



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 11:50 am BST

PDB ID : 6YSU
EMDB ID : EMD-10908
Title : Structure of the P+0 ArfB-ribosome complex in the post-hydrolysis state
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 3.70 Å (reported)
Based on initial models : 5O2R, 4V95, 4RB7, 5AFI

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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

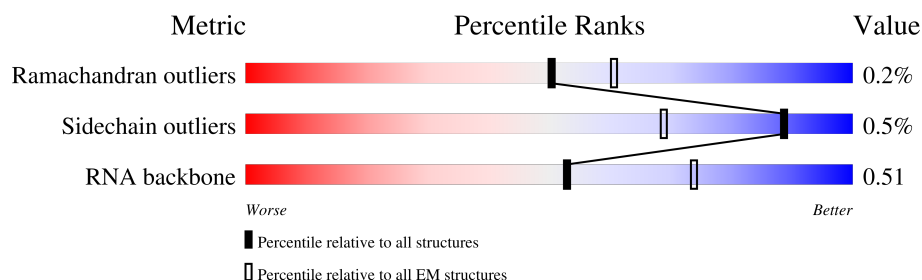
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



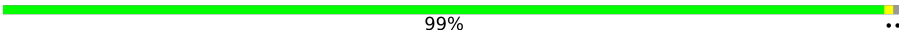
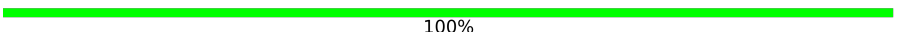
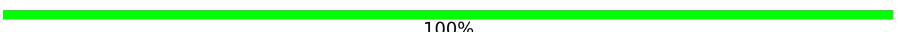
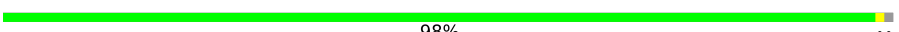
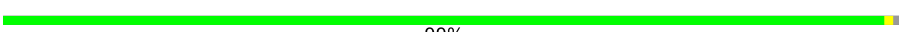







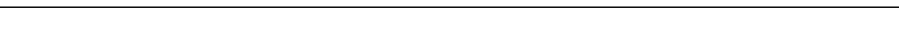

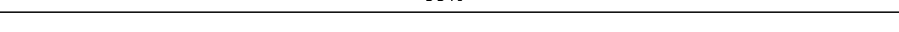
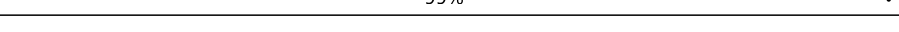
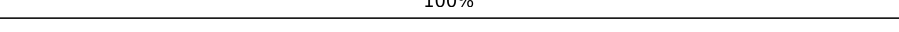
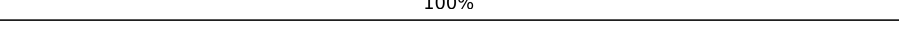
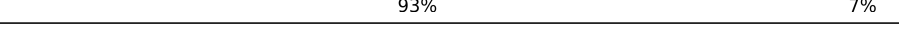
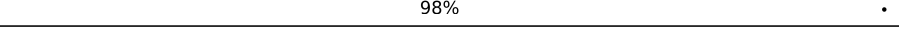
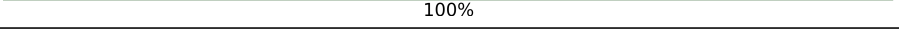

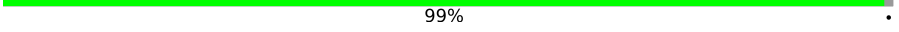
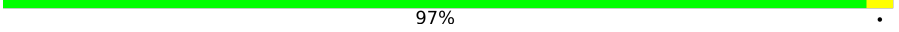
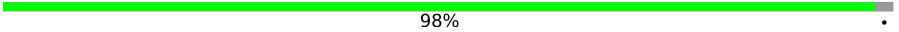
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	57	
2	1	55	
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	A	2903	
8	B	120	



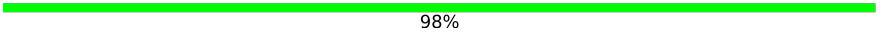
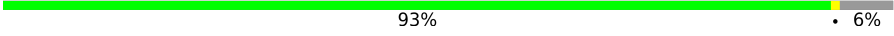


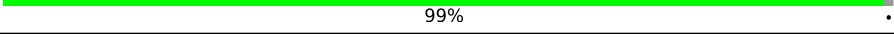
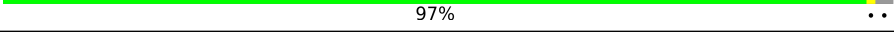
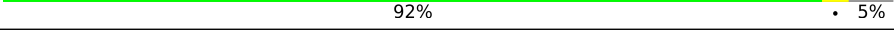
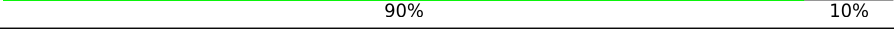
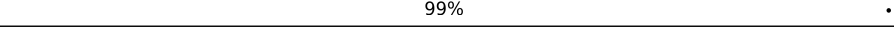
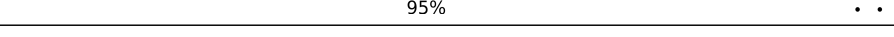
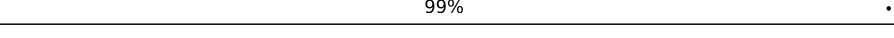
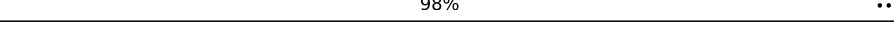
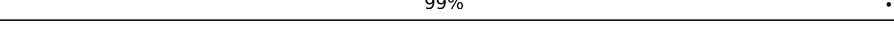
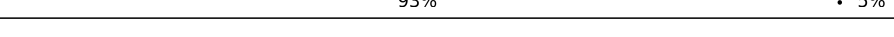

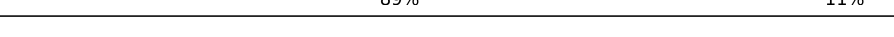
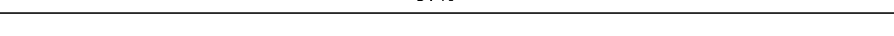

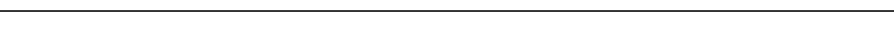

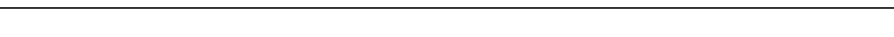
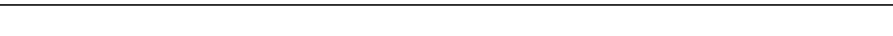
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Mol	Chain	Length	Quality of chain
9	C	273	 99% ..
10	D	209	 100%
11	E	201	 100%
12	F	179	 98% ..
13	G	177	 99% ..
14	H	149	 100%
15	I	142	 99% .
16	J	142	 99% .
17	K	123	 98% ..
18	L	144	 99% ..
19	M	136	 100%
20	N	127	 94% 6%
21	O	117	 97% ..
22	P	115	 99% .
23	Q	118	 99% .
24	R	103	 100%
25	S	110	 100%
26	T	100	 93% 7%
27	U	104	 98% .
28	V	94	 100%
29	W	85	 88% 12%
30	X	78	 99% .
31	Y	63	 97% .
32	Z	59	 98% .
33	a	1542	 73% 26% .

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Mol	Chain	Length	Quality of chain
34	b	240	
35	c	233	
36	d	206	
37	e	167	
38	f	135	
39	g	179	
40	h	130	
41	i	130	
42	j	103	
43	k	129	
44	l	124	
45	m	118	
46	n	102	
47	o	89	
48	p	82	
49	q	84	
50	r	75	
51	s	92	
52	t	87	
53	u	71	
54	v	14	
55	w	76	
56	x	15	
57	y	140	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 146398 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 9 is a protein called 50S ribosomal protein L2.

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

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

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

- Molecule 12 is a protein called 50S ribosomal protein L5.

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

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 17 is a protein called 50S ribosomal protein L14.

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

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

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

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	P	114	Total	C	N	O	S	0
			917	574	179	163	1	0

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Q	117	Total	C	N	O		0
			947	604	192	151		0

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	103	Total	C	N	O	S	0
			816	516	153	145	2	0

- Molecule 25 is a protein called 50S ribosomal protein L22.

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

- Molecule 26 is a protein called 50S ribosomal protein L23.

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

- Molecule 27 is a protein called 50S ribosomal protein L24.

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

- Molecule 28 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 33 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 34 is a protein called 30S ribosomal protein S2.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

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

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
50	r	56	Total	C	N	O	0	0
			464	293	88	83		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 54 is a protein called Api137.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	v	14	Total	C	N	O	0	0
			121	80	25	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	10	ARG	GLN	engineered mutation	UNP Q8WSY8

- Molecule 55 is a RNA chain called P-site tRNAPhe.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 56 is a RNA chain called RNA (5'-R(P*AP*UP*GP*UP*UP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	6	Total	C	N	O	P	0	0
			125	56	19	44	6		

- Molecule 57 is a protein called Alternative stalled-ribosome rescue factor B.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	139	Total	C	N	O	S	0	0
			1078	666	215	195	2		

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	0	2	Total	Mg	0
			2	2	
58	3	1	Total	Mg	0
			1	1	
58	A	244	Total	Mg	0
			244	244	
58	B	5	Total	Mg	0
			5	5	
58	C	2	Total	Mg	0
			2	2	
58	D	2	Total	Mg	0
			2	2	
58	L	1	Total	Mg	0
			1	1	
58	X	1	Total	Mg	0
			1	1	
58	a	93	Total	Mg	0
			93	93	
58	m	1	Total	Mg	0
			1	1	

Continued on next page...

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Mol	Chain	Residues	Atoms		AltConf
58	w	4	Total	Mg	0
			4	4	

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	4	1	Total	Zn	0
			1	1	

- Molecule 60 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
60	A	1	Total	Na	0
			1	1	

3 Residue-property plots [i](#)


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

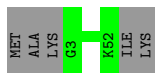
- Molecule 1: 50S ribosomal protein L32

Chain 0:  98% .



- Molecule 2: 50S ribosomal protein L33

Chain 1:  91% 9%



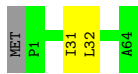
- Molecule 3: 50S ribosomal protein L34

Chain 2:  98% .



- Molecule 4: 50S ribosomal protein L35

Chain 3:  95% . .




