



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 12:13 AM UTC

PDB ID : 5KPV / pdb_00005kpv
EMDB ID : EMD-8280
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure II)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-07-05
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

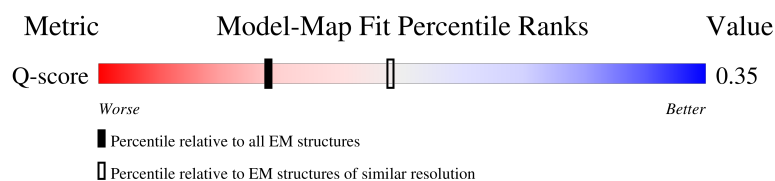
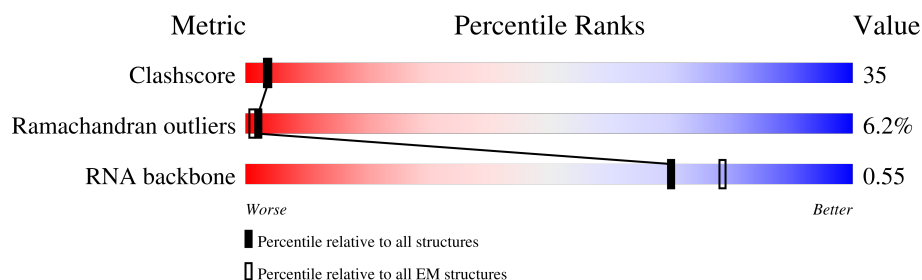
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

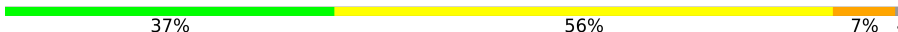
The reported resolution of this entry is 4.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	273	
2	B	209	
3	C	201	
4	D	179	

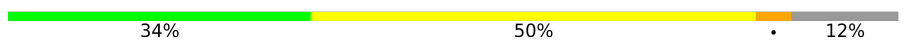
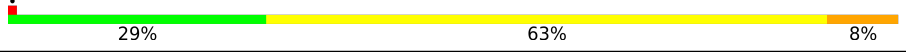
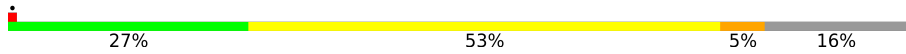
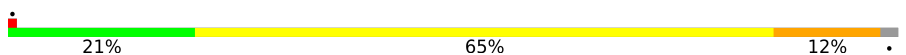
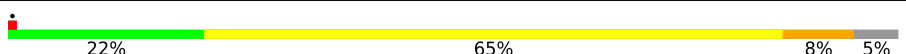
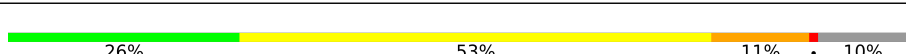
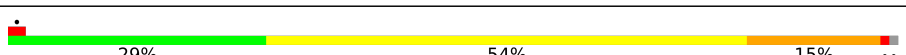
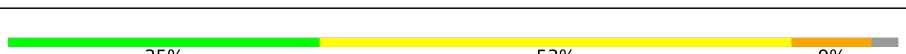
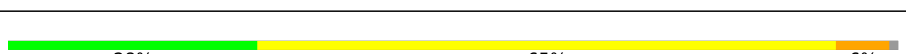
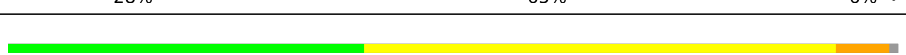
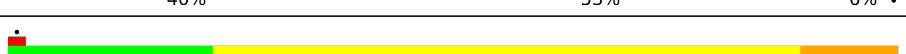
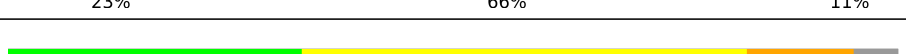
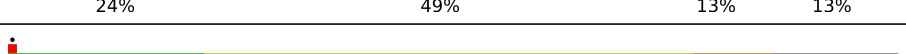
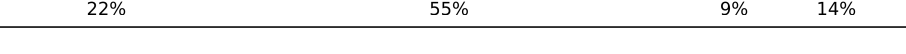
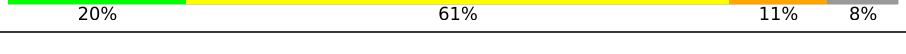
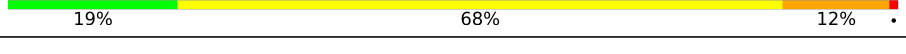
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	E	177	
6	F	149	
7	G	165	
8	H	142	
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
30	4	65	
31	5	38	
32	6	241	
33	7	233	
34	8	206	
35	9	167	
36	10	135	
37	11	179	
38	12	130	
39	13	130	
40	14	103	
41	15	129	
42	16	124	
43	17	118	
44	18	101	
45	19	89	
46	20	82	
47	21	84	
48	22	75	
49	23	92	
50	24	87	
51	25	71	
52	26	1539	
53	27	2903	
54	28	120	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
55	29	20	15% 25% 60% 10% 5%
56	30	76	8% 70% 21%
57	31	77	31% 64% 5%
58	32	77	12% 23% 61% 14%
59	33	750	47% 30% 50% 10% 10%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 154603 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called mRNA.

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

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

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

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

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

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

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

- Molecule 59 is a protein called GTP pyrophosphokinase.

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

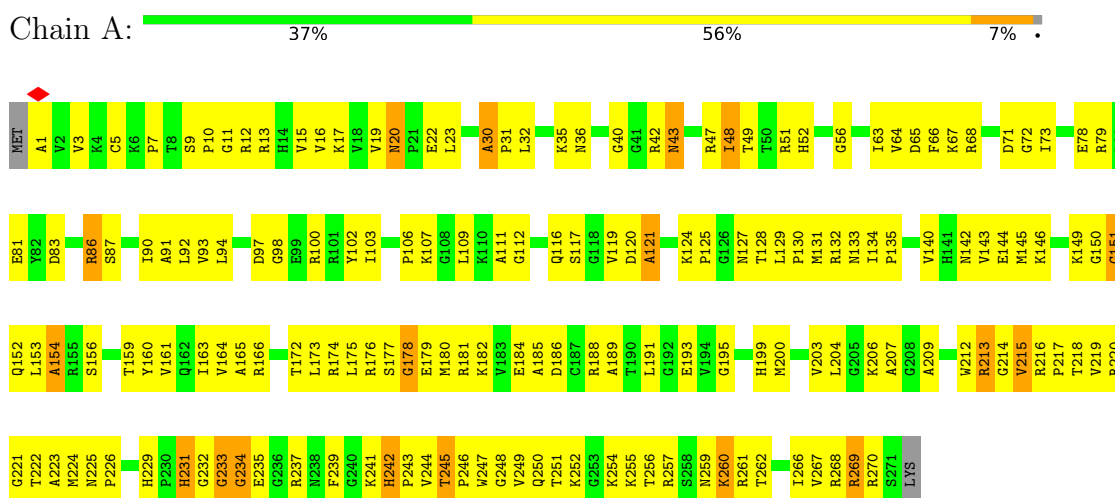
There are 7 discrepancies between the modelled and reference sequences:

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

3 Residue-property plots

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

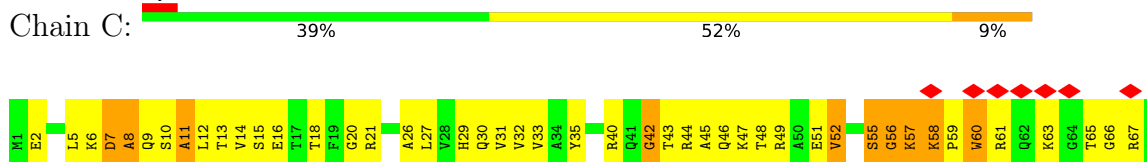
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

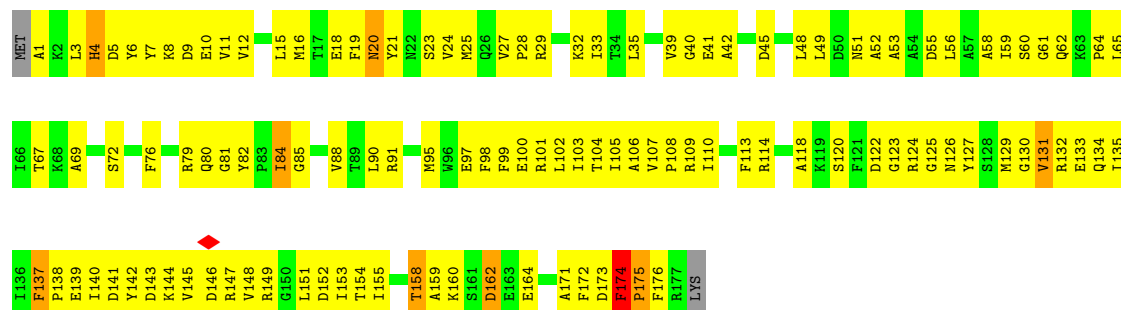


• Molecule 3: 50S ribosomal protein L4

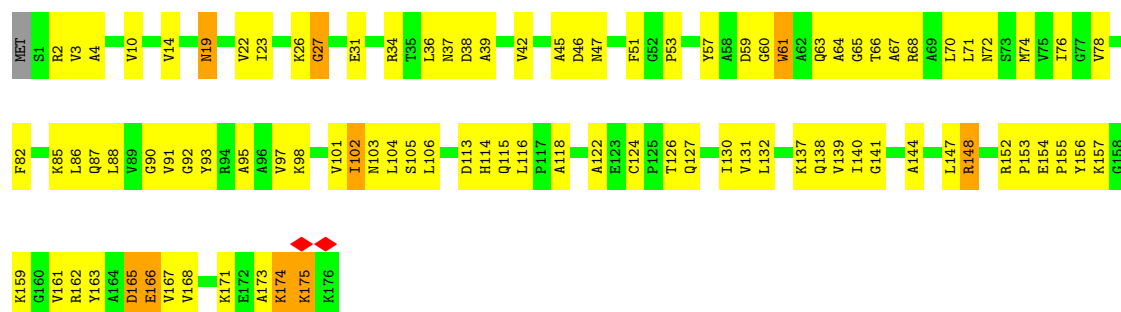




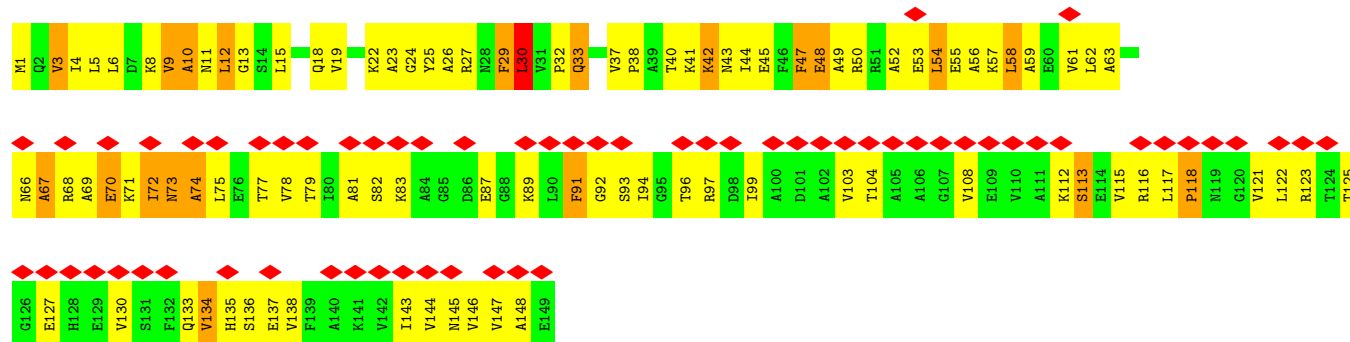
• Molecule 4: 50S ribosomal protein L5



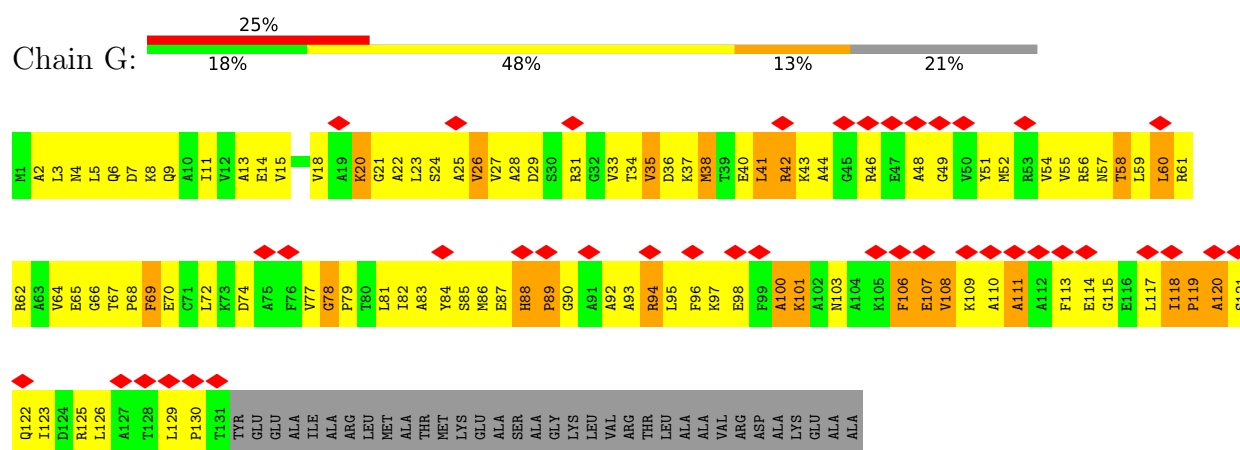
• Molecule 5: 50S ribosomal protein L6



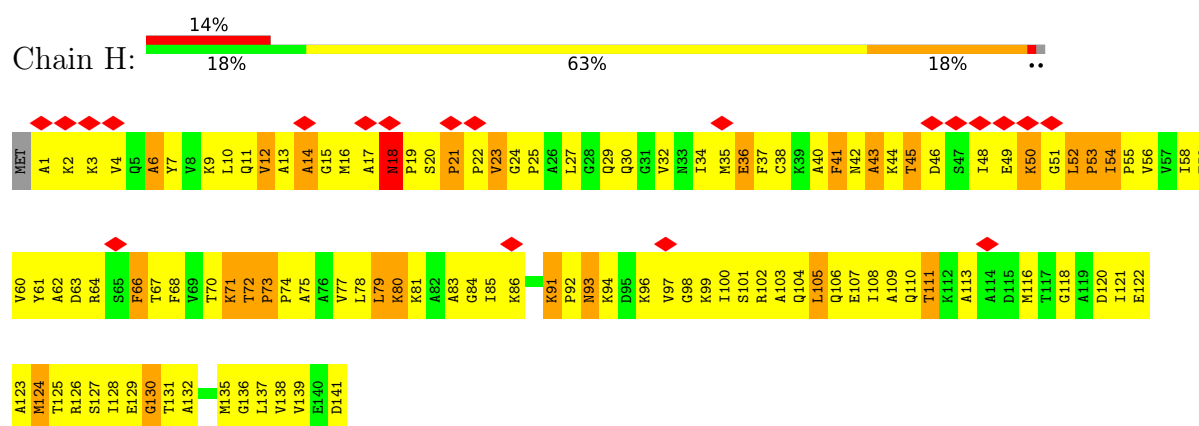
• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L10



