Full wwPDB EM Validation Report (i)

Feb 25, 2024 – 07:25 AM EST

PDB ID	:	7JKQ
EMDB ID	:	EMD-22367
Title	:	Human DPP9-CARD8 complex
Authors	:	Sharif, H.; Hollingsworth, L.R.
Deposited on	:	2020-07-28
Resolution	:	3.30 Å(reported)
Based on initial model	:	6EOQ

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

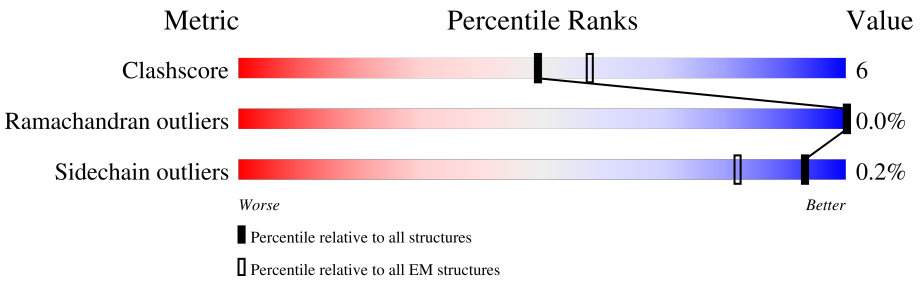
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.30 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 >=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 <=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	863	83% 13% •
1	D	863	• 80% 15% 5%
2	B	537	• 37% 13% 49%
2	C	537	7% 19% 5% 76%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16437 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 Dipeptidyl peptidase 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	827	6650	4277	1128	1216	29	0	0
1	D	822	6611	4249	1123	1210	29	0	0

- Molecule 2 is a protein called Caspase recruitment domain-containing protein 8.

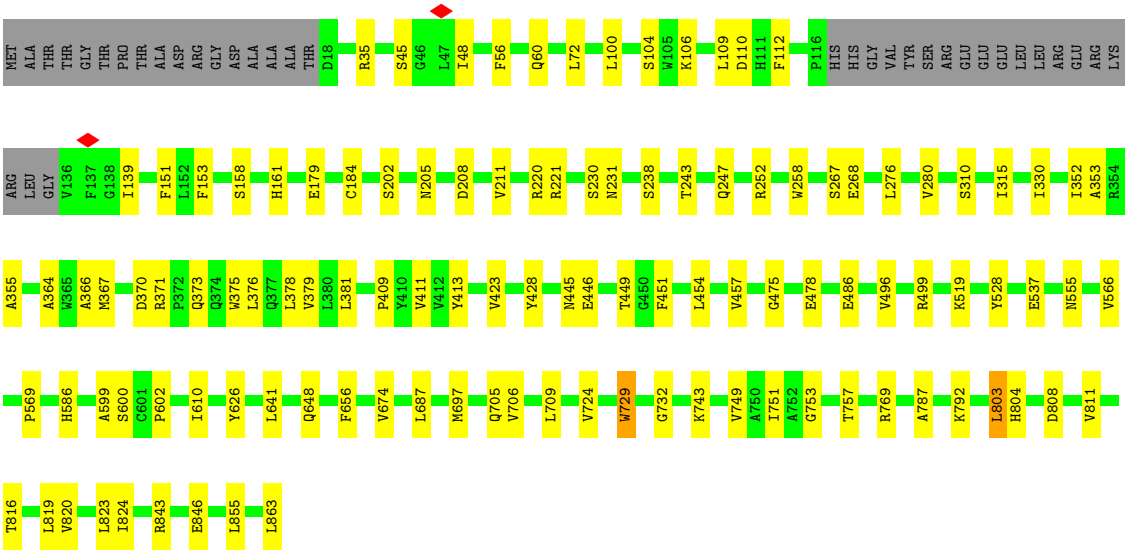
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	272	2153	1390	356	403	4	0	0
2	C	127	1023	661	169	190	3	0	0

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.

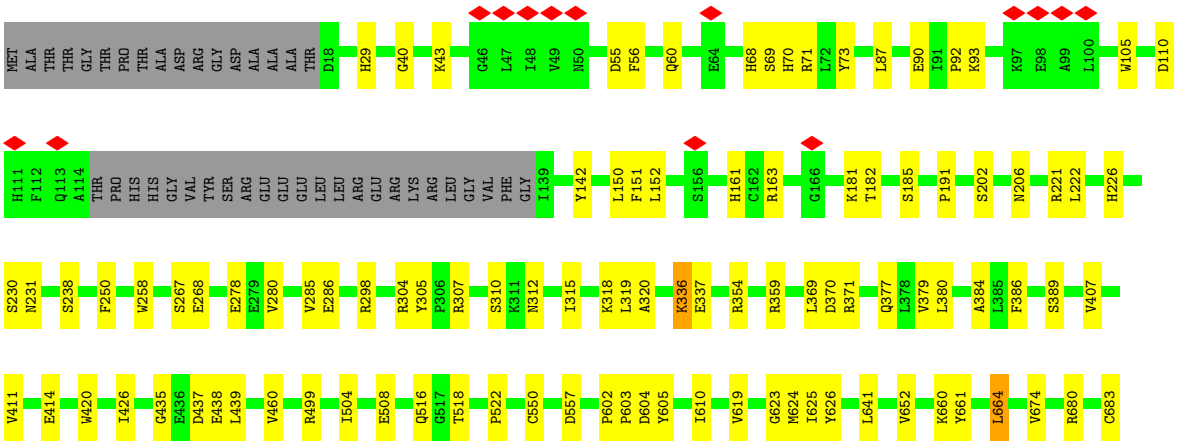
• Molecule 1: Dipeptidyl peptidase 9

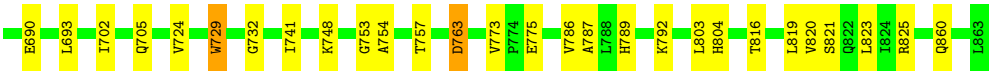
Chain A:



• Molecule 1: Dipeptidyl peptidase 9

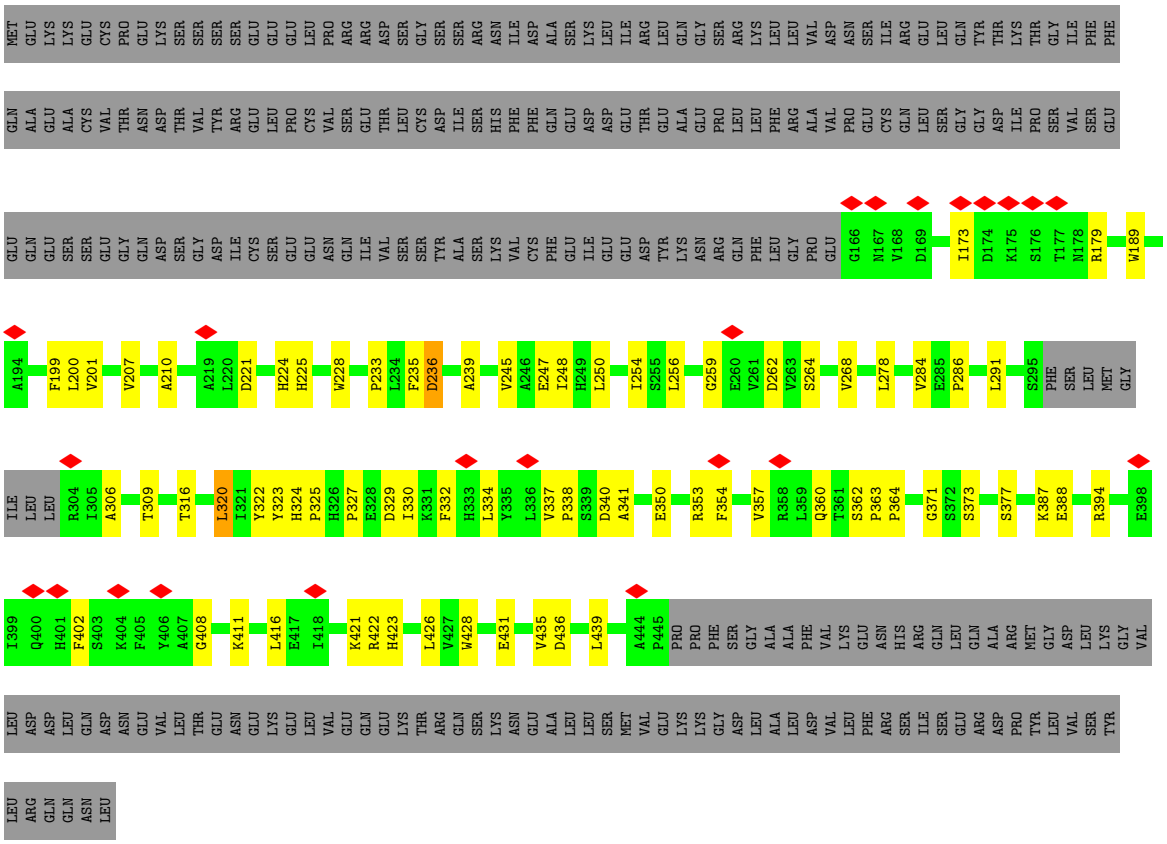
Chain D:





