



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2025 – 06:45 PM EDT

PDB ID : 9B1W
EMDB ID : EMD-44090
Title : HWS19 strain WT mycobacterial ribosome
Authors : Young, I.D.; Chen, Y.; Javid, B.; Fraser, J.S.
Deposited on : 2024-03-14
Resolution : 3.26 Å(reported)
Based on initial models : 5o60, 5o5j

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.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

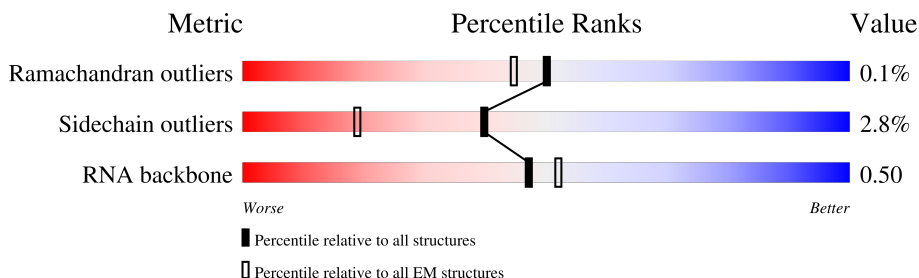
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1511	
2	B	32	
3	C	208	
4	D	200	
5	E	180	
6	F	96	
7	G	155	
8	H	131	

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Mol	Chain	Length	Quality of chain
9	I	126	
10	J	99	
11	K	115	
12	L	122	
13	M	116	
14	N	60	
15	O	88	
16	P	113	
17	Q	94	
18	R	65	
19	S	82	
20	T	85	
21	V	228	
22	X	6	
23	Y	2951	
24	U	118	
25	Z	275	
26	a	214	
27	b	209	
28	c	182	
29	d	176	
30	e	133	
31	f	146	
32	g	122	
33	h	145	

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Mol	Chain	Length	Quality of chain
34	i	136	 5% 96%
35	j	118	 97%
36	k	126	 98%
37	l	113	 95% 5%
38	m	124	 99%
39	n	100	 97%
40	o	114	 96%
41	p	97	 97%
42	q	97	 96%
43	r	192	 6% 98%
44	s	79	 5% 97%
45	t	63	 8% 100%
46	u	64	 97%
47	5	23	 39% 91% 9%
48	v	126	 13% 98%
49	w	59	 97%
50	x	54	 96%
51	y	49	 6% 94% 6%
52	z	46	 7% 98%
53	1	63	 94% 6%
54	2	37	 11% 97%

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 242027 atoms, of which 97267 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 15S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1511	Total	C	H	N	O	P	0	0
			48764	14449	16324	5930	10550	1511		

- Molecule 2 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	32	Total	C	H	N	O	S	0	0
			625	172	345	71	36	1		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	208	Total	C	H	N	O	S	0	0
			3370	1036	1710	322	298	4		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	200	Total	C	H	N	O	S	0	0
			3312	1028	1671	316	295	2		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	180	Total	C	H	N	O	S	0	0
			2659	812	1363	245	235	4		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	96	Total	C	H	N	O	S	0	0
			1567	486	796	138	145	2		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	155	Total	C	H	N	O	S	0	0
			2516	768	1284	241	221	2		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	131	Total	C	H	N	O	S	0	0
			2059	633	1049	189	187	1		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	126	Total	C	H	N	O	S	0	0
			2046	630	1052	194	170			

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	99	Total	C	H	N	O	S	0	0
			1610	495	822	146	144	3		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	115	Total	C	H	N	O	S	0	0
			1721	528	866	170	156	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	122	Total	C	H	N	O	S	0	0
			2004	594	1046	197	165	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	116	Total	C	H	N	O	S	0	0
			1924	572	989	191	169	3		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	60	Total	C	H	N	O	S	0	0
			983	302	506	97	73	5		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	88	Total	C	H	N	O		0	0
			1483	449	763	147	124			

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	113	Total	C	H	N	O		0	0
			1829	570	938	162	159			

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	94	Total	C	H	N	O	S	0	0
			1546	469	798	142	135	2		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	65	Total	C	H	N	O	S	0	0
			1056	318	543	102	90	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	82	Total	C	H	N	O	S	0	0
			1341	425	679	124	112	1		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	85	Total	C	H	N	O		0	0
			1375	402	715	139	119			

- Molecule 21 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	228	Total	C	H	N	O	S	0	0
			3632	1132	1839	322	330	9		

- Molecule 22 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	X	6	Total	C	H	N	O	P	0	0
			180	54	63	13	45	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Y	2951	Total	C	H	N	O	P	0	0
			95279	28252	31894	11671	20511	2951		

- Molecule 24 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	U	118	Total	C	H	N	O	P	0	0
			3807	1126	1285	468	810	118		

- Molecule 25 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	275	Total	C	H	N	O	S	0	0
			4278	1298	2168	438	370	4		

- Molecule 26 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	214	Total	C	H	N	O	S	0	0
			3220	982	1633	310	290	5		

- Molecule 27 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	209	Total	C	H	N	O	S	0	0
			3179	969	1610	295	303	2		

- Molecule 28 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	c	182	Total	C	H	N	O	S	0	0
			2923	907	1478	271	261	6		

- Molecule 29 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	176	Total	C	H	N	O	S	0	0
			2750	845	1402	249	253	1		

- Molecule 30 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	e	133	Total	C	H	N	O	S	0	0
			2014	625	1024	175	187	3		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	f	146	Total	C	H	N	O	S	0	0
			2299	722	1169	207	200	1		

- Molecule 32 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	g	122	Total	C	H	N	O	S	0	0
			1938	586	1000	179	170	3		

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	h	145	Total	C	H	N	O	S	0	0
			2232	676	1154	205	194	3		

- Molecule 34 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	i	136	Total	C	H	N	O	S	0	0
			2220	690	1128	213	187	2		

- Molecule 35 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	118	Total	C	H	N	O	S	
			1902	583	974	180	163	2	
								0	0

- Molecule 36 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	126	Total	C	H	N	O		
			1950	586	994	199	171		
								0	0

- Molecule 37 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	113	Total	C	H	N	O	S	
			1844	570	937	171	165	1	
								0	0

- Molecule 38 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	124	Total	C	H	N	O		
			2029	613	1041	203	172		
								0	0

- Molecule 39 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	100	Total	C	H	N	O		
			1559	478	805	137	139		
								0	0

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	114	Total	C	H	N	O		
			1785	543	912	171	159		
								0	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	97	Total	C	H	N	O		
			1561	479	805	138	139		
								0	0

- Molecule 42 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	q	97	Total	C	H	N	O	S	0	0
			1515	456	783	137	137	2		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	?	-	SER	deletion	UNP A0QSG0
q	?	-	ALA	deletion	UNP A0QSG0
q	?	-	ASN	deletion	UNP A0QSG0
q	?	-	GLU	deletion	UNP A0QSG0
q	?	-	ARG	deletion	UNP A0QSG0
q	?	-	GLY	deletion	UNP A0QSG0
q	?	-	ALA	deletion	UNP A0QSG0
q	?	-	SER	deletion	UNP A0QSG0

- Molecule 43 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	192	Total	C	H	N	O		0	0
			2874	881	1446	255	292			

- Molecule 44 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	s	79	Total	C	H	N	O		0	0
			1189	361	603	123	102			

- Molecule 45 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	t	63	Total	C	H	N	O	S	0	0
			956	283	486	103	80	4		

- Molecule 46 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	u	64	Total	C	H	N	O	S	0	0
			1075	324	544	103	103	1		

- Molecule 47 is a protein called ribosomal protein bL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	23	Total	C	H	N	O	0	0
			397	111	208	50	28		

- Molecule 48 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace	
48	v	126	Total	C	H	N	O	S	0	0
			1877	580	959	156	180	2		

- Molecule 49 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	59	Total	C	H	N	O	0	0
			977	292	503	95	87		

- Molecule 50 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
50	x	54	Total	C	H	N	O	S	0	0
			889	260	466	93	69	1		

- Molecule 51 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace	
51	y	49	Total	C	H	N	O	S	0	0
			819	248	414	82	71	4		

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	z	46	Total	C	H	N	O	S	0	0
			791	225	414	97	54	1		

- Molecule 53 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	63	Total	C	H	N	O	0	0
			1045	302	543	115	85		

- Molecule 54 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	2	37	Total	C	H	N	O	S	0	0
			623	181	324	66	47	5		

- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	210	Total	Mg	0
			210	210	
55	E	1	Total	Mg	0
			1	1	
55	K	1	Total	Mg	0
			1	1	
55	N	2	Total	Mg	0
			2	2	
55	P	1	Total	Mg	0
			1	1	
55	R	1	Total	Mg	0
			1	1	
55	T	1	Total	Mg	0
			1	1	
55	Y	381	Total	Mg	0
			381	381	
55	U	9	Total	Mg	0
			9	9	
55	Z	8	Total	Mg	0
			8	8	
55	b	1	Total	Mg	0
			1	1	
55	c	1	Total	Mg	0
			1	1	
55	i	1	Total	Mg	0
			1	1	
55	o	1	Total	Mg	0
			1	1	
55	p	1	Total	Mg	0
			1	1	
55	s	1	Total	Mg	0
			1	1	
55	t	1	Total	Mg	0
			1	1	
55	1	2	Total	Mg	0
			2	2	

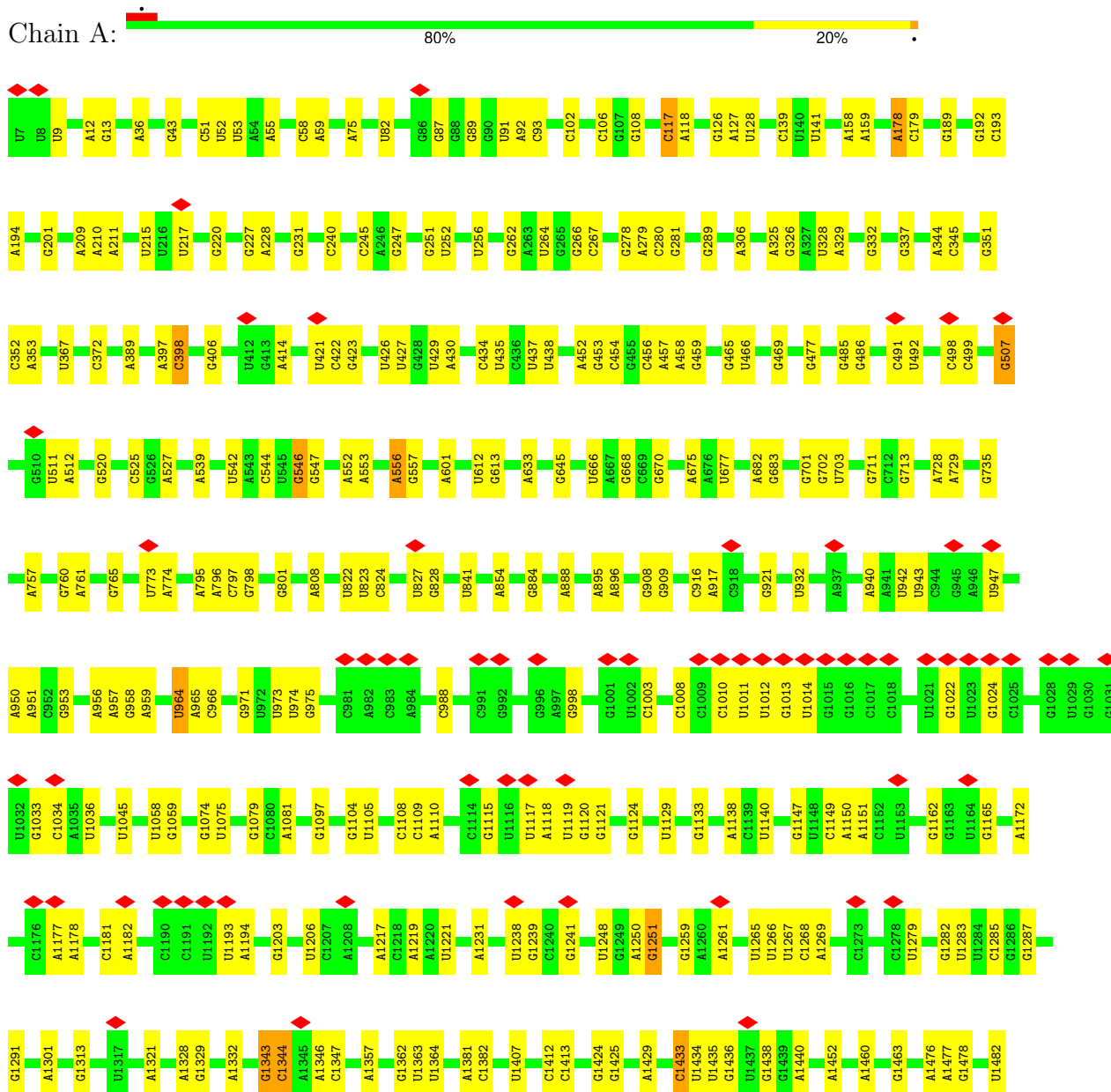
- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