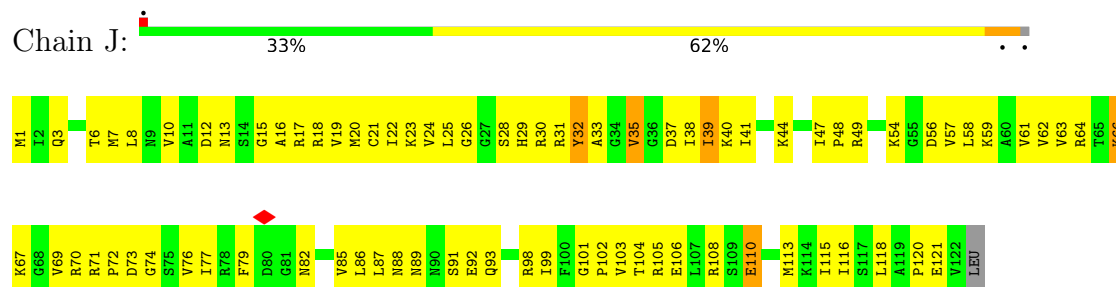
- Molecule 8: 50S ribosomal protein L11



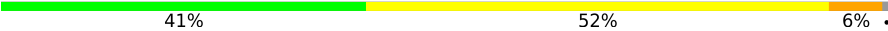
- Molecule 9: 50S ribosomal protein L13

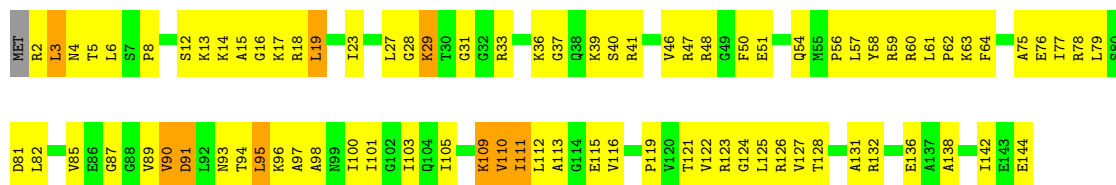


- Molecule 10: 50S ribosomal protein L14

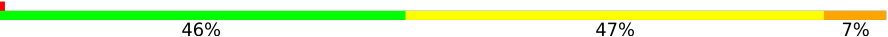


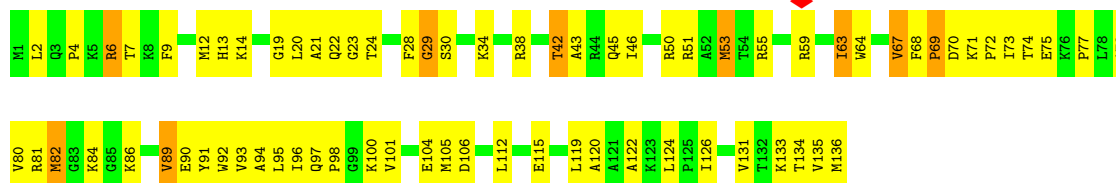
- Molecule 11: 50S ribosomal protein L15

Chain K:  41% 52% 6% •

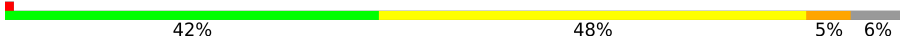


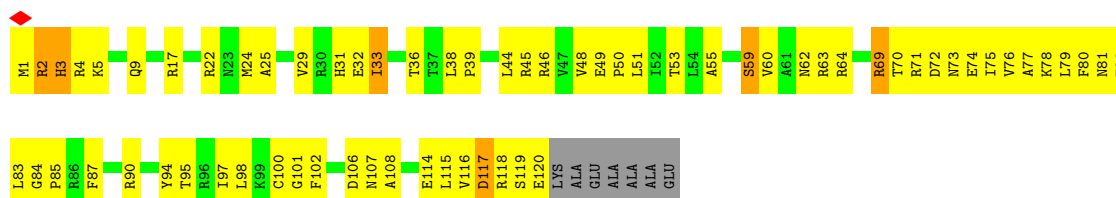
- Molecule 12: 50S ribosomal protein L16

Chain L:  46% 47% 7%



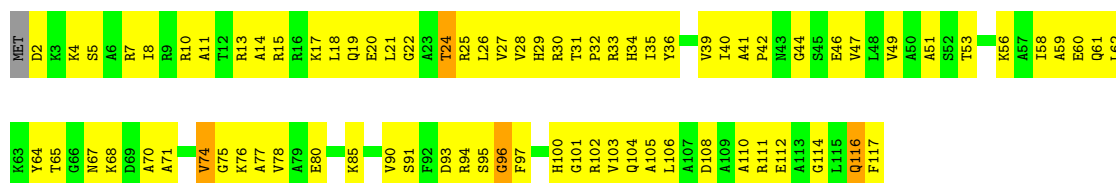
- Molecule 13: 50S ribosomal protein L17

Chain M:  42% 48% 5% 6%



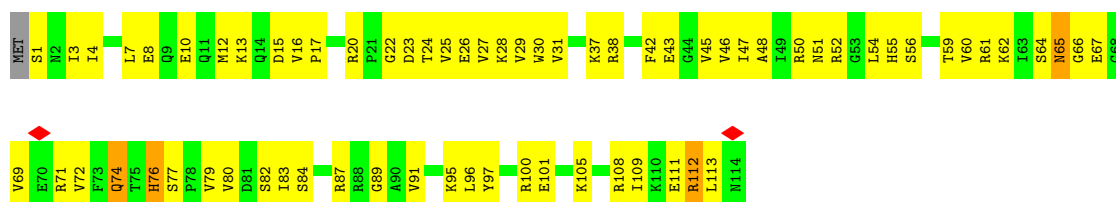
- Molecule 14: 50S ribosomal protein L18

Chain N:  32% 64% • •



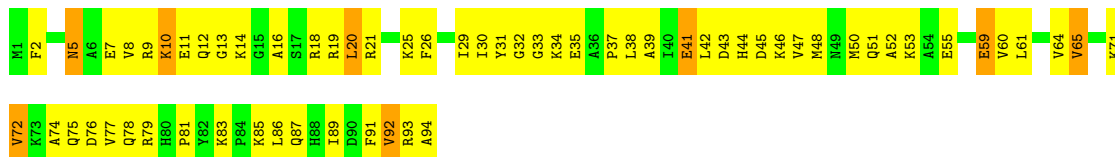
- Molecule 15: 50S ribosomal protein L19

Chain O:  39% 57% • •

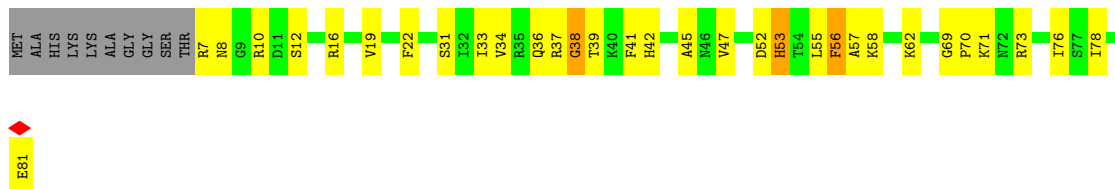




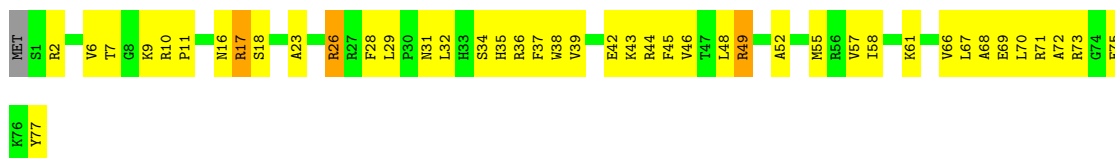
• Molecule 21: 50S ribosomal protein L25



• Molecule 22: 50S ribosomal protein L27



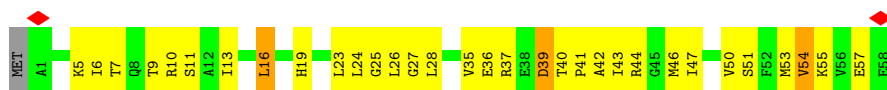
• Molecule 23: 50S ribosomal protein L28



• Molecule 24: 50S ribosomal protein L29

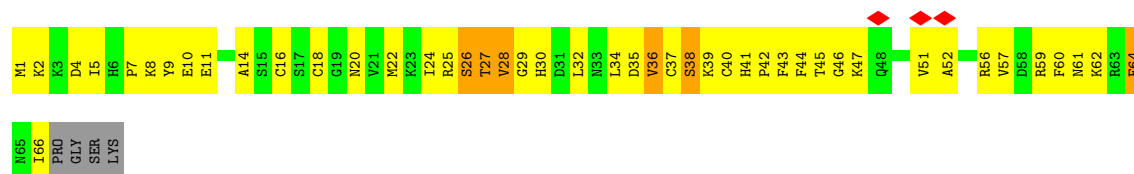


• Molecule 25: 50S ribosomal protein L30

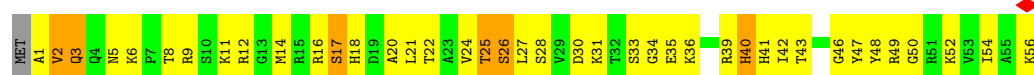


• Molecule 26: 50S ribosomal protein L31





• Molecule 27: 50S ribosomal protein L32



• Molecule 28: 50S ribosomal protein L33



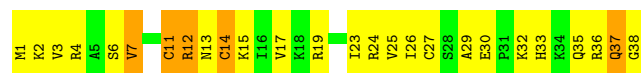
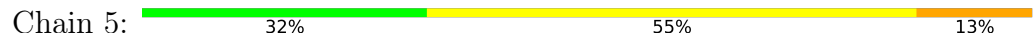
• Molecule 29: 50S ribosomal protein L34



