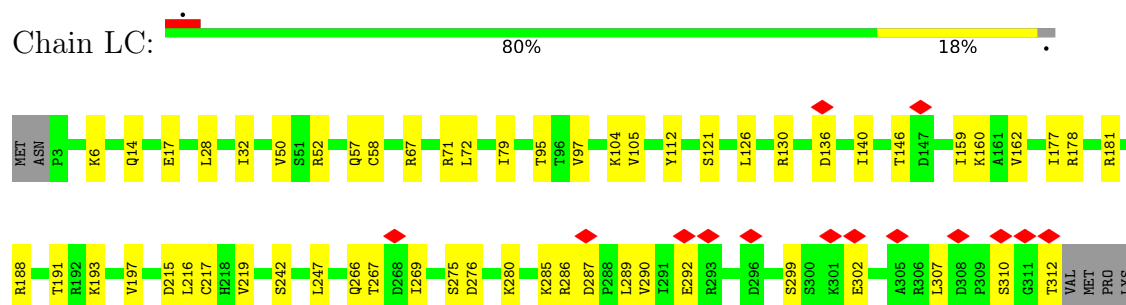
- Molecule 1: Ribosomal protein L2



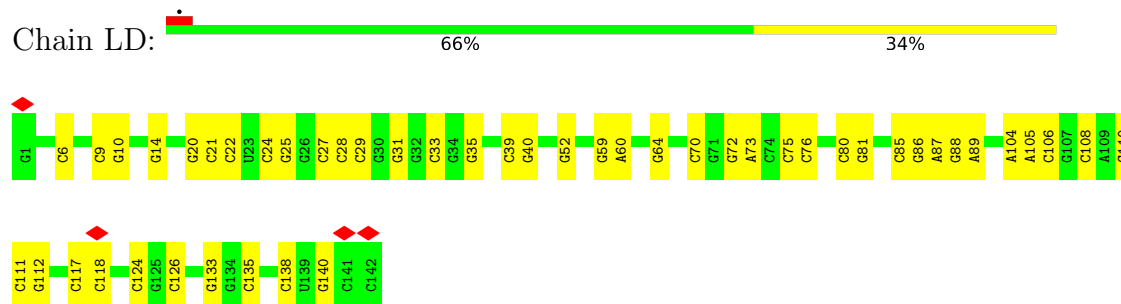
- Molecule 2: Ribosomal protein L3



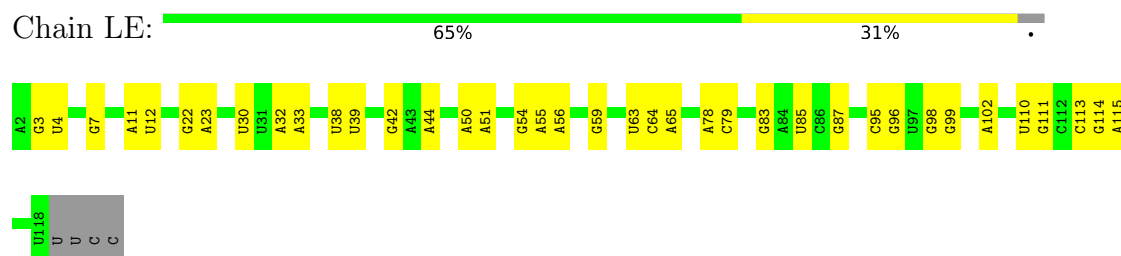
- Molecule 3: Ribosomal protein L4



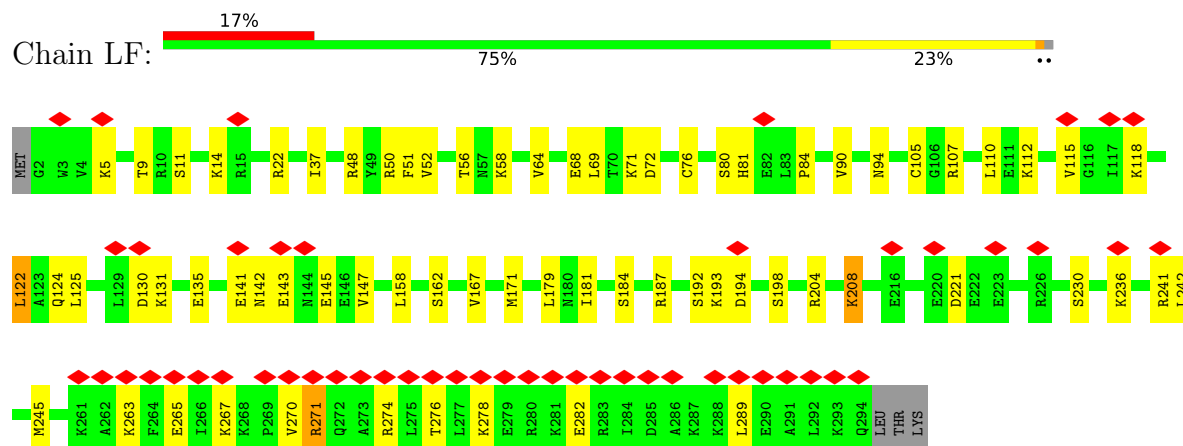
- Molecule 4: 5.8S rRNA



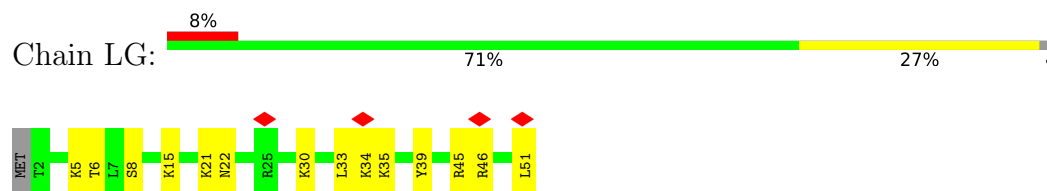
- Molecule 5: 5S rRNA



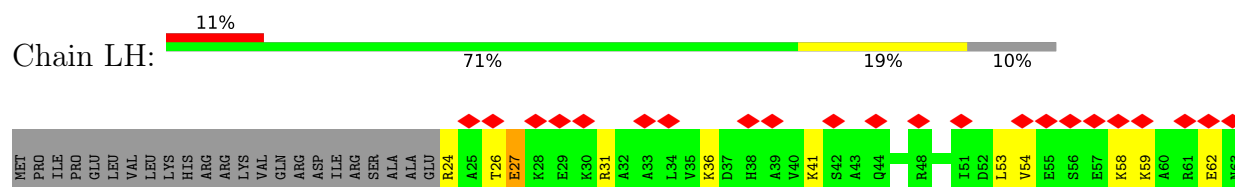
- Molecule 6: Ribosomal protein L5

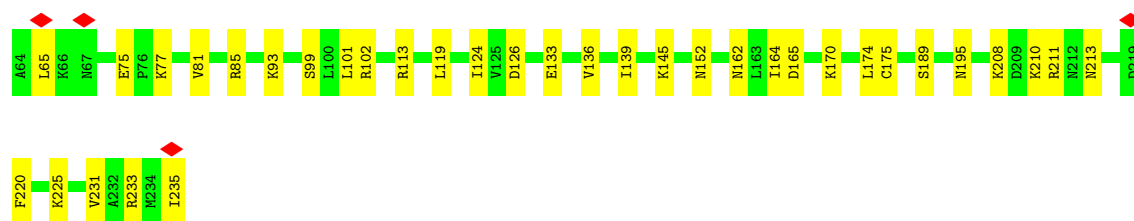


- Molecule 7: Ribosomal protein L39

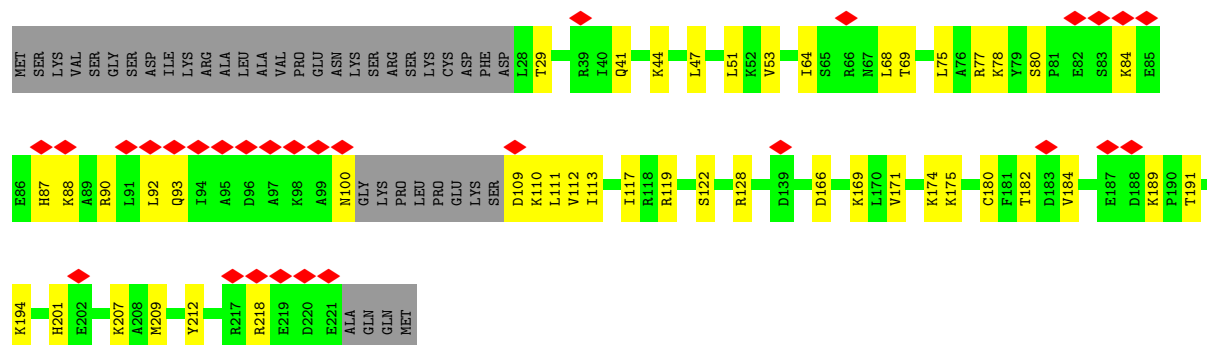


- Molecule 8: Ribosomal protein L7

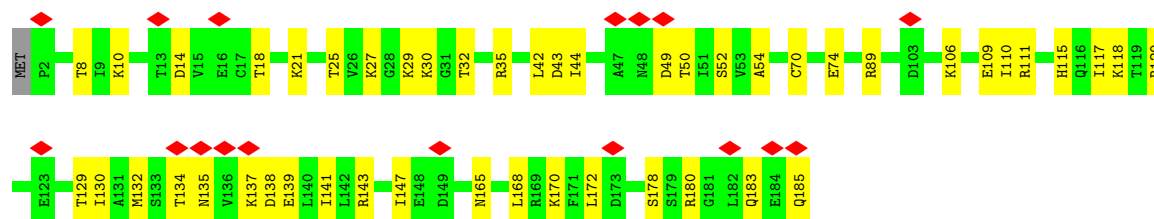
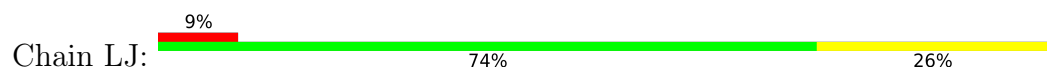




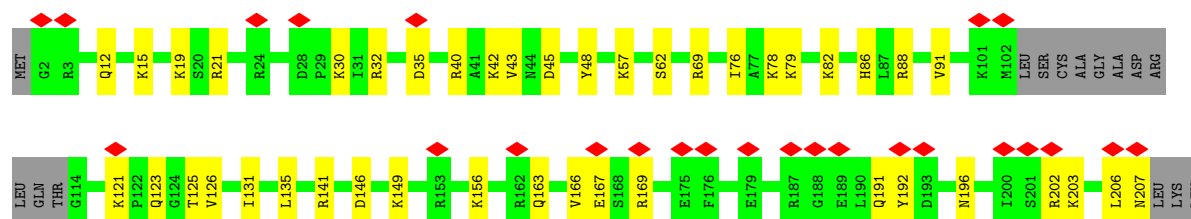
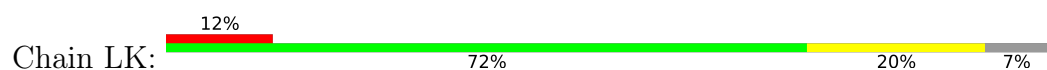
• Molecule 9: Ribosomal protein L7a



• Molecule 10: Ribosomal protein L6

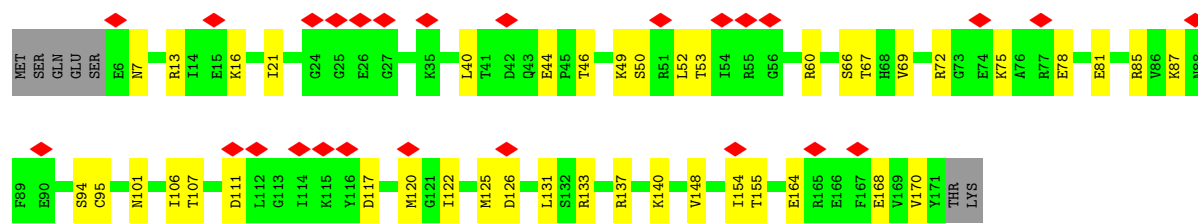


• Molecule 11: Ribosomal protein L10

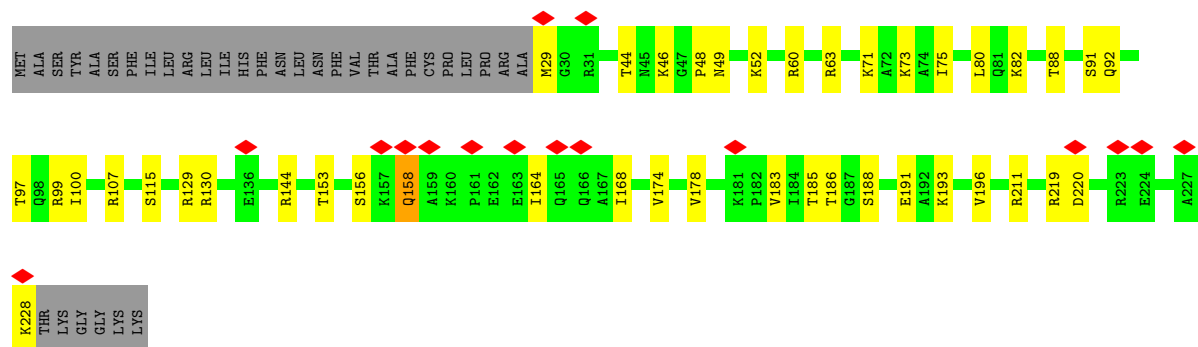


• Molecule 12: Ribosomal protein L11

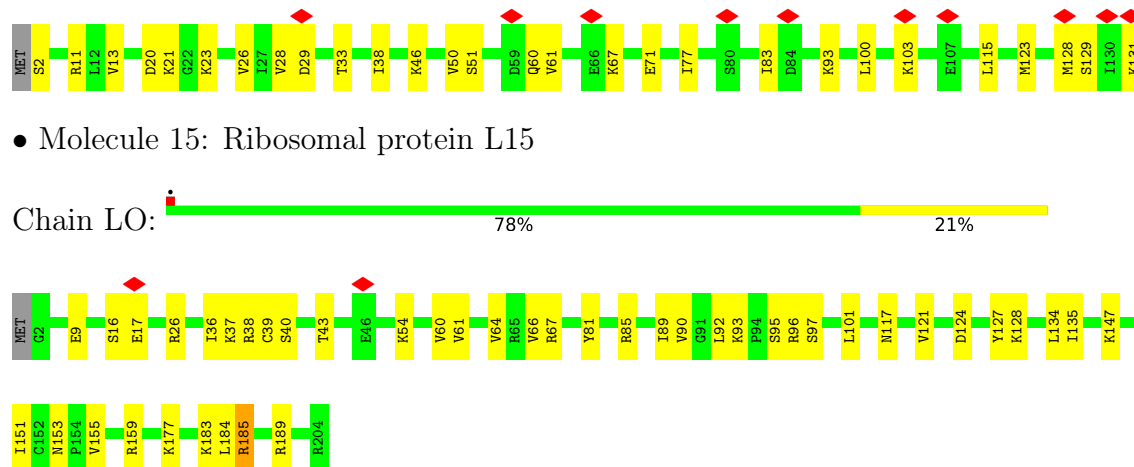
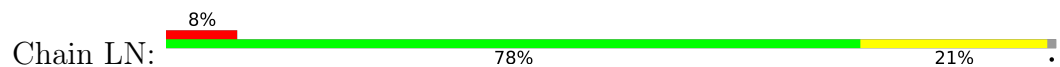




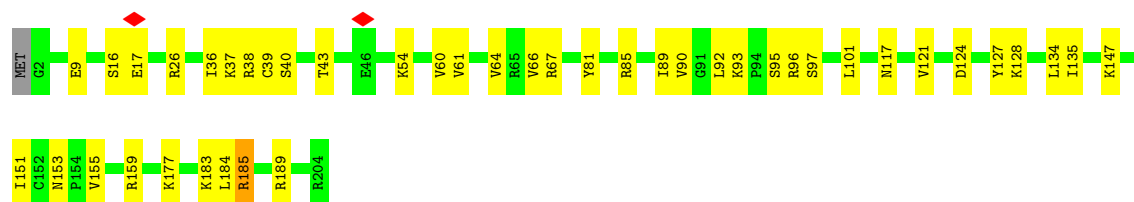
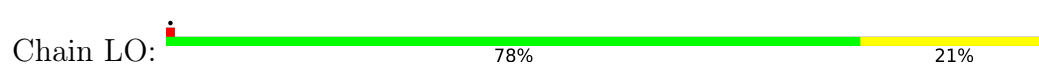
• Molecule 13: Ribosomal protein L13



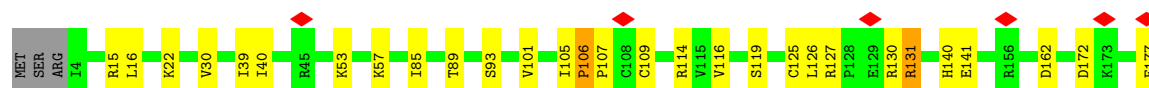
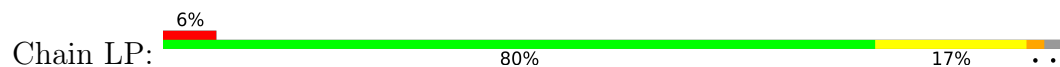
• Molecule 14: Ribosomal protein L14

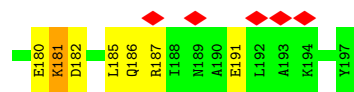


• Molecule 15: Ribosomal protein L15

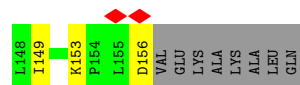
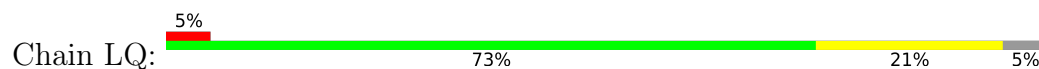


