



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 02:05 PM EDT

PDB ID : 5KPX
EMDB ID : EMD-8282
Title : Structure of RelA bound to ribosome in presence of A/R tRNA (Structure IV)
Authors : Loveland, A.B.; Bah, E.; Madireddy, R.; Zhang, Y.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2016-07-05
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

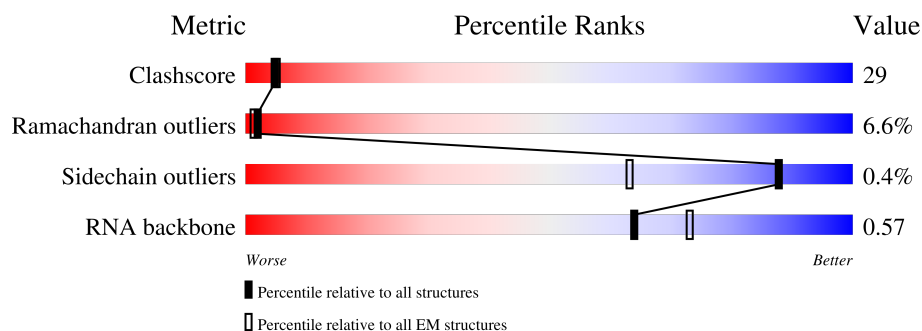
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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






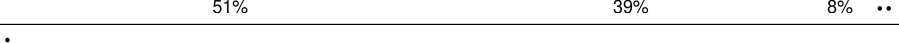
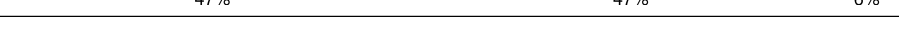
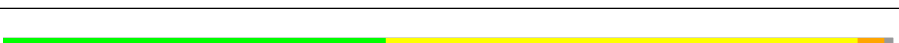
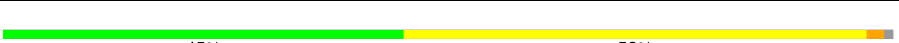



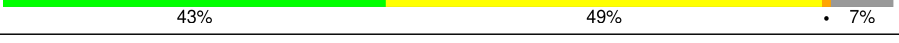
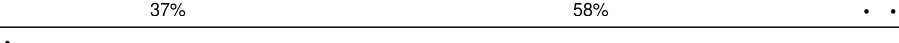
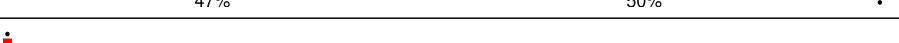

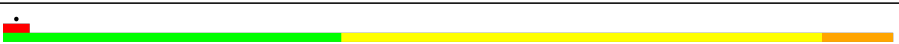


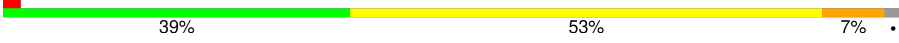


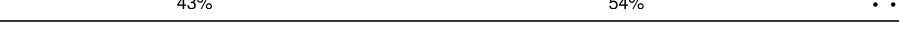
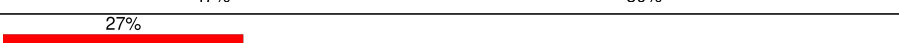



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	273	
2	B	209	
3	C	201	
4	D	179	
5	E	177	
6	F	149	
7	G	165	


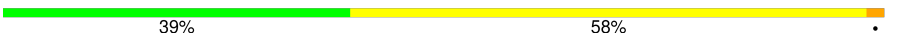

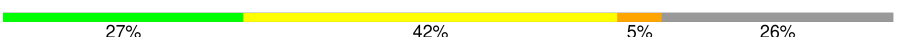


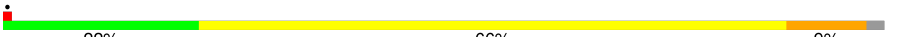
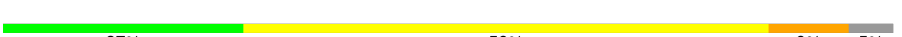
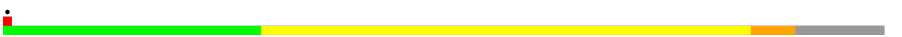

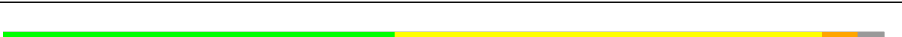
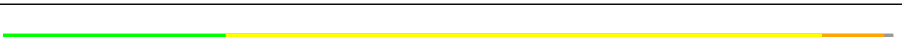

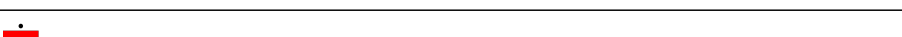
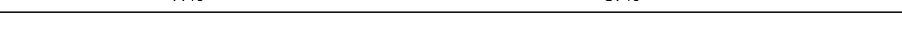
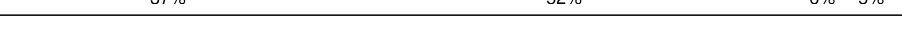
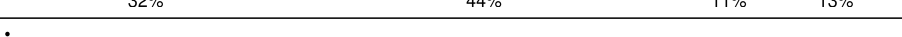


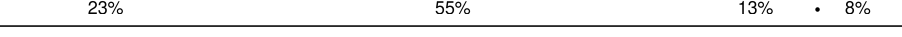


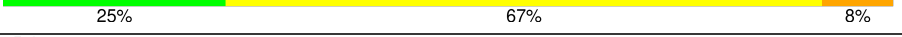

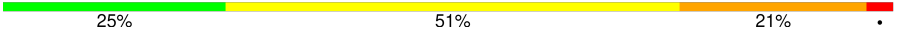
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Mol	Chain	Length	Quality of chain
8	H	142	
9	I	142	
10	J	123	
11	K	144	
12	L	136	
13	M	127	
14	N	117	
15	O	115	
16	P	118	
17	Q	103	
18	R	110	
19	S	100	
20	T	104	
21	U	94	
22	V	85	
23	W	78	
24	X	63	
25	Y	59	
26	Z	70	
27	1	57	
28	2	55	
29	3	46	
30	4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

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

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Mol	Chain	Length	Quality of chain
58	32	77	<div><div></div><div>5%</div><div>17%</div><div>60%</div><div>23%</div></div>
59	33	750	<div><div></div><div>51%</div><div>37%</div><div>46%</div><div>7%</div><div>10%</div></div>

2 Entry composition

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 55 is a RNA chain called mRNA.

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

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

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

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

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

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

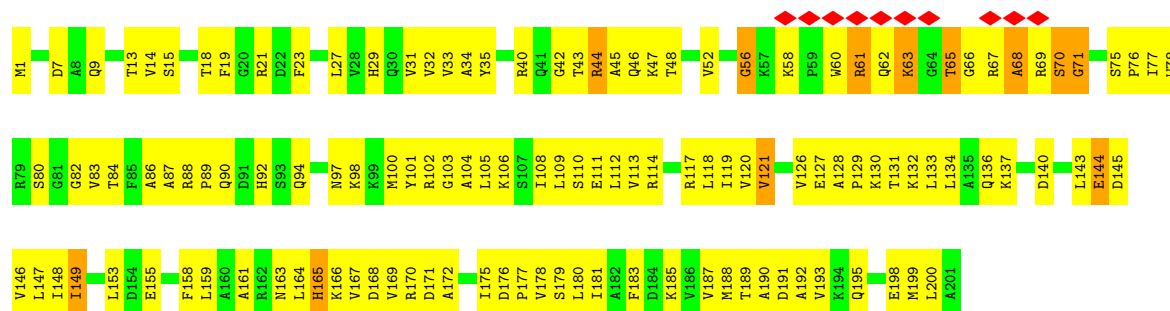
Mol	Chain	Residues	Atoms					AltConf	Trace
58	32	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 59 is a protein called GTP pyrophosphokinase.

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

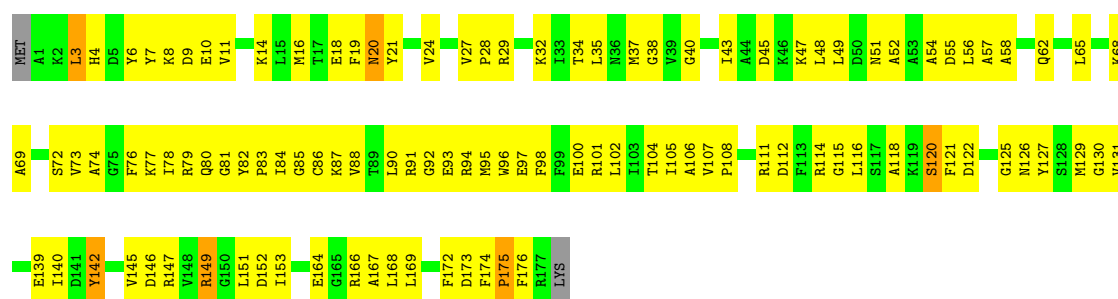
There are 7 discrepancies between the modelled and reference sequences:

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



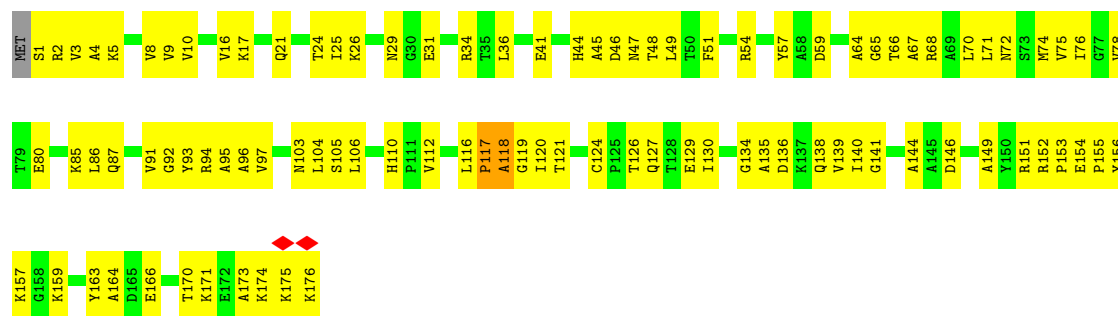
• Molecule 4: 50S ribosomal protein L5

Chain D: 39% 57%



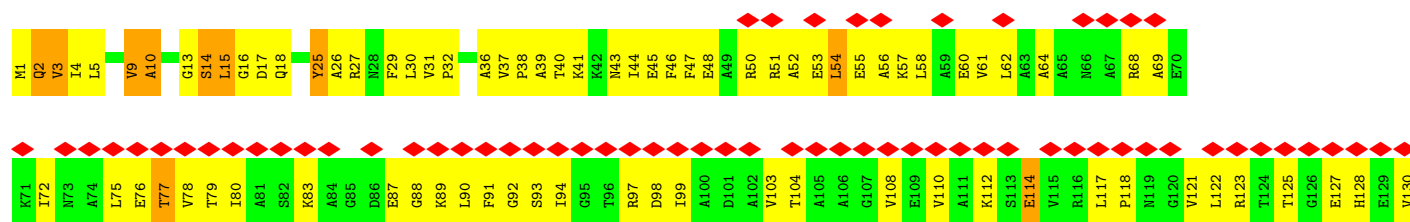
• Molecule 5: 50S ribosomal protein L6

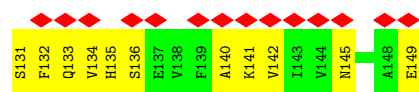
Chain E: 45% 53%



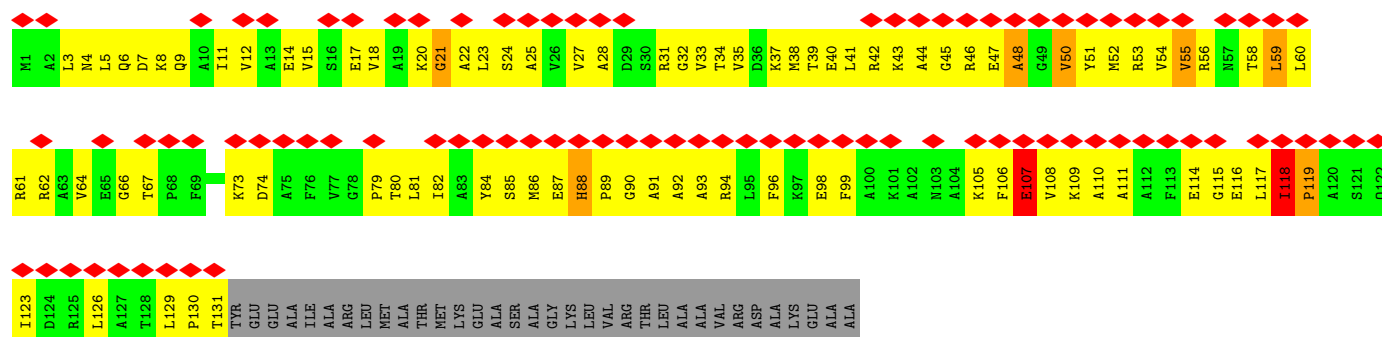
• Molecule 6: 50S ribosomal protein L9

Chain F: 38% 53% 7%

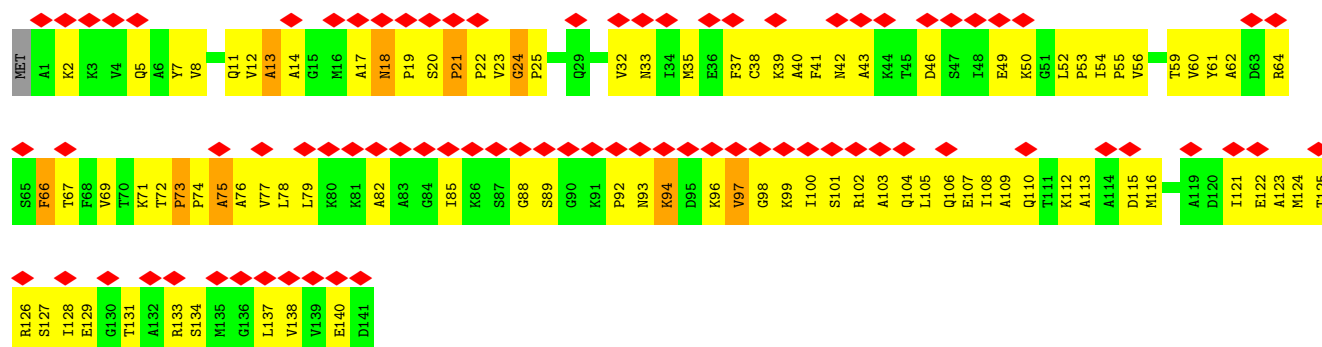




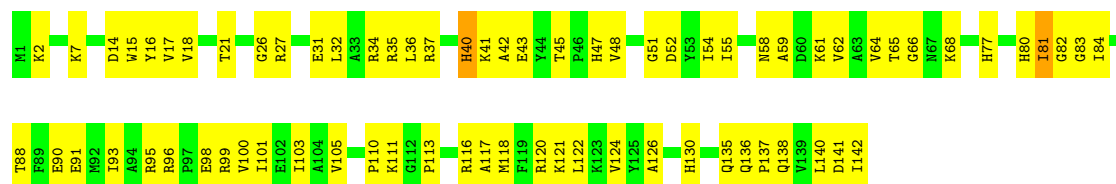
• Molecule 7: 50S ribosomal protein L10



• Molecule 8: 50S ribosomal protein L11



• Molecule 9: 50S ribosomal protein L13



• Molecule 10: 50S ribosomal protein L14





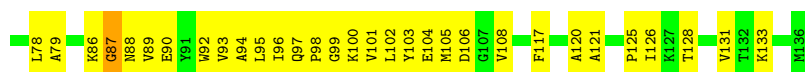
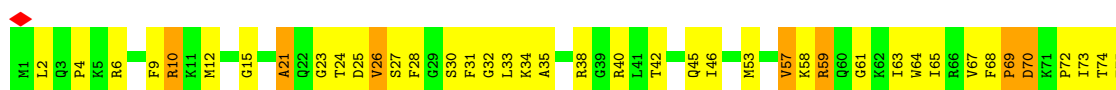
- Molecule 11: 50S ribosomal protein L15

Chain K: 51% 39% 8% ..



