



## wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 01:07 AM EST

PDB ID : 5KPS  
EMDB ID : EMD-8279  
Title : Structure of RelA bound to ribosome in absence of A/R tRNA (Structure I)  
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](mailto: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>.

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

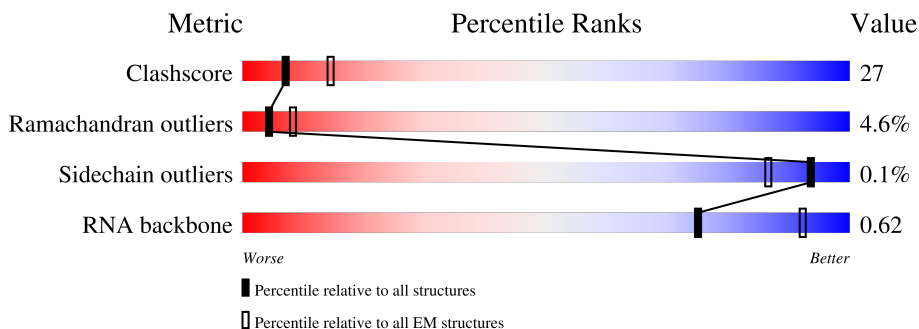
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	750	
2	B	273	
3	C	209	
4	D	201	
5	E	179	
6	F	177	
7	G	149	

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Mol	Chain	Length	Quality of chain
8	H	165	
9	I	142	
10	J	142	
11	K	123	
12	L	144	
13	M	136	
14	N	127	
15	O	117	
16	P	115	
17	Q	118	
18	R	103	
19	S	110	
20	T	100	
21	U	104	
22	V	94	
23	W	85	
24	X	78	
25	Y	63	
26	Z	59	
27	1	70	
28	2	57	
29	3	55	
30	4	46	
31	5	65	
32	6	38	

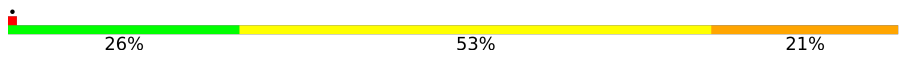
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Mol	Chain	Length	Quality of chain
33	7	241	
34	8	233	
35	9	206	
36	10	167	
37	11	135	
38	12	179	
39	13	130	
40	14	130	
41	15	103	
42	16	129	
43	17	124	
44	18	118	
45	19	101	
46	20	89	
47	21	82	
48	22	84	
49	23	75	
50	24	92	
51	25	87	
52	26	71	
53	27	1539	
54	28	2903	
55	29	120	
56	30	18	
57	31	77	

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Mol	Chain	Length	Quality of chain
58	32	77	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '26%', a yellow segment in the middle labeled '53%', and an orange segment on the right labeled '21%'. A small red dot is visible at the beginning of the green segment.</p>

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 149128 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 GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	143	1103	685	209	204	5	0	0

There are 7 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called 50S ribosomal protein L2.

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

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

- Molecule 4 is a protein called 50S ribosomal protein L4.

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

- Molecule 5 is a protein called 50S ribosomal protein L5.

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

- Molecule 6 is a protein called 50S ribosomal protein L6.

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

- Molecule 7 is a protein called 50S ribosomal protein L9.

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

- Molecule 8 is a protein called 50S ribosomal protein L10.

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

- Molecule 9 is a protein called 50S ribosomal protein L11.

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

- Molecule 10 is a protein called 50S ribosomal protein L13.

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

- Molecule 11 is a protein called 50S ribosomal protein L14.

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

- Molecule 12 is a protein called 50S ribosomal protein L15.

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

- Molecule 13 is a protein called 50S ribosomal protein L16.

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

- Molecule 14 is a protein called 50S ribosomal protein L17.

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

- Molecule 15 is a protein called 50S ribosomal protein L18.

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

- Molecule 16 is a protein called 50S ribosomal protein L19.

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

- Molecule 17 is a protein called 50S ribosomal protein L20.

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

- Molecule 18 is a protein called 50S ribosomal protein L21.

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

- Molecule 19 is a protein called 50S ribosomal protein L22.



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

- Molecule 20 is a protein called 50S ribosomal protein L23.

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

- Molecule 21 is a protein called 50S ribosomal protein L24.

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

- Molecule 22 is a protein called 50S ribosomal protein L25.

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

- Molecule 23 is a protein called 50S ribosomal protein L27.

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

- Molecule 24 is a protein called 50S ribosomal protein L28.

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

- Molecule 25 is a protein called 50S ribosomal protein L29.

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

- Molecule 26 is a protein called 50S ribosomal protein L30.

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

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	3	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	10	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	11	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	12	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	13	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	14	127	1022	634	206	179	3	0	0

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	15	98	786	493	150	142	1	0	0

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	16	116	869	535	173	158	3	0	0

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	17	123	955	590	196	165	4	0	0

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	18	114	883	546	178	156	3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	19	100	805	499	164	139	3	0	0

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	20	88	714	439	144	130	1	0	0

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	21	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	22	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	23	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	24	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	25	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	26	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	27	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	28	2903	62322	27801	11468	20150	2903	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
28	747	C	U	conflict	GB 802133627
28	1847	G	A	conflict	GB 802133627

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
55	29	120	2572	1145	471	836	120	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
29	120	A	-	conflict	GB 1028475309

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	30	18	388	175	76	120	17	0	0

- Molecule 57 is a RNA chain called P site tRNA<sup>fmet</sup>.

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

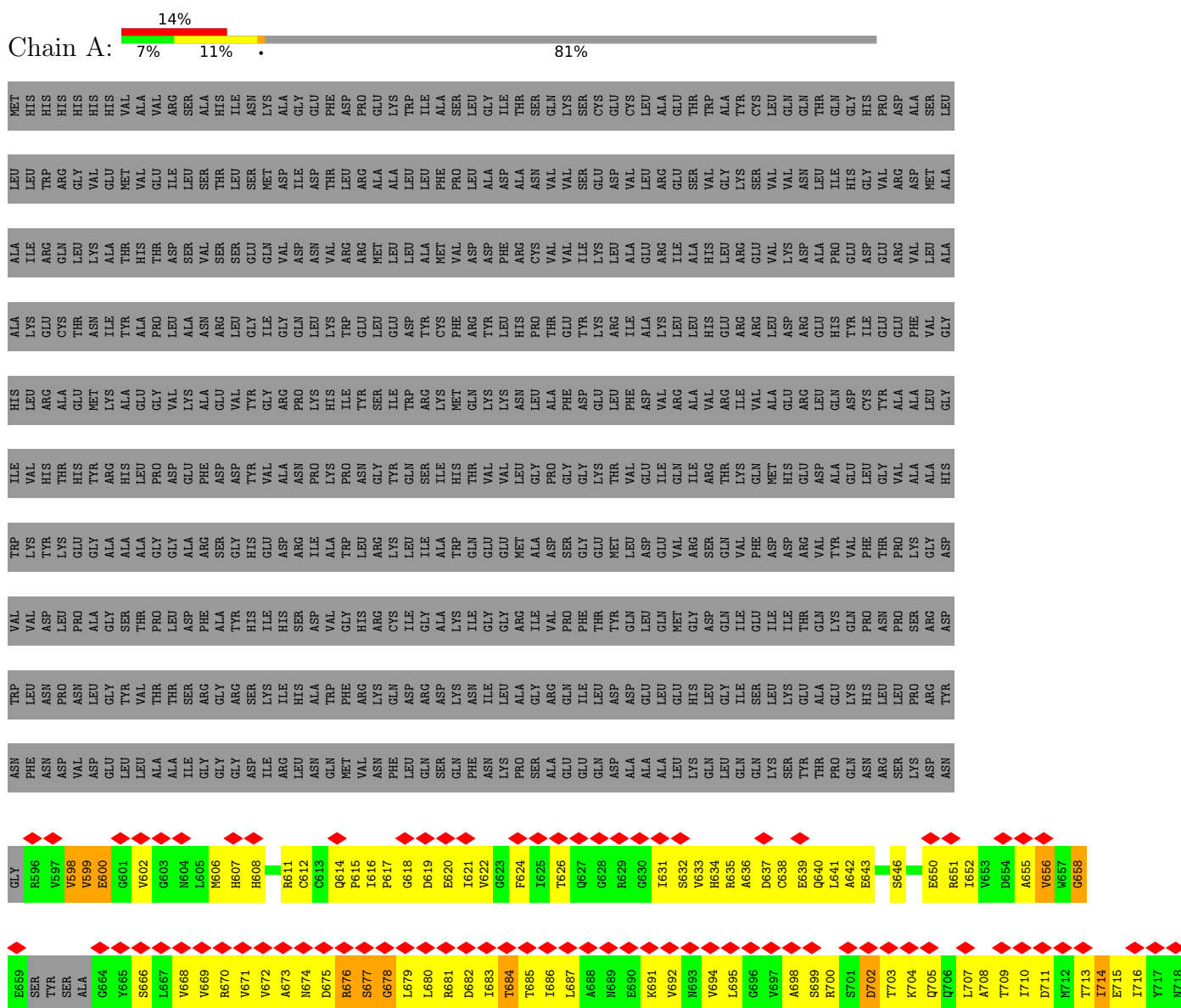
- Molecule 58 is a RNA chain called E-site tRNA<sup>fMet</sup>.

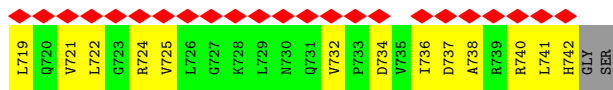
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
58	32	77	1643	732	297	537	77	0	0

### 3 Residue-property plots

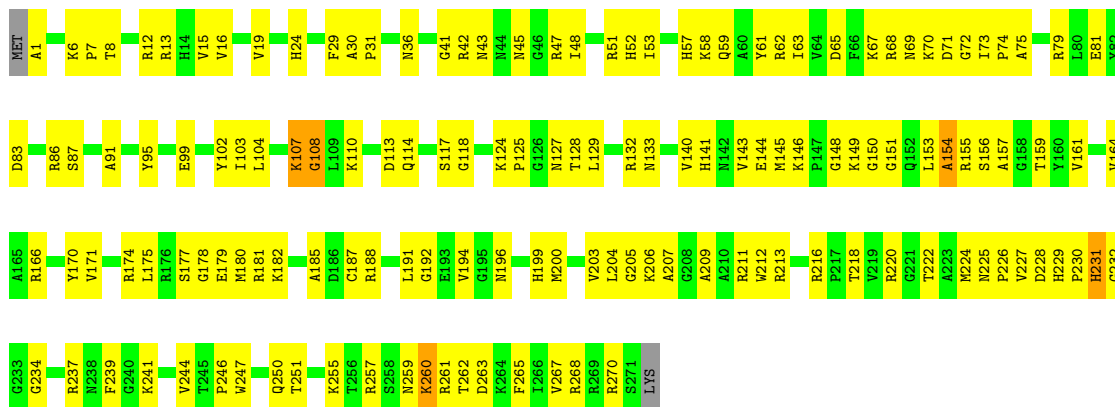
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: GTP pyrophosphokinase

