



## Full wwPDB EM Validation Report ⓘ

Apr 8, 2024 – 04:26 PM JST

PDB ID : 8WYE  
EMDB ID : EMD-37925  
Title : Cryo-EM structure of DSR2-DSAD1 (partial) complex  
Authors : Zhang, J.T.; Jia, N.; Liu, X.Y.  
Deposited on : 2023-10-30  
Resolution : 2.49 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](mailto: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>.

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

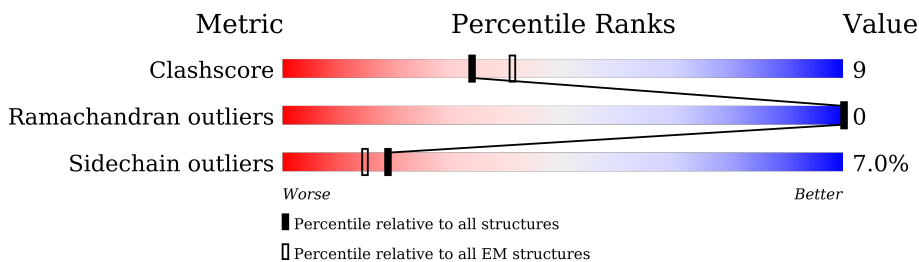
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP)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

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.49 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1005	
1	B	1005	
1	D	1005	
1	E	1005	
2	C	146	

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 21232 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 SIR2 family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	945	7895	5115	1275	1474	31	0	0
1	B	953	7966	5162	1288	1486	30	0	0
1	D	268	2195	1417	355	416	7	0	0
1	E	271	2219	1429	360	423	7	0	0

- Molecule 2 is a protein called Bacillus phage SPbeta DSAD1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	116	957	625	154	175	3	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	121	TRP	-	expression tag	UNP O64191
C	122	SER	-	expression tag	UNP O64191
C	123	HIS	-	expression tag	UNP O64191
C	124	PRO	-	expression tag	UNP O64191
C	125	GLN	-	expression tag	UNP O64191
C	126	PHE	-	expression tag	UNP O64191
C	127	GLU	-	expression tag	UNP O64191
C	128	LYS	-	expression tag	UNP O64191
C	129	GLY	-	expression tag	UNP O64191
C	130	GLY	-	expression tag	UNP O64191
C	131	GLY	-	expression tag	UNP O64191
C	132	SER	-	expression tag	UNP O64191
C	133	GLY	-	expression tag	UNP O64191
C	134	GLY	-	expression tag	UNP O64191
C	135	GLY	-	expression tag	UNP O64191

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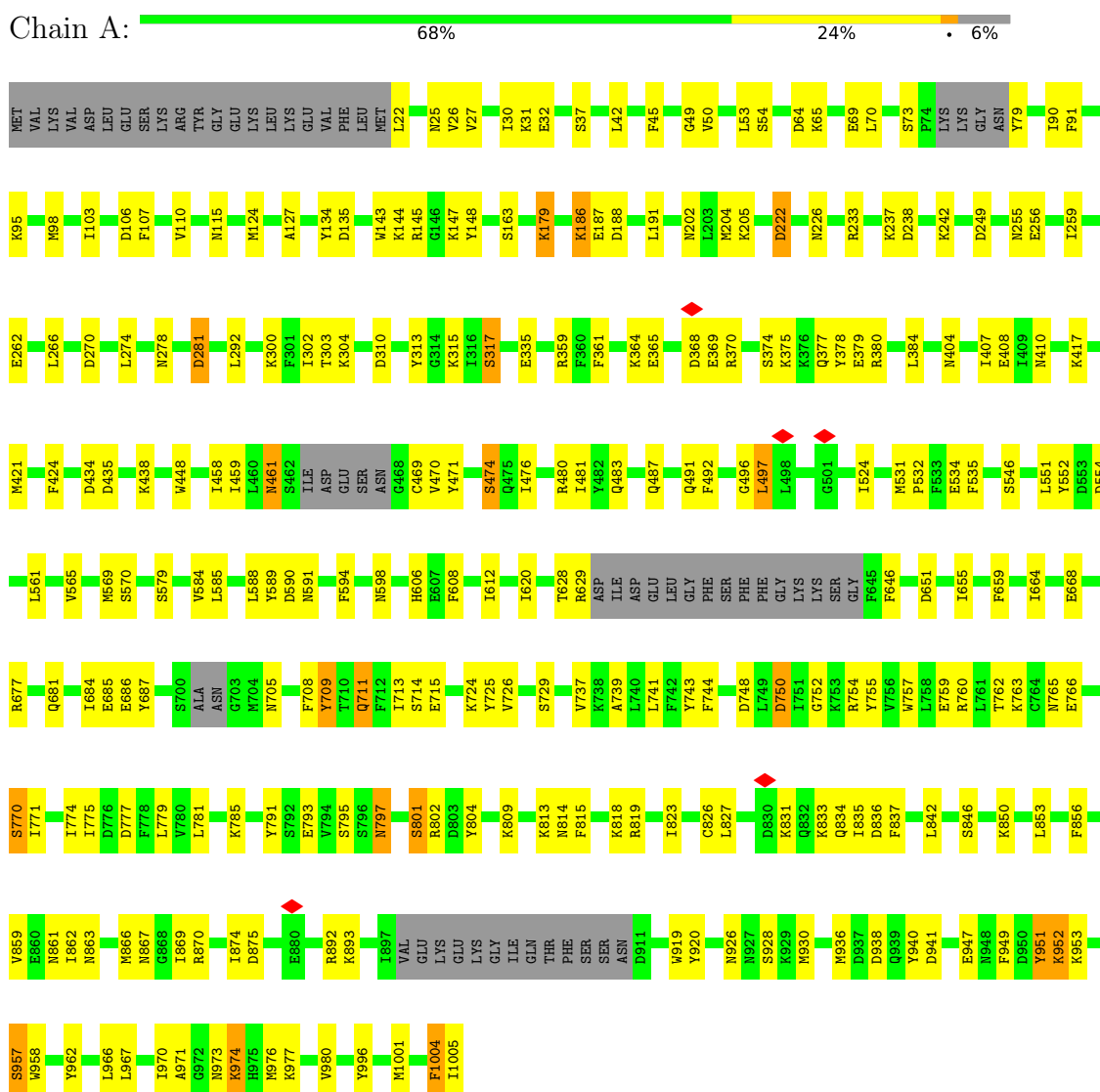
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Chain	Residue	Modelled	Actual	Comment	Reference
C	136	SER	-	expression tag	UNP O64191
C	137	GLY	-	expression tag	UNP O64191
C	138	GLY	-	expression tag	UNP O64191
C	139	TRP	-	expression tag	UNP O64191
C	140	SER	-	expression tag	UNP O64191
C	141	HIS	-	expression tag	UNP O64191
C	142	PRO	-	expression tag	UNP O64191
C	143	GLN	-	expression tag	UNP O64191
C	144	PHE	-	expression tag	UNP O64191
C	145	GLU	-	expression tag	UNP O64191
C	146	LYS	-	expression tag	UNP O64191

### 3 Residue-property plots [i](#)

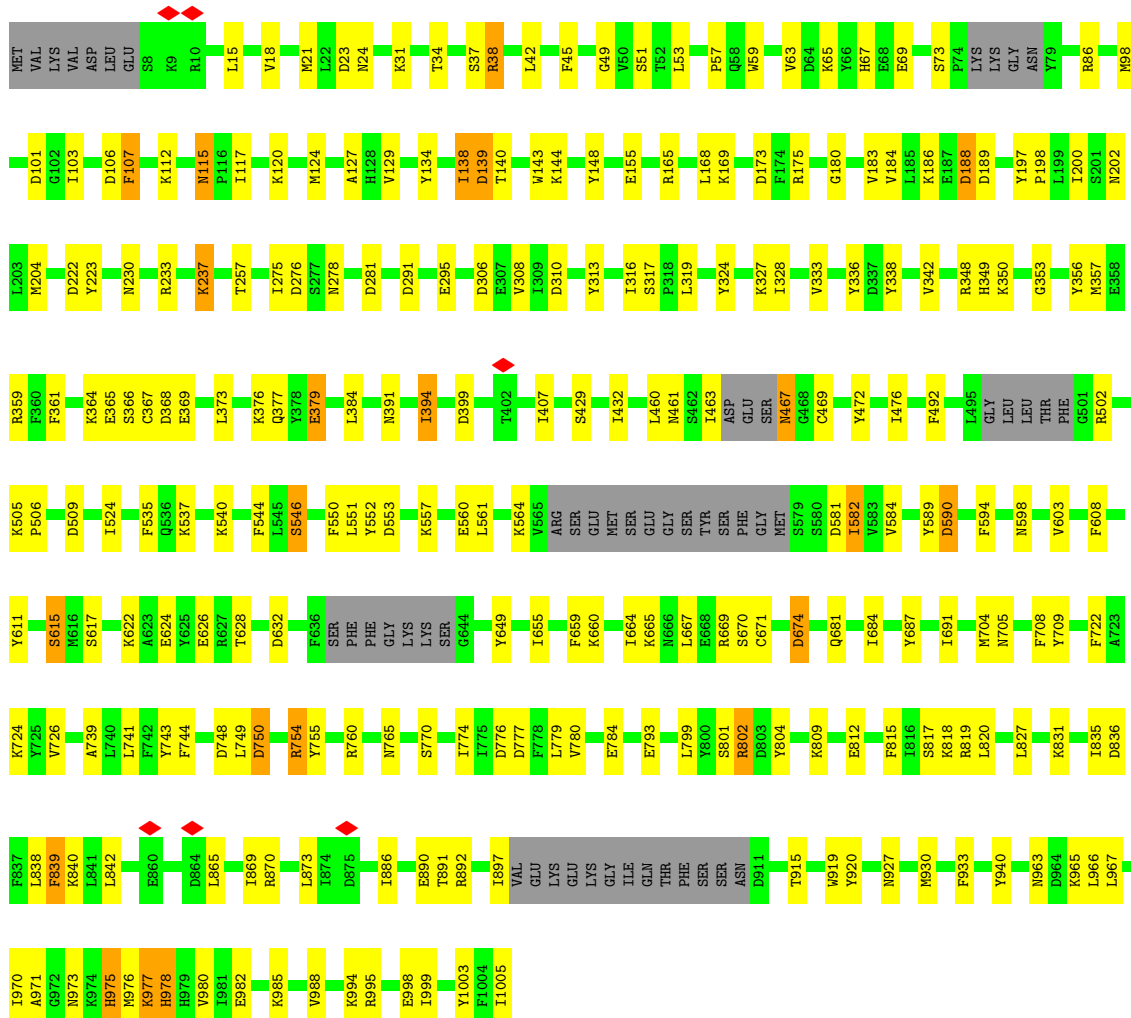
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: SIR2 family protein

