



Full wwPDB EM Validation Report ⓘ

Aug 28, 2025 – 10:20 am BST

PDB ID : 9GSE / pdb_00009gse
EMDB ID : EMD-51545
Title : Cryo-EM structure of mouse PMCA-NPTN complex captured in E1 state without calcium
Authors : Vinayagam, D.; Raunser, S.; Sistel, O.; Schulte, U.; Constantin, C.E.; Prumbaum, D.; Zolles, G.; Fakler, B.
Deposited on : 2024-09-15
Resolution : 3.64 Å (reported)
Based on initial model : 6A69

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.dev126
Mogul : 1.8.4, 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) : 2.45.1

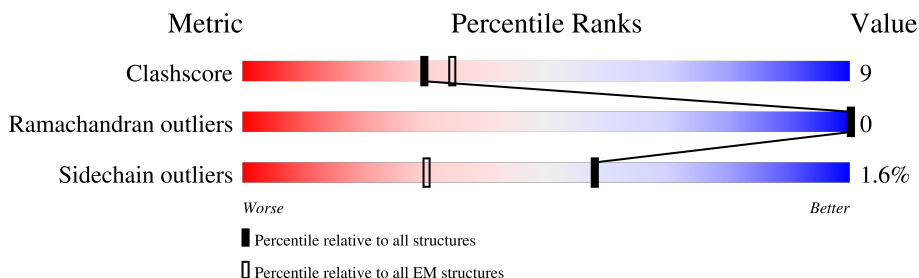
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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	1214	
2	B	413	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9155 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 Plasma membrane calcium-transporting ATPase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	942	Total	C	N	O	S	0	0
			7329	4697	1236	1351	45		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1199	GLU	-	expression tag	UNP Q9R0K7
A	1200	ASN	-	expression tag	UNP Q9R0K7
A	1201	LEU	-	expression tag	UNP Q9R0K7
A	1202	TYR	-	expression tag	UNP Q9R0K7
A	1203	PHE	-	expression tag	UNP Q9R0K7
A	1204	GLN	-	expression tag	UNP Q9R0K7
A	1205	GLY	-	expression tag	UNP Q9R0K7
A	1206	GLY	-	expression tag	UNP Q9R0K7
A	1207	ASP	-	expression tag	UNP Q9R0K7
A	1208	TYR	-	expression tag	UNP Q9R0K7
A	1209	LYS	-	expression tag	UNP Q9R0K7
A	1210	ASP	-	expression tag	UNP Q9R0K7
A	1211	ASP	-	expression tag	UNP Q9R0K7
A	1212	ASP	-	expression tag	UNP Q9R0K7
A	1213	ASP	-	expression tag	UNP Q9R0K7
A	1214	LYS	-	expression tag	UNP Q9R0K7

- Molecule 2 is a protein called Neuroplastin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	214	Total	C	N	O	S	0	0
			1703	1077	292	326	8		

There are 16 discrepancies between the modelled and reference sequences:

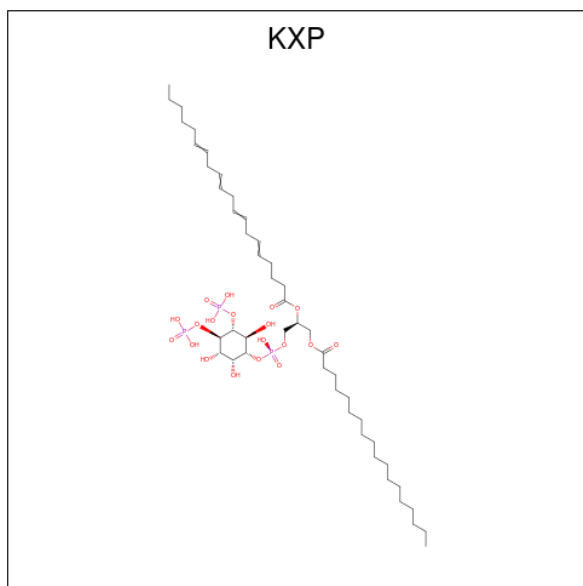
Chain	Residue	Modelled	Actual	Comment	Reference
B	398	GLU	-	expression tag	UNP P97300

