



## wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 08:19 pm BST

PDB ID : 9T5C / pdb\_00009t5c  
EMDB ID : EMD-55100  
Title : Naked mole-rat 80S ribosome in post-translocation non-rotated state  
Authors : Gul, M.; Kudryashev, M.  
Deposited on : 2025-11-05  
Resolution : 2.89 Å (reported)  
Based on initial model : 7CPU

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:

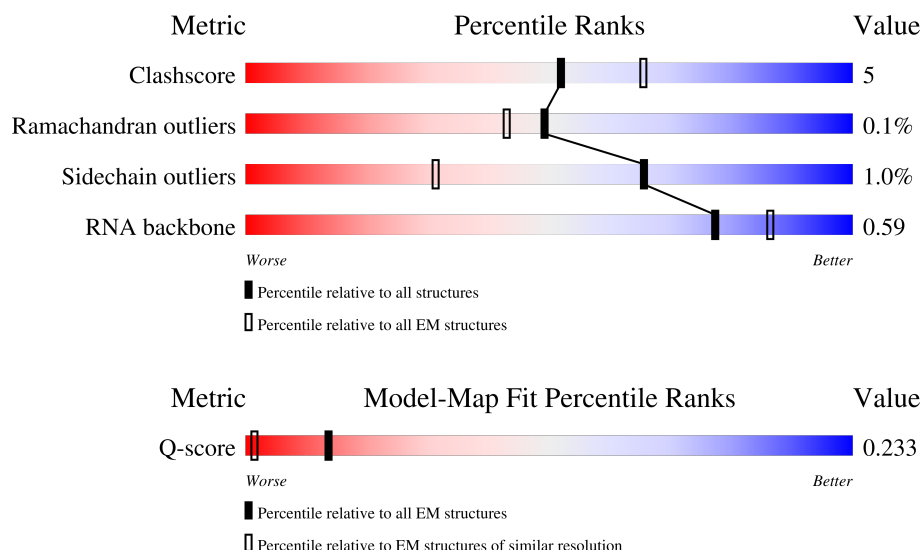
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 2.89 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12148 ( 2.39 - 3.39 )

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	B	10	
2	L5	4731	
3	L7	120	

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Mol	Chain	Length	Quality of chain
4	L8	158	
5	LA	257	
6	LC	419	
7	LD	297	
8	LE	296	
9	LF	270	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	217	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	160	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1870	
47	S6	75	
48	S7	75	
49	SA	295	
50	SB	264	
51	SC	293	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SG	249	
56	SH	194	
57	SI	208	
58	SJ	194	
59	SK	165	
60	SL	158	
61	SN	151	
62	SO	151	
63	SP	145	
64	SQ	146	
65	SR	135	
66	SS	152	
67	ST	145	
68	SU	119	
69	SV	83	
70	SW	130	
71	SX	143	
72	SY	133	
73	SZ	125	
74	Sa	115	
75	Sb	84	
76	Sc	69	
77	Sd	56	
78	Se	133	

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Mol	Chain	Length	Quality of chain
79	Sg	317	<div><div></div><div>50%</div><div>66%</div><div>26%</div><div>8%</div></div>
80	LB	403	<div><div></div><div>80%</div><div>18%</div></div>

## 2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 206721 atoms, of which 38 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	10	Total	C	N	O	P	0	0
			208	94	32	72	10		

- Molecule 2 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	L5	3455	Total	C	H	N	O	P	0	0
			74122	32996	35	13550	24087	3454		

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

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

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

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 6 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	358	Total	C	N	O	S	0	0
			2862	1800	572	475	15		

- Molecule 7 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2389	1509	441	425	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	216	Total	C	N	O	S	0	0
			1743	1115	332	292	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	224	Total	C	N	O	S	0	0
			1813	1156	349	304	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	201	Total	C	N	O	S	0	0
			1633	1037	316	268	12		

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	168	Total	C	N	O	S	0	0
			1349	853	251	239	6		

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	205	Total	C	N	O	S	0	0
			1660	1038	342	276	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL14.

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

- Molecule 16 is a protein called Ribosomal protein L15.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	152	Total	C	N	O	S	0	0
			1231	770	238	214	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LP	40	ASP	HIS	conflict	UNP A0A0P6JH89

- Molecule 19 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 20 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	178	Total	C	N	O	S	0	0
			1490	921	324	236	9		

- Molecule 21 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 23 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 24 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 25 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	131	Total	C	N	O	S	0	0
			1093	686	221	183	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	97	Total	C	N	O	S	0	0
			794	497	171	122	4		

- Molecule 31 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	111	Total	C	N	O	S	0	0
			878	549	181	142	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	121	Total	C	N	O	S	0	0
			1009	640	203	165	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called Ribosomal protein L37.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 45 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	123	Total	C	N	O	S	0	0
			987	611	205	166	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
46	S2	1656	Total	C	H	N	O	P	0	0
			35239	15727	3	6309	11545	1655		

- Molecule 47 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S6	75	Total	C	N	O	P	0	0
			1596	714	291	517	74		

- Molecule 48 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S7	74	Total	C	N	O	P	0	0
			1570	702	280	515	73		

- Molecule 49 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 50 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 51 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SC	220	Total	C	N	O	S	0	0
			1690	1095	290	296	9		

- Molecule 52 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SD	222	Total	C	N	O	S	0	0
			1726	1100	310	309	7		

- Molecule 53 is a protein called Small ribosomal subunit protein eS4.

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

- Molecule 54 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG	220	Total	C	N	O	S	0	0
			1725	1077	346	296	6		

- Molecule 56 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SH	183	Total	C	N	O	S	0	0
			1457	929	267	260	1		

- Molecule 57 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SI	202	Total	C	N	O	S	0	0
			1593	999	312	277	5		

- Molecule 58 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SJ	155	Total	C	N	O	S	0	0
			1258	806	246	204	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SJ	115	LEU	PHE	conflict	UNP G5CBG2

- Molecule 59 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SK	96	Total	C	N	O	S	0	0
			789	513	141	129	6		

- Molecule 60 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SL	134	Total	C	N	O	S	0	0
			1105	705	206	188	6		

- Molecule 61 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 62 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SP	124	Total	C	N	O	S	0	0
			997	632	186	172	7		

- Molecule 64 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 65 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 67 is a protein called Small ribosomal subunit protein eS19.

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

- Molecule 68 is a protein called Small ribosomal subunit protein uS10.



Mol	Chain	Residues	Atoms					AltConf	Trace
68	SU	98	Total	C	N	O	S	0	0
			776	488	145	138	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SU	18	CYS	HIS	conflict	UNP G5B335
SU	19	LEU	ARG	conflict	UNP G5B335
SU	23	ILE	THR	conflict	UNP G5B335

- Molecule 69 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SV	83	Total	C	N	O	S	0	0
			639	393	118	123	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SV	79	ILE	VAL	conflict	UNP Q9CQR2
SV	82	ASP	ASN	conflict	UNP Q9CQR2

- Molecule 70 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SX	139	Total	C	N	O	S	0	0
			1081	682	215	181	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SX	23	ARG	HIS	conflict	UNP A0A0P6J0V6

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SY	119	Total	C	N	O	S	0	0
			979	623	190	161	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SY	10	GLN	ARG	conflict	UNP A0AAX6PA11
SY	15	LYS	ASN	conflict	UNP A0AAX6PA11

- Molecule 73 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	99	Total	C	N	O	S	0	0
			793	492	165	131	5		

- Molecule 75 is a protein called 40S ribosomal protein S27.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	62	Total	C	N	O	S	0	0
			454	279	88	85	2		

- Molecule 77 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 78 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	49	Total	C	N	O	S	0	0
			384	234	87	62	1		

- Molecule 79 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sg	291	Total	C	N	O	S	0	0
			2271	1437	396	426	12		

- Molecule 80 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	B	1	Total	Mg	0
			1	1	
81	L5	226	Total	Mg	0
			226	226	
81	L7	4	Total	Mg	0
			4	4	
81	L8	3	Total	Mg	0
			3	3	
81	LI	1	Total	Mg	0
			1	1	
81	LN	1	Total	Mg	0
			1	1	
81	LP	1	Total	Mg	0
			1	1	
81	Le	2	Total	Mg	0
			2	2	
81	Lg	1	Total	Mg	0
			1	1	
81	S2	86	Total	Mg	0
			86	86	
81	SO	1	Total	Mg	0
			1	1	
81	LB	1	Total	Mg	0
			1	1	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	Lg	1	Total 1	Zn 1	0
82	Lp	1	Total 1	Zn 1	0
82	Sa	1	Total 1	Zn 1	0

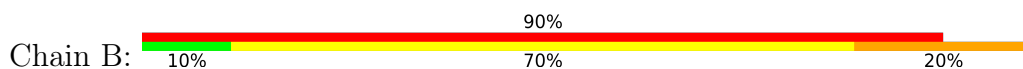
- Molecule 83 is water.

Mol	Chain	Residues	Atoms		AltConf
83	L5	3	Total 3	O 3	0
83	La	1	Total 1	O 1	0
83	S2	2	Total 2	O 2	0

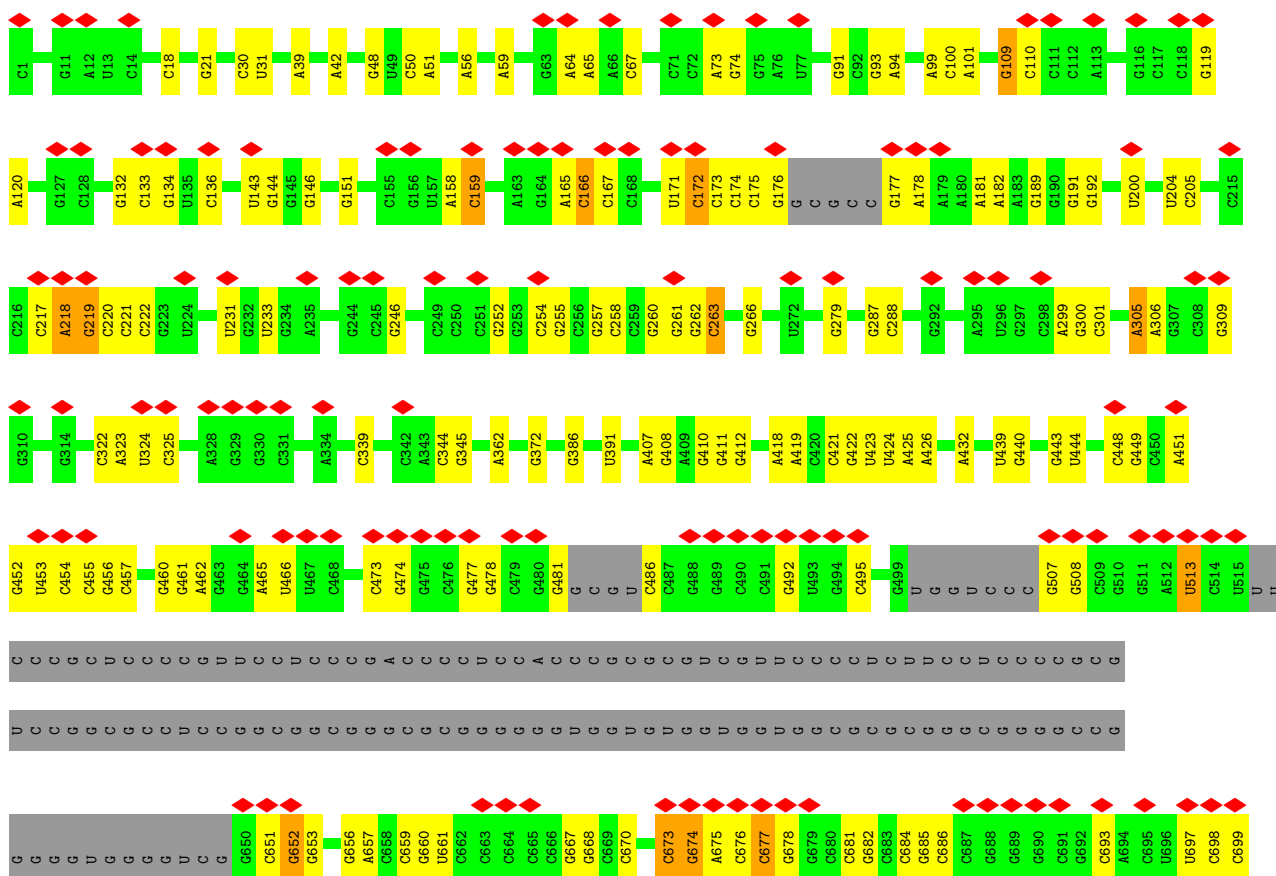
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

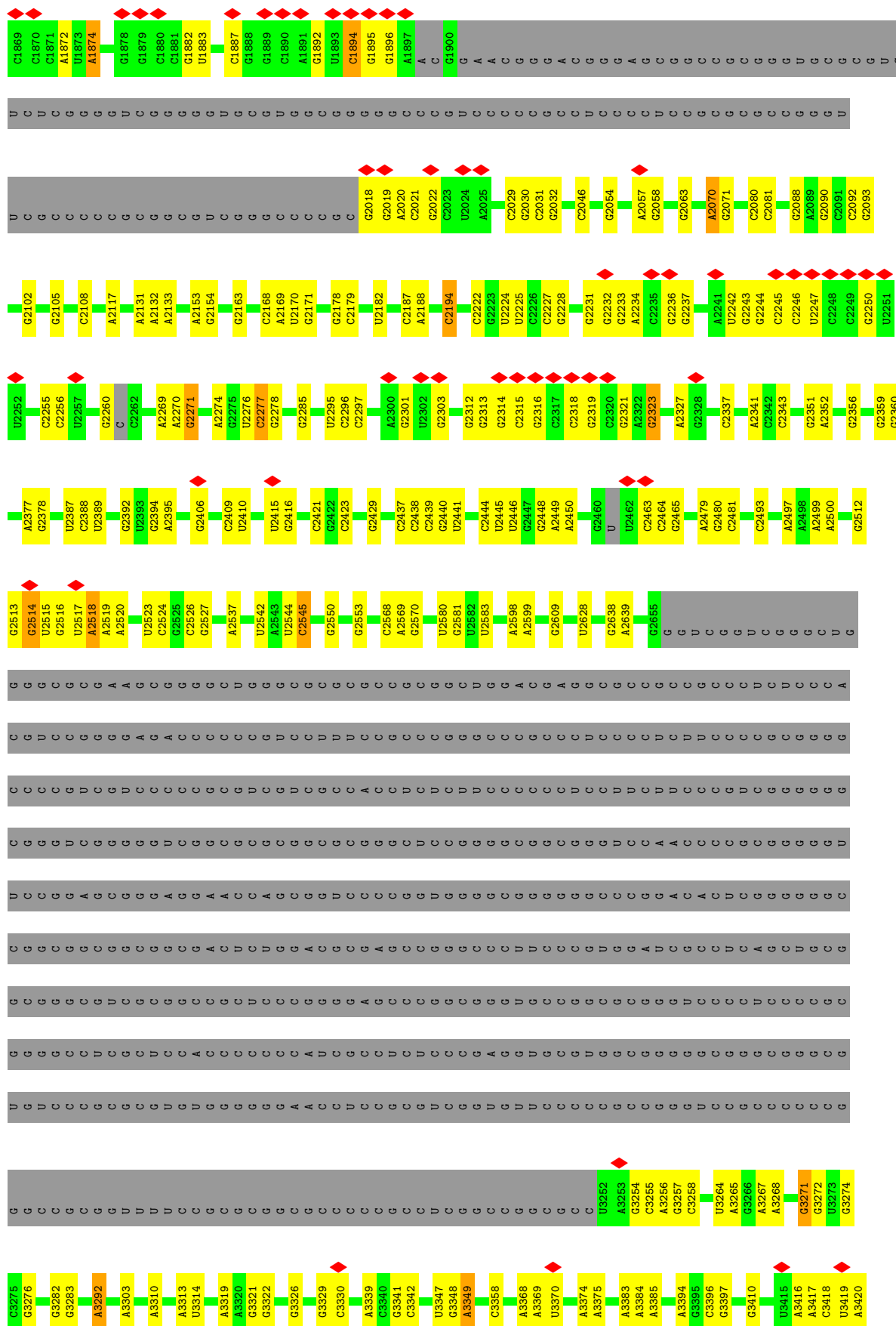
#### • Molecule 1: mRNA



#### • Molecule 2: 28S ribosomal RNA

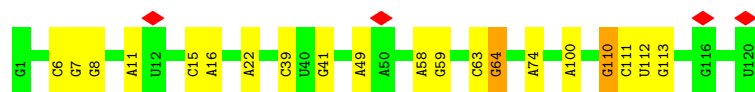




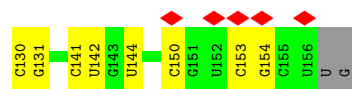
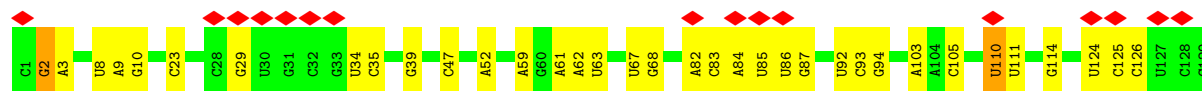
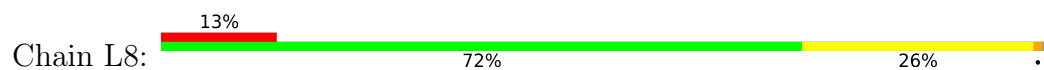


15%

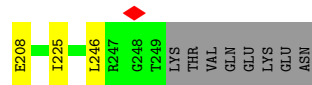
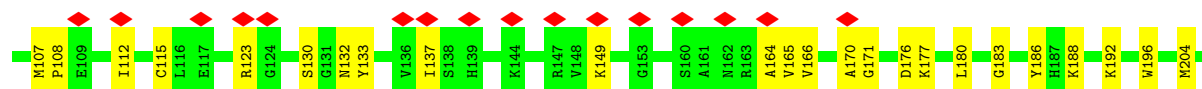
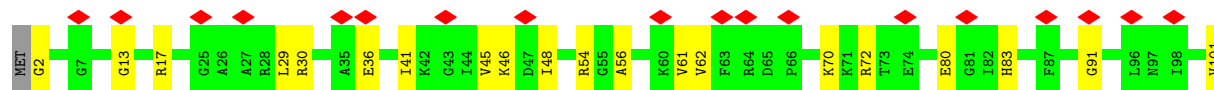
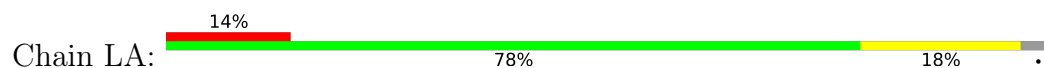




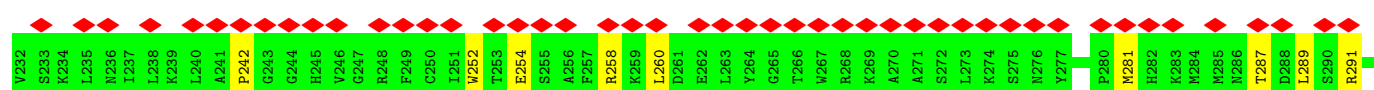
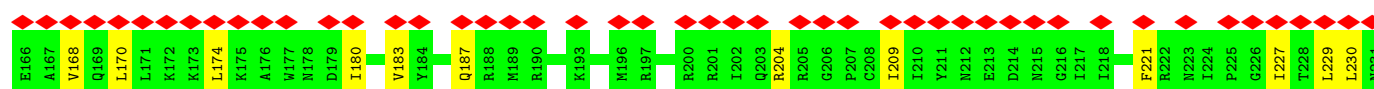
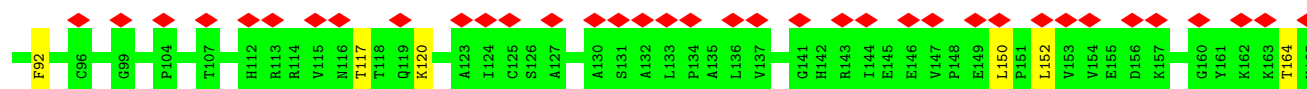
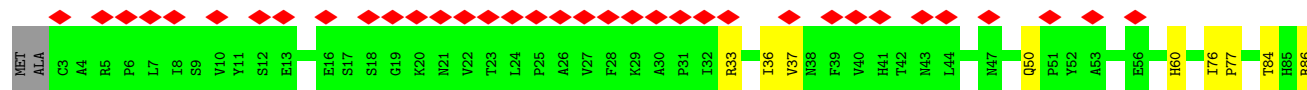
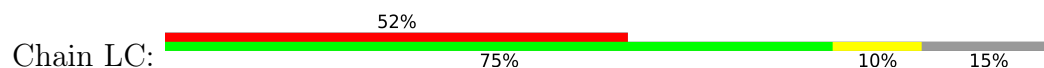
• Molecule 4: 5.8S ribosomal RNA