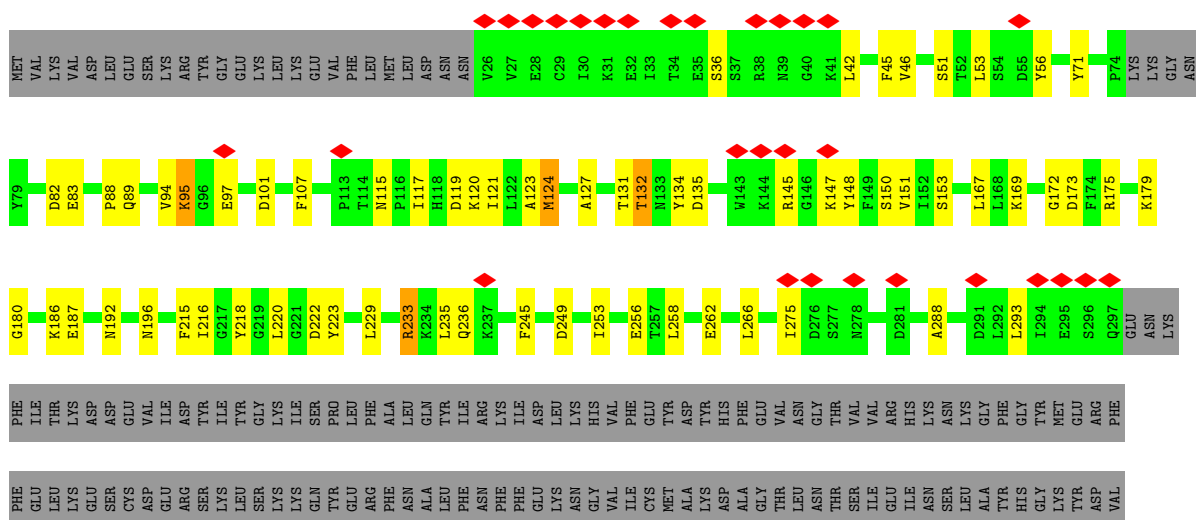


- Molecule 1: SIR2 family protein





• Molecule 1: SIR2 family protein









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	946024	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.550	Depositor
Minimum map value	-2.884	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.087	Depositor
Recommended contour level	0.4	Depositor
Map size ( $\text{\AA}$ )	330.80002, 330.80002, 330.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.827, 0.827, 0.827	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.27	0/8078	0.45	0/10881
1	B	0.27	0/8148	0.44	0/10973
1	D	0.25	0/2249	0.44	0/3049
1	E	0.26	0/2273	0.48	0/3082
2	C	0.27	0/983	0.49	0/1333
All	All	0.27	0/21731	0.45	0/29318

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	7895	0	7731	149	0
1	B	7966	0	7811	149	0
1	D	2195	0	2139	35	0
1	E	2219	0	2155	51	0
2	C	957	0	942	19	0
All	All	21232	0	20778	378	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 9.

