



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 01:16 AM UTC

PDB ID : 9OZZ / pdb_00009ozz
EMDB ID : EMD-71061
Title : Flavobacterium johnsoniae 70S initiation complex with rpsU mRNA containing Shine-Dalgarno sequence. State 2.
Authors : Ortega, J.; Arpin, D.
Deposited on : 2025-06-06
Resolution : 2.50 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:

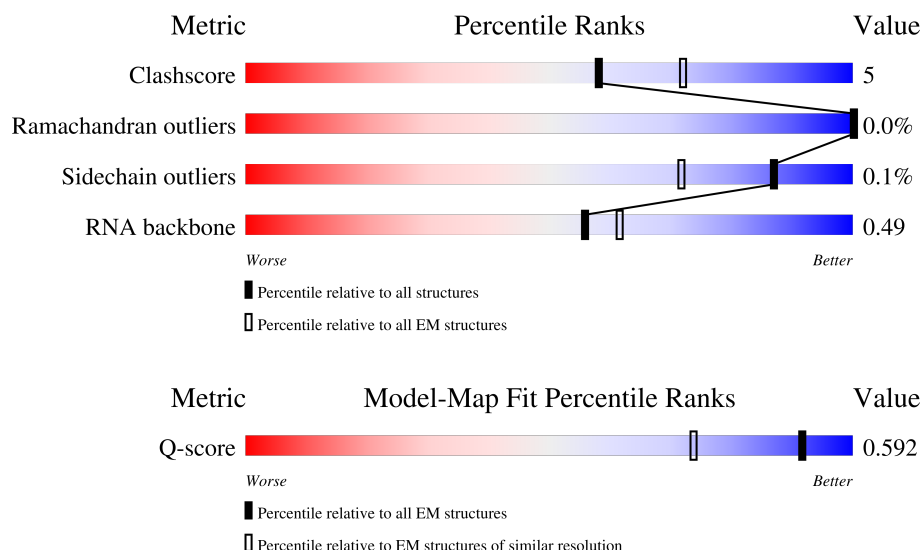
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.50 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.





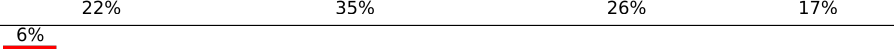
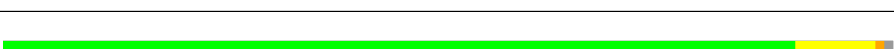



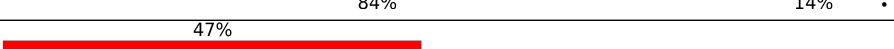


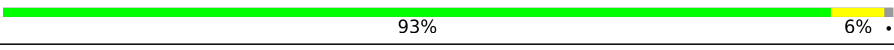
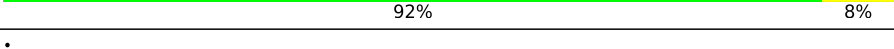

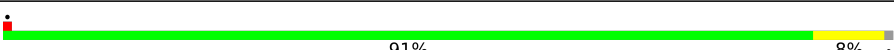


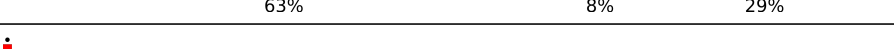







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	1	2862	
2	2	1520	
3	3	111	






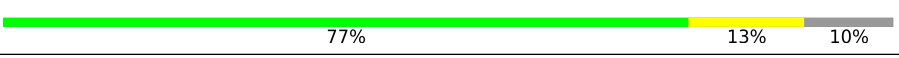
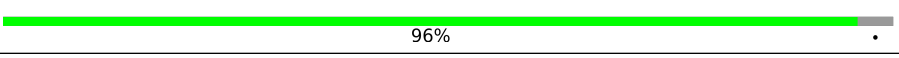
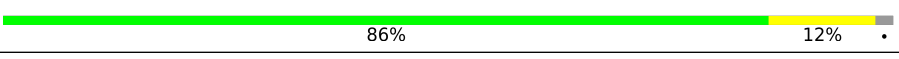
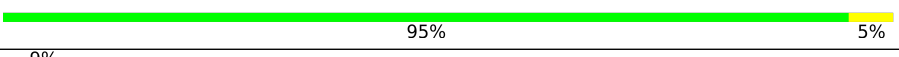


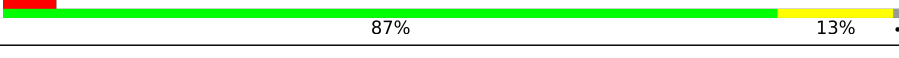


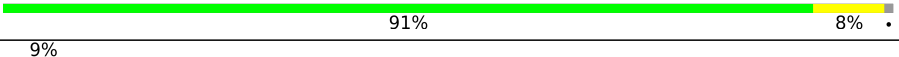



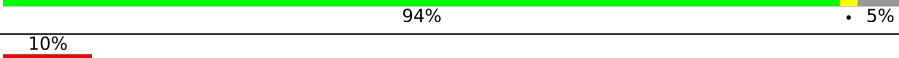
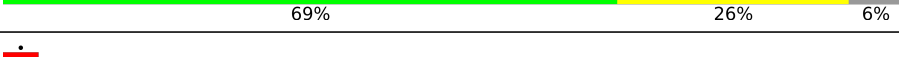
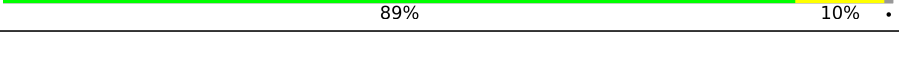
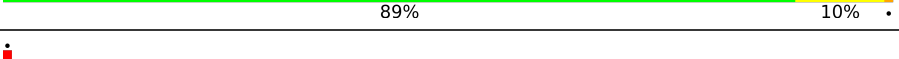

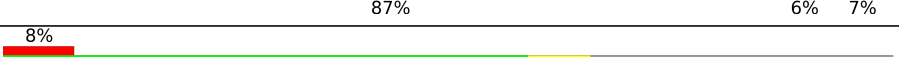

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Mol	Chain	Length	Quality of chain
4	4	50	
5	5	30	
6	6	23	
7	A	77	
8	B	274	
9	C	205	
10	D	209	
11	E	183	
12	F	180	
13	G	146	
14	H	254	
15	J	151	
16	K	122	
17	L	150	
18	M	141	
19	N	163	
20	O	116	
21	P	116	
22	Q	114	
23	R	147	
24	S	137	
25	T	96	
26	U	104	
27	V	203	
28	W	86	

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Mol	Chain	Length	Quality of chain
29	X	78	
30	Y	63	
31	Z	60	
32	a	84	
33	b	64	
34	c	60	
35	d	53	
36	e	65	
37	f	38	
38	h	252	
39	i	201	
40	j	173	
41	k	113	
42	l	158	
43	m	132	
44	n	128	
45	o	101	
46	p	127	
47	q	127	
48	r	124	
49	s	89	
50	t	88	
51	u	188	
52	v	86	
53	w	98	

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Mol	Chain	Length	Quality of chain
54	x	92	<div><div></div><div>7%</div><div>76%</div><div>14%</div><div>10%</div></div>
55	y	83	<div><div></div><div>7%</div><div>82%</div><div>13%</div><div>5%</div></div>

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 138113 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2754	Total	C	N	O	P	0	0
			59085	26384	10861	19086	2754		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	342	A	U	conflict	GB 1735479352
1	406	A	G	conflict	GB 1735479352
1	429	C	U	conflict	GB 1735479352
1	645	C	U	conflict	GB 1735479352
1	925	C	U	conflict	GB 1735479352
1	1510	A	U	conflict	GB 1735479352
1	1687	U	G	conflict	GB 1735479352
1	1745	U	C	conflict	GB 1735479352
1	1746	G	C	conflict	GB 1735479352
1	1753	C	G	conflict	GB 1735479352
1	1754	A	G	conflict	GB 1735479352
1	1815	U	C	conflict	GB 1735479352
1	2098	C	U	conflict	GB 1735479352
1	2209	U	C	conflict	GB 1735479352
1	2471	U	C	conflict	GB 1735479352
1	2569	U	C	conflict	GB 1735479352

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1481	Total	C	N	O	P	0	0
			31728	14167	5801	10279	1481		

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

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

- Molecule 4 is a protein called 50S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	36	Total	C	N	O	S	0	0
			278	183	44	49	2		

- Molecule 5 is a protein called 30S ribosomal protein S22.

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

- Molecule 6 is a RNA chain called rpsU mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	19	Total	C	N	O	P	0	0
			415	184	78	134	19		

- Molecule 7 is a RNA chain called fMet-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	73	Total	C	N	O	P	0	0
			1562	696	286	507	73		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	271	Total	C	N	O	S	0	0
			2053	1277	403	365	8		

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 9 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	204	Total	C	N	O	S	0	0
			1515	956	280	272	7		

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 10 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	D	206	Total	C	N	O	0	0
			1509	964	281	264		

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	E	179	Total	C	N	O	S	0
			1300	836	229	230	5	0

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	F	177	Total	C	N	O	S	0
			1255	805	230	219	1	0

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 13 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	G	122	Total	C	N	O	S	0
			869	559	154	155	1	0

- Molecule 14 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	H	219	Total	C	N	O	S	0
			1676	1067	294	307	8	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	121	Total	C	N	O	S	0	0
			889	559	173	153	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	150	Total	C	N	O	S	0	0
			1048	654	209	183	2		

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	124	Total	C	N	O	S	0	0
			871	570	148	151	2		

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 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	78	Total	C	N	O		0	0
			586	365	119	102			

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

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

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 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	59	Total	C	N	O		0	0
			409	257	80	72			

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	58	Total	C	N	O	S	0	0
			421	271	71	77	2		

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

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

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

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

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

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

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

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

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

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

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	215	Total	C	N	O	S	0	0
			1600	1015	290	289	6		

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	200	Total	C	N	O	S	0	0
			1576	998	291	284	3		

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	172	Total	C	N	O	S	0	0
			1179	744	229	205	1		

- Molecule 41 is a protein called 30S ribosomal protein S6.

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

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	153	Total	C	N	O	S	0	0
			1183	747	231	200	5		

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	125	Total	C	N	O	S	0	0
			972	612	188	168	4		

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	98	Total	C	N	O	S	0	0
			701	450	123	126	2		

- Molecule 46 is a protein called 30S ribosomal protein S11.

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

- Molecule 47 is a protein called 30S ribosomal protein S12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	117	Total	C	N	O	S	0	0
			883	544	181	155	3		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	115	THR	-	expression tag	UNP P0A7T1
r	116	VAL	-	expression tag	UNP P0A7T1
r	117	ALA	-	expression tag	UNP P0A7T1
r	118	ASN	-	expression tag	UNP P0A7T1
r	119	LYS	-	expression tag	UNP P0A7T1
r	120	LYS	-	expression tag	UNP P0A7T1
r	121	LYS	-	expression tag	UNP P0A7T1
r	122	ALA	-	expression tag	UNP P0A7T1
r	123	THR	-	expression tag	UNP P0A7T1
r	124	LYS	-	expression tag	UNP P0A7T1

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	88	Total	C	N	O	S	0	0
			665	416	136	110	3		

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	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 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	u	109	Total	C	N	O	0	0
			783	492	151	140		

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 52 is a protein called 30S ribosomal protein S17.

