Full wwPDB EM Validation Report

Feb 27, 2024 – 08:14 AM EST

PDB ID	:	6V0E
EMDB ID	:	EMD-20995
Title	:	Lipophilic Envelope-spanning Tunnel B (LetB), Model 3
Authors	:	Isom, G.L.; Coudray, N.; MacRae, M.R.; McManus, C.T.; Ekiert, D.C.; Bhabha, G.
Deposited on	:	2019-11-18
Resolution	:	3.06 Å(reported)
Based on initial model	:	5UW2

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 (i) 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 (i)) were used in the production of this report:

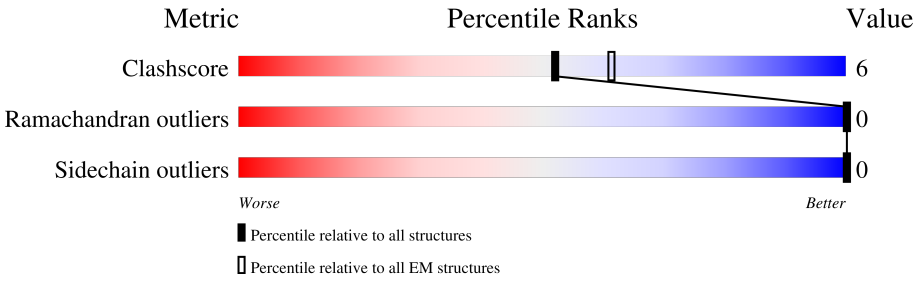
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.06 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

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	832	37% 7% 56%
1	B	832	37% 7% 56%
1	C	832	37% 7% 56%
1	D	832	37% 7% 56%
1	E	832	37% 6% 56%
1	F	832	37% 7% 56%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 16602 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 Intermembrane transport protein YebT.

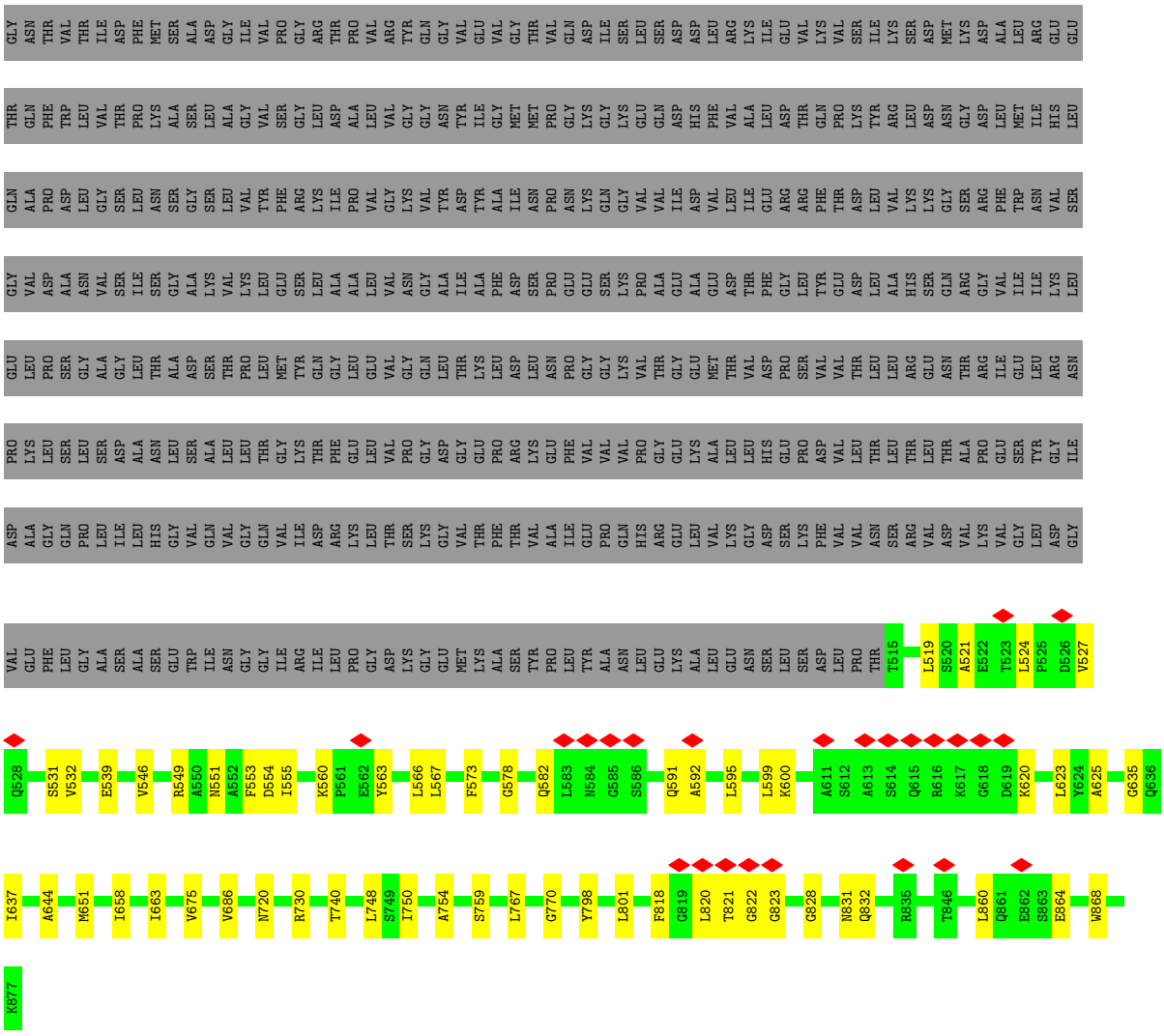
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		
1	B	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		
1	C	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		
1	D	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		
1	E	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		
1	F	363	Total	C	N	O	S	0	0
			2767	1757	487	519	4		

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.

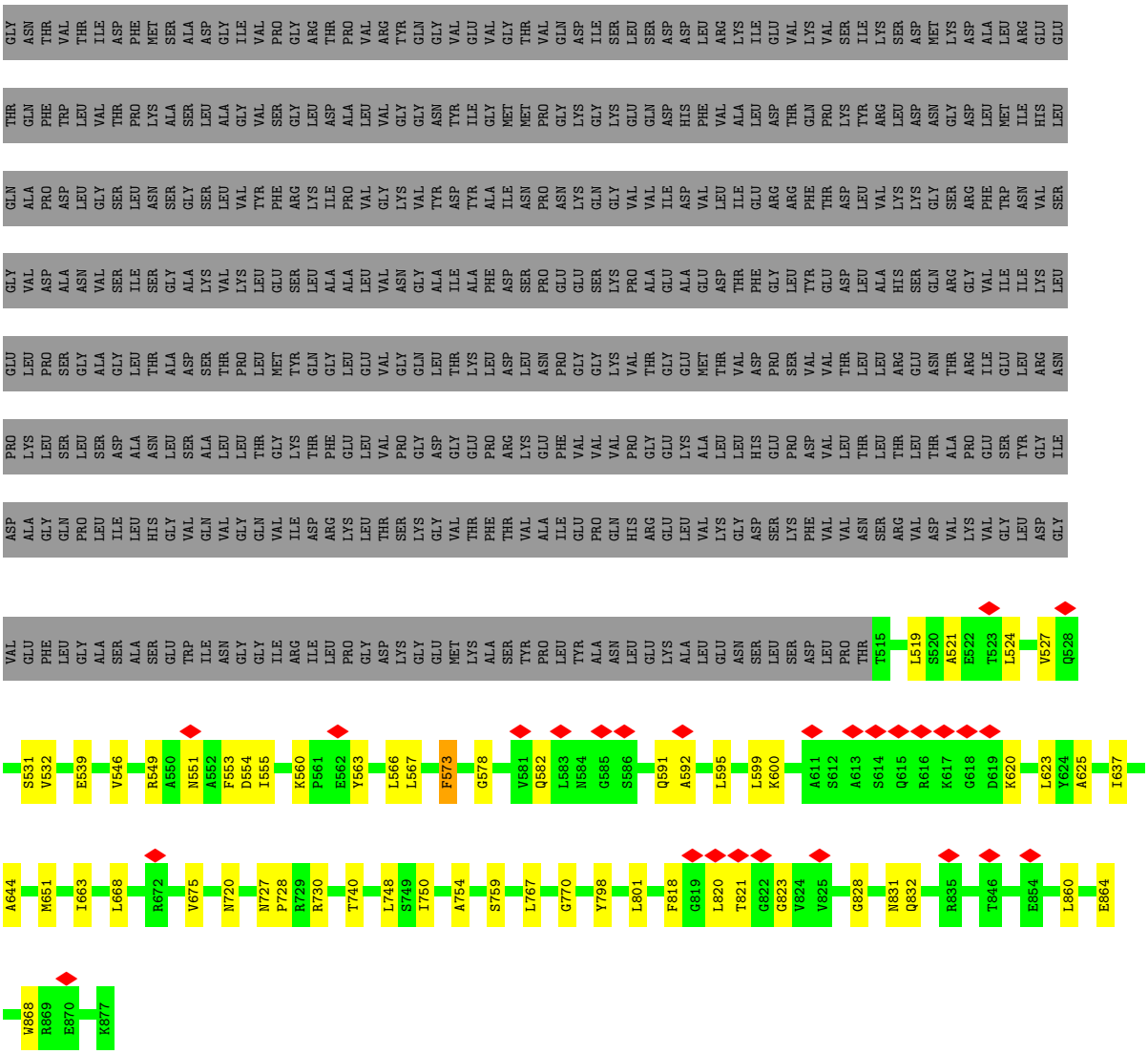
• Molecule 1: Intermembrane transport protein YebT

