



## Full wwPDB EM Validation Report ⓘ

Jan 27, 2025 – 08:16 PM EST

PDB ID : 9ARK  
EMDB ID : EMD-43785  
Title : CryoEM structure of BoNT-NTNH-OrfX2 complex from Clostridium botulinum E1, minor class  
Authors : Gao, L.  
Deposited on : 2024-02-23  
Resolution : 4.10 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.dev113  
MolProbity : 4.02b-467  
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) : 2.40



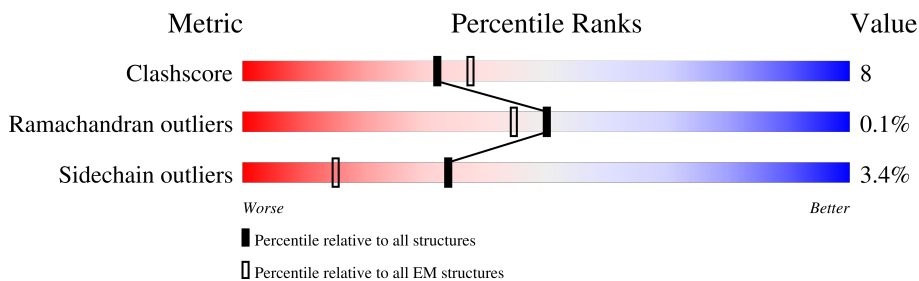
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.10 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	1252	
2	B	1163	
3	C	748	



## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24165 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1245	Total	C	N	O	S	0	0
			9959	6335	1659	1942	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	212	ALA	HIS	engineered mutation	UNP A8Y875
A	213	ALA	GLU	engineered mutation	UNP A8Y875
A	216	ALA	HIS	engineered mutation	UNP A8Y875

- Molecule 2 is a protein called Peptidase M27.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1163	Total	C	N	O	S	0	0
			9662	6233	1553	1852	24		


- Molecule 3 is a protein called Toxin.

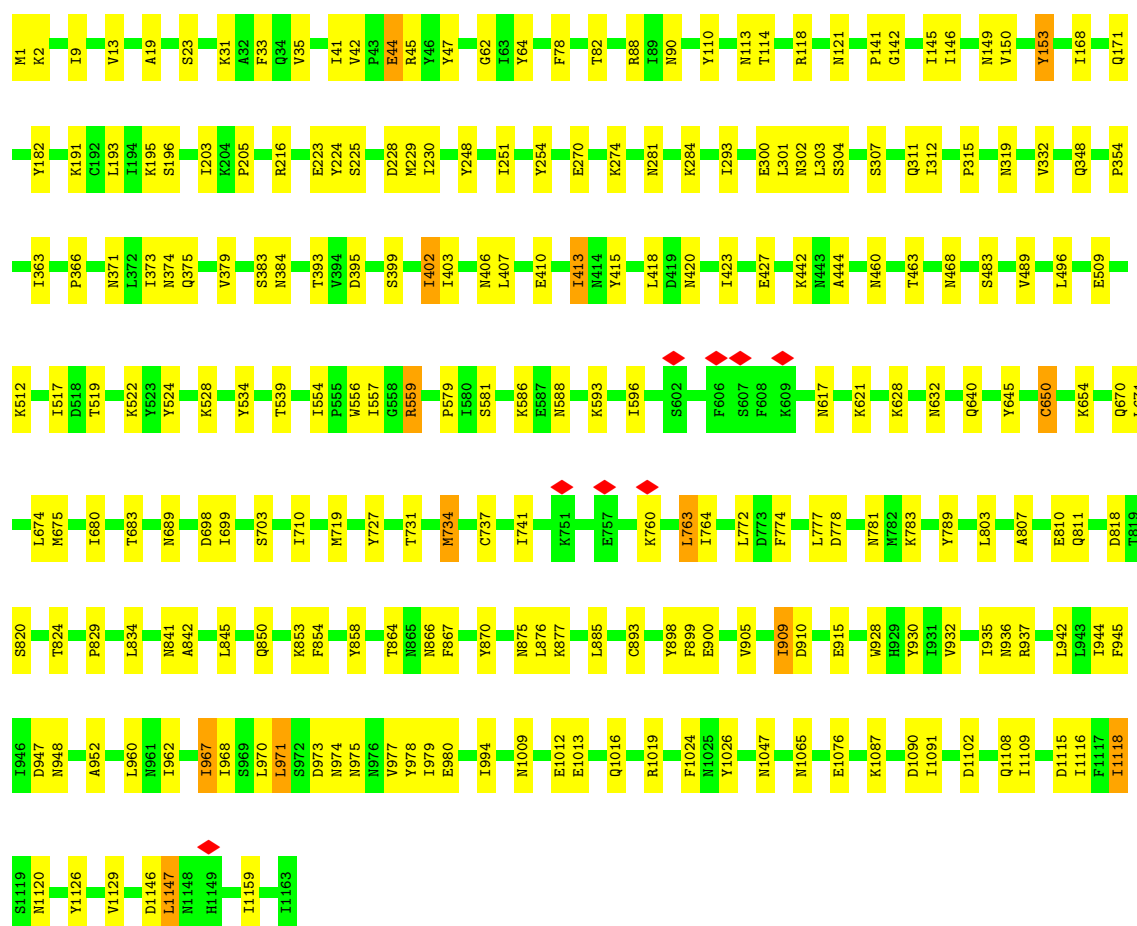
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	578	Total	C	N	O	S	0	0
			4544	2913	749	877	5		





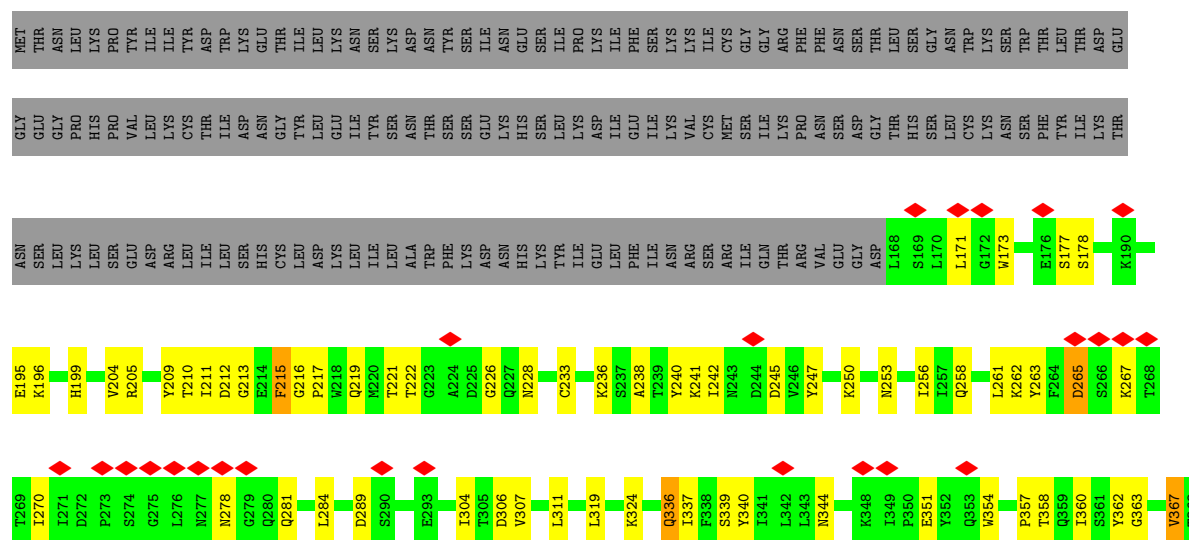


Chain B: 

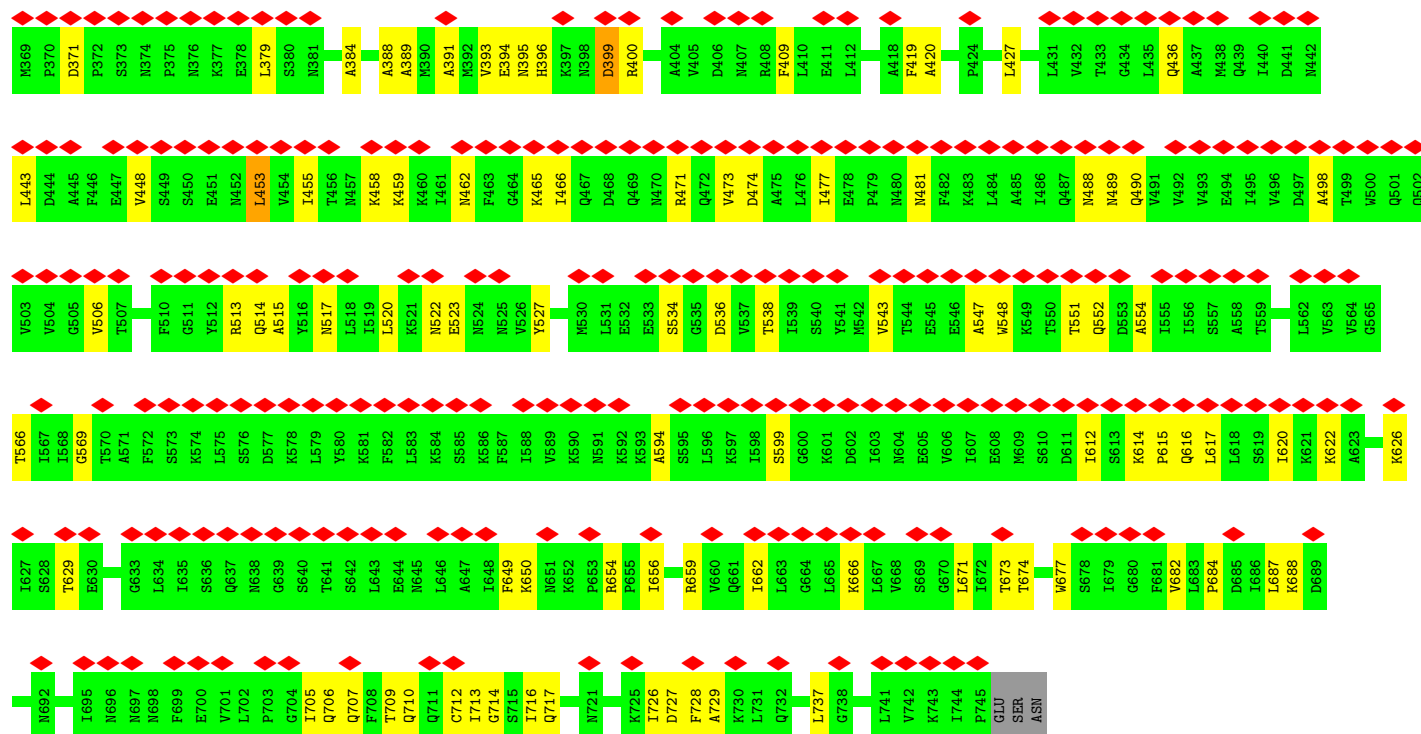


• Molecule 3: Toxin

Chain C: 









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	61340	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	0.526	Depositor
Minimum map value	-0.272	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.055	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	0.26	0/10157	0.45	0/13786
2	B	0.27	0/9876	0.42	0/13391
3	C	0.24	0/4632	0.43	0/6288
All	All	0.26	0/24665	0.43	0/33465

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	9959	0	9681	171	0
2	B	9662	0	9500	149	0
3	C	4544	0	4534	93	0
All	All	24165	0	23715	404	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 8.

