



Full wwPDB EM Validation Report ⓘ

Jul 10, 2025 – 04:15 PM JST

PDB ID : 9KNV / pdb_00009knv
EMDB ID : EMD-62463
Title : AS-136A-bound measles virus L-P complex
Authors : Wang, Y.R.; Zhang, H.Q.
Deposited on : 2024-11-19
Resolution : 3.30 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.dev118
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
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) : 2.44

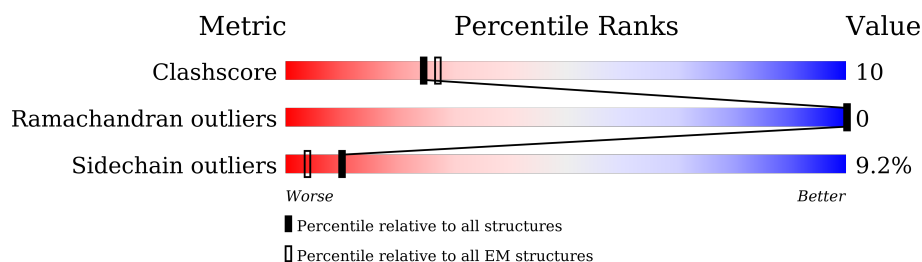
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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	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 ≥ 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	2183	 41% 16% 42%
2	B	507	 94%
2	C	507	 13% 5% 81%
2	D	507	 5% 5% 92%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11528 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	1275	Total	C	N	O	S	0	0
			10241	6535	1771	1876	59		

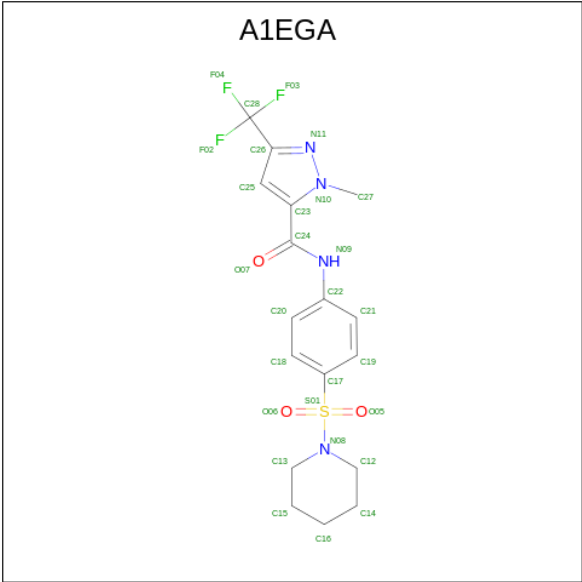
- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	28	Total	C	N	O	S	0	0
			207	129	37	40	1		
2	D	41	Total	C	N	O	S	0	0
			305	188	53	63	1		
2	C	95	Total	C	N	O	S	0	0
			745	476	133	132	4		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is 2-methyl- {N}-(4-piperidin-1-ylsulfonylphenyl)-5-(trifluoromethyl)pyrazole-3-carboxamide (CCD ID: A1EGA) (formula: C₁₇H₁₉F₃N₄O₃S) (labeled as "Ligand of Interest" by depositor).

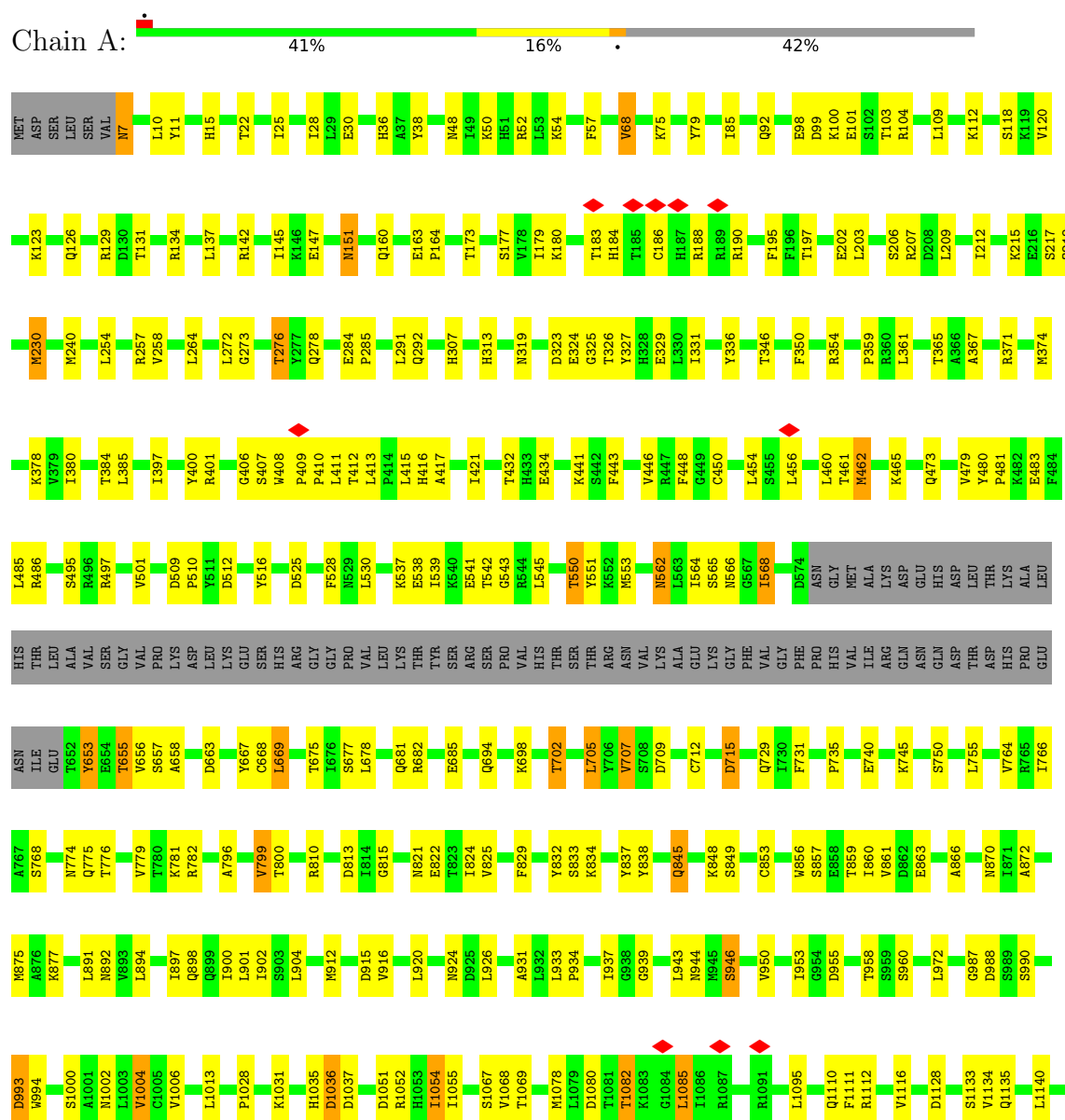


Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	S	
4	A	1	28	17	3	4	3	1	0

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







ASN
ASP
LEU
ALA
LYS
PHE
HIS
GLN
MET
LEU
MET
LYS
ILE
ILE
MET
LYS

● Molecule 2: Phosphoprotein



MET	ALA	LYS	PRO	CYS	GLU	GLN	ALA	ARG	HIS	VAL	ASN	GLY	LEU	CYS	GLY	ALA	ARG	ILE	LYS	GLY	ASP	THR	GLN	ASP	GLY	THR	CYS	LYS	GLU	TYR	HIS	VAL	THR	ASP	GLY	ALA	GLY	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER	LYS	GLY	ILE	GLN	ASP	ALA	ASP	SER	ILE	MET	SER	VAL	GLN	GLY	GLY	ALA	ASP	ILE	THR	ASP	GLY	ASP	GLY	THR	GLN	THR	ALA	SER	PRO	TYR	HIS	VAL	THR	ASP	GLY	ALA	GLY	SER	GLY	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

LYS	GLY	ILE	GLN	ASP	ALA	ASP	SER	ILE	MET	SER	VAL	GLN	GLY	GLY	ALA	ASP	ILE	THR	ASP	GLY	ASP	GLY	THR	GLN	THR	ALA	SER	PRO	TYR	HIS	VAL	THR	ASP	GLY	ALA	GLY	SER	GLY	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ASP	VAL	THR	GLU	THR	GLU	GLY	GLY	GLY	ILE	HIS	VAL	GLN	LEU	LEU	LYS	GLN	SER	ARG	GLY	ASN	VAL	ASP	THR	GLU	ASN	GLY	THR	ALA	ASP	PRO	PHE	ASN	GLY	SER	GLY	THR	LEU	LYS	ASP	GLY	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

THR	GLU	ILE	GLY	ASP	SER	THR	GLY	GLY	ILE	ALA	THR	GLN	CYS	ASP	VAL	ARG	SER	PRO	SER	GLY	PRO	GLY	GLY	ALA	ASN	VAL	THR	GLU	ASN	GLY	THR	ALA	ASP	GLY	THR	LEU	LYS	ASN	VAL	ASP	THR	GLU	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	GLY	GLY	ASP	TYR	TYR	ASP	ASP	GLY	GLY	PHE	THR	SER	ASP	VAL	GLN	GLY	ASP	ILE	THR	GLY	GLY	GLY	ALA	ASN	LYS	ILE	THR	GLU	LEU	ASN	GLY	THR	ALA	ASP	GLY	THR	LEU	LYS	ASN	VAL	ASP	THR	GLU	THR	ASP	GLY	ALA	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER	THR	LEU	GLY	GLY	HIS	LEU	SER	ILE	MET	ILE	ILE	ALA	ILE	PRO	GLY	LEU	GLY	LYS	ASP	PRO	ASN	ASP	THR	ALA	ASP	VAL	GLU	LEU	ASN	GLN	LYS	ASN	P392	D393	L394	K395	P396	I397	D401	S402	G403	R404	E408	K411	LYS	PRO	VAL	ALA	SER	ARG	GLN	THR	ARG	LEU	GLN	GLY	MET	THR	ASN	GLY	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ARG	THR	SER	ARG	GLY	GLN	L433	L434	Q438	L439	K440	G443	K444	K445	V446	S447	V453	A459	S460	V463	I464	I468	K469	S470	S471	R479	M482	T483	D486	D487	M492	K496	F497	H498	G499	M500	L501	M502	K503	K507
-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126133	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.459	Depositor
Minimum map value	-1.151	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.126	Depositor
Map size (Å)	317.99997, 317.99997, 317.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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, A1EGA

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	0.25	0/10470	0.41	0/14193
2	B	0.17	0/208	0.31	0/279
2	C	0.17	0/753	0.39	0/1001
2	D	0.21	0/309	0.54	0/421
All	All	0.24	0/11740	0.41	0/15894

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	10241	0	10251	216	0
2	B	207	0	218	6	0
2	C	745	0	812	16	0
2	D	305	0	305	12	0
3	A	2	0	0	0	0
4	A	28	0	0	0	0
All	All	11528	0	11586	241	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 10.

