



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:54 PM UTC

PDB ID : 8WI7 / pdb_00008wi7
EMDB ID : EMD-37559
Title : Cryo- EM structure of Mycobacterium smegmatis 70S ribosome, bS1 and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

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

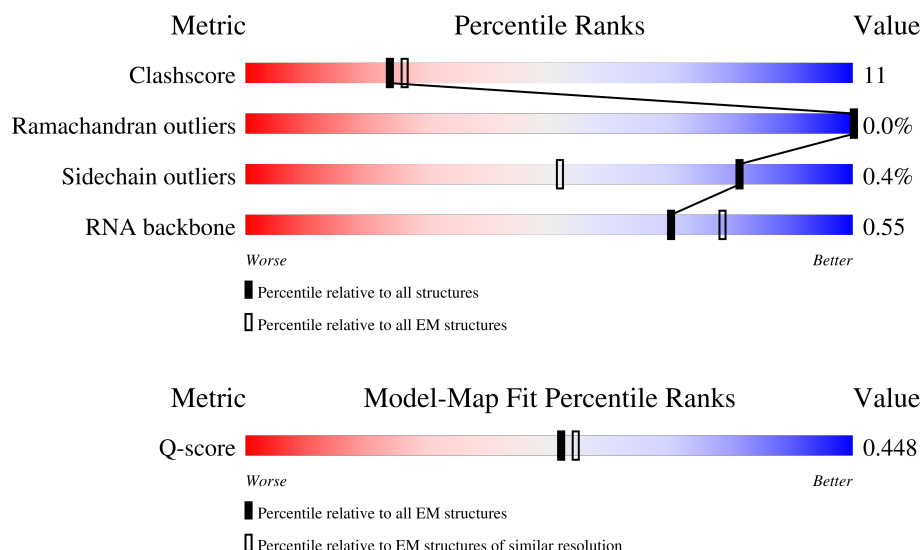
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	E	278	 81% 18%
2	F	217	 84% 13%
3	G	215	 84% 13%

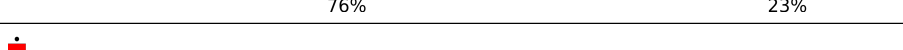
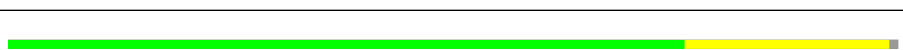
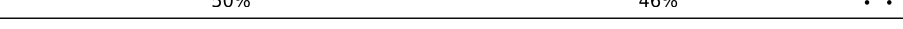
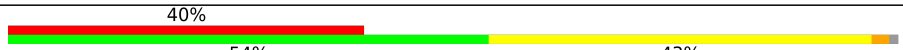
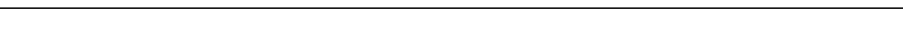
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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

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Mol	Chain	Length	Quality of chain
29	a	1528	
30	b	479	
31	v	33	
32	d	275	
33	e	201	
34	f	214	
35	g	96	
36	h	156	
37	i	132	
38	j	150	
39	k	101	
40	l	138	
41	m	124	
42	n	124	
43	o	101	
44	p	89	
45	q	156	
46	r	98	
47	s	84	
48	t	93	
49	u	86	
50	c	277	
51	w	264	

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 144808 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	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	126	Total	C	N	O	0	0
			956	586	199	171		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	95	Total	C	N	O	0	0
			747	474	136	137		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	93	Total	C	N	O	S	0	0
			710	443	133	132	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	76	Total	C	N	O	0	0
			568	352	120	96		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	62	Total	C	N	O	0	0
			498	300	114	84		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	59	Total	C	N	O	S	0	0
			458	284	84	85	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3025	Total	C	N	O	P	0	0
			64965	28956	11946	21038	3025		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 29 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	1515	Total	C	N	O	P	0	0
			32521	14485	5945	10576	1515		

- Molecule 30 is a protein called 30S ribosomal protein bS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	b	154	Total	C	N	O	0	0
			1193	758	198	237		

- Molecule 31 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	207	Total	C	N	O	S	0	0
			1656	1034	321	297	4		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	168	Total	C	N	O	S	0	0
			1223	769	230	220	4		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	121	Total	C	N	O	S	0	0
			949	588	195	164	2		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 43 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 47 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	u	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 50 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	c	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 51 is a protein called Ribosome hibernation promotion factor RafH.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	255	Total	C	N	O	S	0	0
			2030	1273	387	364	6		

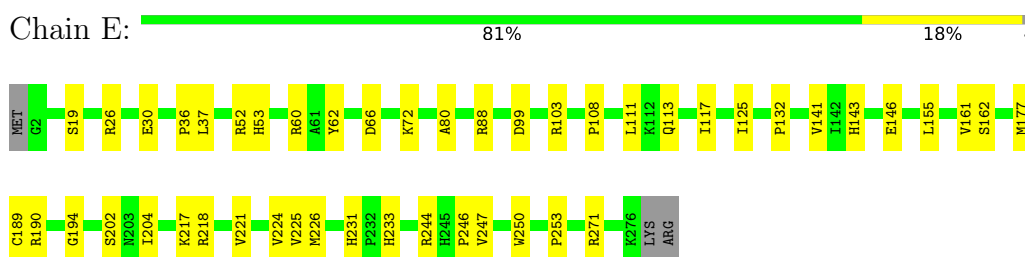
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

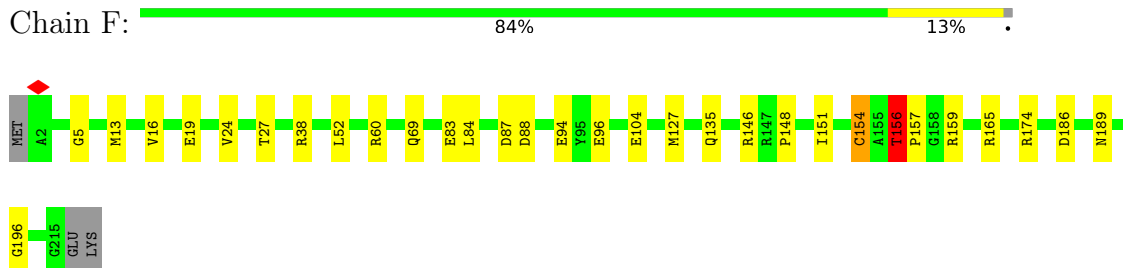
3 Residue-property plots

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.

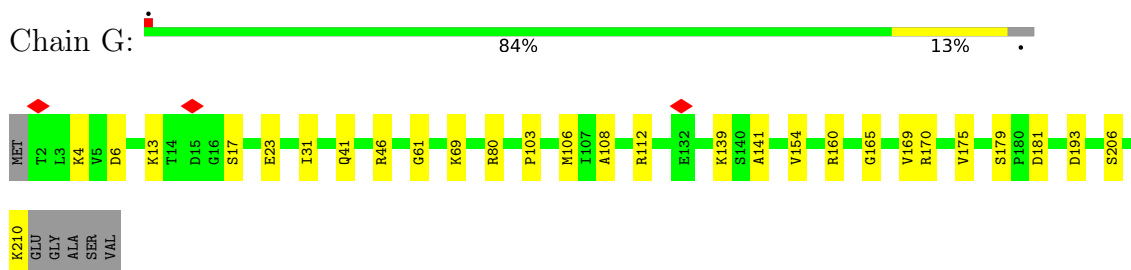
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3



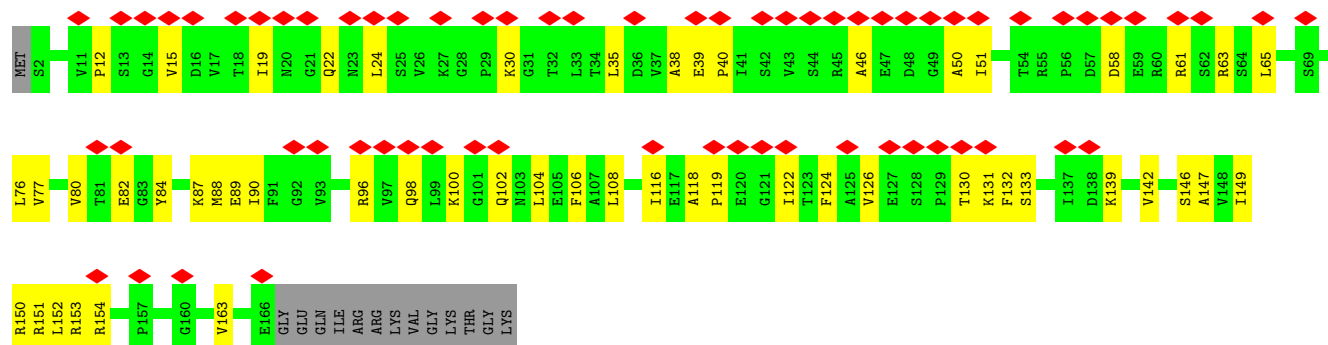
• Molecule 3: 50S ribosomal protein L4



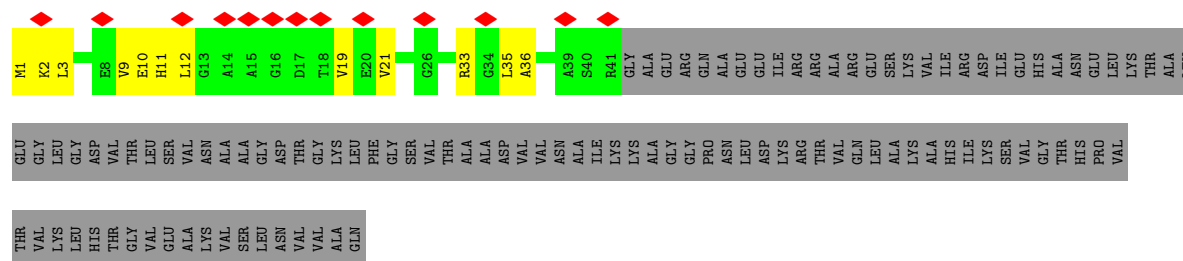
• Molecule 4: 50S ribosomal protein L5



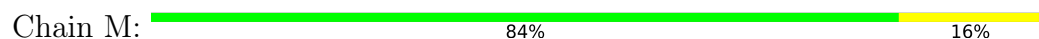
- Molecule 5: 50S ribosomal protein L6



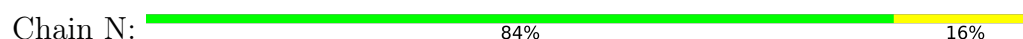
- Molecule 6: 50S ribosomal protein L9



- Molecule 7: 50S ribosomal protein L13

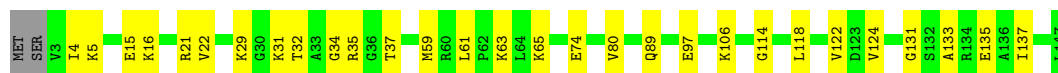


- Molecule 8: 50S ribosomal protein L14

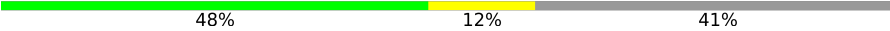


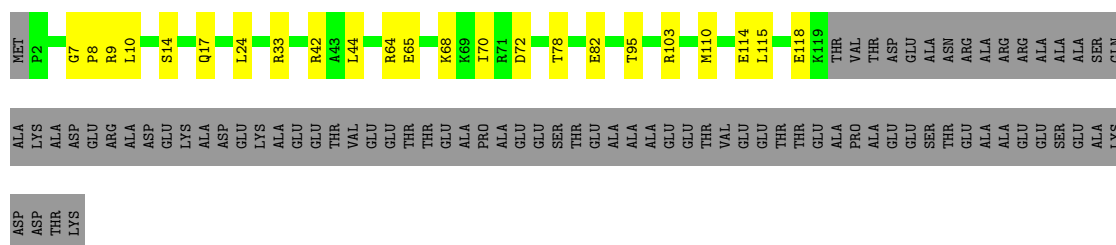
- Molecule 9: 50S ribosomal protein L15

Chain O:  79% 20%



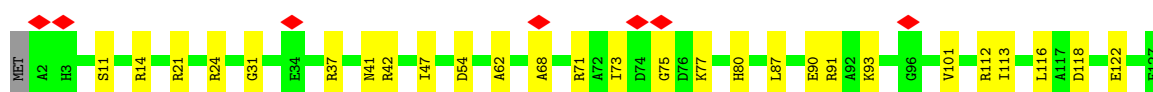
- Molecule 10: 50S ribosomal protein L17

