



Full wwPDB EM Validation Report ⓘ

Mar 4, 2026 – 07:53 PM UTC

PDB ID : 9BDQ / pdb_00009bdq
EMDB ID : EMD-44465
Title : The structure of NiV L-P complex
Authors : Hu, S.; Yang, P.; Yu, Z.; Abraham, J.
Deposited on : 2024-04-12
Resolution : 2.26 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

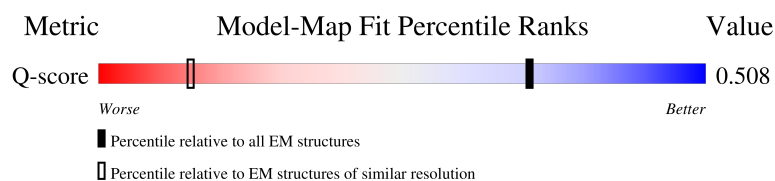
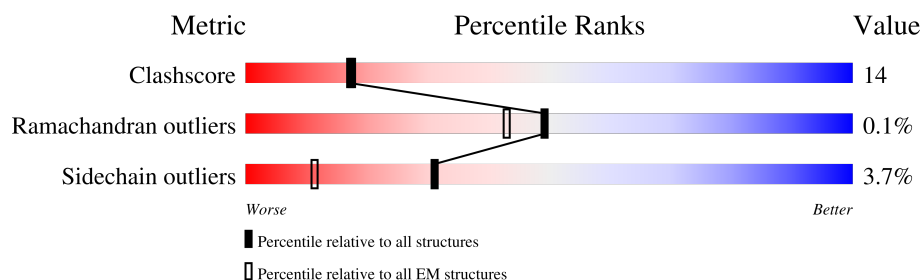
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.26 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3535 (1.76 - 2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2244	
2	B	709	
2	C	709	
2	D	709	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	709	8%7%85%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14667 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1301	Total	C	N	O	S	0	0
			10474	6671	1787	1949	67		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	S	0	0
			932	585	159	181	7		
2	D	103	Total	C	N	O	S	0	0
			826	523	135	161	7		
2	C	200	Total	C	N	O	S	0	0
			1597	999	270	320	8		
2	E	106	Total	C	N	O	S	0	0
			836	526	140	163	7		

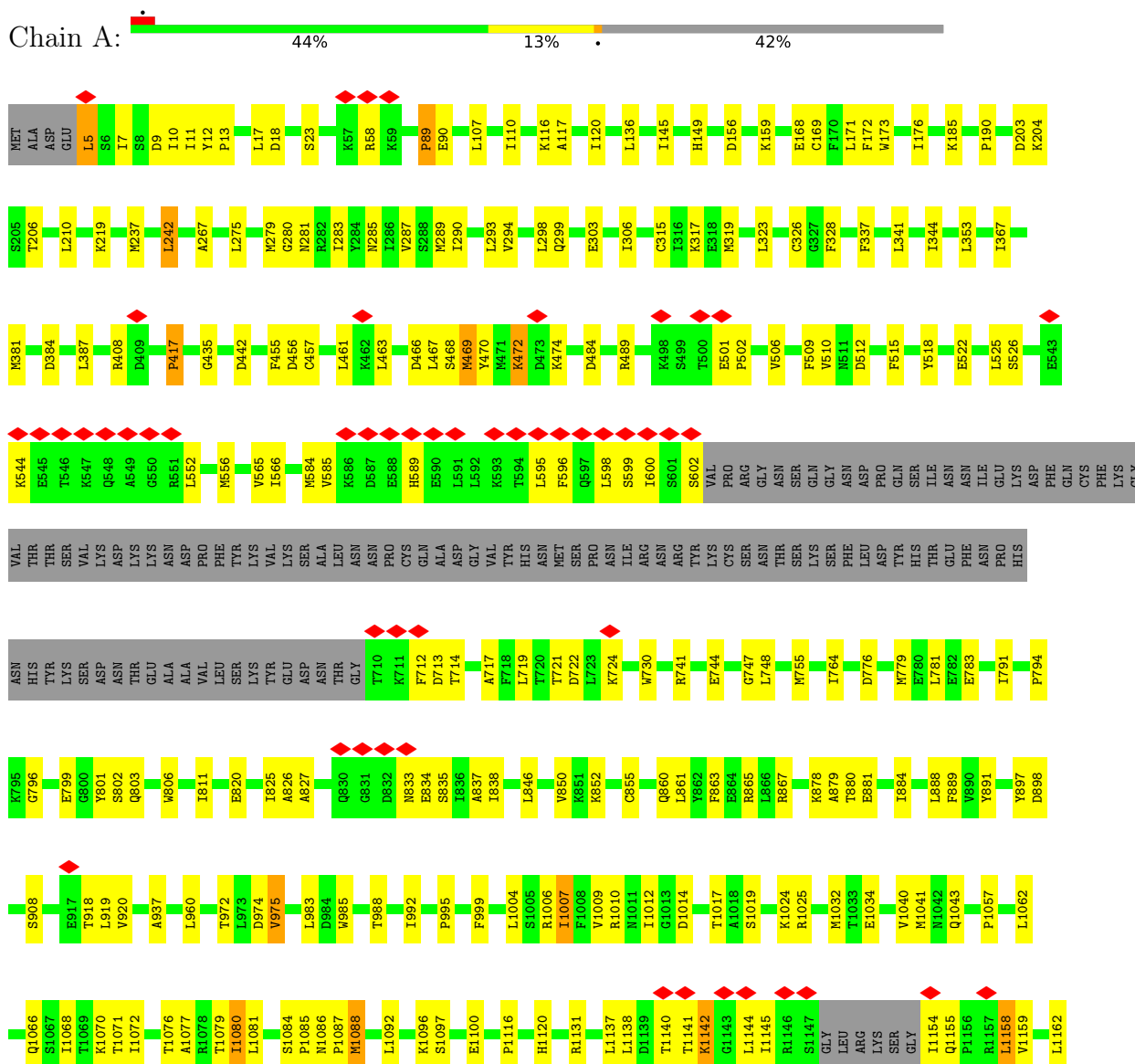
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

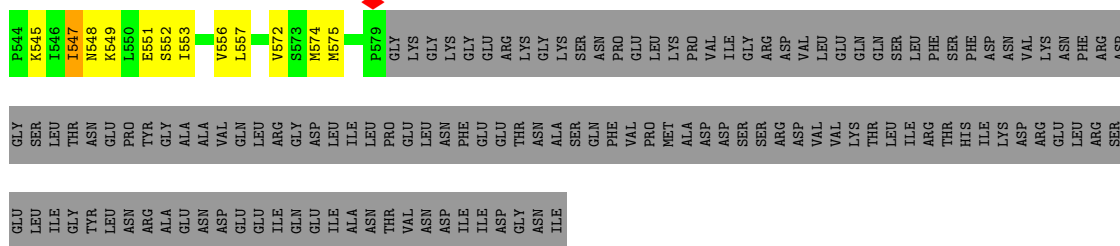
3 Residue-property plots

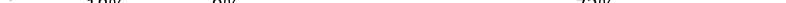
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

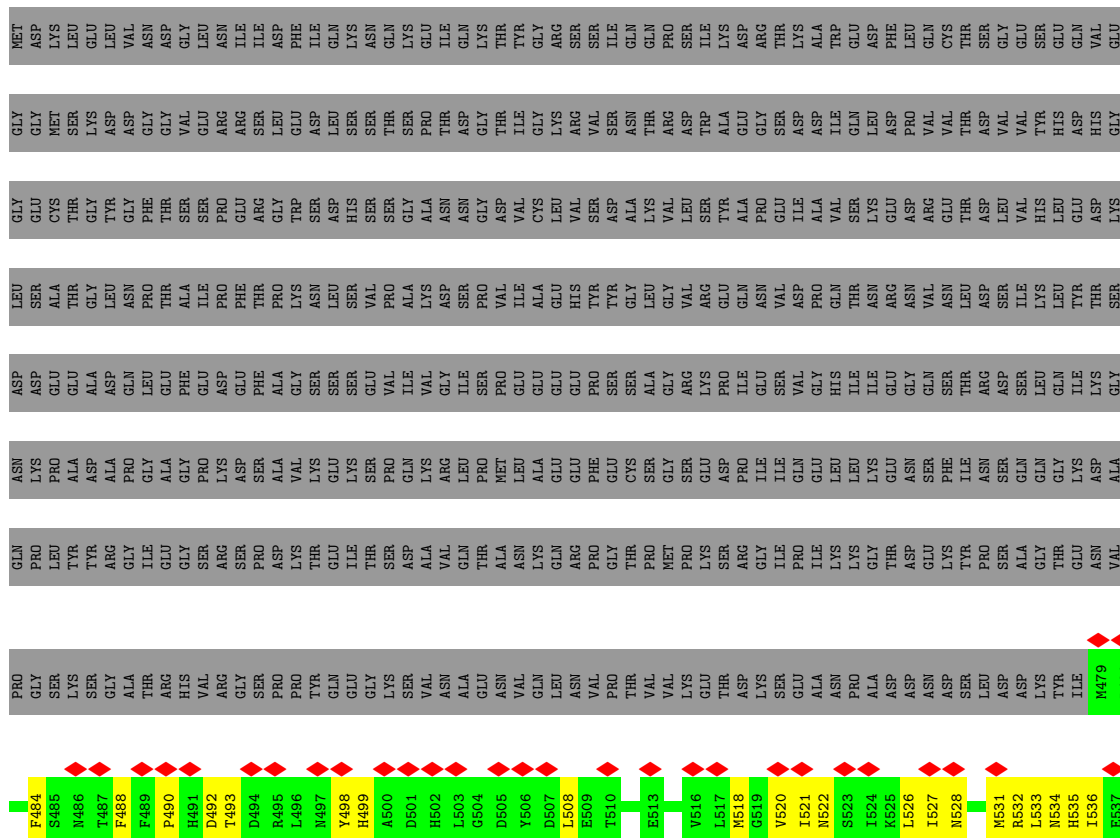
• Molecule 1: RNA-directed RNA polymerase L







Chain C:  6% 18% 9% 72%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	477936	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.583	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	398.4, 398.4, 398.4	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.36	3/10689 (0.0%)	0.52	5/14453 (0.0%)
2	B	0.46	1/947 (0.1%)	0.70	4/1275 (0.3%)
2	C	0.37	1/1618 (0.1%)	0.40	0/2186
2	D	0.25	0/840	0.58	4/1137 (0.4%)
2	E	0.24	0/849	0.51	1/1145 (0.1%)
All	All	0.36	5/14943 (0.0%)	0.53	14/20196 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	544	PRO	N-CD	12.99	1.66	1.47
1	A	89	PRO	N-CD	-9.65	1.34	1.47
1	A	417	PRO	N-CD	9.45	1.60	1.47
2	B	541	LYS	C-O	6.52	1.32	1.24
1	A	599	SER	C-N	-5.93	1.26	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	542	GLU	N-CA-C	-8.06	102.44	111.71
1	A	89	PRO	CA-N-CD	6.79	121.01	111.50
2	B	545	LYS	CA-C-N	6.40	130.78	120.55
2	B	545	LYS	C-N-CA	6.40	130.78	120.55
1	A	469	MET	CA-C-N	-6.38	110.76	122.31
1	A	469	MET	C-N-CA	-6.38	110.76	122.31
2	D	540	VAL	N-CA-C	-5.65	108.35	113.71
2	E	492	ASP	N-CA-C	-5.57	106.53	113.38
2	D	480	PRO	N-CA-CB	-5.50	97.48	103.25
2	B	544	PRO	CA-N-CD	-5.44	104.38	112.00
1	A	466	ASP	N-CA-C	5.16	117.39	107.44

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	542	GLU	CA-C-N	5.11	123.46	120.24
2	D	542	GLU	C-N-CA	5.11	123.46	120.24
1	A	468	SER	N-CA-C	-5.07	105.67	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10474	0	10498	231	0
2	B	932	0	941	63	0
2	C	1597	0	1581	74	0
2	D	826	0	823	46	0
2	E	836	0	838	51	0
3	A	2	0	0	0	0
All	All	14667	0	14681	401	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 14.

