



wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 11:26 AM EDT

PDB ID : 5KPV
EMDB ID : EMD-8280
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure II)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-07-05
Resolution : 4.10 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

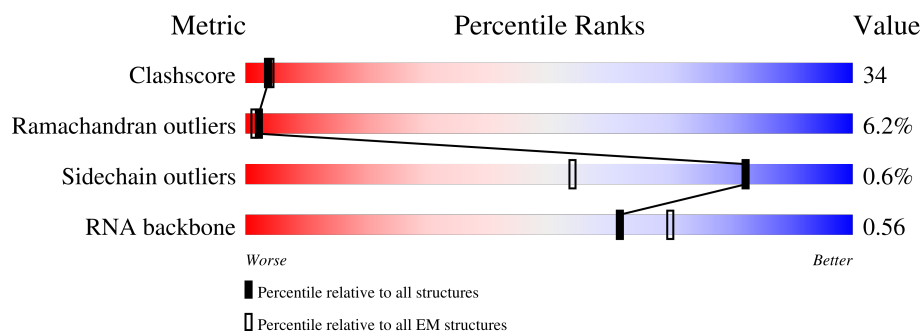
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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.






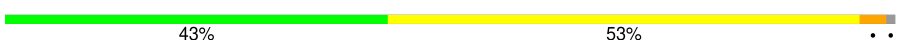




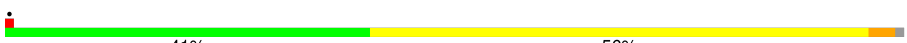
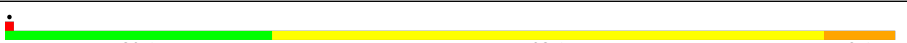
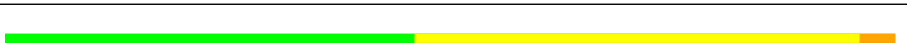
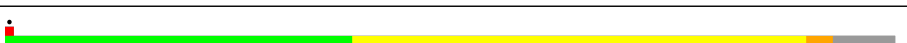
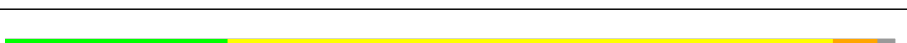
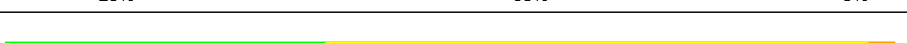
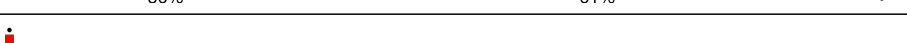

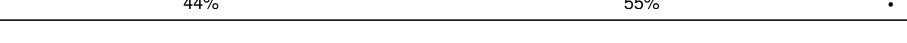
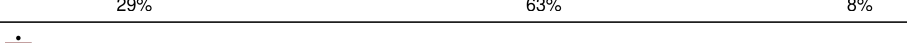







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	273	
2	B	209	
3	C	201	
4	D	179	
5	E	177	
6	F	149	
7	G	165	





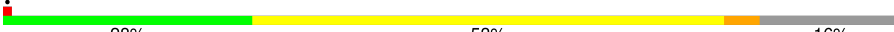
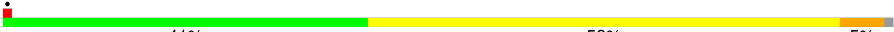
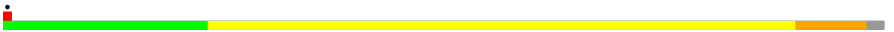





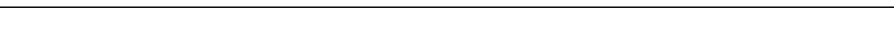

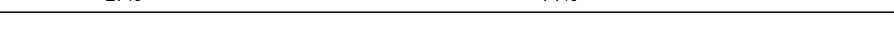

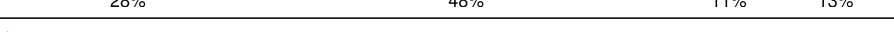




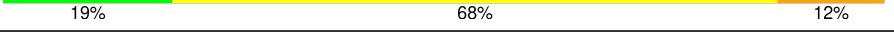


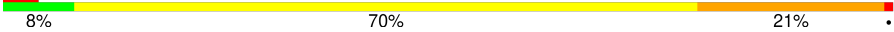
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Mol	Chain	Length	Quality of chain
8	H	142	
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4	65	
31	5	38	
32	6	241	

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Mol	Chain	Length	Quality of chain
33	7	233	
34	8	206	
35	9	167	
36	10	135	
37	11	179	
38	12	130	
39	13	130	
40	14	103	
41	15	129	
42	16	124	
43	17	118	
44	18	101	
45	19	89	
46	20	82	
47	21	84	
48	22	75	
49	23	92	
50	24	87	
51	25	71	
52	26	1539	
53	27	2903	
54	28	120	
55	29	20	
56	30	76	
57	31	77	

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Mol	Chain	Length	Quality of chain
58	32	77	<div><div></div><div>12%</div><div>22%</div><div>61%</div><div>17%</div></div>
59	33	750	<div><div></div><div>47%</div><div>35%</div><div>48%</div><div>6%</div><div>10%</div></div>

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 154603 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	2	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	10	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	11	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	12	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	13	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	14	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	15	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	16	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	17	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	18	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	19	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	20	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	21	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	22	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	23	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	24	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	25	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	26	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	27	2903	Total	C	N	O	P	0	0
			62322	27801	11468	20150	2903		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
27	747	C	U	conflict	GB 802133627
27	1847	G	A	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	28	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
28	120	A	-	conflict	GB 1028475309

- Molecule 55 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	29	20	Total	C	N	O	P	0	0
			432	195	86	132	19		

- Molecule 56 is a RNA chain called A-site tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	30	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 57 is a RNA chain called P-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	31	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 58 is a RNA chain called E-site tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	32	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 59 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	33	675	Total	C	N	O	S	0	0
			4911	3070	904	915	22		

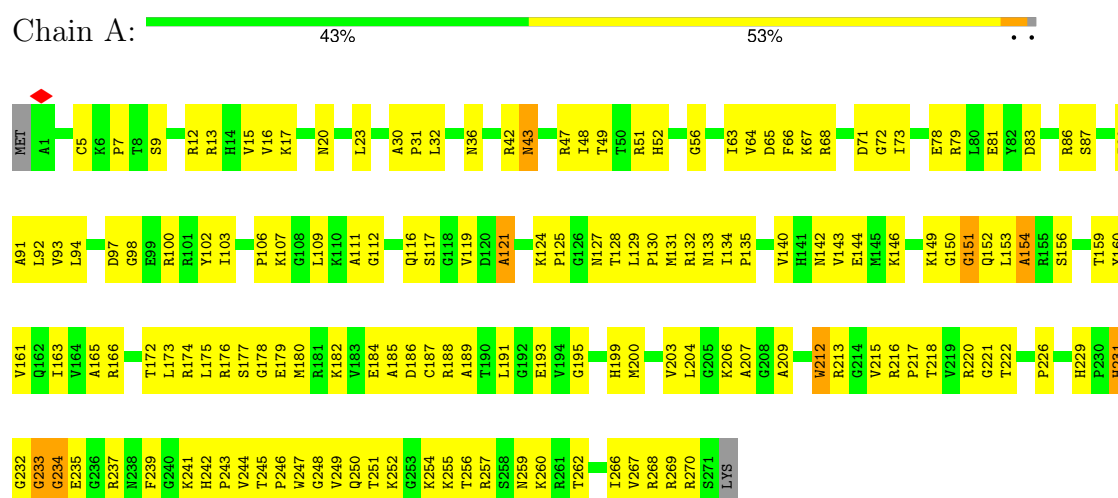
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
33	-5	MET	-	expression tag	UNP P0AG20
33	-4	HIS	-	expression tag	UNP P0AG20
33	-3	HIS	-	expression tag	UNP P0AG20
33	-2	HIS	-	expression tag	UNP P0AG20
33	-1	HIS	-	expression tag	UNP P0AG20
33	0	HIS	-	expression tag	UNP P0AG20
33	1	HIS	-	expression tag	UNP P0AG20

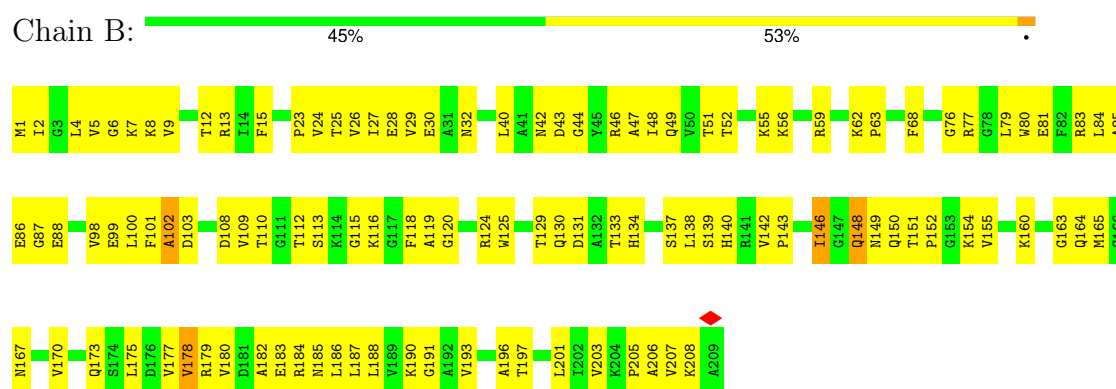
3 Residue-property plots

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.

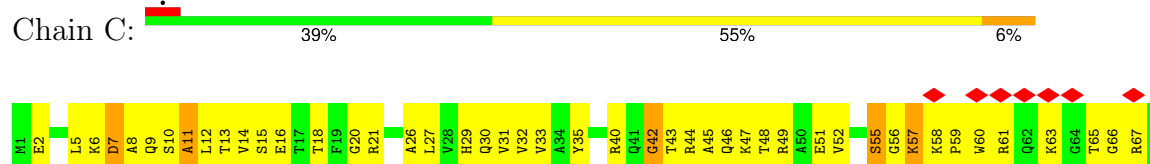
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

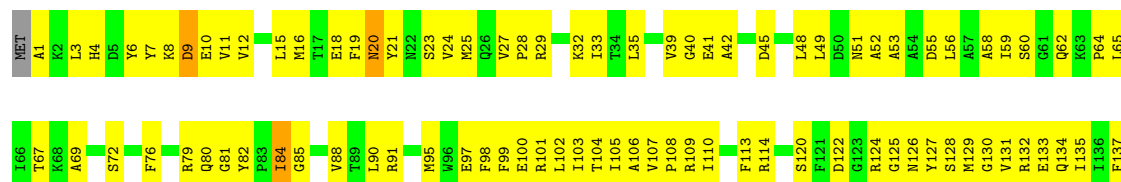


• Molecule 3: 50S ribosomal protein L4

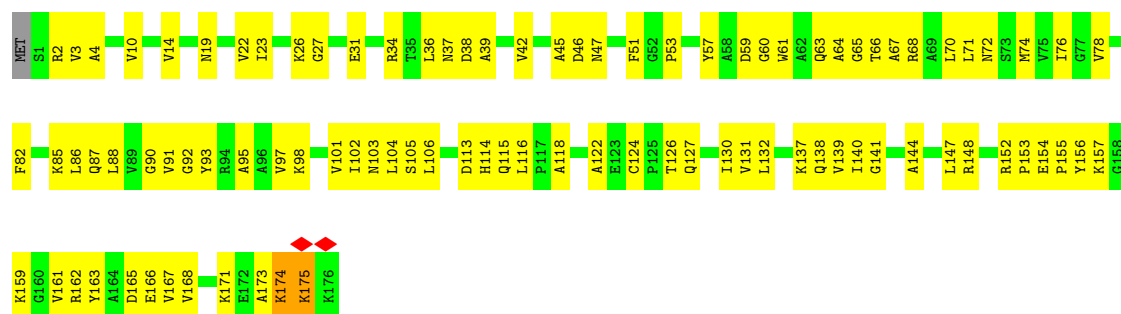




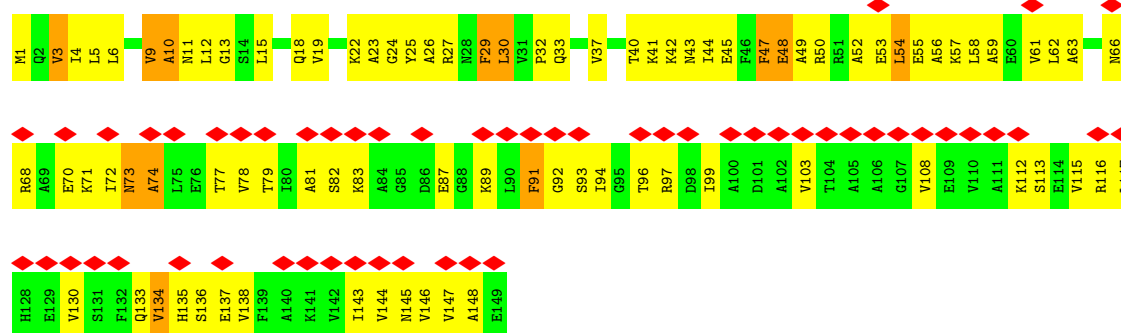
• Molecule 4: 50S ribosomal protein L5



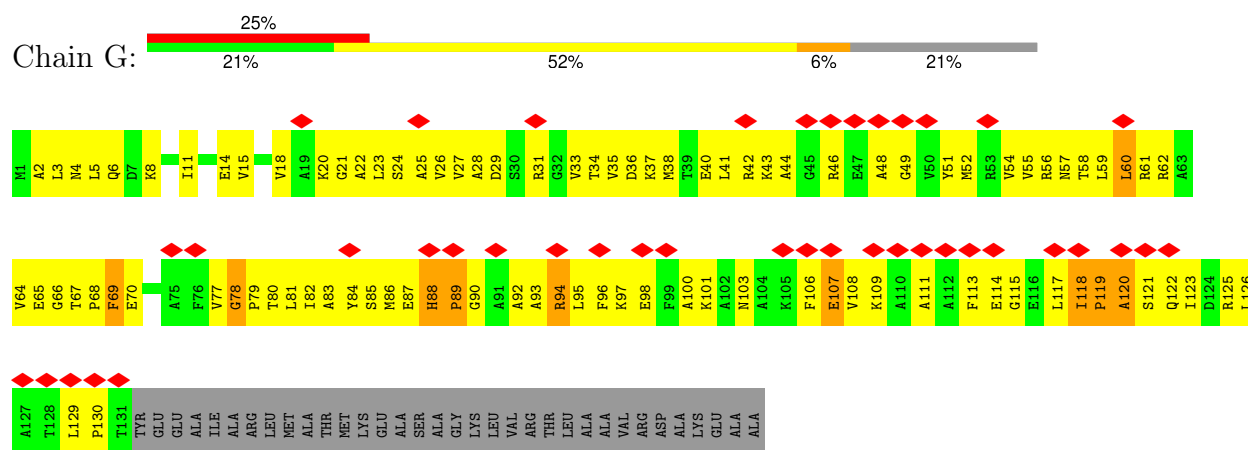
• Molecule 5: 50S ribosomal protein L6



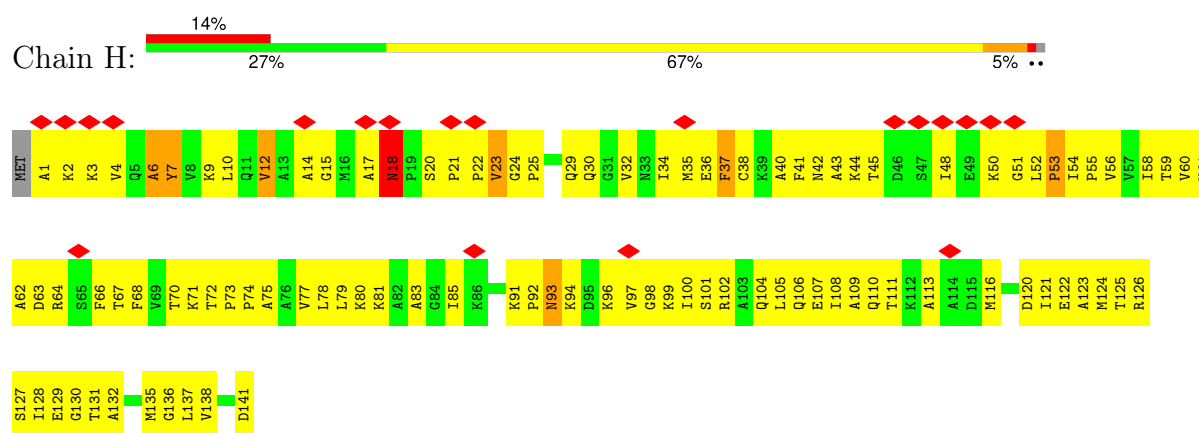
• Molecule 6: 50S ribosomal protein L9



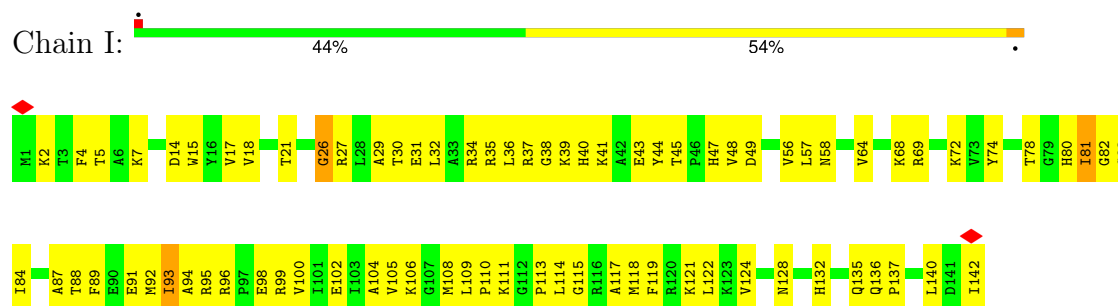
• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13

