



wwPDB EM Validation Summary Report ⓘ

May 16, 2026 – 08:45 am BST

PDB ID : 9RVU / pdb_00009rvu
EMDB ID : EMD-54290
Title : in situ S. pombe hibernating ribosome after 7 days of glucose depletion
Authors : Rosa, H.; Gluc, M.; Jomaa, A.; Mattei, S.
Deposited on : 2025-07-09
Resolution : 3.38 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

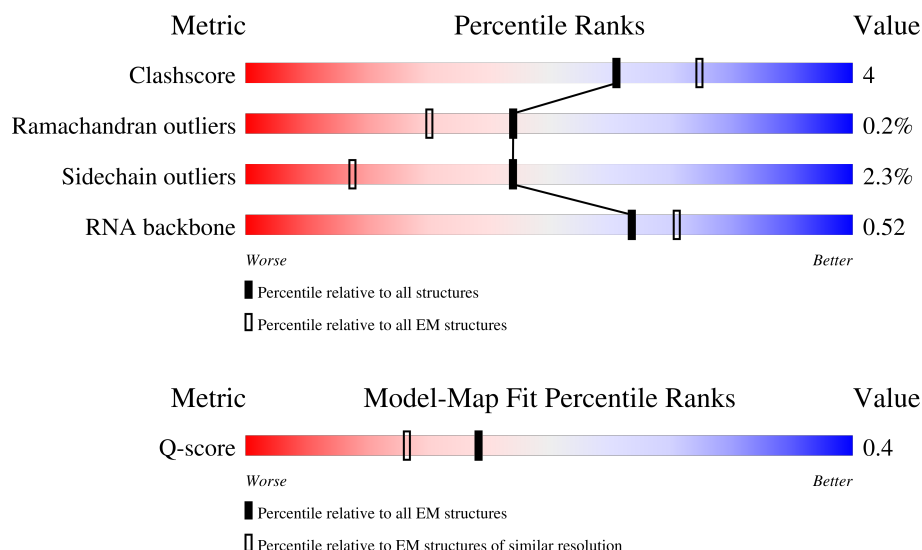
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 3.38 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	14261 (2.88 - 3.88)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1842	
2	AD	292	
3	AE	252	

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Mol	Chain	Length	Quality of chain
4	AF	253	
5	AG	249	
6	AH	262	
7	AI	203	
8	AJ	239	
9	AK	195	
10	AL	200	
11	AM	192	
12	AN	147	
13	AO	152	
14	AP	145	
15	AQ	151	
16	AR	139	
17	AS	154	
18	AT	140	
19	AU	131	
20	AV	152	
21	AW	144	
22	Aa	118	
23	Ab	87	
24	Ac	130	
25	Ad	143	
26	Ae	134	
27	Af	89	
28	Ag	119	

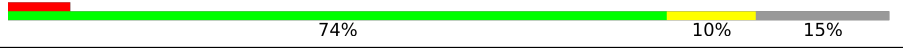
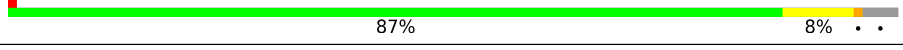
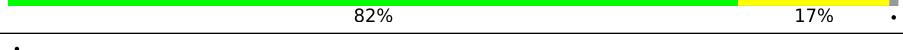
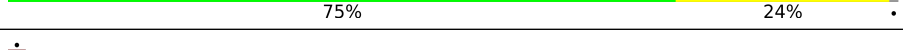
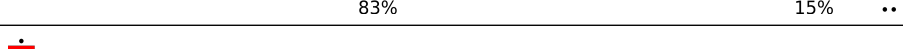
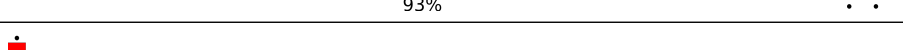
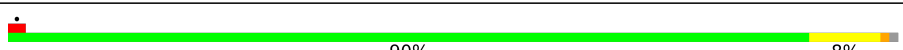
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Mol	Chain	Length	Quality of chain
29	Ah	83	
30	Ai	68	
31	Aj	56	
32	Ak	61	
33	Am	314	
34	B0	106	
35	B1	94	
36	B2	3498	
37	B3	246	
38	B4	165	
39	BN	253	
40	BO	388	
41	BP	363	
42	BQ	294	
43	BR	195	
44	BS	251	
45	BT	259	
46	BV	221	
47	BW	174	
48	BX	208	
49	BY	134	
50	BZ	201	
51	Ba	197	
52	Bc	187	
53	Bd	193	

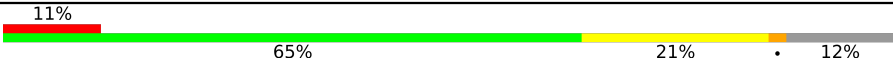
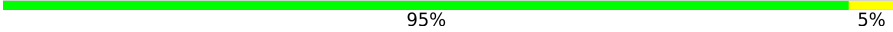
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Mol	Chain	Length	Quality of chain
54	Be	176	
55	Bf	160	
56	Bg	117	
57	Bh	139	
58	Bi	149	
59	Bj	141	
60	Bk	126	
61	Bl	136	
62	Bm	148	
63	Bn	61	
64	Bo	109	
65	Bp	113	
66	Bq	127	
67	Br	108	
68	Bs	111	
69	Bt	122	
70	Bu	99	
71	Bv	91	
72	Bw	74	
73	Bx	51	
74	By	134	
75	H1	284	
76	HE	842	
77	HL	216	
78	HS	106	

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Mol	Chain	Length	Quality of chain
79	HI	157	
80	BA	51	
81	BU	189	
82	Bb	187	
83	A	20	

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 209623 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 small subunit ribosomal RNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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 uS11A.

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	106	Total	C	N	O	S	0	0
			879	546	169	162	2		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13A.

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
21	AW	142	Total	C	N	O	S	0	0
			1119	699	212	205	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Aa	100	Total	C	N	O	S	0	0
			810	508	155	145	2		

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

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

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

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

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

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

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

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

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

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

- 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 eS30A.

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 Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Am	314	Total	C	N	O	S	0	0
			2458	1549	422	478	9		

- Molecule 34 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 36 is a RNA chain called 28S large subunit ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B2	3249	Total	C	N	O	P	0	0
			69470	31043	12521	22657	3249		

- Molecule 37 is a RNA chain called 5S large subunit ribosomal RNA.

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

- Molecule 38 is a RNA chain called 5.8S large subunit ribosomal RNA.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL2A.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL3A.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL18B.

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

- Molecule 43 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	171	Total	C	N	O	S	0	0
			1333	857	244	229	3		

- Molecule 44 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	223	Total	C	N	O	S	0	0
			1814	1158	334	319	3		

- Molecule 45 is a protein called Large ribosomal subunit protein eL8.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	219	Total	C	N	O	S	0	0
			1769	1114	340	305	10		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	201	Total	C	N	O	S	0	0
			1607	1005	320	281	1		

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

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

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

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

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

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

- Molecule 52 is a protein called Large ribosomal subunit protein eL18B.

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

- Molecule 53 is a protein called Large ribosomal subunit protein eL19B.

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

- Molecule 54 is a protein called Large ribosomal subunit protein eL20A.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL21B.

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

- Molecule 56 is a protein called Large ribosomal subunit protein eL22.

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

- Molecule 57 is a protein called Large ribosomal subunit protein uL14A.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL24B.

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

- Molecule 59 is a protein called Large ribosomal subunit protein uL23A.

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

- Molecule 60 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 61 is a protein called Large ribosomal subunit protein eL27A.

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

- Molecule 62 is a protein called Large ribosomal subunit protein uL15B.

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

- Molecule 63 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 64 is a protein called Large ribosomal subunit protein eL30A.

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

- Molecule 65 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 66 is a protein called Large ribosomal subunit protein eL32A.

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

- Molecule 67 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 68 is a protein called Large ribosomal subunit protein eL34B.

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

- Molecule 69 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 70 is a protein called Large ribosomal subunit protein eL36B.

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

- Molecule 71 is a protein called Large ribosomal subunit protein eL37B.

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

- Molecule 72 is a protein called Large ribosomal subunit protein eL38A.

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

- Molecule 73 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 74 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	By	133	Total	C	N	O	S	0	0
			1031	641	203	186	1		

- Molecule 75 is a protein called Ribosome-associated protein oga1.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	H1	100	Total	C	N	O	0	0
			758	449	148	161		

- Molecule 76 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	HE	842	Total	C	N	O	S	0	0
			6544	4134	1132	1239	39		

- Molecule 77 is a protein called Large ribosomal subunit protein uL1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	HL	216	Total	C	N	O	S	0	0
			1679	1072	297	302	8		

- Molecule 78 is a protein called SDO1-like protein C21C3.19.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	HS	106	Total	C	N	O	S	0	0
			834	517	147	167	3		

- Molecule 79 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	HI	138	Total	C	N	O	S	0	0
			1067	658	187	213	9		

- Molecule 80 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BA	51	Total	C	N	O	S	0	0
			413	257	84	67	5		

- Molecule 81 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BU	184	Total	C	N	O	S	0	0
			1461	922	267	267	5		

- Molecule 82 is a protein called Large ribosomal subunit protein uL22A.

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

- Molecule 83 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	A	20	Total	C	N	O	0	0
			149	90	34	25		

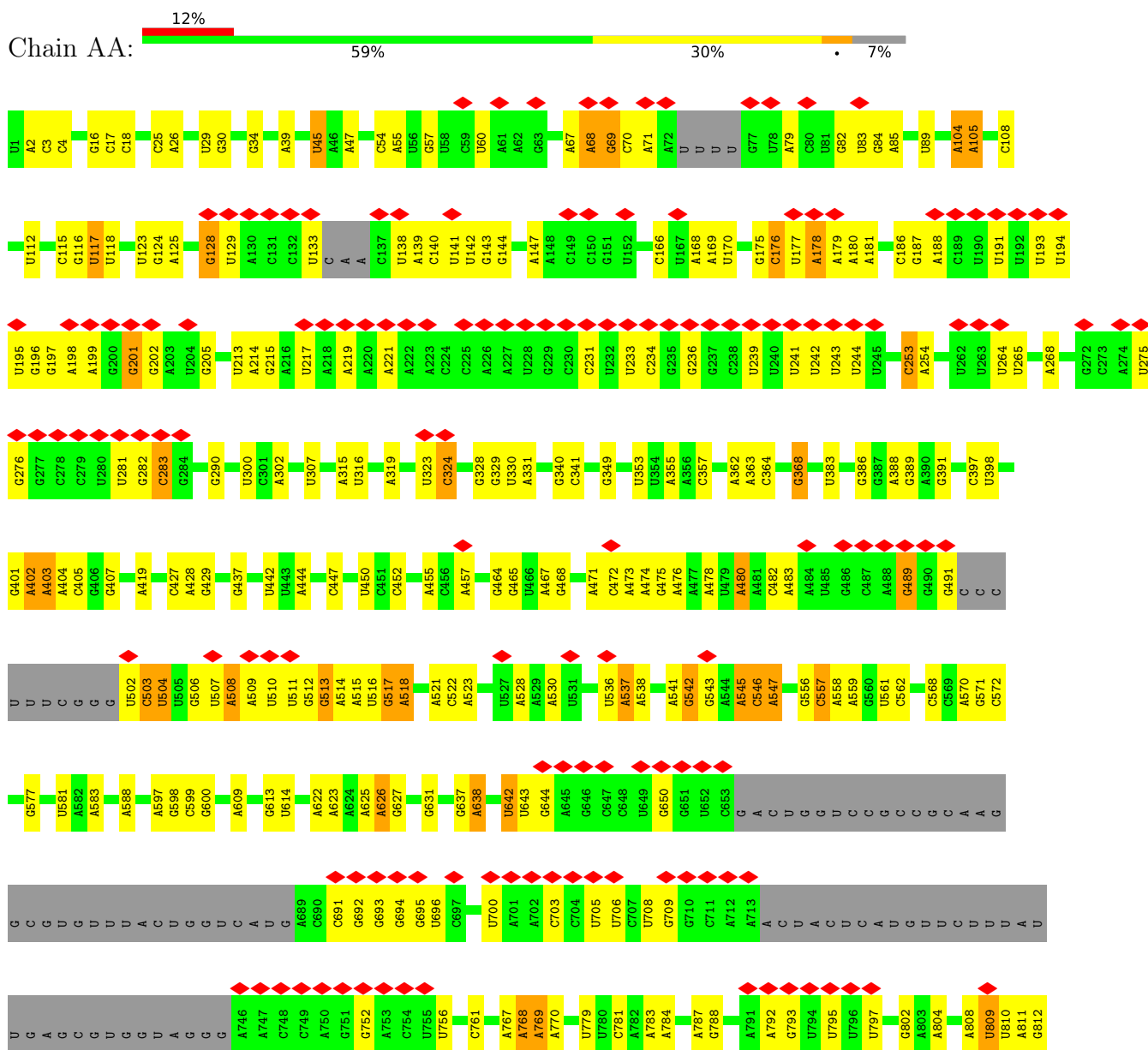
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Ag	1	Total 1	Zn 1	0
84	Ah	1	Total 1	Zn 1	0
84	Aj	1	Total 1	Zn 1	0
84	B0	1	Total 1	Zn 1	0
84	B1	1	Total 1	Zn 1	0
84	Bv	1	Total 1	Zn 1	0

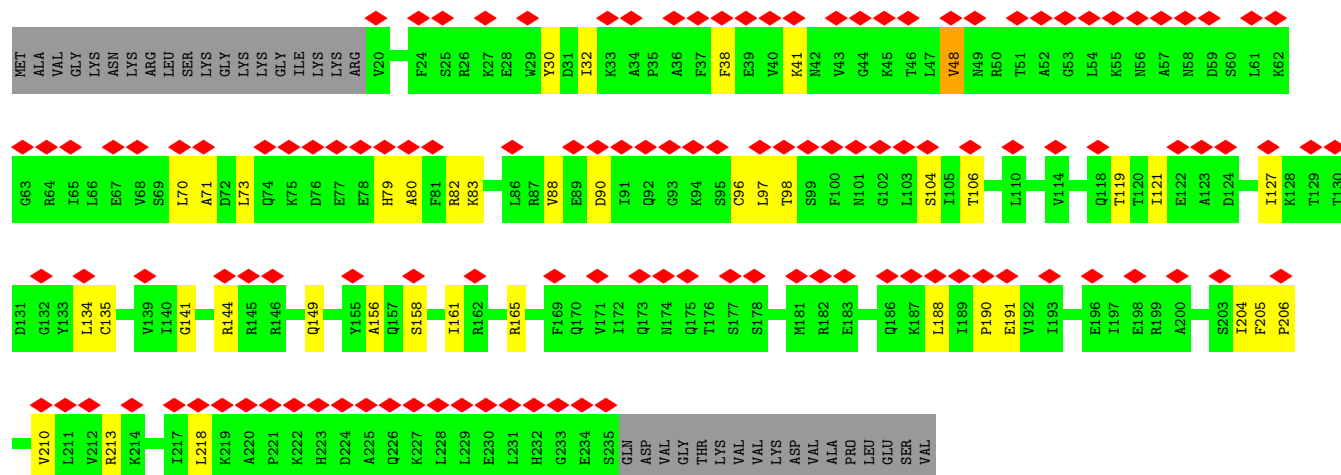
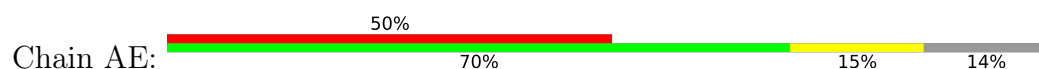
3 Residue-property plots

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.

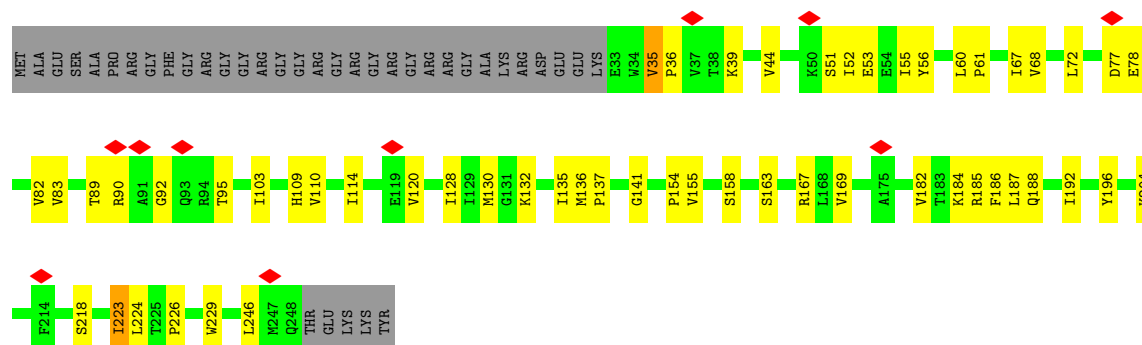
- Molecule 1: 18S small subunit ribosomal RNA



