



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 05:18 pm GMT

PDB ID : 5NWY
EMDB ID : EMD-3713
Title : 2.9 Å cryo-EM structure of VemP-stalled ribosome-nascent chain complex
Authors : Su, T.; Cheng, J.; Sohmen, D.; Hedman, R.; Berninghausen, O.; von Heijne, G.; Wilson, D.N.; Beckmann, R.
Deposited on : 2017-05-08
Resolution : 2.93 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

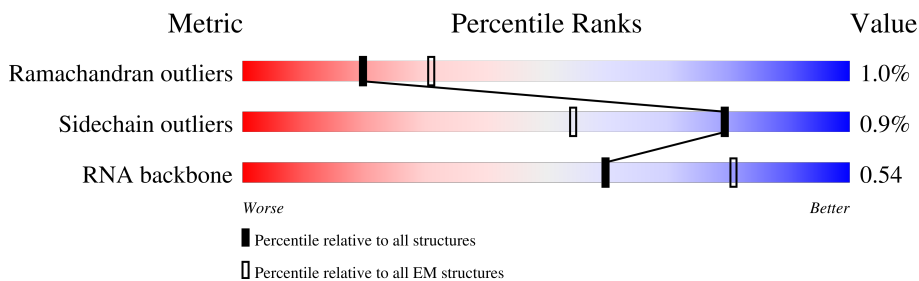
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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.




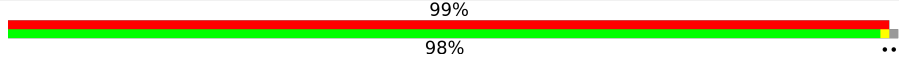
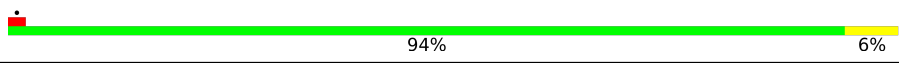
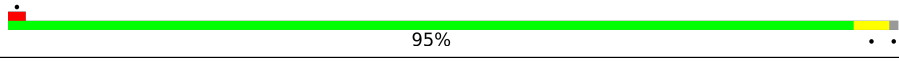
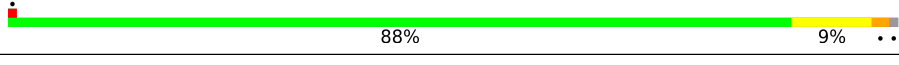
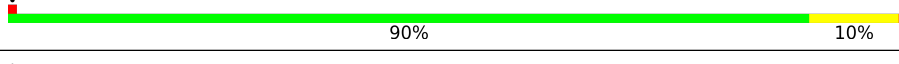
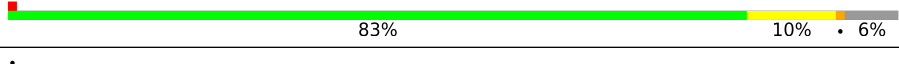
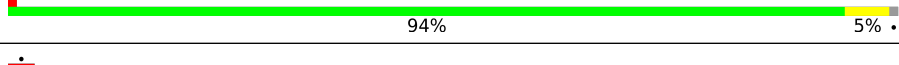
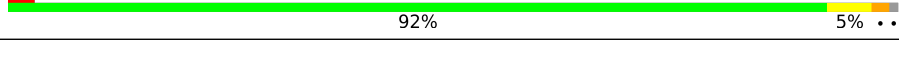
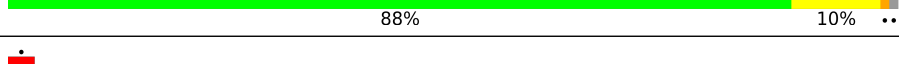
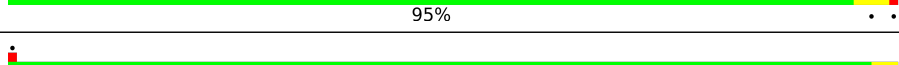
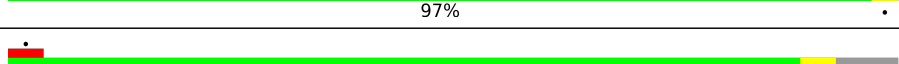

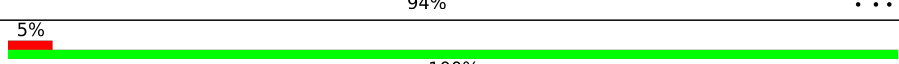
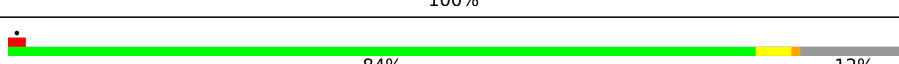
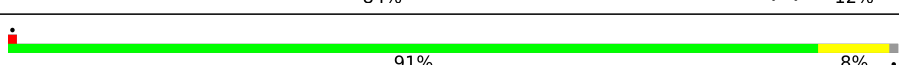
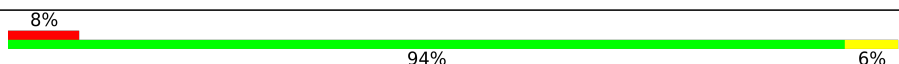
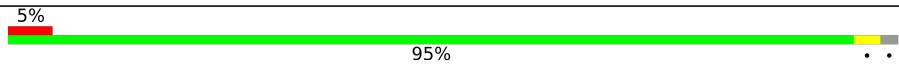
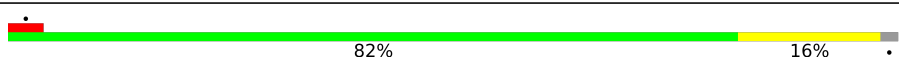

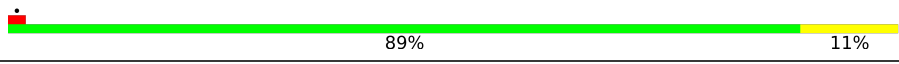
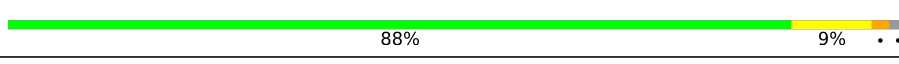
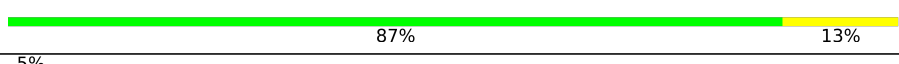


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	s	179	
2	M	75	
3	O	120	
4	P	273	
5	Q	209	
6	R	201	
7	S	179	
8	T	177	

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Mol	Chain	Length	Quality of chain
9	U	149	
10	V	142	
11	W	142	
12	X	123	
13	Y	144	
14	Z	136	
15	a	127	
16	b	117	
17	c	115	
18	d	118	
19	e	103	
20	f	110	
21	g	100	
22	h	104	
23	i	94	
24	j	85	
25	k	78	
26	l	63	
27	m	59	
28	n	57	
29	o	55	
30	p	46	
31	q	65	
32	r	38	
33	N	2903	

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Mol	Chain	Length	Quality of chain
34	L	70	26% 91% 6%
35	0	1539	73% 25%
36	1	233	9% 90% 6%
37	2	233	5% 85% 12%
38	3	206	7% 97%
39	4	166	81% 8% 10%
40	5	131	5% 66% 10% 24%
41	6	156	10% 94%
42	7	130	98%
43	8	130	10% 88% 9%
44	9	103	17% 89% 5% 5%
45	A	129	87% 9%
46	B	124	90% 7%
47	C	118	90% 6%
48	D	101	6% 88% 7% 5%
49	E	89	91% 7%
50	F	82	7% 94% 6%
51	G	84	7% 88% 7% 5%
52	H	75	68% 5% 27%
53	I	92	83% 14%
54	J	87	5% 93%
55	K	71	28% 66% 28%
56	t	4	50% 50%

2 Entry composition i

There are 56 unique types of molecules in this entry. The entry contains 144142 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 VemP nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	s	37	316	198	58	58	2	0	0

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	-2	MET	-	initiating methionine	UNP A0A0P7EF65
s	-1	HIS	-	expression tag	UNP A0A0P7EF65
s	0	HIS	-	expression tag	UNP A0A0P7EF65
s	1	HIS	-	expression tag	UNP A0A0P7EF65
s	2	HIS	-	expression tag	UNP A0A0P7EF65
s	3	HIS	-	expression tag	UNP A0A0P7EF65
s	4	HIS	-	expression tag	UNP A0A0P7EF65
s	5	HIS	-	expression tag	UNP A0A0P7EF65
s	6	HIS	-	expression tag	UNP A0A0P7EF65
s	7	HIS	-	expression tag	UNP A0A0P7EF65
s	8	HIS	-	expression tag	UNP A0A0P7EF65
s	9	GLY	-	expression tag	UNP A0A0P7EF65
s	10	ASP	-	expression tag	UNP A0A0P7EF65
s	11	TYR	-	expression tag	UNP A0A0P7EF65
s	12	LYS	-	expression tag	UNP A0A0P7EF65
s	13	ASP	-	expression tag	UNP A0A0P7EF65
s	14	ASP	-	expression tag	UNP A0A0P7EF65
s	15	ASP	-	expression tag	UNP A0A0P7EF65
s	16	ASP	-	expression tag	UNP A0A0P7EF65
s	17	LYS	-	expression tag	UNP A0A0P7EF65
s	18	GLU	-	expression tag	UNP A0A0P7EF65
s	19	ASN	-	expression tag	UNP A0A0P7EF65
s	20	LEU	-	expression tag	UNP A0A0P7EF65
s	21	TYR	-	expression tag	UNP A0A0P7EF65
s	22	PHE	-	expression tag	UNP A0A0P7EF65
s	23	GLN	-	expression tag	UNP A0A0P7EF65
s	24	GLY	-	expression tag	UNP A0A0P7EF65
s	25	SER	-	expression tag	UNP A0A0P7EF65

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Chain	Residue	Modelled	Actual	Comment	Reference
s	30	GLN	HIS	conflict	UNP A0A0P7EF65
s	59	ALA	VAL	conflict	UNP A0A0P7EF65
s	160	LEU	-	expression tag	UNP A0A0P7EF65
s	161	GLU	-	expression tag	UNP A0A0P7EF65
s	162	VAL	-	expression tag	UNP A0A0P7EF65
s	163	LEU	-	expression tag	UNP A0A0P7EF65
s	164	PHE	-	expression tag	UNP A0A0P7EF65
s	165	GLN	-	expression tag	UNP A0A0P7EF65
s	166	GLY	-	expression tag	UNP A0A0P7EF65
s	167	PRO	-	expression tag	UNP A0A0P7EF65
s	168	TYR	-	expression tag	UNP A0A0P7EF65
s	169	PRO	-	expression tag	UNP A0A0P7EF65
s	170	TYR	-	expression tag	UNP A0A0P7EF65
s	171	ASP	-	expression tag	UNP A0A0P7EF65
s	172	VAL	-	expression tag	UNP A0A0P7EF65
s	173	PRO	-	expression tag	UNP A0A0P7EF65
s	174	ASP	-	expression tag	UNP A0A0P7EF65
s	175	TYR	-	expression tag	UNP A0A0P7EF65
s	176	ALA	-	expression tag	UNP A0A0P7EF65

- Molecule 2 is a RNA chain called Gln-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	M	75	1594	711	281	527	75	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	O	118	2529	1126	464	821	118	0	0

- Molecule 4 is a protein called 50S ribosomal protein L2.

