Full wwPDB EM Validation Report ⓘ

Nov 29, 2022 – 02:34 AM JST

PDB ID	:	7VPZ
EMDB ID	:	EMD-32077
Title	:	Cryo-EM structure of Streptomyces coelicolor transcription initial complex with one Zur dimer
Authors	:	Yang, X.; Zheng, J.
Deposited on	:	2021-10-18
Resolution	:	4.14 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

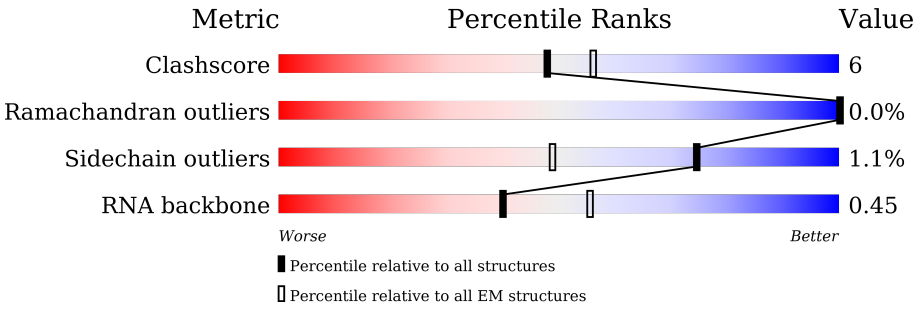
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.14 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)
Clashscore	158937	4297
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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	340	55% 11% 34%
1	B	340	61% 7% 31%
2	C	1161	78% 18%
3	D	1307	81% 16%
4	E	90	72% 13% 14%
5	F	531	47% 10% 43%
6	M	159	18% 70% 12% 18%

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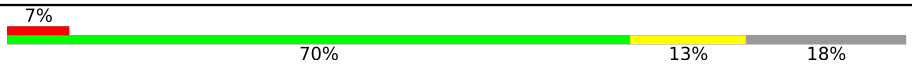
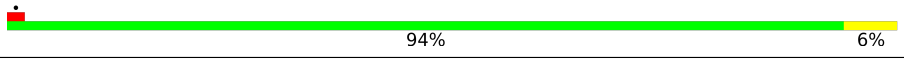
Mol	Chain	Length	Quality of chain
6	N	159	
7	O	84	
8	P	84	
9	Q	5	

2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 30593 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	226	Total	C	N	O	S	0	0
			1742	1102	302	334	4		
1	B	233	Total	C	N	O	S	0	0
			1792	1131	309	347	5		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1116	Total	C	N	O	S	0	0
			8692	5450	1513	1698	31		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1259	Total	C	N	O	S	0	0
			9846	6161	1787	1857	41		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1300	HIS	-	expression tag	UNP Q8CJT1
D	1301	HIS	-	expression tag	UNP Q8CJT1
D	1302	HIS	-	expression tag	UNP Q8CJT1
D	1303	HIS	-	expression tag	UNP Q8CJT1
D	1304	HIS	-	expression tag	UNP Q8CJT1
D	1305	HIS	-	expression tag	UNP Q8CJT1
D	1306	HIS	-	expression tag	UNP Q8CJT1
D	1307	HIS	-	expression tag	UNP Q8CJT1

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	77	Total	C	N	O	0	0
			597	382	98	117		

- Molecule 5 is a protein called RNA polymerase principal sigma factor HrdB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	301	Total	C	N	O	S	0	0
			2396	1509	426	454	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	initiating methionine	UNP P18183
F	-18	GLY	-	expression tag	UNP P18183
F	-17	SER	-	expression tag	UNP P18183
F	-16	SER	-	expression tag	UNP P18183
F	-15	HIS	-	expression tag	UNP P18183
F	-14	HIS	-	expression tag	UNP P18183
F	-13	HIS	-	expression tag	UNP P18183
F	-12	HIS	-	expression tag	UNP P18183
F	-11	HIS	-	expression tag	UNP P18183
F	-10	HIS	-	expression tag	UNP P18183
F	-9	SER	-	expression tag	UNP P18183
F	-8	SER	-	expression tag	UNP P18183
F	-7	GLY	-	expression tag	UNP P18183
F	-6	LEU	-	expression tag	UNP P18183
F	-5	VAL	-	expression tag	UNP P18183
F	-4	PRO	-	expression tag	UNP P18183
F	-3	ARG	-	expression tag	UNP P18183
F	-2	GLY	-	expression tag	UNP P18183
F	-1	SER	-	expression tag	UNP P18183
F	0	HIS	-	expression tag	UNP P18183

- Molecule 6 is a protein called Putative metal uptake regulation protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	131	Total	C	N	O	S	0	0
			984	603	185	190	6		
6	N	131	Total	C	N	O	S	0	0
			984	603	185	190	6		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-19	MET	-	initiating methionine	UNP Q9L2H5
M	-18	GLY	-	expression tag	UNP Q9L2H5
M	-17	SER	-	expression tag	UNP Q9L2H5
M	-16	SER	-	expression tag	UNP Q9L2H5
M	-15	HIS	-	expression tag	UNP Q9L2H5
M	-14	HIS	-	expression tag	UNP Q9L2H5
M	-13	HIS	-	expression tag	UNP Q9L2H5
M	-12	HIS	-	expression tag	UNP Q9L2H5
M	-11	HIS	-	expression tag	UNP Q9L2H5
M	-10	HIS	-	expression tag	UNP Q9L2H5
M	-9	SER	-	expression tag	UNP Q9L2H5
M	-8	SER	-	expression tag	UNP Q9L2H5
M	-7	GLY	-	expression tag	UNP Q9L2H5
M	-6	LEU	-	expression tag	UNP Q9L2H5
M	-5	VAL	-	expression tag	UNP Q9L2H5
M	-4	PRO	-	expression tag	UNP Q9L2H5
M	-3	ARG	-	expression tag	UNP Q9L2H5
M	-2	GLY	-	expression tag	UNP Q9L2H5
M	-1	SER	-	expression tag	UNP Q9L2H5
M	0	HIS	-	expression tag	UNP Q9L2H5
N	-19	MET	-	initiating methionine	UNP Q9L2H5
N	-18	GLY	-	expression tag	UNP Q9L2H5
N	-17	SER	-	expression tag	UNP Q9L2H5
N	-16	SER	-	expression tag	UNP Q9L2H5
N	-15	HIS	-	expression tag	UNP Q9L2H5
N	-14	HIS	-	expression tag	UNP Q9L2H5
N	-13	HIS	-	expression tag	UNP Q9L2H5
N	-12	HIS	-	expression tag	UNP Q9L2H5
N	-11	HIS	-	expression tag	UNP Q9L2H5
N	-10	HIS	-	expression tag	UNP Q9L2H5
N	-9	SER	-	expression tag	UNP Q9L2H5
N	-8	SER	-	expression tag	UNP Q9L2H5
N	-7	GLY	-	expression tag	UNP Q9L2H5
N	-6	LEU	-	expression tag	UNP Q9L2H5
N	-5	VAL	-	expression tag	UNP Q9L2H5
N	-4	PRO	-	expression tag	UNP Q9L2H5
N	-3	ARG	-	expression tag	UNP Q9L2H5
N	-2	GLY	-	expression tag	UNP Q9L2H5
N	-1	SER	-	expression tag	UNP Q9L2H5
N	0	HIS	-	expression tag	UNP Q9L2H5

- Molecule 7 is a DNA chain called DNA (84-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	84	Total 1714	C 810	N 315	O 505	P 84	0	0

- Molecule 8 is a DNA chain called DNA (84-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	84	Total 1729	C 815	N 325	O 505	P 84	0	0

- Molecule 9 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	5	Total 108	C 49	N 22	O 33	P 4	0	0

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	D	1	Total 1	Mg 1	0

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

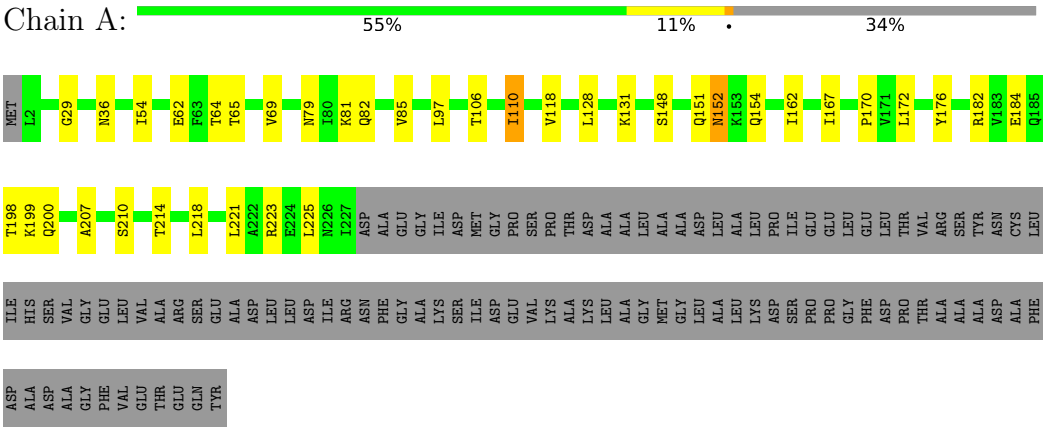
Mol	Chain	Residues	Atoms		AltConf
11	D	2	Total 2	Zn 2	0
11	M	3	Total 3	Zn 3	0
11	N	3	Total 3	Zn 3	0

3 Residue-property plots (i)

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

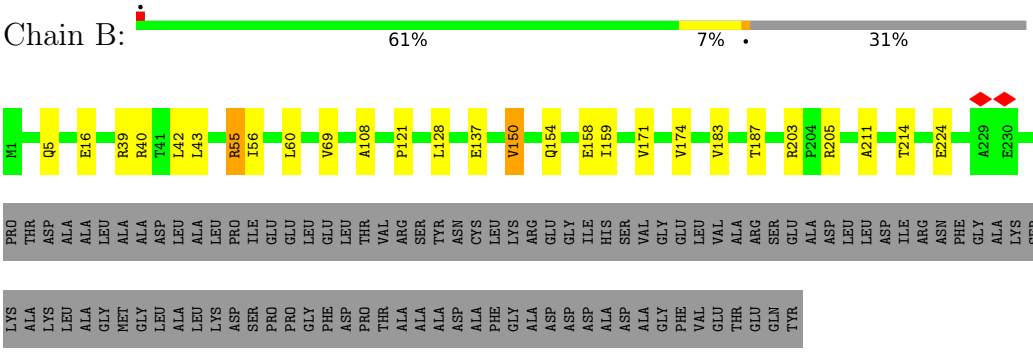
• Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain A:



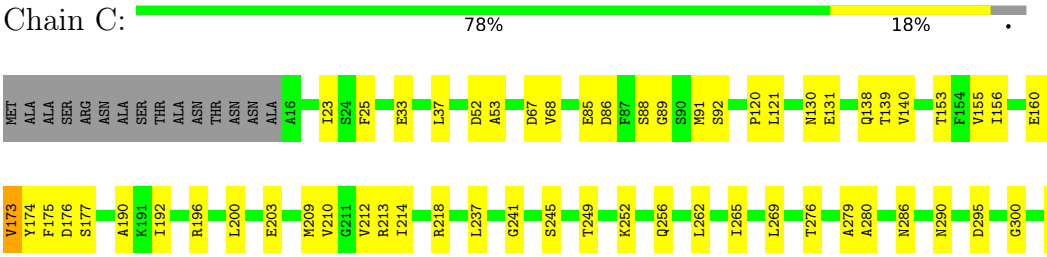
• Molecule 1: DNA-directed RNA polymerase subunit alpha