Chain Q:  48% 12% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R:  6% 78% 21%



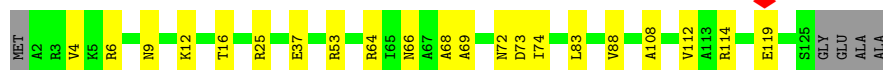
- Molecule 12: 50S ribosomal protein L19

Chain S:  85% 15%



- Molecule 13: 50S ribosomal protein L20

Chain T:  80% 16%



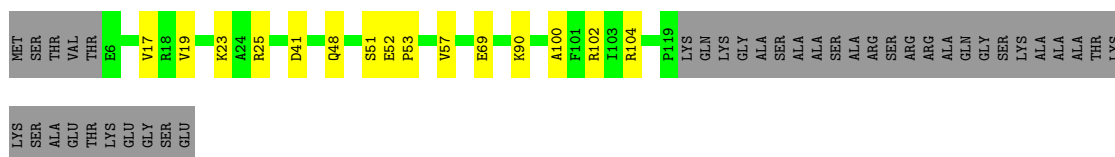
- Molecule 14: 50S ribosomal protein L21

Chain U:  82% 16%



- Molecule 15: 50S ribosomal protein L22

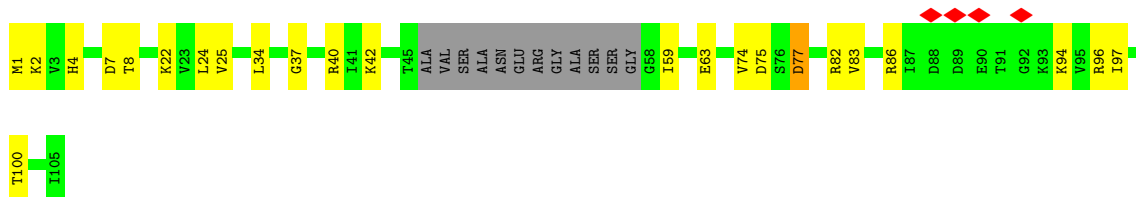
Chain V:  65% 10% 25%



- Molecule 16: 50S ribosomal protein L23



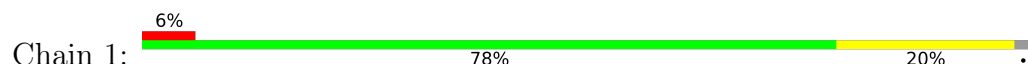
- Molecule 17: 50S ribosomal protein L24



- Molecule 18: 50S ribosomal protein L27



- Molecule 19: 50S ribosomal protein L28



- Molecule 20: 50S ribosomal protein L29

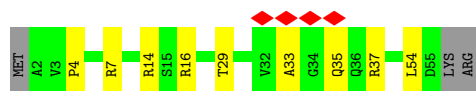
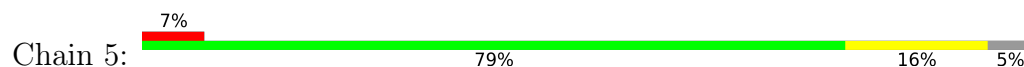


- Molecule 21: 50S ribosomal protein L30

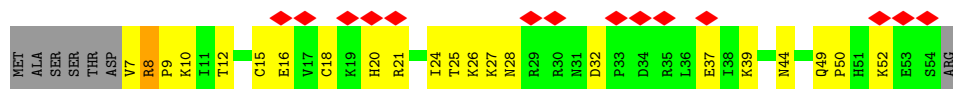




- Molecule 22: 50S ribosomal protein L32



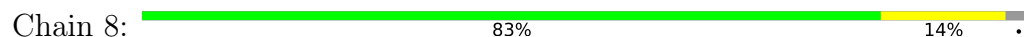
- Molecule 23: 50S ribosomal protein L33A



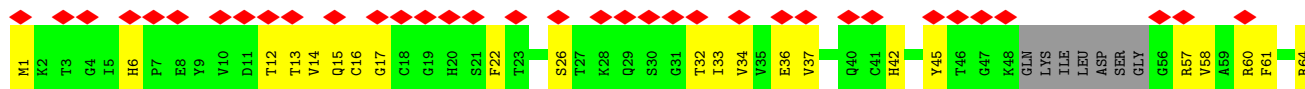
- Molecule 24: 50S ribosomal protein L34



- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31



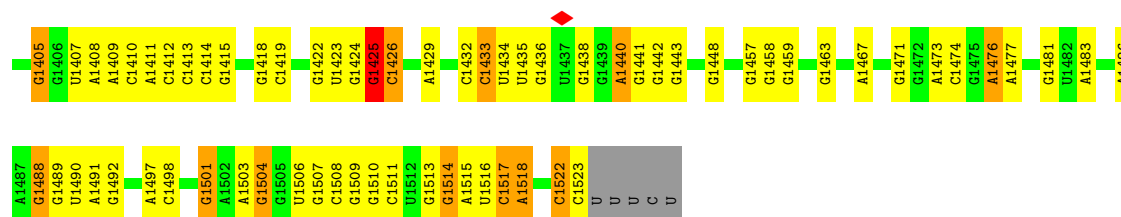
- Molecule 27: 23S rRNA



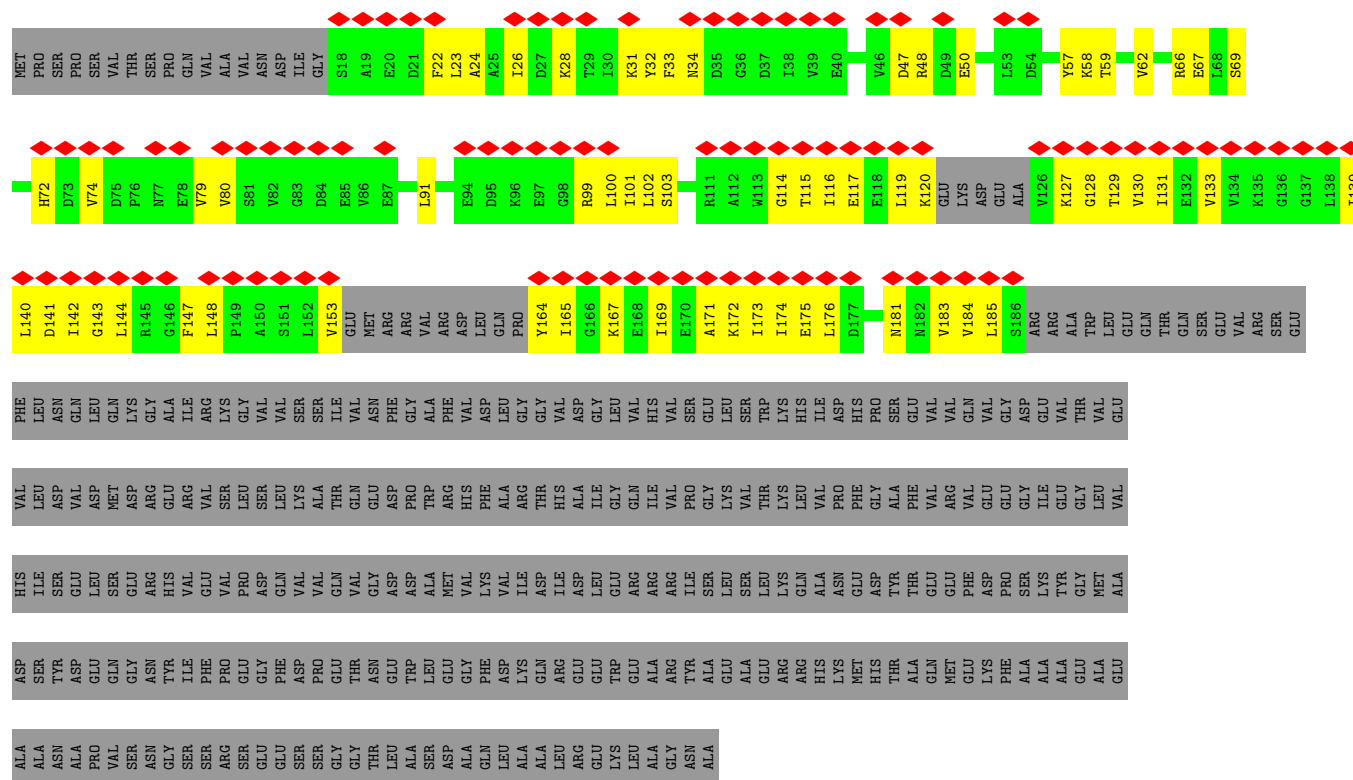
G	G1154	G1073	A994	A907	C813	A725	G643	A545	U451	U365	G297	G217	G114
C	C1155	A1074	U995	A908	A814	A726	G644	G546	G452	G366	G298	A218	A115
U	G1156	A1075	G996	A909	G815	A727	G645	G551	U453	U367	G299	G219	A116
C	U1157	A1076	G997	U911	U818	G728	G646	G554	U454	G369	G300	A221	U117
	U1158	A1077	G998	C912	G819	G730	G647	G555	G460	U370	U301	A222	
	C1161	G1078	G999			A731	G650	G556	A465	G371	U302		A122
	G1162	U1084	C1000	A919	G824	G732	G653	G557		C377	U303		C125
	A1163	G1085	C1001	G920	C825	U733	U654	U654	C470	U377	A227		
	A1164	C1086	C1002	G924	G826	U735	G655	U653	G471	G579	U229		C130
	G1165	A1003	C1003	G927	G827	G736	G656	G564	C472	A380	G307		A131
	A1166	U1088	C1004	C927	G828	A737	U658	A565	C473	A391	U308		C132
		U1089	C1005	U928	U829	A738	U659	A566	C474	A382	G309		
		G1090	A1006	C929	A830	U739	U660	A567	U475	U383	C310		G137
		A1091	G1006	U929	A831	A740	U661	A568	G476	G384	G311		A138
		G1092	G1007	C932	G832	G741	U662	G569	U479	G385	U139		G140
		A1099	G1008	C933	G833	G742	G662	U660	A480	U388	U239		
		C1100	U1009	A934	U839	G743	A663	G587	U481	G389	G242		A148
		A1101	U1010	A935	U840	A747	A664	A588	U482	U316			G149
		G1106	U1011	U942	G841	U748	A665	A589	G483	A392	G248		C150
		A1107	C1012	U943	G844	C749	A666	A590	C484	U393	C249		A151
		G1110	U1013	G945	C845	A750	U668	A591	U485	G394	A251		G152
		C1241	G1014	G946		C752	A670	G593	U487	G399	G254		G153
		C1242	A1015	U947		A753	G671	U594	G488	C400	A255		C154
		C1112	G1016	U948		C754	C672	A595	G489	C401	A256		G155
		C1113	U1017	G948		A755	U674	C596	U493	G402	A257		A159
		G1114	G1018	G951		A756	U675	C597	G494	U403	G263		A164
		U1117	C1019	G954		G757	U676	U598	G499	A404	A265		U165
		A1118	A1020	U954		A758	A678	G599		A406	U266		G176
		C1119	G1021	G960		U760	U680	A601			G264		G183
		G1120	C1022	U961		U764	C681	C604	C502	A412	U270		G184
		C1121	U1025	U965		G765	A682	G605	A503	G413	A271		G187
		C1122	C1030	U966		G766	G684		C504	A422	A272		G188
		G1123	G1033	G967		G768	G685		C505	C423	A273		G189
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		C1130	A1041	G975		U782	G693		C509	G344	A278		G193
		G1131	U1043	U976		G783	A696		C510	G345	U279		A194
		U1137	G1043	A977		G784	G684		U509	G426	G280		A195
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		U1145	A1050	A982		A796	U709		G528	U438	G286		
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		U1149	A1058	A898		A804	A721		A542	U445	G290		G214
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		U1151	U1060	C991		A808	C723		U544	G449	G294		A216
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		U1153									A296		