All (378) 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:531:MET:HG3	1:A:532:PRO:HD2	1.62	0.79
1:B:139:ASP:N	1:B:139:ASP:OD1	2.15	0.78
1:A:313:TYR:O	1:A:317:SER:OG	2.04	0.74
1:B:237:LYS:H	1:B:237:LYS:HE2	1.52	0.74
1:A:98:MET:SD	1:A:98:MET:N	2.62	0.72
1:D:46:VAL:HB	1:D:131:THR:HG22	1.72	0.72
1:A:470:VAL:O	1:A:474:SER:OG	2.10	0.70
1:E:29:CYS:O	1:E:33:ILE:HD12	1.92	0.70
1:A:827:LEU:HD21	1:A:834:GLN:HB3	1.74	0.69
1:B:870:ARG:NH2	2:C:75:ILE:O	2.27	0.68
2:C:103:SER:HA	2:C:111:PRO:HG2	1.77	0.67
1:D:192:ASN:O	1:D:196:ASN:ND2	2.27	0.67
1:A:480:ARG:NH2	1:A:546:SER:O	2.27	0.67
1:B:291:ASP:O	1:B:295:GLU:HG2	1.94	0.67
1:E:26:VAL:O	1:E:30:ILE:HD12	1.95	0.67
1:B:37:SER:OG	1:B:124:MET:O	2.13	0.67
1:B:366:SER:OG	1:B:369:GLU:OE1	2.12	0.67
1:B:975:HIS:O	1:B:976:MET:HG2	1.96	0.66
1:A:233:ARG:NH1	1:E:188:ASP:OD1	2.28	0.66
1:A:424:PHE:O	1:A:438:LYS:NZ	2.28	0.65
1:B:812:GLU:HG2	1:B:815:PHE:HB2	1.80	0.64
1:A:188:ASP:OD1	1:E:233:ARG:NH1	2.26	0.64
1:B:98:MET:SD	1:B:98:MET:N	2.69	0.64
1:A:685:GLU:OE2	1:A:729:SER:OG	2.15	0.64
1:B:364:LYS:NZ	1:B:394:ILE:O	2.31	0.64
1:B:139:ASP:OD2	1:B:169:LYS:NZ	2.31	0.63
1:B:327:LYS:NZ	1:B:391:ASN:O	2.32	0.63
1:E:37:SER:OG	1:E:124:MET:O	2.16	0.63
1:E:123:ALA:HB2	1:E:145:ARG:HH22	1.61	0.63
1:B:23:ASP:OD1	1:B:24:ASN:N	2.31	0.63
1:D:89:GLN:NE2	1:D:187:GLU:O	2.23	0.63
1:A:554:ASP:OD2	1:A:591:ASN:ND2	2.30	0.62
1:B:476:ILE:HD13	1:B:524:ILE:HD11	1.81	0.62
1:B:65:LYS:O	1:B:69:GLU:HG2	1.99	0.62
1:B:65:LYS:HD3	1:B:107:PHE:HE2	1.62	0.62
1:D:151:VAL:HG22	1:D:167:LEU:HD23	1.81	0.62
1:B:827:LEU:HD13	1:B:835:ILE:HG13	1.80	0.62
1:A:777:ASP:OD1	1:A:819:ARG:NH1	2.28	0.61
1:B:467:ASN:N	1:B:467:ASN:HD22	1.97	0.61
1:B:622:LYS:O	1:B:626:GLU:HG2	2.01	0.61
1:D:258:LEU:O	1:D:262:GLU:HG2	2.01	0.61
1:E:132:THR:HG21	1:E:224:ASN:HD22	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:121:ILE:HD11	1:D:216:ILE:HD13	1.83	0.60
1:A:37:SER:OG	1:A:124:MET:O	2.19	0.60
1:A:256:GLU:HA	1:A:259:ILE:HD12	1.84	0.60
1:A:741:LEU:HA	1:A:754:ARG:HD3	1.84	0.60
1:A:359:ARG:NH2	1:A:369:GLU:OE1	2.33	0.59
1:B:472:TYR:OH	1:B:546:SER:OG	2.20	0.59
1:B:1003:TYR:HB2	1:B:1005:ILE:HG13	1.84	0.59
1:A:144:LYS:HA	1:B:460:LEU:HD21	1.85	0.59
1:A:315:LYS:NZ	1:A:335:GLU:OE2	2.35	0.59
1:B:724:LYS:HE3	2:C:124:PRO:HA	1.85	0.59
1:B:222:ASP:OD2	1:B:223:TYR:N	2.36	0.58
1:B:230:ASN:O	1:B:233:ARG:HG2	2.03	0.58
1:A:205:LYS:HB2	1:B:202:ASN:HD21	1.69	0.58
1:E:139:ASP:N	1:E:139:ASP:OD1	2.36	0.58
1:A:793:GLU:OE2	1:A:801:SER:OG	2.21	0.58
1:B:348:ARG:NH2	1:B:353:GLY:O	2.36	0.58
1:A:980:VAL:HG21	1:A:1005:ILE:HG22	1.86	0.58
1:B:336:TYR:O	1:B:349:HIS:ND1	2.35	0.58
1:E:230:ASN:O	1:E:233:ARG:HG2	2.04	0.57
1:A:957:SER:OG	1:B:632:ASP:O	2.22	0.57
2:C:31:ILE:HG22	2:C:83:ILE:HA	1.84	0.57
1:A:938:ASP:OD1	1:A:953:LYS:NZ	2.33	0.57
1:B:324:TYR:OH	1:B:590:ASP:OD1	2.13	0.57
1:B:670:SER:OG	1:B:671:CYS:SG	2.54	0.57
1:B:611:TYR:O	1:B:615:SER:OG	2.23	0.57
1:D:229:LEU:HD21	1:D:266:LEU:HG	1.87	0.57
1:A:819:ARG:O	1:A:823:ILE:HG13	2.04	0.57
1:B:544:PHE:HD2	1:B:550:PHE:HB2	1.69	0.57
1:A:684:ILE:HG21	1:A:726:VAL:HG21	1.87	0.57
1:A:476:ILE:HD13	1:A:524:ILE:HD11	1.85	0.57
1:B:817:SER:OG	1:B:820:LEU:HB2	2.04	0.56
1:B:319:LEU:HD11	1:B:333:VAL:HG21	1.87	0.56
1:E:65:LYS:HD3	1:E:107:PHE:HE2	1.69	0.56
1:A:646:PHE:HB2	1:A:677:ARG:HG2	1.87	0.56
1:A:310:ASP:OD2	1:A:377:GLN:NE2	2.39	0.56
1:A:585:LEU:O	1:A:588:LEU:HB3	2.05	0.56
1:A:370:ARG:HB3	1:A:378:TYR:HE1	1.71	0.56
1:A:861:ASN:OD1	1:A:863:ASN:N	2.35	0.56
1:B:237:LYS:H	1:B:237:LYS:CE	2.19	0.56
2:C:44:PHE:HB3	2:C:64:ILE:HD11	1.88	0.56
2:C:46:LYS:HG3	2:C:113:VAL:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ILE:HG23	1:A:471:TYR:HE1	1.71	0.56
1:D:94:VAL:HG23	1:D:95:LYS:HD2	1.88	0.55
1:A:364:LYS:O	1:A:370:ARG:NH2	2.30	0.55
1:A:869:ILE:HG21	1:A:919:TRP:HZ2	1.70	0.55
1:E:42:LEU:O	1:E:127:ALA:N	2.36	0.55
1:B:724:LYS:HB2	1:B:760:ARG:HB3	1.88	0.54
1:A:417:LYS:O	1:A:421:MET:HG3	2.07	0.54
1:D:123:ALA:HA	1:D:145:ARG:HH12	1.73	0.54
1:E:122:LEU:O	1:E:147:LYS:NZ	2.39	0.54
1:B:561:LEU:HD11	1:B:584:VAL:HG11	1.90	0.54
1:E:229:LEU:HD13	1:E:264:LYS:HB3	1.89	0.54
1:A:687:TYR:OH	1:A:715:GLU:OE2	2.19	0.54
1:A:30:ILE:HD11	1:A:292:LEU:HD21	1.89	0.53
1:A:920:TYR:CD1	1:A:930:MET:HG3	2.43	0.53
1:B:34:THR:O	1:B:38:ARG:HD3	2.07	0.53
1:A:70:LEU:HD21	1:A:91:PHE:HA	1.91	0.53
1:D:135:ASP:O	1:D:169:LYS:NZ	2.40	0.53
1:B:741:LEU:HA	1:B:754:ARG:HD3	1.91	0.53
1:E:46:VAL:HA	1:E:216:ILE:HD12	1.90	0.53
1:B:995:ARG:HD3	2:C:19:LYS:HG3	1.90	0.53
1:A:27:VAL:HG12	1:A:31:LYS:HE3	1.91	0.53
1:A:797:ASN:H	1:A:797:ASN:HD22	1.57	0.53
1:B:684:ILE:HG21	1:B:726:VAL:HG21	1.91	0.53
1:B:980:VAL:HG21	1:B:1005:ILE:HG22	1.89	0.53
1:B:278:ASN:HB2	1:B:281:ASP:HB2	1.91	0.52
1:D:117:ILE:HD13	1:D:120:LYS:HD2	1.89	0.52
1:D:132:THR:OG1	1:D:218:TYR:OH	2.19	0.52
1:A:973:ASN:O	1:A:974:LYS:HG3	2.09	0.52
1:E:50:VAL:HG21	1:E:216:ILE:HD13	1.91	0.52
1:A:480:ARG:NH1	1:A:483:GLN:OE1	2.40	0.52
1:A:739:ALA:HA	1:A:743:TYR:HD2	1.74	0.52
2:C:20:ILE:O	2:C:20:ILE:HD12	2.10	0.52
1:D:101:ASP:OD1	1:D:180:GLY:N	2.42	0.52
1:A:620:ILE:HD11	1:A:655:ILE:HD11	1.92	0.52
1:A:205:LYS:HB2	1:B:202:ASN:ND2	2.25	0.52
1:A:368:ASP:OD1	1:A:369:GLU:N	2.43	0.52
1:E:119:ASP:OD1	1:E:145:ARG:NE	2.39	0.52
1:B:148:TYR:O	1:B:165:ARG:NH1	2.43	0.52
1:B:553:ASP:O	1:B:557:LYS:HG3	2.10	0.51
1:E:136:ASN:O	1:E:140:THR:HG23	2.11	0.51
1:E:139:ASP:OD2	1:E:169:LYS:NZ	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:ASP:O	1:A:226:ASN:ND2	2.32	0.51
1:A:492:PHE:HA	1:A:496:GLY:HA3	1.93	0.51
1:B:665:LYS:NZ	2:C:121:TRP:HE1	2.08	0.51
1:B:802:ARG:HB2	1:B:840:LYS:HB3	1.92	0.51
1:E:56:TYR:CZ	1:E:135:ASP:HB3	2.45	0.51
1:B:967:LEU:HD22	1:B:1005:ILE:HD13	1.93	0.51
2:C:33:LEU:HD11	2:C:39:LEU:HD11	1.93	0.51
1:A:752:GLY:HA3	1:A:797:ASN:HD21	1.75	0.51
1:A:242:LYS:NZ	1:A:262:GLU:O	2.44	0.51
1:A:407:ILE:HD13	1:A:589:TYR:HB3	1.93	0.51
1:E:120:LYS:HZ1	1:E:287:SER:HB3	1.75	0.51
1:B:963:ASN:HD22	1:B:965:LYS:H	1.58	0.51
1:E:247:ARG:CZ	1:E:249:ASP:HB3	2.41	0.51
1:A:836:ASP:OD1	1:A:837:PHE:N	2.43	0.50
1:B:776:ASP:O	1:B:780:VAL:HG23	2.11	0.50
1:D:56:TYR:CZ	1:D:135:ASP:HB3	2.47	0.50
1:A:531:MET:HG2	1:A:535:PHE:CD1	2.47	0.50
1:A:809:LYS:NZ	1:A:815:PHE:O	2.40	0.50
1:B:674:ASP:OD1	1:B:674:ASP:N	2.38	0.50
1:A:65:LYS:O	1:A:69:GLU:HG2	2.12	0.50
1:B:308:VAL:HG13	1:B:356:TYR:HB2	1.93	0.50
1:E:213:ILE:HB	1:E:243:PRO:HB3	1.92	0.49
1:A:831:LYS:O	1:A:835:ILE:HG13	2.12	0.49
1:A:237:LYS:NZ	1:A:238:ASP:OD1	2.42	0.49
1:A:561:LEU:HD12	1:A:584:VAL:HG23	1.92	0.49
1:A:750:ASP:OD1	1:A:750:ASP:N	2.45	0.49
1:A:949:PHE:HB3	1:A:951:TYR:CE2	2.47	0.49
1:A:791:TYR:O	1:A:833:LYS:NZ	2.44	0.49
1:A:802:ARG:HE	1:A:870:ARG:HE	1.60	0.49
1:B:869:ILE:HG21	1:B:919:TRP:CZ2	2.48	0.49
1:A:724:LYS:HB2	1:A:760:ARG:HB3	1.94	0.49
1:A:863:ASN:O	1:A:867:ASN:ND2	2.45	0.49
1:E:94:VAL:HG23	1:E:95:LYS:HG2	1.94	0.49
1:A:459:ILE:HG23	1:A:471:TYR:CE1	2.48	0.49
1:E:151:VAL:HG22	1:E:167:LEU:HD23	1.95	0.49
1:B:836:ASP:OD1	1:B:836:ASP:N	2.46	0.49
1:A:300:LYS:HB2	1:A:302:ILE:HG13	1.95	0.48
1:A:842:LEU:HD13	1:A:853:LEU:HD23	1.95	0.48
1:A:408:GLU:OE1	1:A:410:ASN:ND2	2.45	0.48
1:B:967:LEU:HB3	1:B:1005:ILE:HD11	1.95	0.48
1:E:53:LEU:HD13	1:E:283:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:PHE:O	1:B:365:GLU:HG2	2.13	0.48
2:C:26:ASP:OD2	2:C:89:VAL:HB	2.13	0.48
1:D:145:ARG:HH21	1:D:147:LYS:HG3	1.79	0.48
1:B:755:TYR:HB2	1:B:804:TYR:CZ	2.48	0.48
1:D:253:ILE:HG21	1:D:258:LEU:HD13	1.96	0.48
1:A:361:PHE:O	1:A:365:GLU:HG2	2.12	0.48
1:B:920:TYR:CD1	1:B:930:MET:HG3	2.49	0.48
1:A:608:PHE:O	1:A:612:ILE:HG12	2.14	0.48
1:B:173:ASP:OD2	1:B:175:ARG:HD3	2.14	0.48
1:A:1004:PHE:CE2	1:B:985:LYS:HD3	2.49	0.48
1:B:313:TYR:O	1:B:317:SER:OG	2.30	0.48
1:B:582:ILE:HD13	1:B:582:ILE:HA	1.79	0.47
1:D:51:SER:OG	1:D:135:ASP:OD2	2.24	0.47
1:B:42:LEU:O	1:B:127:ALA:N	2.44	0.47
1:B:755:TYR:HD2	1:B:799:LEU:HD13	1.78	0.47
1:E:204:MET:HE2	1:E:228:LEU:HD21	1.95	0.47
1:E:31:LYS:HE2	1:E:31:LYS:HB2	1.66	0.47
1:B:966:LEU:HD22	2:C:59:PHE:HB2	1.97	0.47
1:B:999:ILE:HG23	1:B:1005:ILE:HD12	1.96	0.47
1:D:115:ASN:OD1	1:D:115:ASN:N	2.39	0.47
1:A:705:ASN:HB3	1:A:708:PHE:HB3	1.96	0.47
1:D:169:LYS:HD2	1:D:173:ASP:HB3	1.95	0.47
1:A:270:ASP:O	1:A:274:LEU:HD13	2.15	0.46
1:A:862:ILE:O	1:A:866:MET:HG2	2.13	0.46
1:B:407:ILE:HD13	1:B:589:TYR:HB3	1.97	0.46
1:A:655:ILE:O	1:A:659:PHE:HB2	2.15	0.46
1:E:184:VAL:HG13	1:E:189:ASP:HB3	1.96	0.46
1:A:54:SER:OG	1:A:54:SER:O	2.32	0.46
1:B:831:LYS:H	1:B:831:LYS:HG2	1.61	0.46
1:D:88:PRO:HB2	1:D:186:LYS:HB3	1.98	0.46
1:A:755:TYR:HB2	1:A:804:TYR:CE1	2.51	0.46
1:A:779:LEU:HD21	1:A:804:TYR:HB2	1.98	0.46
1:B:359:ARG:HD2	1:B:359:ARG:HA	1.81	0.46
1:B:594:PHE:O	1:B:598:ASN:HB2	2.16	0.46
2:C:99:VAL:O	2:C:103:SER:OG	2.28	0.46
1:A:681:GLN:HG2	1:A:726:VAL:HG13	1.97	0.46
1:D:235:LEU:HD13	1:E:199:LEU:HD21	1.96	0.46
1:B:537:LYS:HB3	1:B:537:LYS:HE2	1.60	0.46
1:A:42:LEU:O	1:A:127:ALA:N	2.44	0.46
1:A:379:GLU:OE2	1:A:379:GLU:HA	2.16	0.46
1:B:886:ILE:O	1:B:890:GLU:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:759:GLU:O	1:A:762:THR:OG1	2.25	0.45
1:B:581:ASP:OD1	1:B:622:LYS:NZ	2.29	0.45
1:B:155:GLU:OE2	1:B:198:PRO:HD2	2.16	0.45
1:B:129:VAL:HG11	1:B:138:ILE:HG21	1.97	0.45
1:B:140:THR:O	1:B:144:LYS:HG3	2.16	0.45
1:B:655:ILE:O	1:B:659:PHE:HB2	2.17	0.45
1:D:220:LEU:HD12	1:D:220:LEU:HA	1.83	0.45
1:E:60:TRP:HA	1:E:84:TYR:HE1	1.81	0.45
1:A:186:LYS:HB2	1:A:186:LYS:HE2	1.50	0.45
1:A:310:ASP:OD1	1:A:380:ARG:NH1	2.50	0.45
1:B:376:LYS:O	1:B:379:GLU:HG3	2.16	0.45
1:B:649:TYR:HE1	1:B:687:TYR:HB2	1.82	0.45
1:E:43:VAL:HG22	1:E:128:HIS:HB2	1.99	0.45
1:B:780:VAL:O	1:B:784:GLU:HG3	2.16	0.45
1:E:111:ASP:OD1	1:E:111:ASP:N	2.43	0.45
1:A:589:TYR:OH	1:A:651:ASP:OD1	2.35	0.45
1:A:709:TYR:OH	1:A:748:ASP:OD2	2.27	0.45
1:E:115:ASN:OD1	1:E:115:ASN:N	2.44	0.45
1:A:664:ILE:O	1:A:668:GLU:HG3	2.17	0.45
1:A:771:ILE:O	1:A:775:ILE:HG13	2.17	0.45
1:D:275:ILE:HD13	1:D:288:ALA:HB2	1.99	0.45
1:A:143:TRP:NE1	1:B:460:LEU:O	2.40	0.45
1:B:978:HIS:O	1:B:982:GLU:HG2	2.16	0.45
1:E:224:ASN:OD1	1:E:224:ASN:N	2.50	0.45
1:E:285:ARG:HE	1:E:285:ARG:HB2	1.67	0.45
1:B:31:LYS:HB2	1:B:31:LYS:HE3	1.76	0.45
1:B:188:ASP:OD1	1:D:233:ARG:NH1	2.46	0.45
1:B:617:SER:HA	1:B:667:LEU:HD21	1.99	0.45
1:D:215:PHE:HB2	1:D:245:PHE:HA	1.99	0.45
1:A:737:VAL:HG11	1:A:771:ILE:HG23	1.99	0.44
1:B:101:ASP:OD1	1:B:180:GLY:N	2.39	0.44
1:B:779:LEU:HD21	1:B:804:TYR:HB2	1.98	0.44
1:E:58:GLN:HB3	1:E:60:TRP:CD1	2.52	0.44
1:A:801:SER:HA	1:A:804:TYR:HD1	1.82	0.44
1:D:173:ASP:OD2	1:D:175:ARG:HD3	2.17	0.44
1:A:801:SER:HA	1:A:804:TYR:CD1	2.52	0.44
1:B:49:GLY:O	1:B:53:LEU:HD13	2.18	0.44
1:B:770:SER:O	1:B:774:ILE:HG13	2.17	0.44
1:B:831:LYS:O	1:B:835:ILE:HD12	2.18	0.44
1:D:153:SER:HB2	1:D:172:GLY:HA2	1.99	0.44
1:E:23:ASP:HB3	1:E:26:VAL:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:PRO:HD3	1:B:148:TYR:CG	2.52	0.44
1:A:711:GLN:H	1:A:711:GLN:HG3	1.44	0.44
1:B:313:TYR:HA	1:B:384:LEU:HD21	1.98	0.44
1:D:42:LEU:O	1:D:127:ALA:N	2.43	0.44
1:E:30:ILE:HD12	1:E:30:ILE:H	1.82	0.44
1:A:187:GLU:O	1:A:191:LEU:HD23	2.18	0.44
1:B:143:TRP:HZ3	1:B:148:TYR:HD1	1.66	0.44
1:B:184:VAL:HG13	1:B:189:ASP:HB3	1.98	0.44
1:A:869:ILE:HG21	1:A:919:TRP:CZ2	2.50	0.44
1:B:976:MET:O	1:B:980:VAL:HG22	2.18	0.44
1:B:57:PRO:HD3	1:B:112:LYS:HE3	1.99	0.44
1:B:368:ASP:OD1	1:B:368:ASP:N	2.51	0.44
1:B:624:GLU:O	1:B:628:THR:HG23	2.18	0.44
1:B:705:ASN:HB3	1:B:708:PHE:HB3	1.99	0.44
1:B:965:LYS:HB3	1:B:965:LYS:HE3	1.71	0.44
2:C:120:ASP:OD1	2:C:121:TRP:N	2.51	0.44
1:A:448:TRP:CD1	1:A:481:ILE:HD11	2.53	0.43
1:A:551:LEU:HD11	1:A:608:PHE:HA	2.00	0.43
1:A:892:ARG:HG3	1:A:936:MET:HG2	2.00	0.43
1:A:996:TYR:OH	1:B:632:ASP:OD1	2.28	0.43
1:B:168:LEU:HD11	1:B:200:ILE:HG23	2.00	0.43
1:A:374:SER:OG	1:A:375:LYS:N	2.51	0.43
1:B:660:LYS:O	1:B:664:ILE:HG13	2.18	0.43
1:D:222:ASP:OD1	1:D:223:TYR:N	2.51	0.43
1:A:565:VAL:O	1:A:569:MET:HG3	2.18	0.43
1:A:869:ILE:HD12	1:A:869:ILE:HA	1.86	0.43
1:B:120:LYS:NZ	1:B:291:ASP:OD1	2.42	0.43
1:A:70:LEU:HD23	1:A:91:PHE:HD2	1.82	0.43
1:A:91:PHE:CZ	1:A:103:ILE:HD12	2.53	0.43
1:B:469:CYS:HA	1:B:535:PHE:HE2	1.84	0.43
1:B:777:ASP:OD1	1:B:819:ARG:NH1	2.35	0.43
1:A:202:ASN:ND2	1:B:202:ASN:OD1	2.50	0.43
1:A:606:HIS:NE2	1:B:560:GLU:OE2	2.39	0.43
1:B:15:LEU:HD11	1:B:291:ASP:HB3	2.00	0.43
1:B:65:LYS:HD3	1:B:107:PHE:CE2	2.47	0.43
1:B:505:LYS:HE2	1:B:505:LYS:HB3	1.67	0.43
1:B:820:LEU:HD22	1:B:838:LEU:HD21	1.99	0.43
1:A:941:ASP:OD1	1:A:941:ASP:N	2.51	0.43
1:A:958:TRP:HB3	1:A:962:TYR:OH	2.19	0.43
1:B:971:ALA:O	1:B:977:LYS:HD3	2.19	0.43
1:D:124:MET:CE	1:D:293:LEU:HB3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ASN:HB2	1:A:281:ASP:HB2	2.01	0.43
1:A:781:LEU:O	1:A:785:LYS:HG3	2.18	0.43
1:B:18:VAL:HG21	1:B:275:ILE:HG22	2.01	0.43
1:E:220:LEU:HD23	1:E:220:LEU:HA	1.89	0.43
1:A:64:ASP:OD1	1:A:79:TYR:OH	2.21	0.43
1:A:755:TYR:HB2	1:A:804:TYR:CZ	2.53	0.43
1:A:827:LEU:HD23	1:A:831:LYS:HG3	2.01	0.43
1:B:709:TYR:OH	1:B:748:ASP:OD2	2.16	0.43
1:A:846:SER:O	1:A:850:LYS:HG2	2.19	0.43
1:A:967:LEU:HB3	1:A:1005:ILE:HD11	2.01	0.43
1:B:793:GLU:OE2	1:B:801:SER:HB2	2.19	0.43
1:A:179:LYS:HE2	1:A:179:LYS:HB2	1.90	0.42
1:A:534:GLU:HG2	1:A:535:PHE:N	2.34	0.42
1:A:770:SER:O	1:A:774:ILE:HG13	2.18	0.42
1:A:797:ASN:H	1:A:797:ASN:ND2	2.16	0.42
1:B:117:ILE:HD13	1:B:120:LYS:HD2	2.01	0.42
1:B:930:MET:HB3	1:B:940:TYR:OH	2.19	0.42
1:E:274:LEU:HD23	1:E:274:LEU:HA	1.87	0.42
1:A:461:ASN:OD1	1:A:461:ASN:N	2.51	0.42
1:A:532:PRO:HD3	1:B:148:TYR:CD2	2.54	0.42
1:A:971:ALA:O	1:A:977:LYS:HD2	2.20	0.42
1:E:152:ILE:HD13	1:E:158:VAL:HA	2.01	0.42
1:A:713:ILE:HD12	1:A:713:ILE:HA	1.90	0.42
1:B:492:PHE:CE1	1:B:506:PRO:HG3	2.54	0.42
2:C:20:ILE:O	2:C:22:THR:N	2.52	0.42
1:D:256:GLU:OE1	1:D:256:GLU:N	2.43	0.42
1:A:90:ILE:HG12	1:E:260:TYR:CG	2.55	0.42
1:A:655:ILE:HA	1:A:659:PHE:CD1	2.55	0.42
1:A:966:LEU:O	1:A:970:ILE:HG13	2.20	0.42
1:B:67:HIS:ND1	1:B:73:SER:O	2.53	0.42
1:B:338:TYR:CZ	1:B:357:MET:HB2	2.54	0.42
1:D:153:SER:OG	1:D:175:ARG:NH1	2.52	0.42
1:A:148:TYR:HE2	1:A:163:SER:HG	1.66	0.42
1:A:49:GLY:O	1:A:53:LEU:HD13	2.20	0.42
1:A:313:TYR:HA	1:A:384:LEU:HD21	2.01	0.42
1:A:831:LYS:H	1:A:831:LYS:HG2	1.54	0.42
1:A:974:LYS:HD2	1:A:974:LYS:O	2.20	0.42
1:A:594:PHE:O	1:A:598:ASN:HB2	2.19	0.41
1:A:1001:MET:HE1	1:B:988:VAL:HB	2.02	0.41
1:B:839:PHE:CE2	1:B:873:LEU:HG	2.55	0.41
1:A:25:ASN:OD1	1:A:26:VAL:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:ILE:HA	1:B:106:ASP:OD2	2.20	0.41
1:B:115:ASN:ND2	1:B:117:ILE:HB	2.35	0.41
1:A:552:TYR:CD1	1:B:552:TYR:HA	2.55	0.41
1:B:551:LEU:HD11	1:B:608:PHE:HD1	1.86	0.41
1:B:749:LEU:HD12	1:B:749:LEU:HA	1.90	0.41
1:A:435:ASP:HB3	1:A:458:ILE:HG12	2.02	0.41
1:E:282:TYR:O	1:E:286:TYR:HD2	2.03	0.41
1:A:491:GLN:O	1:A:496:GLY:N	2.52	0.41
1:A:818:LYS:HD3	1:A:818:LYS:N	2.36	0.41
1:B:310:ASP:OD2	1:B:377:GLN:NE2	2.50	0.41
1:B:373:LEU:HB3	1:B:377:GLN:HB3	2.02	0.41
2:C:30:ASP:O	2:C:84:THR:OG1	2.31	0.41
1:E:283:LEU:O	1:E:287:SER:OG	2.32	0.41
1:A:952:LYS:HD3	1:A:952:LYS:N	2.36	0.41
1:B:973:ASN:C	1:B:975:HIS:H	2.24	0.41
2:C:43:TYR:CE2	2:C:67:PHE:HB2	2.56	0.41
1:B:197:TYR:HB3	1:B:200:ILE:HB	2.02	0.41
1:B:750:ASP:O	1:B:754:ARG:HB3	2.21	0.41
1:B:966:LEU:O	1:B:970:ILE:HG13	2.21	0.41
2:C:26:ASP:O	2:C:88:HIS:ND1	2.45	0.41
1:E:45:PHE:HA	1:E:130:ILE:O	2.20	0.41
1:A:668:GLU:OE2	1:A:725:TYR:OH	2.21	0.41
1:A:976:MET:O	1:A:980:VAL:HG22	2.21	0.41
1:B:681:GLN:HG2	1:B:726:VAL:HG13	2.03	0.41
1:B:59:TRP:O	1:B:63:VAL:HG23	2.21	0.40
1:D:53:LEU:HB3	1:D:115:ASN:HD22	1.87	0.40
1:E:206:THR:O	1:E:210:THR:HG23	2.21	0.40
1:E:248:THR:O	1:E:285:ARG:HD2	2.20	0.40
1:A:50:VAL:O	1:A:115:ASN:ND2	2.54	0.40
1:B:461:ASN:OD1	1:B:461:ASN:N	2.54	0.40
1:B:915:THR:HG23	2:C:59:PHE:CE2	2.56	0.40
1:A:266:LEU:HD23	1:A:266:LEU:HA	1.97	0.40
1:A:483:GLN:O	1:A:487:GLN:HG3	2.21	0.40
1:A:866:MET:O	1:A:869:ILE:HG22	2.21	0.40
1:A:947:GLU:H	1:A:947:GLU:CD	2.24	0.40
1:B:257:THR:OG1	1:D:71:TYR:OH	2.35	0.40
1:B:749:LEU:O	1:B:754:ARG:NH2	2.55	0.40
1:B:755:TYR:CD2	1:B:799:LEU:HD13	2.56	0.40
1:B:865:LEU:O	1:B:869:ILE:HD13	2.20	0.40
1:B:869:ILE:HG21	1:B:919:TRP:HZ2	1.85	0.40
1:E:35:GLU:OE1	1:E:39:ASN:ND2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:TYR:O	1:B:350:LYS:HB2	2.21	0.40
1:B:739:ALA:HA	1:B:743:TYR:HD2	1.87	0.40
1:E:124:MET:SD	1:E:293:LEU:HB3	2.62	0.40
1:A:497:LEU:H	1:A:497:LEU:HG	1.61	0.40
1:B:809:LYS:HD2	1:B:809:LYS:HA	1.79	0.40
1:D:151:VAL:HA	1:D:167:LEU:HB3	2.04	0.40
1:E:53:LEU:HA	1:E:53:LEU:HD23	1.85	0.40
1:E:243:PRO:HD2	1:E:265:GLY:O	2.22	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	933/1005 (93%)	915 (98%)	18 (2%)	0	100	100
1	B	939/1005 (93%)	921 (98%)	18 (2%)	0	100	100
1	D	264/1005 (26%)	261 (99%)	3 (1%)	0	100	100
1	E	267/1005 (27%)	264 (99%)	3 (1%)	0	100	100
2	C	114/146 (78%)	110 (96%)	4 (4%)	0	100	100
All	All	2517/4166 (60%)	2471 (98%)	46 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	870/923 (94%)	807 (93%)	63 (7%)	14	28
1	B	877/923 (95%)	817 (93%)	60 (7%)	16	30
1	D	242/923 (26%)	225 (93%)	17 (7%)	15	29
1	E	245/923 (26%)	227 (93%)	18 (7%)	14	27
2	C	111/131 (85%)	105 (95%)	6 (5%)	22	42
All	All	2345/3823 (61%)	2181 (93%)	164 (7%)	19	29