- Molecule 5: 50S ribosomal protein L36

Chain 4:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: 50S ribosomal protein L10

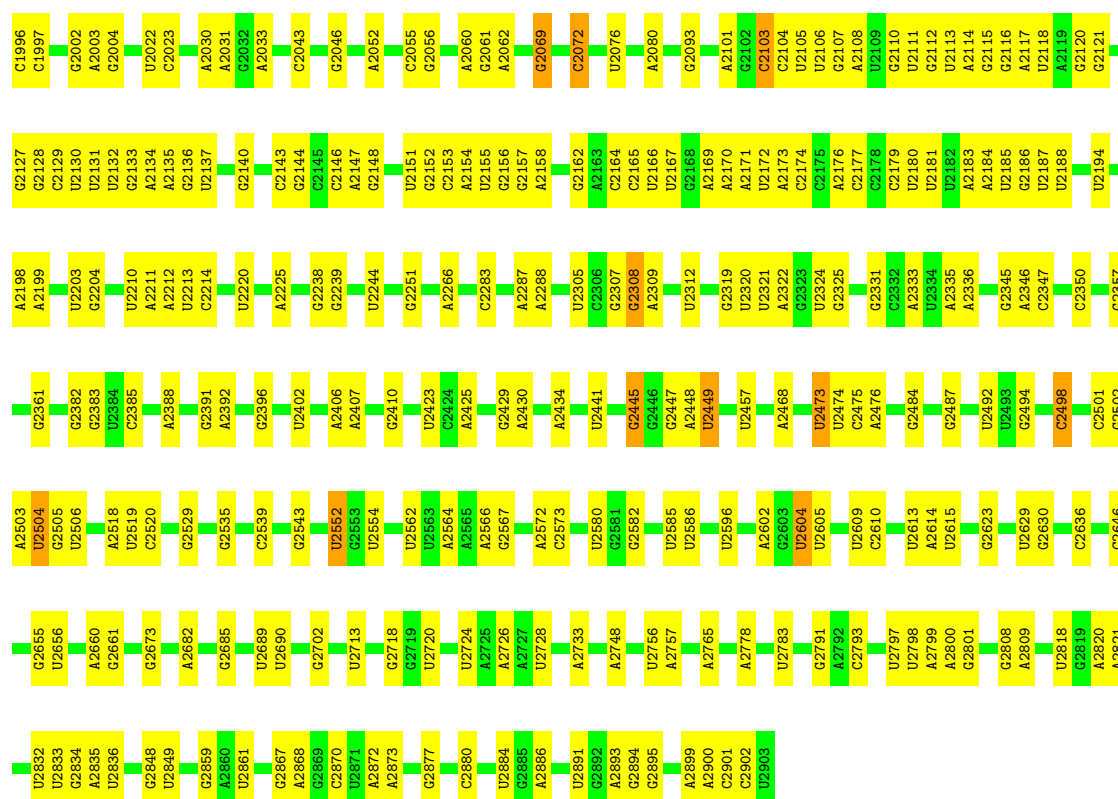
Chain 5:  79% 21%

HI	+
TI31	
TYR	
GLU	
GLU	
ALA	
ILE	
ALA	
ALA	
ARG	
LEU	
MET	
ALA	
THR	
MET	
LYS	
GLU	
ALA	
ALA	
SER	
ALA	
GLY	
LYS	
LEU	
VAL	
ARG	
THR	
LEU	
ALA	
ALA	
VAL	
VAL	
ARG	
ASP	
ALA	
LYS	
GLU	
ALA	
ALA	

• Molecule 7: 23S ribosomal RNA

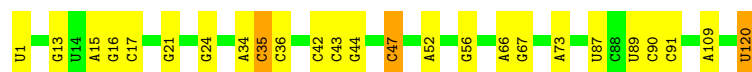
Chain A:  74% 25%

G1857	G1674	U1520	A1395	A1205	U1081	A983	U827	A654	U464	U290	A173	G1
G1869	C1694	G1521	C1399	G1206	U1082	A984	U828	A655	A478	G308	A181	G2
C1870	G1695	U1522	C1399	G1212	U1083	A984	A829	G656	A479	A479	A181	A10
A1871	G1696	G1523	A1403	G1212	G1087	G989	G830	G659	A480	A322	G188	A14
A1872	G1697	G1524	A1403	G1227	A1088	G989	G831	G659	G481	A480	G188	G15
G1873	A1698	A1532	U1406	G1227	A1089	A996	C840	G669	A482	G329	A195	G23
	G1699	C1533	U1406	G1236	A1089	A996	C840	G669	A482	A330	A196	G23
A1877	G1702	U1534	A1413	G1236	A1090	U999	A845	A670	G488	C331	A196	G23
C1878	G1703	A1535	C1414	A1244	G1091	U999	A845	A670	A489	G338	A199	G27
	G1703	C1536	U1415	G1245	U1094	U1003	U847	G682	C490	G338	A199	G27
A1884	U1712	G1537	G1416	A1246	A1095	U1003	U847	G682	G491	A346	U200	C33
U1885	U1713	U1542	A1419	A1247	A1096	C1005	G856	U686	A503	A346	C201	C33
U1886	U1714	U1542	A1419	G1248	U1097	C1005	G857	U686	A504	U34	G215	G35
U1887	G1715	U1554	A1421	U1249	A1098	U1012	G858	G696	A505	C351	G215	G35
A1900	U1716	U1554	G1421	G1250	G1099	C1013	G859	G696	A505	A216	A216	G45
		C1558	A1428	A1253	U1101	A1021	A877	G704	C509	G356	A221	G46
U1911	U1729	U1559	G1429	A1253	C1102	G1022	A878	G704	C510	C357	A221	G46
A1912	C1730	G1560	G1429	G1256	U1103	U1023	A879	A715	U511	U358	A222	U50
A1913	G1731	A1566	C1437	A1265	C1104	A1027	G832	C717	G512	U360	A223	G51
C1914	A1566	A1566	A1452	A1265	G1110	A1027	G832	C717	C527	G361	C225	G55
3TD1915	G1736	G1567	G1452	A1268	G1111	U1033	U834	G725	C527	G363	C228	G55
A1916	G1737	G1568	A1453	A1268	G1112	U1033	C885	G725	C531	C364	C228	C61
U1917	G1738	A1569	C1454	A1453	G1111	U1033	A886	G729	A532	U365	A233	U62
A1918		U1578	U1458	G1271	G1115	A1039	U887	A730	A532	C366	A233	A63
A1919	A1744	U1578	U1458	U1272	G1115	A1039	C888	A734	U546	G367	A241	A71
A1745	A1745	U1578	C1461	U1273	U1119	A1046	C889	A734	A547	A368	A241	A71
		A1583	A1461	A1286	G1122	C1045	C390	G745	U546	U369	A241	A71
G1756	G1756	U1584	C1461	A1286	G1122	C1045	G891	G745	G548	G248	A249	A74
G1929	U1757	C1585	U1467	G1300	G122	C1052	A892	U746	G549	G250	G249	G75
U1758	U1758	C1585	U1468	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
C1764	C1764	C1592	G1475	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
A1936	A1936	A1593	U1476	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
A1937	A1937	A1593	U1476	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
A1938	A1938	A1593	U1476	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
U1939	A1773	A1603	U1476	A1301	U1130	C1053	A892	U746	G555	U373	G250	G75
U1940	U1781	C1607	G1483	A1321	U1130	C1053	A892	U746	G555	U373	G250	G75
C1941	A1808	A1608	U1484	A1321	U1130	C1053	A892	U746	G555	U373	G250	G75
A1609	A1809	U1485	U1485	U1329	U1130	C1053	A892	U746	G555	U373	G250	G75
C1942	A1791	A1610	U1486	C1330	A1142	U1061	A910	A764	U569	G386	A256	G81
		A1610	U1486	C1330	A1142	U1061	A910	A764	U569	G386	A256	G81
U1955	C1800	A1618	U1487	G1331	A1143	G1062	A920	G775	U571	G406	A265	A101
	A1801	A1618	U1487	G1331	A1143	G1062	A920	G775	U571	G406	A265	A101
C1962	A1802	A1626	A1490	G1358	A1151	G1063	A920	G775	U571	G406	A265	A101
U1963	A1802	A1626	A1490	G1358	A1151	G1063	A920	G775	U571	G406	A265	A101
G1964	A1808	A1626	G1491	A1359	A1151	G1063	A920	G775	U571	G406	A265	A101
C1965	A1809	G1633	G1492	A1359	A1155	U1066	A933	A782	A574	A412	A272	A118
A1966	A1809	A1634	A1493	A1365	A1155	U1066	A933	A782	A574	A412	A272	A118
C1967	A1815	A1634	A1494	A1365	A1155	U1066	A933	A782	A574	A412	A272	A118
	C1816	A1634	A1494	A1365	A1155	U1066	A933	A782	A574	A412	A272	A118
A1970	C1816	A1634	A1494	A1365	A1155	U1066	A933	A782	A574	A412	A272	A118
U1971	A1829	G1648	C1498	U1378	U1173	G1071	C946	A800	A614	U448	A278	G134
G1972	A1829	G1649	C1498	U1379	A1175	G1071	C946	A800	A614	U448	A278	G134
	C1833	A1665	A1502	A1383	A1175	G1071	C946	A800	A614	U448	A278	G134
U1982	U1834	A1665	A1502	A1383	C1178	G1074	C957	U807	A627	U451	C281	U139
	G1835	A1665	A1502	A1383	C1178	G1074	C957	U807	A627	U451	C281	U139
U1991	A1508	A1669	C1386	A1386	U1180	C1076	U958	U807	A627	U451	C281	U139
G1992	A1509	A1669	C1386	A1386	U1180	C1076	U958	U807	A627	U451	C281	U139
U1993	G1847	A1392	A1392	A1392	G1182	U1077	C961	U811	A637	A454	A382	C140
	A1848	A1393	A1393	A1393	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C961	U811	A637	A454	A382	C140
		A1545	A1545	A1545	G1182	U1077	C					



• Molecule 8: 5S ribosomal RNA

Chain B: 79% 18%



• Molecule 9: 50S ribosomal protein L2

Chain C: 99%



• Molecule 10: 50S ribosomal protein L3

Chain D: 100%

There are no outlier residues recorded for this chain.

• Molecule 11: 50S ribosomal protein L4

Chain E: 100%



- Molecule 12: 50S ribosomal protein L5

Chain F:  98% ..



- Molecule 13: 50S ribosomal protein L6

Chain G:  99% ..



- Molecule 14: 50S ribosomal protein L9

Chain H:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: 50S ribosomal protein L11

Chain I:  99% .



- Molecule 16: 50S ribosomal protein L13

Chain J:  99% .



- Molecule 17: 50S ribosomal protein L14

Chain K:  98% ..




- Molecule 18: 50S ribosomal protein L15

Chain L:  99% ..



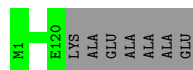
- Molecule 19: 50S ribosomal protein L16

Chain M:  100%

There are no outlier residues recorded for this chain.

- Molecule 20: 50S ribosomal protein L17

Chain N:  94% 6%



- Molecule 21: 50S ribosomal protein L18

Chain O:  97% ..



- Molecule 22: 50S ribosomal protein L19

Chain P:  99% .



- Molecule 23: 50S ribosomal protein L20

Chain Q:  99% .



- Molecule 24: 50S ribosomal protein L21

Chain R:  100%

There are no outlier residues recorded for this chain.

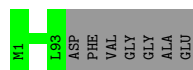
- Molecule 25: 50S ribosomal protein L22

Chain S:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 50S ribosomal protein L23

Chain T:  93% 7%



- Molecule 27: 50S ribosomal protein L24

Chain U:  98%




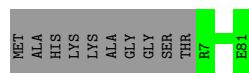
- Molecule 28: 50S ribosomal protein L25

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: 50S ribosomal protein L27

Chain W:  88%



- Molecule 30: 50S ribosomal protein L28

Chain X:  99%



- Molecule 31: 50S ribosomal protein L29

Chain Y:  97%



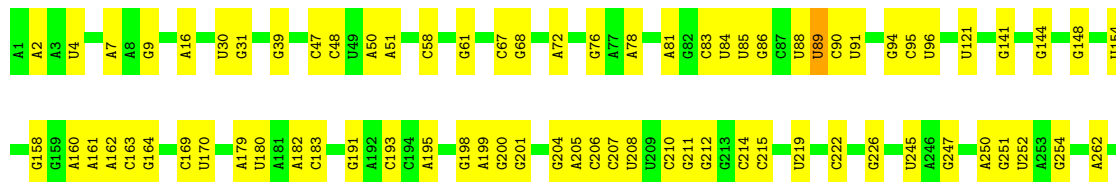
- Molecule 32: 50S ribosomal protein L30