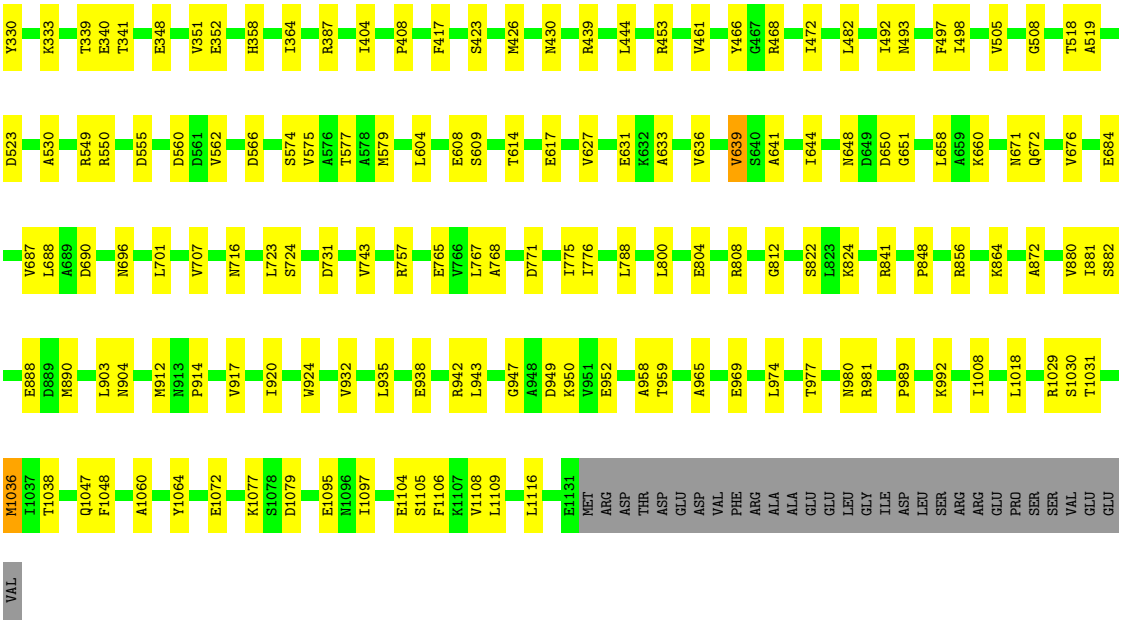
Chain B:



• Molecule 2: DNA-directed RNA polymerase subunit beta

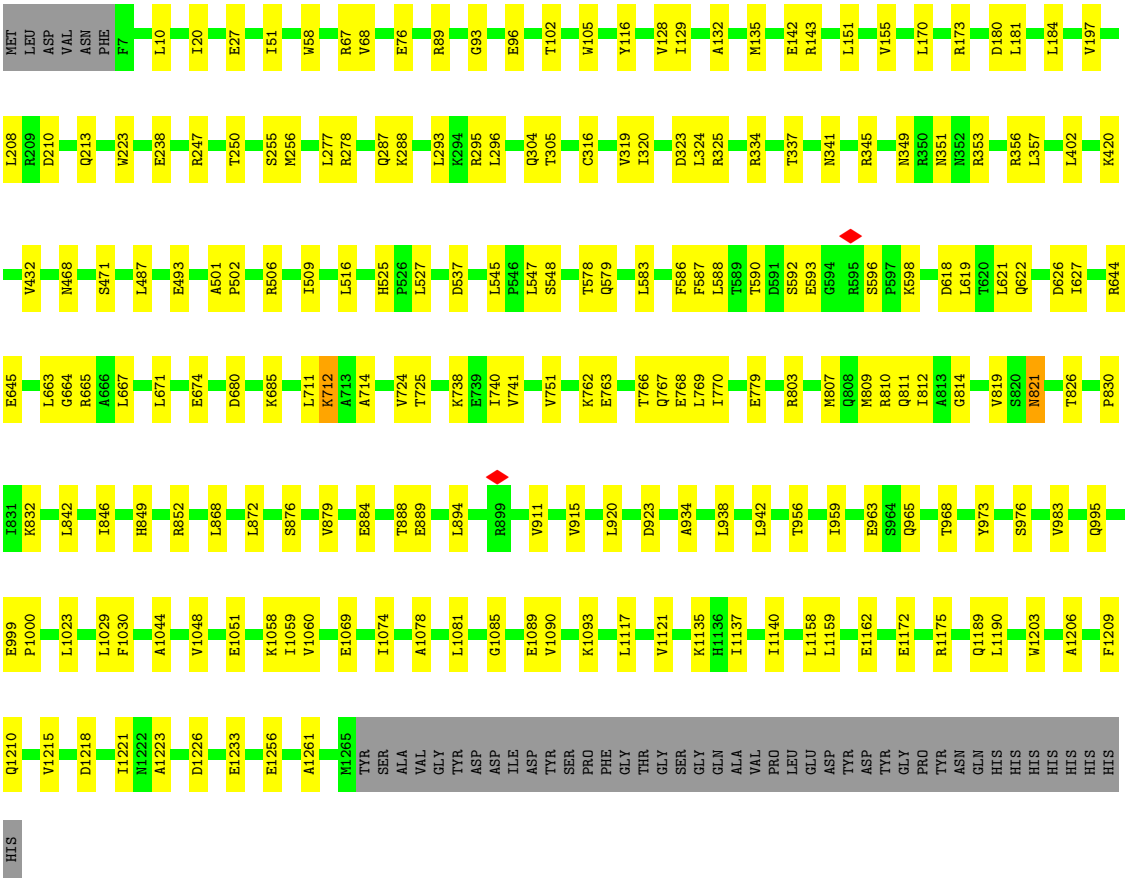
Chain C:





• Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain D:

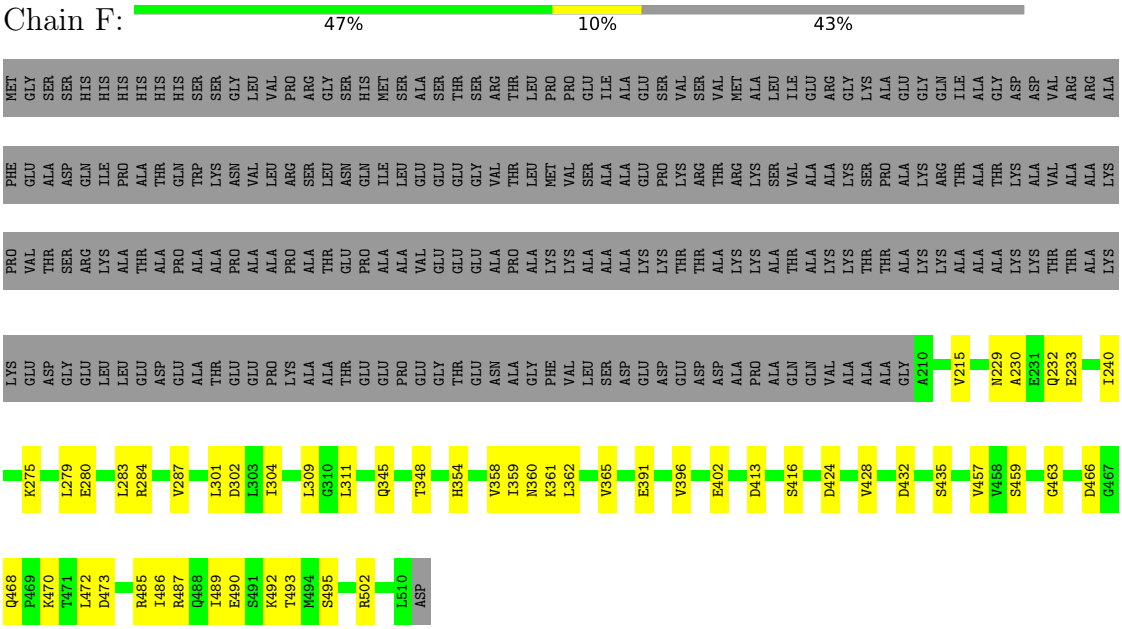


• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:

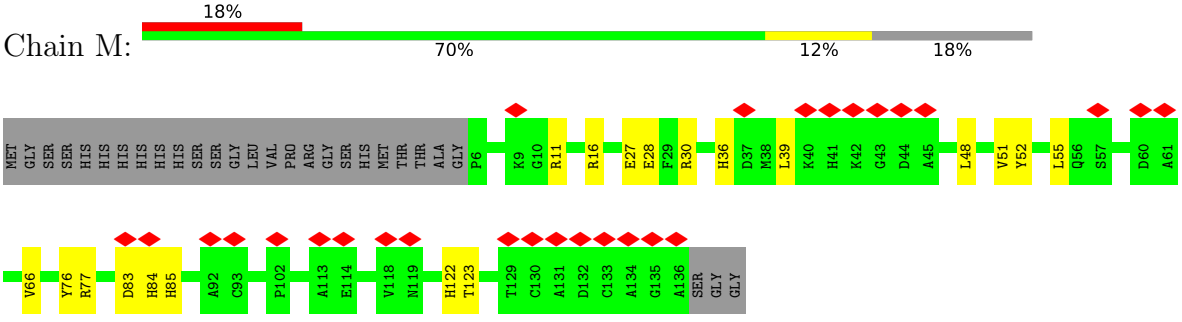
• Molecule 5: RNA polymerase principal sigma factor HrdB

Chain F:



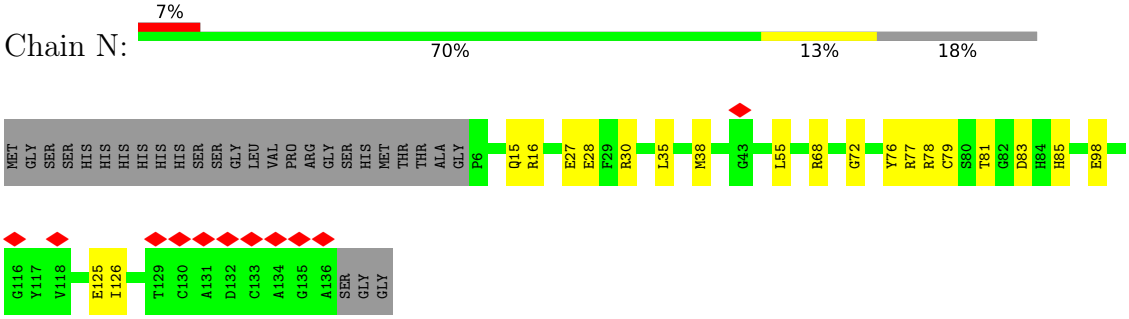
• Molecule 6: Putative metal uptake regulation protein

Chain M:



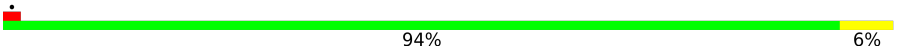
• Molecule 6: Putative metal uptake regulation protein

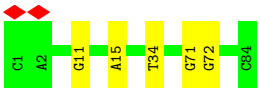
Chain N:



• Molecule 7: DNA (84-MER)

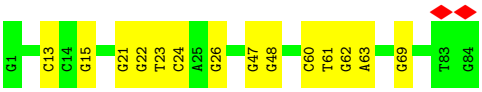
Chain O:





• Molecule 8: DNA (84-MER)

Chain P:



• Molecule 9: RNA

Chain Q:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21494	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40, 40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.751	Depositor
Minimum map value	-1.584	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.29	0/1768	0.58	0/2400
1	B	0.28	0/1818	0.59	0/2467
2	C	0.29	0/8848	0.56	0/11982
3	D	0.28	0/9998	0.59	0/13490
4	E	0.30	0/607	0.53	0/826
5	F	0.27	0/2431	0.56	0/3277
6	M	0.26	0/1001	0.59	0/1355
6	N	0.24	0/1001	0.51	0/1355
7	O	0.68	0/1920	0.95	0/2959
8	P	0.67	0/1940	0.90	0/2994
9	Q	0.24	0/121	0.55	0/188
All	All	0.35	0/31453	0.63	0/43293

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	1742	0	1796	21	0
1	B	1792	0	1841	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	8692	0	8632	133	0
3	D	9846	0	10017	145	0
4	E	597	0	604	10	0
5	F	2396	0	2453	33	0
6	M	984	0	947	14	0
6	N	984	0	947	13	0
7	O	1714	0	940	7	0
8	P	1729	0	940	17	0
9	Q	108	0	55	0	0
10	D	1	0	0	0	0
11	D	2	0	0	0	0
11	M	3	0	0	0	0
11	N	3	0	0	0	0
All	All	30593	0	29172	373	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.