• Molecule 16: Ribosomal protein L13a

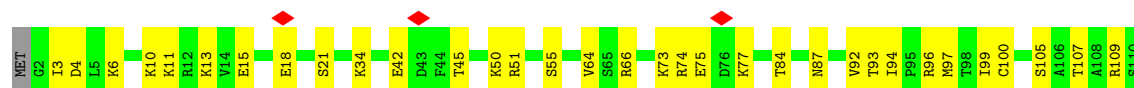




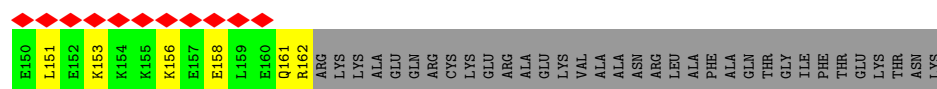
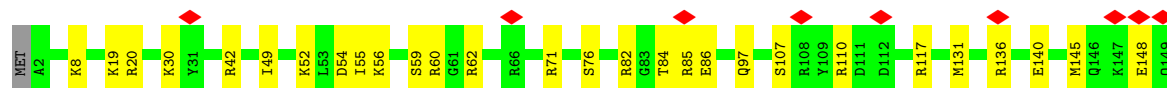
- Molecule 17: Ribosomal protein L17



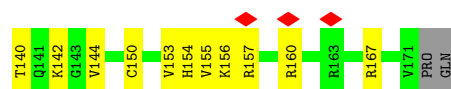
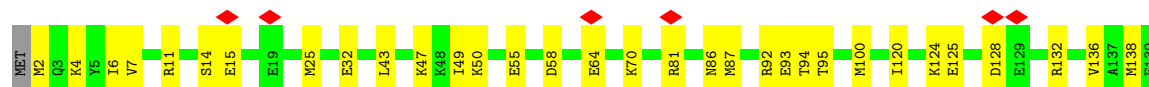
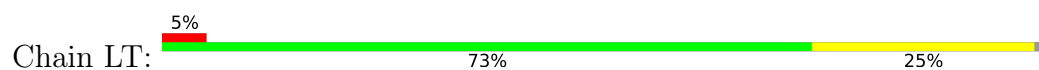
- Molecule 18: Ribosomal protein L18



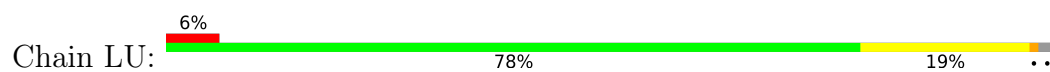
- Molecule 19: Ribosomal protein L19



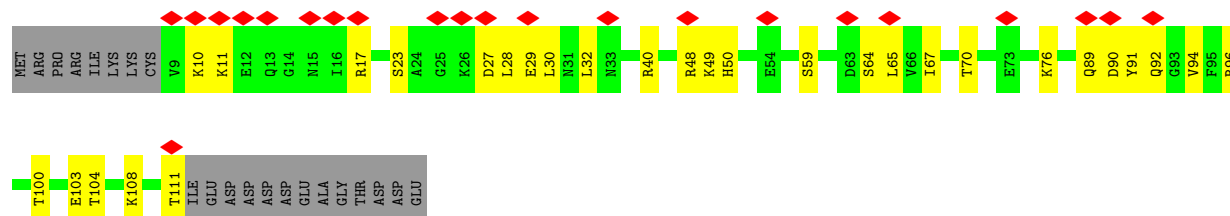
- Molecule 20: Ribosomal protein L18a



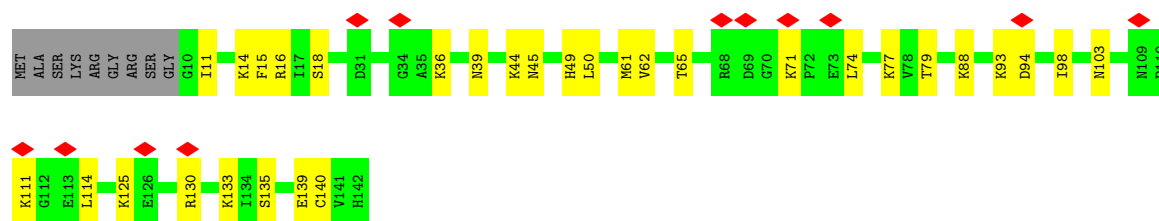
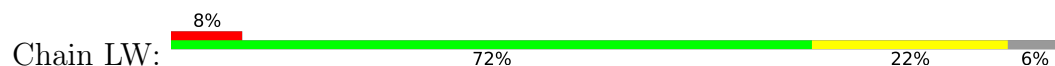
- Molecule 21: Ribosomal protein L21



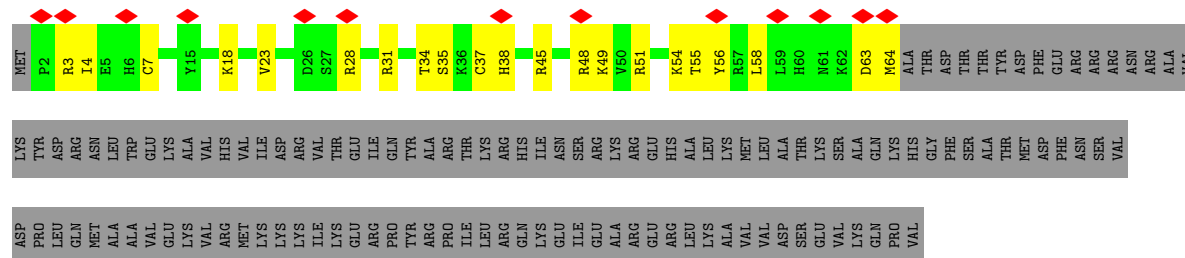
• Molecule 22: Ribosomal protein L22e



• Molecule 23: Ribosomal protein L23

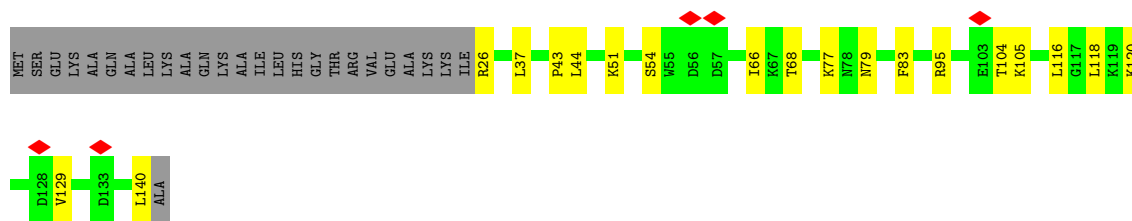


• Molecule 24: Ribosomal protein L24



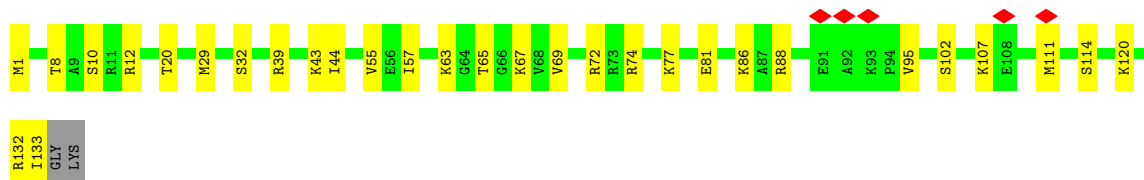
• Molecule 25: Ribosomal protein L23A





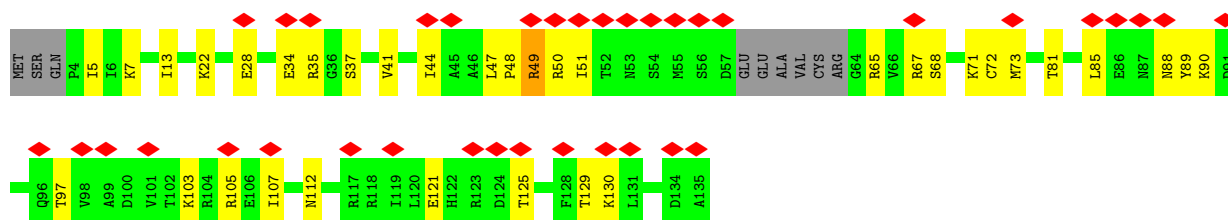
- Molecule 26: Ribosomal protein L26

Chain LZ: 76% 22%



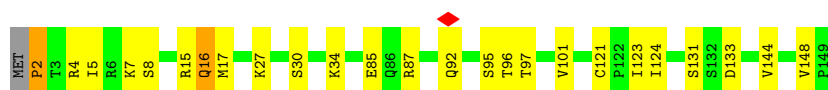
- Molecule 27: Ribosomal protein L27

Chain La: 27% 67% 25% 7%



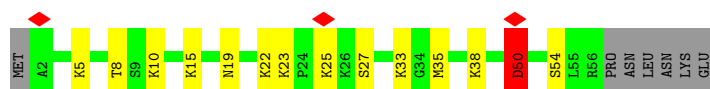
- Molecule 28: Ribosomal protein L27a

Chain Lb: 83% 15%



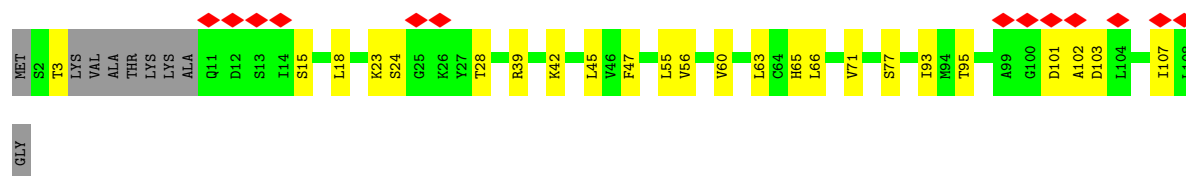
- Molecule 29: Ribosomal protein L29

Chain Lc: 5% 66% 21% 11%

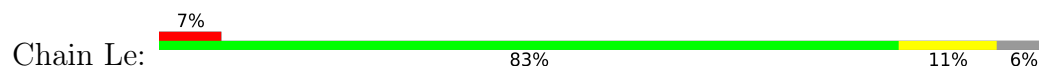


- Molecule 30: Ribosomal protein L30

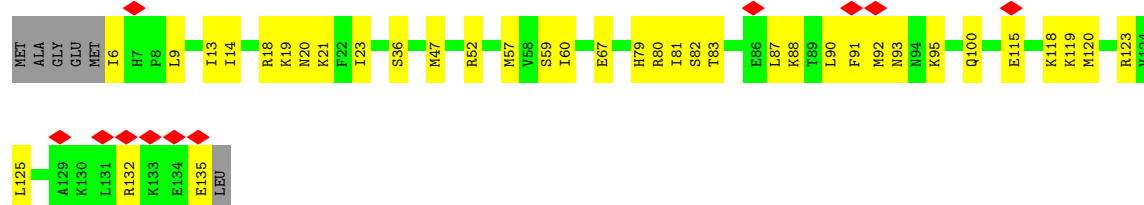
Chain Ld: 12% 70% 22% 8%



• Molecule 31: Ribosomal protein L31B



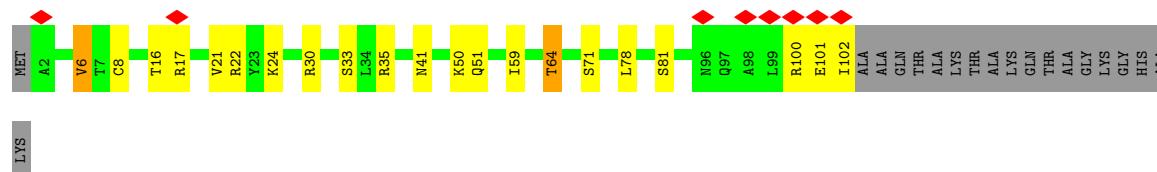
• Molecule 32: Ribosomal protein L32



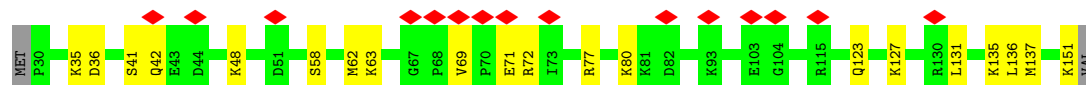
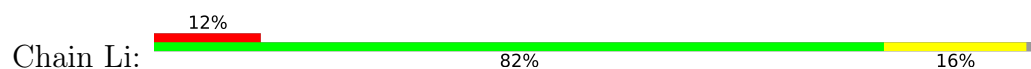
• Molecule 33: Ribosomal protein L35a



