



Full wwPDB EM Validation Report ⓘ

Jul 20, 2025 – 12:15 AM JST

PDB ID : 9J7L / pdb_00009j7l
EMDB ID : EMD-61206
Title : Structure of AAV8 capsid in complex with receptor
Authors : Xu, H.; Wang, G.P.; Su, X.D.
Deposited on : 2024-08-19
Resolution : 2.89 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
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

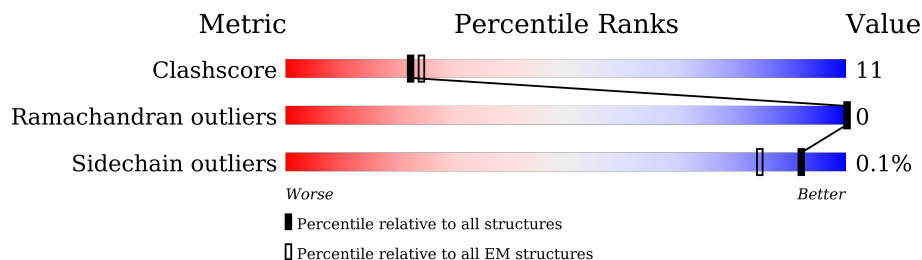
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	5	738	 9% . 88%
1	6	738	 40% 16% 44%
1	7	738	 36% 12% 53%
1	c	738	 12% 5% 83%
1	o	738	 47% 18% 35%
1	p	738	 18% 5% 77%
2	A	470	 6% 52% 21% 27%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15720 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	88	Total	C	N	O	S	0	0
			681	423	119	136	3		
1	6	410	Total	C	N	O	S	0	0
			3336	2129	566	629	12		
1	7	347	Total	C	N	O	S	0	0
			2769	1768	472	519	10		
1	c	126	Total	C	N	O	S	0	0
			986	610	168	203	5		
1	o	481	Total	C	N	O	S	0	0
			3861	2449	664	735	13		
1	p	171	Total	C	N	O	S	0	0
			1352	862	239	246	5		

- Molecule 2 is a protein called Carboxypeptidase D.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	345	Total	C	N	O	S	0	0
			2735	1729	482	516	8		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	494	HIS	-	expression tag	UNP O75976
A	495	HIS	-	expression tag	UNP O75976
A	496	HIS	-	expression tag	UNP O75976
A	497	HIS	-	expression tag	UNP O75976
A	498	HIS	-	expression tag	UNP O75976
A	499	HIS	-	expression tag	UNP O75976
A	500	HIS	-	expression tag	UNP O75976
A	501	HIS	-	expression tag	UNP O75976

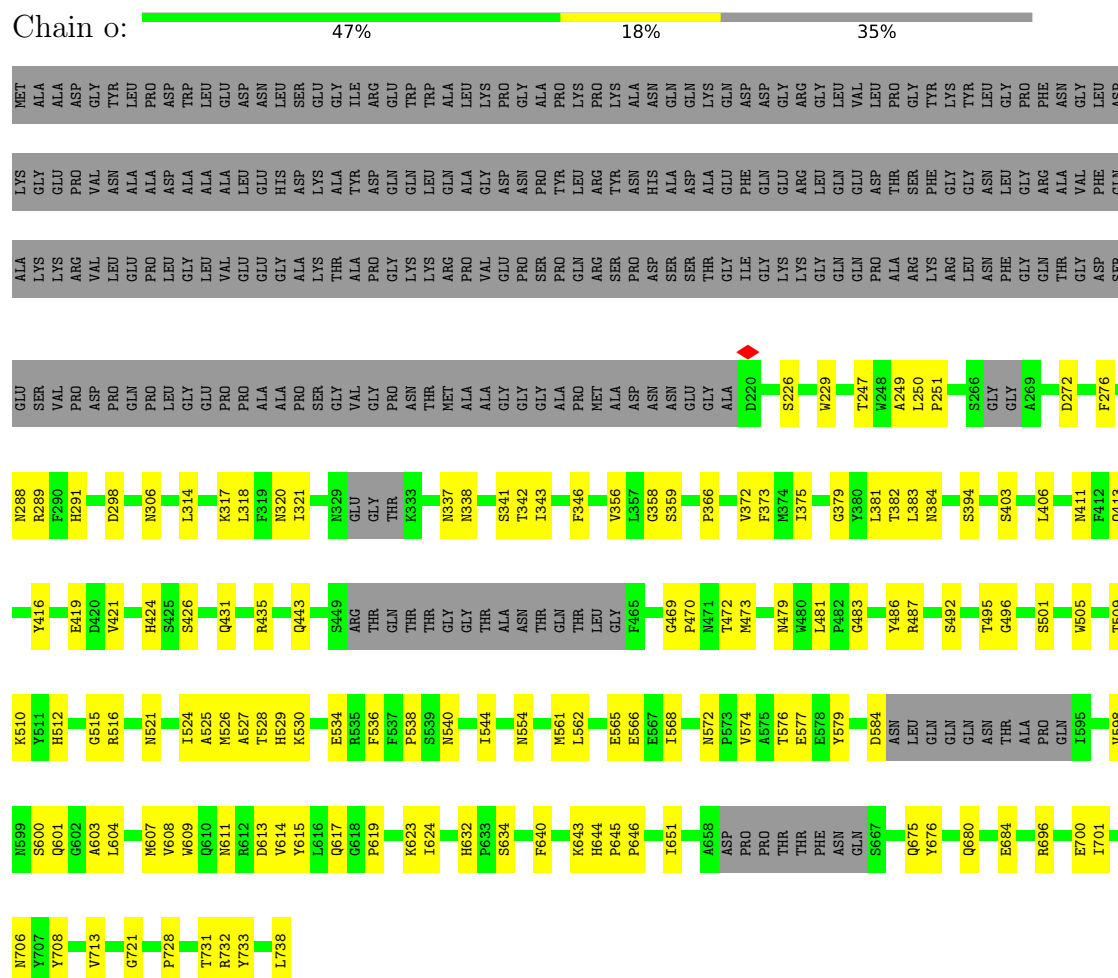
[illegible]

- Molecule 1: Capsid protein

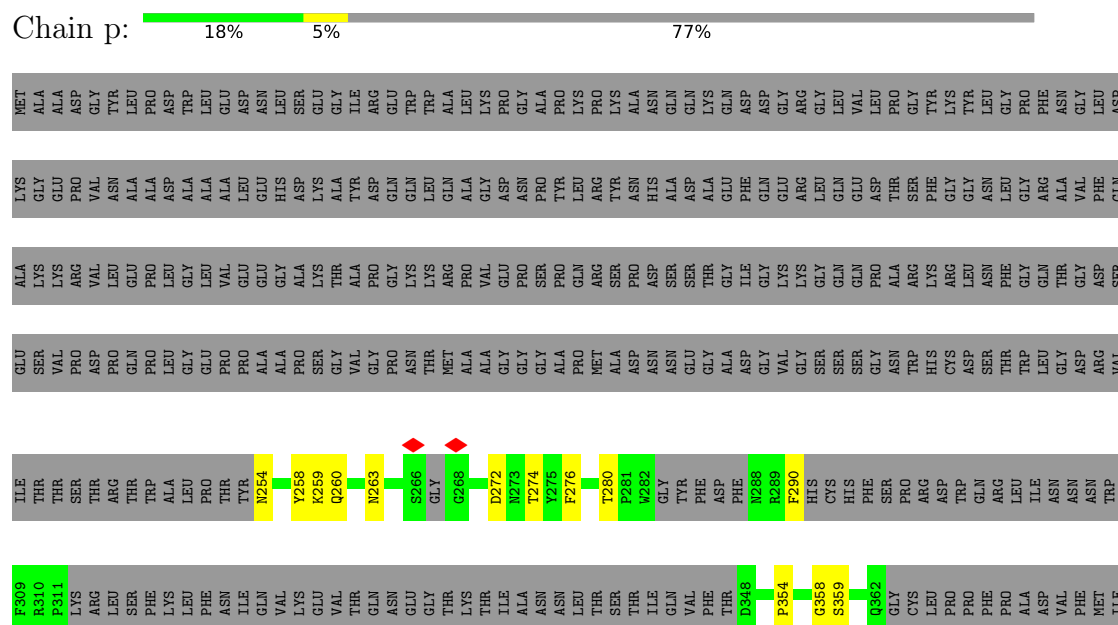
Chain 7: 36% 12% 53%

E326	IIE	GLU	ALA	LYS	MET
Q328	THR	SER	LYS	GLY	ALA
ASN	S244	PRO	ARG	PRO	ASP
GLU		ASP	VAL	VAL	GLY
T332	T247	PRO	LEU	ASN	TYR
N337	N254	GLN	GLU	ALA	LEU
N338		PRO	PRO	ALA	PRO
N339	Y258	LEU	LEU	ASP	ASP
K259	K259	GLY	GLY	ALA	TRP
		GLU	LEU	ALA	LEU
T342		PRO	VAL	ALA	GLU
I343	N263	PRO	GLU	LEU	ASP
F346		ALA	GLU	ASN	ASN
T347	S266	ALA	GLY	HIS	LEU
D348	GLY	PRO	ALA	SER	SER
	A269	SER	LYS	GLY	GLY
L353		GLY	THR	ALA	ILE
P354	D272	VAL	PRO	ASP	ARG
V355	M273	GLY	GLY	GLN	ARG
V356	T274	ASN	LYS	GLN	TRP
L357	Y275	THR	LYS	LEU	TRP
G358		MET	LEU	GLN	ALA
S359	T280	ALA	ARG	ALA	LEU
A360	P281	ALA	VAL	LYS	ALA
H361	W282	GLY	VAL	GLY	PRO
		GLY	PRO	ASN	GLY
P366	N288	GLY	SER	PRO	ALA
		ALA	PRO	TYR	PRO
V372	H291	PRO	GLN	LEU	LYS
F373	C292	MET	ARG	ARG	PRO
	HIS	ALA	SER	TYR	LYS
Y378	PHE	ASP	PRO	ASN	ALA
	SER	ASN	ASP	HIS	ASN
L381	PRO	ASN	SER	ALA	GLN
T382	PRO	GLU	SER	ASP	GLM
L383	ASP	GLY	THR	ALA	GLN
	TRP	ALA	GLY	ALA	LYS
		ASP	ILE	PHE	GLN
S394	GLN	ASP	GLY	ASP	ASP
	ARG	GLY	ILE	GLN	GLY
E399	LEU	VAL	LYS	GLY	GLY
Y400	ILE	GLY	LYS	ARG	ARG
S403	ASN	SER	GLY	LEU	GLY
Q404	ASN	SER	GLN	GLU	LEU
M405	ASN	SER	GLN	GLU	VAL
L406	GLY	GLY	PRO	ASP	LEU
R407	TRP	ASN	ALA	THR	PRO
	GLY	TRP	ARG	SER	GLY
	F309	HIS	LYS	PHE	TYR
	R310	CYS	ARG	GLY	LYS
	P311	ASP	LEU	GLY	TYR
F412	K312	SER	ASN	ASN	TYR
		THR	PHE	LEU	GLY
Y416	L318	THR	THR	GLY	GLY
	F319	TRP	GLY	ARG	PRO
E419	N320	LEU	GLN	PHI	PHI
H424	I321	GLY	THR	ALA	ASN
S425	Q322	ASP	GLY	VAL	GLY
	V323	ARG	ASP	PHE	ASP
SER	Z324	VAL	SER	GLN	LEU

