



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 11:34 AM UTC

PDB ID : 5JM0 / pdb_00005jm0
EMDB ID : EMD-8166
Title : Structure of the *S. cerevisiae* alpha-mannosidase 1
Authors : Schneider, S.; Kosinski, J.; Jakobi, A.J.; Hagen, W.J.H.; Sachse, C.
Deposited on : 2016-04-28
Resolution : 6.30 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

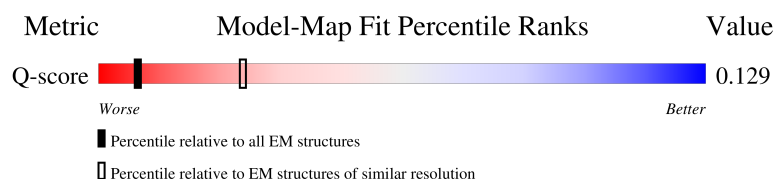
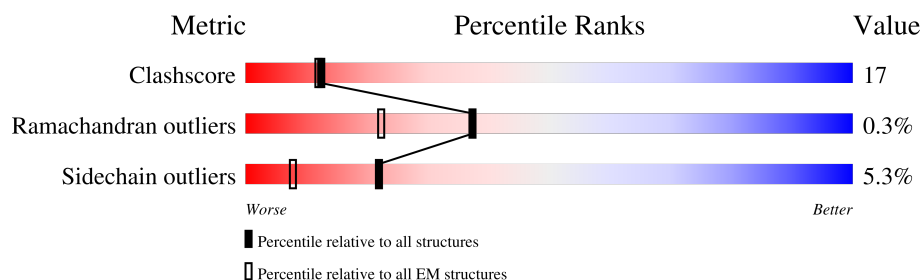
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	550 (5.80 - 6.80)

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

Mol	Chain	Length	Quality of chain
1	A	1096	36% 51% 32% • 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7604 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 Alpha-mannosidase,Alpha-mannosidase,Alpha-mannosidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	940	Total	C	N	O	S	0	0
			7604	4889	1273	1410	32		

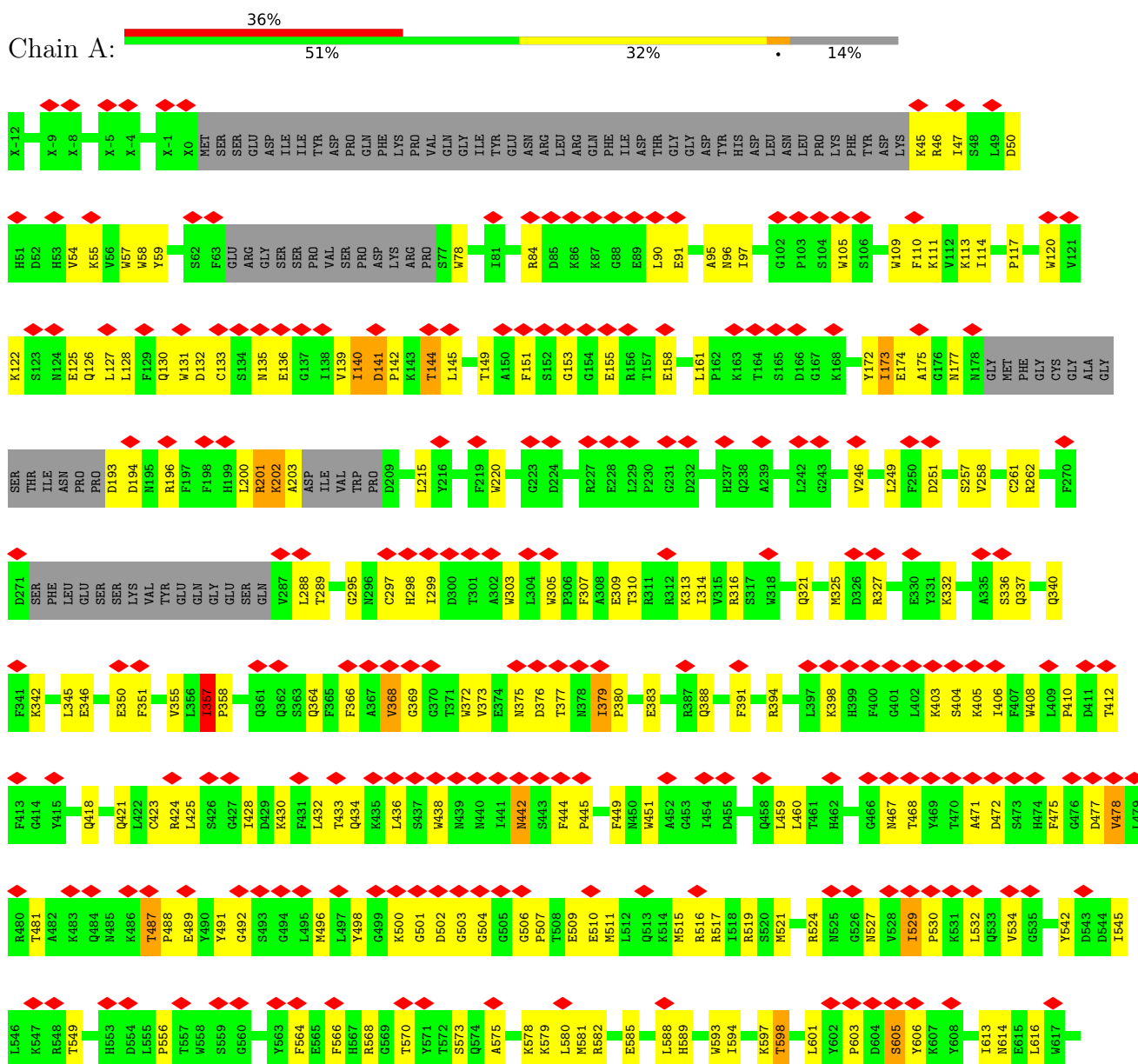
There are 13 discrepancies between the modelled and reference sequences:

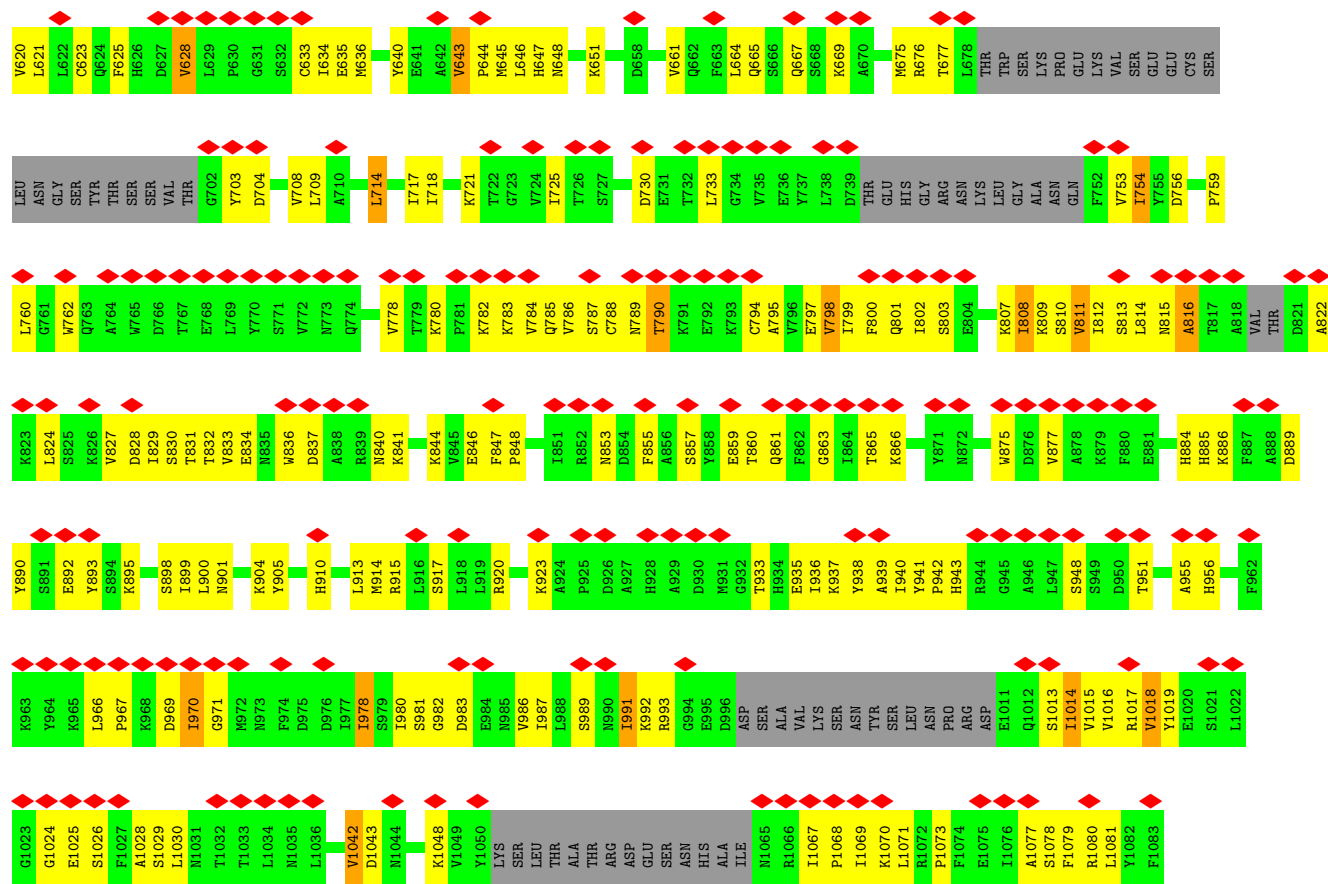
Chain	Residue	Modelled	Actual	Comment	Reference
A	1071	LEU	-	expression tag	UNP P22855
A	1072	ARG	-	expression tag	UNP P22855
A	1073	PRO	-	expression tag	UNP P22855
A	1074	PHE	-	expression tag	UNP P22855
A	1075	GLU	-	expression tag	UNP P22855
A	1076	ILE	-	expression tag	UNP P22855
A	1077	ALA	-	expression tag	UNP P22855
A	1078	SER	-	expression tag	UNP P22855
A	1079	PHE	-	expression tag	UNP P22855
A	1080	ARG	-	expression tag	UNP P22855
A	1081	LEU	-	expression tag	UNP P22855
A	1082	TYR	-	expression tag	UNP P22855
A	1083	PHE	-	expression tag	UNP P22855

