



## Full wwPDB EM Validation Report ⓘ

May 19, 2025 – 12:11 PM EDT

PDB ID : 9ARL / pdb\_00009arl  
EMDB ID : EMD-43786  
Title : CryoEM structure of BoNT-NTNH-OrfX2 complex from Clostridium botulinum strain A1-ST7B, major class  
Authors : Gao, L.  
Deposited on : 2024-02-23  
Resolution : 4.00 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.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

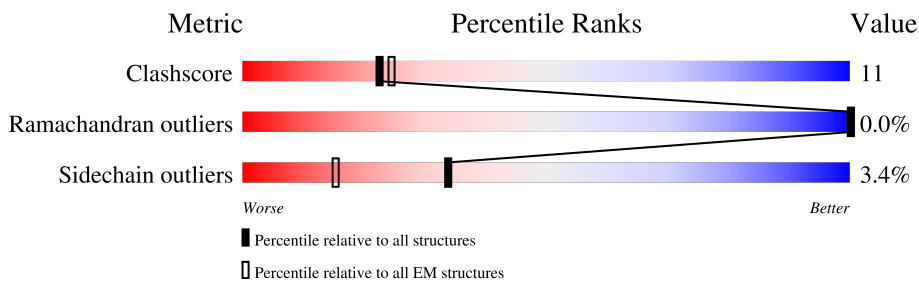
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1296	
2	B	1161	
3	C	750	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24054 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 Botulinum neurotoxin type A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1275	Total	C	N	O	S	0	0
			10336	6634	1704	1965	33		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	224	GLN	GLU	engineered mutation	UNP P0DPI1
A	363	ALA	ARG	engineered mutation	UNP P0DPI1
A	366	PHE	TYR	engineered mutation	UNP P0DPI1

- Molecule 2 is a protein called NtnH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1147	Total	C	N	O	S	0	0
			9349	6013	1485	1820	31		

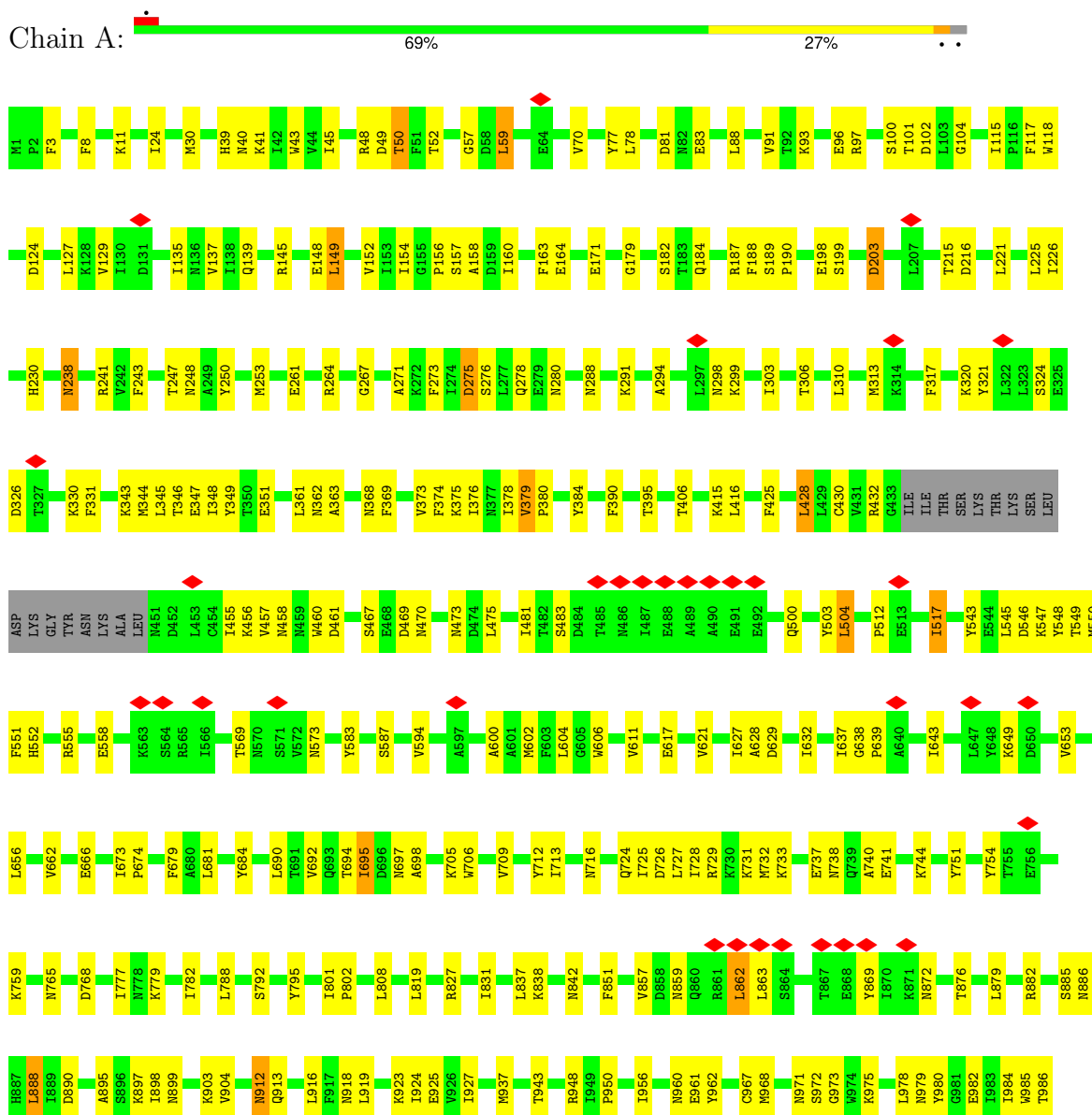
- Molecule 3 is a protein called OrfX2.

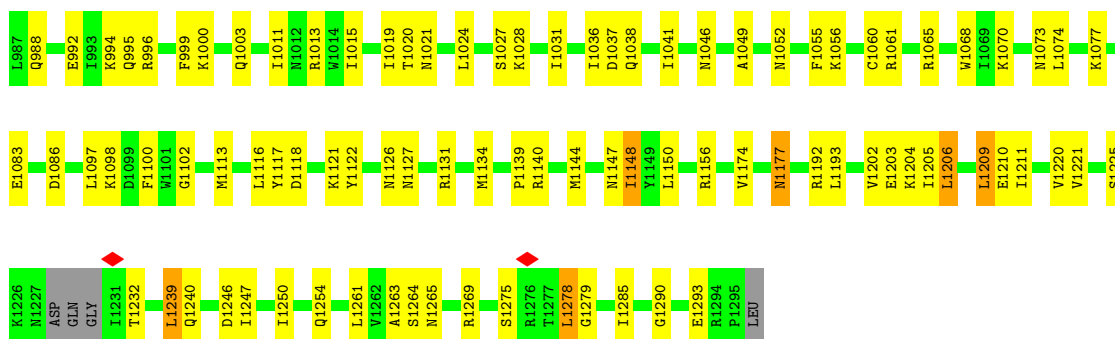
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	561	Total	C	N	O	S	0	0
			4369	2766	735	861	7		

### 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.

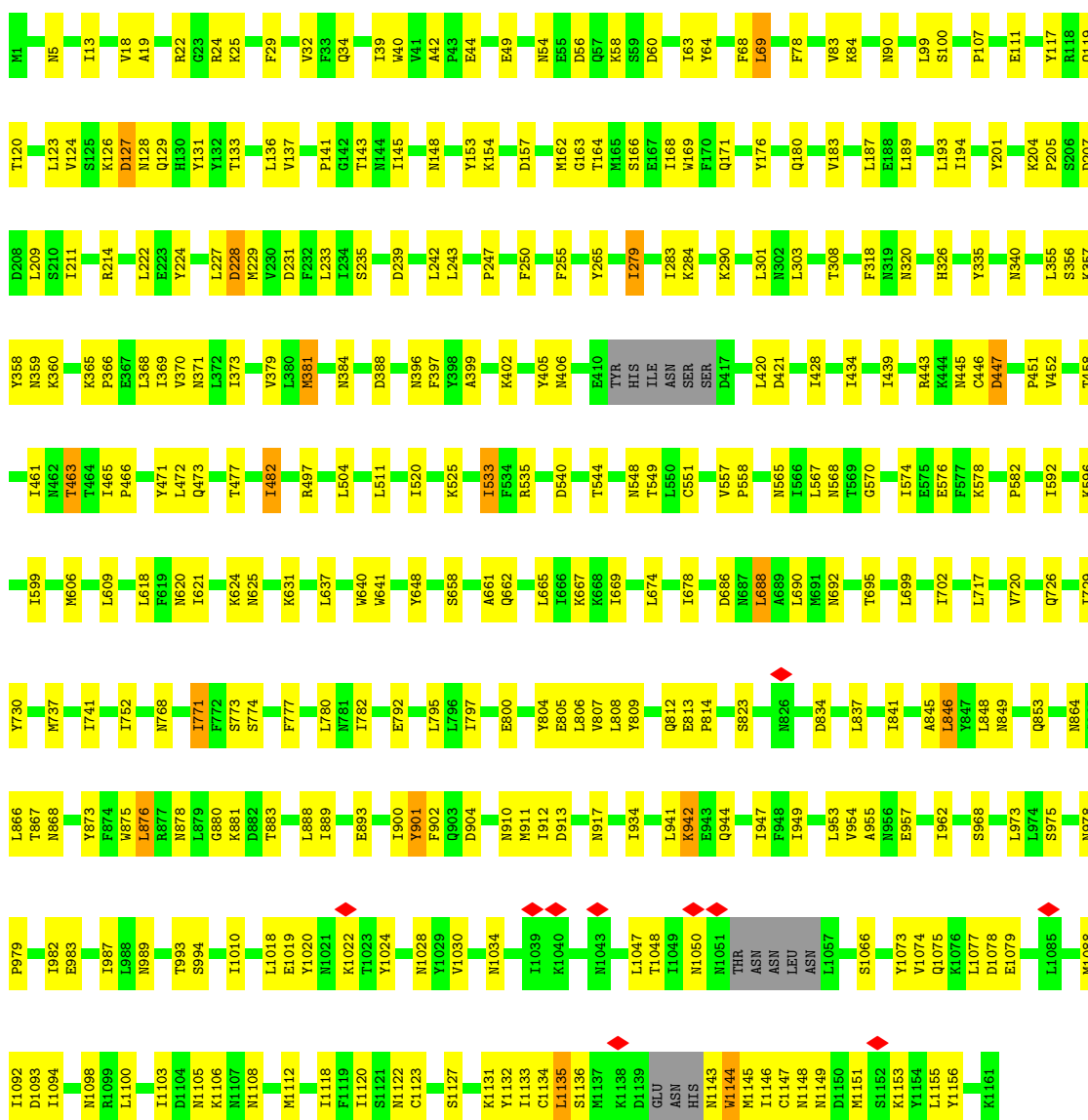
#### • Molecule 1: Botulinum neurotoxin type A





• Molecule 2: NtnH

Chain B: 70% 27%



• Molecule 3: OrfX2



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135181	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.407	Depositor
Minimum map value	-0.223	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size ( $\text{\AA}$ )	403.456, 403.456, 403.456	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.788, 0.788, 0.788	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	0.16	0/10556	0.29	0/14298
2	B	0.17	0/9549	0.28	0/12956
3	C	0.09	0/4443	0.25	0/6008
All	All	0.16	0/24548	0.28	0/33262

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	10336	0	10182	235	0
2	B	9349	0	9070	204	0
3	C	4369	0	4292	98	0
All	All	24054	0	23544	526	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 11.