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Chain	Residue	Modelled	Actual	Comment	Reference
B	399	ASN	-	expression tag	UNP P97300
B	400	LEU	-	expression tag	UNP P97300
B	401	TYR	-	expression tag	UNP P97300
B	402	PHE	-	expression tag	UNP P97300
B	403	GLN	-	expression tag	UNP P97300
B	404	GLY	-	expression tag	UNP P97300
B	405	GLY	-	expression tag	UNP P97300
B	406	HIS	-	expression tag	UNP P97300
B	407	HIS	-	expression tag	UNP P97300
B	408	HIS	-	expression tag	UNP P97300
B	409	HIS	-	expression tag	UNP P97300
B	410	HIS	-	expression tag	UNP P97300
B	411	HIS	-	expression tag	UNP P97300
B	412	HIS	-	expression tag	UNP P97300
B	413	HIS	-	expression tag	UNP P97300

- Molecule 3 is (2S)-1-{[(R)-hydroxy{[(1R,2R,3S,4R,5R,6S)-2,3,6-trihydroxy-4,5-bis(phosphonoxy)cyclohexyl]oxy}phosphoryl]oxy}-3-(octadecanoyloxy)propan-2-yl icoso-5,8,11,14-tetraenoate (CCD ID: KXP) (formula: C₄₇H₈₅O₁₉P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			39	17	19	3	

