



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:01 PM UTC

PDB ID : 3JBO / pdb_00003jbo
EMDB ID : EMD-6452
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P/E-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 5.80 Å (reported)
Based on initial models : 3J79, 3J7A

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
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

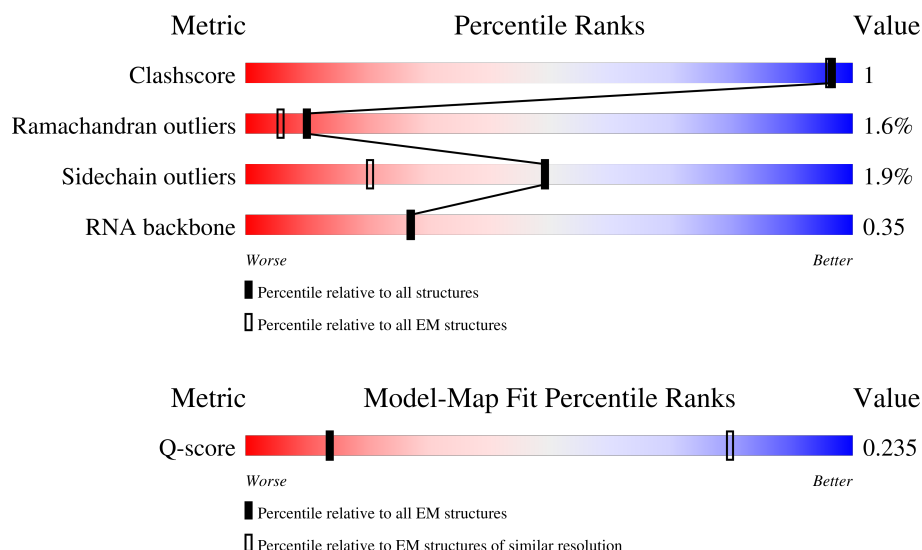
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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	511 (5.30 - 6.30)

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	A	1608	58% 32% 8% .
2	7	75	47% 37% 16%
3	Q	144	17% 92% 8% .

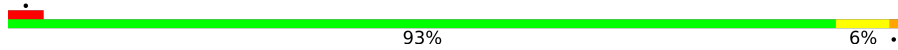
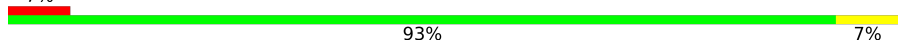
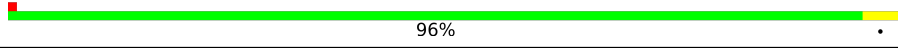
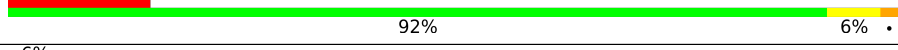
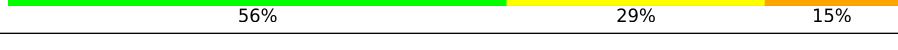
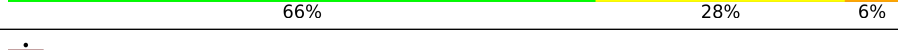
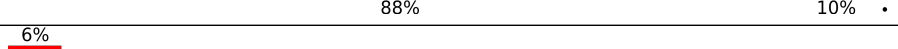
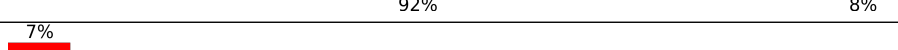
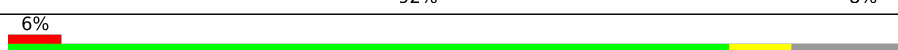
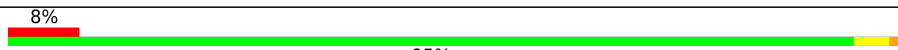
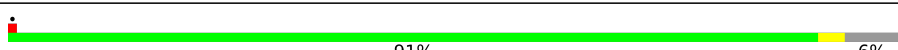
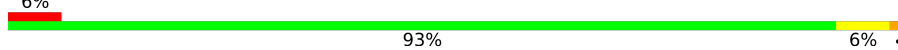
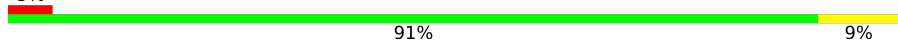
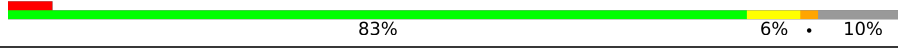
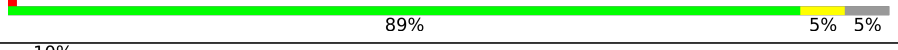
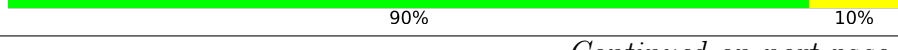
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Mol	Chain	Length	Quality of chain
4	S	128	
5	T	48	
6	M	138	
7	U	149	
8	V	156	
9	E	185	
10	X	103	
11	G	224	
12	W	108	
13	R	114	
14	I	189	
15	O	79	
16	Y	154	
17	Z	72	
18	1	120	
19	2	68	
20	C	195	
21	3	95	
22	4	76	
23	5	65	
24	6	43	
25	B	210	
26	D	209	
27	F	257	
28	H	214	

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Mol	Chain	Length	Quality of chain
29	K	129	
30	J	188	
31	N	98	
32	P	127	
33	L	214	
34	AA	3192	
35	AC	151	
36	AB	118	
37	AL	211	
38	A0	62	
39	AO	147	
40	Ai	95	
41	A2	118	
42	A4	66	
43	A6	98	
44	A7	102	
45	A1	145	
46	AN	146	
47	A8	125	
48	A9	103	
49	Aa	106	
50	Ab	105	
51	Ad	76	
52	Ae	50	
53	Af	51	

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Mol	Chain	Length	Quality of chain
54	AP	204	
55	Ah	85	
56	AI	213	
57	Ac	89	
58	AK	201	
59	AM	132	
60	AS	186	
61	AQ	205	
62	AR	289	
63	AW	170	
64	AY	101	
65	AT	181	
66	AZ	121	
67	A3	119	
68	A5	223	
69	AD	247	
70	AE	380	
71	AF	390	
72	AG	159	
73	AU	180	
74	AH	185	
75	AV	155	
76	Ag	37	
77	AX	97	
78	AJ	244	

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193017 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

- Molecule 2 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	75	Total	C	N	O	P	0	0
			1598	713	290	521	74		

- Molecule 3 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Q	144	Total	C	N	O	S	0	0
			1129	712	222	193	2		

- Molecule 4 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	128	Total	C	N	O	S	0	0
			1047	657	205	181	4		

- Molecule 5 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	T	48	Total	C	N	O	S	0	0
			405	252	85	64	4		

- Molecule 6 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	138	Total	C	N	O	S	0	0
			1099	704	200	194	1		

- Molecule 7 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	U	149	Total	C	N	O	S	0	0
			1202	769	220	210	3		

- Molecule 8 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	146	Total	C	N	O	S	0	0
			1206	772	227	200	7		

- Molecule 9 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	185	Total	C	N	O	S	0	0
			1515	962	290	261	2		

- Molecule 10 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	96	Total	C	N	O	S	0	0
			777	497	137	139	4		

- Molecule 11 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	224	Total	C	N	O	S	0	0
			1758	1132	307	310	9		

- Molecule 12 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	W	95	Total	C	N	O	S	0	0
			786	498	149	136	3		

- Molecule 13 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	98	Total	C	N	O	S	0	0
			747	474	123	146	4		

- Molecule 14 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	180	Total	C	N	O	S	0	0
			1424	893	263	258	10		

- Molecule 15 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	79	Total	C	N	O	S	0	0
			687	450	116	119	2		

- Molecule 16 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Y	154	Total	C	N	O	S	0	0
			1267	811	239	215	2		

- Molecule 17 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Z	72	Total	C	N	O	S	0	0
			557	346	102	105	4		

- Molecule 18 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 19 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2	41	Total	C	N	O	0	0
			321	208	56	57		

- Molecule 20 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	C	195	Total	C	N	O	S	0	0
			1539	990	266	274	9		

- Molecule 21 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 22 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 23 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 24 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 25 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	210	Total	C	N	O	S	0	0
			1714	1097	301	304	12		

- Molecule 26 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	157	Total	C	N	O	S	0	0
			1229	782	225	215	7		

- Molecule 27 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	257	Total	C	N	O	S	0	0
			2062	1320	377	357	8		

- Molecule 28 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	H	204	Total	C	N	O	S	0	0
			1648	1045	313	284	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	158	ILE	-	insertion	UNP Q8IDR9
H	195	ASP	GLU	conflict	UNP Q8IDR9

- Molecule 29 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	K	129	Total	C	N	O	S	0	0
			1037	665	189	178	5		

- Molecule 30 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	J	188	Total	C	N	O	S	0	0
			1529	982	264	279	4		

- Molecule 31 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	98	Total	C	N	O	S	0	0
			772	484	135	148	5		

- Molecule 32 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	127	Total	C	N	O	S	0	0
			954	591	184	176	3		

- Molecule 33 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	171	Total	C	N	O	S	0	0
			1383	872	264	243	4		

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3192	Total	C	N	O	P	0	0
			67862	30436	12049	22217	3160		

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AC	151	Total	C	N	O	P	0	0
			3215	1444	589	1034	148		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	118	Total	C	N	O	P	0	0
			2522	1128	461	816	117		

- Molecule 37 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AL	211	Total	C	N	O	S	0	0
			1757	1116	346	291	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL	19	HIS	ARG	conflict	UNP Q8IAX6
AL	20	ARG	HIS	conflict	UNP Q8IAX6
AL	201	CYS	ARG	conflict	UNP Q8IAX6

- Molecule 38 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A0	62	Total	C	N	O	S	0	0
			522	336	97	88	1		

- Molecule 39 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AO	147	Total	C	N	O	S	0	0
			1172	747	232	189	4		

- Molecule 40 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ai	95	Total	C	N	O	S	0	0
			779	490	152	128	9		

- Molecule 41 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A2	104	Total	C	N	O	S	0	0
			831	529	151	148	3		

- Molecule 42 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 43 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	A6	98	Total	C	N	O	S	0	0
			741	462	132	140	7		

- Molecule 44 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A7	96	Total	C	N	O	S	0	0
			794	508	151	130	5		

- Molecule 45 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 46 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AN	146	Total	C	N	O	S	0	0
			1202	781	210	205	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	LYS	deletion	UNP Q8ILE8

- Molecule 47 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	A8	125	Total	C	N	O	S	0	0
			1037	660	206	164	7		

- Molecule 48 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	A9	103	Total	C	N	O	S	0	0
			845	543	163	136	3		

- Molecule 49 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Aa	106	Total	C	N	O	S	0	0
			859	530	184	139	6		

- Molecule 50 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Ab	95	Total	C	N	O	0	0
			757	477	150	130		

- Molecule 51 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ad	72	Total	C	N	O	S	0	0
			604	395	107	100	2		

- Molecule 52 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Ae	43	Total	C	N	O	S	0	0
			388	243	92	52	1		

- Molecule 53 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Af	51	Total	C	N	O	S	0	0
			414	255	87	67	5		

- Molecule 54 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 55 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ah	85	Total	C	N	O	S	0	0
			659	417	127	108	7		

- Molecule 56 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 57 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ac	89	Total	C	N	O	S	0	0
			710	441	150	114	5		

- Molecule 58 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AK	201	Total	C	N	O	S	0	0
			1660	1064	311	277	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	109	ALA	TYR	conflict	UNP Q8IJZ7

- Molecule 59 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

- Molecule 60 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AS	186	Total	C	N	O	S	0	0
			1503	958	299	241	5		

- Molecule 61 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AQ	189	Total	C	N	O	S	0	0
			1545	984	291	262	8		

- Molecule 62 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AR	252	Total	C	N	O	S	0	0
			2050	1300	385	359	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	?	-	LYS	deletion	UNP Q8ILL3

- Molecule 63 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

- Molecule 64 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AY	101	Total	C	N	O	S	0	0
			797	502	144	145	6		

- Molecule 65 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1001	626	206	166	3		

- Molecule 67 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			995	635	194	164	2		

- Molecule 68 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1867	1166	374	318	9		

- Molecule 70 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3062	1948	575	522	17		

- Molecule 71 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3095	1962	594	528	11		

- Molecule 72 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AG	124	Total	C	N	O	S	0	0
			1011	636	197	172	6		

- Molecule 73 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AU	180	Total	C	N	O	S	0	0
			1497	946	289	255	7		

- Molecule 74 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AH	185	Total	C	N	O	S	0	0
			1476	950	264	256	6		

- Molecule 75 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AV	155	Total	C	N	O	S	0	0
			1276	814	241	215	6		

- Molecule 76 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Ag	37	Total	C	N	O	S	0	0
			343	210	86	45	2		

- Molecule 77 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AX	97	Total	C	N	O	S	0	0
			825	548	135	140	2		

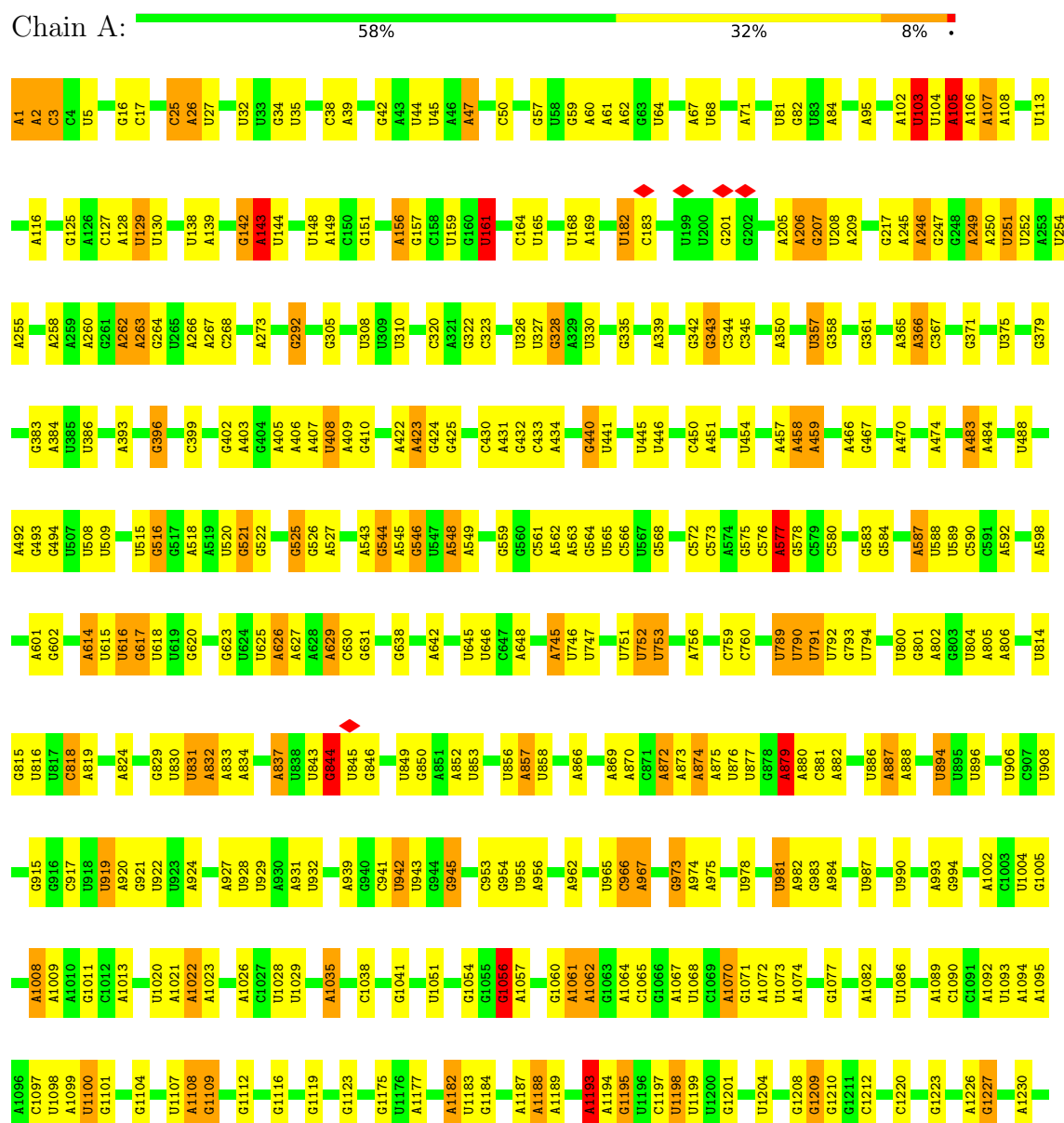
- Molecule 78 is a protein called 60S ribosomal protein eL8.