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

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	T	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	U	47	Total	C	N	O	S	0	0
			359	233	62	63	1		

- Molecule 10 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	W	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Z	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

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

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	b	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	114	Total	C	N	O	S	0	0
			915	573	179	162	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	d	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	e	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

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

- Molecule 22 is a protein called 50S ribosomal protein L24.

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

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	i	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	j	75	Total	C	N	O	S	0	0
			568	353	113	101	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	k	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	l	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	m	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	n	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
29	o	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	p	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	q	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	r	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 33 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
33	N	2897	62215	27754	11448	20115	2898	1	0

- Molecule 34 is a protein called 50S ribosomal protein L31.

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

- Molecule 35 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	0	1539	33015	14725	6052	10699	1539	0	0

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	1	218	1704	1081	305	311	7	0	0

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	2	206	1624	1028	305	288	3	0	0

- Molecule 38 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	3	205	1642	1026	315	297	4	0	0

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	4	150	1105	687	211	201	6	0	0

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	5	100	817	515	148	148	6	0	0

- Molecule 41 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	6	151	1181	735	227	215	4	0	0

- Molecule 42 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	7	129	978	616	173	183	6	0	0

- Molecule 43 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	8	127	1021	634	206	178	3	0	0

- Molecule 44 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	9	98	786	493	150	142	1	0	0

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	A	117	876	540	174	159	3	0	0

- Molecule 46 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	B	123	954	590	196	164	4	0	0

- Molecule 47 is a protein called 30S ribosomal protein S13.

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

- Molecule 48 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	D	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

- Molecule 49 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	E	88	Total	C	N	O	S	0	0
			709	437	143	128	1		

- Molecule 50 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 51 is a protein called 30S ribosomal protein S17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	H	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 53 is a protein called 30S ribosomal protein S19.

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

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	J	85	664	411	137	113	3	0	0

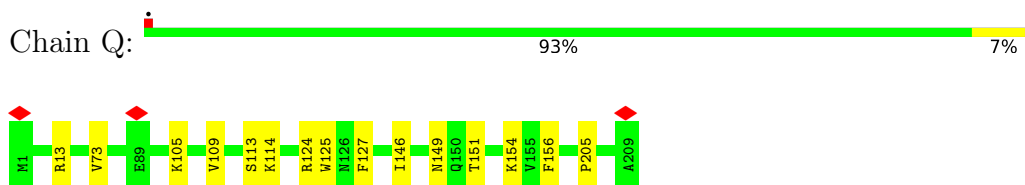
- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	K	51	425	265	86	73	1	0	0

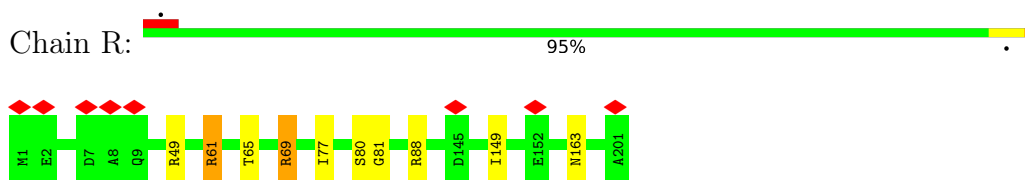
- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	t	4	85	38	15	28	4	0	0

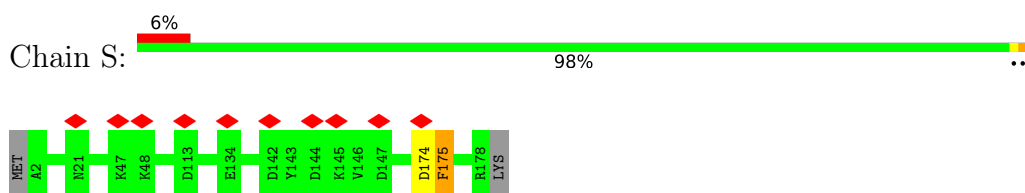
• Molecule 5: 50S ribosomal protein L3



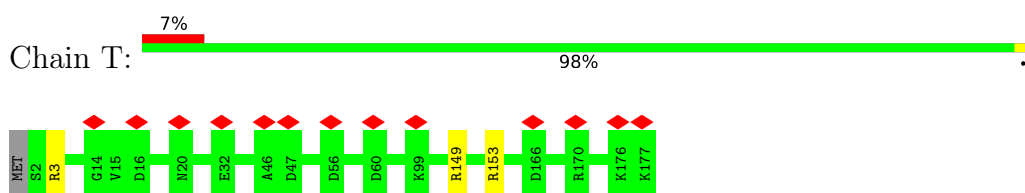
• Molecule 6: 50S ribosomal protein L4



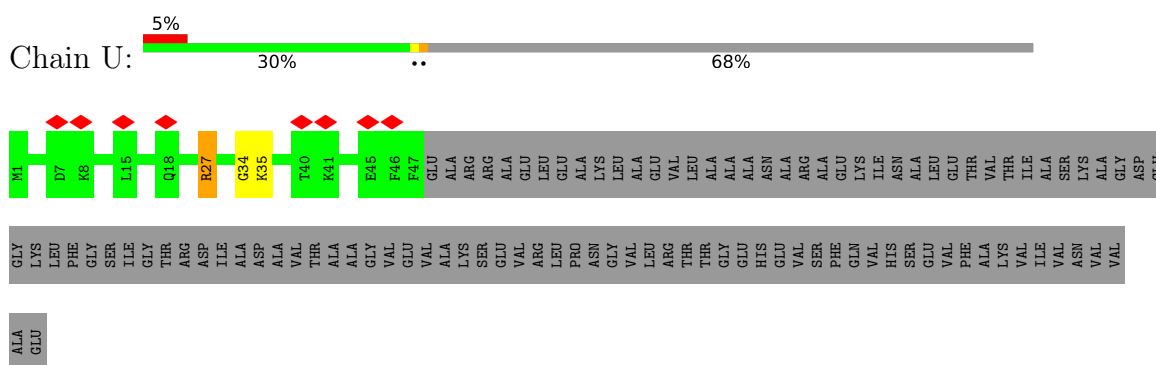
• Molecule 7: 50S ribosomal protein L5



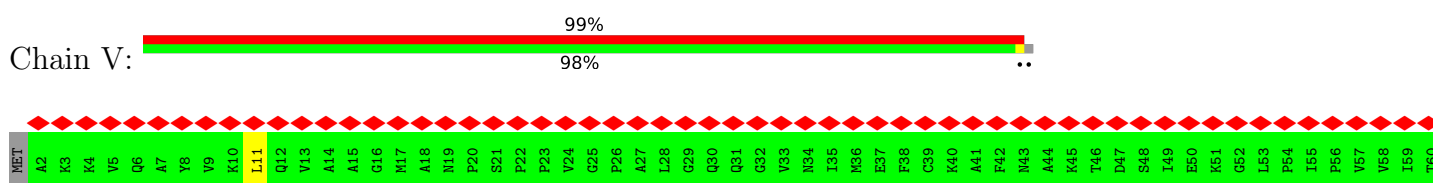
• Molecule 8: 50S ribosomal protein L6

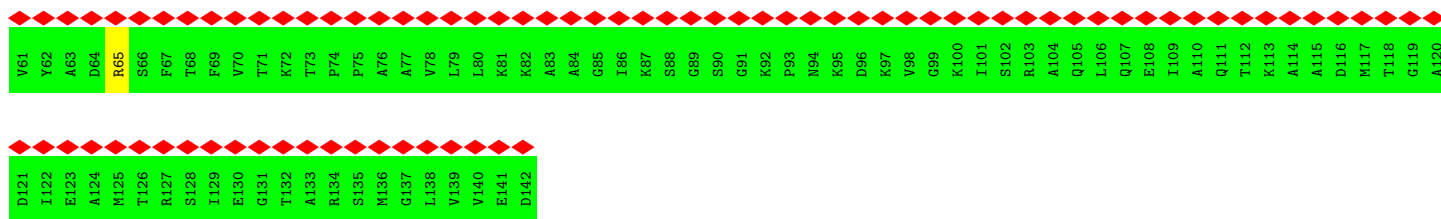


• Molecule 9: 50S ribosomal protein L9

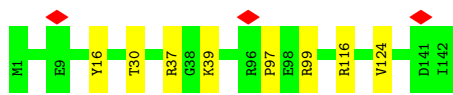


• Molecule 10: 50S ribosomal protein L11

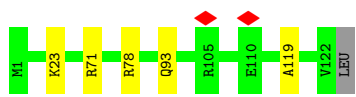




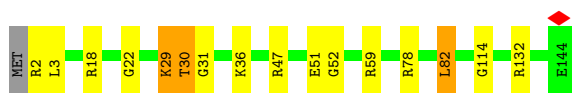
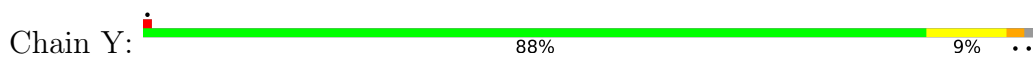
• Molecule 11: 50S ribosomal protein L13



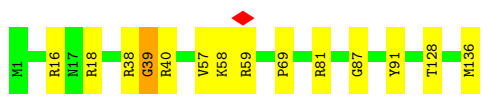
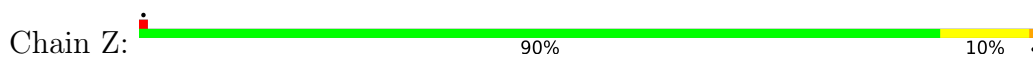
• Molecule 12: 50S ribosomal protein L14



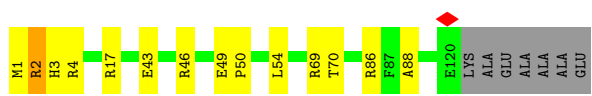
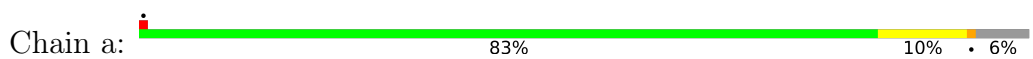
• Molecule 13: 50S ribosomal protein L15



• Molecule 14: 50S ribosomal protein L16



• Molecule 15: 50S ribosomal protein L17

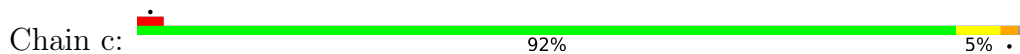


• Molecule 16: 50S ribosomal protein L18

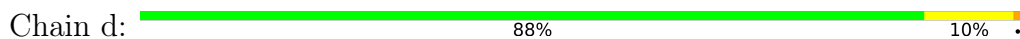




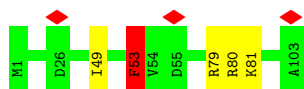
- Molecule 17: 50S ribosomal protein L19



