



wwPDB EM Validation Summary Report ⓘ

Jul 3, 2024 – 09:13 am BST

PDB ID : 6XU8
EMDB ID : EMD-10624
Title : Drosophila melanogaster Ovary 80S ribosome
Authors : Hopes, T.; Agapiou, M.; Norris, K.; McCarthy, C.G.P.; OConnell, M.J.;
Fontana, J.; Aspden, J.L.
Deposited on : 2020-01-17
Resolution : 3.00 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.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

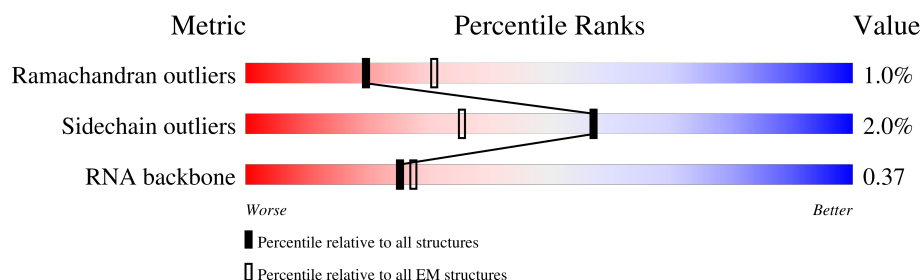
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



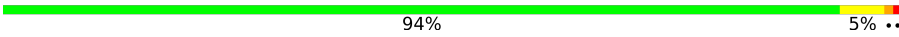
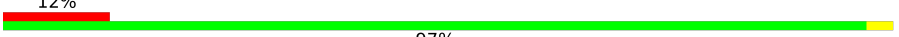

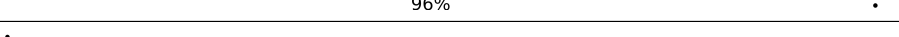


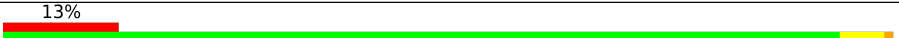
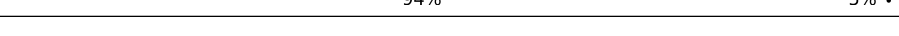
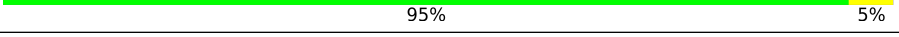
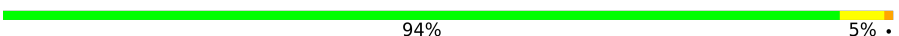

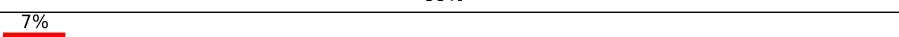

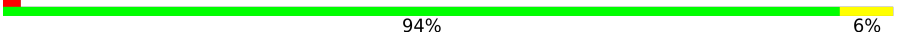



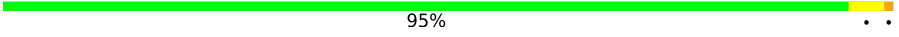
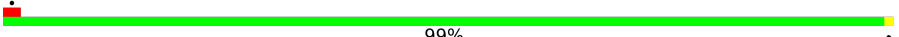

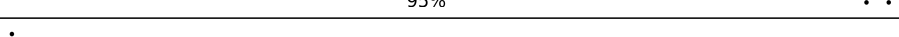



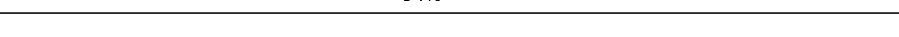
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	CO	205	
2	CL	210	
3	CV	134	
4	CM	159	
5	Ca	149	
6	CN	203	
7	CI	217	
8	CD	290	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	CQ	187	 94% 5% ..
10	CR	203	 12% 97% .
11	CA	253	 96% .
12	CS	173	 85% 14% .
13	CT	158	 92% 7% .
14	CP	185	 13% 94% 5% .
15	CX	120	 95% 5%
16	CY	131	 94% 5% .
17	CZ	134	 99% .
18	Cr	134	 7% 82% 17% .
19	Ch	123	 94% 6%
20	Cb	75	 88% 11% .
21	CB	414	 91% 8%
22	CF	226	 95% ..
23	Cc	100	 99% .
24	Ce	132	 95% ..
25	Cf	157	 84% 15% .
26	Ci	113	 90% 10%
27	Ck	70	 94% ..
28	Cl	50	 98% .
29	CC	392	 91% 8% .
30	Cm	52	 92% 6% .
31	Cn	25	 96% .
32	Cp	91	 95% 5%
33	Co	104	 93% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	CJ	182	
35	CH	190	
36	CE	228	
37	CG	241	
38	A9	30	
39	A7	120	
40	A8	123	
41	Ag	318	
42	AU	102	
43	AO	127	
44	AX	143	
45	AM	119	
46	Ad	52	
47	AN	150	
48	AL	155	
49	AR	120	
50	AP	124	
51	AB	220	
52	AA	218	
53	AV	82	
54	AY	126	
55	AZ	74	
56	Aa	107	
57	Ab	84	
58	AD	227	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	Ae	58	<div> <div>33%</div> <div>95%</div> <div>5%</div> </div>
60	Af	80	<div> <div>52%</div> <div>85%</div> <div>15%</div> </div>
61	AJ	181	<div> <div>8%</div> <div>97%</div> <div>..</div> </div>
62	AE	261	<div> <div>5%</div> <div>97%</div> <div>.</div> </div>
63	AC	227	<div> <div>11%</div> <div>97%</div> <div>.</div> </div>
64	AG	231	<div> <div>18%</div> <div>97%</div> <div>.</div> </div>
65	AH	194	<div> <div>21%</div> <div>95%</div> <div>5%</div> </div>
66	AI	207	<div> <div>17%</div> <div>96%</div> <div>.</div> </div>
67	AQ	148	<div> <div>42%</div> <div>92%</div> <div>8%</div> </div>
68	Cz	217	<div> <div>99%</div> <div>95%</div> <div>5%</div> </div>
69	A5	3703	<div> <div>6%</div> <div>37%</div> <div>46%</div> <div>17%</div> </div>
70	B2	1936	<div> <div>11%</div> <div>63%</div> <div>34%</div> <div>.</div> </div>
71	AW	129	<div> <div>.</div> <div>99%</div> <div>.</div> </div>
72	AT	126	<div> <div>18%</div> <div>94%</div> <div>6%</div> </div>
73	AK	90	<div> <div>7%</div> <div>97%</div> <div>.</div> </div>
74	AF	189	<div> <div>53%</div> <div>95%</div> <div>5%</div> </div>
75	Ac	62	<div> <div>24%</div> <div>92%</div> <div>8%</div> </div>
76	CU	99	<div> <div>6%</div> <div>96%</div> <div>.</div> </div>
77	Cj	87	<div> <div>99%</div> <div>.</div> </div>
78	CW	60	<div> <div>97%</div> <div>.</div> </div>
79	Cg	103	<div> <div>91%</div> <div>8%</div> <div>.</div> </div>
80	Cd	107	<div> <div>93%</div> <div>7%</div> </div>
81	AS	136	<div> <div>18%</div> <div>97%</div> <div>.</div> </div>

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 216955 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 2 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 3 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 4 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 5 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 6 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 7 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 9 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 10 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

- Molecule 12 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 13 is a protein called RE62581p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 14 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 15 is a protein called IP17216p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 16 is a protein called GEO07453p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 17 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

- Molecule 18 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Cr	134	Total	C	N	O	0	0
			1051	670	205	176		

- Molecule 19 is a protein called FI02809p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 20 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 21 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 22 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CF	226	Total	C	N	O	S	0	0
			1895	1216	368	308	3		

- Molecule 23 is a protein called RE25263p.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 25 is a protein called GEO07455p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 26 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 27 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 28 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 29 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

- Molecule 30 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 31 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 32 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 33 is a protein called TA01007p.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 34 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 35 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 36 is a protein called Ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 37 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 38 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

- Molecule 40 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

- Molecule 41 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 42 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 43 is a protein called 40S ribosomal protein S14a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AO	127	Total	C	N	O	S	0	0
			953	587	185	177	4		

- Molecule 44 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 45 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 46 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 47 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 48 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 49 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 50 is a protein called GEO07301p1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

- Molecule 52 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 53 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
AV	80	SER	THR	conflict	UNP O76927

- Molecule 54 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 55 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AZ	74	Total	C	N	O	S	0	0
			608	390	112	106			

- Molecule 56 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

- Molecule 57 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 58 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 59 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Ae	58	Total	C	N	O	S	0	0
			469	289	105	75			

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 62 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 63 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 64 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 65 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 66 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 67 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 68 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

- Molecule 69 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	A5	3703	Total	C	N	O	P	0	0
			77093	34436	13555	25401	3701		

- Molecule 70 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	B2	1936	Total	C	N	O	P	0	0
			39355	17526	6780	13114	1935		

- Molecule 71 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 72 is a protein called 40S ribosomal protein S19a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AT	126	Total	C	N	O	S	0	0
			1000	635	192	170	3		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	ALA	deletion	UNP P39018
AT	?	-	ARG	deletion	UNP P39018
AT	?	-	LEU	deletion	UNP P39018
AT	?	-	VAL	deletion	UNP P39018

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
AT	?	-	GLU	deletion	UNP P39018
AT	?	-	LYS	deletion	UNP P39018
AT	?	-	HIS	deletion	UNP P39018
AT	?	-	PRO	deletion	UNP P39018
AT	?	-	ASP	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018
AT	?	-	GLY	deletion	UNP P39018

- Molecule 73 is a protein called 40S ribosomal protein S10b.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AK	90	Total	C	N	O	S	0	0
			760	500	130	127	3		

- Molecule 74 is a protein called 40S ribosomal protein S5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AF	189	Total	C	N	O	S	0	0
			1481	925	283	266	7		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 76 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	CU	99	Total	C	N	O	S	0	0
			825	530	144	149	2		

- Molecule 77 is a protein called Probable 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cj	87	Total	C	N	O	S	0	0
			704	430	154	115	5		

- Molecule 78 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CW	60	Total	C	N	O	S	0	0
			503	326	95	78	4		

- Molecule 79 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Cg	103	Total	C	N	O	S	0	0
			844	525	176	138	5		

- Molecule 80 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cd	107	Total	C	N	O	S	0	0
			893	556	176	159	2		

- Molecule 81 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AS	136	Total	C	N	O	S	0	0
			1117	701	216	197	3		

3 Residue-property plots [i](#)


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

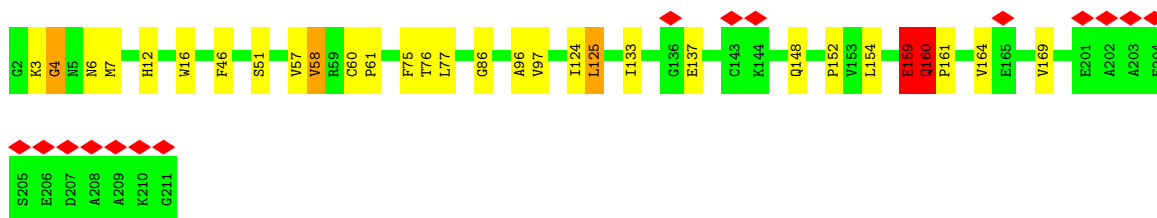
- Molecule 1: 60S ribosomal protein L13a

Chain CO:  94% 5%



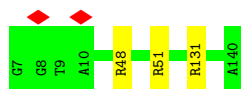
- Molecule 2: 60S ribosomal protein L13

Chain CL:  7% 86% 12% ..



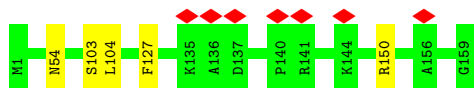
- Molecule 3: 60S ribosomal protein L23

Chain CV:  98% .



- Molecule 4: 60S ribosomal protein L14

Chain CM:  97% .



- Molecule 5: 60S ribosomal protein L27a

Chain Ca:  92% 7% .



- Molecule 6: 60S ribosomal protein L15

Chain CN: 91% 8% .



- Molecule 7: 60S ribosomal protein L10

Chain CI: 6% 96% .



- Molecule 8: 60S ribosomal protein L5

Chain CD: 96% .



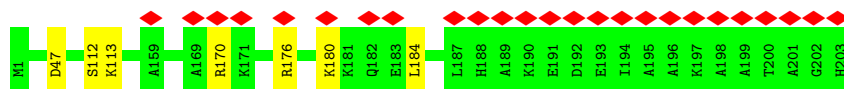
- Molecule 9: 60S ribosomal protein L18

Chain CQ: 94% 5% ..



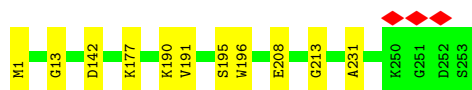
- Molecule 10: 60S ribosomal protein L19

Chain CR: 12% 97% .




- Molecule 11: 60S ribosomal protein L8

Chain CA: 96% .