- Molecule 1: Capsid protein



- Molecule 1: Capsid protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43040	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.103	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size (\AA)	205.44, 205.44, 205.44	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	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	5	0.17	0/693	0.29	0/941
1	6	0.18	0/3439	0.27	0/4679
1	7	0.18	0/2847	0.30	0/3870
1	c	0.18	0/1006	0.32	0/1369
1	o	0.19	0/3975	0.28	0/5413
1	p	0.17	0/1388	0.28	0/1873
2	A	0.13	0/2794	0.31	0/3781
All	All	0.17	0/16142	0.29	0/21926

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	5	681	0	641	17	0
1	6	3336	0	3102	91	0
1	7	2769	0	2615	72	0
1	c	986	0	916	31	0
1	o	3861	0	3635	104	0
1	p	1352	0	1251	31	0
2	A	2735	0	2643	67	0
All	All	15720	0	14803	343	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (343) 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:A:92:ARG:NH1	2:A:185:ASP:OD1	2.16	0.79
1:6:232:ASP:H	1:6:243:THR:HG23	1.47	0.79
1:7:405:MET:SD	1:o:320:ASN:ND2	2.56	0.78
1:5:483:GLY:HA3	1:5:609:TRP:HB3	1.69	0.73
1:6:479:ASN:ND2	1:7:358:GLY:O	2.22	0.73
1:o:250:LEU:HB2	1:o:375:ILE:HD12	1.69	0.72
1:o:700:GLU:N	1:o:700:GLU:OE1	2.24	0.71
2:A:135:VAL:HG13	2:A:179:LEU:HD22	1.73	0.71
1:7:405:MET:HE1	1:o:680:GLN:HG2	1.73	0.70
1:7:405:MET:HE3	1:o:229:TRP:HB2	1.73	0.70
1:c:589:GLN:NE2	1:o:496:GLY:O	2.25	0.69
2:A:255:ASN:HD21	2:A:334:MET:HE2	1.58	0.68
1:c:526:MET:HE2	1:c:575:ALA:HA	1.75	0.68
2:A:285:ASP:OD2	2:A:289:LYS:NZ	2.27	0.67
1:7:382:THR:HG21	1:7:394:SER:H	1.60	0.67
1:o:382:THR:HG21	1:o:394:SER:H	1.60	0.67
1:c:435:ARG:NH2	1:o:272:ASP:O	2.29	0.66
1:o:338:ASN:ND2	1:o:675:GLN:OE1	2.28	0.65
1:6:443:GLN:NE2	1:7:359:SER:O	2.29	0.65
1:p:383:LEU:HD12	1:p:392:ARG:HB3	1.79	0.65
1:p:263:ASN:O	1:p:274:THR:HA	1.96	0.65
1:c:601:GLN:OE1	1:o:600:SER:OG	2.15	0.64
1:6:510:LYS:HB3	1:6:519:LEU:HD23	1.79	0.64
1:7:660:PRO:HG2	1:o:251:PRO:HB3	1.80	0.64
1:6:291:HIS:HD2	1:6:617:GLN:HA	1.62	0.64
1:6:315:SER:HB2	1:6:684:GLU:HG2	1.79	0.63
1:7:338:ASN:ND2	1:7:675:GLN:OE1	2.31	0.63
1:7:342:THR:HG22	1:7:407:ARG:HG2	1.79	0.63
1:5:587:GLN:NE2	1:6:490:ARG:O	2.26	0.63
2:A:62:GLU:OE1	1:c:590:ASN:ND2	2.30	0.63
1:o:289:ARG:HH21	1:o:617:GLN:HB3	1.64	0.63
1:6:487:ARG:NH1	1:6:599:ASN:OD1	2.26	0.62
1:7:247:THR:HB	1:7:372:VAL:HG22	1.79	0.62
1:5:601:GLN:OE1	1:6:600:SER:OG	2.17	0.62
1:7:416:TYR:OH	1:7:644:HIS:O	2.16	0.61
1:7:400:TYR:OH	1:o:298:ASP:OD2	2.18	0.60
2:A:98:ARG:NH1	2:A:122:ALA:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:707:TYR:OH	1:o:566:GLU:OE1	2.18	0.60
2:A:369:ASN:HB3	2:A:373:LEU:HD23	1.84	0.60
1:o:306:ASN:O	1:o:426:SER:OG	2.19	0.60
1:7:657:PRO:HG3	1:o:372:VAL:HG11	1.83	0.59
1:o:479:ASN:ND2	1:p:358:GLY:O	2.35	0.59
2:A:312:ASP:OD1	2:A:313:GLU:N	2.32	0.59
2:A:137:ASN:HB3	2:A:181:SER:HA	1.82	0.59
2:A:255:ASN:O	2:A:349:LEU:N	2.35	0.59
1:o:601:GLN:OE1	1:p:600:SER:OG	2.18	0.59
2:A:166:ARG:NH2	2:A:371:GLU:OE1	2.30	0.59
1:o:505:TRP:O	1:o:510:LYS:NZ	2.35	0.59
1:o:584:ASP:OD1	1:p:599:ASN:ND2	2.36	0.59
1:7:272:ASP:HA	1:7:516:ARG:HG3	1.85	0.59
2:A:215:ASP:HB3	2:A:218:ARG:HB2	1.84	0.58
1:6:452:GLN:HA	1:6:461:GLN:HA	1.84	0.58
2:A:149:LEU:HD21	2:A:256:LEU:HD13	1.86	0.58
1:o:382:THR:HG22	1:o:383:LEU:H	1.69	0.58
1:5:587:GLN:HB3	1:5:593:PRO:HB3	1.84	0.58
1:6:421:VAL:HG21	1:6:640:PHE:HB3	1.84	0.58
1:c:479:ASN:ND2	1:o:358:GLY:O	2.37	0.58
1:7:288:ASN:O	1:7:620:ILE:N	2.37	0.58
2:A:265:TYR:HB2	2:A:288:PHE:HB3	1.85	0.57
1:p:519:LEU:HG	1:p:540:ASN:HD22	1.68	0.57
2:A:142:GLU:OE1	2:A:257:HIS:ND1	2.38	0.57
1:o:272:ASP:HA	1:o:516:ARG:HG3	1.85	0.57
1:o:435:ARG:HD2	1:p:381:LEU:HD13	1.86	0.57
1:6:366:PRO:HG3	1:6:373:PHE:HB3	1.86	0.57
2:A:137:ASN:HD21	2:A:187:PHE:HB2	1.69	0.57
1:c:572:ASN:HD21	1:c:609:TRP:HB2	1.69	0.57
1:6:698:ASN:HD22	1:o:713:VAL:HG11	1.70	0.57
1:7:338:ASN:OD1	1:o:337:ASN:ND2	2.35	0.56
2:A:159:GLY:HA3	2:A:167:LEU:HD12	1.87	0.56
1:6:300:GLN:NE2	1:6:703:TYR:O	2.32	0.56
1:7:382:THR:HG22	1:7:383:LEU:H	1.71	0.56
2:A:350:GLU:OE2	2:A:350:GLU:N	2.38	0.56
2:A:413:THR:HG22	2:A:419:PHE:HB3	1.87	0.56
1:o:470:PRO:HA	1:o:473:MET:HE3	1.86	0.56
1:7:320:ASN:HB2	1:7:680:GLN:HG2	1.87	0.56
1:5:589:GLN:HA	1:6:499:ASN:HA	1.86	0.56
1:6:695:LYS:NZ	1:7:400:TYR:O	2.25	0.56
1:o:421:VAL:HG21	1:o:640:PHE:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:298:ASP:OD2	1:p:400:TYR:OH	2.24	0.55
1:6:698:ASN:HD22	1:o:713:VAL:CG1	2.19	0.55
1:5:443:GLN:NE2	1:6:359:SER:O	2.39	0.55
1:6:437:MET:HE1	1:6:478:LYS:HE3	1.89	0.55
1:o:481:LEU:HB2	1:o:607:MET:HG2	1.87	0.55
1:c:443:GLN:NE2	1:o:359:SER:O	2.36	0.55
2:A:90:GLU:OE2	2:A:90:GLU:N	2.40	0.55
2:A:280:SER:O	2:A:323:ASN:ND2	2.36	0.55
1:c:485:CYS:HB2	1:c:579:TYR:HB2	1.89	0.55
2:A:80:ALA:HB1	2:A:97:LEU:HD11	1.90	0.55
1:c:583:ALA:HB3	1:o:487:ARG:HG2	1.89	0.54
1:o:623:LYS:HB2	1:o:645:PRO:HG3	1.89	0.54
1:6:528:THR:HG23	1:6:538:PRO:HD2	1.90	0.54
1:7:324:LYS:NZ	1:7:337:ASN:OD1	2.40	0.54
1:c:581:ILE:HB	1:o:510:LYS:HB2	1.90	0.54
1:6:416:TYR:OH	1:6:644:HIS:O	2.22	0.54
1:7:419:GLU:OE1	1:7:643:LYS:N	2.41	0.54
1:c:483:GLY:HA3	1:c:609:TRP:HB3	1.90	0.54
2:A:418:ASP:OD1	2:A:418:ASP:N	2.40	0.54
1:6:696:ARG:NE	1:6:698:ASN:OD1	2.40	0.54
1:6:604:LEU:HD22	1:7:524:ILE:HD13	1.90	0.53
1:6:714:ASP:OD2	1:6:727:ARG:NH2	2.41	0.53
1:c:425:SER:HB2	1:c:427:TYR:CE2	2.44	0.53
1:6:483:GLY:HA3	1:6:609:TRP:HB3	1.90	0.53
2:A:261:VAL:HA	2:A:350:GLU:O	2.08	0.53
1:p:603:ALA:HA	1:p:607:MET:HE1	1.90	0.53
1:7:282:TRP:NE1	1:7:399:GLU:OE1	2.40	0.53
1:c:604:LEU:HD22	1:o:524:ILE:HD13	1.90	0.53
1:5:479:ASN:ND2	1:6:358:GLY:O	2.40	0.53
1:6:432:SER:HA	1:6:570:THR:HB	1.90	0.53
