Full wwPDB EM Validation Report

Jun 25, 2025 – 03:21 am BST

PDB ID	:	6RAN / pdb_00006ran
EMDB ID	:	EMD-4781
Title	:	Heterodimeric ABC exporter TmrAB in inward-facing wide conformation
Authors	:	Thomas, C.; Januliene, D.; Mehdipour, A.R.; Hofmann, S.; Hummer, G.; Moeller, A.; Tampe, R.
Deposited on	:	2019-04-06
Resolution	:	4.20 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:

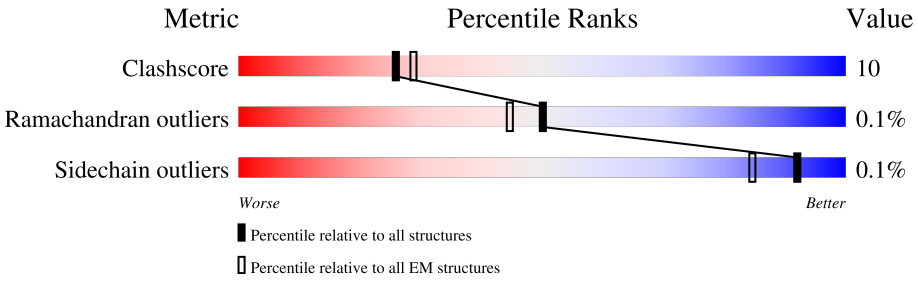
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

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 4.20 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	623	29% 68% 26% • 5%
2	B	578	16% 76% 20% • •
3	C	136	44% 69% 19% • 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10173 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 Multidrug resistance ABC transporter ATP-binding and permease protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	592	Total	C	N	O	S	0	0
			4741	3089	824	820	8		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	523	GLN	GLU	engineered mutation	UNP Q72J05
A	601	LYS	-	expression tag	UNP Q72J05
A	602	LEU	-	expression tag	UNP Q72J05
A	603	GLY	-	expression tag	UNP Q72J05
A	604	GLY	-	expression tag	UNP Q72J05
A	605	GLY	-	expression tag	UNP Q72J05
A	606	GLY	-	expression tag	UNP Q72J05
A	607	GLU	-	expression tag	UNP Q72J05
A	608	ASN	-	expression tag	UNP Q72J05
A	609	LEU	-	expression tag	UNP Q72J05
A	610	TYR	-	expression tag	UNP Q72J05
A	611	PHE	-	expression tag	UNP Q72J05
A	612	GLN	-	expression tag	UNP Q72J05
A	613	GLY	-	expression tag	UNP Q72J05
A	614	HIS	-	expression tag	UNP Q72J05
A	615	HIS	-	expression tag	UNP Q72J05
A	616	HIS	-	expression tag	UNP Q72J05
A	617	HIS	-	expression tag	UNP Q72J05
A	618	HIS	-	expression tag	UNP Q72J05
A	619	HIS	-	expression tag	UNP Q72J05
A	620	HIS	-	expression tag	UNP Q72J05
A	621	HIS	-	expression tag	UNP Q72J05
A	622	HIS	-	expression tag	UNP Q72J05
A	623	HIS	-	expression tag	UNP Q72J05

- Molecule 2 is a protein called Multidrug resistance ABC transporter ATP-binding and permease protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	574	Total	C	N	O	S	0	0
			4535	2930	812	781	12		

- Molecule 3 is a protein called Nanobody Nb9F10.

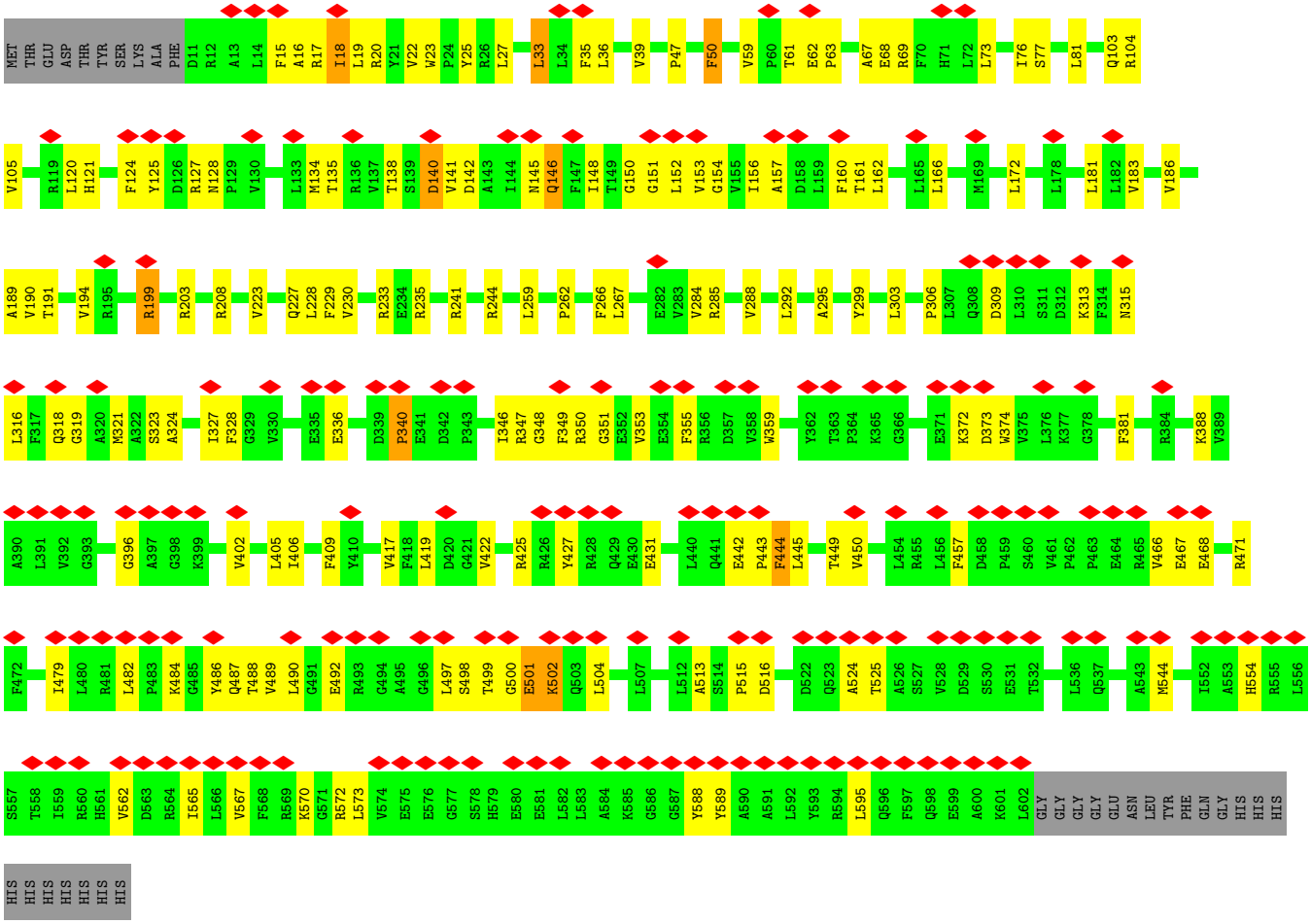
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	121	Total	C	N	O	S	0	0
			897	560	159	173	5		

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.

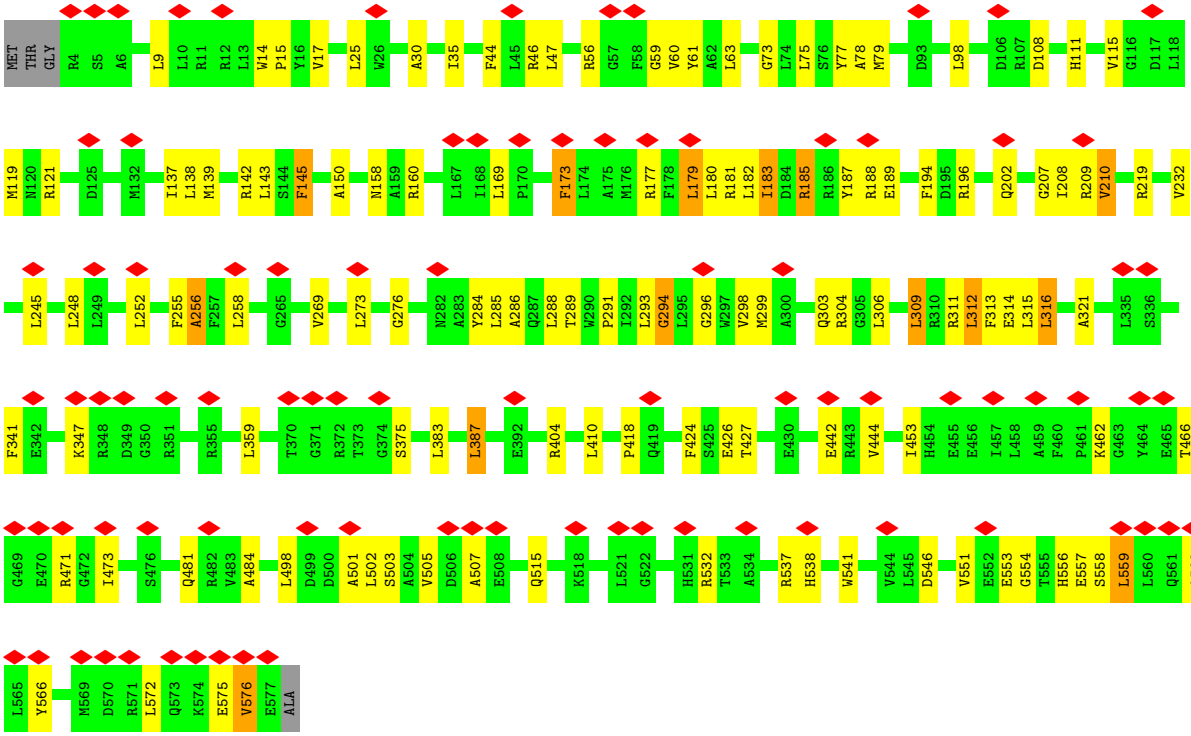
• Molecule 1: Multidrug resistance ABC transporter ATP-binding and permease protein

Chain A:



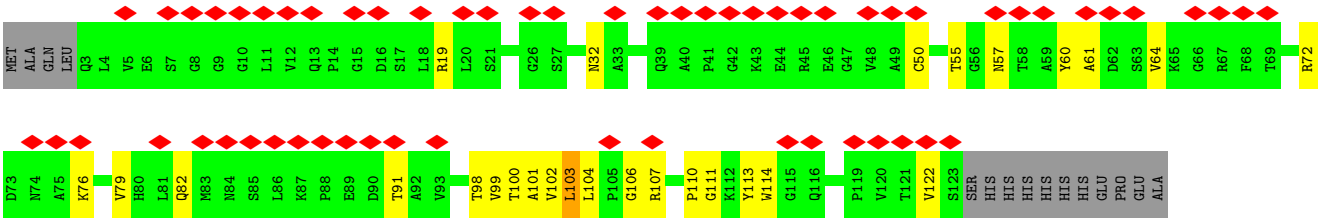
• Molecule 2: Multidrug resistance ABC transporter ATP-binding and permease protein

Chain B:



• Molecule 3: Nanobody Nb9F10

Chain C:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	44733	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction was performed within 3D reconstruction in RELION-3	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	62	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.089	Depositor
Minimum map value	-0.046	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	275.712, 275.712, 275.712	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.077, 1.077, 1.077	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	1.17	1/4846 (0.0%)	1.66	70/6572 (1.1%)
2	B	1.20	0/4624	1.66	72/6260 (1.2%)
3	C	0.50	0/914	0.88	4/1242 (0.3%)
All	All	1.14	1/10384 (0.0%)	1.61	146/14074 (1.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	340	PRO	N-CD	7.04	1.57	1.47

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	210	VAL	N-CA-C	-9.65	103.51	111.81
2	B	442	GLU	N-CA-C	9.21	120.93	111.07
1	A	186	VAL	N-CA-C	8.93	119.00	110.42
2	B	444	VAL	N-CA-CB	8.48	120.47	110.55
2	B	576	VAL	N-CA-C	8.29	119.82	107.80
1	A	17	ARG	N-CA-C	8.24	119.89	111.07
2	B	314	GLU	N-CA-C	-8.16	102.33	111.07
2	B	559	LEU	N-CA-C	-8.00	102.51	111.07
1	A	233	ARG	N-CA-C	7.83	119.82	111.28
1	A	33	LEU	N-CA-C	7.83	120.51	111.11
2	B	59	GLY	N-CA-C	7.58	121.81	112.64
1	A	103	GLN	N-CA-C	7.58	119.54	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	127	ARG	N-CA-C	7.47	120.37	111.33
2	B	303	GLN	N-CA-C	7.37	119.31	111.28
2	B	119	MET	N-CA-C	7.34	118.93	111.07
2	B	284	TYR	N-CA-C	7.25	118.83	111.07
1	A	227	GLN	N-CA-C	7.23	118.80	111.07
1	A	189	ALA	N-CA-C	7.20	118.77	111.07
1	A	50	PHE	N-CA-CB	7.20	120.45	110.01
1	A	105	VAL	N-CA-CB	7.14	118.91	110.55
2	B	471	ARG	N-CA-C	7.14	120.15	108.08
2	B	137	ILE	N-CA-C	7.10	117.86	110.62
1	A	77	SER	N-CA-C	7.03	118.60	111.07
1	A	140	ASP	N-CA-C	6.87	118.42	111.07
1	A	135	THR	N-CA-CB	6.78	120.09	110.12
2	B	311	ARG	N-CA-CB	6.72	120.00	110.12
1	A	208	ARG	N-CA-C	6.68	118.56	111.28
2	B	312	LEU	N-CA-C	6.67	118.21	111.07
2	B	187	TYR	N-CA-C	6.67	118.21	111.07
2	B	444	VAL	N-CA-C	-6.54	104.14	110.42
2	B	453	ILE	N-CA-C	-6.51	106.44	112.43
1	A	142	ASP	N-CA-CB	6.49	119.66	110.12
2	B	309	LEU	N-CA-C	6.49	118.90	111.11
2	B	232	VAL	N-CA-CB	6.46	118.10	110.55
2	B	551	VAL	N-CA-C	-6.45	106.95	113.47
1	A	516	ASP	CA-C-N	6.44	129.30	120.35
1	A	516	ASP	C-N-CA	6.44	129.30	120.35
1	A	340	PRO	N-CA-C	6.43	121.05	111.41
1	A	125	TYR	N-CA-C	-6.33	104.48	111.82
1	A	235	ARG	N-CA-CB	6.33	119.42	110.12
1	A	160	PHE	N-CA-CB	6.31	119.39	110.12
1	A	76	ILE	N-CA-C	6.30	117.04	110.62
1	A	319	GLY	N-CA-C	-6.26	105.19	112.83
2	B	139	MET	N-CA-CB	6.24	119.40	110.16
1	A	191	THR	N-CA-C	-6.24	104.56	111.36
2	B	316	LEU	O-C-N	6.20	128.78	122.09
1	A	160	PHE	N-CA-C	6.19	118.03	111.28
2	B	347	LYS	N-CA-C	6.15	118.44	108.41
2	B	269	VAL	N-CA-C	6.13	116.88	110.62
1	A	124	PHE	N-CA-C	6.10	118.46	111.02
2	B	173	PHE	N-CA-C	6.10	117.92	111.28
2	B	111	HIS	N-CA-C	6.07	117.56	111.07
2	B	145	PHE	N-CA-C	-6.06	105.79	113.43
2	B	294	GLY	N-CA-C	6.04	119.98	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	113	TYR	CB-CA-C	-6.01	100.34	110.19
2	B	185	ARG	N-CA-CB	5.97	118.67	110.01
2	B	25	LEU	N-CA-C	5.97	117.46	111.07
2	B	219	ARG	N-CA-C	5.95	119.36	111.75
1	A	27	LEU	N-CA-CB	5.92	118.60	110.01
2	B	179	LEU	N-CA-C	5.89	117.38	111.07
1	A	25	TYR	CB-CA-C	-5.89	100.51	110.64
1	A	468	GLU	N-CA-CB	5.89	118.54	110.01
2	B	256	ALA	N-CA-CB	5.87	118.52	110.01
3	C	104	LEU	N-CA-C	5.87	120.21	112.35
2	B	304	ARG	CA-C-N	5.84	126.43	119.94
2	B	304	ARG	C-N-CA	5.84	126.43	119.94
2	B	321	ALA	N-CA-C	-5.82	106.18	113.28
2	B	286	ALA	N-CA-CB	5.77	118.70	110.16
1	A	146	GLN	N-CA-CB	5.76	118.59	110.12
1	A	284	VAL	N-CA-C	5.75	118.24	111.05
1	A	229	PHE	N-CA-CB	5.69	119.01	110.53
1	A	515	PRO	N-CA-C	-5.66	108.19	114.92
1	A	145	ASN	N-CA-C	5.64	118.19	111.71
2	B	316	LEU	CA-C-N	5.62	128.38	120.28
2	B	316	LEU	C-N-CA	5.62	128.38	120.28
2	B	121	ARG	N-CA-CB	5.61	118.14	110.01
1	A	67	ALA	N-CA-C	-5.60	105.17	111.28
1	A	121	HIS	CA-C-N	5.58	125.95	119.47
1	A	121	HIS	C-N-CA	5.58	125.95	119.47
1	A	153	VAL	N-CA-C	5.58	118.06	111.09
1	A	162	LEU	N-CA-C	-5.55	104.92	110.97
2	B	418	PRO	CA-C-N	5.54	127.70	120.28
2	B	418	PRO	C-N-CA	5.54	127.70	120.28
2	B	169	LEU	CA-C-N	5.53	126.75	119.84
2	B	169	LEU	C-N-CA	5.53	126.75	119.84
1	A	199	ARG	N-CA-CB	5.53	118.02	110.01
2	B	182	LEU	N-CA-C	5.52	117.30	111.28
1	A	104	ARG	N-CA-C	5.50	118.20	111.82
3	C	103	LEU	N-CA-C	-5.50	100.73	109.59
2	B	44	PHE	CA-CB-CG	-5.48	108.32	113.80
2	B	387	LEU	N-CA-C	-5.48	106.27	113.17
2	B	75	LEU	N-CA-CB	5.47	118.73	110.30
1	A	324	ALA	N-CA-C	5.44	116.89	111.07
2	B	78	ALA	N-CA-C	-5.43	105.44	111.36
2	B	427	THR	CA-C-N	5.43	128.18	120.53
2	B	427	THR	C-N-CA	5.43	128.18	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	457	PHE	CA-CB-CG	-5.42	108.38	113.80
2	B	503	SER	N-CA-C	-5.40	105.91	112.88
2	B	196	ARG	N-CA-C	5.39	116.84	111.07
2	B	30	ALA	CA-C-N	5.39	126.87	120.14
2	B	30	ALA	C-N-CA	5.39	126.87	120.14
1	A	431	GLU	CA-C-N	5.36	127.47	120.28
1	A	431	GLU	C-N-CA	5.36	127.47	120.28
1	A	27	LEU	N-CA-C	-5.35	105.35	111.07
2	B	467	VAL	N-CA-C	5.33	117.30	109.63
1	A	128	ASN	CA-C-N	5.32	125.31	119.89
1	A	128	ASN	C-N-CA	5.32	125.31	119.89
2	B	484	ALA	N-CA-C	5.31	117.98	111.82
2	B	183	ILE	N-CA-C	5.30	117.68	111.05
2	B	150	ALA	CA-C-N	5.29	127.37	120.28
2	B	150	ALA	C-N-CA	5.29	127.37	120.28
1	A	562	VAL	CA-C-N	5.26	127.33	120.28
1	A	562	VAL	C-N-CA	5.26	127.33	120.28
1	A	444	PHE	N-CA-C	-5.26	101.21	109.25
2	B	160	ARG	N-CA-C	5.25	117.43	111.02
1	A	229	PHE	N-CA-C	-5.25	106.93	113.38
1	A	68	GLU	N-CA-C	5.24	117.42	111.02
2	B	17	VAL	CA-C-N	5.24	130.12	120.79
2	B	17	VAL	C-N-CA	5.24	130.12	120.79
2	B	108	ASP	N-CA-C	5.24	116.99	111.28
1	A	500	GLY	N-CA-C	5.23	119.47	112.77
1	A	162	LEU	N-CA-CB	5.22	117.53	109.91
2	B	115	VAL	N-CA-C	5.22	115.94	110.62
1	A	315	ASN	N-CA-C	5.20	116.95	111.28
3	C	113	TYR	N-CA-C	5.19	116.98	108.52
1	A	154	GLY	N-CA-C	-5.19	106.48	112.50
1	A	244	ARG	N-CA-C	5.19	116.93	111.28
2	B	208	ILE	N-CA-C	5.18	115.39	110.42
1	A	501	GLU	N-CA-C	5.17	117.81	111.82
1	A	22	VAL	N-CA-C	-5.17	107.94	112.90
1	A	241	ARG	N-CA-C	5.16	116.90	111.28
1	A	336	GLU	N-CA-C	-5.15	107.65	114.04
1	A	18	ILE	CB-CA-C	-5.14	103.94	112.26
1	A	502	LYS	N-CA-C	-5.13	105.76	111.36
2	B	383	LEU	N-CA-C	5.13	116.56	111.07
2	B	293	LEU	N-CA-C	-5.13	105.58	111.07
2	B	410	LEU	N-CA-C	5.10	116.53	111.07
1	A	166	LEU	CA-C-N	5.08	125.73	119.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	166	LEU	C-N-CA	5.08	125.73	119.99
1	A	120	LEU	CA-C-N	5.07	128.97	120.86
1	A	120	LEU	C-N-CA	5.07	128.97	120.86
1	A	513	ALA	O-C-N	5.07	127.29	122.07
2	B	296	GLY	N-CA-C	-5.07	106.51	112.64
2	B	256	ALA	N-CA-C	-5.06	105.66	111.07
2	B	537	ARG	N-CA-C	-5.04	105.68	111.07
1	A	223	VAL	N-CA-C	5.00	116.32	110.62