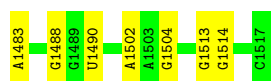
Mol	Chain	Residues	Atoms		AltConf
56	N	1	Total 1	Zn 1	0
56	R	1	Total 1	Zn 1	0
56	t	1	Total 1	Zn 1	0
56	y	1	Total 1	Zn 1	0
56	2	1	Total 1	Zn 1	0

3 Residue-property plots

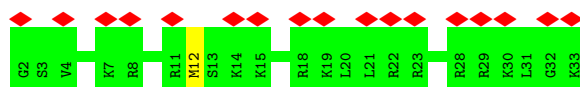
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 15S rRNA

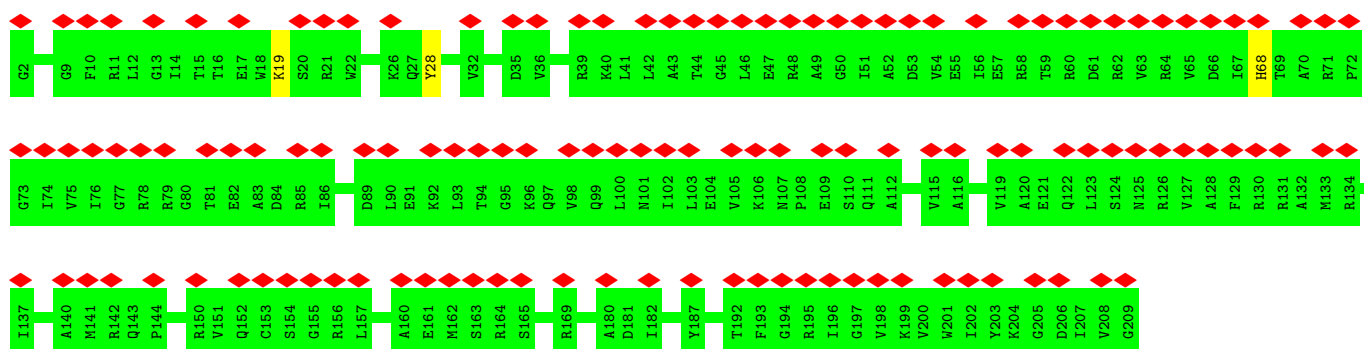




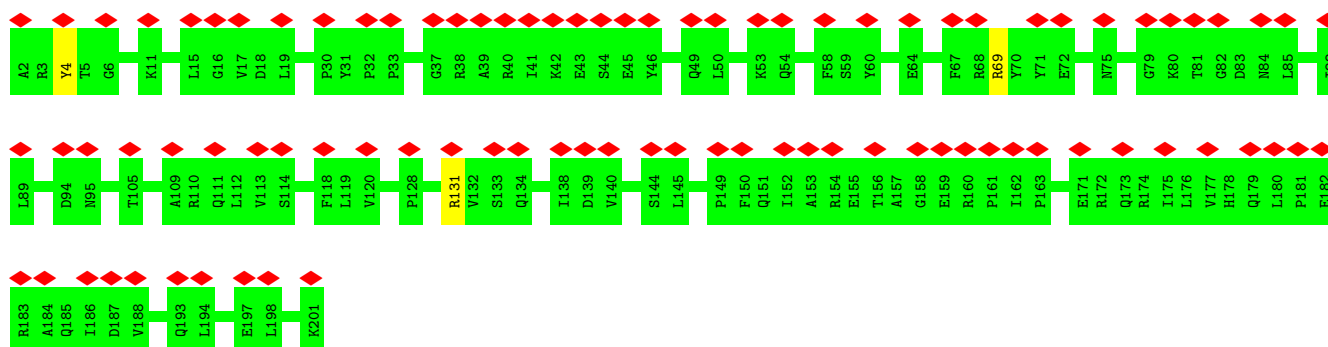
- Molecule 2: Conserved domain protein



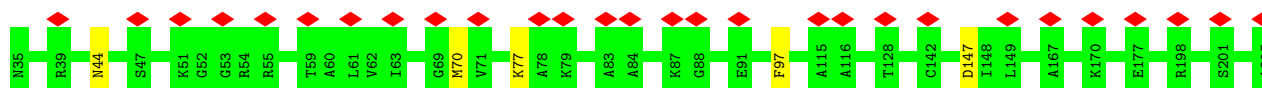
- Molecule 3: Small ribosomal subunit protein uS3

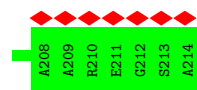


- Molecule 4: Small ribosomal subunit protein uS4

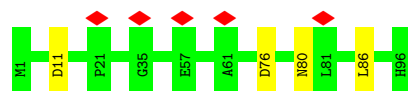


- Molecule 5: Small ribosomal subunit protein uS5

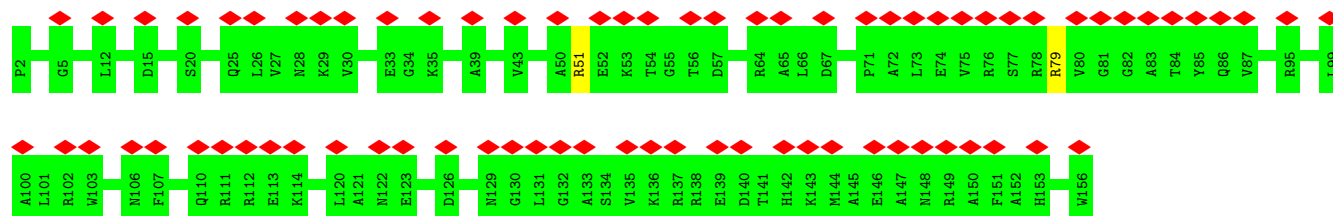




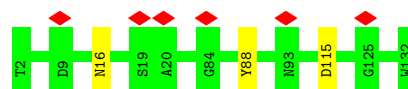
- Molecule 6: Small ribosomal subunit protein bS6



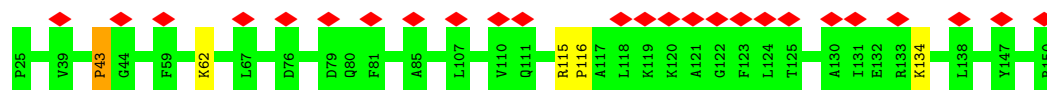
- Molecule 7: Small ribosomal subunit protein uS7



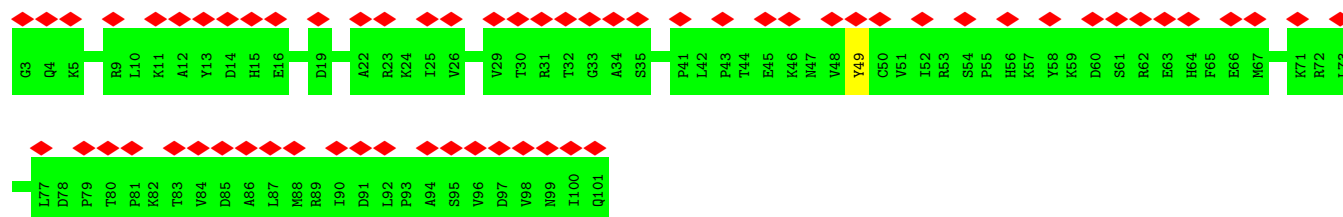
- Molecule 8: Small ribosomal subunit protein uS8



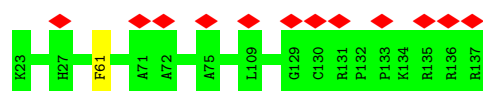
- Molecule 9: Small ribosomal subunit protein uS9



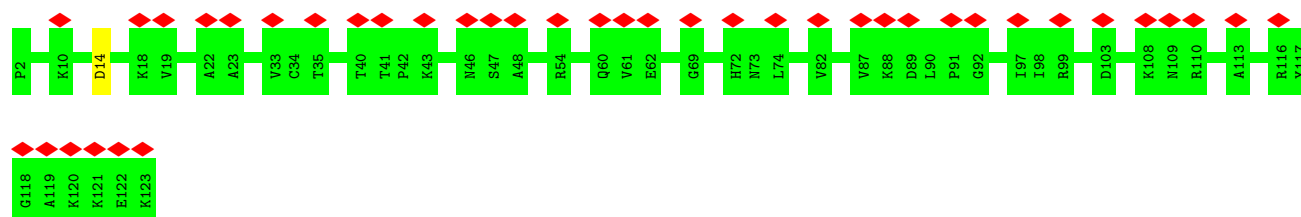
- Molecule 10: Small ribosomal subunit protein uS10



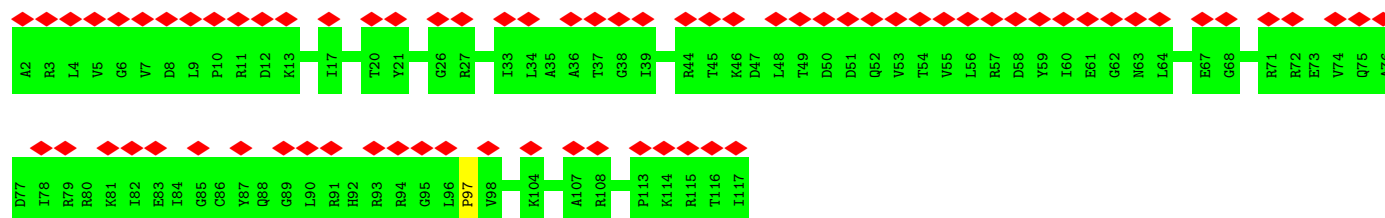
- Molecule 11: Small ribosomal subunit protein uS11



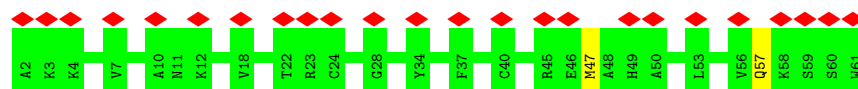
- Molecule 12: Small ribosomal subunit protein uS12



- Molecule 13: Small ribosomal subunit protein uS13



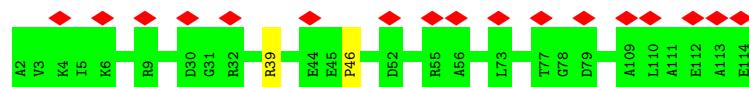
- Molecule 14: Small ribosomal subunit protein uS14B



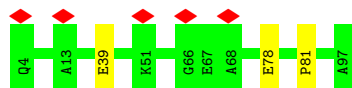
- Molecule 15: Small ribosomal subunit protein uS15



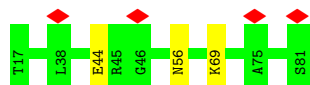
- Molecule 16: Small ribosomal subunit protein bS16



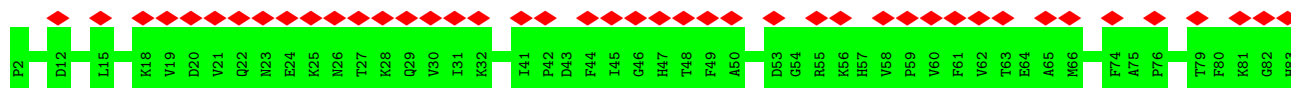
- Molecule 17: Small ribosomal subunit protein uS17