1:7:617:GLN:HE22	1:7:728:PRO:HA	1.74	0.53
1:o:561:MET:HB3	1:o:728:PRO:HD3	1.90	0.53
1:p:623:LYS:HB2	1:p:645:PRO:HG3	1.91	0.53
1:c:463:LEU:HG	1:o:495:THR:HG22	1.91	0.53
1:6:623:LYS:HB2	1:6:645:PRO:HG3	1.91	0.53
1:7:505:TRP:O	1:7:510:LYS:NZ	2.37	0.53
1:6:231:CYS:HA	1:6:244:SER:HA	1.90	0.53
1:6:608:VAL:HG12	1:7:630:ASN:HB3	1.91	0.52
1:7:321:ILE:HD13	1:7:343:ILE:HD11	1.91	0.52
1:7:280:THR:OG1	1:7:378:TYR:O	2.23	0.52
2:A:70:GLU:OE2	2:A:154:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:426:SER:HB2	1:6:731:THR:HG22	1.91	0.52
1:5:462:THR:HA	2:A:274:LYS:HE3	1.92	0.51
1:6:232:ASP:OD1	1:6:233:SER:N	2.38	0.51
1:o:565:GLU:O	1:o:568:ILE:HG12	2.11	0.51
1:o:738:LEU:HD22	1:p:625:PRO:HB3	1.92	0.51
1:o:576:THR:OG1	1:o:577:GLU:OE1	2.27	0.51
2:A:295:TYR:CE2	2:A:302:MET:HE1	2.45	0.51
1:o:416:TYR:OH	1:o:644:HIS:O	2.20	0.51
1:5:600:SER:OG	1:7:601:GLN:OE1	2.28	0.51
1:6:510:LYS:HA	1:6:519:LEU:HA	1.93	0.51
1:o:424:HIS:CE1	1:o:614:VAL:HG13	2.46	0.51
1:o:317:LYS:NZ	1:o:413:GLN:OE1	2.44	0.51
2:A:251:VAL:HG11	2:A:420:TYR:HB2	1.93	0.50
1:7:355:TYR:CE2	1:7:357:LEU:HB2	2.47	0.50
1:o:604:LEU:H	1:o:607:MET:HE2	1.75	0.50
1:p:254:ASN:O	1:p:259:LYS:NZ	2.45	0.50
1:5:477:ALA:HA	1:6:521:ASN:HB3	1.92	0.50
1:7:524:ILE:HA	1:7:636:LEU:HD22	1.94	0.50
1:6:613:ASP:OD1	1:6:731:THR:HB	2.11	0.50
1:7:366:PRO:HG3	1:7:373:PHE:HB3	1.92	0.50
2:A:125:LEU:HD21	2:A:131:GLN:HE21	1.76	0.50
1:o:431:GLN:HE22	1:p:354:PRO:HB3	1.76	0.50
1:5:608:VAL:HG12	1:6:630:ASN:HB3	1.94	0.50
1:c:574:VAL:HG12	1:c:576:THR:H	1.77	0.50
1:7:320:ASN:O	1:7:322:GLN:NE2	2.44	0.50
1:7:382:THR:HG22	1:7:383:LEU:N	2.27	0.50
1:p:280:THR:OG1	1:p:378:TYR:O	2.22	0.50
1:5:473:MET:HA	1:5:476:GLN:HG3	1.94	0.49
1:7:348:ASP:OD2	1:7:353:LEU:N	2.44	0.49
1:6:254:ASN:ND2	1:6:279:SER:O	2.46	0.49
1:6:561:MET:HB3	1:6:728:PRO:HD3	1.94	0.49
2:A:249:LYS:HZ1	2:A:414:GLY:HA2	1.77	0.49
2:A:266:PRO:HD2	2:A:288:PHE:CG	2.48	0.49
1:7:291:HIS:HD2	1:7:617:GLN:HA	1.77	0.49
1:7:503:PHE:HB2	1:7:507:ALA:HB3	1.94	0.49
2:A:67:ALA:O	2:A:70:GLU:HG3	2.13	0.49
2:A:295:TYR:CZ	2:A:349:LEU:HD13	2.48	0.48
1:o:613:ASP:OD1	1:o:731:THR:HB	2.13	0.48
1:6:289:ARG:HH21	1:6:617:GLN:HB3	1.78	0.48
2:A:284:ASP:OD1	2:A:421:ARG:NH2	2.46	0.48
1:o:617:GLN:HE22	1:o:728:PRO:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:492:SER:HB2	1:o:536:PHE:CE1	2.48	0.48
1:c:448:LEU:HD11	1:c:463:LEU:HD22	1.96	0.48
1:o:318:LEU:HD21	1:o:651:ILE:HD12	1.94	0.48
2:A:194:ASP:OD1	2:A:195:CYS:N	2.47	0.48
1:7:519:LEU:CD1	1:7:540:ASN:HD22	2.26	0.48
1:o:431:GLN:NE2	1:p:354:PRO:HB3	2.29	0.48
1:6:346:PHE:HB3	1:6:403:SER:HA	1.96	0.48
1:6:530:LYS:HB3	1:6:574:VAL:HG21	1.96	0.48
1:o:525:ALA:O	1:o:572:ASN:ND2	2.47	0.48
1:o:706:ASN:HB3	1:o:708:TYR:CE1	2.49	0.48
2:A:273:HIS:CE1	2:A:331:GLU:HG3	2.49	0.48
1:o:604:LEU:HD22	1:p:524:ILE:HD13	1.96	0.48
1:6:253:TYR:OH	1:6:375:ILE:O	2.21	0.47
1:o:527:ALA:HB3	1:o:574:VAL:HA	1.94	0.47
1:c:527:ALA:HB3	1:c:574:VAL:HA	1.95	0.47
1:o:250:LEU:HD22	1:o:651:ILE:HG12	1.95	0.47
1:7:399:GLU:O	1:o:229:TRP:NE1	2.41	0.47
2:A:375:THR:HA	2:A:378:GLU:HG2	1.95	0.47
1:5:439:PRO:HB3	1:6:381:LEU:HD21	1.97	0.47
1:6:439:PRO:HB3	1:7:381:LEU:HD21	1.97	0.47
1:7:291:HIS:CD2	1:7:617:GLN:HA	2.50	0.47
2:A:264:SER:HA	2:A:322:THR:O	2.14	0.47
1:6:233:SER:HA	1:6:241:ILE:O	2.14	0.47
1:o:366:PRO:HG3	1:o:373:PHE:HB3	1.97	0.47
1:o:483:GLY:HA3	1:o:609:TRP:HB3	1.97	0.47
1:o:382:THR:HG22	1:o:383:LEU:N	2.30	0.47
1:o:509:THR:H	1:o:540:ASN:HD21	1.63	0.47
1:6:565:GLU:O	1:6:568:ILE:HG12	2.14	0.47
1:c:485:CYS:CB	1:c:579:TYR:HB2	2.43	0.47
1:o:314:LEU:HD21	1:o:646:PRO:HB3	1.97	0.47
1:o:226:SER:HB3	1:o:320:ASN:H	1.81	0.46
1:7:657:PRO:HG2	1:o:249:ALA:HB2	1.97	0.46
1:c:435:ARG:HD2	1:o:381:LEU:HD13	1.97	0.46
1:o:419:GLU:OE2	1:o:643:LYS:N	2.47	0.46
1:6:510:LYS:HD3	1:6:517:ASN:HB3	1.98	0.46
2:A:159:GLY:HA2	2:A:162:ARG:HG2	1.97	0.46
2:A:275:ALA:O	2:A:329:ASP:N	2.45	0.46
1:c:581:ILE:HG22	1:c:595:ILE:HD11	1.97	0.46
1:o:443:GLN:NE2	1:p:359:SER:O	2.47	0.46
1:6:585:ASN:OD1	1:6:594:GLN:N	2.43	0.46
1:6:314:LEU:HA	1:6:684:GLU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:6:570:THR:HG22	1:7:383:LEU:HD21	1.97	0.46
1:7:258:TYR:O	1:7:721:GLY:HA2	2.15	0.46
2:A:192:GLU:HA	2:A:356:TYR:CE1	2.51	0.46
1:7:226:SER:OG	1:7:411:ASN:HB3	2.15	0.46
1:6:448:LEU:HD11	1:6:463:LEU:HD22	1.96	0.46
1:6:263:ASN:HB2	1:6:275:TYR:CE2	2.50	0.46
1:7:312:LYS:HD2	1:7:312:LYS:HA	1.70	0.46
1:7:254:ASN:ND2	1:7:259:LYS:HD2	2.30	0.46
2:A:160:TYR:HA	2:A:168:VAL:HG22	1.98	0.46
2:A:347:ILE:HD12	2:A:349:LEU:HD21	1.98	0.46
2:A:388:VAL:HG12	2:A:457:PHE:HD2	1.80	0.46
1:7:603:ALA:HA	1:7:607:MET:HE2	1.97	0.46
2:A:306:GLU:H	2:A:306:GLU:CD	2.25	0.45
1:7:432:SER:HA	1:7:570:THR:HB	1.99	0.45
1:7:624:ILE:HD12	1:7:643:LYS:HG2	1.98	0.45
1:6:565:GLU:OE2	1:6:615:TYR:OH	2.21	0.45
2:A:295:TYR:HE2	2:A:302:MET:HE1	1.82	0.45
2:A:400:ALA:HB2	2:A:434:LEU:HD22	1.99	0.45
1:7:291:HIS:CD2	1:7:617:GLN:HA	2.51	0.45
1:7:528:THR:HG23	1:7:538:PRO:HD2	1.97	0.45
1:6:305:ASN:HA	1:6:734:LEU:HD11	1.98	0.45
1:6:437:MET:HB2	1:7:361:HIS:NE2	2.32	0.45
1:7:254:ASN:HB3	1:7:259:LYS:NZ	2.30	0.45
1:6:447:TYR:OH	1:6:472:THR:HG21	2.17	0.45
1:6:601:GLN:OE1	1:7:600:SER:OG	2.31	0.45
1:7:527:ALA:O	1:7:575:ALA:N	2.37	0.45
1:7:276:PHE:HB3	1:7:384:ASN:HB3	1.99	0.45
1:7:623:LYS:HB2	1:7:645:PRO:HG3	1.97	0.45
1:7:318:LEU:HB3	1:7:412:PHE:HB3	1.99	0.45
1:7:519:LEU:HD11	1:7:540:ASN:HD22	1.81	0.45
1:7:477:ALA:HA	1:7:521:ASN:HB3	1.99	0.45
1:7:565:GLU:OE2	1:7:615:TYR:OH	2.24	0.45
1:7:512:HIS:NE2	1:7:515:GLY:HA2	2.32	0.44
1:6:271:ASN:OD1	1:6:271:ASN:N	2.50	0.44
2:A:421:ARG:NH1	2:A:422:LEU:O	2.49	0.44
1:7:529:HIS:CE1	1:7:534:GLU:HG3	2.52	0.44