- Molecule 12: 60S ribosomal protein L18a

Chain CS:  85% 14%



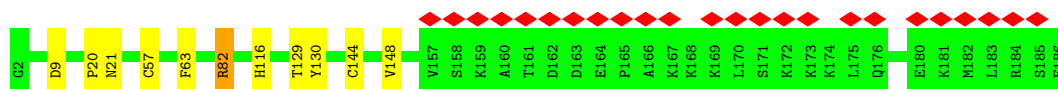
- Molecule 13: RE62581p

Chain CT:  92% 7%



- Molecule 14: 60S ribosomal protein L17

Chain CP:  13% 94% 5%



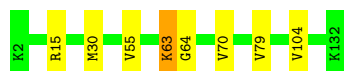
- Molecule 15: IP17216p

Chain CX:  95% 5%



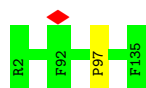
- Molecule 16: GEO07453p1

Chain CY:  94% 5%




- Molecule 17: 60S ribosomal protein L27

Chain CZ:  99%



- Molecule 18: 60S ribosomal protein L28

Chain Cr:  7% 82% 17%




- Molecule 19: FI02809p

Chain Ch:  94% 6%



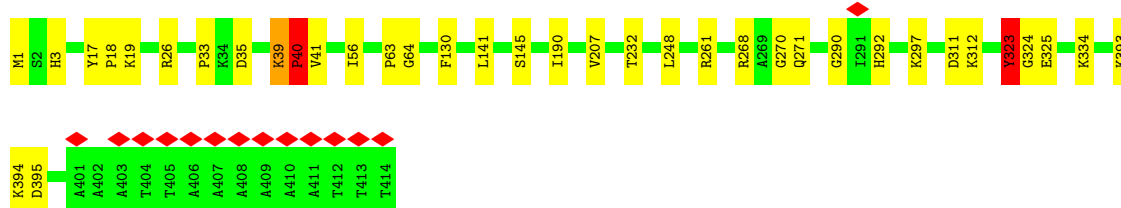
- Molecule 20: 60S ribosomal protein L29

Chain Cb:  88% 11%



- Molecule 21: 60S ribosomal protein L3

Chain CB:  91% 8%



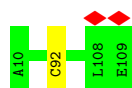
- Molecule 22: 60S ribosomal protein L7

Chain CF:  95%



- Molecule 23: RE25263p

Chain Cc:  99%




- Molecule 24: 60S ribosomal protein L32

Chain Ce:  95%



- Molecule 25: GEO07455p1

Chain Cf:  84% 15%



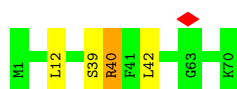
- Molecule 26: 60S ribosomal protein L36

Chain Ci:  90% 10%



- Molecule 27: 60S ribosomal protein L38

Chain Ck:  94%



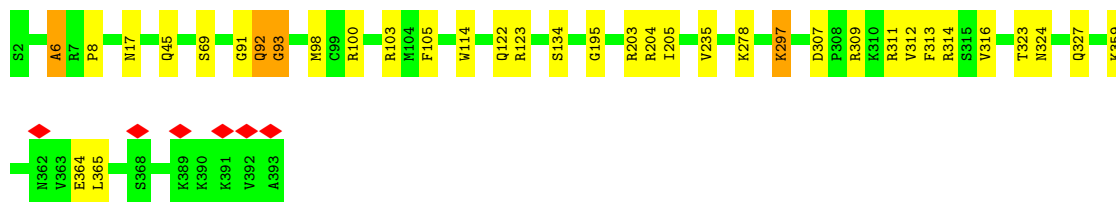
- Molecule 28: 60S ribosomal protein L39

Chain Cl:  98%



- Molecule 29: 60S ribosomal protein L4

Chain CC:  91% 8%



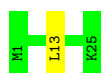
- Molecule 30: Ubiquitin-60S ribosomal protein L40

Chain Cm:  92% 6%

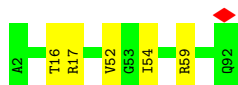


- Molecule 31: 60S ribosomal protein L41

Chain Cn:  96%



- Molecule 32: 60S ribosomal protein L37a



- Molecule 33: TA01007p



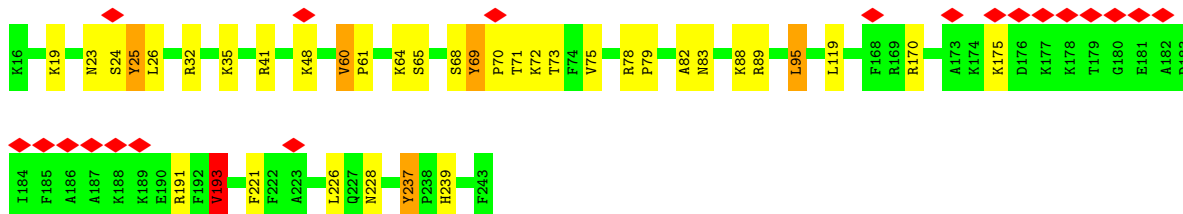
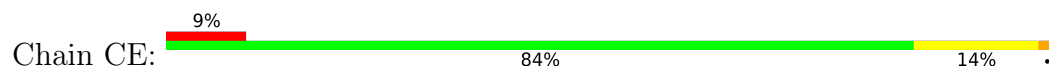
- Molecule 34: 60S ribosomal protein L11



- Molecule 35: 60S ribosomal protein L9

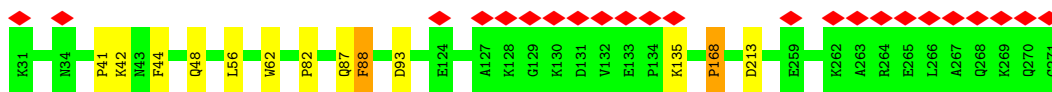


- Molecule 36: Ribosomal protein L6, isoform A



- Molecule 37: 60S ribosomal protein L7a





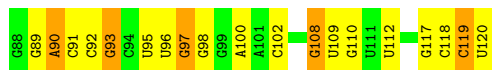
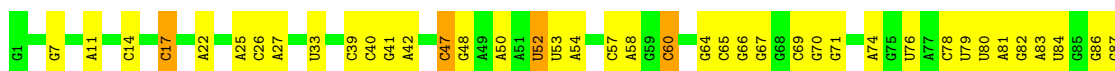
• Molecule 38: 2S ribosomal RNA

Chain A9: 53% 37% 10%



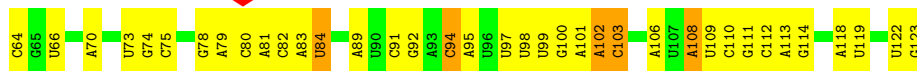
• Molecule 39: 5S ribosomal RNA

Chain A7: 51% 42% 8%



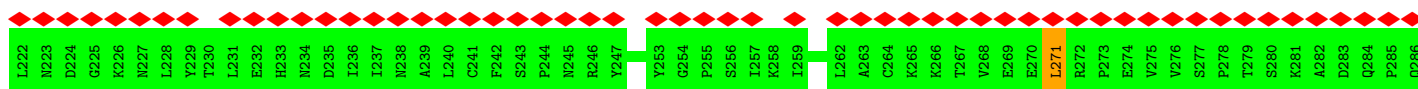
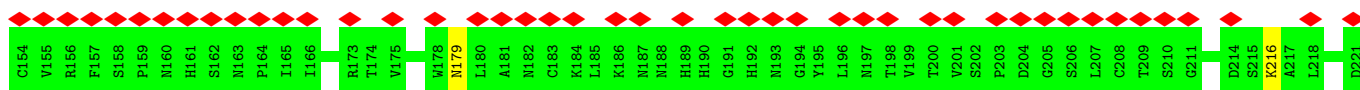
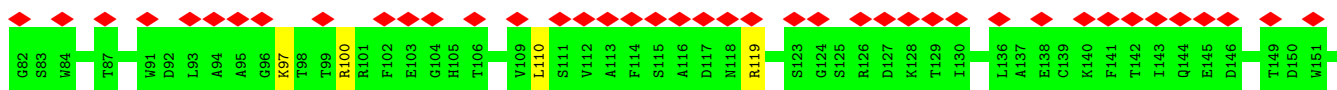
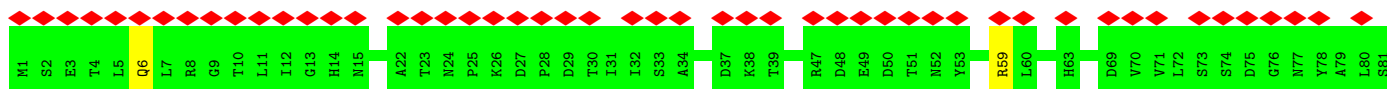
• Molecule 40: 5.8S ribosomal RNA

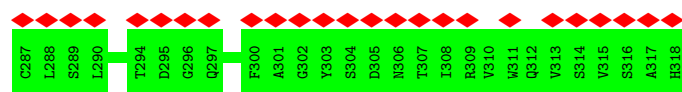
Chain A8: 31% 56% 13%



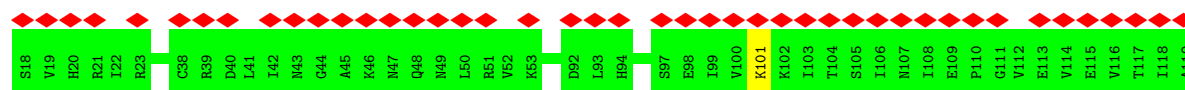
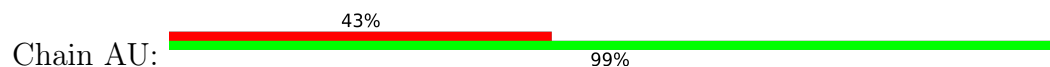
• Molecule 41: Guanine nucleotide-binding protein subunit beta-like protein

Chain Ag: 68% 97%

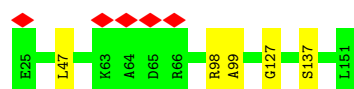




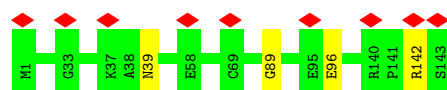
- Molecule 42: 40S ribosomal protein S20



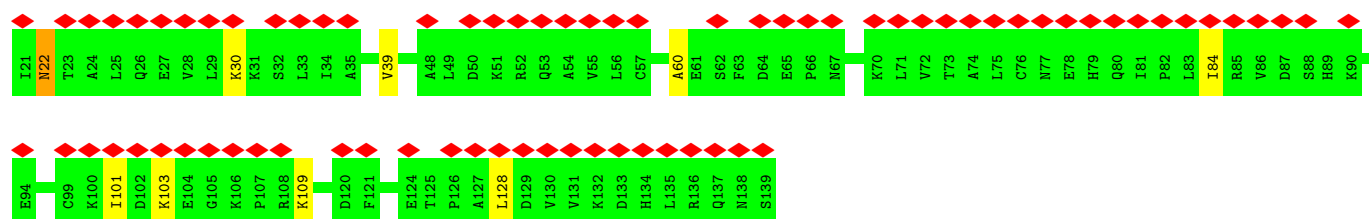
- Molecule 43: 40S ribosomal protein S14a



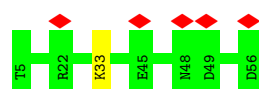
- Molecule 44: 40S ribosomal protein S23



- Molecule 45: 40S ribosomal protein S12

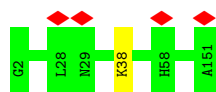


- Molecule 46: 40S ribosomal protein S29

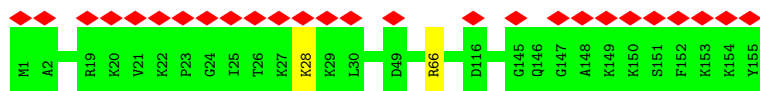


- Molecule 47: 40S ribosomal protein S13

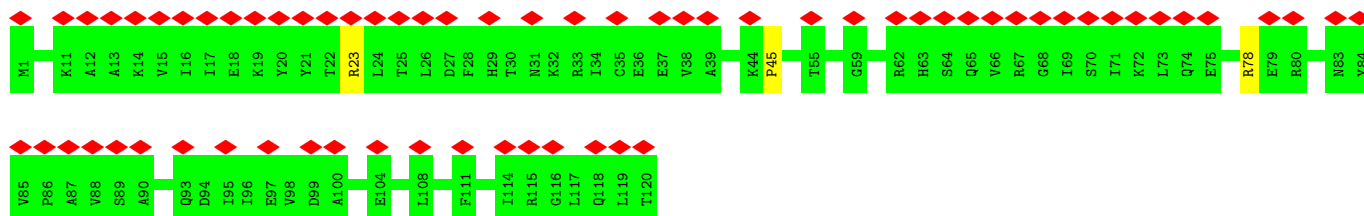




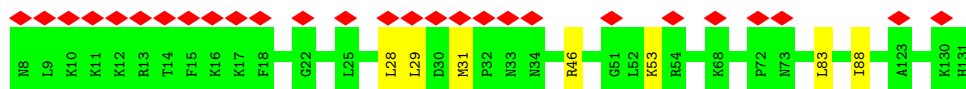
- Molecule 48: 40S ribosomal protein S11



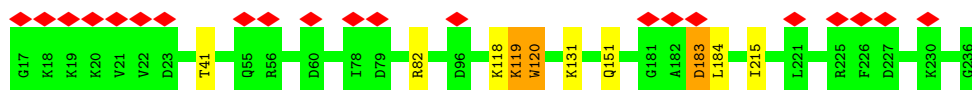
- Molecule 49: 40S ribosomal protein S17



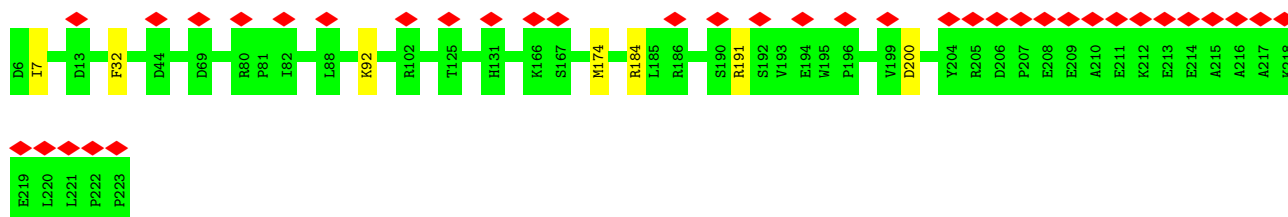
- Molecule 50: GEO07301p1



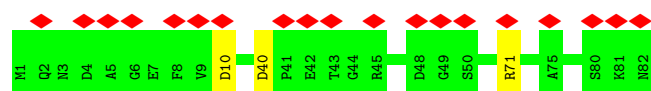
- Molecule 51: 40S ribosomal protein S3a



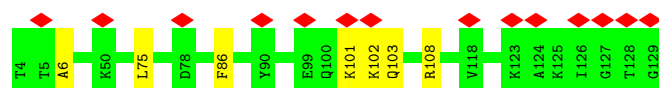
- Molecule 52: 40S ribosomal protein SA



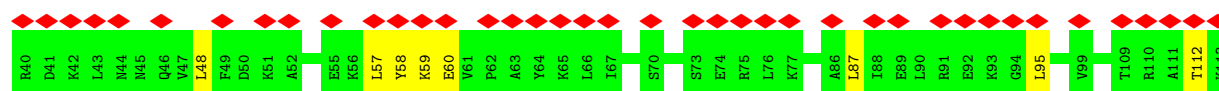
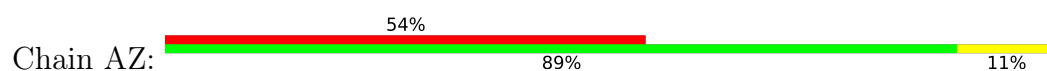
- Molecule 53: 40S ribosomal protein S21