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

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	65	Total	C	N	O	S	0	0
			521	342	96	81	2		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	83	Total	C	N	O	S	0	0
			636	406	118	110	2		

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	79	Total	C	N	O	S	0	0
			615	381	129	104	1		

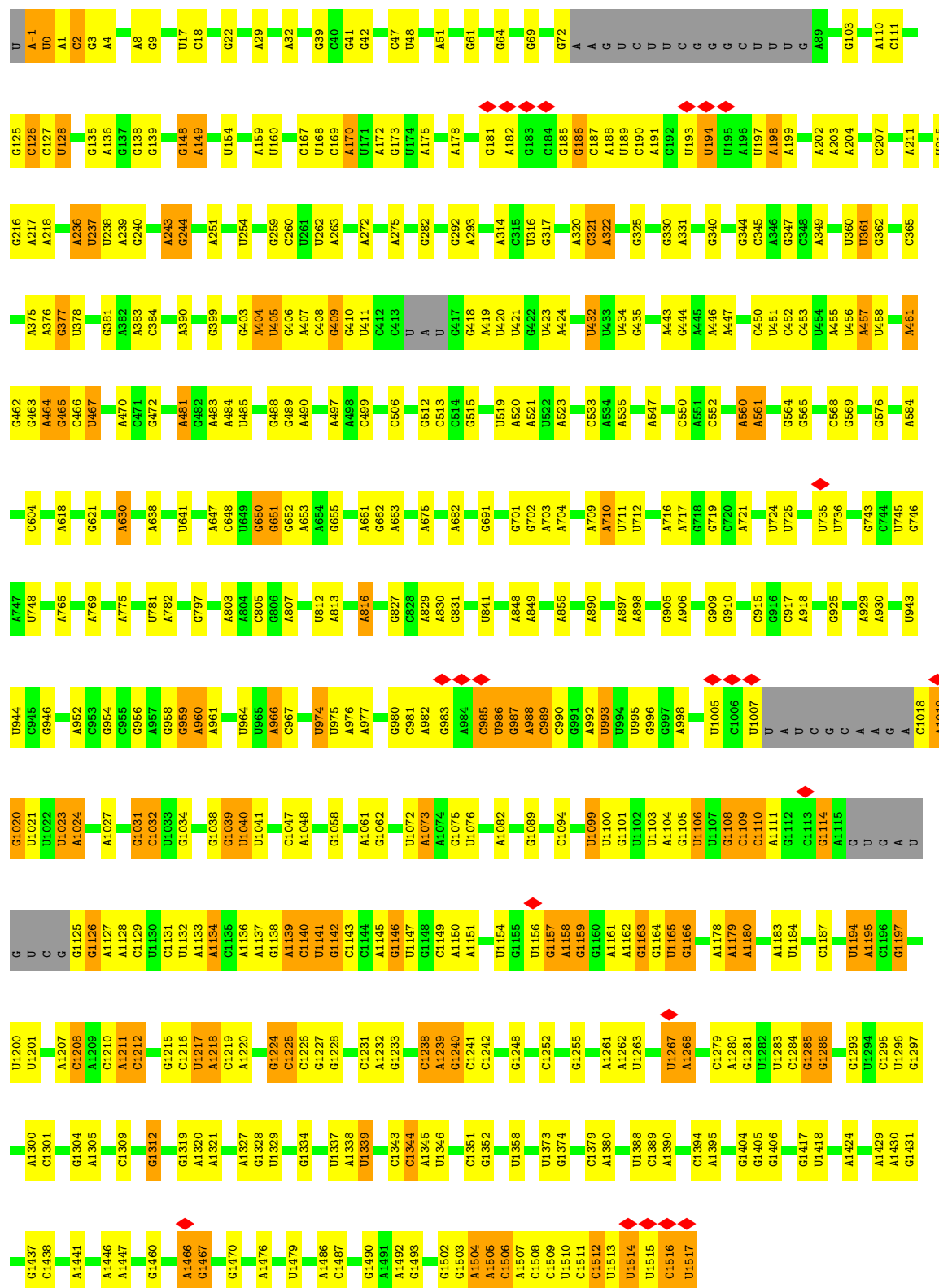
3 Residue-property plots [i](#)

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: 23S rRNA

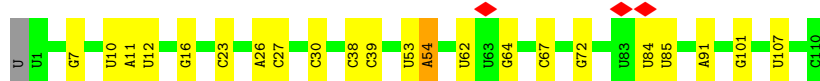




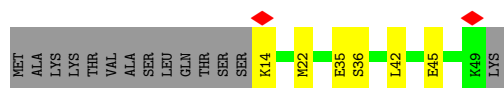


• Molecule 3: 5S rRNA

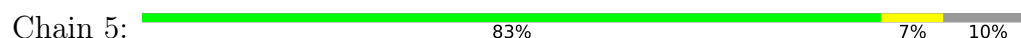
Chain 3: 79% 19% ..



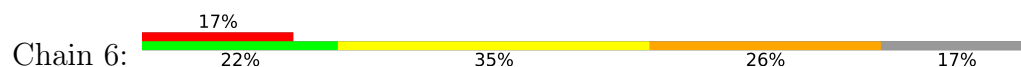
- Molecule 4: 50S ribosomal protein L38



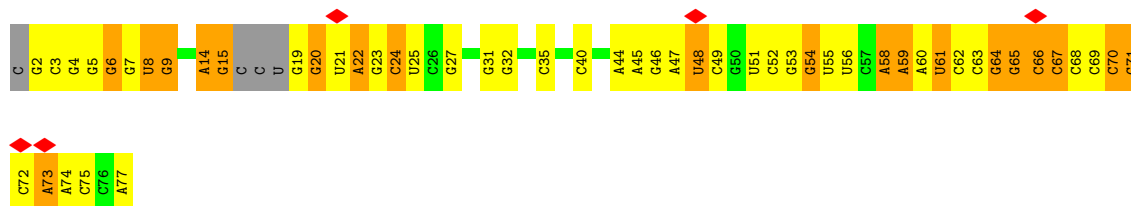
- Molecule 5: 30S ribosomal protein S22



- Molecule 6: rpsU mRNA



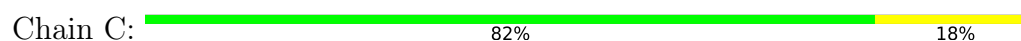
- Molecule 7: fMet-tRNA



- Molecule 8: 50S ribosomal protein L2



- Molecule 9: 50S ribosomal protein L3





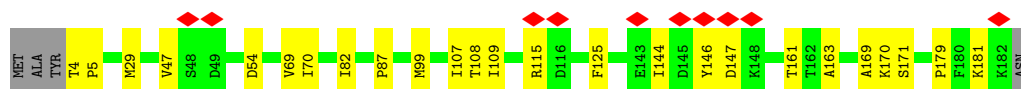
- Molecule 10: 50S ribosomal protein L4

Chain D: 89% 9% .



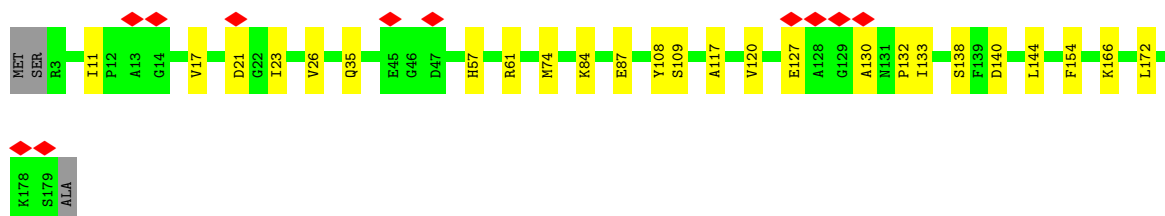
- Molecule 11: 50S ribosomal protein L5

Chain E: 5% 84% 14% .



- Molecule 12: 50S ribosomal protein L6

Chain F: 6% 84% 14% .



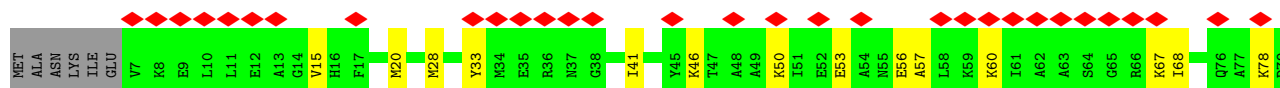
- Molecule 13: 50S ribosomal protein L9

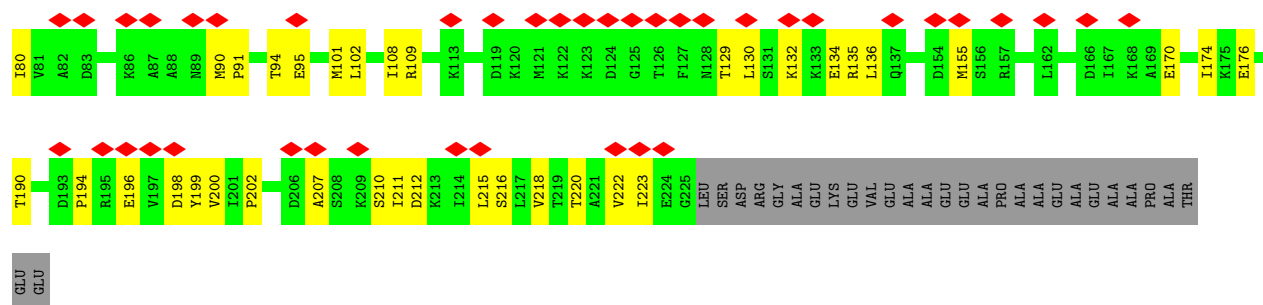
Chain G: 47% 67% 14% 16% .



- Molecule 14: 30S ribosomal protein S2

Chain H: 28% 67% 20% 14% .





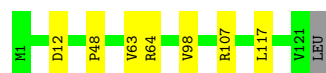
- Molecule 15: 50S ribosomal protein L13

Chain J: 91% 9%



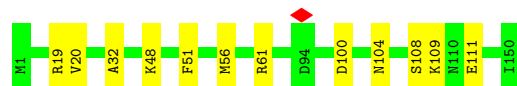
- Molecule 16: 50S ribosomal protein L14

Chain K: 93% 6%



- Molecule 17: 50S ribosomal protein L15

Chain L: 92% 8%



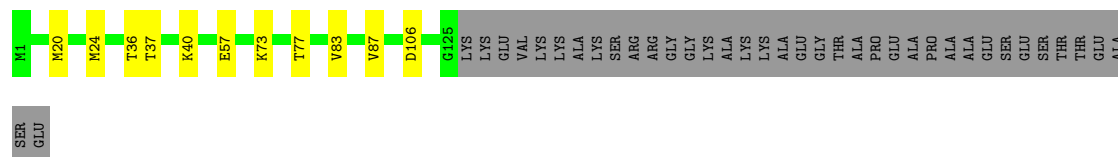
- Molecule 18: 50S ribosomal protein L16

Chain M: 89% 9%




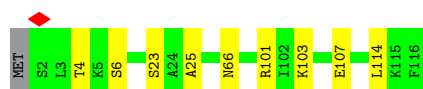
- Molecule 19: 50S ribosomal protein L17

Chain N: 70% 7% 23%




- Molecule 20: 50S ribosomal protein L18

Chain O:  91% 8%




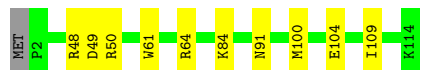
- Molecule 21: 50S ribosomal protein L19

Chain P:  84% 12%



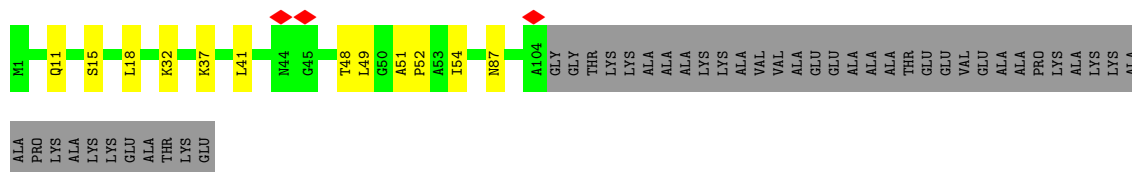
- Molecule 22: 50S ribosomal protein L20