All (373) 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)
2:C:140:VAL:HG21	2:C:404:ILE:HD11	1.57	0.87
2:C:912:MET:SD	3:D:811:GLN:NE2	2.50	0.84
2:C:364:ILE:HD11	2:C:492:ILE:HD12	1.64	0.78
1:B:55:ARG:NH1	1:B:56:ILE:O	2.18	0.77
3:D:502:PRO:HG3	8:P:15:DG:H22	1.51	0.74
3:D:665:ARG:NE	3:D:680:ASP:O	2.21	0.74
3:D:579:GLN:OE1	3:D:803:ARG:NH1	2.21	0.73
2:C:549:ARG:NH2	2:C:555:ASP:OD2	2.21	0.73
2:C:841:ARG:NH2	2:C:848:PRO:O	2.22	0.72
3:D:751:VAL:HG11	3:D:768:GLU:OE2	1.88	0.72
4:E:10:GLY:N	4:E:13:ASN:OD1	2.21	0.72
2:C:200:LEU:HD13	2:C:214:ILE:HD13	1.71	0.72
6:M:27:GLU:O	6:M:77:ARG:NE	2.22	0.72
2:C:1072:GLU:OE2	3:D:547:LEU:N	2.23	0.72
3:D:76:GLU:OE2	3:D:76:GLU:N	2.23	0.72
6:N:78:ARG:NH1	6:N:79:CYS:O	2.23	0.72
6:N:15:GLN:NE2	7:O:11:DG:OP2	2.24	0.70
2:C:765:GLU:N	2:C:765:GLU:OE1	2.24	0.70
2:C:771:ASP:N	2:C:775:ILE:O	2.23	0.70
3:D:1048:VAL:O	3:D:1085:GLY:N	2.25	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:1029:ARG:NH1	2:C:1048:PHE:O	2.25	0.70
6:N:77:ARG:NH1	6:N:79:CYS:SG	2.65	0.69
2:C:339:THR:OG1	2:C:340:GLU:OE1	2.11	0.69
2:C:800:LEU:HD12	2:C:804:GLU:OE1	1.92	0.69
3:D:357:LEU:HD21	5:F:309:LEU:HD21	1.74	0.69
4:E:65:GLU:OE1	4:E:65:GLU:N	2.26	0.68
2:C:617:GLU:OE1	2:C:617:GLU:N	2.27	0.67
3:D:143:ARG:NH1	3:D:250:THR:O	2.28	0.67
2:C:924:TRP:HZ3	2:C:977:THR:HG21	1.60	0.67
5:F:301:LEU:HA	5:F:304:ILE:HD12	1.77	0.67
2:C:256:GLN:N	2:C:256:GLN:OE1	2.29	0.66
3:D:920:LEU:HG	3:D:938:LEU:HD21	1.77	0.66
3:D:923:ASP:OD1	3:D:934:ALA:N	2.28	0.66
3:D:973:TYR:O	3:D:1135:LYS:NZ	2.20	0.66
2:C:33:GLU:OE1	2:C:33:GLU:N	2.29	0.66
2:C:161:ARG:NH2	2:C:423:SER:O	2.29	0.66
2:C:364:ILE:CD1	2:C:492:ILE:HD12	2.27	0.65
3:D:963:GLU:OE2	3:D:965:GLN:NE2	2.30	0.64
2:C:1079:ASP:OD2	3:D:420:LYS:NZ	2.28	0.64
3:D:345:ARG:NH2	5:F:348:THR:O	2.31	0.64
2:C:822:SER:O	2:C:824:LYS:NZ	2.31	0.64
3:D:173:ARG:NE	3:D:208:LEU:HD23	2.12	0.64
2:C:731:ASP:OD1	2:C:864:LYS:NZ	2.27	0.64
3:D:96:GLU:O	3:D:351:ASN:ND2	2.31	0.63
2:C:724:SER:OG	2:C:890:MET:SD	2.53	0.63
6:N:28:GLU:OE1	6:N:30:ARG:NH2	2.32	0.62
1:B:224:GLU:N	1:B:224:GLU:OE1	2.32	0.62
2:C:358:HIS:NE2	2:C:519:ALA:O	2.31	0.62
3:D:502:PRO:HB3	8:P:15:DG:N2	2.14	0.61
2:C:453:ARG:HA	7:O:71:DG:H1'	1.81	0.61
2:C:523:ASP:OD2	2:C:550:ARG:NE	2.33	0.61
2:C:508:GLY:N	2:C:560:ASP:OD1	2.34	0.60
5:F:472:LEU:HD12	8:P:48:DG:OP2	2.00	0.60
1:A:152:ASN:ND2	1:A:152:ASN:O	2.33	0.60
3:D:587:PHE:O	3:D:622:GLN:NE2	2.33	0.60
4:E:36:ARG:NE	4:E:74:GLU:OE1	2.35	0.60
3:D:671:LEU:HD21	3:D:714:ALA:CB	2.31	0.60
1:B:108:ALA:N	1:B:121:PRO:O	2.35	0.60
2:C:196:ARG:HB3	2:C:295:ASP:HB3	1.82	0.60
3:D:1044:ALA:HA	3:D:1090:VAL:HG12	1.84	0.60
2:C:980:ASN:OD1	2:C:981:ARG:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:608:GLU:OE2	2:C:609:SER:N	2.35	0.60
2:C:1077:LYS:NZ	3:D:545:LEU:O	2.25	0.60
2:C:1116:LEU:HD13	3:D:105:TRP:CH2	2.37	0.60
2:C:716:ASN:O	2:C:904:ASN:ND2	2.35	0.59
3:D:1189:GLN:NE2	3:D:1190:LEU:O	2.35	0.59
3:D:884:GLU:OE2	3:D:884:GLU:N	2.32	0.59
2:C:952:GLU:OE1	2:C:952:GLU:N	2.35	0.59
2:C:650:ASP:OD1	2:C:651:GLY:N	2.35	0.59
3:D:618:ASP:OD1	3:D:619:LEU:N	2.36	0.59
6:M:55:LEU:HD13	6:M:76:TYR:HE2	1.66	0.59
3:D:1029:LEU:HD12	3:D:1117:LEU:HD23	1.85	0.59
2:C:23:ILE:O	2:C:958:ALA:N	2.36	0.59
6:M:28:GLU:OE2	6:M:30:ARG:NH2	2.36	0.59
2:C:444:LEU:HD21	2:C:482:LEU:HD13	1.83	0.58
2:C:631:GLU:N	2:C:631:GLU:OE1	2.36	0.58
3:D:586:PHE:O	3:D:590:THR:OG1	2.21	0.58
3:D:671:LEU:HD21	3:D:714:ALA:HB3	1.84	0.58
3:D:493:GLU:OE2	4:E:10:GLY:N	2.37	0.58
3:D:527:LEU:HD21	3:D:712:LYS:HB2	1.84	0.58
1:B:154:GLN:N	1:B:154:GLN:OE1	2.37	0.58
7:O:72:DG:H1	8:P:13:DC:H42	1.52	0.57
2:C:173:VAL:HG12	2:C:192:ILE:HG22	1.87	0.57
2:C:341:THR:N	2:C:348:GLU:OE2	2.36	0.57
2:C:882:SER:OG	3:D:432:VAL:O	2.22	0.57
3:D:626:ASP:OD1	3:D:627:ILE:N	2.38	0.57
6:N:27:GLU:OE1	6:N:77:ARG:NH2	2.37	0.57
3:D:525:HIS:CE1	3:D:527:LEU:HD23	2.40	0.57
3:D:238:GLU:OE1	3:D:238:GLU:N	2.37	0.56
2:C:1036:MET:HB3	5:F:424:ASP:HB3	1.87	0.56
3:D:502:PRO:CG	8:P:15:DG:H22	2.18	0.56
5:F:359:ILE:HD13	5:F:396:VAL:HG12	1.87	0.56
3:D:487:LEU:HD22	3:D:516:LEU:HD11	1.88	0.56
2:C:949:ASP:OD1	2:C:950:LYS:N	2.39	0.55
3:D:1058:LYS:NZ	3:D:1059:ILE:O	2.40	0.55
2:C:352:GLU:N	2:C:352:GLU:OE1	2.40	0.55
2:C:671:ASN:OD1	2:C:672:GLN:N	2.39	0.55
2:C:942:ARG:NH2	2:C:969:GLU:OE2	2.40	0.55
6:M:123:THR:OG1	6:N:125:GLU:O	2.25	0.55
3:D:502:PRO:CB	8:P:15:DG:N2	2.69	0.55
5:F:229:ASN:O	5:F:232:GLN:N	2.40	0.55
8:P:21:DG:H2'	8:P:22:DG:C8	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:430:ASN:HD22	2:C:701:LEU:HD22	1.72	0.54
2:C:472:ILE:CD1	2:C:577:THR:HG21	2.37	0.54
1:A:79:ASN:O	1:A:82:GLN:NE2	2.40	0.54
3:D:770:ILE:HD12	3:D:826:THR:HG21	1.88	0.54
3:D:1261:ALA:HB2	4:E:79:LEU:HD21	1.88	0.54
5:F:354:HIS:O	5:F:358:VAL:HG23	2.07	0.54
1:A:184:GLU:OE2	1:A:184:GLU:N	2.35	0.54
1:A:200:GLN:OE1	1:A:200:GLN:N	2.41	0.54
3:D:277:LEU:HD21	3:D:295:ARG:HE	1.72	0.54
2:C:212:VAL:O	2:C:213:ARG:NE	2.40	0.54
1:A:154:GLN:OE1	1:A:154:GLN:N	2.40	0.54
3:D:1060:VAL:HG13	3:D:1069:GLU:OE2	2.08	0.54
3:D:938:LEU:HD22	3:D:942:LEU:HD22	1.91	0.53
6:M:66:VAL:HG12	6:M:76:TYR:CE1	2.43	0.53
2:C:888:GLU:OE2	2:C:888:GLU:N	2.40	0.53
1:A:170:PRO:O	1:A:198:THR:OG1	2.21	0.53
6:N:81:THR:OG1	6:N:98:GLU:OE1	2.27	0.53
2:C:138:GLN:NE2	2:C:139:THR:O	2.41	0.53
5:F:413:ASP:O	5:F:416:SER:OG	2.20	0.53
3:D:349:ASN:ND2	5:F:345:GLN:OE1	2.41	0.52
3:D:763:GLU:O	3:D:766:THR:OG1	2.22	0.52
3:D:1256:GLU:OE1	3:D:1256:GLU:N	2.43	0.52
4:E:32:TYR:CE2	4:E:75:ILE:HD12	2.44	0.52
6:N:83:ASP:O	6:N:85:HIS:ND1	2.42	0.52
2:C:209:MET:SD	2:C:252:LYS:NZ	2.77	0.52
5:F:215:VAL:HG22	5:F:301:LEU:HB2	1.92	0.52
2:C:472:ILE:HD13	2:C:577:THR:HG21	1.92	0.52
2:C:203:GLU:N	2:C:203:GLU:OE1	2.43	0.51
3:D:128:VAL:HG21	3:D:135:MET:SD	2.50	0.51
2:C:85:GLU:O	2:C:387:ARG:NH1	2.43	0.51
2:C:461:VAL:HG23	3:D:852:ARG:HD2	1.92	0.51
6:M:83:ASP:O	6:M:85:HIS:ND1	2.37	0.51
2:C:992:LYS:HZ3	3:D:725:THR:CB	2.23	0.51
1:A:69:VAL:HG13	1:A:128:LEU:HD23	1.92	0.51
2:C:579:MET:O	2:C:614:THR:OG1	2.20	0.51
5:F:459:SER:O	5:F:463:GLY:N	2.43	0.51
2:C:237:LEU:O	2:C:241:GLY:N	2.43	0.51
3:D:809:MET:HA	3:D:812:ILE:HG22	1.91	0.51
2:C:175:PHE:CE1	2:C:190:ALA:HB2	2.46	0.51
5:F:485:ARG:HB2	7:O:34:DT:H71	1.92	0.51
3:D:879:VAL:O	3:D:879:VAL:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:872:ALA:HB3	2:C:1018:LEU:HD11	1.93	0.50
1:B:158:GLU:OE1	1:B:158:GLU:N	2.44	0.50
8:P:62:DG:H2"	8:P:63:DA:C8	2.46	0.50
3:D:888:THR:OG1	3:D:889:GLU:N	2.44	0.50
2:C:213:ARG:NH2	2:C:218:ARG:O	2.40	0.50
5:F:490:GLU:O	5:F:493:THR:OG1	2.28	0.50
2:C:156:ILE:HD13	2:C:417:PHE:HB3	1.94	0.50
4:E:9:GLU:N	4:E:9:GLU:OE1	2.45	0.50
2:C:676:VAL:HG21	2:C:688:LEU:CD1	2.42	0.50
3:D:210:ASP:O	3:D:213:GLN:NE2	2.44	0.49
1:A:186:ARG:HG3	1:B:150:VAL:HG21	1.93	0.49
3:D:644:ARG:HE	3:D:645:GLU:H	1.60	0.49
2:C:330:TYR:CZ	2:C:351:VAL:HG23	2.46	0.49
2:C:1064:TYR:OH	3:D:506:ARG:O	2.20	0.49
5:F:391:GLU:OE1	5:F:391:GLU:N	2.45	0.49
5:F:457:VAL:HB	5:F:486:ILE:HD11	1.94	0.49
1:B:60:LEU:HD22	1:B:159:ILE:HD13	1.93	0.49
2:C:408:PRO:HG3	8:P:26:DG:H8	1.76	0.49
1:B:39:ARG:O	1:B:43:LEU:HD23	2.12	0.49
2:C:530:ALA:HB2	2:C:566:ASP:HB2	1.94	0.49
3:D:588:LEU:HD21	3:D:664:GLY:O	2.12	0.49
3:D:976:SER:HB2	3:D:983:VAL:HG12	1.93	0.49
6:M:55:LEU:HD13	6:M:76:TYR:CE2	2.45	0.49
3:D:278:ARG:HH21	3:D:296:LEU:HD22	1.78	0.49
1:A:64:THR:OG1	1:A:65:THR:N	2.46	0.48
1:A:207:ALA:O	1:A:210:SER:OG	2.27	0.48
1:B:69:VAL:HG22	1:B:128:LEU:CD1	2.43	0.48
3:D:876:SER:O	3:D:879:VAL:HG12	2.12	0.48
6:N:55:LEU:HD21	6:N:76:TYR:CD1	2.47	0.48
6:N:68:ARG:NH2	6:N:72:GLY:O	2.46	0.48
3:D:89:ARG:N	3:D:323:ASP:OD2	2.46	0.48
2:C:808:ARG:O	2:C:812:GLY:N	2.47	0.48
2:C:1106:PHE:CZ	3:D:10:LEU:HD21	2.48	0.48
3:D:334:ARG:NH2	5:F:402:GLU:O	2.47	0.48
3:D:807:MET:SD	3:D:807:MET:N	2.86	0.48
1:B:39:ARG:NE	1:B:174:VAL:O	2.47	0.48
3:D:1203:TRP:NE1	3:D:1226:ASP:HB2	2.29	0.48
3:D:1233:GLU:OE1	3:D:1233:GLU:N	2.41	0.48
2:C:633:ALA:N	2:C:684:GLU:OE2	2.47	0.48
2:C:992:LYS:HZ1	2:C:1008:ILE:HA	1.78	0.48
3:D:1218:ASP:HA	3:D:1221:ILE:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:262:LEU:HD21	2:C:280:ALA:HB3	1.94	0.48
2:C:723:LEU:HD23	2:C:881:ILE:HD12	1.96	0.48
2:C:959:THR:HG23	2:C:959:THR:O	2.14	0.48
3:D:501:ALA:HB3	3:D:502:PRO:HD3	1.96	0.48
6:M:84:HIS:HE2	6:M:122:HIS:CE1	2.24	0.48
2:C:286:ASN:HA	2:C:290:ASN:HB2	1.96	0.48
2:C:493:ASN:N	2:C:497:PHE:O	2.40	0.48
2:C:914:PRO:O	2:C:917:VAL:HG12	2.14	0.48
3:D:1203:TRP:CD1	3:D:1226:ASP:HB2	2.49	0.48
5:F:279:LEU:HD23	5:F:311:LEU:HD22	1.96	0.48
2:C:160:GLU:O	2:C:426:MET:HB3	2.14	0.47
2:C:641:ALA:HB1	2:C:660:LYS:NZ	2.29	0.47
2:C:91:MET:SD	2:C:92:SER:N	2.87	0.47
2:C:505:VAL:HG11	2:C:562:VAL:HG23	1.96	0.47
3:D:596:SER:O	3:D:598:LYS:N	2.47	0.47
3:D:1089:GLU:N	3:D:1089:GLU:OE1	2.46	0.47
1:B:42:LEU:HD23	1:B:171:VAL:HG21	1.96	0.47
3:D:27:GLU:N	3:D:51:ILE:HD12	2.30	0.47
3:D:740:ILE:HD12	3:D:779:GLU:OE1	2.15	0.47
4:E:32:TYR:CZ	4:E:75:ILE:HD12	2.49	0.47
8:P:62:DG:H2"	8:P:63:DA:N7	2.30	0.47
2:C:707:VAL:HG21	2:C:903:LEU:HD12	1.97	0.47
3:D:506:ARG:N	3:D:995:GLN:OE1	2.48	0.47
3:D:1162:GLU:N	3:D:1162:GLU:OE1	2.48	0.47
3:D:1172:GLU:OE1	3:D:1175:ARG:NH1	2.47	0.47
7:O:71:DG:OP1	7:O:72:DG:P	2.72	0.47
2:C:330:TYR:CE1	2:C:351:VAL:HG23	2.50	0.47
2:C:767:LEU:HD12	2:C:767:LEU:O	2.14	0.47
3:D:304:GLN:NE2	3:D:305:THR:HG23	2.29	0.47
2:C:25:PHE:HD2	2:C:965:ALA:HB2	1.79	0.47
8:P:60:DC:H2'	8:P:61:DT:H72	1.97	0.47
2:C:200:LEU:HD12	2:C:213:ARG:O	2.15	0.46
2:C:468:ARG:HG2	2:C:498:ILE:HB	1.97	0.46
1:B:69:VAL:HG22	1:B:128:LEU:HD13	1.97	0.46
1:B:39:ARG:HE	1:B:43:LEU:HD21	1.79	0.46
3:D:830:PRO:O	3:D:832:LYS:NZ	2.40	0.46
1:B:137:GLU:OE1	1:B:137:GLU:N	2.49	0.46
2:C:209:MET:SD	2:C:249:THR:HG22	2.56	0.46
1:A:214:THR:O	1:A:218:LEU:HD23	2.16	0.46
2:C:1047:GLN:N	2:C:1047:GLN:OE1	2.49	0.46
3:D:142:GLU:OE1	3:D:142:GLU:N	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:674:GLU:N	3:D:674:GLU:OE1	2.44	0.46
2:C:86:ASP:OD2	2:C:88:SER:OG	2.34	0.46
2:C:636:VAL:HG11	2:C:639:VAL:HG13	1.98	0.46
1:A:148:SER:OG	1:A:151:GLN:OE1	2.34	0.46
2:C:265:ILE:O	2:C:269:LEU:HD23	2.16	0.46
2:C:140:VAL:CG2	2:C:404:ILE:HD11	2.35	0.46
2:C:917:VAL:HA	2:C:920:ILE:HG22	1.97	0.46
2:C:1108:VAL:HG13	3:D:324:LEU:HD22	1.97	0.46
5:F:466:ASP:OD1	5:F:470:LYS:NZ	2.49	0.46
1:A:62:GLU:OE1	1:A:62:GLU:N	2.39	0.45
1:A:85:VAL:HG12	1:A:118:VAL:HG22	1.97	0.45
3:D:502:PRO:CB	8:P:15:DG:H22	2.30	0.45
5:F:280:GLU:HA	5:F:283:LEU:HG	1.96	0.45
6:M:27:GLU:OE1	6:M:27:GLU:N	2.48	0.45
2:C:932:VAL:HG13	2:C:935:LEU:HD22	1.98	0.45
2:C:1095:GLU:OE2	2:C:1095:GLU:HA	2.17	0.45
1:A:221:LEU:O	1:A:225:LEU:HD13	2.15	0.45
2:C:176:ASP:OD1	2:C:177:SER:N	2.49	0.45
2:C:938:GLU:OE2	2:C:942:ARG:NE	2.50	0.45
4:E:60:ASP:OD1	4:E:60:ASP:N	2.48	0.45
2:C:648:ASN:ND2	2:C:650:ASP:OD2	2.46	0.45
3:D:93:GLY:C	3:D:319:VAL:HG22	2.37	0.45
3:D:116:TYR:HB2	3:D:295:ARG:HG2	1.99	0.45
3:D:293:LEU:HG	3:D:1159:LEU:HD12	1.98	0.45
3:D:894:LEU:HD13	3:D:956:THR:OG1	2.17	0.45
2:C:776:ILE:HG21	2:C:788:LEU:CD1	2.46	0.45
3:D:320:ILE:O	3:D:325:ARG:NH2	2.49	0.45
1:B:203:ARG:HD3	1:B:205:ARG:HE	1.83	0.45
5:F:492:LYS:O	5:F:495:SER:OG	2.23	0.45
3:D:180:ASP:OD1	3:D:181:LEU:N	2.49	0.44
5:F:428:VAL:O	5:F:428:VAL:HG23	2.17	0.44
6:M:36:HIS:HA	6:M:39:LEU:HG	1.98	0.44
2:C:86:ASP:OD1	2:C:89:GLY:N	2.50	0.44
2:C:173:VAL:HG23	2:C:307:LYS:HG2	1.99	0.44
3:D:58:TRP:CE3	3:D:68:VAL:HG22	2.52	0.44
2:C:1116:LEU:HD21	3:D:402:LEU:HD12	2.00	0.44
3:D:20:ILE:HD13	3:D:316:CYS:O	2.17	0.44
3:D:170:LEU:HD12	3:D:173:ARG:NH2	2.33	0.44
5:F:466:ASP:OD2	5:F:468:GLN:NE2	2.50	0.44
1:A:176:TYR:HB2	1:A:192:LEU:HD11	1.98	0.44
3:D:356:ARG:NE	3:D:356:ARG:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:583:LEU:HD21	3:D:724:VAL:HG11	1.99	0.44
3:D:915:VAL:HG23	3:D:956:THR:HG21	1.99	0.44
2:C:155:VAL:HG22	2:C:160:GLU:OE2	2.17	0.44
3:D:663:LEU:O	3:D:667:LEU:HD23	2.18	0.44
3:D:1074:ILE:HD12	3:D:1078:ALA:HB2	2.00	0.44
3:D:67:ARG:HD3	3:D:67:ARG:HA	1.86	0.44
2:C:974:LEU:HD22	2:C:989:PRO:HA	2.00	0.44
5:F:472:LEU:HD13	5:F:487:ARG:HB2	2.00	0.44
2:C:1104:GLU:OE2	2:C:1105:SER:OG	2.36	0.43
3:D:1051:GLU:N	3:D:1051:GLU:OE1	2.51	0.43
5:F:284:ARG:O	5:F:287:VAL:HG12	2.18	0.43
1:A:29:GLY:O	1:B:40:ARG:NH1	2.49	0.43
2:C:130:ASN:OD1	2:C:131:GLU:N	2.51	0.43
3:D:353:ARG:O	3:D:357:LEU:HD23	2.18	0.43
2:C:210:VAL:HG12	2:C:249:THR:HG21	1.99	0.43
3:D:337:THR:HG23	3:D:341:ASN:HD22	1.84	0.43
3:D:468:ASN:O	3:D:471:SER:OG	2.29	0.43
5:F:486:ILE:HD12	5:F:489:ILE:HD11	2.00	0.43
3:D:920:LEU:CG	3:D:938:LEU:HD21	2.44	0.43
6:M:48:LEU:O	6:M:51:VAL:HG22	2.19	0.43
3:D:155:VAL:HG21	3:D:223:TRP:CH2	2.54	0.43
6:M:122:HIS:HA	6:N:126:ILE:HG22	1.99	0.43
2:C:37:LEU:O	2:C:439:ARG:NE	2.52	0.43
1:B:16:GLU:OE1	1:B:16:GLU:N	2.44	0.43
3:D:151:LEU:HD13	3:D:223:TRP:HH2	1.83	0.43
3:D:583:LEU:HD11	3:D:724:VAL:HG11	2.01	0.43
1:B:5:GLN:OE1	1:B:183:VAL:HG11	2.19	0.43
2:C:943:LEU:O	2:C:947:GLY:N	2.51	0.43
3:D:592:SER:OG	3:D:593:GLU:N	2.52	0.43
3:D:999:GLU:HG3	3:D:1000:PRO:HD3	2.01	0.43
2:C:171:PRO:HB2	2:C:300:GLY:HA3	2.00	0.43
2:C:574:SER:OG	2:C:575:VAL:N	2.52	0.43
2:C:627:VAL:CG2	2:C:687:VAL:HG13	2.49	0.43
2:C:1097:ILE:HD13	3:D:548:SER:HA	2.01	0.43
3:D:911:VAL:HG22	3:D:915:VAL:HG12	2.01	0.43
3:D:1206:ALA:HB3	3:D:1215:VAL:HG21	2.00	0.43
8:P:60:DC:C2'	8:P:61:DT:H72	2.49	0.43
2:C:690:ASP:OD2	2:C:696:ASN:N	2.49	0.42
3:D:959:ILE:HD11	3:D:968:THR:HG21	2.00	0.42
3:D:296:LEU:HD23	3:D:296:LEU:HA	1.91	0.42
3:D:621:LEU:HD11	3:D:664:GLY:CA	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:240:ILE:HD12	5:F:275:LYS:HD3	2.01	0.42
3:D:1158:LEU:H	3:D:1158:LEU:HD23	1.85	0.42
2:C:174:TYR:HE1	2:C:303:LYS:HE3	1.83	0.42
3:D:763:GLU:OE2	3:D:767:GLN:NE2	2.52	0.42
4:E:17:ASP:OD1	4:E:18:GLU:N	2.51	0.42
2:C:276:THR:HB	2:C:279:ALA:HB3	2.02	0.42
3:D:738:LYS:O	3:D:741:VAL:HG12	2.19	0.42
5:F:360:ASN:OD1	5:F:361:LYS:N	2.53	0.42
5:F:473:ASP:OD2	8:P:47:DG:OP2	2.37	0.42
2:C:1030:SER:OG	2:C:1031:THR:N	2.53	0.42
6:M:11:ARG:O	6:M:16:ARG:NH2	2.53	0.42
1:B:211:ALA:O	1:B:214:THR:OG1	2.29	0.42
2:C:245:SER:O	2:C:249:THR:HG23	2.20	0.42
2:C:333:LYS:HE2	2:C:341:THR:HG21	2.01	0.42
2:C:604:LEU:HD23	2:C:604:LEU:H	1.85	0.42
1:A:97:LEU:HB2	1:A:110:ILE:HG13	2.01	0.42
5:F:432:ASP:O	5:F:435:SER:OG	2.26	0.42
2:C:120:PRO:O	2:C:121:LEU:HD22	2.19	0.42
3:D:671:LEU:HD23	3:D:711:LEU:HA	2.00	0.42
3:D:868:LEU:O	3:D:872:LEU:HD23	2.20	0.42
1:A:54:ILE:HD11	1:A:162:ILE:HD11	2.02	0.41
3:D:846:ILE:O	3:D:849:HIS:HB2	2.20	0.41
3:D:1121:VAL:HG11	3:D:1137:ILE:HD12	2.02	0.41
7:O:71:DG:H2'	7:O:71:DG:N3	2.34	0.41
2:C:1116:LEU:CD2	3:D:402:LEU:HD12	2.50	0.41
2:C:1106:PHE:HZ	3:D:10:LEU:HD21	1.85	0.41
3:D:810:ARG:O	3:D:814:GLY:N	2.53	0.41
6:M:52:TYR:O	6:M:55:LEU:HG	2.21	0.41
6:N:35:LEU:HD12	6:N:38:MET:CE	2.50	0.41
1:A:172:LEU:HD21	1:A:199:LYS:HG2	2.01	0.41
2:C:757:ARG:NH2	2:C:768:ALA:O	2.53	0.41
5:F:362:LEU:HA	5:F:365:VAL:HG22	2.02	0.41
2:C:52:ASP:OD1	2:C:53:ALA:N	2.54	0.41
2:C:644:ILE:HG22	2:C:658:LEU:HD11	2.02	0.41
2:C:518:THR:OG1	2:C:519:ALA:N	2.53	0.41
3:D:846:ILE:HD12	3:D:846:ILE:HA	1.85	0.41
3:D:102:THR:HG21	3:D:129:ILE:HD13	2.01	0.41
2:C:880:VAL:HG23	3:D:537:ASP:O	2.21	0.41
3:D:184:LEU:HD22	3:D:197:VAL:HB	2.02	0.41
3:D:288:LYS:HB3	3:D:288:LYS:HE3	1.78	0.41
3:D:751:VAL:HG11	3:D:768:GLU:CD	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:768:GLU:OE2	3:D:769:LEU:HG	2.21	0.41
7:O:15:DA:N6	8:P:69:DG:O6	2.54	0.41
8:P:21:DG:H2'	8:P:22:DG:H8	1.84	0.41
1:A:167:ILE:HG13	1:A:167:ILE:O	2.21	0.41
1:B:42:LEU:HD21	1:B:171:VAL:HG11	2.03	0.41
3:D:578:THR:HG21	3:D:685:LYS:HD3	2.03	0.41
3:D:821:ASN:HD22	3:D:821:ASN:HA	1.63	0.41
5:F:230:ALA:HA	5:F:233:GLU:OE2	2.21	0.41
6:N:35:LEU:HD12	6:N:38:MET:HE1	2.03	0.41
1:B:5:GLN:CD	1:B:183:VAL:HG11	2.42	0.40
2:C:67:ASP:OD1	2:C:68:VAL:N	2.54	0.40
2:C:1060:ALA:HB3	3:D:509:ILE:HD13	2.03	0.40
3:D:353:ARG:NH1	5:F:302:ASP:OD1	2.54	0.40
2:C:676:VAL:HG21	2:C:688:LEU:HD13	2.02	0.40
3:D:255:SER:OG	3:D:256:MET:N	2.54	0.40
3:D:619:LEU:HD21	3:D:663:LEU:HD13	2.03	0.40
3:D:93:GLY:O	3:D:319:VAL:HG22	2.22	0.40
8:P:23:DT:H2'	8:P:24:DC:C2	2.57	0.40
1:B:187:THR:O	1:B:187:THR:HG22	2.22	0.40
3:D:184:LEU:HD22	3:D:197:VAL:CG1	2.51	0.40
3:D:305:THR:HG22	3:D:1223:ALA:HB3	2.03	0.40
3:D:868:LEU:HD22	3:D:1023:LEU:HD11	2.03	0.40
3:D:1030:PHE:CE1	3:D:1140:ILE:HG21	2.56	0.40
3:D:1048:VAL:O	3:D:1085:GLY:CA	2.70	0.40
3:D:1081:LEU:H	3:D:1081:LEU:HD23	1.87	0.40