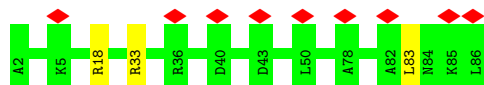
- Molecule 18: Small ribosomal subunit protein bS18B



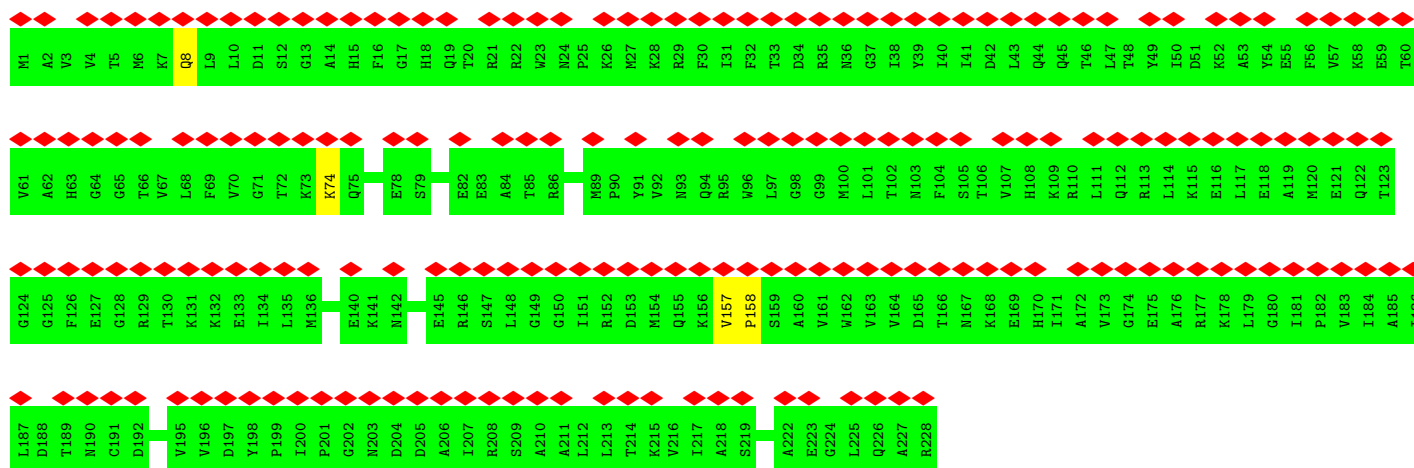
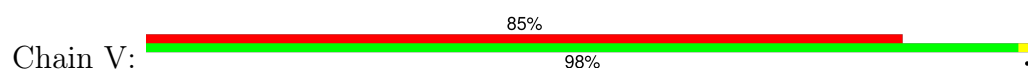
- Molecule 19: Small ribosomal subunit protein uS19



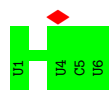
- Molecule 20: Small ribosomal subunit protein bS20



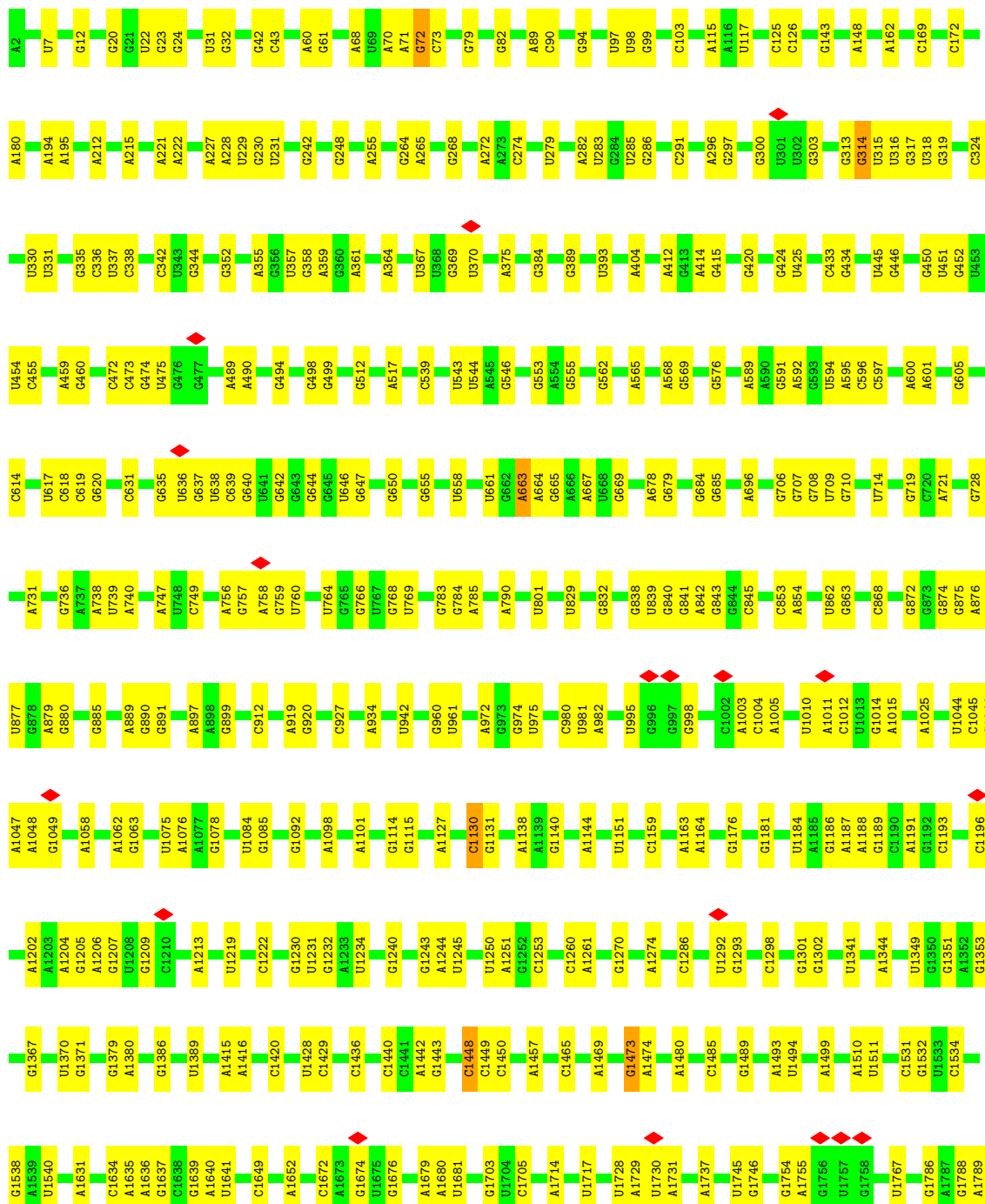
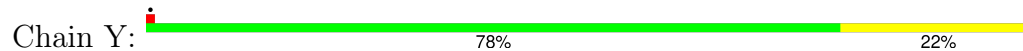
- Molecule 21: Small ribosomal subunit protein uS2

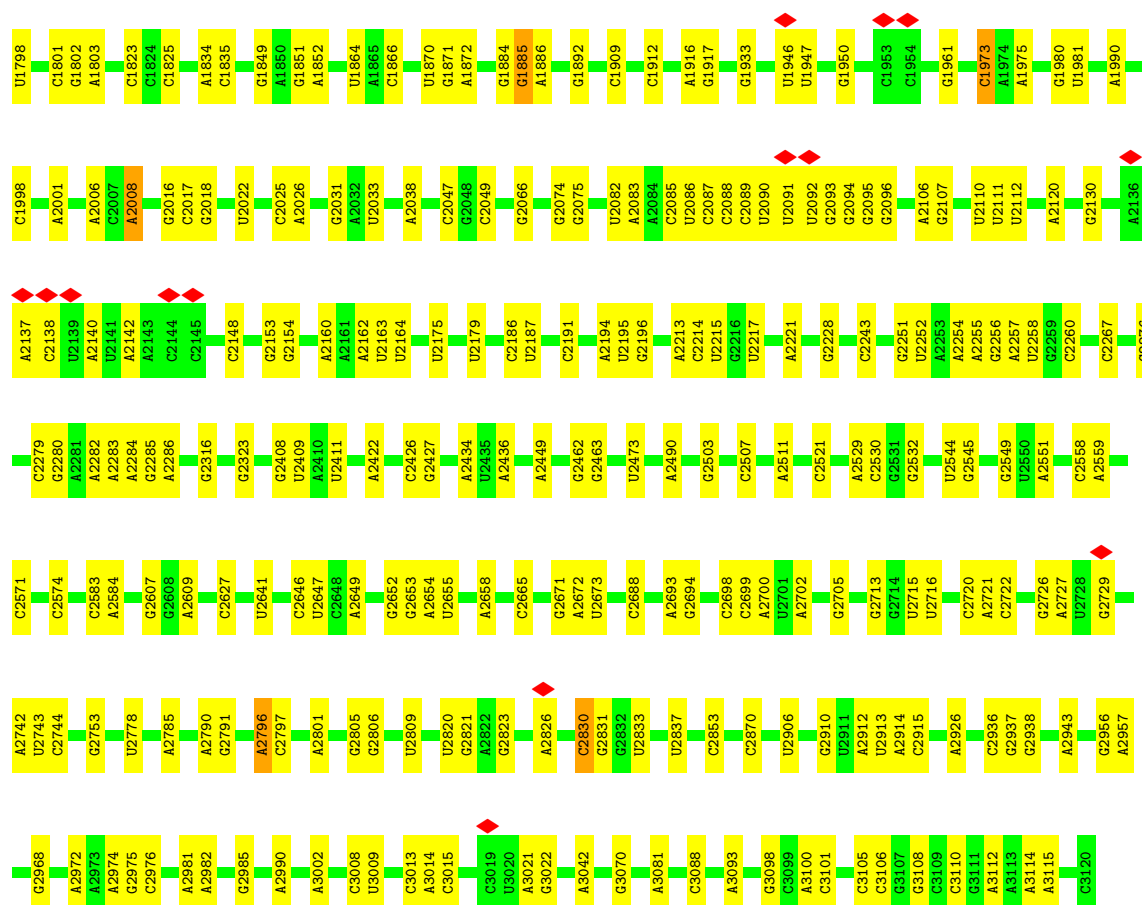


- Molecule 22: mRNA fragment



• Molecule 23: 23S rRNA





- Molecule 24: 5S rRNA

Chain U: 87% 13%



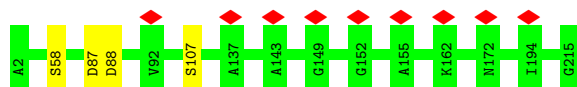
- Molecule 25: Large ribosomal subunit protein uL2

Chain Z: 5% 97%



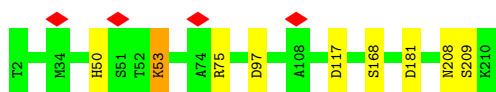
- Molecule 26: Large ribosomal subunit protein uL3

Chain a: 98%



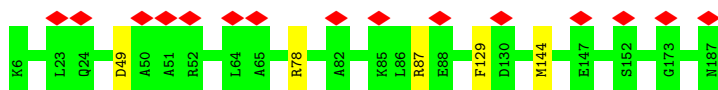
- Molecule 27: Large ribosomal subunit protein uL4

Chain b:  96%



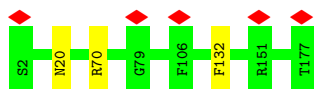
- Molecule 28: Large ribosomal subunit protein uL5

Chain c:  8% 97%

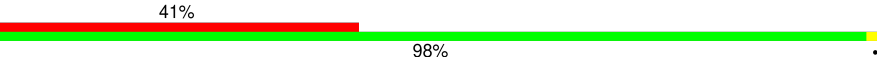


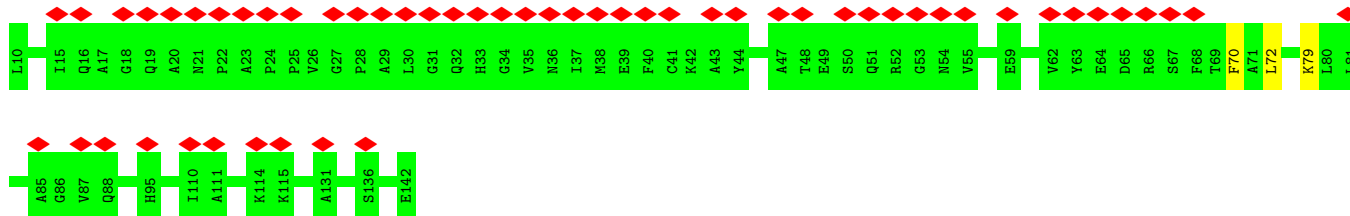
- Molecule 29: Large ribosomal subunit protein uL6