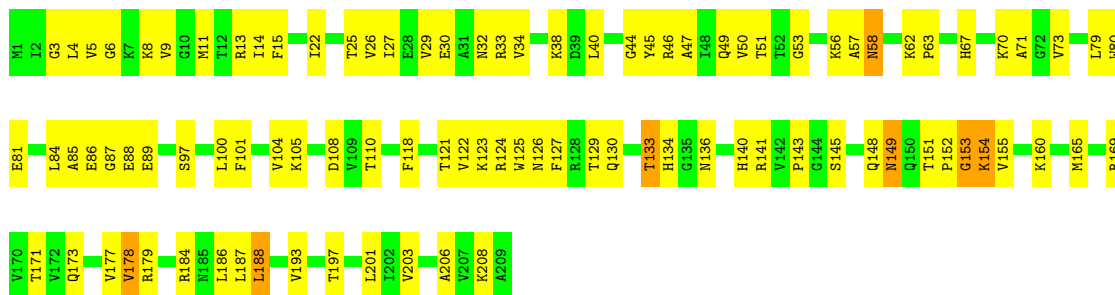




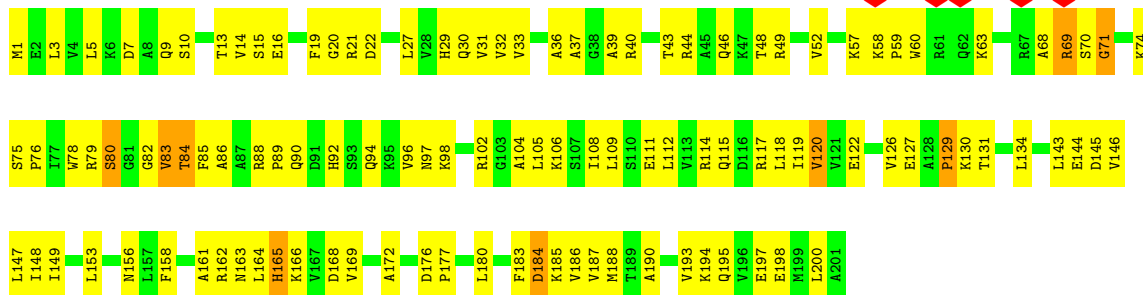
• Molecule 2: 50S ribosomal protein L2



• Molecule 3: 50S ribosomal protein L3



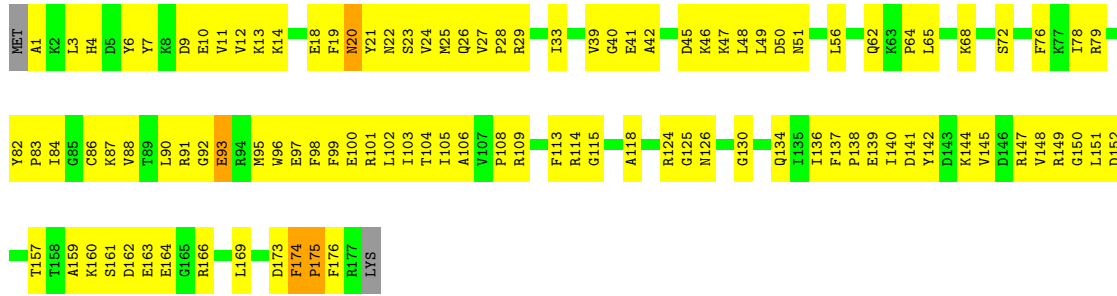
• Molecule 4: 50S ribosomal protein L4



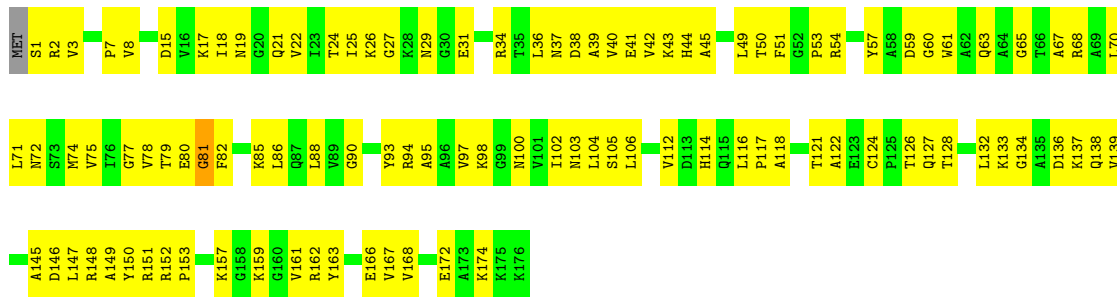
• Molecule 5: 50S ribosomal protein L5



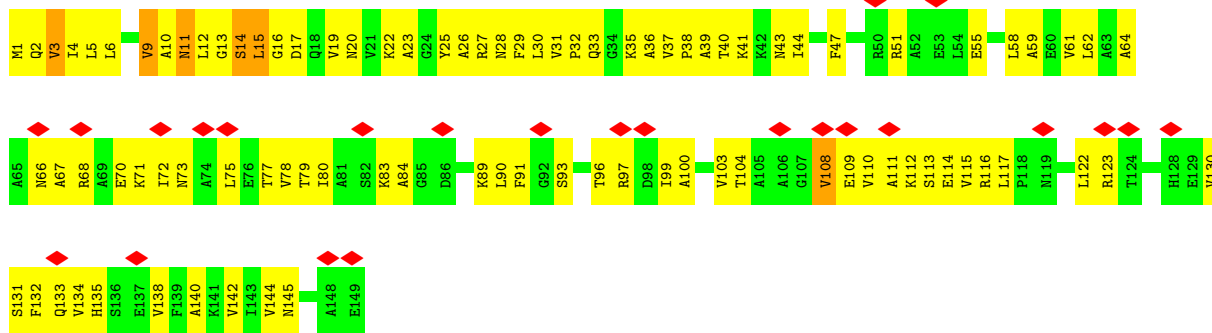




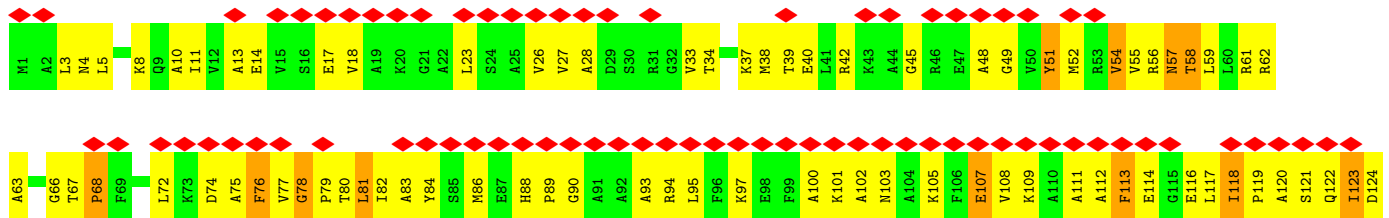
• Molecule 6: 50S ribosomal protein L6

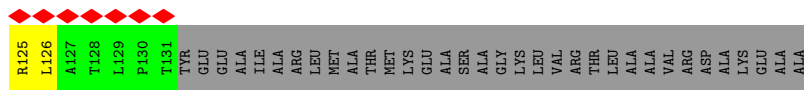


• Molecule 7: 50S ribosomal protein L9



• Molecule 8: 50S ribosomal protein L10

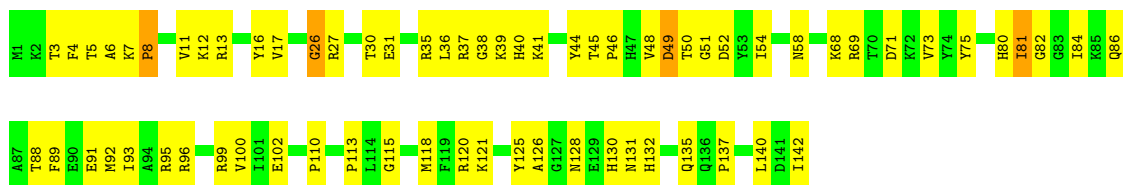




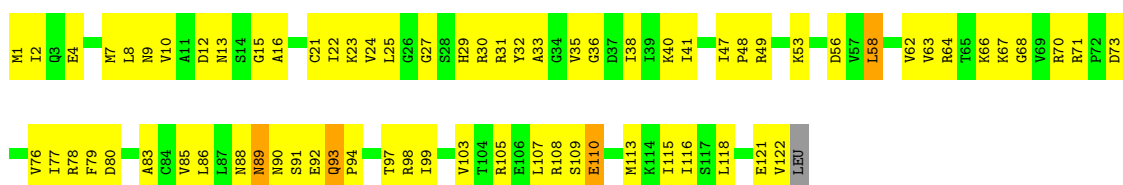
• Molecule 9: 50S ribosomal protein L11



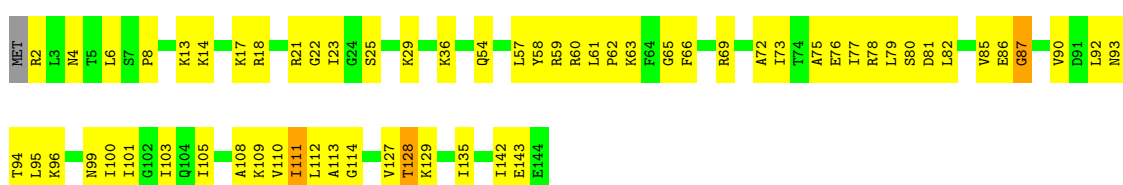
• Molecule 10: 50S ribosomal protein L13



• Molecule 11: 50S ribosomal protein L14

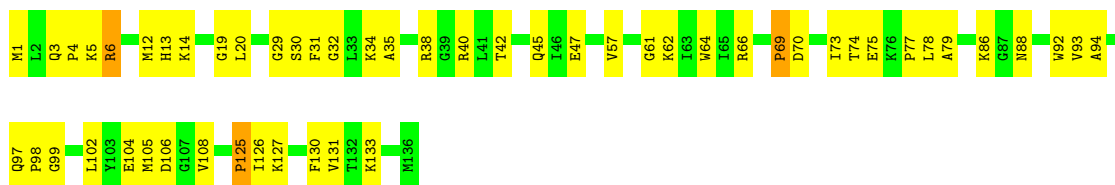


• Molecule 12: 50S ribosomal protein L15



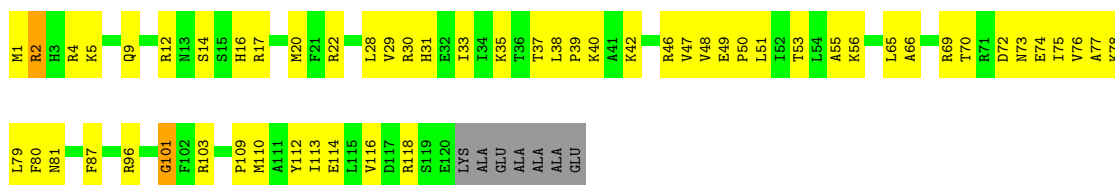
• Molecule 13: 50S ribosomal protein L16

Chain M:  61% 37%



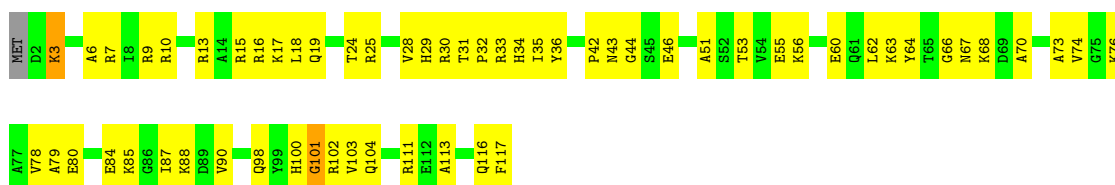
• Molecule 14: 50S ribosomal protein L17

Chain N:  50% 43% 6%



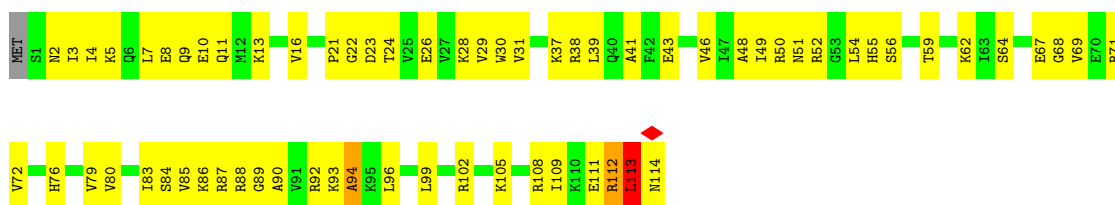
• Molecule 15: 50S ribosomal protein L18

Chain O:  49% 49%



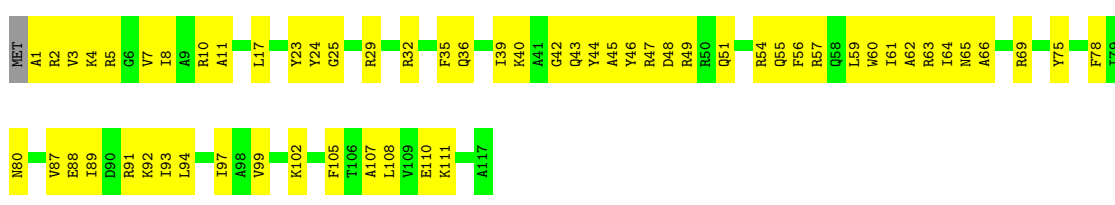
• Molecule 16: 50S ribosomal protein L19

Chain P:  42% 55%

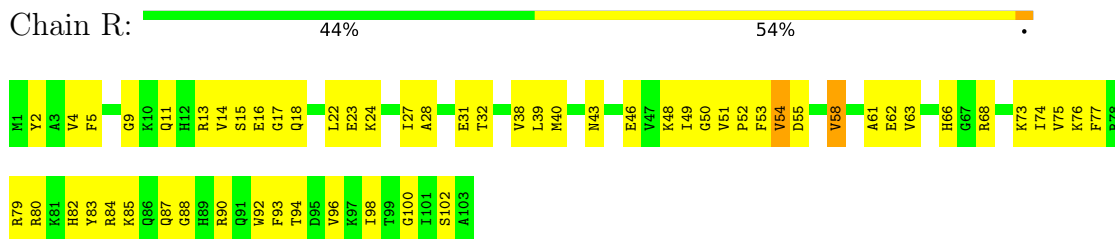


• Molecule 17: 50S ribosomal protein L20

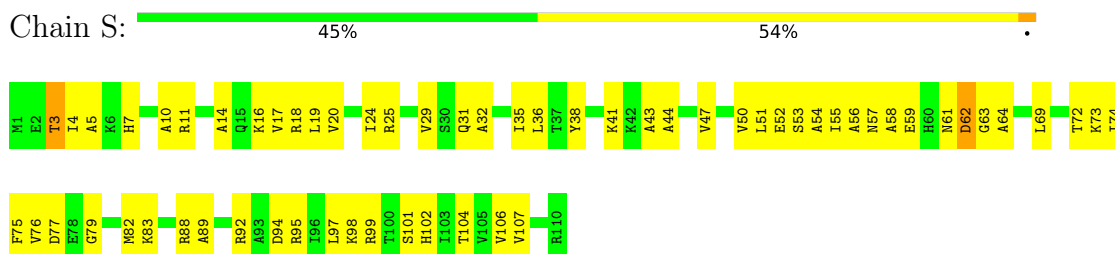
Chain Q:  49% 50%



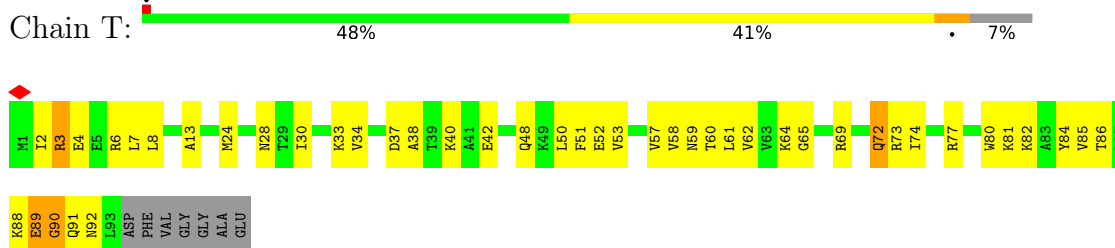
- Molecule 18: 50S ribosomal protein L21



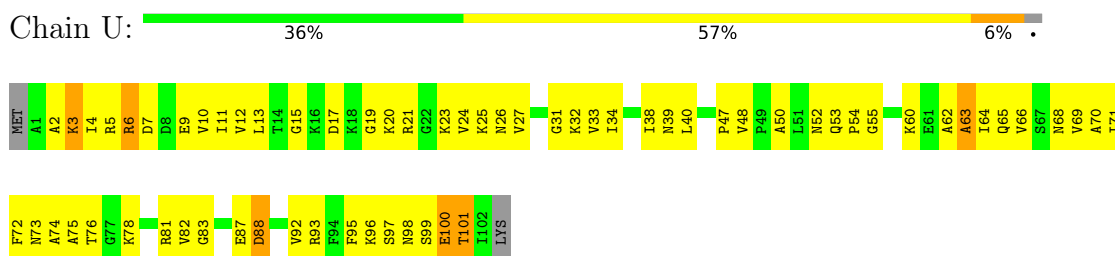
- Molecule 19: 50S ribosomal protein L22



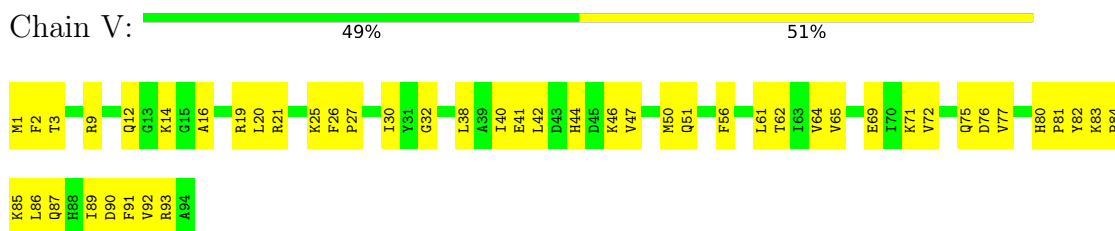
- Molecule 20: 50S ribosomal protein L23



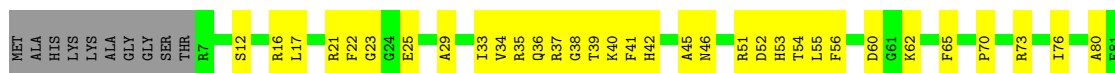
- Molecule 21: 50S ribosomal protein L24