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	A	224/340 (66%)	215 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	231/340 (68%)	224 (97%)	7 (3%)	0	100 100
2	C	1114/1161 (96%)	1064 (96%)	50 (4%)	0	100 100
3	D	1257/1307 (96%)	1207 (96%)	49 (4%)	1 (0%)	51 85
4	E	75/90 (83%)	74 (99%)	1 (1%)	0	100 100
5	F	299/531 (56%)	292 (98%)	7 (2%)	0	100 100
6	M	129/159 (81%)	127 (98%)	2 (2%)	0	100 100
6	N	129/159 (81%)	128 (99%)	1 (1%)	0	100 100
All	All	3458/4087 (85%)	3331 (96%)	126 (4%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	132	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	194/279 (70%)	186 (96%)	8 (4%)	30 56
1	B	199/279 (71%)	197 (99%)	2 (1%)	76 86
2	C	942/979 (96%)	933 (99%)	9 (1%)	76 86
3	D	1054/1095 (96%)	1044 (99%)	10 (1%)	78 88
4	E	64/74 (86%)	64 (100%)	0	100 100
5	F	258/430 (60%)	257 (100%)	1 (0%)	91 94
6	M	99/120 (82%)	99 (100%)	0	100 100
6	N	99/120 (82%)	98 (99%)	1 (1%)	76 86
All	All	2909/3376 (86%)	2878 (99%)	31 (1%)	74 84

