



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:13 PM UTC

PDB ID : 7PIS / pdb_00007pis
EMDB ID : EMD-13449
Title : 70S ribosome with EF-G, A*- and P/E-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 15.00 Å (reported)
Based on initial models : 7OOC, 7OOD, 4V7C, 4V7D

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

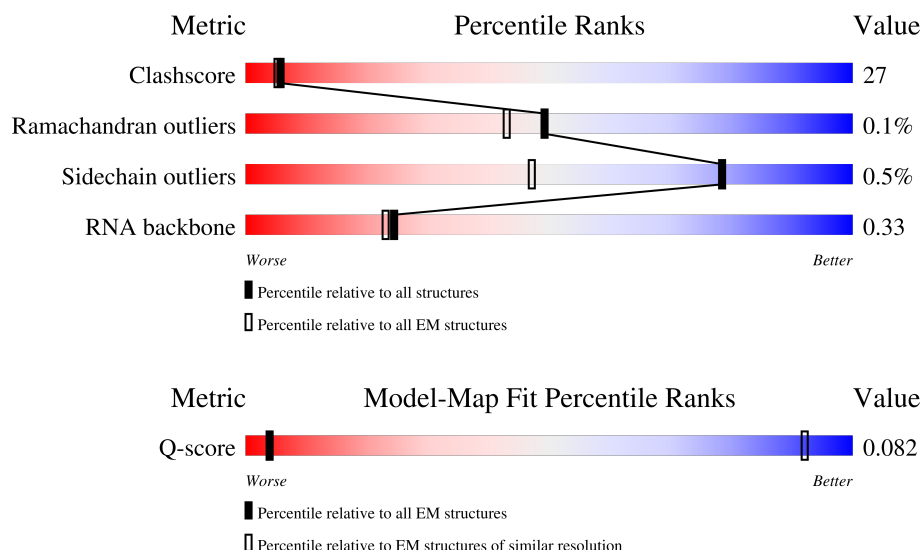
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 15.00 Å.

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



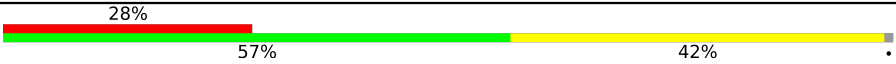
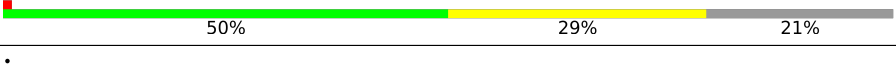
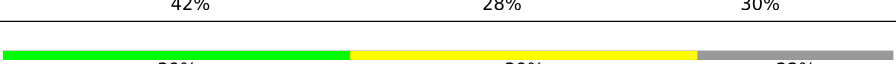
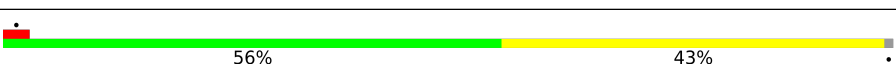
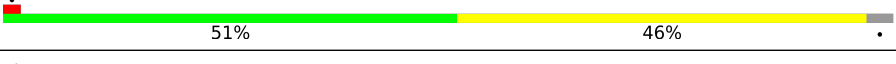
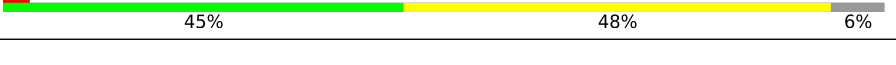
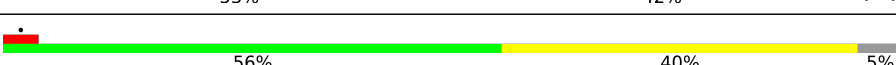
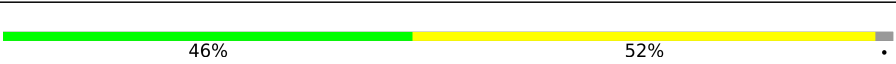
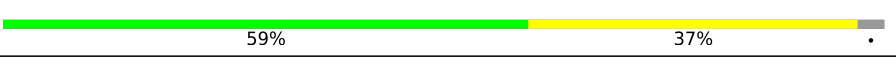
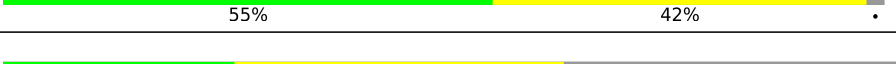
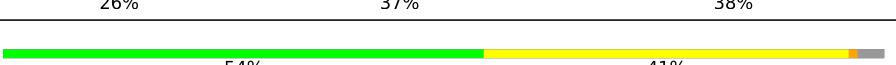
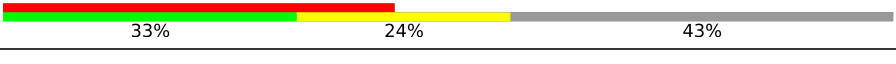
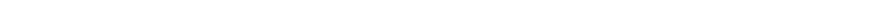
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	37 (14.50 - 15.50)

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	0	48	
2	1	59	
3	2	37	

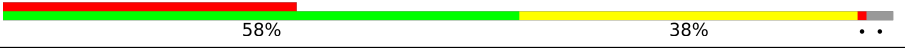
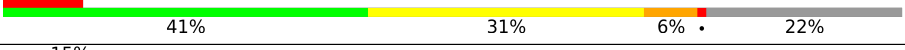
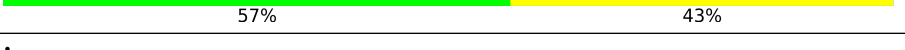
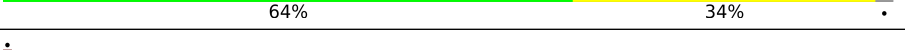
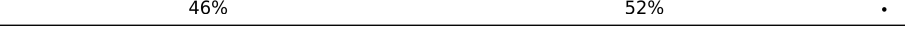
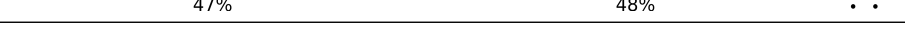
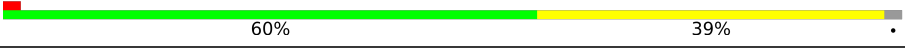
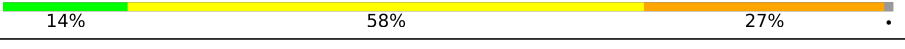
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Mol	Chain	Length	Quality of chain
4	9	688	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	W	122	
26	a	287	
27	b	287	
28	c	212	

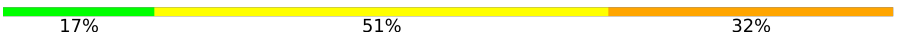
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Mol	Chain	Length	Quality of chain
29	d	180	
30	e	184	
31	f	149	
32	g	161	
33	h	137	
34	i	146	
35	j	122	
36	k	151	
37	l	139	
38	m	124	
39	n	116	
40	o	119	
41	p	127	
42	q	100	
43	r	159	
44	s	237	
45	t	111	
46	u	104	
47	v	65	
48	w	111	
49	x	97	
50	y	57	
51	z	53	
52	3	2907	
53	4	108	

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Mol	Chain	Length	Quality of chain
54	5	1520	 13% 59% 27% .
55	6	76	 17% 51% 32%
55	8	76	 16% 54% 30%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151980 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	682	Total	C	N	O	S	0	0
			5326	3369	911	1021	25		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 11 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 25 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	69	Total	C	N	O	S	0	0
			534	342	87	103	2		

- Molecule 26 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 27 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 28 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 29 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 30 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 31 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 32 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 33 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 34 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 35 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 36 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	148	Total	C	N	O		0	0
			1153	731	226	196			

- Molecule 37 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 38 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 39 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 40 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 41 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 42 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 43 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 44 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 45 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	100	Total	C	N	O		0	0
			818	517	153	148			

- Molecule 49 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 51 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 53 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 54 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

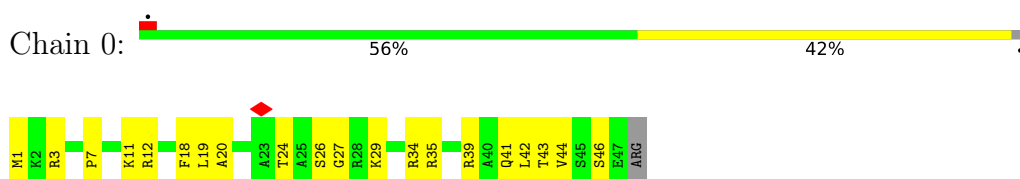
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
55	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

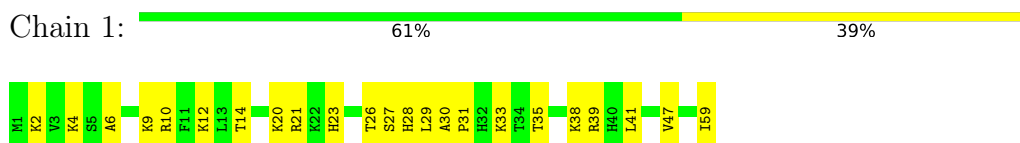
3 Residue-property plots

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.

