



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 04:46 PM EST

PDB ID : 7JIL
EMDB ID : EMD-22345
Title : 70S ribosome *Flavobacterium johnsoniae*
Authors : Ortega, J.
Deposited on : 2020-07-23
Resolution : 2.80 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:

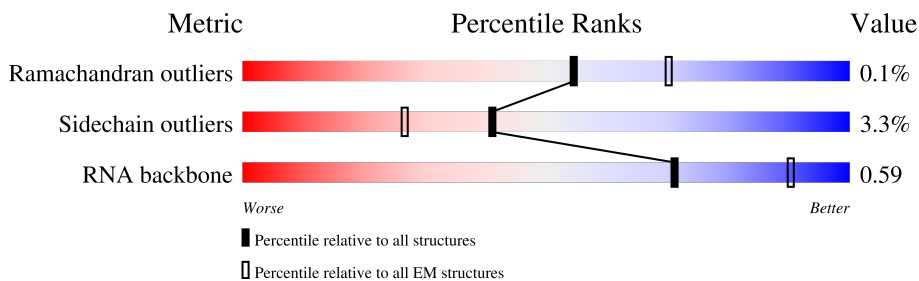
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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	B	274	
2	C	205	
3	D	209	
4	E	183	
5	F	180	
6	G	146	
7	J	151	
8	K	122	

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Mol	Chain	Length	Quality of chain
9	L	150	99%
10	M	141	96%
11	N	163	77% 23%
12	O	116	93% 6%
13	P	116	97%
14	Q	114	97%
15	R	147	70% 29%
16	S	137	93% 7%
17	T	96	86% 11%
18	U	104	88% 10%
19	V	203	60% 39%
20	W	86	85% 13%
21	X	78	97%
22	Y	63	78% 19% 6%
23	Z	60	92% 7%
24	1	2862	80% 15%
25	2	1520	79% 18%
26	3	111	85% 14%
27	4	50	62% 10% 28%
28	5	30	90% 10% 7%
29	a	84	60% 38% 5%
30	b	64	92% 8%
31	c	60	90% 10%
32	d	53	96%
33	e	65	97%

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Mol	Chain	Length	Quality of chain
34	f	38	100%
35	h	252	42% 77% 5% 18%
36	i	201	26% 92%
37	j	173	90% 8%
38	k	113	91% 5%
39	l	158	11% 80% 16%
40	m	132	98%
41	n	128	70% 5% 26%
42	o	101	15% 53% 45%
43	p	127	91% 8%
44	q	127	92% 5%
45	r	124	24% 90% 9%
46	s	89	17% 89% 9%
47	t	88	99%
48	u	188	45% 55%
49	v	86	92% 7%
50	w	98	65% 34%
51	x	92	21% 80% 15%
52	y	83	82% 16%
53	z	64	28% 80% 6% 14%

2 Entry composition i

There are 54 unique types of molecules in this entry. The entry contains 132739 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	271	2018	1258	400	352	8	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	35	SER	ALA	conflict	UNP A0A1B2U0Q0
B	194	GLU	ALA	conflict	UNP A0A1B2U0Q0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	204	1456	927	275	247	7	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	87	ALA	THR	conflict	UNP A0A1M5L9Q4
C	88	ALA	GLU	conflict	UNP A0A1M5L9Q4
C	90	ALA	LYS	conflict	UNP A0A1M5L9Q4
C	138	GLN	ASN	conflict	UNP A0A1M5L9Q4

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	D	206	1484	949	277	258	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	174	Total	C	N	O	S	0	0
			1284	827	224	228	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	176	Total	C	N	O	S	0	0
			1251	802	229	219	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	96	ALA	SER	conflict	UNP A0A1M5L807
F	100	ASN	GLN	conflict	UNP A0A1M5L807
F	128	ALA	LYS	conflict	UNP A0A1M5L807
F	130	ALA	LYS	conflict	UNP A0A1M5L807

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	50	Total	C	N	O	S	0	0
			360	236	61	62	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	150	Total	C	N	O	S	0	0
			1112	705	207	195	5		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	121	Total	C	N	O	S	0	0
			885	557	173	151	4		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	150	Total	C	N	O	S	0	0
			1052	656	209	185	2		

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	M	139	1056	683	199	167	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	96	TRP	ALA	conflict	UNP A0A1B2U0I0

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	N	125	980	615	189	170	6	0	0

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	O	115	846	532	164	150	0	0

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	P	112	848	554	154	140	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	115	LEU	ARG	conflict	UNP A0A1M5PX52

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	Q	113	904	571	185	143	5	0	0

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	R	104	768	499	145	124	0	0

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	S	128	964	600	198	163	3	0	0

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	T	85	647	416	116	114	1	0	0

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	U	94	679	433	134	112	0	0

- Molecule 19 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	V	124	881	577	153	149	2	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	66	ALA	LYS	conflict	UNP A0A1M5HDD0
V	137	ILE	LEU	conflict	UNP A0A1M5HDD0
V	139	GLU	ASP	conflict	UNP A0A1M5HDD0
V	175	ALA	CYS	conflict	UNP A0A1M5HDD0

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	W	75	569	355	116	98	0	0

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	X	76	586	370	114	99	3	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	52	GLN	ALA	conflict	UNP A0A1B2U1R1
X	53	ARG	ALA	conflict	UNP A0A1B2U1R1
X	74	ALA	GLU	conflict	UNP A0A1B2U1R1

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	Y	51	359	226	72	61	0	0

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Z	56	400	254	77	67	2	0	0

- Molecule 24 is a RNA chain called RNA (2862-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
24	1	2742	58828	26270	10817	18999	2742	0	0

- Molecule 25 is a RNA chain called RNA (1519-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	2	1475	31599	14109	5775	10240	1475	0	0

- Molecule 26 is a RNA chain called RNA (111-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	3	110	2339	1043	406	780	110	0	0

- Molecule 27 is a protein called 50S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	4	36	286	189	46	49	2	0	0

- Molecule 28 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	5	27	231	140	61	30	0	0

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	a	52	404	260	65	77	2	0	0

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	b	59	475	300	99	75	1	0	0

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	c	54	415	263	81	70	1	0	0

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	d	51	416	252	101	61	2	0	0

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	e	64	506	322	103	80	1	0	0

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	f	38	305	190	68	45	2	0	0

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	206	Total	C	N	O	S	0	0
			1551	984	282	279	6		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	194	Total	C	N	O	S	0	0
			1540	979	284	274	3		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	159	Total	C	N	O	S	0	0
			1107	700	216	190	1		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	107	Total	C	N	O	S	0	0
			815	534	149	130	2		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	133	Total	C	N	O	S	0	0
			1052	672	203	172	5		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	131	Total	C	N	O	S	0	0
			961	623	167	169	2		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	95	Total	C	N	O	S	0	0
			757	483	149	123	2		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	56	Total	C	N	O	S	0	0
			451	294	82	73	2		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			823	515	160	143	5		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	121	Total	C	N	O	S	0	0
			922	567	195	157	3		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	113	Total	C	N	O	S	0	0
			859	529	177	150	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	81	Total	C	N	O	S	0	0
			615	383	129	100	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	t	88	Total	C	N	O	0	0
			694	443	136	115		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t	71	ARG	LYS	conflict	UNP A0A1M6QTP8

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	u	85	Total	C	N	O	0	0
			653	416	126	111		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	56	ILE	ALA	conflict	UNP A0A1M6QGN9
u	62	GLN	ASN	conflict	UNP A0A1M6QGN9

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			638	404	124	107	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	65	Total	C	N	O	S	0	0
			525	345	97	81	2		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	78	Total	C	N	O	S	0	0
			603	386	110	105	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	70	Total	C	N	O	S	0	0
			550	342	118	89	1		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	z	55	Total	C	N	O	0	0
			429	278	82	69		

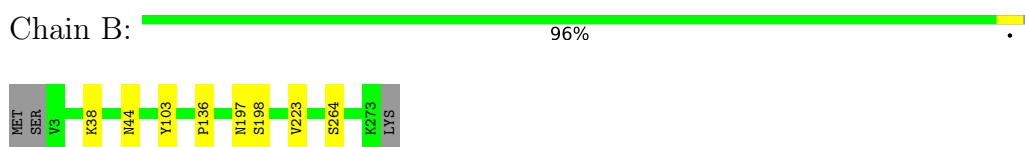
- Molecule 54 is water.

Mol	Chain	Residues	Atoms	AltConf
54	w	1	Total O 1 1	0

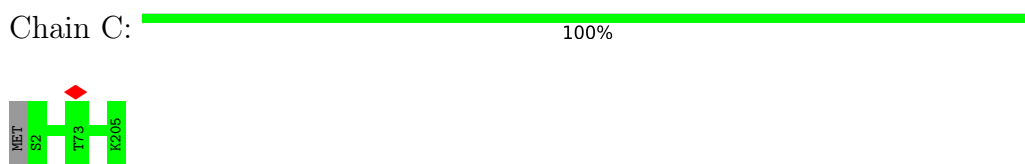
3 Residue-property plots [i](#)

