



wwPDB EM Validation Summary Report ⓘ

Oct 20, 2026 – 05:59 pm BST

PDB ID : 9SVJ / pdb_00009svj
EMDB ID : EMD-55260
Title : Structural characterization of hibernating ribosomes in the Gram-negative pathogen *Acinetobacter baumannii*
Authors : Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G.
Deposited on : 2025-10-03
Resolution : 2.50 Å (reported)
Based on initial model : 8B0X

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:

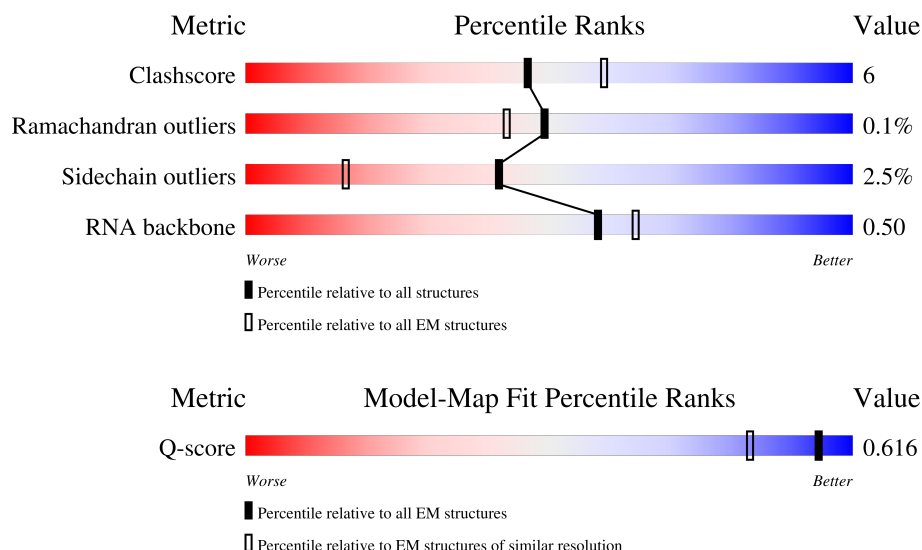
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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	0	51	<div> <div>18%</div> <div>80%</div> <div>20%</div> </div>
2	1	44	<div> <div>91%</div> <div>9%</div> </div>
3	2	64	<div> <div>80%</div> <div>19%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	74	
6	A	1537	
7	B	250	
8	C	215	
9	D	208	
10	E	165	
11	F	127	
12	G	156	
13	H	131	
14	I	128	
15	J	103	
16	K	128	
17	L	124	
18	M	118	
19	N	101	
20	O	89	
21	P	83	
22	Q	85	
23	R	75	
24	S	91	
25	T	88	
26	V	77	
27	W	15	
28	X	116	

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Mol	Chain	Length	Quality of chain
29	a	2893	
30	b	115	
31	c	274	
32	d	212	
33	e	200	
34	f	178	
35	g	177	
36	h	148	
37	i	142	
38	j	122	
39	k	146	
40	l	137	
41	m	125	
42	n	116	
43	o	122	
44	p	119	
45	q	103	
46	r	109	
47	s	106	
48	t	105	
49	u	98	
50	v	85	
51	w	78	
52	x	64	
53	y	58	

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Mol	Chain	Length	Quality of chain
54	z	61	<div><div></div><div>20%</div><div>72%</div><div>16%</div><div>11%</div></div>

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 144017 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			427	274	77	73	3		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			363	222	85	54	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	319	110	76	4		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			295	179	64	48	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	71	Total	C	N	O	S	0	0
			552	343	101	102	6		

- Molecule 6 is a RNA chain called 16S rRNA (1537-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1536	Total	C	N	O	P	0	0
			32947	14705	6016	10690	1536		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	229	Total	C	N	O	S	0	0
			1801	1130	333	332	6		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	215	Total	C	N	O	S	0	0
			1690	1065	318	299	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	207	Total	C	N	O	S	0	0
			1631	1017	313	299	2		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	155	Total	C	N	O	S	0	0
			1129	700	217	207	5		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	106	Total	C	N	O	S	0	0
			878	552	160	162	4		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	153	Total	C	N	O	S	0	0
			1210	758	229	216	7		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	130	Total	C	N	O	S	0	0
			985	615	177	187	6		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	127	Total	C	N	O	S	0	0
			995	621	198	175	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	100	Total	C	N	O	S	0	0
			801	500	150	148	3		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	117	Total	C	N	O	S	0	0
			861	535	166	159	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	118	IAS	ASN	conflict	UNP D0CD20

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			947	581	193	167	6		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	116	Total	C	N	O	S	0	0
			912	564	186	159	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	100	Total	C	N	O	S	0	0
			792	493	158	137	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	88	Total	C	N	O	S	0	0
			705	434	144	126	1		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	82	Total	C	N	O	S	0	0
			644	403	128	112	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	79	Total	C	N	O	S	0	0
			621	390	116	114	1		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	66	Total	C	N	O	S	0	0
			545	349	96	99	1		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	84	Total	C	N	O	S	0	0
			657	419	127	109	2		

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	86	Total	C	N	O	S	0	0
			663	409	139	113	2		

- Molecule 26 is a RNA chain called tRNA (77-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
26	V	77	Total	C	N	O	P	S	0	0
			1644	734	297	535	77	1		

- Molecule 27 is a RNA chain called non-Stop mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	10	Total	C	N	O	P	0	0
			219	97	41	71	10		

- Molecule 28 is a protein called Putative ribosomal subunit interface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	104	Total	C	N	O	S	0	0
			841	519	161	158	3		

- Molecule 29 is a RNA chain called 23S rRNA (2890-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	2890	Total	C	N	O	P	0	0
			61984	27671	11335	20088	2890		

- Molecule 30 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	115	Total	C	N	O	P	0	0
			2450	1095	440	800	115		

- Molecule 31 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	272	Total	C	N	O	S	0	0
			2111	1302	436	365	8		

- Molecule 32 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	211	Total	C	N	O	S	0	0
			1573	973	297	300	3		

- Molecule 33 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	199	Total	C	N	O	S	0	0
			1511	950	280	276	5		

- Molecule 34 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	177	Total	C	N	O	S	0	0
			1395	886	250	251	8		

- Molecule 35 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	175	Total	C	N	O	S	0	0
			1327	838	238	250	1		

- Molecule 36 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	60	Total	C	N	O	S	0	0
			458	287	84	86	1		

- Molecule 37 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	142	Total	C	N	O	S	0	0
			1125	718	200	203	4		

- Molecule 38 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	122	Total	C	N	O	S	0	0
			946	592	180	169	5		

- Molecule 39 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	146	Total	C	N	O	S	0	0
			1089	673	215	200	1		

- Molecule 40 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	137	Total	C	N	O	S	0	0
			1088	687	210	185	6		

- Molecule 41 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	119	Total	C	N	O	S	0	0
			942	590	186	163	3		

- Molecule 42 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	115	Total	C	N	O	S	0	0
			865	532	175	157	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	117	Total	C	N	O	S	0	0
			919	578	177	164			

- Molecule 44 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	117	Total	C	N	O	S	0	0
			934	589	197	146	2		

- Molecule 45 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	103	Total	C	N	O	S	0	0
			807	506	155	143	3		

- Molecule 46 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	109	Total	C	N	O	S	0	0
			826	514	158	150	4		

- Molecule 47 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	92	Total	C	N	O	S	0	0
			717	457	129	130	1		

- Molecule 48 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	t	103	Total	C	N	O		
			766	476	142	148	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	u	97	Total	C	N	O	S		
			760	477	143	139	1	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	78	Total	C	N	O	S		
			589	365	113	109	2	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	77	Total	C	N	O	S		
			632	395	130	105	2	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	62	Total	C	N	O	S		
			498	308	96	93	1	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	58	Total	C	N	O	S		
			463	286	88	85	4	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	54	Total	C	N	O	S		
			447	265	100	81	1	0	0

- Molecule 55 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
55	1	1	Total 1	K 1	0
55	3	1	Total 1	K 1	0
55	A	47	Total 47	K 47	0
55	L	1	Total 1	K 1	0
55	a	111	Total 111	K 111	0
55	b	1	Total 1	K 1	0
55	c	4	Total 4	K 4	0
55	d	2	Total 2	K 2	0
55	t	1	Total 1	K 1	0

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total 1	Zn 1	0
56	4	1	Total 1	Zn 1	0

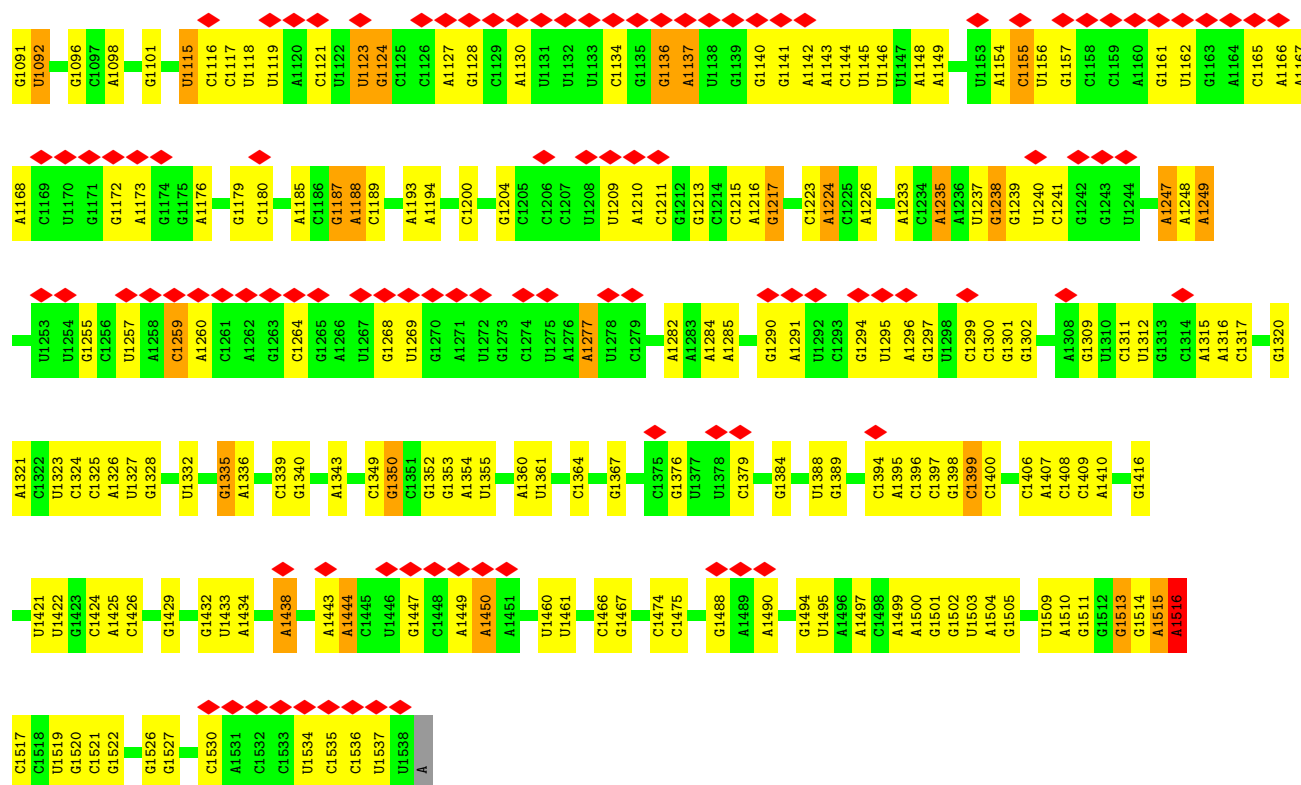
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	95	Total 95	Mg 95	0
57	J	1	Total 1	Mg 1	0
57	M	1	Total 1	Mg 1	0
57	X	1	Total 1	Mg 1	0
57	a	251	Total 251	Mg 251	0
57	b	5	Total 5	Mg 5	0
57	c	1	Total 1	Mg 1	0

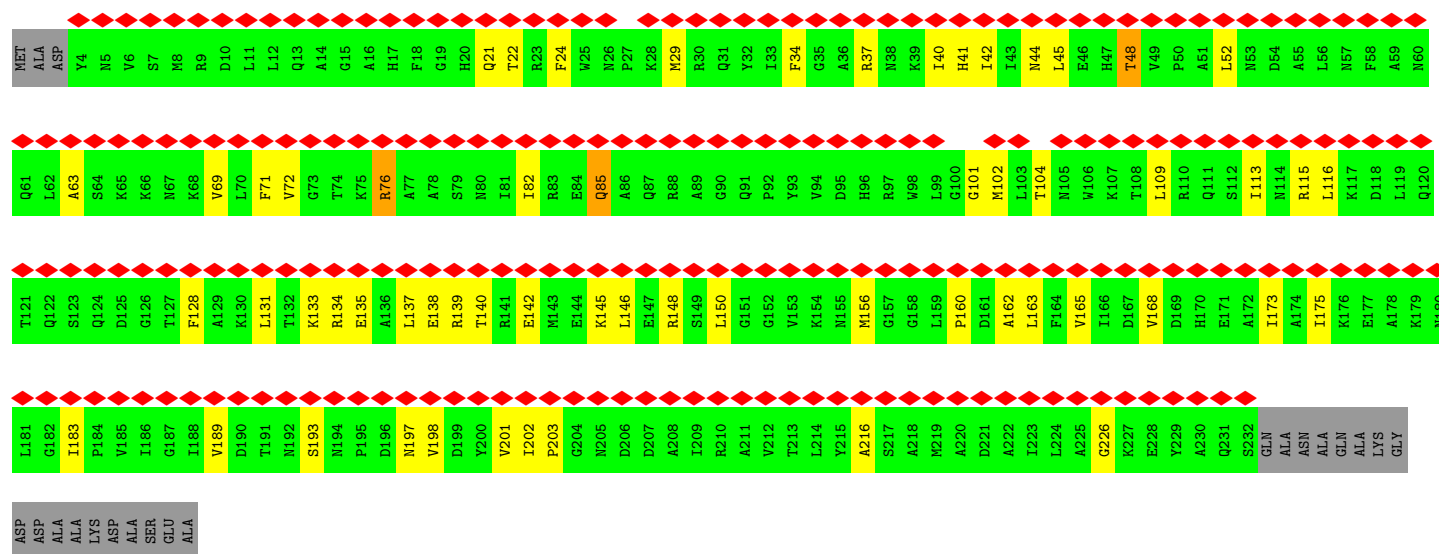
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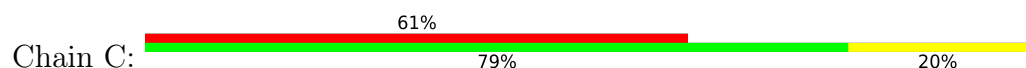
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57	k	1	Total 1	Mg 1	0
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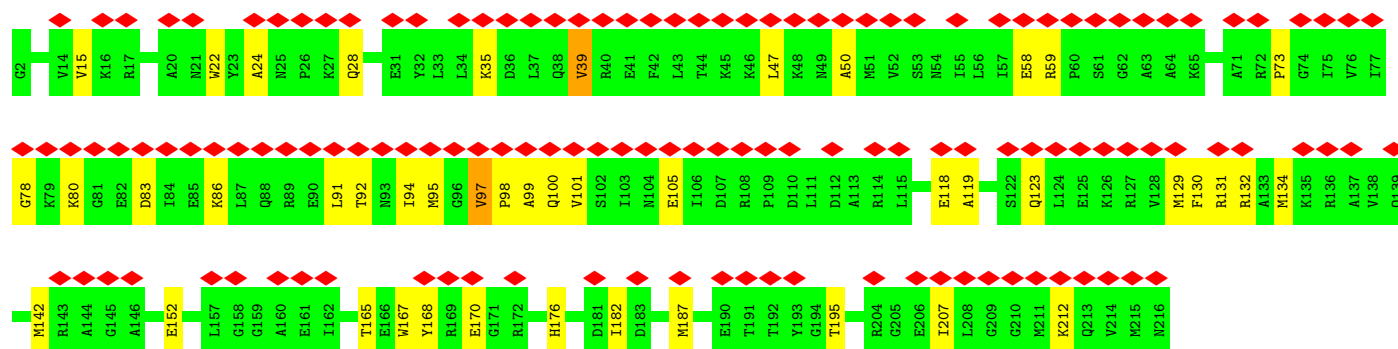