- Molecule 3: Small ribosomal subunit protein eS1B

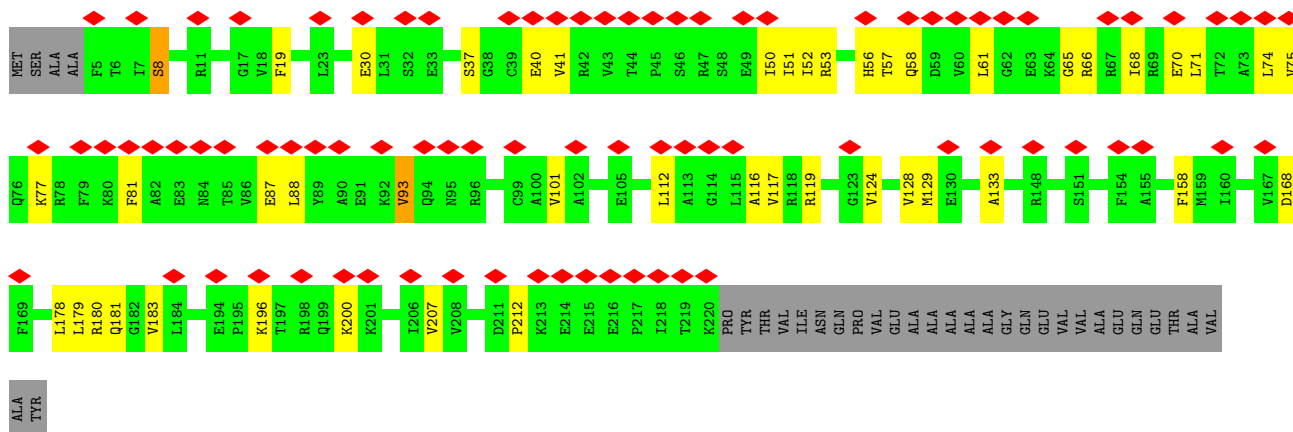


- Molecule 4: Small ribosomal subunit protein uS5

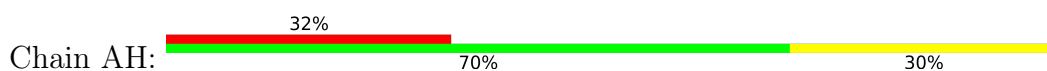


- Molecule 5: Small ribosomal subunit protein uS3

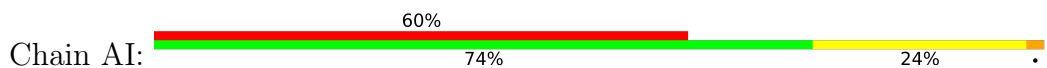


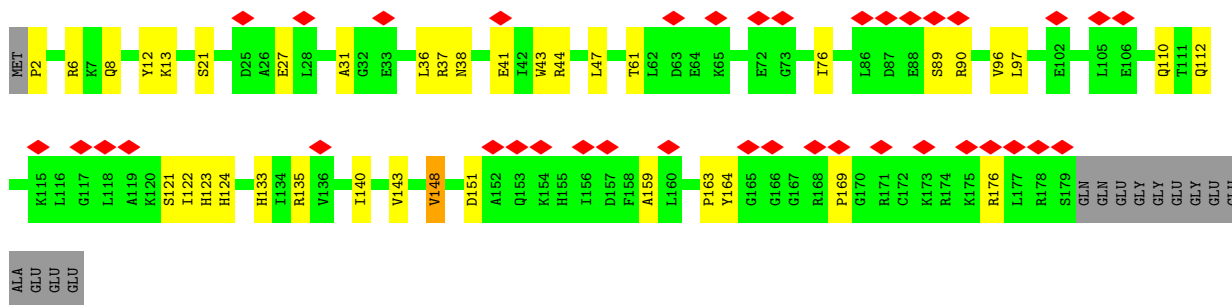


• Molecule 6: Small ribosomal subunit protein eS4C

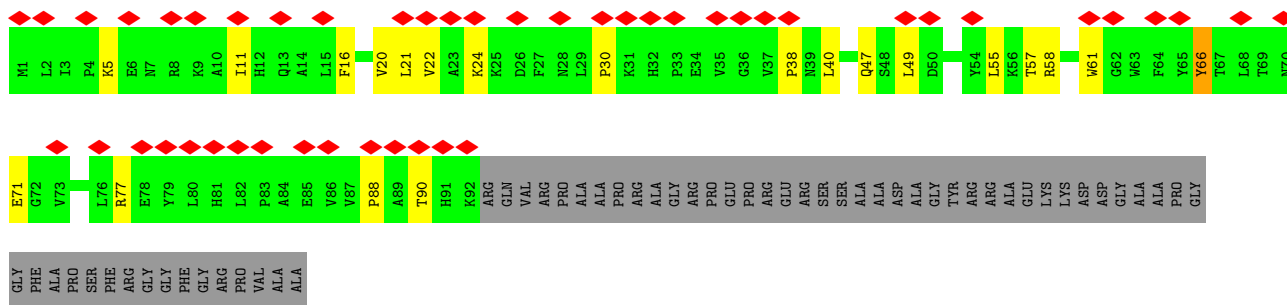


• Molecule 7: Small ribosomal subunit protein uS7A

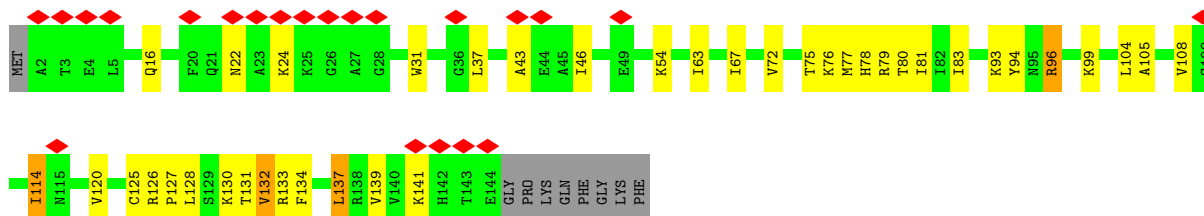




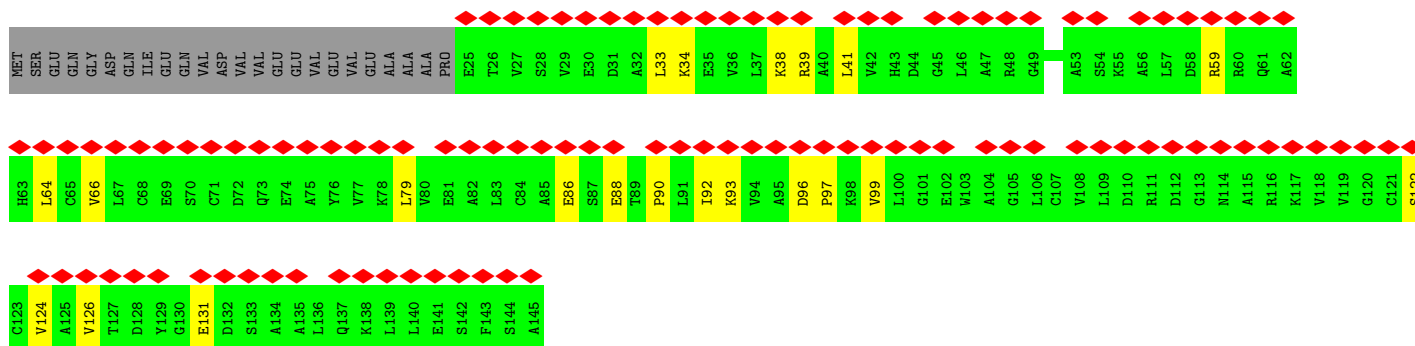
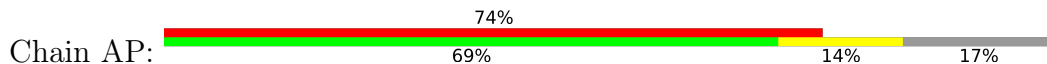
- Molecule 12: Small ribosomal subunit protein eS10B



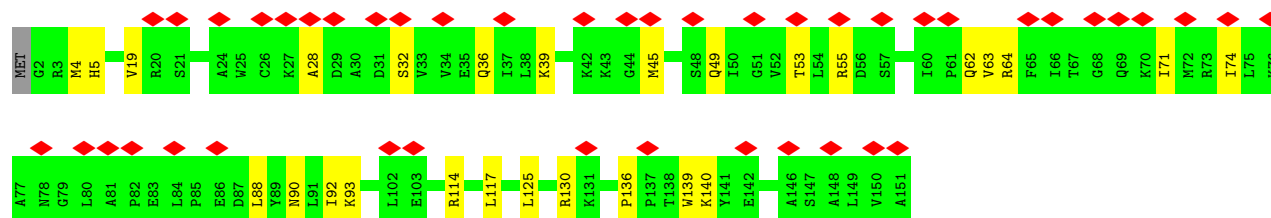
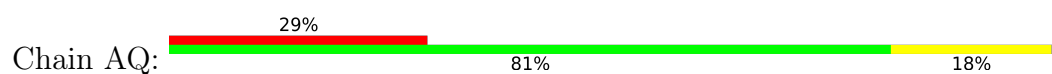
- Molecule 13: Small ribosomal subunit protein uS17A



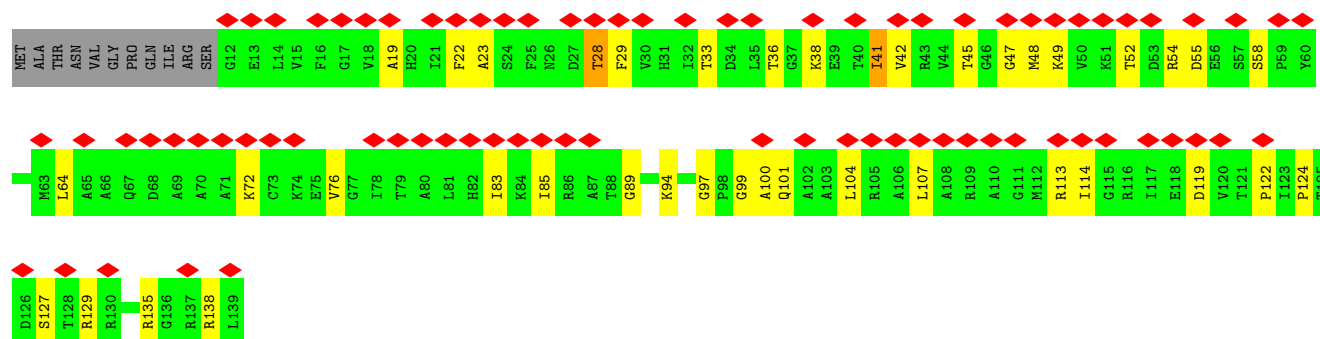
- Molecule 14: Small ribosomal subunit protein eS12A



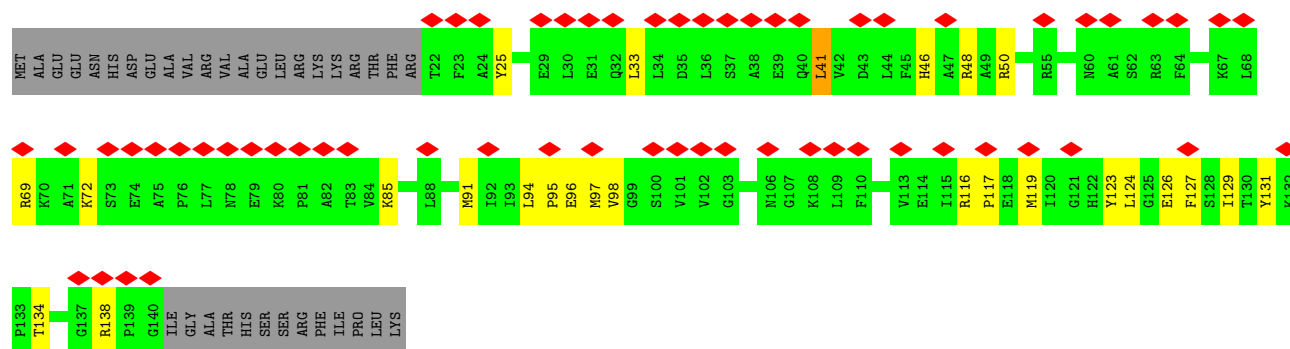
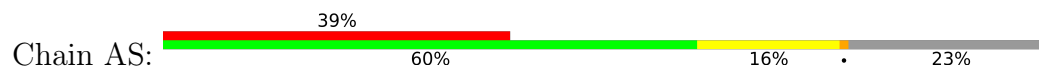
- Molecule 15: Small ribosomal subunit protein uS15



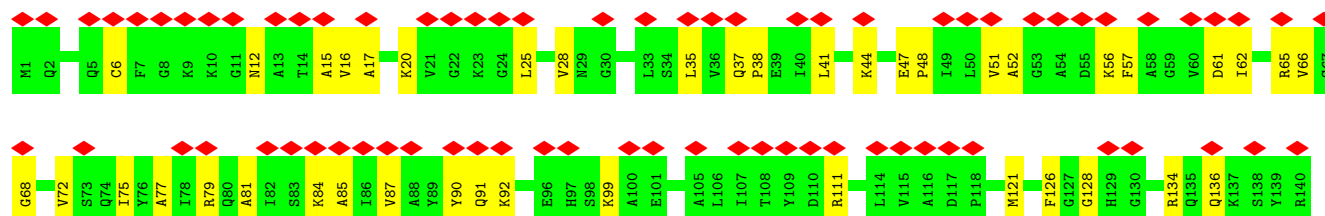
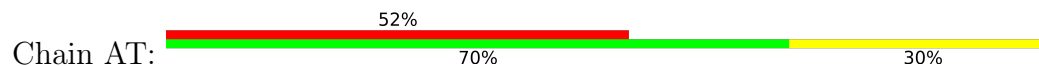
• Molecule 16: Small ribosomal subunit protein uS11A



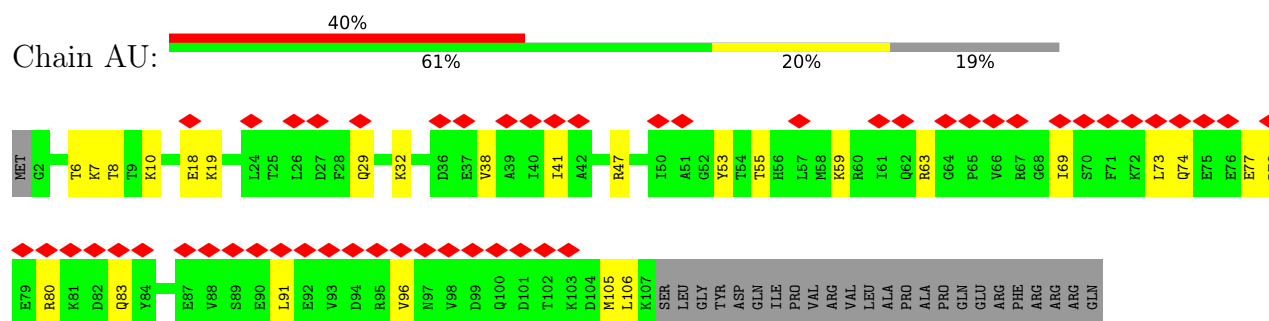
• Molecule 17: Small ribosomal subunit protein uS19B



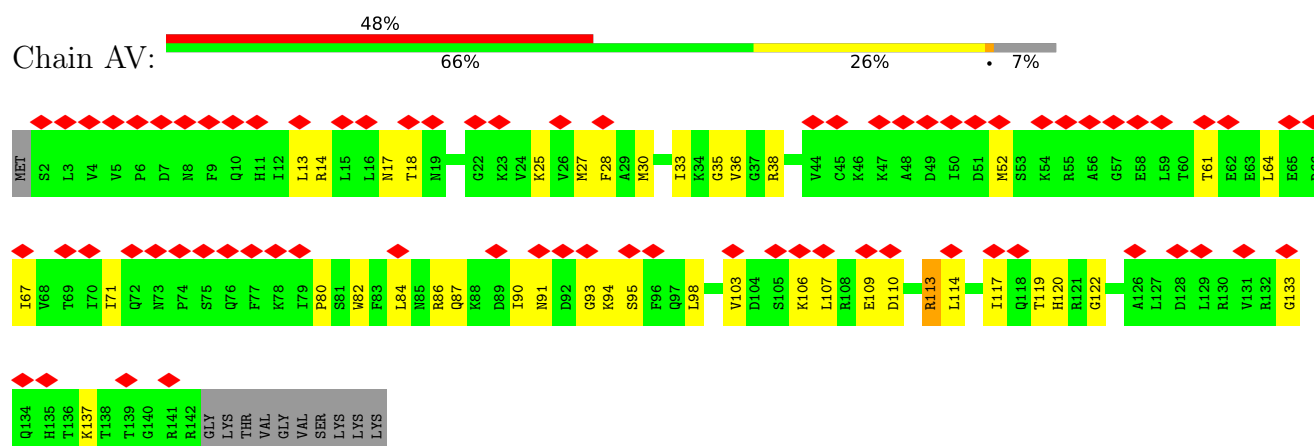
• Molecule 18: Small ribosomal subunit protein uS9A



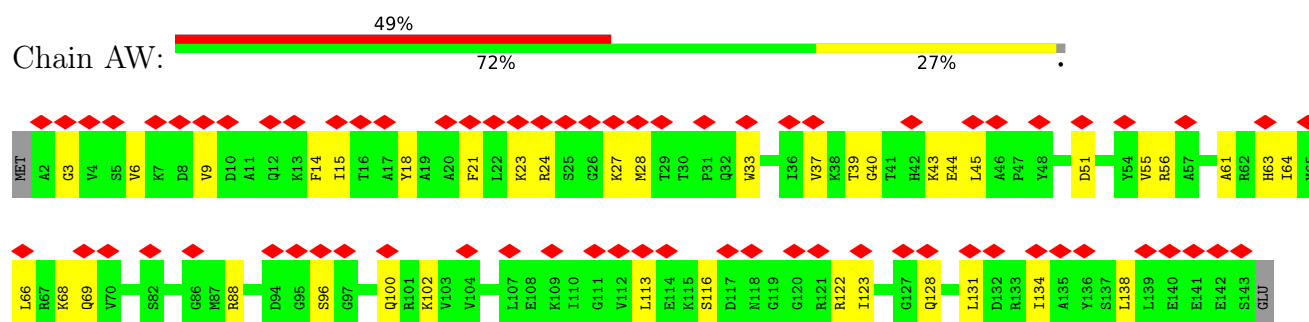
- Molecule 19: Small ribosomal subunit protein eS17A



- Molecule 20: Small ribosomal subunit protein uS13A



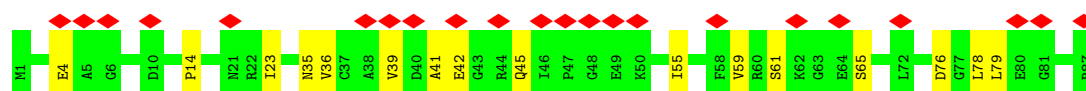
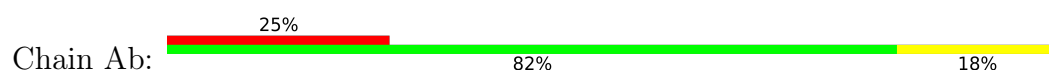
- Molecule 21: Small ribosomal subunit protein eS19A



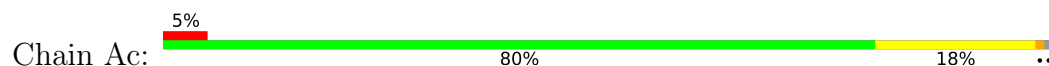
- Molecule 22: Small ribosomal subunit protein uS10