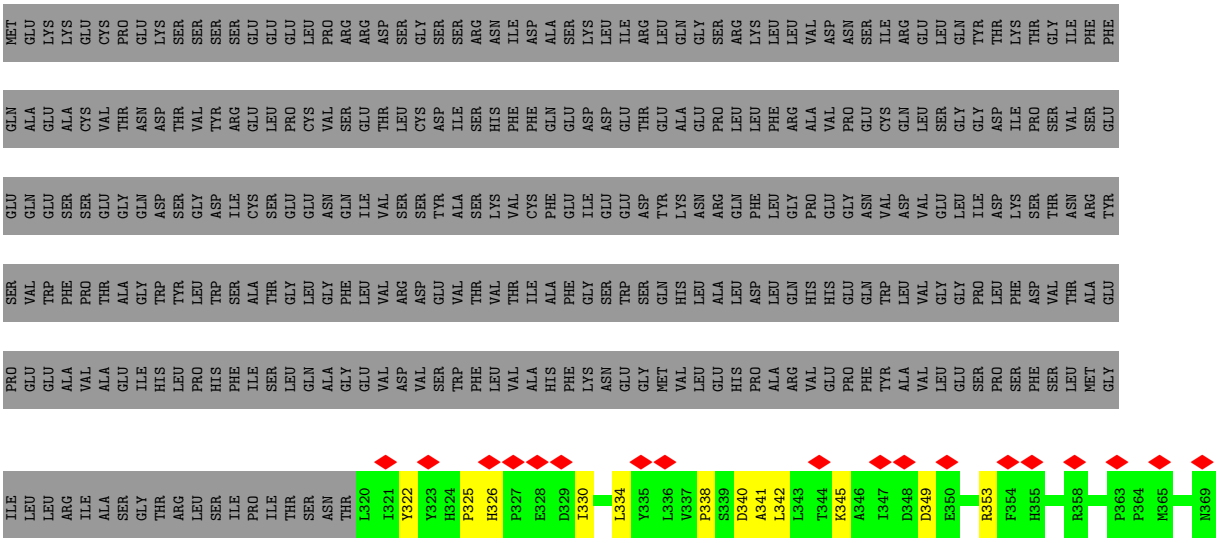
• Molecule 2: Caspase recruitment domain-containing protein 8

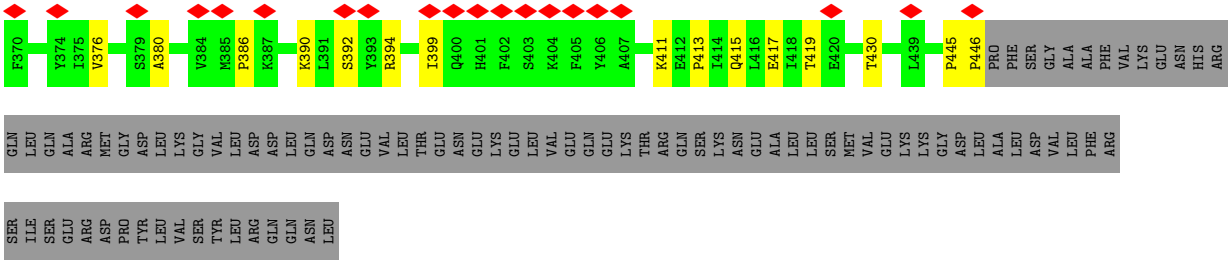
Chain B:



• Molecule 2: Caspase recruitment domain-containing protein 8

Chain C:




F370 Y374 I375 V376 S379 A380 V384 M385 P386 K387 K390 L391 S392 Y393 R394 I399 Q400 H401 F402 S403 K404 F405 Y406 A407 K411 E412 P413 I414 Q415 L416 E417 I418 T419 E420 T430 L439 P445 P446 PRO PHE SER GLY ALA ALA PHE VAL LYS GLU ASN HIS ARG
GLN LEU GLN ALA ARG MET GLY ASP LEU LYS GLY VAL LEU ASP ASP LEU GLN ASP ASN GLU VAL LEU THR GLU ASN GLU LYS GLU LEU VAL GLU GLN GLU LYS THR ARG GLN SER LYS ASN GLU ALA LEU LEU SER MET VAL GLU LYS LYS GLY ASP LEU ALA LEU ASP VAL LEU PHE ARG
SER ILE SER GLU ARG ASP PRO TYR LEU VAL SER TYR LEU ARG GLN GLN ASN LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	120998	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	58.5, 64.99	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	10500	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.067	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	330.0, 330.0, 330.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	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	0.38	0/6852	0.69	2/9307 (0.0%)
1	D	0.35	0/6811	0.69	6/9250 (0.1%)
2	B	0.31	0/2218	0.74	4/3030 (0.1%)
2	C	0.28	0/1053	0.64	1/1432 (0.1%)
All	All	0.35	0/16934	0.69	13/23019 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	D	0	1
2	B	0	1
2	C	0	1
All	All	0	5

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	221	ASP	CB-CG-OD2	7.64	125.18	118.30
1	A	803	LEU	CA-CB-CG	7.38	132.26	115.30
1	D	763	ASP	CB-CG-OD2	6.92	124.53	118.30
1	A	378	LEU	CB-CG-CD1	-6.84	99.37	111.00
2	C	334	LEU	CA-CB-CG	6.35	129.90	115.30
1	D	664	LEU	CA-CB-CG	-6.27	100.89	115.30
1	D	336	LYS	N-CA-CB	-6.02	99.77	110.60
1	D	336	LYS	CA-CB-CG	5.84	126.25	113.40
2	B	320	LEU	CA-CB-CG	5.81	128.67	115.30
1	D	369	LEU	CA-CB-CG	5.65	128.30	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	693	LEU	CA-CB-CG	5.39	127.70	115.30
2	B	236	ASP	CB-CG-OD1	5.33	123.10	118.30
2	B	334	LEU	CA-CB-CG	5.26	127.40	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	599	ALA	Peptide
1	A	729	TRP	Peptide
2	B	362	SER	Peptide
2	C	392	SER	Peptide
1	D	729	TRP	Peptide

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	6650	0	6424	68	0
1	D	6611	0	6380	76	0
2	B	2153	0	2076	43	0
2	C	1023	0	1014	14	0
All	All	16437	0	15894	197	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 6.