All (404) 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:1183:ARG:HG3	1:A:1185:ASN:H	1.43	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:674:LEU:HD21	2:B:680:ILE:HD12	1.67	0.77
2:B:519:THR:CG2	2:B:522:LYS:HG2	2.16	0.75
2:B:650:CYS:SG	2:B:654:LYS:NZ	2.60	0.73
1:A:1067:PRO:O	1:A:1073:LYS:NZ	2.23	0.71
2:B:302:ASN:ND2	2:B:304:SER:OG	2.24	0.70
2:B:293:ILE:HG22	2:B:420:ASN:HB2	1.73	0.70
1:A:1196:ASN:HB3	1:A:1239:PHE:HB3	1.71	0.70
1:A:135:LYS:HG2	1:A:141:GLN:HG2	1.75	0.68
2:B:519:THR:HG23	2:B:522:LYS:HG2	1.74	0.68
3:C:462:ASN:O	3:C:650:LYS:NZ	2.28	0.67
2:B:928:TRP:HB2	2:B:1012:GLU:HB3	1.78	0.66
1:A:654:LEU:O	1:A:659:ASN:ND2	2.29	0.66
2:B:1091:ILE:HG13	2:B:1108:GLN:HG3	1.79	0.65
3:C:649:PHE:O	3:C:659:ARG:NH2	2.29	0.65
3:C:515:ALA:HB3	3:C:536:ASP:HB2	1.79	0.65
2:B:1009:ASN:HD21	2:B:1013:GLU:HB2	1.62	0.65
3:C:477:ILE:HG23	3:C:481:ASN:HD22	1.62	0.65
1:A:955:ASN:HB3	1:A:958:GLU:HG2	1.78	0.65
2:B:517:ILE:O	2:B:517:ILE:HG13	1.97	0.64
1:A:682:TYR:OH	1:A:778:LYS:NZ	2.30	0.64
2:B:311:GLN:NE2	2:B:789:TYR:OH	2.31	0.64
3:C:357:PRO:HA	3:C:393:VAL:HG12	1.79	0.64
3:C:522:ASN:ND2	3:C:727:ASP:O	2.31	0.64
2:B:834:LEU:HD12	2:B:841:ASN:HB3	1.80	0.63
1:A:999:ARG:NH2	1:A:1021:GLY:O	2.30	0.63
3:C:210:THR:HB	3:C:241:LYS:HB3	1.78	0.63
2:B:45:ARG:NH2	2:B:142:GLY:O	2.32	0.63
2:B:248:TYR:O	2:B:628:LYS:NZ	2.32	0.62
1:A:938:THR:HA	1:A:953:SER:HA	1.82	0.62
1:A:20:TYR:HB3	1:A:29:PHE:HB3	1.81	0.62
2:B:1115:ASP:HB3	2:B:1118:ILE:HD12	1.81	0.62
1:A:51:THR:HG22	1:A:53:GLN:H	1.63	0.62
1:A:1183:ARG:NH2	1:A:1204:ASN:OD1	2.31	0.62
2:B:517:ILE:HD11	2:B:670:GLN:OE1	1.99	0.62
1:A:21:ILE:HG12	1:A:134:ILE:HG22	1.81	0.61
2:B:829:PRO:HG2	2:B:850:GLN:HB3	1.83	0.61
2:B:393:THR:HG22	2:B:395:ASP:H	1.66	0.61
1:A:495:ASP:OD1	1:A:495:ASP:N	2.34	0.61
2:B:150:VAL:HG22	2:B:168:ILE:HG12	1.83	0.61
3:C:262:LYS:NZ	3:C:263:TYR:O	2.34	0.61
3:C:709:THR:O	3:C:713:ILE:N	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:278:ASN:ND2	3:C:344:ASN:O	2.34	0.61
3:C:488:ASN:ND2	3:C:490:GLN:OE1	2.33	0.61
1:A:922:ARG:NH2	1:A:1246:GLU:OE1	2.33	0.61
1:A:1207:ASN:ND2	2:B:810:GLU:O	2.34	0.60
1:A:519:VAL:HG21	1:A:700:ARG:HH12	1.65	0.60
2:B:373:ILE:HG12	2:B:460:ASN:HB3	1.81	0.60
1:A:757:ASN:OD1	1:A:757:ASN:N	2.34	0.60
2:B:517:ILE:HD11	2:B:670:GLN:CD	2.22	0.60
1:A:908:TYR:OH	1:A:999:ARG:NH1	2.30	0.59
1:A:517:LEU:O	1:A:611:ASN:ND2	2.35	0.59
1:A:1072:LEU:HD11	1:A:1190:MET:HB3	1.82	0.59
2:B:853:LYS:HD2	2:B:967:ILE:HD11	1.85	0.59
2:B:932:VAL:HB	2:B:945:PHE:HB2	1.85	0.59
3:C:371:ASP:HB2	3:C:379:LEU:HD13	1.85	0.58
1:A:593:VAL:HA	1:A:622:LYS:HE3	1.85	0.58
1:A:835:ILE:HG23	1:A:836:LEU:HD23	1.84	0.58
2:B:930:TYR:O	2:B:947:ASP:N	2.34	0.58
1:A:835:ILE:HG12	1:A:836:LEU:H	1.68	0.58
1:A:684:PHE:O	1:A:688:ASN:ND2	2.34	0.58
3:C:336:GLN:NE2	3:C:337:ILE:O	2.37	0.58
3:C:709:THR:HB	3:C:713:ILE:HD13	1.85	0.58
1:A:1093:LYS:HE2	1:A:1096:ASN:HD22	1.69	0.57
2:B:519:THR:HG22	2:B:522:LYS:HG2	1.84	0.57
3:C:393:VAL:O	3:C:396:HIS:ND1	2.37	0.57
2:B:216:ARG:NE	2:B:225:SER:OG	2.31	0.57
1:A:19:LEU:HD11	1:A:134:ILE:HD12	1.87	0.57
3:C:240:TYR:HB2	3:C:247:TYR:HB2	1.87	0.57
3:C:177:SER:HB2	3:C:389:ALA:HB3	1.85	0.57
2:B:442:LYS:NZ	2:B:444:ALA:O	2.38	0.57
1:A:122:ASN:ND2	1:A:123:GLN:OE1	2.37	0.57
1:A:121:ASP:N	1:A:121:ASP:OD1	2.35	0.57
2:B:193:LEU:O	2:B:196:SER:OG	2.21	0.57
2:B:1024:PHE:HB2	2:B:1159:ILE:HB	1.88	0.56
3:C:340:TYR:HB2	3:C:717:GLN:HB2	1.87	0.56
1:A:939:ILE:HG22	1:A:940:ILE:HG13	1.88	0.56
2:B:930:TYR:HB3	2:B:947:ASP:HA	1.88	0.56
2:B:403:ILE:HD11	2:B:632:ASN:HD22	1.70	0.56
1:A:920:TRP:HB2	1:A:1045:ARG:HG2	1.86	0.56
2:B:935:ILE:HG12	2:B:942:LEU:HD13	1.87	0.56
1:A:910:ASN:ND2	1:A:912:TYR:O	2.37	0.56
2:B:1047:ASN:O	2:B:1047:ASN:ND2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1026:TYR:HD1	2:B:1159:ILE:HD11	1.71	0.56
3:C:726:ILE:HD11	3:C:729:ALA:HB2	1.88	0.56
1:A:1103:ASP:OD1	1:A:1103:ASP:N	2.38	0.55
2:B:332:VAL:HG22	2:B:354:PRO:HG2	1.88	0.55
3:C:242:ILE:HG12	3:C:247:TYR:HE2	1.70	0.55
3:C:351:GLU:O	3:C:354:TRP:NE1	2.39	0.55
1:A:738:TYR:O	1:A:742:GLN:N	2.40	0.55
2:B:182:TYR:O	2:B:348:GLN:NE2	2.38	0.55
2:B:319:ASN:OD1	2:B:319:ASN:N	2.40	0.55
3:C:419:PHE:HB3	3:C:737:LEU:HB2	1.88	0.55
1:A:686:VAL:HG11	1:A:830:TYR:HB3	1.89	0.55
3:C:199:HIS:ND1	3:C:212:ASP:OD1	2.31	0.55
2:B:9:ILE:O	2:B:31:LYS:NZ	2.32	0.55
1:A:818:THR:HG23	1:A:819:LEU:HD22	1.89	0.54
2:B:216:ARG:NH1	2:B:223:GLU:OE2	2.39	0.54
1:A:291:VAL:HG21	1:A:296:LEU:HB3	1.90	0.54
1:A:1121:LEU:N	1:A:1251:GLU:OE2	2.35	0.54
3:C:436:GLN:HE21	3:C:443:LEU:HG	1.73	0.54
2:B:399:SER:O	2:B:593:LYS:NZ	2.37	0.54
2:B:1146:ASP:OD1	2:B:1147:LEU:N	2.39	0.54
3:C:217:PRO:HD3	3:C:236:LYS:HZ1	1.73	0.53
2:B:671:LEU:HD21	2:B:689:ASN:HD22	1.73	0.53
2:B:383:SER:OG	2:B:468:ASN:ND2	2.41	0.53
1:A:287:SER:HB3	1:A:317:TYR:H	1.74	0.53
1:A:855:MET:HG3	1:A:872:ILE:HD13	1.91	0.53
1:A:45:ARG:HH12	1:A:157:LEU:HD21	1.74	0.53
1:A:1126:LYS:HB3	1:A:1153:VAL:HG22	1.91	0.53
2:B:45:ARG:HH12	2:B:145:ILE:HG22	1.74	0.53
1:A:154:GLU:HB2	1:A:155:PRO:HD2	1.91	0.53
1:A:161:ASN:OD1	1:A:162:SER:N	2.42	0.53
1:A:608:LEU:HD23	1:A:608:LEU:H	1.75	0.52
2:B:554:ILE:HB	2:B:557:ILE:HG12	1.91	0.52
3:C:196:LYS:O	3:C:215:PHE:N	2.31	0.52
3:C:448:VAL:HB	3:C:455:ILE:HG12	1.91	0.52
1:A:1102:LYS:HD2	1:A:1102:LYS:H	1.73	0.52
2:B:944:ILE:HB	2:B:952:ALA:HB3	1.92	0.52
3:C:466:ILE:HD11	3:C:656:ILE:HD11	1.92	0.52
3:C:506:VAL:HG13	3:C:547:ALA:HB1	1.91	0.52
3:C:306:ASP:OD1	3:C:307:VAL:N	2.43	0.52
2:B:153:TYR:CD2	2:B:444:ALA:HB2	2.45	0.52
1:A:565:LYS:O	1:A:722:LYS:NZ	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:HIS:ND1	1:A:250:GLU:OE2	2.35	0.52
1:A:1234:ASN:CG	2:B:789:TYR:HH	2.13	0.52
2:B:1:MET:O	2:B:90:ASN:ND2	2.41	0.52
3:C:228:ASN:OD1	3:C:258:GLN:NE2	2.43	0.52
1:A:191:SER:HB3	1:A:360:LEU:HD21	1.92	0.52
1:A:984:SER:O	1:A:989:LYS:NZ	2.38	0.52
1:A:1112:ARG:NH1	1:A:1120:ARG:O	2.42	0.52
3:C:548:TRP:O	3:C:552:GLN:HG2	2.10	0.52
3:C:520:LEU:HD11	3:C:527:TYR:HD2	1.74	0.51
2:B:810:GLU:HG3	2:B:811:GLN:H	1.75	0.51
1:A:853:LEU:HD11	1:A:900:ILE:HG21	1.92	0.51