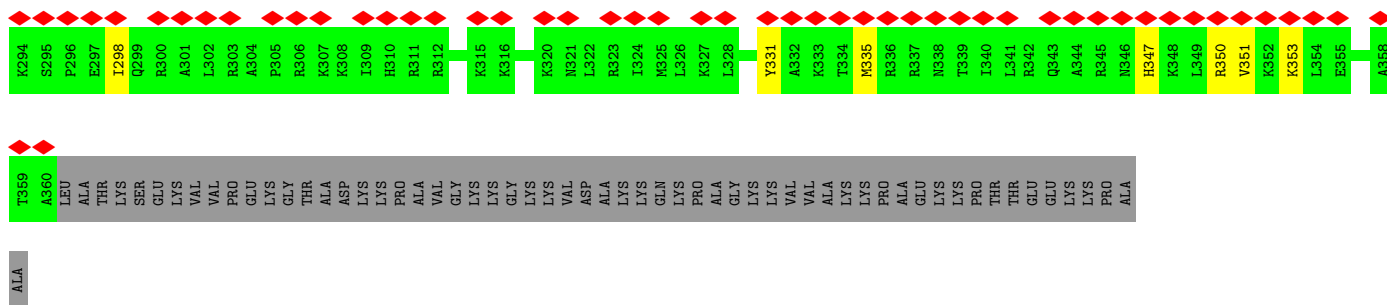


• Molecule 5: Large ribosomal subunit protein uL2

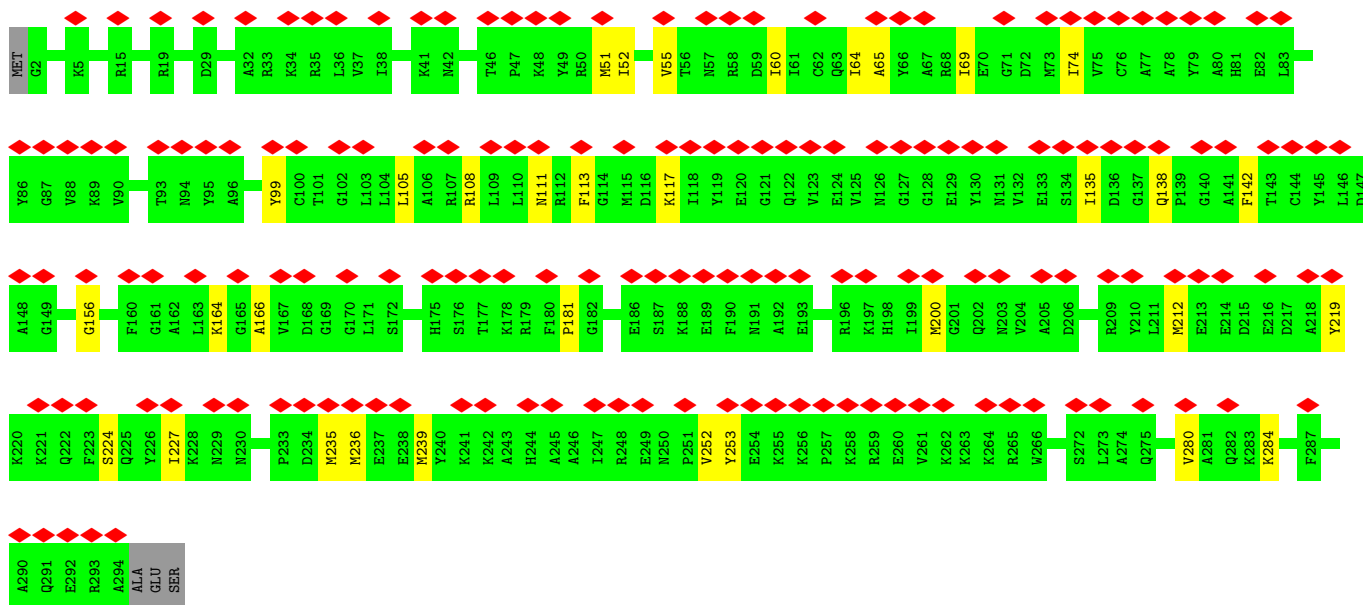
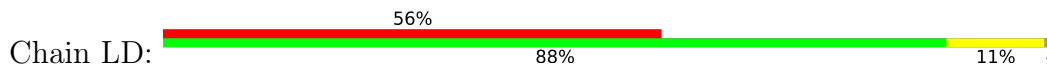


• Molecule 6: Large ribosomal subunit protein uL4

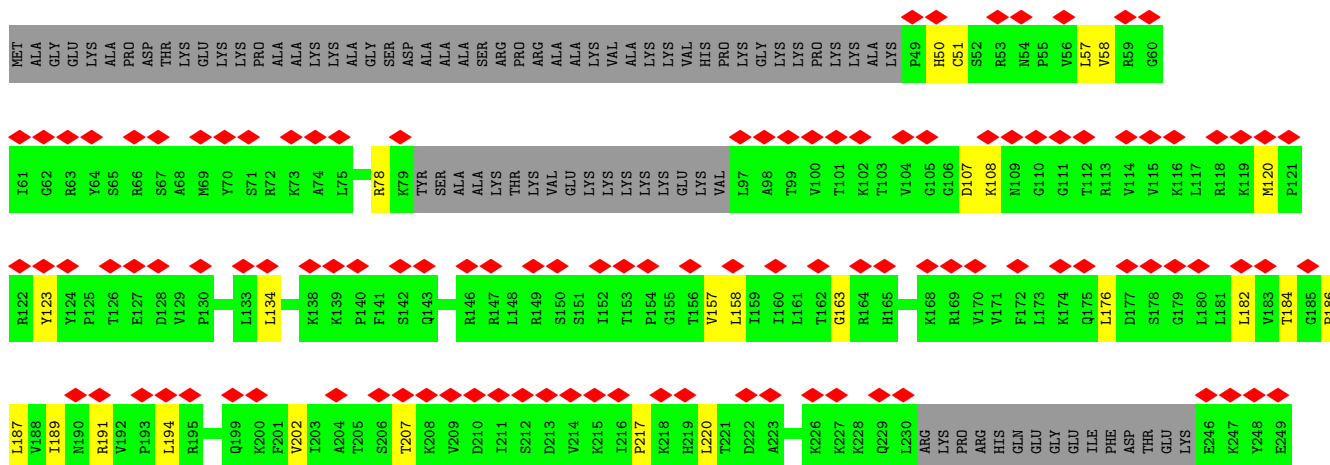




• Molecule 7: Large ribosomal subunit protein uL18

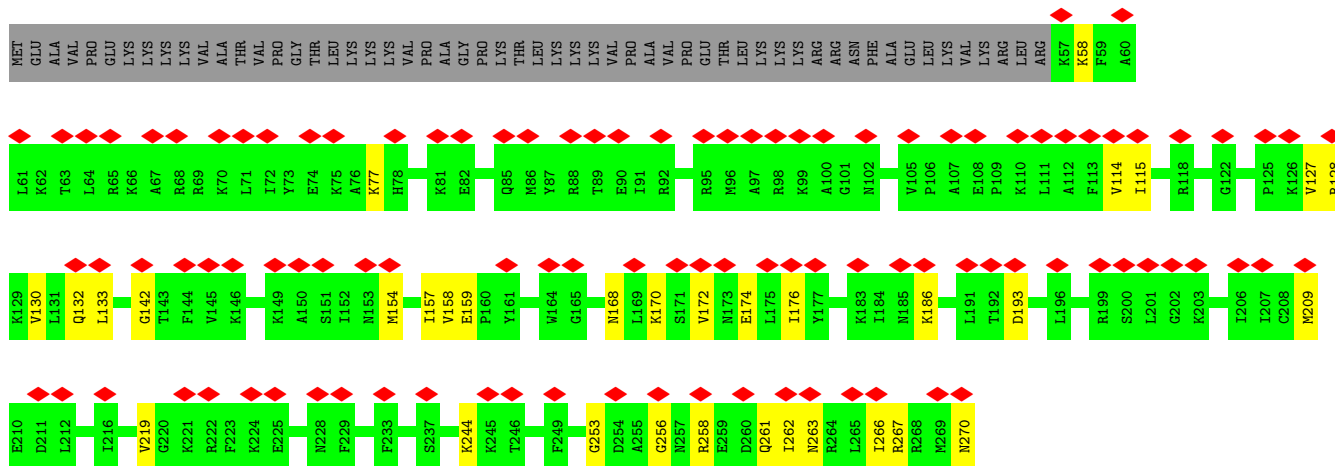
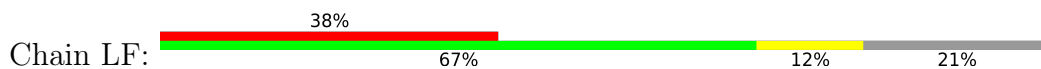


• Molecule 8: Large ribosomal subunit protein eL6

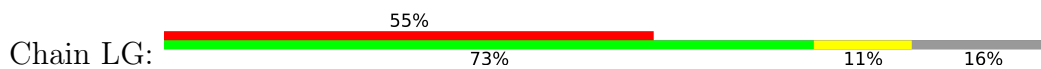




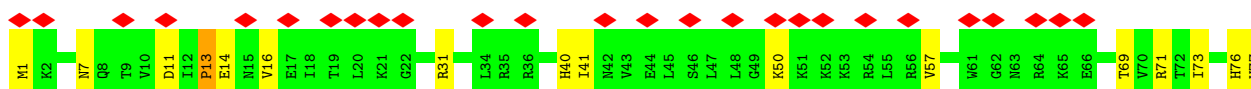
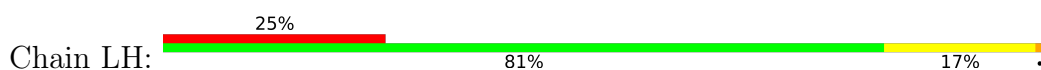
• Molecule 9: Large ribosomal subunit protein uL30

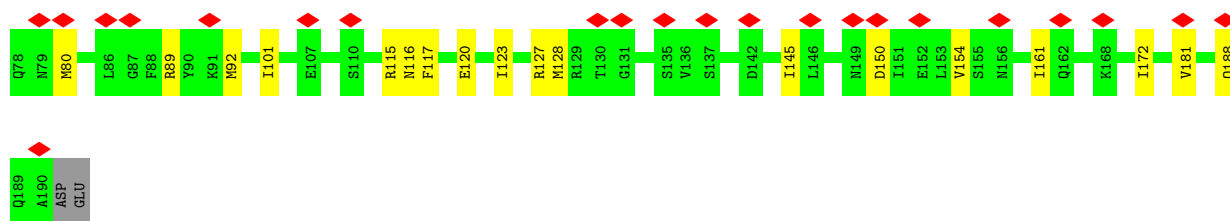


• Molecule 10: Large ribosomal subunit protein eL8

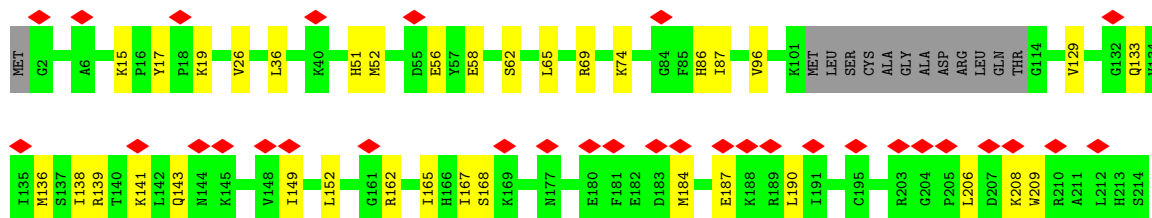
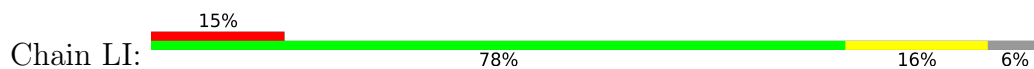


• Molecule 11: Large ribosomal subunit protein uL6

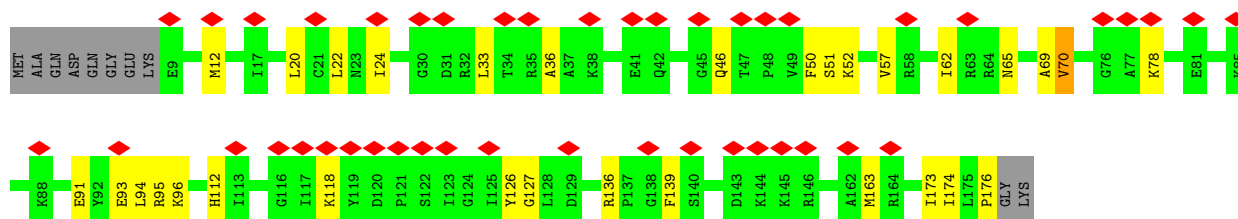
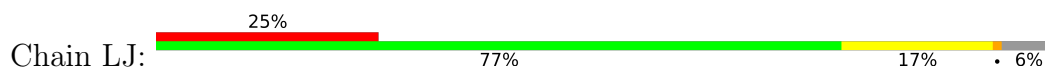




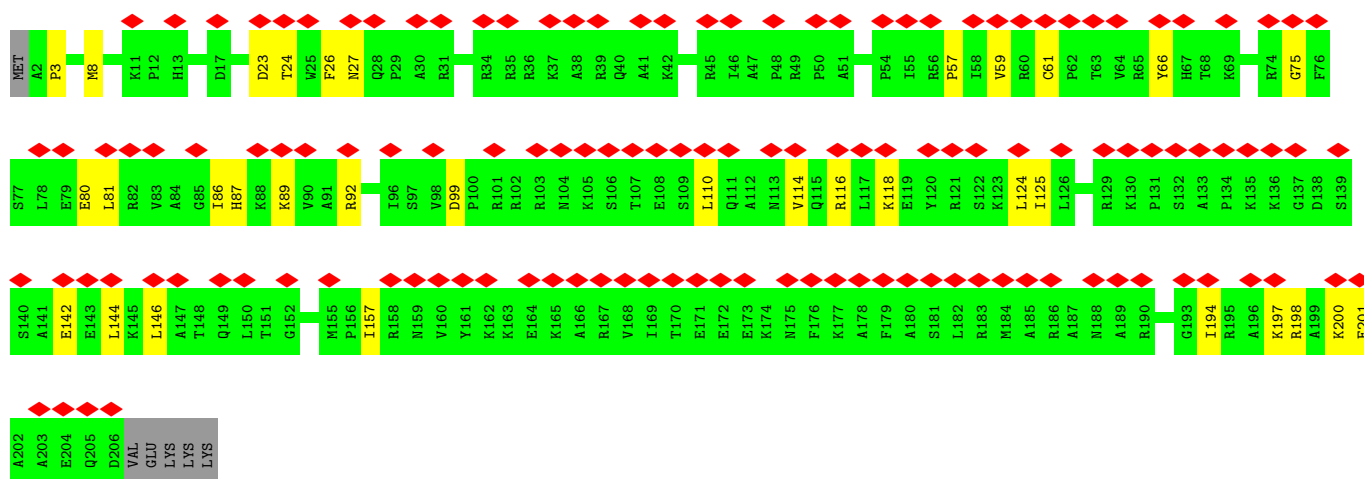
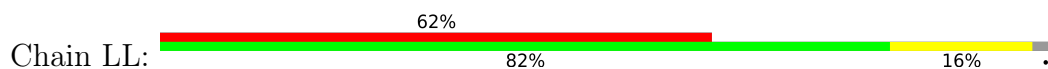
- Molecule 12: 60S ribosomal protein L10



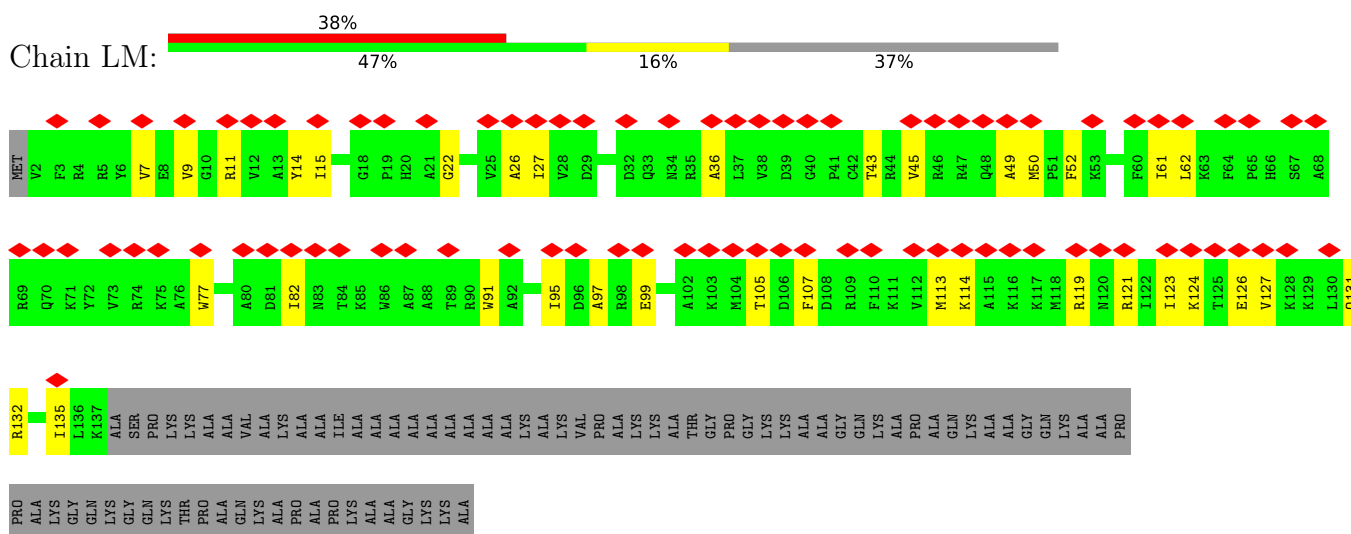
- Molecule 13: Large ribosomal subunit protein uL5



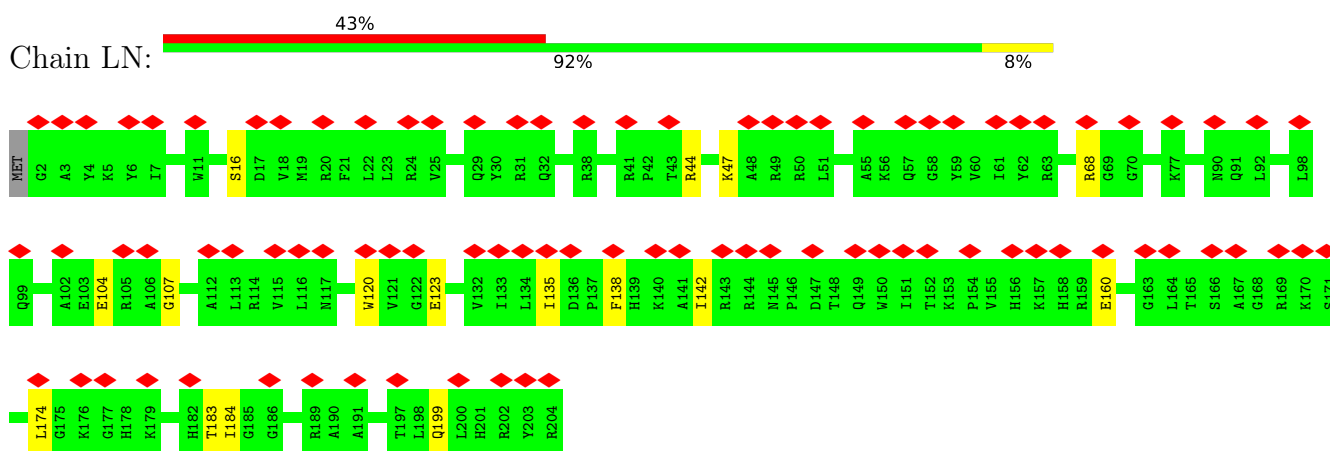
- Molecule 14: Large ribosomal subunit protein eL13



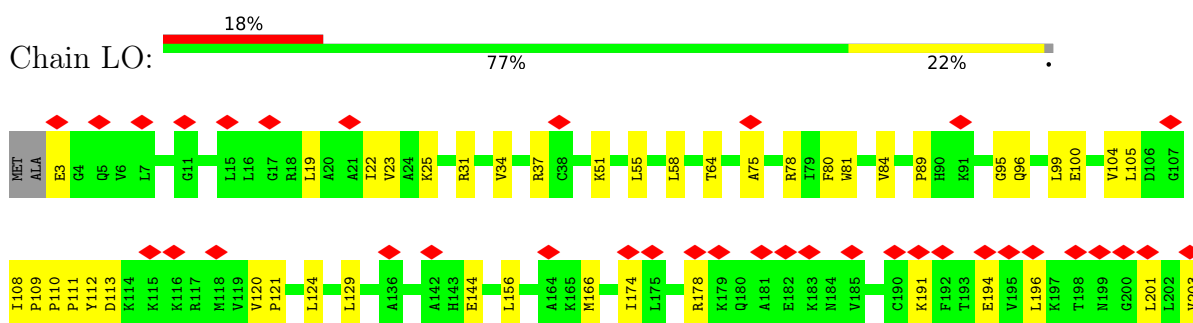
- Molecule 15: Large ribosomal subunit protein eL14