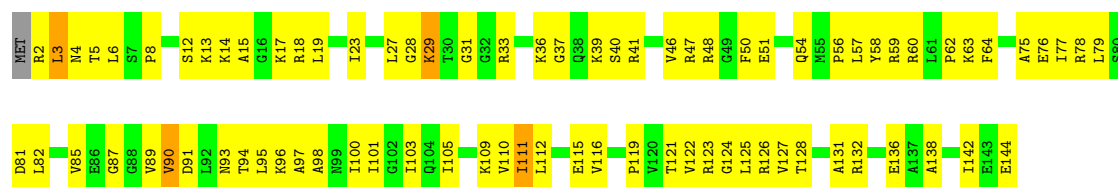


• Molecule 10: 50S ribosomal protein L14



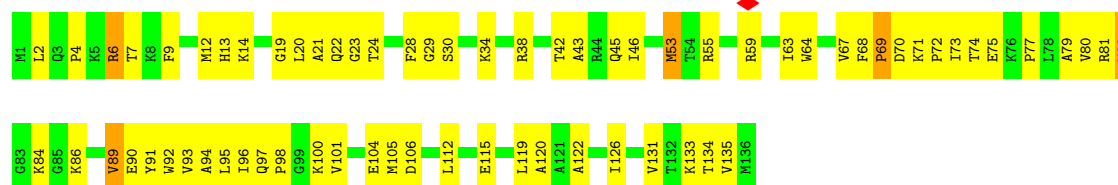
• Molecule 11: 50S ribosomal protein L15

Chain K: 



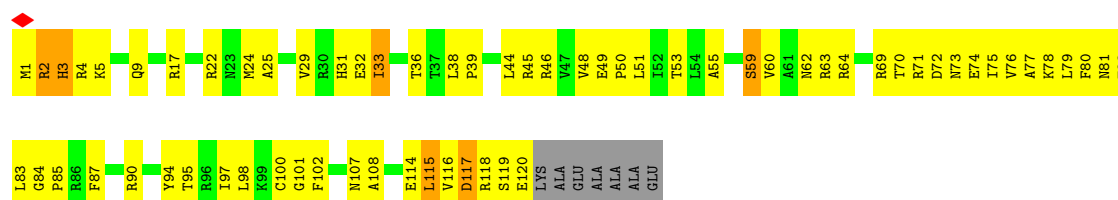
- Molecule 12: 50S ribosomal protein L16

Chain L: 



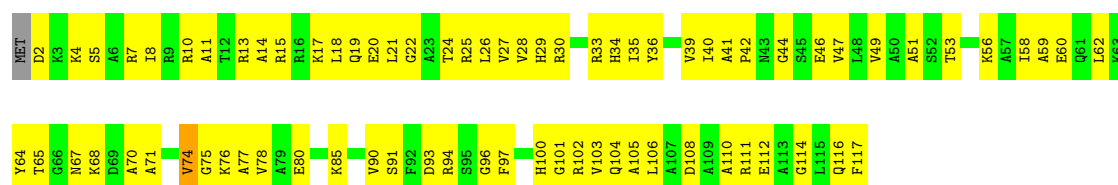
- Molecule 13: 50S ribosomal protein L17

Chain M: 



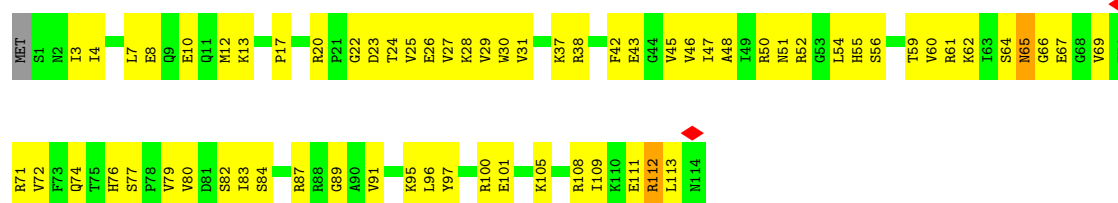
- Molecule 14: 50S ribosomal protein L18

Chain N: 

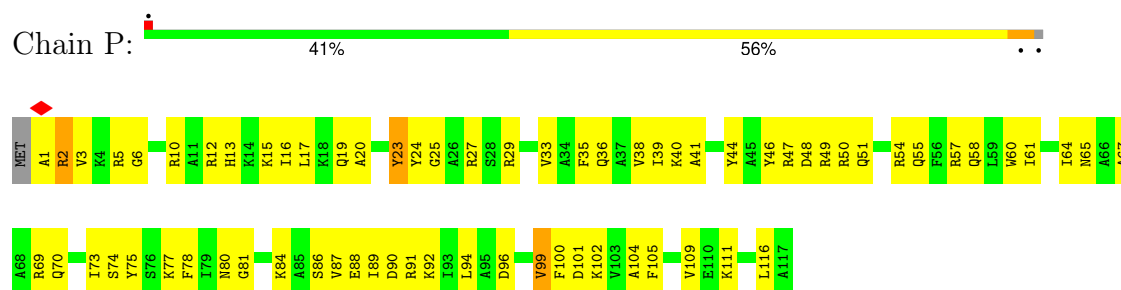


- Molecule 15: 50S ribosomal protein L19

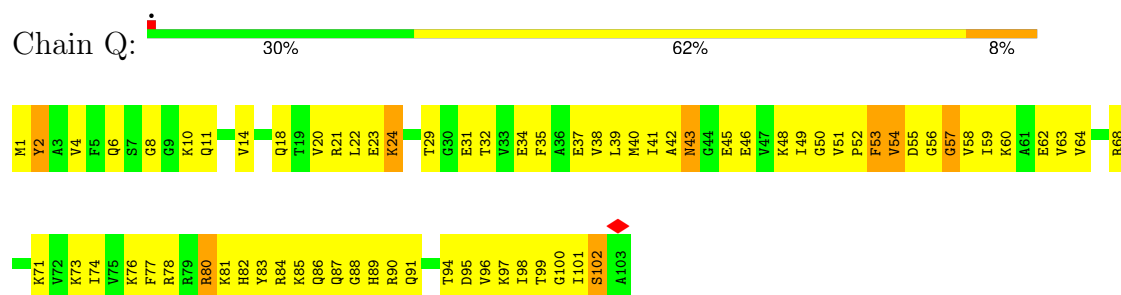
Chain O: 



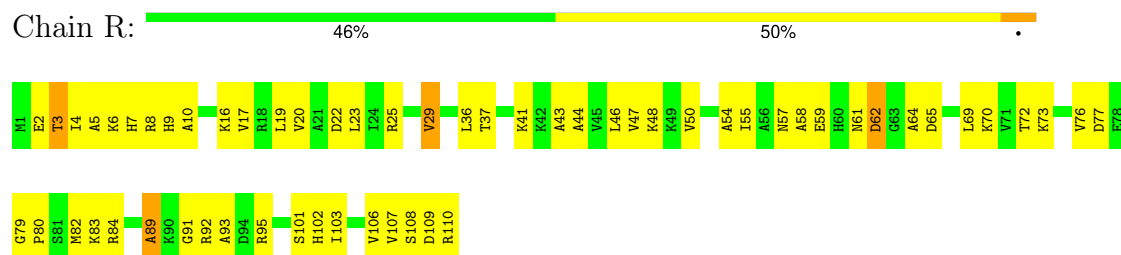
- Molecule 16: 50S ribosomal protein L20



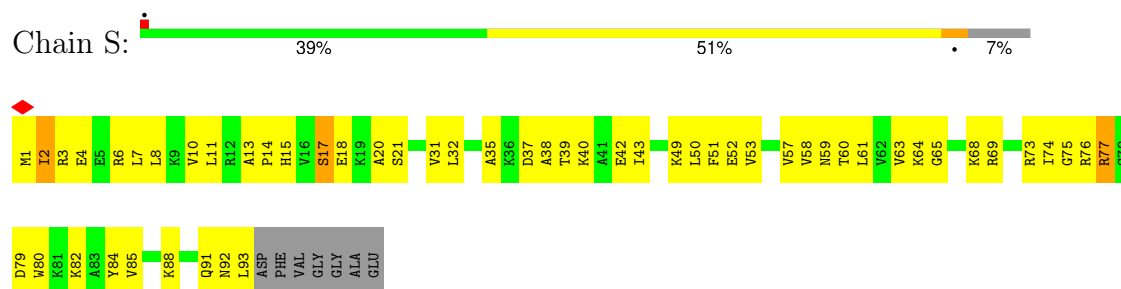
- Molecule 17: 50S ribosomal protein L21



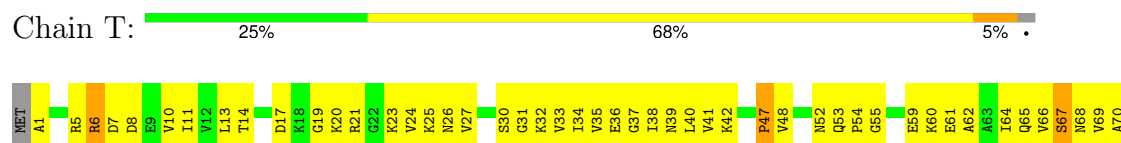
- Molecule 18: 50S ribosomal protein L22

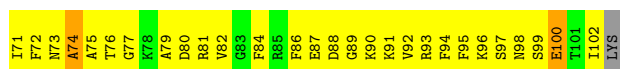


- Molecule 19: 50S ribosomal protein L23

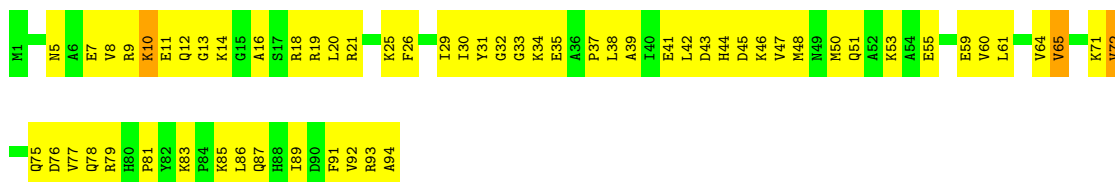


- Molecule 20: 50S ribosomal protein L24

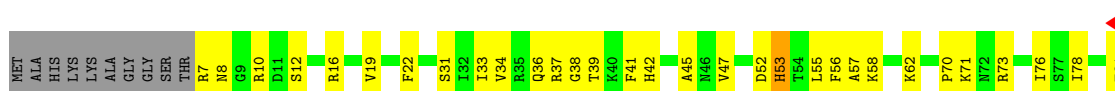




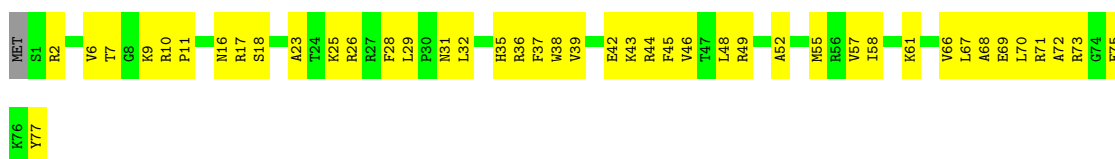
- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



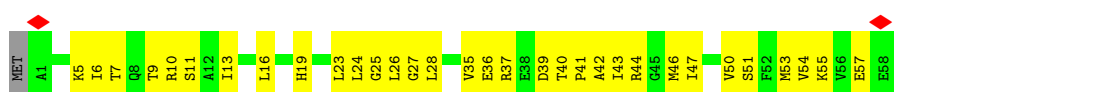
- Molecule 23: 50S ribosomal protein L28



- Molecule 24: 50S ribosomal protein L29

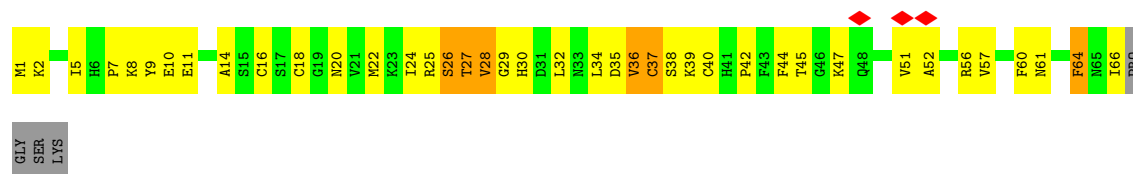


- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L31





- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



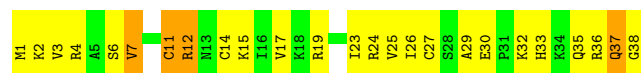
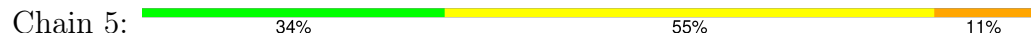
- Molecule 29: 50S ribosomal protein L34



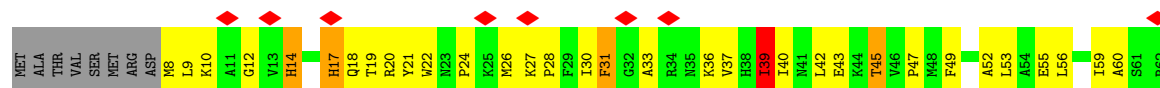
- Molecule 30: 50S ribosomal protein L35

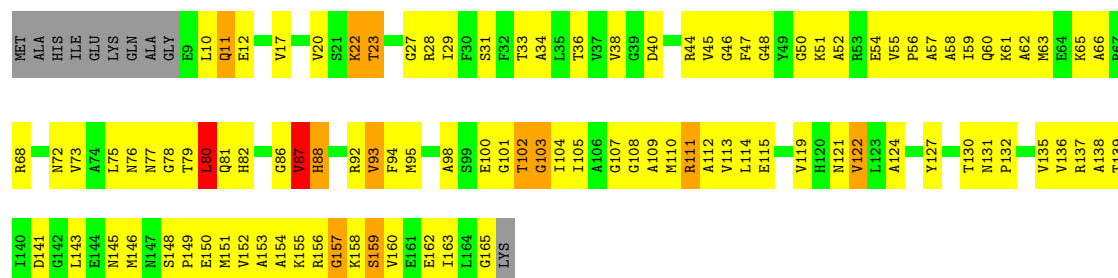


- Molecule 31: 50S ribosomal protein L36

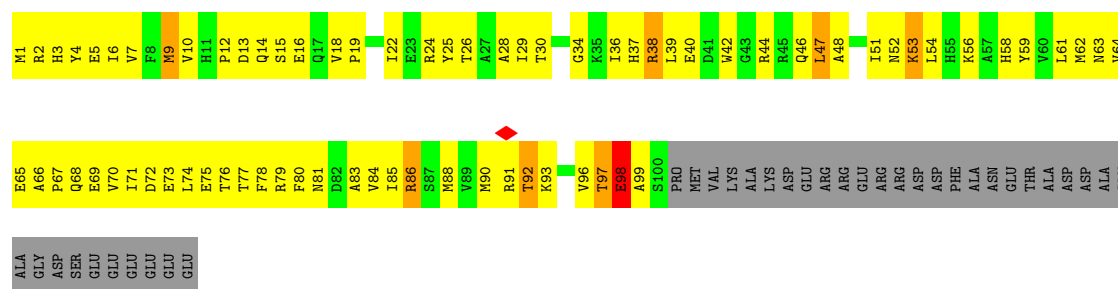
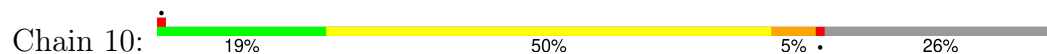


