



# wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 05:46 PM UTC

PDB ID : 9AXT / pdb\_00009axt  
EMDB ID : EMD-43972  
Title : Non-translating *S. pombe* ribosome  
Authors : Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.  
Deposited on : 2024-03-06  
Resolution : 2.40 Å (reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

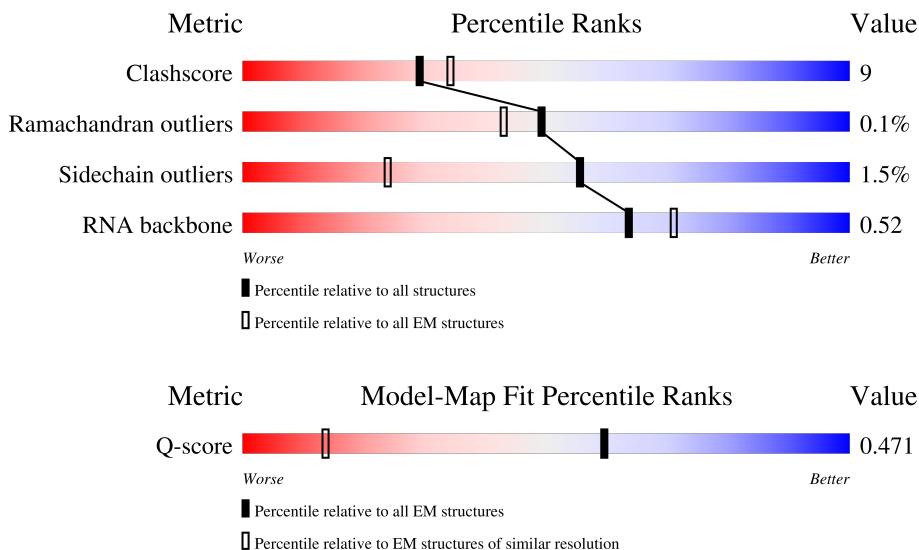
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 2.40 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	5628 ( 1.90 - 2.90 )

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	AA	1842	
2	AD	292	
3	AE	252	

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Mol	Chain	Length	Quality of chain
4	AF	253	24% 66% 18% 15%
5	AG	249	87% 61% 26% 13%
6	AH	262	24% 65% 33%
7	AI	203	99% 70% 30%
8	AJ	239	90% 67% 25% 8%
9	AK	195	79% 75% 23%
10	AL	200	46% 70% 24% 6%
11	AM	192	49% 65% 28% 7%
12	AN	147	63% 46% 16% 37%
13	AO	152	27% 70% 24% 6%
14	AP	145	83% 70% 12% 17%
15	AQ	151	44% 75% 23%
16	AR	139	53% 64% 27% 8%
17	AS	154	77% 44% 32% 23%
18	AT	140	99% 74% 26%
19	AU	131	87% 63% 26% 10%
20	AV	152	93% 64% 29% 7%
21	AW	144	99% 69% 29%
22	Aa	118	85% 64% 21% 14%
23	Ab	87	32% 77% 21%
24	Ac	130	80% 19%
25	Ad	143	82% 73% 25%
26	Ae	134	82% 72% 28%
27	Af	89	78% 61% 15% 22%
28	Ag	119	27% 60% 21% 18%

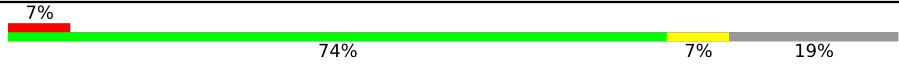

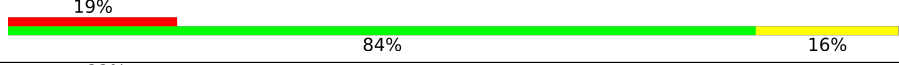

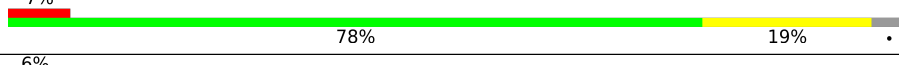

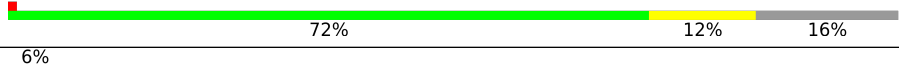

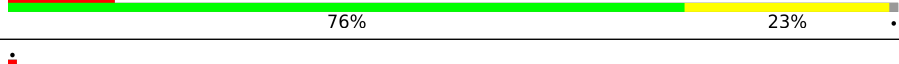


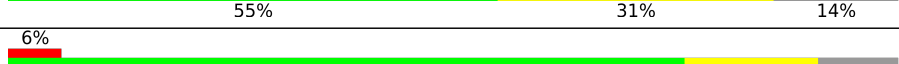
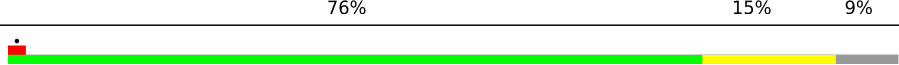
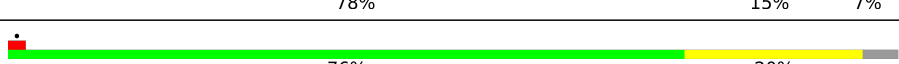

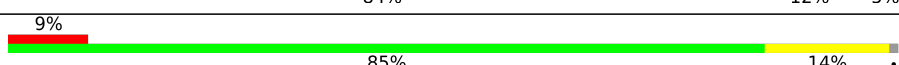
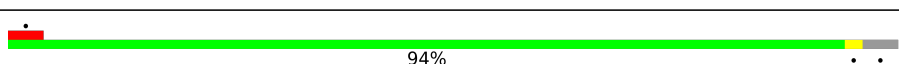
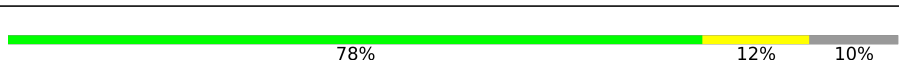
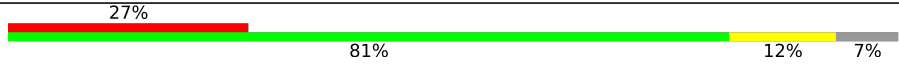



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Mol	Chain	Length	Quality of chain
29	Ah	83	67% 75% 22% ..
30	Ai	68	88% 59% 31% 7%
31	Aj	56	93% 70% 25% 5%
32	Ak	61	98% 72% 26%
33	B0	106	8% 67% 21% 12%
34	B1	94	19% 73% 24% ..
35	B2	3498	16% 46% 38% 8% 8%
36	B3	246	26% 17% 52%
37	B4	165	7% 49% 39% 7% 5%
38	BN	253	81% 17%
39	BO	388	80% 19%
40	BP	363	89% 11%
41	BQ	294	20% 78% 19%
42	BR	195	15% 67% 16% 17%
43	BS	251	9% 75% 18% 7%
44	BT	259	15% 77% 12% 12%
45	BU	189	87% 63% 25% 11%
46	BV	221	79% 63% 23% 14%
47	BW	174	61% 70% 25% ..
48	BX	208	17% 85% 15%
49	BY	134	7% 72% 25%
50	BZ	201	78% 21%
51	Ba	197	88% 12%
52	Bb	187	72% 9% 19%
53	Bc	187	85% 14%

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Mol	Chain	Length	Quality of chain
54	Bd	193	
55	Be	176	
56	Bf	160	
57	Bg	117	
58	Bh	139	
59	Bi	149	
60	Bj	141	
61	Bk	126	
62	Bl	136	
63	Bm	148	
64	Bn	61	
65	Bo	109	
66	Bp	113	
67	Bq	127	
68	Br	108	
69	Bs	111	
70	Bt	122	
71	Bu	99	
72	Bv	91	
73	Bw	74	
74	Bx	51	
75	By	134	

## 2 Entry composition [i](#)

There are 76 unique types of molecules in this entry. The entry contains 194719 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1705	36359	16255	6470	11929	1705	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AD	205	1602	1016	294	287	5	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein eS1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AE	216	1733	1093	319	316	5	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AF	216	1660	1072	289	292	7	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AG	216	1701	1080	308	305	8	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein eS4C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AH	261	2083	1330	391	356	6	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AI	203	1559	972	291	290	6	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein eS6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AJ	221	1784	1123	352	302	7	0	0

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AK	193	1530	967	284	276	3	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein eS8B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AL	188	1506	936	303	264	3	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AM	178	1462	928	291	241	2	0	0

- Molecule 12 is a protein called Small ribosomal subunit protein eS10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AN	92	748	484	132	130	2	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AO	143	1164	743	222	196	3	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein eS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AP	121	Total	C	N	O	S	0	0
			884	549	151	177	7		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	150	Total	C	N	O	S	0	0
			1184	754	222	204	4		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AR	128	Total	C	N	O	S	0	0
			949	587	184	174	4		

- Molecule 17 is a protein called Small ribosomal subunit protein uS19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AS	119	Total	C	N	O	S	0	0
			954	608	179	163	4		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AT	140	Total	C	N	O	S	0	0
			1082	688	203	186	5		

- Molecule 19 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AU	118	Total	C	N	O	S	0	0
			972	606	185	179	2		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AV	141	Total	C	N	O	S	0	0
			1144	714	222	204	4		

- Molecule 21 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AW	142	1119	699	212	205	3	0	0

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Aa	101	815	511	156	146	2	0	0

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Ab	87	672	411	122	135	4	0	0

- Molecule 24 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Ac	129	1028	649	196	179	4	0	0

- Molecule 25 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Ad	142	1095	692	214	187	2	0	0

- Molecule 26 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Ae	133	1078	672	217	185	4	0	0

- Molecule 27 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Af	69	551	350	103	97	1	0	0

- Molecule 28 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ag	97	Total	C	N	O	S	0	0
			795	491	167	132	5		

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ah	81	Total	C	N	O	S	0	0
			619	388	114	108	9		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ai	63	Total	C	N	O	S	0	0
			498	308	99	90	1		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Aj	53	Total	C	N	O	S	0	0
			447	282	91	73	1		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ak	60	Total	C	N	O	S	0	0
			475	296	99	78	2		

- Molecule 33 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B0	93	Total	C	N	O	S	0	0
			758	479	152	122	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	93	Total	C	N	O	S	0	0
			718	442	147	123	6		

- Molecule 35 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	B2	3212	68676	30687	12377	22400	3212	0	0

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	B3	119	2539	1133	454	833	119	0	0

- Molecule 37 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	B4	157	3332	1491	583	1101	157	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	BN	248	1872	1166	377	324	5	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	BO	384	3050	1929	576	535	10	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BP	362	2799	1768	538	490	3	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	BQ	287	2312	1461	410	437	4	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BR	162	1251	802	231	215	3	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	BS	233	1897	1211	349	334	3	0	0

- Molecule 44 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BT	229	1772	1135	325	309	3	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	BU	168	1319	828	244	242	5	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	BV	191	1549	982	291	270	6	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	BW	167	1346	854	252	235	5	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	BX	207	1654	1034	329	290	1	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	BY	130	1038	662	198	174	4	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BZ	200	1676	1050	348	275	3	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Ba	196	1545	991	294	256	4	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Bb	152	1212	770	229	210	3	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
53	Bc	186	1487	937	300	250	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Bd	157	1301	809	275	212	5	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	Be	173	1423	916	268	234	5	0	0

- Molecule 56 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Bf	159	1286	810	247	226	3	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	Bg	99	798	518	138	142		0	0

- Molecule 58 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	Bh	134	999	630	184	177	8	0	0

- Molecule 59 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	Bi	63	523	336	102	82	3	0	0

- Molecule 60 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	Bj	118	947	605	175	166	1	0	0

- Molecule 61 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	Bk	125	998	622	201	173	2	0	0

- Molecule 62 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	Bl	135	1078	698	200	178	2	0	0

- Molecule 63 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Bm	147	1171	740	235	194	2	0	0

- Molecule 64 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Bn	59	495	299	112	84		0	0

- Molecule 65 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Bo	94	705	450	121	130	4	0	0

- Molecule 66 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Bp	103	857	538	167	149	3	0	0

- Molecule 67 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Bq	118	944	591	191	157	5	0	0

- Molecule 68 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Br	104	831	531	160	137	3	0	0

- Molecule 69 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Bs	106	858	538	176	142	2	0	0

- Molecule 70 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	Bt	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 71 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bu	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 72 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bv	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 73 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bw	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 74 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bx	50	Total	C	N	O	S	0	0
			436	273	98	64	1		

- Molecule 75 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	By	134	Total	C	N	O	S	0	0
			1039	646	204	187	2		

- Molecule 76 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
76	Ag	1	Total	Zn	0
			1	1	
76	Ah	1	Total	Zn	0
			1	1	
76	Aj	1	Total	Zn	0
			1	1	

*Continued on next page...*

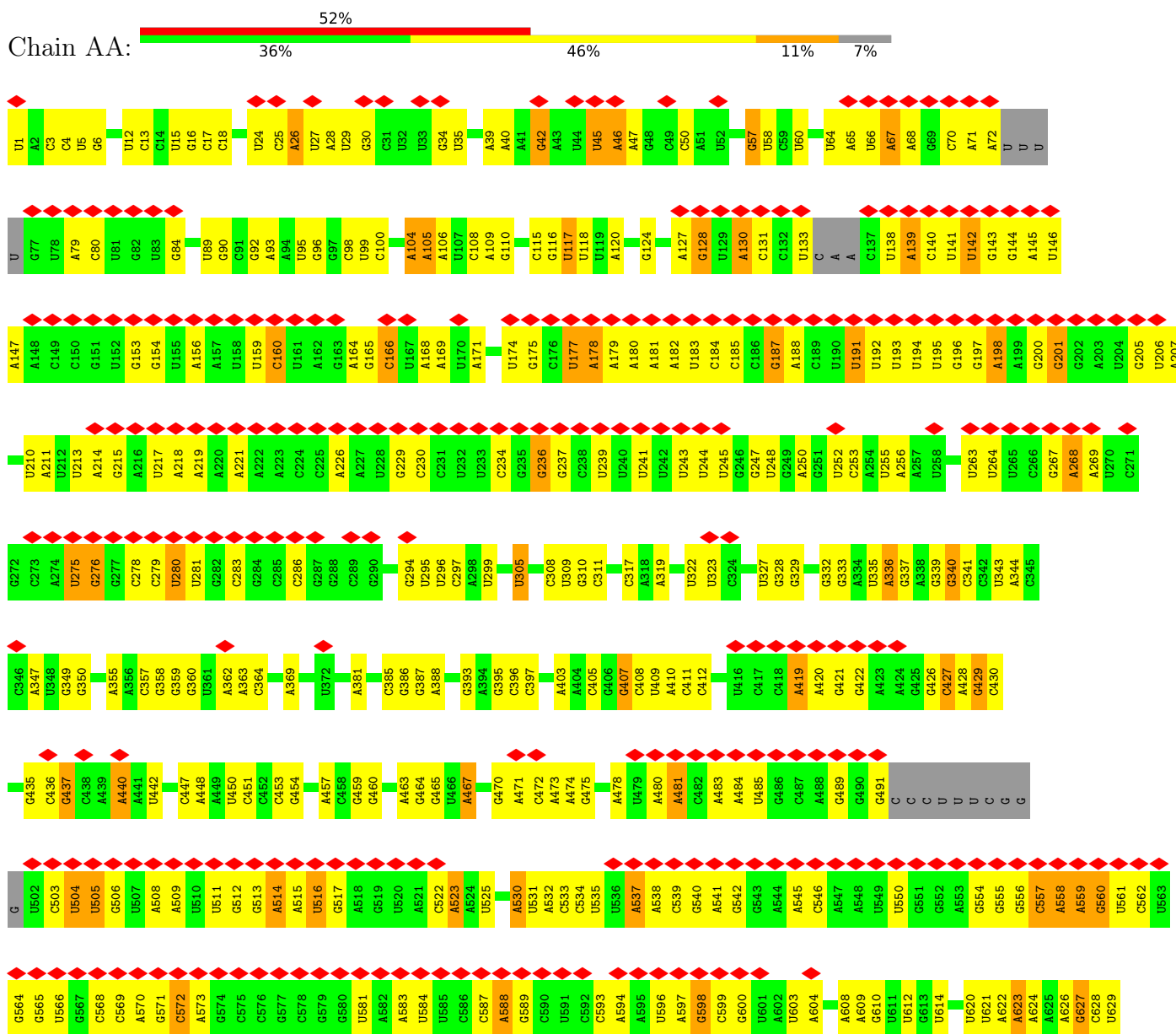
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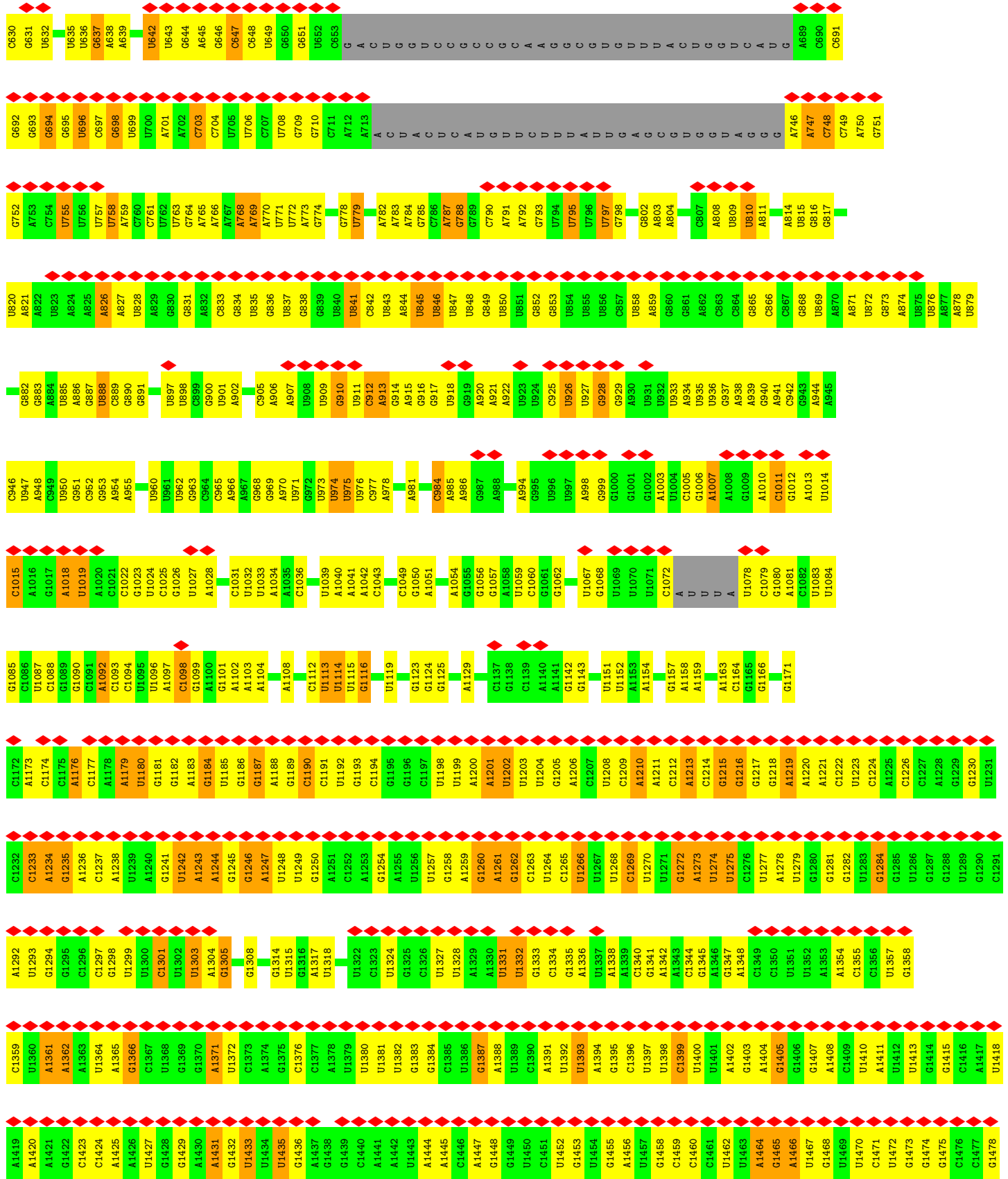
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76	B1	1	Total 1	Zn 1	0
76	Bv	1	Total 1	Zn 1	0