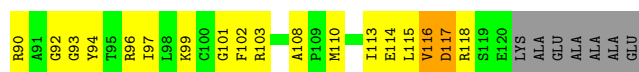
- Molecule 12: 50S ribosomal protein L16

Chain L: 47% 47% 6%



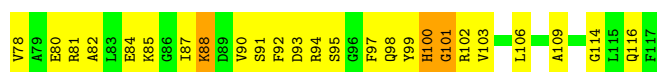
- Molecule 13: 50S ribosomal protein L17

Chain M: 46% 45% 6%



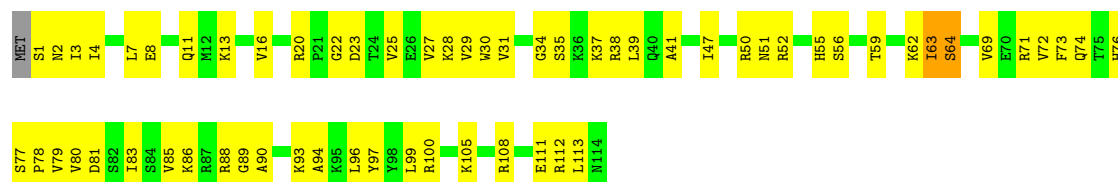
- Molecule 14: 50S ribosomal protein L18

Chain N: 43% 53% 4%

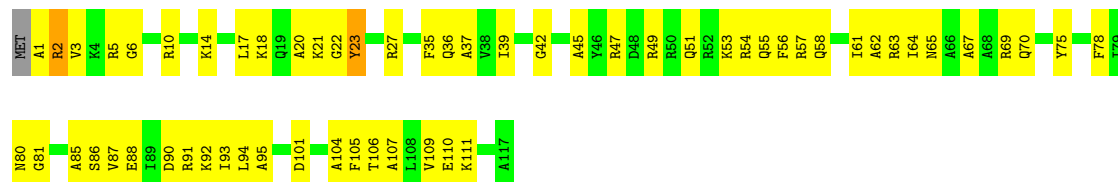


- Molecule 15: 50S ribosomal protein L19

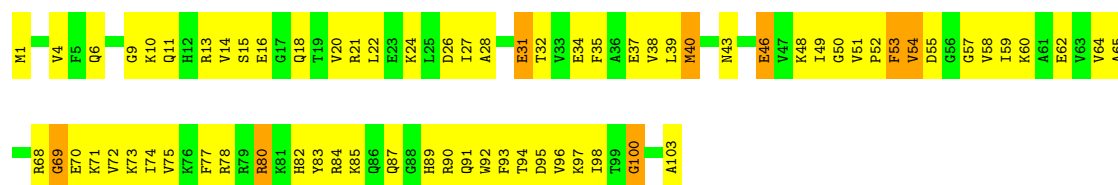
Chain O: 45% 52% 3%



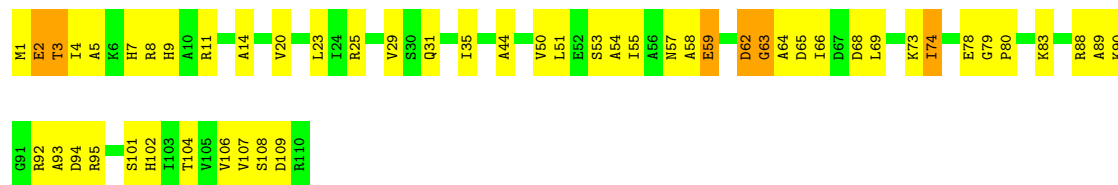
• Molecule 16: 50S ribosomal protein L20



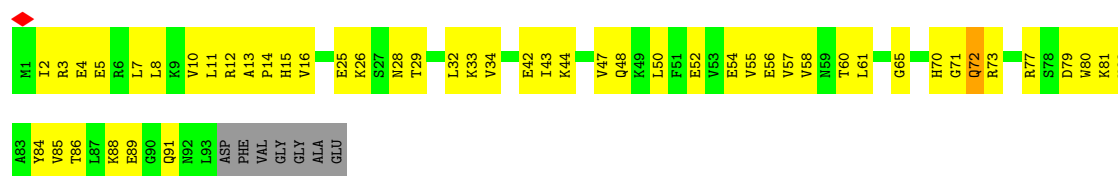
• Molecule 17: 50S ribosomal protein L21



• Molecule 18: 50S ribosomal protein L22

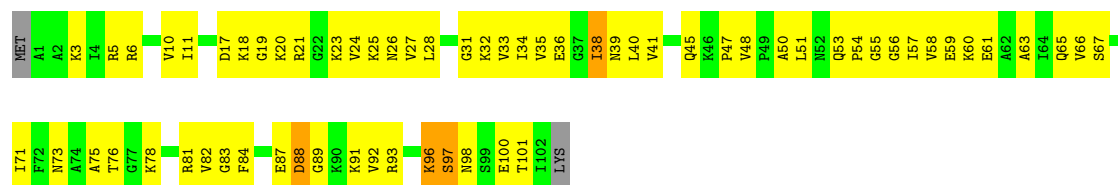


• Molecule 19: 50S ribosomal protein L23



• Molecule 20: 50S ribosomal protein L24

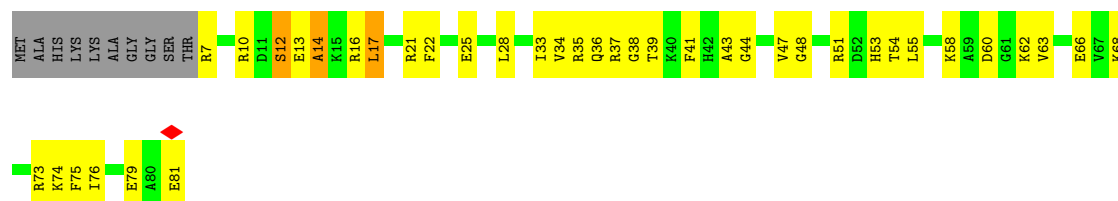




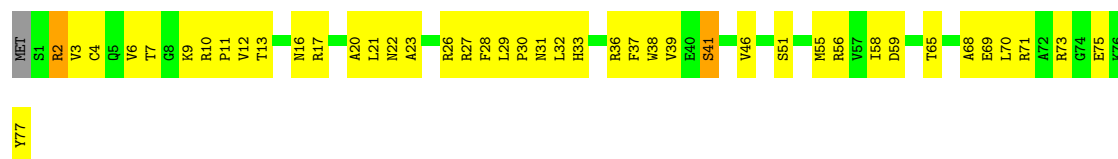
- Molecule 21: 50S ribosomal protein L25



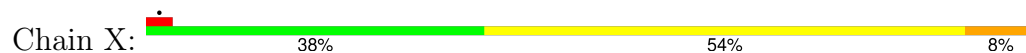
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28

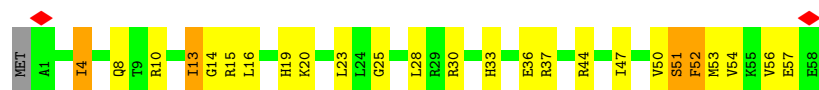


- Molecule 24: 50S ribosomal protein L29

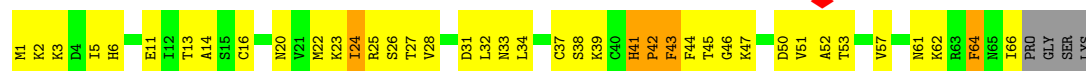
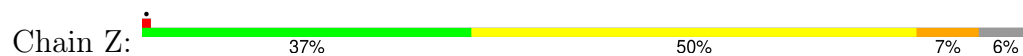


- Molecule 25: 50S ribosomal protein L30

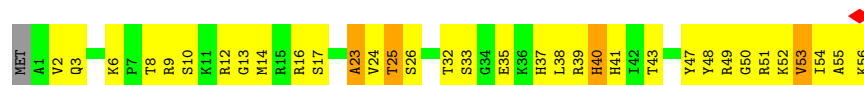




- Molecule 26: 50S ribosomal protein L31



- Molecule 27: 50S ribosomal protein L32



- Molecule 28: 50S ribosomal protein L33



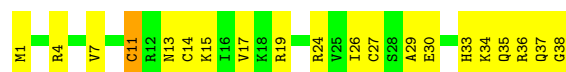
- Molecule 29: 50S ribosomal protein L34



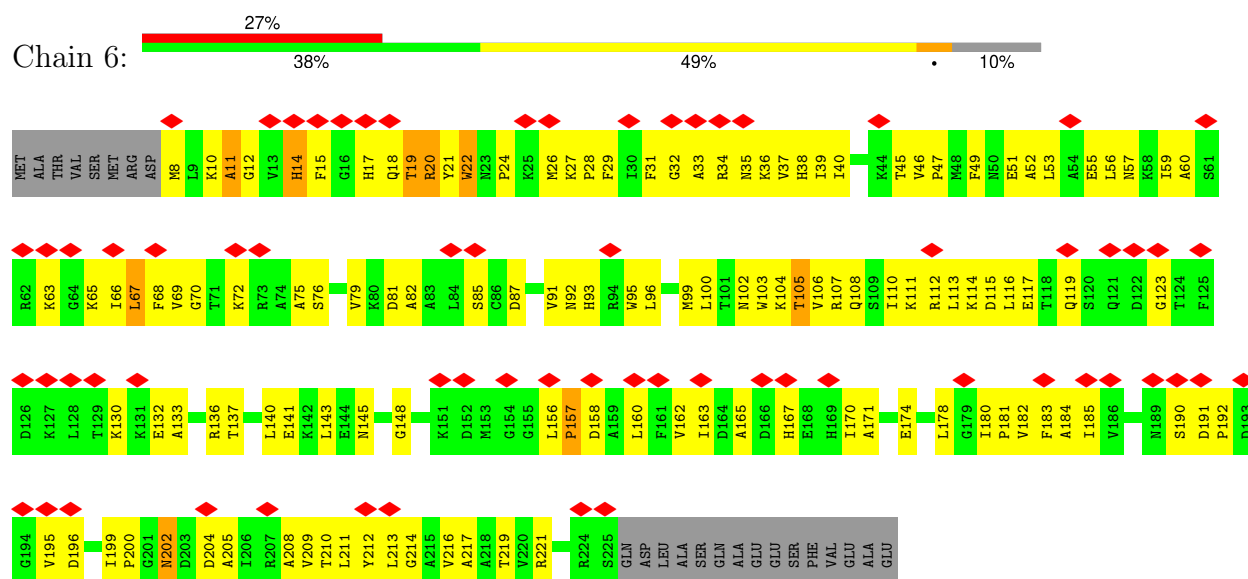
- Molecule 30: 50S ribosomal protein L35



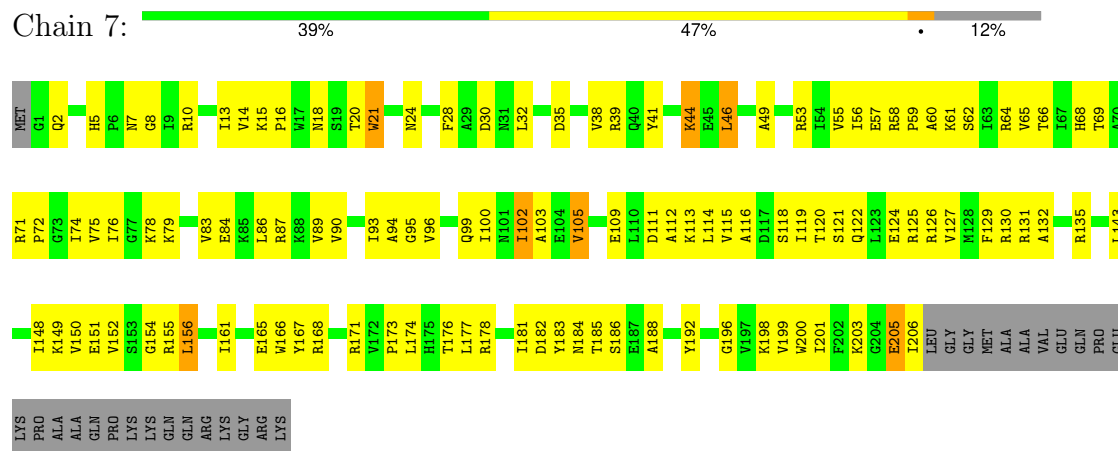
- Molecule 31: 50S ribosomal protein L36