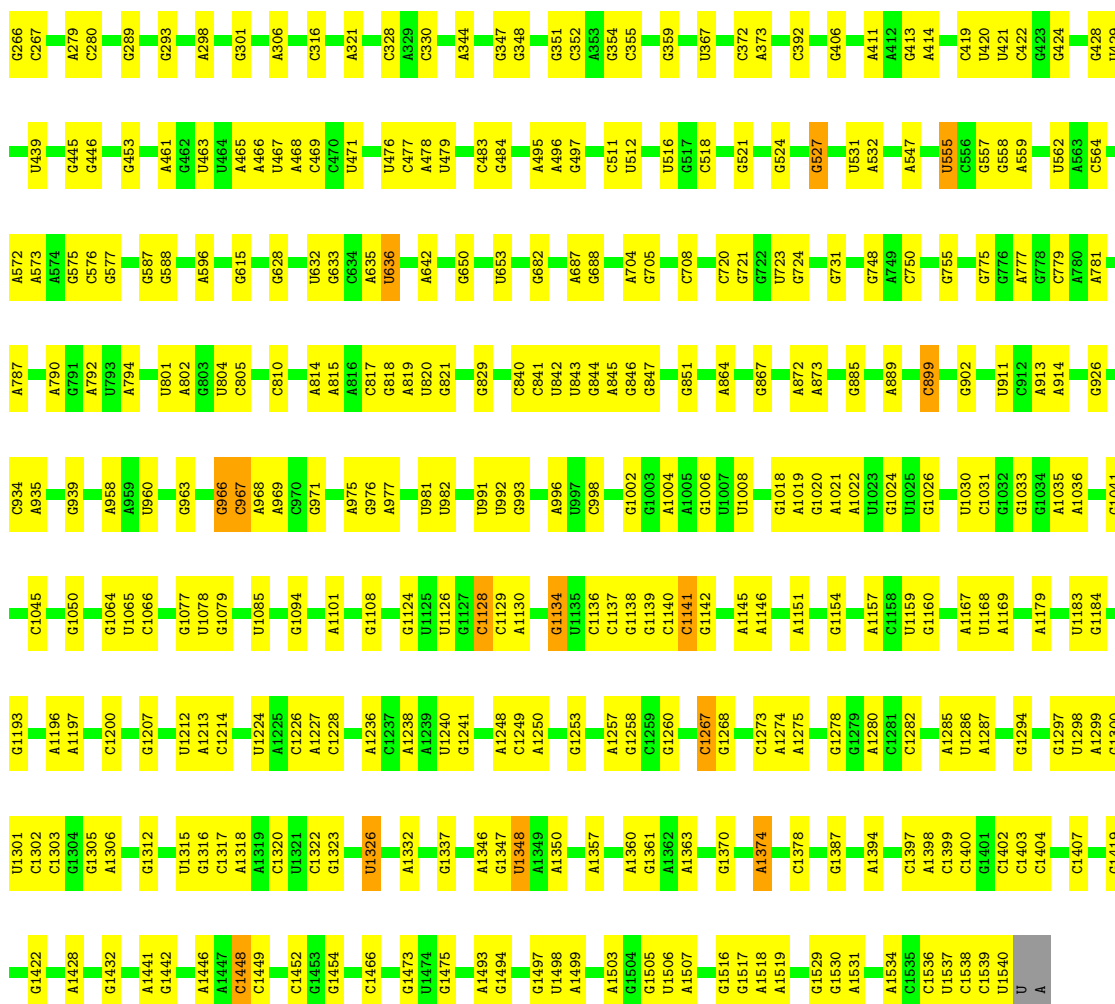
Chain Z:  98%



- Molecule 33: 16S ribosomal RNA

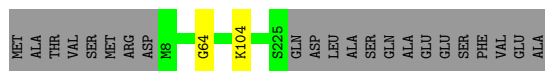
Chain a:  73%





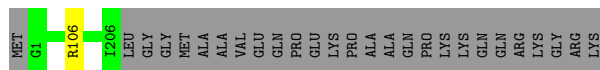
• Molecule 34: 30S ribosomal protein S2

Chain b: 90% 9%



• Molecule 35: 30S ribosomal protein S3

Chain c: 88% 12%



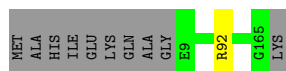
• Molecule 36: 30S ribosomal protein S4

Chain d: 98%



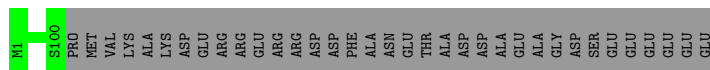
- Molecule 37: 30S ribosomal protein S5

Chain e:  93% • 6%




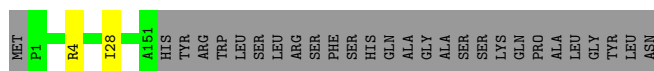
- Molecule 38: 30S ribosomal protein S6

Chain f:  74% 26%



- Molecule 39: 30S ribosomal protein S7

Chain g:  83% • 16%



- Molecule 40: 30S ribosomal protein S8

Chain h:  99% •



- Molecule 41: 30S ribosomal protein S9

Chain i:  97% ••

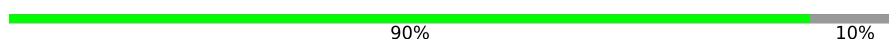


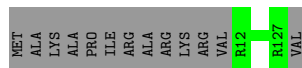
- Molecule 42: 30S ribosomal protein S10

Chain j:  92% • 5%



- Molecule 43: 30S ribosomal protein S11

Chain k:  90% 10%



- Molecule 44: 30S ribosomal protein S12

Chain l:  99%



- Molecule 45: 30S ribosomal protein S13

Chain m:  95%



- Molecule 46: 30S ribosomal protein S14

Chain n:  99%



- Molecule 47: 30S ribosomal protein S15

Chain o:  98%



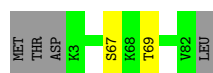
- Molecule 48: 30S ribosomal protein S16

Chain p:  99%



- Molecule 49: 30S ribosomal protein S17

Chain q:  93%




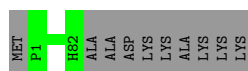
- Molecule 50: 30S ribosomal protein S18

Chain r:  75%



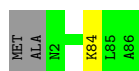
- Molecule 51: 30S ribosomal protein S19

Chain s:  89% 11%




- Molecule 52: 30S ribosomal protein S20

Chain t:  97% ..



- Molecule 53: 30S ribosomal protein S21

Chain u:  90% • 8%



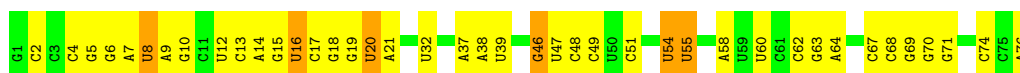
- Molecule 54: Api137

Chain v:  100%

There are no outlier residues recorded for this chain.

- Molecule 55: P-site tRNA^{Phe}

Chain w:  46% 46% 8%



- Molecule 56: RNA (5'-R(P*AP*UP*GP*UP*UP*C)-3')

Chain x:  33% 7% 60%



- Molecule 57: Alternative stalled-ribosome rescue factor B

Chain y:  99% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60692	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	14.417	Depositor
Minimum map value	-7.317	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	347.328, 347.328, 347.328	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.41	0/450	0.55	0/599
2	1	0.41	0/416	0.49	0/554
3	2	0.40	0/380	0.54	0/498
4	3	0.41	0/513	0.53	0/676
5	4	0.38	0/303	0.49	0/397
6	5	0.25	0/646	0.50	0/898
7	A	0.83	9/69263 (0.0%)	0.93	90/108050 (0.1%)
8	B	0.67	2/2873 (0.1%)	0.92	4/4478 (0.1%)
9	C	0.45	0/2121	0.53	0/2852
10	D	0.44	0/1586	0.55	0/2134
11	E	0.39	0/1571	0.49	0/2113
12	F	0.32	0/1434	0.48	0/1926
13	G	0.36	0/1343	0.50	0/1816
14	H	0.34	0/1122	0.53	0/1515
15	I	0.25	0/692	0.44	0/960
16	J	0.44	0/1152	0.50	0/1551
17	K	0.41	0/947	0.53	0/1268
18	L	0.41	0/1054	0.57	0/1403
19	M	0.41	0/1093	0.49	0/1460
20	N	0.41	0/973	0.52	0/1301
21	O	0.34	0/902	0.49	0/1209
22	P	0.41	0/929	0.49	0/1242
23	Q	0.50	0/960	0.46	0/1278
24	R	0.40	0/829	0.51	0/1107
25	S	0.39	0/864	0.49	0/1156
26	T	0.37	0/744	0.50	0/994
27	U	0.39	0/787	0.49	0/1051
28	V	0.40	0/766	0.48	0/1025
29	W	0.42	0/582	0.46	0/769
30	X	0.40	0/635	0.48	0/848
31	Y	0.35	0/510	0.59	1/677 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.38	0/453	0.53	0/605
33	a	0.67	2/36725 (0.0%)	0.89	26/57285 (0.0%)
34	b	0.31	0/1735	0.48	0/2338
35	c	0.34	0/1651	0.47	0/2225
36	d	0.44	0/1665	0.59	3/2227 (0.1%)
37	e	0.38	0/1154	0.53	0/1554
38	f	0.35	0/835	0.50	0/1128
39	g	0.30	0/1195	0.47	0/1602
40	h	0.37	0/989	0.49	0/1326
41	i	0.33	0/1034	0.51	0/1375
42	j	0.32	0/796	0.55	0/1077
43	k	0.34	0/885	0.48	0/1195
44	l	0.40	0/969	0.52	0/1300
45	m	0.29	0/892	0.48	0/1193
46	n	0.32	0/811	0.46	0/1081
47	o	0.32	0/722	0.46	0/964
48	p	0.35	0/659	0.51	0/884
49	q	0.39	0/657	0.55	0/881
50	r	0.35	0/471	0.45	0/633
51	s	0.31	0/675	0.48	0/908
52	t	0.31	0/671	0.44	0/888
53	u	0.30	0/512	0.49	0/683
54	v	0.31	0/128	0.42	0/175
55	w	1.25	12/1650 (0.7%)	1.11	9/2569 (0.4%)
56	x	0.61	0/138	0.86	0/212
57	y	0.28	0/1090	0.45	0/1461
All	All	0.69	25/157602 (0.0%)	0.83	133/235574 (0.1%)

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
36	d	0	2

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	w	20	U	C2-N3	17.27	1.49	1.37
55	w	16	U	C5-C6	16.84	1.49	1.34
55	w	16	U	C2-N3	16.80	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	w	20	U	C5-C6	16.74	1.49	1.34
55	w	20	U	N1-C2	16.43	1.53	1.38

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2449	U	C2-N3-C4	-13.54	118.87	127.00
7	A	366	C	C2-N1-C1'	11.70	131.67	118.80
55	w	16	U	C2-N3-C4	-11.70	119.98	127.00
55	w	20	U	C2-N3-C4	-11.60	120.04	127.00
7	A	366	C	N1-C2-O2	10.94	125.46	118.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	d	70	GLN	Mainchain
36	d	71	PHE	Mainchain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/65 (95%)	52 (84%)	8 (13%)	2 (3%)	4	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	104 (81%)	25 (19%)	0	100	100
9	C	269/273 (98%)	237 (88%)	31 (12%)	1 (0%)	34	69
10	D	207/209 (99%)	182 (88%)	25 (12%)	0	100	100
11	E	199/201 (99%)	181 (91%)	18 (9%)	0	100	100
12	F	175/179 (98%)	152 (87%)	23 (13%)	0	100	100
13	G	174/177 (98%)	159 (91%)	14 (8%)	1 (1%)	25	62
14	H	147/149 (99%)	115 (78%)	32 (22%)	0	100	100
15	I	139/142 (98%)	110 (79%)	29 (21%)	0	100	100
16	J	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
17	K	120/123 (98%)	102 (85%)	18 (15%)	0	100	100
18	L	141/144 (98%)	117 (83%)	23 (16%)	1 (1%)	22	59
19	M	134/136 (98%)	107 (80%)	27 (20%)	0	100	100
20	N	118/127 (93%)	106 (90%)	12 (10%)	0	100	100
21	O	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
22	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
23	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
24	R	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
25	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
26	T	91/100 (91%)	74 (81%)	17 (19%)	0	100	100
27	U	100/104 (96%)	87 (87%)	13 (13%)	0	100	100
28	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
29	W	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
30	X	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
31	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
32	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
34	b	216/240 (90%)	188 (87%)	27 (12%)	1 (0%)	29	66
35	c	204/233 (88%)	188 (92%)	16 (8%)	0	100	100
36	d	203/206 (98%)	170 (84%)	32 (16%)	1 (0%)	29	66
37	e	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
38	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	g	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
40	h	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
41	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
42	j	96/103 (93%)	72 (75%)	22 (23%)	2 (2%)	7	38
43	k	114/129 (88%)	101 (89%)	13 (11%)	0	100	100
44	l	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
45	m	112/118 (95%)	94 (84%)	18 (16%)	0	100	100
46	n	99/102 (97%)	87 (88%)	12 (12%)	0	100	100
47	o	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
48	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
49	q	78/84 (93%)	60 (77%)	16 (20%)	2 (3%)	5	34
50	r	54/75 (72%)	48 (89%)	6 (11%)	0	100	100
51	s	80/92 (87%)	73 (91%)	7 (9%)	0	100	100
52	t	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
53	u	63/71 (89%)	53 (84%)	10 (16%)	0	100	100
54	v	12/14 (86%)	8 (67%)	4 (33%)	0	100	100
57	y	137/140 (98%)	132 (96%)	5 (4%)	0	100	100
All	All	5926/6304 (94%)	5198 (88%)	717 (12%)	11 (0%)	50	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	3	31	ILE
49	q	67	SER
4	3	32	LEU
18	L	128	THR
49	q	69	THR