Chain Q:  90% 9%




- Molecule 23: 50S ribosomal protein L21

Chain R:  63% 8% 29%




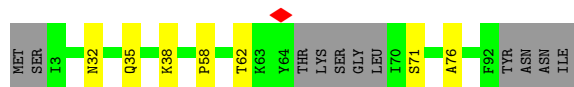
- Molecule 24: 50S ribosomal protein L22

Chain S:  85% 9% 7%




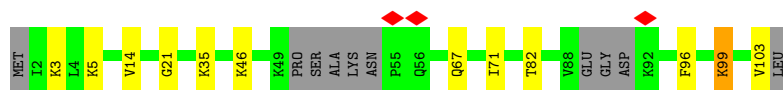
- Molecule 25: 50S ribosomal protein L23

Chain T:  81% 7% 11%

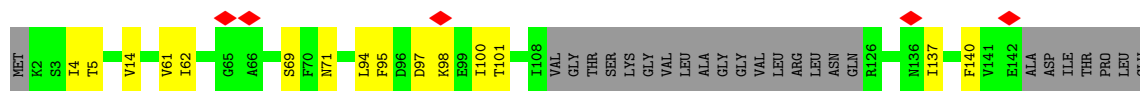


- Molecule 26: 50S ribosomal protein L24

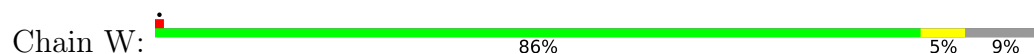
Chain U:  79% 11% 10%



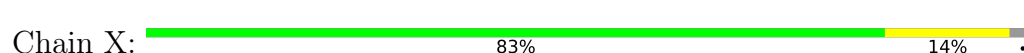
- Molecule 27: 50S ribosomal protein L25



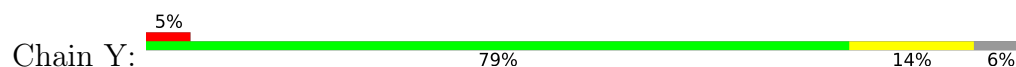
- Molecule 28: 50S ribosomal protein L27



- Molecule 29: 50S ribosomal protein L28



- Molecule 30: 50S ribosomal protein L29




- Molecule 31: 50S ribosomal protein L30



- Molecule 32: 50S ribosomal protein L31




- Molecule 33: 50S ribosomal protein L32

Chain b:  80% 11% 8%



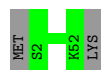
- Molecule 34: 50S ribosomal protein L33

Chain c:  77% 13% 10%




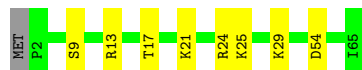
- Molecule 35: 50S ribosomal protein L34

Chain d:  96%



- Molecule 36: 50S ribosomal protein L35

Chain e:  86% 12%



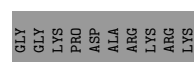
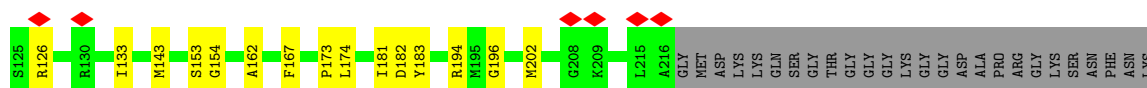
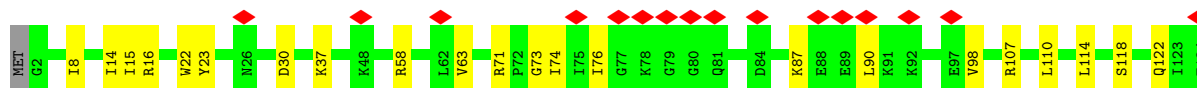
- Molecule 37: 50S ribosomal protein L36

Chain f:  95% 5%

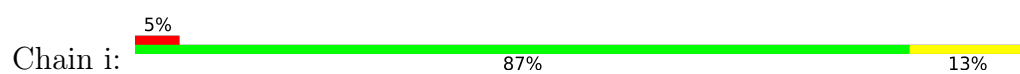


- Molecule 38: 30S ribosomal protein S3

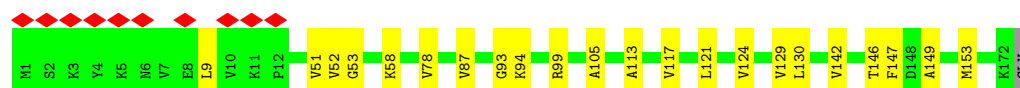
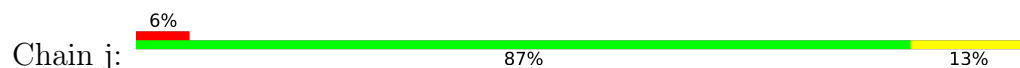
Chain h:  9% 71% 15% 15%



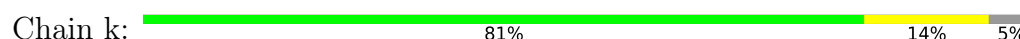
- Molecule 39: 30S ribosomal protein S4



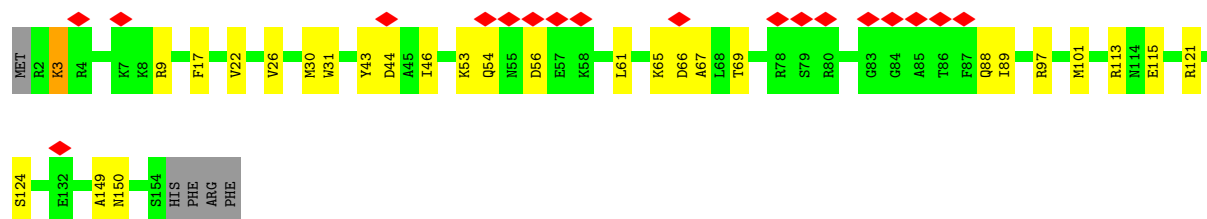
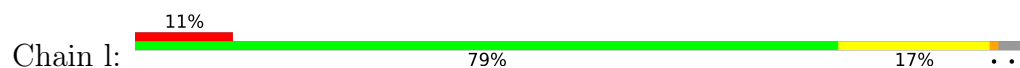
- Molecule 40: 30S ribosomal protein S5



- Molecule 41: 30S ribosomal protein S6



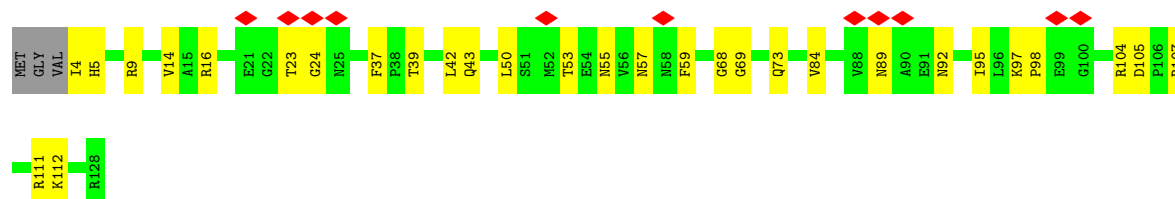
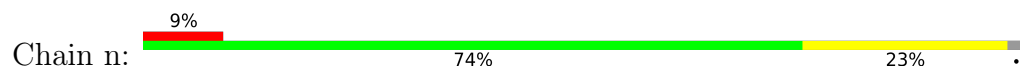
- Molecule 42: 30S ribosomal protein S7



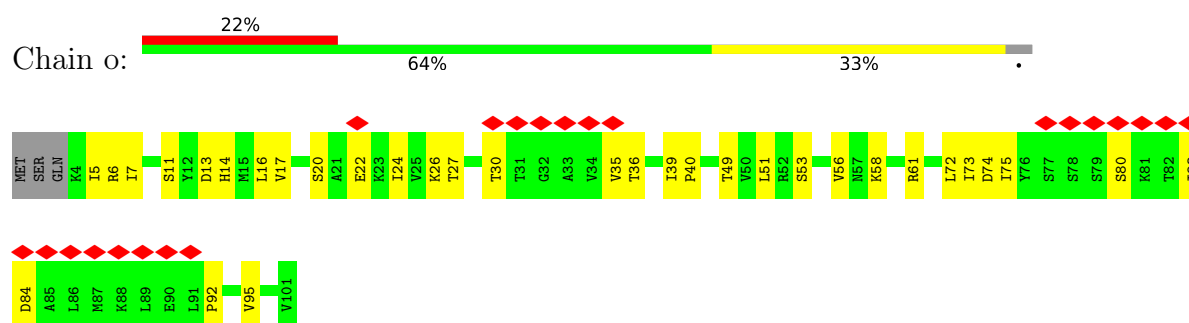
- Molecule 43: 30S ribosomal protein S8



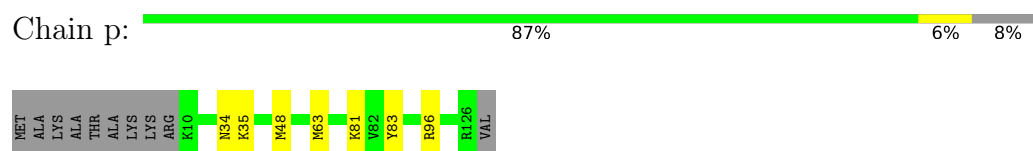
- Molecule 44: 30S ribosomal protein S9



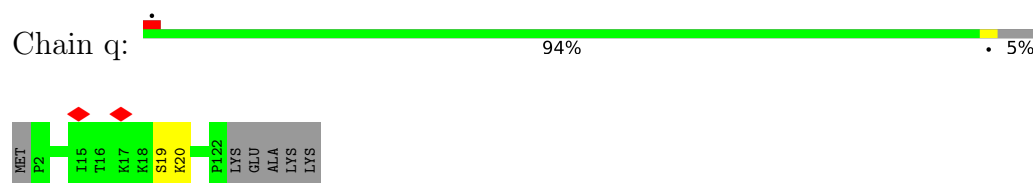
- Molecule 45: 30S ribosomal protein S10



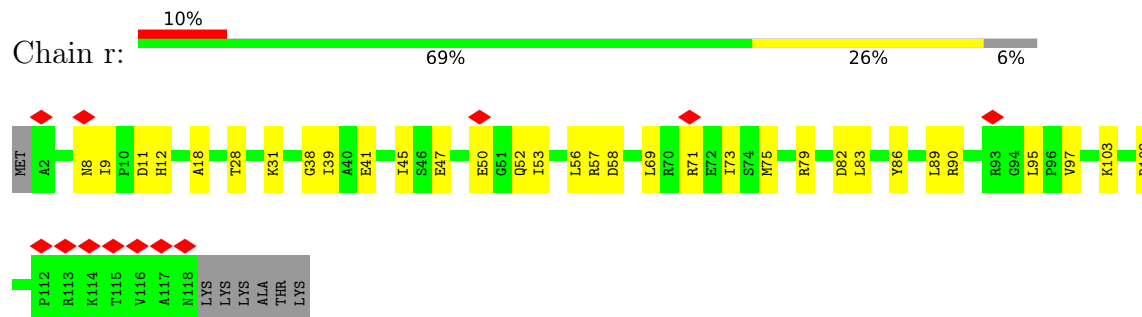
- Molecule 46: 30S ribosomal protein S11



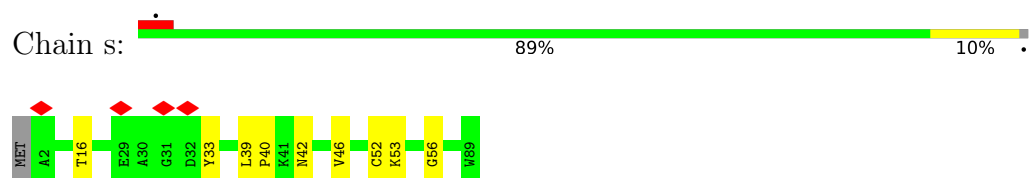
- Molecule 47: 30S ribosomal protein S12



