



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:54 PM UTC

PDB ID : 7VT0 / pdb_00007vt0
EMDB ID : EMD-32117
Title : Dimer structure of SORLA
Authors : Xi, Z.; Cang, W.; Chuang, L.
Deposited on : 2021-10-27
Resolution : 3.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

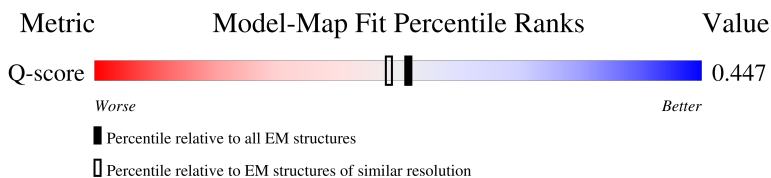
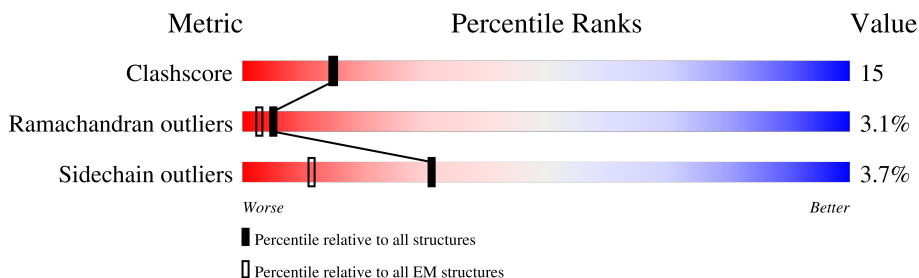
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	664	19% 71% 24% ..
1	B	664	18% 63% 29% 6% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10536 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 Sortilin-related receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	663	Total	C	N	O	S	0	0
			5268	3345	898	1003	22		
1	B	663	Total	C	N	O	S	0	0
			5268	3345	898	1003	22		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	751415	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.291	Depositor
Minimum map value	-3.495	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.394	Depositor
Map size (Å)	344.32, 344.32, 344.32	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.076, 1.076, 1.076	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	0.76	28/5405 (0.5%)	0.75	15/7328 (0.2%)
1	B	0.77	23/5405 (0.4%)	0.85	30/7328 (0.4%)
All	All	0.76	51/10810 (0.5%)	0.80	45/14656 (0.3%)

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	B	0	1

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	362	CYS	CA-C	-18.79	1.35	1.53
1	A	363	VAL	CA-C	-11.86	1.37	1.52
1	B	662	ASN	CA-C	-9.94	1.39	1.52
1	B	667	ASP	CA-C	-9.82	1.39	1.52
1	A	386	LEU	CA-C	-9.79	1.39	1.52
1	A	361	VAL	C-O	-7.91	1.14	1.24
1	A	363	VAL	N-CA	-7.81	1.36	1.46
1	A	364	SER	N-CA	-7.77	1.36	1.46
1	A	373	TYR	C-O	-7.77	1.14	1.24
1	A	366	SER	CA-C	-7.76	1.44	1.53
1	B	668	ARG	CA-C	-7.23	1.43	1.52
1	B	655	THR	CA-C	-7.17	1.43	1.53
1	B	636	SER	N-CA	7.14	1.55	1.46
1	A	662	ASN	CA-C	-7.04	1.36	1.52
1	B	545	HIS	CA-C	-6.84	1.44	1.53
1	B	633	TRP	CA-C	-6.74	1.44	1.52
1	B	629	ASP	N-CA	-6.55	1.36	1.46
1	A	429	ILE	N-CA	6.50	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	371	ASN	N-CA	-6.49	1.37	1.46
1	A	427	THR	CA-C	-6.48	1.45	1.52
1	A	389	VAL	CA-CB	-6.44	1.45	1.54
1	A	361	VAL	CA-C	-6.35	1.44	1.52
1	A	372	LEU	CA-C	-6.29	1.45	1.52
1	A	660	CYS	CA-C	6.25	1.60	1.52
1	A	654	ARG	CA-C	-6.17	1.44	1.52
1	B	625	CYS	CA-C	-6.10	1.45	1.53
1	B	545	HIS	C-O	-6.09	1.15	1.23
1	A	625	CYS	CA-C	-6.09	1.45	1.53
1	A	362	CYS	C-O	-6.06	1.17	1.23
1	A	427	THR	C-O	-6.04	1.16	1.23
1	B	466	ASN	CA-C	-6.01	1.44	1.52
1	B	634	SER	CA-CB	-6.01	1.44	1.53
1	B	545	HIS	CA-CB	-6.00	1.44	1.53
1	B	653	ARG	C-O	-6.00	1.16	1.24
1	A	349	TYR	C-O	-5.92	1.17	1.23
1	A	371	ASN	CA-C	-5.86	1.45	1.52
1	B	545	HIS	N-CA	-5.83	1.38	1.46
1	B	609	SER	N-CA	-5.71	1.38	1.46
1	B	630	TYR	CA-C	-5.59	1.46	1.53
1	B	544	ASP	C-N	-5.57	1.26	1.33
1	B	652	LYS	CA-C	-5.54	1.45	1.53
1	B	629	ASP	CA-CB	-5.48	1.46	1.54
1	B	657	HIS	CA-C	-5.47	1.45	1.52
1	A	387	GLU	CA-C	-5.45	1.46	1.53
1	A	372	LEU	C-O	-5.37	1.17	1.23
1	B	455	ALA	CA-CB	-5.36	1.45	1.53
1	A	386	LEU	C-O	-5.33	1.17	1.23
1	B	660	CYS	CA-C	5.25	1.59	1.52
1	A	372	LEU	N-CA	-5.12	1.39	1.46
1	A	629	ASP	C-O	-5.04	1.15	1.23
1	A	361	VAL	CA-CB	-5.02	1.47	1.54

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	365	HIS	N-CA-C	-20.07	83.42	111.52
1	B	629	ASP	N-CA-C	-11.32	100.19	114.56
1	B	668	ARG	CA-C-N	-11.28	105.74	119.84
1	B	668	ARG	C-N-CA	-11.28	105.74	119.84
1	B	666	PHE	N-CA-C	8.93	129.83	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	662	ASN	N-CA-C	-8.72	102.55	113.01
1	B	581	VAL	CB-CA-C	-8.68	98.31	110.12
1	A	362	CYS	N-CA-C	-8.65	92.13	107.28
1	B	592	GLU	O-C-N	8.62	133.84	122.73
1	A	370	THR	N-CA-C	-7.72	94.37	110.80
1	B	643	CYS	N-CA-C	7.60	121.37	107.99
1	B	609	SER	N-CA-C	-7.60	94.62	110.80
1	A	363	VAL	CB-CA-C	-7.21	99.47	111.29
1	A	427	THR	CB-CA-C	-7.18	101.75	110.94
1	B	637	ASP	N-CA-C	6.99	118.86	110.19
1	B	632	LEU	N-CA-C	6.98	119.75	107.61
1	B	581	VAL	N-CA-C	6.91	118.08	107.78
1	B	665	ASP	N-CA-C	6.74	119.05	107.93
1	B	661	PHE	CB-CA-C	-6.68	100.78	110.06
1	A	674	ASN	N-CA-C	-6.65	104.79	113.17
1	B	678	THR	N-CA-C	6.57	116.54	107.73
1	A	429	ILE	N-CA-C	6.57	118.17	108.45
1	B	455	ALA	CA-C-N	6.49	126.07	119.19
1	B	455	ALA	C-N-CA	6.49	126.07	119.19
1	B	515	ALA	CB-CA-C	-6.26	109.33	116.54
1	B	672	VAL	N-CA-C	-6.24	106.65	112.83
1	B	653	ARG	N-CA-CB	-6.07	101.04	110.57
1	A	366	SER	CB-CA-C	-6.02	103.39	111.88
1	B	668	ARG	N-CA-C	5.97	123.01	109.81
1	B	645	LEU	N-CA-C	5.94	123.45	110.80
1	B	653	ARG	N-CA-C	5.94	118.63	109.07
1	A	363	VAL	N-CA-C	5.83	121.46	109.34
1	B	124	SER	CB-CA-C	-5.74	109.98	116.63
1	A	624	PRO	CA-C-O	-5.63	115.13	121.43
1	B	652	LYS	CB-CA-C	-5.61	101.89	111.31
1	B	666	PHE	CB-CA-C	-5.60	99.27	110.42
1	A	654	ARG	CA-C-N	5.56	129.13	120.68
1	A	654	ARG	C-N-CA	5.56	129.13	120.68
1	A	484	LEU	CB-CA-C	-5.38	110.39	116.63
1	B	667	ASP	CB-CA-C	-5.36	99.76	110.42
1	B	668	ARG	CB-CA-C	-5.25	99.83	110.17
1	A	386	LEU	CB-CA-C	-5.24	101.56	109.99
1	A	362	CYS	CB-CA-C	-5.22	104.30	111.51
1	B	727	GLY	N-CA-C	-5.19	107.83	114.37
1	B	657	HIS	N-CA-C	5.01	118.55	112.23