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

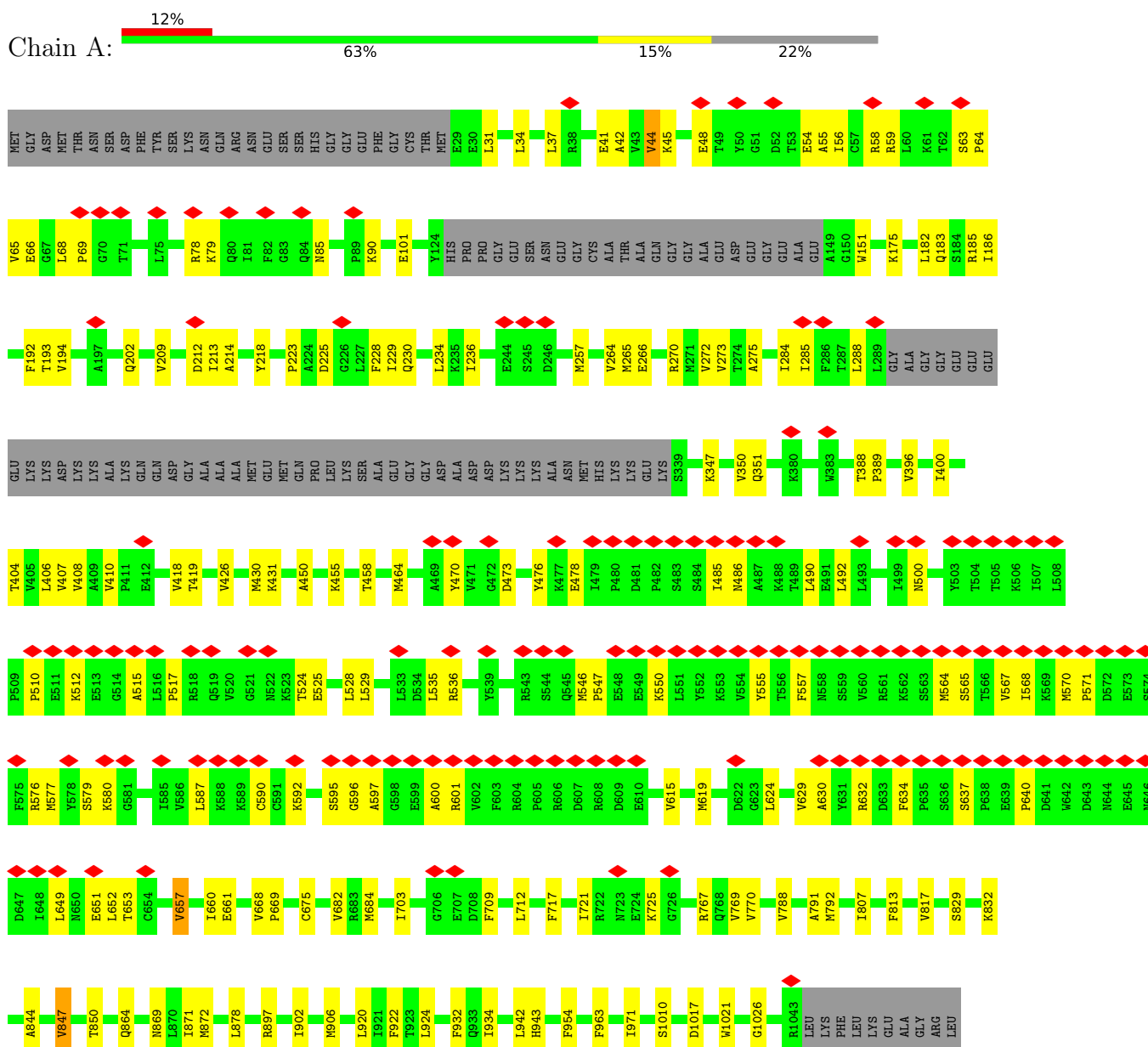


Mol	Chain	Residues	Atoms				AltConf
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	

3 Residue-property plots [i](#)

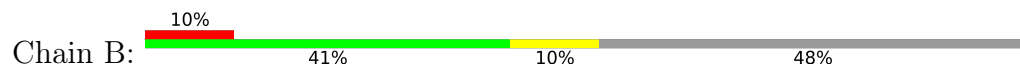
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Plasma membrane calcium-transporting ATPase 2



LEU	THR	THR	ASP	THR	SER	LYS	SER	ALA	THR	SER	SER	SER	PRO	GLY	SER	PRO	ILE	HIS	SER	SER	LEU	GLU	THR	THR	SER	SER	LEU	GLU	ASN	LEU	TYR	PHE	GLN	GLY	GLY	ASP	TYR	LYS	ASP	ASP	ASP	ASP	LYS
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- Molecule 2: Neuroplastin



GLU	ILE	GLN	TRP	TRP	TYR	ALA	GLU	VAL	ASN	ARG	ALA	GLU	SER	PHE	ARG	GLN	LEU	TRP	ASP	GLY	ALA	ALA	ARG	LYS	ARG	ARG	VAL	VAL	THR	THR	ASN	ASN	THR	ALA	ALA	GLY	TYR	SER	ASN	GLY	VAL	VAL	SER	SER	LEU	ARG	ILE	THR	ARG	LEU	THR	LEU	GLU	ASP	SER	GLY	GLY	TYR	TYR	GLU	CYS	ARG	ALA	ALA	SER	ASN
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Category	Item	Value	Color	Label
A	V188	1.00	Red	ASP
	E189	1.00	Red	PRO
	L190	1.00	Red	LYS
	T191	1.00	Red	ARG
	A192	1.00	Red	ASN
	T193	1.00	Red	ASP
	R194	1.00	Red	LEU
	K195	1.00	Red	ARG
	N196	1.00	Red	GLN
	A197	1.00	Red	ASN
B	S198	1.00	Red	PRO
	N199	1.00	Red	SER
	M200	1.00	Yellow	ILE
	R203	1.00	Red	THR
	I204	1.00	Orange	TRP
	N205	1.00	Orange	ILE
	K206	1.00	Orange	ARG
	P207	1.00	Grey	ALA
	R208	1.00	Grey	ALA
	A209	1.00	Grey	THR
C	G213	1.00	Red	ILE
	E214	1.00	Red	ILE
	Y215	1.00	Red	ALA
	H216	1.00	Green	ALA
	V217	1.00	Green	THR
	C218	1.00	Green	THR
	Y219	1.00	Green	ILE
	H220	1.00	Green	SER
	F221	1.00	Green	VAL
	V222	1.00	Green	LEU
D	S223	1.00	Red	GLN
	A224	1.00	Red	K147
	P225	1.00	Red	P148
	K226	1.00	Red	R149
	A227	1.00	Red	T150
	N228	1.00	Red	V151
	A229	1.00	Green	E154
	K234	1.00	Red	R159
	I239	1.00	Yellow	E160
	M256	1.00	Yellow	S161
E	Y263	1.00	Red	L162
	P264	1.00	Red	L163
	W268	1.00	Red	P164
	I269	1.00	Red	Q168
	R270	1.00	Red	L171
	K271	1.00	Red	T172
	K272	1.00	Red	S173
	N275	1.00	Red	S174
	F278	1.00	Red	S175
	E279	1.00	Red	H176