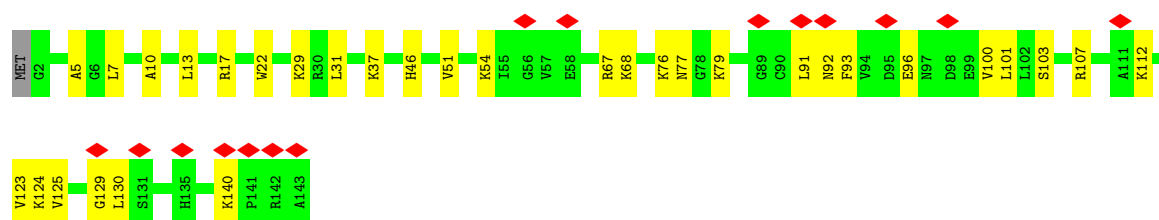
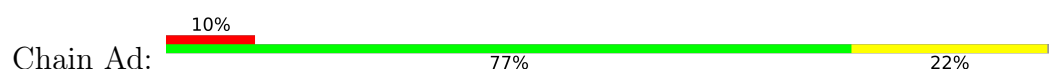
- Molecule 23: Small ribosomal subunit protein eS21



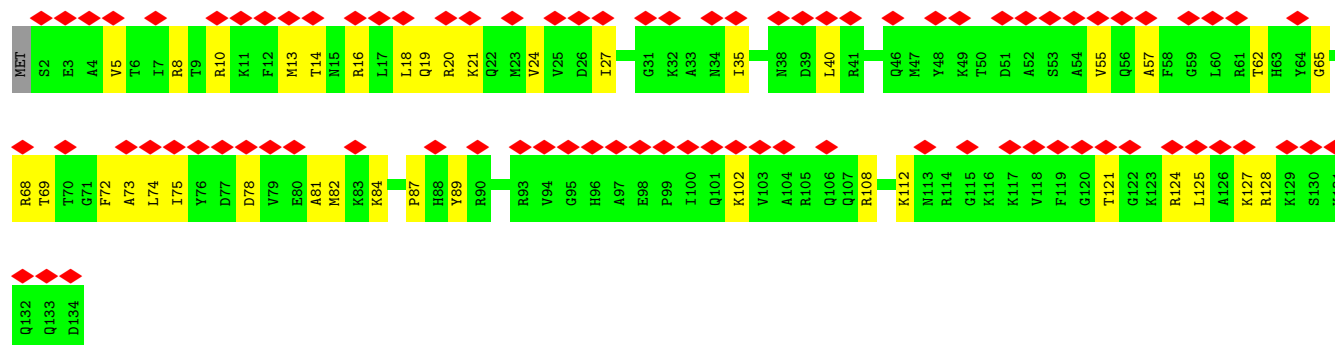
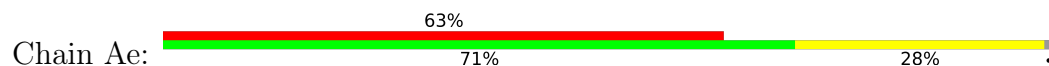
- Molecule 24: Small ribosomal subunit protein uS8A



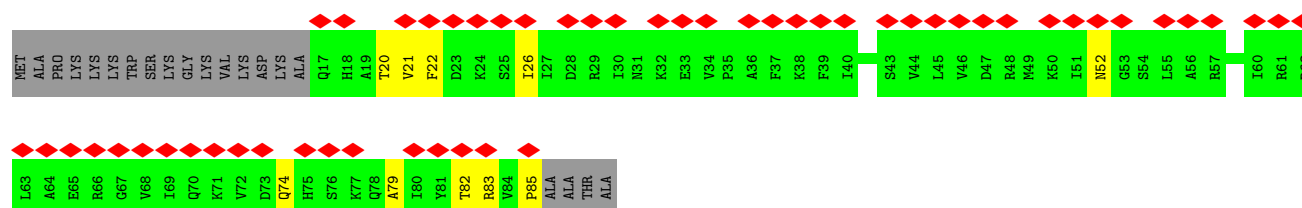
- Molecule 25: Small ribosomal subunit protein uS12A



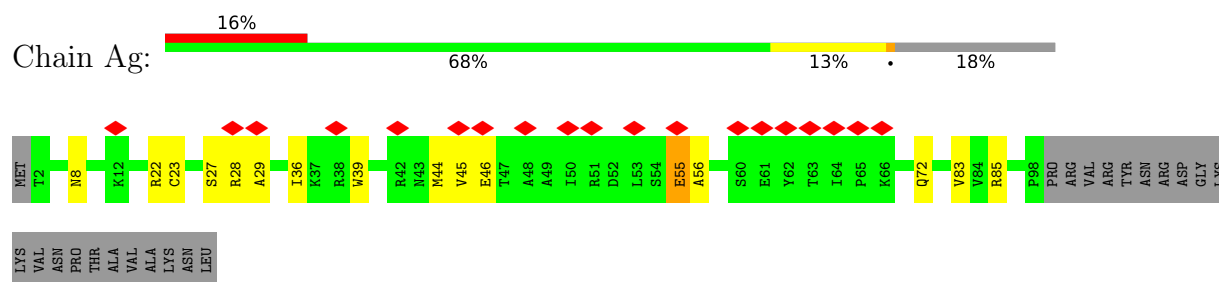
- Molecule 26: Small ribosomal subunit protein eS24A



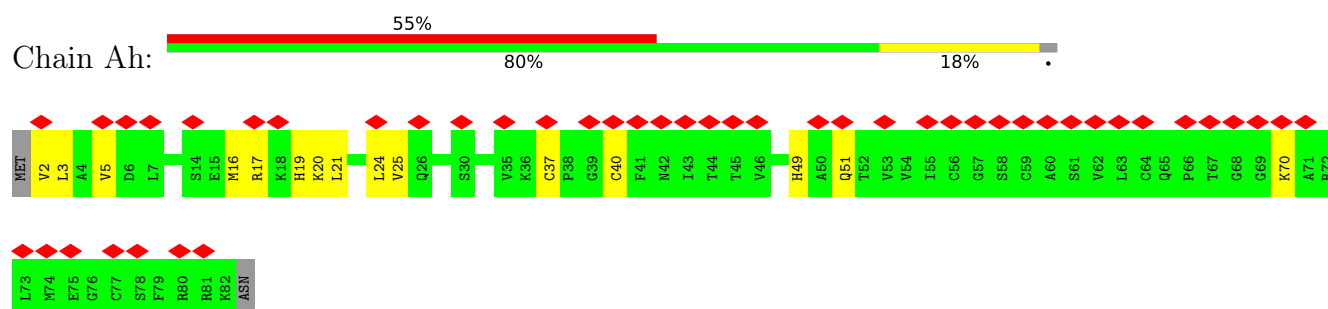
- Molecule 27: Small ribosomal subunit protein eS25A



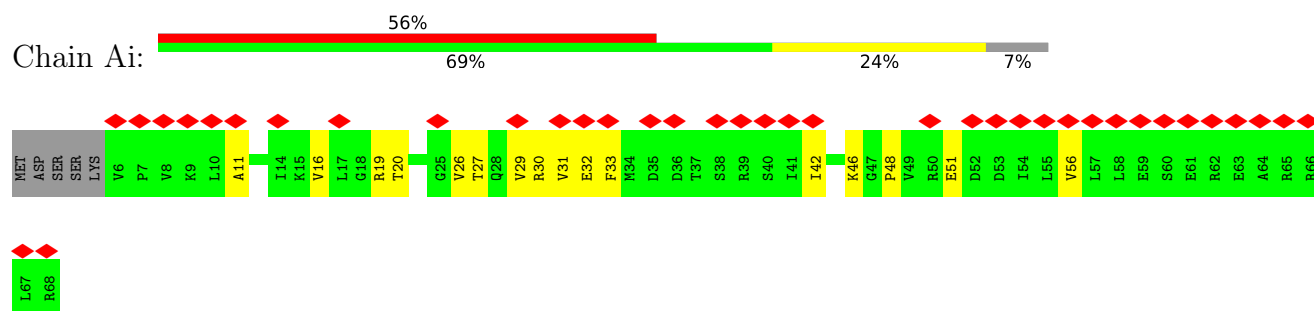
- Molecule 28: Small ribosomal subunit protein eS26B



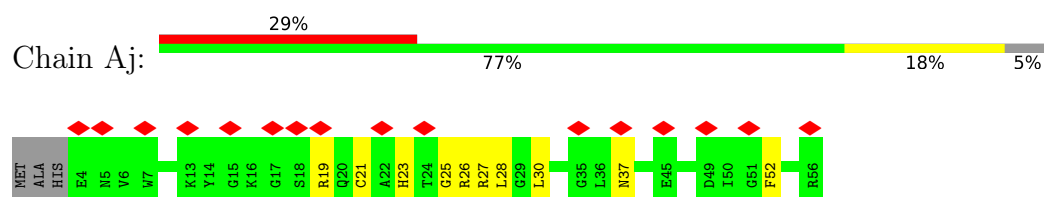
- Molecule 29: Small ribosomal subunit protein eS27



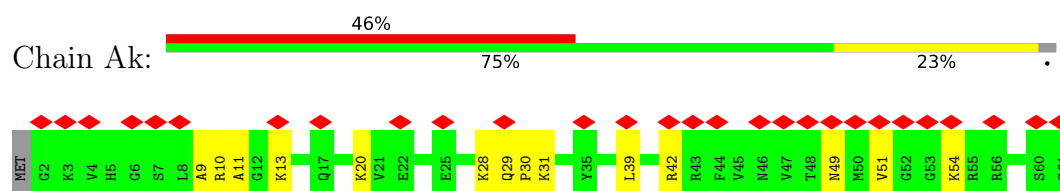
- Molecule 30: Small ribosomal subunit protein eS28A



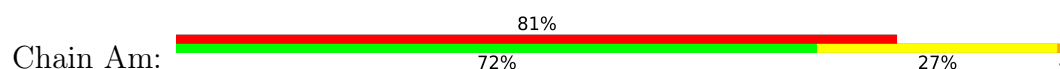
- Molecule 31: Small ribosomal subunit protein uS14

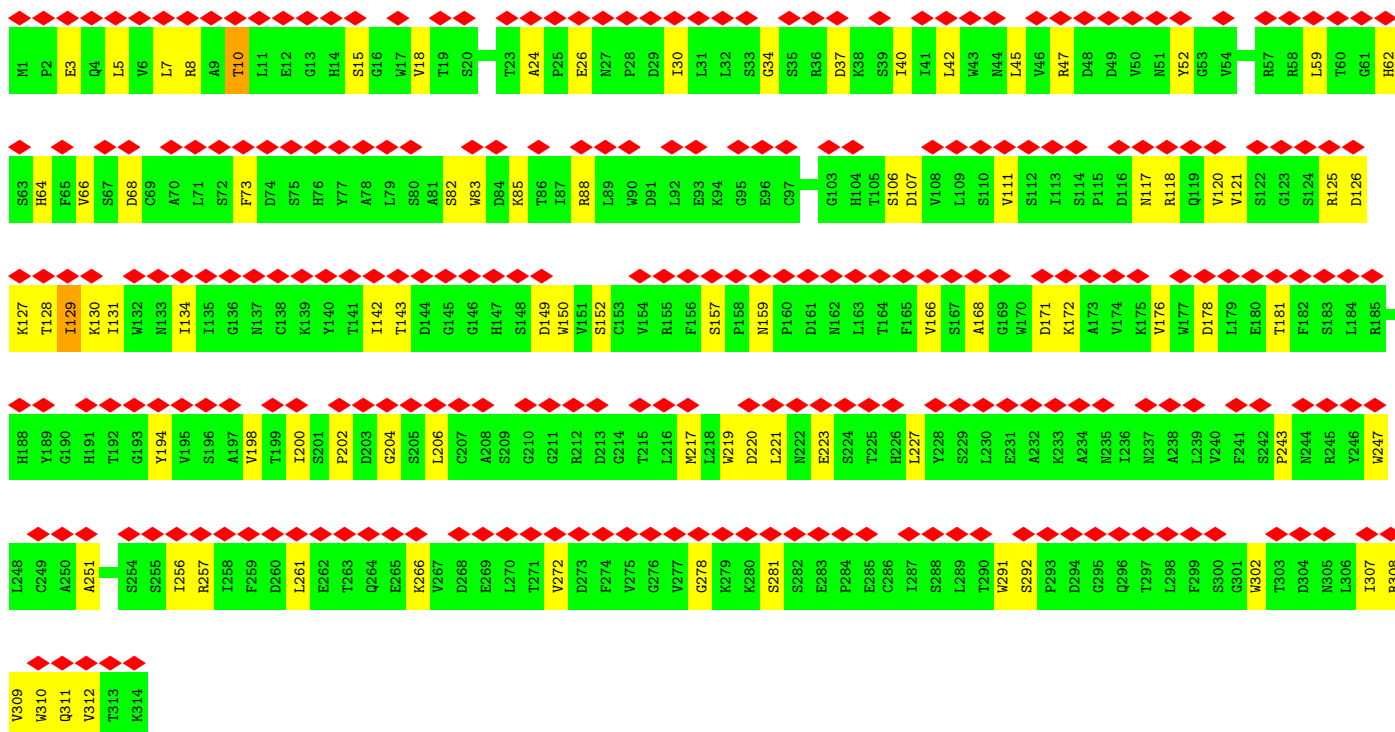


- Molecule 32: Small ribosomal subunit protein eS30A

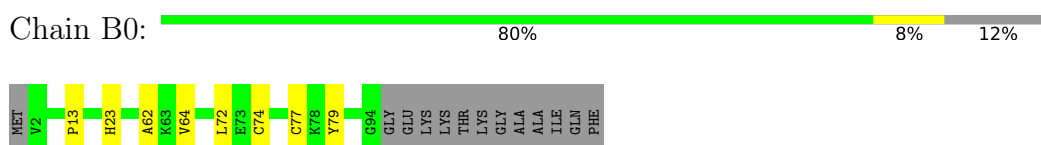


- Molecule 33: Small ribosomal subunit protein RACK1

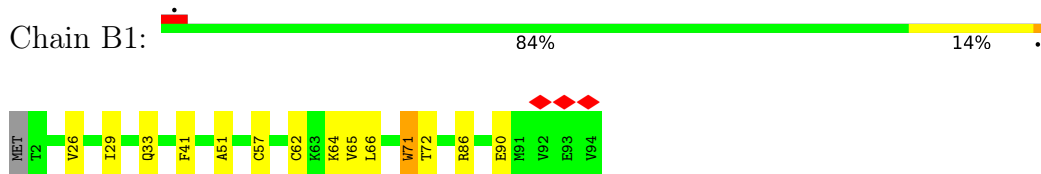




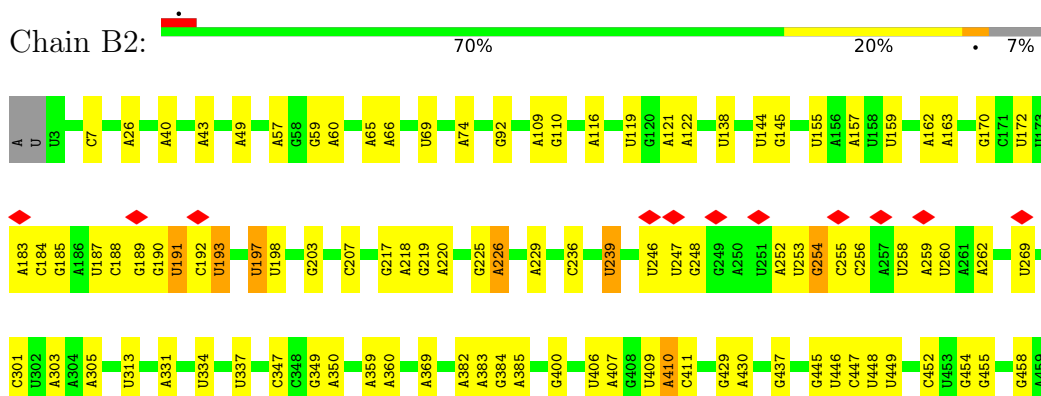
- Molecule 34: Large ribosomal subunit protein eL42



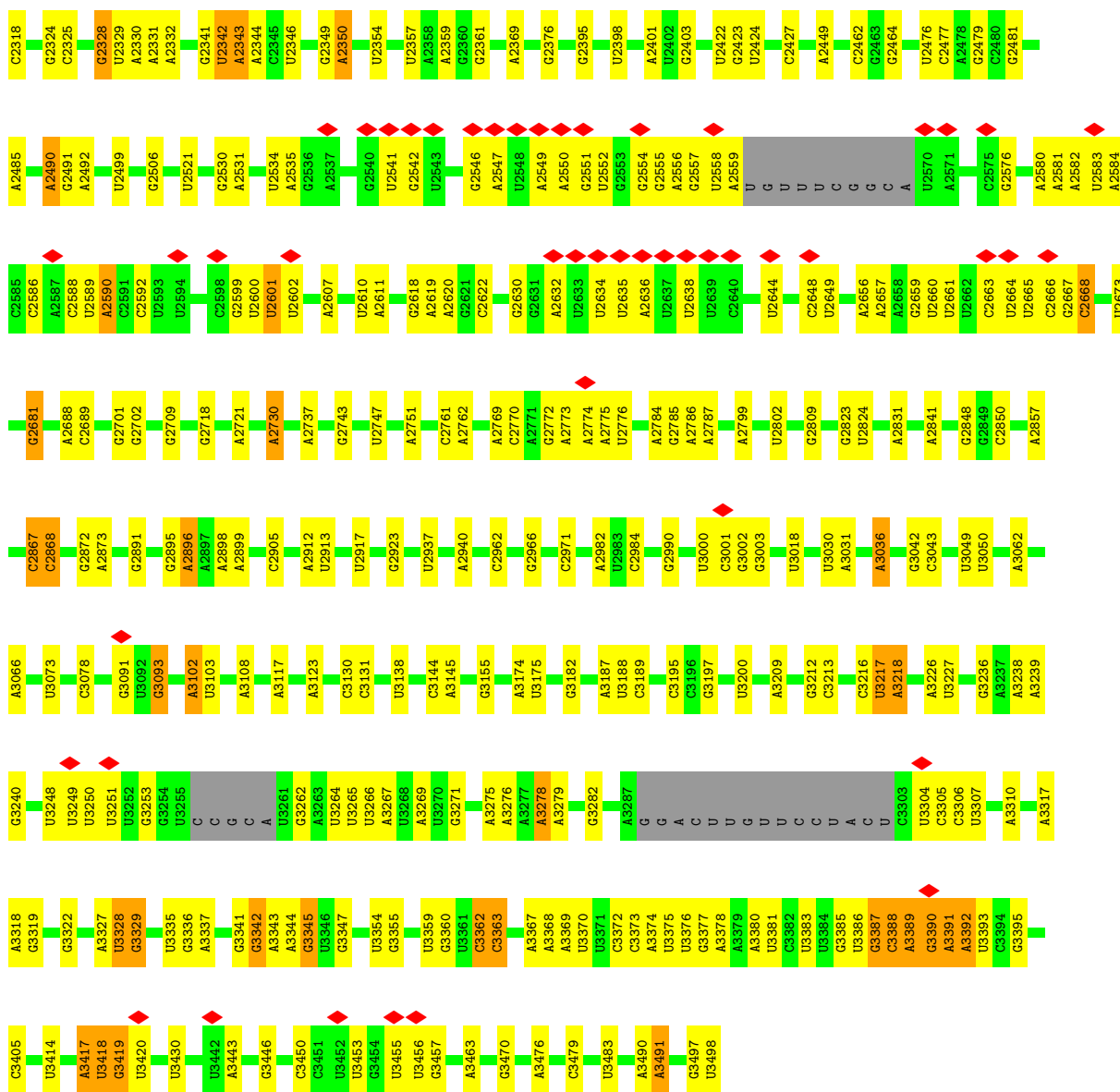
- Molecule 35: Large ribosomal subunit protein eL43A