- Molecule 32: 30S ribosomal protein S2

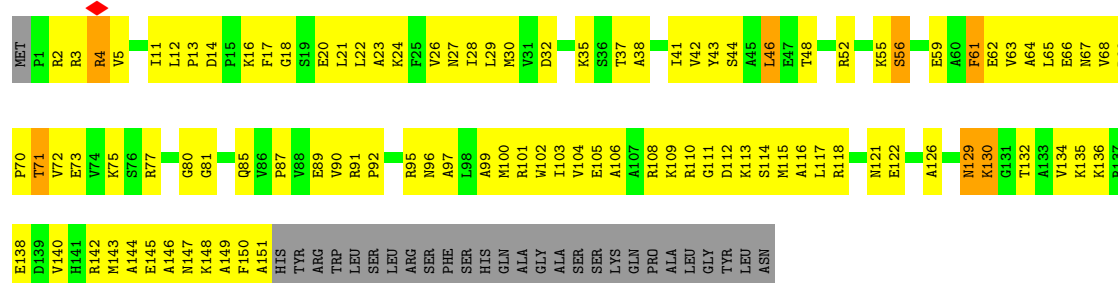




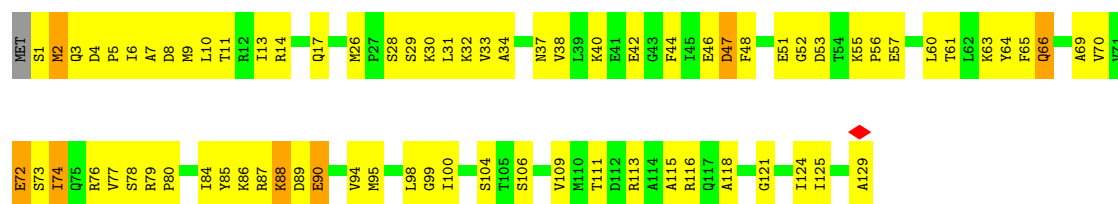
• Molecule 36: 30S ribosomal protein S6



• Molecule 37: 30S ribosomal protein S7

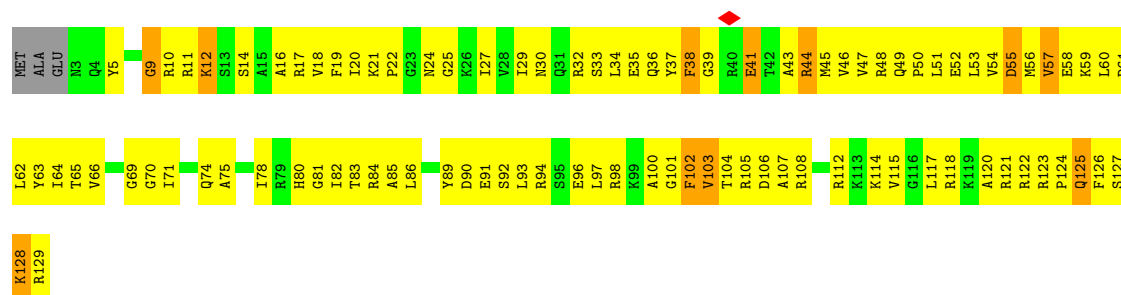


• Molecule 38: 30S ribosomal protein S8

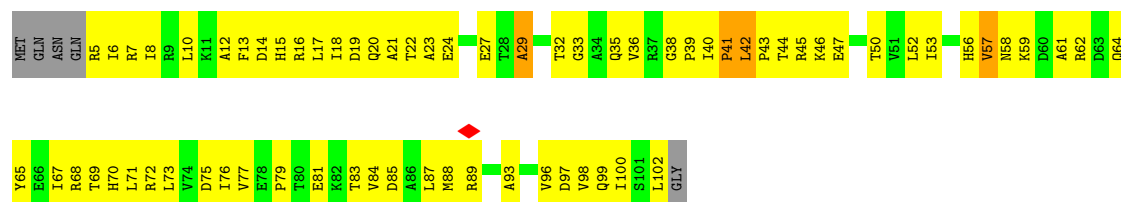


• Molecule 39: 30S ribosomal protein S9

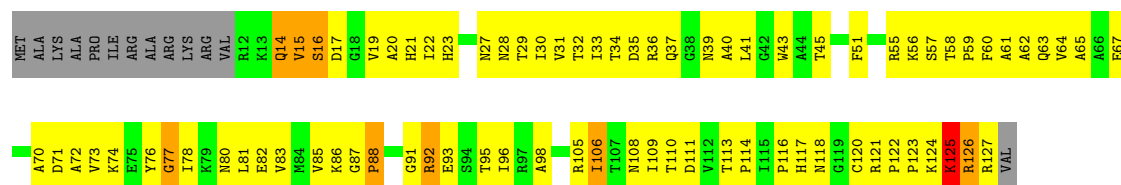




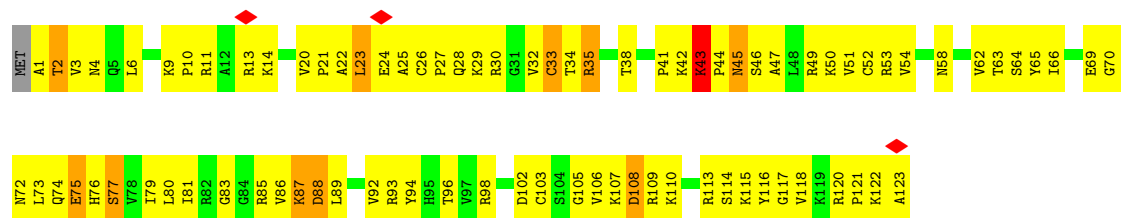
- Molecule 40: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S11

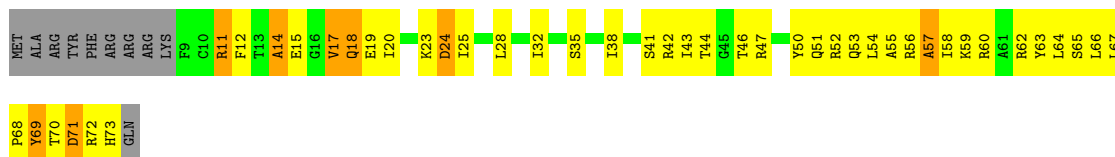


- Molecule 42: 30S ribosomal protein S12

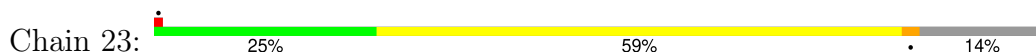


- Molecule 43: 30S ribosomal protein S13

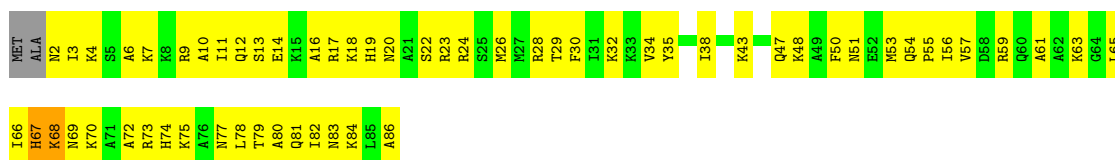




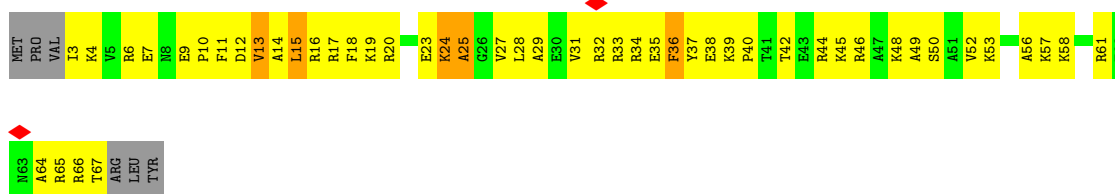
- Molecule 49: 30S ribosomal protein S19



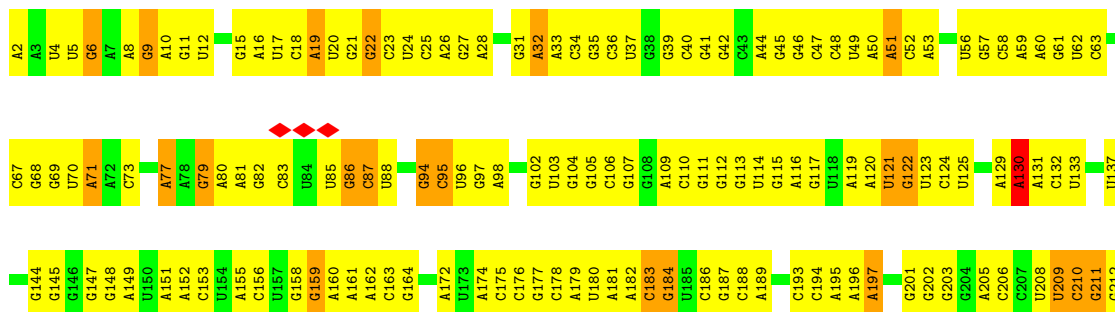
- Molecule 50: 30S ribosomal protein S20



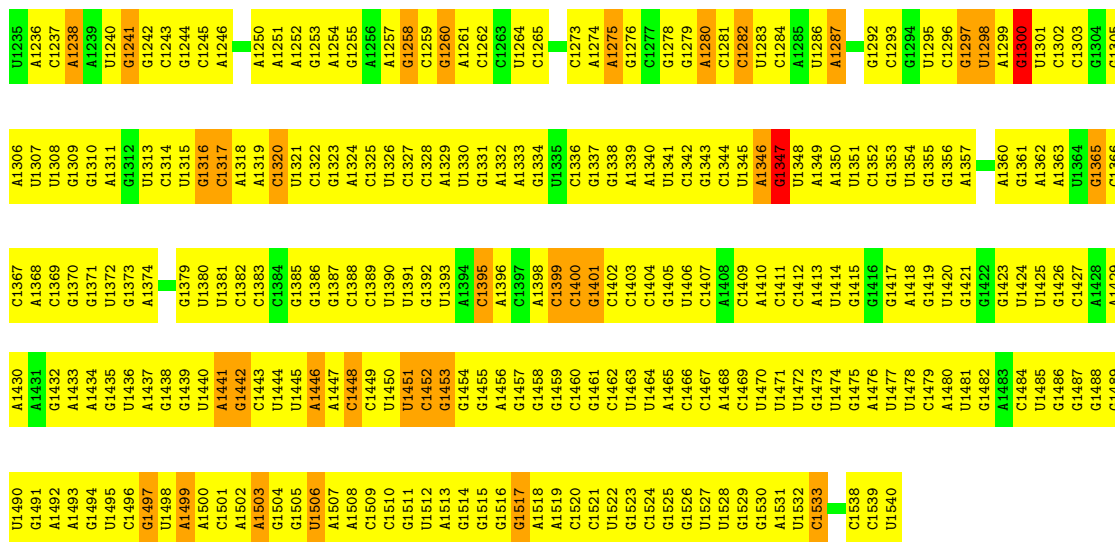
- Molecule 51: 30S ribosomal protein S21