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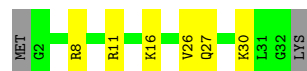
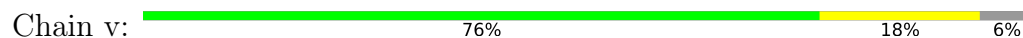




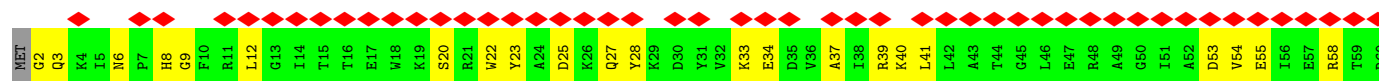
• Molecule 30: 30S ribosomal protein bS1

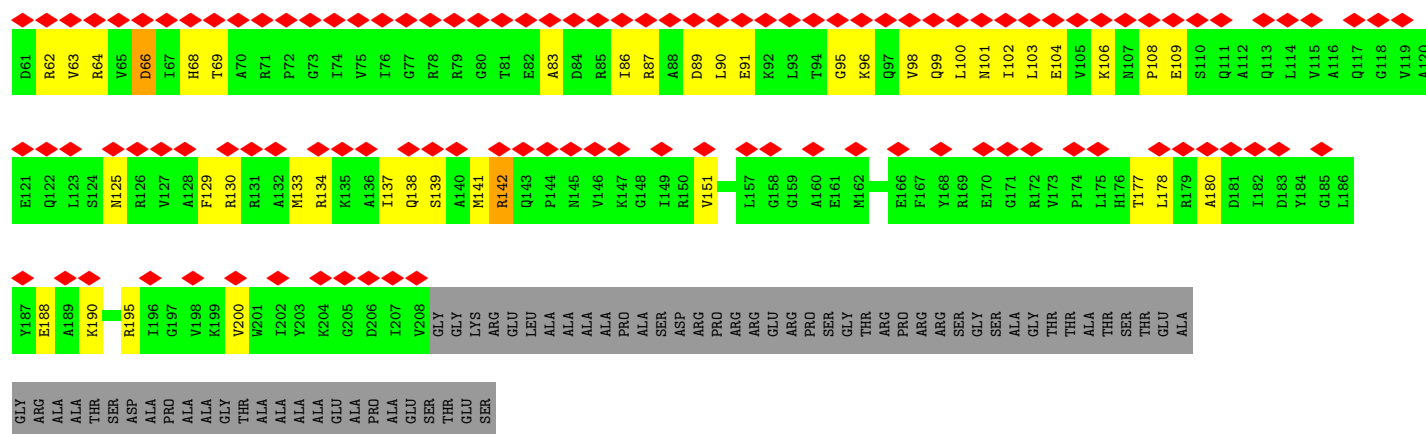


• Molecule 31: 30S ribosomal protein S22

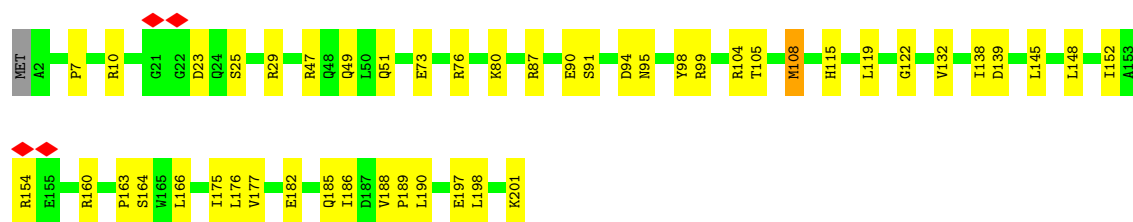
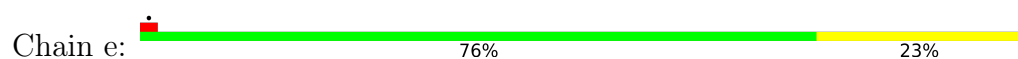


• Molecule 32: 30S ribosomal protein S3

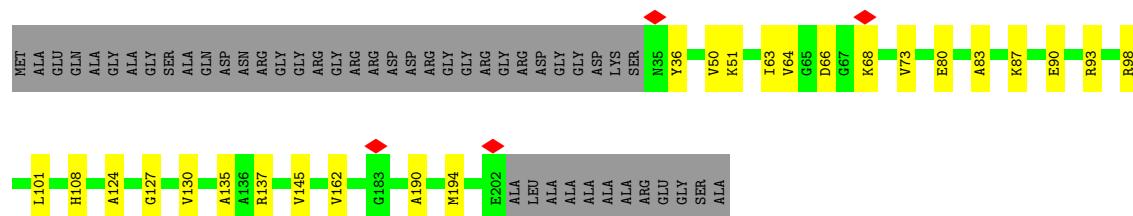




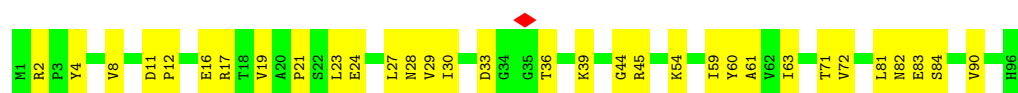
• Molecule 33: 30S ribosomal protein S4



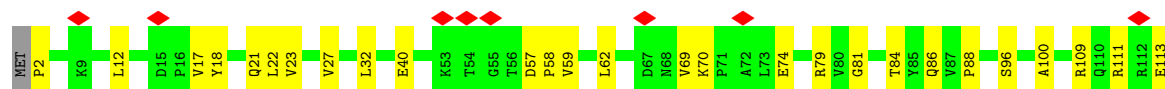
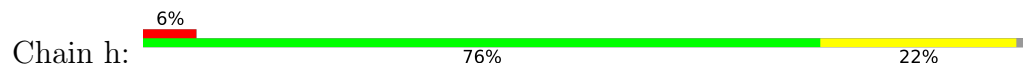
• Molecule 34: 30S ribosomal protein S5

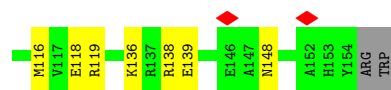


• Molecule 35: 30S ribosomal protein S6



• Molecule 36: 30S ribosomal protein S7





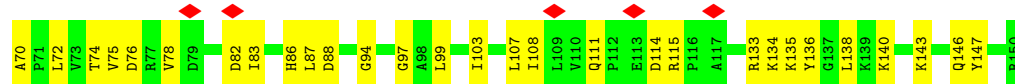
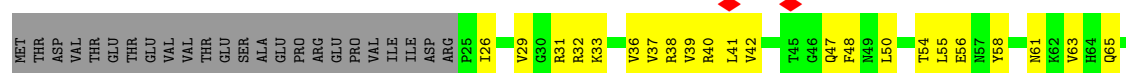
- Molecule 37: 30S ribosomal protein S8

Chain i: 76% 23%



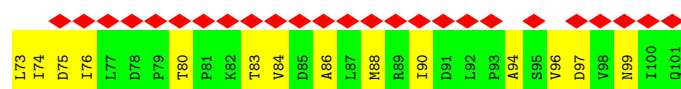
- Molecule 38: 30S ribosomal protein S9

Chain j: 5% 50% 34% 16%



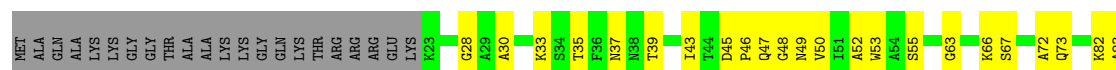
- Molecule 39: 30S ribosomal protein S10

Chain k: 45% 50% 46%



- Molecule 40: 30S ribosomal protein S11

Chain l: 50% 33% 17%

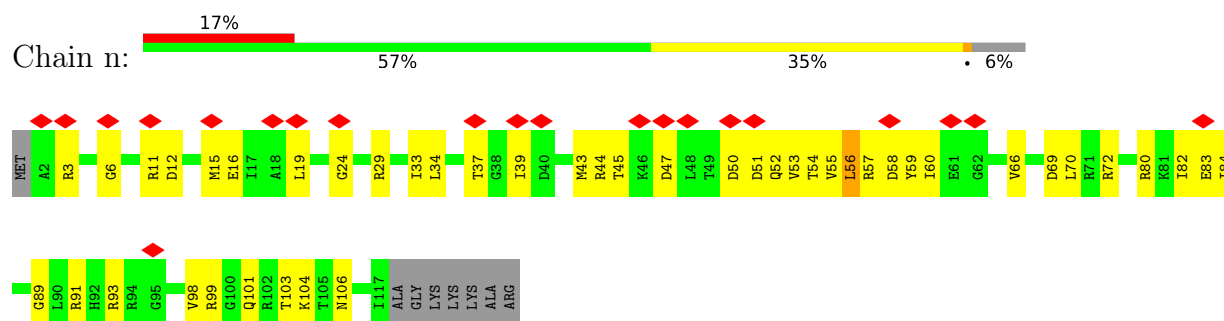


- Molecule 41: 30S ribosomal protein S12

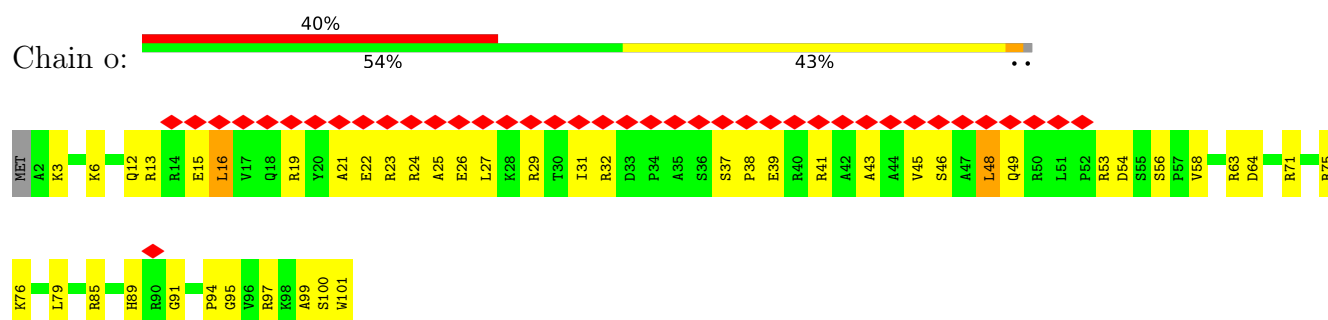
Chain m: 76% 22%



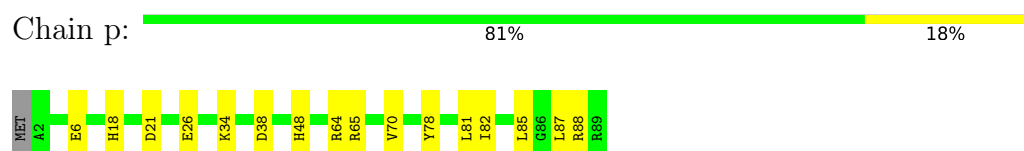
- Molecule 42: 30S ribosomal protein S13