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

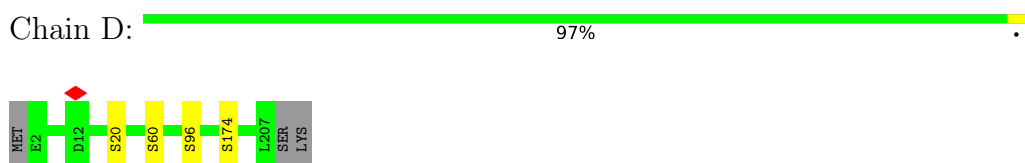
- Molecule 1: 50S ribosomal protein L2



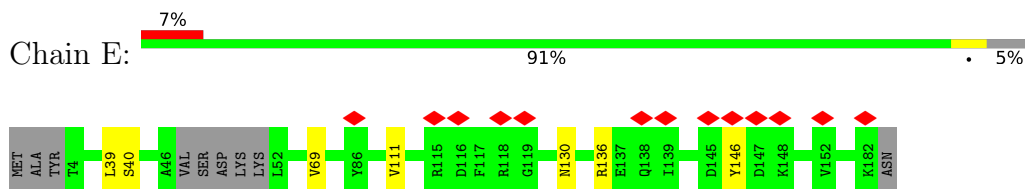
- Molecule 2: 50S ribosomal protein L3



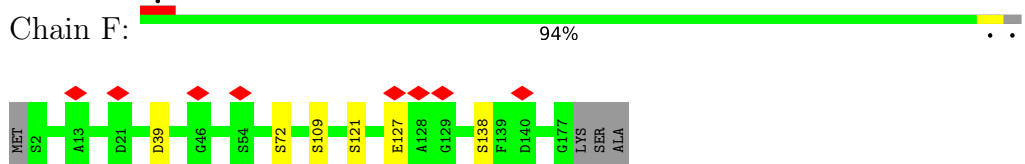
- Molecule 3: 50S ribosomal protein L4



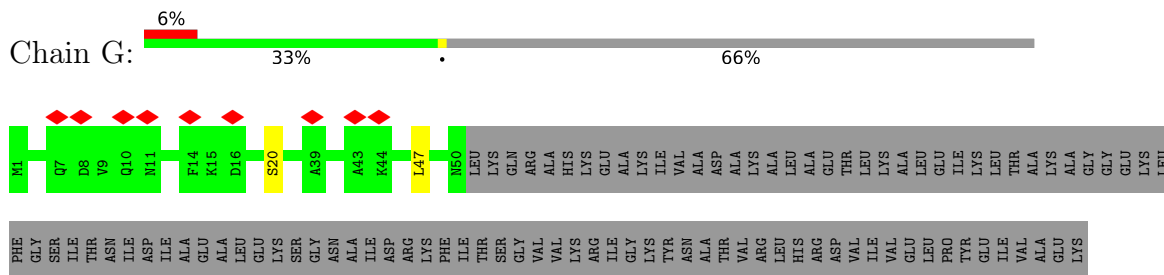
- Molecule 4: 50S ribosomal protein L5



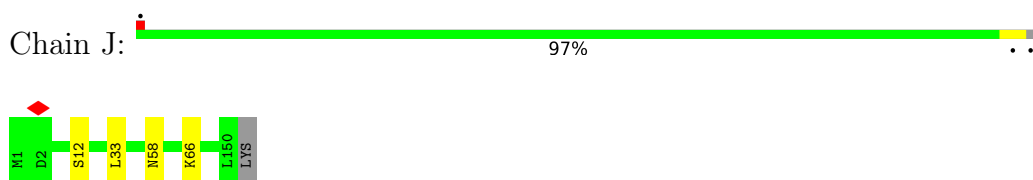
- Molecule 5: 50S ribosomal protein L6



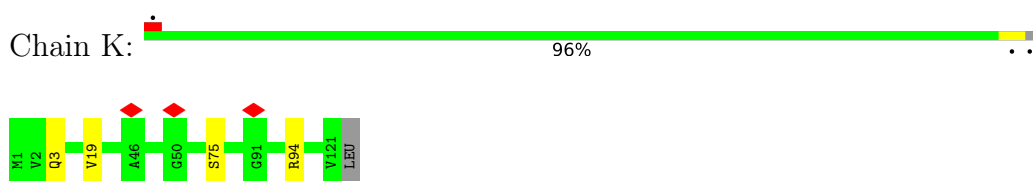
• Molecule 6: 50S ribosomal protein L9



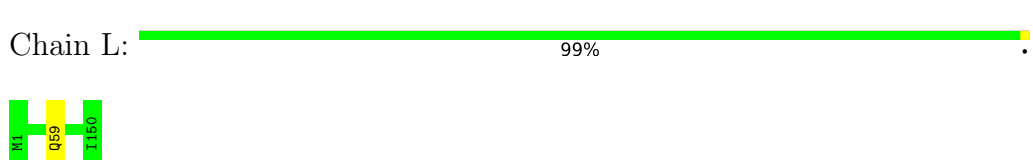
• Molecule 7: 50S ribosomal protein L13



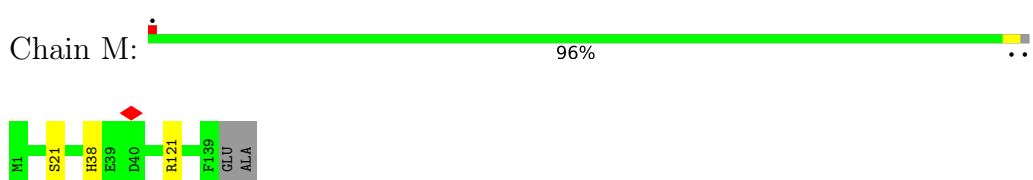
• Molecule 8: 50S ribosomal protein L14



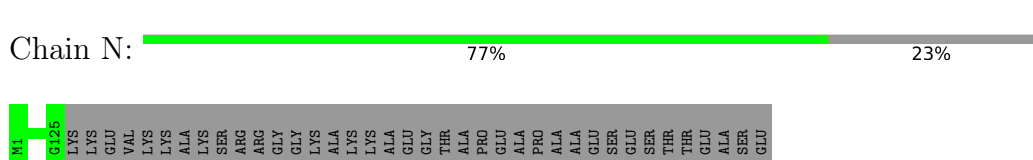
• Molecule 9: 50S ribosomal protein L15



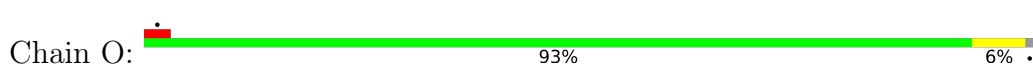
• Molecule 10: 50S ribosomal protein L16

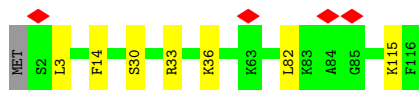


• Molecule 11: 50S ribosomal protein L17

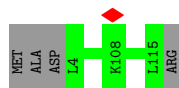


• Molecule 12: 50S ribosomal protein L18





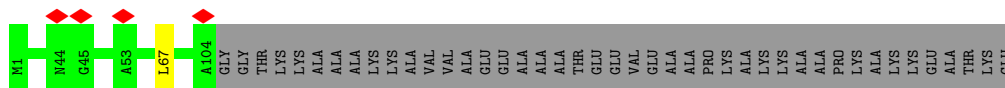
- Molecule 13: 50S ribosomal protein L19



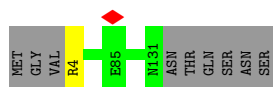
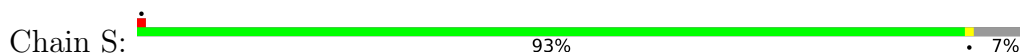
- Molecule 14: 50S ribosomal protein L20



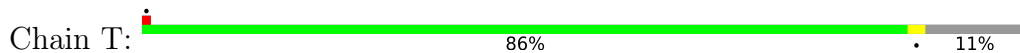
- Molecule 15: 50S ribosomal protein L21



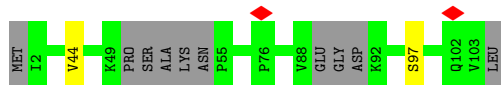
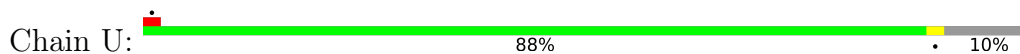
- Molecule 16: 50S ribosomal protein L22



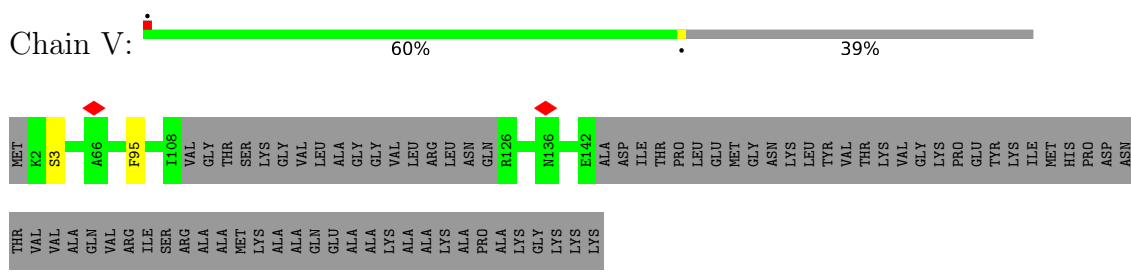
- Molecule 17: 50S ribosomal protein L23



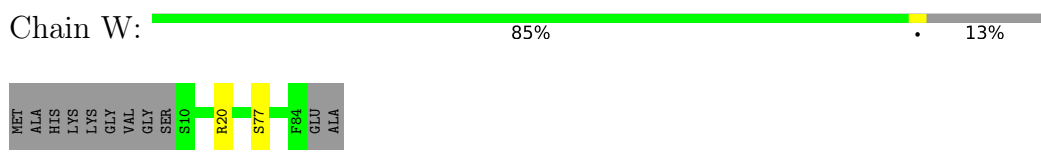
- Molecule 18: 50S ribosomal protein L24



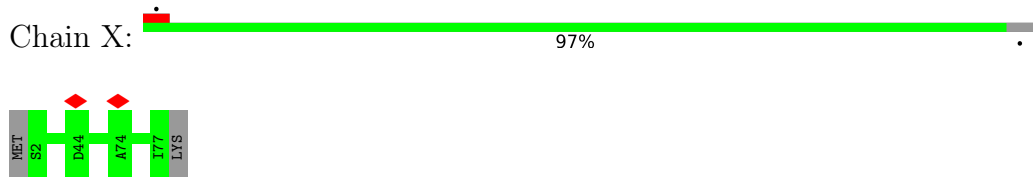
- Molecule 19: 50S ribosomal protein L25



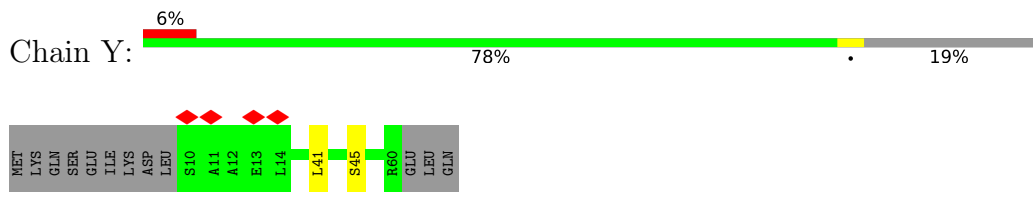
• Molecule 20: 50S ribosomal protein L27



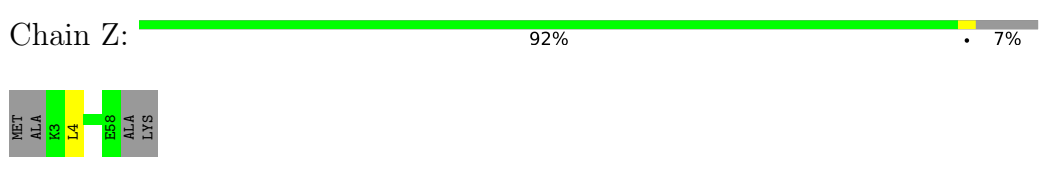
• Molecule 21: 50S ribosomal protein L28



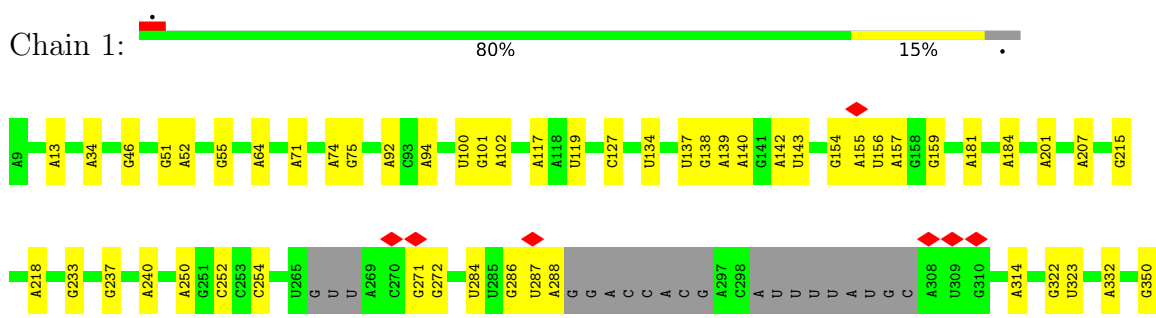
• Molecule 22: 50S ribosomal protein L29