3 Residue-property plots

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

- Molecule 1: Alpha-mannosidase,Alpha-mannosidase,Alpha-mannosidase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	33588	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.135	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.064	Depositor
Map size (Å)	270.0, 270.0, 270.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.31	0/7723	0.77	11/10429 (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
1	A	0	3

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	966	LEU	CA-C-N	7.43	129.12	119.84
1	A	966	LEU	C-N-CA	7.43	129.12	119.84
1	A	251	ASP	CA-C-N	-7.17	114.41	121.65
1	A	251	ASP	C-N-CA	-7.17	114.41	121.65
1	A	837	ASP	CB-CA-C	-5.57	109.66	117.23
1	A	468	THR	CB-CA-C	-5.54	108.59	116.34
1	A	141	ASP	CA-C-N	5.52	125.69	119.90
1	A	141	ASP	C-N-CA	5.52	125.69	119.90
1	A	605	SER	N-CA-C	-5.41	106.53	113.02
1	A	357	ILE	CA-C-N	-5.25	114.26	119.56
1	A	357	ILE	C-N-CA	-5.25	114.26	119.56

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	144	THR	Peptide
1	A	442	ASN	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	605	SER	Peptide

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	7604	0	7356	253	0
All	All	7604	0	7356	253	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 17.

All (253) 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)
1:A:151:PHE:HB3	1:A:316:ARG:HE	1.42	0.84
1:A:815:ASN:HB2	1:A:824:LEU:HB2	1.59	0.82
1:A:886:LYS:NZ	1:A:955:ALA:O	2.13	0.81
1:A:643:VAL:HG22	1:A:644:PRO:HD2	1.64	0.80
1:A:487:THR:HG23	1:A:488:PRO:HD3	1.67	0.77
1:A:899:ILE:HG13	1:A:914:MET:HG2	1.67	0.77
1:A:900:LEU:HB3	1:A:939:ALA:HB3	1.65	0.77
1:A:718:ILE:HG12	1:A:725:ILE:HG12	1.67	0.76
1:A:580:LEU:HD22	1:A:646:LEU:HB3	1.69	0.74
1:A:570:THR:HA	1:A:573:SER:HB3	1.69	0.74
1:A:992:LYS:NZ	1:A:993:ARG:O	2.20	0.72
1:A:327:ARG:NH1	1:A:510:GLU:O	2.23	0.72
1:A:78:TRP:CZ2	1:A:78:TRP:CZ3	2.77	0.71
1:A:105:TRP:CZ2	1:A:105:TRP:CZ3	2.77	0.71
1:A:295:GLY:HA2	1:A:498:TYR:HB3	1.74	0.70
1:A:131:TRP:CZ3	1:A:131:TRP:CZ2	2.77	0.70
1:A:588:LEU:HD22	1:A:620:VAL:HG21	1.75	0.69
1:A:58:TRP:CZ2	1:A:58:TRP:CZ3	2.77	0.69
1:A:391:PHE:HE1	1:A:394:ARG:HH11	1.41	0.69
1:A:220:TRP:CZ2	1:A:220:TRP:CZ3	2.77	0.69
1:A:120:TRP:CZ2	1:A:120:TRP:CZ3	2.77	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:TYR:HD2	1:A:704:ASP:H	1.40	0.68
1:A:57:TRP:CZ2	1:A:57:TRP:CZ3	2.77	0.67
1:A:109:TRP:CZ2	1:A:109:TRP:CZ3	2.77	0.67
1:A:128:LEU:HD11	1:A:158:GLU:HB3	1.76	0.67
1:A:847:PHE:HB2	1:A:914:MET:HB3	1.76	0.67
1:A:451:TRP:N	1:A:459:LEU:O	2.26	0.67
1:A:110:PHE:HB3	1:A:173:ILE:HG23	1.76	0.66
1:A:139:VAL:HG23	1:A:149:THR:HB	1.76	0.66
1:A:830:SER:HA	1:A:937:LYS:HA	1.78	0.66
1:A:900:LEU:HD12	1:A:955:ALA:HA	1.78	0.66
1:A:57:TRP:HB2	1:A:111:LYS:HB2	1.76	0.65
1:A:875:TRP:NE1	1:A:877:VAL:O	2.30	0.65
1:A:901:ASN:HA	1:A:938:TYR:HA	1.79	0.64
1:A:788:CYS:SG	1:A:789:ASN:N	2.70	0.64
1:A:585:GLU:O	1:A:589:HIS:ND1	2.30	0.63
1:A:754:ILE:HG23	1:A:846:GLU:HB2	1.79	0.63
1:A:406:ILE:HD11	1:A:432:LEU:HB2	1.80	0.63
1:A:1024:GLY:H	1:A:1073:PRO:HB3	1.63	0.63
1:A:193:ASP:OD2	1:A:194:ASP:N	2.31	0.63
1:A:847:PHE:N	1:A:914:MET:O	2.28	0.62
1:A:993:ARG:HA	1:A:1014:ILE:HA	1.82	0.62
1:A:633:CYS:SG	1:A:634:ILE:N	2.72	0.62
1:A:733:LEU:HB3	1:A:895:LYS:HD3	1.81	0.62
1:A:445:PRO:HG2	1:A:556:PRO:HG3	1.82	0.61
1:A:759:PRO:HA	1:A:841:LYS:HA	1.82	0.61
1:A:368:VAL:HG21	1:A:408:TRP:HB2	1.81	0.61
1:A:249:LEU:HB3	1:A:257:SER:HB3	1.82	0.61
1:A:853:ASN:ND2	1:A:855:PHE:O	2.34	0.61
1:A:516:ARG:HD2	1:A:534:VAL:HG12	1.82	0.61
1:A:834:GLU:HA	1:A:933:THR:HA	1.83	0.60
1:A:811:VAL:HG12	1:A:830:SER:H	1.65	0.60
1:A:844:LYS:HG2	1:A:917:SER:HA	1.82	0.60
1:A:418:GLN:OE1	1:A:421:GLN:NE2	2.35	0.59
1:A:410:PRO:O	1:A:434:GLN:NE2	2.35	0.59
1:A:372:TRP:HD1	1:A:373:VAL:HG13	1.66	0.59
1:A:379:ILE:HG23	1:A:380:PRO:HD3	1.83	0.59
1:A:406:ILE:HA	1:A:430:LYS:HB3	1.85	0.59
1:A:529:ILE:HG12	1:A:530:PRO:HD2	1.84	0.59
1:A:368:VAL:HG23	1:A:406:ILE:HG23	1.86	0.58
1:A:910:HIS:HB2	1:A:913:LEU:HB3	1.85	0.58
1:A:126:GLN:H	1:A:203:ALA:HB3	1.67	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:TRP:HB3	1:A:991:ILE:HG23	1.86	0.58
1:A:782:LYS:NZ	1:A:784:VAL:HG22	2.18	0.58