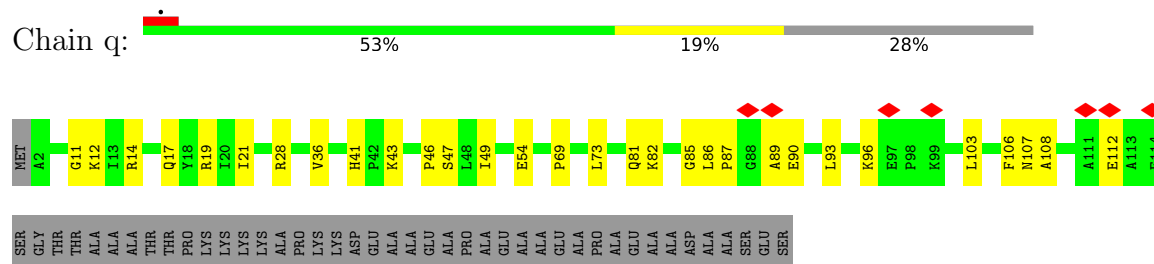
- Molecule 43: 30S ribosomal protein S14A



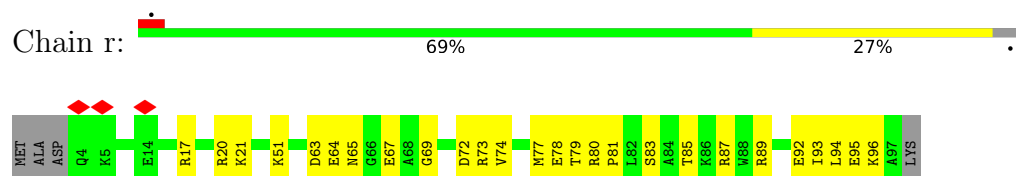
- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16

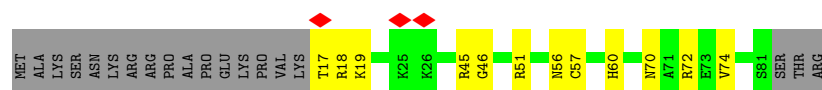


- Molecule 46: 30S ribosomal protein S17

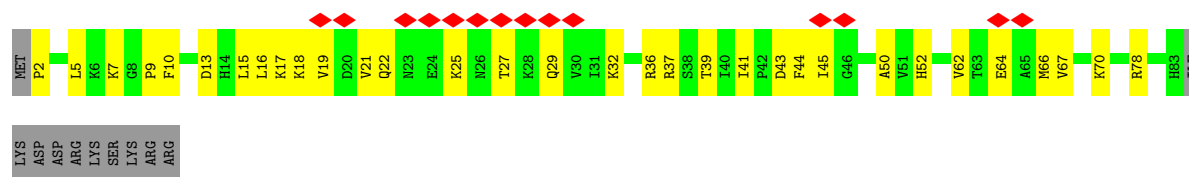


- Molecule 47: 30S ribosomal protein S18B

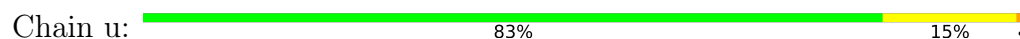




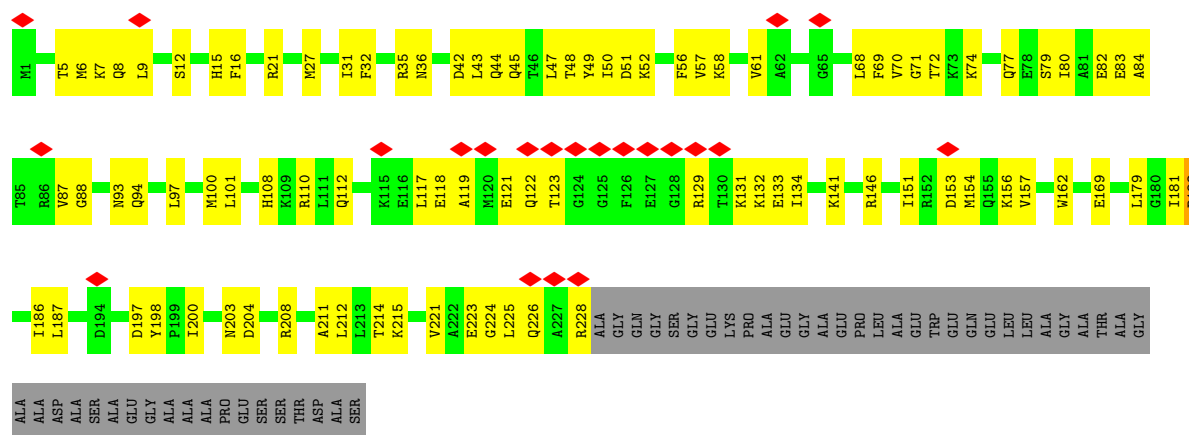
• Molecule 48: 30S ribosomal protein S19



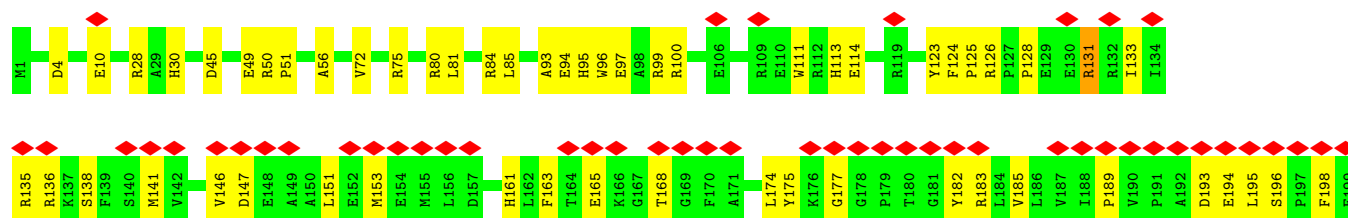
• Molecule 49: 30S ribosomal protein S20

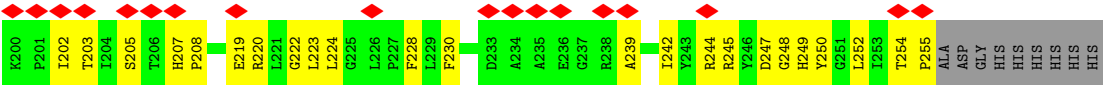


• Molecule 50: 30S ribosomal protein S2



• Molecule 51: Ribosome hibernation promotion factor Rahf





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction in Relion	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.212	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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	E	0.13	0/2153	0.27	0/2895
2	F	0.17	0/1609	0.41	0/2165
3	G	0.12	0/1592	0.27	0/2153
4	H	0.13	0/1467	0.35	0/1973
5	I	0.13	0/1281	0.35	0/1733
6	J	0.22	0/311	0.46	0/419
7	M	0.14	0/1157	0.32	0/1567
8	N	0.13	0/946	0.29	0/1268
9	O	0.13	0/1091	0.37	0/1457
10	Q	0.13	0/945	0.30	0/1267
11	R	0.15	0/966	0.43	0/1298
12	S	0.15	0/921	0.34	0/1236
13	T	0.14	0/1000	0.29	0/1341
14	U	0.15	0/764	0.30	0/1030
15	V	0.13	0/887	0.30	0/1204
16	W	0.15	0/757	0.33	0/1018
17	X	0.14	0/716	0.35	0/957
18	Z	0.15	0/577	0.31	0/774
19	1	0.12	0/478	0.30	0/641
20	2	0.13	0/534	0.32	0/713
21	3	0.15	0/477	0.32	0/640
22	5	0.13	0/427	0.28	0/572
23	6	0.19	0/405	0.47	0/542
24	7	0.11	0/380	0.29	0/500
25	8	0.10	0/503	0.27	0/667
26	4	0.15	0/467	0.36	0/626
27	A	0.12	0/72743	0.26	0/113499
28	B	0.11	0/2821	0.24	0/4396
29	a	0.12	0/36400	0.27	1/56798 (0.0%)
30	b	0.16	0/1201	0.48	0/1615
31	v	0.11	0/271	0.25	0/348
32	d	0.15	0/1680	0.37	1/2256 (0.0%)
33	e	0.12	0/1672	0.29	0/2251
34	f	0.13	0/1239	0.29	0/1673

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.14	0/782	0.36	0/1059
36	h	0.13	0/1225	0.36	1/1653 (0.1%)
37	i	0.13	0/1025	0.29	0/1385
38	j	0.16	0/1012	0.41	0/1362
39	k	0.23	0/789	0.49	0/1069
40	l	0.16	0/873	0.38	0/1180
41	m	0.13	0/960	0.31	0/1283
42	n	0.14	0/942	0.40	0/1260
43	o	0.26	0/830	0.45	0/1106
44	p	0.14	0/729	0.32	0/977
45	q	0.14	0/908	0.36	0/1226
46	r	0.12	0/759	0.32	0/1016
47	s	0.12	0/518	0.28	0/693
48	t	0.14	0/680	0.37	0/915
49	u	0.16	0/663	0.40	0/882
50	c	0.14	0/1822	0.40	1/2457 (0.0%)
51	w	0.14	0/2078	0.33	0/2816
All	All	0.13	0/157433	0.29	4/235831 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	c	182	PRO	CA-N-CD	-8.06	100.71	112.00
36	h	58	PRO	CA-N-CD	-8.04	100.74	112.00
32	d	108	PRO	CA-N-CD	-6.88	102.36	112.00
29	a	1425	G	C4'-C3'-O3'	-5.11	105.34	113.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1587	0	1630	28	0
3	G	1569	0	1607	21	0
4	H	1445	0	1476	43	0
5	I	1260	0	1300	41	0
6	J	308	0	323	10	0
7	M	1130	0	1167	25	0
8	N	938	0	1000	15	0
9	O	1078	0	1151	25	0
10	Q	928	0	972	14	0
11	R	956	0	991	22	0
12	S	907	0	938	22	0
13	T	988	0	1038	22	0
14	U	754	0	802	11	0
15	V	873	0	909	12	0
16	W	747	0	794	7	0
17	X	710	0	760	18	0
18	Z	568	0	586	11	0
19	1	470	0	484	11	0
20	2	531	0	541	12	0
21	3	474	0	500	12	0
22	5	423	0	463	9	0
23	6	397	0	407	20	0
24	7	377	0	411	17	0
25	8	498	0	538	7	0
26	4	458	0	447	92	0
27	A	64965	0	32687	1010	0
28	B	2522	0	1285	40	0
29	a	32521	0	16366	603	0
30	b	1193	0	1238	46	0
31	v	271	0	329	7	0
32	d	1656	0	1704	62	0
33	e	1641	0	1668	36	0
34	f	1223	0	1287	25	0
35	g	771	0	797	47	0
36	h	1207	0	1259	25	0
37	i	1010	0	1046	23	0
38	j	994	0	1050	55	0
39	k	775	0	808	54	0
40	l	855	0	863	40	0
41	m	949	0	1032	21	0
42	n	935	0	985	109	0
43	o	819	0	866	84	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	p	720	0	760	14	0
45	q	891	0	935	28	0
46	r	748	0	795	20	0
47	s	513	0	540	9	0
48	t	662	0	677	41	0
49	u	660	0	712	11	0
50	c	1793	0	1839	66	0
51	w	2030	0	2023	86	0
All	All	144808	0	96951	2581	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 11.