- Molecule 52: 16S ribosomal RNA

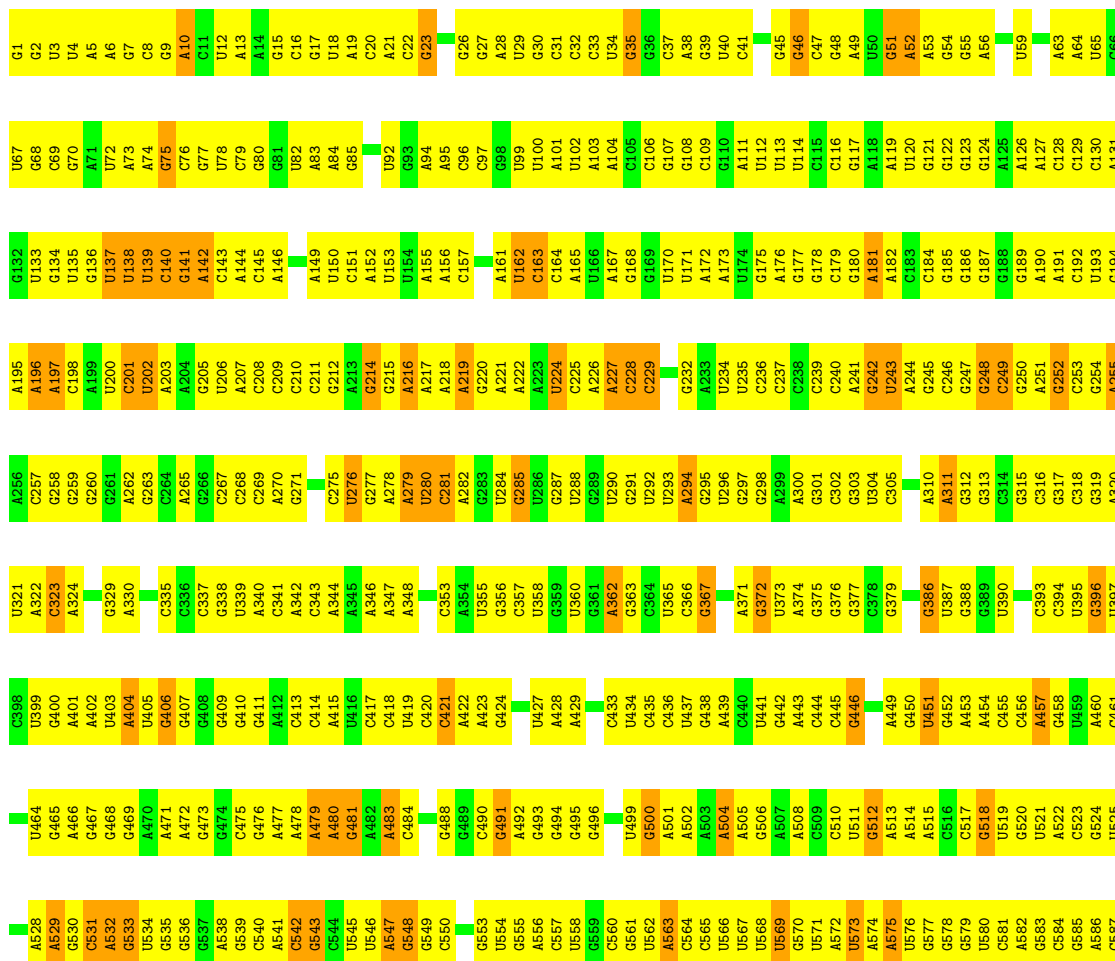


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	A1110	G1047	C980	A918	C858	A790	A728	A665	A596	A532	A468	G404	U340			C215
G1174	A1111	G1048	C981	A919	C859	G791	A729	A666	A597	A533	C469	U405	U341			U216
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	C1113	G1050		U921	C861	U793	G731	G668	U598	A535	U471	U407				U218
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G1181	U1115	U1052	C987	A923	U863	G795		G670	A600	G537	U473	U409	G346			C220
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G1184	U1118	A1055	C990	G926	C866	U798	G737	U673	G604	G540	U476	A412	C352			A288
G1185	C1119	U1056	U991	G927	C867	G799	C738	G674	G605	G541	U477	G413	A353			U224
G1186	U1120	G1057	U992	G928	C868	G800	C739	G675	G606	G542	C478	A414	G354			C225
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A1191	C1124	G1061	A996	G933	A872		C736	U679	G610	C546	G484	G418	G358			U229
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A1204	G1139	U1076	U1011	A946	C885	U820	C756	U692	U625	A498	A499	A431	C371			C307
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C1208	G1143	A1080	G1015	U950	A889	G824	G760	A696	A629	C563	A502	U435	U375			C311
C1209	U1144	A1081	A1016	G951	C890	A825	G761	U697	A630	C564	C503	G436	U376			A250
G1210	A1145	U1082		U952	U891	C826	U762	G698	C631	U565	C504	U437	G377			G251
U1211	C1146	U1083	A1019	G953	A892	U827	G763	C699	C632	G566	G505	U438	G378			U252
U1212	U1147	G1084	G1020	U955	C894	U828	C764		G633	G567	G506	U439	C379			A253
A1213	C1148	U1085		U956	C895	G829	G765	G703	C634	U508	C507	C440	G380			G254
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C1217	C1151	G1088	U1025	C959	C898	G832	A768	G706	C637	U571	A511	G445	A383			U256
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A1219	A1155	U1090	C1027	U961	A900	U835	G771	U709	A642	A574	C513	G447	C385			G258
G1220	G1156	U1091	U1028	C962	A901	G836	U772	G710	C643	G575	C514	G448	C386			G259
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G1222	U1158	G1093	U1030	A964	G903	C838		A712	G645	G577	U516	A451	G388			U323
C1223	C1159	U1094	C1031	U965	U904	C839	G776	G713	G646	C578	G517	A452	A389			G324
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A1225	C1161	C1096	G1033	A966	A906	C841	G778	A715	A648	C580		A456	G391			G264
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A1227	C1163	C1098	C970	U908	A908	U843	A780	U717	U653	G521		A458	A393			C328
C1228	U1164	G1099	G971	A909	C844	A781	G780	A718		C522		U459	G394			A329
A1229	G1165	G1100	C972	C910	A845	A782	G783	U719	U657	A523		A461	C395			U268
C1230	U1166	A1102	G1039	U911	G846	C783	G785	G721	G658	G524		A462	C396			C269
G1231	C1167	C1103	U1040	C912	G847	A784	G786	G722	U659	G525		G462	C397			A270
U1232	A1168	U975	G1041	A913	U854	G785		U723	C660	C526		U463	U398			C271
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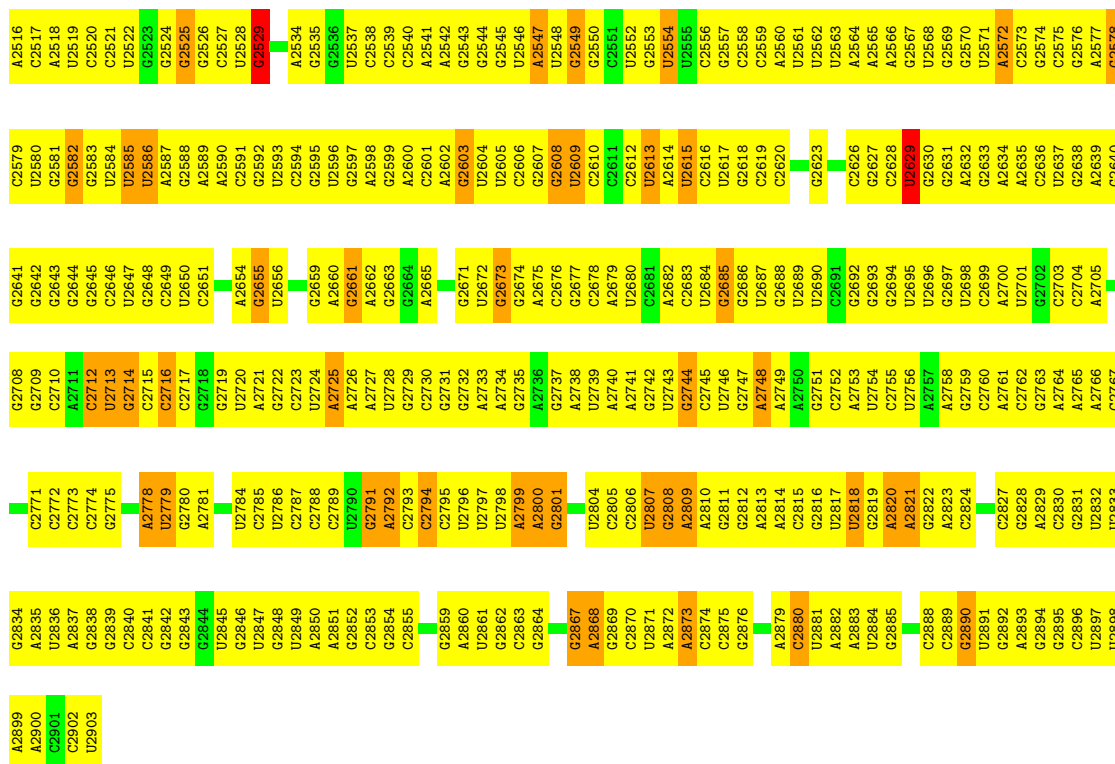
• Molecule 53: 23S ribosomal RNA

Chain 27: 19% 68% 12%



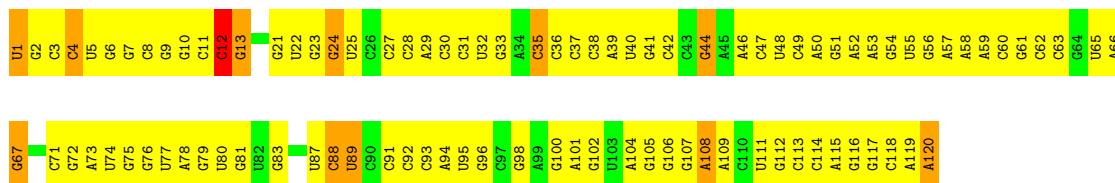
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C1498	A1367	G1295	G1301	C1045	A980	A918	U850	G786	U724	U658	A590
A1499	G1368	G1236	A1302	A1046	A981	U919	C851	C787	G725	G659	U591
G1500	G1369	A1237	G1303	G1047	A982	A920	U852	A788	G726	C660	A592
G1501	C1370	G1238	G1306	A1048	A983	G921	C853	G727	A727	A661	U593
A1502	G1371	G1239	A1307	C1049	A984	G922	C854	G728	G728	G662	U594
A1503	A1372	U1240	G1308	A1050	C985	G923	G855	A792	A730	G663	C595
A1504	A1373	A1241	A1309	G1051	A988	G924	G856	A793	G729	G664	U596
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C1507	G1376	G1244	G1311	G1054	A990	A927	G859	C796	G733	U667	A599
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G1445	A1378	G1314	C1321	A1057	C992	U930	G862	G799	C736	A670	A602
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A1452	A1387	U1255	G1128	G1063	U999	A936	U873	C806	A743	A677	A609
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G1455	U1390	G1258	G1131	U1066	C1005	G940	G875	G809	U746	C680	G612
U1520	G1391	G1259	U1132	A1067	C1006	A941	C876	U810	C747	G681	A613
U1521	A1392	A1260	A1133	G1068	C1007	G942	A877	U811	G748	G682	A614
A1522	A1395	C1261	A1134	A1069	C1008	A943	A878	C812	A749	U615	A616
U1523	G1396	A1262	C1135	A1070	A1009	U946	G879	U813	G684	G685	G617
G1524	C1398	U1263	G1136	G1071	A1010	C946	G880	C814	A752	U666	G622
A1525	G1399	A1264	G1137	C1072	A1011	A947	G881	C815	A753	C687	G623
C1526	U1400	A1265	U1138	A1073	U1012	C948	G882	C816	U754	U668	A626
G1527	G1401	G1266	G1139	G1074	C1013	G949	G883	C817	U755	C687	A627
U1468	U1402	U1267	C1140	C1075	U1014	U950	U884	A818	A756	A689	G628
A1469	A1403	A1268	U1141	C1076	U1015	C951	C885	A819	G757	G690	G629
C1531	U1340	A1269	A1142	A1077	U1015	G954	U886	A820	C758	C691	G630
A1532	G1341	C1270	A1144	U1078	U1018	U955	U887	A821	G759	A693	A631
C1533	A1342	A1271	C1145	A1080	U1019	G956	C888	G822	U760	G694	A632
U1534	G1343	A1272	U1146	U1081	A1020	G957	C889	C823	A761	G695	A633
A1535	U1344	U1273	A1147	U1082	A1021	C958	C890	U824	U762	G696	A634
C1536	G1345	C1278	U1148	U1083	G1022	U958	C891	A825	G763	G697	C635
G1537	A1346	G1279	G1149	A1084	U1023	A959	A892	U826	A764	U703	G636
U1478	A1347	G1280	C1150	A1085	G1024	A960	C893	U827	C765	G704	A637
G1479	C1348	G1281	A1151	A1086	G1025	C961	U894	U828	U766	A705	U638
C1480	U1349	U1282	C1152	G1087	G1026	G962	U895	A829	U767	G706	C640
U1481	C1350	G1283	C1153	A1088	A1027	U963	A896	G830	G768	G707	U641
A1548	G1351	A1284	G1154	A1089	A1028	C964	C897	G831	U769	U709	C645
A1549	A1419	A1285	U1217	A1090	A1029	C965	C898	U832	U770	G713	U646
C1550	U1484	A1286	A1155	A1091	G1030	G966	A899	A833	G771	U714	G647
A1551	U1485	A1287	G1156	C1092	G1031	U967	A900	G834	G772	U715	G648
A1552	G1422	G1288	G1157	C1093	A1032	C968	C901	G834	G773	G716	G649
U1553	G1423	C1289	C1158	G1094	U1033	G969	C902	U839	G774	A718	C650
U1554	G1424	C1290	U1159	A1095	G1036	U970	A909	C840	G775	C719	A654
U1555	G1425	G1291	G1160	A1096	U1037	G971	G841	G776	G776	U720	A655
U1556	A1426	C1293	C1161	U1097	G1038	A972	A911	G777	U777	A721	
U1557	U1427	U1294	G1162	U1097	C1039	A973	C912	U778	U779		
U1558	C1428	C1295	A1165	C1100	A1039	C974	C912	G843	G780		
U1559	G1429	G1296	G1166	U1101	A975	A976	U913	A844	G781		
U1560	U1430	C1297	C1167	C1102	G1041	G976	U914	A845	A782		
C1561	A1431	C1298	G1168	A1103	G1042	G977	C915	U847	A783		

C2452	C2453	C2391	C2390	U2329	U2262	A2199	U2132	A2070	A2009	G1949	A1885	U1820	C1760	U1692	C1564
A2453	C2392	C2264	C2330	G2330	C2263	C2200	C2133	A2071	C2010	G1950		A1821	C1761	U1693	C1565
C2454	C2393	C2265	G2331	G2337	C2264	C2201	A2134	C2072	U2011	U1951	G1888	C1822	U1762	C1694	A1566
C2455	C2394	C2266	C2332	U2265	U2203	C2202	C2135	C2073	G2012	A1952	G1889	G1823	C1763	C1695	C1567
C2456	C2395	C2267	C2333	C2266	G2204	C2204	U2136	U2074	A2013	A1953	A1890	G1824	C1764	G1696	G1568
C2457	C2396	C2267	U2334	U2267			U2137	U2075	A2014	G1954	G1891	U1825	U1765	C1697	A1569
C2458	C2396	C2268							A2015	U1955	C1892	G1826	C1766	A1698	A1570
C2459	C2397					C2208	G2144	C2078	U2016	U1956	C1893	U1827	C1767	C1699	A1571
U2398	C2398					C2209	C2145	U2079	U2017	C1957	C1894	G1828	C1768	A1700	C1638
A2461	C2399	U2272	C2338	U2210	C2271	C2210	C2146	A2080	G2018	C1958	C1895	U1829	C1769	A1701	A1572
C2462	C2400	A2273				C2211	A2147	U2081	A2019	C1959	C1896	C1830	C1770	A1640	C1574
C2463	C2401					C2212	C2148	C2082	A2020	G1960	G1897	G1831	C1771	G1703	C1575
C2464	U2402					C2213	U2149	C2083	C2021	C1961	U1898	C1832	A1772	C1704	U1576
C2465	C2403					C2214		C2084	U2022	C1962	A1899	C1833	A1773		
C2466	U2404					C2215	C2152	U2085	C2023	U1963	A1900		C1774	C1706	C1577
C2467	C2405					C2216	C2153	U2086	G2024	G1964	A1901	C1837	C1775	G1707	U1578
C2468	C2406					C2217	A2154	C2087	C2025	C1965	C1902	C1838	C1776	C1708	A1580
A2469	A2407					C2218	U2155	C2088	U2026	A1966	G1903	G1839	U1777	U1709	G1581
C2470	U2408					U2219	C2156	C2089	G2027	C1967	G1904	G1840	U1778	G1710	C1582
C2471	C2409					U2220	C2157	C2090	U2028	G1968	C1905	U1841	U1779	A1711	G1651
C2472	G2410					C2221	A2158	C2091	G2029	A1969	G1906	G1842	U1780	U1712	C1585
	A2411					C2222	C2159	U2092	A2030	A1970	C1907	C1843	U1781		
C2475	A2412					C2223	C2160	G2093	A2031	U1971		C1844	U1782	G1715	C1586
A2476	C2413					C2224	C2161	A2094		G1972		C1845	U1783	U1716	C1587
U2477	G2414					A2225	C2162	A2095	U2034	C1973	A1912	G1846	A1784	A1717	C1588
A2478	C2415					C2226	A2163	C2096	C2035	C1974	A1913	C1847	U1785	C1718	U1589
C2479	C2416					C2227	C2164	C2097	C2036	G1975	C1914	A1848	U1786	G1719	A1591
C2480	C2417					G2228	U2098	U2098	A2037	U1976	U1915	C1849	U1787	U1720	C1592
C2481	A2418					U2229	C2166	U2099	G2038	A1977	A1916	G1850	C1788	G1721	A1593
C2482	U2419					C2230	U2167	G2100	U2039	A1978	U1917	U1851	A1789	A1722	U1594
	C2420					U2231	C2168	A2101	G2040	U1979	A1918	U1852	C1790		
	G2421					C2232	A2169	C2102	U2041	G1980	A1919	C1853	U1791	C1728	C1595
C2485	C2422					U2233	C2170	C2103	C2043	U1981	A1920	C1854	C1792	U1729	A1596
C2486	U2423					C2234	A2171	C2104	A2043	C1982	G1921		C1793	C1730	A1597
C2488	C2424					G2235	U2172	U2105	C2044	G1983	G1922	G1857	U1794	G1731	A1598
	A2425						A2173	U2106	C2045	G1984	U1923	A1858	C1795	C1732	C1600
U2489	C2426					C2238	C2174		G2046	C1985	C1924	U1859	U1796	G1733	A1601
C2490	U2427					C2239	C2175	U2109	C2047	C1986	C1925	C1860	C1797		C1666
U2491	C2428					U2240	A2176	G2110	G2048	A1987	U1926	G1861	U1798	U1736	A1602
C2492	C2429					C2241	C2177	U2111	C2049	G1988	A1927	G1862	C1799	C1671	A1603
C2493	U2430					C2242	C2178	G2112	C2050	G1989	A1928	C1862	C1800	G1738	C1604
C2494	A2431					U2243	C2179	U2113	A2051	C1990	G1929	A1866	A1801	A1739	C1605
C2495	U2432					U2244		A2114	C2052	U1991	G1930	C1867	A1802	C1740	C1606
	A2432					U2245		C2115	C2053	G1992	U1931	C1868	A1803	C1741	C1607
C2498	C2433					G2246	A2183	G2116	A2054	C1993	A1932	G1869	C1804	U1742	A1608
C2499	U2436					C2247	C2184	A2117	C2055	U1993	G1933	C1870	A1805	G1743	A1609
U2500	C2437					U2248	U2185	U2118	C2056	U1995	C1934	A1871	C1806	A1744	A1610
C2501	U2438					C2249	C2186	A2119	G2057	C1996	G1935	A1872	C1807	U1745	C1611
C2502	C2438					U2250	U2187	G2120	A2058	C1997	A1936	C1873	U1808	A1746	C1612
A2503	U2439					G2251	U2188	G2121	C2059	C1998	A1937	G1874	A1808	U1747	G1613
C2504	C2440					C2252	U2189	U2122	A2060	C1999	U1938	C1875	A1809	U1747	C1614
U2505	U2441					C2253	C2190	C2123	G2061	C2000	A1937	G1875	C1810	C1748	A1615
C2506	C2442					C2254	A2191	G2124	C2062	C2001	U1940	A1877	U1812	U1748	A1616
C2507	U2443					G2255	U2192	C2125	C2063	C2002		G1878	C1813	G1753	C1617
C2508	C2444					U2256	C2193	A2126	C2064	A2003		C1879	G1814	C1754	A1818
C2509						C2257	U2194	C2127	C2065	U1944	U1943	U1880	C1815	A1754	G1619
	G2447					U2258	U2195	G2128	C2066	A2005	C2004	U1887	C1816	G1756	C1620
C2512	U2448					C2259	C2196	C2129	C2067	C2006	U1946	U1882	G1817	A1757	U1688
A2513	C2449					C2260	U2197	U2130	G2067	U2007	C1947	U1883	U1818	U1758	G1622
C2514	A2450					C2261	C2198	U2131	U2068	C2008	C1948	C1894	C1819	U1759	A1689
	C2451					C2262	U2199	U2132		C2009	C1949	C1894	U1815	U1760	G1623