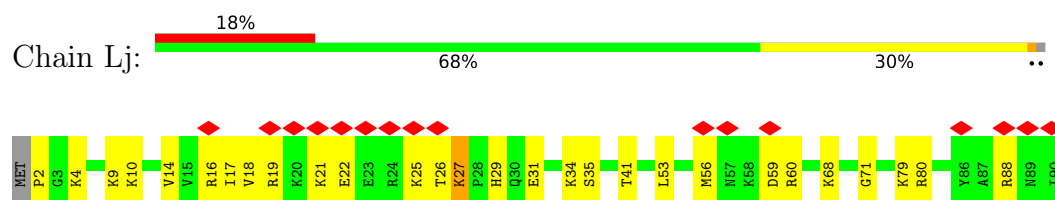
• Molecule 34: Ribosomal protein L34



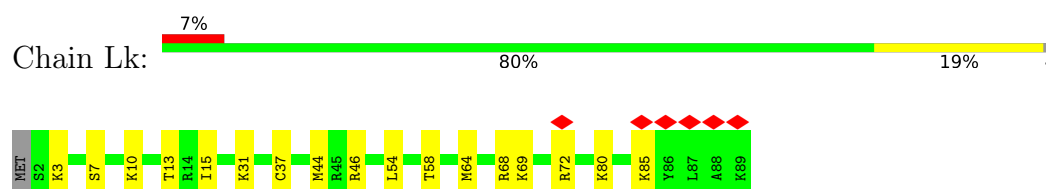
• Molecule 35: Ribosomal protein L29



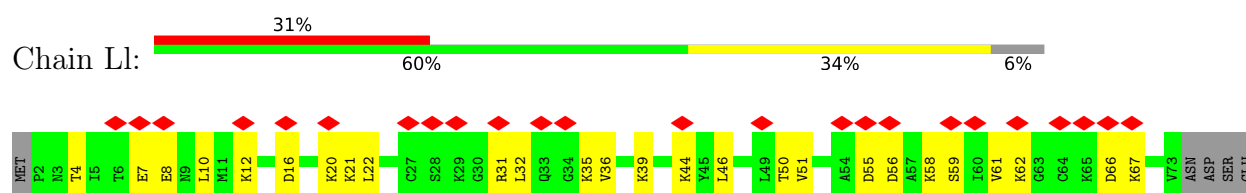
- Molecule 36: Ribosomal protein L36-1



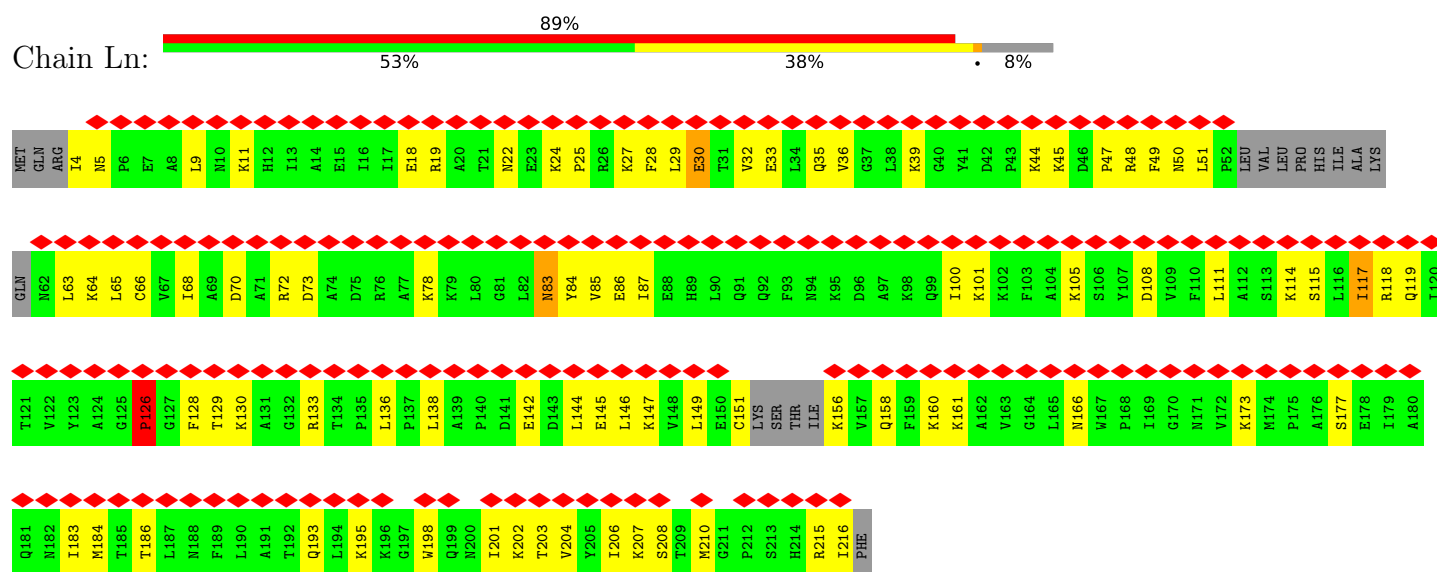
- Molecule 37: Ribosomal protein L37



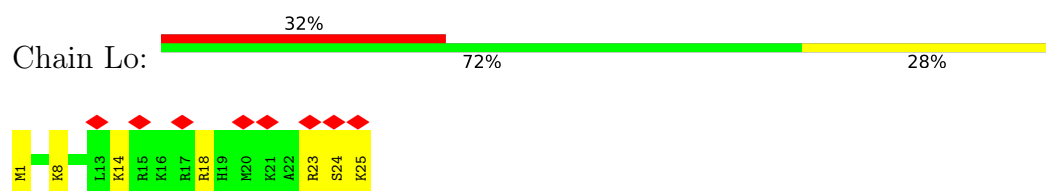
- Molecule 38: Ribosomal protein L38e



- Molecule 39: Ribosomal protein L10a

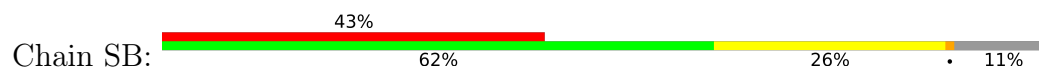


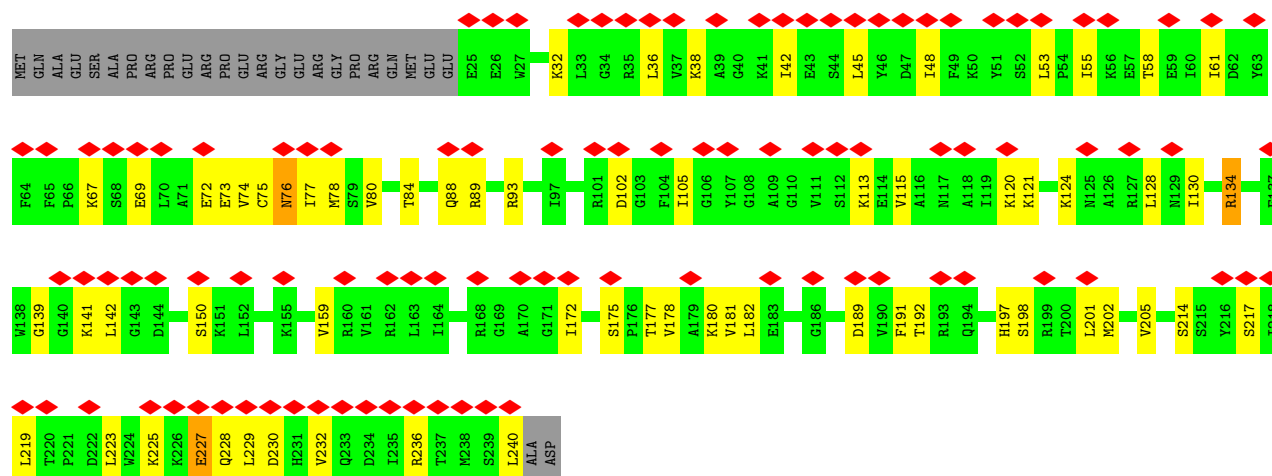
- Molecule 40: Ribosomal protein L41



- Molecule 41: Ribosomal protein L44



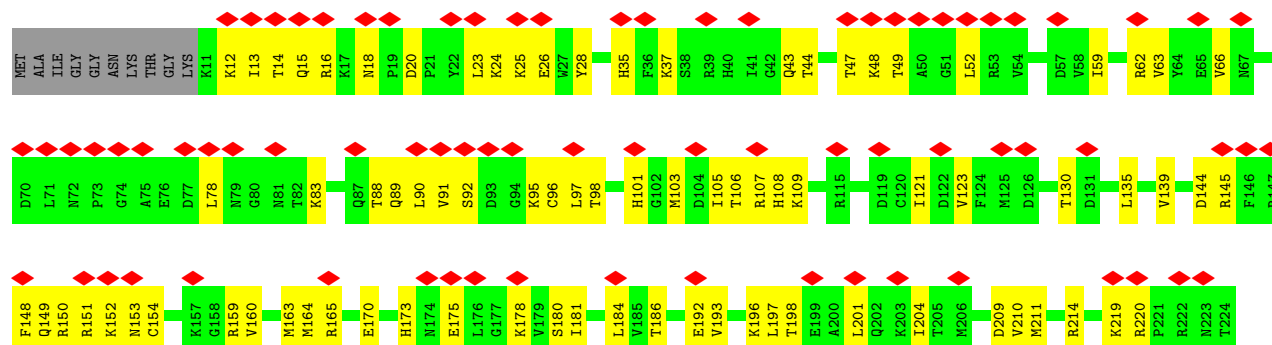


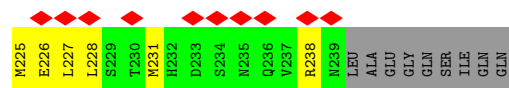


• Molecule 47: Ribosomal protein S3

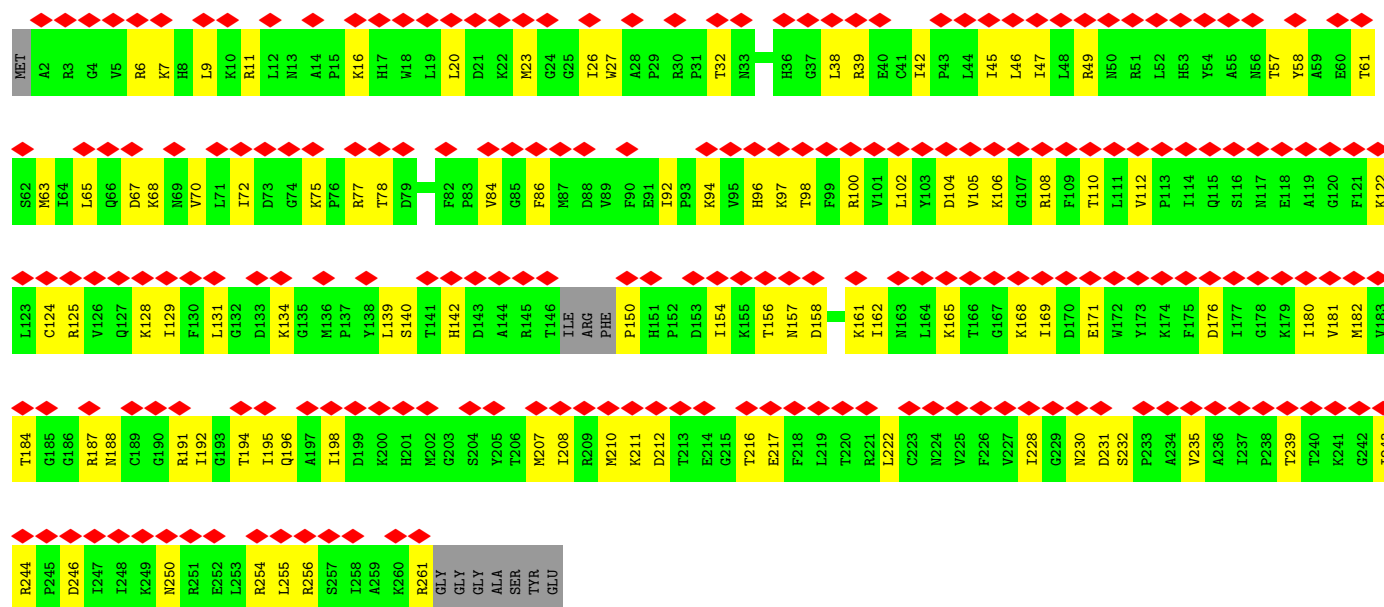
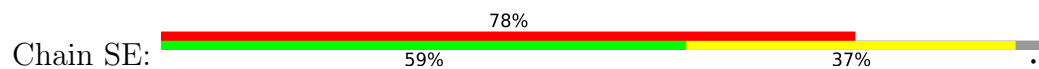


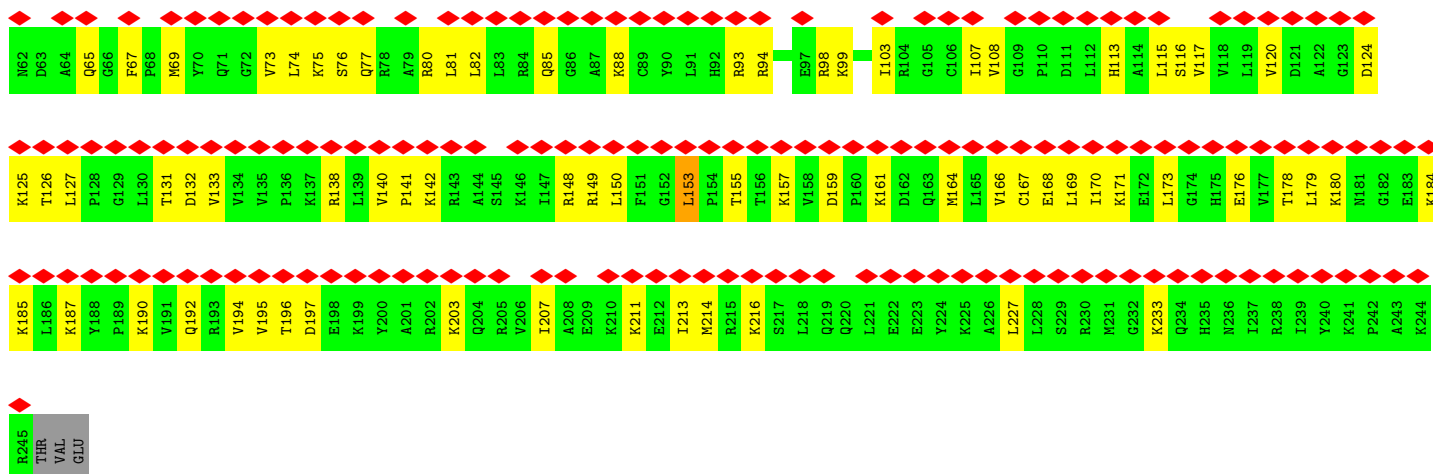
• Molecule 48: Ribosomal protein S3a



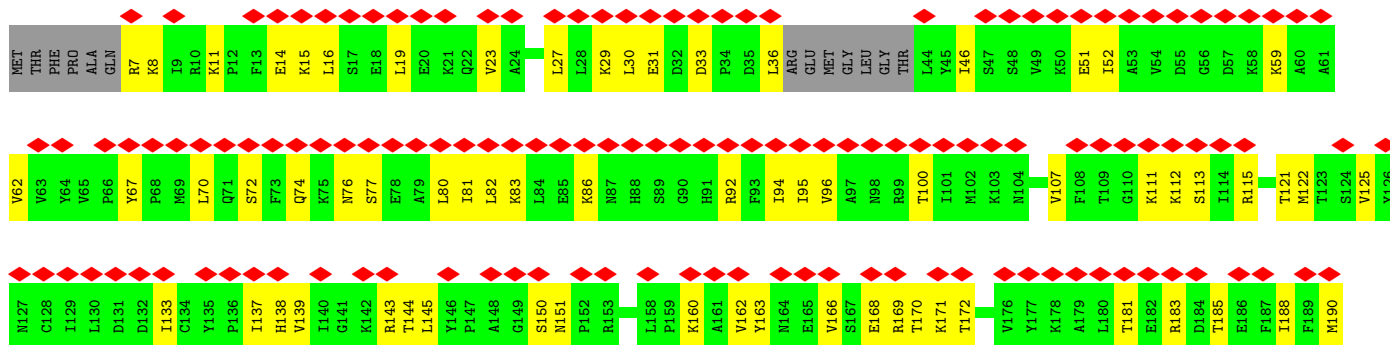
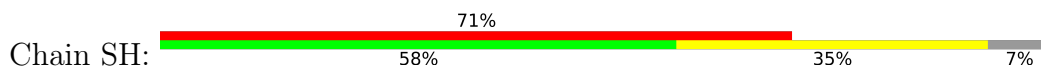


• Molecule 49: Ribosomal protein S4

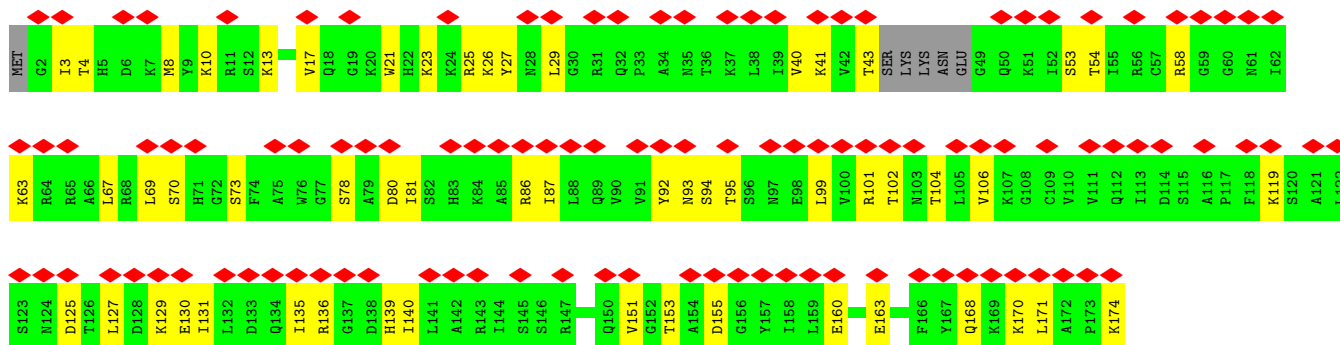




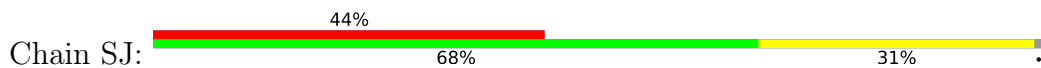
• Molecule 52: Ribosomal protein S7

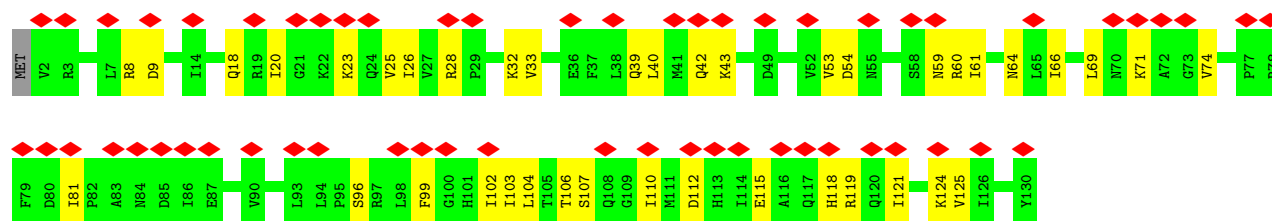


• Molecule 53: Ribosomal protein S8

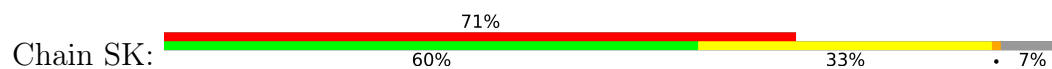


• Molecule 54: Ribosomal protein S15A

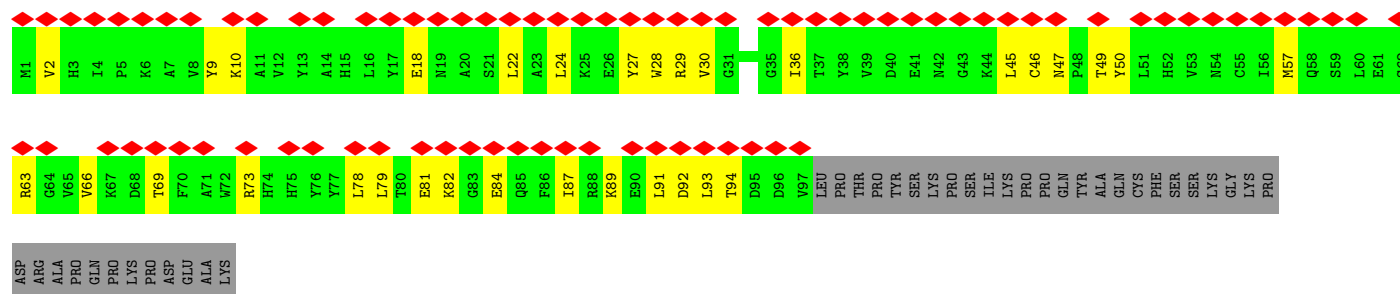




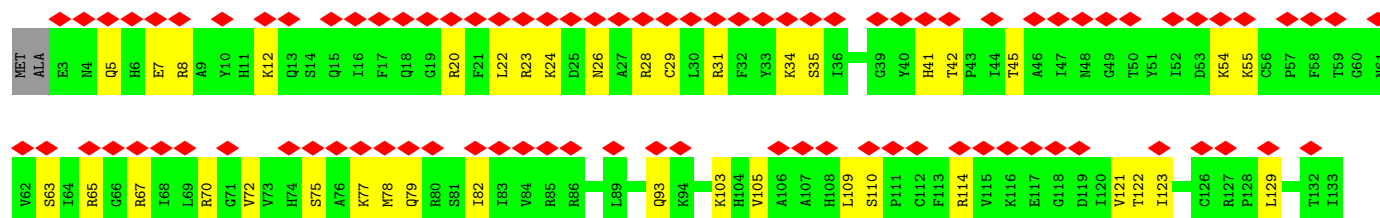
• Molecule 55: Ribosomal protein S9



• Molecule 56: Ribosomal protein S10B

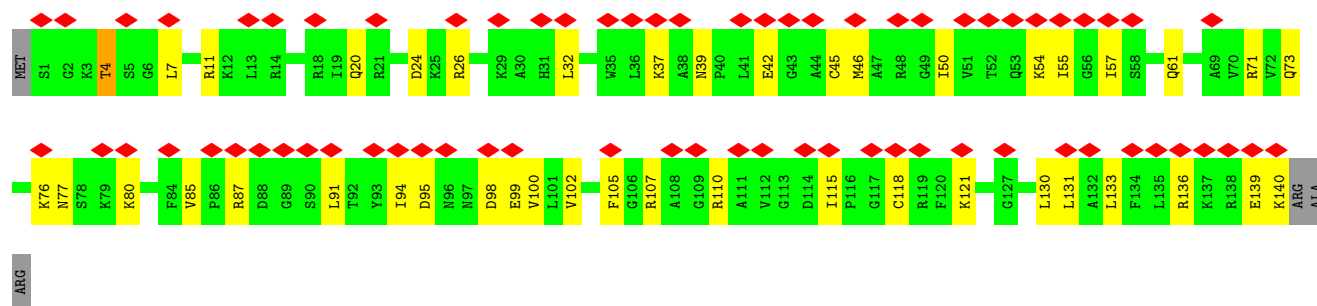


• Molecule 57: Ribosomal protein S11

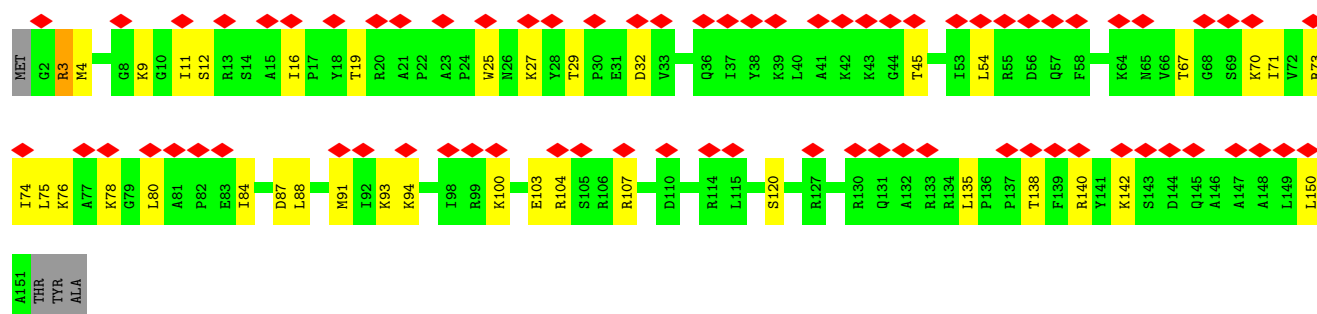
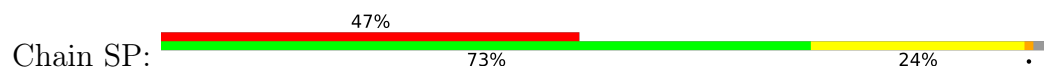




