



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 10:59 PM EDT

PDB ID : 5U9G
EMDB ID : EMD-8522
Title : 3.2 Å cryo-EM ArfA-RF2 ribosome rescue complex (Structure I)
Authors : Demo, G.; Svidritskiy, E.; Madireddy, R.; Diaz-Avalos, R.; Grant, T.; Grigorieff, N.; Sousa, D.; Korostelev, A.A.
Deposited on : 2016-12-16
Resolution : 3.20 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:

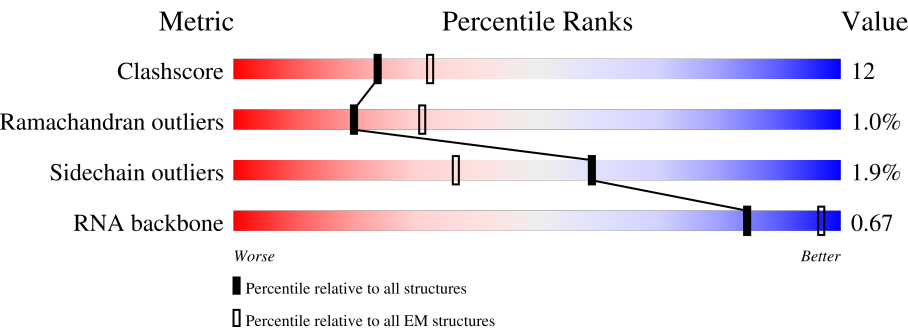
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.20 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.













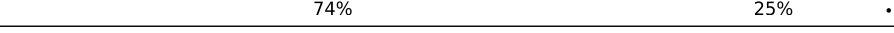
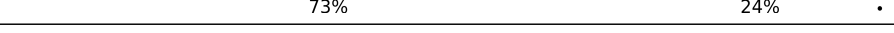
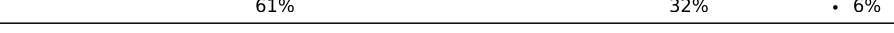


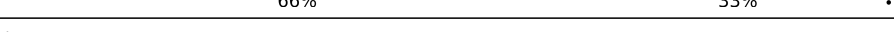









Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 ≥ 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	1539	<div><div></div><div>63%33%5%</div></div>
2	01	2903	<div><div></div><div>61%33%6%</div></div>
3	02	119	<div><div></div><div>66%32%. </div></div>
4	Y	72	<div><div>33%</div><div>10%56%</div></div>
5	W	77	<div><div></div><div>65%31%. </div></div>
5	X	77	<div><div>18%</div><div>60%34%6%</div></div>
6	03	234	<div><div>56%</div><div>74%19%. 6%</div></div>




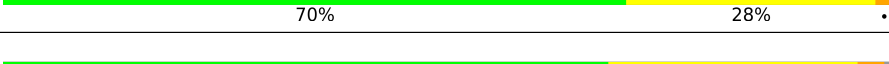
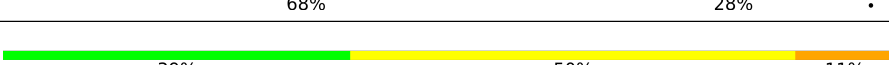


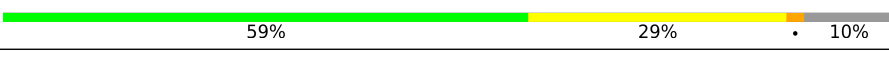


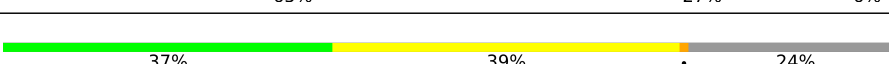
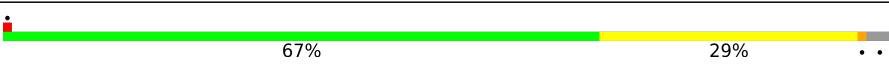




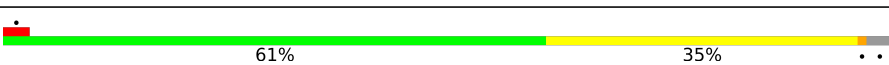

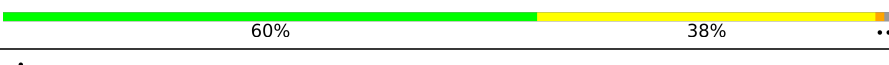

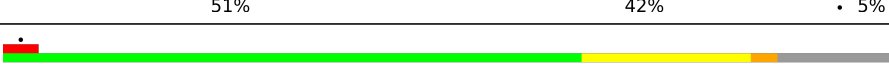



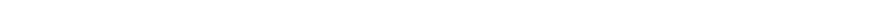
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Mol	Chain	Length	Quality of chain
7	04	273	
8	05	209	
9	06	201	
10	07	179	
11	08	177	
12	09	149	
13	10	165	
14	11	142	
15	12	142	
16	13	123	
17	14	144	
18	15	136	
19	16	127	
20	17	117	
21	18	115	
22	19	118	
23	20	103	
24	21	110	
25	22	100	
26	23	104	
27	24	94	
28	25	85	
29	26	78	
30	27	63	
31	28	59	

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Mol	Chain	Length	Quality of chain
32	29	70	
33	30	57	
34	31	55	
35	32	46	
36	33	65	
37	34	38	
38	V	14	
39	Z	365	
40	B	241	
41	C	233	
42	D	206	
43	E	167	
44	F	131	
45	G	156	
46	H	130	
47	I	130	
48	J	103	
49	K	129	
50	L	124	
51	M	118	
52	N	101	
53	O	89	
54	P	82	
55	Q	84	
56	R	75	

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Mol	Chain	Length	Quality of chain
57	S	92	<div><div></div><div>50%</div><div>36%</div><div>14%</div></div>
58	T	87	<div><div></div><div>60%</div><div>37%</div><div>..</div></div>
59	U	71	<div><div></div><div>51%</div><div>35%</div><div>6%</div><div>8%</div></div>

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 152649 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	01	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	1847	G	A	conflict	GB 42756

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	02	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 4 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	32	Total	C	N	O	S	0	0
			249	155	53	40	1		

- Molecule 5 is a RNA chain called fMet-tRNA (P- and E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	77	Total	C	N	O	P	0	0
			1622	723	289	534	76		
5	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	03	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	04	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	07	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	16	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	22	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	23	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	29	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	31	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a RNA chain called truncated mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	14	Total	C	N	O	P	0	0
			306	138	64	91	13		

- Molecule 39 is a protein called Peptide chain release factor RF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	361	Total	C	N	O	S	0	0
			2814	1728	499	578	9		

- Molecule 40 is a protein called 30S ribosomal protein S2.

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

- Molecule 41 is a protein called 30S ribosomal protein S3.

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

- Molecule 42 is a protein called 30S ribosomal protein S4.

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

- Molecule 43 is a protein called 30S ribosomal protein S5.

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

- Molecule 44 is a protein called 30S ribosomal protein S6.

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

- Molecule 45 is a protein called 30S ribosomal protein S7.

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

- Molecule 46 is a protein called 30S ribosomal protein S8.

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

- Molecule 47 is a protein called 30S ribosomal protein S9.

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

- Molecule 48 is a protein called 30S ribosomal protein S10.

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

- Molecule 49 is a protein called 30S ribosomal protein S11.

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

- Molecule 50 is a protein called 30S ribosomal protein S12.

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

- Molecule 51 is a protein called 30S ribosomal protein S13.

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

- Molecule 52 is a protein called 30S ribosomal protein S14.

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

- Molecule 53 is a protein called 30S ribosomal protein S15.

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

- Molecule 54 is a protein called 30S ribosomal protein S16.

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

- Molecule 55 is a protein called 30S ribosomal protein S17.

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

- Molecule 56 is a protein called 30S ribosomal protein S18.

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

- Molecule 57 is a protein called 30S ribosomal protein S19.

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

- Molecule 58 is a protein called 30S ribosomal protein S20.

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

- Molecule 59 is a protein called 30S ribosomal protein S21.

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

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	A	97	Total	Mg	0
			97	97	
60	01	239	Total	Mg	0
			239	239	
60	02	4	Total	Mg	0
			4	4	
60	X	2	Total	Mg	0
			2	2	
60	14	1	Total	Mg	0
			1	1	
60	25	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
60	30	1	Total 1	Mg 1	0
60	W	2	Total 2	Mg 2	0
60	H	1	Total 1	Mg 1	0

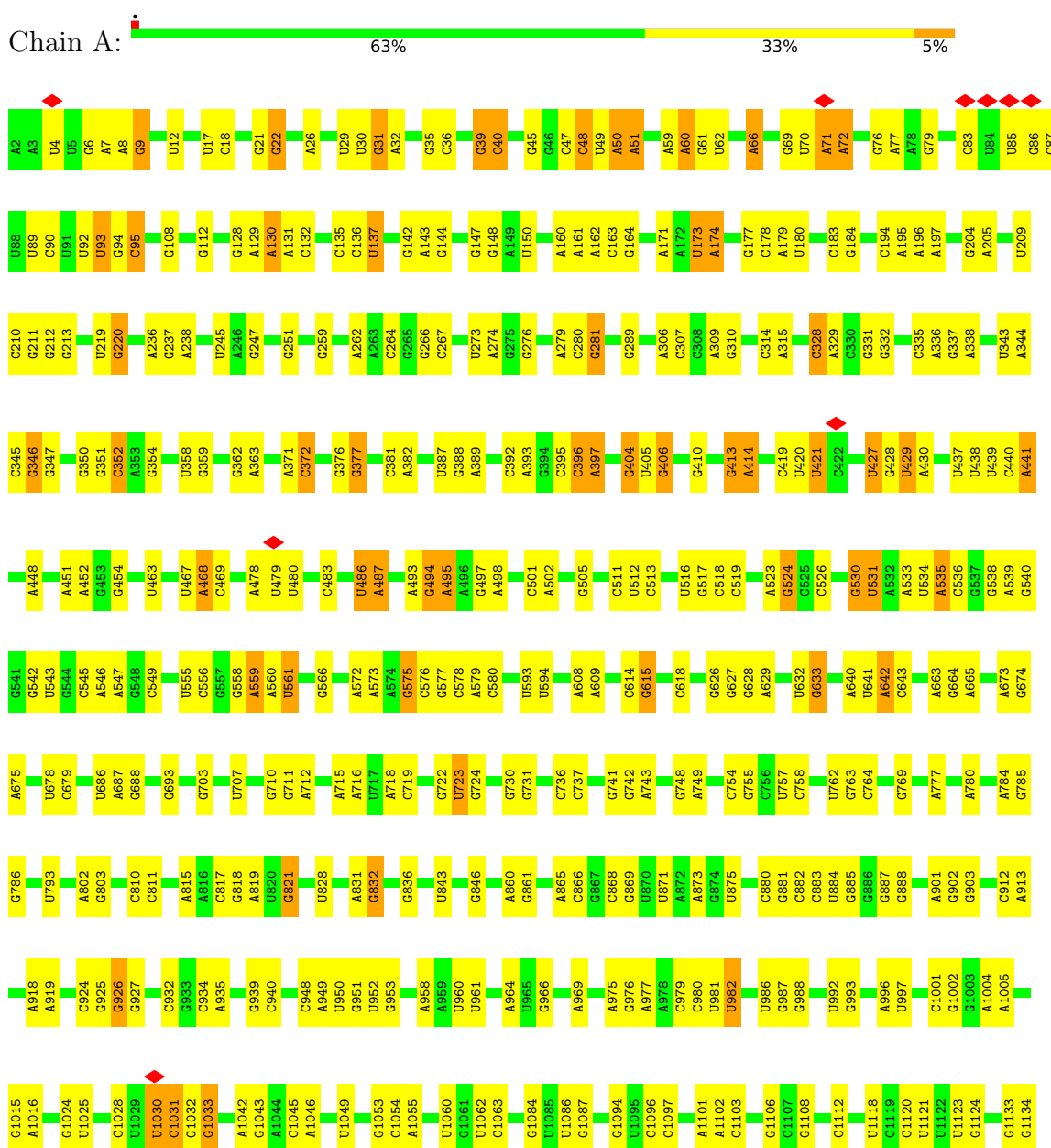
- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