All (241) 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:284:GLU:HG3	1:A:285:PRO:HD3	1.56	0.86
1:A:257:ARG:NH1	1:A:336:TYR:O	2.10	0.84
1:A:401:ARG:HG3	1:A:406:GLY:HA2	1.62	0.81
1:A:378:LYS:NZ	1:A:815:GLY:O	2.19	0.76
1:A:658:ALA:HB3	1:A:800:THR:HG21	1.66	0.74
1:A:1253:ASP:OD1	1:A:1253:ASP:N	2.12	0.74
1:A:1167:ARG:NH1	1:A:1366:GLU:OE2	2.24	0.70
1:A:441:LYS:NZ	2:B:364:GLU:OE2	2.25	0.70
1:A:1186:ASN:N	1:A:1186:ASN:OD1	2.25	0.70
1:A:1307:VAL:O	1:A:1311:THR:OG1	2.09	0.70
1:A:1180:CYS:SG	1:A:1364:HIS:NE2	2.63	0.69
1:A:768:SER:OG	1:A:775:GLN:NE2	2.25	0.69
1:A:715:ASP:OD1	1:A:729:GLN:NE2	2.25	0.69
1:A:384:THR:HG21	1:A:813:ASP:HB3	1.75	0.68
1:A:653:TYR:O	1:A:782:ARG:NH2	2.28	0.66
1:A:184:HIS:O	1:A:188:ARG:NH2	2.27	0.66
1:A:1002:ASN:OD1	1:A:1145:TRP:NE1	2.20	0.66
1:A:1036:ASP:OD1	1:A:1036:ASP:N	2.30	0.65
1:A:1192:VAL:HG23	1:A:1310:TYR:HB3	1.79	0.65
1:A:79:TYR:OH	1:A:202:GLU:OE2	2.14	0.64
1:A:1031:LYS:O	1:A:1395:ASN:ND2	2.31	0.64
1:A:15:HIS:NE2	1:A:856:TRP:O	2.28	0.64
1:A:833:SER:HB2	1:A:837:TYR:HB2	1.81	0.63
1:A:681:GLN:NE2	1:A:685:GLU:OE2	2.30	0.63
1:A:400:TYR:HE2	1:A:409:PRO:HD2	1.63	0.63
1:A:408:TRP:HB3	1:A:411:LEU:HB2	1.79	0.63
1:A:990:SER:OG	1:A:993:ASP:OD1	2.15	0.63
1:A:147:GLU:OE1	1:A:151:ASN:ND2	2.33	0.62
1:A:416:HIS:CE1	2:D:362:THR:HA	2.35	0.61
1:A:380:ILE:HD11	2:B:372:ILE:HD12	1.81	0.61
1:A:1028:PRO:HA	1:A:1031:LYS:HG2	1.83	0.61
1:A:1173:ARG:NH2	1:A:1174:HIS:O	2.34	0.60
1:A:955:ASP:HB3	1:A:958:THR:HG22	1.84	0.60
1:A:112:LYS:NZ	1:A:924:ASN:OD1	2.34	0.60
1:A:417:ALA:HB1	1:A:421:ILE:HG23	1.82	0.60
1:A:131:THR:HG23	1:A:1163:LEU:HD21	1.84	0.59
2:C:401:ASP:HB2	2:C:404:ARG:HG3	1.84	0.59
1:A:933:LEU:HB3	1:A:939:GLY:HA3	1.85	0.59
1:A:367:ALA:HB2	1:A:707:VAL:HG11	1.85	0.58
1:A:1054:ILE:HG12	1:A:1153:PRO:HG2	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:PHE:HE2	1:A:483:GLU:HG3	1.66	0.58
1:A:1274:LEU:O	1:A:1278:THR:HG23	2.04	0.58
2:B:371:MET:HB2	2:C:397:ILE:HG12	1.84	0.58
1:A:656:VAL:HG23	1:A:796:ALA:HB2	1.86	0.57
1:A:705:LEU:HD11	1:A:735:PRO:HG3	1.86	0.57
2:C:487:ASP:OD1	2:C:487:ASP:N	2.38	0.57
1:A:456:LEU:HD11	1:A:510:PRO:HB2	1.87	0.57
1:A:432:THR:HG23	1:A:434:GLU:H	1.69	0.56
1:A:987:GLY:HA2	1:A:1004:VAL:HG13	1.87	0.56
1:A:123:LYS:HB2	1:A:972:LEU:HD13	1.86	0.56
1:A:371:ARG:NH1	1:A:731:PHE:O	2.38	0.56
1:A:1200:ASP:OD1	1:A:1201:ILE:N	2.35	0.56
1:A:677:SER:OG	2:D:372:ILE:O	2.16	0.55
1:A:101:GLU:HG3	1:A:104:ARG:HH21	1.72	0.54
1:A:1199:ASP:OD1	1:A:1200:ASP:N	2.39	0.54
1:A:273:GLY:O	1:A:276:THR:OG1	2.22	0.54
2:C:492:ASN:O	2:C:496:LYS:HG2	2.07	0.54
1:A:1180:CYS:SG	1:A:1362:HIS:ND1	2.80	0.54
1:A:203:LEU:HD23	1:A:212:ILE:HG12	1.89	0.53
1:A:461:THR:O	1:A:465:LYS:HG2	2.08	0.53
1:A:904:LEU:HD11	1:A:920:LEU:HD13	1.89	0.53
2:C:479:ARG:O	2:C:483:THR:HG23	2.08	0.53
1:A:495:SER:HB2	1:A:501:VAL:HG22	1.91	0.53
1:A:1302:THR:O	1:A:1302:THR:OG1	2.24	0.53
1:A:291:LEU:HD13	1:A:346:THR:HG21	1.90	0.52
1:A:1145:TRP:CE3	1:A:1147:ARG:HB3	2.44	0.52
1:A:11:TYR:HE1	1:A:180:LYS:HE3	1.75	0.52
1:A:1256:TRP:HZ3	1:A:1274:LEU:HD22	1.74	0.52
1:A:1321:VAL:HG12	1:A:1322:ILE:H	1.75	0.52
1:A:142:ARG:HB2	1:A:145:ILE:HG13	1.92	0.51
1:A:397:ILE:HD11	1:A:412:THR:HG23	1.92	0.51
2:C:459:ALA:O	2:C:463:VAL:HG23	2.10	0.51
1:A:1002:ASN:HB3	1:A:1145:TRP:CD1	2.46	0.51
1:A:1067:SER:OG	1:A:1068:VAL:N	2.43	0.51
1:A:1082:THR:HG23	1:A:1085:LEU:H	1.74	0.51
1:A:179:ILE:O	1:A:183:THR:HG23	2.10	0.51
1:A:1270:SER:HB3	1:A:1273:GLU:HG3	1.92	0.51
1:A:454:LEU:HD13	2:D:390:LEU:HD21	1.93	0.51
1:A:542:THR:OG1	1:A:543:GLY:N	2.44	0.51
2:B:364:GLU:HB2	2:D:363:LEU:HG	1.92	0.51
1:A:126:GLN:OE1	1:A:129:ARG:NH2	2.44	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:GLY:O	1:A:329:GLU:HG3	2.11	0.51
1:A:480:TYR:HB2	1:A:485:LEU:HD11	1.93	0.50
1:A:1198:LEU:HD23	1:A:1306:ARG:HD2	1.93	0.50
1:A:206:SER:OG	1:A:207:ARG:N	2.39	0.50
1:A:1145:TRP:CE3	1:A:1148:LEU:HG	2.47	0.49
1:A:1080:ASP:OD1	1:A:1080:ASP:N	2.46	0.49
1:A:292:GLN:NE2	1:A:825:VAL:O	2.45	0.49
1:A:550:THR:HG22	1:A:551:TYR:H	1.77	0.49
1:A:1245:TYR:OH	1:A:1259:ALA:HA	2.13	0.49
2:C:460:SER:O	2:C:464:ILE:HG13	2.11	0.49
1:A:50:LYS:O	1:A:54:LYS:HG2	2.12	0.49
1:A:380:ILE:HG12	2:B:372:ILE:HB	1.95	0.49
1:A:1177:CYS:HB2	1:A:1180:CYS:HB2	1.95	0.49
1:A:821:ASN:HB3	1:A:822:GLU:OE2	2.13	0.49
1:A:79:TYR:HE2	1:A:215:LYS:HA	1.77	0.49
1:A:1282:THR:HG21	1:A:1326:LYS:HD3	1.94	0.49
1:A:900:ILE:HD12	1:A:931:ALA:HB2	1.94	0.48
1:A:934:PRO:HB2	1:A:960:SER:HB3	1.95	0.48
1:A:460:LEU:HG	1:A:1397:LEU:HD11	1.94	0.48
1:A:1173:ARG:NE	1:A:1174:HIS:H	2.11	0.48
1:A:1051:ASP:OD2	1:A:1384:ARG:NH1	2.47	0.48
1:A:1385:LYS:HD2	1:A:1386:LEU:H	1.79	0.48
2:C:483:THR:HA	2:C:486:ASP:OD2	2.13	0.48
1:A:354:ARG:NH1	1:A:537:LYS:O	2.43	0.48
1:A:1266:ARG:O	1:A:1399:TYR:HB2	2.13	0.48
1:A:374:MET:HE3	1:A:669:LEU:HD22	1.96	0.48
2:C:468:ILE:O	2:C:471:SER:OG	2.31	0.48
1:A:916:VAL:O	1:A:920:LEU:HB2	2.14	0.47
1:A:313:HIS:HB2	1:A:327:TYR:CE1	2.50	0.47
1:A:7:ASN:OD1	1:A:7:ASN:N	2.48	0.47
1:A:1245:TYR:CZ	1:A:1262:LEU:HB2	2.50	0.47
1:A:845:GLN:NE2	1:A:848:LYS:HD2	2.30	0.47
1:A:11:TYR:CE1	1:A:180:LYS:HE3	2.49	0.47
1:A:99:ASP:OD1	1:A:100:LYS:N	2.46	0.47
1:A:413:LEU:O	1:A:413:LEU:HD12	2.15	0.47
1:A:779:VAL:HB	1:A:800:THR:HG22	1.97	0.47
1:A:1140:LEU:O	1:A:1144:MET:HB2	2.15	0.47
1:A:1179:ILE:HG23	1:A:1364:HIS:CE1	2.50	0.47
1:A:272:LEU:HD11	1:A:319:ASN:HD22	1.80	0.46
1:A:516:TYR:OH	1:A:525:ASP:OD2	2.24	0.46
1:A:655:THR:HG22	1:A:782:ARG:HE	1.79	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1256:TRP:CZ3	1:A:1274:LEU:HD22	2.49	0.46
1:A:877:LYS:HB2	1:A:877:LYS:HE3	1.64	0.46
1:A:1051:ASP:OD1	1:A:1152:ARG:NH1	2.30	0.46
1:A:950:VAL:HG11	1:A:1162:VAL:HG11	1.97	0.46
1:A:1354:THR:O	1:A:1354:THR:OG1	2.29	0.46
1:A:564:ILE:HG23	1:A:745:LYS:HB2	1.97	0.46
1:A:1343:VAL:HA	1:A:1346:THR:HG22	1.97	0.46
1:A:254:LEU:O	1:A:258:VAL:HG23	2.16	0.46
1:A:1329:THR:HG21	1:A:1333:TYR:H	1.81	0.46
1:A:407:SER:C	1:A:408:TRP:HD1	2.24	0.46
2:D:374:ILE:HG23	2:D:374:ILE:O	2.16	0.46
2:C:393:ASP:O	2:C:394:LEU:HD23	2.16	0.46
1:A:497:ARG:O	1:A:501:VAL:HG23	2.16	0.46
1:A:915:ASP:OD1	1:A:915:ASP:N	2.47	0.46
1:A:810:ARG:HA	1:A:810:ARG:HD3	1.81	0.46
1:A:872:ALA:HB1	1:A:943:LEU:HB2	1.98	0.45
1:A:481:PRO:HB2	1:A:483:GLU:OE2	2.17	0.45
1:A:1052:ARG:O	1:A:1152:ARG:NH1	2.48	0.45
1:A:668:CYS:SG	1:A:740:GLU:HB3	2.57	0.45
1:A:1263:ALA:HB3	1:A:1274:LEU:HD11	1.98	0.45
1:A:1269:VAL:HG22	1:A:1273:GLU:HB2	1.98	0.45
1:A:57:PHE:CE2	1:A:483:GLU:HG3	2.49	0.45
1:A:1283:SER:OG	1:A:1285:ASN:O	2.33	0.45
2:D:371:MET:HA	2:D:374:ILE:HG22	1.98	0.45
1:A:781:LYS:HD2	1:A:782:ARG:N	2.32	0.45
1:A:1268:ASN:HD22	1:A:1403:PRO:HD2	1.82	0.44
1:A:860:ILE:HG13	1:A:861:VAL:HG23	1.99	0.44
1:A:678:LEU:HG	2:D:373:ALA:HB2	1.98	0.44
1:A:25:ILE:H	1:A:25:ILE:HG13	1.60	0.44
1:A:52:ARG:HA	1:A:52:ARG:HD3	1.85	0.44
1:A:190:ARG:NH1	1:A:190:ARG:HA	2.32	0.44
2:D:383:ASP:OD1	2:D:383:ASP:N	2.42	0.44
1:A:473:GLN:HB2	1:A:528:PHE:O	2.17	0.44
1:A:764:VAL:HG11	1:A:799:VAL:HG13	2.00	0.44
1:A:461:THR:HA	1:A:1078:MET:HE3	2.00	0.44
1:A:1197:GLN:NE2	1:A:1201:ILE:HD12	2.32	0.44
1:A:359:PRO:HD2	1:A:538:GLU:O	2.18	0.44
1:A:1035:HIS:HB2	1:A:1037:ASP:OD1	2.17	0.44
1:A:11:TYR:CE2	1:A:861:VAL:HG13	2.53	0.43
2:D:368:SER:O	2:D:372:ILE:HG12	2.18	0.43
1:A:1173:ARG:H	1:A:1173:ARG:HG3	1.38	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:447:SER:OG	2:C:453:VAL:O	2.36	0.43
1:A:151:ASN:OD1	1:A:151:ASN:N	2.48	0.43
1:A:407:SER:C	1:A:409:PRO:HD3	2.43	0.43
1:A:568:ILE:H	1:A:568:ILE:HG13	1.33	0.43
1:A:1135:GLN:OE1	1:A:1135:GLN:N	2.50	0.43
1:A:1252:ASP:OD1	1:A:1379:ARG:HG2	2.19	0.43
1:A:857:SER:HB2	1:A:870:ASN:HB3	2.00	0.43
1:A:565:SER:HB2	1:A:745:LYS:HE2	1.99	0.43
1:A:796:ALA:O	1:A:800:THR:HG23	2.19	0.43
1:A:845:GLN:HE21	1:A:848:LYS:HD2	1.84	0.43
1:A:1054:ILE:HB	1:A:1380:ILE:HG21	2.01	0.43
1:A:1266:ARG:HG2	1:A:1399:TYR:CD2	2.54	0.43
1:A:36:HIS:HD2	1:A:38:TYR:HB2	1.84	0.43
2:C:503:LYS:HB3	2:C:503:LYS:HE2	1.74	0.43
1:A:307:HIS:HB3	1:A:821:ASN:ND2	2.34	0.42
1:A:421:ILE:HD11	1:A:443:PHE:CZ	2.54	0.42
1:A:409:PRO:HB2	1:A:410:PRO:HD3	2.01	0.42
1:A:1258:GLU:HG2	1:A:1386:LEU:HD13	2.00	0.42
1:A:988:ASP:HA	1:A:1145:TRP:HZ2	1.84	0.42
2:B:377:LEU:HD23	2:B:377:LEU:HA	1.86	0.42
1:A:75:LYS:HD2	1:A:195:PHE:CG	2.54	0.42
1:A:894:LEU:O	1:A:898:GLN:HG2	2.20	0.42
1:A:912:MET:HE1	1:A:1111:PHE:CD2	2.55	0.42
1:A:68:VAL:HG11	1:A:209:LEU:HD21	2.01	0.42
1:A:112:LYS:HE3	1:A:901:LEU:HD21	2.01	0.42
1:A:1000:SER:O	1:A:1000:SER:OG	2.28	0.42
1:A:137:LEU:HD11	1:A:1343:VAL:HG23	2.02	0.42
1:A:509:ASP:HB3	1:A:512:ASP:HB2	2.01	0.42
1:A:944:ASN:HD21	1:A:953:ILE:HD13	1.84	0.42
1:A:1274:LEU:HA	1:A:1277:ILE:HG22	2.02	0.42
2:C:411:LYS:HB3	2:C:434:LEU:HB3	2.01	0.42
1:A:755:LEU:HB3	1:A:766:ILE:HD11	2.01	0.42
1:A:1145:TRP:CZ3	1:A:1147:ARG:HB3	2.55	0.42
1:A:1112:ARG:O	1:A:1116:VAL:HG23	2.20	0.42
2:C:395:LYS:HD2	2:C:395:LYS:HA	1.91	0.42
1:A:994:TRP:HZ3	1:A:1145:TRP:CD1	2.38	0.42
1:A:1195:GLY:H	1:A:1354:THR:HG23	1.85	0.42
1:A:1344:LEU:HD23	1:A:1344:LEU:HA	1.93	0.42
1:A:1362:HIS:HB3	1:A:1364:HIS:CE1	2.55	0.41
1:A:278:GLN:NE2	1:A:541:GLU:OE2	2.35	0.41
1:A:1306:ARG:NH2	1:A:1345:GLU:OE2	2.47	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:MET:HE2	1:A:853:CYS:SG	2.60	0.41
1:A:448:PHE:HD2	1:A:682:ARG:HD3	1.84	0.41
1:A:1013:LEU:HD12	1:A:1013:LEU:HA	1.84	0.41
1:A:380:ILE:HD12	1:A:385:LEU:HD22	2.02	0.41
1:A:1002:ASN:HB3	1:A:1145:TRP:HD1	1.84	0.41
2:D:354:ASN:OD1	2:D:354:ASN:N	2.53	0.41
1:A:134:ARG:NH1	1:A:1164:GLU:O	2.52	0.41
1:A:323:ASP:OD1	1:A:324:GLU:N	2.53	0.41
1:A:421:ILE:HD11	1:A:443:PHE:CE2	2.55	0.41
1:A:163:GLU:HB2	1:A:164:PRO:HD3	2.02	0.41
1:A:462:MET:H	1:A:462:MET:HG2	1.49	0.41
1:A:702:THR:O	1:A:702:THR:OG1	2.28	0.41
1:A:781:LYS:HD2	1:A:782:ARG:H	1.86	0.41
1:A:272:LEU:HD12	1:A:272:LEU:HA	1.93	0.41
1:A:663:ASP:HA	1:A:774:ASN:HA	2.02	0.41
1:A:1134:VAL:HG13	1:A:1158:GLU:HB3	2.02	0.41
2:C:469:LYS:HB2	2:C:469:LYS:HE3	1.67	0.41
1:A:230:MET:HE3	1:A:230:MET:HB3	1.73	0.41
1:A:562:ASN:OD1	1:A:566:ASN:ND2	2.53	0.41
1:A:1195:GLY:H	1:A:1354:THR:CG2	2.33	0.41
1:A:397:ILE:HD11	1:A:412:THR:CG2	2.50	0.41
1:A:694:GLN:HG3	1:A:698:LYS:HD2	2.02	0.41
1:A:833:SER:CB	1:A:837:TYR:HB2	2.49	0.41
1:A:946:SER:HB2	1:A:953:ILE:HG22	2.02	0.41
2:D:352:GLN:HA	2:D:355:ARG:NH2	2.36	0.41
2:D:366:HIS:O	2:D:370:ILE:HB	2.20	0.41
1:A:75:LYS:O	1:A:75:LYS:HG3	2.21	0.41
1:A:48:ASN:OD1	1:A:486:ARG:NH1	2.53	0.40
1:A:30:GLU:HG2	1:A:36:HIS:CE1	2.57	0.40
1:A:829:PHE:HB3	1:A:838:TYR:CD2	2.56	0.40
1:A:1315:ASN:HB2	1:A:1333:TYR:OH	2.21	0.40
1:A:715:ASP:OD1	1:A:715:ASP:N	2.32	0.40
1:A:1398:ILE:HD13	1:A:1398:ILE:HA	1.85	0.40
2:C:498:HIS:NE2	2:C:502:MET:SD	2.95	0.40
1:A:859:THR:OG1	1:A:860:ILE:N	2.55	0.40
1:A:863:GLU:HG3	1:A:866:ALA:HB3	2.02	0.40
1:A:1162:VAL:HG22	1:A:1339:LEU:HD22	2.04	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	1267/2183 (58%)	1179 (93%)	88 (7%)	0	100	100
2	B	26/507 (5%)	25 (96%)	1 (4%)	0	100	100
2	C	91/507 (18%)	84 (92%)	7 (8%)	0	100	100
2	D	39/507 (8%)	33 (85%)	6 (15%)	0	100	100
All	All	1423/3704 (38%)	1321 (93%)	102 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	1137/1945 (58%)	1033 (91%)	104 (9%)	7	27
2	B	24/416 (6%)	21 (88%)	3 (12%)	3	16
2	C	83/416 (20%)	78 (94%)	5 (6%)	16	42
2	D	36/416 (9%)	30 (83%)	6 (17%)	2	8
All	All	1280/3193 (40%)	1162 (91%)	118 (9%)	10	26