All (401) 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:1379:PHE:HD2	1:A:1386:VAL:CG1	1.43	1.30
1:A:1379:PHE:CD2	1:A:1386:VAL:CG1	2.27	1.16
1:A:1379:PHE:HD2	1:A:1386:VAL:HG12	1.00	1.16
1:A:506:VAL:HG11	1:A:1138:LEU:HD13	1.33	1.09
2:B:542:GLU:HB2	2:E:543:ILE:HG21	1.31	1.08
1:A:1379:PHE:CE2	1:A:1381:ILE:HB	1.89	1.08
2:C:557:LEU:O	2:C:560:THR:HG22	1.51	1.08
1:A:1379:PHE:CD2	1:A:1386:VAL:HG12	1.92	1.03
2:B:542:GLU:HB2	2:E:543:ILE:CG2	1.90	1.00
1:A:1379:PHE:CZ	1:A:1381:ILE:HB	1.99	0.97
2:B:540:VAL:O	2:B:544:PRO:HD3	1.63	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1374:ASN:OD1	1:A:1396:MET:SD	2.25	0.95
1:A:1379:PHE:CE2	1:A:1381:ILE:CG2	2.50	0.94
1:A:918:THR:HG23	1:A:920:VAL:O	1.69	0.92
2:C:488:PHE:HE1	2:C:492:ASP:HB2	1.34	0.92
1:A:1379:PHE:HE2	1:A:1381:ILE:CG2	1.84	0.91
1:A:1379:PHE:CD2	1:A:1386:VAL:HG11	2.03	0.90
2:B:541:LYS:C	2:B:544:PRO:HD2	1.97	0.90
1:A:1379:PHE:HE2	1:A:1381:ILE:HG21	1.39	0.88
1:A:1379:PHE:CE2	1:A:1381:ILE:CB	2.55	0.88
2:B:541:LYS:O	2:B:544:PRO:HD2	1.80	0.82
2:B:575:MET:HG2	2:D:574:MET:HE1	1.62	0.82
2:E:488:PHE:HE1	2:E:490:PRO:HA	1.45	0.81
2:C:488:PHE:CE1	2:C:492:ASP:HB2	2.16	0.79
1:A:203:ASP:OD1	1:A:204:LYS:N	2.16	0.79
2:C:557:LEU:O	2:C:560:THR:CG2	2.31	0.79
2:B:482:ASP:HA	2:B:485:SER:HB3	1.65	0.79
1:A:267:ALA:HB1	1:A:344:ILE:HD13	1.64	0.78
1:A:469:MET:HE1	1:A:566:ILE:HA	1.65	0.78
2:E:488:PHE:CE1	2:E:490:PRO:HA	2.20	0.77
2:C:577:MET:HE1	2:C:592:PRO:HA	1.66	0.77
2:B:540:VAL:O	2:B:544:PRO:CD	2.33	0.77
1:A:206:THR:OG1	1:A:219:LYS:HG3	1.85	0.76
1:A:717:ALA:HB2	1:A:855:CYS:SG	2.25	0.76
2:C:540:VAL:O	2:C:544:PRO:HD3	1.85	0.76
1:A:918:THR:CG2	1:A:920:VAL:O	2.32	0.76
1:A:1092:LEU:O	1:A:1131:ARG:HD3	1.85	0.76
1:A:319:MET:HE1	1:A:341:LEU:HD23	1.67	0.76
1:A:58:ARG:HH21	1:A:489:ARG:HG2	1.52	0.75
1:A:156:ASP:HB2	1:A:159:LYS:HE2	1.68	0.75
1:A:1140:THR:HA	1:A:1144:LEU:HD12	1.68	0.75
1:A:467:LEU:HD21	1:A:1088:MET:HB3	1.69	0.74
1:A:169:CYS:HB3	1:A:242:LEU:HD22	1.70	0.72
2:C:557:LEU:C	2:C:560:THR:HG22	2.14	0.72
1:A:1299:ARG:HA	1:A:1302:THR:HG22	1.72	0.72
2:B:502:HIS:ND1	2:B:502:HIS:O	2.23	0.72
1:A:461:LEU:HD13	1:A:463:LEU:HG	1.71	0.71
1:A:506:VAL:CG1	1:A:1138:LEU:HD13	2.18	0.71
1:A:722:ASP:OD1	1:A:724:LYS:HG3	1.91	0.71
1:A:298:LEU:HD23	1:A:353:LEU:HD23	1.72	0.71
1:A:58:ARG:NH2	1:A:489:ARG:HG2	2.05	0.70
1:A:898:ASP:O	1:A:1368:ARG:NH1	2.23	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:508:LEU:HB3	2:E:508:LEU:HD21	1.73	0.70
1:A:510:VAL:O	1:A:1085:PRO:HD2	1.92	0.69
2:B:479:MET:HE1	2:B:481:SER:HB3	1.75	0.69
1:A:1291:THR:HG23	1:A:1294:LEU:HB2	1.75	0.69
2:B:541:LYS:CA	2:B:544:PRO:HD2	2.23	0.69
2:D:479:MET:HE3	2:D:479:MET:HA	1.75	0.68
1:A:1374:ASN:OD1	1:A:1396:MET:CG	2.41	0.68
1:A:469:MET:HG3	1:A:470:TYR:N	2.07	0.67
1:A:275:LEU:HD12	1:A:283:ILE:HD12	1.77	0.67
1:A:799:GLU:CD	1:A:799:GLU:H	2.02	0.67
2:B:542:GLU:CB	2:E:543:ILE:HG21	2.18	0.66
2:C:676:GLU:OE1	2:C:676:GLU:N	2.24	0.66
1:A:1249:PHE:HB2	1:A:1420:TYR:HB3	1.77	0.66
2:B:534:ASN:OD1	2:D:532:ARG:NH2	2.30	0.65
1:A:461:LEU:HD11	1:A:518:TYR:HE1	1.62	0.65
2:C:602:VAL:HG12	2:C:603:LEU:N	2.10	0.64
1:A:289:MET:O	1:A:293:LEU:HG	1.97	0.64
1:A:408:ARG:NH1	1:A:435:GLY:O	2.31	0.64
1:A:825:ILE:HG22	1:A:838:ILE:HG13	1.79	0.64
2:D:534:ASN:HB2	2:C:532:ARG:HH12	1.63	0.63
1:A:285:ASN:O	1:A:289:MET:HG2	1.99	0.62
1:A:860:GLN:HB2	2:C:650:SER:HB2	1.81	0.62
2:B:502:HIS:CE1	2:D:477:TYR:HB2	2.34	0.62
1:A:1379:PHE:CE2	1:A:1386:VAL:HG11	2.33	0.62
1:A:456:ASP:OD1	1:A:457:CYS:N	2.33	0.62
1:A:1365:ARG:NH2	1:A:1407:PHE:O	2.34	0.61
2:B:516:VAL:HG22	2:D:515:SER:HB2	1.83	0.61
2:C:682:ILE:O	2:C:686:ASN:ND2	2.34	0.61
1:A:267:ALA:HB1	1:A:344:ILE:CD1	2.31	0.61
1:A:1381:ILE:HG12	1:A:1382:GLU:HG3	1.83	0.60
2:B:526:LEU:HD13	2:E:526:LEU:HD21	1.84	0.60
2:B:541:LYS:HA	2:B:544:PRO:HD2	1.83	0.60
1:A:455:PHE:HB2	1:A:744:GLU:HG3	1.84	0.59
1:A:1438:GLN:NE2	1:A:1440:ASP:OD1	2.31	0.59
1:A:1172:ILE:HA	1:A:1175:LYS:HE2	1.85	0.59
2:B:519:GLY:C	2:D:518:MET:HE1	2.27	0.59
2:B:526:LEU:HD21	2:D:526:LEU:HD13	1.83	0.59
2:B:540:VAL:CG1	2:D:539:GLN:HB2	2.32	0.59
1:A:89:PRO:HG3	1:A:281:ASN:HA	1.85	0.59
1:A:1295:ARG:O	1:A:1298:ILE:HG13	2.01	0.59
1:A:1081:LEU:O	1:A:1084:SER:HB3	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:490:PRO:O	2:E:491:HIS:C	2.46	0.58
2:E:506:TYR:HB2	2:E:510:THR:HB	1.86	0.58
1:A:1154:ILE:HB	1:A:1158:LEU:HD22	1.84	0.58
2:C:664:VAL:O	2:C:668:ILE:HG12	2.04	0.58
1:A:58:ARG:HH21	1:A:489:ARG:CG	2.16	0.58
1:A:279:MET:HE3	1:A:326:CYS:SG	2.43	0.58
2:D:532:ARG:O	2:D:535:HIS:ND1	2.35	0.58
2:E:533:LEU:HA	2:E:536:ILE:HG22	1.84	0.58
1:A:17:LEU:O	1:A:544:LYS:NZ	2.35	0.57
2:C:567:ILE:HD11	2:E:567:ILE:HD13	1.86	0.57
1:A:107:LEU:HG	1:A:171:LEU:HD22	1.87	0.57
1:A:467:LEU:HG	1:A:1456:LEU:HD21	1.85	0.57
1:A:747:GLY:HA2	2:B:589:LYS:HE3	1.84	0.57
1:A:467:LEU:HD12	1:A:1456:LEU:HD11	1.87	0.57
1:A:1141:THR:O	1:A:1145:ILE:HG12	2.05	0.57
1:A:719:LEU:HD21	1:A:863:PHE:HB2	1.86	0.57
1:A:1154:ILE:HG22	1:A:1155:GLN:HG3	1.86	0.57
2:B:518:MET:HE2	2:E:520:VAL:HG22	1.87	0.57
2:C:664:VAL:HB	2:C:685:LEU:HD11	1.87	0.57
1:A:717:ALA:CB	1:A:855:CYS:SG	2.92	0.56
2:B:488:PHE:CE2	2:B:492:ASP:HB3	2.39	0.56
2:B:488:PHE:HB3	2:B:493:THR:CG2	2.35	0.56
1:A:156:ASP:CB	1:A:159:LYS:HE2	2.34	0.56
2:C:488:PHE:CD1	2:C:493:THR:HG23	2.40	0.56
1:A:173:TRP:HD1	1:A:242:LEU:HD13	1.70	0.56
1:A:381:MET:HE3	1:A:794:PRO:HB2	1.88	0.56
1:A:1068:ILE:HD13	1:A:1162:LEU:HA	1.86	0.56
1:A:267:ALA:CB	1:A:344:ILE:HD13	2.32	0.56
1:A:1140:THR:HG23	1:A:1144:LEU:HB2	1.87	0.56
1:A:1290:PRO:HG3	1:A:1294:LEU:HD12	1.88	0.56
2:C:535:HIS:O	2:C:538:GLU:HG3	2.06	0.56
1:A:1154:ILE:HG22	1:A:1155:GLN:N	2.20	0.56
2:E:541:LYS:O	2:E:541:LYS:HG2	2.05	0.56
1:A:279:MET:CE	1:A:326:CYS:SG	2.94	0.56
2:B:556:VAL:HG11	2:E:557:LEU:HB3	1.86	0.56
2:D:525:LYS:C	2:D:525:LYS:HZ2	2.14	0.56
1:A:461:LEU:HD11	1:A:518:TYR:CE1	2.40	0.55
2:E:489:PHE:O	2:E:490:PRO:C	2.49	0.55
1:A:173:TRP:CD1	1:A:242:LEU:HD13	2.42	0.55
2:B:499:HIS:HD2	2:D:479:MET:SD	2.29	0.55