Chain d:  98%



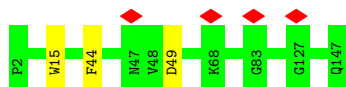
- Molecule 30: Large ribosomal subunit protein uL11

Chain e:  41% 98%



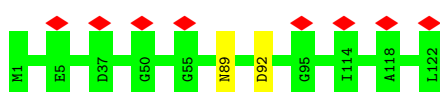
- Molecule 31: 50S ribosomal protein L13

Chain f:  98%



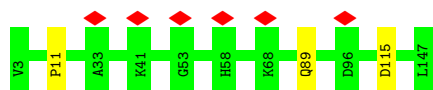
- Molecule 32: Large ribosomal subunit protein uL14

Chain g:  7% 98%



- Molecule 33: 50S ribosomal protein L15

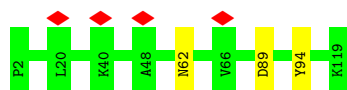
Chain h:  98%



- Molecule 34: Large ribosomal subunit protein uL16



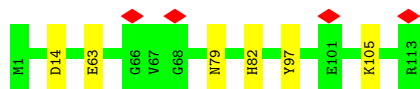
- Molecule 35: Large ribosomal subunit protein bL17



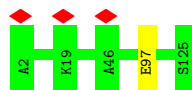
- Molecule 36: Large ribosomal subunit protein uL18



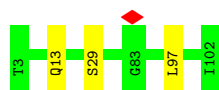
- Molecule 37: Large ribosomal subunit protein bL19



- Molecule 38: Large ribosomal subunit protein bL20

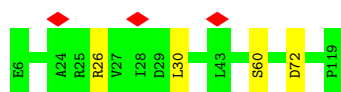


- Molecule 39: Large ribosomal subunit protein bL21



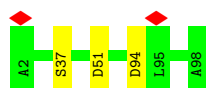
- Molecule 40: 50S ribosomal protein L22

Chain o:  96%



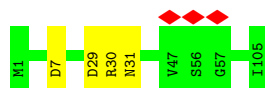
- Molecule 41: Large ribosomal subunit protein uL23

Chain p:  97%



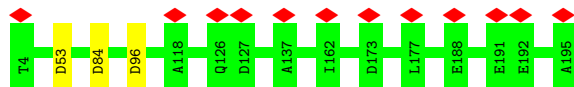
- Molecule 42: Large ribosomal subunit protein uL24

Chain q:  96%



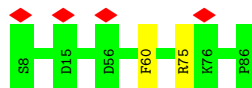
- Molecule 43: Large ribosomal subunit protein bL25

Chain r:  6% 98%



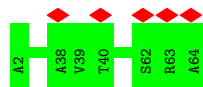
- Molecule 44: Large ribosomal subunit protein bL27

Chain s:  5% 97%



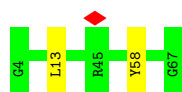
- Molecule 45: Large ribosomal subunit protein bL28

Chain t:  8% 100%

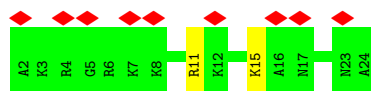
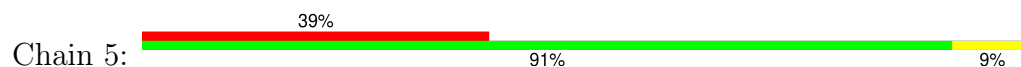


- Molecule 46: Large ribosomal subunit protein uL29

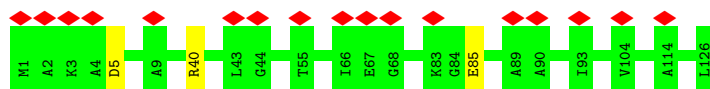
Chain u:  97%



- Molecule 47: ribosomal protein bL37



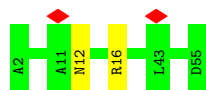
- Molecule 48: Large ribosomal subunit protein uL10



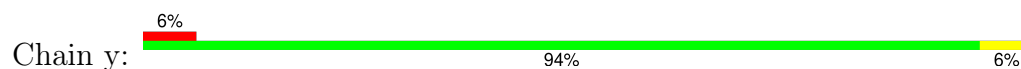
- Molecule 49: Large ribosomal subunit protein uL30



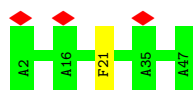
- Molecule 50: Large ribosomal subunit protein bL32



- Molecule 51: Large ribosomal subunit protein bL33A

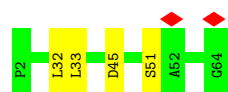


- Molecule 52: 50S ribosomal protein L34



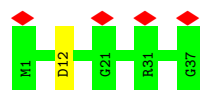
- Molecule 53: Large ribosomal subunit protein bL35

Chain 1:  94% 6%



- Molecule 54: 50S ribosomal protein L36

Chain 2:  11% 97% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	130579	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 ($e^-/\text{\AA}^2$)	72.704	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	14.991	Depositor
Minimum map value	-12.917	Depositor
Average map value	-0.016	Depositor
Map value standard deviation	0.429	Depositor
Recommended contour level	0.927	Depositor
Map size (\AA)	573.696, 573.696, 573.696	wwPDB
Map dimensions	864, 864, 864	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.664, 0.664, 0.664	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G7M, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/36282	0.74	15/56612 (0.0%)
2	B	0.28	0/280	0.69	0/359
3	C	0.25	0/1684	0.57	0/2261
4	D	0.26	0/1672	0.56	0/2251
5	E	0.25	0/1312	0.55	0/1772
6	F	0.25	0/782	0.56	0/1059
7	G	0.24	0/1252	0.56	0/1690
8	H	0.28	0/1025	0.59	0/1385
9	I	0.62	3/1012 (0.3%)	1.11	6/1362 (0.4%)
10	J	0.25	0/802	0.53	0/1086
11	K	0.32	0/873	0.54	0/1180
12	L	0.26	0/969	0.63	0/1294
13	M	0.27	0/942	0.68	2/1260 (0.2%)
14	N	0.26	0/488	0.54	0/650
15	O	0.28	0/729	0.66	0/977
16	P	0.30	0/908	0.65	1/1226 (0.1%)
17	Q	0.30	0/759	0.66	1/1016 (0.1%)
18	R	0.28	0/518	0.60	0/693
19	S	0.24	0/680	0.48	0/915
20	T	0.27	0/663	0.65	0/882
21	V	0.25	0/1822	0.53	1/2457 (0.0%)
22	X	0.11	0/128	0.67	0/196
23	Y	0.24	0/70951	0.77	48/110641 (0.0%)
24	U	0.21	0/2821	0.74	0/4396
25	Z	0.27	0/2153	0.60	0/2895
26	a	0.26	0/1609	0.58	0/2165
27	b	0.31	1/1592 (0.1%)	0.56	0/2153
28	c	0.26	0/1467	0.57	0/1973
29	d	0.28	0/1369	0.57	0/1848
30	e	0.24	0/986	0.45	0/1303
31	f	0.26	0/1157	0.54	0/1567
32	g	0.26	0/946	0.59	0/1268

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.28	0/1091	0.63	1/1457 (0.1%)
34	i	0.26	0/1118	0.58	0/1506
35	j	0.27	0/945	0.56	0/1267
36	k	0.28	0/966	0.59	0/1298
37	l	0.27	0/921	0.59	0/1236
38	m	0.28	0/1000	0.59	0/1341
39	n	0.25	0/764	0.49	0/1030
40	o	0.27	0/887	0.59	0/1204
41	p	0.26	0/766	0.54	0/1030
42	q	0.25	0/738	0.51	0/987
43	r	0.25	0/1443	0.53	0/1970
44	s	0.27	0/595	0.61	0/798
45	t	0.25	0/478	0.56	0/641
46	u	0.32	0/534	0.62	0/713
47	5	0.25	0/191	0.63	0/247
48	v	0.26	0/925	0.46	0/1246
49	w	0.28	0/477	0.61	0/640
50	x	0.30	0/427	0.63	0/572
51	y	0.27	0/413	0.57	0/553
52	z	0.26	0/380	0.70	0/500
53	1	0.26	0/507	0.66	0/672
54	2	0.28	0/303	0.64	0/401
All	All	0.24	4/156502 (0.0%)	0.72	75/234101 (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
40	o	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	116	PRO	CG-CD	-12.15	1.10	1.50
9	I	116	PRO	CB-CG	-9.84	1.00	1.50
9	I	116	PRO	N-CD	8.09	1.59	1.47
27	b	53	LYS	CE-NZ	-5.33	1.35	1.49

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	116	PRO	CB-CG-CD	18.83	179.94	106.50
9	I	116	PRO	N-CD-CG	-17.14	77.48	103.20
9	I	116	PRO	CA-CB-CG	-16.09	73.43	104.00
9	I	116	PRO	CA-N-CD	-12.58	93.89	111.50
16	P	46	PRO	CA-N-CD	-11.46	95.45	111.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	o	26	ARG	Sidechain