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	674	ASN	Mainchain

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	5268	0	5066	141	0
1	B	5268	0	5064	168	0
All	All	10536	0	10130	309	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 15.

All (309) 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:386:LEU:HD23	1:A:389:VAL:HG22	1.51	0.91
1:A:364:SER:HB3	1:A:366:SER:HB2	1.54	0.90
1:B:665:ASP:O	1:B:666:PHE:HB3	1.77	0.84
1:B:636:SER:HA	1:B:642:GLU:HG2	1.60	0.83
1:A:363:VAL:O	1:A:364:SER:C	2.23	0.81
1:A:361:VAL:HG12	1:A:362:CYS:H	1.50	0.76
1:A:360:PHE:HB3	1:A:372:LEU:HD11	1.67	0.75
1:B:592:GLU:O	1:B:593:LYS:HB2	1.86	0.74
1:B:340:PHE:HE2	1:B:363:VAL:HG21	1.53	0.73
1:B:364:SER:HB2	1:B:370:THR:HA	1.69	0.72
1:B:644:LEU:HB3	1:B:739:GLY:HA2	1.72	0.72
1:B:689:LYS:HG2	1:B:700:VAL:HG22	1.71	0.71
1:B:459:THR:HB	1:B:463:GLU:HB2	1.73	0.70
1:A:268:ARG:HE	1:A:278:PHE:HE2	1.40	0.70
1:A:676:SER:O	1:A:677:CYS:C	2.33	0.70
1:B:484:LEU:HB2	1:B:491:ARG:HD2	1.73	0.70
1:A:346:ILE:HG23	1:A:364:SER:HA	1.74	0.70
1:B:723:ARG:HH12	1:B:725:THR:HB	1.57	0.70
1:A:294:LEU:HD21	1:A:311:LYS:HD2	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:396:GLY:HA3	1:B:400:ASP:HB2	1.74	0.69
1:B:641:ASN:C	1:B:643:CYS:H	2.01	0.68
1:A:510:VAL:HB	1:A:517:LYS:H	1.58	0.68
1:B:726:ARG:NH1	1:B:745:LEU:O	2.27	0.68
1:A:348:GLU:HG3	1:A:365:HIS:CD2	2.29	0.67
1:A:636:SER:HA	1:A:642:GLU:HG2	1.75	0.67
1:B:255:ILE:HG22	1:B:257:PRO:HD2	1.77	0.67
1:A:453:LEU:HD22	1:A:530:TRP:HE1	1.58	0.67
1:B:443:THR:HG21	1:B:447:GLY:HA2	1.77	0.66
1:B:713:PRO:HB3	1:B:719:GLY:HA2	1.77	0.66
1:B:601:GLY:O	1:B:611:LEU:HB2	1.96	0.66
1:B:682:TYR:CZ	1:B:728:TYR:HB3	2.31	0.65
1:B:386:LEU:HD22	1:B:389:VAL:HG23	1.78	0.65
1:B:358:GLN:NE2	1:B:375:SER:O	2.30	0.65
1:B:609:SER:O	1:B:610:TRP:C	2.36	0.65
1:B:605:GLU:O	1:B:606:ASN:C	2.40	0.64
1:B:725:THR:HG23	1:B:727:GLY:H	1.63	0.63
1:B:668:ARG:NH1	1:B:670:VAL:HG12	2.13	0.63
1:B:581:VAL:HG12	1:B:603:ASN:HA	1.79	0.63
1:B:726:ARG:HH21	1:B:728:TYR:HD2	1.46	0.63
1:B:211:LEU:HG	1:B:219:LEU:HD22	1.79	0.63
1:B:473:CYS:HA	1:B:511:GLY:O	1.98	0.62
1:B:490:ARG:HD3	1:B:491:ARG:HG3	1.81	0.62
1:B:469:LEU:C	1:B:471:GLN:H	2.08	0.62
1:B:661:PHE:C	1:B:663:GLY:N	2.56	0.62
1:B:638:GLU:O	1:B:639:ARG:C	2.42	0.62
1:A:661:PHE:C	1:A:663:GLY:H	2.07	0.62
1:B:607:VAL:HG13	1:B:608:HIS:CD2	2.35	0.62
1:A:364:SER:CB	1:A:366:SER:HB2	2.29	0.62
1:B:468:GLU:HG3	1:B:470:SER:H	1.65	0.62
1:B:304:ASP:OD1	1:B:305:LYS:NZ	2.31	0.61
1:A:371:ASN:O	1:A:372:LEU:C	2.39	0.61
1:A:248:VAL:HG22	1:A:266:ILE:HD11	1.82	0.61
1:A:468:GLU:OE1	1:A:469:LEU:N	2.33	0.61
1:A:358:GLN:NE2	1:A:375:SER:O	2.34	0.61
1:A:120:LEU:HD22	1:A:167:PHE:HD1	1.65	0.61
1:A:437:ASN:HB3	1:A:439:ARG:HH22	1.65	0.60
1:A:347:ASN:C	1:A:348:GLU:HG2	2.26	0.60
1:A:363:VAL:O	1:A:365:HIS:N	2.35	0.60
1:A:364:SER:O	1:A:365:HIS:HB3	2.01	0.59
1:A:456:PRO:HD3	1:A:475:LEU:HD12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:678:THR:O	1:B:679:ARG:C	2.44	0.59
1:A:364:SER:HB3	1:A:366:SER:CB	2.31	0.59
1:A:376:GLU:HG2	1:A:378:GLU:H	1.66	0.59
1:A:429:ILE:HG12	1:A:430:ASN:N	2.16	0.59
1:B:356:GLU:OE1	1:B:424:TYR:OH	2.20	0.59
1:B:661:PHE:C	1:B:663:GLY:H	2.10	0.59
1:A:267:GLU:HG2	1:A:275:SER:HB2	1.85	0.59
1:B:300:PHE:O	1:B:404:ARG:NH2	2.35	0.58
1:B:315:LEU:HD22	1:B:321:GLN:HA	1.85	0.58
1:B:526:ALA:HB2	1:B:633:TRP:HH2	1.68	0.58
1:B:633:TRP:CH2	1:B:635:PRO:HA	2.39	0.57
1:A:361:VAL:HG12	1:A:362:CYS:N	2.16	0.57
1:A:255:ILE:HG22	1:A:257:PRO:HD2	1.87	0.57
1:A:697:GLU:O	1:A:728:TYR:OH	2.23	0.57
1:B:190:THR:HB	1:B:197:LEU:HD23	1.86	0.57
1:A:346:ILE:O	1:A:347:ASN:ND2	2.38	0.57
1:B:170:SER:OG	1:B:173:ASP:O	2.21	0.57
1:A:378:GLU:OE2	1:A:380:LEU:N	2.37	0.56
1:B:641:ASN:O	1:B:643:CYS:N	2.37	0.56
1:A:329:SER:OG	1:A:335:MET:SD	2.58	0.56
1:B:668:ARG:CZ	1:B:670:VAL:HG12	2.34	0.56
1:B:390:LEU:HD12	1:B:429:ILE:HD13	1.86	0.56
1:B:468:GLU:C	1:B:470:SER:H	2.14	0.56
1:B:468:GLU:C	1:B:470:SER:N	2.62	0.56
1:A:443:THR:HG22	1:A:445:ASP:H	1.71	0.56
1:A:483:GLN:HG3	1:A:487:LEU:HD22	1.87	0.55
1:B:690:MET:SD	1:B:691:SER:N	2.79	0.55
1:A:538:HIS:HD2	1:A:553:ALA:HA	1.71	0.55
1:B:637:ASP:HB2	1:B:641:ASN:O	2.06	0.55
1:B:586:LEU:HD12	1:B:599:ILE:HG12	1.87	0.54
1:B:721:THR:HA	1:B:751:PRO:HA	1.89	0.54
1:A:371:ASN:OD1	1:A:384:LEU:HD11	2.06	0.54
1:B:189:ILE:HD11	1:B:237:PHE:HD2	1.73	0.54
1:B:673:SER:O	1:B:675:CYS:N	2.41	0.54
1:A:346:ILE:HG22	1:A:347:ASN:H	1.72	0.54
1:A:104:GLN:HE22	1:A:125:LEU:HD23	1.73	0.53
1:A:364:SER:O	1:A:365:HIS:C	2.44	0.53
1:B:444:PHE:CE2	1:B:638:GLU:HB2	2.43	0.53
1:B:360:PHE:HD2	1:B:372:LEU:HD21	1.74	0.53
1:A:266:ILE:O	1:A:277:VAL:HA	2.09	0.53