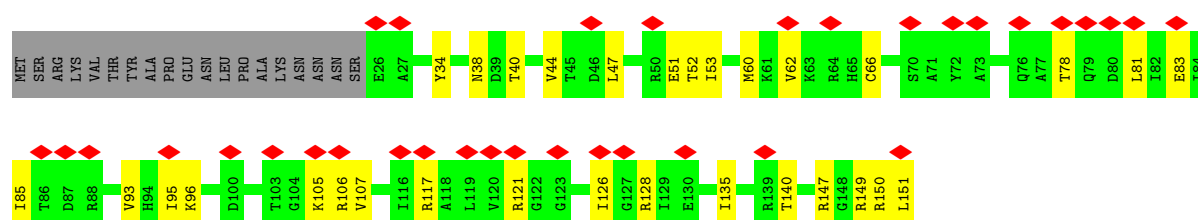
- Molecule 58: Ribosomal protein S23



- Molecule 59: Ribosomal protein S13



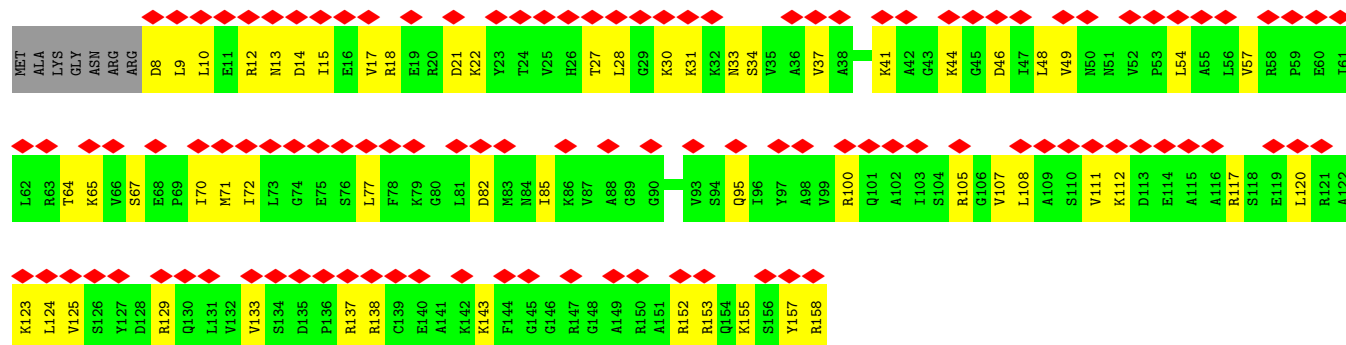
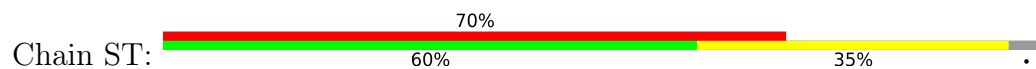
- Molecule 60: Ribosomal protein S14



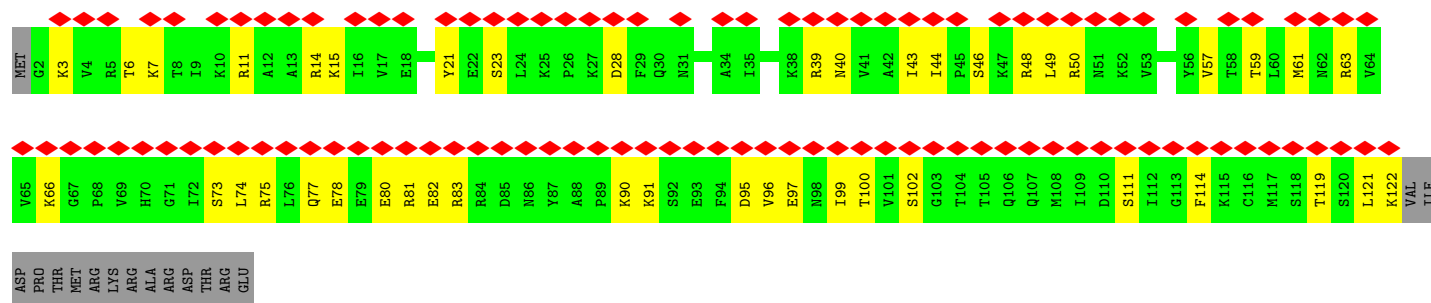
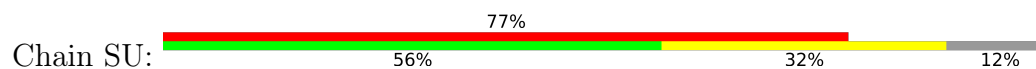
- Molecule 61: Ribosomal protein S15



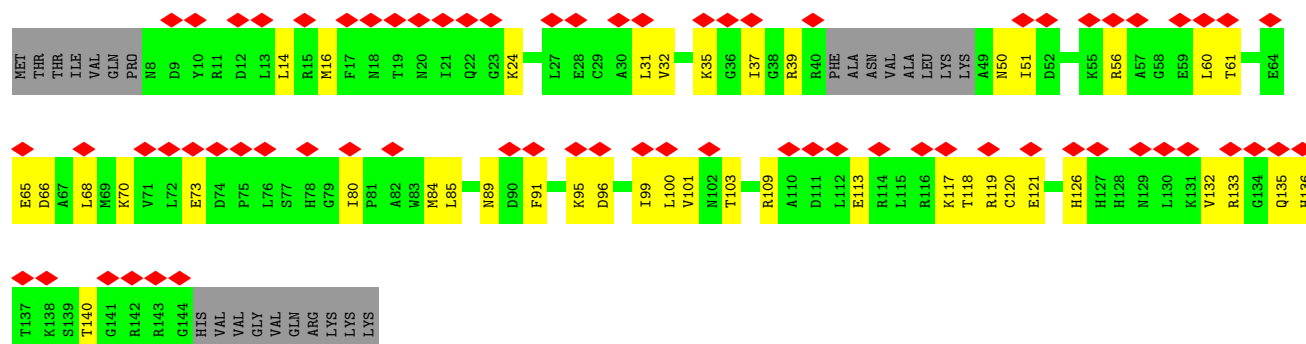
- Molecule 62: Ribosomal protein S16



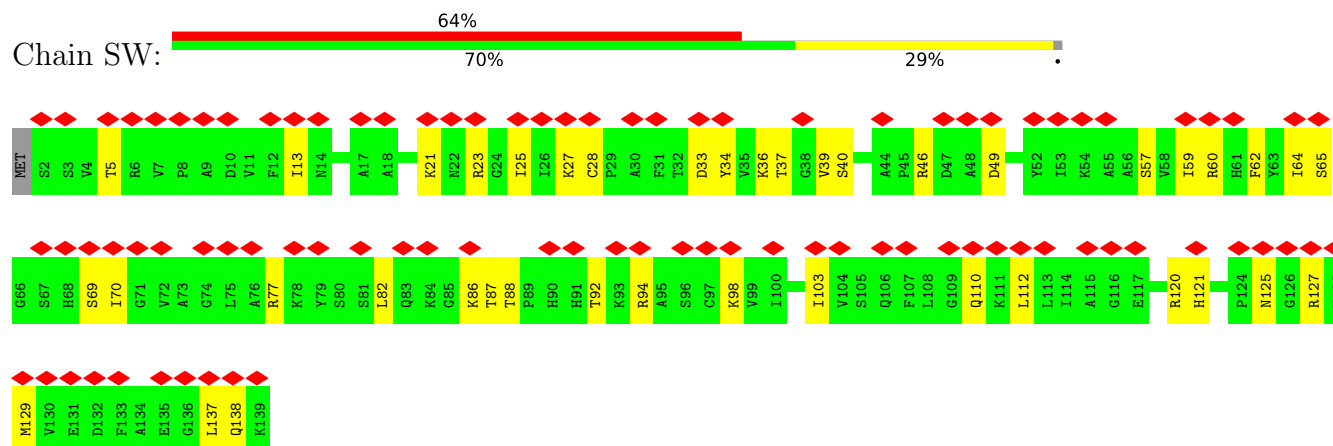
- Molecule 63: Ribosomal protein S17



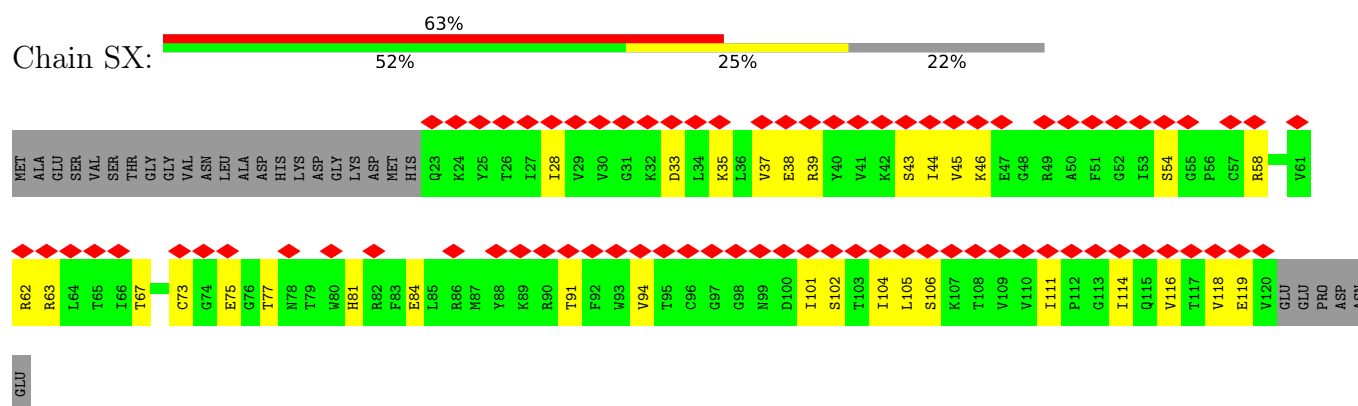
- Molecule 64: Ribosomal protein S18



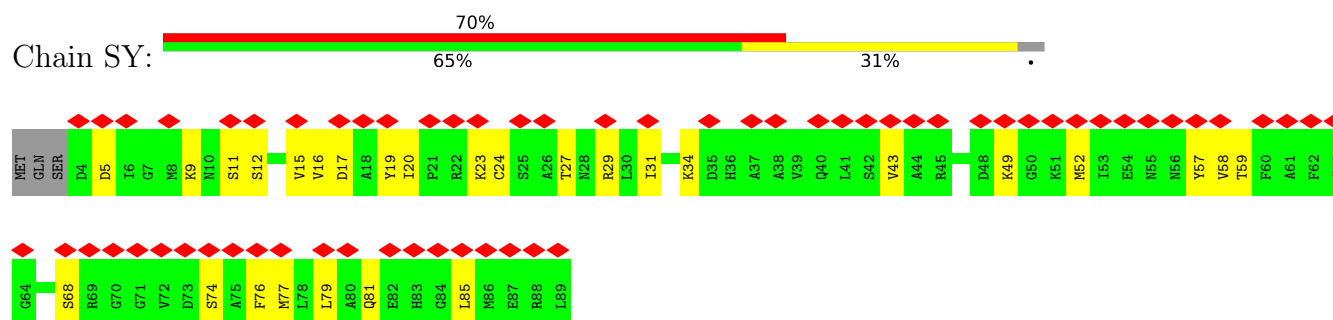
- Molecule 65: Ribosomal protein S19e



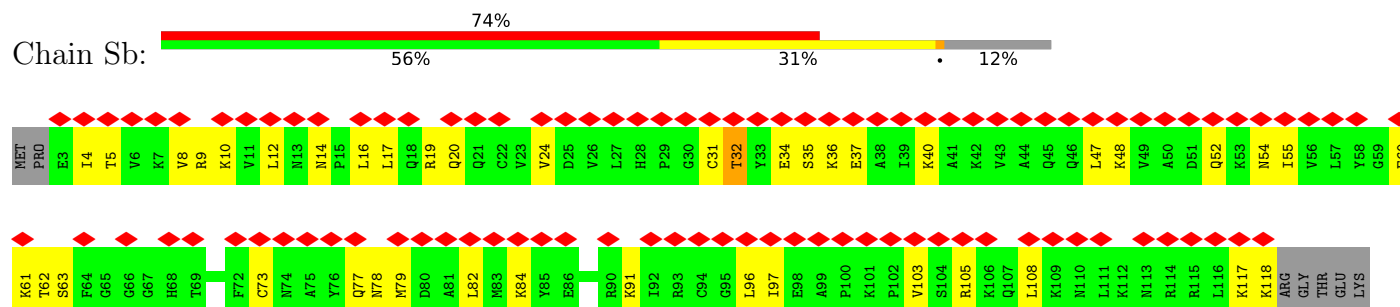
- Molecule 66: Ribosomal protein S20



- Molecule 67: Ribosomal protein S21



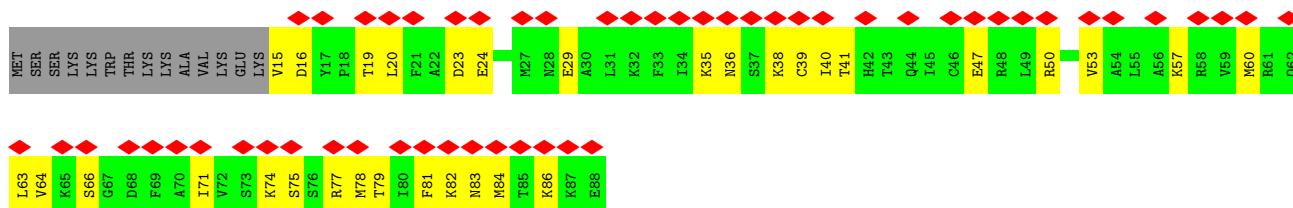
- Molecule 68: Ribosomal protein S24



ALA
THR
VAL
THR
LEU
GLY
ALA
LYS
LYS

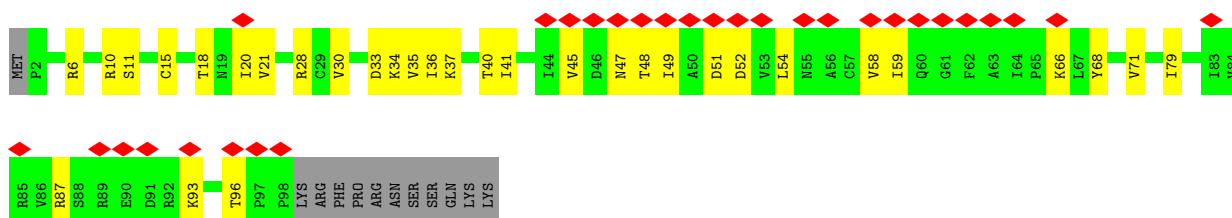
• Molecule 69: Ribosomal protein S25

Chain Sc: 




• Molecule 70: Ribosomal protein S26

Chain Sd: 



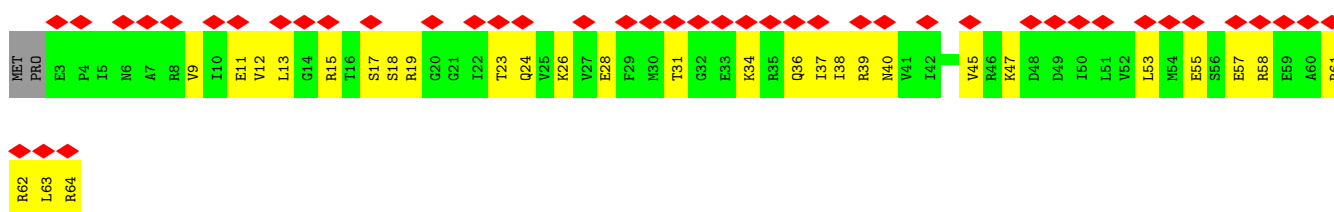
• Molecule 71: Ribosomal protein S27

Chain Se: 