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	81	LYS
1	A	106	THR
1	A	110	ILE
1	A	131	LYS
1	A	152	ASN
1	A	182	ARG
1	A	223	ARG
1	B	55	ARG
1	B	150	VAL
2	C	153	THR
2	C	173	VAL
2	C	466	TYR
2	C	639	VAL
2	C	743	VAL
2	C	856	ARG
2	C	1036	MET
2	C	1038	THR
2	C	1109	LEU
3	D	247	ARG
3	D	287	GLN
3	D	712	LYS
3	D	762	LYS
3	D	819	VAL
3	D	821	ASN
3	D	842	LEU
3	D	1093	LYS
3	D	1209	PHE
3	D	1210	GLN
5	F	502	ARG
6	N	16	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
3	D	103	HIS
3	D	287	GLN
3	D	525	HIS
3	D	821	ASN
5	F	282	ASN
5	F	499	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	Q	4/5 (80%)	1 (25%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	Q	5	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 9 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

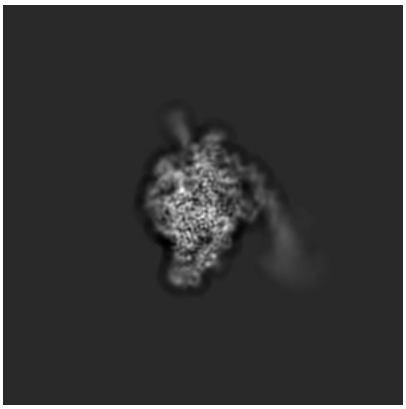
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-32077. These allow visual inspection of the internal detail of the map and identification of artifacts.

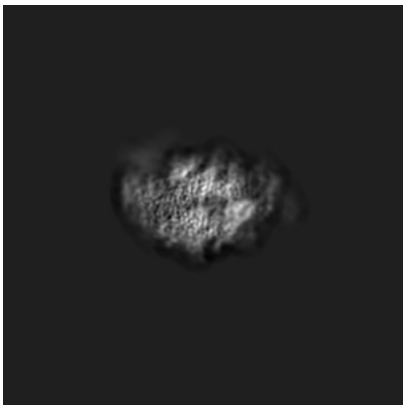
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

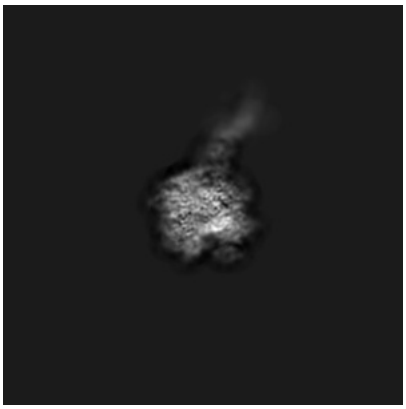
6.1.1 Primary map



X

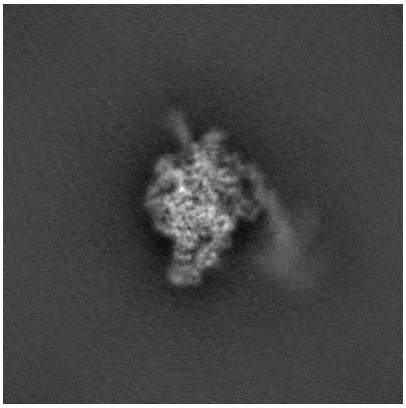


Y

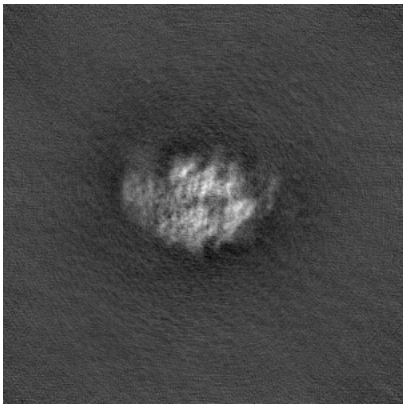


Z

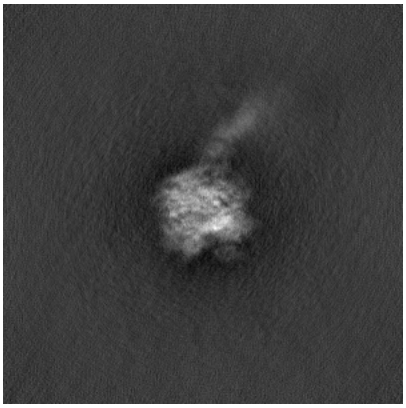
6.1.2 Raw map



X



Y

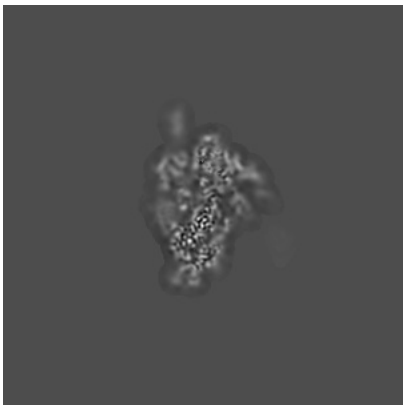


Z

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

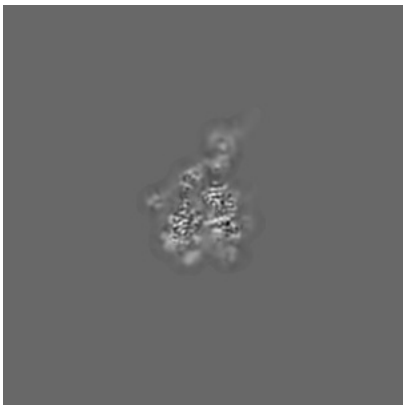
6.2 Central slices (i)