• Molecule 54: 5S ribosomal RNA

Chain 28: 20% 70% 9%



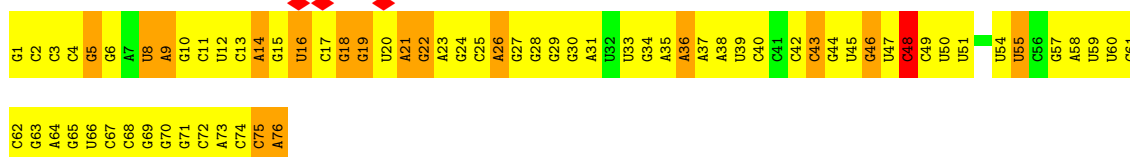
• Molecule 55: mRNA

Chain 29: 15% 25% 60% 15%



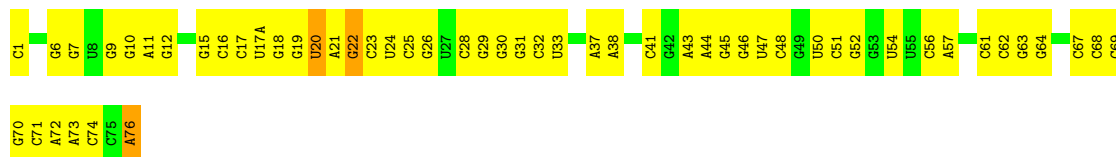
• Molecule 56: A-site tRNA^{Phe}

Chain 30: 8% 70% 21%

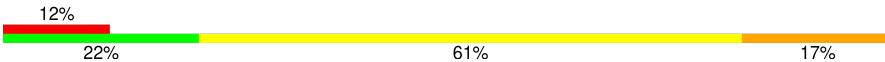


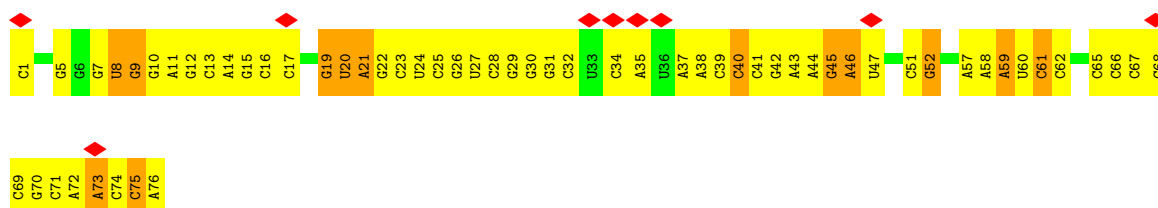
- Molecule 57: P-site tRNAfMet

Chain 31: 



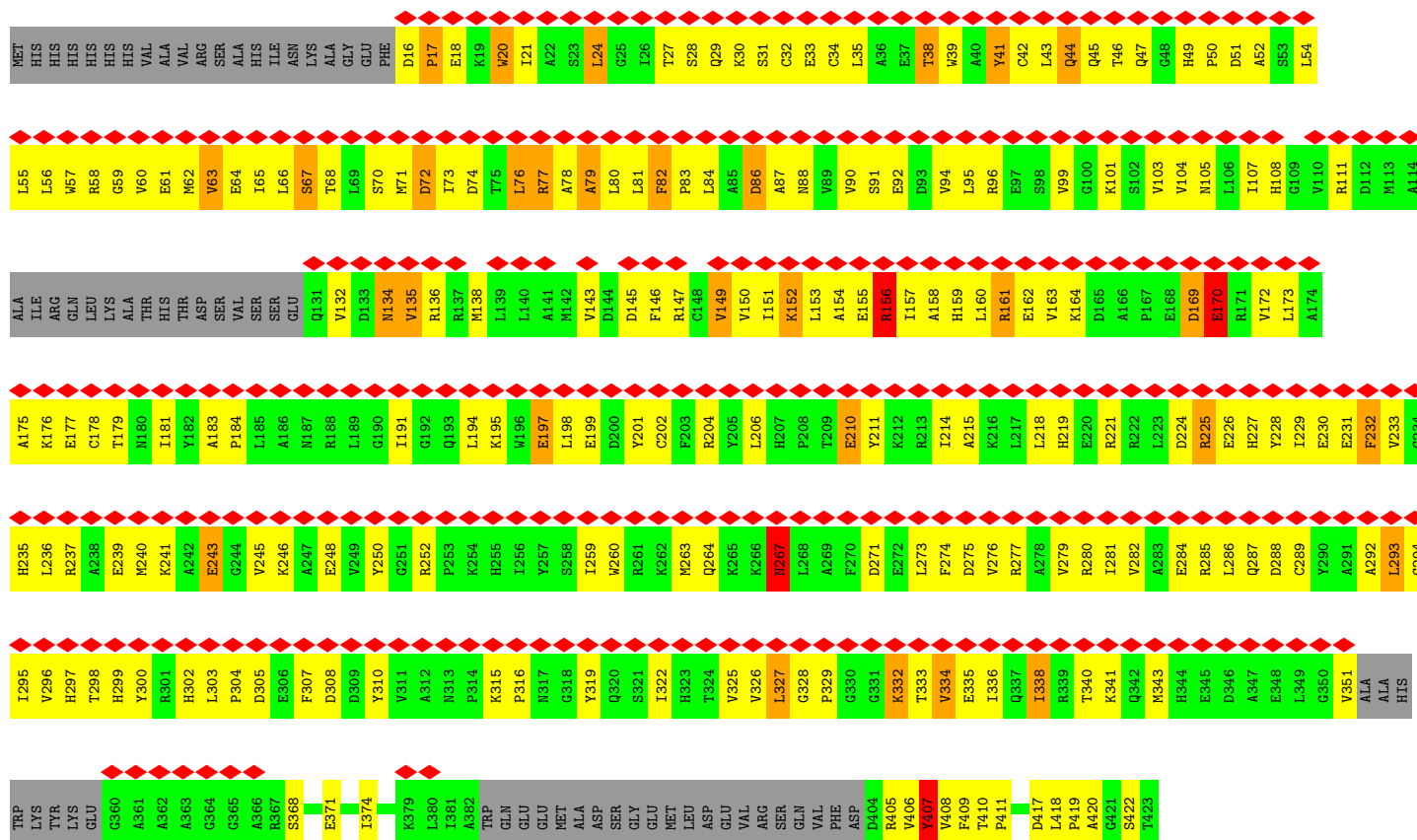
- Molecule 58: E-site tRNAfMet

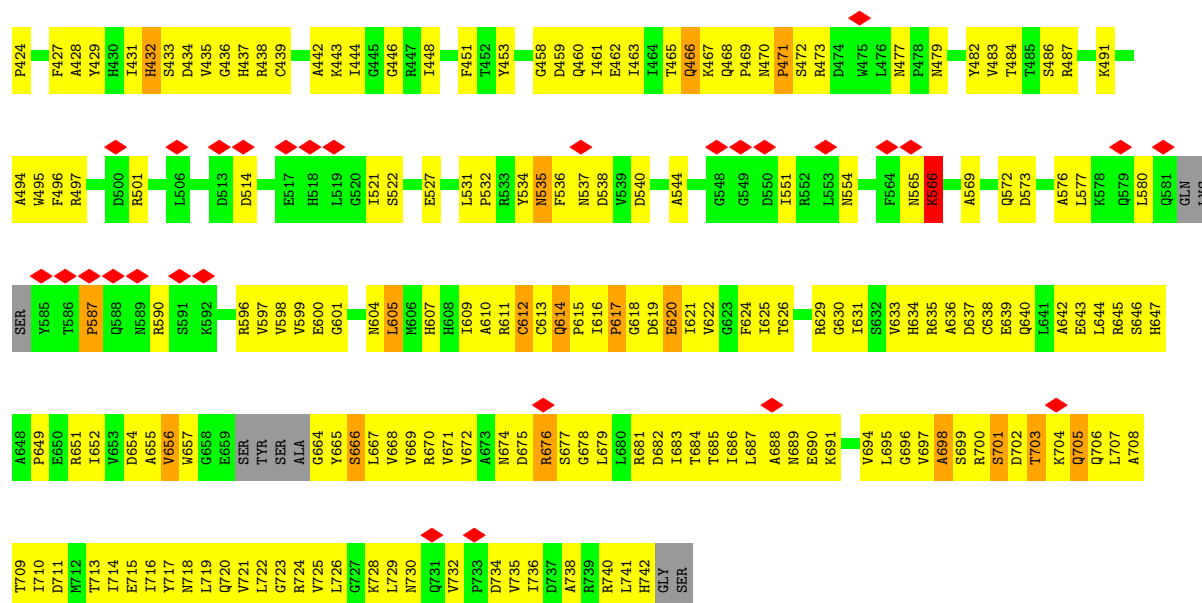
Chain 32: 



- Molecule 59: GTP pyrophosphokinase

Chain 33: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46935	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.503	Depositor
Minimum map value	-0.155	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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	0.34	0/2121	0.71	0/2852
2	B	0.37	0/1586	0.70	0/2134
3	C	0.39	0/1571	0.70	0/2113
4	D	0.35	0/1434	0.62	0/1926
5	E	0.32	0/1343	0.65	0/1816
6	F	0.40	0/1122	0.66	0/1515
7	G	0.45	0/1001	0.79	3/1350 (0.2%)
8	H	0.42	0/1046	0.79	1/1410 (0.1%)
9	I	0.33	0/1152	0.64	0/1551
10	J	0.32	0/947	0.68	0/1268
11	K	0.34	0/1054	0.71	1/1403 (0.1%)
12	L	0.36	0/1093	0.64	0/1460
13	M	0.35	0/973	0.65	1/1301 (0.1%)
14	N	0.33	0/902	0.63	0/1209
15	O	0.35	0/929	0.67	0/1242
16	P	0.38	0/960	0.60	0/1278
17	Q	0.36	0/829	0.79	1/1107 (0.1%)
18	R	0.32	0/864	0.67	0/1156
19	S	0.34	0/744	0.76	0/994
20	T	0.35	0/787	0.68	0/1051
21	U	0.35	0/766	0.66	1/1025 (0.1%)
22	V	0.39	0/582	0.68	0/769
23	W	0.34	0/635	0.65	0/848
24	X	0.32	0/510	0.62	0/677
25	Y	0.33	0/453	0.68	0/605
26	Z	0.40	0/531	0.76	0/709
27	1	0.31	0/450	0.71	0/599
28	2	0.38	0/416	0.68	0/554
29	3	0.39	0/380	0.67	0/498
30	4	0.35	0/513	0.62	0/676
31	5	0.33	0/303	0.74	0/397
32	6	0.40	0/1735	0.67	1/2338 (0.0%)
33	7	0.35	0/1651	0.64	0/2225
34	8	0.33	0/1665	0.68	2/2227 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	9	0.33	0/1169	0.67	0/1573
36	10	0.35	0/835	0.75	1/1128 (0.1%)
37	11	0.32	0/1195	0.62	0/1602
38	12	0.35	0/989	0.70	0/1326
39	13	0.35	0/1034	0.71	0/1375
40	14	0.35	0/796	0.71	1/1077 (0.1%)
41	15	0.36	0/885	0.73	1/1195 (0.1%)
42	16	0.36	0/969	0.76	1/1300 (0.1%)
43	17	0.31	0/892	0.70	0/1193
44	18	0.46	0/817	0.61	0/1088
45	19	0.32	0/722	0.58	0/964
46	20	0.37	0/659	0.71	0/884
47	21	0.35	0/657	0.72	0/881
48	22	0.38	0/544	0.62	0/731
49	23	0.36	0/652	0.72	0/877
50	24	0.33	0/671	0.55	0/888
51	25	0.41	0/550	0.73	1/728 (0.1%)
52	26	0.51	1/36967 (0.0%)	0.72	4/57666 (0.0%)
53	27	0.54	3/69801 (0.0%)	0.72	7/108894 (0.0%)
54	28	0.41	1/2876 (0.0%)	0.71	1/4483 (0.0%)
55	29	0.97	0/486	0.74	0/757
56	30	0.65	1/1813 (0.1%)	0.77	0/2823
57	31	0.44	1/1836 (0.1%)	0.70	0/2859
58	32	0.89	2/1835 (0.1%)	0.77	1/2857 (0.0%)
59	33	0.65	6/4985 (0.1%)	1.09	37/6770 (0.5%)
All	All	0.50	15/167683 (0.0%)	0.72	66/250202 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
52	26	0	13
53	27	0	34
56	30	0	1
59	33	0	3
All	All	0	51

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.66	1.19	1.33
59	33	152	LYS	CD-CE	-7.76	1.31	1.51
53	27	1379	U	O3'-P	-7.76	1.51	1.61
59	33	17	PRO	CA-CB	-7.25	1.39	1.53
52	26	2	A	OP3-P	-7.00	1.52	1.61

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.76	130.18	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.83	104.19	119.40
59	33	17	PRO	N-CA-CB	-11.16	89.90	103.30
59	33	17	PRO	CA-CB-CG	10.28	124.33	104.80
59	33	63	VAL	CG1-CB-CG2	-9.25	96.11	110.90

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	130	A	Sidechain
52	26	159	G	Sidechain
52	26	266	G	Sidechain
52	26	820	U	Sidechain
52	26	88	U	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	2082	0	2157	183	0
2	B	1565	0	1616	121	0
3	C	1552	0	1619	137	0
4	D	1410	0	1447	150	0
5	E	1323	0	1374	88	0
6	F	1111	0	1148	83	0
7	G	988	0	1025	124	0
8	H	1032	0	1088	136	0
9	I	1129	0	1162	89	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	90	0
11	K	1045	0	1117	89	0
12	L	1074	0	1157	70	0
13	M	960	0	1000	75	0
14	N	892	0	923	73	0
15	O	917	0	965	78	0
16	P	947	0	1022	94	0
17	Q	816	0	839	90	0
18	R	857	0	922	52	0
19	S	738	0	807	55	0
20	T	779	0	834	79	0
21	U	753	0	780	71	0
22	V	575	0	592	29	0
23	W	625	0	655	45	0
24	X	509	0	543	60	0
25	Y	449	0	491	41	0
26	Z	522	0	521	52	0
27	1	444	0	461	52	0
28	2	409	0	440	20	0
29	3	377	0	418	33	0
30	4	504	0	574	33	0
31	5	302	0	343	30	0
32	6	1704	0	1732	124	0
33	7	1624	0	1699	111	0
34	8	1643	0	1710	168	0
35	9	1156	0	1199	110	0
36	10	817	0	808	98	0
37	11	1181	0	1240	97	0
38	12	979	0	1034	84	0
39	13	1022	0	1070	130	0
40	14	786	0	828	92	0
41	15	869	0	878	89	0
42	16	955	0	1019	118	0
43	17	883	0	944	97	0
44	18	805	0	847	95	0
45	19	714	0	737	54	0
46	20	649	0	666	87	0
47	21	648	0	691	52	0
48	22	535	0	552	54	0
49	23	637	0	665	71	0
50	24	665	0	714	67	0
51	25	544	0	579	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	1573	0
53	27	62322	0	31345	2882	0
54	28	2572	0	1302	116	0
55	29	432	0	218	14	0
56	30	1623	0	821	75	0
57	31	1644	0	836	46	0
58	32	1643	0	836	66	0
59	33	4911	0	4550	655	0
All	All	154603	0	105189	8829	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 34.