• Molecule 30: 50S ribosomal protein L35

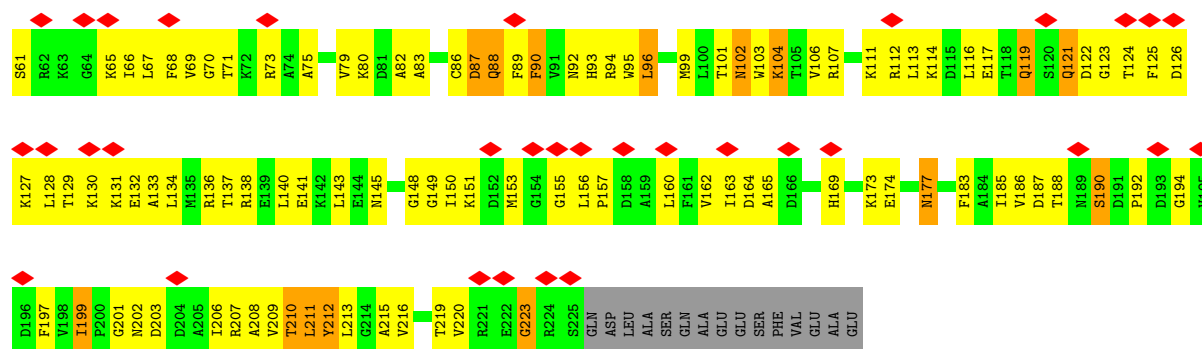


• Molecule 31: 50S ribosomal protein L36



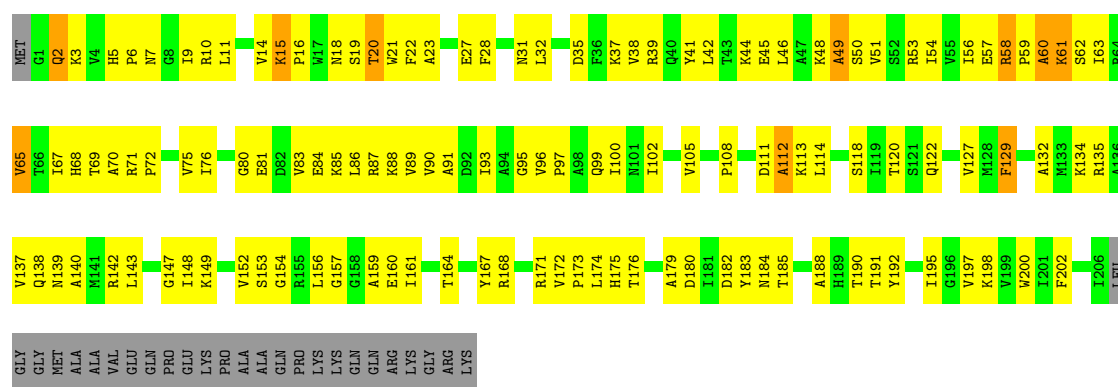
• Molecule 32: 30S ribosomal protein S2





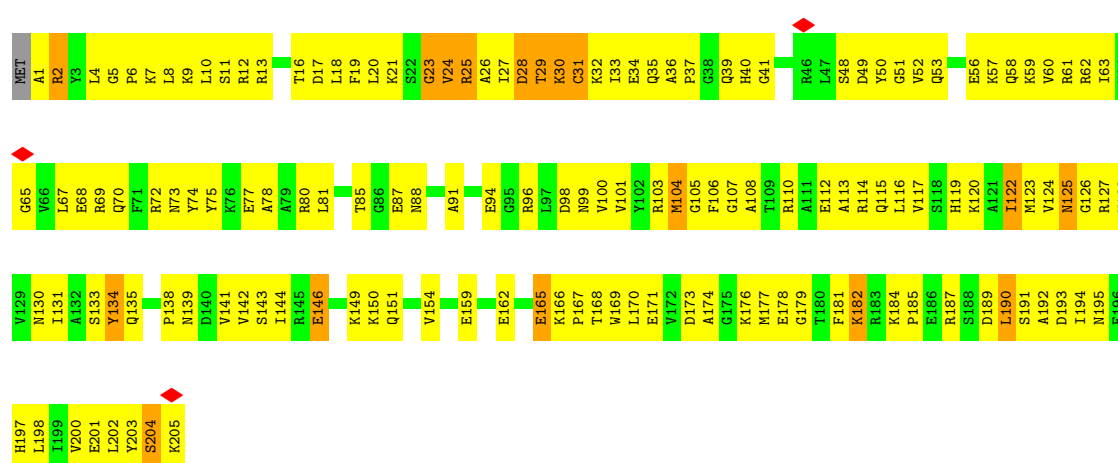
- Molecule 33: 30S ribosomal protein S3

Chain 7: 34% 50% 12%



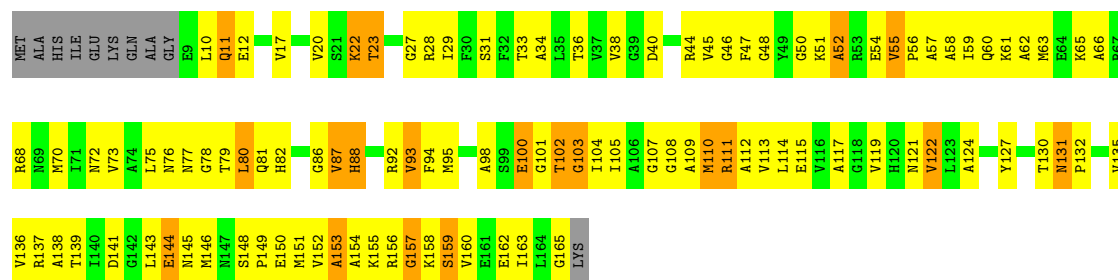
- Molecule 34: 30S ribosomal protein S4

Chain 8: 29% 63% 8%

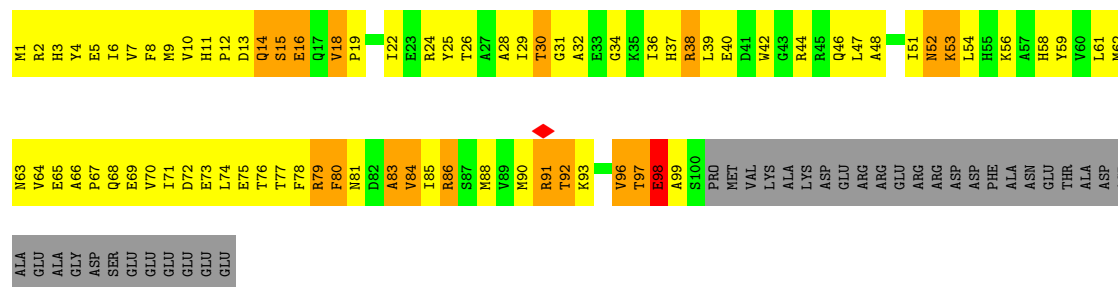
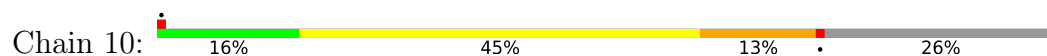


- Molecule 35: 30S ribosomal protein S5

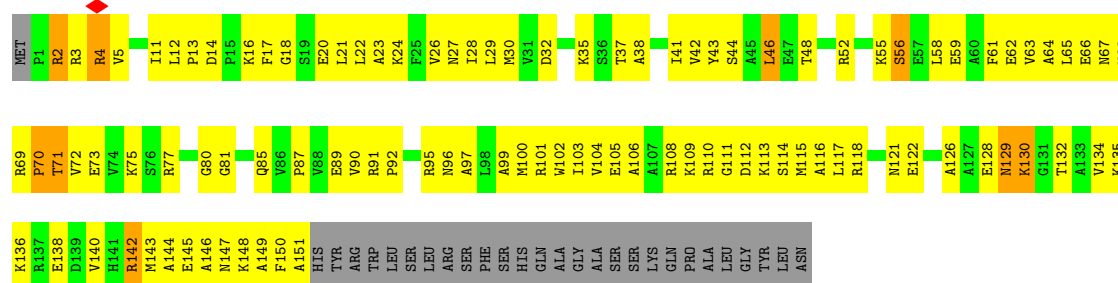
Chain 9: 31% 51% 12% 6%



- Molecule 36: 30S ribosomal protein S6



- Molecule 37: 30S ribosomal protein S7

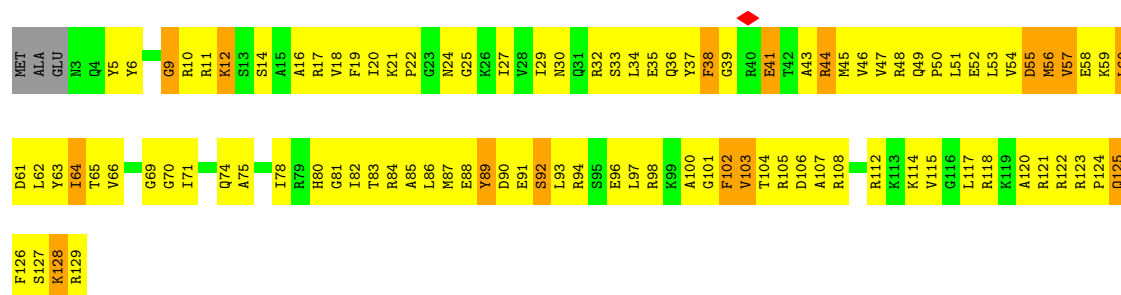


- Molecule 38: 30S ribosomal protein S8

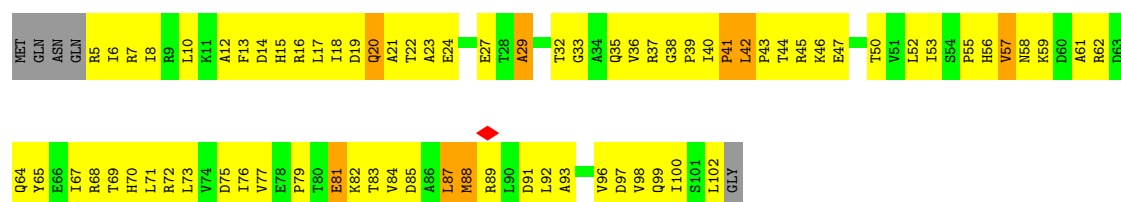


- Molecule 39: 30S ribosomal protein S9

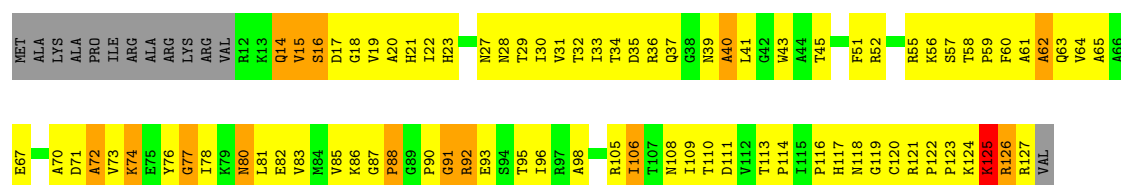




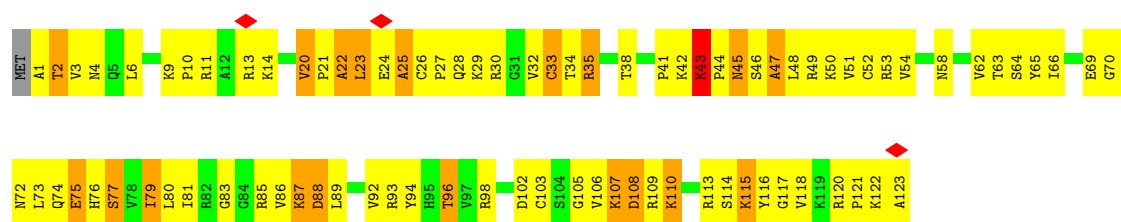
- Molecule 40: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S11

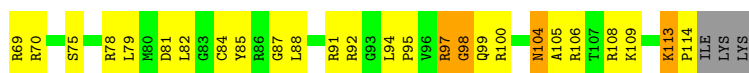


- Molecule 42: 30S ribosomal protein S12



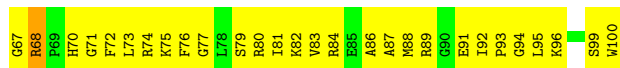
- Molecule 43: 30S ribosomal protein S13





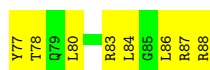
- Molecule 44: 30S ribosomal protein S14

Chain 18: 28% 65% 6%



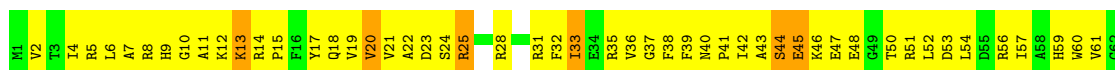
- Molecule 45: 30S ribosomal protein S15

Chain 19: 40% 53% 6%



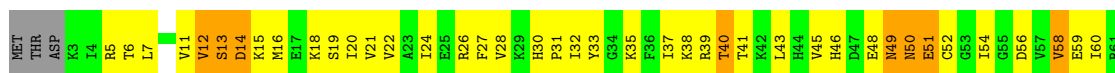
- Molecule 46: 30S ribosomal protein S16

Chain 20: 23% 66% 11%



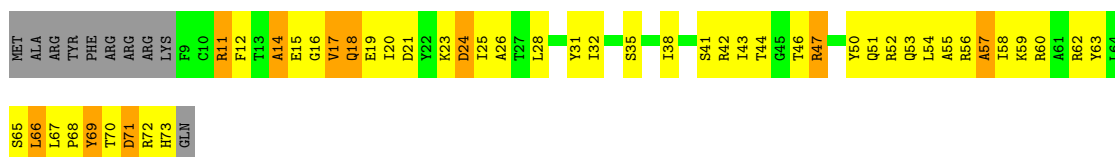
- Molecule 47: 30S ribosomal protein S17

Chain 21: 33% 50% 12% 5%

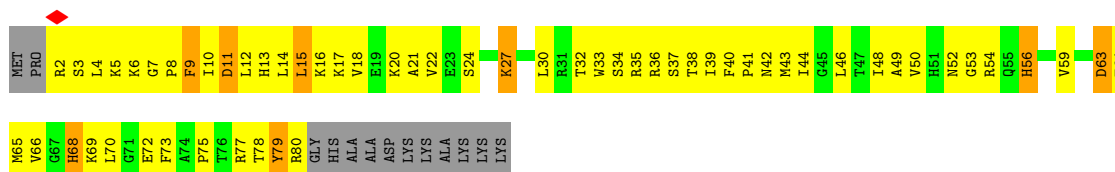


- Molecule 48: 30S ribosomal protein S18

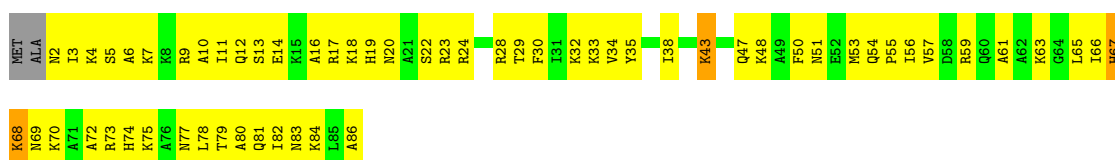
Chain 22: 24% 49% 13% 13%



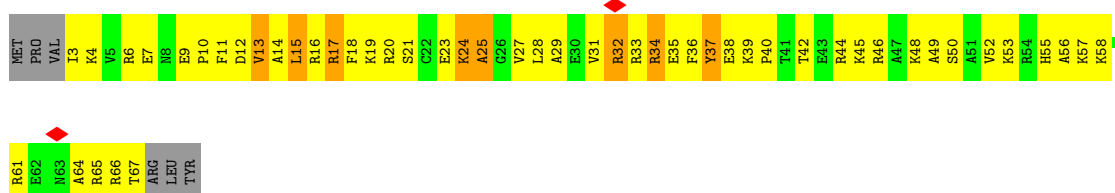
- Molecule 49: 30S ribosomal protein S19



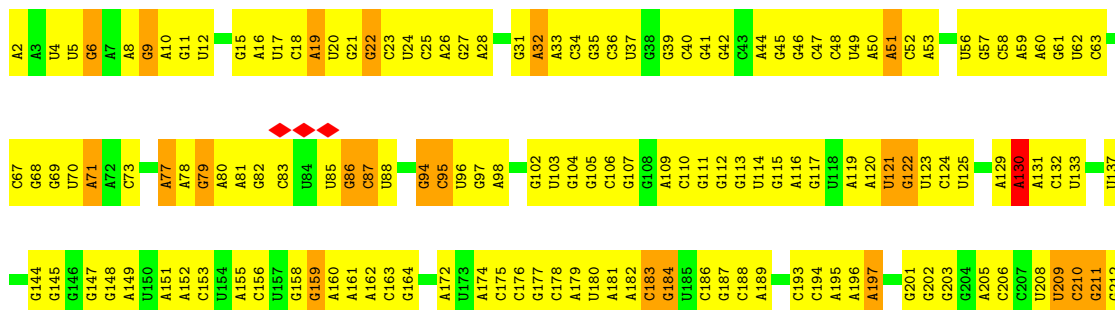
- Molecule 50: 30S ribosomal protein S20



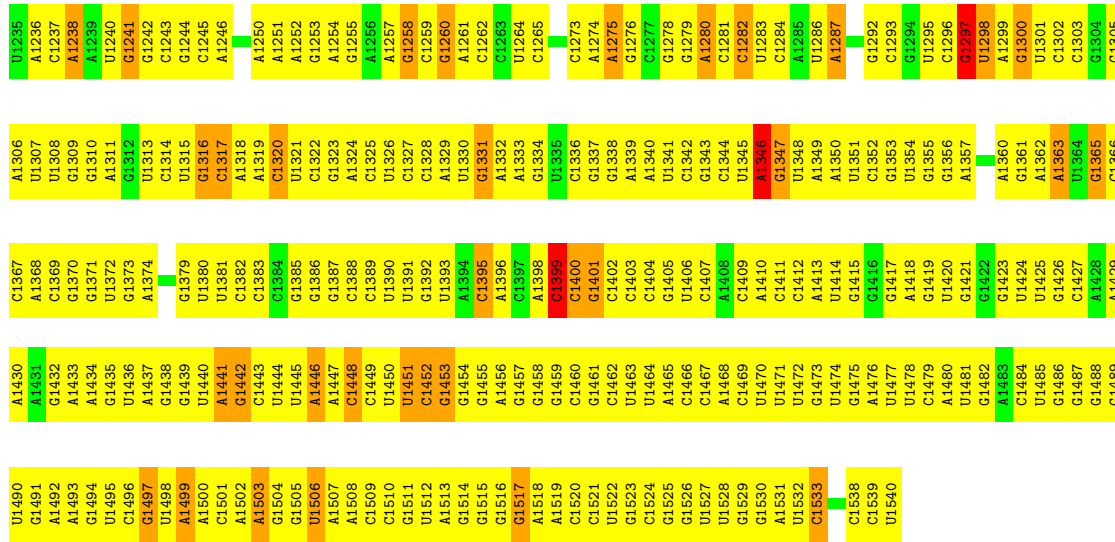
- Molecule 51: 30S ribosomal protein S21