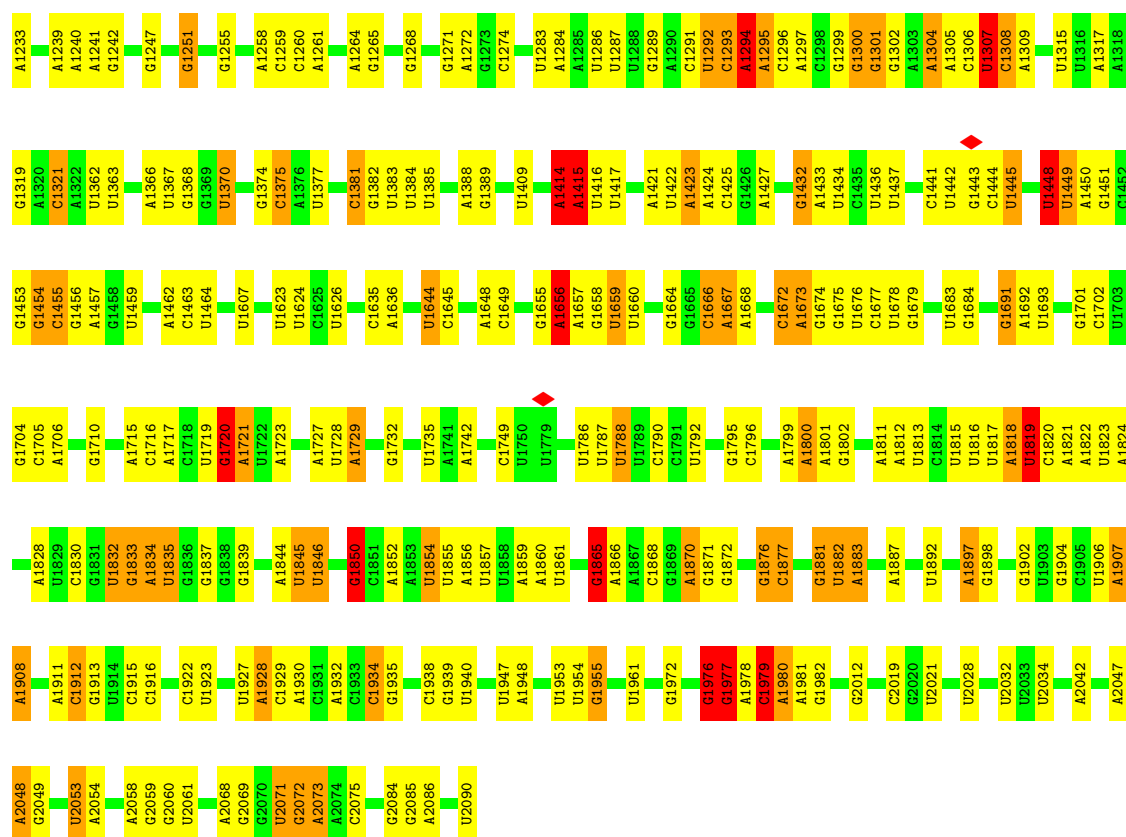
Mol	Chain	Residues	Atoms					AltConf	Trace
78	AJ	222	Total	C	N	O	S	0	0
			1813	1174	323	309	7		

3 Residue-property plots

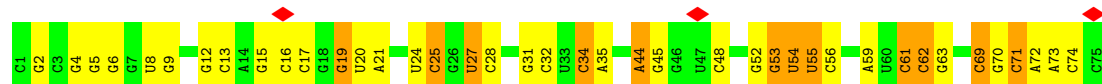
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S ribosomal RNA

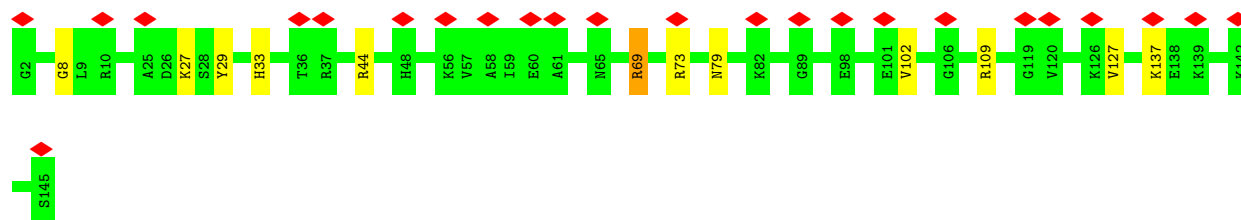
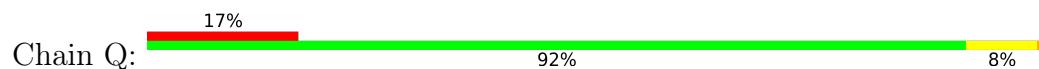




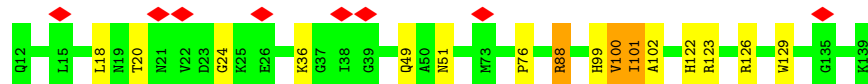
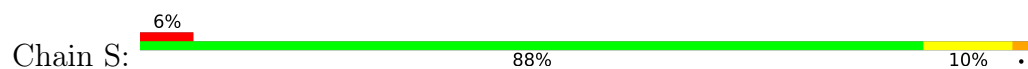
• Molecule 2: P/E-tRNA



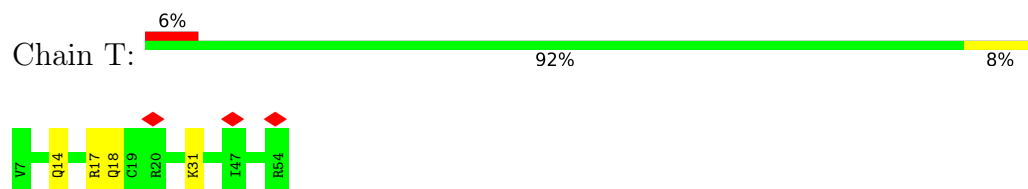
• Molecule 3: 40S ribosomal protein uS12



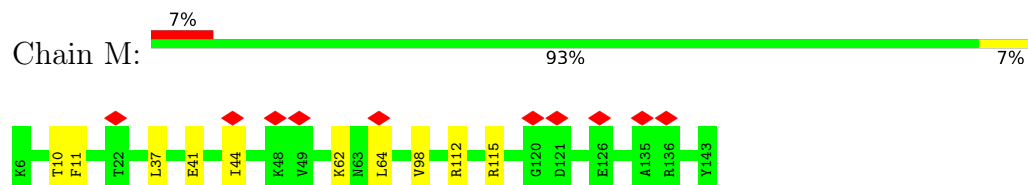
• Molecule 4: 40S ribosomal protein uS13



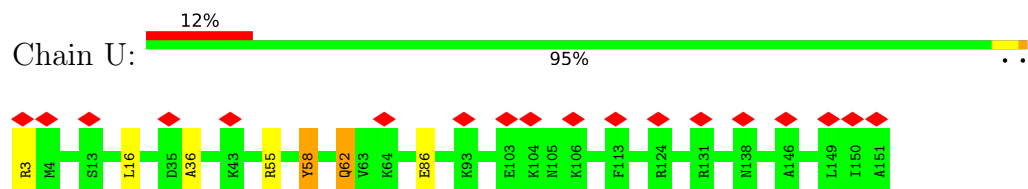
- Molecule 5: 40S ribosomal protein uS14



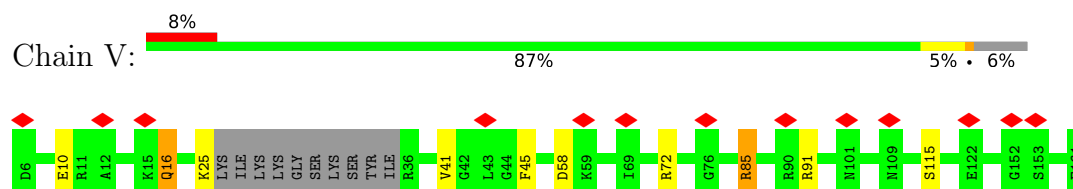
- Molecule 6: 40S ribosomal protein uS9



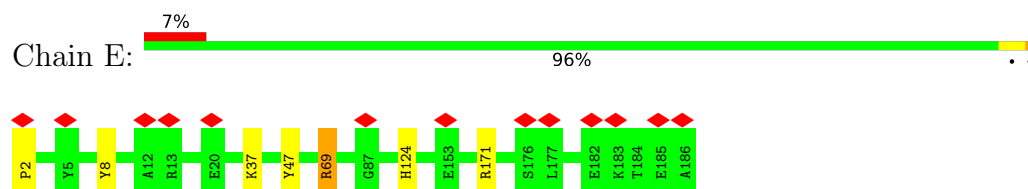
- Molecule 7: 40S ribosomal protein uS15



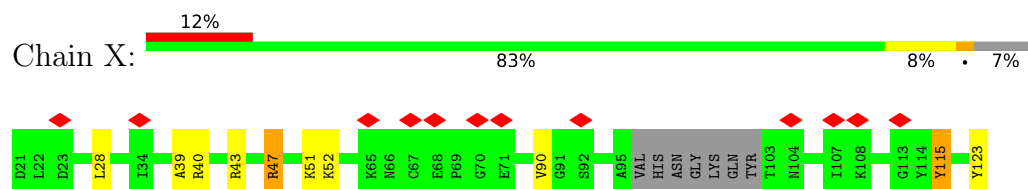
- Molecule 8: 40S ribosomal protein uS17



- Molecule 9: 40S ribosomal protein uS4

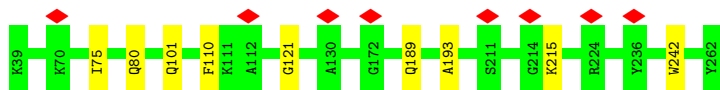


- Molecule 10: 40S ribosomal protein uS19

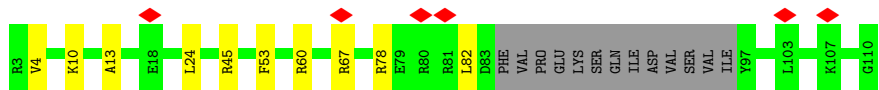
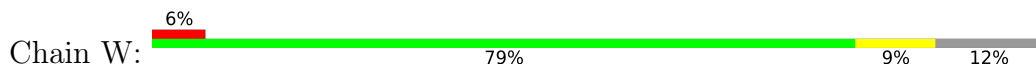


- Molecule 11: 40S ribosomal protein uS5

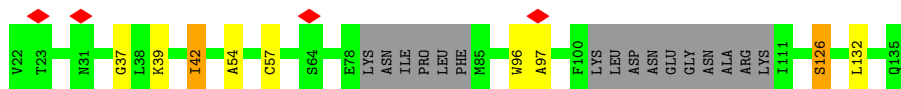
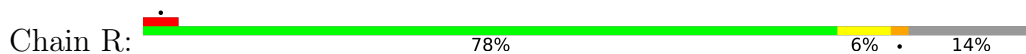




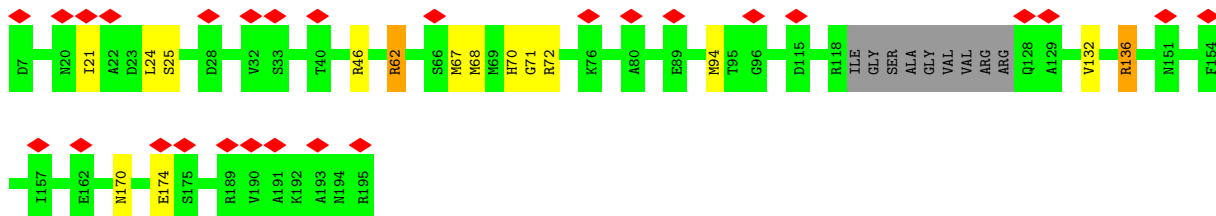
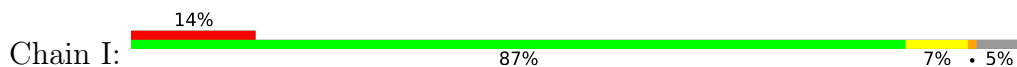
- Molecule 12: 40S ribosomal protein eS17



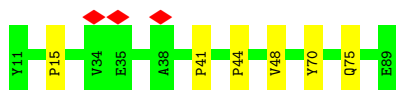
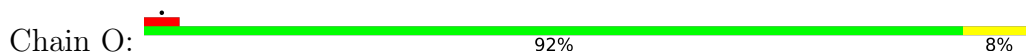
- Molecule 13: 40S ribosomal protein eS12



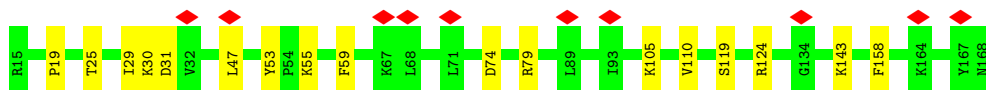
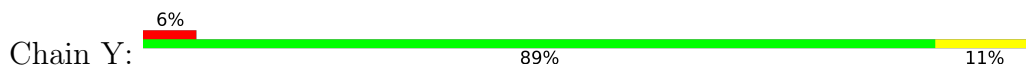
- Molecule 14: 40S ribosomal protein uS7



- Molecule 15: 40S ribosomal protein eS10

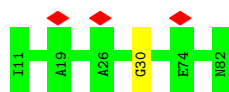


- Molecule 16: 40S ribosomal protein eS19

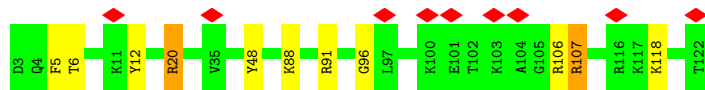
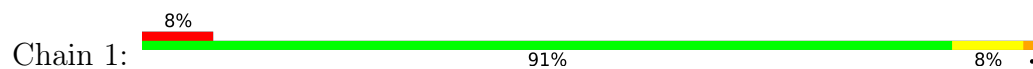


- Molecule 17: 40S ribosomal protein eS21

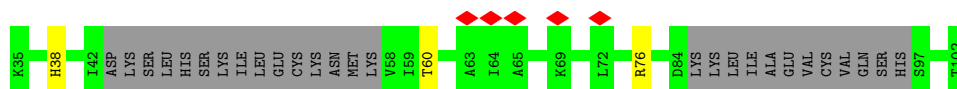




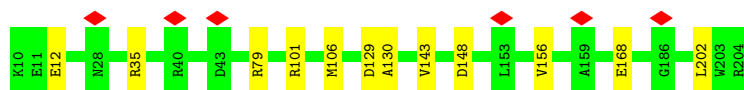
- Molecule 18: 40S ribosomal protein eS24