1:A:22:LYS:HB3	1:A:133:GLU:HG3	1.92	0.51
1:A:320:ASN:H	1:A:320:ASN:HD22	1.57	0.51
1:A:232:THR:HA	1:A:248:ASN:HA	1.93	0.51
1:A:1133:ASN:HB3	2:B:1065:ASN:HD22	1.74	0.51
1:A:47:VAL:HG12	1:A:55:PHE:HZ	1.76	0.51
1:A:165:ILE:HD13	1:A:181:ILE:HB	1.93	0.51
2:B:300:GLU:CD	2:B:415:TYR:HB2	2.31	0.51
2:B:406:ASN:OD1	2:B:407:LEU:N	2.39	0.51
3:C:265:ASP:OD1	3:C:265:ASP:N	2.43	0.51
1:A:65:ASP:N	1:A:65:ASP:OD1	2.44	0.51
1:A:899:ASN:HD21	1:A:1028:ASN:HB3	1.76	0.51
1:A:994:THR:HG21	1:A:1059:ILE:HD12	1.92	0.50
3:C:367:VAL:HG11	3:C:384:ALA:HB3	1.93	0.50
1:A:1144:LYS:NZ	1:A:1192:SER:OG	2.24	0.50
2:B:23:SER:HB3	2:B:47:TYR:CZ	2.46	0.50
2:B:311:GLN:HE22	2:B:789:TYR:HH	1.59	0.50
3:C:213:GLY:HA3	3:C:238:ALA:HA	1.94	0.50
1:A:876:GLY:HA3	1:A:895:LEU:O	2.10	0.50
2:B:509:GLU:HA	2:B:512:LYS:HG3	1.93	0.50
2:B:588:ASN:OD1	2:B:640:GLN:NE2	2.44	0.50
2:B:64:TYR:HD1	2:B:363:ILE:HD13	1.76	0.50
3:C:261:LEU:HB3	3:C:284:LEU:HD11	1.93	0.50
2:B:581:SER:HA	2:B:586:LYS:HE3	1.94	0.50
1:A:82:ARG:NH2	1:A:362:ASN:OD1	2.41	0.50
2:B:866:ASN:ND2	2:B:936:ASN:OD1	2.44	0.49
1:A:168:ARG:HA	1:A:497:TYR:HB2	1.93	0.49
1:A:1149:TYR:HE1	1:A:1161:PRO:HB3	1.77	0.49
2:B:818:ASP:OD1	2:B:820:SER:N	2.44	0.49
2:B:875:ASN:HA	2:B:977:VAL:HG12	1.94	0.49
1:A:671:LEU:HD13	1:A:818:THR:HG21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:961:TRP:CE2	1:A:995:ILE:HG21	2.47	0.49
1:A:1055:ASP:OD1	1:A:1055:ASP:N	2.40	0.49
1:A:113:TYR:HE1	1:A:286:LEU:HD23	1.78	0.49
1:A:705:TYR:HB2	1:A:755:MET:HE1	1.95	0.49
1:A:836:LEU:HD21	2:B:945:PHE:HE2	1.78	0.49
1:A:443:TYR:OH	1:A:691:THR:OG1	2.24	0.48
2:B:534:TYR:HH	2:B:703:SER:HG	1.60	0.48
1:A:923:ILE:HD12	1:A:954:LEU:HD21	1.95	0.48
1:A:1172:GLU:HG2	1:A:1215:LYS:HD3	1.96	0.48
2:B:517:ILE:HD11	2:B:670:GLN:CG	2.44	0.48
3:C:674:THR:O	3:C:677:TRP:NE1	2.46	0.48
2:B:35:VAL:HG11	2:B:41:ILE:HD12	1.95	0.48
3:C:215:PHE:CE1	3:C:233:CYS:HB3	2.49	0.48
1:A:1056:GLU:OE2	1:A:1060:GLN:NE2	2.46	0.48
1:A:1106:LEU:HD21	1:A:1177:ILE:HD11	1.95	0.48
1:A:320:ASN:HD21	1:A:323:LYS:HD3	1.79	0.48
1:A:248:ASN:OD1	1:A:248:ASN:N	2.46	0.47
2:B:141:PRO:HG3	2:B:171:GLN:HB2	1.96	0.47
3:C:612:ILE:HD11	3:C:617:LEU:HD13	1.96	0.47
3:C:471:ARG:HB3	3:C:473:VAL:HG22	1.94	0.47
1:A:704:MET:HG2	1:A:758:ILE:HG21	1.96	0.47
1:A:875:ASN:HB2	1:A:897:GLU:HG2	1.94	0.47
1:A:1171:LYS:NZ	1:A:1223:THR:OG1	2.39	0.47
2:B:579:PRO:O	2:B:645:TYR:OH	2.29	0.47
2:B:858:TYR:OH	2:B:866:ASN:O	2.32	0.47
1:A:453:GLU:HG3	1:A:650:ILE:HG12	1.96	0.47
1:A:674:ARG:NH2	1:A:786:ASP:OD2	2.44	0.47
1:A:143:ILE:HG12	1:A:492:ILE:HG23	1.97	0.47
1:A:368:ILE:HG23	1:A:395:ILE:HG22	1.96	0.47
1:A:903:ASN:OD1	1:A:903:ASN:N	2.45	0.47
2:B:596:ILE:HD13	2:B:741:ILE:HD11	1.97	0.47
2:B:698:ASP:OD2	2:B:864:THR:OG1	2.28	0.47
2:B:971:LEU:HD23	2:B:971:LEU:H	1.79	0.47
3:C:211:ILE:HD11	3:C:319:LEU:HG	1.96	0.47
3:C:393:VAL:HG23	3:C:394:GLU:HG3	1.97	0.47
3:C:458:LYS:HG3	3:C:459:LYS:HG3	1.96	0.47
1:A:837:ILE:HD11	2:B:948:ASN:HD22	1.79	0.47
1:A:196:ASP:OD1	1:A:196:ASP:N	2.47	0.47
1:A:249:ILE:HA	1:A:252:PHE:HD2	1.80	0.47
1:A:332:TYR:O	1:A:466:ASN:ND2	2.45	0.47
2:B:191:LYS:HB2	2:B:303:LEU:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:216:ARG:HE	2:B:225:SER:HG	1.61	0.47
3:C:253:ASN:HB2	3:C:304:ILE:HA	1.96	0.47
1:A:15:ASP:OD1	1:A:15:ASP:N	2.49	0.46
1:A:354:GLN:HG2	1:A:432:GLY:O	2.15	0.46
2:B:23:SER:HB3	2:B:47:TYR:CE1	2.50	0.46
2:B:731:THR:HG23	2:B:774:PHE:HE1	1.78	0.46
3:C:673:THR:HG21	3:C:687:LEU:HD23	1.97	0.46
1:A:1106:LEU:HD12	1:A:1175:ILE:HD11	1.96	0.46
2:B:224:TYR:HE1	2:B:640:GLN:HE22	1.63	0.46
3:C:662:ILE:HG22	3:C:666:LYS:HE3	1.96	0.46
2:B:1076:GLU:HB3	2:B:1109:ILE:HD11	1.96	0.46
3:C:569:GLY:HA3	3:C:620:ILE:HG21	1.97	0.46
1:A:30:TYR:CG	1:A:44:GLU:HG3	2.51	0.46
2:B:307:SER:OG	2:B:312:ILE:O	2.24	0.46
2:B:807:ALA:HB1	2:B:834:LEU:HD11	1.98	0.46
2:B:876:LEU:HD11	2:B:978:TYR:CZ	2.50	0.46
3:C:517:ASN:HB2	3:C:534:SER:HB3	1.96	0.46
2:B:734:MET:HA	2:B:737:CYS:HB3	1.96	0.46
1:A:450:THR:HG22	1:A:646:LEU:HD22	1.97	0.46
2:B:45:ARG:HH22	2:B:145:ILE:HG22	1.81	0.46
2:B:110:TYR:HB3	2:B:118:ARG:HB3	1.98	0.46
2:B:371:ASN:HB3	2:B:379:VAL:HG12	1.97	0.46
2:B:375:GLN:OE1	2:B:375:GLN:N	2.40	0.46
1:A:107:LEU:O	1:A:147:ASN:ND2	2.27	0.46
2:B:719:MET:HE1	2:B:783:LYS:HG2	1.98	0.46
2:B:909:ILE:HB	2:B:915:GLU:HG3	1.98	0.46
2:B:113:ASN:OD1	2:B:114:THR:N	2.46	0.46
2:B:1016:GLN:OE1	2:B:1019:ARG:NH2	2.48	0.46
1:A:480:ALA:N	1:A:481:PRO:HD2	2.31	0.45
1:A:994:THR:HB	1:A:1006:TYR:HB2	1.96	0.45
1:A:1009:GLY:HA2	1:A:1059:ILE:HG22	1.97	0.45
3:C:527:TYR:OH	3:C:706:GLN:N	2.49	0.45
1:A:1027:ASP:OD1	1:A:1027:ASP:N	2.28	0.45
2:B:867:PHE:CZ	2:B:935:ILE:HD12	2.52	0.45
2:B:1126:TYR:O	2:B:1129:VAL:HG22	2.16	0.45
1:A:628:LEU:HB2	1:A:632:ILE:HD11	1.97	0.45
2:B:778:ASP:HB3	2:B:781:ASN:HB2	1.99	0.45
3:C:177:SER:N	3:C:389:ALA:O	2.49	0.45
3:C:481:ASN:HD21	3:C:498:ALA:HB2	1.81	0.45
1:A:873:ASN:N	1:A:873:ASN:OD1	2.49	0.45
1:A:972:LYS:HB3	2:B:772:LEU:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:877:LYS:HD3	2:B:975:ASN:HA	1.99	0.45
1:A:468:LEU:O	1:A:472:ILE:HG12	2.17	0.45
2:B:42:VAL:HG12	2:B:44:GLU:HG2	1.97	0.45
3:C:250:LYS:HZ2	3:C:307:VAL:HG12	1.81	0.45
1:A:115:GLY:HA2	1:A:125:HIS:HB3	1.98	0.45
1:A:407:LYS:HB3	1:A:431:ASN:HB2	1.99	0.45
1:A:821:ASN:ND2	2:B:900:GLU:OE1	2.45	0.45
1:A:910:ASN:HD21	1:A:913:LYS:HB3	1.81	0.45
3:C:358:THR:HG21	3:C:395:ASN:H	1.81	0.45
1:A:1131:ARG:CZ	1:A:1136:SER:HB3	2.47	0.45
2:B:596:ILE:HG21	2:B:741:ILE:HD11	1.97	0.45
2:B:885:LEU:HD11	2:B:979:ILE:HD11	1.99	0.45
3:C:513:ARG:NH1	3:C:536:ASP:HB3	2.31	0.45
1:A:924:PRO:O	1:A:1040:ARG:NH2	2.45	0.44
1:A:1100:ARG:HG3	1:A:1177:ILE:HD12	1.99	0.44
2:B:31:LYS:HE2	2:B:33:PHE:HE1	1.83	0.44
3:C:427:LEU:HG	3:C:453:LEU:HD11	1.99	0.44
1:A:39:ILE:HG23	1:A:148:VAL:HG22	1.99	0.44
1:A:879:TYR:HB2	1:A:891:TYR:OH	2.17	0.44
2:B:556:TRP:CH2	2:B:710:ILE:HD11	2.52	0.44
2:B:617:ASN:O	2:B:621:LYS:HG2	2.17	0.44
3:C:538:THR:HG23	3:C:599:SER:HB3	1.99	0.44
1:A:1125:ILE:HG13	1:A:1152:PHE:CE1	2.53	0.44
2:B:1120:ASN:OD1	2:B:1120:ASN:N	2.46	0.44
3:C:204:VAL:HG12	3:C:209:TYR:HE2	1.81	0.44