1:A:156:ASP:HB2	1:A:159:LYS:HB3	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:MET:CE	1:A:341:LEU:HD23	2.35	0.55
1:A:461:LEU:O	1:A:461:LEU:HD12	2.06	0.55
1:A:878:LYS:HD3	1:A:881:GLU:OE2	2.06	0.55
2:B:528:ASN:HA	2:B:531:MET:SD	2.46	0.55
2:C:674:ASP:HB3	2:C:677:LEU:HB3	1.89	0.55
1:A:1328:ILE:HG13	1:A:1462:PRO:HB3	1.87	0.55
2:B:488:PHE:HE2	2:B:492:ASP:HB3	1.73	0.54
1:A:721:THR:OG1	1:A:834:GLU:OE1	2.23	0.54
1:A:972:THR:OG1	1:A:974:ASP:OD1	2.23	0.54
2:B:484:PHE:HE2	2:C:520:VAL:HG13	1.72	0.54
2:C:550:LEU:O	2:C:553:ILE:HG22	2.07	0.54
2:E:518:MET:O	2:E:521:ILE:HG13	2.07	0.54
2:B:541:LYS:HA	2:B:544:PRO:CD	2.38	0.54
1:A:556:MET:HE2	1:A:801:TYR:CZ	2.43	0.54
1:A:11:ILE:HD11	1:A:919:LEU:HD12	1.88	0.54
2:B:484:PHE:HZ	2:E:496:LEU:HB3	1.72	0.54
2:C:526:LEU:HB3	2:E:525:LYS:HE3	1.89	0.54
2:E:490:PRO:O	2:E:493:THR:N	2.40	0.54
1:A:501:GLU:HG2	1:A:502:PRO:HD2	1.89	0.54
1:A:172:PHE:O	1:A:176:ILE:HG12	2.08	0.53
1:A:1262:LYS:HG2	1:A:1263:GLU:N	2.23	0.53
1:A:387:LEU:HD22	2:E:578:ILE:HD11	1.90	0.53
1:A:741:ARG:NE	1:A:744:GLU:OE2	2.34	0.53
1:A:275:LEU:HD12	1:A:283:ILE:CD1	2.39	0.53
2:B:479:MET:HE3	2:B:482:ASP:H	1.73	0.53
1:A:867:ARG:NH2	2:C:640:PRO:O	2.42	0.53
2:C:563:ALA:O	2:C:567:ILE:HG23	2.09	0.53
1:A:306:ILE:HD11	2:C:651:GLN:HB2	1.89	0.53
2:B:488:PHE:HB3	2:B:493:THR:HG23	1.90	0.53
1:A:776:ASP:OD1	1:A:776:ASP:N	2.39	0.53
2:C:598:ILE:HG12	2:E:574:MET:HG2	1.91	0.53
2:C:608:LEU:HD13	2:E:577:MET:HB3	1.90	0.53
1:A:1379:PHE:CE2	1:A:1381:ILE:HG22	2.39	0.53
2:C:602:VAL:CG1	2:C:603:LEU:N	2.70	0.53
2:B:535:HIS:O	2:B:539:GLN:HG2	2.09	0.52
2:C:499:HIS:O	2:C:499:HIS:ND1	2.42	0.52
1:A:9:ASP:OD2	1:A:190:PRO:HD3	2.09	0.52
2:B:509:GLU:HG2	2:B:510:THR:HG23	1.91	0.52
2:E:504:GLY:HA3	2:E:506:TYR:CZ	2.45	0.52
1:A:145:ILE:O	1:A:149:HIS:CD2	2.63	0.52
2:D:507:ASP:O	2:D:510:THR:OG1	2.23	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1116:PRO:HG2	1:A:1216:LEU:HD11	1.92	0.52
1:A:1250:PHE:HB3	1:A:1371:ASN:HB2	1.92	0.51
1:A:203:ASP:CG	1:A:204:LYS:H	2.16	0.51
2:B:537:GLU:HG2	2:D:536:ILE:HD11	1.92	0.51
1:A:1066:GLN:NE2	1:A:1070:LYS:HG2	2.25	0.51
1:A:1202:HIS:HD2	1:A:1203:MET:HG2	1.76	0.51
1:A:1068:ILE:O	1:A:1072:ILE:HG12	2.11	0.51
2:D:551:GLU:OE1	2:C:549:LYS:NZ	2.41	0.51
1:A:999:PHE:HE1	1:A:1173:LEU:HD22	1.76	0.51
2:E:483:ASP:O	2:E:486:ASN:ND2	2.44	0.51
1:A:298:LEU:CD2	1:A:353:LEU:HD23	2.41	0.51
1:A:747:GLY:HA3	2:B:592:PRO:HD3	1.93	0.51
1:A:1043:GLN:HB3	1:A:1176:LEU:HD13	1.92	0.51
2:D:545:LYS:HA	2:D:548:ASN:ND2	2.26	0.50
2:C:533:LEU:HA	2:C:536:ILE:HG22	1.92	0.50
1:A:525:LEU:HD21	1:A:748:LEU:HB3	1.92	0.50
2:B:537:GLU:HA	2:D:536:ILE:HD11	1.92	0.50
2:E:495:ARG:HH21	2:E:496:LEU:HD23	1.77	0.50
1:A:1068:ILE:HA	1:A:1071:THR:HG23	1.94	0.50
1:A:1333:LEU:O	1:A:1337:THR:HG23	2.12	0.50
2:B:481:SER:N	2:E:514:GLU:OE2	2.44	0.50
2:C:557:LEU:HA	2:C:560:THR:HG22	1.93	0.50
2:C:534:ASN:N	2:E:532:ARG:HH22	2.09	0.50
2:D:479:MET:N	2:D:480:PRO:HD3	2.26	0.50
2:D:533:LEU:HD11	2:C:533:LEU:HD12	1.93	0.50
1:A:206:THR:OG1	1:A:219:LYS:CG	2.58	0.50
1:A:417:PRO:HB2	1:A:456:ASP:HB3	1.94	0.50
1:A:472:LYS:HE3	1:A:474:LYS:HE2	1.94	0.50
1:A:1364:ASN:OD1	1:A:1367:SER:OG	2.22	0.50
2:B:559:LYS:HB3	2:E:561:ASN:HD21	1.77	0.50
1:A:136:LEU:O	1:A:1420:TYR:OH	2.29	0.49
1:A:384:ASP:OD1	2:E:580:GLY:N	2.43	0.49
2:D:488:PHE:HE1	2:D:492:ASP:HB3	1.75	0.49
2:B:576:ILE:HD11	2:B:583:LYS:HB3	1.95	0.49
1:A:1077:ALA:O	1:A:1080:ILE:HG13	2.12	0.49
2:B:540:VAL:HA	2:B:543:ILE:HB	1.93	0.49
2:E:480:PRO:HD2	2:E:483:ASP:HB2	1.93	0.49
1:A:1092:LEU:HG	1:A:1131:ARG:HG2	1.95	0.49
2:E:551:GLU:HB3	2:E:555:ARG:HH12	1.78	0.49
2:E:558:ALA:O	2:E:562:THR:HG23	2.13	0.49
1:A:512:ASP:HB3	1:A:515:PHE:HB2	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:GLU:HG3	1:A:280:GLY:HA2	1.94	0.48
1:A:1096:LYS:O	1:A:1100:GLU:HG3	2.13	0.48
2:C:488:PHE:HE1	2:C:492:ASP:CB	2.16	0.48
1:A:1154:ILE:HG21	1:A:1158:LEU:HD13	1.95	0.48
1:A:1415:ASP:OD1	1:A:1415:ASP:N	2.34	0.48
1:A:290:ILE:O	1:A:294:VAL:HG23	2.14	0.48
1:A:23:SER:HB2	1:A:367:ILE:HG12	1.96	0.48
1:A:298:LEU:HB3	1:A:888:LEU:HD11	1.95	0.48
1:A:116:LYS:O	1:A:120:ILE:HG13	2.14	0.48
1:A:1066:GLN:OE1	1:A:1071:THR:HG22	2.14	0.48
2:C:700:THR:O	2:C:704:ILE:HD12	2.13	0.48
2:B:592:PRO:HG2	2:B:595:LYS:HZ1	1.78	0.48
2:C:543:ILE:O	2:C:546:ILE:HG12	2.14	0.48
2:E:524:ILE:HA	2:E:527:ILE:HD12	1.96	0.48
1:A:584:MET:HE3	1:A:811:ILE:HG23	1.95	0.47
1:A:484:ASP:OD1	1:A:484:ASP:N	2.47	0.47
1:A:1076:THR:O	1:A:1080:ILE:HG23	2.14	0.47
1:A:596:PHE:O	1:A:600:ILE:HG13	2.13	0.47
2:B:541:LYS:O	2:B:544:PRO:CD	2.59	0.47
2:D:501:ASP:OD1	2:D:502:HIS:N	2.48	0.47
2:C:602:VAL:CG1	2:C:603:LEU:H	2.28	0.47
1:A:469:MET:HE1	1:A:566:ILE:CA	2.38	0.47
1:A:598:LEU:O	1:A:602:SER:OG	2.30	0.47
2:D:520:VAL:HG13	2:E:484:PHE:HZ	1.79	0.47
2:C:527:ILE:HG13	2:E:525:LYS:HZ1	1.80	0.47
1:A:992:ILE:HG13	1:A:1032:MET:HE1	1.97	0.47
2:C:642:LEU:HD23	2:C:642:LEU:HA	1.72	0.47
1:A:589:HIS:HB3	1:A:891:TYR:CD2	2.50	0.47
2:B:518:MET:HE3	2:E:520:VAL:HA	1.96	0.47
1:A:203:ASP:CG	1:A:204:LYS:N	2.73	0.47
1:A:17:LEU:HD22	1:A:237:MET:HB2	1.98	0.46
1:A:975:VAL:HG23	1:A:1171:LEU:HD13	1.97	0.46
1:A:1320:TYR:OH	1:A:1447:GLU:OE1	2.31	0.46
1:A:1246:TYR:HB3	1:A:1423:HIS:CG	2.50	0.46
1:A:1290:PRO:HD2	1:A:1295:ARG:HG3	1.98	0.46
2:B:560:THR:OG1	2:E:561:ASN:OD1	2.27	0.46
1:A:323:LEU:O	1:A:328:PHE:HB2	2.16	0.46
1:A:1088:MET:HG2	1:A:1456:LEU:CD2	2.46	0.46
2:B:540:VAL:HG11	2:D:539:GLN:HB2	1.97	0.46
2:C:557:LEU:CA	2:C:560:THR:HG22	2.46	0.46
1:A:1014:ASP:HB3	1:A:1017:THR:HG22	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:764:ILE:HG23	1:A:791:ILE:HB	1.98	0.46
2:C:518:MET:HA	2:C:521:ILE:HG22	1.98	0.46
2:D:478:ILE:HD11	2:D:482:ASP:HB2	1.96	0.46
2:D:534:ASN:ND2	2:C:532:ARG:HH22	2.14	0.46
1:A:5:LEU:HD13	1:A:9:ASP:HB3	1.98	0.46
1:A:283:ILE:O	1:A:287:VAL:HG23	2.15	0.46
2:B:511:LEU:HD12	2:B:511:LEU:HA	1.80	0.46
2:C:552:SER:OG	2:C:555:ARG:NH2	2.47	0.46
2:B:502:HIS:O	2:B:502:HIS:CG	2.69	0.46
1:A:58:ARG:NH2	1:A:489:ARG:CG	2.78	0.45
1:A:820:GLU:HG3	1:A:865:ARG:HD3	1.98	0.45
2:C:534:ASN:OD1	2:E:532:ARG:NH1	2.34	0.45
2:B:543:ILE:HG22	2:B:544:PRO:N	2.31	0.45
