



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 03:05 PM UTC

PDB ID : 8GJK / pdb_00008gjk
EMDB ID : EMD-40092
Title : Multi-drug efflux pump RE-CmeB bound with ampicillin
Authors : Zhang, Z.
Deposited on : 2023-03-16
Resolution : 3.16 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:

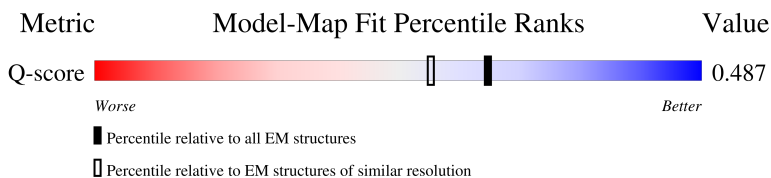
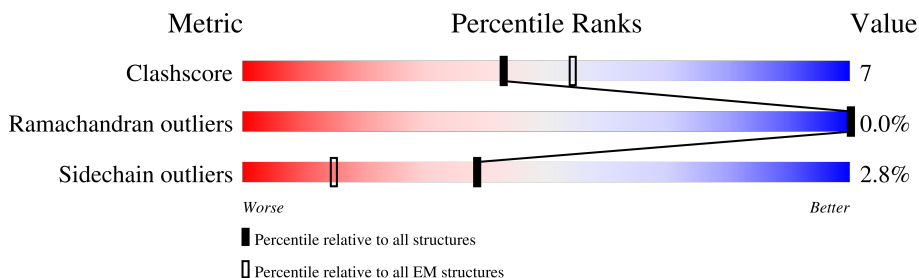
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.16 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	14474 (2.66 - 3.66)

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	1039	 81% 17% ..
1	B	1039	 78% 20% ..
1	C	1039	 80% 18% ..

2 Entry composition [i](#)

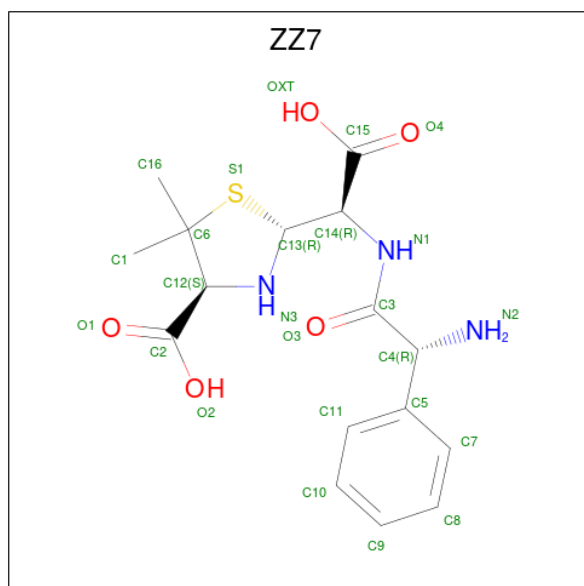
There are 2 unique types of molecules in this entry. The entry contains 23920 atoms, of which 19 are hydrogens and 0 are deuteriums.

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 Efflux pump membrane transporter.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1032	Total	C	N	O	S	0	0
			7954	5161	1280	1485	28		
1	A	1032	Total	C	N	O	S	0	0
			7952	5158	1280	1486	28		
1	C	1032	Total	C	N	O	S	0	0
			7970	5170	1287	1485	28		

- Molecule 2 is (2R,4S)-2-[(R)-{[(2R)-2-amino-2-phenylacetyl]amino}(carboxymethyl)-5,5-dimethyl-1,3-thiazolidine-4-carboxylic acid (CCD ID: ZZ7) (formula: C₁₆H₂₁N₃O₅S).

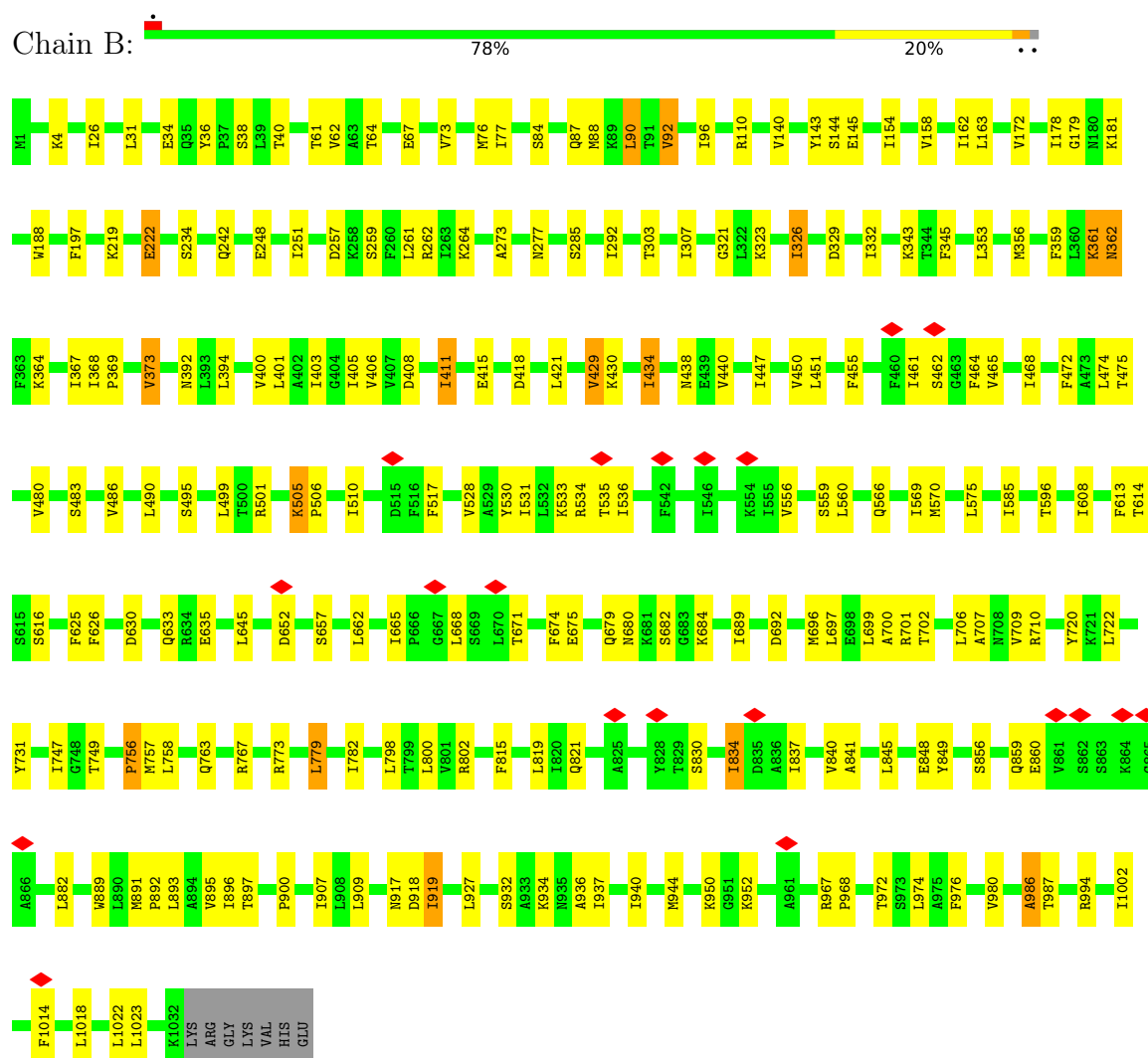


Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	H	N	O S	0
			44	16	19	3	5 1	

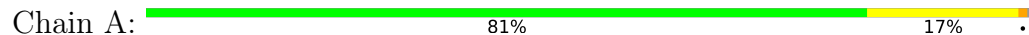
3 Residue-property plots

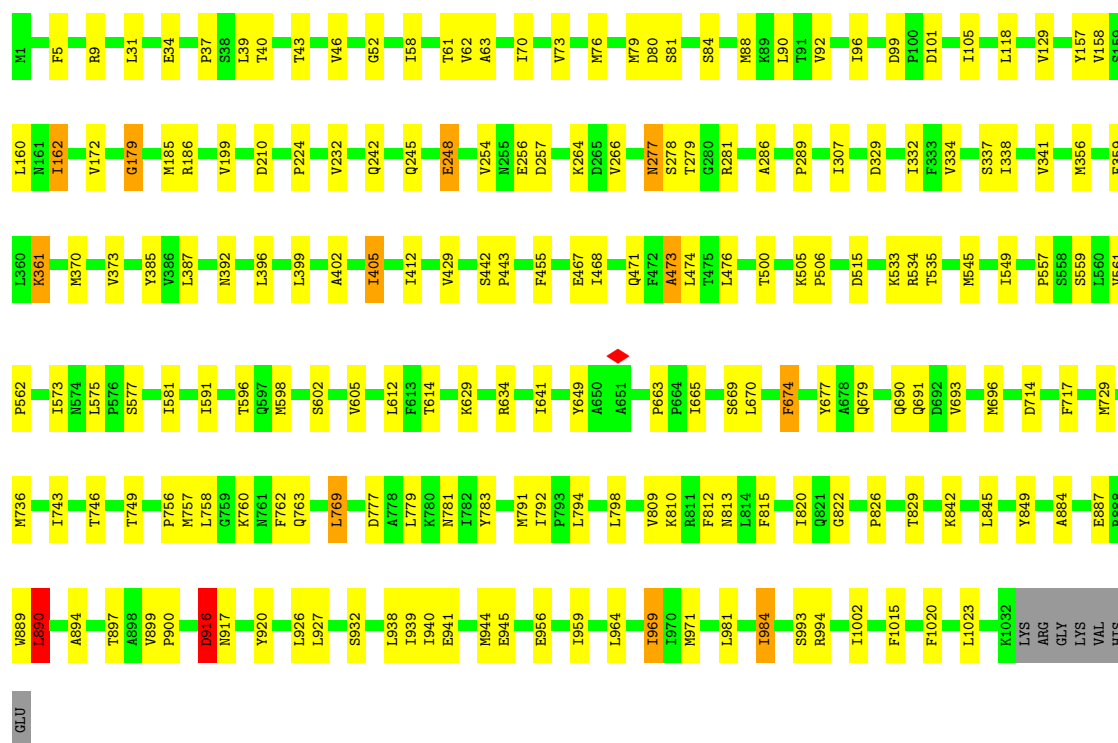
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Efflux pump membrane transporter

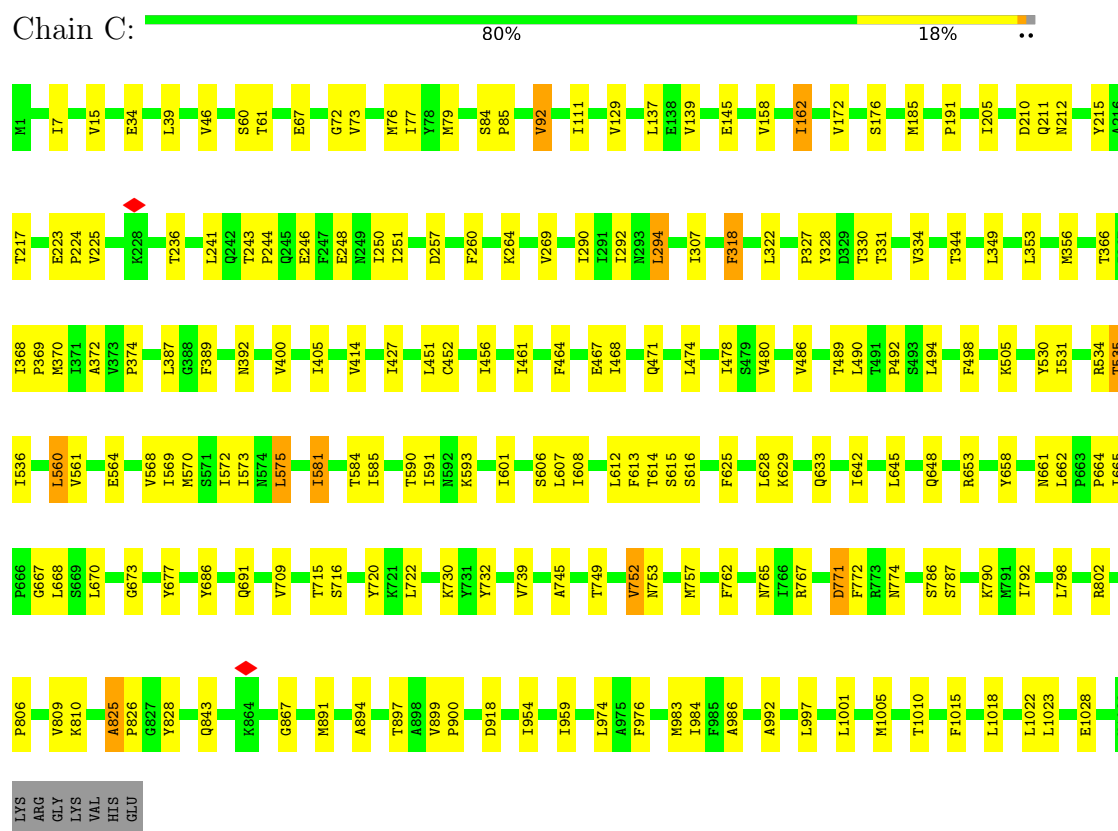


• Molecule 1: Efflux pump membrane transporter





• Molecule 1: Efflux pump membrane transporter



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18424	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 ($e^-/\text{\AA}^2$)	36.1	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.009	Depositor
Minimum map value	-0.472	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.034	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZZ7

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	0.65	0/8105	1.01	50/11014 (0.5%)
1	B	0.63	0/8108	1.02	53/11019 (0.5%)
1	C	0.57	0/8124	0.94	36/11037 (0.3%)
All	All	0.62	0/24337	0.99	139/33070 (0.4%)

There are no bond length outliers.