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	172	LEU	Mainchain

5.2 Too-close contacts (i)

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	4741	0	4874	122	0
2	B	4535	0	4701	84	0
3	C	897	0	887	24	0
All	All	10173	0	10462	207	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 10.

All (207) 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:484:LYS:HB2	1:A:488:THR:HB	1.37	1.04
1:A:288:VAL:HB	1:A:292:LEU:HD23	1.43	0.96
3:C:100:THR:OG1	3:C:111:GLY:HA2	1.69	0.92
2:B:79:MET:HG2	2:B:138:LEU:HD11	1.53	0.91
1:A:388:LYS:HE3	1:A:544:MET:HE2	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:ASP:O	1:A:313:LYS:HG2	1.76	0.85
2:B:179:LEU:HD11	2:B:248:LEU:HD13	1.60	0.84
1:A:492:GLU:HG3	1:A:497:LEU:HD22	1.58	0.83
3:C:50:CYS:HB3	3:C:99:VAL:HG21	1.59	0.83
1:A:346:ILE:HG22	1:A:348:GLY:H	1.42	0.82
2:B:466:THR:OG1	2:B:473:ILE:HG13	1.79	0.82
1:A:309:ASP:HB3	1:A:313:LYS:HE2	1.60	0.80
1:A:230:VAL:HG12	1:A:230:VAL:O	1.81	0.78
3:C:98:THR:O	3:C:111:GLY:HA3	1.83	0.78
2:B:294:GLY:O	2:B:298:VAL:HG23	1.85	0.77
3:C:60:TYR:O	3:C:106:GLY:HA2	1.84	0.77
2:B:173:PHE:HZ	2:B:299:MET:HE1	1.52	0.75
1:A:18:ILE:HG13	1:A:328:PHE:HZ	1.54	0.73
2:B:502:LEU:HD23	2:B:505:VAL:HG21	1.70	0.72
1:A:199:ARG:HD3	1:A:203:ARG:NH2	2.05	0.72
2:B:177:ARG:NH1	2:B:181:ARG:HH21	1.91	0.69
2:B:177:ARG:HH11	2:B:181:ARG:HH21	1.39	0.68
3:C:110:PRO:HB3	3:C:114:TRP:HZ2	1.59	0.68
1:A:323:SER:O	1:A:327:ILE:HG12	1.93	0.67
2:B:553:GLU:HG3	3:C:102:VAL:HB	1.76	0.67
3:C:50:CYS:CB	3:C:99:VAL:HG21	2.25	0.67
3:C:110:PRO:HB3	3:C:114:TRP:CZ2	2.29	0.67
1:A:353:VAL:HG22	1:A:419:LEU:CD2	2.25	0.66
1:A:353:VAL:HG22	1:A:419:LEU:HD22	1.78	0.66
1:A:405:LEU:HD21	1:A:417:VAL:CG2	2.25	0.66
2:B:180:LEU:HD21	2:B:245:LEU:HD21	1.78	0.66
1:A:15:PHE:CD1	1:A:19:LEU:HD11	2.31	0.65
1:A:595:LEU:HD12	2:B:575:GLU:OE1	1.96	0.65
1:A:355:PHE:CD1	1:A:417:VAL:HG13	2.31	0.65
1:A:449:THR:HG22	1:A:487:GLN:O	1.96	0.65
1:A:450:VAL:HB	1:A:486:TYR:O	1.96	0.65
1:A:492:GLU:HG3	1:A:497:LEU:CD2	2.27	0.65
1:A:355:PHE:CZ	1:A:405:LEU:HD23	2.33	0.63
1:A:405:LEU:HD21	1:A:417:VAL:HG21	1.79	0.63
2:B:79:MET:CG	2:B:138:LEU:HD11	2.28	0.63
1:A:59:VAL:HG23	1:A:62:GLU:HA	1.79	0.62
3:C:91:THR:HG22	3:C:122:VAL:H	1.65	0.62
2:B:467:VAL:O	2:B:473:ILE:HB	2.00	0.61
1:A:524:ALA:C	1:A:554:HIS:HB2	2.25	0.61
1:A:140:ASP:HB3	1:A:327:ILE:HD11	1.83	0.60
1:A:355:PHE:CE2	1:A:405:LEU:HD23	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:285:LEU:HA	2:B:288:LEU:HB2	1.83	0.60
2:B:46:ARG:HG3	2:B:276:GLY:C	2.26	0.60
2:B:462:LYS:HB2	2:B:466:THR:HB	1.82	0.60
1:A:572:ARG:HG2	1:A:573:LEU:O	2.01	0.60
1:A:190:VAL:O	1:A:194:VAL:HG23	2.02	0.59
1:A:355:PHE:HZ	1:A:406:ILE:HG13	1.67	0.59
2:B:576:VAL:HG23	2:B:576:VAL:O	2.03	0.59
1:A:59:VAL:CG2	1:A:62:GLU:HA	2.32	0.59
1:A:347:ARG:HG3	1:A:350:ARG:HH22	1.67	0.59
2:B:553:GLU:CG	3:C:102:VAL:HB	2.32	0.59
1:A:81:LEU:HD11	2:B:255:PHE:HE1	1.67	0.59
1:A:396:GLY:HA2	1:A:570:LYS:H	1.68	0.58
2:B:56:ARG:O	2:B:56:ARG:HG3	2.03	0.58
1:A:355:PHE:CD2	1:A:381:PHE:CZ	2.92	0.58
2:B:501:ALA:C	2:B:502:LEU:HD12	2.28	0.58
1:A:15:PHE:O	1:A:19:LEU:HG	2.02	0.58
1:A:484:LYS:HB2	1:A:488:THR:CB	2.23	0.57
1:A:340:PRO:HB3	1:A:425:ARG:O	2.04	0.57
2:B:79:MET:HE1	2:B:142:ARG:HD3	1.86	0.57
1:A:228:LEU:HD21	2:B:387:LEU:HD21	1.86	0.57
2:B:309:LEU:HD11	2:B:313:PHE:CZ	2.40	0.57
1:A:35:PHE:O	1:A:39:VAL:HG23	2.05	0.56
1:A:405:LEU:HD11	1:A:417:VAL:HG21	1.88	0.56
1:A:81:LEU:HD13	2:B:258:LEU:CD1	2.36	0.56
2:B:473:ILE:HG22	2:B:473:ILE:O	2.06	0.56
1:A:59:VAL:HG21	1:A:63:PRO:HD2	1.87	0.56
1:A:36:LEU:HD21	1:A:156:ILE:HG22	1.88	0.56
1:A:16:ALA:HA	1:A:19:LEU:HD12	1.89	0.55
1:A:349:PHE:C	1:A:351:GLY:H	2.13	0.55
1:A:498:SER:O	1:A:499:THR:C	2.50	0.55
1:A:347:ARG:HG3	1:A:347:ARG:O	2.07	0.55
2:B:173:PHE:CZ	2:B:299:MET:HE1	2.38	0.54
2:B:562:ALA:HB1	3:C:107:ARG:HE	1.73	0.54
2:B:60:VAL:O	2:B:63:LEU:HB3	2.08	0.54
2:B:341:PHE:CE1	2:B:359:LEU:HD23	2.43	0.53
2:B:79:MET:HE3	2:B:138:LEU:HD21	1.91	0.53
2:B:553:GLU:OE2	3:C:57:ASN:HB2	2.09	0.53
1:A:259:LEU:HB3	2:B:77:TYR:CE1	2.44	0.53
2:B:481:GLN:HG3	2:B:501:ALA:O	2.09	0.53
3:C:19:ARG:NH1	3:C:82:GLN:OE1	2.42	0.53
1:A:61:THR:O	1:A:62:GLU:HB3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:LEU:HD13	2:B:258:LEU:HD13	1.91	0.52
1:A:288:VAL:CB	1:A:292:LEU:HD23	2.28	0.52
3:C:100:THR:HG1	3:C:111:GLY:HA2	1.71	0.52
1:A:355:PHE:HD1	1:A:417:VAL:HG13	1.73	0.52
2:B:35:ILE:CG1	2:B:142:ARG:HG3	2.40	0.52
1:A:140:ASP:CB	1:A:327:ILE:HD11	2.40	0.51
3:C:61:ALA:HB3	3:C:64:VAL:HG22	1.93	0.51
2:B:558:SER:HB2	3:C:101:ALA:HB2	1.92	0.50
1:A:62:GLU:N	1:A:63:PRO:HD3	2.26	0.50
2:B:207:GLY:O	2:B:210:VAL:HB	2.10	0.50
2:B:14:TRP:N	2:B:15:PRO:CD	2.75	0.50
2:B:481:GLN:CG	2:B:501:ALA:O	2.59	0.50
1:A:228:LEU:CD2	2:B:387:LEU:HD21	2.42	0.50
1:A:18:ILE:HG13	1:A:328:PHE:CZ	2.42	0.50
1:A:33:LEU:C	1:A:33:LEU:HD23	2.38	0.49
1:A:69:ARG:O	1:A:73:LEU:HB3	2.11	0.49
1:A:266:PHE:CD2	1:A:267:LEU:HD12	2.47	0.49
1:A:498:SER:O	1:A:502:LYS:HG3	2.11	0.49
1:A:262:PRO:HB3	2:B:73:GLY:O	2.12	0.49
1:A:466:VAL:HG12	1:A:486:TYR:CE2	2.47	0.49
1:A:497:LEU:HD21	1:A:502:LYS:HD2	1.94	0.49
1:A:595:LEU:HG	2:B:572:LEU:CD1	2.42	0.49