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	32	GLU
1	A	45	PHE
1	A	73	SER
1	A	95	LYS
1	A	106	ASP
1	A	107	PHE
1	A	110	VAL
1	A	134	TYR
1	A	135	ASP
1	A	145	ARG
1	A	147	LYS
1	A	179	LYS
1	A	186	LYS
1	A	204	MET
1	A	222	ASP
1	A	249	ASP
1	A	255	ASN
1	A	281	ASP
1	A	303	THR
1	A	304	LYS
1	A	317	SER
1	A	404	ASN
1	A	434	ASP
1	A	461	ASN
1	A	469	CYS
1	A	474	SER
1	A	497	LEU
1	A	570	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	579	SER
1	A	590	ASP
1	A	628	THR
1	A	629	ARG
1	A	686	GLU
1	A	709	TYR
1	A	711	GLN
1	A	714	SER
1	A	744	PHE
1	A	750	ASP
1	A	757	TRP
1	A	763	LYS
1	A	765	ASN
1	A	766	GLU
1	A	770	SER
1	A	795	SER
1	A	797	ASN
1	A	801	SER
1	A	813	LYS
1	A	814	ASN
1	A	826	CYS
1	A	856	PHE
1	A	859	VAL
1	A	874	ILE
1	A	875	ASP
1	A	893	LYS
1	A	926	ASN
1	A	928	SER
1	A	940	TYR
1	A	951	TYR
1	A	952	LYS
1	A	957	SER
1	A	974	LYS
1	A	1004	PHE
1	B	21	MET
1	B	38	ARG
1	B	45	PHE
1	B	51	SER
1	B	86	ARG
1	B	107	PHE
1	B	115	ASN
1	B	134	TYR