- Molecule 36: 28S large subunit ribosomal RNA

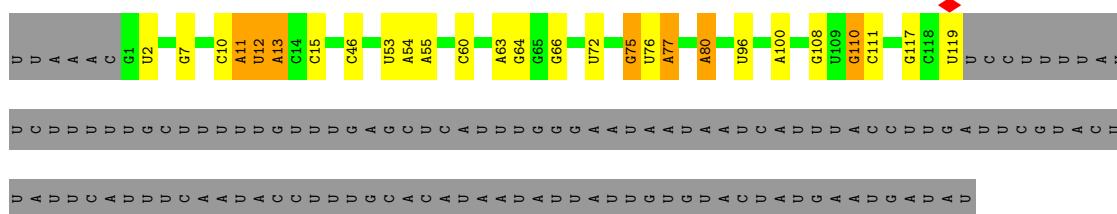






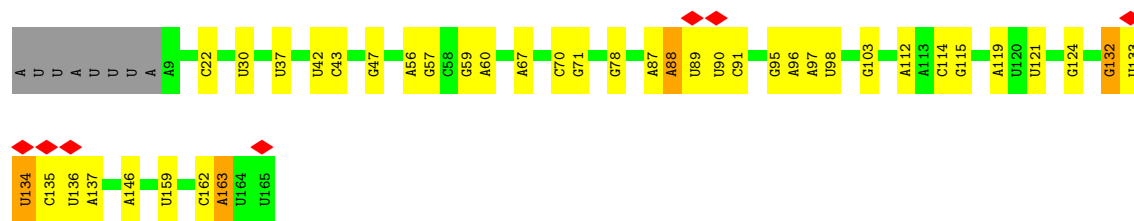
• Molecule 37: 5S large subunit ribosomal RNA

Chain B3: 37% 8% 52%



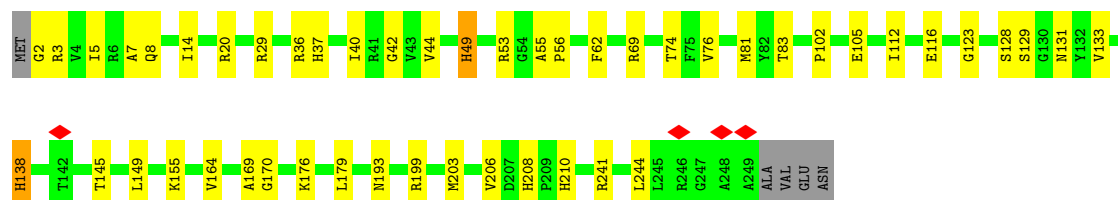
• Molecule 38: 5.8S large subunit ribosomal RNA

Chain B4: 71% 22% 5%



- Molecule 39: Large ribosomal subunit protein uL2A

Chain BN: 79% 19%



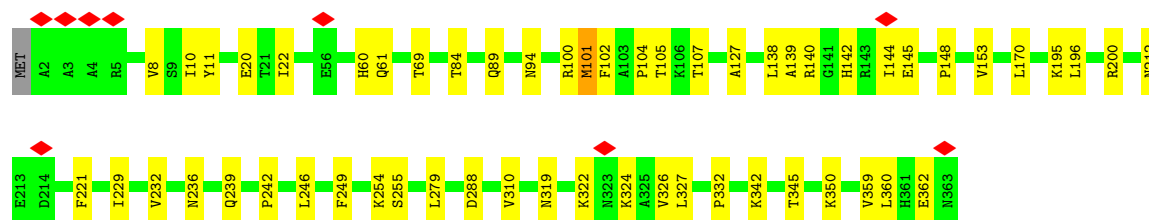
- Molecule 40: Large ribosomal subunit protein uL3A

Chain BO: 83% 16%



- Molecule 41: Large ribosomal subunit protein uL4A

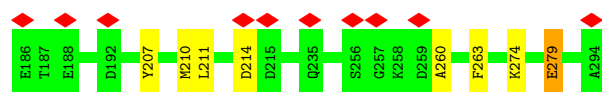
Chain BP: 84% 15%



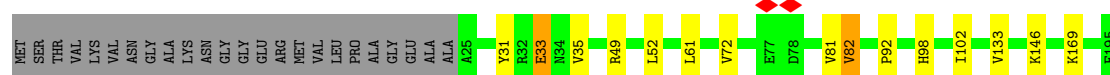
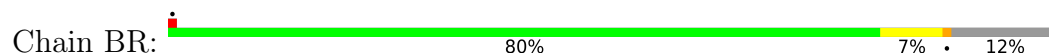
- Molecule 42: Large ribosomal subunit protein uL18B

Chain BQ: 5% 86% 11%

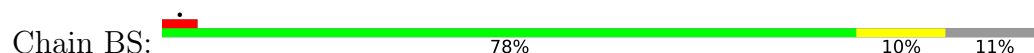




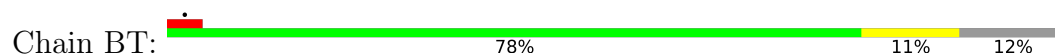
- Molecule 43: Large ribosomal subunit protein eL6



- Molecule 44: Large ribosomal subunit protein uL30C



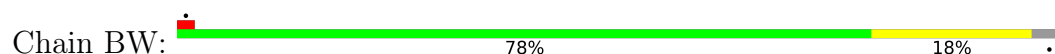
- Molecule 45: Large ribosomal subunit protein eL8



- Molecule 46: Large ribosomal subunit protein uL16A



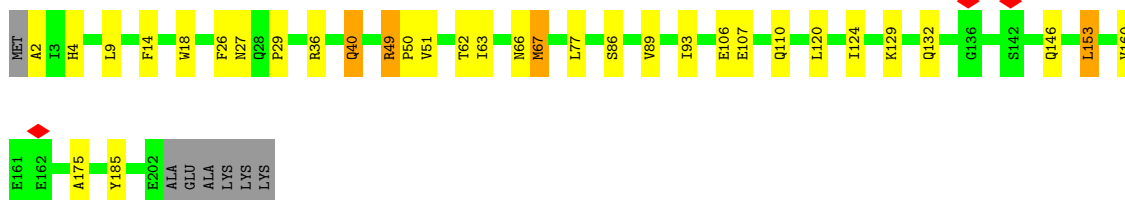
- Molecule 47: Large ribosomal subunit protein uL5A





- Molecule 48: Large ribosomal subunit protein eL13

Chain BX: 81% 14% ..



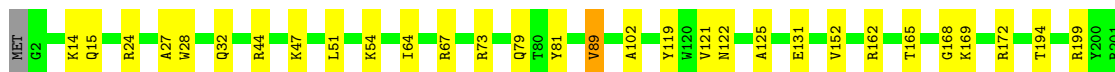
- Molecule 49: Large ribosomal subunit protein eL14

Chain BY: 87% 10% .



- Molecule 50: Large ribosomal subunit protein eL15B

Chain BZ: 85% 14%



- Molecule 51: Large ribosomal subunit protein uL13A

Chain Ba: 86% 14%



- Molecule 52: Large ribosomal subunit protein eL18B

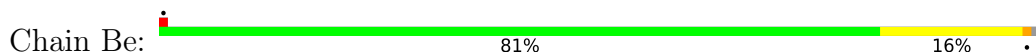
Chain Bc: 85% 14% ..



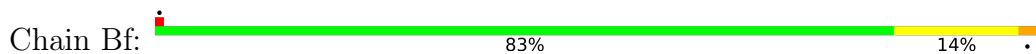
- Molecule 53: Large ribosomal subunit protein eL19B

Chain Bd: 73% 9% 19%

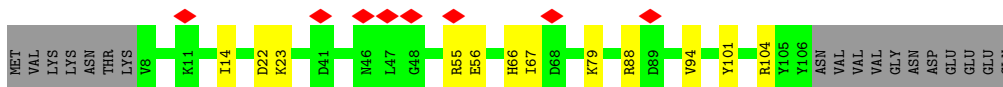
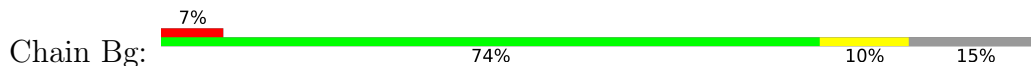
- Molecule 54: Large ribosomal subunit protein eL20A



- Molecule 55: Large ribosomal subunit protein eL21B



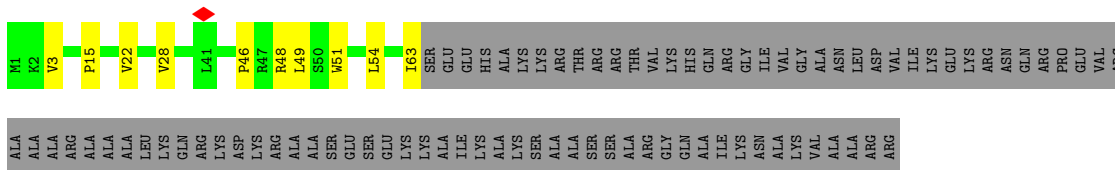
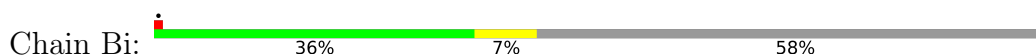
- Molecule 56: Large ribosomal subunit protein eL22



- Molecule 57: Large ribosomal subunit protein uL14A

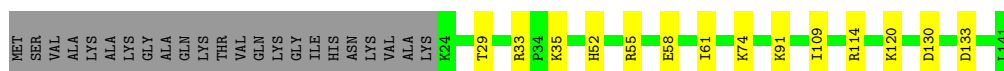


- Molecule 58: Large ribosomal subunit protein eL24B

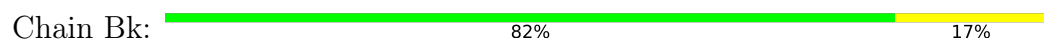


- Molecule 59: Large ribosomal subunit protein uL23A





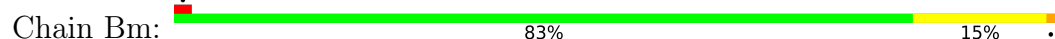
- Molecule 60: Large ribosomal subunit protein uL24



- Molecule 61: Large ribosomal subunit protein eL27A



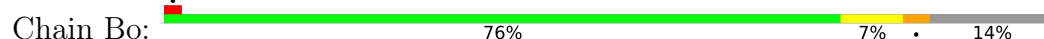
- Molecule 62: Large ribosomal subunit protein uL15B



- Molecule 63: Large ribosomal subunit protein eL29



- Molecule 64: Large ribosomal subunit protein eL30A

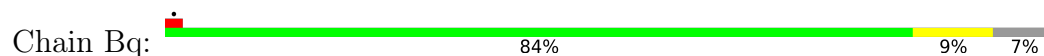


- Molecule 65: Large ribosomal subunit protein eL31

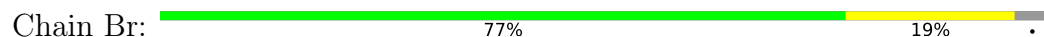




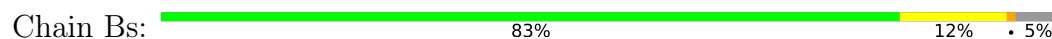
- Molecule 66: Large ribosomal subunit protein eL32A



- Molecule 67: Large ribosomal subunit protein eL33A



- Molecule 68: Large ribosomal subunit protein eL34B



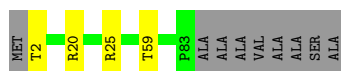
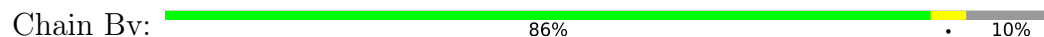
- Molecule 69: Large ribosomal subunit protein uL29



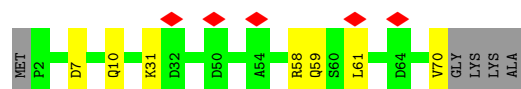
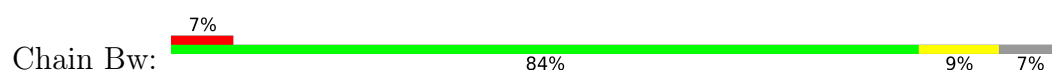
- Molecule 70: Large ribosomal subunit protein eL36B



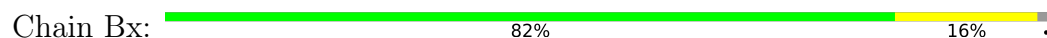
- Molecule 71: Large ribosomal subunit protein eL37B



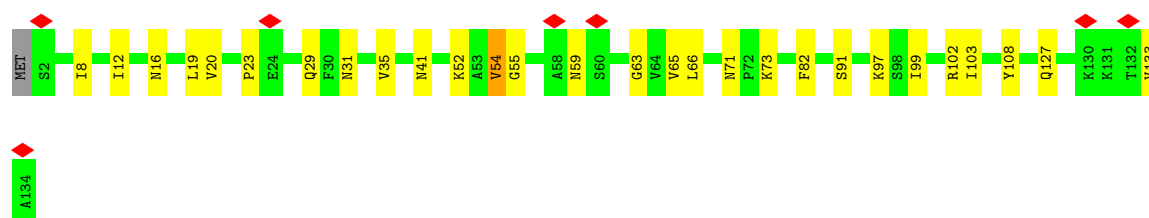
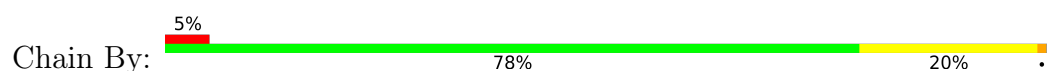
- Molecule 72: Large ribosomal subunit protein eL38A



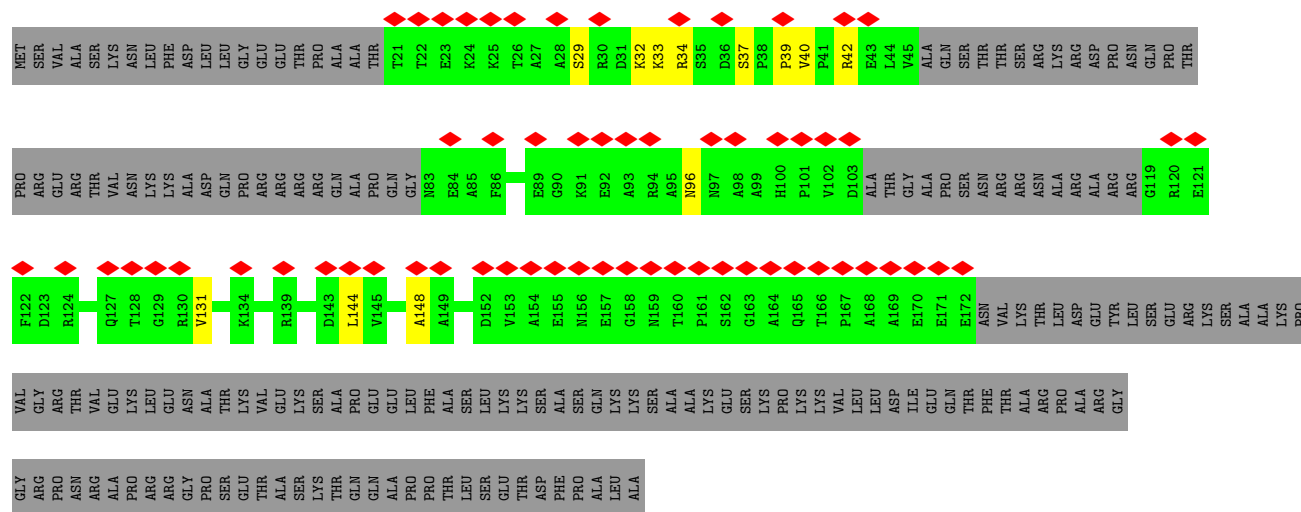
- Molecule 73: Large ribosomal subunit protein eL39



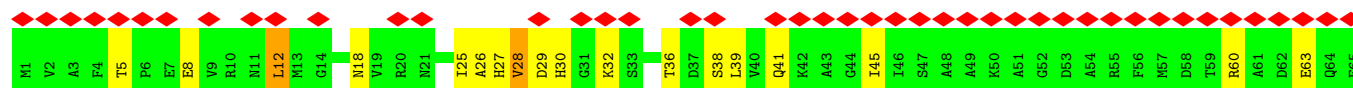
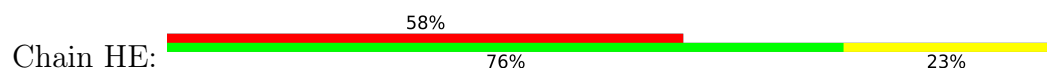
- Molecule 74: Large ribosomal subunit protein eL28