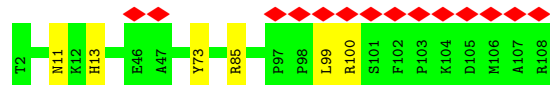
- Molecule 54: 40S ribosomal protein S24



- Molecule 55: 40S ribosomal protein S25



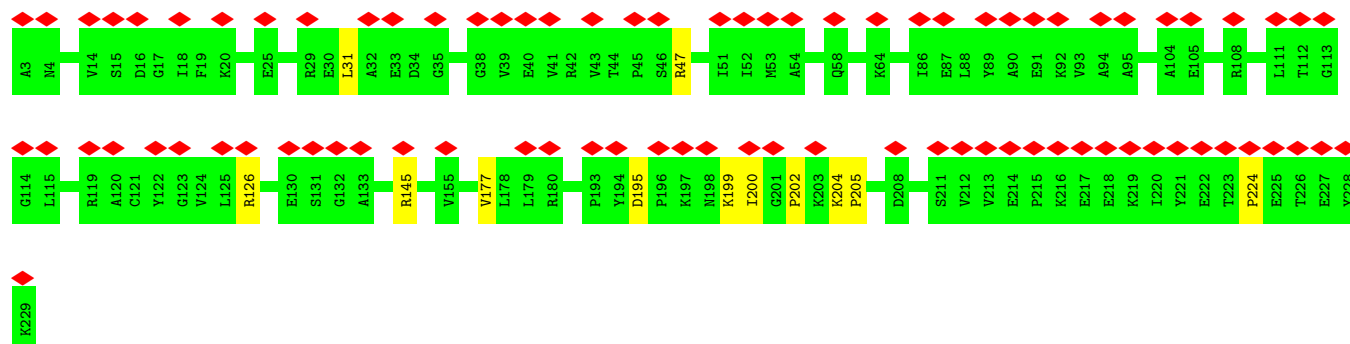
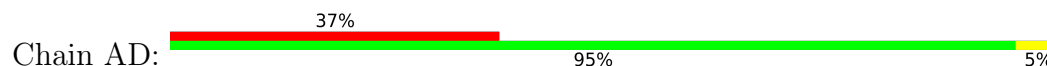
- Molecule 56: 40S ribosomal protein S26



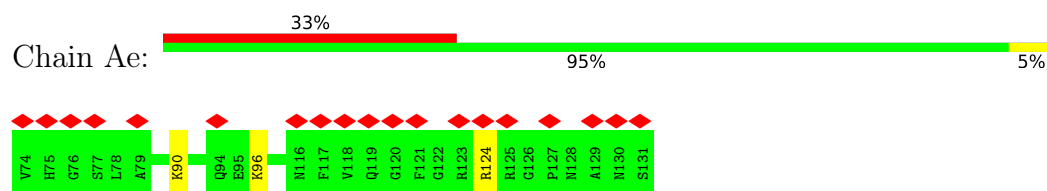
- Molecule 57: 40S ribosomal protein S27



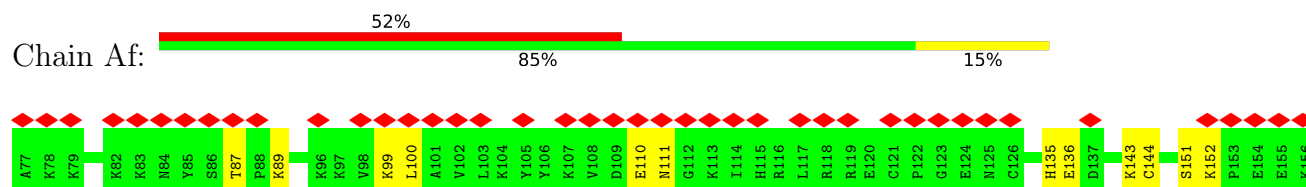
- Molecule 58: 40S ribosomal protein S3



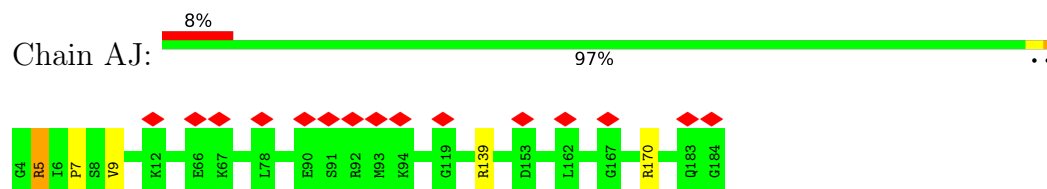
- Molecule 59: 40S ribosomal protein S30



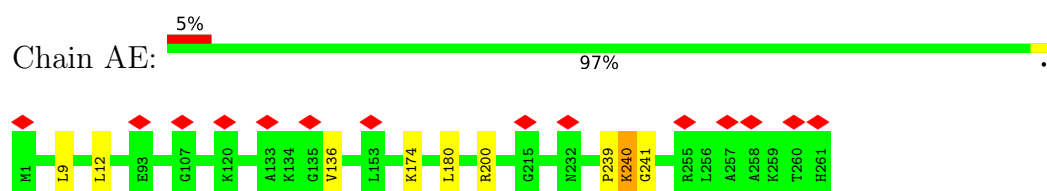
- Molecule 60: Ubiquitin-40S ribosomal protein S27a



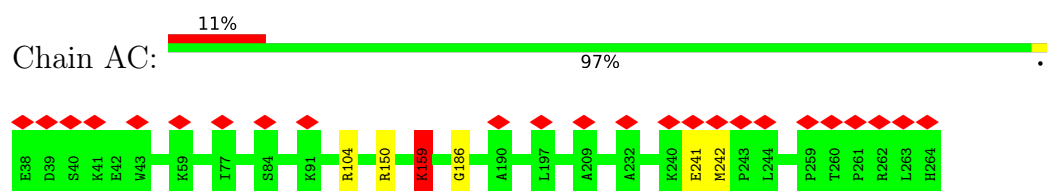
- Molecule 61: 40S ribosomal protein S9



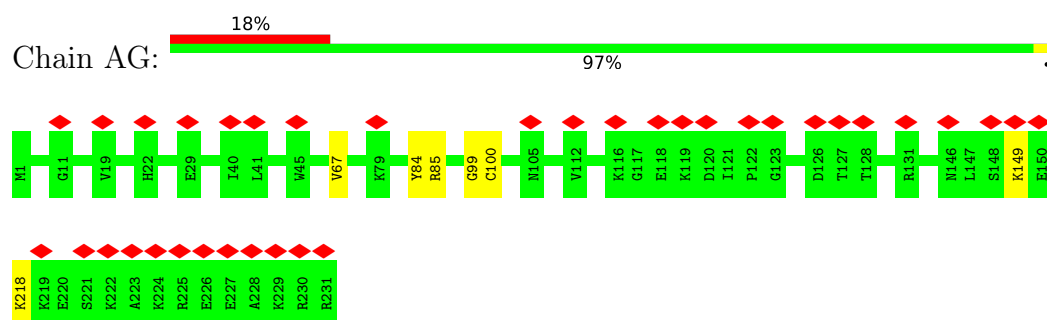
- Molecule 62: 40S ribosomal protein S4



- Molecule 63: 40S ribosomal protein S2

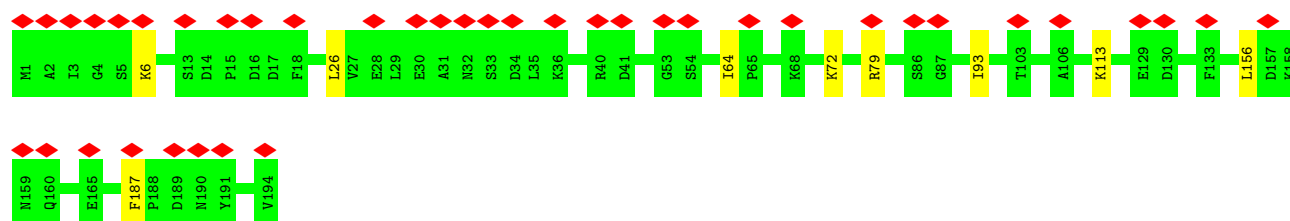


- Molecule 64: 40S ribosomal protein S6



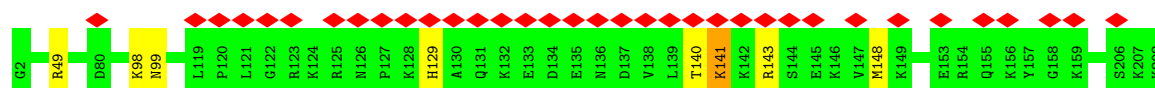
- Molecule 65: 40S ribosomal protein S7

Chain AH: 

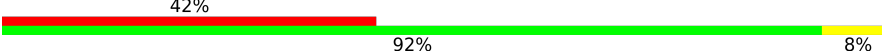


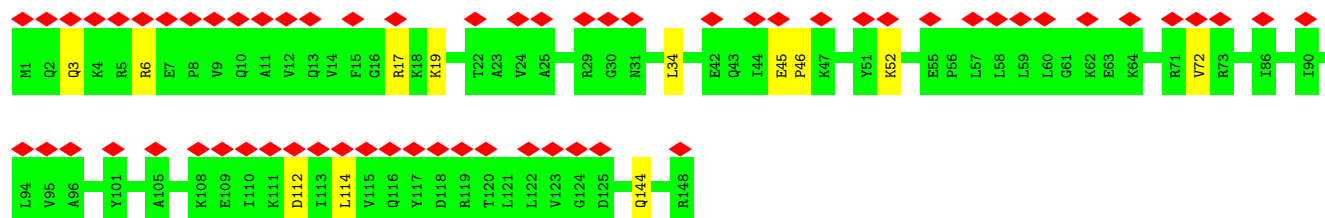
- Molecule 66: 40S ribosomal protein S8

Chain AI: 



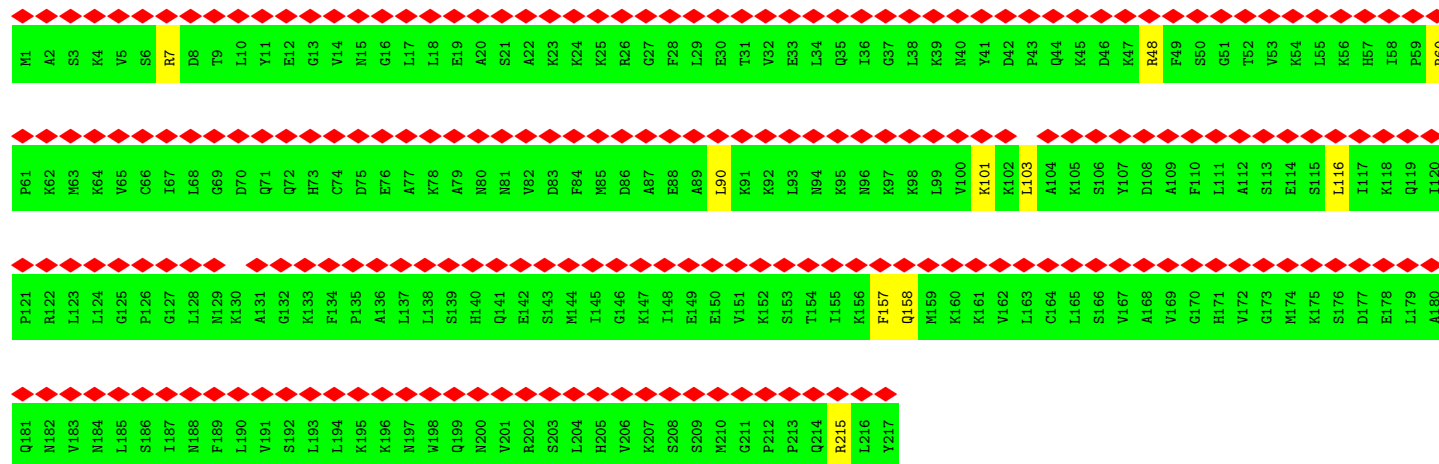
- Molecule 67: 40S ribosomal protein S16

Chain AQ: 



- Molecule 68: 60S ribosomal protein L10a-2

Chain Cz: 



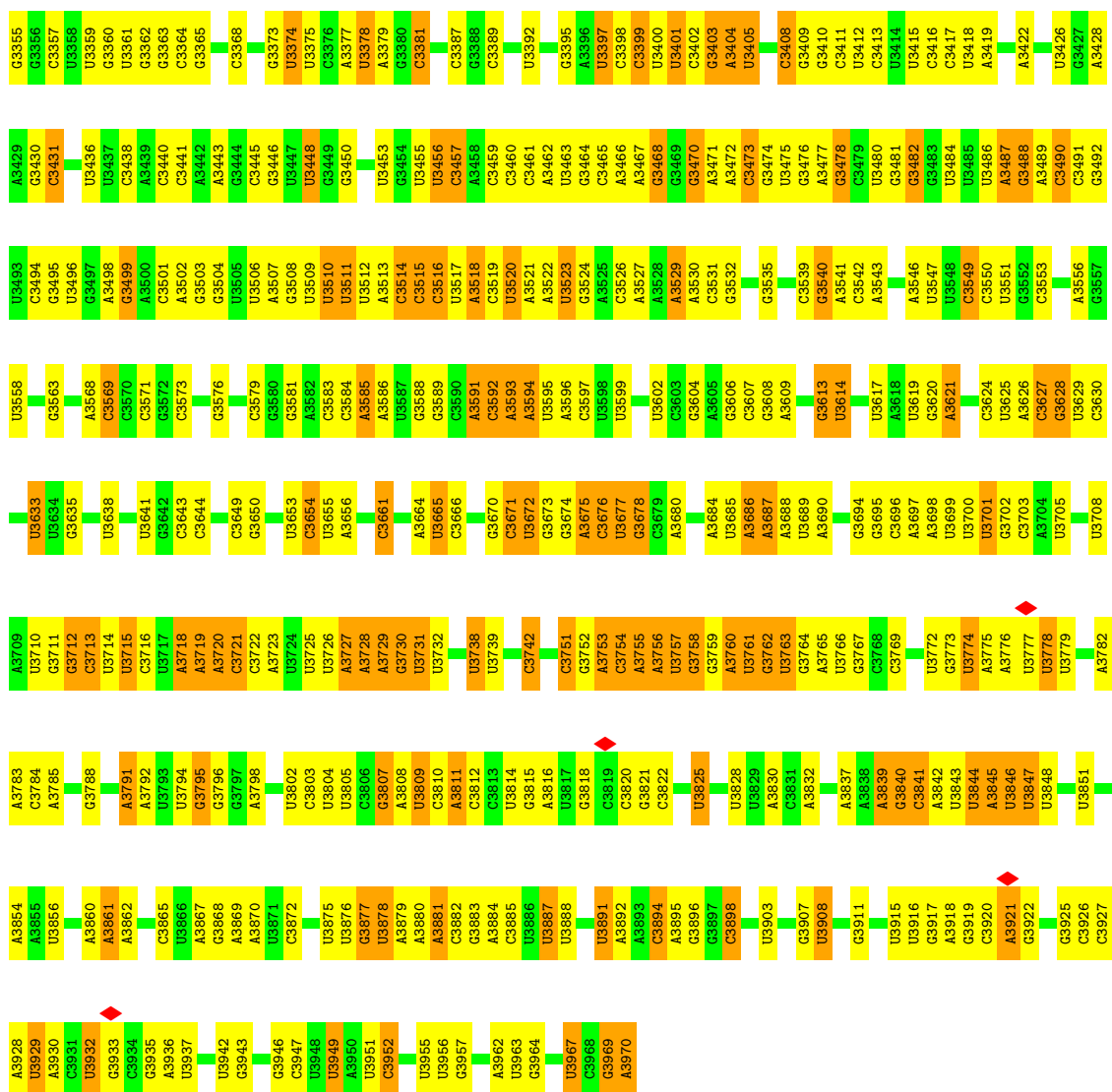
- Molecule 69: 28S ribosomal RNA

Chain A5: 