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	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	37 (97%)	1 (3%)	46	69
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
9	C	216/218 (99%)	215 (100%)	1 (0%)	88	94
10	D	164/164 (100%)	164 (100%)	0	100	100
11	E	165/165 (100%)	164 (99%)	1 (1%)	86	93
12	F	148/150 (99%)	146 (99%)	2 (1%)	67	82
13	G	137/138 (99%)	137 (100%)	0	100	100
14	H	114/114 (100%)	114 (100%)	0	100	100
16	J	116/116 (100%)	115 (99%)	1 (1%)	78	88
17	K	103/104 (99%)	102 (99%)	1 (1%)	76	86
18	L	102/103 (99%)	102 (100%)	0	100	100
19	M	109/109 (100%)	109 (100%)	0	100	100
20	N	100/103 (97%)	100 (100%)	0	100	100
21	O	86/87 (99%)	84 (98%)	2 (2%)	50	71
22	P	99/100 (99%)	99 (100%)	0	100	100
23	Q	89/90 (99%)	89 (100%)	0	100	100
24	R	84/84 (100%)	84 (100%)	0	100	100
25	S	93/93 (100%)	93 (100%)	0	100	100
26	T	80/84 (95%)	80 (100%)	0	100	100
27	U	83/85 (98%)	83 (100%)	0	100	100
28	V	78/78 (100%)	78 (100%)	0	100	100
29	W	57/63 (90%)	57 (100%)	0	100	100
30	X	67/68 (98%)	67 (100%)	0	100	100
31	Y	55/55 (100%)	54 (98%)	1 (2%)	59	77
32	Z	48/49 (98%)	48 (100%)	0	100	100
34	b	180/198 (91%)	179 (99%)	1 (1%)	86	93
35	c	170/190 (90%)	169 (99%)	1 (1%)	86	93
36	d	172/173 (99%)	171 (99%)	1 (1%)	86	93
37	e	114/126 (90%)	113 (99%)	1 (1%)	78	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	f	87/116 (75%)	87 (100%)	0	100	100
39	g	124/147 (84%)	122 (98%)	2 (2%)	62	80
40	h	104/105 (99%)	104 (100%)	0	100	100
41	i	105/107 (98%)	104 (99%)	1 (1%)	76	86
42	j	86/90 (96%)	85 (99%)	1 (1%)	71	84
43	k	89/99 (90%)	89 (100%)	0	100	100
44	l	103/104 (99%)	103 (100%)	0	100	100
45	m	92/96 (96%)	90 (98%)	2 (2%)	52	72
46	n	79/84 (94%)	79 (100%)	0	100	100
47	o	76/77 (99%)	75 (99%)	1 (1%)	69	83
48	p	65/65 (100%)	64 (98%)	1 (2%)	65	81
49	q	74/78 (95%)	74 (100%)	0	100	100
50	r	49/65 (75%)	49 (100%)	0	100	100
51	s	72/79 (91%)	72 (100%)	0	100	100
52	t	65/66 (98%)	64 (98%)	1 (2%)	65	81
53	u	46/61 (75%)	45 (98%)	1 (2%)	52	72
54	v	14/14 (100%)	14 (100%)	0	100	100
57	y	112/115 (97%)	112 (100%)	0	100	100
All	All	4686/4896 (96%)	4662 (100%)	24 (0%)	89	94

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	g	4	ARG
42	j	32	THR
41	i	11	ARG
45	m	10	ASP
17	K	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
47	o	61	GLN
48	p	79	ASN
22	P	65	ASN

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Mol	Chain	Res	Type
22	P	9	GLN
49	q	46	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	a	1536/1542 (99%)	395 (25%)	0
55	w	74/76 (97%)	38 (51%)	0
56	x	5/15 (33%)	1 (20%)	0
7	A	2898/2903 (99%)	710 (24%)	49 (1%)
8	B	119/120 (99%)	23 (19%)	1 (0%)
All	All	4632/4656 (99%)	1167 (25%)	50 (1%)

5 of 1167 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	2	G
7	A	10	A
7	A	14	A
7	A	15	G
7	A	23	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1877	A
7	A	2185	U
8	B	34	A
7	A	1941	C
7	A	2128	G

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

41 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
7	2MA	A	2503	7,58	17,25,26	2.50	5 (29%)	17,37,40	1.29	2 (11%)
7	PSU	A	2605	7	18,21,22	1.05	2 (11%)	22,30,33	1.87	5 (22%)
7	6MZ	A	2030	7	18,25,26	1.78	5 (27%)	16,36,39	2.45	4 (25%)
7	PSU	A	746	7,58	18,21,22	1.05	2 (11%)	22,30,33	1.70	3 (13%)
7	OMC	A	2498	7,58	19,22,23	2.78	7 (36%)	26,31,34	0.93	2 (7%)
7	5MC	A	747	7	18,22,23	3.40	7 (38%)	26,32,35	1.17	3 (11%)
55	5MU	w	54	55	19,22,23	4.84	7 (36%)	28,32,35	3.64	8 (28%)
7	2MG	A	1835	7	18,26,27	2.36	7 (38%)	16,38,41	1.46	4 (25%)
7	PSU	A	2504	7	18,21,22	1.09	2 (11%)	22,30,33	1.80	4 (18%)
33	4OC	a	1402	33	20,23,24	3.17	8 (40%)	26,32,35	0.89	1 (3%)
55	MIA	w	37	55	24,31,32	2.53	4 (16%)	26,44,47	3.07	8 (30%)
7	6MZ	A	1618	7	18,25,26	1.76	4 (22%)	16,36,39	1.94	4 (25%)
7	OMU	A	2552	7,58	19,22,23	2.85	7 (36%)	26,31,34	1.83	4 (15%)
7	PSU	A	2457	7	18,21,22	0.98	2 (11%)	22,30,33	1.75	4 (18%)
33	5MC	a	967	33	18,22,23	3.52	7 (38%)	26,32,35	1.03	1 (3%)
7	PSU	A	2580	7	18,21,22	1.11	3 (16%)	22,30,33	1.93	6 (27%)
55	G7M	w	46	55	20,26,27	2.13	6 (30%)	17,39,42	1.22	3 (17%)
7	PSU	A	1911	7	18,21,22	1.05	1 (5%)	22,30,33	1.84	5 (22%)
7	2MG	A	2445	7	18,26,27	2.37	7 (38%)	16,38,41	1.47	4 (25%)
33	2MG	a	1207	33	18,26,27	2.49	7 (38%)	16,38,41	1.46	4 (25%)
7	5MU	A	1939	7,58	19,22,23	4.59	7 (36%)	28,32,35	3.81	10 (35%)
55	PSU	w	55	55	18,21,22	1.11	1 (5%)	22,30,33	1.82	5 (22%)
7	PSU	A	1917	7	18,21,22	1.08	1 (5%)	22,30,33	1.90	4 (18%)
7	G7M	A	2069	7	20,26,27	3.87	9 (45%)	17,39,42	1.00	1 (5%)
33	UR3	a	1498	33	19,22,23	2.69	6 (31%)	26,32,35	1.59	4 (15%)
55	PSU	w	32	55	18,21,22	1.47	3 (16%)	22,30,33	1.94	4 (18%)
33	MA6	a	1518	33	18,26,27	1.35	2 (11%)	19,38,41	3.17	2 (10%)
33	G7M	a	527	33	20,26,27	3.99	10 (50%)	17,39,42	1.03	1 (5%)
33	PSU	a	516	33,58	18,21,22	1.03	2 (11%)	22,30,33	1.71	5 (22%)
33	MA6	a	1519	33	18,26,27	1.35	2 (11%)	19,38,41	3.28	2 (10%)
55	PSU	w	39	55	18,21,22	1.03	1 (5%)	22,30,33	1.70	2 (9%)
7	3TD	A	1915	7	18,22,23	4.43	7 (38%)	22,32,35	1.74	4 (18%)
7	PSU	A	2604	7	18,21,22	1.34	2 (11%)	22,30,33	1.94	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	4SU	w	8	55	18,21,22	3.70	8 (44%)	26,30,33	2.20	4 (15%)
7	5MC	A	1962	7	18,22,23	3.46	7 (38%)	26,32,35	1.12	1 (3%)
33	2MG	a	966	33	18,26,27	2.39	7 (38%)	16,38,41	1.46	4 (25%)
33	2MG	a	1516	33	18,26,27	2.40	7 (38%)	16,38,41	1.41	4 (25%)
7	PSU	A	955	7	18,21,22	1.07	3 (16%)	22,30,33	1.67	4 (18%)
7	1MG	A	745	7	18,26,27	2.57	5 (27%)	19,39,42	1.51	4 (21%)
33	5MC	a	1407	33	18,22,23	3.54	7 (38%)	26,32,35	1.06	2 (7%)
7	OMG	A	2251	55,7,58	18,26,27	2.48	8 (44%)	19,38,41	1.54	4 (21%)