- Molecule 18: 50S ribosomal protein L20



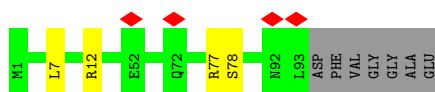
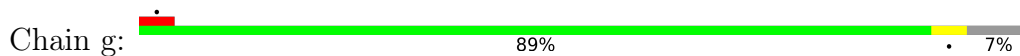
- Molecule 19: 50S ribosomal protein L21



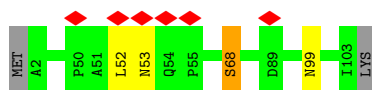
- Molecule 20: 50S ribosomal protein L22



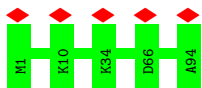
- Molecule 21: 50S ribosomal protein L23



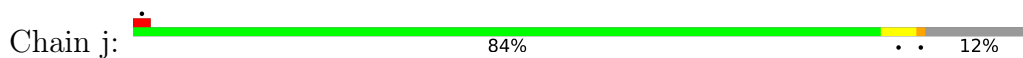
- Molecule 22: 50S ribosomal protein L24



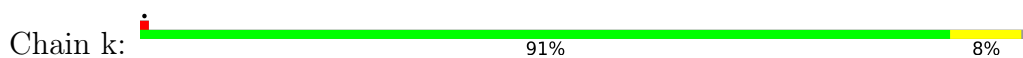
- Molecule 23: 50S ribosomal protein L25



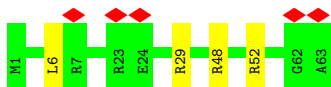
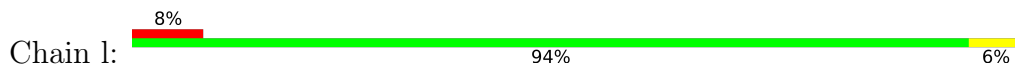
- Molecule 24: 50S ribosomal protein L27



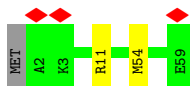
- Molecule 25: 50S ribosomal protein L28



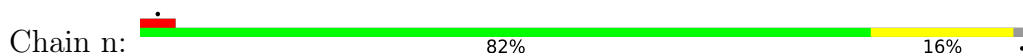
- Molecule 26: 50S ribosomal protein L29



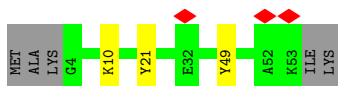
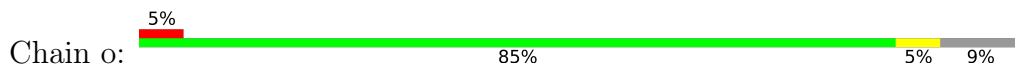
- Molecule 27: 50S ribosomal protein L30



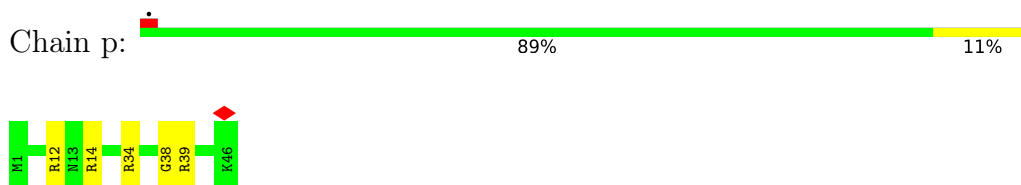
- Molecule 28: 50S ribosomal protein L32



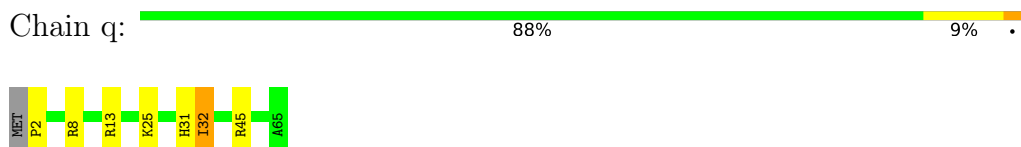
- Molecule 29: 50S ribosomal protein L33



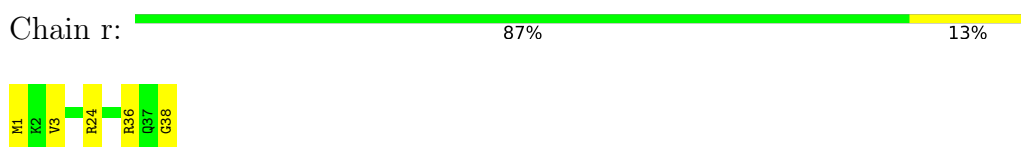
• Molecule 30: 50S ribosomal protein L34



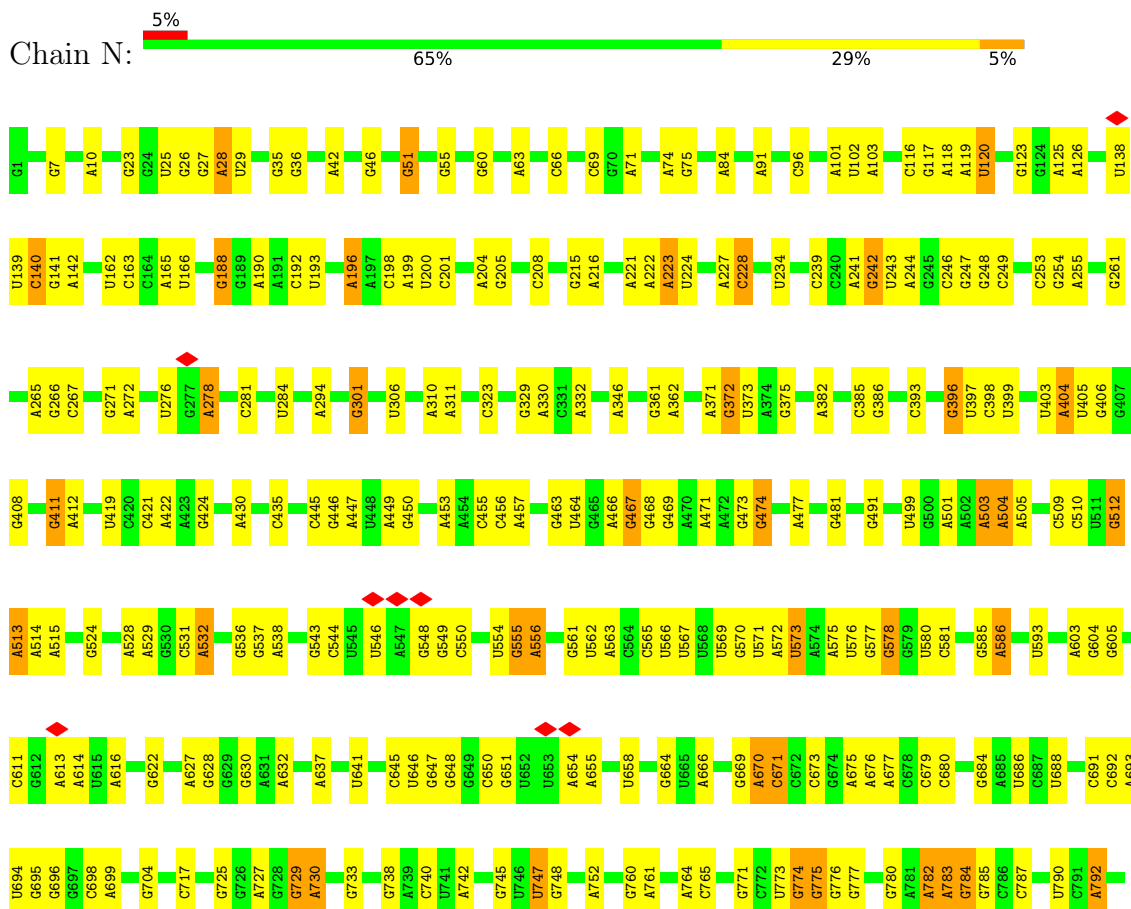
• Molecule 31: 50S ribosomal protein L35

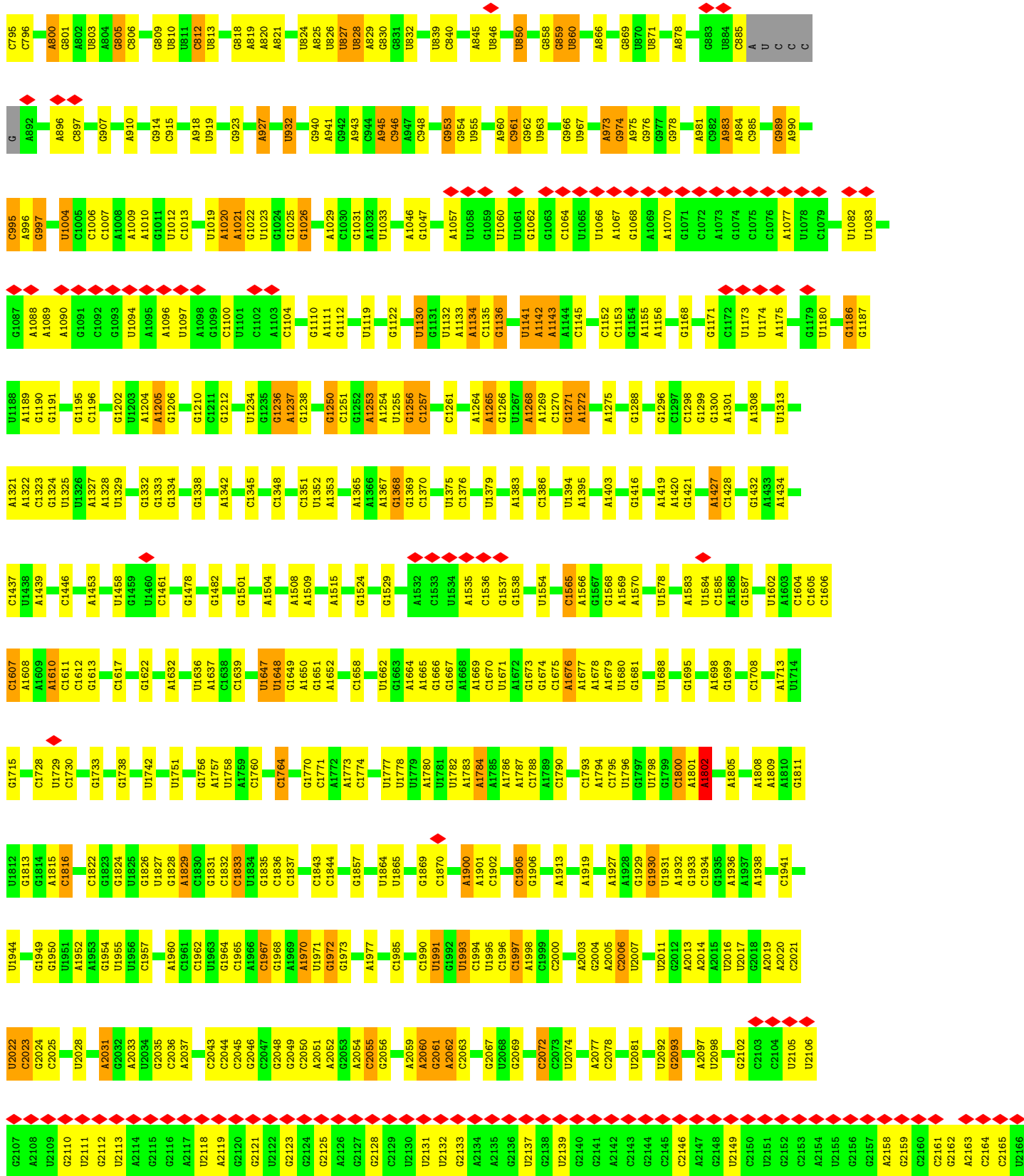


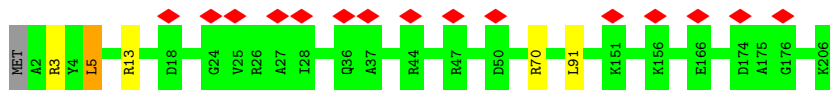
• Molecule 32: 50S ribosomal protein L36