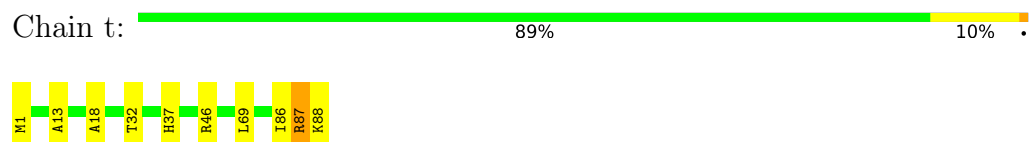
- Molecule 48: 30S ribosomal protein S13



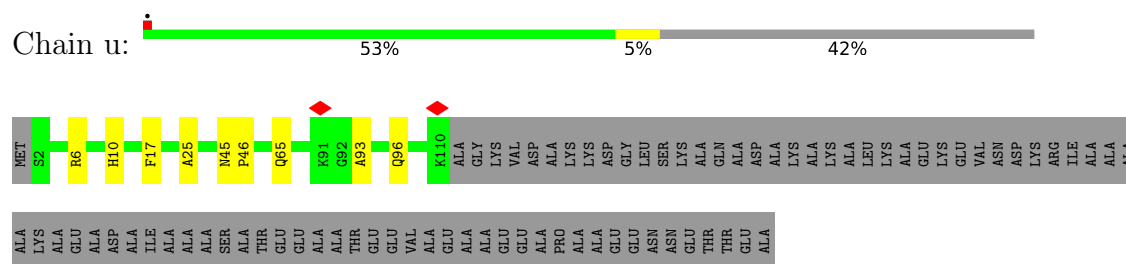
- Molecule 49: 30S ribosomal protein S14



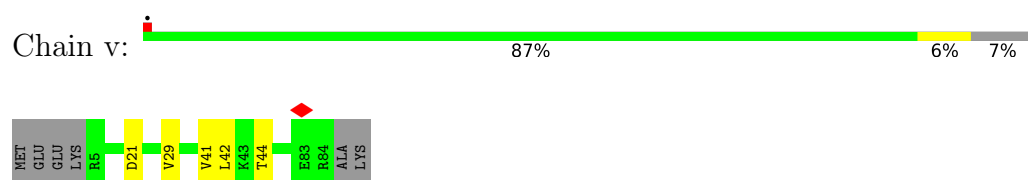
- Molecule 50: 30S ribosomal protein S15



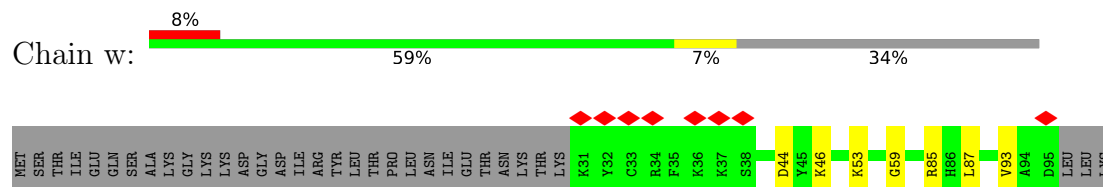
• Molecule 51: 30S ribosomal protein S16



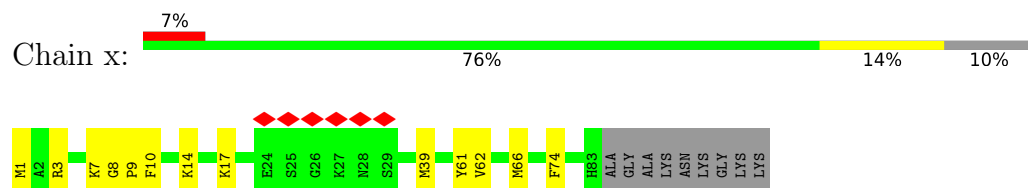
• Molecule 52: 30S ribosomal protein S17



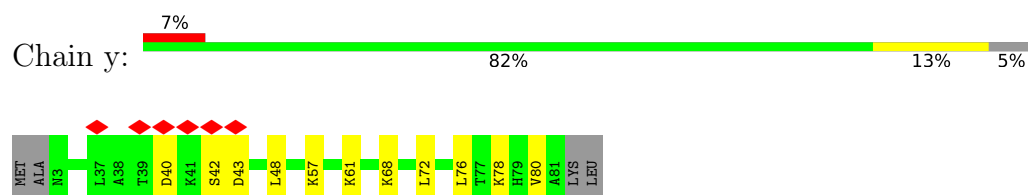
• Molecule 53: 30S ribosomal protein S18



• Molecule 54: 30S ribosomal protein S19



• Molecule 55: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	129125	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.467	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	410.40002, 410.40002, 410.40002	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8550001, 0.8550001, 0.8550001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.27	0/66183	0.33	0/103212
2	2	0.24	1/35523 (0.0%)	0.34	2/55388 (0.0%)
3	3	0.20	0/2611	0.25	0/4067
4	4	0.24	0/282	0.56	0/377
5	5	0.20	0/234	0.37	0/301
6	6	0.34	0/464	0.58	0/719
7	A	0.37	0/1745	0.61	0/2717
8	B	0.26	0/2090	0.38	0/2815
9	C	0.27	0/1538	0.41	0/2061
10	D	0.23	0/1530	0.36	0/2065
11	E	0.21	0/1321	0.42	0/1789
12	F	0.17	0/1272	0.32	0/1720
13	G	0.23	0/878	0.51	0/1192
14	H	0.18	0/1702	0.45	1/2300 (0.0%)
15	J	0.26	0/1130	0.43	0/1529
16	K	0.24	0/896	0.35	0/1204
17	L	0.24	0/1060	0.35	0/1422
18	M	0.23	0/1077	0.37	0/1442
19	N	0.27	0/994	0.40	0/1331
20	O	0.18	0/854	0.32	0/1144
21	P	0.24	0/863	0.36	0/1163
22	Q	0.26	0/918	0.37	0/1220
23	R	0.23	0/778	0.41	0/1045
24	S	0.24	0/974	0.36	0/1305
25	T	0.21	0/652	0.35	0/877
26	U	0.19	0/682	0.40	1/911 (0.1%)
27	V	0.19	0/888	0.35	0/1216
28	W	0.24	0/594	0.36	0/794
29	X	0.24	0/593	0.39	0/794
30	Y	0.17	0/412	0.45	0/561
31	Z	0.25	0/403	0.45	0/545
32	a	0.16	0/431	0.31	0/586
33	b	0.25	0/488	0.43	1/657 (0.2%)
34	c	0.21	0/421	0.34	0/569

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	d	0.25	0/422	0.33	0/553
36	e	0.25	0/512	0.43	0/672
37	f	0.22	0/307	0.35	0/405
38	h	0.19	0/1623	0.40	0/2190
39	i	0.18	0/1606	0.30	0/2157
40	j	0.22	0/1194	0.35	0/1615
41	k	0.22	0/834	0.40	0/1129
42	l	0.19	0/1204	0.42	1/1619 (0.1%)
43	m	0.21	0/976	0.33	0/1324
44	n	0.19	0/986	0.39	0/1322
45	o	0.23	0/712	0.56	1/973 (0.1%)
46	p	0.18	0/837	0.33	0/1134
47	q	0.21	0/935	0.33	0/1258
48	r	0.22	0/891	0.53	0/1192
49	s	0.20	0/676	0.38	0/906
50	t	0.22	0/704	0.37	0/946
51	u	0.19	0/799	0.38	0/1086
52	v	0.18	0/646	0.34	0/866
53	w	0.21	0/531	0.31	0/710
54	x	0.19	0/652	0.37	0/881
55	y	0.19	0/619	0.32	0/825
All	All	0.25	1/150147 (0.0%)	0.35	7/224801 (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
13	G	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1504	A	O3'-P	-7.16	1.50	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1504	A	O3'-P-O5'	12.07	122.10	104.00
2	2	1504	A	OP1-P-O3'	-8.05	83.84	108.00
33	b	32	ILE	N-CA-C	-6.19	106.73	111.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	l	3	LYS	CB-CA-C	-6.13	109.52	116.63
26	U	99	LYS	N-CA-C	-5.36	108.51	114.62

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	G	39	ALA	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	59085	0	29705	309	0
2	2	31728	0	15978	221	0
3	3	2339	0	1181	6	0
4	4	278	0	295	6	0
5	5	231	0	268	1	0
6	6	415	0	206	18	0
7	A	1562	0	794	35	0
8	B	2053	0	2127	20	0
9	C	1515	0	1548	27	0
10	D	1509	0	1532	15	0
11	E	1300	0	1267	18	0
12	F	1255	0	1275	17	0
13	G	869	0	863	32	0
14	H	1676	0	1718	37	0
15	J	1112	0	1149	11	0
16	K	889	0	946	9	0
17	L	1048	0	1048	8	0
18	M	1056	0	1109	10	0
19	N	980	0	1017	11	0
20	O	846	0	873	5	0
21	P	848	0	846	8	0
22	Q	904	0	956	10	0
23	R	768	0	810	9	0
24	S	964	0	992	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	T	647	0	696	4	0
26	U	679	0	733	8	0
27	V	871	0	839	11	0
28	W	586	0	607	4	0
29	X	586	0	618	9	0
30	Y	409	0	405	5	0
31	Z	400	0	416	8	0
32	a	421	0	384	3	0
33	b	475	0	468	6	0
34	c	415	0	432	11	0
35	d	416	0	449	0	0
36	e	506	0	574	9	0
37	f	305	0	337	2	0
38	h	1600	0	1604	26	0
39	i	1576	0	1592	18	0
40	j	1179	0	1185	15	0
41	k	815	0	780	14	0
42	l	1183	0	1192	21	0
43	m	961	0	978	7	0
44	n	972	0	1005	22	0
45	o	701	0	694	25	0
46	p	823	0	820	5	0
47	q	922	0	973	1	0
48	r	883	0	921	28	0
49	s	665	0	669	7	0
50	t	694	0	703	8	0
51	u	783	0	739	6	0
52	v	638	0	684	3	0
53	w	521	0	553	5	0
54	x	636	0	628	11	0
55	y	615	0	672	9	0
All	All	138113	0	91853	1080	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1080 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:14:LEU:HD21	41:k:84:ARG:HD3	1.11	1.05
1:1:272:G:H22	13:G:52:LYS:NZ	1.54	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:k:14:LEU:HD21	41:k:84:ARG:CD	1.90	1.02
41:k:14:LEU:CD2	41:k:84:ARG:HD3	1.88	1.01
1:1:272:G:N2	13:G:52:LYS:NZ	2.09	1.00