1:A:297:CYS:SG	1:A:506:GLY:N	2.76	0.58
1:A:451:TRP:O	1:A:459:LEU:N	2.35	0.58
1:A:782:LYS:HD2	1:A:798:VAL:HG23	1.86	0.57
1:A:582:ARG:NH2	1:A:885:HIS:O	2.38	0.57
1:A:500:LYS:HG2	1:A:502:ASP:H	1.70	0.56
1:A:1017:ARG:HA	1:A:1078:SER:HA	1.86	0.56
1:A:423:CYS:SG	1:A:424:ARG:N	2.78	0.56
1:A:831:THR:HB	1:A:936:ILE:HB	1.87	0.56
1:A:889:ASP:OD1	1:A:890:TYR:N	2.38	0.56
1:A:594:ILE:HG13	1:A:597:LYS:HE2	1.87	0.56
1:A:644:PRO:HA	1:A:647:HIS:HB2	1.88	0.56
1:A:787:SER:HB3	1:A:795:ALA:HB3	1.88	0.56
1:A:721:LYS:H	1:A:782:LYS:HE3	1.70	0.56
1:A:377:THR:O	1:A:861:GLN:NE2	2.39	0.56
1:A:669:LYS:HB2	1:A:969:ASP:OD2	2.06	0.55
1:A:810:SER:HA	1:A:831:THR:HA	1.89	0.55
1:A:593:TRP:NE1	1:A:675:MET:SD	2.80	0.54
1:A:110:PHE:N	1:A:173:ILE:O	2.41	0.54
1:A:59:TYR:HB3	1:A:109:TRP:HB2	1.89	0.54
1:A:780:LYS:HD2	1:A:801:GLN:HB3	1.89	0.54
1:A:55:LYS:HD3	1:A:113:LYS:HZ2	1.73	0.54
1:A:126:GLN:HE22	1:A:128:LEU:HD13	1.72	0.54
1:A:900:LEU:O	1:A:939:ALA:N	2.38	0.54
1:A:109:TRP:CD2	1:A:174:GLU:HB3	2.43	0.53
1:A:313:LYS:HD3	1:A:504:GLY:HA3	1.90	0.53
1:A:521:MET:O	1:A:524:ARG:NH2	2.41	0.53
1:A:831:THR:N	1:A:936:ILE:O	2.41	0.53
1:A:1016:VAL:O	1:A:1079:PHE:N	2.35	0.53
1:A:139:VAL:HG12	1:A:173:ILE:HB	1.91	0.53
1:A:844:LYS:HD3	1:A:915:ARG:HG2	1.91	0.53
1:A:177:ASN:ND2	1:A:193:ASP:OD1	2.43	0.52
1:A:904:LYS:HZ1	1:A:938:TYR:HB3	1.75	0.52
1:A:840:ASN:HD21	1:A:923:LYS:HE2	1.75	0.52
1:A:1030:LEU:HB2	1:A:1071:LEU:HG	1.92	0.52
1:A:989:SER:HB2	1:A:1019:TYR:HE2	1.73	0.52
1:A:136:GLU:HA	1:A:316:ARG:HH12	1.75	0.52
1:A:303:TRP:HZ3	1:A:503:GLY:H	1.58	0.51
1:A:436:LEU:HA	1:A:564:PHE:HB2	1.91	0.51
1:A:814:LEU:HB3	1:A:827:VAL:HG23	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:901:ASN:ND2	1:A:904:LYS:HB2	2.24	0.51
1:A:634:ILE:HG12	1:A:635:GLU:H	1.76	0.51
1:A:117:PRO:HB2	1:A:122:LYS:HD2	1.91	0.51
1:A:289:THR:HB	1:A:530:PRO:HB3	1.93	0.51
1:A:714:LEU:HD11	1:A:942:PRO:HB3	1.92	0.51
1:A:667:GLN:HG3	1:A:971:GLY:HA3	1.93	0.50
1:A:581:MET:O	1:A:585:GLU:N	2.41	0.50
1:A:983:ASP:HB3	1:A:986:VAL:HG12	1.94	0.50
1:A:573:SER:O	1:A:578:LYS:NZ	2.45	0.50
1:A:332:LYS:HD3	1:A:364:GLN:HA	1.93	0.50
1:A:785:GLN:O	1:A:797:GLU:N	2.38	0.50
1:A:848:PRO:HA	1:A:913:LEU:HA	1.93	0.50
1:A:603:PRO:HA	1:A:606:TYR:HA	1.94	0.50
1:A:901:ASN:HD22	1:A:904:LYS:HE2	1.76	0.50
1:A:144:THR:HG23	1:A:145:LEU:H	1.77	0.50
1:A:1028:ALA:O	1:A:1071:LEU:N	2.36	0.49
1:A:298:HIS:HB3	1:A:501:GLY:HA2	1.94	0.49
1:A:375:ASN:HD21	1:A:388:GLN:HE22	1.61	0.49
1:A:721:LYS:N	1:A:782:LYS:HE3	2.28	0.49
1:A:132:ASP:HB3	1:A:196:ARG:HA	1.94	0.49
1:A:884:HIS:N	1:A:905:TYR:O	2.31	0.49
1:A:1014:ILE:HD11	1:A:1081:LEU:HD12	1.95	0.49
1:A:357:ILE:HG23	1:A:358:PRO:HD3	1.95	0.49
1:A:288:LEU:HD13	1:A:527:ASN:HD21	1.78	0.48
1:A:451:TRP:HB3	1:A:459:LEU:HB3	1.94	0.48
1:A:517:ARG:HG2	1:A:521:MET:HE3	1.94	0.48
1:A:756:ASP:OD2	1:A:915:ARG:NH2	2.46	0.48
1:A:813:SER:O	1:A:828:ASP:N	2.33	0.48
1:A:901:ASN:ND2	1:A:904:LYS:O	2.24	0.48
1:A:901:ASN:HD22	1:A:904:LYS:HB2	1.79	0.48
1:A:130:GLN:HE21	1:A:201:ARG:HD2	1.79	0.48
1:A:45:LYS:NZ	1:A:125:GLU:OE2	2.45	0.48
1:A:993:ARG:HG2	1:A:1014:ILE:HG22	1.96	0.48
1:A:730:ASP:HB2	1:A:733:LEU:HB2	1.95	0.48
1:A:802:ILE:HG12	1:A:803:SER:H	1.79	0.48
1:A:1069:ILE:HG23	1:A:1070:LYS:HG3	1.94	0.48
1:A:709:LEU:HD11	1:A:794:CYS:HB3	1.95	0.47
1:A:981:SER:OG	1:A:982:GLY:N	2.46	0.47
1:A:430:LYS:NZ	1:A:460:LEU:HG	2.29	0.47
1:A:898:SER:HB3	1:A:941:TYR:HB3	1.96	0.47
1:A:175:ALA:HB2	1:A:196:ARG:HD3	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:815:ASN:HD22	1:A:822:ALA:HB1	1.79	0.47
1:A:127:LEU:HB3	1:A:161:LEU:HD12	1.95	0.47
1:A:648:ASN:HA	1:A:651:LYS:HB2	1.95	0.47
1:A:425:LEU:HB3	1:A:1043:ASP:HB2	1.96	0.47
1:A:1030:LEU:N	1:A:1069:ILE:O	2.48	0.47
1:A:50:ASP:OD2	1:A:200:LEU:HD23	2.16	0.46
1:A:136:GLU:OE2	1:A:309:GLU:HB3	2.15	0.46
1:A:643:VAL:HG13	1:A:645:MET:H	1.80	0.46
1:A:1013:SER:OG	1:A:1081:LEU:O	2.26	0.46
1:A:460:LEU:HD21	1:A:545:ILE:HD13	1.97	0.46
1:A:886:LYS:HG2	1:A:956:HIS:HA	1.98	0.46
1:A:1025:GLU:HG2	1:A:1026:SER:N	2.31	0.46
1:A:307:PHE:HA	1:A:310:THR:HG22	1.98	0.46
1:A:332:LYS:HD2	1:A:366:PHE:HE2	1.81	0.46
1:A:640:TYR:HA	1:A:643:VAL:HB	1.98	0.46
1:A:109:TRP:HA	1:A:174:GLU:HA	1.98	0.45