Chain A:

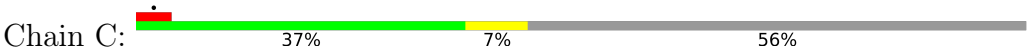


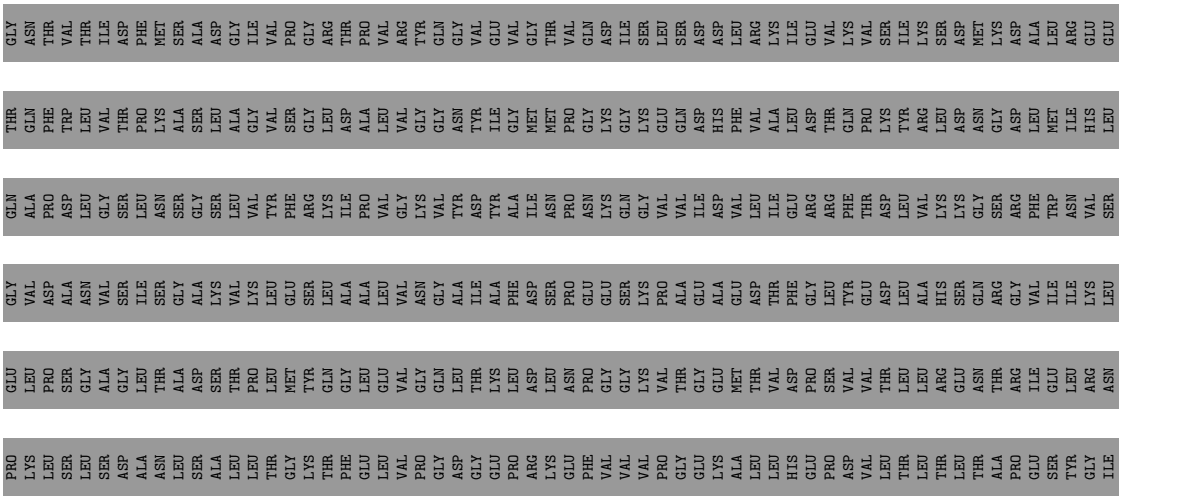
• Molecule 1: Intermembrane transport protein YebT

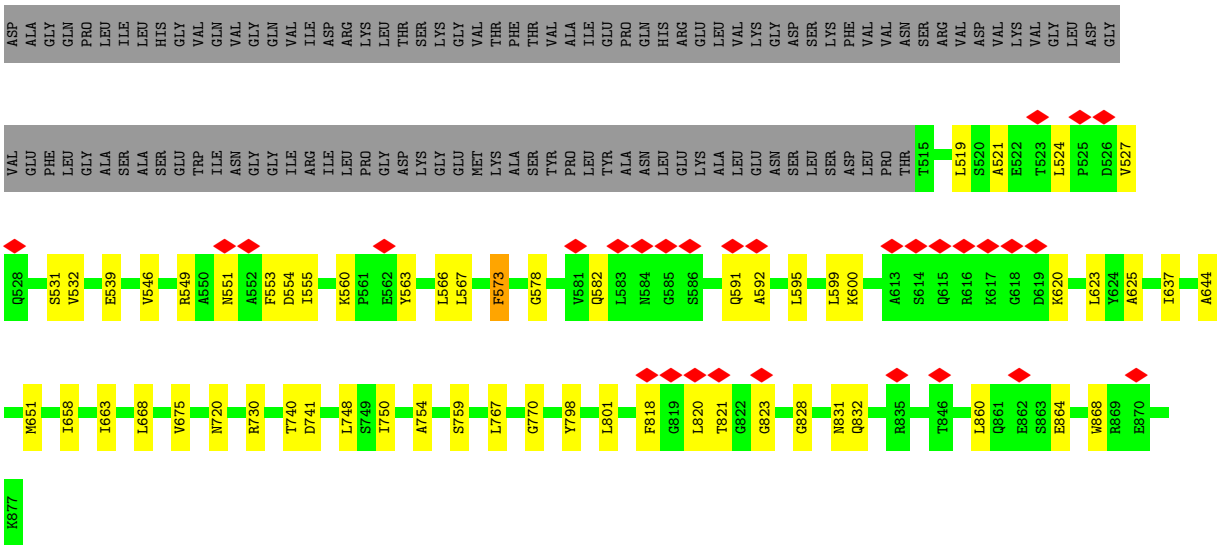
Chain B:



• Molecule 1: Intermembrane transport protein YebT

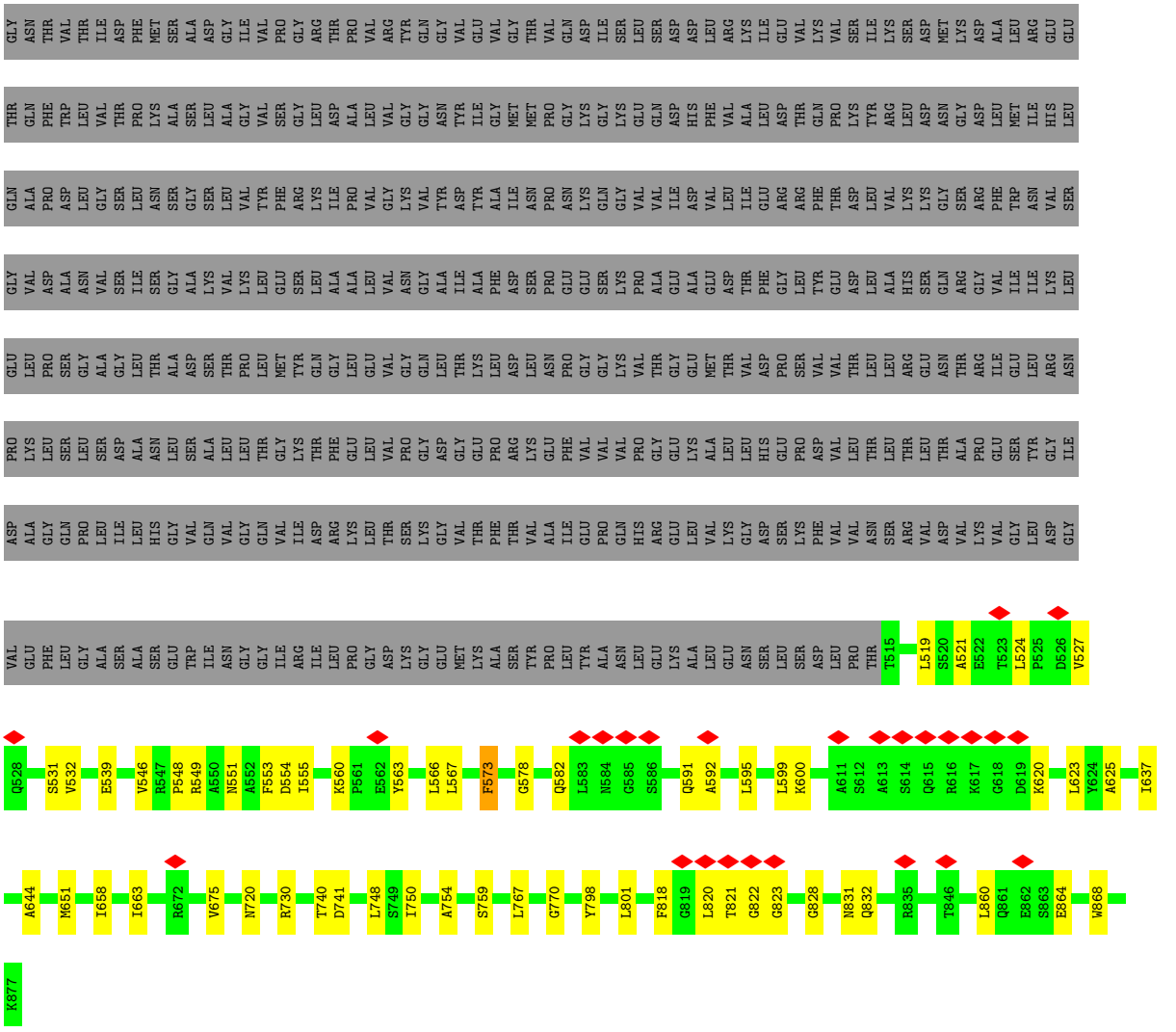






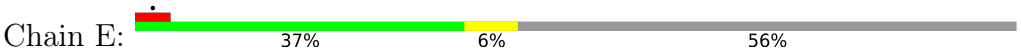
• Molecule 1: Intermembrane transport protein YebT