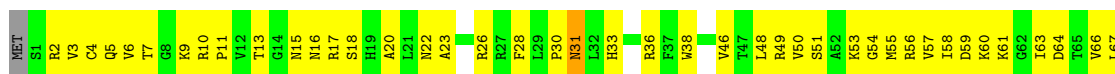
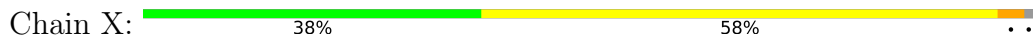
- Molecule 22: 50S ribosomal protein L25



- Molecule 23: 50S ribosomal protein L27



• Molecule 24: 50S ribosomal protein L28



• Molecule 25: 50S ribosomal protein L29



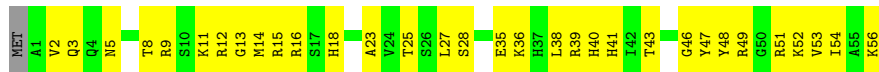
• Molecule 26: 50S ribosomal protein L30



• Molecule 27: 50S ribosomal protein L31



• Molecule 28: 50S ribosomal protein L32



• Molecule 29: 50S ribosomal protein L33

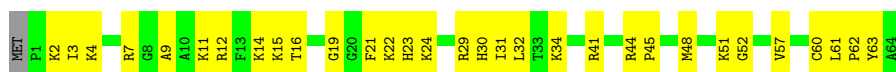




• Molecule 30: 50S ribosomal protein L34



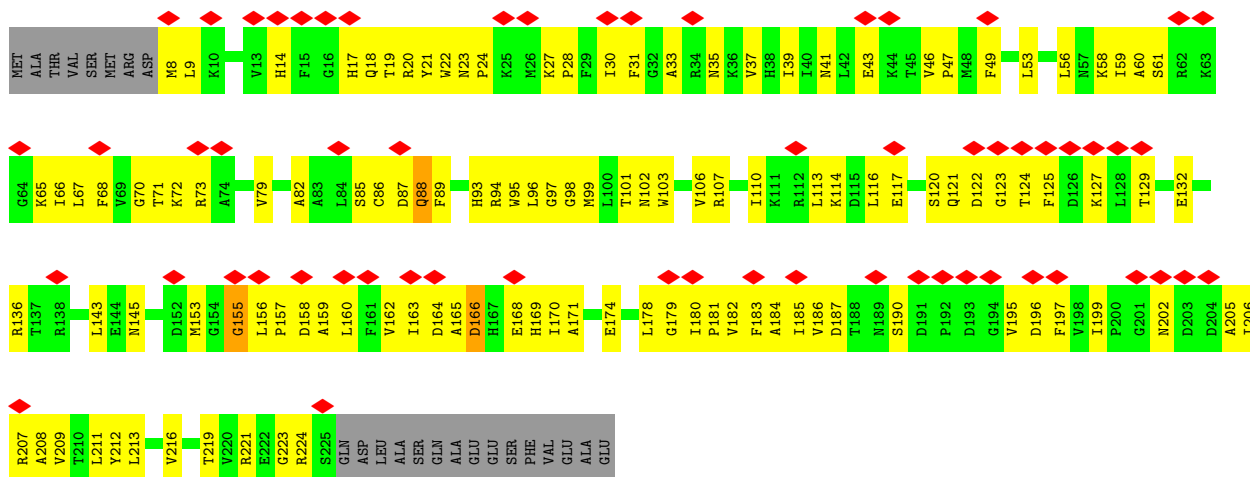
• Molecule 31: 50S ribosomal protein L35



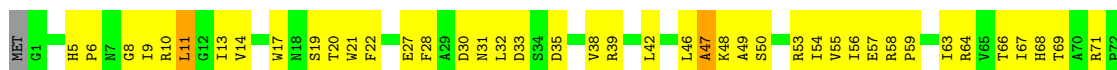
• Molecule 32: 50S ribosomal protein L36



• Molecule 33: 30S ribosomal protein S2

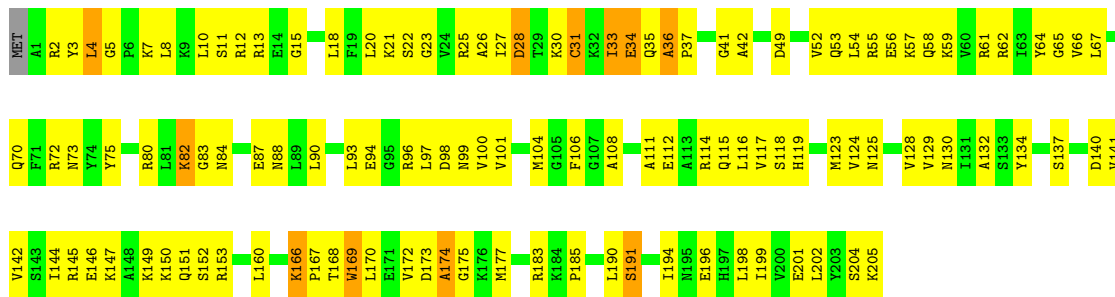


• Molecule 34: 30S ribosomal protein S3

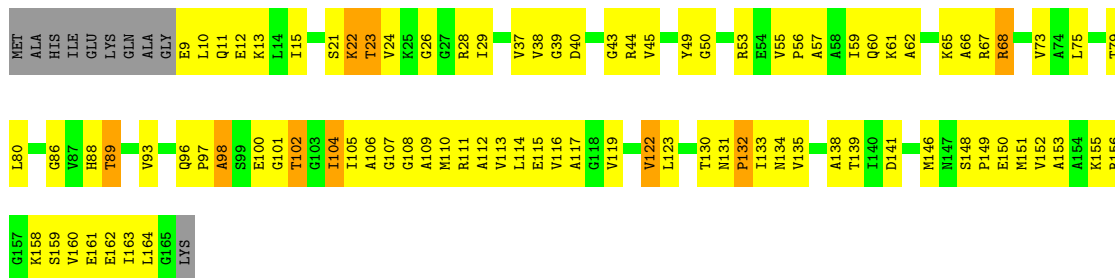




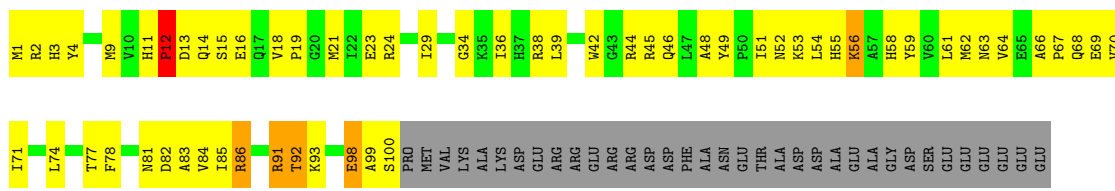
• Molecule 35: 30S ribosomal protein S4



• Molecule 36: 30S ribosomal protein S5

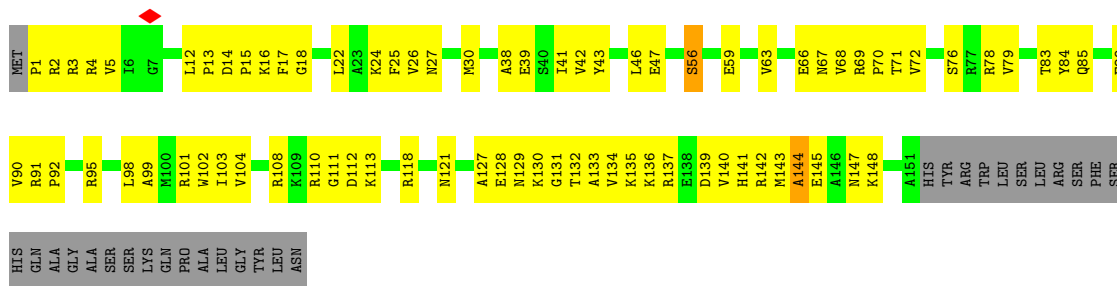


• Molecule 37: 30S ribosomal protein S6

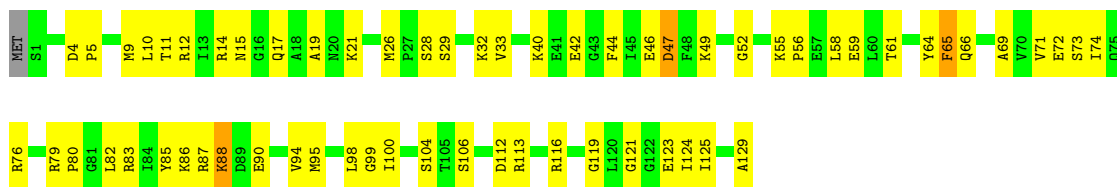


• Molecule 38: 30S ribosomal protein S7

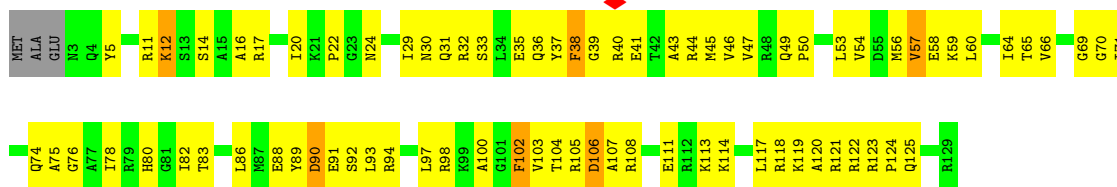




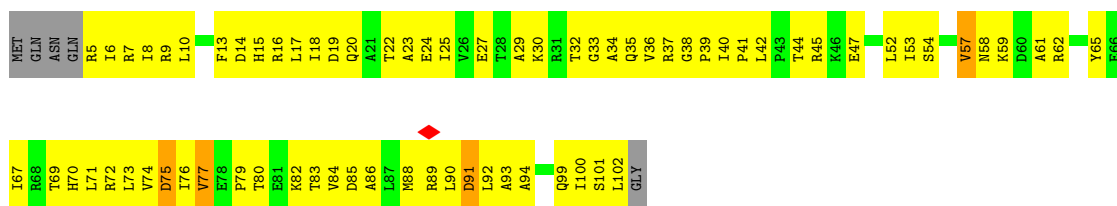
• Molecule 39: 30S ribosomal protein S8



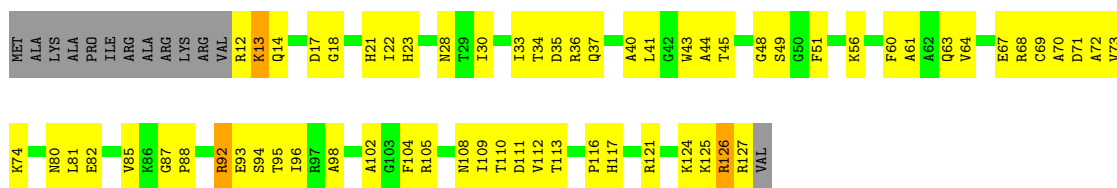
• Molecule 40: 30S ribosomal protein S9



• Molecule 41: 30S ribosomal protein S10

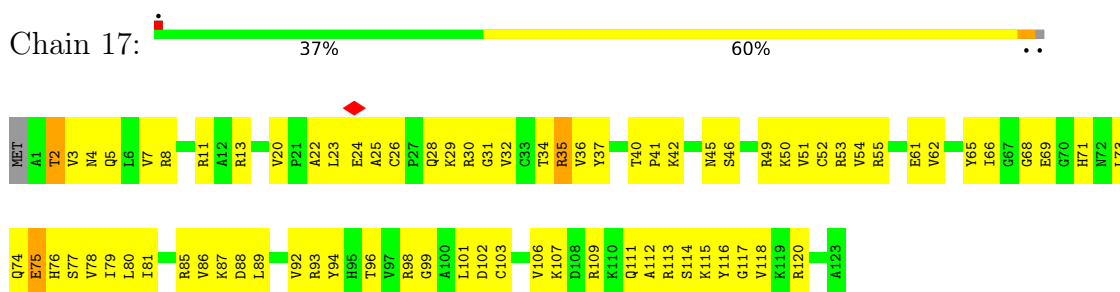


• Molecule 42: 30S ribosomal protein S11

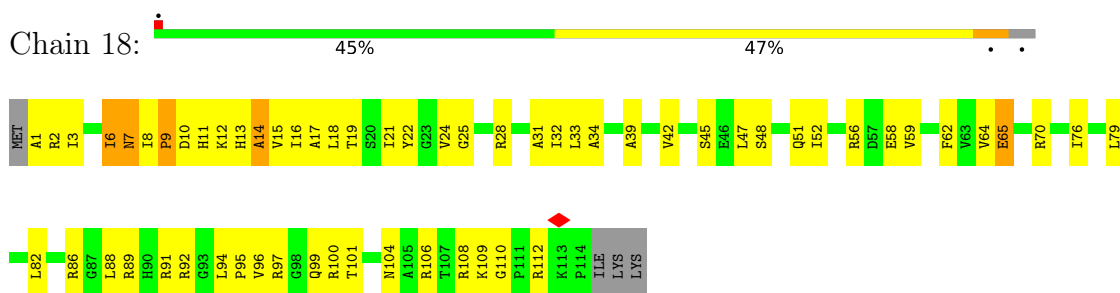




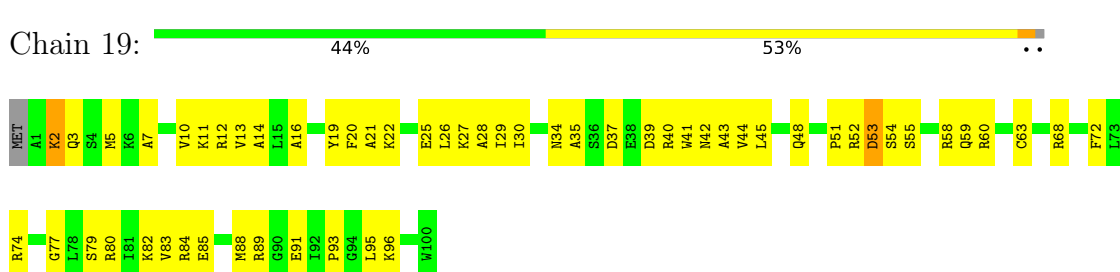
• Molecule 43: 30S ribosomal protein S12



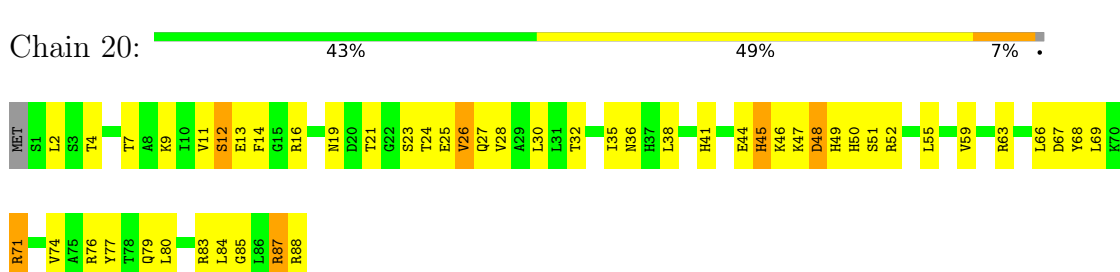
• Molecule 44: 30S ribosomal protein S13