The worst 5 of 8829 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)
53:27:45:G:H5''	53:27:46:G:H5'	1.22	1.18
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.17
7:G:55:VAL:HA	53:27:1084:A:H5'	1.26	1.15
53:27:1702:G:H2'	53:27:1703:G:H5''	1.15	1.14
59:33:24:LEU:HD21	59:33:70:SER:HA	1.19	1.12

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	269/273 (98%)	218 (81%)	41 (15%)	10 (4%)	2	23
2	B	207/209 (99%)	172 (83%)	28 (14%)	7 (3%)	3	24
3	C	199/201 (99%)	147 (74%)	32 (16%)	20 (10%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	27 (15%)	5 (3%)	3	27
5	E	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	3	27
6	F	147/149 (99%)	108 (74%)	20 (14%)	19 (13%)	0	4
7	G	129/165 (78%)	93 (72%)	25 (19%)	11 (8%)	0	10
8	H	139/142 (98%)	104 (75%)	25 (18%)	10 (7%)	1	13
9	I	140/142 (99%)	120 (86%)	14 (10%)	6 (4%)	2	21
10	J	120/123 (98%)	97 (81%)	16 (13%)	7 (6%)	1	17
11	K	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	12
12	L	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	2	20
13	M	118/127 (93%)	91 (77%)	22 (19%)	5 (4%)	2	21
14	N	114/117 (97%)	98 (86%)	15 (13%)	1 (1%)	14	50
15	O	112/115 (97%)	93 (83%)	15 (13%)	4 (4%)	3	23
16	P	115/118 (98%)	103 (90%)	7 (6%)	5 (4%)	2	21
17	Q	101/103 (98%)	77 (76%)	16 (16%)	8 (8%)	1	12
18	R	108/110 (98%)	87 (81%)	15 (14%)	6 (6%)	1	17
19	S	91/100 (91%)	71 (78%)	16 (18%)	4 (4%)	2	20
20	T	100/104 (96%)	79 (79%)	14 (14%)	7 (7%)	1	13
21	U	92/94 (98%)	76 (83%)	11 (12%)	5 (5%)	1	18
22	V	73/85 (86%)	65 (89%)	7 (10%)	1 (1%)	9	40
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	4	28
24	X	61/63 (97%)	49 (80%)	7 (12%)	5 (8%)	1	11
25	Y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
26	Z	64/70 (91%)	47 (73%)	7 (11%)	10 (16%)	0	3
27	1	54/57 (95%)	43 (80%)	6 (11%)	5 (9%)	0	10
28	2	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
29	3	44/46 (96%)	32 (73%)	11 (25%)	1 (2%)	5	31
30	4	62/65 (95%)	51 (82%)	8 (13%)	3 (5%)	2	19
31	5	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	3
32	6	216/241 (90%)	170 (79%)	32 (15%)	14 (6%)	1	15
33	7	204/233 (88%)	175 (86%)	22 (11%)	7 (3%)	3	24
34	8	203/206 (98%)	157 (77%)	30 (15%)	16 (8%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	109 (70%)	33 (21%)	13 (8%)	0	10
36	10	98/135 (73%)	77 (79%)	14 (14%)	7 (7%)	1	13
37	11	149/179 (83%)	123 (83%)	14 (9%)	12 (8%)	1	11
38	12	127/130 (98%)	110 (87%)	8 (6%)	9 (7%)	1	13
39	13	125/130 (96%)	93 (74%)	19 (15%)	13 (10%)	0	7
40	14	96/103 (93%)	76 (79%)	15 (16%)	5 (5%)	1	18
41	15	114/129 (88%)	90 (79%)	13 (11%)	11 (10%)	0	9
42	16	121/124 (98%)	95 (78%)	13 (11%)	13 (11%)	0	6
43	17	112/118 (95%)	88 (79%)	14 (12%)	10 (9%)	0	10
44	18	98/101 (97%)	72 (74%)	21 (21%)	5 (5%)	1	18
45	19	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	1	17
46	20	80/82 (98%)	59 (74%)	18 (22%)	3 (4%)	2	22
47	21	78/84 (93%)	54 (69%)	19 (24%)	5 (6%)	1	15
48	22	63/75 (84%)	50 (79%)	5 (8%)	8 (13%)	0	4
49	23	77/92 (84%)	64 (83%)	11 (14%)	2 (3%)	4	29
50	24	83/87 (95%)	75 (90%)	6 (7%)	2 (2%)	5	30
51	25	63/71 (89%)	40 (64%)	19 (30%)	4 (6%)	1	16
59	33	663/750 (88%)	557 (84%)	60 (9%)	46 (7%)	1	14
All	All	6509/6970 (93%)	5226 (80%)	879 (14%)	404 (6%)	2	16

5 of 404 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	86	GLU
2	B	102	ALA
3	C	6	LYS
3	C	11	ALA
3	C	57	LYS

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	216/218 (99%)	215 (100%)	1 (0%)	86	90
2	B	164/164 (100%)	164 (100%)	0	100	100
3	C	165/165 (100%)	165 (100%)	0	100	100
4	D	148/150 (99%)	146 (99%)	2 (1%)	62	76
5	E	137/138 (99%)	137 (100%)	0	100	100
6	F	114/114 (100%)	114 (100%)	0	100	100
7	G	100/123 (81%)	100 (100%)	0	100	100
8	H	109/110 (99%)	107 (98%)	2 (2%)	54	71
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	102 (99%)	1 (1%)	73	81
11	K	102/103 (99%)	102 (100%)	0	100	100
12	L	109/109 (100%)	109 (100%)	0	100	100
13	M	100/103 (97%)	99 (99%)	1 (1%)	73	81
14	N	86/87 (99%)	86 (100%)	0	100	100
15	O	99/100 (99%)	99 (100%)	0	100	100
16	P	89/90 (99%)	89 (100%)	0	100	100
17	Q	84/84 (100%)	83 (99%)	1 (1%)	67	79
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	80 (100%)	0	100	100
20	T	83/85 (98%)	82 (99%)	1 (1%)	67	79
21	U	78/78 (100%)	78 (100%)	0	100	100
22	V	57/63 (90%)	57 (100%)	0	100	100
23	W	67/68 (98%)	67 (100%)	0	100	100
24	X	55/55 (100%)	55 (100%)	0	100	100
25	Y	48/49 (98%)	48 (100%)	0	100	100
26	Z	59/62 (95%)	58 (98%)	1 (2%)	56	72
27	1	47/48 (98%)	47 (100%)	0	100	100
28	2	45/49 (92%)	45 (100%)	0	100	100
29	3	38/38 (100%)	38 (100%)	0	100	100
30	4	51/52 (98%)	50 (98%)	1 (2%)	50	68
31	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	178 (99%)	2 (1%)	70	80
33	7	170/190 (90%)	169 (99%)	1 (1%)	84	88
34	8	172/173 (99%)	172 (100%)	0	100	100
35	9	119/126 (94%)	117 (98%)	2 (2%)	56	72
36	10	87/116 (75%)	85 (98%)	2 (2%)	45	64
37	11	124/147 (84%)	123 (99%)	1 (1%)	79	84
38	12	104/105 (99%)	103 (99%)	1 (1%)	73	81
39	13	105/107 (98%)	104 (99%)	1 (1%)	73	81
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	89 (100%)	0	100	100
42	16	103/104 (99%)	103 (100%)	0	100	100
43	17	92/96 (96%)	92 (100%)	0	100	100
44	18	83/84 (99%)	80 (96%)	3 (4%)	30	53
45	19	76/77 (99%)	75 (99%)	1 (1%)	65	77
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	73 (99%)	1 (1%)	62	76
48	22	56/65 (86%)	55 (98%)	1 (2%)	54	71
49	23	70/79 (89%)	70 (100%)	0	100	100
50	24	65/66 (98%)	65 (100%)	0	100	100
51	25	55/61 (90%)	54 (98%)	1 (2%)	54	71
59	33	452/635 (71%)	449 (99%)	3 (1%)	81	86
All	All	5303/5698 (93%)	5272 (99%)	31 (1%)	82	88

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	9	80	LEU
51	25	36	PHE
36	10	47	LEU
59	33	338	ILE
45	19	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
50	24	47	GLN
59	33	88	ASN
16	P	58	GLN
16	P	55	GLN
59	33	264	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	205 (13%)	9 (0%)
53	27	2902/2903 (99%)	447 (15%)	24 (0%)
54	28	119/120 (99%)	14 (11%)	1 (0%)
55	29	19/20 (95%)	5 (26%)	1 (5%)
56	30	75/76 (98%)	19 (25%)	0
57	31	76/77 (98%)	8 (10%)	0
58	32	76/77 (98%)	19 (25%)	1 (1%)
All	All	4805/4812 (99%)	717 (14%)	36 (0%)

5 of 717 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	4	U
52	26	6	G
52	26	9	G
52	26	19	A
52	26	22	G

5 of 36 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	2406	A
58	32	20	U
53	27	2655	G
53	27	2867	G
53	27	490	C

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 [i](#)

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](#)

There are no chain breaks in this entry.

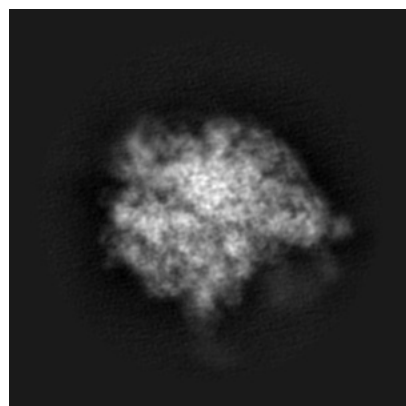
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8280. These allow visual inspection of the internal detail of the map and identification of artifacts.

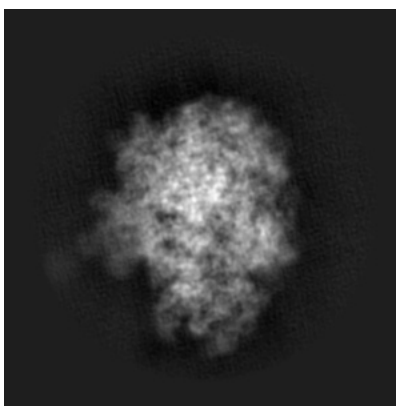
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

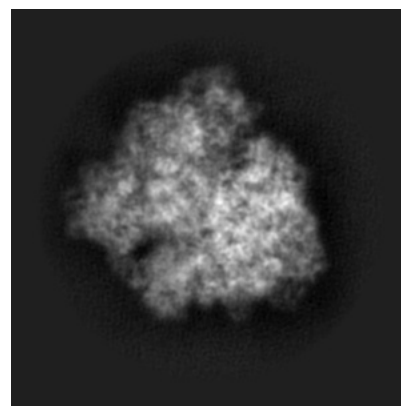
6.1.1 Primary map



X

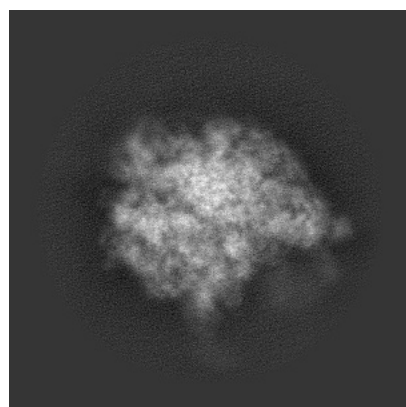


Y

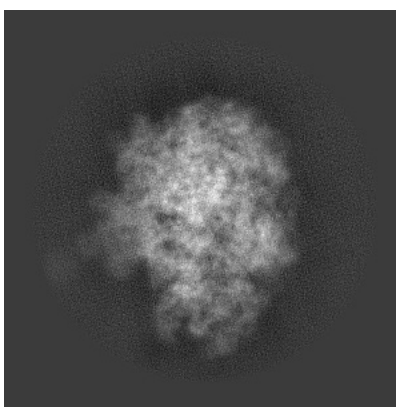


Z

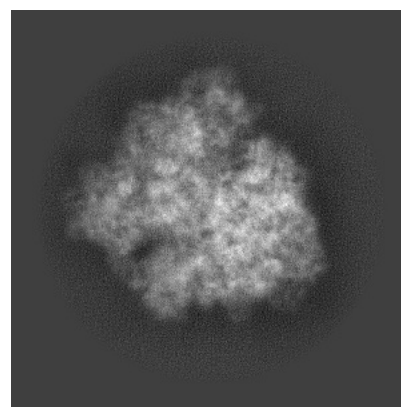
6.1.2 Raw map



X



Y

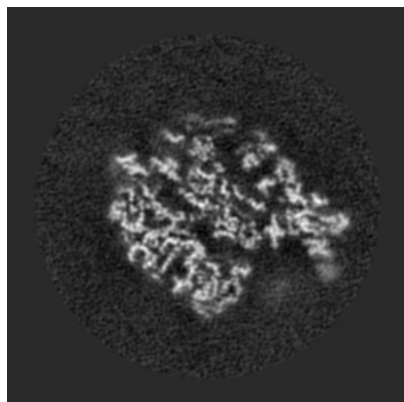


Z

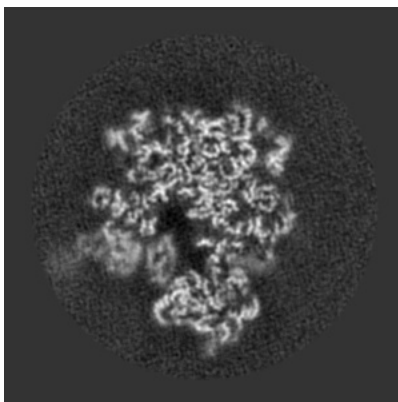
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

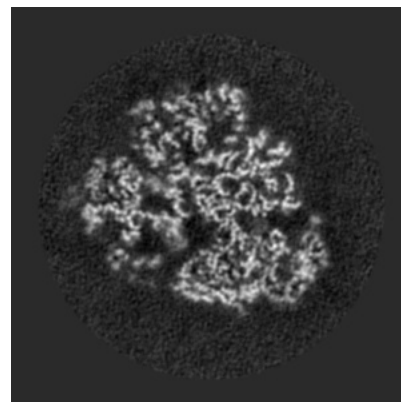
6.2.1 Primary map



X Index: 240

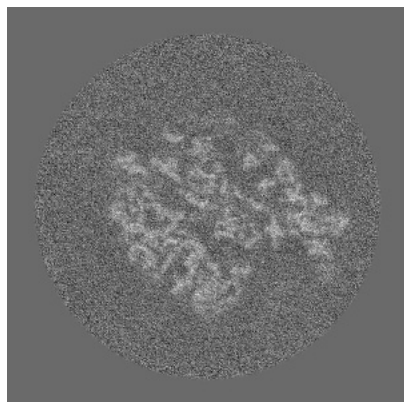


Y Index: 240

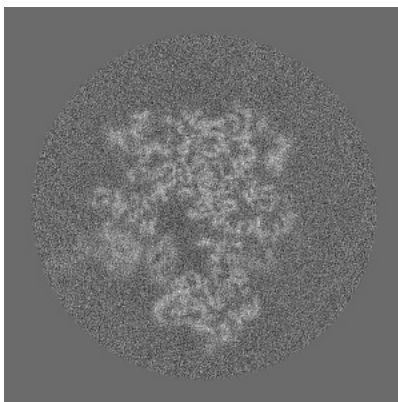


Z Index: 240

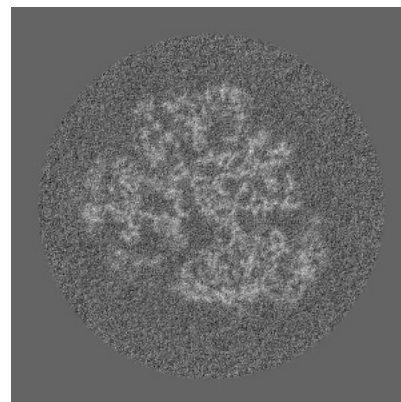
6.2.2 Raw map



X Index: 240



Y Index: 240

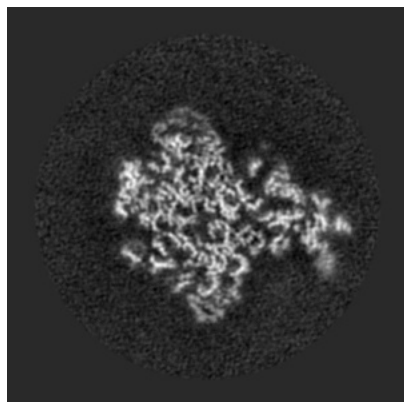


Z Index: 240

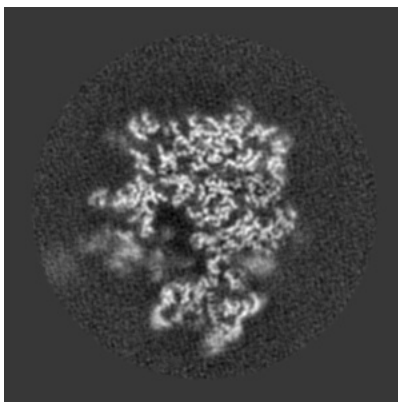
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