The worst 5 of 2581 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)
26:4:37:VAL:HB	42:n:57:ARG:CZ	1.41	1.51
26:4:37:VAL:HB	42:n:57:ARG:NH1	1.19	1.46
26:4:36:GLU:C	42:n:57:ARG:HH22	1.23	1.46
26:4:37:VAL:N	42:n:57:ARG:HH22	1.16	1.42
27:A:1611:A:H2	35:g:17:ARG:NH2	1.22	1.34

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	E	273/278 (98%)	265 (97%)	8 (3%)	0	100 100
2	F	212/217 (98%)	204 (96%)	7 (3%)	1 (0%)	24 57
3	G	207/215 (96%)	205 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	H	180/187 (96%)	173 (96%)	7 (4%)	0	100	100
5	I	163/179 (91%)	162 (99%)	1 (1%)	0	100	100
6	J	39/151 (26%)	39 (100%)	0	0	100	100
7	M	144/147 (98%)	141 (98%)	3 (2%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	131 (92%)	12 (8%)	0	100	100
10	Q	116/199 (58%)	114 (98%)	2 (2%)	0	100	100
11	R	124/127 (98%)	124 (100%)	0	0	100	100
12	S	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
13	T	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
14	U	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
15	V	112/153 (73%)	111 (99%)	1 (1%)	0	100	100
16	W	93/100 (93%)	92 (99%)	1 (1%)	0	100	100
17	X	89/105 (85%)	88 (99%)	1 (1%)	0	100	100
18	Z	74/88 (84%)	71 (96%)	3 (4%)	0	100	100
19	1	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
20	2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
21	3	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
23	6	46/55 (84%)	42 (91%)	4 (9%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	60/64 (94%)	58 (97%)	2 (3%)	0	100	100
26	4	55/75 (73%)	54 (98%)	1 (2%)	0	100	100
30	b	148/479 (31%)	143 (97%)	5 (3%)	0	100	100
31	v	29/33 (88%)	29 (100%)	0	0	100	100
32	d	205/275 (74%)	196 (96%)	9 (4%)	0	100	100
33	e	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
34	f	166/214 (78%)	162 (98%)	4 (2%)	0	100	100
35	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
36	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
37	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	j	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
39	k	95/101 (94%)	90 (95%)	4 (4%)	1 (1%)	11	43
40	l	113/138 (82%)	107 (95%)	6 (5%)	0	100	100
41	m	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
42	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
43	o	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
44	p	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
45	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
46	r	92/98 (94%)	89 (97%)	3 (3%)	0	100	100
47	s	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
48	t	80/93 (86%)	77 (96%)	3 (4%)	0	100	100
49	u	83/86 (96%)	83 (100%)	0	0	100	100
50	c	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
51	w	253/264 (96%)	240 (95%)	13 (5%)	0	100	100
All	All	5634/6731 (84%)	5444 (97%)	188 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	156	THR
39	k	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	E	215/218 (99%)	215 (100%)	0	100	100
2	F	160/163 (98%)	158 (99%)	2 (1%)	61	72
3	G	169/173 (98%)	169 (100%)	0	100	100
4	H	151/156 (97%)	150 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	I	139/150 (93%)	139 (100%)	0	100	100
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	118 (99%)	1 (1%)	73	77
8	N	100/100 (100%)	100 (100%)	0	100	100
9	O	112/114 (98%)	112 (100%)	0	100	100
10	Q	97/158 (61%)	97 (100%)	0	100	100
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	100/100 (100%)	100 (100%)	0	100	100
13	T	97/99 (98%)	97 (100%)	0	100	100
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	90/117 (77%)	90 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	78 (99%)	1 (1%)	61	72
18	Z	55/63 (87%)	55 (100%)	0	100	100
19	1	50/51 (98%)	50 (100%)	0	100	100
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	52 (100%)	0	100	100
22	5	43/46 (94%)	43 (100%)	0	100	100
23	6	46/52 (88%)	45 (98%)	1 (2%)	45	65
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	51/63 (81%)	51 (100%)	0	100	100
30	b	132/407 (32%)	131 (99%)	1 (1%)	73	77
31	v	29/31 (94%)	29 (100%)	0	100	100
32	d	170/212 (80%)	167 (98%)	3 (2%)	51	69
33	e	175/176 (99%)	173 (99%)	2 (1%)	65	74
34	f	123/147 (84%)	123 (100%)	0	100	100
35	g	85/85 (100%)	85 (100%)	0	100	100
36	h	129/132 (98%)	129 (100%)	0	100	100
37	i	107/108 (99%)	107 (100%)	0	100	100
38	j	102/125 (82%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	k	88/90 (98%)	86 (98%)	2 (2%)	44	64
40	l	89/105 (85%)	89 (100%)	0	100	100
41	m	102/105 (97%)	102 (100%)	0	100	100
42	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
43	o	85/86 (99%)	83 (98%)	2 (2%)	43	64
44	p	76/77 (99%)	76 (100%)	0	100	100
45	q	92/118 (78%)	92 (100%)	0	100	100
46	r	80/83 (96%)	78 (98%)	2 (2%)	42	63
47	s	55/72 (76%)	55 (100%)	0	100	100
48	t	73/84 (87%)	73 (100%)	0	100	100
49	u	69/70 (99%)	68 (99%)	1 (1%)	59	71
50	c	191/218 (88%)	191 (100%)	0	100	100
51	w	208/215 (97%)	207 (100%)	1 (0%)	81	80
All	All	4718/5467 (86%)	4697 (100%)	21 (0%)	81	81

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	n	56	LEU
46	r	92	GLU
51	w	131	ARG
46	r	94	LEU
43	o	48	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
37	i	16	ASN
42	n	101	GLN
37	i	63	GLN
40	l	31	HIS
45	q	107	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3022/3119 (96%)	539 (17%)	17 (0%)
28	B	117/118 (99%)	16 (13%)	1 (0%)
29	a	1514/1528 (99%)	268 (17%)	0
All	All	4653/4765 (97%)	823 (17%)	18 (0%)

5 of 823 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	12	G
27	A	20	G
27	A	31	U
27	A	32	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	2350	G
28	B	10	G
27	A	2729	G
27	A	1002	C
27	A	2094	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 ⓘ

There are no chain breaks in this entry.

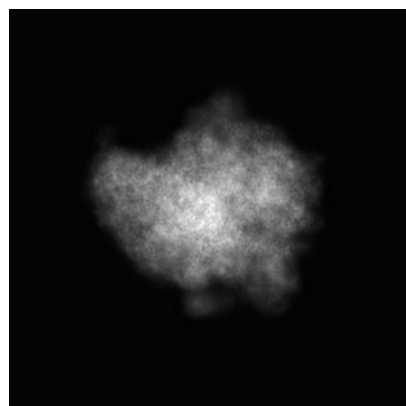
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37559. These allow visual inspection of the internal detail of the map and identification of artifacts.

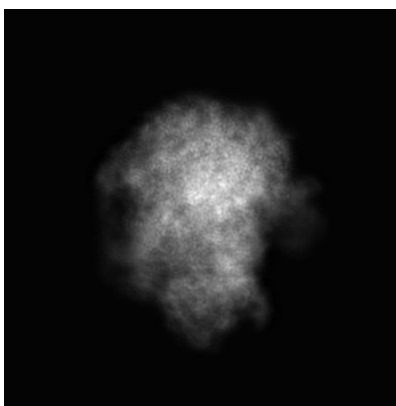
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

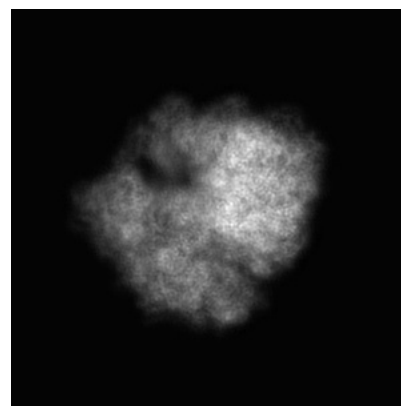
6.1.1 Primary map



X

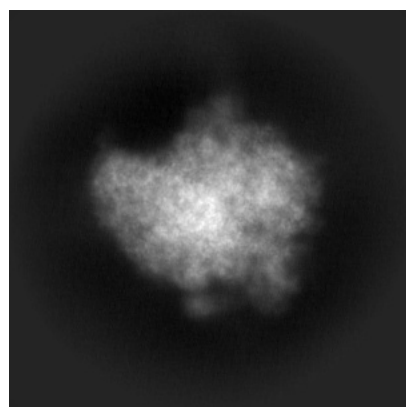


Y

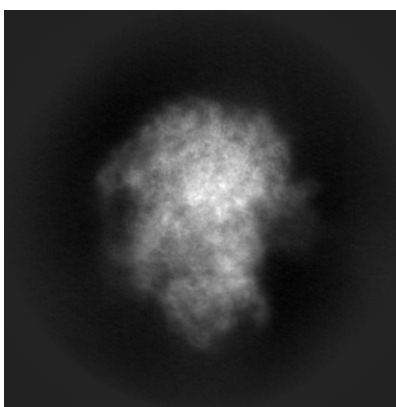


Z

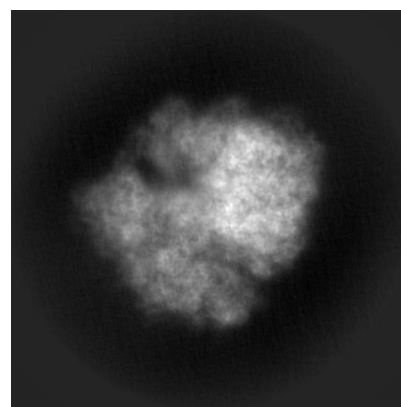
6.1.2 Raw map



X



Y

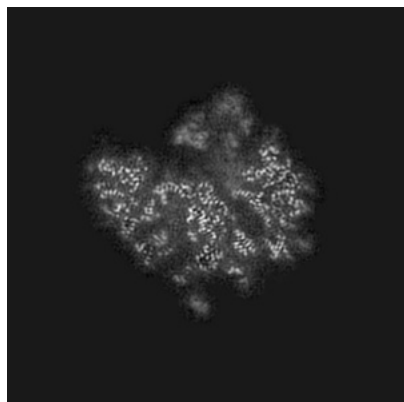


Z

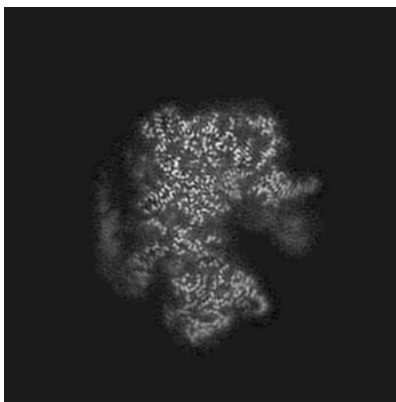
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

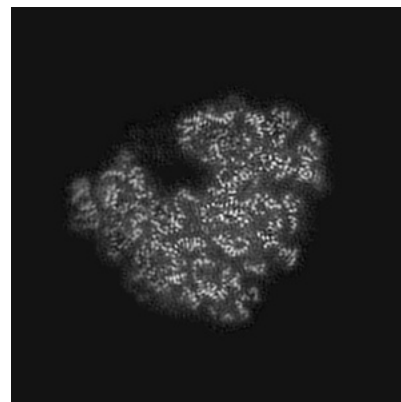
6.2.1 Primary map



X Index: 190

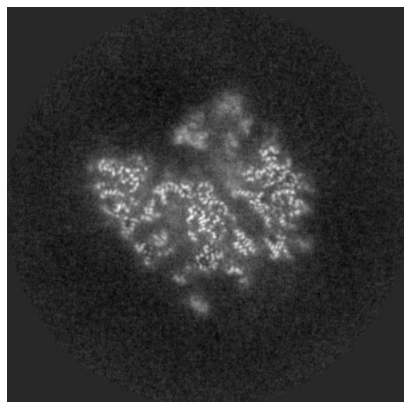


Y Index: 190

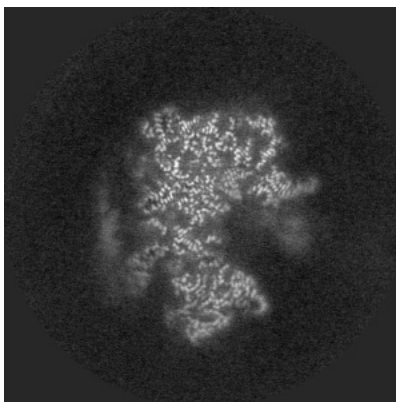


Z Index: 190

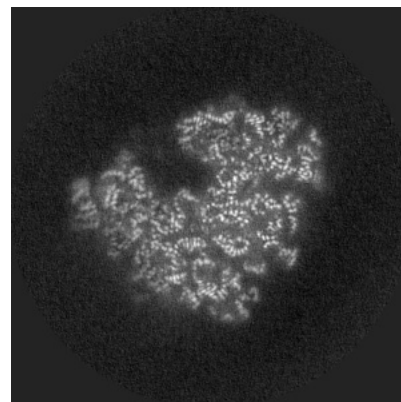
6.2.2 Raw map



X Index: 190



Y Index: 190

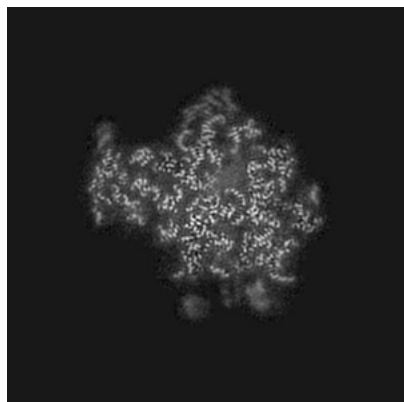


Z Index: 190

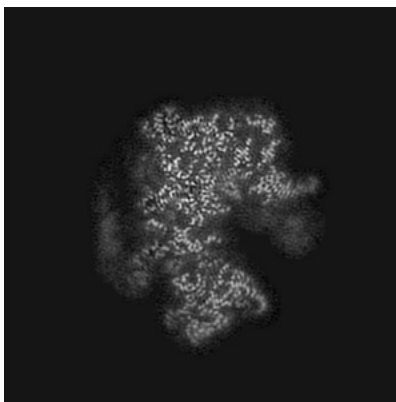
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