2:B:47:LEU:HB3	2:B:61:TYR:CE2	2.48	0.49
2:B:188:ARG:HG3	2:B:189:GLU:N	2.27	0.49
1:A:81:LEU:HB2	2:B:258:LEU:HD12	1.93	0.48
1:A:409:PHE:CE2	2:B:209:ARG:HD3	2.48	0.48
1:A:492:GLU:HA	1:A:497:LEU:HB3	1.95	0.48
2:B:9:LEU:CD1	2:B:306:LEU:HD11	2.43	0.48
1:A:422:VAL:HG11	1:A:427:TYR:OH	2.13	0.48
1:A:396:GLY:HA2	1:A:570:LYS:N	2.28	0.48
1:A:405:LEU:HD21	1:A:417:VAL:HG22	1.95	0.48
1:A:442:GLU:HG3	1:A:442:GLU:O	2.13	0.48
1:A:497:LEU:HD21	1:A:502:LYS:HG2	1.95	0.48
1:A:47:PRO:O	1:A:50:PHE:N	2.45	0.47
2:B:9:LEU:HD12	2:B:306:LEU:HD11	1.96	0.47
1:A:349:PHE:C	1:A:351:GLY:N	2.73	0.47
2:B:256:ALA:HB1	2:B:285:LEU:HD23	1.96	0.47
3:C:100:THR:OG1	3:C:111:GLY:CA	2.53	0.47
1:A:492:GLU:HG3	1:A:497:LEU:HB3	1.95	0.47
1:A:501:GLU:OE1	1:A:504:LEU:HD23	2.14	0.47
3:C:103:LEU:HB2	3:C:107:ARG:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:498:LEU:HB3	2:B:501:ALA:HB2	1.97	0.47
1:A:47:PRO:HB2	1:A:299:TYR:CE2	2.50	0.47
2:B:179:LEU:CD1	2:B:248:LEU:HD13	2.36	0.47
1:A:36:LEU:HD21	1:A:156:ILE:CG2	2.45	0.46
1:A:372:LYS:C	1:A:374:TRP:H	2.23	0.46
1:A:309:ASP:HB3	1:A:313:LYS:CE	2.37	0.46
1:A:148:ILE:O	1:A:152:LEU:HB3	2.16	0.46
1:A:449:THR:HB	1:A:487:GLN:HA	1.98	0.46
2:B:185:ARG:O	2:B:189:GLU:HG2	2.15	0.46
1:A:15:PHE:CE1	1:A:19:LEU:HD11	2.50	0.46
2:B:375:SER:OG	2:B:546:ASP:HA	2.16	0.46
1:A:565:ILE:HD13	1:A:589:TYR:OH	2.15	0.45
2:B:138:LEU:C	2:B:138:LEU:HD23	2.42	0.45
2:B:256:ALA:HB1	2:B:285:LEU:CD2	2.47	0.45
1:A:157:ALA:O	1:A:161:THR:HG22	2.17	0.45
2:B:98:LEU:HD22	2:B:315:LEU:HD22	1.99	0.45
1:A:466:VAL:HG12	1:A:486:TYR:HE2	1.81	0.45
3:C:76:LYS:HB2	3:C:76:LYS:HE2	1.77	0.45
2:B:424:PHE:HB2	2:B:426:GLU:HG2	1.99	0.45
1:A:199:ARG:HD3	1:A:203:ARG:CZ	2.46	0.45
1:A:20:ARG:HA	1:A:23:TRP:HB2	1.99	0.44
1:A:146:GLN:O	1:A:150:GLY:N	2.32	0.44
1:A:359:TRP:HB3	1:A:374:TRP:CZ3	2.53	0.44
1:A:303:LEU:O	1:A:306:PRO:HD2	2.17	0.44
1:A:295:ALA:O	1:A:299:TYR:HD2	2.00	0.44
2:B:558:SER:CB	3:C:101:ALA:HB2	2.48	0.44
1:A:497:LEU:HD21	1:A:502:LYS:CD	2.48	0.44
2:B:180:LEU:O	2:B:183:ILE:HG13	2.18	0.44
2:B:288:LEU:C	2:B:291:PRO:HD2	2.43	0.44
1:A:141:VAL:O	1:A:141:VAL:HG22	2.17	0.44
2:B:341:PHE:CD1	2:B:359:LEU:HD23	2.52	0.44
1:A:151:GLY:HA2	1:A:316:LEU:HD12	2.00	0.43
1:A:134:MET:CE	2:B:202:GLN:HB2	2.48	0.43
1:A:355:PHE:HE2	1:A:402:VAL:HG13	1.83	0.43
1:A:492:GLU:HA	1:A:497:LEU:CB	2.48	0.43
2:B:312:LEU:O	2:B:315:LEU:HB3	2.18	0.43
1:A:443:PRO:HD2	1:A:502:LYS:HE2	1.99	0.43
2:B:35:ILE:HG13	2:B:142:ARG:HG3	1.99	0.43
1:A:355:PHE:CE1	1:A:417:VAL:HG13	2.53	0.43
1:A:396:GLY:HA2	1:A:570:LYS:HA	2.00	0.43
2:B:158:ASN:HD22	2:B:273:LEU:HD21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:554:GLY:HA3	2:B:559:LEU:HD21	2.00	0.43
1:A:444:PHE:HB3	2:B:210:VAL:HG21	2.01	0.43
2:B:313:PHE:HD1	2:B:316:LEU:HD12	1.84	0.43
2:B:556:HIS:CD2	2:B:557:GLU:HG3	2.53	0.43
1:A:181:LEU:C	1:A:183:VAL:N	2.76	0.43
2:B:562:ALA:CB	3:C:107:ARG:HE	2.32	0.43
2:B:553:GLU:HG3	2:B:553:GLU:O	2.18	0.43
3:C:72:ARG:HB3	3:C:79:VAL:HG23	2.01	0.43
1:A:497:LEU:HD21	1:A:502:LYS:CG	2.49	0.43
1:A:138:THR:HG23	2:B:194:PHE:HZ	1.84	0.42
1:A:525:THR:HA	1:A:554:HIS:O	2.19	0.42
1:A:62:GLU:HG2	1:A:62:GLU:O	2.18	0.42
2:B:98:LEU:CD2	2:B:315:LEU:HD22	2.50	0.42
1:A:346:ILE:HD11	1:A:427:TYR:HB3	2.01	0.42
2:B:541:TRP:CZ3	3:C:32:ASN:HB2	2.55	0.42
1:A:318:GLN:O	1:A:321:MET:N	2.53	0.42
1:A:36:LEU:CD2	1:A:156:ILE:CG2	2.98	0.41
1:A:396:GLY:HA2	1:A:570:LYS:CA	2.50	0.41
2:B:559:LEU:HD13	2:B:566:TYR:CG	2.55	0.41
2:B:248:LEU:C	2:B:248:LEU:HD23	2.45	0.41
2:B:507:ALA:HB2	2:B:532:ARG:HH22	1.84	0.41
1:A:285:ARG:O	1:A:285:ARG:HG2	2.20	0.41
1:A:501:GLU:CD	1:A:504:LEU:HD23	2.45	0.41
1:A:161:THR:HG23	1:A:306:PRO:HG3	2.03	0.41
1:A:181:LEU:C	1:A:183:VAL:H	2.29	0.41
1:A:422:VAL:HG11	1:A:427:TYR:CZ	2.56	0.41
1:A:489:VAL:HG22	1:A:490:LEU:N	2.36	0.41
1:A:492:GLU:O	1:A:497:LEU:HB3	2.21	0.41
2:B:515:GLN:HA	2:B:538:HIS:NE2	2.36	0.41
1:A:567:VAL:HG12	1:A:588:TYR:HE2	1.86	0.40
1:A:467:GLU:HG3	1:A:471:ARG:HH12	1.87	0.40
1:A:479:ILE:HA	1:A:482:LEU:HD13	2.03	0.40
2:B:143:LEU:C	2:B:145:PHE:H	2.29	0.40
2:B:285:LEU:O	2:B:289:THR:HG23	2.22	0.40
2:B:359:LEU:CD1	3:C:55:THR:HG22	2.52	0.40
1:A:445:LEU:CB	1:A:490:LEU:HD11	2.52	0.40
2:B:79:MET:SD	2:B:138:LEU:HD21	2.61	0.40
2:B:248:LEU:HD21	2:B:252:LEU:HD11	2.02	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	590/623 (95%)	566 (96%)	23 (4%)	1 (0%)	44 77
2	B	572/578 (99%)	551 (96%)	21 (4%)	0	100 100
3	C	119/136 (88%)	116 (98%)	3 (2%)	0	100 100
All	All	1281/1337 (96%)	1233 (96%)	47 (4%)	1 (0%)	50 82

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	373	ASP

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	496/521 (95%)	496 (100%)	0	100 100
2	B	462/464 (100%)	461 (100%)	1 (0%)	92 94
3	C	96/109 (88%)	96 (100%)	0	100 100
All	All	1054/1094 (96%)	1053 (100%)	1 (0%)	92 94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	404	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	121	HIS
1	A	302	GLN
1	A	308	GLN
1	A	413	GLN
1	A	596	GLN
1	A	598	GLN
2	B	400	HIS
3	C	3	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 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.