1:6:553:ASP:N	1:6:553:ASP:OD1	2.49	0.44
1:7:346:PHE:HB3	1:7:403:SER:HA	1.99	0.44
1:6:262:SER:OG	1:6:263:ASN:N	2.51	0.44
1:6:357:LEU:HD13	1:6:648:GLN:HB3	2.00	0.44
1:6:453:THR:OG1	1:6:460:THR:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:608:VAL:HG12	1:p:630:ASN:HB3	1.97	0.44
1:6:696:ARG:NH1	1:7:394:SER:OG	2.50	0.44
1:c:572:ASN:ND2	1:c:609:TRP:HB2	2.32	0.44
1:p:258:TYR:OH	1:p:399:GLU:OE1	2.31	0.44
1:p:519:LEU:HG	1:p:540:ASN:ND2	2.32	0.44
1:o:696:ARG:NH1	1:p:394:SER:OG	2.50	0.44
1:p:421:VAL:HG11	1:p:642:LEU:HD23	1.99	0.44
1:7:406:LEU:HD21	1:7:412:PHE:HB2	1.99	0.44
2:A:61:GLU:OE2	2:A:92:ARG:NH2	2.47	0.44
1:5:466:SER:HA	1:6:553:ASP:HA	2.00	0.44
1:7:254:ASN:HD22	1:7:259:LYS:HD2	1.83	0.44
2:A:64:LEU:HB2	2:A:146:ARG:HH21	1.83	0.44
1:6:721:GLY:HA2	1:p:258:TYR:O	2.18	0.43
1:7:528:THR:HG23	1:7:538:PRO:HD2	1.99	0.43
1:o:247:THR:HB	1:o:372:VAL:HG22	1.99	0.43
1:o:435:ARG:HA	1:o:435:ARG:HD3	1.76	0.43
1:c:604:LEU:HB3	1:o:524:ILE:HG21	1.98	0.43
1:6:617:GLN:HE22	1:6:728:PRO:HA	1.83	0.43
1:7:553:ASP:OD1	1:7:553:ASP:N	2.52	0.43
2:A:267:PHE:CG	2:A:282:THR:HG22	2.52	0.43
2:A:359:ALA:HA	2:A:362:LEU:HG	2.01	0.43
1:p:522:PRO:HA	1:p:540:ASN:O	2.18	0.43
1:7:659:ASP:OD1	1:7:659:ASP:N	2.51	0.43
2:A:170:LEU:HD21	2:A:377:ILE:HB	1.99	0.43
1:6:472:THR:HG22	1:6:475:ASN:HB2	2.00	0.43
1:o:701:ILE:HG22	1:o:733:TYR:HD1	1.84	0.43
1:6:259:LYS:HB3	1:6:259:LYS:HE3	1.82	0.43
1:o:342:THR:HA	1:o:406:LEU:O	2.18	0.43
1:5:451:THR:HG21	1:6:503:PHE:CE2	2.54	0.43
1:6:471:ASN:OD1	1:7:263:ASN:ND2	2.53	0.42
1:6:692:GLU:HG2	1:6:734:LEU:HD13	2.01	0.42
1:c:470:PRO:HA	1:c:473:MET:HE3	2.01	0.42
1:6:312:LYS:HB3	1:6:312:LYS:HE3	1.76	0.42
1:6:529:HIS:CE1	1:6:534:GLU:HG3	2.54	0.42
1:o:604:LEU:HB2	1:o:607:MET:HG3	2.01	0.42
2:A:125:LEU:CD2	2:A:131:GLN:HE21	2.30	0.42
1:c:451:THR:OG1	1:o:501:SER:O	2.37	0.42
1:o:338:ASN:ND2	1:o:341:SER:OG	2.53	0.42
1:o:530:LYS:HB3	1:o:574:VAL:HG21	2.01	0.42
1:7:325:GLU:HG3	1:7:338:ASN:HB2	2.00	0.42
1:7:424:HIS:CE1	1:7:614:VAL:HG13	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:o:544:ILE:HG23	1:o:562:LEU:HD23	2.01	0.42
1:6:239:ARG:NE	1:6:686:GLU:OE2	2.36	0.42
2:A:75:GLY:C	2:A:161:ARG:HH21	2.28	0.42
1:6:291:HIS:N	1:6:616:LEU:O	2.53	0.42
1:6:495:THR:HA	1:6:498:ASN:HD22	1.85	0.42
2:A:61:GLU:OE2	2:A:92:ARG:NE	2.43	0.42
1:o:321:ILE:HD13	1:o:343:ILE:HD11	2.02	0.42
1:o:469:GLY:H	1:o:472:THR:HG23	1.83	0.42
1:o:609:TRP:HE1	1:o:632:HIS:CD2	2.36	0.42
1:6:486:TYR:O	1:6:526:MET:HE1	2.20	0.42
1:o:579:TYR:HB3	1:o:598:VAL:HG23	2.02	0.42
1:6:288:ASN:O	1:6:619:PRO:HA	2.20	0.42
1:o:314:LEU:HA	1:o:684:GLU:O	2.19	0.42
1:o:479:ASN:OD1	1:p:637:MET:HB2	2.19	0.42
1:7:263:ASN:O	1:7:274:THR:HA	2.19	0.41
2:A:61:GLU:C	2:A:63:GLU:H	2.27	0.41
2:A:300:PRO:HA	2:A:303:LYS:NZ	2.35	0.41
1:6:291:HIS:CD2	1:6:617:GLN:HA	2.49	0.41
1:7:311:PRO:HA	1:7:687:TRP:HA	2.01	0.41
2:A:145:SER:O	2:A:149:LEU:HD23	2.20	0.41
1:c:567:GLU:OE2	1:c:567:GLU:N	2.44	0.41
1:o:356:VAL:HG11	1:o:379:GLY:O	2.20	0.41
1:6:461:GLN:H	1:6:461:GLN:HG3	1.71	0.41
2:A:312:ASP:OD2	2:A:315:GLU:HB2	2.20	0.41
1:o:346:PHE:HB3	1:o:403:SER:HA	2.01	0.41
1:o:509:THR:N	1:o:540:ASN:HD21	2.18	0.41
1:p:272:ASP:HA	1:p:516:ARG:HG2	2.02	0.41
1:p:290:PHE:CE2	1:p:620:ILE:HA	2.55	0.41
1:6:244:SER:HB2	1:6:246:ARG:NH1	2.36	0.41
1:6:453:THR:HG1	1:6:460:THR:N	2.18	0.41
2:A:216:LEU:HD22	2:A:238:VAL:HG23	2.01	0.41
2:A:305:GLY:HA3	2:A:317:PHE:O	2.20	0.41
1:6:374:MET:HB3	1:p:669:LEU:HD11	2.02	0.41
1:6:466:SER:HA	1:7:553:ASP:HA	2.02	0.41
1:7:717:VAL:HB	1:7:721:GLY:HA2	2.03	0.41
1:o:288:ASN:O	1:o:619:PRO:HA	2.20	0.41
1:o:632:HIS:O	1:o:634:SER:N	2.49	0.41
1:p:632:HIS:O	1:p:634:SER:N	2.51	0.41
1:5:473:MET:HE3	1:5:473:MET:HB2	1.91	0.41
1:6:258:TYR:HA	1:6:279:SER:O	2.21	0.41
2:A:193:GLY:H	2:A:356:TYR:HD1	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:379:LYS:HD3	2:A:379:LYS:HA	1.88	0.41
1:c:580:GLY:C	1:c:581:ILE:HD13	2.46	0.41
1:o:486:TYR:O	1:o:526:MET:HE1	2.20	0.41
1:6:479:ASN:ND2	1:7:637:MET:HE2	2.36	0.41
1:7:643:LYS:HE3	1:7:643:LYS:HB2	1.82	0.41
1:c:468:GLY:HA3	1:c:476:GLN:HG2	2.02	0.41
1:6:615:TYR:CD1	1:6:730:GLY:HA2	2.57	0.40
1:7:657:PRO:O	1:o:676:TYR:OH	2.29	0.40
1:o:611:ASN:OD1	1:o:632:HIS:NE2	2.47	0.40
1:7:263:ASN:HB2	1:7:275:TYR:CE2	2.56	0.40
1:7:522:PRO:HA	1:7:540:ASN:O	2.21	0.40
1:o:611:ASN:O	1:o:732:ARG:NH2	2.47	0.40
1:p:260:GLN:NE2	1:p:276:PHE:HE2	2.19	0.40
2:A:64:LEU:HB2	2:A:146:ARG:NH2	2.37	0.40
2:A:260:SER:O	2:A:350:GLU:HB3	2.21	0.40
1:5:604:LEU:HD22	1:6:524:ILE:HD13	2.03	0.40
1:6:580:GLY:HA3	1:7:511:TYR:HA	2.02	0.40
1:7:511:TYR:CE1	1:7:518:SER:HB3	2.57	0.40
2:A:166:ARG:NH2	2:A:378:GLU:OE2	2.55	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	5	80/738 (11%)	78 (98%)	2 (2%)	0	100	100
1	6	388/738 (53%)	376 (97%)	12 (3%)	0	100	100
1	7	325/738 (44%)	314 (97%)	11 (3%)	0	100	100
1	c	118/738 (16%)	112 (95%)	6 (5%)	0	100	100
1	o	469/738 (64%)	455 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	p	145/738 (20%)	142 (98%)	3 (2%)	0	100	100
2	A	329/470 (70%)	307 (93%)	22 (7%)	0	100	100
All	All	1854/4898 (38%)	1784 (96%)	70 (4%)	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	5	74/618 (12%)	74 (100%)	0	100	100
1	6	362/618 (59%)	362 (100%)	0	100	100
1	7	304/618 (49%)	304 (100%)	0	100	100
1	c	109/618 (18%)	109 (100%)	0	100	100
1	o	423/618 (68%)	422 (100%)	1 (0%)	92	98
1	p	143/618 (23%)	143 (100%)	0	100	100
2	A	291/382 (76%)	291 (100%)	0	100	100
All	All	1706/4090 (42%)	1705 (100%)	1 (0%)	92	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	o	554	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	5	452	GLN
1	5	590	ASN
1	6	377	GLN
1	6	521	ASN