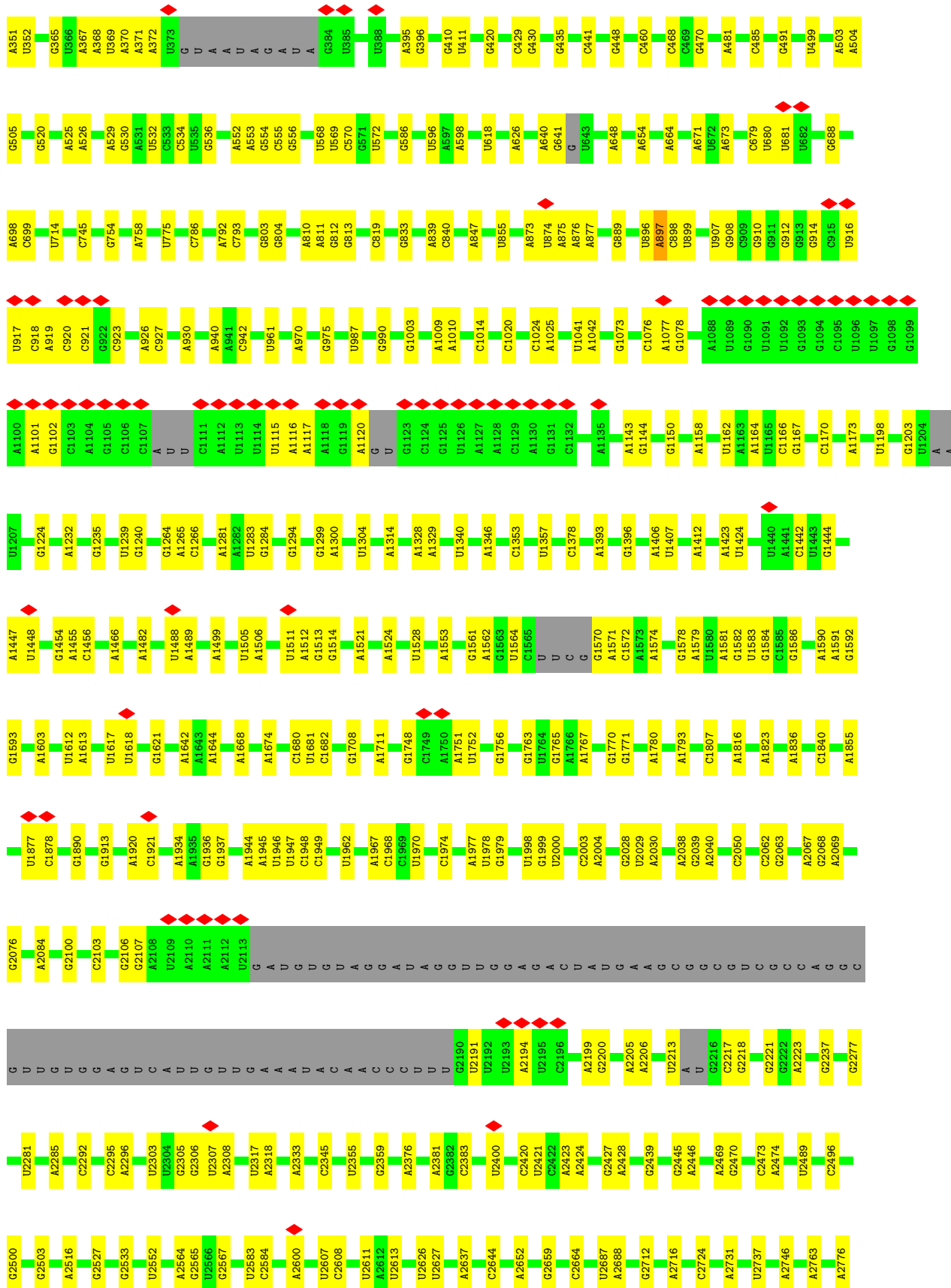


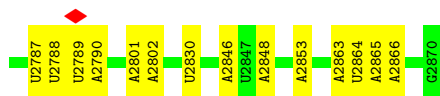
• Molecule 23: 50S ribosomal protein L30



• Molecule 24: RNA (2862-MER)

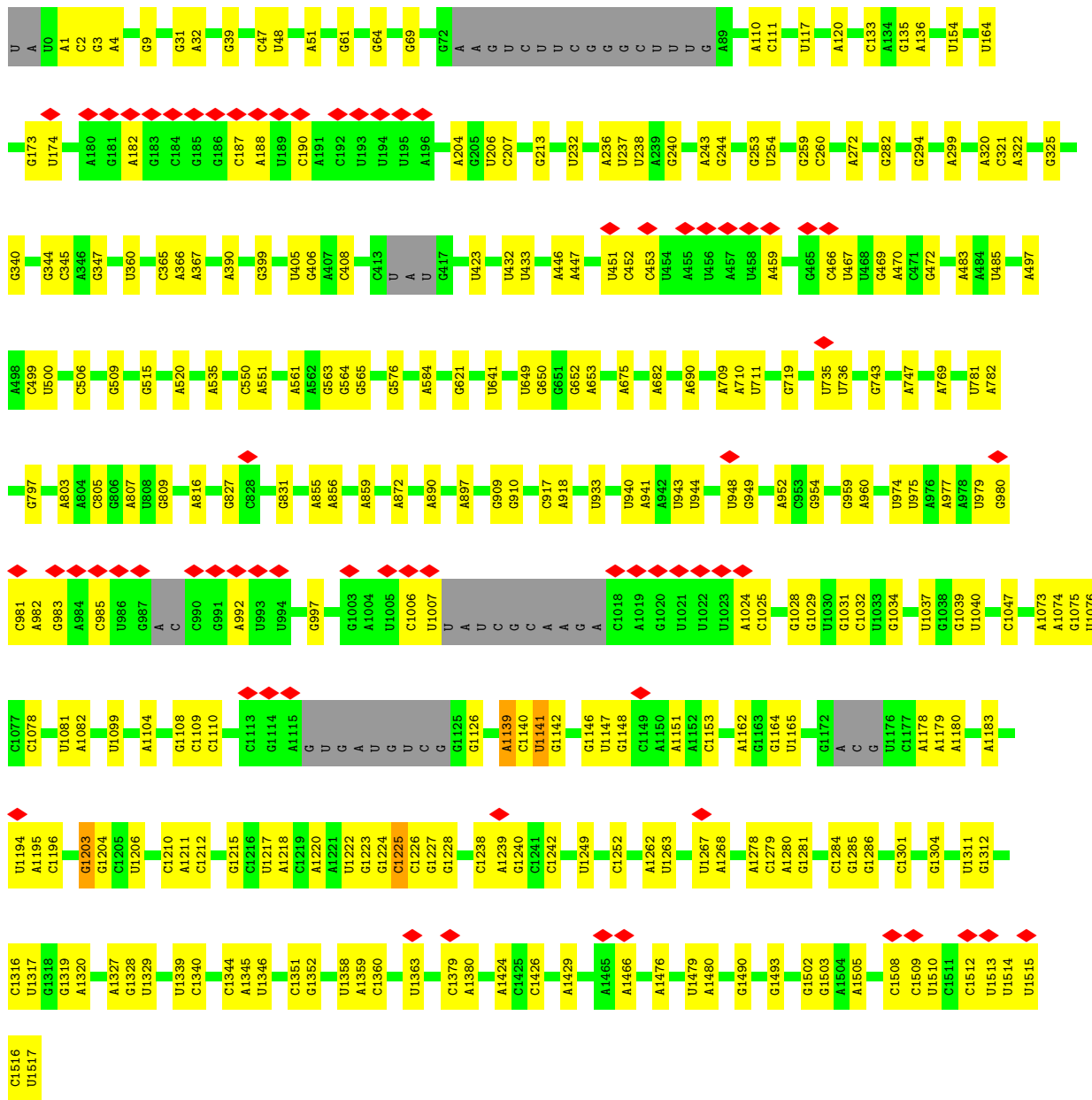






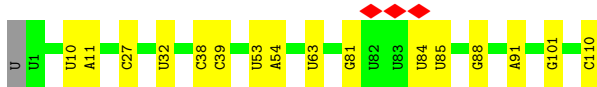
● Molecule 25: RNA (1519-MER)

Chain 2: 79% 18%

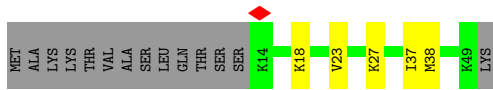


● Molecule 26: RNA (111-MER)

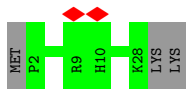
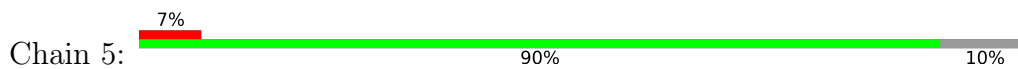
Chain 3: 85% 14%



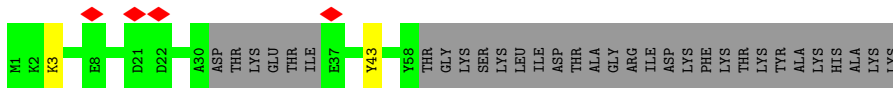
- Molecule 27: 50S ribosomal protein L38



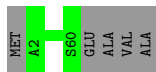
- Molecule 28: 30S ribosomal protein S22



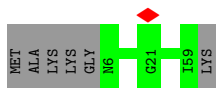
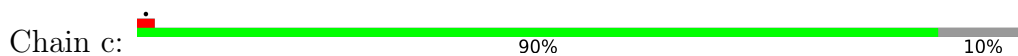
- Molecule 29: 50S ribosomal protein L31