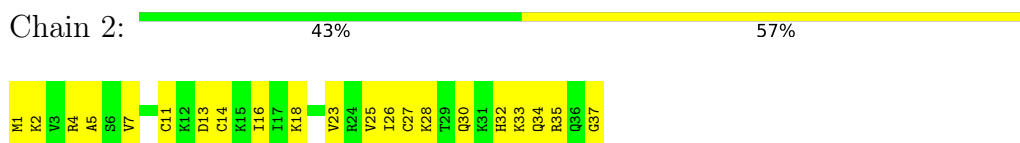
- Molecule 1: 50S ribosomal protein L34



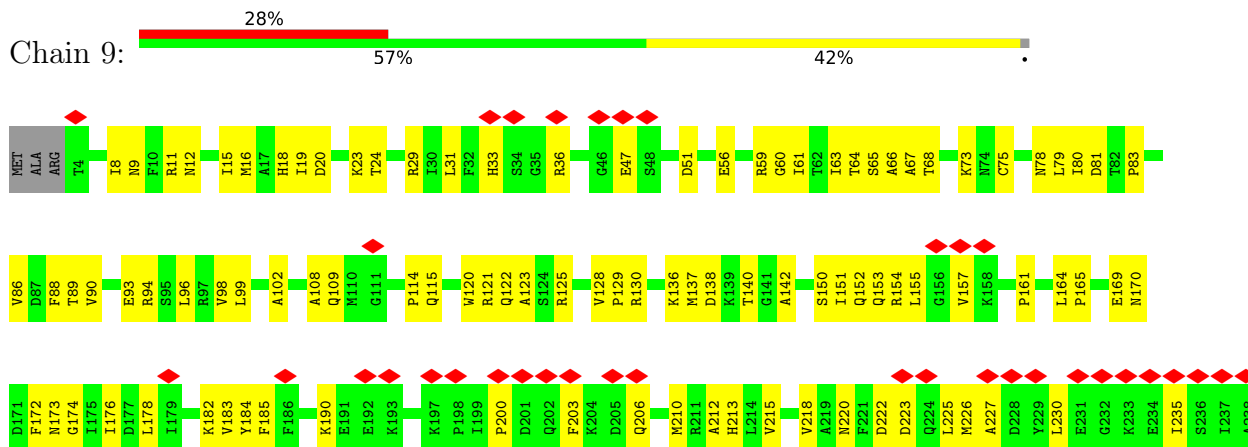
- Molecule 2: 50S ribosomal protein L35

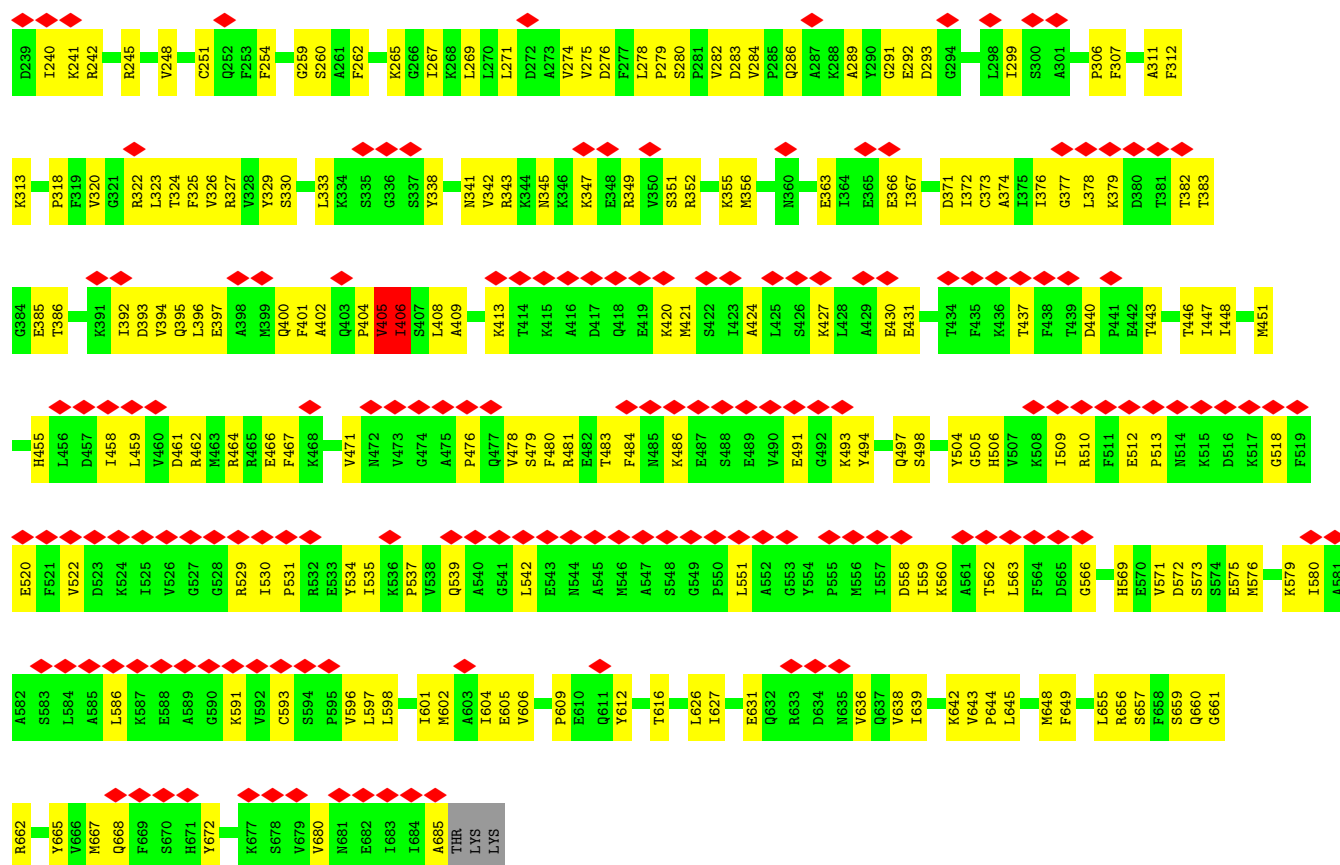


- Molecule 3: 50S ribosomal protein L36



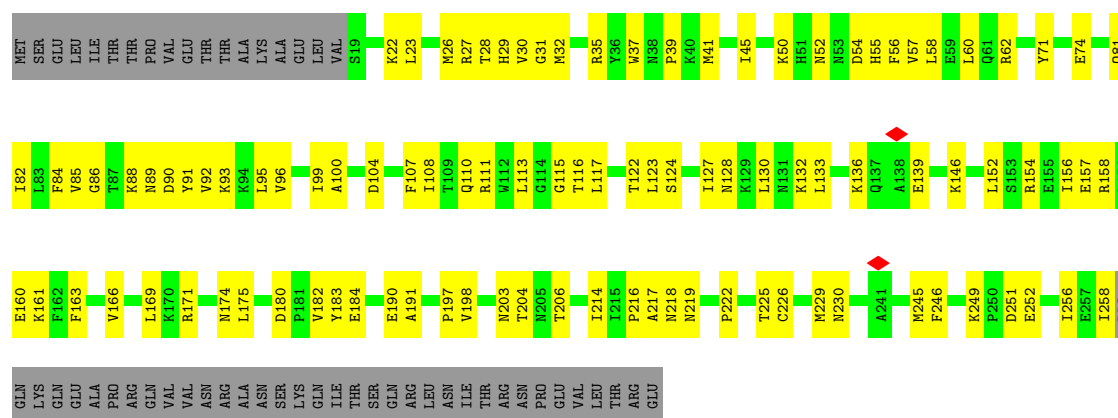
- Molecule 4: Elongation factor G





• Molecule 5: 30S ribosomal protein S2

Chain A: 47% 34% 18%

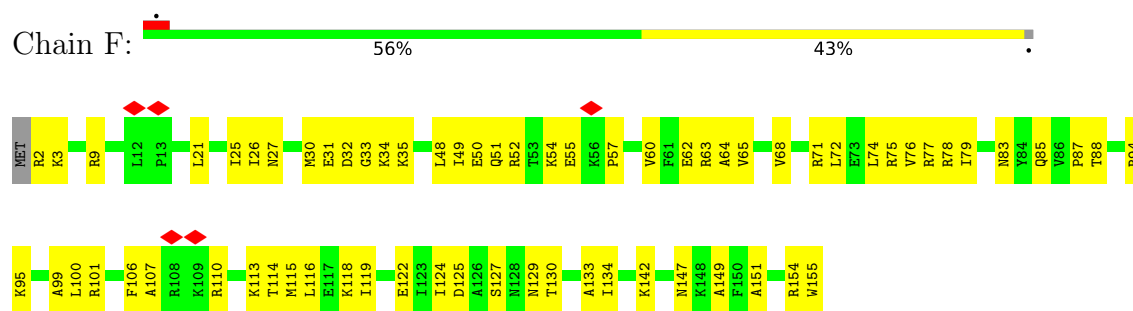


• Molecule 6: 30S ribosomal protein S3

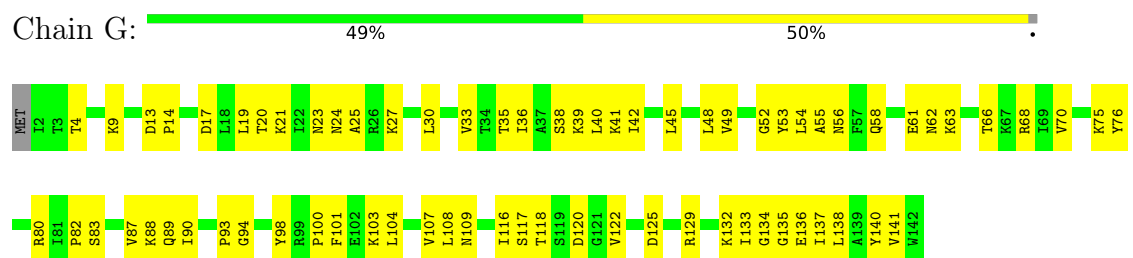
Chain B: 50% 29% 21%



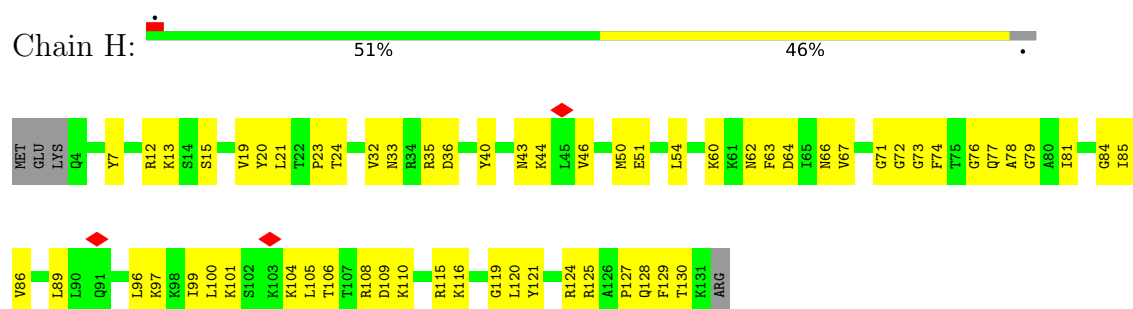
- Molecule 10: 30S ribosomal protein S7



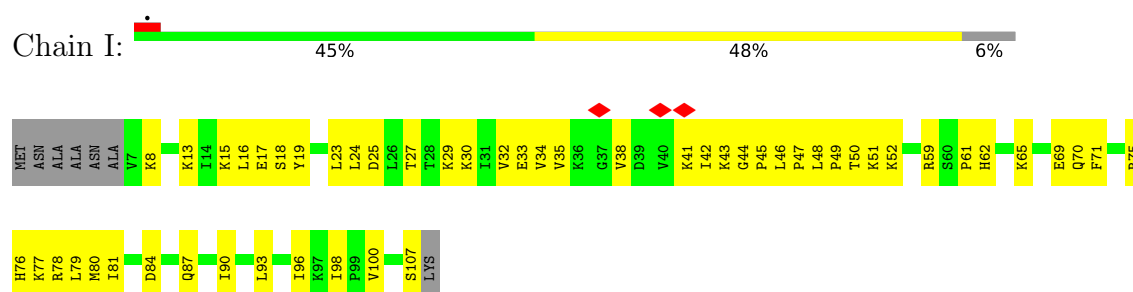
- Molecule 11: 30S ribosomal protein S8



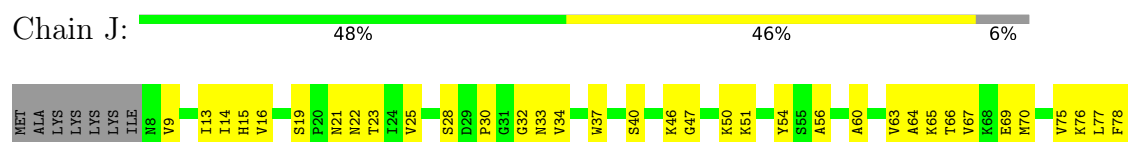
- Molecule 12: 30S ribosomal protein S9



- Molecule 13: 30S ribosomal protein S10

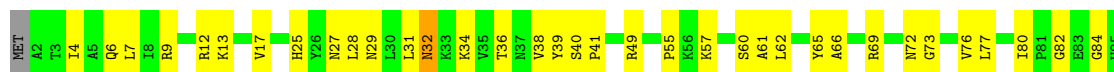


- Molecule 14: 30S ribosomal protein S11

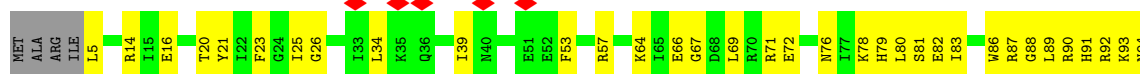




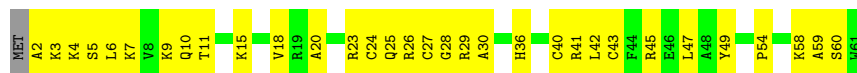
- Molecule 15: 30S ribosomal protein S12



- Molecule 16: 30S ribosomal protein S13



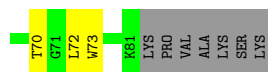
- Molecule 17: 30S ribosomal protein S14 type Z



- Molecule 18: 30S ribosomal protein S15



- Molecule 19: 30S ribosomal protein S16

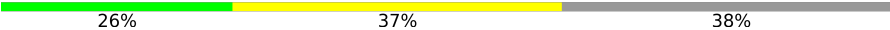


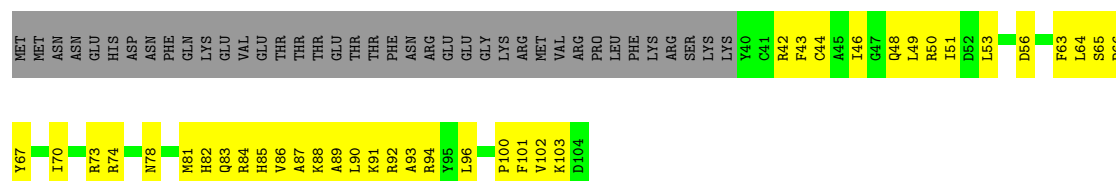
- Molecule 20: 30S ribosomal protein S17

Chain P:  55% 42%



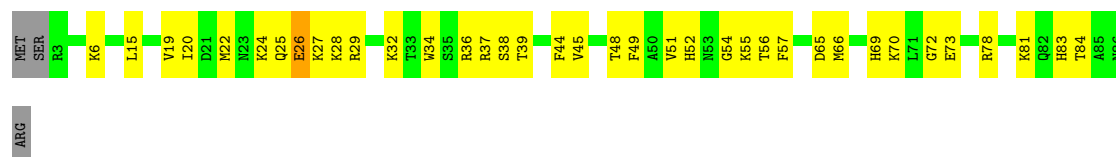
- Molecule 21: 30S ribosomal protein S18

Chain Q:  26% 37% 38%



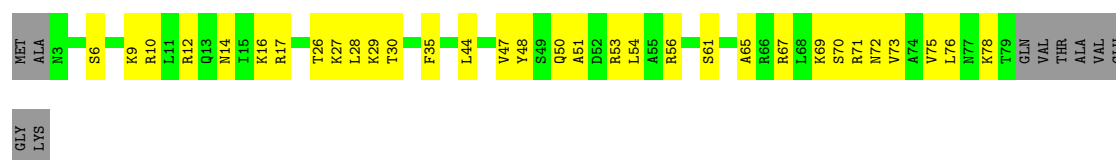
- Molecule 22: 30S ribosomal protein S19

Chain R:  54% 41%



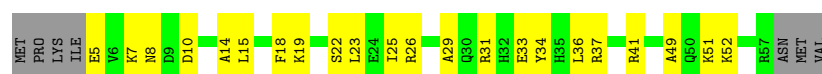
- Molecule 23: 30S ribosomal protein S20

Chain S:  52% 37% 11%

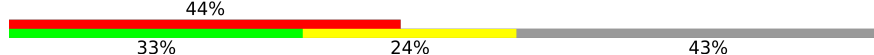


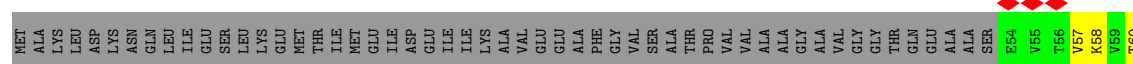
- Molecule 24: 30S ribosomal protein S21