All (526) 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)
2:B:848:LEU:O	2:B:979:PRO:HA	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1239:LEU:HD12	1:A:1247:ILE:HD11	1.63	0.79
3:C:533:PRO:HD2	3:C:602:VAL:HG11	1.65	0.78
1:A:1117:TYR:HD1	1:A:1278:LEU:HD11	1.53	0.73
1:A:1278:LEU:HD12	1:A:1278:LEU:C	2.13	0.73
1:A:838:LYS:O	1:A:842:ASN:ND2	2.20	0.73
1:A:1203:GLU:HG3	1:A:1264:SER:HB2	1.71	0.73
3:C:535:ILE:HB	3:C:597:ILE:HB	1.71	0.73
2:B:1131:LYS:HE2	2:B:1148:ASN:HA	1.71	0.72
2:B:678:ILE:HD11	2:B:692:ASN:HD21	1.54	0.72
2:B:1047:LEU:HB2	2:B:1145:MET:HE1	1.73	0.71
3:C:616:LEU:O	3:C:620:ASN:ND2	2.21	0.70
1:A:904:VAL:HG11	1:A:924:ILE:HD11	1.74	0.69
1:A:275:ASP:OD1	1:A:275:ASP:N	2.15	0.69
1:A:695:ILE:HG22	1:A:819:LEU:HD11	1.75	0.68
2:B:58:LYS:O	2:B:365:LYS:NZ	2.26	0.68
2:B:618:LEU:HD11	2:B:752:ILE:HD11	1.76	0.68
2:B:120:THR:HG23	2:B:445:ASN:HB2	1.75	0.67
3:C:355:TRP:HB2	3:C:420:LEU:HD21	1.76	0.67
1:A:101:THR:HG23	1:A:104:GLY:H	1.58	0.67
1:A:288:ASN:HA	1:A:291:LYS:HE3	1.76	0.67
1:A:379:VAL:HG13	1:A:380:PRO:HD3	1.77	0.67
3:C:286:LEU:HB3	3:C:339:PHE:HB2	1.77	0.67
3:C:342:ILE:HG21	3:C:361:ILE:HG21	1.76	0.66
1:A:1192:ARG:HG2	1:A:1211:ILE:HG13	1.76	0.66
3:C:224:THR:H	3:C:375:PRO:HB3	1.61	0.66
1:A:264:ARG:HD2	1:A:346:THR:HB	1.76	0.66
2:B:849:ASN:H	2:B:853:GLN:HG3	1.59	0.66
3:C:548:GLU:OE2	3:C:583:ARG:NH1	2.28	0.66
2:B:133:THR:HG21	2:B:434:ILE:HD12	1.77	0.66
2:B:582:PRO:HB3	2:B:720:VAL:HG13	1.77	0.66
2:B:229:MET:HE2	2:B:255:PHE:HZ	1.61	0.65
3:C:582:ILE:HA	3:C:585:LYS:HZ3	1.61	0.65
3:C:350:ILE:HD13	3:C:677:GLY:HA3	1.79	0.65
1:A:182:SER:O	1:A:184:GLN:NE2	2.29	0.65
1:A:344:MET:HA	1:A:348:ILE:HD12	1.79	0.65
1:A:550:MET:HE1	1:A:728:ILE:HG12	1.78	0.65
1:A:972:SER:HA	1:A:988:GLN:O	1.98	0.64
1:A:294:ALA:O	1:A:298:ASN:ND2	2.30	0.64
2:B:504:LEU:HD22	2:B:540:ASP:HB3	1.78	0.64
2:B:640:TRP:HB2	2:B:729:ILE:HG12	1.79	0.64
3:C:502:VAL:HG11	3:C:551:ILE:HG12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:597:ILE:HG23	3:C:601:ASN:HB3	1.80	0.63
3:C:231:ILE:HG13	3:C:263:LEU:HG	1.80	0.63
1:A:629:ASP:OD1	2:B:944:GLN:NE2	2.32	0.63
1:A:982:GLU:HG2	1:A:1000:LYS:HG2	1.81	0.62
1:A:712:TYR:O	1:A:716:ASN:ND2	2.30	0.62
2:B:674:LEU:HD21	2:B:692:ASN:HD22	1.65	0.62
3:C:353:TYR:HB3	3:C:356:LEU:HD12	1.81	0.62
1:A:230:HIS:NE2	1:A:345:LEU:O	2.33	0.62
1:A:276:SER:O	1:A:280:ASN:ND2	2.28	0.62
1:A:897:LYS:HB2	1:A:927:ILE:HB	1.81	0.62
2:B:128:ASN:ND2	3:C:318:ASP:OD2	2.32	0.62
2:B:768:ASN:HA	2:B:771:ILE:HD11	1.82	0.62
1:A:59:LEU:HD13	1:A:158:ALA:HA	1.81	0.62
1:A:1139:PRO:O	1:A:1156:ARG:NH2	2.32	0.62
1:A:726:ASP:OD1	1:A:729:ARG:NH1	2.32	0.61
2:B:127:ASP:OD1	2:B:127:ASP:N	2.23	0.61
2:B:357:LYS:O	2:B:360:LYS:NZ	2.33	0.61
1:A:1097:LEU:HD13	1:A:1174:VAL:HG12	1.80	0.61
1:A:306:THR:HB	1:A:517:ILE:HG22	1.81	0.61
1:A:1037:ASP:OD1	1:A:1038:GLN:N	2.32	0.61
1:A:913:GLN:HG2	1:A:1070:LYS:HD3	1.83	0.61
3:C:460:LYS:HD2	3:C:468:ASN:HB3	1.83	0.61
2:B:402:LYS:HE2	2:B:596:LYS:HG2	1.81	0.61
3:C:436:ILE:HD12	3:C:441:ILE:HB	1.82	0.61
1:A:24:ILE:HG22	1:A:135:ILE:HD11	1.81	0.60
1:A:1027:SER:HB3	1:A:1041:ILE:HD13	1.82	0.60
1:A:1117:TYR:CD1	1:A:1278:LEU:HD11	2.36	0.60
2:B:136:LEU:HD11	2:B:168:ILE:HG13	1.83	0.60
1:A:628:ALA:HA	2:B:942:LYS:HB3	1.82	0.60
2:B:69:LEU:HD21	2:B:78:PHE:HB2	1.82	0.60
2:B:883:THR:HG23	2:B:904:ASP:HA	1.84	0.60
1:A:1193:LEU:HG	1:A:1206:LEU:HD21	1.84	0.60
1:A:428:LEU:HD12	1:A:456:LYS:HG2	1.84	0.60
1:A:979:ASN:OD1	1:A:980:TYR:N	2.35	0.59
1:A:1204:LYS:HZ1	1:A:1263:ALA:HB3	1.67	0.59
2:B:1127:SER:HA	2:B:1132:TYR:HA	1.83	0.59
1:A:681:LEU:HD23	1:A:694:THR:HG22	1.84	0.59
1:A:1275:SER:HB3	2:B:795:LEU:HD13	1.83	0.59
2:B:120:THR:O	2:B:445:ASN:ND2	2.29	0.59
2:B:621:ILE:O	2:B:625:ASN:ND2	2.26	0.59
1:A:706:TRP:CE3	1:A:808:LEU:HD13	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:923:LYS:HA	1:A:1055:PHE:O	2.03	0.59
3:C:259:ILE:HG22	3:C:300:ILE:HG12	1.84	0.59
3:C:512:TYR:HB3	3:C:527:LEU:HD11	1.83	0.59
1:A:1239:LEU:HD23	1:A:1250:ILE:HD11	1.84	0.58
3:C:186:MET:HE3	3:C:190:ILE:HD11	1.83	0.58
1:A:326:ASP:OD1	1:A:330:LYS:N	2.36	0.58
2:B:368:LEU:HD21	2:B:461:ILE:HD12	1.83	0.58
2:B:154:LYS:HD3	2:B:157:ASP:HB2	1.85	0.58
2:B:548:ASN:O	2:B:578:LYS:NZ	2.33	0.58
1:A:995:GLN:HG2	1:A:1041:ILE:HG22	1.84	0.58
1:A:1134:MET:HB3	1:A:1261:LEU:HB2	1.85	0.58
2:B:1100:LEU:HD21	2:B:1133:ILE:HD13	1.85	0.58
1:A:230:HIS:ND1	1:A:261:GLU:OE2	2.26	0.58
1:A:115:ILE:HD11	1:A:512:PRO:HB3	1.85	0.58
2:B:592:ILE:HG13	2:B:729:ILE:HG13	1.86	0.58
3:C:690:ILE:HA	3:C:693:MET:HG2	1.86	0.58
3:C:661:ILE:HG22	3:C:665:LYS:HE2	1.85	0.57
2:B:22:ARG:HB3	2:B:124:VAL:HG23	1.85	0.57
2:B:145:ILE:O	2:B:171:GLN:NE2	2.37	0.57
1:A:24:ILE:H	1:A:30:MET:HE1	1.69	0.57
3:C:619:ILE:HG12	3:C:622:ARG:HH21	1.69	0.57
3:C:303:TYR:HE2	3:C:317:LYS:HB3	1.70	0.57
2:B:356:SER:O	2:B:359:ASN:ND2	2.37	0.57
1:A:351:GLU:OE2	1:A:362:ASN:ND2	2.36	0.57
1:A:979:ASN:HB3	1:A:982:GLU:HB2	1.85	0.57
1:A:673:ILE:HD12	1:A:674:PRO:HD2	1.87	0.57
1:A:768:ASP:OD2	1:A:937:MET:N	2.38	0.56
2:B:1134:CYS:HB2	2:B:1155:LEU:HB3	1.87	0.56
3:C:173:LEU:HD13	3:C:397:SER:HB2	1.86	0.56
2:B:279:ILE:HB	2:B:284:LYS:HZ1	1.70	0.56
2:B:396:ASN:OD1	2:B:399:ALA:N	2.38	0.56
1:A:1013:ARG:NE	1:A:1100:PHE:O	2.38	0.56
2:B:511:LEU:HD21	2:B:533:ILE:HD11	1.87	0.56
2:B:49:GLU:HG2	2:B:451:PRO:HB3	1.86	0.56
1:A:549:THR:OG1	1:A:550:MET:N	2.38	0.56
1:A:948:ARG:HB3	1:A:1068:TRP:HB2	1.87	0.56
1:A:600:ALA:HA	1:A:754:TYR:CZ	2.41	0.56
3:C:429:ALA:HB1	3:C:666:ILE:HG23	1.88	0.56
1:A:1220:VAL:HB	1:A:1240:GLN:O	2.06	0.56
2:B:808:LEU:HD21	2:B:846:LEU:HD21	1.88	0.56
1:A:882:ARG:NH1	1:A:1073:ASN:OD1	2.32	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:436:ILE:HG22	3:C:456:ILE:HG21	1.87	0.55
1:A:11:LYS:NZ	1:A:81:ASP:OD2	2.39	0.55
2:B:1019:GLU:N	2:B:1024:TYR:OH	2.36	0.55
2:B:1151:MET:SD	2:B:1151:MET:N	2.79	0.55
3:C:272:ILE:HD13	3:C:341:TYR:HB3	1.87	0.55
1:A:961:GLU:OE2	1:A:996:ARG:NH2	2.39	0.55
1:A:1028:LYS:HB3	1:A:1038:GLN:HB3	1.87	0.55
1:A:583:TYR:OH	1:A:639:PRO:O	2.22	0.55
3:C:229:ARG:HH21	3:C:262:ASP:HB3	1.71	0.55
1:A:238:ASN:OD1	1:A:238:ASN:N	2.40	0.55
2:B:726:GLN:HE22	2:B:780:LEU:HD11	1.72	0.55
1:A:8:PHE:HB3	1:A:88:LEU:HD21	1.88	0.55
1:A:164:GLU:OE2	1:A:187:ARG:NH1	2.40	0.55
2:B:239:ASP:HA	2:B:242:LEU:HD12	1.88	0.55
2:B:606:MET:HA	2:B:609:LEU:HD23	1.89	0.55
2:B:730:TYR:CZ	2:B:780:LEU:HB2	2.42	0.55
2:B:806:LEU:HD23	2:B:987:ILE:HD13	1.88	0.55
3:C:363:TYR:HA	3:C:384:ALA:HA	1.89	0.54
2:B:301:LEU:HD11	2:B:420:LEU:HD21	1.88	0.54
3:C:541:GLU:HG2	3:C:593:LYS:HE2	1.88	0.54
1:A:1240:GLN:NE2	1:A:1246:ASP:OD1	2.41	0.54
2:B:381:MET:HE1	2:B:473:GLN:HB3	1.90	0.54
2:B:477:THR:OG1	2:B:497:ARG:NH1	2.39	0.54
2:B:29:PHE:CE2	2:B:126:LYS:HA	2.43	0.54
2:B:405:TYR:HE2	2:B:599:ILE:HG23	1.73	0.54
1:A:467:SER:O	1:A:470:ASN:ND2	2.38	0.54
2:B:686:ASP:OD1	2:B:686:ASP:N	2.39	0.54
1:A:375:LYS:HB2	1:A:416:LEU:HD11	1.88	0.53
2:B:227:LEU:HD21	2:B:320:ASN:HD22	1.72	0.53
2:B:910:ASN:HD21	2:B:912:ILE:HD11	1.72	0.53
1:A:918:ASN:ND2	1:A:1060:CYS:O	2.32	0.53
2:B:1034:ASN:ND2	2:B:1050:ASN:O	2.33	0.53
3:C:363:TYR:O	3:C:398:HIS:ND1	2.41	0.53
1:A:93:LYS:NZ	1:A:378:ILE:O	2.33	0.53
1:A:779:LYS:O	1:A:782:ILE:HG22	2.08	0.53
2:B:888:LEU:HA	2:B:975:SER:HA	1.90	0.53
2:B:889:ILE:HD12	2:B:973:LEU:HD13	1.91	0.53
3:C:604:GLN:NE2	3:C:608:ASP:OD2	2.42	0.53
2:B:1122:ASN:N	2:B:1122:ASN:OD1	2.42	0.53
3:C:422:ILE:HG23	3:C:426:LEU:HD12	1.91	0.53
2:B:111:GLU:HB3	2:B:117:TYR:CE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:543:GLN:HE21	3:C:551:ILE:HG21	1.74	0.53
3:C:417:SER:HB2	3:C:419:PRO:HD2	1.90	0.53
1:A:1118:ASP:HB2	1:A:1121:LYS:HE2	1.90	0.53
1:A:48:ARG:NH1	1:A:77:TYR:O	2.42	0.52
1:A:303:ILE:HD11	1:A:310:LEU:HA	1.90	0.52
1:A:555:ARG:NH1	1:A:558:GLU:OE2	2.41	0.52
1:A:611:VAL:HG12	1:A:1024:LEU:HD11	1.91	0.52
2:B:849:ASN:OD1	2:B:853:GLN:NE2	2.41	0.52
1:A:999:PHE:HD1	1:A:1036:ILE:HG21	1.75	0.52
1:A:604:LEU:HD11	1:A:937:MET:HE1	1.91	0.52