• Molecule 7: Small ribosomal subunit protein uS2

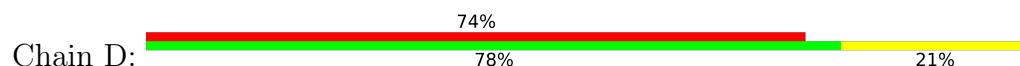
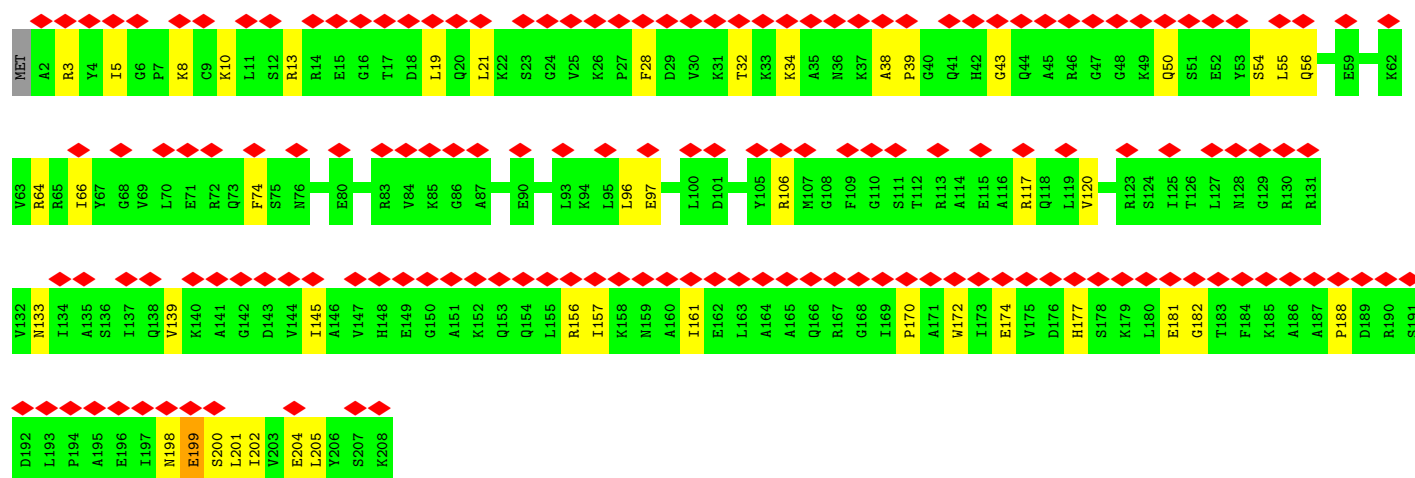


• Molecule 8: Small ribosomal subunit protein uS3

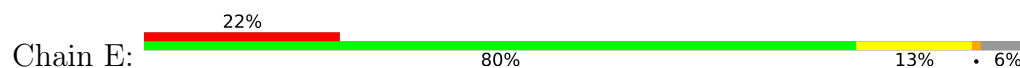
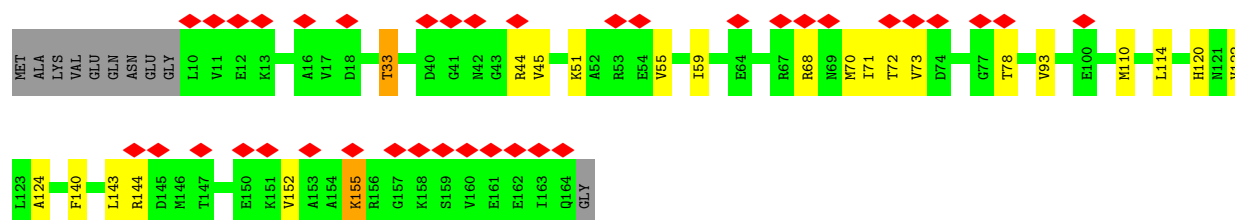




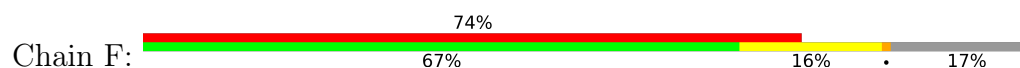
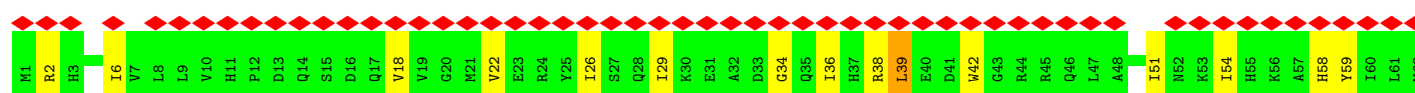
• Molecule 9: Small ribosomal subunit protein uS4

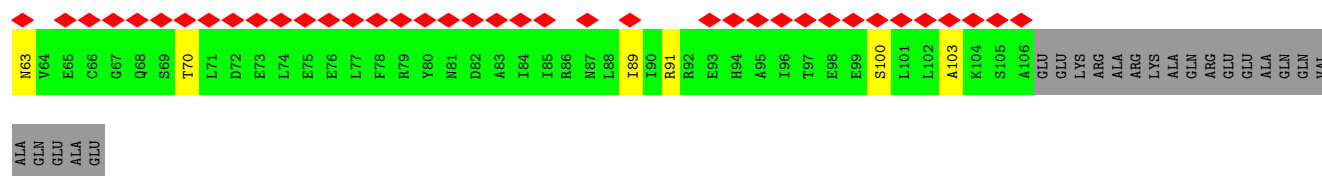


• Molecule 10: Small ribosomal subunit protein uS5

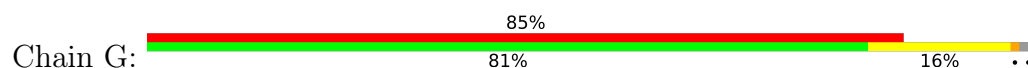
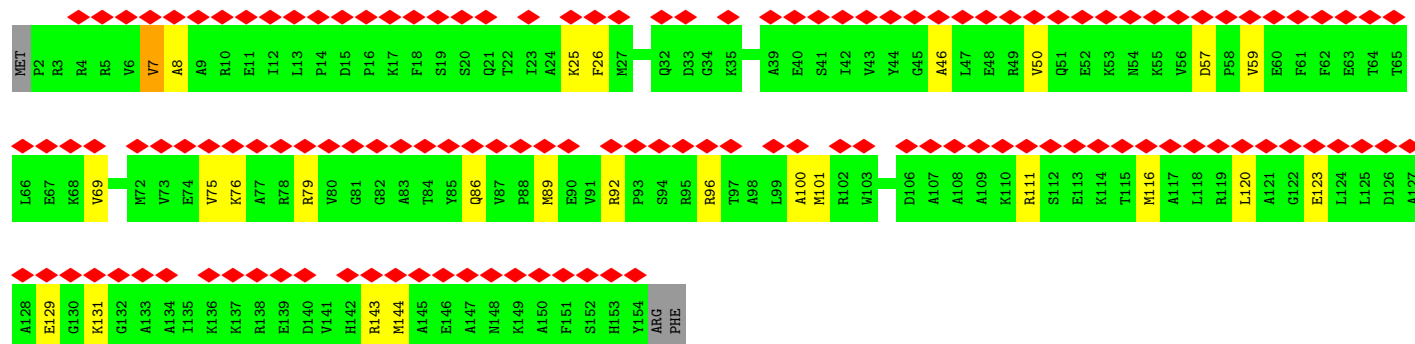


• Molecule 11: Small ribosomal subunit protein bS6

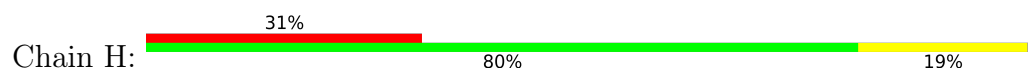
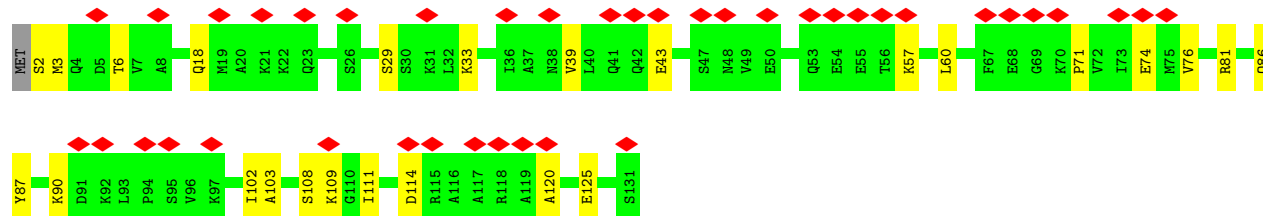




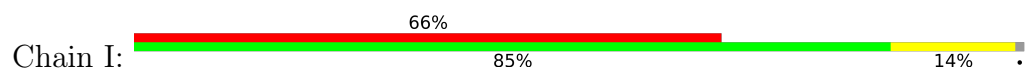
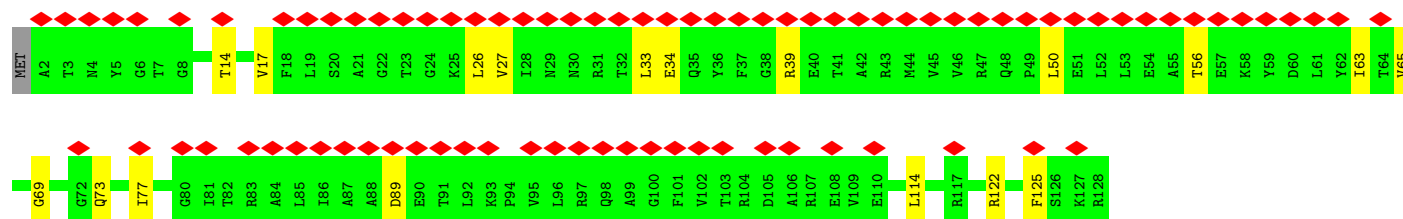
• Molecule 12: Small ribosomal subunit protein uS7



• Molecule 13: Small ribosomal subunit protein uS8

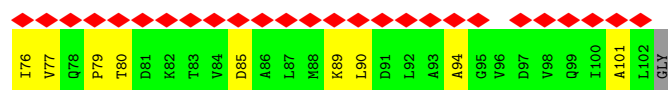


• Molecule 14: Small ribosomal subunit protein uS9

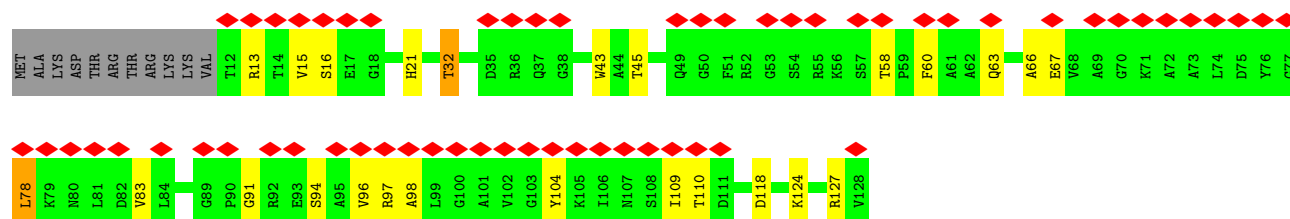


• Molecule 15: Small ribosomal subunit protein uS10

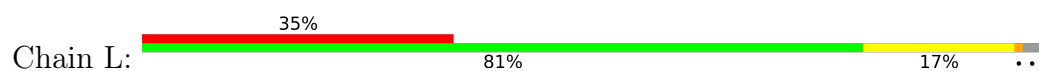
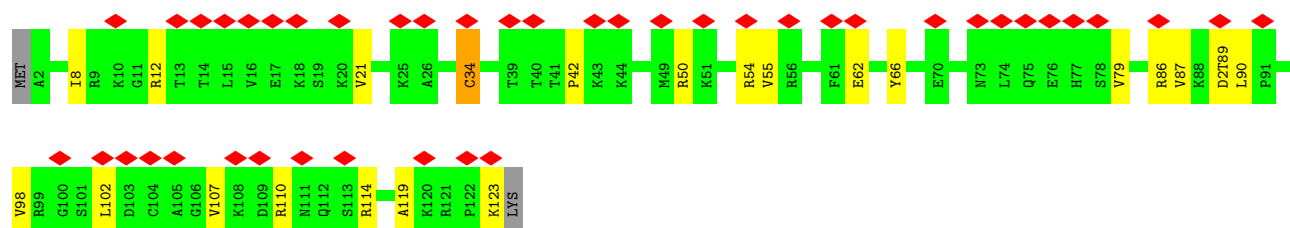




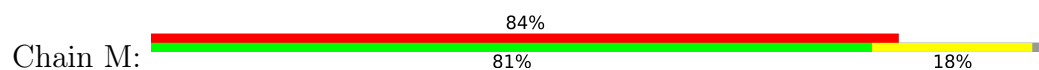
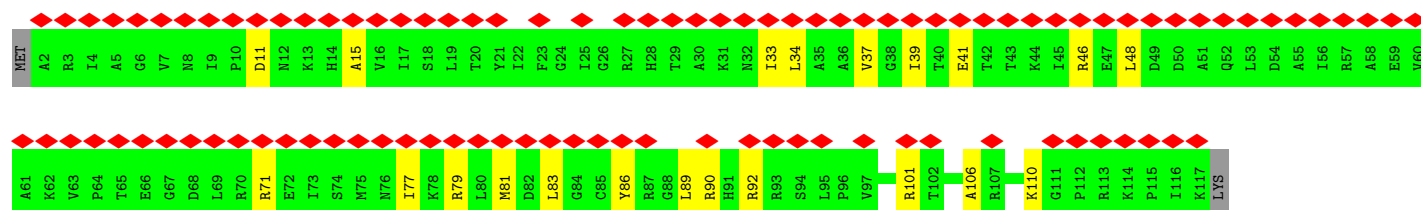
- Molecule 16: Small ribosomal subunit protein uS11



- Molecule 17: Small ribosomal subunit protein uS12



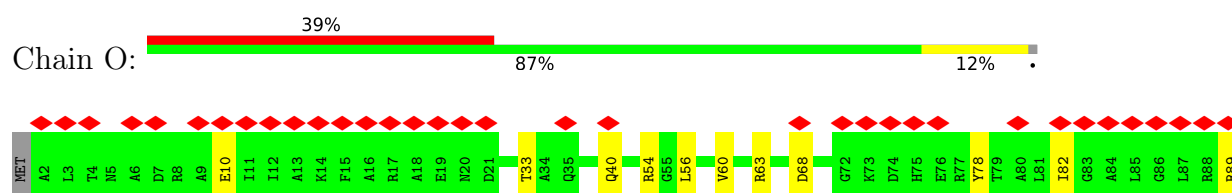
- Molecule 18: Small ribosomal subunit protein uS13