All (139) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	257	ASP	N-CA-C	-11.78	97.69	112.88
1	C	257	ASP	N-CA-C	-10.64	100.54	112.57
1	A	777	ASP	N-CA-C	-9.46	101.05	111.36
1	C	427	ILE	N-CA-C	9.10	121.22	109.30
1	A	61	THR	CA-C-N	-8.84	114.15	123.08
1	A	61	THR	C-N-CA	-8.84	114.15	123.08
1	B	178	ILE	N-CA-C	8.44	119.23	110.62
1	B	747	ILE	N-CA-C	-8.43	104.53	112.96
1	C	1015	PHE	N-CA-C	8.29	120.39	111.36
1	C	787	SER	N-CA-C	-8.04	103.45	113.18
1	A	792	ILE	CA-C-N	-7.75	112.36	120.03
1	A	792	ILE	C-N-CA	-7.75	112.36	120.03
1	A	890	LEU	N-CA-C	7.62	119.67	111.36
1	C	673	GLY	N-CA-C	7.46	121.69	111.54
1	A	62	VAL	CB-CA-C	-7.38	104.43	111.44
1	C	145	GLU	N-CA-C	-7.17	103.39	111.07
1	C	774	ASN	N-CA-C	7.16	120.92	111.75
1	C	372	ALA	N-CA-C	7.06	119.06	111.36
1	C	498	PHE	N-CA-C	7.04	118.74	111.14
1	A	277	ASN	N-CA-C	7.01	118.61	110.97
1	B	919	ILE	CB-CA-C	-6.94	103.00	111.88

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	ASP	N-CA-C	-6.87	104.01	112.88
1	B	455	PHE	N-CA-C	6.86	119.60	111.71
1	B	84	SER	CA-C-N	-6.85	112.04	119.98
1	B	84	SER	C-N-CA	-6.85	112.04	119.98
1	B	277	ASN	N-CA-C	6.84	118.81	111.36
1	C	162	ILE	N-CA-C	6.81	117.56	110.62
1	C	505	LYS	CA-C-N	-6.78	113.72	120.98
1	C	505	LYS	C-N-CA	-6.78	113.72	120.98
1	B	373	VAL	CA-C-N	-6.75	112.82	119.64
1	B	373	VAL	C-N-CA	-6.75	112.82	119.64
1	B	505	LYS	N-CA-C	6.74	120.18	109.40
1	A	210	ASP	N-CA-C	6.74	118.62	111.28
1	A	577	SER	N-CA-C	6.71	118.59	111.28
1	B	475	THR	N-CA-C	-6.66	103.83	112.23
1	A	535	THR	N-CA-C	6.66	118.53	111.28
1	A	665	ILE	N-CA-C	-6.56	100.31	108.05
1	A	245	GLN	N-CA-C	-6.53	105.28	113.18
1	A	361	LYS	N-CA-C	6.52	118.05	111.07
1	B	434	ILE	N-CA-C	-6.50	104.51	110.82
1	A	40	THR	N-CA-C	6.50	119.05	109.50
1	B	368	ILE	CA-C-N	-6.46	113.06	120.04
1	B	368	ILE	C-N-CA	-6.46	113.06	120.04
1	B	665	ILE	N-CA-C	-6.43	100.57	107.77
1	C	61	THR	N-CA-C	6.42	118.36	111.36
1	A	157	TYR	N-CA-C	-6.40	103.55	112.45
1	A	691	GLN	N-CA-C	-6.40	105.30	113.23
1	B	707	ALA	N-CA-C	6.36	118.01	111.14
1	A	674	PHE	N-CA-C	6.32	119.63	110.28
1	A	981	LEU	CA-C-N	-6.31	113.19	119.56
1	A	981	LEU	C-N-CA	-6.31	113.19	119.56
1	A	84	SER	CA-C-N	-6.30	111.20	120.46
1	A	84	SER	C-N-CA	-6.30	111.20	120.46
1	B	731	TYR	N-CA-C	-6.28	104.88	112.54
1	C	467	GLU	N-CA-C	-6.26	104.54	111.36
1	B	61	THR	N-CA-C	6.23	118.15	111.36
1	A	1015	PHE	N-CA-C	6.20	119.01	111.82
1	A	248	GLU	N-CA-C	-6.18	104.80	112.90
1	C	77	ILE	N-CA-C	6.17	116.33	110.53
1	A	916	ASP	N-CA-C	6.13	119.15	110.50
1	A	932	SER	N-CA-C	-6.11	104.53	112.23
1	C	959	ILE	N-CA-C	-6.11	105.11	111.58
1	B	635	GLU	N-CA-C	6.10	118.01	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	763	GLN	N-CA-C	6.09	118.64	110.35
1	C	752	VAL	N-CA-C	6.05	116.22	110.53
1	A	405	ILE	N-CA-C	6.04	116.82	110.72
1	B	361	LYS	N-CA-C	5.99	117.81	111.28
1	C	899	VAL	CA-C-N	-5.99	113.64	119.87
1	C	899	VAL	C-N-CA	-5.99	113.64	119.87
1	B	652	ASP	N-CA-C	-5.97	104.60	112.24
1	A	179	GLY	N-CA-C	5.94	121.86	114.37
1	C	825	ALA	N-CA-C	-5.89	102.63	109.93
1	B	917	ASN	N-CA-C	-5.88	101.34	110.10
1	C	691	GLN	N-CA-C	-5.88	105.20	112.90
1	B	891	MET	N-CA-C	5.86	121.65	113.57
1	A	429	VAL	N-CA-C	5.82	116.56	110.62
1	B	64	THR	CA-C-N	-5.79	113.06	119.19
1	B	64	THR	C-N-CA	-5.79	113.06	119.19
1	A	763	GLN	N-CA-C	5.75	118.60	110.50
1	B	145	GLU	N-CA-C	-5.69	104.46	111.40
1	B	932	SER	N-CA-C	-5.68	105.84	112.89
1	B	162	ILE	N-CA-C	5.65	117.57	111.58
1	C	210	ASP	N-CA-C	5.64	117.11	111.07
1	B	179	GLY	N-CA-C	5.63	119.49	112.73
1	B	40	THR	CA-C-N	-5.61	114.60	120.38
1	B	40	THR	C-N-CA	-5.61	114.60	120.38
1	B	438	ASN	N-CA-C	-5.61	105.17	112.23
1	C	60	SER	N-CA-C	5.61	117.19	111.14
1	A	815	PHE	CA-C-N	-5.59	114.02	119.78
1	A	815	PHE	C-N-CA	-5.59	114.02	119.78
1	B	26	ILE	N-CA-C	-5.56	104.94	110.62
1	A	515	ASP	N-CA-C	-5.56	105.22	112.23
1	B	465	VAL	N-CA-C	-5.51	105.00	110.62
1	B	596	THR	N-CA-C	-5.50	106.52	113.18
1	A	473	ALA	N-CA-C	5.47	118.17	111.82
1	C	891	MET	CA-C-N	-5.46	114.19	119.87
1	C	891	MET	C-N-CA	-5.46	114.19	119.87
1	B	536	ILE	N-CA-C	5.45	116.18	110.62
1	B	285	SER	N-CA-C	5.45	117.91	110.55
1	B	251	ILE	N-CA-C	5.44	116.21	107.73
1	B	31	LEU	N-CA-C	5.43	116.53	109.64
1	A	746	THR	N-CA-C	5.39	116.96	111.14
1	B	756	PRO	N-CA-C	5.39	118.96	110.50
1	B	657	SER	N-CA-C	5.38	118.24	110.28
1	B	462	SER	N-CA-C	5.34	117.24	109.71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	986	ALA	N-CA-C	5.33	117.96	109.96
1	A	162	ILE	N-CA-C	5.32	115.53	110.53
1	A	889	TRP	N-CA-C	-5.30	106.49	113.12
1	C	716	SER	N-CA-C	5.30	117.97	111.82
1	B	367	ILE	CA-C-N	-5.29	116.09	120.33
1	B	367	ILE	C-N-CA	-5.29	116.09	120.33
1	C	891	MET	N-CA-C	5.29	121.50	109.81
1	B	434	ILE	CB-CA-C	-5.28	105.13	112.04
1	A	917	ASN	N-CA-C	-5.27	101.87	110.20
1	B	613	PHE	N-CA-C	5.26	116.70	111.07
1	C	560	LEU	N-CA-C	5.23	116.67	111.07
1	A	99	ASP	CA-C-N	-5.23	113.65	119.19
1	A	99	ASP	C-N-CA	-5.23	113.65	119.19
1	C	489	THR	N-CA-C	5.21	119.31	111.96
1	C	828	TYR	N-CA-C	5.20	117.84	110.50
1	A	826	PRO	CA-C-N	-5.13	116.15	123.08
1	A	826	PRO	C-N-CA	-5.13	116.15	123.08
1	C	575	LEU	CA-C-N	-5.12	114.44	119.92
1	C	575	LEU	C-N-CA	-5.12	114.44	119.92
1	C	1010	THR	N-CA-C	5.11	116.66	111.14
1	A	596	THR	N-CA-C	-5.10	105.80	112.23
1	C	843	GLN	N-CA-C	5.10	116.65	111.14
1	A	781	ASN	N-CA-C	5.10	116.84	111.28
1	C	536	ILE	N-CA-C	5.07	115.79	110.62
1	B	62	VAL	N-CA-C	5.07	116.17	111.81
1	B	326	ILE	CA-C-N	-5.06	113.71	118.97
1	B	326	ILE	C-N-CA	-5.06	113.71	118.97
1	A	899	VAL	CA-C-N	-5.05	114.87	119.82
1	A	899	VAL	C-N-CA	-5.05	114.87	119.82
1	C	986	ALA	N-CA-C	5.05	117.54	109.96
1	A	185	MET	N-CA-C	-5.04	101.54	109.25
1	A	969	ILE	CB-CA-C	-5.03	105.44	112.02
1	B	259	SER	N-CA-C	-5.02	101.13	109.46
1	A	602	SER	N-CA-C	5.01	116.56	111.14

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	7952	0	8115	92	0
1	B	7954	0	8113	113	0
1	C	7970	0	8146	117	0
2	C	25	19	19	1	0
All	All	23901	19	24393	318	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 7.