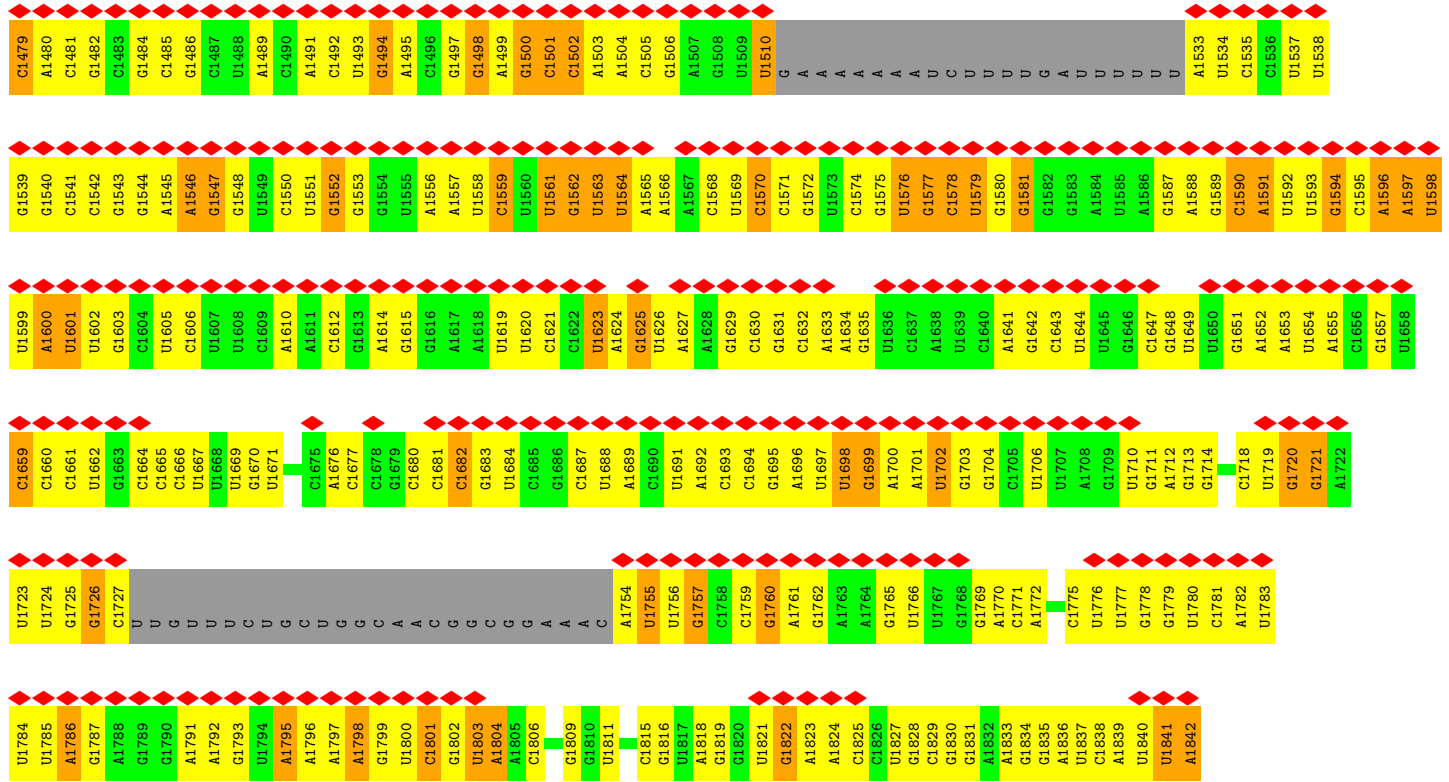
### 3 Residue-property plots

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

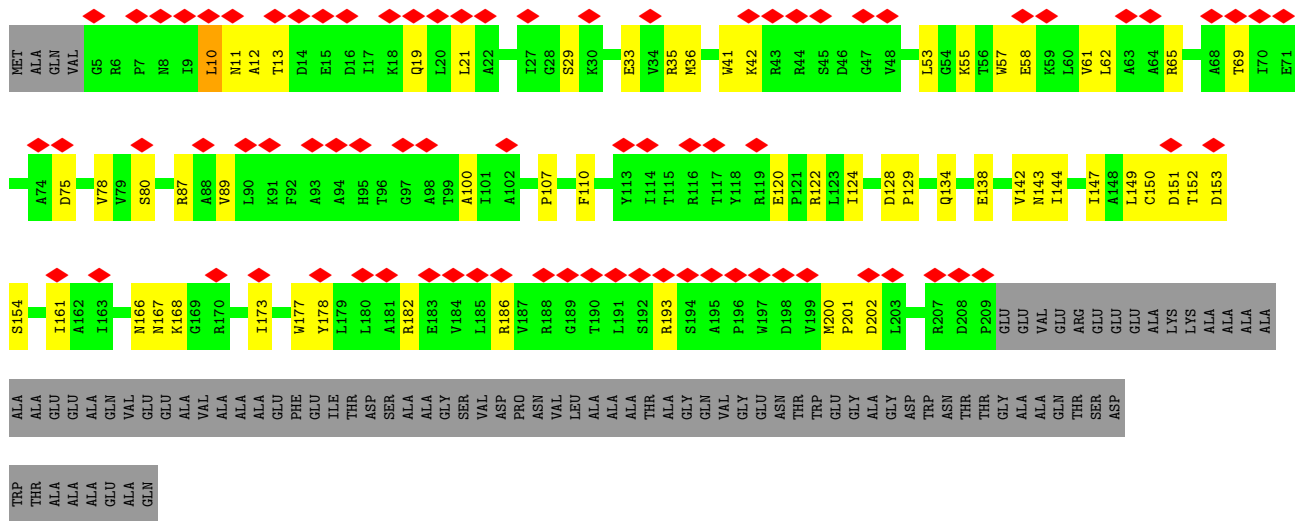
- Molecule 1: 18S ribosomal RNA





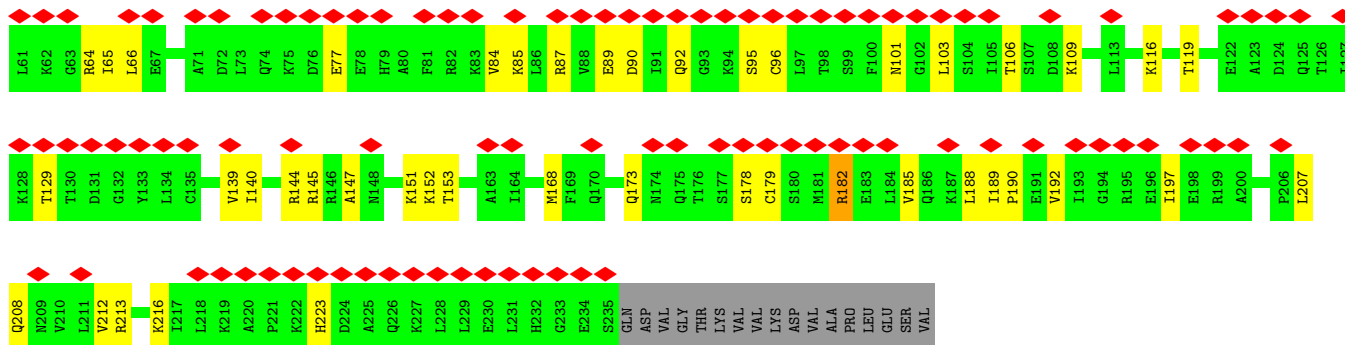


• Molecule 2: Small ribosomal subunit protein uS2A

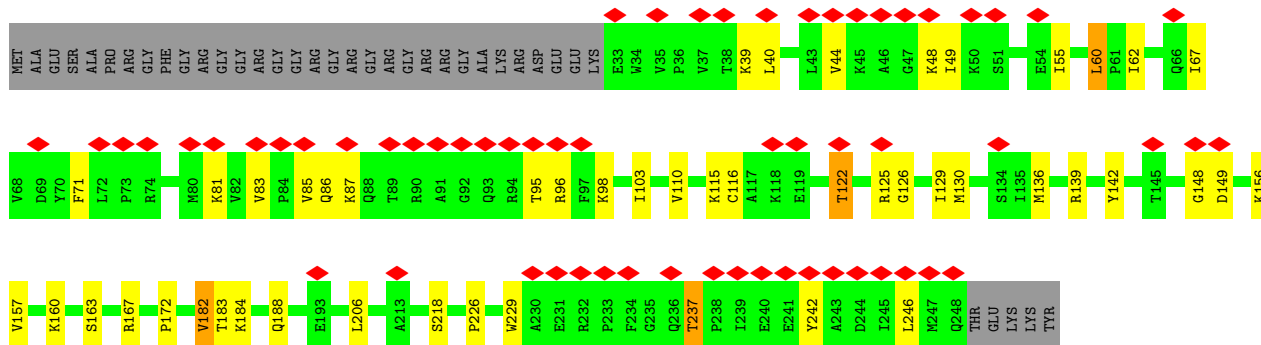


• Molecule 3: Small ribosomal subunit protein eS1B





• Molecule 4: Small ribosomal subunit protein uS5

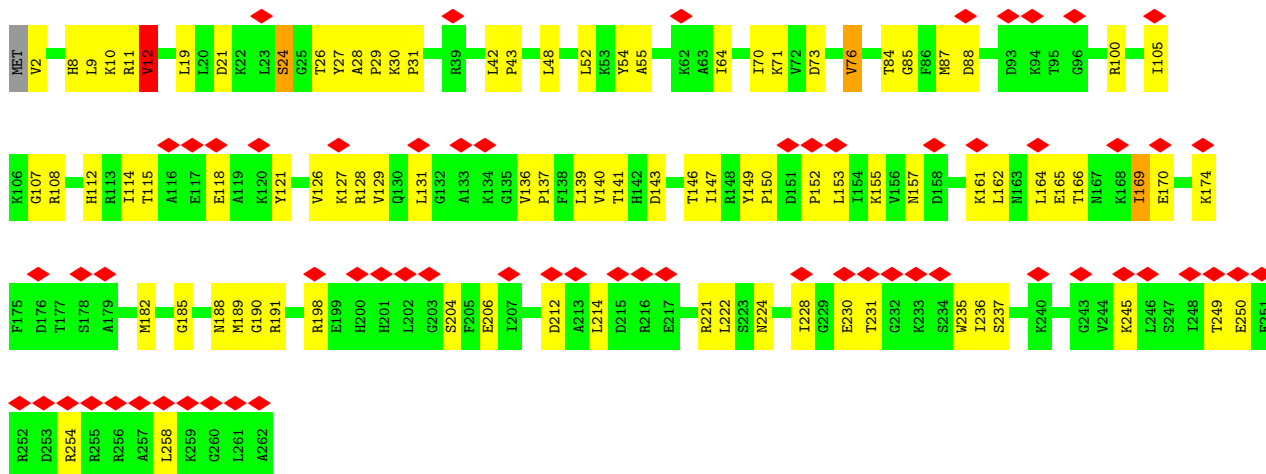


• Molecule 5: Small ribosomal subunit protein uS3

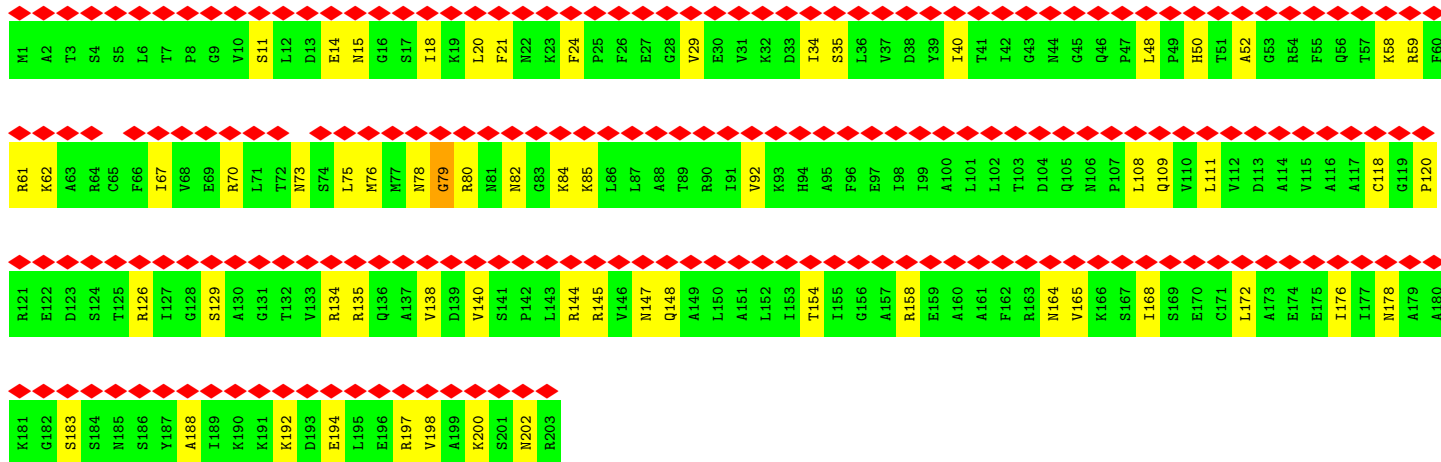


• Molecule 6: Small ribosomal subunit protein eS4C

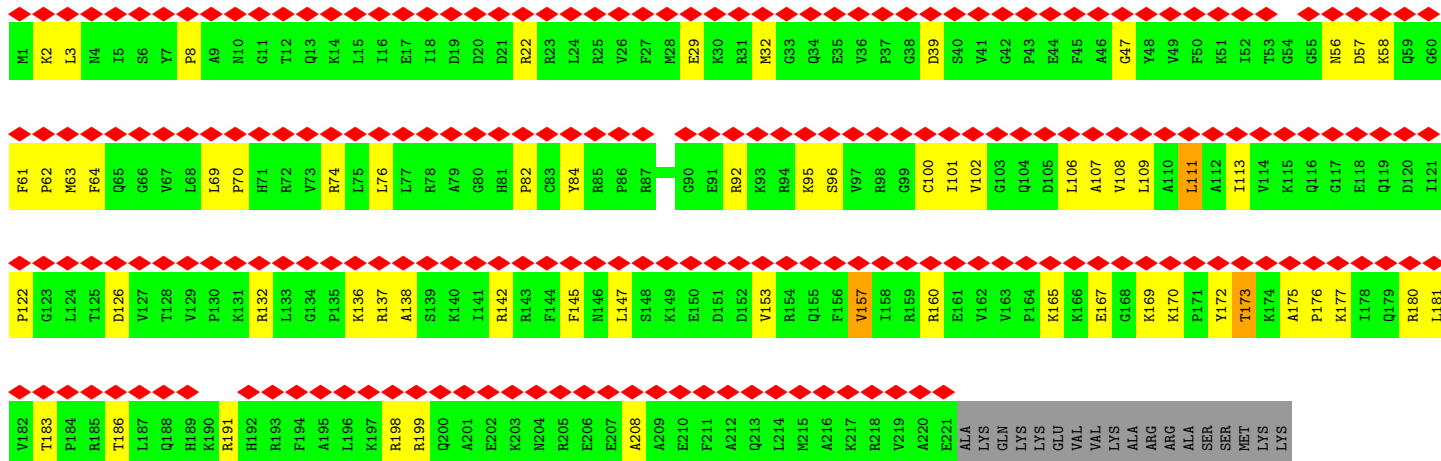
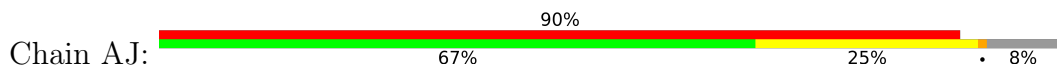




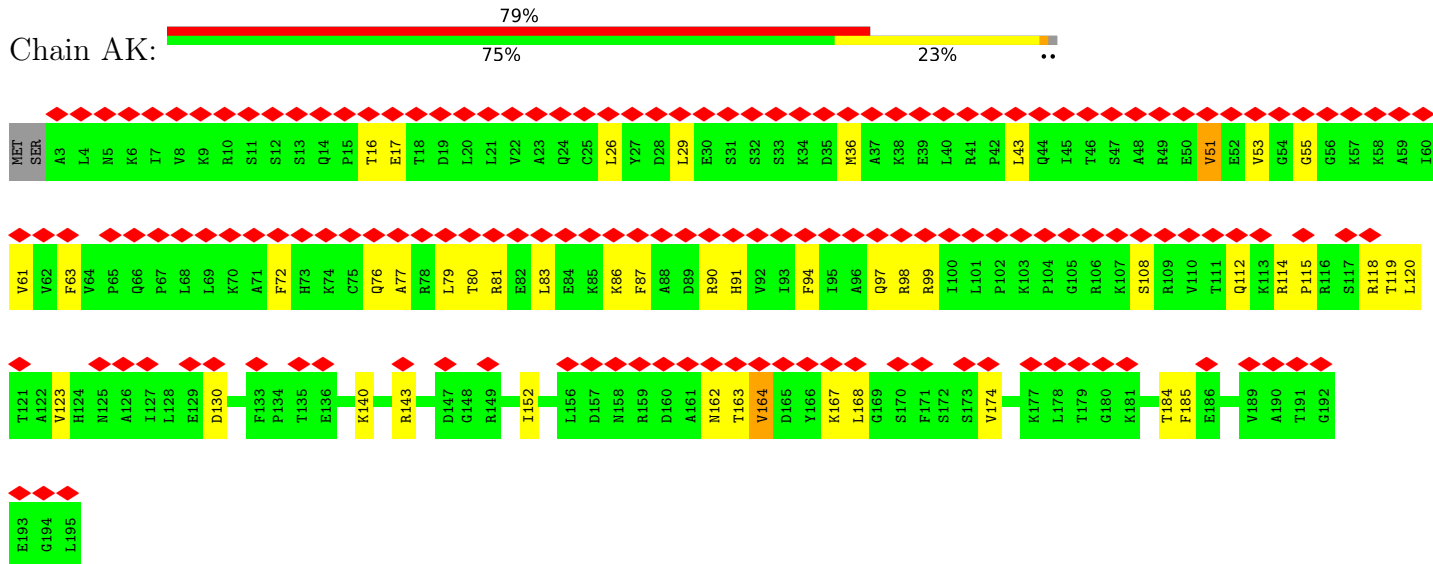
• Molecule 7: Small ribosomal subunit protein uS7A



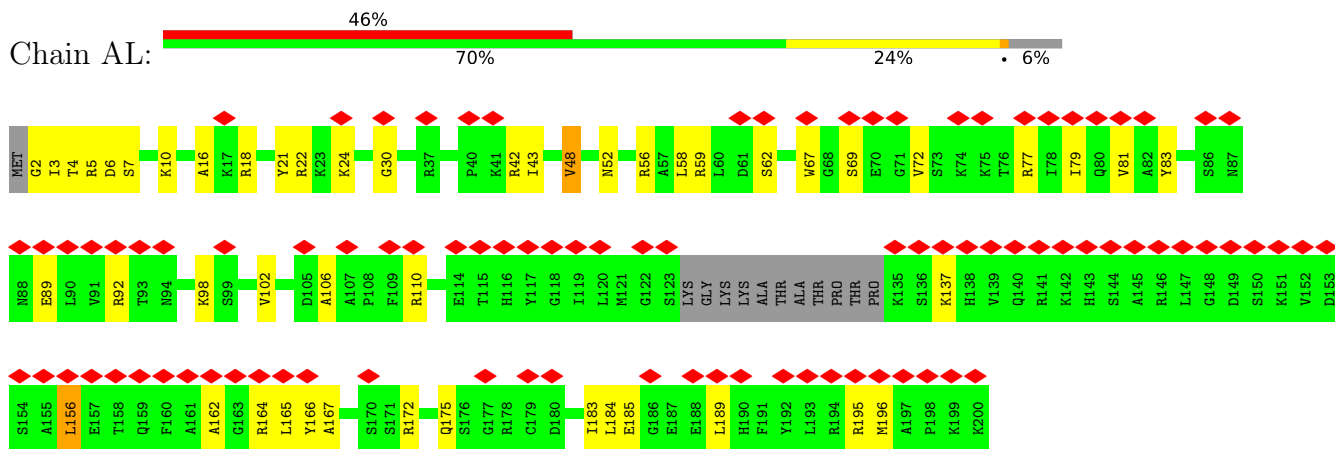
• Molecule 8: Small ribosomal subunit protein eS6B



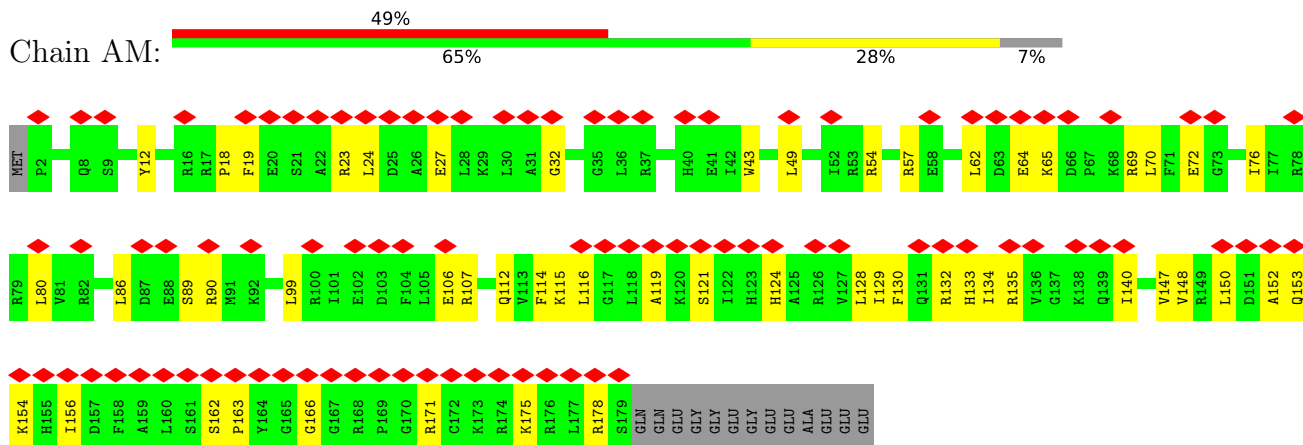
• Molecule 9: Small ribosomal subunit protein eS7