All (197) 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:C:326:HIS:HB3	2:C:345:LYS:O	1.78	0.84
2:B:329:ASP:HA	2:B:341:ALA:O	1.79	0.83
2:B:332:PHE:O	2:B:338:PRO:HA	1.91	0.71
2:B:426:LEU:HB2	2:B:436:ASP:HB3	1.74	0.69
1:A:139:ILE:HD13	1:A:153:PHE:CD2	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:152:LEU:HD21	1:D:191:PRO:HB2	1.79	0.65
2:B:210:ALA:HB3	2:B:236:ASP:HB3	1.79	0.64
1:A:184:CYS:SG	1:A:205:ASN:ND2	2.73	0.62
1:A:379:VAL:HG22	1:A:411:VAL:HG22	1.82	0.62
2:B:225:HIS:HB3	2:B:228:TRP:HB2	1.81	0.60
1:D:641:LEU:HD21	1:D:705:GLN:HB3	1.84	0.59
2:B:330:ILE:O	2:B:340:ASP:HA	2.03	0.59
1:A:310:SER:O	1:A:371:ARG:NH2	2.35	0.58
1:A:569:PRO:HG2	1:A:600:SER:HA	1.85	0.58
1:A:753:GLY:HA2	1:A:803:LEU:HB2	1.86	0.57
2:B:322:TYR:HA	2:B:377:SER:HA	1.86	0.57
2:B:421:LYS:HE2	2:B:439:LEU:HG	1.86	0.57
1:D:757:THR:HB	1:D:787:ALA:HB2	1.85	0.56
1:D:438:GLU:HG3	1:D:460:VAL:HG12	1.86	0.56
2:B:360:GLN:HA	2:B:364:PRO:HD3	1.88	0.56
1:A:230:SER:OG	1:A:231:ASN:N	2.40	0.55
1:A:243:THR:O	1:A:247:GLN:HB2	2.06	0.55
1:A:252:ARG:NH1	1:A:352:ILE:O	2.39	0.55
2:B:199:PHE:HE2	2:B:207:VAL:HG21	1.73	0.54
2:B:189:TRP:HA	2:B:200:LEU:HD23	1.89	0.54
1:D:310:SER:O	1:D:371:ARG:NH2	2.41	0.54
1:A:373:GLN:OE1	1:A:769:ARG:NH1	2.40	0.54
1:D:87:LEU:HD13	1:D:105:TRP:HB3	1.89	0.54
1:D:222:LEU:HD23	1:D:320:ALA:HB1	1.90	0.54
1:D:380:LEU:HD11	1:D:439:LEU:HD22	1.90	0.53
2:C:415:GLN:NE2	2:C:417:GLU:O	2.37	0.53
1:D:221:ARG:NH2	1:D:226:HIS:O	2.41	0.53
1:A:276:LEU:HD22	1:A:364:ALA:HB1	1.90	0.53
1:D:69:SER:HB3	1:D:93:LYS:HB3	1.90	0.53
1:D:312:ASN:OD1	1:D:371:ARG:NH1	2.41	0.53
1:A:537:GLU:OE2	1:A:586:HIS:NE2	2.36	0.52
2:C:330:ILE:HB	2:C:341:ALA:HB3	1.91	0.52
1:A:808:ASP:OD2	1:A:811:VAL:N	2.42	0.52
1:D:56:PHE:HA	1:D:73:TYR:O	2.10	0.52
1:D:499:ARG:NH2	1:D:683:CYS:SG	2.73	0.52
1:D:624:MET:HG3	1:D:652:VAL:HG12	1.91	0.52
1:D:757:THR:HG21	1:D:819:LEU:HB2	1.92	0.51
1:A:35:ARG:NH2	2:C:430:THR:O	2.43	0.51
2:C:380:ALA:HB3	2:C:399:ILE:HB	1.93	0.51
1:D:518:THR:HB	1:D:522:PRO:HA	1.93	0.51
1:A:475:GLY:H	1:A:478:GLU:HG2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:259:GLY:O	2:B:322:TYR:OH	2.24	0.51
2:B:224:HIS:NE2	2:C:322:TYR:O	2.44	0.51
1:D:202:SER:HB3	1:D:258:TRP:HE1	1.75	0.51
1:D:379:VAL:HG22	1:D:411:VAL:HG22	1.92	0.51
1:D:821:SER:OG	1:D:825:ARG:NH2	2.44	0.50
1:A:158:SER:OG	1:A:179:GLU:OE1	2.28	0.50
1:D:40:GLY:HA2	1:D:43:LYS:HE3	1.93	0.50
1:D:337:GLU:HG3	1:D:389:SER:HB3	1.93	0.50
1:A:757:THR:HG21	1:A:819:LEU:HB2	1.93	0.50
1:D:623:GLY:HA2	1:D:652:VAL:HG11	1.94	0.50
2:B:388:GLU:OE2	2:B:422:ARG:NH1	2.44	0.50
2:B:394:ARG:HG3	2:B:411:LYS:HD3	1.93	0.50
1:D:604:ASP:OD1	1:D:604:ASP:N	2.45	0.50
1:A:220:ARG:HD2	1:A:330:ILE:HD13	1.93	0.50
1:A:449:THR:HG23	1:A:451:PHE:H	1.76	0.49
2:B:327:PRO:HD2	2:B:371:GLY:H	1.77	0.49
1:A:499:ARG:HH12	1:A:648:GLN:HG2	1.76	0.49
1:D:286:GLU:OE1	1:D:307:ARG:NE	2.43	0.49
2:B:200:LEU:HD12	2:B:247:GLU:HB2	1.95	0.49
1:A:48:ILE:HD12	1:A:602:PRO:HD3	1.95	0.49
1:A:757:THR:HB	1:A:787:ALA:HB2	1.93	0.49
2:B:207:VAL:HG23	2:B:239:ALA:HB2	1.95	0.49
2:B:316:THR:HG22	2:B:320:LEU:HD21	1.94	0.49
1:D:71:ARG:NE	1:D:90:GLU:OE2	2.46	0.49
1:D:661:TYR:HB3	1:D:664:LEU:HD12	1.94	0.49
1:A:56:PHE:HB3	1:A:72:LEU:HD11	1.95	0.49
1:A:202:SER:HB3	1:A:211:VAL:HG12	1.95	0.49
1:D:377:GLN:NE2	1:D:414:GLU:OE2	2.36	0.48
2:B:330:ILE:HB	2:B:341:ALA:HB3	1.96	0.48
1:D:250:PHE:O	1:D:354:ARG:NH1	2.43	0.48
1:D:238:SER:HB3	1:D:280:VAL:HG23	1.95	0.48
1:A:315:ILE:HD12	1:A:352:ILE:HG13	1.94	0.48
2:B:387:LYS:HB2	2:B:423:HIS:HB3	1.96	0.48
1:A:820:VAL:HA	1:A:823:LEU:HD12	1.95	0.48
1:A:100:LEU:HB3	2:B:278:LEU:HB2	1.95	0.47
1:D:29:HIS:N	1:D:860:GLN:OE1	2.40	0.47
1:D:336:LYS:HG3	1:D:386:PHE:HB3	1.96	0.47
1:A:208:ASP:OD2	1:A:221:ARG:NH2	2.47	0.47
1:A:792:LYS:HE2	1:A:792:LYS:HB3	1.72	0.47
1:D:60:GLN:OE1	1:D:70:HIS:NE2	2.47	0.47
1:A:60:GLN:OE1	1:A:555:ASN:ND2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:402:PHE:HZ	2:B:408:GLY:HA2	1.79	0.47
1:D:619:VAL:HG21	1:D:680:ARG:HD2	1.96	0.47
1:D:285:VAL:HG13	1:D:304:ARG:HD2	1.96	0.47
1:D:804:HIS:CE1	1:D:816:THR:HG1	2.31	0.47
1:D:185:SER:O	1:D:206:ASN:ND2	2.47	0.46
2:B:262:ASP:OD2	2:B:264:SER:OG	2.26	0.46
2:C:386:PRO:HG3	2:C:390:LYS:HG2	1.98	0.46
1:D:319:LEU:O	1:D:336:LYS:HB3	2.14	0.46
1:A:202:SER:HG	1:A:258:TRP:HE1	1.63	0.46
1:A:370:ASP:HB2	1:A:375:TRP:HE3	1.79	0.46
1:D:267:SER:OG	1:D:268:GLU:N	2.49	0.46
1:A:454:LEU:HD12	1:A:496:VAL:HG21	1.98	0.46
2:B:329:ASP:N	2:B:329:ASP:OD1	2.48	0.46
1:D:384:ALA:HB3	1:D:407:VAL:HG21	1.98	0.46