All (318) 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:585:ILE:HG12	1:C:608:ILE:HD13	1.54	0.88
1:C:572:ILE:HG13	1:C:613:PHE:CZ	2.19	0.77
1:B:706:LEU:HD23	1:B:709:VAL:HG22	1.66	0.77
1:B:674:PHE:CE2	1:B:830:SER:HB2	2.21	0.76
1:B:468:ILE:HG21	1:B:919:ILE:HD13	1.70	0.73
1:C:664:PRO:HG2	1:C:670:LEU:HD11	1.73	0.71
1:B:773:ARG:HH22	1:A:224:PRO:HD2	1.55	0.70
1:B:834:ILE:HA	1:B:837:ILE:HD12	1.74	0.69
1:B:697:LEU:HG	1:B:709:VAL:CG1	2.22	0.69
1:B:570:MET:HE1	1:B:671:THR:HG22	1.74	0.68
1:C:570:MET:HE2	1:C:625:PHE:CE1	2.30	0.67
1:C:677:TYR:HE2	1:C:810:LYS:HD3	1.60	0.65
1:C:590:THR:HA	1:C:593:LYS:HE3	1.78	0.65
1:C:732:TYR:HB3	1:C:792:ILE:HD13	1.79	0.65
1:C:570:MET:HE2	1:C:625:PHE:HE1	1.63	0.64
1:C:572:ILE:HG21	1:C:613:PHE:CE2	2.33	0.64
1:C:356:MET:HE1	1:C:414:VAL:HG11	1.80	0.63
1:B:706:LEU:CD2	1:B:709:VAL:HG22	2.28	0.63
1:B:706:LEU:HD23	1:B:709:VAL:CG2	2.28	0.62
1:C:292:ILE:N	1:C:292:ILE:HD12	2.13	0.62
1:C:139:VAL:O	1:C:327:PRO:HD2	2.00	0.62
1:C:46:VAL:HG22	1:C:129:VAL:HG22	1.81	0.62
1:B:242:GLN:HG2	1:B:756:PRO:HG2	1.81	0.62
1:B:675:GLU:HB3	1:B:819:LEU:HD11	1.81	0.61
1:B:401:LEU:HD12	1:B:472:PHE:HZ	1.64	0.61
1:B:556:VAL:HG11	1:B:907:ILE:HD11	1.83	0.61
1:C:585:ILE:HG12	1:C:608:ILE:HG21	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:421:LEU:HD22	1:B:501:ARG:HG3	1.81	0.61
1:A:80:ASP:HB3	1:A:812:PHE:HD1	1.65	0.60
1:A:714:ASP:HB3	1:A:717:PHE:HE1	1.65	0.60
1:B:585:ILE:HG12	1:B:608:ILE:HG21	1.83	0.60
1:C:569:ILE:HD11	1:C:628:LEU:HD11	1.83	0.60
1:B:531:ILE:HD12	1:B:1014:PHE:HB3	1.82	0.60
1:A:679:GLN:NE2	1:A:813:ASN:HB2	2.15	0.60
1:A:359:PHE:HB3	1:A:971:MET:HE3	1.84	0.60
1:A:614:THR:HG22	1:A:614:THR:O	2.02	0.60
1:A:70:ILE:O	1:A:73:VAL:HG23	2.03	0.59
1:A:677:TYR:HE2	1:A:810:LYS:HD3	1.67	0.59
1:B:720:TYR:HE1	1:B:802:ARG:HG2	1.68	0.59
1:B:421:LEU:HD21	1:B:429:VAL:HA	1.84	0.58
1:C:331:THR:HA	1:C:334:VAL:HG12	1.85	0.58
1:B:674:PHE:HE2	1:B:830:SER:HB2	1.67	0.58
1:A:158:VAL:HG22	1:A:162:ILE:HD12	1.85	0.58
1:B:570:MET:HE2	1:B:662:LEU:HD23	1.86	0.58
1:C:185:MET:HE2	1:C:269:VAL:HG12	1.85	0.58
1:B:697:LEU:HG	1:B:709:VAL:HG12	1.85	0.57
1:A:37:PRO:HG3	1:A:471:GLN:HG3	1.86	0.57
1:C:158:VAL:HG13	1:C:290:ILE:HD11	1.87	0.57
1:B:36:TYR:C	1:B:38:SER:H	2.12	0.57
1:C:172:VAL:HG13	1:C:292:ILE:HG23	1.87	0.57
1:A:179:GLY:HA2	1:A:278:SER:HB3	1.87	0.56
1:C:368:ILE:HG23	1:C:494:LEU:HB2	1.87	0.56
1:B:73:VAL:HG22	1:B:110:ARG:HD3	1.87	0.56
1:A:31:LEU:HD21	1:A:385:TYR:HA	1.86	0.56
1:A:729:MET:HE1	1:A:736:MET:HG2	1.87	0.56
1:A:940:ILE:HD12	1:A:1020:PHE:HB2	1.88	0.56
1:B:674:PHE:CZ	1:B:830:SER:HB2	2.40	0.56
1:B:67:GLU:HG3	1:B:90:LEU:HD11	1.86	0.56
1:A:248:GLU:HB3	1:A:264:LYS:HB3	1.88	0.56
1:C:248:GLU:HB3	1:C:264:LYS:HB3	1.88	0.55
1:B:486:VAL:HG13	1:B:490:LEU:HB3	1.88	0.55
1:B:329:ASP:HB3	1:B:332:ILE:HG12	1.88	0.55
1:A:561:VAL:HG13	1:A:562:PRO:HD2	1.89	0.55
1:B:697:LEU:HG	1:B:709:VAL:HG11	1.89	0.54
1:C:572:ILE:HG13	1:C:613:PHE:CE2	2.42	0.54
1:B:415:GLU:HA	1:B:418:ASP:OD2	2.08	0.54
1:B:722:LEU:HD21	1:B:798:LEU:HD22	1.89	0.54
1:C:328:TYR:HE2	1:C:330:THR:HG23	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:841:ALA:O	1:B:845:LEU:HB2	2.07	0.54
1:A:70:ILE:HB	1:A:79:MET:HE1	1.90	0.54
1:A:629:LYS:HB2	1:A:634:ARG:HG2	1.90	0.53
1:A:39:LEU:O	1:A:96:ILE:HD13	2.08	0.53
1:B:630:ASP:HB3	1:B:633:GLN:HG2	1.89	0.53
1:B:570:MET:CE	1:B:671:THR:HG22	2.38	0.53
1:A:845:LEU:HB3	1:A:849:TYR:HB2	1.90	0.53
1:C:575:LEU:HD13	1:C:584:THR:HG23	1.90	0.53
1:B:569:ILE:HG13	1:B:626:PHE:HB2	1.91	0.53
1:C:667:GLY:O	1:C:668:LEU:HD23	2.08	0.53
1:B:895:VAL:HG13	1:B:936:ALA:HB3	1.91	0.52
1:C:720:TYR:HE1	1:C:802:ARG:HG2	1.75	0.52
1:C:137:LEU:HD22	1:C:294:LEU:HB2	1.91	0.52
1:C:568:VAL:HB	1:C:662:LEU:HD22	1.92	0.52
1:C:614:THR:O	1:C:615:SER:C	2.50	0.52
1:C:615:SER:O	1:C:616:SER:HB3	2.10	0.52
1:A:884:ALA:HB2	1:C:15:VAL:HG21	1.90	0.52
1:C:601:ILE:HG12	1:C:628:LEU:CD2	2.40	0.52
1:C:757:MET:HB3	1:C:762:PHE:HD2	1.75	0.52
1:B:893:LEU:HA	1:B:896:ILE:HG12	1.92	0.51
1:C:715:THR:HG22	1:C:806:PRO:HG3	1.93	0.51
1:C:405:ILE:HG21	1:C:480:VAL:HG12	1.92	0.51
1:C:570:MET:SD	1:C:612:LEU:HD23	2.50	0.51
1:B:560:LEU:HD12	1:B:919:ILE:HG13	1.93	0.51
1:C:211:GLN:CD	1:C:250:ILE:HG23	2.34	0.51
1:A:402:ALA:HB2	1:A:476:LEU:HD23	1.93	0.51
1:C:162:ILE:HD11	1:C:318:PHE:HE1	1.74	0.51
1:C:353:LEU:HD22	1:C:366:THR:HB	1.93	0.51
1:C:897:THR:O	1:C:900:PRO:HD2	2.10	0.51
1:A:341:VAL:HG22	1:A:994:ARG:HE	1.76	0.51
1:A:690:GLN:HA	1:A:693:VAL:HG22	1.91	0.50
1:B:361:LYS:HA	1:B:510:ILE:HD13	1.92	0.50
1:C:158:VAL:CG1	1:C:290:ILE:HD11	2.41	0.50
1:B:219:LYS:HE3	1:B:234:SER:HB2	1.94	0.50
1:B:248:GLU:HB3	1:B:264:LYS:HB3	1.93	0.50
1:A:545:MET:O	1:A:549:ILE:HG13	2.12	0.50
1:C:217:THR:HG22	1:C:236:THR:HA	1.94	0.50
1:A:199:VAL:HG21	1:A:266:VAL:HG11	1.93	0.50
1:C:72:GLY:H	1:C:76:MET:HE1	1.76	0.50
1:C:745:ALA:O	1:C:767:ARG:HA	2.11	0.49
1:B:700:ALA:HB2	1:B:840:VAL:HG11	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:LEU:HD22	1:C:246:GLU:HB3	1.94	0.49
1:B:570:MET:HG2	1:B:625:PHE:CD2	2.47	0.49
1:A:81:SER:HB2	1:A:90:LEU:HD13	1.95	0.49
1:C:569:ILE:HD12	1:C:628:LEU:HD21	1.95	0.48
1:B:495:SER:O	1:B:499:LEU:HB2	2.13	0.48
1:A:5:PHE:HA	1:A:9:ARG:HH21	1.79	0.48
1:C:176:SER:O	1:C:290:ILE:HA	2.13	0.48
1:B:856:SER:O	1:B:859:GLN:HG2	2.13	0.48
1:C:176:SER:O	1:C:290:ILE:HG23	2.14	0.48
1:A:329:ASP:HB3	1:A:332:ILE:HG13	1.95	0.48
1:B:197:PHE:HB3	1:B:261:LEU:HD21	1.95	0.48
1:A:356:MET:HE1	1:A:370:MET:HG2	1.95	0.48
1:A:412:ILE:HD13	1:A:938:LEU:HD21	1.95	0.48
1:C:356:MET:HG3	1:C:369:PRO:HG2	1.96	0.48
1:C:686:TYR:CZ	1:C:809:VAL:HG13	2.49	0.48
1:C:954:ILE:HD11	1:C:1028:GLU:HG3	1.95	0.48
1:C:368:ILE:HB	1:C:369:PRO:HD3	1.96	0.48
1:B:219:LYS:HB2	1:B:222:GLU:HG3	1.95	0.48
1:C:185:MET:HE1	1:C:244:PRO:HG3	1.96	0.48
1:C:212:ASN:HB3	1:C:753:ASN:ND2	2.29	0.48
1:B:4:LYS:HG3	1:B:434:ILE:HD12	1.96	0.47
1:B:421:LEU:HD11	1:B:429:VAL:HG13	1.96	0.47
1:B:559:SER:O	1:B:918:ASP:HA	2.14	0.47
1:B:34:GLU:O	1:B:392:ASN:HA	2.13	0.47
1:C:452:CYS:O	1:C:456:ILE:HG12	2.14	0.47
1:A:842:LYS:HE3	1:A:842:LYS:HB2	1.74	0.47
1:C:223:GLU:HG3	1:C:224:PRO:HA	1.96	0.47
1:B:614:THR:C	1:B:616:SER:H	2.23	0.47
1:B:172:VAL:HG13	1:B:292:ILE:HG23	1.97	0.47
1:A:674:PHE:CZ	1:A:822:GLY:HA3	2.50	0.47
1:C:564:GLU:HG2	1:C:992:ALA:HB3	1.97	0.47
1:A:612:LEU:HB3	1:A:670:LEU:HD21	1.97	0.47
1:B:701:ARG:HG2	1:B:702:THR:HG23	1.96	0.47
1:A:557:PRO:HB2	1:A:829:THR:HG21	1.97	0.47
1:A:829:THR:HG21	1:A:916:ASP:HB3	1.96	0.47
1:C:531:ILE:HG22	1:C:1018:LEU:HD13	1.97	0.47
1:C:569:ILE:CD1	1:C:628:LEU:HD11	2.45	0.47
1:C:39:LEU:HD13	1:C:468:ILE:HG12	1.97	0.47
1:B:779:LEU:HD22	1:B:800:LEU:HG	1.97	0.47
1:C:474:LEU:HD23	1:C:474:LEU:HA	1.76	0.47
1:B:144:SER:HA	1:B:321:GLY:O	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:SER:HB2	1:A:443:PRO:HD3	1.98	0.46
1:A:561:VAL:CG1	1:A:562:PRO:HD2	2.46	0.46
1:B:353:LEU:HD23	1:B:356:MET:HE2	1.98	0.46
1:B:359:PHE:HE2	1:B:974:LEU:HD12	1.81	0.46
1:C:370:MET:O	1:C:374:PRO:HD2	2.15	0.46
1:C:568:VAL:HB	1:C:662:LEU:CD2	2.46	0.46
1:C:612:LEU:HG	2:C:1101:ZZ7:H12C	1.97	0.46
1:A:186:ARG:HH22	1:A:749:THR:HG22	1.80	0.46
1:A:679:GLN:HE22	1:A:813:ASN:HB2	1.81	0.46
1:C:205:ILE:HD11	1:C:745:ALA:HB2	1.98	0.46
1:B:369:PRO:O	1:B:373:VAL:HG23	2.15	0.46