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Mol	Chain	Res	Type
1	6	611	ASN
1	6	644	HIS
1	7	362	GLN
1	7	548	GLN
1	7	549	ASN
1	7	630	ASN
1	7	632	HIS
2	A	299	HIS
1	o	322	GLN
1	o	338	ASN
1	o	344	GLN
1	o	431	GLN
1	o	497	GLN
1	o	500	ASN
1	o	540	ASN
1	o	702	GLN
1	p	488	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

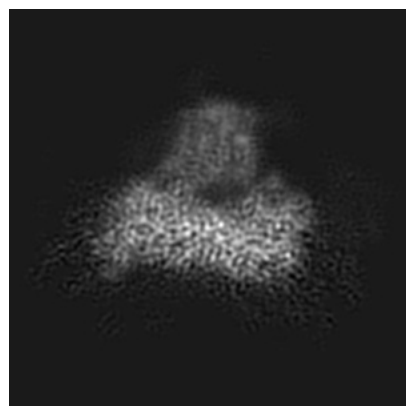
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61206. These allow visual inspection of the internal detail of the map and identification of artifacts.

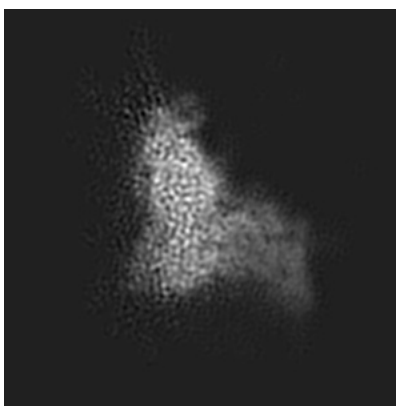
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

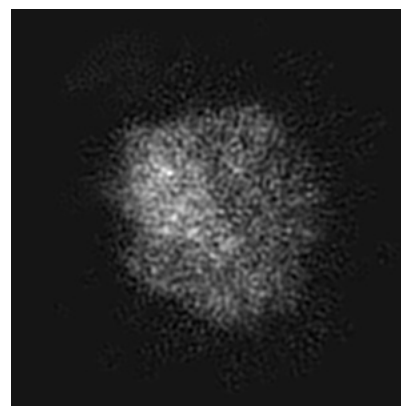
6.1.1 Primary map



X

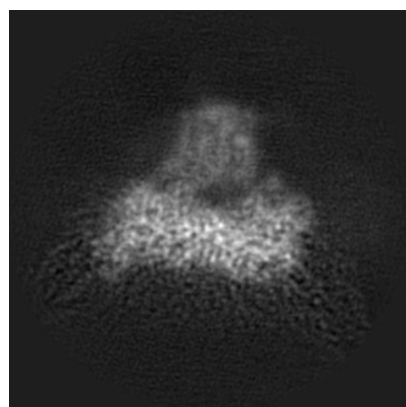


Y

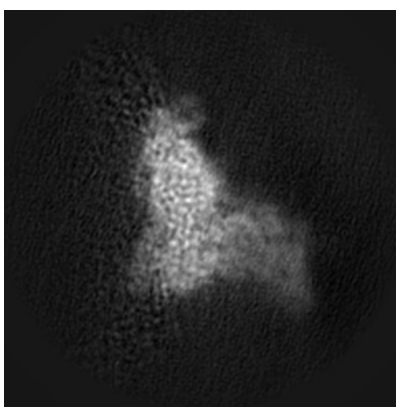


Z

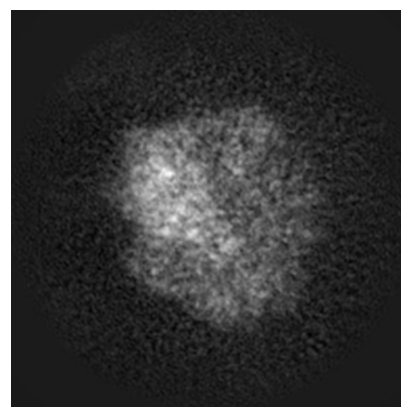
6.1.2 Raw map



X



Y

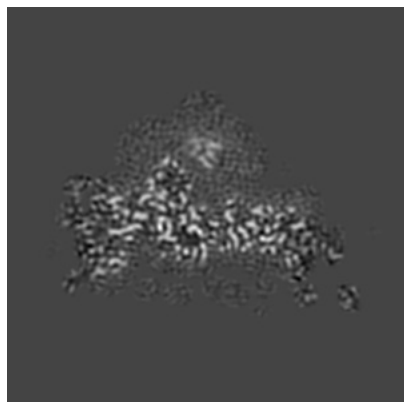


Z

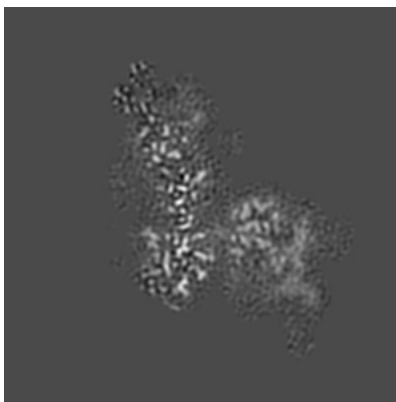
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

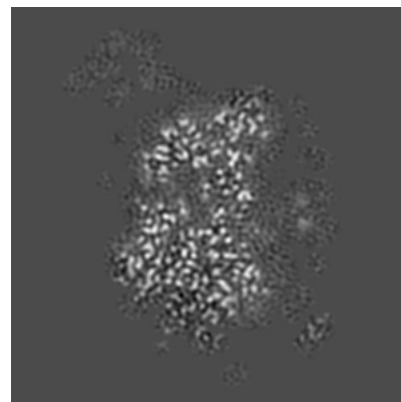
6.2.1 Primary map



X Index: 96

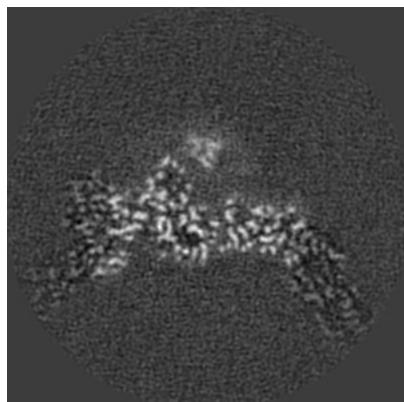


Y Index: 96

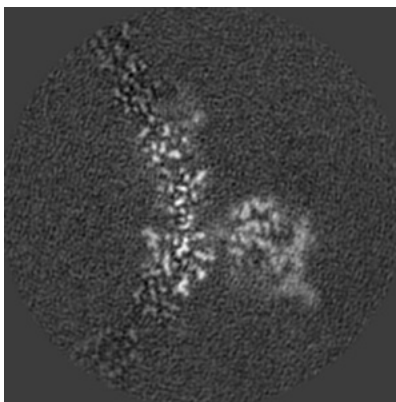


Z Index: 96

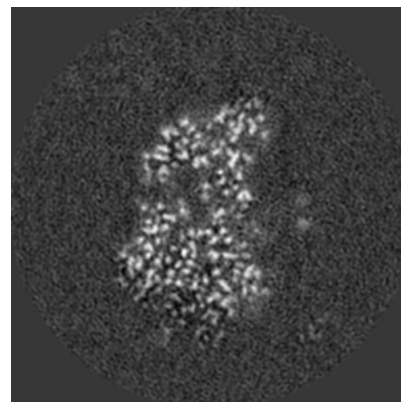
6.2.2 Raw map



X Index: 96



Y Index: 96

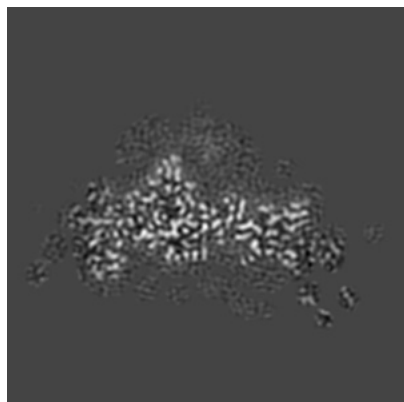


Z Index: 96

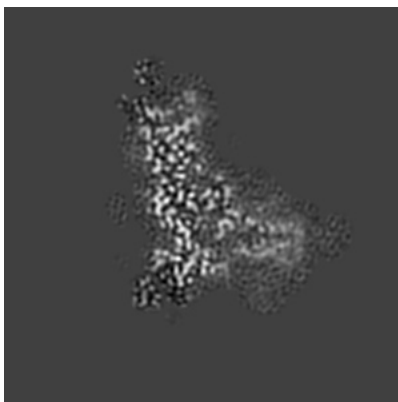
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

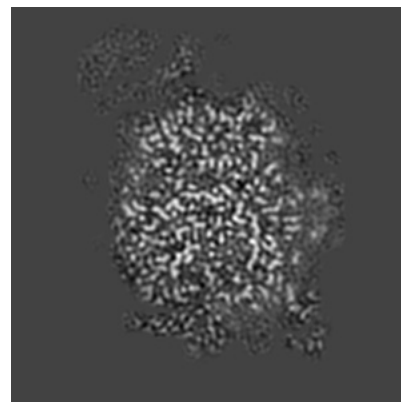
6.3.1 Primary map



X Index: 100

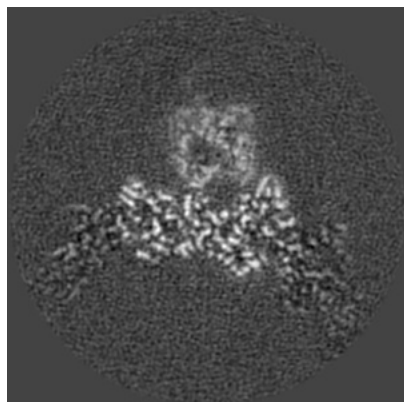


Y Index: 85

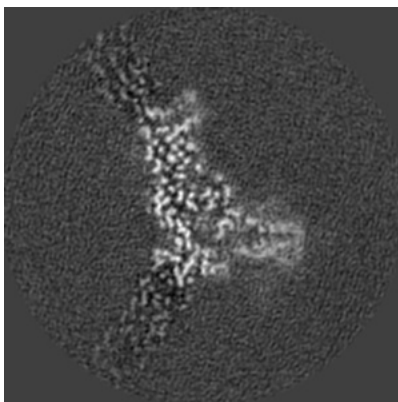


Z Index: 87

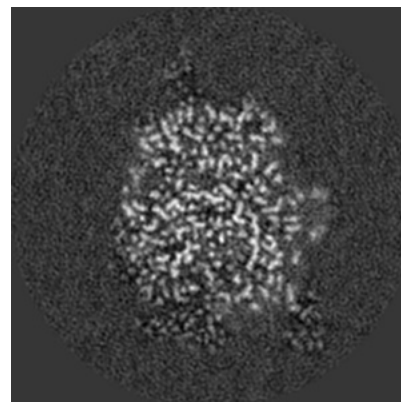
6.3.2 Raw map



X Index: 74



Y Index: 85

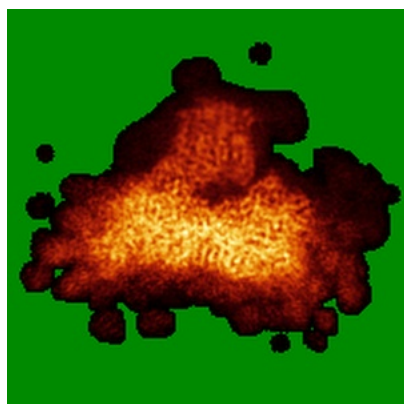


Z Index: 87

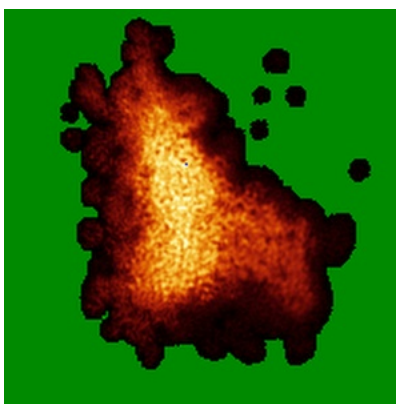
The images above show the largest variance slices of the map in three orthogonal directions.