3:C:419:PHE:CZ	3:C:712:CYS:HB3	2.52	0.44
3:C:465:LYS:NZ	3:C:650:LYS:HB3	2.33	0.44
3:C:677:TRP:O	3:C:707:GLN:NE2	2.49	0.44
1:A:395:ILE:HG13	1:A:396:ILE:HG23	1.98	0.44
1:A:1055:ASP:O	1:A:1059:ILE:HG12	2.17	0.44
1:A:1249:TRP:CD1	1:A:1251:GLU:HG3	2.53	0.44
3:C:654:ARG:HB2	3:C:659:ARG:HH11	1.82	0.44
1:A:222:TYR:CD1	1:A:331:LEU:HD21	2.53	0.44
2:B:366:PRO:HB3	2:B:384:ASN:HB3	2.00	0.44
3:C:419:PHE:HE2	3:C:716:ILE:HD11	1.82	0.44
1:A:862:TYR:HD2	1:A:874:ILE:HD11	1.83	0.44
2:B:910:ASP:HA	2:B:962:ILE:HG22	2.00	0.44
3:C:216:GLY:HA2	3:C:236:LYS:HG3	1.99	0.44
3:C:270:ILE:HD12	3:C:717:GLN:HG3	1.99	0.44
2:B:1087:LYS:NZ	2:B:1102:ASP:OD1	2.43	0.44
2:B:374:ASN:OD1	2:B:374:ASN:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:399:ASP:O	3:C:400:ARG:NH1	2.43	0.43
3:C:363:GLY:N	3:C:388:ALA:O	2.37	0.43
1:A:7:PHE:CD1	1:A:18:ILE:HD11	2.52	0.43
1:A:528:VAL:HG21	1:A:717:THR:HG21	2.00	0.43
1:A:957:ASN:ND2	1:A:979:ASN:H	2.16	0.43
2:B:1090:ASP:OD1	2:B:1091:ILE:N	2.52	0.43
3:C:489:ASN:O	3:C:490:GLN:NE2	2.52	0.43
1:A:537:LEU:HB2	1:A:560:ILE:HG23	1.99	0.43
1:A:1104:SER:OG	1:A:1177:ILE:O	2.36	0.43
2:B:423:ILE:O	2:B:427:GLU:HG2	2.18	0.43
1:A:376:ASN:HB3	1:A:381:LYS:HA	2.01	0.43
1:A:892:ASN:HB3	1:A:1033:ILE:HB	2.01	0.43
2:B:13:VAL:HG23	2:B:19:ALA:HA	2.01	0.43
2:B:149:ASN:OD1	2:B:150:VAL:N	2.51	0.43
3:C:543:VAL:HG23	3:C:594:ALA:HB3	2.01	0.43
1:A:126:ILE:HD11	1:A:296:LEU:HD11	1.99	0.43
1:A:185:THR:O	1:A:185:THR:OG1	2.37	0.43
1:A:599:ILE:HD11	1:A:630:ALA:HB2	2.01	0.43
1:A:893:ASP:OD1	1:A:893:ASP:N	2.52	0.43
2:B:205:PRO:HG3	2:B:254:TYR:CZ	2.54	0.43
2:B:727:TYR:CZ	2:B:777:LEU:HB2	2.54	0.43
2:B:970:LEU:HD11	2:B:979:ILE:HD12	2.01	0.43
2:B:803:LEU:HD13	2:B:824:THR:HG21	2.00	0.43
3:C:629:THR:HA	3:C:688:LYS:NZ	2.33	0.43
1:A:47:VAL:HG12	1:A:55:PHE:CZ	2.54	0.43
1:A:346:LYS:HD2	1:A:346:LYS:HA	1.89	0.43
1:A:445:ASP:HB3	1:A:643:PRO:HG3	2.00	0.43
1:A:17:THR:HG22	1:A:34:ASN:HD22	1.84	0.42
2:B:402:ILE:H	2:B:402:ILE:HG13	1.56	0.42
3:C:289:ASP:N	3:C:289:ASP:OD1	2.52	0.42
1:A:74:LEU:HD22	1:A:74:LEU:HA	1.75	0.42
1:A:1098:ILE:HD11	1:A:1240:TRP:CZ3	2.54	0.42
1:A:650:ILE:HG13	1:A:792:TYR:HE2	1.85	0.42
1:A:693:ILE:HG12	1:A:769:TYR:CE2	2.54	0.42
1:A:738:TYR:HE1	1:A:743:ILE:HG21	1.84	0.42
1:A:892:ASN:ND2	1:A:1038:TYR:O	2.47	0.42
2:B:315:PRO:HB2	2:B:319:ASN:HB3	2.01	0.42
2:B:483:SER:HB2	2:B:496:LEU:HD22	2.01	0.42
2:B:842:ALA:HB2	2:B:980:GLU:HB2	2.00	0.42
2:B:898:TYR:HB2	2:B:905:VAL:HB	2.00	0.42
3:C:394:GLU:HB2	3:C:396:HIS:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:LYS:NZ	1:A:517:LEU:HG	2.34	0.42
2:B:228:ASP:OD1	2:B:229:MET:N	2.52	0.42
3:C:261:LEU:HB2	3:C:362:TYR:CZ	2.54	0.42
1:A:1013:ASP:OD1	1:A:1014:GLN:N	2.52	0.42
2:B:195:LYS:HG3	2:B:230:ILE:HG21	2.01	0.42
2:B:675:MET:O	3:C:324:LYS:NZ	2.46	0.42
1:A:68:TYR:HB2	1:A:158:PHE:CE2	2.55	0.42
1:A:260:LEU:HD12	1:A:260:LEU:HA	1.90	0.42
2:B:121:ASN:OD1	2:B:121:ASN:N	2.53	0.42
2:B:556:TRP:HH2	2:B:710:ILE:HD11	1.85	0.42
2:B:519:THR:CG2	2:B:522:LYS:NZ	2.83	0.42
2:B:973:ASP:O	2:B:974:ASN:ND2	2.53	0.42
1:A:446:ASP:N	1:A:446:ASP:OD1	2.48	0.42
1:A:551:ILE:HD13	1:A:551:ILE:HA	1.95	0.42
1:A:1002:ASP:HA	1:A:1016:SER:HA	2.02	0.42
2:B:524:TYR:HB2	2:B:960:LEU:HD13	2.02	0.42
2:B:893:CYS:SG	3:C:205:ARG:NH2	2.93	0.42
3:C:671:LEU:O	3:C:674:THR:OG1	2.37	0.42
3:C:253:ASN:HD22	3:C:304:ILE:HG22	1.85	0.41
1:A:164:ASN:HD21	1:A:220:GLY:HA3	1.84	0.41
1:A:660:LYS:HB3	1:A:660:LYS:HE3	1.70	0.41
1:A:1203:ASN:OD1	1:A:1204:ASN:N	2.53	0.41
3:C:178:SER:HA	3:C:388:ALA:HA	2.02	0.41
2:B:410:GLU:OE1	2:B:410:GLU:N	2.47	0.41
3:C:240:TYR:OH	3:C:253:ASN:ND2	2.53	0.41
1:A:81:ASP:O	1:A:85:LYS:HG2	2.21	0.41
1:A:297:ASN:N	1:A:298:PRO:HD2	2.36	0.41
1:A:1056:GLU:O	1:A:1060:GLN:HG2	2.20	0.41
2:B:932:VAL:HG11	2:B:994:ILE:HG12	2.02	0.41
3:C:226:GLY:HA2	3:C:363:GLY:HA2	2.01	0.41
3:C:682:VAL:HG12	3:C:684:PRO:HD2	2.01	0.41
3:C:705:ILE:HG13	3:C:709:THR:HG23	2.02	0.41
1:A:601:ILE:HG12	1:A:760:ARG:NH1	2.35	0.41
3:C:221:THR:OG1	3:C:222:THR:N	2.53	0.41
2:B:62:GLY:HA2	2:B:146:ILE:HD11	2.02	0.41
2:B:1115:ASP:OD1	2:B:1116:ILE:N	2.53	0.41
2:B:78:PHE:O	2:B:82:THR:HG22	2.21	0.41
2:B:281:ASN:HA	2:B:284:LYS:HE3	2.01	0.41
2:B:301:LEU:HD11	2:B:418:LEU:HD21	2.03	0.41
2:B:870:TYR:HB3	2:B:932:VAL:HG13	2.03	0.41
3:C:409:PHE:HZ	3:C:420:ALA:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:471:ARG:NH1	3:C:471:ARG:HA	2.36	0.41
1:A:914:ASN:HB3	1:A:998:ASP:HA	2.03	0.41
1:A:74:LEU:HD13	1:A:80:LYS:HG2	2.03	0.41
1:A:1075:PHE:CG	1:A:1243:ILE:HG12	2.56	0.41
2:B:203:ILE:O	2:B:254:TYR:OH	2.28	0.41
2:B:556:TRP:HB3	2:B:559:ARG:HH21	1.86	0.41
3:C:284:LEU:HB3	3:C:339:SER:H	1.85	0.41
3:C:714:GLY:O	3:C:717:GLN:NE2	2.53	0.41
1:A:138:ASN:OD1	1:A:138:ASN:N	2.50	0.41
1:A:278:ASP:O	1:A:282:ILE:HG12	2.20	0.41
2:B:763:LEU:HD12	2:B:763:LEU:HA	1.89	0.41
1:A:561:ASN:OD1	1:A:562:ASN:N	2.54	0.40
1:A:1092:LEU:HD23	1:A:1214:PHE:CE1	2.56	0.40
2:B:118:ARG:HD3	2:B:118:ARG:HA	1.87	0.40
2:B:251:ILE:HD13	2:B:251:ILE:HA	1.95	0.40
3:C:462:ASN:ND2	3:C:474:ASP:OD2	2.55	0.40
1:A:48:ILE:O	1:A:50:THR:HG23	2.21	0.40
1:A:107:LEU:HD13	1:A:107:LEU:HA	1.91	0.40
1:A:738:TYR:O	1:A:741:LYS:N	2.48	0.40
3:C:622:LYS:O	3:C:626:LYS:HG2	2.21	0.40
2:B:534:TYR:CE2	2:B:699:ILE:HG23	2.56	0.40
2:B:760:LYS:O	2:B:764:ILE:HG12	2.21	0.40
3:C:551:THR:OG1	3:C:554:ALA:HB3	2.21	0.40
3:C:612:ILE:HA	3:C:616:GLN:HE21	1.86	0.40
1:A:61:LEU:HB2	1:A:407:LYS:HB2	2.03	0.40
1:A:612:ILE:HG22	1:A:632:ILE:HG22	2.04	0.40
1:A:751:VAL:O	1:A:755:MET:HG2	2.22	0.40
1:A:1126:LYS:HE3	1:A:1126:LYS:HB2	1.87	0.40
2:B:270:GLU:HA	2:B:274:LYS:HE3	2.04	0.40
2:B:528:LYS:NZ	2:B:937:ARG:O	2.50	0.40
2:B:854:PHE:HB2	2:B:968:ILE:HG23	2.02	0.40
1:A:665:LYS:O	1:A:669:ASN:ND2	2.32	0.40
3:C:360:ILE:HA	3:C:391:ALA:HA	2.02	0.40
3:C:614:LYS:N	3:C:615:PRO:HD2	2.37	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	1241/1252 (99%)	1172 (94%)	67 (5%)	2 (0%)	44	77
2	B	1161/1163 (100%)	1118 (96%)	42 (4%)	1 (0%)	48	82
3	C	576/748 (77%)	564 (98%)	12 (2%)	0	100	100
All	All	2978/3163 (94%)	2854 (96%)	121 (4%)	3 (0%)	50	82