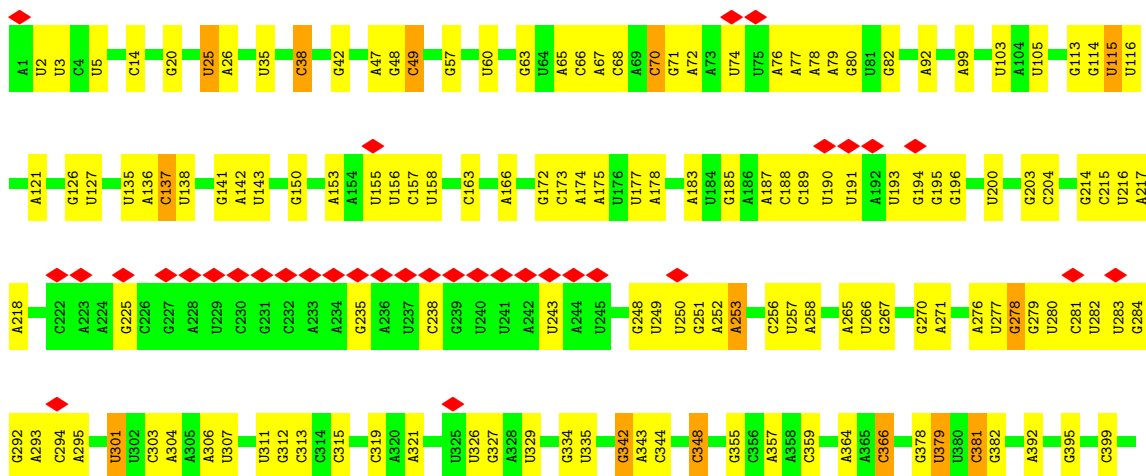


	A1889	A1778	G1715	G1650	G1581	A1516	C1447	U1376	A1313	C1245	A1167	G1107
A2075	U1890	G1779	G1718	C1651	A1588	A1517	G1448	A1377	A1314	U1246	G1168	G1108
A2076	C1891	U1780	G1719	U1652	A1589	A1518	G1449	U1378	A1315	C1260	C1169	G1109
A2077	C1892	U1781	G1720	G1653	A1590	A1519	U1450	U1379	A1316		U1170	G1110
C2078	C1893	C1782	A1721	C1654	A1591	U1520	G1451	G1380	A1317	A1253	G1171	C1111
U2079		C1720	A1655	A1655	U1592	G1522	A1452	U1381	A1318	U1254	G1172	G1112
U2082	C1898	U1722	U1656	U1657	U1593	G1523	U1453	U1382	A1319	U1255	U1173	A1113
A2083	C1899	U1723	G1658	G1659	U1594	U1524	C1454	A1383	U1320		G1174	A1114
U2084	G1786	A1724	G1659	U1659	U1595	A1525	A1455	C1394	G1321	C1288	G1175	A1115
U2094	C1787	G1725	G1660	A1596	G1526	G1525	U1456	U1386	C1324	A1258	A1176	G1116
	U1903	U1726	G1661	A1597	C1527	G1526	G1457	U1387	A1197	A1260	A1177	A1117
C2087		U1728	U1662	A1598	G1528	G1528	G1458	C1388	A1326	A1261	A1182	C1118
G2088	A1908	G1729	G1663	C1599	C1529	G1528	A1459	C1389	G1327	C1262	U1183	C1119
A2089	U1909	A1730	C1664		U1530	C1529	A1460	C1390	U1328	U1263	A1192	A1120
U2090	C1911	G1731	C1665	G1604	U1531	U1531	G1461	A1391	U1329	U1264	A1193	A1121
A2091	G1793	A1732	C1666	U1605	A1532	A1532	U1462	A1392	G1330	U1265	A1194	C1123
U2092	U1913	A1733	U1667	G1606	A1533	A1533	C1463	A1393	G1331		U1195	G1124
U2093	A1796	G1734	U1668	A1607	G1534	G1534	G1464	U1394	C1332	U1269	A1196	A1125
U2094	A1797	G1735	U1669	G1608	U1535	U1535	G1465	U1395	C1333	G1270	A1197	A1126
U2095	U1915	G1736	G1670	U1609	U1536	U1536	A1466	A1396	C1334	G1271	U1198	C1127
	G1916	U1737	U1671	A1610	U1538	U1538	A1467			U1272	U1199	C1128
U1917	U1917	U1738	A1672	G1611	U1539	U1539	A1468	A1399	U1338	A1274	A1199	A1129
U1918	U1800	U1739	C1673	G1612	A1539	A1539	A1467		U1339	U1275	C1199	
A1919	U1801	U1740	A1674	A1613	U1540	U1540	A1467	U1402	U1339	A1276	A1202	U1130
U1920	G1803	G1741	G1675	A1614	A1541	A1541		C1403	U1339	A1277	U1203	C1131
	A1804	G1745	U1676	G1615	C1542	C1542	G1471	U1404	G1341	G1276	C1204	U1132
	U1807	A1746	U1677	G1616	C1543	C1543	C1472	U1405	U1342	A1278	U1205	A1133
A1923	A1808	A1747	U1678	U1617	U1544	U1544	C1473	A1406	A1343	C1279	G1206	G1134
A1924	A1809	G1748	U1679	U1618	A1545	A1545	A1474	C1407	G1345		G1207	U1135
U1925	A1810	A1749	U1680	C1619	U1546	U1546	A1475	A1408	C1346	U1282	U1208	A1136
U1926	A1811	G1750	U1681	A1620	A1547	A1547	G1476	G1409	A1347	A1283	A1209	G1137
U1927	C1812	G1751	U1682	A1621	U1548	U1548	G1477	A1410	U1348	A1284	A1210	C1138
	A1813	G1752	U1683	G1622	U1549	A1549	A1478	U1411	A1410	A1285	A1211	U1139
	U1859	G1753	G1684	G1623	U1550	G1479	G1479	A1412	A1349		G1212	G1140
	U1860	U1754	G1685	G1624	U1551	U1551	U1480	C1413	A1350		C1213	G1141
	A1861	G1755	U1686	U1625	A1552	A1552	U1481	C1414	C1351	U1288	G1214	U1143
	U1862	U1756	U1687	A1626	A1553	C1553	U1482	A1415	U1352	C1289		C1144
	U1863	A1757	G1688	U1627	C1554	C1554	U1483	U1416	U1290	U1290	C1145	C1144
	U1864	G1758	G1689	G1628	G1555	G1555	U1484	G1417	U1291	G1292	U1220	C1146
	U1865	U1759	U1690	C1629	A1558	A1558	A1485	A1418	U1292	A1222	U1221	U1147
	G1866	C1761	G1692	G1630	A1563	A1563	A1486	U1420	A1293	A1223	G1223	C1148
	A1867	G1762	C1693	U1631	G1564	G1564	C1487	G1421	U1294	U1294	G1149	G1150
	C1868	A1763	A1694	G1632	U1565	U1565	A1488	G1422	U1295	G1297	A1151	A1151
	C1869	G1764	A1695	G1633	U1566	U1566	A1489	C1423	G1361	A1298	G1228	A1152
	G1870	U1765	A1696	A1634	U1567	G1567		G1424	G1362	A1299	U1229	G1153
	A1871	U1766	U1697	A1635	A1568	A1568	C1492	U1425	G1363	G1300	U1230	U1154
	A1872	A1767	A1698		U1569	U1569	A1493	U1426	A1364	A1301	A1231	U1155
	A1873	G1768	U1699	G1638	U1570	U1570	C1498	G1427	U1365	U1302	G1232	U1156
	G1875	U1769	U1700	U1640	U1573	U1573			G1366	G1303	G1233	C1157
	U1876	G1770	G1702	U1641	U1574	U1574	A1501	U1430	A1367	A1304	G1234	C1158
	A1877	G1771		G1642	A1575	A1575	A1502	A1435	A1368	A1305	A1159	C1159
	U1878	U1772	G1710	C1644	U1576	U1576	A1505	A1436	C1369	G1306	U1160	U1160
	A1880	C1774	G1711	U1645	U1577	A1577		A1437	C1370	U1308	A1161	A1161
	C1881	U1775	C1712	U1646	A1578	A1578	A1509	A1438	A1371	U1309	G1162	G1163
	G1882	U1776	U1713	A1647	U1579	U1579	G1510		A1372	A1310	C1241	G1164
	U1885	A1777	U1714	G1649	U1580	U1580	C1512	C1442	A1373	G1311	A1242	A1165
							U1513		G1374	G1312	A1243	U1166
							U1514		G1375		U1244	
							U1515					

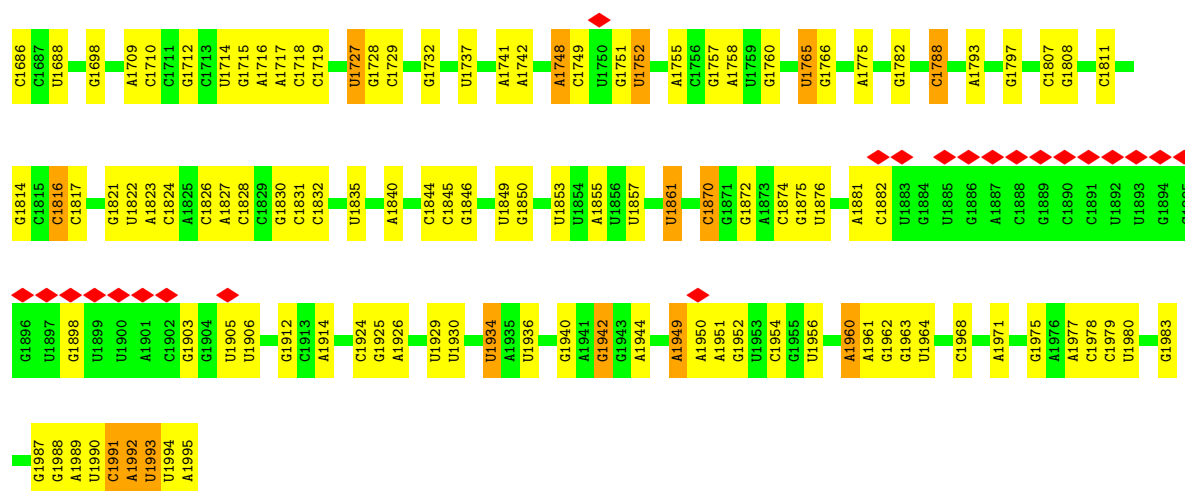




• Molecule 70: 18S ribosomal RNA

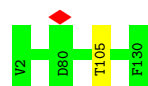






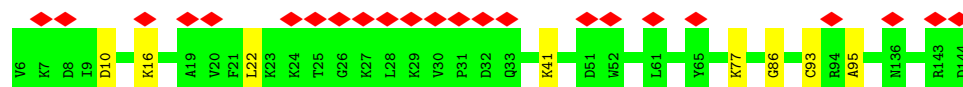
- Molecule 71: 40S ribosomal protein S15Aa

Chain AW: 99%



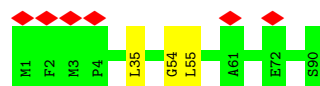
- Molecule 72: 40S ribosomal protein S19a

Chain AT: 18% 94% 6%



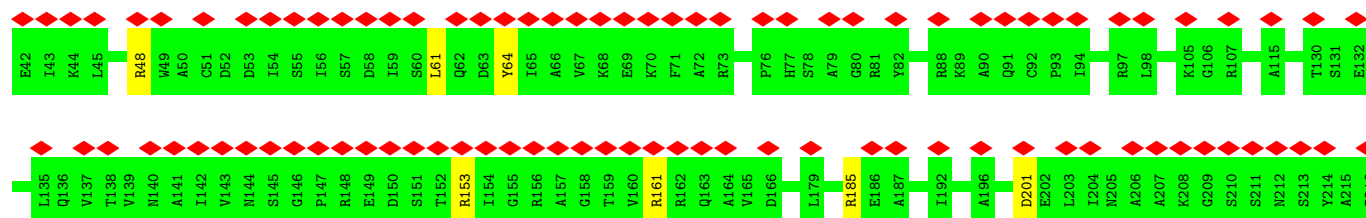
- Molecule 73: 40S ribosomal protein S10b

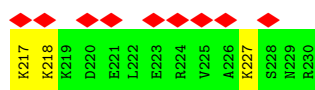
Chain AK: 7% 97% 5%



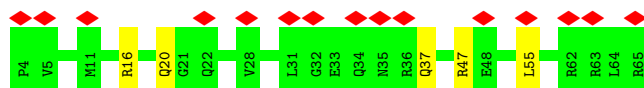
- Molecule 74: 40S ribosomal protein S5b