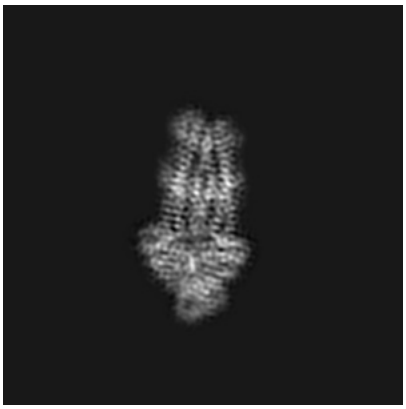
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4781. These allow visual inspection of the internal detail of the map and identification of artifacts.

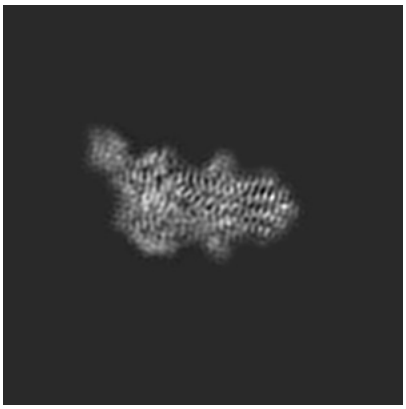
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

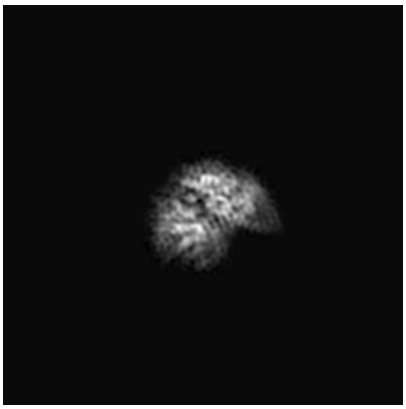
6.1.1 Primary map



X

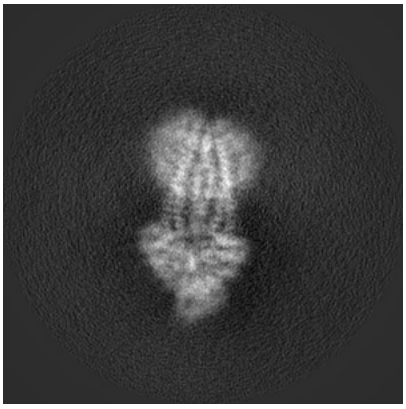


Y

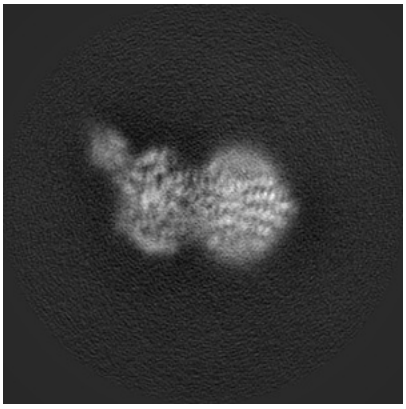


Z

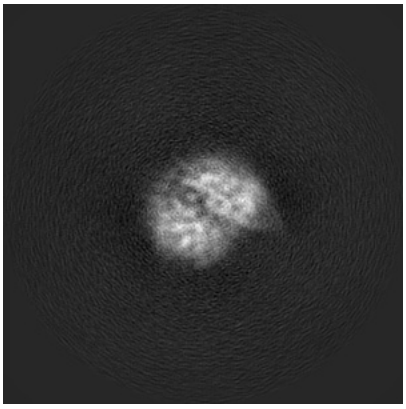
6.1.2 Raw map



X



Y



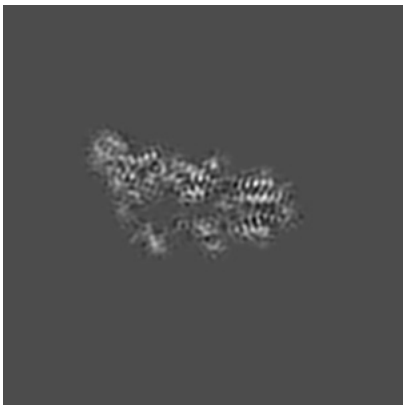
Z

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

6.2 Central slices (i)

6.2.1 Primary map

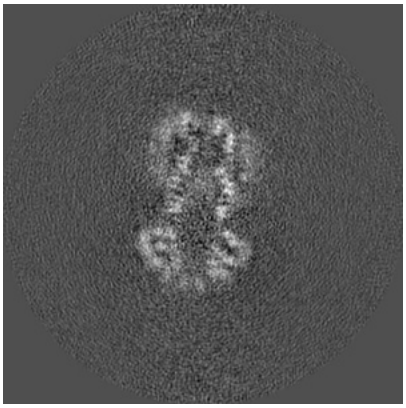
X Index: 128



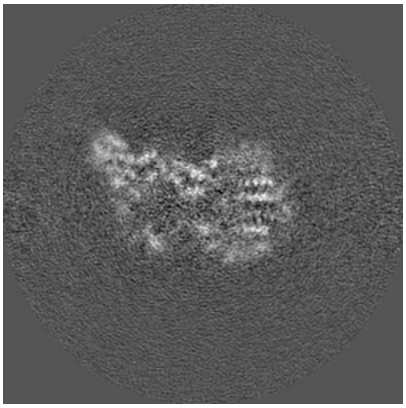
Y Index: 128

Z Index: 128

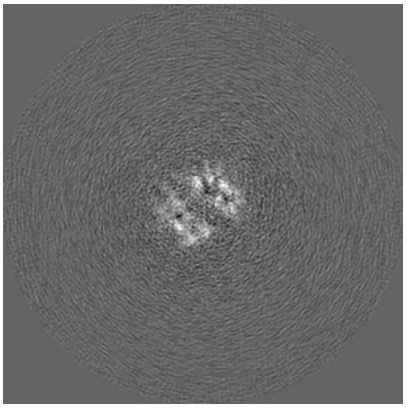
6.2.2 Raw map



X Index: 128



Y Index: 128



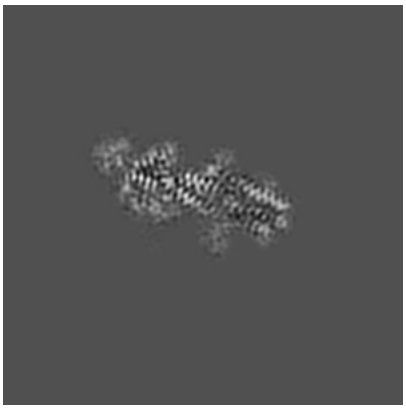
Z Index: 128

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

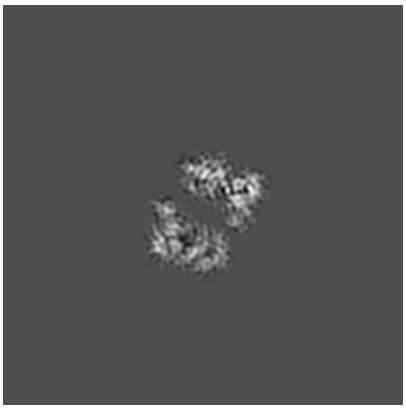
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 136

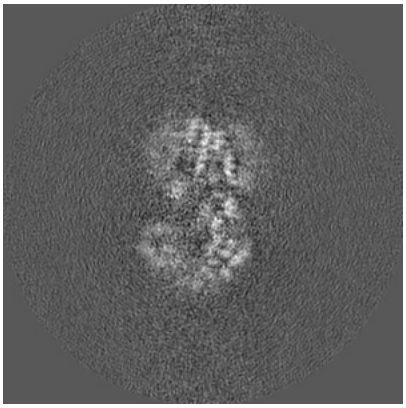


Y Index: 137

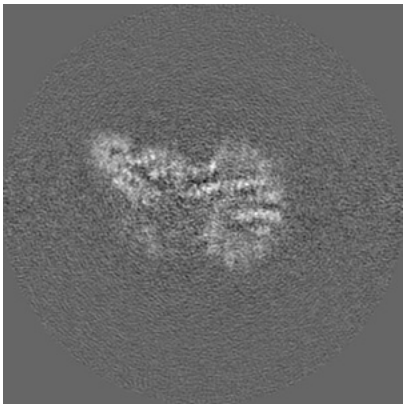


Z Index: 102

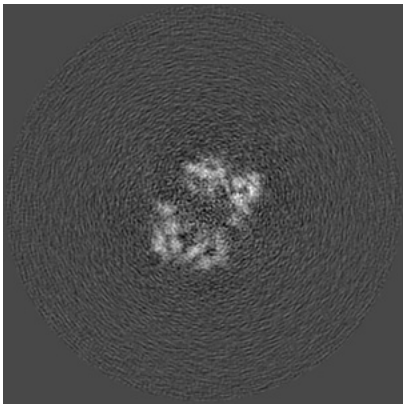
6.3.2 Raw map



X Index: 133



Y Index: 131

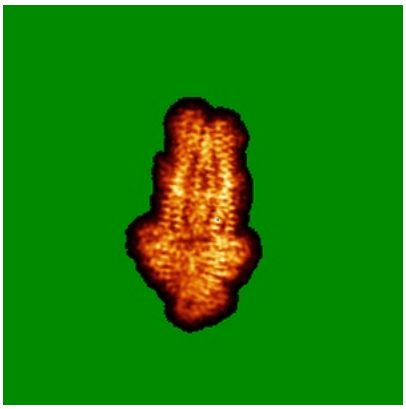


Z Index: 102

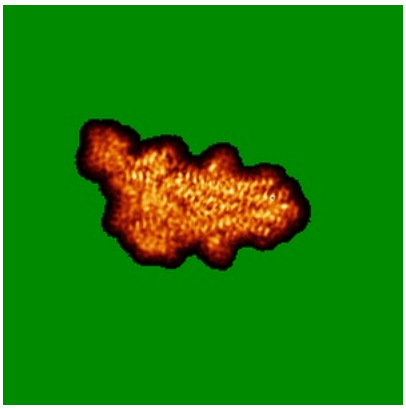
The images above show the largest variance slices of the map in three orthogonal directions.