- Molecule 52: 16S ribosomal RNA

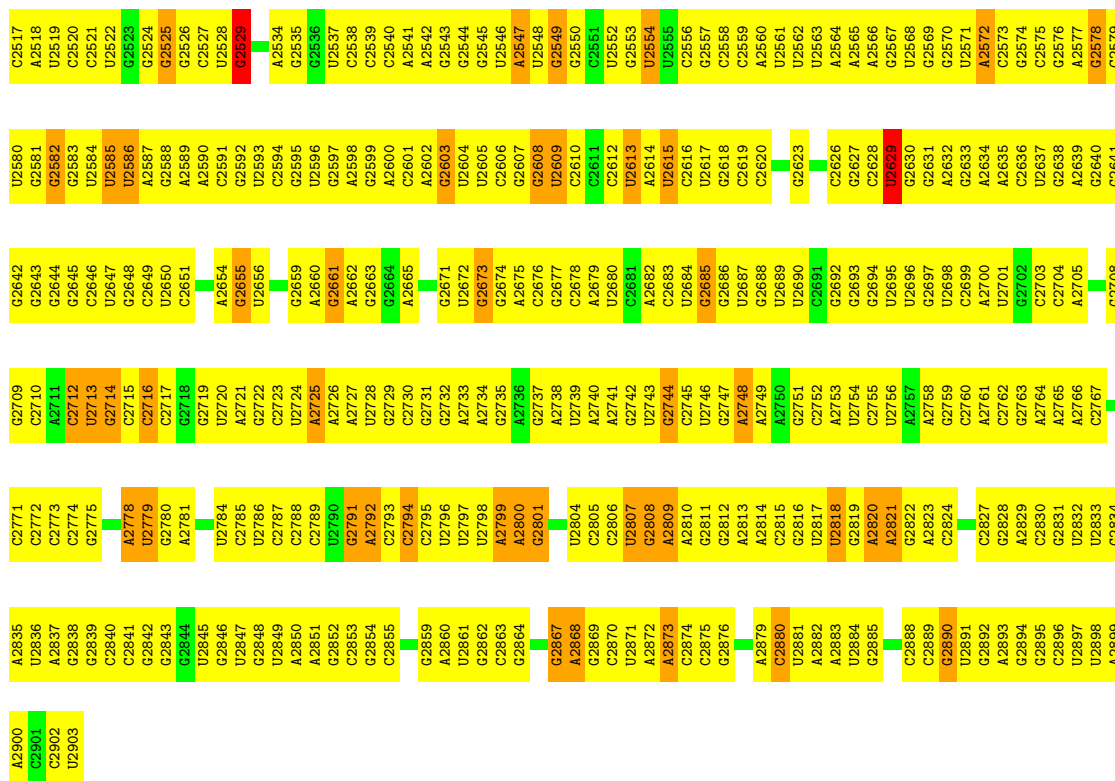


A1170	A1171	G1108	C1045	A978	U916	C856	U788	C726	A663	U593	G530	A466	G402	A338		G213
G1174	G1175	A1110	G1047	C979	G917	C857	U789	G727	G664	U594	U531	A467	C403	U340	A279	C214
		A1111	G1048	C980	A918	C858	A790	A728	A665	U595	A532	A468	G404	U340	C280	C215
		C1112	U1049	U981	A919	C859	G791	A729	G666	A596	A533	C469	U405	C341	G281	U216
		C1113	G1050		U920	A860	A792	G730	G667	U598	U534	C470	G406	C342	A282	C217
		C1114	C1051	U986	G921	C861	U793	G731	G668	U598	A535	U471	U407		U283	U218
		U1115	U1052	U986	G922	C862	A794	C732	G669	C599	C536	U472	A408	C345	C284	U219
		U1116	C1053	C987	A923	U863	G795		G670	A600	G537	U473	U409	G346	C285	G220
		U1117	G1054	U988	C924	A864	C796	C735	G671	G601	G538	U474	G410	G347	C286	C221
		A1118	C1055	U989	G925	A865	C797	C736	U672	A539	C475	C475	A411		U287	C222
		C1119	U1056	C990	G926	C866	U798	G737	G673	G604	G540	U476	A412	C352	A288	A223
		U1119	A1057	U991	G927	G867	G799	C738	G674	U605	G541	C477	G413	A353	G289	U224
		C1120	G1057	U992	G928	C868	G800	C739	A675	G606	G542	A476	A414	C354	C290	C225
		U1121	C1058	G993	G929	C869	U801	U740	U676	A607	U543		A415	C355	U291	G226
		U1122	U1059	A994		U870	A802	G741	U677	A608	G544	C483	G416	C356	G292	G227
		U1123	G1060	C995	C932	U871	G803	C742	U678	A609	C545	G484	C417	A357	G293	A228
		G1126	A1061	A996	G933	A872		A743	C679	U610	A546	U485	C418	G357	U294	U229
		U1127	U1062	U997	G934	A873	A807	G744	A681	C613	G548	A487	U420	G359	C295	G230
		C1128	C1063	C998	A935	G874	C808	G745	G682	C614	C549	C488	U421	G361	U296	U231
		U1129	G1064	A1000	C936	U875	G809	A746	G683		C549	C488	U422	G362	A298	G232
		A1130	U1065	C1001	A937	C876	C810	A747	U684	G617	G550	C489	G423	A363	G299	C233
		C1131	C1066		A938	C877	C811	G754	G685	C618	U552	G491	G424	A364	A300	C234
		U1132	G1067		G939	A878	G812	A749	U686	U619	A553	C492	G425	U365	G301	A236
		C1133		A1004	C940	C879	U820	C756	U692	C620	A554	A493	U426	A366	G302	G237
		U1134	U1070	A1005	G941	C880	A815	U751	A687	C621	U555	C494	U427	U367	A303	A238
		C1135	G1071	G1006	G942	C881	A816	G752	G688	A621	C556	G495	U428	U368	U304	U239
		U1136	U1072	U1007	U943	C882	C817	A753	C689	A622	C556	G495	G428	U368	G305	G242
		C1137	C1073	A1008	G944	C883	G818	C754	G690	C623	G557	A496	U429	G369	A306	A243
		U1138	G1074	U1009	G945	U884	A819	G755	G691	C624	G558	C497	A430	C370	G307	
		G1139	U1075	U1010	A946	C885	U820	C756	U692	U625	A559	A498	A431	A371	C307	
		C1140	G1077	C1011	G947	C886	G821	U757	A693	G626	A560	A499	A432	C372	C308	
		U1141	U1078	A1012	C948	C887	U822	C758	A694	G627	G561	G500	G433	A373	A309	A246
		C1142	G1079	G1013	A949	C888	C823	A759	A695	G628	U562	C501	U434	A374	G310	G247
		U1143	A1080	U1014	U950	A889	G824	G760	A696	A629	A563	A502	U435	U375	C311	
		G1144	A1081	G1015	G951	C890	A825	G761	U697	C630	C564	C503	C436	G376	C312	
		C1210	A1082	A1016	U952	U891	C826	U762	G698	C631	U565	C504	U437	G377	A313	A250
		U1211	U1083		G953	A892	U827	G763	C699	C632	G566	C505	U438	G378	U252	G251
		C1212	G1084	A1019	U954	C893	U828	C764		G633	G567	C379	U439	G380	C314	U253
		A1213	U1085	G1020	U955	G894	G829	G765	G703	C634	C507	C440	C440	G380	A315	G254
		G1214	U1086	U1023	U956	C895	A830	A766	A704	A635	G569	U508	A441	G377	U317	G255
		C1215	U1087	G1024	U957	C896	A831	A767	G705	U636	C570	A509		A382	G318	U256
		U1216	U1087	U1025	A958	C897	G832	A768	G706	C637	U571	A510	G445	A383	G319	G257
		C1217	U1088	U1026	A959	C898	G833	G769	U707	U638	A572	G384	G446	A383	G320	G258
		G1218	G1089	G1026	C999	U834	U835	C770	C708		C511	G385	G447	C386	A321	G259
		A1154	U1090	C1027	A900	U901	U835	G771	U709	A642	A573	C513	A448	C386	C322	G260
		C1155	U1091	G962	U961	A901	G836	U772	G710	C643	G575	C514	G449	U387	U323	U261
		U1156	A1092	U1029	G963	G902	U837	G773	G711	U644	C576	G515	G450	G388	G324	A262
		C1222	A1093	U1030	A964	G903	C838		A712	G645	G577	U516	A451	A389	A325	A263
		U1158	G1094	C1031	U904	U903	C839	G776	G713	G646	C578	G517	A452	U390	G326	C264
		C1223	U1095	G1032	U905	A906	C840	A777	G714	C647	A579			G391	G326	G265
		U1224	C1096	G1033	A906	U906	C841	G778	A715	A648	C580	A520	A456	C392	A327	G266
		C1225	C1097	G1034	A969	A907	U842	C779	A716	U653	G581	G521	A457	A393	A329	C267
		U1226	A908	U1037	C970	U908	U843	A780	U717	C522	G394	C330	U458	G394	U268	
		C1227	G1098	C1037	G971	A909	G844	A781	A718	G584	A523	A459	A459	C395	C331	C269
		U1228	A1163	U1039	G972	C910	A845	A782	G721	U657	G585	G524	A461	C396	G332	A270
		C1229	G1164	G1039	C911	U911	G846	C783	G722	U659	C586	G525	A461	A397	U333	C271
		U1165	A1101	U1040	G973	C912	G847	A784	G723	U659	G587	C526	G462	U388	C334	C272
		C1166	A1102	U1041	A975	A913	G785	G785	U723	C660	U463	G527	U463	G399	C335	U273
		U1232	C1103	G1041	A975	A914	U854	G724	G724	G661	C528	G528	U464	A336	A274	
		C1233	A1169	A1044	G976	U915	U855	A787	G725	U662	G592	C400	A465	C400	C337	G275