1:A:848:PRO:HB3	1:A:913:LEU:HD12	1.98	0.45
1:A:676:ARG:HG2	1:A:677:THR:N	2.31	0.45
1:A:1018:VAL:O	1:A:1077:ALA:N	2.42	0.45
1:A:142:PRO:HB2	1:A:144:THR:O	2.17	0.45
1:A:215:LEU:HD23	1:A:258:VAL:HG13	1.99	0.45
1:A:345:LEU:HD13	1:A:398:LYS:NZ	2.32	0.45
1:A:376:ASP:HA	1:A:412:THR:HG23	1.99	0.45
1:A:1015:VAL:HA	1:A:1080:ARG:HA	1.99	0.45
1:A:299:ILE:HG21	1:A:314:ILE:HD13	1.98	0.45
1:A:449:PHE:HD1	1:A:556:PRO:HB2	1.81	0.45
1:A:634:ILE:HG23	1:A:636:MET:H	1.82	0.45
1:A:809:LYS:O	1:A:832:THR:N	2.40	0.45
1:A:1067:ILE:HD12	1:A:1067:ILE:H	1.82	0.45
1:A:573:SER:HB2	1:A:920:ARG:HB3	1.99	0.44
1:A:991:ILE:HD12	1:A:1016:VAL:HG22	1.99	0.44
1:A:408:TRP:CH2	1:A:410:PRO:HG3	2.52	0.44
1:A:478:VAL:HA	1:A:515:MET:HE1	1.99	0.44
1:A:807:LYS:H	1:A:836:TRP:HZ3	1.65	0.44
1:A:593:TRP:HB3	1:A:991:ILE:O	2.17	0.44
1:A:857:SER:N	1:A:889:ASP:O	2.49	0.44
1:A:141:ASP:OD1	1:A:141:ASP:N	2.49	0.44
1:A:321:GLN:O	1:A:325:MET:HG2	2.18	0.44
1:A:783:LYS:H	1:A:799:ILE:HG22	1.81	0.44
1:A:808:ILE:HA	1:A:833:VAL:HG22	1.99	0.44
1:A:337:GLN:HB2	1:A:340:GLN:HB2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:LYS:HG2	1:A:404:SER:H	1.83	0.44
1:A:613:ILE:HG13	1:A:616:LEU:HD12	1.99	0.44
1:A:215:LEU:HD22	1:A:262:ARG:HB2	2.00	0.43
1:A:202:LYS:HB2	1:A:202:LYS:NZ	2.32	0.43
1:A:857:SER:HB3	1:A:889:ASP:HB3	2.00	0.43
1:A:336:SER:HA	1:A:368:VAL:HG13	1.99	0.43
1:A:430:LYS:HZ1	1:A:460:LEU:HG	1.83	0.43
1:A:467:ASN:HB3	1:A:471:ALA:HB2	1.99	0.43
1:A:664:LEU:HD23	1:A:664:LEU:HA	1.87	0.43
1:A:1042:VAL:HG22	1:A:1048:LYS:HA	1.99	0.43
1:A:545:ILE:O	1:A:549:THR:HG22	2.18	0.43
1:A:438:TRP:HB3	1:A:442:ASN:HD21	1.84	0.43
1:A:816:ALA:H	1:A:822:ALA:HB3	1.84	0.43
1:A:992:LYS:O	1:A:1015:VAL:N	2.39	0.43
1:A:789:ASN:O	1:A:790:THR:HG23	2.19	0.43
1:A:860:THR:OG1	1:A:861:GLN:N	2.52	0.43
1:A:978:ILE:HD12	1:A:978:ILE:H	1.84	0.43
1:A:84:ARG:HB3	1:A:90:LEU:HD12	2.01	0.42
1:A:96:ASN:OD1	1:A:97:ILE:HG23	2.19	0.42
1:A:506:GLY:HA2	1:A:507:PRO:HD3	1.84	0.42
1:A:58:TRP:HB3	1:A:95:ALA:HB2	2.01	0.42
1:A:475:PHE:CE1	1:A:477:ASP:HB2	2.53	0.42
1:A:566:PHE:CD2	1:A:568:ARG:HG2	2.54	0.42
1:A:95:ALA:O	1:A:96:ASN:ND2	2.52	0.42
1:A:760:LEU:HD23	1:A:762:TRP:H	1.85	0.42
1:A:246:VAL:HA	1:A:261:CYS:SG	2.59	0.42
1:A:1068:PRO:HD2	1:A:1079:PHE:HE1	1.83	0.42
1:A:59:TYR:CE2	1:A:91:GLU:HB2	2.54	0.42
1:A:369:GLY:HA2	1:A:428:ILE:HD12	2.01	0.42
1:A:444:PHE:HA	1:A:445:PRO:HD3	1.79	0.42
1:A:811:VAL:N	1:A:830:SER:O	2.53	0.42
1:A:342:LYS:HE3	1:A:346:GLU:OE2	2.19	0.42
1:A:423:CYS:SG	1:A:459:LEU:HG	2.60	0.42
1:A:509:GLU:HG2	1:A:511:MET:HG2	2.01	0.42
1:A:598:THR:OG1	1:A:664:LEU:HD21	2.19	0.42
1:A:133:CYS:HB3	1:A:155:GLU:HA	2.02	0.41
1:A:625:PHE:HB2	1:A:628:VAL:HG23	2.03	0.41
1:A:135:ASN:HD21	1:A:305:TRP:CD1	2.38	0.41
1:A:519:ARG:HG2	1:A:532:LEU:HG	2.02	0.41
1:A:573:SER:HB2	1:A:920:ARG:HE	1.86	0.41
1:A:491:TYR:CG	1:A:492:GLY:N	2.88	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:ASP:HB2	1:A:496:MET:HE3	2.01	0.41
1:A:623:CYS:HB2	1:A:645:MET:HE2	2.02	0.41
1:A:718:ILE:HA	1:A:725:ILE:HA	2.03	0.41
1:A:140:ILE:N	1:A:172:TYR:O	2.48	0.41
1:A:405:LYS:O	1:A:428:ILE:HG13	2.20	0.41
1:A:579:LYS:NZ	1:A:935:GLU:H	2.19	0.41
1:A:667:GLN:HA	1:A:970:ILE:O	2.21	0.41
1:A:153:GLY:HA2	1:A:507:PRO:HB3	2.03	0.41
1:A:373:VAL:HG11	1:A:621:LEU:HB3	2.02	0.41
1:A:394:ARG:NH1	1:A:614:ASN:HD21	2.19	0.41
1:A:54:VAL:HG23	1:A:55:LYS:HG3	2.02	0.41
1:A:408:TRP:CD1	1:A:432:LEU:HD22	2.56	0.41
1:A:644:PRO:O	1:A:648:ASN:N	2.47	0.41
1:A:844:LYS:HB3	1:A:915:ARG:HG2	2.02	0.41
1:A:46:ARG:HG2	1:A:47:ILE:H	1.85	0.41
1:A:1029:SER:HA	1:A:1070:LYS:HA	2.03	0.41
1:A:430:LYS:HG2	1:A:542:TYR:CZ	2.56	0.40
1:A:859:GLU:HG2	1:A:863:GLY:O	2.20	0.40
1:A:1025:GLU:HG2	1:A:1026:SER:H	1.86	0.40
1:A:298:HIS:HB2	1:A:408:TRP:HH2	1.86	0.40
1:A:475:PHE:CZ	1:A:481:THR:HG22	2.57	0.40
1:A:351:PHE:O	1:A:355:VAL:HG23	2.22	0.40
1:A:575:ALA:O	1:A:579:LYS:HG3	2.21	0.40
1:A:665:GLN:NE2	1:A:967:PRO:HD3	2.37	0.40
1:A:753:VAL:HG22	1:A:847:PHE:CE1	2.57	0.40
1:A:855:PHE:CD1	1:A:866:LYS:HG3	2.56	0.40
1:A:943:HIS:CE1	1:A:948:SER:HA	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	907/1096 (83%)	814 (90%)	90 (10%)	3 (0%)	36 72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	478	VAL
1	A	816	ALA
1	A	980	ILE