3:C:586:ALA:HA	3:C:595:ILE:HG22	1.91	0.52
2:B:58:LYS:HD2	2:B:64:TYR:CD2	2.45	0.52
1:A:550:MET:HE2	1:A:731:LYS:HD2	1.90	0.52
2:B:667:LYS:HG2	2:B:699:LEU:HD22	1.92	0.52
3:C:477:LYS:HD2	3:C:492:PHE:HB2	1.90	0.52
3:C:186:MET:O	3:C:190:ILE:HG12	2.09	0.52
3:C:483:GLN:HB2	3:C:488:VAL:HG21	1.90	0.52
1:A:430:CYS:O	1:A:545:LEU:N	2.43	0.52
1:A:558:GLU:HG2	1:A:738:ASN:HD21	1.75	0.52
1:A:587:SER:OG	1:A:617:GLU:OE2	2.22	0.52
2:B:1131:LYS:HA	2:B:1149:ASN:HD21	1.74	0.52
2:B:84:LYS:NZ	2:B:335:TYR:O	2.29	0.51
2:B:807:VAL:HG22	2:B:823:SER:HB3	1.92	0.51
2:B:812:GLN:NE2	2:B:837:LEU:O	2.43	0.51
1:A:139:GLN:HE21	1:A:145:ARG:HD3	1.74	0.51
2:B:127:ASP:HB2	2:B:129:GLN:HE22	1.74	0.51
1:A:163:PHE:HD1	1:A:188:PHE:HA	1.74	0.51
1:A:483:SER:HB3	1:A:684:TYR:HE2	1.76	0.51
2:B:63:ILE:HG21	2:B:358:TYR:HB3	1.91	0.51
2:B:737:MET:HE2	2:B:777:PHE:HB3	1.92	0.51
3:C:459:GLY:N	3:C:471:SER:OG	2.43	0.51
1:A:916:LEU:HD11	1:A:1055:PHE:HB3	1.93	0.51
1:A:967:CYS:SG	1:A:1049:ALA:HB1	2.51	0.51
1:A:1147:ASN:ND2	2:B:620:ASN:OD1	2.44	0.51
2:B:239:ASP:OD1	2:B:641:TRP:NE1	2.41	0.51
3:C:709:GLN:HA	3:C:712:ILE:HG12	1.92	0.51
1:A:984:ILE:HG21	1:A:996:ARG:HE	1.75	0.51
2:B:388:ASP:OD1	2:B:388:ASP:N	2.42	0.51
1:A:638:GLY:HA2	1:A:643:ILE:HG22	1.92	0.50
1:A:765:ASN:OD1	1:A:765:ASN:N	2.44	0.50
1:A:97:ARG:O	1:A:100:SER:OG	2.21	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:LYS:HG3	1:A:986:THR:HB	1.93	0.50
1:A:216:ASP:OD1	1:A:384:TYR:OH	2.25	0.50
3:C:538:TYR:CD1	3:C:594:LYS:HD2	2.45	0.50
3:C:486:LEU:HD13	3:C:511:GLU:HB3	1.93	0.50
1:A:637:ILE:HG12	1:A:732:MET:HE2	1.94	0.50
2:B:235:SER:OG	2:B:320:ASN:ND2	2.34	0.50
2:B:54:ASN:ND2	2:B:56:ASP:OD1	2.44	0.49
2:B:678:ILE:HG12	2:B:688:LEU:HD12	1.94	0.49
3:C:190:ILE:HD12	3:C:337:GLN:HG2	1.94	0.49
3:C:381:ILE:HD12	3:C:405:LEU:HG	1.94	0.49
1:A:504:LEU:HD21	2:B:1135:LEU:HD12	1.94	0.49
1:A:751:TYR:CZ	1:A:759:LYS:HG3	2.47	0.49
1:A:1193:LEU:HD11	1:A:1206:LEU:HD11	1.94	0.49
2:B:866:LEU:HG	2:B:867:THR:HG23	1.93	0.49
2:B:805:GLU:OE2	2:B:989:ASN:ND2	2.27	0.49
3:C:629:GLU:HG2	3:C:632:ARG:HH21	1.76	0.49
2:B:373:ILE:HG22	2:B:379:VAL:HA	1.93	0.49
3:C:350:ILE:HD12	3:C:676:VAL:HG12	1.95	0.49
2:B:549:THR:C	2:B:551:CYS:H	2.20	0.49
2:B:876:LEU:HD22	2:B:934:ILE:HD11	1.94	0.49
1:A:45:ILE:HB	1:A:154:ILE:HG13	1.95	0.49
1:A:857:VAL:HG12	1:A:859:ASN:H	1.78	0.49
1:A:198:GLU:OE1	1:A:199:SER:N	2.45	0.49
1:A:374:PHE:CE2	1:A:406:THR:HG21	2.48	0.49
1:A:473:ASN:HD22	1:A:475:LEU:HD12	1.76	0.49
1:A:1015:ILE:HG23	1:A:1031:ILE:HG23	1.94	0.49
2:B:544:THR:HG22	2:B:557:VAL:HG22	1.95	0.49
1:A:692:VAL:HA	1:A:695:ILE:HD11	1.94	0.49
2:B:878:ASN:OD1	2:B:880:GLY:N	2.45	0.49
2:B:1135:LEU:HD11	2:B:1143:ASN:HB3	1.95	0.49
2:B:1136:SER:HB3	2:B:1146:ILE:HG23	1.95	0.49
3:C:471:SER:HB2	3:C:494:LEU:HD11	1.95	0.49
1:A:288:ASN:O	1:A:291:LYS:HG2	2.13	0.48
1:A:481:ILE:HD13	1:A:698:ALA:HA	1.94	0.48
1:A:662:VAL:HG22	1:A:795:TYR:HE2	1.78	0.48
1:A:1269:ARG:HG2	2:B:809:TYR:CZ	2.48	0.48
2:B:124:VAL:HG12	2:B:131:TYR:CE2	2.48	0.48
1:A:118:TRP:CD2	1:A:129:VAL:HG22	2.48	0.48
2:B:1092:ILE:HD11	2:B:1100:LEU:HD23	1.94	0.48
1:A:924:ILE:HB	1:A:1055:PHE:HB2	1.93	0.48
2:B:308:THR:HA	2:B:792:GLU:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:684:TYR:CD2	1:A:690:LEU:HB3	2.49	0.48
1:A:985:TRP:CE2	1:A:1019:ILE:HG21	2.48	0.48
2:B:5:ASN:HA	2:B:83:VAL:HG11	1.95	0.48
2:B:279:ILE:HB	2:B:284:LYS:NZ	2.29	0.48
2:B:957:GLU:N	2:B:957:GLU:OE1	2.46	0.48
3:C:355:TRP:HA	3:C:389:GLU:HG3	1.95	0.48
2:B:845:ALA:HB2	2:B:983:GLU:HB2	1.95	0.48
2:B:973:LEU:HD21	2:B:982:ILE:HG21	1.95	0.48
1:A:160:ILE:HD12	1:A:160:ILE:H	1.78	0.48
1:A:363:ALA:HB1	1:A:368:ASN:HB3	1.96	0.48
1:A:483:SER:O	1:A:697:ASN:ND2	2.46	0.48
1:A:124:ASP:O	1:A:299:LYS:NZ	2.46	0.48
2:B:864:ASN:HD22	2:B:868:ASN:HD21	1.61	0.48
3:C:419:PRO:O	3:C:423:GLU:HG2	2.14	0.48
2:B:366:PRO:HB3	2:B:384:ASN:HB3	1.95	0.48
3:C:283:GLN:HE21	3:C:285:ASN:HD21	1.60	0.48
3:C:431:LEU:HD11	3:C:438:VAL:HA	1.96	0.48
1:A:267:GLY:HA2	1:A:271:ALA:HB2	1.96	0.47
1:A:78:LEU:N	1:A:83:GLU:OE1	2.47	0.47
1:A:248:ASN:O	1:A:543:TYR:OH	2.31	0.47
2:B:463:THR:OG1	2:B:465:ILE:O	2.31	0.47
2:B:1091:TYR:HE2	2:B:1106:LYS:HA	1.79	0.47
1:A:1031:ILE:HB	1:A:1036:ILE:HG13	1.97	0.47
1:A:432:ARG:HG2	1:A:546:ASP:HA	1.96	0.47
1:A:882:ARG:HH22	1:A:1073:ASN:HD21	1.61	0.47
3:C:223:THR:HG22	3:C:377:LEU:HD11	1.96	0.47
3:C:623:ASN:HA	3:C:626:ILE:HG22	1.95	0.47
3:C:666:ILE:O	3:C:669:THR:OG1	2.31	0.47
1:A:705:LYS:O	1:A:709:VAL:HG12	2.15	0.47
1:A:740:ALA:HB2	1:A:777:ILE:HD11	1.96	0.47
1:A:962:TYR:CG	1:A:1060:CYS:HB2	2.50	0.47
2:B:148:ASN:HA	2:B:169:TRP:O	2.15	0.47
3:C:224:THR:HG23	3:C:367:SER:HB2	1.97	0.47
1:A:148:GLU:OE1	1:A:148:GLU:N	2.44	0.47
1:A:481:ILE:HD11	1:A:679:PHE:CD2	2.50	0.47
1:A:956:ILE:HD11	1:A:1061:ARG:HD2	1.96	0.47
1:A:968:MET:HE2	1:A:971:ASN:HA	1.97	0.47
2:B:520:ILE:HG23	2:B:525:LYS:HB2	1.96	0.47
3:C:353:TYR:CG	3:C:676:VAL:HG13	2.50	0.47
1:A:985:TRP:NE1	1:A:1021:ASN:HD21	2.12	0.47
2:B:741:ILE:HD13	2:B:777:PHE:HE2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:359:THR:HG21	3:C:390:ASN:H	1.80	0.47
3:C:231:ILE:HD11	3:C:363:TYR:HE2	1.80	0.47
1:A:733:LYS:O	1:A:737:GLU:HG2	2.15	0.47
3:C:709:GLN:O	3:C:713:GLY:N	2.44	0.46
1:A:1177:ASN:OD1	1:A:1177:ASN:N	2.47	0.46
2:B:558:PRO:HB3	2:B:574:ILE:HD11	1.97	0.46
2:B:1120:ILE:HG21	2:B:1123:CYS:HB2	1.97	0.46
2:B:204:LYS:NZ	2:B:207:ASP:OD1	2.41	0.46
2:B:1075:GLN:N	2:B:1075:GLN:OE1	2.49	0.46
1:A:1122:TYR:OH	1:A:1156:ARG:NH2	2.48	0.46
2:B:22:ARG:HB2	2:B:29:PHE:CE2	2.50	0.46
2:B:40:TRP:HB2	2:B:137:VAL:HG22	1.97	0.46
2:B:902:PHE:CE2	2:B:978:ASN:HB2	2.50	0.46
1:A:879:LEU:HB3	1:A:1074:LEU:HB3	1.97	0.46
1:A:547:LYS:HG2	1:A:548:TYR:O	2.15	0.46
1:A:1131:ARG:H	1:A:1131:ARG:HD3	1.81	0.46
2:B:366:PRO:HG2	2:B:369:ILE:HD11	1.97	0.46
1:A:1204:LYS:HE2	1:A:1247:ILE:HB	1.98	0.46
1:A:985:TRP:CD2	1:A:1019:ILE:HG21	2.50	0.46
2:B:368:LEU:HD11	2:B:461:ILE:HG13	1.98	0.46
2:B:661:ALA:O	2:B:665:LEU:HG	2.16	0.46
2:B:841:ILE:HG13	2:B:875:TRP:CE3	2.51	0.46
1:A:962:TYR:OH	1:A:1065:ARG:HD3	2.15	0.46
2:B:107:PRO:HB3	2:B:163:GLY:O	2.16	0.46
1:A:737:GLU:O	1:A:741:GLU:HG2	2.16	0.46
2:B:947:ILE:HB	2:B:955:ALA:HB3	1.97	0.46
1:A:91:VAL:HG23	1:A:190:PRO:HG3	1.97	0.45
1:A:457:VAL:HG21	1:A:551:PHE:HB3	1.98	0.45
2:B:1020:TYR:CZ	2:B:1066:SER:HB2	2.51	0.45
3:C:358:PRO:HA	3:C:388:VAL:HG12	1.99	0.45
3:C:676:VAL:HG11	3:C:710:GLN:HG3	1.98	0.45
1:A:872:ASN:O	1:A:876:THR:OG1	2.22	0.45
1:A:937:MET:HE2	1:A:937:MET:HB3	1.81	0.45
1:A:1122:TYR:HD1	1:A:1140:ARG:HD2	1.81	0.45
2:B:620:ASN:O	2:B:624:LYS:HG2	2.16	0.45
1:A:156:PRO:HG3	1:A:160:ILE:HG23	1.98	0.45
3:C:232:ARG:HH21	3:C:258:LEU:HB3	1.82	0.45
2:B:1105:ASN:HB3	2:B:1108:ASN:HB3	1.99	0.45
3:C:458:PHE:CZ	3:C:659:ILE:HG12	2.52	0.45
1:A:594:VAL:HA	1:A:606:TRP:HZ2	1.82	0.45
1:A:1098:LYS:NZ	1:A:1102:GLY:O	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1018:LEU:HD23	2:B:1019:GLU:N	2.32	0.45
2:B:141:PRO:HA	2:B:169:TRP:HB3	1.97	0.45
2:B:726:GLN:HE22	2:B:780:LEU:HD21	1.82	0.45
2:B:804:TYR:O	2:B:823:SER:HB2	2.17	0.45
1:A:157:SER:OG	1:A:158:ALA:N	2.50	0.45
1:A:1077:LYS:NZ	1:A:1083:GLU:OE1	2.50	0.45
1:A:1118:ASP:OD1	1:A:1118:ASP:N	2.50	0.45
2:B:567:LEU:HB3	2:B:576:GLU:CD	2.42	0.45
3:C:502:VAL:HG13	3:C:543:GLN:HG3	1.98	0.45
3:C:422:ILE:HD12	3:C:448:LEU:HD22	1.98	0.45
1:A:569:THR:O	1:A:583:TYR:HA	2.16	0.44
1:A:999:PHE:CD1	1:A:1036:ILE:HG21	2.52	0.44
2:B:1079:GLU:HA	2:B:1112:MET:O	2.17	0.44
2:B:1091:TYR:CE2	2:B:1106:LYS:HA	2.51	0.44
2:B:1093:ASP:HB2	2:B:1103:ILE:HD13	1.99	0.44
1:A:912:ASN:O	1:A:912:ASN:ND2	2.36	0.44
2:B:888:LEU:HD13	2:B:902:PHE:CZ	2.53	0.44
1:A:324:SER:O	1:A:331:PHE:HA	2.17	0.44
1:A:1211:ILE:HD12	1:A:1211:ILE:H	1.82	0.44
1:A:1221:VAL:HG22	1:A:1239:LEU:HD22	1.99	0.44
1:A:980:TYR:OH	1:A:1148:ILE:O	2.21	0.44
1:A:1097:LEU:HG	1:A:1225:SER:HB2	1.99	0.44
2:B:123:LEU:HD11	2:B:137:VAL:HG21	1.99	0.44
1:A:226:ILE:HG12	1:A:349:TYR:O	2.18	0.44