E294 Y313 A317 T318 I0319 A324 S325 Y326 E360 LVS ARG ARG LVS ARG ARG PRO ASP ASP ASP ASP ASP GLU PRO PRO ALA GLY PRO MET LVS LVS THR THR SER THR THR ASN ASN ASN ASN LVS LVS ASP ASN ASN LEU ARG GLN GLM ASN THR THR ASN ASN GLU GLU ASN LEU TYR PHE GLM GLY GLY THR

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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	292379	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.096	Depositor
Minimum map value	-1.670	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.312	Depositor
Map size (\AA)	273.0, 273.0, 273.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.91, 0.91, 0.91	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.17	0/7462	0.37	0/10116
2	B	0.17	0/1741	0.45	0/2366
All	All	0.17	0/9203	0.38	0/12482

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

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	7329	0	7554	129	0
2	B	1703	0	1672	35	0
3	A	39	0	0	0	0
4	B	84	0	78	1	0
All	All	9155	0	9304	164	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 9.

All (164) 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:55:ALA:HA	1:A:58:ARG:HE	1.41	0.84
2:B:206:LYS:HA	2:B:206:LYS:HE2	1.61	0.81
1:A:668:VAL:HG23	1:A:669:PRO:HD3	1.69	0.74
1:A:192:PHE:HD1	1:A:193:THR:N	1.90	0.68
2:B:181:SER:HB2	2:B:200:MET:HE3	1.77	0.67
2:B:256:MET:HE1	2:B:313:TYR:HB2	1.77	0.66
1:A:570:MET:HE3	1:A:571:PRO:HD3	1.75	0.66
1:A:54:GLU:O	1:A:58:ARG:HG3	1.96	0.65
1:A:192:PHE:HD1	1:A:193:THR:H	1.43	0.65
1:A:535:LEU:HA	1:A:536:ARG:HH21	1.62	0.65
1:A:65:VAL:HG21	1:A:230:GLN:HE22	1.61	0.65
1:A:902:ILE:HG23	1:A:906:MET:HE2	1.80	0.64
1:A:592:LYS:HB2	1:A:653:THR:HG22	1.79	0.64
1:A:577:MET:HE2	1:A:632:ARG:HD2	1.79	0.63
2:B:214:GLU:HB2	2:B:263:TYR:HE2	1.63	0.63
1:A:59:ARG:O	1:A:59:ARG:HD2	1.97	0.63
1:A:225:ASP:HB2	1:A:275:ALA:HB3	1.80	0.63
2:B:263:TYR:CD1	2:B:264:PRO:HA	2.33	0.63
2:B:219:TYR:O	2:B:226:LYS:HA	1.99	0.62
1:A:182:LEU:HD22	1:A:426:VAL:HG11	1.81	0.62
2:B:164:PRO:HB3	2:B:205:ASN:HA	1.82	0.61
1:A:725:LYS:N	1:A:725:LYS:HD3	2.16	0.61
1:A:632:ARG:HH21	1:A:651:GLU:HB3	1.64	0.61
2:B:271:ARG:HD2	2:B:278:PHE:HB3	1.82	0.60