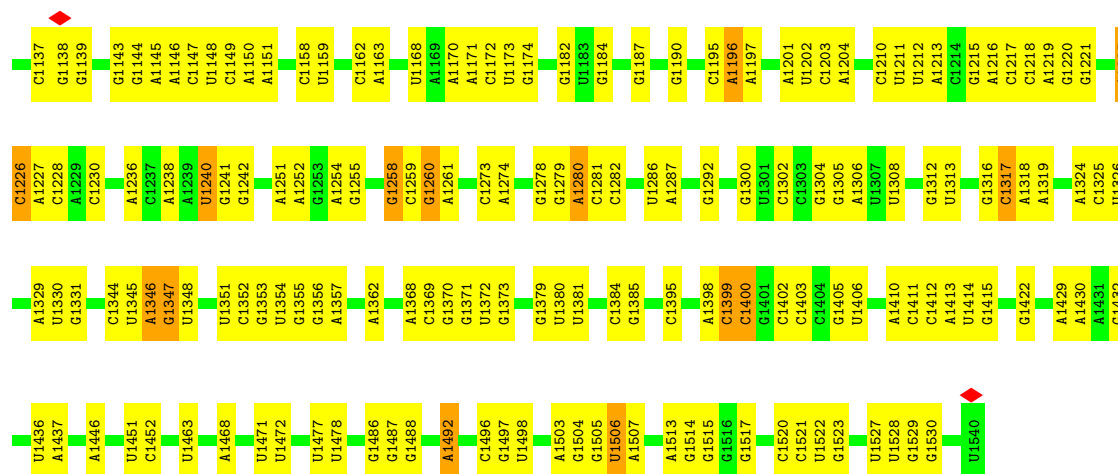
Mol	Chain	Residues	Atoms		AltConf
61	34	1	Total 1	Zn 1	0

3 Residue-property plots

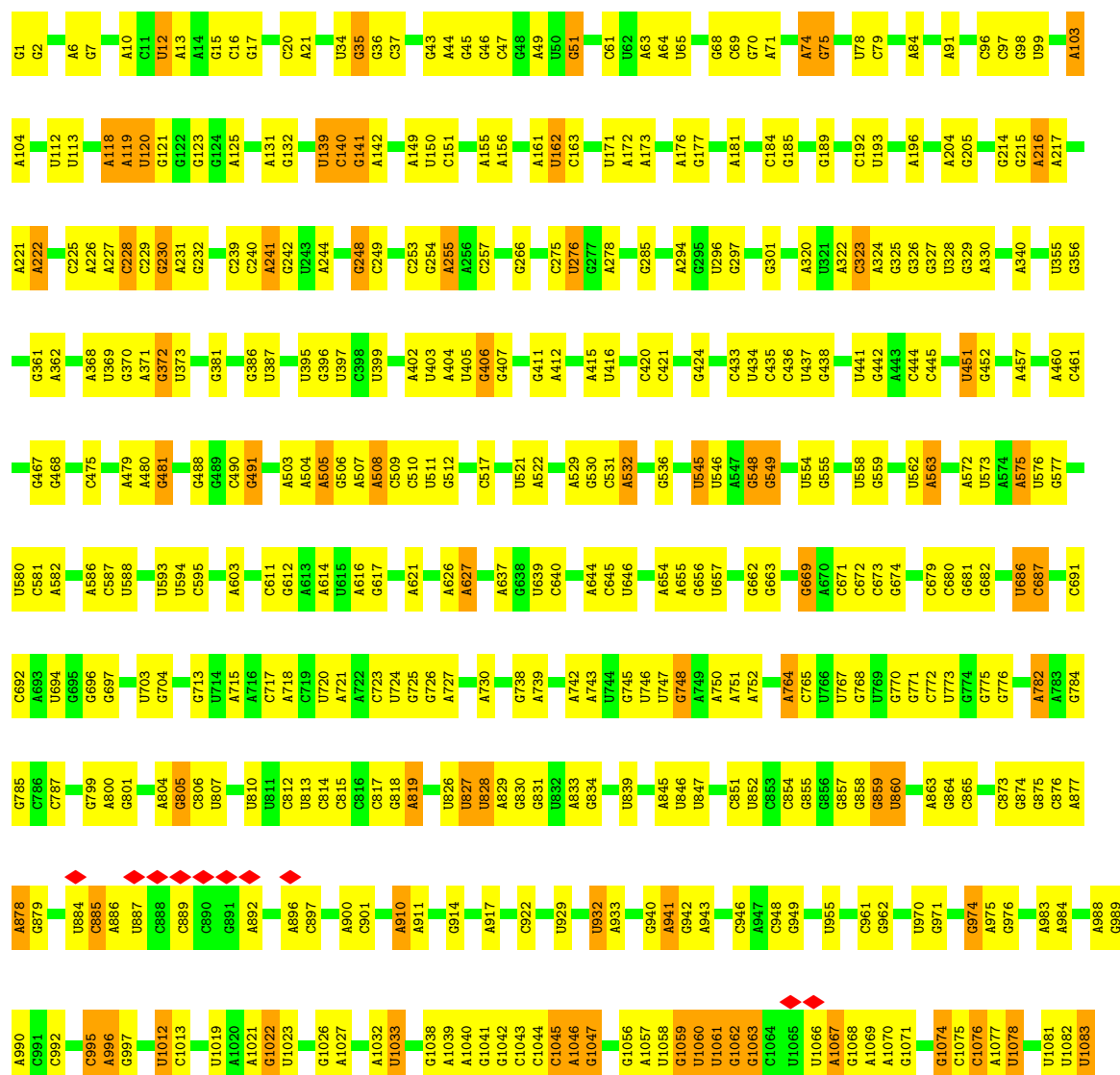
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S ribosomal RNA

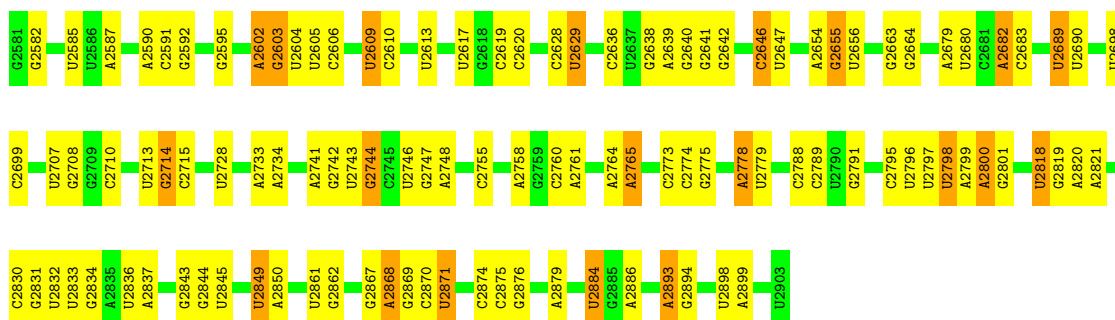




• Molecule 2: 23S ribosomal RNA



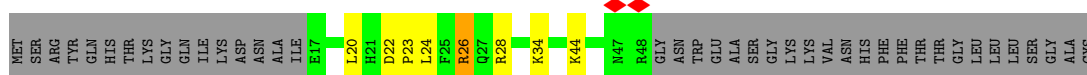
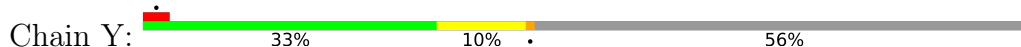
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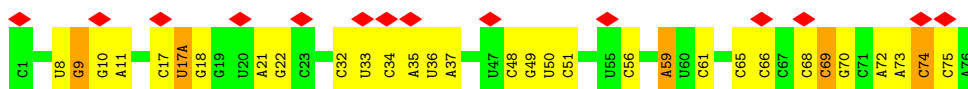
• Molecule 3: 5S ribosomal RNA



• Molecule 4: Alternative ribosome-rescue factor A



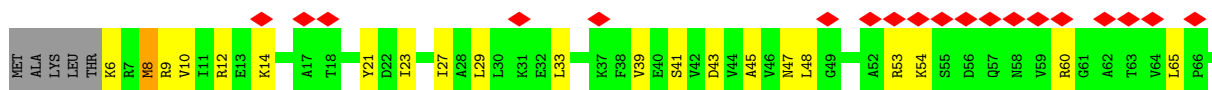
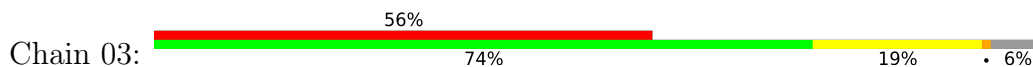
• Molecule 5: fMet-tRNA (P- and E-site)

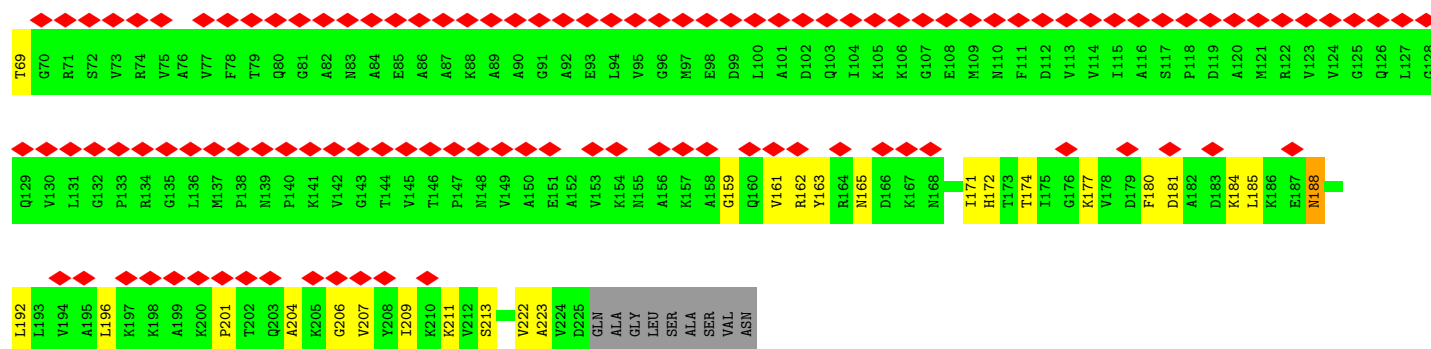


• Molecule 5: fMet-tRNA (P- and E-site)