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
7	2MA	A	2503	7,58	-	2/3/25/26	0/3/3/3
7	PSU	A	2605	7	-	0/7/25/26	0/2/2/2
7	6MZ	A	2030	7	-	5/5/27/28	0/3/3/3
7	PSU	A	746	7,58	-	3/7/25/26	0/2/2/2
7	OMC	A	2498	7,58	-	4/9/27/28	0/2/2/2
7	5MC	A	747	7	-	3/7/25/26	0/2/2/2
55	5MU	w	54	55	-	3/7/25/26	0/2/2/2
7	2MG	A	1835	7	-	2/5/27/28	0/3/3/3
7	PSU	A	2504	7	-	2/7/25/26	0/2/2/2
33	4OC	a	1402	33	-	1/9/29/30	0/2/2/2
55	MIA	w	37	55	-	4/11/33/34	0/3/3/3
7	6MZ	A	1618	7	-	3/5/27/28	0/3/3/3
7	OMU	A	2552	7,58	-	5/9/27/28	0/2/2/2
7	PSU	A	2457	7	-	0/7/25/26	0/2/2/2
33	5MC	a	967	33	-	2/7/25/26	0/2/2/2
7	PSU	A	2580	7	-	0/7/25/26	0/2/2/2
55	G7M	w	46	55	-	3/3/25/26	0/3/3/3
7	PSU	A	1911	7	-	0/7/25/26	0/2/2/2
7	2MG	A	2445	7	-	2/5/27/28	0/3/3/3
33	2MG	a	1207	33	-	0/5/27/28	0/3/3/3
7	5MU	A	1939	7,58	-	2/7/25/26	0/2/2/2
55	PSU	w	55	55	-	5/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PSU	A	1917	7	-	0/7/25/26	0/2/2/2
7	G7M	A	2069	7	-	1/3/25/26	0/3/3/3
33	UR3	a	1498	33	-	4/7/25/26	0/2/2/2
55	PSU	w	32	55	-	2/7/25/26	0/2/2/2
33	MA6	a	1518	33	-	2/7/29/30	0/3/3/3
33	G7M	a	527	33	-	3/3/25/26	0/3/3/3
33	PSU	a	516	33,58	-	0/7/25/26	0/2/2/2
33	MA6	a	1519	33	-	2/7/29/30	0/3/3/3
55	PSU	w	39	55	-	3/7/25/26	0/2/2/2
7	3TD	A	1915	7	-	2/7/25/26	0/2/2/2
7	PSU	A	2604	7	-	2/7/25/26	0/2/2/2
55	4SU	w	8	55	-	2/7/25/26	0/2/2/2
7	5MC	A	1962	7	-	4/7/25/26	0/2/2/2
33	2MG	a	966	33	-	0/5/27/28	0/3/3/3
33	2MG	a	1516	33	-	0/5/27/28	0/3/3/3
7	PSU	A	955	7	-	0/7/25/26	0/2/2/2
7	1MG	A	745	7	-	0/3/25/26	0/3/3/3
33	5MC	a	1407	33	-	0/7/25/26	0/2/2/2
7	OMG	A	2251	55,7,58	-	0/5/27/28	0/3/3/3

The worst 5 of 205 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1915	3TD	C6-C5	14.14	1.51	1.35
55	w	54	5MU	C2-N1	11.21	1.56	1.38
55	w	54	5MU	C6-N1	10.36	1.55	1.38
55	w	54	5MU	C4-C5	10.11	1.61	1.44
33	a	527	G7M	C8-N7	9.86	1.51	1.33

The worst 5 of 154 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1519	MA6	N1-C6-N6	-13.08	103.29	117.06
33	a	1518	MA6	N1-C6-N6	-12.51	103.89	117.06
7	A	1939	5MU	C5-C4-N3	12.43	125.92	115.31
55	w	54	5MU	C5-C4-N3	12.17	125.70	115.31
7	A	1939	5MU	C5-C6-N1	-11.04	111.99	123.34

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	746	PSU	C2'-C1'-C5-C6
7	A	747	5MC	C3'-C4'-C5'-O5'
7	A	1618	6MZ	N1-C6-N6-C9
7	A	1915	3TD	O4'-C1'-C5-C4
7	A	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 358 ligands modelled in this entry, 358 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](#)

There are no chain breaks in this entry.

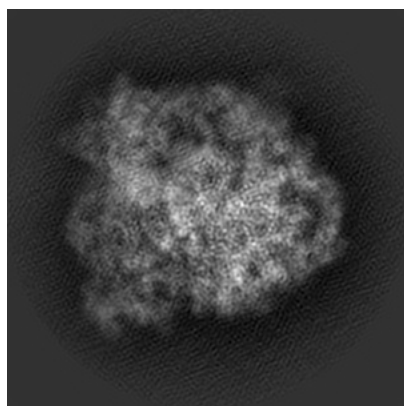
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10908. These allow visual inspection of the internal detail of the map and identification of artifacts.

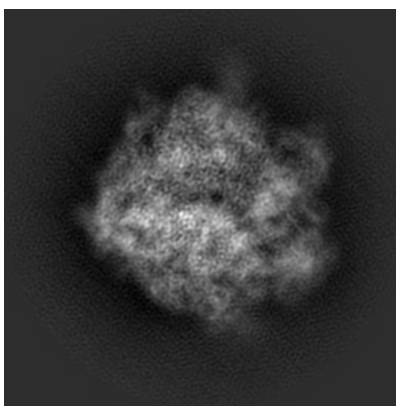
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

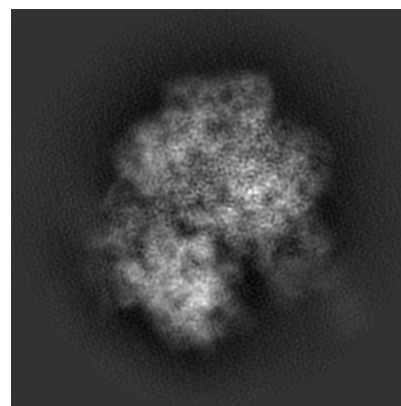
6.1.1 Primary map



X

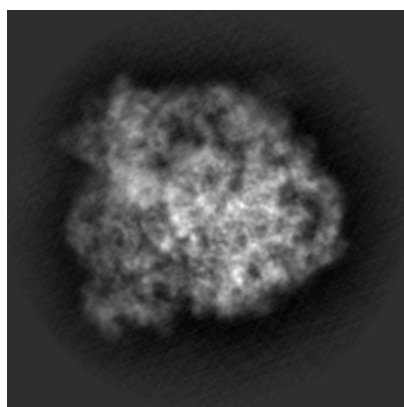


Y

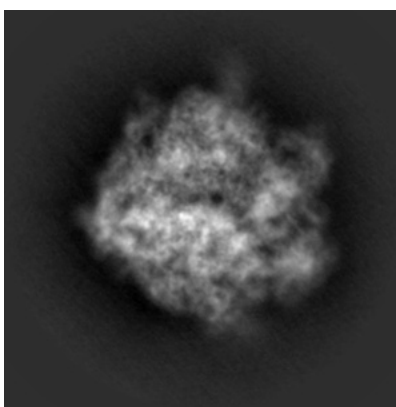


Z

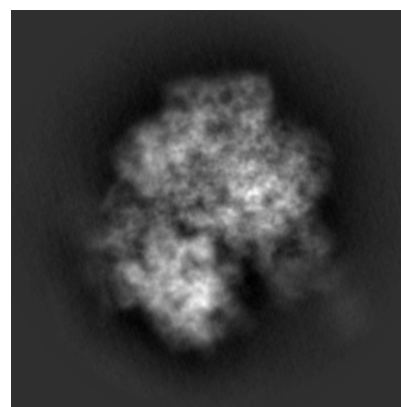
6.1.2 Raw map



X



Y

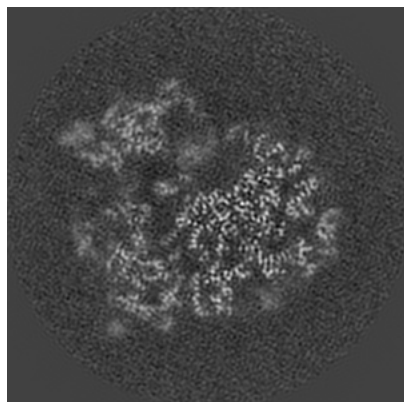


Z

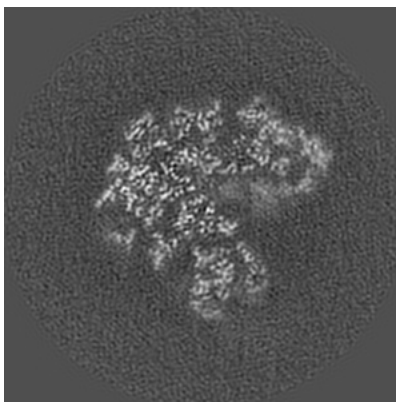
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

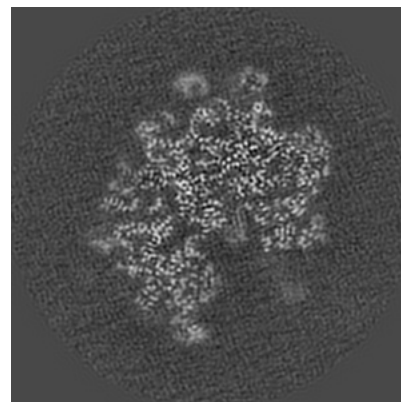
6.2.1 Primary map



X Index: 162

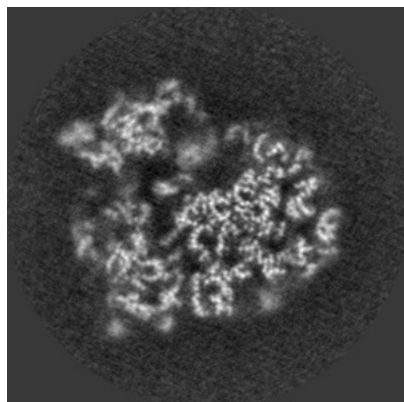


Y Index: 162

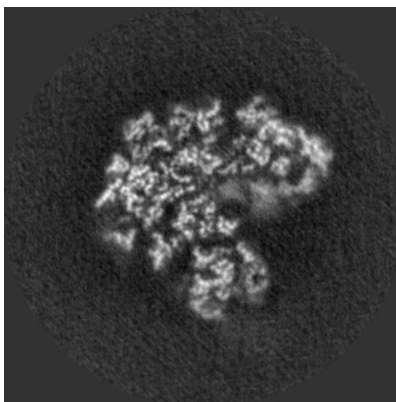


Z Index: 162

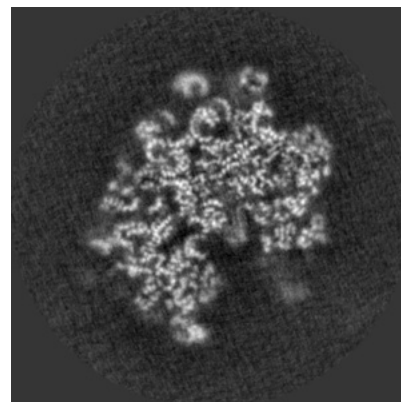
6.2.2 Raw map



X Index: 162



Y Index: 162

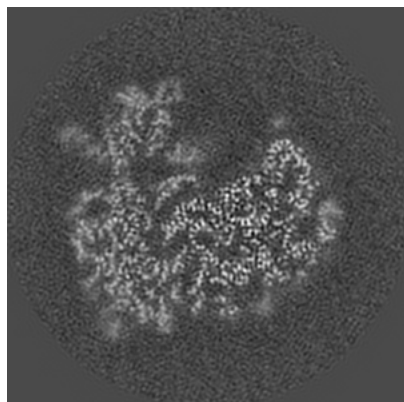


Z Index: 162

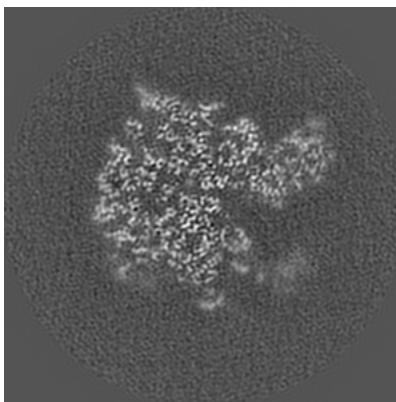
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