- Molecule 19: 40S ribosomal protein eS25



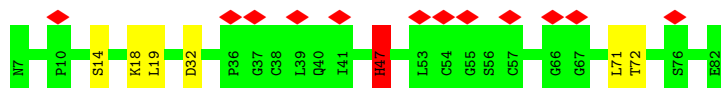
- Molecule 20: 40S ribosomal protein uS2



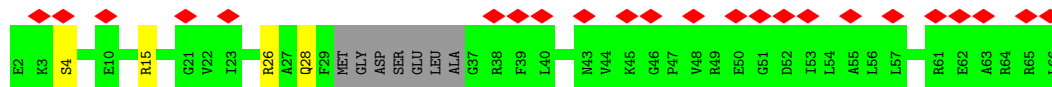
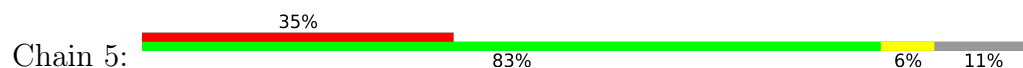
- Molecule 21: 40S ribosomal protein eS26



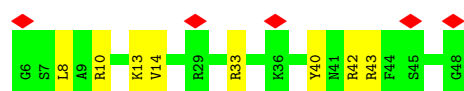
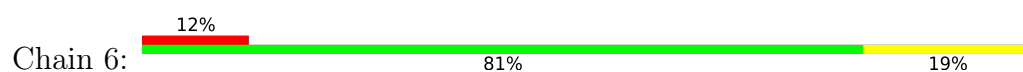
- Molecule 22: 40S ribosomal protein eS27



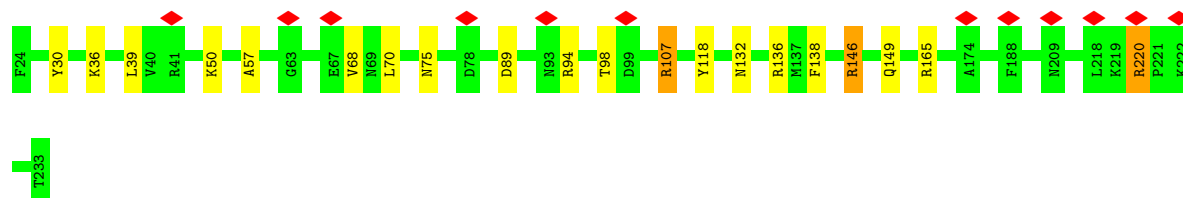
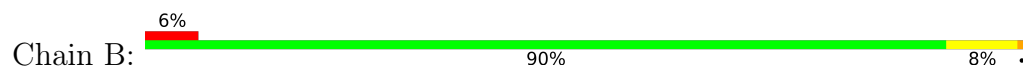
- Molecule 23: 40S ribosomal protein eS28



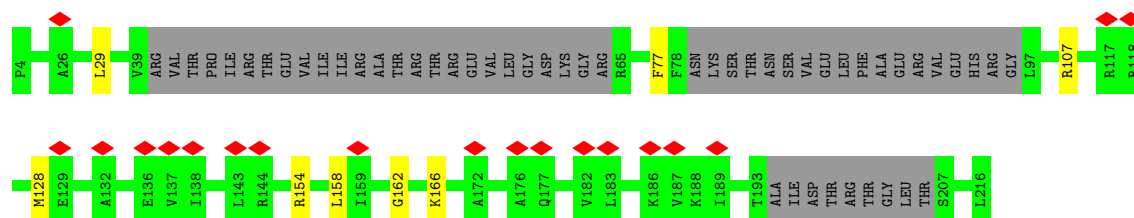
- Molecule 24: 40S ribosomal protein eS30



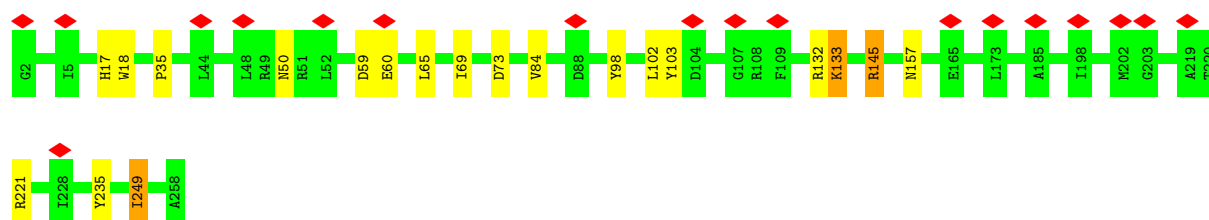
- Molecule 25: 40S ribosomal protein eS1



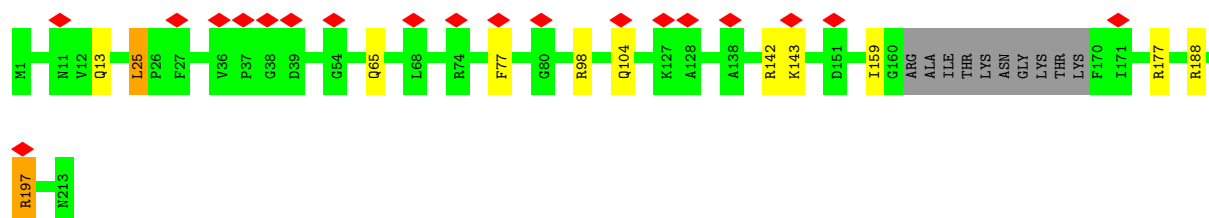
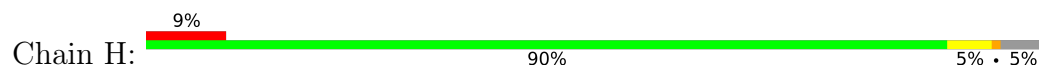
- Molecule 26: 40S ribosomal protein uS3



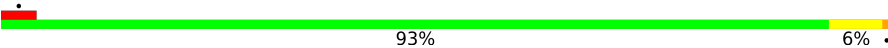
- Molecule 27: 40S ribosomal protein eS4

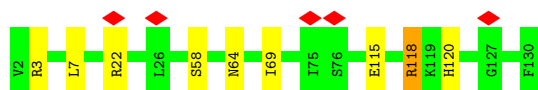


- Molecule 28: 40S ribosomal protein eS6

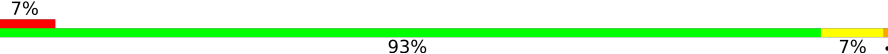


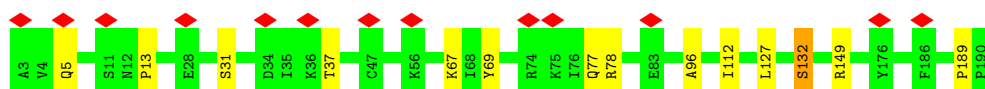
- Molecule 29: 40S ribosomal protein uS8

Chain K:  93% 6%

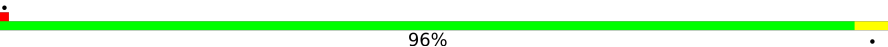


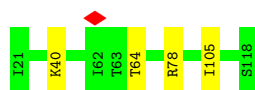
- Molecule 30: 40S ribosomal protein eS7

Chain J:  93% 7% 7%

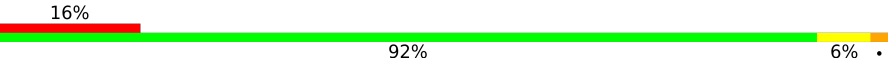


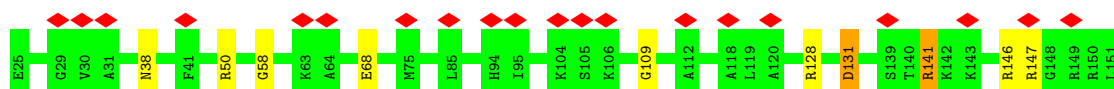
- Molecule 31: 40S ribosomal protein uS10

Chain N:  96%



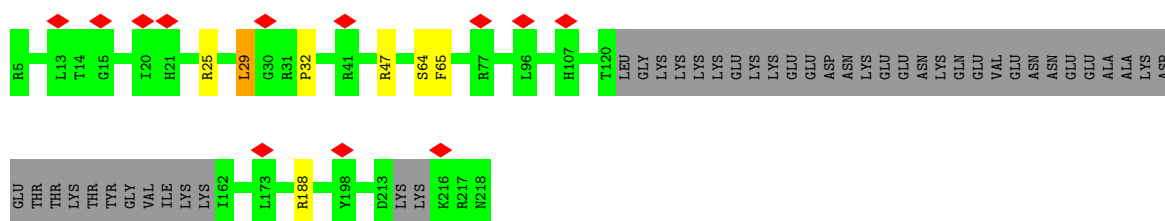
- Molecule 32: 40S ribosomal protein uS11

Chain P:  92% 6% 16%



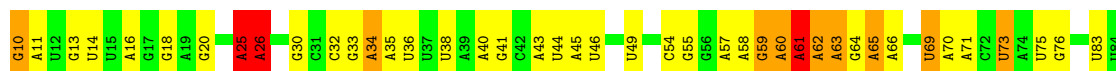
- Molecule 33: 40S ribosomal protein eS8

Chain L:  77% 20% 6%



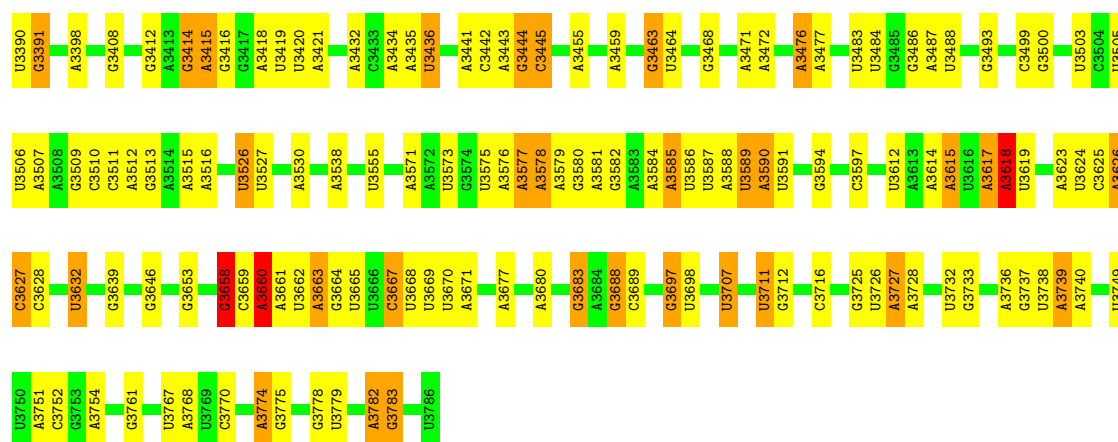
- Molecule 34: 28S ribosomal RNA

Chain AA:  56% 33% 9%



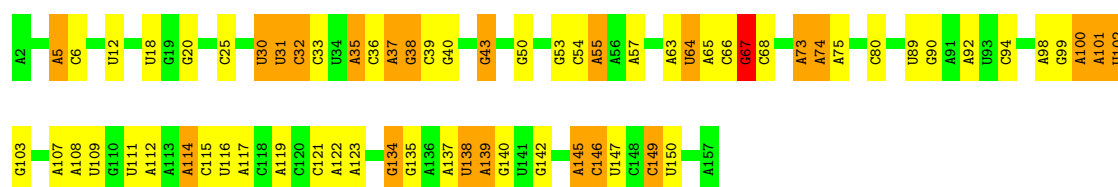
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A1468	U1210	U1109	U1209	U1110	U1013	G915	A799	C621	U530	G435	U336	U254	A168	U87
U1459	U1211	G1111	U1210	A1015	A1014	U916	A800	U622	U531	G436	U337	U255	U173	A88
A1460	U1212	G1112	U1211	A1016	A1015	U917	U801	U623	C532	U439	U338	C256	U174	G92
U1309	U1213	G1113	U1212	A1017	U1017	U918	U802	U628	A534	A440	G342	U257	G175	C93
A1310	U1214	G1114	C1214	A1018	U1017	U919	A803	U629	U535	A441	G343	U258	C181	G94
U1470	U1215	G1115	U1215	A1019	U1018	U920	A804	U630	A536	A442	G344	A261	U182	A99
A1473	U1216	G1116	C1216	U1020	U1019	U921	U805	U631	A537	A443	G345	U262	U183	U184
U1476	U1217	G1117	U1217	U1021	U1020	U922	G806	U632	A538	A444	G346	U263	U184	G105
A1479	U1218	G1118	U1218	U1022	U1021	U923	A809	U633	G539	A445	U264	U264	A185	U109
G1480	U1219	G1119	U1219	U1023	U1022	U924	U810	U636	A542	A446	U265	U265	A186	G110
A1481	U1220	G1120	U1220	U1024	U1023	U925	A811	U637	U543	A447	U266	U266	U189	C111
A1486	U1221	G1121	U1221	U1025	U1024	U926	U812	U641	U544	A448	U267	U267	G190	U112
U1497	U1222	G1122	U1222	U1026	U1025	U927	U813	U642	C544	A449	U268	U268	G191	U113
U1498	U1223	G1123	U1223	U1027	U1026	U928	U814	U643	C545	A450	U269	U269	G192	C113
U1499	U1224	G1124	U1224	U1028	U1027	U929	U815	U644	C546	A451	U270	U270	G193	A116
A1503	U1225	G1125	U1225	U1029	U1028	U930	U816	U645	C547	A452	U271	U271	C194	U119
U1504	U1226	G1126	U1226	U1030	U1029	U931	U817	U646	C548	A453	U272	U272	A195	U120
U1505	U1227	G1127	U1227	U1031	U1030	U932	U818	U647	U573	A454	U273	U273	G196	U121
C1506	U1228	G1128	U1228	U1032	U1031	U933	U819	U648	U574	A455	U274	U274	U197	U122
U1507	U1229	G1129	U1229	U1033	U1032	U934	U820	U649	U575	A456	U275	U275	U198	A123
U1510	U1230	G1130	U1230	U1034	U1033	U935	U821	U650	U576	A457	U276	U276	G201	U124
G1516	U1231	G1131	U1231	U1035	U1034	U936	U822	U651	U577	A458	U277	U277	A206	U130
U1524	U1232	G1132	U1232	U1036	U1035	U937	U823	U652	U578	A459	U278	U278	G205	U131
U1534	U1233	G1133	U1233	U1037	U1036	U938	U824	U653	C579	A460	U279	U279	A207	U132
G1535	U1234	G1134	U1234	U1038	U1037	U939	U825	U654	U580	A461	U280	U280	U211	U133
U1536	U1235	G1135	U1235	U1039	U1038	U940	U826	U655	U581	A462	U281	U281	A208	G135
U1538	U1236	G1136	U1236	U1040	U1039	U941	U827	U656	C581	A463	U282	U282	C214	U136
G1540	U1237	G1137	U1237	U1041	U1040	U942	U828	U657	U582	A464	U283	U283	G215	G137
U1549	U1238	G1138	U1238	U1042	U1041	U943	U829	U658	U583	A465	U284	U284	C216	G138
A1550	U1239	G1139	U1239	U1043	U1042	U944	U830	U659	U584	A466	U285	U285	A217	A139
G1552	U1240	G1140	U1240	U1044	U1043	U945	U831	U660	U585	A467	U286	U286	U218	A140
G1556	U1241	G1141	U1241	U1045	U1044	U946	U832	U661	U586	A468	U287	U287	A219	A141
U1563	U1242	G1142	U1242	U1046	U1045	U947	U833	U662	U587	A469	U288	U288	G309	C142
G1564	U1243	G1143	U1243	U1047	U1046	U948	U834	U663	U588	A470	U289	U289	U310	G143
G1565	U1244	G1144	U1244	U1048	U1047	U949	U835	U664	U589	A471	U290	U290	G311	U144
A1567	U1245	G1145	U1245	U1049	U1048	U950	U836	U665	U590	A472	U291	U291	A312	U145
C1568	U1246	G1146	U1246	U1050	U1049	U951	U837	U666	U591	A473	U292	U292	U313	U146
C1571	U1247	G1147	U1247	U1051	U1050	U952	U838	U667	U592	A474	U293	U293	A314	C147
									U593	A475	U294	U294	A227	G148
									C594	A476	U295	U295	A228	U155
									U595	A477	U296	U296	A229	U156
									U596	A478	U297	U297	C241	G157
									U597	A479	U298	U298	U240	U162
									U598	A480	U299	U299	U241	U163
									U599	A481	U300	U300	U242	G163
									U600	A482	U301	U301	U243	A165
									U601	A483	U302	U302	U244	
									U602	A484	U303	U303	U245	
									U603	A485	U304	U304	U246	
									U604	A486	U305	U305	U247	
									U605	A487	U306	U306	U248	
									U606	A488	U307	U307	U249	
									U607	A489	U308	U308	U250	
									U608	A490	U309	U309	U251	
									U609	A491	U310	U310	U252	
									U610	A492	U311	U311	U253	
									U611	A493	U312	U312	U254	
									U612	A494	U313	U313	U255	
									U613	A495	U314	U314	U256	
									U614	A496	U315	U315	U257	
									U615	A497	U316	U316	U258	
									U616	A498	U317	U317	U259	
									U617	A499	U318	U318	U260	
									U618	A500	U319	U319	U261	
									U619	A501	U320	U320	U262	
									U620	A502	U321	U321	U263	
									U621	A503	U322	U322	U264	
									U622	A504	U323	U323	U265	
									U623	A505	U324	U324	U266	
									U624	A506	U325	U325	U267	
									U625	A507	U326	U326	U268	
									U626	A508	U327	U327	U269	
									U627	A509	U328	U328	U270	
									U628	A510	U329	U329	U271	
									U629	A511	U330	U330	U272	
									U630	A512	U331	U331	U273	
									U631	A513	U332	U332	U274	
									U632	A514	U333	U333	U275	
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									U635	A517	U336	U336	U278	
									U636	A518	U337	U337	U279	
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									U638	A520	U339	U339	U281	
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									U640	A522	U341	U341	U283	
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									U645	A527	U346	U346	U288	
									U646	A528	U347	U347	U289	
									U647	A529	U348	U348	U290	
									U648	A530	U349	U349	U291	
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									U650	A532	U351	U351	U293	
									U651	A533	U352	U352	U294	
									U652	A534	U353	U353	U295	
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									U655	A537	U356	U356	U298	
									U656	A538	U357	U357	U299	
									U657	A539	U358	U358	U300	
									U658	A540	U359	U359	U301	
									U659	A541	U360	U360	U302	
									U660	A542	U361	U361	U303	
									U661	A543	U362	U362	U304	
									U662	A544	U363	U363	U305	
									U663	A545	U364	U364	U306	
									U664	A546	U365	U365	U307	
									U665	A547	U366	U366	U308	
									U666	A548	U367	U367	U309	
									U667	A549	U368	U368	U310	