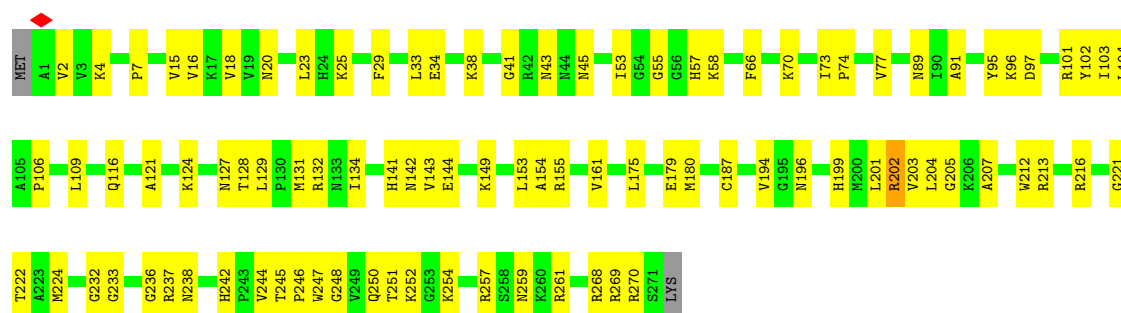
• Molecule 6: 50S ribosomal protein L1





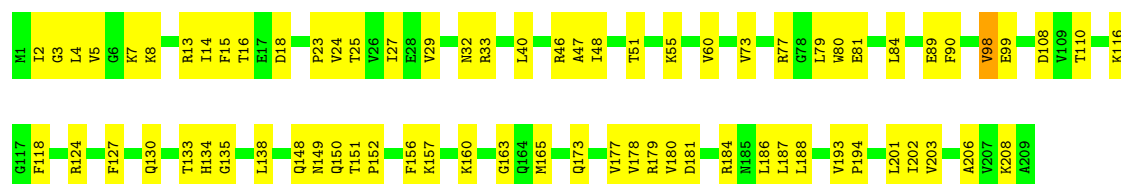
• Molecule 7: 50S ribosomal protein L2

Chain 04: 65% 34%



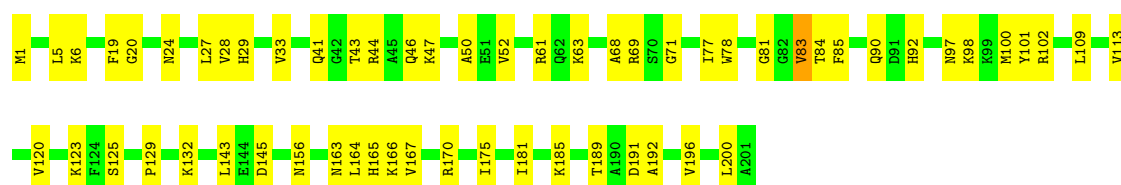
• Molecule 8: 50S ribosomal protein L3

Chain 05: 65% 34%



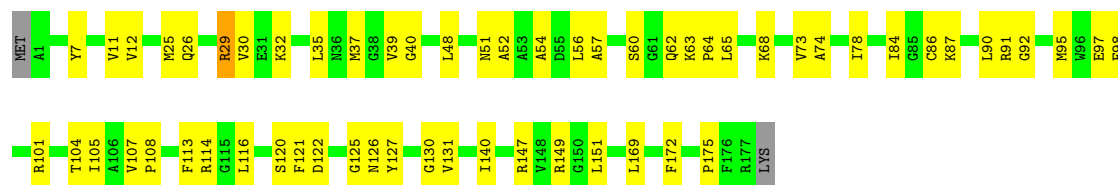
• Molecule 9: 50S ribosomal protein L4

Chain 06: 71% 29%

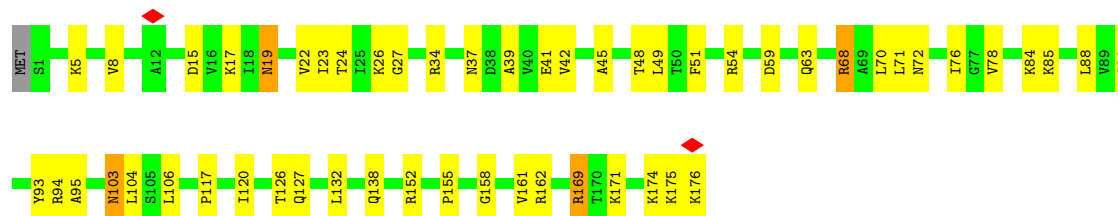


• Molecule 10: 50S ribosomal protein L5

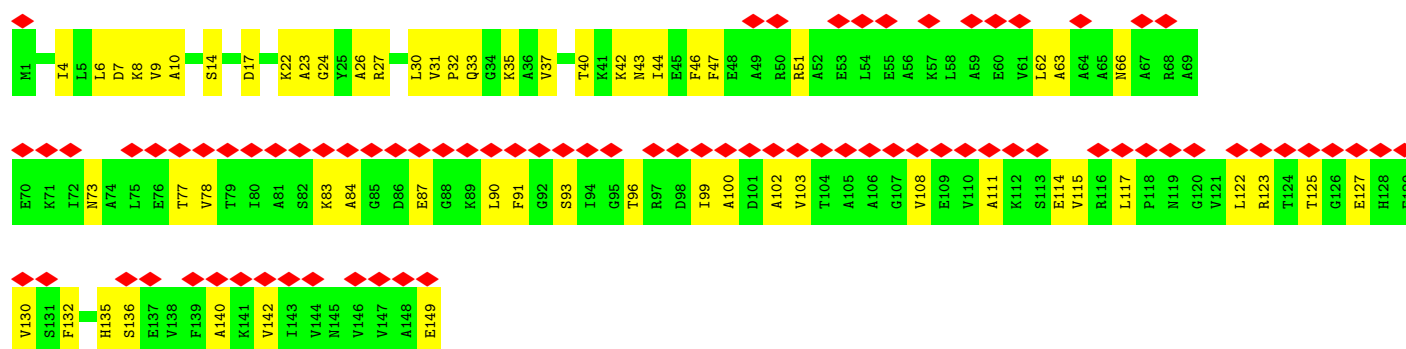
Chain 07: 66% 32%



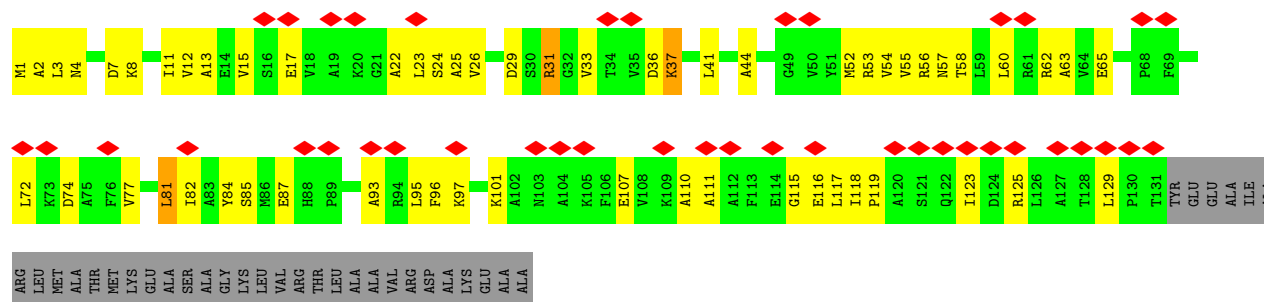
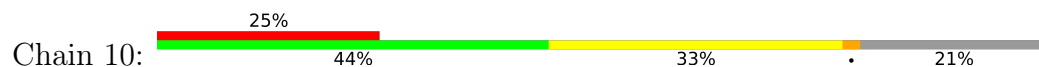
• Molecule 11: 50S ribosomal protein L6



• Molecule 12: 50S ribosomal protein L9

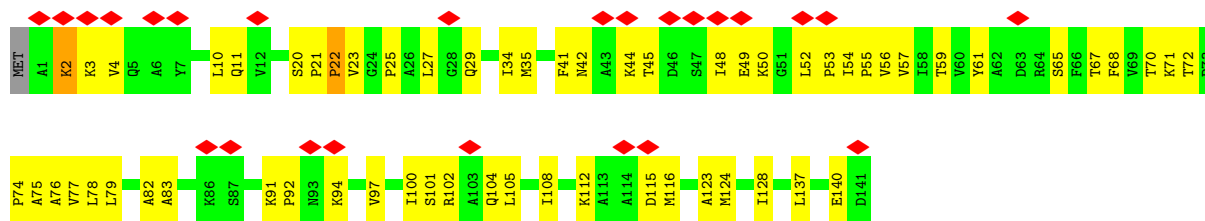


• Molecule 13: 50S ribosomal protein L10



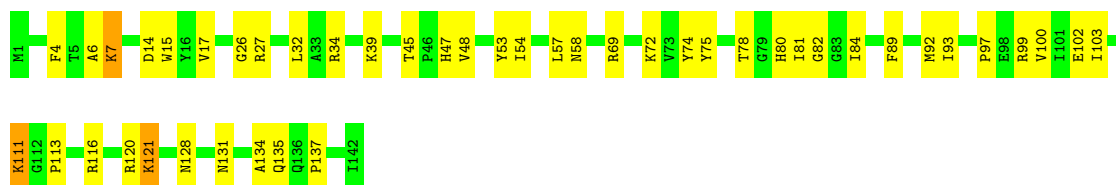
• Molecule 14: 50S ribosomal protein L11





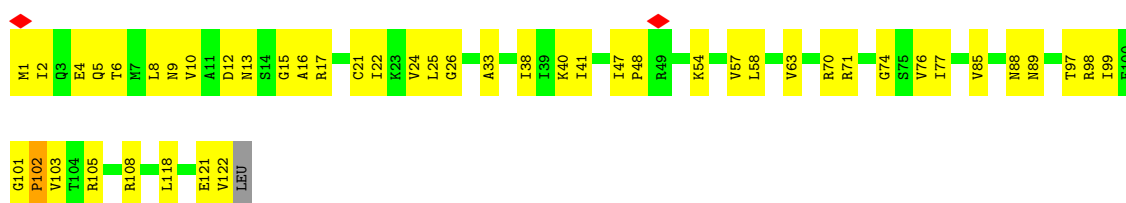
- Molecule 15: 50S ribosomal protein L13

Chain 12: 68% 30% .



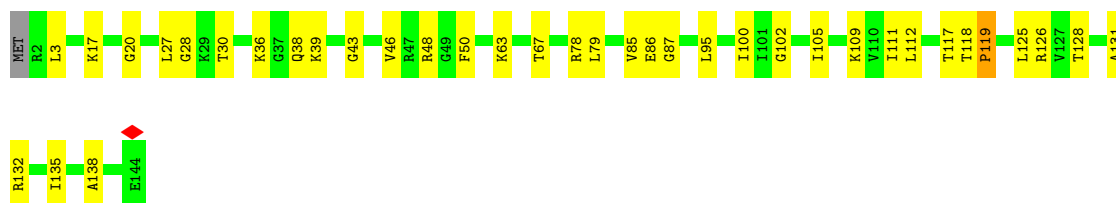
- Molecule 16: 50S ribosomal protein L14

Chain 13: 61% 37% ..



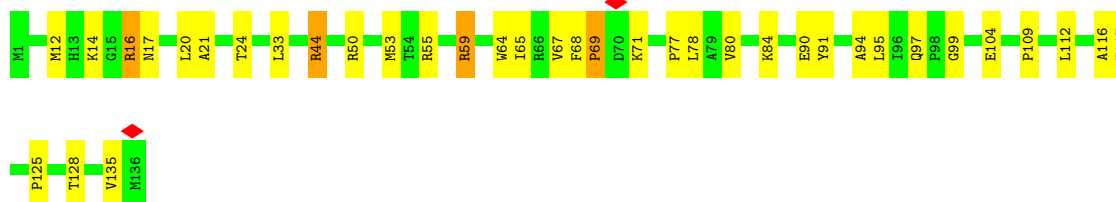
- Molecule 17: 50S ribosomal protein L15

Chain 14: 74% 25% ..

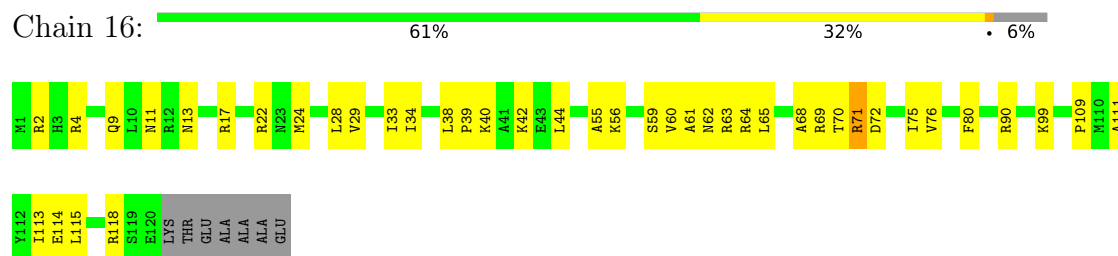


- Molecule 18: 50S ribosomal protein L16

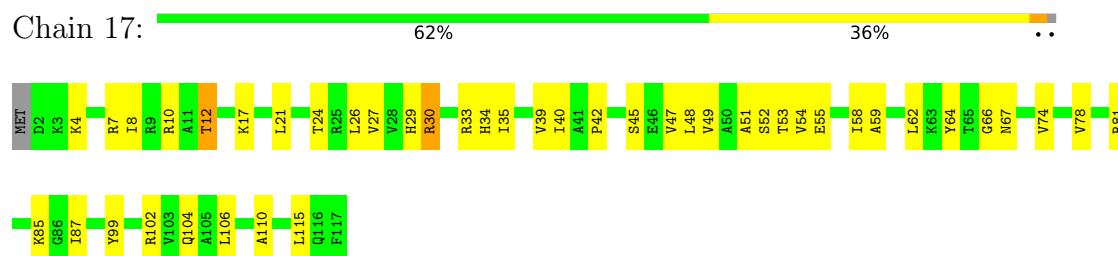
Chain 15: 73% 24% .