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

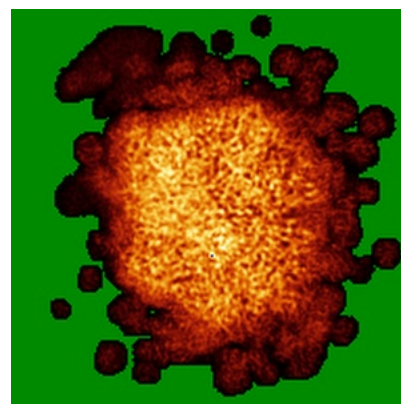
6.4.1 Primary map



X

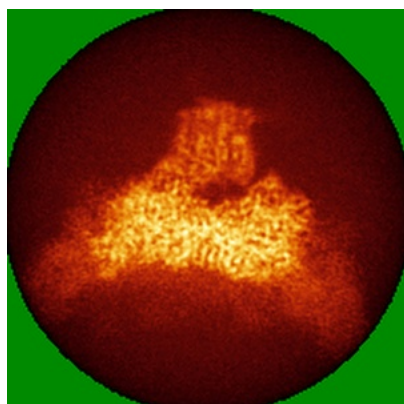


Y

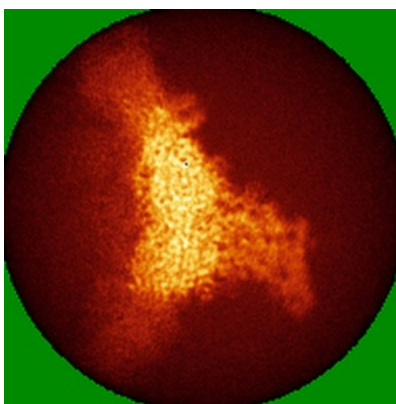


Z

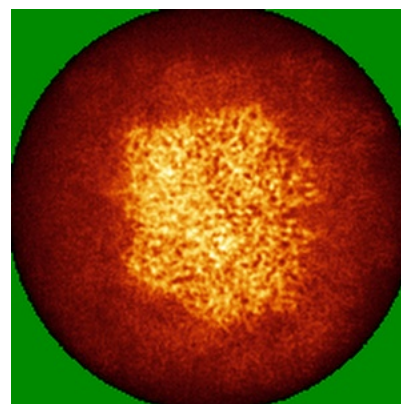
6.4.2 Raw map



X



Y

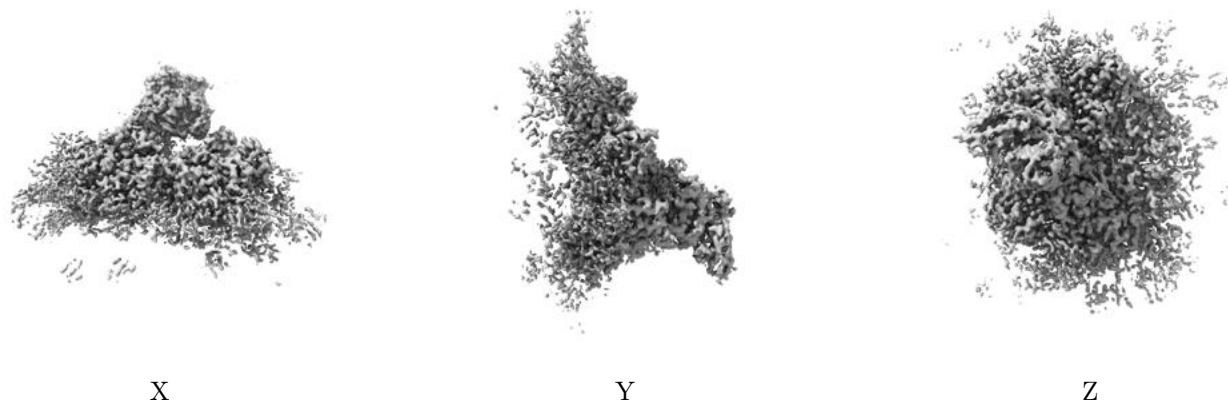


Z

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.

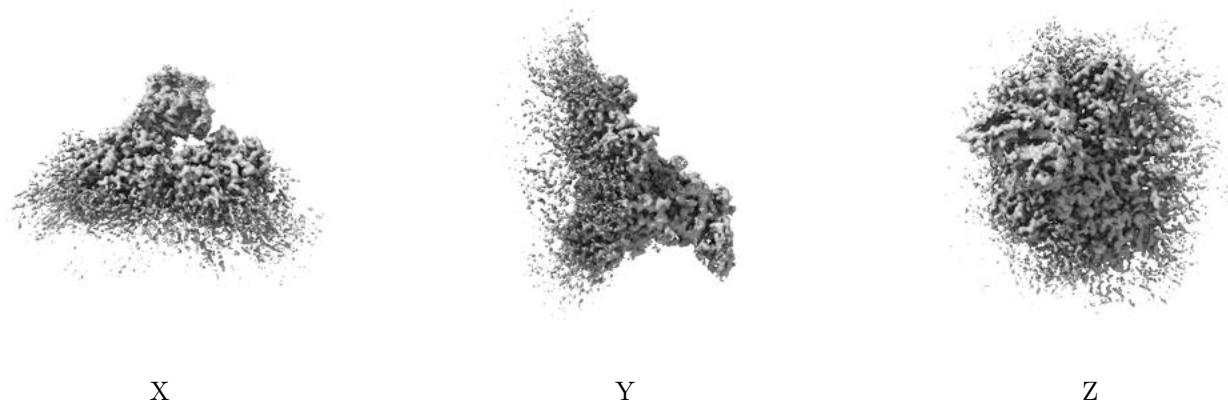
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

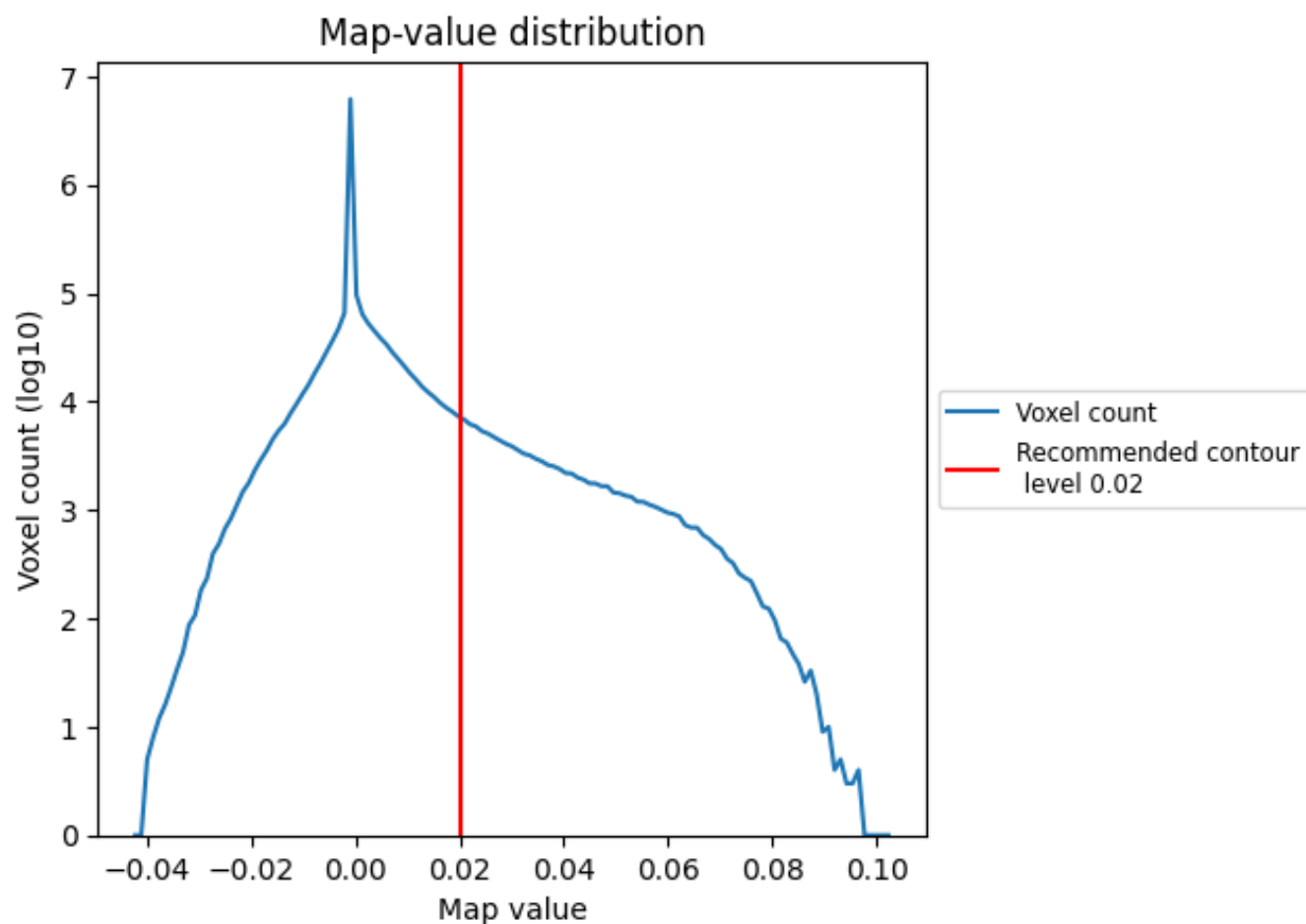
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