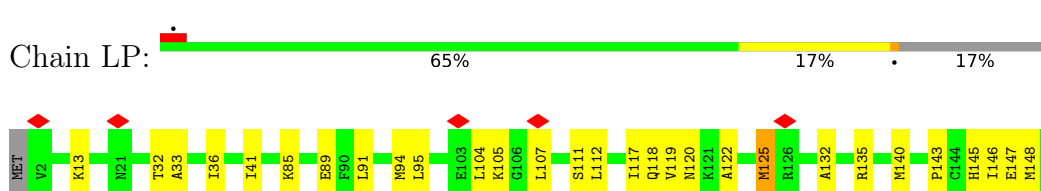
- Molecule 16: Ribosomal protein L15



- Molecule 17: Large ribosomal subunit protein uL13

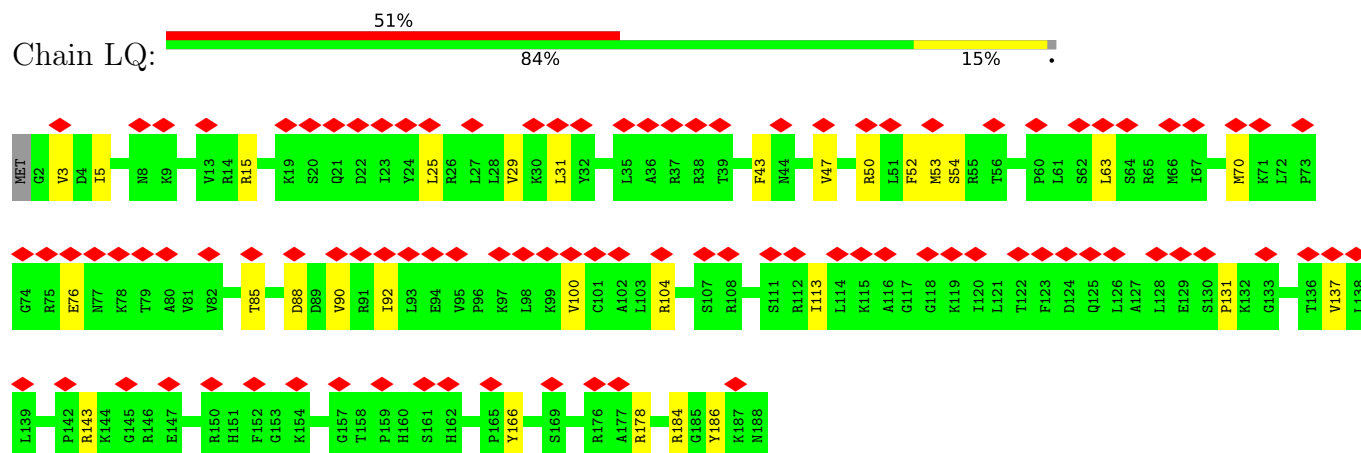


- Molecule 18: Large ribosomal subunit protein uL22

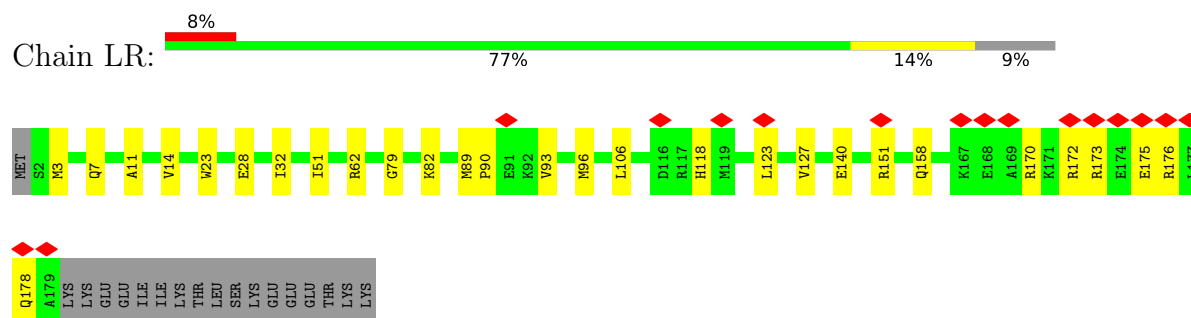


GLN  
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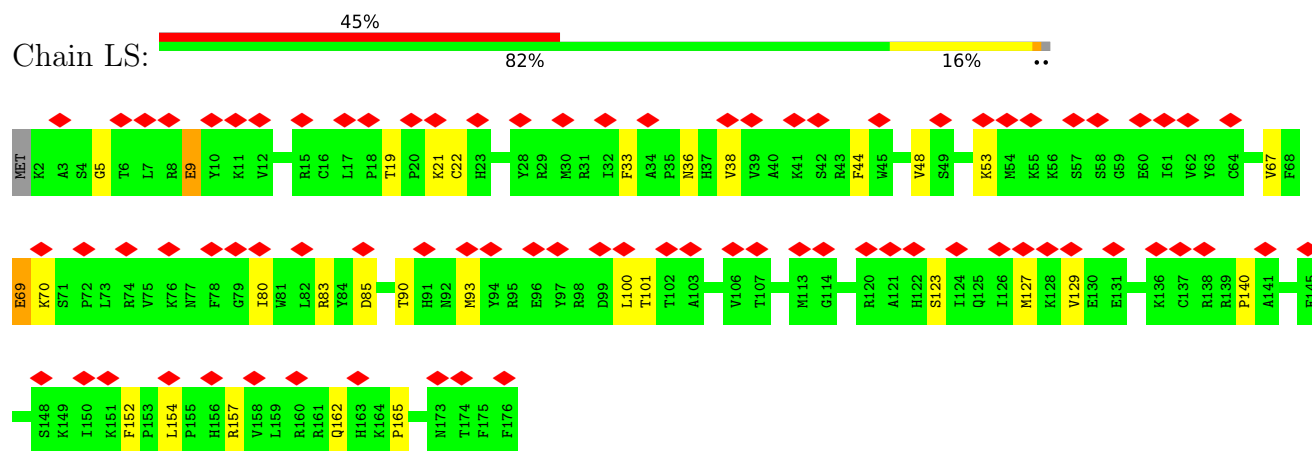
• Molecule 19: Large ribosomal subunit protein eL18



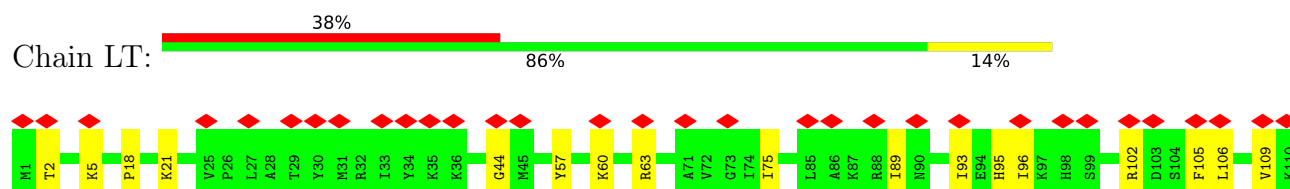
• Molecule 20: Ribosomal protein L19

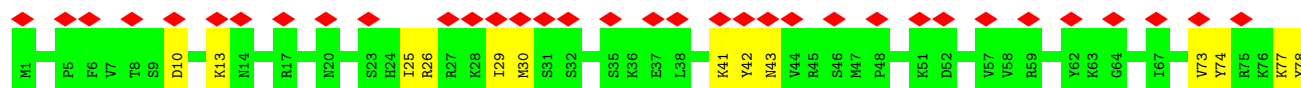


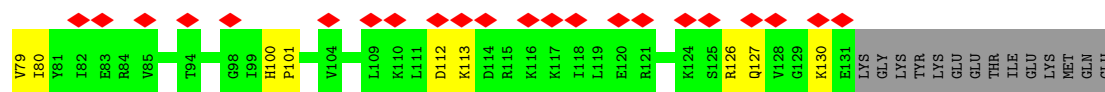
• Molecule 21: Large ribosomal subunit protein eL20



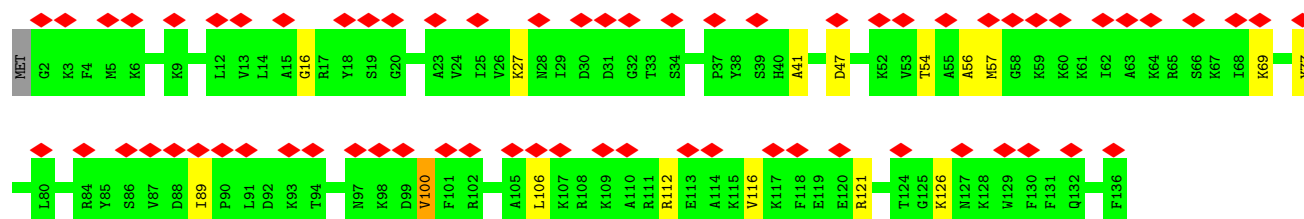
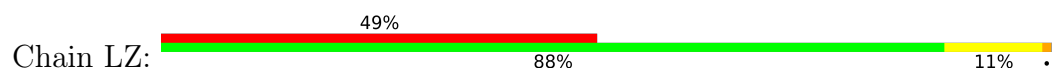
• Molecule 22: Large ribosomal subunit protein eL21



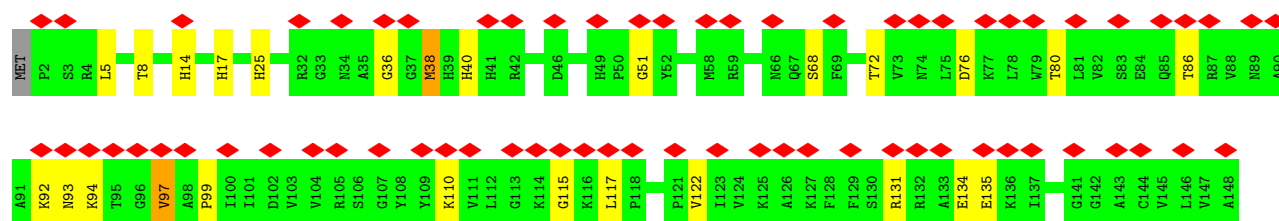
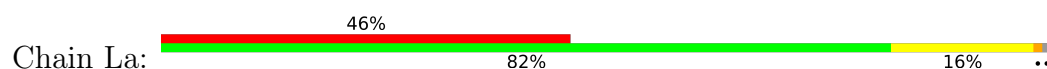




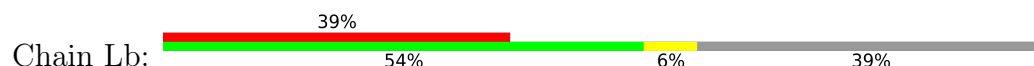
- Molecule 28: 60S ribosomal protein L27



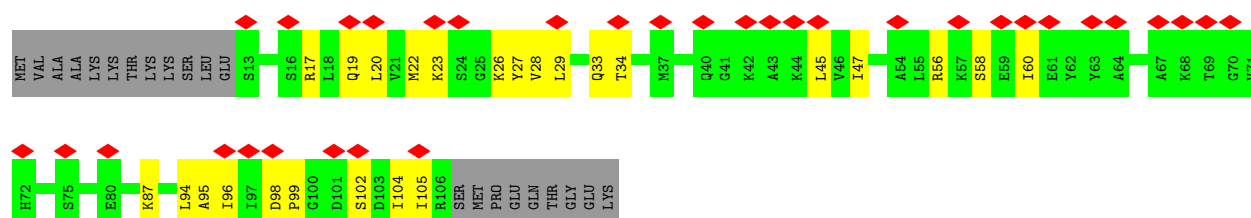
- Molecule 29: Large ribosomal subunit protein uL15



- Molecule 30: Large ribosomal subunit protein eL29

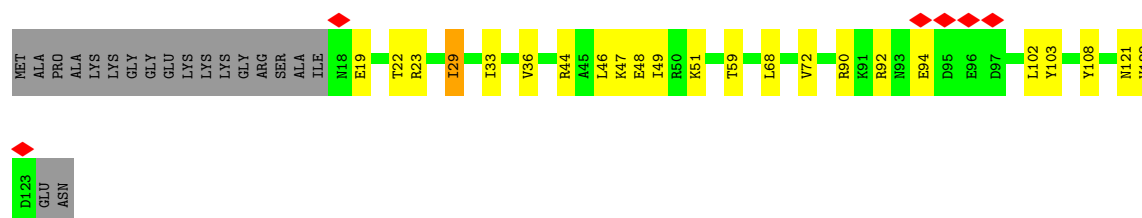


- Molecule 31: Large ribosomal subunit protein eL30

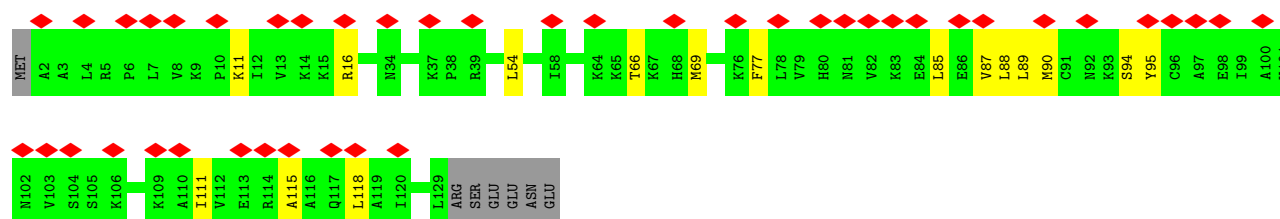
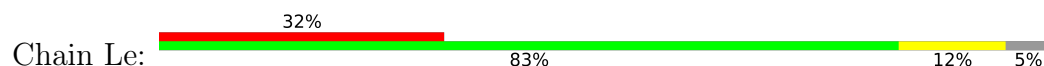




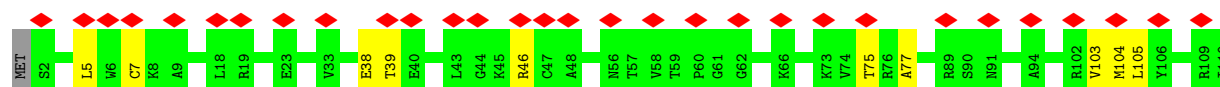
- Molecule 32: Large ribosomal subunit protein eL31



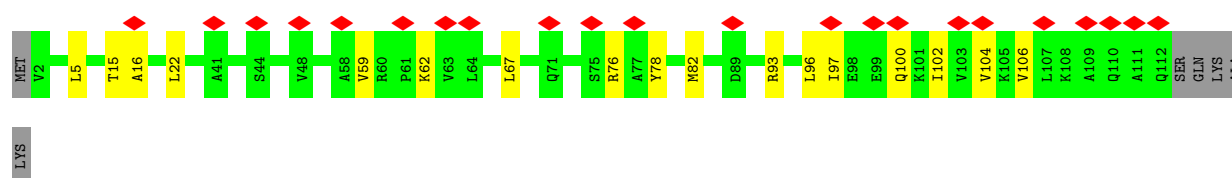
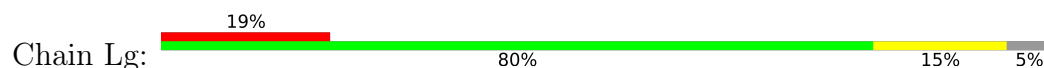
- Molecule 33: 60S ribosomal protein L32



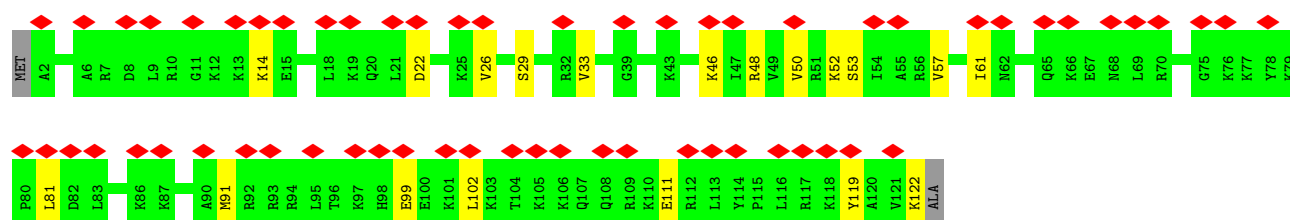
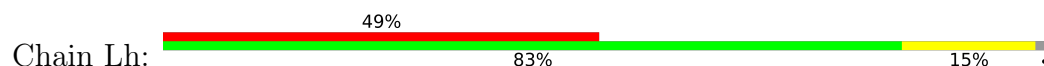
- Molecule 34: Large ribosomal subunit protein eL33



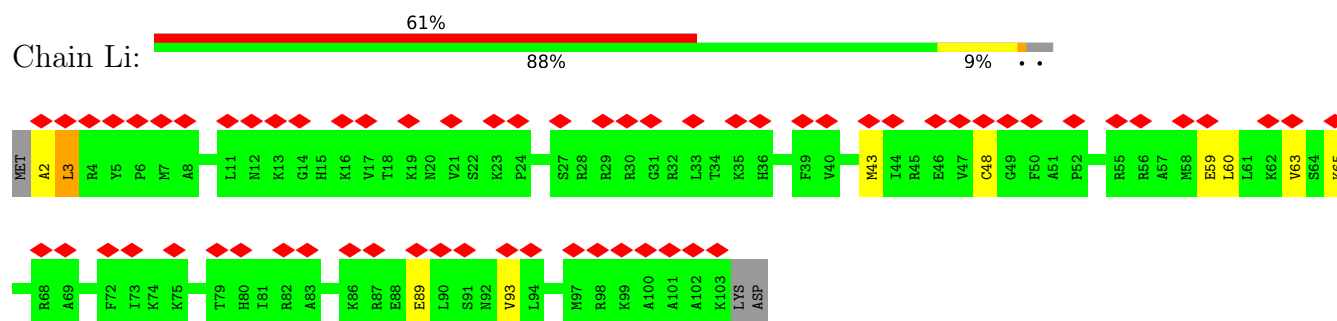
- Molecule 35: Large ribosomal subunit protein eL34



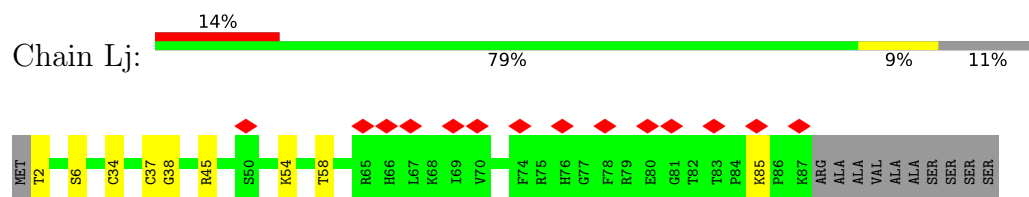
- Molecule 36: Large ribosomal subunit protein uL29



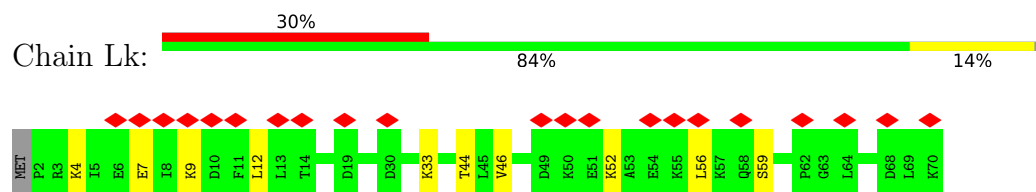
- Molecule 37: 60S ribosomal protein L36



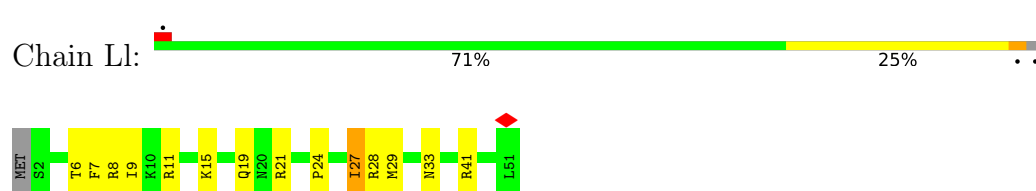
- Molecule 38: Ribosomal protein L37



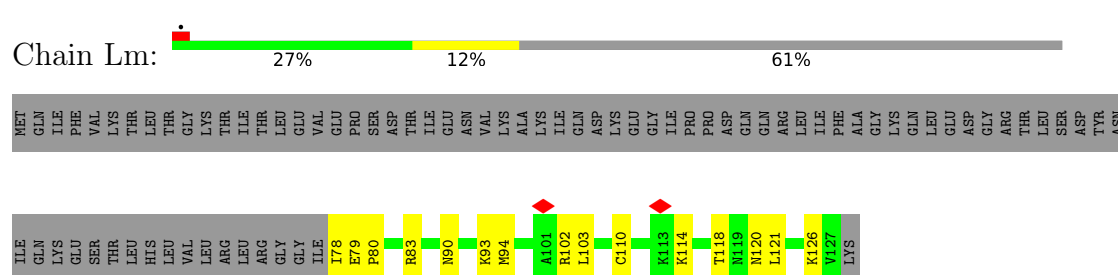
- Molecule 39: Large ribosomal subunit protein eL38