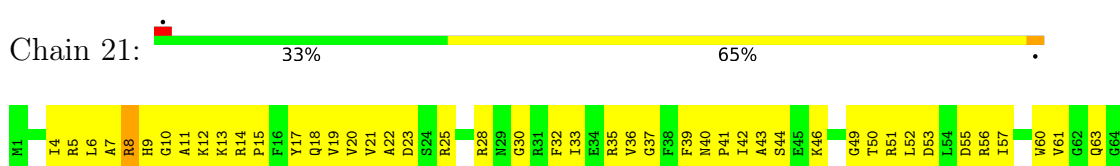
• Molecule 45: 30S ribosomal protein S14



• Molecule 46: 30S ribosomal protein S15



• Molecule 47: 30S ribosomal protein S16

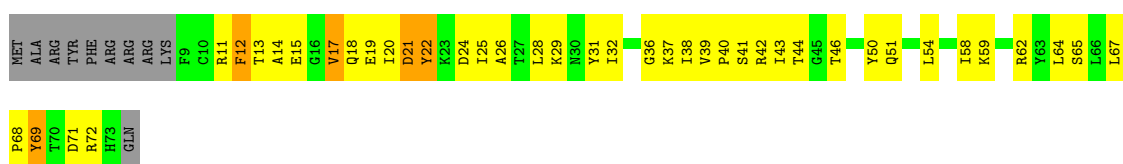




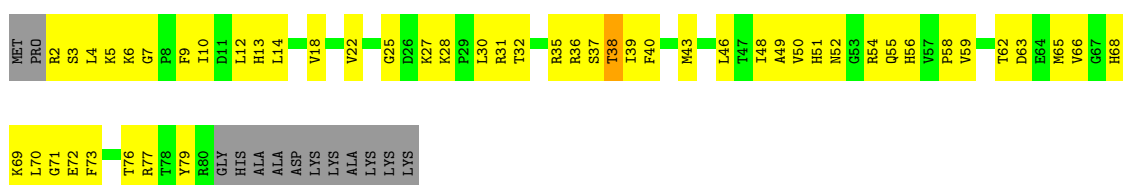
• Molecule 48: 30S ribosomal protein S17



• Molecule 49: 30S ribosomal protein S18



• Molecule 50: 30S ribosomal protein S19



• Molecule 51: 30S ribosomal protein S20

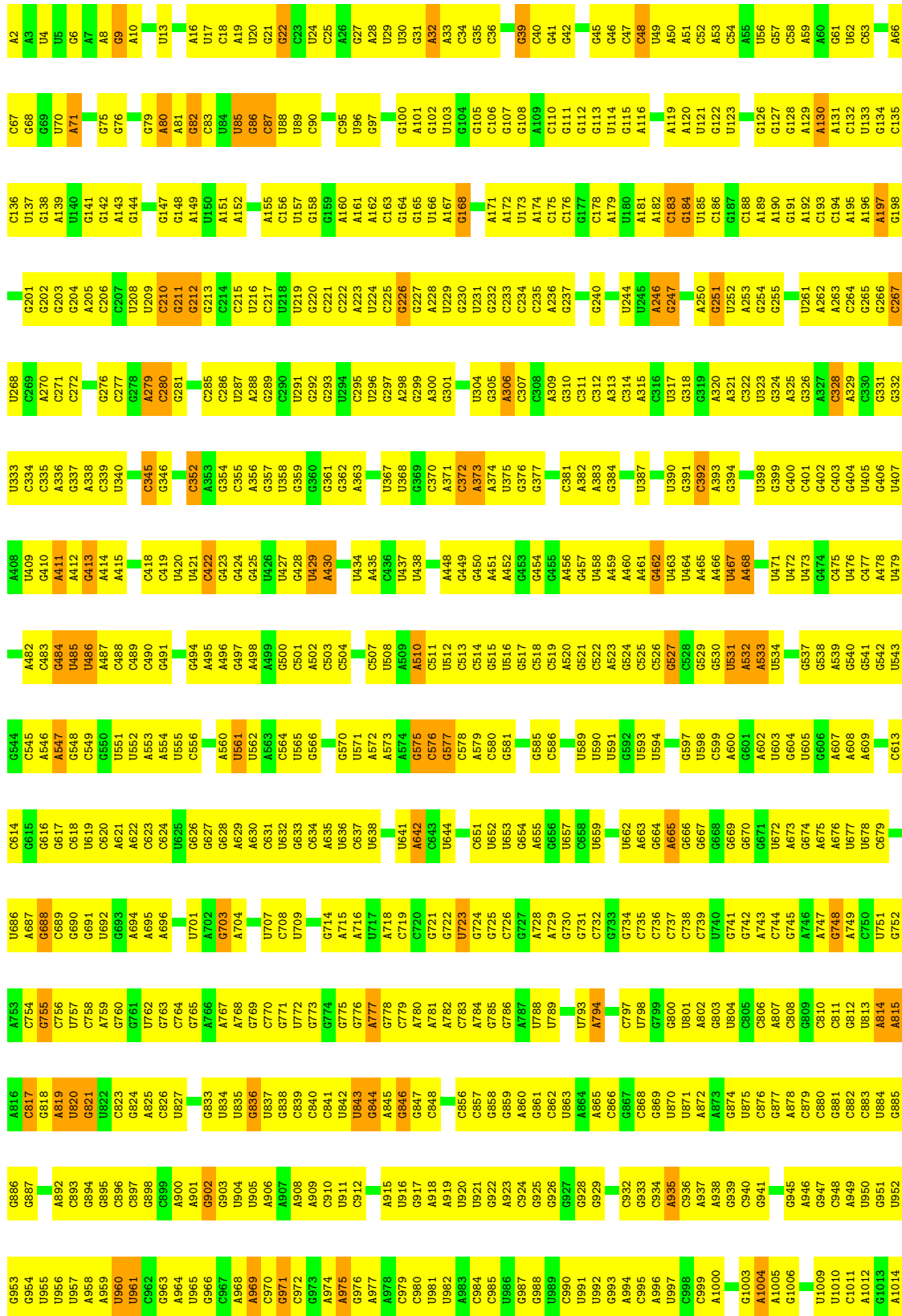


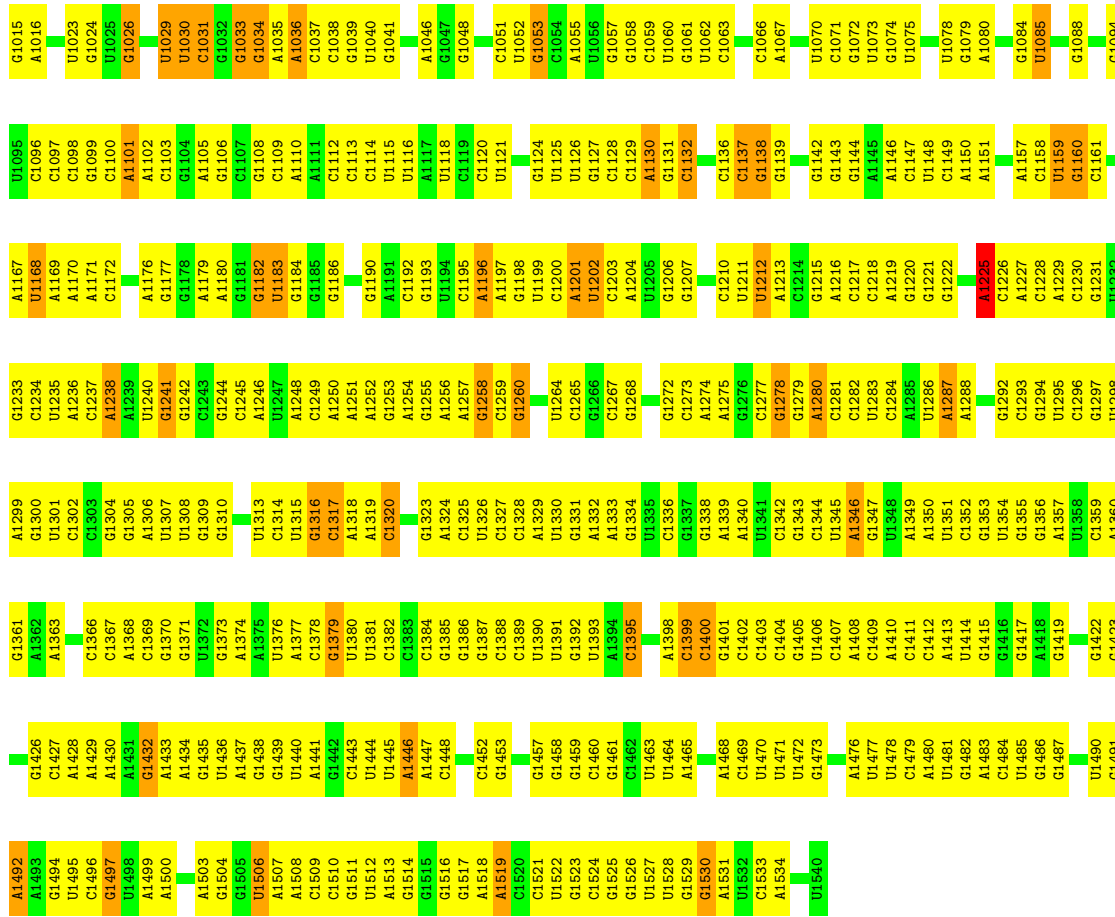
• Molecule 52: 30S ribosomal protein S21



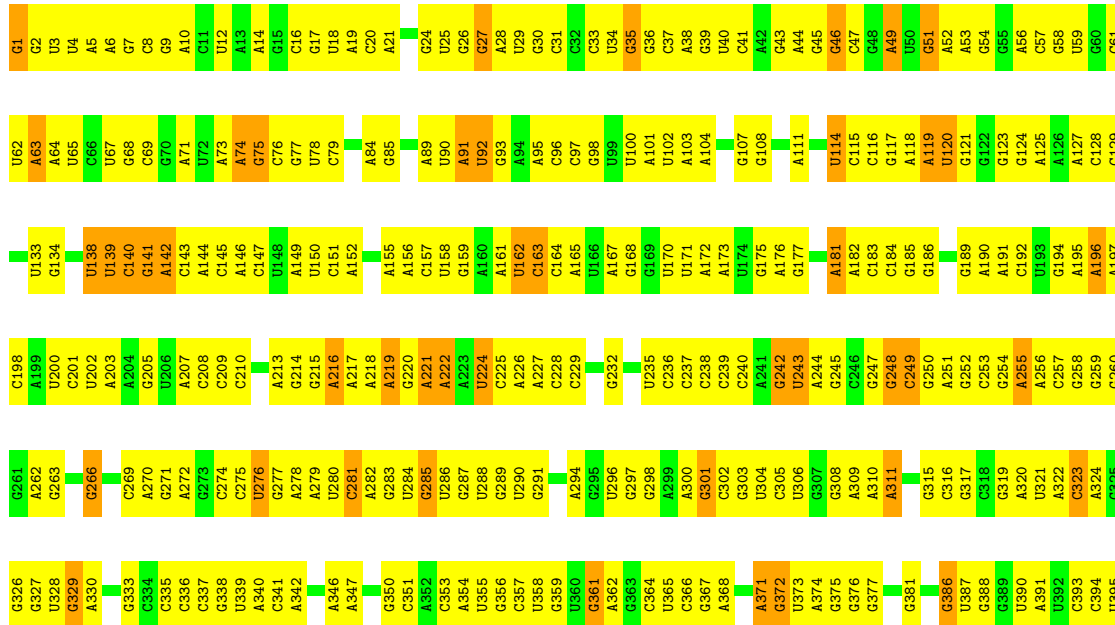
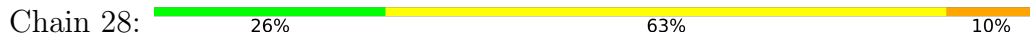
• Molecule 53: 16S ribosomal RNA

Chain 27:  27% 65% 8%



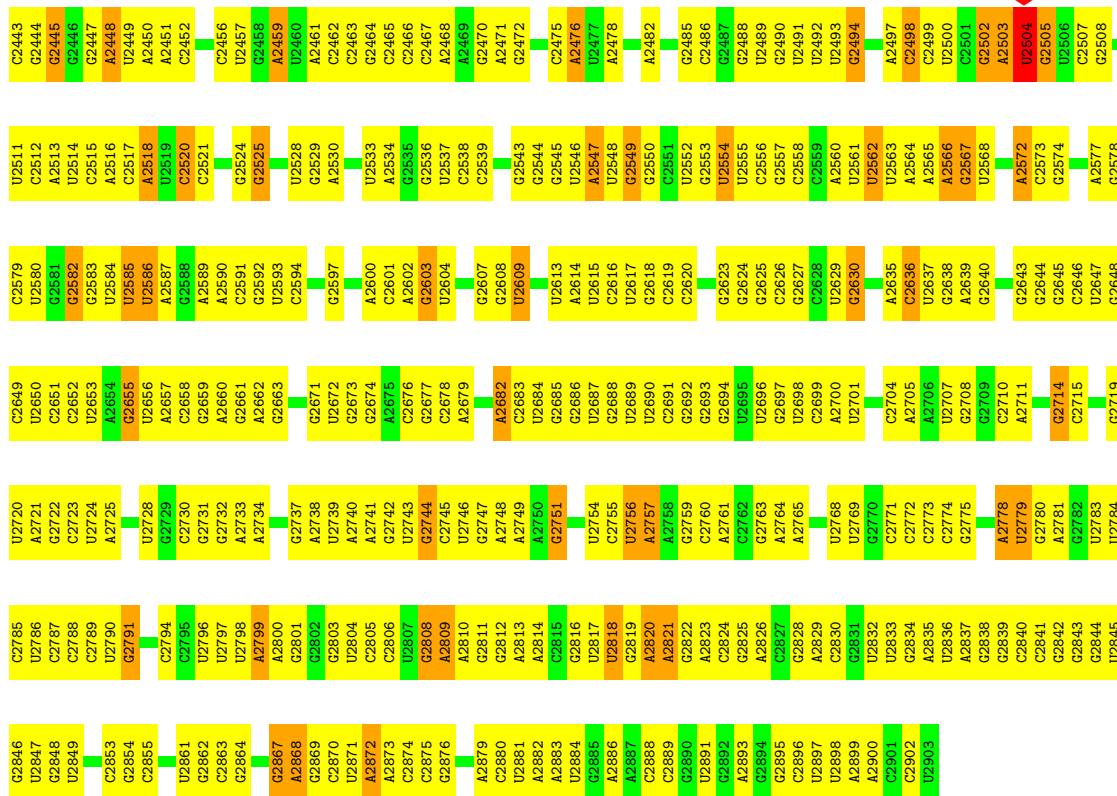


● Molecule 54: 23S ribosomal RNA

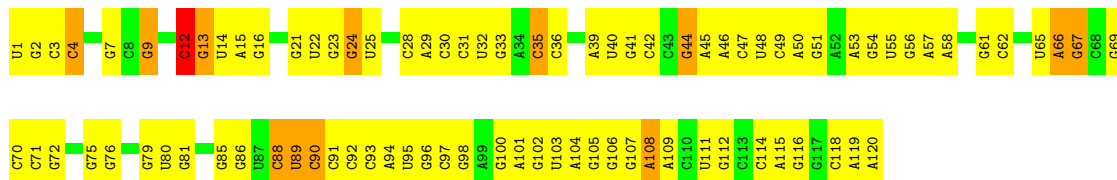
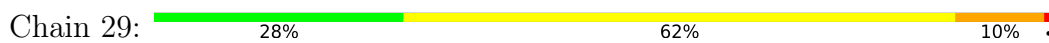