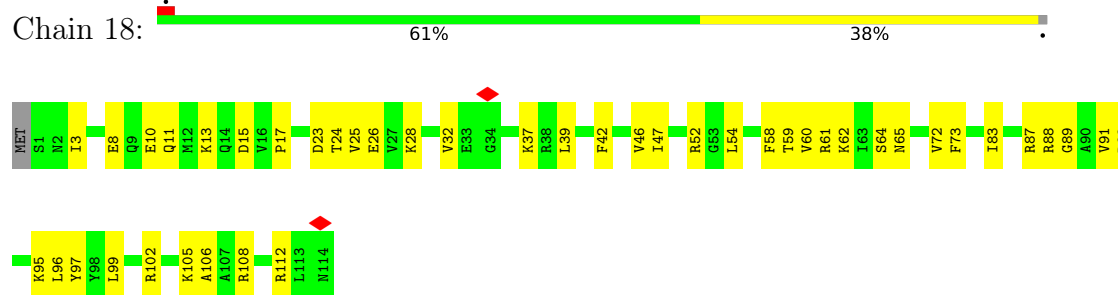
- Molecule 19: 50S ribosomal protein L17



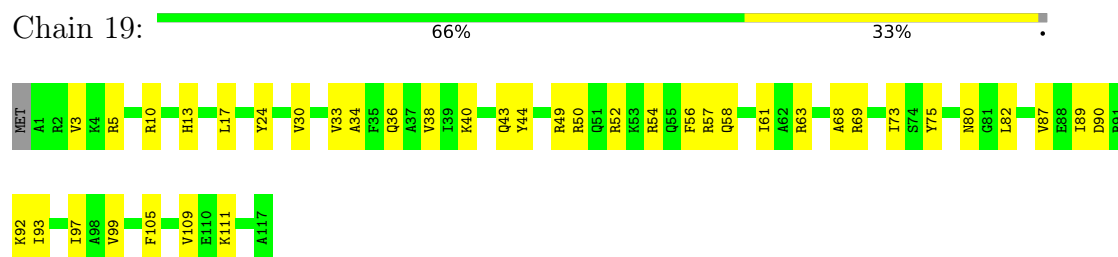
- Molecule 20: 50S ribosomal protein L18



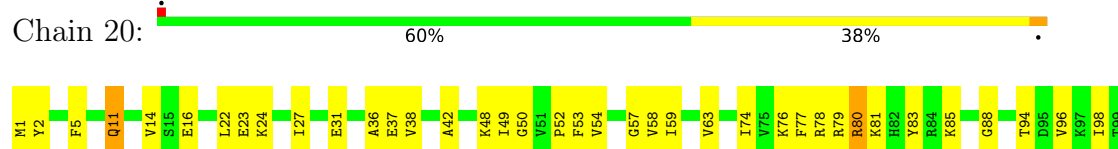
- Molecule 21: 50S ribosomal protein L19



- Molecule 22: 50S ribosomal protein L20

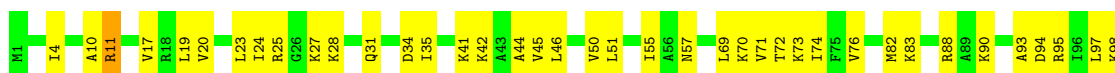


- Molecule 23: 50S ribosomal protein L21

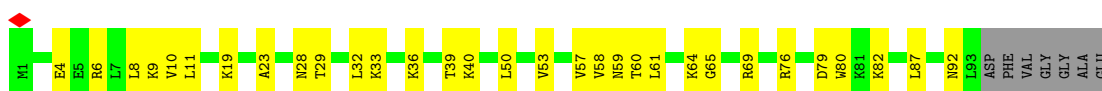




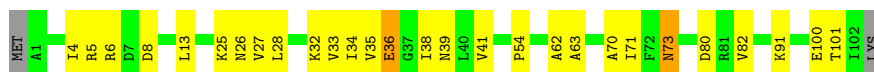
- Molecule 24: 50S ribosomal protein L22



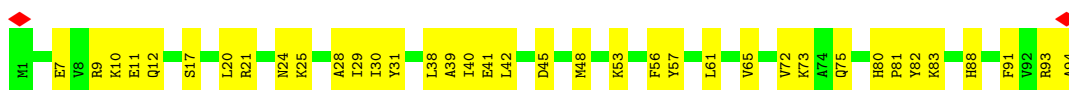
- Molecule 25: 50S ribosomal protein L23



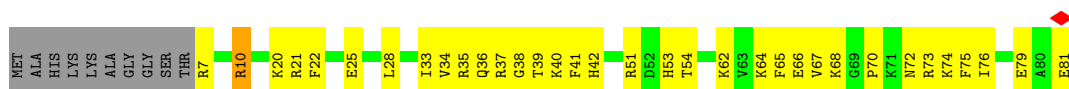
- Molecule 26: 50S ribosomal protein L24



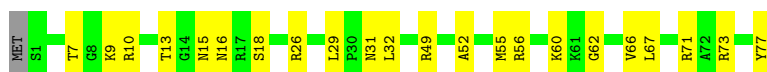
- Molecule 27: 50S ribosomal protein L25



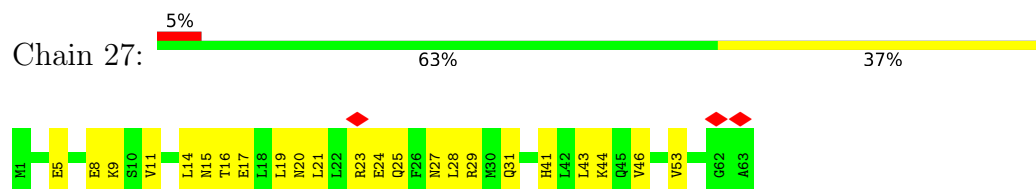
- Molecule 28: 50S ribosomal protein L27



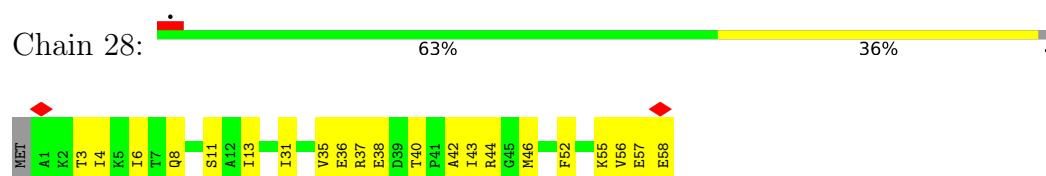
- Molecule 29: 50S ribosomal protein L28



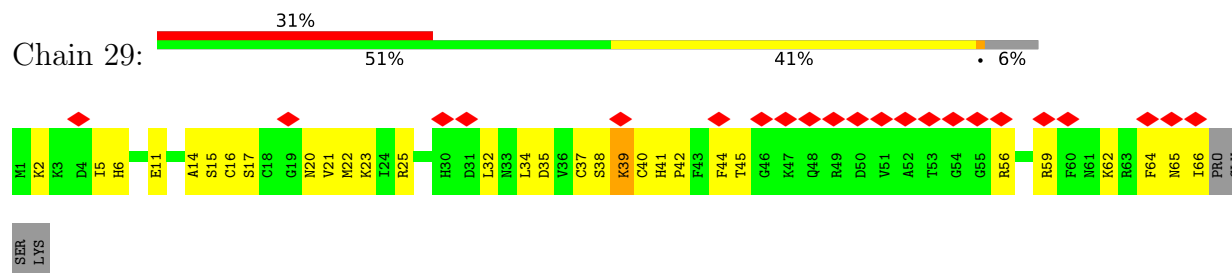
- Molecule 30: 50S ribosomal protein L29



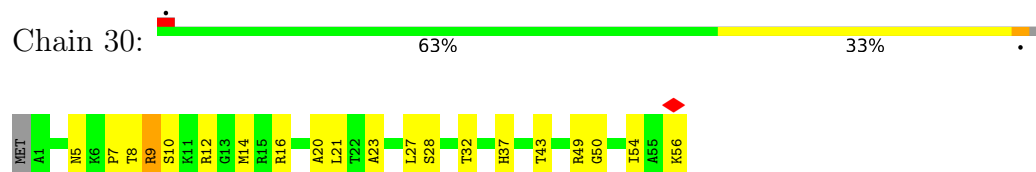
- Molecule 31: 50S ribosomal protein L30



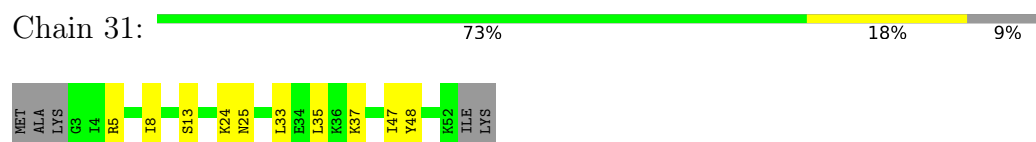
- Molecule 32: 50S ribosomal protein L31



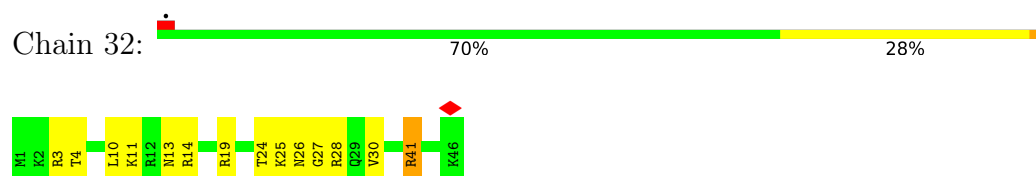
- Molecule 33: 50S ribosomal protein L32



- Molecule 34: 50S ribosomal protein L33



- Molecule 35: 50S ribosomal protein L34



- Molecule 36: 50S ribosomal protein L35





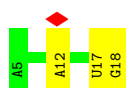
- Molecule 37: 50S ribosomal protein L36

Chain 34: 39% 50% 11%



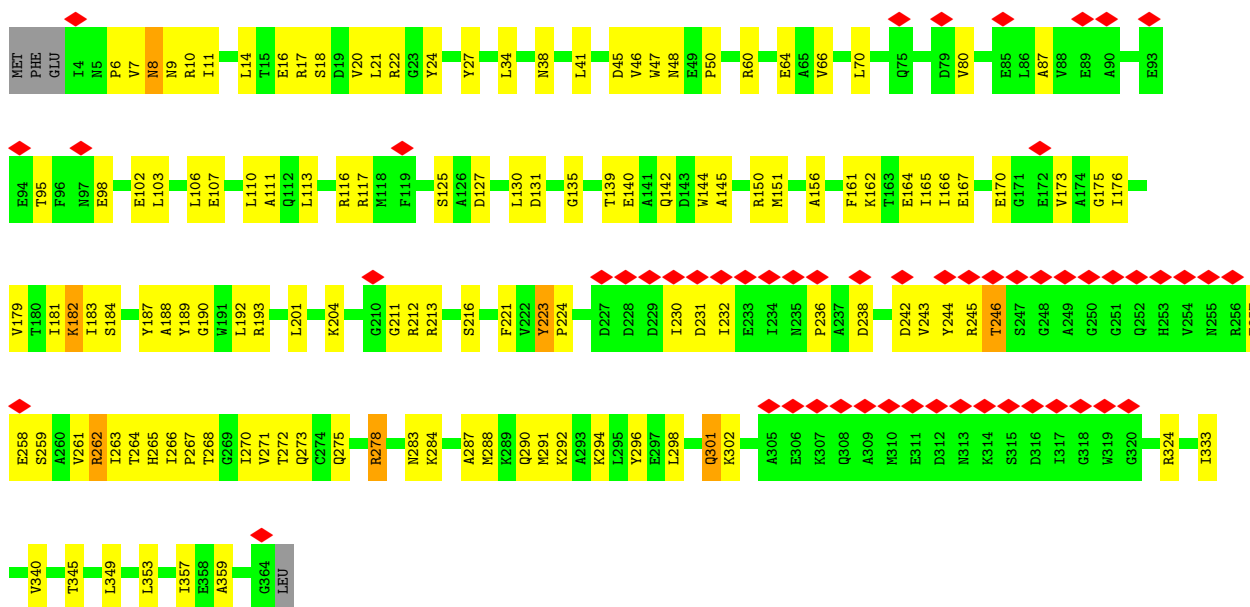
- Molecule 38: truncated mRNA

Chain V: 7% 79% 21%



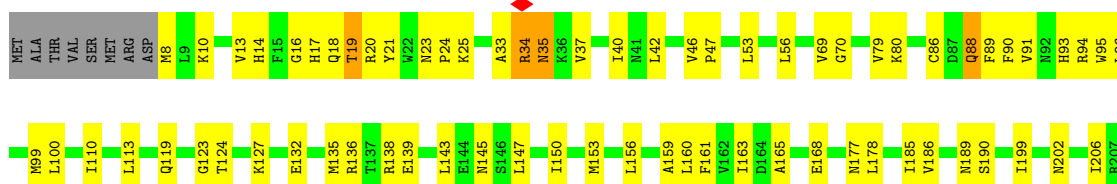
- Molecule 39: Peptide chain release factor RF2

Chain Z: 15% 63% 34%



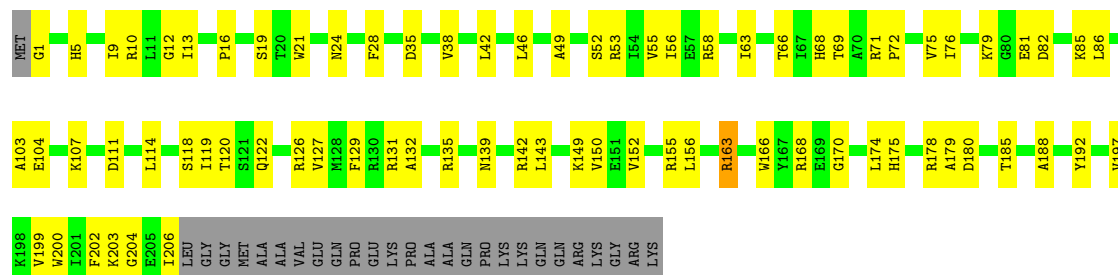
- Molecule 40: 30S ribosomal protein S2

Chain B: 59% 29% 10%



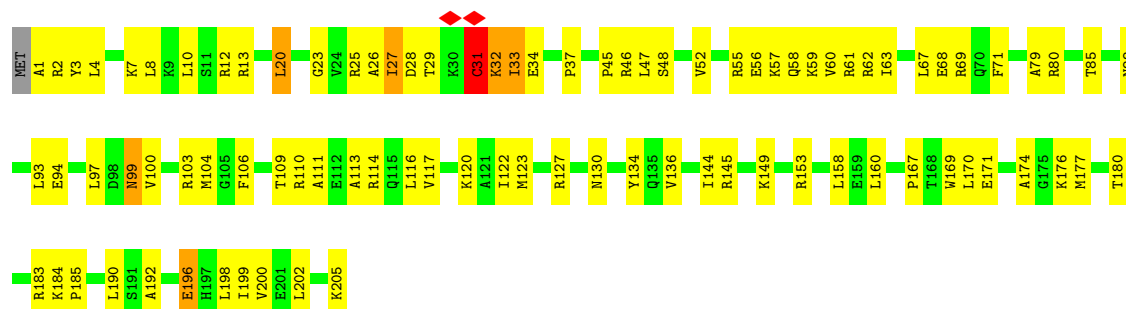
- Molecule 41: 30S ribosomal protein S3

Chain C:  56% 32% 12%



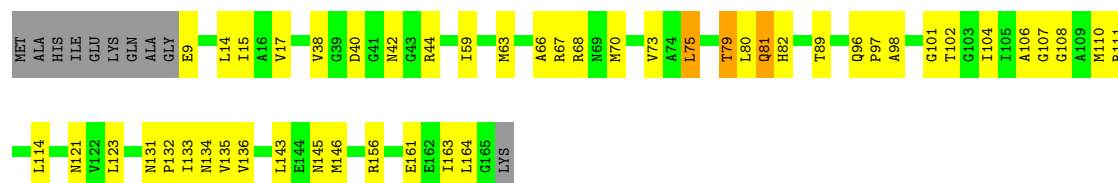
- Molecule 42: 30S ribosomal protein S4

Chain D:  56% 40% .