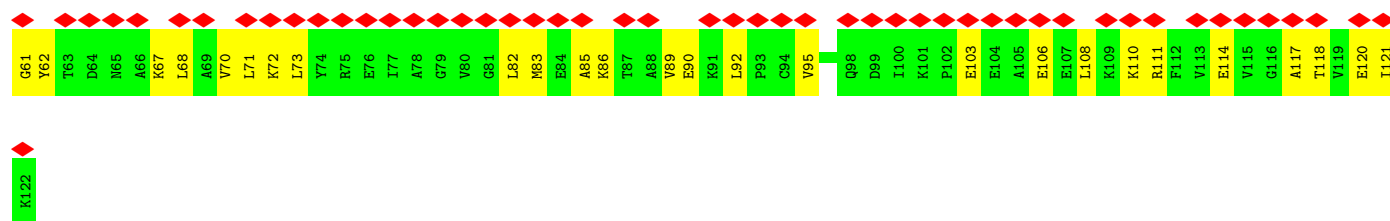
Chain T:  52% 37% 12%



- Molecule 25: 50S ribosomal protein L7/L12

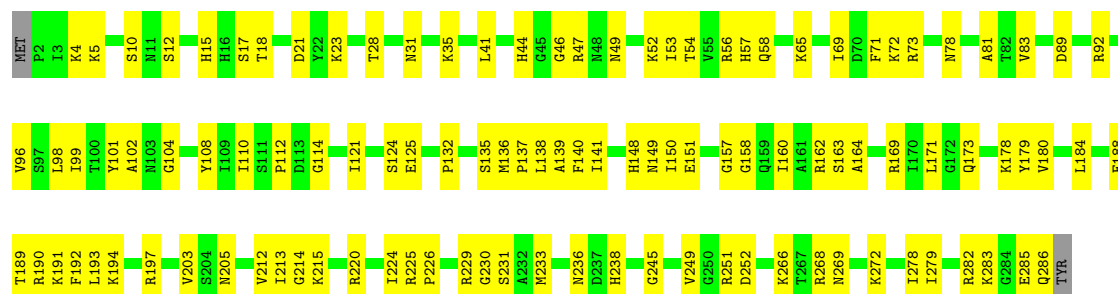
Chain W:  33% 24% 43%





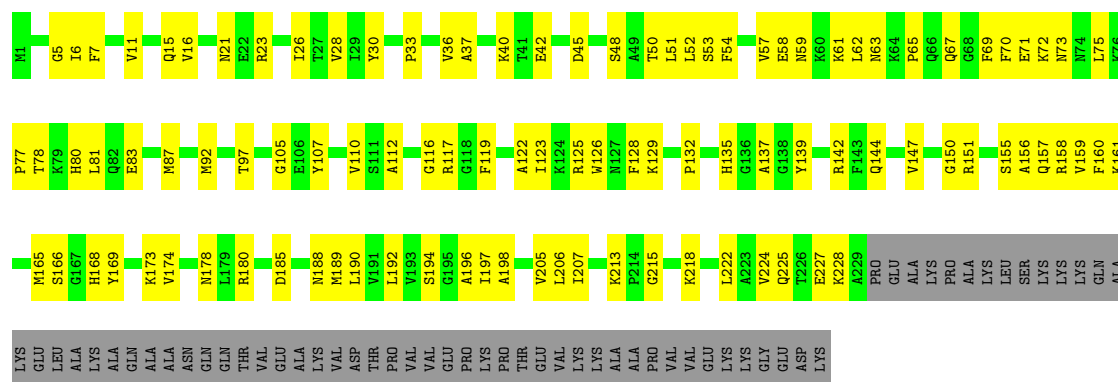
• Molecule 26: 50S ribosomal protein L2

Chain a: 61% 38%



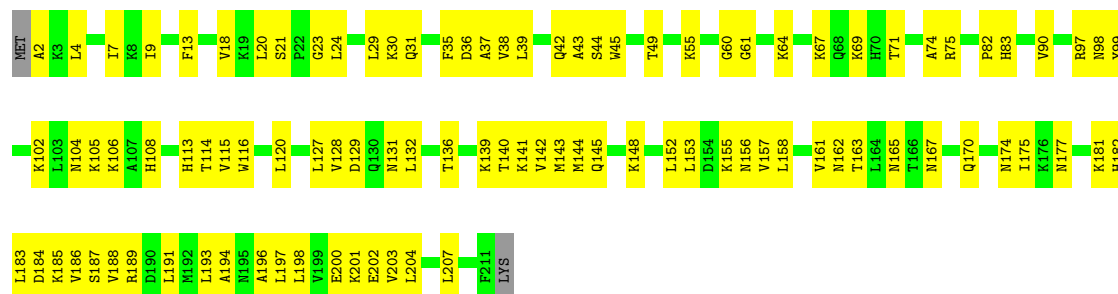
• Molecule 27: 50S ribosomal protein L3

Chain b: 44% 36% 20%

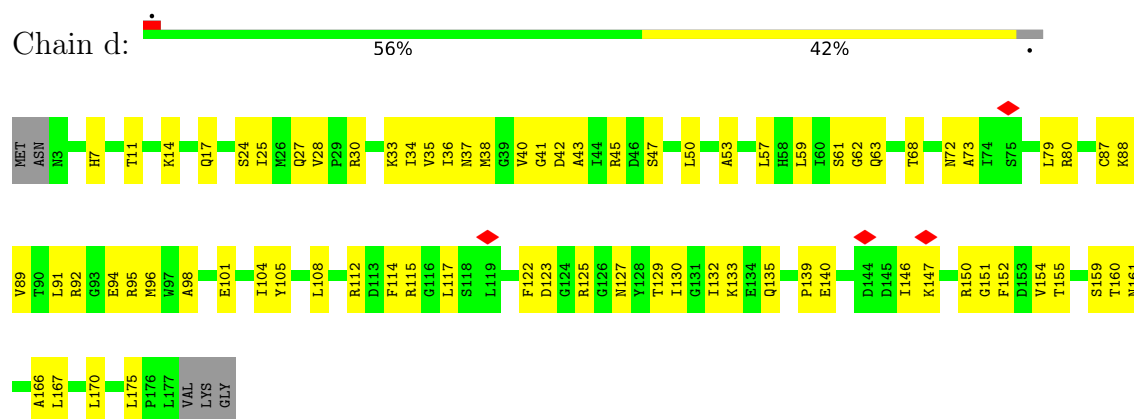


• Molecule 28: 50S ribosomal protein L4

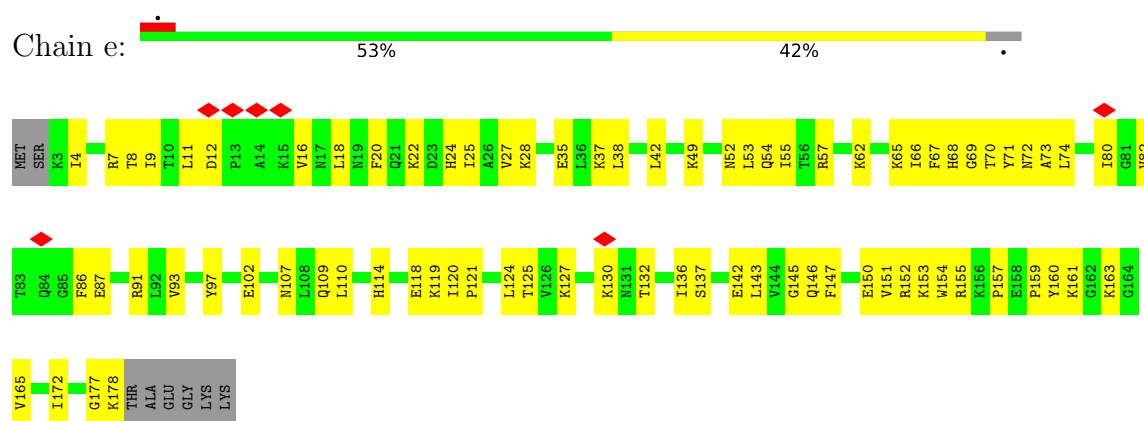
Chain c: 53% 46%



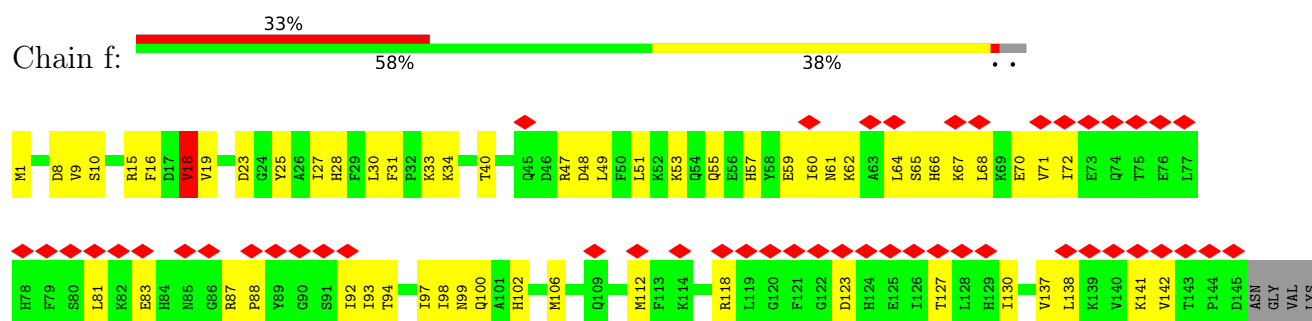
• Molecule 29: 50S ribosomal protein L5



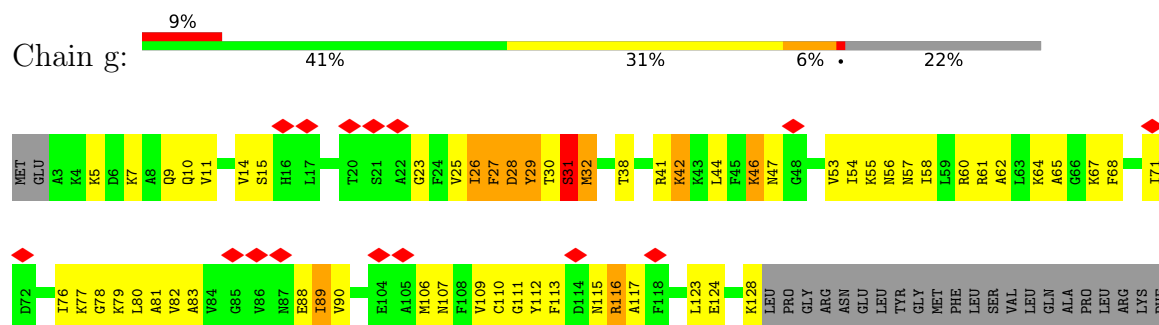
• Molecule 30: 50S ribosomal protein L6



• Molecule 31: 50S ribosomal protein L9



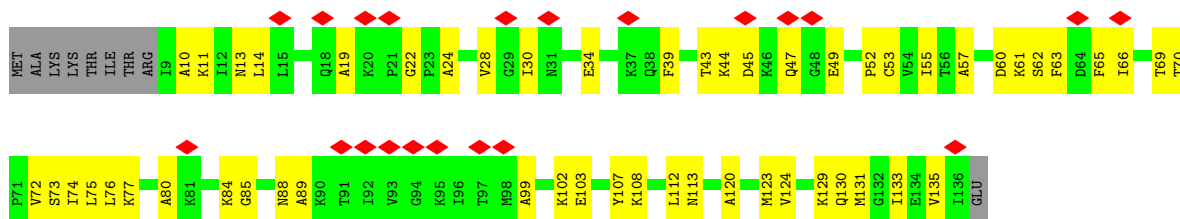
• Molecule 32: 50S ribosomal protein L10



LEU
TYR
ALA
LEU
GLU
ALA
VAL
LYS
ALA
ALA
LYS

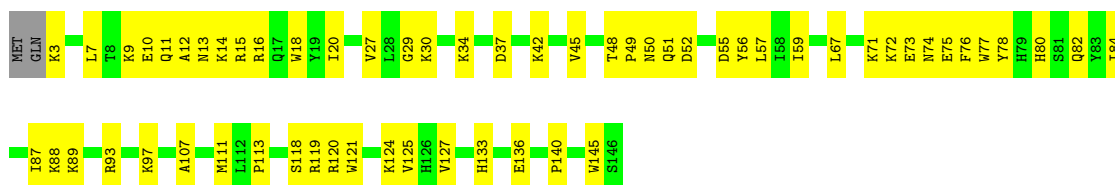
• Molecule 33: 50S ribosomal protein L11

Chain h: 15% 54% 39% 7%



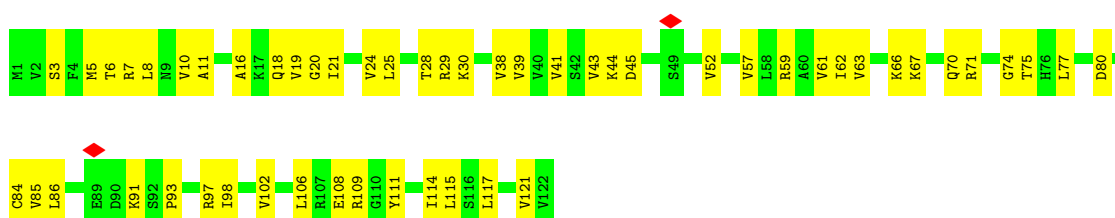
• Molecule 34: 50S ribosomal protein L13

Chain i: 58% 40%



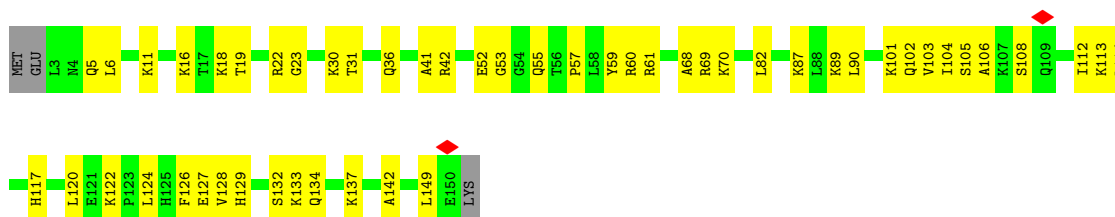
• Molecule 35: 50S ribosomal protein L14

Chain j: 57% 43%



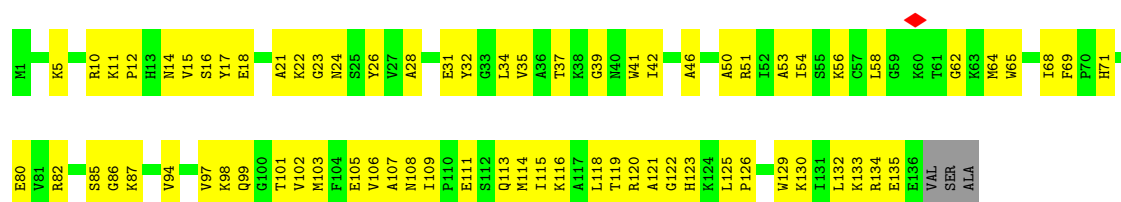
• Molecule 36: 50S ribosomal protein L15

Chain k: 64% 34%



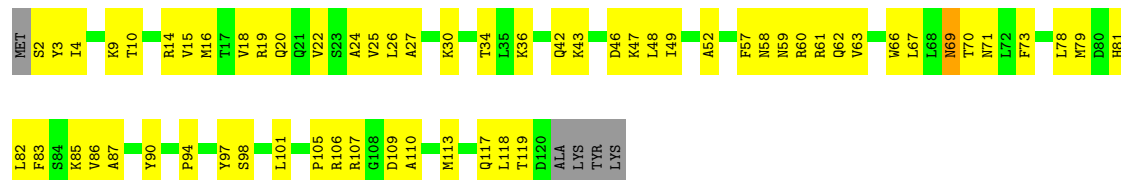
• Molecule 37: 50S ribosomal protein L16

Chain l: 46% 52%



• Molecule 38: 50S ribosomal protein L17

Chain m: 47% 48%



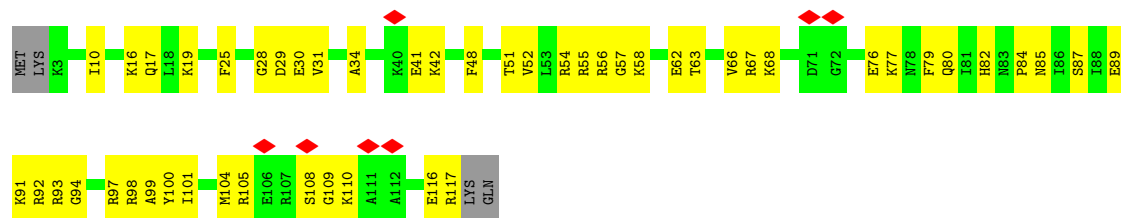
• Molecule 39: 50S ribosomal protein L18

Chain n: 49% 47%



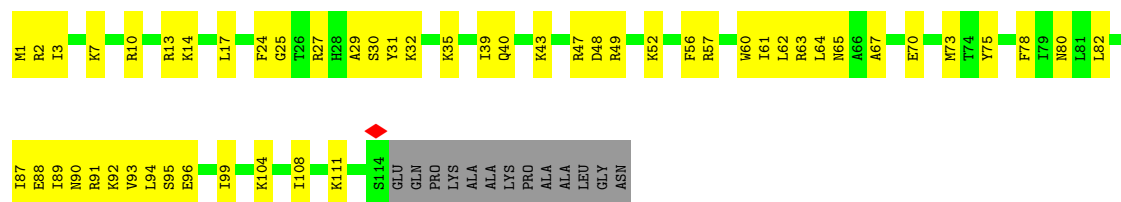
• Molecule 40: 50S ribosomal protein L19

Chain o: 6% 54% 43%

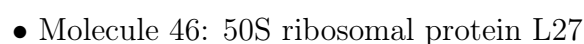
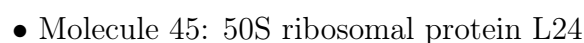
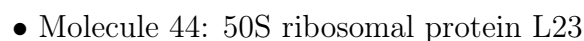
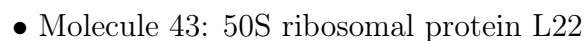


• Molecule 41: 50S ribosomal protein L20

Chain p: 49% 41% 10%



• Molecule 42: 50S ribosomal protein L21





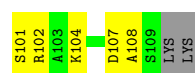
- Molecule 47: 50S ribosomal protein L28

Chain v: 57% 40% .



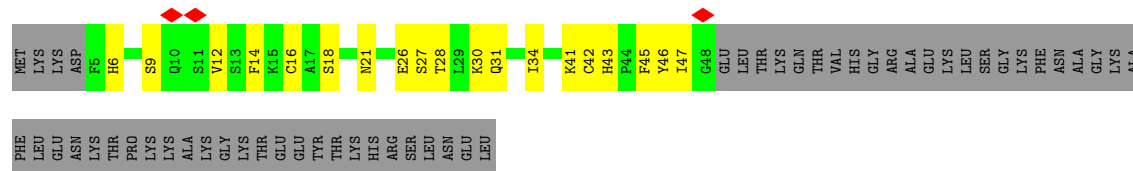
- Molecule 48: 50S ribosomal protein L29

Chain w: 57% 33% 10%



- Molecule 49: 50S ribosomal protein L31

Chain x: 26% 20% 55%



- Molecule 50: 50S ribosomal protein L32

Chain y: 60% 39% .