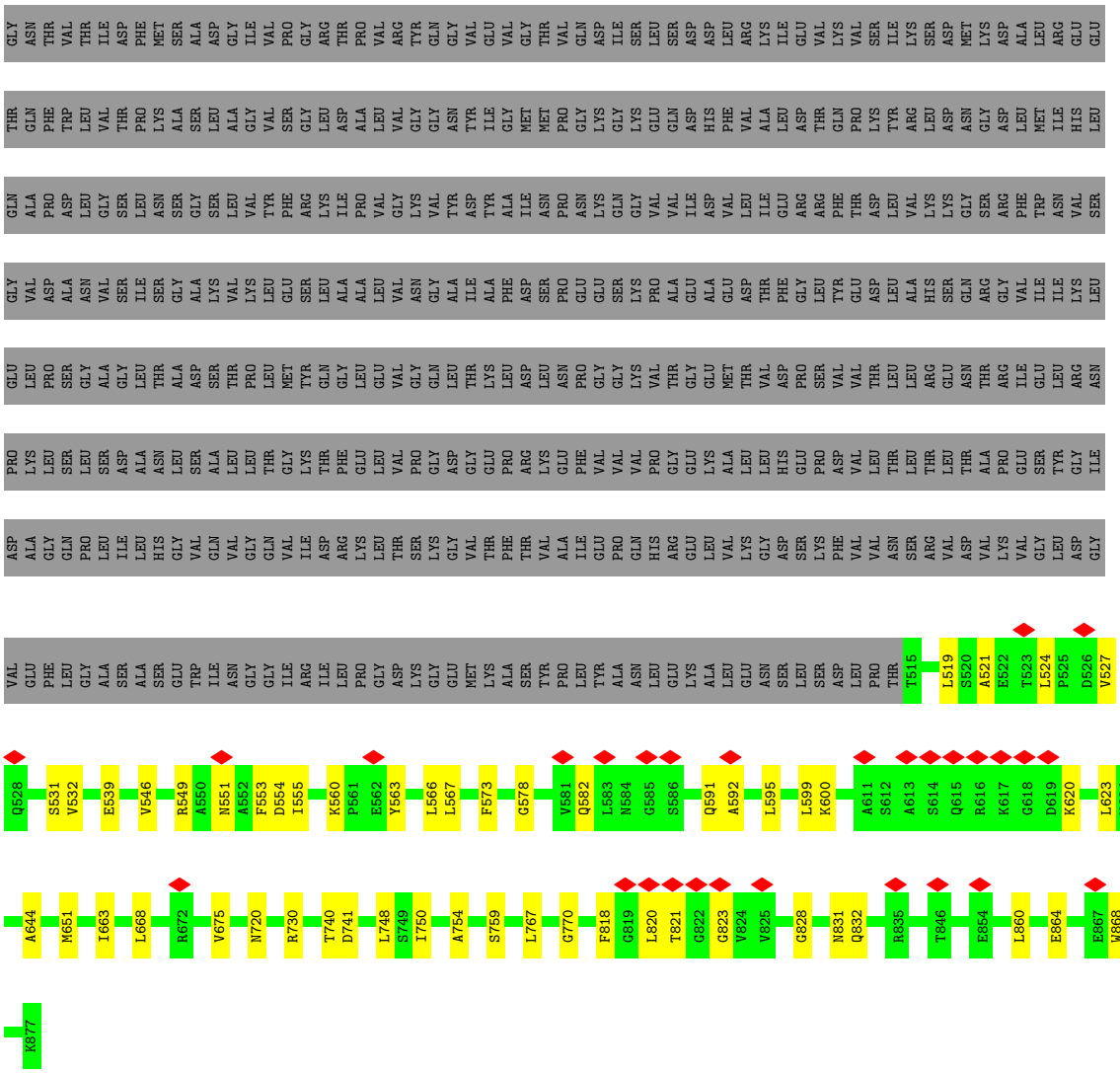
Chain D:



• Molecule 1: Intermembrane transport protein YebT

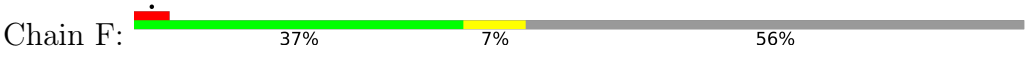
Chain E:

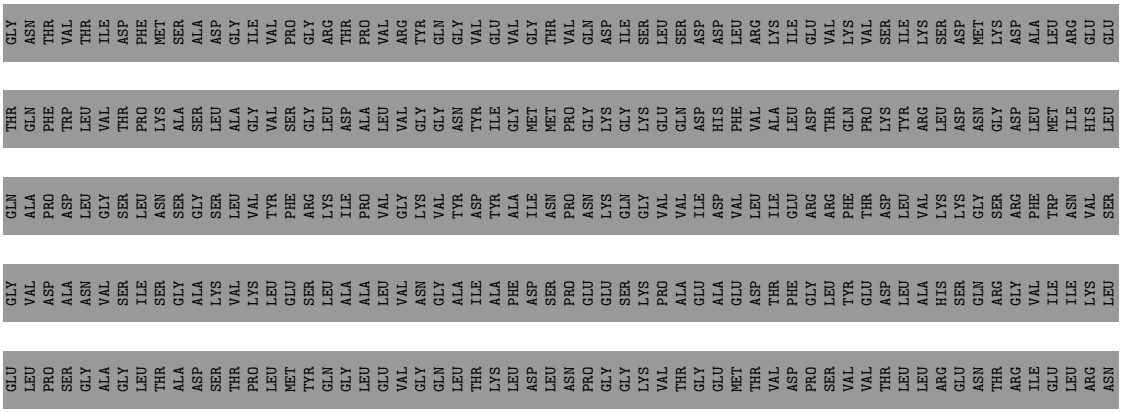


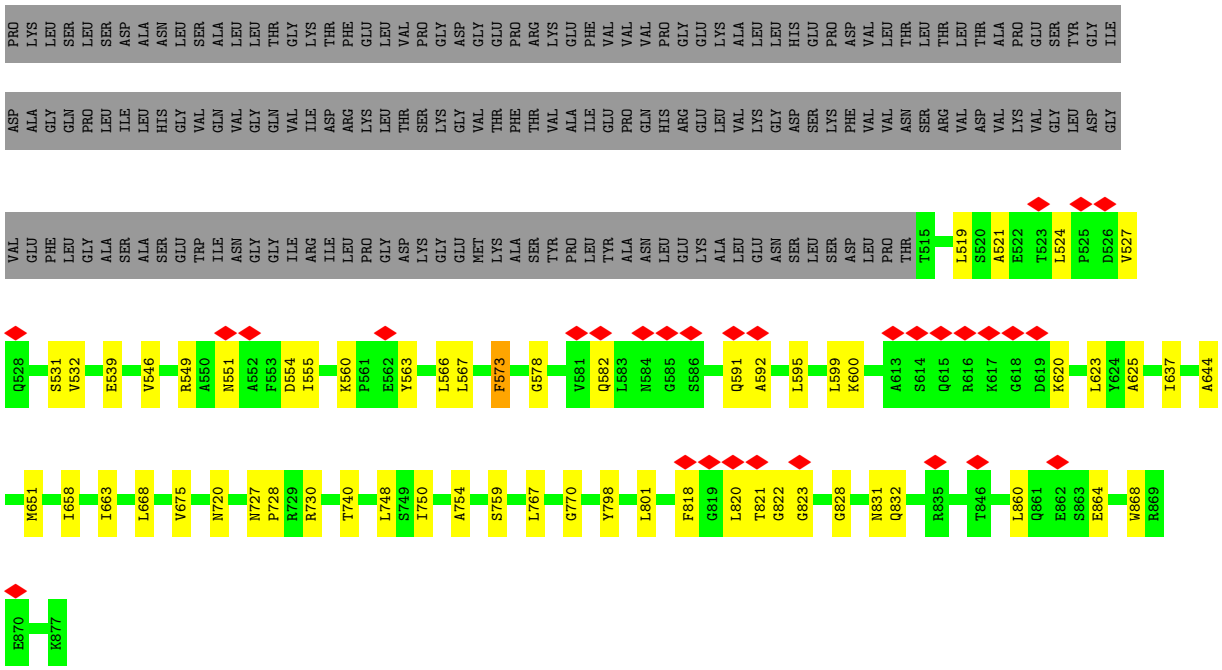


• Molecule 1: Intermembrane transport protein YebT

Chain F:






PRO LYS LEU SER LEU SER ASP ALA ASN LEU SER ALA LEU LEU THR GLY LYS THR PHE GLU LEU VAL PRO GLY ASP GLY GLU PRO ARG LYS GLU PHE VAL VAL PRO GLY GLU LYS ALA LEU LEU HIS GLU PRO ASP VAL LEU THR LEU THR LEU THR ALA PRO GLU SER TYR GLY ILE
ASP ALA GLY GLN PRO LEU ILE LEU HIS GLY VAL GLN VAL GLY GLN VAL ILE ASP ARG LYS LEU THR SER LYS GLY VAL THR PHE THR VAL ALA ILE GLU PRO GLN HIS ARG GLU LEU VAL LYS GLY ASP SER LYS PHE VAL VAL ASN SER ARG VAL ASP VAL LYS VAL GLY LEU ASP GLY
VAL GLU PHE LEU GLY ALA SER ALA SER GLU TRP ILE ASN GLY GLY ILE ARG ILE LEU PRO GLY ASP LYS GLY GLU MET LYS ALA SER TYR PRO LEU TYR ALA ASN LEU GLU LYS ALA LEU GLU ASN SER LEU SER ASP LEU PRO THR T515 L519 S520 A521 E522 T523 L524 P525 D526 V527
Q528 S531 V532 E539 V546 R549 A550 N551 A552 F553 D554 I555 K560 P561 E562 Y563 L566 L567 F573 G578 V581 Q582 L583 N584 G585 S586 Q591 A592 L595 L599 K600 A613 S614 Q615 R616 K617 G618 D619 K620 L623 Y624 A625 I637 T A644
M651 I658 I663 L668 V675 N720 N727 P728 R729 R730 T740 L748 S749 I750 A754 S759 L767 G770 Y798 L801 F818 G819 L820 T821 G822 G823 G828 N831 Q832 R835 T846 L860 Q861 E862 S863 E864 W868 R869
E870 K877

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	101464	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 ($e^-/Å^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.385	Depositor
Minimum map value	-0.184	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	366.8, 366.8, 366.8	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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	0.41	0/2822	0.62	1/3831 (0.0%)
1	B	0.41	0/2822	0.62	2/3831 (0.1%)
1	C	0.41	0/2822	0.62	2/3831 (0.1%)
1	D	0.41	0/2822	0.62	2/3831 (0.1%)
1	E	0.41	0/2822	0.62	1/3831 (0.0%)
1	F	0.41	0/2822	0.62	2/3831 (0.1%)
All	All	0.41	0/16932	0.62	10/22986 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	567	LEU	CA-CB-CG	5.89	128.86	115.30
1	B	567	LEU	CA-CB-CG	5.89	128.85	115.30
1	D	567	LEU	CA-CB-CG	5.89	128.84	115.30
1	C	567	LEU	CA-CB-CG	5.88	128.82	115.30
1	A	567	LEU	CA-CB-CG	5.88	128.81	115.30
1	F	567	LEU	CA-CB-CG	5.87	128.81	115.30
1	C	573	PHE	CB-CG-CD1	5.09	124.36	120.80
1	F	573	PHE	CB-CG-CD1	5.06	124.34	120.80
1	D	573	PHE	CB-CG-CD1	5.06	124.34	120.80
1	B	573	PHE	CB-CG-CD1	5.01	124.31	120.80