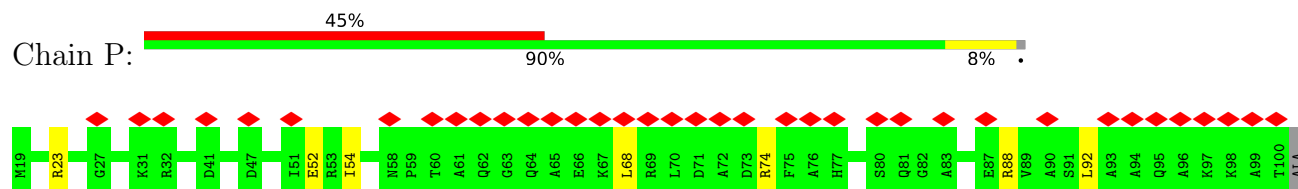
- Molecule 19: Small ribosomal subunit protein uS14



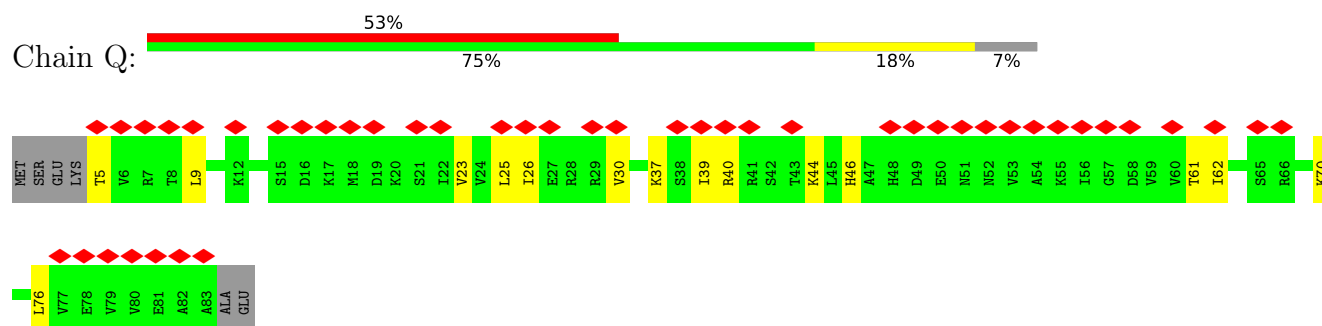
- Molecule 20: Small ribosomal subunit protein uS15



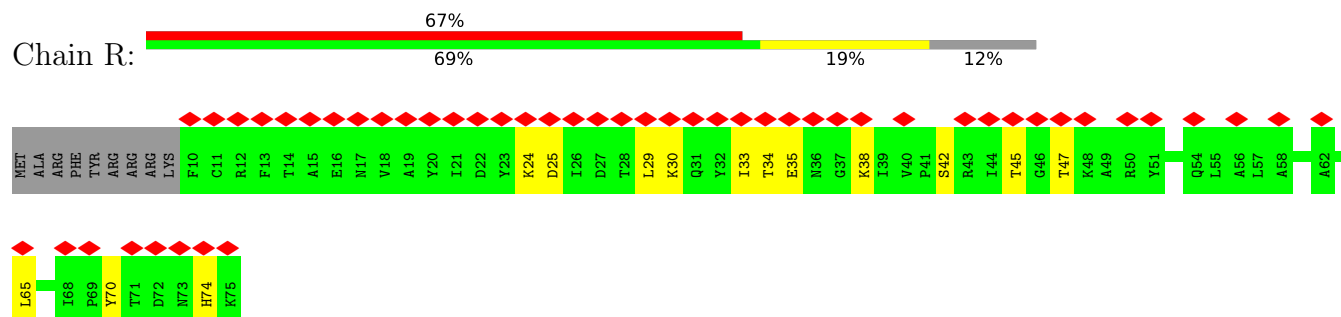
- Molecule 21: Small ribosomal subunit protein bS16



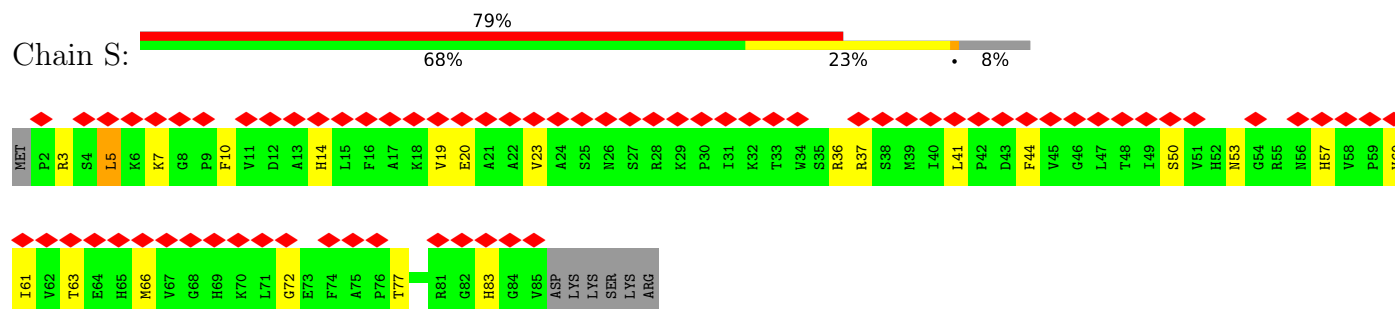
- Molecule 22: Small ribosomal subunit protein uS17



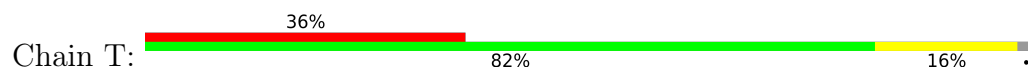
- Molecule 23: Small ribosomal subunit protein bS18

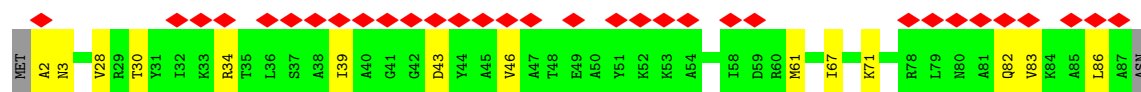


- Molecule 24: Small ribosomal subunit protein uS19

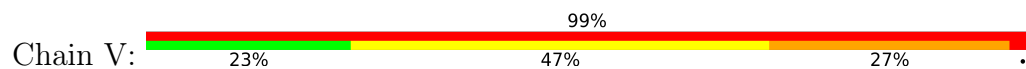
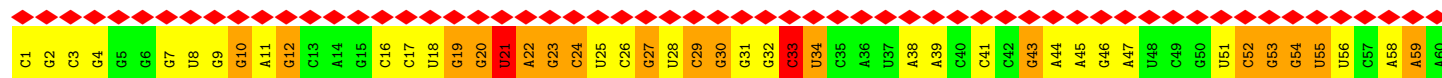


- Molecule 25: Small ribosomal subunit protein bS20

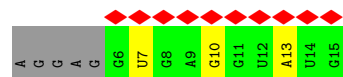




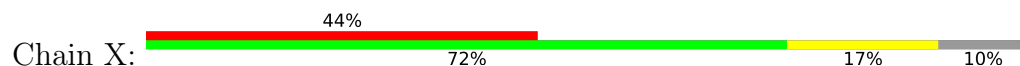
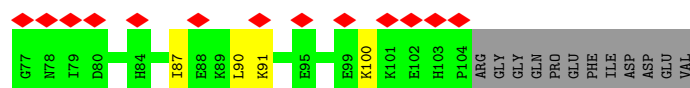
• Molecule 26: tRNA (77-MER)



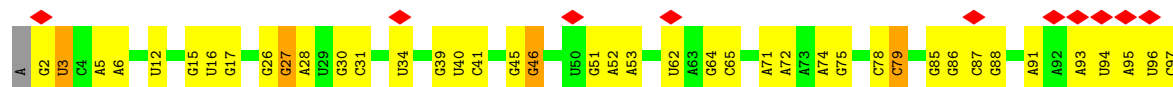
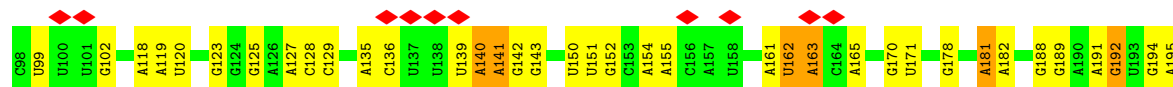
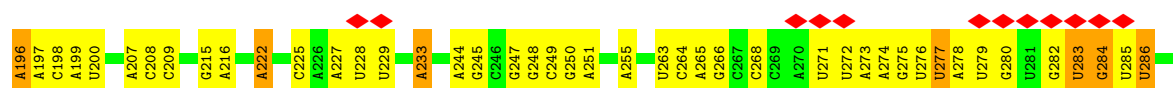
• Molecule 27: non-Stop mRNA



• Molecule 28: Putative ribosomal subunit interface protein

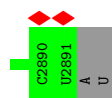


• Molecule 29: 23S rRNA (2890-MER)

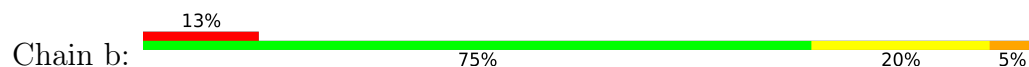




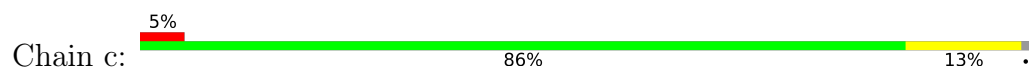
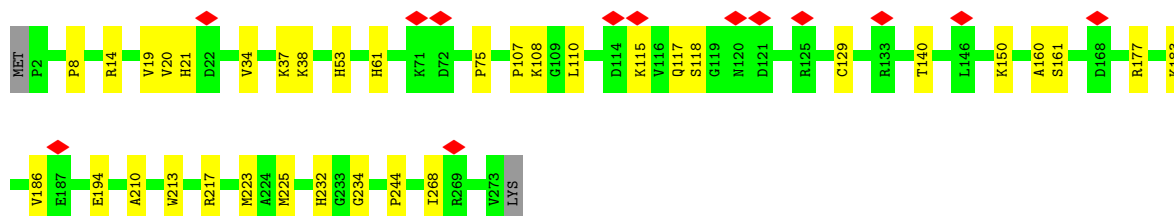
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A1907	A1908	U1912	C1913	A1917	G1918	G1919	U1920	A1921	C1922	A1925	A1926	A1927	U1928	U1929	U1932	G1938	G1939	G1943	U1944	U1952	G1953	C1956	A1959	U1960	G1961	U1971	U1980	G1981	U1982	U1983	U1984	C1985	C1986	A2003	A2004	U2011	C2012	G2013	C2014	U2015	A2019	A2020	G2021	A2022	U2023														
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U2107	A2108	G2109	G2110	U2111	G2112	G2113	G2114	A2115	G2116	G2117	C2118	U2119	U2120	U2121	G2122	A2123	A2124	G2125	C2126	U2127	G2128	G2129	A2130	A2131	C2132	G2133	C2134	U2135	A2136	G2137	U2138	U2139	C2140	C2141	A2142	G2143	U2144	G2145	G2146	A2147	G2148	C2149	C2150	G2151	U2152	C2153	C2154	U2155	U2156	G2157	A2158	A2159	A2160	U2161	A2162	C2163	C2164	A2165	C2166
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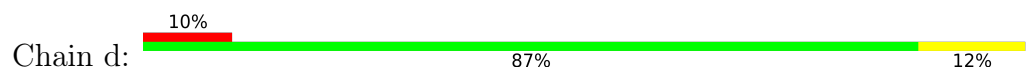
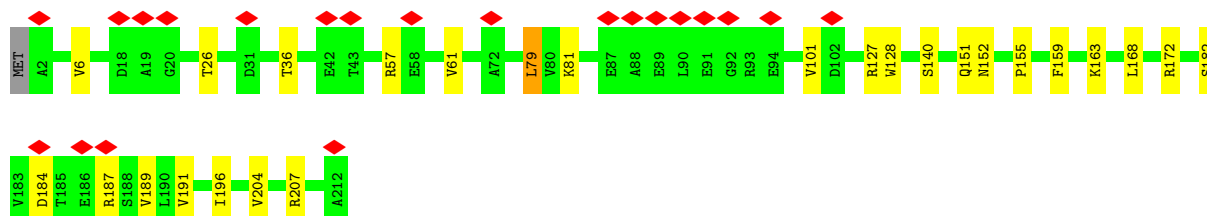
- Molecule 30: 5S rRNA



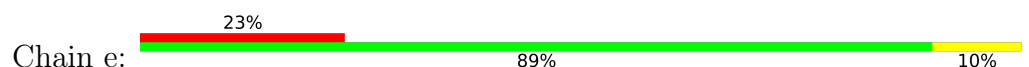
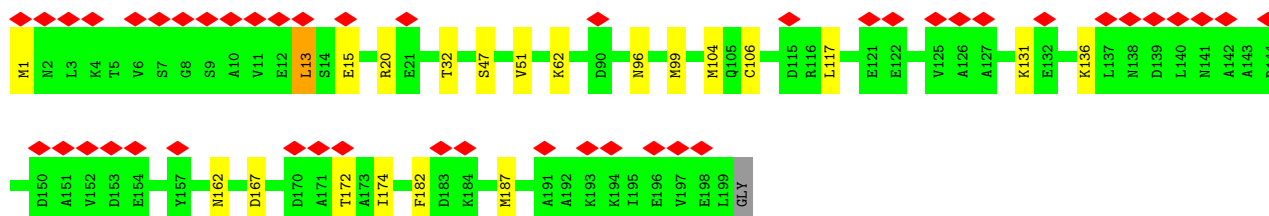
- Molecule 31: Large ribosomal subunit protein uL2



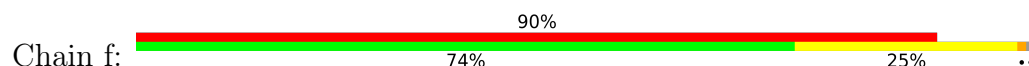
- Molecule 32: Large ribosomal subunit protein uL3