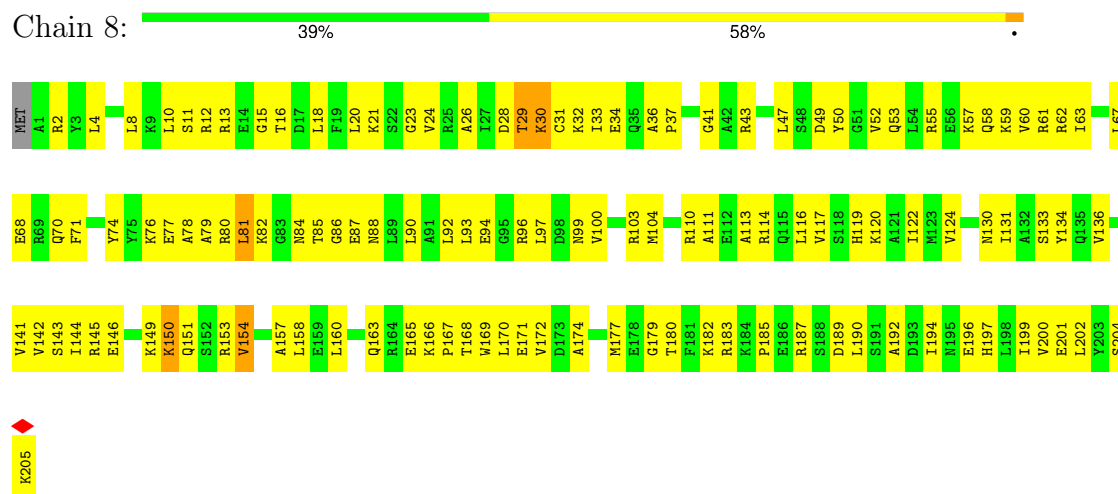
- Molecule 32: 30S ribosomal protein S2



• Molecule 33: 30S ribosomal protein S3

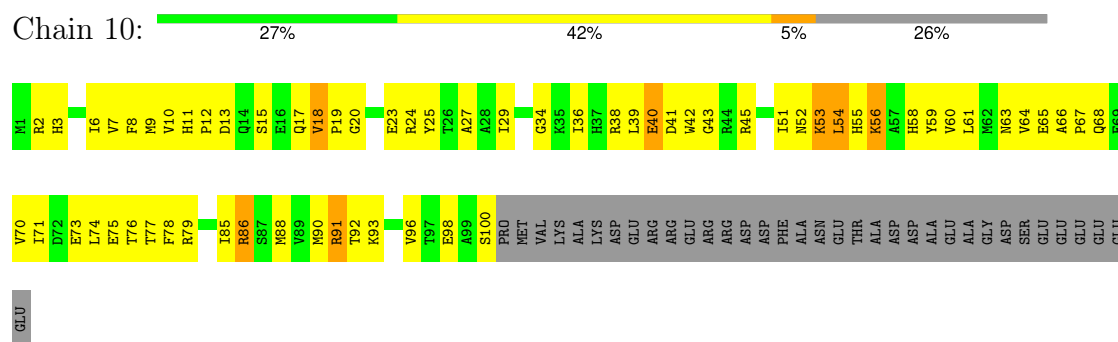


• Molecule 34: 30S ribosomal protein S4

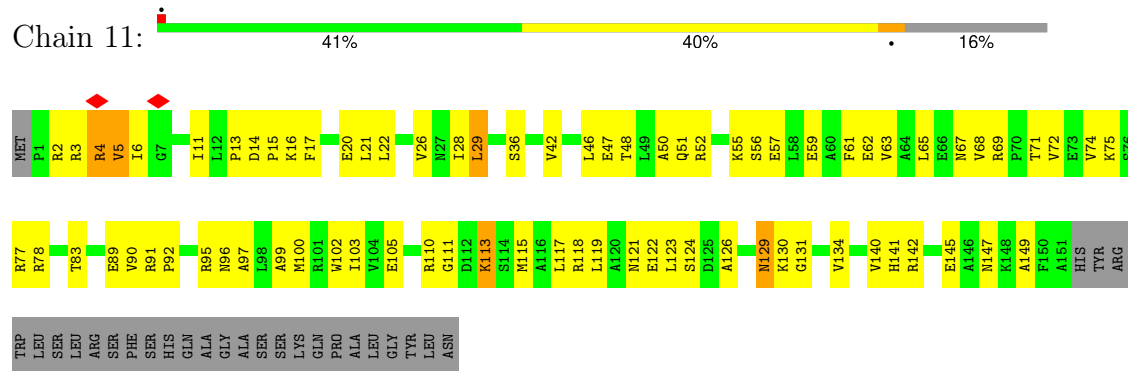


• Molecule 35: 30S ribosomal protein S5

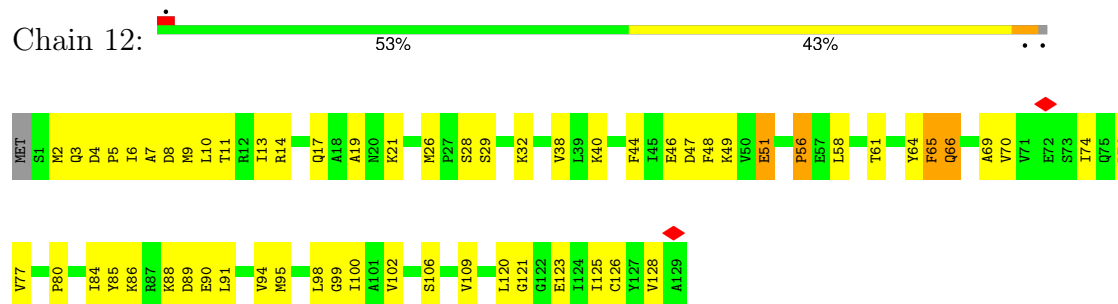
- Molecule 36: 30S ribosomal protein S6



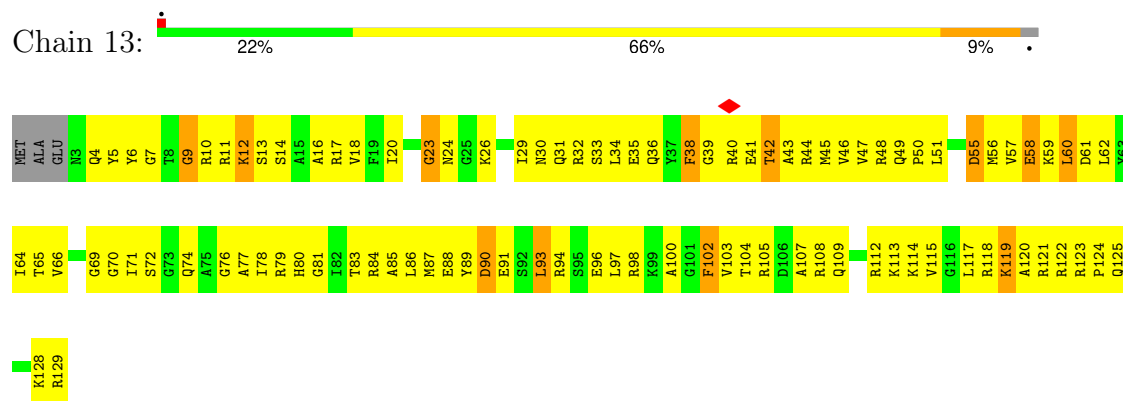
- Molecule 37: 30S ribosomal protein S7



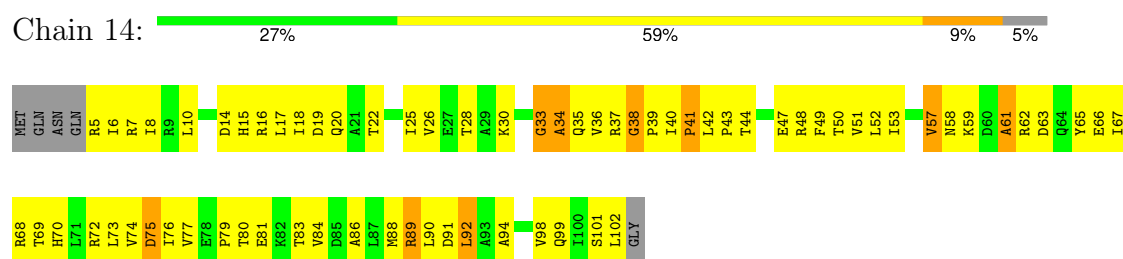
- Molecule 38: 30S ribosomal protein S8



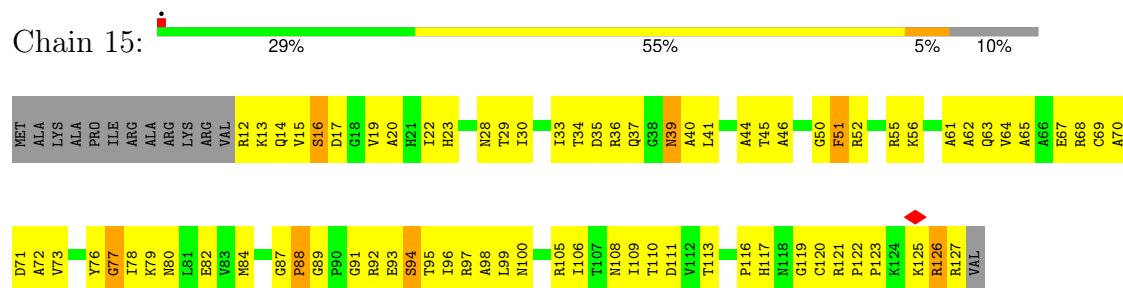
- Molecule 39: 30S ribosomal protein S9



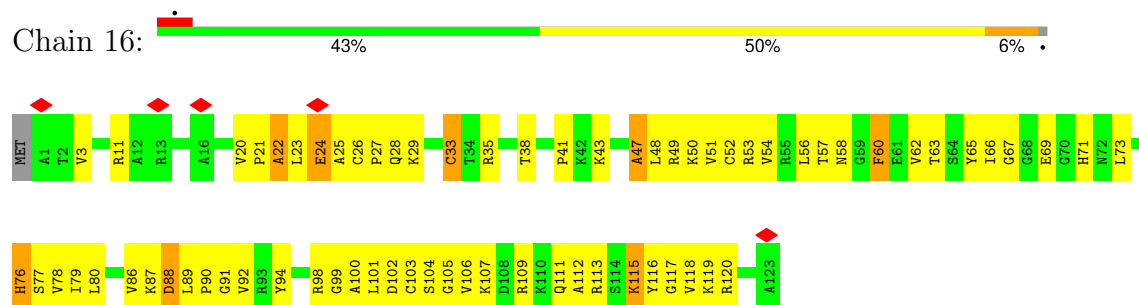
• Molecule 40: 30S ribosomal protein S10



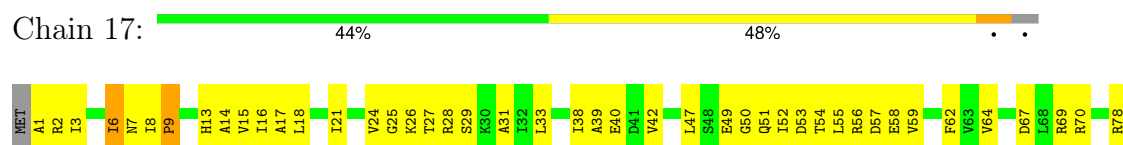
• Molecule 41: 30S ribosomal protein S11



• Molecule 42: 30S ribosomal protein S12



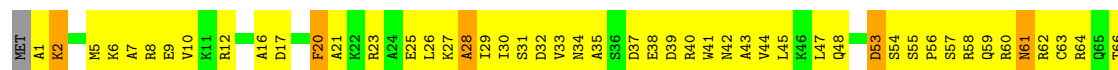
• Molecule 43: 30S ribosomal protein S13





• Molecule 44: 30S ribosomal protein S14

Chain 18: 25% 67% 7%



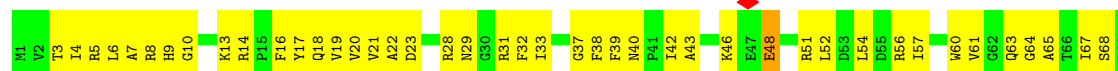
• Molecule 45: 30S ribosomal protein S15

Chain 19: 56% 42%



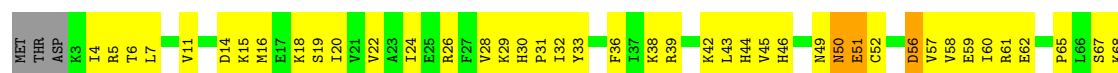
• Molecule 46: 30S ribosomal protein S16

Chain 20: 41% 57%



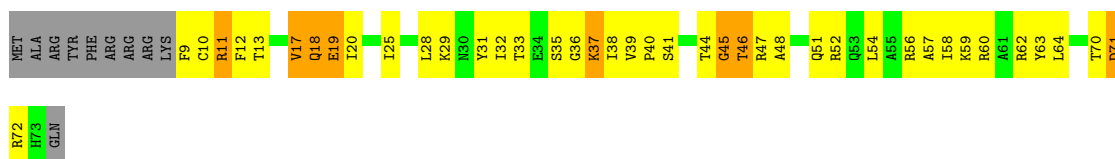
• Molecule 47: 30S ribosomal protein S17

Chain 21: 37% 52% 6% 5%

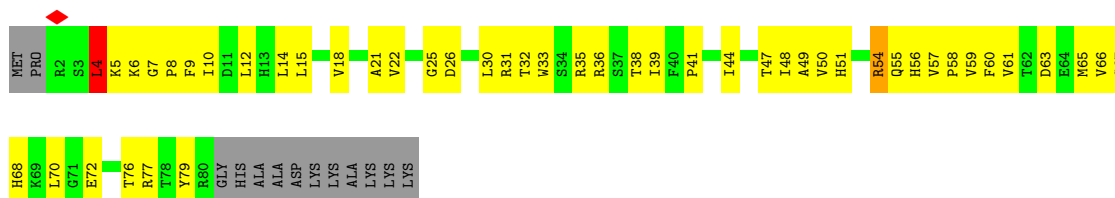


• Molecule 48: 30S ribosomal protein S18

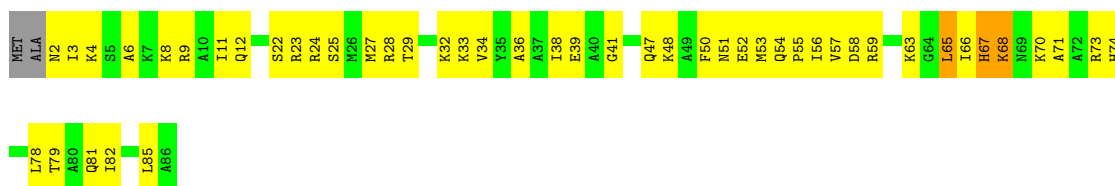
Chain 22: 32% 44% 11% 13%



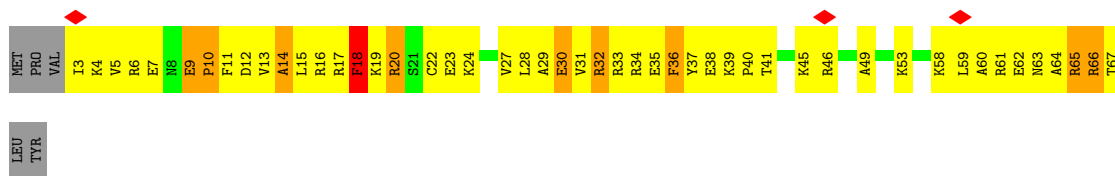
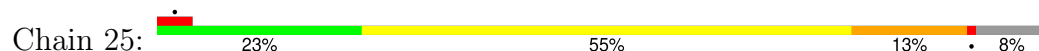
- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