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	10	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	22	THR
1	A	28	ILE
1	A	68	VAL
1	A	85	ILE
1	A	92	GLN
1	A	98	GLU
1	A	103	THR
1	A	109	LEU
1	A	118	SER
1	A	120	VAL
1	A	151	ASN
1	A	160	GLN
1	A	173	THR
1	A	177	SER
1	A	186	CYS
1	A	197	THR
1	A	217	SER
1	A	218	GLN
1	A	230	MET
1	A	264	LEU
1	A	276	THR
1	A	326	THR
1	A	331	ILE
1	A	350	PHE
1	A	361	LEU
1	A	365	THR
1	A	415	LEU
1	A	446	VAL
1	A	450	CYS
1	A	462	MET
1	A	479	VAL
1	A	530	LEU
1	A	539	ILE
1	A	545	LEU
1	A	550	THR
1	A	553	MET
1	A	562	ASN
1	A	568	ILE
1	A	653	TYR
1	A	655	THR
1	A	657	SER
1	A	667	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	669	LEU
1	A	675	THR
1	A	702	THR
1	A	705	LEU
1	A	707	VAL
1	A	709	ASP
1	A	712	CYS
1	A	715	ASP
1	A	750	SER
1	A	776	THR
1	A	799	VAL
1	A	824	ILE
1	A	832	TYR
1	A	834	LYS
1	A	845	GLN
1	A	849	SER
1	A	875	MET
1	A	891	LEU
1	A	892	ASN
1	A	897	ILE
1	A	902	ILE
1	A	926	LEU
1	A	937	ILE
1	A	946	SER
1	A	993	ASP
1	A	1004	VAL
1	A	1006	VAL
1	A	1036	ASP
1	A	1054	ILE
1	A	1055	ILE
1	A	1069	THR
1	A	1082	THR
1	A	1085	LEU
1	A	1095	LEU
1	A	1110	GLN
1	A	1128	ASP
1	A	1133	SER
1	A	1159	VAL
1	A	1163	LEU
1	A	1164	GLU
1	A	1173	ARG
1	A	1177	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1186	ASN
1	A	1233	ARG
1	A	1240	ARG
1	A	1241	ILE
1	A	1243	THR
1	A	1253	ASP
1	A	1269	VAL
1	A	1273	GLU
1	A	1280	ILE
1	A	1313	ILE
1	A	1321	VAL
1	A	1332	ILE
1	A	1343	VAL
1	A	1354	THR
1	A	1359	THR
1	A	1365	VAL
1	A	1372	ILE
1	A	1375	ILE
2	B	355	ARG
2	B	363	LEU
2	B	377	LEU
2	D	353	ILE
2	D	356	GLN
2	D	357	ASN
2	D	368	SER
2	D	370	ILE
2	D	390	LEU
2	C	397	ILE
2	C	408	GLU
2	C	438	GLN
2	C	453	VAL
2	C	482	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	36	HIS
1	A	91	ASN
1	A	114	ASN
1	A	218	GLN
1	A	376	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	425	GLN
1	A	473	GLN
1	A	697	HIS
1	A	775	GLN
1	A	816	HIS
1	A	817	HIS
1	A	821	ASN
1	A	845	GLN
1	A	899	GLN
1	A	1257	ASN
1	A	1268	ASN
1	A	1317	ASN
1	A	1395	ASN
1	A	1401	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	A1EGA	A	2203	-	29,30,30	4.19	16 (55%)	40,45,45	3.23	15 (37%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1EGA	A	2203	-	-	9/23/34/34	0/3/3/3