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4	34/50 (68%)	33 (97%)	1 (3%)	0	100	100
5	5	25/30 (83%)	25 (100%)	0	0	100	100
8	B	269/274 (98%)	250 (93%)	18 (7%)	1 (0%)	30	49
9	C	202/205 (98%)	188 (93%)	14 (7%)	0	100	100
10	D	204/209 (98%)	193 (95%)	11 (5%)	0	100	100
11	E	177/183 (97%)	163 (92%)	14 (8%)	0	100	100
12	F	175/180 (97%)	169 (97%)	6 (3%)	0	100	100
13	G	116/146 (80%)	107 (92%)	9 (8%)	0	100	100
14	H	217/254 (85%)	209 (96%)	8 (4%)	0	100	100
15	J	148/151 (98%)	130 (88%)	18 (12%)	0	100	100
16	K	119/122 (98%)	113 (95%)	6 (5%)	0	100	100
17	L	148/150 (99%)	131 (88%)	17 (12%)	0	100	100
18	M	137/141 (97%)	128 (93%)	9 (7%)	0	100	100
19	N	123/163 (76%)	115 (94%)	8 (6%)	0	100	100
20	O	113/116 (97%)	105 (93%)	8 (7%)	0	100	100
21	P	110/116 (95%)	100 (91%)	10 (9%)	0	100	100
22	Q	111/114 (97%)	104 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	R	102/147 (69%)	89 (87%)	13 (13%)	0	100	100
24	S	126/137 (92%)	124 (98%)	2 (2%)	0	100	100
25	T	81/96 (84%)	75 (93%)	6 (7%)	0	100	100
26	U	88/104 (85%)	81 (92%)	7 (8%)	0	100	100
27	V	120/203 (59%)	116 (97%)	4 (3%)	0	100	100
28	W	76/86 (88%)	75 (99%)	1 (1%)	0	100	100
29	X	74/78 (95%)	69 (93%)	5 (7%)	0	100	100
30	Y	57/63 (90%)	53 (93%)	4 (7%)	0	100	100
31	Z	54/60 (90%)	48 (89%)	6 (11%)	0	100	100
32	a	56/84 (67%)	52 (93%)	4 (7%)	0	100	100
33	b	57/64 (89%)	51 (90%)	6 (10%)	0	100	100
34	c	52/60 (87%)	51 (98%)	1 (2%)	0	100	100
35	d	49/53 (92%)	49 (100%)	0	0	100	100
36	e	62/65 (95%)	54 (87%)	8 (13%)	0	100	100
37	f	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
38	h	213/252 (84%)	199 (93%)	14 (7%)	0	100	100
39	i	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
40	j	170/173 (98%)	157 (92%)	13 (8%)	0	100	100
41	k	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
42	l	151/158 (96%)	142 (94%)	9 (6%)	0	100	100
43	m	129/132 (98%)	123 (95%)	6 (5%)	0	100	100
44	n	123/128 (96%)	115 (94%)	8 (6%)	0	100	100
45	o	96/101 (95%)	90 (94%)	6 (6%)	0	100	100
46	p	115/127 (91%)	109 (95%)	6 (5%)	0	100	100
47	q	119/127 (94%)	111 (93%)	8 (7%)	0	100	100
48	r	115/124 (93%)	109 (95%)	6 (5%)	0	100	100
49	s	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
50	t	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
51	u	107/188 (57%)	106 (99%)	1 (1%)	0	100	100
52	v	78/86 (91%)	74 (95%)	4 (5%)	0	100	100
53	w	63/98 (64%)	62 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	x	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
55	y	77/83 (93%)	75 (97%)	2 (3%)	0	100	100
All	All	5630/6302 (89%)	5292 (94%)	337 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	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	
4	4	30/44 (68%)	30 (100%)	0	100	100
5	5	23/26 (88%)	23 (100%)	0	100	100
8	B	215/225 (96%)	214 (100%)	1 (0%)	81	92
9	C	156/162 (96%)	156 (100%)	0	100	100
10	D	150/181 (83%)	150 (100%)	0	100	100
11	E	121/156 (78%)	121 (100%)	0	100	100
12	F	121/148 (82%)	121 (100%)	0	100	100
13	G	80/118 (68%)	78 (98%)	2 (2%)	42	69
14	H	174/207 (84%)	174 (100%)	0	100	100
15	J	115/128 (90%)	115 (100%)	0	100	100
16	K	89/100 (89%)	89 (100%)	0	100	100
17	L	93/115 (81%)	93 (100%)	0	100	100
18	M	102/116 (88%)	102 (100%)	0	100	100
19	N	101/131 (77%)	101 (100%)	0	100	100
20	O	79/90 (88%)	79 (100%)	0	100	100
21	P	78/98 (80%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	Q	89/94 (95%)	89 (100%)	0	100	100
23	R	72/112 (64%)	72 (100%)	0	100	100
24	S	93/116 (80%)	93 (100%)	0	100	100
25	T	70/85 (82%)	70 (100%)	0	100	100
26	U	68/89 (76%)	68 (100%)	0	100	100
27	V	81/163 (50%)	81 (100%)	0	100	100
28	W	60/69 (87%)	60 (100%)	0	100	100
29	X	62/69 (90%)	62 (100%)	0	100	100
30	Y	36/55 (66%)	36 (100%)	0	100	100
31	Z	41/52 (79%)	41 (100%)	0	100	100
32	a	40/75 (53%)	40 (100%)	0	100	100
33	b	44/53 (83%)	44 (100%)	0	100	100
34	c	45/56 (80%)	45 (100%)	0	100	100
35	d	42/46 (91%)	42 (100%)	0	100	100
36	e	55/59 (93%)	54 (98%)	1 (2%)	51	77
37	f	31/34 (91%)	31 (100%)	0	100	100
38	h	153/201 (76%)	153 (100%)	0	100	100
39	i	163/173 (94%)	163 (100%)	0	100	100
40	j	111/138 (80%)	111 (100%)	0	100	100
41	k	74/101 (73%)	74 (100%)	0	100	100
42	l	114/136 (84%)	114 (100%)	0	100	100
43	m	93/111 (84%)	93 (100%)	0	100	100
44	n	99/107 (92%)	99 (100%)	0	100	100
45	o	72/94 (77%)	72 (100%)	0	100	100
46	p	80/102 (78%)	80 (100%)	0	100	100
47	q	97/107 (91%)	97 (100%)	0	100	100
48	r	87/100 (87%)	87 (100%)	0	100	100
49	s	61/73 (84%)	61 (100%)	0	100	100
50	t	66/79 (84%)	65 (98%)	1 (2%)	57	80
51	u	68/136 (50%)	68 (100%)	0	100	100
52	v	71/81 (88%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	w	52/87 (60%)	52 (100%)	0	100	100
54	x	67/78 (86%)	67 (100%)	0	100	100
55	y	65/72 (90%)	65 (100%)	0	100	100
All	All	4249/5248 (81%)	4244 (100%)	5 (0%)	87	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	B	103	TYR
13	G	49	GLU
13	G	51	LEU
36	e	54	ASP
50	t	87	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
23	R	11	GLN
48	r	100	GLN
26	U	101	ASN
39	i	36	HIS
24	S	122	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2746/2862 (95%)	458 (16%)	25 (0%)
2	2	1477/1520 (97%)	289 (19%)	30 (2%)
3	3	109/111 (98%)	15 (13%)	0
6	6	17/23 (73%)	8 (47%)	0
7	A	71/77 (92%)	35 (49%)	0
All	All	4420/4593 (96%)	805 (18%)	55 (1%)

5 of 805 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	28	A
1	1	34	A

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Mol	Chain	Res	Type
1	1	46	G
1	1	55	G

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	110	A
2	2	1023	U
2	2	1466	A
2	2	1280	A
2	2	236	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

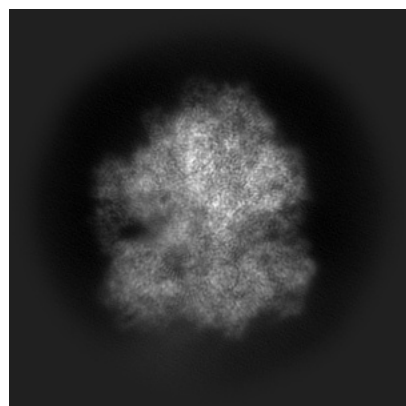
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71061. These allow visual inspection of the internal detail of the map and identification of artifacts.

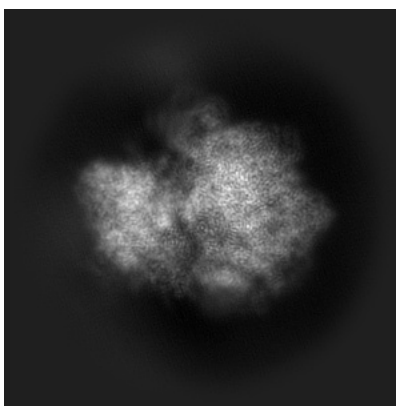
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

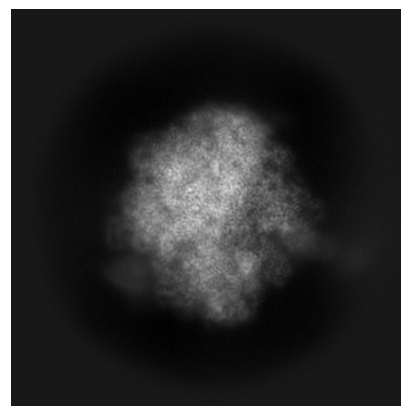
6.1.1 Primary map



X

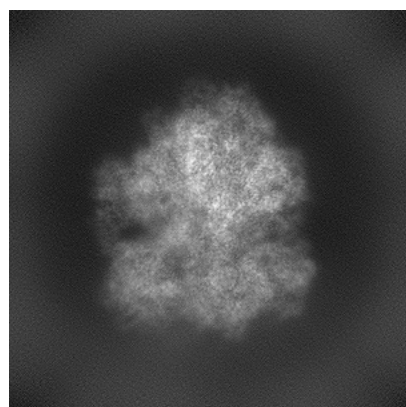


Y

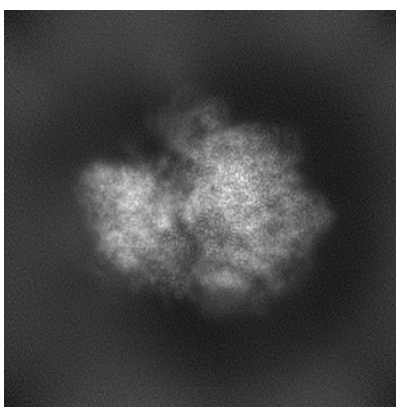


Z

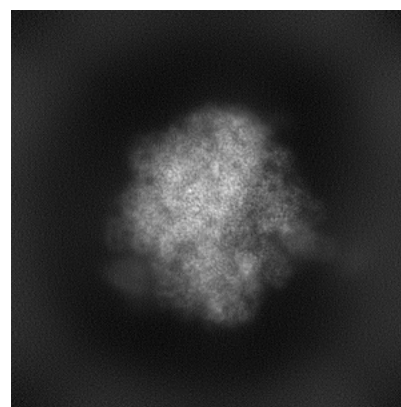
6.1.2 Raw map



X



Y

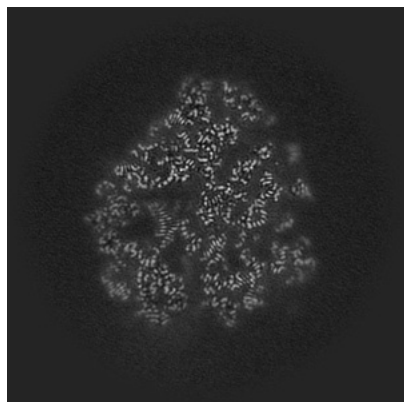


Z

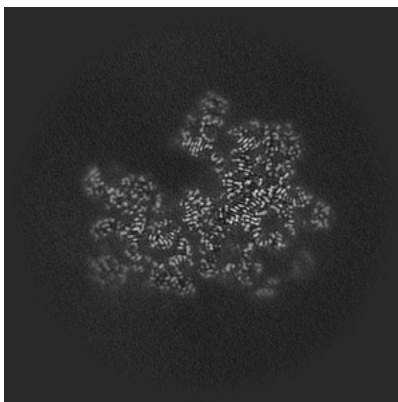
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