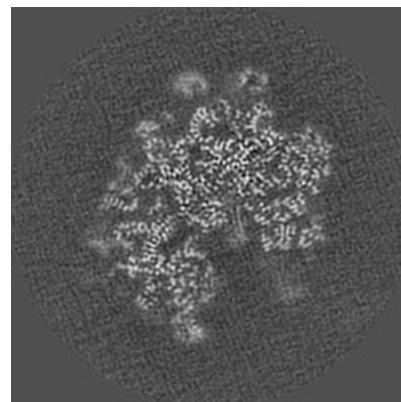
6.3.1 Primary map



X Index: 156

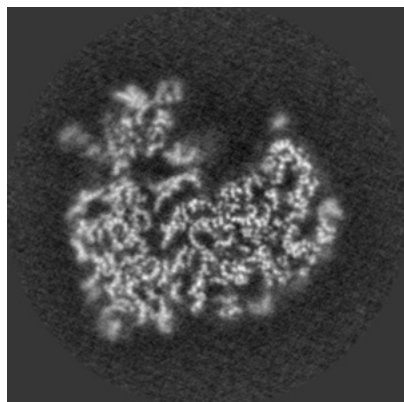


Y Index: 180

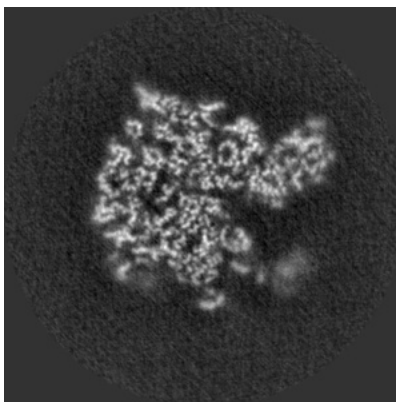


Z Index: 163

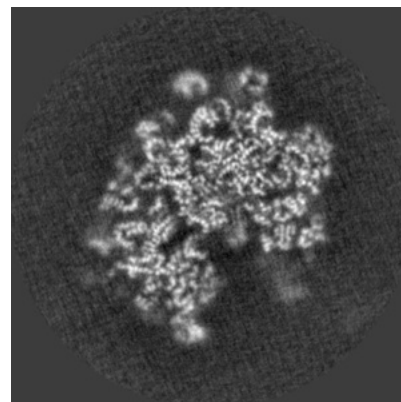
6.3.2 Raw map



X Index: 155



Y Index: 180

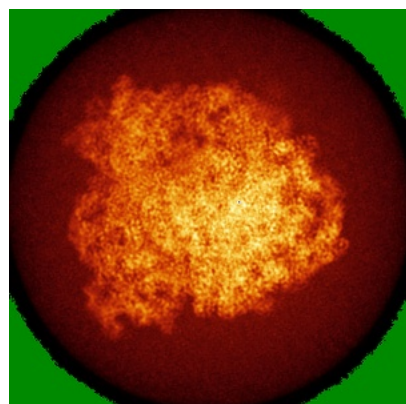


Z Index: 163

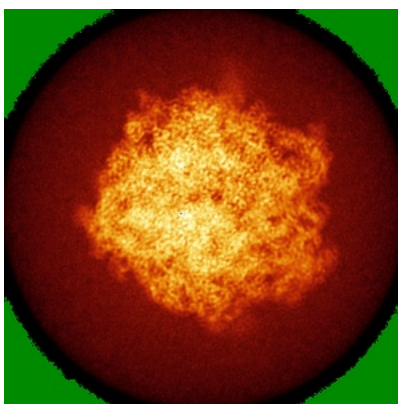
The images above show the largest variance slices of the map in three orthogonal directions.

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

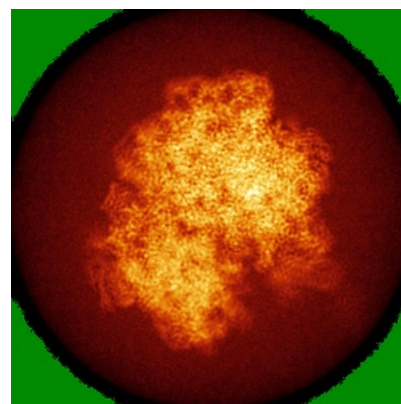
6.4.1 Primary map



X

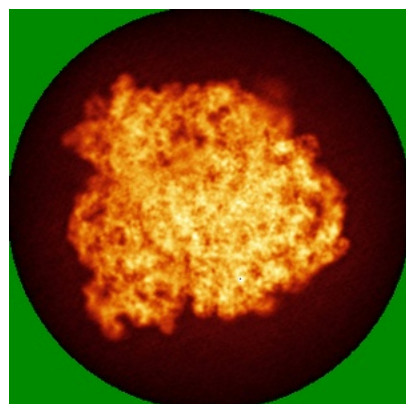


Y

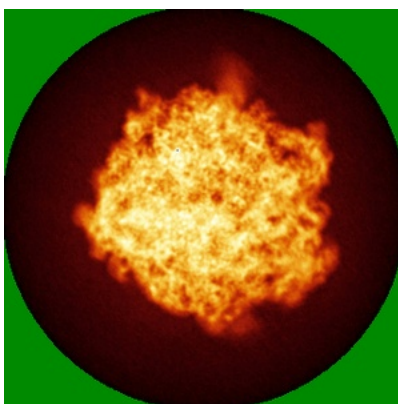


Z

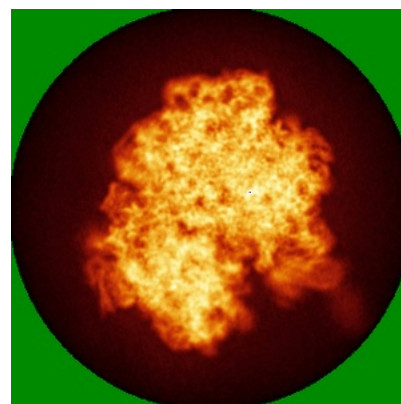
6.4.2 Raw map



X



Y

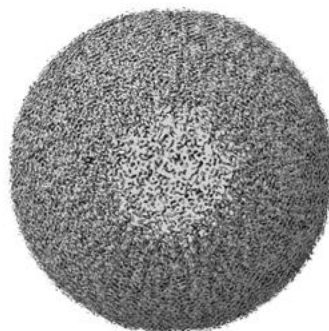


Z

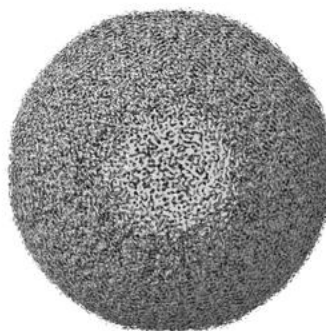
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

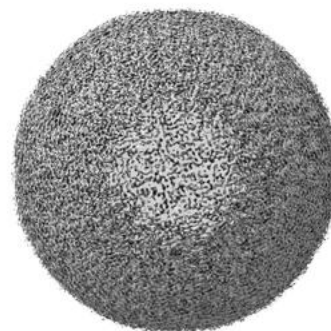
6.5.1 Primary map



X



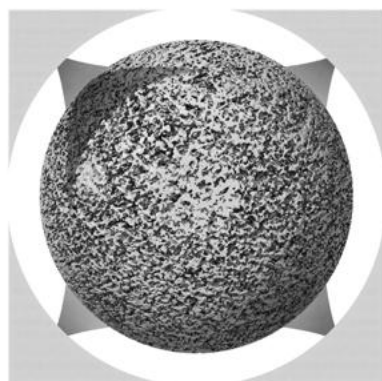
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

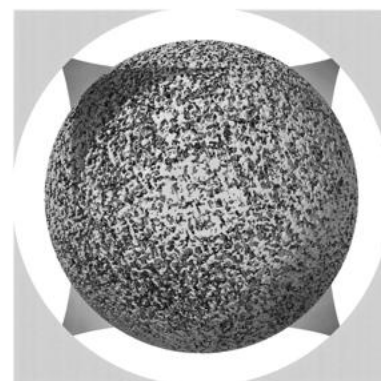
6.5.2 Raw map



X



Y



Z

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.

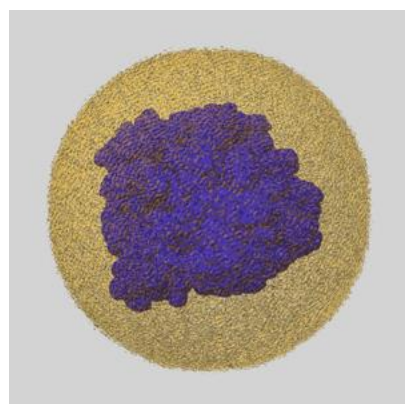
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

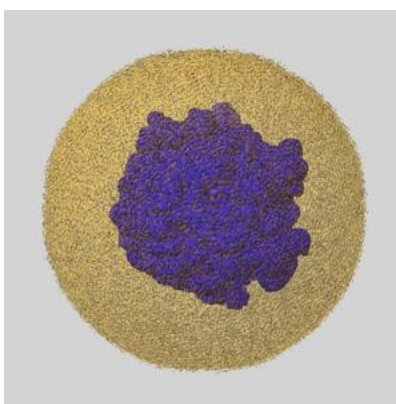
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

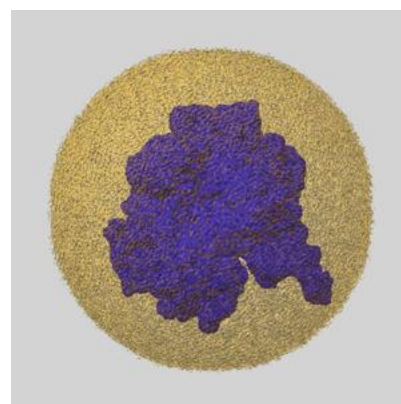
6.6.1 emd_10908_msk_1.map [i](#)