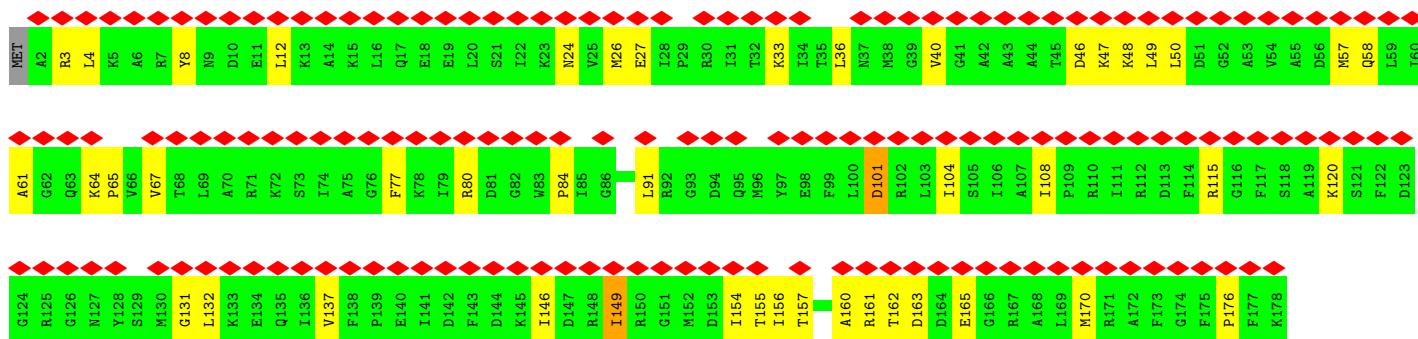


- Molecule 33: Large ribosomal subunit protein uL4

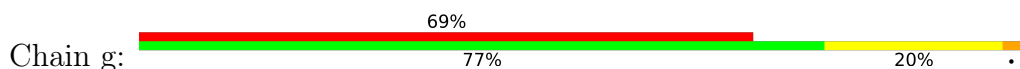


- Molecule 34: Large ribosomal subunit protein uL5

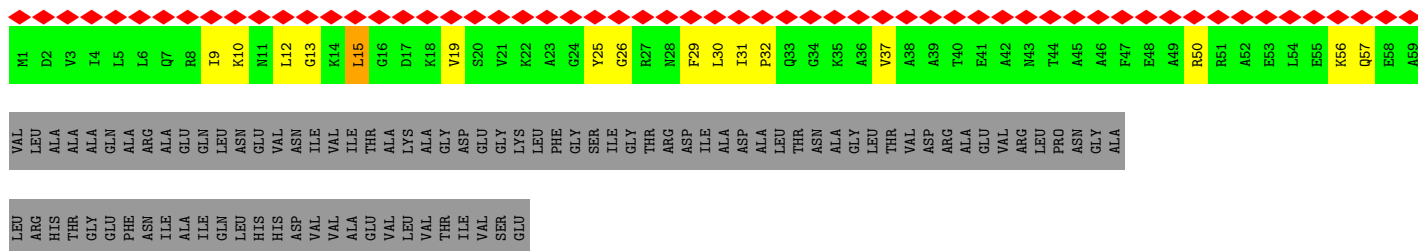




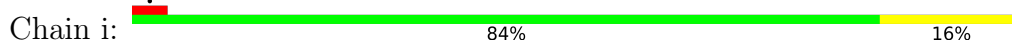
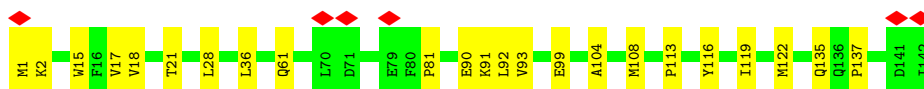
• Molecule 35: Large ribosomal subunit protein uL6



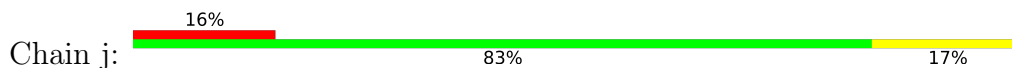
• Molecule 36: Large ribosomal subunit protein bL9

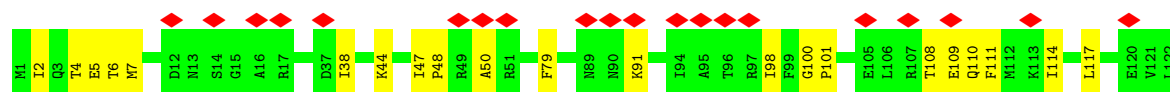


• Molecule 37: Large ribosomal subunit protein uL13

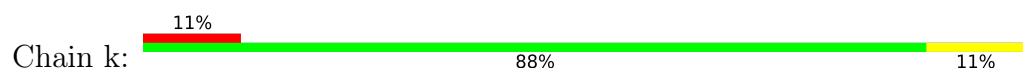
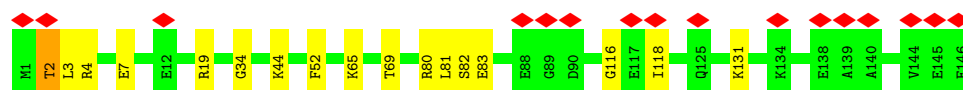


• Molecule 38: Large ribosomal subunit protein uL14

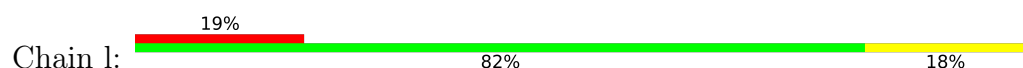
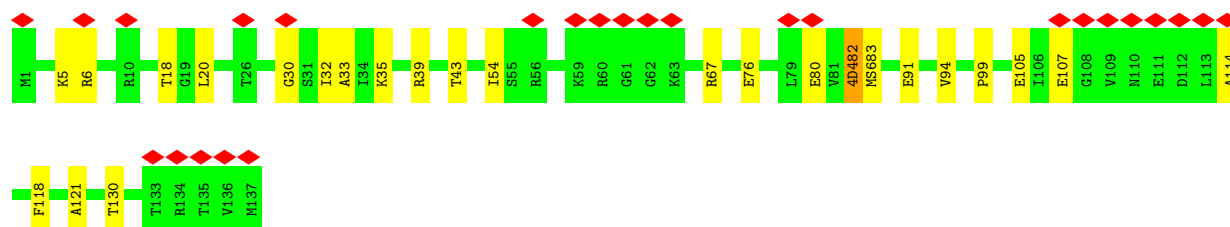




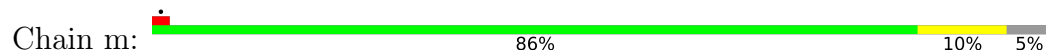
- Molecule 39: Large ribosomal subunit protein uL15



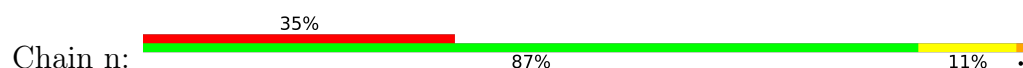
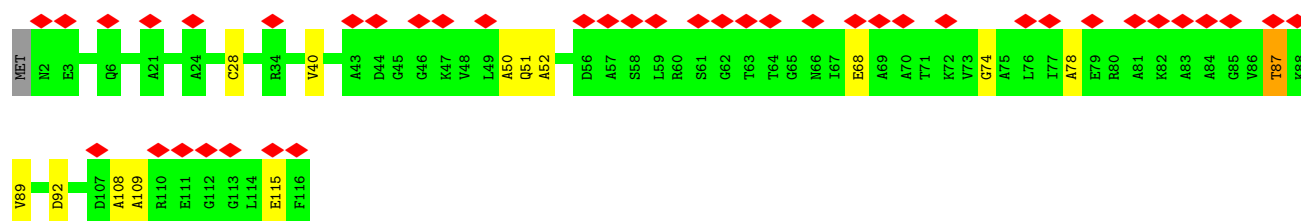
- Molecule 40: Large ribosomal subunit protein uL16



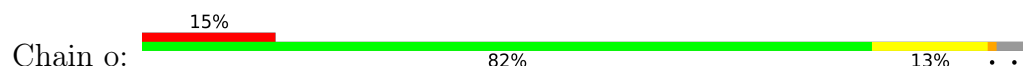
- Molecule 41: Large ribosomal subunit protein bL17



- Molecule 42: Large ribosomal subunit protein uL18



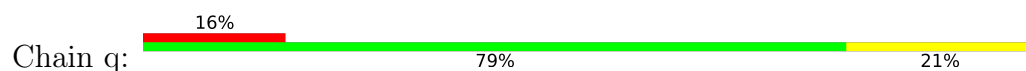
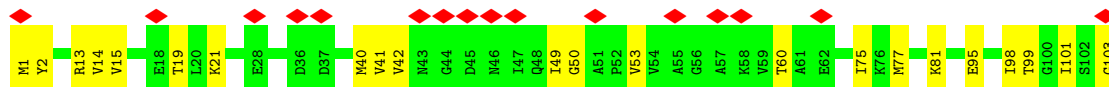
- Molecule 43: Large ribosomal subunit protein bL19



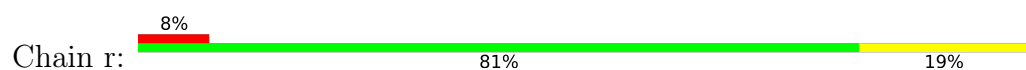
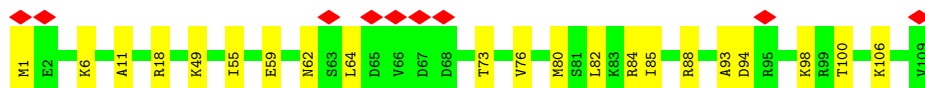
- Molecule 44: Large ribosomal subunit protein bL20



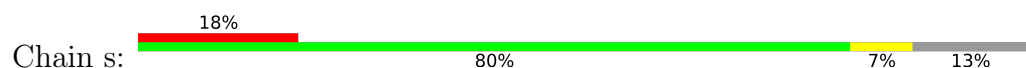
- Molecule 45: Large ribosomal subunit protein bL21



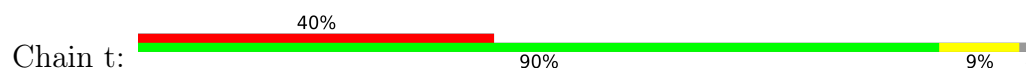
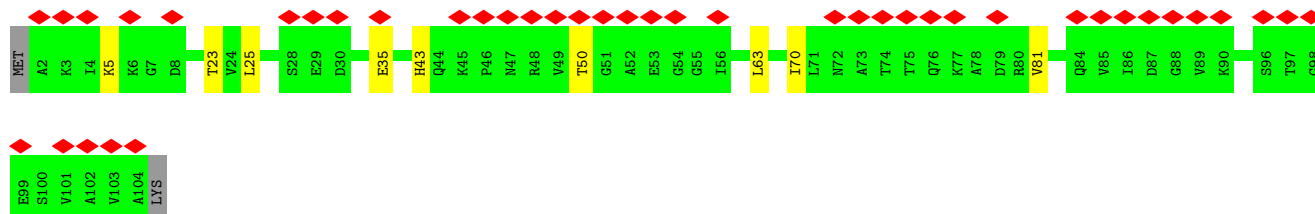
- Molecule 46: Large ribosomal subunit protein uL22



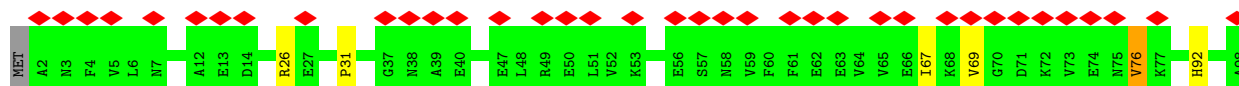
- Molecule 47: Large ribosomal subunit protein uL23



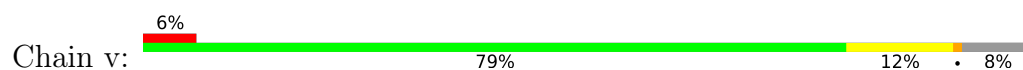
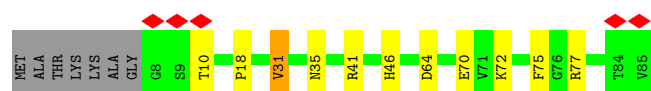
- Molecule 48: Large ribosomal subunit protein uL24



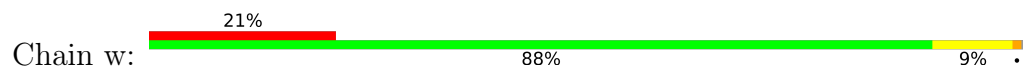
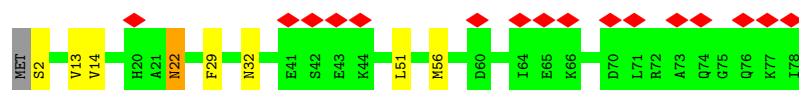
- Molecule 49: Large ribosomal subunit protein bL25



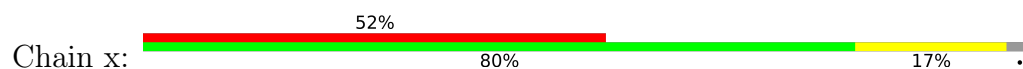
- Molecule 50: Large ribosomal subunit protein bL27



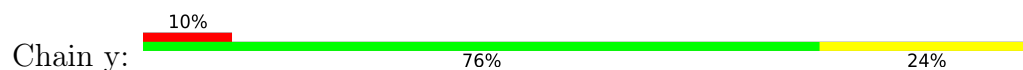
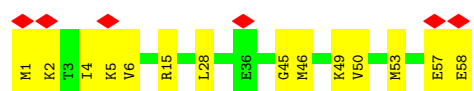
- Molecule 51: Large ribosomal subunit protein bL28



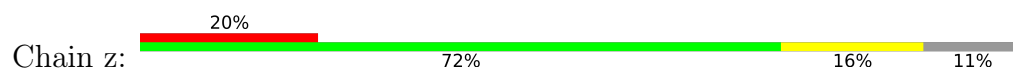
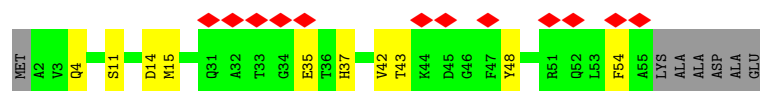
- Molecule 52: Large ribosomal subunit protein uL29



- Molecule 53: Large ribosomal subunit protein uL30



- Molecule 54: Large ribosomal subunit protein bL32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	225259	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 ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.429	Depositor
Minimum map value	-1.526	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.077	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, MS6, MEQ, UR3, 2MG, 6MZ, K, 2MA, OMC, ZN, 4D4, OMG, PSU, H2U, 3TD, IAS, OMU, D2T, 5MC, MA6, G7M, 4OC, MG, 4SU, 1MG

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	0	0.21	0/434	0.38	0/573
2	1	0.24	0/367	0.30	0/481
3	2	0.22	0/515	0.34	0/678
4	3	0.22	0/296	0.27	0/389
5	4	0.13	0/561	0.37	0/750
6	A	0.46	0/36630	0.75	5/57129 (0.0%)
7	B	0.13	0/1832	0.30	0/2474
8	C	0.16	0/1714	0.30	0/2304
9	D	0.15	0/1653	0.29	0/2213
10	E	0.20	0/1141	0.31	0/1537
11	F	0.15	0/893	0.28	0/1204
12	G	0.13	0/1229	0.27	0/1647
13	H	0.17	0/993	0.28	0/1331
14	I	0.16	0/1006	0.28	0/1346
15	J	0.17	0/811	0.30	0/1096
16	K	0.17	0/869	0.33	0/1175
17	L	0.18	0/949	0.38	0/1270
18	M	0.14	0/922	0.29	0/1237
19	N	0.16	0/803	0.29	0/1071
20	O	0.18	0/715	0.30	0/958
21	P	0.16	0/655	0.29	0/879
22	Q	0.16	0/628	0.32	0/847
23	R	0.16	0/555	0.32	0/749
24	S	0.15	0/675	0.32	0/912
25	T	0.19	0/669	0.24	0/892
26	V	0.29	0/1724	0.81	1/2687 (0.0%)
27	W	0.29	0/245	0.77	0/381
28	X	0.16	0/858	0.26	0/1150
29	a	0.59	0/68962	0.79	32/107563 (0.0%)
30	b	0.46	0/2739	0.76	0/4266
31	c	0.23	0/2152	0.33	0/2891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	d	0.23	0/1580	0.33	0/2127
33	e	0.22	0/1532	0.31	0/2068
34	f	0.20	0/1415	0.44	0/1895
35	g	0.15	0/1346	0.29	0/1818
36	h	0.12	0/461	0.35	0/616
37	i	0.23	0/1151	0.35	0/1551
38	j	0.22	0/956	0.30	0/1286
39	k	0.21	0/1097	0.31	0/1461
40	l	0.20	0/1084	0.30	0/1448
41	m	0.23	0/956	0.35	0/1282
42	n	0.19	0/873	0.32	0/1167
43	o	0.20	0/931	0.31	0/1249
44	p	0.24	0/947	0.32	0/1262
45	q	0.22	0/818	0.35	0/1094
46	r	0.22	0/831	0.36	0/1113
47	s	0.19	0/723	0.26	0/967
48	t	0.16	0/770	0.26	0/1034
49	u	0.19	0/770	0.34	0/1036
50	v	0.22	0/597	0.29	0/798
51	w	0.22	0/642	0.29	0/856
52	x	0.17	0/499	0.26	0/662
53	y	0.23	0/468	0.39	0/624
54	z	0.23	0/453	0.32	0/604
All	All	0.47	0/155095	0.69	38/232098 (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	l	0	1