- Molecule 30: 50S ribosomal protein L32



- Molecule 31: 50S ribosomal protein L33

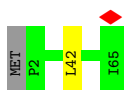


- Molecule 32: 50S ribosomal protein L34



- Molecule 33: 50S ribosomal protein L35

Chain e:  97%




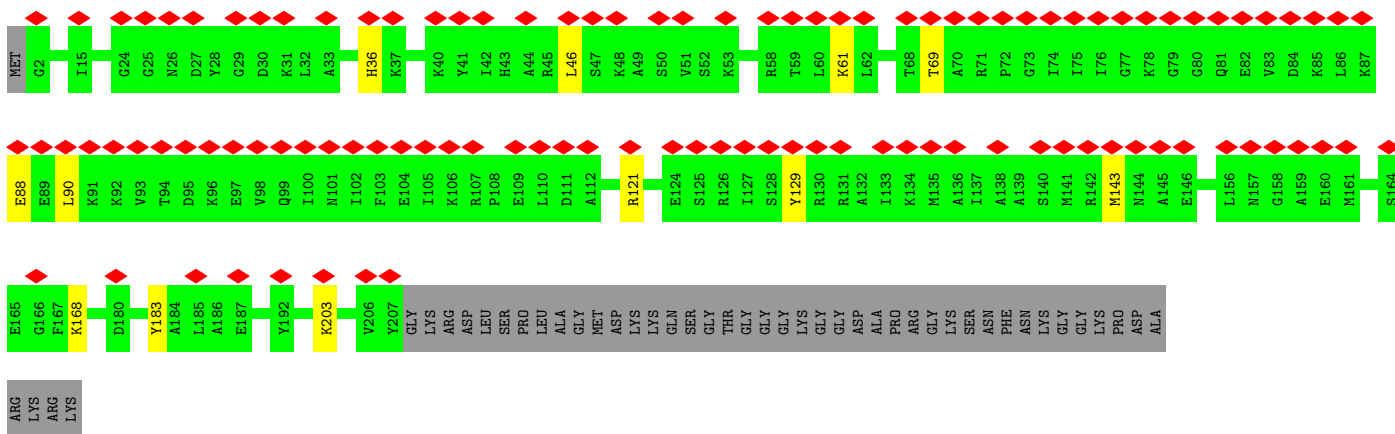
- Molecule 34: 50S ribosomal protein L36

Chain f:  100%

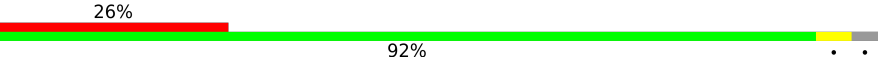
There are no outlier residues recorded for this chain.

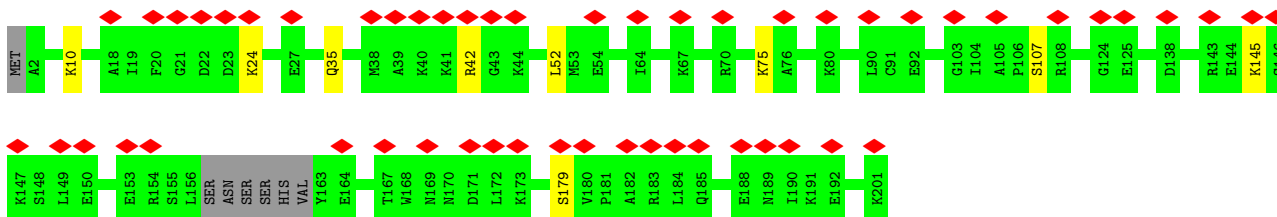
- Molecule 35: 30S ribosomal protein S3

Chain h:  42% 77% 5% 18%




- Molecule 36: 30S ribosomal protein S4

Chain i:  26% 92%

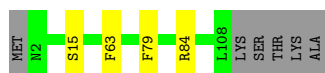
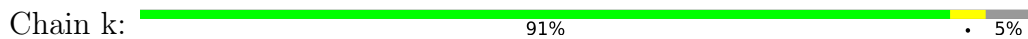


- Molecule 37: 30S ribosomal protein S5

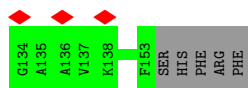
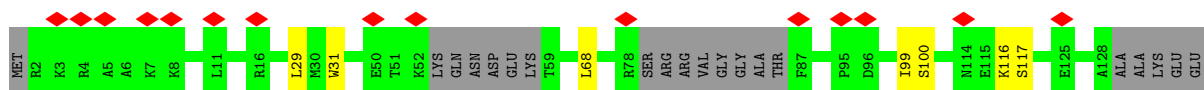
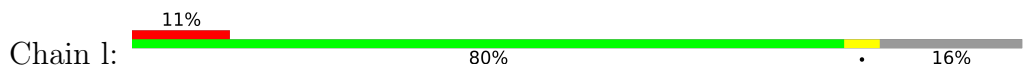
Chain j:  90% 8%



- Molecule 38: 30S ribosomal protein S6



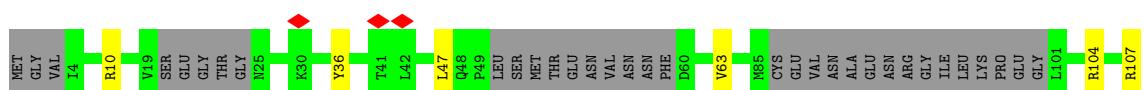
- Molecule 39: 30S ribosomal protein S7



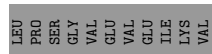
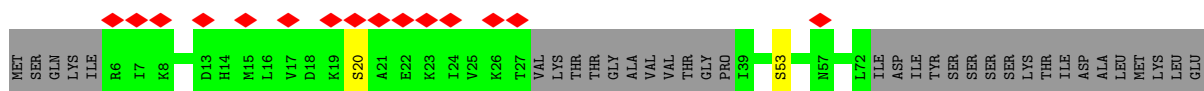
- Molecule 40: 30S ribosomal protein S8



- Molecule 41: 30S ribosomal protein S9

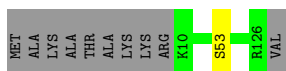


- Molecule 42: 30S ribosomal protein S10

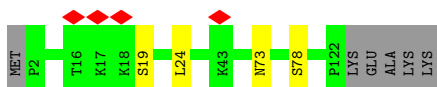
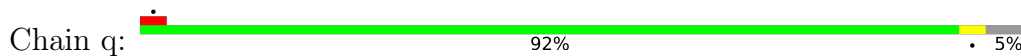


- Molecule 43: 30S ribosomal protein S11

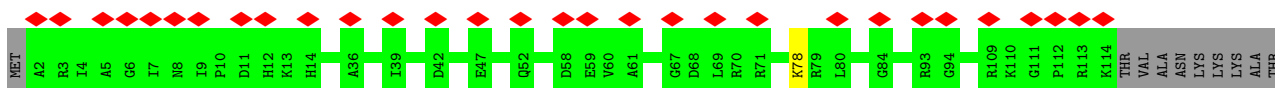
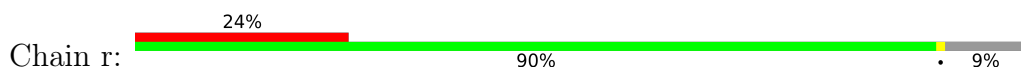




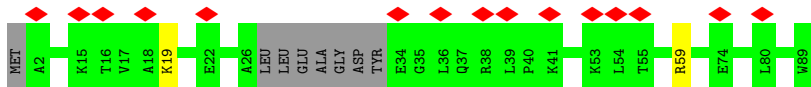
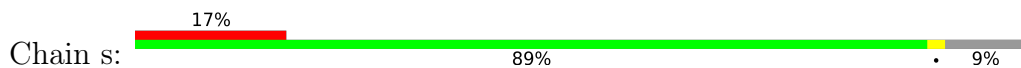
- Molecule 44: 30S ribosomal protein S12



- Molecule 45: 30S ribosomal protein S13



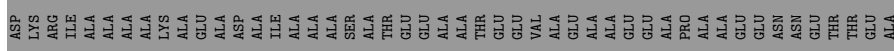
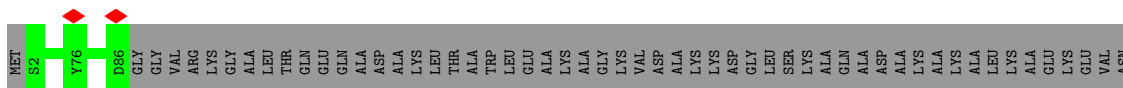
- Molecule 46: 30S ribosomal protein S14



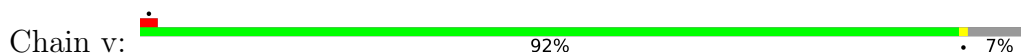
- Molecule 47: 30S ribosomal protein S15

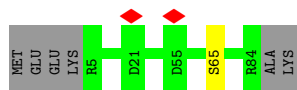


- Molecule 48: 30S ribosomal protein S16

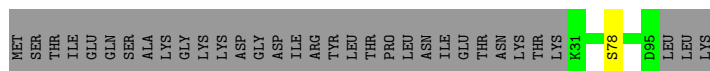


- Molecule 49: 30S ribosomal protein S17

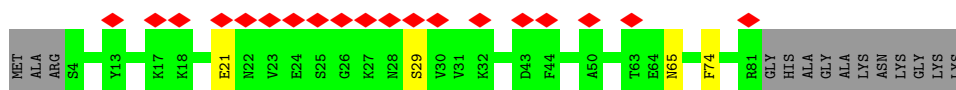
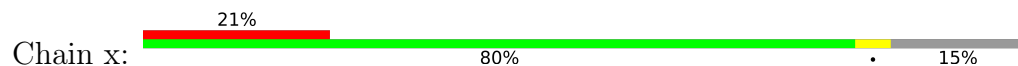




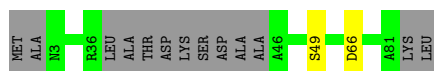
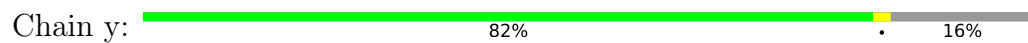
- Molecule 50: 30S ribosomal protein S18



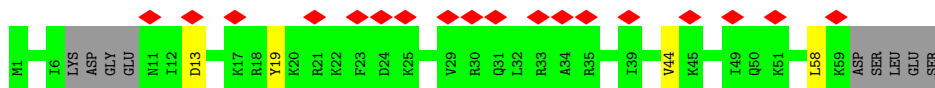
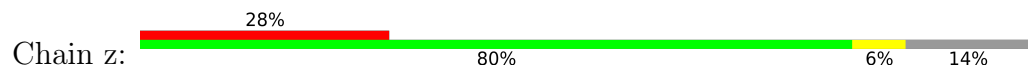
- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	705543	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 ($e^-/\text{\AA}^2$)	50	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	26.299	Depositor
Minimum map value	-15.121	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.8	Depositor
Map size (Å)	386.27997, 386.27997, 386.27997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.073, 1.073, 1.073	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	B	0.26	0/2055	0.46	0/2773
2	C	0.25	0/1479	0.45	0/1989
3	D	0.25	0/1505	0.43	0/2035
4	E	0.26	0/1305	0.46	0/1764
5	F	0.25	0/1268	0.44	0/1714
6	G	0.28	0/366	0.47	0/497
7	J	0.24	0/1130	0.43	0/1529
8	K	0.25	0/892	0.46	0/1199
9	L	0.25	0/1064	0.44	0/1427
10	M	0.24	0/1077	0.44	0/1442
11	N	0.23	0/994	0.41	0/1331
12	O	0.27	0/854	0.47	0/1144
13	P	0.26	0/863	0.45	0/1163
14	Q	0.24	0/918	0.37	0/1220
15	R	0.25	0/778	0.45	0/1045
16	S	0.23	0/974	0.40	0/1305
17	T	0.25	0/652	0.43	0/877
18	U	0.23	0/682	0.42	0/911
19	V	0.25	0/898	0.44	0/1226
20	W	0.25	0/577	0.45	0/771
21	X	0.24	0/593	0.42	0/794
22	Y	0.23	0/362	0.40	0/492
23	Z	0.23	0/403	0.45	0/545
24	1	0.23	0/65892	0.74	1/102748 (0.0%)
25	2	0.20	1/35376 (0.0%)	0.75	6/55154 (0.0%)
26	3	0.21	0/2611	0.71	0/4067
27	4	0.21	0/290	0.33	0/385
28	5	0.20	0/234	0.37	0/301
29	a	0.24	0/413	0.41	0/557
30	b	0.25	0/488	0.41	0/657
31	c	0.23	0/421	0.45	0/569
32	d	0.23	0/422	0.39	0/553
33	e	0.23	0/512	0.44	0/672
34	f	0.24	0/307	0.46	0/405