X



Y

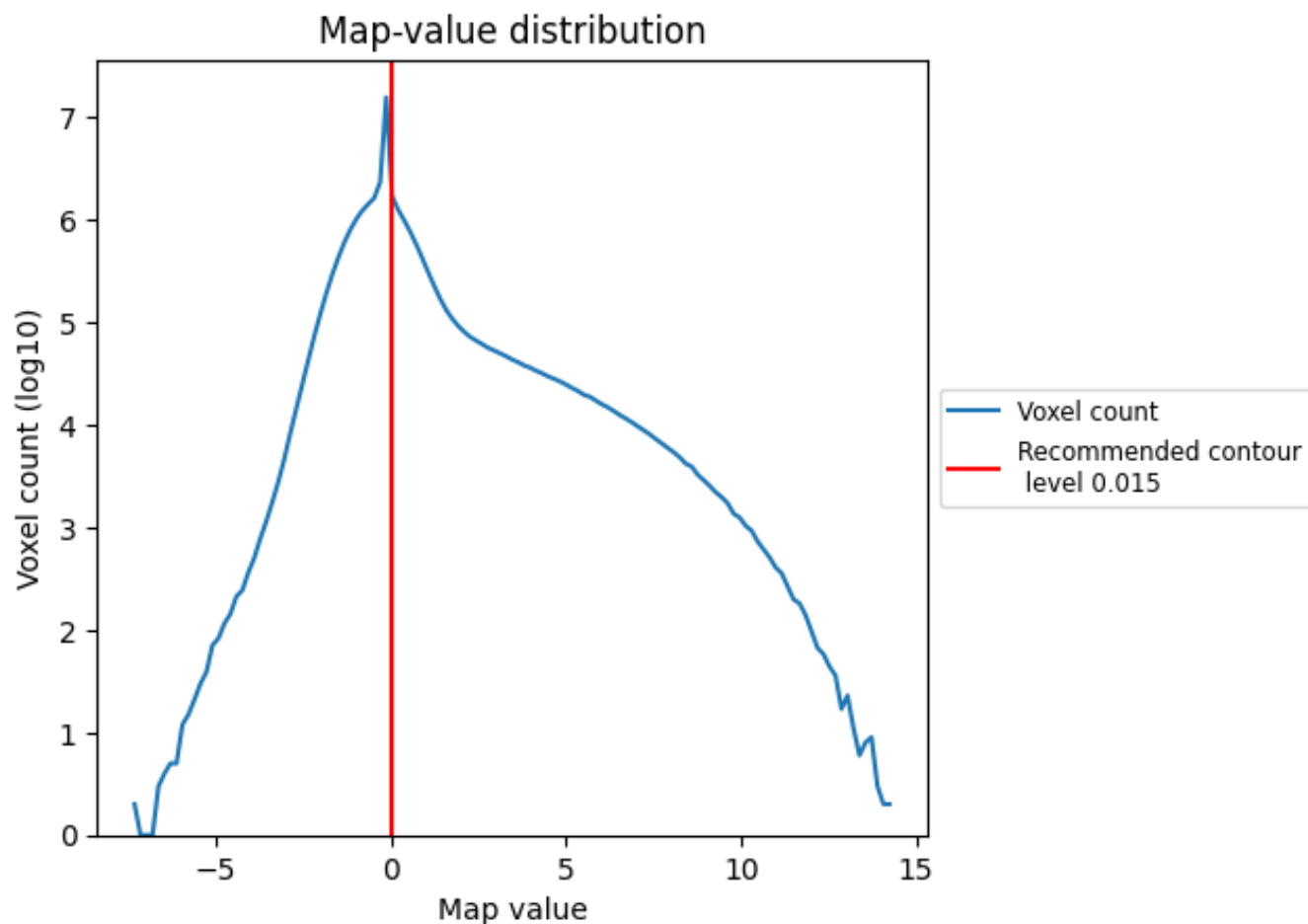


Z

7 Map analysis [i](#)

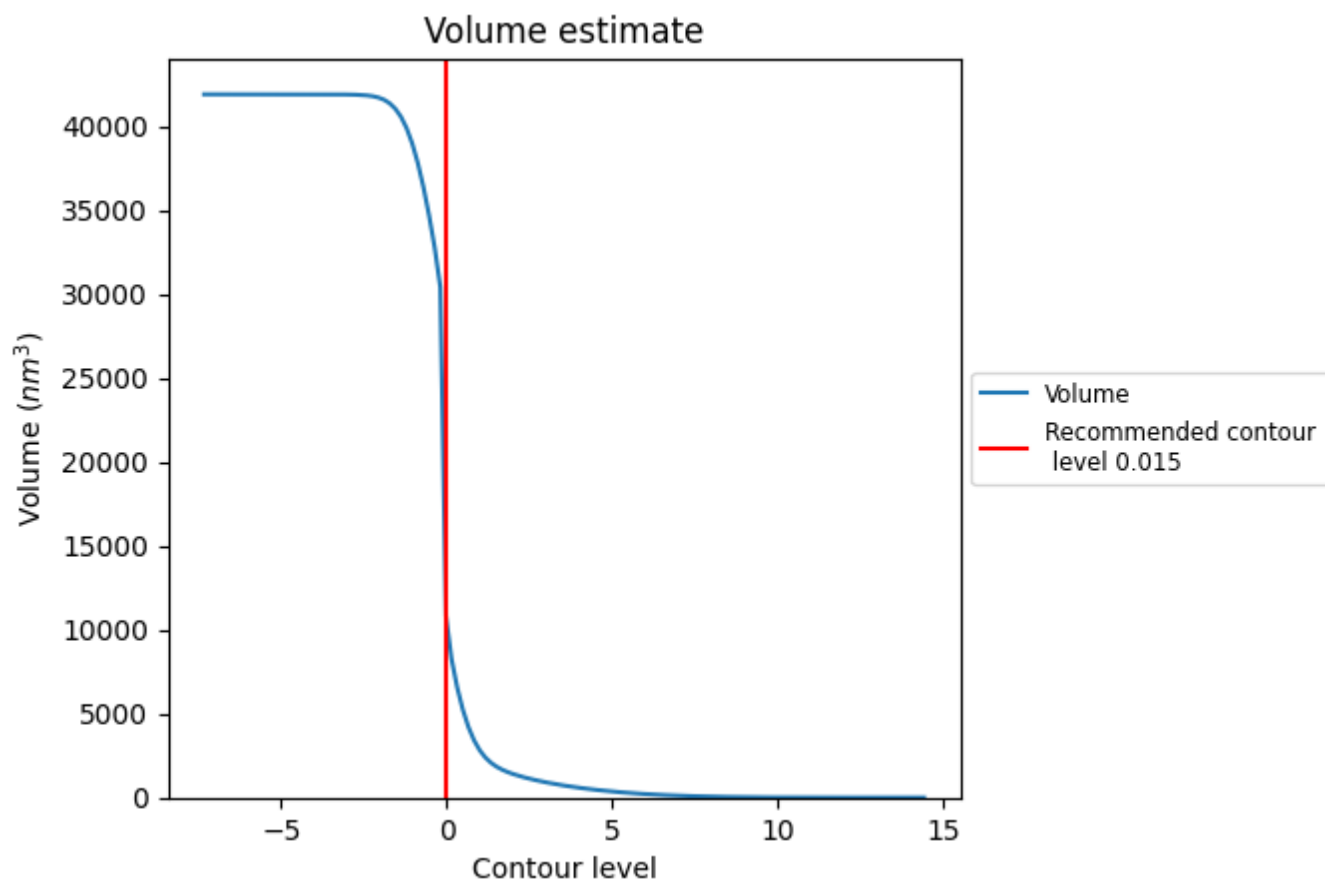
This section contains the results of statistical analysis of the map.

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.

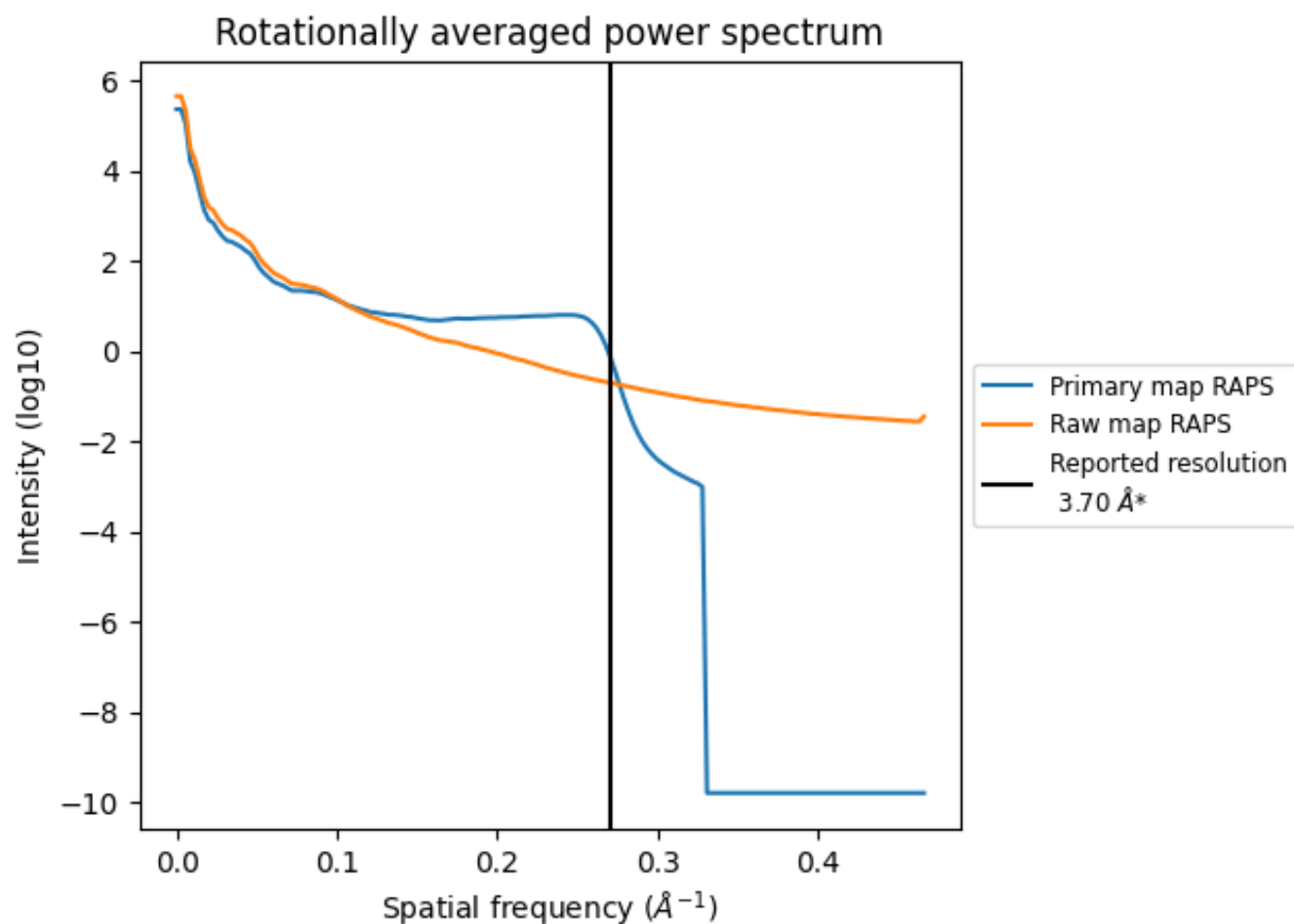
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10367 nm³; this corresponds to an approximate mass of 9365 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 ⓘ