*Continued on next page...*

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	138	ILE
1	B	139	ASP
1	B	183	VAL
1	B	186	LYS
1	B	188	ASP
1	B	204	MET
1	B	237	LYS
1	B	276	ASP
1	B	306	ASP
1	B	316	ILE
1	B	328	ILE
1	B	342	VAL
1	B	367	CYS
1	B	379	GLU
1	B	394	ILE
1	B	399	ASP
1	B	429	SER
1	B	432	ILE
1	B	463	ILE
1	B	467	ASN
1	B	502	ARG
1	B	509	ASP
1	B	540	LYS
1	B	546	SER
1	B	564	LYS
1	B	582	ILE
1	B	590	ASP
1	B	603	VAL
1	B	615	SER
1	B	669	ARG
1	B	674	ASP
1	B	691	ILE
1	B	704	MET
1	B	722	PHE
1	B	744	PHE
1	B	750	ASP
1	B	754	ARG
1	B	765	ASN
1	B	802	ARG
1	B	818	LYS
1	B	839	PHE
1	B	842	LEU

*Continued on next page...*

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	891	THR
1	B	892	ARG
1	B	897	ILE
1	B	927	ASN
1	B	933	PHE
1	B	975	HIS
1	B	977	LYS
1	B	978	HIS
1	B	994	LYS
1	B	998	GLU
2	C	36	SER
2	C	52	ARG
2	C	62	SER
2	C	71	LYS
2	C	72	ARG
2	C	108	SER
1	D	36	SER
1	D	45	PHE
1	D	82	ASP
1	D	83	GLU
1	D	95	LYS
1	D	97	GLU
1	D	107	PHE
1	D	119	ASP
1	D	124	MET
1	D	132	THR
1	D	134	TYR
1	D	148	TYR
1	D	150	SER
1	D	179	LYS
1	D	233	ARG
1	D	236	GLN
1	D	249	ASP
1	E	35	GLU
1	E	41	LYS
1	E	45	PHE
1	E	68	GLU
1	E	82	ASP
1	E	90	ILE
1	E	107	PHE
1	E	119	ASP
1	E	134	TYR

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Mol	Chain	Res	Type
1	E	139	ASP
1	E	165	ARG
1	E	186	LYS
1	E	191	LEU
1	E	202	ASN
1	E	225	ILE
1	E	251	SER
1	E	273	SER
1	E	295	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	202	ASN
1	A	797	ASN
1	B	963	ASN
1	D	196	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

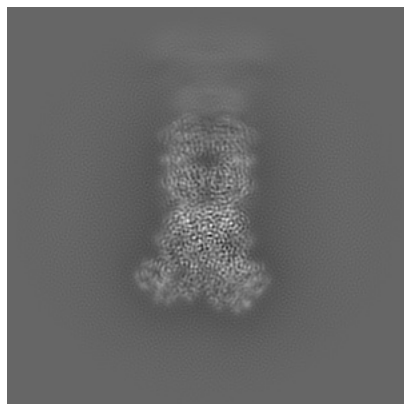
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37925. These allow visual inspection of the internal detail of the map and identification of artifacts.

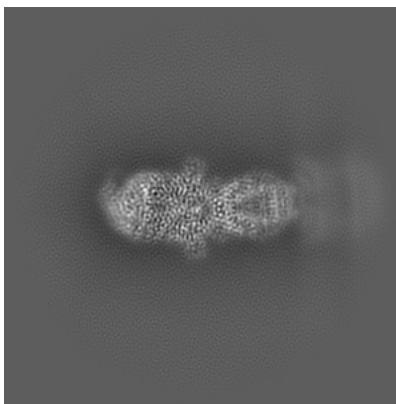
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

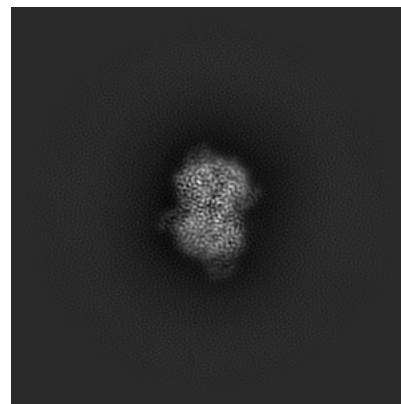
#### 6.1.1 Primary map



X

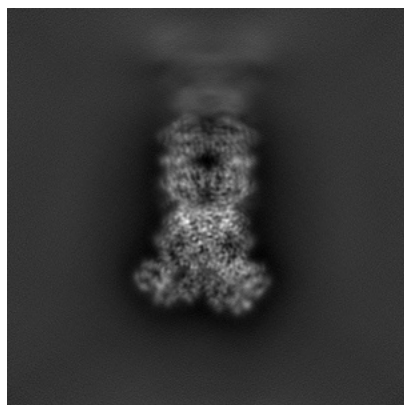


Y

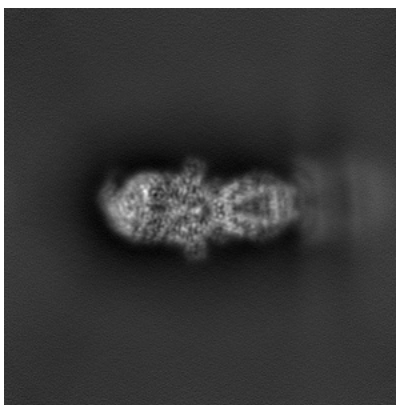


Z

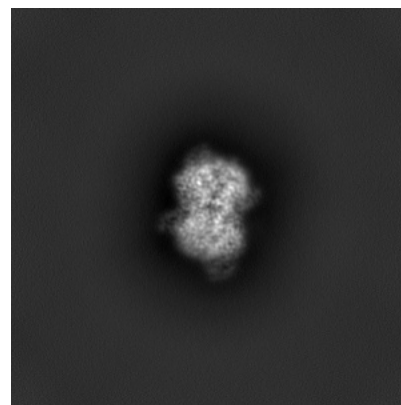
#### 6.1.2 Raw map



X



Y

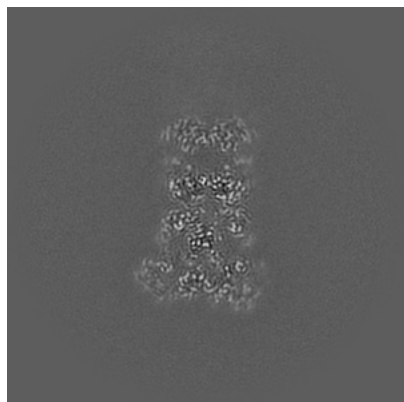


Z

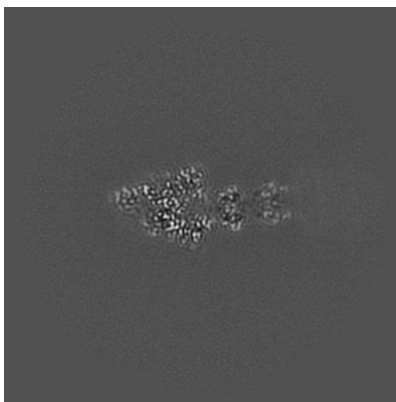
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

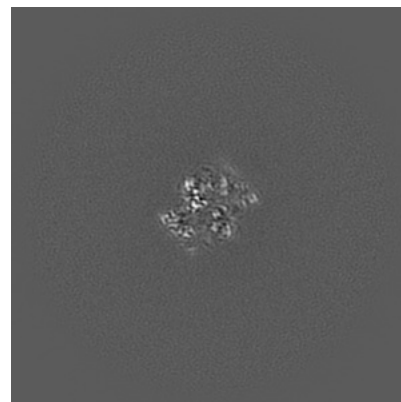
### 6.2.1 Primary map



X Index: 200

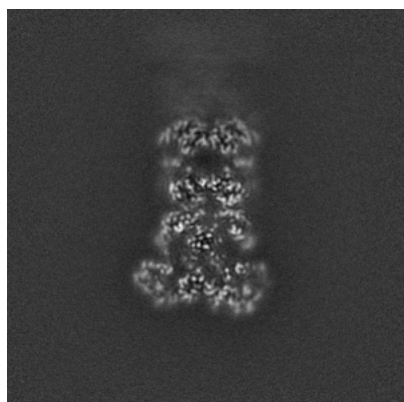


Y Index: 200

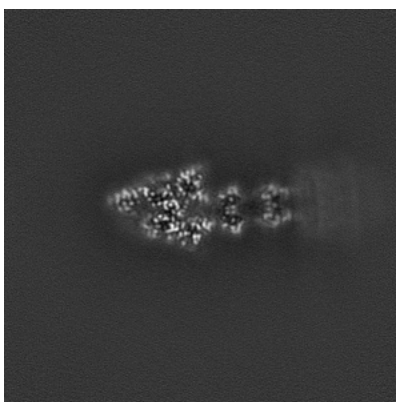


Z Index: 200

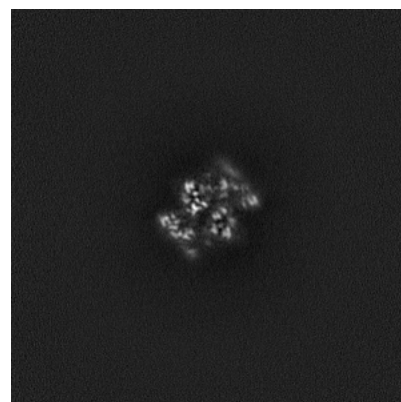
### 6.2.2 Raw map



X Index: 200



Y Index: 200

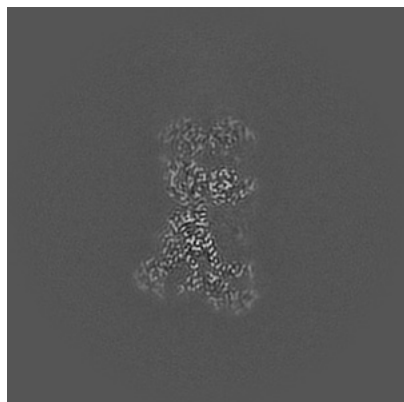


Z Index: 200

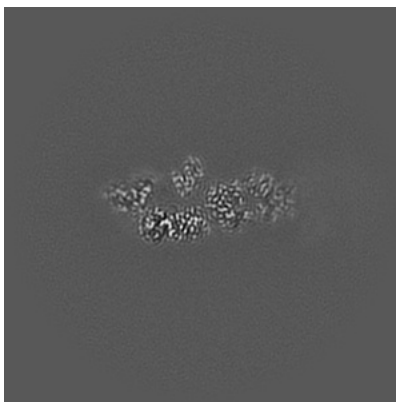
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