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	2767	0	2795	37	0
1	B	2767	0	2795	36	0
1	C	2767	0	2795	37	0
1	D	2767	0	2795	38	0
1	E	2767	0	2795	36	0
1	F	2767	0	2795	38	0
All	All	16602	0	16770	190	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 (190) 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:C:818:PHE:HB3	1:D:823:GLY:H	1.55	0.71
1:A:823:GLY:H	1:F:818:PHE:HB3	1.57	0.69
1:A:818:PHE:HB3	1:B:823:GLY:H	1.58	0.68
1:D:818:PHE:HB3	1:E:823:GLY:H	1.60	0.66
1:C:546:VAL:HG23	1:C:555:ILE:HG12	1.80	0.63
1:E:546:VAL:HG23	1:E:555:ILE:HG12	1.80	0.63
1:D:546:VAL:HG23	1:D:555:ILE:HG12	1.80	0.63
1:F:546:VAL:HG23	1:F:555:ILE:HG12	1.80	0.63
1:B:546:VAL:HG23	1:B:555:ILE:HG12	1.80	0.63
1:A:546:VAL:HG23	1:A:555:ILE:HG12	1.81	0.61
1:A:637:ILE:HG22	1:A:730:ARG:HG3	1.83	0.61
1:D:637:ILE:HG22	1:D:730:ARG:HG3	1.83	0.61
1:E:637:ILE:HG22	1:E:730:ARG:HG3	1.83	0.61
1:E:818:PHE:HB3	1:F:823:GLY:H	1.64	0.61
1:F:637:ILE:HG22	1:F:730:ARG:HG3	1.83	0.61
1:B:637:ILE:HG22	1:B:730:ARG:HG3	1.83	0.60
1:B:818:PHE:HB3	1:C:823:GLY:H	1.66	0.60
1:C:637:ILE:HG22	1:C:730:ARG:HG3	1.83	0.60
1:A:754:ALA:HB2	1:A:860:LEU:HD13	1.86	0.58
1:E:521:ALA:HB2	1:E:623:LEU:HB3	1.86	0.58
1:E:651:MET:HB3	1:E:663:ILE:HD12	1.86	0.58
1:F:651:MET:HB3	1:F:663:ILE:HD12	1.86	0.58
1:A:651:MET:HB3	1:A:663:ILE:HD12	1.86	0.58
1:C:754:ALA:HB2	1:C:860:LEU:HD13	1.85	0.58
1:D:521:ALA:HB2	1:D:623:LEU:HB3	1.86	0.58
1:D:759:SER:OG	1:E:828:GLY:O	2.22	0.58
1:F:754:ALA:HB2	1:F:860:LEU:HD13	1.86	0.58
1:D:651:MET:HB3	1:D:663:ILE:HD12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:521:ALA:HB2	1:C:623:LEU:HB3	1.86	0.57
1:D:754:ALA:HB2	1:D:860:LEU:HD13	1.86	0.57
1:B:754:ALA:HB2	1:B:860:LEU:HD13	1.85	0.57
1:F:521:ALA:HB2	1:F:623:LEU:HB3	1.86	0.57
1:A:759:SER:OG	1:B:828:GLY:O	2.22	0.57
1:B:651:MET:HB3	1:B:663:ILE:HD12	1.86	0.57
1:C:651:MET:HB3	1:C:663:ILE:HD12	1.86	0.57
1:D:527:VAL:HG21	1:D:531:SER:H	1.70	0.56
1:B:521:ALA:HB2	1:B:623:LEU:HB3	1.86	0.56
1:B:527:VAL:HG21	1:B:531:SER:H	1.71	0.56
1:C:527:VAL:HG21	1:C:531:SER:H	1.70	0.56
1:A:527:VAL:HG21	1:A:531:SER:H	1.71	0.56
1:F:527:VAL:HG21	1:F:531:SER:H	1.70	0.56
1:E:527:VAL:HG21	1:E:531:SER:H	1.70	0.56
1:E:754:ALA:HB2	1:E:860:LEU:HD13	1.86	0.56
1:A:521:ALA:HB2	1:A:623:LEU:HB3	1.86	0.56
1:A:560:LYS:HB2	1:A:563:TYR:HD2	1.71	0.56
1:D:578:GLY:HA2	1:E:592:ALA:HB2	1.88	0.56
1:E:759:SER:OG	1:F:828:GLY:O	2.24	0.55
1:A:821:THR:HA	1:F:820:LEU:HB3	1.89	0.55
1:D:560:LYS:HB2	1:D:563:TYR:HD2	1.72	0.55
1:F:560:LYS:HB2	1:F:563:TYR:HD2	1.71	0.55
1:B:560:LYS:HB2	1:B:563:TYR:HD2	1.72	0.55
1:C:820:LEU:HB3	1:D:821:THR:HA	1.88	0.55
1:E:560:LYS:HB2	1:E:563:TYR:HD2	1.71	0.54
1:B:759:SER:OG	1:C:828:GLY:O	2.25	0.54
1:C:560:LYS:HB2	1:C:563:TYR:HD2	1.72	0.53
1:D:644:ALA:HB2	1:D:675:VAL:HG11	1.91	0.53
1:D:554:ASP:OD1	1:D:620:LYS:NZ	2.39	0.53
1:A:644:ALA:HB2	1:A:675:VAL:HG11	1.91	0.53
1:B:578:GLY:HA2	1:C:592:ALA:HB2	1.91	0.53
1:C:554:ASP:OD1	1:C:620:LYS:NZ	2.39	0.53
1:C:720:ASN:HD21	1:C:740:THR:HA	1.74	0.52
1:F:644:ALA:HB2	1:F:675:VAL:HG11	1.91	0.52
1:F:720:ASN:HD21	1:F:740:THR:HA	1.75	0.52
1:A:549:ARG:HH12	1:A:551:ASN:HD22	1.56	0.52
1:A:720:ASN:HD21	1:A:740:THR:HA	1.74	0.52
1:E:554:ASP:OD1	1:E:620:LYS:NZ	2.39	0.52
1:C:644:ALA:HB2	1:C:675:VAL:HG11	1.91	0.52
1:A:578:GLY:HA2	1:B:592:ALA:HB2	1.92	0.52
1:D:720:ASN:HD21	1:D:740:THR:HA	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:820:LEU:HB3	1:B:821:THR:HA	1.92	0.52
1:B:720:ASN:HD21	1:B:740:THR:HA	1.74	0.52
1:E:644:ALA:HB2	1:E:675:VAL:HG11	1.91	0.52
1:E:720:ASN:HD21	1:E:740:THR:HA	1.74	0.52
1:E:549:ARG:HH12	1:E:551:ASN:HD22	1.56	0.52
1:D:820:LEU:HB3	1:E:821:THR:HA	1.92	0.52
1:B:549:ARG:HH12	1:B:551:ASN:HD22	1.56	0.52
1:B:644:ALA:HB2	1:B:675:VAL:HG11	1.91	0.51
1:A:831:ASN:OD1	1:A:832:GLN:NE2	2.43	0.51
1:B:831:ASN:OD1	1:B:832:GLN:NE2	2.43	0.51
1:C:549:ARG:HH12	1:C:551:ASN:HD22	1.56	0.51
1:D:549:ARG:HH12	1:D:551:ASN:HD22	1.56	0.51
1:E:831:ASN:OD1	1:E:832:GLN:NE2	2.43	0.51
1:F:549:ARG:HH12	1:F:551:ASN:HD22	1.56	0.51
1:C:831:ASN:OD1	1:C:832:GLN:NE2	2.43	0.51
1:D:831:ASN:OD1	1:D:832:GLN:NE2	2.43	0.51
1:F:831:ASN:OD1	1:F:832:GLN:NE2	2.43	0.50
1:A:828:GLY:O	1:F:759:SER:OG	2.28	0.50
1:C:759:SER:OG	1:D:828:GLY:O	2.29	0.50
1:E:578:GLY:HA2	1:F:592:ALA:HB2	1.93	0.50
1:A:554:ASP:OD1	1:A:620:LYS:NZ	2.39	0.49
1:B:554:ASP:OD1	1:B:620:LYS:NZ	2.39	0.49
1:B:521:ALA:HB1	1:B:524:LEU:HD12	1.95	0.49
1:C:818:PHE:HD2	1:D:822:GLY:HA2	1.78	0.49
1:B:748:LEU:HD13	1:B:750:ILE:HG23	1.95	0.48
1:C:521:ALA:HB1	1:C:524:LEU:HD12	1.95	0.48
1:A:748:LEU:HD13	1:A:750:ILE:HG23	1.95	0.48
1:E:748:LEU:HD13	1:E:750:ILE:HG23	1.95	0.48
1:F:521:ALA:HB1	1:F:524:LEU:HD12	1.95	0.48
1:C:578:GLY:HA2	1:D:592:ALA:HB2	1.96	0.48
1:E:521:ALA:HB1	1:E:524:LEU:HD12	1.95	0.47
1:F:554:ASP:OD1	1:F:620:LYS:NZ	2.39	0.47
1:A:822:GLY:HA2	1:F:818:PHE:HD2	1.79	0.47
1:A:592:ALA:HB2	1:F:578:GLY:HA2	1.96	0.47
1:B:563:TYR:HA	1:B:566:LEU:HD13	1.97	0.47
1:D:864:GLU:OE2	1:D:868:TRP:NE1	2.33	0.47
1:A:563:TYR:HA	1:A:566:LEU:HD13	1.97	0.47
1:A:521:ALA:HB1	1:A:524:LEU:HD12	1.95	0.47
1:C:748:LEU:HD13	1:C:750:ILE:HG23	1.95	0.47
1:D:521:ALA:HB1	1:D:524:LEU:HD12	1.95	0.47
1:D:748:LEU:HD13	1:D:750:ILE:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:532:VAL:HG21	1:E:539:GLU:HB3	1.97	0.47
1:C:563:TYR:HA	1:C:566:LEU:HD13	1.97	0.47
1:E:864:GLU:OE2	1:E:868:TRP:NE1	2.33	0.47
1:E:820:LEU:HB3	1:F:821:THR:HA	1.97	0.47
1:F:748:LEU:HD13	1:F:750:ILE:HG23	1.95	0.46
1:F:532:VAL:HG21	1:F:539:GLU:HB3	1.97	0.46
1:D:532:VAL:HG21	1:D:539:GLU:HB3	1.97	0.46
1:B:532:VAL:HG21	1:B:539:GLU:HB3	1.97	0.46
1:F:563:TYR:HA	1:F:566:LEU:HD13	1.97	0.46
1:A:532:VAL:HG21	1:A:539:GLU:HB3	1.97	0.45
1:B:820:LEU:HB3	1:C:821:THR:HA	1.98	0.45
1:D:563:TYR:HA	1:D:566:LEU:HD13	1.97	0.45
1:B:524:LEU:HD23	1:B:524:LEU:HA	1.85	0.45
1:D:519:LEU:HD11	1:D:573:PHE:HD2	1.81	0.45
1:E:563:TYR:HA	1:E:566:LEU:HD13	1.97	0.45
1:C:532:VAL:HG21	1:C:539:GLU:HB3	1.97	0.45
1:E:668:LEU:HB2	1:F:658:ILE:HG13	1.97	0.45
1:F:767:LEU:HD23	1:F:770:GLY:HA2	1.98	0.45
1:E:519:LEU:HD11	1:E:573:PHE:HD2	1.82	0.45
1:B:527:VAL:HG23	1:B:600:LYS:HD2	1.99	0.45
1:C:519:LEU:HD11	1:C:573:PHE:HD2	1.81	0.45
1:E:767:LEU:HD23	1:E:770:GLY:HA2	1.99	0.45
1:E:527:VAL:HG23	1:E:600:LYS:HD2	1.99	0.45
1:B:668:LEU:HB2	1:C:658:ILE:HG13	1.99	0.45
1:D:767:LEU:HD23	1:D:770:GLY:HA2	1.98	0.45
1:C:767:LEU:HD23	1:C:770:GLY:HA2	1.98	0.44
1:D:527:VAL:HG23	1:D:600:LYS:HD2	1.99	0.44
1:A:527:VAL:HG23	1:A:600:LYS:HD2	1.99	0.44
1:F:519:LEU:HD11	1:F:573:PHE:HD2	1.82	0.44
1:B:767:LEU:HD23	1:B:770:GLY:HA2	1.99	0.44
1:B:519:LEU:HD11	1:B:573:PHE:HD2	1.82	0.44
1:A:595:LEU:HG	1:A:599:LEU:HD13	2.00	0.44
1:C:527:VAL:HG23	1:C:600:LYS:HD2	1.99	0.44
1:D:595:LEU:HG	1:D:599:LEU:HD13	2.00	0.44
1:C:595:LEU:HG	1:C:599:LEU:HD13	2.00	0.43
1:F:527:VAL:HG23	1:F:600:LYS:HD2	1.99	0.43
1:F:595:LEU:HG	1:F:599:LEU:HD13	2.00	0.43
1:A:519:LEU:HD11	1:A:573:PHE:HD2	1.81	0.43
1:B:595:LEU:HG	1:B:599:LEU:HD13	2.00	0.43
1:E:595:LEU:HG	1:E:599:LEU:HD13	2.00	0.43
1:A:658:ILE:HG13	1:F:668:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:767:LEU:HD23	1:A:770:GLY:HA2	1.99	0.43
1:B:864:GLU:OE2	1:B:868:TRP:NE1	2.33	0.43
1:D:521:ALA:O	1:D:553:PHE:N	2.48	0.43
1:E:521:ALA:O	1:E:553:PHE:N	2.48	0.42
1:C:668:LEU:HB2	1:D:658:ILE:HG13	2.01	0.42
1:E:582:GLN:HE22	1:E:591:GLN:HE22	1.68	0.42
1:D:524:LEU:HD21	1:D:625:ALA:HA	2.01	0.42
1:D:582:GLN:HE22	1:D:591:GLN:HE22	1.68	0.42
1:F:524:LEU:HA	1:F:524:LEU:HD23	1.85	0.42
1:F:582:GLN:HE22	1:F:591:GLN:HE22	1.68	0.42
1:F:864:GLU:OE2	1:F:868:TRP:NE1	2.33	0.42
1:C:582:GLN:HE22	1:C:591:GLN:HE22	1.68	0.41
1:E:524:LEU:HD21	1:E:625:ALA:HA	2.01	0.41
1:C:864:GLU:OE2	1:C:868:TRP:NE1	2.33	0.41
1:C:524:LEU:HD21	1:C:625:ALA:HA	2.01	0.41
1:F:524:LEU:HD21	1:F:625:ALA:HA	2.01	0.41
1:A:582:GLN:HE22	1:A:591:GLN:HE22	1.68	0.41
1:B:521:ALA:O	1:B:553:PHE:N	2.47	0.41
1:B:727:ASN:HA	1:B:728:PRO:HD3	1.95	0.41
1:C:521:ALA:O	1:C:553:PHE:N	2.48	0.41
1:A:521:ALA:O	1:A:553:PHE:N	2.47	0.41
1:A:524:LEU:HA	1:A:524:LEU:HD23	1.85	0.41
1:B:582:GLN:HE22	1:B:591:GLN:HE22	1.68	0.41
1:E:818:PHE:HD2	1:F:822:GLY:HA2	1.86	0.41
1:D:548:PRO:HG2	1:E:563:TYR:HE1	1.85	0.41
1:F:727:ASN:HA	1:F:728:PRO:HD3	1.95	0.41
1:A:524:LEU:HD21	1:A:625:ALA:HA	2.02	0.41
1:A:798:TYR:HB3	1:A:801:LEU:HD12	2.03	0.41
1:A:864:GLU:OE2	1:A:868:TRP:NE1	2.33	0.41
1:B:524:LEU:HD21	1:B:625:ALA:HA	2.01	0.41
1:B:798:TYR:HB3	1:B:801:LEU:HD12	2.03	0.41
1:C:741:ASP:OD1	1:C:741:ASP:N	2.55	0.40
1:C:798:TYR:HB3	1:C:801:LEU:HD12	2.03	0.40
1:D:741:ASP:OD1	1:D:741:ASP:N	2.55	0.40
1:A:635:GLY:HA3	1:A:686:VAL:HG21	2.04	0.40
1:F:798:TYR:HB3	1:F:801:LEU:HD12	2.03	0.40
1:D:524:LEU:HD23	1:D:524:LEU:HA	1.85	0.40
1:D:798:TYR:HB3	1:D:801:LEU:HD12	2.03	0.40
1:E:741:ASP:OD1	1:E:741:ASP:N	2.55	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	361/832 (43%)	341 (94%)	20 (6%)	0	100	100
1	B	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	C	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	D	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	E	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
1	F	361/832 (43%)	342 (95%)	19 (5%)	0	100	100
All	All	2166/4992 (43%)	2051 (95%)	115 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	291/683 (43%)	291 (100%)	0	100	100
1	B	291/683 (43%)	291 (100%)	0	100	100
1	C	291/683 (43%)	291 (100%)	0	100	100
1	D	291/683 (43%)	291 (100%)	0	100	100
1	E	291/683 (43%)	291 (100%)	0	100	100
1	F	291/683 (43%)	291 (100%)	0	100	100
All	All	1746/4098 (43%)	1746 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	551	ASN
1	A	591	GLN
1	A	832	GLN
1	B	551	ASN
1	B	591	GLN
1	B	832	GLN
1	C	551	ASN
1	C	591	GLN
1	C	832	GLN
1	D	551	ASN
1	D	591	GLN
1	D	832	GLN
1	E	551	ASN
1	E	591	GLN
1	E	832	GLN
1	F	551	ASN
1	F	591	GLN
1	F	832	GLN