Chain AF: 53% 95% 5%

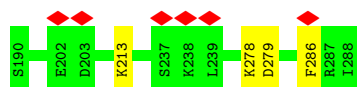




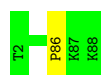
- Molecule 75: 40S ribosomal protein S28



- Molecule 76: 60S ribosomal protein L22



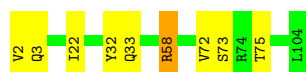
- Molecule 77: Probable 60S ribosomal protein L37-A



- Molecule 78: 60S ribosomal protein L24



- Molecule 79: 60S ribosomal protein L34

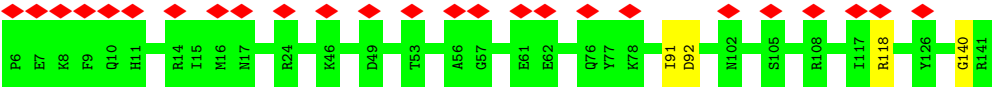


- Molecule 80: 60S ribosomal protein L31



- Molecule 81: 40S ribosomal protein S18





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	185913	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.861	Depositor
Minimum map value	-0.593	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.035	Depositor
Map size (\AA)	426.00003, 426.00003, 426.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.065, 1.065, 1.065	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CO	0.89	0/1700	0.90	5/2277 (0.2%)
2	CL	0.74	1/1726 (0.1%)	1.02	5/2308 (0.2%)
3	CV	0.77	0/1014	0.79	1/1362 (0.1%)
4	CM	0.67	0/1326	0.77	0/1780
5	Ca	0.98	1/1235 (0.1%)	1.00	5/1640 (0.3%)
6	CN	1.02	4/1750 (0.2%)	0.99	2/2335 (0.1%)
7	CI	0.53	1/1827 (0.1%)	0.66	1/2447 (0.0%)
8	CD	0.61	0/2379	0.68	1/3196 (0.0%)
9	CQ	0.96	1/1544 (0.1%)	0.93	3/2069 (0.1%)
10	CR	0.61	0/1703	0.67	1/2255 (0.0%)
11	CA	0.84	1/1970 (0.1%)	0.83	3/2635 (0.1%)
12	CS	0.85	0/1491	1.00	4/1998 (0.2%)
13	CT	0.83	1/1326 (0.1%)	0.85	3/1773 (0.2%)
14	CP	0.92	2/1529 (0.1%)	0.87	2/2042 (0.1%)
15	CX	0.66	0/1001	0.84	3/1348 (0.2%)
16	CY	0.79	0/1094	0.81	2/1456 (0.1%)
17	CZ	0.51	0/1141	0.67	0/1517
18	Cr	0.88	2/1069 (0.2%)	1.13	3/1432 (0.2%)
19	Ch	0.65	0/1024	0.78	0/1353
20	Cb	0.62	0/628	0.95	1/832 (0.1%)
21	CB	0.79	1/3356 (0.0%)	0.91	8/4494 (0.2%)
22	CF	0.90	0/1931	0.84	4/2587 (0.2%)
23	Cc	0.55	0/779	0.64	0/1048
24	Ce	1.04	1/1132 (0.1%)	0.94	2/1508 (0.1%)
25	Cf	0.92	2/1270 (0.2%)	1.07	4/1696 (0.2%)
26	Ci	0.58	0/944	0.89	3/1250 (0.2%)
27	Ck	0.60	0/583	0.79	2/774 (0.3%)
28	Cl	0.89	0/445	0.89	1/589 (0.2%)
29	CC	0.91	1/3163 (0.0%)	0.95	8/4253 (0.2%)
30	Cm	0.57	0/435	0.78	0/575
31	Cn	0.57	0/237	0.74	1/300 (0.3%)
32	Cp	0.85	0/719	0.87	0/954
33	Co	0.76	0/887	0.88	1/1162 (0.1%)
34	CJ	0.42	0/1494	0.76	3/2001 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	CH	0.61	0/1519	0.80	3/2042 (0.1%)
36	CE	0.65	1/1883 (0.1%)	0.97	5/2514 (0.2%)
37	CG	0.58	1/1968 (0.1%)	0.77	0/2637
38	A9	1.48	2/714 (0.3%)	1.50	18/1112 (1.6%)
39	A7	1.53	15/2854 (0.5%)	1.51	59/4447 (1.3%)
40	A8	1.93	42/2932 (1.4%)	1.72	96/4568 (2.1%)
41	Ag	0.32	0/2574	0.70	3/3506 (0.1%)
42	AU	0.31	0/825	0.64	0/1111
43	AO	0.35	0/965	0.70	0/1295
44	AX	0.36	0/1152	0.69	0/1540
45	AM	0.34	0/937	0.79	2/1260 (0.2%)
46	Ad	0.33	0/443	0.64	0/589
47	AN	0.38	0/1225	0.63	0/1641
48	AL	0.45	0/1296	0.64	0/1725
49	AR	0.34	0/993	0.74	0/1333
50	AP	0.32	0/1036	0.76	3/1383 (0.2%)
51	AB	0.33	0/1825	0.69	1/2448 (0.0%)
52	AA	0.33	0/1777	0.64	0/2422
53	AV	0.34	0/622	0.64	0/835
54	AY	0.30	0/1032	0.69	1/1373 (0.1%)
55	AZ	0.33	0/616	0.85	3/826 (0.4%)
56	Aa	0.41	0/883	0.69	0/1184
57	Ab	0.30	0/668	0.65	0/898
58	AD	0.31	0/1808	0.71	1/2427 (0.0%)
59	Ae	0.31	0/475	0.65	0/625
60	Af	0.33	0/672	0.74	1/887 (0.1%)
61	AJ	0.32	0/1526	0.64	1/2037 (0.0%)
62	AE	0.34	0/2096	0.67	2/2819 (0.1%)
63	AC	0.37	0/1785	0.70	1/2415 (0.0%)
64	AG	0.32	0/1891	0.67	1/2519 (0.0%)
65	AH	0.32	0/1593	0.68	2/2145 (0.1%)
66	AI	0.41	0/1689	0.80	1/2250 (0.0%)
67	AQ	0.33	0/1202	0.79	3/1608 (0.2%)
68	Cz	0.33	0/1727	0.75	3/2308 (0.1%)
69	A5	1.84	1826/86147 (2.1%)	1.78	3112/134004 (2.3%)
70	B2	0.69	4/43887 (0.0%)	1.11	255/68161 (0.4%)
71	AW	0.37	0/1046	0.60	0/1402
72	AT	0.29	0/1019	0.66	0/1367
73	AK	0.33	0/786	0.78	3/1064 (0.3%)
74	AF	0.33	0/1501	0.70	1/2017 (0.0%)
75	Ac	0.36	0/502	0.75	1/670 (0.1%)
76	CU	0.45	0/838	0.79	1/1123 (0.1%)
77	Cj	1.06	0/717	0.85	0/950

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	CW	0.68	0/515	0.77	0/683
79	Cg	0.80	0/855	0.84	2/1142 (0.2%)
80	Cd	0.27	0/908	0.46	0/1221
81	AS	0.28	0/1135	0.67	2/1521 (0.1%)
All	All	1.26	1910/232911 (0.8%)	1.34	3669/341300 (1.1%)

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
1	CO	0	9
2	CL	0	14
4	CM	0	2
5	Ca	0	5
6	CN	0	7
7	CI	0	5
8	CD	0	5
9	CQ	0	5
10	CR	0	3
11	CA	0	4
12	CS	0	11
13	CT	0	8
14	CP	0	3
16	CY	0	2
18	Cr	0	15
19	Ch	0	5
20	Cb	0	4
21	CB	0	18
22	CF	0	4
24	Ce	0	3
25	Cf	0	11
26	Ci	0	7
27	Ck	0	2
29	CC	0	15
30	Cm	0	2
33	Co	0	3
34	CJ	0	4
35	CH	0	4
36	CE	0	25
37	CG	0	9

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
43	AO	0	4
44	AX	0	1
45	AM	0	3
46	Ad	0	1
50	AP	0	3
51	AB	0	4
52	AA	0	2
53	AV	0	2
54	AY	0	1
55	AZ	0	4
56	Aa	0	2
57	Ab	0	1
58	AD	0	6
59	Ae	0	1
60	Af	0	10
61	AJ	0	4
62	AE	0	1
63	AC	0	2
64	AG	0	2
65	AH	0	3
66	AI	0	2
67	AQ	0	5
68	Cz	0	2
72	AT	0	3
74	AF	0	2
75	Ac	0	1
76	CU	0	1
78	CW	0	1
79	Cg	0	1
80	Cd	0	1
All	All	0	290

The worst 5 of 1910 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	A5	1313	A	N9-C4	-13.10	1.29	1.37
69	A5	1795	A	C5-C6	-12.81	1.29	1.41
69	A5	1689	G	N7-C5	-12.62	1.31	1.39
69	A5	1686	A	N9-C4	-11.02	1.31	1.37
69	A5	754	A	N9-C4	-10.88	1.31	1.37

The worst 5 of 3669 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
69	A5	1699	A	N1-C6-N6	-37.41	96.15	118.60
69	A5	3472	A	C8-N9-C4	-20.68	97.53	105.80
69	A5	1699	A	C5-C6-N6	20.58	140.17	123.70
69	A5	840	U	O5'-P-OP1	-19.48	87.32	110.70
69	A5	33	C	C6-N1-C2	-17.17	113.43	120.30

There are no chirality outliers.

5 of 290 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CO	109	GLY	Peptide
1	CO	111	PRO	Peptide
1	CO	112	SER	Peptide
1	CO	177	LYS	Peptide
1	CO	190	ALA	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CO	203/205 (99%)	177 (87%)	24 (12%)	2 (1%)	15	53
2	CL	208/210 (99%)	154 (74%)	42 (20%)	12 (6%)	1	10
3	CV	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
4	CM	157/159 (99%)	129 (82%)	27 (17%)	1 (1%)	25	64
5	Ca	147/149 (99%)	113 (77%)	33 (22%)	1 (1%)	22	60
6	CN	201/203 (99%)	166 (83%)	32 (16%)	3 (2%)	10	42
7	CI	215/217 (99%)	183 (85%)	30 (14%)	2 (1%)	17	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	CD	288/290 (99%)	247 (86%)	39 (14%)	2 (1%)	22	60
9	CQ	185/187 (99%)	160 (86%)	25 (14%)	0	100	100
10	CR	201/203 (99%)	183 (91%)	18 (9%)	0	100	100
11	CA	251/253 (99%)	211 (84%)	39 (16%)	1 (0%)	34	72
12	CS	171/173 (99%)	126 (74%)	37 (22%)	8 (5%)	2	14
13	CT	156/158 (99%)	130 (83%)	25 (16%)	1 (1%)	25	64
14	CP	183/185 (99%)	163 (89%)	19 (10%)	1 (0%)	29	68
15	CX	118/120 (98%)	98 (83%)	19 (16%)	1 (1%)	19	57
16	CY	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	19	57
17	CZ	132/134 (98%)	110 (83%)	21 (16%)	1 (1%)	19	57
18	Cr	132/134 (98%)	81 (61%)	47 (36%)	4 (3%)	4	24
19	Ch	121/123 (98%)	106 (88%)	15 (12%)	0	100	100
20	Cb	73/75 (97%)	59 (81%)	11 (15%)	3 (4%)	3	16
21	CB	412/414 (100%)	346 (84%)	56 (14%)	10 (2%)	6	29
22	CF	224/226 (99%)	199 (89%)	20 (9%)	5 (2%)	6	31
23	Cc	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
24	Ce	130/132 (98%)	118 (91%)	11 (8%)	1 (1%)	19	57
25	Cf	155/157 (99%)	113 (73%)	36 (23%)	6 (4%)	3	17
26	Ci	111/113 (98%)	82 (74%)	28 (25%)	1 (1%)	17	55
27	Ck	68/70 (97%)	61 (90%)	7 (10%)	0	100	100
28	Cl	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
29	CC	390/392 (100%)	318 (82%)	67 (17%)	5 (1%)	12	45
30	Cm	50/52 (96%)	43 (86%)	6 (12%)	1 (2%)	7	34
31	Cn	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
32	Cp	89/91 (98%)	80 (90%)	9 (10%)	0	100	100
33	Co	102/104 (98%)	82 (80%)	18 (18%)	2 (2%)	7	34
34	CJ	180/182 (99%)	149 (83%)	30 (17%)	1 (1%)	25	64
35	CH	188/190 (99%)	164 (87%)	21 (11%)	3 (2%)	9	40
36	CE	226/228 (99%)	157 (70%)	62 (27%)	7 (3%)	4	23
37	CG	239/241 (99%)	194 (81%)	43 (18%)	2 (1%)	19	57
41	Ag	316/318 (99%)	265 (84%)	51 (16%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	AU	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
43	AO	125/127 (98%)	100 (80%)	25 (20%)	0	100	100
44	AX	141/143 (99%)	120 (85%)	20 (14%)	1 (1%)	22	60
45	AM	117/119 (98%)	85 (73%)	32 (27%)	0	100	100
46	Ad	50/52 (96%)	33 (66%)	17 (34%)	0	100	100
47	AN	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
48	AL	153/155 (99%)	133 (87%)	19 (12%)	1 (1%)	22	60
49	AR	118/120 (98%)	92 (78%)	25 (21%)	1 (1%)	19	57
50	AP	122/124 (98%)	96 (79%)	26 (21%)	0	100	100
51	AB	218/220 (99%)	176 (81%)	37 (17%)	5 (2%)	6	30
52	AA	216/218 (99%)	179 (83%)	36 (17%)	1 (0%)	29	68
53	AV	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
54	AY	124/126 (98%)	101 (82%)	22 (18%)	1 (1%)	19	57
55	AZ	72/74 (97%)	56 (78%)	16 (22%)	0	100	100
56	Aa	105/107 (98%)	86 (82%)	18 (17%)	1 (1%)	15	53
57	Ab	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
58	AD	225/227 (99%)	179 (80%)	44 (20%)	2 (1%)	17	55
59	Ae	56/58 (97%)	39 (70%)	17 (30%)	0	100	100
60	Af	78/80 (98%)	57 (73%)	21 (27%)	0	100	100
61	AJ	179/181 (99%)	152 (85%)	26 (14%)	1 (1%)	25	64
62	AE	259/261 (99%)	215 (83%)	42 (16%)	2 (1%)	19	57
63	AC	225/227 (99%)	188 (84%)	35 (16%)	2 (1%)	17	55
64	AG	229/231 (99%)	197 (86%)	30 (13%)	2 (1%)	17	55
65	AH	192/194 (99%)	161 (84%)	31 (16%)	0	100	100
66	AI	205/207 (99%)	161 (78%)	41 (20%)	3 (2%)	10	42
67	AQ	146/148 (99%)	116 (80%)	29 (20%)	1 (1%)	22	60
68	Cz	215/217 (99%)	175 (81%)	40 (19%)	0	100	100
71	AW	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
72	AT	122/126 (97%)	92 (75%)	29 (24%)	1 (1%)	19	57
73	AK	88/90 (98%)	64 (73%)	24 (27%)	0	100	100
74	AF	187/189 (99%)	146 (78%)	41 (22%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Ac	60/62 (97%)	49 (82%)	11 (18%)	0	100	100
76	CU	97/99 (98%)	73 (75%)	23 (24%)	1 (1%)	15	53
77	Cj	85/87 (98%)	74 (87%)	10 (12%)	1 (1%)	13	48
78	CW	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
79	Cg	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	15	53
80	Cd	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
81	AS	134/136 (98%)	117 (87%)	16 (12%)	1 (1%)	22	60
All	All	11596/11750 (99%)	9587 (83%)	1892 (16%)	117 (1%)	20	53