2:C:660:SER:O	2:C:664:VAL:HG23	2.17	0.45
1:A:985:TRP:HA	1:A:988:THR:HG22	1.97	0.45
1:A:1221:ALA:HB1	1:A:1398:LEU:HD22	1.98	0.45
2:D:523:SER:OG	2:C:522:ASN:OD1	2.27	0.45
2:C:596:PRO:HB2	2:E:574:MET:SD	2.56	0.45
1:A:110:ILE:HG23	1:A:960:LEU:HB3	1.99	0.45
1:A:117:ALA:HA	1:A:120:ILE:HD12	1.99	0.45
1:A:1142:LYS:HB2	1:A:1142:LYS:HE2	1.70	0.45
2:D:518:MET:O	2:D:521:ILE:HG22	2.17	0.45
2:C:545:LYS:HB2	2:C:548:ASN:HD21	1.82	0.45
1:A:1299:ARG:HA	1:A:1302:THR:CG2	2.43	0.45
1:A:168:GLU:H	1:A:168:GLU:CD	2.25	0.45
1:A:1072:ILE:HG13	1:A:1162:LEU:HD13	1.98	0.45
1:A:1202:HIS:CD2	1:A:1203:MET:HG2	2.52	0.45
2:D:547:ILE:HD13	2:D:547:ILE:HA	1.83	0.45
2:C:544:PRO:HB3	2:E:539:GLN:NE2	2.32	0.45
2:C:560:THR:HG23	2:C:561:ASN:N	2.31	0.45
1:A:999:PHE:CE1	1:A:1173:LEU:HD22	2.52	0.44
2:B:521:ILE:HD13	2:D:484:PHE:HD2	1.83	0.44
2:B:540:VAL:O	2:B:543:ILE:HB	2.17	0.44
2:C:678:ARG:O	2:C:682:ILE:HG13	2.17	0.44
1:A:1175:LYS:HE2	1:A:1175:LYS:HB2	1.81	0.44
1:A:12:TYR:CE1	1:A:185:LYS:HE2	2.52	0.44
2:D:536:ILE:HD13	2:D:536:ILE:HA	1.81	0.44
2:D:553:ILE:CG2	2:C:553:ILE:HD11	2.47	0.44
1:A:908:SER:HB2	1:A:937:ALA:HB2	1.98	0.44
1:A:1057:PRO:HG3	1:A:1120:HIS:HB2	1.98	0.44
1:A:730:TRP:O	1:A:796:GLY:HA2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1433:VAL:O	1:A:1433:VAL:HG13	2.18	0.44
1:A:1455:HIS:O	1:A:1456:LEU:HG	2.17	0.44
2:B:520:VAL:O	2:B:524:ILE:HG12	2.17	0.44
1:A:299:GLN:NE2	1:A:884:ILE:O	2.44	0.44
2:D:534:ASN:HB2	2:C:532:ARG:NH1	2.31	0.44
1:A:303:GLU:HB2	1:A:852:LYS:HE3	2.00	0.44
1:A:1006:ARG:HA	1:A:1009:VAL:O	2.18	0.44
2:C:540:VAL:HG21	2:E:536:ILE:HG13	1.99	0.43
1:A:1391:ILE:O	1:A:1394:GLN:HG2	2.18	0.43
2:C:571:LEU:O	2:C:574:MET:HG2	2.18	0.43
2:E:507:ASP:OD1	2:E:508:LEU:N	2.50	0.43
1:A:833:ASN:OD1	1:A:833:ASN:N	2.52	0.43
1:A:1171:LEU:HD12	1:A:1171:LEU:HA	1.85	0.43
2:B:539:GLN:O	2:B:542:GLU:HG2	2.19	0.43
2:D:548:ASN:OD1	2:D:549:LYS:N	2.51	0.43
1:A:584:MET:SD	1:A:827:ALA:HB3	2.58	0.43
2:B:508:LEU:HD11	2:E:509:GLU:H	1.84	0.43
2:C:602:VAL:HG12	2:C:603:LEU:H	1.81	0.43
2:E:488:PHE:HE1	2:E:494:ASP:HB3	1.84	0.43
1:A:995:PRO:HG2	1:A:1019:SER:OG	2.19	0.43
2:D:543:ILE:HG12	2:C:543:ILE:HB	2.01	0.43
2:B:518:MET:HE1	2:D:484:PHE:HE2	1.83	0.43
2:D:477:TYR:HB3	2:D:478:ILE:HG22	2.00	0.43
2:C:528:ASN:HA	2:C:531:MET:HG3	2.00	0.43
1:A:585:VAL:HG13	1:A:595:LEU:HD11	2.01	0.43
1:A:1017:THR:HG21	1:A:1218:VAL:O	2.17	0.43
1:A:1230:ILE:HD13	1:A:1230:ILE:HA	1.80	0.43
2:C:604:GLU:HB3	2:E:579:PRO:HB3	2.01	0.43
2:E:542:GLU:HG2	2:E:545:LYS:HE2	2.01	0.43
2:C:498:TYR:CE2	2:E:479:MET:HE1	2.54	0.42
1:A:18:ASP:CG	1:A:18:ASP:O	2.62	0.42
1:A:323:LEU:HD11	1:A:337:PHE:CD2	2.54	0.42
1:A:510:VAL:HG11	1:A:1080:ILE:HD12	2.01	0.42
1:A:803:GLN:HA	1:A:806:TRP:CD1	2.54	0.42
1:A:897:TYR:CE1	1:A:1259:GLN:HG2	2.53	0.42
2:B:559:LYS:HE3	2:B:559:LYS:HB2	1.82	0.42
2:C:564:LEU:HD23	2:C:564:LEU:HA	1.88	0.42
1:A:1100:GLU:CD	1:A:1449:THR:H	2.27	0.42
1:A:210:LEU:C	1:A:210:LEU:HD12	2.44	0.42
1:A:472:LYS:O	1:A:506:VAL:HG23	2.20	0.42
1:A:755:MET:HE1	1:A:806:TRP:CZ2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1389:ASN:OD1	1:A:1389:ASN:N	2.53	0.42
2:B:541:LYS:C	2:B:543:ILE:N	2.71	0.42
2:E:488:PHE:CE1	2:E:494:ASP:HB3	2.55	0.42
2:D:553:ILE:HG21	2:C:553:ILE:HD11	2.02	0.42
2:C:548:ASN:OD1	2:C:549:LYS:N	2.53	0.42
1:A:293:LEU:HD23	1:A:315:CYS:HB3	2.01	0.42
1:A:1253:ARG:HD3	1:A:1415:ASP:O	2.19	0.42
2:B:579:PRO:HG2	2:C:600:ARG:CZ	2.50	0.42
2:C:533:LEU:HA	2:C:536:ILE:CG2	2.49	0.42
1:A:522:GLU:O	1:A:526:SER:OG	2.28	0.41
1:A:878:LYS:HD3	1:A:881:GLU:CD	2.44	0.41
2:D:525:LYS:HE3	2:D:525:LYS:HB3	1.84	0.41
2:D:520:VAL:HG13	2:E:484:PHE:CZ	2.55	0.41
2:D:572:VAL:HA	2:D:575:MET:HG3	2.01	0.41
1:A:303:GLU:HB2	1:A:852:LYS:HG3	2.01	0.41
1:A:467:LEU:HD23	1:A:509:PHE:HZ	1.85	0.41
1:A:1372:ILE:HD11	1:A:1400:LEU:HD11	2.02	0.41
1:A:12:TYR:HA	1:A:13:PRO:HD3	1.89	0.41
1:A:781:LEU:HD12	1:A:781:LEU:HA	1.88	0.41
1:A:1012:ILE:HA	1:A:1012:ILE:HD13	1.80	0.41
1:A:1062:LEU:HD12	1:A:1203:MET:HE2	2.02	0.41
1:A:1193:VAL:HG13	1:A:1217:GLU:HB3	2.03	0.41
1:A:1329:ASP:OD1	1:A:1329:ASP:N	2.45	0.41
1:A:1392:TYR:CD1	1:A:1392:TYR:N	2.88	0.41
2:C:490:PRO:O	2:C:493:THR:OG1	2.32	0.41
1:A:826:ALA:O	1:A:837:ALA:N	2.52	0.41
1:A:1080:ILE:HD11	1:A:1138:LEU:HD22	2.01	0.41
1:A:1293:ALA:HB1	1:A:1325:ARG:O	2.21	0.41
1:A:1447:GLU:OE1	1:A:1447:GLU:HA	2.20	0.41
2:D:478:ILE:C	2:D:480:PRO:HD3	2.45	0.41
2:D:552:SER:O	2:D:556:VAL:HG13	2.19	0.41
1:A:846:LEU:HD22	1:A:850:VAL:HG11	2.02	0.41
1:A:1097:SER:OG	1:A:1131:ARG:NE	2.54	0.41
1:A:863:PHE:HZ	1:A:879:ALA:HA	1.85	0.41
2:C:528:ASN:O	2:C:531:MET:HG3	2.20	0.41
1:A:1137:LEU:HA	1:A:1137:LEU:HD12	1.85	0.41
1:A:1262:LYS:HG2	1:A:1263:GLU:H	1.85	0.41
1:A:467:LEU:CD2	1:A:509:PHE:HZ	2.34	0.41
1:A:719:LEU:HD13	1:A:838:ILE:HD13	2.03	0.41
1:A:779:MET:HE2	1:A:779:MET:HB3	1.90	0.41
1:A:1321:LEU:HD23	1:A:1321:LEU:HA	1.90	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:526:LEU:HB3	2:D:525:LYS:HE2	2.02	0.41
2:D:557:LEU:HD23	2:D:557:LEU:HA	1.92	0.41
2:C:636:ASP:OD1	2:C:636:ASP:N	2.53	0.41
1:A:861:LEU:HD23	1:A:861:LEU:HA	1.83	0.41
1:A:1024:LYS:HB3	1:A:1024:LYS:HE3	1.93	0.41
1:A:1290:PRO:HD2	1:A:1295:ARG:HD3	2.03	0.41
2:C:574:MET:HG3	2:C:596:PRO:HB3	2.03	0.41
2:C:604:GLU:HG2	2:E:581:LYS:HB2	2.01	0.41
1:A:835:SER:OG	1:A:889:PHE:HE1	2.05	0.40
1:A:1088:MET:HE3	1:A:1088:MET:HB2	1.68	0.40
1:A:744:GLU:OE1	2:B:583:LYS:NZ	2.49	0.40
2:B:524:ILE:HD11	2:C:484:PHE:CZ	2.56	0.40
1:A:472:LYS:NZ	1:A:565:VAL:HB	2.36	0.40
1:A:1041:MET:HE1	1:A:1198:ALA:HB3	2.03	0.40
1:A:1086:ASN:HA	1:A:1087:PRO:HD3	1.89	0.40
1:A:1421:HIS:HB3	1:A:1423:HIS:CD2	2.57	0.40
2:C:499:HIS:CD2	2:E:479:MET:HE3	2.56	0.40
2:C:557:LEU:HA	2:C:560:THR:CG2	2.52	0.40
1:A:1004:LEU:O	1:A:1007:ILE:HG12	2.21	0.40
2:B:517:LEU:HD13	2:D:480:PRO:HA	2.03	0.40
2:D:536:ILE:O	2:D:540:VAL:HG23	2.22	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	1291/2244 (58%)	1249 (97%)	42 (3%)	0	100	100
2	B	116/709 (16%)	114 (98%)	2 (2%)	0	100	100
2	C	194/709 (27%)	189 (97%)	5 (3%)	0	100	100
2	D	101/709 (14%)	93 (92%)	7 (7%)	1 (1%)	12	10