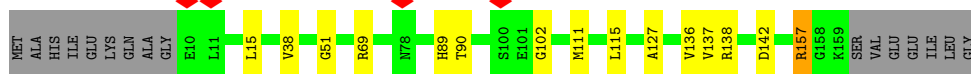
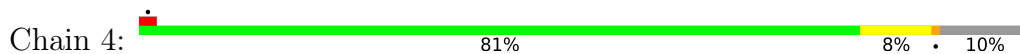
• Molecule 33: 23S rRNA







• Molecule 39: 30S ribosomal protein S5

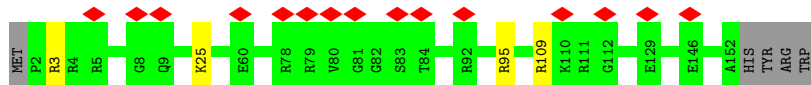


• Molecule 40: 30S ribosomal protein S6



GLU

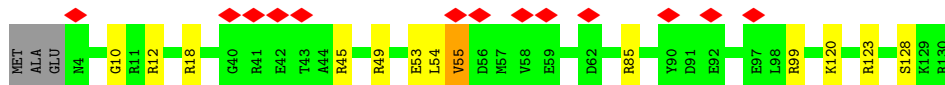
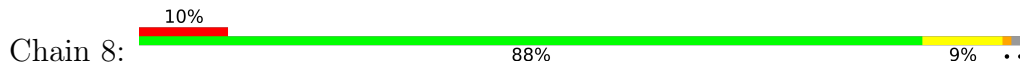
• Molecule 41: 30S ribosomal protein S7



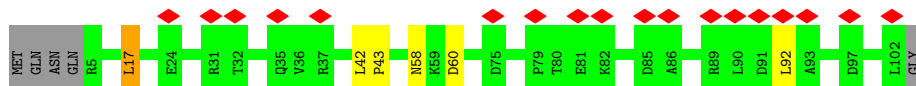
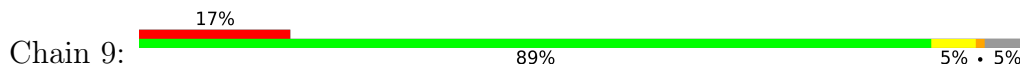
• Molecule 42: 30S ribosomal protein S8



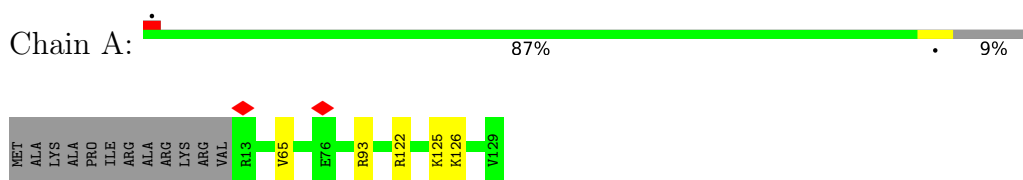
• Molecule 43: 30S ribosomal protein S9



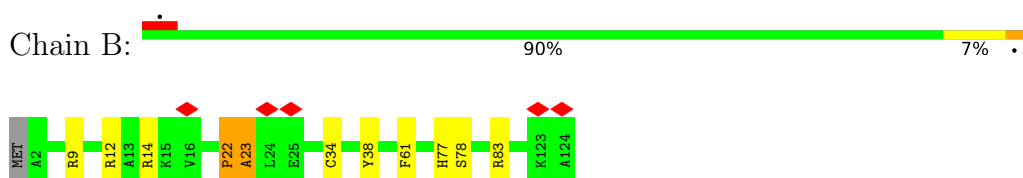
• Molecule 44: 30S ribosomal protein S10



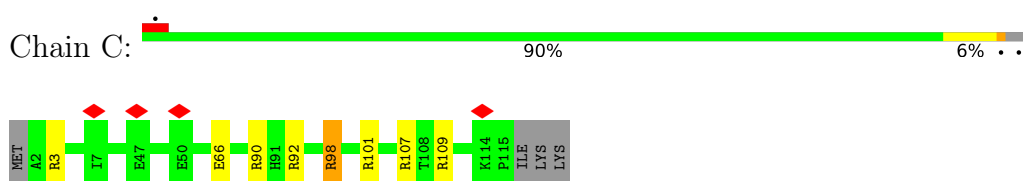
- Molecule 45: 30S ribosomal protein S11



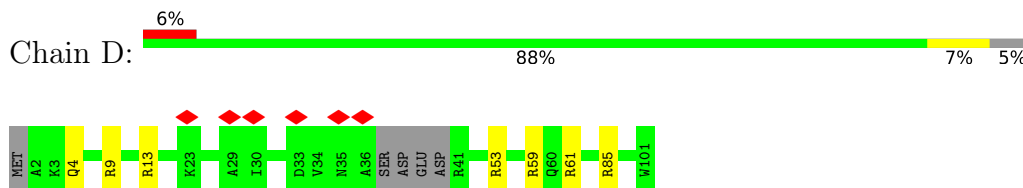
- Molecule 46: 30S ribosomal protein S12



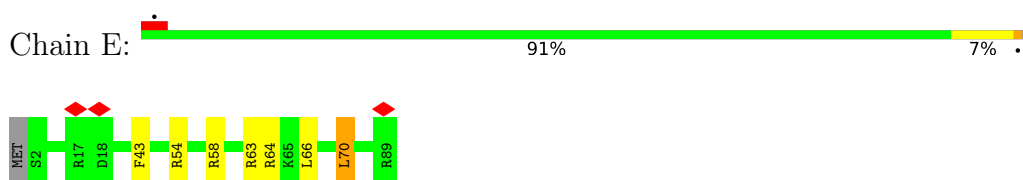
- Molecule 47: 30S ribosomal protein S13



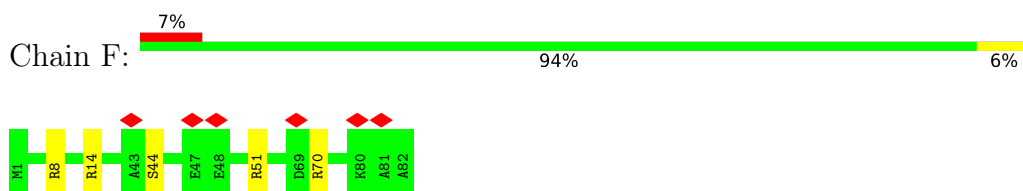
- Molecule 48: 30S ribosomal protein S14



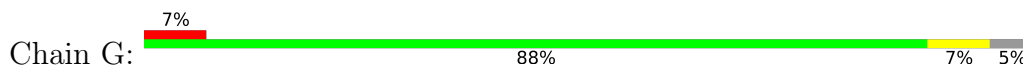
- Molecule 49: 30S ribosomal protein S15



- Molecule 50: 30S ribosomal protein S16

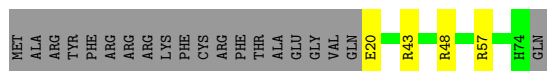


- Molecule 51: 30S ribosomal protein S17

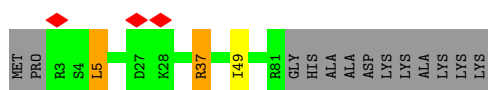
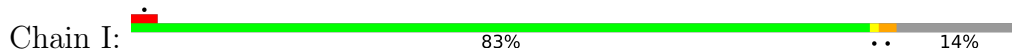




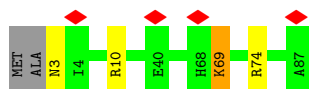
• Molecule 52: 30S ribosomal protein S18



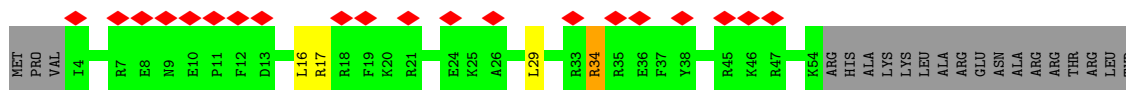
• Molecule 53: 30S ribosomal protein S19



• Molecule 54: 30S ribosomal protein S20



• Molecule 55: 30S ribosomal protein S21



• Molecule 56: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	400024	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.318	Depositor
Minimum map value	-0.174	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.03	Depositor
Map size (\AA)	398.912, 398.912, 398.912	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	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	s	0.89	1/326 (0.3%)	0.80	1/441 (0.2%)
2	M	0.63	3/1779 (0.2%)	0.83	2/2768 (0.1%)
3	O	0.79	2/2828 (0.1%)	0.87	6/4410 (0.1%)
4	P	1.41	22/2121 (1.0%)	1.32	27/2852 (0.9%)
5	Q	1.18	3/1585 (0.2%)	1.13	8/2134 (0.4%)
6	R	0.97	3/1571 (0.2%)	1.02	9/2113 (0.4%)
7	S	0.67	0/1434	0.85	0/1926
8	T	0.67	0/1342	0.83	4/1816 (0.2%)
9	U	0.76	0/364	1.05	1/490 (0.2%)
10	V	0.52	0/1045	0.65	0/1410
11	W	1.10	4/1151 (0.3%)	1.10	7/1551 (0.5%)
12	X	1.15	0/947	1.19	5/1268 (0.4%)
13	Y	1.30	3/1053 (0.3%)	1.38	13/1403 (0.9%)
14	Z	1.13	2/1092 (0.2%)	1.19	7/1460 (0.5%)
15	a	1.28	3/973 (0.3%)	1.30	10/1301 (0.8%)
16	b	0.84	2/901 (0.2%)	1.08	8/1209 (0.7%)
17	c	1.09	3/927 (0.3%)	1.19	7/1240 (0.6%)
18	d	1.32	5/959 (0.5%)	1.37	15/1278 (1.2%)
19	e	1.08	2/828 (0.2%)	1.08	3/1107 (0.3%)
20	f	1.02	1/864 (0.1%)	1.09	1/1156 (0.1%)
21	g	0.91	0/744	1.01	2/994 (0.2%)
22	h	0.82	1/787 (0.1%)	0.89	0/1051
23	i	0.78	0/765	0.86	0/1025
24	j	1.21	2/575 (0.3%)	1.29	6/762 (0.8%)
25	k	1.09	1/634 (0.2%)	1.15	6/848 (0.7%)
26	l	0.71	0/509	1.05	4/677 (0.6%)
27	m	0.86	0/452	1.08	2/605 (0.3%)
28	n	1.16	2/449 (0.4%)	1.42	7/599 (1.2%)
29	o	1.31	7/416 (1.7%)	0.96	1/554 (0.2%)
30	p	1.38	3/379 (0.8%)	1.75	6/498 (1.2%)
31	q	1.14	0/512	1.26	6/676 (0.9%)
32	r	1.15	1/302 (0.3%)	1.35	5/397 (1.3%)
33	N	1.24	512/69681 (0.7%)	1.04	347/108706 (0.3%)
34	L	0.61	0/531	0.85	0/709