6.2.1 Primary map



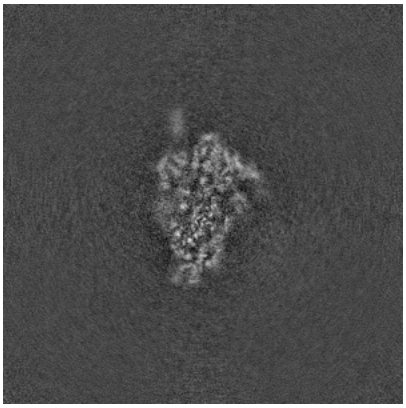
X Index: 192

Y Index: 192

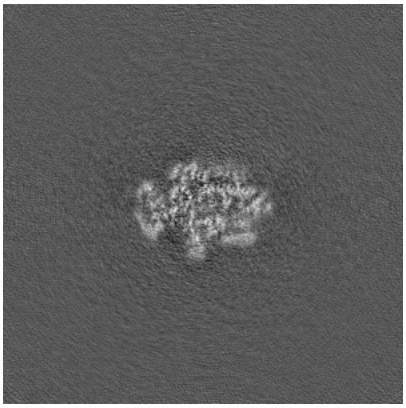


Z Index: 192

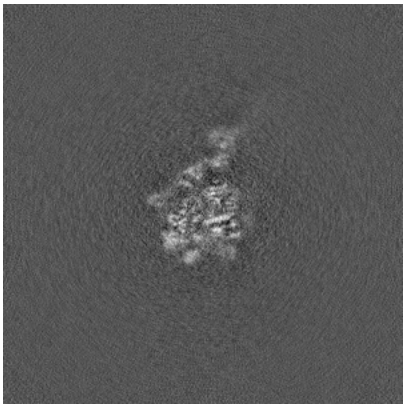
6.2.2 Raw map



X Index: 192



Y Index: 192

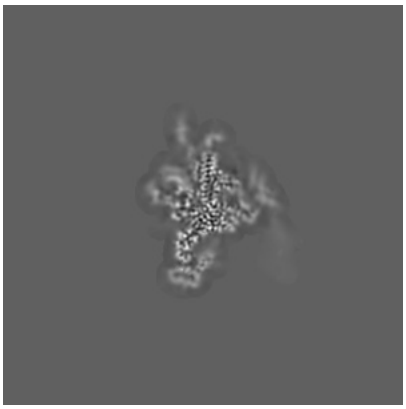


Z Index: 192

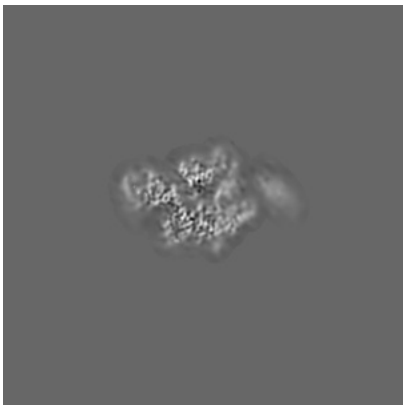
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

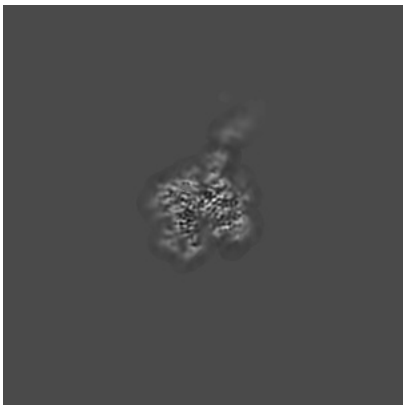
6.3.1 Primary map



X Index: 204

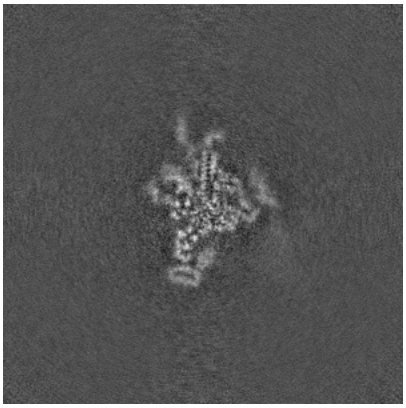


Y Index: 171

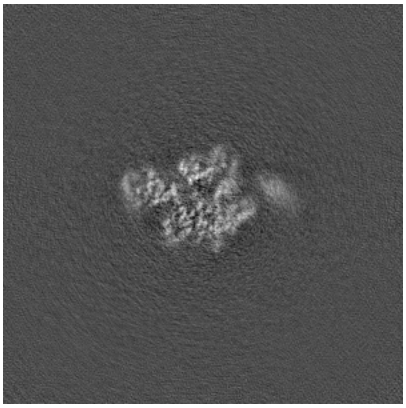


Z Index: 179

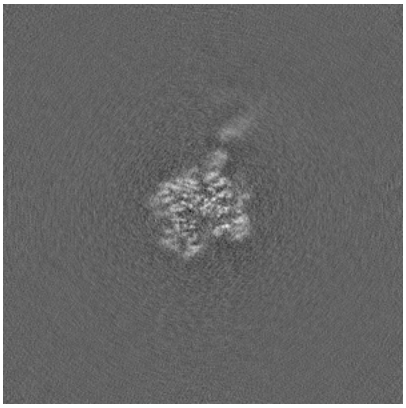
6.3.2 Raw map



X Index: 204



Y Index: 171

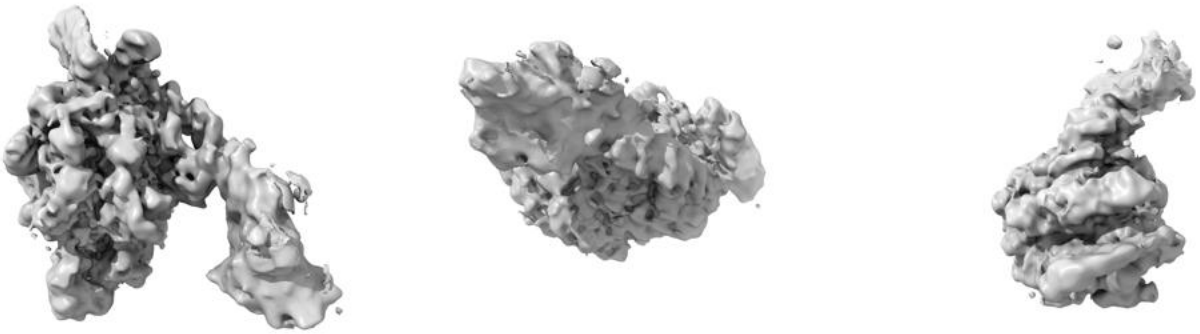


Z Index: 179

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

6.4 Orthogonal surface views (i)

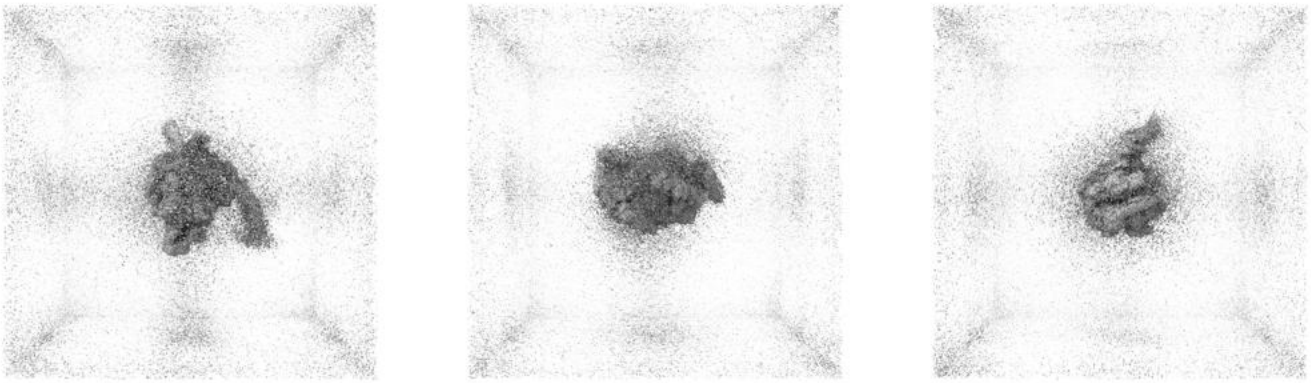
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

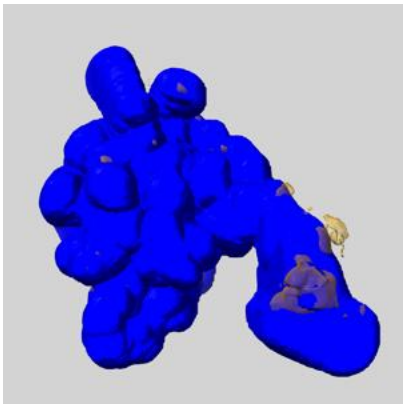
6.5 Mask visualisation (i)

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

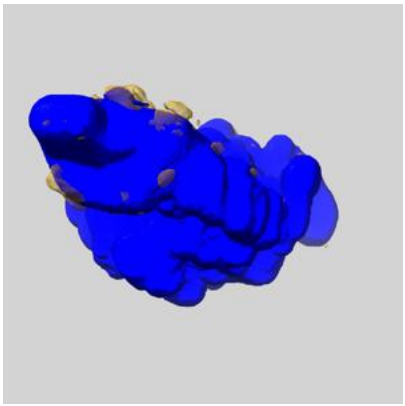
A mask typically either:

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

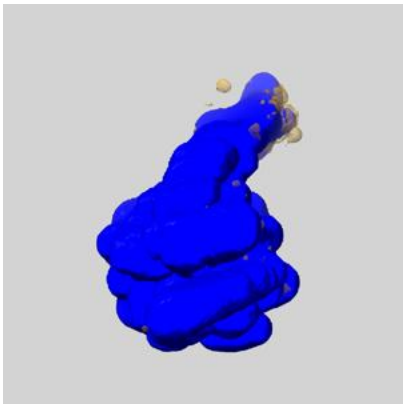
6.5.1 emd_32077_msk_1.map (i)