- Molecule 51: 50S ribosomal protein L33 1

Chain z: 47% 47% 6%



- Molecule 52: 23S ribosomal RNA

Chain 3: 14% 58% 27%

U939	U940	A943	U944	U945	A946	A947	A948	C949	U950	C951	U952	G953	A954	A955	U956	U957	C958	C959	A960	U961	U962	U963	A964	U965	U966	U967	A968	U969	U970	U971	C972	U973	G974	G975	C976	A977	G978	U979	C980	A981	G982	A983	C984	A985	C986	U987	G988	G989	G990	G991	G992	A993	U994	A995	U996	U997	U999																																																																																																																																																																																																																																																																																																																																																																																																																																								
U819	U820	C821	C822	A823	A824	U825	C826	C827	C828	A829	A830	U831	C832	C833	C834	U835	U836	A837	U838	A839	C840	C841	U842	U843	C844	U845	U846	C847	U848	C849	U850	C851	C852	A853	C854	A855	A856	U857	A858	C859	C860	U861	U862	U863	C864	C865	C866	C867	C868	U869	U870	A871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000																																																																																																																																																																																																																																																																																																												
U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000																																																																																																																																																																																																																																																
U619	U620	C621	C622	A623	A624	U625	C626	C627	C628	A629	A630	U631	C632	C633	C634	U635	U636	A637	U638	A639	C640	C641	U642	U643	C644	U645	U646	C647	U648	C649	U650	C651	C652	A653	C654	A655	A656	U657	A658	C659	C660	U661	U662	U663	C664	C665	C666	C667	C668	U669	U670	A671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000																																																																																																				
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G1876	G1814	A1750	C1432	A1370	C1247	A1186	G1124	A1063	U1000
G1879	U1815	A1751		G1371	A1248	C1187	U1125	A1064	C1001
A1880	A1816	A1752	A1435	U1372	A1249	G1189	G1126	G1065	A1002
C1881	A1817	G1753	C1436	C1373	U1250	G1189	C1127	G1066	U1003
G1882	G1818		A1437	U1374	G1252	G1191	U1128	A1067	U1004
A1883	G1819		G1438	G1375	G1252	G1191	G1129	U1068	G1005
A1884	U1820	C1759	A1439	G1376	G1253	U1192	A1130	G1069	U1006
A1885	G1821	G1760	U1440	U1377	U1254	U1193	A1131	C1007	C1007
C1886	A1822	G1698	A1441	C1378	G1255	U1194	C1132	A1008	A1008
U1887	U1823	A1762	A1442	C1379	A1256	U1196	A1133	A1009	A1009
G1887	G1824	G1763	A1443	U1380	G1257	U1196	G1134	G1010	G1010
A1888	U1825	U1764	C1444	A1381	G1258	G1197		A1011	A1011
U1889	A1826	G1765	U1445	A1382	A1259	G1198	G1137	U1076	
U1890	U1827	A1766	G1446	G1383	U1260	A1199	A1138	G1077	G1012
A1891	A1828	A1767	A1447	C1384	U1261	U1200	C1139	C1078	A1016
A1892	U1829	G1768	U1448	U1385	G1262	A1201	U1140	U1079	
C1893	G1830	A1769	G1449	G1386	G1263		U1141	A1080	A1019
A1894	G1831	A1770	G1450	G1387	U1264	A1204	U1142	A1081	G1020
G1895	G1832	C1771	A1451	G1388	G1265	U1205	U1143	A1082	C1021
A1896	G1833	G1772	A1452	G1389	G1266	U1206	C1144	A1083	G1022
A1897	U1834	A1773	U1453		A1267	U1207	G1145	C1084	C1023
G1898	G1835	G1774	G1454	A1393	U1268	A1208	A1146	A1085	A1024
	A1836	A1775	A1455	A1394	C1269	U1209	G1147	G1086	G1025
A1902	C1837	G1776	C1456	A1395	A1270	A1210	U1148	C1087	A1026
A1903	A1838	G1777	A1457	A1396	A1271	U1211	G1149	A1088	U1027
G1906	G1839	G1778	A1458	G1397	A1272	C1212	U1150	A1089	C1028
A1907	C1840	G1779	A1459	C1398	U1273	U1213	U1151	G1090	A1029
A1908	U1841	G1780	C1531	G1399	A1274	U1214		G1091	U1030
G1909	G1842	C1781	G1464	U1400	C1275	G1215	U1154	A1092	A1031
G1910	C1843	U1782	U1465	A1401	A1276	U1216	G1155	U1093	A1032
G1911	C1844	G1783	U1466	G1402	A1277	G1217	C1156	G1094	A1033
A1912	A1845	U1784	U1467	G1403	G1278	G1218	G1157	U1095	A1034
G1913	G1846	U1785		C1404	U1279	U1219	C1158	U1096	U1035
G1914	U1847	U1786	C1472	G1405	G1280	U1220	G1159	G1097	A1036
G1915	G1848	A1787	C1473	A1406	A1281	G1221	G1160	G1098	A1037
C1916	G1849	A1788	C1474	U1407	G1282	A1222	A1161	C1099	G1038
G1917	G1850	G1789	C1475	G1408	A1283	C1223	A1162	U1100	G1039
	U1851	U1790	A1541	G1409	A1284	G1224	G1163	U1101	U1040
	G1852	A1791	G1542	A1410	U1285	A1225	A1164	A1102	C1041
		A1792	U1543	C1411	G1286	G1226	U1165	G1103	C1042
A1920	A1855	A1793	G1544	A1412		C1227	G1166	A1104	C1043
C1921	G1856	A1794	A1545	A1413	G1289	U1228	U1167	A1105	C1044
U1922	G1857	G1795	U1546	C1414	G1290	U1229	A1168	G1106	A1045
A1923	A1860	A1796	G1547	A1415	C1291	U1230	A1169	C1107	A1046
U1924	A1861	C1797	U1481	G1416	A1292	G1231	C1170	A1108	A1047
A1925	A1862		U1482		U1293	U1232	G1171	G1109	A1048
A1926	G1863	G1677	G1483	G1417	U1294	A1233	G1172	C1110	U1049
C1927	A1864	U1677	U1484	U1418	A1295	U1234	G1173	C1111	A1050
G1928	G1865	U1678	A1485	A1419	G1296	U1235	G1174	A1112	U1051
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U1930	G1867	A1680	U1487	U1421	A1298	G1237	U1176	G1114	C1053
	U1617	U1618	U1488	U1422	A1299	A1238	A1177	G1115	U1054
	U1618	G1615	G1552	A1423	A1299	G1239	U1178	U1116	A1055
	A1619	A1619	U1556	U1424	C1300	U1240	G1179	U1117	A1056
	U1743	G1683	G1557	U1425	G1301	U1241	G1180	U1118	G1057
	U1744	A1684	A1558	C1426	U1302	G1242	A1181	A1119	U1058
	A1745	A1685	A1559	A1495	U1303	A1243	U1182	G1059	A1120
	U1746	U1686	U1496	A1496	U1304	G1244	A1183	A1121	G1060
	U1747	G1687	A1497	A1497	G1305	A1245	U1184	G1122	A1061
	U1748	A1688	U1498	G1429	G1306				
	A1749	A1689	C1499	A1431	G1307	U1246	U1185	A1123	A1062

A2814	G2753	G2629	G2668	U2508	A2443	A2382	A2318	G2254	U2193	A2130	A2067	C2003	G1940
G2815	U2754	U2630	A2669	C2609	G2444	G2382	A2319	A2255	G2194	G2131	G2068	G2004	C1941
A2816	G2755	G2631	U2670	G2510	G2445	A2384	A2320	C2256	U2195	G2132	G2069	G2005	G1942
C2819	G2756	C2632	U2571	A2511	U2449	A2385	C2321	U2257	G2196	A2133	C2070	C2006	A1943
G2820	A2757	G2633	A2572	U2512	C2450	A2386	G2322	G2258	U2197	G2134	C2071	U2007	A1944
U2821	G2758	C2634	A2573	G2513	C2451	U2387	U2323	G2259	G2198		C2072	A2008	A1945
U2822	G2759	G2635	A2574	U2514	G2452	C2388	A2324	G2260	C2199		C2073	U2009	U1946
C2823	G2760	U2636	G2575	C2515	G2453	A2389	A2325	G2261	U2200	A2137	G2074	A2010	
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G2825	C2700	G2638	G2577	C2517	A2455	U2391	U2327	G2263	U2202	G2139	G2076	A2012	G1952
A2826	A2762	A2639	A2578	A2518	G2456	U2392	A2328		U2203	A2141	A2077		U1953
G2827	U2764	U2579	A2579	U2519	U2457	C2393	G2329	C2266	C2204	U2142	A2078	C2015	G1954
A2828	A2765	A2580	A2458	C2520	A2458	A2394	A2330	G2267	U2005	G2143	G2079	G2016	G1955
C2828	G2642	C2581		A2521		U2395	G2331	C2268	A2206	C2144	C2080	G2017	G1956
G2829	A2643		A2461	A2522	A2461	A2396	U2332	C2269	U2207	A2145	U2081	U2018	U1957
A2830	G2705	G2684	G2582	C2523	G2582	A2397	G2333	C2270	U2208	A2146	U2082	G2019	U1958
U2831	U2706	U2644	A2583	U2524	G2463	U2398	U2334	C2271			U2083	A2020	A1959
G2832	A2707	U2645	G2584	G2525	G2464	C2403	A2335	C2272	U2216	U2148	A2084	A2021	A1960
A2833	G2708	G2646	G2585	C2526	U2465	A2400	A2336	C2273	G2217	U2149		A2022	A1961
C2834	C2709	A2647	A2586	A2527	U2466	U2401	U2337	A2274	U2218	C2150	G2087		U1962
G2835	G2710	U2648	U2587	G2528	G2467	C2402	G2338	A2275			U2088	C2025	U1963
A2836	G2711	G2649	U2588	C2529	A2468	U2403	A2339	A2276	A2214	A2151	A2089	A2026	C1964
U2837	A2712	A2650	G2589	U2530	U2469	G2404	G2340	A2277	C2215	U2152	G2090	G2027	C1965
G2838	G2713	G2651	G2590	U2531	A2470	U2405	G2341	A2278	U2216	G2153	C2091	G2028	G1966
A2839	U2716	U2652	U2592	C2532	C2471	U2406	U2342	G2279	G2217	A2154	U2092	U2029	U1967
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A2841	C2718	U2654	C2594	G2534	C2473	C2408	A2344	U2281	U2219	G2156	U2094	C2031	C1969
G2842	U2718	U2655	A2595	G2535	C2474	U2409	A2345	A2282	U2220	A2157	A2095	G2032	C1970
C2843	A2719	G2656	A2596	C2536	C2475	G2410	G2346	A2283	C2222	C2158	U2096	G2033	G1971
U2844	G2720	C2657	G2597	U2536	A2476	C2411	G2347	G2284	C2223	U2160	A2097	C2034	C1972
A2845	C2721	G2658	C2598	G2537	A2477	C2412	U2348	G2285	A2224	G2161	U2098	U2035	U1973
U2846	G2722	U2659	C2599	A2538	A2477	A2413	U2349	A2286	C2225	U2162	U2099	U2036	U1974
A2847			G2600	C2539	C2478	G2414	G2340	G2287	U2226	U2163	U2100	A2037	G1975
G2848	G2725	A2662	U2601	G2540	A2479	U2414	C2349		U2227	G2164	A2101	A2038	A1976
U2849	G2726	G2663	C2602	C2541	G2480	U2415	U2351	U2291	U2228	A2165	U2102	G2039	A1977
G2850	G2727	U2664	A2603	G2542		U2416	U2352	A2292	C2229		C2103	A2040	U1978
A2851	U2728	A2665	G2604	G2543	C2483	G2417	G2353	C2293	A2230	G2169	A2104	C2041	G1979
U2852	G2729	C2666	G2605	U2544	A2484	G2418	A2354	C2294	A2231	A2170	G2105	A2042	G1980
G2853	G2730	G2667	A2606	U2545	U2485	A2419	C2355	A2296	G2232	A2171	G2106	C2043	U1981
U2854	U2731	A2668	G2607	U2546	A2486	A2420	U2356	A2297	C2233	A2172	A2107	C2044	G1982
A2855	A2732	G2669	A2608	C2547	U2487	U2421	G2357	G2298	C2234	G2173	C2108	C2045	U1983
G2856	G2733	A2670	C2609	G2548	C2488	G2422	U2358	G2299	A2235	G2174	A2109	G2046	A1984
U2857	C2734	G2671	A2610	A2549	G2489	G2423	G2359	U2299	G2236	U2175	U2110	U2047	A1985
A2858	G2735	A2672	G2611	G2550	A2490	C2425		A2300	U2237	G2176	U2111	C1986	C1986
U2859	U2736	C2673	G2612	G2551	C2491	A2426	A2362		G2238	G2177	A2112	G2050	C1987
	G2737	A2674	U2613	G2552	G2492	A2427		U2303	U2239		U2113	G2051	A1988
G2860	U2738	C2675	U2614	U2553	C2493	U2428	A2366	U2304	U2240	A2178	C2114	C2052	U1989
U2861	C2739	G2676	G2615	G2554	G2494	G2429		G2305	A2241	U2180	A2115	G2053	C1990
A2862	U2740	A2677	A2616	U2555	A2495	G2430	G2369	A2306	G2242	A2181	U2116	C2054	U1991
G2863	A2741	U2678	U2617	C2556	G2496		U2371	G2307	G2243	C2182	G2117	A2055	C1992
U2864	U2742		C2618	G2557	U2497	C2425		U2308	U2244	U2183		A2056	U1993
A2865	U2743	G2681	C2619	G2558	G2498	A2433	C2372	U2309	G2245	A2184	A2121	C2057	U1994
U2866	U2744	A2682	C2620	C2559	U2499	A2434	G2373	A2308	U2246		G2122	G2058	G1995
G2867	A2745	G2683	U2621	U2560	U2500	C2435	A2374	C2310	G2247	C2185	A2123	G2059	A1996
U2868	G2746	A2684	A2622	G2561	U2501	G2436	A2375	G2311	C2248	C2186	A2124	G2060	C1997
A2869	U2747	G2685	G2623	U2562	G2502	G2437	C2376	U2312	C2249	C2187	A2125	A2061	U1998
U2870	A2748	A2686	U2624	U2563	G2503	A2438	A2377	U2313	G2250	U2188	A2126	G2062	G1999
G2871	U2749	U2687	U2625	C2564	C2504	U2439	G2378	U2314	U2251	U2189	G2127	C2063	U2000
A2872	A2750	A2688	A2626	G2565	A2505	A2440	G2379	G2315	U2252	G2190			C2001
U2873	G2751	C2689	U2627	C2566	C2506	A2441	U2380	G2316	U2253	G2191			U2002
G2874	G2752	U2690	U2628	C2567	C2507	A2442	G2381	A2317	U2253	U2192	U2129	A2066	

G2876	G2877	G2878	G2879	A2880	A2881	U2882	A2883	C2884	U2885	A2886	A2887	U2888	U2889	C2890	C2891	U2892	C2893	G2894	A2895	G2896	G2897	A2898	C2899	U2900	U	A	U	U	U	G	G	A
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• Molecule 53: 5S ribosomal RNA

Chain 4: 15% 50% 32%

U1	U2	U3	G4	G5	U6	G7	C8	C9	G10	G11	G12	U13	U14	C15	G16	G19	U20	G21	G22	A23	A24	A25	C26	A27	C28	C29	U30	G31	G32	U33	U34	C35	U38	U39	U40	C41	C42	A43	A44	C45	C46	C47	A48	G49	C50	U53	U54	A55	A56	G57	C58	A59	C60	A61	G62	U63
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G64	G65	A66	G67	C68	C69	G70	A71	A72	G73	G74	U75	A76	G77	C78	U79	G80	U	U	C84	A85	G88	A89	G90	A91	A92	U93	A94	G95	G96	A97	A98	A99	G100	C101	A102	C103	G104	A105	A106	C107	C108
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• Molecule 54: 16S ribosomal RNA