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	832/971 (86%)	788 (95%)	44 (5%)	20 41

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	ILE
1	A	140	ILE
1	A	173	ILE
1	A	201	ARG
1	A	202	LYS
1	A	350	GLU
1	A	357	ILE
1	A	368	VAL
1	A	379	ILE
1	A	383	GLU
1	A	433	THR
1	A	487	THR
1	A	489	GLU
1	A	529	ILE
1	A	598	THR
1	A	601	LEU
1	A	628	VAL
1	A	643	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	661	VAL
1	A	708	VAL
1	A	714	LEU
1	A	717	ILE
1	A	754	ILE
1	A	778	VAL
1	A	786	VAL
1	A	790	THR
1	A	798	VAL
1	A	800	PHE
1	A	808	ILE
1	A	811	VAL
1	A	812	ILE
1	A	829	ILE
1	A	865	THR
1	A	892	GLU
1	A	893	TYR
1	A	940	ILE
1	A	951	THR
1	A	970	ILE
1	A	978	ILE
1	A	987	ILE
1	A	991	ILE
1	A	1014	ILE
1	A	1018	VAL
1	A	1042	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	HIS
1	A	60	GLN
1	A	99	GLN
1	A	130	GLN
1	A	235	GLN
1	A	237	HIS
1	A	361	GLN
1	A	362	GLN
1	A	375	ASN
1	A	388	GLN
1	A	393	GLN
1	A	458	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	484	GLN
1	A	522	ASN
1	A	527	ASN
1	A	533	GLN
1	A	576	GLN
1	A	614	ASN
1	A	662	GLN
1	A	665	GLN
1	A	785	GLN
1	A	840	ASN
1	A	861	GLN
1	A	959	ASN
1	A	973	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

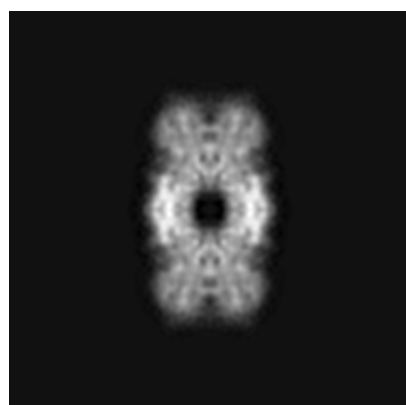
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8166. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

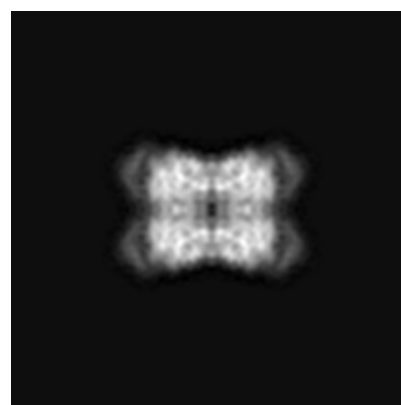
6.1.1 Primary map



X



Y

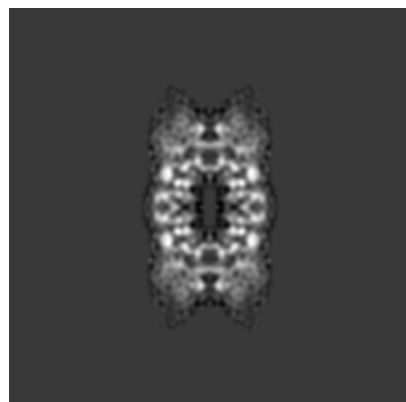


Z

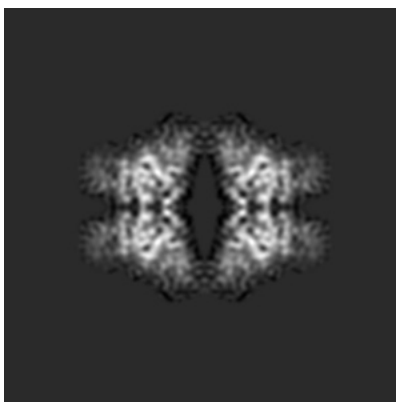
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 125



Y Index: 125

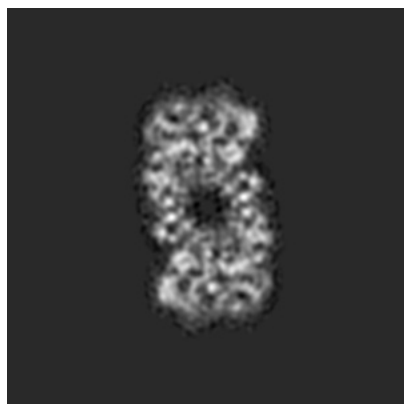


Z Index: 125

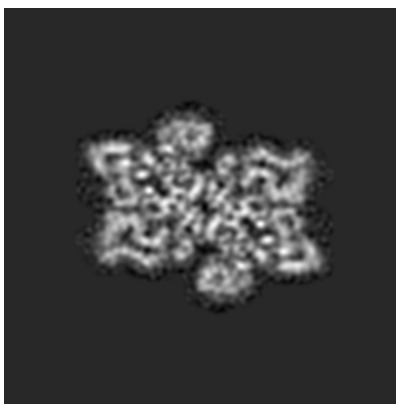
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

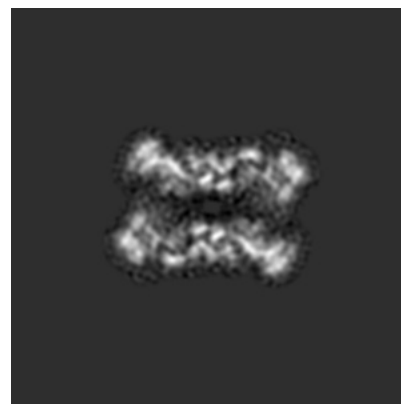
6.3.1 Primary map



X Index: 104



Y Index: 110

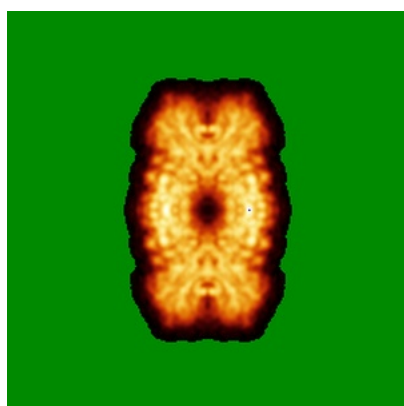


Z Index: 133

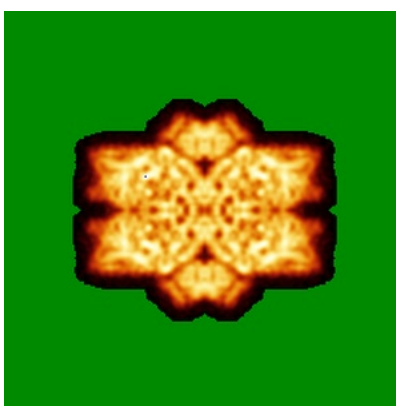
The images above show the largest variance slices of the map in three orthogonal directions.

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

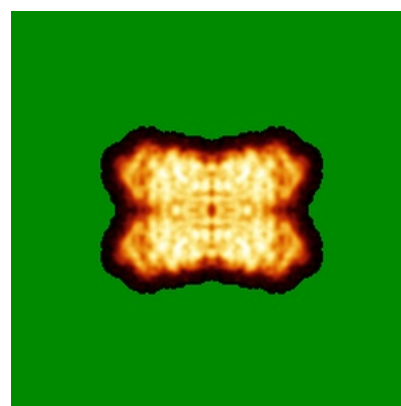
6.4.1 Primary map



X



Y

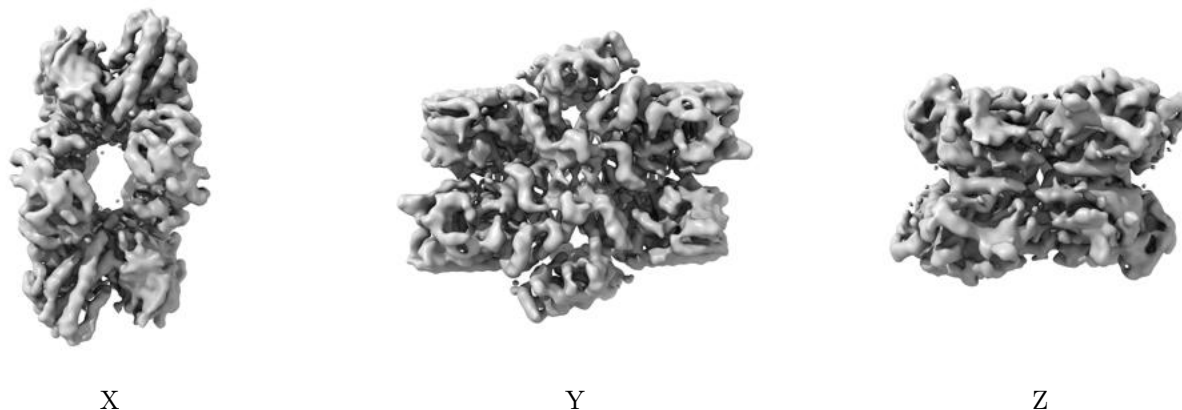


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.064. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