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	a	1301	U	C2-N1-C1'	7.27	126.43	117.70
6	A	415	C	N3-C2-O2	-6.72	117.20	121.90
29	a	875	U	N3-C2-O2	-6.44	117.69	122.20
29	a	781	U	C2-N1-C1'	6.26	125.21	117.70
29	a	520	A	C2-N3-C4	-6.07	107.57	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
40	l	82	4D4	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	427	0	462	7	0
2	1	363	0	401	5	0
3	2	509	0	566	8	0
4	3	295	0	325	8	0
5	4	552	0	552	10	0
6	A	32947	0	16585	343	0
7	B	1801	0	1814	33	0
8	C	1690	0	1774	24	0
9	D	1631	0	1691	29	0
10	E	1129	0	1174	12	0
11	F	878	0	878	14	0
12	G	1210	0	1255	19	0
13	H	985	0	1047	14	0
14	I	995	0	1053	14	0
15	J	801	0	832	18	0
16	K	861	0	873	16	0
17	L	947	0	997	14	0
18	M	912	0	975	16	0
19	N	792	0	833	23	0
20	O	705	0	712	6	0
21	P	644	0	655	5	0
22	Q	621	0	665	8	0
23	R	545	0	556	11	0
24	S	657	0	675	20	0
25	T	663	0	715	9	0
26	V	1644	0	842	42	0
27	W	219	0	108	2	0
28	X	841	0	824	11	0
29	a	61984	0	31148	551	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	b	2450	0	1241	14	0
31	c	2111	0	2176	23	0
32	d	1573	0	1611	14	0
33	e	1511	0	1566	12	0
34	f	1395	0	1450	33	0
35	g	1327	0	1386	21	0
36	h	458	0	480	7	0
37	i	1125	0	1148	14	0
38	j	946	0	1007	14	0
39	k	1089	0	1158	12	0
40	l	1088	0	1150	16	0
41	m	942	0	987	7	0
42	n	865	0	905	6	0
43	o	919	0	973	12	0
44	p	934	0	997	7	0
45	q	807	0	842	12	0
46	r	826	0	894	13	0
47	s	717	0	777	4	0
48	t	766	0	816	4	0
49	u	760	0	783	4	0
50	v	589	0	592	6	0
51	w	632	0	667	8	0
52	x	498	0	537	6	0
53	y	463	0	488	7	0
54	z	447	0	435	5	0
55	1	1	0	0	0	0
55	3	1	0	0	0	0
55	A	47	0	0	0	0
55	L	1	0	0	0	0
55	a	111	0	0	2	0
55	b	1	0	0	0	0
55	c	4	0	0	0	0
55	d	2	0	0	0	0
55	t	1	0	0	1	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
57	A	95	0	0	0	0
57	J	1	0	0	0	0
57	M	1	0	0	0	0
57	X	1	0	0	0	0
57	a	251	0	0	2	0
57	b	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	c	1	0	0	0	0
57	d	1	0	0	0	0
57	k	1	0	0	0	0
57	p	1	0	0	0	0
57	v	1	0	0	0	0
57	z	1	0	0	0	0
All	All	144017	0	96053	1458	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 6.

The worst 5 of 1458 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)
29:a:1059:A:H1'	29:a:1086:A:H4'	1.54	0.89
26:V:51:U:H3	26:V:65:G:H1	0.92	0.88
29:a:1925:A:H2	29:a:1932:U:H3	1.20	0.86
6:A:74:G:H8	6:A:93:A:H62	1.22	0.85
43:o:30:VAL:HG22	43:o:47:GLU:HG3	1.59	0.84

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	
1	0	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
2	1	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
3	2	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
4	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
5	4	69/74 (93%)	61 (88%)	8 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	B	227/250 (91%)	212 (93%)	14 (6%)	1 (0%)	30	49
8	C	213/215 (99%)	207 (97%)	6 (3%)	0	100	100
9	D	205/208 (99%)	198 (97%)	7 (3%)	0	100	100
10	E	153/165 (93%)	152 (99%)	1 (1%)	0	100	100
11	F	104/127 (82%)	102 (98%)	2 (2%)	0	100	100
12	G	151/156 (97%)	141 (93%)	10 (7%)	0	100	100
13	H	128/131 (98%)	123 (96%)	5 (4%)	0	100	100
14	I	125/128 (98%)	115 (92%)	10 (8%)	0	100	100
15	J	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
16	K	113/128 (88%)	105 (93%)	8 (7%)	0	100	100
17	L	119/124 (96%)	114 (96%)	5 (4%)	0	100	100
18	M	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
19	N	98/101 (97%)	91 (93%)	7 (7%)	0	100	100
20	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
21	P	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
22	Q	77/85 (91%)	76 (99%)	1 (1%)	0	100	100
23	R	64/75 (85%)	64 (100%)	0	0	100	100
24	S	82/91 (90%)	81 (99%)	1 (1%)	0	100	100
25	T	84/88 (96%)	84 (100%)	0	0	100	100
28	X	102/116 (88%)	100 (98%)	2 (2%)	0	100	100
31	c	270/274 (98%)	260 (96%)	10 (4%)	0	100	100
32	d	208/212 (98%)	202 (97%)	5 (2%)	1 (0%)	24	43
33	e	197/200 (98%)	196 (100%)	1 (0%)	0	100	100
34	f	175/178 (98%)	158 (90%)	17 (10%)	0	100	100
35	g	173/177 (98%)	167 (96%)	5 (3%)	1 (1%)	21	38
36	h	58/148 (39%)	53 (91%)	5 (9%)	0	100	100
37	i	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
38	j	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
39	k	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
40	l	133/137 (97%)	131 (98%)	2 (2%)	0	100	100
41	m	117/125 (94%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	n	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
43	o	115/122 (94%)	113 (98%)	2 (2%)	0	100	100
44	p	115/119 (97%)	115 (100%)	0	0	100	100
45	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
46	r	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
47	s	90/106 (85%)	89 (99%)	1 (1%)	0	100	100
48	t	101/105 (96%)	98 (97%)	3 (3%)	0	100	100
49	u	95/98 (97%)	90 (95%)	5 (5%)	0	100	100
50	v	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
51	w	75/78 (96%)	75 (100%)	0	0	100	100
52	x	60/64 (94%)	59 (98%)	1 (2%)	0	100	100
53	y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
54	z	52/61 (85%)	50 (96%)	2 (4%)	0	100	100
All	All	5571/5937 (94%)	5384 (97%)	184 (3%)	3 (0%)	49	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	B	128	PHE
32	d	152	ASN
35	g	86	LYS

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	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	36/36 (100%)	35 (97%)	1 (3%)	38	66
3	2	52/53 (98%)	52 (100%)	0	100	100
4	3	33/33 (100%)	32 (97%)	1 (3%)	36	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	60/63 (95%)	60 (100%)	0	100	100
7	B	188/200 (94%)	177 (94%)	11 (6%)	18	37
8	C	175/175 (100%)	167 (95%)	8 (5%)	24	48
9	D	170/171 (99%)	167 (98%)	3 (2%)	51	77
10	E	113/120 (94%)	109 (96%)	4 (4%)	32	58
11	F	95/111 (86%)	93 (98%)	2 (2%)	47	74
12	G	125/128 (98%)	123 (98%)	2 (2%)	55	79
13	H	108/109 (99%)	104 (96%)	4 (4%)	30	57
14	I	99/100 (99%)	97 (98%)	2 (2%)	48	75
15	J	89/91 (98%)	85 (96%)	4 (4%)	24	49
16	K	87/97 (90%)	84 (97%)	3 (3%)	32	60
17	L	103/105 (98%)	101 (98%)	2 (2%)	50	76
18	M	96/98 (98%)	96 (100%)	0	100	100
19	N	81/82 (99%)	78 (96%)	3 (4%)	30	57
20	O	71/72 (99%)	68 (96%)	3 (4%)	26	52
21	P	63/63 (100%)	63 (100%)	0	100	100
22	Q	71/76 (93%)	67 (94%)	4 (6%)	19	39
23	R	58/66 (88%)	57 (98%)	1 (2%)	53	78
24	S	71/78 (91%)	68 (96%)	3 (4%)	26	52
25	T	65/67 (97%)	63 (97%)	2 (3%)	35	62
28	X	92/102 (90%)	90 (98%)	2 (2%)	45	73
31	c	218/220 (99%)	216 (99%)	2 (1%)	70	87
32	d	165/166 (99%)	159 (96%)	6 (4%)	31	58
33	e	155/155 (100%)	151 (97%)	4 (3%)	40	68
34	f	146/147 (99%)	141 (97%)	5 (3%)	32	60
35	g	140/142 (99%)	134 (96%)	6 (4%)	26	51
36	h	45/112 (40%)	41 (91%)	4 (9%)	9	20
37	i	118/118 (100%)	117 (99%)	1 (1%)	73	88
38	j	103/103 (100%)	103 (100%)	0	100	100
39	k	108/108 (100%)	106 (98%)	2 (2%)	50	76
40	l	111/111 (100%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	m	96/101 (95%)	96 (100%)	0	100	100
42	n	84/85 (99%)	81 (96%)	3 (4%)	31	58
43	o	99/102 (97%)	97 (98%)	2 (2%)	48	75
44	p	85/86 (99%)	85 (100%)	0	100	100
45	q	84/84 (100%)	83 (99%)	1 (1%)	63	83
46	r	88/88 (100%)	88 (100%)	0	100	100
47	s	78/87 (90%)	78 (100%)	0	100	100
48	t	83/85 (98%)	80 (96%)	3 (4%)	31	58
49	u	79/80 (99%)	77 (98%)	2 (2%)	42	69
50	v	60/64 (94%)	56 (93%)	4 (7%)	15	31
51	w	69/70 (99%)	67 (97%)	2 (3%)	37	65
52	x	54/55 (98%)	52 (96%)	2 (4%)	30	57
53	y	54/54 (100%)	53 (98%)	1 (2%)	50	76
54	z	46/50 (92%)	44 (96%)	2 (4%)	26	51
All	All	4616/4816 (96%)	4499 (98%)	117 (2%)	42	69

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	R	25	ASP
51	w	2	SER
32	d	140	SER
50	v	70	GLU
43	o	36	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
36	h	11	ASN
39	k	71	GLN
54	z	4	GLN
36	h	57	GLN
37	i	67	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	V	76/77 (98%)	35 (46%)	1 (1%)
27	W	9/15 (60%)	1 (11%)	0
29	a	2889/2893 (99%)	540 (18%)	0
30	b	114/115 (99%)	15 (13%)	0
6	A	1534/1537 (99%)	275 (17%)	13 (0%)
All	All	4622/4637 (99%)	866 (18%)	14 (0%)

5 of 866 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	6	C
6	A	9	A
6	A	10	A
6	A	11	G
6	A	24	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	876	C
6	A	989	U
26	V	20	G
6	A	1187	G
6	A	1449	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

39 non-standard protein/DNA/RNA residues are 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
29	PSU	a	2569	29	18,21,22	2.14	8 (44%)	22,30,33	1.98	5 (22%)
26	PSU	V	56	26	18,21,22	1.91	7 (38%)	22,30,33	1.80	3 (13%)
32	MEQ	d	153	32	8,9,10	0.85	0	5,10,12	0.76	0
29	G7M	a	2058	29	23,26,27	2.17	5 (21%)	35,39,42	1.88	7 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
40	4D4	l	82	40	9,11,12	0.79	0	8,13,15	1.66	2 (25%)
29	OMG	a	2240	29,55	23,26,27	2.34	6 (26%)	33,38,41	1.88	10 (30%)
29	PSU	a	945	29	18,21,22	2.08	7 (38%)	22,30,33	1.84	3 (13%)
26	OMC	V	33	26	19,22,23	1.76	3 (15%)	26,31,34	0.96	2 (7%)
6	5MC	A	964	6	18,22,23	1.90	6 (33%)	26,32,35	1.35	2 (7%)
29	3TD	a	1904	29	18,22,23	2.72	7 (38%)	22,32,35	1.74	2 (9%)
29	H2U	a	2438	29	18,21,22	4.09	5 (27%)	21,30,33	5.05	7 (33%)
29	1MG	a	736	29	22,26,27	2.47	6 (27%)	33,39,42	2.00	7 (21%)
40	MS6	l	83	40	5,7,8	0.60	0	2,7,9	1.73	1 (50%)
26	4SU	V	8	26	18,21,22	3.75	8 (44%)	26,30,33	2.17	4 (15%)
6	MA6	A	1516	6	23,26,27	1.23	3 (13%)	34,38,41	2.24	9 (26%)
29	PSU	a	1900	29	18,21,22	2.01	7 (38%)	22,30,33	1.82	3 (13%)
17	D2T	L	89	17	7,9,10	1.31	1 (14%)	6,11,13	1.46	1 (16%)
29	6MZ	a	2019	29	22,25,26	2.34	3 (13%)	30,36,39	2.41	9 (30%)
29	OMC	a	2487	29,57	19,22,23	1.75	3 (15%)	26,31,34	1.05	2 (7%)
29	PSU	a	2594	29	18,21,22	2.11	7 (38%)	22,30,33	1.84	3 (13%)
6	PSU	A	513	57,6	18,21,22	2.01	7 (38%)	22,30,33	1.86	4 (18%)
29	PSU	a	737	29,57	18,21,22	2.10	8 (44%)	22,30,33	1.84	3 (13%)
29	PSU	a	2493	29,55	18,21,22	2.08	7 (38%)	22,30,33	1.77	5 (22%)
6	UR3	A	1495	6	19,22,23	2.54	6 (31%)	26,32,35	1.32	2 (7%)
26	H2U	V	21	26	18,21,22	4.33	5 (27%)	21,30,33	4.86	7 (33%)
29	PSU	a	2446	29	18,21,22	2.16	7 (38%)	22,30,33	1.90	5 (22%)
6	2MG	A	963	6	23,26,27	2.56	4 (17%)	32,38,41	2.10	10 (31%)
16	IAS	K	118	16	5,6,8	1.89	1 (20%)	3,6,10	3.31	1 (33%)
29	OMU	a	2541	29	19,22,23	2.61	7 (36%)	26,31,34	1.76	5 (19%)
6	MA6	A	1515	6	23,26,27	1.21	3 (13%)	34,38,41	2.24	9 (26%)
29	2MA	a	2492	29,55	22,25,26	1.34	3 (13%)	33,37,40	2.04	7 (21%)
6	2MG	A	1513	6	23,26,27	2.57	6 (26%)	32,38,41	2.15	11 (34%)
29	2MG	a	2434	29	23,26,27	2.58	7 (30%)	32,38,41	2.04	10 (31%)
6	2MG	A	1204	55,6	23,26,27	2.57	5 (21%)	32,38,41	2.13	11 (34%)
6	G7M	A	524	55,6	23,26,27	2.15	5 (21%)	35,39,42	1.83	7 (20%)
26	5MU	V	55	26	19,22,23	2.35	7 (36%)	28,32,35	3.74	10 (35%)
6	4OC	A	1399	6	20,23,24	2.20	4 (20%)	26,32,35	1.07	2 (7%)
29	PSU	a	1906	29	18,21,22	2.04	7 (38%)	22,30,33	1.83	3 (13%)
29	5MU	a	1928	29,55	19,22,23	2.54	7 (36%)	28,32,35	3.75	10 (35%)