• Molecule 72: Ribosomal protein S28

Chain Sg: 



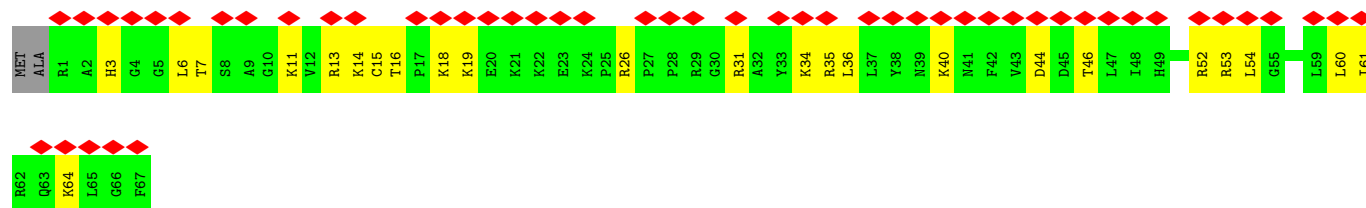
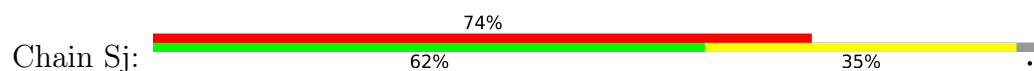
• Molecule 73: Ribosomal protein S29A

Chain Sh: 

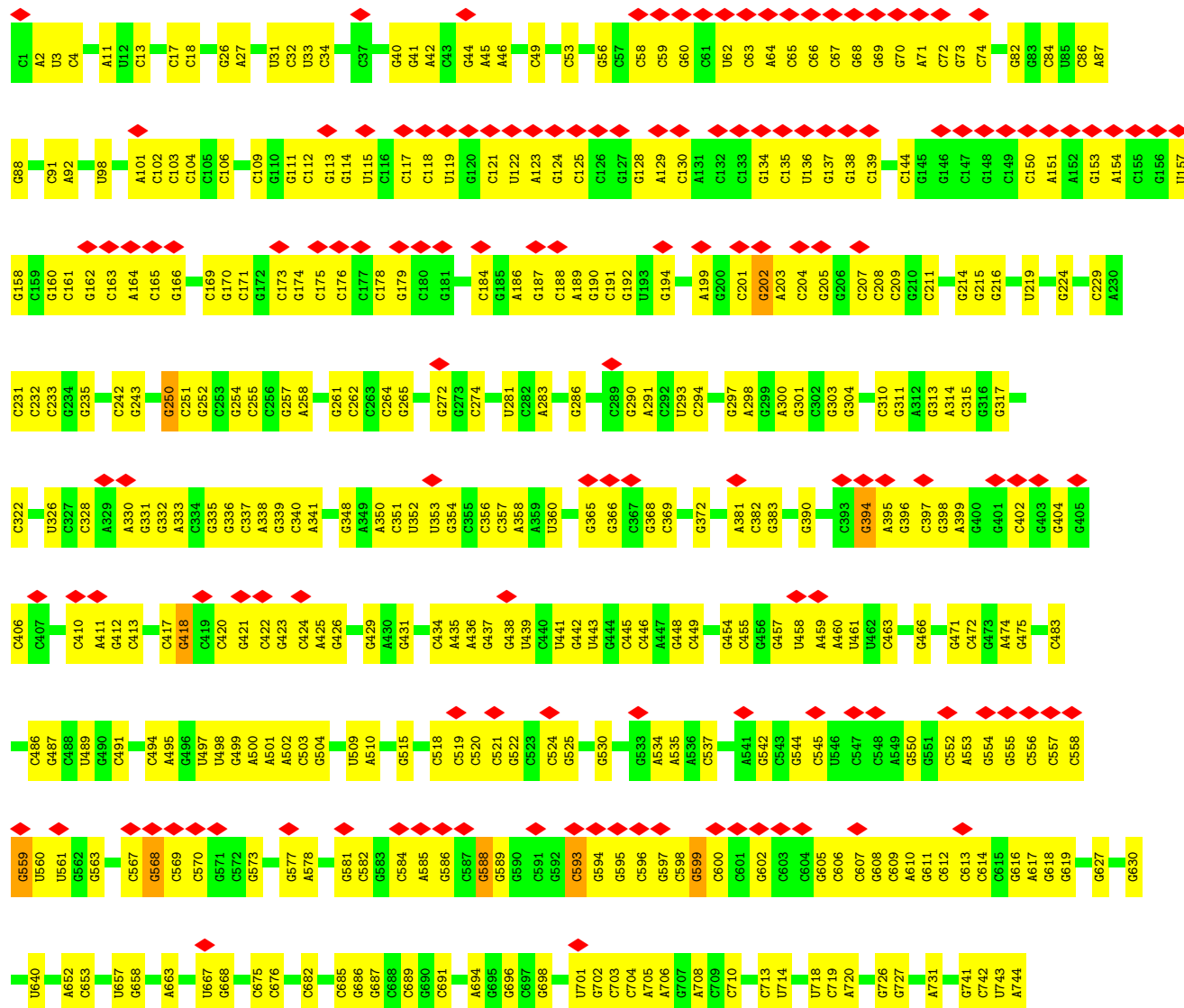


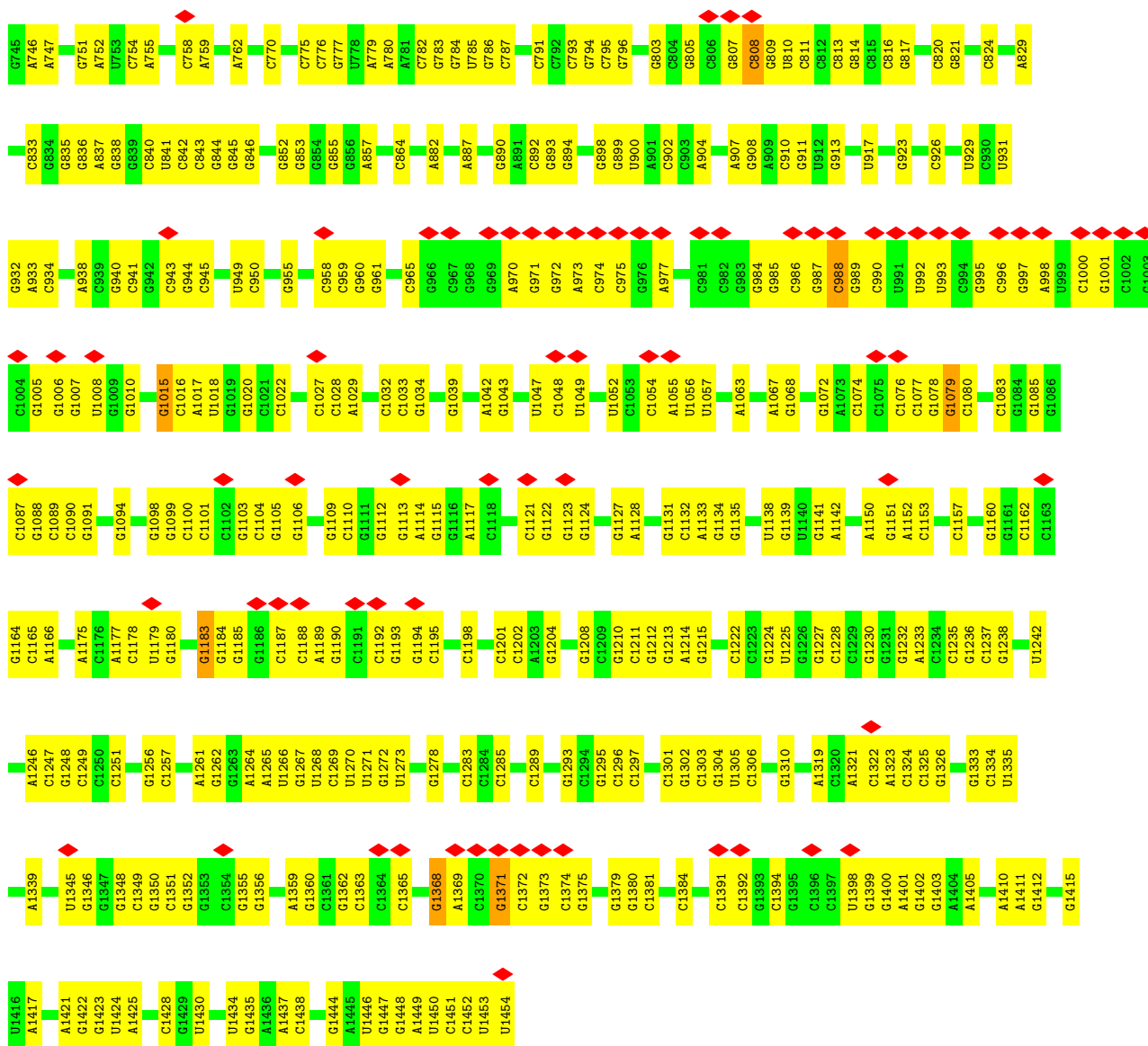


• Molecule 74: Ribosomal protein S30

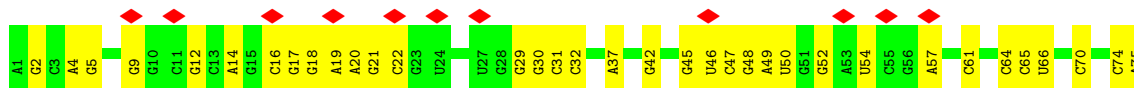


• Molecule 75: Small Subunit rRNA

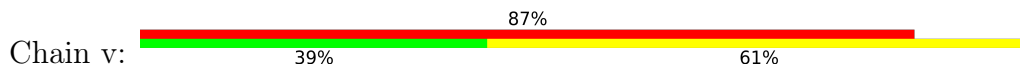


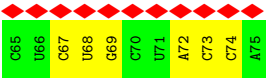


• Molecule 76: tRNA

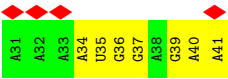


• Molecule 77: tRNA





● Molecule 78: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31100	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	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	18.685	Depositor
Minimum map value	-9.239	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.87	Depositor
Map size (Å)	410.0, 410.0, 410.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0/1888	0.85	0/2538
2	LB	0.56	0/3058	0.84	3/4129 (0.1%)
3	LC	0.59	0/2466	0.82	0/3345
4	LD	0.59	0/3393	0.86	0/5292
5	LE	0.58	0/2798	0.82	0/4361
6	LF	0.56	0/2398	0.78	0/3216
7	LG	0.53	0/450	0.83	0/601
8	LH	0.57	0/1747	0.83	0/2355
9	LI	0.58	0/1513	0.82	0/2044
10	LJ	0.59	0/1479	0.83	0/1997
11	LK	0.56	0/1630	0.77	0/2181
12	LL	0.58	0/1359	0.79	0/1825
13	LM	0.57	0/1623	0.85	0/2173
14	LN	0.56	0/1037	0.74	0/1390
15	LO	0.57	0/1751	0.79	1/2346 (0.0%)
16	LP	0.56	0/1610	0.82	1/2160 (0.0%)
17	LQ	0.59	0/1273	0.81	0/1703
18	LR	0.60	0/1425	0.86	1/1907 (0.1%)
19	LS	0.56	0/1357	0.73	0/1796
20	LT	0.55	0/1457	0.81	1/1957 (0.1%)
21	LU	0.55	0/1283	0.85	0/1725
22	LV	0.57	0/861	0.83	0/1158
23	LW	0.57	0/1039	0.81	0/1401
24	LX	0.55	0/553	0.93	0/736
25	LY	0.55	0/951	0.81	0/1286
26	LZ	0.57	0/1091	0.77	0/1454
27	La	0.59	0/1021	0.85	0/1376
28	Lb	0.58	0/1231	0.88	1/1647 (0.1%)
29	Lc	0.57	0/463	0.93	1/612 (0.2%)
30	Ld	0.61	0/760	0.79	0/1027
31	Le	0.56	0/832	0.78	0/1118
32	Lf	0.59	0/1101	0.79	0/1467
33	Lg	0.56	0/793	0.87	0/1062
34	Lh	0.60	0/830	0.87	0/1115

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Li	0.54	0/996	0.77	0/1328
36	Lj	0.57	0/741	0.84	0/982
37	Lk	0.63	0/727	0.83	0/963
38	Ll	0.56	0/562	0.90	0/749
39	Ln	0.62	0/1621	0.85	2/2183 (0.1%)
40	Lo	0.49	0/229	0.73	0/291
41	Lp	0.56	0/778	0.82	0/1029
42	Lq	0.57	0/717	0.91	0/955
43	Ls	0.56	0/392	1.02	0/522
44	Lt	0.59	0/62214	0.88	57/97098 (0.1%)
45	SA	0.60	0/1612	0.78	0/2190
46	SB	0.60	0/1700	0.81	0/2293
47	SC	0.59	0/1662	0.80	0/2231
48	SD	0.56	0/1890	0.80	0/2546
49	SE	0.60	0/2099	0.85	0/2829
50	SF	0.61	0/1422	0.79	0/1912
51	SG	0.60	0/1915	0.82	1/2560 (0.0%)
52	SH	0.59	0/1456	0.82	0/1962
53	SI	0.61	0/1336	0.84	0/1792
54	SJ	0.60	0/1048	0.81	0/1412
55	SK	0.61	0/1443	0.84	1/1930 (0.1%)
56	SL	0.60	0/819	0.75	0/1112
57	SM	0.60	0/1289	0.79	0/1724
58	SO	0.58	0/1104	0.81	0/1478
59	SP	0.58	0/1218	0.79	0/1640
60	SQ	0.61	0/932	0.87	0/1251
61	SR	0.58	0/938	0.79	0/1253
62	ST	0.63	0/1192	0.78	0/1594
63	SU	0.62	0/975	0.84	0/1303
64	SV	0.58	0/1040	0.86	0/1392
65	SW	0.62	0/1104	0.79	0/1484
66	SX	0.61	0/790	0.77	0/1067
67	SY	0.63	0/659	0.81	0/883
68	Sb	0.61	0/937	0.83	1/1254 (0.1%)
69	Sc	0.60	0/594	0.90	1/791 (0.1%)
70	Sd	0.57	0/800	0.80	0/1077
71	Se	0.60	0/635	0.80	0/861
72	Sg	0.60	0/500	0.85	0/666
73	Sh	0.58	0/417	0.87	3/553 (0.5%)
74	Sj	0.56	0/553	0.84	0/736
75	St	0.62	2/34858 (0.0%)	0.88	22/54401 (0.0%)
76	u	0.55	0/1795	0.80	0/2798
77	v	0.54	0/1792	0.82	0/2793

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	y	0.56	0/274	0.96	0/426
All	All	0.59	2/190296 (0.0%)	0.85	97/278794 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	St	418	G	O3'-P	5.18	1.67	1.61
75	St	559	G	O3'-P	5.10	1.67	1.61

The worst 5 of 97 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	Lb	2	PRO	CA-N-CD	-9.21	98.61	111.50
75	St	1183	G	O4'-C1'-N9	8.97	115.38	108.20
44	Lt	691	G	C2'-C3'-O3'	8.95	129.18	109.50
29	Lc	50	ASP	CB-CA-C	8.94	128.28	110.40
44	Lt	1252	G	C2'-C3'-O3'	8.71	128.66	109.50