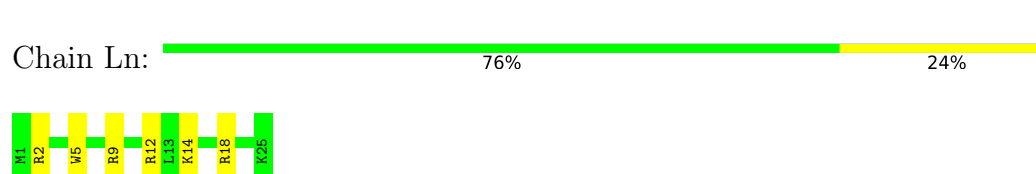
- Molecule 40: Large ribosomal subunit protein eL39



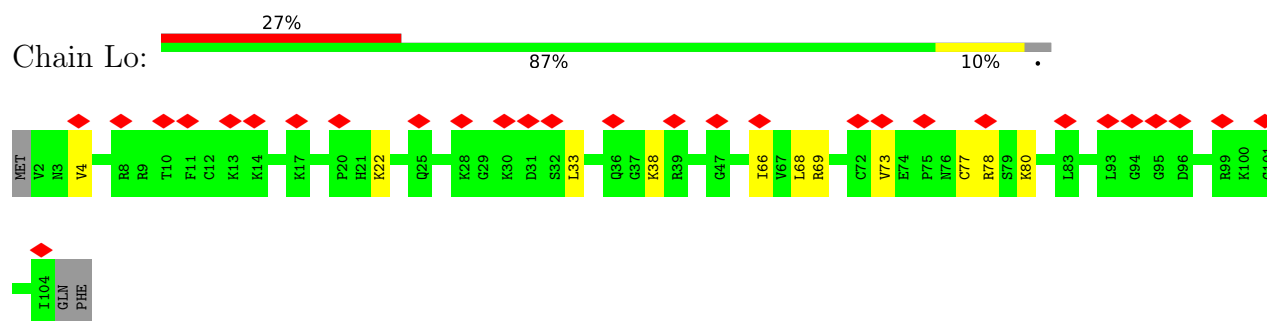
- Molecule 41: Ubiquitin-ribosomal protein eL40 fusion protein



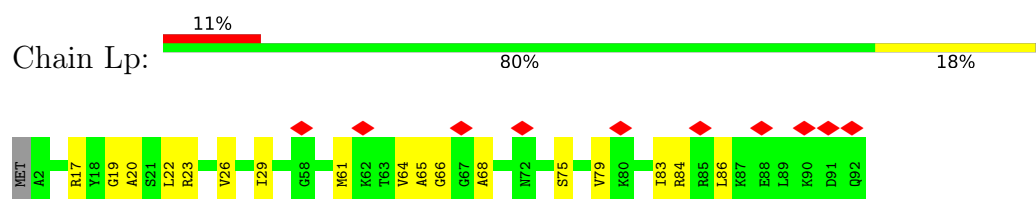
- Molecule 42: 60S ribosomal protein L41



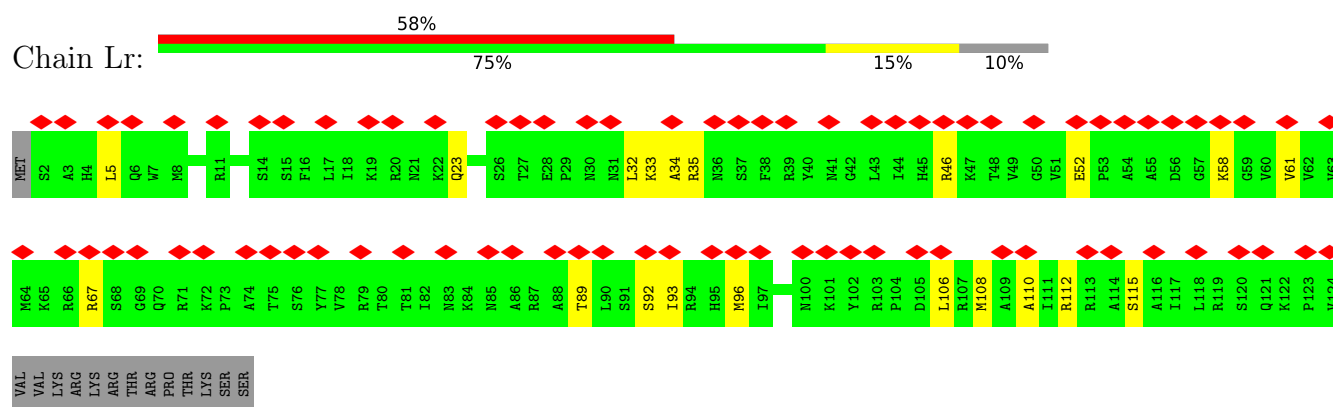
- Molecule 43: 60S ribosomal protein L36a



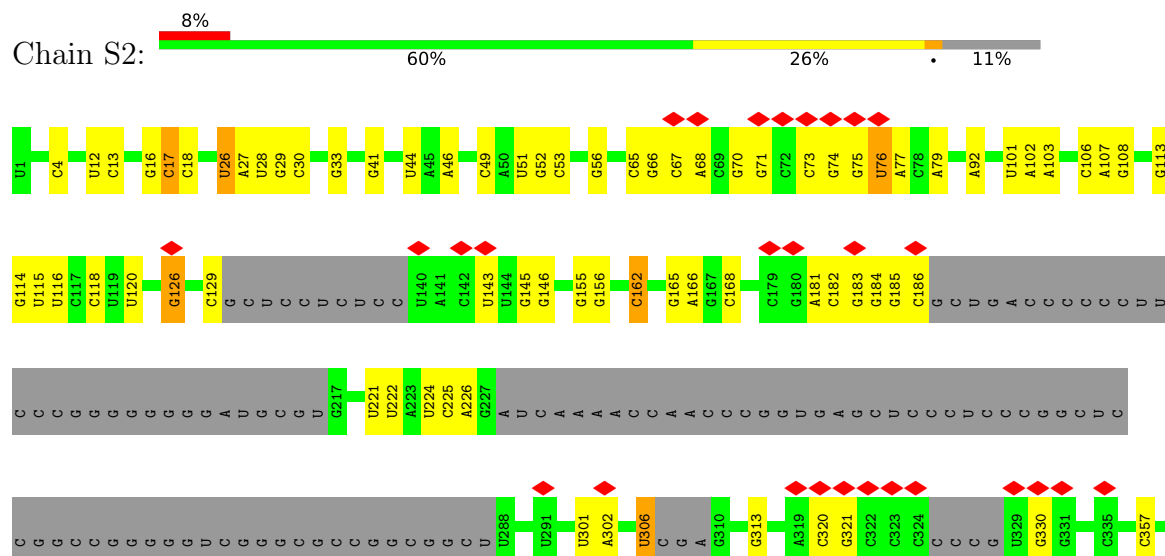
- Molecule 44: Large ribosomal subunit protein eL43

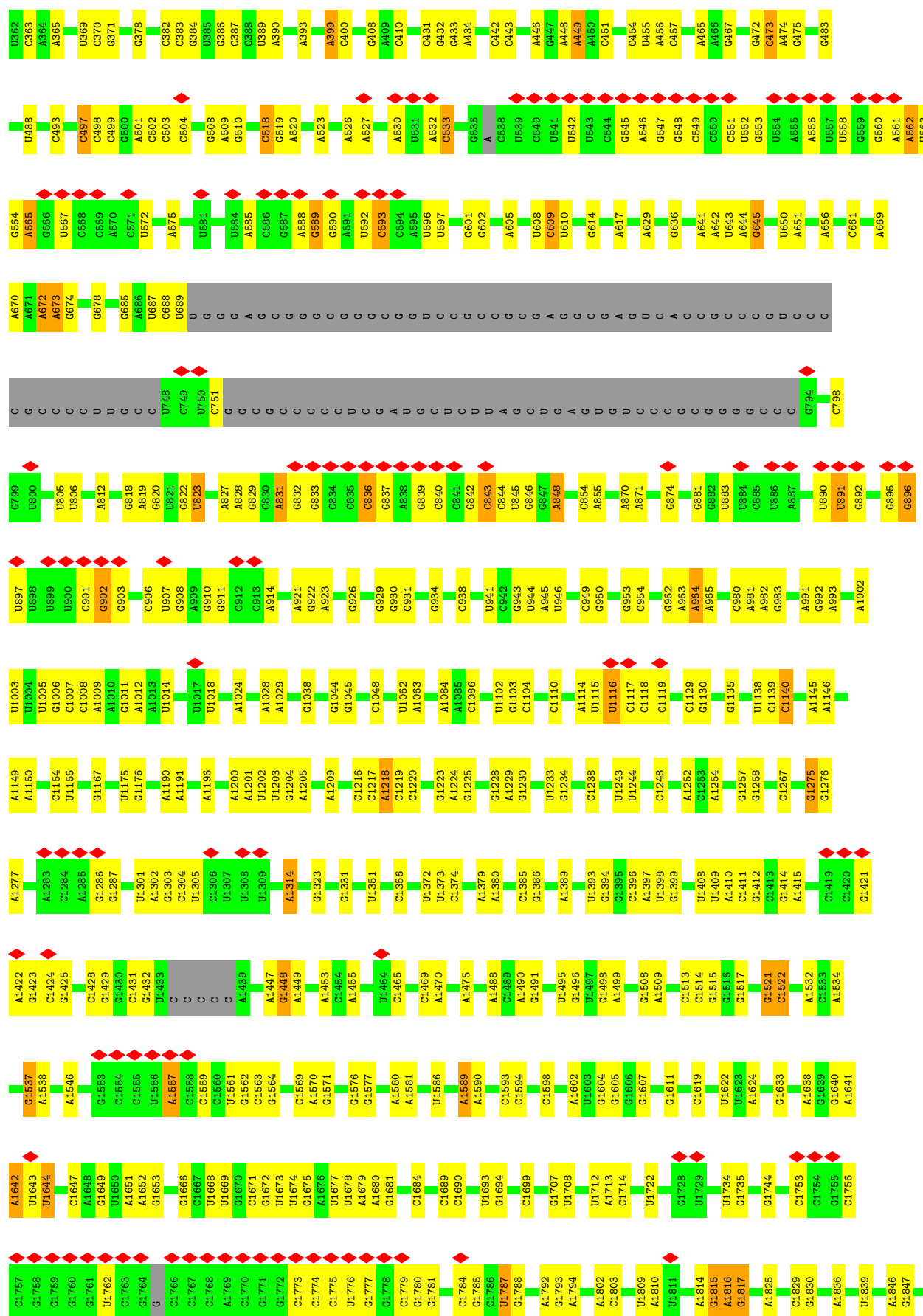


- Molecule 45: Large ribosomal subunit protein eL28



- Molecule 46: 18S ribosomal RNA





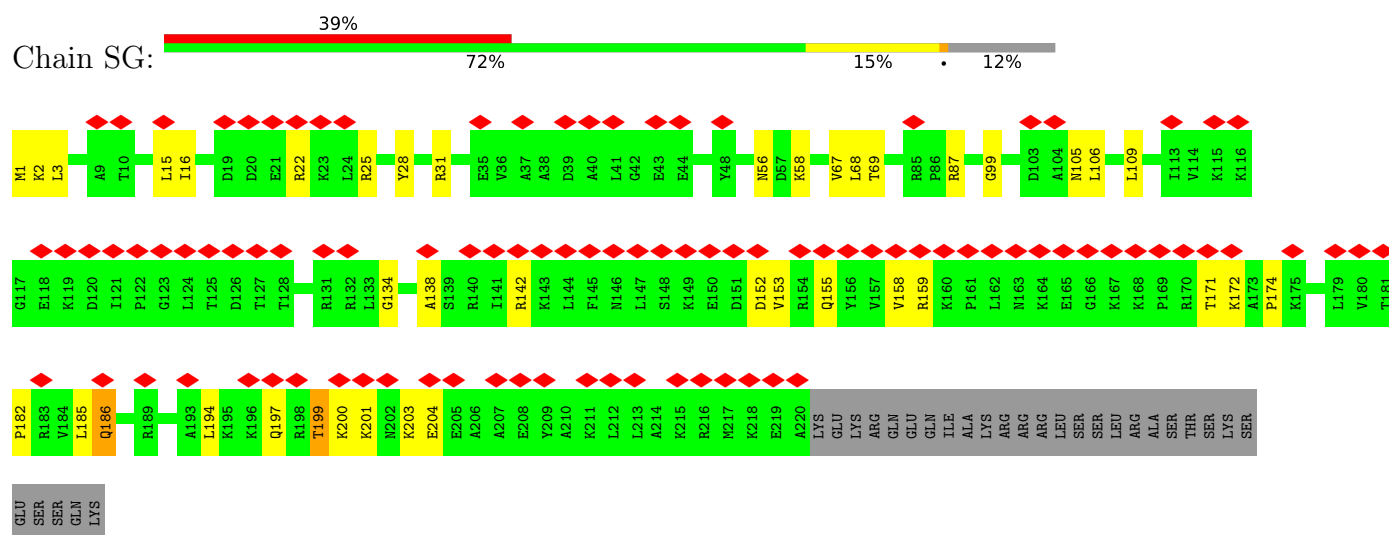




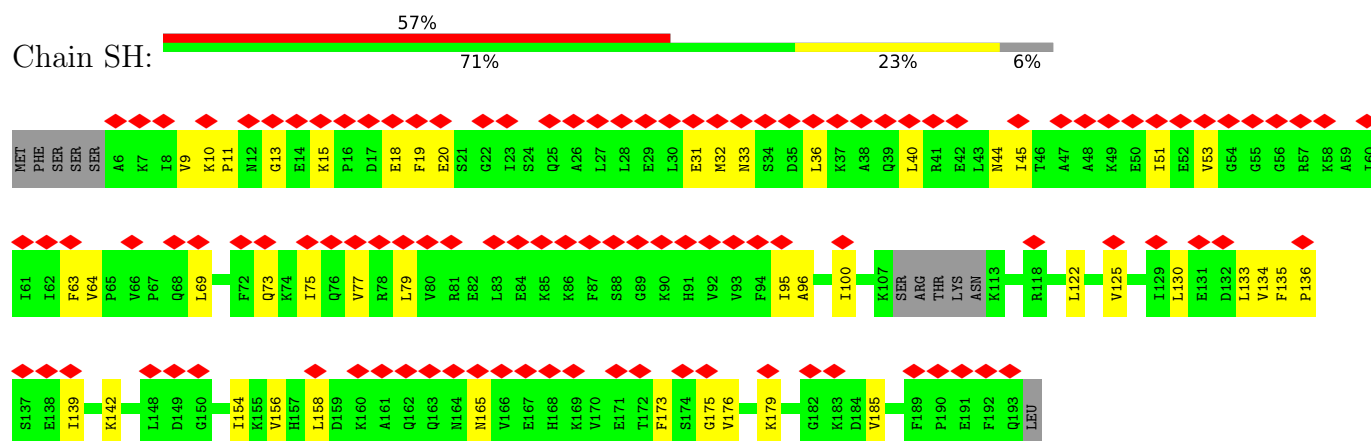
- Molecule 54: Small ribosomal subunit protein uS7



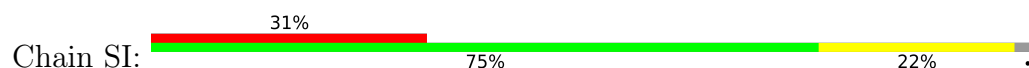
- Molecule 55: 40S ribosomal protein S6

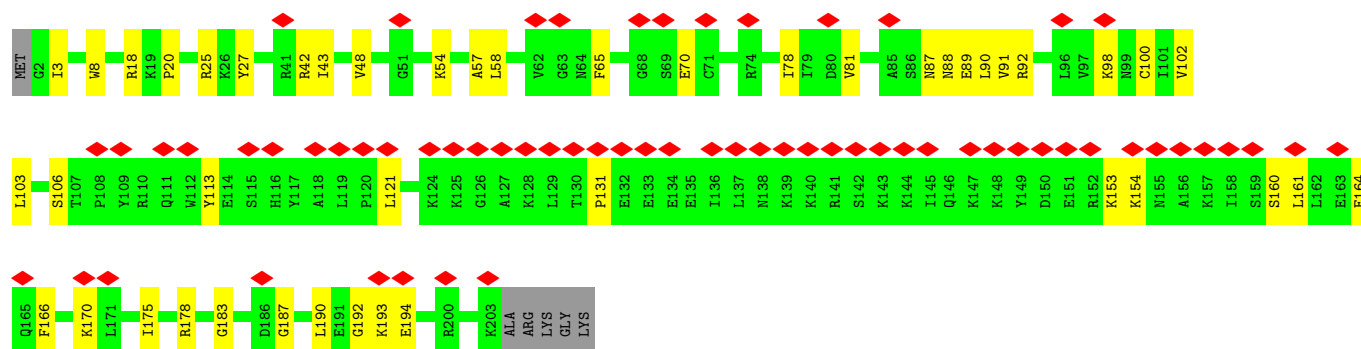


- Molecule 56: 40S ribosomal protein S7

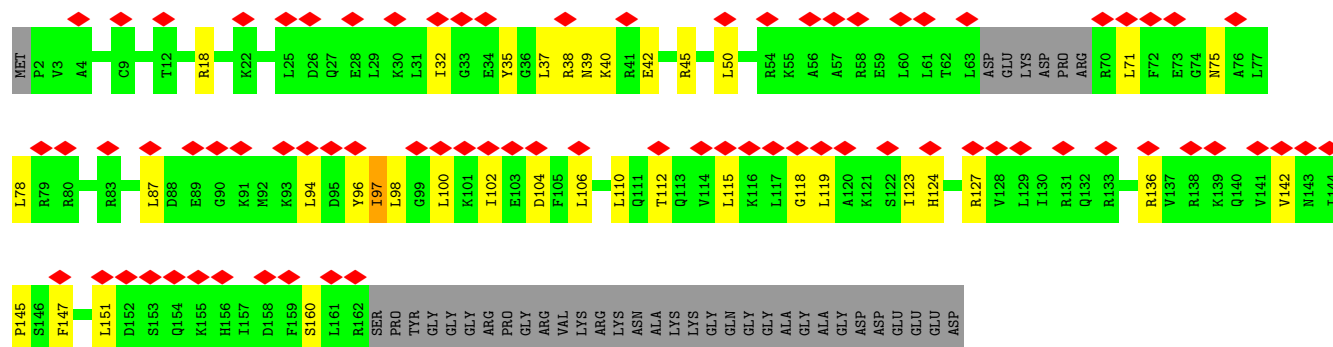
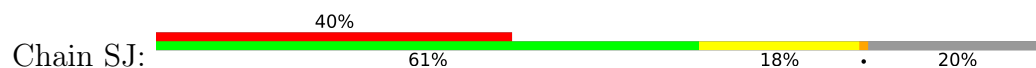


- Molecule 57: Small ribosomal subunit protein eS8

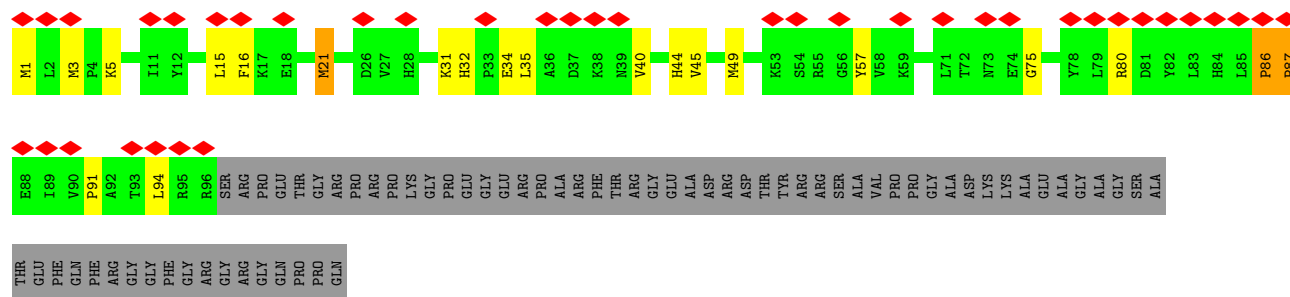




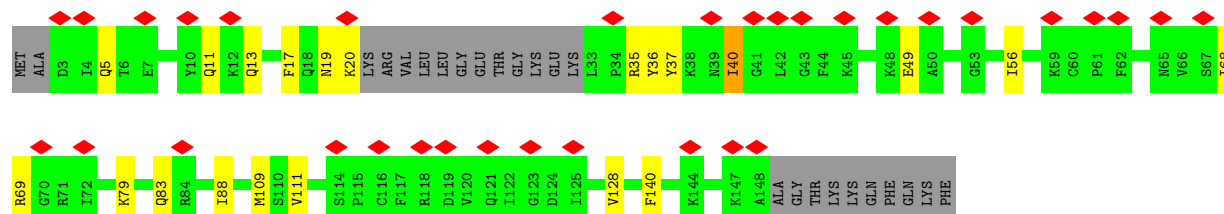
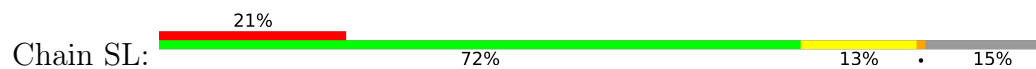
• Molecule 58: Small ribosomal subunit protein uS4