1:A:243:PHE:CZ	1:A:273:PHE:HB3	2.53	0.44
2:B:443:ARG:HH22	3:C:316:ASP:CG	2.26	0.44
2:B:1019:GLU:HA	2:B:1073:TYR:HA	2.00	0.44
3:C:430:LEU:O	3:C:433:SER:OG	2.32	0.44
3:C:539:VAL:HG12	3:C:593:LYS:HB2	2.00	0.44
1:A:376:ILE:HD12	1:A:390:PHE:HZ	1.82	0.44
1:A:117:PHE:HA	1:A:317:PHE:CZ	2.53	0.44
1:A:198:GLU:HG2	1:A:361:LEU:HD11	2.00	0.43
1:A:801:ILE:N	1:A:802:PRO:HD2	2.33	0.43
1:A:869:TYR:OH	1:A:1086:ASP:OD2	2.28	0.43
2:B:100:SER:HB3	2:B:428:ILE:HD12	1.99	0.43
2:B:162:MET:HG2	2:B:265:TYR:CZ	2.53	0.43
3:C:276:THR:HG21	3:C:709:GLN:HB3	2.00	0.43
1:A:49:ASP:HB3	1:A:187:ARG:HD3	2.00	0.43
1:A:662:VAL:HG22	1:A:795:TYR:CE2	2.53	0.43
2:B:340:ASN:N	2:B:340:ASN:OD1	2.51	0.43
2:B:1028:ASN:OD1	2:B:1030:VAL:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:ILE:HD13	1:A:552:HIS:HA	2.00	0.43
2:B:893:GLU:HB2	2:B:968:SER:HB2	1.99	0.43
1:A:455:ILE:HD12	1:A:555:ARG:HG3	2.00	0.43
1:A:725:ILE:HG13	1:A:792:SER:OG	2.19	0.43
1:A:1144:MET:HB2	1:A:1150:LEU:HD13	2.01	0.43
2:B:214:ARG:HG2	2:B:318:PHE:CE1	2.54	0.43
2:B:582:PRO:O	2:B:648:TYR:OH	2.35	0.43
3:C:507:ASP:HB2	3:C:536:GLU:HB2	1.99	0.43
1:A:725:ILE:HG23	1:A:788:LEU:HB3	2.00	0.43
1:A:885:SER:OG	1:A:886:ASN:N	2.48	0.43
2:B:32:VAL:HG12	2:B:42:ALA:HB2	2.01	0.43
1:A:602:MET:SD	1:A:602:MET:N	2.83	0.43
1:A:1000:LYS:HE3	1:A:1000:LYS:HB3	1.85	0.43
3:C:227:ASP:OD1	3:C:227:ASP:N	2.52	0.43
1:A:903:LYS:HD3	1:A:919:LEU:HD13	2.01	0.43
2:B:834:ASP:O	2:B:853:GLN:NE2	2.48	0.43
2:B:901:TYR:OH	2:B:910:ASN:ND2	2.33	0.43
1:A:548:TYR:OH	1:A:573:ASN:ND2	2.52	0.43
1:A:890:ASP:HB3	1:A:895:ALA:HA	2.01	0.43
1:A:1117:TYR:HB2	1:A:1279:GLY:HA2	2.01	0.43
2:B:34:GLN:HB2	2:B:40:TRP:CE2	2.54	0.43
2:B:565:ASN:HA	2:B:568:ASN:OD1	2.19	0.43
2:B:837:LEU:HD21	2:B:846:LEU:HD23	2.00	0.43
2:B:846:LEU:HD12	2:B:982:ILE:HG23	1.99	0.43
1:A:39:HIS:CG	1:A:40:ASN:H	2.37	0.43
1:A:863:LEU:HD12	1:A:863:LEU:H	1.84	0.43
2:B:466:PRO:HB2	2:B:471:TYR:HE1	1.83	0.43
2:B:567:LEU:HD13	2:B:576:GLU:HB3	2.01	0.43
3:C:242:TYR:CE2	3:C:251:SER:HB3	2.53	0.43
3:C:285:ASN:HB3	3:C:338:ILE:HG23	2.01	0.43
1:A:888:LEU:HD23	1:A:898:ILE:HG21	2.00	0.42
1:A:1036:ILE:O	2:B:782:ILE:HG12	2.19	0.42
2:B:119:GLN:NE2	2:B:283:ILE:HD11	2.34	0.42
2:B:176:TYR:CE1	2:B:183:VAL:HG21	2.54	0.42
2:B:813:GLU:HG3	2:B:814:PRO:HD2	2.00	0.42
3:C:254:GLU:OE1	3:C:254:GLU:N	2.50	0.42
3:C:512:TYR:CE1	3:C:529:VAL:HG12	2.54	0.42
1:A:203:ASP:OD1	1:A:203:ASP:N	2.52	0.42
1:A:744:LYS:HE2	1:A:744:LYS:HB2	1.77	0.42
1:A:950:PRO:HB3	1:A:1290:GLY:HA2	2.01	0.42
1:A:994:LYS:HE3	1:A:994:LYS:HB3	1.80	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:LYS:O	2:B:164:THR:HG21	2.19	0.42
2:B:187:LEU:HD12	2:B:187:LEU:HA	1.90	0.42
2:B:205:PRO:HB3	2:B:209:LEU:HD23	2.00	0.42
2:B:235:SER:O	2:B:303:LEU:HB2	2.19	0.42
2:B:1153:LYS:HA	2:B:1156:TYR:CE2	2.54	0.42
3:C:258:LEU:HD12	3:C:302:THR:HB	2.01	0.42
3:C:421:PHE:O	3:C:425:PHE:HB3	2.19	0.42
2:B:250:PHE:HE2	2:B:397:PHE:HZ	1.67	0.42
2:B:535:ARG:NE	2:B:941:LEU:O	2.49	0.42
1:A:1254:GLN:N	1:A:1254:GLN:OE1	2.52	0.42
2:B:107:PRO:HB3	2:B:163:GLY:C	2.45	0.42
2:B:717:LEU:HD23	2:B:717:LEU:HA	1.83	0.42
3:C:298:VAL:HG21	3:C:332:ILE:HD13	2.00	0.42
1:A:3:PHE:N	1:A:96:GLU:OE2	2.53	0.42
1:A:156:PRO:HA	1:A:187:ARG:HB3	2.02	0.42
1:A:899:ASN:OD1	1:A:927:ILE:HD11	2.19	0.42
1:A:1205:ILE:HD12	1:A:1205:ILE:HA	1.84	0.42
2:B:42:ALA:O	2:B:44:GLU:N	2.49	0.42
2:B:439:ILE:O	3:C:207:ARG:NH2	2.50	0.42
2:B:482:ILE:HD11	2:B:669:ILE:HG13	2.01	0.42
2:B:875:TRP:HB2	2:B:983:GLU:HB3	2.01	0.42
1:A:171:GLU:H	1:A:171:GLU:HG2	1.67	0.42
1:A:709:VAL:O	1:A:713:ILE:HG13	2.20	0.42
2:B:228:ASP:OD1	2:B:228:ASP:N	2.53	0.42
2:B:1020:TYR:CE2	2:B:1074:VAL:HG22	2.55	0.42
2:B:1048:THR:HB	2:B:1144:TRP:HD1	1.85	0.42
1:A:637:ILE:HG22	1:A:643:ILE:HG21	2.02	0.42
1:A:1003:GLN:HA	1:A:1011:ILE:HD11	2.02	0.42
2:B:574:ILE:HD12	2:B:574:ILE:H	1.84	0.42
3:C:212:THR:HB	3:C:243:ASP:HB3	2.01	0.42
3:C:218:ASP:HB2	3:C:236:PRO:HG2	2.02	0.42
3:C:628:ALA:O	3:C:632:ARG:HG3	2.20	0.42
1:A:819:LEU:HD12	1:A:819:LEU:HA	1.83	0.42
1:A:925:GLU:OE2	1:A:1052:ASN:ND2	2.34	0.42
1:A:1265:ASN:ND2	2:B:813:GLU:OE2	2.53	0.42
2:B:13:ILE:HG23	2:B:19:ALA:HA	2.01	0.42
2:B:25:LYS:HE2	2:B:446:CYS:SG	2.60	0.42
2:B:366:PRO:HG3	2:B:384:ASN:OD1	2.20	0.42
2:B:1010:ILE:HD13	2:B:1010:ILE:HA	1.87	0.42
1:A:50:THR:HG22	1:A:57:GLY:HA2	2.01	0.42
2:B:949:ILE:HB	2:B:954:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:423:GLU:OE1	3:C:443:ALA:HB1	2.19	0.42
3:C:655:THR:O	3:C:659:ILE:HG13	2.20	0.42
1:A:458:ASN:HB3	1:A:461:ASP:HB2	2.02	0.41
2:B:250:PHE:CE2	2:B:397:PHE:HZ	2.38	0.41
2:B:371:ASN:OD1	2:B:379:VAL:HG13	2.20	0.41
3:C:183:PHE:HB2	3:C:377:LEU:HA	2.02	0.41
3:C:433:SER:HA	3:C:665:LYS:HE3	2.02	0.41
3:C:600:SER:HB3	3:C:603:ARG:HH21	1.85	0.41
1:A:247:THR:HG23	1:A:253:MET:O	2.20	0.41
1:A:923:LYS:HB3	1:A:1056:LYS:HB3	2.02	0.41
1:A:1209:LEU:HD22	1:A:1209:LEU:HA	1.82	0.41
2:B:90:ASN:HB2	2:B:99:LEU:HD12	2.02	0.41
2:B:1098:ASN:HB3	2:B:1147:CYS:HB3	2.00	0.41
1:A:988:GLN:NE2	1:A:992:GLU:OE1	2.53	0.41
2:B:180:GLN:NE2	2:B:797:ILE:HD13	2.35	0.41
2:B:421:ASP:OD1	2:B:421:ASP:N	2.52	0.41
3:C:277:GLY:HA2	3:C:349:LYS:H	1.85	0.41
3:C:458:PHE:CE1	3:C:491:LEU:HD21	2.55	0.41
1:A:343:LYS:NZ	1:A:347:GLU:OE2	2.38	0.41
2:B:64:TYR:CD1	2:B:143:THR:HG22	2.55	0.41
2:B:189:LEU:O	2:B:193:LEU:HG	2.20	0.41
2:B:570:GLY:N	2:B:576:GLU:OE2	2.34	0.41
2:B:1093:ASP:OD1	2:B:1094:ILE:N	2.53	0.41
3:C:561:SER:O	3:C:656:GLY:HA3	2.21	0.41
1:A:188:PHE:CD2	1:A:221:LEU:HD13	2.55	0.41
1:A:1127:ASN:OD1	1:A:1127:ASN:N	2.53	0.41
1:A:1209:LEU:HD13	1:A:1210:GLU:N	2.35	0.41
1:A:801:ILE:HG13	1:A:851:PHE:CD2	2.55	0.41
2:B:888:LEU:HB3	2:B:900:ILE:O	2.21	0.41
2:B:913:ASP:OD1	2:B:917:ASN:N	2.54	0.41
2:B:1020:TYR:OH	2:B:1078:ASP:OD2	2.37	0.41
1:A:102:ASP:HB3	1:A:503:TYR:CD1	2.55	0.41
1:A:179:GLY:O	1:A:321:TYR:OH	2.20	0.41
1:A:369:PHE:CD2	1:A:460:TRP:HB3	2.55	0.41
2:B:873:TYR:HA	2:B:934:ILE:O	2.21	0.41
1:A:374:PHE:HD1	1:A:415:LYS:HA	1.85	0.41
1:A:649:LYS:O	1:A:653:VAL:HG23	2.20	0.41
2:B:68:PHE:CE2	2:B:69:LEU:HD23	2.56	0.41
2:B:222:LEU:HD11	2:B:224:TYR:HE1	1.86	0.41
1:A:43:TRP:HB2	1:A:152:VAL:HG22	2.02	0.41
2:B:24:ARG:NH1	2:B:447:ASP:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:136:LEU:HD13	2:B:166:SER:OG	2.21	0.41
2:B:247:PRO:HB2	2:B:631:LYS:HE2	2.03	0.41
2:B:846:LEU:H	2:B:846:LEU:HG	1.64	0.41
2:B:911:MET:SD	2:B:962:ILE:HG21	2.61	0.41
3:C:556:VAL:HG13	3:C:560:PHE:CD1	2.55	0.41
1:A:241:ARG:NH2	1:A:278:GLN:OE1	2.54	0.41
1:A:425:PHE:HD2	1:A:460:TRP:HH2	1.69	0.41
1:A:862:LEU:H	1:A:862:LEU:HD22	1.86	0.41
1:A:1278:LEU:C	1:A:1278:LEU:CD1	2.85	0.41
2:B:993:THR:OG1	2:B:994:SER:N	2.53	0.41
1:A:163:PHE:HE1	1:A:189:SER:H	1.68	0.40
2:B:201:TYR:CZ	2:B:290:LYS:HG3	2.55	0.40
2:B:773:SER:OG	2:B:774:SER:N	2.54	0.40
3:C:512:TYR:HE1	3:C:529:VAL:HG12	1.84	0.40
1:A:41:LYS:HB3	1:A:149:LEU:HA	2.02	0.40
1:A:250:TYR:CG	1:A:545:LEU:HD21	2.56	0.40
1:A:374:PHE:CD2	1:A:406:THR:HG21	2.57	0.40
1:A:960:ASN:ND2	1:A:1061:ARG:HG3	2.36	0.40
1:A:968:MET:HA	1:A:973:GLY:HA3	2.03	0.40
2:B:658:SER:O	2:B:662:GLN:HG2	2.22	0.40
2:B:695:THR:O	2:B:699:LEU:HG	2.21	0.40
3:C:353:TYR:CZ	3:C:676:VAL:HA	2.56	0.40
3:C:508:PHE:CZ	3:C:510:GLN:HB2	2.56	0.40
1:A:1100:PHE:HB2	1:A:1285:ILE:HG13	2.04	0.40
2:B:231:ASP:O	2:B:235:SER:OG	2.32	0.40
2:B:690:LEU:HD12	2:B:690:LEU:HA	1.89	0.40
2:B:1022:LYS:HD3	2:B:1024:TYR:CZ	2.57	0.40
3:C:226:ALA:HB2	3:C:232:ARG:H	1.85	0.40
3:C:544:TRP:O	3:C:548:GLU:HB2	2.22	0.40
1:A:666:GLU:H	1:A:724:GLN:NE2	2.20	0.40
1:A:725:ILE:HD13	1:A:725:ILE:HA	1.93	0.40
1:A:727:LEU:HD11	1:A:731:LYS:HE2	2.03	0.40
1:A:320:LYS:HD3	1:A:321:TYR:CE2	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	1269/1296 (98%)	1226 (97%)	42 (3%)	1 (0%)	48	81
2	B	1139/1161 (98%)	1084 (95%)	55 (5%)	0	100	100
3	C	553/750 (74%)	547 (99%)	6 (1%)	0	100	100
All	All	2961/3207 (92%)	2857 (96%)	103 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1278	LEU