• Molecule 10: Small ribosomal subunit protein eS8B

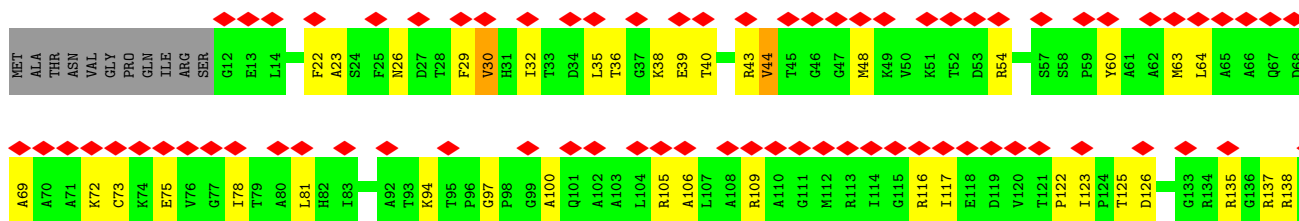


• Molecule 11: Small ribosomal subunit protein uS4B

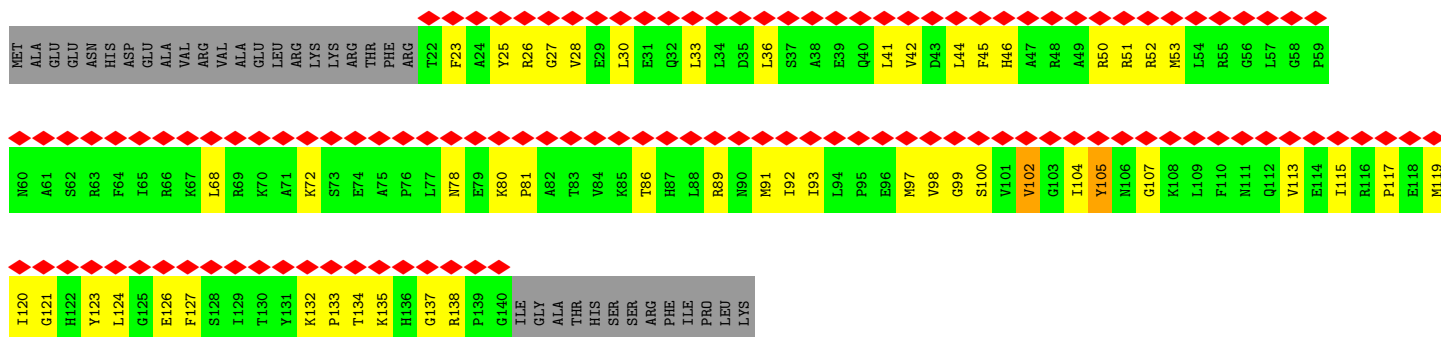
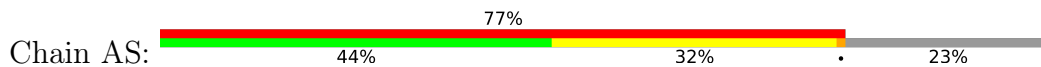


• Molecule 12: Small ribosomal subunit protein eS10B

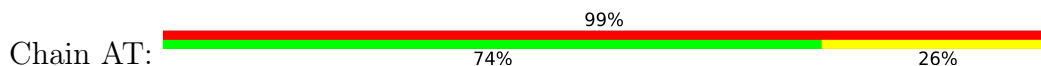




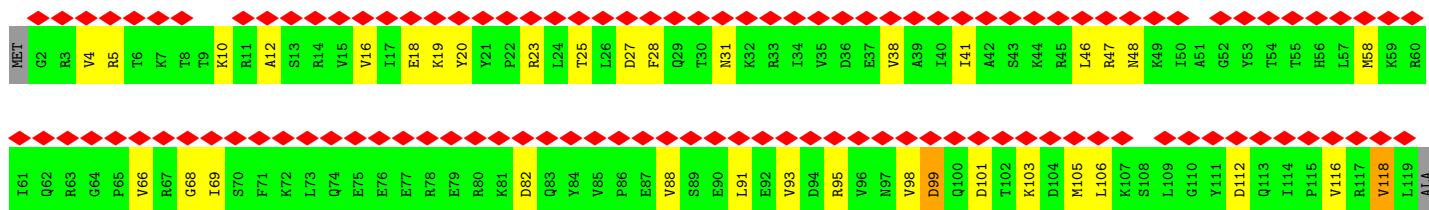
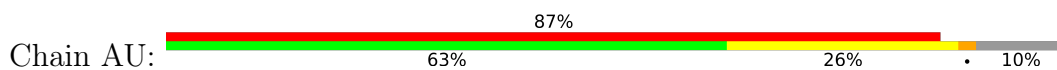
• Molecule 17: Small ribosomal subunit protein uS19B



• Molecule 18: Small ribosomal subunit protein uS9A

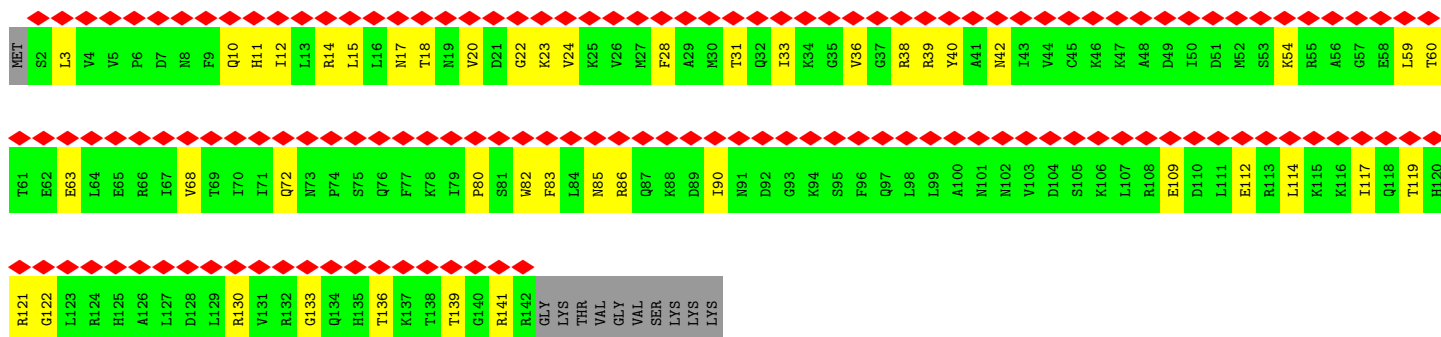


• Molecule 19: Small ribosomal subunit protein eS17A

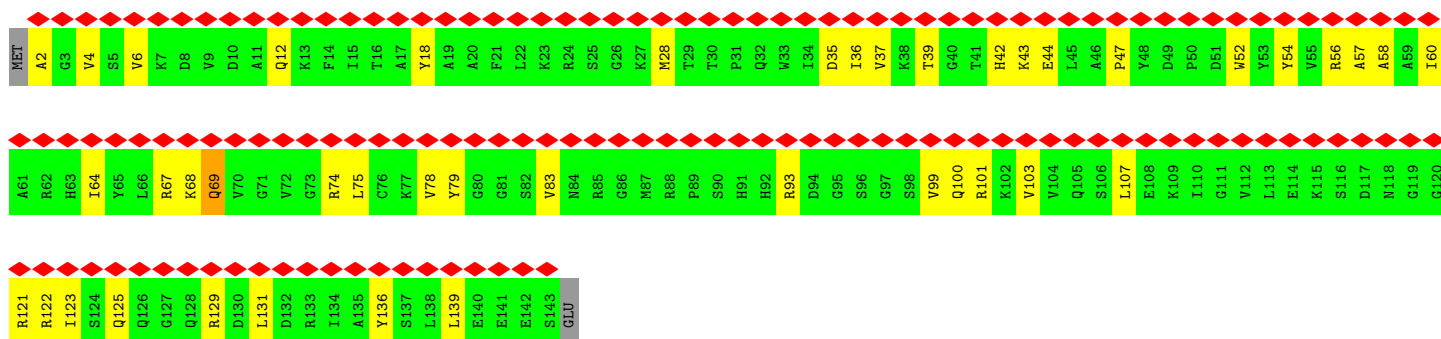
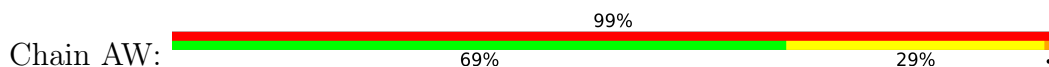


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ALA  
PRO  
GLN  
GLU  
ARG  
PHE  
ARG  
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GLN

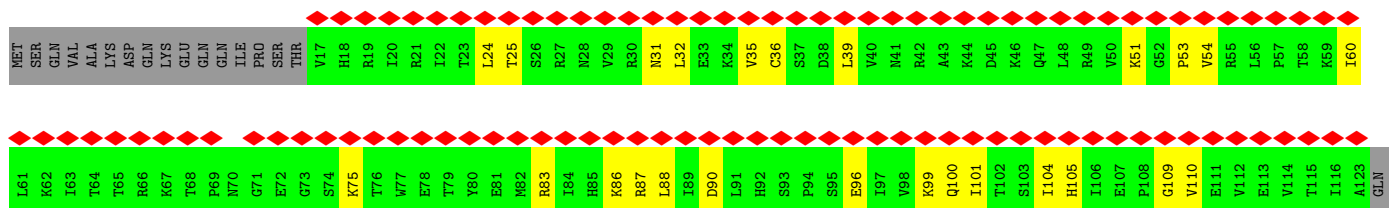
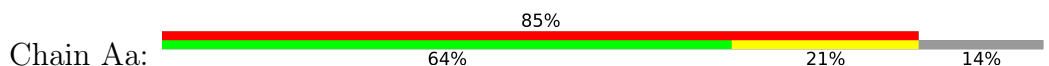
• Molecule 20: Small ribosomal subunit protein uS13B



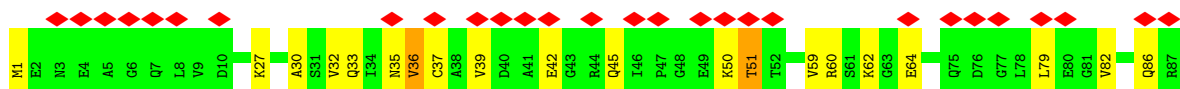
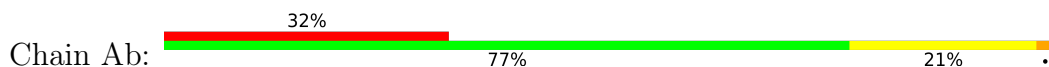
• Molecule 21: Small ribosomal subunit protein eS19A



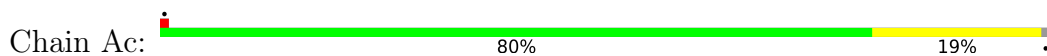
• Molecule 22: Small ribosomal subunit protein uS10



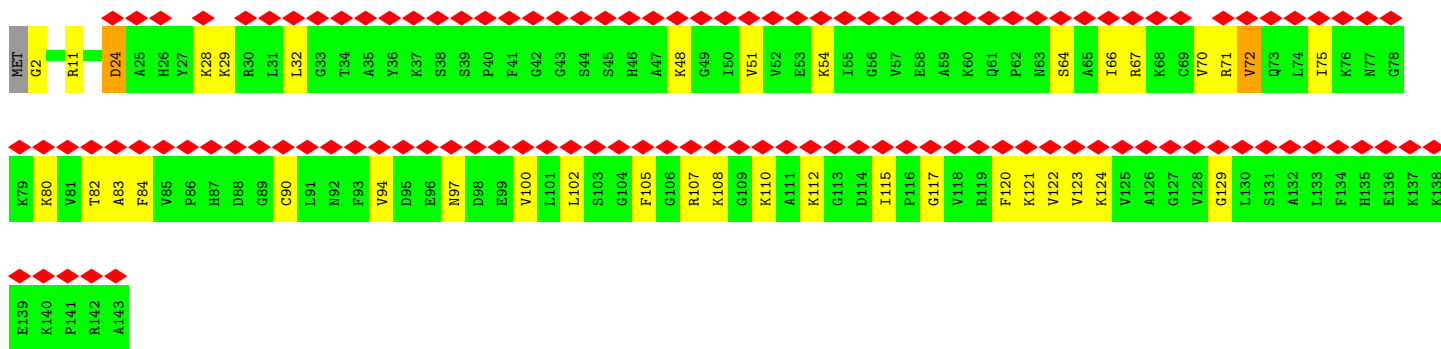
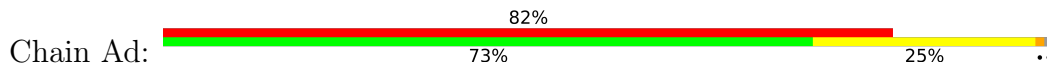
• Molecule 23: Small ribosomal subunit protein eS21



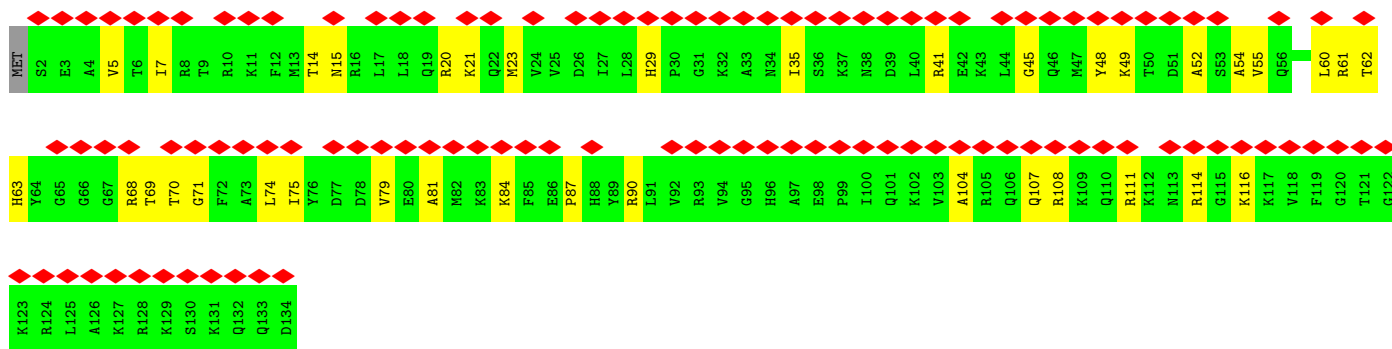
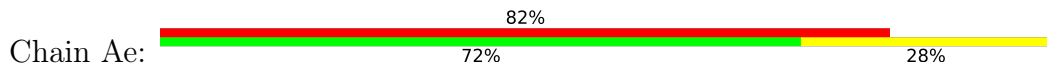
• Molecule 24: Small ribosomal subunit protein uS8A



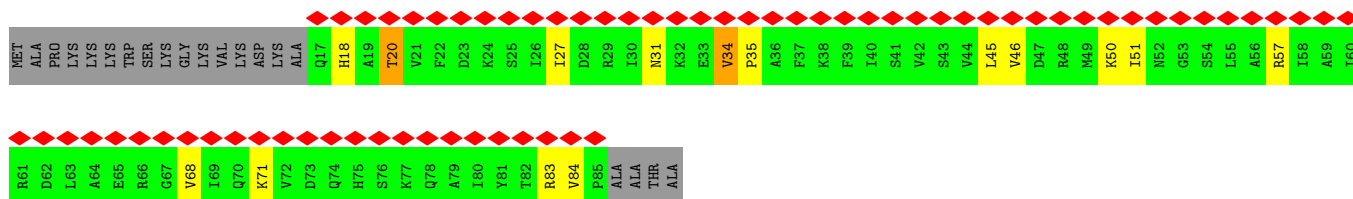
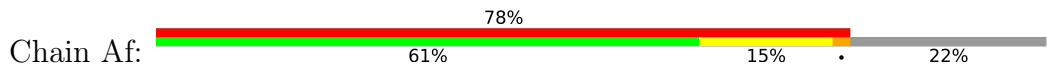
• Molecule 25: Small ribosomal subunit protein uS12A



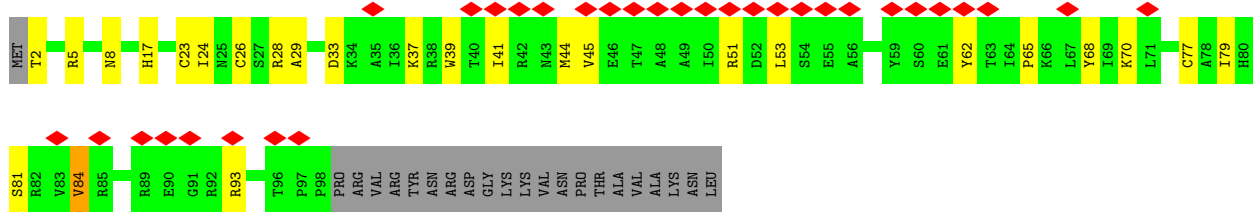
• Molecule 26: Small ribosomal subunit protein eS24A



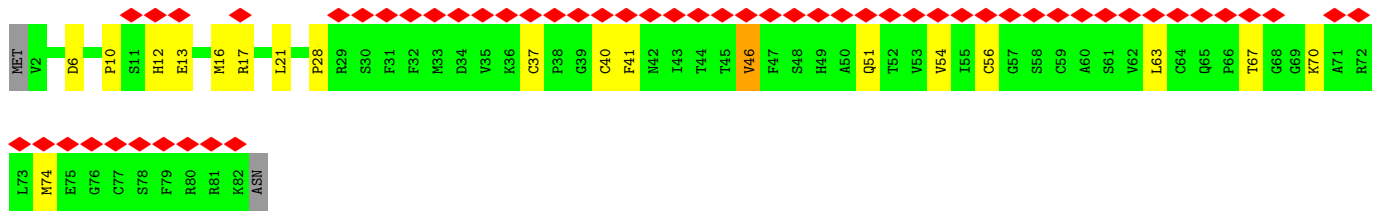
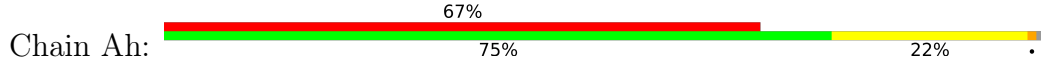
• Molecule 27: Small ribosomal subunit protein eS25A



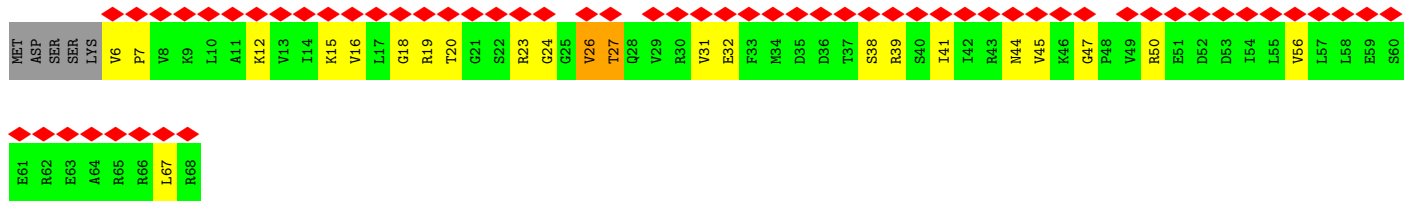
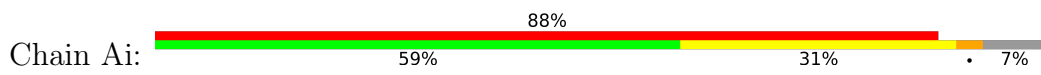
• Molecule 28: Small ribosomal subunit protein eS26B



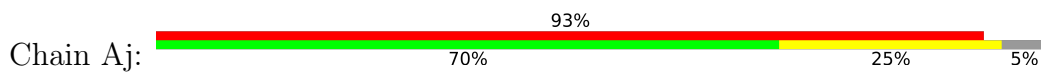
• Molecule 29: Small ribosomal subunit protein eS27



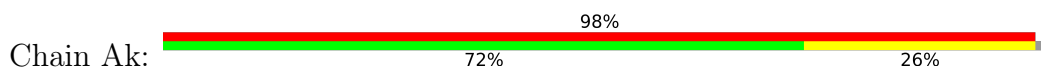
• Molecule 30: Small ribosomal subunit protein eS28A



• Molecule 31: Small ribosomal subunit protein uS14



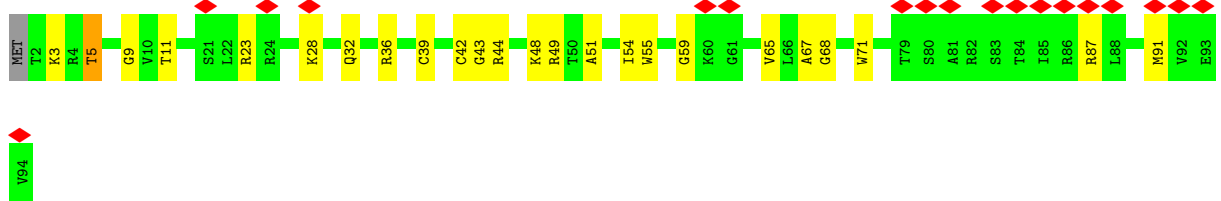
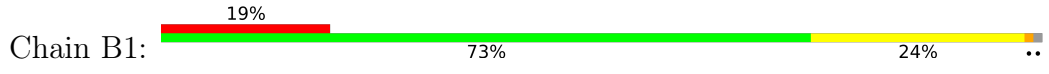
• Molecule 32: Small ribosomal subunit protein eS30B