1:A:632:ARG:HB3	1:A:652:LEU:HD23	1.84	0.60
1:A:832:LYS:HB3	1:A:971:ILE:HD11	1.84	0.59
1:A:767:ARG:HB3	1:A:897:ARG:HH12	1.66	0.59
1:A:550:LYS:HB3	1:A:568:ILE:HG13	1.84	0.59
1:A:512:LYS:HB3	1:A:515:ALA:HB3	1.84	0.59
2:B:180:TYR:HE1	2:B:182:TYR:HB3	1.68	0.59
1:A:284:ILE:HG13	1:A:285:ILE:HD12	1.85	0.58
2:B:263:TYR:HD1	2:B:264:PRO:HA	1.67	0.58
2:B:214:GLU:HB2	2:B:263:TYR:CE2	2.39	0.58
1:A:668:VAL:HG12	1:A:813:PHE:HB3	1.86	0.58
1:A:703:ILE:HG13	1:A:709:PHE:HD1	1.68	0.58
2:B:183:TRP:HD1	2:B:193:THR:HB	1.69	0.58
1:A:486:ASN:HD21	1:A:597:ALA:HA	1.68	0.58
1:A:284:ILE:O	1:A:288:LEU:HG	2.04	0.57
1:A:450:ALA:HB3	1:A:770:VAL:HG12	1.85	0.57
1:A:257:MET:HA	1:A:257:MET:HE3	1.86	0.57
1:A:408:VAL:HG22	1:A:869:ASN:HB2	1.85	0.57
1:A:192:PHE:CD1	1:A:193:THR:N	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:624:LEU:HG	1:A:661:GLU:HB3	1.88	0.56
1:A:942:LEU:HD12	1:A:943:HIS:N	2.20	0.56
1:A:577:MET:HE3	1:A:652:LEU:HD21	1.89	0.55
1:A:194:VAL:HG12	1:A:214:ALA:HA	1.87	0.55
1:A:229:ILE:HD11	1:A:272:VAL:HG12	1.88	0.55
1:A:347:LYS:O	1:A:351:GLN:HG2	2.07	0.55
1:A:577:MET:HE1	1:A:649:LEU:HA	1.89	0.55
1:A:942:LEU:HD12	1:A:943:HIS:H	1.71	0.55
1:A:571:PRO:HG3	1:A:576:ARG:HG2	1.88	0.54
1:A:185:ARG:O	1:A:185:ARG:HD2	2.07	0.54
1:A:524:THR:O	1:A:528:LEU:HG	2.08	0.54
1:A:183:GLN:O	1:A:186:ILE:HG22	2.08	0.54
1:A:265:MET:HB3	1:A:266:GLU:OE2	2.07	0.54
2:B:213:GLY:HA2	2:B:263:TYR:HD2	1.73	0.53
2:B:200:MET:HE2	2:B:217:CYS:HB2	1.91	0.53
1:A:464:MET:HB3	1:A:660:ILE:HD11	1.91	0.53
1:A:175:LYS:HD2	1:A:419:THR:HG22	1.89	0.52
1:A:791:ALA:HB3	1:A:807:ILE:HG22	1.91	0.52
1:A:63:SER:HB3	1:A:68:LEU:HA	1.91	0.52
1:A:192:PHE:HD2	1:A:223:PRO:HG3	1.73	0.51
2:B:271:ARG:HG2	2:B:279:GLU:C	2.35	0.51
1:A:557:PHE:HB2	1:A:564:MET:HB2	1.92	0.51
2:B:263:TYR:HD1	2:B:264:PRO:CA	2.22	0.51
2:B:268:TRP:CZ3	2:B:317:ALA:HB2	2.46	0.51
2:B:200:MET:CE	2:B:217:CYS:HB2	2.41	0.50
1:A:492:LEU:HD11	1:A:576:ARG:HH22	1.77	0.50
1:A:78:ARG:HG3	1:A:209:VAL:HG21	1.94	0.50
1:A:632:ARG:HD3	1:A:634:PHE:CE1	2.47	0.50
2:B:317:ALA:HB3	2:B:324:ALA:O	2.11	0.50
1:A:510:PRO:HA	1:A:517:PRO:HA	1.93	0.49
1:A:485:ILE:HG21	1:A:490:LEU:HD13	1.95	0.49