A2450	A2451	A2388	A2389	A2327	C2260	U2197	U2130	U2088	U2007	C1947	U1883	U1818	U1758	A1690	G1623	U1562
G2452	G2453	G2390	G2391	A2328	C2261	A2198	U2131	G2069	C2008	G1948	G1884	A1819	A1759	C1691	G1623	U1563
G2454	G2455	G2392	G2393	G2263	U2262	C2200	U2132	A2070	A2009	G1949	A1885	A1820	C1760	U1692	A1630	C1564
G2456	G2457	G2394	G2395	C2264	U2265	G2201	A2134	C2072	G2010	G1950	G1888	C1822	C1762	C1694	G1631	C1565
G2458	G2459	G2396	G2397	A2266	U2266	U2203	A2135	C2073	G2012	A1952	G1889	G1823	G1763	G1695	G1632	G1567
G2460	G2461	G2398	G2399	A2267	U2267	G2204	U2136	U2074	A2013	A1953	A1890	G1824	C1764	G1696	A1634	G1568
G2462	G2463	G2400	G2401	A2273	G2271	C2208	G2144	C2078	A2015	G1994	G1891	U1825	U1765	A1698	A1635	A1569
G2464	G2465	G2402	G2403	A2277	U2271	G2209	G2145	U2079	A2016	U1956	C1892	G1826	G1766	U1570	A1636	A1570
G2466	G2467	G2404	G2405	A2278	U2272	G2210	G2146	A2080	U2017	U1957	C1893	G1827	G1767	A1571	A1637	A1572
G2468	G2469	G2406	G2407	A2279	U2273	G2211	A2147	U2081	G2018	C1958	C1894	G1828	G1768	A1700	C1638	A1573
G2470	G2471	G2408	G2409	A2280	U2274	G2212	G2148	A2082	A2019	G1959	C1895	A1829	U1769	A1701	C1639	G1574
G2472	G2473	G2410	G2411	A2281	U2275	G2213	U2149	U2083	G2020	A1960	G1896	G1831	G1770	G1702	A1640	C1574
G2475	G2476	G2412	G2413	A2282	U2276	G2214	G2152	G2084	C2021	C1961	G1897	G1832	C1771	G1703	C1575	C1576
G2477	G2478	G2414	G2415	A2283	U2277	G2215	G2153	G2085	C2022	C1962	U1898	A1833	A1772	C1704	U1576	C1577
G2479	G2480	G2416	G2417	A2284	U2278	G2216	C2154	U2086	G2023	U1963	A1899	G1837	A1773	A1705	A1578	A1579
G2481	G2482	G2418	G2419	A2285	U2279	G2217	A2154	G2087	G2024	G1964	A1901	G1837	G1774	C1706	U1580	U1581
G2483	G2484	G2420	G2421	A2286	U2280	G2218	U2155	A2088	C2025	C1965	C1902	C1838	G1775	C1707	G1582	G1583
G2485	G2486	G2422	G2423	A2287	U2281	U2219	G2156	A2089	U2026	A1966	C1903	G1839	U1777	C1708	G1584	G1585
G2487	G2488	G2424	G2425	A2288	U2282	G2220	G2157	A2090	G2027	C1967	G1904	G1840	U1778	G1709	A1650	C1586
G2489	G2490	G2426	G2427	A2289	U2283	G2221	A2158	A2091	U2028	G1968	C1905	G1841	U1779	G1710	G1651	G1652
G2491	G2492	G2428	G2429	A2290	U2284	G2222	G2159	A2092	G2029	A1969	G1906	G1842	A1780	U1712	A1652	C1585
G2493	G2494	G2430	G2431	A2291	U2285	G2223	G2160	G2093	A2030	A1970	G1907	C1843	U1781	G1721	G1653	A1586
G2495	G2496	G2432	G2433	A2292	U2286	G2224	G2161	A2094	A2031	U1971	G1908	C1844	U1782	G1722	A1654	G1587
G2497	G2498	G2434	G2435	A2293	U2287	G2225	G2162	A2095	U2034	G1972	U1911	G1845	A1783	U1716	A1655	G1588
G2499	G2500	G2436	G2437	A2294	U2288	G2226	A2163	C2096	G2035	G1973	A1912	G1846	A1784	U1717	C1656	U1589
G2501	G2502	G2438	G2439	A2295	U2289	G2227	A2164	A2097	G2036	G1974	A1913	G1847	A1785	G1718	U1657	A1590
G2503	G2504	G2440	G2441	A2296	U2290	G2228	G2165	U2098	A2037	G1975	C1914	A1848	A1786	G1719	C1658	A1591
G2505	G2506	G2442	G2443	A2297	U2291	G2229	G2166	U2099	G2038	U1976	G1915	G1849	A1787	G1720	C1659	C1592
G2507	G2508	G2444	G2445	A2298	U2292	G2230	U2167	G2100	U2039	A1977	A1916	G1850	A1788	G1721	A1593	U1594
G2509	G2510	G2446	G2447	A2299	U2293	G2231	U2168	G2101	G2040	U1978	U1917	U1851	A1789	A1722	U1660	U1594
G2511	G2512	G2448	G2449	A2300	U2294	G2232	A2170	G2102	U2041	U1979	A1918	U1852	C1790	A1723	C1595	C1596
G2513	G2514	G2450	G2451	A2301	U2295	G2233	A2171	U2105	C2043	G1982	G1921	A1854	A1791	C1728	A1596	A1597
G2515	G2516	G2452	G2453	A2302	U2296	G2234	U2172	U2106	C2044	G1983	G1922	G1857	C1792	C1730	A1665	A1598
G2517	G2518	G2454	G2455	A2303	U2297	G2235	A2173	U2107	C2045	G1984	G1923	A1858	A1794	G1731	G1666	U1599
G2519	G2520	G2456	G2457	A2304	U2298	G2236	C2174	U2108	G2046	C1985	C1924	U1859	A1795	C1732	C1600	C1601
G2521	G2522	G2458	G2459	A2305	U2299	G2237	C2175	U2109	C2047	C1986	C1925	G1860	G1797	G1733	G1667	G1602
G2523	G2524	G2460	G2461	A2306	U2300	G2238	A2176	G2110	G2048	A1987	G1926	G1861	U1798	U1736	A1603	C1604
G2525	G2526	G2462	G2463	A2307	U2301	G2239	C2177	U2111	G2049	G1988	A1927	G1862	G1799	G1737	C1605	C1606
G2527	G2528	G2464	G2465	A2308	U2302	G2240	C2178	G2112	C2050	G1989	A1928	G1863	C1800	G1738	A1672	G1606
G2529	G2530	G2466	G2467	A2309	U2303	G2241	C2179	U2113	A2051	C1990	G1929	A1866	A1801	A1739	G1673	C1607
G2531	G2532	G2468	G2469	A2310	U2304	G2242	U2182	G2114	A2052	U1991	G1930	G1867	A1802	G1740	G1674	C1608
G2533	G2534	G2470	G2471	A2311	U2305	G2243	A2183	G2115	G2053	C1992	U1931	C1868	A1803	C1741	C1675	A1609
G2535	G2536	G2472	G2473	A2312	U2306	G2244	A2184	G2116	A2054	U1993	A1932	G1869	C1804	U1742	A1676	A1610
G2537	G2538	G2474	G2475	A2313	U2307	G2245	U2185	U2117	C2055	C1994	G1933	C1870	A1805	U1743	A1677	A1611
G2539	G2540	G2476	G2477	A2314	U2308	G2246	U2186	A2119	G2056	U1995	G1934	A1871	C1806	A1744	A1678	C1612
G2541	G2542	G2478	G2479	A2315	U2309	G2247	U2187	A2120	G2057	C1996	G1935	G1872	G1807	A1745	A1679	C1613
G2543	G2544	G2480	G2481	A2316	U2310	G2248	U2188	G2121	A2058	C1997	A1936	G1873	A1808	U1746	U1680	G1614
G2545	G2546	G2482	G2483	A2317	U2311	G2249	U2189	G2122	A2059	C1998	U1937	C1874	A1809	U1747	G1681	A1615
G2547	G2548	G2484	G2485	A2318	U2312	G2250	U2190	U2123	G2060	C1999	A1938	G1875	A1810	C1748	C1682	C1616
G2549	G2550	G2486	G2487	A2319	U2313	G2251	G2191	G2124	G2061	C2000	U1939	A1876	G1811	U1749	U1683	A1617
G2551	G2552	G2488	G2489	A2320	U2314	G2252	A2191	G2125	A2062	C2001	U1940	A1877	U1812	C1752	G1684	C1618
G2553	G2554	G2490	G2491	A2321	U2315	G2253	U2192	G2126	C2063	A2003	U1943	G1878	G1813	G1753	C1685	G1619
G2555	G2556	G2492	G2493	A2322	U2316	G2254	U2193	A2126	C2064	G2004	U1944	G1879	G1814	A1754	C1686	G1620
G2557	G2558	G2494	G2495	A2323	U2317	G2255	U2194	G2127	C2065	U1945	U1946	U1880	G1815	G1755	U1687	G1621
G2559	G2560	G2496	G2497	A2324	U2318	G2256	U2195	G2128	C2066	A2005	U1947	U1881	C1816	A1756	G1688	U1622
G2561	G2562	G2498	G2499	A2325	U2319	G2257	C2196	C2129	G2067	C2006	U1948	U1882	G1817	A1757	A1689	



• Molecule 54: 5S ribosomal RNA

Chain 28: 20% 71% 8%



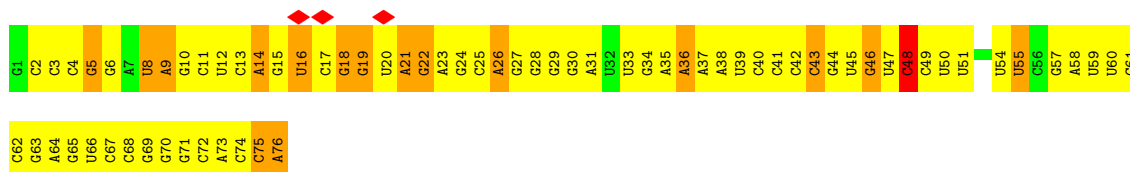
• Molecule 55: mRNA

Chain 29: 15% 25% 60% 10% 5%



• Molecule 56: A-site tRNA^{Phe}

Chain 30: 8% 70% 21%



L695	G696	V697	A698	S699	R700	S701	D702	T703	K704	Q705	Q706	L707	A708	T709	I710	D711	V712	I713	I714	E715	I716	V717	N718	L719	Q720	V721	L722	G723	R724	V725	L726	K727	L728	L729	N730	Q731	V732	V733	D734	I735	I736	D737	A738	R739	L740	H741	GLY	SER										
H634	R635	A636	D637	C638	E639	Q640	L641	A642	E643	L644	R645	S646	H647	A648	P649	E650	R651	I652	V653	D654	A655	V656	W657	G658	E659	SER	TYR	SER	ALA	G664	Y665	S666	L667	V668	V669	R670	V671	V672	A673	N674	D675	R676	G677	G678	L679	L680	R681	D682	I683	T684	T685	I686	L687	A688	N689	E690	K691	V694
Q572	D573	A576	L577	K578	Q579	L580	Q581	GLN	LYS	SER	Y585	T586	P587	Q588	N589	R590	S591	K592	D593	N594	G595	R596	V597	V598	V599	E600	G601	N604	L605	M606	Y534	H607	H608	I609	A610	R611	C612	C613	Q614	P615	I616	P617	G618	D619	E620	I621	V622	G623	F624	I625	T626	R629	G630	I631	S632	V633		
T485	S486	R487	K491	I492	H493	A494	W495	F496	R497	D500	R501	L506	D513	D514	E517	H518	L519	G520	I521	S522	E527	K528	H529	L530	L531	P532	R533	Y534	N535	F536	N537	D538	V539	D540	E541	A544	G548	G549	D550	I551	R552	L553	N554	F559	F564	N565	K566	A569										
A420	G421	S422	T423	P424	F427	A428	Y429	H430	I431	H432	S433	D434	V435	G436	H437	C439	I440	G441	A442	K443	I444	G445	G446	R447	I448	F451	T452	Y453	G458	D459	Q460	I461	E462	I463	T465	Q466	K467	Q468	P469	M470	P471	S472	R473	D474	W475	L476	M477	P478	M479	L480	G481	Y482	V483	T484				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46935	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	30488	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.503	Depositor
Minimum map value	-0.155	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.38	0/2121	1.08	22/2852 (0.8%)
2	B	0.39	0/1586	1.09	12/2134 (0.6%)
3	C	0.41	0/1571	1.07	8/2113 (0.4%)
4	D	0.35	0/1434	1.02	12/1926 (0.6%)
5	E	0.36	0/1343	1.04	7/1816 (0.4%)
6	F	0.45	0/1122	1.13	13/1515 (0.9%)
7	G	0.51	0/1001	1.40	21/1350 (1.6%)
8	H	0.54	0/1046	1.49	34/1410 (2.4%)
9	I	0.38	0/1152	1.03	10/1551 (0.6%)
10	J	0.36	0/947	1.09	7/1268 (0.6%)
11	K	0.37	0/1054	1.21	10/1403 (0.7%)
12	L	0.38	0/1093	1.03	7/1460 (0.5%)
13	M	0.38	0/973	1.07	2/1301 (0.2%)
14	N	0.35	0/902	0.99	4/1209 (0.3%)
15	O	0.35	0/929	1.01	5/1242 (0.4%)
16	P	0.37	0/960	1.01	8/1278 (0.6%)
17	Q	0.37	0/829	1.21	12/1107 (1.1%)
18	R	0.35	0/864	1.03	6/1156 (0.5%)
19	S	0.37	0/744	1.17	8/994 (0.8%)
20	T	0.37	0/787	1.05	6/1051 (0.6%)
21	U	0.36	0/766	1.06	6/1025 (0.6%)
22	V	0.38	0/582	1.09	4/769 (0.5%)
23	W	0.35	0/635	1.05	4/848 (0.5%)
24	X	0.35	0/510	1.00	3/677 (0.4%)
25	Y	0.39	0/453	1.09	4/605 (0.7%)
26	Z	0.45	0/531	1.24	7/709 (1.0%)
27	1	0.35	0/450	1.09	3/599 (0.5%)
28	2	0.37	0/416	1.03	3/554 (0.5%)
29	3	0.43	0/380	1.05	2/498 (0.4%)
30	4	0.35	0/513	0.93	0/676
31	5	0.37	0/303	1.13	2/397 (0.5%)
32	6	0.42	0/1735	1.15	24/2338 (1.0%)
33	7	0.39	0/1651	1.07	9/2225 (0.4%)
34	8	0.36	0/1665	1.11	13/2227 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	9	0.36	0/1169	1.05	10/1573 (0.6%)
36	10	0.42	0/835	1.22	18/1128 (1.6%)
37	11	0.34	0/1195	1.04	3/1602 (0.2%)
38	12	0.40	0/989	1.14	8/1326 (0.6%)
39	13	0.37	0/1034	1.14	8/1375 (0.6%)
40	14	0.41	0/796	1.12	8/1077 (0.7%)
41	15	0.39	0/885	1.19	9/1195 (0.8%)
42	16	0.39	0/969	1.22	10/1300 (0.8%)
43	17	0.37	0/892	1.14	6/1193 (0.5%)
44	18	0.47	0/817	0.99	7/1088 (0.6%)
45	19	0.33	0/722	0.94	3/964 (0.3%)
46	20	0.40	0/659	1.15	10/884 (1.1%)
47	21	0.40	0/657	1.08	6/881 (0.7%)
48	22	0.40	0/544	1.02	5/731 (0.7%)
49	23	0.39	0/652	1.18	9/877 (1.0%)
50	24	0.38	0/671	0.96	2/888 (0.2%)
51	25	0.45	0/550	1.23	7/728 (1.0%)
52	26	0.45	0/36967	0.59	14/57666 (0.0%)
53	27	0.47	1/69801 (0.0%)	0.60	18/108894 (0.0%)
54	28	0.43	0/2876	0.58	1/4483 (0.0%)
55	29	0.75	0/486	0.76	1/757 (0.1%)
56	30	0.55	0/1813	0.64	1/2823 (0.0%)
57	31	0.44	0/1836	0.52	1/2859 (0.0%)
58	32	0.66	0/1835	0.67	2/2857 (0.1%)
59	33	0.82	15/4985 (0.3%)	1.39	80/6770 (1.2%)
All	All	0.46	16/167683 (0.0%)	0.79	545/250202 (0.2%)

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

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

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.96	1.19	1.33
59	33	17	PRO	CA-CB	-9.93	1.39	1.53
59	33	20	TRP	NE1-CE2	-7.69	1.28	1.37
59	33	152	LYS	CD-CE	-6.87	1.31	1.52
59	33	159	HIS	CG-ND1	-6.55	1.31	1.38

The worst 5 of 545 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	119	SER	N-CA-C	-14.91	94.35	112.54
42	16	20	VAL	N-CA-C	13.84	122.41	107.60
7	G	60	LEU	N-CA-C	-12.53	96.17	113.20
59	33	17	PRO	N-CA-CB	-12.21	89.90	103.33
39	13	87	MET	N-CA-C	-12.05	98.56	113.38

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	130	A	Sidechain
52	26	159	G	Sidechain
52	26	266	G	Sidechain
52	26	820	U	Sidechain
52	26	88	U	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2082	0	2157	191	0
2	B	1565	0	1616	124	0
3	C	1552	0	1619	141	0
4	D	1410	0	1447	151	0
5	E	1323	0	1374	90	0
6	F	1111	0	1148	86	0
7	G	988	0	1025	127	0
8	H	1032	0	1088	140	0
9	I	1129	0	1162	94	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	93	0
11	K	1045	0	1117	88	0
12	L	1074	0	1157	77	0
13	M	960	0	1000	78	0
14	N	892	0	923	75	0
15	O	917	0	965	79	0
16	P	947	0	1022	96	0
17	Q	816	0	839	94	0
18	R	857	0	922	54	0
19	S	738	0	807	54	0
20	T	779	0	834	80	0
21	U	753	0	780	77	0
22	V	575	0	592	30	0
23	W	625	0	655	45	0
24	X	509	0	543	62	0
25	Y	449	0	491	41	0
26	Z	522	0	521	53	0
27	1	444	0	461	53	0
28	2	409	0	440	20	0
29	3	377	0	418	32	0
30	4	504	0	574	33	0
31	5	302	0	343	29	0
32	6	1704	0	1732	130	0
33	7	1624	0	1699	114	0
34	8	1643	0	1710	176	0
35	9	1156	0	1199	113	0
36	10	817	0	808	104	0
37	11	1181	0	1240	100	0
38	12	979	0	1034	90	0
39	13	1022	0	1070	135	0
40	14	786	0	828	92	0
41	15	869	0	878	94	0
42	16	955	0	1019	120	0
43	17	883	0	944	99	0
44	18	805	0	847	101	0
45	19	714	0	737	57	0
46	20	649	0	666	90	0
47	21	648	0	691	55	0
48	22	535	0	552	56	0
49	23	637	0	665	72	0
50	24	665	0	714	67	0
51	25	544	0	579	82	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	1573	0
53	27	62322	0	31345	2871	0
54	28	2572	0	1302	116	0
55	29	432	0	218	14	0
56	30	1623	0	821	75	0
57	31	1644	0	836	46	0
58	32	1643	0	836	66	0
59	33	4911	0	4550	671	0
All	All	154603	0	105189	8961	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 35.