### 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	1147/1177 (98%)	1100 (96%)	47 (4%)	26	49
2	B	1055/1093 (96%)	1015 (96%)	40 (4%)	28	51
3	C	474/667 (71%)	470 (99%)	4 (1%)	79	84
All	All	2676/2937 (91%)	2585 (97%)	91 (3%)	34	54

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	THR
1	A	52	THR

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Mol	Chain	Res	Type
1	A	59	LEU
1	A	70	VAL
1	A	127	LEU
1	A	137	VAL
1	A	149	LEU
1	A	203	ASP
1	A	215	THR
1	A	225	LEU
1	A	238	ASN
1	A	275	ASP
1	A	313	MET
1	A	373	VAL
1	A	379	VAL
1	A	395	THR
1	A	428	LEU
1	A	469	ASP
1	A	500	GLN
1	A	504	LEU
1	A	517	ILE
1	A	621	VAL
1	A	627	ILE
1	A	632	ILE
1	A	656	LEU
1	A	695	ILE
1	A	827	ARG
1	A	831	ILE
1	A	837	LEU
1	A	862	LEU
1	A	888	LEU
1	A	912	ASN
1	A	943	THR
1	A	978	LEU
1	A	1020	THR
1	A	1046	ASN
1	A	1113	MET
1	A	1116	LEU
1	A	1126	ASN
1	A	1148	ILE
1	A	1177	ASN
1	A	1202	VAL
1	A	1206	LEU
1	A	1209	LEU

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Mol	Chain	Res	Type
1	A	1232	THR
1	A	1239	LEU
1	A	1293	GLU
2	B	18	VAL
2	B	39	ILE
2	B	60	ASP
2	B	69	LEU
2	B	127	ASP
2	B	153	TYR
2	B	194	ILE
2	B	211	ILE
2	B	228	ASP
2	B	233	LEU
2	B	243	LEU
2	B	279	ILE
2	B	326	HIS
2	B	355	LEU
2	B	370	VAL
2	B	381	MET
2	B	406	ASN
2	B	447	ASP
2	B	452	VAL
2	B	458	THR
2	B	463	THR
2	B	472	LEU
2	B	482	ILE
2	B	533	ILE
2	B	637	LEU
2	B	688	LEU
2	B	702	ILE
2	B	771	ILE
2	B	800	GLU
2	B	846	LEU
2	B	876	LEU
2	B	881	LYS
2	B	901	TYR
2	B	942	LYS
2	B	953	LEU
2	B	1077	LEU
2	B	1088	MET
2	B	1118	ILE
2	B	1135	LEU

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Mol	Chain	Res	Type
2	B	1144	TRP
3	C	173	LEU
3	C	374	GLU
3	C	431	LEU
3	C	552	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	15	ASN
1	A	39	HIS
1	A	139	GLN
1	A	311	GLN
1	A	724	GLN
1	A	760	ASN
1	A	790	GLN
1	A	1021	ASN
1	A	1147	ASN
1	A	1265	ASN
2	B	15	ASN
2	B	80	GLN
2	B	128	ASN
2	B	171	GLN
2	B	180	GLN
2	B	320	ASN
2	B	348	GLN
2	B	406	ASN
2	B	571	ASN
2	B	604	ASN
2	B	692	ASN
2	B	715	ASN
2	B	726	GLN
2	B	728	ASN
2	B	769	GLN
2	B	817	ASN
2	B	864	ASN
2	B	895	ASN
2	B	1149	ASN
3	C	176	ASN
3	C	285	ASN
3	C	331	ASN

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Mol	Chain	Res	Type
3	C	391	ASN
3	C	402	ASN
3	C	498	GLN
3	C	601	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.

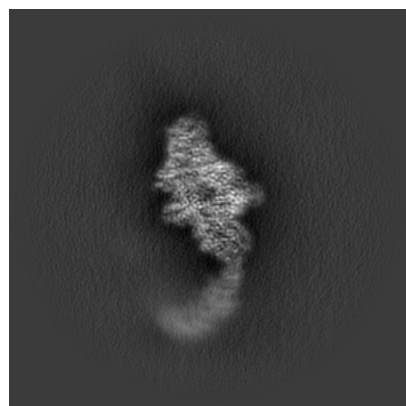
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43786. These allow visual inspection of the internal detail of the map and identification of artifacts.

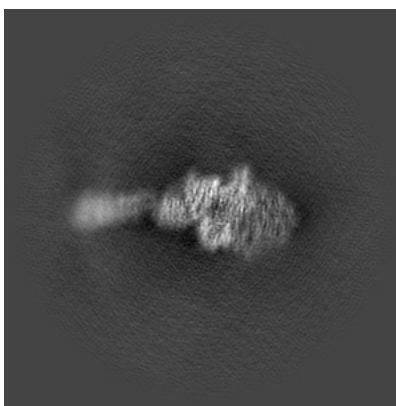
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

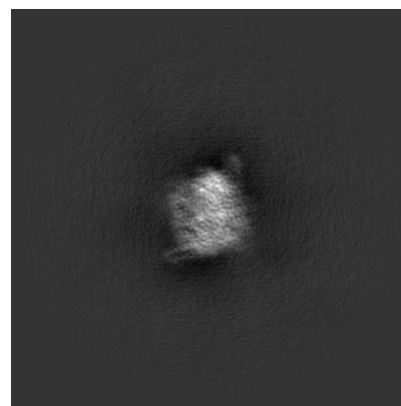
#### 6.1.1 Primary map



X

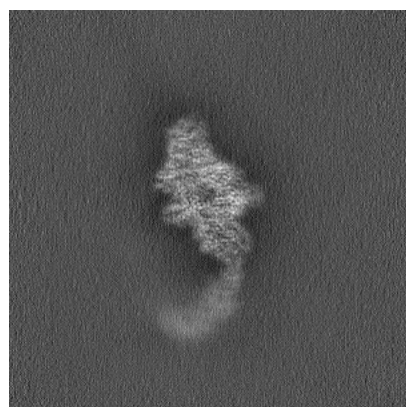


Y

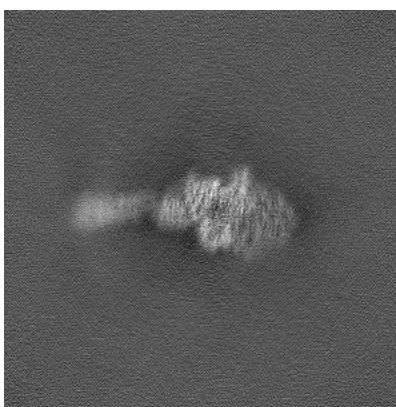


Z

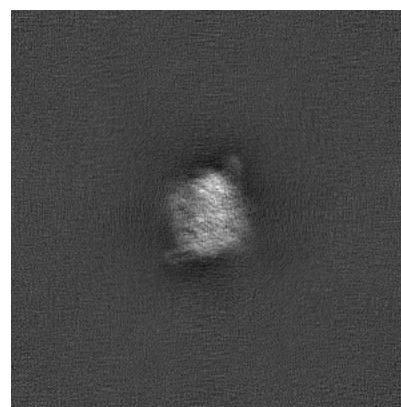
#### 6.1.2 Raw map



X



Y



Z

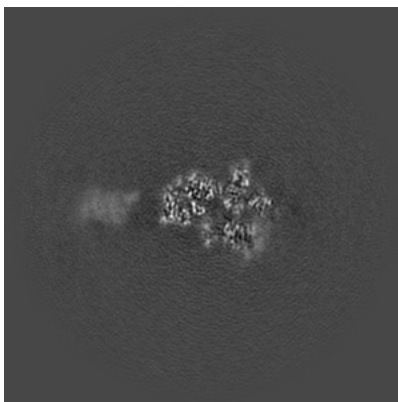
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