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C1345	C1270	G1202	C1140	A1077	C998	A933	C865	G799	C732	A670	A599	A536	A536	G468	U397
C1351	G1272	A1205	U1141	U1078	U999	U934	A866	A800	G733	C671	G600	C549	C549	G469	U398
A1352	A1278	C1208	A1144	C1079	A1000	C935	C867	U803	C737	C672	C601	C541	C541	A470	G400
A1354	C1279	U1209	A1143	A1080	A936	A936	U868	A804	A738	C673	A603	C542	C542	A471	A401
G1355	G1280	C1210	C1145	U1081	G937	G938	U871	C805	G740	G674	A602	C543	C543	A472	A402
C1357	G1281	U1082	C1146	U1082	G939	G939	U872	C806	U741	A677	U607	C544	C544	A473	U403
C1358	U1282	U1083	A1147	U1083	G940	G940	C873	U807	U741	C678	A608	U545	U545	A474	A404
A1359	G1283	A1213	A1148	A1085	A941	A941	C876	G808	A743	C679	A609	U546	U546	A477	G406
G1360	A1284	A1214	A1149	A1085	A942	A942	C877	G809	A743	C680	C610	U546	U546	A478	G406
A1361	A1285	G1215	A1150	A1086	A943	A943	A877	U810	U744	G681	C611	U548	U548	A479	G409
G1362	A1286	U1087	A1151	G1087	C946	C946	A878	U811	G745	U683	G612	U549	U549	A480	G410
C1363	A1287	A1088	U1082	U1088	A947	A947	C879	C812	U746	U684	A613	C550	C550	G481	G411
C1364	G1288	A1089	C1013	A1089	C948	C948	C883	U813	C747	A685	A614	G551	G551	G488	G411
G1365	G1289	A1010	A1014	A1090	C949	C949	U884	U814	A748	U686	A616	U552	U552	G489	C414
A1366	A1155	U1019	U1019	U1095	G950	G950	C885	C815	A749	C687	G617	U554	U554	C490	A415
A1367	G1157	A1020	A1020	A1096	C951	C951	A886	C817	A752	U688	G620	U556	U556	U416	U416
G1368	C1158	A1021	A1021	A1097	G952	G952	U887	C818	A753	A689	G620	U557	U557	C417	C417
C1369	U1159	G1022	G1022	U1097	G953	G953	C889	U819	U754	G690	A621	U558	U558	G493	C418
C1370	G1160	U1023	U1023	A1098	C954	C954	C890	A820	U755	C691	G622	U558	U558	G494	U419
G1371	G1161	G1024	G1024	A1098	U955	U955	C891	A821	A756	C692	G623	U559	U559	G495	C420
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A1373	G1163	C1026	C1026	C1100	C957	C957	C893	C823	C758	U694	G625	G561	G561	A422	A422
C1376	C1164	A1027	A1027	U1101	U958	U958	C894	U824	G759	G695	A626	U562	U562	A423	A423
A1377	A1165	A1028	A1028	U1102	A959	A959	U894	A825	G760	G696	A627	U563	U563	G500	G424
G1378	G1166	A1029	A1029	A1103	A960	A960	U895	A826	G763	G697	C564	C564	C564	U427	U427
U1379	C1167	A1030	A1030	U1105	C961	C961	A896	U827	U763	G698	A503	A503	A503	A503	A503
A1383	G1168	G1031	G1031	U1106	C962	C962	C897	U828	U764	A699	A504	A504	A504	A504	A504
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A1386	G1171	G1037	G1037	U1109	C965	C965	A900	C831	U767	U702	A507	A507	A507	A507	A507
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U1394	U1174	U1039	U1039	G1111	U968	U968	C902	A834	U770	A705	A510	A510	A510	A510	A510
A1395	A1175	A1040	A1040	G1112	C969	C969	U906	C835	G771	A706	A511	A511	A511	A511	A511
A1396	U1176	C1045	C1045	U1113	U970	U970	A909	C836	G774	A707	A512	A512	A512	A512	A512
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C1398	C1178	G1047	G1047	C1118	A972	A972	A911	U839	G776	U709	A514	A514	A514	A514	A514
G1401	U1179	A1048	A1048	U1119	A973	A973	C912	C840	G777	U710	A515	A515	A515	A515	A515
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A1403	U1181	U1053	U1053	C1121	A975	A975	C914	C842	U779	A644	A517	A517	A517	A517	A517
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U1405	U1183	U1055	U1055	C1123	A979	A979	C916	C844	U781	U714	A519	A519	A519	A519	A519
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U1407	U1185	A1057	A1057	C1125	A981	A981	C918	C846	A783	A716	A521	A521	A521	A521	A521
G1408	G1186	U1058	U1058	G1126	A982	A982	C919	C847	A784	A717	A522	A522	A522	A522	A522
U1409	U1187	A1059	A1059	A1127	A983	A983	C920	C848	G785	C719	A523	A523	A523	A523	A523
U1410	G1188	U1060	U1060	C1128	A984	A984	C921	C849	U786	U720	A524	A524	A524	A524	A524
U1411	A1189	C1061	C1061	G1129	C985	C985	C922	C853	C787	A721	A525	A525	A525	A525	A525
U1412	G1190	U1062	U1062	U1130	C986	C986	C923	C854	A788	A722	A526	A526	A526	A526	A526
G1413	U1191	G1063	G1063	C1131	A987	A987	C924	C855	A789	C723	A527	A527	A527	A527	A527
A1414	C1195	C1064	C1064	U1132	A988	A988	C925	C856	U790	U724	A528	A528	A528	A528	A528
A1415	G1196	A1133	A1133	A1133	A989	A989	C926	C857	C791	G725	A529	A529	A529	A529	A529
U1416	G1197	A1134	A1134	A1134	A990	A990	A927	C858	A794	G726	A530	A530	A530	A530	A530
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A1418	U1199	U1137	U1137	U1136	C991	C991	A929	C860	A795	A728	A532	A532	A532	A532	A532
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U1433	U1213	U1151	U1151	U1149	C1006	C1006	A944	C875	C810	A743	A547	A547	A547	A547	A547
U1434	U1214	U1152	U1152	U1150	C1007	C1007	A945	C876	C811	A744	A548	A548	A548	A548	A548
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U1437	U1217	U1155	U1155	U1153	C1010	C1010	A948	C879	C814	A747	A551	A551	A551	A551	A551
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U1443	U1223	U1161	U1161	U1159	C1016	C1016	A954	C885	C820	A753	A557	A557	A557	A557	A557
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U1447	U1227	U1165	U1165	U1163	C1020	C1020	A958	C889	C824	A757	A561	A561	A561	A561	A561
U1448	U1228	U1166	U1166	U1164	C1021	C1021	A959	C890	C825	A758	A562	A562	A562	A562</	





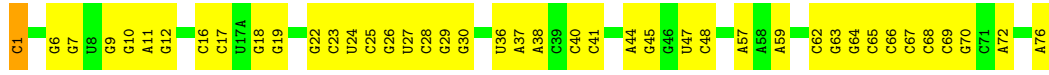
• Molecule 55: 5S ribosomal RNA



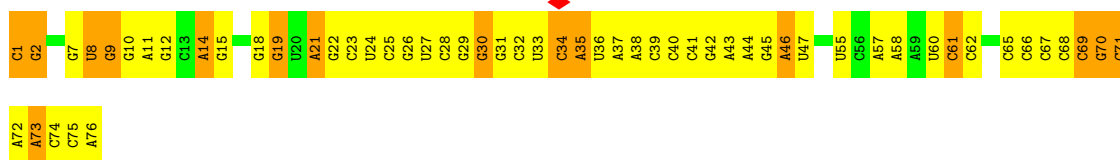
• Molecule 56: mRNA



• Molecule 57: P site tRNA<sup>fmet</sup>



• Molecule 58: E-site tRNA<sup>fMet</sup>





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76158	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	0.465	Depositor
Minimum map value	-0.124	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.08	Depositor
Map size ( $\text{\AA}$ )	393.6, 393.6, 393.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.82, 0.82, 0.82	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.63	1/1115 (0.1%)	0.83	1/1510 (0.1%)
2	B	0.38	0/2121	0.71	0/2852
3	C	0.39	0/1586	0.69	1/2134 (0.0%)
4	D	0.44	0/1571	0.71	1/2113 (0.0%)
5	E	0.40	0/1434	0.64	0/1926
6	F	0.38	0/1343	0.67	1/1816 (0.1%)
7	G	0.49	0/1122	0.73	0/1515
8	H	0.60	0/1001	0.75	0/1350
9	I	0.60	0/1046	0.86	2/1410 (0.1%)
10	J	0.40	0/1152	0.64	0/1551
11	K	0.35	0/947	0.63	0/1268
12	L	0.36	0/1054	0.68	0/1403
13	M	0.39	0/1093	0.64	0/1460
14	N	0.37	0/973	0.62	0/1301
15	O	0.36	0/902	0.59	0/1209
16	P	0.37	0/929	0.67	1/1242 (0.1%)
17	Q	0.42	0/960	0.57	0/1278
18	R	0.41	0/829	0.70	1/1107 (0.1%)
19	S	0.34	0/864	0.60	0/1156
20	T	0.36	0/744	0.63	0/994
21	U	0.37	0/787	0.69	0/1051
22	V	0.40	0/766	0.61	0/1025
23	W	0.40	0/582	0.65	0/769
24	X	0.38	0/635	0.62	0/848
25	Y	0.40	0/510	0.60	0/677
26	Z	0.35	0/453	0.61	0/605
27	1	0.55	0/531	0.81	0/709
28	2	0.34	0/450	0.66	0/599
29	3	0.41	0/416	0.65	0/554
30	4	0.42	0/380	0.67	0/498
31	5	0.38	0/513	0.62	0/676
32	6	0.53	0/303	0.91	2/397 (0.5%)
33	7	0.46	0/1735	0.64	0/2338
34	8	0.39	0/1651	0.62	0/2225

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	9	0.37	0/1665	0.63	0/2227
36	10	0.36	0/1169	0.67	1/1573 (0.1%)
37	11	0.39	0/835	0.70	0/1128
38	12	0.35	0/1195	0.59	0/1602
39	13	0.35	0/989	0.66	0/1326
40	14	0.37	0/1034	0.64	0/1375
41	15	0.38	0/796	0.67	0/1077
42	16	0.38	0/885	0.71	0/1195
43	17	0.38	0/969	0.66	1/1300 (0.1%)
44	18	0.39	0/892	0.66	0/1193
45	19	0.38	0/817	0.57	0/1088
46	20	0.34	0/722	0.61	0/964
47	21	0.39	0/659	0.62	0/884
48	22	0.36	0/657	0.67	0/881
49	23	0.42	0/544	0.66	0/731
50	24	0.48	0/652	0.70	0/877
51	25	0.37	0/671	0.52	0/888
52	26	0.45	0/550	0.64	0/728
53	27	0.46	1/36967 (0.0%)	0.67	1/57666 (0.0%)
54	28	0.49	1/69801 (0.0%)	0.67	5/108894 (0.0%)
55	29	0.40	1/2876 (0.0%)	0.66	0/4483
56	30	0.62	0/436	0.69	0/679
57	31	0.45	1/1836 (0.1%)	0.66	0/2859
58	32	0.71	1/1835 (0.1%)	0.68	0/2857
All	All	0.46	6/161950 (0.0%)	0.67	18/242041 (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
53	27	0	6
54	28	0	9
55	29	0	1
All	All	0	16

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	29	1	U	OP3-P	-6.99	1.52	1.61
53	27	2	A	OP3-P	-6.92	1.52	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	31	1	C	OP3-P	-6.89	1.52	1.61
54	28	1	G	OP3-P	-6.88	1.52	1.61
58	32	1	C	OP3-P	-6.86	1.52	1.61

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	28	2504	U	N1-C1'-C2'	7.12	123.26	114.00
32	6	19	ARG	NE-CZ-NH1	-6.43	117.09	120.30
43	17	115	LYS	N-CA-C	-5.96	94.89	111.00
1	A	678	GLY	N-CA-C	5.72	127.41	113.10
16	P	113	LEU	CA-CB-CG	5.67	128.34	115.30

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	27	80	A	Sidechain
53	27	82	G	Sidechain
53	27	820	U	Sidechain
53	27	898	G	Sidechain
53	27	938	A	Sidechain

## 5.2 Too-close contacts

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	1103	0	1130	102	0
2	B	2082	0	2157	138	0
3	C	1565	0	1616	96	0
4	D	1552	0	1619	118	0
5	E	1410	0	1447	121	0
6	F	1323	0	1374	92	0
7	G	1111	0	1148	84	0
8	H	988	0	1025	127	0
9	I	1032	0	1088	128	0
10	J	1129	0	1162	70	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	938	0	1012	68	0
12	L	1045	0	1117	73	0
13	M	1074	0	1157	47	0
14	N	960	0	1000	52	0
15	O	892	0	923	57	0
16	P	917	0	965	80	0
17	Q	947	0	1022	71	0
18	R	816	0	839	60	0
19	S	857	0	922	53	0
20	T	738	0	807	39	0
21	U	779	0	834	64	0
22	V	753	0	780	37	0
23	W	575	0	592	33	0
24	X	625	0	655	44	0
25	Y	509	0	543	38	0
26	Z	449	0	491	25	0
27	1	522	0	521	47	0
28	2	444	0	461	40	0
29	3	409	0	440	14	0
30	4	377	0	418	29	0
31	5	504	0	574	27	0
32	6	302	0	343	26	0
33	7	1704	0	1732	104	0
34	8	1624	0	1699	99	0
35	9	1643	0	1710	121	0
36	10	1156	0	1199	90	0
37	11	817	0	808	71	0
38	12	1181	0	1240	79	0
39	13	979	0	1034	64	0
40	14	1022	0	1070	98	0
41	15	786	0	828	81	0
42	16	869	0	878	67	0
43	17	955	0	1019	100	0
44	18	883	0	944	73	0
45	19	805	0	847	58	0
46	20	714	0	737	46	0
47	21	649	0	666	59	0
48	22	648	0	691	55	0
49	23	535	0	552	44	0
50	24	637	0	665	72	0
51	25	665	0	714	46	0
52	26	544	0	579	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	27	33016	0	16617	1316	0
54	28	62322	0	31345	2457	0
55	29	2572	0	1302	116	0
56	30	388	0	196	10	0
57	31	1644	0	836	31	0
58	32	1643	0	836	66	0
All	All	149128	0	100926	6677	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