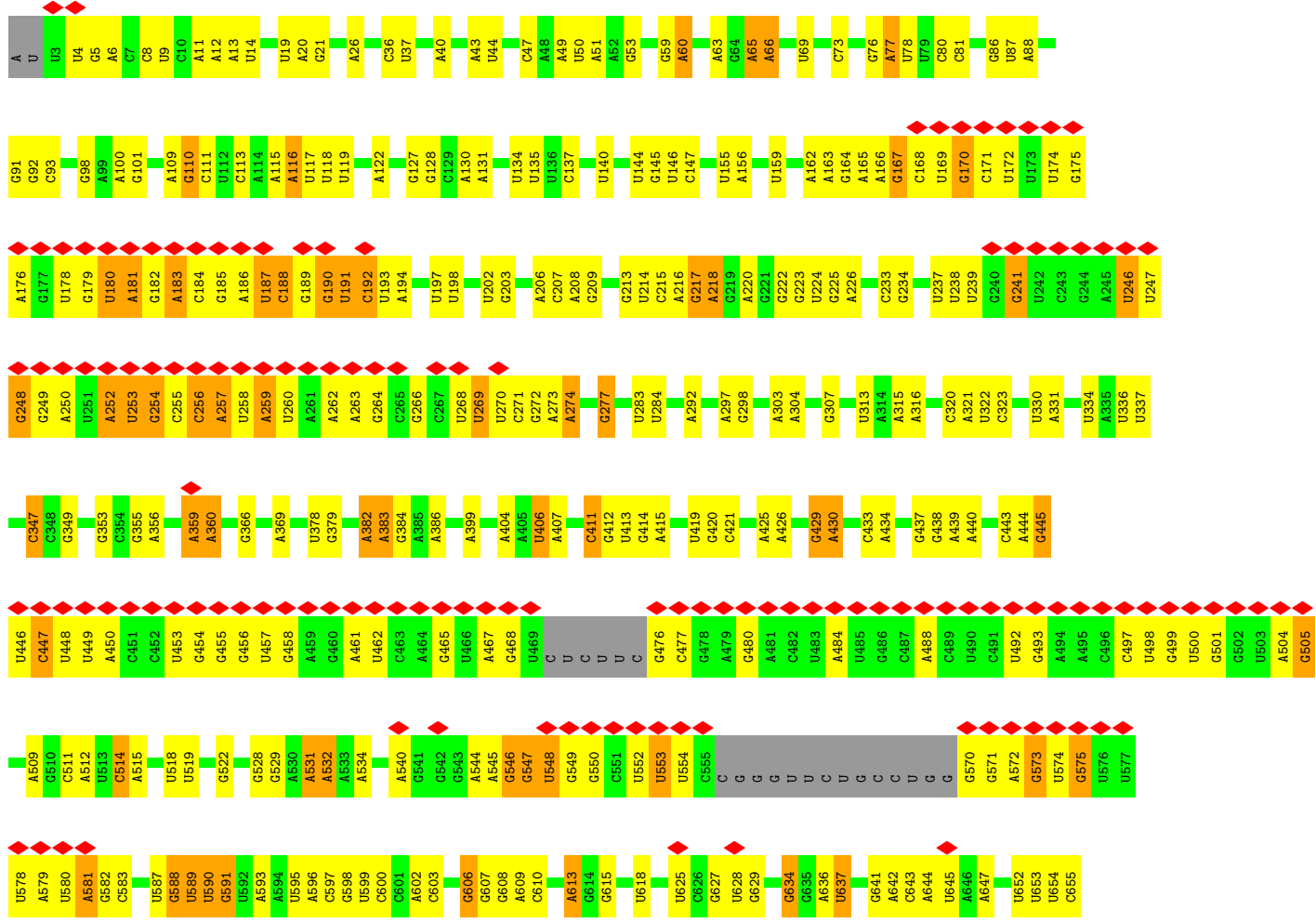
• Molecule 33: Large ribosomal subunit protein eL42

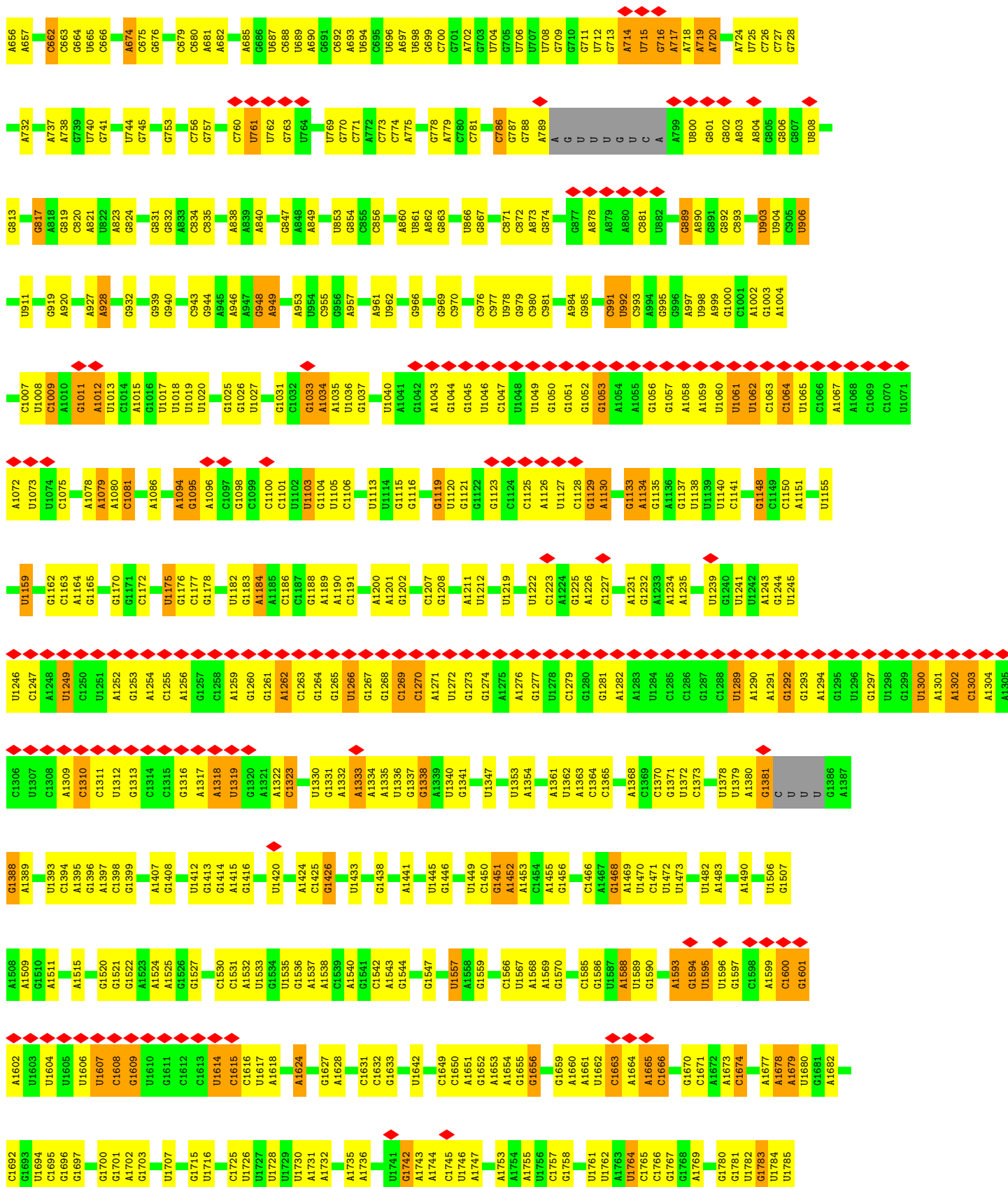


• Molecule 34: Large ribosomal subunit protein eL43A

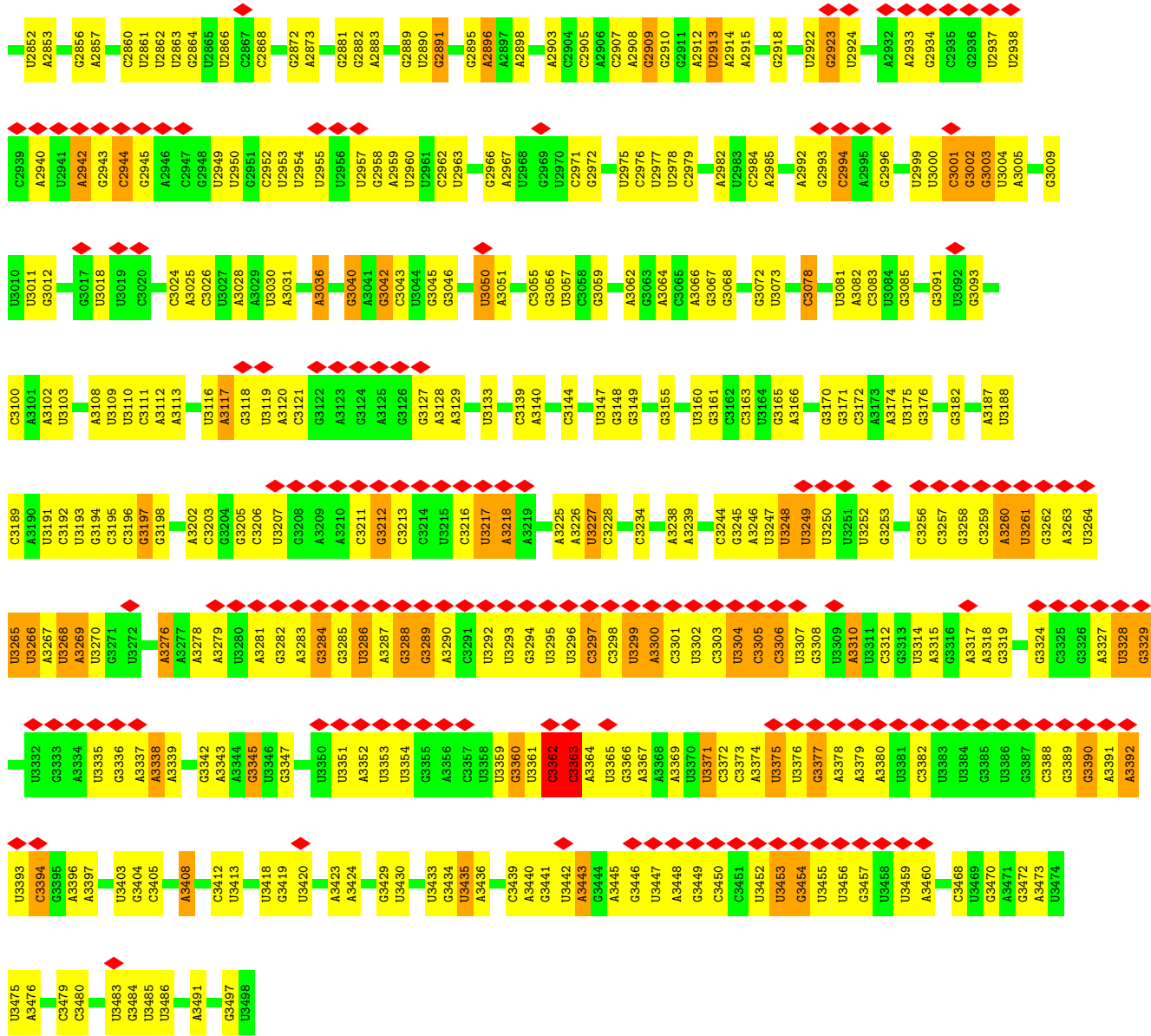


• Molecule 35: 28S ribosomal RNA

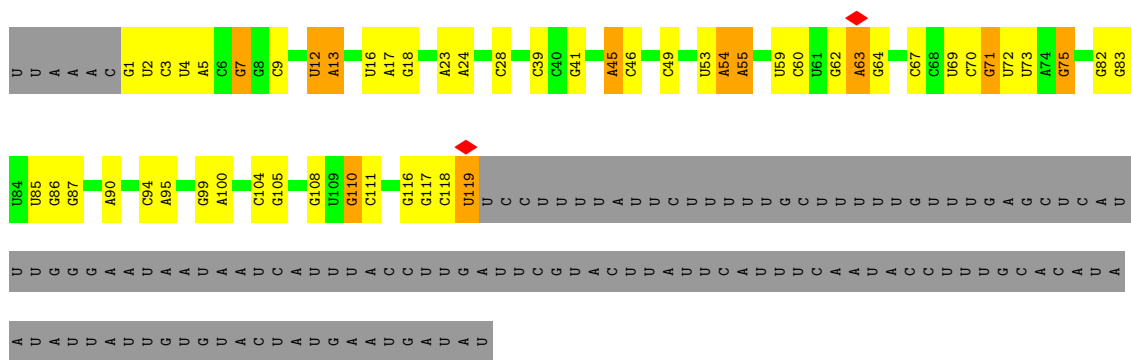




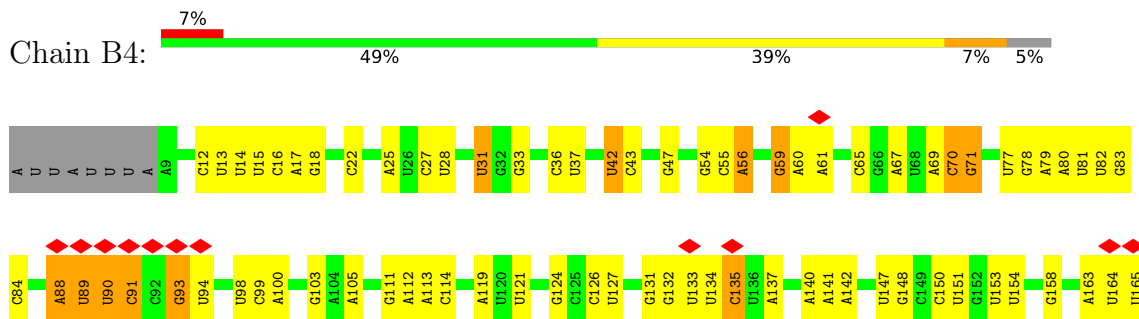




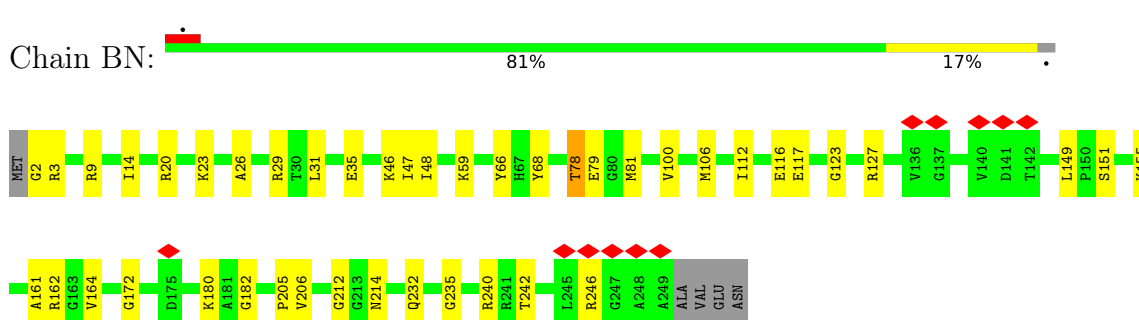
● Molecule 36: 5S ribosomal RNA



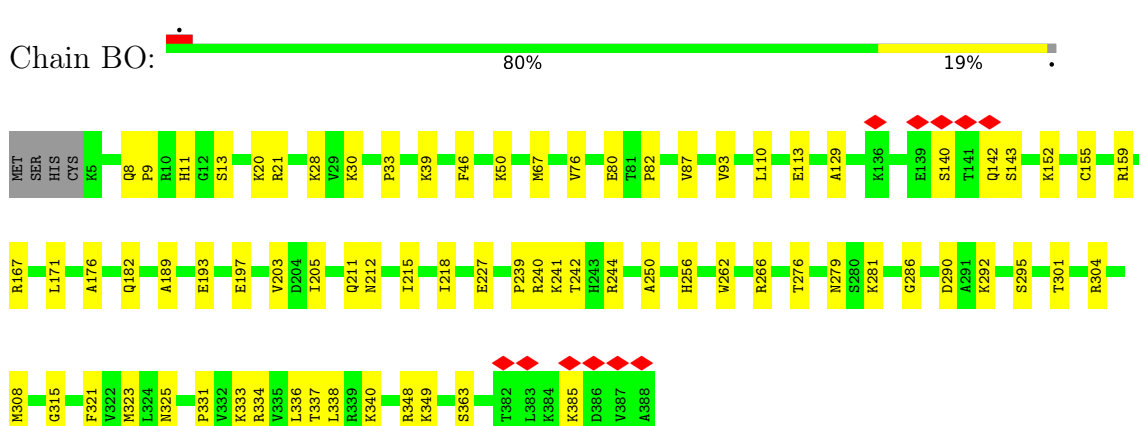
• Molecule 37: 5.8S ribosomal RNA



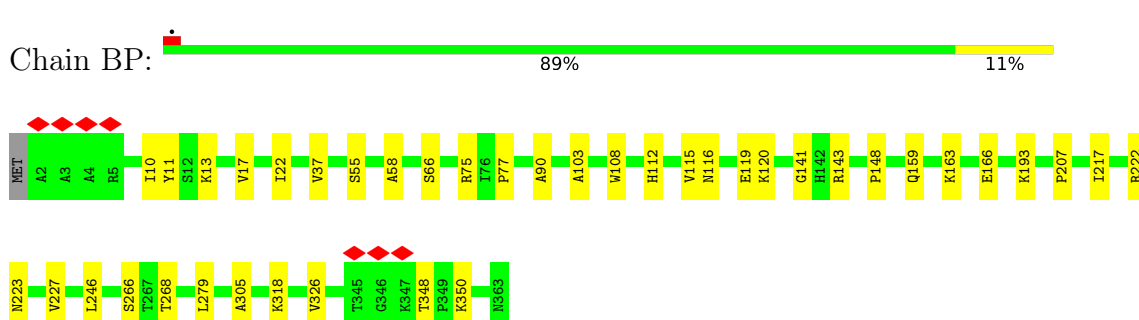
• Molecule 38: Large ribosomal subunit protein uL2C



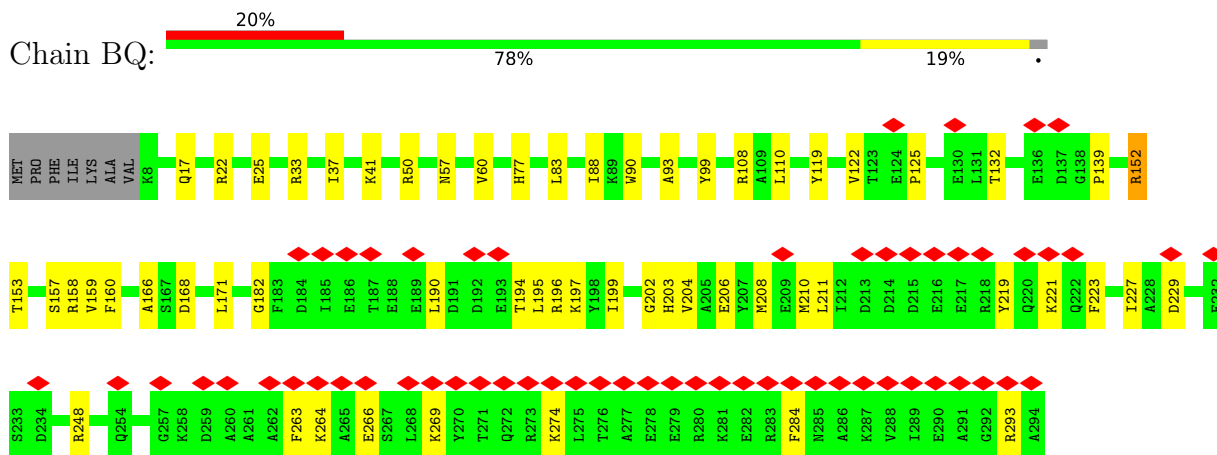
• Molecule 39: Large ribosomal subunit protein uL3A



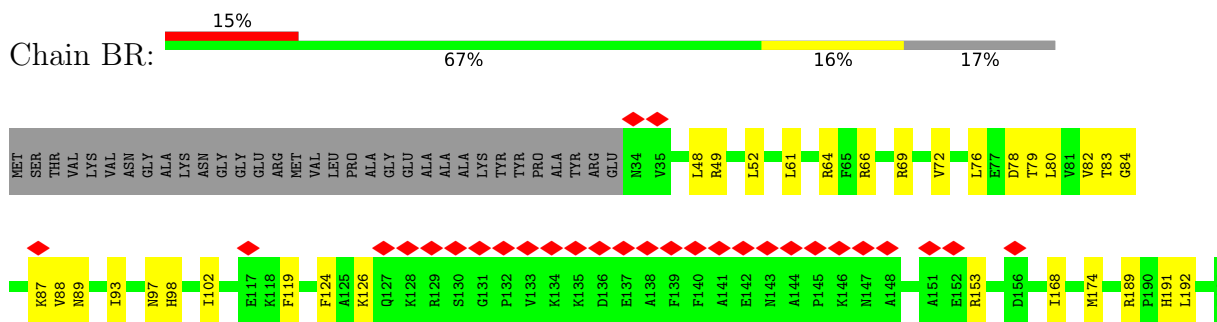
• Molecule 40: Large ribosomal subunit protein uL4A



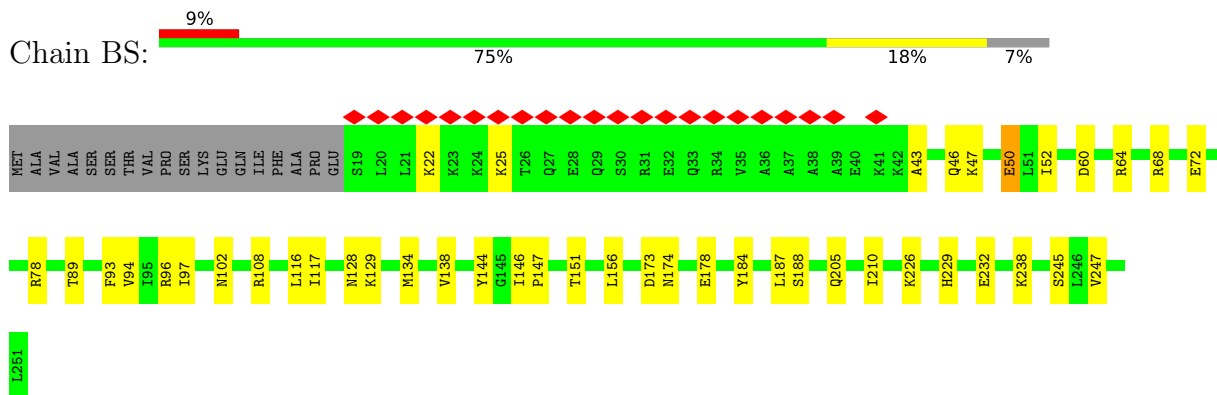
• Molecule 41: Large ribosomal subunit protein uL18B