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	245/251 (98%)	234 (96%)	10 (4%)	1 (0%)	30	60
2	LB	376/379 (99%)	358 (95%)	16 (4%)	2 (0%)	25	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	LC	308/316 (98%)	298 (97%)	10 (3%)	0	100	100
6	LF	291/297 (98%)	276 (95%)	12 (4%)	3 (1%)	13	41
7	LG	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
8	LH	210/235 (89%)	201 (96%)	6 (3%)	3 (1%)	9	34
9	LI	182/225 (81%)	171 (94%)	9 (5%)	2 (1%)	12	39
10	LJ	182/185 (98%)	168 (92%)	11 (6%)	3 (2%)	8	31
11	LK	191/210 (91%)	180 (94%)	11 (6%)	0	100	100
12	LL	164/173 (95%)	157 (96%)	7 (4%)	0	100	100
13	LM	198/234 (85%)	187 (94%)	8 (4%)	3 (2%)	8	33
14	LN	128/131 (98%)	121 (94%)	7 (6%)	0	100	100
15	LO	201/204 (98%)	193 (96%)	7 (4%)	1 (0%)	25	56
16	LP	192/197 (98%)	182 (95%)	6 (3%)	4 (2%)	5	26
17	LQ	153/164 (93%)	146 (95%)	7 (5%)	0	100	100
18	LR	176/179 (98%)	168 (96%)	8 (4%)	0	100	100
19	LS	159/196 (81%)	158 (99%)	1 (1%)	0	100	100
20	LT	168/173 (97%)	164 (98%)	3 (2%)	1 (1%)	22	52
21	LU	154/159 (97%)	140 (91%)	12 (8%)	2 (1%)	10	35
22	LV	101/124 (82%)	92 (91%)	8 (8%)	1 (1%)	13	41
23	LW	131/142 (92%)	125 (95%)	6 (5%)	0	100	100
24	LX	61/189 (32%)	60 (98%)	0	1 (2%)	8	31
25	LY	113/141 (80%)	105 (93%)	6 (5%)	2 (2%)	7	30
26	LZ	131/135 (97%)	123 (94%)	8 (6%)	0	100	100
27	La	122/135 (90%)	110 (90%)	10 (8%)	2 (2%)	8	31
28	Lb	146/149 (98%)	135 (92%)	9 (6%)	2 (1%)	9	34
29	Lc	53/62 (86%)	49 (92%)	3 (6%)	1 (2%)	6	29
30	Ld	96/109 (88%)	91 (95%)	3 (3%)	2 (2%)	5	26
31	Le	98/106 (92%)	91 (93%)	7 (7%)	0	100	100
32	Lf	128/136 (94%)	119 (93%)	9 (7%)	0	100	100
33	Lg	96/123 (78%)	92 (96%)	4 (4%)	0	100	100
34	Lh	99/120 (82%)	90 (91%)	6 (6%)	3 (3%)	3	20
35	Li	120/124 (97%)	114 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lj	87/90 (97%)	78 (90%)	7 (8%)	2 (2%)	5	24
37	Lk	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
38	Ll	70/77 (91%)	63 (90%)	7 (10%)	0	100	100
39	Ln	194/217 (89%)	176 (91%)	13 (7%)	5 (3%)	4	22
40	Lo	23/25 (92%)	23 (100%)	0	0	100	100
41	Lp	91/106 (86%)	90 (99%)	1 (1%)	0	100	100
42	Lq	89/94 (95%)	82 (92%)	7 (8%)	0	100	100
43	Ls	45/127 (35%)	40 (89%)	2 (4%)	3 (7%)	1	6
45	SA	195/245 (80%)	183 (94%)	9 (5%)	3 (2%)	8	33
46	SB	214/242 (88%)	203 (95%)	6 (3%)	5 (2%)	5	24
47	SC	204/217 (94%)	191 (94%)	10 (5%)	3 (2%)	8	33
48	SD	227/248 (92%)	218 (96%)	8 (4%)	1 (0%)	30	60
49	SE	253/268 (94%)	233 (92%)	19 (8%)	1 (0%)	30	60
50	SF	175/190 (92%)	165 (94%)	8 (5%)	2 (1%)	12	39
51	SG	236/248 (95%)	221 (94%)	13 (6%)	2 (1%)	16	45
52	SH	173/190 (91%)	165 (95%)	6 (4%)	2 (1%)	11	37
53	SI	164/174 (94%)	153 (93%)	8 (5%)	3 (2%)	7	30
54	SJ	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	8	31
55	SK	174/189 (92%)	167 (96%)	4 (2%)	3 (2%)	7	30
56	SL	95/134 (71%)	90 (95%)	5 (5%)	0	100	100
57	SM	150/154 (97%)	133 (89%)	17 (11%)	0	100	100
58	SO	138/144 (96%)	133 (96%)	4 (3%)	1 (1%)	19	49
59	SP	148/154 (96%)	139 (94%)	8 (5%)	1 (1%)	19	49
60	SQ	124/145 (86%)	110 (89%)	11 (9%)	3 (2%)	5	23
61	SR	109/145 (75%)	102 (94%)	5 (5%)	2 (2%)	7	30
62	ST	149/158 (94%)	142 (95%)	6 (4%)	1 (1%)	19	49
63	SU	119/137 (87%)	111 (93%)	5 (4%)	3 (2%)	4	23
64	SV	125/154 (81%)	107 (86%)	16 (13%)	2 (2%)	8	31
65	SW	136/139 (98%)	127 (93%)	9 (7%)	0	100	100
66	SX	96/126 (76%)	95 (99%)	1 (1%)	0	100	100
67	SY	84/89 (94%)	77 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Sb	114/132 (86%)	103 (90%)	9 (8%)	2 (2%)	7	30
69	Sc	72/88 (82%)	69 (96%)	3 (4%)	0	100	100
70	Sd	95/109 (87%)	91 (96%)	3 (3%)	1 (1%)	12	39
71	Se	77/81 (95%)	74 (96%)	3 (4%)	0	100	100
72	Sg	60/64 (94%)	52 (87%)	7 (12%)	1 (2%)	7	30
73	Sh	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
74	Sj	65/69 (94%)	60 (92%)	4 (6%)	1 (2%)	8	33
All	All	10051/11193 (90%)	9452 (94%)	505 (5%)	94 (1%)	17	43

5 of 94 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	LA	15	VAL
2	LB	303	LYS
16	LP	181	LYS
29	Lc	50	ASP
34	Lh	6	VAL

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	188/192 (98%)	151 (80%)	37 (20%)	1	4
2	LB	312/313 (100%)	226 (72%)	86 (28%)	0	1
3	LC	257/263 (98%)	200 (78%)	57 (22%)	1	3
6	LF	238/242 (98%)	168 (71%)	70 (29%)	0	1
7	LG	47/48 (98%)	33 (70%)	14 (30%)	0	1
8	LH	183/204 (90%)	139 (76%)	44 (24%)	0	2
9	LI	164/198 (83%)	121 (74%)	43 (26%)	0	1
10	LJ	163/164 (99%)	118 (72%)	45 (28%)	0	1
11	LK	165/177 (93%)	122 (74%)	43 (26%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	LL	142/149 (95%)	100 (70%)	42 (30%)	0	1
13	LM	169/197 (86%)	129 (76%)	40 (24%)	0	2
14	LN	110/111 (99%)	82 (74%)	28 (26%)	0	1
15	LO	174/175 (99%)	132 (76%)	42 (24%)	0	2
16	LP	162/165 (98%)	128 (79%)	34 (21%)	1	3
17	LQ	132/139 (95%)	97 (74%)	35 (26%)	0	1
18	LR	154/155 (99%)	103 (67%)	51 (33%)	0	0
19	LS	139/167 (83%)	105 (76%)	34 (24%)	0	2
20	LT	151/154 (98%)	110 (73%)	41 (27%)	0	1
21	LU	130/133 (98%)	99 (76%)	31 (24%)	0	2
22	LV	91/110 (83%)	62 (68%)	29 (32%)	0	1
23	LW	108/114 (95%)	77 (71%)	31 (29%)	0	1
24	LX	61/174 (35%)	41 (67%)	20 (33%)	0	1
25	LY	104/123 (85%)	87 (84%)	17 (16%)	2	8
26	LZ	114/115 (99%)	84 (74%)	30 (26%)	0	1
27	La	111/119 (93%)	77 (69%)	34 (31%)	0	1
28	Lb	126/127 (99%)	102 (81%)	24 (19%)	1	5
29	Lc	50/57 (88%)	36 (72%)	14 (28%)	0	1
30	Ld	86/92 (94%)	64 (74%)	22 (26%)	0	1
31	Le	88/92 (96%)	76 (86%)	12 (14%)	3	13
32	Lf	116/120 (97%)	79 (68%)	37 (32%)	0	1
33	Lg	82/103 (80%)	67 (82%)	15 (18%)	1	5
34	Lh	89/100 (89%)	69 (78%)	20 (22%)	1	3
35	Li	105/107 (98%)	85 (81%)	20 (19%)	1	5
36	Lj	77/78 (99%)	50 (65%)	27 (35%)	0	0
37	Lk	73/74 (99%)	56 (77%)	17 (23%)	0	2
38	Ll	63/68 (93%)	37 (59%)	26 (41%)	0	0
39	Ln	173/189 (92%)	89 (51%)	84 (49%)	0	0
40	Lo	22/22 (100%)	15 (68%)	7 (32%)	0	1
41	Lp	83/93 (89%)	61 (74%)	22 (26%)	0	1
42	Lq	71/73 (97%)	37 (52%)	34 (48%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
43	Ls	43/110 (39%)	29 (67%)	14 (33%)	0	1	
45	SA	172/217 (79%)	126 (73%)	46 (27%)	0	1	
46	SB	179/201 (89%)	115 (64%)	64 (36%)	0	0	
47	SC	172/182 (94%)	102 (59%)	70 (41%)	0	0	
48	SD	207/220 (94%)	120 (58%)	87 (42%)	0	0	
49	SE	225/232 (97%)	126 (56%)	99 (44%)	0	0	
50	SF	150/157 (96%)	100 (67%)	50 (33%)	0	0	
51	SG	204/213 (96%)	117 (57%)	87 (43%)	0	0	
52	SH	160/170 (94%)	96 (60%)	64 (40%)	0	0	
53	SI	142/148 (96%)	89 (63%)	53 (37%)	0	0	
54	SJ	114/115 (99%)	76 (67%)	38 (33%)	0	0	
55	SK	155/164 (94%)	95 (61%)	60 (39%)	0	0	
56	SL	86/119 (72%)	54 (63%)	32 (37%)	0	0	
57	SM	135/136 (99%)	90 (67%)	45 (33%)	0	0	
58	SO	111/114 (97%)	68 (61%)	43 (39%)	0	0	
59	SP	124/129 (96%)	86 (69%)	38 (31%)	0	1	
60	SQ	86/112 (77%)	58 (67%)	28 (33%)	0	1	
61	SR	102/128 (80%)	66 (65%)	36 (35%)	0	0	
62	ST	125/130 (96%)	70 (56%)	55 (44%)	0	0	
63	SU	109/124 (88%)	68 (62%)	41 (38%)	0	0	
64	SV	109/131 (83%)	69 (63%)	40 (37%)	0	0	
65	SW	114/115 (99%)	73 (64%)	41 (36%)	0	0	
66	SX	87/110 (79%)	55 (63%)	32 (37%)	0	0	
67	SY	69/72 (96%)	41 (59%)	28 (41%)	0	0	
68	Sb	101/113 (89%)	61 (60%)	40 (40%)	0	0	
69	Sc	66/79 (84%)	35 (53%)	31 (47%)	0	0	
70	Sd	91/103 (88%)	60 (66%)	31 (34%)	0	0	
71	Se	71/73 (97%)	43 (61%)	28 (39%)	0	0	
72	Sg	55/57 (96%)	27 (49%)	28 (51%)	0	0	
73	Sh	43/45 (96%)	21 (49%)	22 (51%)	0	0	
74	Sj	57/58 (98%)	34 (60%)	23 (40%)	0	0	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	8737/9573 (91%)	5984 (68%)	2753 (32%)	1 1

5 of 2753 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	SG	170	ILE
61	SR	51	SER
52	SH	94	ILE
51	SG	168	GLU
55	SK	146	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
51	SG	10	ASN
61	SR	128	HIS
51	SG	65	GLN
53	SI	134	GLN
64	SV	89	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	LD	141/142 (99%)	48 (34%)	4 (2%)
44	Lt	2588/2697 (95%)	980 (37%)	0
5	LE	116/121 (95%)	37 (31%)	4 (3%)
75	St	1453/1454 (99%)	711 (48%)	0
76	u	74/75 (98%)	35 (47%)	0
77	v	74/75 (98%)	46 (62%)	0
78	y	10/11 (90%)	7 (70%)	0
All	All	4456/4575 (97%)	1864 (41%)	8 (0%)

5 of 1864 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	LD	6	C
4	LD	9	C
4	LD	10	G
4	LD	14	G
4	LD	20	G

5 of 8 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	LE	114	G
5	LE	110	U
5	LE	63	U
4	LD	88	G
5	LE	85	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.

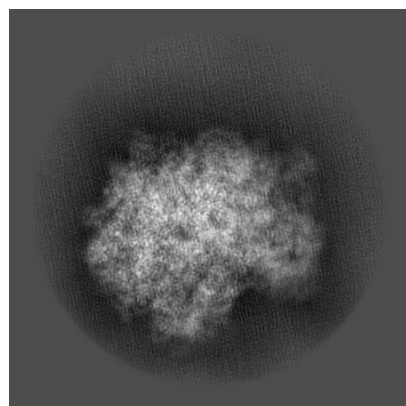
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16235. These allow visual inspection of the internal detail of the map and identification of artifacts.

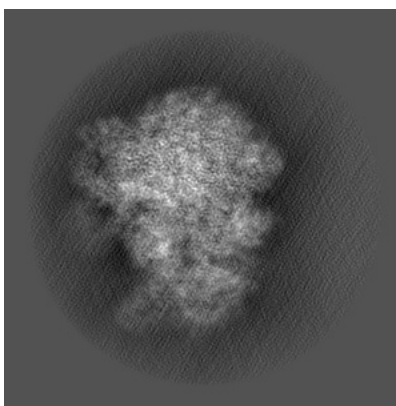
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

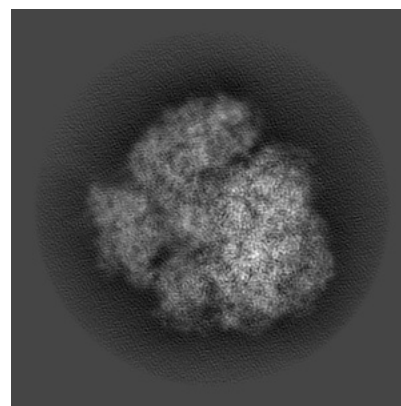
6.1.1 Primary map



X

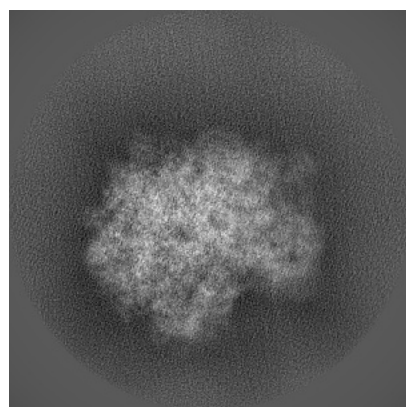


Y

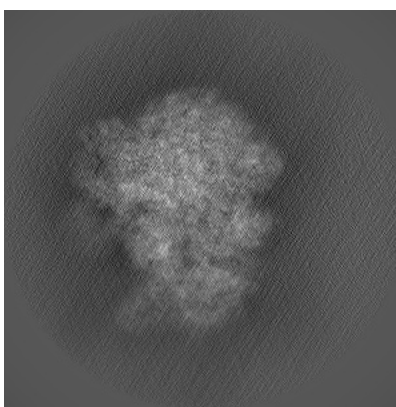


Z

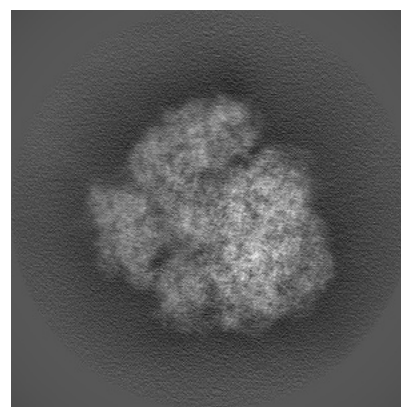
6.1.2 Raw map



X



Y

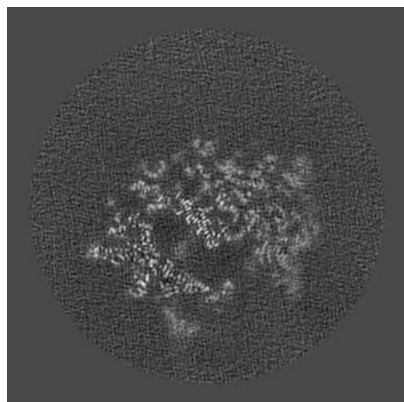


Z

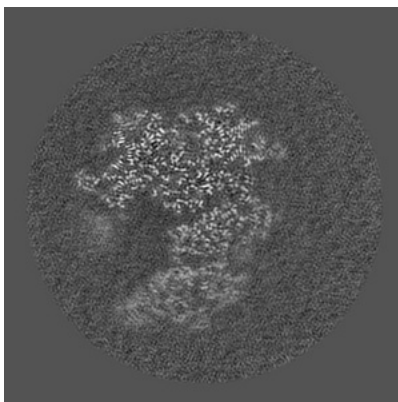
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

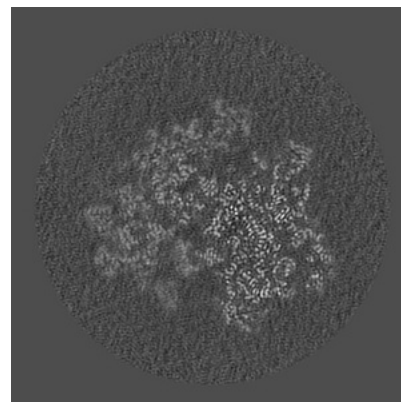
6.2.1 Primary map



X Index: 250

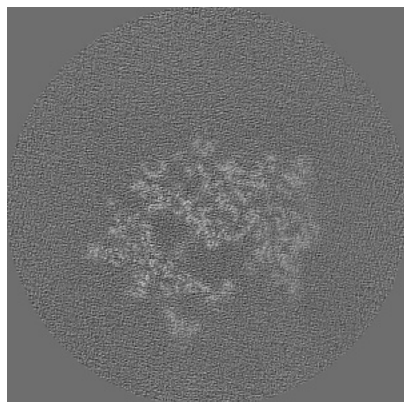


Y Index: 250

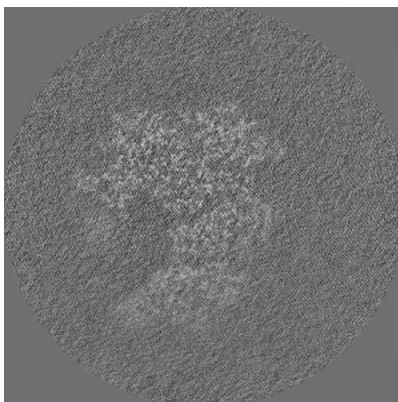


Z Index: 250

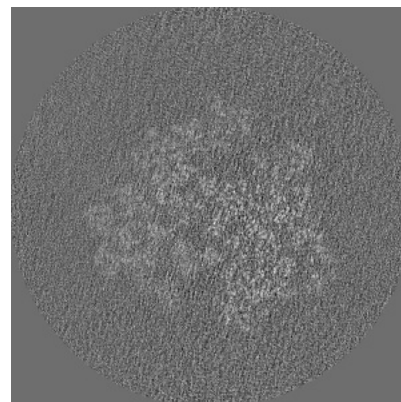
6.2.2 Raw map



X Index: 250



Y Index: 250

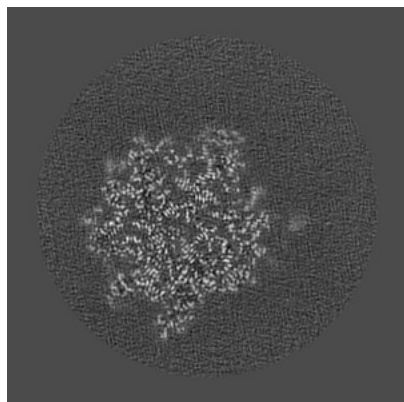


Z Index: 250

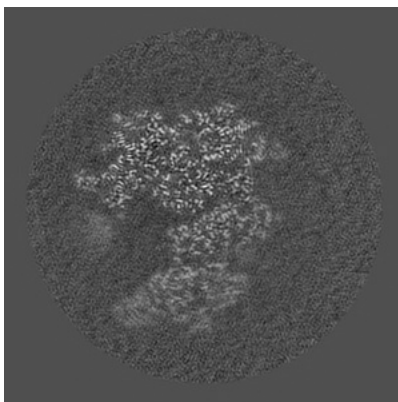
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