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	
2	B	30/32 (94%)	29 (97%)	1 (3%)	0	100	100
3	C	206/208 (99%)	192 (93%)	14 (7%)	0	100	100
4	D	198/200 (99%)	191 (96%)	7 (4%)	0	100	100
5	E	178/180 (99%)	168 (94%)	10 (6%)	0	100	100
6	F	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
7	G	153/155 (99%)	147 (96%)	6 (4%)	0	100	100
8	H	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
9	I	124/126 (98%)	114 (92%)	9 (7%)	1 (1%)	16	45
10	J	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
11	K	113/115 (98%)	108 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
13	M	114/116 (98%)	108 (95%)	6 (5%)	0	100	100
14	N	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
15	O	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
16	P	111/113 (98%)	105 (95%)	6 (5%)	0	100	100
17	Q	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
18	R	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
19	S	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
20	T	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
21	V	226/228 (99%)	220 (97%)	5 (2%)	1 (0%)	30	60
25	Z	273/275 (99%)	260 (95%)	12 (4%)	1 (0%)	30	60
26	a	212/214 (99%)	198 (93%)	14 (7%)	0	100	100
27	b	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
28	c	180/182 (99%)	170 (94%)	10 (6%)	0	100	100
29	d	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
30	e	96/133 (72%)	92 (96%)	4 (4%)	0	100	100
31	f	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
32	g	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
33	h	143/145 (99%)	129 (90%)	14 (10%)	0	100	100
34	i	134/136 (98%)	124 (92%)	9 (7%)	1 (1%)	19	49
35	j	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
36	k	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
37	l	111/113 (98%)	106 (96%)	5 (4%)	0	100	100
38	m	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
39	n	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
40	o	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
41	p	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
42	q	93/97 (96%)	93 (100%)	0	0	100	100
43	r	190/192 (99%)	189 (100%)	1 (0%)	0	100	100
44	s	77/79 (98%)	72 (94%)	5 (6%)	0	100	100
45	t	61/63 (97%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	u	62/64 (97%)	62 (100%)	0	0	100	100
47	5	21/23 (91%)	20 (95%)	1 (5%)	0	100	100
48	v	124/126 (98%)	121 (98%)	2 (2%)	1 (1%)	16	45
49	w	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
50	x	52/54 (96%)	52 (100%)	0	0	100	100
51	y	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
52	z	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
53	1	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
54	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
All	All	5740/5877 (98%)	5485 (96%)	250 (4%)	5 (0%)	50	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	Z	221	VAL
34	i	29	PHE
48	v	85	GLU
9	I	43	PRO
21	V	157	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	30/30 (100%)	29 (97%)	1 (3%)	33	58
3	C	170/170 (100%)	167 (98%)	3 (2%)	54	72
4	D	175/175 (100%)	172 (98%)	3 (2%)	56	73
5	E	127/127 (100%)	122 (96%)	5 (4%)	27	53
6	F	85/85 (100%)	81 (95%)	4 (5%)	22	49
7	G	131/131 (100%)	129 (98%)	2 (2%)	60	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	107/107 (100%)	104 (97%)	3 (3%)	38	62
9	I	102/102 (100%)	100 (98%)	2 (2%)	50	70
10	J	89/89 (100%)	88 (99%)	1 (1%)	70	81
11	K	89/89 (100%)	88 (99%)	1 (1%)	70	81
12	L	103/103 (100%)	102 (99%)	1 (1%)	73	82
13	M	99/99 (100%)	99 (100%)	0	100	100
14	N	49/49 (100%)	47 (96%)	2 (4%)	26	52
15	O	76/76 (100%)	72 (95%)	4 (5%)	19	45
16	P	92/92 (100%)	91 (99%)	1 (1%)	70	81
17	Q	80/80 (100%)	78 (98%)	2 (2%)	42	65
18	R	55/55 (100%)	52 (94%)	3 (6%)	18	44
19	S	73/73 (100%)	73 (100%)	0	100	100
20	T	69/69 (100%)	66 (96%)	3 (4%)	25	51
21	V	191/191 (100%)	189 (99%)	2 (1%)	73	82
25	Z	215/215 (100%)	208 (97%)	7 (3%)	33	58
26	a	160/160 (100%)	156 (98%)	4 (2%)	42	65
27	b	169/169 (100%)	160 (95%)	9 (5%)	19	45
28	c	151/151 (100%)	146 (97%)	5 (3%)	33	58
29	d	148/148 (100%)	145 (98%)	3 (2%)	50	70
30	e	102/102 (100%)	99 (97%)	3 (3%)	37	61
31	f	119/119 (100%)	116 (98%)	3 (2%)	42	65
32	g	100/100 (100%)	98 (98%)	2 (2%)	50	70
33	h	112/112 (100%)	110 (98%)	2 (2%)	54	72
34	i	114/114 (100%)	110 (96%)	4 (4%)	31	56
35	j	97/97 (100%)	94 (97%)	3 (3%)	35	59
36	k	93/93 (100%)	91 (98%)	2 (2%)	47	68
37	l	100/100 (100%)	94 (94%)	6 (6%)	16	41
38	m	97/97 (100%)	96 (99%)	1 (1%)	73	82
39	n	81/81 (100%)	78 (96%)	3 (4%)	29	55
40	o	90/90 (100%)	87 (97%)	3 (3%)	33	58
41	p	83/83 (100%)	80 (96%)	3 (4%)	30	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	q	81/81 (100%)	77 (95%)	4 (5%)	21	48
43	r	155/155 (100%)	152 (98%)	3 (2%)	52	71
44	s	58/58 (100%)	56 (97%)	2 (3%)	32	57
45	t	50/50 (100%)	50 (100%)	0	100	100
46	u	58/58 (100%)	56 (97%)	2 (3%)	32	57
47	5	18/18 (100%)	16 (89%)	2 (11%)	5	19
48	v	89/89 (100%)	87 (98%)	2 (2%)	47	68
49	w	52/52 (100%)	50 (96%)	2 (4%)	28	54
50	x	43/43 (100%)	41 (95%)	2 (5%)	22	49
51	y	47/47 (100%)	44 (94%)	3 (6%)	14	39
52	z	35/35 (100%)	34 (97%)	1 (3%)	37	61
53	1	53/53 (100%)	49 (92%)	4 (8%)	11	33
54	2	35/35 (100%)	34 (97%)	1 (3%)	37	61
All	All	4797/4797 (100%)	4663 (97%)	134 (3%)	40	62

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	u	13	LEU
48	v	5	ASP
53	1	33	LEU
25	Z	237	GLU
25	Z	198	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
51	y	20	HIS
53	1	63	ASN
28	c	83	GLN
31	f	132	HIS
38	m	122	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1509/1511 (99%)	294 (19%)	21 (1%)
22	X	5/6 (83%)	0	0
23	Y	2923/2951 (99%)	608 (20%)	38 (1%)
24	U	117/118 (99%)	13 (11%)	2 (1%)
All	All	4554/4586 (99%)	915 (20%)	61 (1%)

5 of 915 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	U
1	A	12	A
1	A	13	G
1	A	36	A
1	A	43	G

5 of 61 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	Y	445	U
23	Y	2693	A
23	Y	981	U
23	Y	2282	A
24	U	10	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	G7M	A	507	1	20,26,27	0.94	1 (5%)	16,39,42	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	G7M	A	507	1	-	2/3/25/26	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	507	G7M	C8-N9	3.01	1.38	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	507	G7M	O4'-C4'-C5'-O5'
1	A	507	G7M	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 629 ligands modelled in this entry, 629 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	Y	28
30	e	20
42	q	1
1	A	1

The worst 5 of 50 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	2325:U	O3'	2407:C	P	20.88
1	Y	1541:G	O3'	1629:G	P	11.64
1	Y	1008:G	O3'	1009:U	P	10.75
1	e	22:PRO	C	23:ALA	N	10.53
1	e	15:ILE	C	16:GLN	N	8.57

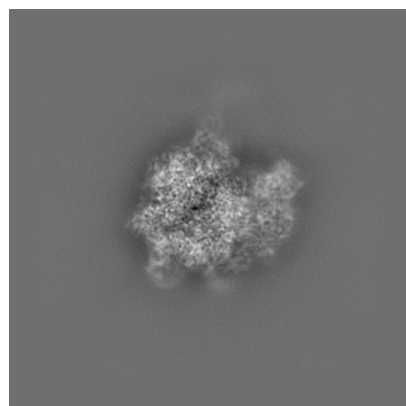
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44090. These allow visual inspection of the internal detail of the map and identification of artifacts.

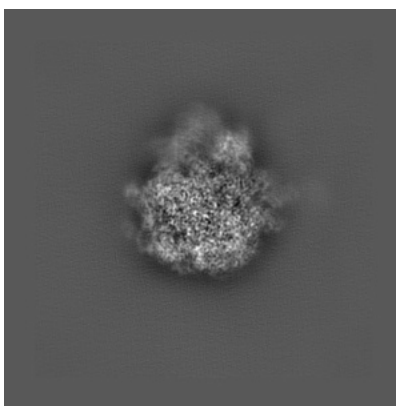
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

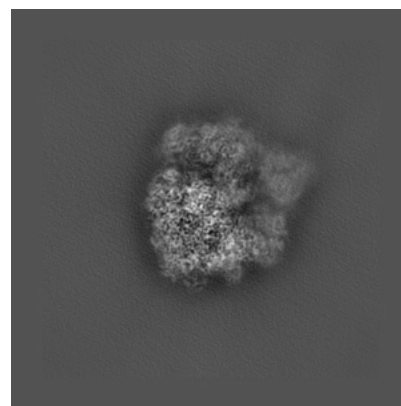
6.1.1 Primary map



X

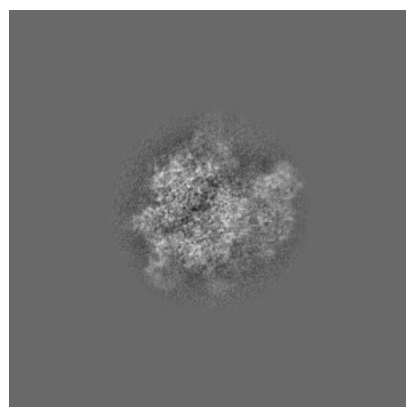


Y

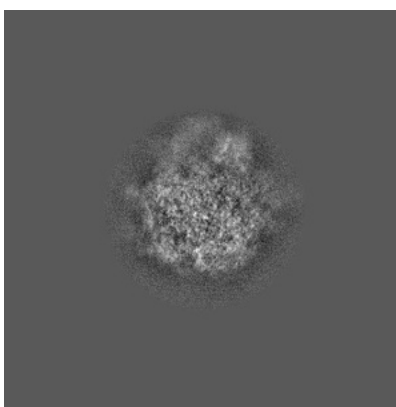


Z

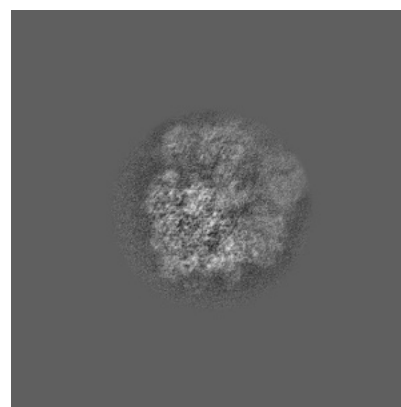
6.1.2 Raw map



X



Y

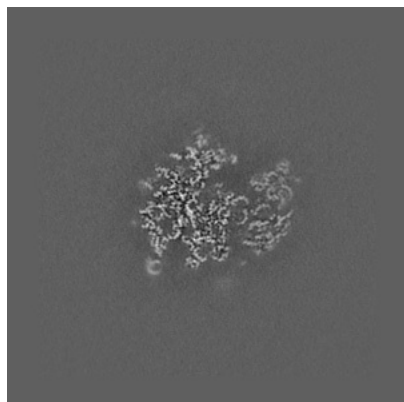


Z

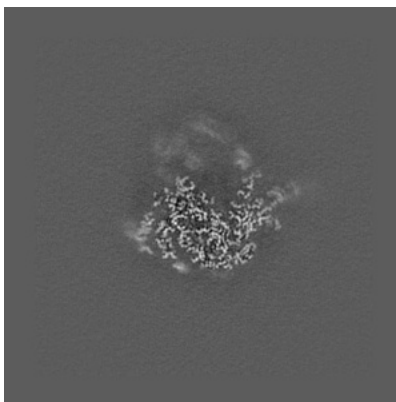
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

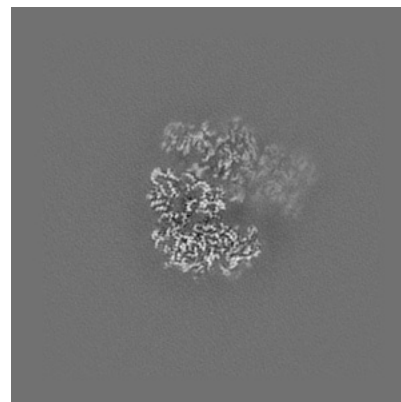
6.2.1 Primary map



X Index: 432

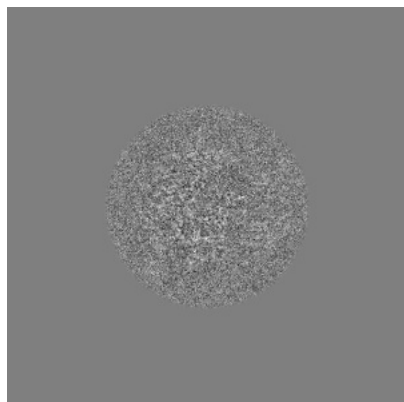


Y Index: 432

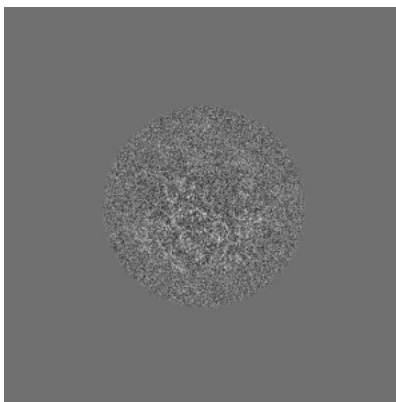


Z Index: 432

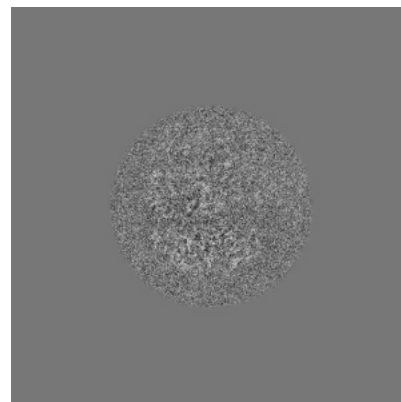
6.2.2 Raw map



X Index: 432



Y Index: 432

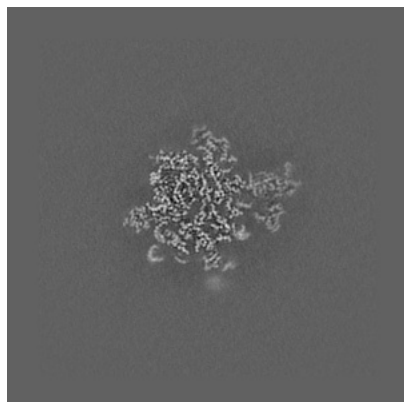


Z Index: 432

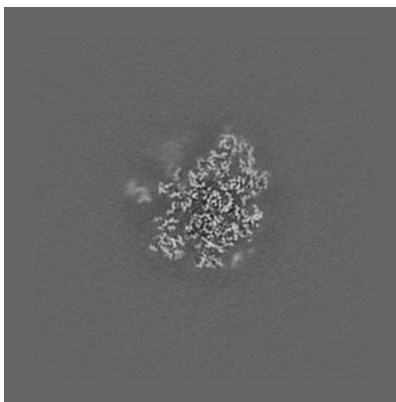
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