• Molecule 59: Small ribosomal subunit protein eS10

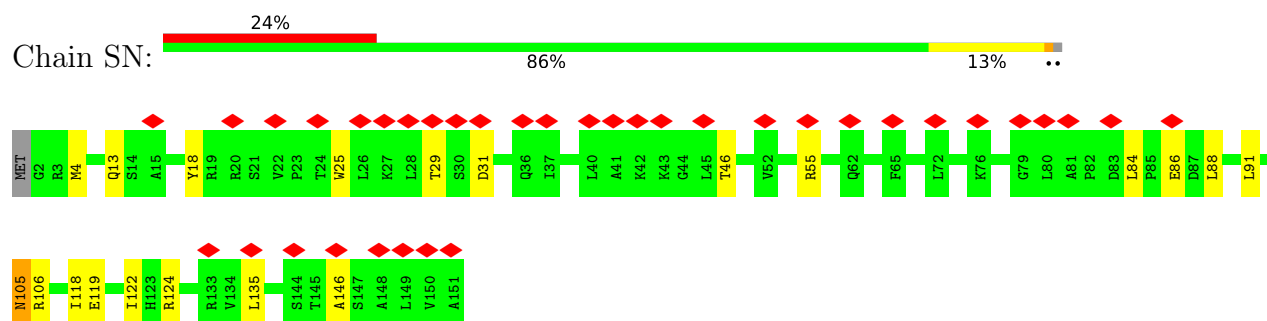


• Molecule 60: Small ribosomal subunit protein uS17

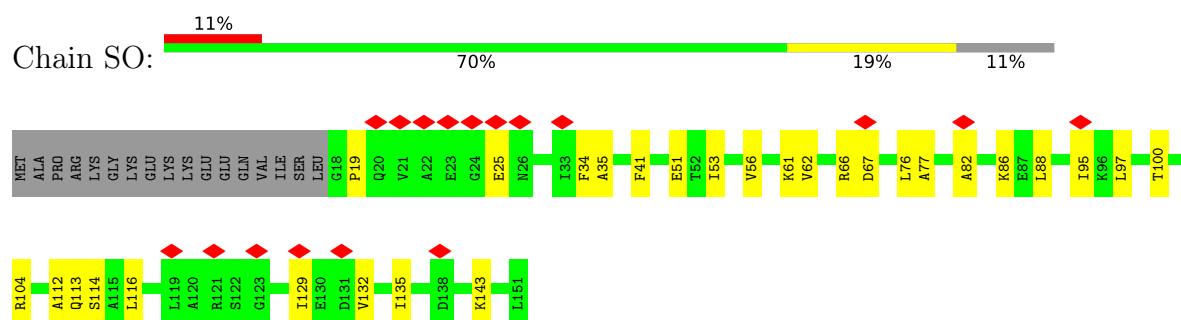




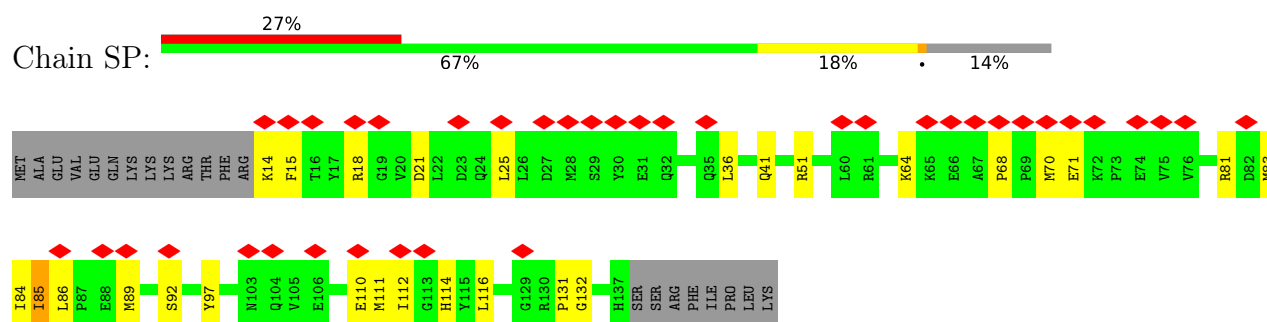
- Molecule 61: Small ribosomal subunit protein uS15



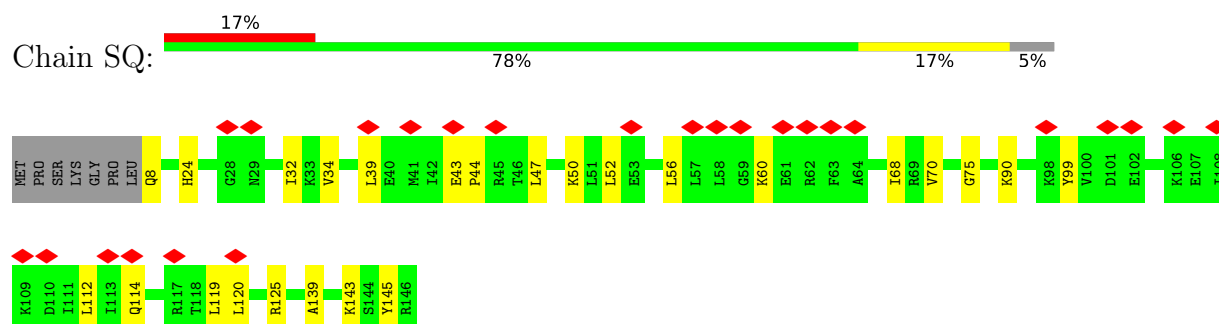
- Molecule 62: Small ribosomal subunit protein uS11



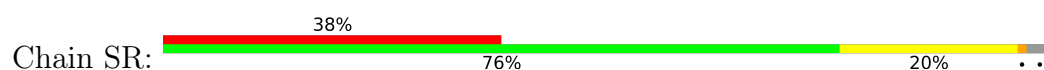
- Molecule 63: 40S ribosomal protein S15

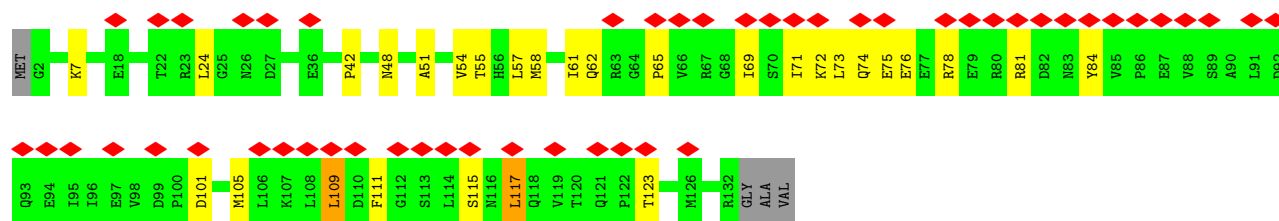


- Molecule 64: Small ribosomal subunit protein uS9

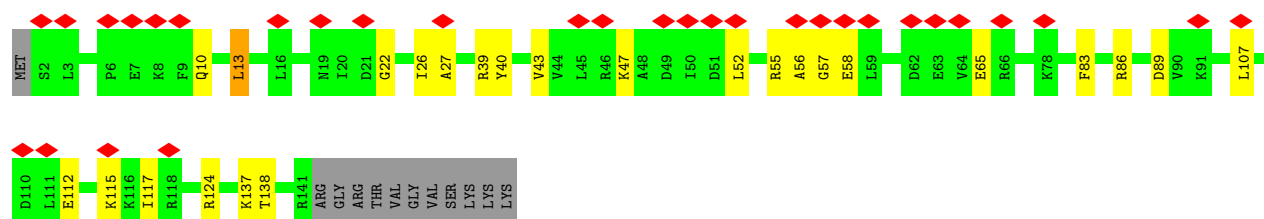
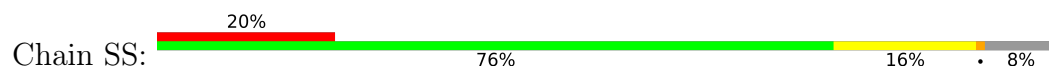


- Molecule 65: Small ribosomal subunit protein eS17

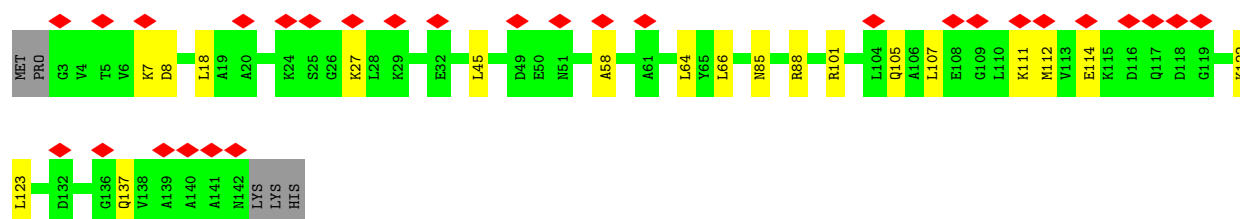
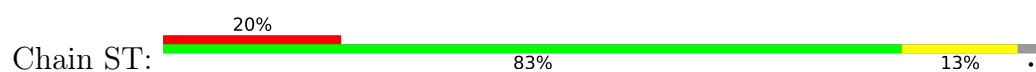




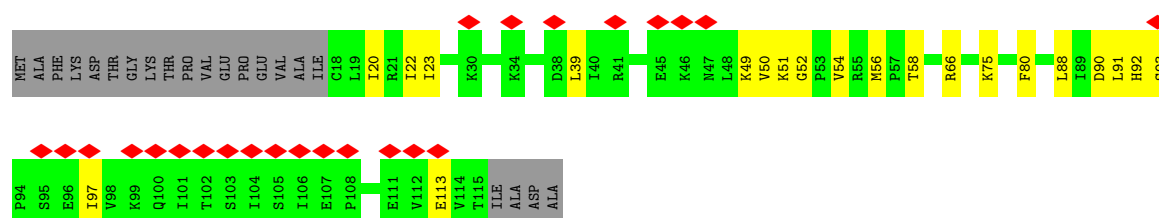
- Molecule 66: Small ribosomal subunit protein uS13



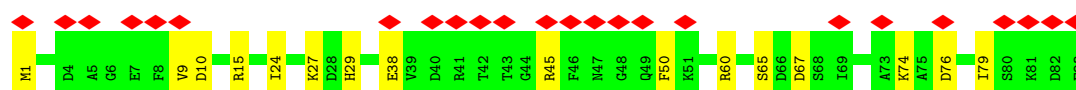
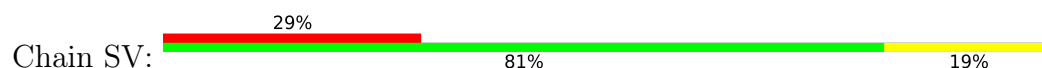
- Molecule 67: Small ribosomal subunit protein eS19




- Molecule 68: Small ribosomal subunit protein uS10

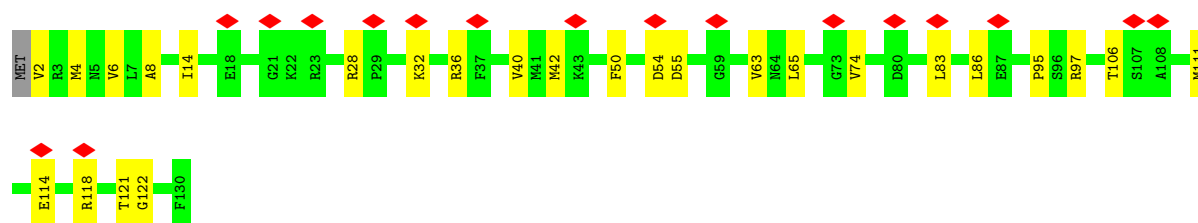


- Molecule 69: Small ribosomal subunit protein eS21




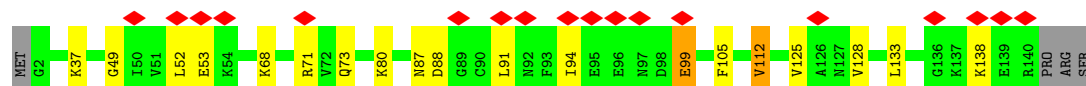
- Molecule 70: Small ribosomal subunit protein uS8

Chain SW: 



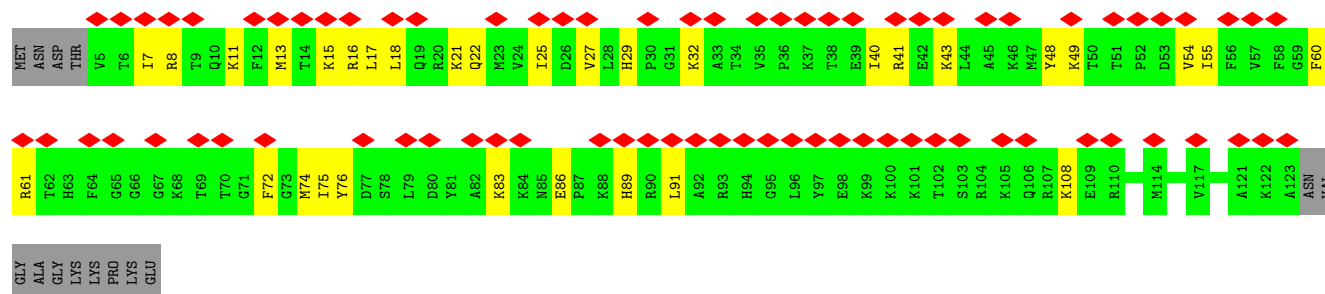
- Molecule 71: Small ribosomal subunit protein uS12

Chain SX: 



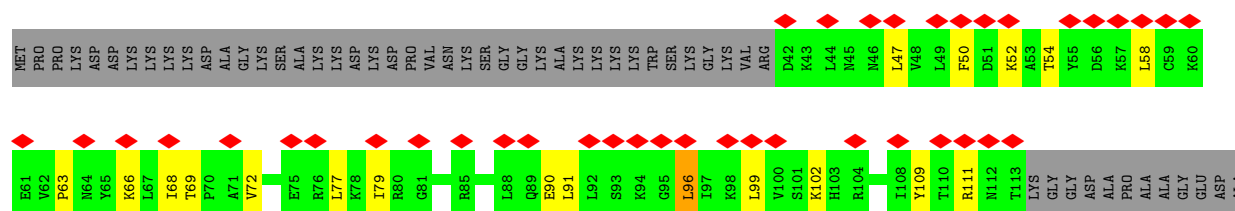
- Molecule 72: 40S ribosomal protein S24

Chain SY: 



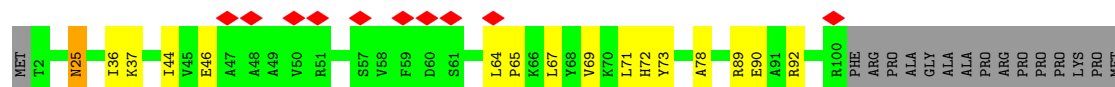
- Molecule 73: Small ribosomal subunit protein eS25

Chain SZ: 




- Molecule 74: 40S ribosomal protein S26

Chain Sa: 




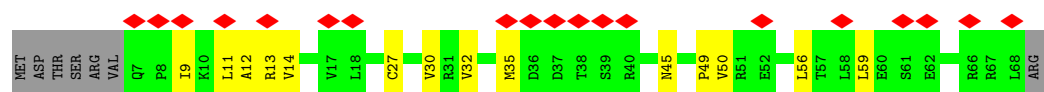
- Molecule 75: 40S ribosomal protein S27

Chain Sb: 




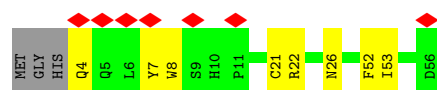
- Molecule 76: Small ribosomal subunit protein eS28

Chain Sc: 



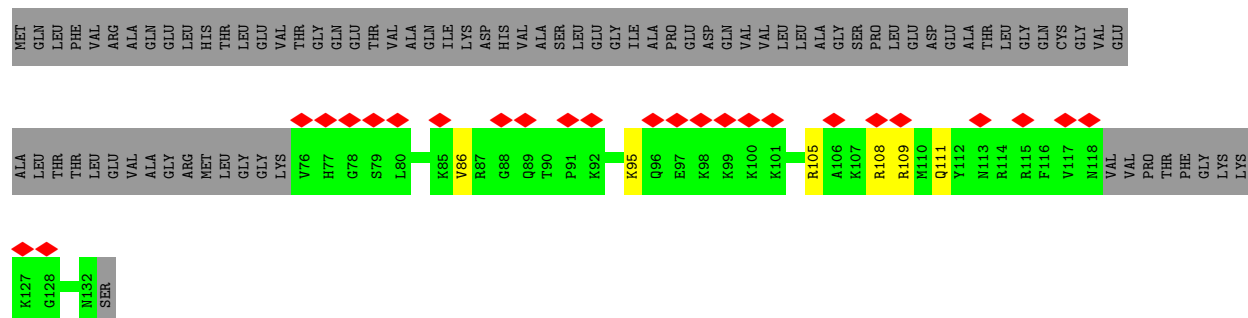
- Molecule 77: Small ribosomal subunit protein uS14

Chain Sd: 



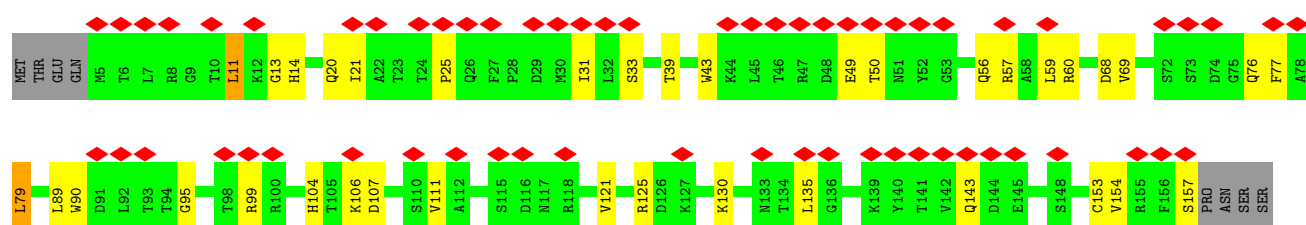
- Molecule 78: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

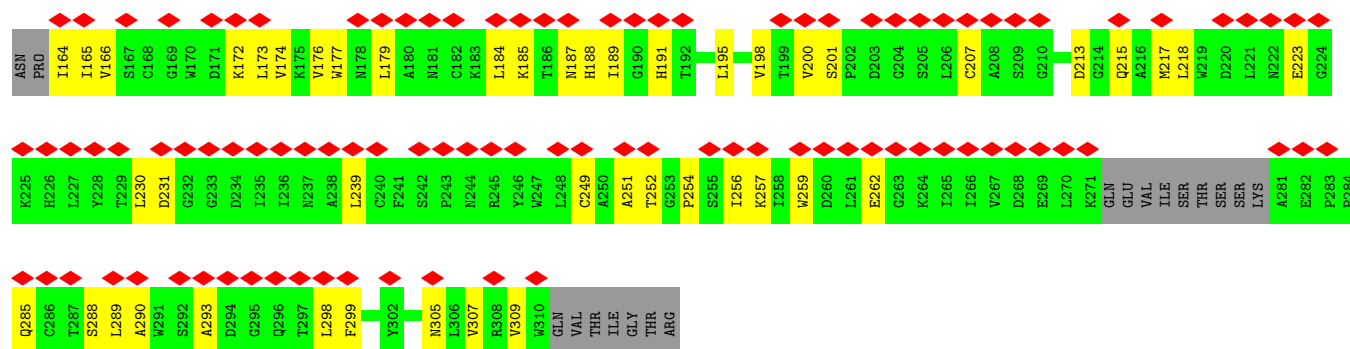
Chain Se: 



- Molecule 79: Small ribosomal subunit protein RACK1

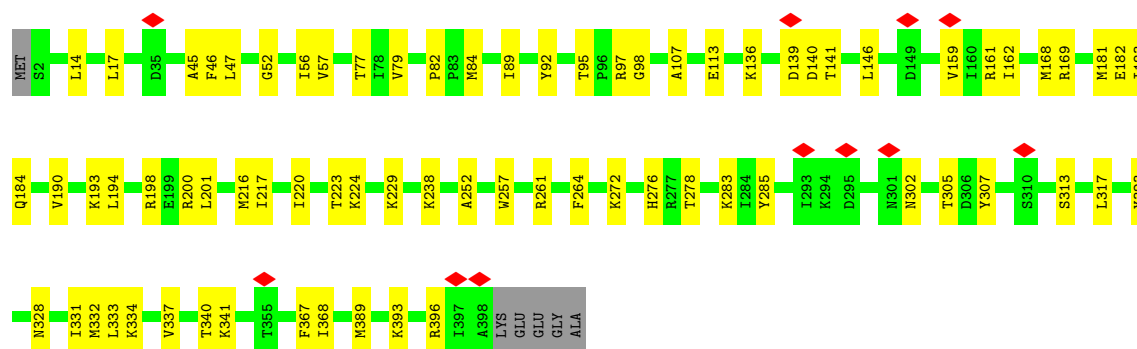
Chain Sg: 