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2203	A1EGA	C19-C17	8.71	1.52	1.38
4	A	2203	A1EGA	C18-C17	8.28	1.51	1.38
4	A	2203	A1EGA	C21-C22	8.00	1.52	1.39
4	A	2203	A1EGA	C20-C22	7.73	1.52	1.39
4	A	2203	A1EGA	C19-C21	7.46	1.52	1.38
4	A	2203	A1EGA	C18-C20	7.41	1.52	1.38
4	A	2203	A1EGA	S01-N08	4.84	1.70	1.63
4	A	2203	A1EGA	C13-N08	4.43	1.52	1.47
4	A	2203	A1EGA	C12-N08	4.32	1.52	1.47
4	A	2203	A1EGA	C25-C26	-3.41	1.35	1.39
4	A	2203	A1EGA	C24-N09	3.13	1.44	1.35
4	A	2203	A1EGA	C25-C23	-2.57	1.35	1.39
4	A	2203	A1EGA	O07-C24	-2.50	1.18	1.23
4	A	2203	A1EGA	C17-S01	2.47	1.79	1.76
4	A	2203	A1EGA	O05-S01	2.41	1.46	1.43
4	A	2203	A1EGA	O06-S01	2.37	1.46	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2203	A1EGA	O06-S01-O05	-10.48	102.54	119.52
4	A	2203	A1EGA	C28-C26-N11	7.44	128.47	119.72
4	A	2203	A1EGA	O05-S01-N08	6.85	112.93	106.69
4	A	2203	A1EGA	C22-N09-C24	-6.13	110.65	126.58
4	A	2203	A1EGA	O06-S01-N08	5.99	112.15	106.69
4	A	2203	A1EGA	C26-N11-N10	4.67	107.87	104.37
4	A	2203	A1EGA	C25-C26-C28	-4.34	123.30	127.93
4	A	2203	A1EGA	O06-S01-C17	3.58	112.58	108.05
4	A	2203	A1EGA	C13-N08-S01	3.33	123.09	117.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2203	A1EGA	C12-N08-S01	3.21	122.88	117.05
4	A	2203	A1EGA	O07-C24-N09	-2.86	117.17	123.71
4	A	2203	A1EGA	C25-C23-C24	-2.60	120.44	128.55
4	A	2203	A1EGA	F02-C28-C26	-2.40	108.36	112.47
4	A	2203	A1EGA	C25-C26-N11	-2.19	108.23	111.41
4	A	2203	A1EGA	C18-C17-S01	-2.18	117.46	119.76

There are no chirality outliers.

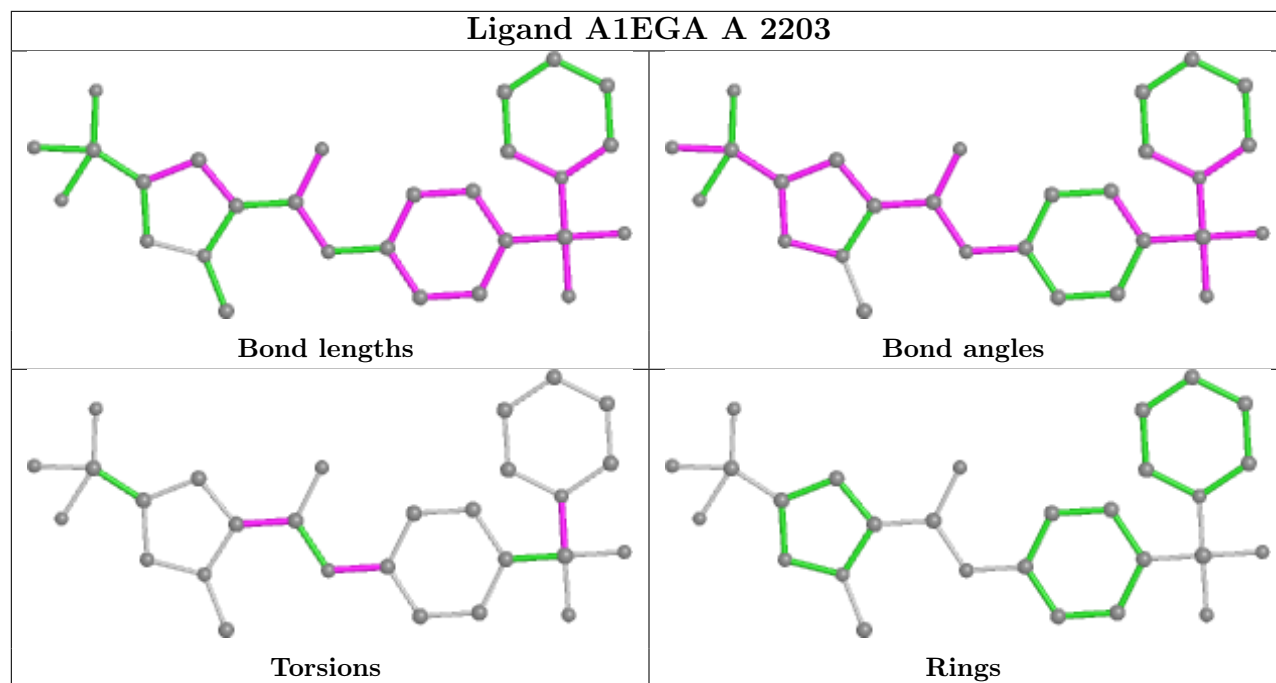
All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2203	A1EGA	C12-N08-S01-O05
4	A	2203	A1EGA	C13-N08-S01-O06
4	A	2203	A1EGA	C12-N08-S01-C17
4	A	2203	A1EGA	C20-C22-N09-C24
4	A	2203	A1EGA	C21-C22-N09-C24
4	A	2203	A1EGA	C12-N08-S01-O06
4	A	2203	A1EGA	C13-N08-S01-C17
4	A	2203	A1EGA	C13-N08-S01-O05
4	A	2203	A1EGA	C25-C23-C24-O07

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

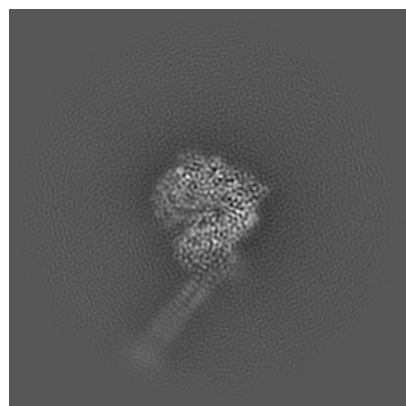
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62463. These allow visual inspection of the internal detail of the map and identification of artifacts.