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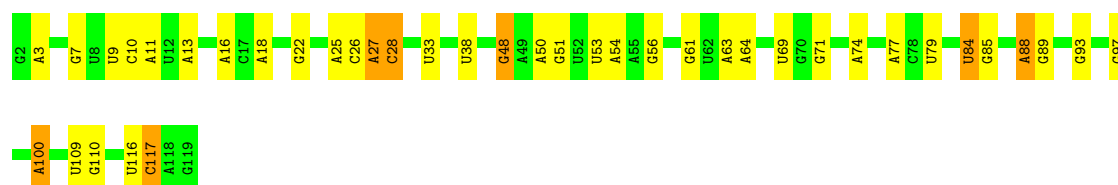
• Molecule 35: 5.8S ribosomal RNA

Chain AC: 56% 29% 15%



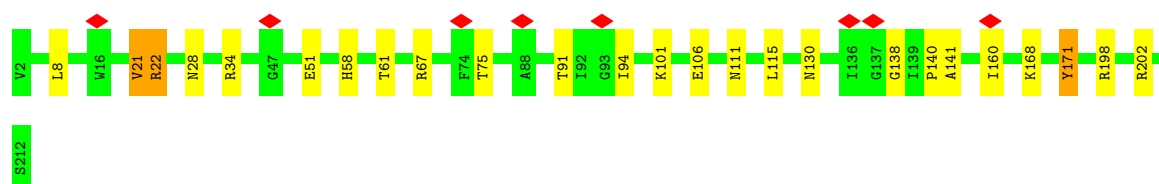
• Molecule 36: 5S ribosomal RNA

Chain AB: 66% 28% 6%



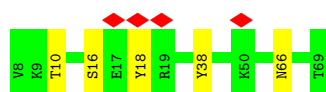
• Molecule 37: 60S ribosomal protein eL13

Chain AL: 88% 10%

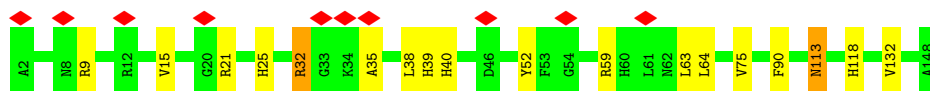
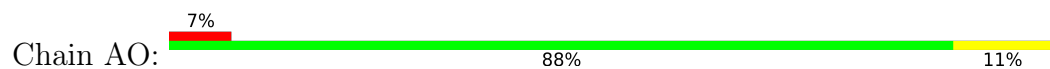


• Molecule 38: 60S ribosomal protein eL24

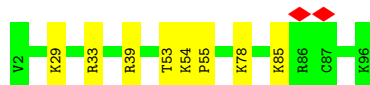
Chain A0: 6% 92% 8%



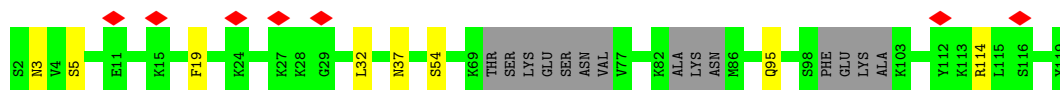
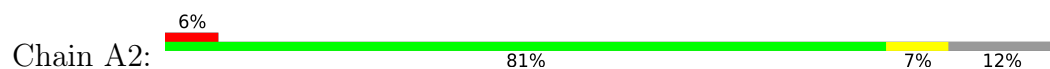
- Molecule 39: 60S ribosomal protein uL15



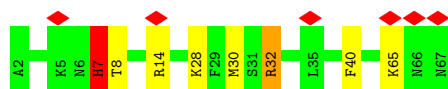
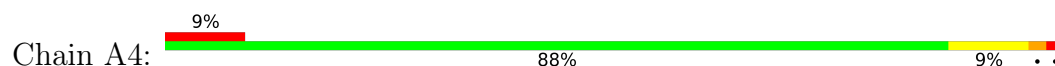
- Molecule 40: 60S ribosomal protein eL44



- Molecule 41: 60S ribosomal protein eL28



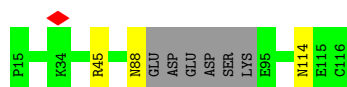
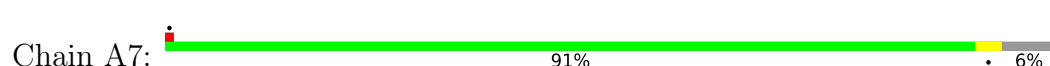
- Molecule 42: 60S ribosomal protein eL29



- Molecule 43: 60S ribosomal protein eL30

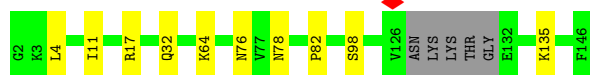


- Molecule 44: 60S ribosomal protein eL31



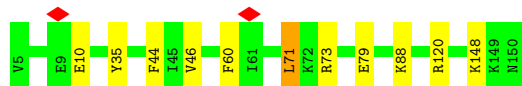
- Molecule 45: 60S ribosomal protein eL27

Chain A1:  90% 7%



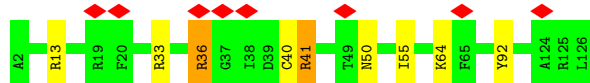
- Molecule 46: 60S ribosomal protein eL14

Chain AN:  92% 7%



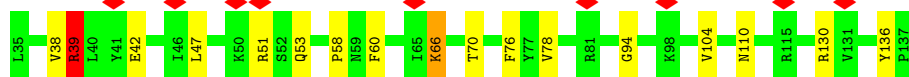
- Molecule 47: 60S ribosomal protein eL32

Chain A8:  6% 93% 6%



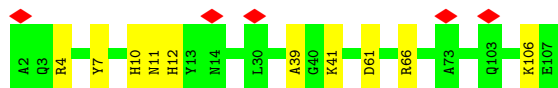
- Molecule 48: 60S ribosomal protein eL33

Chain A9:  9% 83% 15% ..



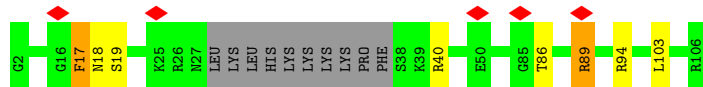
- Molecule 49: 60S ribosomal protein eL34

Chain Aa:  5% 91% 9%



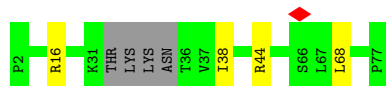
- Molecule 50: 60S ribosomal protein eL36

Chain Ab:  5% 83% 6% 10%

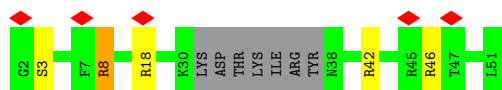
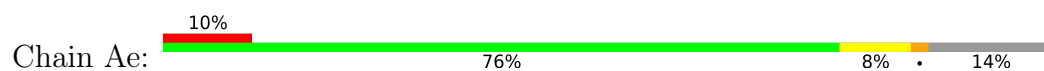


- Molecule 51: 60S ribosomal protein eL38

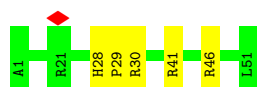
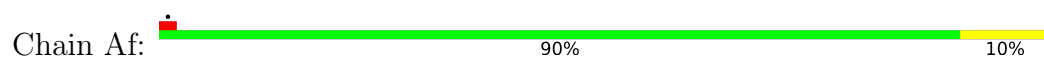
Chain Ad:  89% 5% 5%



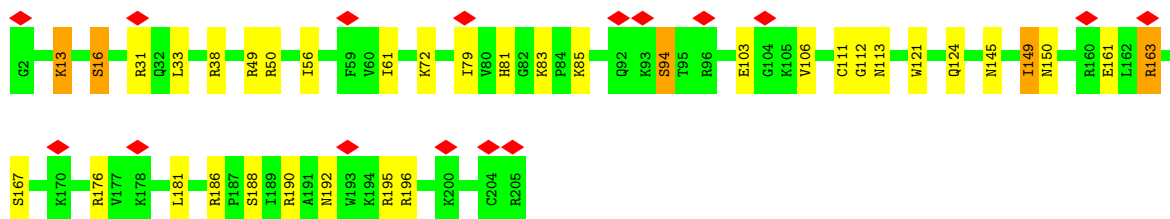
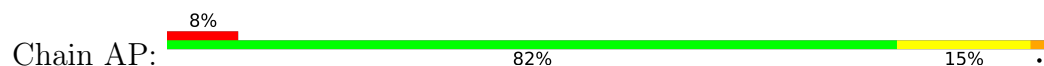
- Molecule 52: 60S ribosomal protein eL39



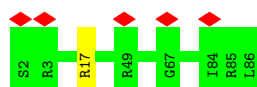
- Molecule 53: 60S ribosomal protein eL40



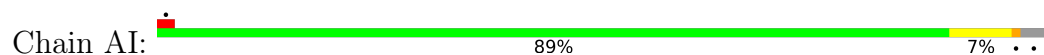
- Molecule 54: 60S ribosomal protein eL15



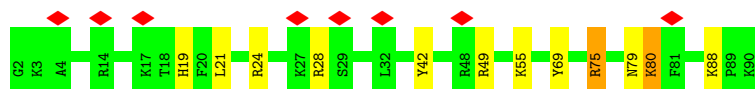
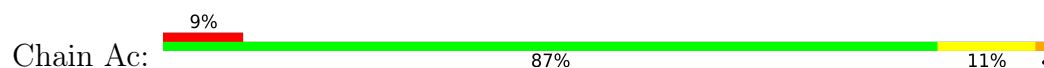
- Molecule 55: 60S ribosomal protein eL43



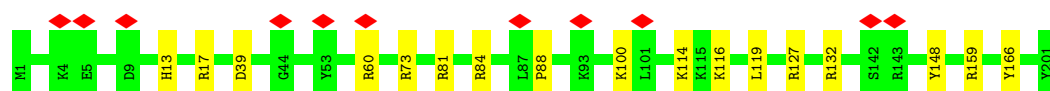
- Molecule 56: 60S ribosomal protein eL6



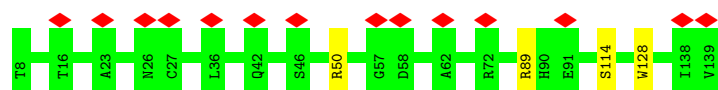
- Molecule 57: 60S ribosomal protein eL37



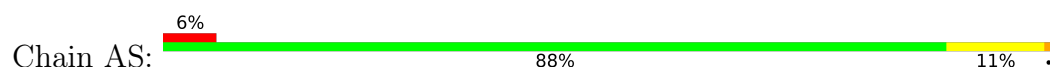
- Molecule 58: 60S ribosomal protein uL13



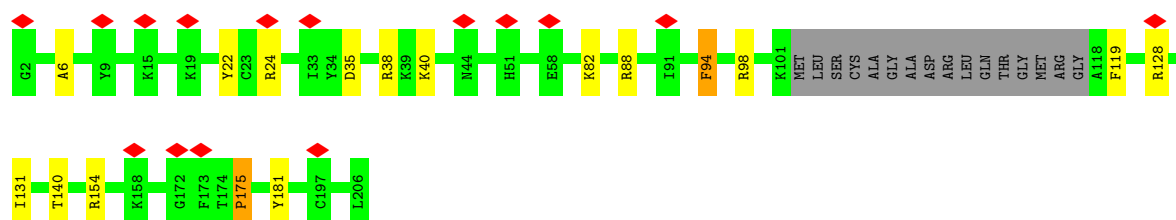
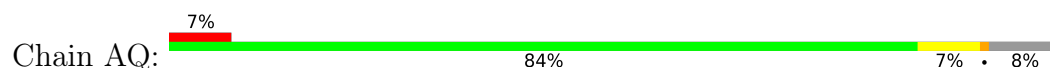
- Molecule 59: 60S ribosomal protein uL14



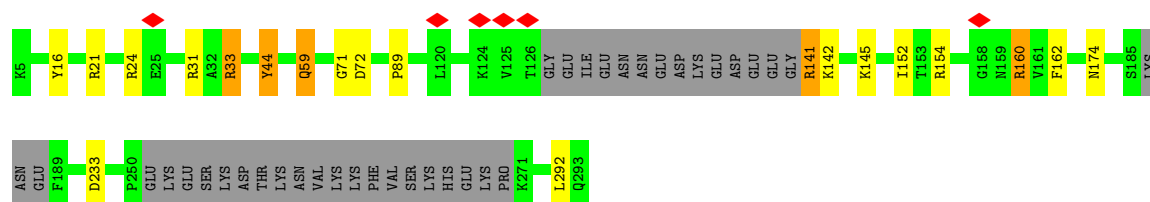
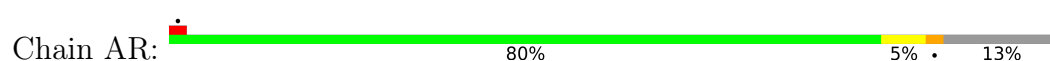
- Molecule 60: 60S ribosomal protein eL18



- Molecule 61: 60S ribosomal protein uL16



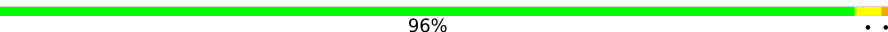
- Molecule 62: 60S ribosomal protein uL18

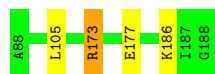


- Molecule 63: 60S ribosomal protein uL22

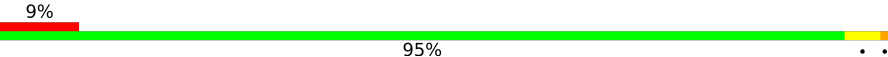


- Molecule 64: 60S ribosomal protein uL23

Chain AY:  96% ..