2:B:193:THR:H	2:B:194:ARG:NH1	2.09	0.49
2:B:180:TYR:CE1	2:B:182:TYR:HB3	2.47	0.49
2:B:197:ALA:HB1	2:B:200:MET:HG3	1.94	0.49
1:A:577:MET:SD	1:A:649:LEU:HD22	2.53	0.49
1:A:64:PRO:HG2	1:A:66:GLU:OE1	2.13	0.48
1:A:34:LEU:HD12	1:A:34:LEU:O	2.13	0.48
1:A:632:ARG:NH2	1:A:651:GLU:HB3	2.28	0.48
1:A:79:LYS:NZ	1:A:85:ASN:HD21	2.11	0.48
1:A:101:GLU:OE2	1:A:101:GLU:HA	2.14	0.48
1:A:590:CYS:HA	1:A:652:LEU:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:MET:HG3	1:A:524:THR:HA	1.96	0.47
2:B:264:PRO:HD2	2:B:319:ASN:ND2	2.29	0.47
1:A:218:TYR:HA	1:A:264:VAL:HG12	1.96	0.47
1:A:228:PHE:HE1	1:A:230:GLN:C	2.23	0.47
1:A:864:GLN:HE21	1:A:1010:SER:HB2	1.80	0.46
1:A:525:GLU:O	1:A:529:LEU:HG	2.15	0.46
1:A:767:ARG:HH11	1:A:897:ARG:HH11	1.63	0.46
1:A:717:PHE:O	1:A:721:ILE:HG12	2.16	0.46
1:A:675:CYS:SG	1:A:817:VAL:HG22	2.56	0.46
1:A:767:ARG:HH11	1:A:897:ARG:NH1	2.13	0.46
1:A:580:LYS:HG2	1:A:629:VAL:HG22	1.97	0.46
1:A:41:GLU:O	1:A:44:VAL:HG22	2.17	0.45
1:A:920:LEU:HD12	1:A:920:LEU:HA	1.66	0.45
2:B:159:ARG:HG3	2:B:160:GLU:H	1.81	0.45
1:A:637:SER:HB2	1:A:640:PRO:HG3	1.99	0.45
2:B:272:LYS:HD3	2:B:313:TYR:HE1	1.82	0.45
1:A:455:LYS:HB2	1:A:684:MET:HE3	1.98	0.44
1:A:473:ASP:N	1:A:595:SER:HB2	2.32	0.44
1:A:712:LEU:HD23	1:A:712:LEU:H	1.82	0.44
1:A:350:VAL:HG23	1:A:351:GLN:OE1	2.16	0.44
1:A:430:MET:HE2	1:A:430:MET:HB3	1.65	0.44
2:B:214:GLU:CB	2:B:263:TYR:HE2	2.26	0.44
1:A:236:ILE:HG23	1:A:264:VAL:HA	1.99	0.44
1:A:192:PHE:CD2	1:A:223:PRO:HG3	2.53	0.44
1:A:485:ILE:HG13	1:A:486:ASN:H	1.82	0.44
1:A:546:MET:HE1	1:A:550:LYS:HB2	2.00	0.44
1:A:213:ILE:HA	1:A:213:ILE:HD13	1.84	0.44
2:B:185:ARG:HD2	2:B:215:TYR:CZ	2.53	0.44
1:A:212:ASP:O	1:A:273:VAL:HG22	2.18	0.43
1:A:458:THR:OG1	1:A:792:MET:HE1	2.18	0.43
1:A:470:TYR:HB3	1:A:657:VAL:HG23	1.99	0.43
1:A:230:GLN:NE2	1:A:270:ARG:HD2	2.34	0.43
1:A:151:TRP:H	1:A:151:TRP:CD1	2.36	0.43
1:A:546:MET:HE3	1:A:547:PRO:O	2.18	0.43
1:A:630:ALA:HB1	1:A:652:LEU:HB3	2.01	0.43
1:A:202:GLN:N	1:A:202:GLN:CD	2.76	0.43
1:A:492:LEU:HD11	1:A:576:ARG:NH2	2.33	0.43
1:A:596:GLY:HA3	1:A:601:ARG:HD3	2.01	0.43
1:A:79:LYS:HZ2	1:A:85:ASN:HD21	1.67	0.43
1:A:228:PHE:CD1	1:A:228:PHE:C	2.95	0.43