1:A:368:ASN:HB2	1:A:369:ARG:HH21	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:LEU:HD12	1:A:599:ILE:HG12	1.89	0.53
1:A:239:GLN:N	1:A:239:GLN:OE1	2.42	0.53
1:A:510:VAL:HG23	1:A:515:ALA:HA	1.90	0.53
1:B:116:VAL:HA	1:B:138:SER:O	2.08	0.53
1:B:641:ASN:C	1:B:643:CYS:N	2.67	0.53
1:B:436:GLU:OE1	1:B:436:GLU:N	2.39	0.52
1:B:436:GLU:O	1:B:513:ASN:HB2	2.09	0.52
1:A:387:GLU:O	1:A:388:ASN:C	2.52	0.52
1:B:693:ASP:HB3	1:B:696:LEU:HG	1.90	0.52
1:B:634:SER:O	1:B:642:GLU:HB3	2.10	0.52
1:B:657:HIS:O	1:B:658:ALA:C	2.51	0.51
1:A:370:THR:O	1:A:371:ASN:ND2	2.44	0.51
1:B:468:GLU:O	1:B:470:SER:N	2.43	0.51
1:B:584:TYR:HE2	1:B:602:SER:HG	1.58	0.51
1:A:367:ASN:O	1:A:368:ASN:HB2	2.10	0.51
1:B:324:VAL:HG11	1:B:401:THR:HG21	1.92	0.51
1:B:358:GLN:HG3	1:B:446:LYS:HE2	1.92	0.51
1:B:641:ASN:CG	1:B:643:CYS:HB2	2.36	0.51
1:A:340:PHE:CD2	1:A:363:VAL:HG11	2.46	0.51
1:A:363:VAL:HG21	1:A:373:TYR:CD2	2.46	0.51
1:A:376:GLU:OE1	1:A:381:LYS:HB3	2.10	0.51
1:B:469:LEU:C	1:B:471:GLN:N	2.69	0.51
1:A:478:ALA:HB2	1:A:490:ARG:HD3	1.93	0.51
1:B:637:ASP:HB2	1:B:641:ASN:C	2.36	0.51
1:B:723:ARG:HH11	1:B:747:GLY:HA2	1.76	0.51
1:A:179:PHE:HB2	1:A:188:TRP:HB2	1.91	0.50
1:B:96:VAL:HG11	1:B:145:PHE:HB2	1.93	0.50
1:B:531:ARG:HG2	1:B:532:GLU:H	1.76	0.50
1:B:607:VAL:HG13	1:B:608:HIS:CG	2.46	0.50
1:B:643:CYS:C	1:B:644:LEU:HG	2.37	0.50
1:A:674:ASN:OD1	1:A:736:CYS:HA	2.11	0.50
1:A:363:VAL:CG2	1:A:373:TYR:HD2	2.25	0.50
1:A:313:VAL:HG12	1:A:314:HIS:H	1.77	0.50
1:B:239:GLN:N	1:B:239:GLN:OE1	2.45	0.50
1:B:630:TYR:O	1:B:631:LYS:HB3	2.11	0.50
1:A:277:VAL:HG13	1:A:293:ILE:HB	1.94	0.50
1:B:473:CYS:O	1:B:474:SER:C	2.52	0.50
1:A:626:THR:HG22	1:A:627:GLU:N	2.27	0.49
1:A:550:THR:HG23	1:A:586:LEU:HD21	1.92	0.49
1:A:102:HIS:HB3	1:A:122:ARG:O	2.12	0.49
1:A:432:SER:OG	1:A:436:GLU:OE2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:LYS:O	1:B:247:HIS:N	2.40	0.49
1:A:360:PHE:HB3	1:A:372:LEU:CD1	2.41	0.49
1:A:346:ILE:HG22	1:A:347:ASN:N	2.27	0.49
1:A:260:LYS:O	1:A:263:THR:OG1	2.23	0.48
1:B:634:SER:O	1:B:635:PRO:C	2.55	0.48
1:B:333:LYS:HB3	1:B:334:PRO:HD2	1.95	0.48
1:B:686:PHE:C	1:B:688:PHE:H	2.20	0.48
1:B:187:LEU:HG	1:B:202:ILE:HD13	1.96	0.48
1:B:726:ARG:NH2	1:B:728:TYR:HD2	2.10	0.48
1:A:461:TYR:HB3	1:A:532:GLU:OE1	2.14	0.48
1:B:302:LEU:HD13	1:B:307:MET:HE3	1.95	0.48
1:A:124:SER:O	1:A:125:LEU:HB3	2.13	0.48
1:B:655:THR:O	1:B:656:PRO:C	2.56	0.48
1:B:223:ASP:N	1:B:223:ASP:OD1	2.46	0.48
1:B:302:LEU:HD11	1:B:332:ARG:HH12	1.79	0.48
1:B:635:PRO:O	1:B:642:GLU:HB3	2.13	0.48
1:A:545:HIS:CE1	1:A:593:LYS:HG2	2.49	0.48
1:B:487:LEU:HG	1:B:488:GLN:H	1.78	0.48
1:B:626:THR:HG22	1:B:627:GLU:N	2.29	0.48
1:B:386:LEU:HD12	1:B:450:TRP:CD2	2.49	0.48
1:B:677:CYS:HB3	1:B:736:CYS:HB3	1.78	0.48
1:A:133:SER:HG	1:A:164:ILE:H	1.58	0.47
1:B:386:LEU:HD12	1:B:450:TRP:CG	2.50	0.47
1:B:638:GLU:C	1:B:640:GLY:N	2.69	0.47
1:B:468:GLU:HG3	1:B:469:LEU:N	2.29	0.47
1:B:688:PHE:CZ	1:B:701:PRO:HB3	2.49	0.47
1:A:278:PHE:CE1	1:A:292:VAL:HG22	2.49	0.47
1:B:311:LYS:HD3	1:B:327:TRP:CE2	2.49	0.47
1:B:376:GLU:N	1:B:376:GLU:OE2	2.47	0.47
1:B:726:ARG:HH12	1:B:746:GLU:HA	1.78	0.47
1:A:678:THR:OG1	1:A:679:ARG:N	2.46	0.47
1:B:667:ASP:OD1	1:B:668:ARG:N	2.48	0.47
1:A:192:ASP:N	1:A:192:ASP:OD1	2.48	0.47
1:A:348:GLU:C	1:A:349:TYR:CD1	2.93	0.47
1:A:413:ASP:HB3	1:A:479:GLN:HG2	1.97	0.47
1:A:458:PHE:HE1	1:A:465:ILE:HG13	1.79	0.47
1:A:106:VAL:HG23	1:A:120:LEU:HB3	1.96	0.47
1:A:479:GLN:HG3	1:A:480:ARG:H	1.80	0.47
1:B:472:GLY:O	1:B:512:LYS:HG3	2.14	0.47
1:A:173:ASP:OD1	1:A:175:LYS:NZ	2.43	0.47
1:A:552:ILE:HG21	1:A:583:VAL:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:LYS:HB3	1:A:664:GLU:HG2	1.97	0.47
1:B:731:ILE:HD12	1:B:731:ILE:H	1.79	0.47
1:A:91:LYS:NZ	1:A:619:ASP:HB2	2.30	0.46
1:B:260:LYS:O	1:B:263:THR:OG1	2.26	0.46
1:B:220:LEU:HG	1:B:253:TRP:CZ2	2.50	0.46
1:B:682:TYR:CE1	1:B:728:TYR:HB3	2.50	0.46
1:A:626:THR:HG22	1:A:627:GLU:H	1.80	0.46
1:A:676:SER:O	1:A:678:THR:N	2.47	0.46
1:B:277:VAL:HG13	1:B:293:ILE:HB	1.96	0.46
1:A:187:LEU:HG	1:A:202:ILE:HD13	1.98	0.46
1:A:333:LYS:HB3	1:A:334:PRO:HD2	1.98	0.46
1:A:582:PHE:CE1	1:A:605:GLU:HG3	2.50	0.46
1:A:443:THR:HG21	1:A:447:GLY:N	2.31	0.46
1:A:313:VAL:HG12	1:A:314:HIS:CD2	2.50	0.46
1:A:360:PHE:C	1:A:361:VAL:O	2.56	0.46
1:B:644:LEU:CB	1:B:739:GLY:HA2	2.44	0.46
1:B:713:PRO:HA	1:B:718:VAL:HG23	1.97	0.46
1:B:550:THR:HG23	1:B:586:LEU:HD21	1.98	0.46
1:B:473:CYS:O	1:B:510:VAL:HG12	2.16	0.45
1:B:688:PHE:CG	1:B:701:PRO:HA	2.51	0.45
1:B:156:LEU:HA	1:B:159:ARG:HH22	1.81	0.45
1:B:469:LEU:O	1:B:471:GLN:N	2.50	0.45
1:A:203:PRO:HD2	1:A:241:TRP:CD1	2.51	0.45
1:A:364:SER:C	1:A:366:SER:N	2.56	0.45