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 monosaccharides 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.

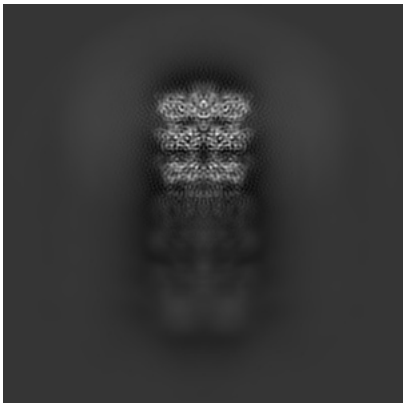
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20995. These allow visual inspection of the internal detail of the map and identification of artifacts.

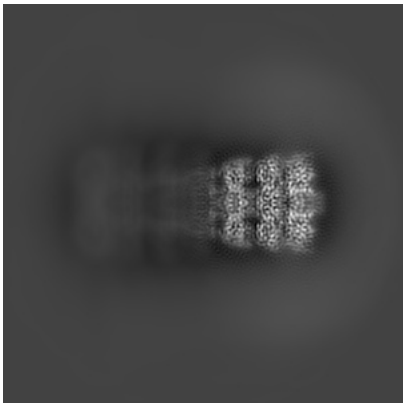
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

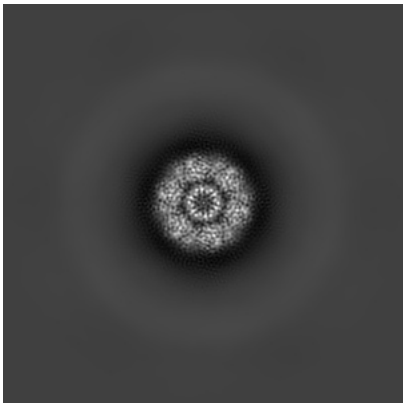
6.1.1 Primary map



X



Y



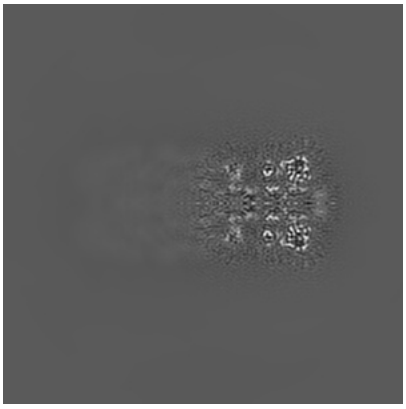
Z

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

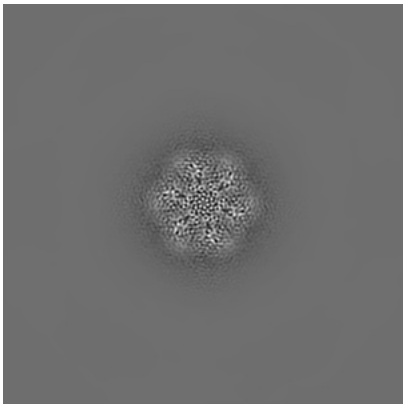
6.2 Central slices

6.2.1 Primary map

X Index: 140



Y Index: 140



Z Index: 140

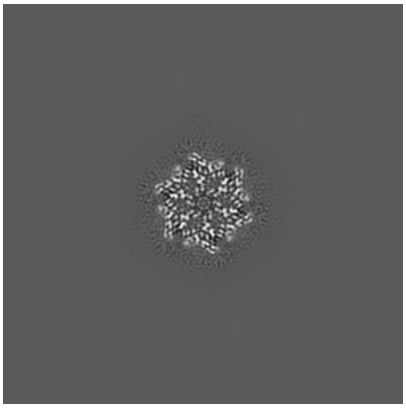
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 121

Y Index: 134



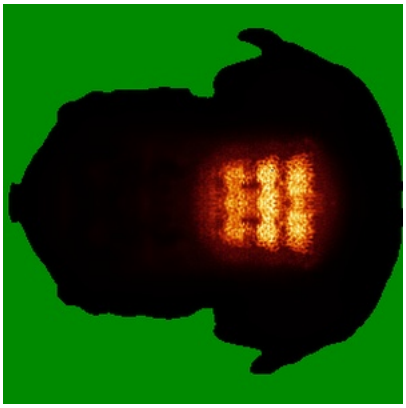
Z Index: 188

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

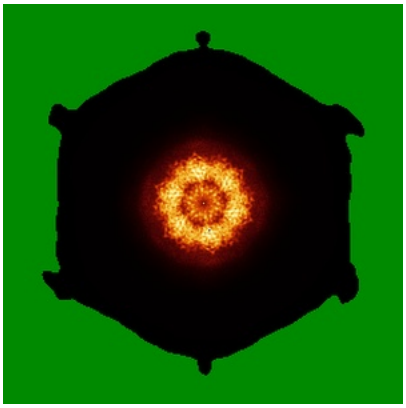
6.4 Orthogonal standard-deviation projections (False-color) (i)

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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

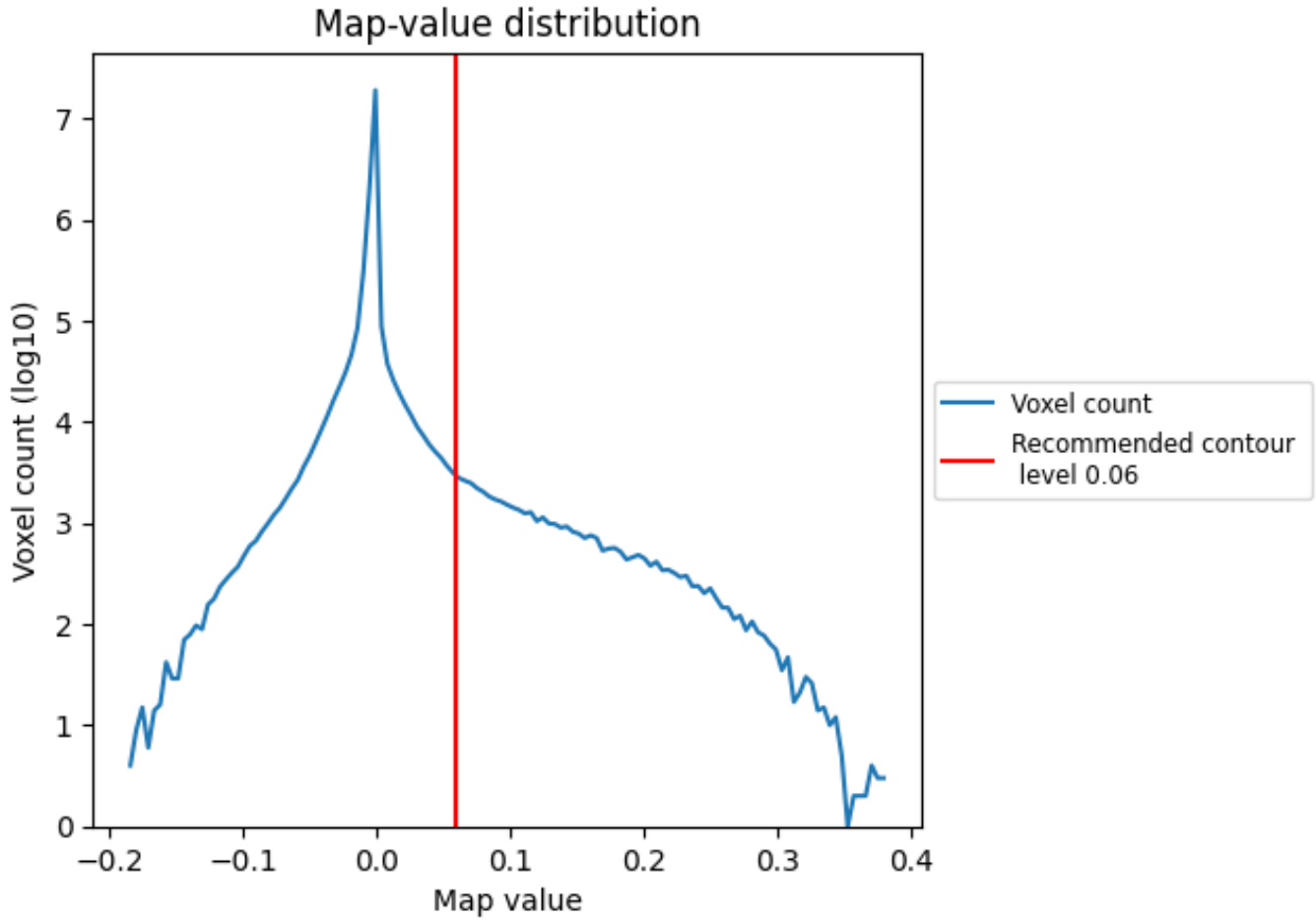
6.6 Mask visualisation (i)