1:A:598:MET:HE2	1:A:641:ILE:HG23	1.97	0.46
1:A:939:ILE:HG13	1:A:969:ILE:HD11	1.97	0.46
1:B:450:VAL:HG11	1:B:937:ILE:HD11	1.97	0.46
1:A:757:MET:HB3	1:A:762:PHE:HD2	1.81	0.46
1:C:322:LEU:HD12	1:C:322:LEU:HA	1.77	0.46
1:B:362:ASN:HD22	1:B:362:ASN:H	1.64	0.45
1:B:140:VAL:HG13	1:B:326:ILE:HG12	1.98	0.45
1:A:894:ALA:HB2	1:A:1023:LEU:HD12	1.98	0.45
1:C:530:TYR:HA	1:C:534:ARG:HH21	1.80	0.45
1:A:46:VAL:HG22	1:A:129:VAL:HG22	1.98	0.45
1:A:63:ALA:HB2	1:A:88:MET:HG3	1.98	0.45
1:A:897:THR:O	1:A:900:PRO:HD2	2.16	0.45
1:C:137:LEU:HD12	1:C:330:THR:OG1	2.16	0.45
1:C:212:ASN:HB3	1:C:753:ASN:HD21	1.82	0.45
1:C:585:ILE:HG12	1:C:608:ILE:CD1	2.36	0.45
1:A:476:LEU:HD13	1:A:927:LEU:HD13	1.98	0.45
1:A:402:ALA:HA	1:A:405:ILE:HG13	1.99	0.45
1:C:7:ILE:HG12	1:C:492:PRO:HB2	1.99	0.45
1:B:345:PHE:CD1	1:B:403:ILE:HD11	2.52	0.45
1:C:749:THR:HG22	1:C:765:ASN:HB3	1.98	0.45
1:B:710:ARG:HG3	1:B:821:GLN:HG3	1.99	0.45
1:B:986:ALA:HB1	1:B:994:ARG:HE	1.81	0.44
1:A:714:ASP:HB3	1:A:717:PHE:CE1	2.49	0.44
1:A:984:ILE:HD12	1:A:1002:ILE:HD12	1.99	0.44
1:B:757:MET:HG2	1:B:758:LEU:HG	1.98	0.44
1:A:396:LEU:HD23	1:A:399:LEU:HD12	1.98	0.44
1:A:783:TYR:HB3	1:A:791:MET:HE3	1.99	0.44
1:C:76:MET:HE2	1:C:76:MET:HB3	1.76	0.44
1:C:568:VAL:O	1:C:662:LEU:HD13	2.18	0.44
1:C:722:LEU:HD11	1:C:798:LEU:HB3	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:LYS:H	1:A:361:LYS:HG3	1.51	0.44
1:A:387:LEU:HD12	1:A:474:LEU:HD21	2.00	0.44
1:B:36:TYR:C	1:B:38:SER:N	2.74	0.44
1:B:697:LEU:CG	1:B:709:VAL:HG12	2.48	0.44
1:A:677:TYR:CE2	1:A:810:LYS:HD3	2.51	0.44
1:C:251:ILE:HG23	1:C:260:PHE:HB3	2.00	0.44
1:C:573:ILE:HG12	1:C:591:ILE:HD13	2.00	0.44
1:C:642:ILE:HD11	1:C:661:ASN:OD1	2.17	0.44
1:B:505:LYS:HA	1:B:506:PRO:HD3	1.88	0.43
1:B:680:ASN:ND2	1:B:684:LYS:HG2	2.33	0.43
1:C:328:TYR:CE2	1:C:330:THR:HG23	2.52	0.43
1:C:629:LYS:HE3	1:C:633:GLN:HB3	2.00	0.43
1:B:406:VAL:HG12	1:B:483:SER:HB3	1.99	0.43
1:B:696:MET:HG3	1:B:841:ALA:HA	1.99	0.43
1:B:968:PRO:O	1:B:972:THR:HG23	2.19	0.43
1:B:976:PHE:O	1:B:980:VAL:HG22	2.18	0.43
1:A:890:LEU:HA	1:A:890:LEU:HD12	1.86	0.43
1:B:394:LEU:HD13	1:B:394:LEU:HA	1.86	0.43
1:C:572:ILE:HB	1:C:658:TYR:HD2	1.83	0.43
1:C:664:PRO:CG	1:C:670:LEU:HD11	2.45	0.43
1:A:455:PHE:HB3	1:A:473:ALA:HB1	2.01	0.43
1:A:562:PRO:HG2	1:A:993:SER:HA	2.00	0.43
1:C:486:VAL:HG13	1:C:490:LEU:HB3	2.01	0.43
1:A:88:MET:HE3	1:A:88:MET:HB3	1.95	0.43
1:C:568:VAL:HG12	1:C:662:LEU:HD11	2.00	0.43
1:C:976:PHE:HD2	1:C:1005:MET:HE3	1.84	0.43
1:B:517:PHE:CZ	1:B:967:ARG:HA	2.54	0.43
1:A:956:GLU:HA	1:A:959:ILE:HG12	2.00	0.43
1:C:387:LEU:HD12	1:C:478:ILE:HD11	2.00	0.43
1:C:464:PHE:O	1:C:468:ILE:HG13	2.18	0.43
1:C:894:ALA:HB2	1:C:1023:LEU:HD12	2.00	0.43
1:B:682:SER:HB2	1:B:848:GLU:HG3	2.01	0.43
1:A:729:MET:HB3	1:A:729:MET:HE2	1.61	0.43
1:A:591:ILE:HA	1:A:649:TYR:OH	2.19	0.43
1:A:614:THR:O	1:A:614:THR:CG2	2.67	0.43
1:C:344:THR:HG21	1:C:400:VAL:HG13	2.00	0.43
1:C:569:ILE:CG1	1:C:628:LEU:HD11	2.49	0.43
1:B:679:GLN:HE21	1:B:815:PHE:HB2	1.84	0.42
1:A:76:MET:HE2	1:A:76:MET:HB3	1.94	0.42
1:A:561:VAL:HG13	1:A:920:TYR:HE2	1.84	0.42
1:A:696:MET:HE1	1:A:820:ILE:HG12	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:535:THR:CG2	1:C:1022:LEU:HD11	2.49	0.42
1:A:634:ARG:H	1:A:634:ARG:HG3	1.78	0.42
1:C:665:ILE:HG21	1:C:668:LEU:HD12	2.01	0.42
1:B:345:PHE:HB2	1:B:400:VAL:HG22	2.01	0.42
1:B:950:LYS:HB2	1:B:950:LYS:HE3	1.81	0.42
1:B:364:LYS:HD3	1:B:364:LYS:HA	1.82	0.42
1:B:535:THR:HA	1:B:1018:LEU:HD11	2.01	0.42
1:A:101:ASP:O	1:A:105:ILE:HG12	2.19	0.42
1:A:533:LYS:HE2	1:A:534:ARG:HH12	1.85	0.42
1:C:606:SER:O	1:C:607:LEU:HD23	2.19	0.42
1:B:430:LYS:O	1:B:434:ILE:HG12	2.20	0.42
1:A:281:ARG:HD3	1:A:286:ALA:HA	2.01	0.42
1:A:757:MET:HG2	1:A:758:LEU:HG	2.01	0.42
1:B:533:LYS:HA	1:B:533:LYS:HD3	1.88	0.42
1:B:689:ILE:HA	1:B:849:TYR:OH	2.19	0.42
1:A:160:LEU:HD22	1:A:760:LYS:HG3	2.02	0.42
1:A:573:ILE:HD13	1:A:591:ILE:HD12	2.01	0.42
1:A:769:LEU:HD12	1:C:225:VAL:HG22	2.01	0.42
1:B:447:ILE:HD13	1:B:934:LYS:HG3	2.00	0.42
1:B:499:LEU:HD12	1:B:499:LEU:HA	1.87	0.42
1:A:794:LEU:HB3	1:A:798:LEU:HD12	2.01	0.42
1:C:585:ILE:CG1	1:C:608:ILE:HG21	2.49	0.42
1:B:88:MET:HE3	1:B:88:MET:HB3	1.98	0.42
1:B:566:GLN:HB3	1:B:662:LEU:HD12	2.02	0.42
1:C:581:ILE:O	1:C:585:ILE:HG13	2.19	0.42
1:B:461:ILE:HD12	1:B:461:ILE:HA	1.96	0.42
1:B:950:LYS:HD2	1:B:952:LYS:HD3	2.02	0.42
1:A:545:MET:HE2	1:A:545:MET:HB3	1.89	0.42
1:B:720:TYR:CE1	1:B:802:ARG:HG2	2.52	0.41
1:B:889:TRP:O	1:B:892:PRO:HD2	2.20	0.41
1:B:303:THR:O	1:B:307:ILE:HG13	2.20	0.41
1:A:52:GLY:O	1:C:215:TYR:HB2	2.20	0.41
1:A:277:ASN:O	1:A:581:ILE:HG12	2.20	0.41
1:C:389:PHE:HE2	1:C:471:GLN:HA	1.85	0.41
1:B:77:ILE:HD12	1:B:77:ILE:HA	1.93	0.41
1:B:154:ILE:O	1:B:158:VAL:HG13	2.19	0.41
1:B:882:LEU:HB2	1:B:892:PRO:HB3	2.02	0.41
1:A:941:GLU:HA	1:A:944:MET:HE3	2.02	0.41
1:C:76:MET:HG3	1:C:92:VAL:HG12	2.01	0.41
1:C:461:ILE:HD13	1:C:867:GLY:HA3	2.02	0.41
1:B:940:ILE:O	1:B:944:MET:HG2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:LYS:HA	1:A:506:PRO:HD3	1.88	0.41
1:C:84:SER:O	1:C:85:PRO:C	2.62	0.41
1:B:401:LEU:HB3	1:B:927:LEU:HD22	2.02	0.41
1:A:34:GLU:O	1:A:392:ASN:HA	2.21	0.41
1:A:337:SER:O	1:A:341:VAL:HG23	2.21	0.41
1:B:143:TYR:CE1	1:B:323:LYS:HB2	2.56	0.41
1:B:401:LEU:HD23	1:B:401:LEU:HA	1.85	0.41
1:A:186:ARG:HE	1:A:186:ARG:HB3	1.57	0.41
1:C:825:ALA:O	1:C:826:PRO:C	2.64	0.41
1:A:46:VAL:HG21	1:A:70:ILE:HD11	2.02	0.41
1:A:242:GLN:HG3	1:A:756:PRO:HG2	2.03	0.41
1:C:34:GLU:O	1:C:392:ASN:HA	2.21	0.41
1:B:893:LEU:HD23	1:B:896:ILE:HD11	2.03	0.41
1:C:328:TYR:HE2	1:C:330:THR:CG2	2.34	0.41
1:B:692:ASP:HB3	1:B:845:LEU:HD23	2.03	0.41
1:A:79:MET:HB2	1:A:90:LEU:HD11	2.02	0.41
1:A:172:VAL:HG21	1:A:307:ILE:HD11	2.03	0.41
1:C:389:PHE:CE2	1:C:471:GLN:HA	2.56	0.41
1:C:645:LEU:HD23	1:C:648:GLN:HE21	1.85	0.41
1:C:786:SER:HB3	1:C:790:LYS:H	1.86	0.41
1:B:76:MET:HG3	1:B:92:VAL:HG12	2.03	0.41
1:B:261:LEU:HD12	1:B:261:LEU:HA	1.89	0.41
1:B:474:LEU:HD12	1:B:474:LEU:HA	1.68	0.41
1:B:897:THR:O	1:B:900:PRO:HD2	2.20	0.41
1:A:663:PRO:HG3	1:A:669:SER:O	2.21	0.41
1:C:983:MET:HE1	1:C:997:LEU:HD23	2.02	0.41
1:B:181:LYS:HA	1:B:273:ALA:HB1	2.02	0.40
1:B:262:ARG:HB2	1:B:264:LYS:HG2	2.02	0.40
1:C:677:TYR:CE2	1:C:810:LYS:HD3	2.49	0.40
1:C:67:GLU:HG3	1:C:79:MET:SD	2.61	0.40
1:C:349:LEU:O	1:C:353:LEU:HG	2.21	0.40
1:C:572:ILE:HG21	1:C:613:PHE:CD2	2.56	0.40
1:C:1001:LEU:HD12	1:C:1001:LEU:HA	1.96	0.40
1:B:188:TRP:HA	1:B:767:ARG:O	2.21	0.40
1:B:530:TYR:CE1	1:B:534:ARG:HG3	2.57	0.40
1:A:940:ILE:O	1:A:944:MET:HG3	2.21	0.40
1:C:730:LYS:HD2	1:C:730:LYS:HA	1.82	0.40
1:A:559:SER:HB3	1:A:829:THR:HB	2.02	0.40
1:C:191:PRO:HD2	1:C:772:PHE:CD2	2.56	0.40
1:C:771:ASP:N	1:C:771:ASP:OD1	2.54	0.40
1:B:140:VAL:HA	1:B:326:ILE:HA	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:405:ILE:HG21	1:B:480:VAL:HG22	2.02	0.40
1:B:408:ASP:HA	1:B:411:ILE:HB	2.03	0.40
1:A:334:VAL:O	1:A:338:ILE:HG12	2.21	0.40
1:C:591:ILE:HD11	1:C:653:ARG:HH22	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1030/1039 (99%)	1013 (98%)	16 (2%)	1 (0%)	48	76
1	B	1030/1039 (99%)	998 (97%)	32 (3%)	0	100	100
1	C	1030/1039 (99%)	1009 (98%)	21 (2%)	0	100	100
All	All	3090/3117 (99%)	3020 (98%)	69 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	289	PRO