1:B:212:HIS:HB3	1:B:215:ALA:O	2.16	0.45
1:B:324:VAL:HG23	1:B:349:TYR:HE2	1.81	0.45
1:A:461:TYR:HB2	1:A:535:PRO:HB3	1.98	0.45
1:A:367:ASN:O	1:A:368:ASN:CB	2.64	0.45
1:A:691:SER:OG	1:A:693:ASP:O	2.35	0.45
1:B:712:PRO:O	1:B:714:VAL:N	2.45	0.45
1:A:229:LYS:HB2	1:A:247:HIS:HA	1.99	0.45
1:B:176:ARG:NH1	1:B:216:SER:OG	2.50	0.45
1:B:451:GLU:OE1	1:B:638:GLU:HG3	2.17	0.45
1:B:647:HIS:HB2	1:B:648:LYS:H	1.48	0.45
1:B:684:CYS:HB3	1:B:699:CYS:HB3	1.50	0.45
1:A:363:VAL:HB	1:A:364:SER:H	0.99	0.44
1:A:439:ARG:HA	1:A:476:HIS:CE1	2.51	0.44
1:B:380:LEU:O	1:B:380:LEU:HG	2.17	0.44
1:A:178:ILE:HG12	1:A:189:ILE:HG22	1.99	0.44
1:A:433:MET:HG3	1:A:434:ASN:OD1	2.17	0.44
1:A:387:GLU:O	1:A:389:VAL:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:657:HIS:C	1:B:658:ALA:O	2.61	0.44
1:B:230:GLN:CD	1:B:243:MET:HE1	2.43	0.44
1:B:313:VAL:HG11	1:B:325:GLN:HG3	2.00	0.44
1:A:443:THR:HG21	1:A:447:GLY:H	1.82	0.44
1:B:443:THR:HG23	1:B:450:TRP:CE3	2.53	0.44
1:A:531:ARG:HG2	1:A:532:GLU:H	1.83	0.44
1:B:300:PHE:H	1:B:404:ARG:HH21	1.64	0.44
1:B:439:ARG:HG2	1:B:439:ARG:HH11	1.82	0.44
1:A:190:THR:HB	1:A:197:LEU:HD23	1.99	0.43
1:A:122:ARG:HH21	1:A:125:LEU:HD22	1.82	0.43
1:B:392:TYR:HB2	1:B:481:LEU:HD21	2.00	0.43
1:B:682:TYR:HE1	1:B:729:ARG:C	2.27	0.43
1:B:566:ASN:HB3	1:B:569:GLU:OE1	2.19	0.43
1:A:258:TYR:CZ	1:A:305:LYS:HE3	2.54	0.43
1:A:688:PHE:HB3	1:A:699:CYS:HB3	2.00	0.43
1:B:519:ASN:OD1	1:B:535:PRO:HA	2.19	0.43
1:A:151:LYS:HE2	1:A:197:LEU:HD12	2.01	0.43
1:B:348:GLU:HG3	1:B:365:HIS:HB2	2.00	0.43
1:A:386:LEU:HD21	1:A:428:LEU:HD11	2.01	0.43
1:A:389:VAL:HG12	1:A:390:LEU:H	1.84	0.43
1:A:517:LYS:HE2	1:A:517:LYS:HA	2.01	0.43
1:A:537:PRO:HB2	1:A:554:GLN:HE21	1.83	0.43
1:A:505:ILE:HG23	1:A:522:ILE:HG12	2.00	0.43
1:A:685:ASP:OD2	1:A:729:ARG:NH2	2.42	0.43
1:B:266:ILE:HG22	1:B:278:PHE:HB2	2.01	0.43
1:B:559:ASN:OD1	1:B:559:ASN:N	2.52	0.43
1:A:255:ILE:HD12	1:A:255:ILE:H	1.84	0.43
1:A:369:ARG:HB3	1:A:370:THR:H	1.52	0.42
1:A:388:ASN:ND2	1:A:388:ASN:H	2.17	0.42
1:B:623:VAL:O	1:B:624:PRO:C	2.62	0.42
1:B:627:GLU:H	1:B:627:GLU:CD	2.27	0.42
1:A:423:VAL:HA	1:A:443:THR:O	2.20	0.42
1:A:603:ASN:HB3	1:A:604:LYS:H	1.65	0.42
1:B:386:LEU:HD23	1:B:387:GLU:O	2.19	0.42
1:B:581:VAL:O	1:B:582:PHE:C	2.62	0.42
1:A:364:SER:HB3	1:A:366:SER:N	2.34	0.42
1:B:464:LYS:HD2	1:B:464:LYS:HA	1.86	0.42
1:B:473:CYS:O	1:B:474:SER:O	2.38	0.42
1:B:616:ASN:OD1	1:B:617:ALA:N	2.53	0.42
1:B:726:ARG:HH22	1:B:746:GLU:HB3	1.84	0.42
1:A:340:PHE:HD2	1:A:363:VAL:HG11	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:ASN:HD21	1:B:124:SER:HA	1.85	0.42
1:A:245:GLN:HB2	1:A:284:PHE:CD2	2.55	0.42
1:A:269:HIS:ND1	1:A:270:GLU:N	2.68	0.42
1:B:673:SER:C	1:B:675:CYS:N	2.78	0.42
1:A:376:GLU:OE1	1:A:376:GLU:N	2.49	0.42
1:B:115:ASN:HB3	1:B:141:TYR:H	1.84	0.42
1:B:645:LEU:HD23	1:B:645:LEU:HA	1.64	0.42
1:A:230:GLN:HE21	1:A:243:MET:CE	2.32	0.41
1:B:539:TYR:N	1:B:552:ILE:O	2.53	0.41
1:B:742:GLU:O	1:B:746:GLU:HG2	2.20	0.41
1:B:354:ALA:HB2	1:B:359:VAL:HG23	2.01	0.41
1:A:278:PHE:HE1	1:A:292:VAL:HG22	1.85	0.41
1:A:370:THR:HG21	1:A:389:VAL:HB	2.02	0.41
1:B:179:PHE:HB2	1:B:188:TRP:HB2	2.01	0.41
1:B:642:GLU:H	1:B:642:GLU:HG3	1.25	0.41
1:A:712:PRO:O	1:A:714:VAL:N	2.49	0.41
1:B:140:ASP:OD1	1:B:140:ASP:N	2.52	0.41
1:A:497:LYS:HB2	1:A:542:TRP:HZ2	1.86	0.41
1:B:314:HIS:HB2	1:B:319:GLU:H	1.86	0.41
1:A:521:TYR:CE2	1:A:532:GLU:HG2	2.55	0.41
1:A:534:LEU:HB3	1:A:538:HIS:CE1	2.55	0.41
1:B:276:THR:HG23	1:B:295:GLU:HG3	2.02	0.41
1:B:405:TYR:HB3	1:B:411:PHE:HD2	1.85	0.41
1:A:674:ASN:CG	1:A:737:SER:H	2.28	0.41
1:B:370:THR:HG21	1:B:391:TYR:HB3	2.02	0.41
1:B:686:PHE:C	1:B:688:PHE:N	2.77	0.41
1:A:376:GLU:HG2	1:A:378:GLU:N	2.35	0.41
1:A:386:LEU:HD13	1:A:450:TRP:CD2	2.56	0.41
1:A:519:ASN:OD1	1:A:535:PRO:HA	2.21	0.41
1:B:249:LYS:HE3	1:B:249:LYS:HB2	1.84	0.41
1:A:390:LEU:HD12	1:A:429:ILE:HB	2.03	0.41
1:A:674:ASN:CG	1:A:674:ASN:O	2.64	0.41
1:B:219:LEU:HD21	1:B:237:PHE:CE1	2.56	0.41
1:B:314:HIS:C	1:B:316:LEU:H	2.28	0.41
1:B:644:LEU:HB2	1:B:645:LEU:H	1.73	0.41
1:A:730:LYS:HE2	1:A:736:CYS:SG	2.61	0.40
1:A:730:LYS:HE3	1:A:730:LYS:HB2	1.33	0.40
1:B:142:GLY:HA2	1:B:145:PHE:HE1	1.86	0.40
1:B:218:LEU:O	1:B:219:LEU:HD23	2.20	0.40
1:B:661:PHE:O	1:B:663:GLY:N	2.54	0.40
1:A:661:PHE:C	1:A:663:GLY:N	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:468:GLU:CG	1:B:470:SER:H	2.32	0.40
1:A:370:THR:HG22	1:A:371:ASN:N	2.36	0.40
1:B:233:LYS:HE2	1:B:283:PHE:CG	2.56	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	661/664 (100%)	553 (84%)	89 (14%)	19 (3%)	3	19
1	B	661/664 (100%)	539 (82%)	100 (15%)	22 (3%)	3	17
All	All	1322/1328 (100%)	1092 (83%)	189 (14%)	41 (3%)	5	18