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	104/709 (15%)	95 (91%)	9 (9%)	0	100	100
All	All	1806/5080 (36%)	1740 (96%)	65 (4%)	1 (0%)	49	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	480	PRO

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	1171/2044 (57%)	1136 (97%)	35 (3%)	36	45
2	B	108/621 (17%)	94 (87%)	14 (13%)	4	3
2	C	185/621 (30%)	180 (97%)	5 (3%)	39	49
2	D	97/621 (16%)	95 (98%)	2 (2%)	47	58
2	E	97/621 (16%)	92 (95%)	5 (5%)	21	22
All	All	1658/4528 (37%)	1597 (96%)	61 (4%)	31	37

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	7	ILE
1	A	10	ILE
1	A	242	LEU
1	A	317	LYS
1	A	442	ASP
1	A	472	LYS
1	A	552	LEU
1	A	712	PHE
1	A	713	ASP
1	A	714	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	783	GLU
1	A	802	SER
1	A	880	THR
1	A	975	VAL
1	A	983	LEU
1	A	1007	ILE
1	A	1010	ARG
1	A	1025	ARG
1	A	1034	GLU
1	A	1040	VAL
1	A	1079	THR
1	A	1080	ILE
1	A	1088	MET
1	A	1142	LYS
1	A	1158	LEU
1	A	1159	VAL
1	A	1180	ARG
1	A	1291	THR
1	A	1294	LEU
1	A	1305	THR
1	A	1323	SER
1	A	1378	ASP
1	A	1385	LYS
1	A	1451	VAL
2	B	487	THR
2	B	488	PHE
2	B	491	HIS
2	B	494	ASP
2	B	512	CYS
2	B	525	LYS
2	B	531	MET
2	B	540	VAL
2	B	541	LYS
2	B	542	GLU
2	B	543	ILE
2	B	545	LYS
2	B	559	LYS
2	B	572	VAL
2	D	503	LEU
2	D	547	ILE
2	C	540	VAL
2	C	545	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	C	573	SER
2	C	642	LEU
2	C	690	ASN
2	E	491	HIS
2	E	506	TYR
2	E	547	ILE
2	E	552	SER
2	E	560	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	ASN
1	A	149	HIS
1	A	213	ASN
1	A	427	HIS
1	A	589	HIS
1	A	792	HIS
1	A	1029	HIS
1	A	1086	ASN
1	A	1125	ASN
1	A	1324	GLN
2	D	561	ASN
2	C	497	ASN
2	C	606	GLN
2	C	690	ASN
2	E	497	ASN
2	E	499	HIS
2	E	534	ASN
2	E	548	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

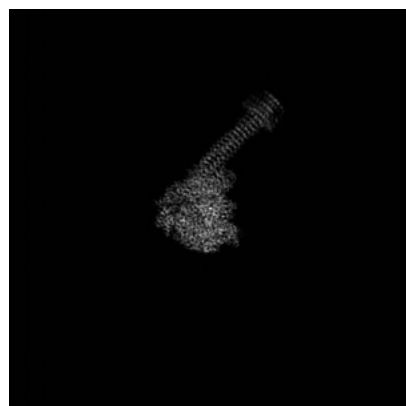
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44465. These allow visual inspection of the internal detail of the map and identification of artifacts.

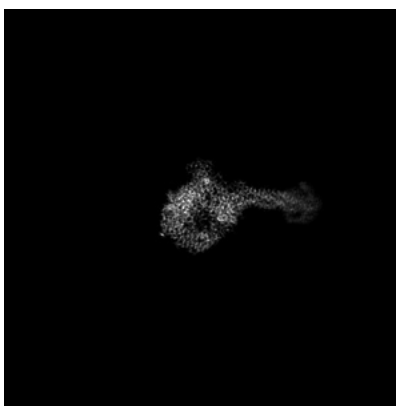
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

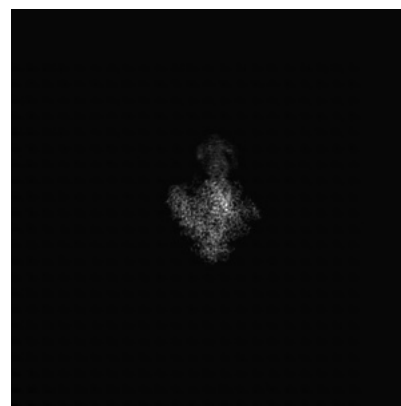
6.1.1 Primary map



X

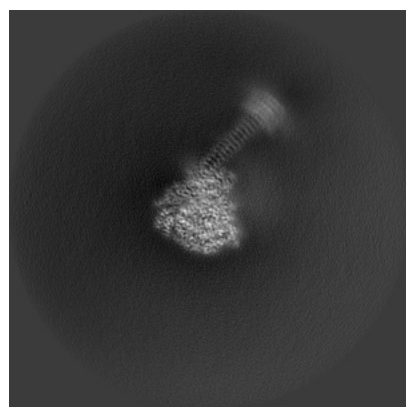


Y

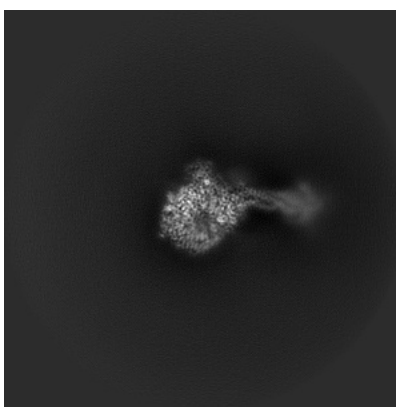


Z

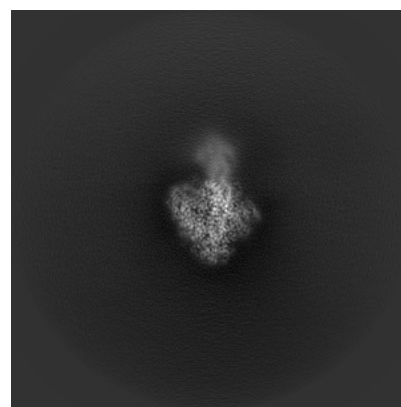
6.1.2 Raw map



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: 240

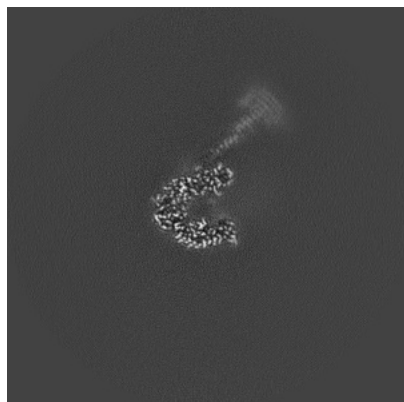


Y Index: 240

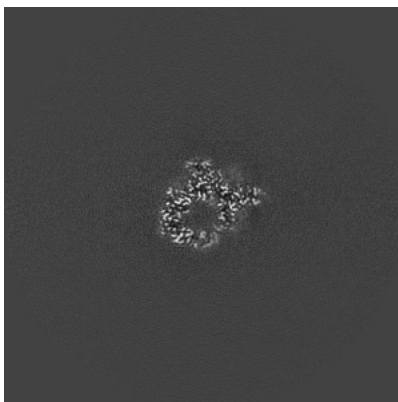


Z Index: 240

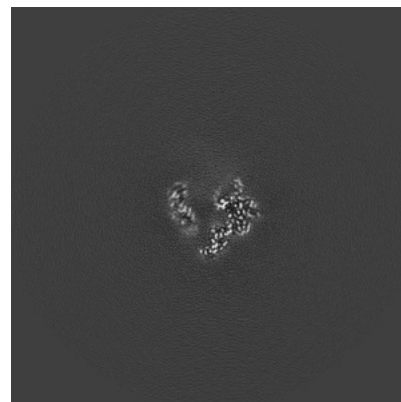
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