2:B:208:ARG:HG3	2:B:209:ALA:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:VAL:HG22	1:A:577:MET:HB2	2.01	0.42
2:B:294:GLU:OE2	4:B:502:NAG:H61	2.19	0.42
1:A:568:ILE:HG12	1:A:570:MET:H	1.84	0.42
1:A:844:ALA:O	1:A:847:VAL:HG12	2.19	0.42
1:A:565:SER:HB3	1:A:579:SER:HA	2.01	0.42
1:A:675:CYS:HG	1:A:817:VAL:HG22	1.85	0.42
1:A:615:VAL:O	1:A:619:MET:HG2	2.20	0.42
2:B:204:ILE:HD11	2:B:207:PRO:HA	2.01	0.42
1:A:37:LEU:HD13	1:A:42:ALA:H	1.83	0.42
1:A:476:TYR:HB3	1:A:478:GLU:O	2.20	0.42
1:A:932:PHE:HB2	1:A:934:ILE:HG12	2.00	0.42
1:A:587:LEU:HD12	1:A:587:LEU:HA	1.89	0.42
1:A:564:MET:O	1:A:564:MET:HE3	2.19	0.42
1:A:500:ASN:HD22	1:A:580:LYS:HG3	1.85	0.42
1:A:44:VAL:O	1:A:48:GLU:HG2	2.20	0.41
2:B:180:TYR:HE2	2:B:220:HIS:HD1	1.67	0.41
1:A:406:LEU:O	1:A:410:VAL:HG12	2.19	0.41
2:B:183:TRP:CD1	2:B:193:THR:HB	2.50	0.41
1:A:234:LEU:HD23	1:A:234:LEU:HA	1.89	0.41
1:A:850:THR:HG21	1:A:922:PHE:CZ	2.56	0.41
1:A:388:THR:N	1:A:389:PRO:HD2	2.36	0.41
1:A:41:GLU:O	1:A:45:LYS:HG2	2.20	0.41
1:A:59:ARG:HD2	1:A:59:ARG:C	2.46	0.41
1:A:864:GLN:HB3	1:A:954:PHE:CE1	2.55	0.41
1:A:68:LEU:HD12	1:A:69:PRO:HD2	2.02	0.41
1:A:90:LYS:HE2	1:A:90:LYS:HB2	1.89	0.41
1:A:185:ARG:NE	1:A:430:MET:HE1	2.35	0.41
1:A:404:THR:O	1:A:407:VAL:HG12	2.21	0.41
1:A:555:TYR:HD2	1:A:565:SER:OG	2.04	0.40
1:A:570:MET:N	1:A:571:PRO:HD2	2.36	0.40
1:A:592:LYS:HD2	1:A:600:ALA:HB1	2.02	0.40
1:A:829:SER:O	1:A:832:LYS:HG2	2.22	0.40
1:A:1017:ASP:OD1	1:A:1021:TRP:CD1	2.74	0.40
2:B:234:LYS:HB3	2:B:263:TYR:O	2.21	0.40
1:A:592:LYS:HG3	1:A:651:GLU:OE2	2.21	0.40
1:A:963:PHE:HD2	1:A:1026:GLY:C	2.30	0.40
1:A:431:LYS:HE2	1:A:431:LYS:HB2	1.96	0.40
2:B:239:ILE:HG21	2:B:326:VAL:HG21	2.04	0.40
1:A:878:LEU:HD23	1:A:878:LEU:HA	1.97	0.40
2:B:269:ILE:N	2:B:269:ILE:HD12	2.37	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	936/1214 (77%)	896 (96%)	40 (4%)	0	100	100
2	B	212/413 (51%)	205 (97%)	7 (3%)	0	100	100
All	All	1148/1627 (71%)	1101 (96%)	47 (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	A	817/1046 (78%)	803 (98%)	14 (2%)	56	73
2	B	191/361 (53%)	189 (99%)	2 (1%)	73	83
All	All	1008/1407 (72%)	992 (98%)	16 (2%)	58	74