All (41) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	242	ILE
1	A	364	SER
1	A	388	ASN
1	B	242	ILE
1	B	389	VAL
1	B	635	PRO
1	B	642	GLU
1	B	658	ALA
1	B	666	PHE
1	B	701	PRO
1	A	363	VAL
1	A	370	THR
1	A	468	GLU
1	A	489	LEU
1	A	509	SER

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Mol	Chain	Res	Type
1	A	607	VAL
1	A	676	SER
1	A	677	CYS
1	A	695	SER
1	B	474	SER
1	B	593	LYS
1	B	631	LYS
1	B	674	ASN
1	B	683	GLU
1	A	368	ASN
1	B	606	ASN
1	B	610	TRP
1	B	667	ASP
1	B	682	TYR
1	B	737	SER
1	A	297	VAL
1	A	371	ASN
1	A	453	LEU
1	A	675	CYS
1	B	644	LEU
1	B	679	ARG
1	B	681	ASP
1	B	686	PHE
1	A	457	ALA
1	B	469	LEU
1	A	124	SER

5.3.2 Protein sidechains ⓘ

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	575/576 (100%)	564 (98%)	11 (2%)	50	66
1	B	575/576 (100%)	544 (95%)	31 (5%)	20	47
All	All	1150/1152 (100%)	1108 (96%)	42 (4%)	31	55

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	346	ILE
1	A	348	GLU
1	A	362	CYS
1	A	363	VAL
1	A	365	HIS
1	A	366	SER
1	A	367	ASN
1	A	372	LEU
1	A	429	ILE
1	A	675	CYS
1	A	730	LYS
1	B	467	CYS
1	B	468	GLU
1	B	469	LEU
1	B	510	VAL
1	B	581	VAL
1	B	593	LYS
1	B	607	VAL
1	B	608	HIS
1	B	637	ASP
1	B	638	GLU
1	B	639	ARG
1	B	642	GLU
1	B	644	LEU
1	B	645	LEU
1	B	647	HIS
1	B	648	LYS
1	B	649	THR
1	B	650	VAL
1	B	656	PRO
1	B	664	GLU
1	B	665	ASP
1	B	675	CYS
1	B	678	THR
1	B	682	TYR
1	B	683	GLU
1	B	684	CYS
1	B	686	PHE
1	B	689	LYS
1	B	690	MET
1	B	699	CYS
1	B	700	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	HIS
1	A	158	ASN
1	A	247	HIS
1	A	388	ASN
1	A	437	ASN
1	A	486	ASN
1	A	554	GLN
1	A	647	HIS
1	B	108	HIS
1	B	158	ASN
1	B	483	GLN
1	B	545	HIS
1	B	662	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

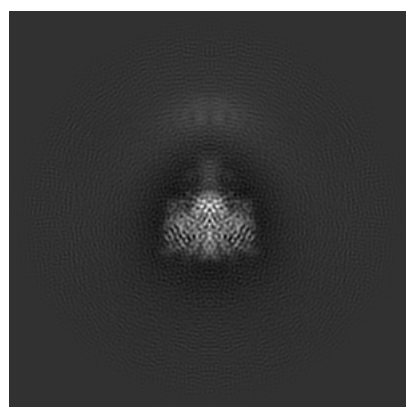
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32117. These allow visual inspection of the internal detail of the map and identification of artifacts.