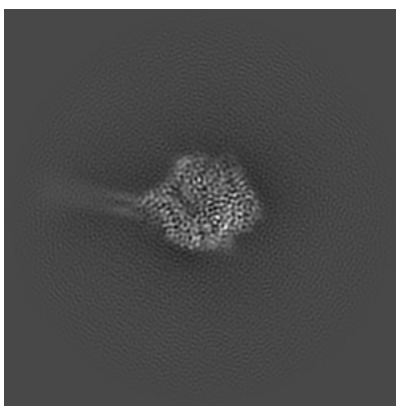
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

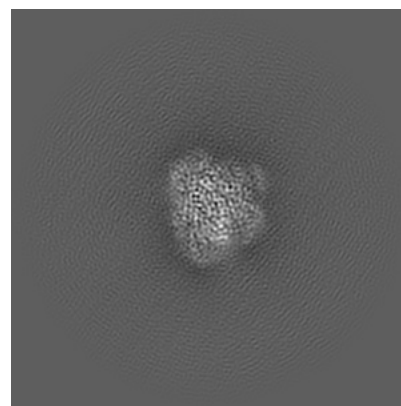
6.1.1 Primary map



X

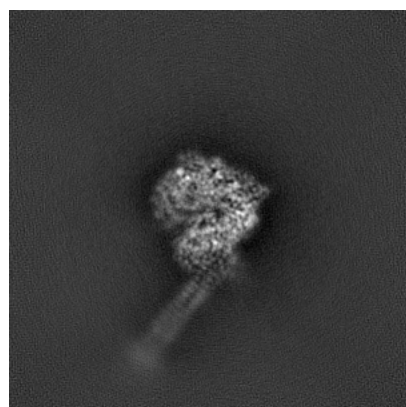


Y

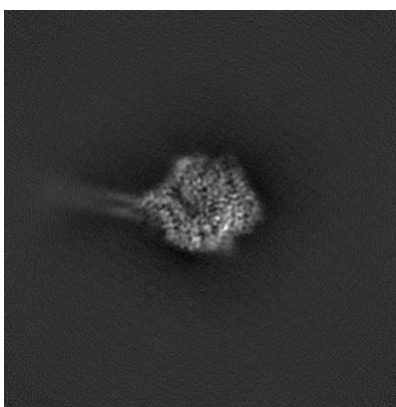


Z

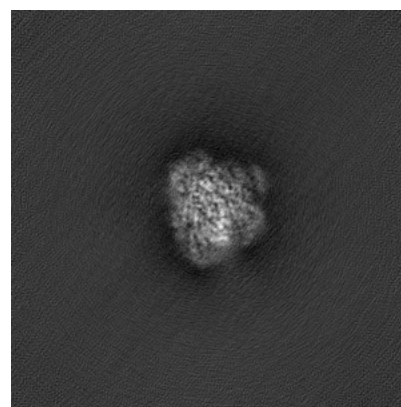
6.1.2 Raw map



X



Y

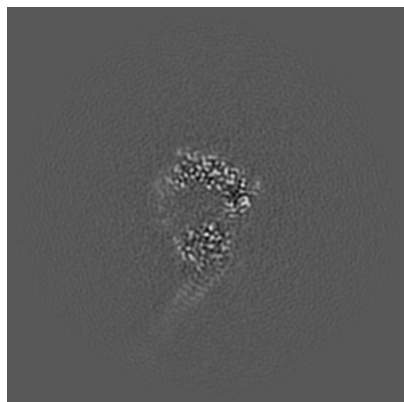


Z

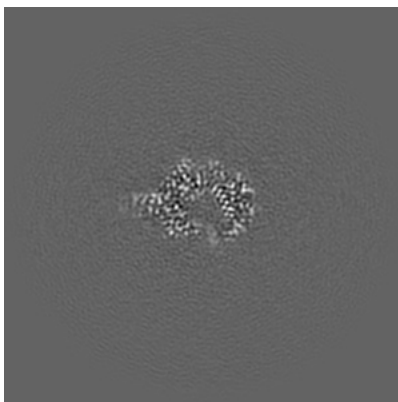
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

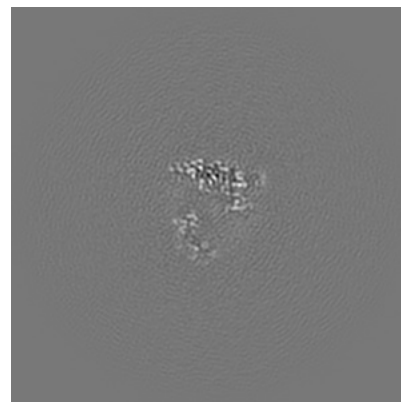
6.2.1 Primary map



X Index: 150

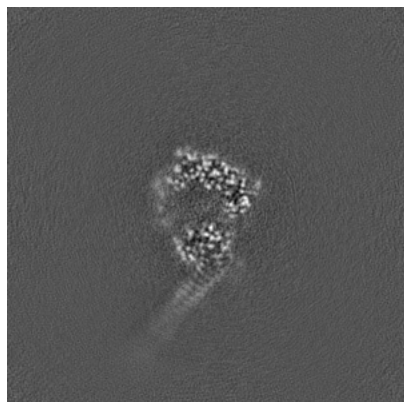


Y Index: 150

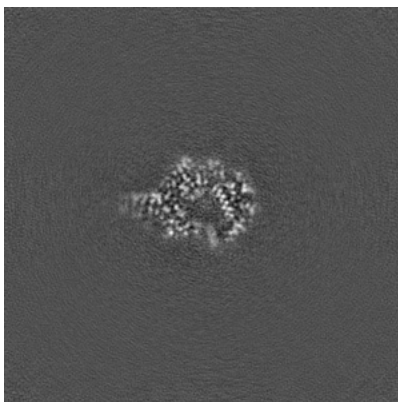


Z Index: 150

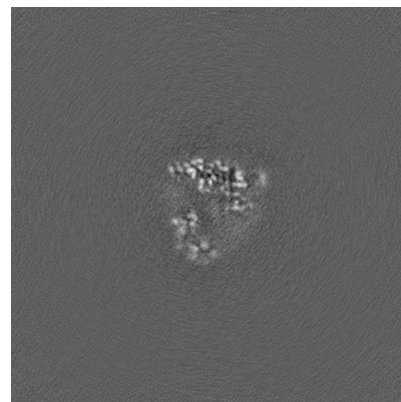
6.2.2 Raw map



X Index: 150



Y Index: 150

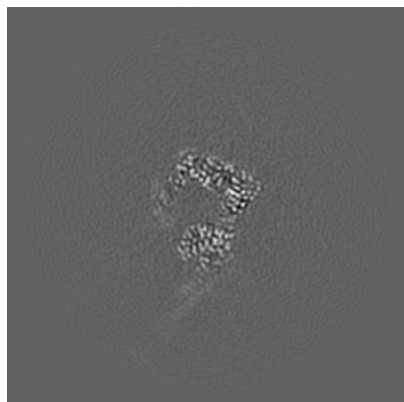


Z Index: 150

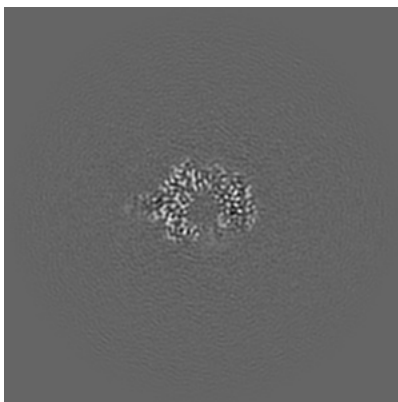
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

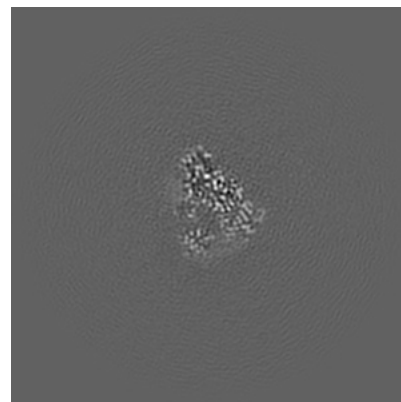
6.3.1 Primary map



X Index: 148



Y Index: 153

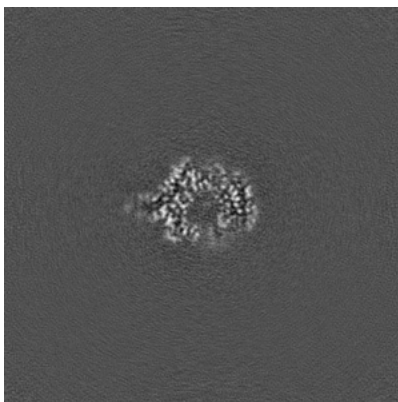


Z Index: 163

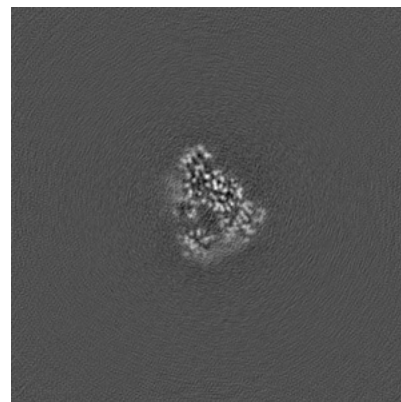
6.3.2 Raw map



X Index: 148



Y Index: 153

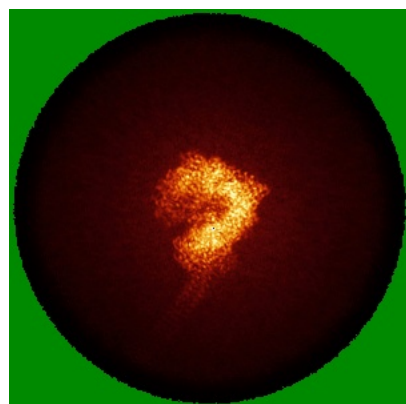


Z Index: 163

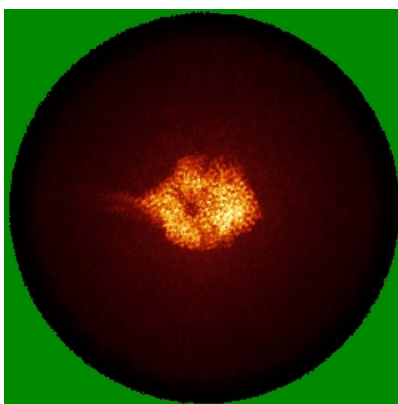
The images above show the largest variance slices of the map in three orthogonal directions.