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.25	0/1573	0.49	0/2119
36	i	0.24	0/1569	0.41	0/2105
37	j	0.25	0/1121	0.45	0/1513
38	k	0.24	0/834	0.42	0/1129
39	l	0.23	0/1070	0.41	0/1436
40	m	0.25	0/976	0.43	0/1324
41	n	0.24	0/766	0.44	0/1020
42	o	0.25	0/459	0.47	0/614
43	p	0.25	0/837	0.45	0/1134
44	q	0.24	0/935	0.47	0/1258
45	r	0.24	0/867	0.48	0/1158
46	s	0.23	0/624	0.43	0/833
47	t	0.23	0/704	0.38	0/946
48	u	0.24	0/669	0.44	0/906
49	v	0.22	0/646	0.44	0/866
50	w	0.24	0/535	0.38	0/714
51	x	0.25	0/618	0.45	0/836
52	y	0.22	0/553	0.38	0/735
53	z	0.24	0/433	0.39	0/580
All	All	0.23	1/144444 (0.0%)	0.68	7/216487 (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	1	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	2	1517	U	C1'-N1	5.83	1.57	1.48

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	2	1225	C	P-O3'-C3'	7.35	128.52	119.70
25	2	1203	G	C2'-C3'-O3'	6.68	124.39	113.70
25	2	1139	A	P-O3'-C3'	6.50	127.50	119.70
25	2	1225	C	N1-C2-O2	5.85	122.41	118.90
25	2	1141	U	P-O3'-C3'	5.47	126.26	119.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
39	1	99	ILE	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	B	269/274 (98%)	244 (91%)	22 (8%)	3 (1%)	14	41
2	C	202/205 (98%)	173 (86%)	29 (14%)	0	100	100
3	D	204/209 (98%)	187 (92%)	17 (8%)	0	100	100
4	E	170/183 (93%)	145 (85%)	25 (15%)	0	100	100
5	F	174/180 (97%)	156 (90%)	18 (10%)	0	100	100
6	G	48/146 (33%)	37 (77%)	11 (23%)	0	100	100
7	J	148/151 (98%)	134 (90%)	14 (10%)	0	100	100
8	K	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
9	L	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
10	M	137/141 (97%)	128 (93%)	9 (7%)	0	100	100
11	N	123/163 (76%)	118 (96%)	5 (4%)	0	100	100
12	O	113/116 (97%)	93 (82%)	20 (18%)	0	100	100
13	P	110/116 (95%)	97 (88%)	13 (12%)	0	100	100
14	Q	111/114 (97%)	105 (95%)	6 (5%)	0	100	100
15	R	102/147 (69%)	89 (87%)	13 (13%)	0	100	100
16	S	126/137 (92%)	124 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	T	81/96 (84%)	71 (88%)	10 (12%)	0	100	100
18	U	88/104 (85%)	79 (90%)	9 (10%)	0	100	100
19	V	120/203 (59%)	112 (93%)	8 (7%)	0	100	100
20	W	73/86 (85%)	64 (88%)	9 (12%)	0	100	100
21	X	74/78 (95%)	70 (95%)	4 (5%)	0	100	100
22	Y	49/63 (78%)	42 (86%)	7 (14%)	0	100	100
23	Z	54/60 (90%)	48 (89%)	6 (11%)	0	100	100
27	4	34/50 (68%)	32 (94%)	2 (6%)	0	100	100
28	5	25/30 (83%)	24 (96%)	1 (4%)	0	100	100
29	a	48/84 (57%)	39 (81%)	9 (19%)	0	100	100
30	b	57/64 (89%)	53 (93%)	4 (7%)	0	100	100
31	c	52/60 (87%)	49 (94%)	3 (6%)	0	100	100
32	d	49/53 (92%)	46 (94%)	3 (6%)	0	100	100
33	e	62/65 (95%)	53 (86%)	9 (14%)	0	100	100
34	f	36/38 (95%)	36 (100%)	0	0	100	100
35	h	204/252 (81%)	173 (85%)	31 (15%)	0	100	100
36	i	190/201 (94%)	173 (91%)	17 (9%)	0	100	100
37	j	157/173 (91%)	145 (92%)	12 (8%)	0	100	100
38	k	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
39	l	125/158 (79%)	107 (86%)	18 (14%)	0	100	100
40	m	129/132 (98%)	119 (92%)	10 (8%)	0	100	100
41	n	87/128 (68%)	74 (85%)	13 (15%)	0	100	100
42	o	52/101 (52%)	44 (85%)	8 (15%)	0	100	100
43	p	115/127 (91%)	90 (78%)	25 (22%)	0	100	100
44	q	119/127 (94%)	107 (90%)	12 (10%)	0	100	100
45	r	111/124 (90%)	100 (90%)	11 (10%)	0	100	100
46	s	77/89 (86%)	65 (84%)	12 (16%)	0	100	100
47	t	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
48	u	83/188 (44%)	78 (94%)	5 (6%)	0	100	100
49	v	78/86 (91%)	73 (94%)	5 (6%)	0	100	100
50	w	63/98 (64%)	63 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	x	76/92 (83%)	68 (90%)	8 (10%)	0	100	100
52	y	66/83 (80%)	57 (86%)	8 (12%)	1 (2%)	10	33
53	z	51/64 (80%)	50 (98%)	1 (2%)	0	100	100
All	All	5180/6112 (85%)	4661 (90%)	515 (10%)	4 (0%)	54	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	197	ASN
1	B	198	SER
52	y	66	ASP
1	B	136	PRO

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	B	204/225 (91%)	199 (98%)	5 (2%)	47	80
2	C	139/162 (86%)	139 (100%)	0	100	100
3	D	143/181 (79%)	139 (97%)	4 (3%)	43	77
4	E	122/156 (78%)	115 (94%)	7 (6%)	20	50
5	F	122/148 (82%)	116 (95%)	6 (5%)	25	57
6	G	35/118 (30%)	33 (94%)	2 (6%)	20	50
7	J	115/128 (90%)	111 (96%)	4 (4%)	36	70
8	K	88/100 (88%)	84 (96%)	4 (4%)	27	60
9	L	94/115 (82%)	93 (99%)	1 (1%)	73	92
10	M	102/116 (88%)	99 (97%)	3 (3%)	42	76
11	N	101/131 (77%)	101 (100%)	0	100	100
12	O	79/90 (88%)	72 (91%)	7 (9%)	9	28
13	P	78/98 (80%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	Q	89/94 (95%)	87 (98%)	2 (2%)	52	83
15	R	72/112 (64%)	71 (99%)	1 (1%)	67	90
16	S	93/116 (80%)	92 (99%)	1 (1%)	73	92
17	T	70/85 (82%)	68 (97%)	2 (3%)	42	76
18	U	68/89 (76%)	66 (97%)	2 (3%)	42	76
19	V	83/163 (51%)	81 (98%)	2 (2%)	49	81
20	W	58/69 (84%)	56 (97%)	2 (3%)	37	71
21	X	62/69 (90%)	62 (100%)	0	100	100
22	Y	32/55 (58%)	30 (94%)	2 (6%)	18	46
23	Z	41/52 (79%)	40 (98%)	1 (2%)	49	81
27	4	32/44 (73%)	27 (84%)	5 (16%)	2	8
28	5	23/26 (88%)	23 (100%)	0	100	100
29	a	43/75 (57%)	41 (95%)	2 (5%)	26	59
30	b	44/53 (83%)	44 (100%)	0	100	100
31	c	45/56 (80%)	45 (100%)	0	100	100
32	d	42/46 (91%)	42 (100%)	0	100	100
33	e	55/59 (93%)	54 (98%)	1 (2%)	59	86
34	f	31/34 (91%)	31 (100%)	0	100	100
35	h	150/201 (75%)	138 (92%)	12 (8%)	12	34
36	i	159/173 (92%)	150 (94%)	9 (6%)	20	50
37	j	107/138 (78%)	103 (96%)	4 (4%)	34	68
38	k	74/101 (73%)	70 (95%)	4 (5%)	22	53
39	l	104/136 (76%)	98 (94%)	6 (6%)	20	50
40	m	93/111 (84%)	91 (98%)	2 (2%)	52	83
41	n	76/107 (71%)	70 (92%)	6 (8%)	12	34
42	o	50/94 (53%)	48 (96%)	2 (4%)	31	65
43	p	80/102 (78%)	79 (99%)	1 (1%)	69	91
44	q	97/107 (91%)	93 (96%)	4 (4%)	30	64
45	r	85/100 (85%)	84 (99%)	1 (1%)	71	92
46	s	57/73 (78%)	55 (96%)	2 (4%)	36	70
47	t	66/79 (84%)	65 (98%)	1 (2%)	65	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	u	63/136 (46%)	63 (100%)	0	100	100
49	v	71/81 (88%)	70 (99%)	1 (1%)	67	90
50	w	53/87 (61%)	52 (98%)	1 (2%)	57	85
51	x	65/78 (83%)	61 (94%)	4 (6%)	18	47
52	y	58/72 (81%)	57 (98%)	1 (2%)	60	87
53	z	42/56 (75%)	38 (90%)	4 (10%)	8	25
All	All	3955/5097 (78%)	3824 (97%)	131 (3%)	41	72

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	q	78	SER
47	t	34	ARG
53	z	58	LEU
17	T	61	SER
17	T	17	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
38	k	18	GLN
45	r	8	ASN
39	l	88	GLN
41	n	25	ASN
48	u	61	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	1	2731/2862 (95%)	435 (15%)	24 (0%)
25	2	1468/1520 (96%)	262 (17%)	31 (2%)
26	3	109/111 (98%)	16 (14%)	0
All	All	4308/4493 (95%)	713 (16%)	55 (1%)