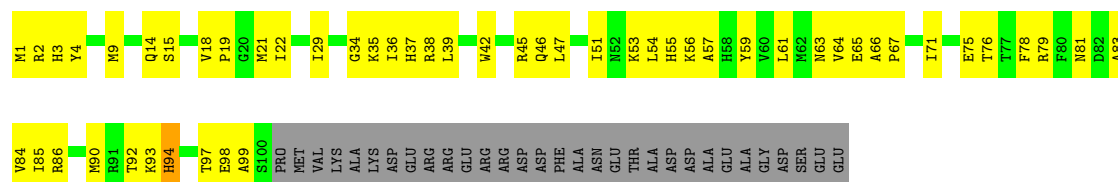
- Molecule 43: 30S ribosomal protein S5

Chain E:  65% 27% 6%



- Molecule 44: 30S ribosomal protein S6

Chain F:  37% 39% • 24%



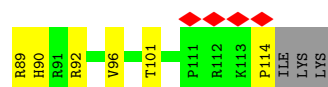
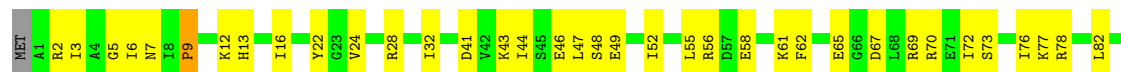
- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | ALA | LYS | ALA | PRO | ILE | ARG | ALA | ARG | LYS | ARG | VAL | R12 | R13 | K14 | V19 | A20 | H21 | I22 | H23 | A24 | S25 | F26 | T29 | I30 | I33 | T34 | D35 | R36 | A40 | W43 | A44 | T45 | T58 | P59 | F60 | D63 | V64 | C69 | A72 | V73 | K74 | N80 | L81 | E82 | V83 | K86 | G87 | P98 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



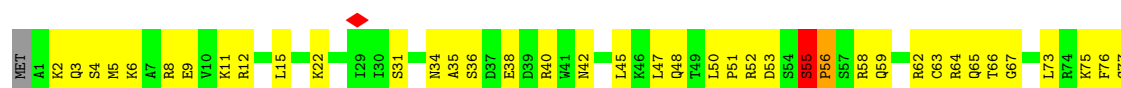
- Molecule 50: 30S ribosomal protein S12



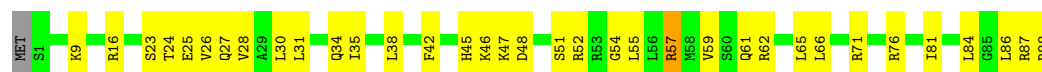
- Molecule 51: 30S ribosomal protein S13



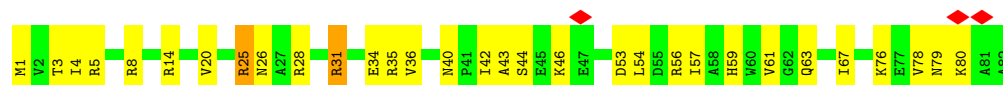
- Molecule 52: 30S ribosomal protein S14



- Molecule 53: 30S ribosomal protein S15

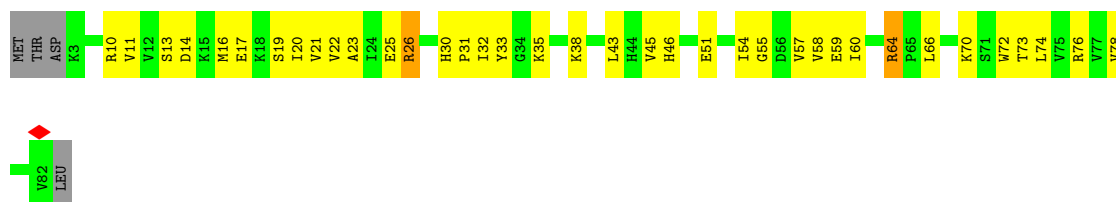


- Molecule 54: 30S ribosomal protein S16



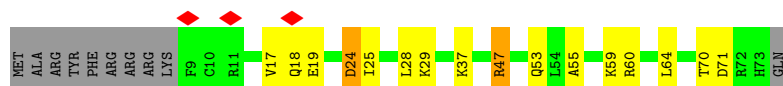
- Molecule 55: 30S ribosomal protein S17

Chain Q:  51% 42% 5%



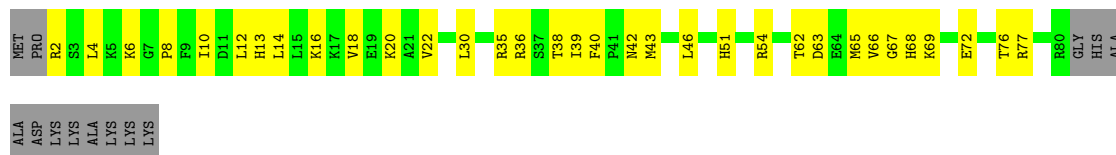
- Molecule 56: 30S ribosomal protein S18

Chain R:  65% 19% 13%



- Molecule 57: 30S ribosomal protein S19

Chain S:  50% 36% 14%



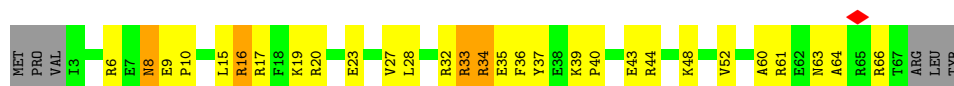
- Molecule 58: 30S ribosomal protein S20

Chain T:  60% 37% 2%



- Molecule 59: 30S ribosomal protein S21

Chain U:  51% 35% 6% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	139861	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 ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	29000	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	17.734	Depositor
Minimum map value	-5.902	Depositor
Average map value	-1.160	Depositor
Map value standard deviation	1.507	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.215, 1.215, 1.215	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.25	0/36963	0.65	0/57662
2	01	0.24	0/69797	0.65	1/108890 (0.0%)
3	02	0.25	0/2847	0.65	0/4440
4	Y	0.31	0/253	0.54	0/330
5	W	0.25	0/1832	0.64	0/2855
5	X	0.29	0/1811	0.67	1/2822 (0.0%)
6	03	0.28	0/1361	0.58	1/1796 (0.1%)
7	04	0.29	0/2121	0.59	0/2852
8	05	0.33	0/1586	0.57	0/2134
9	06	0.30	0/1571	0.58	1/2113 (0.0%)
10	07	0.32	0/1434	0.54	0/1926
11	08	0.29	0/1343	0.55	0/1816
12	09	0.31	0/1122	0.57	0/1515
13	10	0.35	0/1001	0.64	0/1350
14	11	0.31	0/1046	0.58	0/1410
15	12	0.30	0/1152	0.56	0/1551
16	13	0.30	0/947	0.60	0/1268
17	14	0.32	0/1054	0.59	0/1403
18	15	0.32	0/1093	0.59	0/1460
19	16	0.30	0/973	0.55	0/1301
20	17	0.28	0/902	0.55	0/1209
21	18	0.31	0/929	0.54	0/1242
22	19	0.29	0/960	0.46	0/1278
23	20	0.33	0/829	0.63	1/1107 (0.1%)
24	21	0.28	0/864	0.56	0/1156
25	22	0.30	0/744	0.54	0/994
26	23	0.33	0/787	0.61	0/1051
27	24	0.30	0/766	0.55	0/1025
28	25	0.34	0/582	0.58	0/769
29	26	0.30	0/635	0.52	0/848
30	27	0.28	0/510	0.47	0/677
31	28	0.27	0/453	0.51	0/605

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	29	0.31	0/531	0.52	0/709
33	30	0.31	0/450	0.58	0/599
34	31	0.30	0/416	0.52	0/554
35	32	0.30	0/380	0.51	0/498
36	33	0.31	0/513	0.61	0/676
37	34	0.23	0/303	0.40	0/397
38	V	0.21	0/345	0.60	0/538
39	Z	0.31	0/2854	0.56	0/3842
40	B	0.31	0/1735	0.57	0/2338
41	C	0.30	0/1651	0.54	0/2225
42	D	0.29	0/1665	0.59	0/2227
43	E	0.31	0/1169	0.59	0/1573
44	F	0.32	0/835	0.62	0/1128
45	G	0.29	0/1195	0.55	0/1602
46	H	0.30	0/989	0.57	0/1326
47	I	0.31	0/1034	0.59	0/1375
48	J	0.30	0/796	0.64	0/1077
49	K	0.31	0/885	0.60	0/1195
50	L	0.31	0/969	0.67	1/1300 (0.1%)
51	M	0.28	0/892	0.57	0/1193
52	N	0.34	0/817	0.64	3/1088 (0.3%)
53	O	0.28	0/722	0.52	0/964
54	P	0.32	0/659	0.57	0/884
55	Q	0.30	0/657	0.58	0/881
56	R	0.30	0/544	0.57	0/731
57	S	0.32	0/652	0.56	0/877
58	T	0.28	0/671	0.44	0/888
59	U	0.37	0/550	0.67	0/728
All	All	0.27	0/165147	0.63	9/246268 (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
39	Z	0	2
52	N	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	06	81	GLY	N-CA-C	-7.61	94.08	113.10
52	N	55	SER	C-N-CD	-7.29	104.56	120.60
6	03	206	GLY	N-CA-C	-6.01	98.08	113.10
2	01	1178	C	N1-C1'-C2'	5.90	121.67	114.00
5	X	17(A)	U	N1-C1'-C2'	5.89	121.66	114.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	N	55	SER	Mainchain
39	Z	236	PRO	Peptide
39	Z	246	THR	Peptide

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	33012	0	16618	430	0
2	01	62318	0	31345	807	0
3	02	2546	0	1292	41	0
4	Y	249	0	255	13	0
5	W	1640	0	837	15	0
5	X	1622	0	827	17	0
6	03	1353	0	1159	38	0
7	04	2082	0	2157	79	0
8	05	1565	0	1616	69	0
9	06	1552	0	1619	47	0
10	07	1410	0	1447	56	0
11	08	1323	0	1374	54	0
12	09	1111	0	1148	51	0
13	10	988	0	1025	57	0
14	11	1032	0	1088	49	0
15	12	1129	0	1162	44	0
16	13	938	0	1012	38	0
17	14	1045	0	1117	30	0
18	15	1074	0	1157	31	0
19	16	960	0	1000	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	17	892	0	923	35	0
21	18	917	0	965	45	0
22	19	947	0	1022	35	0
23	20	816	0	839	36	0
24	21	857	0	922	38	0
25	22	738	0	807	30	0
26	23	779	0	834	17	0
27	24	753	0	780	34	0
28	25	575	0	592	30	0
29	26	625	0	655	22	0
30	27	509	0	543	19	0
31	28	449	0	491	18	0
32	29	522	0	524	28	0
33	30	444	0	461	26	0
34	31	409	0	440	8	0
35	32	377	0	418	22	0
36	33	504	0	574	16	0
37	34	302	0	340	30	0
38	V	306	0	154	1	0
39	Z	2814	0	2682	105	0
40	B	1704	0	1732	66	0
41	C	1624	0	1699	64	0
42	D	1643	0	1710	78	0
43	E	1156	0	1199	42	0
44	F	817	0	808	51	0
45	G	1181	0	1240	43	0
46	H	979	0	1034	28	0
47	I	1022	0	1070	59	0
48	J	786	0	828	52	0
49	K	869	0	878	42	0
50	L	955	0	1019	36	0
51	M	883	0	944	48	0
52	N	805	0	847	55	0
53	O	714	0	737	31	0
54	P	649	0	666	28	0
55	Q	648	0	691	36	0
56	R	535	0	552	18	0
57	S	637	0	665	30	0
58	T	665	0	714	29	0
59	U	544	0	579	32	0
60	01	239	0	0	0	0
60	02	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	14	1	0	0	0	0
60	25	1	0	0	0	0
60	30	1	0	0	0	0
60	A	97	0	0	0	0
60	H	1	0	0	0	0
60	W	2	0	0	0	0
60	X	2	0	0	0	0
61	34	1	0	0	0	0
All	All	152649	0	103833	3103	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 12.