Chain 5: 13% 59% 27%

U	U	U	U	U5	C6	U7	G8	A9	G10	G11	G12	U13	U14	U15	G16	A17	U18	C19	C20	U21	G22	G23	C24	U25	C26	A27	C28	C29	U30	G31	G32	A33	A34	C35	G36	C37	U38	C39	G40	C41	G42	G43	C44	A45	U46	G47	C48	C49	U50	A51	A52	U53	A54	C55	A56	U57	G58	C59	A60	C61
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G62	U63	C64	G65	A66	U67	C68	G69	A70	G71	G72	G73	U74	A75	G76	A79	U80	A81	C82	U83	U84	G85	G86	C87	A88	G89	G90	C91	G92	A93	A94	C95	G96	G97	U98	U99	G100	A101	G102	U103	A104	A105	C106	A107	C108	U109	U110	A111	U112	A51	C113	A114	A115	A116	C55	U117	C118	U119	A120	C121	C122
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U123	U124	A125	U126	A127	A128	U129	G130	G131	G132	G133	G134	A135	U136	A137	A138	U141	G142	U143	U144	G145	A148	G149	G154	C155	G156	U157	A158	U159	A160	U166	A167	U168	G169	A170	A171	C172	U173	U174	A175	U179	G180	U180	C	A	U	G185	A186	G187	A188	U189	A190	U195	G196
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A197	A198	A199	G200	G201	C204	U205	G206	A209	G212	U213	U214	G215	G216	U217	U218	A219	U220	U221	G222	U223	G224	A225	U226	G226	A227	G228	G229	A230	U231	G232	C233	C236	A237	U238	A239	U240	A241	A242	G243	C244	U245	A246	G247	U248	U249	A250	G251	U252	G253	G254	G255	U256	U257	A258	C260
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G261	G262	C263	G264	A265	G271	G272	C273	A274	U275	U276	G277	A278	C279	G280	U281	G282	U283	A284	G285	G286	U287	A288	U289	G290	C291	U292	G293	A294	U295	A296	A297	G298	U299	A300	G301	A302	A303	U304	A305	G306	C307	C308	A309	C310	A311	A312	U313	G314	G315	G316	A317	C318	U319	G320	A321	G322	A323
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C324	A325	C326	G327	C328	C329	C330	C331	A332	U333	A334	C335	U336	C337	C338	U339	A340	C341	G342	C343	G344	A345	G346	U347	C348	A349	C350	C351	A352	G353	U354	A355	G356	G357	A358	A359	U360	U361	U362	U363	U364	U365	C366	A367	C368	A369	A370	U371	G372	A373	G374	C375	G376	U377	A378	U379	C380	C381	U382	U383
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G384	A385	U386	G387	A388	A389	C390	C391	A392	A393	U394	G395	C396	C397	C398	C399	A400	U401	G402	A403	A404	U405	G406	U407	U408	C409	A410	A411	G412	G413	U414	C415	U416	U417	U418	U419	A420	C421	A422	U423	U424	U425	U426	A429	C430	U431	U432	U433	C434	U435	U436	U437	U438	A439	U440	U441	G442	G443	G444
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A445	A446	G447	C448	A449	U450	G451	A452	C453	U454	C455	A456	U457	G458	C459	A460	G461	C462	U463	A464	A465	U466	G467	A468	C469	U470	A471	G472	A473	U476	U477	G478	C479	U480	A481	U482	U483	A484	C485	C486	A487	U488	U489	U490	U491	G492	A493	A494	U495	A496	A497	U498	A499	U500	U501	C502	G503	A504	C505
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U506	A507	U508	C509	A510	U511	U514	C515	C516	C517	A518	G519	C520	A521	U522	U523	C524	G525	C526	A527	U528	U529	A530	C531	U532	A533	C534	A535	U536	C537	U538	G539	U540	C541	C542	C543	A544	A545	C546	C547	U548	U549	U552	C553	C554	C555	C556	A557	U558	U559	U560	U561	A562	C563	U564	C565	C566	C567
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G568	U569	A570	C571	A572	U573	C574	A575	A576	C577	C578	G579	C580	A581	U582	G583	C584	G585	C586	A587	U588	U589	G590	A591	A592	A593	A594	C595	U596	C597	U598	G599	C600	U601	C602	U603	U604	A605	A606	A607	U608	G609	C610	A611	U612	U613	U614	C615	C616	U617	U618	A619	A620	C621	A622	U623	U624	U625	G626	A627
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A628	U629	G630	C631	A632	U633	U634	G635	G636	A637	A638	C639	C640	U641	A642	U643	U644	U647	C648	U649	A650	G651	A652	G653	U654	G655	U656	G657	C658	U659	A660	G661	C662	A663	A664	G665	U666	U667	U668	U669	G670	G671	A672	A673	U674	U675	U676	C677	U680	U681	G682	C683	A684	G685	C686	G687	G688	U689
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G690	A813	G874	U938	G1003	G1063	G1123	C1184	A1244	G1305	U1365	A1432	A1493
A691	C814	G875	G939	U1004	U1064	U1124	C1185	A1245	A1306	U1366	G1433	A1494
A692	G815	G753	G940	U1005	G1065	C1125	U1186	A1246	A1307	G1367	G1434	C1495
A693	A941	U754	A941	U1006	U1066	U1126	U1187	A1247	G1308	G1368	G1435	G1496
G695	U817	U755	G942	U1007	G1067	G1128	A1188	U1248	A1309	A1369	A1436	U1497
	U818	G879	G943	G1008	G1068	G1129	U1189		C1310	C1370	A1437	G1498
	G819	G881	A944	G1009	U1069	C1129	G1190	G1251	G1311	A1371	U1438	G1499
U698	A820	U882	U945	A1010	G1070	G1130	U1191	C1252	G1312	C1372	U1439	G1500
A699	U821	A883	G946	A1011	A1071	G1131	C1192	A1253	A1313	A1373	U1440	G1501
G700	A822	G762	U947	A1012	G1072	G1132	U1192	A1254	A1314	C1374	C1441	U1502
A701	C823	A763	U948	C1013	A1073	G1133	A1194	A1255	A1315	C1375	A1442	U1503
U702	U824	A764	G949	U1014	G1074	C1134	G1195	U1256	A1316	G1376	A1443	G1504
A703	A825	A765	G950	U1015	U1075	U1135	G1196	U1257	C1317	C1377	G1444	G1505
U704	G826	G766	U951	A1016	U1076	G1136	G1197	U1258	C1318	C1378	G1445	G1506
	C827	U767	U952	U1017	U1077	G1137	U1198	U1259	U1319	C1379	U1446	U1507
A705	U828	G768	A953	U1018	G1078	U1138	U1199	U1260	A1320	G1380	U1447	C1508
G706	G829	U769	A954	G1019	G1079	A1139	G1200	A1261	G1321	U1381	A1448	A1509
A707	U830	G770	U955	G	G	U1141	C1201	A1262	U1322	G1382	G1449	C
G708	C831	G771	U956	A	U1081	U1142	A1202	G1263	A1323	A1383	C1450	U
A709	G832	G772	C957	A895	U1082	G1143	A1203	G1264	U1324	A1384	A1451	U
G710	G833	G773	G958	G896	A1083	C1144	C1204	U1265	U1325	A1385	C1452	C
G711	G834	A774	G961	A897	A1084	A1144	G1205	U1266	C1326	C1386	G1453	U
A712	G835	G775		A898	U1085	A1145	G1206	G1267	G1327	U1387	G1454	C
A713	C836	C776		U899	U1086	A1146	G1207	G1268	C1328	A1388	G1455	U
C714	G837	A777		G900	C1087	U1147	G1208	U1269	G1329	U1389	U1456	U
A715	A838			A901	C1088	U1148	C1209	G1270	A1330	G1390	G1457	C
C716	U839	A778		A902	C1089	U1149	U1210	U1271	U1331		A1458	U
C717	U839	A779		A903	G1090	G1150	A1211	C1272	U1332	A1393		A
A718	C840	U780		C904	G1091	G1151	C1212	A1273	A1333	G1394	G1461	G1461
G719	C841	A781		U905	A1092	G1152	G1213	G1274	C1334	C1395	G1462	G1462
U720	C842	G782		C906	A1093	G1153	A1214	U1275	G1335		A1463	A1463
G721	C843	G783		A907	C1094	A1154	U1215	U1276	C1336	A1401	G1464	G1464
G722	C844	A784		A908	G1095	A1155	G1216	C1277	U1337	U1402	G1465	G1465
	C845	U785		A909	A1096	G1156	G1217	G1278	A1338	A1403	U1466	U1466
G723	G846	A786		C910	G1097	G1157	C1218	G1279	U1339	U1404	A1467	A1467
A724	U847	G787		G911	C1098	A1158	C1219	A1280	G1340	U1405	A1468	A1468
G725	G848	A788			G1099	U1159	A1220	U1281	U1341	U1406	G1469	G1469
A726	U849	G789			C1100	G1160	A1221	U1282	C1342	A1407	U1470	U1470
G727	G850	U790			A1101	G1161	U1222	G1283	G1343	A1408	C1471	C1471
G728	U851	A791			C1102	G1162	A1223	A1284	C1344		G1472	G1472
C729	G852	C792			C1103	U1163	C1224	G1285	G1345	A1411	U1473	U1473
G730	A853	A731			C1104	U1164	A1225	G1286	G1346	C1412	A1474	A1474
A731	A854	G793			C1105	U1165	A1226	G1287	U1347	G1413	A1475	A1475
G732	G855	C794			U1106	A1166	A1227	C1288	G1348	U1414	A1476	A1476
A733		U795			U1107	C1167	A1228	U1289	U1349	G1415	A1477	A1477
C734		A796			A1108	G1168	A1229	G1290	A1350	U1416	A1478	A1478
C735	U858	G797			U1109	U1169	G1230	C1291	U1351	U1417	G1479	G1479
U736	C860	U798			C1110	C1170	U1231	A1292	A1352	G1418	G1480	G1480
G737	A861	U799			U1051	A1171	C1232	U1293	C1353		U1481	U1481
A738	C862	G800			G1111	A1172	G1233	U1294	G1354	A1421	A1482	A1482
G739	U801	U801			U1112	C1173	C1234	U1295	U1355	A1422	C1483	C1483
G740	C802	C803			U1113	U1174	C1235	C1296	G1356	C1423	G1484	G1484
C741	A803	A804			A1114	C1175	A1236	U1297	U1357	A1424	C1485	C1485
G742	C805	A743			G1115	A1176	G1237	U1298	U1358	A1425	C1486	C1486
A743	A806	U744			U1116	U1177	G1238	U1299	C1359	U1427	U1487	U1487
U744	G807	U745			C1057	A1118	U1239	G1300	G1360	U1428	A1488	A1488
G807	G808	U746			A933	C1178	U1301	U1301	G1361	A1428	C1489	C1489
U745	C809	G747			G934	A1179	G1241	C1302	U1362	G1429	G1490	G1490
A746	U810	U748			U1060	U1180	U1242	A1303	U1363	A1491	G1491	G1491
G747	U811	G749			C1061	G1181	A1243	U1304	C1364	A1431	G1492	G1492
U748	A812	A812			C1062	U1122						

● Molecule 55: tRNA-Phe

Chain 6:

17%

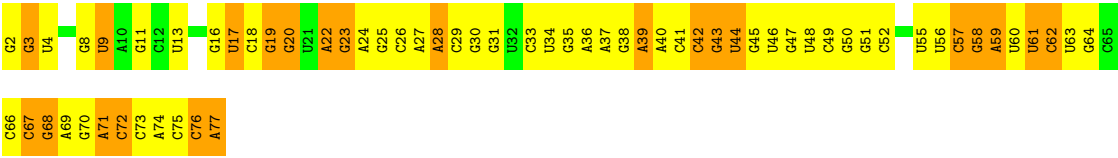
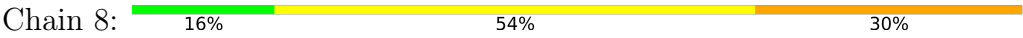
51%

32%

G2	U55
G3	U56
U4	C57
	G58
G8	A59
U9	U60
U10	U61
G11	U62
C12	U63
U13	G64
	C65
G16	G66
U17	
C18	
G19	
G20	
U21	
A22	
G23	
C24	
G25	
C26	
A27	
A28	
C29	
G30	
C33	
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G35	
A36	
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G38	
A39	
A40	
C41	
C42	
G43	
U44	
G45	
U46	
G47	
U48	
C49	
G50	
G51	
C52	
U55	
U56	
C57	
G58	
A59	
U60	
U61	
C62	
U63	
G64	
C65	
G66	



● Molecule 55: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	627	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.988	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0	0.30	0/383	0.51	0/504
2	1	0.15	0/484	0.41	0/637
3	2	0.17	0/306	0.40	0/401
4	9	0.22	0/5419	0.51	3/7307 (0.0%)
5	A	0.17	0/1954	0.44	0/2642
6	B	0.13	0/1721	0.38	0/2323
7	C	0.17	0/1691	0.47	0/2267
8	D	0.17	0/1188	0.44	0/1593
9	E	0.17	0/1384	0.48	0/1867
10	F	0.16	0/1266	0.46	0/1700
11	G	0.21	0/1126	0.44	0/1517
12	H	0.17	0/1044	0.45	0/1395
13	I	0.15	0/820	0.45	1/1103 (0.1%)
14	J	0.17	0/844	0.51	2/1136 (0.2%)
15	K	0.34	0/1094	0.61	0/1468
16	L	0.16	0/962	0.48	0/1289
17	M	0.14	0/483	0.43	0/643
18	N	0.15	0/679	0.42	0/907
19	O	0.14	0/659	0.47	0/885
20	P	0.15	0/684	0.44	0/913
21	Q	0.26	0/545	0.66	0/730
22	R	0.20	0/698	0.55	1/936 (0.1%)
23	S	0.16	0/631	0.37	0/838
24	T	0.22	0/475	0.46	0/621
25	W	0.21	0/538	0.59	0/722
26	a	0.15	0/2267	0.45	0/3044
27	b	0.15	0/1795	0.45	0/2412
28	c	0.17	0/1671	0.47	0/2246
29	d	0.17	0/1409	0.49	0/1894
30	e	0.16	0/1420	0.43	0/1912
31	f	0.24	0/1183	0.51	0/1587
32	g	0.49	0/969	0.82	2/1295 (0.2%)
33	h	0.17	0/968	0.53	1/1298 (0.1%)
34	i	0.14	0/1186	0.39	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.15	0/953	0.45	0/1275
36	k	0.16	0/1170	0.44	0/1559
37	l	0.21	0/1104	0.56	0/1481
38	m	0.15	0/973	0.44	0/1309
39	n	0.23	0/897	0.52	0/1198
40	o	0.23	0/948	0.54	0/1262
41	p	0.17	0/961	0.46	0/1278
42	q	0.18	0/828	0.54	0/1111
43	r	0.15	0/1077	0.47	0/1441
44	s	0.15	0/732	0.47	0/988
45	t	0.15	0/879	0.49	0/1165
46	u	0.15	0/665	0.39	0/884
47	v	0.17	0/519	0.46	0/695
48	w	0.17	0/826	0.45	0/1104
49	x	0.17	0/353	0.47	0/474
50	y	0.34	0/457	0.55	0/601
51	z	0.23	0/412	0.49	0/547
52	3	0.12	0/69073	0.30	0/107710
53	4	0.12	0/2505	0.34	0/3902
54	5	0.12	0/35768	0.30	0/55764
55	6	0.16	0/1808	0.42	0/2817
55	8	0.16	0/1808	0.42	0/2817
All	All	0.15	0/164662	0.37	10/245006 (0.0%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	R	26	GLU	N-CA-C	-7.13	100.71	111.34
33	h	28	VAL	N-CA-C	-6.92	106.06	112.43
32	g	30	THR	CB-CA-C	6.81	121.56	111.89
14	J	118	LYS	CA-C-N	6.19	129.28	120.49
14	J	118	LYS	C-N-CA	6.19	129.28	120.49

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	0	380	0	429	24	0
2	1	477	0	530	26	0
3	2	304	0	350	21	0
4	9	5326	0	5343	241	0
5	A	1921	0	1973	76	0
6	B	1698	0	1768	55	0
7	C	1660	0	1719	119	0
8	D	1173	0	1267	55	0
9	E	1362	0	1377	85	0
10	F	1246	0	1308	61	0
11	G	1110	0	1226	59	0
12	H	1028	0	1094	56	0
13	I	809	0	894	50	0
14	J	829	0	855	55	0
15	K	1076	0	1170	69	0
16	L	951	0	1014	54	0
17	M	474	0	509	40	0
18	N	673	0	730	33	0
19	O	646	0	677	37	0
20	P	675	0	728	31	0
21	Q	535	0	562	62	0
22	R	682	0	691	40	0
23	S	629	0	681	33	0
24	T	471	0	522	19	0
25	W	534	0	572	22	0
26	a	2225	0	2301	98	0
27	b	1762	0	1808	99	0
28	c	1644	0	1731	106	0
29	d	1388	0	1469	78	0
30	e	1396	0	1481	69	0
31	f	1160	0	1172	44	0
32	g	960	0	1014	51	0
33	h	959	0	1039	51	0
34	i	1164	0	1192	55	0
35	j	944	0	1019	50	0
36	k	1153	0	1256	53	0
37	l	1079	0	1134	68	0
38	m	958	0	1011	53	0
39	n	889	0	952	50	0
40	o	938	0	1008	62	0
41	p	947	0	1028	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	q	811	0	858	45	0
43	r	1068	0	1150	55	0
44	s	720	0	803	28	0
45	t	872	0	972	54	0
46	u	657	0	695	28	0
47	v	513	0	560	31	0
48	w	818	0	870	38	0
49	x	344	0	333	16	0
50	y	452	0	472	32	0
51	z	408	0	440	36	0
52	3	61664	0	30954	3017	0
53	4	2239	0	1137	103	0
54	5	31943	0	16058	1639	0
55	6	1618	0	821	60	0
55	8	1618	0	821	55	0
All	All	151980	0	105548	6675	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 27.