X



Y

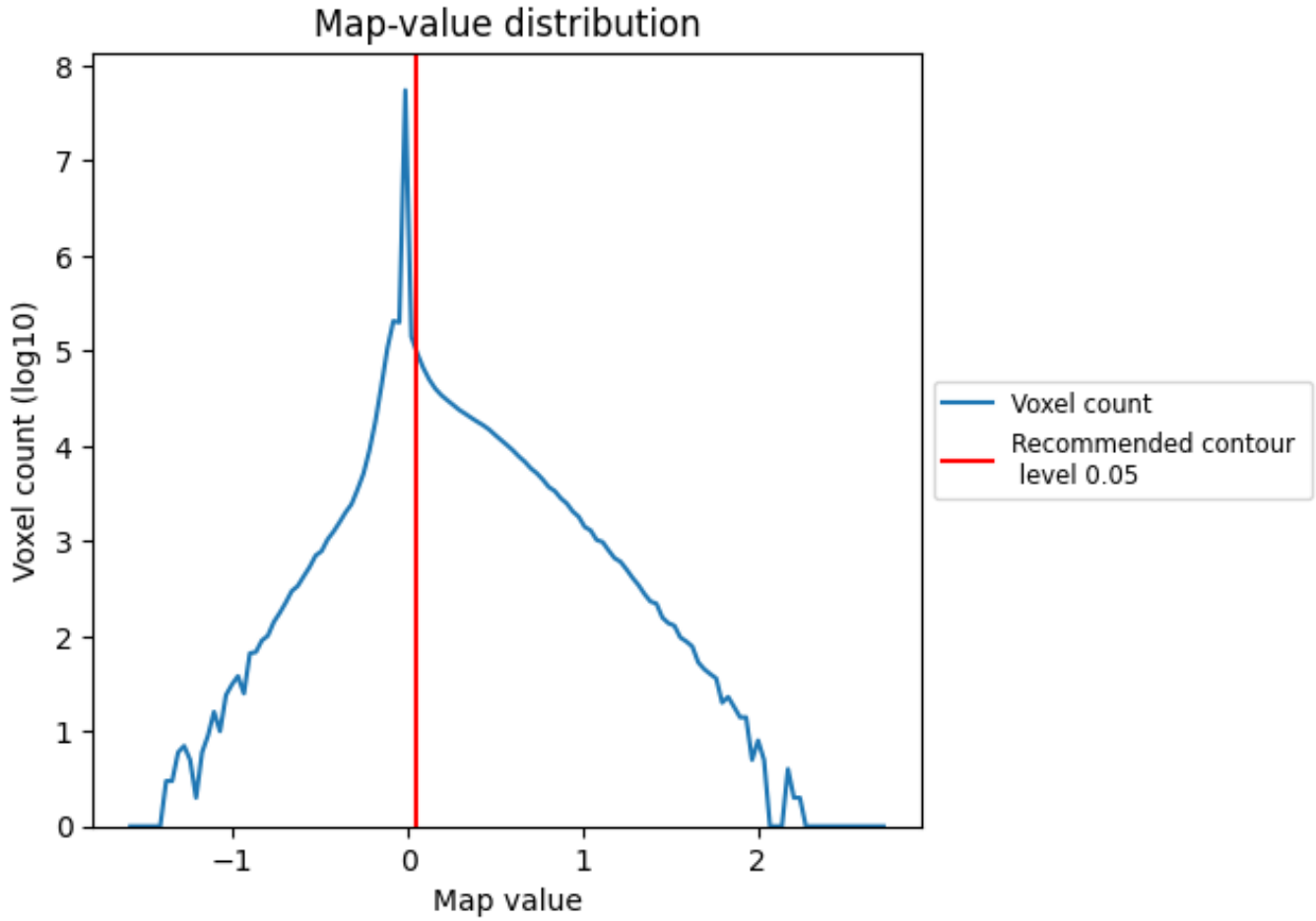


Z

7 Map analysis

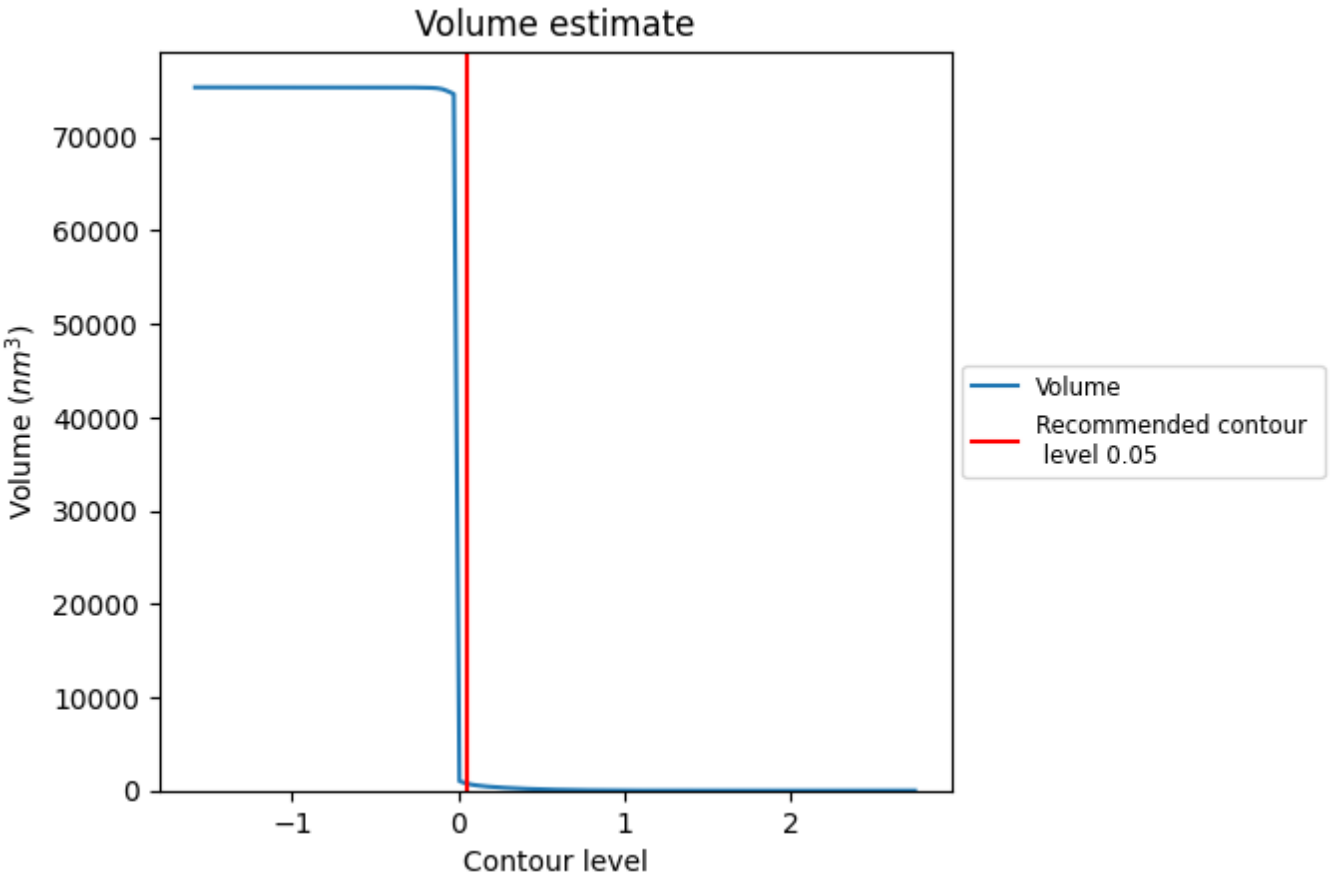
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

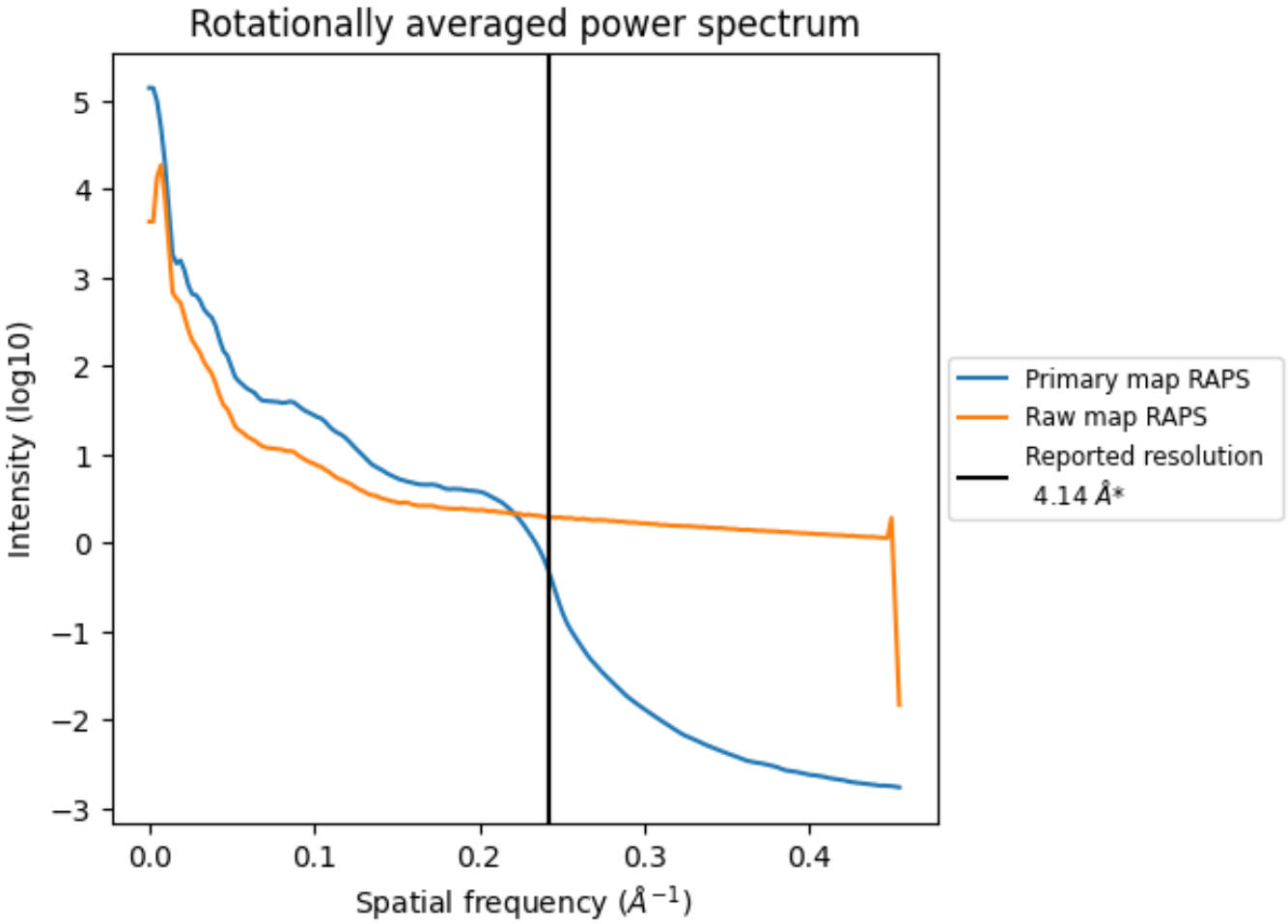
7.2 Volume estimate



The volume at the recommended contour level is 770 nm^3; this corresponds to an approximate mass of 695 kDa.