- Molecule 80: Large ribosomal subunit protein uL3

Chain LB: 80% 18%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	118185	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60.04	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.956	Depositor
Minimum map value	-1.484	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.147	Depositor
Recommended contour level	0.584	Depositor
Map size ( $\text{\AA}$ )	528.0, 528.0, 528.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.1, 1.1, 1.1	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	B	0.15	0/231	0.35	0/356
2	L5	0.16	0/82867	0.22	0/129223
3	L7	0.16	0/2858	0.20	0/4455
4	L8	0.15	0/3701	0.19	0/5766
5	LA	0.22	0/1936	0.46	0/2596
6	LC	0.19	0/2916	0.40	0/3914
7	LD	0.19	0/2435	0.39	0/3260
8	LE	0.18	0/1775	0.38	0/2381
9	LF	0.20	0/1805	0.38	0/2408
10	LG	0.18	0/1844	0.39	0/2483
11	LH	0.18	0/1537	0.37	0/2065
12	LI	0.20	0/1671	0.42	0/2230
13	LJ	0.18	0/1372	0.43	0/1836
14	LL	0.18	0/1691	0.39	0/2264
15	LM	0.20	0/1146	0.50	0/1531
16	LN	0.21	0/1746	0.40	0/2338
17	LO	0.22	0/1670	0.50	0/2232
18	LP	0.23	0/1256	0.48	0/1684
19	LQ	0.19	0/1539	0.40	0/2053
20	LR	0.19	0/1506	0.42	0/1991
21	LS	0.21	0/1491	0.39	0/2000
22	LT	0.19	0/1335	0.41	0/1781
23	LU	0.34	1/831 (0.1%)	0.60	0/1115
24	LV	0.21	0/987	0.39	0/1324
25	LW	0.19	0/532	0.39	0/708
26	LX	0.18	0/984	0.42	0/1323
27	LY	0.21	0/1110	0.49	0/1477
28	LZ	0.19	0/1130	0.39	0/1507
29	La	0.23	0/1193	0.51	2/1593 (0.1%)
30	Lb	0.18	0/808	0.45	0/1065
31	Lc	0.18	0/742	0.41	0/996
32	Ld	0.23	0/894	0.46	0/1204

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.19	0/1071	0.36	0/1429
34	Lf	0.20	0/895	0.41	0/1198
35	Lg	0.19	0/888	0.39	0/1185
36	Lh	0.19	0/1017	0.39	0/1343
37	Li	0.21	0/843	0.50	0/1115
38	Lj	0.20	0/720	0.38	0/952
39	Lk	0.20	0/574	0.47	0/760
40	Ll	0.20	0/454	0.44	0/599
41	Lm	0.22	0/417	0.49	0/553
42	Ln	0.18	0/240	0.31	0/305
43	Lo	0.18	0/855	0.36	0/1128
44	Lp	0.19	0/718	0.42	0/953
45	Lr	0.17	0/1002	0.38	0/1343
46	S2	0.17	0/39392	0.22	0/61373
47	S6	0.11	0/1784	0.27	0/2779
48	S7	0.12	0/1753	0.27	0/2730
49	SA	0.23	0/1679	0.44	0/2283
50	SB	0.20	0/1749	0.43	0/2340
51	SC	0.21	0/1726	0.44	0/2335
52	SD	0.18	0/1754	0.40	0/2362
53	SE	0.21	0/2092	0.48	1/2816 (0.0%)
54	SF	0.21	0/1436	0.50	0/1930
55	SG	0.25	0/1747	0.50	3/2337 (0.1%)
56	SH	0.21	0/1478	0.46	0/1981
57	SI	0.22	0/1621	0.57	1/2172 (0.0%)
58	SJ	0.23	0/1275	0.51	0/1710
59	SK	0.34	0/810	0.63	2/1091 (0.2%)
60	SL	0.21	0/1125	0.43	0/1507
61	SN	0.26	0/1232	0.43	0/1656
62	SO	0.22	0/1015	0.47	0/1361
63	SP	0.27	0/1015	0.54	2/1357 (0.1%)
64	SQ	0.24	0/1126	0.49	0/1506
65	SR	0.23	0/1078	0.50	0/1447
66	SS	0.22	0/1175	0.48	0/1575
67	ST	0.24	0/1108	0.55	1/1486 (0.1%)
68	SU	0.22	0/785	0.44	0/1054
69	SV	0.21	0/646	0.48	0/864
70	SW	0.21	0/1051	0.47	0/1406
71	SX	0.21	0/1097	0.46	0/1463
72	SY	0.21	0/996	0.50	0/1321
73	SZ	0.21	0/580	0.56	0/780
74	Sa	0.22	0/806	0.41	0/1080
75	Sb	0.22	0/665	0.53	0/891



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Sc	0.20	0/456	0.52	0/615
77	Sd	0.21	0/455	0.47	0/603
78	Se	0.18	0/386	0.37	0/505
79	Sg	0.20	0/2324	0.52	2/3159 (0.1%)
80	LB	0.19	0/3269	0.43	0/4375
All	All	0.18	1/221919 (0.0%)	0.32	14/326272 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	LM	0	1
19	LQ	0	1
20	LR	0	1
62	SO	0	1
75	Sb	0	1
79	Sg	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	LU	30	GLU	CB-CG	-5.06	1.37	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SK	87	PRO	N-CA-CB	7.40	111.02	103.25
59	SK	86	PRO	N-CA-CB	7.38	110.24	103.08
57	SI	131	PRO	N-CA-CB	7.21	110.82	103.25
63	SP	131	PRO	N-CA-CB	6.78	110.49	103.38
29	La	38	MET	CA-C-N	-6.49	112.82	122.56

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	LM	9	VAL	Peptide
19	LQ	184	ARG	Peptide

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Mol	Chain	Res	Type	Group
20	LR	151	ARG	Sidechain
62	SO	25	GLU	Peptide
75	Sb	72	ARG	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	208	0	105	1	0
2	L5	74087	35	37416	478	0
3	L7	2558	0	1296	11	0
4	L8	3314	0	1683	17	0
5	LA	1898	0	1993	34	0
6	LC	2862	0	3035	29	0
7	LD	2389	0	2420	23	0
8	LE	1743	0	1880	19	0
9	LF	1771	0	1886	20	0
10	LG	1813	0	1944	18	0
11	LH	1519	0	1603	20	0
12	LI	1633	0	1679	21	0
13	LJ	1349	0	1383	17	0
14	LL	1660	0	1762	24	0
15	LM	1125	0	1202	23	0
16	LN	1701	0	1749	11	0
17	LO	1640	0	1792	30	0
18	LP	1231	0	1265	23	0
19	LQ	1515	0	1639	21	0
20	LR	1490	0	1638	19	0
21	LS	1451	0	1488	20	0
22	LT	1307	0	1380	15	0
23	LU	817	0	839	16	0
24	LV	973	0	1034	11	0
25	LW	519	0	533	10	0
26	LX	967	0	1040	8	0
27	LY	1093	0	1176	16	0
28	LZ	1107	0	1182	11	0
29	La	1164	0	1213	17	0
30	Lb	794	0	860	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Lc	732	0	769	15	0
32	Ld	879	0	924	13	0
33	Le	1053	0	1147	12	0
34	Lf	876	0	912	7	0
35	Lg	878	0	961	11	0
36	Lh	1009	0	1151	11	0
37	Li	832	0	917	6	0
38	Lj	705	0	741	5	0
39	Lk	568	0	635	7	0
40	Ll	444	0	483	12	0
41	Lm	411	0	445	11	0
42	Ln	239	0	289	3	0
43	Lo	842	0	916	6	0
44	Lp	708	0	756	15	0
45	Lr	987	0	1048	16	0
46	S2	35236	3	17778	264	0
47	S6	1596	0	815	13	0
48	S7	1570	0	802	17	0
49	SA	1642	0	1646	28	0
50	SB	1722	0	1794	26	0
51	SC	1690	0	1763	30	0
52	SD	1726	0	1816	32	0
53	SE	2050	0	2156	36	0
54	SF	1416	0	1458	37	0
55	SG	1725	0	1822	28	0
56	SH	1457	0	1533	28	0
57	SI	1593	0	1603	30	0
58	SJ	1258	0	1333	24	0
59	SK	789	0	790	16	0
60	SL	1105	0	1160	17	0
61	SN	1208	0	1294	16	0
62	SO	1002	0	1023	23	0
63	SP	997	0	1024	17	0
64	SQ	1109	0	1174	17	0
65	SR	1064	0	1118	29	0
66	SS	1157	0	1213	17	0
67	ST	1090	0	1116	14	0
68	SU	776	0	846	12	0
69	SV	639	0	635	10	0
70	SW	1034	0	1080	18	0
71	SX	1081	0	1153	12	0
72	SY	979	0	1055	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	SZ	574	0	627	12	0
74	Sa	793	0	841	13	0
75	Sb	651	0	668	14	0
76	Sc	454	0	457	11	0
77	Sd	445	0	442	5	0
78	Se	384	0	415	7	0
79	Sg	2271	0	2226	57	0
80	LB	3202	0	3347	47	0
81	B	1	0	0	0	0
81	L5	226	0	0	0	0
81	L7	4	0	0	0	0
81	L8	3	0	0	0	0
81	LB	1	0	0	0	0
81	LI	1	0	0	0	0
81	LN	1	0	0	0	0
81	LP	1	0	0	0	0
81	Le	2	0	0	0	0
81	Lg	1	0	0	0	0
81	S2	86	0	0	0	0
81	SO	1	0	0	0	0
82	Lg	1	0	0	0	0
82	Lp	1	0	0	0	0
82	Sa	1	0	0	0	0
83	L5	3	0	0	0	0
83	La	1	0	0	0	0
83	S2	2	0	0	0	0
All	All	206683	38	152232	1927	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1927 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:S2:70:G:H21	46:S2:79:A:H62	1.20	0.86
2:L5:1895:G:N2	2:L5:1896:G:C4	2.45	0.84
71:SX:94:ILE:HG22	71:SX:125:VAL:HG21	1.58	0.83
2:L5:176:G:H1	2:L5:260:G:H1	1.22	0.82
54:SF:35:LEU:HD13	54:SF:117:ILE:HG22	1.60	0.82

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LA	246/257 (96%)	228 (93%)	18 (7%)	0	100	100
6	LC	356/419 (85%)	338 (95%)	18 (5%)	0	100	100
7	LD	291/297 (98%)	284 (98%)	7 (2%)	0	100	100
8	LE	210/296 (71%)	193 (92%)	17 (8%)	0	100	100
9	LF	212/270 (78%)	205 (97%)	6 (3%)	1 (0%)	24	54
10	LG	220/266 (83%)	215 (98%)	5 (2%)	0	100	100
11	LH	188/192 (98%)	177 (94%)	10 (5%)	1 (0%)	24	54
12	LI	197/214 (92%)	193 (98%)	4 (2%)	0	100	100
13	LJ	166/178 (93%)	147 (89%)	16 (10%)	3 (2%)	6	25
14	LL	203/211 (96%)	192 (95%)	11 (5%)	0	100	100
15	LM	134/217 (62%)	125 (93%)	9 (7%)	0	100	100
16	LN	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
17	LO	199/203 (98%)	189 (95%)	10 (5%)	0	100	100
18	LP	150/184 (82%)	142 (95%)	8 (5%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	176/196 (90%)	166 (94%)	10 (6%)	0	100	100
21	LS	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
22	LT	158/160 (99%)	150 (95%)	8 (5%)	0	100	100
23	LU	98/128 (77%)	86 (88%)	12 (12%)	0	100	100
24	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
25	LW	60/157 (38%)	58 (97%)	2 (3%)	0	100	100
26	LX	116/156 (74%)	112 (97%)	4 (3%)	0	100	100
27	LY	129/145 (89%)	127 (98%)	2 (2%)	0	100	100
28	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	Lb	93/160 (58%)	90 (97%)	3 (3%)	0	100	100
31	Lc	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
32	Ld	104/125 (83%)	100 (96%)	4 (4%)	0	100	100
33	Le	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
34	Lf	107/110 (97%)	102 (95%)	4 (4%)	1 (1%)	14	41
35	Lg	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
36	Lh	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	3 (3%)	1 (1%)	12	39
38	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	48/128 (38%)	46 (96%)	2 (4%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	121/137 (88%)	118 (98%)	3 (2%)	0	100	100
49	SA	206/295 (70%)	198 (96%)	8 (4%)	0	100	100
50	SB	210/264 (80%)	208 (99%)	2 (1%)	0	100	100
51	SC	218/293 (74%)	206 (94%)	12 (6%)	0	100	100
52	SD	220/243 (90%)	209 (95%)	11 (5%)	0	100	100
53	SE	256/263 (97%)	242 (94%)	14 (6%)	0	100	100
54	SF	175/204 (86%)	160 (91%)	15 (9%)	0	100	100
55	SG	218/249 (88%)	201 (92%)	16 (7%)	1 (0%)	24	54
56	SH	179/194 (92%)	162 (90%)	17 (10%)	0	100	100
57	SI	200/208 (96%)	182 (91%)	18 (9%)	0	100	100
58	SJ	151/194 (78%)	137 (91%)	14 (9%)	0	100	100
59	SK	94/165 (57%)	81 (86%)	11 (12%)	2 (2%)	5	21
60	SL	130/158 (82%)	117 (90%)	13 (10%)	0	100	100
61	SN	148/151 (98%)	146 (99%)	1 (1%)	1 (1%)	18	48
62	SO	132/151 (87%)	119 (90%)	13 (10%)	0	100	100
63	SP	122/145 (84%)	119 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	SQ	137/146 (94%)	127 (93%)	10 (7%)	0	100	100
65	SR	129/135 (96%)	118 (92%)	11 (8%)	0	100	100
66	SS	138/152 (91%)	135 (98%)	3 (2%)	0	100	100
67	ST	138/145 (95%)	131 (95%)	7 (5%)	0	100	100
68	SU	96/119 (81%)	93 (97%)	3 (3%)	0	100	100
69	SV	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
70	SW	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
71	SX	137/143 (96%)	133 (97%)	4 (3%)	0	100	100
72	SY	117/133 (88%)	114 (97%)	3 (3%)	0	100	100
73	SZ	70/125 (56%)	66 (94%)	4 (6%)	0	100	100
74	Sa	97/115 (84%)	93 (96%)	4 (4%)	0	100	100
75	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
76	Sc	60/69 (87%)	53 (88%)	7 (12%)	0	100	100
77	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
78	Se	45/133 (34%)	45 (100%)	0	0	100	100
79	Sg	285/317 (90%)	253 (89%)	31 (11%)	1 (0%)	30	59
80	LB	395/403 (98%)	373 (94%)	21 (5%)	1 (0%)	36	65
All	All	10748/12499 (86%)	10172 (95%)	563 (5%)	13 (0%)	49	77

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	SG	152	ASP
59	SK	87	PRO
80	LB	140	ASP
11	LH	13	PRO
13	LJ	78	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	
5	LA	190/199 (96%)	190 (100%)	0	100	100
6	LC	301/348 (86%)	300 (100%)	1 (0%)	86	96
7	LD	246/249 (99%)	245 (100%)	1 (0%)	84	94
8	LE	194/256 (76%)	194 (100%)	0	100	100
9	LF	185/234 (79%)	185 (100%)	0	100	100
10	LG	193/223 (86%)	191 (99%)	2 (1%)	68	89
11	LH	169/171 (99%)	167 (99%)	2 (1%)	63	86
12	LI	171/181 (94%)	171 (100%)	0	100	100
13	LJ	142/149 (95%)	140 (99%)	2 (1%)	59	85
14	LL	172/178 (97%)	171 (99%)	1 (1%)	78	93
15	LM	116/157 (74%)	115 (99%)	1 (1%)	70	90
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	172/173 (99%)	171 (99%)	1 (1%)	78	93
18	LP	133/163 (82%)	132 (99%)	1 (1%)	73	90
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	157/175 (90%)	154 (98%)	3 (2%)	50	79
21	LS	155/156 (99%)	152 (98%)	3 (2%)	50	79
22	LT	140/140 (100%)	140 (100%)	0	100	100
23	LU	90/114 (79%)	88 (98%)	2 (2%)	45	77
24	LV	100/107 (94%)	100 (100%)	0	100	100
25	LW	54/126 (43%)	54 (100%)	0	100	100
26	LX	106/133 (80%)	105 (99%)	1 (1%)	70	90
27	LY	122/135 (90%)	121 (99%)	1 (1%)	73	90
28	LZ	117/118 (99%)	115 (98%)	2 (2%)	53	82
29	La	120/121 (99%)	116 (97%)	4 (3%)	33	67
30	Lb	82/124 (66%)	80 (98%)	2 (2%)	43	75
31	Lc	79/97 (81%)	79 (100%)	0	100	100
32	Ld	97/110 (88%)	96 (99%)	1 (1%)	68	89
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	94/100 (94%)	94 (100%)	0	100	100
36	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	47	77
41	Lm	46/116 (40%)	46 (100%)	0	100	100
42	Ln	24/24 (100%)	24 (100%)	0	100	100
43	Lo	91/94 (97%)	91 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	107/121 (88%)	107 (100%)	0	100	100
49	SA	174/242 (72%)	171 (98%)	3 (2%)	53	82
50	SB	193/229 (84%)	192 (100%)	1 (0%)	81	93
51	SC	181/224 (81%)	178 (98%)	3 (2%)	53	82
52	SD	186/202 (92%)	186 (100%)	0	100	100
53	SE	221/225 (98%)	218 (99%)	3 (1%)	59	85
54	SF	152/170 (89%)	145 (95%)	7 (5%)	24	57
55	SG	178/218 (82%)	176 (99%)	2 (1%)	65	88
56	SH	159/174 (91%)	157 (99%)	2 (1%)	61	86
57	SI	159/180 (88%)	157 (99%)	2 (1%)	61	86
58	SJ	130/168 (77%)	129 (99%)	1 (1%)	73	90
59	SK	80/136 (59%)	79 (99%)	1 (1%)	61	86
60	SL	123/142 (87%)	122 (99%)	1 (1%)	73	90
61	SN	130/131 (99%)	128 (98%)	2 (2%)	57	84
62	SO	104/119 (87%)	103 (99%)	1 (1%)	68	89
63	SP	105/130 (81%)	103 (98%)	2 (2%)	50	79
64	SQ	115/121 (95%)	113 (98%)	2 (2%)	53	82
65	SR	119/121 (98%)	116 (98%)	3 (2%)	42	74
66	SS	122/132 (92%)	118 (97%)	4 (3%)	33	67
67	ST	110/115 (96%)	110 (100%)	0	100	100
68	SU	91/107 (85%)	87 (96%)	4 (4%)	25	59
69	SV	67/67 (100%)	65 (97%)	2 (3%)	36	70
70	SW	112/113 (99%)	110 (98%)	2 (2%)	51	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	SX	111/115 (96%)	109 (98%)	2 (2%)	51	80
72	SY	104/115 (90%)	103 (99%)	1 (1%)	68	89
73	SZ	64/103 (62%)	62 (97%)	2 (3%)	35	69
74	Sa	87/99 (88%)	83 (95%)	4 (5%)	24	57
75	Sb	75/76 (99%)	75 (100%)	0	100	100
76	Sc	47/62 (76%)	47 (100%)	0	100	100
77	Sd	47/49 (96%)	46 (98%)	1 (2%)	47	77
78	Se	37/106 (35%)	37 (100%)	0	100	100
79	Sg	250/275 (91%)	247 (99%)	3 (1%)	63	86
80	LB	344/348 (99%)	344 (100%)	0	100	100
All	All	9332/10620 (88%)	9238 (99%)	94 (1%)	65	89

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	SK	21	MET
66	SS	47	LYS
61	SN	105	ASN
64	SQ	114	GLN
68	SU	39	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
53	SE	50	ASN
56	SH	186	ASN
53	SE	142	HIS
55	SG	177	GLN
60	SL	100	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	9/10 (90%)	9 (100%)	1 (11%)
2	L5	3424/4731 (72%)	445 (12%)	7 (0%)
3	L7	119/120 (99%)	6 (5%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	L8	155/158 (98%)	22 (14%)	0
46	S2	1637/1870 (87%)	246 (15%)	3 (0%)
47	S6	74/75 (98%)	15 (20%)	2 (2%)
48	S7	73/75 (97%)	21 (28%)	0
All	All	5491/7039 (78%)	764 (13%)	13 (0%)

5 of 764 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	-2	U
1	B	-1	U
1	B	0	U
1	B	1	U
1	B	2	U

5 of 13 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L5	4352	U
46	S2	546	A
47	S6	54	A
46	S2	1521	G
47	S6	22	G

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 331 ligands modelled in this entry, 331 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	L5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	L5	183:A	O3'	189:G	P	5.53

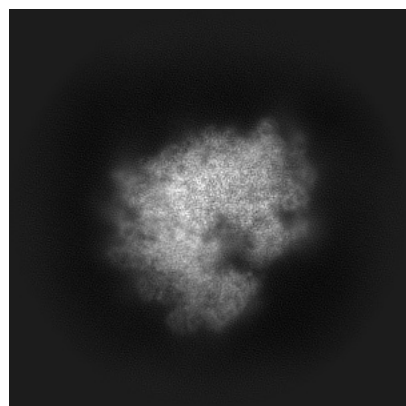
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55100. These allow visual inspection of the internal detail of the map and identification of artifacts.