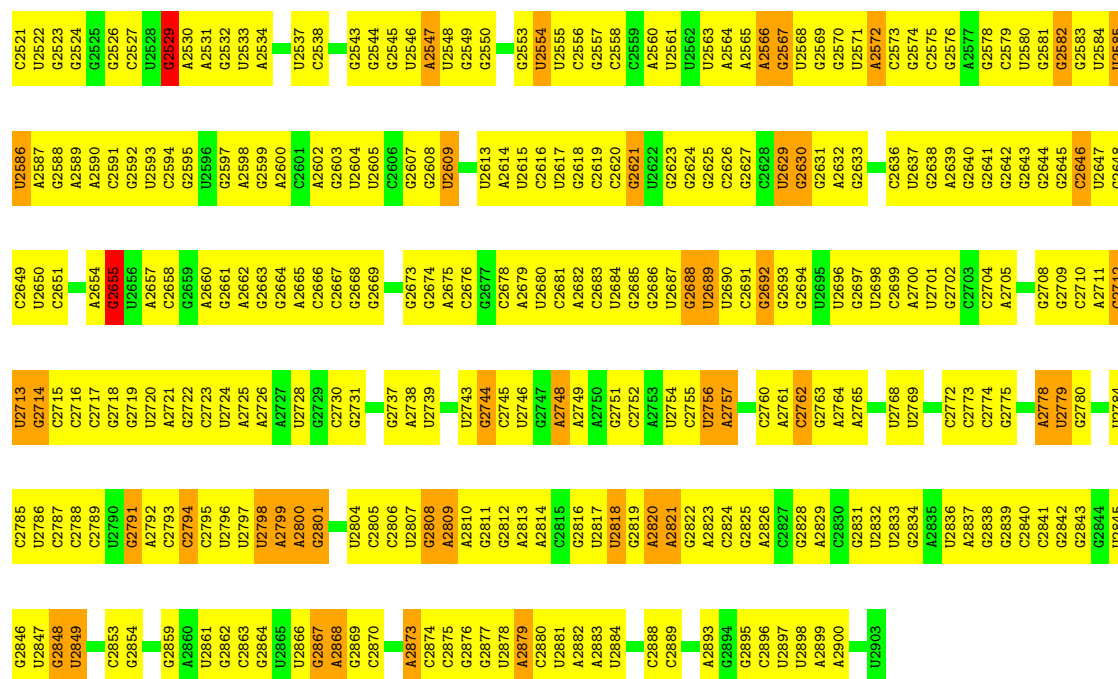
- Molecule 52: 16S ribosomal RNA



G1139	G1074	A1005	A937	U875	C811	C744	A596	A532	C403	C339	C271	C207
C1140	U1075	G1006	G942	C876	G812	G745	G597	A533	G404	U340		U208
G1141	U1076	U1007	C942	G877		G746	U598	U534	U405	C341	C277	G209
G1142	U1077	U1008	U943	C878	A815	A747	C599	U535	G406	C342	G278	C210
G1143	U1078	U1009	C879	A879	A816	G748	A600	C536	U407	U343	A279	G211
G1144	U1079	U1010	G945	C880	C817	A749	G601	G537	A408	A344	C280	G212
A1145	A1080	C1011	A946	C881	G818	C750	A602	G538	U409	C345	G281	G213
A1146	A1081		G947	C882	A819	C751	A603	U476	U410	G346		C214
C1147	G1084	A1014	C948	U883	U820	A752	G604	C477	A411	A349	C284	U216
U1085	U1085	G1015	A949	U884	G821	A753	U605	A478	A412	G350	C285	U217
			U950	G885		C754	G606	U479	G413	G351	C286	C217
			G951	G886	G824	C755	A607	U543	A414	G352	U287	U218
			U952		A825	C756	A608	G544		A288		U219
			G953	A889	C826	C757	A609	A481	C418	G349		G220
			G954	G890	C826	C757		A482	C419	A353	G289	G221
			C954	G890	U827	C758		A483	U420	G354	C290	C221
			U955	U891	U828	A759		G484	U420	C355	U291	C222
			U956	A892	G829		G614	U485	U421	A356		A223
			U957	C893	G830	U762	G615	C549	C422	G357		U224
			A958	G894	A831	C763	G616	G550	G423	U358		C225
			U959	C895	G832	C764	G617	U551	G424	G359		G326
			U960	G896	G833	C765	C618	C489	G425	G360		G227
			U961	C897	U834	A766		C490	U426	G361		A228
			C962	G898	U835	A767	A621	A554	U427	G362		U229
			G963	C899	G836	A768	A622	C492	G428	A363		G230
			A964	A900	U837	C769	C623	A493	U429	A364		U231
			U965	G901	G838	C770	G624	G494	A430			G232
			C966	A902	C839	A705	U625	A495	A431	U367		C233
			U968	G903	C840	C772	G626	A558	A432	A306		C234
			A968	U904	C841	G773	G627	A560	A432	C307		C235
			U969	U905	U842	G774	G628	U561	U434	C308		A236
			C970	A906	U843	C775	A629	C562	A435	A371		G237
			G971	U907	G844	C776	G710	A563	G310	G372		A238
			C972	A908	A845	A777	A630	C501	U437	A373		U239
			G973	C903	G846	C778	G631	C502	C311	C312		G240
			A974	U910	G847	C779	G633	C503	U438	A313		
			U975	U911	C848	A780	C634	G567	U439	U375		
			C976	C912	G849	A781	A635	C568	C440	C376		
			A977	A913	U850	A782	U636	C569	A441	A315		
			U978	A914	C851	C783		A510	G442	C316		A246
			C979	A915	G852	A784	C643	C511	C443	C317		G247
			U980	U916	C853	C785	G722	U512	G318	U317		C248
			C981	C917	U854	C786	U723	C513	A320	U317		C249
			U982	A918	C856	A787	G724	C514	A321	G380		A250
			A919	U920	C857	C788	G645	G575	A321	G381		G251
			C984	C984	G858	A792	G656	U516	A322	A322		U252
				U921	G859	C793	G725	G577	G324	A323		G253
				G922		A794	G727	C578	G450	U323		G255
				A923		C795	A728	C518	A451	G324		U256
				G924				C519	A452	A325		G257
				C924				A520	G453	U389		G258
				G925				G581	C453	G391		G259
				C926						A327		G260
				G927					U458	C392		G261
				C928					A459	A393		U261
				G929					A460	A329		A262
				C930					A461	C394		A263
				G931					G324	C395		G264
				C932					G462	C396		G265
				G933					U463	U397		G266
				C934					G527	A398		C267
				G935					A465	G399		U268
				C936					U591	C400		G269
				G937					U467	C401		A270
				C938					G530	G397		G271
				G939					U531	C402		G272
				C940					A468	A398		G273
				G941					G532	C403		G274
				C942					A469	A399		G275
				G943					G533	C404		G276
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				C946					A471	A399		G279
				G947					G535	C406		G280
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				G961					G542	C413		G294
				C962					A479	A399		G295
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				C964					A480	A399		G297
				G965					G544	C415		G298
				C966					A481	A399		G299
				G967					G545	C416		G300
				C968					A482	A399		G301
				G969					G546	C417		G302
				C970					A483	A399		G303
				G971					G547	C418		G304
				C972					A484	A399		G305
				G973					G548	C419		G306
				A974					A485	A399		G307
				U975					G549	C420		G308
				C976					A486	A399		G309
				G977					G550	C421		G310
				C978					A487	A399		G311
				G979					G551	C422		G312
				C980					A488	A399		G313
				U981					G552	C423		G314
				C982					A489	A399		G315
				G983					G553	C424		G316
				C984					A490	A399		G317
				U985					G554	C425		G318
				C986					A491	A399		G319
				G987					G555	C426		G320
				C988					A492	A399		G321
				U989					G556	C427		G322
				C990					A493	A399		G323
				G991					G557	C428		G324
				C992					A494	A399		G325
				U993					G558	C429		G326
				C994					A495	A399		G327
				G995					G559	C430		G328
				C996					A496	A399		G329
				U997					G560	C431		G330
				C998					A497	A399		G331
				G999					G561	C432		G332
				C1000					A498	A399		G333
				U999					G562	C433		G334
				C1001					A499	A399		G335
				G1002					G563	C434		G336
				C1003					A500	A399		G337
				U999					G564	C435		G338
				C1004					A501	A399		G339
				G1005					G565	C436		G340
				C1006					A502	A399		G341
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				G1008					G567	C438		G344
				C1009					A504	A399		G345
				U999					G568	C439		G346
				C1010					A505	A399		G347
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				C1012					A506	A399		G349
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				G1017					G573	C444		G356
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				C1019					A511	A399		G359
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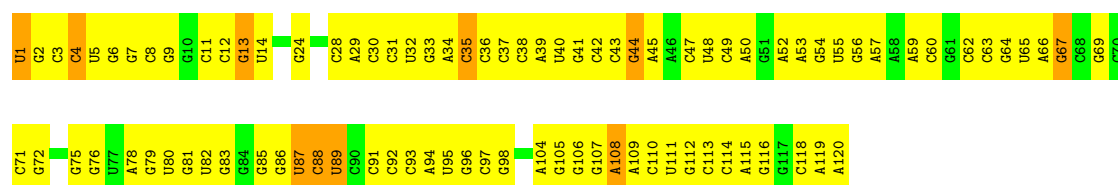
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U2511	G2373	G2234	G2234	G2168	C2104	C2104	A2033	U1963	C1893	C1822	C1761	C1686	C1615
C2512	C2374			A2169	U2105	U2105	U2034	G1964	G1894	G1823	A1762	G1687	A1616
A2513		G2237	G2237	A2170	U2106	U2106	G2036	C1967	G1896	G1824	U1763	U1688	C1617
U2514	A2381	G2238	G2238	A2171	G2107	G2107	C2037	G1968	G1896	U1825	C1764	A1689	A1618
C2515	U2312	G2239	G2239	U2172	A2108	A2108	U2038	A1969	A1900	G1826	U1765	A1690	G1619
A2516	C2313	U2340	U2340	A2173	A2109	A2109	G2039	A1970	A1901	U1827	G1766	C1691	G1620
C2517	U2384	A2241	A2241	C2174	U2109	U2109	G2040	U1971	C1902	G1828	U1692	U1692	U1621
A2518	C2385	G2242	G2242	C2175	G2110	G2110	U2041	G1972	G1903	A1829	U1769	U1693	G1622
U2519	A2317	U2243	U2243	A2176	U2111	U2111	A2042	G1973	G1904	C1830	C1770	G1694	G1623
C2520	U2387	U2244	U2244	C2177	G2112	G2112	C2043	C1974	C1905	G1831	A1772	G1695	U1629