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	481	PRO
2	B	413	ILE
1	A	743	ILE

### 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	1114/1150 (97%)	1063 (95%)	51 (5%)	23	46
2	B	1099/1103 (100%)	1078 (98%)	21 (2%)	52	69
3	C	505/677 (75%)	485 (96%)	20 (4%)	27	50
All	All	2718/2930 (93%)	2626 (97%)	92 (3%)	34	54

All (92) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	65	ASP
1	A	74	LEU
1	A	93	ARG
1	A	107	LEU
1	A	121	ASP
1	A	142	ASP
1	A	148	VAL
1	A	168	ARG
1	A	169	ASN
1	A	172	MET
1	A	185	THR
1	A	201	GLU
1	A	248	ASN
1	A	260	LEU
1	A	286	LEU
1	A	289	VAL
1	A	295	LEU
1	A	296	LEU
1	A	299	TYR
1	A	320	ASN
1	A	377	ILE
1	A	456	ASP
1	A	463	ASN
1	A	465	GLU
1	A	660	LYS
1	A	672	LYS
1	A	728	LEU
1	A	735	THR
1	A	738	TYR
1	A	757	ASN
1	A	795	ASN
1	A	800	HIS
1	A	839	TYR
1	A	899	ASN
1	A	910	ASN
1	A	914	ASN
1	A	930	ILE
1	A	932	ASN
1	A	939	ILE
1	A	1024	HIS
1	A	1027	ASP
1	A	1116	LEU
1	A	1125	ILE

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	A	1133	ASN
1	A	1143	ARG
1	A	1149	TYR
1	A	1153	VAL
1	A	1172	GLU
1	A	1175	ILE
1	A	1208	ASN
1	A	1234	ASN
2	B	2	LYS
2	B	44	GLU
2	B	88	ARG
2	B	153	TYR
2	B	402	ILE
2	B	413	ILE
2	B	463	THR
2	B	489	VAL
2	B	539	THR
2	B	559	ARG
2	B	650	CYS
2	B	683	THR
2	B	734	MET
2	B	763	LEU
2	B	845	LEU
2	B	899	PHE
2	B	909	ILE
2	B	967	ILE
2	B	971	LEU
2	B	1118	ILE
2	B	1147	LEU
3	C	171	LEU
3	C	173	TRP
3	C	195	GLU
3	C	215	PHE
3	C	219	GLN
3	C	245	ASP
3	C	256	ILE
3	C	265	ASP
3	C	267	LYS
3	C	281	GLN
3	C	311	LEU
3	C	336	GLN
3	C	367	VAL

*Continued on next page...*



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Mol	Chain	Res	Type
3	C	399	ASP
3	C	453	LEU
3	C	514	GLN
3	C	523	GLU
3	C	566	THR
3	C	710	GLN
3	C	728	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	ASN
1	A	125	HIS
1	A	235	GLN
1	A	320	ASN
1	A	463	ASN
1	A	709	GLN
1	A	899	ASN
1	A	902	GLN
1	A	928	ASN
1	A	946	ASN
1	A	981	ASN
1	A	1096	ASN
1	A	1130	GLN
1	A	1151	ASN
1	A	1196	ASN
1	A	1234	ASN
2	B	34	GLN
2	B	302	ASN
2	B	311	GLN
2	B	400	ASN
2	B	632	ASN
2	B	640	GLN
2	B	811	GLN
2	B	813	ASN
2	B	1050	ASN
3	C	185	ASN
3	C	253	ASN
3	C	480	ASN
3	C	481	ASN
3	C	488	ASN
3	C	710	GLN



### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

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

There are no ligands in this entry.

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

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



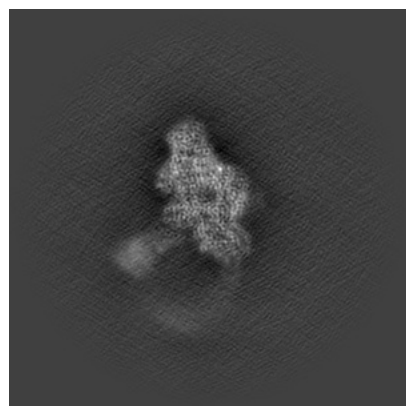
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43785. These allow visual inspection of the internal detail of the map and identification of artifacts.

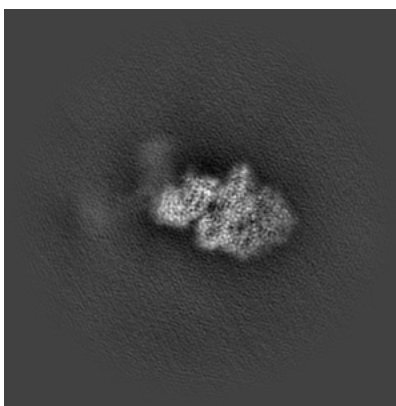
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