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

7 Map analysis

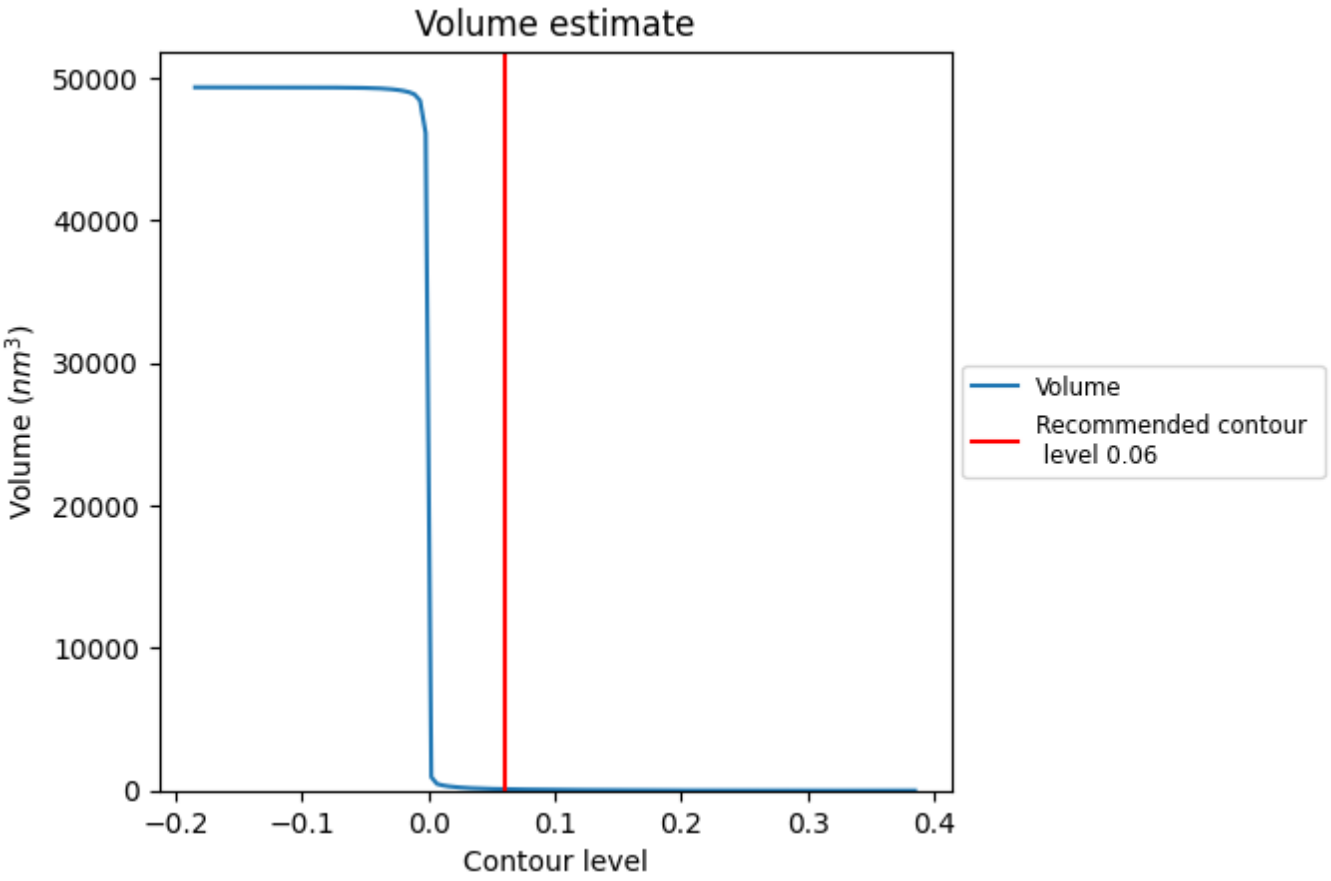
This section contains the results of statistical analysis of the map.

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.

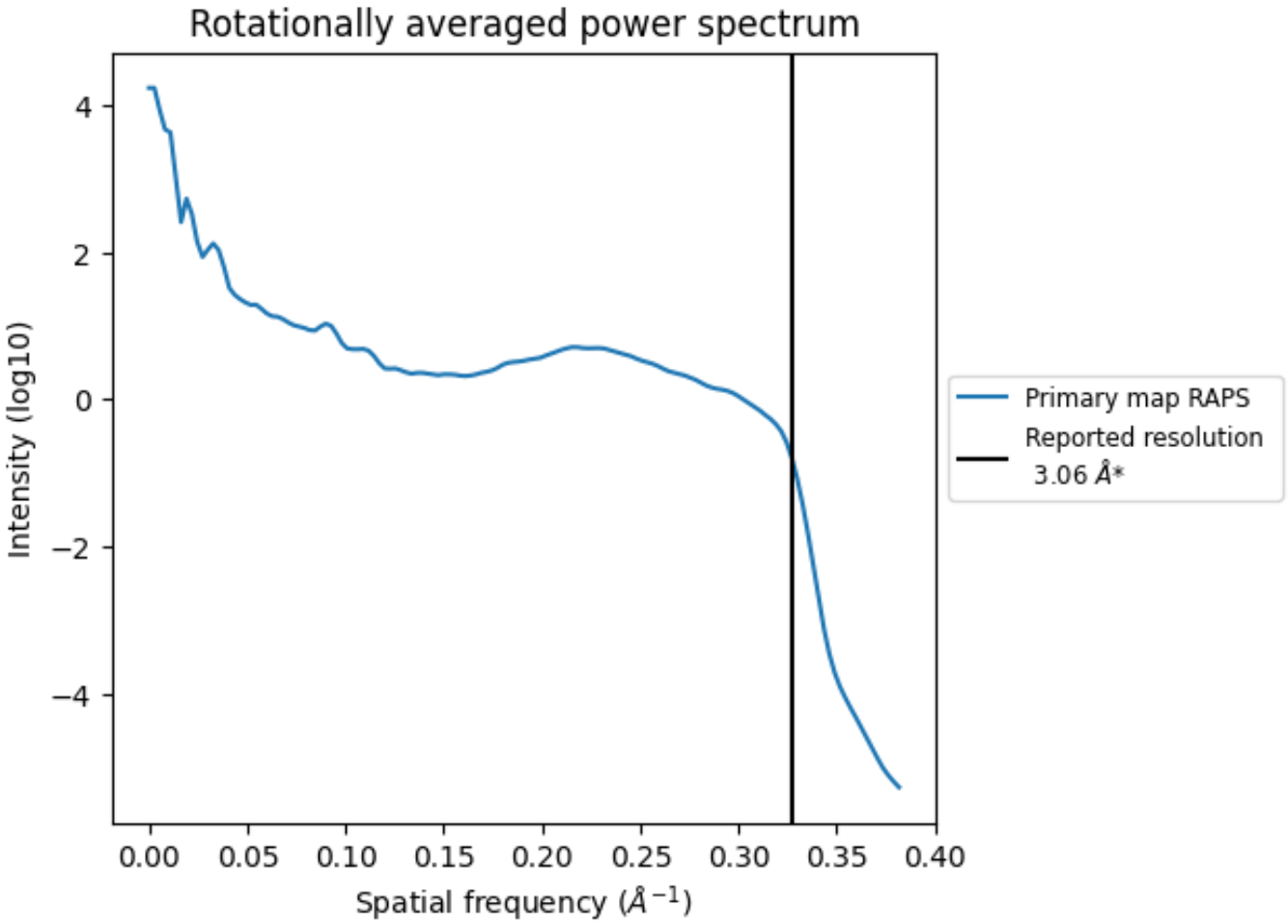
7.2 Volume estimate



The volume at the recommended contour level is 99 nm^3; this corresponds to an approximate mass of 89 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 0.327 Å^{-1}

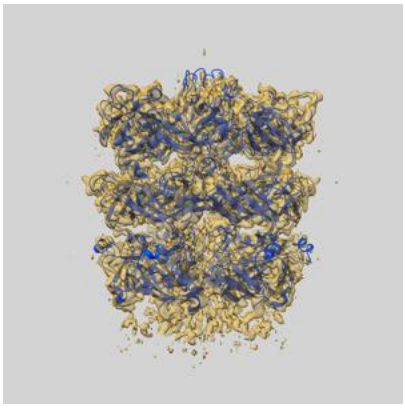
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

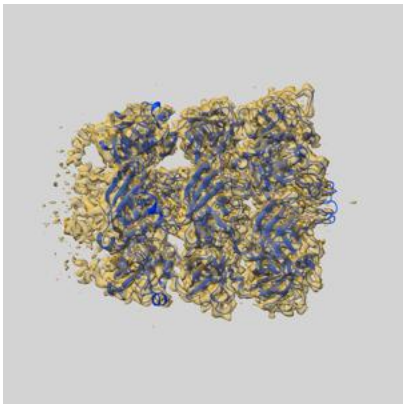
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20995 and PDB model 6V0E. Per-residue inclusion information can be found in section 3 on page 4.