5 of 713 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	1	13	A

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Mol	Chain	Res	Type
24	1	34	A
24	1	46	G
24	1	51	G
24	1	52	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	2	236	A
25	2	1109	C
25	2	1379	C
25	2	1280	A
25	2	243	A

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

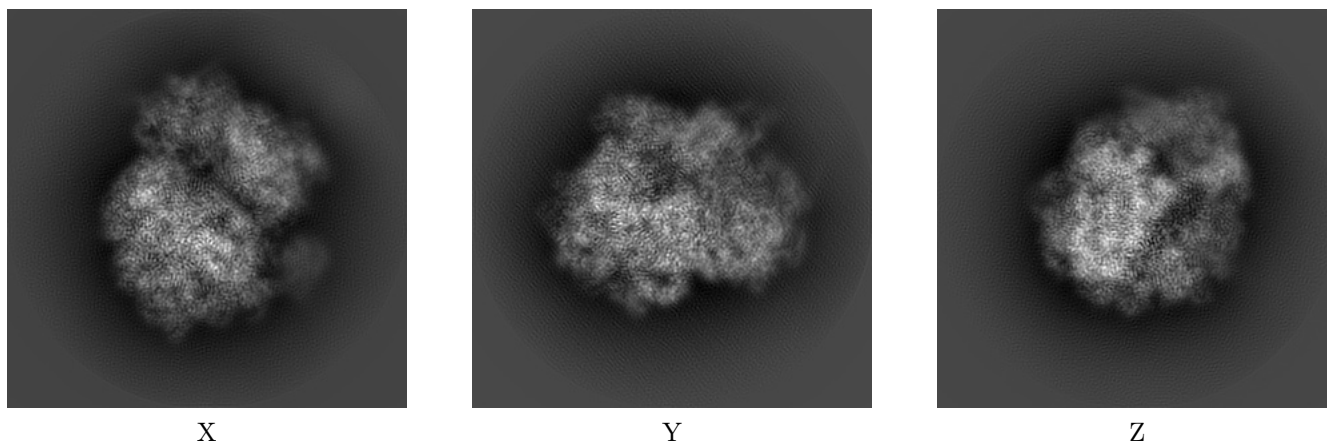
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22345. 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](#)

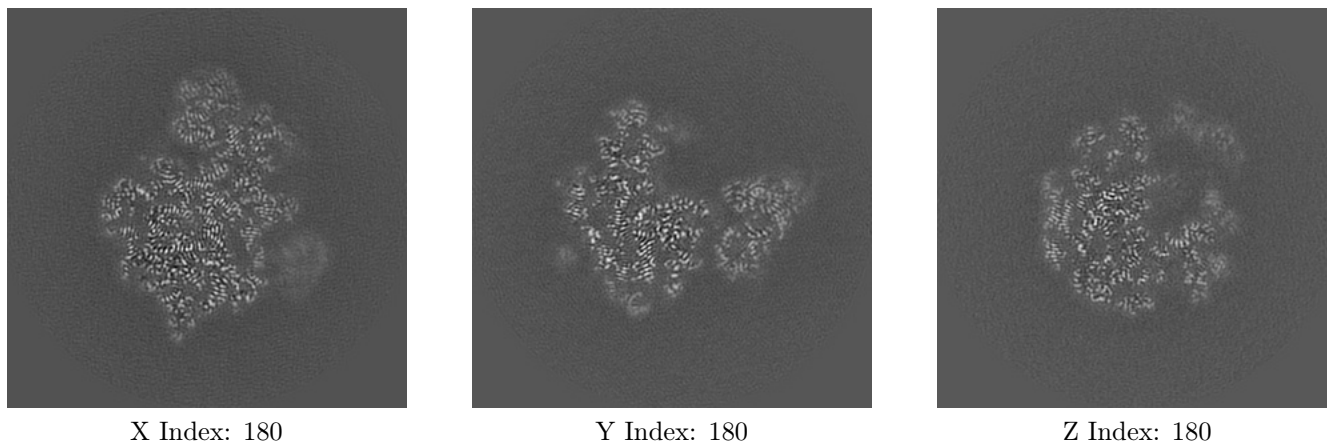
6.1.1 Primary map



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

6.2 Central slices [i](#)

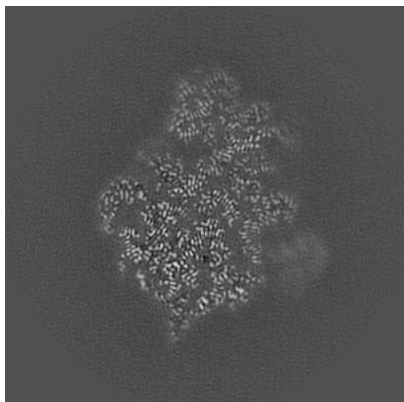
6.2.1 Primary map



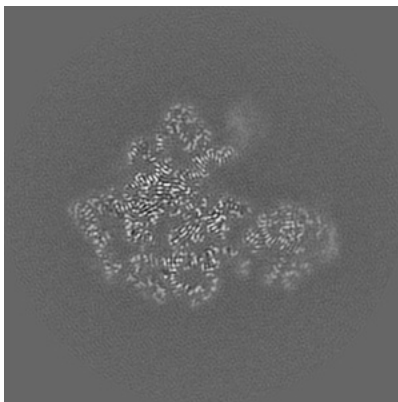
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