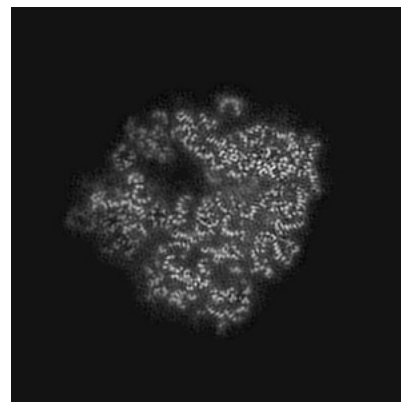
6.3.1 Primary map



X Index: 210

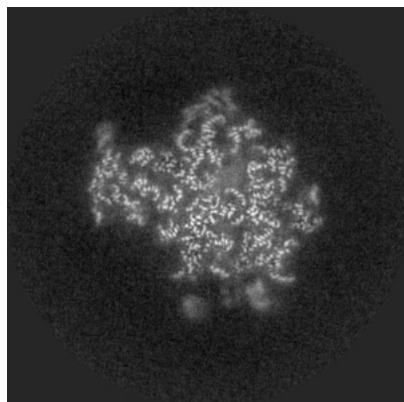


Y Index: 191

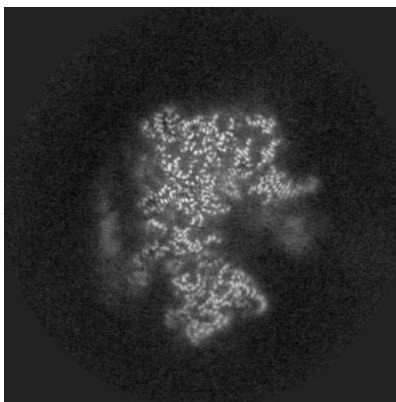


Z Index: 200

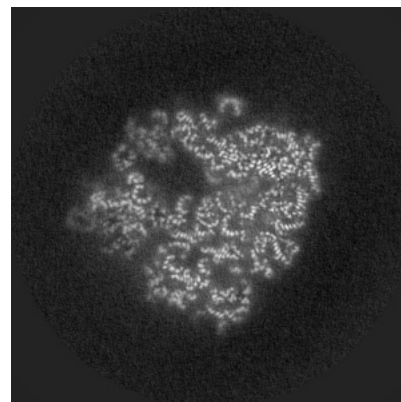
6.3.2 Raw map



X Index: 210



Y Index: 191

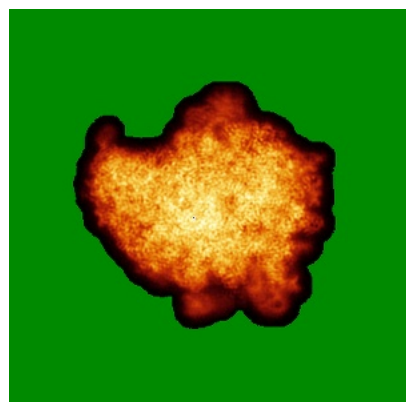


Z Index: 200

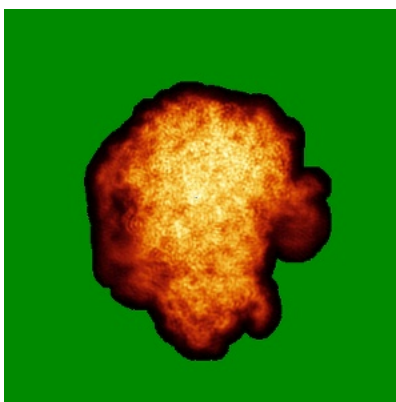
The images above show the largest variance slices of the map in three orthogonal directions.

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

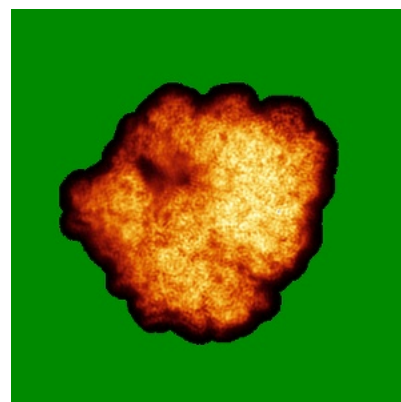
6.4.1 Primary map



X

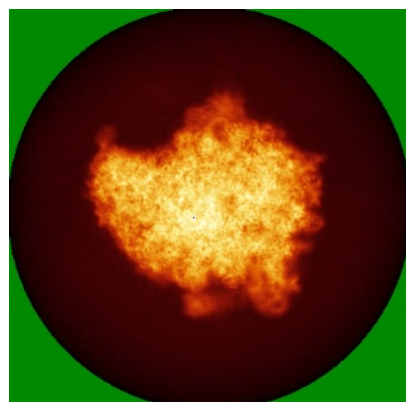


Y

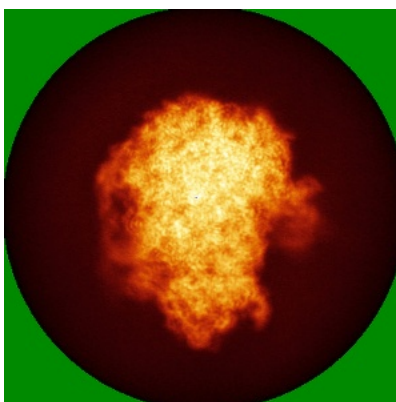


Z

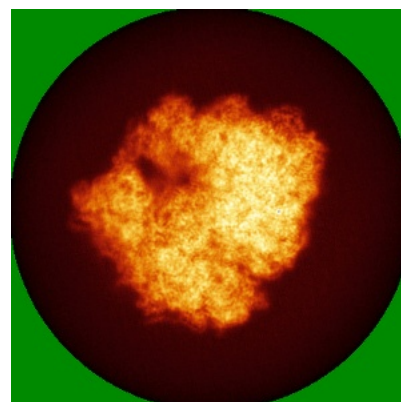
6.4.2 Raw map



X



Y

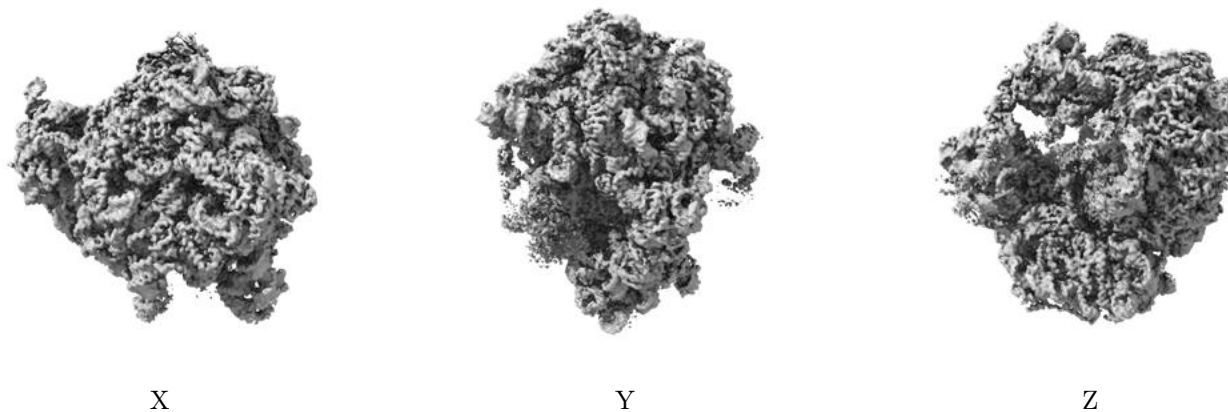


Z

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

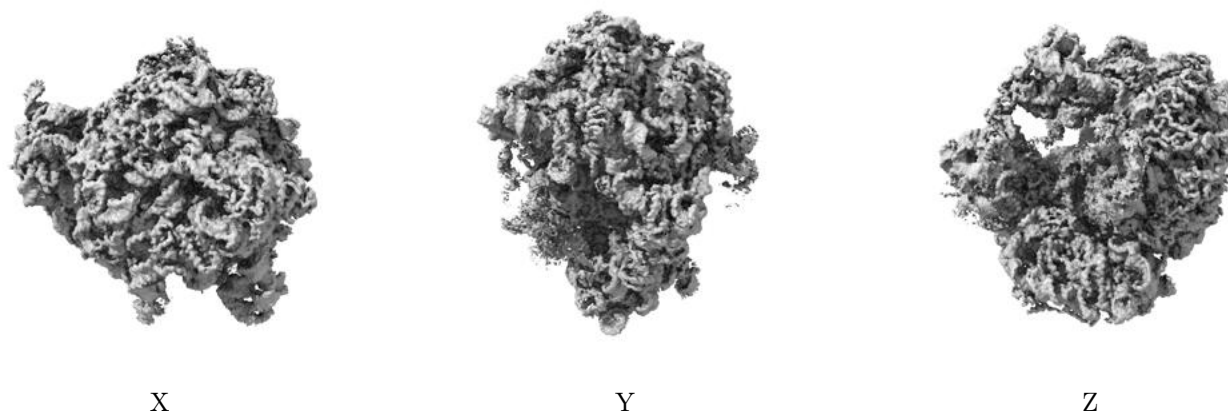
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