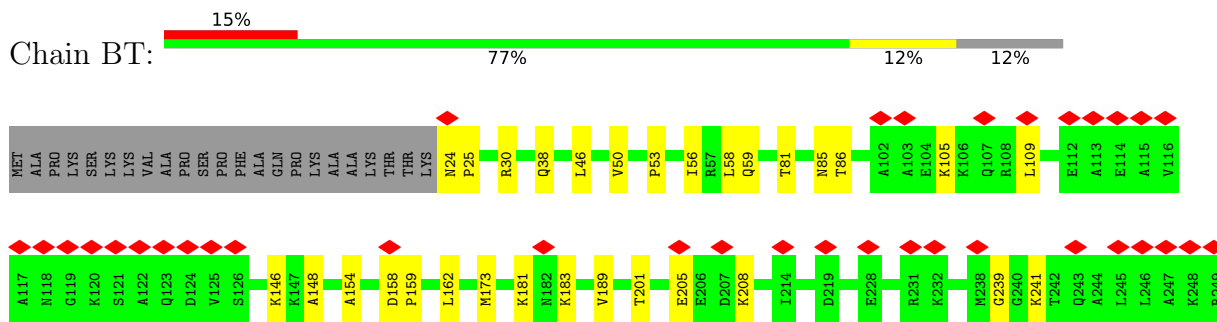
• Molecule 42: Large ribosomal subunit protein eL6



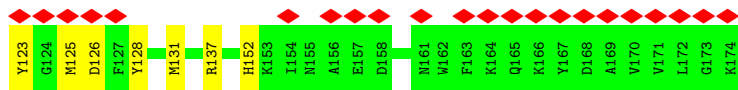
• Molecule 43: Large ribosomal subunit protein uL30C



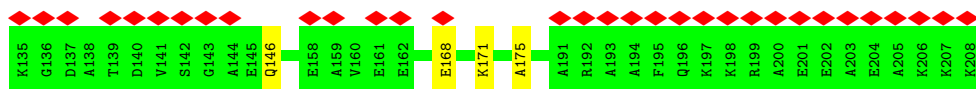
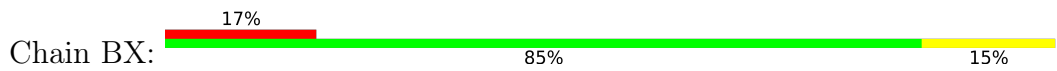
• Molecule 44: Large ribosomal subunit protein eL8



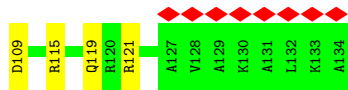
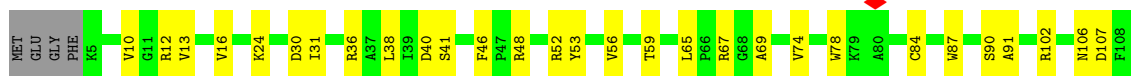
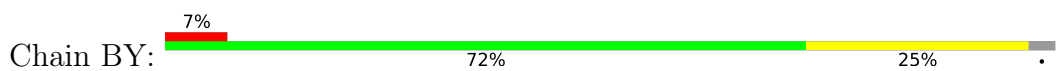




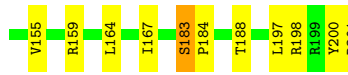
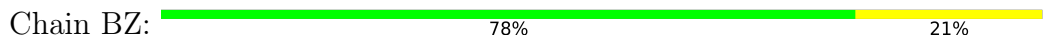
• Molecule 48: Large ribosomal subunit protein eL13



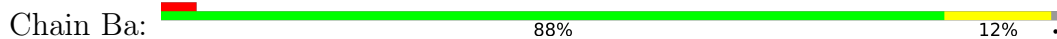
• Molecule 49: Large ribosomal subunit protein eL14



• Molecule 50: Large ribosomal subunit protein eL15B



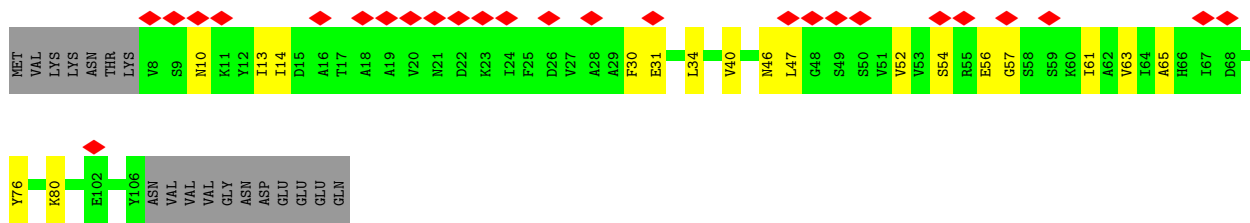
• Molecule 51: Large ribosomal subunit protein uL13A



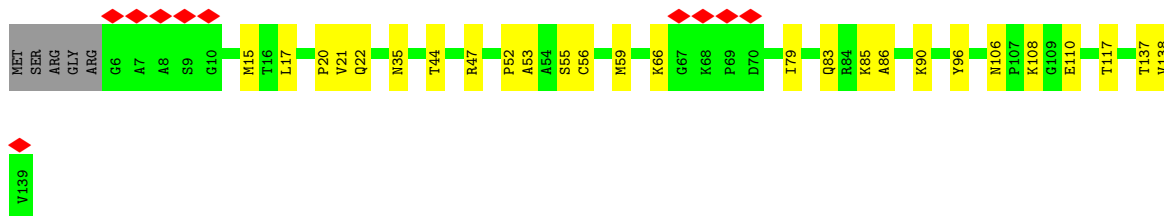
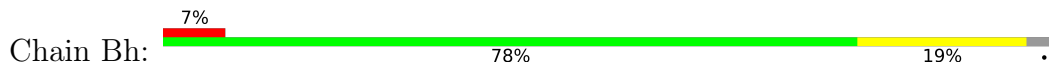
• Molecule 52: Large ribosomal subunit protein uL22A



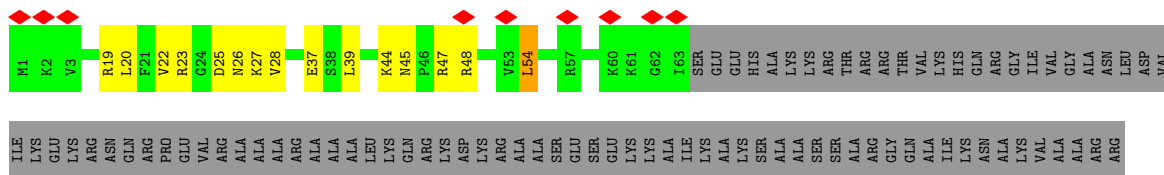
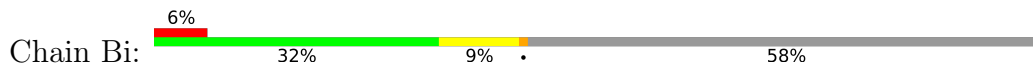




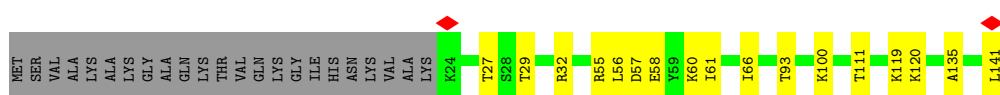
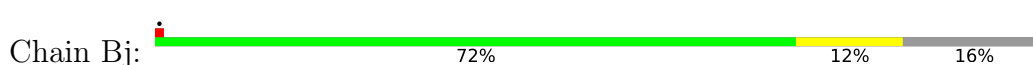
• Molecule 58: Large ribosomal subunit protein uL14B



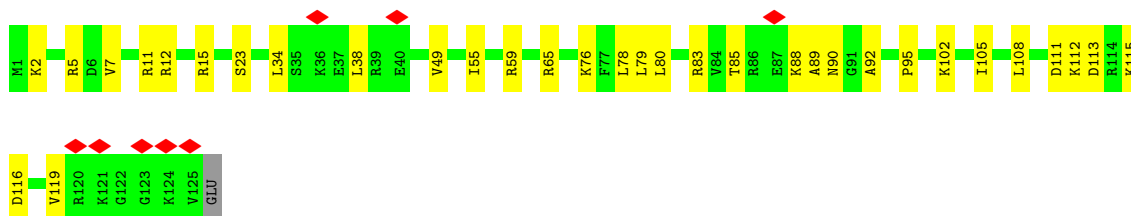
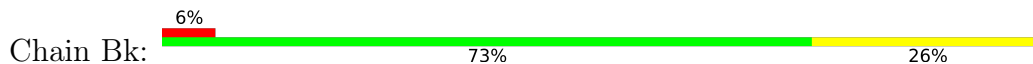
• Molecule 59: Large ribosomal subunit protein eL24B



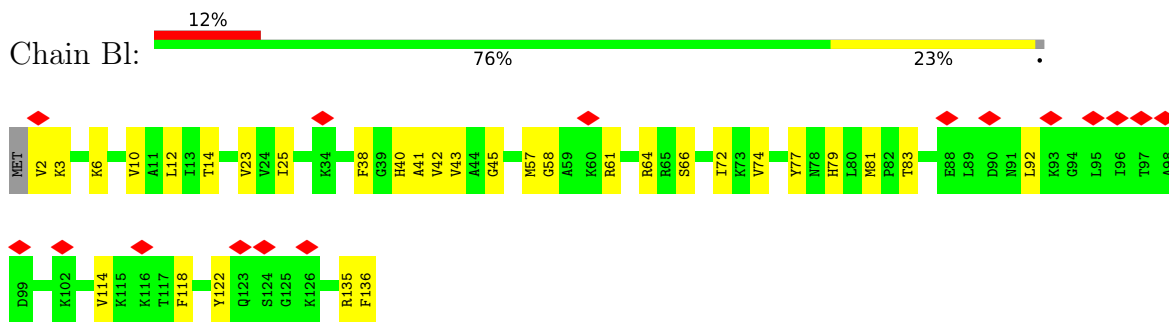
• Molecule 60: Large ribosomal subunit protein uL23A



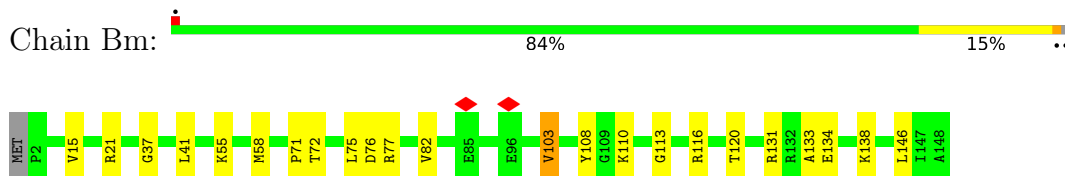
• Molecule 61: Large ribosomal subunit protein uL24



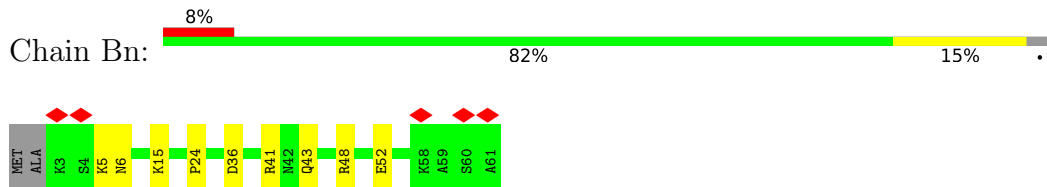
• Molecule 62: Large ribosomal subunit protein eL27A



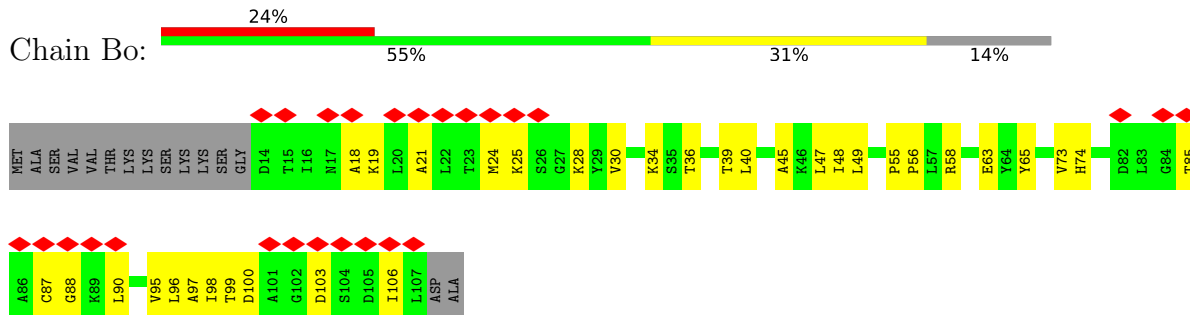
• Molecule 63: Large ribosomal subunit protein uL15B



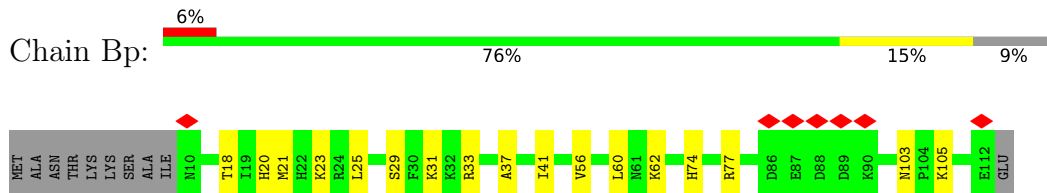
• Molecule 64: Large ribosomal subunit protein eL29



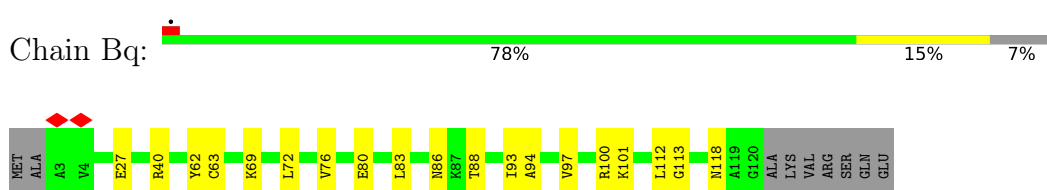
• Molecule 65: Large ribosomal subunit protein eL30A



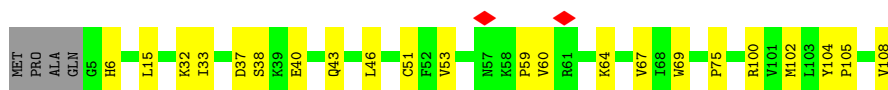
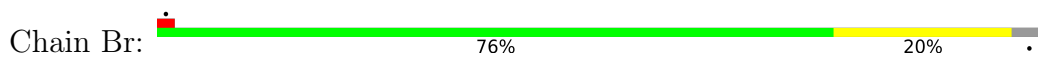
• Molecule 66: Large ribosomal subunit protein eL31



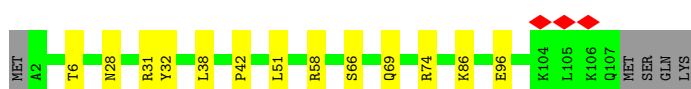
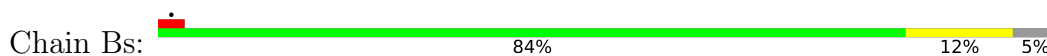
• Molecule 67: Large ribosomal subunit protein eL32A



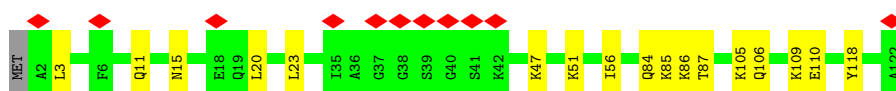
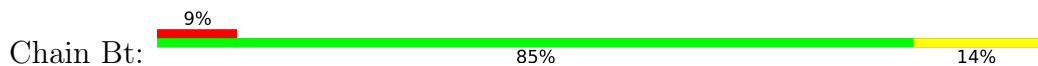
- Molecule 68: Large ribosomal subunit protein eL33A



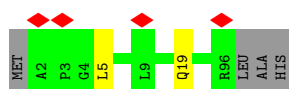
- Molecule 69: Large ribosomal subunit protein eL34B



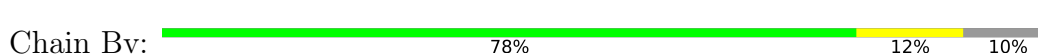
- Molecule 70: Large ribosomal subunit protein uL29



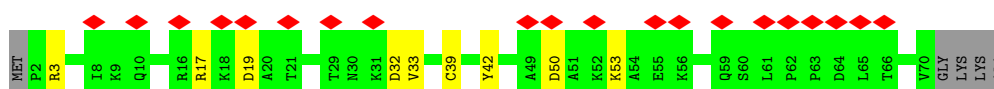
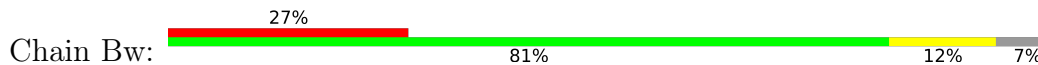
- Molecule 71: Large ribosomal subunit protein eL36B



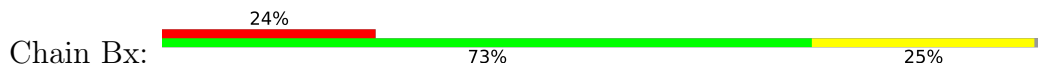
- Molecule 72: Large ribosomal subunit protein eL37B

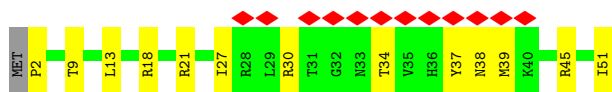


- Molecule 73: Large ribosomal subunit protein eL38A

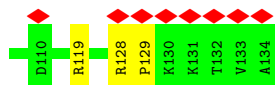
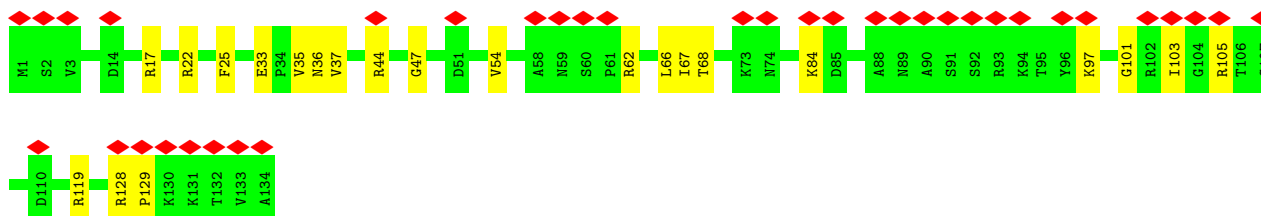
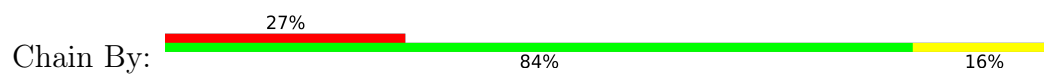