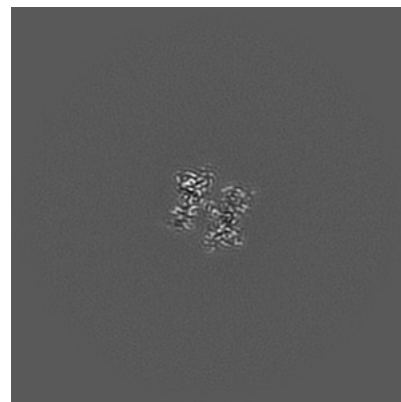
### 6.3.1 Primary map



X Index: 207

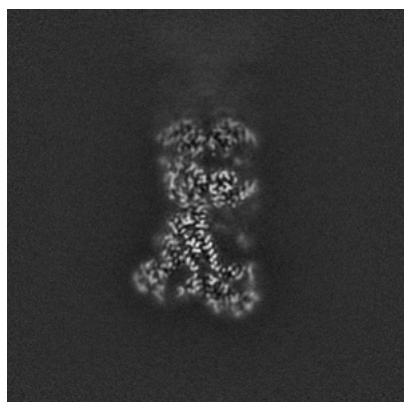


Y Index: 216

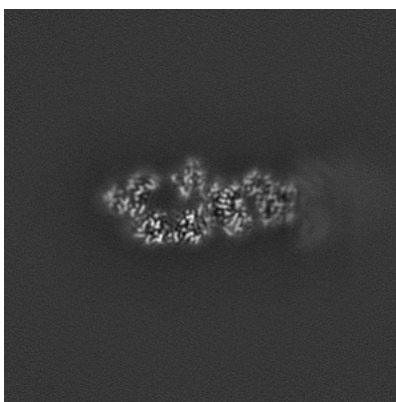


Z Index: 178

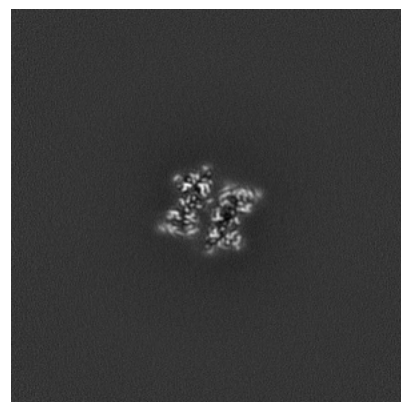
### 6.3.2 Raw map



X Index: 207



Y Index: 219

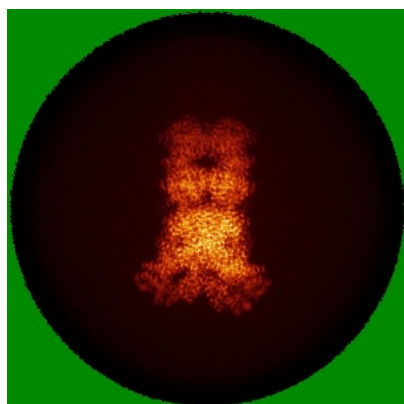


Z Index: 183

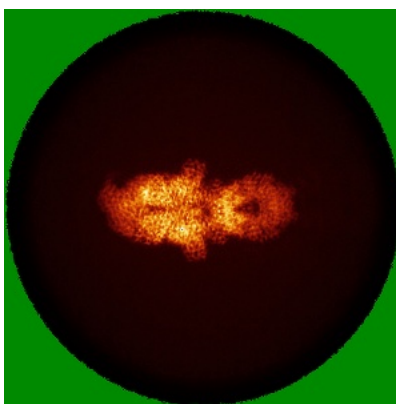
The images above show the largest variance slices of the map in three orthogonal directions.

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

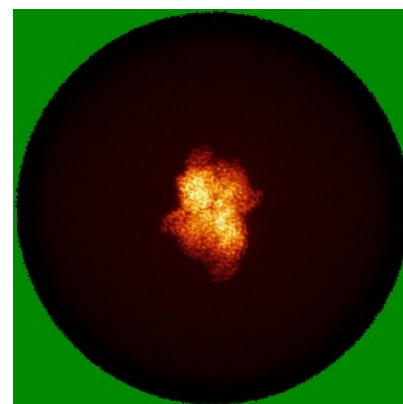
### 6.4.1 Primary map



X

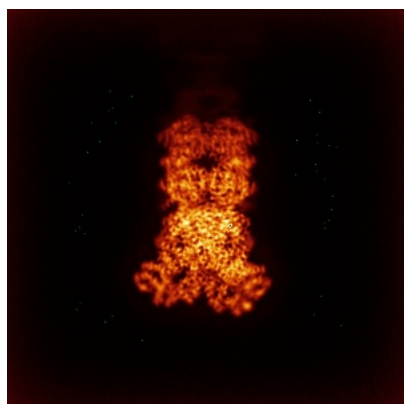


Y

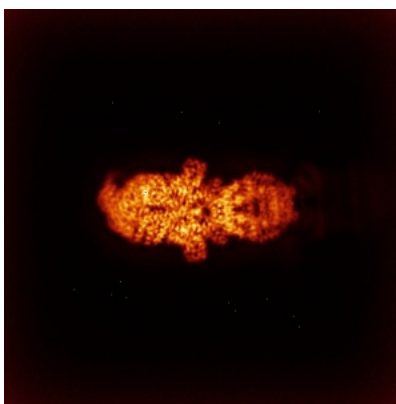


Z

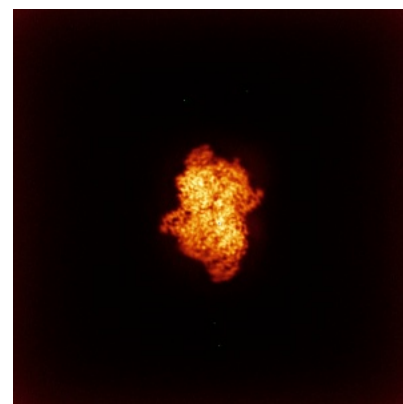
### 6.4.2 Raw map



X



Y

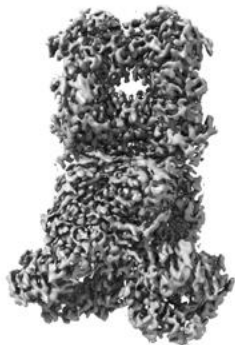


Z

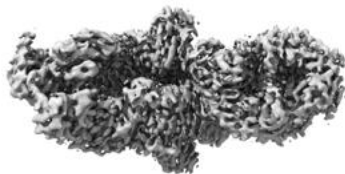
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

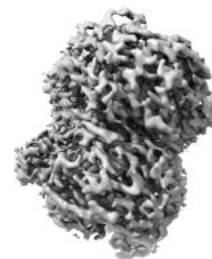
### 6.5.1 Primary map



X



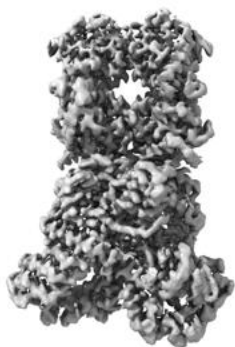
Y



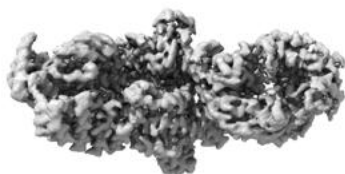
Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

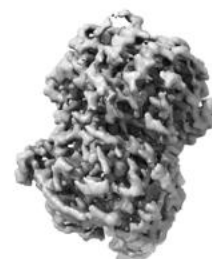
### 6.5.2 Raw map



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.

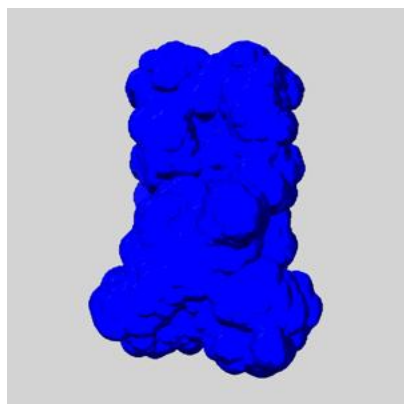
## 6.6 Mask visualisation [i](#)

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

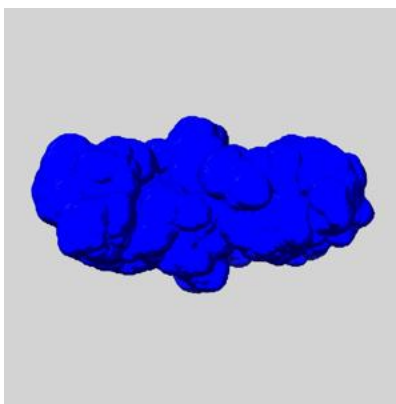
A mask typically either:

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

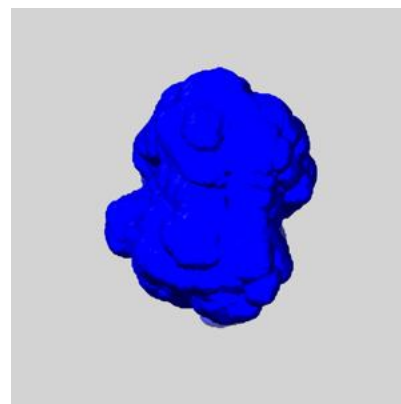
### 6.6.1 emd\_37925\_msk\_1.map [i](#)