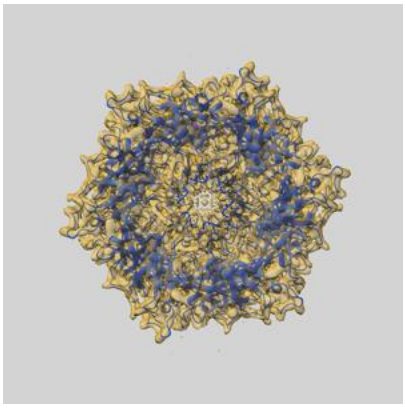
9.1 Map-model overlay



X



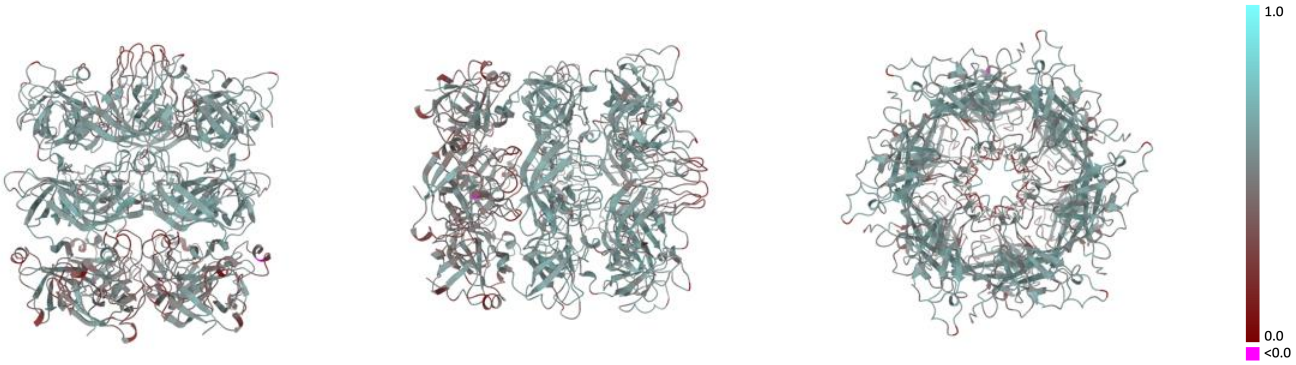
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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.

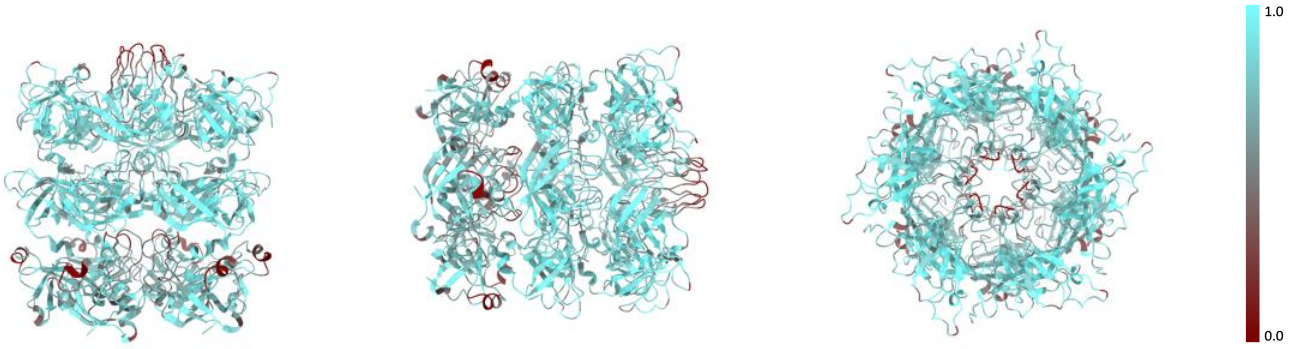
9.2 Q-score mapped to coordinate model (i)



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.

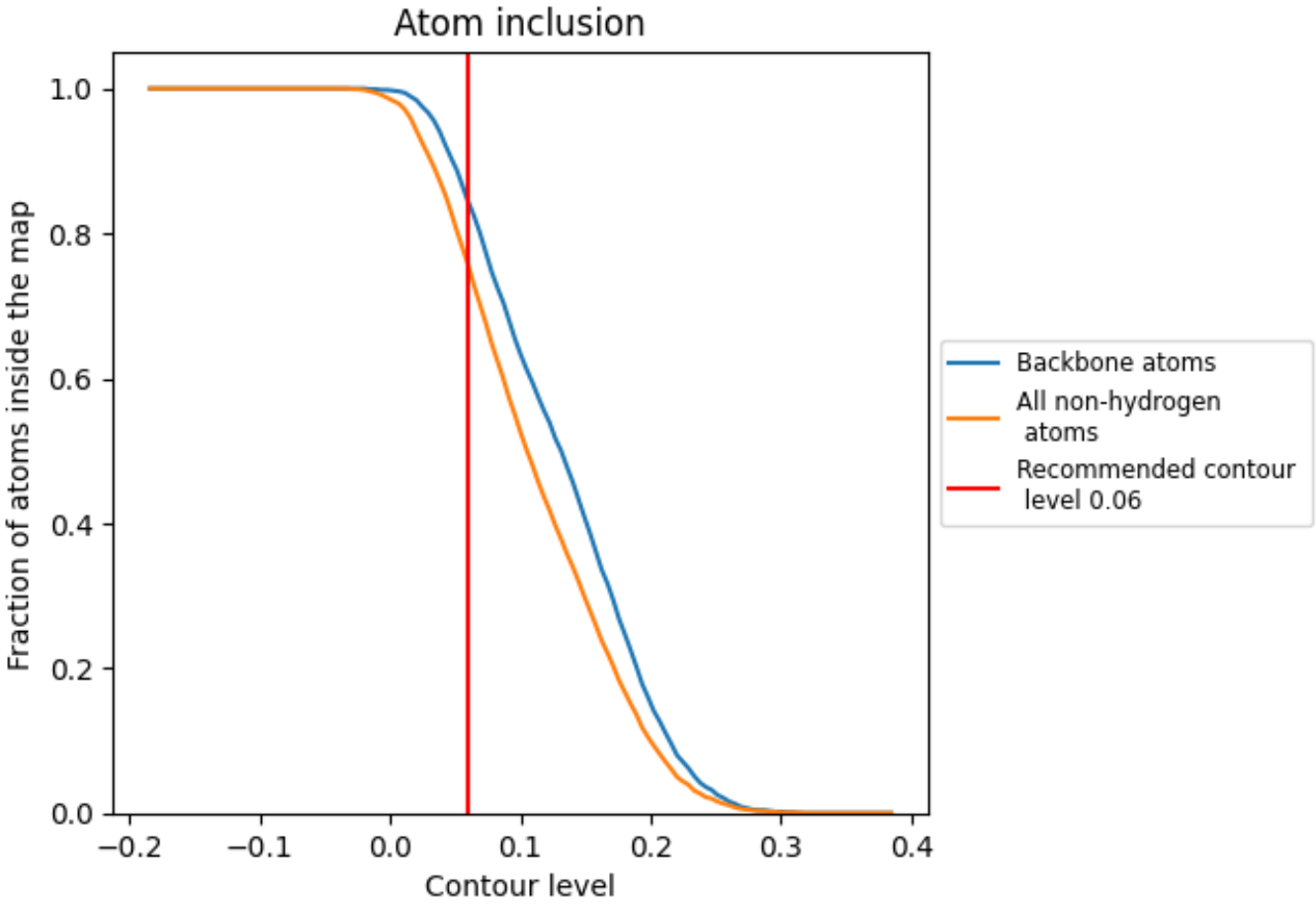
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.06).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7560	0.5010
A	0.7570	0.5040
B	0.7560	0.5010
C	0.7550	0.5000
D	0.7580	0.5040
E	0.7550	0.4990
F	0.7550	0.5000