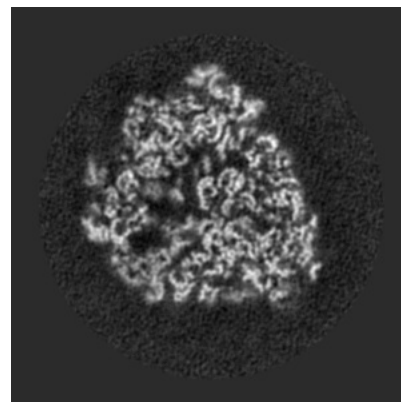
6.3.1 Primary map



X Index: 250

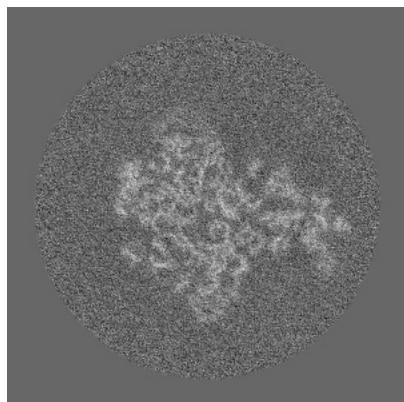


Y Index: 247

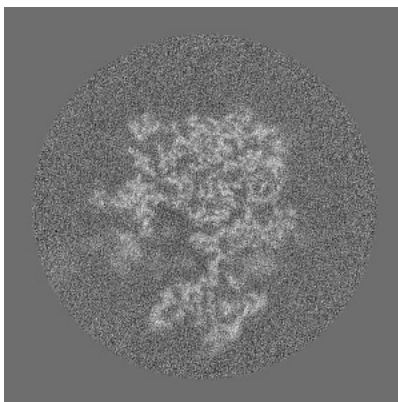


Z Index: 226

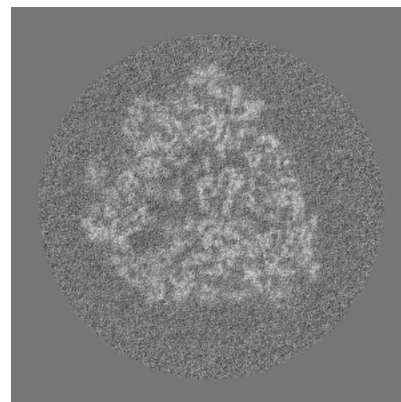
6.3.2 Raw map



X Index: 250



Y Index: 249

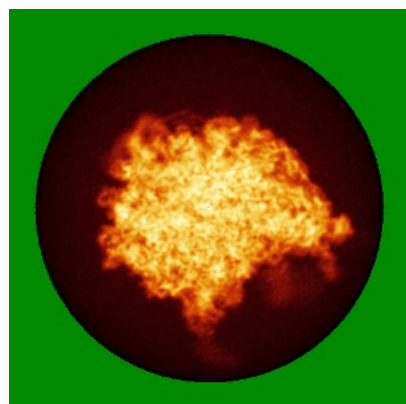


Z Index: 226

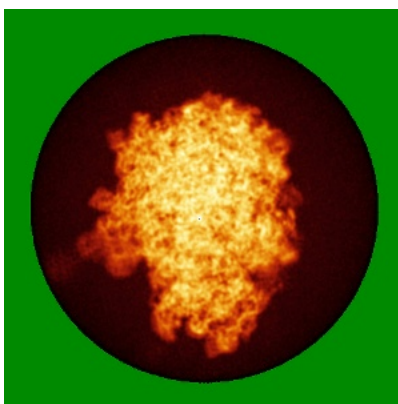
The images above show the largest variance slices of the map in three orthogonal directions.

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

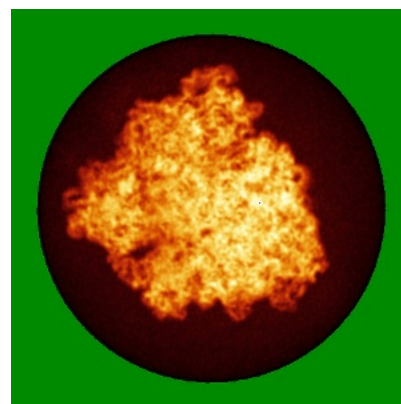
6.4.1 Primary map



X

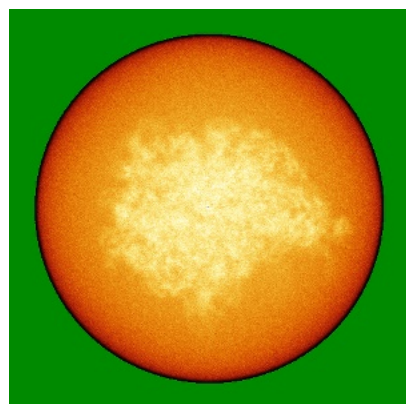


Y

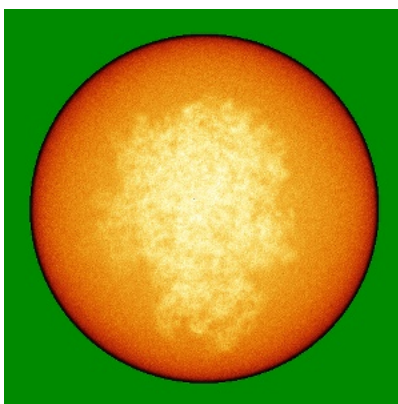


Z

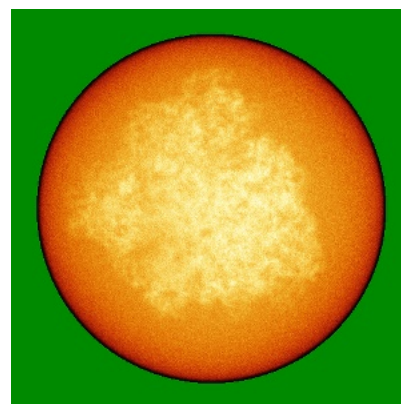
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

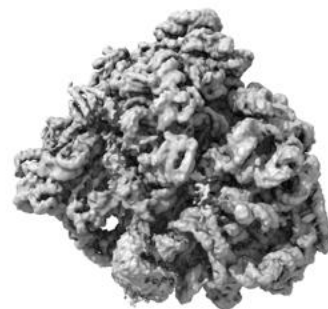
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

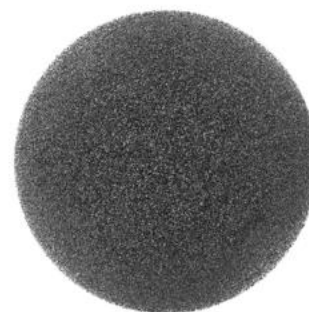
6.5.2 Raw map



X



Y



Z

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

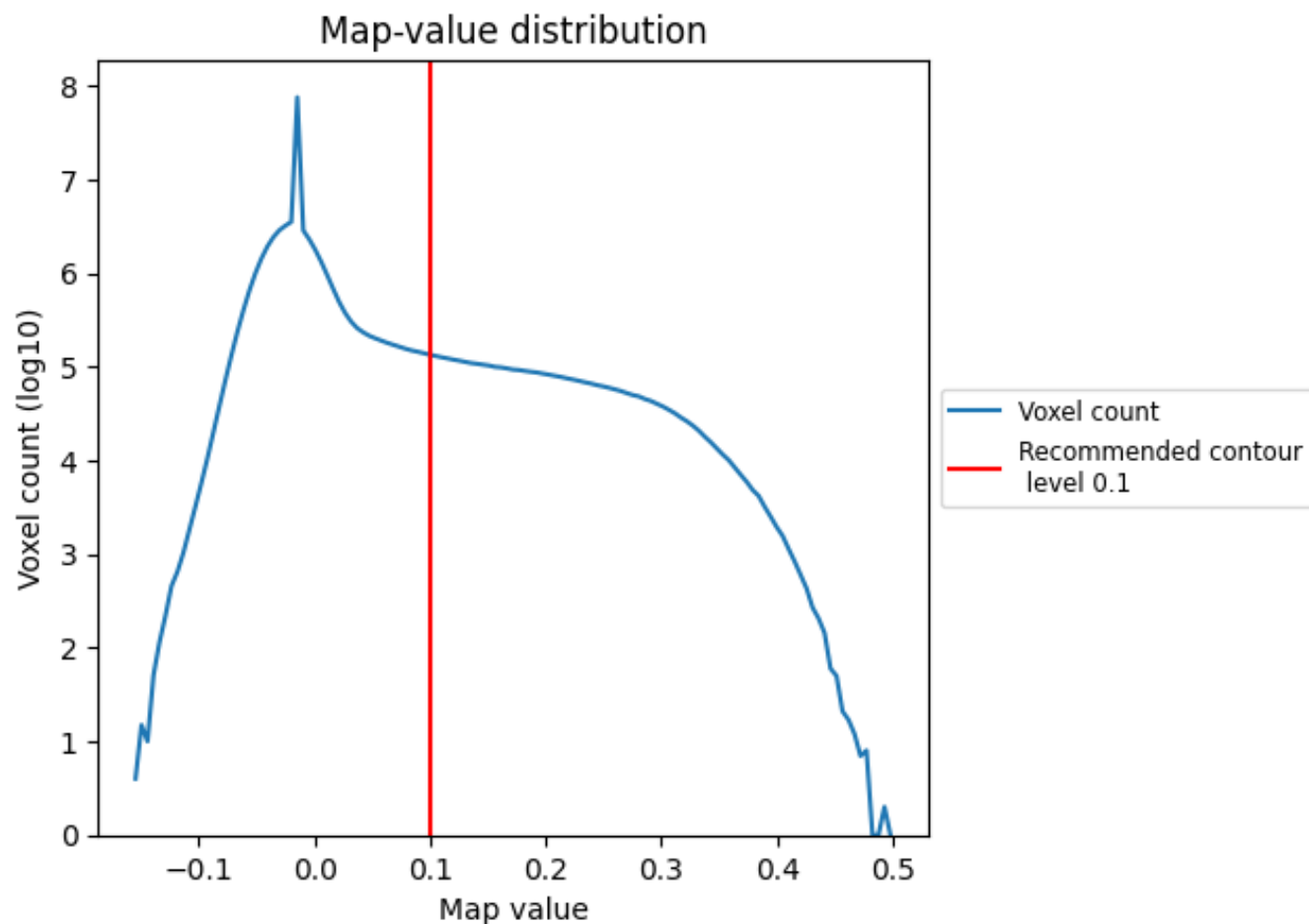
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

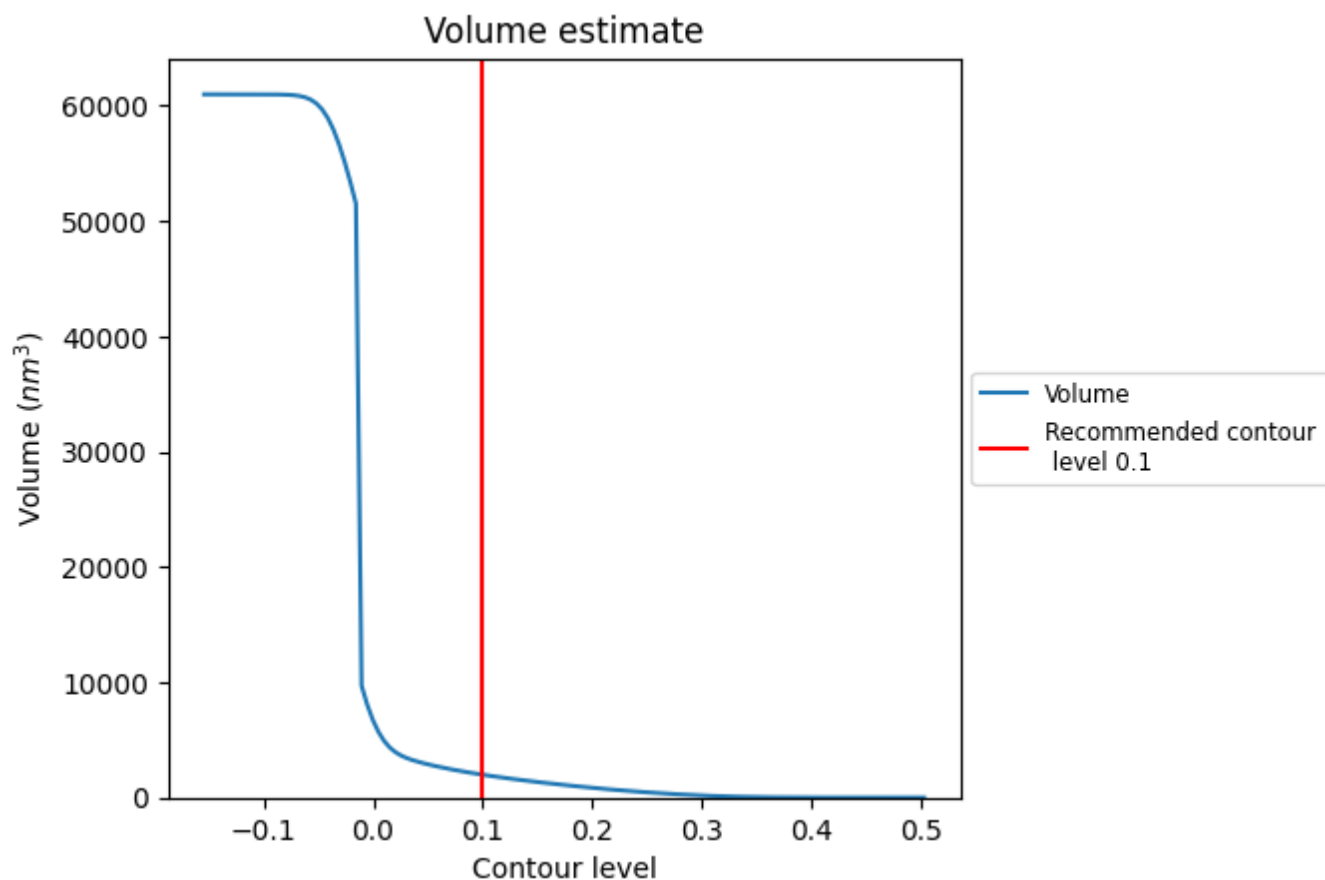
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

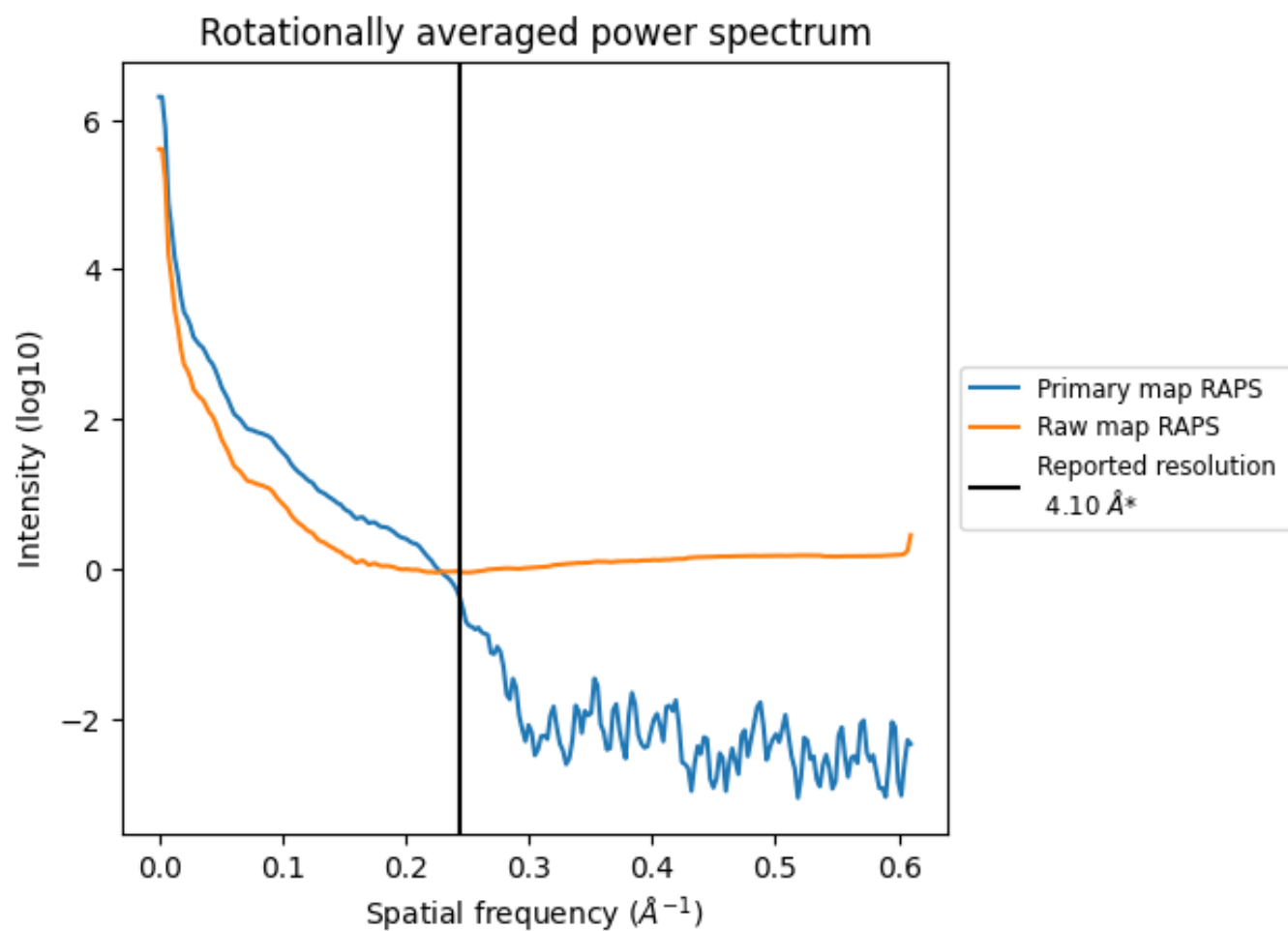
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1983 nm³; this corresponds to an approximate mass of 1791 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 ⓘ