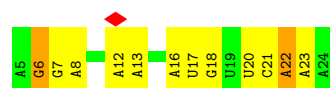
• Molecule 54: 5S ribosomal RNA

Chain 28: 25% 67% 8%



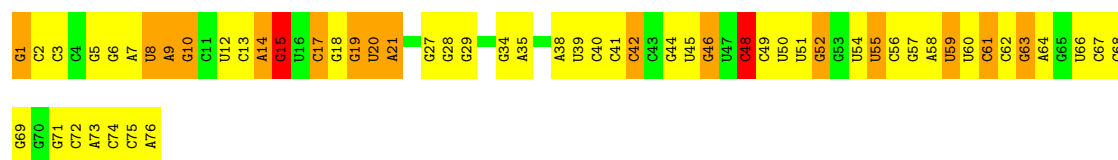
• Molecule 55: mRNA

Chain 29: 5% 40% 50% 10%



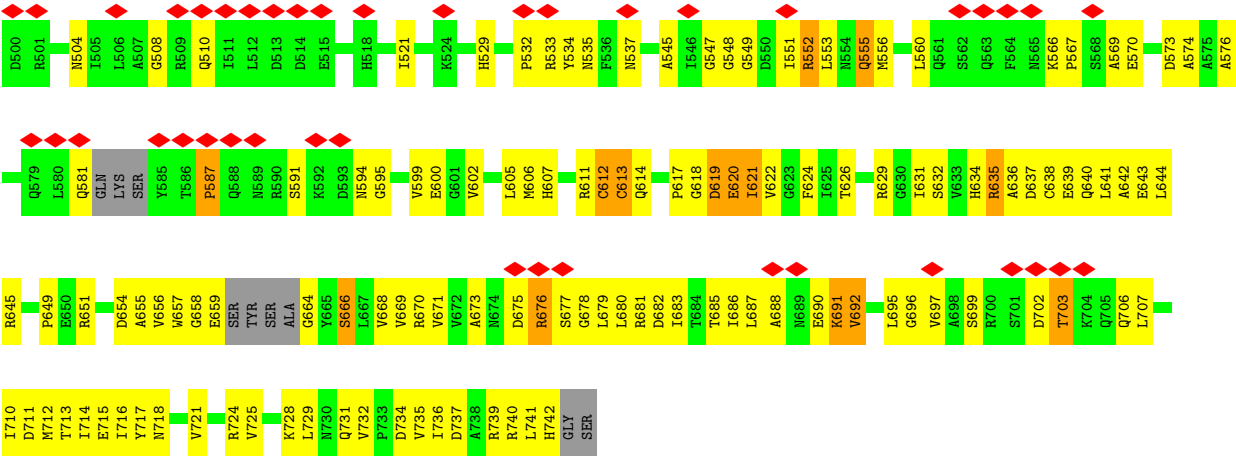
• Molecule 56: A-site tRNA^{Phe}

Chain 30: 25% 51% 21%



• Molecule 57: P-site tRNA^{fMet}

Chain 31: 35% 60% 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57430	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	0.490	Depositor
Minimum map value	-0.157	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.34	0/2121	0.70	0/2852
2	B	0.37	0/1586	0.67	0/2134
3	C	0.39	0/1571	0.71	1/2113 (0.0%)
4	D	0.36	0/1434	0.66	0/1926
5	E	0.35	0/1343	0.69	0/1816
6	F	0.44	0/1122	0.64	0/1515
7	G	0.50	0/1001	0.79	2/1350 (0.1%)
8	H	0.49	0/1046	0.69	1/1410 (0.1%)
9	I	0.33	0/1152	0.63	0/1551
10	J	0.35	0/947	0.68	0/1268
11	K	0.36	0/1054	0.71	1/1403 (0.1%)
12	L	0.35	0/1093	0.64	0/1460
13	M	0.33	0/973	0.64	0/1301
14	N	0.32	0/902	0.63	0/1209
15	O	0.34	0/929	0.73	1/1242 (0.1%)
16	P	0.37	0/960	0.57	0/1278
17	Q	0.39	0/829	0.77	1/1107 (0.1%)
18	R	0.33	0/864	0.68	0/1156
19	S	0.34	0/744	0.66	0/994
20	T	0.35	0/787	0.76	1/1051 (0.1%)
21	U	0.36	0/766	0.63	0/1025
22	V	0.37	0/582	0.62	0/769
23	W	0.37	0/635	0.70	0/848
24	X	0.36	0/510	0.62	0/677
25	Y	0.34	0/453	0.62	0/605
26	Z	0.42	0/531	0.71	1/709 (0.1%)
27	1	0.35	0/450	0.72	0/599
28	2	0.37	0/416	0.60	0/554
29	3	0.41	0/380	0.64	0/498
30	4	0.35	0/513	0.70	0/676
31	5	0.33	0/303	0.68	0/397
32	6	0.42	0/1735	0.68	1/2338 (0.0%)
33	7	0.35	0/1651	0.63	1/2225 (0.0%)
34	8	0.36	0/1665	0.64	0/2227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	9	0.35	0/1169	0.69	0/1573
36	10	0.38	0/835	0.69	0/1128
37	11	0.34	0/1195	0.65	0/1602
38	12	0.34	0/989	0.68	0/1326
39	13	0.36	0/1034	0.72	0/1375
40	14	0.38	0/796	0.72	1/1077 (0.1%)
41	15	0.36	0/885	0.75	0/1195
42	16	0.36	0/969	0.76	3/1300 (0.2%)
43	17	0.32	0/892	0.62	0/1193
44	18	0.33	0/817	0.58	0/1088
45	19	0.33	0/722	0.60	0/964
46	20	0.39	0/659	0.67	0/884
47	21	0.36	0/657	0.71	0/881
48	22	0.38	0/544	0.73	0/731
49	23	0.37	0/652	0.70	1/877 (0.1%)
50	24	0.32	0/671	0.56	0/888
51	25	0.42	0/550	0.73	1/728 (0.1%)
52	26	0.55	1/36967 (0.0%)	0.71	3/57666 (0.0%)
53	27	0.60	1/69801 (0.0%)	0.72	10/108894 (0.0%)
54	28	0.45	1/2876 (0.0%)	0.69	1/4483 (0.0%)
55	29	0.63	0/486	0.67	0/757
56	30	0.67	1/1813 (0.1%)	0.78	1/2823 (0.0%)
57	31	0.49	1/1836 (0.1%)	0.69	1/2859 (0.0%)
58	32	0.87	1/1835 (0.1%)	0.78	0/2857
59	33	0.67	6/4985 (0.1%)	1.09	37/6770 (0.5%)
All	All	0.54	12/167683 (0.0%)	0.72	70/250202 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
52	26	0	16
53	27	0	37
56	30	0	2
58	32	0	1
59	33	0	2
All	All	0	58

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	33	156	ARG	CZ-NH2	-10.57	1.19	1.33
59	33	152	LYS	CD-CE	-7.77	1.31	1.51
59	33	17	PRO	CA-CB	-7.25	1.39	1.53
57	31	1	C	OP3-P	-6.97	1.52	1.61
56	30	1	G	OP3-P	-6.93	1.52	1.61

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	33	156	ARG	NE-CZ-NH1	19.92	130.26	120.30
59	33	156	ARG	NH1-CZ-NH2	-13.88	104.13	119.40
59	33	17	PRO	N-CA-CB	-11.14	89.93	103.30
59	33	17	PRO	CA-CB-CG	10.28	124.33	104.80
59	33	63	VAL	CG1-CB-CG2	-9.24	96.12	110.90

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	26	117	G	Sidechain
52	26	159	G	Sidechain
52	26	239	U	Sidechain
52	26	266	G	Sidechain
52	26	438	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	166	0
2	B	1565	0	1616	126	0
3	C	1552	0	1619	123	0
4	D	1410	0	1447	111	0
5	E	1323	0	1374	81	0
6	F	1111	0	1148	85	0
7	G	988	0	1025	114	0
8	H	1032	0	1088	101	0
9	I	1129	0	1162	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	938	0	1012	59	0
11	K	1045	0	1117	85	0
12	L	1074	0	1157	67	0
13	M	960	0	1000	65	0
14	N	892	0	923	68	0
15	O	917	0	965	75	0
16	P	947	0	1022	82	0
17	Q	816	0	839	86	0
18	R	857	0	922	47	0
19	S	738	0	807	48	0
20	T	779	0	834	50	0
21	U	753	0	780	49	0
22	V	575	0	592	35	0
23	W	625	0	655	39	0
24	X	509	0	543	33	0
25	Y	449	0	491	18	0
26	Z	522	0	521	46	0
27	1	444	0	461	39	0
28	2	409	0	440	25	0
29	3	377	0	418	35	0
30	4	504	0	574	41	0
31	5	302	0	343	33	0
32	6	1704	0	1732	105	0
33	7	1624	0	1699	111	0
34	8	1643	0	1710	145	0
35	9	1156	0	1199	122	0
36	10	817	0	808	74	0
37	11	1181	0	1240	74	0
38	12	979	0	1034	70	0
39	13	1022	0	1070	109	0
40	14	786	0	828	82	0
41	15	869	0	878	90	0
42	16	955	0	1019	97	0
43	17	883	0	944	77	0
44	18	805	0	847	104	0
45	19	714	0	737	31	0
46	20	649	0	666	70	0
47	21	648	0	691	64	0
48	22	535	0	552	51	0
49	23	637	0	665	55	0
50	24	665	0	714	60	0
51	25	544	0	579	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	26	33016	0	16617	1357	0
53	27	62322	0	31345	2394	0
54	28	2572	0	1302	112	0
55	29	432	0	218	15	0
56	30	1623	0	821	58	0
57	31	1644	0	836	33	0
58	32	1643	0	836	78	0
59	33	4911	0	4550	627	0
All	All	154603	0	105189	7602	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 29.

The worst 5 of 7602 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)
59:33:188:ARG:NH1	59:33:377:LEU:HA	1.23	1.40
59:33:24:LEU:HD21	59:33:70:SER:HA	1.19	1.16
59:33:17:PRO:HB3	59:33:39:TRP:NE1	1.58	1.15
34:8:84:ASN:HD22	34:8:87:GLU:HG3	0.98	1.15
59:33:188:ARG:NH1	59:33:377:LEU:CA	2.09	1.14

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%)	34 (13%)	17 (6%)	1	16
2	B	207/209 (99%)	175 (84%)	25 (12%)	7 (3%)	3	25
3	C	199/201 (99%)	157 (79%)	23 (12%)	19 (10%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	175/179 (98%)	143 (82%)	23 (13%)	9 (5%)	1	18
5	E	174/177 (98%)	148 (85%)	19 (11%)	7 (4%)	2	22
6	F	147/149 (99%)	116 (79%)	20 (14%)	11 (8%)	1	13
7	G	129/165 (78%)	91 (70%)	27 (21%)	11 (8%)	0	10
8	H	139/142 (98%)	107 (77%)	21 (15%)	11 (8%)	1	12
9	I	140/142 (99%)	120 (86%)	16 (11%)	4 (3%)	3	27
10	J	120/123 (98%)	94 (78%)	19 (16%)	7 (6%)	1	16
11	K	141/144 (98%)	108 (77%)	18 (13%)	15 (11%)	0	6
12	L	134/136 (98%)	104 (78%)	17 (13%)	13 (10%)	0	8
13	M	118/127 (93%)	95 (80%)	18 (15%)	5 (4%)	2	21
14	N	114/117 (97%)	92 (81%)	16 (14%)	6 (5%)	1	18
15	O	112/115 (97%)	96 (86%)	13 (12%)	3 (3%)	4	29
16	P	115/118 (98%)	99 (86%)	13 (11%)	3 (3%)	4	29
17	Q	101/103 (98%)	74 (73%)	19 (19%)	8 (8%)	1	12
18	R	108/110 (98%)	84 (78%)	17 (16%)	7 (6%)	1	15
19	S	91/100 (91%)	76 (84%)	13 (14%)	2 (2%)	5	32
20	T	100/104 (96%)	81 (81%)	11 (11%)	8 (8%)	1	12
21	U	92/94 (98%)	75 (82%)	13 (14%)	4 (4%)	2	21
22	V	73/85 (86%)	64 (88%)	5 (7%)	4 (6%)	1	18
23	W	75/78 (96%)	65 (87%)	7 (9%)	3 (4%)	2	22
24	X	61/63 (97%)	53 (87%)	2 (3%)	6 (10%)	0	8
25	Y	56/59 (95%)	48 (86%)	4 (7%)	4 (7%)	1	14
26	Z	64/70 (91%)	49 (77%)	8 (12%)	7 (11%)	0	6
27	1	54/57 (95%)	39 (72%)	9 (17%)	6 (11%)	0	6
28	2	48/55 (87%)	39 (81%)	8 (17%)	1 (2%)	5	33
29	3	44/46 (96%)	38 (86%)	4 (9%)	2 (4%)	2	20
30	4	62/65 (95%)	49 (79%)	11 (18%)	2 (3%)	3	26
31	5	36/38 (95%)	28 (78%)	5 (14%)	3 (8%)	0	11
32	6	216/241 (90%)	158 (73%)	40 (18%)	18 (8%)	0	11
33	7	204/233 (88%)	174 (85%)	24 (12%)	6 (3%)	3	27
34	8	203/206 (98%)	166 (82%)	27 (13%)	10 (5%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	9	155/167 (93%)	119 (77%)	20 (13%)	16 (10%)	0	7
36	10	98/135 (73%)	71 (72%)	18 (18%)	9 (9%)	0	10
37	11	149/179 (83%)	125 (84%)	16 (11%)	8 (5%)	1	18
38	12	127/130 (98%)	109 (86%)	14 (11%)	4 (3%)	3	26
39	13	125/130 (96%)	93 (74%)	16 (13%)	16 (13%)	0	4
40	14	96/103 (93%)	74 (77%)	10 (10%)	12 (12%)	0	4
41	15	114/129 (88%)	89 (78%)	15 (13%)	10 (9%)	0	10
42	16	121/124 (98%)	90 (74%)	21 (17%)	10 (8%)	0	11
43	17	112/118 (95%)	89 (80%)	15 (13%)	8 (7%)	1	14
44	18	98/101 (97%)	74 (76%)	16 (16%)	8 (8%)	1	11
45	19	86/89 (97%)	73 (85%)	10 (12%)	3 (4%)	3	24
46	20	80/82 (98%)	59 (74%)	20 (25%)	1 (1%)	10	41
47	21	78/84 (93%)	57 (73%)	14 (18%)	7 (9%)	0	10
48	22	63/75 (84%)	44 (70%)	11 (18%)	8 (13%)	0	4
49	23	77/92 (84%)	62 (80%)	11 (14%)	4 (5%)	1	18
50	24	83/87 (95%)	71 (86%)	9 (11%)	3 (4%)	3	24
51	25	63/71 (89%)	36 (57%)	14 (22%)	13 (21%)	0	1
59	33	663/750 (88%)	559 (84%)	61 (9%)	43 (6%)	1	15
All	All	6509/6970 (93%)	5217 (80%)	860 (13%)	432 (7%)	2	15

5 of 432 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	97	ASP
1	A	107	LYS
1	A	121	ALA
1	A	143	VAL
1	A	154	ALA

5.3.2 Protein sidechains ⓘ

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

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

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	216/218 (99%)	215 (100%)	1 (0%)	86	90
2	B	164/164 (100%)	164 (100%)	0	100	100
3	C	165/165 (100%)	163 (99%)	2 (1%)	67	78
4	D	148/150 (99%)	147 (99%)	1 (1%)	81	86
5	E	137/138 (99%)	137 (100%)	0	100	100
6	F	114/114 (100%)	114 (100%)	0	100	100
7	G	100/123 (81%)	99 (99%)	1 (1%)	73	81
8	H	109/110 (99%)	109 (100%)	0	100	100
9	I	116/116 (100%)	116 (100%)	0	100	100
10	J	103/104 (99%)	103 (100%)	0	100	100
11	K	102/103 (99%)	101 (99%)	1 (1%)	73	81
12	L	109/109 (100%)	109 (100%)	0	100	100
13	M	100/103 (97%)	99 (99%)	1 (1%)	73	81
14	N	86/87 (99%)	86 (100%)	0	100	100
15	O	99/100 (99%)	99 (100%)	0	100	100
16	P	89/90 (99%)	89 (100%)	0	100	100
17	Q	84/84 (100%)	84 (100%)	0	100	100
18	R	93/93 (100%)	93 (100%)	0	100	100
19	S	80/84 (95%)	80 (100%)	0	100	100
20	T	83/85 (98%)	83 (100%)	0	100	100
21	U	78/78 (100%)	78 (100%)	0	100	100
22	V	57/63 (90%)	57 (100%)	0	100	100
23	W	67/68 (98%)	67 (100%)	0	100	100
24	X	55/55 (100%)	55 (100%)	0	100	100
25	Y	48/49 (98%)	48 (100%)	0	100	100
26	Z	59/62 (95%)	57 (97%)	2 (3%)	32	55
27	1	47/48 (98%)	47 (100%)	0	100	100
28	2	45/49 (92%)	45 (100%)	0	100	100
29	3	38/38 (100%)	38 (100%)	0	100	100
30	4	51/52 (98%)	51 (100%)	0	100	100
31	5	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	6	180/199 (90%)	179 (99%)	1 (1%)	84	88
33	7	170/190 (90%)	169 (99%)	1 (1%)	84	88
34	8	172/173 (99%)	172 (100%)	0	100	100
35	9	119/126 (94%)	117 (98%)	2 (2%)	56	72
36	10	87/116 (75%)	87 (100%)	0	100	100
37	11	124/147 (84%)	124 (100%)	0	100	100
38	12	104/105 (99%)	104 (100%)	0	100	100
39	13	105/107 (98%)	103 (98%)	2 (2%)	52	70
40	14	86/90 (96%)	86 (100%)	0	100	100
41	15	89/99 (90%)	87 (98%)	2 (2%)	47	65
42	16	103/104 (99%)	103 (100%)	0	100	100
43	17	92/96 (96%)	92 (100%)	0	100	100
44	18	83/84 (99%)	83 (100%)	0	100	100
45	19	76/77 (99%)	76 (100%)	0	100	100
46	20	65/65 (100%)	65 (100%)	0	100	100
47	21	74/78 (95%)	73 (99%)	1 (1%)	62	75
48	22	56/65 (86%)	56 (100%)	0	100	100
49	23	70/79 (89%)	70 (100%)	0	100	100
50	24	65/66 (98%)	65 (100%)	0	100	100
51	25	55/61 (90%)	54 (98%)	1 (2%)	54	71
59	33	452/635 (71%)	448 (99%)	4 (1%)	75	83
All	All	5303/5698 (93%)	5280 (100%)	23 (0%)	88	91