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

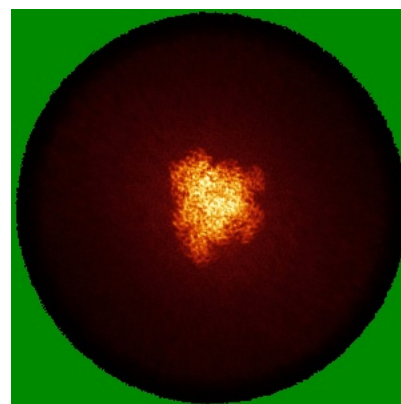
6.4.1 Primary map



X

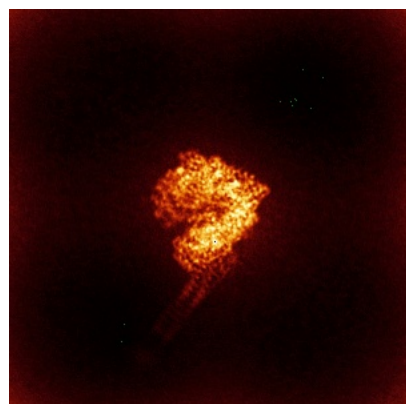


Y

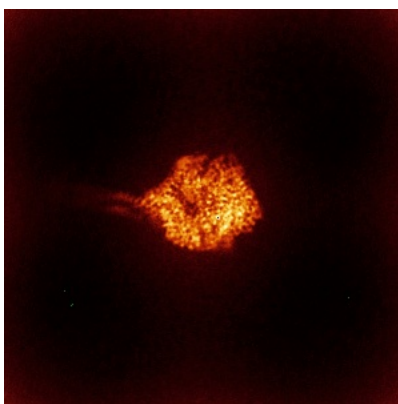


Z

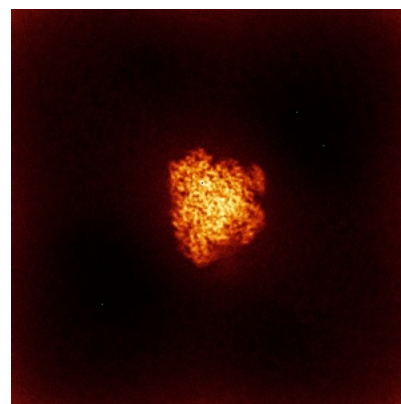
6.4.2 Raw map



X



Y

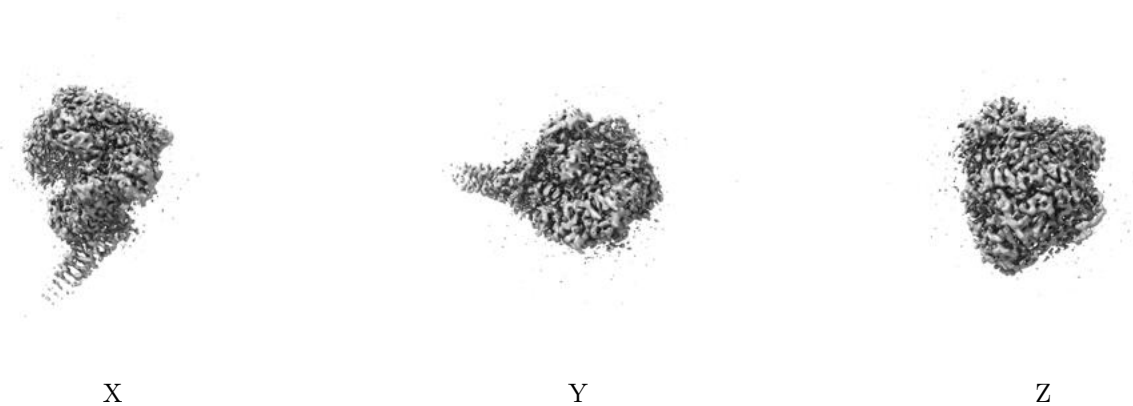


Z

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.

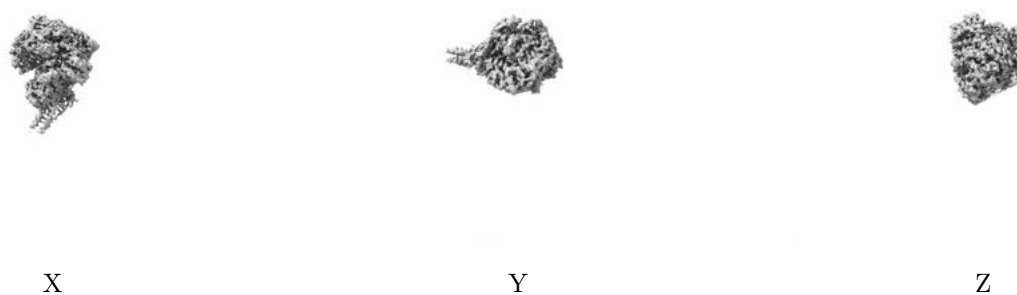
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.126. 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.

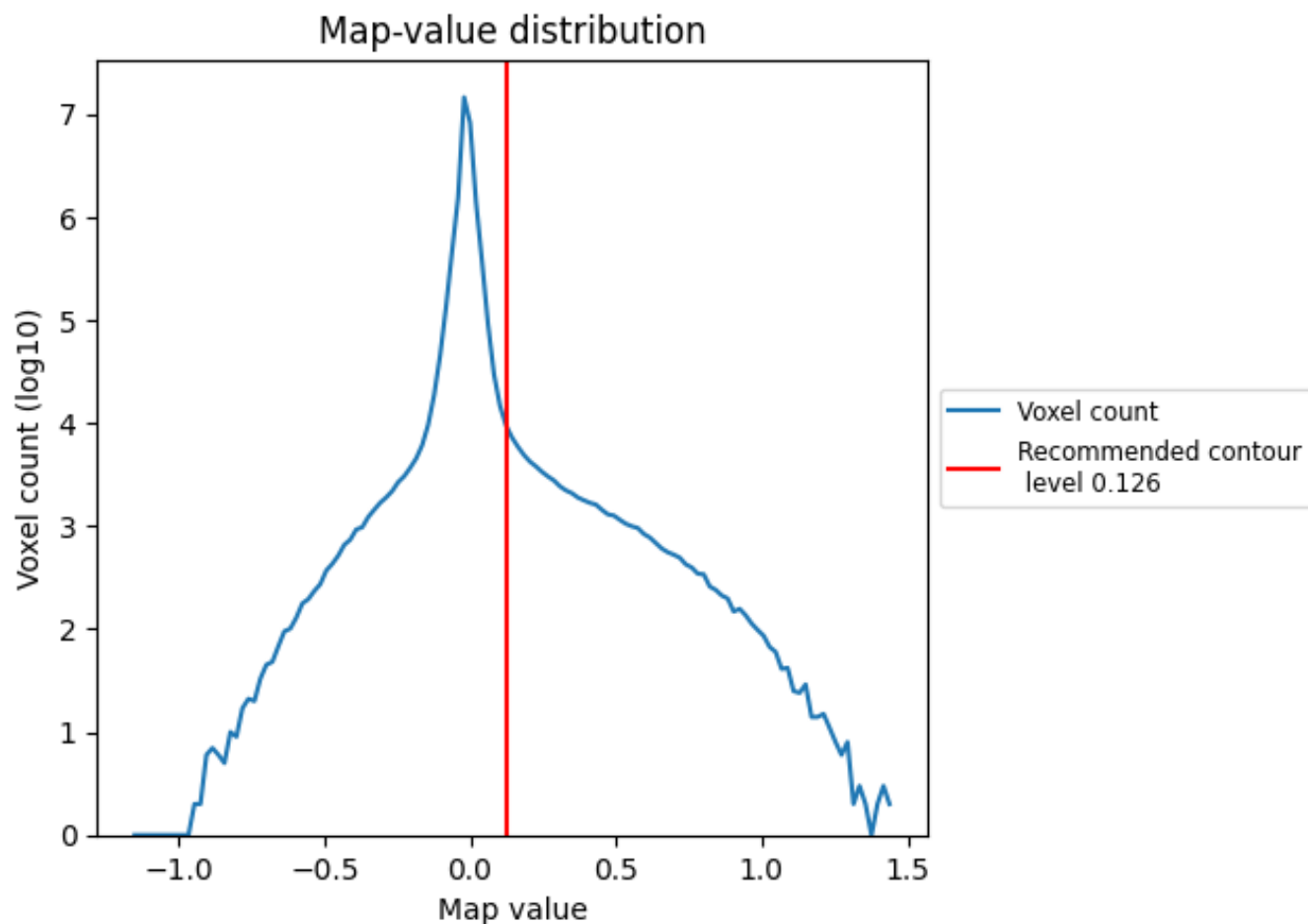
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