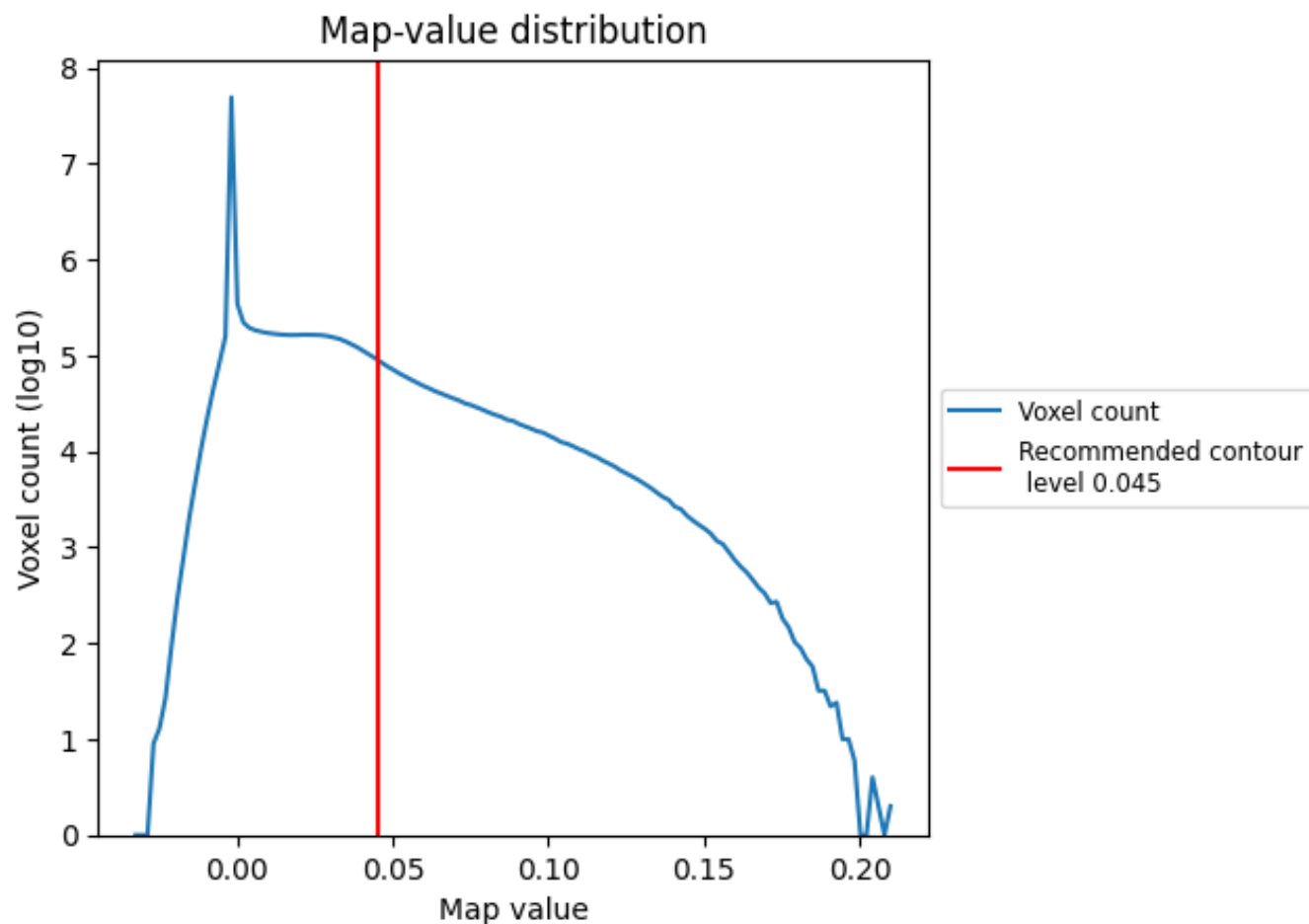
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

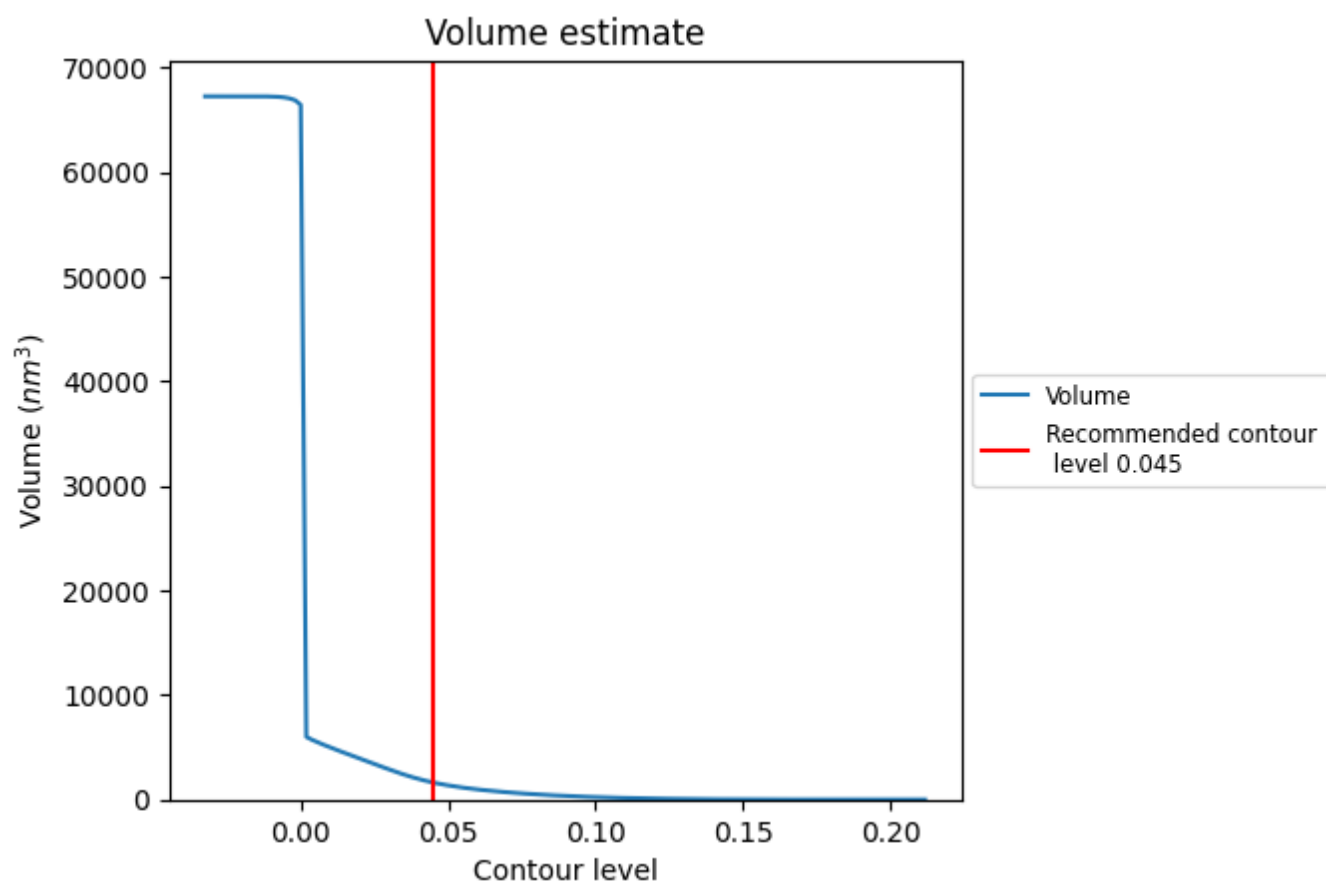
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

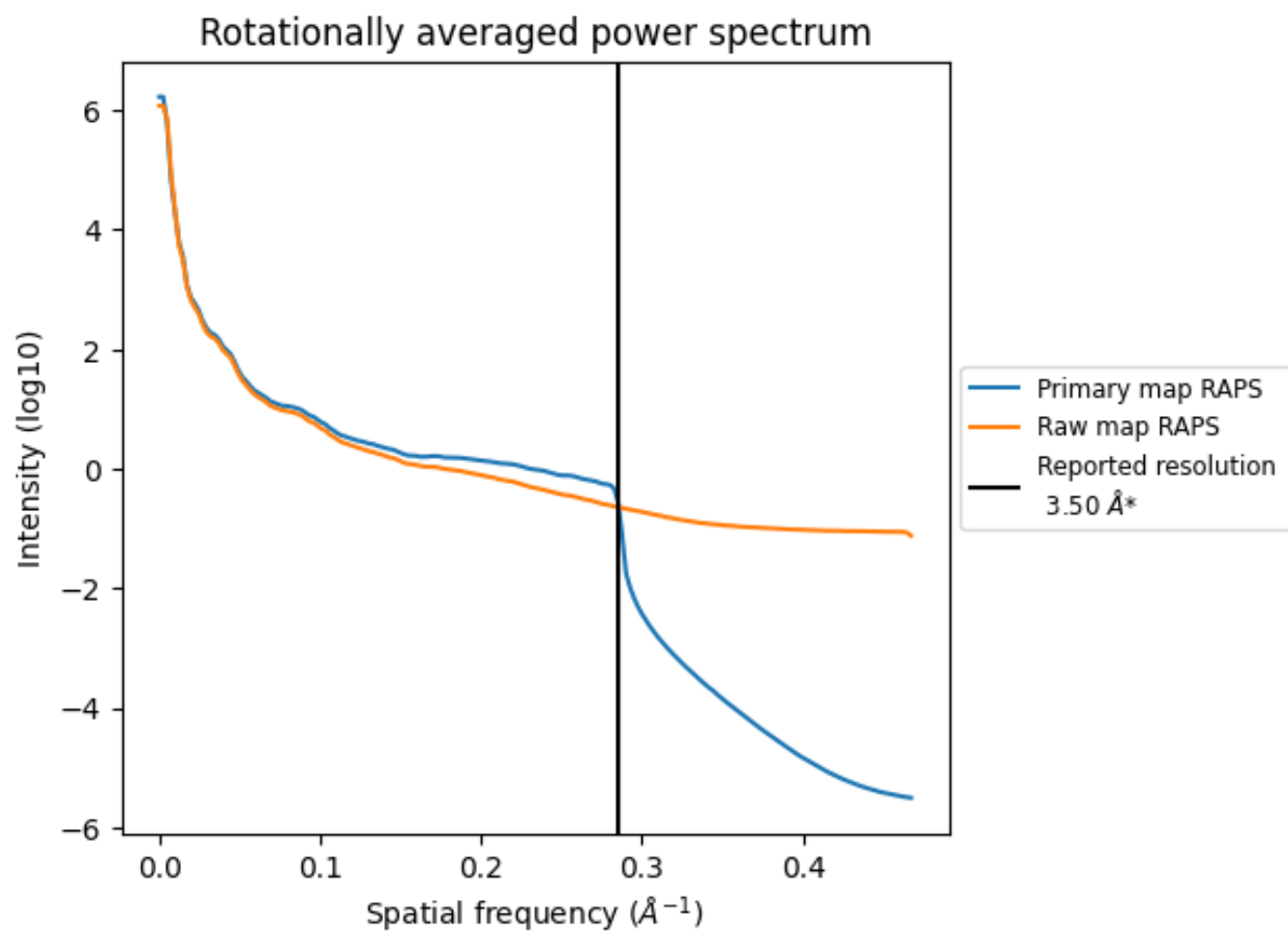
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1622 nm³; this corresponds to an approximate mass of 1465 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 ⓘ