1:D:319:LEU:HB2	1:D:336:LYS:HB3	1.98	0.45
2:C:325:PRO:HG3	2:C:376:VAL:HG22	1.98	0.45
1:D:55:ASP:HB3	1:D:142:TYR:HE1	1.82	0.45
1:D:230:SER:OG	1:D:231:ASN:N	2.49	0.45
2:C:338:PRO:HB2	2:C:415:GLN:HE21	1.81	0.45
1:D:820:VAL:HA	1:D:823:LEU:HD12	1.98	0.45
1:D:625:ILE:HA	1:D:674:VAL:O	2.17	0.45
1:A:804:HIS:CG	1:A:816:THR:HG1	2.32	0.45
1:D:110:ASP:OD1	1:D:110:ASP:N	2.47	0.45
1:D:151:PHE:O	1:D:161:HIS:HA	2.16	0.45
2:B:248:ILE:HB	2:B:291:LEU:HB3	1.98	0.44
1:D:602:PRO:HB2	1:D:605:TYR:HB2	2.00	0.44
1:A:353:ALA:HB1	1:A:423:VAL:HG11	1.99	0.44
1:A:457:VAL:HG22	1:A:486:GLU:HG3	2.00	0.44
2:B:256:LEU:HD21	2:B:284:VAL:HG12	2.00	0.44
1:A:367:MET:HE3	1:A:376:LEU:HD11	1.99	0.44
1:D:359:ARG:NH1	1:D:508:GLU:OE2	2.51	0.44
1:D:516:GLN:HE22	1:D:550:CYS:H	1.66	0.44
1:D:754:ALA:HA	1:D:804:HIS:ND1	2.33	0.44
1:A:706:VAL:HG21	1:A:743:LYS:HG3	1.99	0.44
1:A:729:TRP:O	1:A:732:GLY:N	2.41	0.44
2:B:256:LEU:HD13	2:B:286:PRO:HA	1.99	0.44
1:A:370:ASP:OD1	1:A:371:ARG:N	2.50	0.43
1:A:749:VAL:HG22	1:A:863:LEU:HD13	2.00	0.43
1:D:435:GLY:O	1:D:437:ASP:N	2.47	0.43
1:A:381:LEU:HD23	1:A:409:PRO:HB3	2.00	0.43
1:A:110:ASP:OD1	1:A:110:ASP:N	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:370:ASP:OD1	1:D:371:ARG:N	2.50	0.43
2:B:201:VAL:HG12	2:B:245:VAL:HG13	1.99	0.43
1:A:519:LYS:HB3	1:A:528:TYR:CZ	2.53	0.43
1:D:305:TYR:CZ	1:D:763:ASP:HB3	2.54	0.43
1:D:557:ASP:OD1	1:D:557:ASP:N	2.51	0.43
1:A:48:ILE:HD11	1:A:656:PHE:HE2	1.84	0.43
1:A:626:TYR:HB2	1:A:674:VAL:HB	2.00	0.43
2:B:173:ILE:HB	2:B:179:ARG:HG3	2.01	0.43
1:D:516:GLN:NE2	1:D:550:CYS:H	2.16	0.43
2:B:268:VAL:HG11	2:B:291:LEU:HD12	2.00	0.43
1:A:151:PHE:O	1:A:161:HIS:HA	2.19	0.43
1:A:566:VAL:HG21	1:A:610:ILE:HD11	2.00	0.42
2:B:337:VAL:HG22	2:B:416:LEU:HA	2.01	0.42
1:A:641:LEU:HD21	1:A:705:GLN:HB3	2.00	0.42
1:A:843:ARG:HD3	1:A:843:ARG:HA	1.85	0.42
2:B:254:ILE:HA	2:B:323:TYR:HB2	2.02	0.42
1:D:626:TYR:HB2	1:D:674:VAL:HB	2.00	0.42
1:A:202:SER:OG	1:A:258:TRP:NE1	2.50	0.42
2:B:363:PRO:HA	2:B:364:PRO:HD3	1.82	0.42
1:D:181:LYS:NZ	1:D:182:THR:O	2.46	0.42
2:B:373:SER:OG	2:B:435:VAL:O	2.38	0.42
2:C:340:ASP:HB2	2:C:413:PRO:HG2	2.00	0.42
1:D:773:VAL:HG12	1:D:775:GLU:H	1.84	0.42
2:B:350:GLU:HA	2:B:353:ARG:HG2	2.01	0.42
1:D:150:LEU:HD12	1:D:163:ARG:HB3	2.01	0.42
1:D:729:TRP:O	1:D:732:GLY:N	2.41	0.42
2:C:417:GLU:HG3	2:C:419:THR:HG23	2.02	0.42
1:D:426:ILE:HD12	1:D:504:ILE:HG23	2.01	0.42
1:D:702:ILE:HD12	1:D:702:ILE:HA	1.90	0.42
1:A:267:SER:OG	1:A:268:GLU:N	2.50	0.42
2:B:428:TRP:HE3	2:B:431:GLU:HB3	1.85	0.42
1:D:278:GLU:HB2	1:D:315:ILE:HD11	2.02	0.42
1:D:724:VAL:O	1:D:748:LYS:N	2.53	0.42
1:D:753:GLY:HA2	1:D:803:LEU:HB2	2.02	0.42
2:B:324:HIS:HA	2:B:325:PRO:HD3	1.95	0.41
2:C:349:ASP:O	2:C:353:ARG:NH2	2.46	0.41
1:D:420:TRP:HZ2	1:D:690:GLU:HG2	1.85	0.41
1:A:413:TYR:OH	1:A:445:ASN:ND2	2.47	0.41
1:A:499:ARG:NH1	1:A:648:GLN:HG2	2.35	0.41
2:C:445:PRO:HA	2:C:446:PRO:HD2	1.97	0.41
1:A:104:SER:OG	1:A:106:LYS:NZ	2.44	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:SER:HB2	1:A:280:VAL:HG13	2.03	0.41
1:A:446:GLU:HG2	1:A:687:LEU:HB2	2.02	0.41
1:A:709:LEU:HD21	1:A:724:VAL:HG11	2.03	0.41
1:A:45:SER:HA	1:A:48:ILE:HG22	2.01	0.41
2:C:342:LEU:HB3	2:C:411:LYS:HB3	2.02	0.41
1:D:602:PRO:HA	1:D:603:PRO:HD3	1.97	0.41
1:A:751:ILE:HG21	1:A:855:LEU:HD13	2.02	0.41
2:B:354:PHE:HA	2:B:357:VAL:HG22	2.03	0.41
1:D:318:LYS:HE3	1:D:337:GLU:HG2	2.02	0.41
1:D:610:ILE:HD13	1:D:624:MET:HG2	2.02	0.41
1:A:139:ILE:CD1	1:A:153:PHE:CE2	3.04	0.41
1:A:355:ALA:HA	1:A:366:ALA:HA	2.02	0.41
1:D:757:THR:HA	1:D:786:VAL:HG12	2.02	0.41
1:A:697:MET:HB2	1:A:697:MET:HE2	1.95	0.41
1:A:846:GLU:HG3	1:D:825:ARG:HA	2.02	0.41
2:B:250:LEU:HD21	2:B:309:THR:H	1.86	0.41
2:B:233:PRO:HG2	2:B:235:PHE:CZ	2.55	0.41
1:D:68:HIS:CG	1:D:90:GLU:HB3	2.56	0.41
1:A:109:LEU:HB3	1:A:112:PHE:HE1	1.86	0.40
2:B:330:ILE:HG21	2:B:364:PRO:HA	2.03	0.40
1:D:789:HIS:HB3	1:D:792:LYS:HE2	2.02	0.40
1:D:286:GLU:OE2	1:D:307:ARG:NH2	2.54	0.40
1:D:741:ILE:HG23	1:D:792:LYS:HB2	2.03	0.40
1:A:820:VAL:O	1:A:824:ILE:HG12	2.21	0.40
1:A:109:LEU:HB3	1:A:112:PHE:CE1	2.56	0.40
1:A:139:ILE:HD13	1:A:153:PHE:CE2	2.57	0.40
2:B:236:ASP:HA	2:B:306:ALA:HA	2.03	0.40
1:D:68:HIS:HA	1:D:92:PRO:HA	2.03	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	823/863 (95%)	780 (95%)	42 (5%)	1 (0%)	51	81
1	D	818/863 (95%)	775 (95%)	43 (5%)	0	100	100
2	B	268/537 (50%)	241 (90%)	27 (10%)	0	100	100
2	C	125/537 (23%)	111 (89%)	14 (11%)	0	100	100
All	All	2034/2800 (73%)	1907 (94%)	126 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	428	TYR