X



Y



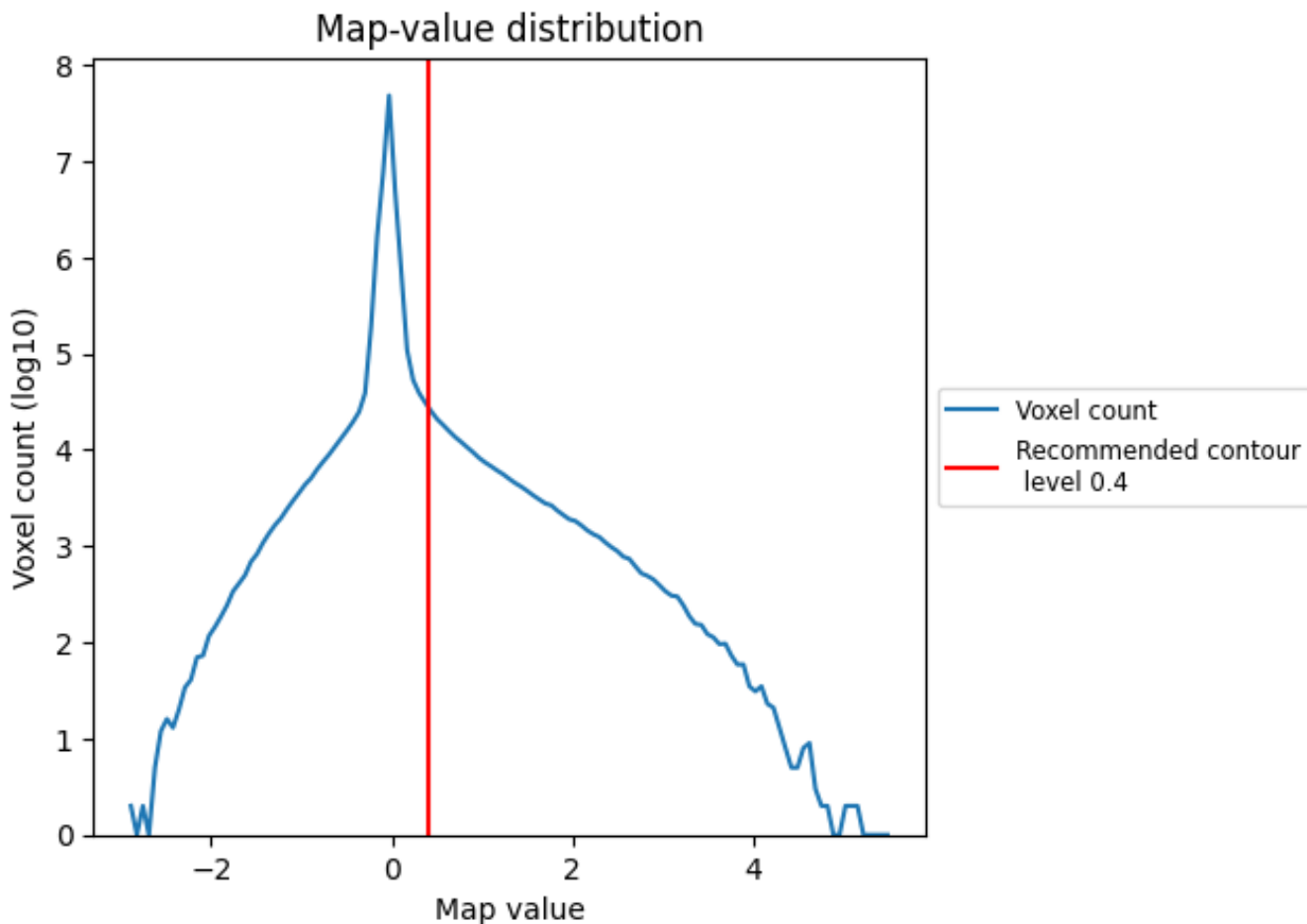
Z



## 7 Map analysis [i](#)

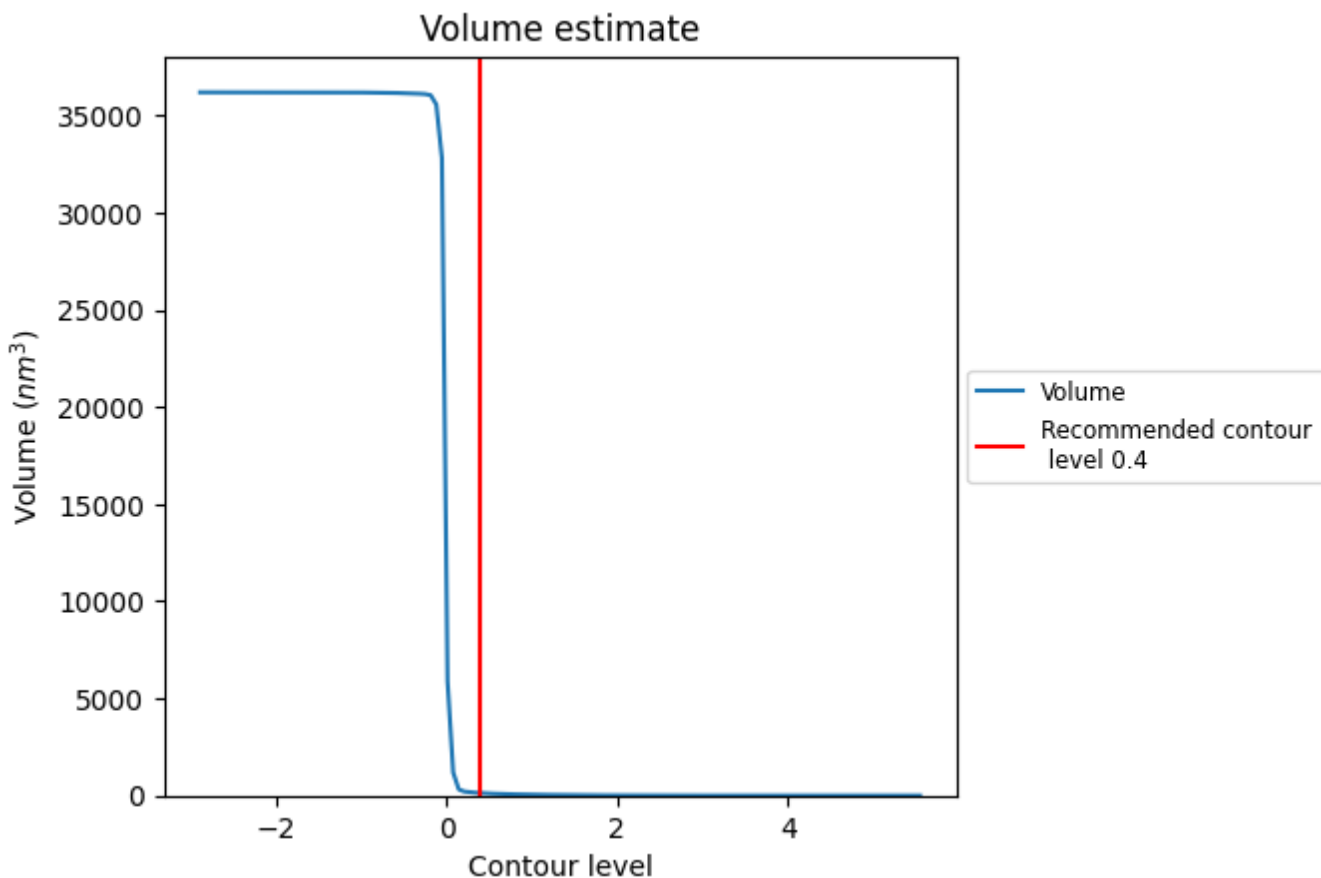
This section contains the results of statistical analysis of the map.

### 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.

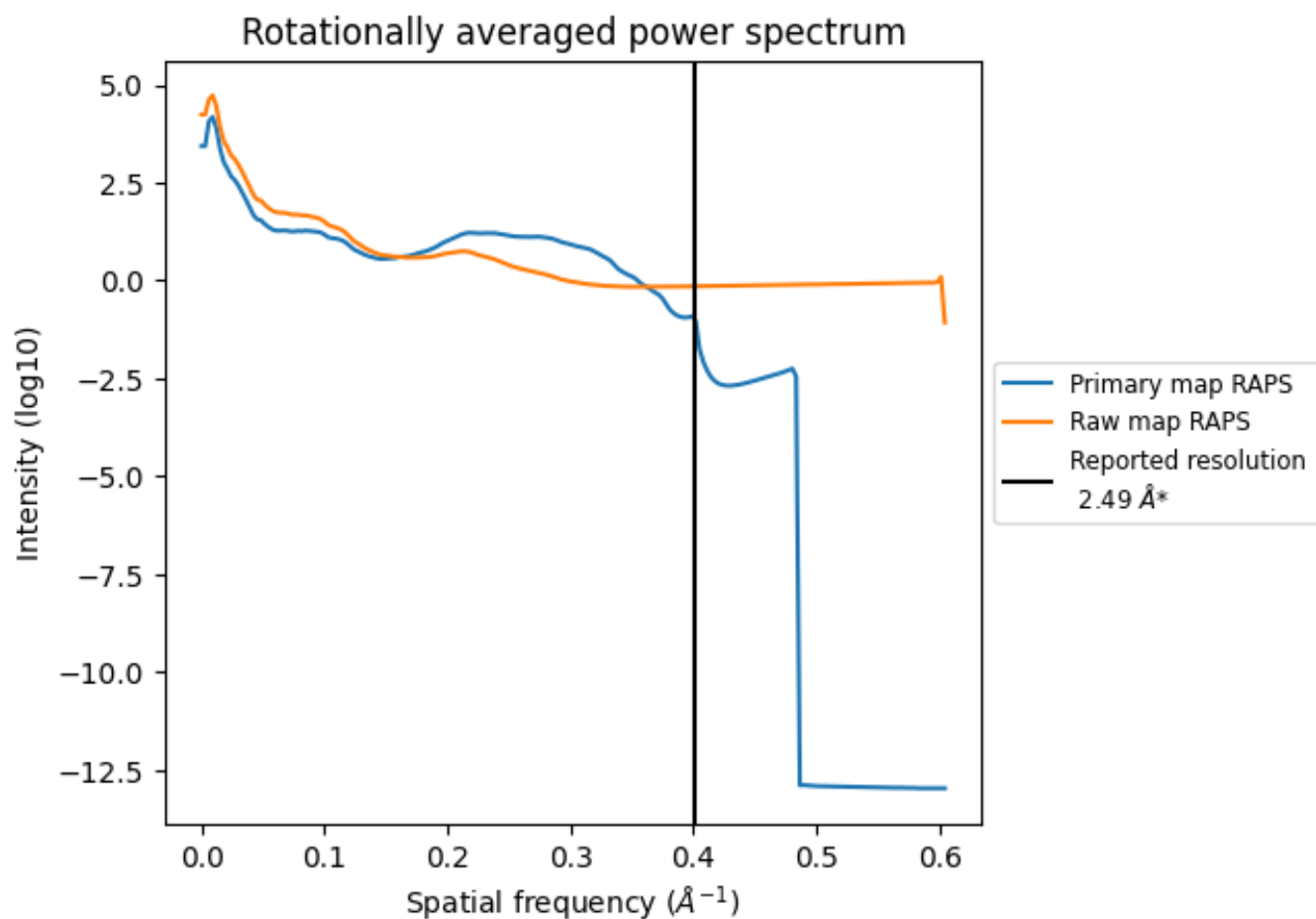
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130 nm<sup>3</sup>; this corresponds to an approximate mass of 117 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](#)