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

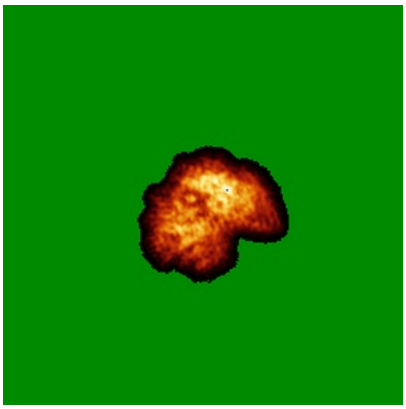
6.4.1 Primary map



X

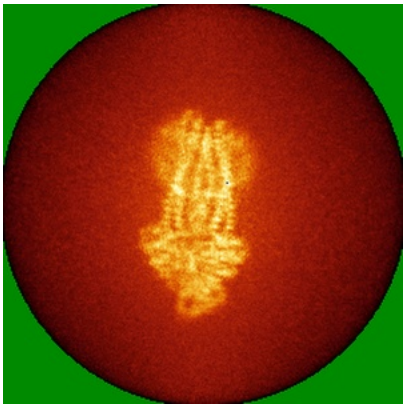


Y

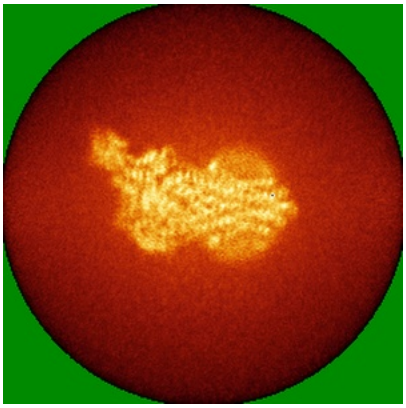


Z

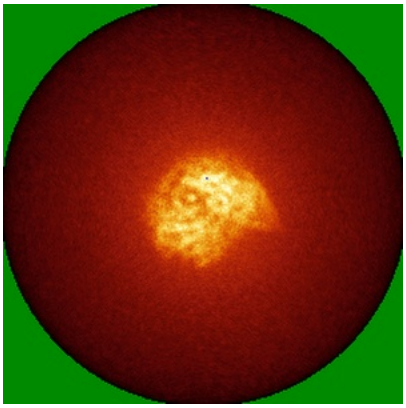
6.4.2 Raw map



X



Y

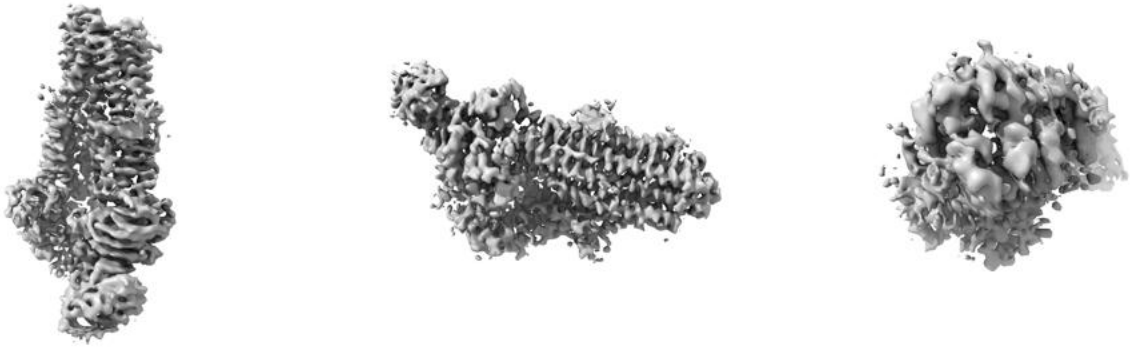


Z

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

6.5 Orthogonal surface views (i)

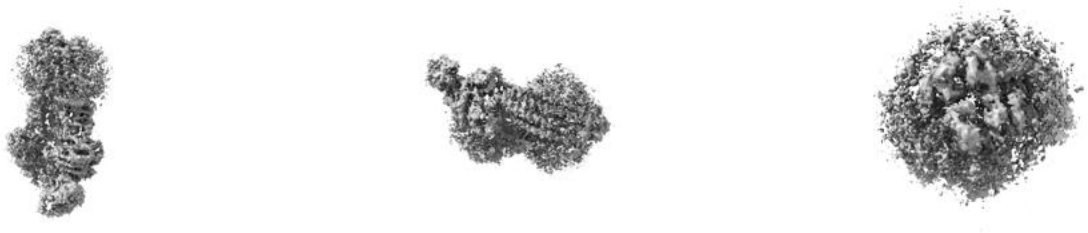
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

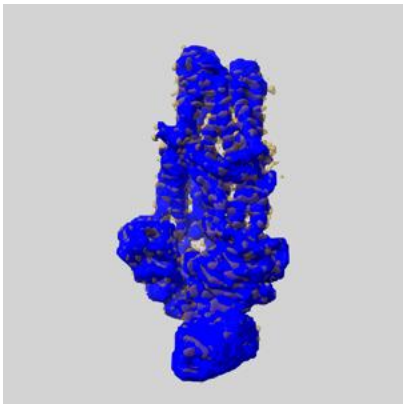
6.6 Mask visualisation (i)

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

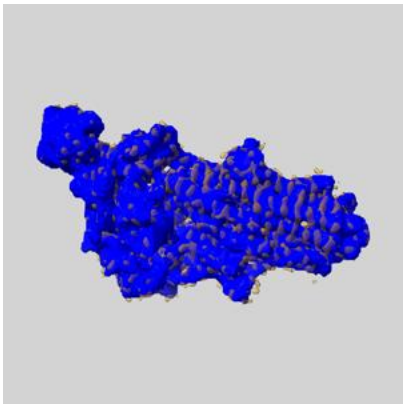
A mask typically either:

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

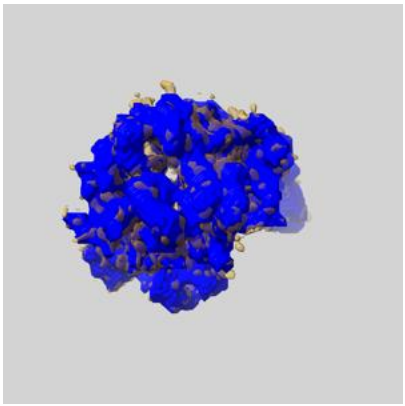
6.6.1 emd_4781_msk_1.map (i)