The worst 5 of 8961 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:27:45:G:H5''	53:27:46:G:H5'	1.22	1.18
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.57	1.17
7:G:55:VAL:HA	53:27:1084:A:H5'	1.26	1.15
53:27:1702:G:H2'	53:27:1703:G:H5''	1.15	1.14
59:33:24:LEU:HD21	59:33:70:SER:HA	1.19	1.12

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	269/273 (98%)	218 (81%)	41 (15%)	10 (4%)	2	22
2	B	207/209 (99%)	172 (83%)	28 (14%)	7 (3%)	3	23
3	C	199/201 (99%)	147 (74%)	32 (16%)	20 (10%)	0	7

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	27 (15%)	5 (3%)	3	26
5	E	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	3	26
6	F	147/149 (99%)	108 (74%)	20 (14%)	19 (13%)	0	3
7	G	129/165 (78%)	93 (72%)	25 (19%)	11 (8%)	0	10
8	H	139/142 (98%)	104 (75%)	25 (18%)	10 (7%)	1	13
9	I	140/142 (99%)	120 (86%)	14 (10%)	6 (4%)	2	20
10	J	120/123 (98%)	97 (81%)	16 (13%)	7 (6%)	1	16
11	K	141/144 (98%)	110 (78%)	20 (14%)	11 (8%)	1	12
12	L	134/136 (98%)	113 (84%)	15 (11%)	6 (4%)	2	19
13	M	118/127 (93%)	91 (77%)	22 (19%)	5 (4%)	2	20
14	N	114/117 (97%)	98 (86%)	15 (13%)	1 (1%)	14	49
15	O	112/115 (97%)	93 (83%)	15 (13%)	4 (4%)	2	22
16	P	115/118 (98%)	103 (90%)	7 (6%)	5 (4%)	2	20
17	Q	101/103 (98%)	77 (76%)	16 (16%)	8 (8%)	1	11
18	R	108/110 (98%)	87 (81%)	15 (14%)	6 (6%)	1	17
19	S	91/100 (91%)	71 (78%)	16 (18%)	4 (4%)	2	20
20	T	100/104 (96%)	79 (79%)	14 (14%)	7 (7%)	1	13
21	U	92/94 (98%)	76 (83%)	11 (12%)	5 (5%)	1	17
22	V	73/85 (86%)	65 (89%)	7 (10%)	1 (1%)	9	39
23	W	75/78 (96%)	67 (89%)	6 (8%)	2 (3%)	4	28
24	X	61/63 (97%)	49 (80%)	7 (12%)	5 (8%)	0	10
25	Y	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
26	Z	64/70 (91%)	47 (73%)	7 (11%)	10 (16%)	0	2
27	1	54/57 (95%)	43 (80%)	6 (11%)	5 (9%)	0	9
28	2	48/55 (87%)	41 (85%)	7 (15%)	0	100	100
29	3	44/46 (96%)	32 (73%)	11 (25%)	1 (2%)	5	31
30	4	62/65 (95%)	51 (82%)	8 (13%)	3 (5%)	2	18
31	5	36/38 (95%)	26 (72%)	5 (14%)	5 (14%)	0	3
32	6	216/241 (90%)	170 (79%)	32 (15%)	14 (6%)	1	15
33	7	204/233 (88%)	175 (86%)	22 (11%)	7 (3%)	3	23
34	8	203/206 (98%)	157 (77%)	30 (15%)	16 (8%)	1	11

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	109 (70%)	33 (21%)	13 (8%)	0	10
36	10	98/135 (73%)	77 (79%)	14 (14%)	7 (7%)	1	13
37	11	149/179 (83%)	123 (83%)	14 (9%)	12 (8%)	1	11
38	12	127/130 (98%)	110 (87%)	8 (6%)	9 (7%)	1	13
39	13	125/130 (96%)	93 (74%)	19 (15%)	13 (10%)	0	7
40	14	96/103 (93%)	76 (79%)	15 (16%)	5 (5%)	1	17
41	15	114/129 (88%)	90 (79%)	13 (11%)	11 (10%)	0	8
42	16	121/124 (98%)	95 (78%)	13 (11%)	13 (11%)	0	6
43	17	112/118 (95%)	88 (79%)	14 (12%)	10 (9%)	0	10
44	18	98/101 (97%)	72 (74%)	21 (21%)	5 (5%)	1	17
45	19	86/89 (97%)	70 (81%)	11 (13%)	5 (6%)	1	16
46	20	80/82 (98%)	59 (74%)	18 (22%)	3 (4%)	2	21
47	21	78/84 (93%)	54 (69%)	19 (24%)	5 (6%)	1	15
48	22	63/75 (84%)	50 (79%)	5 (8%)	8 (13%)	0	4
49	23	77/92 (84%)	64 (83%)	11 (14%)	2 (3%)	4	28
50	24	83/87 (95%)	75 (90%)	6 (7%)	2 (2%)	4	30
51	25	63/71 (89%)	40 (64%)	19 (30%)	4 (6%)	1	15
59	33	663/750 (88%)	557 (84%)	60 (9%)	46 (7%)	1	13
All	All	6509/6970 (93%)	5226 (80%)	879 (14%)	404 (6%)	2	15

5 of 404 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

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

5 of 717 RNA backbone outliers are listed below:

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

5 of 36 RNA pucker outliers are listed below:

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

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

There are no chain breaks in this entry.

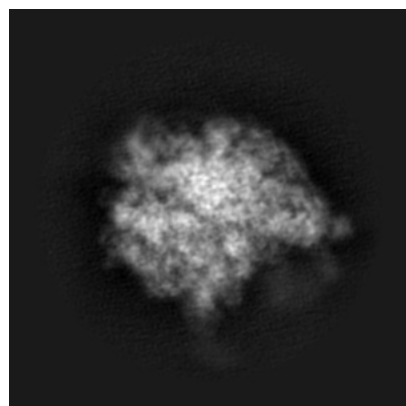
6 Map visualisation [i](#)

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

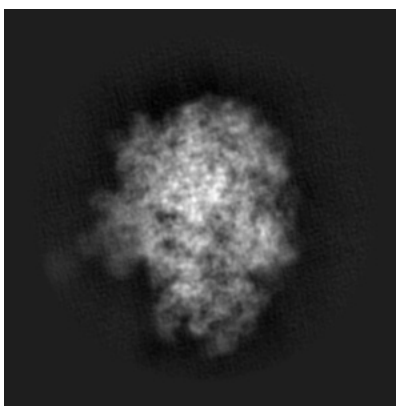
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

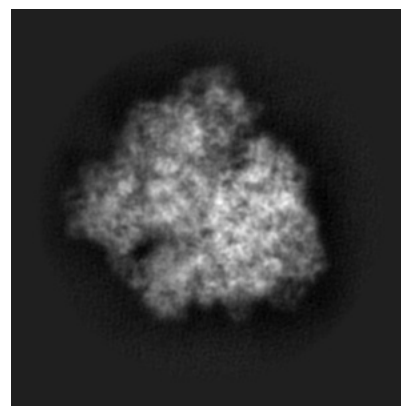
6.1.1 Primary map



X

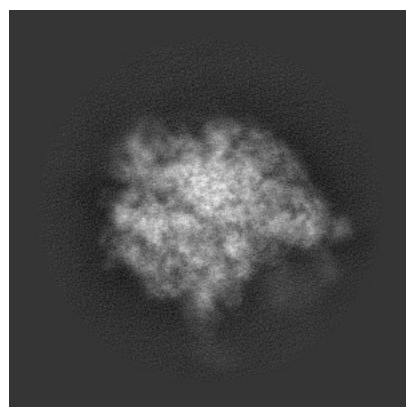


Y

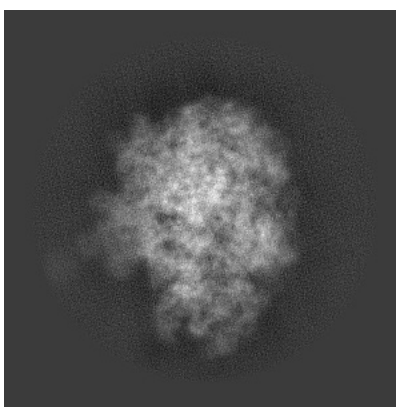


Z

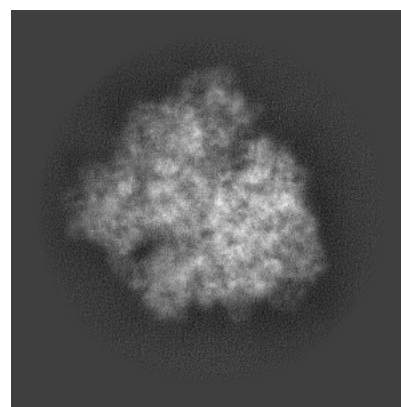
6.1.2 Raw map



X



Y

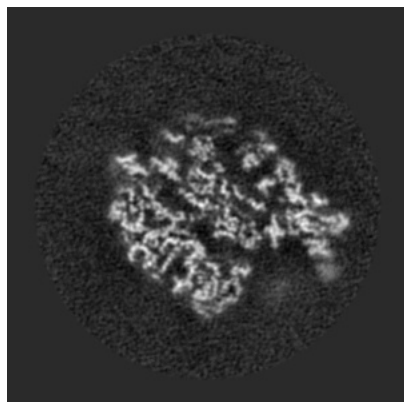


Z

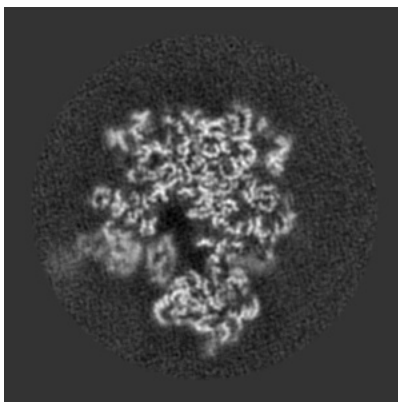
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

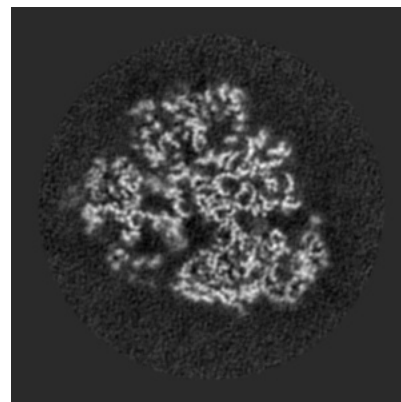
6.2.1 Primary map



X Index: 240

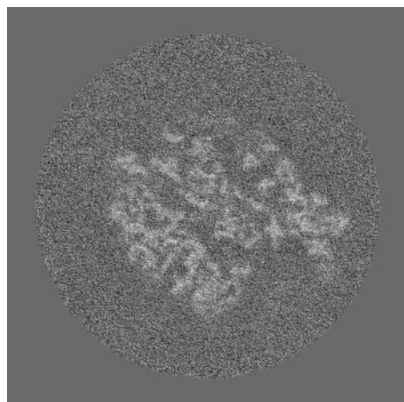


Y Index: 240

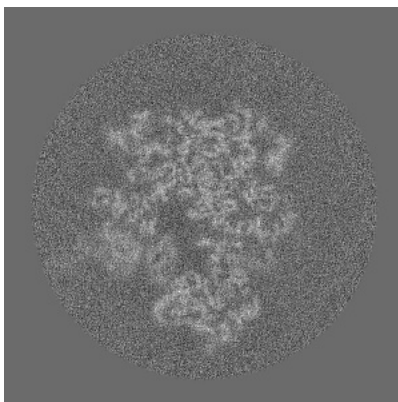


Z Index: 240

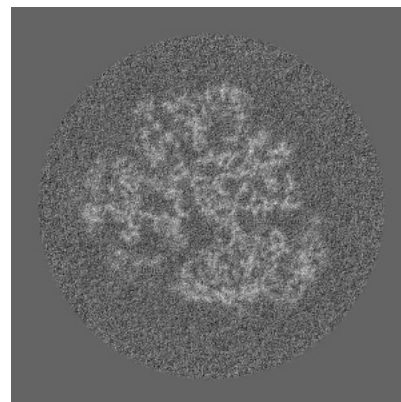
6.2.2 Raw map



X Index: 240



Y Index: 240

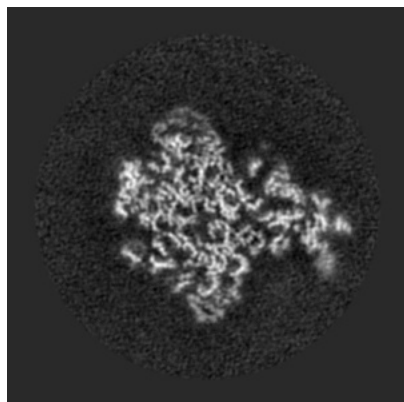


Z Index: 240

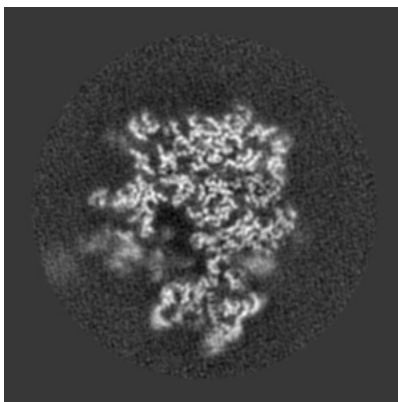
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