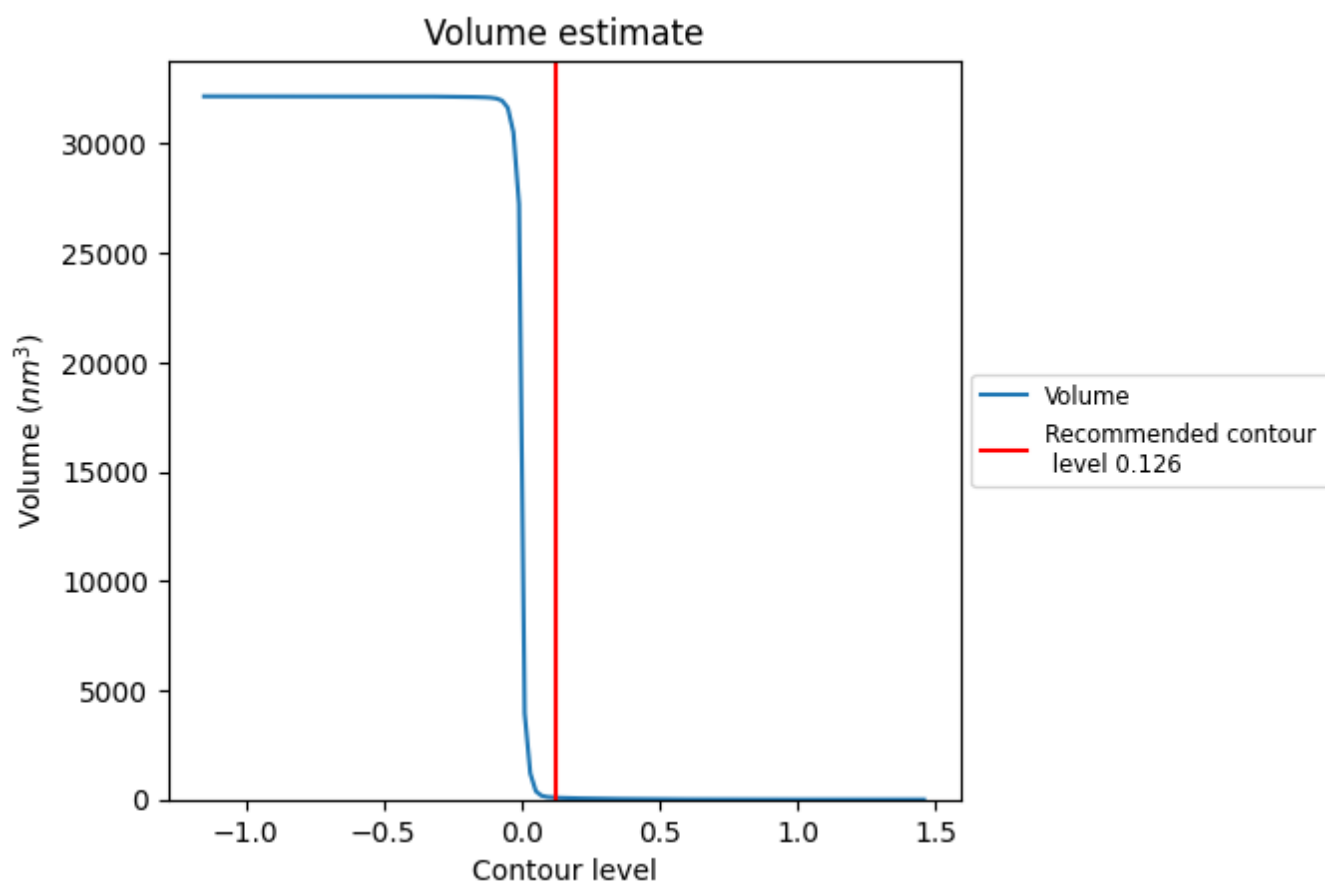
This section contains the results of statistical analysis of the map.

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.

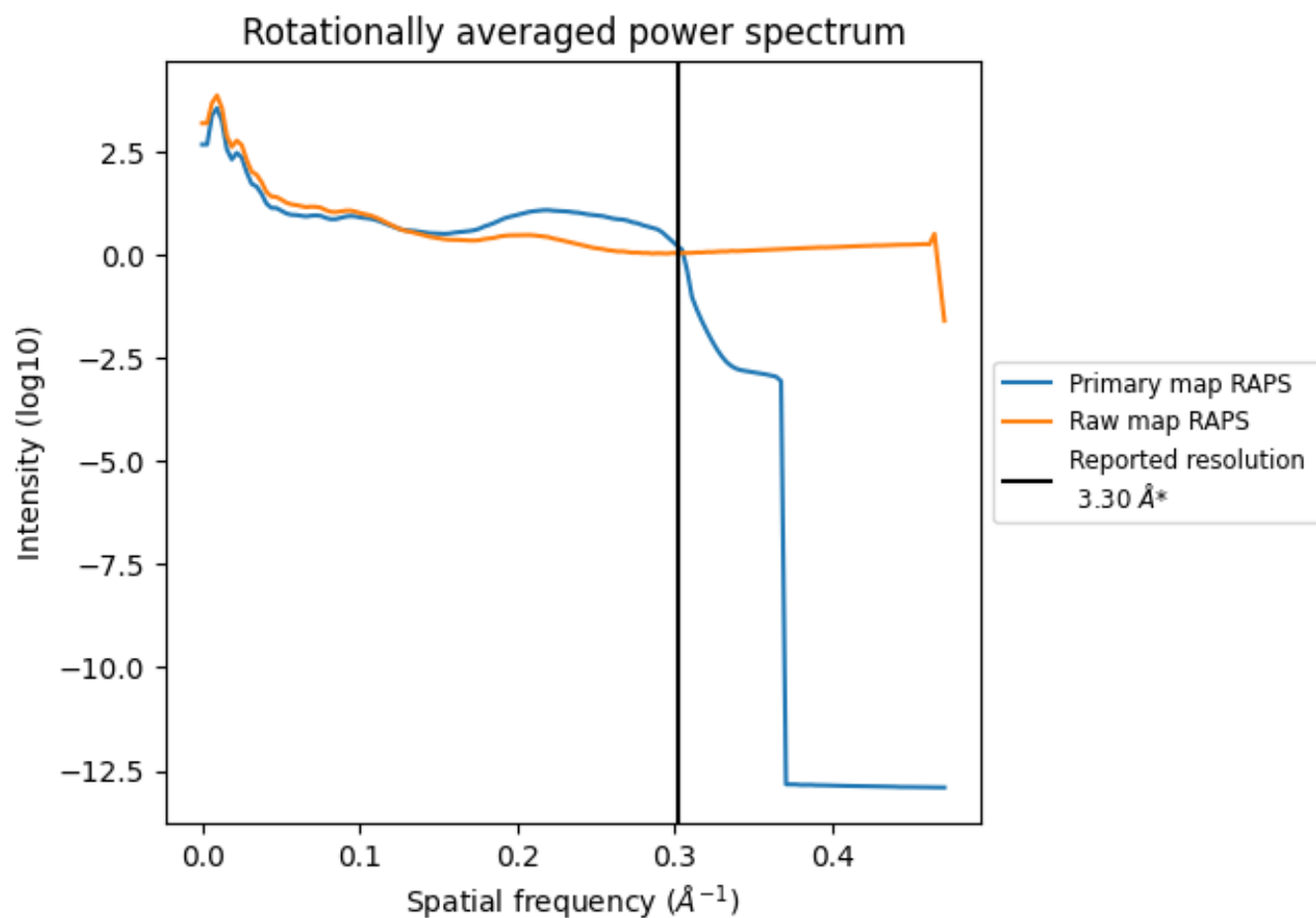
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 88 nm³; this corresponds to an approximate mass of 79 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 ⓘ