- Molecule 74: Large ribosomal subunit protein eL39





- Molecule 75: Large ribosomal subunit protein eL28



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73376	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.236	Depositor
Minimum map value	-1.145	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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	AA	0.08	0/40661	0.22	0/63326
2	AD	0.12	0/1635	0.34	0/2228
3	AE	0.11	0/1756	0.31	0/2358
4	AF	0.11	0/1695	0.28	0/2297
5	AG	0.09	0/1726	0.25	0/2316
6	AH	0.11	0/2125	0.31	0/2858
7	AI	0.10	0/1577	0.27	0/2123
8	AJ	0.10	0/1815	0.27	0/2428
9	AK	0.12	0/1554	0.32	0/2091
10	AL	0.08	0/1534	0.24	0/2050
11	AM	0.13	0/1487	0.32	0/1990
12	AN	0.10	0/769	0.31	0/1043
13	AO	0.10	0/1190	0.27	0/1602
14	AP	0.08	0/892	0.27	0/1208
15	AQ	0.80	2/1208 (0.2%)	0.97	5/1624 (0.3%)
16	AR	0.09	0/961	0.28	0/1293
17	AS	0.12	0/973	0.37	0/1307
18	AT	0.09	0/1100	0.25	0/1474
19	AU	0.10	0/983	0.34	0/1318
20	AV	0.09	0/1158	0.26	0/1552
21	AW	0.07	0/1139	0.23	0/1531
22	Aa	0.08	0/826	0.26	0/1114
23	Ab	0.06	0/680	0.20	0/918
24	Ac	0.08	0/1042	0.21	0/1399
25	Ad	0.09	0/1115	0.27	0/1489
26	Ae	0.12	0/1093	0.29	0/1453
27	Af	0.09	0/558	0.27	0/750
28	Ag	0.08	0/808	0.24	0/1083
29	Ah	0.34	1/630 (0.2%)	0.52	1/845 (0.1%)
30	Ai	0.10	0/500	0.26	0/669
31	Aj	0.09	0/458	0.26	0/610
32	Ak	0.07	0/482	0.24	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	B0	0.10	0/772	0.23	0/1025
34	B1	0.09	0/727	0.27	0/973
35	B2	0.10	0/76871	0.25	5/119827 (0.0%)
36	B3	0.09	0/2838	0.22	0/4422
37	B4	0.09	0/3723	0.23	0/5796
38	BN	0.08	0/1910	0.25	0/2575
39	BO	0.08	0/3116	0.23	0/4190
40	BP	0.08	0/2852	0.22	0/3850
41	BQ	0.08	0/2361	0.22	0/3173
42	BR	0.10	0/1275	0.28	0/1719
43	BS	0.09	0/1929	0.22	0/2583
44	BT	0.09	0/1801	0.22	0/2430
45	BU	0.07	0/1330	0.22	0/1789
46	BV	0.07	0/1579	0.21	0/2115
47	BW	0.52	2/1369 (0.1%)	0.58	4/1830 (0.2%)
48	BX	0.08	0/1686	0.21	0/2267
49	BY	0.06	0/1054	0.16	0/1413
50	BZ	0.08	0/1717	0.22	0/2306
51	Ba	0.09	0/1575	0.24	0/2109
52	Bb	0.08	0/1237	0.23	0/1661
53	Bc	0.07	0/1511	0.23	0/2021
54	Bd	0.07	0/1320	0.18	0/1757
55	Be	0.08	0/1458	0.22	0/1961
56	Bf	0.08	0/1314	0.22	0/1771
57	Bg	0.10	0/812	0.28	0/1090
58	Bh	0.10	0/1015	0.27	0/1369
59	Bi	0.07	0/534	0.22	0/709
60	Bj	0.09	0/963	0.26	0/1296
61	Bk	0.07	0/1008	0.19	0/1341
62	Bl	0.07	0/1101	0.22	0/1477
63	Bm	0.09	0/1200	0.22	0/1611
64	Bn	0.06	0/503	0.19	0/664
65	Bo	0.13	0/714	0.33	0/961
66	Bp	0.06	0/872	0.19	0/1172
67	Bq	0.08	0/958	0.21	0/1278
68	Br	0.50	2/853 (0.2%)	1.02	3/1146 (0.3%)
69	Bs	0.11	0/870	0.26	0/1165
70	Bt	0.07	0/1008	0.21	0/1340
71	Bu	0.06	0/766	0.18	0/1017
72	Bv	0.08	0/666	0.24	0/881
73	Bw	0.11	0/566	0.27	0/757
74	Bx	0.09	0/447	0.31	0/597
75	By	0.07	0/1053	0.21	0/1414

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
All	All	0.12	7/209364 (0.0%)	0.27	18/307834 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	AQ	61	PRO	CG-CD	-24.01	0.69	1.50
47	BW	45	PRO	CG-CD	-17.74	0.90	1.50
68	Br	59	PRO	CB-CG	-11.22	0.93	1.49
15	AQ	61	PRO	CB-CG	11.20	2.05	1.49
29	Ah	10	PRO	CG-CD	-6.59	1.28	1.50

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AQ	61	PRO	N-CD-CG	-26.75	63.07	103.20
68	Br	59	PRO	CB-CG-CD	23.09	179.98	106.10
15	AQ	61	PRO	CA-CB-CG	-19.31	67.80	104.50
47	BW	45	PRO	N-CD-CG	-17.52	76.92	103.20
68	Br	59	PRO	N-CD-CG	-17.04	77.63	103.20

There are no chirality outliers.

There are no planarity outliers.

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

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	AA	36359	0	18308	752	0
2	AD	1602	0	1625	40	0
3	AE	1733	0	1816	34	0
4	AF	1660	0	1736	35	0
5	AG	1701	0	1777	51	0
6	AH	2083	0	2192	63	0
7	AI	1559	0	1624	46	0
8	AJ	1784	0	1879	44	0
9	AK	1530	0	1609	31	0
10	AL	1506	0	1538	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AM	1462	0	1562	39	0
12	AN	748	0	735	16	0
13	AO	1164	0	1201	26	0
14	AP	884	0	872	12	0
15	AQ	1184	0	1252	31	0
16	AR	949	0	986	35	0
17	AS	954	0	993	46	0
18	AT	1082	0	1142	34	0
19	AU	972	0	1011	25	0
20	AV	1144	0	1197	37	0
21	AW	1119	0	1130	30	0
22	Aa	815	0	876	18	0
23	Ab	672	0	660	17	0
24	Ac	1028	0	1080	19	0
25	Ad	1095	0	1149	29	0
26	Ae	1078	0	1133	26	0
27	Af	551	0	583	16	0
28	Ag	795	0	832	20	0
29	Ah	619	0	635	12	0
30	Ai	498	0	539	17	0
31	Aj	447	0	443	17	0
32	Ak	475	0	517	11	0
33	B0	758	0	815	13	0
34	B1	718	0	751	20	0
35	B2	68676	0	34523	1023	0
36	B3	2539	0	1283	43	0
37	B4	3332	0	1684	59	0
38	BN	1872	0	1917	35	0
39	BO	3050	0	3125	53	0
40	BP	2799	0	2925	27	0
41	BQ	2312	0	2272	39	0
42	BR	1251	0	1337	24	0
43	BS	1897	0	1984	29	0
44	BT	1772	0	1866	19	0
45	BU	1319	0	1389	32	0
46	BV	1549	0	1591	35	0
47	BW	1346	0	1397	31	0
48	BX	1654	0	1705	23	0
49	BY	1038	0	1115	20	0
50	BZ	1676	0	1712	31	0
51	Ba	1545	0	1641	19	0
52	Bb	1212	0	1239	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	Bc	1487	0	1597	17	0
54	Bd	1301	0	1393	11	0
55	Be	1423	0	1488	23	0
56	Bf	1286	0	1310	20	0
57	Bg	798	0	834	10	0
58	Bh	999	0	1047	18	0
59	Bi	523	0	555	8	0
60	Bj	947	0	1012	11	0
61	Bk	998	0	1090	25	0
62	Bl	1078	0	1154	22	0
63	Bm	1171	0	1215	17	0
64	Bn	495	0	504	9	0
65	Bo	705	0	746	24	0
66	Bp	857	0	891	11	0
67	Bq	944	0	1005	12	0
68	Br	831	0	858	14	0
69	Bs	858	0	925	10	0
70	Bt	999	0	1092	13	0
71	Bu	759	0	840	2	0
72	Bv	652	0	663	10	0
73	Bw	560	0	608	5	0
74	Bx	436	0	463	14	0
75	By	1039	0	1092	15	0
76	Ag	1	0	0	0	0
76	Ah	1	0	0	0	0
76	Aj	1	0	0	0	0
76	B0	1	0	0	0	0
76	B1	1	0	0	0	0
76	Bv	1	0	0	0	0
All	All	194719	0	143285	3089	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 9.

The worst 5 of 3089 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)
1:AA:127:A:H62	1:AA:294:G:H21	1.09	1.00
35:B2:787:G:H1	35:B2:804:A:H61	1.07	0.97
1:AA:127:A:H62	1:AA:294:G:N2	1.65	0.94
37:B4:132:G:H1	37:B4:137:A:H61	0.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1719:U:H3	1:AA:1765:G:H1	1.15	0.92

There are no symmetry-related clashes.

## 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	
2	AD	203/292 (70%)	183 (90%)	20 (10%)	0	100	100
3	AE	214/252 (85%)	197 (92%)	16 (8%)	1 (0%)	24	37
4	AF	214/253 (85%)	205 (96%)	8 (4%)	1 (0%)	24	37
5	AG	214/249 (86%)	201 (94%)	13 (6%)	0	100	100
6	AH	259/262 (99%)	249 (96%)	9 (4%)	1 (0%)	30	43
7	AI	201/203 (99%)	187 (93%)	13 (6%)	1 (0%)	24	37
8	AJ	219/239 (92%)	210 (96%)	9 (4%)	0	100	100
9	AK	191/195 (98%)	181 (95%)	10 (5%)	0	100	100
10	AL	184/200 (92%)	179 (97%)	5 (3%)	0	100	100
11	AM	176/192 (92%)	166 (94%)	9 (5%)	1 (1%)	21	32
12	AN	90/147 (61%)	77 (86%)	12 (13%)	1 (1%)	11	18
13	AO	141/152 (93%)	126 (89%)	15 (11%)	0	100	100
14	AP	119/145 (82%)	103 (87%)	14 (12%)	2 (2%)	7	10
15	AQ	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
16	AR	126/139 (91%)	117 (93%)	9 (7%)	0	100	100
17	AS	117/154 (76%)	102 (87%)	15 (13%)	0	100	100
18	AT	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
19	AU	116/131 (88%)	107 (92%)	7 (6%)	2 (2%)	7	10
20	AV	139/152 (91%)	129 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	AW	140/144 (97%)	131 (94%)	9 (6%)	0	100	100
22	Aa	99/118 (84%)	97 (98%)	2 (2%)	0	100	100
23	Ab	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Ad	140/143 (98%)	135 (96%)	5 (4%)	0	100	100
26	Ae	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
27	Af	67/89 (75%)	66 (98%)	1 (2%)	0	100	100
28	Ag	95/119 (80%)	91 (96%)	4 (4%)	0	100	100
29	Ah	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
30	Ai	61/68 (90%)	57 (93%)	4 (7%)	0	100	100
31	Aj	51/56 (91%)	45 (88%)	6 (12%)	0	100	100
32	Ak	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	10
33	B0	91/106 (86%)	88 (97%)	3 (3%)	0	100	100
34	B1	91/94 (97%)	84 (92%)	7 (8%)	0	100	100
38	BN	246/253 (97%)	231 (94%)	15 (6%)	0	100	100
39	BO	382/388 (98%)	369 (97%)	13 (3%)	0	100	100
40	BP	360/363 (99%)	346 (96%)	14 (4%)	0	100	100
41	BQ	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
42	BR	160/195 (82%)	143 (89%)	17 (11%)	0	100	100
43	BS	231/251 (92%)	226 (98%)	5 (2%)	0	100	100
44	BT	227/259 (88%)	222 (98%)	5 (2%)	0	100	100
45	BU	162/189 (86%)	157 (97%)	5 (3%)	0	100	100
46	BV	187/221 (85%)	183 (98%)	4 (2%)	0	100	100
47	BW	165/174 (95%)	157 (95%)	8 (5%)	0	100	100
48	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
49	BY	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
50	BZ	198/201 (98%)	191 (96%)	6 (3%)	1 (0%)	24	37
51	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
52	Bb	150/187 (80%)	145 (97%)	5 (3%)	0	100	100
53	Bc	184/187 (98%)	178 (97%)	6 (3%)	0	100	100
54	Bd	155/193 (80%)	151 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	Be	171/176 (97%)	168 (98%)	3 (2%)	0	100	100
56	Bf	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
57	Bg	97/117 (83%)	87 (90%)	10 (10%)	0	100	100
58	Bh	132/139 (95%)	127 (96%)	5 (4%)	0	100	100
59	Bi	61/149 (41%)	60 (98%)	1 (2%)	0	100	100
60	Bj	116/141 (82%)	109 (94%)	7 (6%)	0	100	100
61	Bk	123/126 (98%)	121 (98%)	2 (2%)	0	100	100
62	Bl	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
63	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
64	Bn	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
65	Bo	92/109 (84%)	91 (99%)	1 (1%)	0	100	100
66	Bp	101/113 (89%)	98 (97%)	3 (3%)	0	100	100
67	Bq	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
68	Br	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
69	Bs	104/111 (94%)	101 (97%)	3 (3%)	0	100	100
70	Bt	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
71	Bu	93/99 (94%)	91 (98%)	2 (2%)	0	100	100
72	Bv	80/91 (88%)	74 (92%)	6 (8%)	0	100	100
73	Bw	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
74	Bx	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	By	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
All	All	10389/11466 (91%)	9904 (95%)	473 (5%)	12 (0%)	49	64

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AH	12	VAL
19	AU	118	VAL
3	AE	147	ALA
7	AI	79	GLY
50	BZ	183	SER

### 5.3.2 Protein sidechains [i](#)

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
2	AD	170/228 (75%)	168 (99%)	2 (1%)	63 81
3	AE	193/223 (86%)	189 (98%)	4 (2%)	47 69
4	AF	175/199 (88%)	166 (95%)	9 (5%)	21 37
5	AG	181/203 (89%)	178 (98%)	3 (2%)	53 74
6	AH	226/227 (100%)	217 (96%)	9 (4%)	28 47
7	AI	169/169 (100%)	168 (99%)	1 (1%)	78 89
8	AJ	188/204 (92%)	184 (98%)	4 (2%)	47 69
9	AK	169/171 (99%)	164 (97%)	5 (3%)	36 58
10	AL	157/166 (95%)	155 (99%)	2 (1%)	61 80
11	AM	155/165 (94%)	152 (98%)	3 (2%)	50 71
12	AN	77/116 (66%)	77 (100%)	0	100 100
13	AO	124/131 (95%)	121 (98%)	3 (2%)	43 65
14	AP	92/118 (78%)	90 (98%)	2 (2%)	45 67
15	AQ	127/128 (99%)	126 (99%)	1 (1%)	73 86
16	AR	95/104 (91%)	93 (98%)	2 (2%)	47 69
17	AS	101/131 (77%)	99 (98%)	2 (2%)	48 70
18	AT	111/111 (100%)	109 (98%)	2 (2%)	51 73
19	AU	107/120 (89%)	106 (99%)	1 (1%)	70 85
20	AV	127/136 (93%)	125 (98%)	2 (2%)	55 76
21	AW	117/119 (98%)	113 (97%)	4 (3%)	32 54
22	Aa	95/111 (86%)	95 (100%)	0	100 100
23	Ab	73/73 (100%)	71 (97%)	2 (3%)	39 62
24	Ac	114/115 (99%)	112 (98%)	2 (2%)	51 73
25	Ad	112/113 (99%)	109 (97%)	3 (3%)	39 62
26	Ae	112/113 (99%)	111 (99%)	1 (1%)	70 85
27	Af	61/75 (81%)	59 (97%)	2 (3%)	33 55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	Ag	87/106 (82%)	84 (97%)	3 (3%)	32	54
29	Ah	71/73 (97%)	70 (99%)	1 (1%)	59	79
30	Ai	56/61 (92%)	51 (91%)	5 (9%)	9	15
31	Aj	45/47 (96%)	45 (100%)	0	100	100
32	Ak	51/52 (98%)	50 (98%)	1 (2%)	48	70
33	B0	84/93 (90%)	81 (96%)	3 (4%)	31	52
34	B1	74/75 (99%)	73 (99%)	1 (1%)	59	79
38	BN	188/192 (98%)	187 (100%)	1 (0%)	81	91
39	BO	318/326 (98%)	316 (99%)	2 (1%)	78	89
40	BP	293/294 (100%)	291 (99%)	2 (1%)	76	88
41	BQ	235/241 (98%)	231 (98%)	4 (2%)	53	74
42	BR	132/155 (85%)	130 (98%)	2 (2%)	57	77
43	BS	198/213 (93%)	196 (99%)	2 (1%)	68	84
44	BT	182/212 (86%)	181 (100%)	1 (0%)	81	91
45	BU	149/168 (89%)	146 (98%)	3 (2%)	48	70
46	BV	165/187 (88%)	164 (99%)	1 (1%)	78	89
47	BW	141/146 (97%)	139 (99%)	2 (1%)	59	79
48	BX	166/167 (99%)	165 (99%)	1 (1%)	78	89
49	BY	110/113 (97%)	110 (100%)	0	100	100
50	BZ	175/176 (99%)	174 (99%)	1 (1%)	78	89
51	Ba	159/160 (99%)	159 (100%)	0	100	100
52	Bb	124/149 (83%)	123 (99%)	1 (1%)	73	86
53	Bc	157/158 (99%)	156 (99%)	1 (1%)	78	89
54	Bd	136/163 (83%)	136 (100%)	0	100	100
55	Be	151/154 (98%)	151 (100%)	0	100	100
56	Bf	138/139 (99%)	137 (99%)	1 (1%)	76	88
57	Bg	86/103 (84%)	85 (99%)	1 (1%)	63	81
58	Bh	103/107 (96%)	101 (98%)	2 (2%)	50	71
59	Bi	57/121 (47%)	55 (96%)	2 (4%)	32	53
60	Bj	105/122 (86%)	103 (98%)	2 (2%)	50	71
61	Bk	110/111 (99%)	109 (99%)	1 (1%)	70	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	Bl	114/115 (99%)	112 (98%)	2 (2%)	51	73
63	Bm	122/123 (99%)	118 (97%)	4 (3%)	33	55
64	Bn	50/51 (98%)	50 (100%)	0	100	100
65	Bo	75/87 (86%)	73 (97%)	2 (3%)	39	62
66	Bp	94/102 (92%)	94 (100%)	0	100	100
67	Bq	100/107 (94%)	98 (98%)	2 (2%)	48	70
68	Br	91/94 (97%)	89 (98%)	2 (2%)	45	67
69	Bs	91/96 (95%)	90 (99%)	1 (1%)	65	82
70	Bt	106/107 (99%)	106 (100%)	0	100	100
71	Bu	81/84 (96%)	81 (100%)	0	100	100
72	Bv	68/71 (96%)	68 (100%)	0	100	100
73	Bw	63/66 (96%)	62 (98%)	1 (2%)	55	76
74	Bx	46/47 (98%)	46 (100%)	0	100	100
75	By	113/113 (100%)	112 (99%)	1 (1%)	70	85
All	All	8888/9616 (92%)	8755 (98%)	133 (2%)	55	77

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	Bj	29	THR
62	Bl	72	ILE
69	Bs	32	TYR
16	AR	30	VAL
15	AQ	145	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
40	BP	201	HIS
70	Bt	13	GLN
44	BT	182	ASN
70	Bt	11	GLN
72	Bv	76	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1690/1842 (91%)	415 (24%)	16 (0%)
35	B2	3204/3498 (91%)	644 (20%)	26 (0%)
36	B3	118/246 (47%)	17 (14%)	1 (0%)
37	B4	156/165 (94%)	26 (16%)	1 (0%)
All	All	5168/5751 (89%)	1102 (21%)	44 (0%)

5 of 1102 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	C
1	AA	4	C
1	AA	25	C
1	AA	26	A
1	AA	34	G

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	B2	1269	C
35	B2	3217	U
35	B2	1272	U
35	B2	2661	U
35	B2	3292	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](#)

Of 6 ligands modelled in this entry, 6 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
1	AA	9

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	537:A	O3'	538:A	P	4.50
1	AA	546:C	O3'	547:A	P	4.24
1	AA	1419:A	O3'	1420:A	P	4.11
1	AA	1359:C	O3'	1360:U	P	3.79
1	AA	1483:C	O3'	1484:G	P	3.67

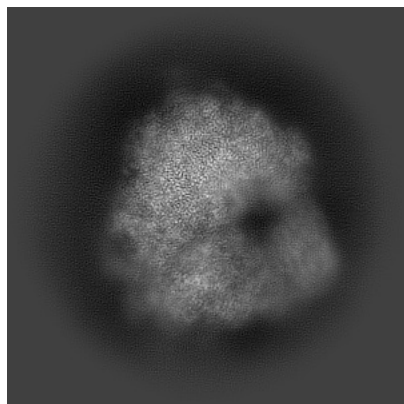
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43972. These allow visual inspection of the internal detail of the map and identification of artifacts.