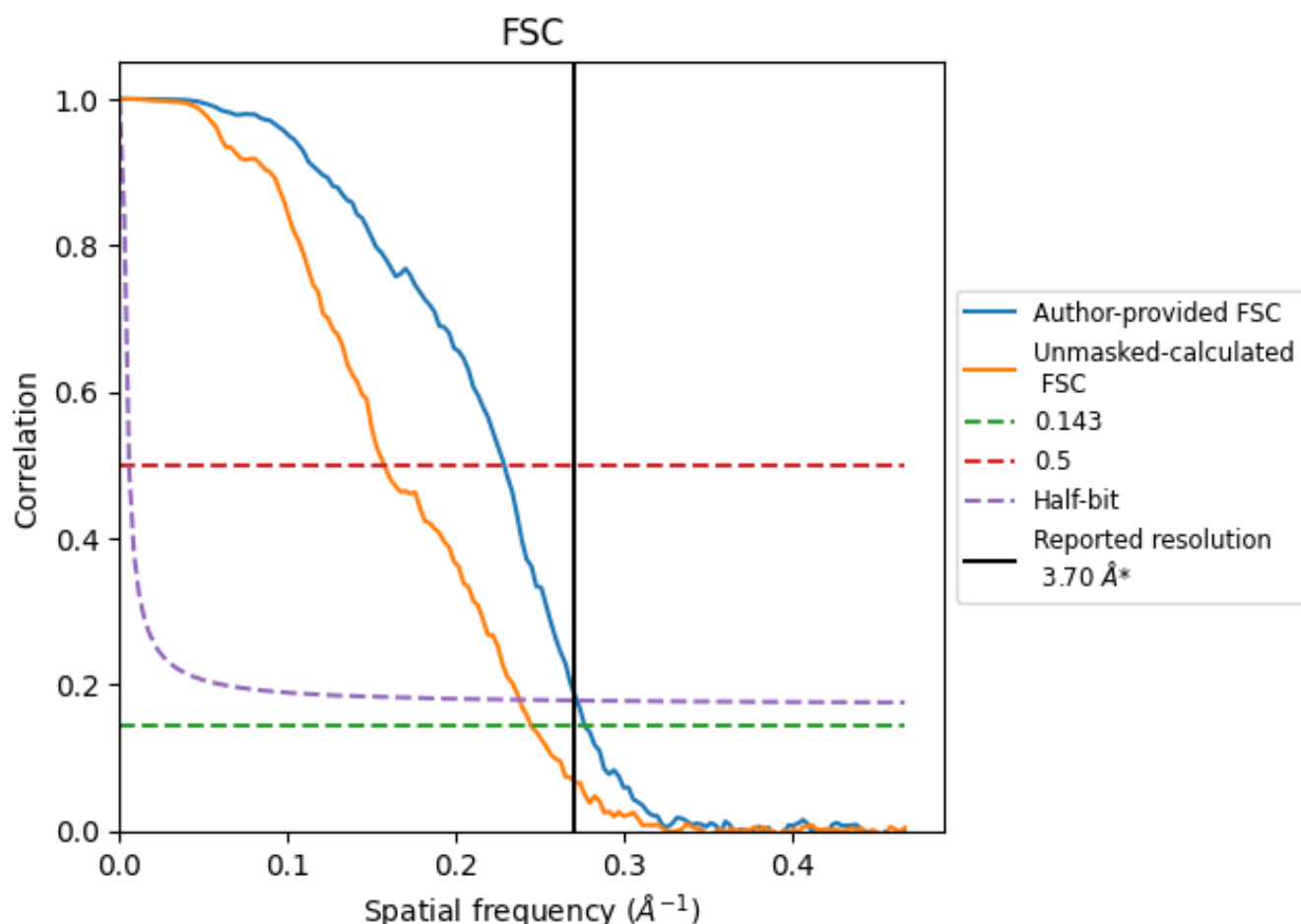


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

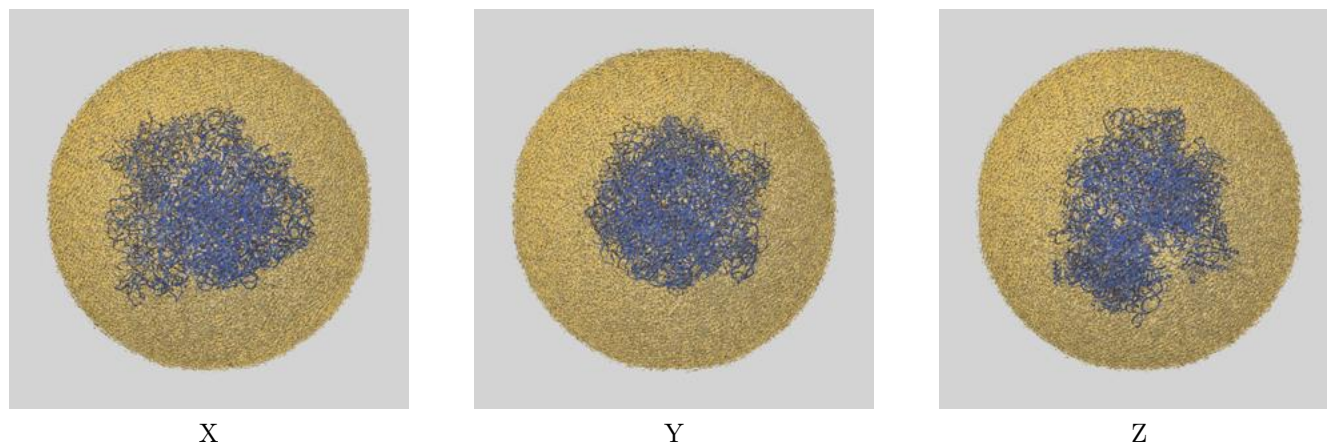
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.62	4.38	3.68
Unmasked-calculated*	4.09	6.37	4.21

*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 4.09 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

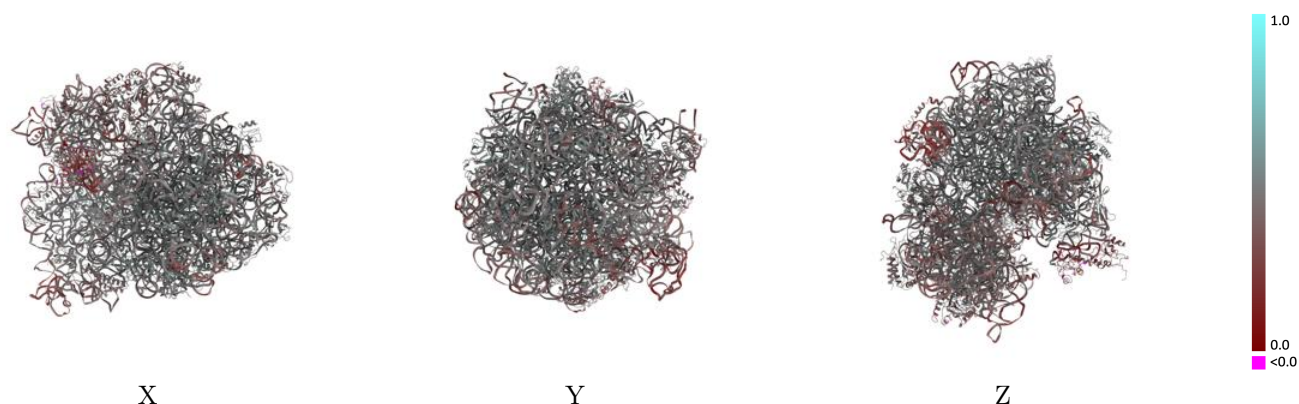
This section contains information regarding the fit between EMDB map EMD-10908 and PDB model 6YSU. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



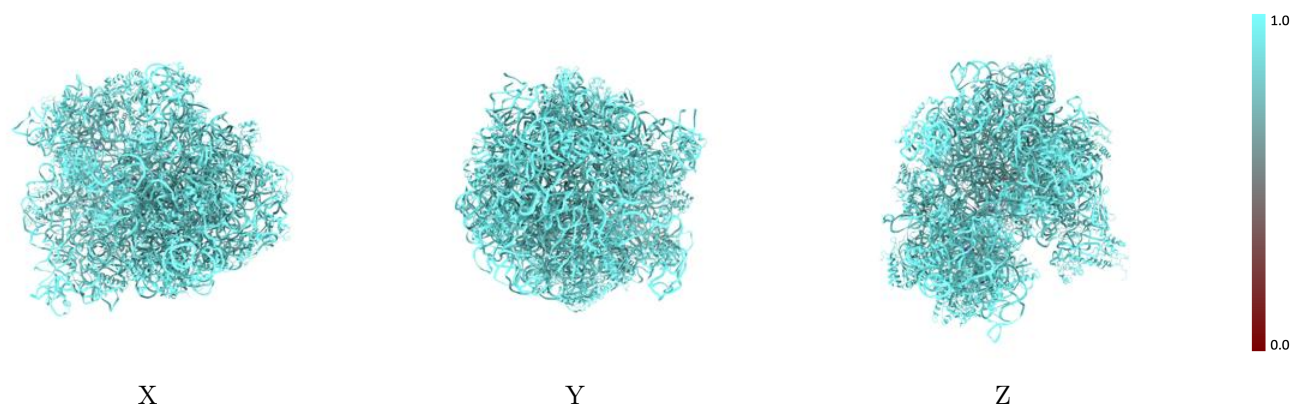
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



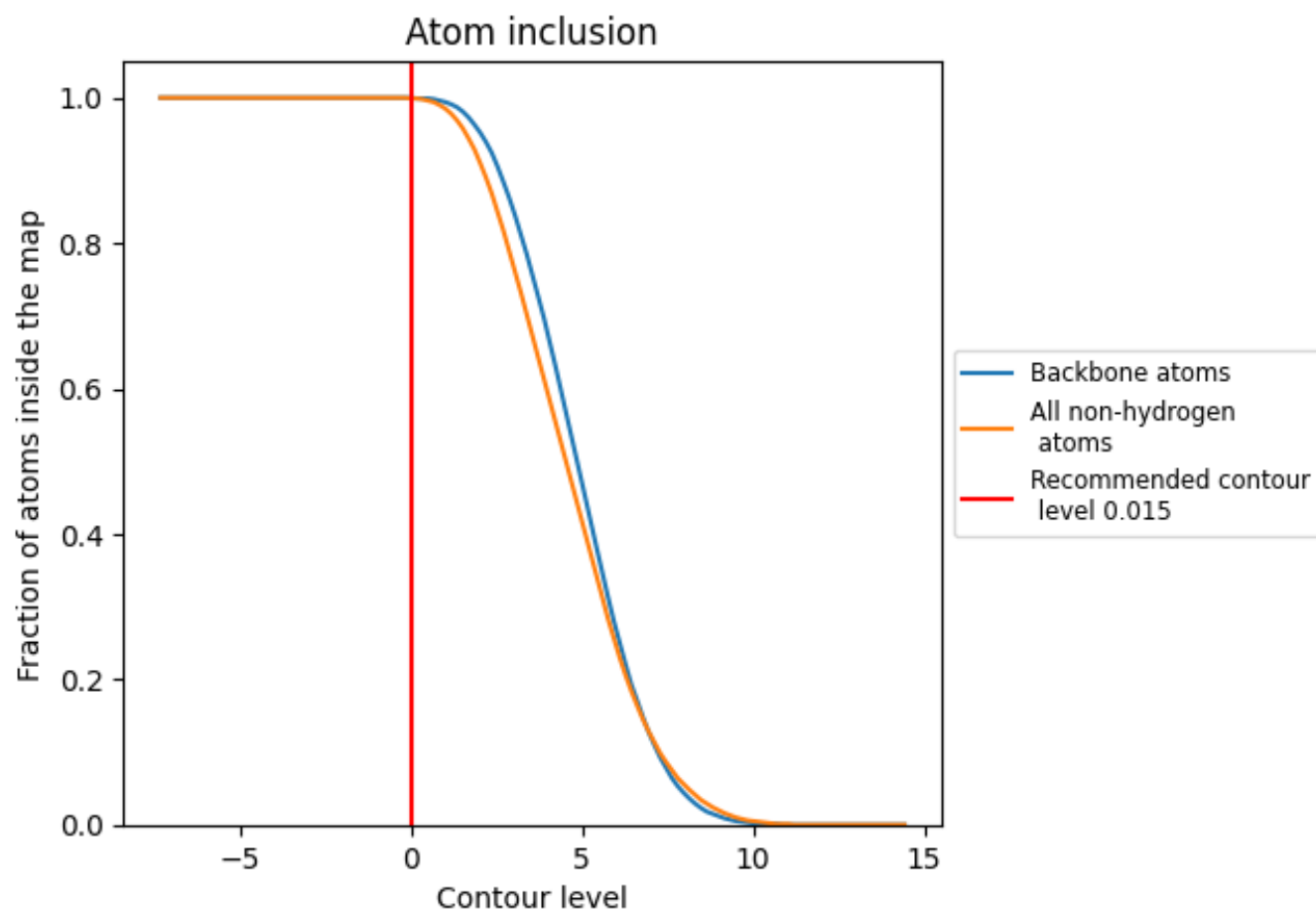
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9990	 0.4460
0	 1.0000	 0.5050
1	 0.9950	 0.4970
2	 0.9970	 0.5250
3	 0.9980	 0.5170
4	 1.0000	 0.5120
5	 1.0000	 0.2850
A	 1.0000	 0.4500
B	 1.0000	 0.4160
C	 0.9980	 0.5170
D	 0.9990	 0.5070
E	 1.0000	 0.4880
F	 1.0000	 0.3980
G	 1.0000	 0.4570
H	 0.9980	 0.3960
I	 0.9970	 0.2800
J	 0.9980	 0.5100
K	 0.9990	 0.5110
L	 0.9970	 0.4980
M	 0.9970	 0.5030
N	 0.9990	 0.5050
O	 1.0000	 0.4360
P	 1.0000	 0.5050
Q	 1.0000	 0.5010
R	 1.0000	 0.5000
S	 0.9980	 0.5050
T	 1.0000	 0.4930
U	 0.9990	 0.4640
V	 0.9990	 0.4740
W	 1.0000	 0.5200
X	 0.9950	 0.4990
Y	 1.0000	 0.4320
Z	 1.0000	 0.4980
a	 1.0000	 0.4270
b	 0.9960	 0.4300



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Chain	Atom inclusion	Q-score
c	 0.9980	 0.4500
d	 0.9990	 0.4480
e	 0.9980	 0.4820
f	 0.9990	 0.4410
g	 0.9990	 0.3910
h	 0.9990	 0.4810
i	 0.9980	 0.4130
j	 0.9960	 0.4000
k	 0.9980	 0.4630
l	 0.9980	 0.4920
m	 1.0000	 0.4030
n	 1.0000	 0.4340
o	 1.0000	 0.4570
p	 1.0000	 0.4610
q	 0.9980	 0.4560
r	 1.0000	 0.4780
s	 1.0000	 0.4230
t	 0.9990	 0.4400
u	 1.0000	 0.4180
v	 1.0000	 0.4260
w	 0.9950	 0.3300
x	 1.0000	 0.4530
y	 0.9880	 0.4320