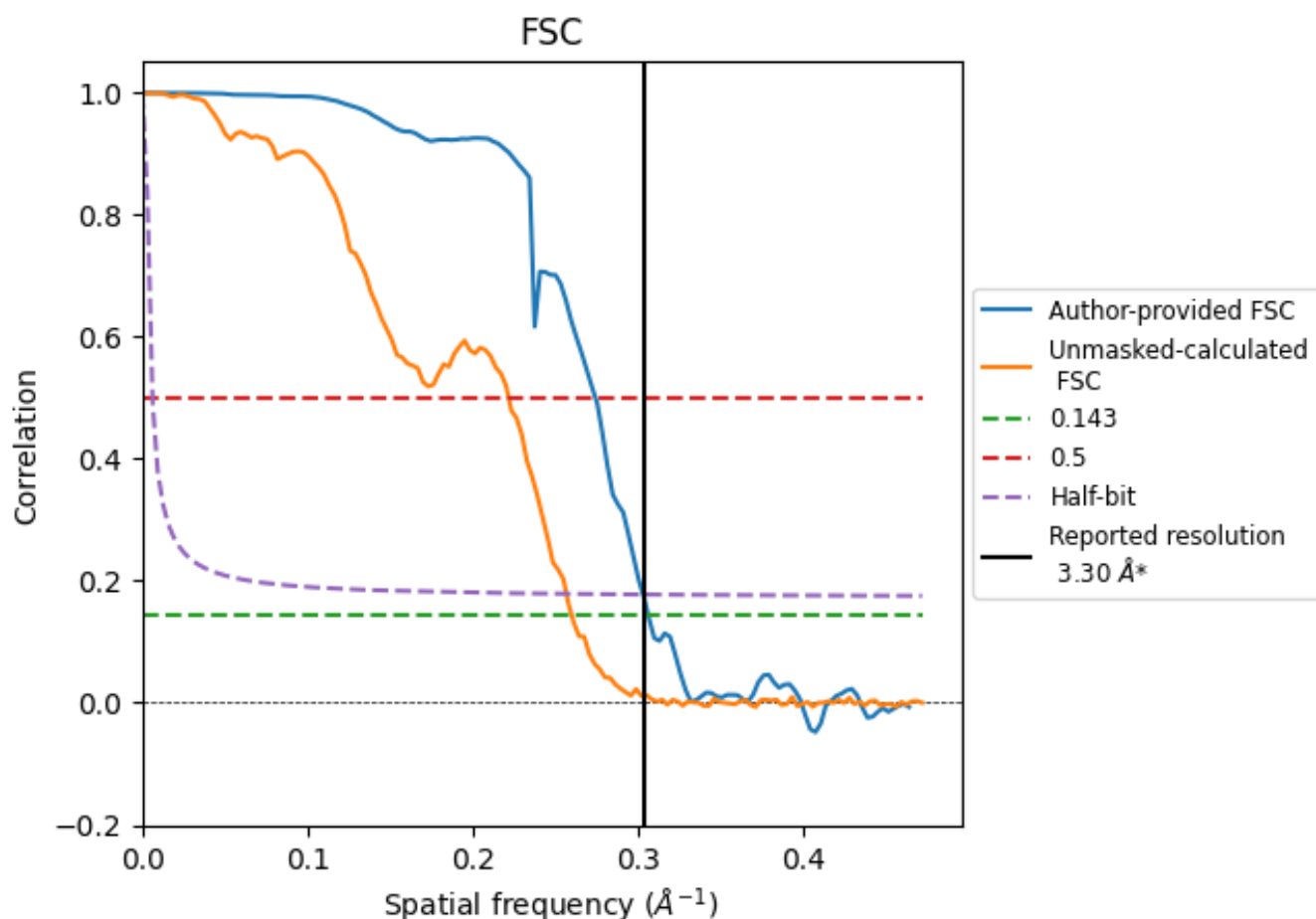


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

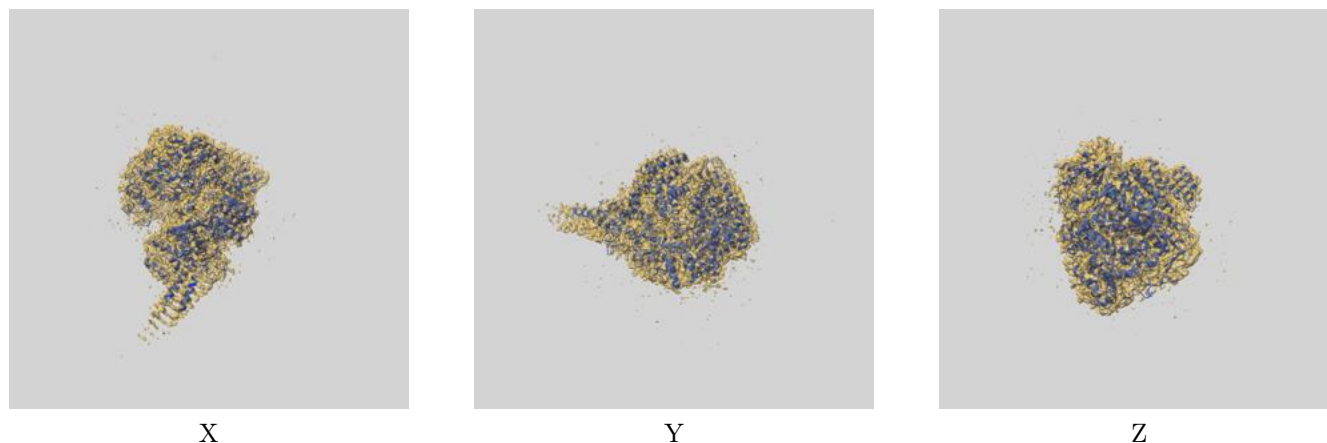
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.27	3.65	3.30
Unmasked-calculated*	3.85	4.51	3.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.85 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

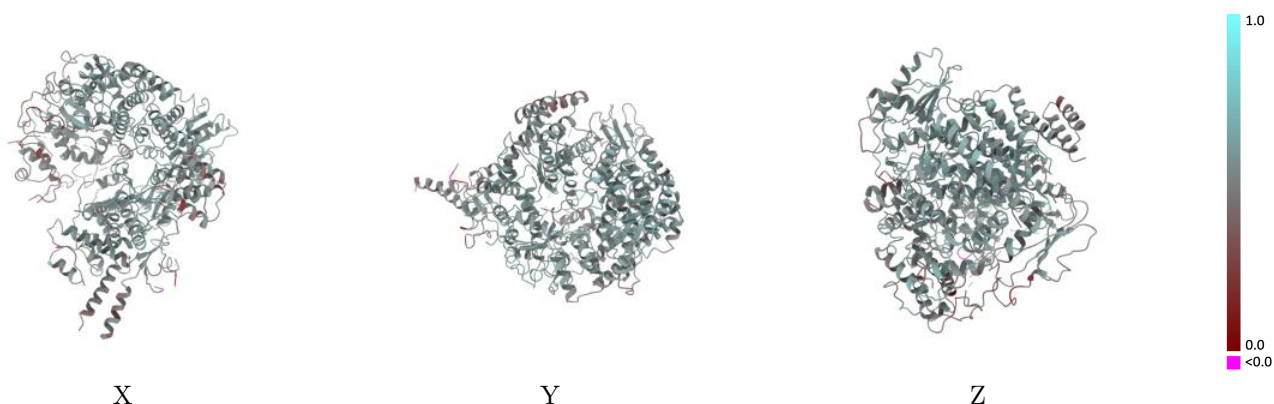
This section contains information regarding the fit between EMDB map EMD-62463 and PDB model 9KNV. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



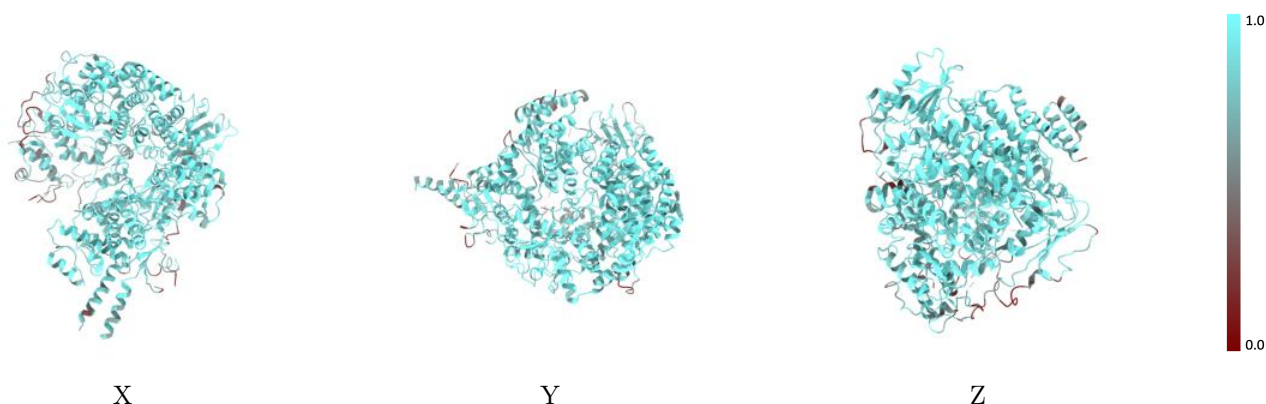
The images above show the 3D surface view of the map at the recommended contour level 0.126 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



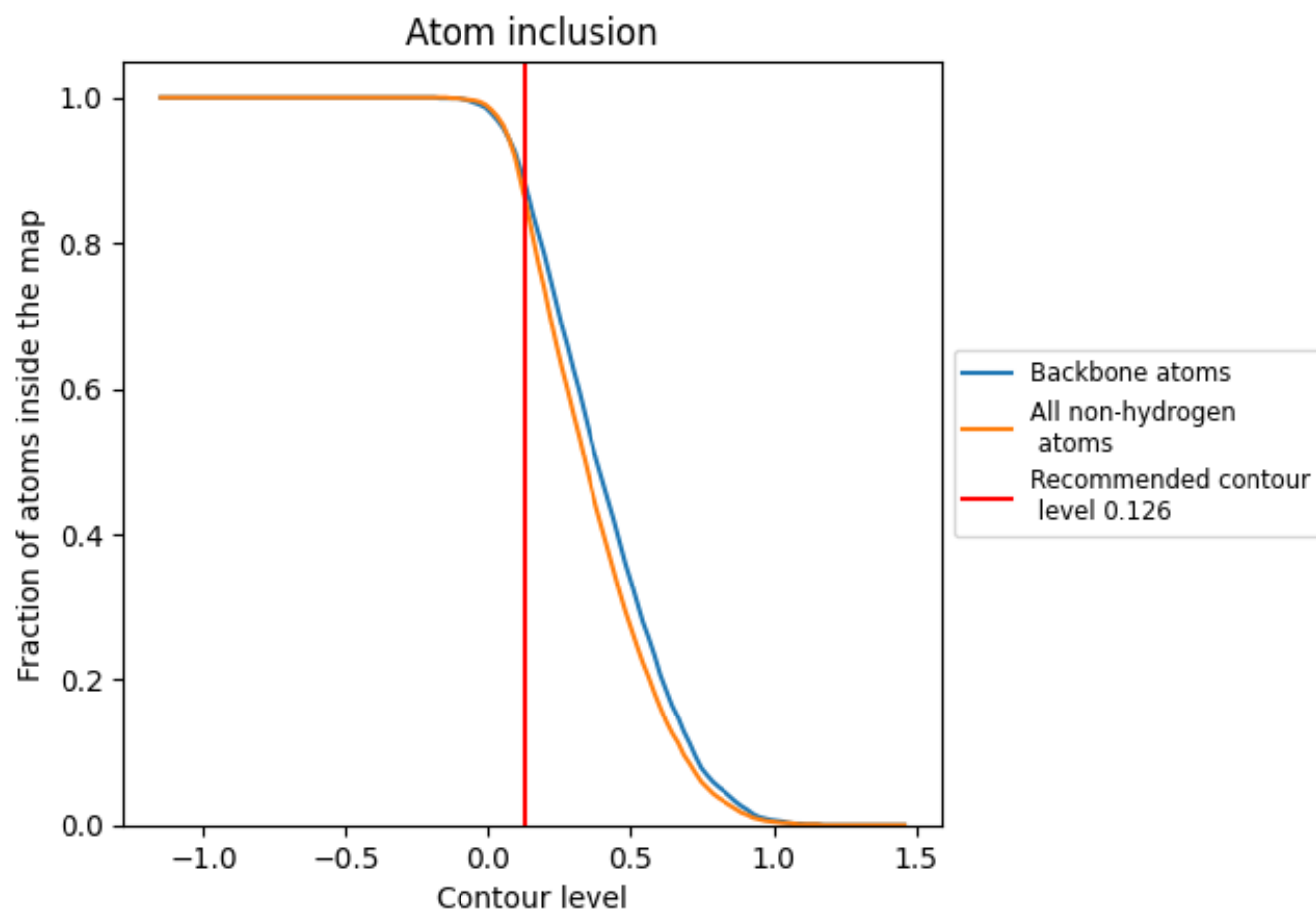
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.126).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% 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 (0.126) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8630	<div></div> 0.5240
A	<div></div> 0.8790	<div></div> 0.5310
B	<div></div> 0.7800	<div></div> 0.4950
C	<div></div> 0.7300	<div></div> 0.4640
D	<div></div> 0.6960	<div></div> 0.4550