The worst 5 of 6677 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)
9:I:7:TYR:HA	9:I:58:ILE:O	1.26	1.26
22:V:75:GLN:HB3	22:V:90:ASP:O	1.47	1.13
9:I:90:GLY:HA2	54:28:1064:C:H1'	1.26	1.13
9:I:133:ARG:NH1	54:28:1079:C:H4'	1.63	1.12
53:27:1259:C:H3'	53:27:1260:G:H5''	1.31	1.11

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	139/750 (18%)	106 (76%)	21 (15%)	12 (9%)	1	13
2	B	269/273 (98%)	227 (84%)	31 (12%)	11 (4%)	3	27
3	C	207/209 (99%)	183 (88%)	17 (8%)	7 (3%)	3	31
4	D	199/201 (99%)	162 (81%)	28 (14%)	9 (4%)	2	25
5	E	175/179 (98%)	140 (80%)	31 (18%)	4 (2%)	6	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	174/177 (98%)	145 (83%)	27 (16%)	2 (1%)	14	51
7	G	147/149 (99%)	115 (78%)	23 (16%)	9 (6%)	1	20
8	H	129/165 (78%)	85 (66%)	29 (22%)	15 (12%)	0	6
9	I	139/142 (98%)	112 (81%)	21 (15%)	6 (4%)	2	26
10	J	140/142 (99%)	123 (88%)	13 (9%)	4 (3%)	4	33
11	K	120/123 (98%)	102 (85%)	12 (10%)	6 (5%)	2	23
12	L	141/144 (98%)	110 (78%)	25 (18%)	6 (4%)	2	26
13	M	134/136 (98%)	115 (86%)	16 (12%)	3 (2%)	6	38
14	N	118/127 (93%)	96 (81%)	18 (15%)	4 (3%)	3	31
15	O	114/117 (97%)	100 (88%)	10 (9%)	4 (4%)	3	30
16	P	112/115 (97%)	99 (88%)	11 (10%)	2 (2%)	8	42
17	Q	115/118 (98%)	105 (91%)	10 (9%)	0	100	100
18	R	101/103 (98%)	84 (83%)	13 (13%)	4 (4%)	3	27
19	S	108/110 (98%)	95 (88%)	8 (7%)	5 (5%)	2	25
20	T	91/100 (91%)	77 (85%)	8 (9%)	6 (7%)	1	19
21	U	100/104 (96%)	83 (83%)	8 (8%)	9 (9%)	1	13
22	V	92/94 (98%)	79 (86%)	12 (13%)	1 (1%)	14	51
23	W	73/85 (86%)	66 (90%)	6 (8%)	1 (1%)	11	46
24	X	75/78 (96%)	67 (89%)	5 (7%)	3 (4%)	3	27
25	Y	61/63 (97%)	53 (87%)	5 (8%)	3 (5%)	2	24
26	Z	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	8	42
27	1	64/70 (91%)	48 (75%)	10 (16%)	6 (9%)	0	12
28	2	54/57 (95%)	46 (85%)	7 (13%)	1 (2%)	8	41
29	3	48/55 (87%)	45 (94%)	2 (4%)	1 (2%)	7	39
30	4	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
31	5	62/65 (95%)	54 (87%)	6 (10%)	2 (3%)	4	32
32	6	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	5	34
33	7	216/241 (90%)	170 (79%)	36 (17%)	10 (5%)	2	25
34	8	204/233 (88%)	179 (88%)	20 (10%)	5 (2%)	5	36
35	9	203/206 (98%)	167 (82%)	22 (11%)	14 (7%)	1	17
36	10	155/167 (93%)	117 (76%)	26 (17%)	12 (8%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	11	98/135 (73%)	77 (79%)	13 (13%)	8 (8%)	1	14
38	12	149/179 (83%)	127 (85%)	18 (12%)	4 (3%)	5	35
39	13	127/130 (98%)	116 (91%)	8 (6%)	3 (2%)	6	37
40	14	125/130 (96%)	105 (84%)	10 (8%)	10 (8%)	1	15
41	15	96/103 (93%)	75 (78%)	16 (17%)	5 (5%)	2	23
42	16	114/129 (88%)	95 (83%)	13 (11%)	6 (5%)	2	22
43	17	121/124 (98%)	91 (75%)	24 (20%)	6 (5%)	2	23
44	18	112/118 (95%)	98 (88%)	8 (7%)	6 (5%)	2	22
45	19	98/101 (97%)	80 (82%)	13 (13%)	5 (5%)	2	23
46	20	86/89 (97%)	62 (72%)	14 (16%)	10 (12%)	0	6
47	21	80/82 (98%)	64 (80%)	11 (14%)	5 (6%)	1	19
48	22	78/84 (93%)	60 (77%)	13 (17%)	5 (6%)	1	19
49	23	63/75 (84%)	52 (82%)	6 (10%)	5 (8%)	1	15
50	24	77/92 (84%)	64 (83%)	11 (14%)	2 (3%)	5	35
51	25	83/87 (95%)	77 (93%)	6 (7%)	0	100	100
52	26	63/71 (89%)	39 (62%)	15 (24%)	9 (14%)	0	4
All	All	5985/6970 (86%)	4958 (83%)	749 (12%)	278 (5%)	4	25

5 of 278 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	599	VAL
1	A	666	SER
1	A	677	SER
1	A	702	ASP
2	B	107	LYS

### 5.3.2 Protein sidechains [i](#)

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

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



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	121/635 (19%)	121 (100%)	0	100	100
2	B	216/218 (99%)	216 (100%)	0	100	100
3	C	164/164 (100%)	164 (100%)	0	100	100
4	D	165/165 (100%)	165 (100%)	0	100	100
5	E	148/150 (99%)	147 (99%)	1 (1%)	84	90
6	F	137/138 (99%)	136 (99%)	1 (1%)	84	90
7	G	114/114 (100%)	114 (100%)	0	100	100
8	H	100/123 (81%)	100 (100%)	0	100	100
9	I	109/110 (99%)	109 (100%)	0	100	100
10	J	116/116 (100%)	116 (100%)	0	100	100
11	K	103/104 (99%)	102 (99%)	1 (1%)	76	86
12	L	102/103 (99%)	102 (100%)	0	100	100
13	M	109/109 (100%)	109 (100%)	0	100	100
14	N	100/103 (97%)	100 (100%)	0	100	100
15	O	86/87 (99%)	86 (100%)	0	100	100
16	P	99/100 (99%)	98 (99%)	1 (1%)	76	86
17	Q	89/90 (99%)	89 (100%)	0	100	100
18	R	84/84 (100%)	84 (100%)	0	100	100
19	S	93/93 (100%)	93 (100%)	0	100	100
20	T	80/84 (95%)	80 (100%)	0	100	100
21	U	83/85 (98%)	83 (100%)	0	100	100
22	V	78/78 (100%)	78 (100%)	0	100	100
23	W	57/63 (90%)	57 (100%)	0	100	100
24	X	67/68 (98%)	67 (100%)	0	100	100
25	Y	55/55 (100%)	55 (100%)	0	100	100
26	Z	48/49 (98%)	48 (100%)	0	100	100
27	1	59/62 (95%)	58 (98%)	1 (2%)	60	78
28	2	47/48 (98%)	47 (100%)	0	100	100
29	3	45/49 (92%)	45 (100%)	0	100	100
30	4	38/38 (100%)	38 (100%)	0	100	100
31	5	51/52 (98%)	51 (100%)	0	100	100
32	6	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	7	180/199 (90%)	180 (100%)	0	100	100
34	8	170/190 (90%)	170 (100%)	0	100	100
35	9	172/173 (99%)	172 (100%)	0	100	100
36	10	119/126 (94%)	119 (100%)	0	100	100
37	11	87/116 (75%)	86 (99%)	1 (1%)	73	84
38	12	124/147 (84%)	124 (100%)	0	100	100
39	13	104/105 (99%)	104 (100%)	0	100	100
40	14	105/107 (98%)	105 (100%)	0	100	100
41	15	86/90 (96%)	86 (100%)	0	100	100
42	16	89/99 (90%)	89 (100%)	0	100	100
43	17	103/104 (99%)	103 (100%)	0	100	100
44	18	92/96 (96%)	92 (100%)	0	100	100
45	19	83/84 (99%)	83 (100%)	0	100	100
46	20	76/77 (99%)	76 (100%)	0	100	100
47	21	65/65 (100%)	65 (100%)	0	100	100
48	22	74/78 (95%)	74 (100%)	0	100	100
49	23	56/65 (86%)	56 (100%)	0	100	100
50	24	70/79 (89%)	70 (100%)	0	100	100
51	25	65/66 (98%)	65 (100%)	0	100	100
52	26	55/61 (90%)	55 (100%)	0	100	100
All	All	4972/5698 (87%)	4966 (100%)	6 (0%)	93	97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	P	113	LEU
27	1	37	CYS
37	11	12	PRO
6	F	117	PRO
5	E	174	PHE

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

Mol	Chain	Res	Type
33	7	189	ASN
40	14	4	GLN
35	9	73	ASN
37	11	63	ASN
42	16	80	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	27	1538/1539 (99%)	171 (11%)	7 (0%)
54	28	2902/2903 (99%)	386 (13%)	20 (0%)
55	29	119/120 (99%)	12 (10%)	3 (2%)
56	30	17/18 (94%)	3 (17%)	0
57	31	76/77 (98%)	5 (6%)	0
58	32	76/77 (98%)	17 (22%)	0
All	All	4728/4734 (99%)	594 (12%)	30 (0%)

5 of 594 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	27	4	U
53	27	6	G
53	27	9	G
53	27	13	U
53	27	22	G

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	28	1378	A
55	29	44	G
54	28	1730	C
55	29	88	C
54	28	2566	A

## 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 monosaccharides 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.

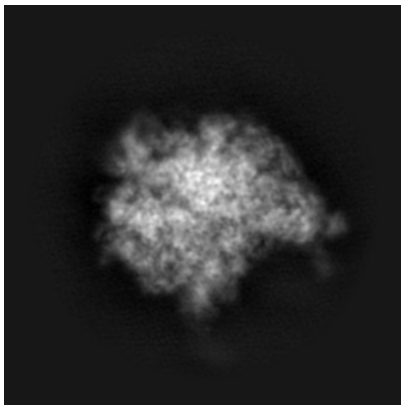
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8279. These allow visual inspection of the internal detail of the map and identification of artifacts.

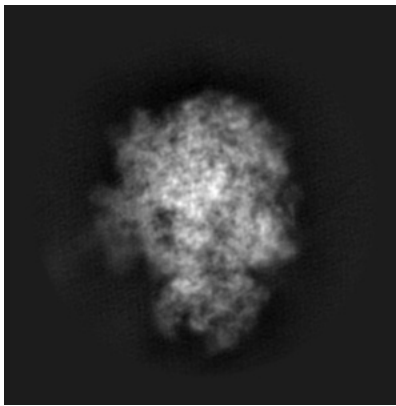
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

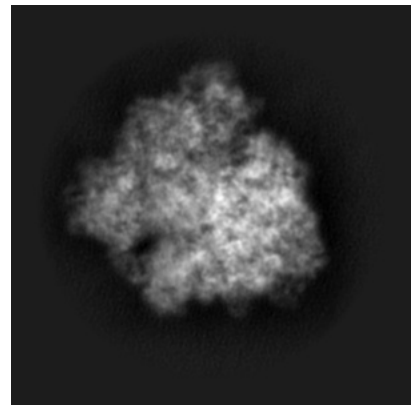
#### 6.1.1 Primary map



X

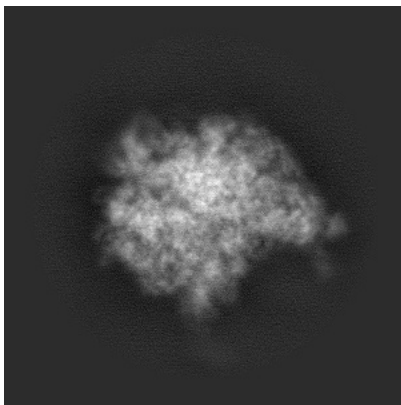


Y

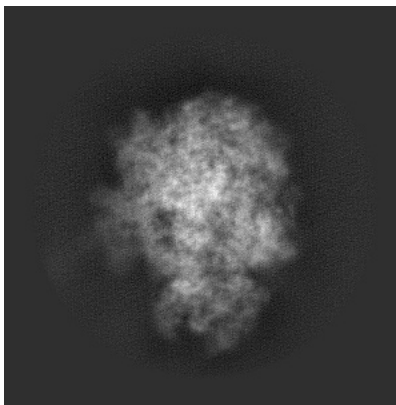


Z

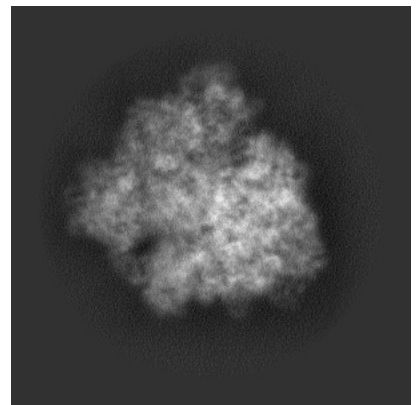
#### 6.1.2 Raw map



X



Y

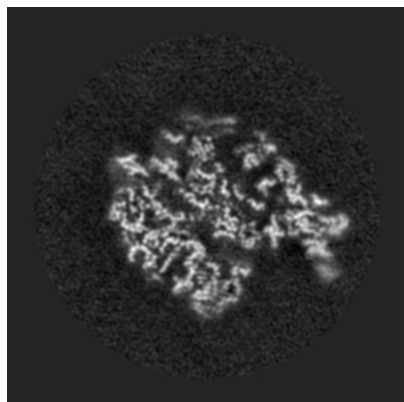


Z

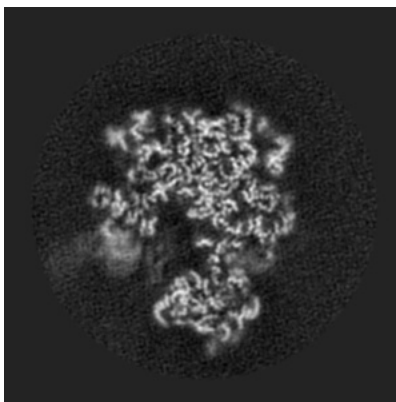
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