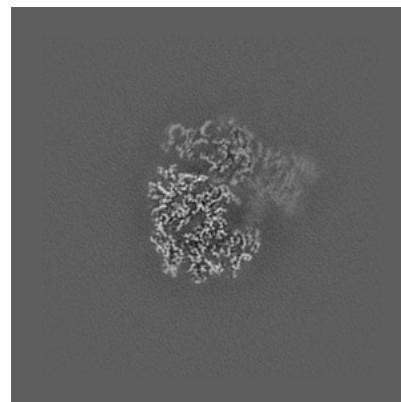
6.3.1 Primary map



X Index: 399

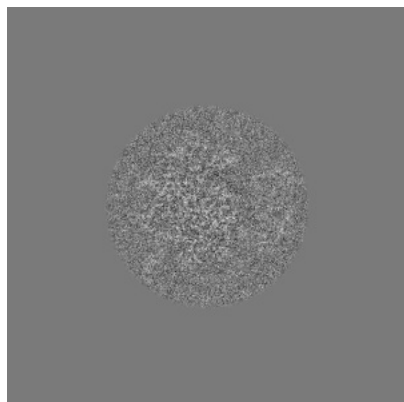


Y Index: 361

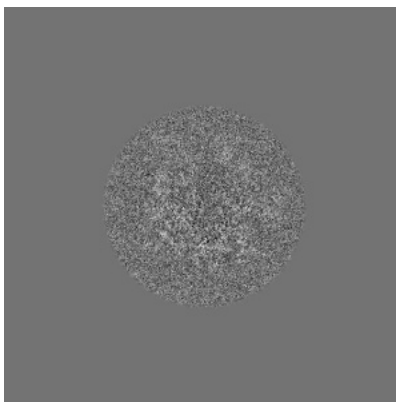


Z Index: 423

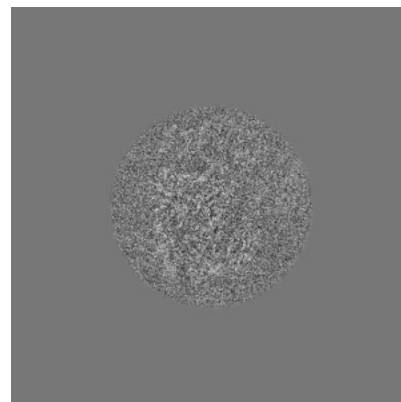
6.3.2 Raw map



X Index: 423



Y Index: 413



Z Index: 422

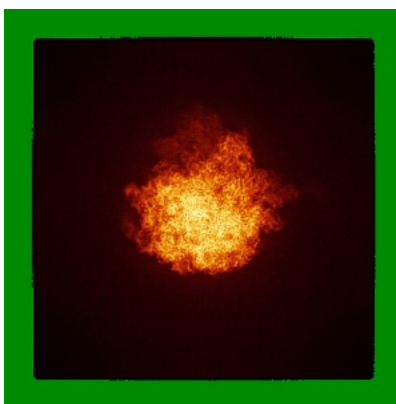
The images above show the largest variance slices of the map in three orthogonal directions.

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

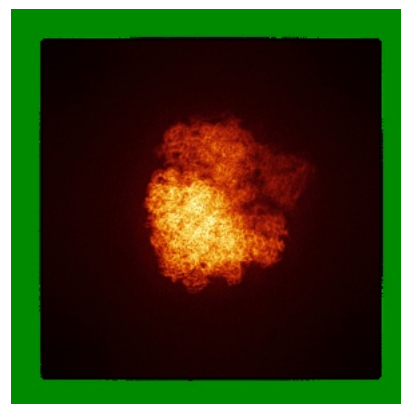
6.4.1 Primary map



X

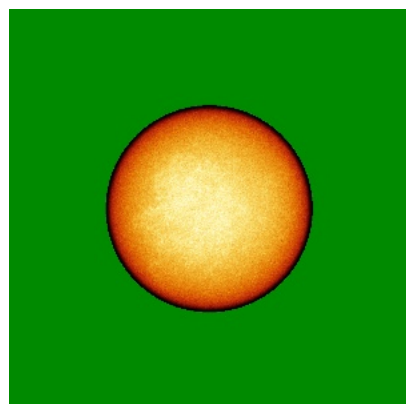


Y

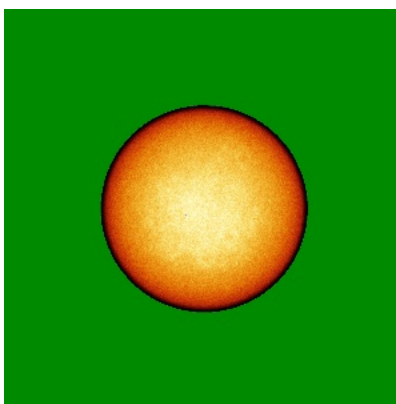


Z

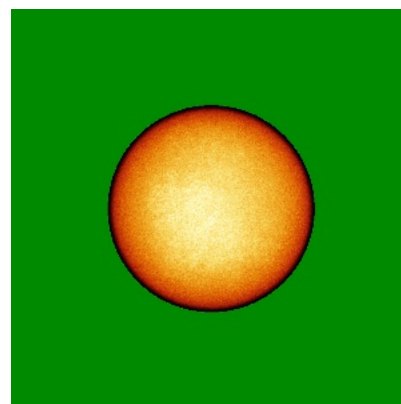
6.4.2 Raw map



X



Y

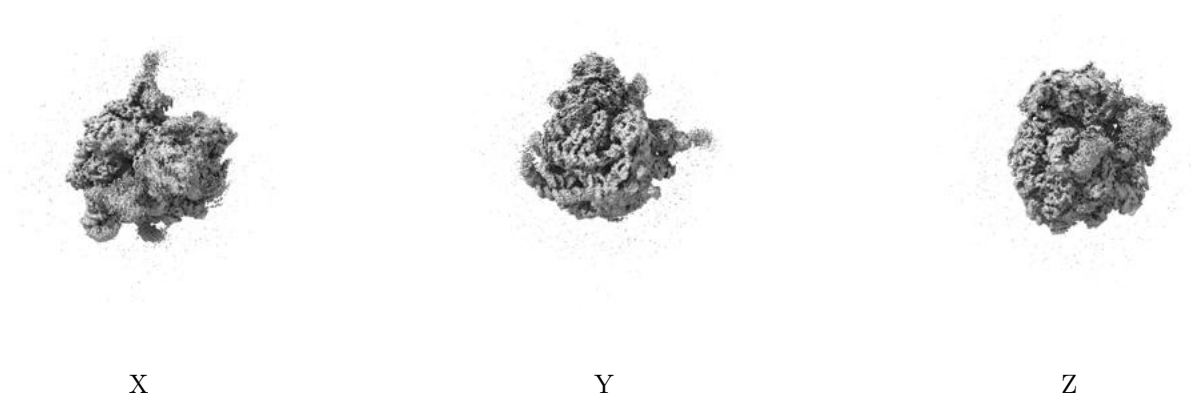


Z

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.

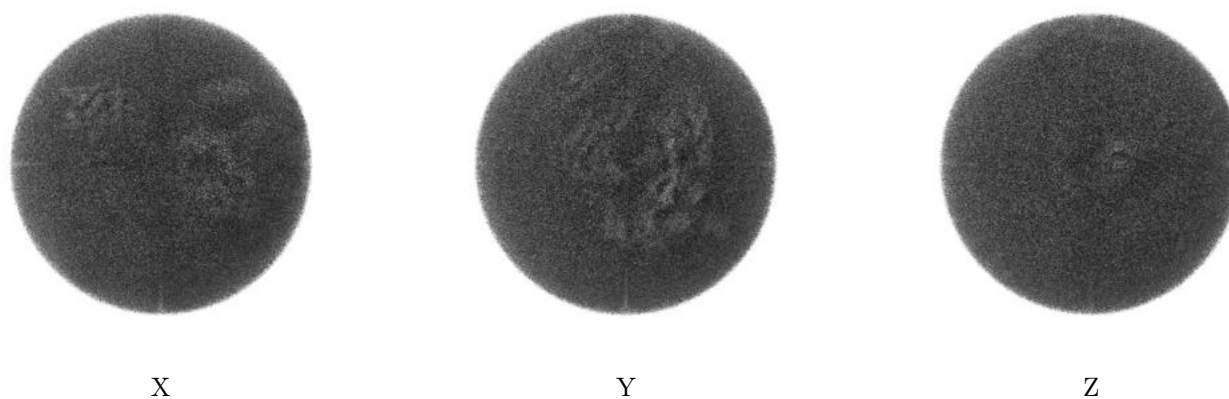
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.927. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

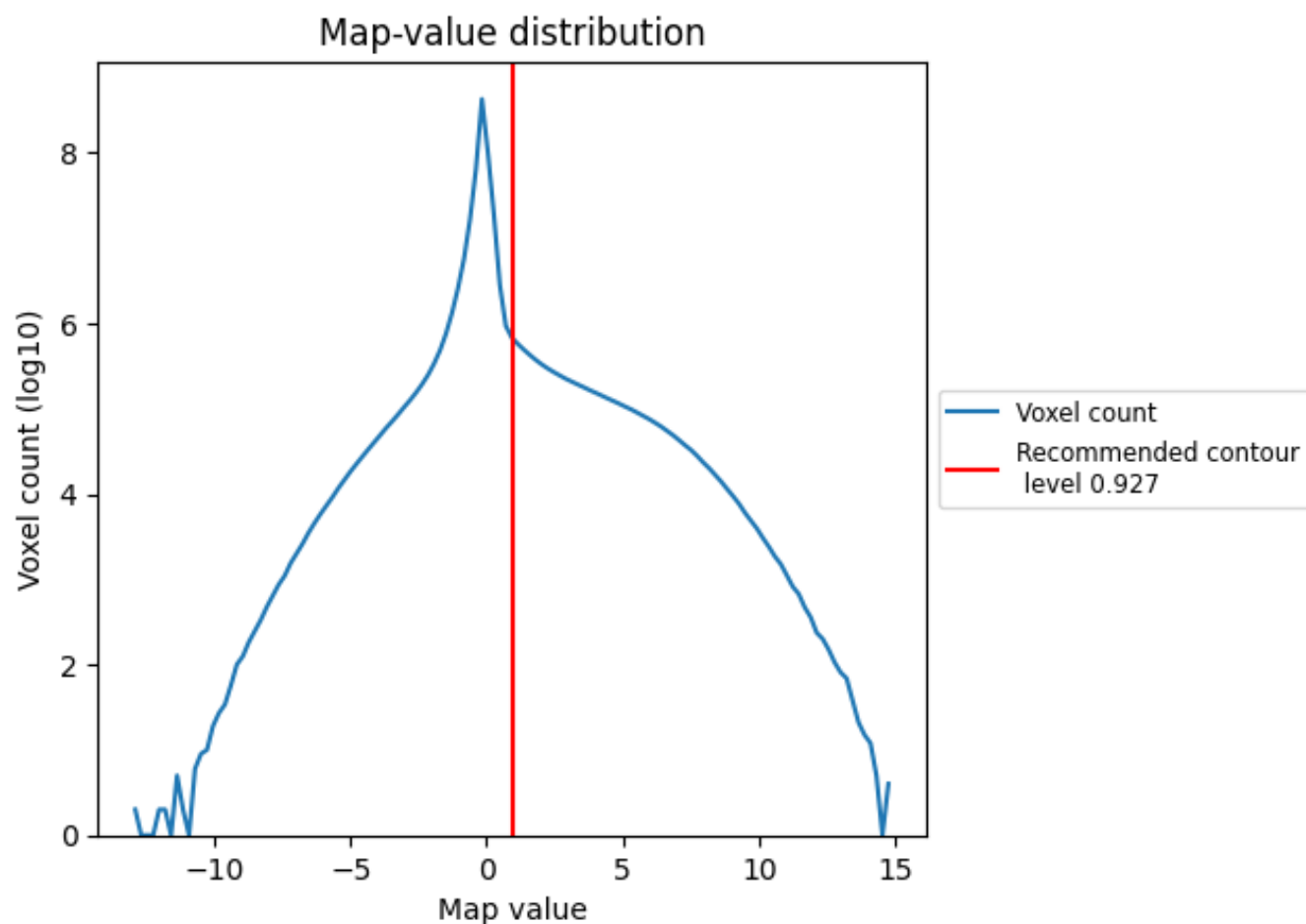
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