The worst 5 of 6675 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)
54:5:661:G:H1	54:5:738:A:N6	1.27	1.32
54:5:69:G:N2	54:5:137:A:C2	1.98	1.31
40:o:92:ARG:CD	40:o:116:GLU:O	1.77	1.31
52:3:1762:A:N6	52:3:2702:G:H21	1.40	1.19
52:3:1762:A:H61	52:3:2702:G:N2	1.39	1.18

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	680/688 (99%)	620 (91%)	58 (8%)	2 (0%)	36	72
5	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
6	B	213/273 (78%)	205 (96%)	8 (4%)	0	100	100
7	C	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
8	D	151/219 (69%)	138 (91%)	13 (9%)	0	100	100
9	E	165/215 (77%)	139 (84%)	26 (16%)	0	100	100
10	F	152/155 (98%)	137 (90%)	15 (10%)	0	100	100
11	G	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
12	H	126/132 (96%)	121 (96%)	5 (4%)	0	100	100
13	I	99/108 (92%)	93 (94%)	6 (6%)	0	100	100
14	J	112/121 (93%)	108 (96%)	4 (4%)	0	100	100
15	K	134/139 (96%)	109 (81%)	25 (19%)	0	100	100
16	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
17	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
18	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
19	O	78/94 (83%)	67 (86%)	11 (14%)	0	100	100
20	P	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
21	Q	63/104 (61%)	56 (89%)	7 (11%)	0	100	100
22	R	82/87 (94%)	63 (77%)	19 (23%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	61 (91%)	6 (9%)	0	100	100
26	a	283/287 (99%)	257 (91%)	26 (9%)	0	100	100
27	b	227/287 (79%)	199 (88%)	28 (12%)	0	100	100
28	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
29	d	173/180 (96%)	154 (89%)	19 (11%)	0	100	100
30	e	174/184 (95%)	166 (95%)	8 (5%)	0	100	100
31	f	143/149 (96%)	133 (93%)	8 (6%)	2 (1%)	9	40
32	g	124/161 (77%)	109 (88%)	13 (10%)	2 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	h	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
34	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
35	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
36	k	146/151 (97%)	131 (90%)	15 (10%)	0	100	100
37	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
38	m	117/124 (94%)	103 (88%)	14 (12%)	0	100	100
39	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
40	o	113/119 (95%)	100 (88%)	13 (12%)	0	100	100
41	p	112/127 (88%)	106 (95%)	6 (5%)	0	100	100
42	q	97/100 (97%)	88 (91%)	8 (8%)	1 (1%)	12	49
43	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
44	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
45	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
46	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
47	v	61/65 (94%)	52 (85%)	9 (15%)	0	100	100
48	w	96/111 (86%)	84 (88%)	12 (12%)	0	100	100
49	x	42/97 (43%)	39 (93%)	3 (7%)	0	100	100
50	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
51	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6567/7480 (88%)	6003 (91%)	557 (8%)	7 (0%)	49	83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	9	406	ILE
4	9	572	ASP
32	g	31	SER
31	f	18	VAL
32	g	116	ARG

5.3.2 Protein sidechains [i](#)

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	579/584 (99%)	576 (100%)	3 (0%)	81	83
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	122 (99%)	1 (1%)	73	80
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	111 (95%)	6 (5%)	21	42
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	73 (99%)	1 (1%)	59	72
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	241 (100%)	0	100	100
27	b	186/233 (80%)	186 (100%)	0	100	100
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	150 (100%)	0	100	100
30	e	153/159 (96%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	f	123/134 (92%)	122 (99%)	1 (1%)	73	80
32	g	101/129 (78%)	87 (86%)	14 (14%)	3	14
33	h	102/110 (93%)	102 (100%)	0	100	100
34	i	126/128 (98%)	126 (100%)	0	100	100
35	j	103/103 (100%)	103 (100%)	0	100	100
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	113 (100%)	0	100	100
38	m	105/109 (96%)	104 (99%)	1 (1%)	68	78
39	n	96/99 (97%)	96 (100%)	0	100	100
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	100 (100%)	0	100	100
42	q	90/91 (99%)	90 (100%)	0	100	100
43	r	116/132 (88%)	116 (100%)	0	100	100
44	s	82/208 (39%)	82 (100%)	0	100	100
45	t	96/96 (100%)	96 (100%)	0	100	100
46	u	69/85 (81%)	69 (100%)	0	100	100
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	87 (100%)	0	100	100
49	x	41/86 (48%)	41 (100%)	0	100	100
50	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5700 (100%)	30 (0%)	78	83

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	g	28	ASP
50	y	47	MET
32	g	32	MET
50	y	52	ARG
32	g	90	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
29	d	174	ASN
34	i	126	HIS
30	e	146	GLN
33	h	47	GLN
36	k	14	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	1011 (35%)	30 (1%)
53	4	103/108 (95%)	41 (39%)	4 (3%)
54	5	1490/1520 (98%)	492 (33%)	10 (0%)
55	6	75/76 (98%)	40 (53%)	4 (5%)
55	8	75/76 (98%)	40 (53%)	4 (5%)
All	All	4618/4687 (98%)	1624 (35%)	52 (1%)

5 of 1624 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	12	A
52	3	14	U
52	3	15	A
52	3	28	G
52	3	29	G

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	2721	C
54	5	166	U
55	8	18	C
52	3	2897	G
53	4	59	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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-13449. These allow visual inspection of the internal detail of the map and identification of artifacts.

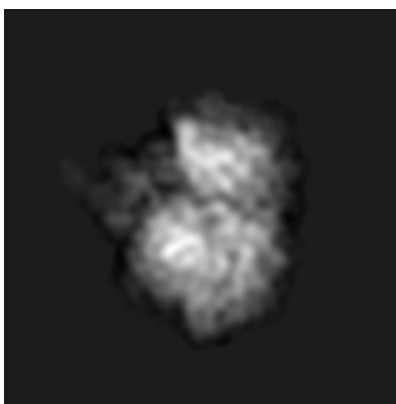
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

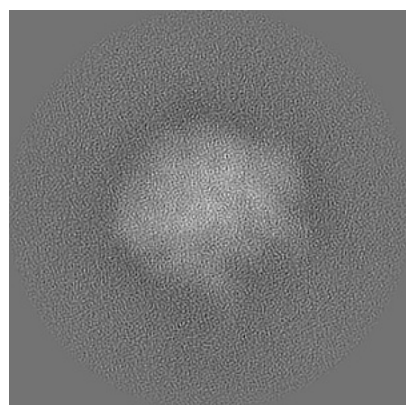


Y

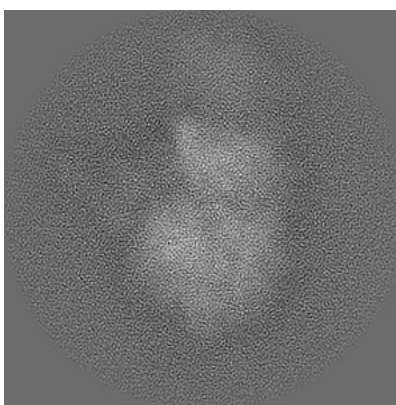


Z

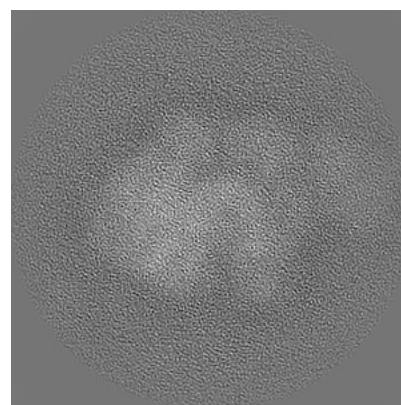
6.1.2 Raw map



X



Y

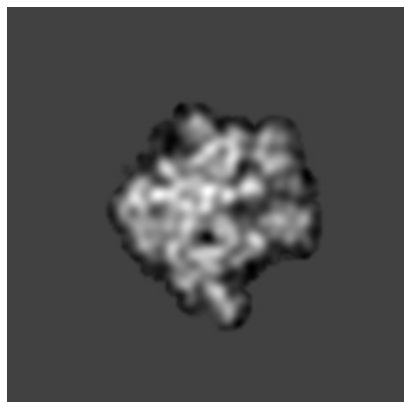


Z

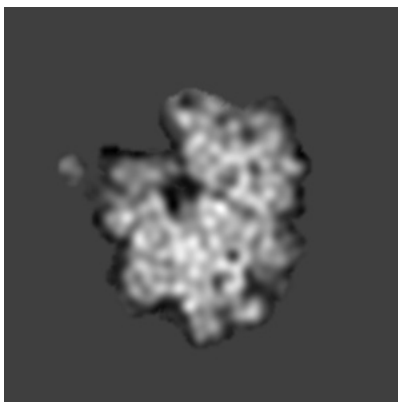
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

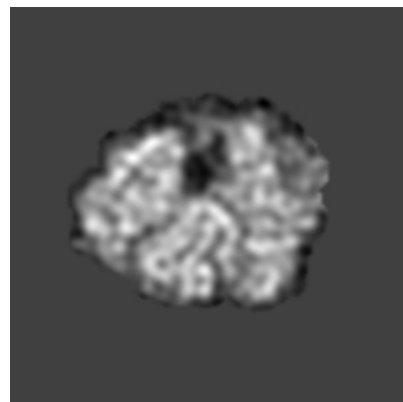
6.2.1 Primary map



X Index: 128

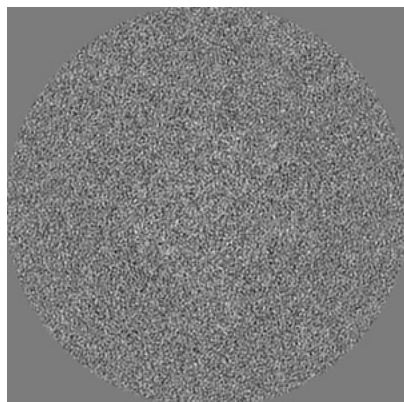


Y Index: 128

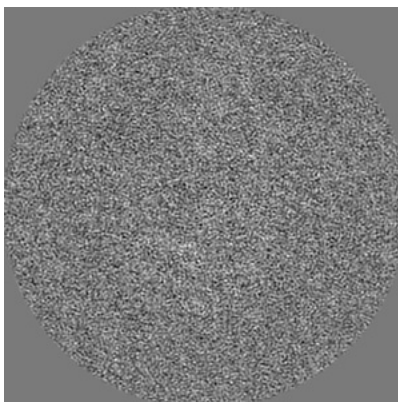


Z Index: 128

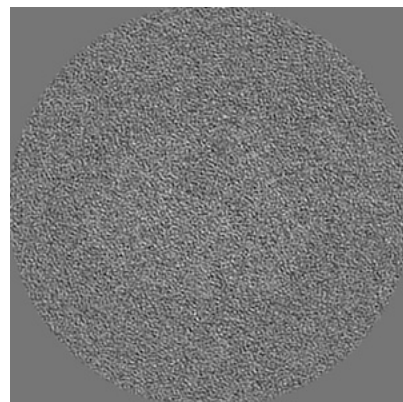
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

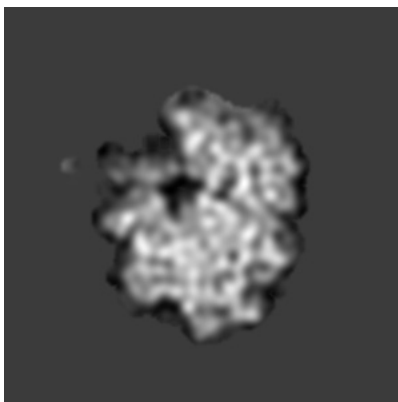
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

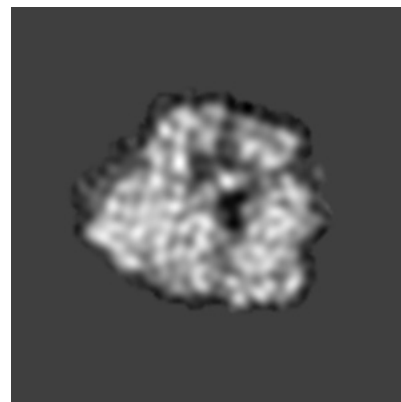
6.3.1 Primary map



X Index: 102

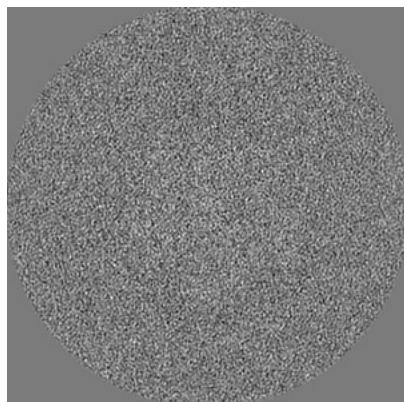


Y Index: 125

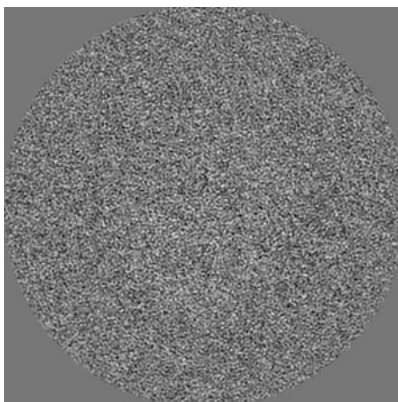


Z Index: 119

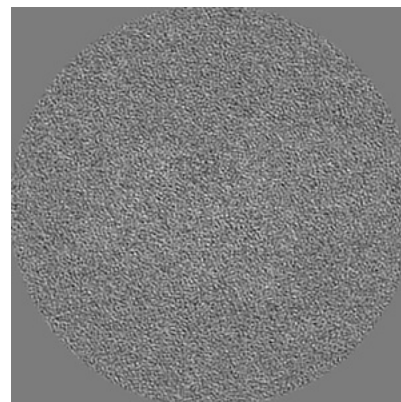
6.3.2 Raw map



X Index: 118



Y Index: 118



Z Index: 130

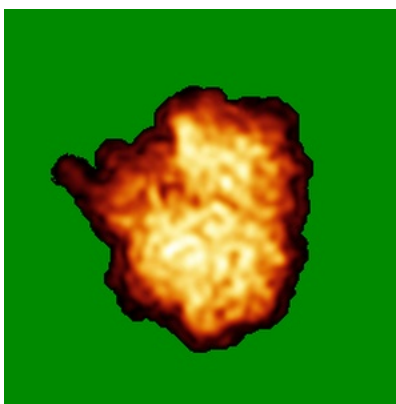
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