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	0	0.96	132/36966 (0.4%)	0.93	107/57666 (0.2%)
36	1	0.82	2/1735 (0.1%)	0.94	3/2338 (0.1%)
37	2	0.85	1/1651 (0.1%)	0.95	4/2225 (0.2%)
38	3	0.75	0/1664	0.98	6/2227 (0.3%)
39	4	1.11	1/1118 (0.1%)	1.21	6/1504 (0.4%)
40	5	0.90	1/835 (0.1%)	1.04	4/1128 (0.4%)
41	6	0.66	0/1195	0.95	5/1602 (0.3%)
42	7	0.88	0/988	0.99	2/1326 (0.2%)
43	8	0.85	0/1033	1.13	7/1375 (0.5%)
44	9	0.74	0/796	1.01	3/1077 (0.3%)
45	A	0.85	1/892 (0.1%)	1.03	3/1205 (0.2%)
46	B	1.09	3/968 (0.3%)	1.22	7/1300 (0.5%)
47	C	0.85	1/892 (0.1%)	1.12	9/1193 (0.8%)
48	D	0.86	0/784	1.14	7/1043 (0.7%)
49	E	0.94	0/717	1.14	8/959 (0.8%)
50	F	0.94	0/658	1.16	5/884 (0.6%)
51	G	0.82	0/657	1.02	0/881
52	H	0.98	1/462 (0.2%)	1.11	2/621 (0.3%)
53	I	0.81	0/652	1.05	3/877 (0.3%)
54	J	0.89	0/670	1.06	3/888 (0.3%)
55	K	1.07	1/430 (0.2%)	1.24	4/570 (0.7%)
56	t	0.87	0/94	0.96	1/144 (0.7%)
All	All	1.10	732/156683 (0.5%)	1.03	725/234467 (0.3%)

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
4	P	0	3
5	Q	0	1
7	S	0	2
9	U	0	1
10	V	0	1
13	Y	0	2
14	Z	0	2
22	h	0	1
31	q	0	1
33	N	0	7
35	0	0	5
36	1	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
37	2	0	2
39	4	0	5
40	5	0	2
43	8	0	4
45	A	0	1
46	B	0	2
51	G	0	2
53	I	0	1
54	J	0	1
55	K	0	1
All	All	0	50

The worst 5 of 732 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	N	2873	A	C6-N1	-20.61	1.21	1.35
33	N	2765	A	C6-N1	-18.53	1.22	1.35
33	N	2502	G	P-OP2	16.69	1.77	1.49
33	N	503	A	C6-N1	-15.32	1.24	1.35
33	N	1156	A	P-OP2	15.22	1.74	1.49

The worst 5 of 725 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	N	2506[A]	U	OP1-P-O3'	17.15	142.94	105.20
33	N	2506[B]	U	OP1-P-O3'	17.15	142.94	105.20
30	p	39	ARG	NE-CZ-NH1	16.10	128.35	120.30
30	p	39	ARG	NE-CZ-NH2	-14.77	112.91	120.30
2	M	73	C	O3'-P-O5'	14.38	131.32	104.00

There are no chirality outliers.

5 of 50 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	P	195	VAL	Peptide
4	P	234	GLY	Peptide
4	P	238	ARG	Peptide
5	Q	151	THR	Peptide
7	S	174	ASP	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	s	35/179 (20%)	32 (91%)	3 (9%)	0	100	100
4	P	269/273 (98%)	247 (92%)	18 (7%)	4 (2%)	10	32
5	Q	207/209 (99%)	195 (94%)	11 (5%)	1 (0%)	29	60
6	R	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
7	S	175/179 (98%)	163 (93%)	11 (6%)	1 (1%)	25	56
8	T	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
9	U	45/149 (30%)	35 (78%)	9 (20%)	1 (2%)	6	23
10	V	139/142 (98%)	112 (81%)	27 (19%)	0	100	100
11	W	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
12	X	120/123 (98%)	109 (91%)	9 (8%)	2 (2%)	9	29
13	Y	141/144 (98%)	121 (86%)	16 (11%)	4 (3%)	5	17
14	Z	134/136 (98%)	118 (88%)	11 (8%)	5 (4%)	3	12
15	a	118/127 (93%)	102 (86%)	14 (12%)	2 (2%)	9	29
16	b	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
17	c	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
18	d	115/118 (98%)	115 (100%)	0	0	100	100
19	e	101/103 (98%)	92 (91%)	8 (8%)	1 (1%)	15	43
20	f	108/110 (98%)	100 (93%)	7 (6%)	1 (1%)	17	46
21	g	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	6	23
22	h	100/104 (96%)	84 (84%)	14 (14%)	2 (2%)	7	25
23	i	92/94 (98%)	89 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	j	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
25	k	75/78 (96%)	71 (95%)	3 (4%)	1 (1%)	12	35
26	l	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
27	m	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
28	n	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	8	26
29	o	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
30	p	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
31	q	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	9	30
32	r	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
34	L	64/70 (91%)	56 (88%)	7 (11%)	1 (2%)	9	30
36	1	216/233 (93%)	187 (87%)	28 (13%)	1 (0%)	29	60
37	2	204/233 (88%)	186 (91%)	16 (8%)	2 (1%)	15	43
38	3	203/206 (98%)	182 (90%)	21 (10%)	0	100	100
39	4	148/166 (89%)	116 (78%)	30 (20%)	2 (1%)	11	34
40	5	98/131 (75%)	81 (83%)	11 (11%)	6 (6%)	1	4
41	6	149/156 (96%)	139 (93%)	10 (7%)	0	100	100
42	7	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
43	8	125/130 (96%)	103 (82%)	20 (16%)	2 (2%)	9	30
44	9	96/103 (93%)	84 (88%)	9 (9%)	3 (3%)	4	15
45	A	115/129 (89%)	102 (89%)	13 (11%)	0	100	100
46	B	121/124 (98%)	104 (86%)	15 (12%)	2 (2%)	9	29
47	C	112/118 (95%)	103 (92%)	8 (7%)	1 (1%)	17	46
48	D	92/101 (91%)	77 (84%)	14 (15%)	1 (1%)	14	40
49	E	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
50	F	80/82 (98%)	69 (86%)	10 (12%)	1 (1%)	12	35
51	G	78/84 (93%)	66 (85%)	9 (12%)	3 (4%)	3	11
52	H	53/75 (71%)	49 (92%)	3 (6%)	1 (2%)	8	26
53	I	77/92 (84%)	73 (95%)	4 (5%)	0	100	100
54	J	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	13	38
55	K	49/71 (69%)	40 (82%)	9 (18%)	0	100	100
All	All	5614/6198 (91%)	5069 (90%)	489 (9%)	56 (1%)	20	43

5 of 56 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	P	239	ASN
13	Y	36	LYS
14	Z	58	LYS
19	e	53	PHE
28	n	55	ILE

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	s	34/158 (22%)	34 (100%)	0	100	100
4	P	216/218 (99%)	215 (100%)	1 (0%)	88	96
5	Q	164/164 (100%)	161 (98%)	3 (2%)	59	82
6	R	165/165 (100%)	161 (98%)	4 (2%)	49	77
7	S	148/150 (99%)	148 (100%)	0	100	100
8	T	137/138 (99%)	137 (100%)	0	100	100
9	U	38/114 (33%)	37 (97%)	1 (3%)	46	75
10	V	109/110 (99%)	108 (99%)	1 (1%)	78	92
11	W	116/116 (100%)	116 (100%)	0	100	100
12	X	103/104 (99%)	103 (100%)	0	100	100
13	Y	102/103 (99%)	102 (100%)	0	100	100
14	Z	109/109 (100%)	108 (99%)	1 (1%)	78	92
15	a	100/103 (97%)	97 (97%)	3 (3%)	41	72
16	b	86/87 (99%)	86 (100%)	0	100	100
17	c	98/100 (98%)	95 (97%)	3 (3%)	40	71
18	d	89/90 (99%)	88 (99%)	1 (1%)	73	90
19	e	84/84 (100%)	82 (98%)	2 (2%)	49	77
20	f	93/93 (100%)	93 (100%)	0	100	100
21	g	80/84 (95%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	h	83/85 (98%)	82 (99%)	1 (1%)	71	89
23	i	78/78 (100%)	78 (100%)	0	100	100
24	j	56/63 (89%)	55 (98%)	1 (2%)	59	82
25	k	67/68 (98%)	67 (100%)	0	100	100
26	l	55/55 (100%)	55 (100%)	0	100	100
27	m	48/49 (98%)	48 (100%)	0	100	100
28	n	47/48 (98%)	46 (98%)	1 (2%)	53	79
29	o	45/49 (92%)	45 (100%)	0	100	100
30	p	38/38 (100%)	38 (100%)	0	100	100
31	q	51/52 (98%)	49 (96%)	2 (4%)	32	63
32	r	34/34 (100%)	34 (100%)	0	100	100
34	L	59/62 (95%)	58 (98%)	1 (2%)	60	83
36	1	180/192 (94%)	179 (99%)	1 (1%)	86	95
37	2	170/190 (90%)	169 (99%)	1 (1%)	86	95
38	3	172/173 (99%)	171 (99%)	1 (1%)	86	95
39	4	113/125 (90%)	110 (97%)	3 (3%)	44	74
40	5	87/112 (78%)	86 (99%)	1 (1%)	73	90
41	6	124/129 (96%)	123 (99%)	1 (1%)	81	93
42	7	104/105 (99%)	104 (100%)	0	100	100
43	8	105/107 (98%)	104 (99%)	1 (1%)	76	91
44	9	86/90 (96%)	85 (99%)	1 (1%)	71	89
45	A	90/99 (91%)	89 (99%)	1 (1%)	73	90
46	B	103/104 (99%)	103 (100%)	0	100	100
47	C	92/96 (96%)	91 (99%)	1 (1%)	73	90
48	D	79/84 (94%)	79 (100%)	0	100	100
49	E	75/77 (97%)	74 (99%)	1 (1%)	69	88
50	F	65/65 (100%)	65 (100%)	0	100	100
51	G	74/78 (95%)	73 (99%)	1 (1%)	67	86
52	H	48/65 (74%)	48 (100%)	0	100	100
53	I	70/79 (89%)	68 (97%)	2 (3%)	42	73
54	J	65/66 (98%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
55	K	44/61 (72%)	43 (98%)	1 (2%)	50 78
All	All	4678/5068 (92%)	4635 (99%)	43 (1%)	79 92

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	3	5	LEU
44	9	17	LEU
39	4	15	LEU
40	5	9	MET
47	C	98	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
40	5	55	HIS
51	G	31	HIS
41	6	28	ASN
47	C	8	ASN
9	U	11	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	M	74/75 (98%)	11 (14%)	0
3	O	117/120 (97%)	21 (17%)	1 (0%)
33	N	2894/2903 (99%)	536 (18%)	34 (1%)
35	0	1538/1539 (99%)	279 (18%)	22 (1%)
56	t	3/4 (75%)	1 (33%)	0
All	All	4626/4641 (99%)	848 (18%)	57 (1%)

5 of 848 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	M	9	C
2	M	10	G
2	M	15	G
2	M	16	C
2	M	17	G

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
33	N	2286	G
35	0	1493	A
35	0	64	G
35	0	1491	G
35	0	1190	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](#)

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.