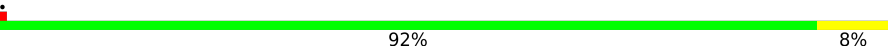


- Molecule 65: 60S ribosomal protein eL19

Chain AT:  95% ..

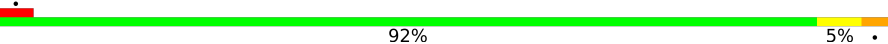


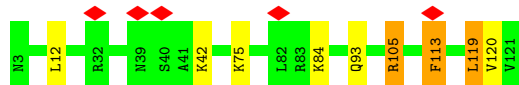
- Molecule 66: 60S ribosomal protein uL24

Chain AZ:  92% 8%



- Molecule 67: 60S ribosomal protein uL29

Chain A3:  92% 5%

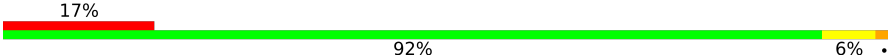


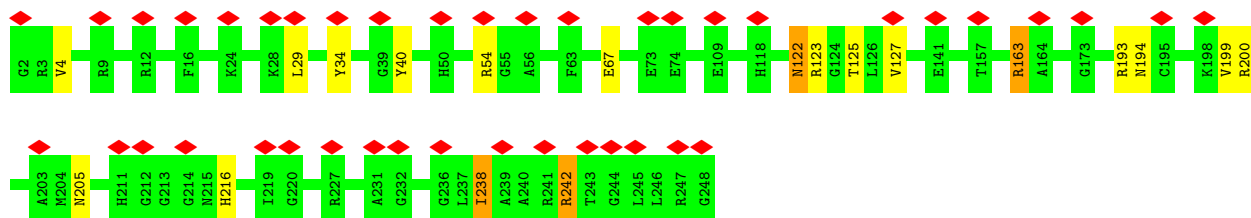
- Molecule 68: 60S ribosomal protein uL30

Chain A5:  92% 7%

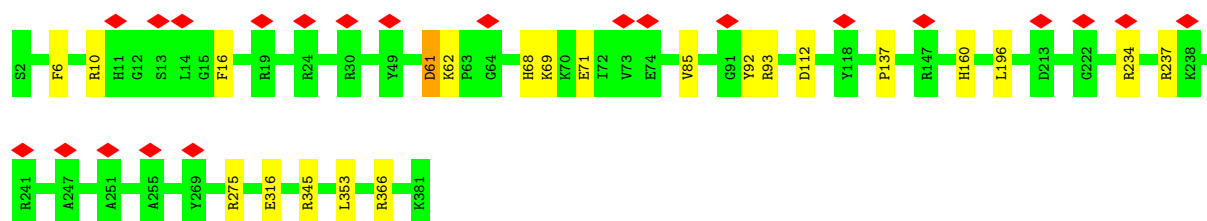


- Molecule 69: 60S ribosomal protein uL2

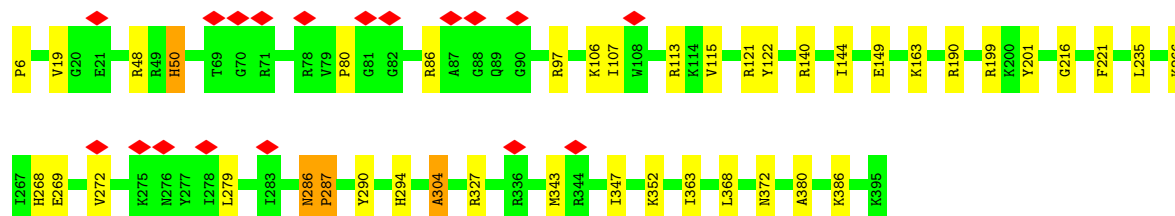
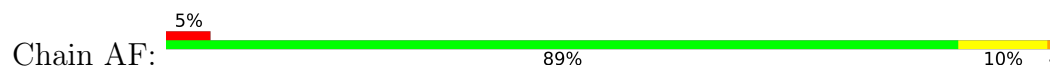
Chain AD:  92% 6%



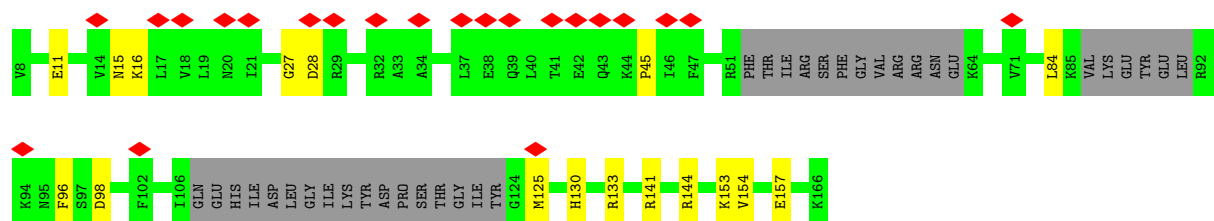
- Molecule 70: 60S ribosomal protein uL3



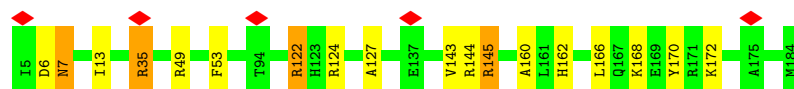
- Molecule 71: 60S ribosomal protein uL4



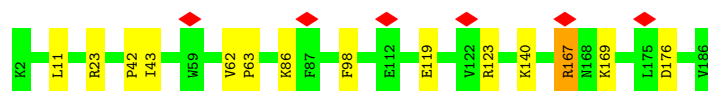
- Molecule 72: 60S ribosomal protein uL5



- Molecule 73: 60S ribosomal protein eL20



- Molecule 74: 60S ribosomal protein uL6

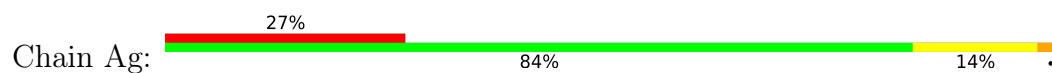


- Molecule 75: 60S ribosomal protein eL21





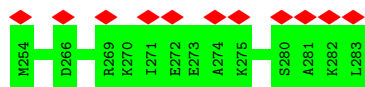
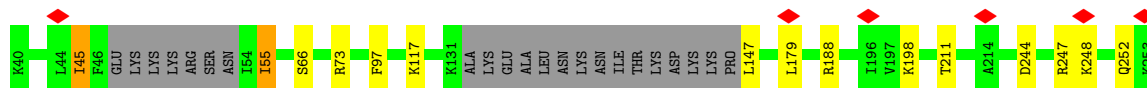
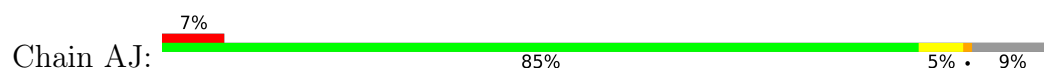
- Molecule 76: 60S ribosomal protein eL41



- Molecule 77: 60S ribosomal protein eL22



- Molecule 78: 60S ribosomal protein eL8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22793	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	30120	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.117	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	491.36, 491.36, 491.36	wwPDB
Map dimensions	296, 296, 296	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.66, 1.66, 1.66	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	A	0.95	0/38275	1.12	124/59596 (0.2%)
2	7	0.97	0/1785	1.25	16/2782 (0.6%)
3	Q	0.85	0/1149	1.46	1/1532 (0.1%)
4	S	0.87	0/1063	1.63	6/1425 (0.4%)
5	T	0.94	0/412	1.46	1/544 (0.2%)
6	M	0.83	0/1114	1.48	5/1487 (0.3%)
7	U	0.81	0/1223	1.56	4/1634 (0.2%)
8	V	0.86	0/1233	1.40	1/1645 (0.1%)
9	E	0.85	0/1539	1.53	1/2055 (0.0%)
10	X	0.84	0/788	1.61	5/1050 (0.5%)
11	G	0.80	0/1800	1.48	3/2429 (0.1%)
12	W	0.86	0/793	1.59	8/1053 (0.8%)
13	R	0.89	0/755	1.65	8/1013 (0.8%)
14	I	0.86	0/1443	1.56	8/1936 (0.4%)
15	O	0.86	0/706	1.47	1/950 (0.1%)
16	Y	0.85	0/1295	1.59	8/1742 (0.5%)
17	Z	0.83	0/565	1.42	0/758
18	1	0.85	0/999	1.48	4/1321 (0.3%)
19	2	0.93	0/324	1.53	0/435
20	C	0.82	0/1570	1.54	10/2129 (0.5%)
21	3	0.93	0/794	1.51	2/1055 (0.2%)
22	4	0.81	0/597	1.45	3/801 (0.4%)
23	5	0.87	0/459	1.30	1/606 (0.2%)
24	6	0.88	0/349	1.72	6/458 (1.3%)
25	B	0.82	0/1738	1.49	11/2321 (0.5%)
26	D	0.89	0/1241	1.44	4/1652 (0.2%)
27	F	0.84	0/2098	1.48	4/2819 (0.1%)
28	H	0.83	0/1665	1.47	9/2210 (0.4%)
29	K	0.86	0/1054	1.50	3/1411 (0.2%)
30	J	0.82	0/1545	1.46	6/2064 (0.3%)
31	N	0.84	0/780	1.53	4/1053 (0.4%)
32	P	0.87	0/966	1.56	6/1295 (0.5%)
33	L	0.86	0/1407	1.43	5/1879 (0.3%)
34	AA	0.96	7/75922 (0.0%)	1.12	262/118216 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	0.93	0/3599	1.16	20/5603 (0.4%)
36	AB	0.95	0/2823	1.06	6/4400 (0.1%)
37	AL	0.84	0/1789	1.57	8/2381 (0.3%)
38	A0	0.83	0/534	1.48	4/711 (0.6%)
39	AO	0.85	0/1199	1.58	15/1597 (0.9%)
40	Ai	0.81	0/789	1.39	2/1032 (0.2%)
41	A2	0.86	0/840	1.46	4/1114 (0.4%)
42	A4	0.86	0/564	1.71	6/737 (0.8%)
43	A6	0.85	0/749	1.53	2/1001 (0.2%)
44	A7	0.88	0/806	1.47	1/1073 (0.1%)
45	A1	0.82	0/1151	1.45	8/1531 (0.5%)
46	AN	0.81	0/1218	1.45	5/1621 (0.3%)
47	A8	0.85	0/1054	1.53	5/1399 (0.4%)
48	A9	0.86	0/865	1.50	9/1160 (0.8%)
49	Aa	0.86	0/872	1.54	6/1161 (0.5%)
50	Ab	0.88	0/763	1.53	2/1008 (0.2%)
51	Ad	0.84	0/612	1.45	0/812
52	Ae	0.96	0/396	1.64	3/521 (0.6%)
53	Af	0.83	0/419	1.45	0/556
54	AP	0.89	0/1735	1.62	20/2320 (0.9%)
55	Ah	0.83	0/668	1.46	0/887
56	AI	0.81	0/1708	1.56	12/2274 (0.5%)
57	Ac	0.87	0/723	1.62	11/951 (1.2%)
58	AK	0.84	0/1690	1.48	3/2260 (0.1%)
59	AM	0.81	0/1012	1.42	3/1363 (0.2%)
60	AS	0.86	0/1531	1.49	12/2040 (0.6%)
61	AQ	0.86	0/1580	1.48	4/2113 (0.2%)
62	AR	0.85	0/2079	1.53	7/2777 (0.3%)
63	AW	0.87	0/1244	1.49	2/1663 (0.1%)
64	AY	0.81	0/806	1.41	1/1074 (0.1%)
65	AT	0.85	0/1525	1.56	8/2016 (0.4%)
66	AZ	0.86	0/1013	1.49	2/1339 (0.1%)
67	A3	0.83	0/1005	1.60	7/1329 (0.5%)
68	A5	0.86	0/1917	1.53	7/2562 (0.3%)
69	AD	0.85	0/1902	1.48	7/2544 (0.3%)
70	AE	0.83	0/3130	1.50	8/4195 (0.2%)
71	AF	0.85	0/3145	1.55	23/4205 (0.5%)
72	AG	0.90	0/1021	1.63	11/1349 (0.8%)
73	AU	0.85	0/1527	1.51	12/2043 (0.6%)
74	AH	0.82	0/1501	1.52	10/2025 (0.5%)
75	AV	0.83	0/1301	1.52	5/1732 (0.3%)
76	Ag	1.01	0/348	1.66	3/448 (0.7%)
77	AX	0.81	0/842	1.46	5/1125 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	AJ	1.19	1/1840 (0.1%)	1.57	7/2456 (0.3%)
All	All	0.92	8/207281 (0.0%)	1.28	836/303864 (0.3%)

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	A	0	141
2	7	1	5
3	Q	0	4
5	T	0	1
6	M	0	2
7	U	0	1
8	V	0	3
9	E	0	3
10	X	0	2
12	W	0	3
14	I	0	3
16	Y	0	2
18	1	0	3
19	2	0	1
21	3	0	2
23	5	0	1
24	6	0	4
25	B	1	4
27	F	0	4
28	H	0	4
29	K	0	1
32	P	0	5
33	L	0	2
34	AA	1	328
35	AC	0	13
36	AB	0	8
37	AL	0	7
38	A0	0	1
39	AO	0	1
40	Ai	0	3
41	A2	2	0
42	A4	0	5
43	A6	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	A7	0	1
46	AN	0	3
47	A8	0	3
48	A9	0	3
49	Aa	0	2
50	Ab	0	3
51	Ad	0	2
52	Ae	0	2
53	Af	0	2
54	AP	0	7
55	Ah	0	1
56	AI	0	2
57	Ac	0	3
58	AK	0	8
60	AS	0	9
61	AQ	0	6
62	AR	0	7
63	AW	0	4
64	AY	0	1
65	AT	0	3
66	AZ	0	4
67	A3	0	1
68	A5	0	5
69	AD	0	4
70	AE	0	6
71	AF	0	10
72	AG	0	3
73	AU	0	5
74	AH	0	2
75	AV	0	6
76	Ag	0	3
77	AX	0	1
78	AJ	0	2
All	All	5	692