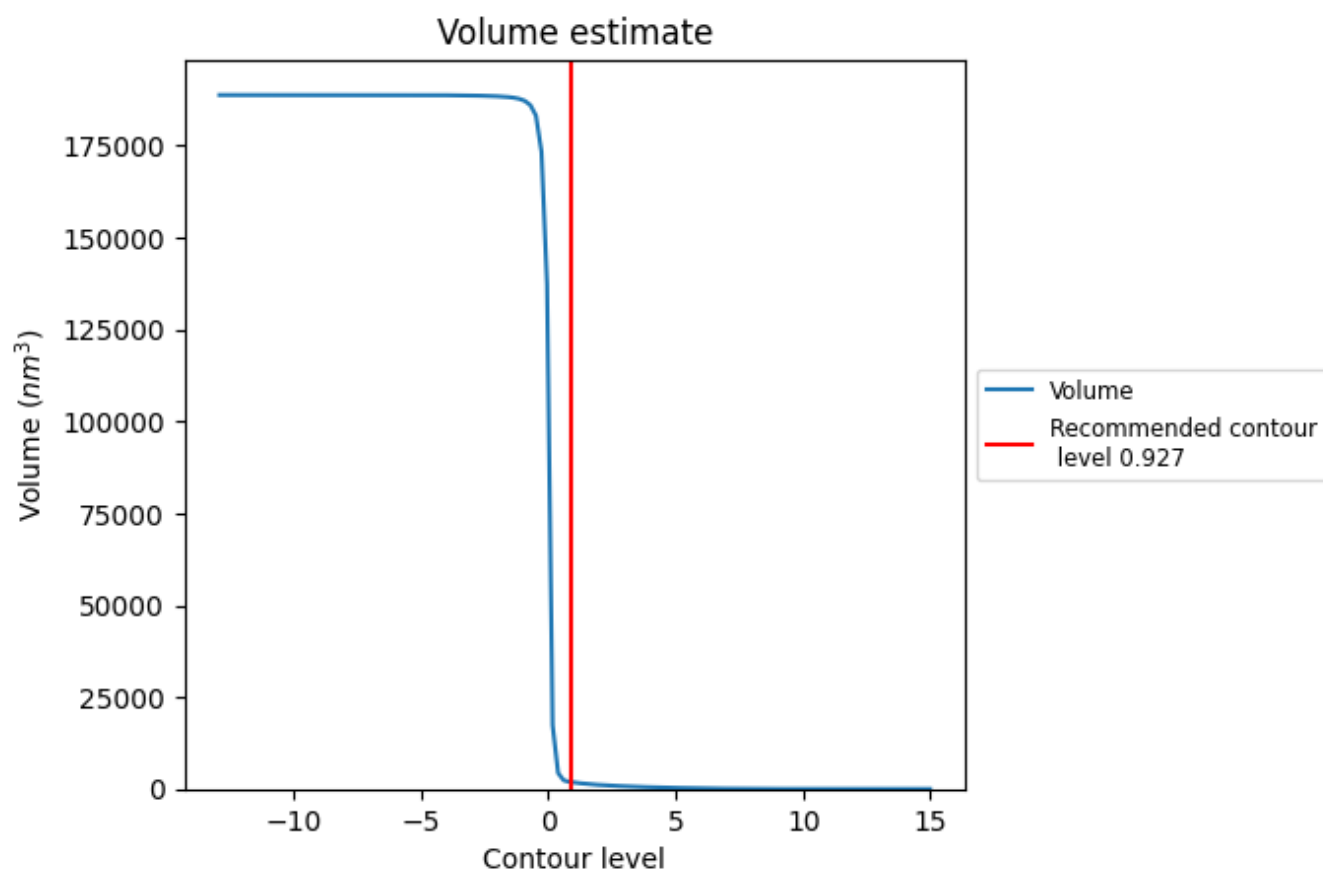
This section contains the results of statistical analysis of the map.

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.

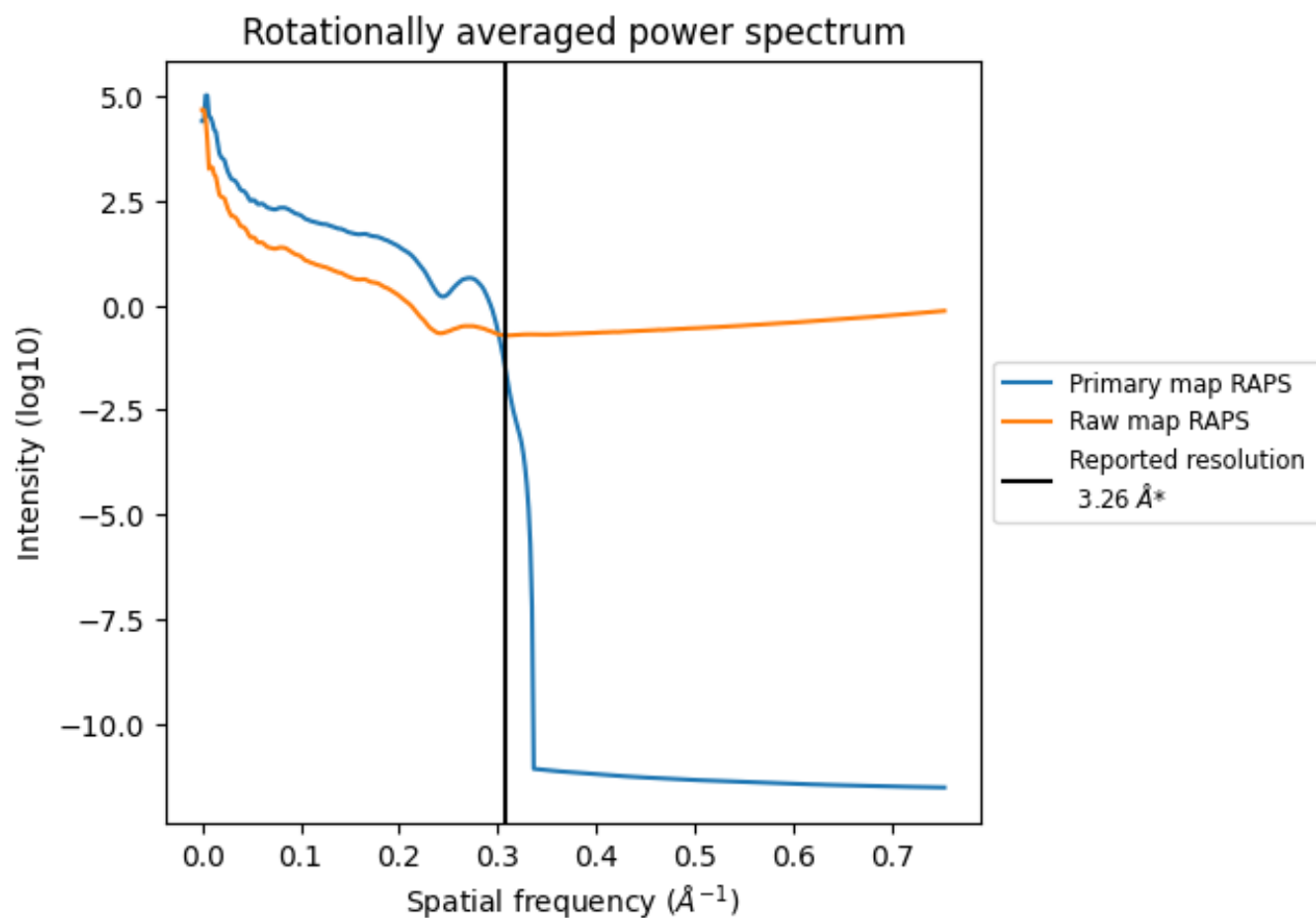
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1838 nm^3 ; this corresponds to an approximate mass of 1660 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 ⓘ