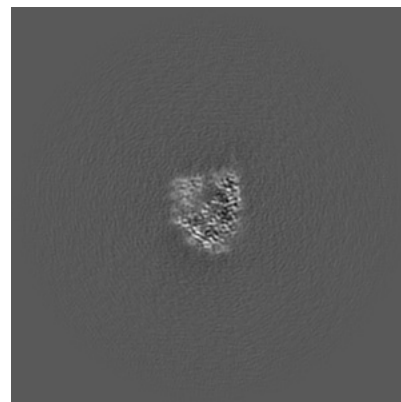
### 6.2.1 Primary map



X Index: 256

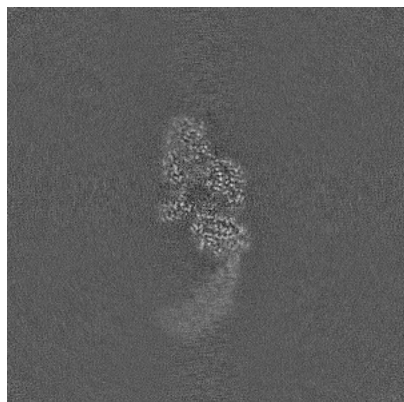


Y Index: 256

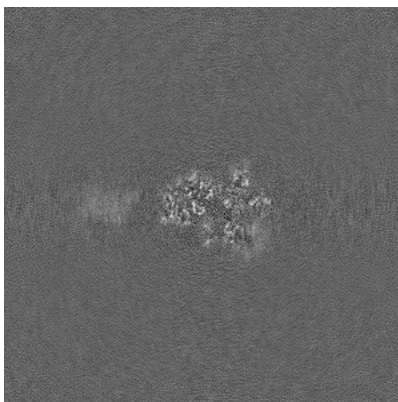


Z Index: 256

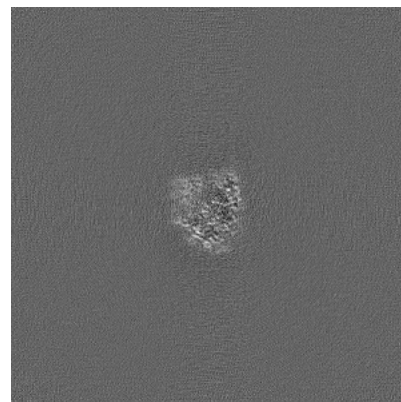
### 6.2.2 Raw map



X Index: 256



Y Index: 256

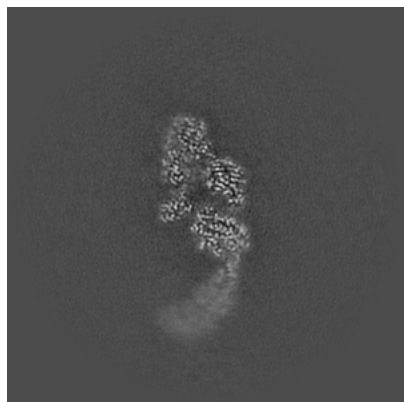


Z Index: 256

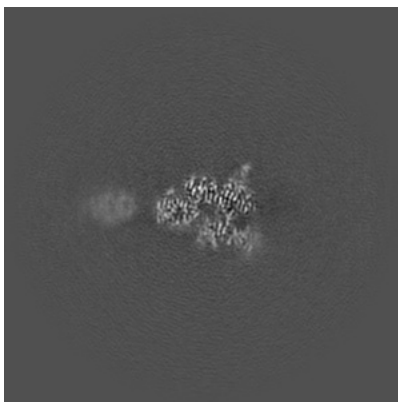
The images above show central slices of the map in three orthogonal directions.

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

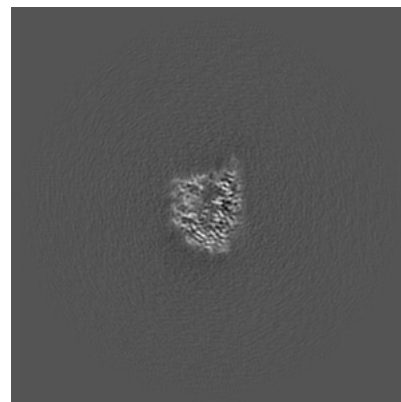
### 6.3.1 Primary map



X Index: 255



Y Index: 266

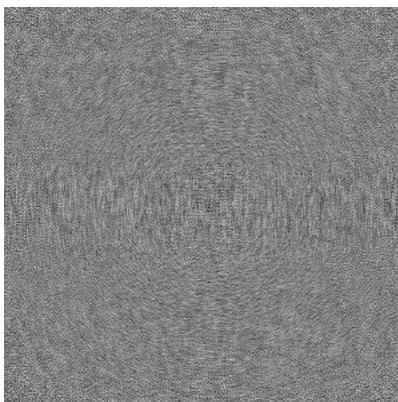


Z Index: 258

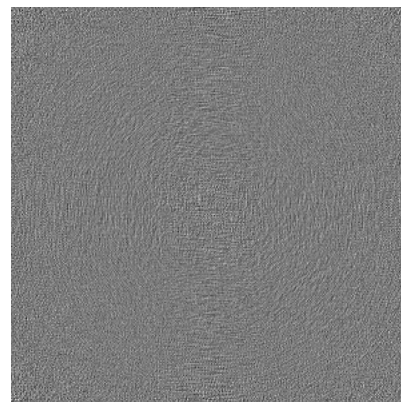
### 6.3.2 Raw map



X Index: 255



Y Index: 0



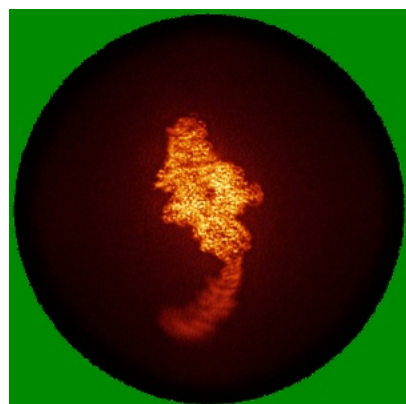
Z Index: 511

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

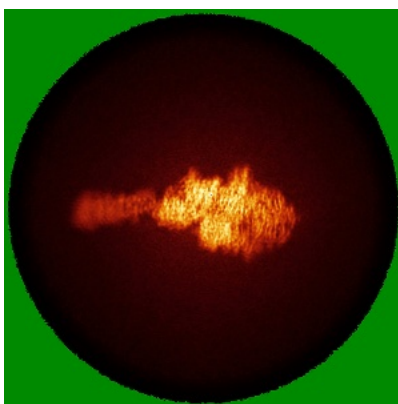


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

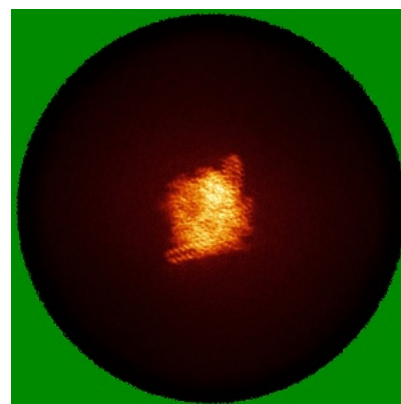
### 6.4.1 Primary map



X

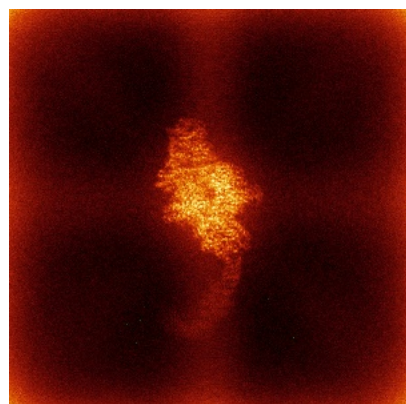


Y

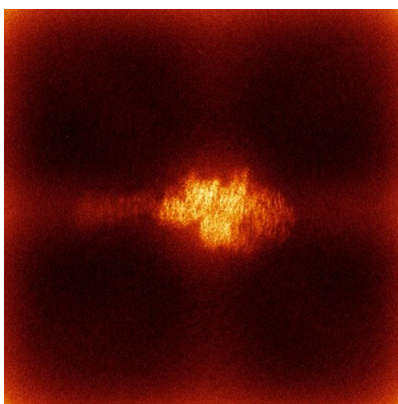


Z

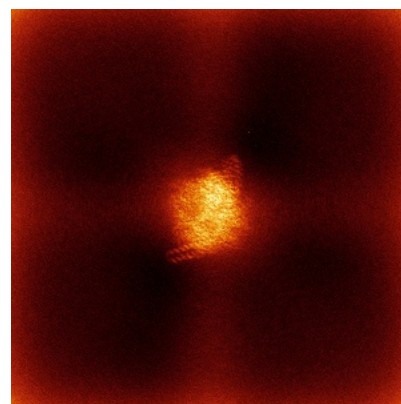
### 6.4.2 Raw map



X



Y

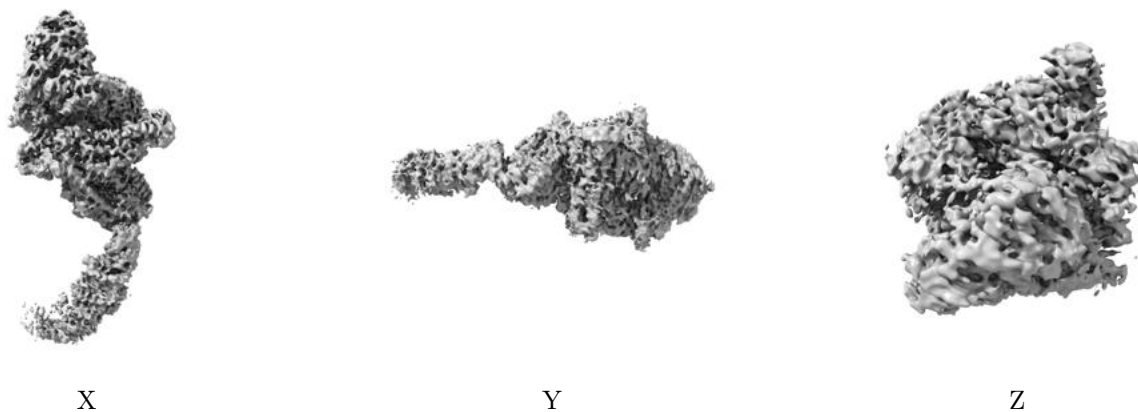


Z

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.