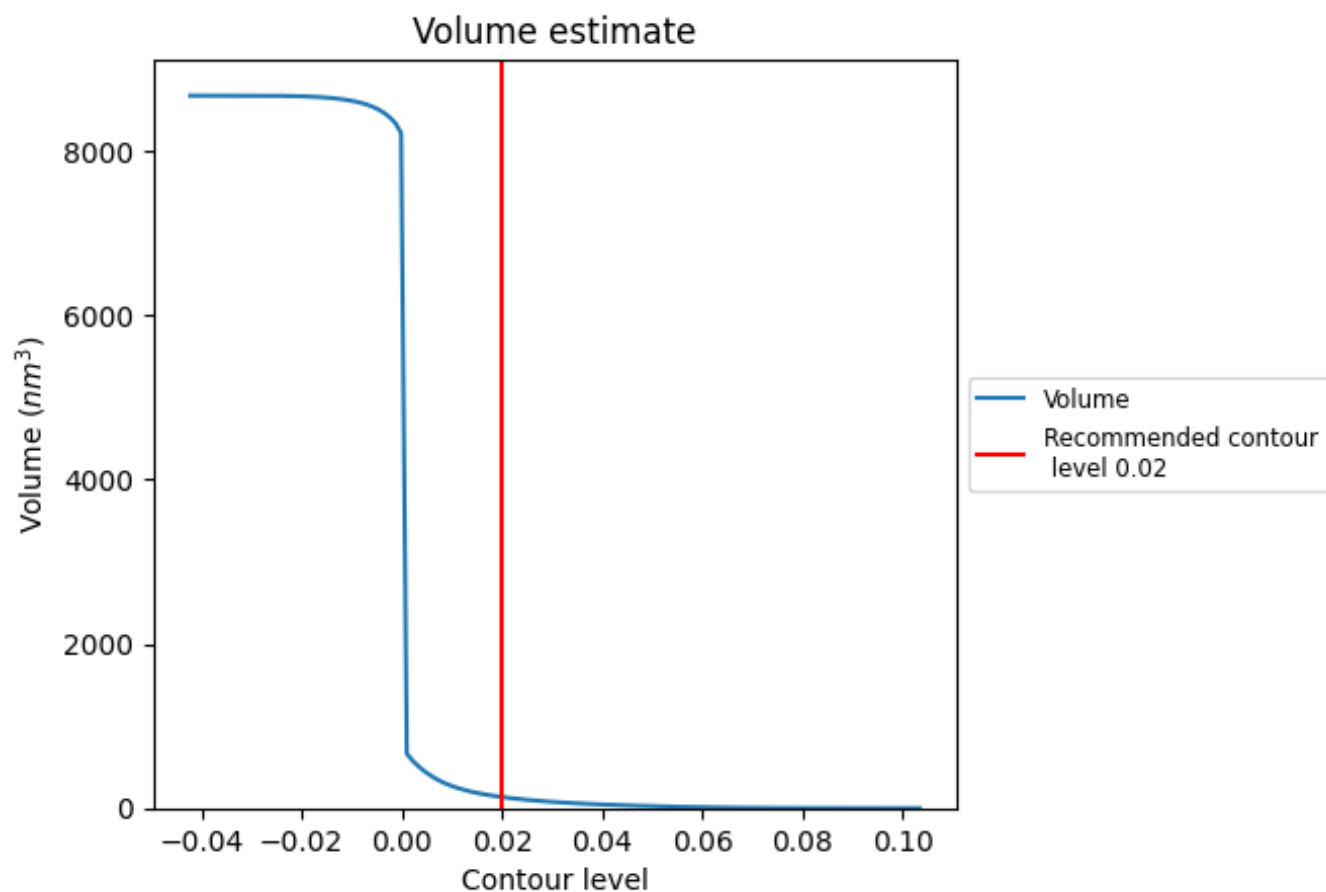
This section contains the results of statistical analysis of the map.

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.

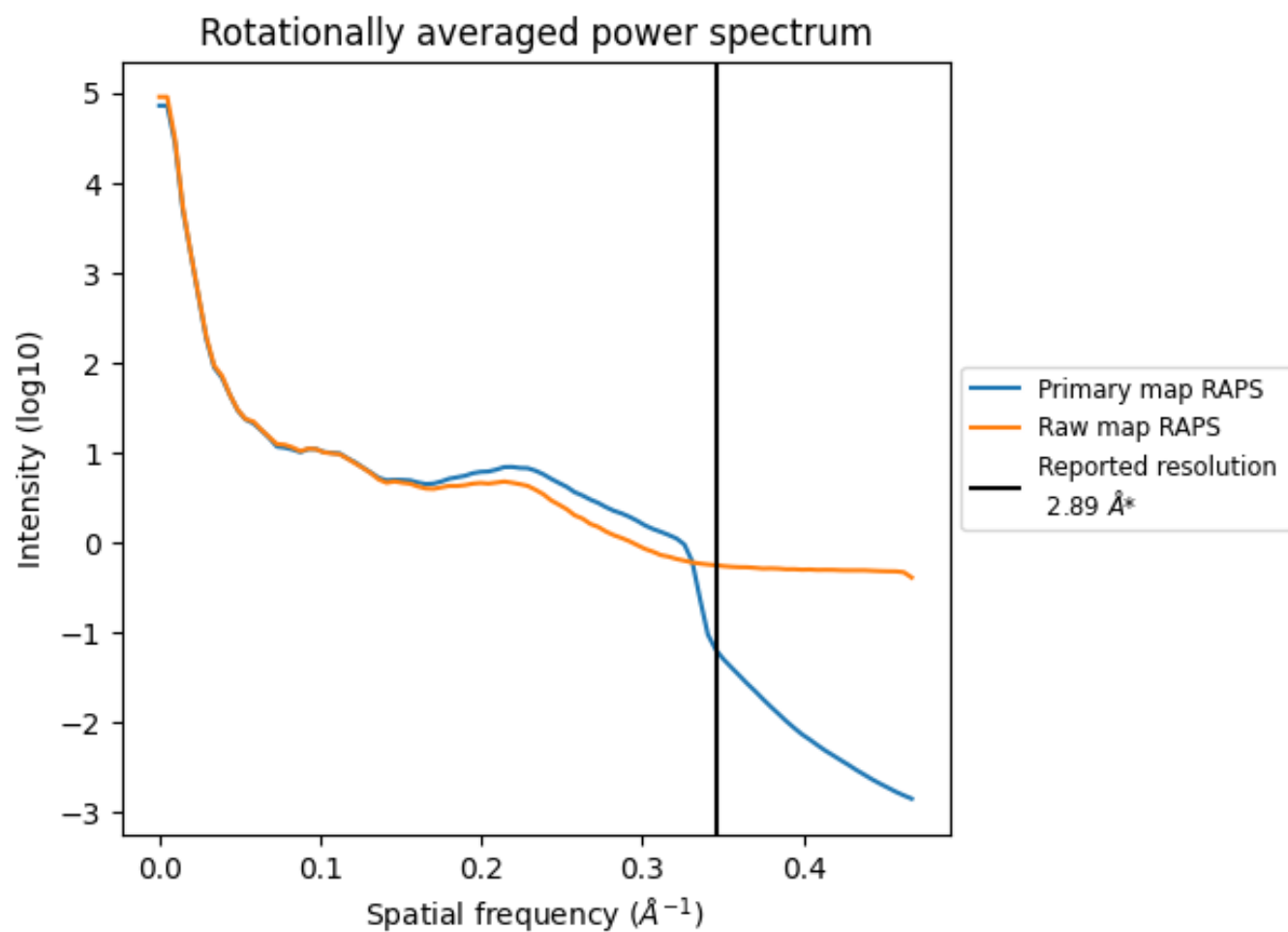
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 135 nm³; this corresponds to an approximate mass of 122 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 ⓘ

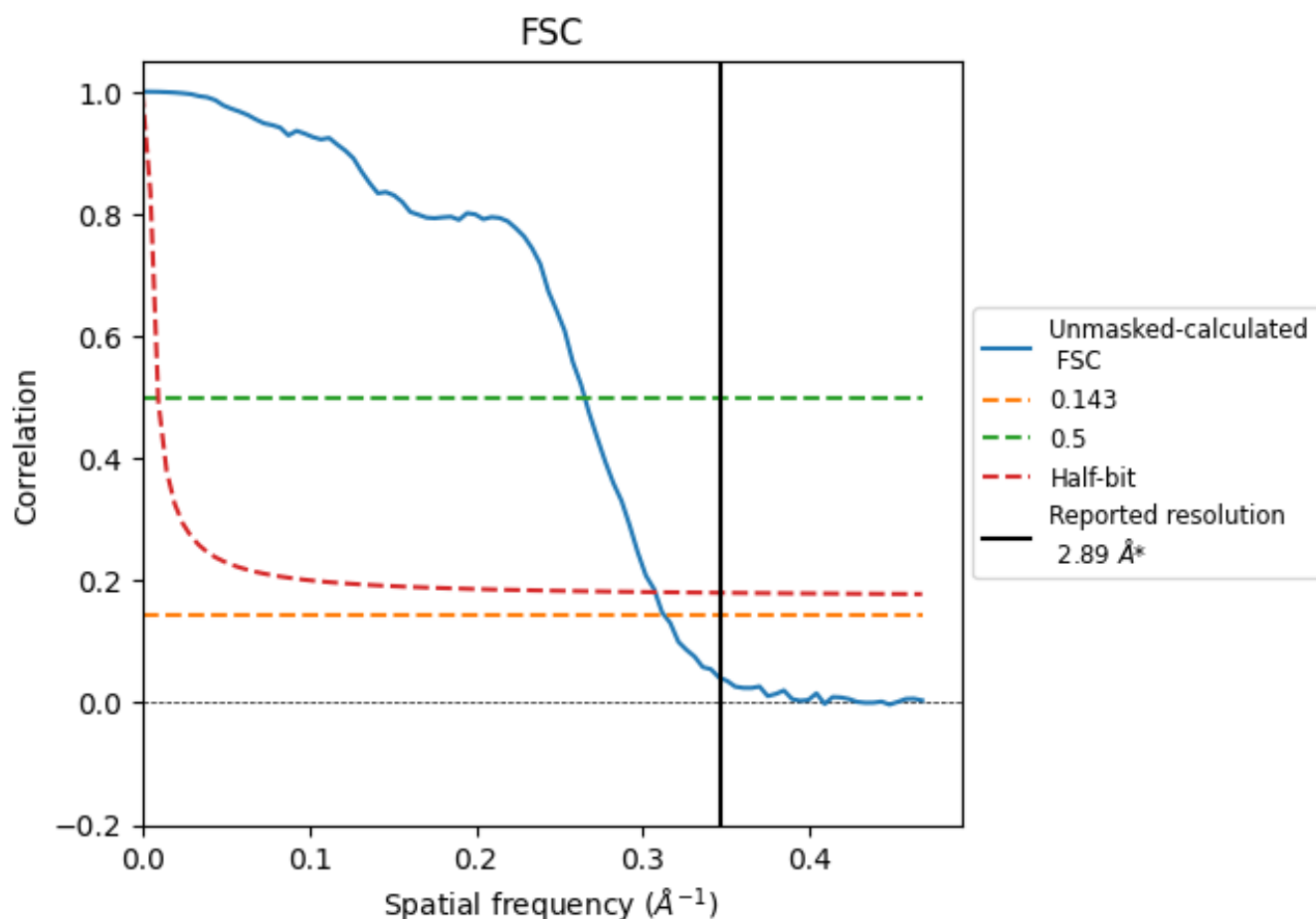


*Reported resolution corresponds to spatial frequency of 0.346 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