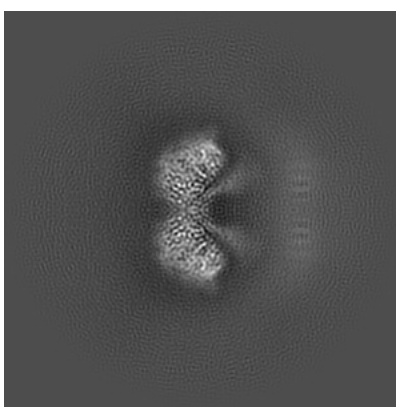
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

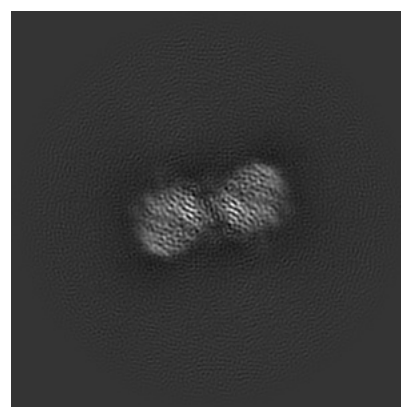
6.1.1 Primary map



X



Y

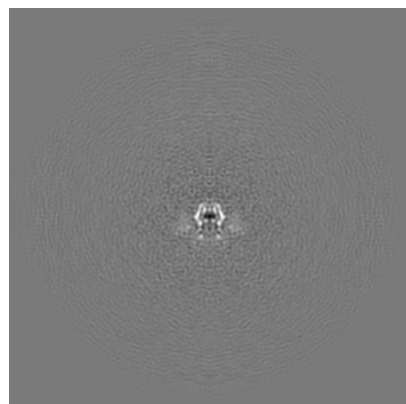


Z

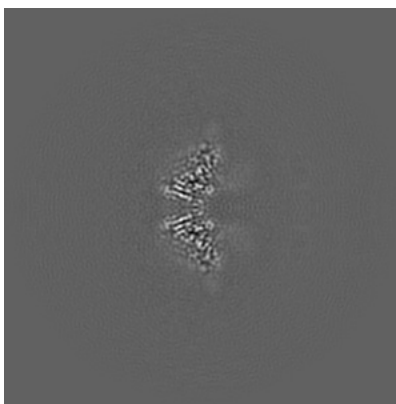
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

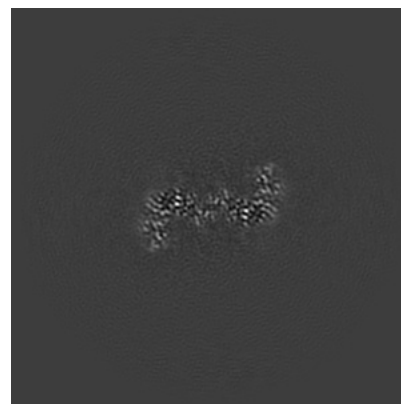
6.2.1 Primary map



X Index: 160



Y Index: 160

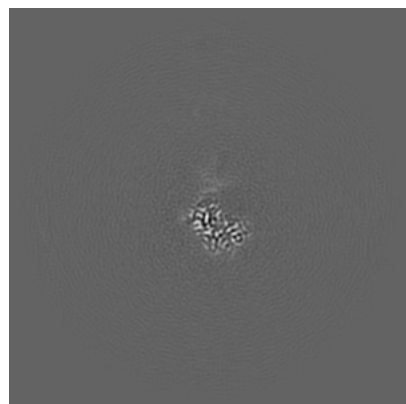


Z Index: 160

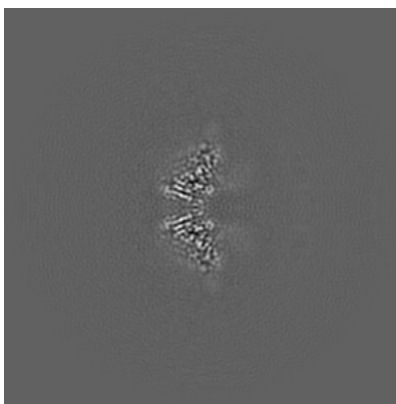
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

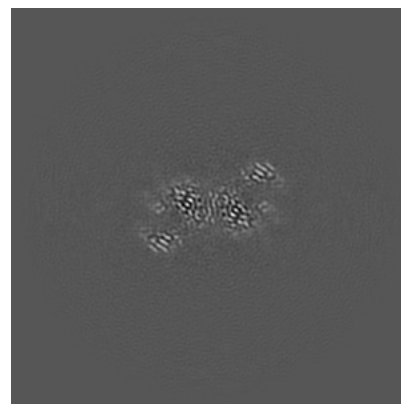
6.3.1 Primary map



X Index: 180



Y Index: 160

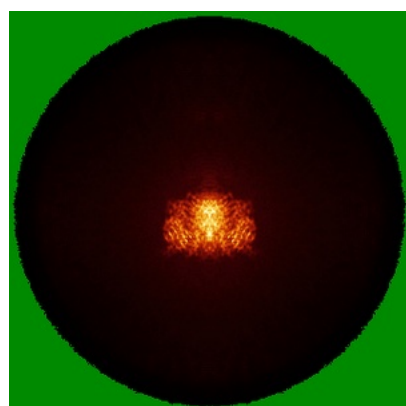


Z Index: 151

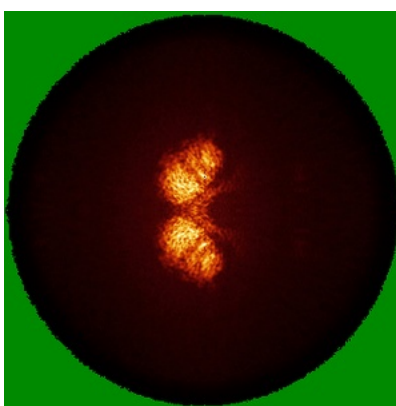
The images above show the largest variance slices of the map in three orthogonal directions.

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

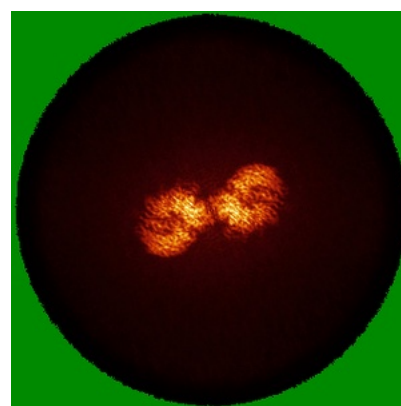
6.4.1 Primary map



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

This section was not generated.