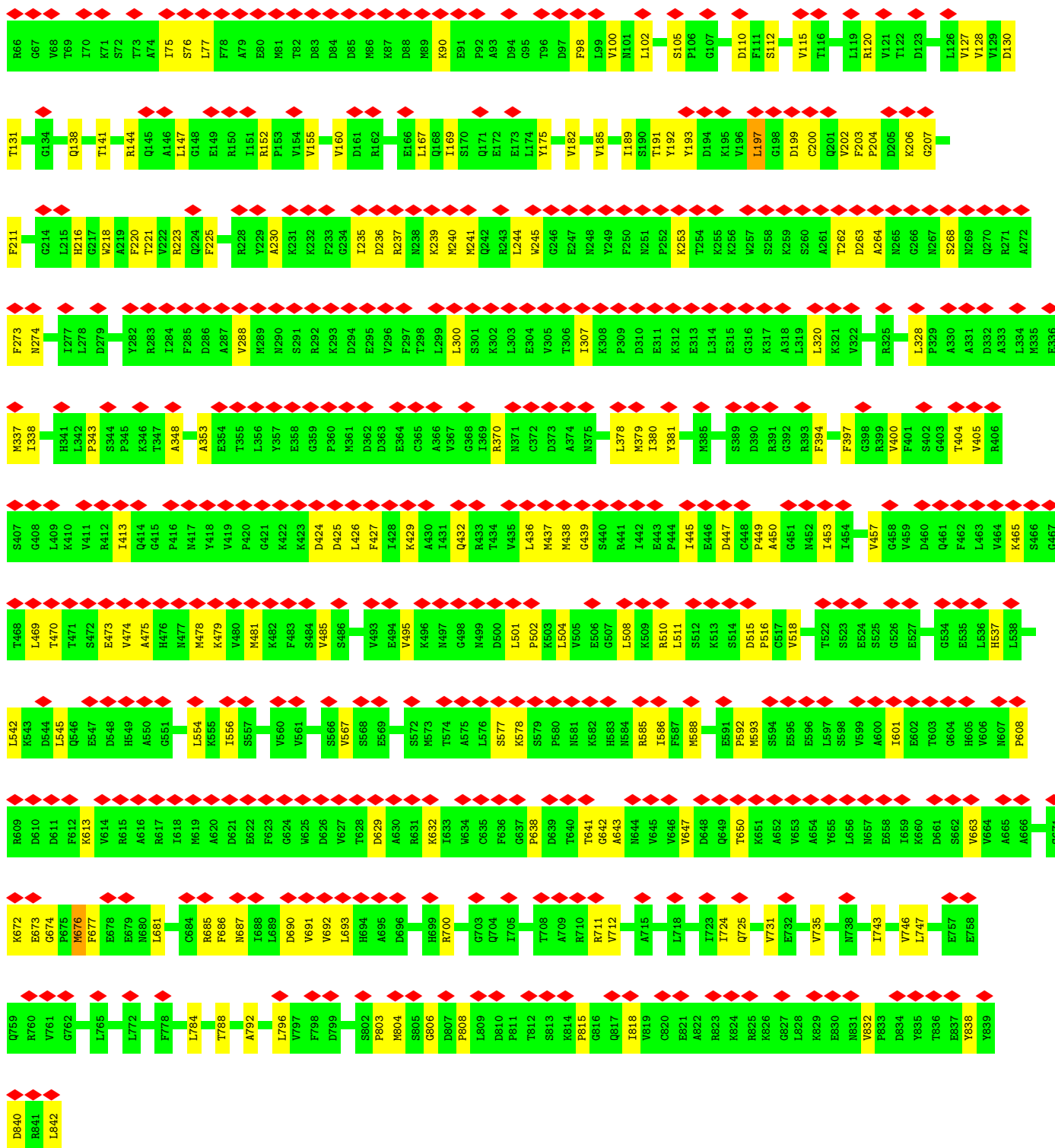


- Molecule 75: Ribosome-associated protein oga1

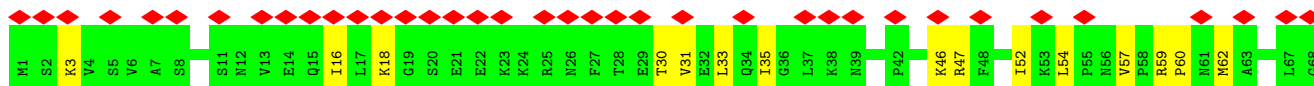


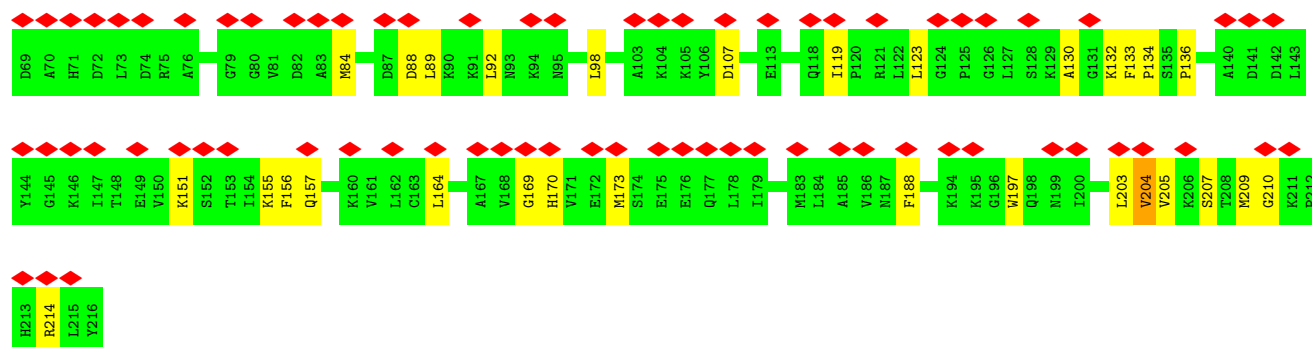
- Molecule 76: Elongation factor 2





- Molecule 77: Large ribosomal subunit protein uL1B





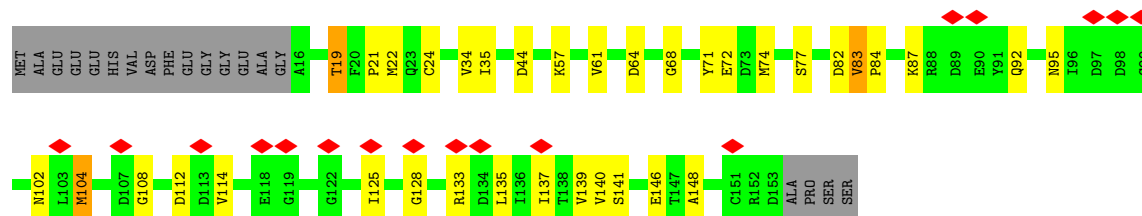
- Molecule 78: SDO1-like protein C21C3.19

Chain HS: 86% 13% .



- Molecule 79: Eukaryotic translation initiation factor 5A-1

Chain HI: 11% 65% 21% 12% .



- Molecule 80: Large ribosomal subunit protein eL40A

Chain BA: 90% 10% .



- Molecule 81: Large ribosomal subunit protein uL6B

Chain BU: 89% 8% .



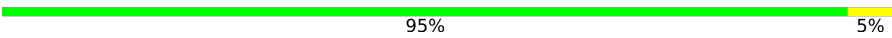
- Molecule 82: Large ribosomal subunit protein uL22A

Chain Bb: 71% 10% 19% .



ALA
ARG
ASN
LEU
ALA
ALA
ARG
LYS
ALA
ILE
THR
ALA
ALA

- Molecule 83: Large ribosomal subunit protein uL22A

Chain A:  95% 5%

V164
S165
R166
A183

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	88206	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; 3D CTF Estimation done in Warp	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	140	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	81000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.004	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.000494	Depositor
Map size ($\text{\AA}$)	585.8, 585.8, 585.8	wwPDB
Map dimensions	580, 580, 580	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.01, 1.01, 1.01	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, 5CT

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	0.06	0/40670	0.14	0/63362
2	AD	0.14	0/1635	0.44	0/2228
3	AE	0.08	0/1756	0.25	0/2358
4	AF	0.10	0/1695	0.29	0/2297
5	AG	0.11	0/1726	0.30	0/2316
6	AH	0.11	0/2125	0.33	0/2858
7	AI	0.12	0/1577	0.37	0/2123
8	AJ	0.08	0/1815	0.25	0/2428
9	AK	0.09	0/1554	0.28	0/2091
10	AL	0.08	0/1534	0.23	0/2050
11	AM	0.10	0/1487	0.30	0/1990
12	AN	0.11	0/769	0.33	0/1043
13	AO	0.09	0/1190	0.30	0/1602
14	AP	0.10	0/892	0.30	0/1208
15	AQ	0.12	0/1208	0.26	0/1624
16	AR	0.07	0/961	0.24	0/1293
17	AS	0.10	0/973	0.30	0/1307
18	AT	0.11	0/1100	0.35	0/1474
19	AU	0.12	0/888	0.39	0/1188
20	AV	0.18	0/1158	0.41	0/1552
21	AW	0.11	0/1139	0.28	0/1531
22	Aa	0.08	0/821	0.23	0/1107
23	Ab	0.09	0/680	0.24	0/918
24	Ac	0.14	0/1042	0.36	0/1399
25	Ad	0.11	0/1115	0.28	0/1489
26	Ae	0.11	0/1093	0.30	0/1453
27	Af	0.09	0/558	0.27	0/750
28	Ag	0.11	0/808	0.33	0/1083
29	Ah	0.07	0/630	0.20	0/845
30	Ai	0.21	0/500	0.44	0/669
31	Aj	0.08	0/458	0.24	0/610
32	Ak	0.13	0/482	0.44	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Am	0.09	0/2520	0.25	0/3434
34	B0	0.07	0/772	0.22	0/1025
35	B1	0.11	0/727	0.34	0/973
36	B2	0.07	0/77761	0.16	0/121212
37	B3	0.07	0/2838	0.13	0/4422
38	B4	0.06	0/3723	0.11	0/5796
39	BN	0.10	0/1910	0.27	0/2575
40	BO	0.10	0/3116	0.27	0/4190
41	BP	0.09	0/2852	0.26	0/3850
42	BQ	0.10	0/2361	0.28	0/3173
43	BR	0.13	0/1361	0.35	0/1836
44	BS	0.09	0/1846	0.23	0/2475
45	BT	0.10	0/1801	0.28	0/2430
46	BV	0.11	0/1804	0.34	1/2416 (0.0%)
47	BW	0.12	0/1369	0.30	0/1830
48	BX	0.08	0/1639	0.21	0/2208
49	BY	0.09	0/1054	0.24	0/1413
50	BZ	0.10	0/1717	0.24	0/2306
51	Ba	0.09	0/1575	0.24	0/2109
52	Bc	0.11	0/1511	0.28	0/2021
53	Bd	0.09	0/1320	0.25	0/1757
54	Be	0.10	0/1458	0.26	0/1961
55	Bf	0.11	0/1314	0.28	0/1771
56	Bg	0.10	0/812	0.31	0/1090
57	Bh	0.10	0/1015	0.27	0/1369
58	Bi	0.09	0/534	0.26	0/709
59	Bj	0.08	0/963	0.25	0/1296
60	Bk	0.11	0/1008	0.32	0/1341
61	Bl	0.12	0/1101	0.29	0/1477
62	Bm	0.10	0/1200	0.27	0/1611
63	Bn	0.07	0/503	0.21	0/664
64	Bo	0.09	0/714	0.25	0/961
65	Bp	0.09	0/872	0.25	0/1172
66	Bq	0.10	0/958	0.25	0/1278
67	Br	0.09	0/853	0.22	0/1146
68	Bs	0.08	0/870	0.20	0/1165
69	Bt	0.08	0/1008	0.20	0/1340
70	Bu	0.07	0/766	0.21	0/1017
71	Bv	0.10	0/666	0.30	0/881
72	Bw	0.07	0/566	0.22	0/757
73	Bx	0.08	0/447	0.26	0/597
74	By	0.10	0/1045	0.26	0/1404
75	H1	0.10	0/768	0.26	0/1035

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	HE	0.10	0/6670	0.29	0/9031
77	HL	0.10	0/1704	0.32	0/2285
78	HS	0.09	0/847	0.34	0/1144
79	HI	0.12	0/1066	0.32	0/1437
80	BA	0.09	0/419	0.23	0/554
81	BU	0.08	0/1479	0.24	0/1993
82	Bb	0.14	0/1237	0.42	0/1661
83	A	0.10	0/148	0.30	0/193
All	All	0.08	0/224627	0.22	1/328676 (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
20	AV	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	BV	5	PRO	N-CA-CB	7.06	110.66	103.25

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	AV	113	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	AA	36359	0	18299	209	0
2	AD	1602	0	1625	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	AE	1733	0	1816	22	0
4	AF	1660	0	1736	31	0
5	AG	1701	0	1777	28	0
6	AH	2083	0	2192	51	0
7	AI	1559	0	1624	44	0
8	AJ	1784	0	1879	22	0
9	AK	1530	0	1609	29	0
10	AL	1506	0	1538	19	0
11	AM	1462	0	1562	21	0
12	AN	748	0	735	15	0
13	AO	1164	0	1201	34	0
14	AP	884	0	872	12	0
15	AQ	1184	0	1252	20	0
16	AR	949	0	986	26	0
17	AS	954	0	993	16	0
18	AT	1082	0	1142	31	0
19	AU	879	0	918	17	0
20	AV	1144	0	1197	32	0
21	AW	1119	0	1130	26	0
22	Aa	810	0	871	11	0
23	Ab	672	0	660	11	0
24	Ac	1028	0	1080	23	0
25	Ad	1095	0	1149	23	0
26	Ae	1078	0	1133	30	0
27	Af	551	0	583	6	0
28	Ag	795	0	832	11	0
29	Ah	619	0	635	12	0
30	Ai	498	0	539	11	0
31	Aj	447	0	443	9	0
32	Ak	475	0	517	9	0
33	Am	2458	0	2370	50	0
34	B0	758	0	815	4	0
35	B1	718	0	751	9	0
36	B2	69470	0	34918	185	0
37	B3	2539	0	1283	12	0
38	B4	3332	0	1684	10	0
39	BN	1872	0	1917	34	0
40	BO	3050	0	3125	35	0
41	BP	2799	0	2925	30	0
42	BQ	2312	0	2272	23	0
43	BR	1333	0	1413	9	0
44	BS	1814	0	1884	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	BT	1772	0	1866	16	0
46	BV	1769	0	1804	10	0
47	BW	1346	0	1397	23	0
48	BX	1607	0	1650	25	0
49	BY	1038	0	1115	5	0
50	BZ	1676	0	1712	20	0
51	Ba	1545	0	1641	17	0
52	Bc	1487	0	1597	15	0
53	Bd	1301	0	1393	8	0
54	Be	1423	0	1488	21	0
55	Bf	1286	0	1310	16	0
56	Bg	798	0	834	6	0
57	Bh	999	0	1047	9	0
58	Bi	523	0	555	5	0
59	Bj	947	0	1012	13	0
60	Bk	998	0	1090	13	0
61	Bl	1078	0	1154	20	0
62	Bm	1171	0	1215	17	0
63	Bn	495	0	504	2	0
64	Bo	705	0	746	6	0
65	Bp	857	0	891	4	0
66	Bq	944	0	1005	7	0
67	Br	831	0	858	14	0
68	Bs	858	0	925	8	0
69	Bt	999	0	1092	9	0
70	Bu	759	0	840	4	0
71	Bv	652	0	663	2	0
72	Bw	560	0	608	4	0
73	Bx	436	0	463	5	0
74	By	1031	0	1080	22	0
75	H1	758	0	712	11	0
76	HE	6544	0	6571	113	0
77	HL	1679	0	1795	27	0
78	HS	834	0	833	7	0
79	HI	1067	0	1056	20	0
80	BA	413	0	455	3	0
81	BU	1461	0	1527	9	0
82	Bb	1212	0	1239	13	0
83	A	149	0	169	2	0
84	Ag	1	0	0	0	0
84	Ah	1	0	0	0	0
84	Aj	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	B0	1	0	0	0	0
84	B1	1	0	0	0	0
84	Bv	1	0	0	0	0
All	All	209623	0	157794	1629	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 4.

The worst 5 of 1629 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)
20:AV:110:ASP:HA	20:AV:113:ARG:HD2	1.49	0.91
18:AT:37:GLN:HG3	18:AT:38:PRO:HD3	1.54	0.89
1:AA:572:C:H41	25:Ad:67:ARG:HH12	1.30	0.80
76:HE:110:ASP:HB3	76:HE:537:HIS:HB2	1.64	0.79
1:AA:1102:A:H5'	4:AF:163:SER:HB3	1.65	0.79