8.2 Resolution estimates [i](#)

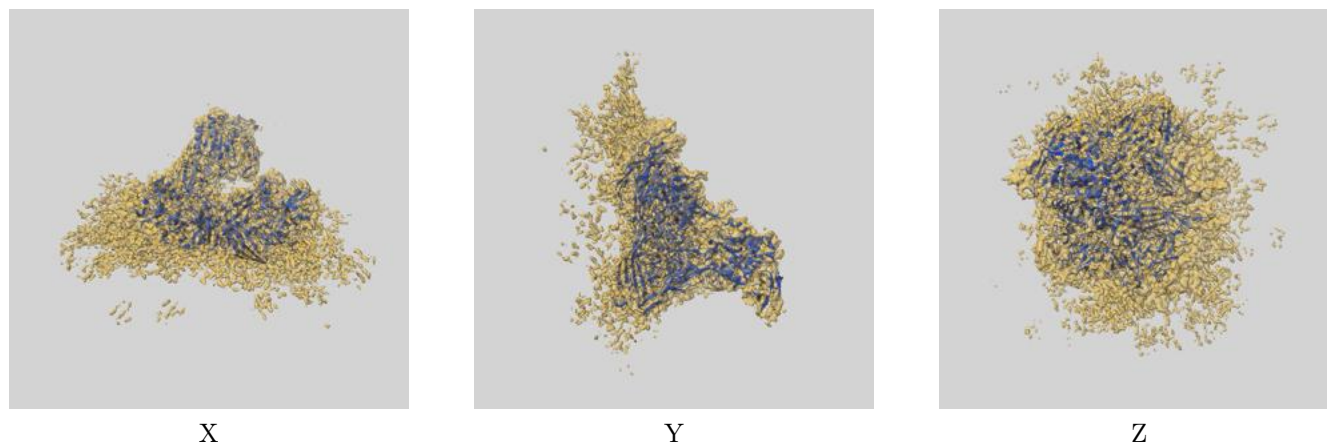
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.20	3.77	3.25

*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 3.20 differs from the reported value 2.89 by more than 10 %

9 Map-model fit [i](#)

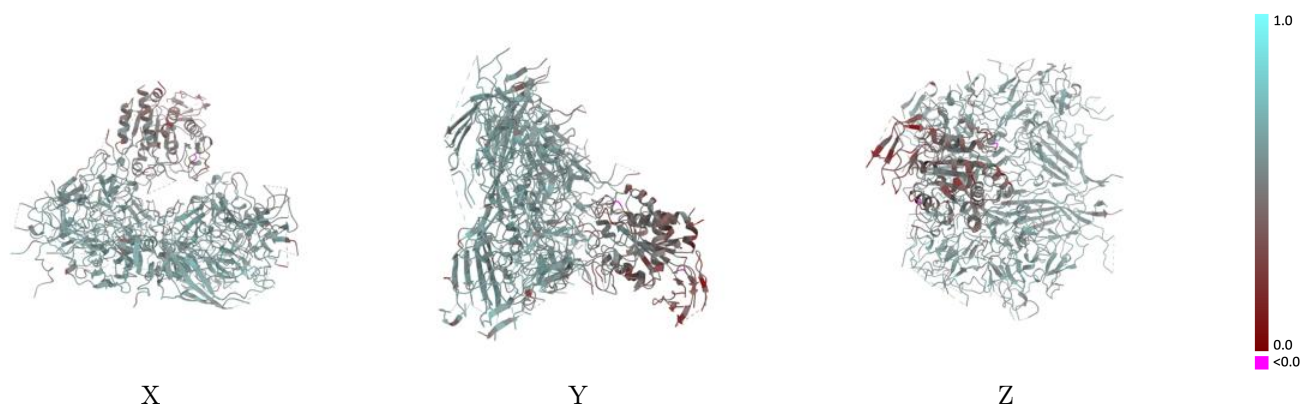
This section contains information regarding the fit between EMDB map EMD-61206 and PDB model 9J7L. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



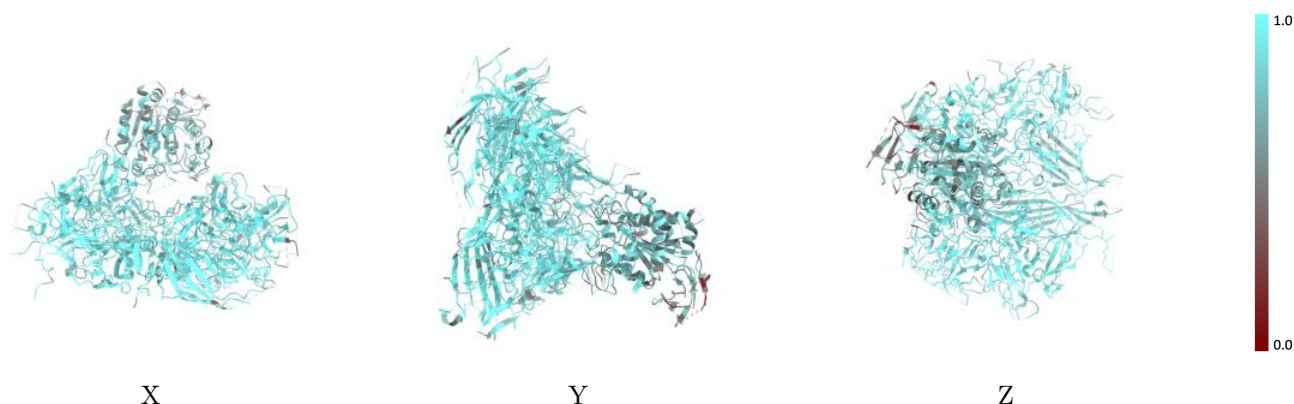
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



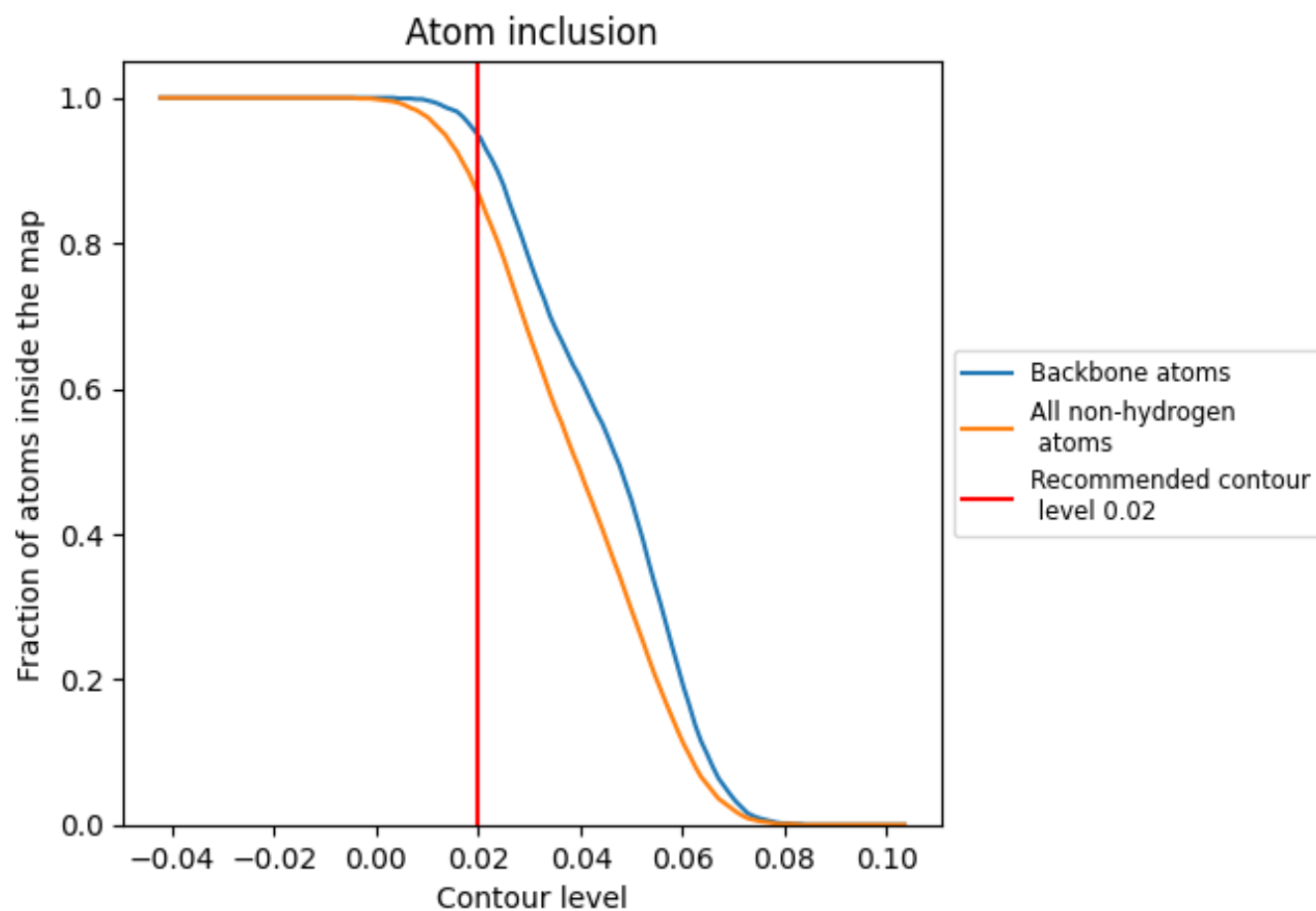
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8680	<div><div></div></div> 0.5400
5	<div><div></div></div> 0.8970	<div><div></div></div> 0.5450
6	<div><div></div></div> 0.8980	<div><div></div></div> 0.5710
7	<div><div></div></div> 0.8930	<div><div></div></div> 0.5700
A	<div><div></div></div> 0.7000	<div><div></div></div> 0.4070
c	<div><div></div></div> 0.8900	<div><div></div></div> 0.5460
o	<div><div></div></div> 0.9190	<div><div></div></div> 0.5750
p	<div><div></div></div> 0.8970	<div><div></div></div> 0.5690

1.0

0.0

<0.0