5 of 117 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CO	112	SER
1	CO	113	PRO
2	CL	7	MET
2	CL	148	GLN
2	CL	160	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CO	175/175 (100%)	175 (100%)	0	100	100
2	CL	173/173 (100%)	168 (97%)	5 (3%)	42	76
3	CV	101/101 (100%)	99 (98%)	2 (2%)	55	83
4	CM	138/138 (100%)	136 (99%)	2 (1%)	67	88
5	Ca	122/122 (100%)	121 (99%)	1 (1%)	81	93
6	CN	174/174 (100%)	169 (97%)	5 (3%)	42	76
7	CI	187/187 (100%)	187 (100%)	0	100	100
8	CD	241/241 (100%)	238 (99%)	3 (1%)	71	90
9	CQ	164/164 (100%)	159 (97%)	5 (3%)	41	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	CR	176/176 (100%)	173 (98%)	3 (2%)	60	85
11	CA	195/195 (100%)	192 (98%)	3 (2%)	65	87
12	CS	156/156 (100%)	152 (97%)	4 (3%)	46	78
13	CT	137/137 (100%)	135 (98%)	2 (2%)	65	87
14	CP	160/160 (100%)	155 (97%)	5 (3%)	40	75
15	CX	106/106 (100%)	103 (97%)	3 (3%)	43	77
16	CY	116/116 (100%)	112 (97%)	4 (3%)	37	72
17	CZ	121/121 (100%)	121 (100%)	0	100	100
18	Cr	112/112 (100%)	110 (98%)	2 (2%)	59	85
19	Ch	112/112 (100%)	110 (98%)	2 (2%)	59	85
20	Cb	67/67 (100%)	65 (97%)	2 (3%)	41	75
21	CB	349/349 (100%)	342 (98%)	7 (2%)	55	83
22	CF	200/200 (100%)	198 (99%)	2 (1%)	76	91
23	Cc	84/84 (100%)	83 (99%)	1 (1%)	71	90
24	Ce	120/120 (100%)	119 (99%)	1 (1%)	81	93
25	Cf	123/123 (100%)	119 (97%)	4 (3%)	38	73
26	Ci	100/100 (100%)	100 (100%)	0	100	100
27	Ck	65/65 (100%)	64 (98%)	1 (2%)	65	87
28	Cl	45/45 (100%)	45 (100%)	0	100	100
29	CC	323/323 (100%)	311 (96%)	12 (4%)	34	70
30	Cm	48/48 (100%)	46 (96%)	2 (4%)	30	66
31	Cn	23/23 (100%)	23 (100%)	0	100	100
32	Cp	74/74 (100%)	69 (93%)	5 (7%)	16	48
33	Co	94/94 (100%)	93 (99%)	1 (1%)	73	90
34	CJ	155/155 (100%)	154 (99%)	1 (1%)	86	95
35	CH	169/169 (100%)	167 (99%)	2 (1%)	71	90
36	CE	197/197 (100%)	190 (96%)	7 (4%)	35	70
37	CG	210/210 (100%)	207 (99%)	3 (1%)	67	88
41	Ag	280/280 (100%)	272 (97%)	8 (3%)	42	76
42	AU	95/95 (100%)	94 (99%)	1 (1%)	73	90
43	AO	98/98 (100%)	97 (99%)	1 (1%)	76	91

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	AX	116/116 (100%)	114 (98%)	2 (2%)	60	85
45	AM	104/104 (100%)	99 (95%)	5 (5%)	25	62
46	Ad	45/45 (100%)	45 (100%)	0	100	100
47	AN	130/130 (100%)	129 (99%)	1 (1%)	81	93
48	AL	138/138 (100%)	137 (99%)	1 (1%)	84	94
49	AR	108/108 (100%)	106 (98%)	2 (2%)	57	84
50	AP	111/111 (100%)	110 (99%)	1 (1%)	78	92
51	AB	199/199 (100%)	196 (98%)	3 (2%)	65	87
52	AA	190/190 (100%)	186 (98%)	4 (2%)	53	82
53	AV	67/67 (100%)	66 (98%)	1 (2%)	65	87
54	AY	105/106 (99%)	101 (96%)	4 (4%)	33	69
55	AZ	67/67 (100%)	66 (98%)	1 (2%)	65	87
56	Aa	94/94 (100%)	91 (97%)	3 (3%)	39	74
57	Ab	72/72 (100%)	72 (100%)	0	100	100
58	AD	192/192 (100%)	189 (98%)	3 (2%)	62	86
59	Ae	47/47 (100%)	45 (96%)	2 (4%)	29	66
60	Af	70/70 (100%)	69 (99%)	1 (1%)	67	88
61	AJ	161/161 (100%)	161 (100%)	0	100	100
62	AE	220/220 (100%)	215 (98%)	5 (2%)	50	80
63	AC	188/188 (100%)	185 (98%)	3 (2%)	62	86
64	AG	200/200 (100%)	197 (98%)	3 (2%)	65	87
65	AH	175/175 (100%)	171 (98%)	4 (2%)	50	80
66	AI	175/175 (100%)	172 (98%)	3 (2%)	60	85
67	AQ	122/122 (100%)	119 (98%)	3 (2%)	47	79
68	Cz	190/190 (100%)	185 (97%)	5 (3%)	46	78
71	AW	113/113 (100%)	112 (99%)	1 (1%)	78	92
72	AT	104/104 (100%)	100 (96%)	4 (4%)	33	69
73	AK	81/81 (100%)	81 (100%)	0	100	100
74	AF	157/157 (100%)	150 (96%)	7 (4%)	27	64
75	Ac	54/54 (100%)	51 (94%)	3 (6%)	21	56
76	CU	92/92 (100%)	91 (99%)	1 (1%)	73	90

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	Cj	74/74 (100%)	74 (100%)	0	100	100
78	CW	54/54 (100%)	53 (98%)	1 (2%)	57	84
79	Cg	95/95 (100%)	88 (93%)	7 (7%)	13	44
80	Cd	99/99 (100%)	93 (94%)	6 (6%)	18	53
81	AS	122/122 (100%)	121 (99%)	1 (1%)	81	93
All	All	10116/10117 (100%)	9913 (98%)	203 (2%)	57	83

5 of 203 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	AM	30	LYS
59	Ae	90	LYS
80	Cd	83	VAL
47	AN	38	LYS
52	AA	191	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
81	AS	73	ASN
81	AS	87	GLN
81	AS	135	HIS
55	AZ	46	GLN
66	AI	64	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
38	A9	29/30 (96%)	8 (27%)	1 (3%)
39	A7	119/120 (99%)	30 (25%)	1 (0%)
40	A8	122/123 (99%)	45 (36%)	1 (0%)
69	A5	3561/3703 (96%)	1353 (37%)	81 (2%)
70	B2	1792/1936 (92%)	630 (35%)	32 (1%)
All	All	5623/5912 (95%)	2066 (36%)	116 (2%)

5 of 2066 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
38	A9	4	U
38	A9	9	C
38	A9	20	U
38	A9	21	G
38	A9	22	A

5 of 116 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
69	A5	2125	G
70	B2	1673	U
69	A5	3608	G
70	B2	1595	G
70	B2	1185	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
69	A5	7
70	B2	5
72	AT	1
7	CI	1

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AT	107:LEU	C	121:ARG	N	19.55
1	A5	2293:C	O3'	2390:U	P	18.82
1	A5	2941:G	O3'	2976:A	P	18.19
1	B2	738:A	O3'	757:U	P	14.79
1	A5	2406:A	O3'	2452:A	P	13.09

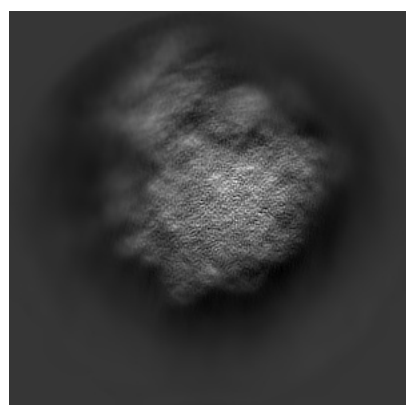
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10624. These allow visual inspection of the internal detail of the map and identification of artifacts.

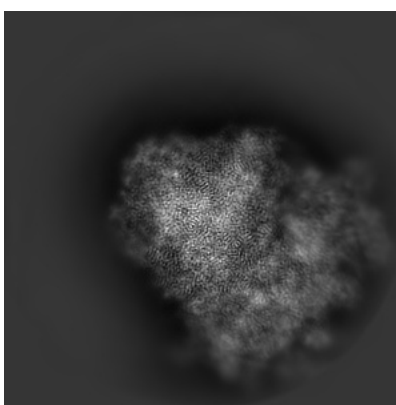
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

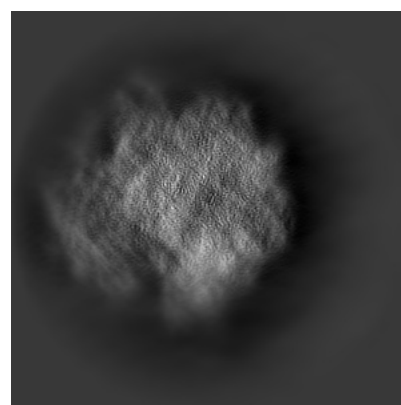
6.1.1 Primary map



X



Y

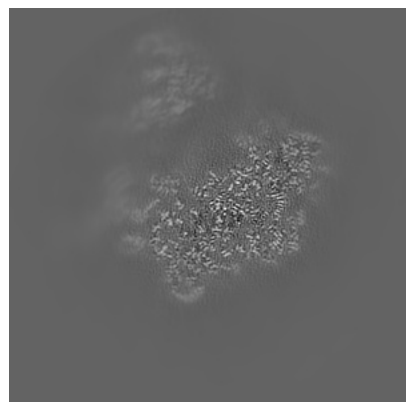


Z

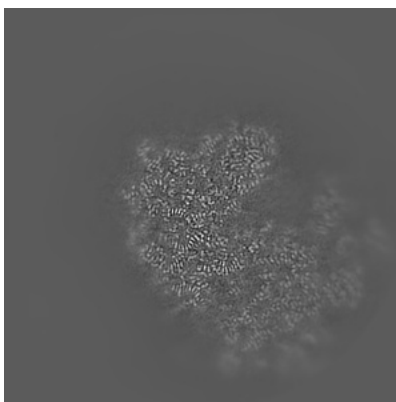
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

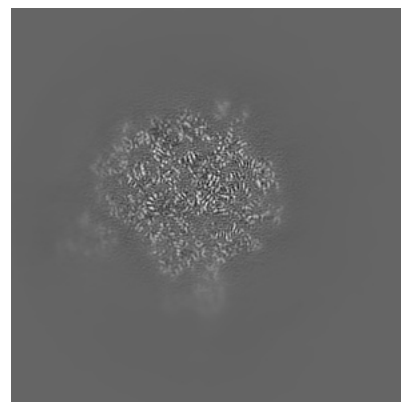
6.2.1 Primary map



X Index: 200



Y Index: 200

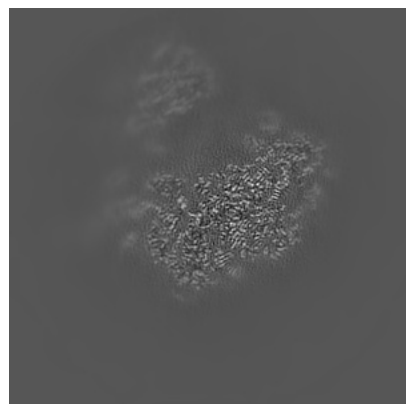


Z Index: 200

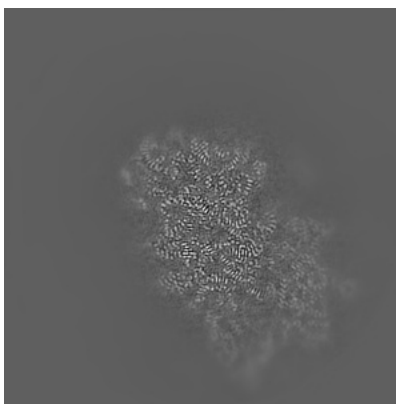
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

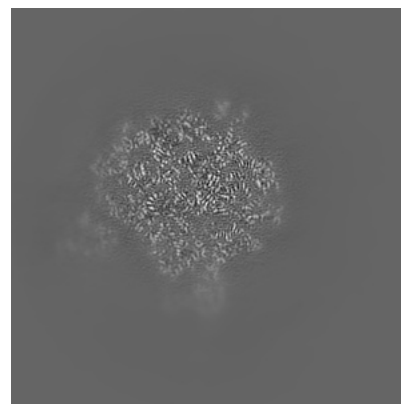
6.3.1 Primary map



X Index: 206



Y Index: 225

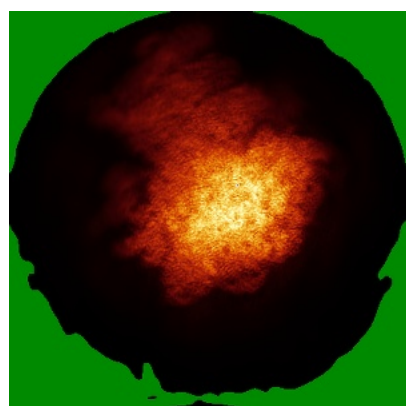


Z Index: 200

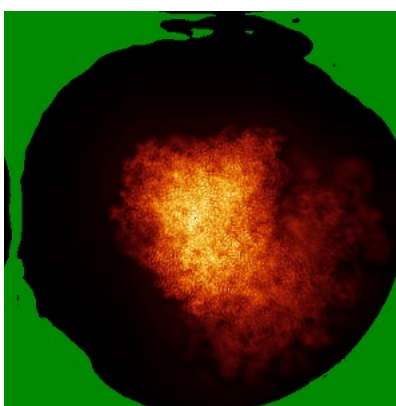
The images above show the largest variance slices of the map in three orthogonal directions.