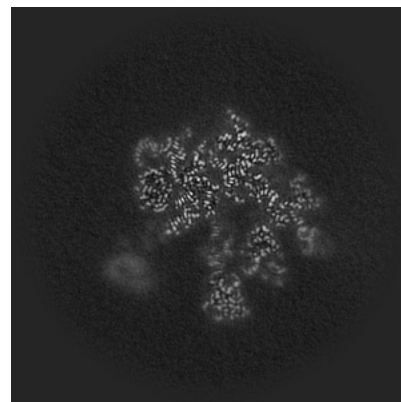
6.2.1 Primary map



X Index: 240

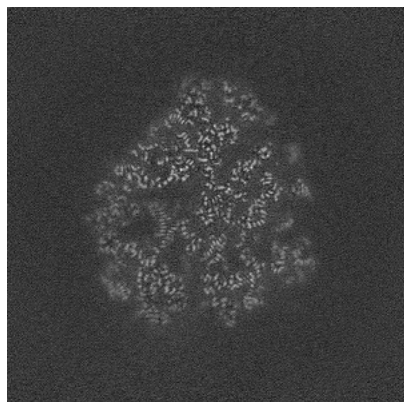


Y Index: 240

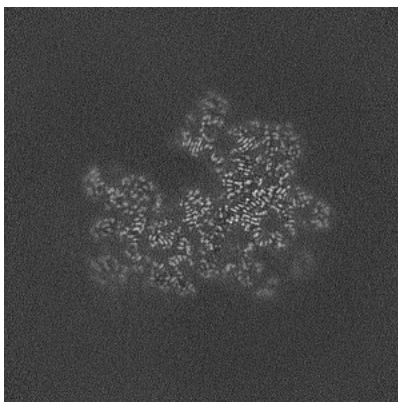


Z Index: 240

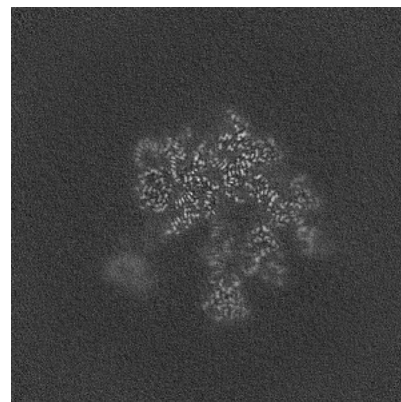
6.2.2 Raw map



X Index: 240



Y Index: 240

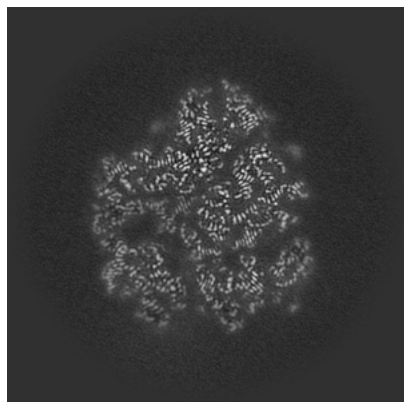


Z Index: 240

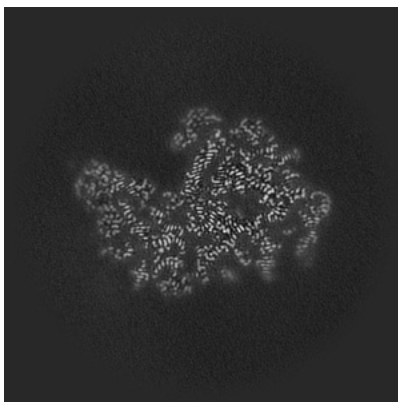
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

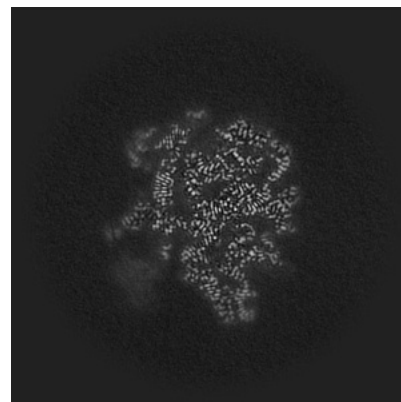
6.3.1 Primary map



X Index: 246

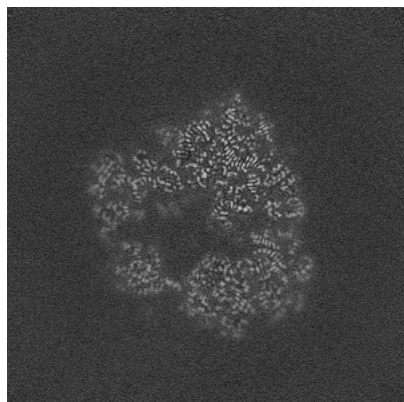


Y Index: 261

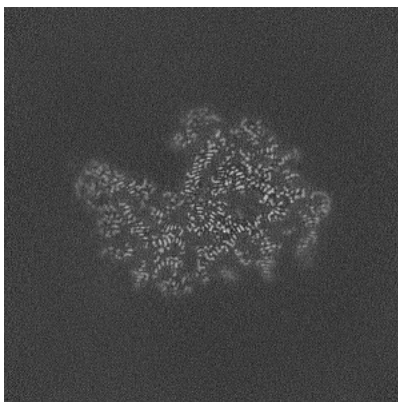


Z Index: 285

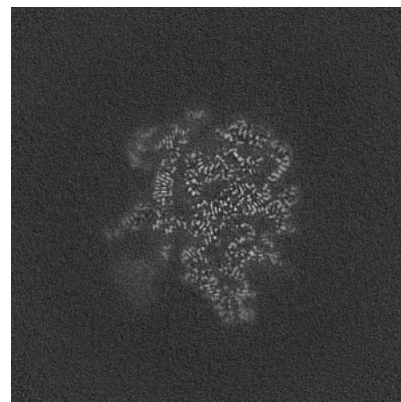
6.3.2 Raw map



X Index: 263



Y Index: 261

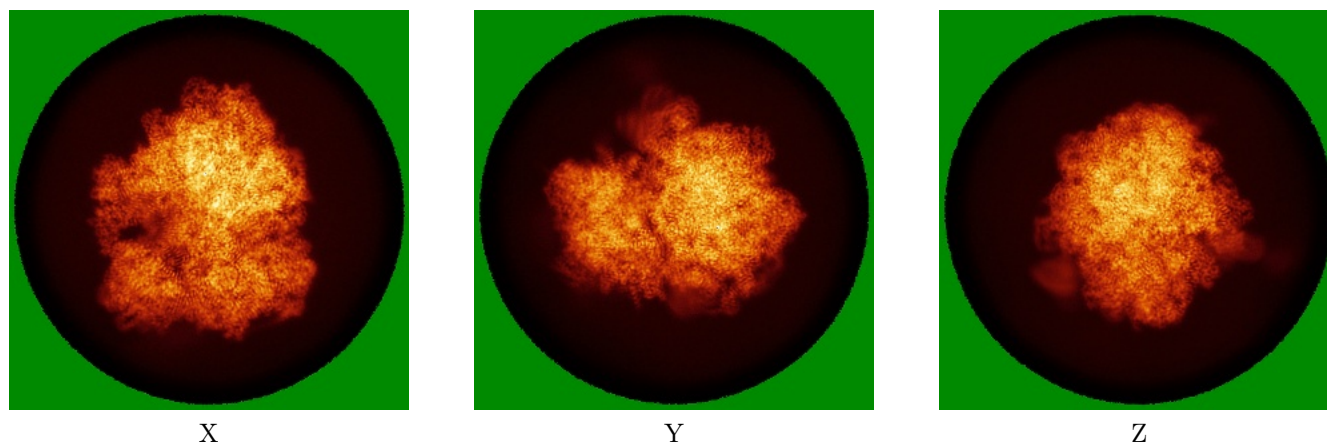


Z Index: 285

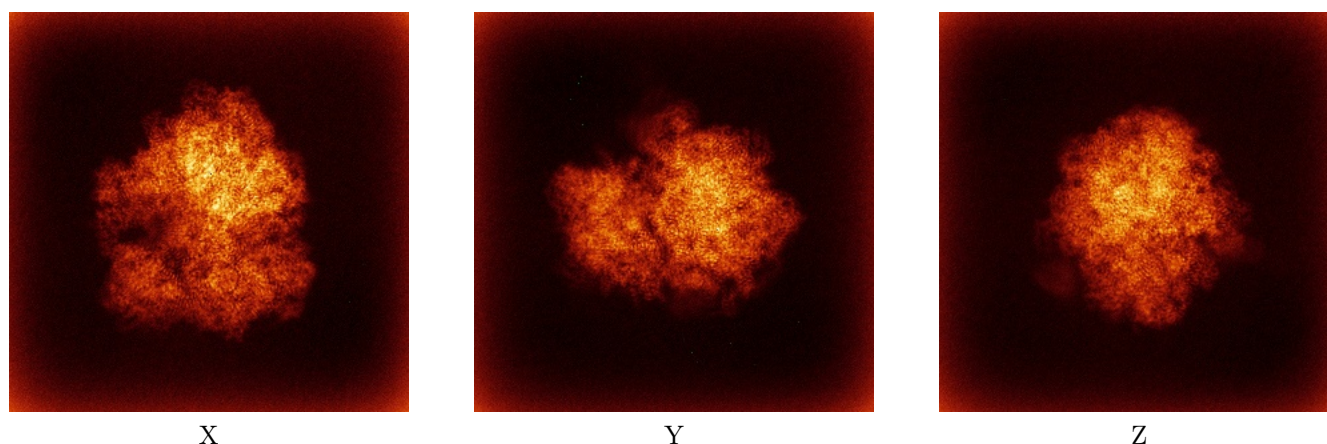
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

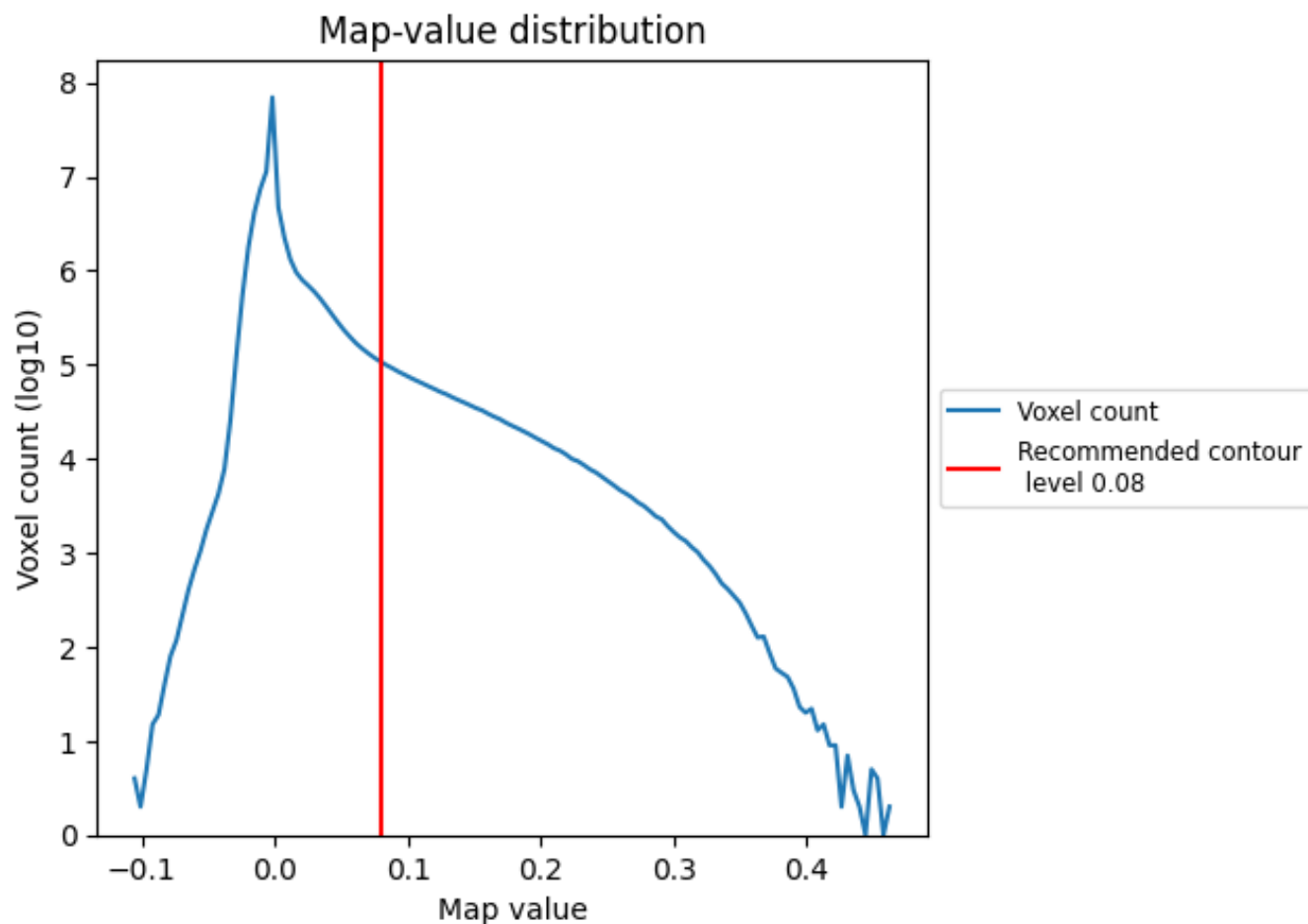
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