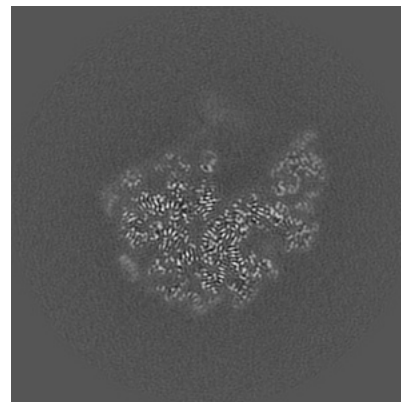
6.3.1 Primary map



X Index: 178



Y Index: 151

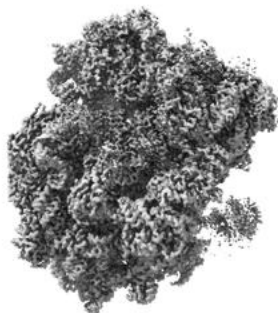


Z Index: 155

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

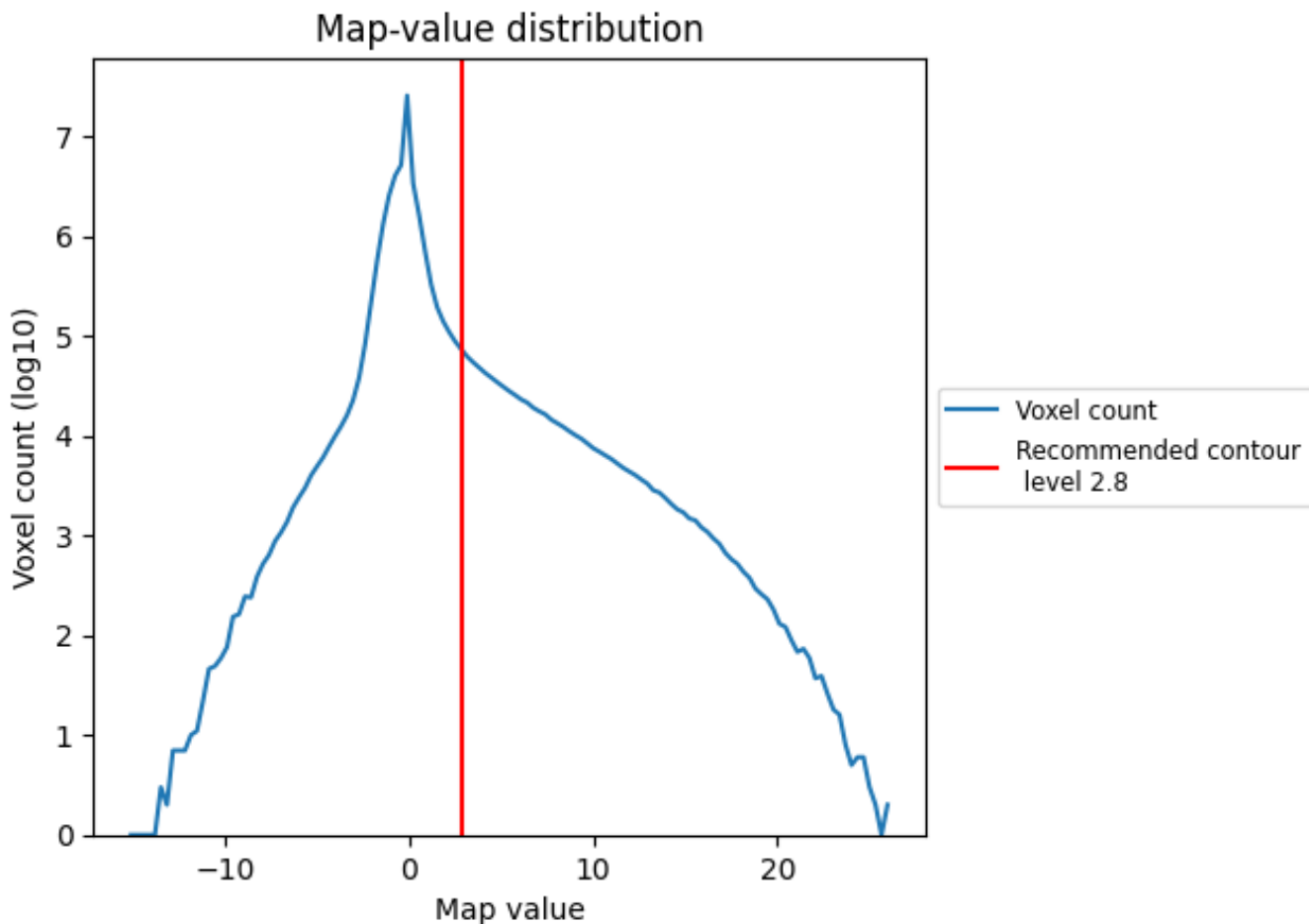
6.5 Mask visualisation

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

7 Map analysis [i](#)

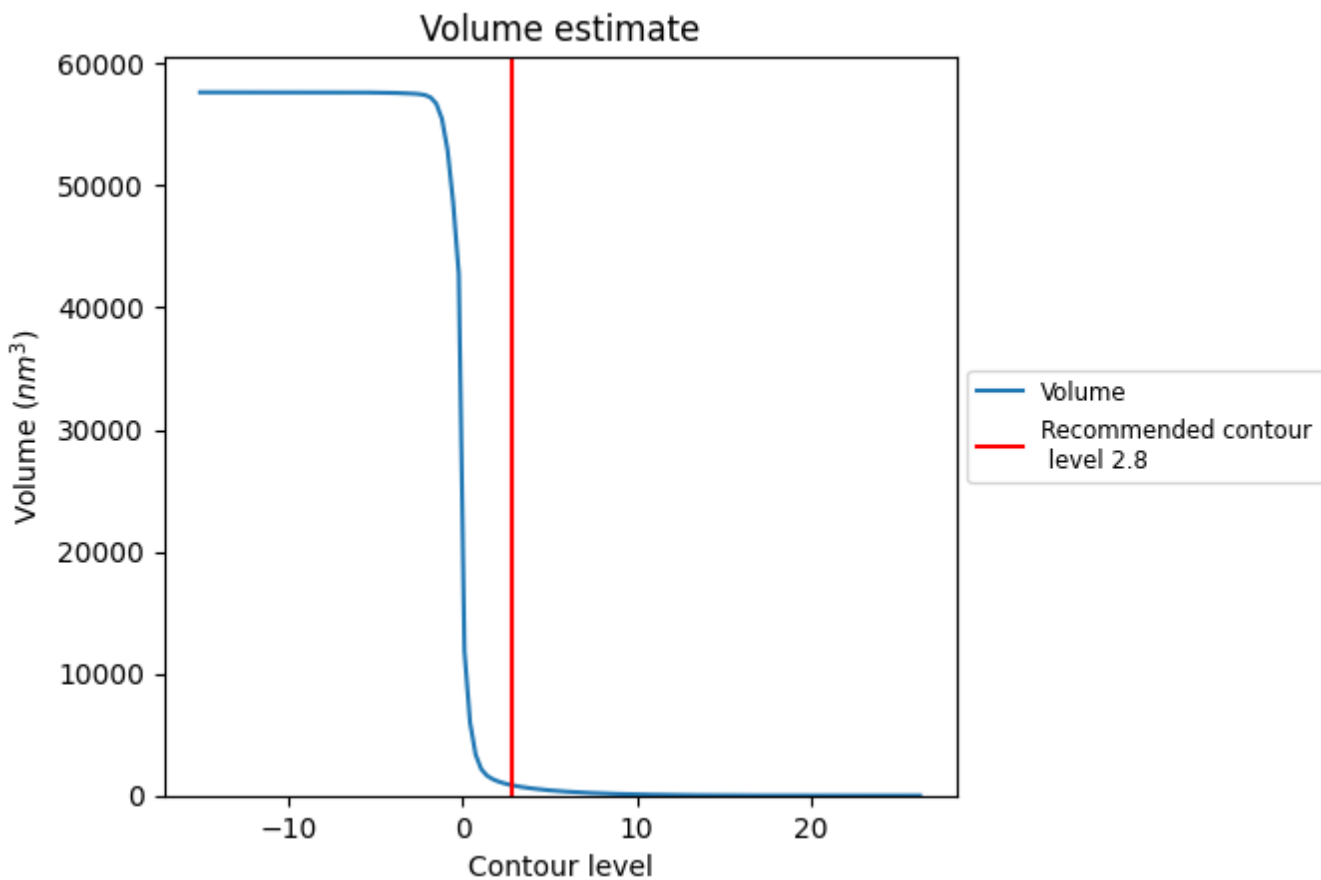
This section contains the results of statistical analysis of the map.

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.

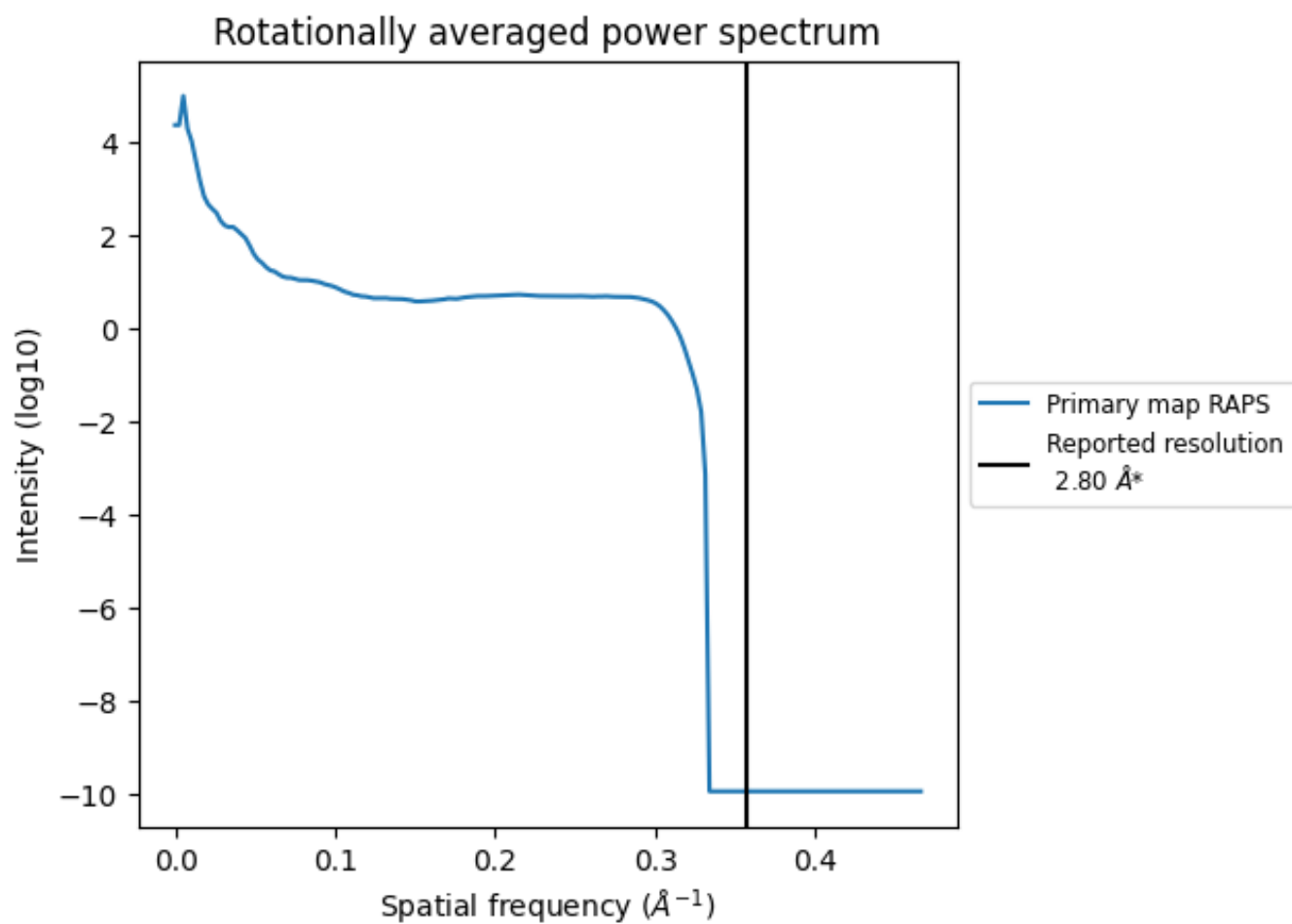
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 857 nm³; this corresponds to an approximate mass of 774 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](#)