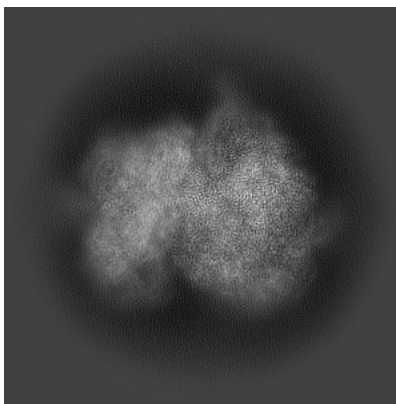
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

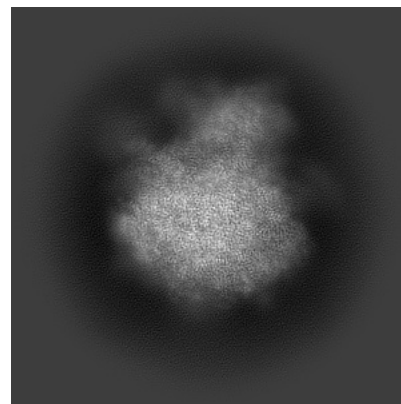
#### 6.1.1 Primary map



X

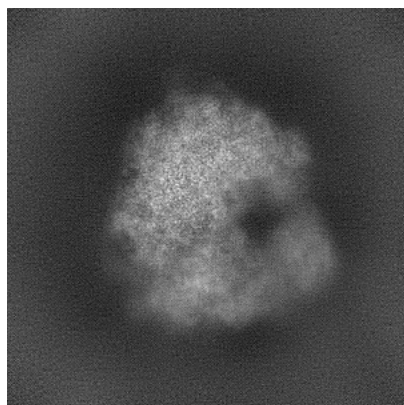


Y

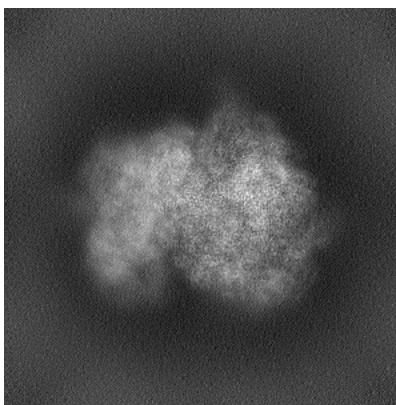


Z

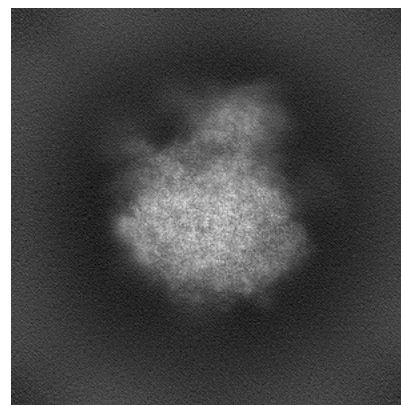
#### 6.1.2 Raw map



X



Y

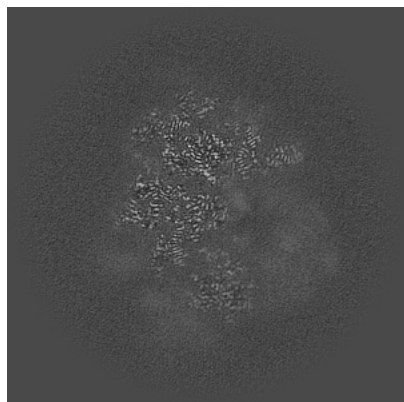


Z

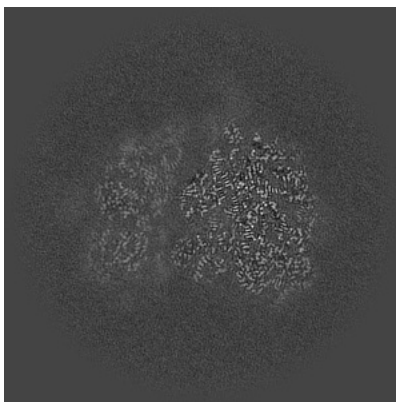
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

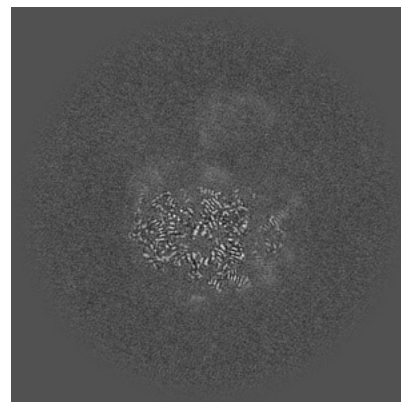
### 6.2.1 Primary map



X Index: 256

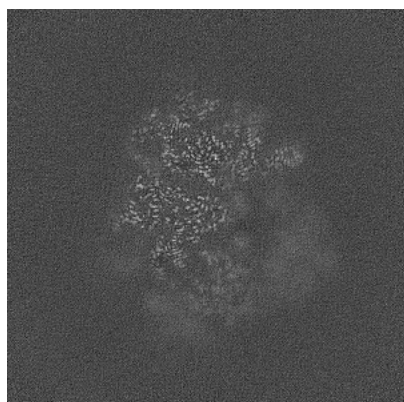


Y Index: 256

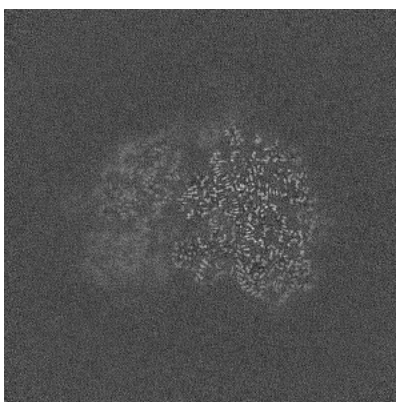


Z Index: 256

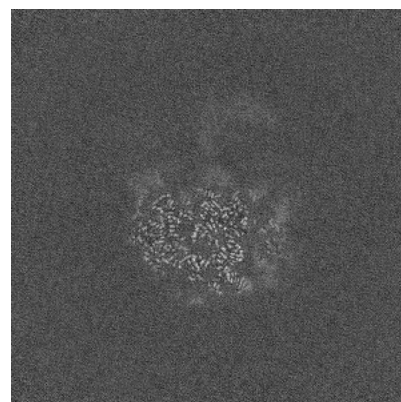
### 6.2.2 Raw map



X Index: 256



Y Index: 256

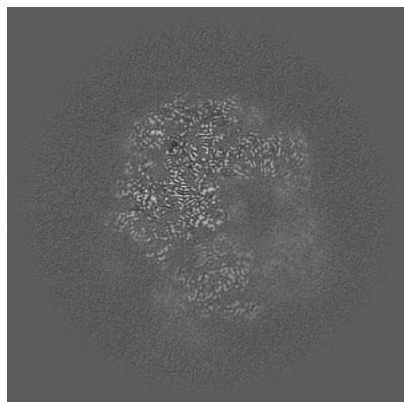


Z Index: 256

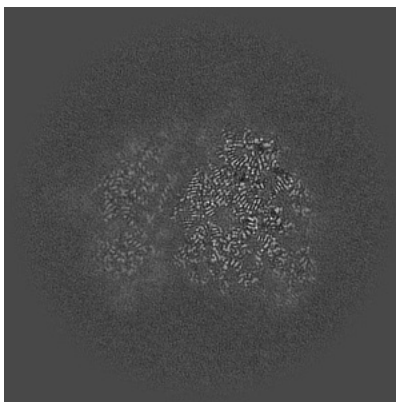
The images above show central slices of the map in three orthogonal directions.

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

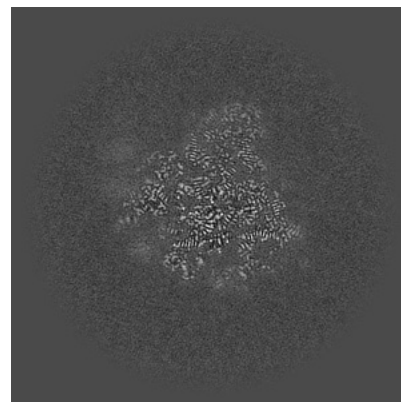
### 6.3.1 Primary map



X Index: 275

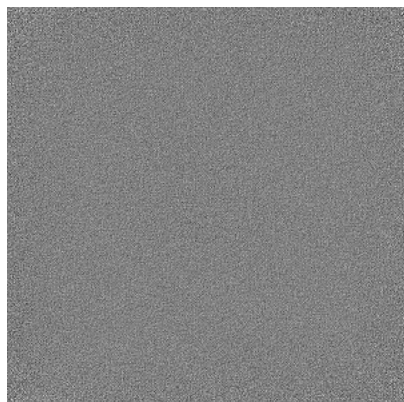


Y Index: 247

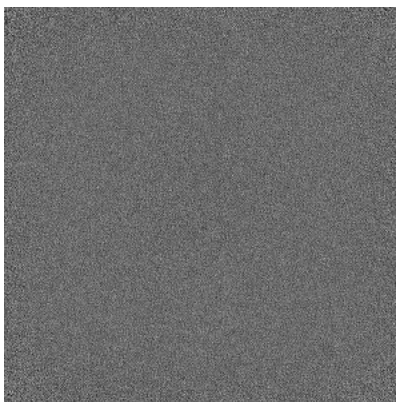


Z Index: 323

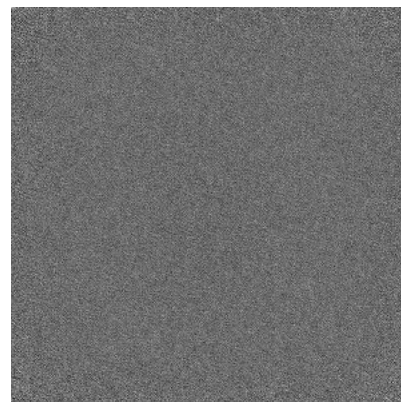
### 6.3.2 Raw map



X Index: 0



Y Index: 0

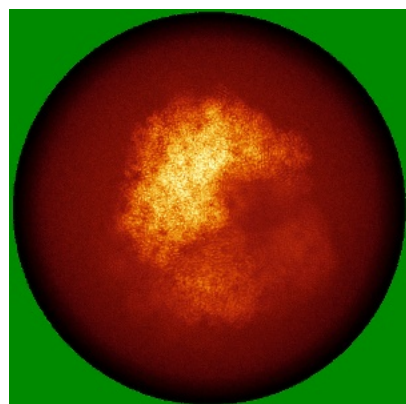


Z Index: 0

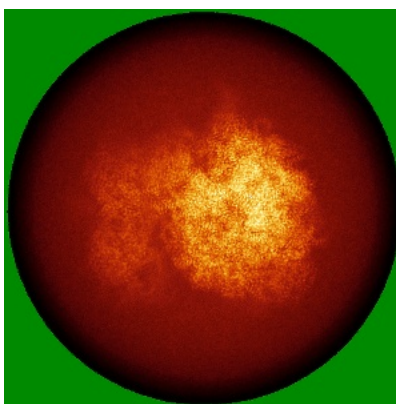
The images above show the largest variance slices of the map in three orthogonal directions.

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

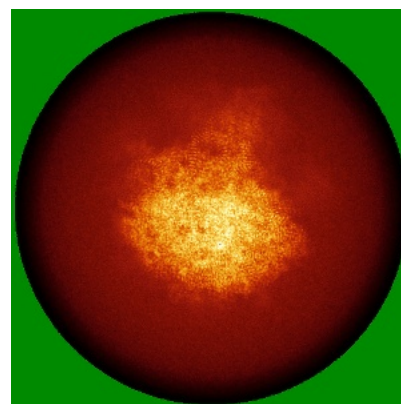
### 6.4.1 Primary map



X

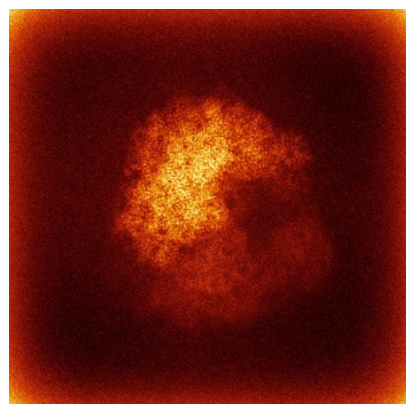


Y

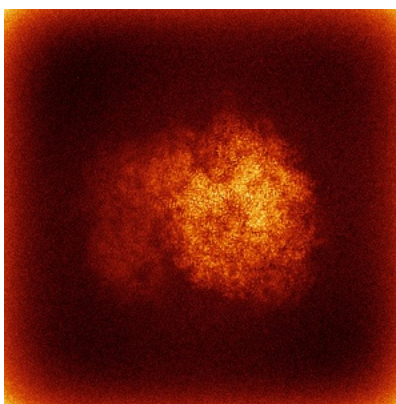


Z

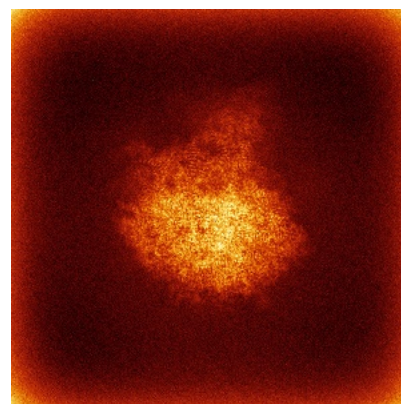
### 6.4.2 Raw map



X



Y

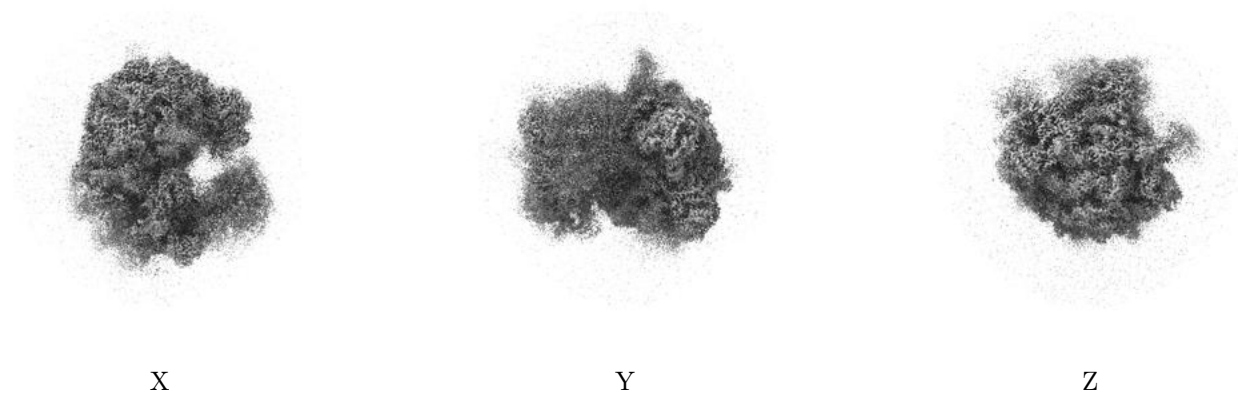


Z

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.

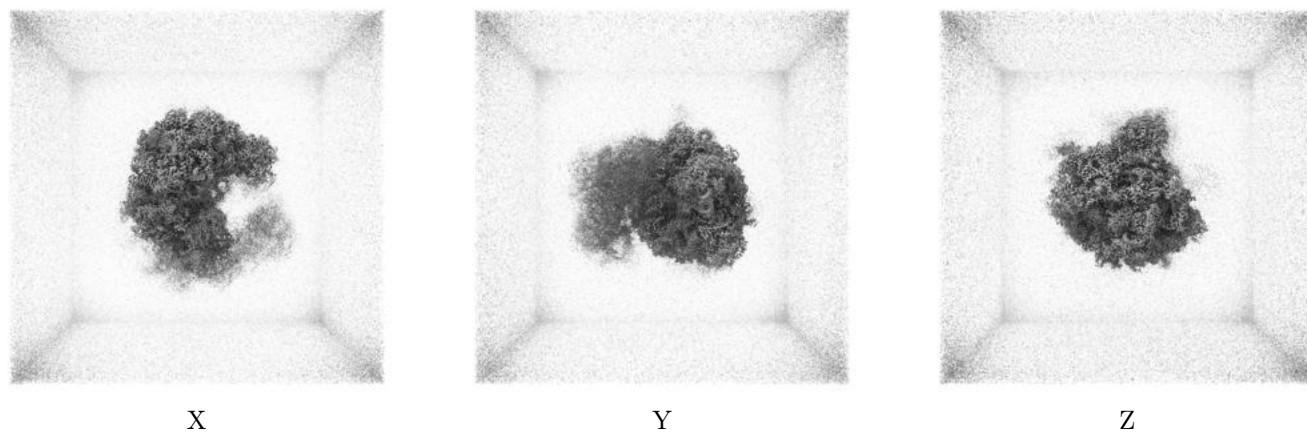
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.26. 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.

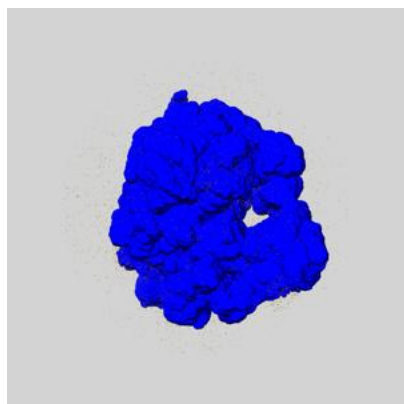
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

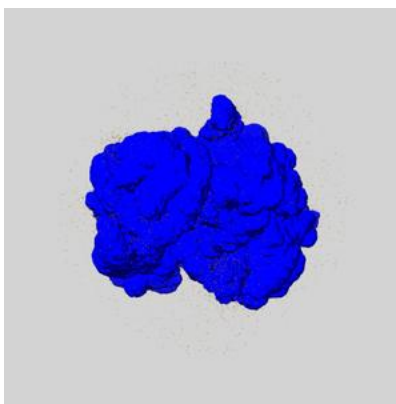
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

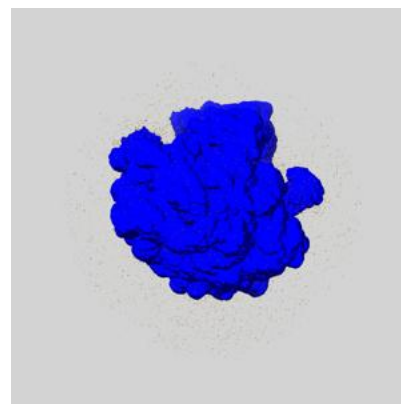
### 6.6.1 emd\_43972\_msk\_1.map [i](#)



X



Y

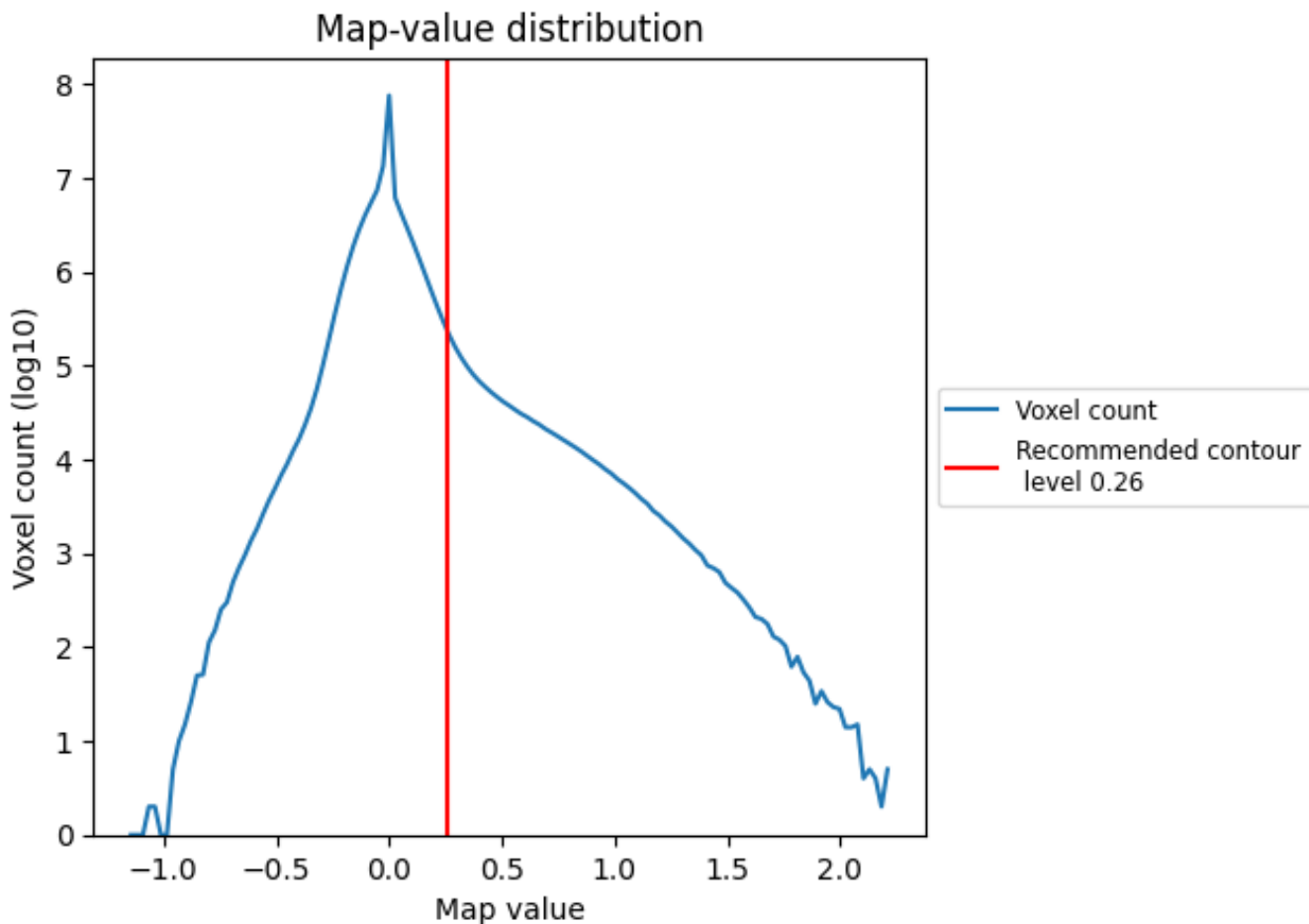


Z

## 7 Map analysis [i](#)

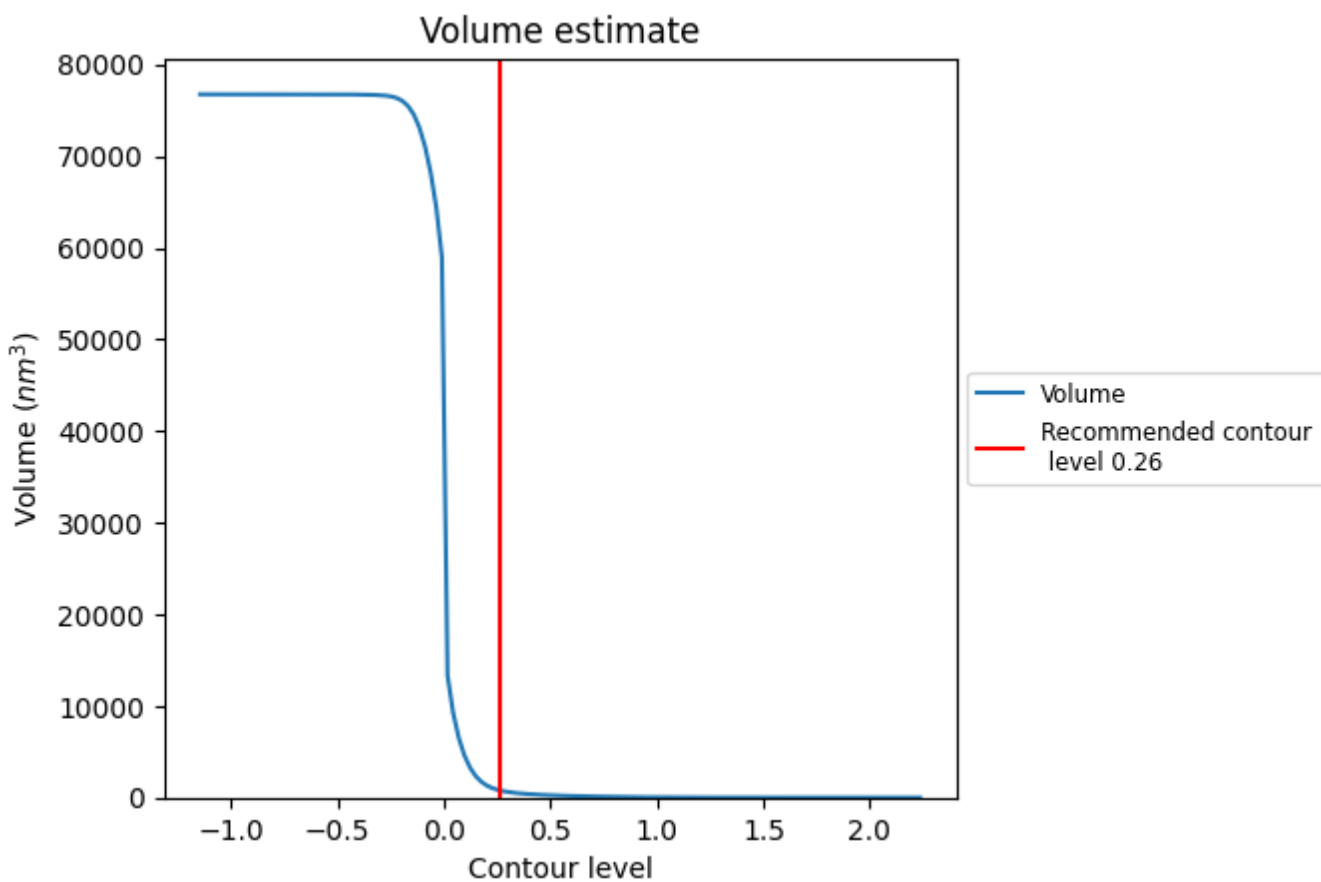
This section contains the results of statistical analysis of the map.