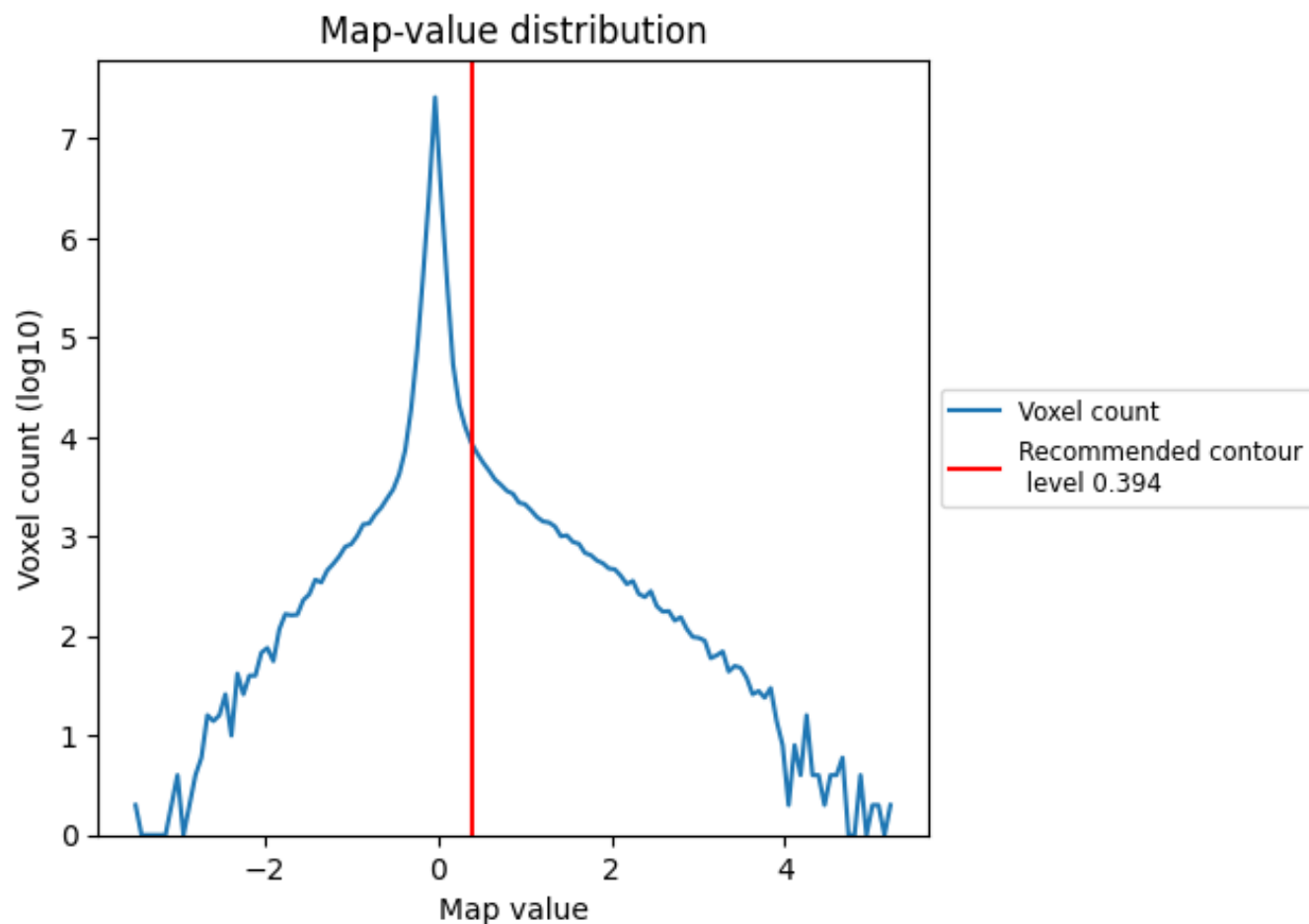
6.6 Mask visualisation

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

7 Map analysis [i](#)

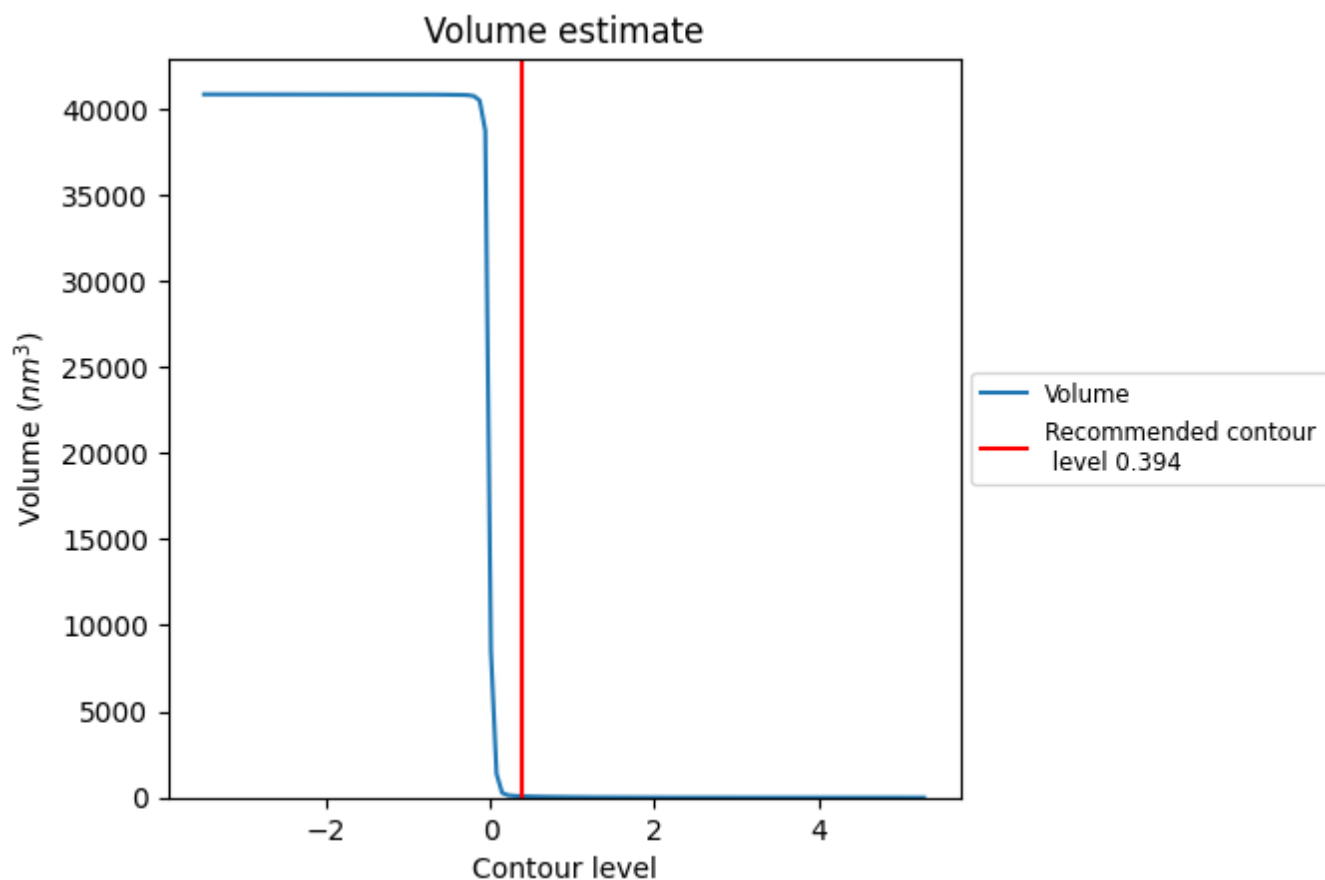
This section contains the results of statistical analysis of the map.

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.