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	721/753 (96%)	721 (100%)	0	100	100
1	D	716/753 (95%)	714 (100%)	2 (0%)	92	96
2	B	234/479 (49%)	234 (100%)	0	100	100
2	C	115/479 (24%)	114 (99%)	1 (1%)	78	87
All	All	1786/2464 (72%)	1783 (100%)	3 (0%)	93	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	394	ARG
1	D	298	ARG
1	D	660	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	857	HIS

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Mol	Chain	Res	Type
1	D	84	ASN
1	D	525	HIS

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 (i)

There are no chain breaks in this entry.

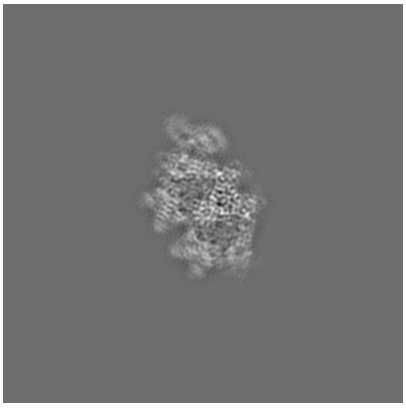
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-22367. These allow visual inspection of the internal detail of the map and identification of artifacts.

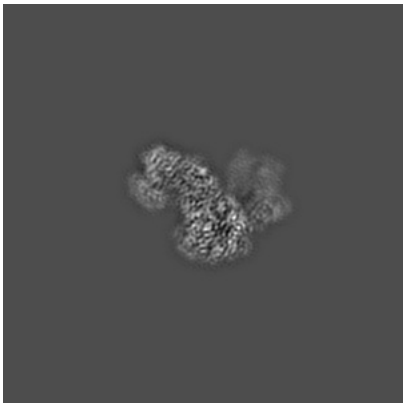
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

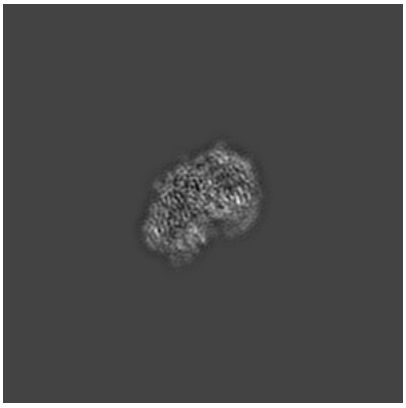
6.1.1 Primary map



X



Y

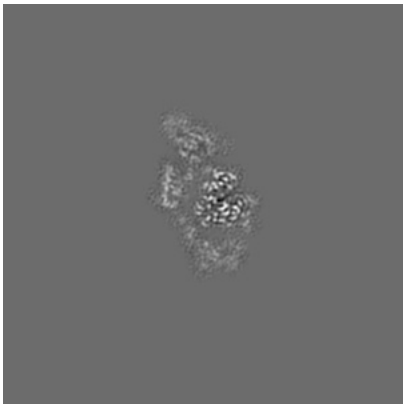


Z

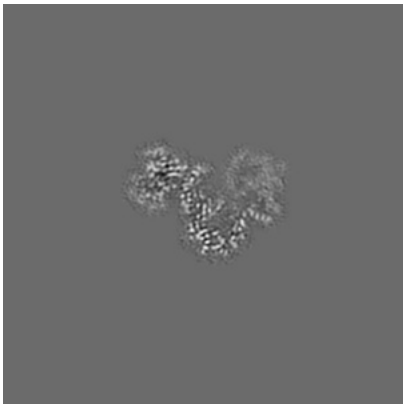
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

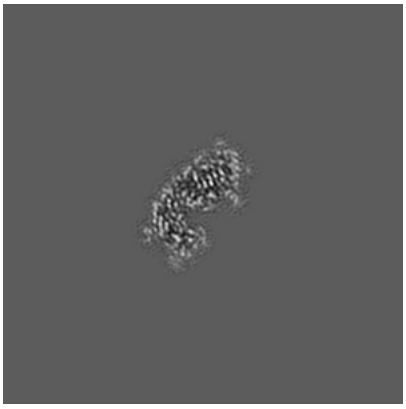
6.2.1 Primary map



X Index: 200



Y Index: 200

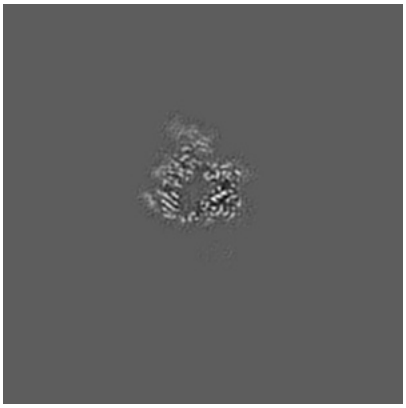


Z Index: 200

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

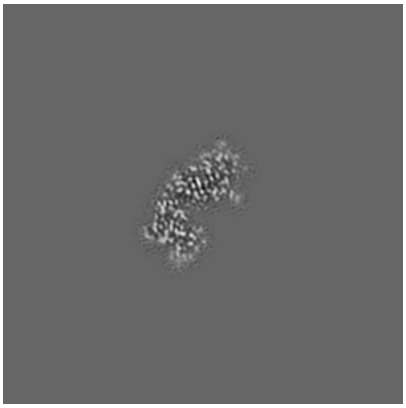
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 186

Y Index: 212

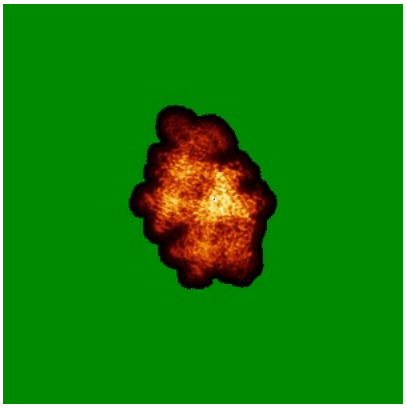


Z Index: 203

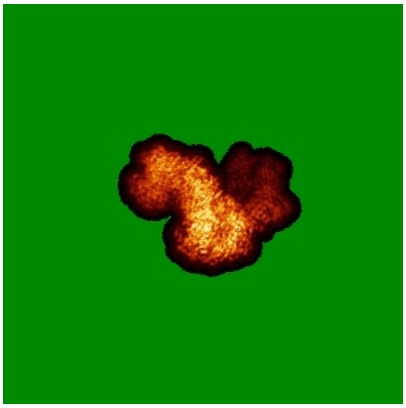
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

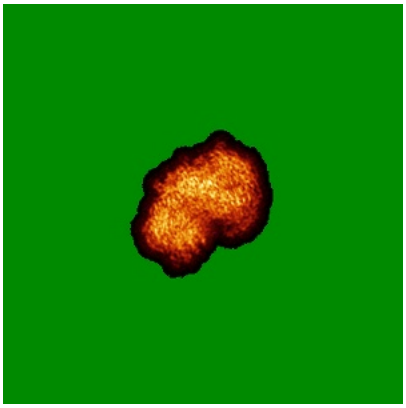
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (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 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