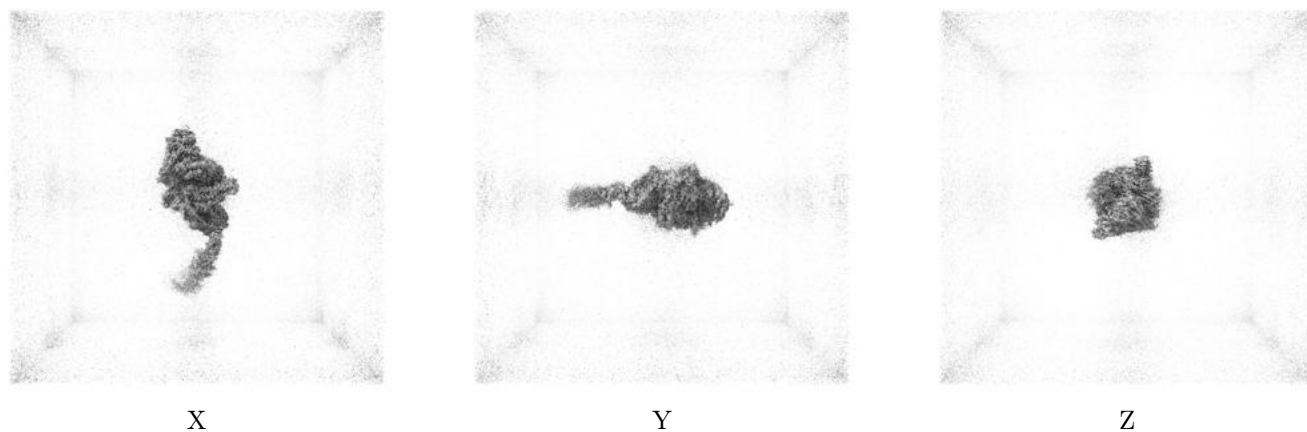
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

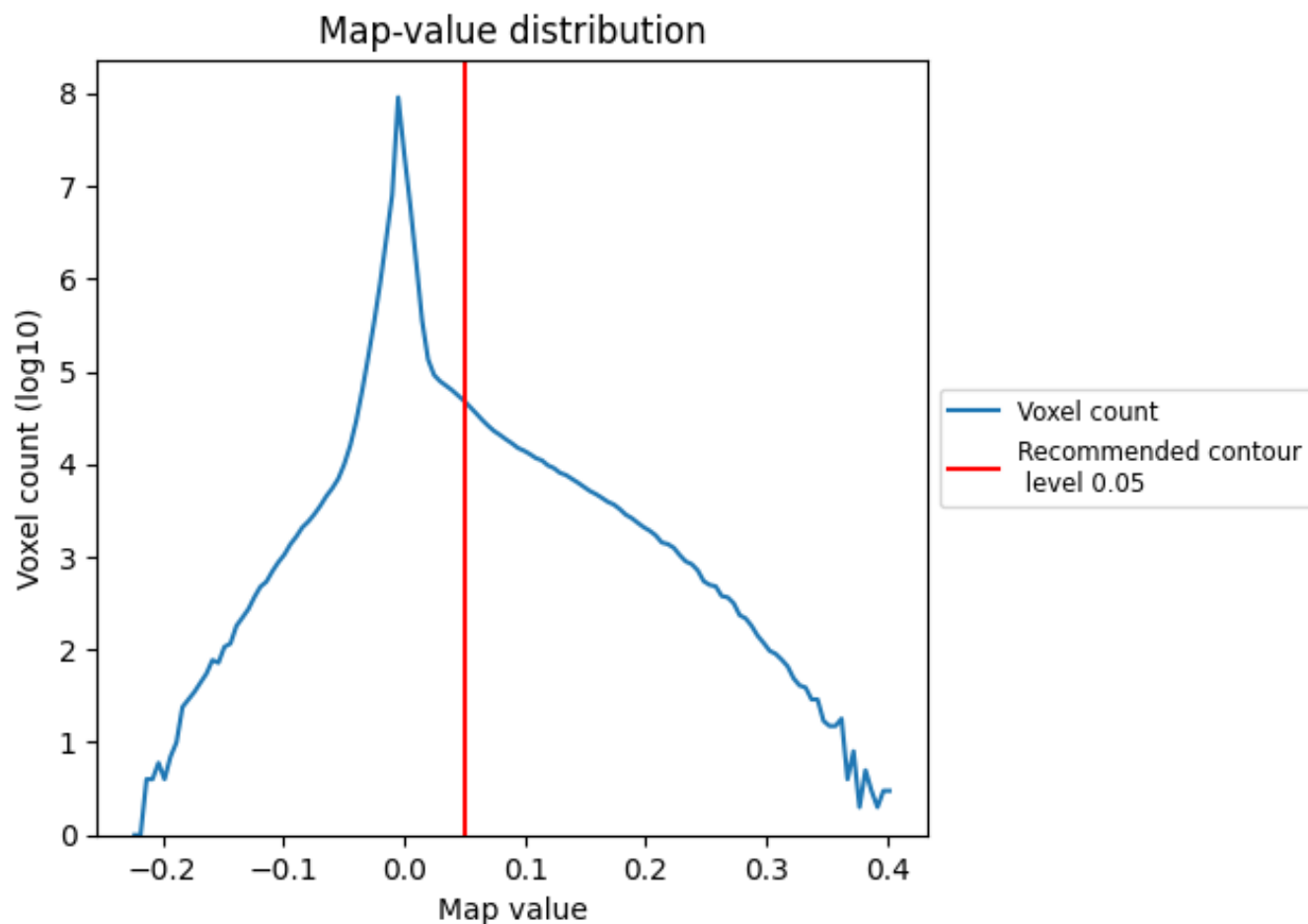
## 6.6 Mask visualisation [i](#)

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.

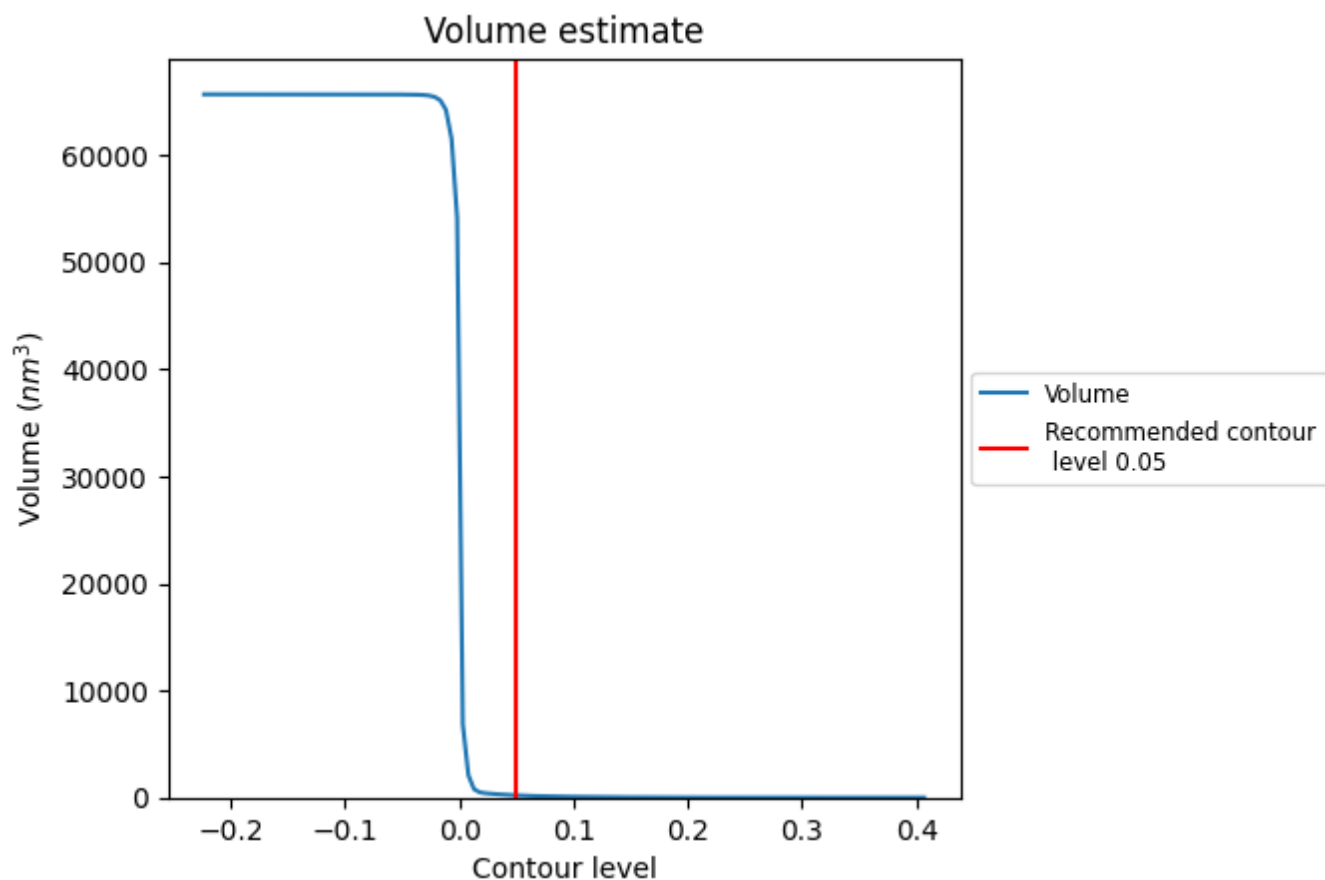
### 7.1 Map-value distribution [i](#)



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.



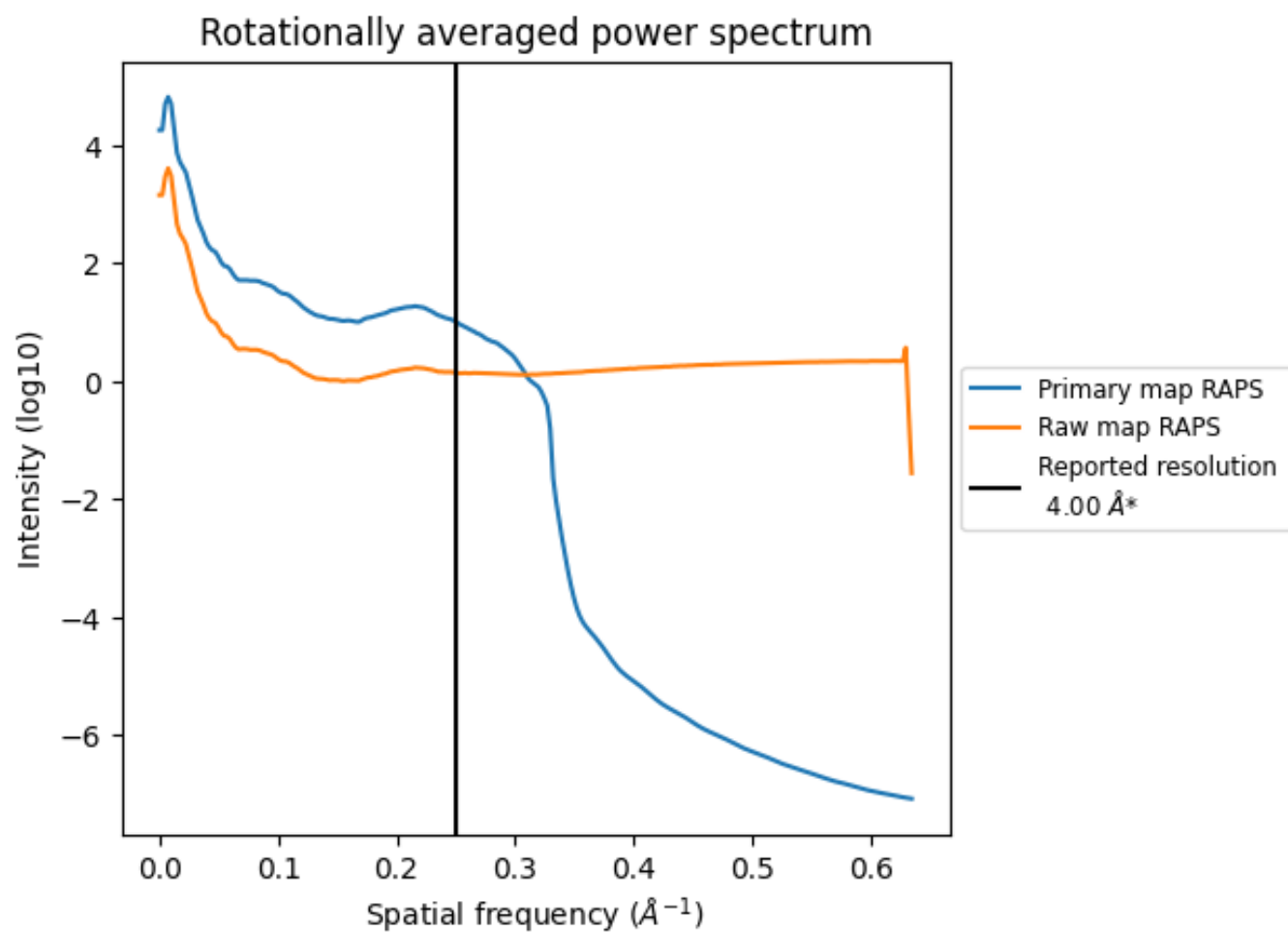
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 208 nm<sup>3</sup>; this corresponds to an approximate mass of 188 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](#)