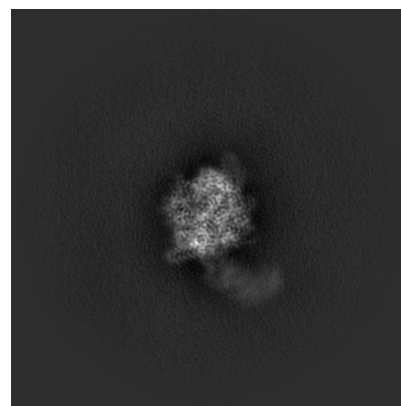
#### 6.1.1 Primary map



X

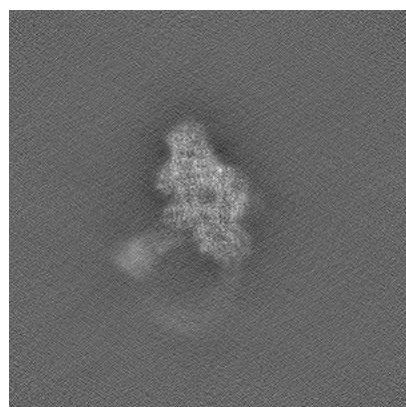


Y

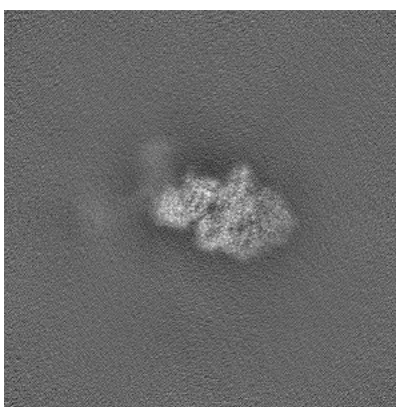


Z

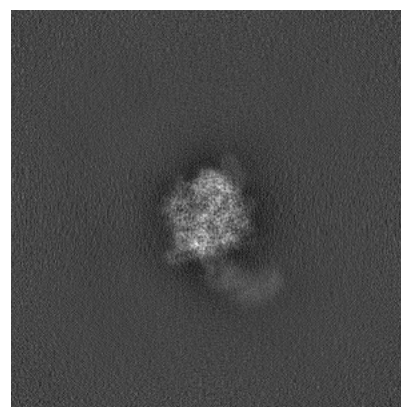
#### 6.1.2 Raw map



X



Y



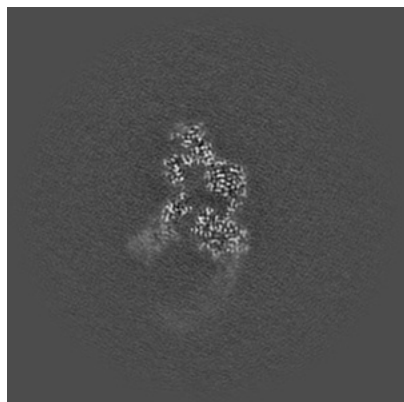
Z

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

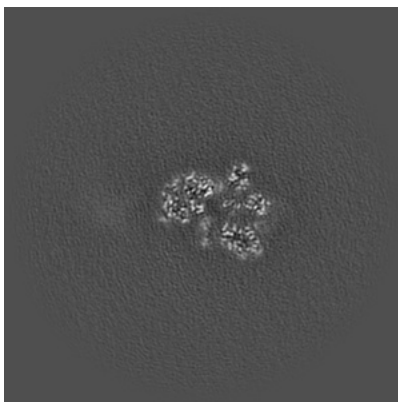


## 6.2 Central slices [i](#)

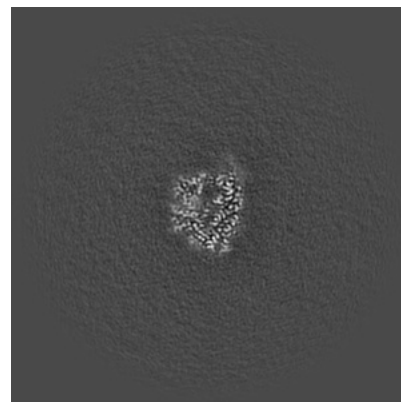
### 6.2.1 Primary map



X Index: 256

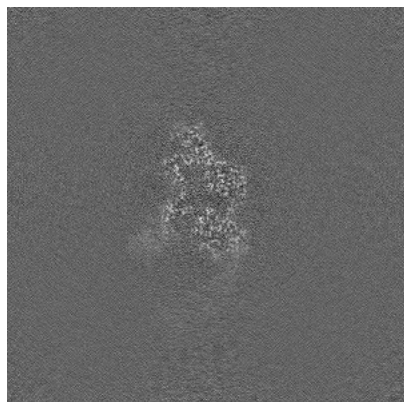


Y Index: 256

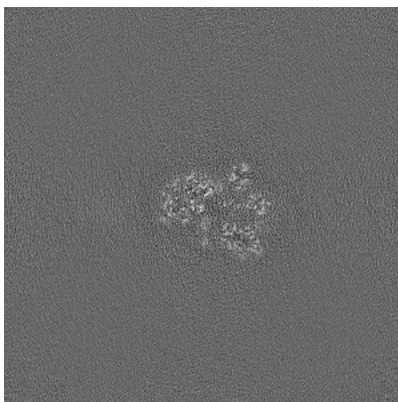


Z Index: 256

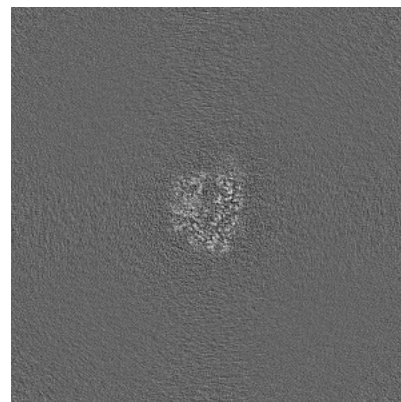
### 6.2.2 Raw map



X Index: 256



Y Index: 256



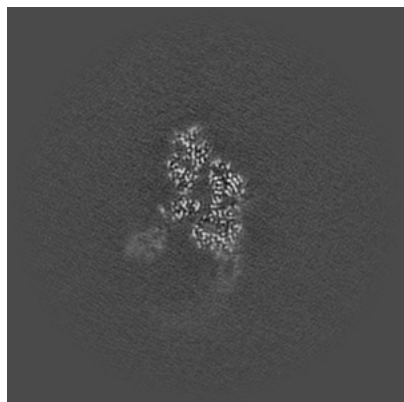
Z Index: 256

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

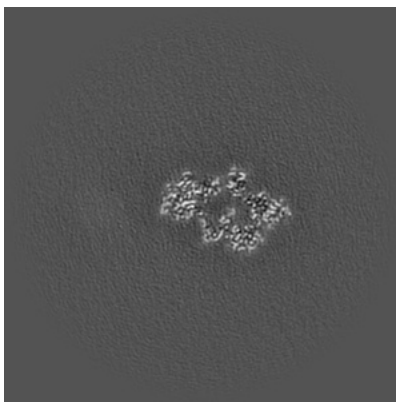


## 6.3 Largest variance slices [i](#)

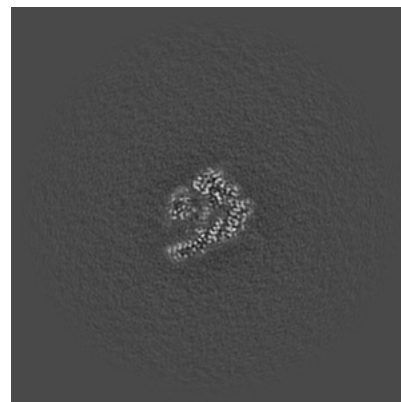
### 6.3.1 Primary map



X Index: 266

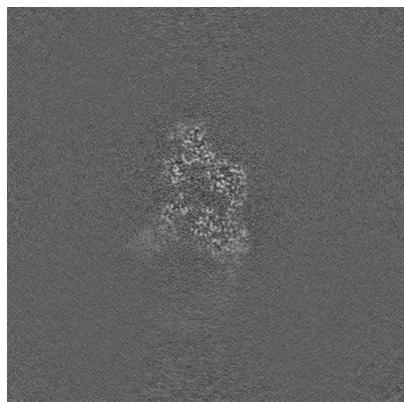


Y Index: 247

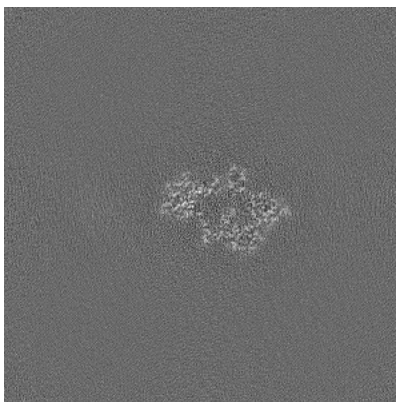


Z Index: 292

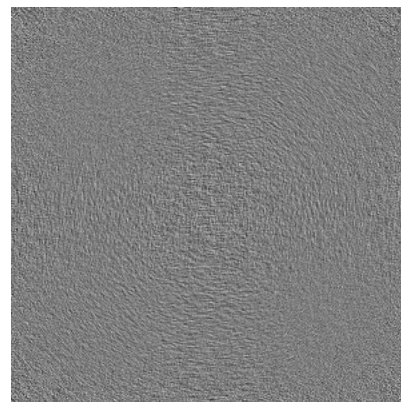
### 6.3.2 Raw map



X Index: 255



Y Index: 248



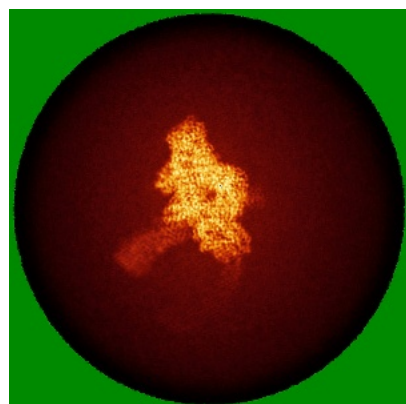
Z Index: 511

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

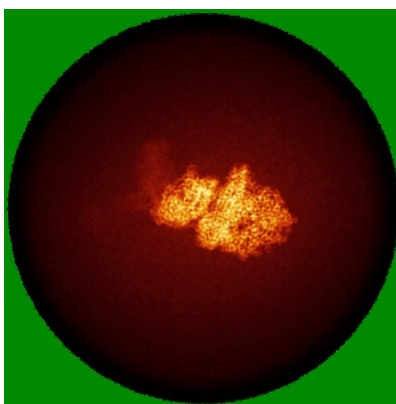


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

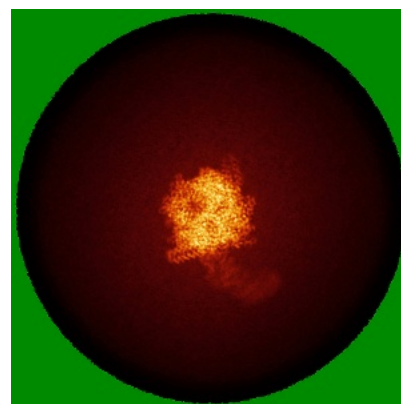
### 6.4.1 Primary map



X

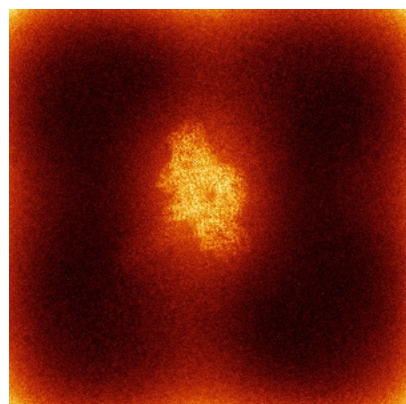


Y

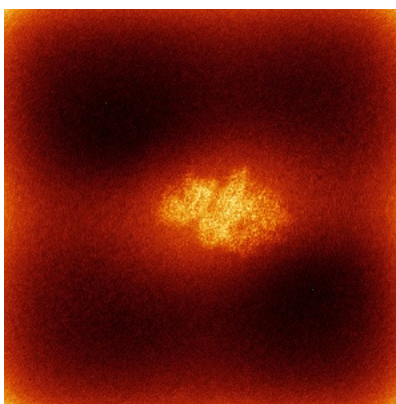


Z

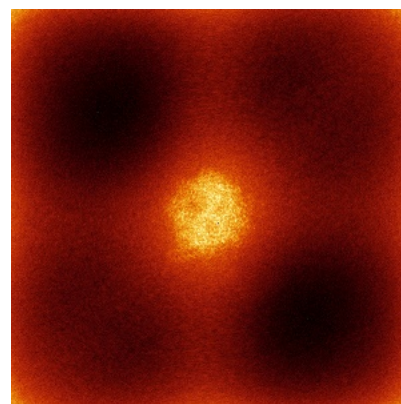
### 6.4.2 Raw map



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.



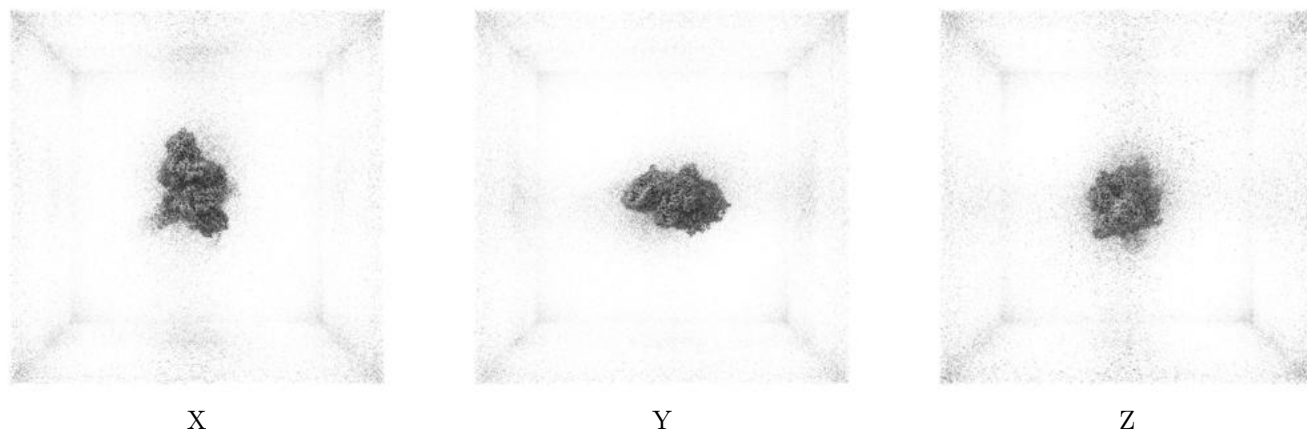
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.055. 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](#)

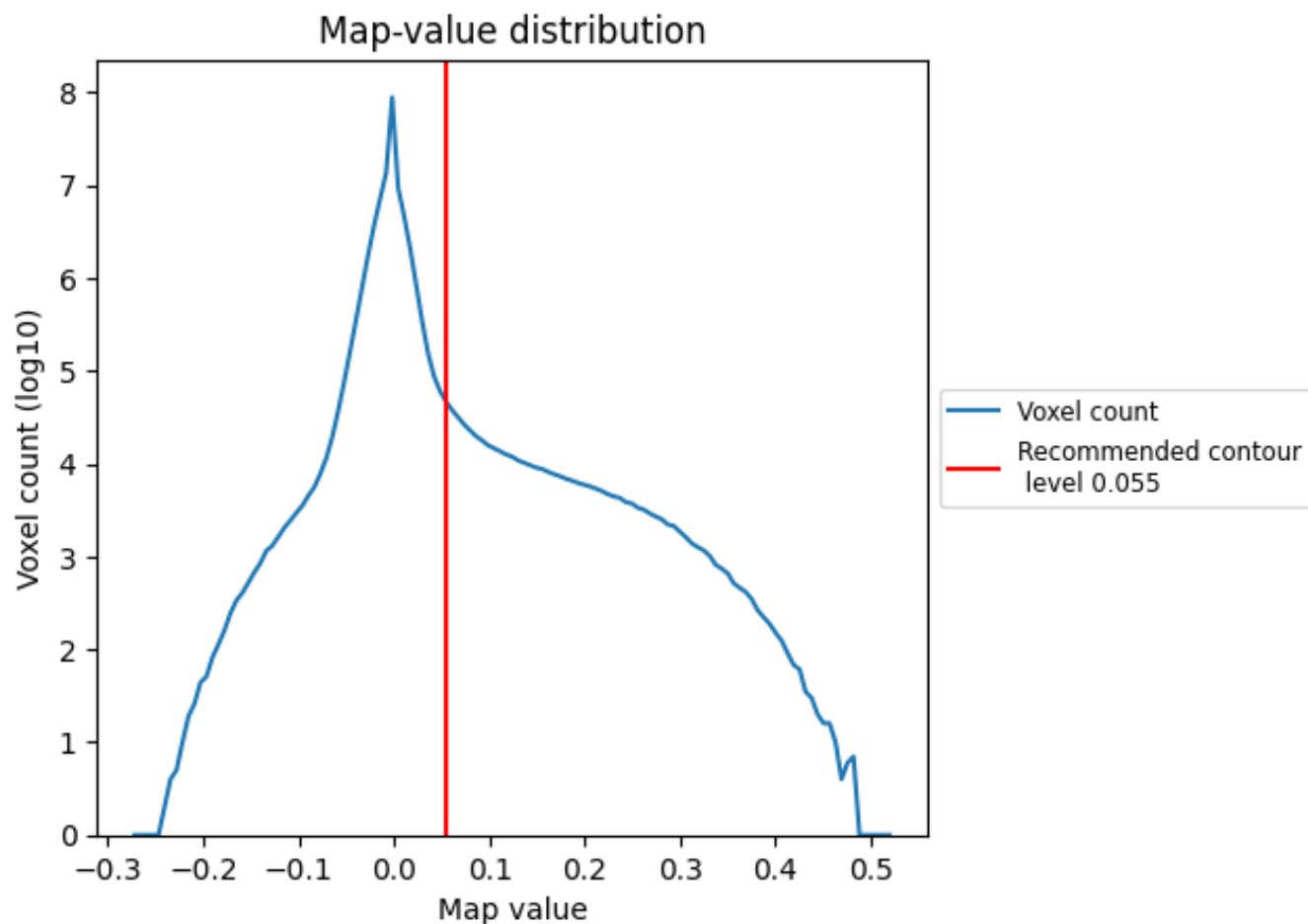
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