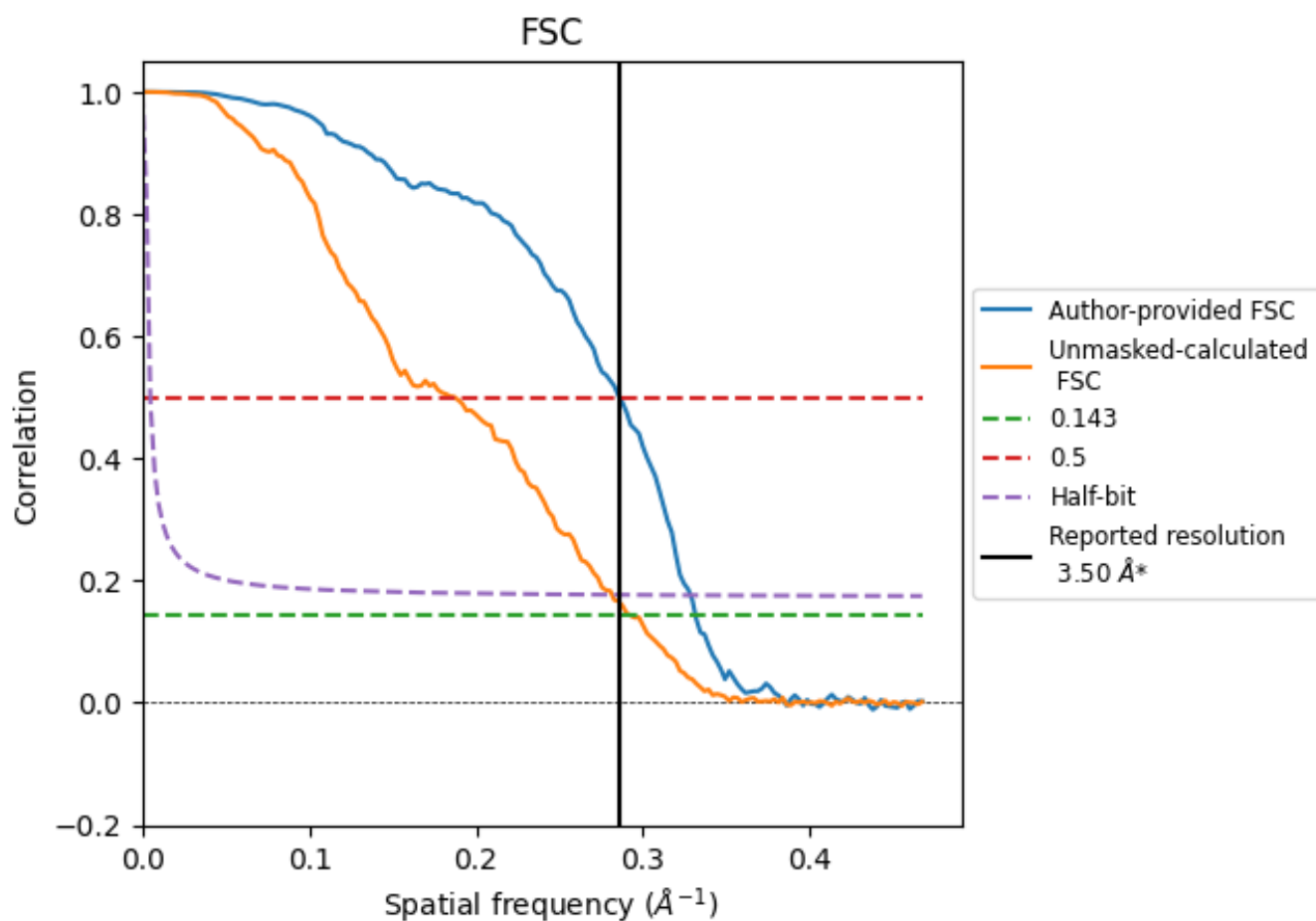


*Reported resolution corresponds to spatial frequency of $0.286 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

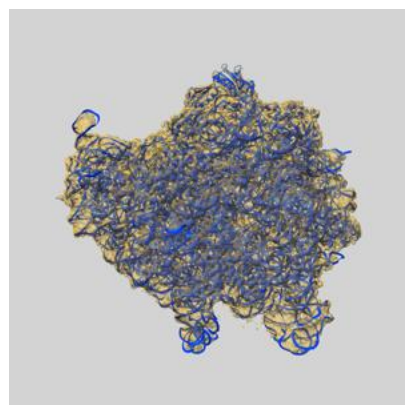
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.02	3.50	3.04
Unmasked-calculated*	3.42	5.34	3.55

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.02 differs from the reported value 3.5 by more than 10 %

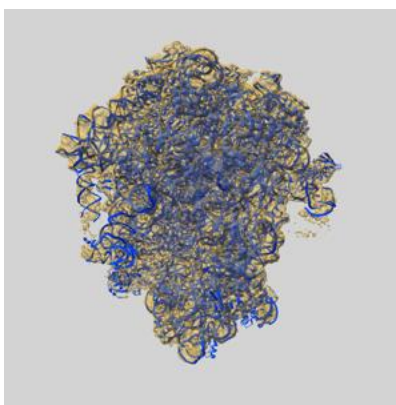
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37559 and PDB model 8WI7. Per-residue inclusion information can be found in section [3](#) on page [13](#).

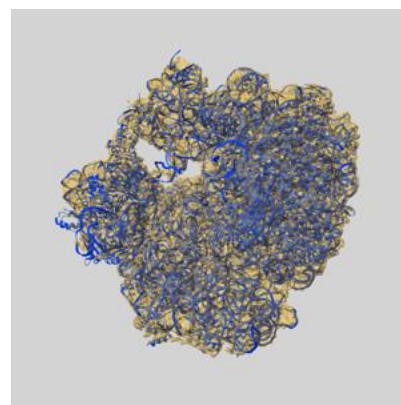
9.1 Map-model overlay [i](#)



X



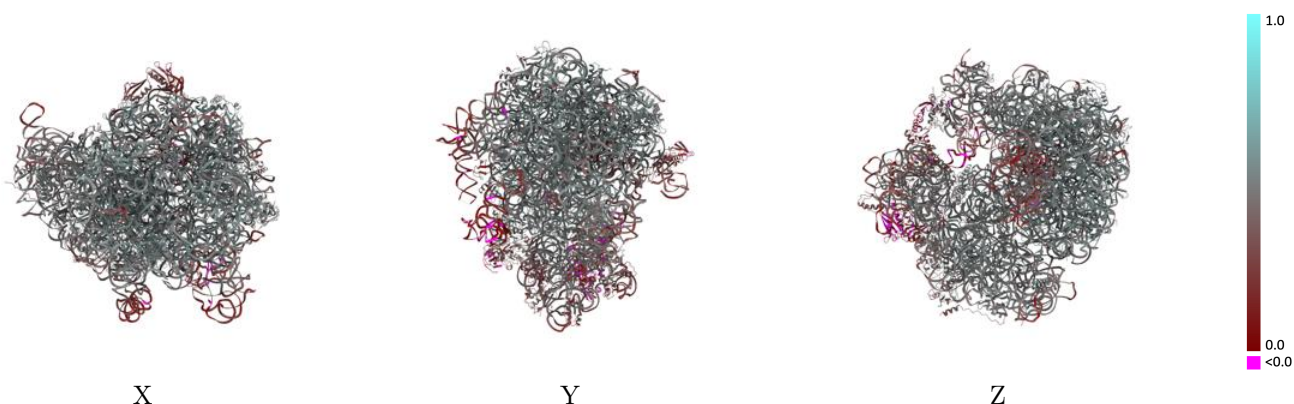
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.045 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](#)



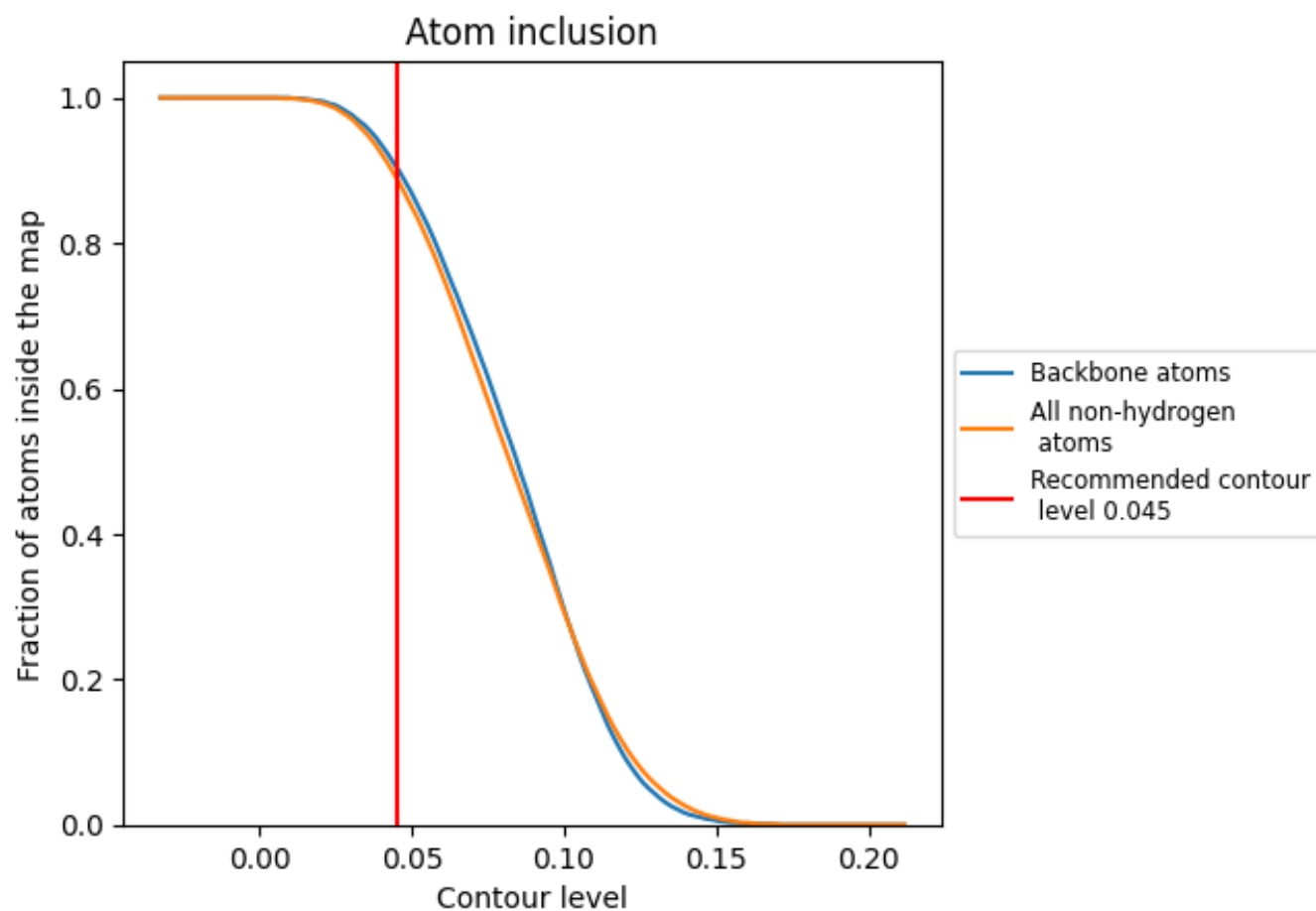
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 89% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.4480
1	 0.8870	 0.4740
2	 0.8290	 0.4720
3	 0.8870	 0.5080
4	 0.3240	 0.1470
5	 0.8530	 0.5140
6	 0.5620	 0.2770
7	 0.9940	 0.4920
8	 0.8930	 0.5180
A	 0.9260	 0.4580
B	 0.9440	 0.4300
E	 0.9670	 0.5360
F	 0.9220	 0.5300
G	 0.8930	 0.5060
H	 0.7810	 0.4110
I	 0.4780	 0.2610
J	 0.5430	 0.2690
M	 0.9280	 0.5110
N	 0.9360	 0.5230
O	 0.8900	 0.5000
Q	 0.9610	 0.5370
R	 0.8100	 0.4400
S	 0.8970	 0.4870
T	 0.9340	 0.5160
U	 0.8860	 0.5350
V	 0.9680	 0.5370
W	 0.8960	 0.5170
X	 0.8200	 0.4780
Z	 0.9450	 0.5260
a	 0.9630	 0.4570
b	 0.2710	 0.2050
c	 0.6970	 0.3630
d	 0.2170	 0.0800
e	 0.8310	 0.4530
f	 0.8400	 0.4590



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Chain	Atom inclusion	Q-score
g	 0.8130	 0.4670
h	 0.7130	 0.3330
i	 0.9200	 0.5010
j	 0.7630	 0.3970
k	 0.5080	 0.4090
l	 0.8630	 0.4680
m	 0.8930	 0.4950
n	 0.6820	 0.2270
o	 0.4980	 0.3780
p	 0.8760	 0.4820
q	 0.8450	 0.4760
r	 0.8790	 0.4500
s	 0.8080	 0.4180
t	 0.6910	 0.3250
u	 0.8840	 0.4770
v	 0.9680	 0.4840
w	 0.6440	 0.3880