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	AJ	55	ILE	CG1-CD1	36.58	2.94	1.51
34	AA	2915	U	C4-C5	30.17	2.03	1.43
34	AA	2915	U	N1-C2	27.44	1.93	1.38
34	AA	2915	U	N1-C6	25.70	1.89	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2915	U	N3-C4	25.41	1.89	1.38

The worst 5 of 836 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	AB	27	A	O3'-P-O5'	-11.35	86.98	104.00
34	AA	181	C	P-O3'-C3'	11.22	137.03	120.20
1	A	981	U	P-O3'-C3'	11.07	136.81	120.20
1	A	844	G	P-O3'-C3'	10.86	136.49	120.20
1	A	1912	C	P-O3'-C3'	10.85	136.47	120.20

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	7	31	G	C3'
25	B	225	ILE	CB
34	AA	3018	A	C3'
41	A2	55	THR	CA
41	A2	116	SER	CA

5 of 692 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	C	Sidechain
1	A	38	C	Sidechain
1	A	39	A	Sidechain
1	A	47	A	Sidechain
1	A	62	A	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34207	0	17266	43	0
2	7	1598	0	816	1	0
3	Q	1129	0	1196	3	0
4	S	1047	0	1101	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	T	405	0	419	0	0
6	M	1099	0	1183	1	0
7	U	1202	0	1299	1	0
8	V	1206	0	1239	1	0
9	E	1515	0	1605	0	0
10	X	777	0	832	2	0
11	G	1758	0	1811	1	0
12	W	786	0	858	0	0
13	R	747	0	754	0	0
14	I	1424	0	1471	0	0
15	O	687	0	695	0	0
16	Y	1267	0	1316	0	0
17	Z	557	0	558	0	0
18	1	986	0	1076	1	0
19	2	321	0	338	0	0
20	C	1539	0	1600	0	0
21	3	782	0	820	1	0
22	4	586	0	604	1	0
23	5	458	0	496	0	0
24	6	346	0	381	0	0
25	B	1714	0	1838	3	0
26	D	1229	0	1311	0	0
27	F	2062	0	2200	3	0
28	H	1648	0	1803	0	0
29	K	1037	0	1099	2	0
30	J	1529	0	1680	1	0
31	N	772	0	813	0	0
32	P	954	0	997	1	0
33	L	1383	0	1434	0	0
34	AA	67862	0	34233	154	0
35	AC	3215	0	1633	6	0
36	AB	2522	0	1275	2	0
37	AL	1757	0	1888	1	0
38	A0	522	0	539	0	0
39	AO	1172	0	1230	1	0
40	Ai	779	0	861	0	0
41	A2	831	0	887	1	0
42	A4	555	0	599	3	0
43	A6	741	0	763	1	0
44	A7	794	0	869	0	0
45	A1	1134	0	1245	1	0
46	AN	1202	0	1316	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	A8	1037	0	1139	1	0
48	A9	845	0	886	1	0
49	Aa	859	0	912	2	0
50	Ab	757	0	842	1	0
51	Ad	604	0	686	0	0
52	Ae	388	0	421	0	0
53	Af	414	0	452	1	0
54	AP	1697	0	1802	2	0
55	Ah	659	0	727	0	0
56	AI	1685	0	1849	0	0
57	Ac	710	0	761	0	0
58	AK	1660	0	1785	1	0
59	AM	996	0	1044	0	0
60	AS	1503	0	1636	0	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	2	0
63	AW	1319	0	1303	0	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	1	0
67	A3	995	0	1121	1	0
68	A5	1879	0	2005	0	0
69	AD	1867	0	1964	1	0
70	AE	3062	0	3205	6	0
71	AF	3095	0	3333	3	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	0	0
75	AV	1276	0	1355	1	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	1	0
78	AJ	1813	0	1985	25	0
All	All	193017	0	144286	254	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 1.

The worst 5 of 254 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)
34:AA:2915:U:C5	34:AA:2915:U:C4	2.03	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:2915:U:N3	34:AA:2915:U:C2	1.87	1.42
34:AA:2915:U:N1	34:AA:2915:U:C6	1.89	1.39
34:AA:2915:U:C4	34:AA:2915:U:N3	1.89	1.37
34:AA:2915:U:C2	34:AA:2915:U:N1	1.93	1.35

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Q	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	9	40
4	S	126/128 (98%)	107 (85%)	11 (9%)	8 (6%)	1	12
5	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
6	M	136/138 (99%)	128 (94%)	6 (4%)	2 (2%)	8	39
7	U	147/149 (99%)	144 (98%)	2 (1%)	1 (1%)	18	56
8	V	142/156 (91%)	134 (94%)	4 (3%)	4 (3%)	4	24
9	E	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
10	X	92/103 (89%)	82 (89%)	6 (6%)	4 (4%)	2	17
11	G	222/224 (99%)	209 (94%)	10 (4%)	3 (1%)	9	40
12	W	91/108 (84%)	87 (96%)	3 (3%)	1 (1%)	11	45
13	R	92/114 (81%)	78 (85%)	10 (11%)	4 (4%)	2	17
14	I	176/189 (93%)	166 (94%)	7 (4%)	3 (2%)	7	36
15	O	77/79 (98%)	70 (91%)	3 (4%)	4 (5%)	1	14
16	Y	152/154 (99%)	141 (93%)	7 (5%)	4 (3%)	4	25
17	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	9	40
18	1	118/120 (98%)	109 (92%)	7 (6%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	2	35/68 (52%)	32 (91%)	1 (3%)	2 (6%)	1	13
20	C	193/195 (99%)	180 (93%)	11 (6%)	2 (1%)	12	48
21	3	93/95 (98%)	81 (87%)	12 (13%)	0	100	100
22	4	74/76 (97%)	67 (90%)	4 (5%)	3 (4%)	2	17
23	5	54/65 (83%)	52 (96%)	1 (2%)	1 (2%)	6	31
24	6	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
25	B	208/210 (99%)	188 (90%)	16 (8%)	4 (2%)	6	31
26	D	149/209 (71%)	143 (96%)	4 (3%)	2 (1%)	9	41
27	F	255/257 (99%)	244 (96%)	10 (4%)	1 (0%)	30	67
28	H	200/214 (94%)	186 (93%)	13 (6%)	1 (0%)	24	63
29	K	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	7	37
30	J	186/188 (99%)	175 (94%)	7 (4%)	4 (2%)	5	28
31	N	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
32	P	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
33	L	165/214 (77%)	149 (90%)	15 (9%)	1 (1%)	21	59
37	AL	209/211 (99%)	190 (91%)	13 (6%)	6 (3%)	3	23
38	A0	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
39	AO	145/147 (99%)	134 (92%)	8 (6%)	3 (2%)	5	29
40	Ai	93/95 (98%)	84 (90%)	6 (6%)	3 (3%)	3	21
41	A2	96/118 (81%)	92 (96%)	3 (3%)	1 (1%)	12	48
42	A4	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
43	A6	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
44	A7	92/102 (90%)	90 (98%)	2 (2%)	0	100	100
45	A1	136/145 (94%)	131 (96%)	5 (4%)	0	100	100
46	AN	144/146 (99%)	138 (96%)	4 (3%)	2 (1%)	9	40
47	A8	123/125 (98%)	111 (90%)	10 (8%)	2 (2%)	7	37
48	A9	101/103 (98%)	93 (92%)	5 (5%)	3 (3%)	3	22
49	Aa	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
50	Ab	91/105 (87%)	86 (94%)	3 (3%)	2 (2%)	5	28
51	Ad	68/76 (90%)	65 (96%)	2 (3%)	1 (2%)	8	39
52	Ae	39/50 (78%)	38 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Af	49/51 (96%)	44 (90%)	5 (10%)	0	100	100
54	AP	202/204 (99%)	182 (90%)	11 (5%)	9 (4%)	2	16
55	Ah	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	AI	203/213 (95%)	188 (93%)	10 (5%)	5 (2%)	4	25
57	Ac	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	20
58	AK	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	63
59	AM	130/132 (98%)	122 (94%)	7 (5%)	1 (1%)	16	54
60	AS	184/186 (99%)	166 (90%)	13 (7%)	5 (3%)	4	25
61	AQ	185/205 (90%)	169 (91%)	11 (6%)	5 (3%)	4	25
62	AR	244/289 (84%)	219 (90%)	19 (8%)	6 (2%)	4	25
63	AW	149/170 (88%)	137 (92%)	10 (7%)	2 (1%)	9	41
64	AY	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12	48
65	AT	179/181 (99%)	174 (97%)	3 (2%)	2 (1%)	11	45
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	16	54
67	A3	117/119 (98%)	110 (94%)	5 (4%)	2 (2%)	7	36
68	A5	221/223 (99%)	197 (89%)	19 (9%)	5 (2%)	5	27
69	AD	245/247 (99%)	232 (95%)	9 (4%)	4 (2%)	7	37
70	AE	378/380 (100%)	350 (93%)	27 (7%)	1 (0%)	36	72
71	AF	388/390 (100%)	355 (92%)	24 (6%)	9 (2%)	5	27
72	AG	116/159 (73%)	106 (91%)	7 (6%)	3 (3%)	4	25
73	AU	178/180 (99%)	162 (91%)	12 (7%)	4 (2%)	5	28
74	AH	183/185 (99%)	163 (89%)	17 (9%)	3 (2%)	7	37
75	AV	153/155 (99%)	142 (93%)	10 (6%)	1 (1%)	18	56
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	3	23
77	AX	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
78	AJ	216/244 (88%)	201 (93%)	12 (6%)	3 (1%)	9	40
All	All	10111/10698 (94%)	9380 (93%)	565 (6%)	166 (2%)	10	37

5 of 166 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	41	GLU
8	V	41	VAL

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Mol	Chain	Res	Type
10	X	52	LYS
13	R	42	ILE
14	I	70	HIS

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	
3	Q	120/120 (100%)	119 (99%)	1 (1%)	73	79
4	S	114/114 (100%)	111 (97%)	3 (3%)	40	61
5	T	43/43 (100%)	41 (95%)	2 (5%)	23	44
6	M	116/116 (100%)	113 (97%)	3 (3%)	40	61
7	U	132/132 (100%)	130 (98%)	2 (2%)	57	71
8	V	131/140 (94%)	129 (98%)	2 (2%)	57	71
9	E	161/164 (98%)	157 (98%)	4 (2%)	42	62
10	X	88/94 (94%)	88 (100%)	0	100	100
11	G	191/191 (100%)	188 (98%)	3 (2%)	55	69
12	W	86/99 (87%)	86 (100%)	0	100	100
13	R	83/97 (86%)	83 (100%)	0	100	100
14	I	154/160 (96%)	150 (97%)	4 (3%)	40	61
15	O	76/76 (100%)	75 (99%)	1 (1%)	61	73
16	Y	137/137 (100%)	132 (96%)	5 (4%)	31	52
17	Z	60/60 (100%)	60 (100%)	0	100	100
18	1	104/104 (100%)	100 (96%)	4 (4%)	29	50
19	2	35/61 (57%)	35 (100%)	0	100	100
20	C	167/167 (100%)	164 (98%)	3 (2%)	51	67
21	3	87/87 (100%)	87 (100%)	0	100	100
22	4	70/70 (100%)	68 (97%)	2 (3%)	37	57
23	5	47/52 (90%)	46 (98%)	1 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	6	36/36 (100%)	36 (100%)	0	100	100
25	B	195/195 (100%)	192 (98%)	3 (2%)	57	71
26	D	132/177 (75%)	129 (98%)	3 (2%)	44	63
27	F	233/233 (100%)	223 (96%)	10 (4%)	26	47
28	H	182/190 (96%)	179 (98%)	3 (2%)	55	69
29	K	115/115 (100%)	114 (99%)	1 (1%)	70	78
30	J	177/177 (100%)	173 (98%)	4 (2%)	44	63
31	N	91/91 (100%)	90 (99%)	1 (1%)	65	75
32	P	99/99 (100%)	97 (98%)	2 (2%)	48	66
33	L	151/190 (80%)	150 (99%)	1 (1%)	76	81
37	AL	190/190 (100%)	184 (97%)	6 (3%)	34	55
38	A0	53/53 (100%)	52 (98%)	1 (2%)	50	66
39	AO	121/121 (100%)	119 (98%)	2 (2%)	53	68
40	Ai	87/87 (100%)	86 (99%)	1 (1%)	65	75
41	A2	97/109 (89%)	95 (98%)	2 (2%)	47	65
42	A4	60/60 (100%)	59 (98%)	1 (2%)	53	68
43	A6	83/83 (100%)	81 (98%)	2 (2%)	43	63
44	A7	90/96 (94%)	89 (99%)	1 (1%)	65	75
45	A1	127/131 (97%)	125 (98%)	2 (2%)	55	69
46	AN	135/135 (100%)	133 (98%)	2 (2%)	57	71
47	A8	114/114 (100%)	113 (99%)	1 (1%)	70	78
48	A9	90/90 (100%)	85 (94%)	5 (6%)	19	40
49	Aa	89/89 (100%)	89 (100%)	0	100	100
50	Ab	82/92 (89%)	80 (98%)	2 (2%)	43	63
51	Ad	69/73 (94%)	68 (99%)	1 (1%)	59	72
52	Ae	40/47 (85%)	38 (95%)	2 (5%)	22	42
53	Af	45/45 (100%)	44 (98%)	1 (2%)	45	64
54	AP	179/179 (100%)	170 (95%)	9 (5%)	22	42
55	Ah	70/70 (100%)	70 (100%)	0	100	100
56	AI	189/195 (97%)	184 (97%)	5 (3%)	40	61
57	Ac	74/74 (100%)	73 (99%)	1 (1%)	59	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AK	181/181 (100%)	178 (98%)	3 (2%)	53	68
59	AM	106/106 (100%)	105 (99%)	1 (1%)	70	78
60	AS	158/158 (100%)	155 (98%)	3 (2%)	50	66
61	AQ	165/176 (94%)	160 (97%)	5 (3%)	36	57
62	AR	215/250 (86%)	212 (99%)	3 (1%)	59	72
63	AW	128/128 (100%)	123 (96%)	5 (4%)	28	49
64	AY	90/90 (100%)	88 (98%)	2 (2%)	45	64
65	AT	162/162 (100%)	162 (100%)	0	100	100
66	AZ	111/111 (100%)	109 (98%)	2 (2%)	51	67
67	A3	110/110 (100%)	108 (98%)	2 (2%)	51	67
68	A5	201/201 (100%)	199 (99%)	2 (1%)	68	77
69	AD	191/191 (100%)	184 (96%)	7 (4%)	30	51
70	AE	335/335 (100%)	334 (100%)	1 (0%)	86	85
71	AF	336/336 (100%)	329 (98%)	7 (2%)	47	65
72	AG	110/142 (78%)	107 (97%)	3 (3%)	39	60
73	AU	162/162 (100%)	162 (100%)	0	100	100
74	AH	168/168 (100%)	166 (99%)	2 (1%)	63	75
75	AV	140/140 (100%)	137 (98%)	3 (2%)	47	65
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	37	57
77	AX	92/92 (100%)	91 (99%)	1 (1%)	65	75
78	AJ	204/224 (91%)	200 (98%)	4 (2%)	48	66
All	All	9096/9417 (97%)	8924 (98%)	172 (2%)	49	66

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	AK	39	ASP
69	AD	34	TYR
60	AS	91	LEU
63	AW	16	LYS
70	AE	237	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
56	AI	160	ASN
63	AW	147	GLN
75	AV	96	HIS
58	AK	175	ASN
62	AR	94	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	484 (30%)	100 (6%)
2	7	74/75 (98%)	33 (44%)	5 (6%)
34	AA	3165/3192 (99%)	984 (31%)	189 (5%)
35	AC	148/151 (98%)	49 (33%)	10 (6%)
36	AB	117/118 (99%)	29 (24%)	2 (1%)
All	All	5092/5144 (98%)	1579 (31%)	306 (6%)

5 of 1579 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	C
1	A	5	U
1	A	17	C
1	A	26	A

5 of 306 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2665	A
34	AA	3667	C
34	AA	2886	A
34	AA	3309	G
35	AC	114	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	36.79

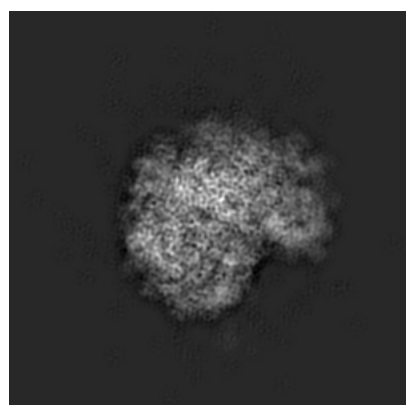
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6452. These allow visual inspection of the internal detail of the map and identification of artifacts.