The worst 5 of 3103 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)
2:01:45:G:H5''	2:01:46:G:H5'	1.26	1.16
1:A:376:G:H2'	1:A:377:G:H5''	1.33	1.08
2:01:1173:U:H2'	2:01:1174:U:H4'	1.36	1.04
1:A:9:G:H5'	43:E:107:GLY:HA3	1.44	1.00
18:15:50:ARG:HD3	18:15:65:ILE:HD11	1.41	1.00

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	
4	Y	30/72 (42%)	26 (87%)	4 (13%)	0	100	100
6	03	218/234 (93%)	192 (88%)	25 (12%)	1 (0%)	29	67
7	04	269/273 (98%)	244 (91%)	22 (8%)	3 (1%)	14	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	05	207/209 (99%)	181 (87%)	24 (12%)	2 (1%)	15	54
9	06	199/201 (99%)	179 (90%)	18 (9%)	2 (1%)	15	54
10	07	175/179 (98%)	148 (85%)	26 (15%)	1 (1%)	25	64
11	08	174/177 (98%)	164 (94%)	10 (6%)	0	100	100
12	09	147/149 (99%)	136 (92%)	9 (6%)	2 (1%)	11	46
13	10	129/165 (78%)	94 (73%)	32 (25%)	3 (2%)	6	34
14	11	139/142 (98%)	121 (87%)	17 (12%)	1 (1%)	22	61
15	12	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
16	13	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	5	32
17	14	141/144 (98%)	126 (89%)	13 (9%)	2 (1%)	11	46
18	15	134/136 (98%)	122 (91%)	11 (8%)	1 (1%)	22	61
19	16	118/127 (93%)	102 (86%)	15 (13%)	1 (1%)	19	58
20	17	114/117 (97%)	106 (93%)	7 (6%)	1 (1%)	17	56
21	18	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
22	19	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
23	20	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
24	21	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
25	22	91/100 (91%)	84 (92%)	6 (7%)	1 (1%)	14	51
26	23	100/104 (96%)	87 (87%)	12 (12%)	1 (1%)	15	54
27	24	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
28	25	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
29	26	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
30	27	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
31	28	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
32	29	64/70 (91%)	54 (84%)	9 (14%)	1 (2%)	9	43
33	30	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
34	31	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
35	32	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
36	33	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	9	43
37	34	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	5	29
39	Z	359/365 (98%)	310 (86%)	49 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	B	216/241 (90%)	188 (87%)	26 (12%)	2 (1%)	17	56
41	C	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
42	D	203/206 (98%)	176 (87%)	24 (12%)	3 (2%)	10	44
43	E	155/167 (93%)	137 (88%)	18 (12%)	0	100	100
44	F	98/131 (75%)	83 (85%)	14 (14%)	1 (1%)	15	54
45	G	149/156 (96%)	133 (89%)	16 (11%)	0	100	100
46	H	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
47	I	125/130 (96%)	107 (86%)	17 (14%)	1 (1%)	19	58
48	J	96/103 (93%)	78 (81%)	11 (12%)	7 (7%)	1	7
49	K	114/129 (88%)	96 (84%)	16 (14%)	2 (2%)	8	41
50	L	121/124 (98%)	99 (82%)	19 (16%)	3 (2%)	5	32
51	M	112/118 (95%)	100 (89%)	9 (8%)	3 (3%)	5	30
52	N	98/101 (97%)	80 (82%)	13 (13%)	5 (5%)	2	15
53	O	86/89 (97%)	82 (95%)	3 (4%)	1 (1%)	13	49
54	P	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
55	Q	78/84 (93%)	61 (78%)	17 (22%)	0	100	100
56	R	63/75 (84%)	52 (82%)	10 (16%)	1 (2%)	9	43
57	S	77/92 (84%)	67 (87%)	10 (13%)	0	100	100
58	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
59	U	63/71 (89%)	46 (73%)	12 (19%)	5 (8%)	1	6
All	All	6453/6864 (94%)	5709 (88%)	682 (11%)	62 (1%)	20	54

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	03	207	VAL
9	06	61	ARG
9	06	83	VAL
13	10	123	ILE
16	13	89	ASN

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	
4	Y	24/59 (41%)	23 (96%)	1 (4%)	30	65
6	03	106/181 (59%)	103 (97%)	3 (3%)	43	74
7	04	216/218 (99%)	213 (99%)	3 (1%)	67	86
8	05	164/164 (100%)	164 (100%)	0	100	100
9	06	165/165 (100%)	165 (100%)	0	100	100
10	07	148/150 (99%)	147 (99%)	1 (1%)	84	94
11	08	137/138 (99%)	133 (97%)	4 (3%)	42	74
12	09	114/114 (100%)	112 (98%)	2 (2%)	59	82
13	10	100/123 (81%)	98 (98%)	2 (2%)	55	80
14	11	109/110 (99%)	108 (99%)	1 (1%)	78	91
15	12	116/116 (100%)	113 (97%)	3 (3%)	46	76
16	13	103/104 (99%)	102 (99%)	1 (1%)	76	90
17	14	102/103 (99%)	102 (100%)	0	100	100
18	15	109/109 (100%)	106 (97%)	3 (3%)	43	74
19	16	100/104 (96%)	100 (100%)	0	100	100
20	17	86/87 (99%)	84 (98%)	2 (2%)	50	78
21	18	99/100 (99%)	99 (100%)	0	100	100
22	19	89/90 (99%)	88 (99%)	1 (1%)	73	88
23	20	84/84 (100%)	82 (98%)	2 (2%)	49	77
24	21	93/93 (100%)	92 (99%)	1 (1%)	73	88
25	22	80/84 (95%)	80 (100%)	0	100	100
26	23	83/85 (98%)	80 (96%)	3 (4%)	35	69
27	24	78/78 (100%)	78 (100%)	0	100	100
28	25	57/63 (90%)	55 (96%)	2 (4%)	36	69
29	26	67/68 (98%)	65 (97%)	2 (3%)	41	73
30	27	55/55 (100%)	55 (100%)	0	100	100
31	28	48/49 (98%)	48 (100%)	0	100	100
32	29	59/62 (95%)	58 (98%)	1 (2%)	60	83
33	30	47/48 (98%)	46 (98%)	1 (2%)	53	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	31	45/49 (92%)	45 (100%)	0	100	100
35	32	38/38 (100%)	37 (97%)	1 (3%)	46	76
36	33	51/52 (98%)	49 (96%)	2 (4%)	32	67
37	34	34/34 (100%)	31 (91%)	3 (9%)	10	36
39	Z	296/311 (95%)	290 (98%)	6 (2%)	55	80
40	B	180/199 (90%)	176 (98%)	4 (2%)	52	79
41	C	170/190 (90%)	168 (99%)	2 (1%)	71	88
42	D	172/173 (99%)	164 (95%)	8 (5%)	26	62
43	E	119/126 (94%)	113 (95%)	6 (5%)	24	60
44	F	87/112 (78%)	85 (98%)	2 (2%)	50	78
45	G	124/129 (96%)	123 (99%)	1 (1%)	81	93
46	H	104/105 (99%)	101 (97%)	3 (3%)	42	74
47	I	105/107 (98%)	104 (99%)	1 (1%)	76	90
48	J	86/90 (96%)	85 (99%)	1 (1%)	71	88
49	K	89/99 (90%)	84 (94%)	5 (6%)	21	57
50	L	103/104 (99%)	101 (98%)	2 (2%)	57	81
51	M	92/96 (96%)	92 (100%)	0	100	100
52	N	83/84 (99%)	83 (100%)	0	100	100
53	O	76/77 (99%)	74 (97%)	2 (3%)	46	76
54	P	65/65 (100%)	62 (95%)	3 (5%)	27	63
55	Q	74/78 (95%)	72 (97%)	2 (3%)	44	75
56	R	56/65 (86%)	54 (96%)	2 (4%)	35	69
57	S	70/79 (89%)	70 (100%)	0	100	100
58	T	65/66 (98%)	63 (97%)	2 (3%)	40	72
59	U	55/61 (90%)	53 (96%)	2 (4%)	35	69
All	All	5277/5593 (94%)	5178 (98%)	99 (2%)	59	81

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	D	20	LEU
44	F	14	GLN
42	D	31	CYS

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Mol	Chain	Res	Type
43	E	9	GLU
46	H	113	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
47	I	24	ASN
48	J	58	ASN
53	O	27	GLN
22	19	80	ASN
22	19	43	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	176 (11%)	3 (0%)
2	01	2902/2903 (99%)	332 (11%)	3 (0%)
3	02	118/119 (99%)	9 (7%)	0
38	V	13/14 (92%)	1 (7%)	0
5	W	76/77 (98%)	8 (10%)	0
5	X	76/77 (98%)	14 (18%)	0
All	All	4723/4729 (99%)	540 (11%)	6 (0%)

5 of 540 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	6	G
1	A	7	A
1	A	9	G
1	A	22	G

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	01	490	C
2	01	859	G
2	01	2326	C
1	A	343	U
1	A	69	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 349 ligands modelled in this entry, 349 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

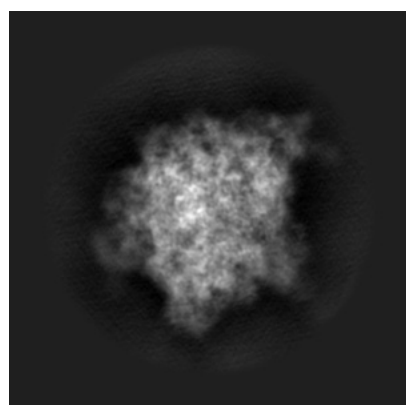
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8522. These allow visual inspection of the internal detail of the map and identification of artifacts.

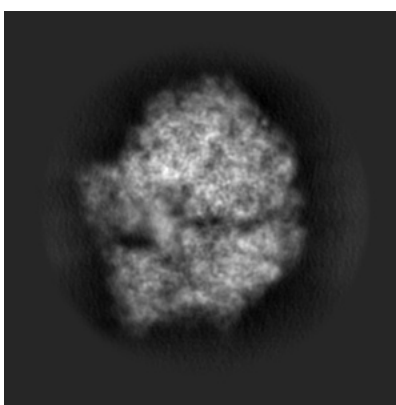
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

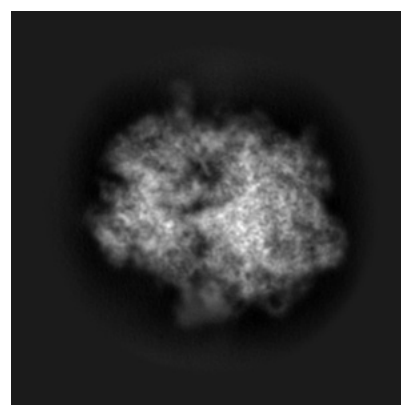
6.1.1 Primary map



X



Y

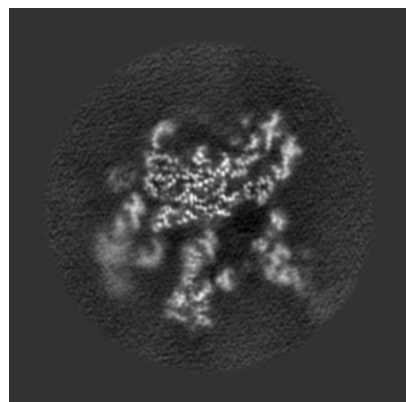


Z

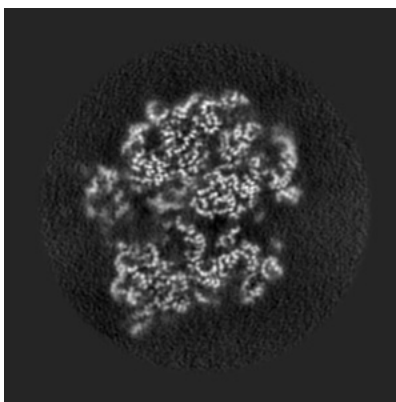
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