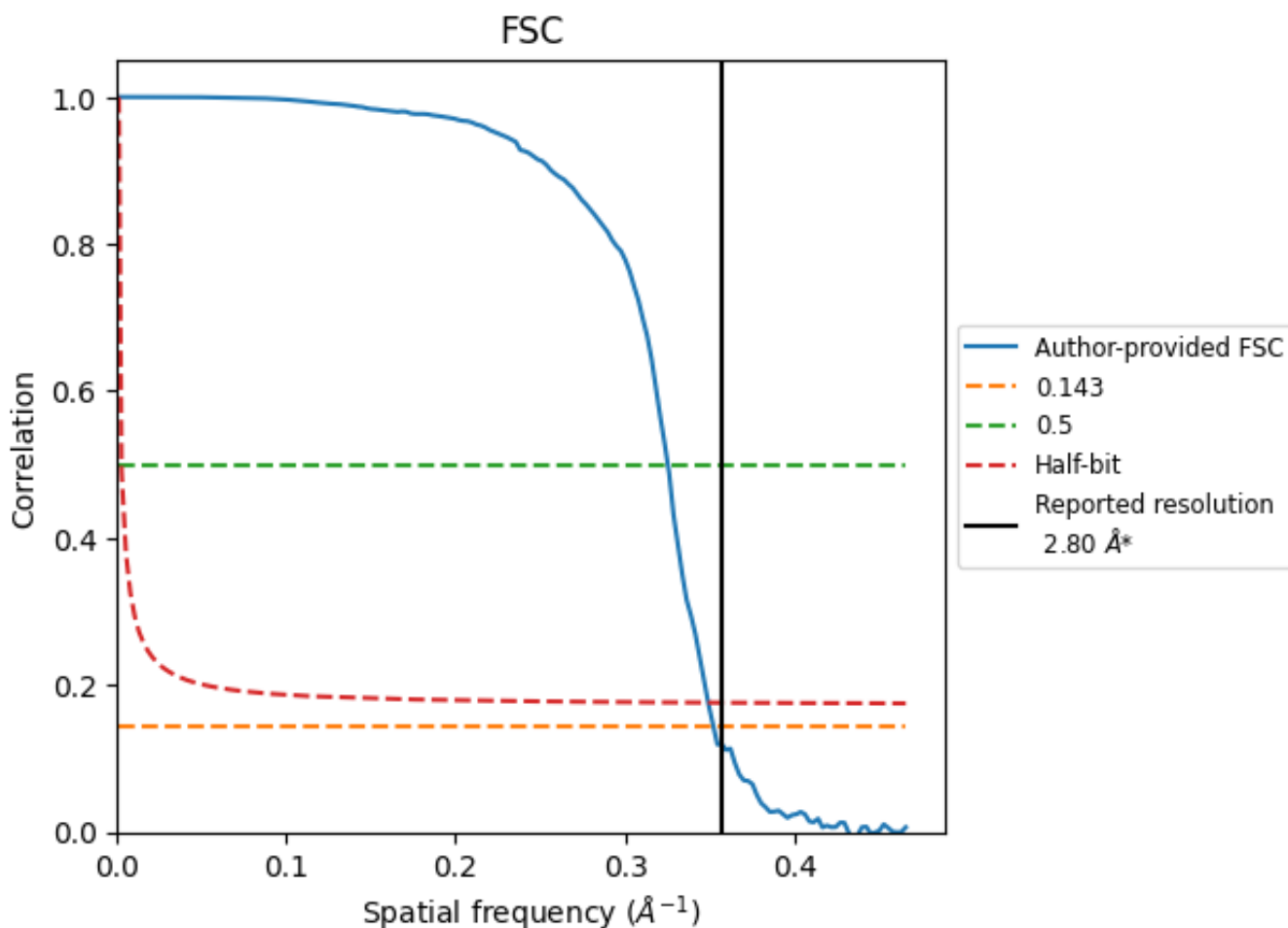


*Reported resolution corresponds to spatial frequency of 0.357\AA^{-1}

8 Fourier-Shell correlation [\(i\)](#)

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

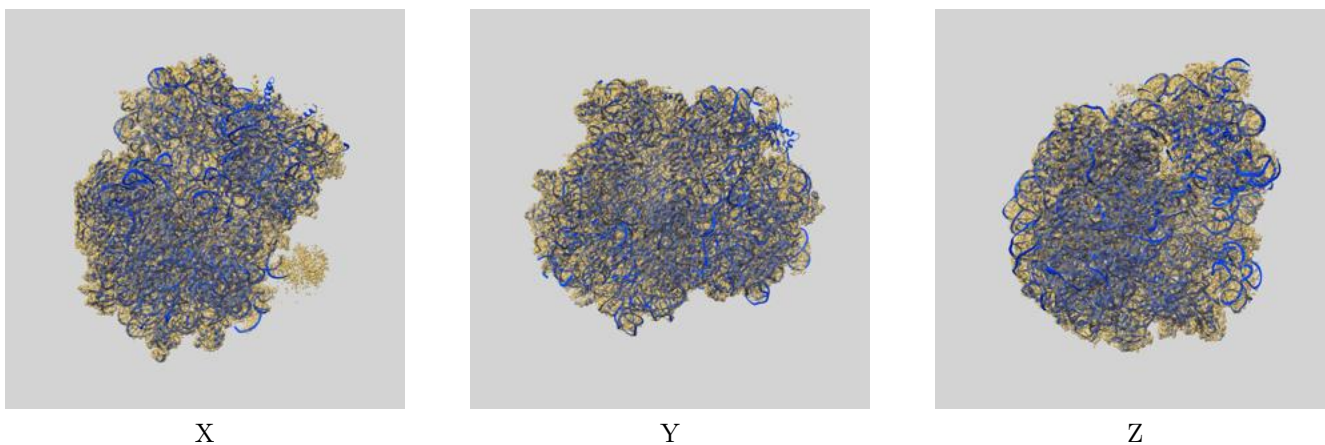
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.07	2.86
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

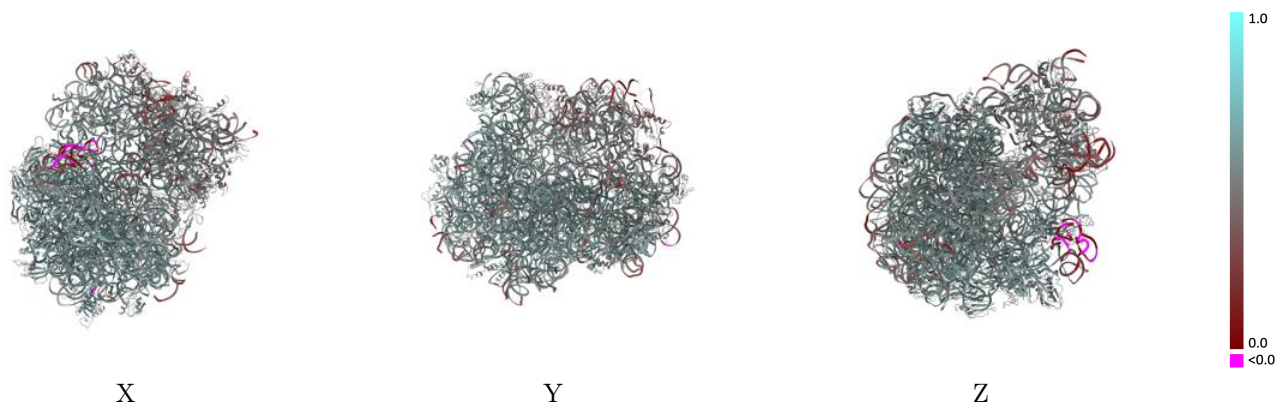
This section contains information regarding the fit between EMDB map EMD-22345 and PDB model 7JIL. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



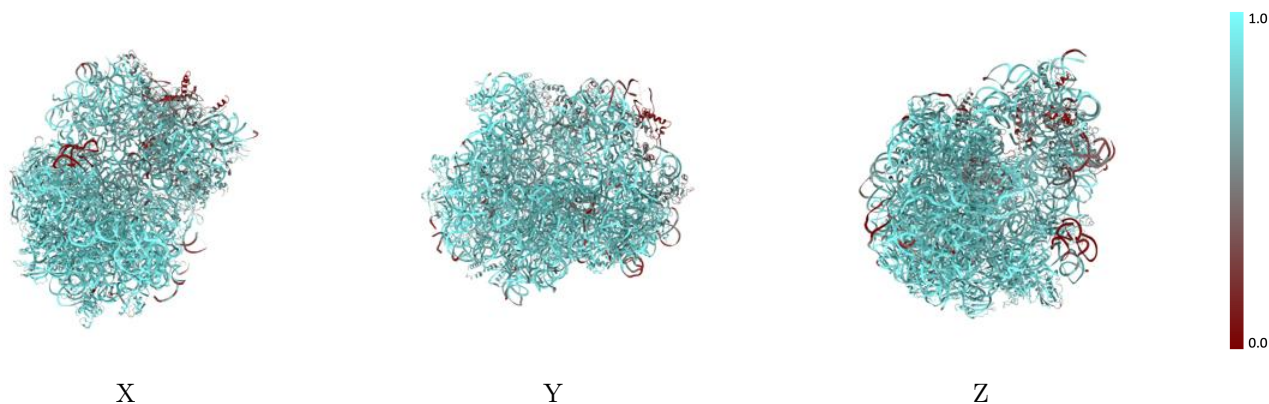
The images above show the 3D surface view of the map at the recommended contour level 2.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



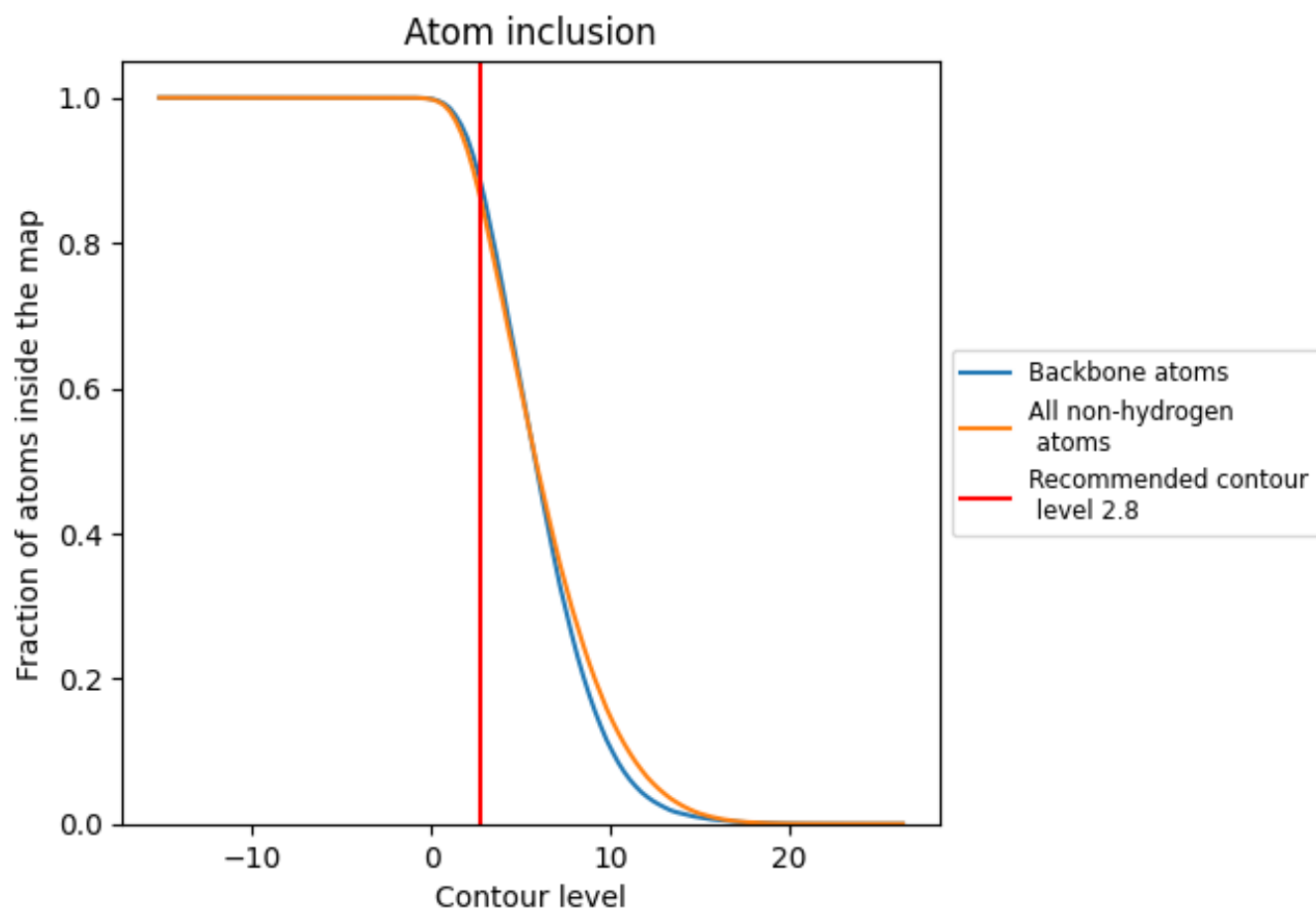
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.8).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (2.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.5340
1	 0.9127	 0.5510
2	 0.8520	 0.5020
3	 0.9132	 0.5370
4	 0.6855	 0.4670
5	 0.7489	 0.5550
B	 0.8873	 0.5790
C	 0.8831	 0.5720
D	 0.8732	 0.5650
E	 0.7267	 0.4760
F	 0.7808	 0.5260
G	 0.6359	 0.4640
J	 0.8601	 0.5640
K	 0.8265	 0.5640
L	 0.8682	 0.5700
M	 0.8642	 0.5710
N	 0.8920	 0.5770
O	 0.8270	 0.5370
P	 0.8466	 0.5580
Q	 0.9049	 0.5800
R	 0.8660	 0.5630
S	 0.8759	 0.5680
T	 0.7896	 0.5490
U	 0.7973	 0.5520
V	 0.7904	 0.5420
W	 0.8863	 0.5720
X	 0.8706	 0.5670
Y	 0.7529	 0.5160
Z	 0.8858	 0.5740
a	 0.7118	 0.4740
b	 0.9231	 0.5890
c	 0.8719	 0.5640
d	 0.9086	 0.6020
e	 0.8815	 0.5780
f	 0.8966	 0.5850



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Chain	Atom inclusion	Q-score
h	 0.3894	 0.4360
i	 0.5313	 0.4780
j	 0.7699	 0.5310
k	 0.8577	 0.5580
l	 0.6650	 0.4700
m	 0.8006	 0.5380
n	 0.7004	 0.4970
o	 0.5372	 0.4930
p	 0.8114	 0.5380
q	 0.7517	 0.5300
r	 0.5719	 0.4290
s	 0.6017	 0.4940
t	 0.8316	 0.5340
u	 0.8053	 0.5210
v	 0.7690	 0.5340
w	 0.8563	 0.5640
x	 0.5608	 0.4360
y	 0.8187	 0.5260
z	 0.5156	 0.5150