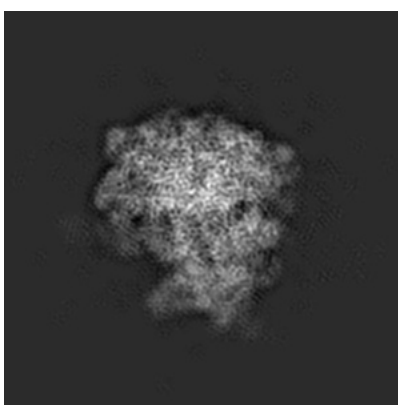
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

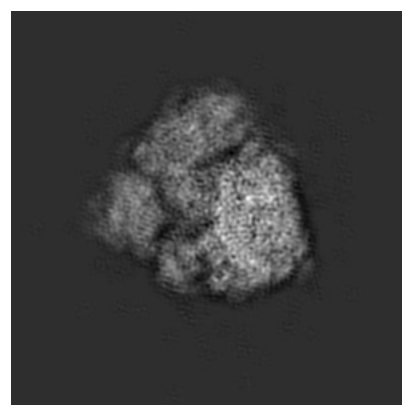
6.1.1 Primary map



X



Y

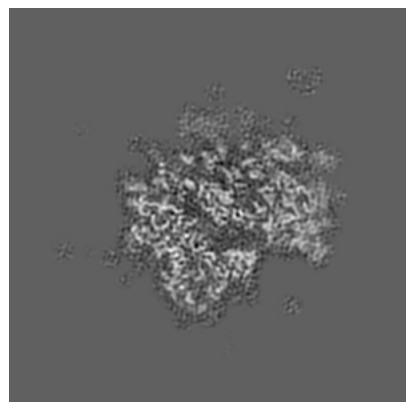


Z

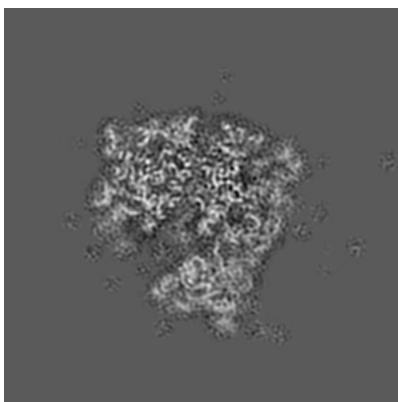
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

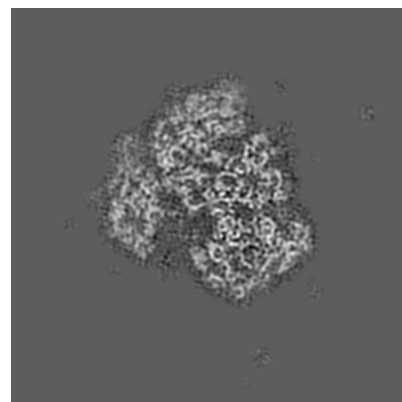
6.2.1 Primary map



X Index: 148



Y Index: 148

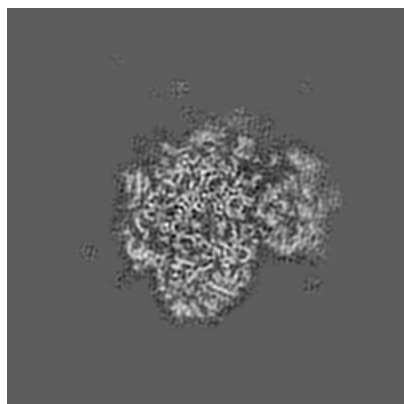


Z Index: 148

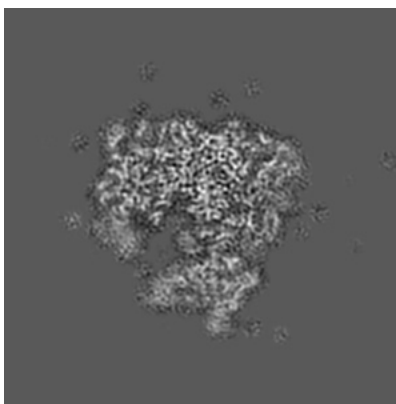
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

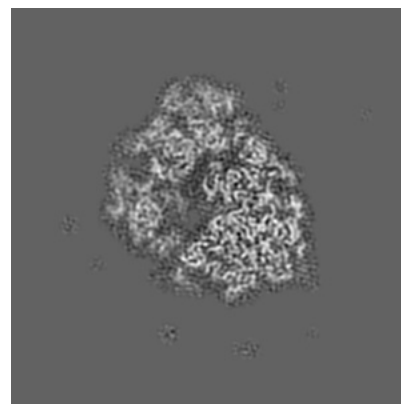
6.3.1 Primary map



X Index: 157



Y Index: 154

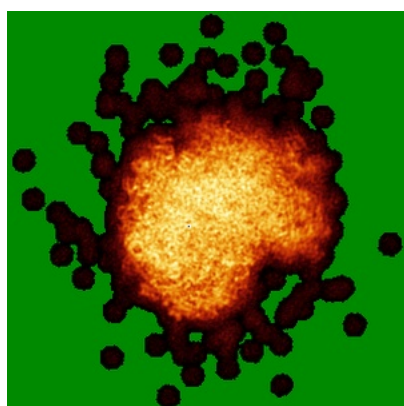


Z Index: 137

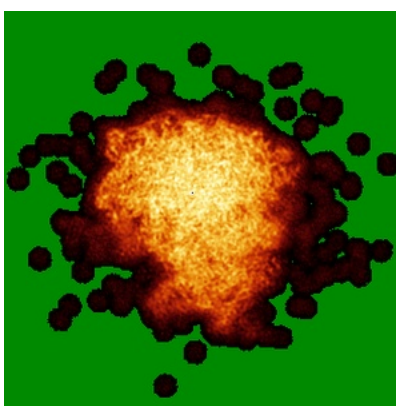
The images above show the largest variance slices of the map in three orthogonal directions.

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

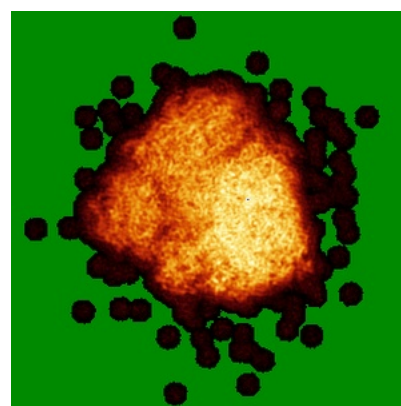
6.4.1 Primary map



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

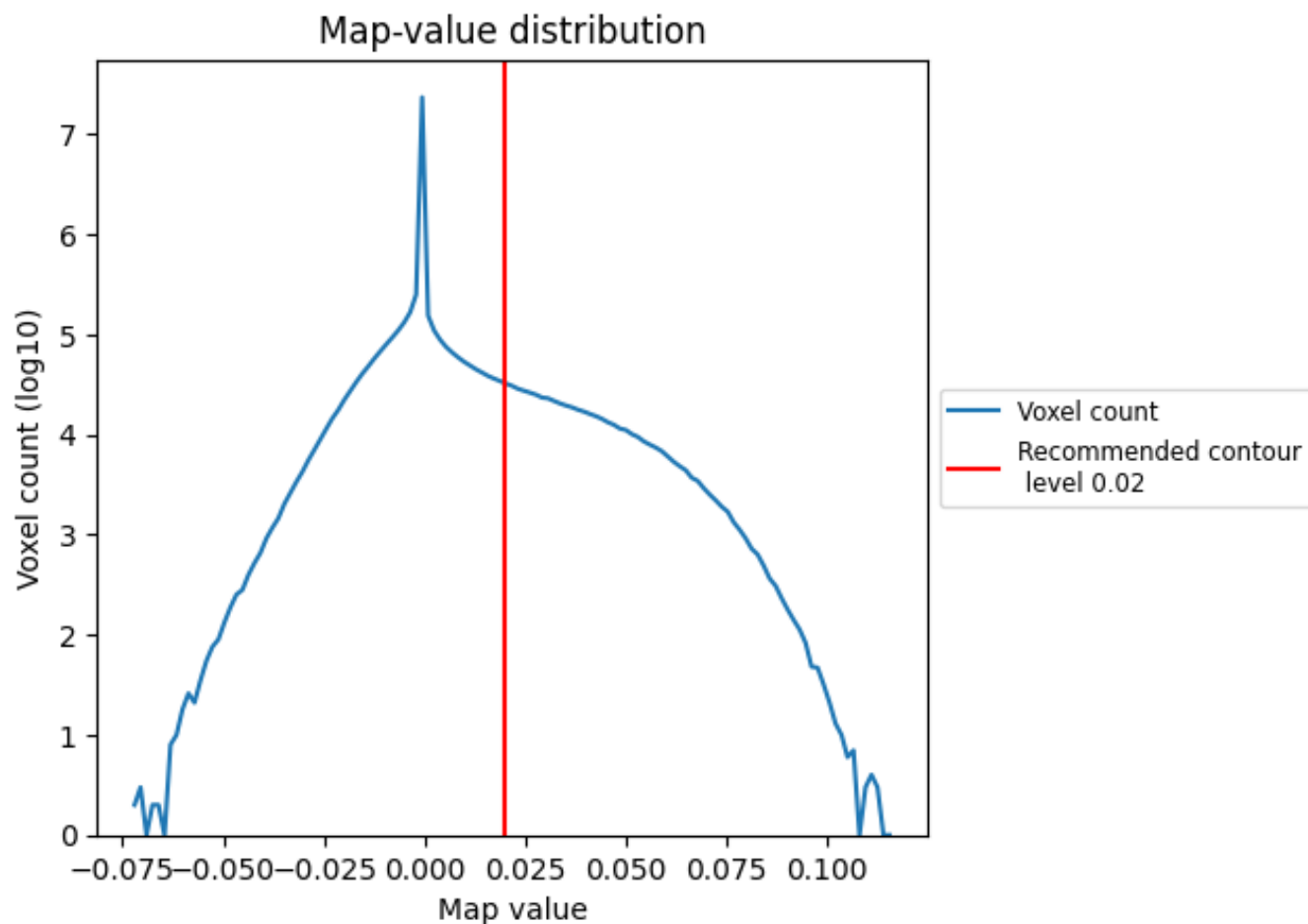
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

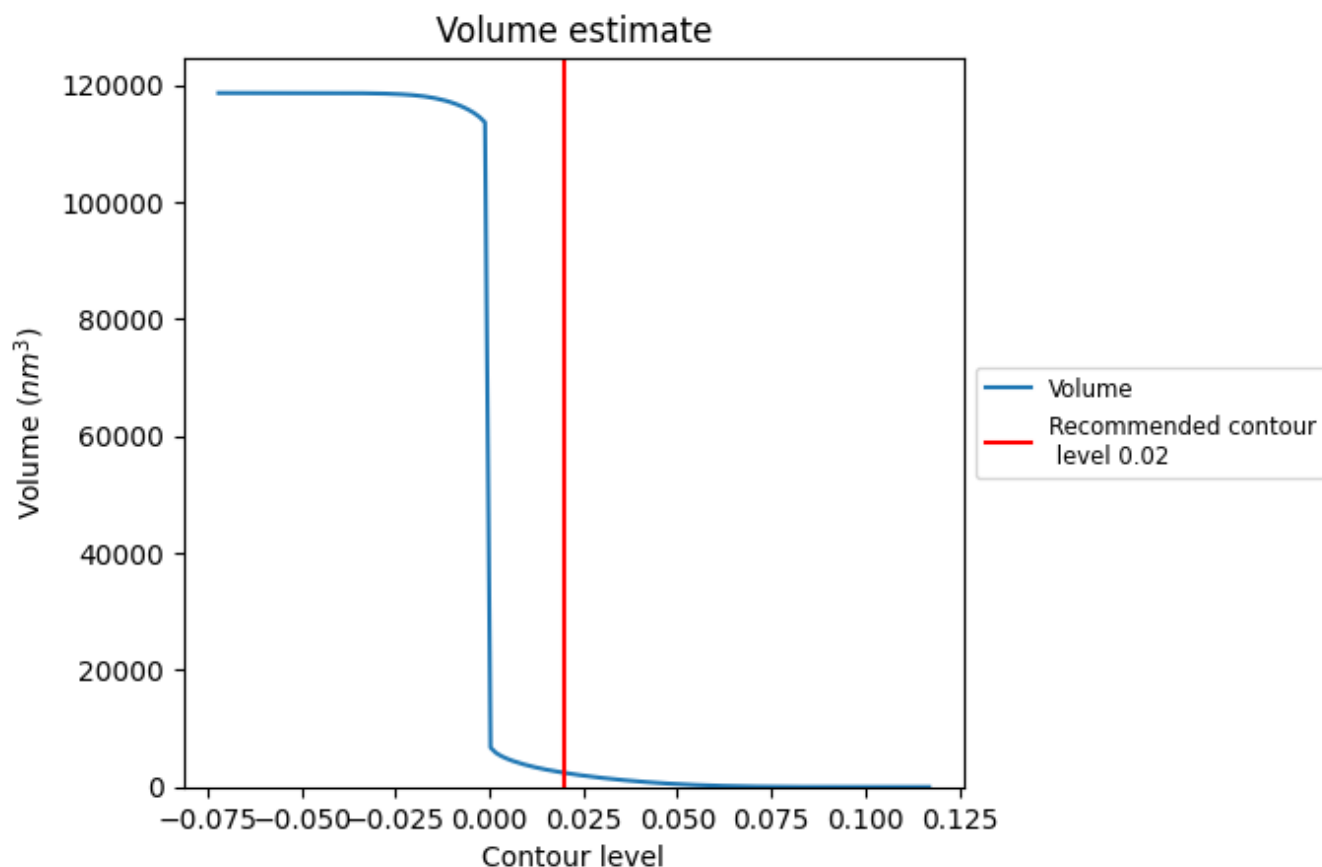
This section contains the results of statistical analysis of the map.

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.