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%)	165 (81%)	34 (17%)	4 (2%)	6	24
3	AE	214/252 (85%)	203 (95%)	11 (5%)	0	100	100
4	AF	214/253 (85%)	205 (96%)	8 (4%)	1 (0%)	24	53
5	AG	214/249 (86%)	192 (90%)	20 (9%)	2 (1%)	14	41
6	AH	259/262 (99%)	235 (91%)	23 (9%)	1 (0%)	30	58
7	AI	201/203 (99%)	179 (89%)	15 (8%)	7 (4%)	3	16
8	AJ	219/239 (92%)	212 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AK	191/195 (98%)	180 (94%)	11 (6%)	0	100	100
10	AL	184/200 (92%)	179 (97%)	5 (3%)	0	100	100
11	AM	176/192 (92%)	163 (93%)	13 (7%)	0	100	100
12	AN	90/147 (61%)	82 (91%)	8 (9%)	0	100	100
13	AO	141/152 (93%)	130 (92%)	11 (8%)	0	100	100
14	AP	119/145 (82%)	106 (89%)	13 (11%)	0	100	100
15	AQ	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
16	AR	126/139 (91%)	117 (93%)	9 (7%)	0	100	100
17	AS	117/154 (76%)	110 (94%)	6 (5%)	1 (1%)	14	41
18	AT	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
19	AU	104/131 (79%)	92 (88%)	11 (11%)	1 (1%)	12	39
20	AV	139/152 (91%)	132 (95%)	7 (5%)	0	100	100
21	AW	140/144 (97%)	134 (96%)	6 (4%)	0	100	100
22	Aa	98/118 (83%)	93 (95%)	5 (5%)	0	100	100
23	Ab	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Ad	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
26	Ae	131/134 (98%)	119 (91%)	12 (9%)	0	100	100
27	Af	67/89 (75%)	62 (92%)	5 (8%)	0	100	100
28	Ag	95/119 (80%)	93 (98%)	1 (1%)	1 (1%)	11	37
29	Ah	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
30	Ai	61/68 (90%)	56 (92%)	5 (8%)	0	100	100
31	Aj	51/56 (91%)	51 (100%)	0	0	100	100
32	Ak	58/61 (95%)	50 (86%)	6 (10%)	2 (3%)	3	16
33	Am	312/314 (99%)	294 (94%)	18 (6%)	0	100	100
34	B0	91/106 (86%)	87 (96%)	4 (4%)	0	100	100
35	B1	91/94 (97%)	83 (91%)	8 (9%)	0	100	100
39	BN	246/253 (97%)	232 (94%)	14 (6%)	0	100	100
40	BO	382/388 (98%)	363 (95%)	19 (5%)	0	100	100
41	BP	360/363 (99%)	345 (96%)	15 (4%)	0	100	100
42	BQ	285/294 (97%)	264 (93%)	21 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	BR	169/195 (87%)	151 (89%)	17 (10%)	1 (1%)	21	49
44	BS	221/251 (88%)	216 (98%)	5 (2%)	0	100	100
45	BT	227/259 (88%)	217 (96%)	10 (4%)	0	100	100
46	BV	217/221 (98%)	204 (94%)	12 (6%)	1 (0%)	24	53
47	BW	165/174 (95%)	153 (93%)	12 (7%)	0	100	100
48	BX	199/208 (96%)	198 (100%)	1 (0%)	0	100	100
49	BY	128/134 (96%)	127 (99%)	1 (1%)	0	100	100
50	BZ	198/201 (98%)	191 (96%)	7 (4%)	0	100	100
51	Ba	194/197 (98%)	192 (99%)	2 (1%)	0	100	100
52	Bc	184/187 (98%)	179 (97%)	5 (3%)	0	100	100
53	Bd	155/193 (80%)	152 (98%)	3 (2%)	0	100	100
54	Be	171/176 (97%)	167 (98%)	4 (2%)	0	100	100
55	Bf	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
56	Bg	97/117 (83%)	85 (88%)	12 (12%)	0	100	100
57	Bh	132/139 (95%)	131 (99%)	1 (1%)	0	100	100
58	Bi	61/149 (41%)	55 (90%)	6 (10%)	0	100	100
59	Bj	116/141 (82%)	115 (99%)	1 (1%)	0	100	100
60	Bk	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
61	Bl	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
62	Bm	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
63	Bn	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
64	Bo	92/109 (84%)	90 (98%)	2 (2%)	0	100	100
65	Bp	101/113 (89%)	100 (99%)	1 (1%)	0	100	100
66	Bq	116/127 (91%)	110 (95%)	6 (5%)	0	100	100
67	Br	102/108 (94%)	95 (93%)	7 (7%)	0	100	100
68	Bs	104/111 (94%)	102 (98%)	2 (2%)	0	100	100
69	Bt	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
70	Bu	93/99 (94%)	92 (99%)	1 (1%)	0	100	100
71	Bv	80/91 (88%)	75 (94%)	5 (6%)	0	100	100
72	Bw	67/74 (90%)	66 (98%)	1 (2%)	0	100	100
73	Bx	48/51 (94%)	46 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	By	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
75	H1	94/284 (33%)	86 (92%)	7 (7%)	1 (1%)	11	37
76	HE	840/842 (100%)	783 (93%)	54 (6%)	3 (0%)	30	58
77	HL	214/216 (99%)	204 (95%)	10 (5%)	0	100	100
78	HS	104/106 (98%)	92 (88%)	11 (11%)	1 (1%)	12	39
79	HI	135/157 (86%)	119 (88%)	16 (12%)	0	100	100
80	BA	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
81	BU	182/189 (96%)	180 (99%)	2 (1%)	0	100	100
82	Bb	150/187 (80%)	141 (94%)	9 (6%)	0	100	100
83	A	18/20 (90%)	18 (100%)	0	0	100	100
All	All	12184/13456 (90%)	11513 (94%)	644 (5%)	27 (0%)	44	70

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AD	143	ASN
7	AI	24	PHE
28	Ag	55	GLU
46	BV	5	PRO
76	HE	28	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AD	170/228 (75%)	158 (93%)	12 (7%)	13	39
3	AE	193/223 (86%)	190 (98%)	3 (2%)	55	68
4	AF	175/199 (88%)	169 (97%)	6 (3%)	32	58
5	AG	181/203 (89%)	173 (96%)	8 (4%)	25	51
6	AH	226/227 (100%)	220 (97%)	6 (3%)	39	61
7	AI	169/169 (100%)	168 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AJ	188/204 (92%)	185 (98%)	3 (2%)	55	68
9	AK	169/171 (99%)	167 (99%)	2 (1%)	63	72
10	AL	157/166 (95%)	156 (99%)	1 (1%)	78	80
11	AM	155/165 (94%)	150 (97%)	5 (3%)	34	59
12	AN	77/116 (66%)	74 (96%)	3 (4%)	28	53
13	AO	124/131 (95%)	120 (97%)	4 (3%)	34	59
14	AP	92/118 (78%)	92 (100%)	0	100	100
15	AQ	127/128 (99%)	125 (98%)	2 (2%)	55	68
16	AR	95/104 (91%)	93 (98%)	2 (2%)	47	64
17	AS	101/131 (77%)	100 (99%)	1 (1%)	68	75
18	AT	111/111 (100%)	110 (99%)	1 (1%)	70	76
19	AU	97/120 (81%)	96 (99%)	1 (1%)	68	75
20	AV	127/136 (93%)	127 (100%)	0	100	100
21	AW	117/119 (98%)	117 (100%)	0	100	100
22	Aa	95/111 (86%)	92 (97%)	3 (3%)	34	59
23	Ab	73/73 (100%)	70 (96%)	3 (4%)	27	52
24	Ac	114/115 (99%)	112 (98%)	2 (2%)	51	67
25	Ad	112/113 (99%)	108 (96%)	4 (4%)	31	56
26	Ae	112/113 (99%)	110 (98%)	2 (2%)	51	67
27	Af	61/75 (81%)	61 (100%)	0	100	100
28	Ag	87/106 (82%)	84 (97%)	3 (3%)	32	58
29	Ah	71/73 (97%)	70 (99%)	1 (1%)	59	70
30	Ai	56/61 (92%)	55 (98%)	1 (2%)	51	67
31	Aj	45/47 (96%)	45 (100%)	0	100	100
32	Ak	51/52 (98%)	51 (100%)	0	100	100
33	Am	276/276 (100%)	271 (98%)	5 (2%)	51	67
34	B0	84/93 (90%)	82 (98%)	2 (2%)	43	62
35	B1	74/75 (99%)	71 (96%)	3 (4%)	27	52
39	BN	188/192 (98%)	181 (96%)	7 (4%)	30	55
40	BO	318/326 (98%)	309 (97%)	9 (3%)	38	60
41	BP	293/294 (100%)	283 (97%)	10 (3%)	32	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	BQ	235/241 (98%)	233 (99%)	2 (1%)	70	76
43	BR	139/155 (90%)	134 (96%)	5 (4%)	31	56
44	BS	188/213 (88%)	183 (97%)	5 (3%)	39	61
45	BT	182/212 (86%)	180 (99%)	2 (1%)	65	74
46	BV	185/187 (99%)	181 (98%)	4 (2%)	45	63
47	BW	141/146 (97%)	135 (96%)	6 (4%)	26	51
48	BX	162/167 (97%)	156 (96%)	6 (4%)	30	55
49	BY	110/113 (97%)	104 (94%)	6 (6%)	19	46
50	BZ	175/176 (99%)	173 (99%)	2 (1%)	65	74
51	Ba	159/160 (99%)	156 (98%)	3 (2%)	50	66
52	Bc	157/158 (99%)	151 (96%)	6 (4%)	29	54
53	Bd	136/163 (83%)	131 (96%)	5 (4%)	30	55
54	Be	151/154 (98%)	146 (97%)	5 (3%)	33	58
55	Bf	138/139 (99%)	132 (96%)	6 (4%)	26	51
56	Bg	86/103 (84%)	86 (100%)	0	100	100
57	Bh	103/107 (96%)	101 (98%)	2 (2%)	50	66
58	Bi	57/121 (47%)	55 (96%)	2 (4%)	32	56
59	Bj	105/122 (86%)	105 (100%)	0	100	100
60	Bk	110/111 (99%)	108 (98%)	2 (2%)	51	67
61	Bl	114/115 (99%)	111 (97%)	3 (3%)	40	61
62	Bm	122/123 (99%)	119 (98%)	3 (2%)	42	62
63	Bn	50/51 (98%)	50 (100%)	0	100	100
64	Bo	75/87 (86%)	70 (93%)	5 (7%)	15	41
65	Bp	94/102 (92%)	93 (99%)	1 (1%)	65	74
66	Bq	100/107 (94%)	99 (99%)	1 (1%)	68	75
67	Br	91/94 (97%)	88 (97%)	3 (3%)	33	58
68	Bs	91/96 (95%)	87 (96%)	4 (4%)	25	51
69	Bt	106/107 (99%)	104 (98%)	2 (2%)	50	66
70	Bu	81/84 (96%)	77 (95%)	4 (5%)	22	49
71	Bv	68/71 (96%)	66 (97%)	2 (3%)	37	60
72	Bw	63/66 (96%)	62 (98%)	1 (2%)	55	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Bx	46/47 (98%)	45 (98%)	1 (2%)	45	63
74	By	112/113 (99%)	110 (98%)	2 (2%)	51	67
75	H1	78/230 (34%)	78 (100%)	0	100	100
76	HE	720/720 (100%)	709 (98%)	11 (2%)	57	69
77	HL	188/188 (100%)	185 (98%)	3 (2%)	55	68
78	HS	97/97 (100%)	94 (97%)	3 (3%)	35	59
79	HI	118/131 (90%)	113 (96%)	5 (4%)	26	52
80	BA	46/46 (100%)	45 (98%)	1 (2%)	45	63
81	BU	164/168 (98%)	162 (99%)	2 (1%)	63	72
82	Bb	124/149 (83%)	121 (98%)	3 (2%)	43	62
83	A	14/14 (100%)	14 (100%)	0	100	100
All	All	10442/11318 (92%)	10197 (98%)	245 (2%)	44	63

5 of 245 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	BP	326	VAL
76	HE	202	VAL
48	BX	51	VAL
76	HE	147	LEU
79	HI	104	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 189 such sidechains are listed below:

Mol	Chain	Res	Type
50	BZ	32	GLN
64	Bo	74	HIS
50	BZ	95	GLN
53	Bd	67	HIS
68	Bs	3	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1696/1842 (92%)	410 (24%)	14 (0%)
36	B2	3240/3498 (92%)	635 (19%)	21 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	B3	118/246 (47%)	16 (13%)	1 (0%)
38	B4	156/165 (94%)	28 (17%)	1 (0%)
All	All	5210/5751 (90%)	1089 (20%)	37 (0%)

5 of 1089 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	3	C
1	AA	4	C
1	AA	25	C
1	AA	26	A

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	B2	3001	C
37	B3	12	U
36	B2	3217	U
36	B2	3328	U
1	AA	1580	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
79	5CT	HI	52	79	13,14,15	0.49	0	9,15,17	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	5CT	HI	52	79	-	8/13/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	HI	52	5CT	C2-C1-NZ-CE
79	HI	52	5CT	NZ-C1-C2-C3
79	HI	52	5CT	C-CA-CB-CG
79	HI	52	5CT	N-CA-CB-CG
79	HI	52	5CT	CD-CE-NZ-C1

There are no ring outliers.

No monomer is involved in short contacts.

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

There are no chain breaks in this entry.

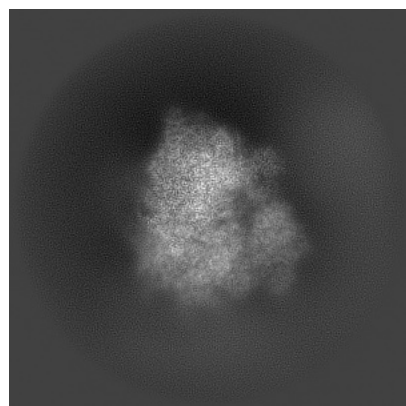
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54290. These allow visual inspection of the internal detail of the map and identification of artifacts.

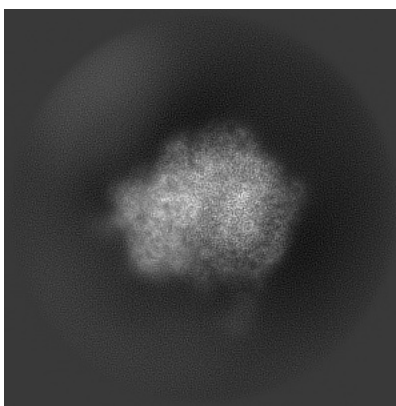
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

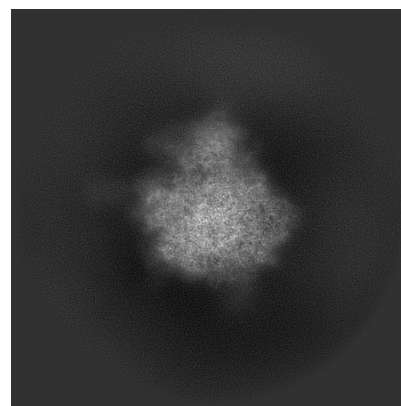
6.1.1 Primary map



X

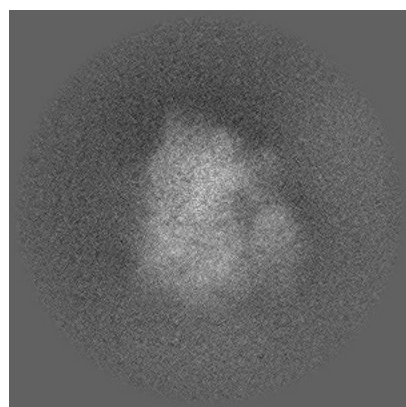


Y

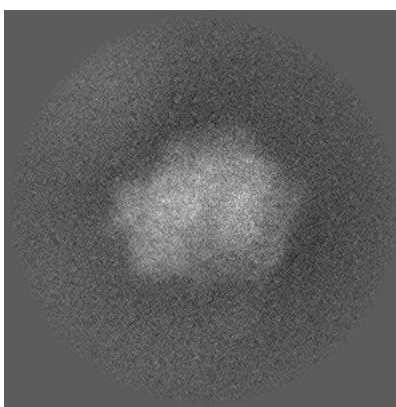


Z

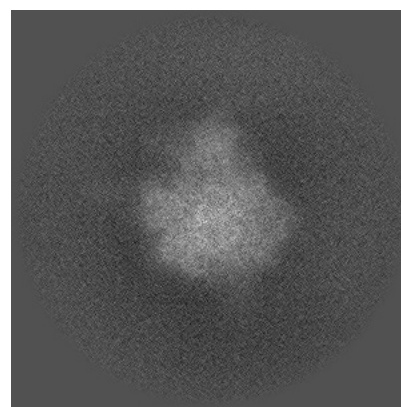
6.1.2 Raw map



X



Y

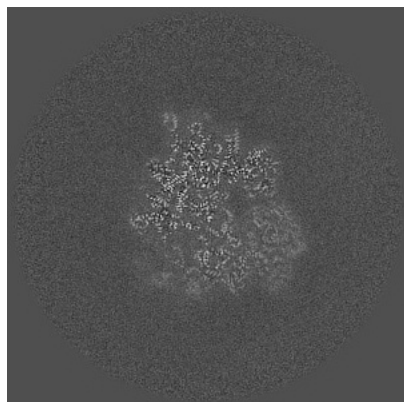


Z

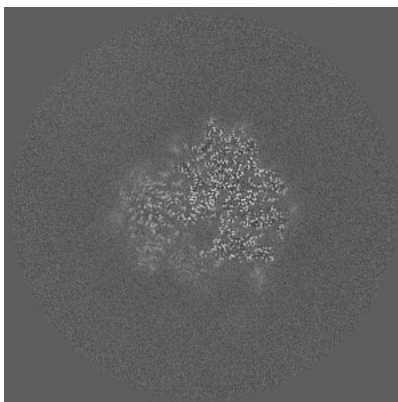
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

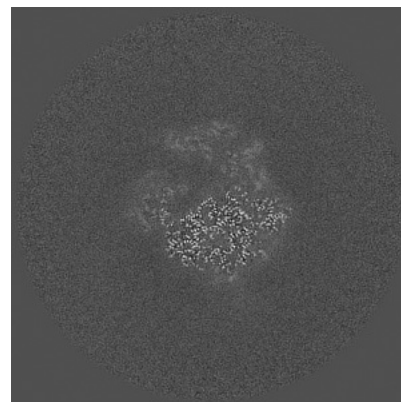
6.2.1 Primary map



X Index: 290

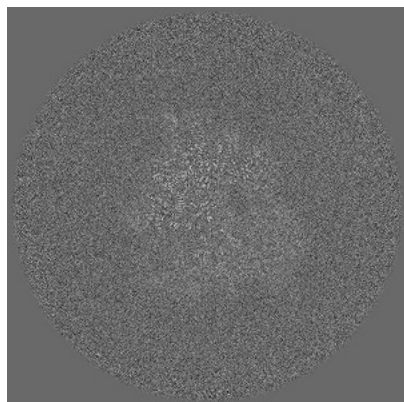


Y Index: 290

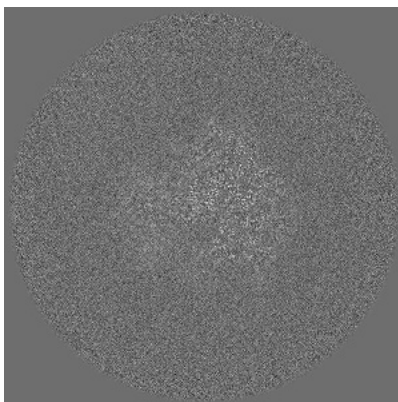


Z Index: 290

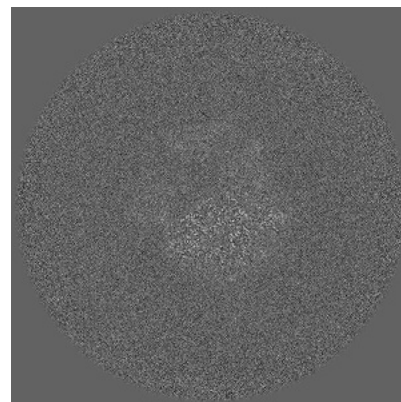
6.2.2 Raw map



X Index: 290



Y Index: 290

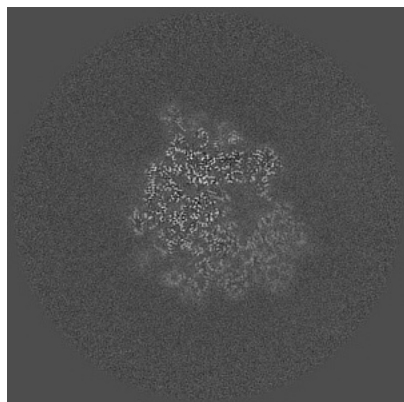


Z Index: 290

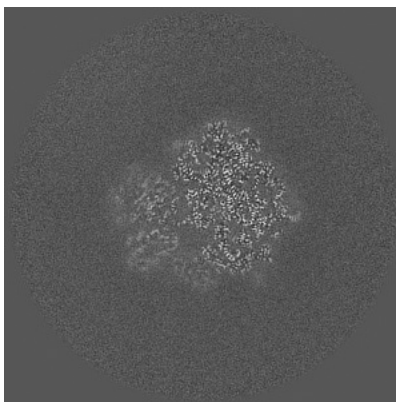
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