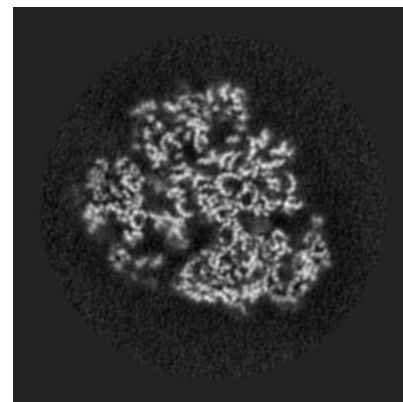
### 6.2.1 Primary map



X Index: 240

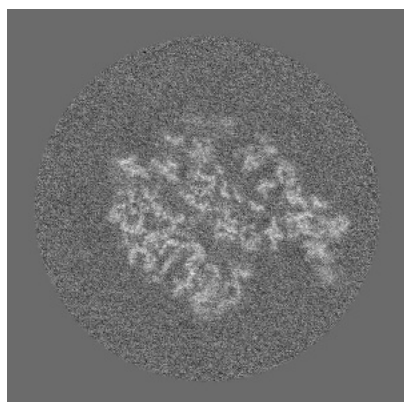


Y Index: 240

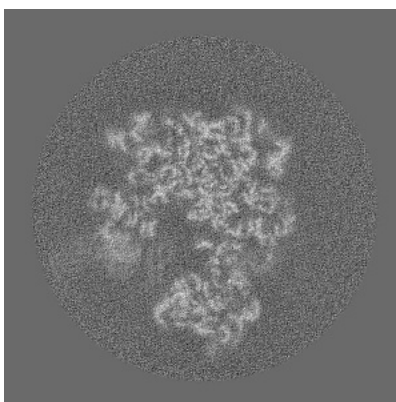


Z Index: 240

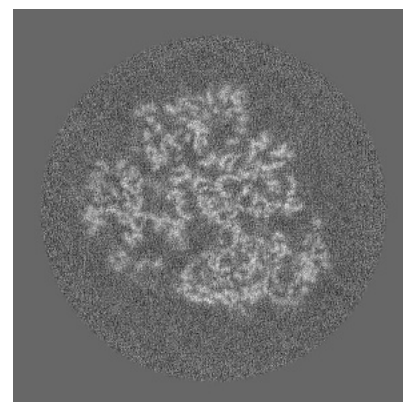
### 6.2.2 Raw map



X Index: 240



Y Index: 240

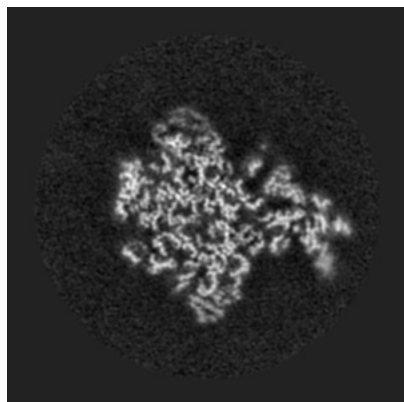


Z Index: 240

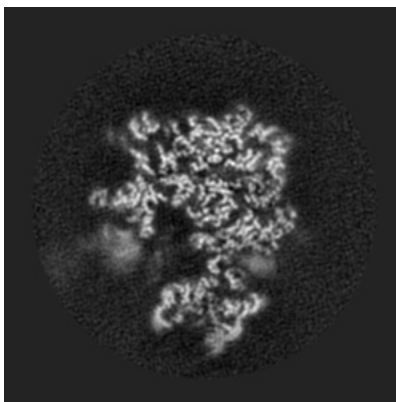
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

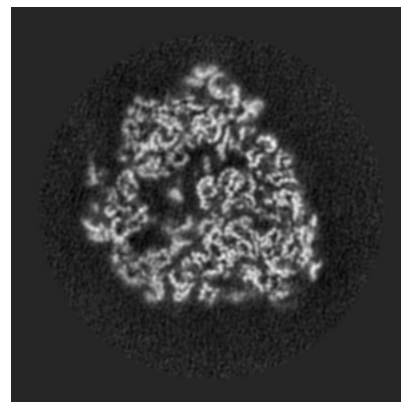
### 6.3.1 Primary map



X Index: 249

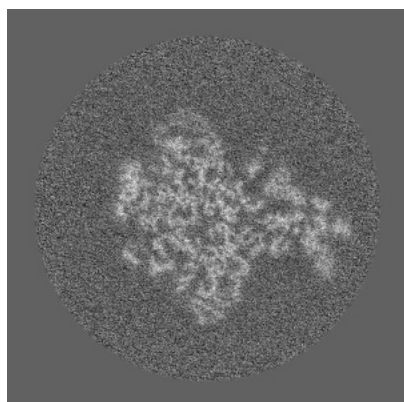


Y Index: 247

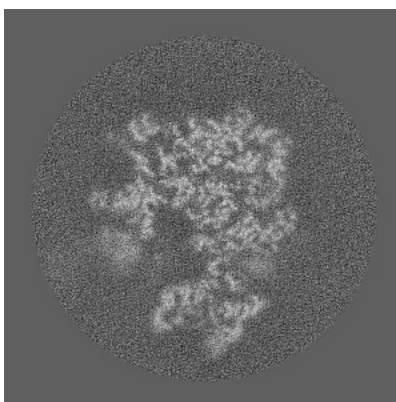


Z Index: 225

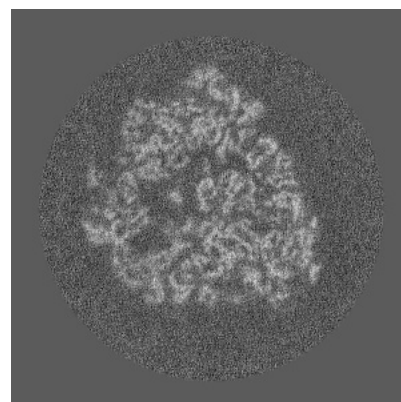
### 6.3.2 Raw map



X Index: 249



Y Index: 247



Z Index: 225

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



## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



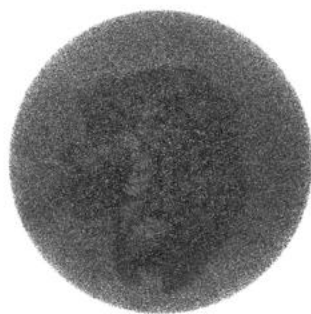
Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

## 6.5 Mask visualisation [i](#)

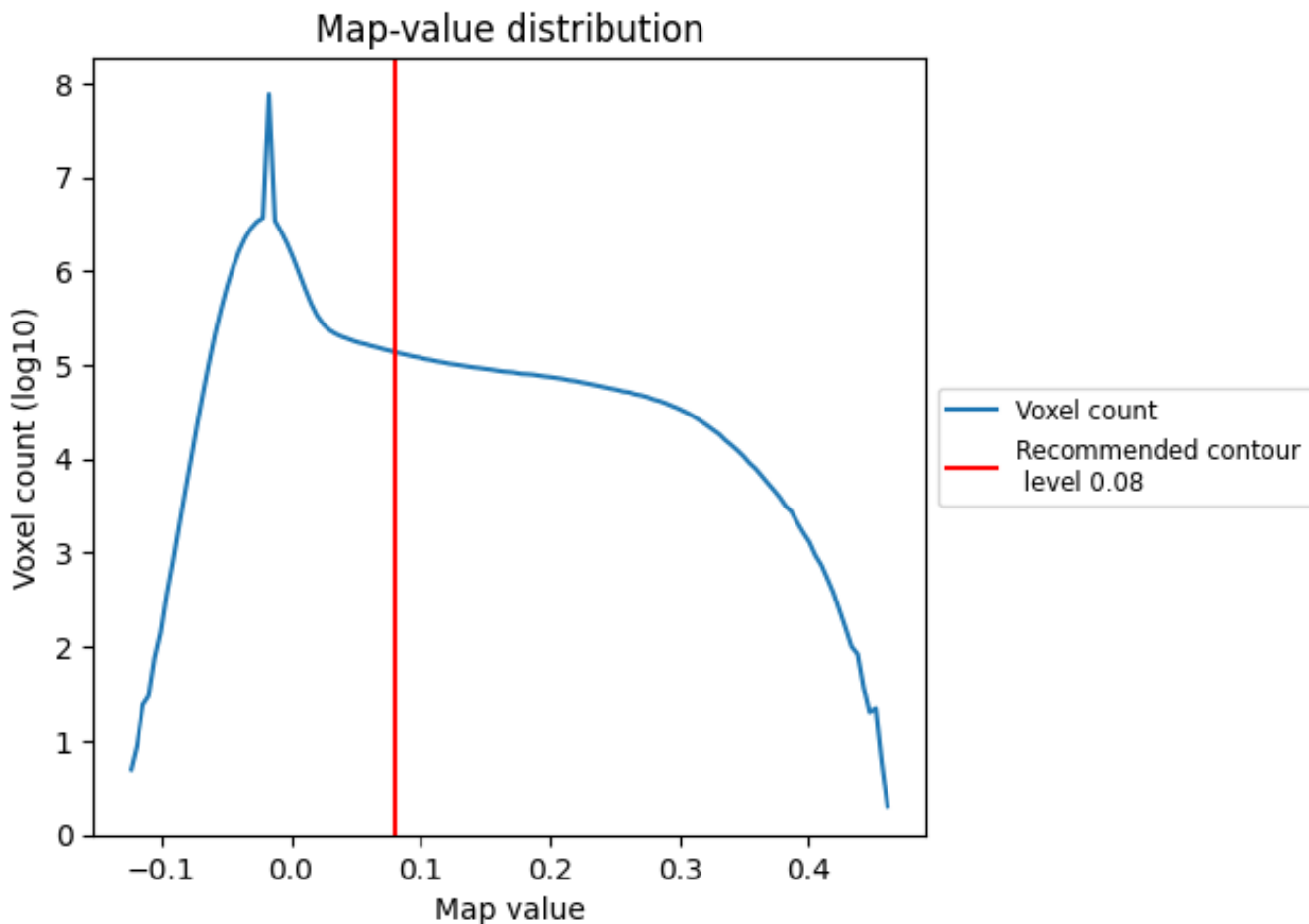
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

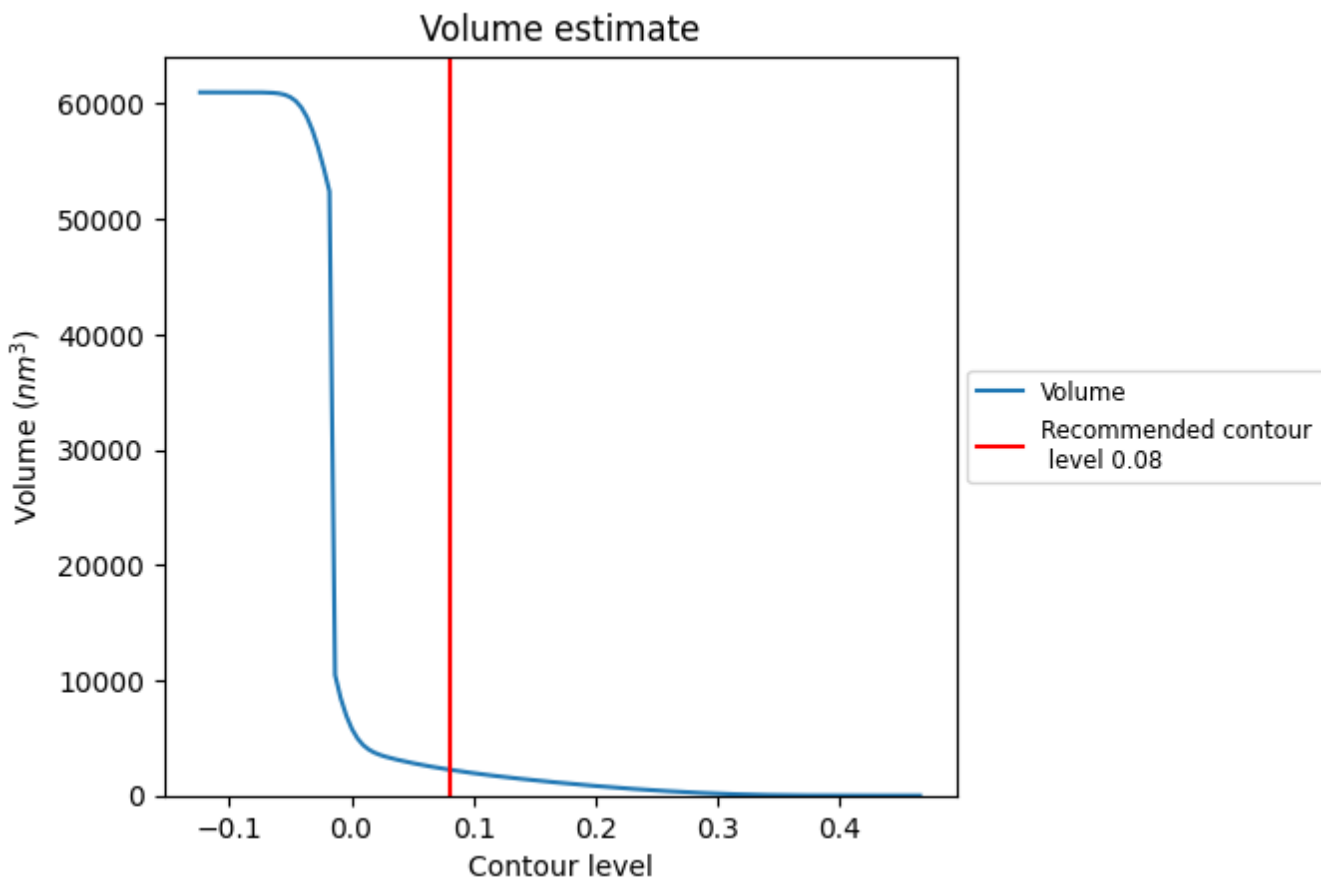
This section contains the results of statistical analysis of the map.