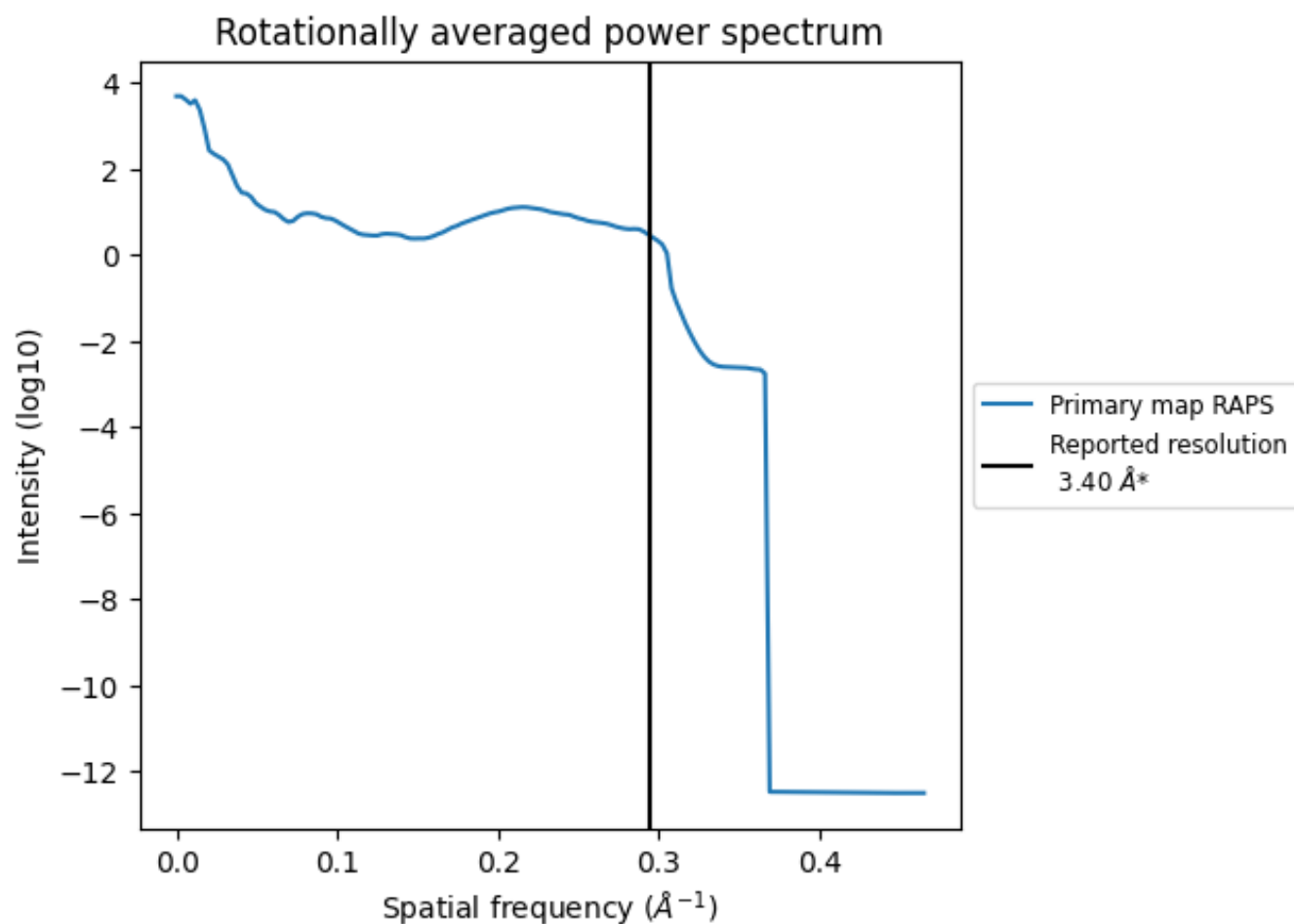
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm³; this corresponds to an approximate mass of 67 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 0.294 $\text{\AA}^{-1}$

8 Fourier-Shell correlation ⓘ

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

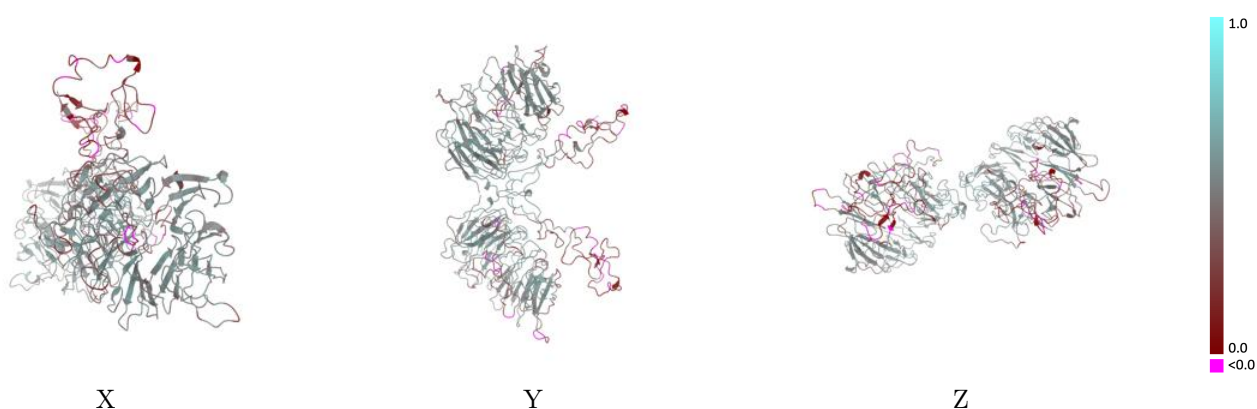
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32117 and PDB model 7VT0. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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

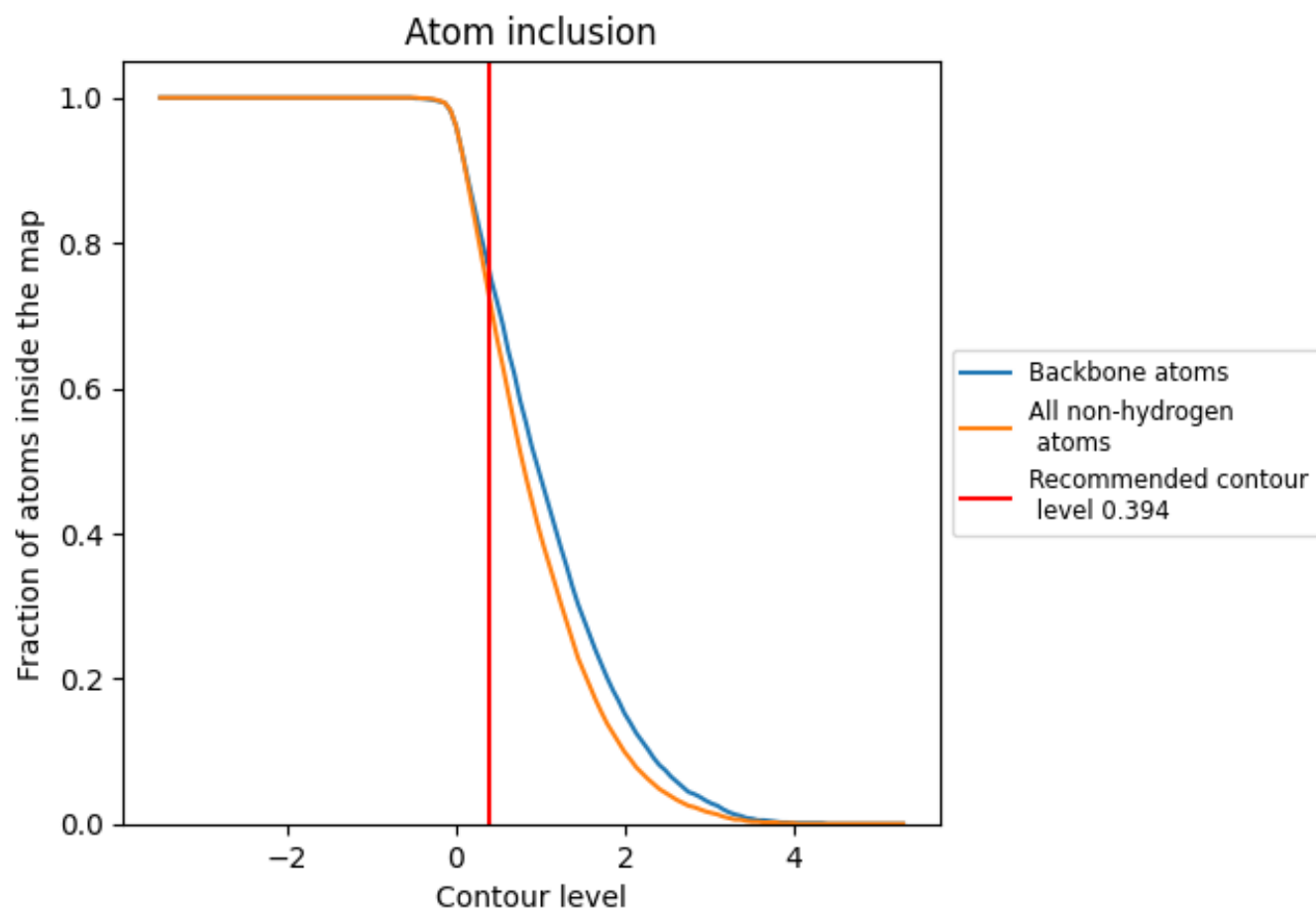


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (0.394) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7250	0.4470
A	0.7210	0.4390
B	0.7290	0.4540