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	871/883 (99%)	846 (97%)	25 (3%)	37	63
1	B	871/883 (99%)	843 (97%)	28 (3%)	34	61
1	C	874/883 (99%)	855 (98%)	19 (2%)	45	67
All	All	2616/2649 (99%)	2544 (97%)	72 (3%)	38	63

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	87	GLN
1	B	90	LEU
1	B	92	VAL
1	B	96	ILE
1	B	163	LEU
1	B	222	GLU
1	B	343	LYS
1	B	362	ASN
1	B	411	ILE
1	B	429	VAL
1	B	440	VAL
1	B	451	LEU
1	B	464	PHE
1	B	528	VAL
1	B	575	LEU
1	B	645	LEU
1	B	668	LEU
1	B	699	LEU
1	B	749	THR
1	B	779	LEU
1	B	782	ILE
1	B	834	ILE
1	B	860	GLU
1	B	909	LEU
1	B	987	THR
1	B	1002	ILE
1	B	1022	LEU
1	B	1023	LEU
1	A	43	THR
1	A	58	ILE
1	A	92	VAL
1	A	118	LEU
1	A	232	VAL
1	A	254	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	256	GLU
1	A	279	THR
1	A	373	VAL
1	A	467	GLU
1	A	468	ILE
1	A	500	THR
1	A	575	LEU
1	A	605	VAL
1	A	743	ILE
1	A	769	LEU
1	A	779	LEU
1	A	809	VAL
1	A	887	GLU
1	A	890	LEU
1	A	916	ASP
1	A	926	LEU
1	A	945	GLU
1	A	964	LEU
1	A	984	ILE
1	C	73	VAL
1	C	92	VAL
1	C	111	ILE
1	C	243	THR
1	C	294	LEU
1	C	307	ILE
1	C	318	PHE
1	C	451	LEU
1	C	535	THR
1	C	560	LEU
1	C	561	VAL
1	C	581	ILE
1	C	709	VAL
1	C	739	VAL
1	C	752	VAL
1	C	771	ASP
1	C	918	ASP
1	C	974	LEU
1	C	984	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (55) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	108	ASN
1	B	150	ASN
1	B	295	GLN
1	B	362	ASN
1	B	392	ASN
1	B	438	ASN
1	B	502	ASN
1	B	511	GLN
1	B	514	ASN
1	B	597	GLN
1	B	679	GLN
1	B	680	ASN
1	B	690	GLN
1	B	691	GLN
1	B	753	ASN
1	B	821	GLN
1	B	832	GLN
1	B	843	GLN
1	B	859	GLN
1	B	960	ASN
1	B	1027	ASN
1	A	87	GLN
1	A	202	ASN
1	A	255	ASN
1	A	277	ASN
1	A	293	ASN
1	A	295	GLN
1	A	320	GLN
1	A	325	GLN
1	A	422	HIS
1	A	426	ASN
1	A	594	ASN
1	A	633	GLN
1	A	737	GLN
1	A	795	ASN
1	C	45	GLN
1	C	245	GLN
1	C	293	ASN
1	C	308	ASN
1	C	312	GLN
1	C	325	GLN
1	C	362	ASN
1	C	471	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	511	GLN
1	C	514	ASN
1	C	566	GLN
1	C	574	ASN
1	C	582	HIS
1	C	654	ASN
1	C	691	GLN
1	C	694	ASN
1	C	708	ASN
1	C	753	ASN
1	C	843	GLN
1	C	917	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ZZ7	C	1101	-	20,26,26	1.69	3 (15%)	26,38,38	0.92	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ZZ7	C	1101	-	-	0/20/39/39	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1101	ZZ7	C6-S1	-4.12	1.77	1.85
2	C	1101	ZZ7	C5-C4	-3.93	1.48	1.52
2	C	1101	ZZ7	C13-S1	-3.55	1.76	1.84

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1101	ZZ7	C12-C6-S1	2.89	109.36	103.86

There are no chirality outliers.

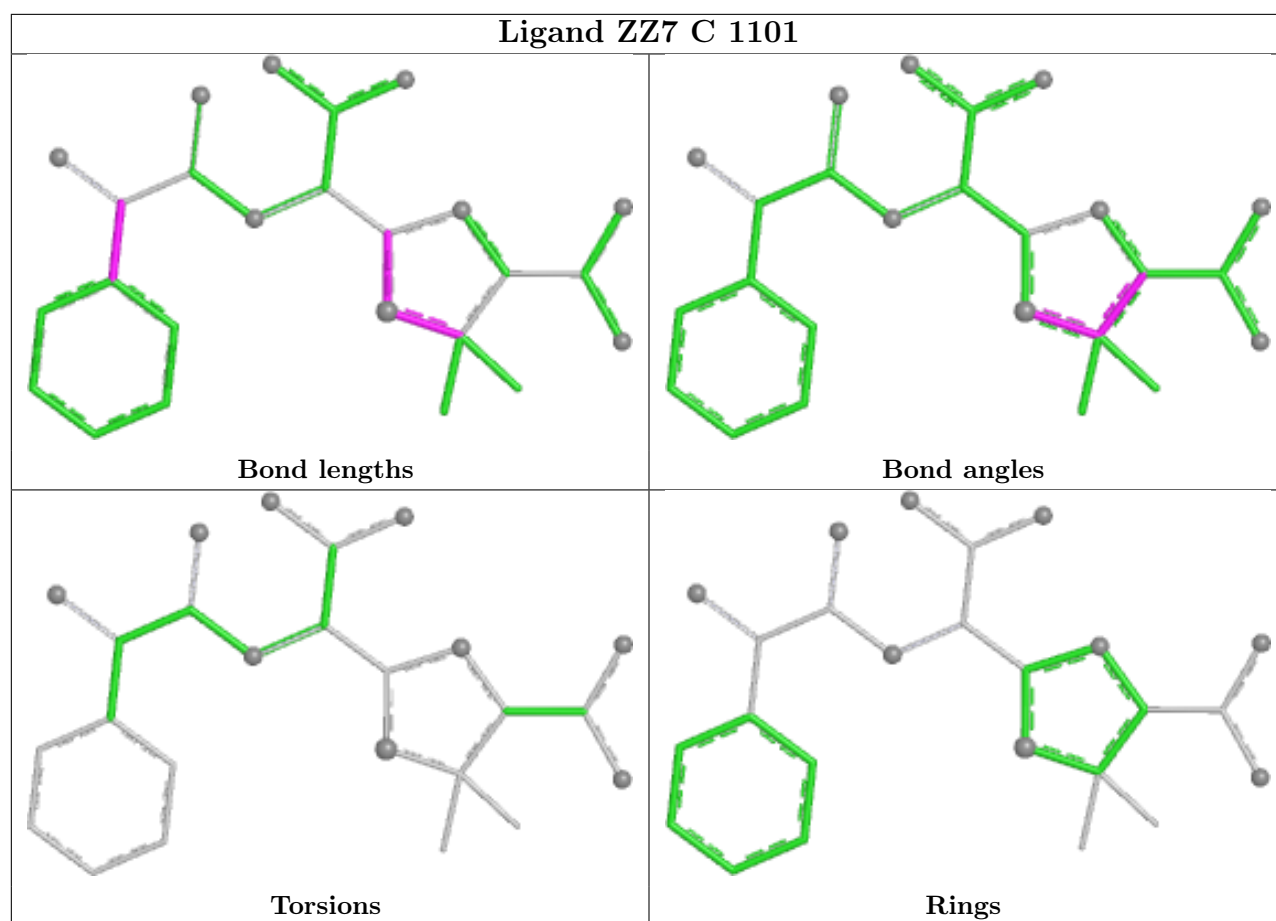
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1101	ZZ7	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

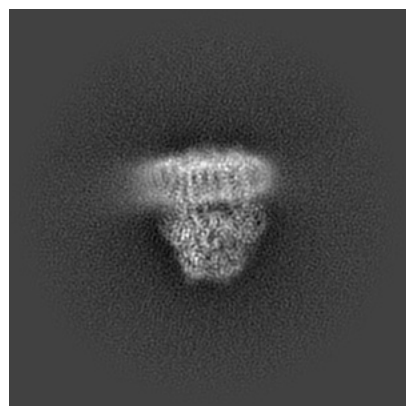
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40092. These allow visual inspection of the internal detail of the map and identification of artifacts.

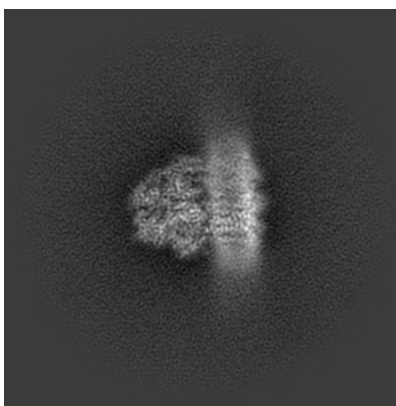
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

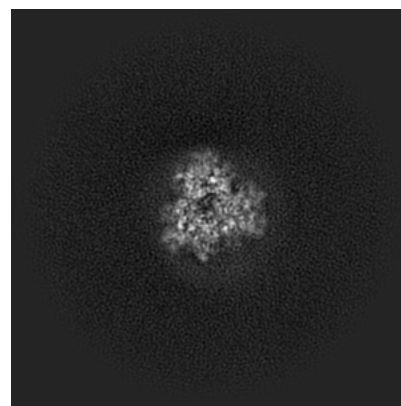
6.1.1 Primary map



X

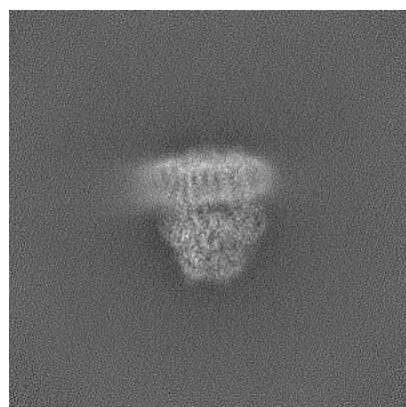


Y

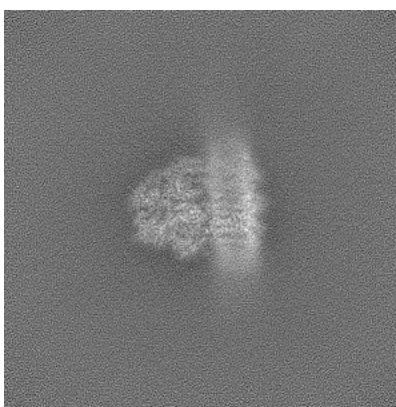


Z

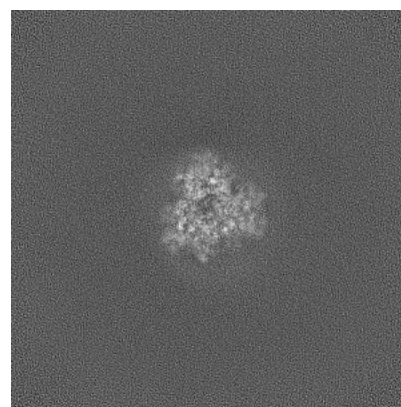
6.1.2 Raw map



X



Y

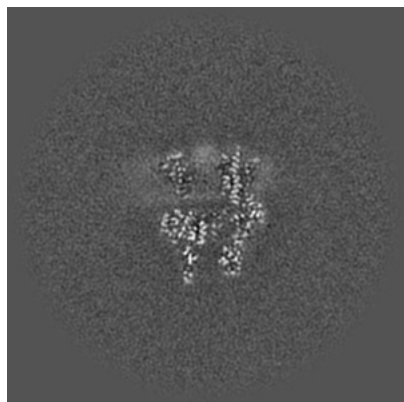


Z

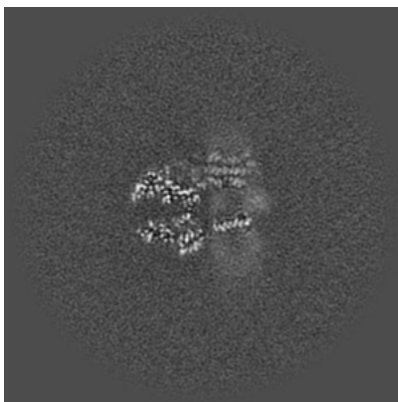
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