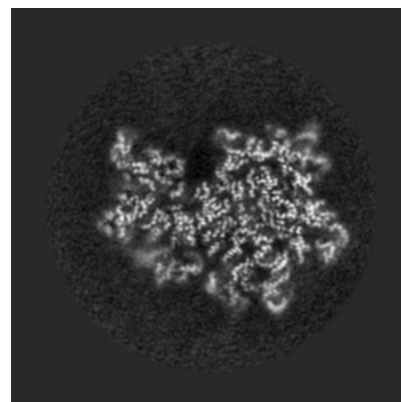
6.2.1 Primary map



X Index: 160



Y Index: 160

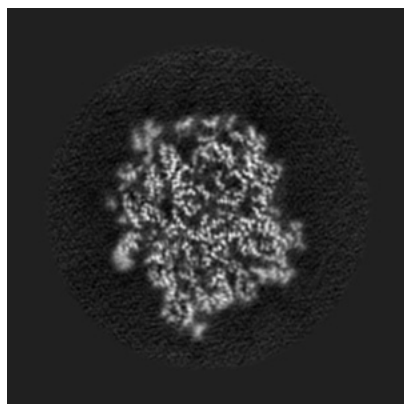


Z Index: 160

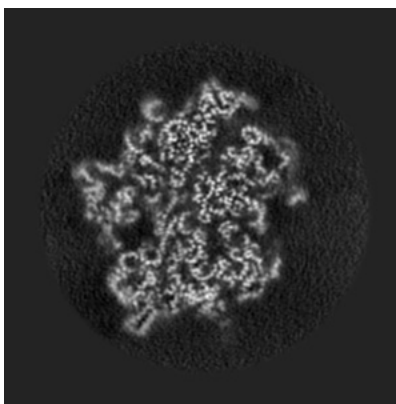
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

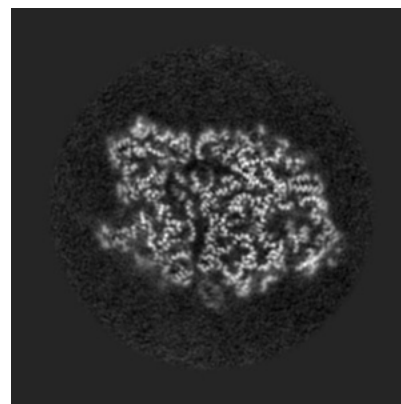
6.3.1 Primary map



X Index: 188



Y Index: 154



Z Index: 185

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 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

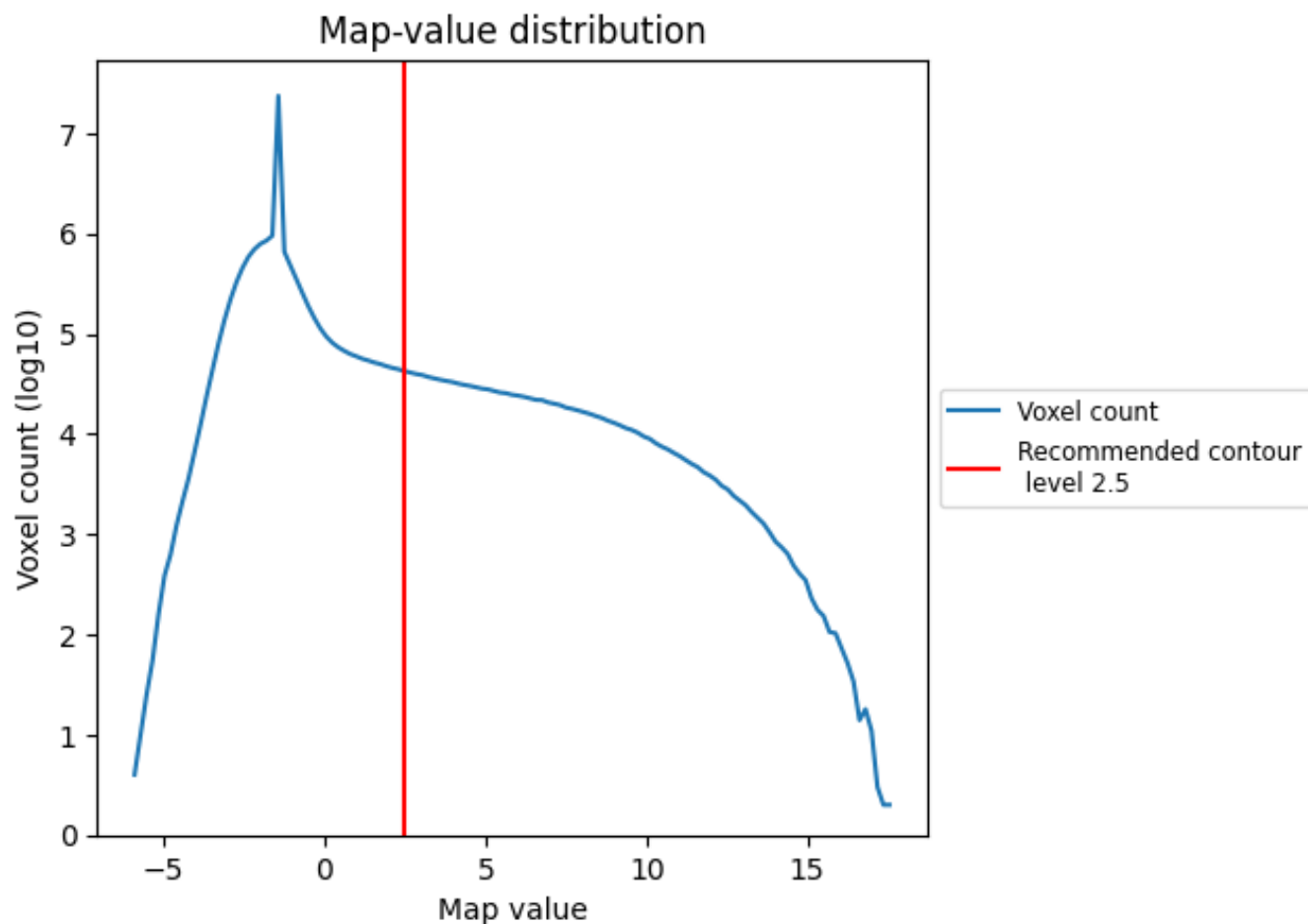
6.5 Mask visualisation

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

7 Map analysis [i](#)

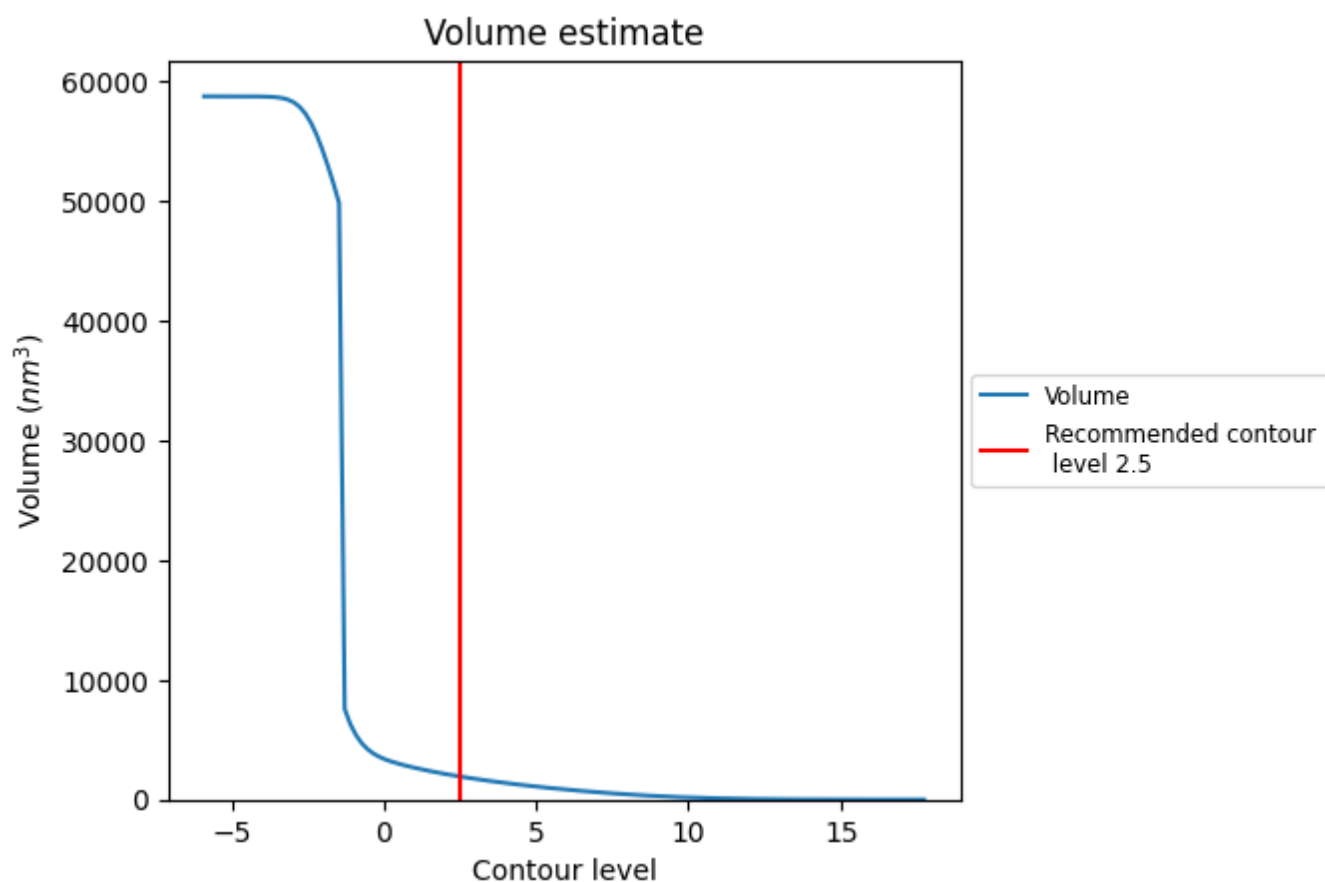
This section contains the results of statistical analysis of the map.

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.

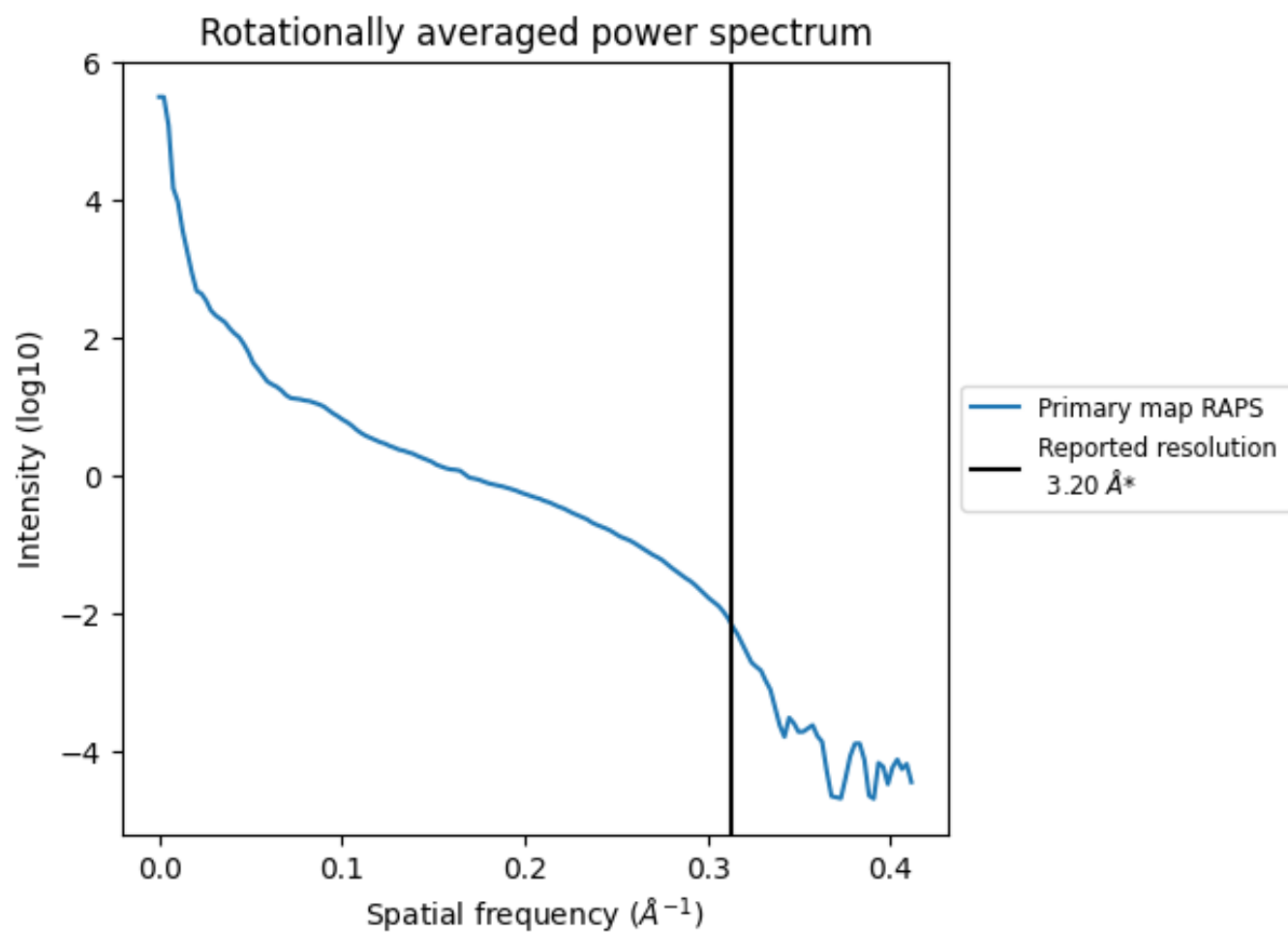
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1927 nm³; this corresponds to an approximate mass of 1740 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 0.312 Å⁻¹