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

7.3 Rotationally averaged power spectrum (i)

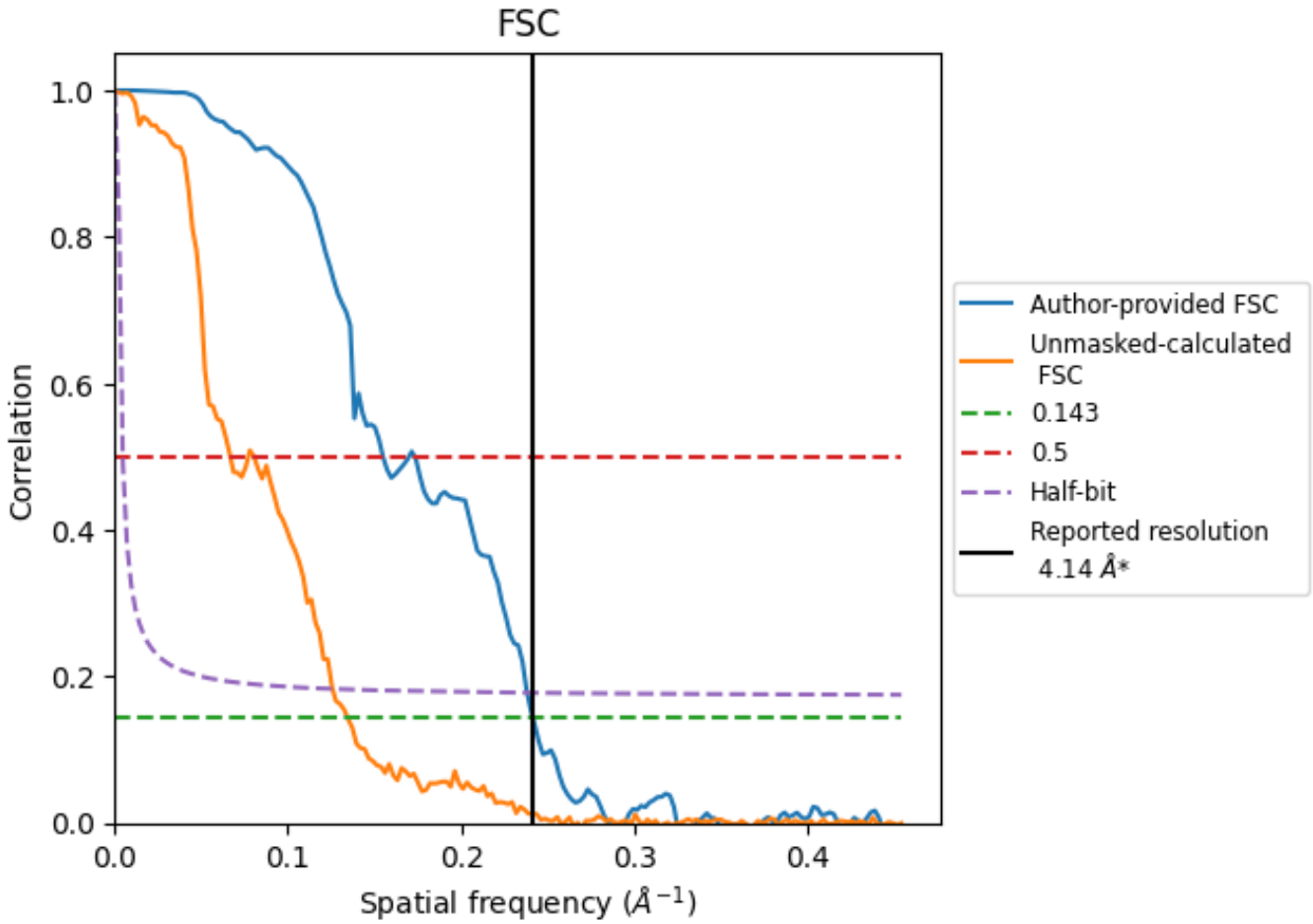


*Reported resolution corresponds to spatial frequency of 0.242 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.242 Å^{-1}

8.2 Resolution estimates (i)

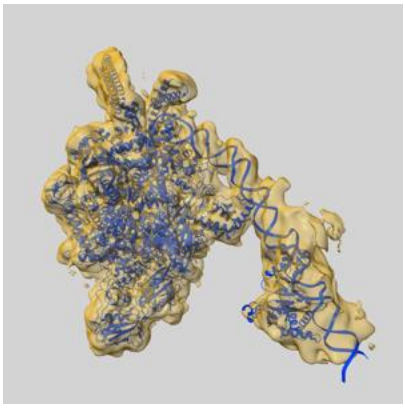
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.14	-	-
Author-provided FSC curve	4.14	6.46	4.20
Unmasked-calculated*	7.43	14.99	7.95

*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 7.43 differs from the reported value 4.14 by more than 10 %

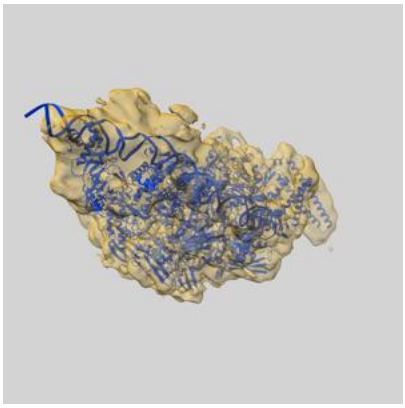
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-32077 and PDB model 7VPZ. Per-residue inclusion information can be found in section 3 on page 8.

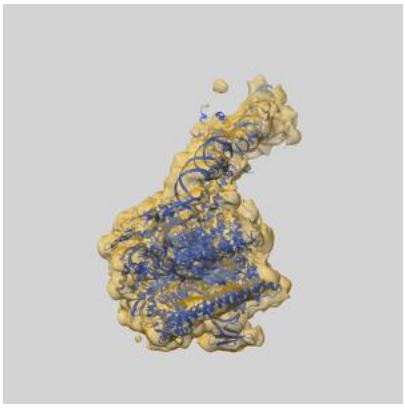
9.1 Map-model overlay



X



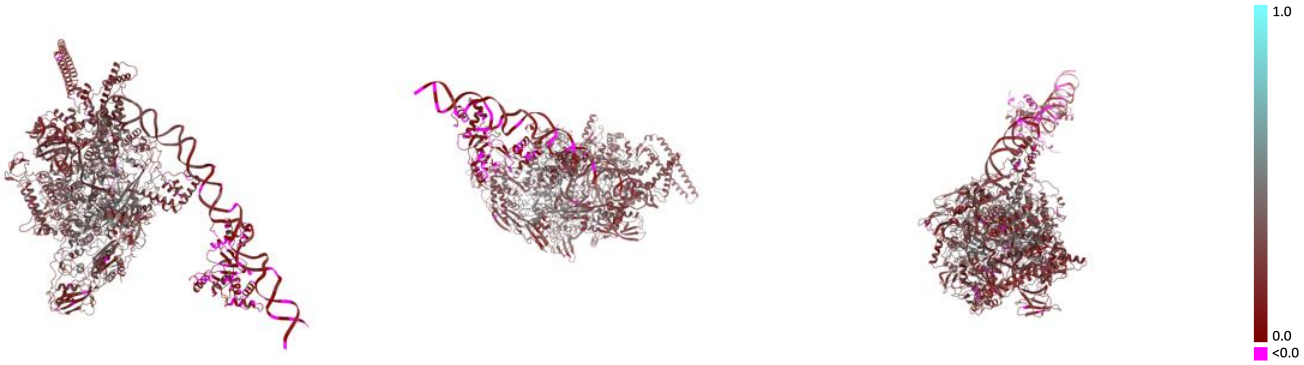
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

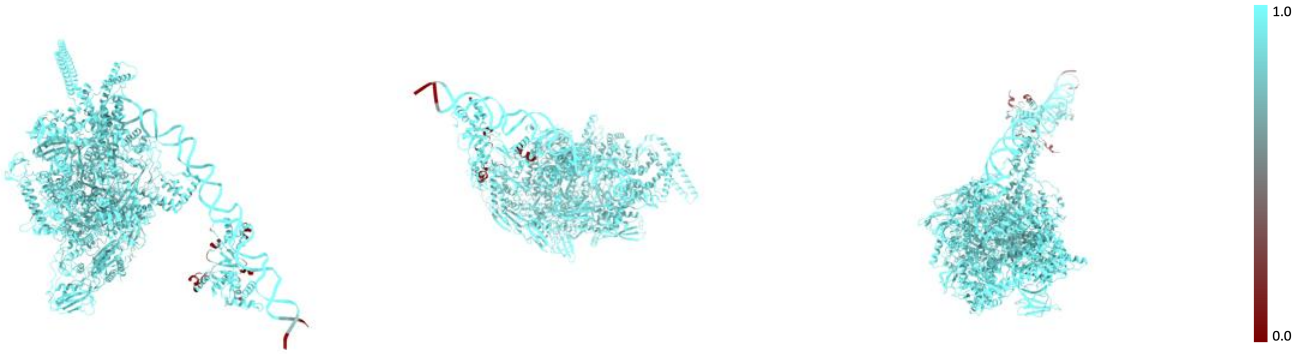
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

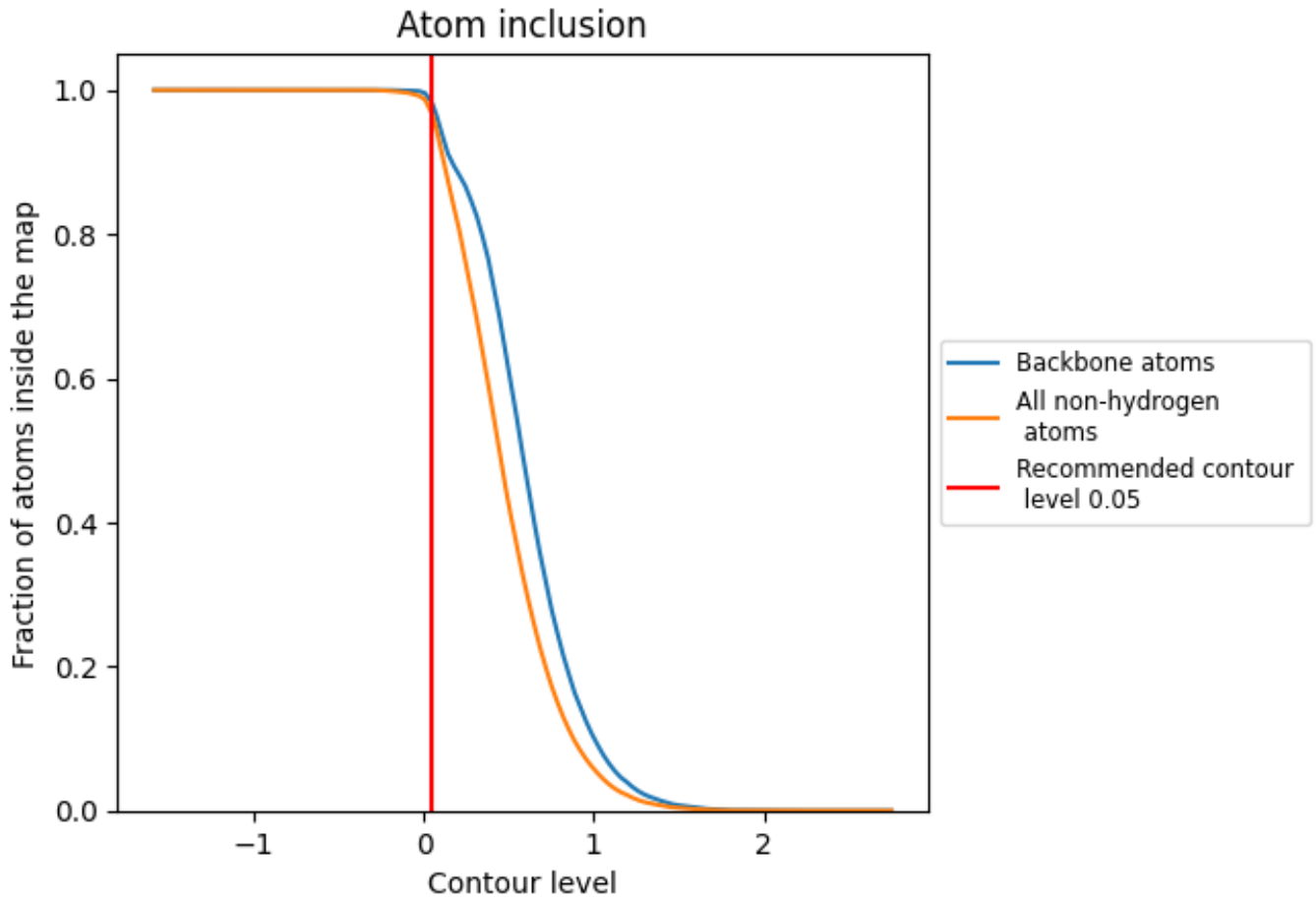
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9667	0.2620
A	0.9772	0.2750
B	0.9801	0.2360
C	0.9828	0.3180
D	0.9777	0.3000
E	0.9488	0.2760
F	0.9713	0.2160
M	0.7751	0.0390
N	0.9016	0.0610
O	0.9597	0.1780
P	0.9526	0.1570
Q	0.9537	0.2770