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

6.3 Largest variance slices [i](#)

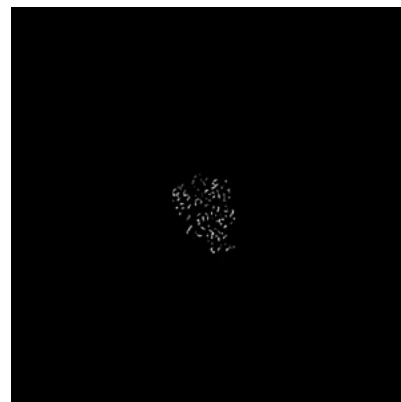
6.3.1 Primary map



X Index: 245

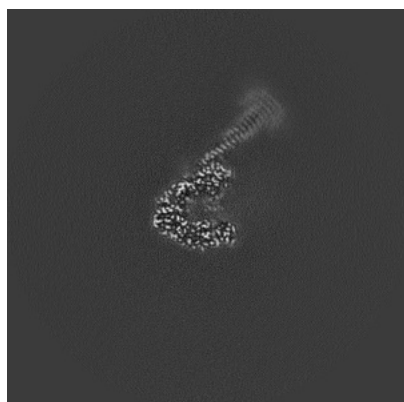


Y Index: 241

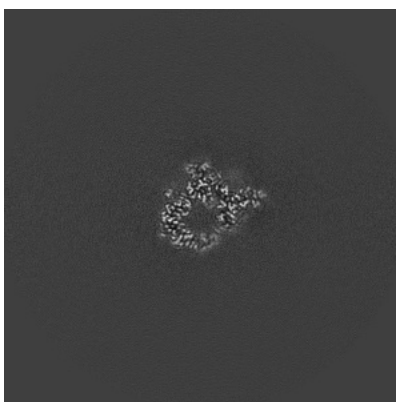


Z Index: 215

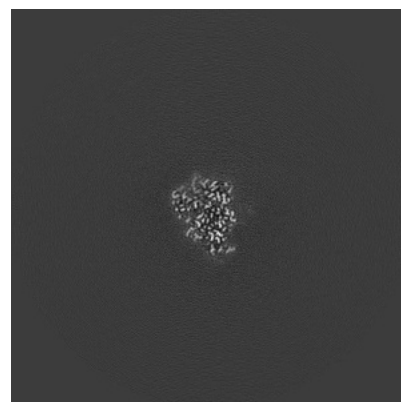
6.3.2 Raw map



X Index: 245



Y Index: 241

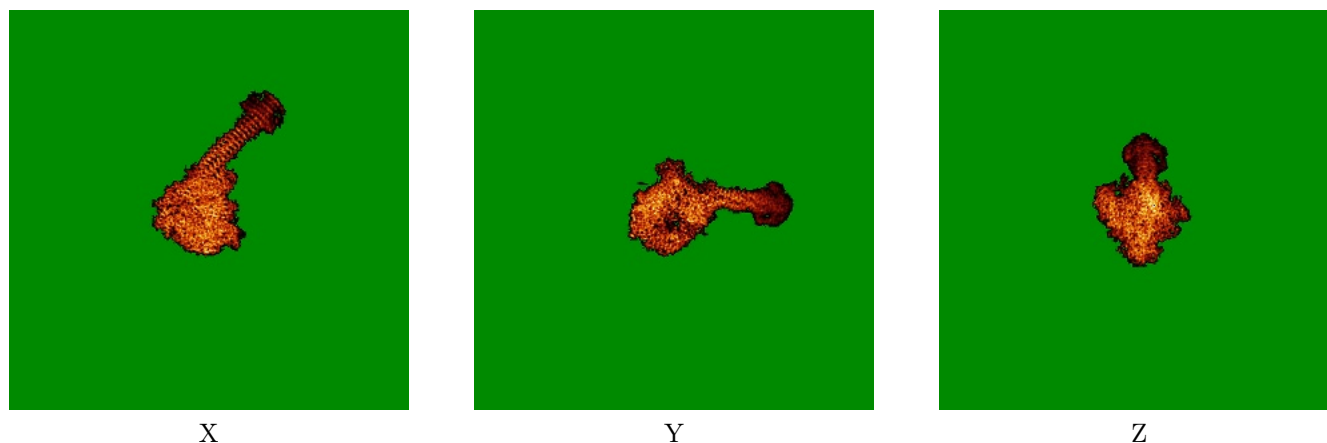


Z Index: 214

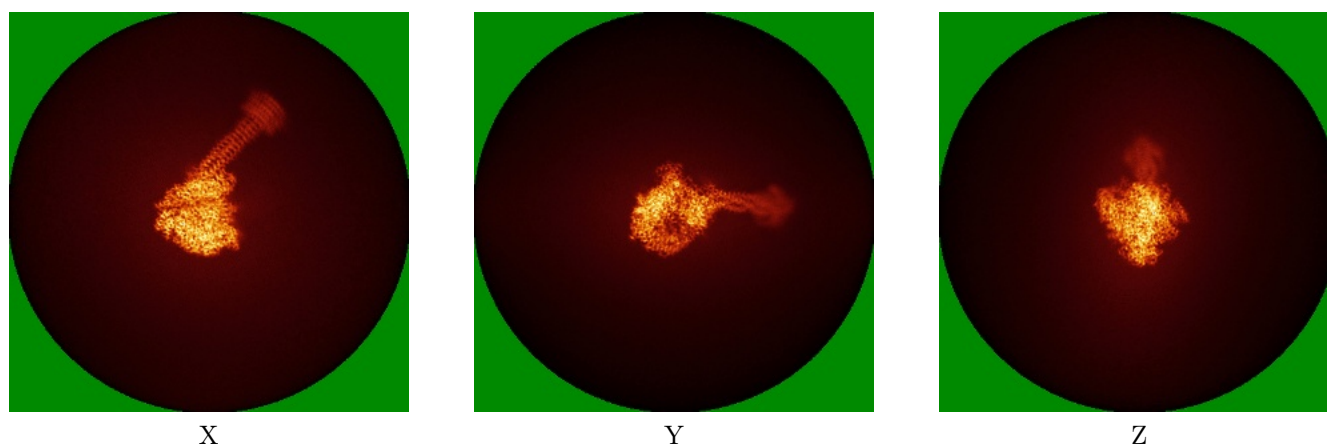
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

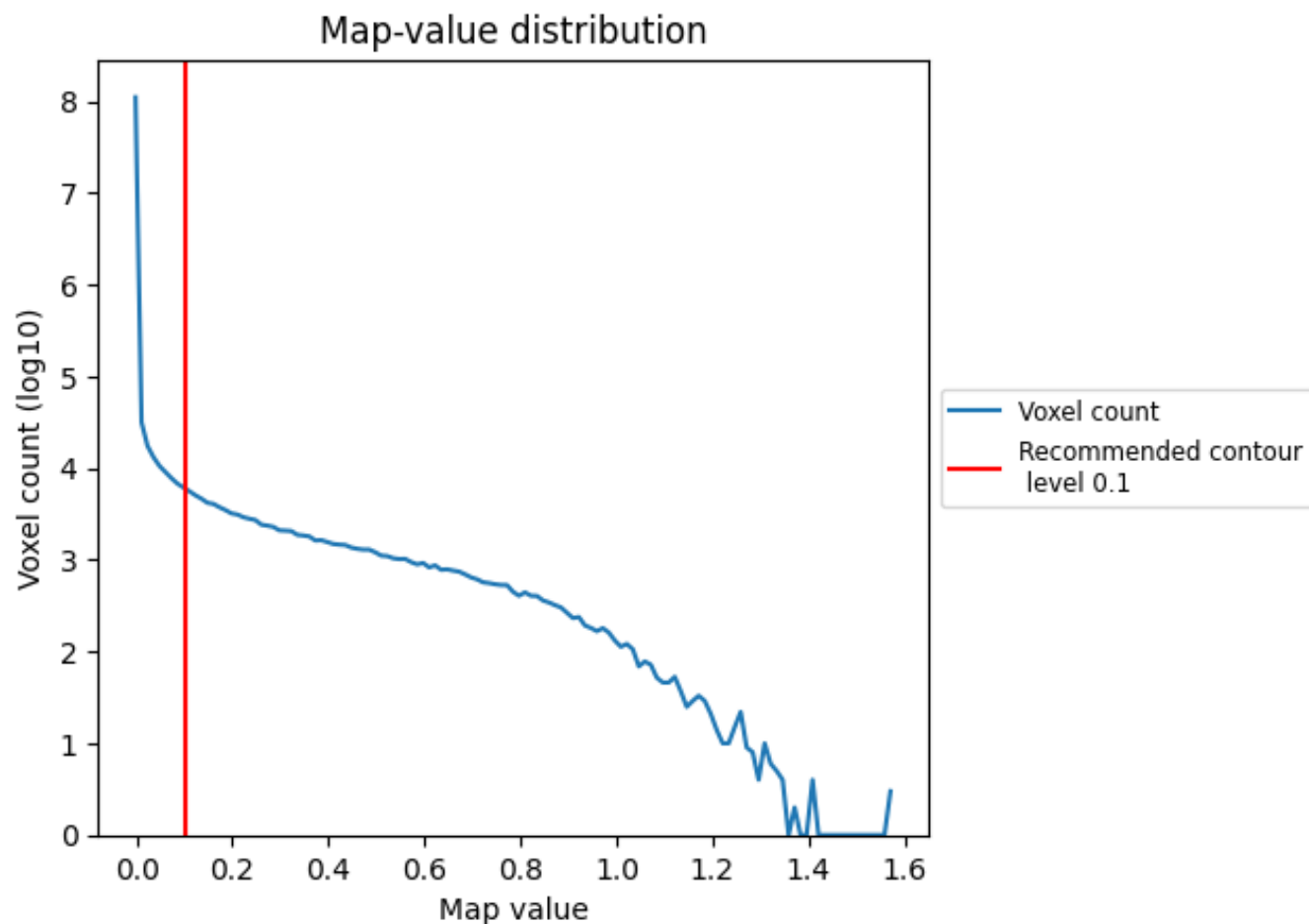
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