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
29	PSU	a	2569	29	-	0/7/25/26	0/2/2/2
26	PSU	V	56	26	-	0/7/25/26	0/2/2/2
32	MEQ	d	153	32	-	4/8/9/11	-
29	G7M	a	2058	29	-	2/7/25/26	0/3/3/3
40	4D4	l	82	40	-	3/11/12/14	-
29	OMG	a	2240	29,55	-	1/9/27/28	0/3/3/3
29	PSU	a	945	29	-	0/7/25/26	0/2/2/2
26	OMC	V	33	26	-	0/9/27/28	0/2/2/2
6	5MC	A	964	6	-	0/7/25/26	0/2/2/2
29	3TD	a	1904	29	-	0/7/25/26	0/2/2/2
29	H2U	a	2438	29	-	1/7/38/39	0/2/2/2
29	1MG	a	736	29	-	0/7/25/26	0/3/3/3
40	MS6	l	83	40	-	2/4/6/8	-
26	4SU	V	8	26	-	0/7/25/26	0/2/2/2
6	MA6	A	1516	6	-	1/11/29/30	0/3/3/3
29	PSU	a	1900	29	-	0/7/25/26	0/2/2/2
17	D2T	L	89	17	-	4/7/12/14	-
29	6MZ	a	2019	29	-	2/9/27/28	0/3/3/3
29	OMC	a	2487	29,57	-	0/9/27/28	0/2/2/2
29	PSU	a	2594	29	-	0/7/25/26	0/2/2/2
6	PSU	A	513	57,6	-	0/7/25/26	0/2/2/2
29	PSU	a	737	29,57	-	1/7/25/26	0/2/2/2
29	PSU	a	2493	29,55	-	2/7/25/26	0/2/2/2
6	UR3	A	1495	6	-	0/7/25/26	0/2/2/2
26	H2U	V	21	26	-	4/7/38/39	0/2/2/2
29	PSU	a	2446	29	-	0/7/25/26	0/2/2/2
6	2MG	A	963	6	-	0/9/27/28	0/3/3/3
16	IAS	K	118	16	-	2/3/5/8	-
29	OMU	a	2541	29	-	2/9/27/28	0/2/2/2
6	MA6	A	1515	6	-	0/11/29/30	0/3/3/3
29	2MA	a	2492	29,55	-	3/7/25/26	0/3/3/3
6	2MG	A	1513	6	-	0/9/27/28	0/3/3/3
29	2MG	a	2434	29	-	1/9/27/28	0/3/3/3
6	2MG	A	1204	55,6	-	2/9/27/28	0/3/3/3
6	G7M	A	524	55,6	-	3/7/25/26	0/3/3/3
26	5MU	V	55	26	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	4OC	A	1399	6	-	0/9/29/30	0/2/2/2
29	PSU	a	1906	29	-	0/7/25/26	0/2/2/2
29	5MU	a	1928	29,55	-	0/7/25/26	0/2/2/2

The worst 5 of 198 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	V	21	H2U	O4-C4	10.17	1.43	1.23
29	a	2438	H2U	O4-C4	9.84	1.43	1.23
29	a	2019	6MZ	C6-N6	9.55	1.44	1.34
6	A	1204	2MG	O6-C6	9.09	1.40	1.23
6	A	1513	2MG	O6-C6	8.99	1.40	1.23

The worst 5 of 204 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	a	2438	H2U	C4-N3-C2	-14.75	113.55	125.79
26	V	21	H2U	C4-N3-C2	-13.64	114.48	125.79
26	V	21	H2U	O2-C2-N1	-11.70	108.42	123.11
29	a	2438	H2U	O2-C2-N1	-10.62	109.78	123.11
29	a	1928	5MU	C4-N3-C2	-8.74	116.04	127.35

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	L	89	D2T	CA-CB-CG-OD1
17	L	89	D2T	CA-CB-CG-OD2
17	L	89	D2T	SB-CB-CG-OD2
32	d	153	MEQ	O-C-CA-CB
6	A	524	G7M	C3'-C4'-C5'-O5'

There are no ring outliers.

12 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	a	2240	OMG	1	0
26	V	33	OMC	5	0
29	a	1904	3TD	1	0
29	a	2438	H2U	1	0
6	A	1516	MA6	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	a	2019	6MZ	2	0
26	V	21	H2U	2	0
29	a	2541	OMU	2	0
6	A	1515	MA6	1	0
6	A	1513	2MG	1	0
26	V	55	5MU	1	0
6	A	1399	4OC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 531 ligands modelled in this entry, 531 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1530:C	O3'	1531:A	P	4.72

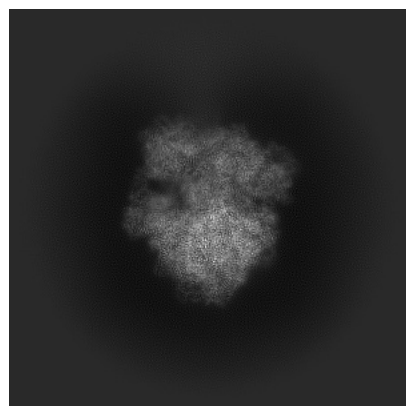
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55260. These allow visual inspection of the internal detail of the map and identification of artifacts.

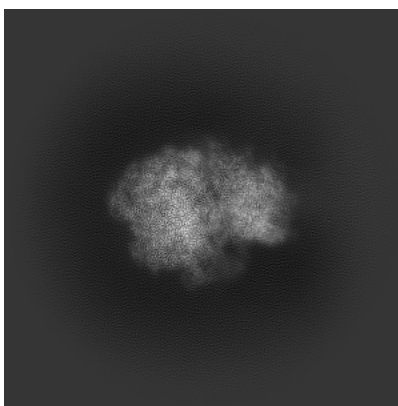
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

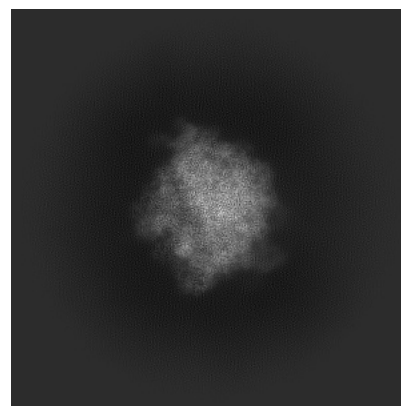
6.1.1 Primary map



X

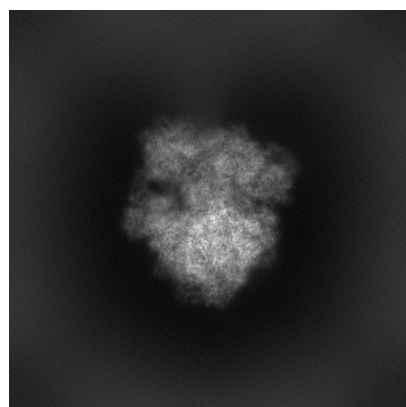


Y

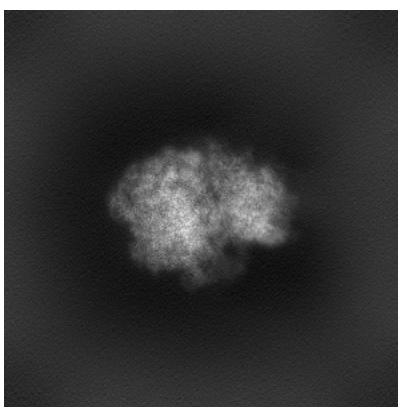


Z

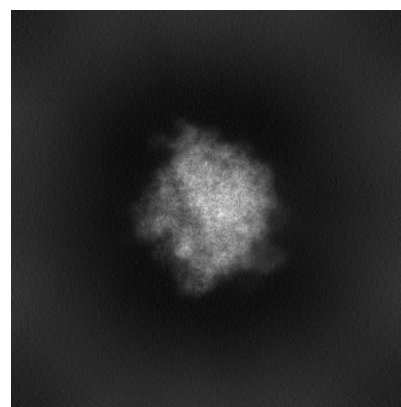
6.1.2 Raw map



X



Y

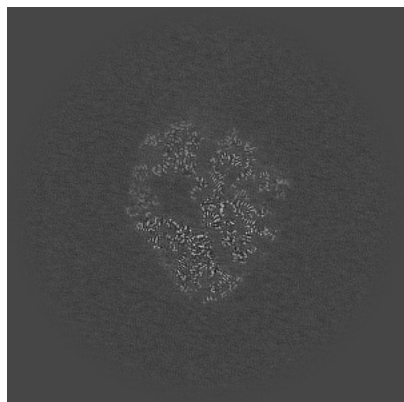


Z

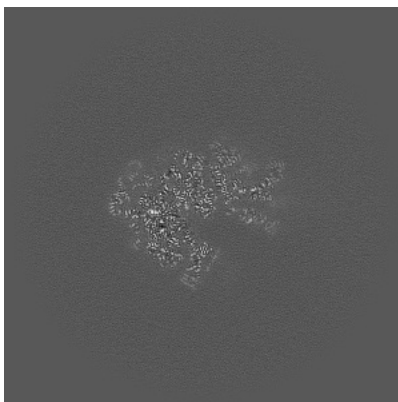
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

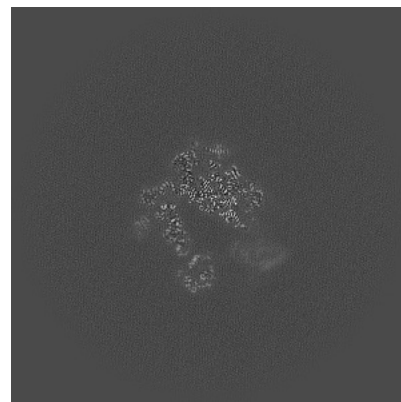
6.2.1 Primary map



X Index: 256

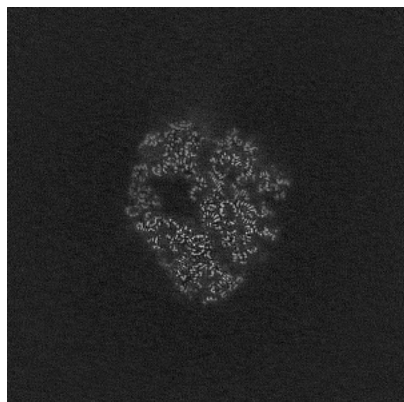


Y Index: 256

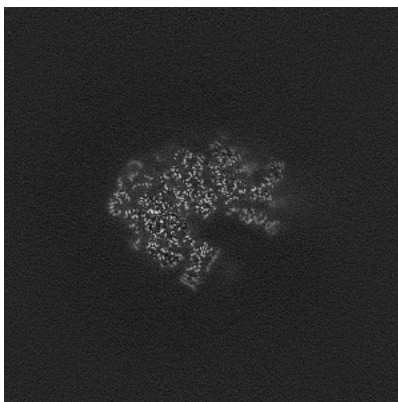


Z Index: 256

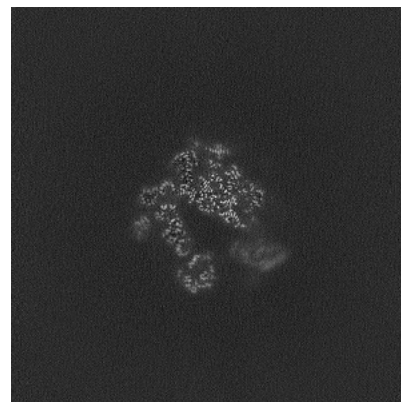
6.2.2 Raw map



X Index: 256



Y Index: 256

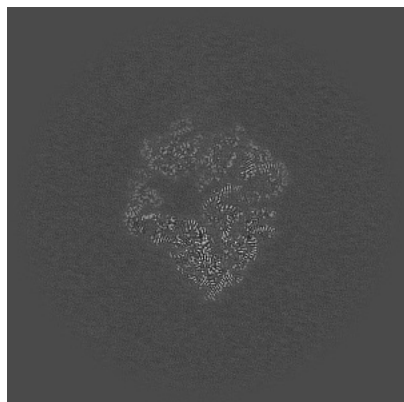


Z Index: 256

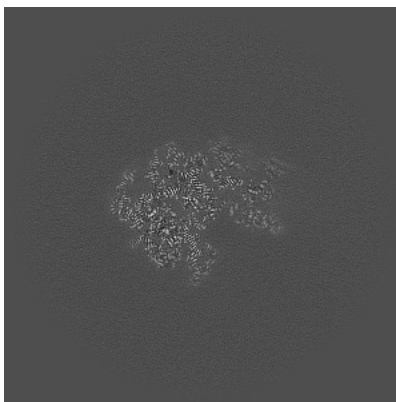
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

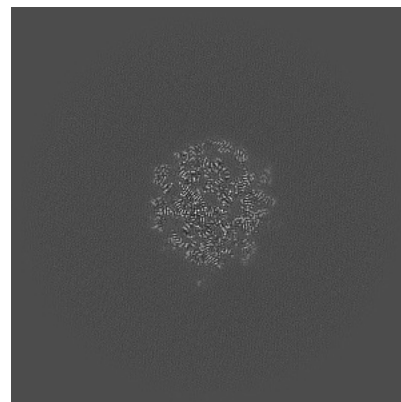
6.3.1 Primary map



X Index: 248

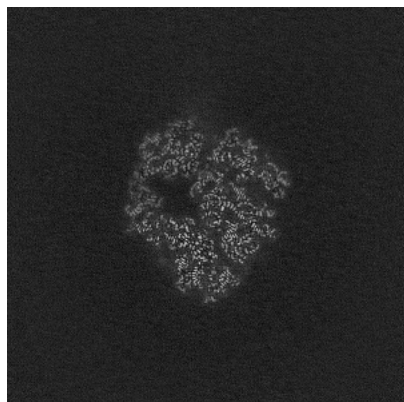


Y Index: 262

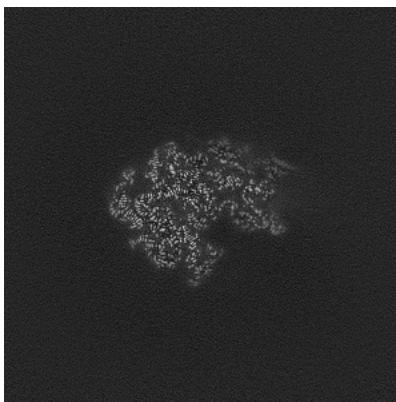


Z Index: 216

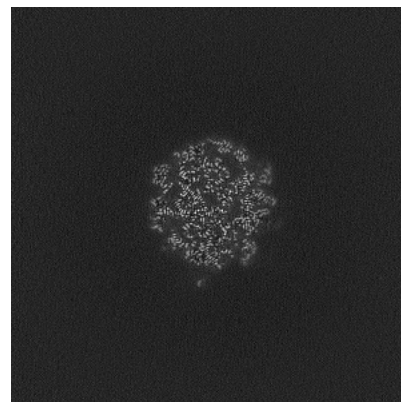
6.3.2 Raw map



X Index: 253



Y Index: 263

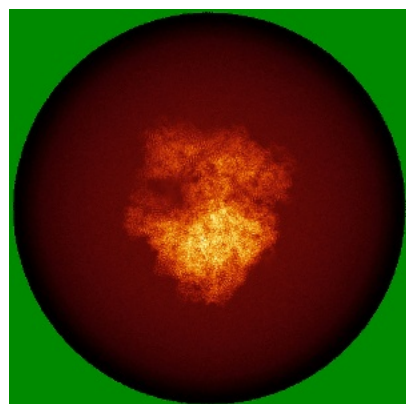


Z Index: 216

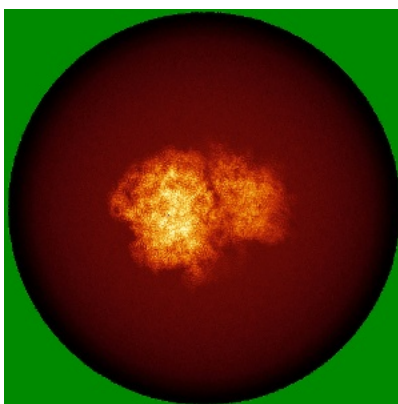
The images above show the largest variance slices of the map in three orthogonal directions.