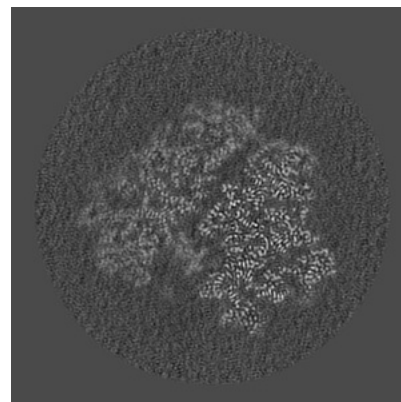
6.3.1 Primary map



X Index: 314

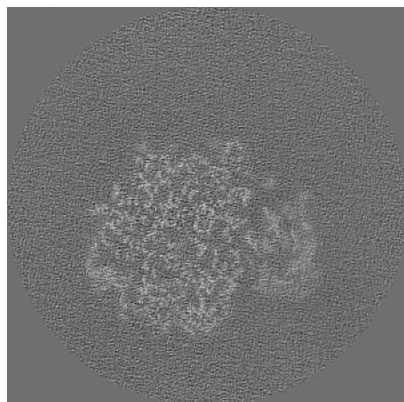


Y Index: 249

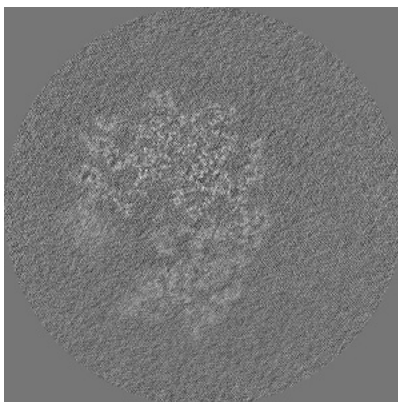


Z Index: 240

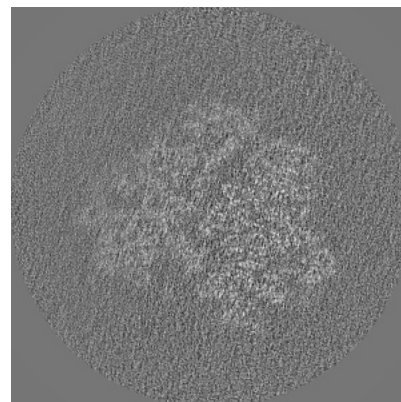
6.3.2 Raw map



X Index: 280



Y Index: 230

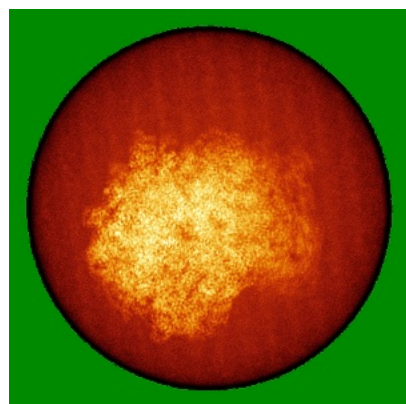


Z Index: 240

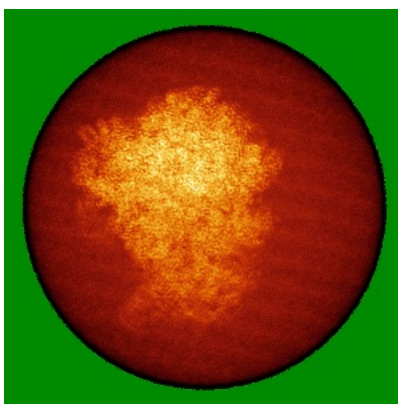
The images above show the largest variance slices of the map in three orthogonal directions.

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

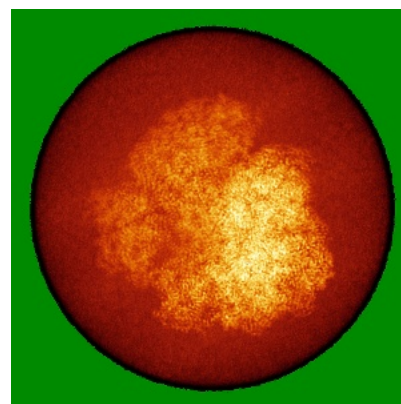
6.4.1 Primary map



X

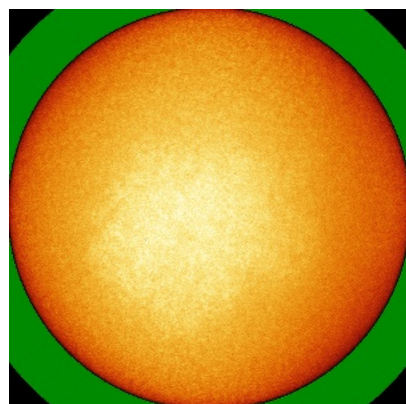


Y

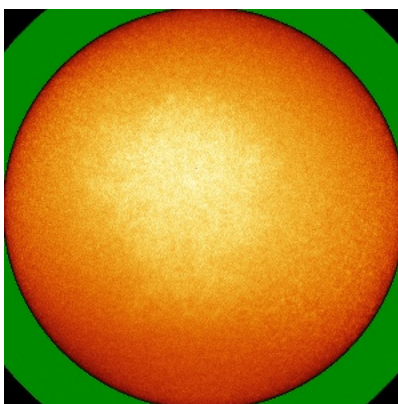


Z

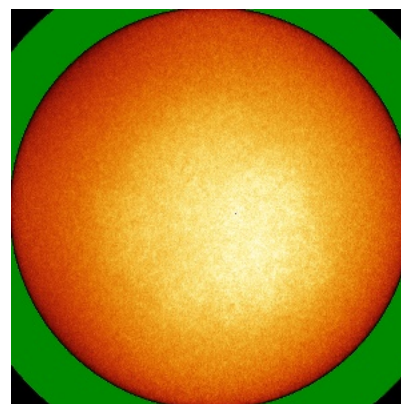
6.4.2 Raw map



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.

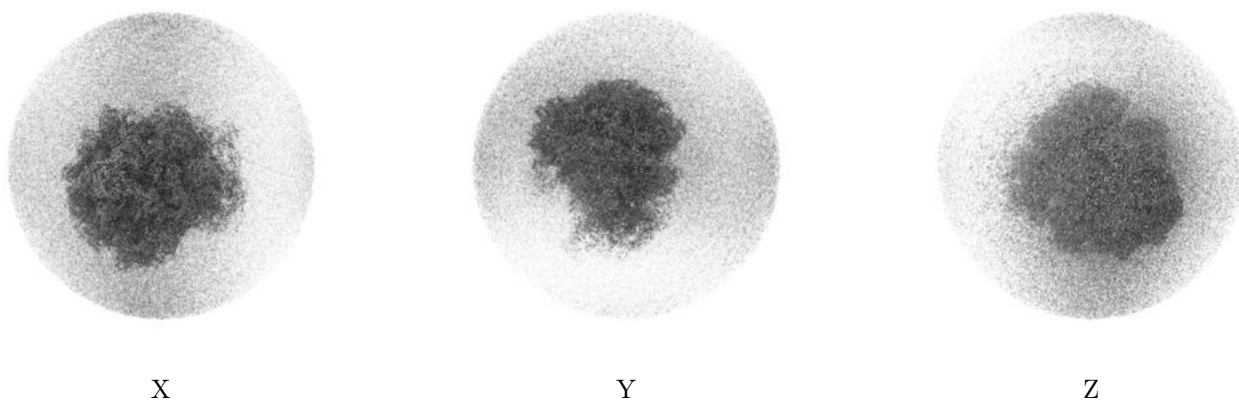
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.87. 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.

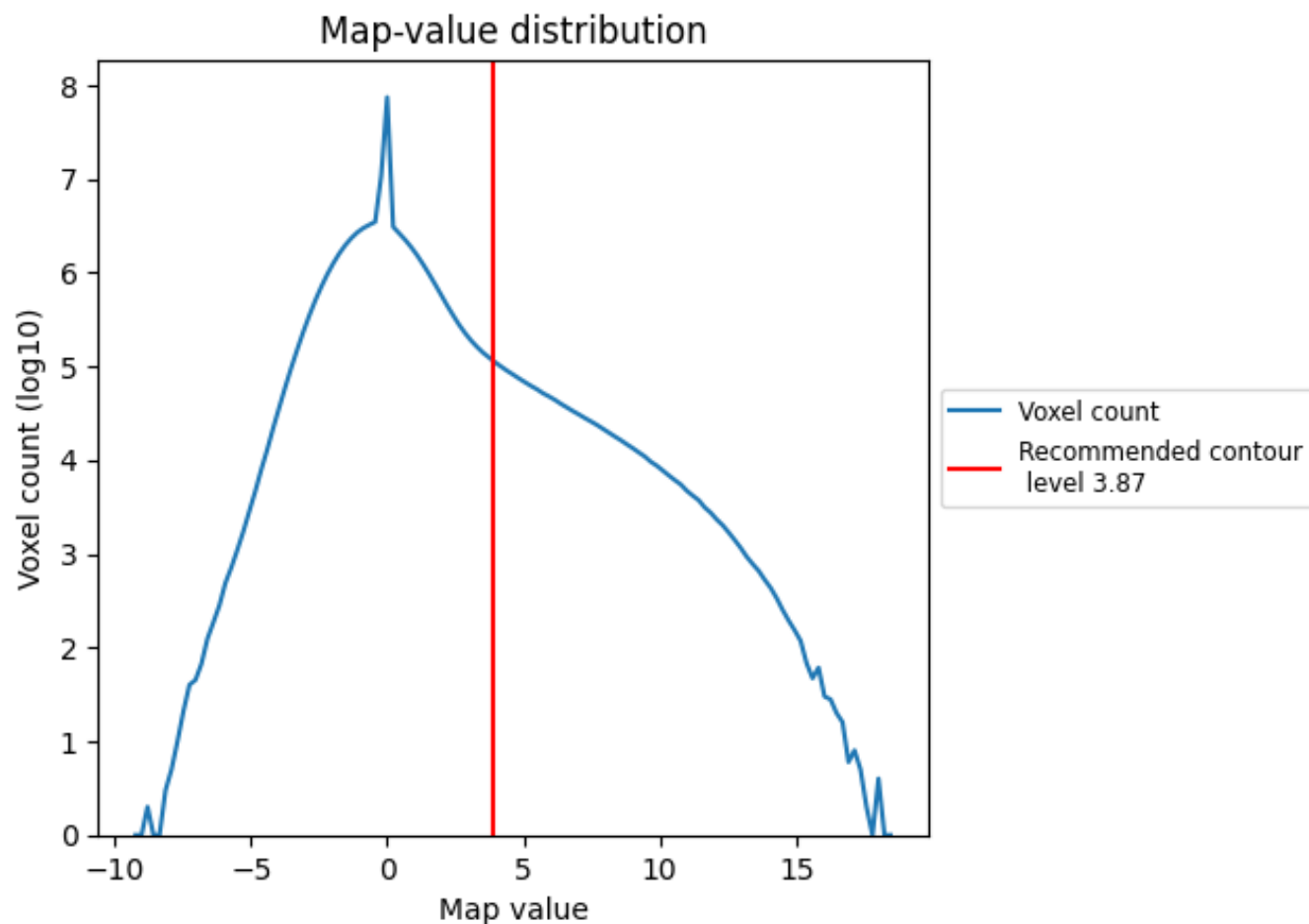
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

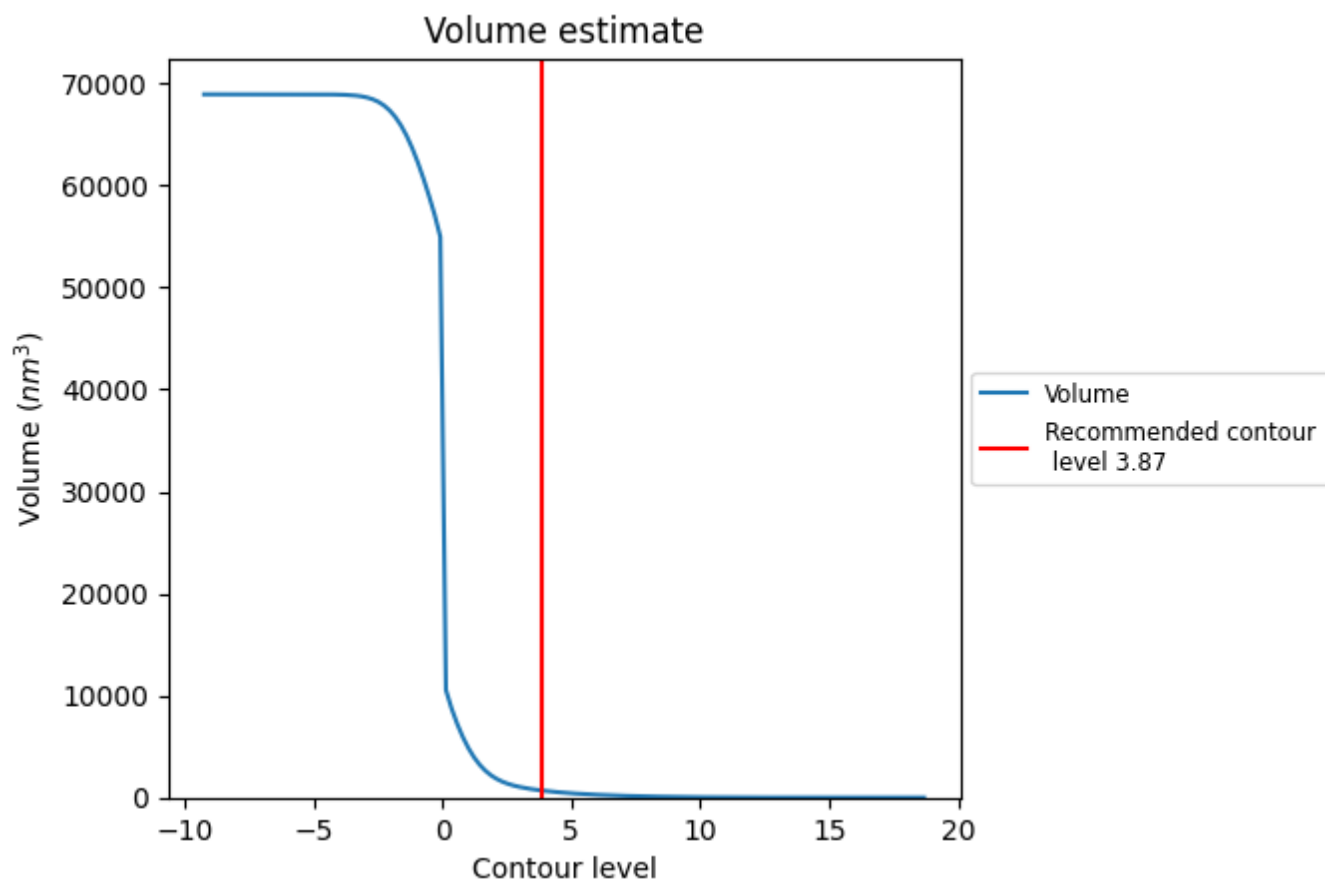
This section contains the results of statistical analysis of the map.

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.