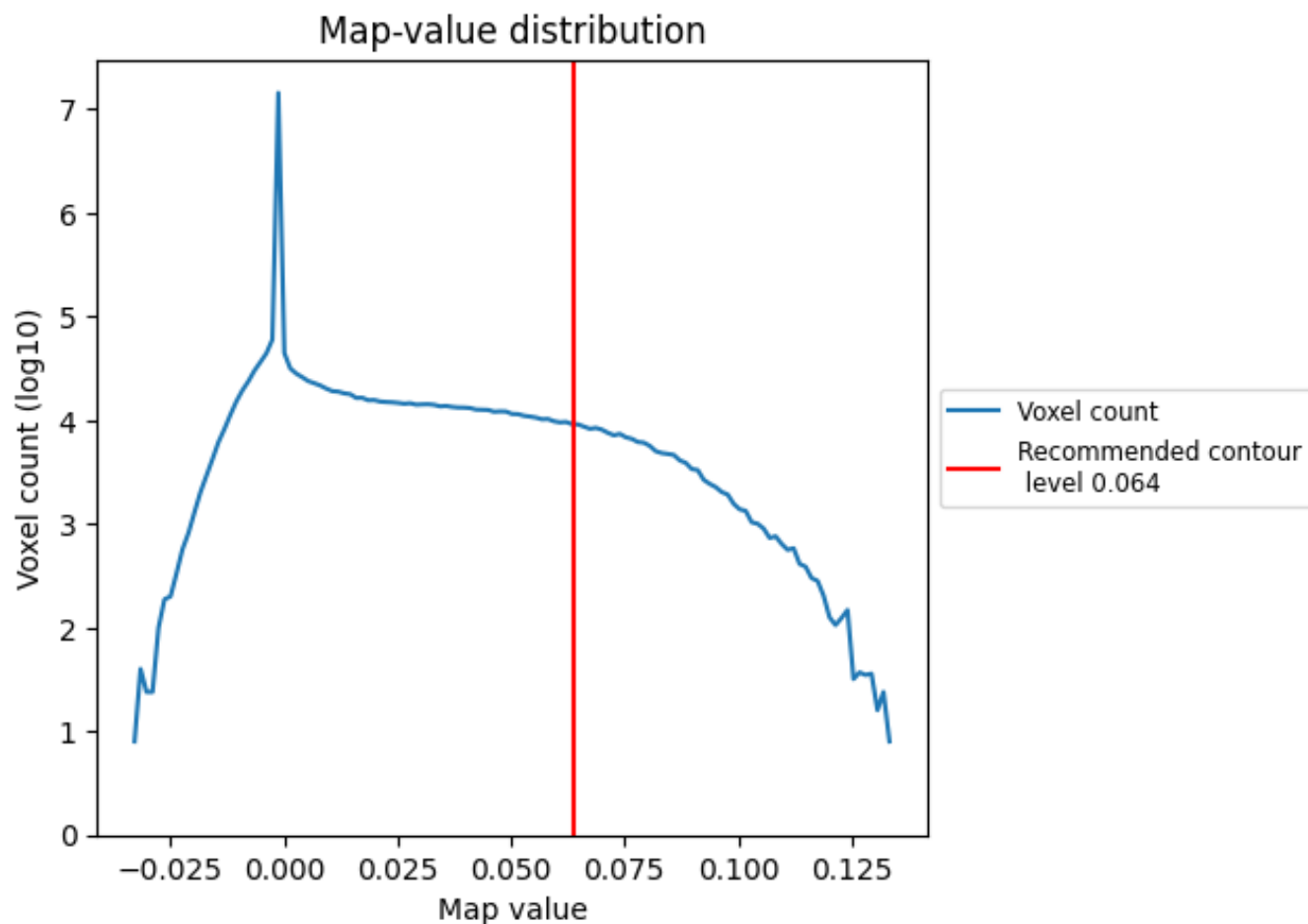
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

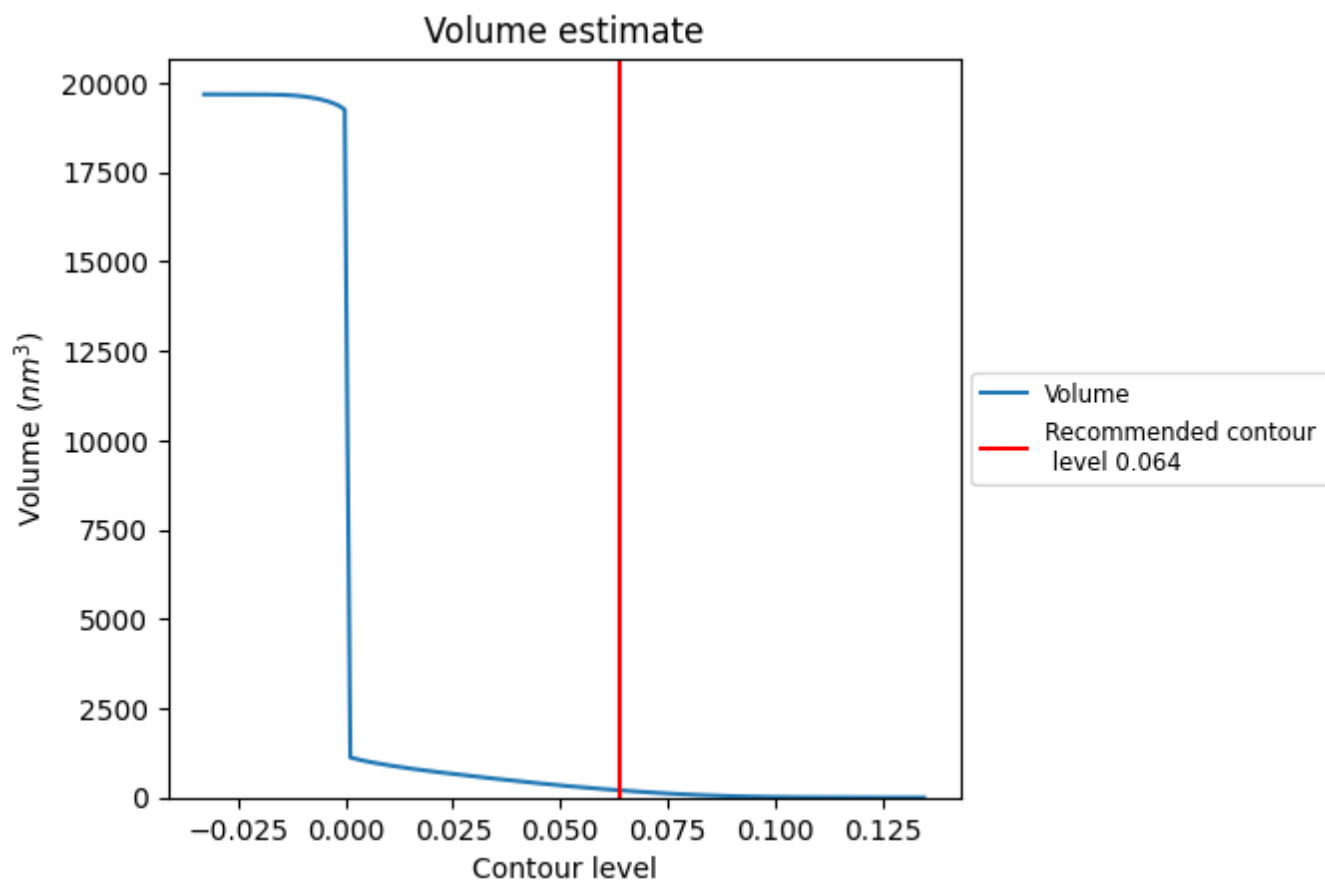
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