X



Y

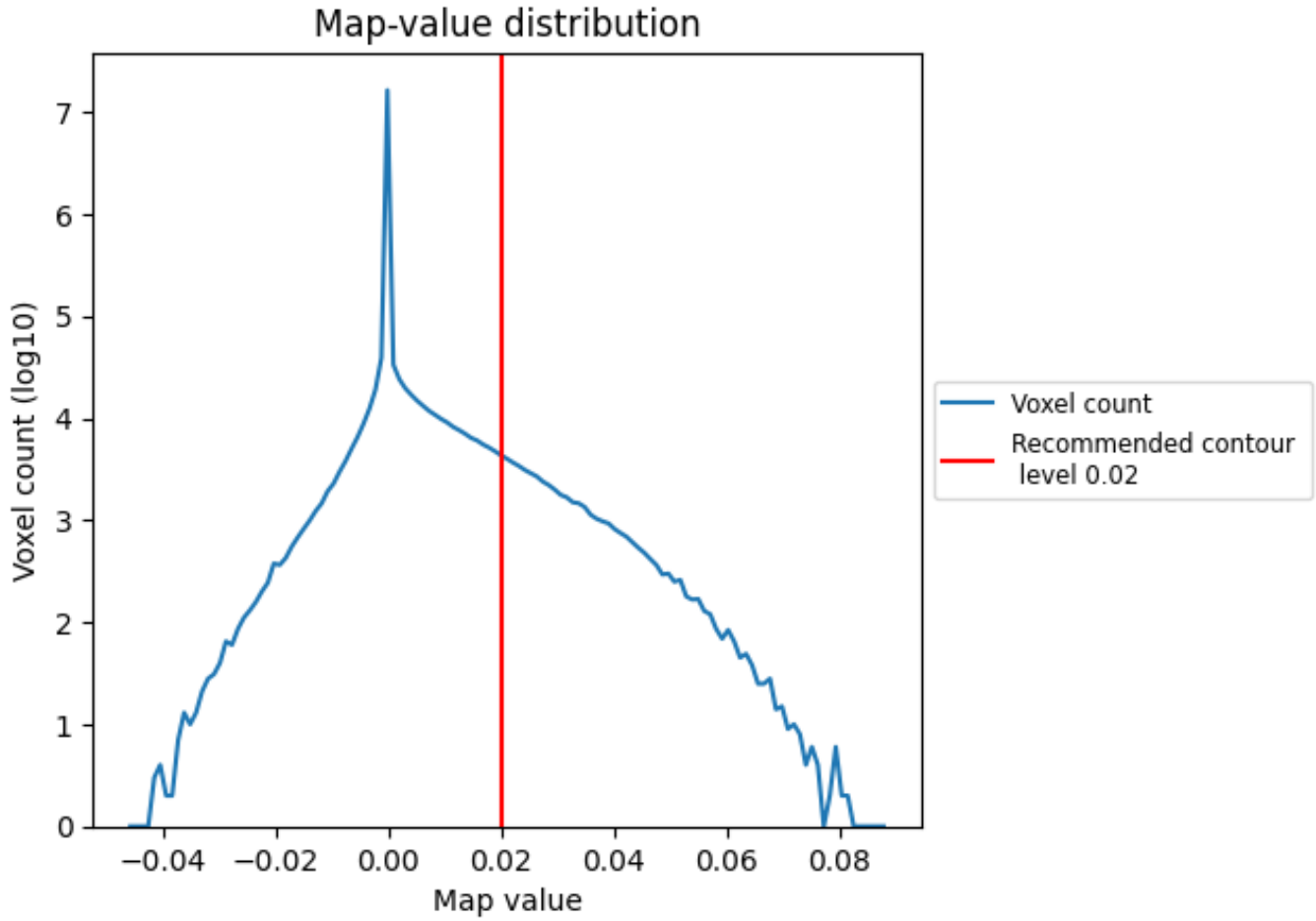


Z

7 Map analysis

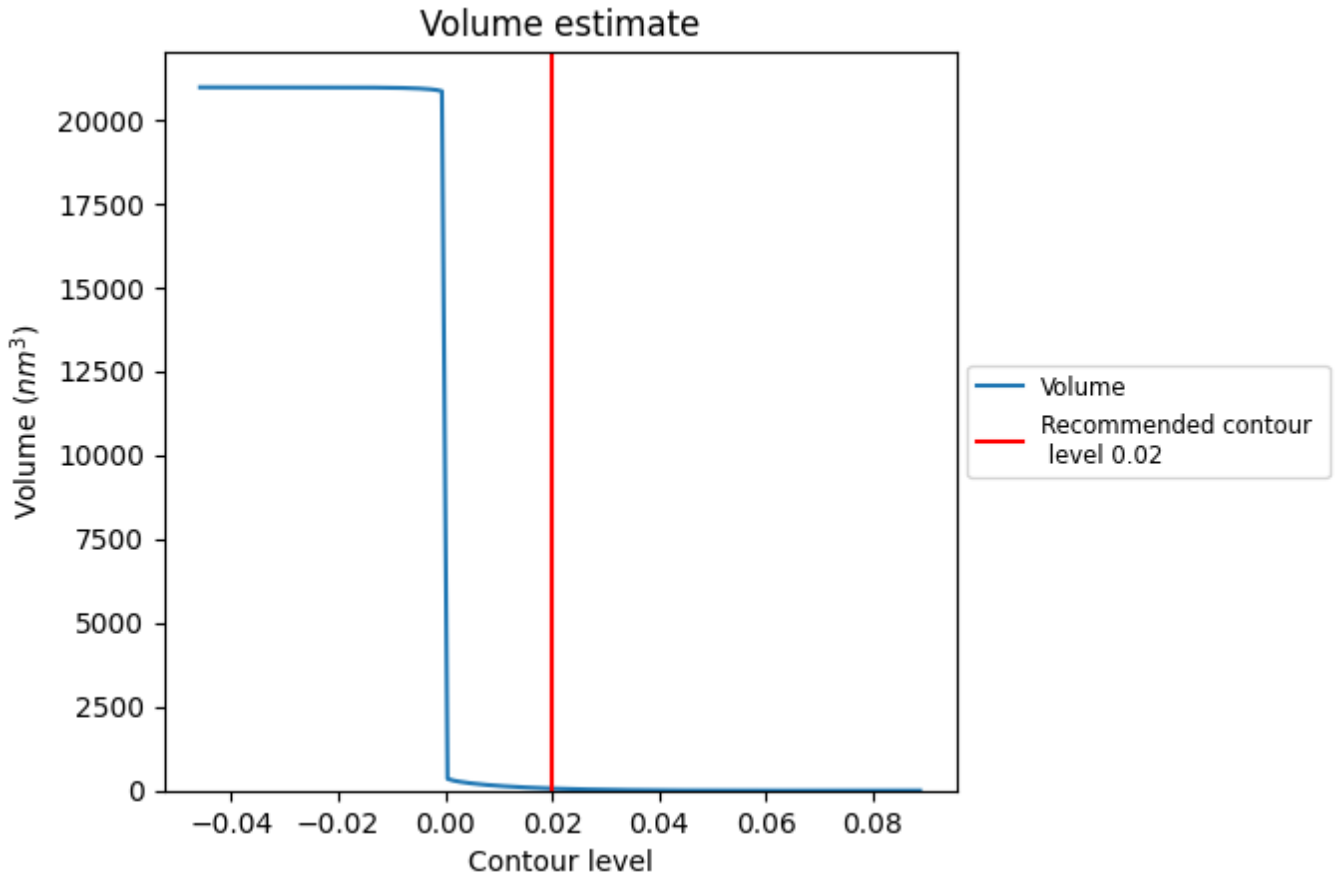
This section contains the results of statistical analysis of the map.

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.

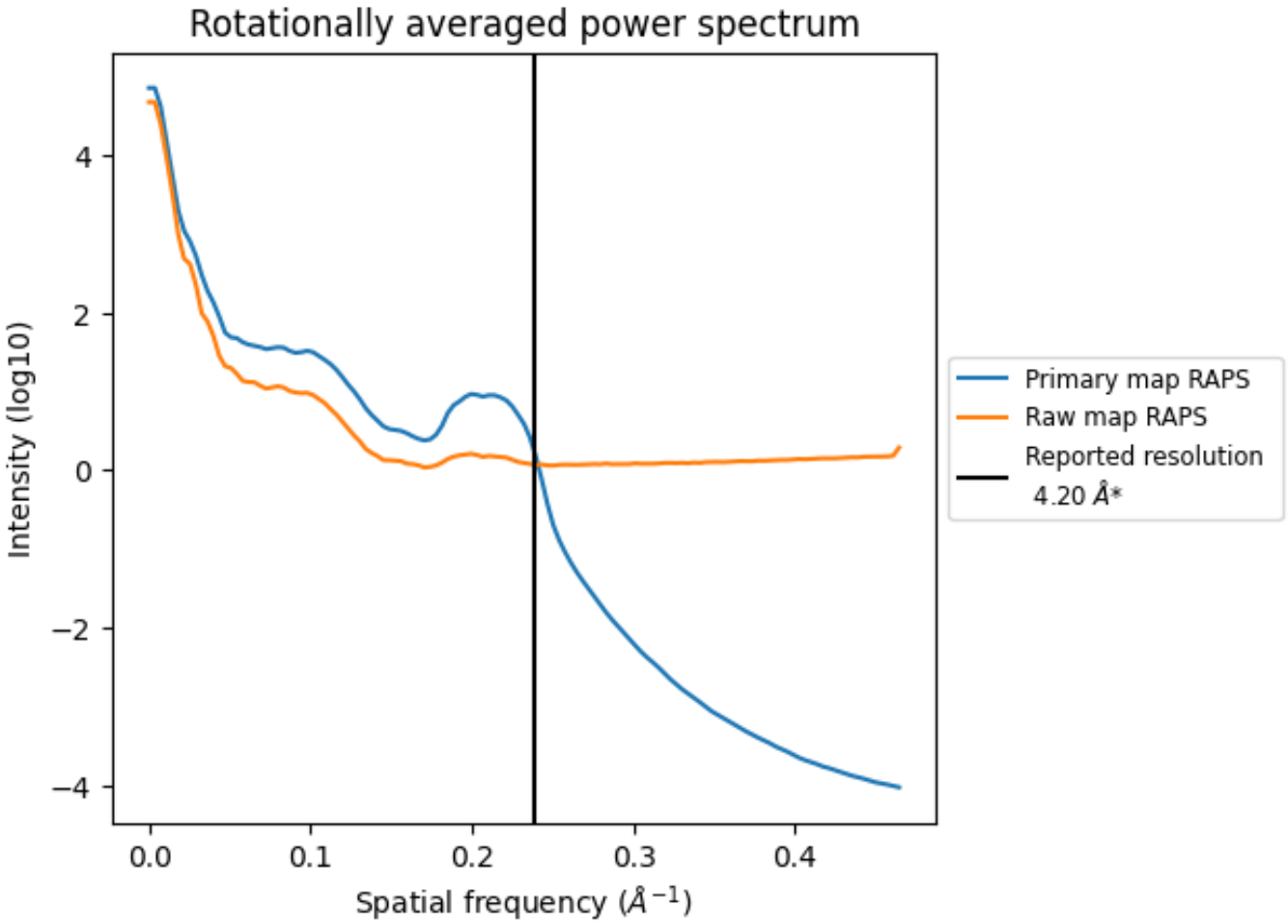
7.2 Volume estimate



The volume at the recommended contour level is 62 nm^3; this corresponds to an approximate mass of 56 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)