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

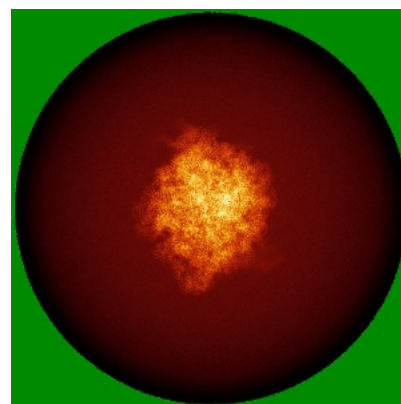
6.4.1 Primary map



X

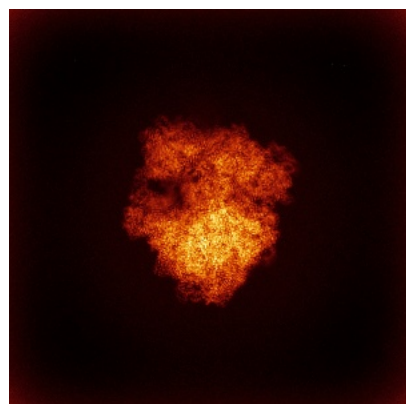


Y

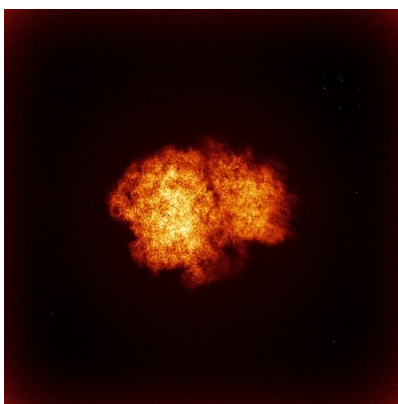


Z

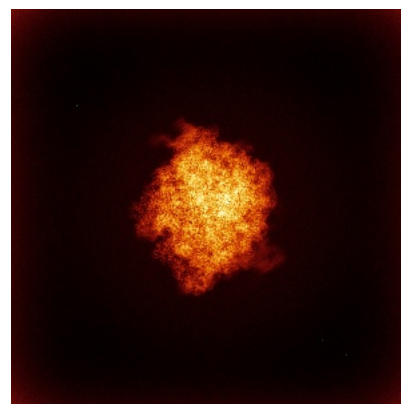
6.4.2 Raw map



X



Y

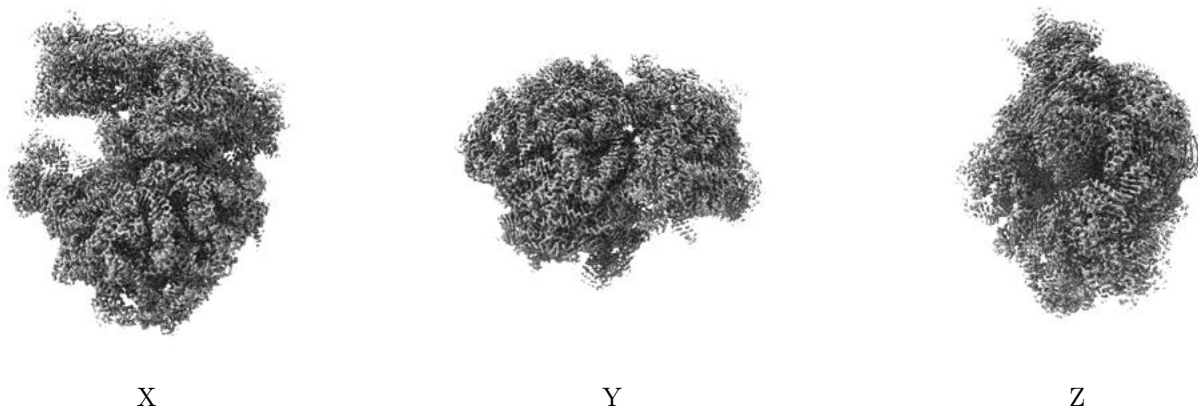


Z

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 0.55. 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.

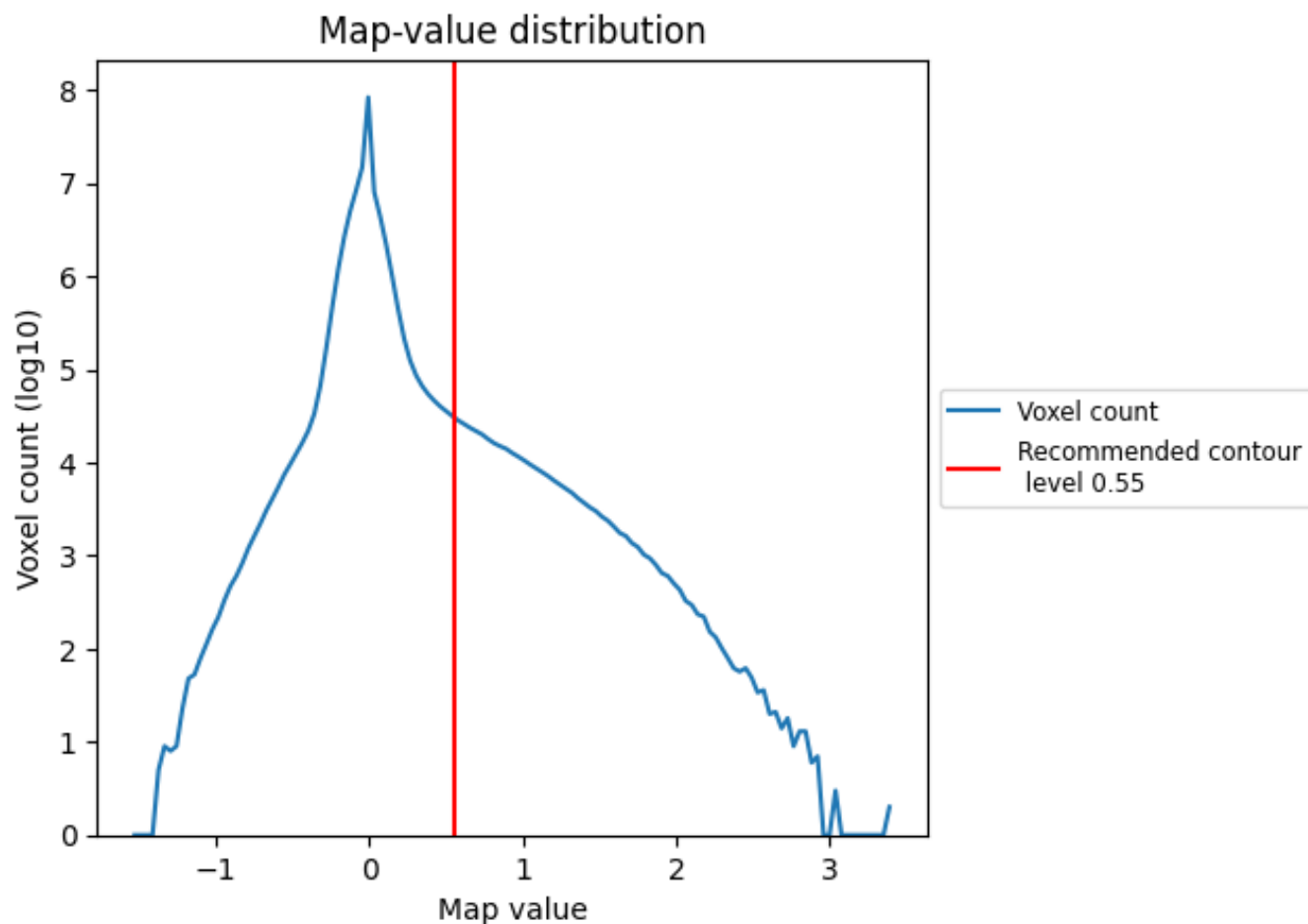
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

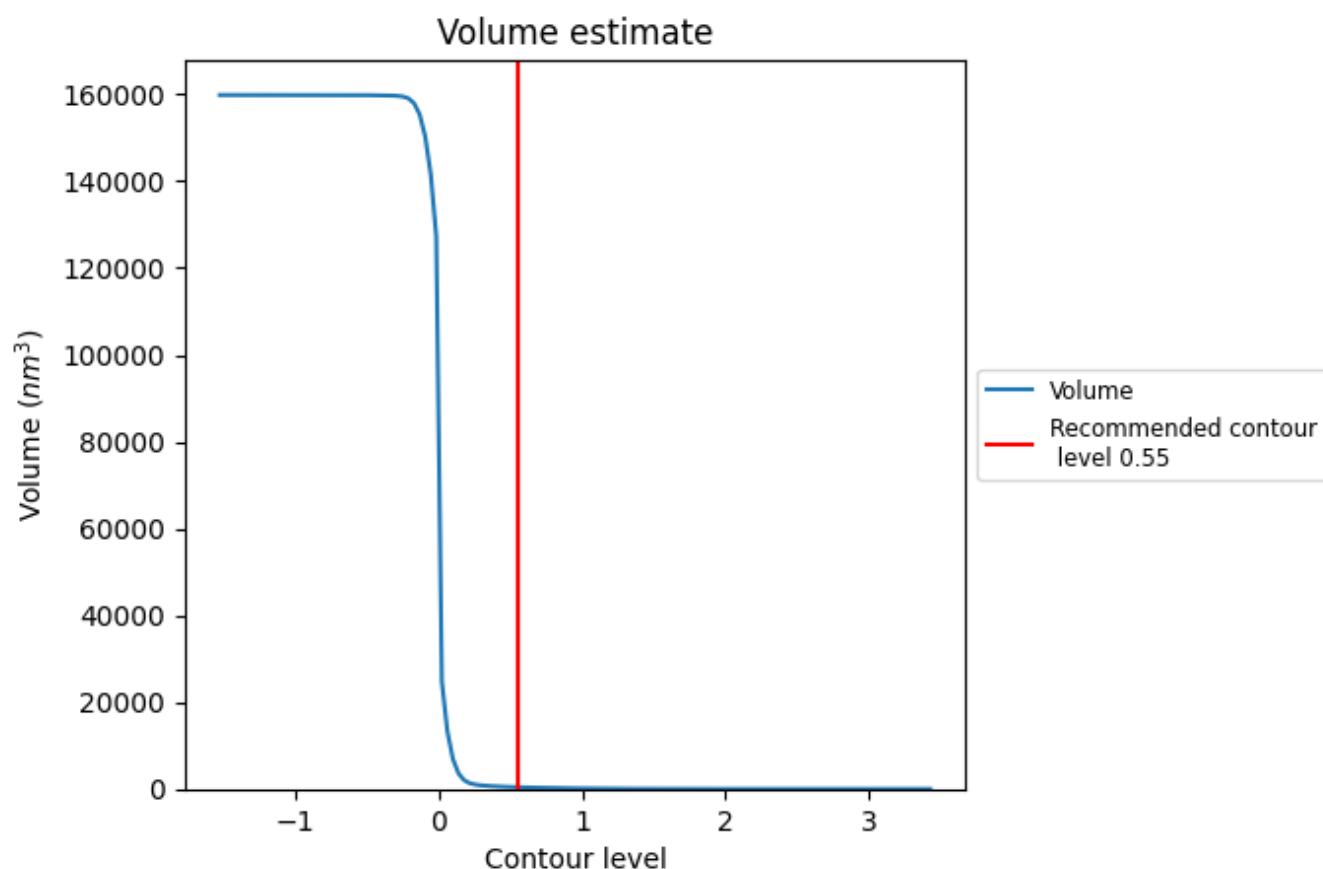
This section contains the results of statistical analysis of the map.

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.

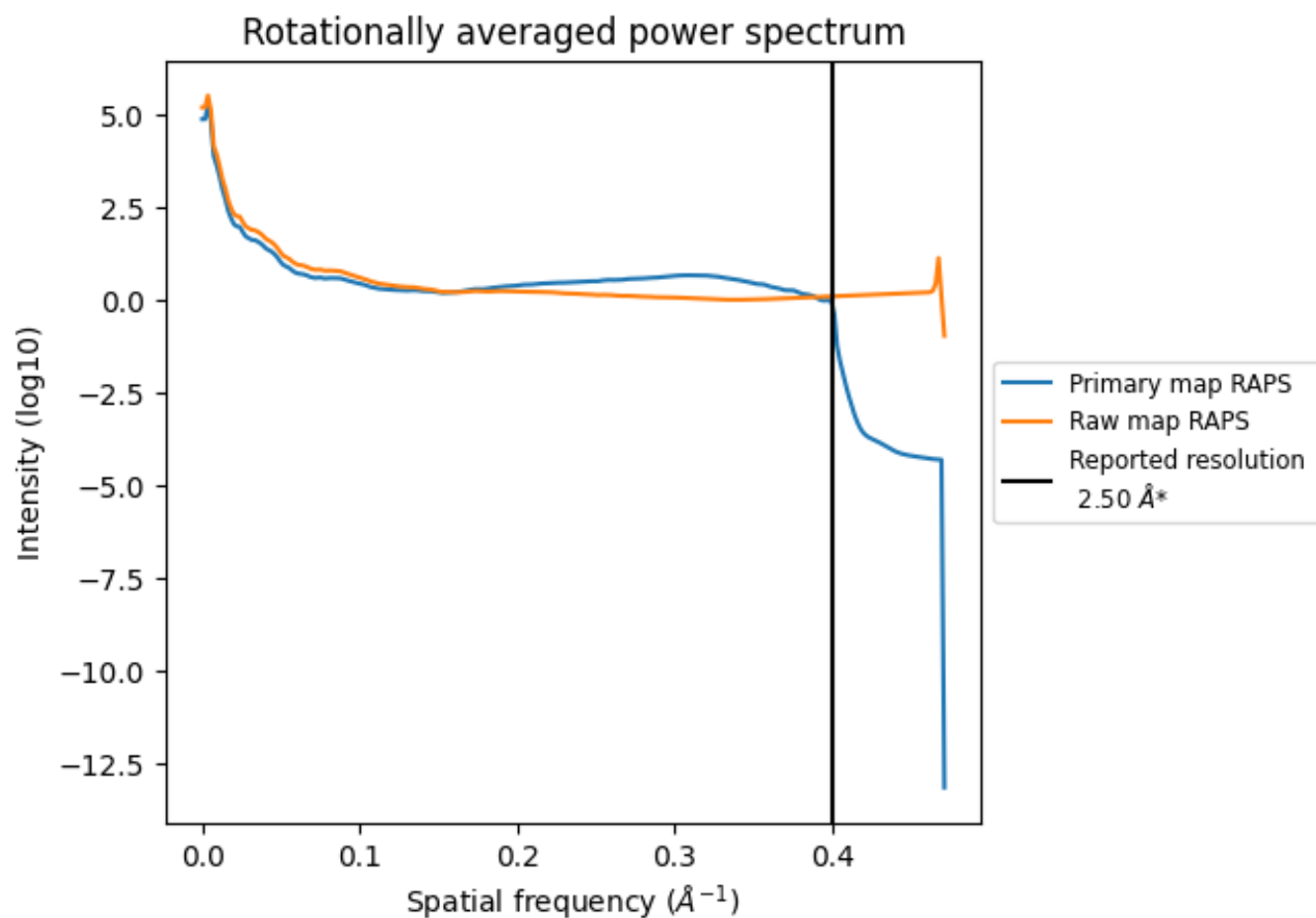
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 397 nm³; this corresponds to an approximate mass of 359 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 ⓘ