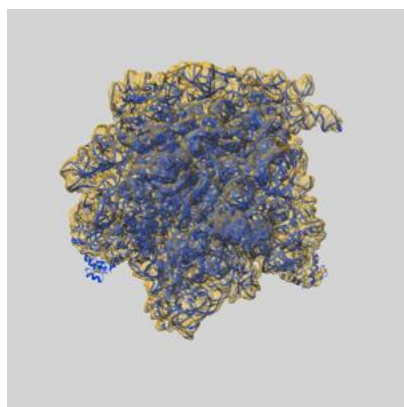
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

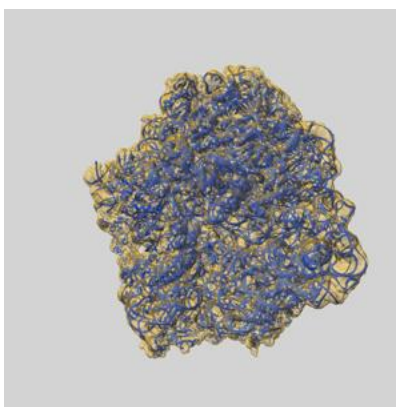
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8522 and PDB model 5U9G. Per-residue inclusion information can be found in section 3 on page 16.

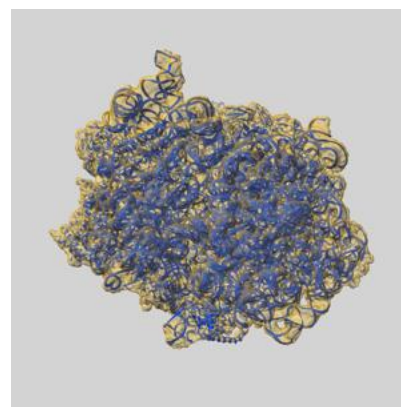
9.1 Map-model overlay [i](#)



X



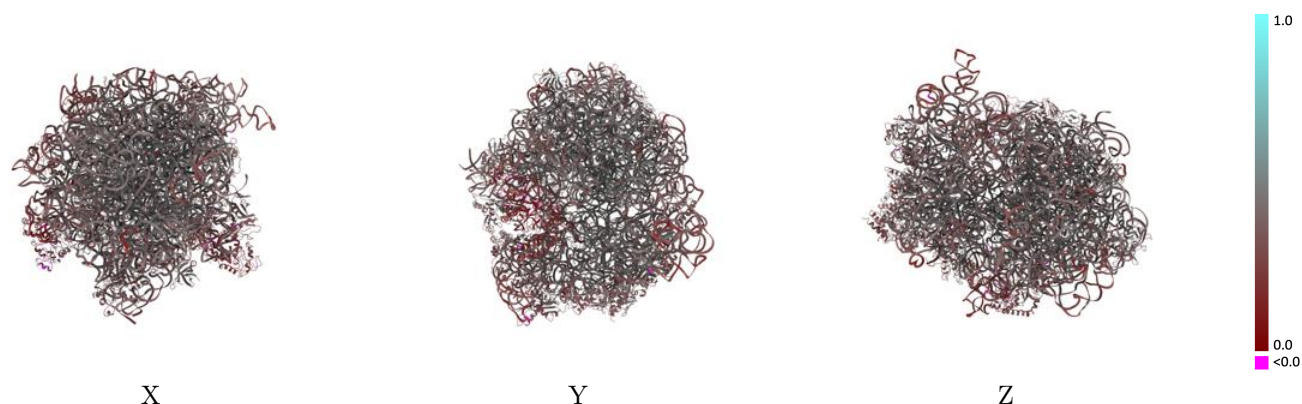
Y



Z

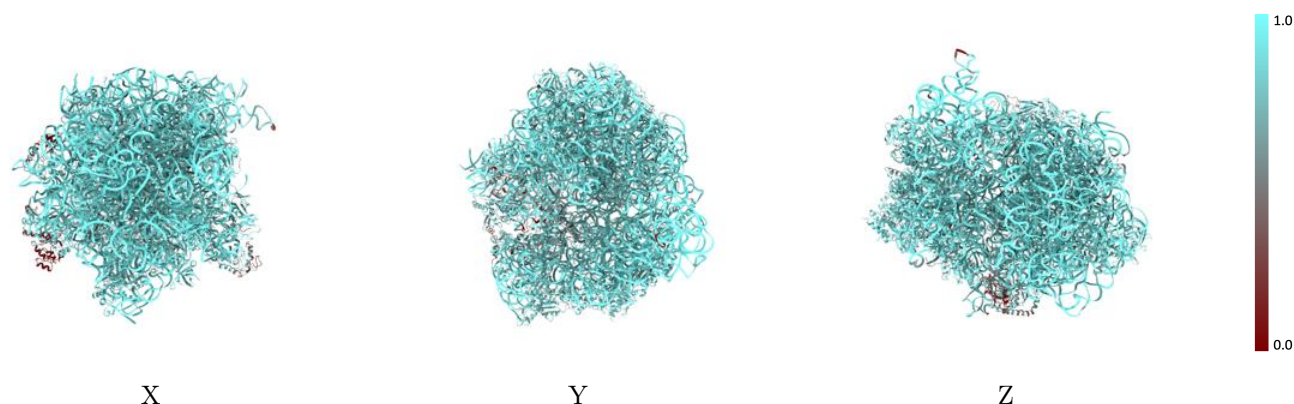
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



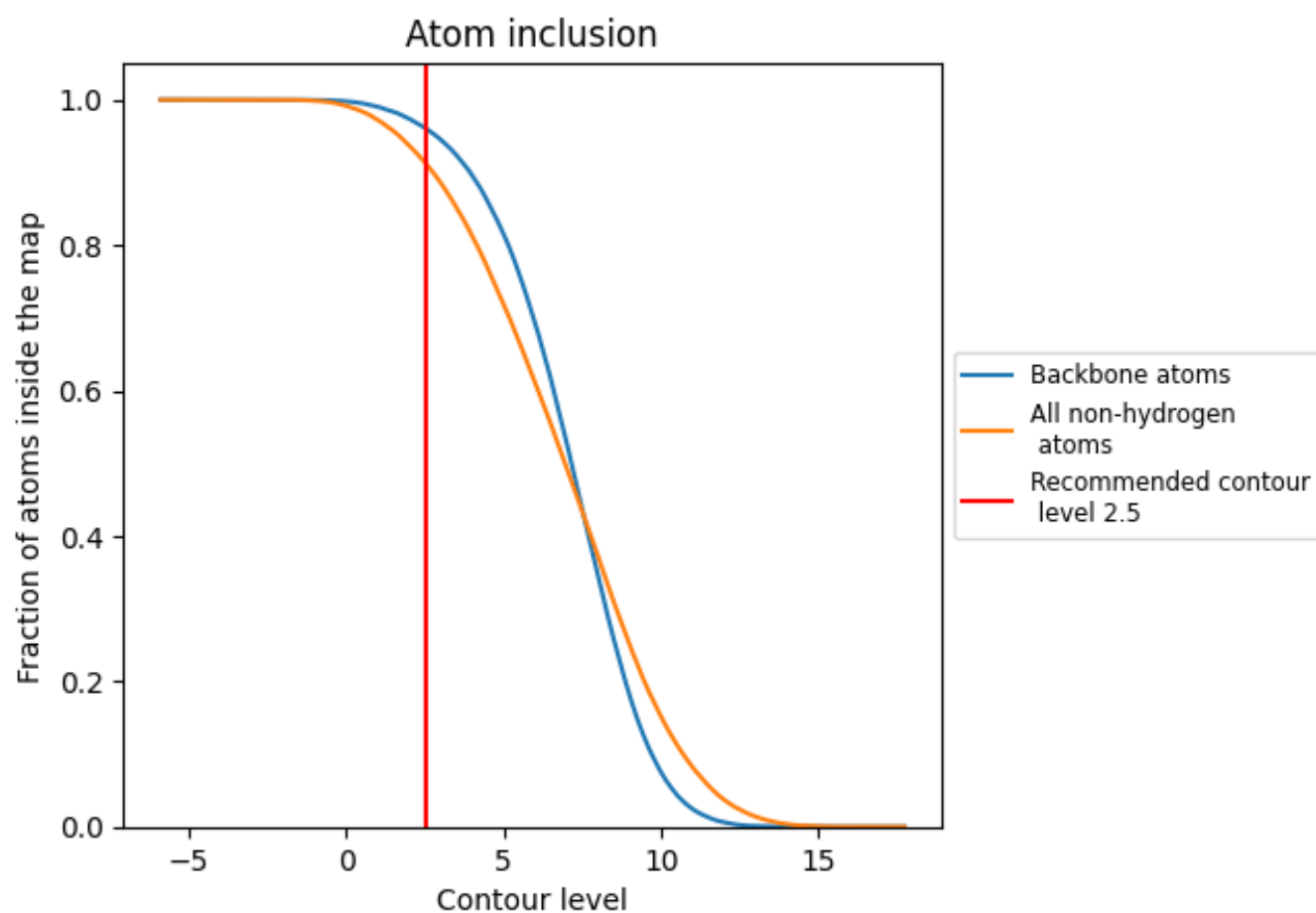
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9136	 0.3870
01	 0.9762	 0.4080
02	 0.9839	 0.3710
03	 0.4326	 0.2010
04	 0.8393	 0.4400
05	 0.8687	 0.4320
06	 0.8592	 0.3960
07	 0.8602	 0.3290
08	 0.8458	 0.3660
09	 0.3896	 0.3110
10	 0.5424	 0.2010
11	 0.6898	 0.2190
12	 0.8755	 0.4110
13	 0.7853	 0.4230
14	 0.8682	 0.4130
15	 0.8244	 0.4150
16	 0.8807	 0.3950
17	 0.8934	 0.3600
18	 0.8367	 0.4100
19	 0.8943	 0.4060
20	 0.8783	 0.4170
21	 0.8254	 0.4100
22	 0.7950	 0.3750
23	 0.8475	 0.3900
24	 0.8686	 0.3900
25	 0.9125	 0.4380
26	 0.8469	 0.4180
27	 0.8089	 0.3180
28	 0.8604	 0.4030
29	 0.5225	 0.2850
30	 0.8671	 0.4190
31	 0.7855	 0.4030
32	 0.8620	 0.4390
33	 0.8798	 0.4370
34	 0.8396	 0.4150



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Chain	Atom inclusion	Q-score
A	 0.9760	 0.3940
B	 0.8078	 0.3340
C	 0.8169	 0.3840
D	 0.8340	 0.3630
E	 0.8580	 0.4040
F	 0.8128	 0.3560
G	 0.8024	 0.3250
H	 0.8678	 0.3970
I	 0.8621	 0.3430
J	 0.8187	 0.3360
K	 0.8568	 0.3880
L	 0.8100	 0.4200
M	 0.7861	 0.3240
N	 0.8475	 0.3470
O	 0.8623	 0.3550
P	 0.8852	 0.3970
Q	 0.8544	 0.3840
R	 0.8268	 0.3740
S	 0.8647	 0.3550
T	 0.8385	 0.3400
U	 0.7408	 0.2680
V	 0.8856	 0.3090
W	 0.9111	 0.3830
X	 0.6201	 0.2200
Y	 0.7934	 0.3870
Z	 0.6488	 0.2770