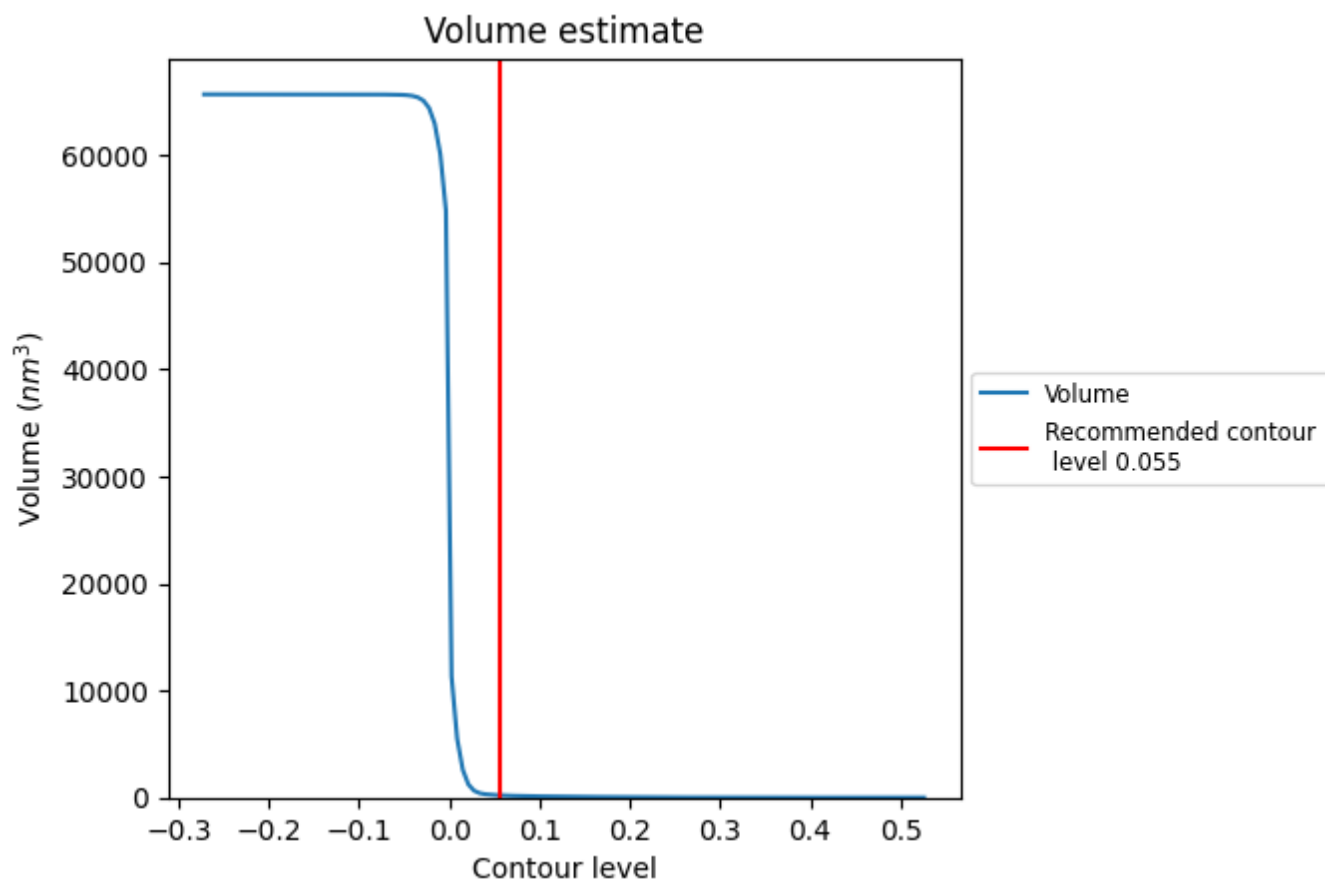
### 7.1 Map-value distribution [i](#)



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](#)

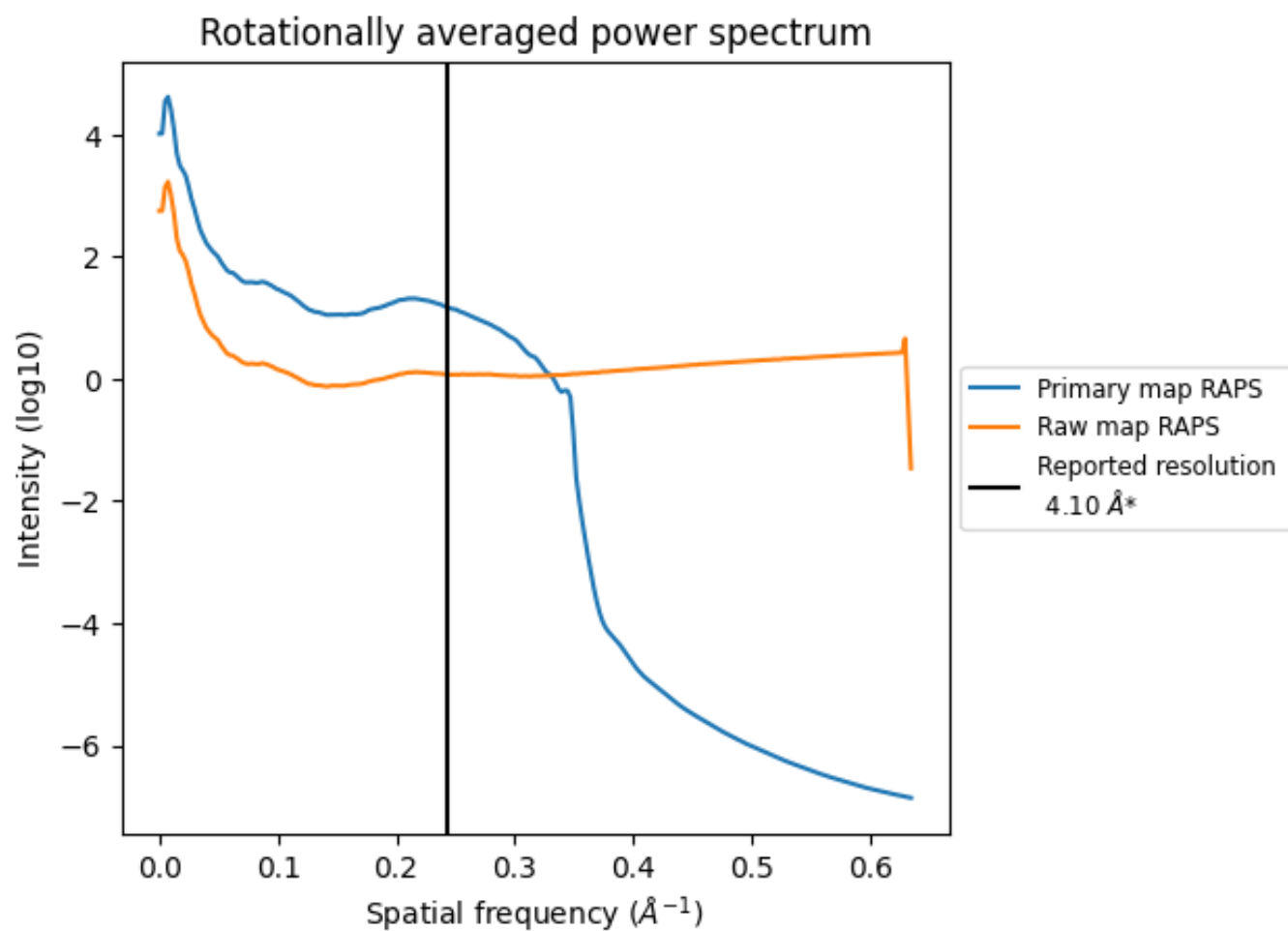


The volume at the recommended contour level is 215  $\text{nm}^3$ ; this corresponds to an approximate mass of 194 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



### 7.3 Rotationally averaged power spectrum ⓘ



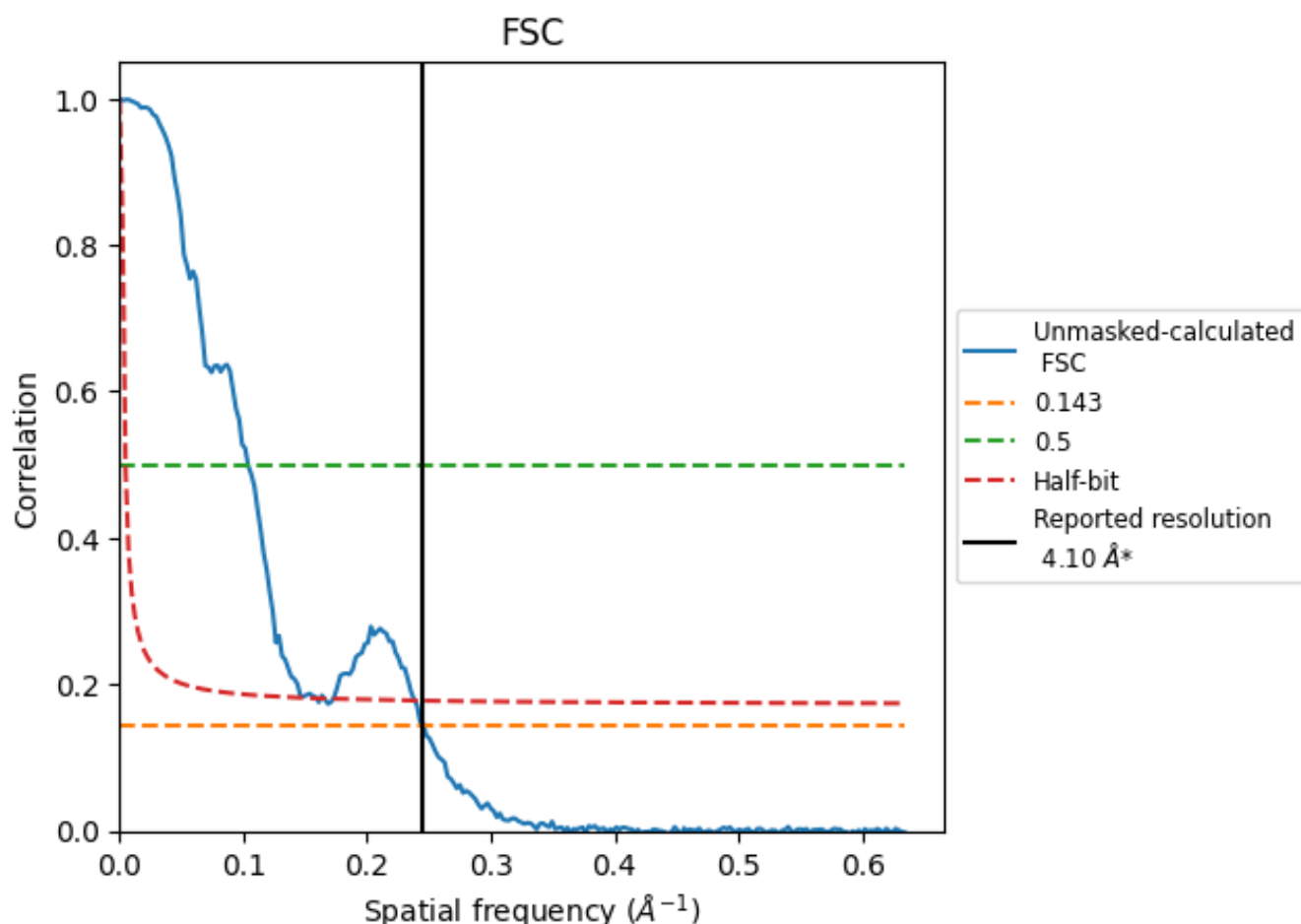
\*Reported resolution corresponds to spatial frequency of 0.244 Å<sup>-1</sup>