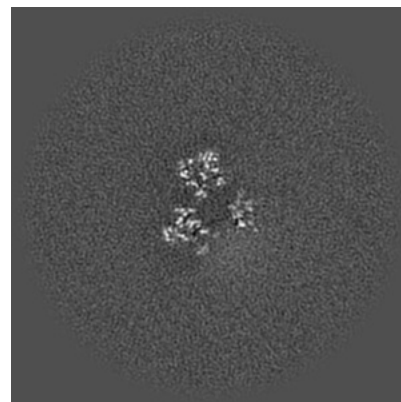
6.2.1 Primary map



X Index: 175

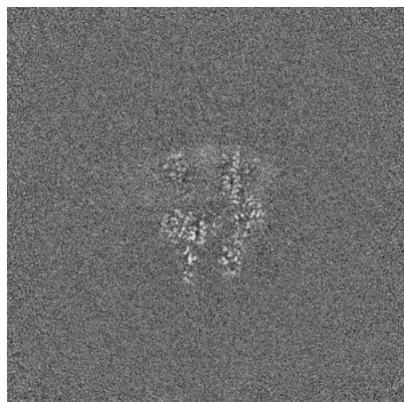


Y Index: 175

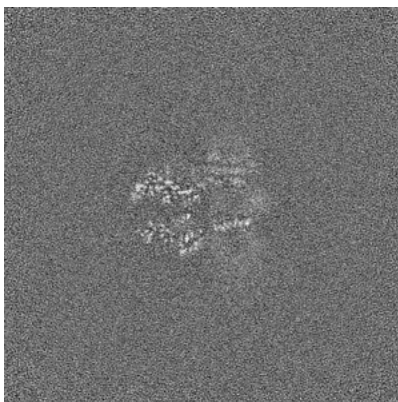


Z Index: 175

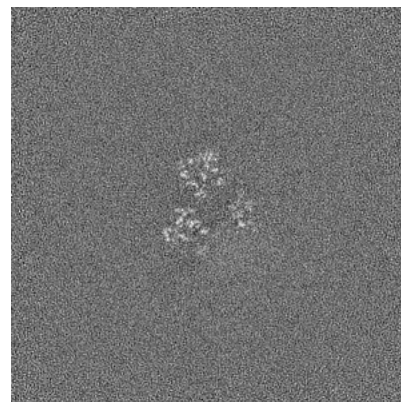
6.2.2 Raw map



X Index: 175



Y Index: 175

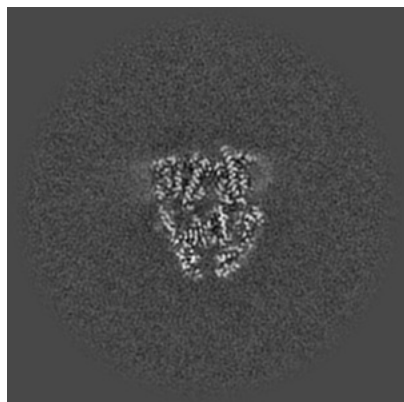


Z Index: 175

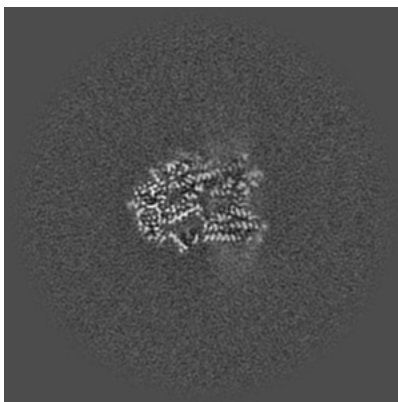
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

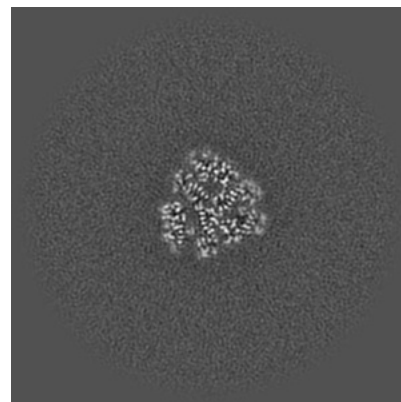
6.3.1 Primary map



X Index: 164

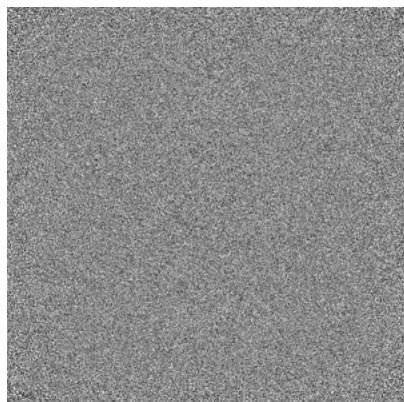


Y Index: 160

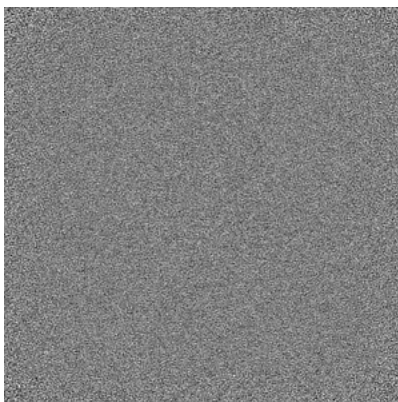


Z Index: 156

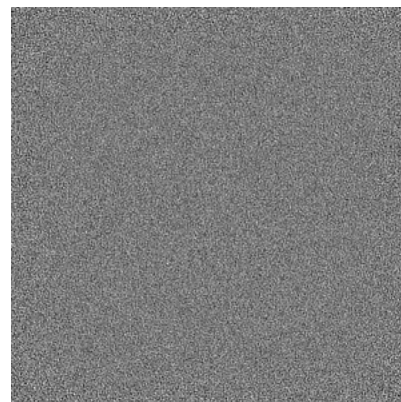
6.3.2 Raw map



X Index: 0



Y Index: 0

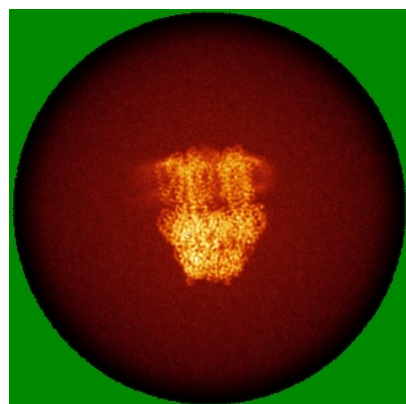


Z Index: 0

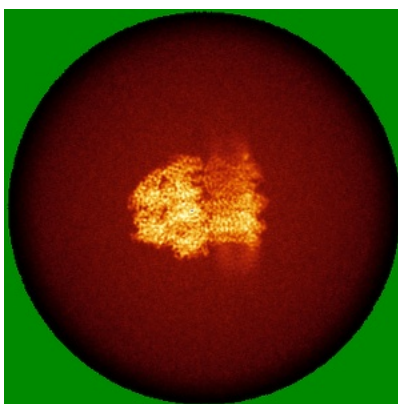
The images above show the largest variance slices of the map in three orthogonal directions.

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

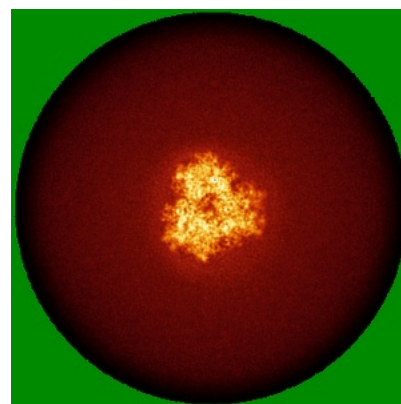
6.4.1 Primary map



X

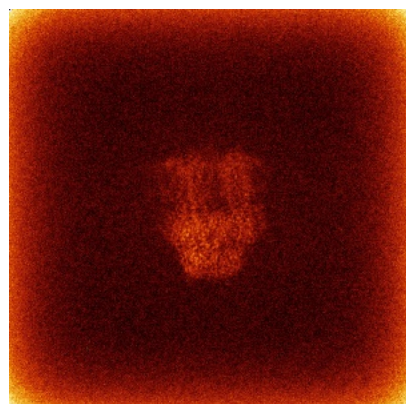


Y

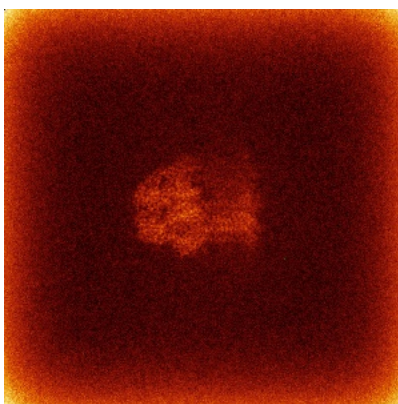


Z

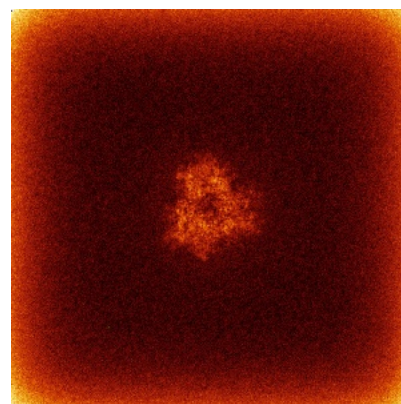
6.4.2 Raw map



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.

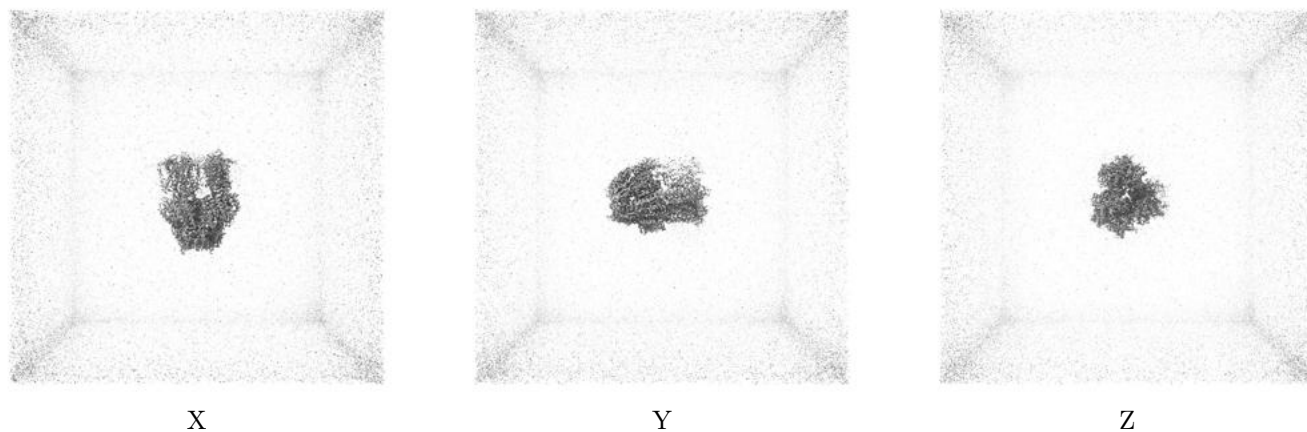
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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



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.