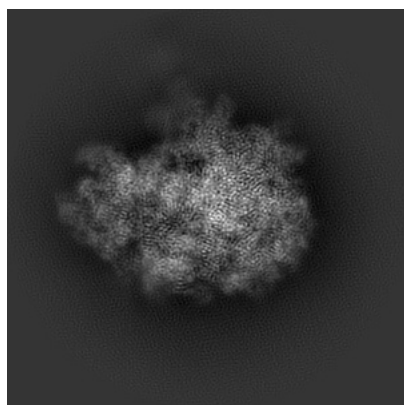
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3713. These allow visual inspection of the internal detail of the map and identification of artifacts.

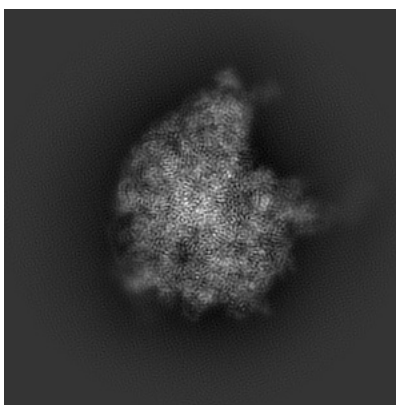
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

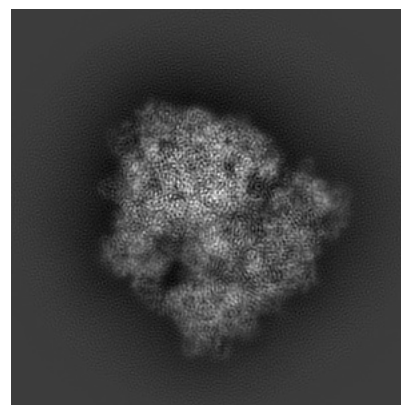
6.1.1 Primary map



X



Y

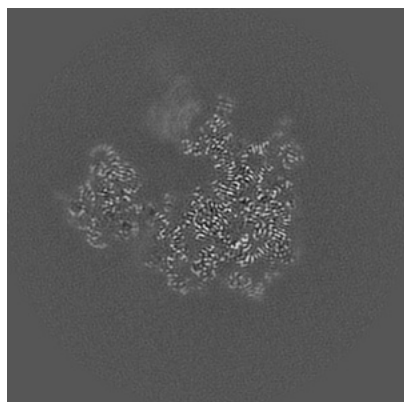


Z

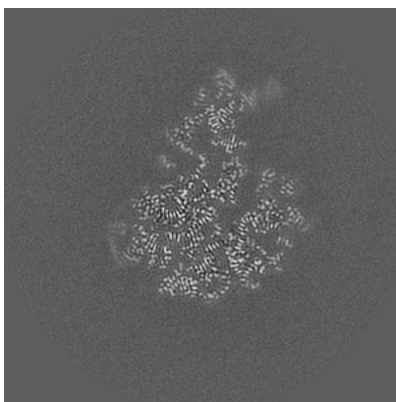
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

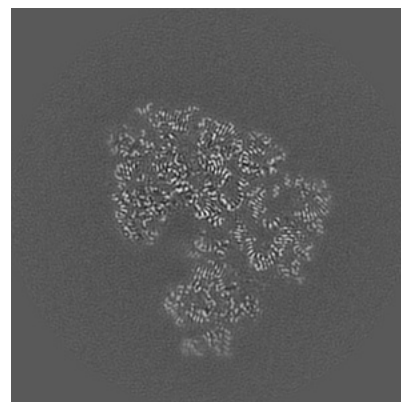
6.2.1 Primary map



X Index: 184



Y Index: 184

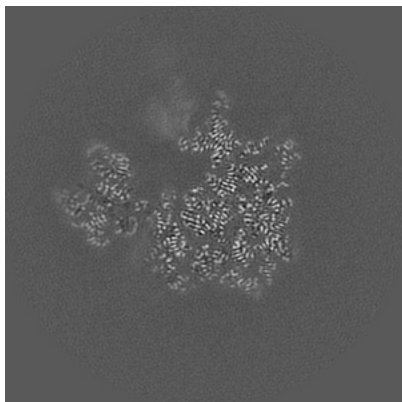


Z Index: 184

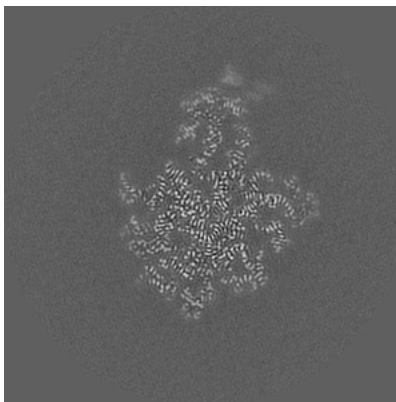
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

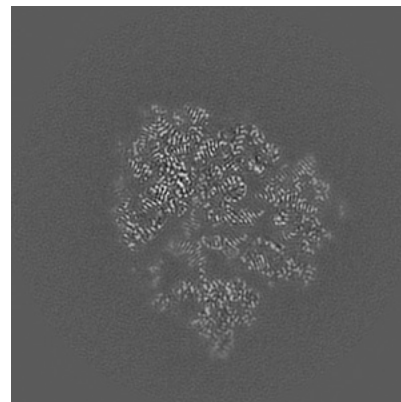
6.3.1 Primary map



X Index: 187



Y Index: 199



Z Index: 193

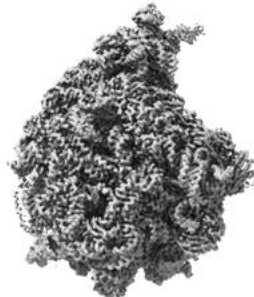
The images above show the largest variance slices of the map in three orthogonal directions.