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	13	93	LEU
47	21	78	VAL
41	15	117	HIS
51	25	18	PHE
13	M	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
34	8	70	GLN
39	13	125	GLN
34	8	99	ASN
37	11	67	ASN
43	17	13	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	26	1538/1539 (99%)	190 (12%)	8 (0%)
53	27	2902/2903 (99%)	410 (14%)	22 (0%)
54	28	119/120 (99%)	9 (7%)	1 (0%)
55	29	19/20 (95%)	4 (21%)	0
56	30	75/76 (98%)	20 (26%)	1 (1%)
57	31	76/77 (98%)	6 (7%)	0
58	32	76/77 (98%)	22 (28%)	1 (1%)
All	All	4805/4812 (99%)	661 (13%)	33 (0%)

5 of 661 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	26	9	G
52	26	13	U
52	26	22	G
52	26	32	A
52	26	39	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	27	2756	U
53	27	2873	A
58	32	16	C
53	27	858	G
53	27	774	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

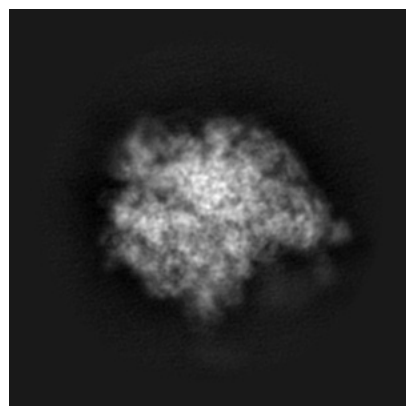
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8282. These allow visual inspection of the internal detail of the map and identification of artifacts.

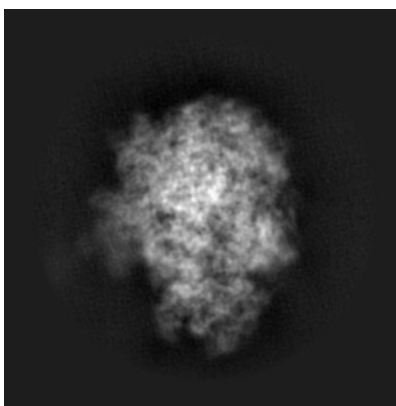
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

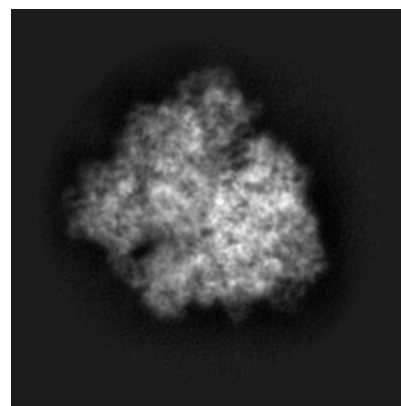
6.1.1 Primary map



X

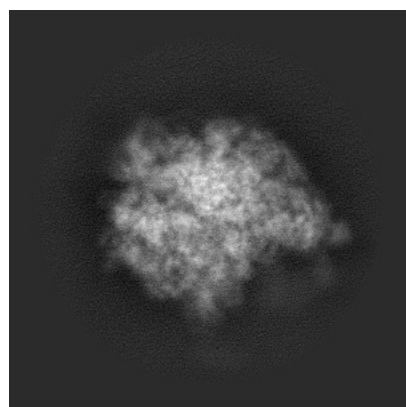


Y

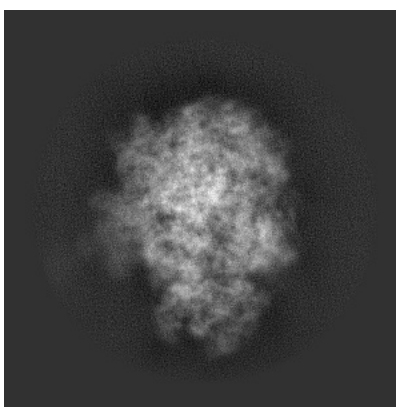


Z

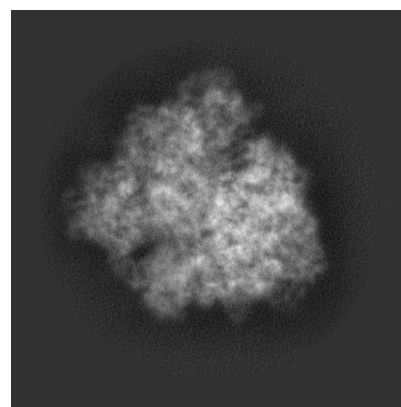
6.1.2 Raw map



X



Y

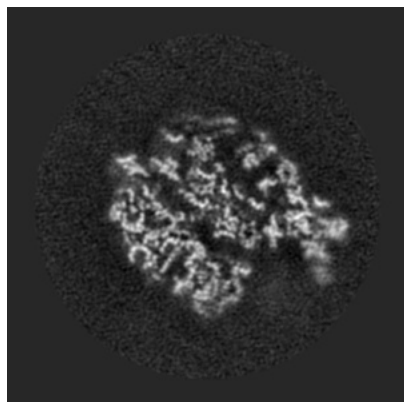


Z

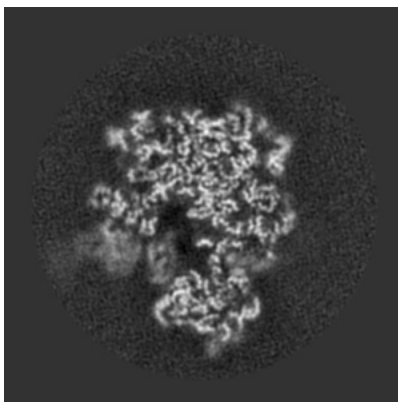
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

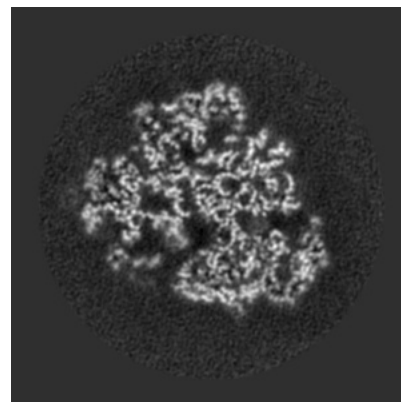
6.2.1 Primary map



X Index: 240

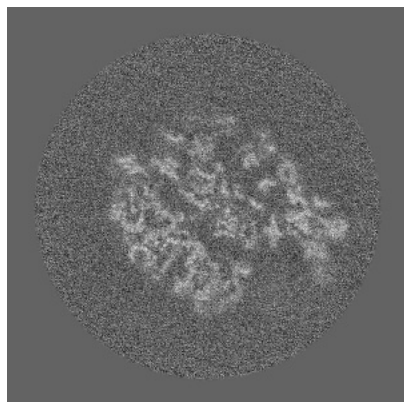


Y Index: 240

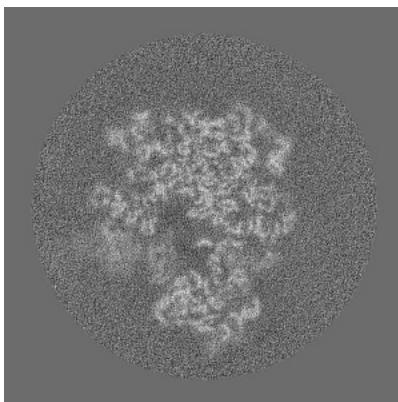


Z Index: 240

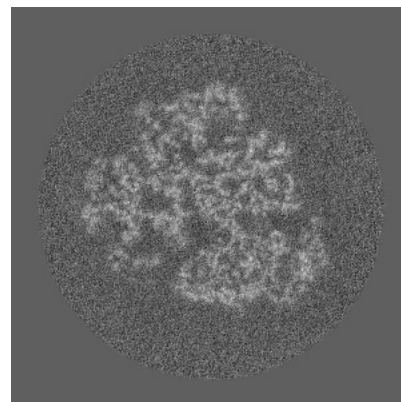
6.2.2 Raw map



X Index: 240



Y Index: 240

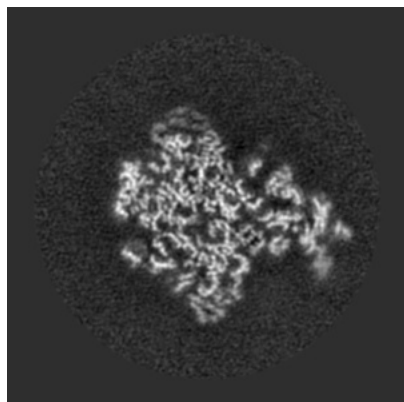


Z Index: 240

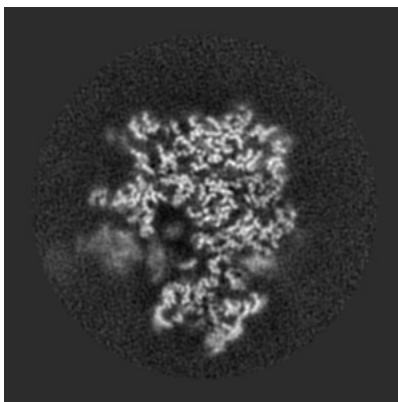
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

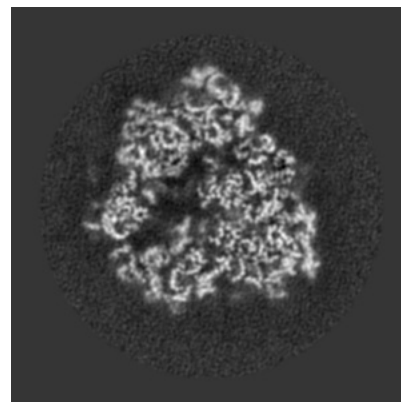
6.3.1 Primary map



X Index: 250

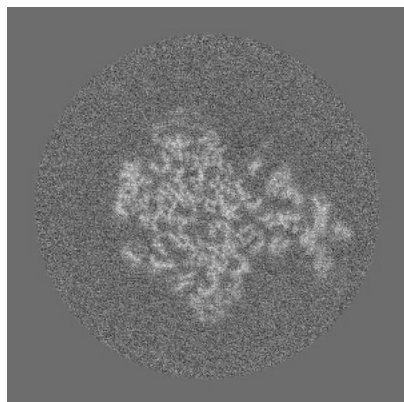


Y Index: 247

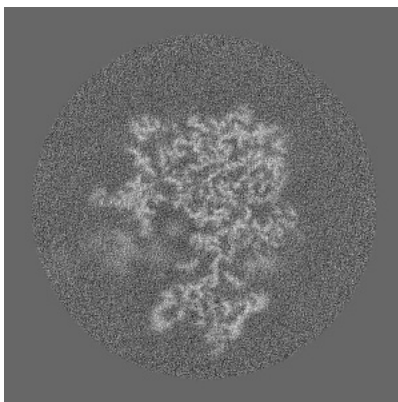


Z Index: 220

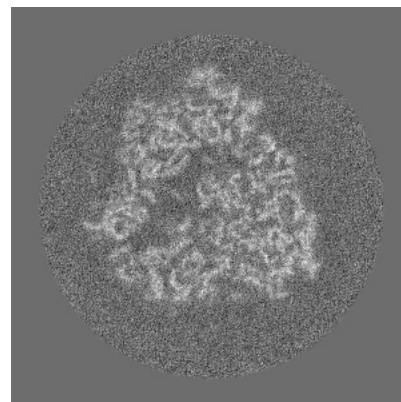
6.3.2 Raw map



X Index: 250



Y Index: 250

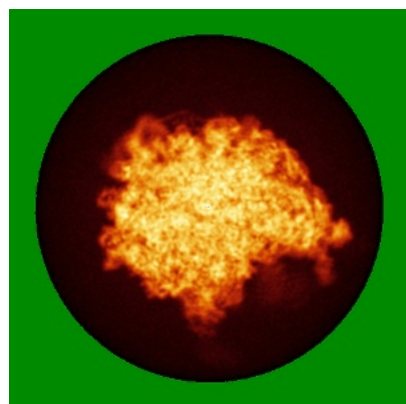


Z Index: 222

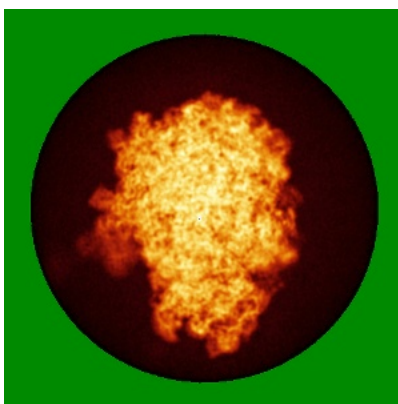
The images above show the largest variance slices of the map in three orthogonal directions.