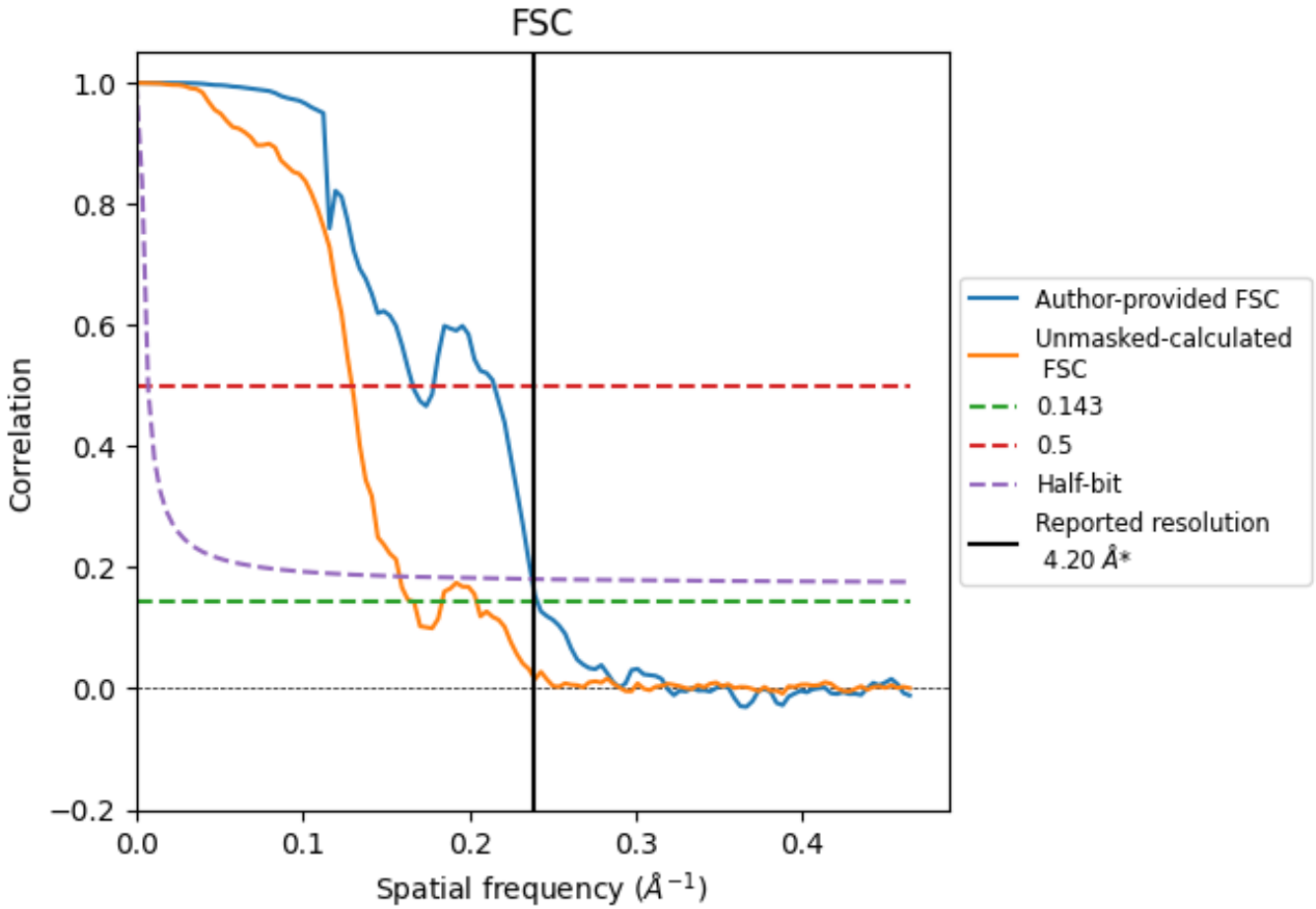


*Reported resolution corresponds to spatial frequency of 0.238 Å^{-1}

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 0.238 Å^{-1}

8.2 Resolution estimates (i)

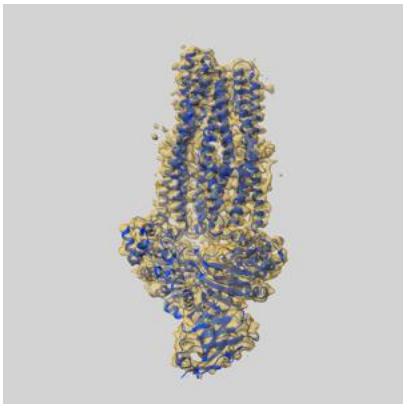
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	4.15	6.02	4.21
Unmasked-calculated*	5.99	7.72	6.32

*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 5.99 differs from the reported value 4.2 by more than 10 %

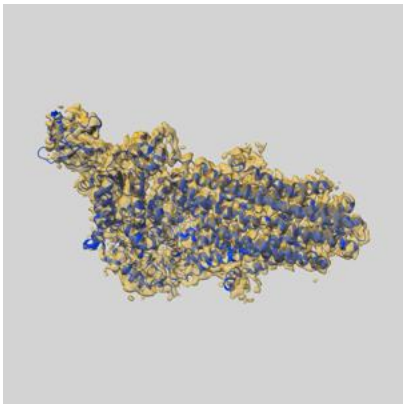
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4781 and PDB model 6RAN. Per-residue inclusion information can be found in section 3 on page 5.

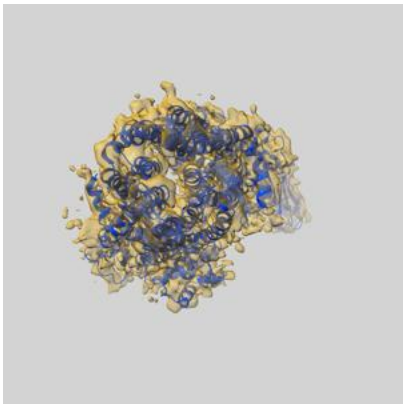
9.1 Map-model overlay



X



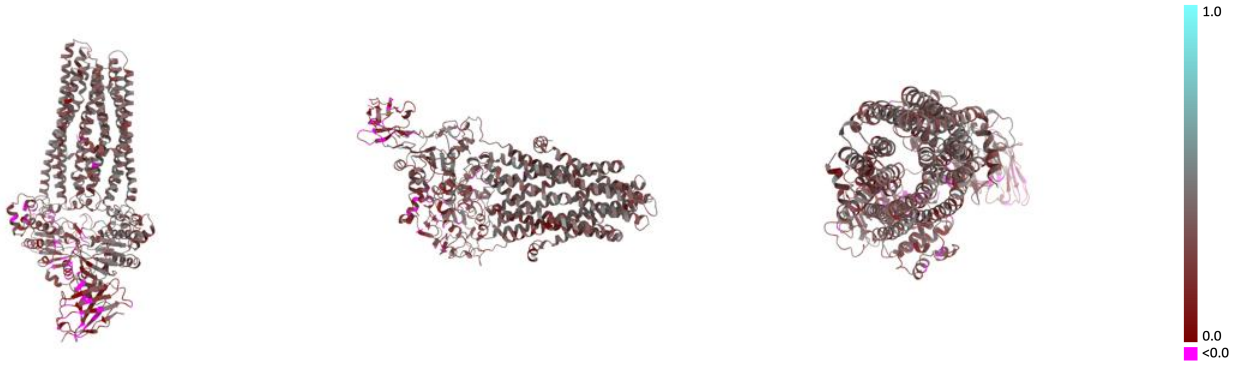
Y



Z

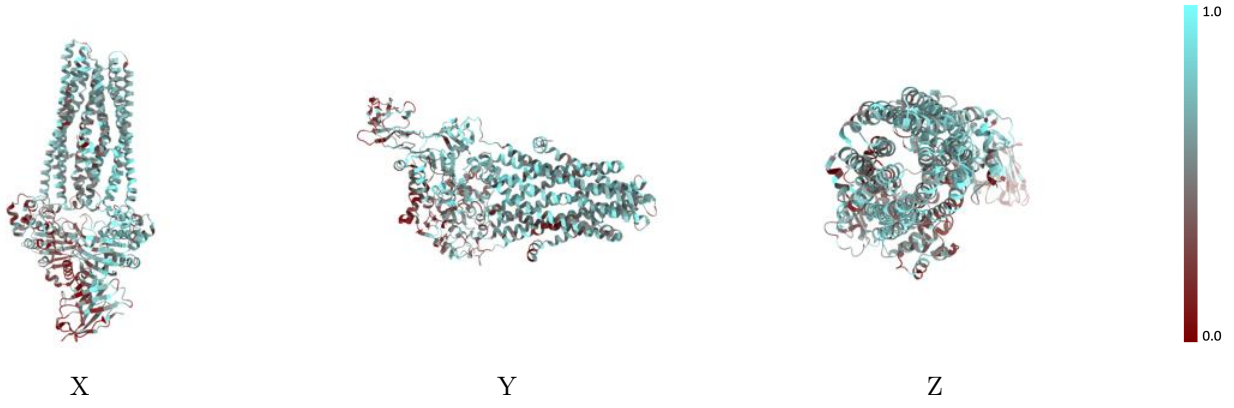
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



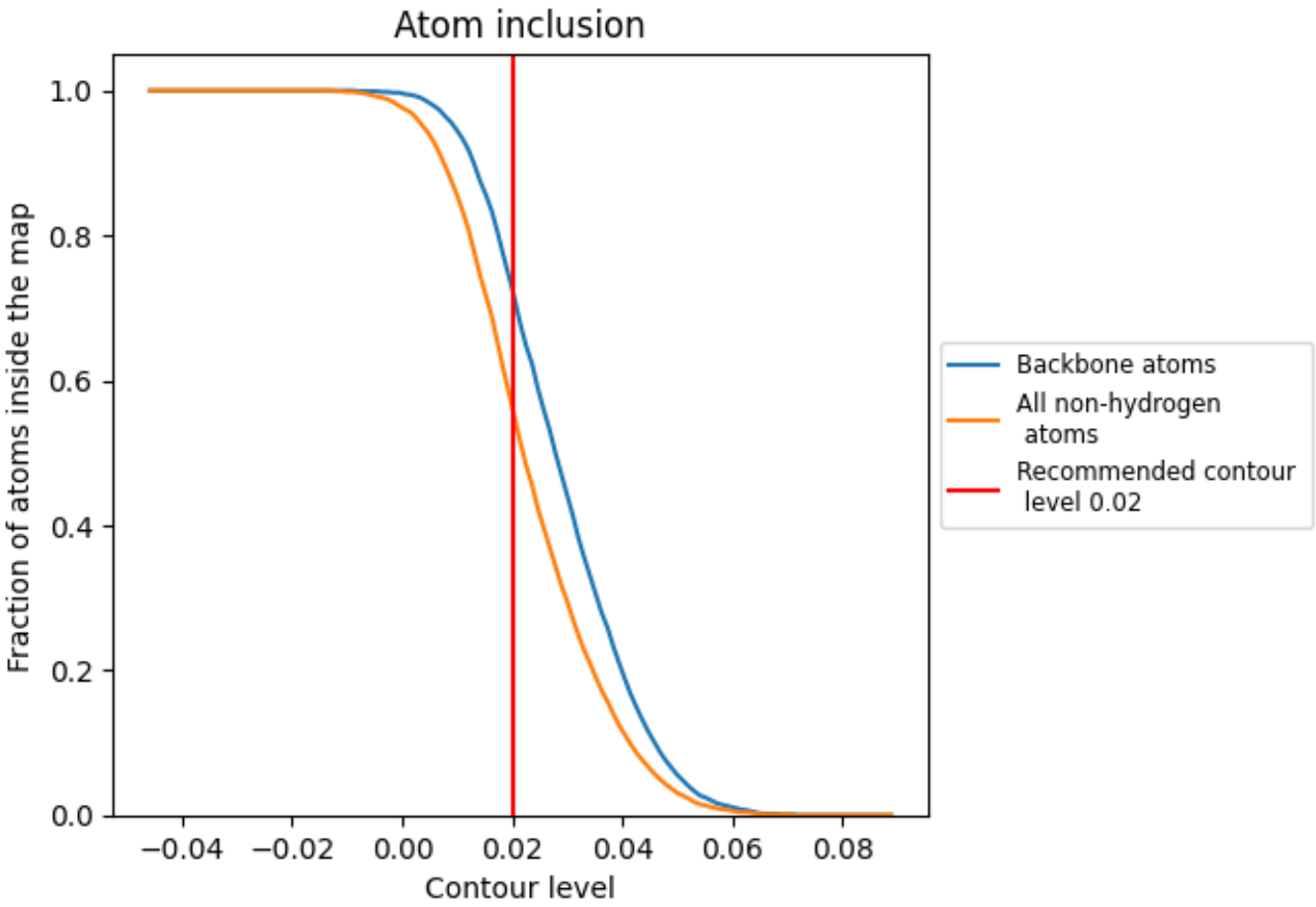
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 73% of all backbone atoms, 56% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5630	0.3060
A	0.5270	0.2970
B	0.6290	0.3390
C	0.4250	0.1840