### 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.

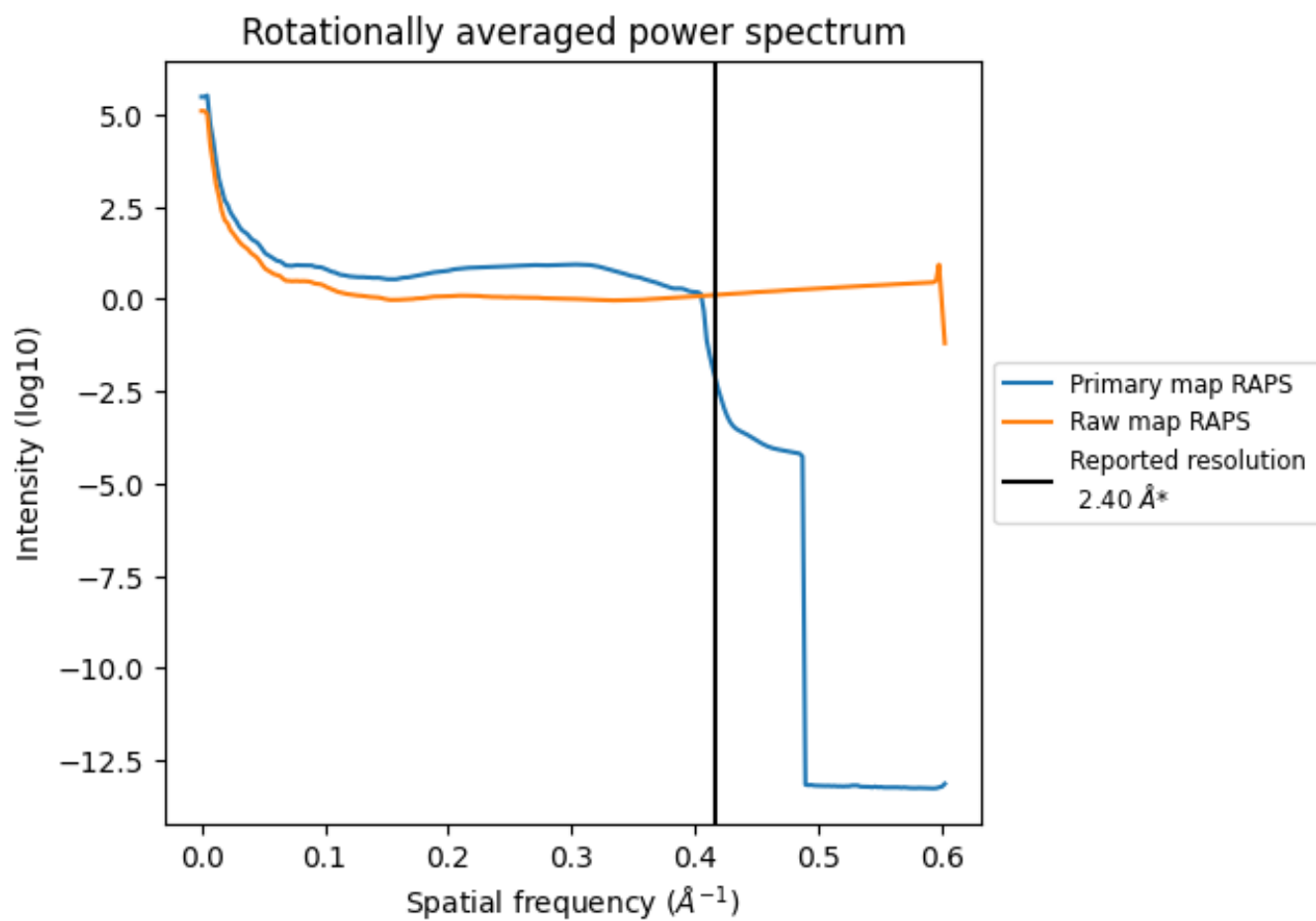
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 798 nm<sup>3</sup>; this corresponds to an approximate mass of 720 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 [i](#)

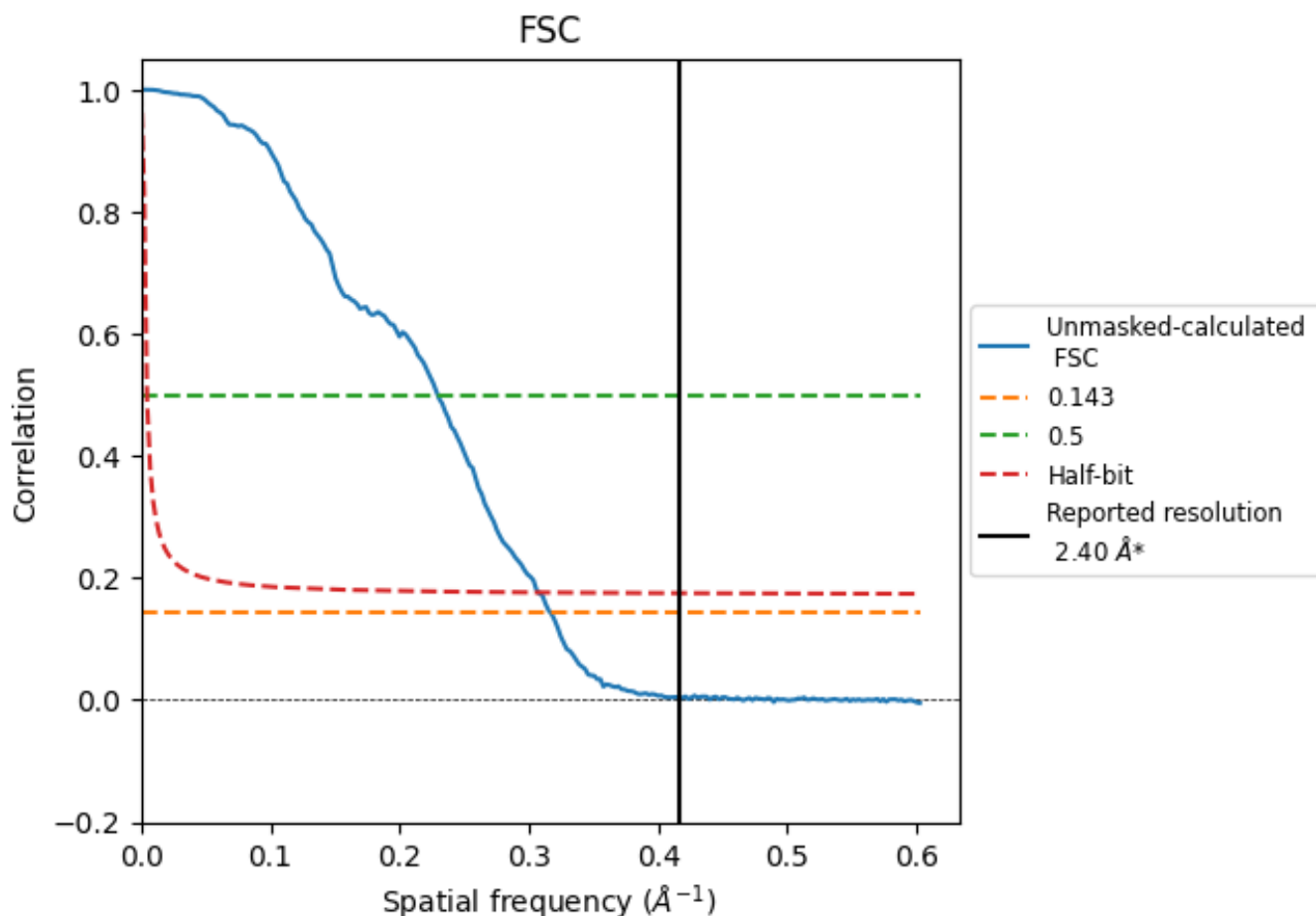


\*Reported resolution corresponds to spatial frequency of 0.417 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.417 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

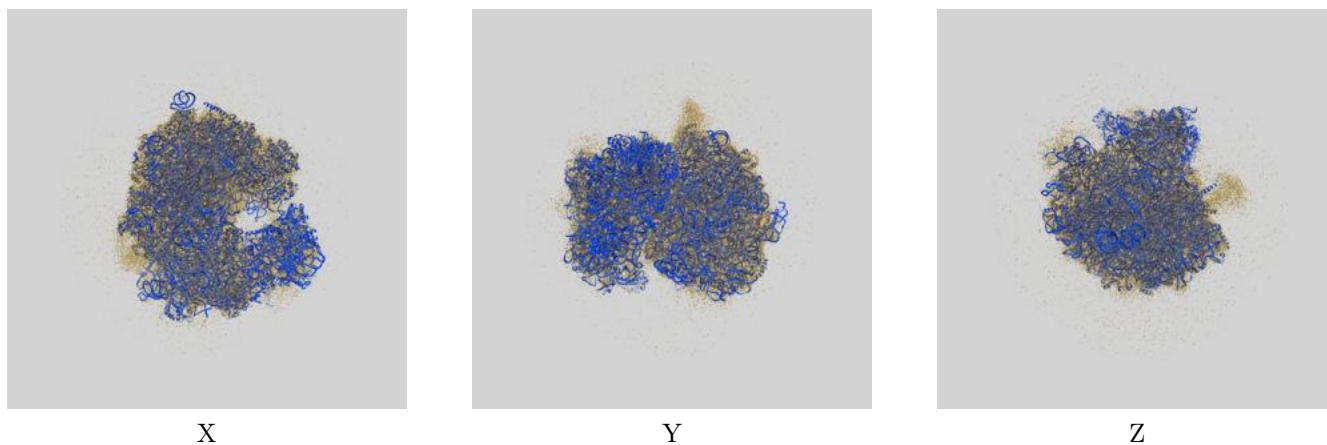
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	4.36	3.25

\*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 3.16 differs from the reported value 2.4 by more than 10 %

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

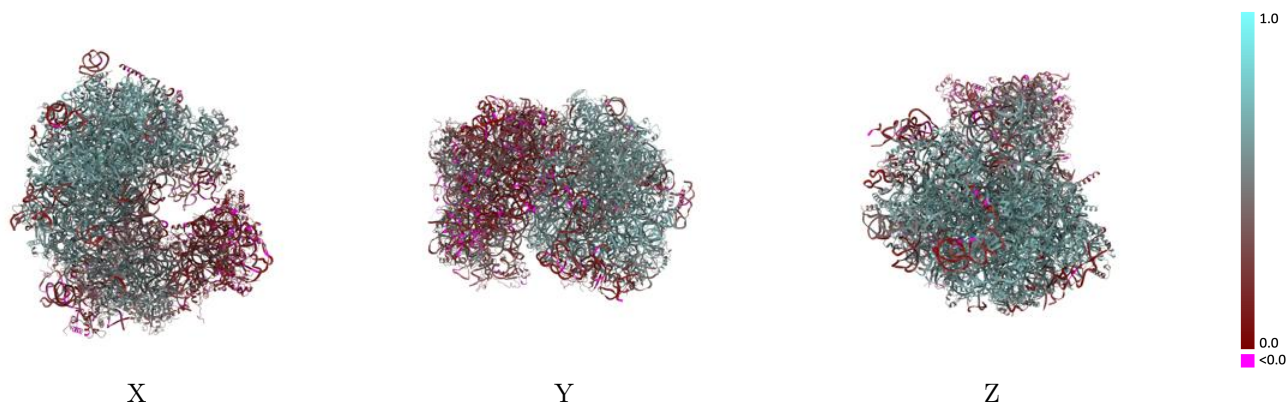
This section contains information regarding the fit between EMDB map EMD-43972 and PDB model 9AXT. Per-residue inclusion information can be found in section 3 on page 18.

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



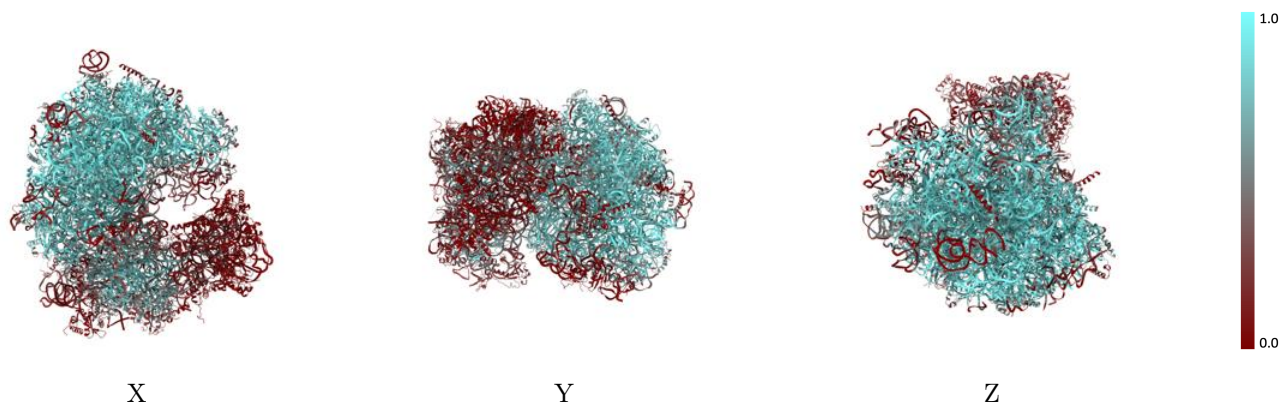
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



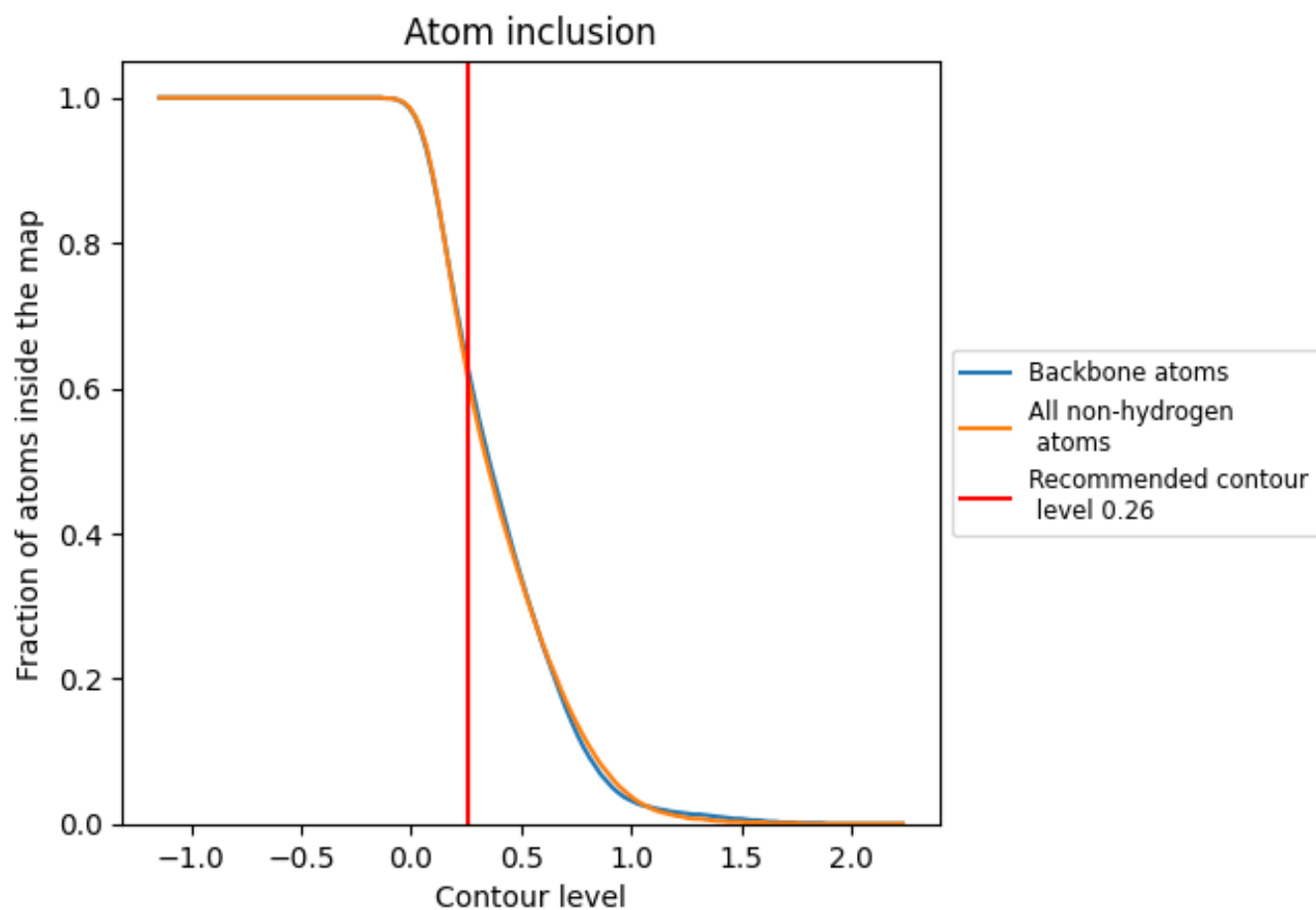
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.26).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 61% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6110	0.4710
AA	0.3830	0.3040
AD	0.4760	0.4750
AE	0.3310	0.4020
AF	0.5420	0.4860
AG	0.0350	0.1970
AH	0.5600	0.4930
AI	0.0700	0.2400
AJ	0.0850	0.2720
AK	0.1760	0.3090
AL	0.4000	0.4120
AM	0.3840	0.4250
AN	0.0180	0.1400
AO	0.5670	0.4850
AP	0.0020	0.1310
AQ	0.4300	0.4500
AR	0.3800	0.4060
AS	0.0380	0.1410
AT	0.0660	0.2240
AU	0.1050	0.2880
AV	0.0490	0.1830
AW	0.0630	0.2100
Aa	0.0760	0.2020
Ab	0.5120	0.4800
Ac	0.7430	0.5550
Ad	0.1950	0.3170
Ae	0.2370	0.3540
Af	0.0200	0.1580
Ag	0.4830	0.4510
Ah	0.2880	0.4020
Ai	0.0820	0.3060
Aj	0.0540	0.2630
Ak	0.0220	0.2230
B0	0.7550	0.5840
B1	0.7120	0.5720



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Chain	Atom inclusion	Q-score
B2	0.7780	0.5350
B3	0.8450	0.5590
B4	0.8680	0.5760
BN	0.9080	0.6490
BO	0.9010	0.6430
BP	0.8980	0.6450
BQ	0.6680	0.5380
BR	0.6630	0.5350
BS	0.8430	0.6070
BT	0.7310	0.5850
BU	0.0610	0.2580
BV	0.1460	0.3590
BW	0.3270	0.3660
BX	0.7540	0.5940
BY	0.7320	0.5710
BZ	0.9730	0.6700
Ba	0.8950	0.6410
Bb	0.9090	0.6520
Bc	0.9020	0.6490
Bd	0.8390	0.6140
Be	0.8170	0.6100
Bf	0.7600	0.5740
Bg	0.5590	0.5040
Bh	0.8420	0.6260
Bi	0.7280	0.5810
Bj	0.8640	0.6230
Bk	0.8030	0.6140
Bl	0.7320	0.5650
Bm	0.9360	0.6580
Bn	0.8620	0.6210
Bo	0.6070	0.5150
Bp	0.8550	0.6230
Bq	0.9110	0.6470
Br	0.9230	0.6500
Bs	0.8970	0.6480
Bt	0.8000	0.6100
Bu	0.8170	0.6170
Bv	0.9600	0.6670
Bw	0.5920	0.5100
Bx	0.7080	0.5240
By	0.6030	0.5620