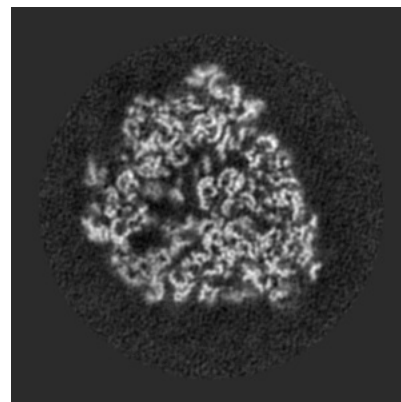
6.3.1 Primary map



X Index: 250

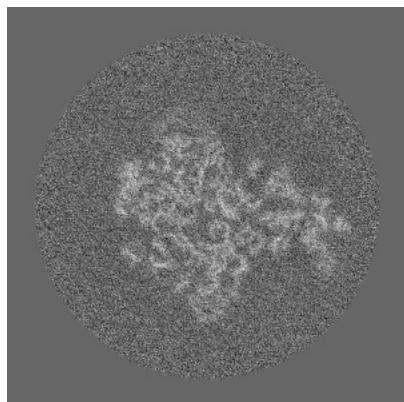


Y Index: 247

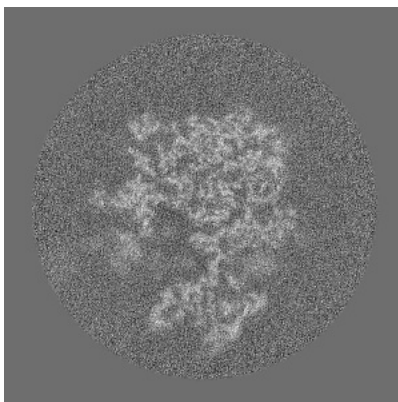


Z Index: 226

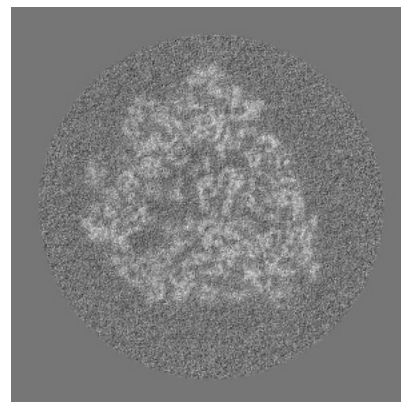
6.3.2 Raw map



X Index: 250



Y Index: 249

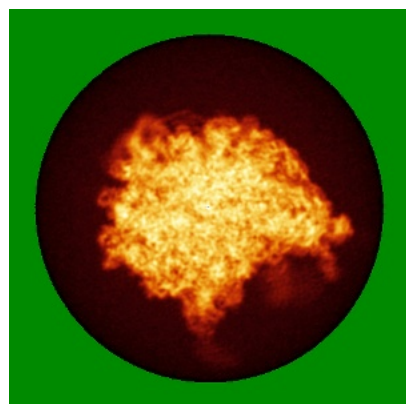


Z Index: 226

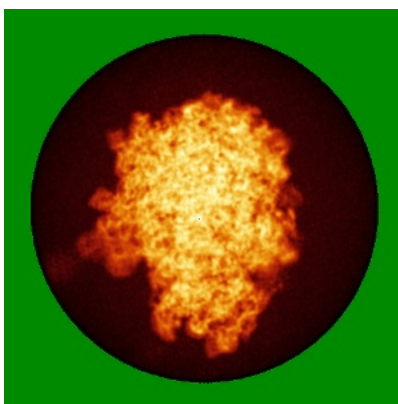
The images above show the largest variance slices of the map in three orthogonal directions.

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

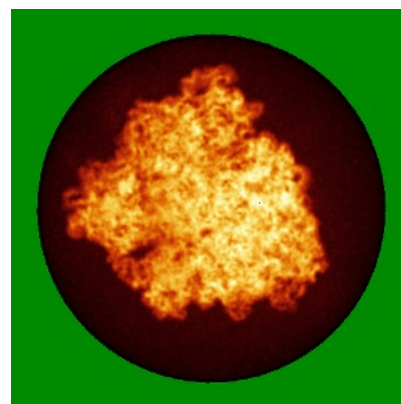
6.4.1 Primary map



X

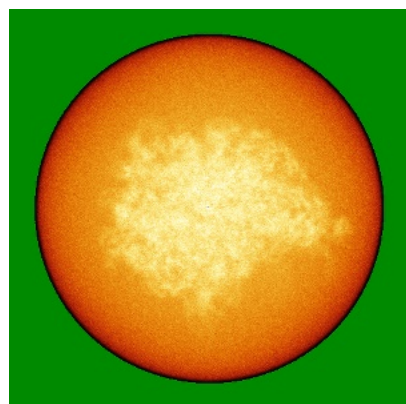


Y

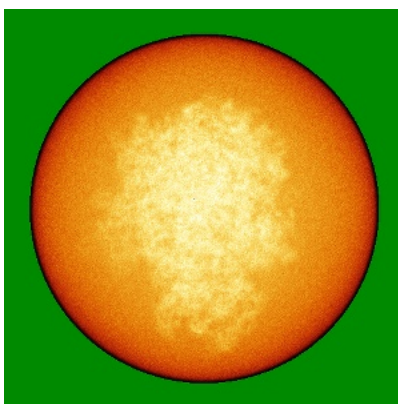


Z

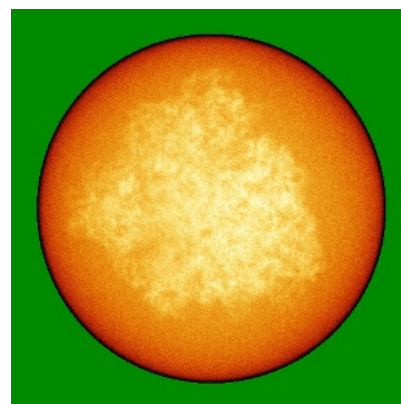
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

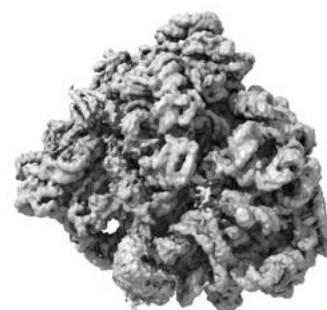
6.5.1 Primary map



X



Y



Z

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

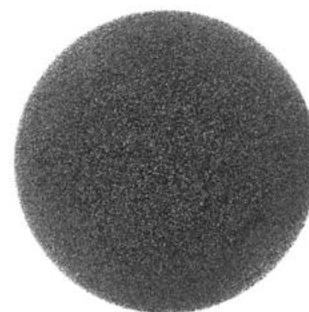
6.5.2 Raw map



X



Y



Z

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

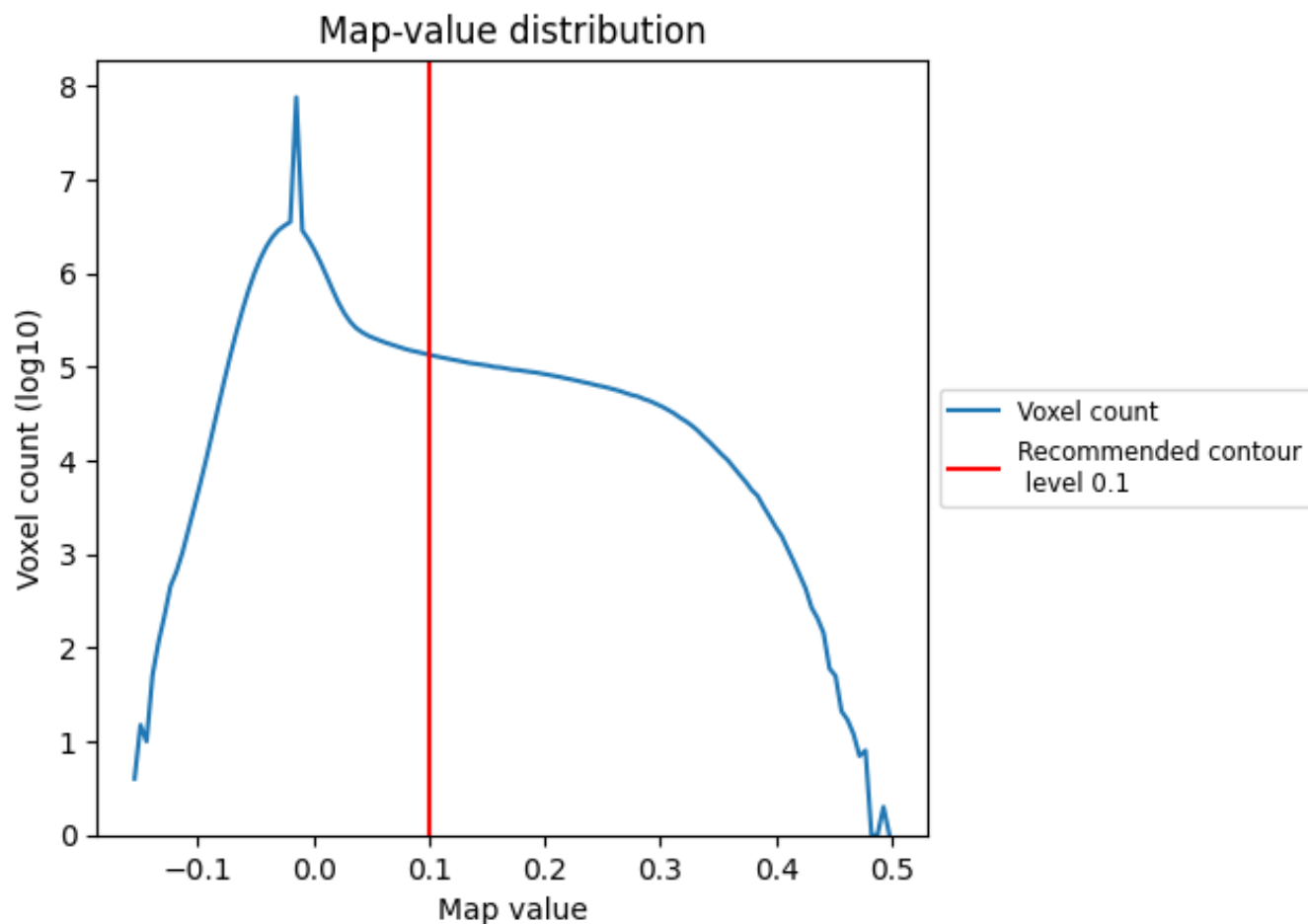
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

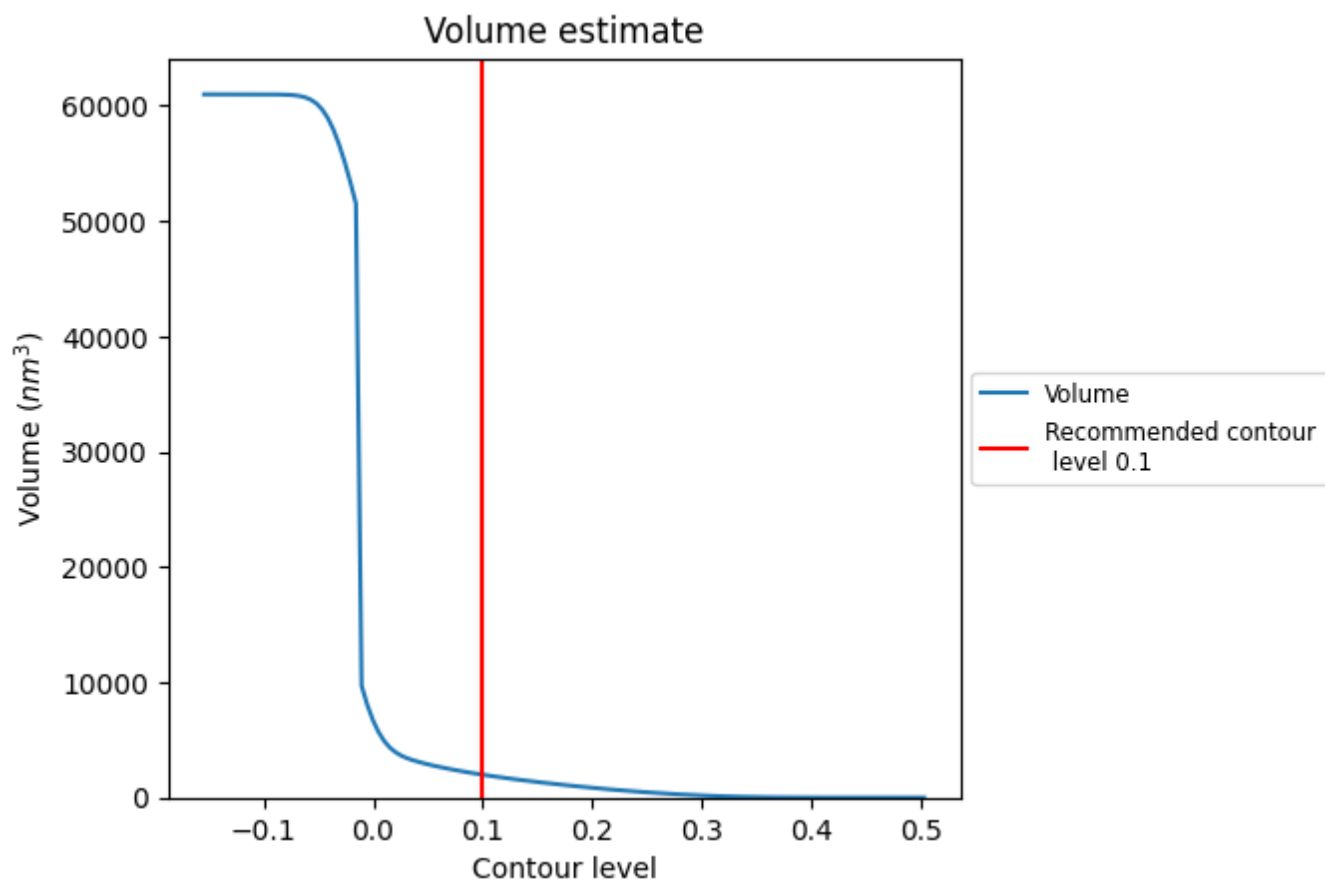
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