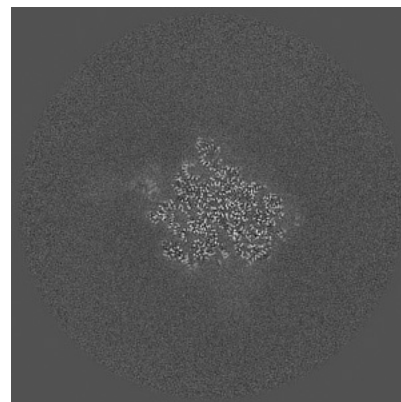
6.3.1 Primary map



X Index: 301

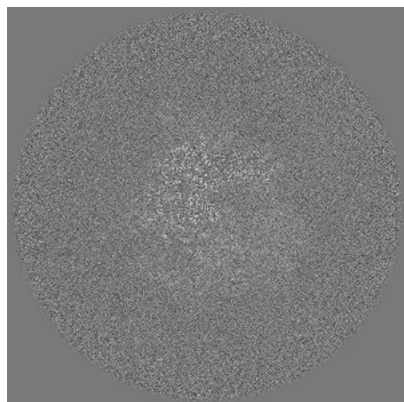


Y Index: 280

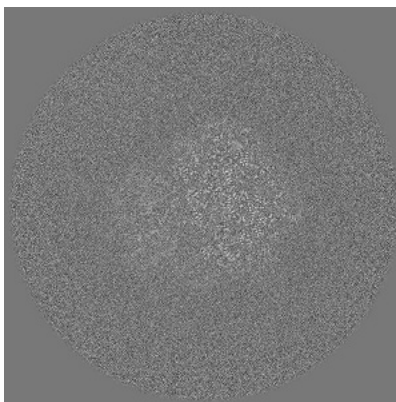


Z Index: 327

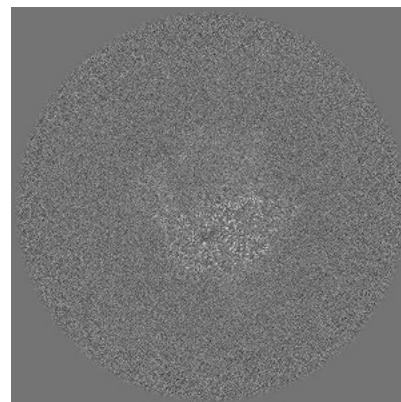
6.3.2 Raw map



X Index: 297



Y Index: 280

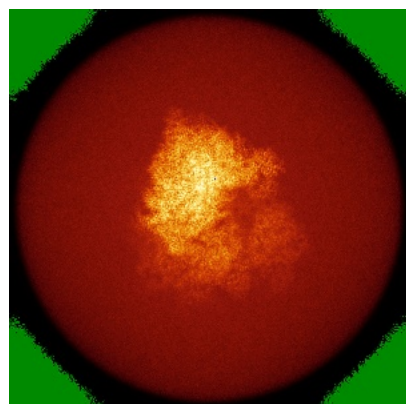


Z Index: 300

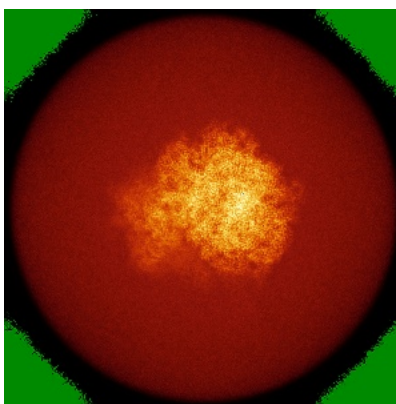
The images above show the largest variance slices of the map in three orthogonal directions.

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

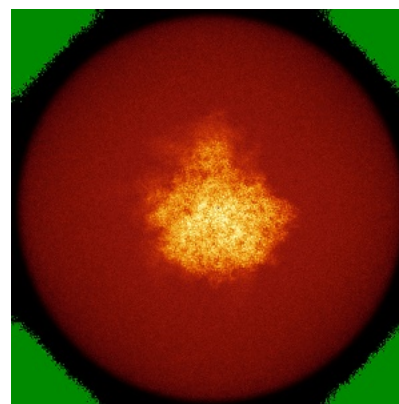
6.4.1 Primary map



X

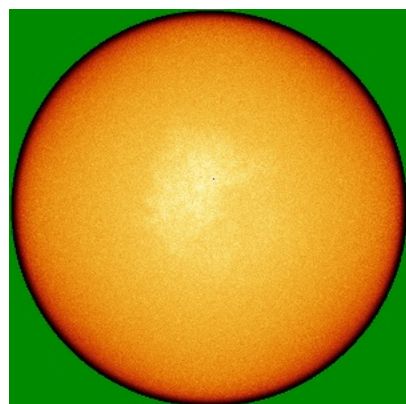


Y

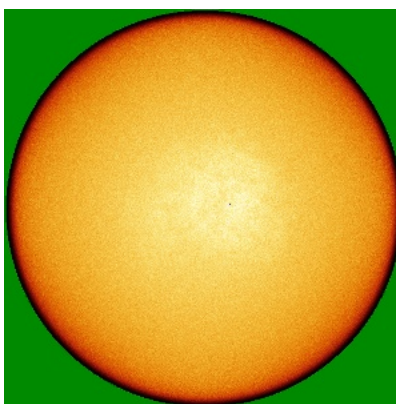


Z

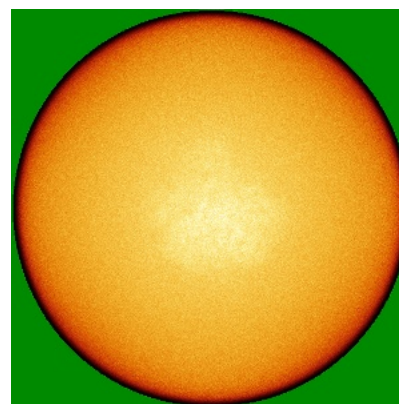
6.4.2 Raw map



X



Y

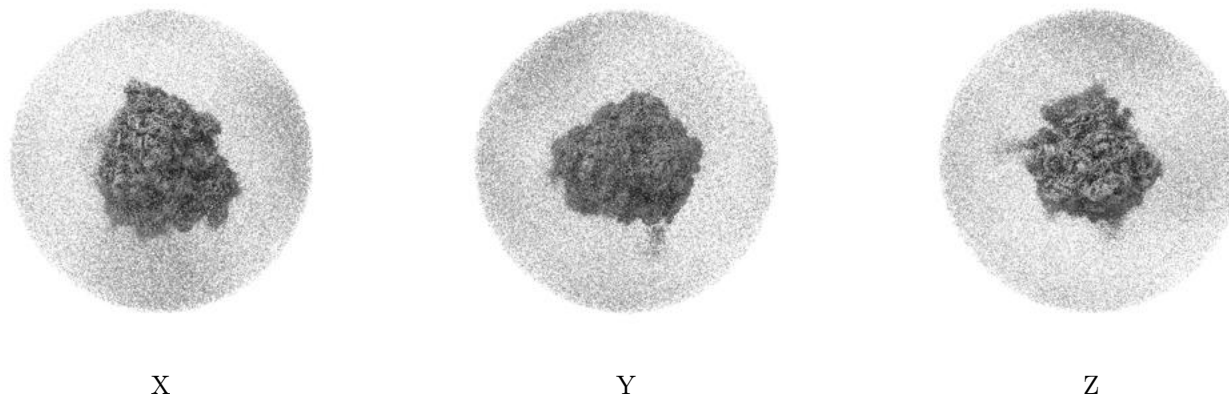


Z

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.

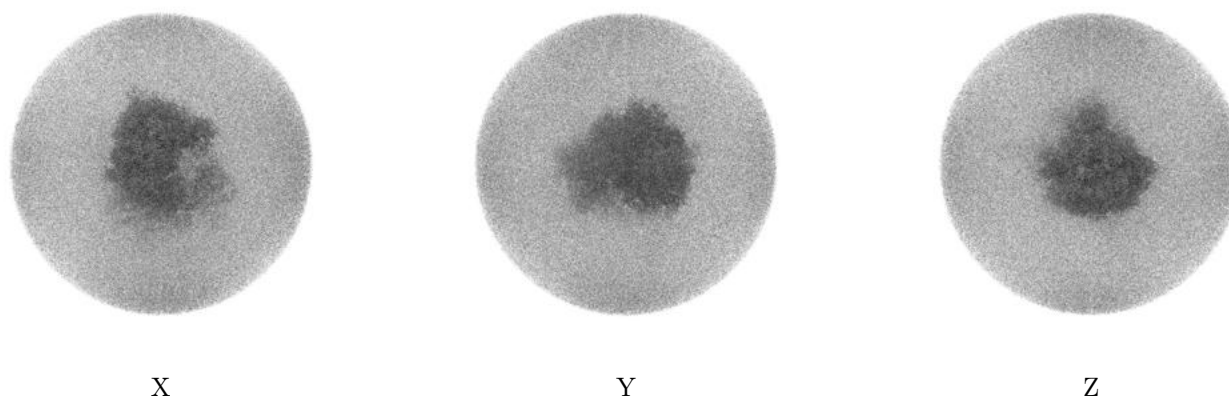
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.000494. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

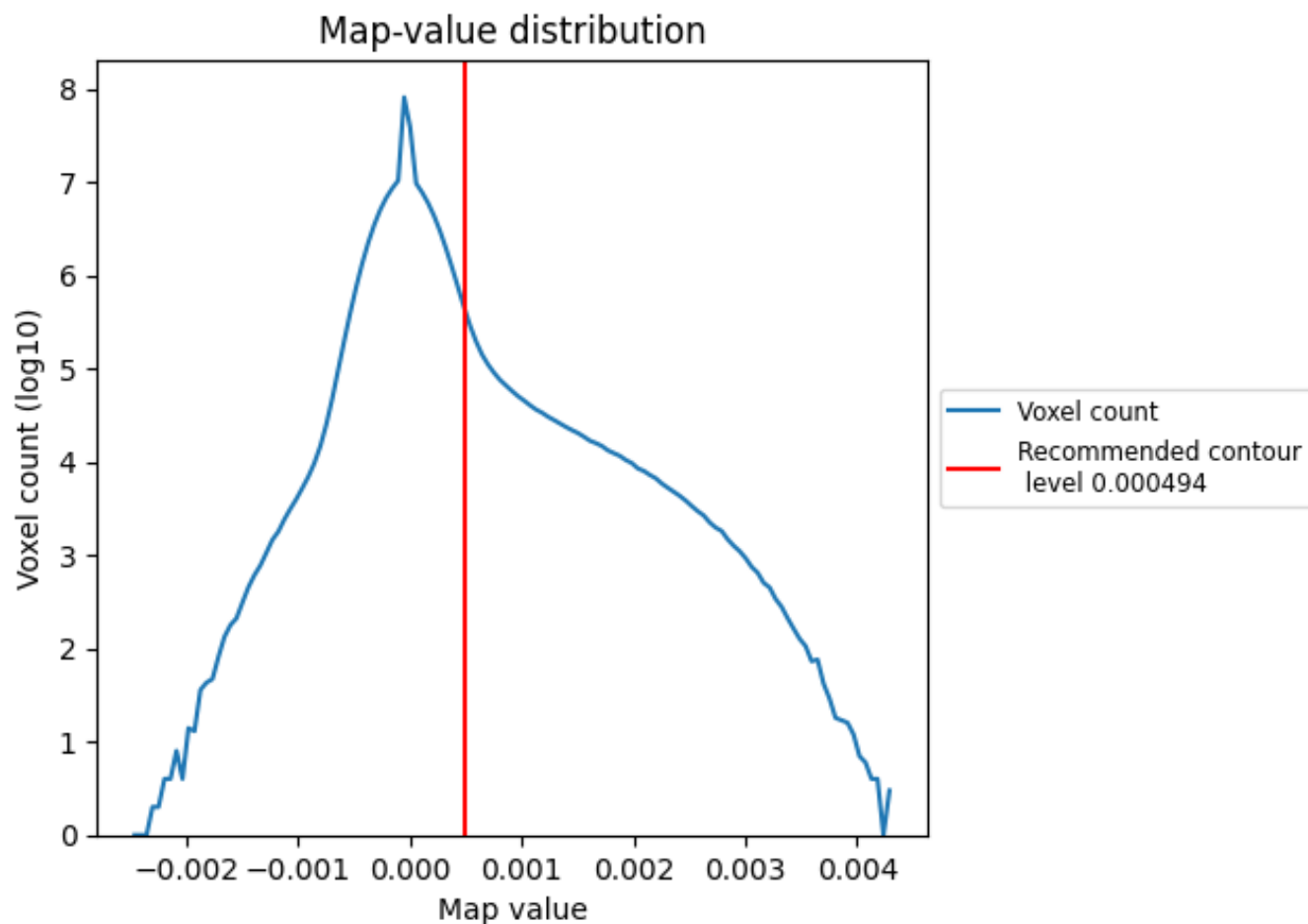
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

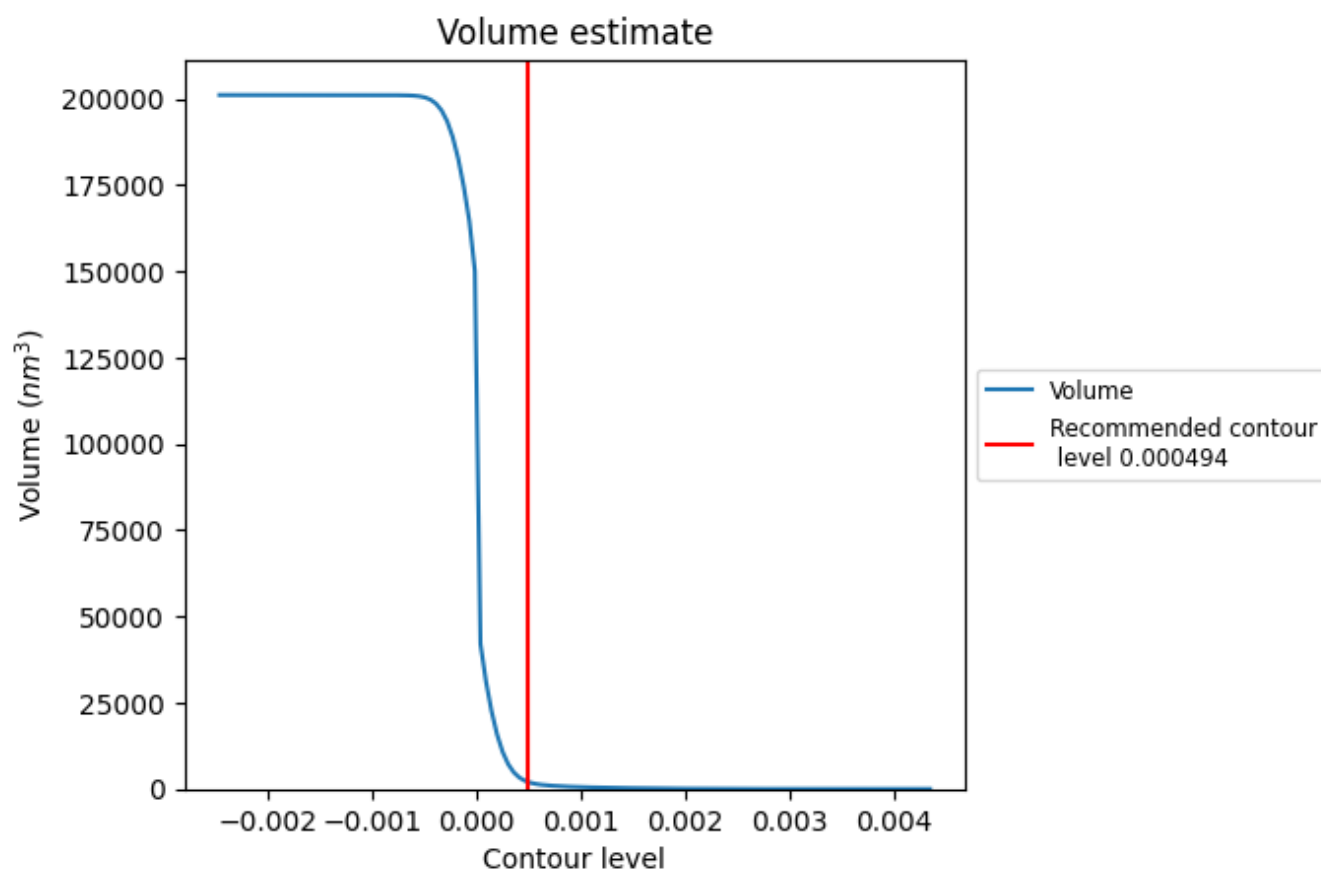
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