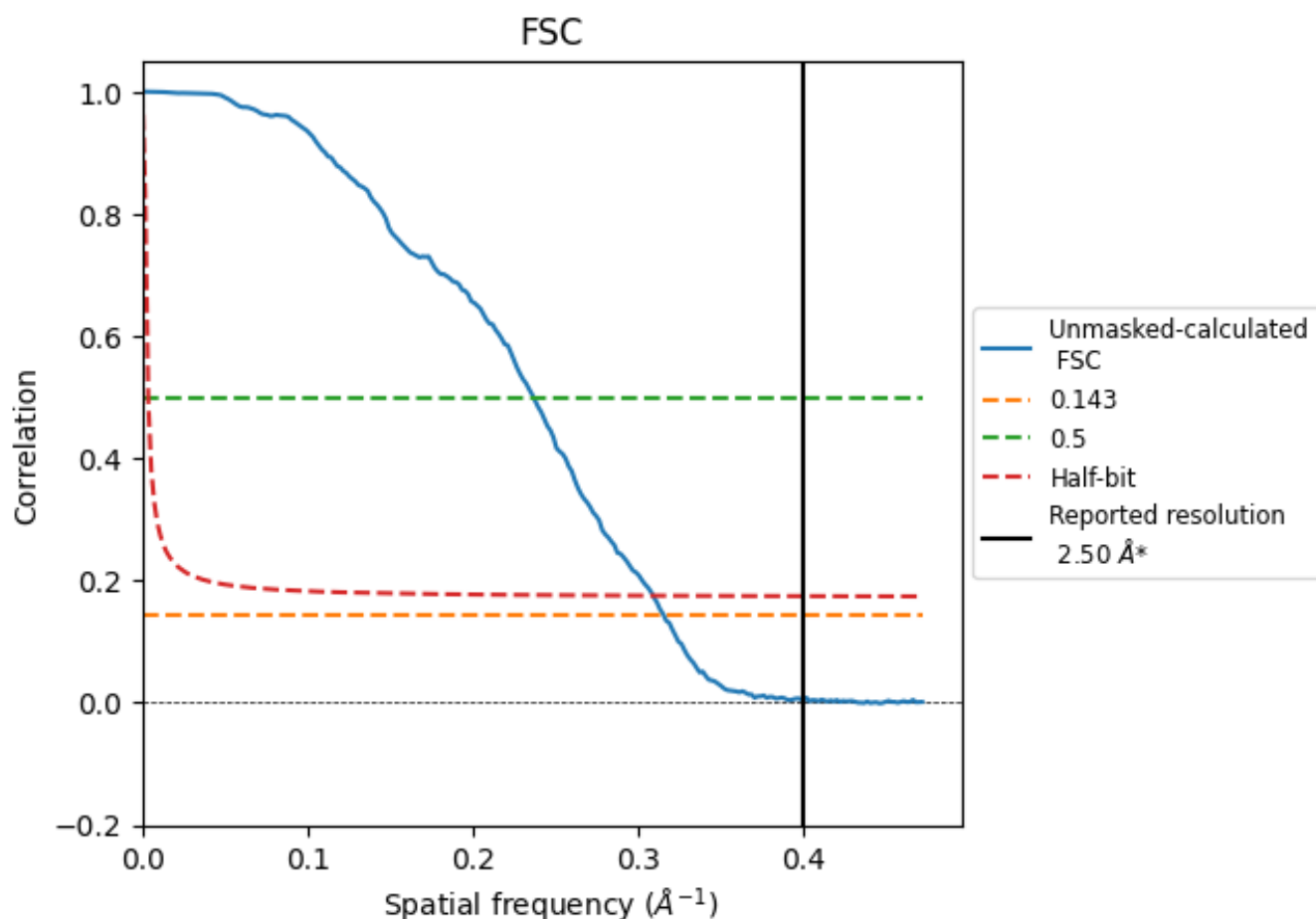


*Reported resolution corresponds to spatial frequency of 0.400 Å⁻¹

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 $0.400 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

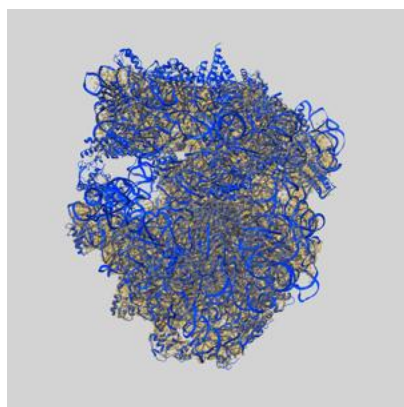
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.17	4.23	3.24

*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 3.17 differs from the reported value 2.5 by more than 10 %

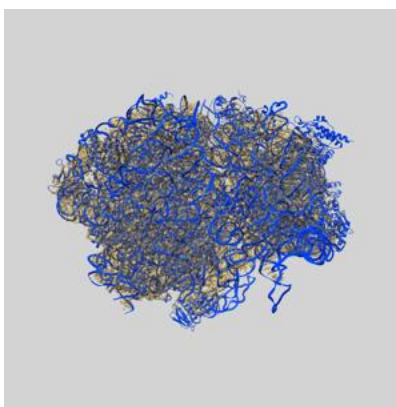
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55260 and PDB model 9SVJ. Per-residue inclusion information can be found in section [3](#) on page [16](#).

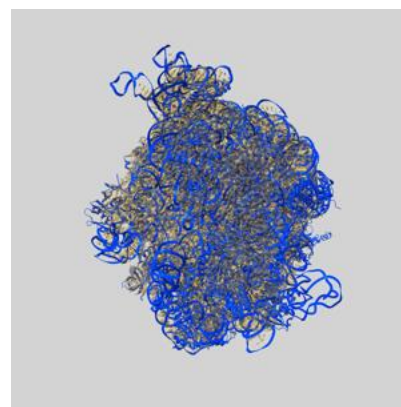
9.1 Map-model overlay [i](#)



X



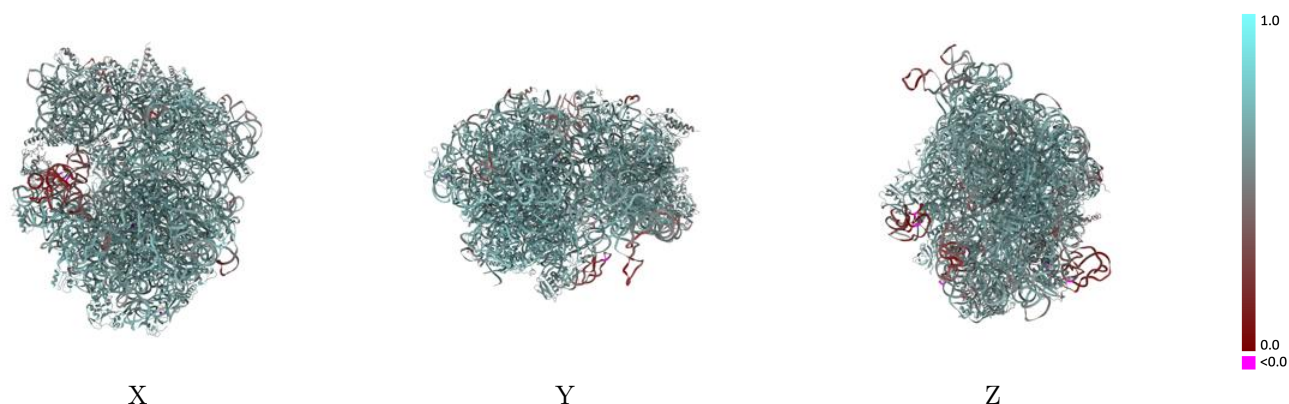
Y



Z

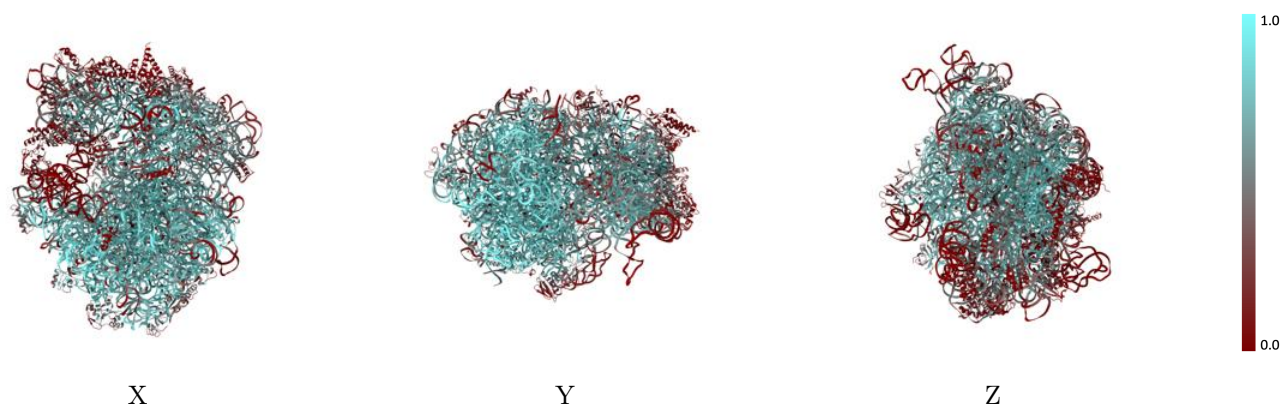
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



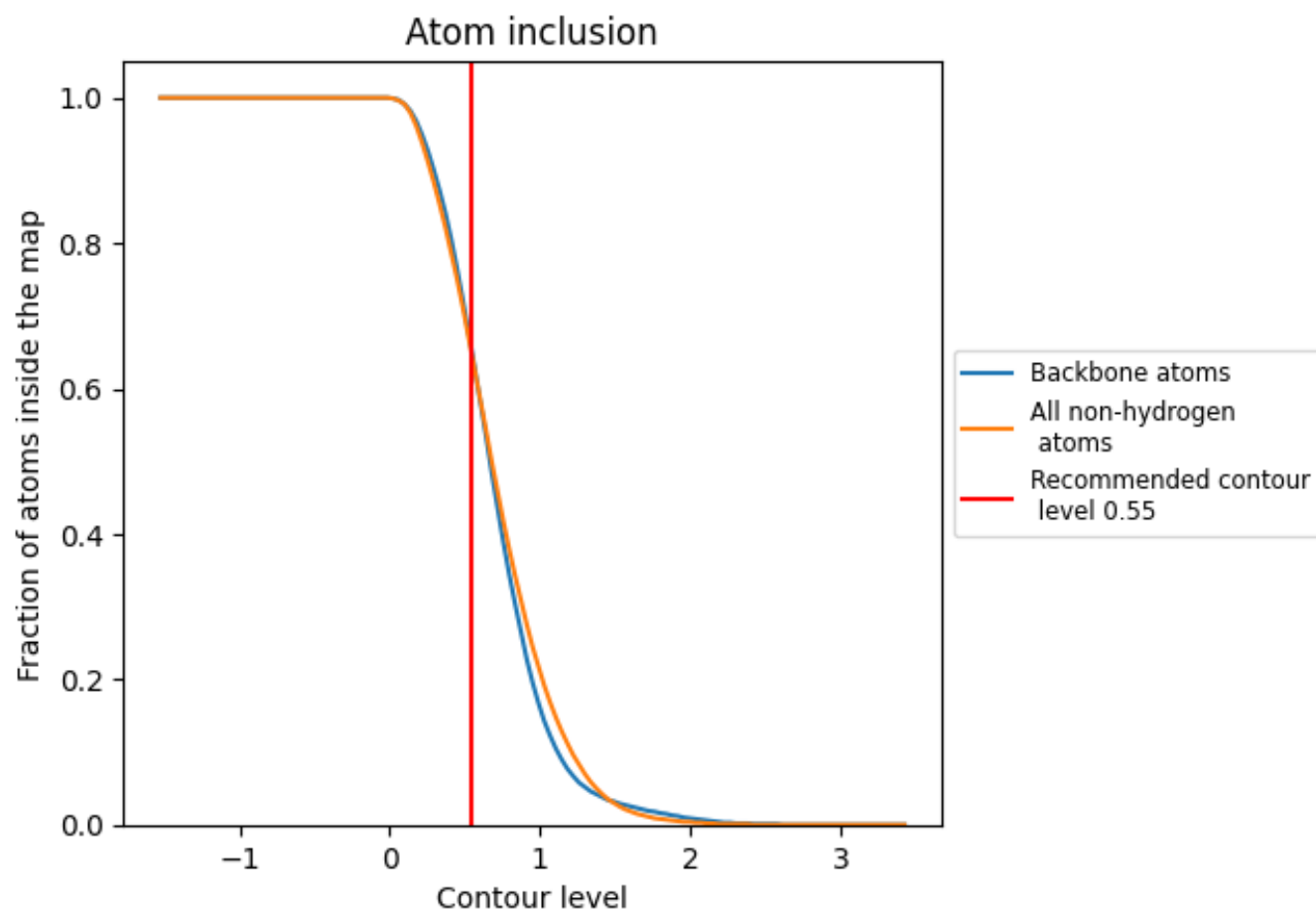
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 64% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6450	 0.6160
0	 0.6040	 0.6470
1	 0.8690	 0.6750
2	 0.8710	 0.6840
3	 0.7140	 0.6590
4	 0.0060	 0.4620
A	 0.6290	 0.6060
B	 0.0420	 0.5440
C	 0.3540	 0.6030
D	 0.2580	 0.5880
E	 0.5920	 0.6450
F	 0.1780	 0.5830
G	 0.1850	 0.5690
H	 0.5220	 0.6430
I	 0.3270	 0.5980
J	 0.2910	 0.5750
K	 0.3730	 0.6080
L	 0.5010	 0.6350
M	 0.1960	 0.5800
N	 0.3410	 0.5900
O	 0.5120	 0.6340
P	 0.4650	 0.6180
Q	 0.3570	 0.6160
R	 0.2550	 0.6000
S	 0.1540	 0.5660
T	 0.4770	 0.6320
V	 0.0100	 0.3630
W	 0.0320	 0.4320
X	 0.4280	 0.6230
a	 0.7770	 0.6230
b	 0.6540	 0.6210
c	 0.7980	 0.6740
d	 0.7850	 0.6700
e	 0.6540	 0.6590
f	 0.1430	 0.5580



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Chain	Atom inclusion	Q-score
g	 0.2950	 0.6010
h	 0.0040	 0.4380
i	 0.7760	 0.6670
j	 0.6890	 0.6650
k	 0.7170	 0.6630
l	 0.6630	 0.6600
m	 0.8320	 0.6800
n	 0.5410	 0.6340
o	 0.6640	 0.6610
p	 0.8460	 0.6840
q	 0.7180	 0.6630
r	 0.7490	 0.6700
s	 0.6060	 0.6480
t	 0.4390	 0.6130
u	 0.5140	 0.6300
v	 0.7930	 0.6740
w	 0.6930	 0.6640
x	 0.4320	 0.6200
y	 0.7220	 0.6620
z	 0.7280	 0.6650