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

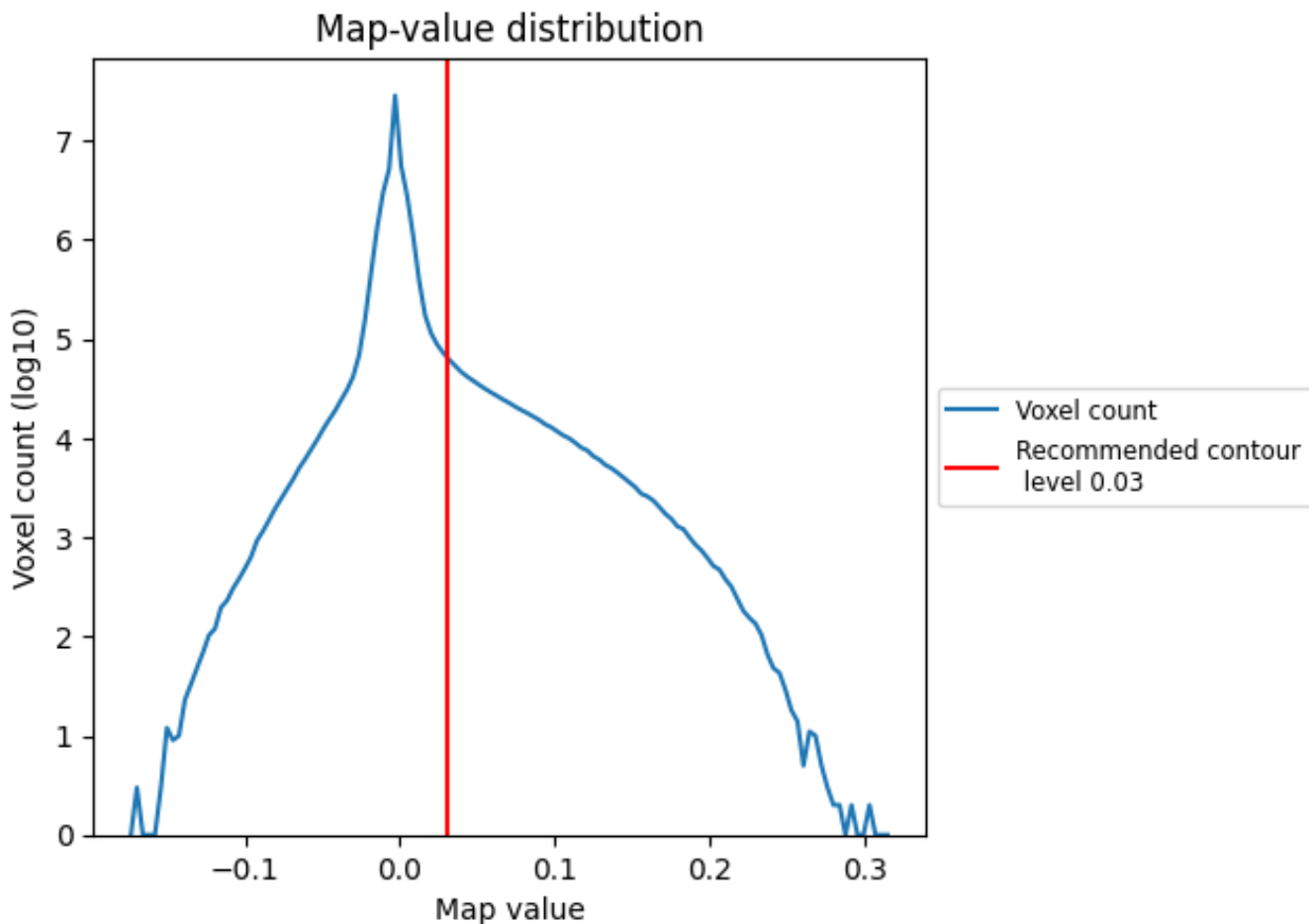
6.5 Mask visualisation

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

7 Map analysis [i](#)

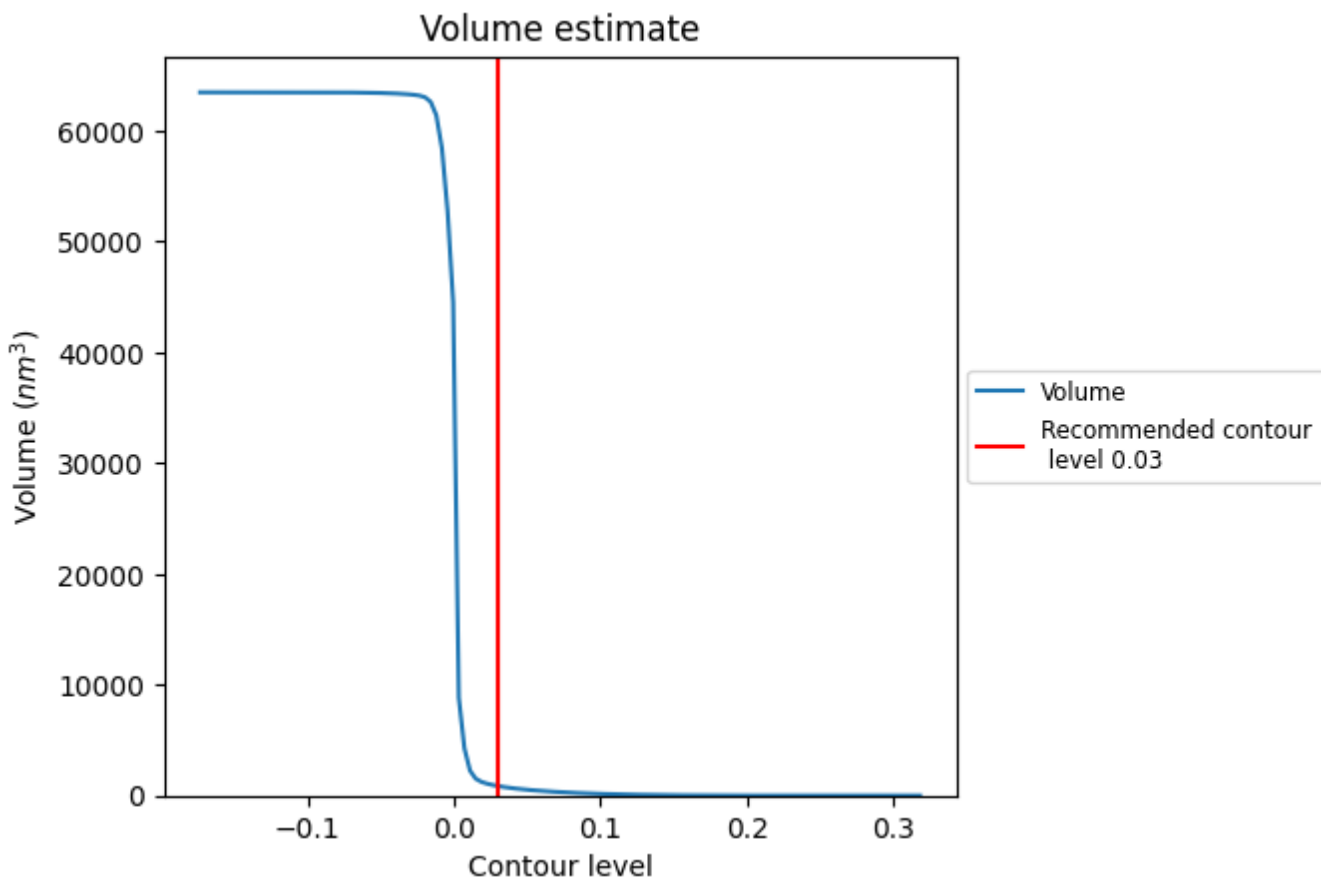
This section contains the results of statistical analysis of the map.

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.

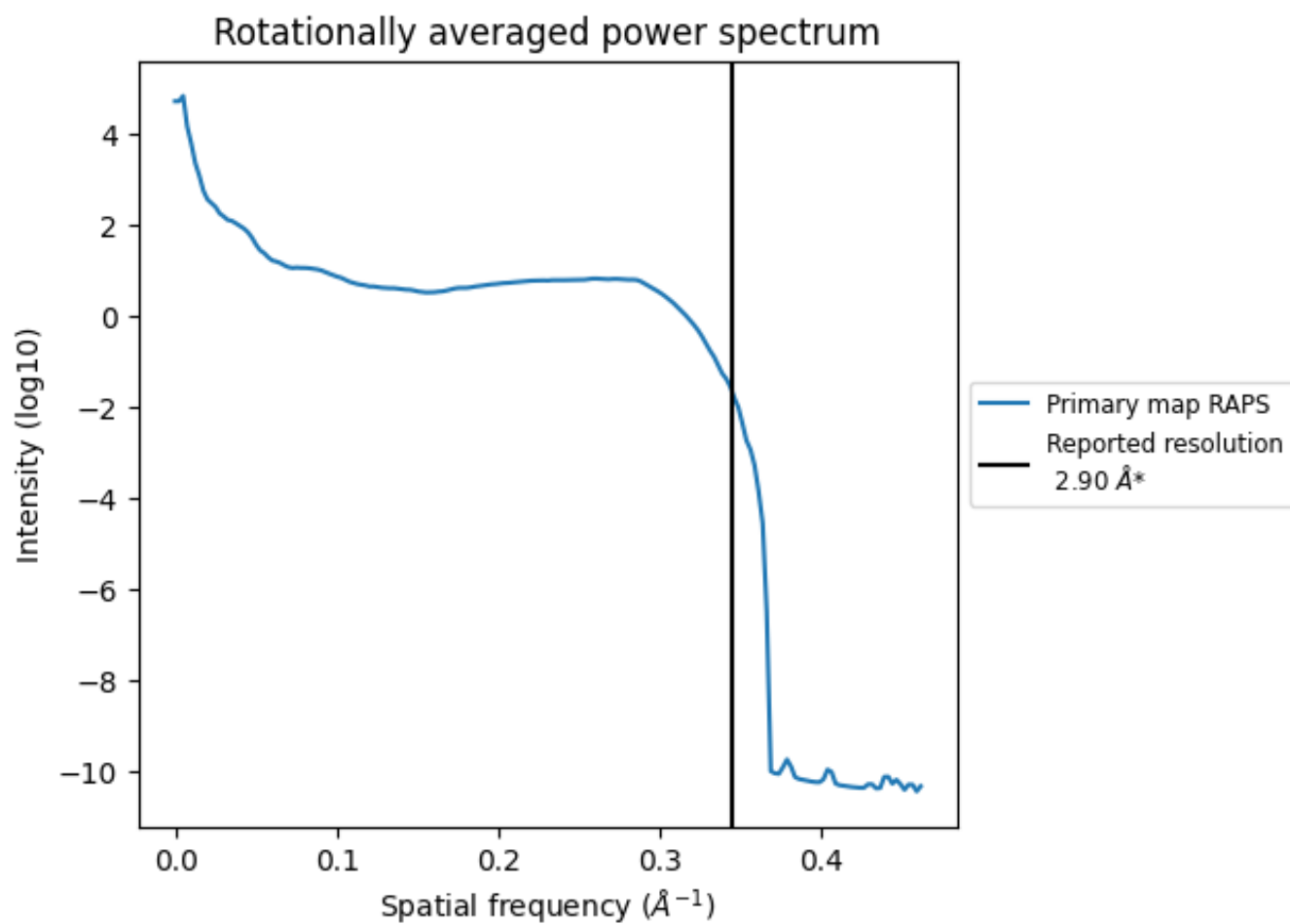
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 859 nm^3 ; this corresponds to an approximate mass of 776 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