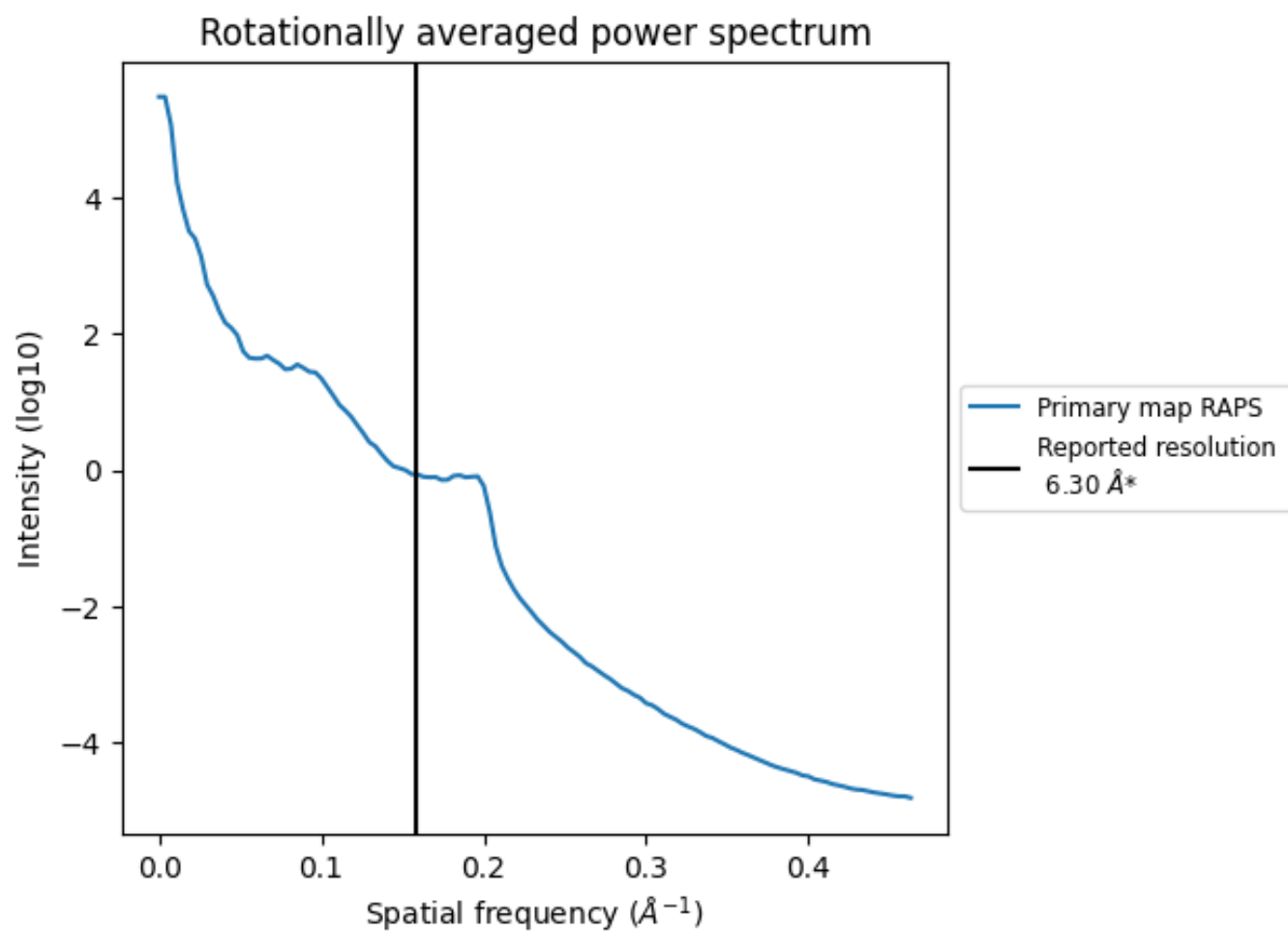
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 201 nm³; this corresponds to an approximate mass of 182 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 ⓘ

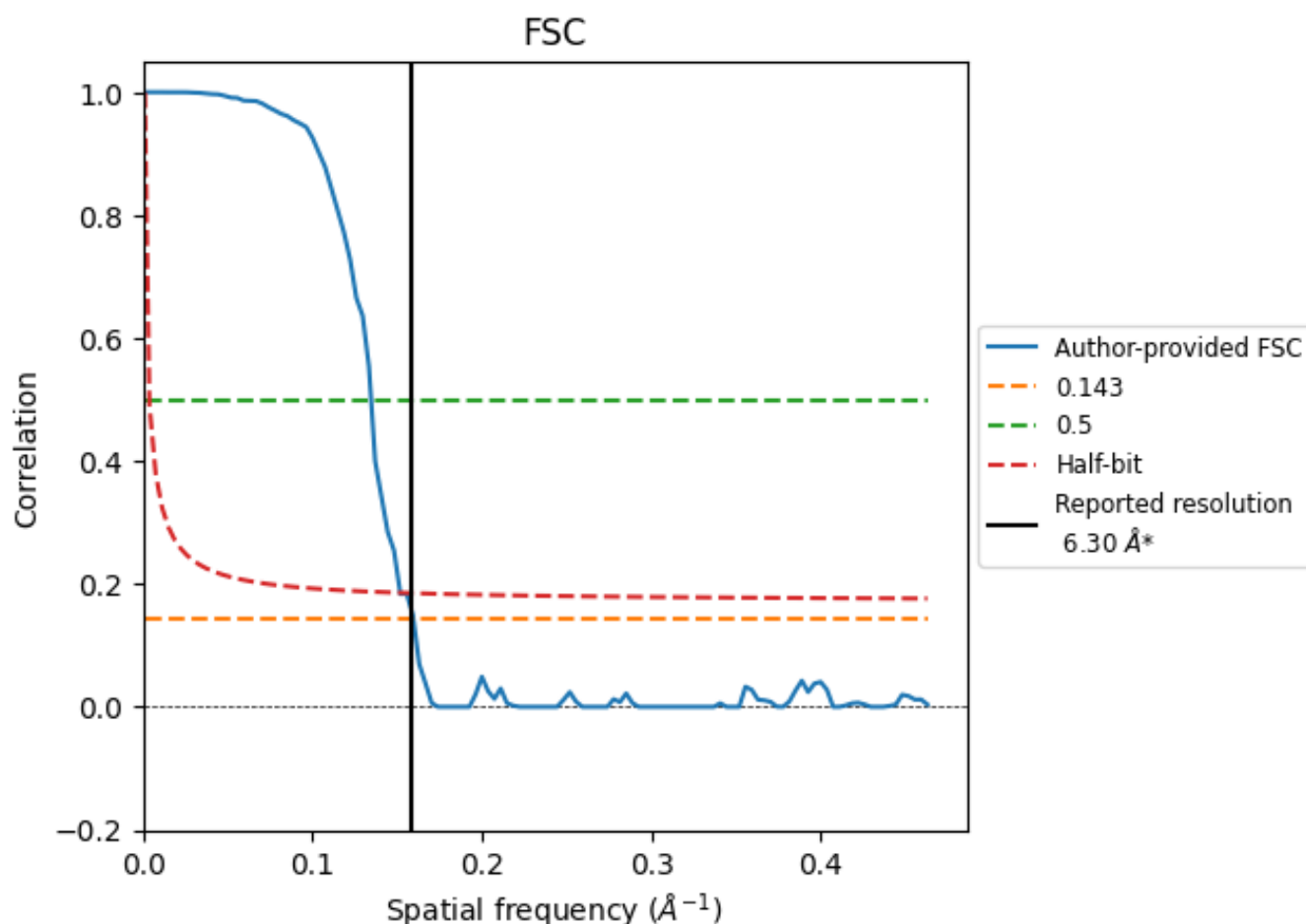


*Reported resolution corresponds to spatial frequency of 0.159 Å⁻¹

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 0.159 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	6.27	7.43	6.59
Unmasked-calculated*	-	-	-

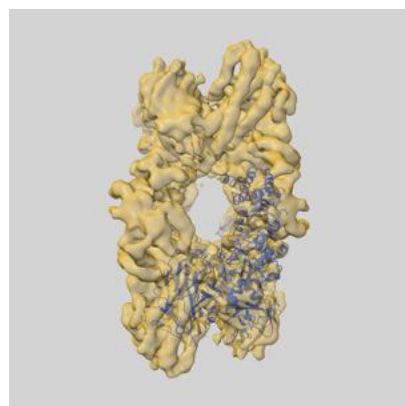
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit ⓘ