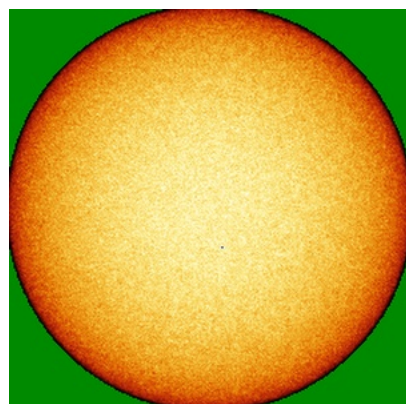


Y

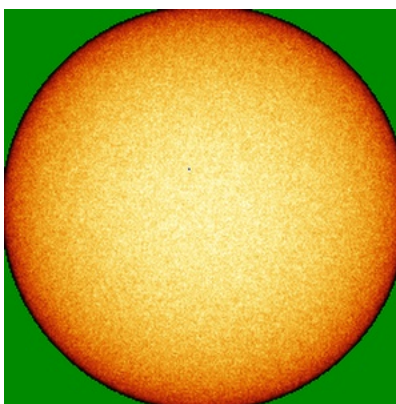


Z

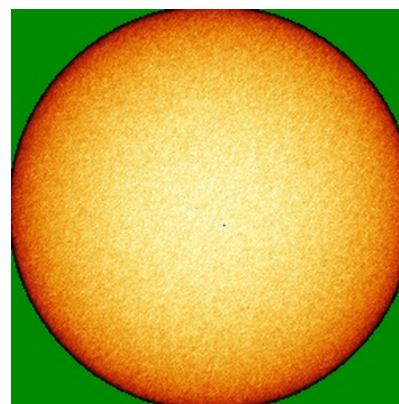
6.4.2 Raw map



X



Y

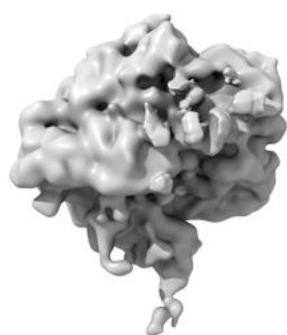


Z

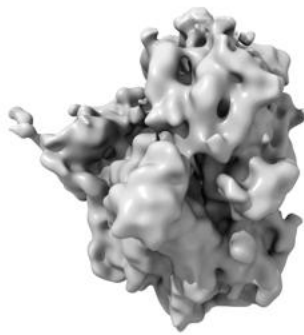
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

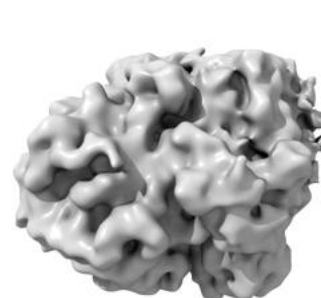
6.5.1 Primary map



X



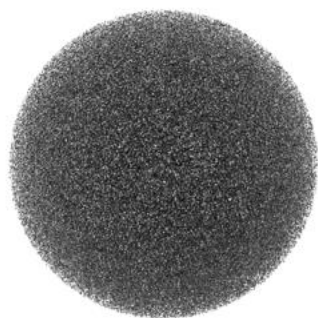
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

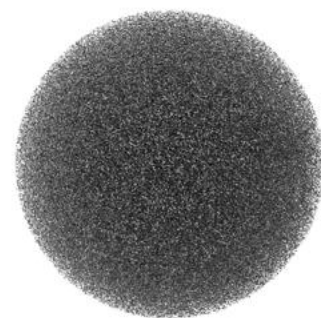
6.5.2 Raw map



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.

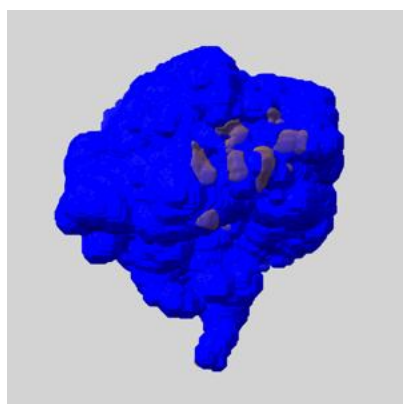
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

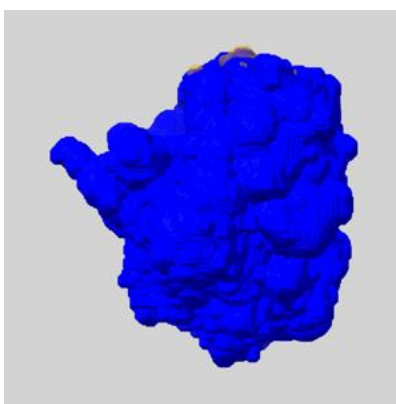
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

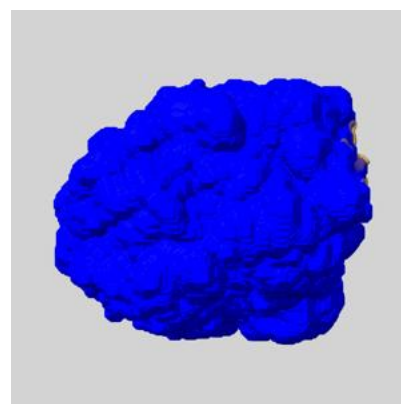
6.6.1 emd_13449_msk_1.map [i](#)



X



Y

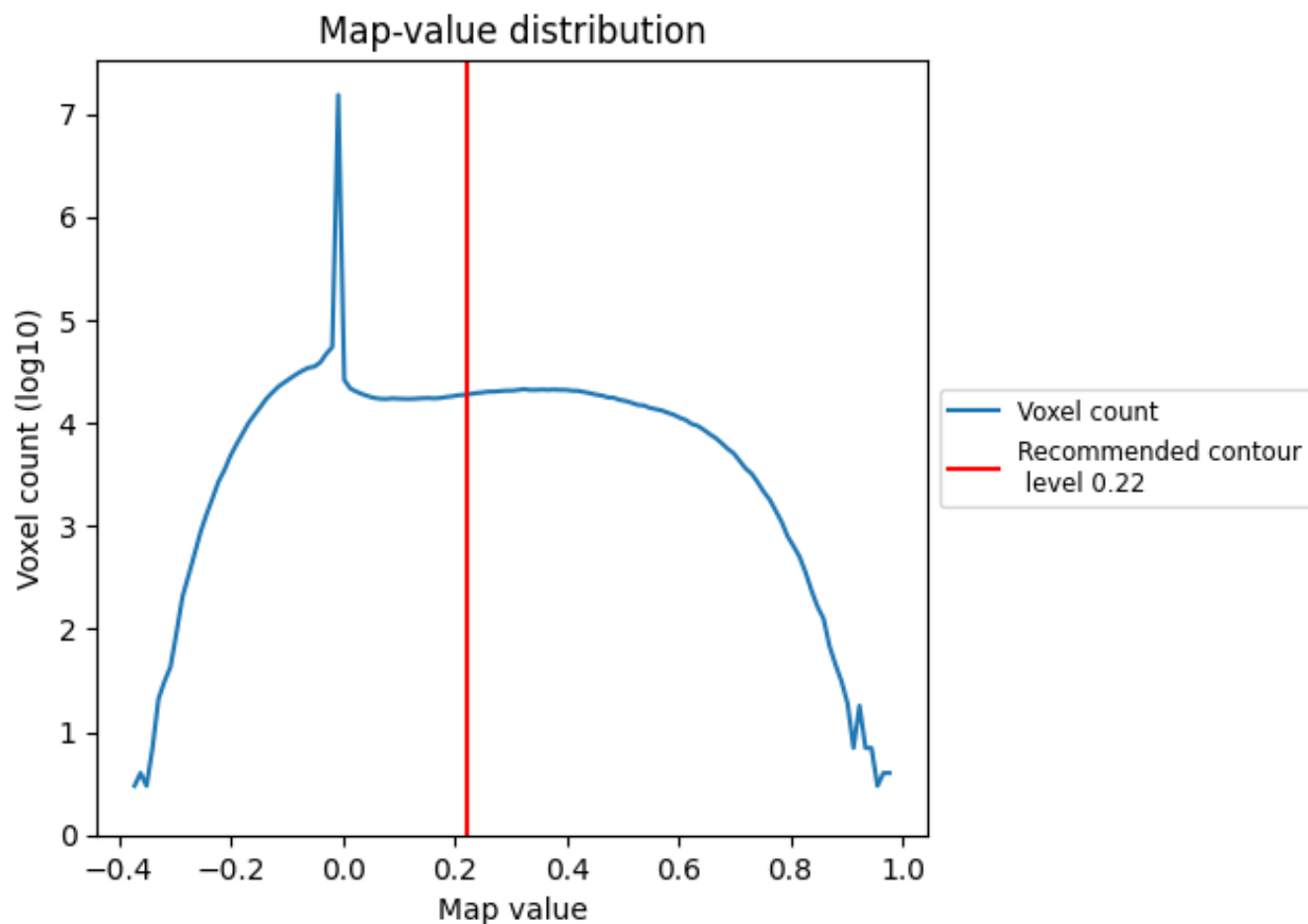


Z

7 Map analysis [i](#)

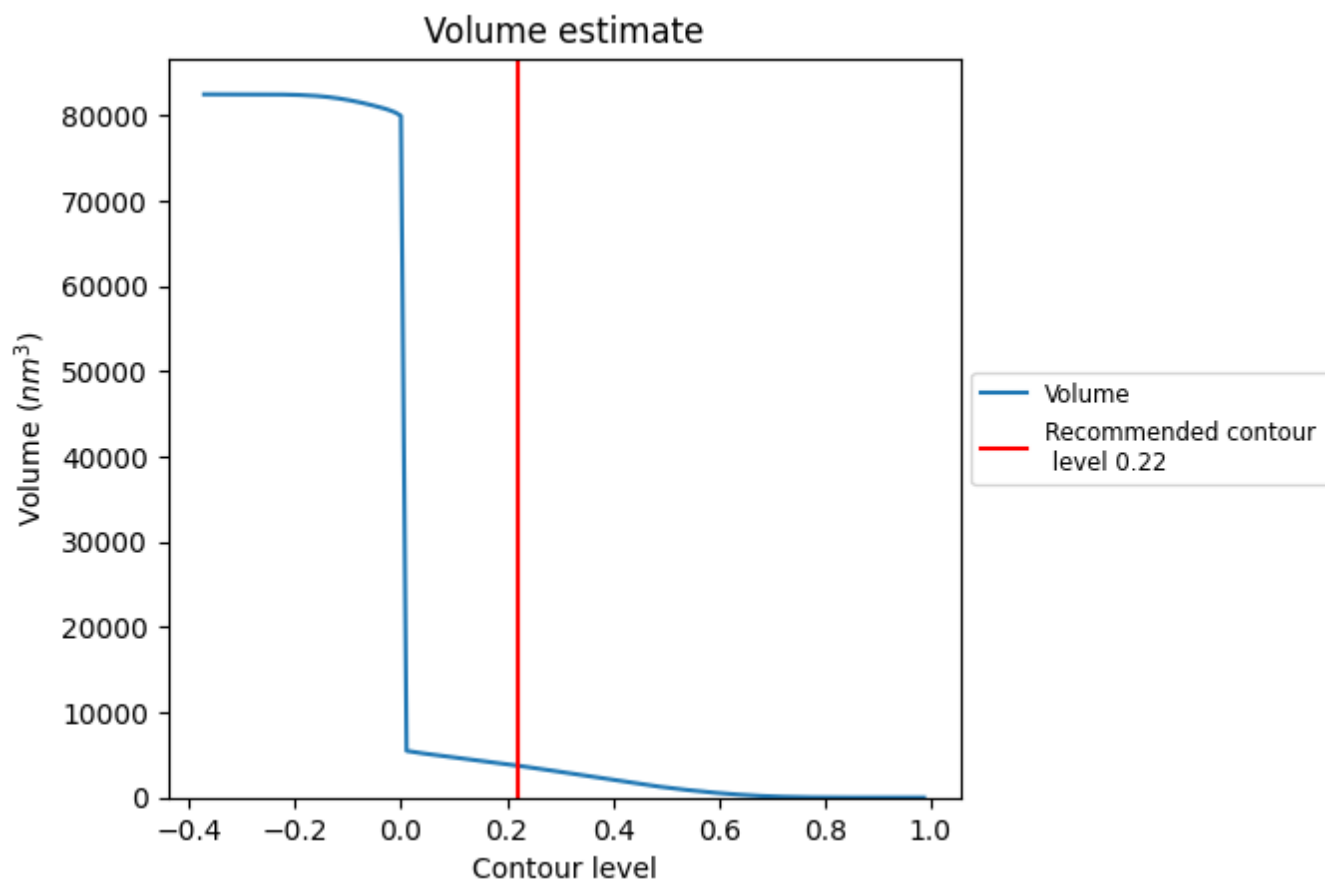
This section contains the results of statistical analysis of the map.

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.

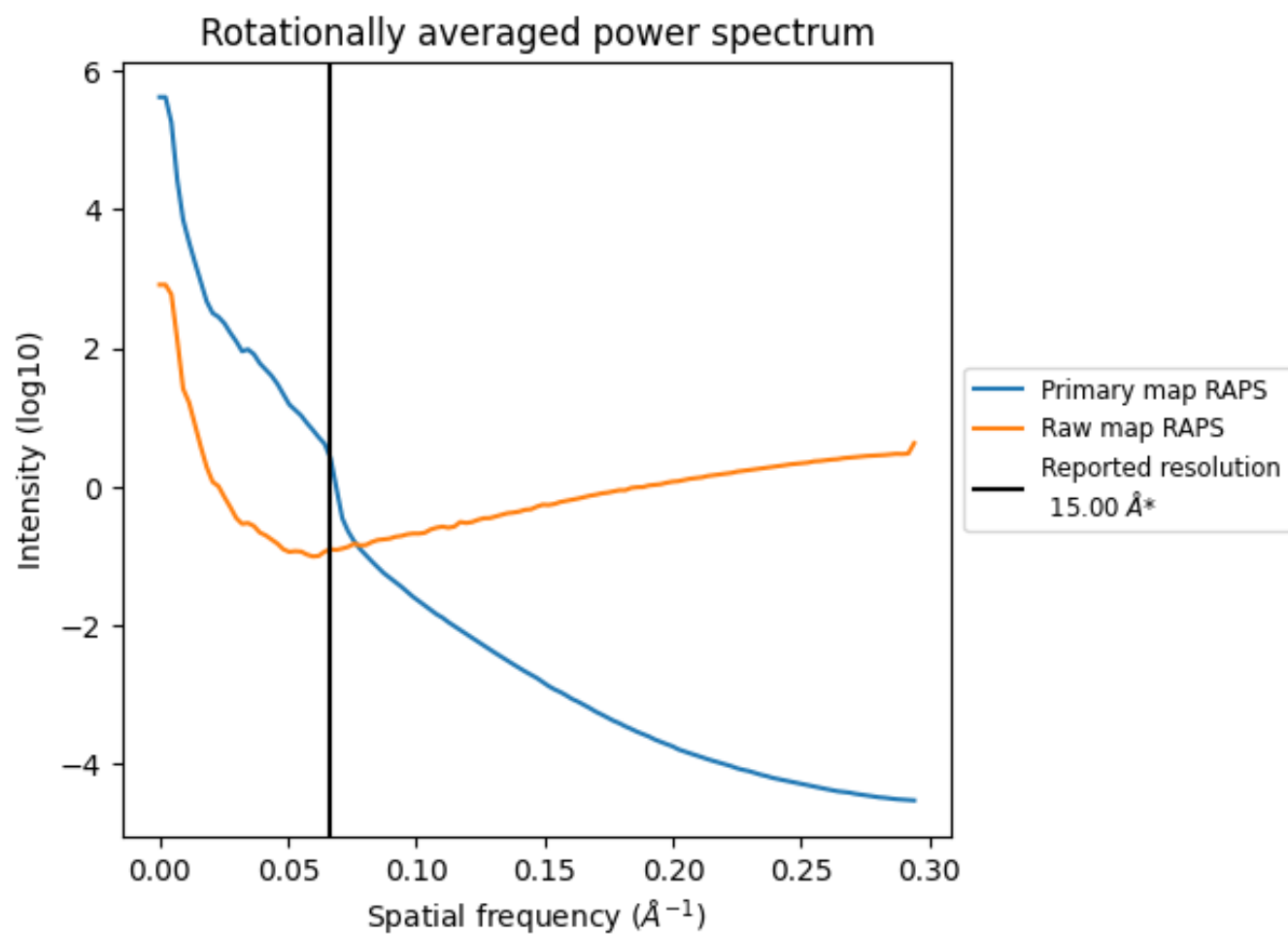
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3746 nm³; this corresponds to an approximate mass of 3384 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 ⓘ