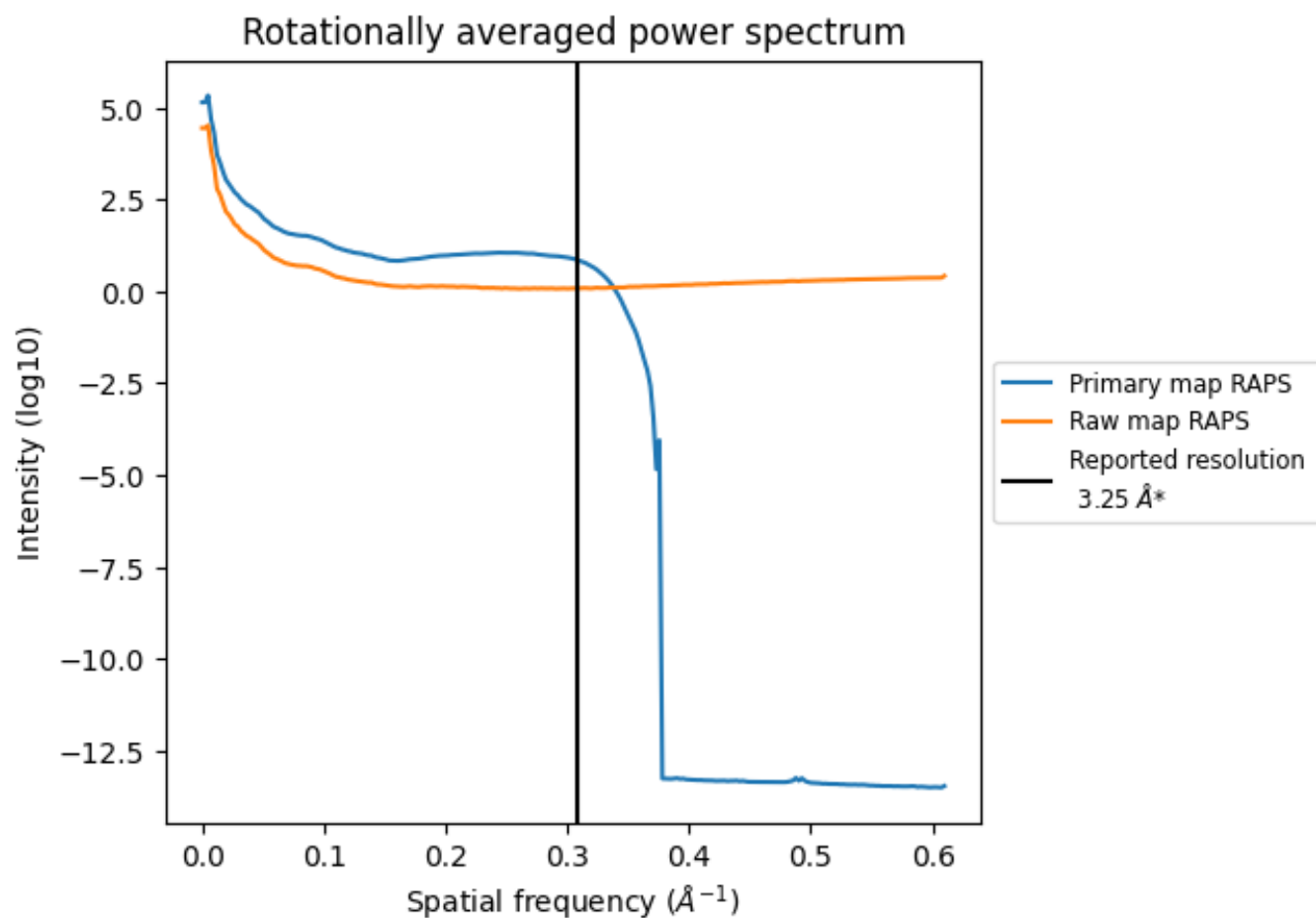
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 689 nm³; this corresponds to an approximate mass of 622 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 ⓘ

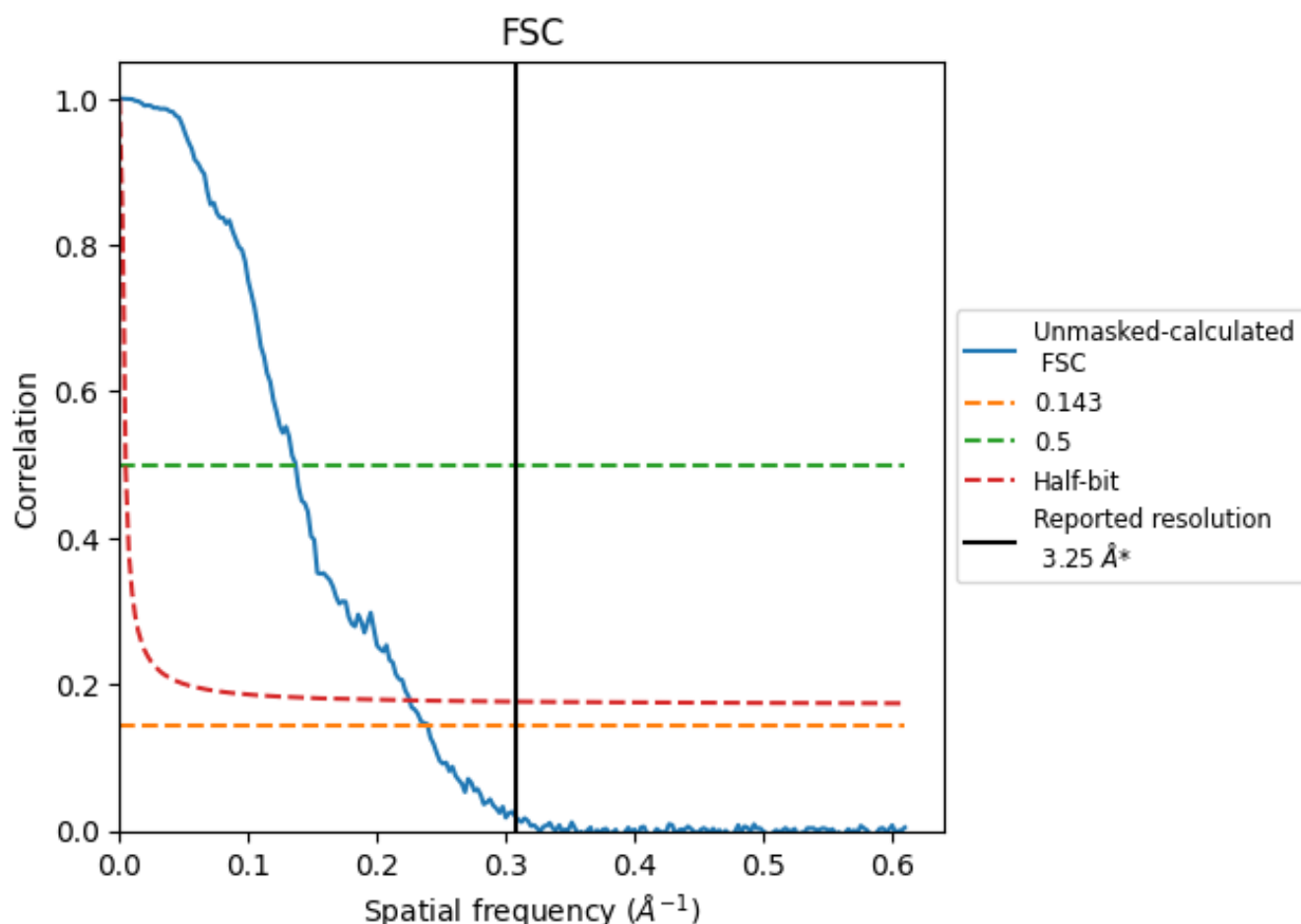


*Reported resolution corresponds to spatial frequency of 0.308 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.308 Å⁻¹

8.2 Resolution estimates [i](#)

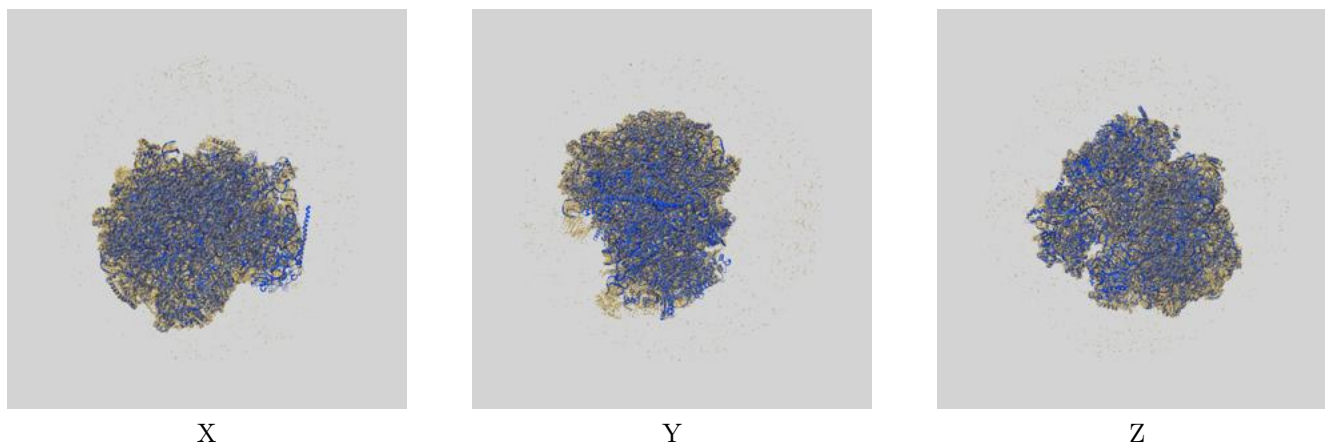
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.25	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.18	7.32	4.44

*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 4.18 differs from the reported value 3.25 by more than 10 %

9 Map-model fit [i](#)

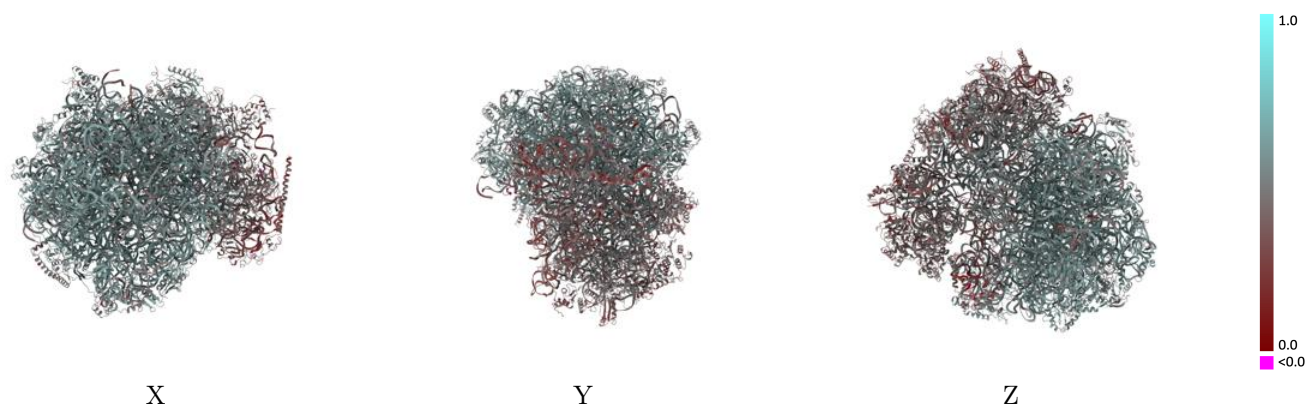
This section contains information regarding the fit between EMDB map EMD-16235 and PDB model 8BTR. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



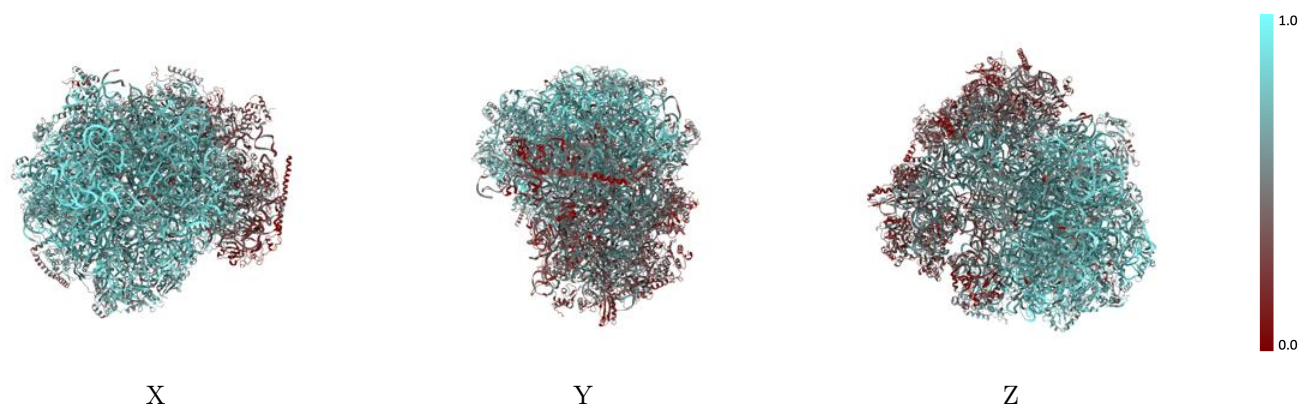
The images above show the 3D surface view of the map at the recommended contour level 3.87 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



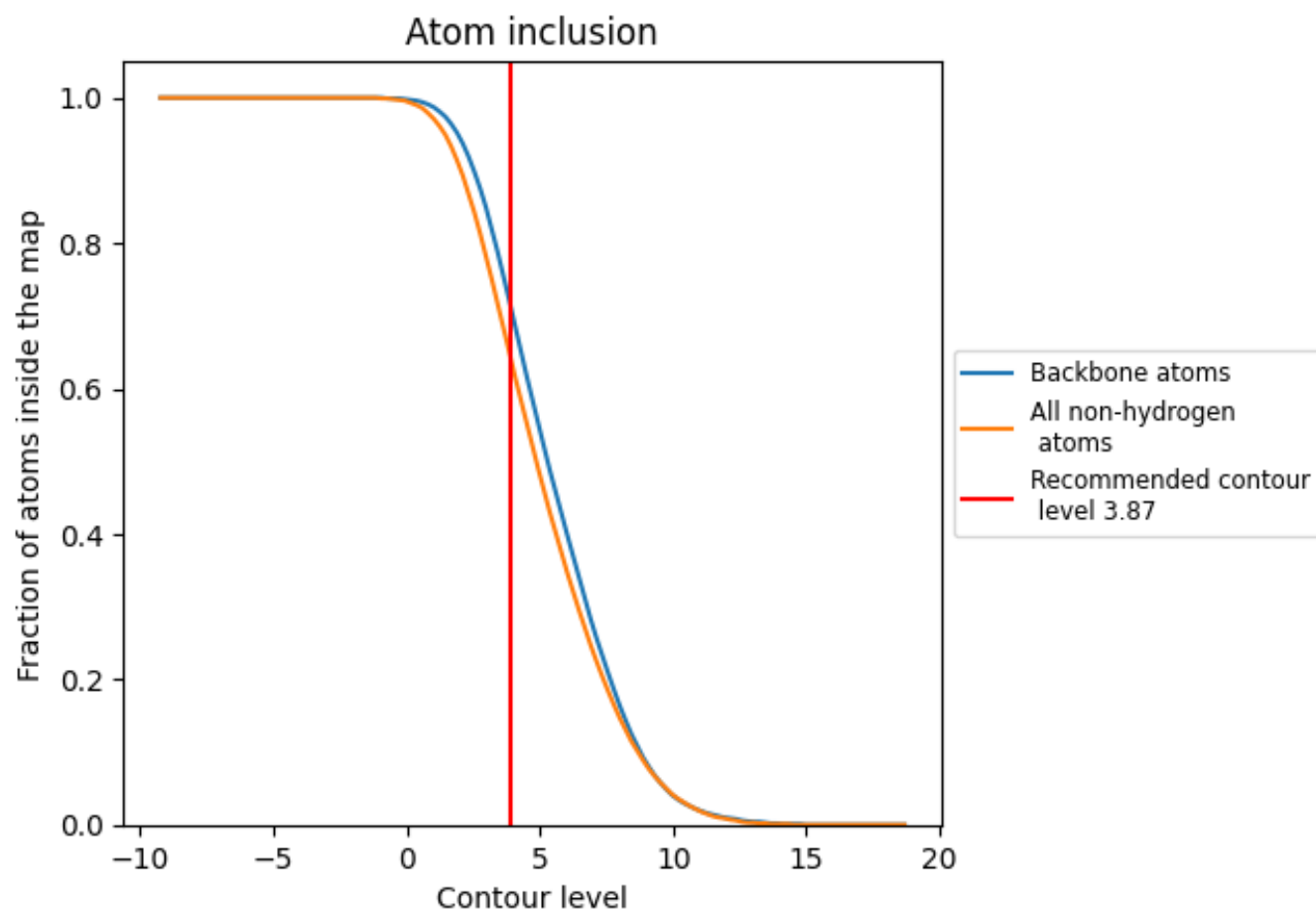
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.87).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 65% 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 (3.87) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6470	 0.4990
LA	 0.7210	 0.5800
LB	 0.7110	 0.5580
LC	 0.7320	 0.5590
LD	 0.8410	 0.5500
LE	 0.8710	 0.5560
LF	 0.6150	 0.5260
LG	 0.7380	 0.5760
LH	 0.6450	 0.5370
LI	 0.6250	 0.5280
LJ	 0.6470	 0.5410
LK	 0.6300	 0.5410
LL	 0.6040	 0.5250
LM	 0.7040	 0.5480
LN	 0.6520	 0.5300
LO	 0.7830	 0.5850
LP	 0.6840	 0.5450
LQ	 0.6990	 0.5530
LR	 0.7020	 0.5650
LS	 0.6540	 0.5420
LT	 0.6900	 0.5500
LU	 0.6980	 0.5570
LV	 0.5390	 0.4780
LW	 0.6490	 0.5340
LX	 0.6340	 0.5130
LY	 0.7040	 0.5560
LZ	 0.7270	 0.5530
La	 0.5110	 0.4950
Lb	 0.7760	 0.5760
Lc	 0.7010	 0.5570
Ld	 0.5950	 0.5160
Le	 0.6960	 0.5590
Lf	 0.6960	 0.5550
Lg	 0.7320	 0.5740
Lh	 0.6880	 0.5700







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Chain	Atom inclusion	Q-score
Li	 0.6330	 0.5390
Lj	 0.5930	 0.5140
Lk	 0.7440	 0.5710
Ll	 0.5080	 0.4610
Ln	 0.0950	 0.3020
Lo	 0.5280	 0.5350
Lp	 0.7320	 0.5800
Lq	 0.6890	 0.5510
Ls	 0.7220	 0.5310
Lt	 0.8420	 0.5540
SA	 0.3440	 0.4060
SB	 0.4270	 0.4500
SC	 0.3470	 0.4080
SD	 0.4680	 0.4620
SE	 0.2440	 0.3790
SF	 0.3320	 0.4280
SG	 0.1510	 0.3560
SH	 0.2690	 0.4050
SI	 0.3240	 0.4270
SJ	 0.4460	 0.4630
SK	 0.2910	 0.3820
SL	 0.2540	 0.3360
SM	 0.3240	 0.4390
SO	 0.4120	 0.4790
SP	 0.4130	 0.4530
SQ	 0.5220	 0.4920
SR	 0.3260	 0.4150
ST	 0.2850	 0.3990
SU	 0.1820	 0.3570
SV	 0.3930	 0.4230
SW	 0.3380	 0.4010
SX	 0.2380	 0.3790
SY	 0.3160	 0.4230
Sb	 0.2210	 0.3650
Sc	 0.2910	 0.3920
Sd	 0.5340	 0.4990
Se	 0.2870	 0.4310
Sg	 0.2760	 0.4070
Sh	 0.4190	 0.4250
Sj	 0.2700	 0.4140
St	 0.6090	 0.4320
u	 0.5660	 0.4250

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Chain	Atom inclusion	Q-score
v	 0.2280	 0.3370
y	 0.4940	 0.4370