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

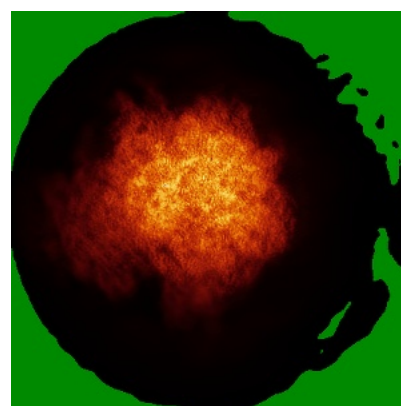
6.4.1 Primary map



X



Y



Z

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 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

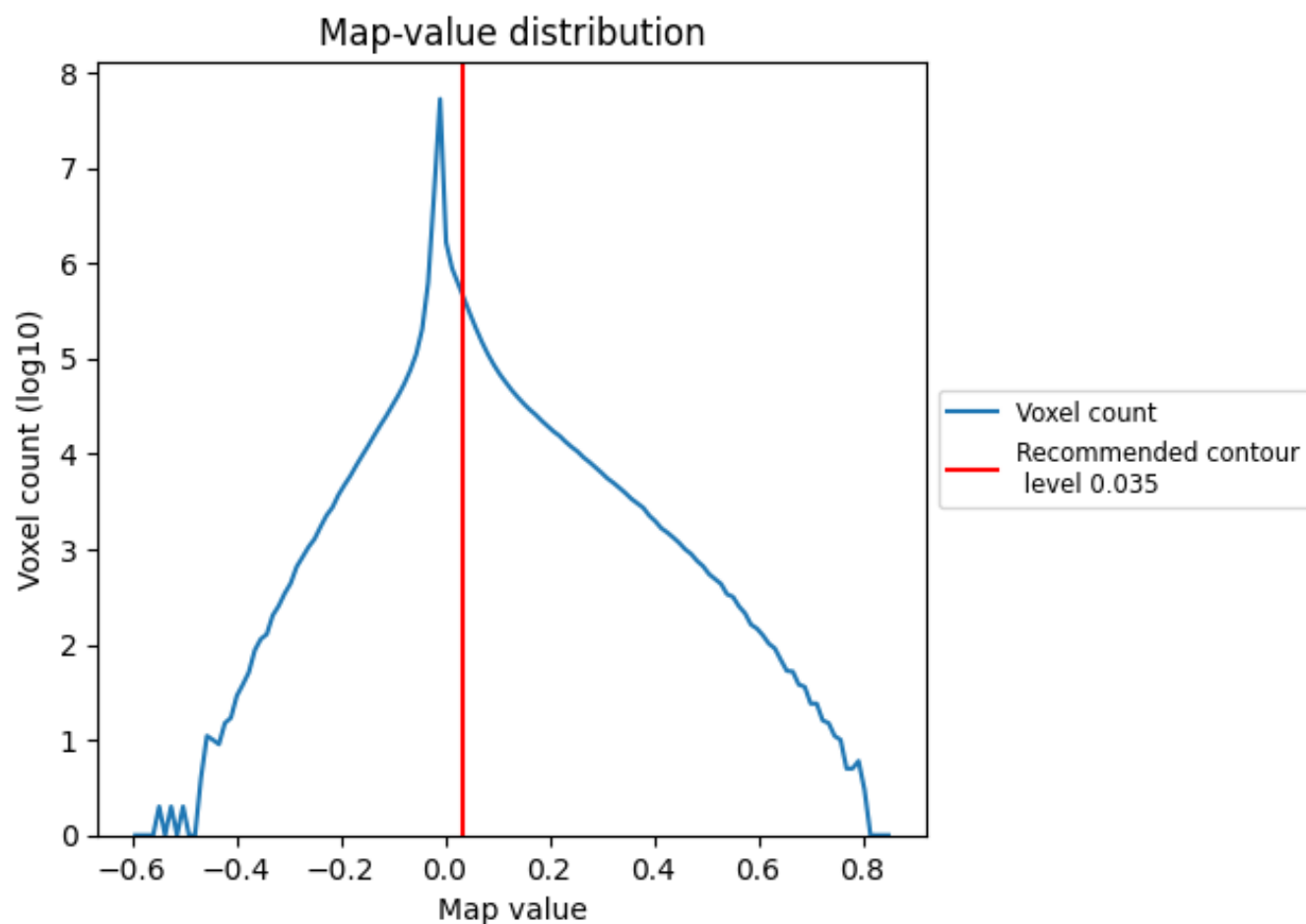
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

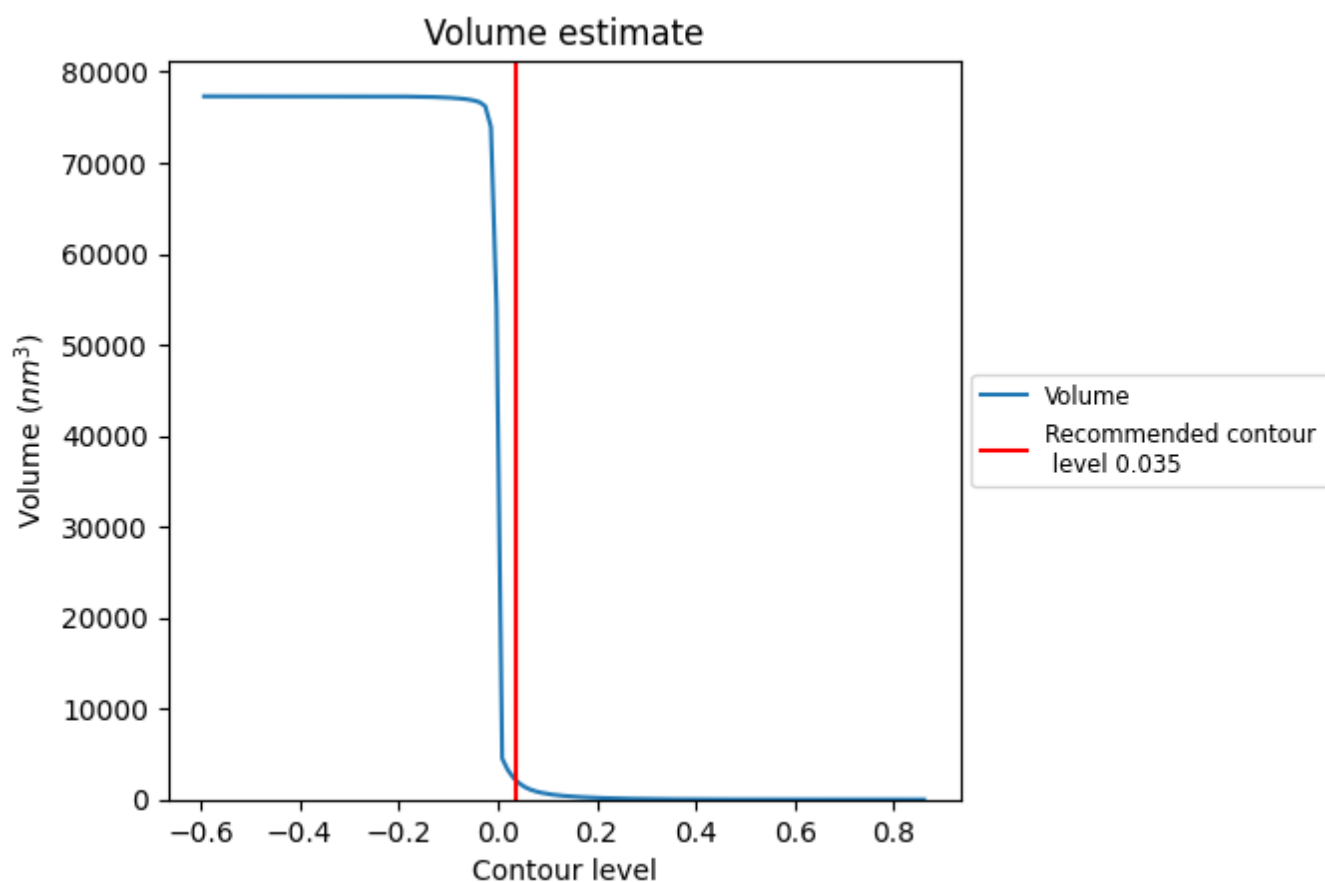
This section contains the results of statistical analysis of the map.

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.

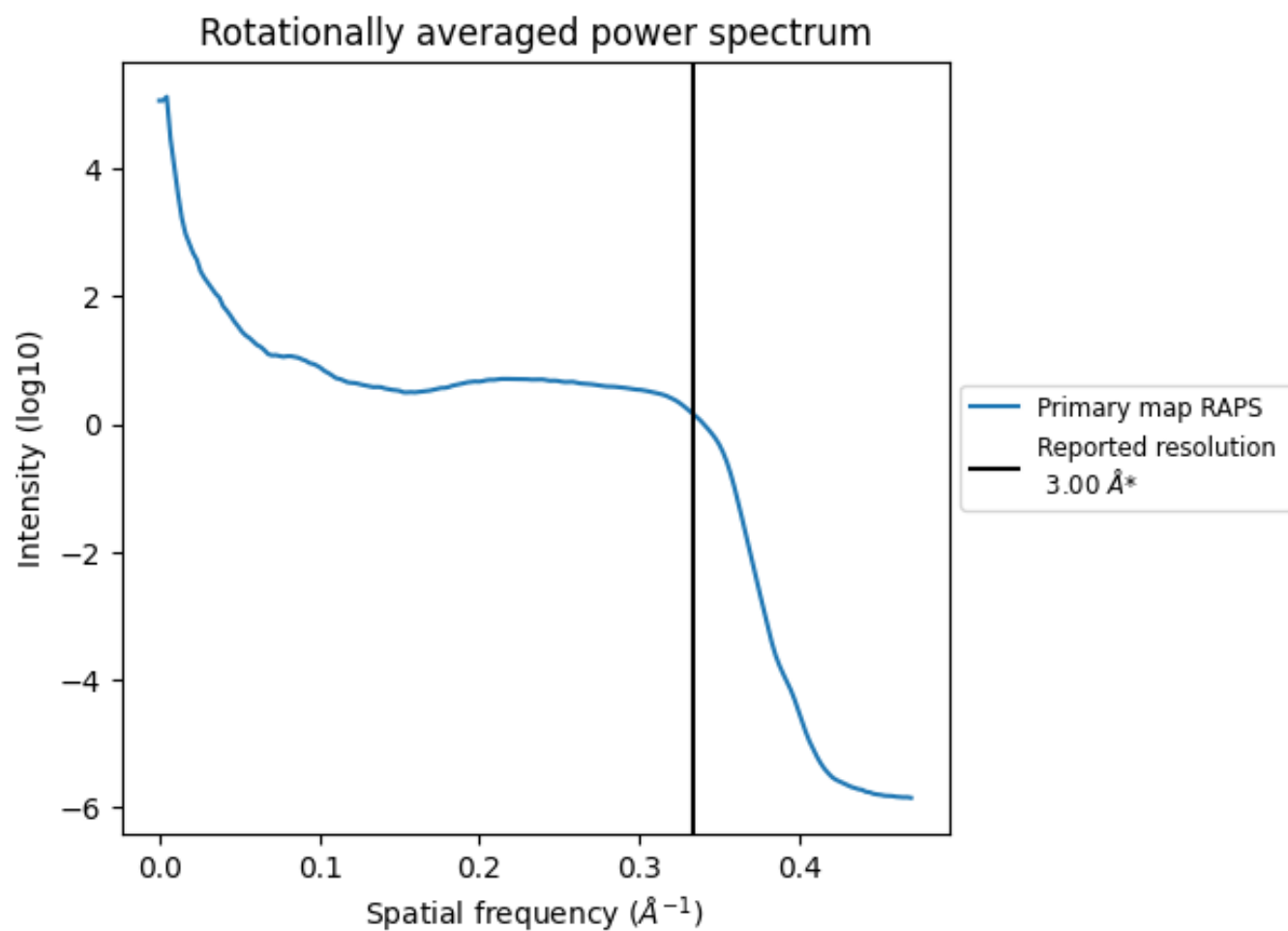
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2221 nm³; this corresponds to an approximate mass of 2007 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 ⓘ