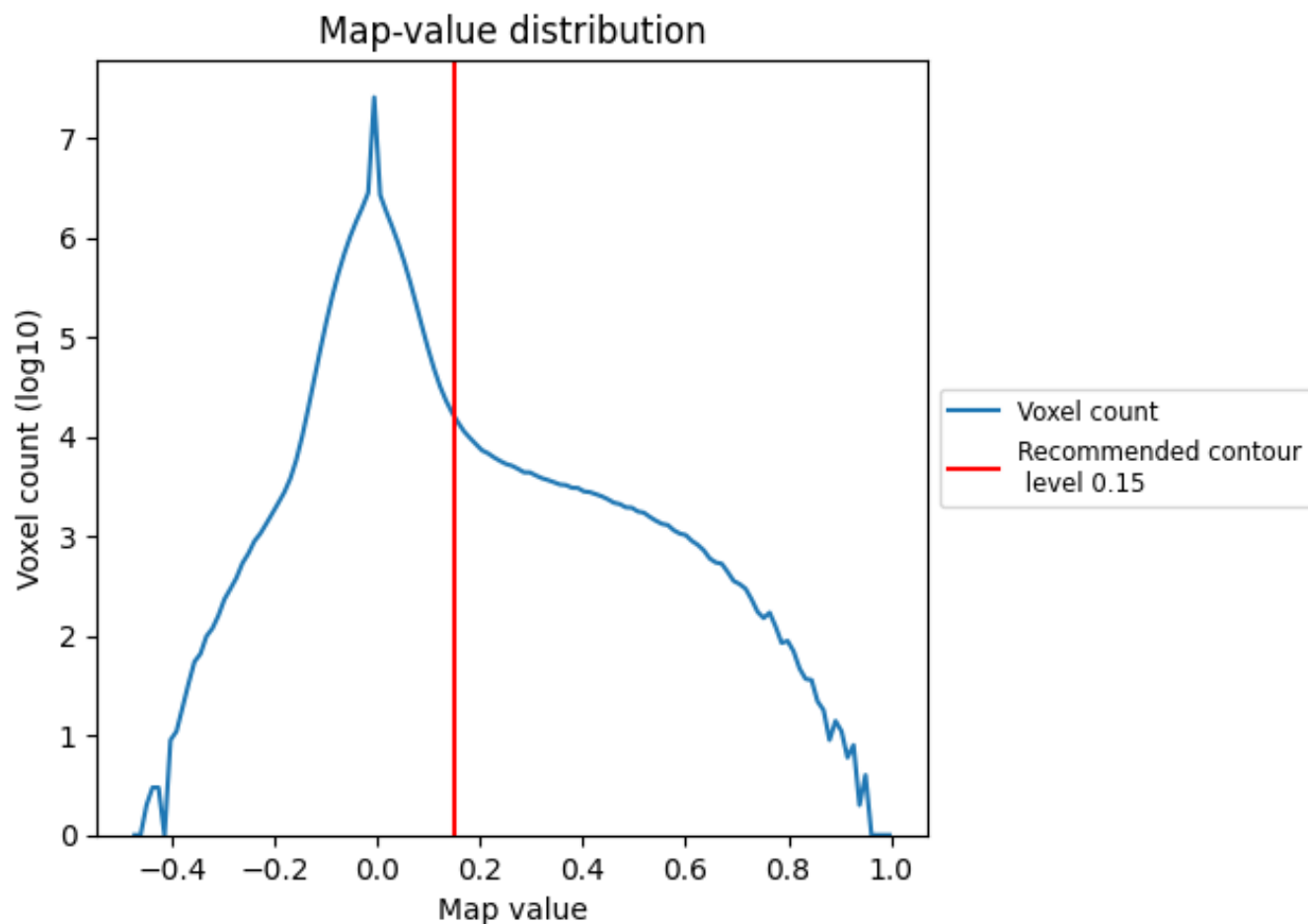
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

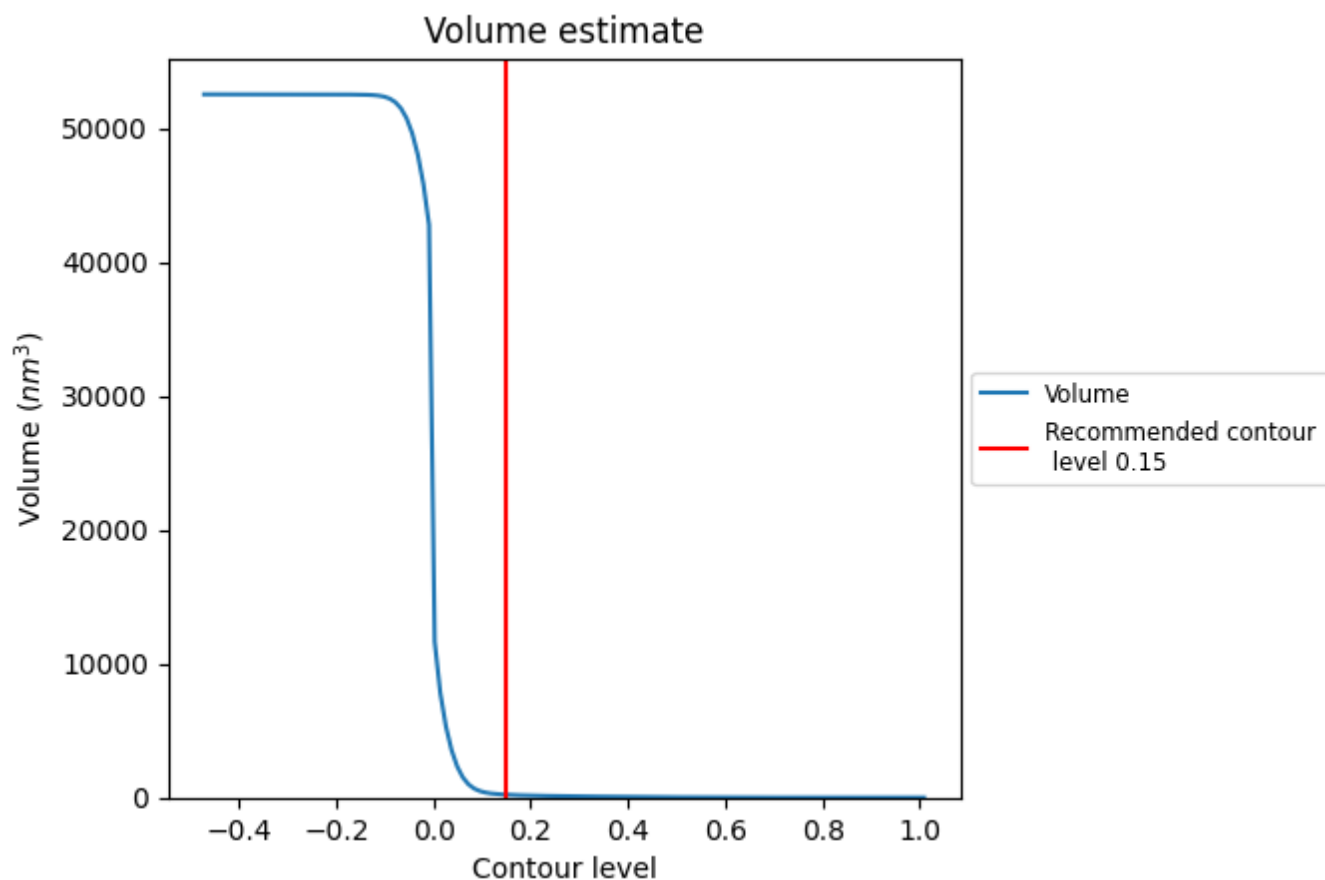
This section contains the results of statistical analysis of the map.

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.

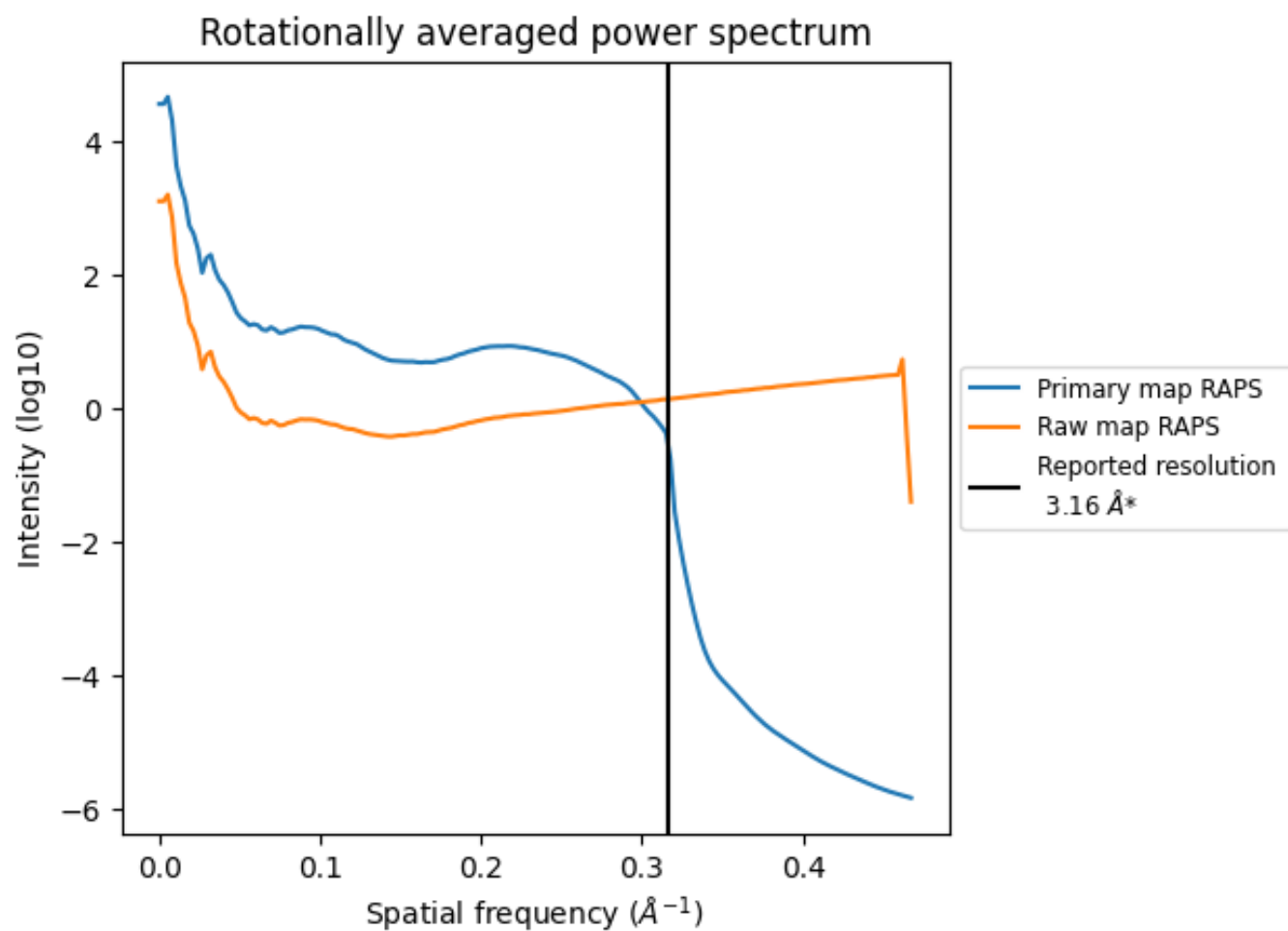
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 212 nm³; this corresponds to an approximate mass of 191 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 ⓘ