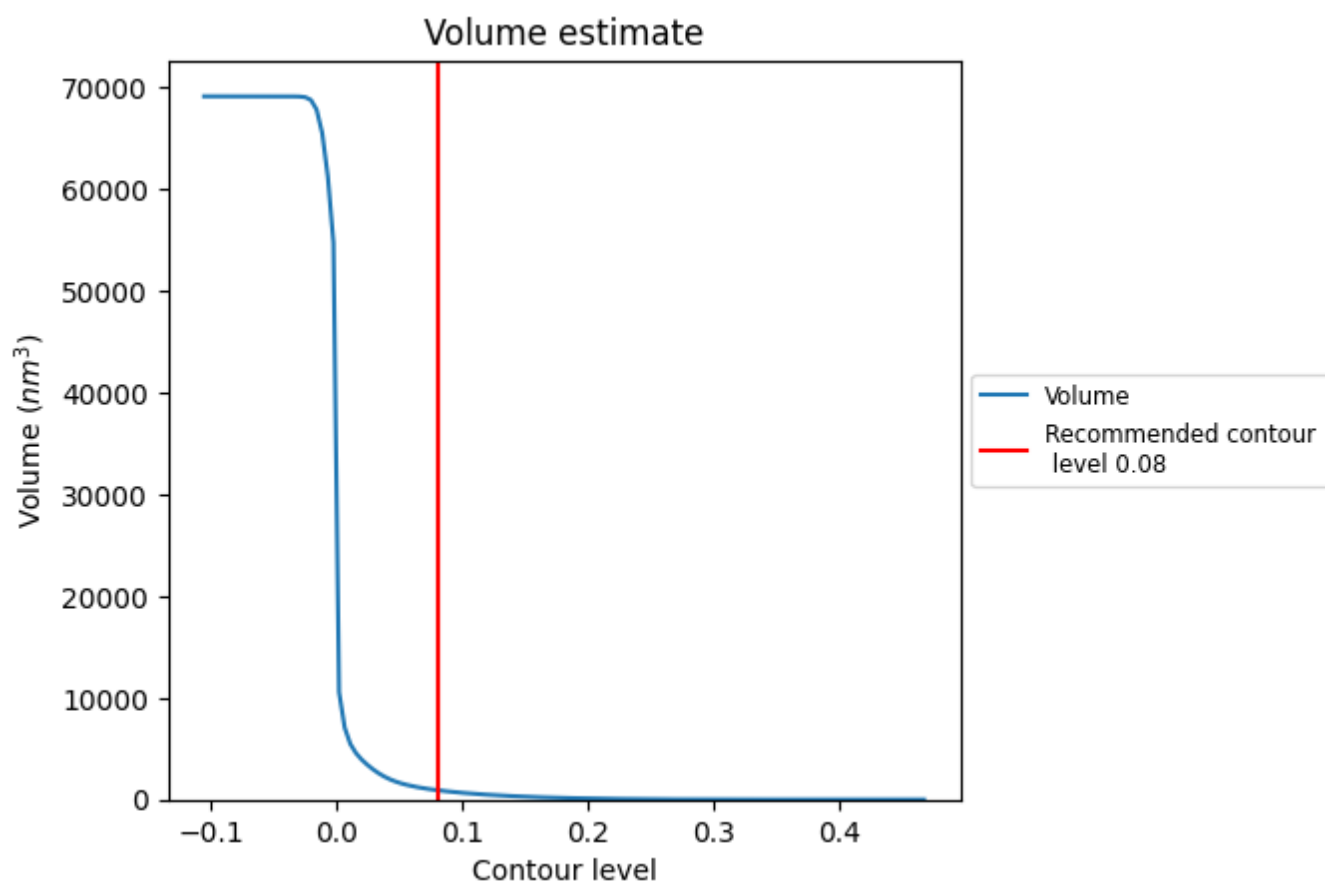
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

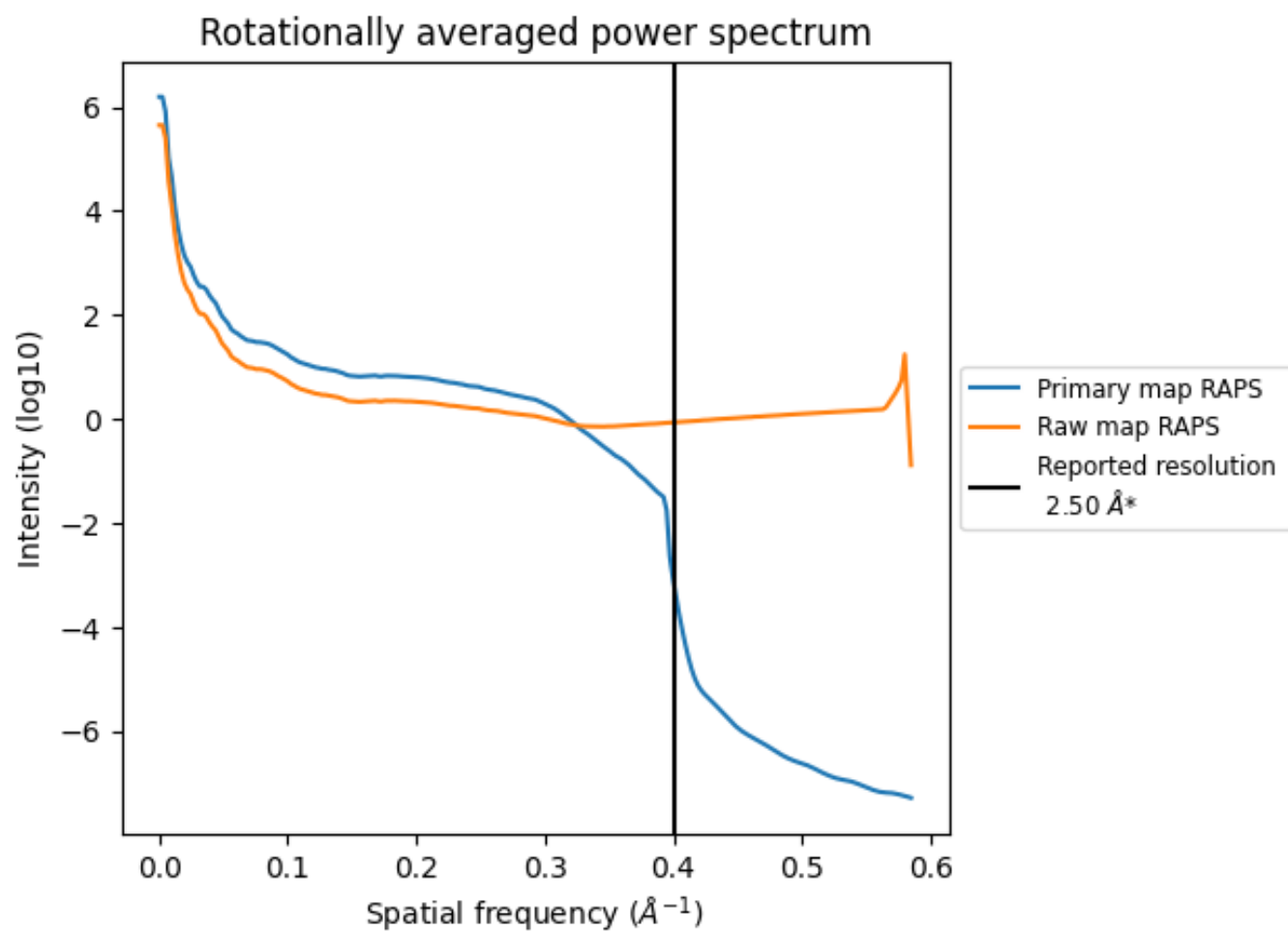
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 919 nm³; this corresponds to an approximate mass of 831 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

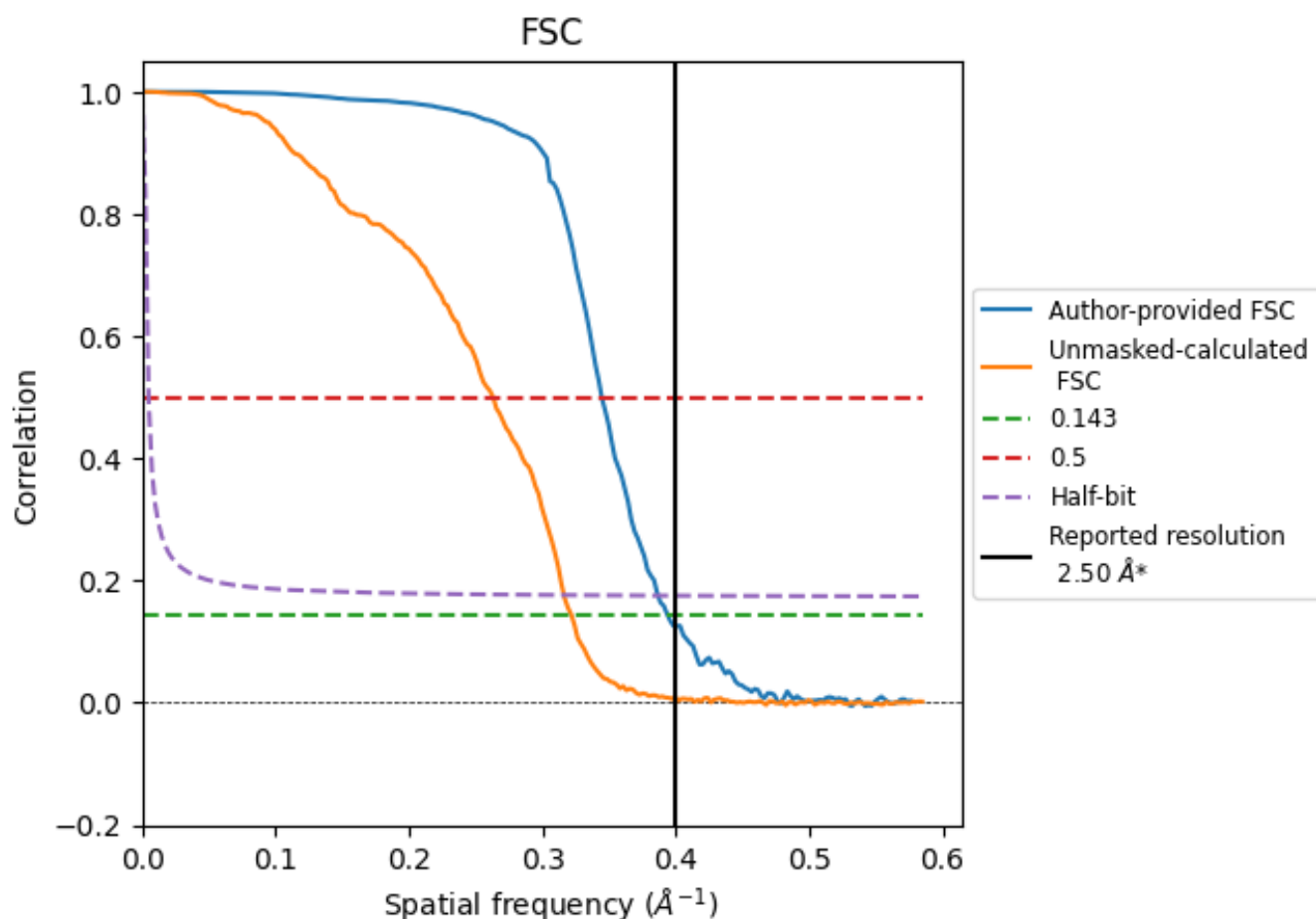


*Reported resolution corresponds to spatial frequency of 0.400 \AA^{-1}

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 0.400 \AA^{-1}

8.2 Resolution estimates [i](#)

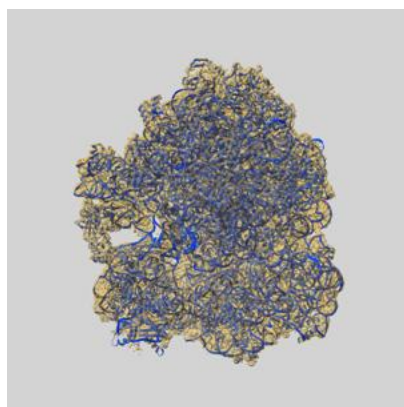
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.54	2.90	2.59
Unmasked-calculated*	3.11	3.80	3.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.11 differs from the reported value 2.5 by more than 10 %