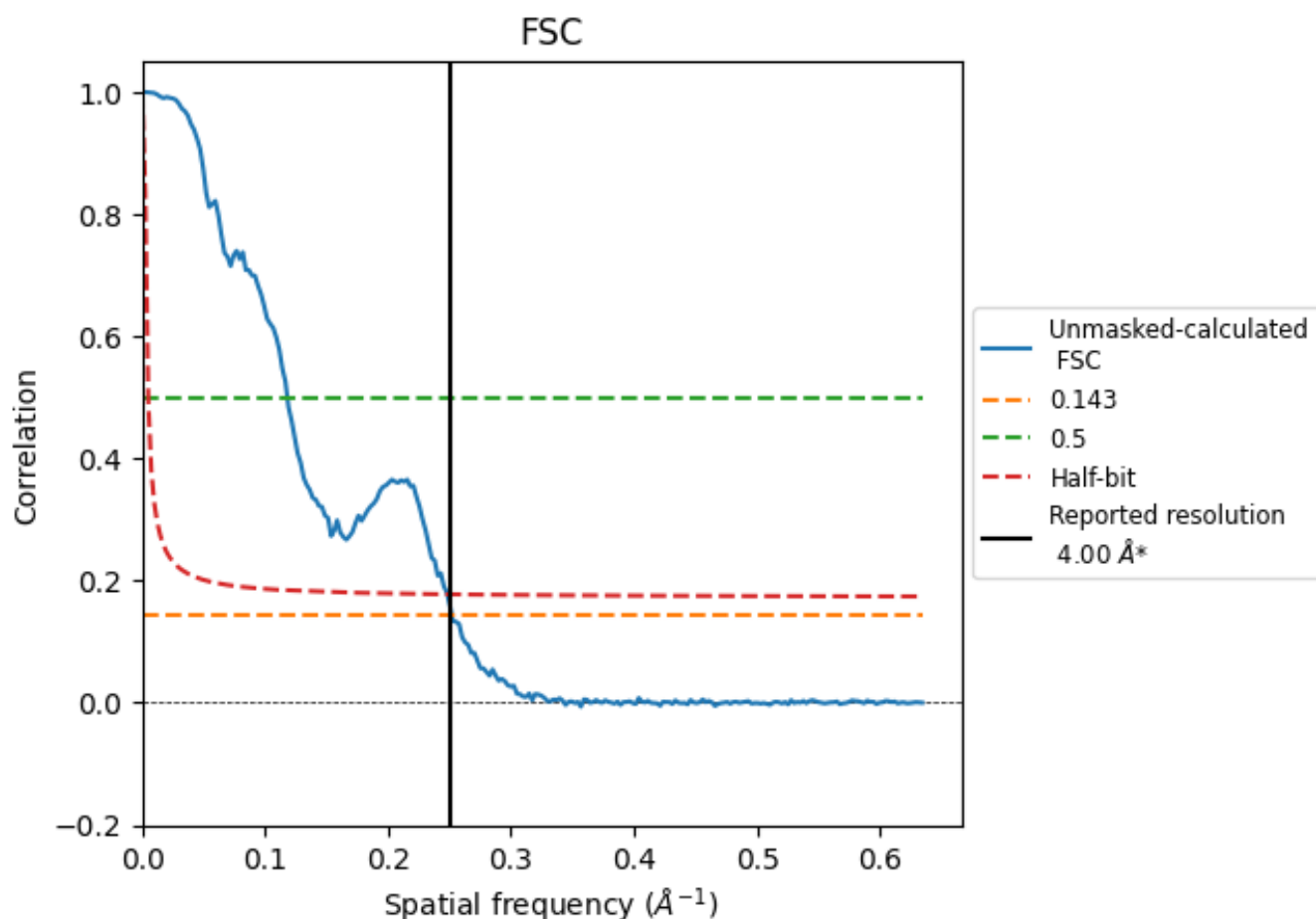


\*Reported resolution corresponds to spatial frequency of 0.250  $\text{\AA}^{-1}$

## 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 0.250  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

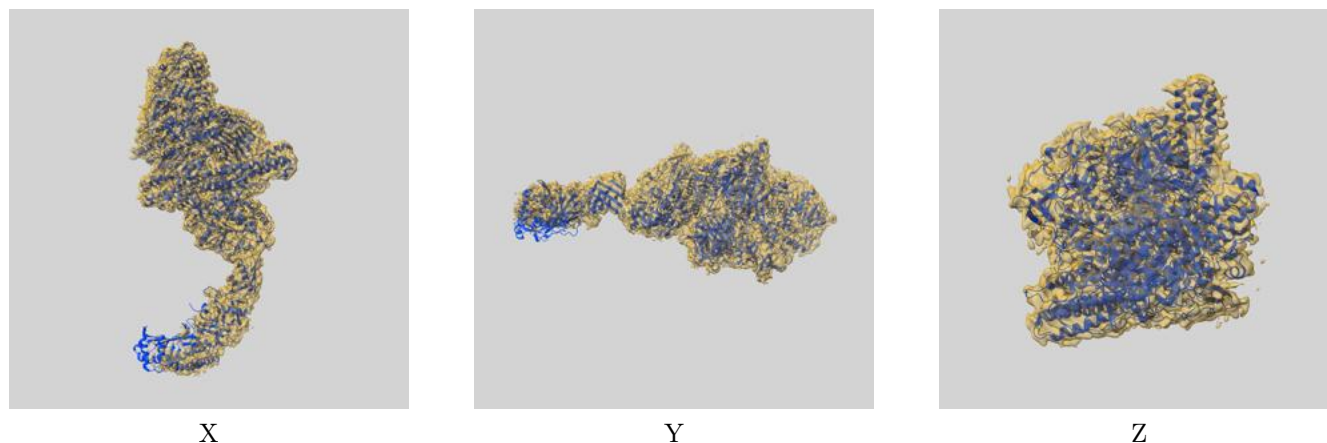
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.97	8.47	4.03

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

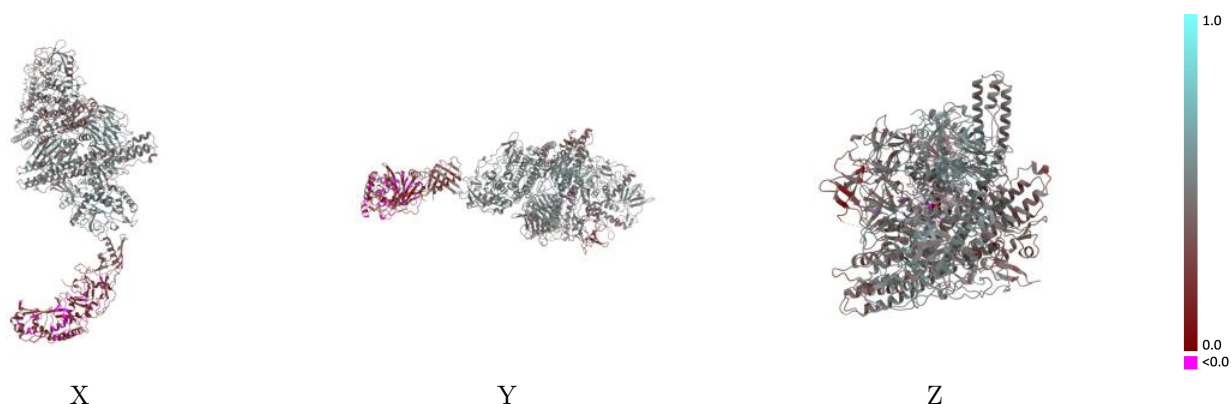
This section contains information regarding the fit between EMDB map EMD-43786 and PDB model 9ARL. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

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



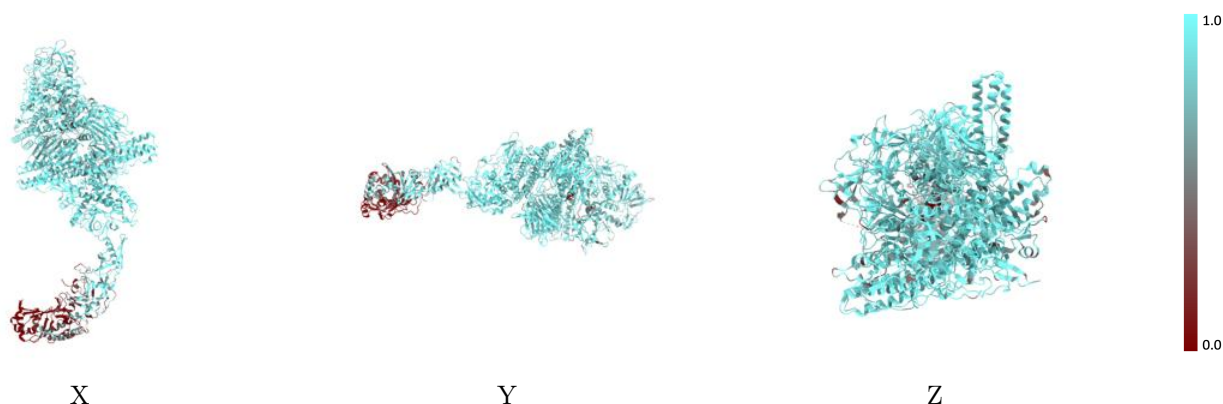
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



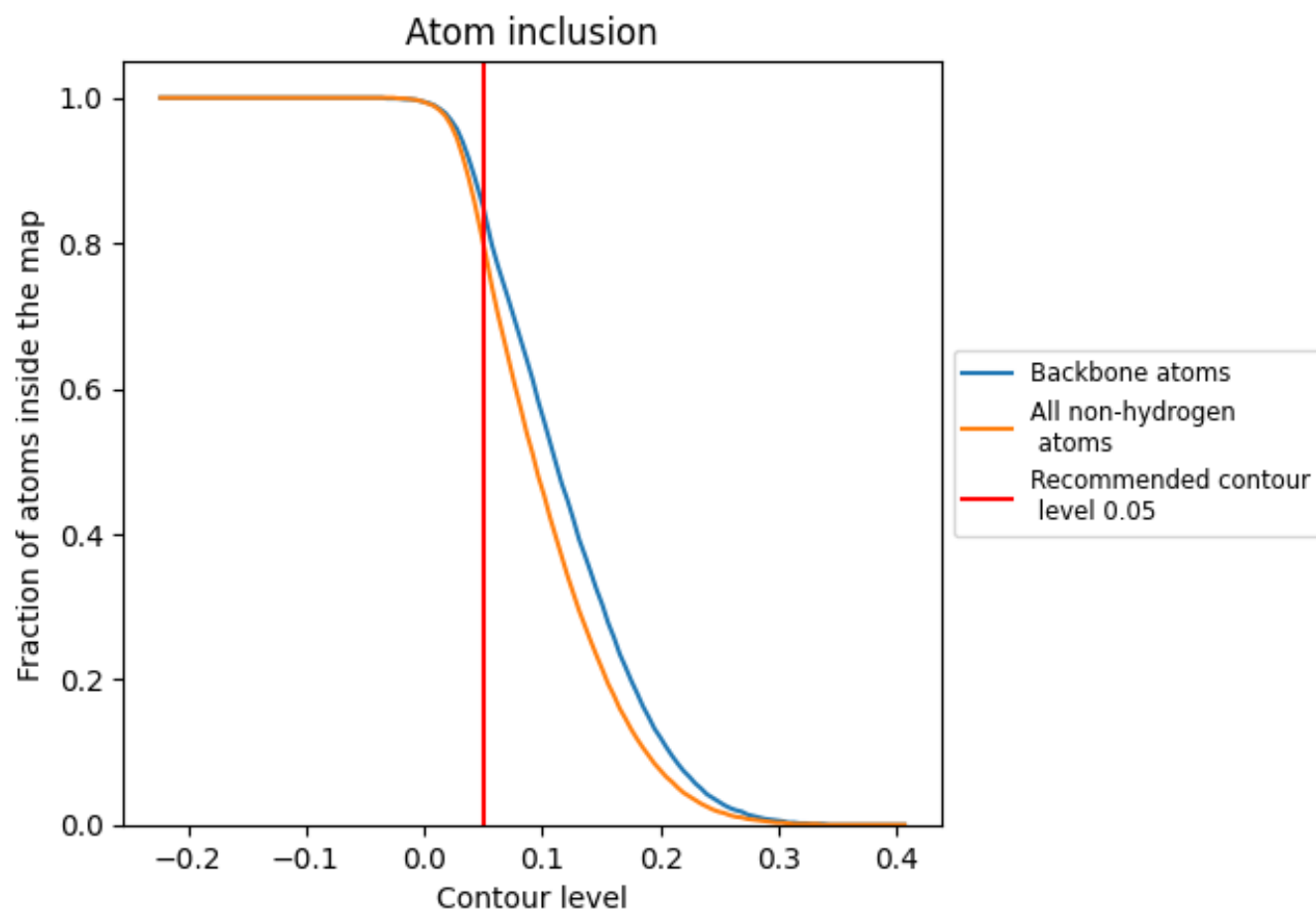
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8010	<div></div> 0.4230
A	<div></div> 0.8680	<div></div> 0.4640
B	<div></div> 0.9040	<div></div> 0.4810
C	<div></div> 0.4250	<div></div> 0.2000