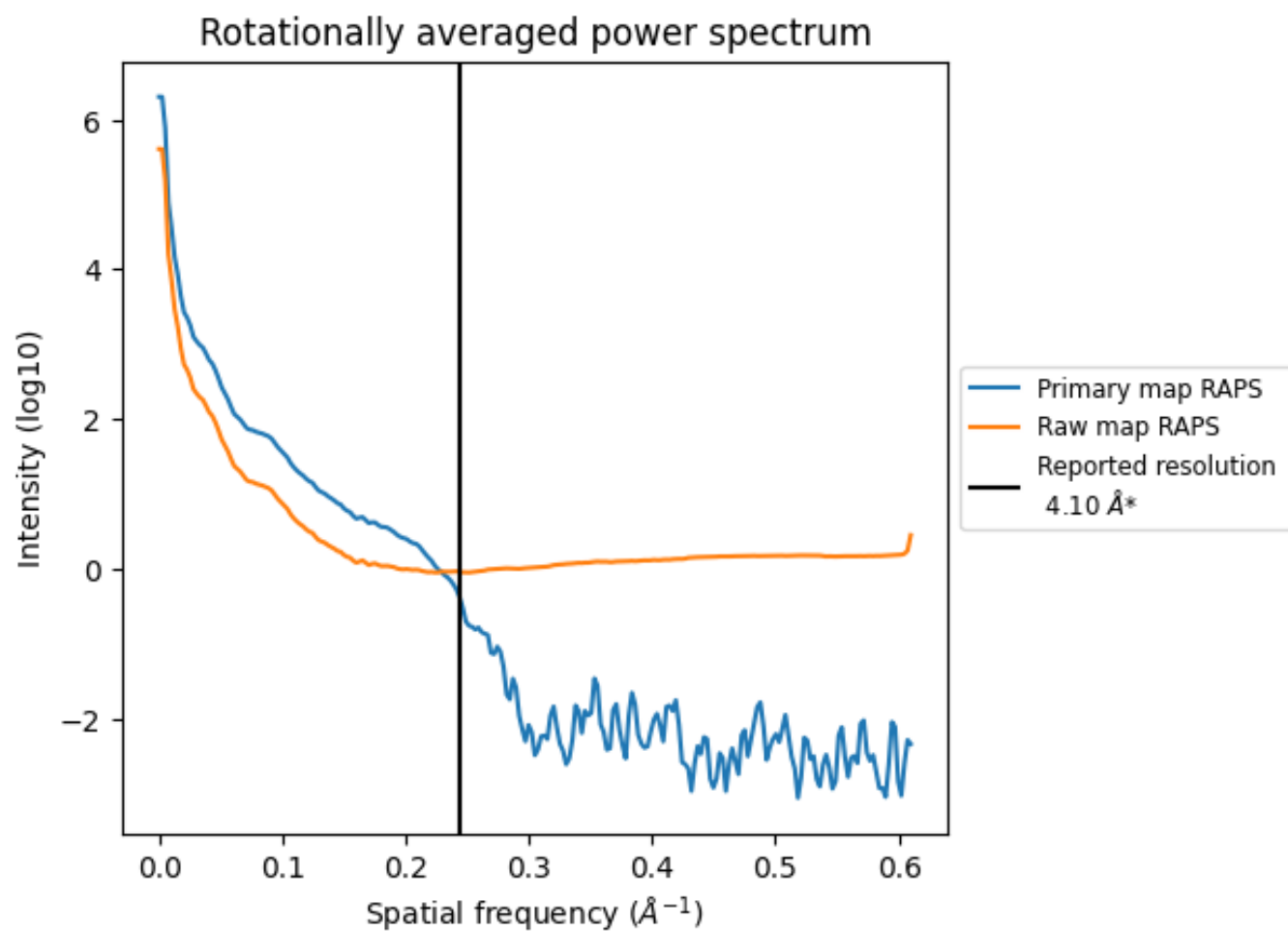
7.2 Volume estimate [i](#)



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

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

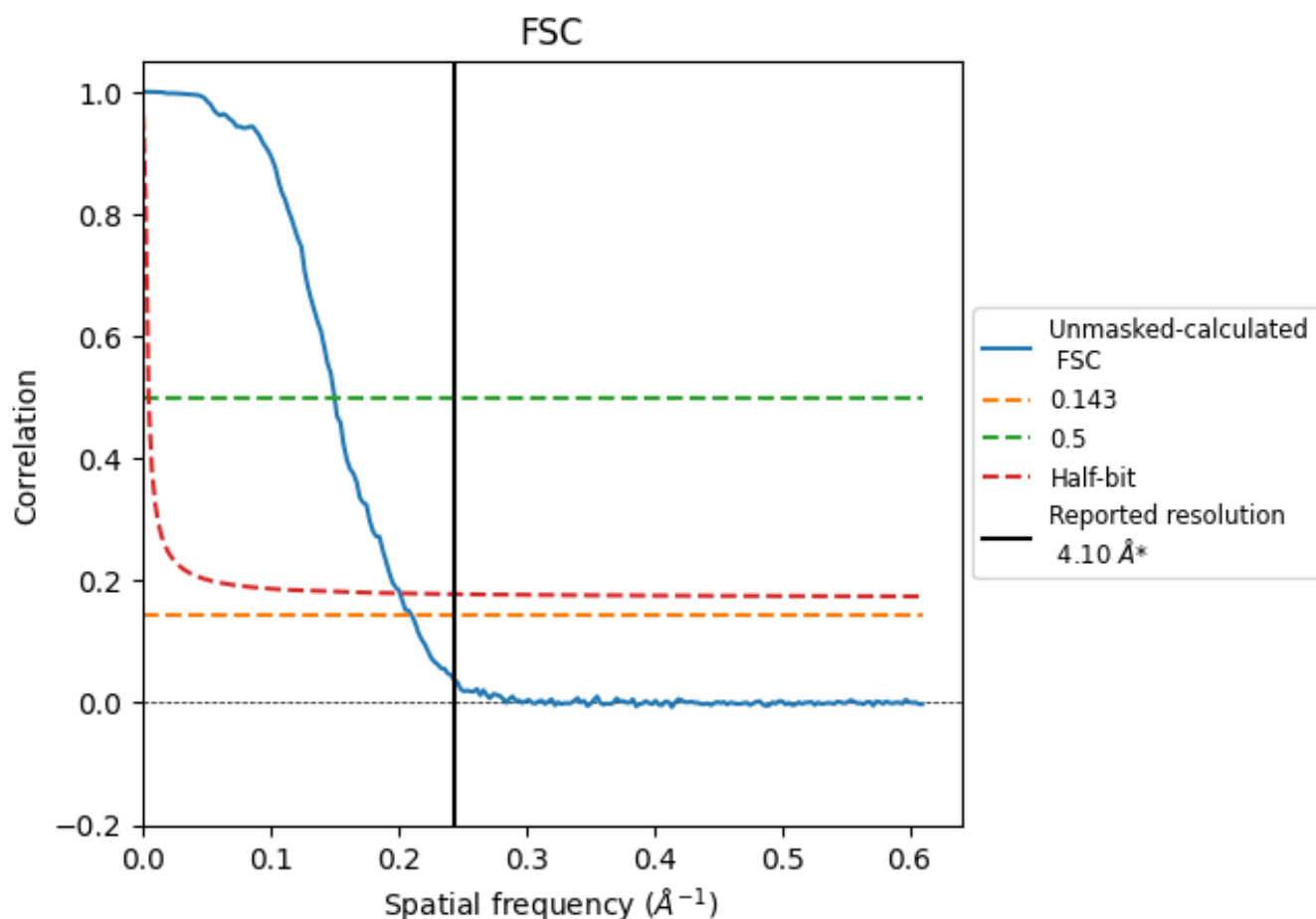


*Reported resolution corresponds to spatial frequency of $0.244 \text{ \AA}^{-1}$

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 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

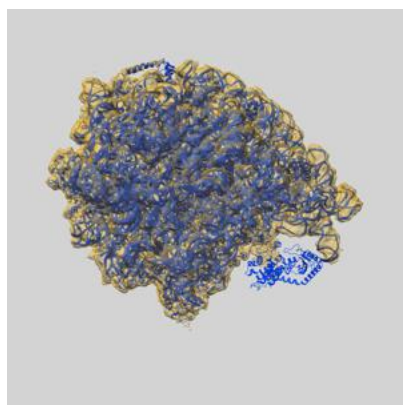
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.75	6.65	4.96

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

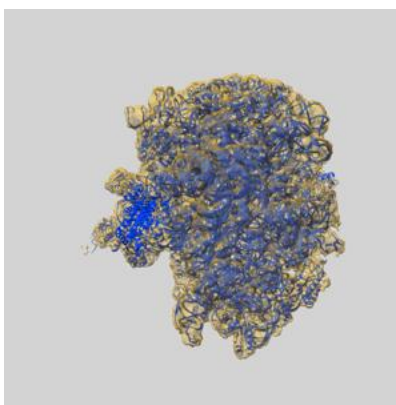
9 Map-model fit [i](#)

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

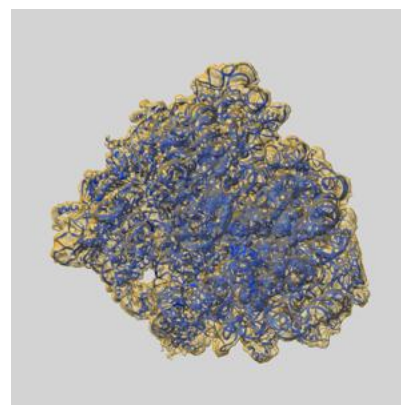
9.1 Map-model overlay [i](#)



X



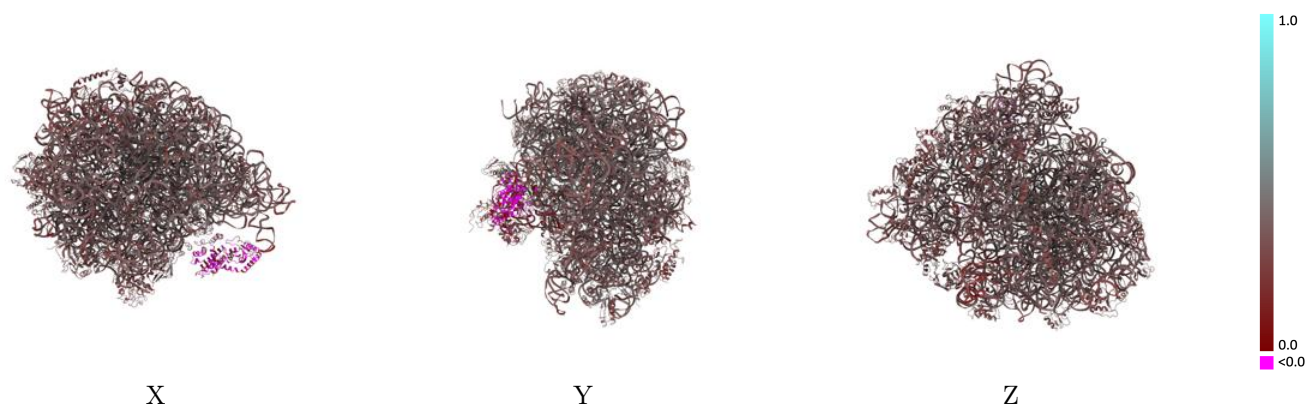
Y



Z

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

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

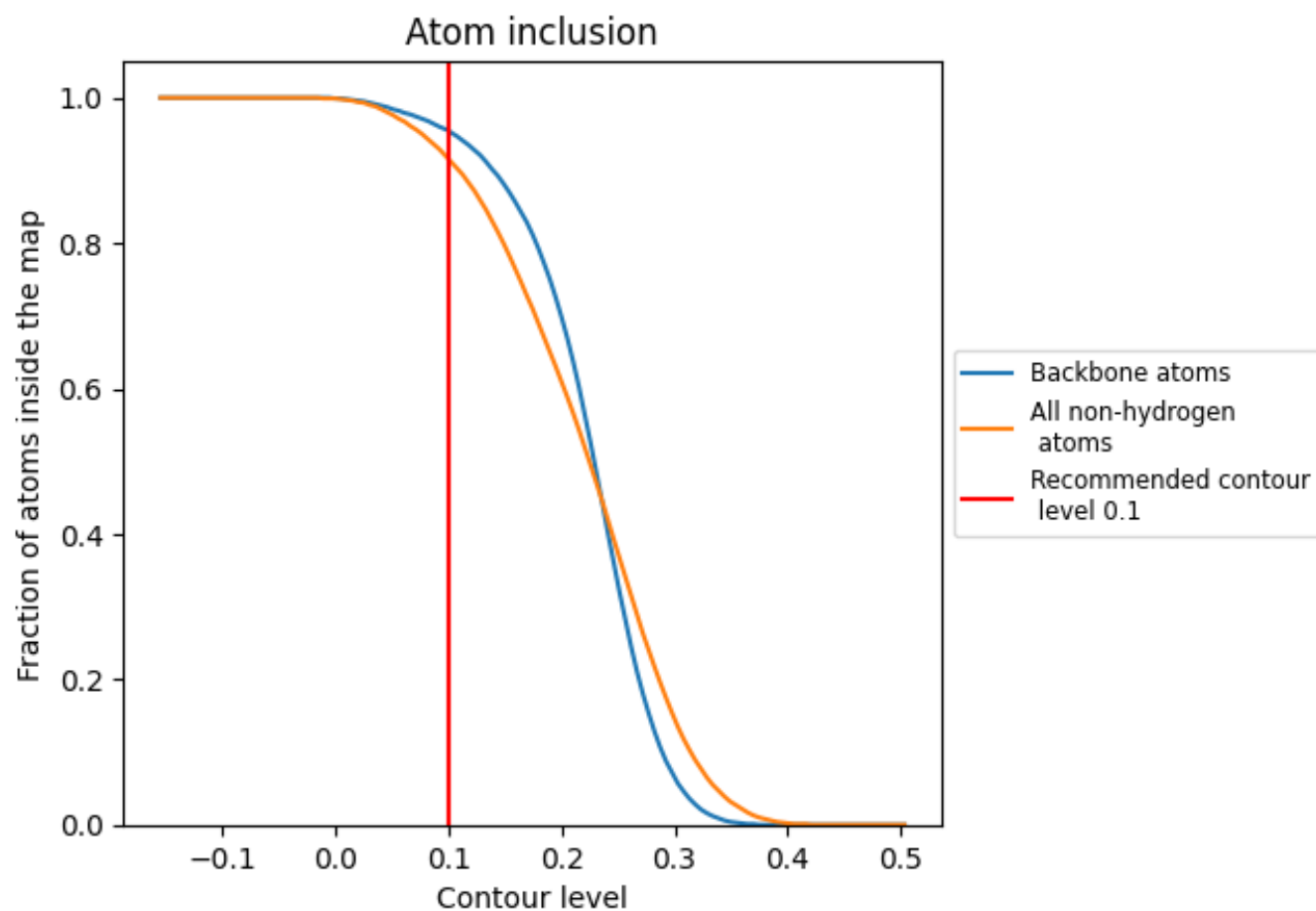


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

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



Continued on next page...

Continued from previous page...

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