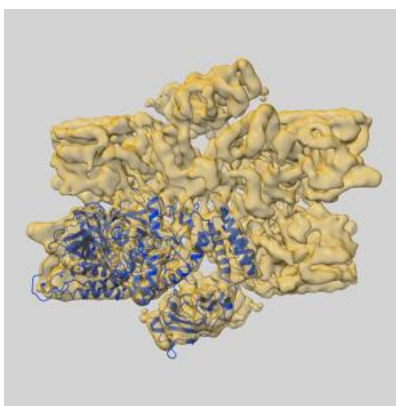
This section contains information regarding the fit between EMDB map EMD-8166 and PDB model 5JM0. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlays

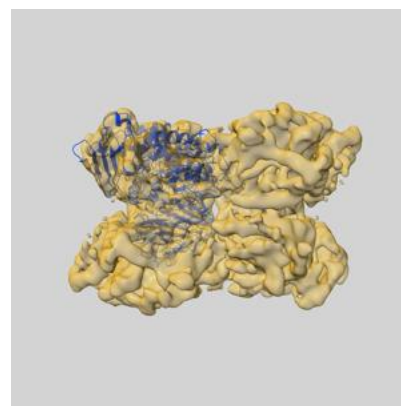
9.1.1 Map-model overlay ⓘ



X

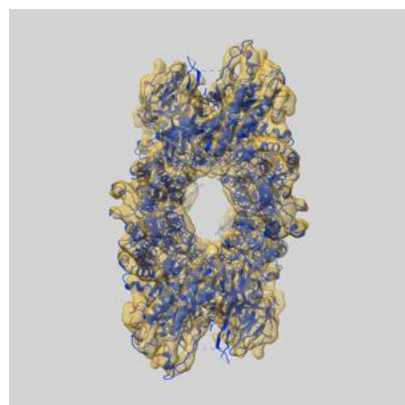


Y

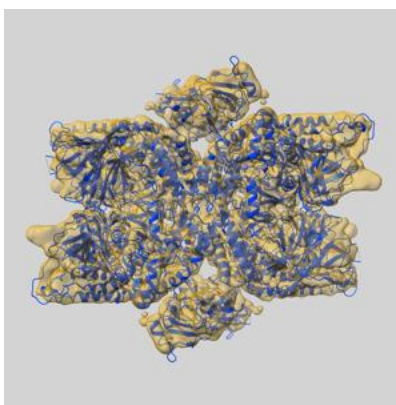


Z

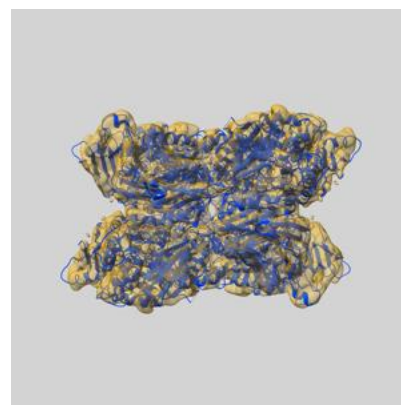
9.1.2 Map-model assembly overlay ⓘ



X



Y



Z

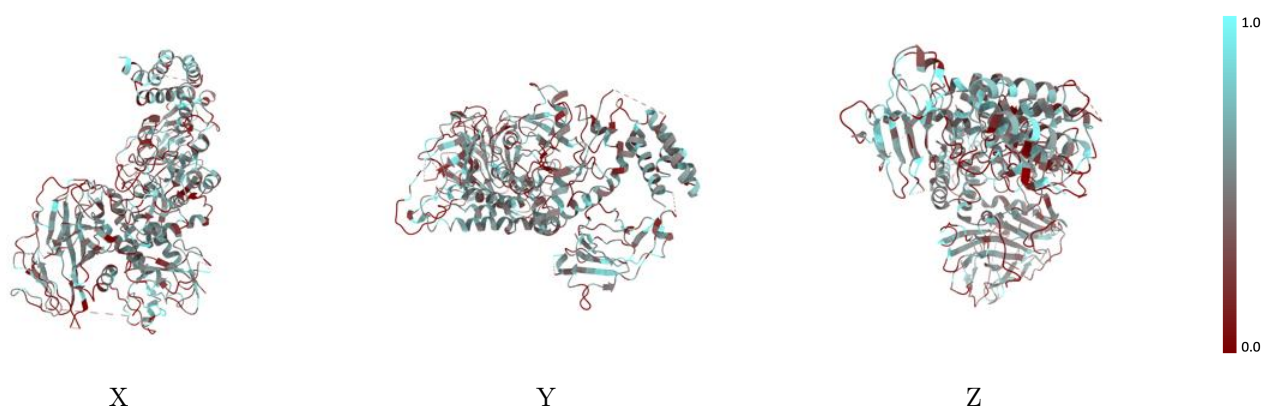
The images above show the 3D surface view of the map at the recommended contour level 0.064 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



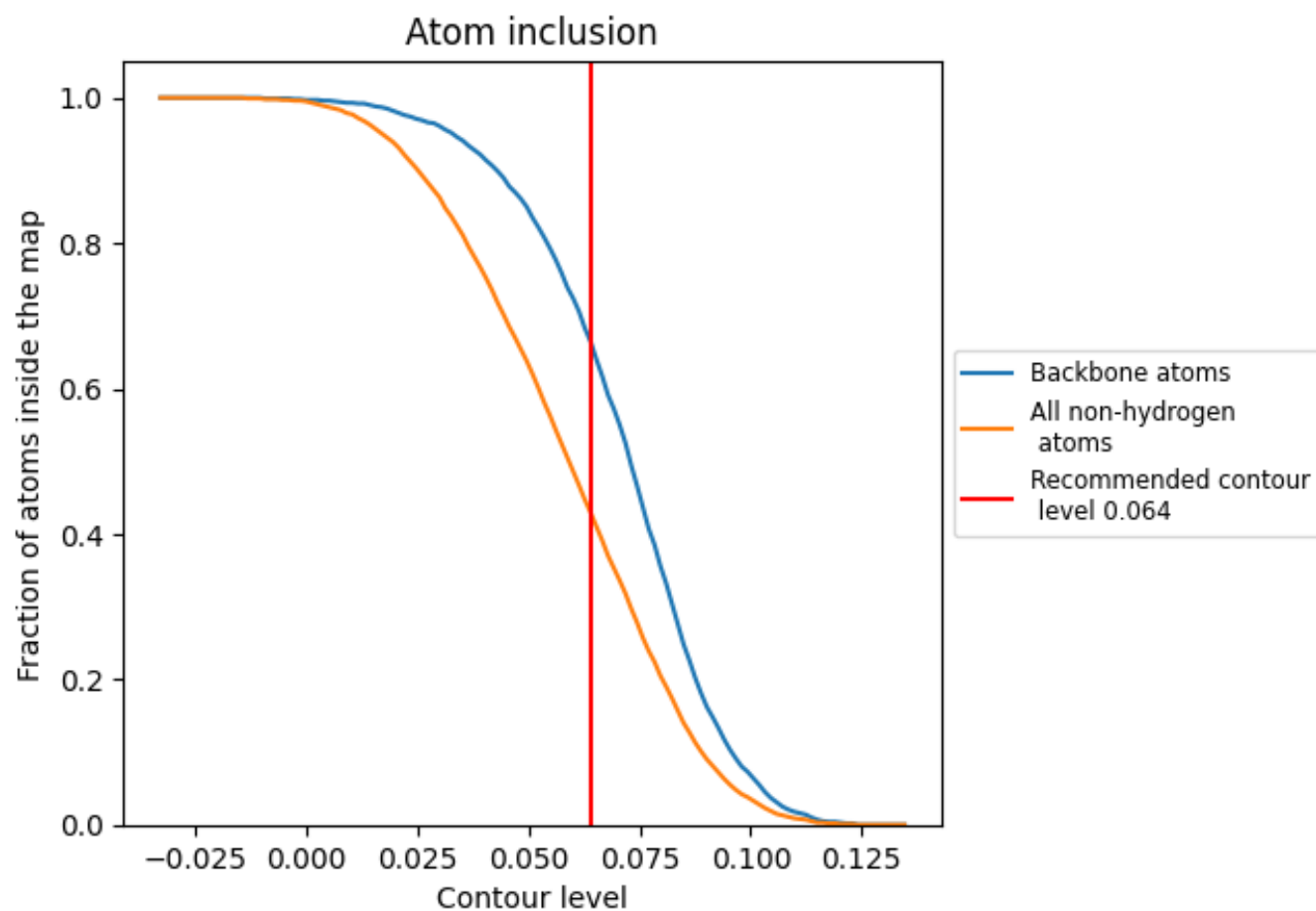
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.064).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 43% 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 (0.064) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4290	0.1290
A	0.4290	0.1290