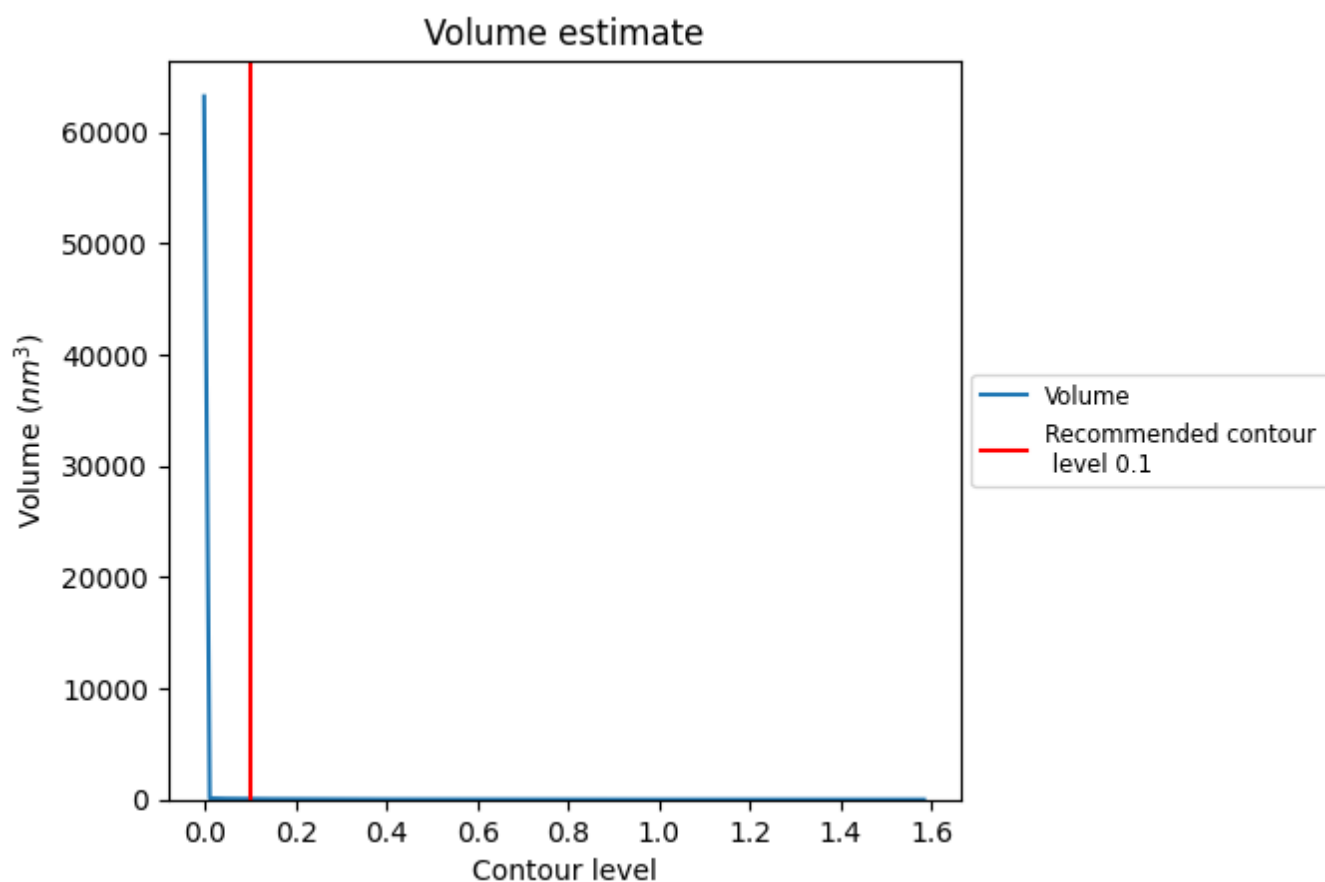
This section contains the results of statistical analysis of the map.

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.

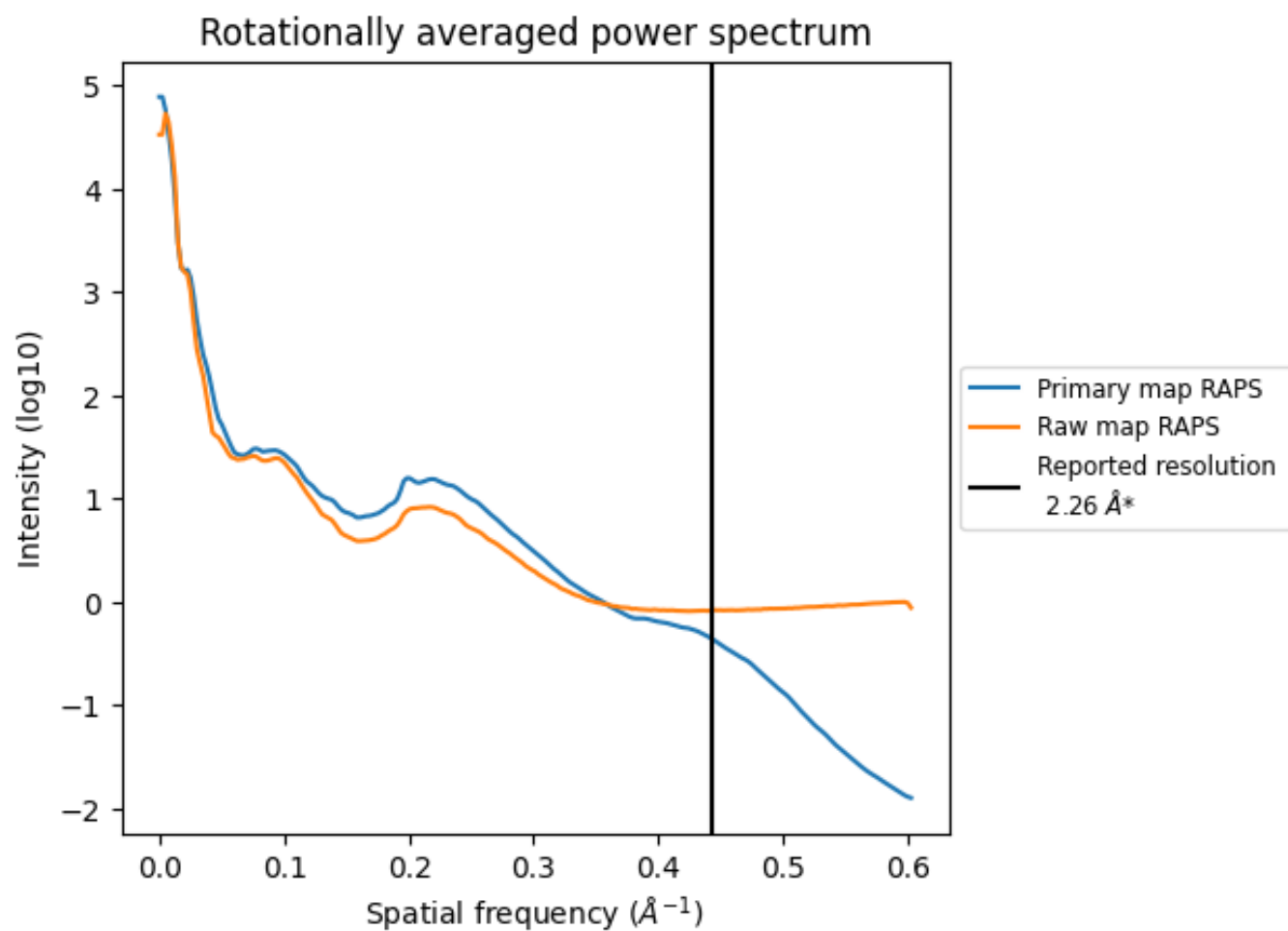
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 62 nm^3 ; this corresponds to an approximate mass of 56 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 ⓘ

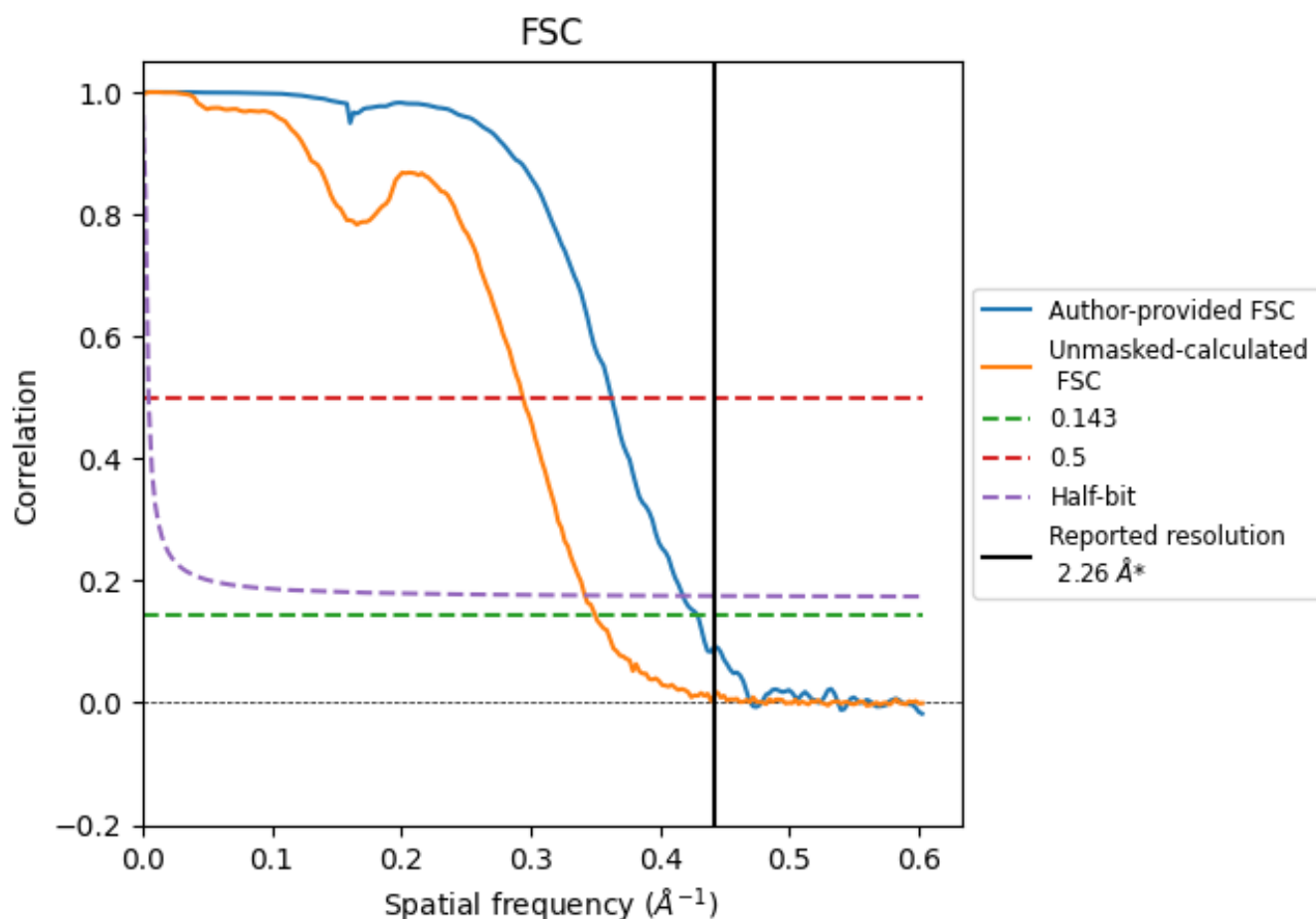


*Reported resolution corresponds to spatial frequency of 0.442 Å⁻¹

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 0.442 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