## 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 0.244 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	4.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	9.62	6.28

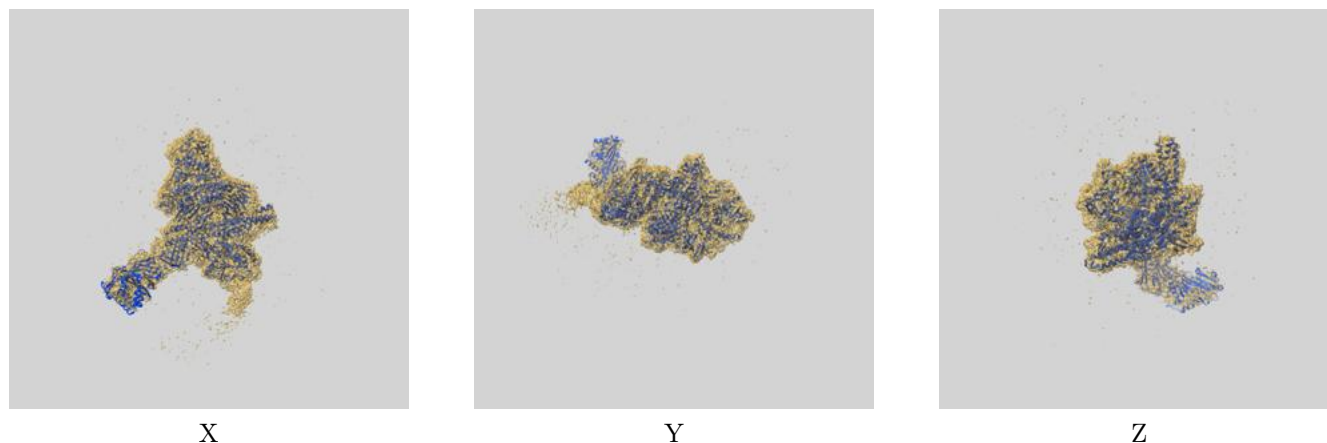
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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

This section contains information regarding the fit between EMDB map EMD-43785 and PDB model 9ARK. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

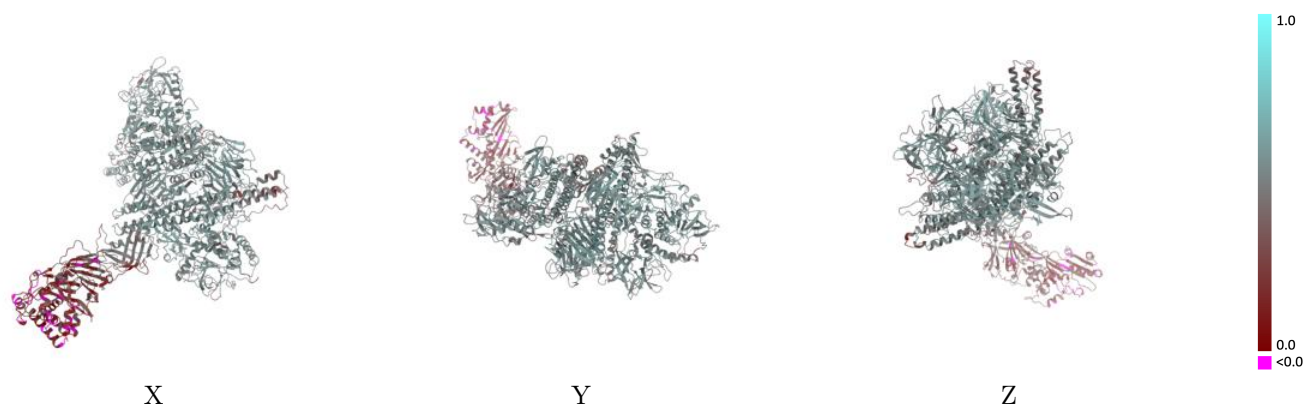
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.055 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.

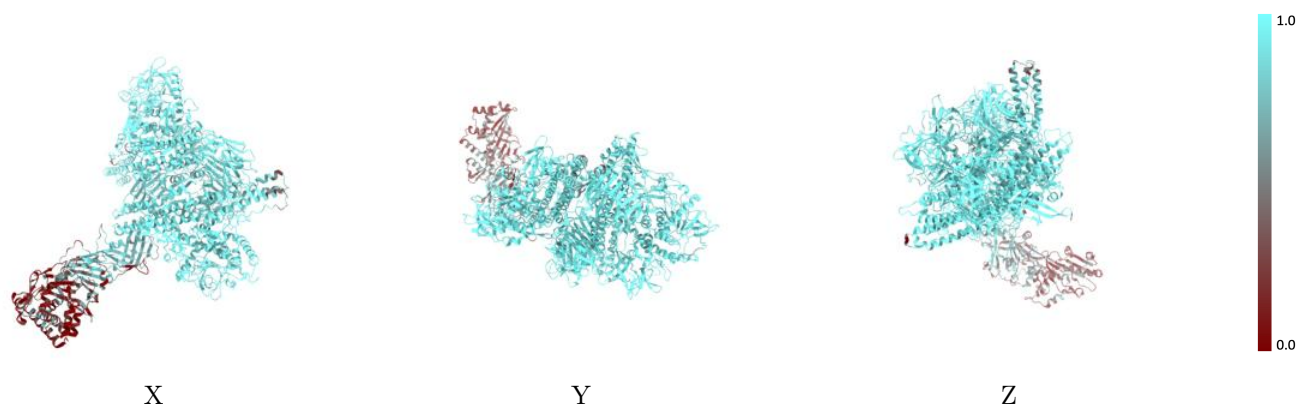


## 9.2 Q-score mapped to coordinate model [i](#)



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.

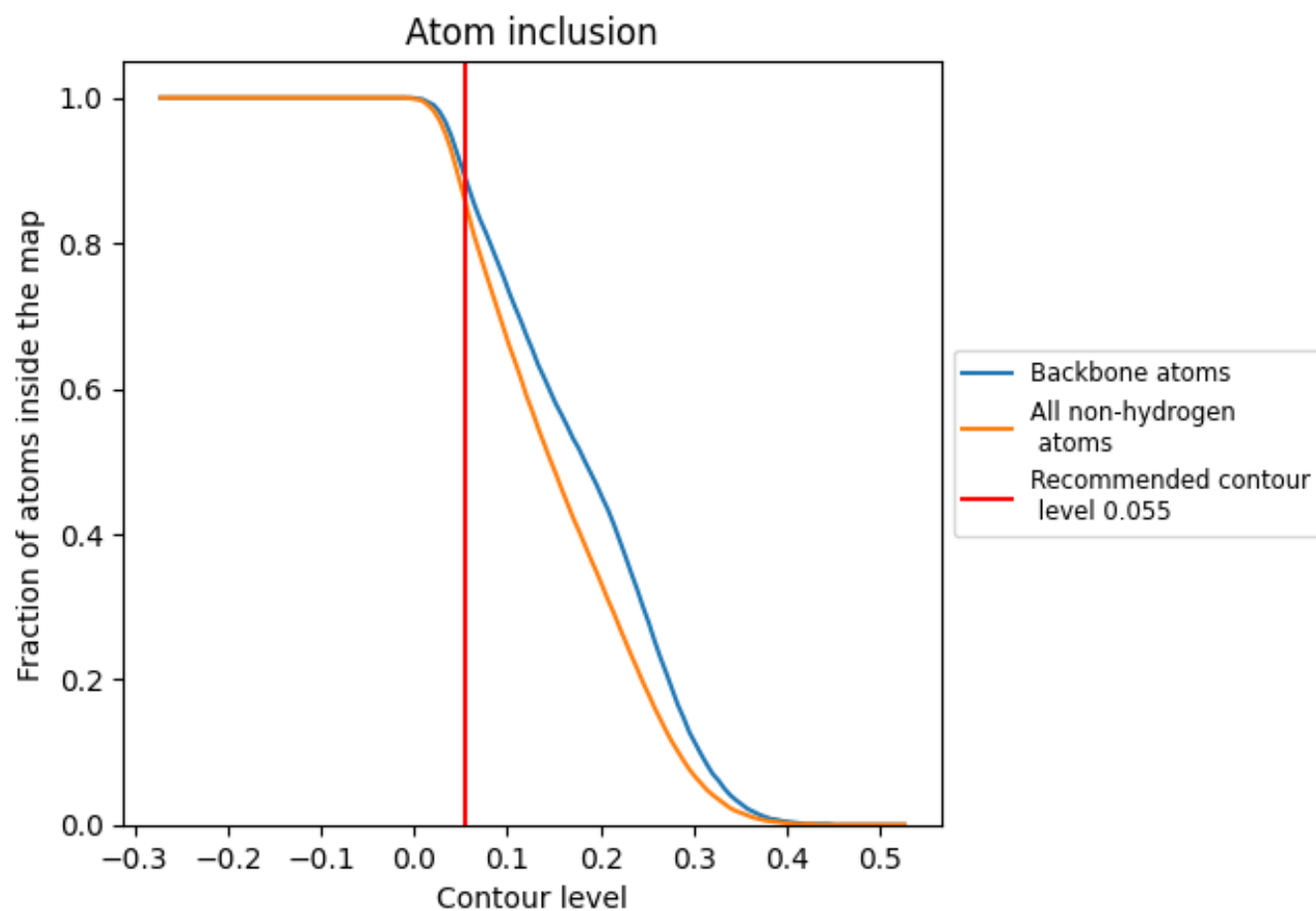
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.055).



## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8570	<div></div> 0.4860
A	<div></div> 0.9560	<div></div> 0.5350
B	<div></div> 0.9490	<div></div> 0.5360
C	<div></div> 0.4480	<div></div> 0.2710