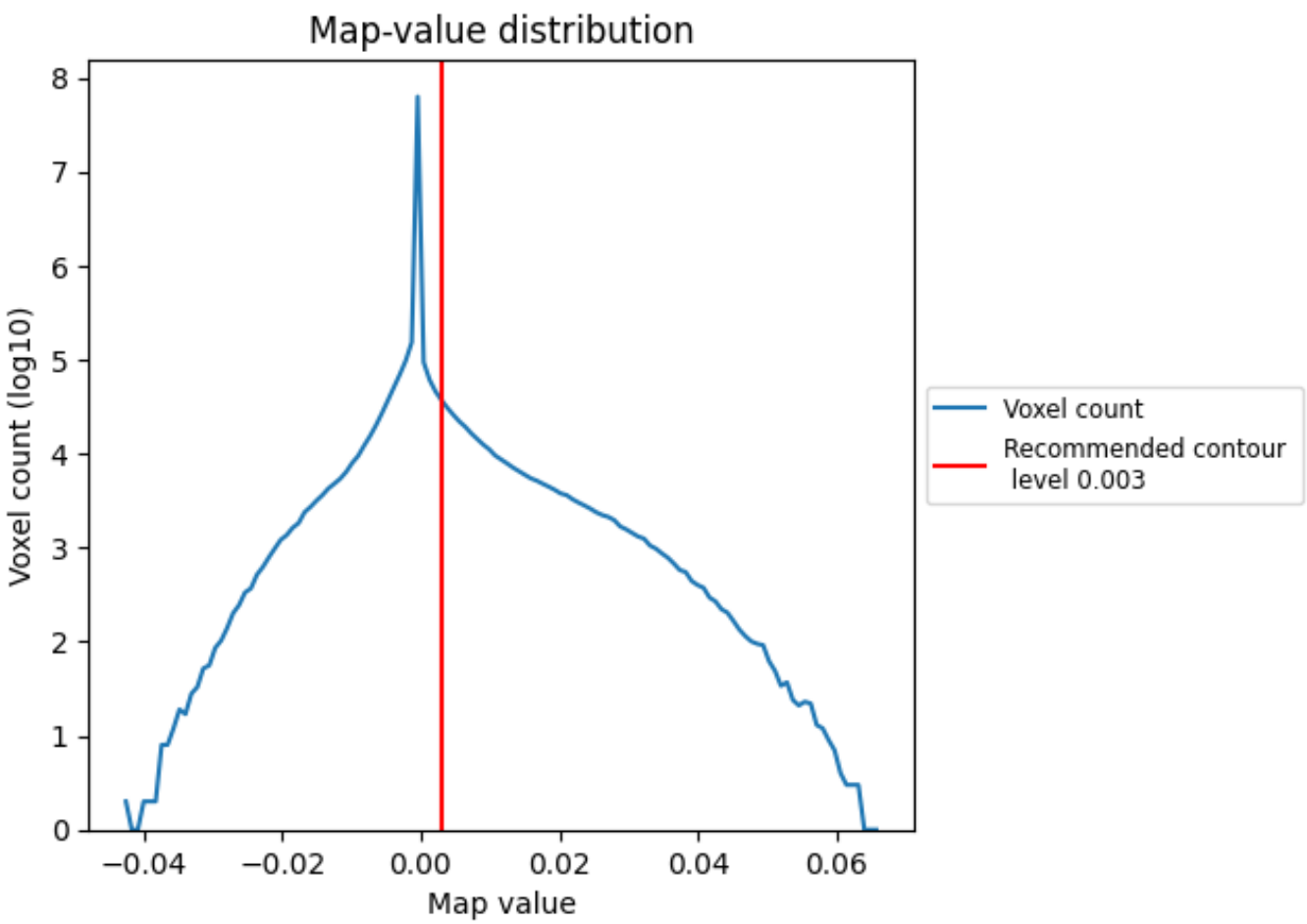
6.6 Mask visualisation (i)

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

7 Map analysis (i)

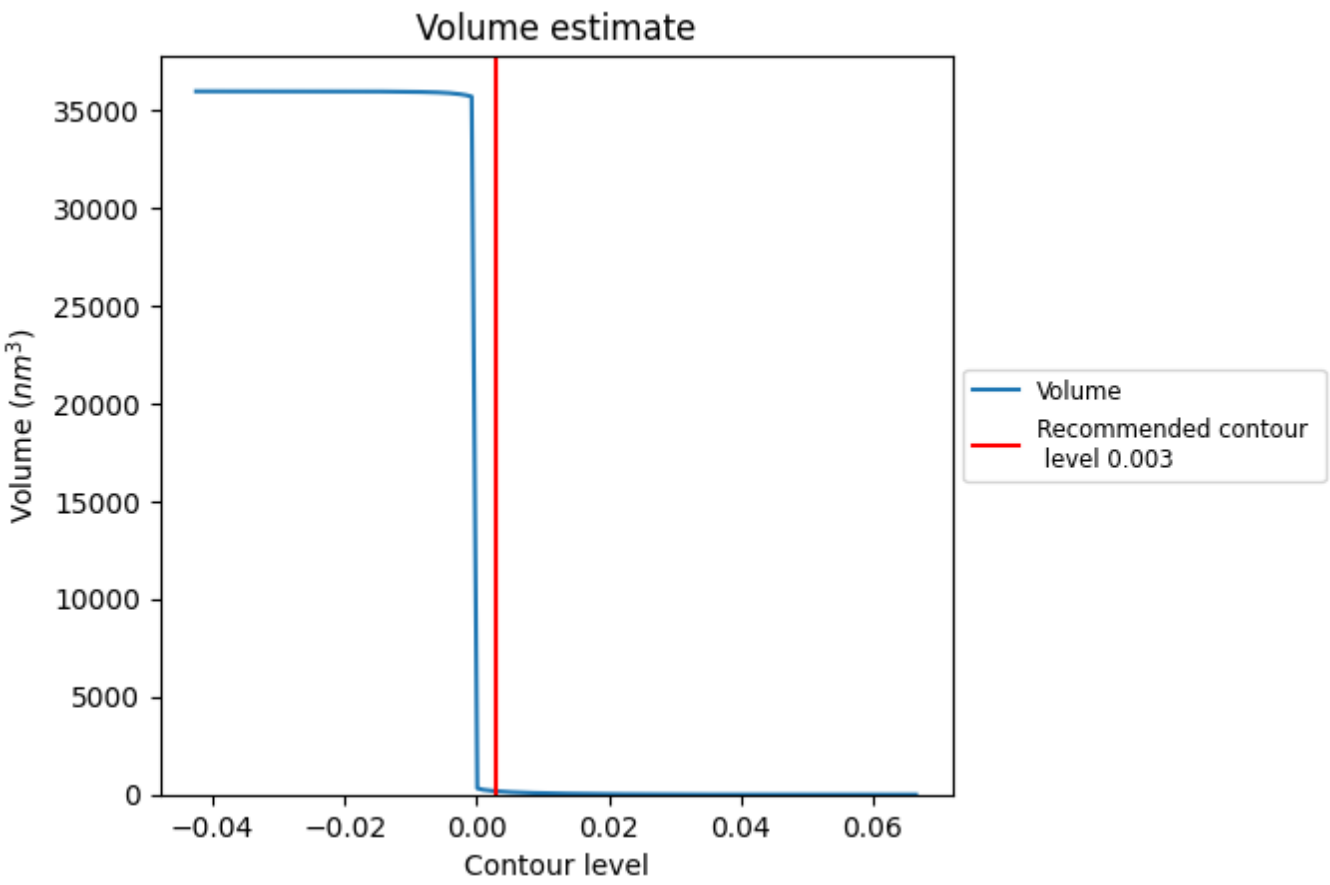
This section contains the results of statistical analysis of the map.

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.