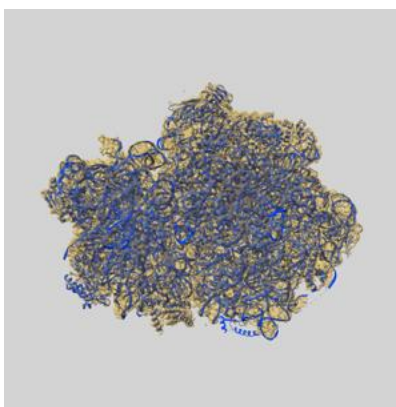
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-71061 and PDB model 9OZZ. Per-residue inclusion information can be found in section [3](#) on page [16](#).

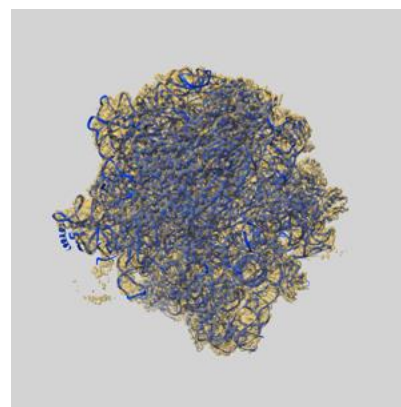
9.1 Map-model overlay [i](#)



X



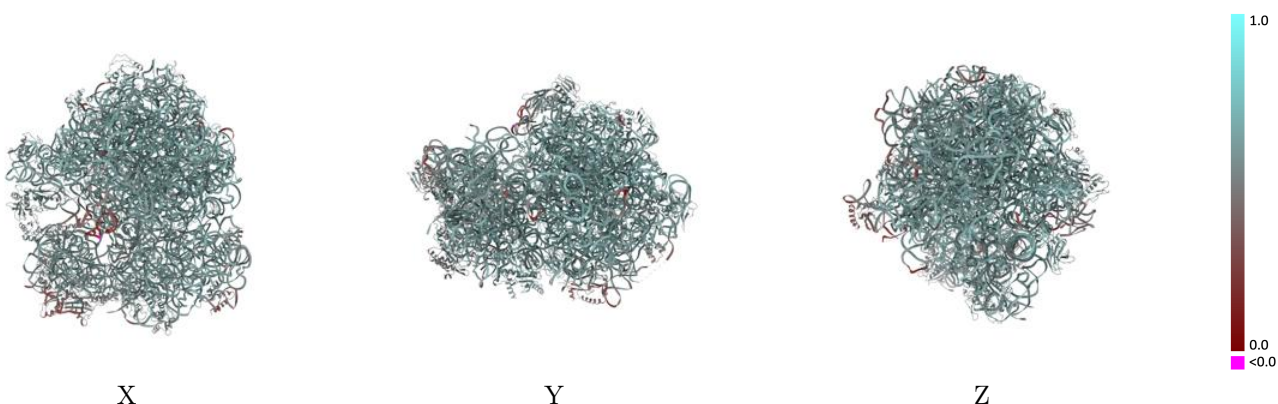
Y



Z

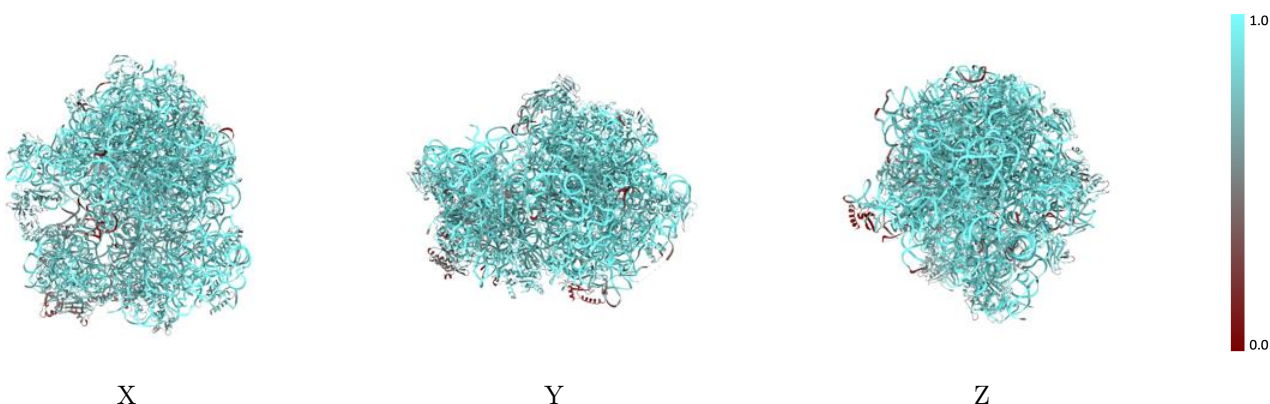
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



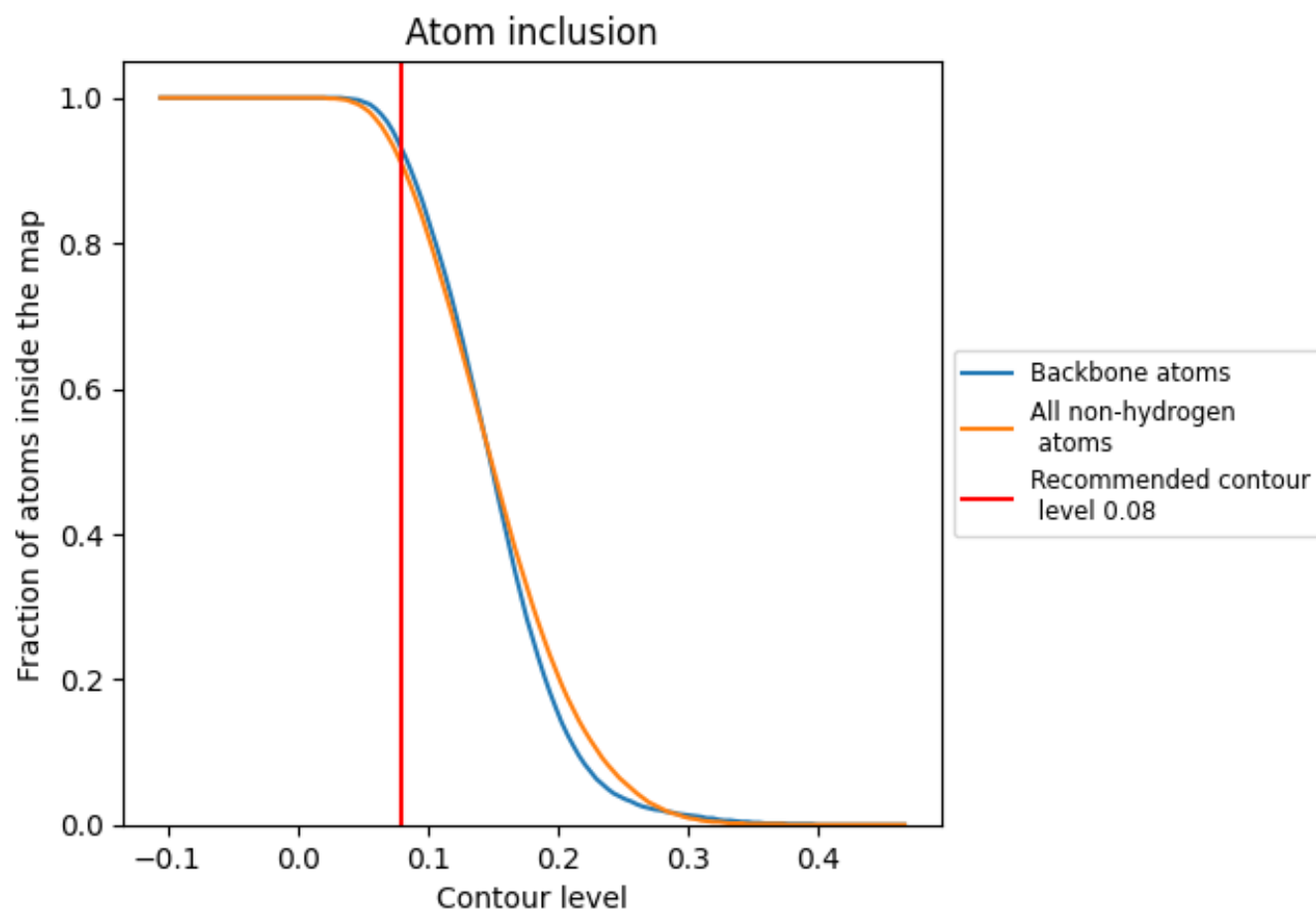
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ











































The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.5920
1	 0.9540	 0.6060
2	 0.9530	 0.5880
3	 0.9510	 0.5890
4	 0.7020	 0.5300
5	 0.8900	 0.6150
6	 0.6650	 0.4630
A	 0.7510	 0.5650
B	 0.9430	 0.6270
C	 0.9040	 0.6140
D	 0.9070	 0.5970
E	 0.7620	 0.5530
F	 0.7400	 0.5500
G	 0.3770	 0.4340
H	 0.4940	 0.4990
J	 0.9060	 0.6000
K	 0.9040	 0.6170
L	 0.8970	 0.6070
M	 0.9120	 0.6120
N	 0.9360	 0.6160
O	 0.8100	 0.5760
P	 0.8900	 0.6120
Q	 0.9290	 0.6120
R	 0.8750	 0.6020
S	 0.9180	 0.6060
T	 0.8560	 0.5720
U	 0.7850	 0.5600
V	 0.7940	 0.5670
W	 0.9210	 0.6160
X	 0.9070	 0.6030
Y	 0.7760	 0.5290
Z	 0.9360	 0.5970
a	 0.6710	 0.5490
b	 0.9560	 0.6270
c	 0.8720	 0.5980



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Chain	Atom inclusion	Q-score
d	 0.9820	 0.6470
e	 0.9600	 0.6230
f	 0.9170	 0.6150
h	 0.7040	 0.5340
i	 0.7520	 0.5580
j	 0.8540	 0.5830
k	 0.8580	 0.5850
l	 0.6850	 0.5420
m	 0.9120	 0.6010
n	 0.7380	 0.5450
o	 0.6480	 0.4990
p	 0.8230	 0.5850
q	 0.8750	 0.6080
r	 0.7120	 0.5390
s	 0.8260	 0.5650
t	 0.8880	 0.5940
u	 0.8570	 0.5500
v	 0.8420	 0.5930
w	 0.7660	 0.5770
x	 0.7460	 0.5420
y	 0.8170	 0.5560