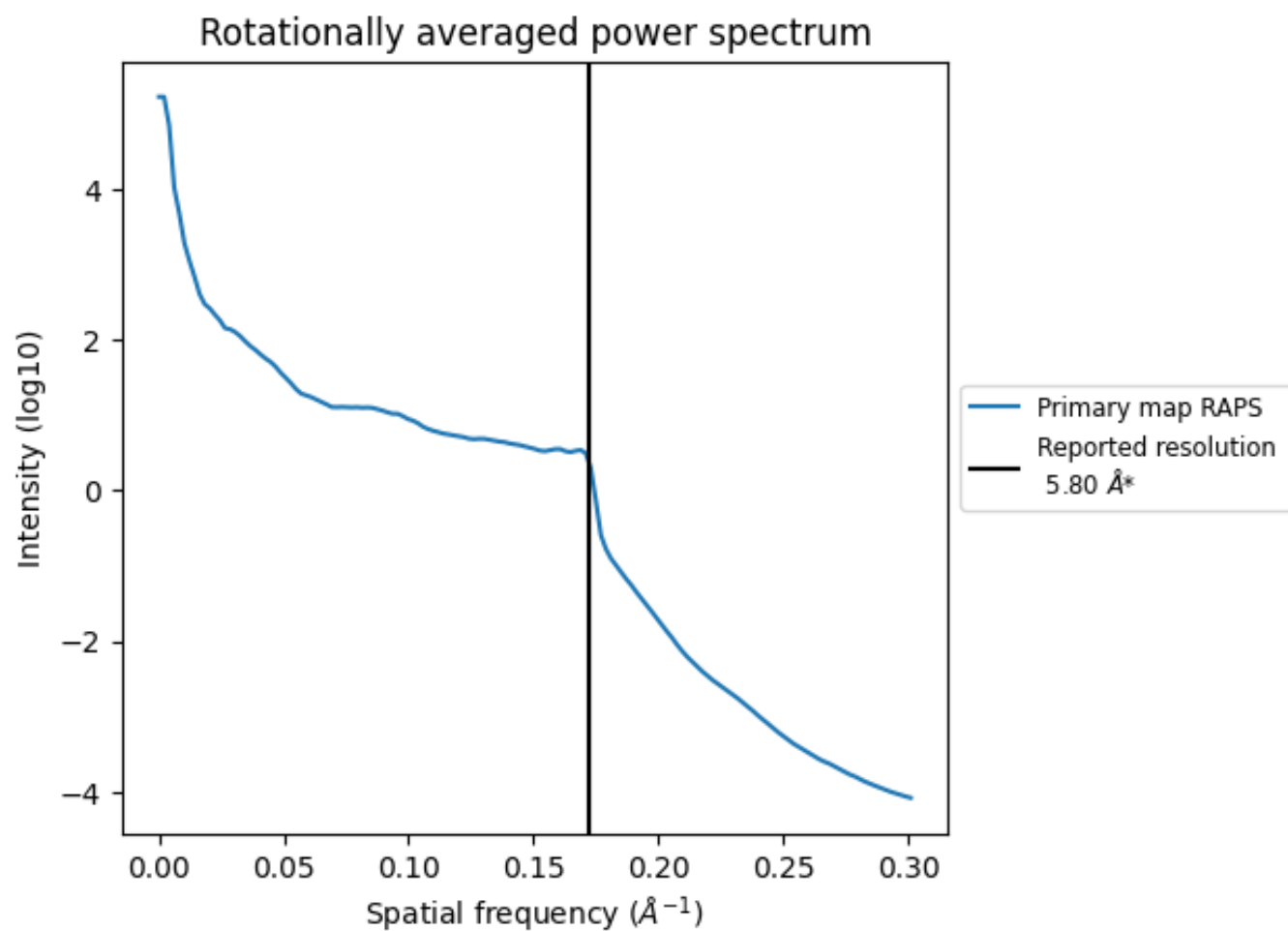
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2413 nm³; this corresponds to an approximate mass of 2180 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 0.172 Å⁻¹

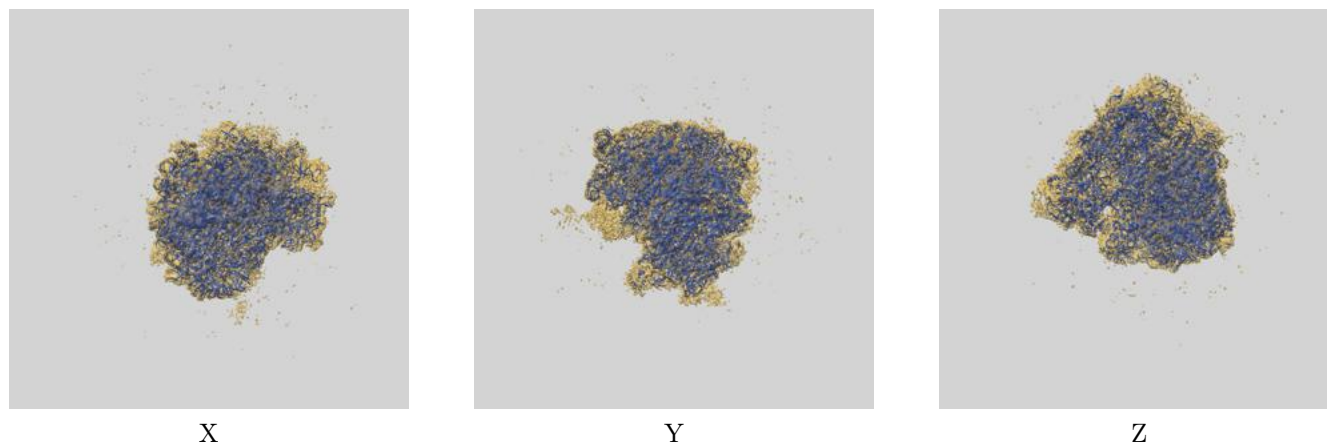
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

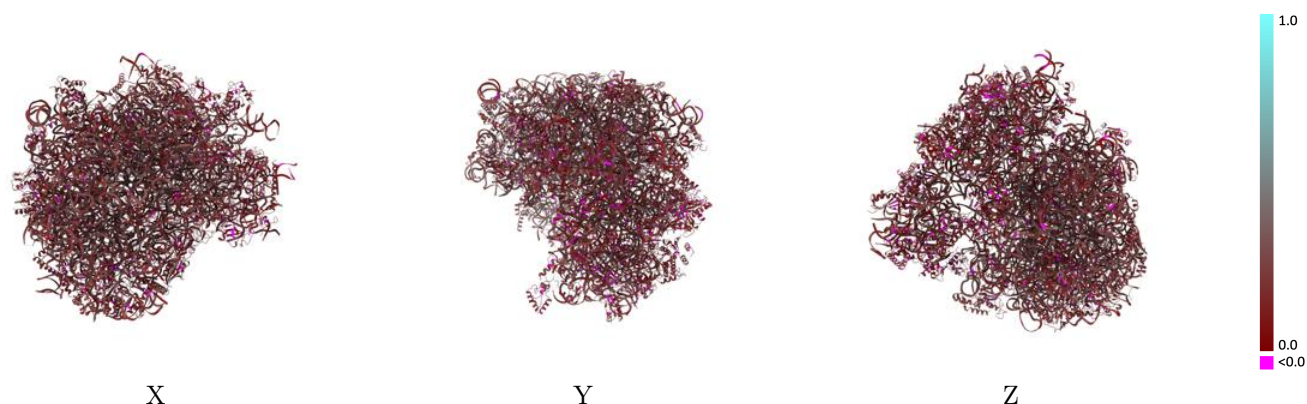
This section contains information regarding the fit between EMDB map EMD-6452 and PDB model 3JBO. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



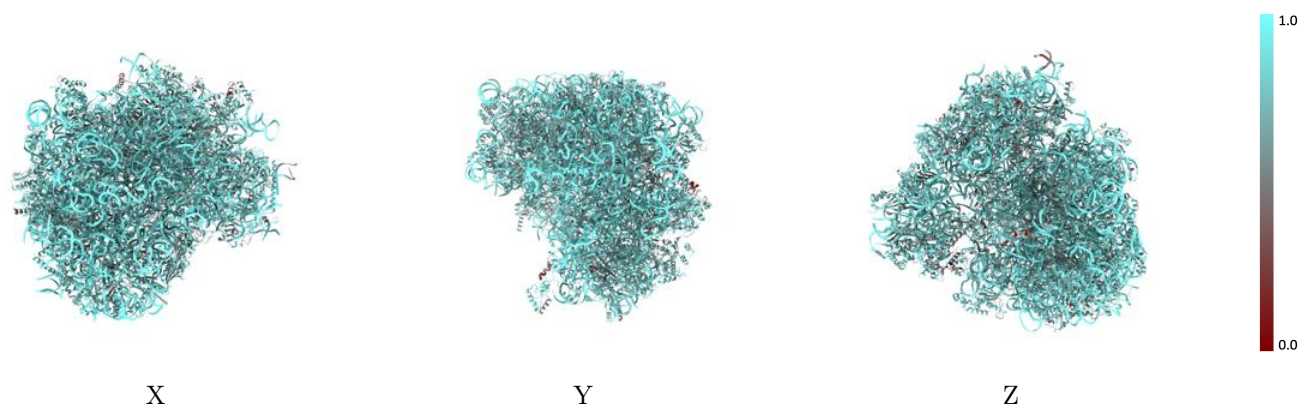
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



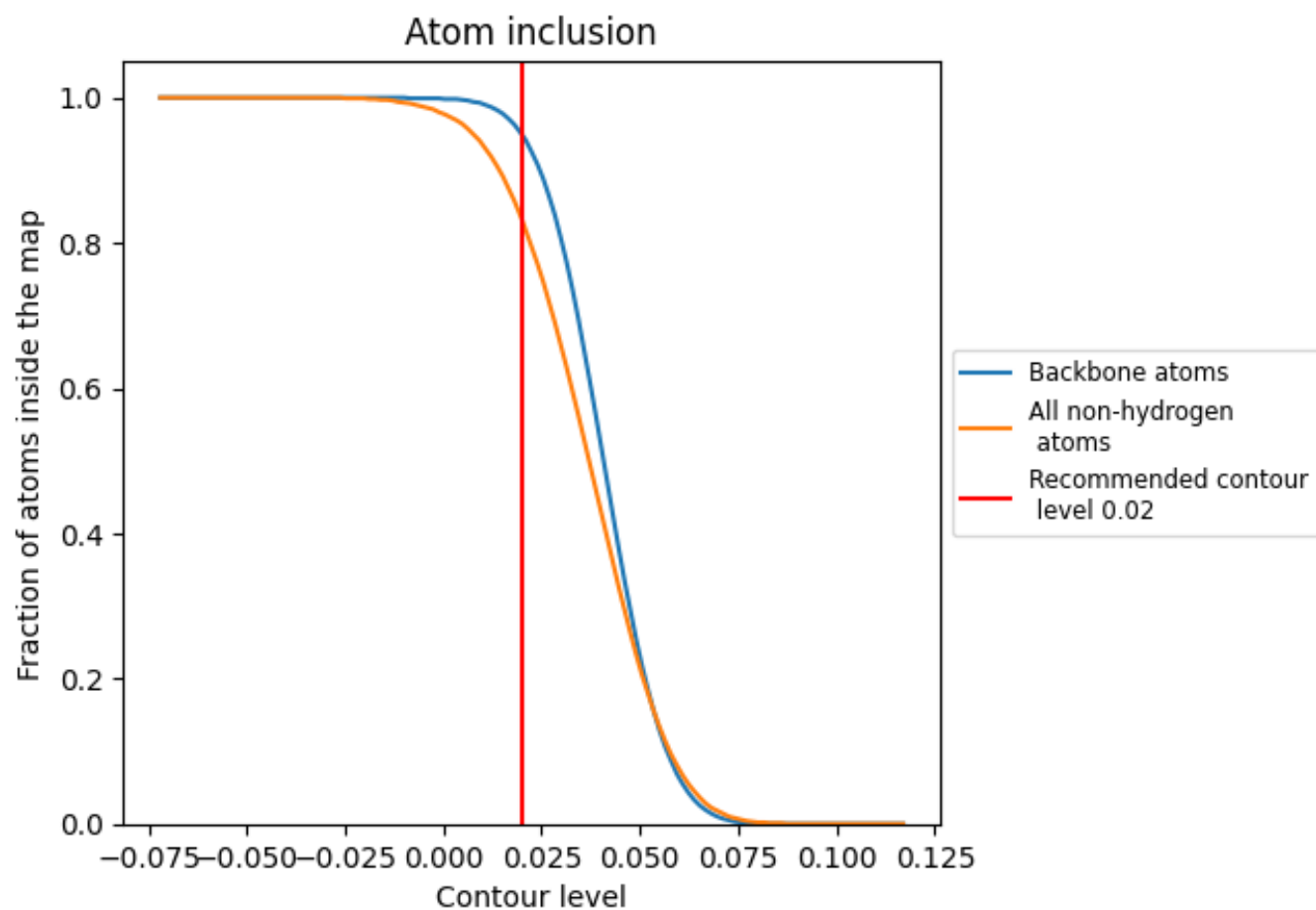
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8320	 0.2350
1	 0.7240	 0.1750
2	 0.7350	 0.2180
3	 0.6570	 0.2160
4	 0.7020	 0.2110
5	 0.4790	 0.1990
6	 0.6700	 0.2340
7	 0.7770	 0.2280
A	 0.9220	 0.2420
A0	 0.7200	 0.2300
A1	 0.7180	 0.2170
A2	 0.7690	 0.2350
A3	 0.7210	 0.1910
A4	 0.6860	 0.2280
A5	 0.7050	 0.2010
A6	 0.6820	 0.2190
A7	 0.7110	 0.1910
A8	 0.6500	 0.2200
A9	 0.7000	 0.2040
AA	 0.9290	 0.2660
AB	 0.9700	 0.2630
AC	 0.9480	 0.2660
AD	 0.5990	 0.2000
AE	 0.6930	 0.2120
AF	 0.7100	 0.2030
AG	 0.7160	 0.2170
AH	 0.7420	 0.2140
AI	 0.7470	 0.2030
AJ	 0.7300	 0.2300
AK	 0.6760	 0.1910
AL	 0.7420	 0.2230
AM	 0.6470	 0.2270
AN	 0.7530	 0.2140
AO	 0.6980	 0.2100
AP	 0.6680	 0.1850



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Chain	Atom inclusion	Q-score
AQ	 0.6970	 0.2270
AR	 0.7590	 0.2030
AS	 0.6810	 0.2040
AT	 0.6580	 0.2020
AU	 0.7220	 0.2160
AV	 0.6990	 0.2270
AW	 0.7290	 0.2080
AX	 0.7160	 0.2030
AY	 0.7160	 0.2360
AZ	 0.7600	 0.2110
Aa	 0.6910	 0.2250
Ab	 0.7320	 0.2120
Ac	 0.6590	 0.1940
Ad	 0.7620	 0.2280
Ae	 0.6970	 0.2200
Af	 0.7100	 0.1950
Ag	 0.5760	 0.1850
Ah	 0.6420	 0.1970
Ai	 0.6770	 0.2060
B	 0.6640	 0.1960
C	 0.7410	 0.2030
D	 0.6850	 0.2100
E	 0.7120	 0.1910
F	 0.7300	 0.1900
G	 0.7380	 0.2160
H	 0.7220	 0.1770
I	 0.6440	 0.1850
J	 0.7140	 0.1950
K	 0.6770	 0.1930
L	 0.7160	 0.2060
M	 0.7170	 0.1660
N	 0.7380	 0.1730
O	 0.7770	 0.2150
P	 0.6460	 0.1980
Q	 0.6000	 0.1980
R	 0.8210	 0.2190
S	 0.7550	 0.1920
T	 0.7600	 0.1870
U	 0.6560	 0.1920
V	 0.6900	 0.2190
W	 0.7460	 0.2010
X	 0.7280	 0.2290

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Chain	Atom inclusion	Q-score
Y	 0.7860	 0.1900
Z	 0.7310	 0.2160