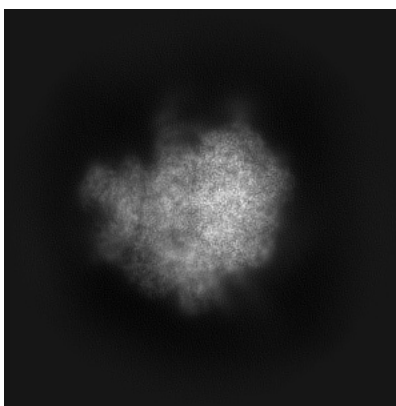
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

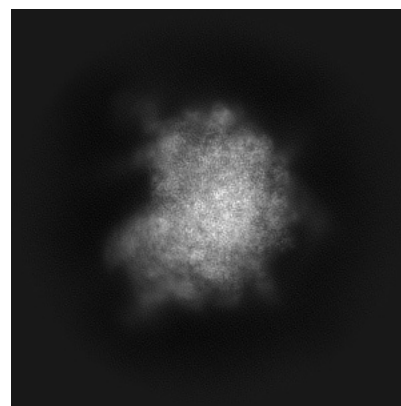
#### 6.1.1 Primary map



X

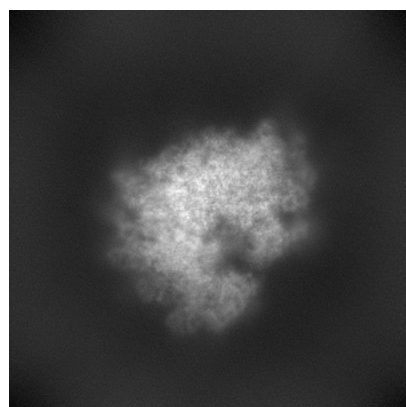


Y

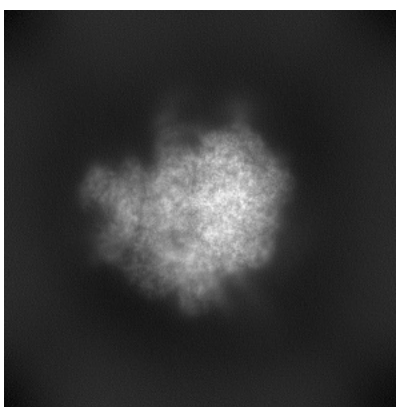


Z

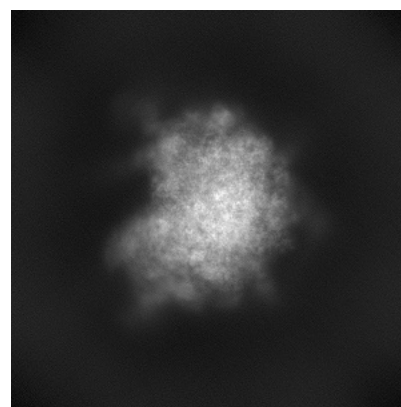
#### 6.1.2 Raw map



X



Y

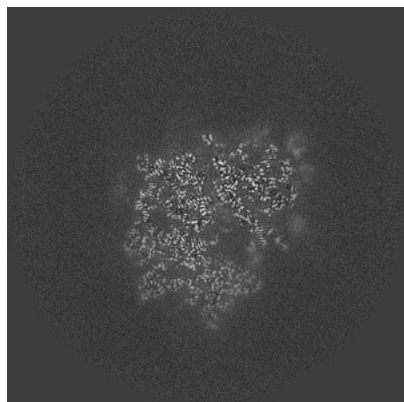


Z

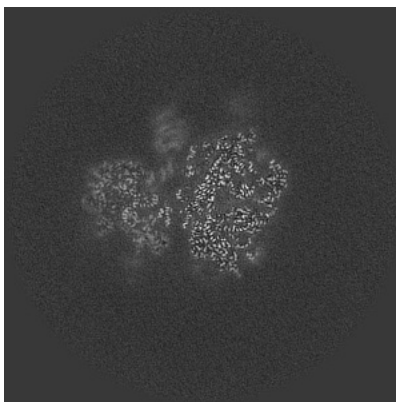
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

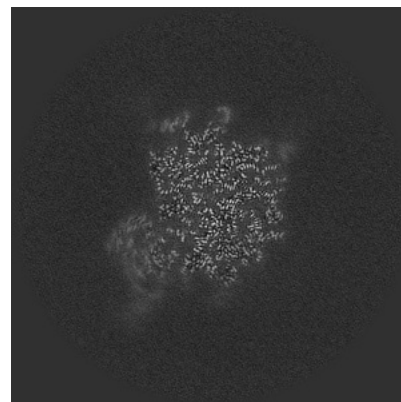
### 6.2.1 Primary map



X Index: 240

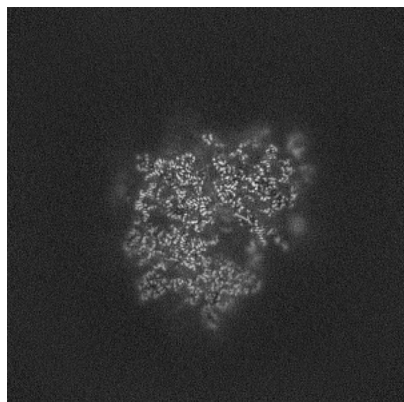


Y Index: 240

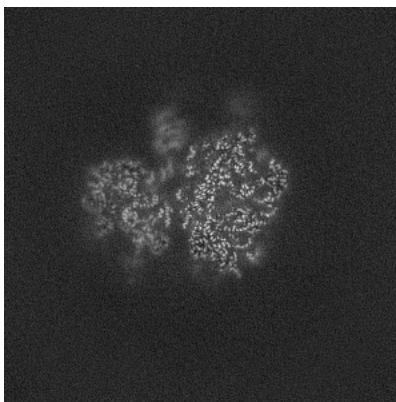


Z Index: 240

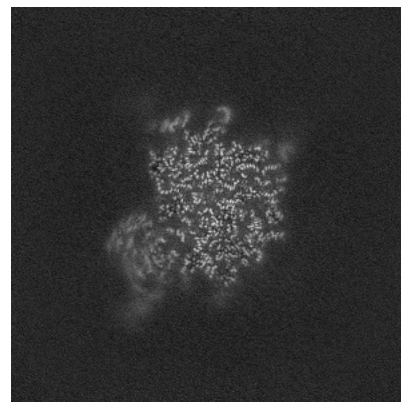
### 6.2.2 Raw map



X Index: 240



Y Index: 240



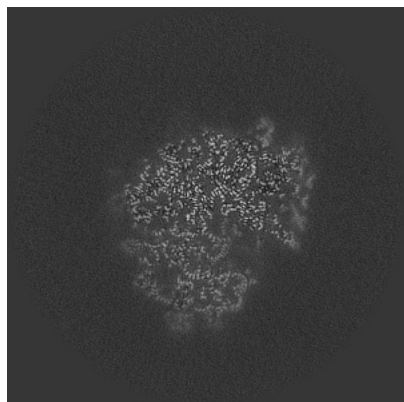
Z Index: 240

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

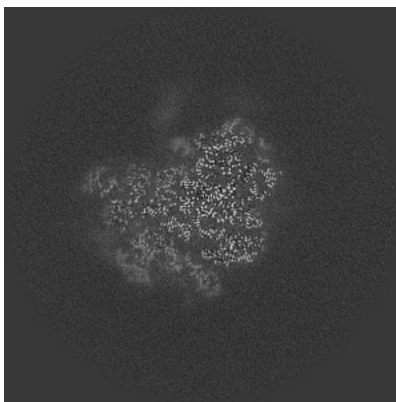


## 6.3 Largest variance slices [i](#)

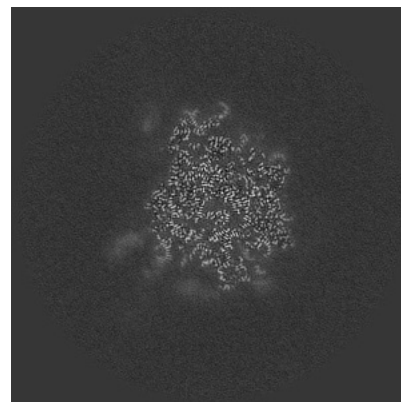
### 6.3.1 Primary map



X Index: 253

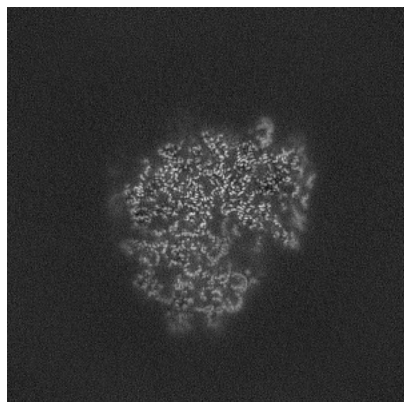


Y Index: 226

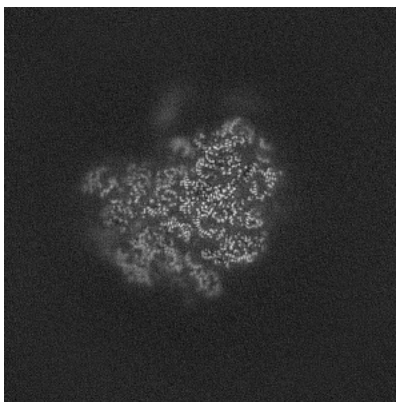


Z Index: 263

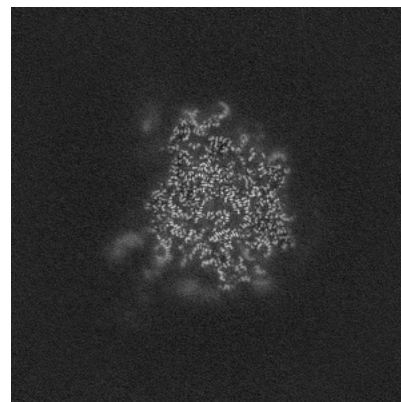
### 6.3.2 Raw map



X Index: 252



Y Index: 226

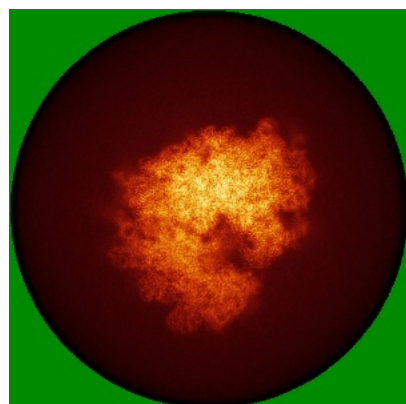


Z Index: 263

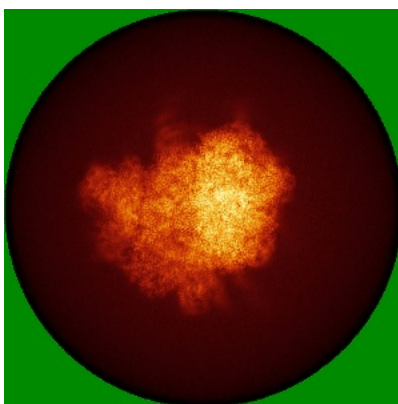
The images above show the largest variance slices of the map in three orthogonal directions.

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

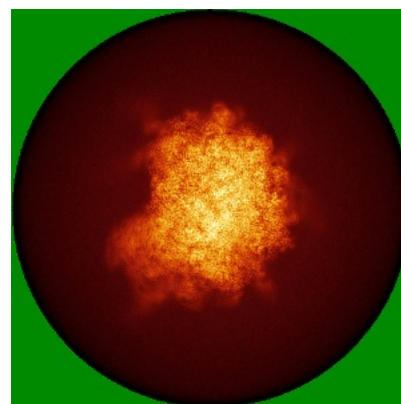
### 6.4.1 Primary map



X

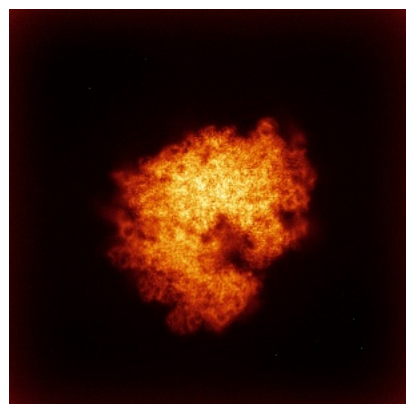


Y

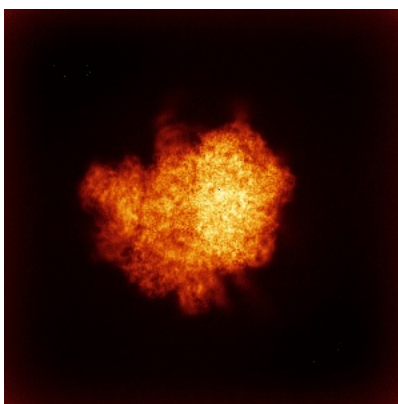


Z

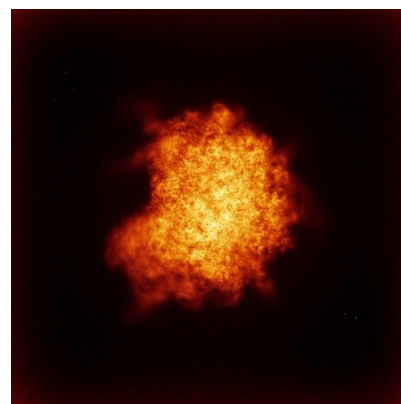
### 6.4.2 Raw map



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.

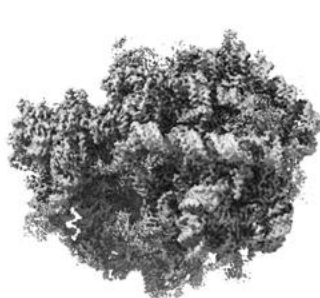


## 6.5 Orthogonal surface views [i](#)

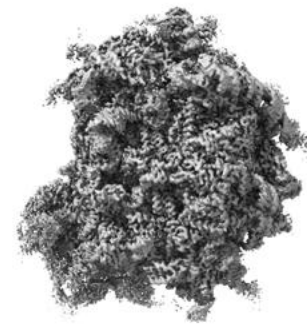
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.584. 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



X



Y



Z

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.

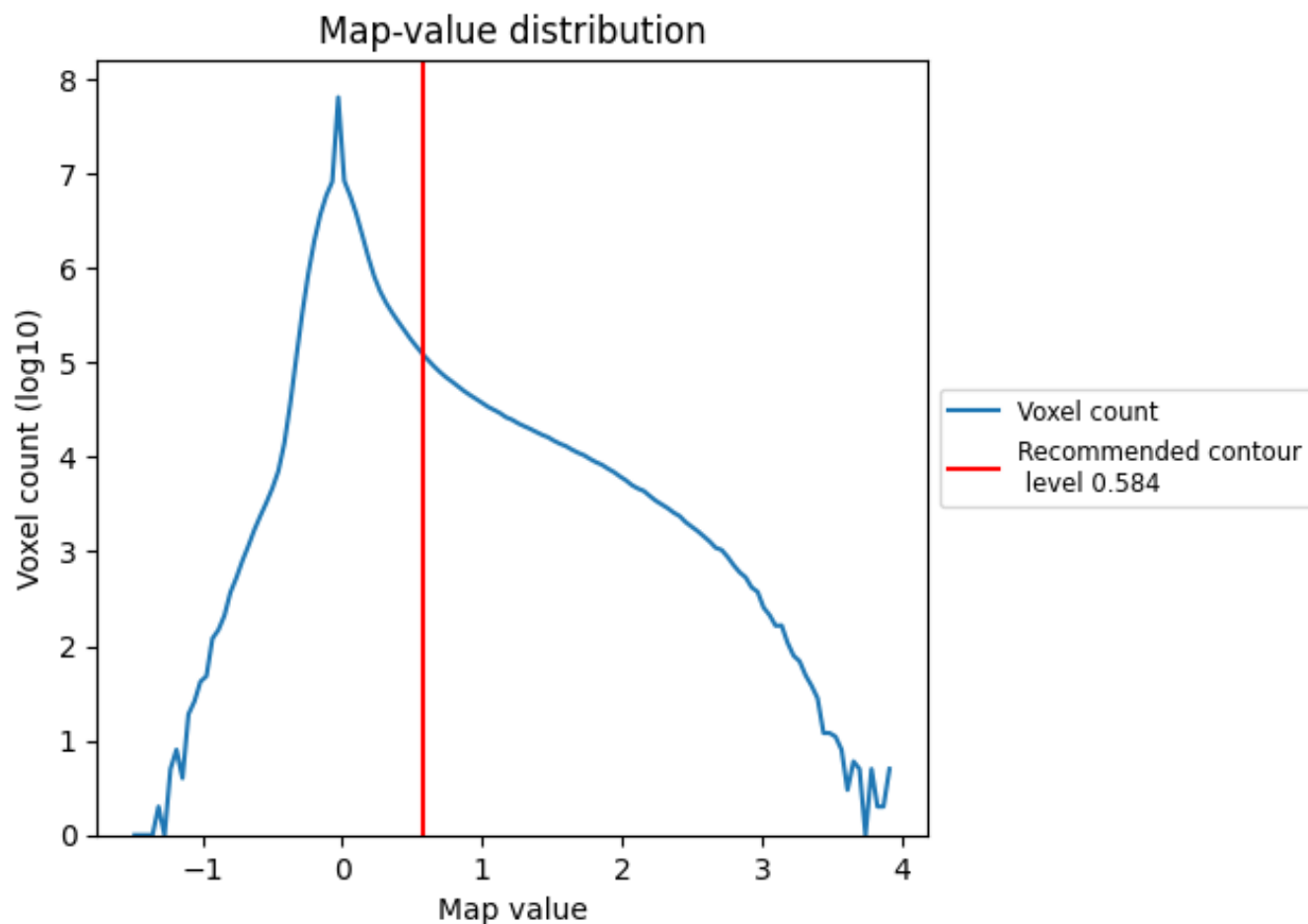
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

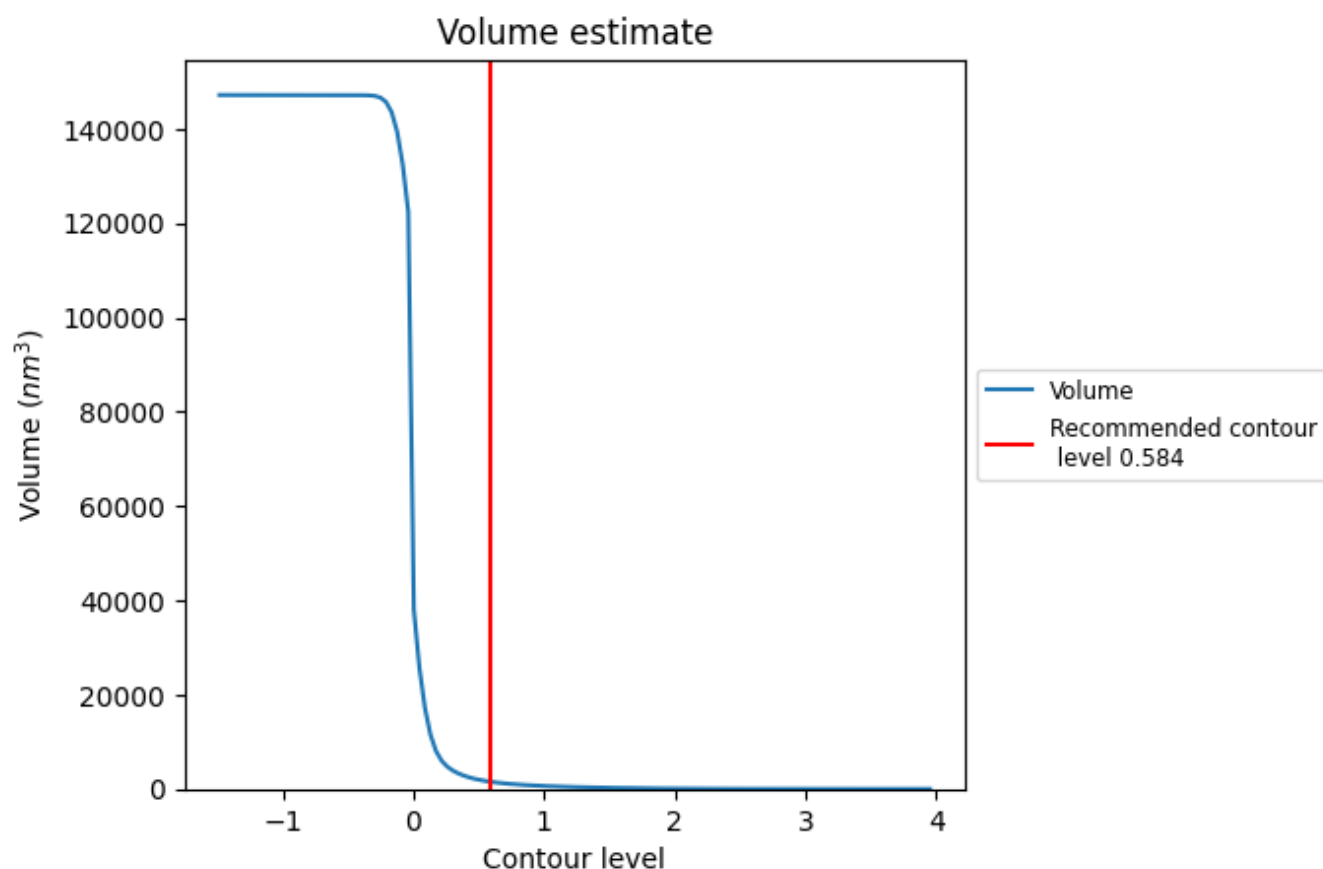
This section contains the results of statistical analysis of the map.