### 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.

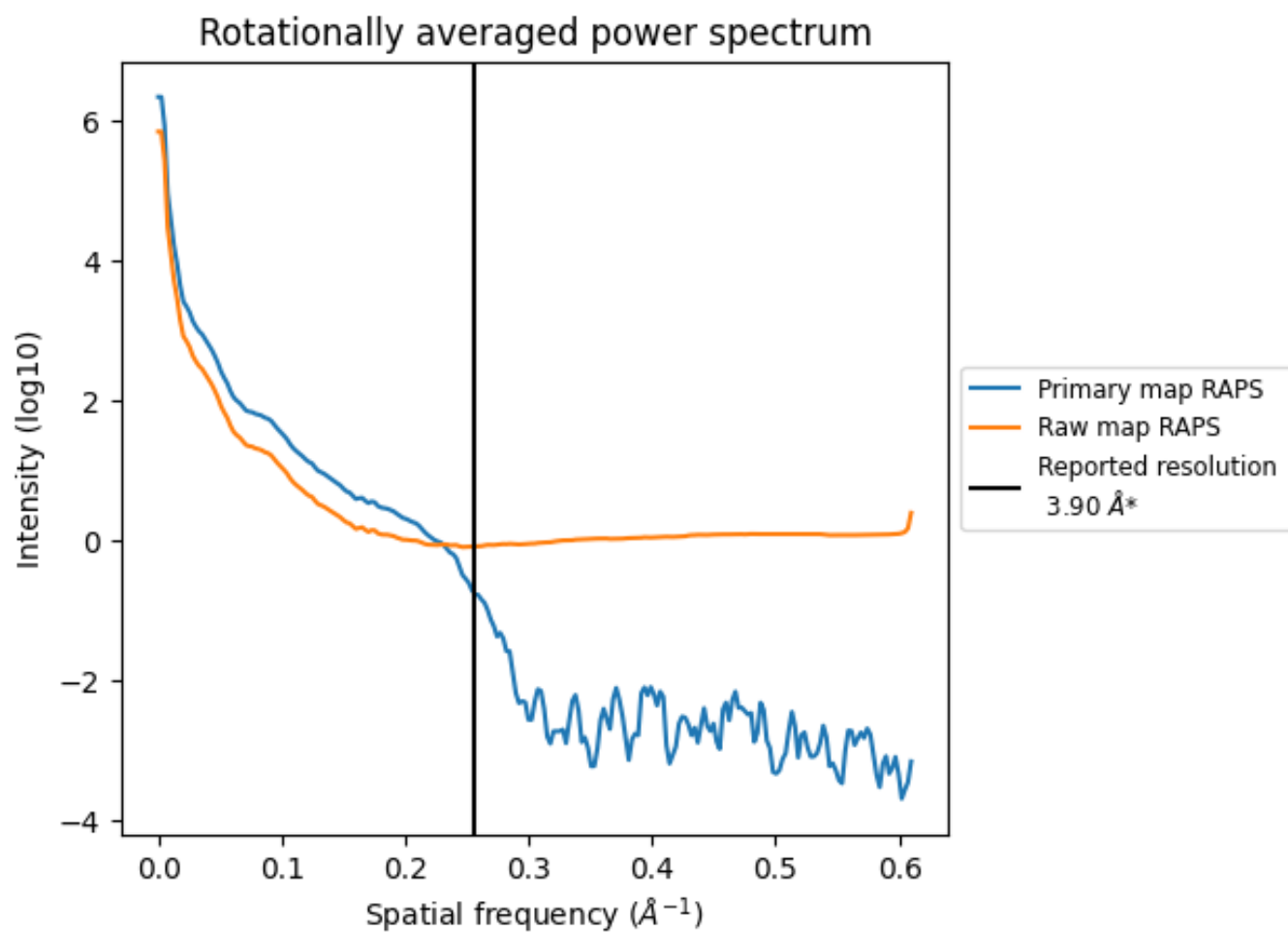
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2253 nm<sup>3</sup>; this corresponds to an approximate mass of 2035 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 i

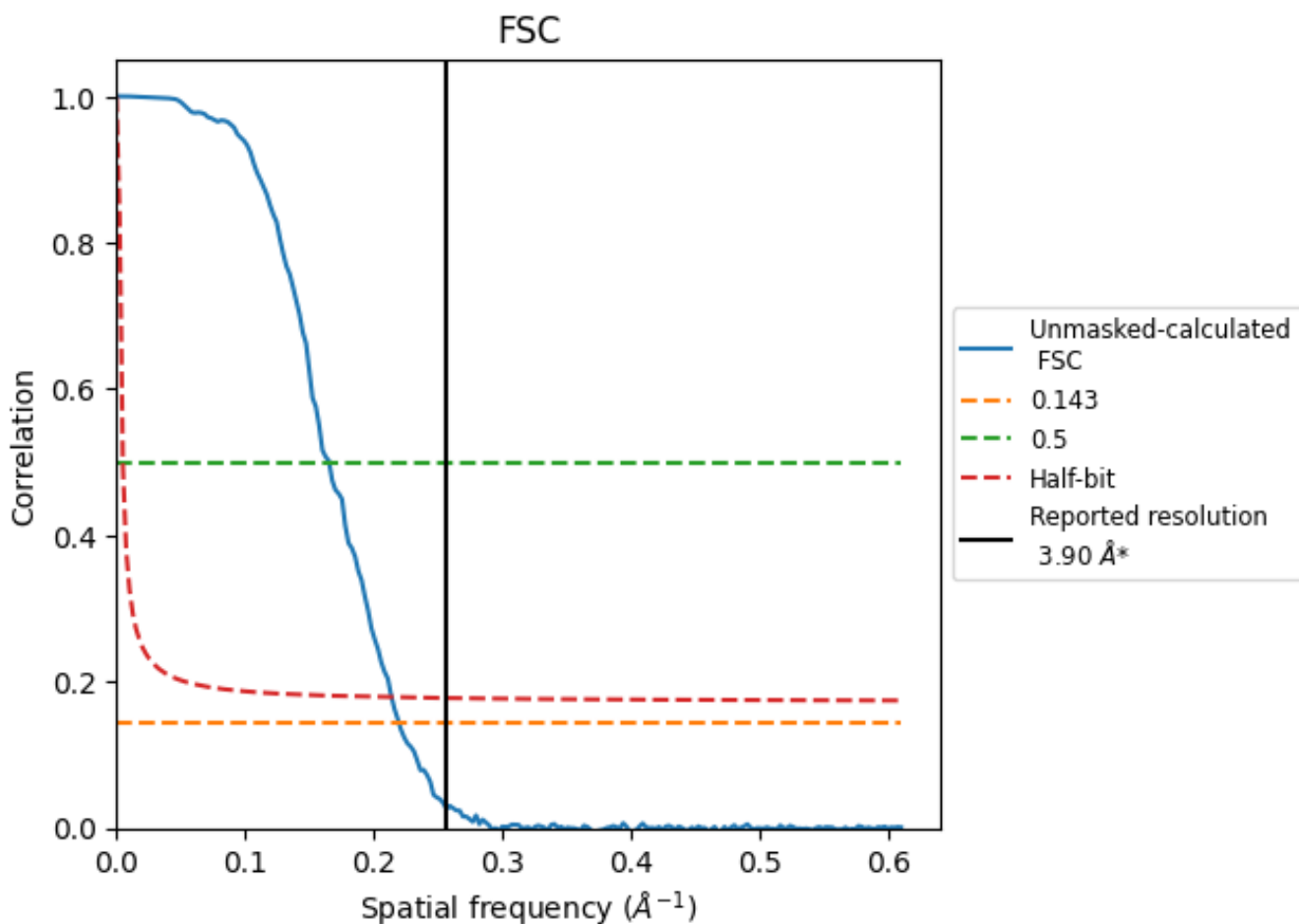


\*Reported resolution corresponds to spatial frequency of 0.256 Å<sup>-1</sup>

## 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<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

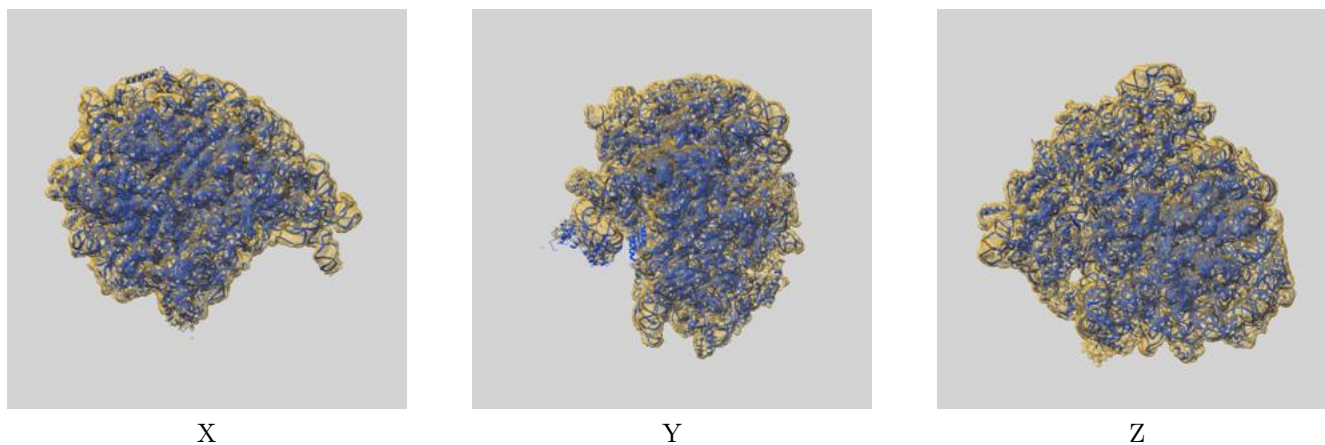
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.55	6.05	4.68

\*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 4.55 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-8279 and PDB model 5KPS. Per-residue inclusion information can be found in section 3 on page 15.

### 9.1 Map-model overlay [i](#)

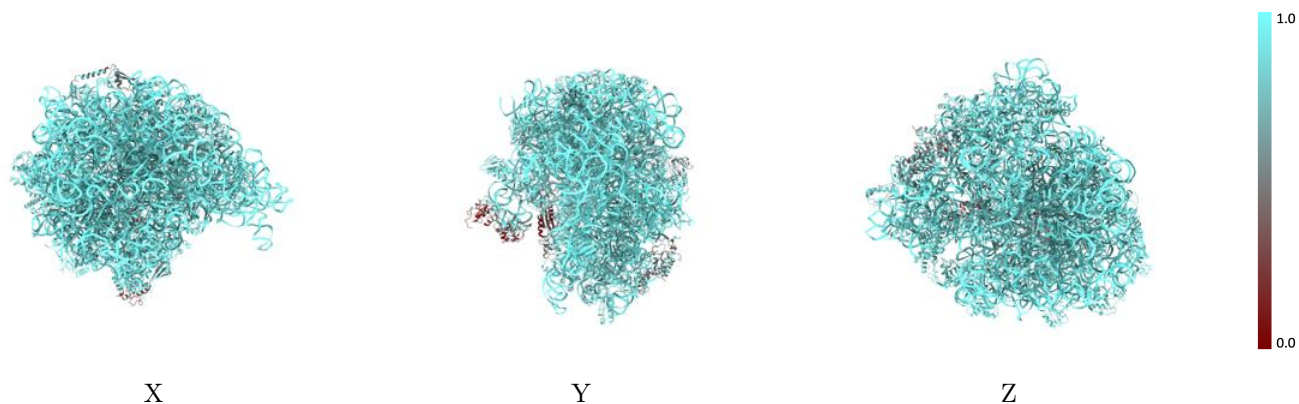


The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

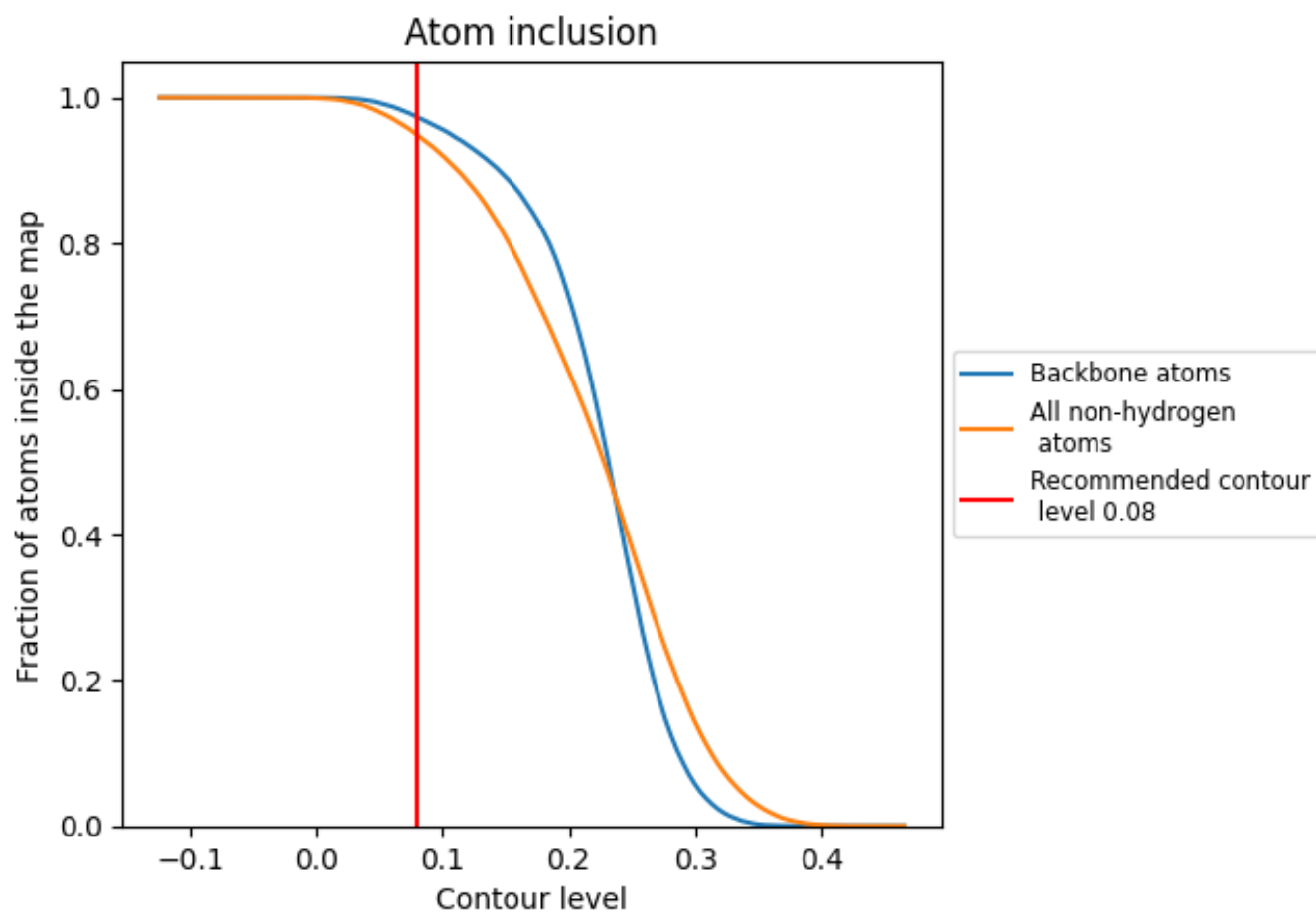
This section was not generated.

## 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 (0.08).

## 9.4 Atom inclusion [i](#)






































At the recommended contour level, 97% of all backbone atoms, 95% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.9490
1	 0.9198
10	 0.9012
11	 0.9196
12	 0.8995
13	 0.9062
14	 0.9265
15	 0.8371
16	 0.9290
17	 0.8686
18	 0.9201
19	 0.8992
2	 0.9206
20	 0.9290
21	 0.9314
22	 0.9209
23	 0.9514
24	 0.9114
25	 0.9169
26	 0.8124
27	 0.9962
28	 0.9954
29	 0.9988
3	 0.8903
30	 0.8814
31	 0.9848
32	 0.9410
4	 0.9268
5	 0.9185
6	 0.9281
7	 0.5331
8	 0.8523
9	 0.8912
A	 0.2626
B	 0.9167



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion
C	 0.9233
D	 0.8757
E	 0.9199
F	 0.9337
G	 0.6670
H	 0.3171
I	 0.4129
J	 0.9082
K	 0.8894
L	 0.9232
M	 0.8906
N	 0.9252
O	 0.9432
P	 0.9133
Q	 0.9328
R	 0.9222
S	 0.8684
T	 0.9072
U	 0.9166
V	 0.9255
W	 0.9195
X	 0.9151
Y	 0.9014
Z	 0.8970