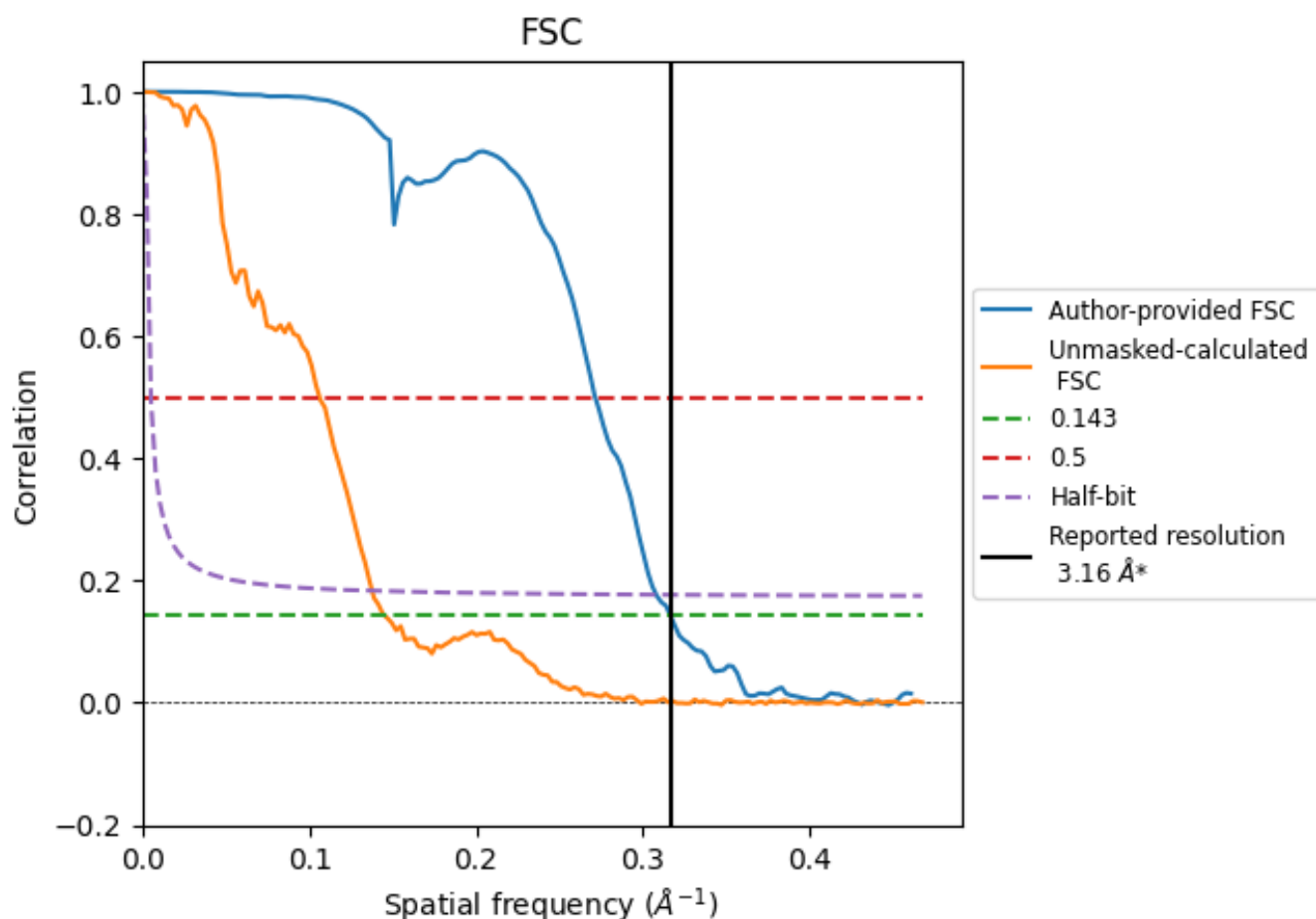


*Reported resolution corresponds to spatial frequency of 0.316 Å⁻¹

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 $0.316 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

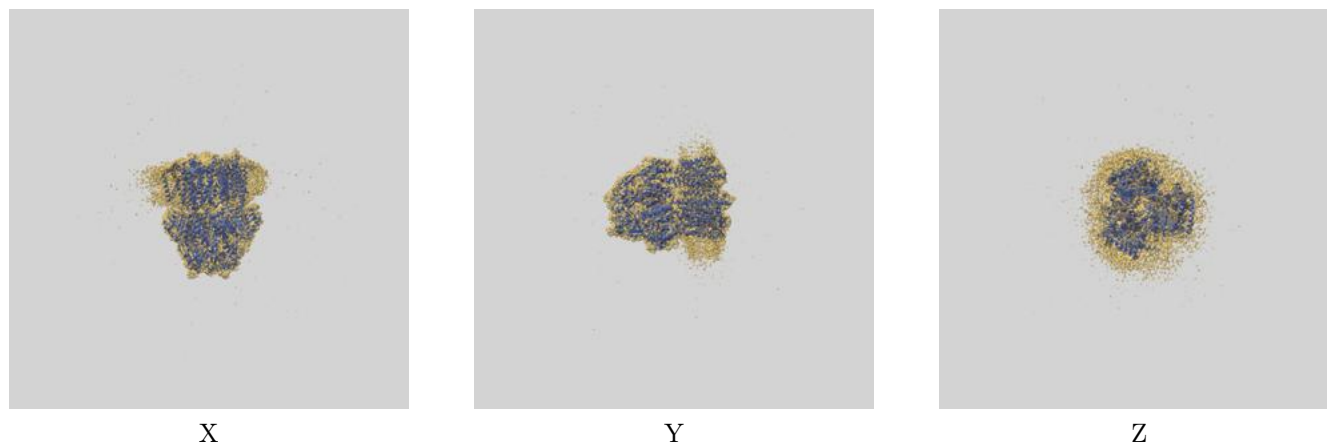
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.16	-	-
Author-provided FSC curve	3.16	3.68	3.25
Unmasked-calculated*	6.90	9.41	7.26

*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 6.90 differs from the reported value 3.16 by more than 10 %

9 Map-model fit [i](#)

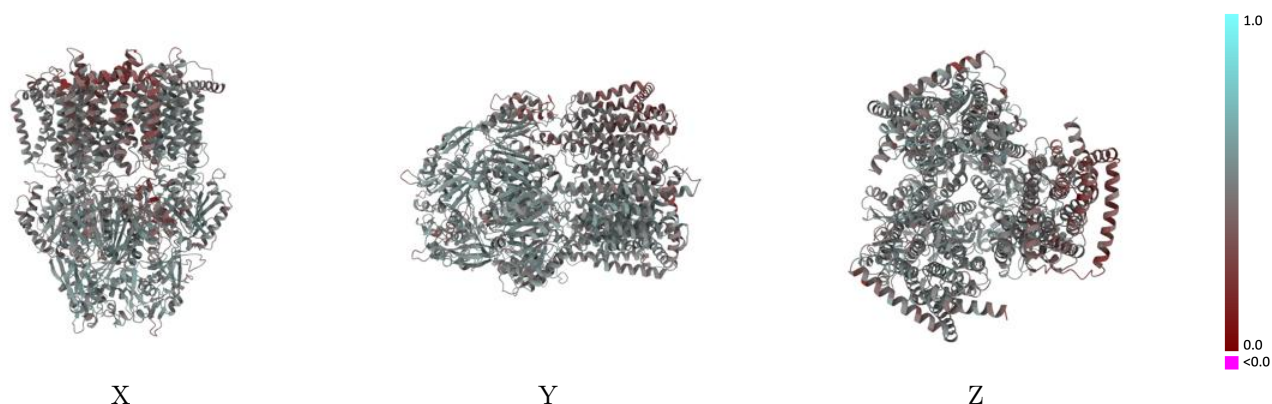
This section contains information regarding the fit between EMDB map EMD-40092 and PDB model 8GJK. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



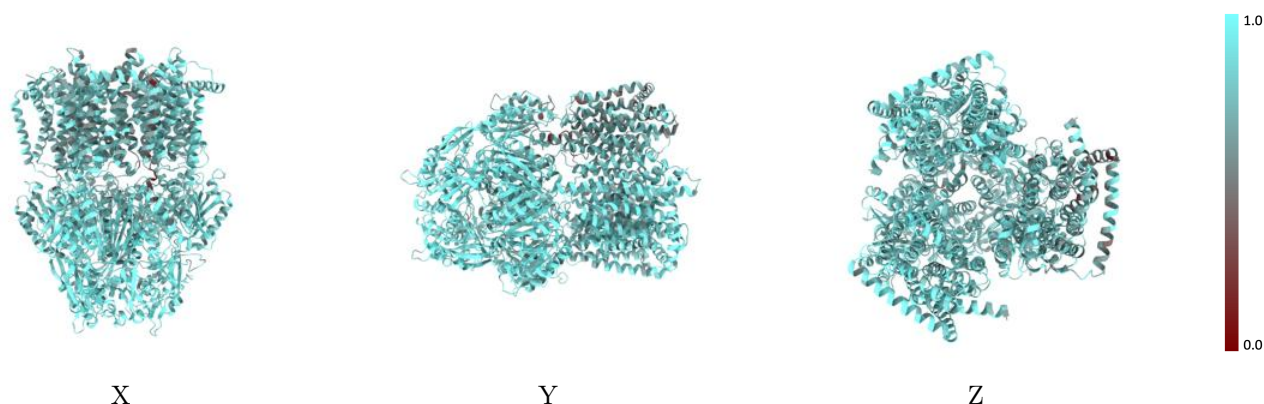
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



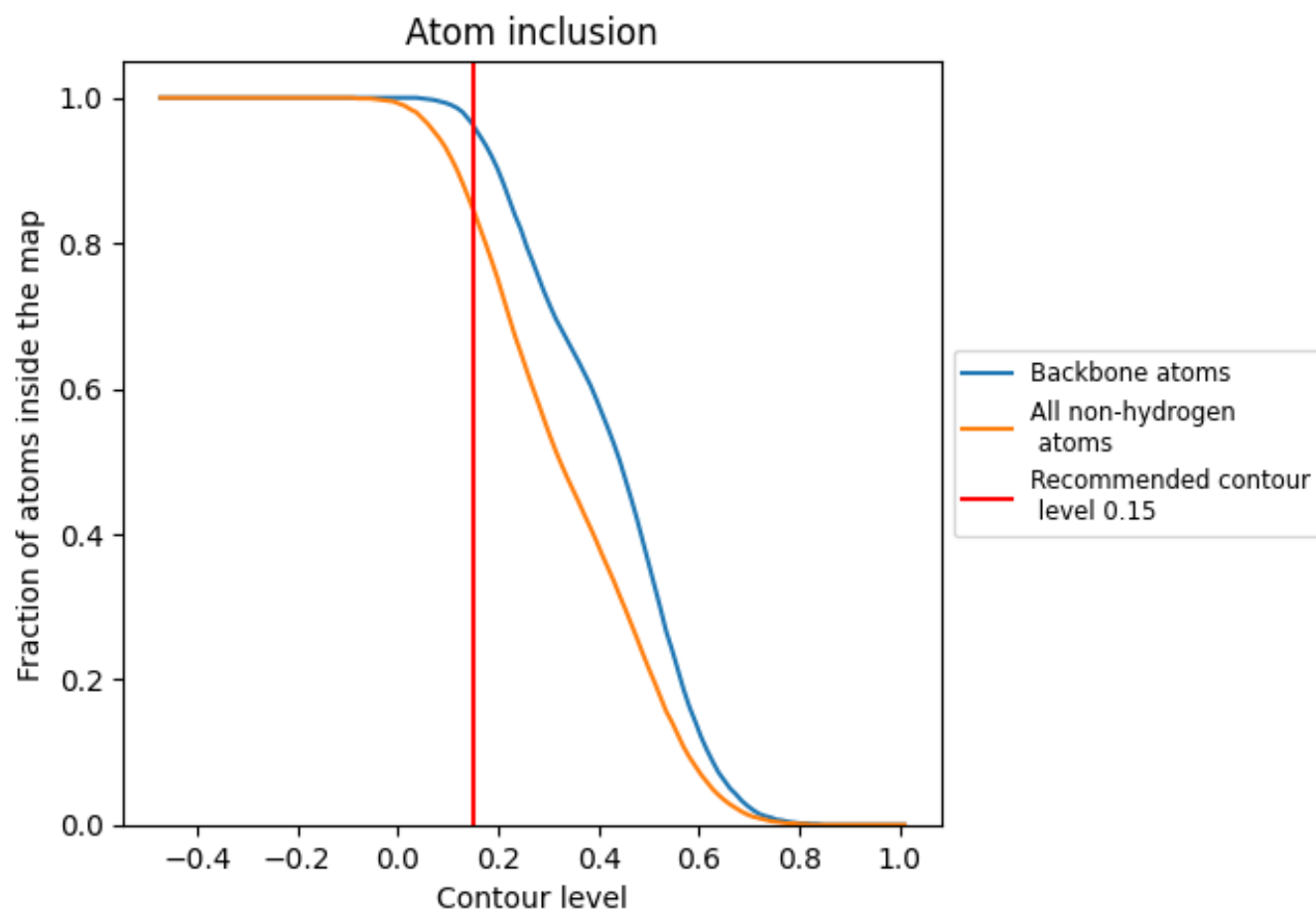
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 85% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8470	0.4870
A	0.8710	0.5040
B	0.8100	0.4610
C	0.8610	0.4950