### 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.

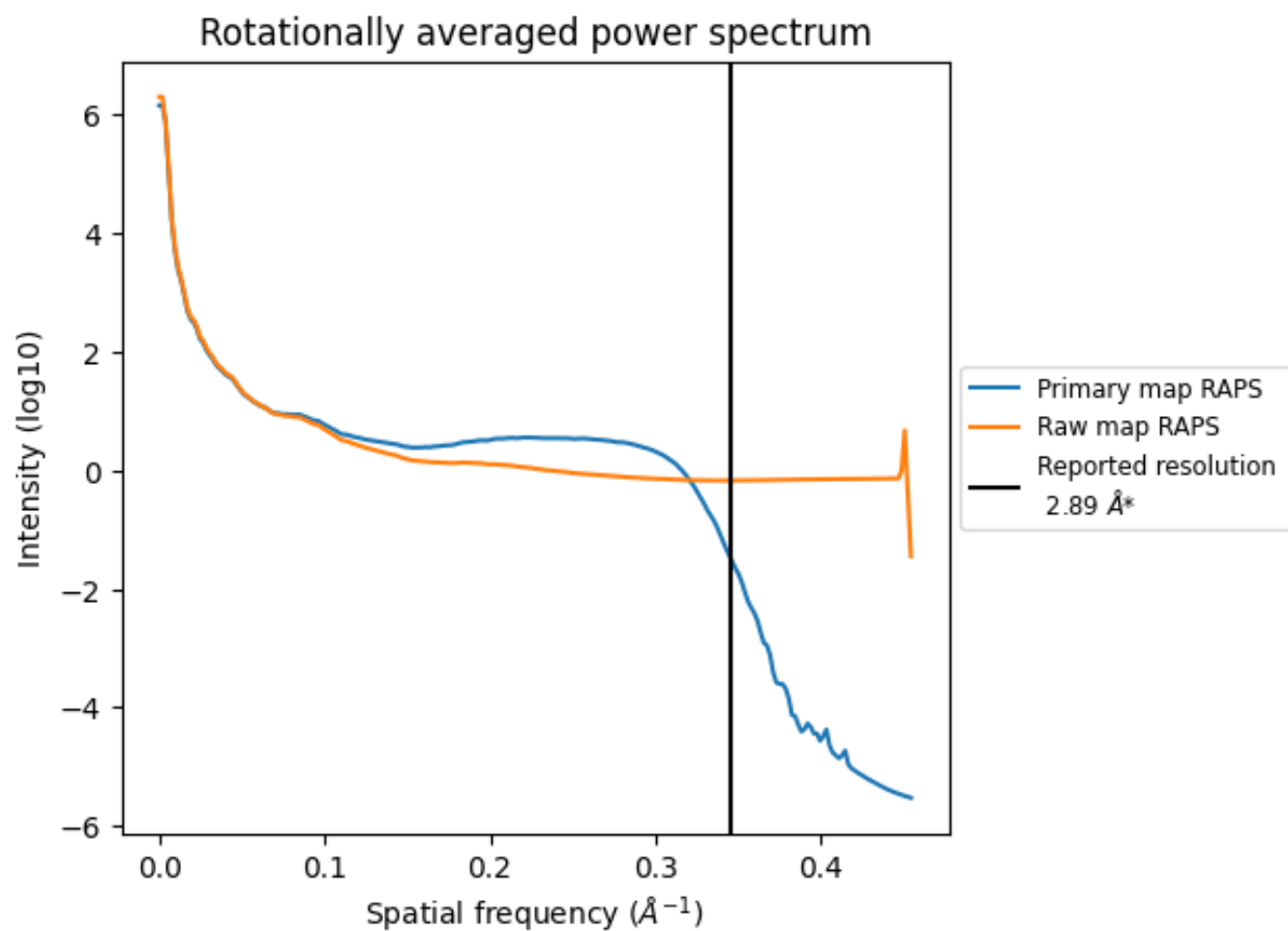
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1551  $\text{nm}^3$ ; this corresponds to an approximate mass of 1401 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 ⓘ

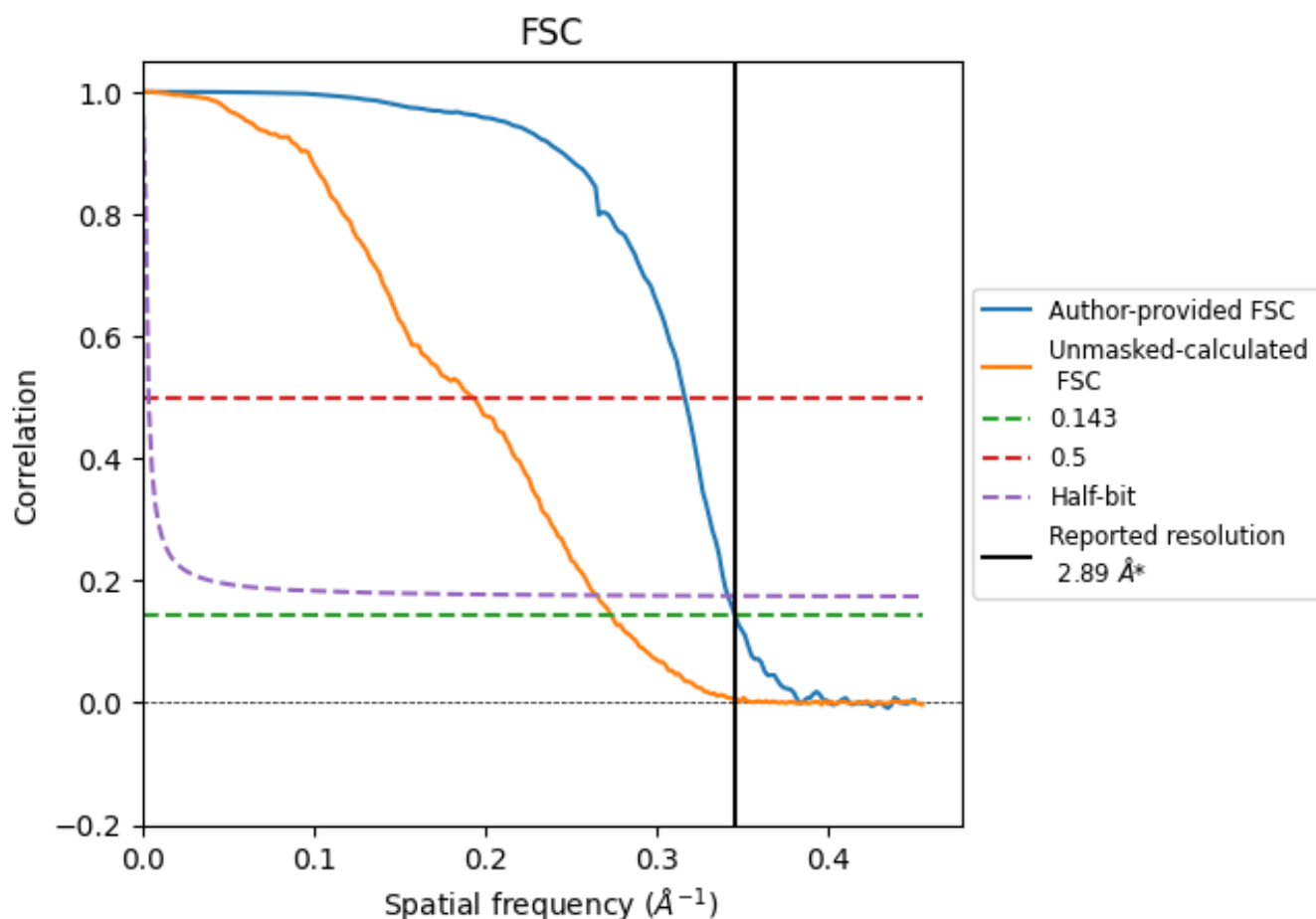


\*Reported resolution corresponds to spatial frequency of 0.346  $\text{\AA}^{-1}$

## 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 0.346  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

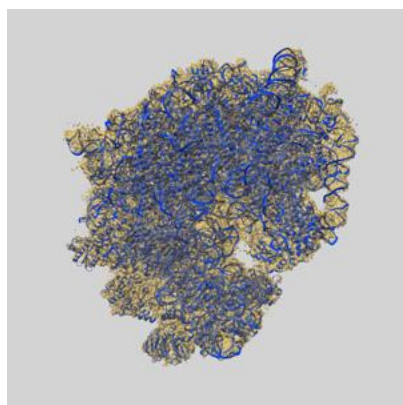
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	2.89	3.16	2.93
Unmasked-calculated*	3.66	5.19	3.78

\*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 3.66 differs from the reported value 2.89 by more than 10 %

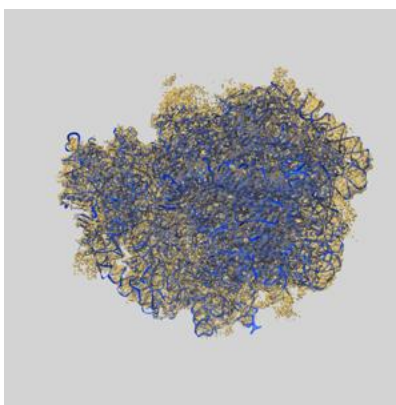
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55100 and PDB model 9T5C. Per-residue inclusion information can be found in section [3](#) on page [21](#).

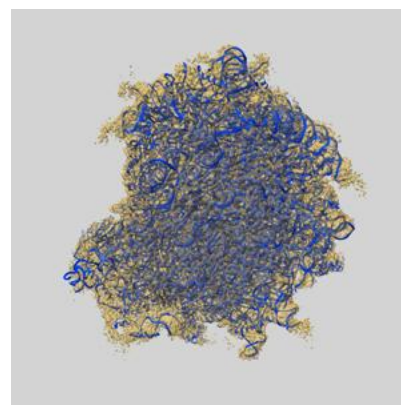
### 9.1 Map-model overlay [i](#)



X



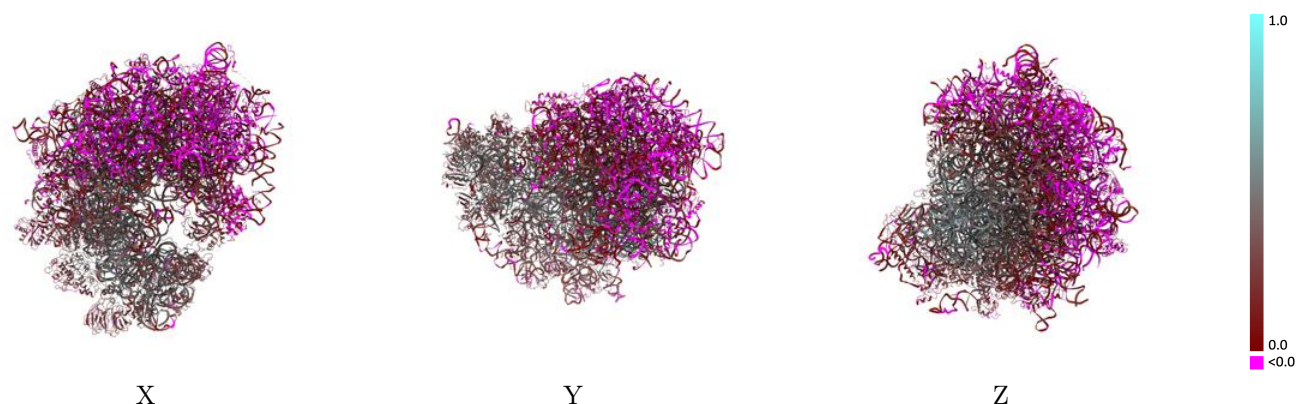
Y



Z

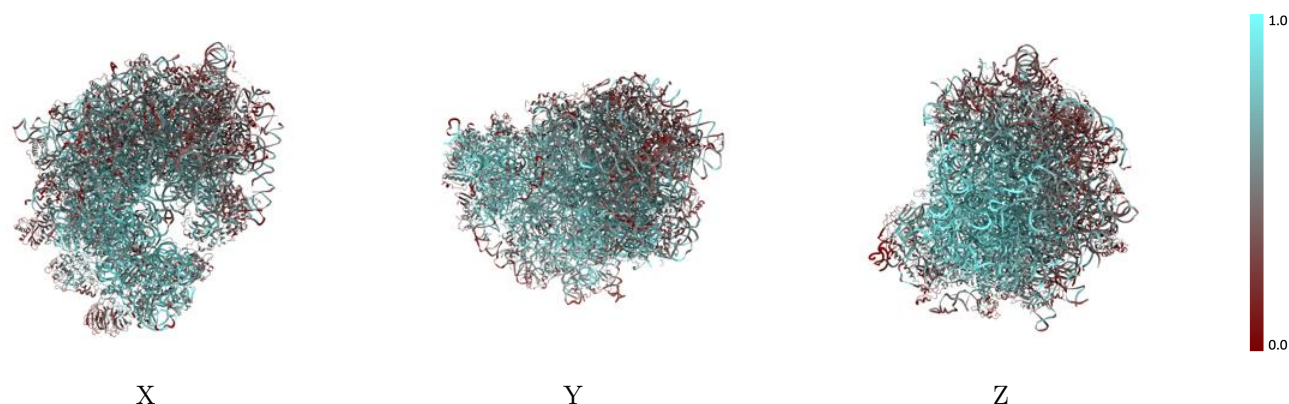
The images above show the 3D surface view of the map at the recommended contour level 0.584 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



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

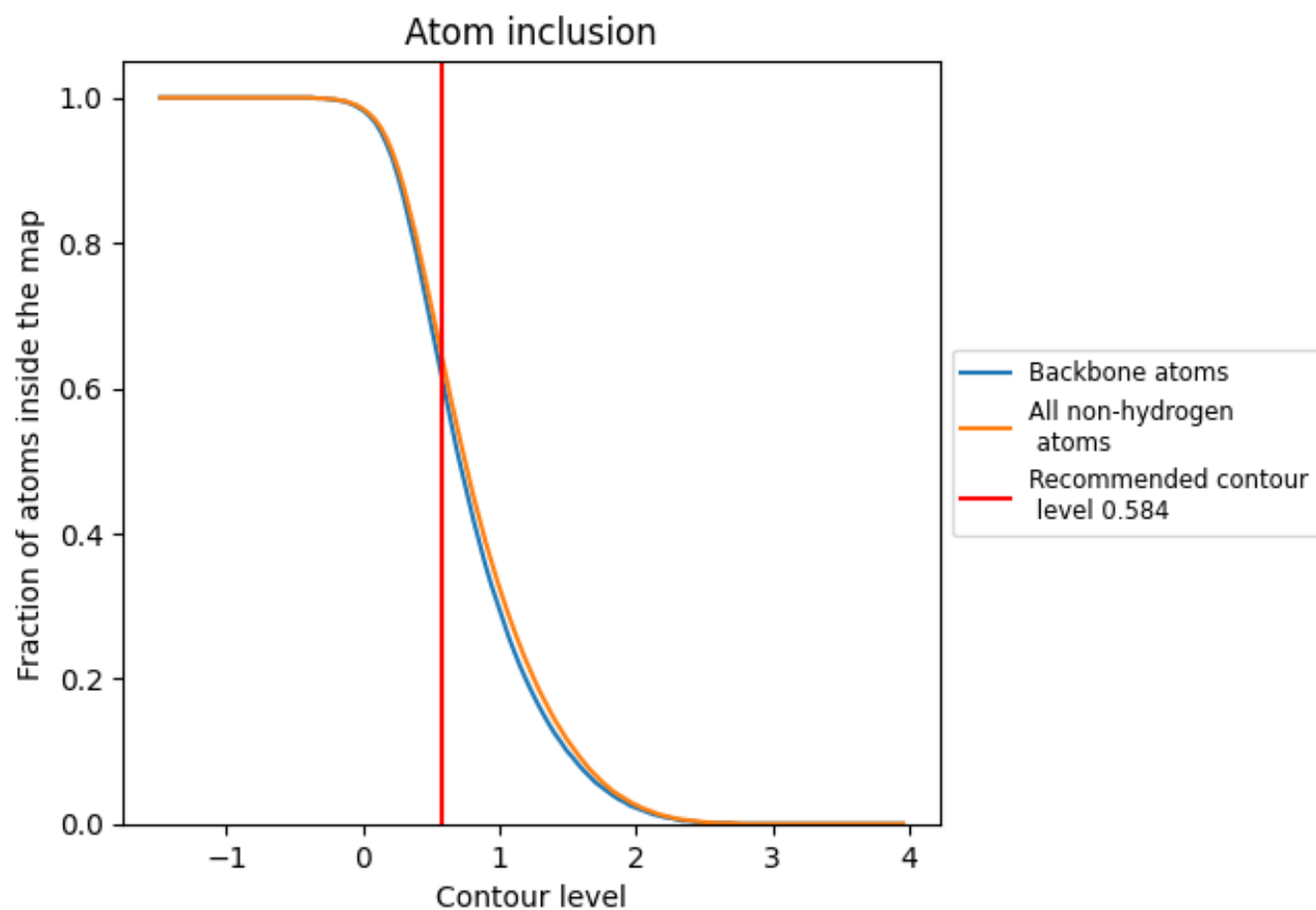
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.584).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.584) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6390	 0.2330
B	 0.2780	 0.0640
L5	 0.6960	 0.2130
L7	 0.6450	 0.1350
L8	 0.6200	 0.0880
LA	 0.6660	 0.2500
LB	 0.7980	 0.4400
LC	 0.3830	 -0.0020
LD	 0.3850	 0.0500
LE	 0.3230	 -0.0180
LF	 0.4260	 0.0220
LG	 0.3310	 -0.0220
LH	 0.5330	 0.1820
LI	 0.6320	 0.2520
LJ	 0.5590	 0.2390
LL	 0.3390	 -0.0130
LM	 0.3590	 -0.0150
LN	 0.4580	 0.0300
LO	 0.6360	 0.2190
LP	 0.8040	 0.3880
LQ	 0.4100	 0.0140
LR	 0.7190	 0.3630
LS	 0.4490	 0.0480
LT	 0.4620	 0.0840
LU	 0.6530	 0.3600
LV	 0.8430	 0.4900
LW	 0.8380	 0.4880
LX	 0.5680	 0.1680
LY	 0.4480	 0.0770
LZ	 0.4240	 0.0740
La	 0.4460	 0.0490
Lb	 0.3130	 0.0330
Lc	 0.5290	 0.1600
Ld	 0.8230	 0.5030
Le	 0.5300	 0.1090











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Chain	Atom inclusion	Q-score
Lf	 0.5300	 0.1280
Lg	 0.6510	 0.2230
Lh	 0.4500	 0.0600
Li	 0.3350	 -0.0070
Lj	 0.6500	 0.1880
Lk	 0.5070	 0.1800
Ll	 0.7260	 0.2870
Lm	 0.6780	 0.2640
Ln	 0.8940	 0.5200
Lo	 0.5530	 0.1750
Lp	 0.7000	 0.2860
Lr	 0.3520	 -0.0170
S2	 0.8020	 0.3560
S6	 0.6990	 0.2430
S7	 0.6030	 0.2580
SA	 0.5920	 0.3160
SB	 0.5360	 0.2580
SC	 0.6860	 0.3810
SD	 0.5610	 0.3620
SE	 0.3300	 0.1330
SF	 0.5910	 0.3310
SG	 0.4620	 0.2570
SH	 0.3440	 0.1710
SI	 0.5490	 0.2410
SJ	 0.4270	 0.1620
SK	 0.4900	 0.3070
SL	 0.5760	 0.2580
SN	 0.5800	 0.2530
SO	 0.6610	 0.3400
SP	 0.5550	 0.3200
SQ	 0.6550	 0.3780
SR	 0.4910	 0.3010
SS	 0.5670	 0.3090
ST	 0.6290	 0.3610
SU	 0.5930	 0.4010
SV	 0.5200	 0.3010
SW	 0.6310	 0.3110
SX	 0.7070	 0.3920
SY	 0.3220	 0.1640
SZ	 0.4120	 0.2720
Sa	 0.7520	 0.4110
Sb	 0.4180	 0.1970

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Chain	Atom inclusion	Q-score
Sc	 0.5750	 0.3450
Sd	 0.7450	 0.4380
Se	 0.4200	 0.2160
Sg	 0.3820	 0.2780