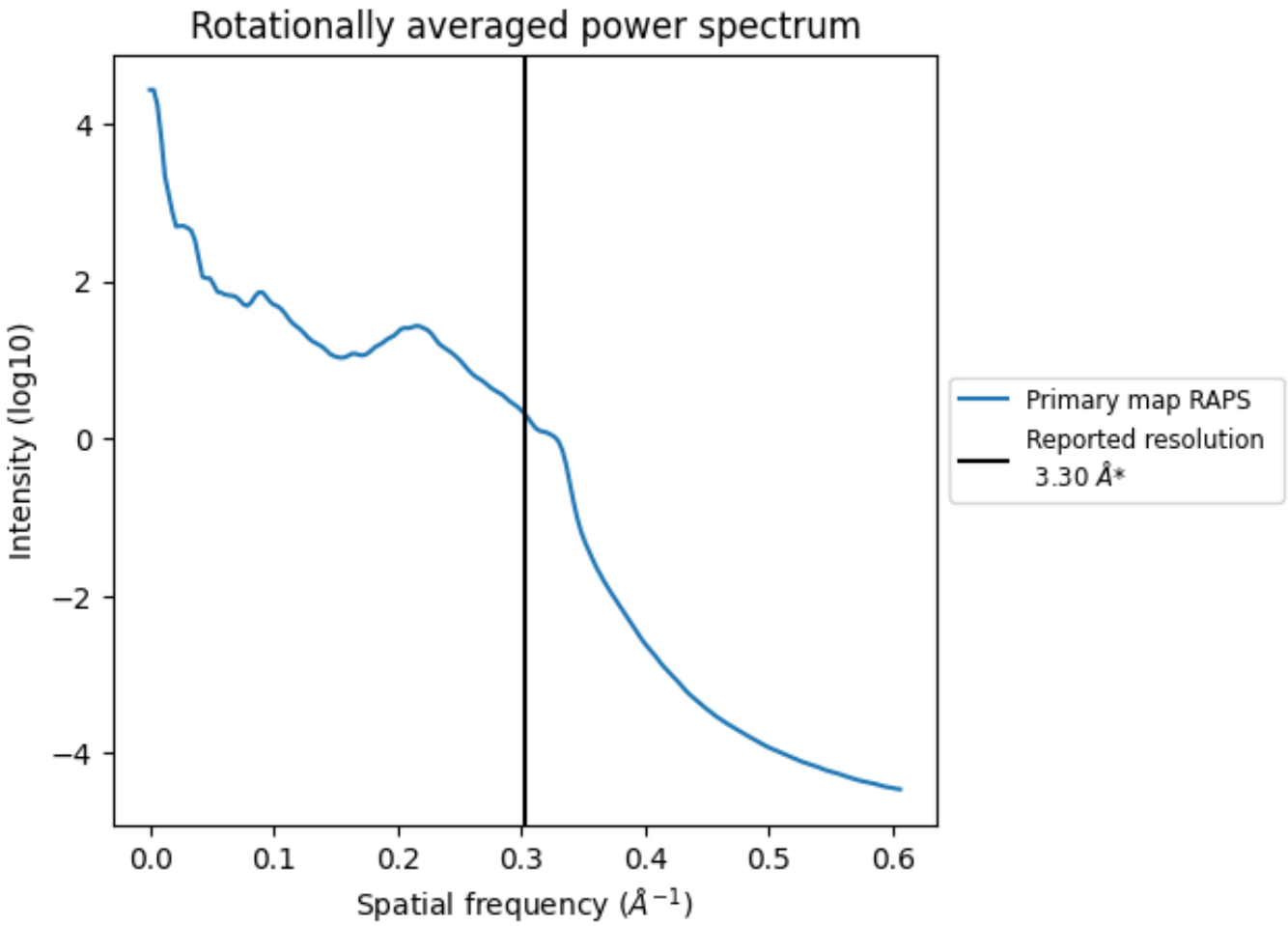
7.2 Volume estimate (i)



The volume at the recommended contour level is 171 nm^3; this corresponds to an approximate mass of 155 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)

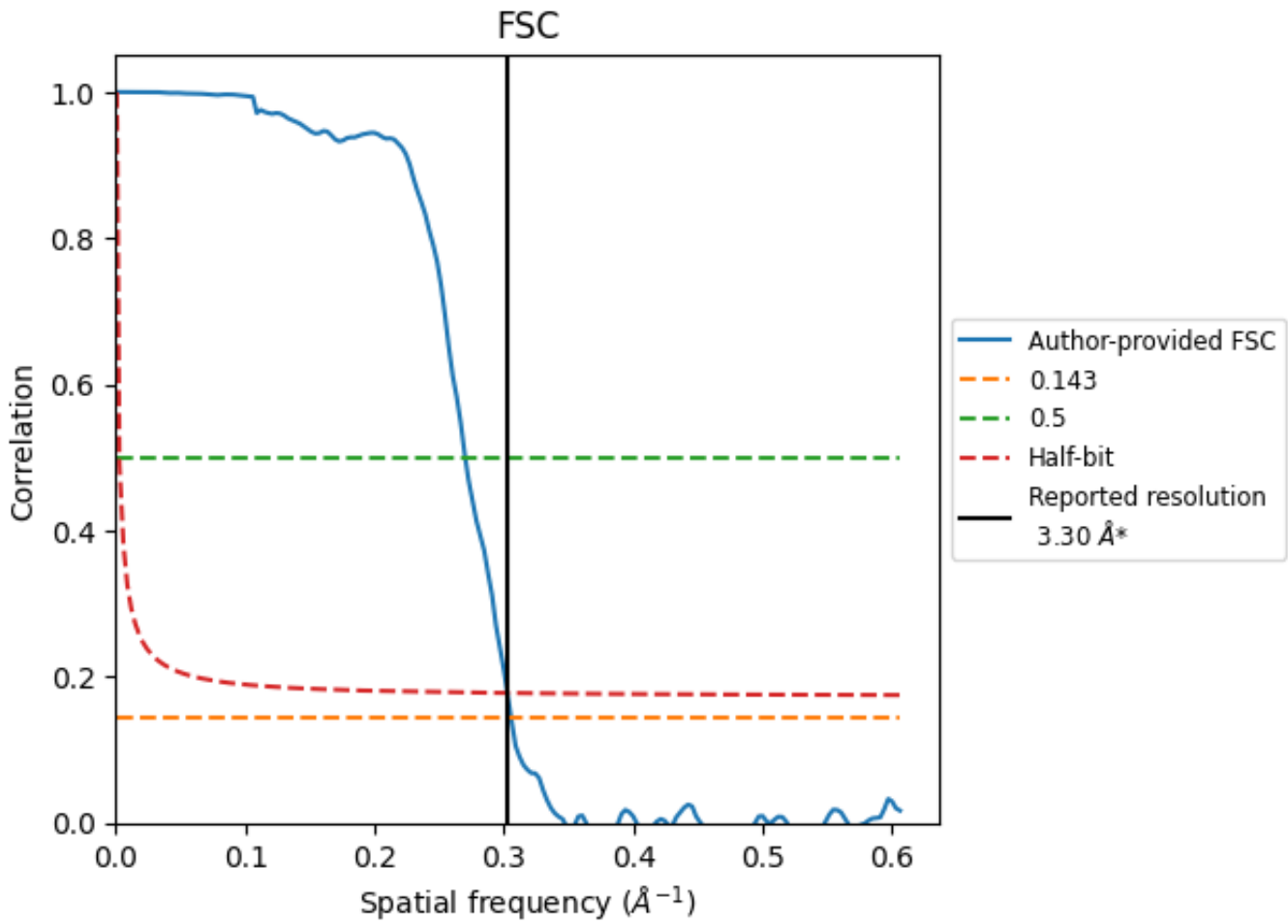


*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.303 Å^{-1}

8.2 Resolution estimates (i)

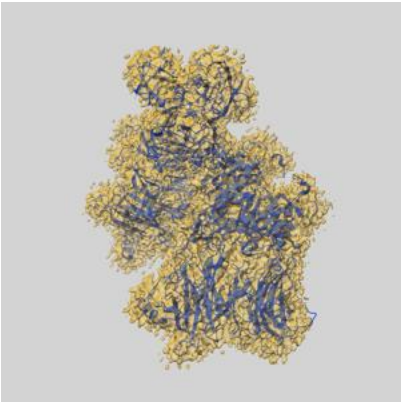
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.27	3.70	3.30
Unmasked-calculated*	-	-	-

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

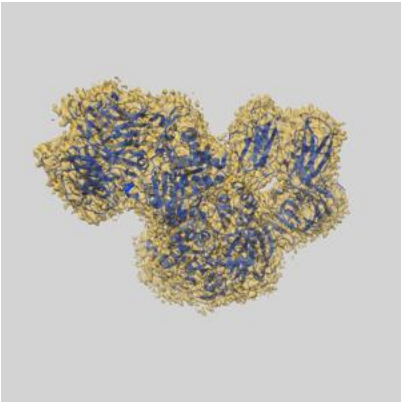
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-22367 and PDB model 7JKQ. Per-residue inclusion information can be found in section 3 on page 4.