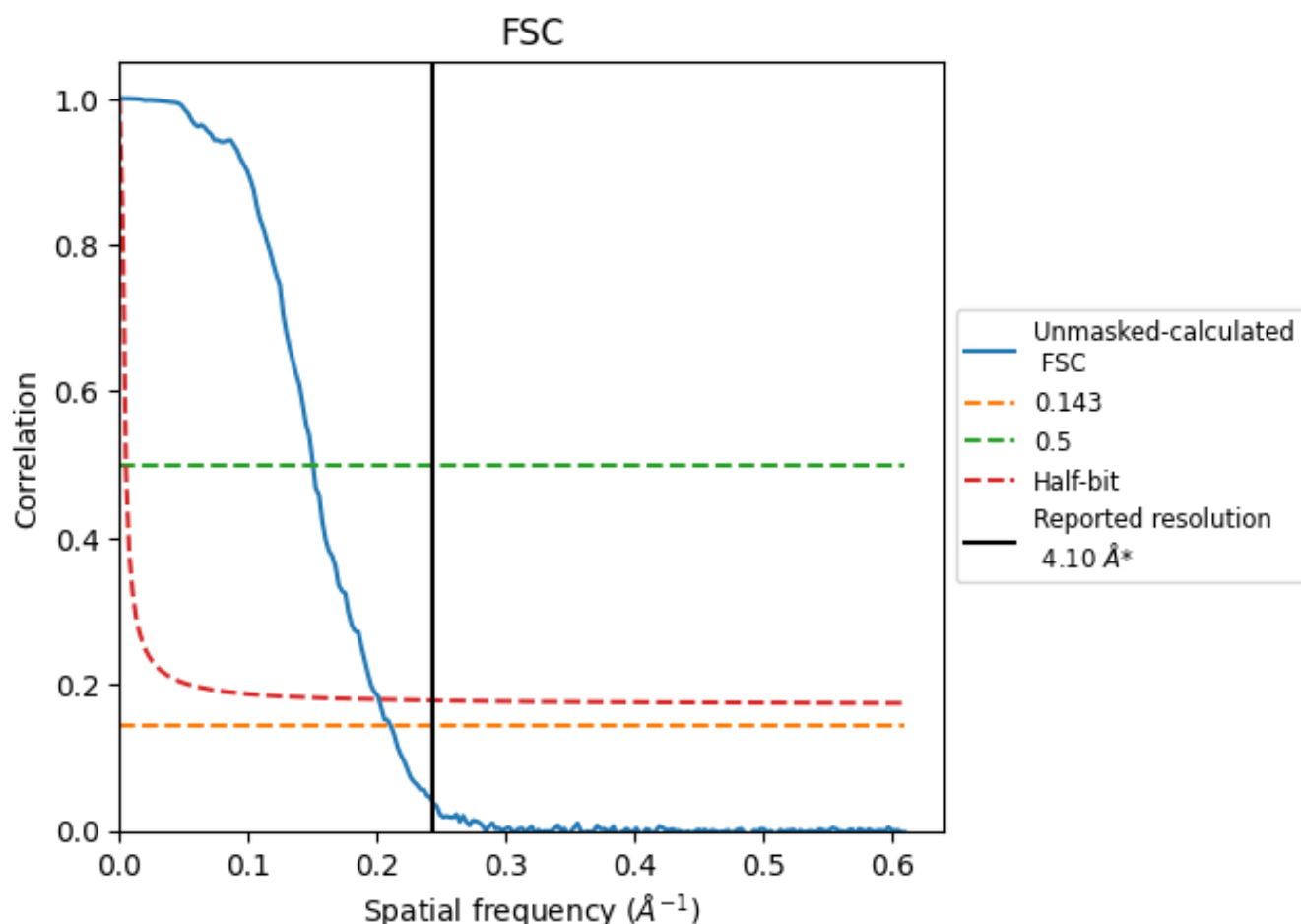


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

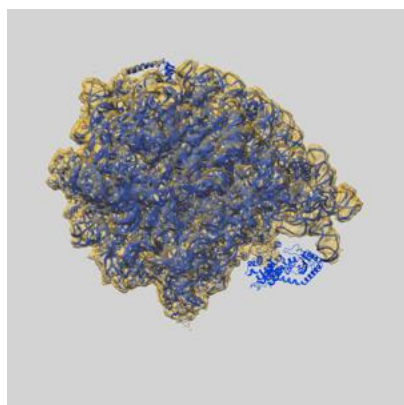
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.75	6.65	4.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.75 differs from the reported value 4.1 by more than 10 %

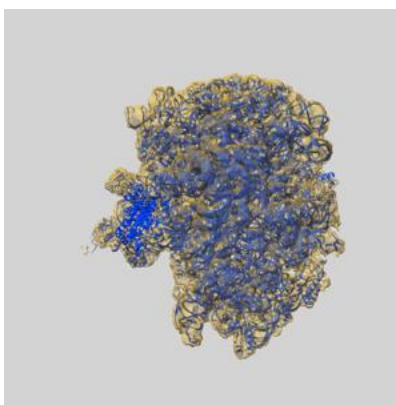
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8280 and PDB model 5KPV. Per-residue inclusion information can be found in section [3](#) on page [15](#).

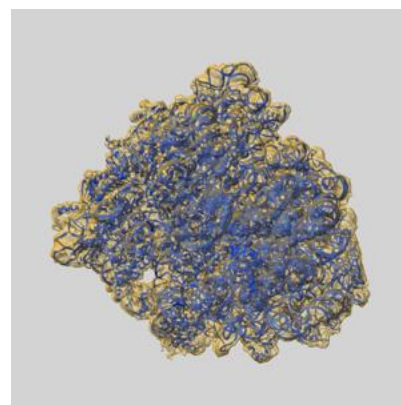
9.1 Map-model overlay [i](#)



X



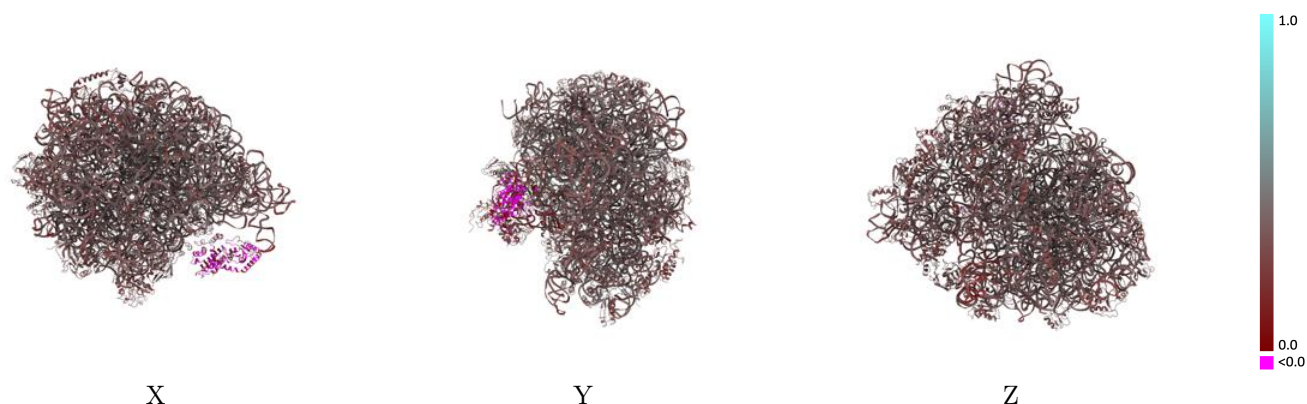
Y



Z

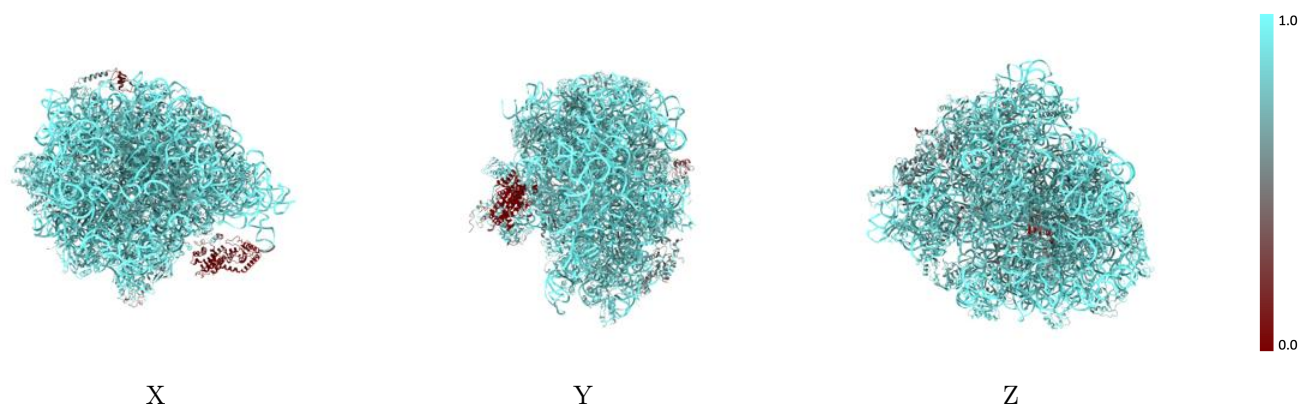
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



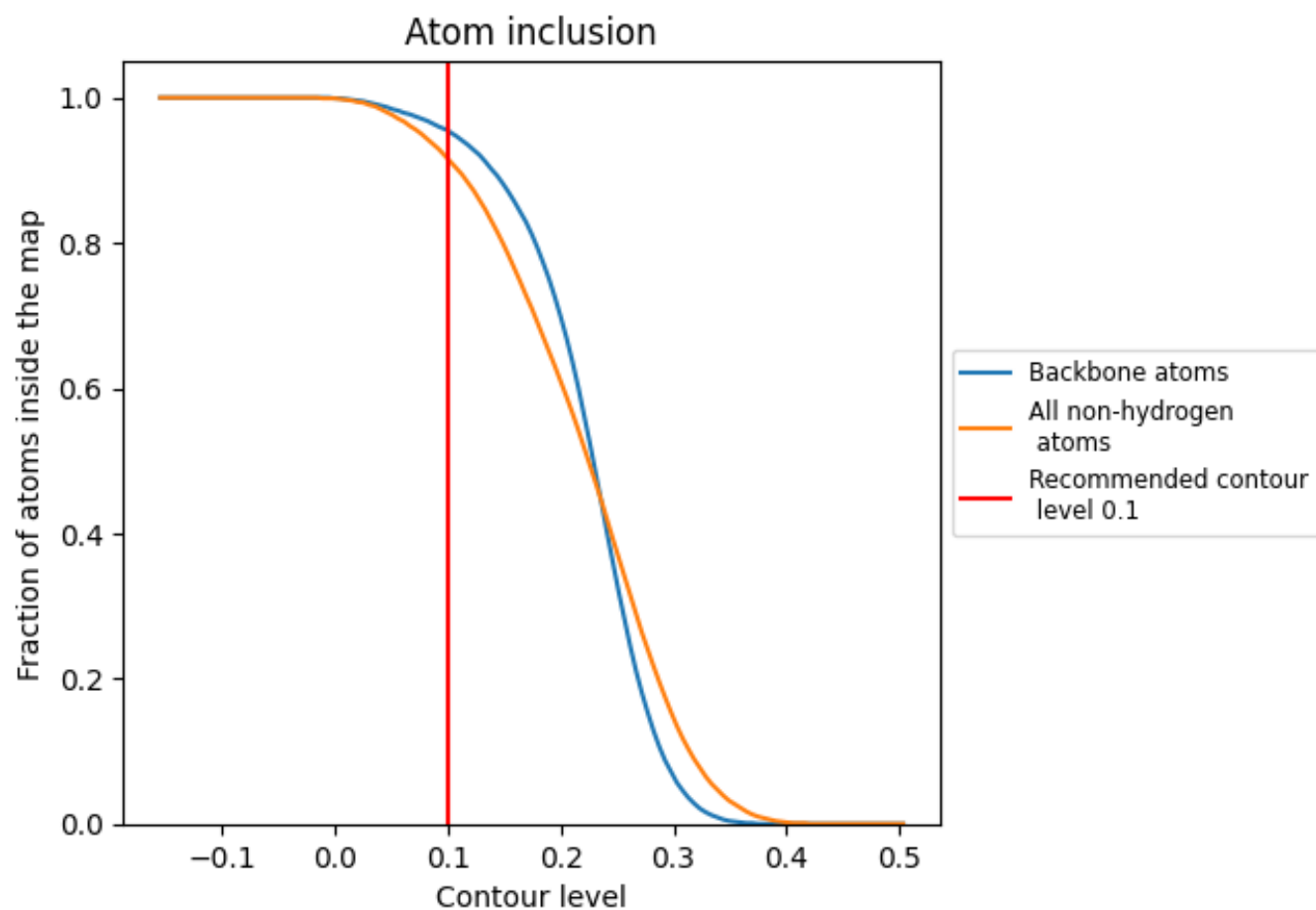
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.3500
1	 0.8760	 0.3710
10	 0.8770	 0.3530
11	 0.8570	 0.3250
12	 0.8490	 0.3570
13	 0.8850	 0.3410
14	 0.7990	 0.3440
15	 0.8650	 0.3510
16	 0.7910	 0.3770
17	 0.8460	 0.3370
18	 0.8450	 0.3360
19	 0.8570	 0.3220
2	 0.7280	 0.3520
20	 0.8710	 0.3510
21	 0.8510	 0.3640
22	 0.8930	 0.3520
23	 0.8810	 0.3430
24	 0.8680	 0.3230
25	 0.7350	 0.3160
26	 0.9880	 0.3630
27	 0.9920	 0.3650
28	 0.9940	 0.3590
29	 0.7680	 0.2970
3	 0.8840	 0.3610
30	 0.8740	 0.2400
31	 0.9580	 0.3470
32	 0.7270	 0.2370
33	 0.4050	 0.1560
4	 0.8190	 0.3740
5	 0.8220	 0.3680
6	 0.5650	 0.3130
7	 0.8030	 0.3620
8	 0.8230	 0.3300
9	 0.8430	 0.3680
A	 0.8460	 0.3840



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Chain	Atom inclusion	Q-score
B	 0.8480	 0.3850
C	 0.7850	 0.3360
D	 0.8540	 0.3440
E	 0.8740	 0.3680
F	 0.4760	 0.3210
G	 0.5700	 0.2520
H	 0.7230	 0.2430
I	 0.8570	 0.3670
J	 0.8040	 0.3940
K	 0.8730	 0.3700
L	 0.8250	 0.3810
M	 0.8720	 0.3580
N	 0.8900	 0.3430
O	 0.8550	 0.3900
P	 0.8700	 0.3390
Q	 0.8810	 0.3770
R	 0.8110	 0.3610
S	 0.8660	 0.3670
T	 0.8810	 0.3540
U	 0.8790	 0.3640
V	 0.8610	 0.3790
W	 0.8590	 0.3650
X	 0.8550	 0.3070
Y	 0.8540	 0.3640
Z	 0.8360	 0.3290