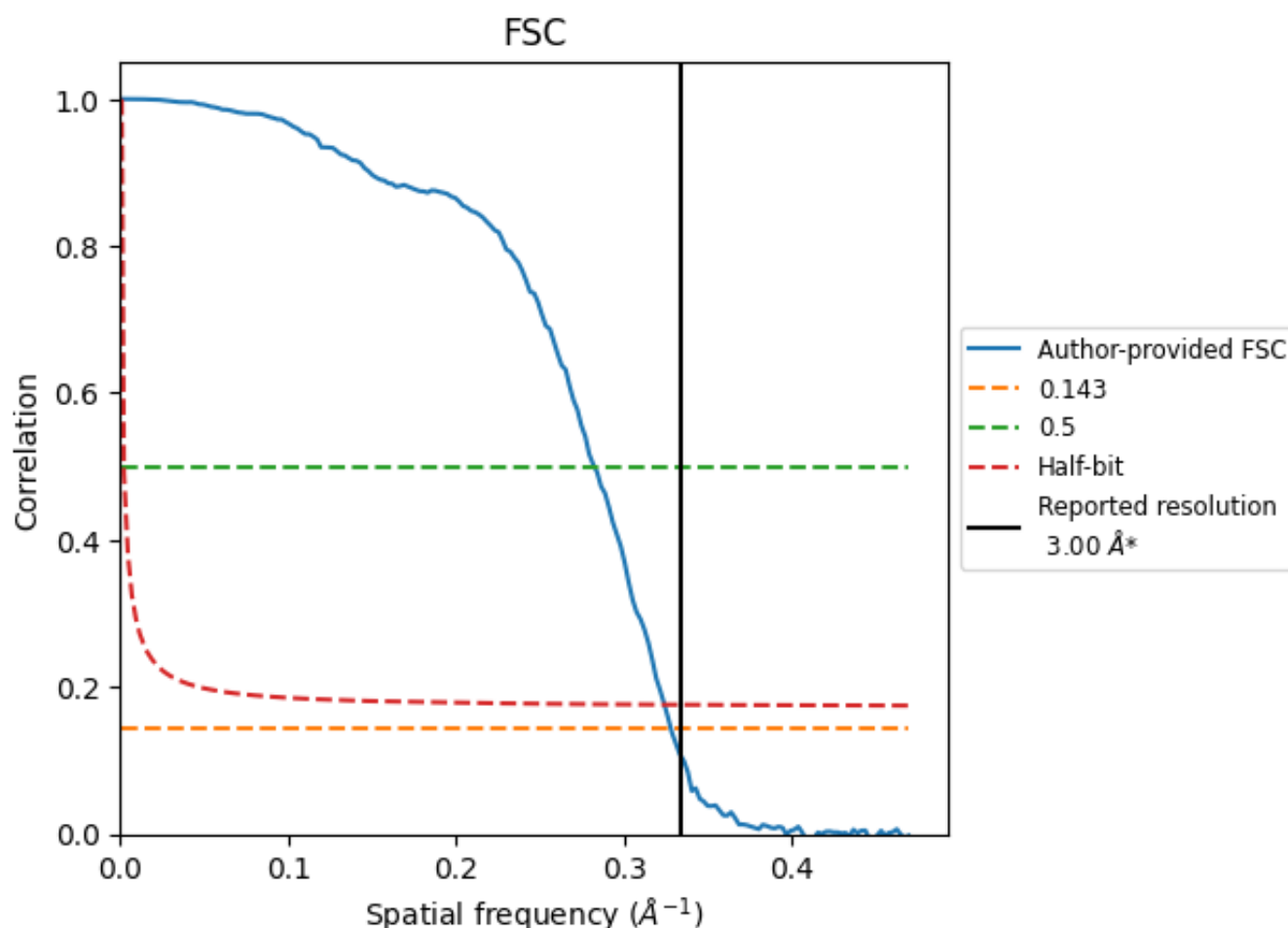


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

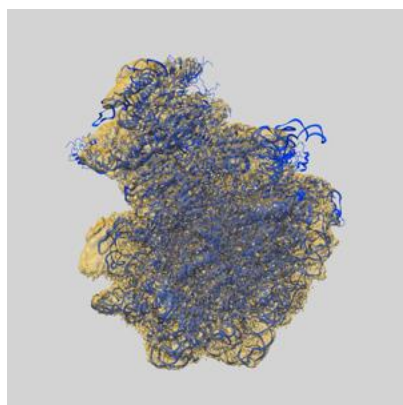
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.05	3.54	3.09
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

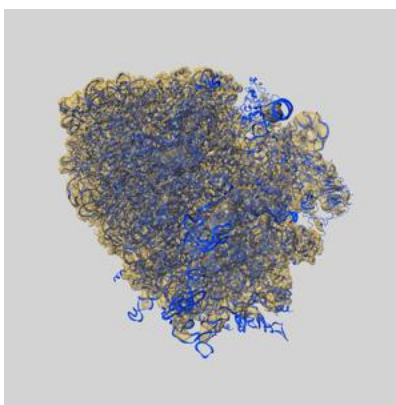
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10624 and PDB model 6XU8. Per-residue inclusion information can be found in section [3](#) on page [19](#).

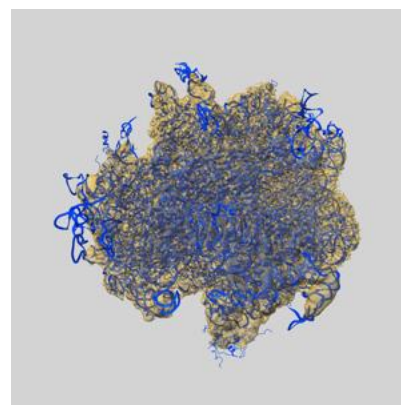
9.1 Map-model overlay [i](#)



X



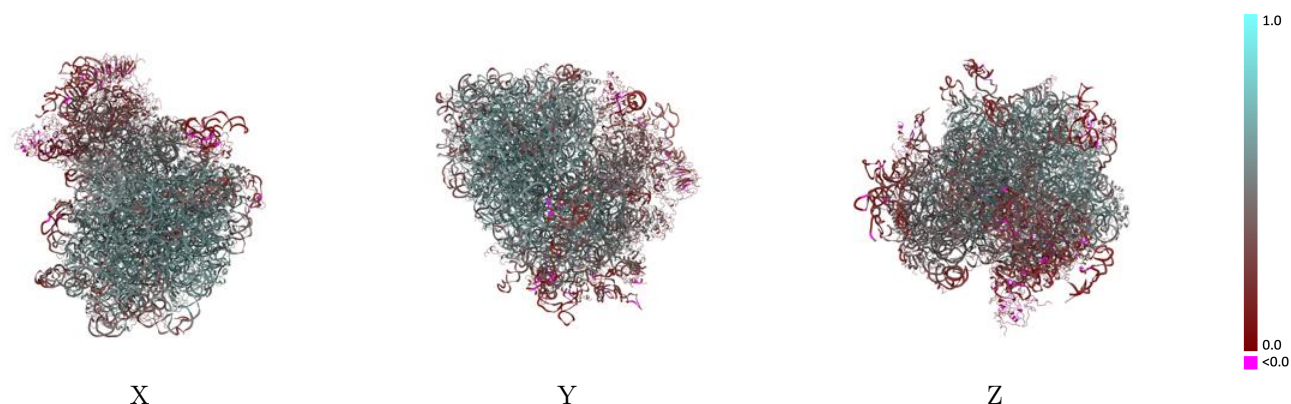
Y



Z

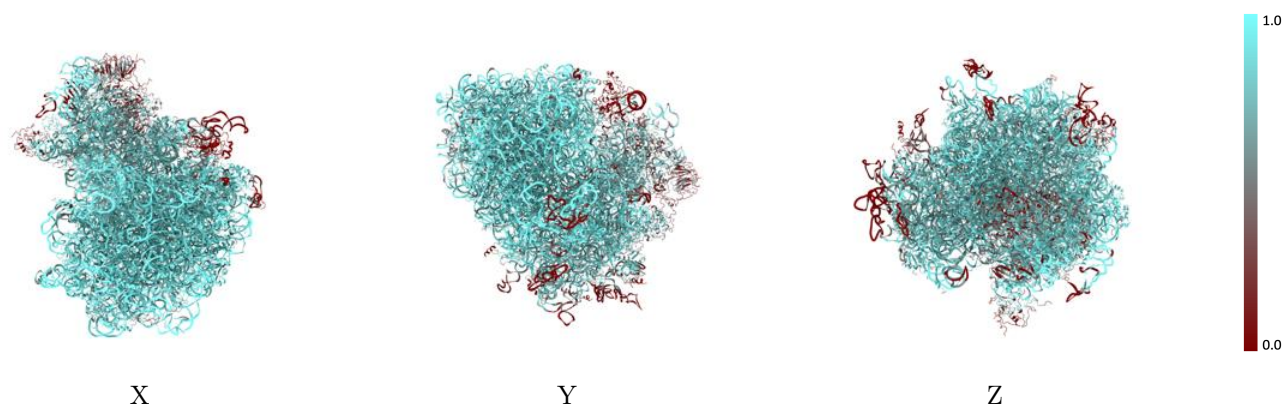
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



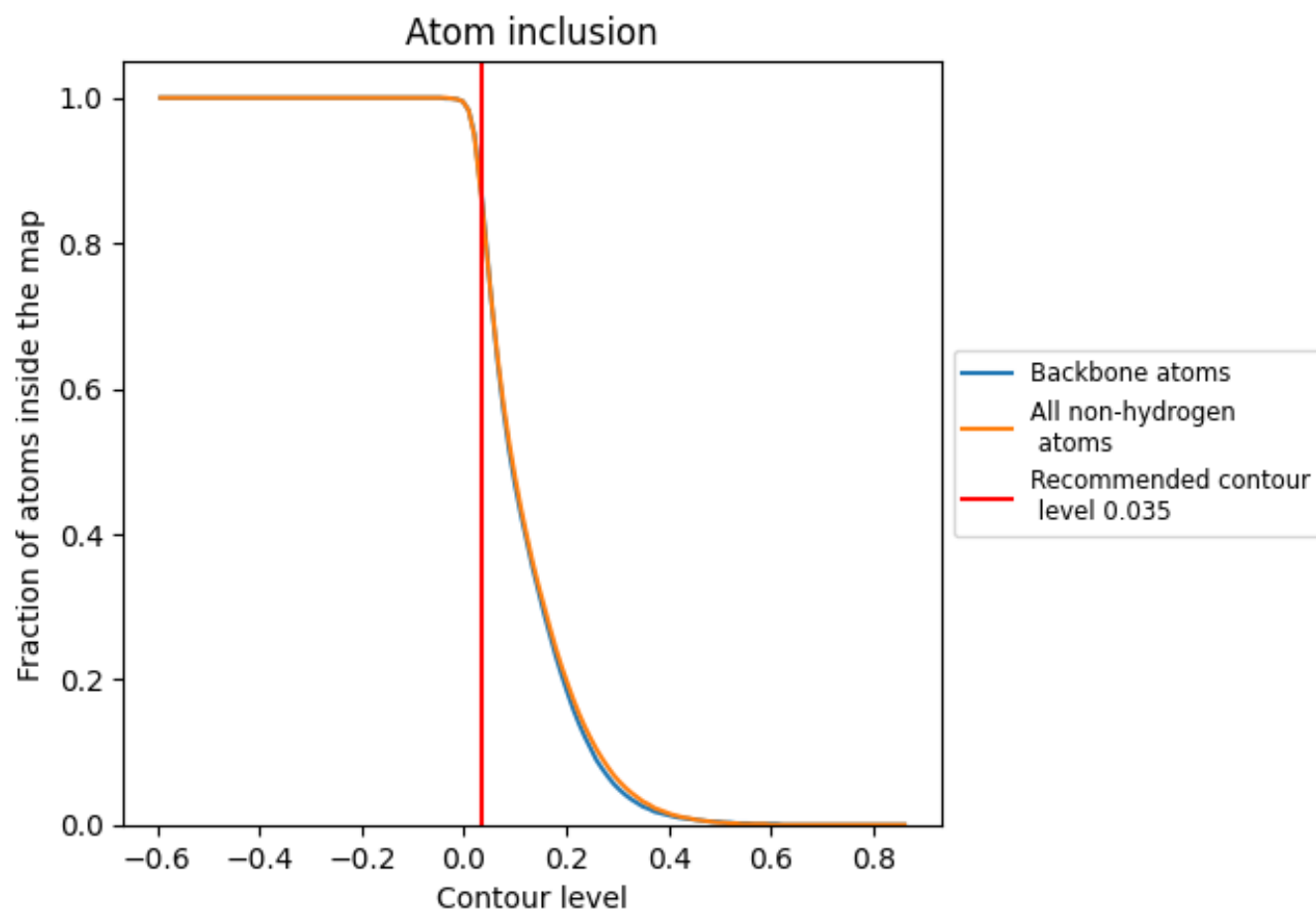
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.4690
A5	 0.9300	 0.5240
A7	 0.9890	 0.5620
A8	 0.9790	 0.5900
A9	 0.9890	 0.5630
AA	 0.6440	 0.3570
AB	 0.7850	 0.4240
AC	 0.7080	 0.4180
AD	 0.4960	 0.2880
AE	 0.7810	 0.4400
AF	 0.4030	 0.2890
AG	 0.6770	 0.3620
AH	 0.6720	 0.3350
AI	 0.7140	 0.4450
AJ	 0.7860	 0.3840
AK	 0.8310	 0.1820
AL	 0.7310	 0.4760
AM	 0.3340	 0.0880
AN	 0.8370	 0.4940
AO	 0.8010	 0.4400
AP	 0.6410	 0.2030
AQ	 0.4760	 0.2430
AR	 0.3860	 0.2720
AS	 0.6640	 0.2790
AT	 0.6780	 0.2540
AU	 0.4620	 0.2850
AV	 0.6100	 0.3970
AW	 0.8340	 0.4890
AX	 0.7800	 0.4840
AY	 0.7450	 0.3580
AZ	 0.3970	 0.2280
Aa	 0.7760	 0.4720
Ab	 0.7900	 0.3890
Ac	 0.5360	 0.3050
Ad	 0.8290	 0.3120













Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ae	 0.6000	 0.3500
Af	 0.4230	 0.0970
Ag	 0.2740	 0.1760
B2	 0.8560	 0.3880
CA	 0.9590	 0.5900
CB	 0.9340	 0.5680
CC	 0.9430	 0.5700
CD	 0.8930	 0.4970
CE	 0.8360	 0.4500
CF	 0.9770	 0.5970
CG	 0.8210	 0.4880
CH	 0.9590	 0.5270
CI	 0.8560	 0.4890
CJ	 0.8410	 0.4420
CL	 0.8710	 0.5180
CM	 0.9020	 0.4850
CN	 0.9670	 0.5880
CO	 0.9580	 0.5830
CP	 0.8400	 0.5490
CQ	 0.9720	 0.5970
CR	 0.8270	 0.4900
CS	 0.9540	 0.5590
CT	 0.9520	 0.5600
CU	 0.8200	 0.4670
CV	 0.9580	 0.5910
CW	 0.9510	 0.5770
CX	 0.9120	 0.5480
CY	 0.9670	 0.5800
CZ	 0.9260	 0.5180
Ca	 0.9520	 0.5710
Cb	 0.9330	 0.5120
Cc	 0.9350	 0.5380
Cd	 0.9530	 0.5620
Ce	 0.9680	 0.6060
Cf	 0.9070	 0.5050
Cg	 0.9730	 0.5870
Ch	 0.9340	 0.5600
Ci	 0.8650	 0.4810
Cj	 0.9780	 0.6210
Ck	 0.8650	 0.4890
Cl	 0.9810	 0.6090
Cm	 0.9740	 0.5340

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Cn	 0.9350	 0.5760
Co	 0.9480	 0.5650
Cp	 0.9560	 0.5900
Cr	 0.8540	 0.5020
Cz	 0.0230	 0.1440