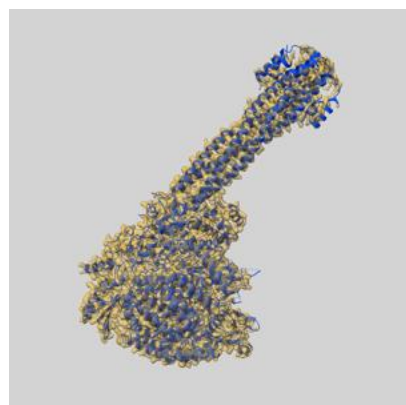
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.26	-	-
Author-provided FSC curve	2.33	2.76	2.39
Unmasked-calculated*	2.86	3.40	2.92

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.86 differs from the reported value 2.26 by more than 10 %

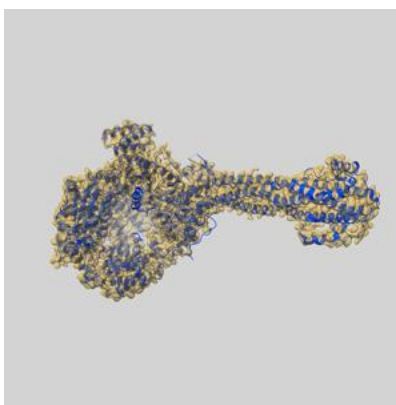
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44465 and PDB model 9BDQ. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

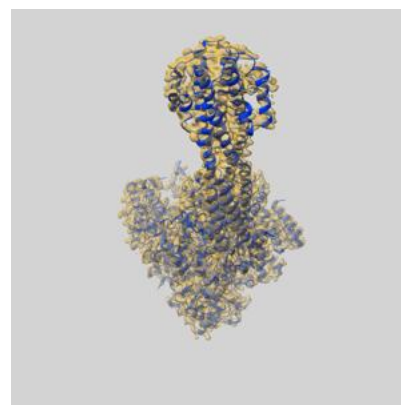
9.1 Map-model overlay [i](#)



X



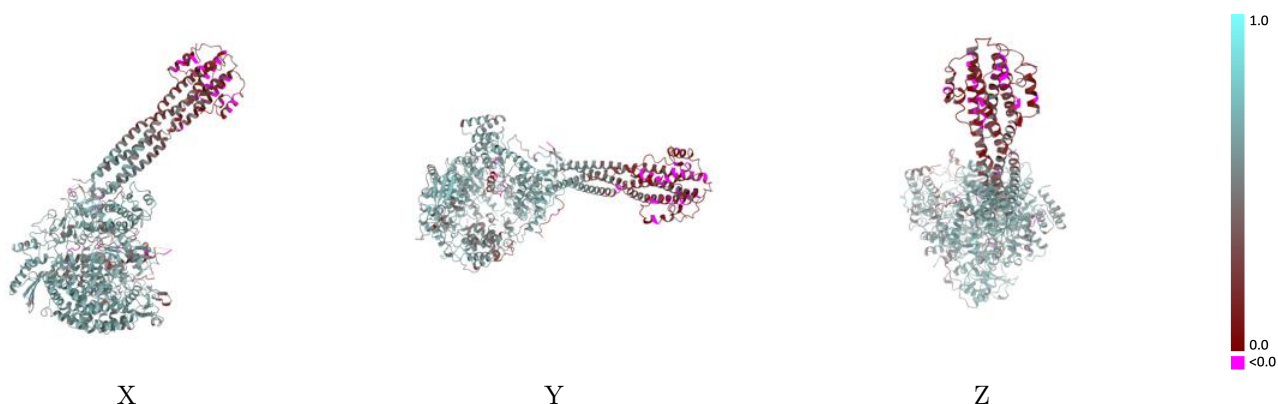
Y



Z

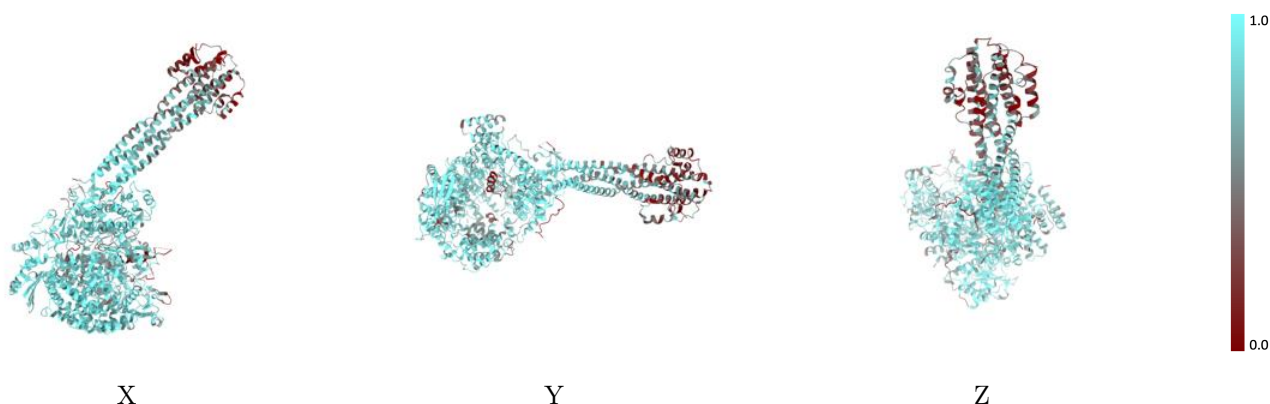
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



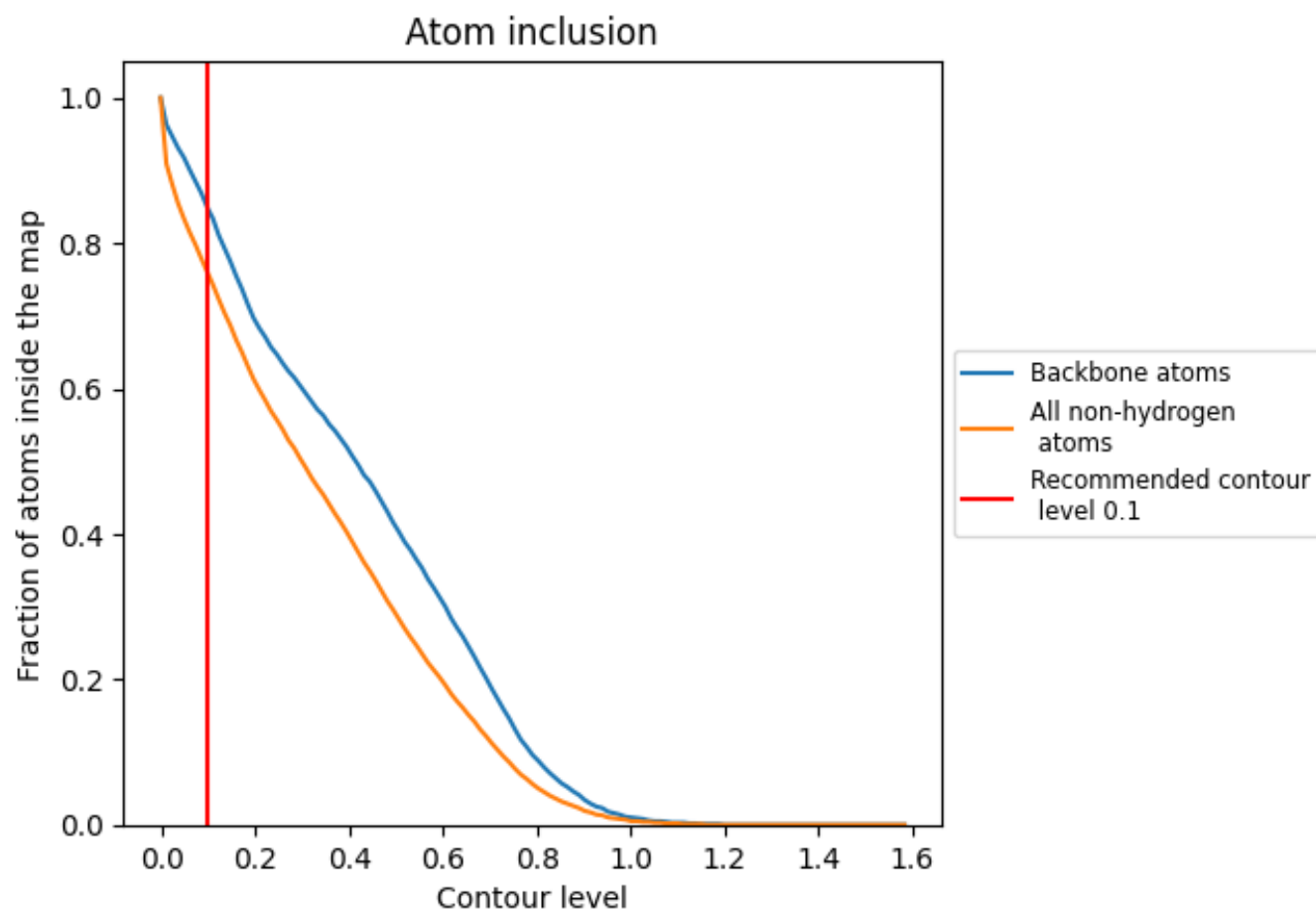
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 85% of all backbone atoms, 76% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7570	0.5080
A	0.8290	0.5750
B	0.4780	0.2960
C	0.6360	0.4020
D	0.5290	0.2930
E	0.6210	0.3280