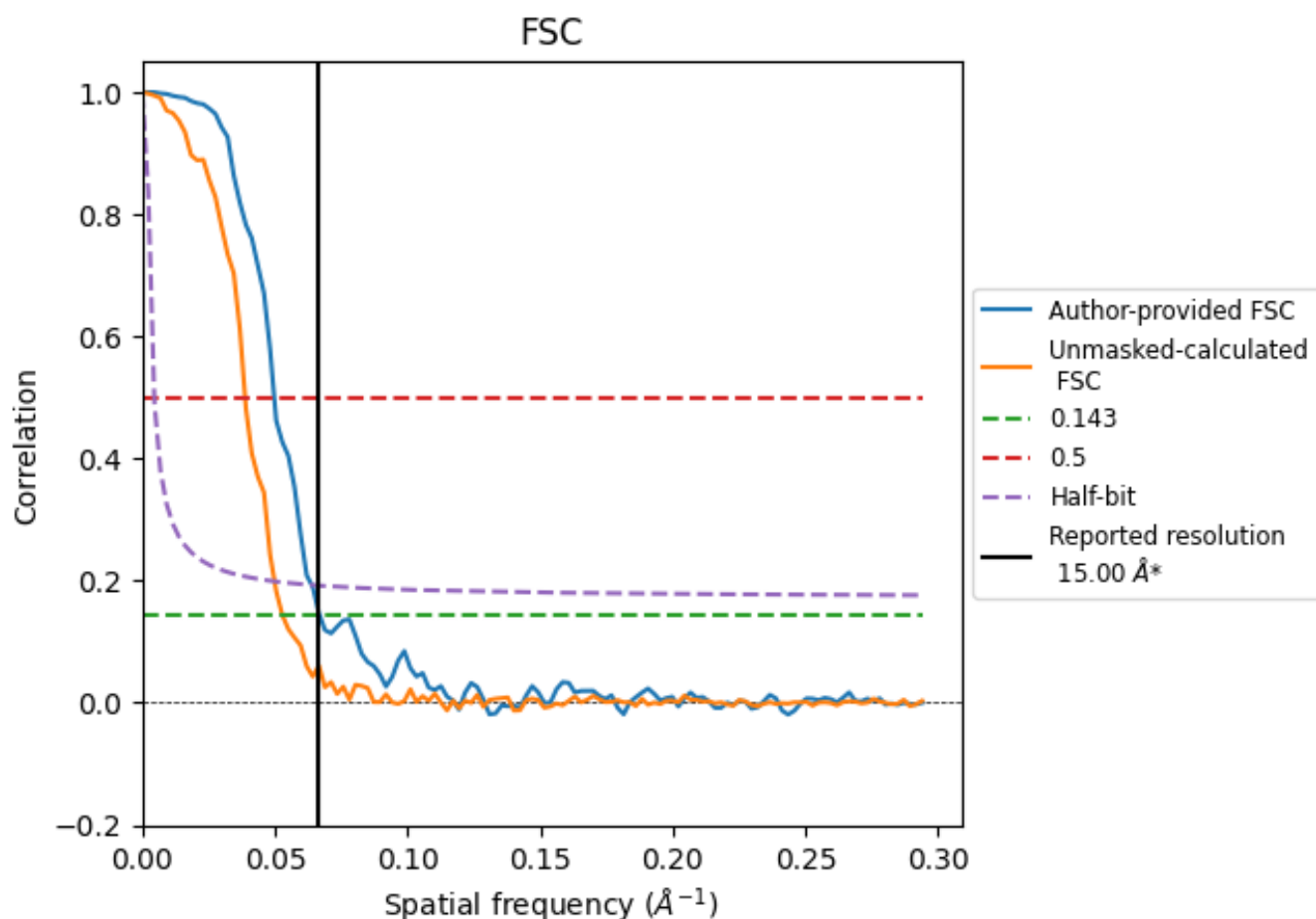


*Reported resolution corresponds to spatial frequency of 0.067 $\text{\AA}^{-1}$

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 0.067 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

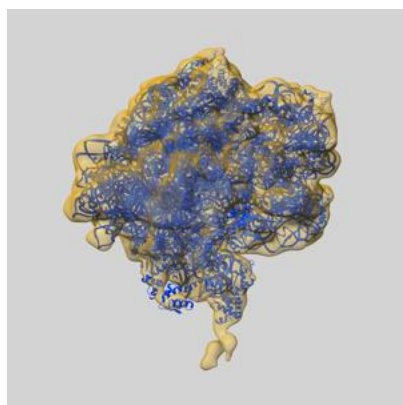
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	15.00	-	-
Author-provided FSC curve	14.95	20.08	15.62
Unmasked-calculated*	18.90	25.84	20.04

*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 18.90 differs from the reported value 15.0 by more than 10 %

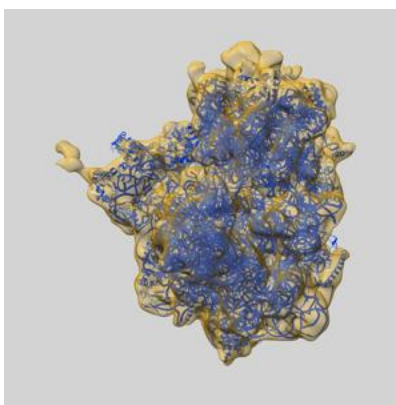
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13449 and PDB model 7PIS. Per-residue inclusion information can be found in section 3 on page 14.

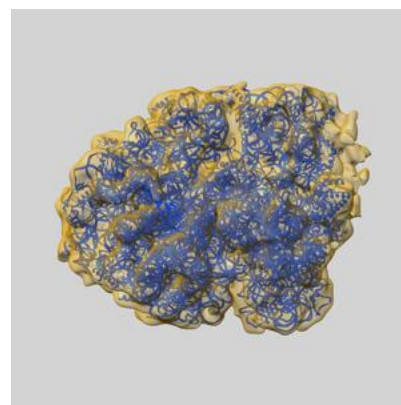
9.1 Map-model overlay [i](#)



X



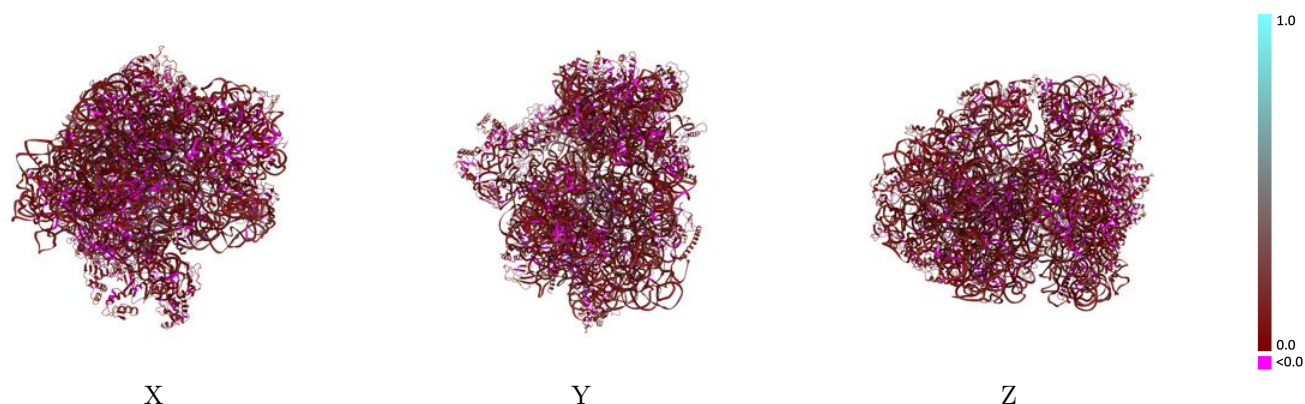
Y



Z

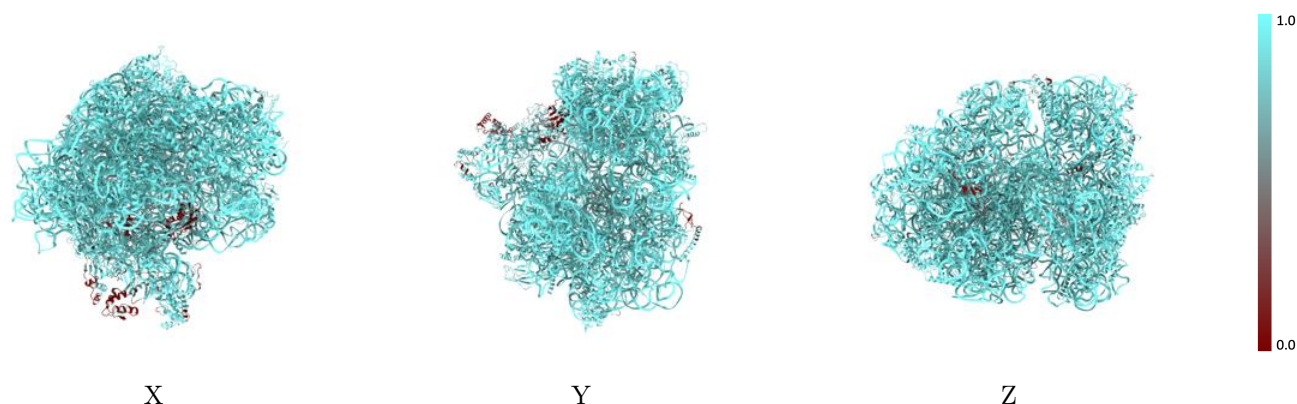
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



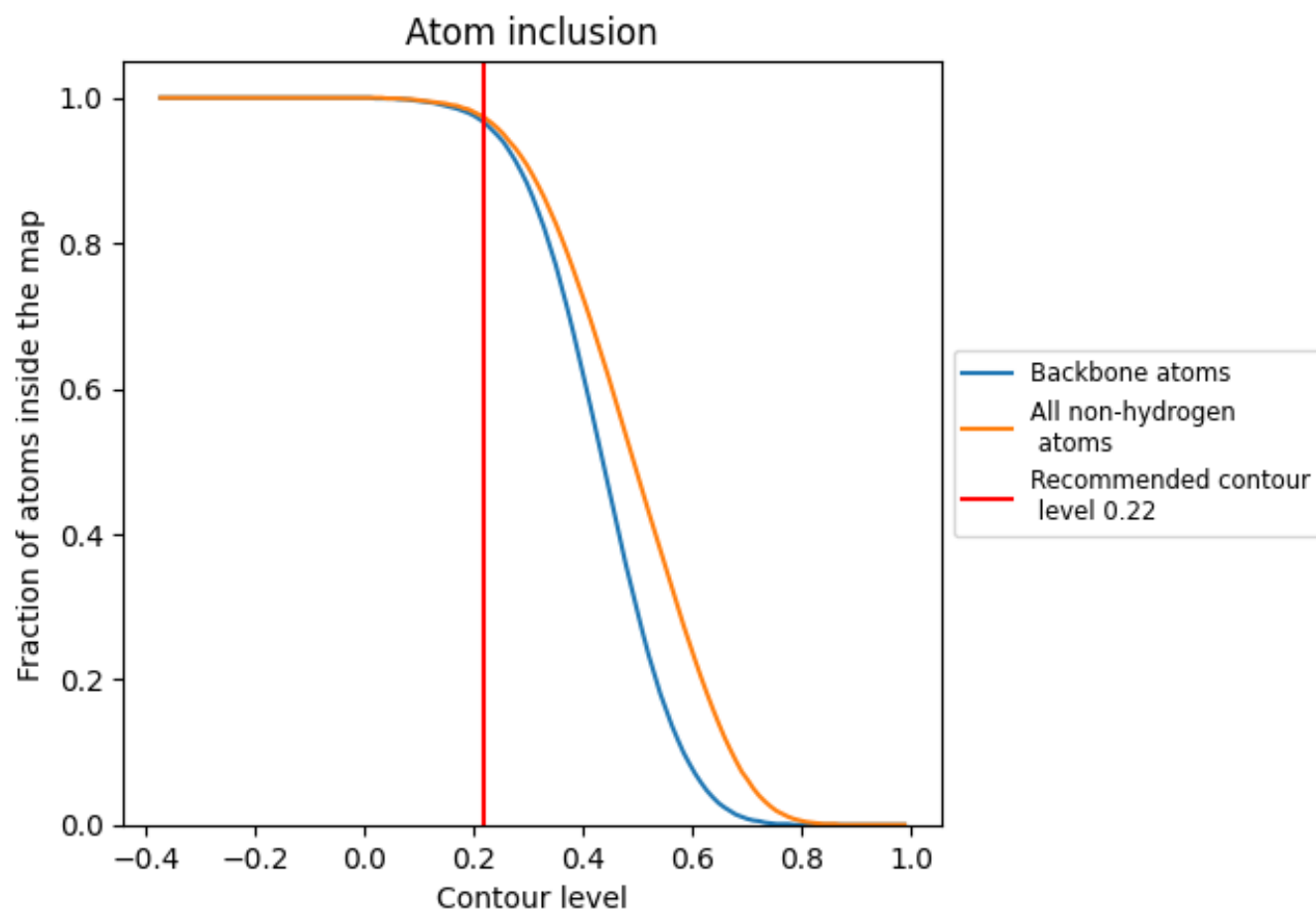
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.0820
0	 0.9920	 0.0050
1	 1.0000	 0.0320
2	 1.0000	 0.0070
3	 0.9990	 0.0970
4	 1.0000	 0.1040
5	 0.9980	 0.1000
6	 0.9880	 0.0950
8	 0.9840	 0.0790
9	 0.6770	 0.0620
A	 0.9830	 0.0770
B	 0.9770	 0.0530
C	 0.9880	 0.0340
D	 0.9900	 0.0530
E	 0.9630	 0.0830
F	 0.9500	 0.0770
G	 0.9990	 0.0570
H	 0.9450	 0.0480
I	 0.9480	 0.0380
J	 0.9890	 0.0460
K	 0.9880	 0.0270
L	 0.9080	 0.0510
M	 1.0000	 0.0280
N	 0.9940	 0.0500
O	 1.0000	 0.0400
P	 0.9570	 0.0600
Q	 0.9850	 0.0700
R	 0.9940	 0.0610
S	 0.9950	 0.0440
T	 0.9890	 0.0700
W	 0.1690	 0.0900
a	 1.0000	 0.0280
b	 0.9930	 0.0380
c	 0.9960	 0.0580
d	 0.9630	 0.0700



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Chain	Atom inclusion	Q-score
e	 0.9290	 0.0580
f	 0.6120	 0.0700
g	 0.8340	 0.0780
h	 0.7950	 0.0770
i	 0.9940	 0.0450
j	 0.9760	 0.0240
k	 0.9820	 0.0370
l	 0.9900	 0.0490
m	 0.9940	 0.0260
n	 0.9860	 0.0590
o	 0.9310	 0.0400
p	 0.9800	 0.0390
q	 0.9470	 0.0690
r	 0.9980	 0.0510
s	 1.0000	 0.0370
t	 0.9170	 0.0620
u	 0.9750	 0.0320
v	 1.0000	 0.0320
w	 0.9880	 0.0950
x	 0.9010	 0.1130
y	 0.9890	 0.0720
z	 1.0000	 0.0290