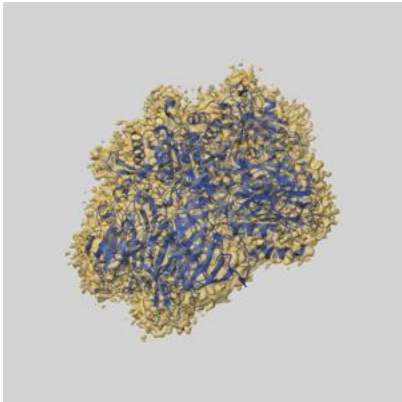
9.1 Map-model overlay (i)



X



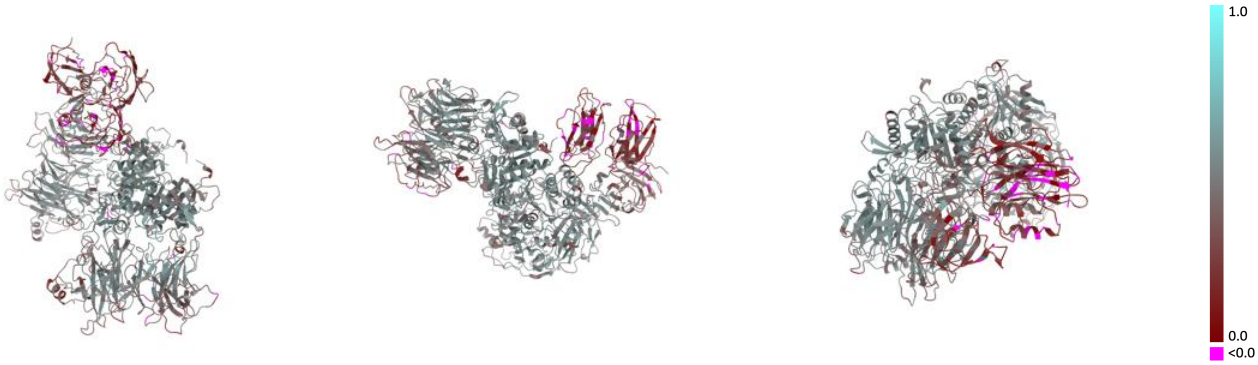
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.003 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.

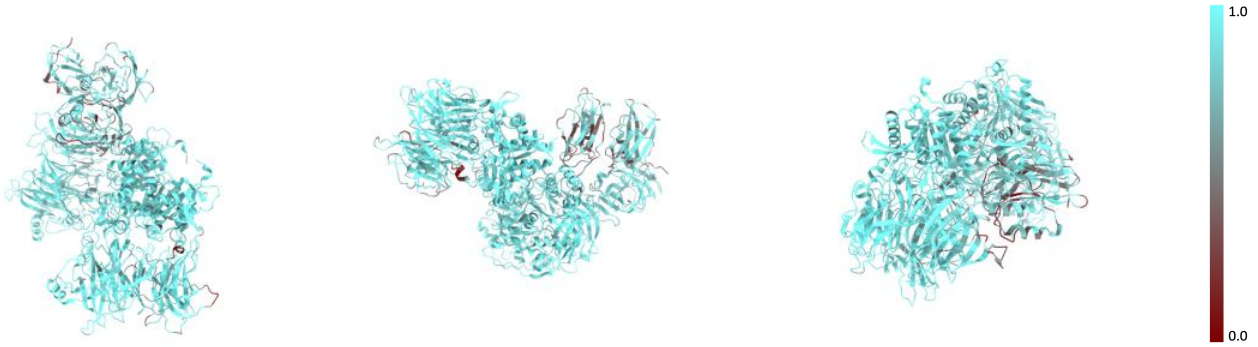
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

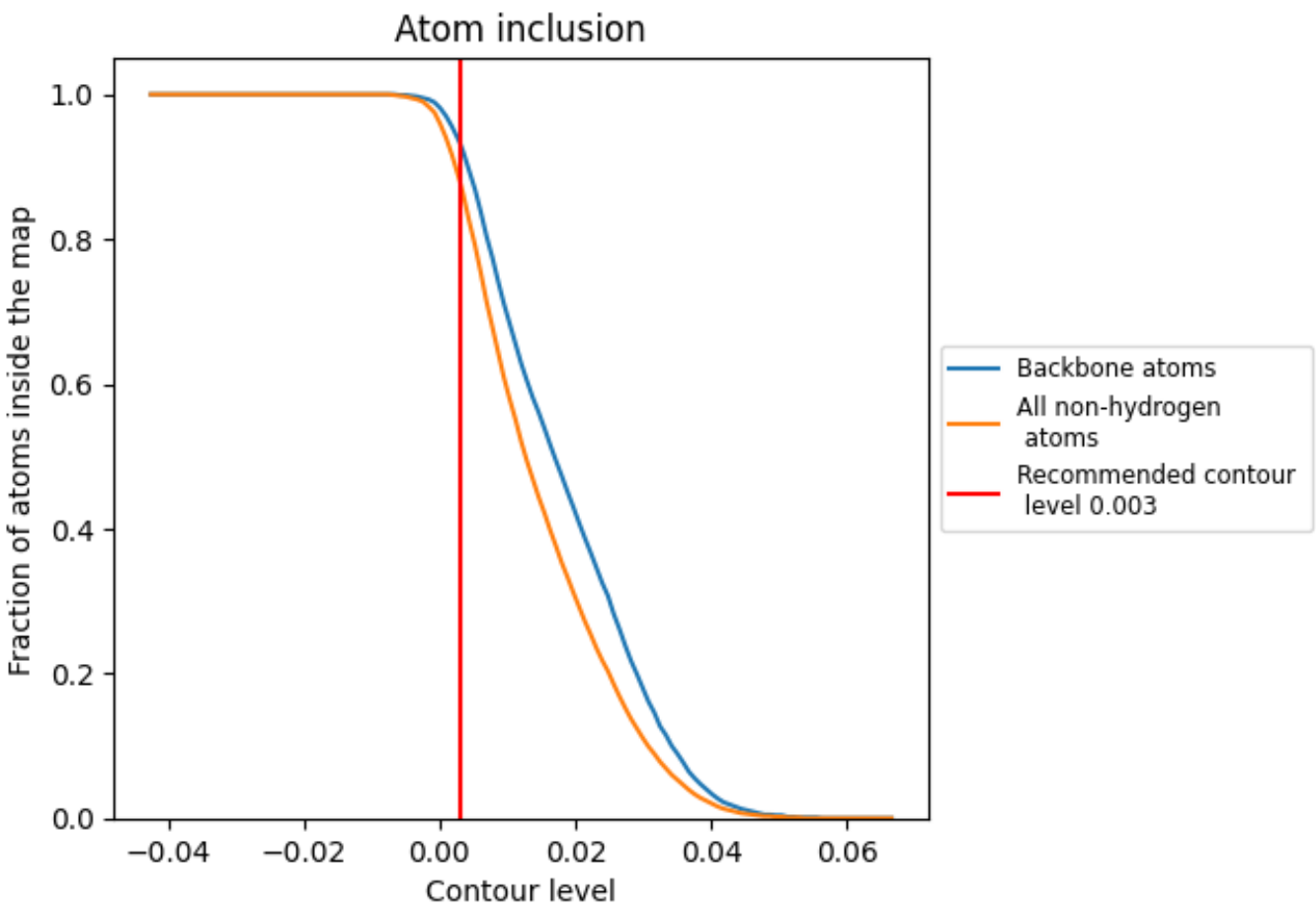
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.003).

9.4 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8800	0.4340
A	0.9330	0.4980
B	0.7760	0.2720
C	0.5650	0.1460
D	0.9100	0.4680