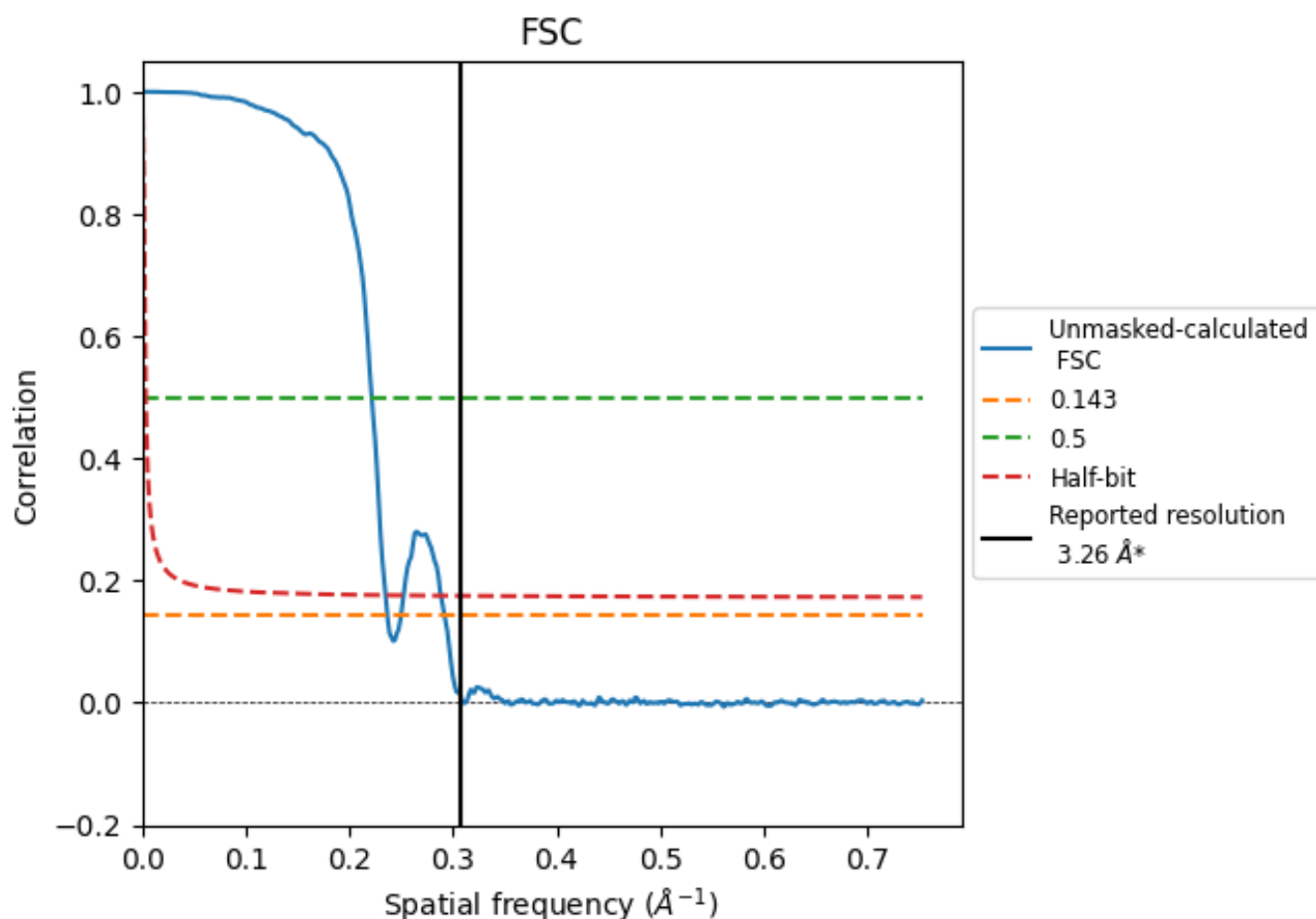


*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.307 Å⁻¹

8.2 Resolution estimates [i](#)

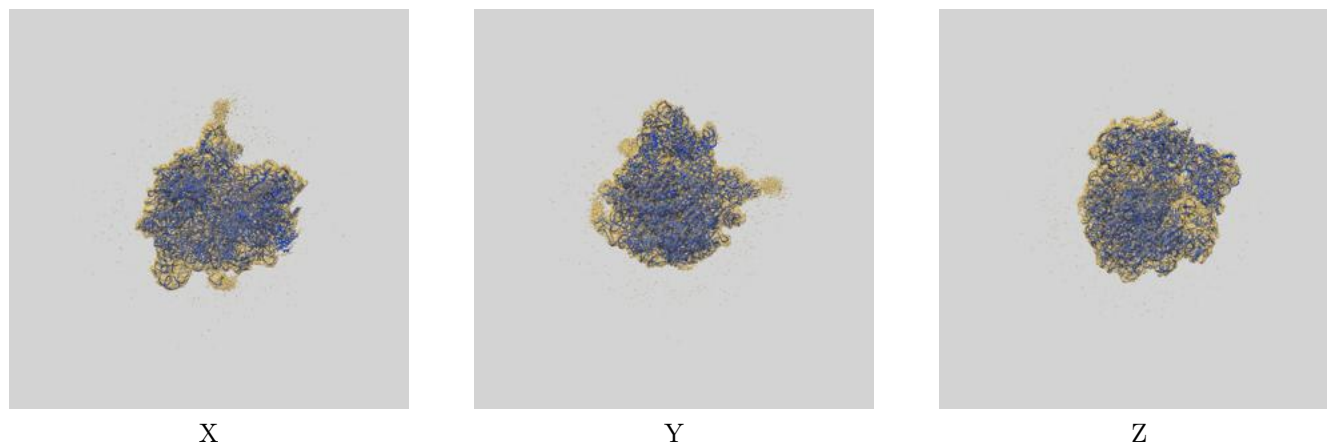
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.26	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.22	4.51	4.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.22 differs from the reported value 3.26 by more than 10 %

9 Map-model fit [i](#)

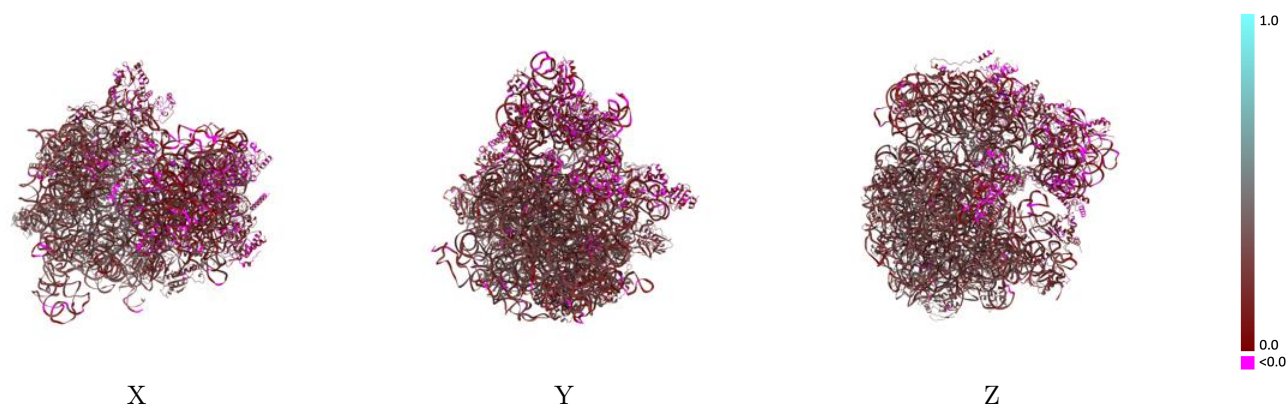
This section contains information regarding the fit between EMDB map EMD-44090 and PDB model 9B1W. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



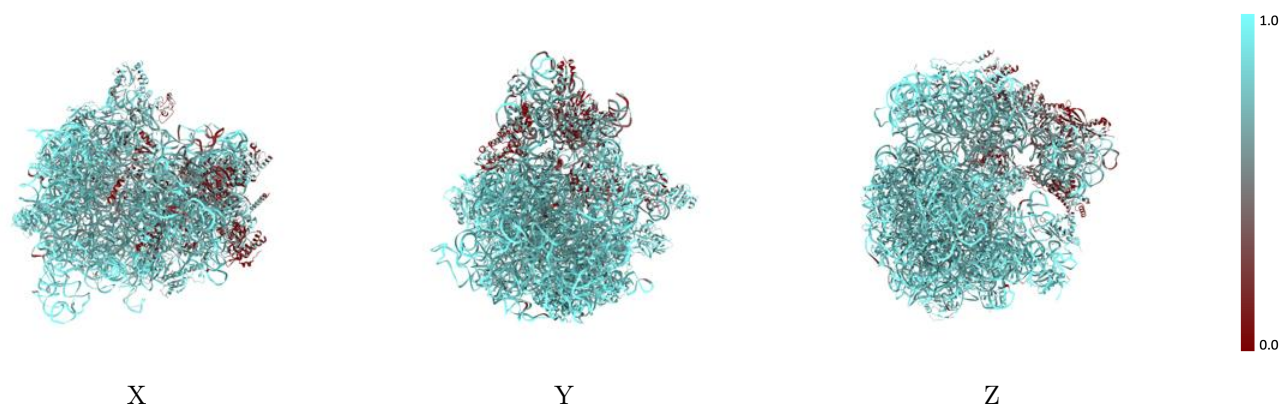
The images above show the 3D surface view of the map at the recommended contour level 0.927 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



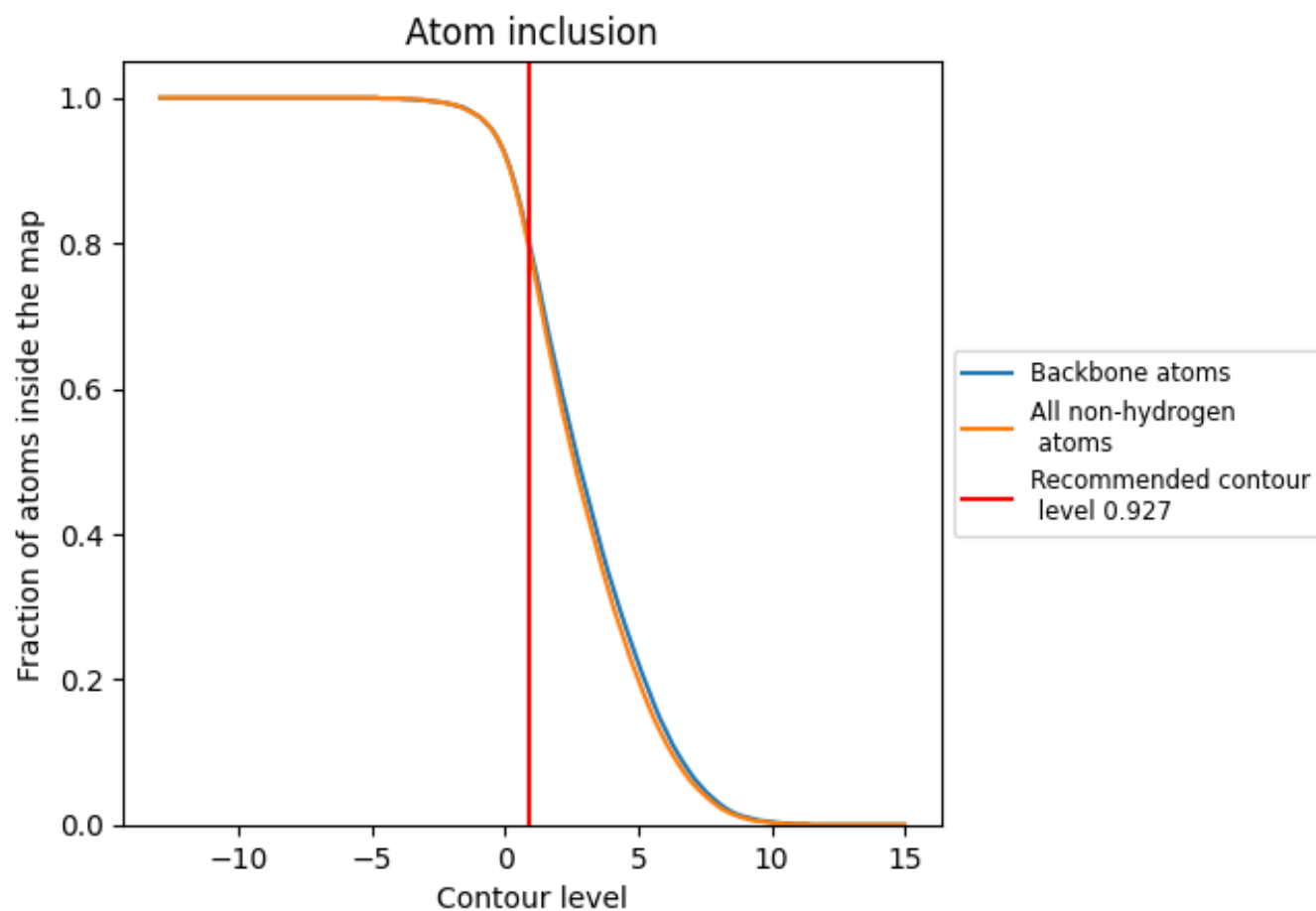
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.927).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 79% 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 (0.927) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7910	 0.2240
1	 0.7880	 0.2980
2	 0.7600	 0.2130
5	 0.5700	 0.2210
A	 0.8120	 0.1940
B	 0.3780	 0.1420
C	 0.3300	 0.1030
D	 0.4880	 0.0500
E	 0.6530	 0.1910
F	 0.7760	 0.2770
G	 0.4640	 0.1160
H	 0.7920	 0.2450
I	 0.6480	 0.1190
J	 0.3050	 0.0590
K	 0.7490	 0.2300
L	 0.5230	 0.2090
M	 0.3350	 0.0530
N	 0.4690	 0.1060
O	 0.7790	 0.2660
P	 0.7160	 0.1700
Q	 0.7410	 0.2560
R	 0.8230	 0.2460
S	 0.3930	 0.0580
T	 0.6910	 0.1690
U	 0.9140	 0.2490
V	 0.1620	 0.0990
X	 0.5560	 0.1530
Y	 0.8720	 0.2550
Z	 0.7700	 0.2540
a	 0.7880	 0.2590
b	 0.8190	 0.2890
c	 0.7610	 0.1550
d	 0.8330	 0.2270
e	 0.4980	 0.0760
f	 0.8100	 0.2780



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Chain	Atom inclusion	Q-score
g	 0.7470	 0.2370
h	 0.8070	 0.2770
i	 0.7160	 0.2120
j	 0.8040	 0.2770
k	 0.8360	 0.2400
l	 0.7840	 0.2430
m	 0.7830	 0.2580
n	 0.8460	 0.2690
o	 0.7990	 0.2840
p	 0.8310	 0.3000
q	 0.8390	 0.2860
r	 0.7620	 0.2120
s	 0.7780	 0.2560
t	 0.7500	 0.2520
u	 0.8240	 0.2710
v	 0.7320	 0.0940
w	 0.8170	 0.2720
x	 0.8260	 0.3000
y	 0.7750	 0.2210
z	 0.7990	 0.2990