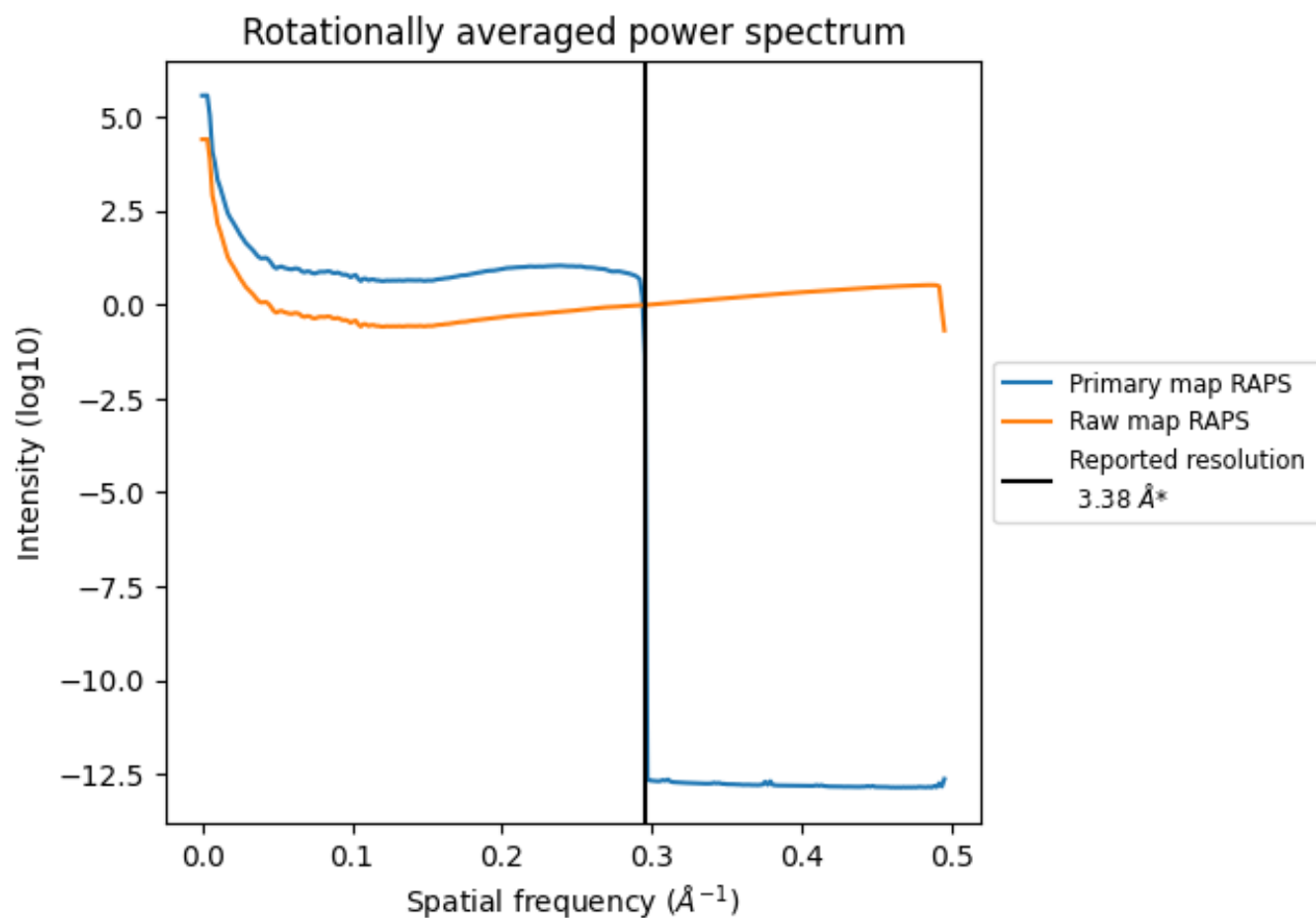
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2034 nm³; this corresponds to an approximate mass of 1837 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 ⓘ

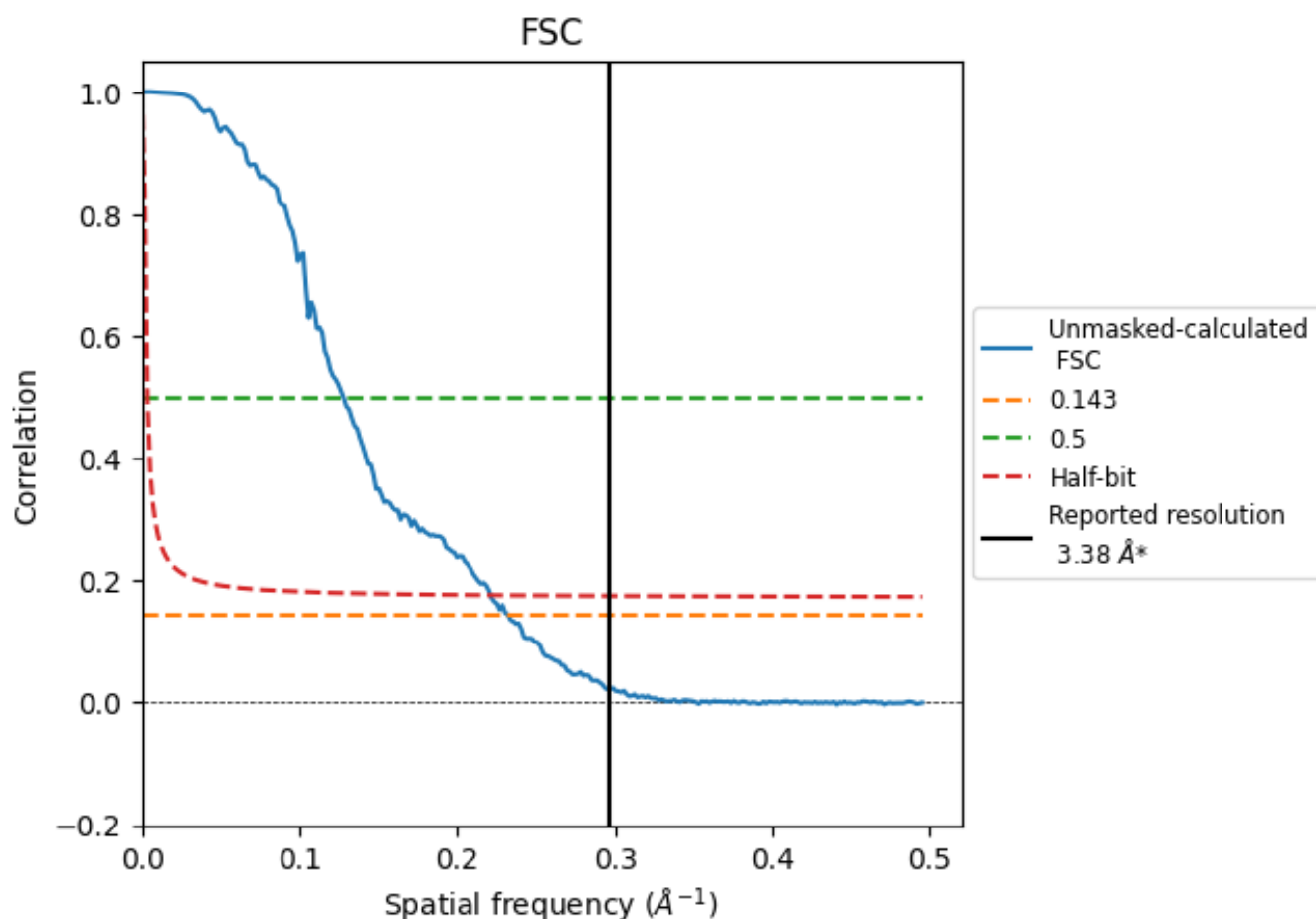


*Reported resolution corresponds to spatial frequency of 0.296 $\text{\AA}^{-1}$

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 0.296 Å⁻¹

8.2 Resolution estimates [i](#)

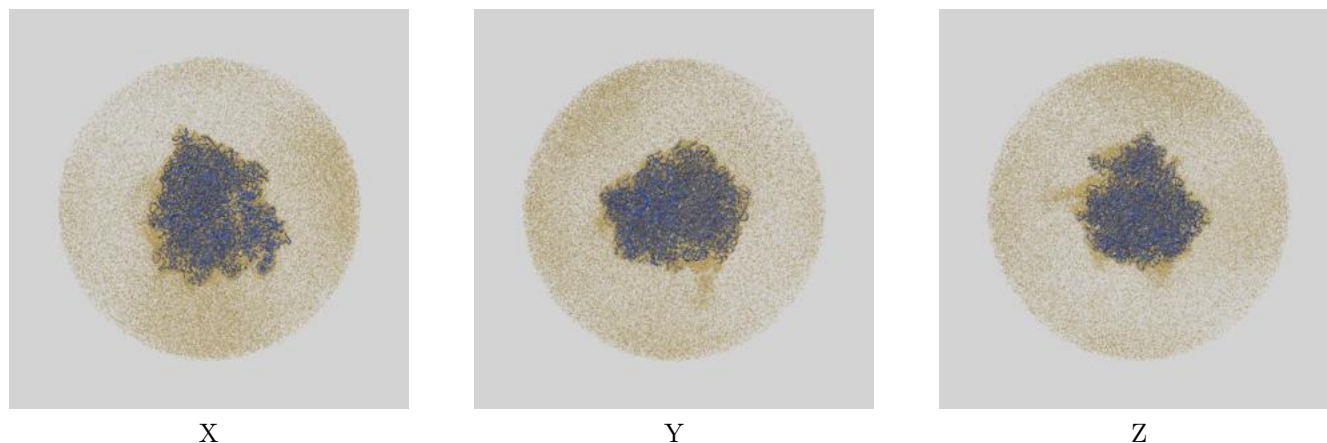
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.38	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.30	7.82	4.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.30 differs from the reported value 3.38 by more than 10 %

9 Map-model fit [i](#)

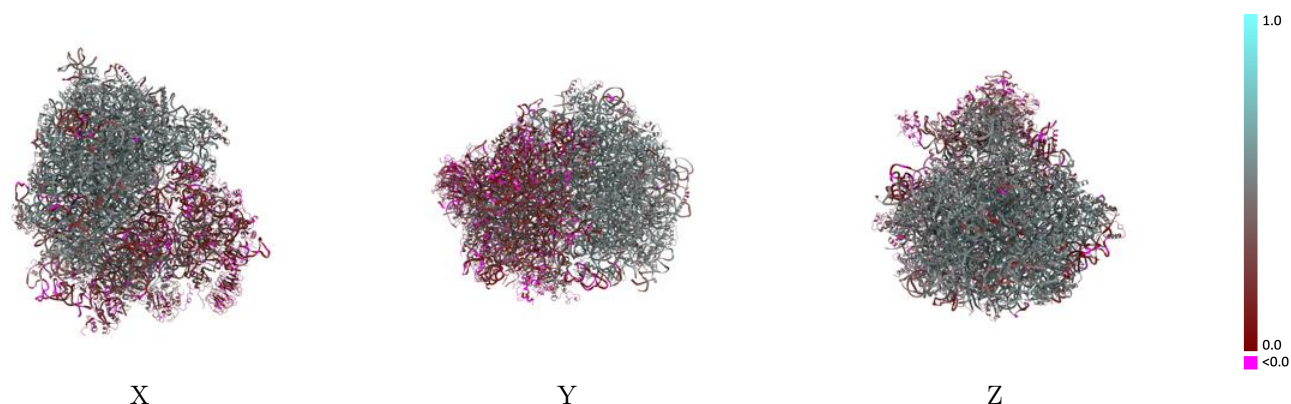
This section contains information regarding the fit between EMDB map EMD-54290 and PDB model 9RVU. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



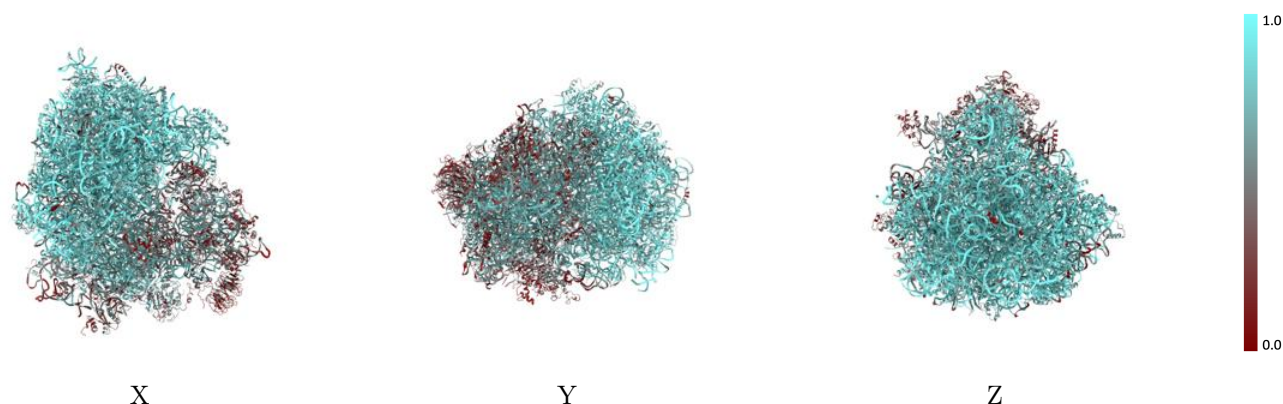
The images above show the 3D surface view of the map at the recommended contour level 0.000494 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



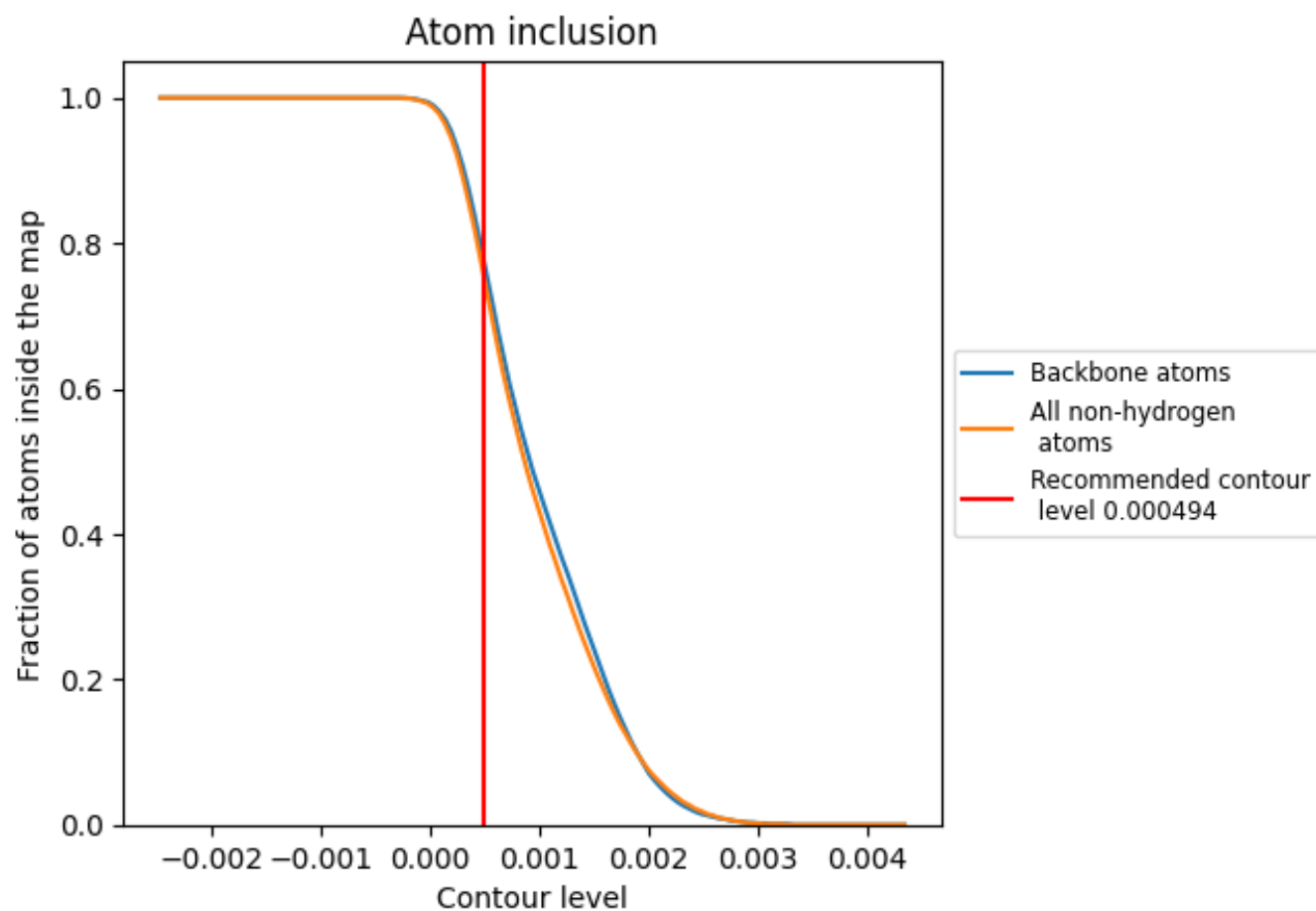
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.000494).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 76% 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 (0.000494) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7550	 0.4000
A	 0.8250	 0.4990
AA	 0.7160	 0.2870
AD	 0.5460	 0.2730
AE	 0.3620	 0.1780
AF	 0.7230	 0.4160
AG	 0.4830	 0.2590
AH	 0.5200	 0.2760
AI	 0.3650	 0.2010
AJ	 0.4050	 0.2170
AK	 0.4320	 0.2470
AL	 0.6880	 0.3720
AM	 0.5970	 0.3080
AN	 0.4080	 0.1860
AO	 0.6930	 0.3810
AP	 0.1480	 0.0160
AQ	 0.5660	 0.2630
AR	 0.3710	 0.1420
AS	 0.4160	 0.1770
AT	 0.3940	 0.2050
AU	 0.3940	 0.2020
AV	 0.4010	 0.1960
AW	 0.4190	 0.1910
Aa	 0.3910	 0.1510
Ab	 0.5980	 0.3230
Ac	 0.7060	 0.4000
Ad	 0.7140	 0.3940
Ae	 0.3460	 0.1360
Af	 0.2570	 0.1260
Ag	 0.6470	 0.2980
Ah	 0.3700	 0.1850
Ai	 0.3290	 0.2080
Aj	 0.5860	 0.2720
Ak	 0.4340	 0.2020
Am	 0.2330	 0.1420



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Chain	Atom inclusion	Q-score
B0	 0.8940	 0.5230
B1	 0.8420	 0.4930
B2	 0.8950	 0.4800
B3	 0.9350	 0.5010
B4	 0.9100	 0.4940
BA	 0.9080	 0.5500
BN	 0.8790	 0.5210
BO	 0.8690	 0.5190
BP	 0.8620	 0.5130
BQ	 0.8030	 0.4640
BR	 0.8260	 0.5010
BS	 0.8170	 0.5060
BT	 0.7980	 0.4550
BU	 0.8510	 0.5290
BV	 0.8620	 0.5000
BW	 0.8010	 0.4820
BX	 0.8470	 0.5030
BY	 0.8230	 0.4780
BZ	 0.9040	 0.5400
Ba	 0.8750	 0.5230
Bb	 0.8940	 0.5560
Bc	 0.8760	 0.5250
Bd	 0.8740	 0.4990
Be	 0.8720	 0.5340
Bf	 0.8520	 0.5100
Bg	 0.7070	 0.3690
Bh	 0.8600	 0.5140
Bi	 0.8770	 0.4930
Bj	 0.8420	 0.5070
Bk	 0.8510	 0.5060
Bl	 0.8170	 0.4800
Bm	 0.8690	 0.5140
Bn	 0.8850	 0.5330
Bo	 0.8390	 0.4820
Bp	 0.8480	 0.5010
Bq	 0.8790	 0.5100
Br	 0.8910	 0.5290
Bs	 0.8870	 0.5300
Bt	 0.8240	 0.5010
Bu	 0.8490	 0.5150
Bv	 0.9270	 0.5400
Bw	 0.7450	 0.4450

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Chain	Atom inclusion	Q-score
Bx	 0.8460	 0.4940
By	 0.7700	 0.4780
H1	 0.3320	 0.1500
HE	 0.3530	 0.2500
HI	 0.7170	 0.4550
HL	 0.3990	 0.2320
HS	 0.8270	 0.5210