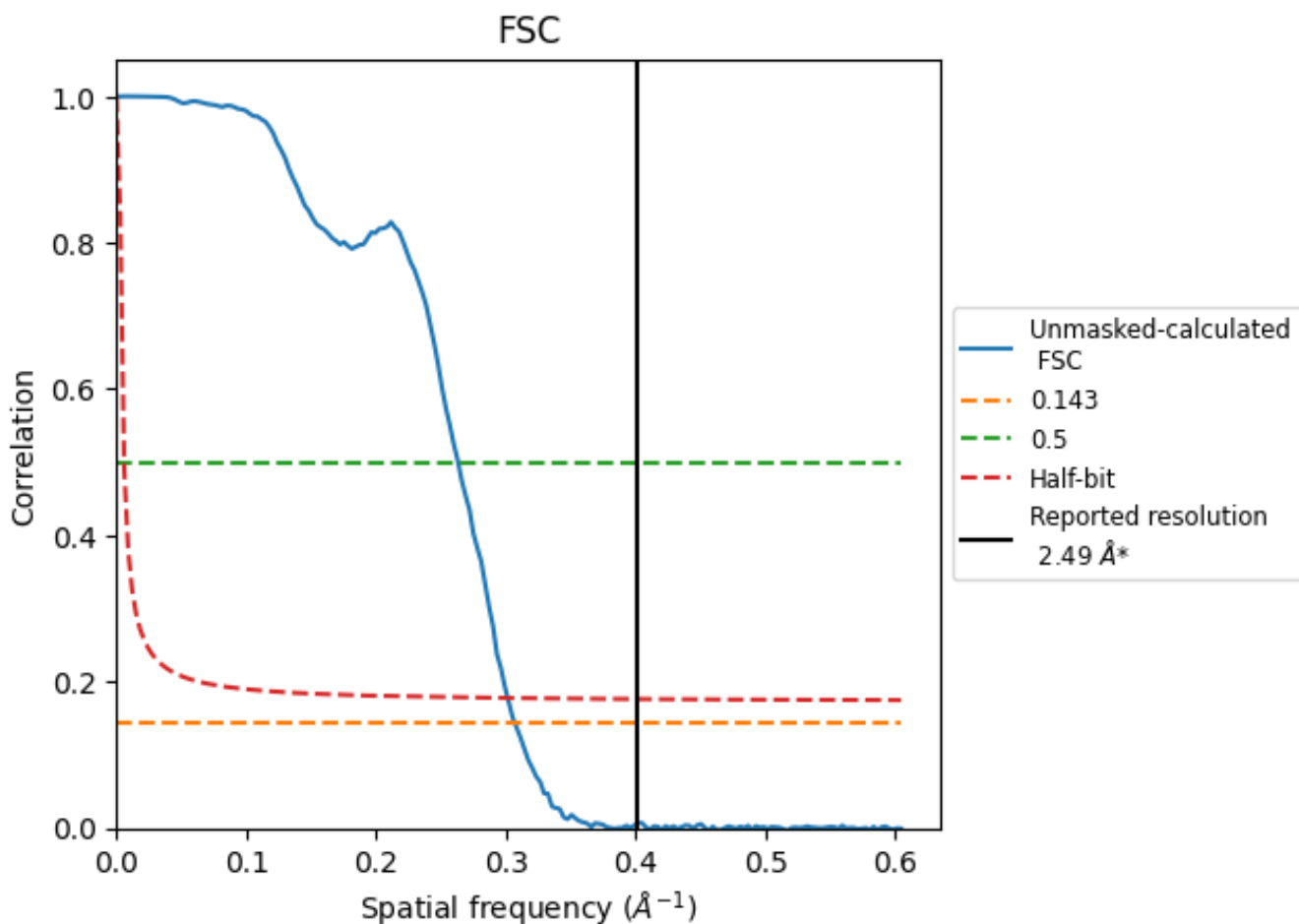


\*Reported resolution corresponds to spatial frequency of 0.402 Å<sup>-1</sup>

## 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 0.402 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

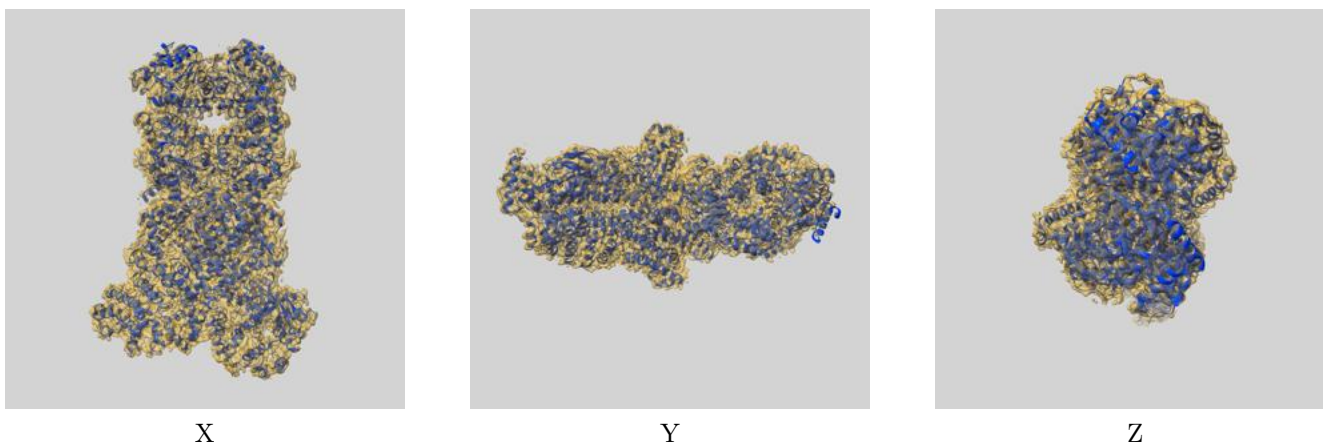
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.49	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.26	3.80	3.32

\*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 3.26 differs from the reported value 2.49 by more than 10 %

## 9 Map-model fit [i](#)

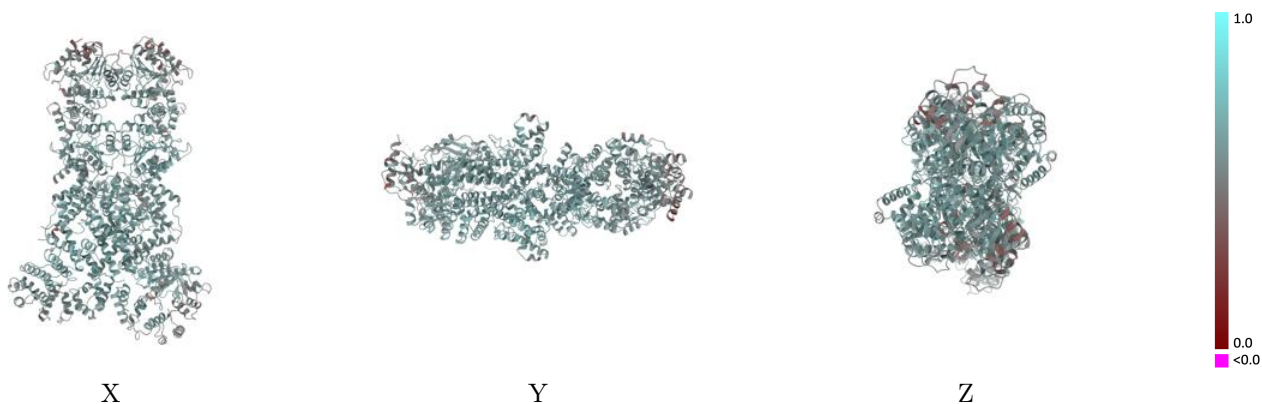
This section contains information regarding the fit between EMDB map EMD-37925 and PDB model 8WYE. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



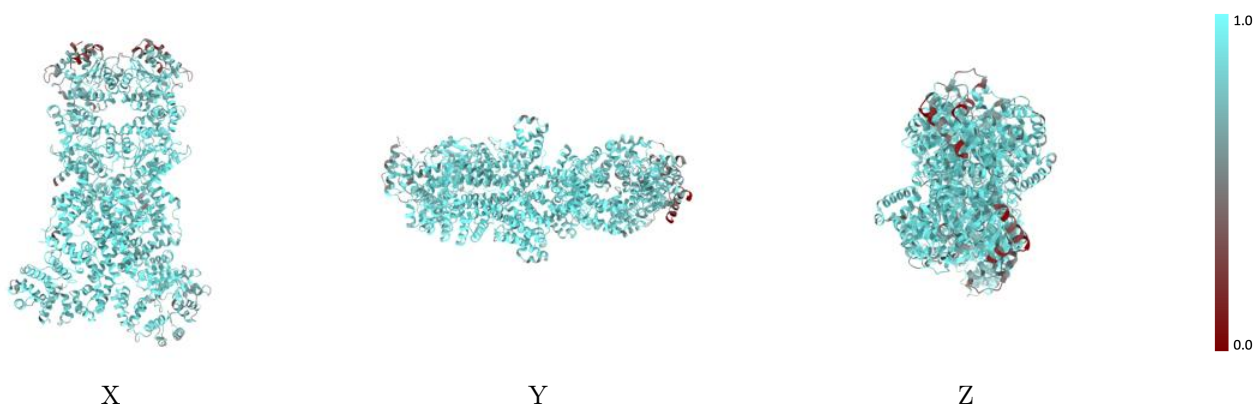
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



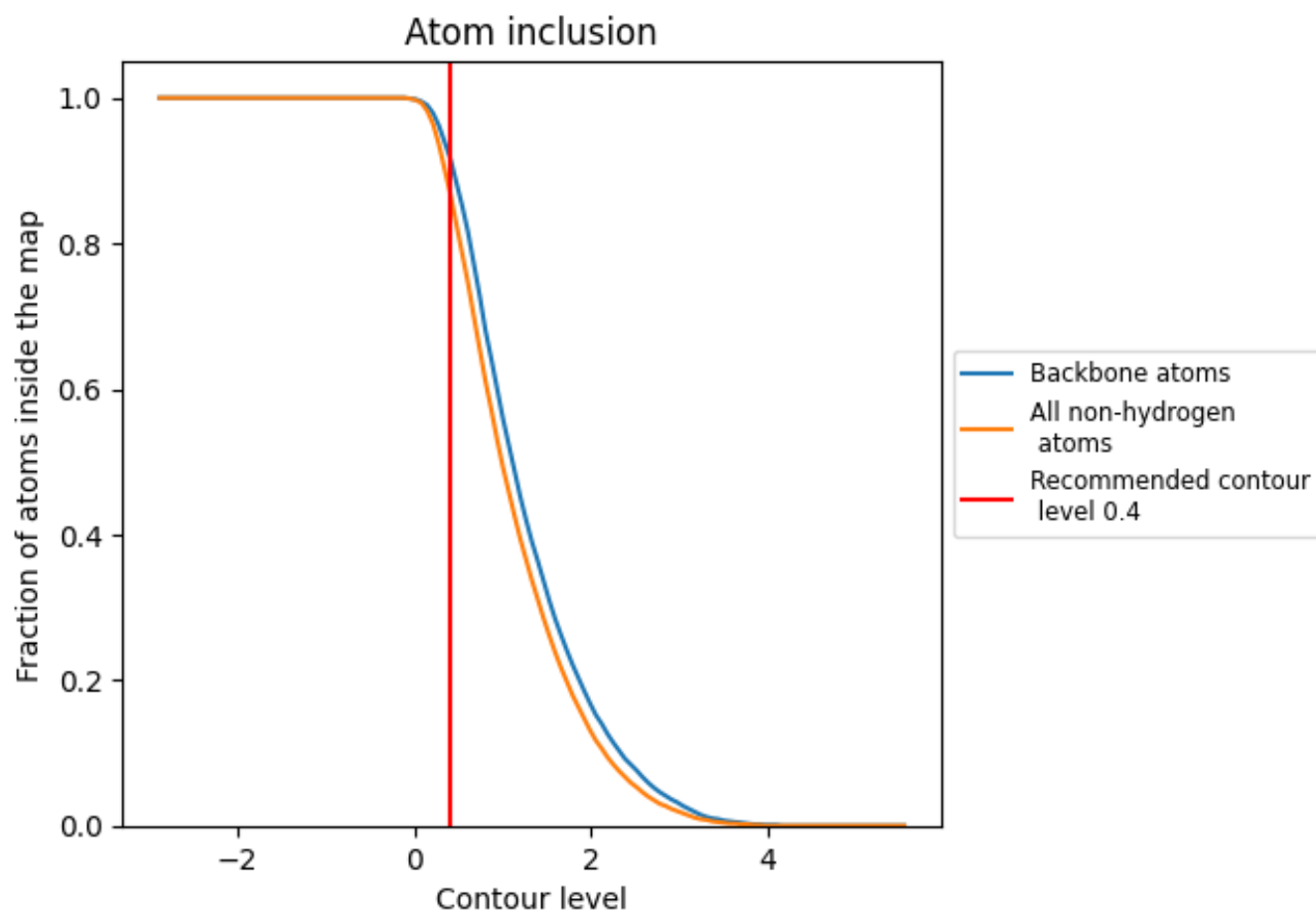
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

## 9.4 Atom inclusion [i](#)















At the recommended contour level, 92% of all backbone atoms, 87% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8730	 0.5840
A	 0.9120	 0.5970
B	 0.9100	 0.5970
C	 0.8270	 0.5610
D	 0.7470	 0.5390
E	 0.7510	 0.5420