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

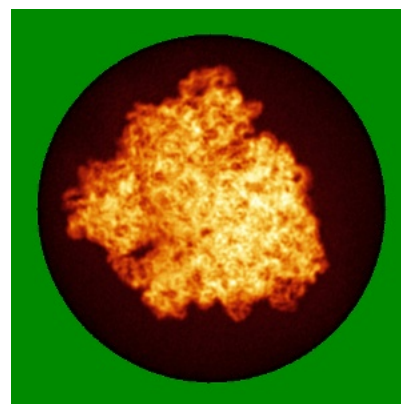
6.4.1 Primary map



X

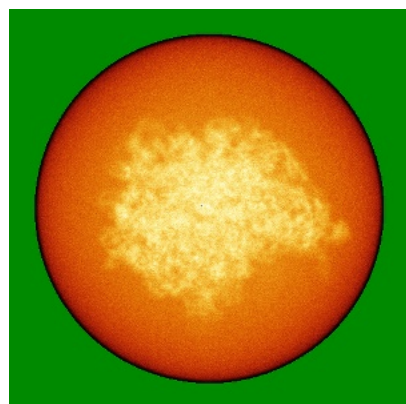


Y

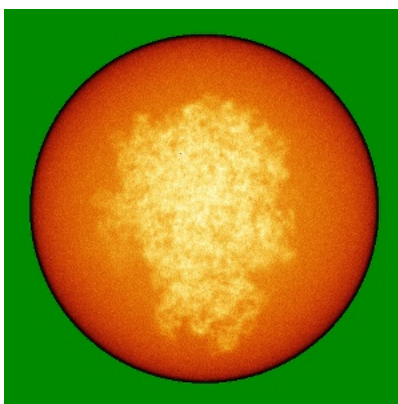


Z

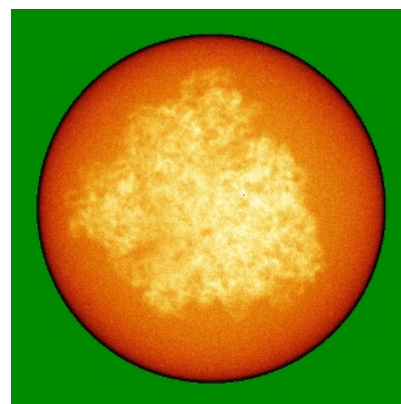
6.4.2 Raw map



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



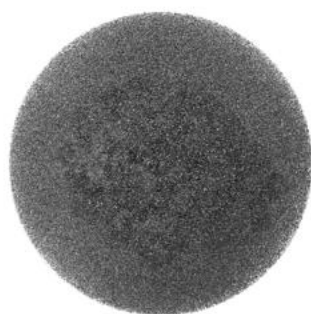
Y



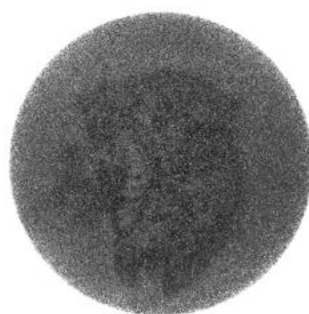
Z

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.

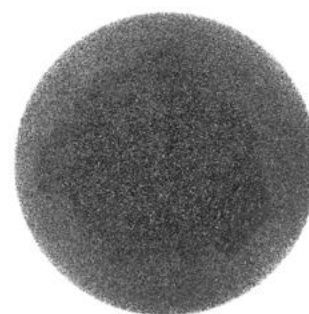
6.5.2 Raw map



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.

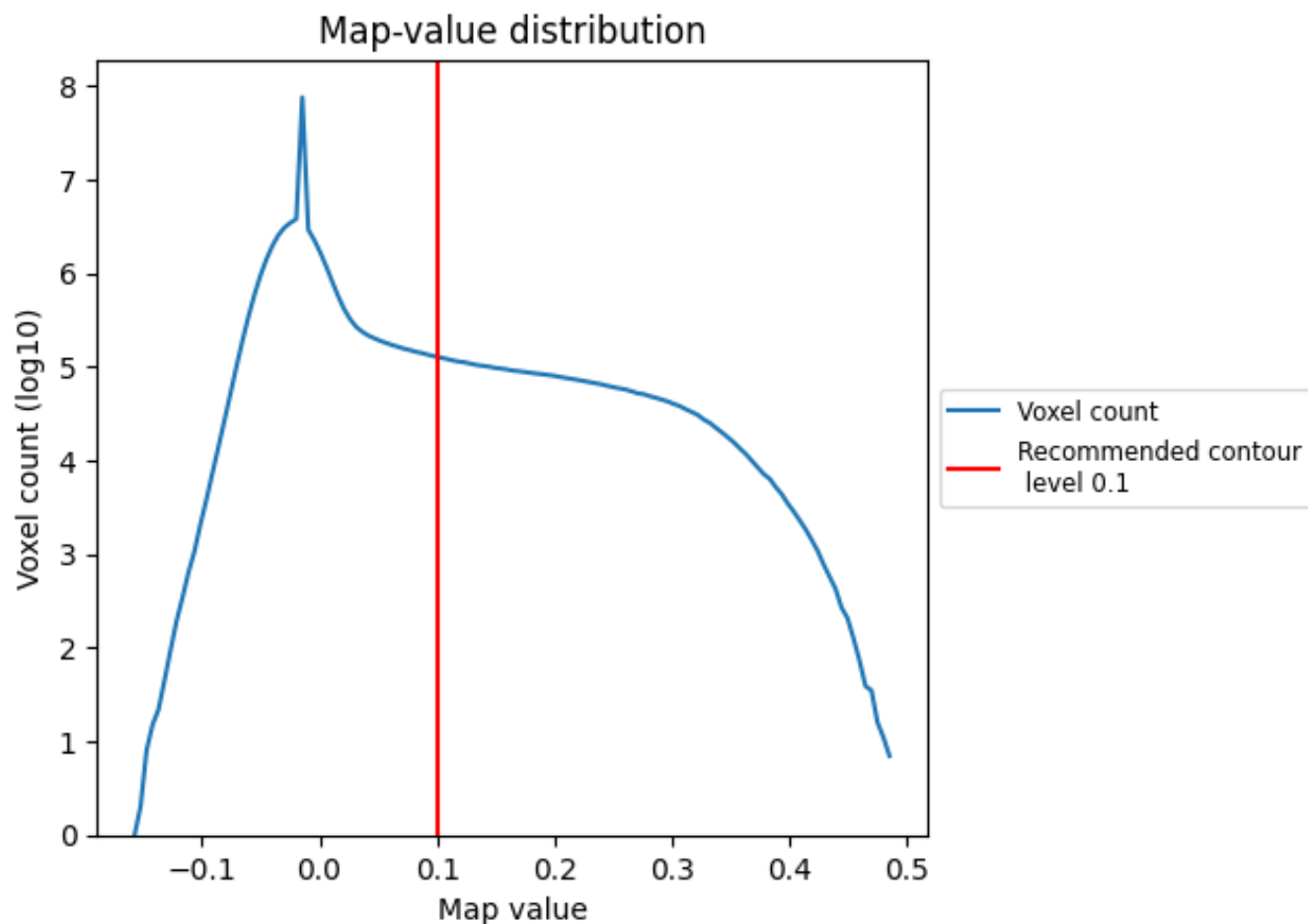
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

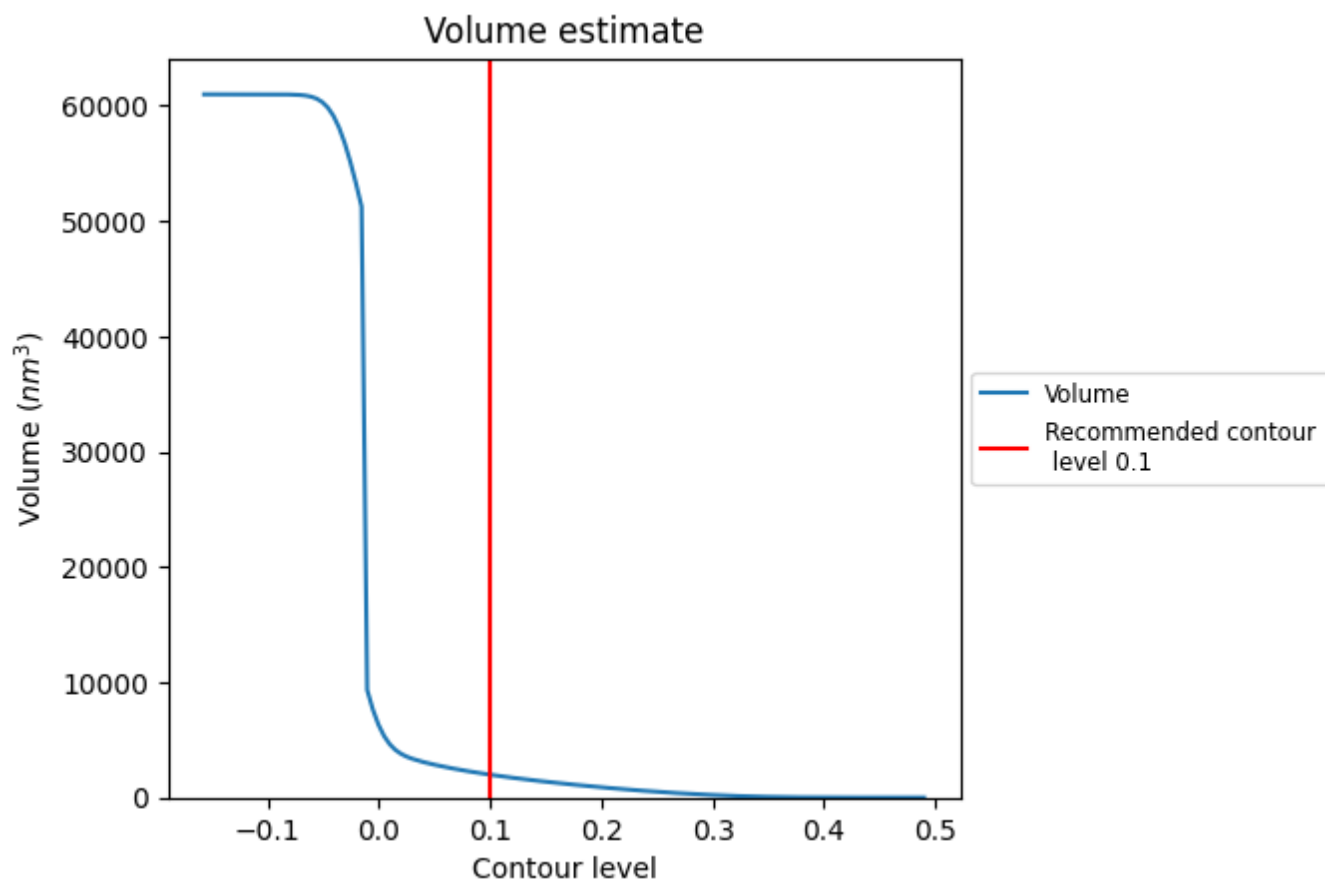
This section contains the results of statistical analysis of the map.

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.

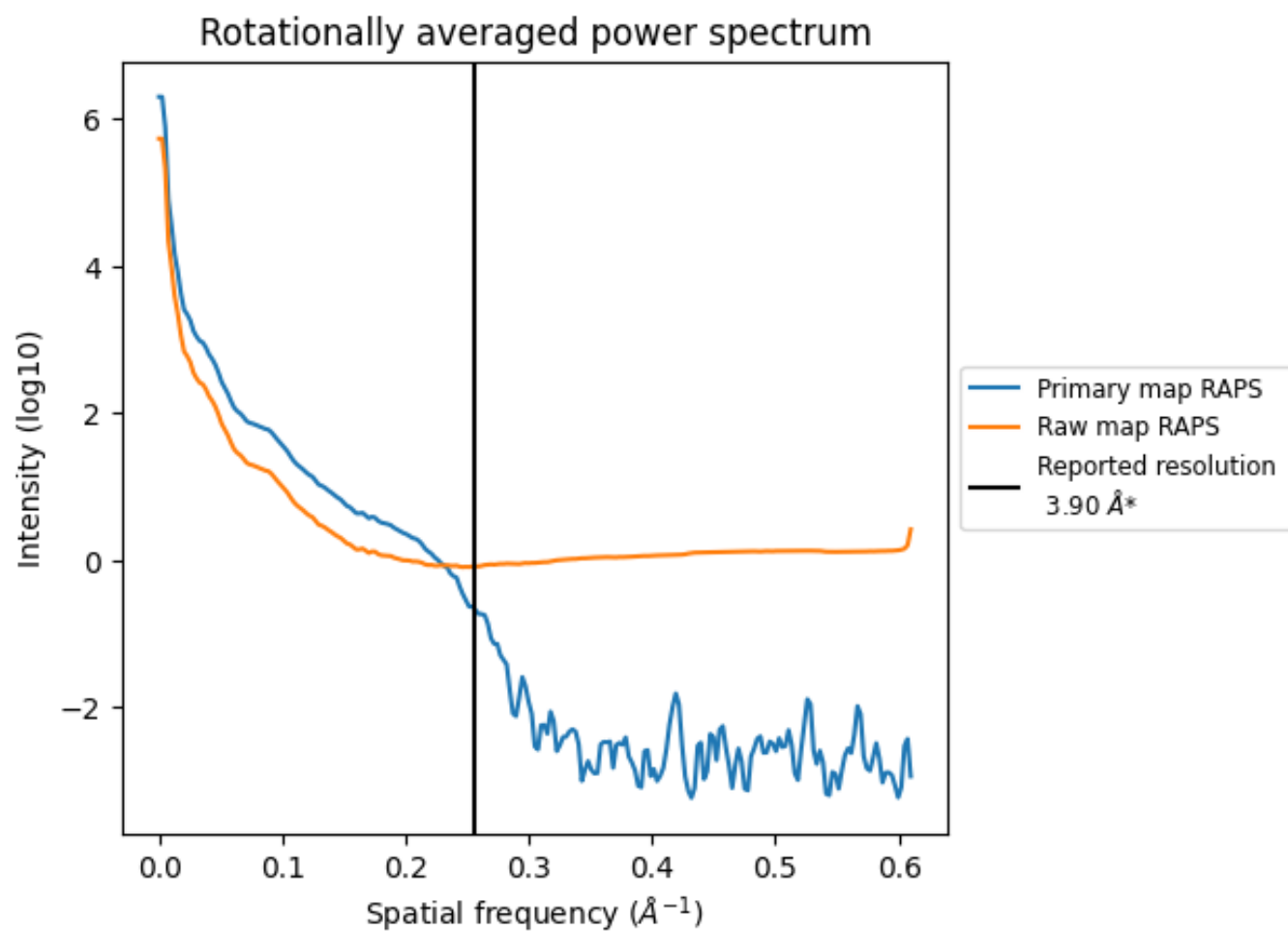
7.2 Volume estimate [i](#)