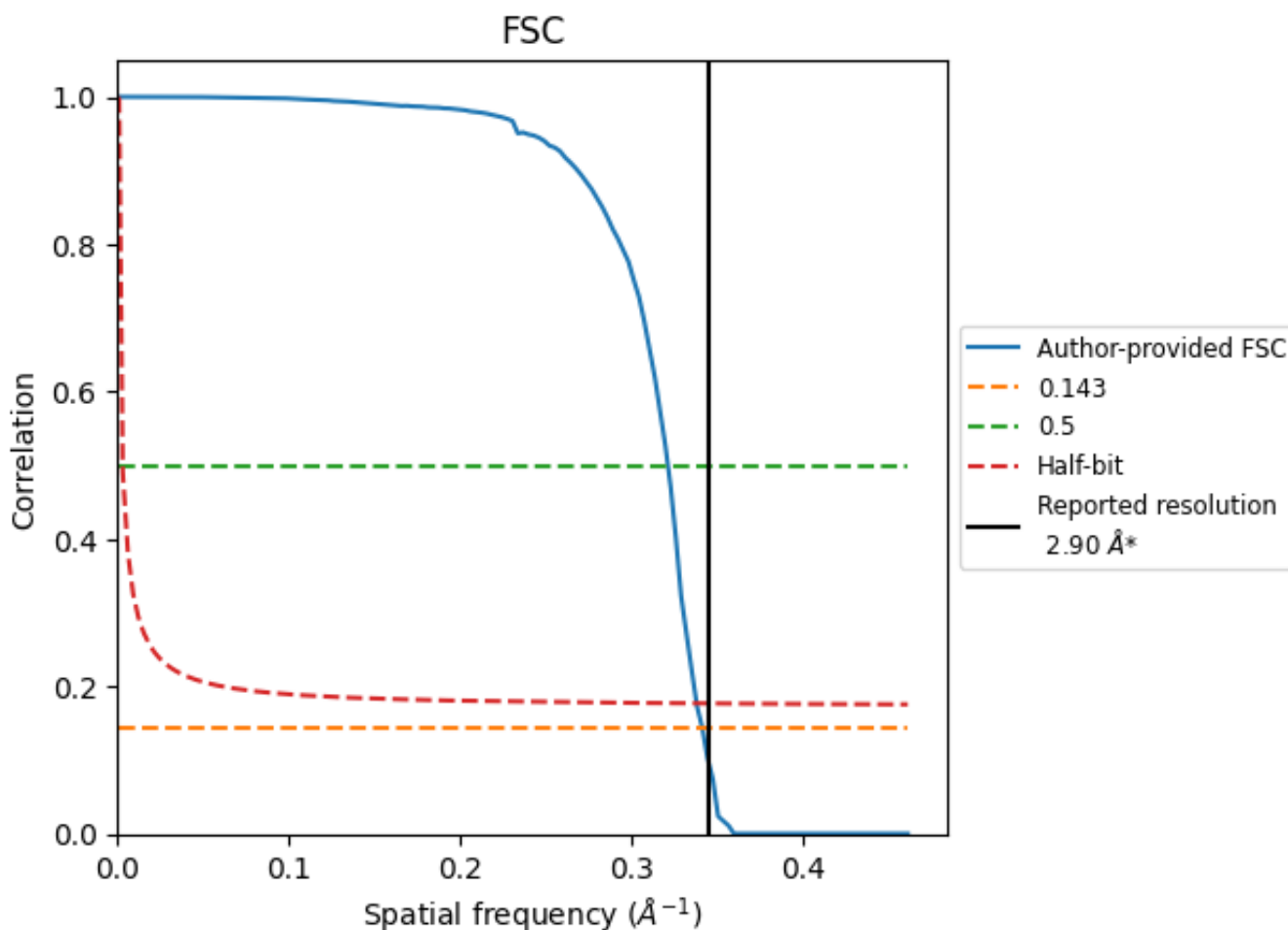


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

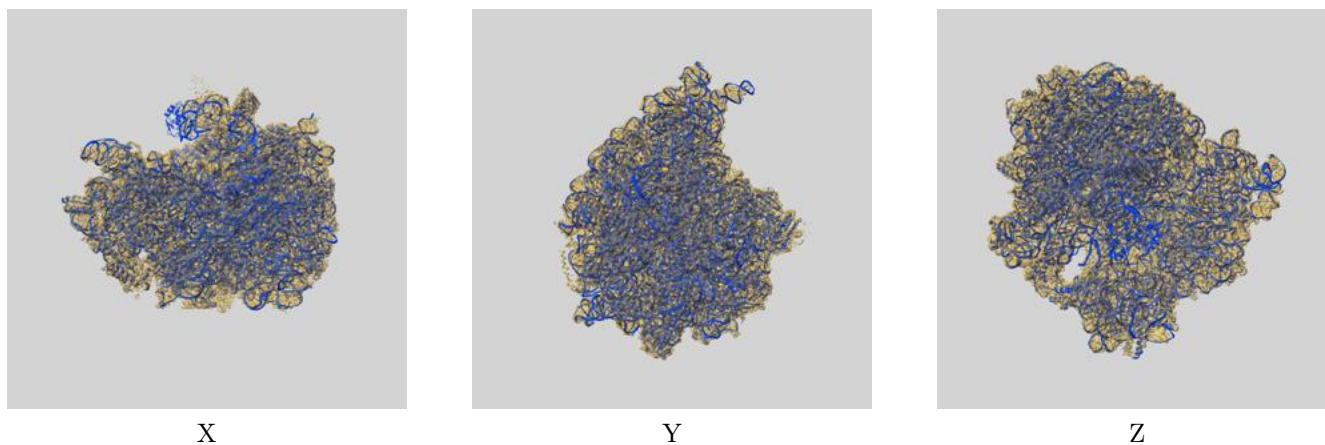
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.93	3.11	2.96
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

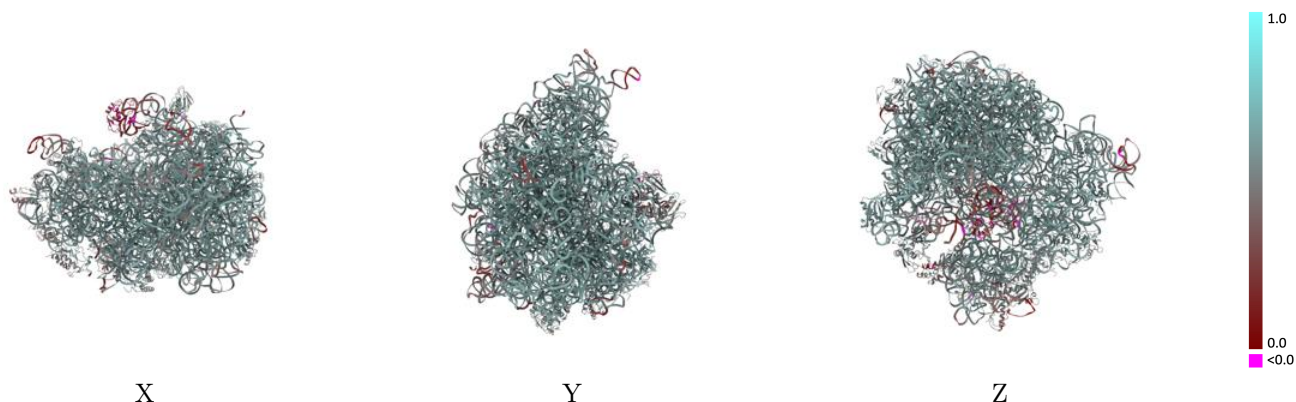
This section contains information regarding the fit between EMDB map EMD-3713 and PDB model 5NWY. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



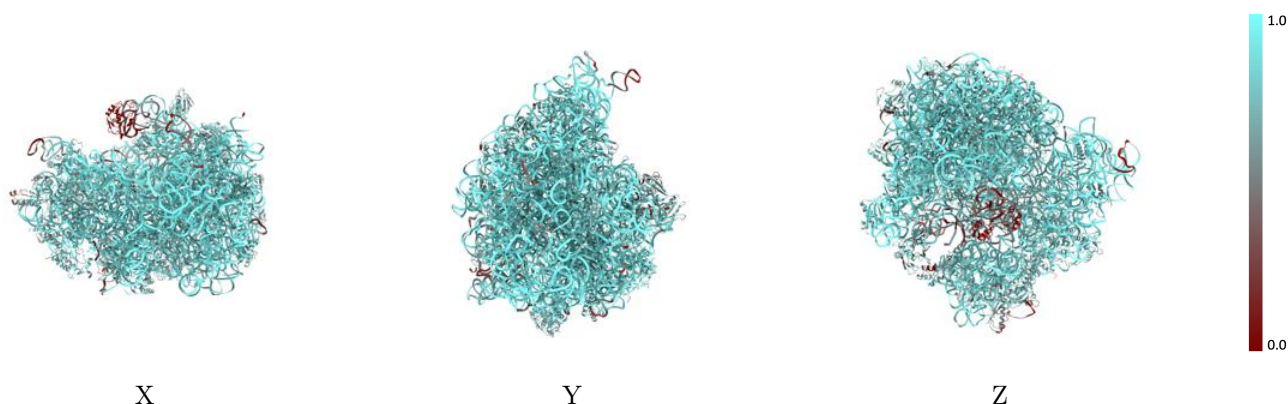
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



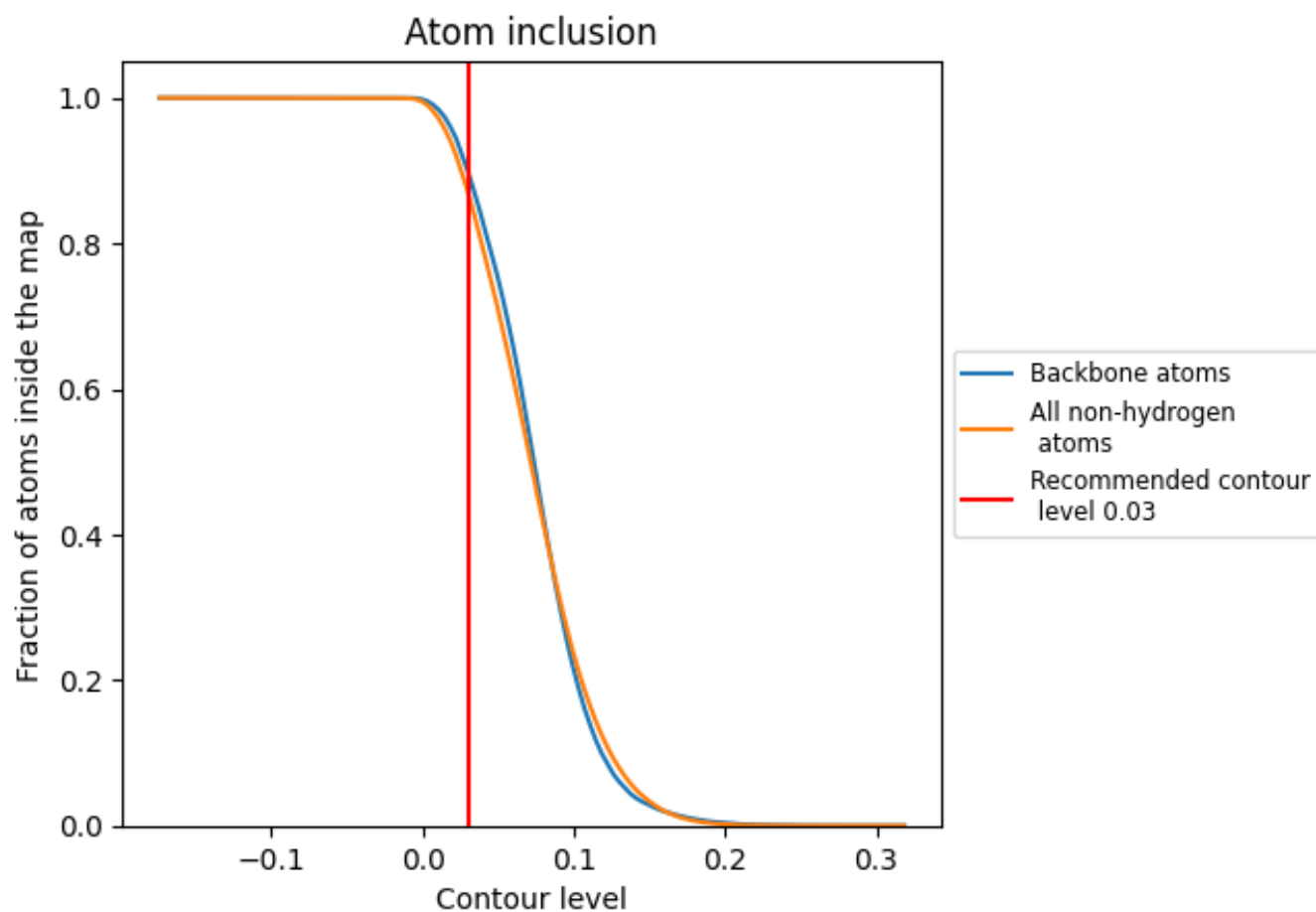
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 87% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8712	 0.5580
0	 0.9264	 0.5680
1	 0.6770	 0.4790
2	 0.7490	 0.5300
3	 0.7432	 0.5250
4	 0.8199	 0.5570
5	 0.7299	 0.4990
6	 0.6573	 0.4860
7	 0.8113	 0.5570
8	 0.7382	 0.4890
9	 0.6347	 0.4720
A	 0.7676	 0.5310
B	 0.8065	 0.5630
C	 0.7391	 0.4970
D	 0.7884	 0.5180
E	 0.8015	 0.5410
F	 0.7875	 0.5270
G	 0.7500	 0.5280
H	 0.8142	 0.5480
I	 0.7536	 0.5100
J	 0.7643	 0.5280
K	 0.4680	 0.3800
L	 0.5519	 0.4100
M	 0.7999	 0.5240
N	 0.9143	 0.5700
O	 0.9450	 0.5730
P	 0.8814	 0.5940
Q	 0.8751	 0.5870
R	 0.7842	 0.5620
S	 0.7232	 0.5120
T	 0.7238	 0.5210
U	 0.6657	 0.4780
V	 0.0108	 0.1470
W	 0.8599	 0.5820
X	 0.8467	 0.5720



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Chain	Atom inclusion	Q-score
Y	 0.8443	 0.5730
Z	 0.8434	 0.5760
a	 0.8774	 0.5890
b	 0.8225	 0.5640
c	 0.8318	 0.5770
d	 0.8831	 0.6000
e	 0.8254	 0.5570
f	 0.8325	 0.5790
g	 0.7839	 0.5470
h	 0.7497	 0.5340
i	 0.7965	 0.5550
j	 0.8845	 0.5970
k	 0.8583	 0.5790
l	 0.7319	 0.5080
m	 0.8096	 0.5710
n	 0.8478	 0.5720
o	 0.7706	 0.5490
p	 0.8842	 0.6010
q	 0.9082	 0.6130
r	 0.8660	 0.5800
s	 0.6494	 0.5340
t	 0.8941	 0.5800