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 ⓘ

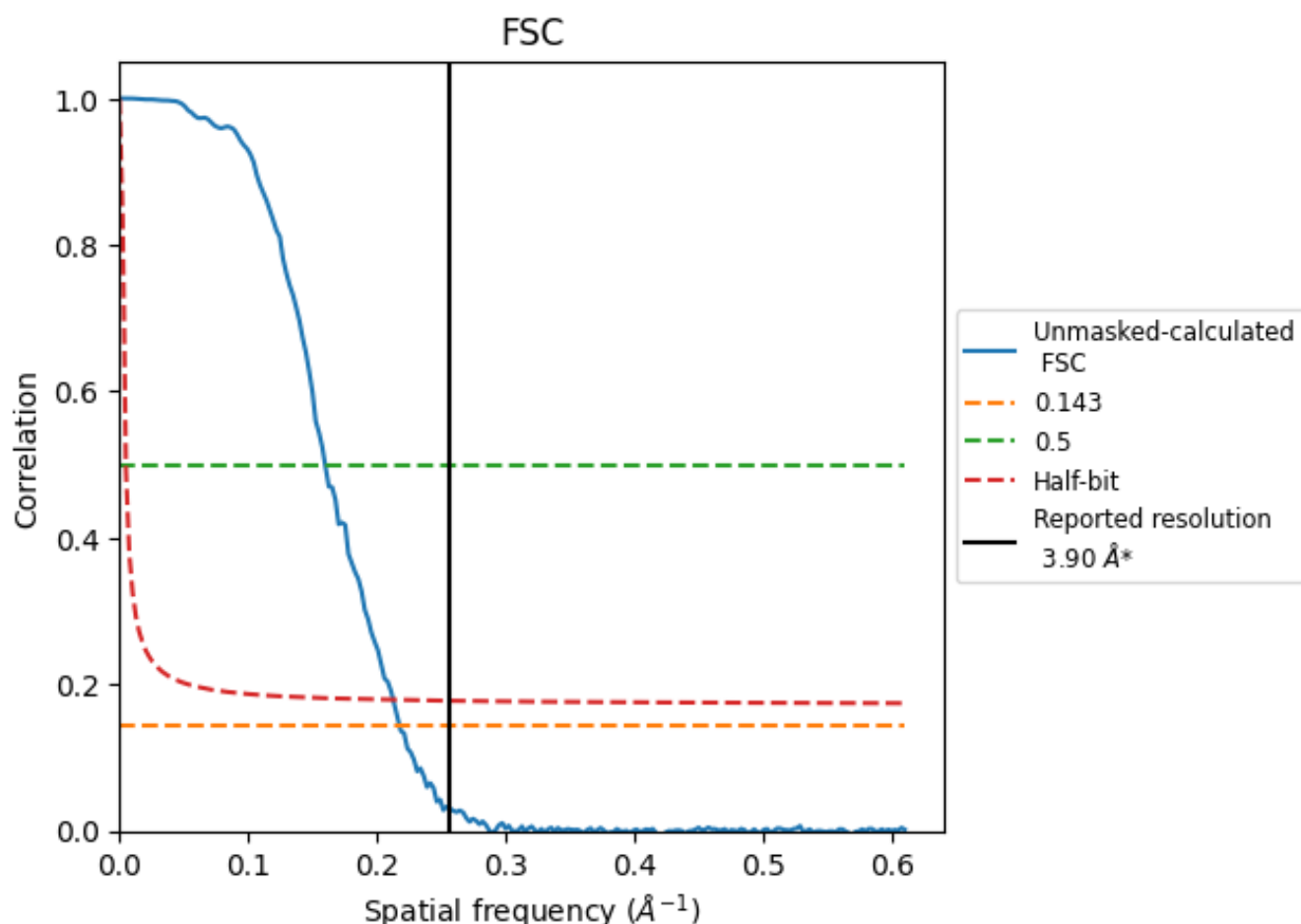


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

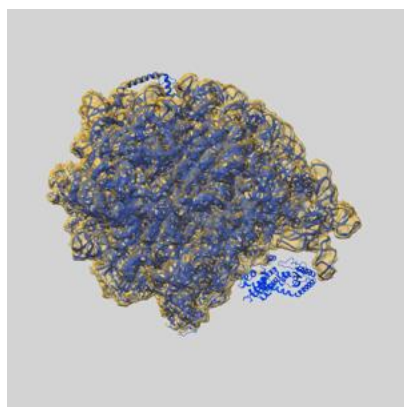
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.60	6.27	4.70

*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 4.60 differs from the reported value 3.9 by more than 10 %

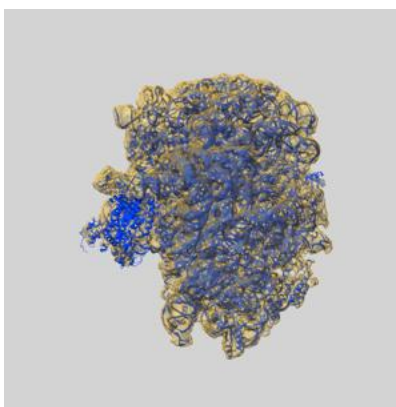
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8282 and PDB model 5KPX. Per-residue inclusion information can be found in section [3](#) on page [15](#).

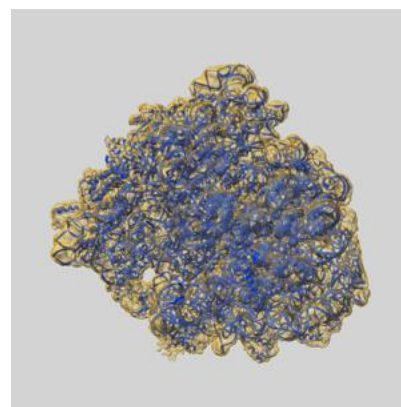
9.1 Map-model overlay [i](#)



X



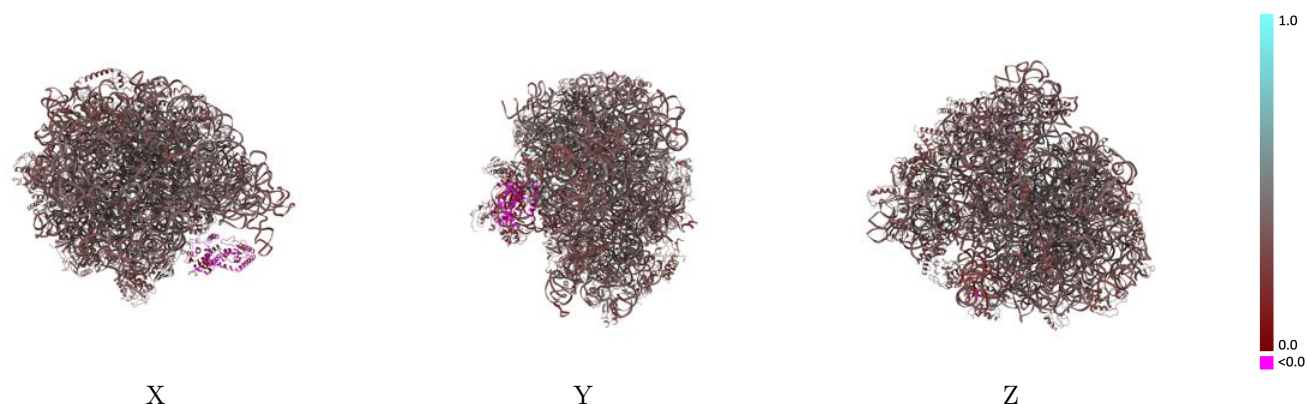
Y



Z

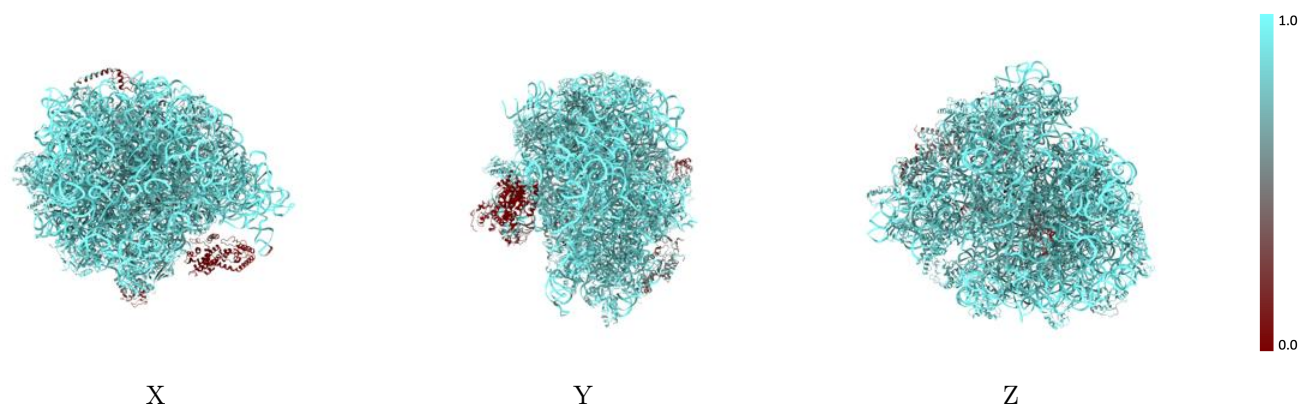
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



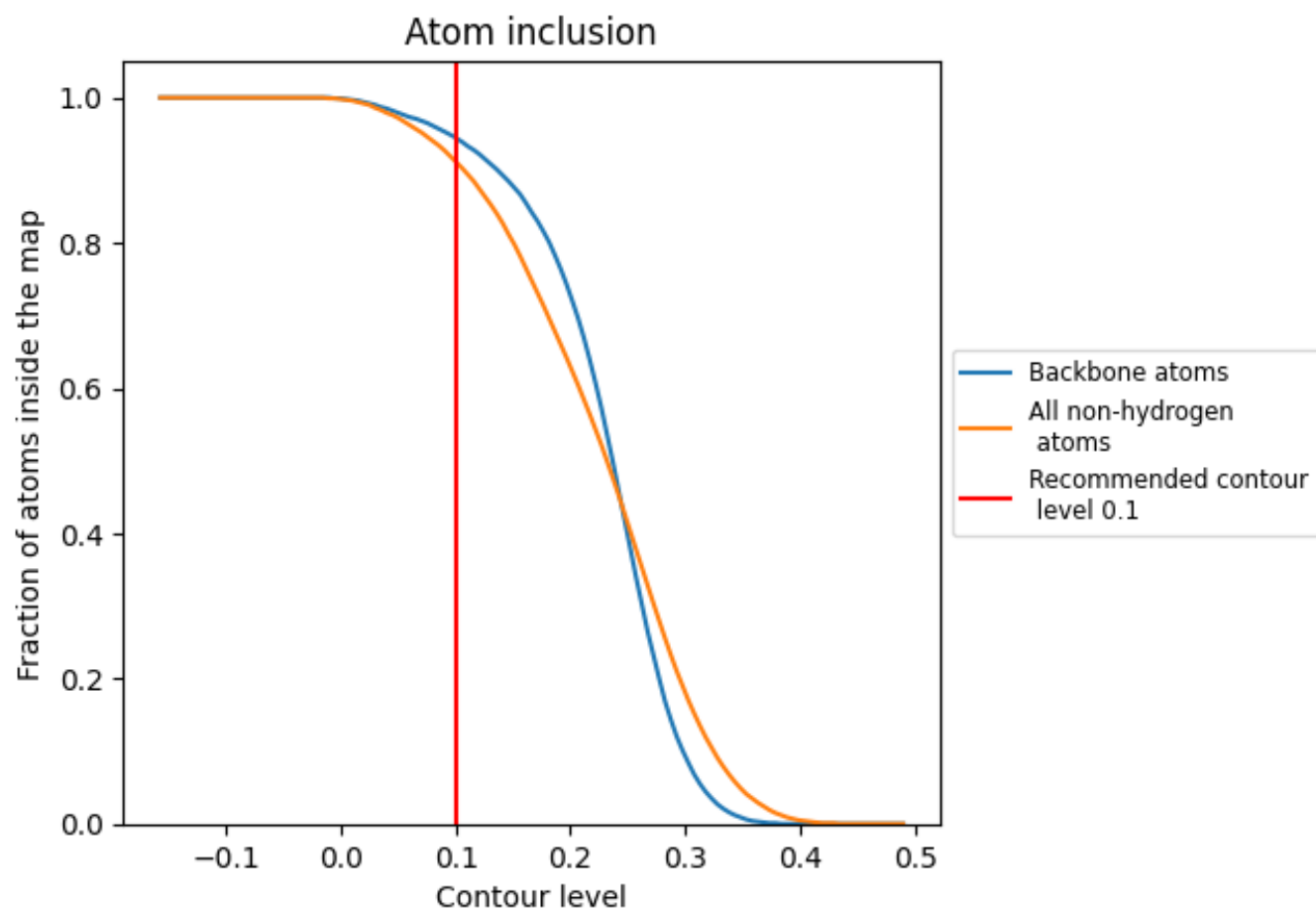
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% 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	 0.9120	 0.3580
1	 0.8690	 0.3750
10	 0.8790	 0.3680
11	 0.8610	 0.3410
12	 0.8490	 0.3650
13	 0.8740	 0.3400
14	 0.8200	 0.3440
15	 0.8770	 0.3640
16	 0.7890	 0.3860
17	 0.8580	 0.3420
18	 0.8590	 0.3500
19	 0.8670	 0.3410
2	 0.7850	 0.3840
20	 0.8610	 0.3570
21	 0.8590	 0.3780
22	 0.8870	 0.3740
23	 0.8650	 0.3510
24	 0.8620	 0.3240
25	 0.7700	 0.3200
26	 0.9900	 0.3690
27	 0.9880	 0.3720
28	 0.9940	 0.3690
29	 0.9260	 0.3270
3	 0.8730	 0.3670
30	 0.9530	 0.2870
31	 0.9650	 0.3590
32	 0.8090	 0.2580
33	 0.3570	 0.1640
4	 0.8330	 0.3790
5	 0.8600	 0.3810
6	 0.4950	 0.3230
7	 0.8330	 0.3720
8	 0.8290	 0.3240
9	 0.8540	 0.3800
A	 0.8500	 0.3970



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Chain	Atom inclusion	Q-score
B	 0.8620	 0.3950
C	 0.7900	 0.3460
D	 0.8670	 0.3520
E	 0.8760	 0.3640
F	 0.4120	 0.3110
G	 0.2890	 0.2640
H	 0.3830	 0.2580
I	 0.8740	 0.3680
J	 0.8010	 0.4000
K	 0.8680	 0.3750
L	 0.8240	 0.3960
M	 0.8850	 0.3680
N	 0.8920	 0.3440
O	 0.8580	 0.3920
P	 0.8770	 0.3470
Q	 0.8790	 0.3790
R	 0.8210	 0.3720
S	 0.8640	 0.3700
T	 0.8890	 0.3650
U	 0.8350	 0.3680
V	 0.8640	 0.3950
W	 0.8700	 0.3670
X	 0.8430	 0.2950
Y	 0.8470	 0.3630
Z	 0.8650	 0.3540