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	44	VAL
1	A	56	ILE
1	A	396	VAL
1	A	400	ILE
1	A	418	VAL
1	A	657	VAL
1	A	682	VAL

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Mol	Chain	Res	Type
1	A	769	VAL
1	A	788	VAL
1	A	847	VAL
1	A	871	ILE
1	A	872	MET
1	A	924	LEU
2	B	199	ASN
2	B	204	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	230	GLN
1	A	691	ASN
1	A	835	GLN
1	A	909	ASN
2	B	292	ASN
2	B	303	ASN
2	B	305	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](#)

7 ligands are modelled in this entry.

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	NAG	B	501	2	14,14,15	0.66	0	17,19,21	2.54	5 (29%)
3	KXP	A	1401	-	39,39,69	2.50	16 (41%)	51,56,87	6.16	4 (7%)
4	NAG	B	503	2	14,14,15	0.73	0	17,19,21	2.45	4 (23%)
4	NAG	B	505	2	14,14,15	0.71	0	17,19,21	0.85	0
4	NAG	B	506	2	14,14,15	0.72	0	17,19,21	0.90	0
4	NAG	B	502	2	14,14,15	0.66	0	17,19,21	1.05	1 (5%)
4	NAG	B	504	2	14,14,15	0.69	0	17,19,21	0.80	0

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	NAG	B	501	2	-	2/6/23/26	0/1/1/1
3	KXP	A	1401	-	-	19/35/59/90	0/1/1/1
4	NAG	B	503	2	-	1/6/23/26	0/1/1/1
4	NAG	B	505	2	-	1/6/23/26	0/1/1/1
4	NAG	B	506	2	-	2/6/23/26	0/1/1/1
4	NAG	B	502	2	-	3/6/23/26	0/1/1/1
4	NAG	B	504	2	-	0/6/23/26	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1401	KXP	P42-O41	7.13	1.72	1.59
3	A	1401	KXP	O50-C49	5.94	1.47	1.22
3	A	1401	KXP	C21-C22	4.89	1.65	1.50
3	A	1401	KXP	P37-O36	3.97	1.66	1.59
3	A	1401	KXP	P42-O43	-3.89	1.39	1.54
3	A	1401	KXP	P42-O45	-3.60	1.38	1.50
3	A	1401	KXP	C6-C3	-3.09	1.24	1.49
3	A	1401	KXP	C30-C29	3.01	1.60	1.52
3	A	1401	KXP	P25-O28	2.82	1.67	1.60
3	A	1401	KXP	O20-C18	2.67	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1401	KXP	P37-O39	-2.65	1.44	1.54
3	A	1401	KXP	O48-C49	2.59	1.39	1.33
3	A	1401	KXP	O20-C21	2.30	1.50	1.45
3	A	1401	KXP	O1-C18	-2.21	1.16	1.22
3	A	1401	KXP	O46-C31	2.16	1.48	1.43
3	A	1401	KXP	O24-C23	-2.01	1.37	1.44

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1401	KXP	O48-C49-O50	42.46	179.63	125.57
3	A	1401	KXP	C6-C3-C5	8.62	178.88	113.42
4	B	501	NAG	C2-N2-C7	7.42	133.47	122.90
4	B	503	NAG	C2-N2-C7	7.21	133.17	122.90
4	B	503	NAG	C1-C2-N2	4.43	118.06	110.49
4	B	501	NAG	C1-C2-N2	4.41	118.02	110.49
4	B	503	NAG	C1-O5-C5	3.66	117.15	112.19
4	B	501	NAG	O5-C1-C2	-3.33	106.03	111.29
3	A	1401	KXP	O20-C18-C1	2.89	120.97	111.91
4	B	501	NAG	O7-C7-N2	2.55	126.65	121.95
4	B	501	NAG	C4-C3-C2	-2.49	107.37	111.02
4	B	503	NAG	O7-C7-N2	2.45	126.46	121.95
4	B	502	NAG	O5-C1-C2	-2.31	107.64	111.29
3	A	1401	KXP	O27-P25-O26	-2.11	101.80	112.24

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1401	KXP	C31-C32-O41-P42
3	A	1401	KXP	O50-C49-O48-C22
3	A	1401	KXP	C23-O24-P25-O26
3	A	1401	KXP	C29-O28-P25-O27
4	B	501	NAG	C1-C2-N2-C7
4	B	503	NAG	C1-C2-N2-C7
4	B	502	NAG	C8-C7-N2-C2
4	B	502	NAG	O7-C7-N2-C2
4	B	506	NAG	C8-C7-N2-C2
4	B	506	NAG	O7-C7-N2-C2
3	A	1401	KXP	C1-C2-C4-C5
3	A	1401	KXP	C18-C1-C2-C4
3	A	1401	KXP	C29-O28-P25-O24

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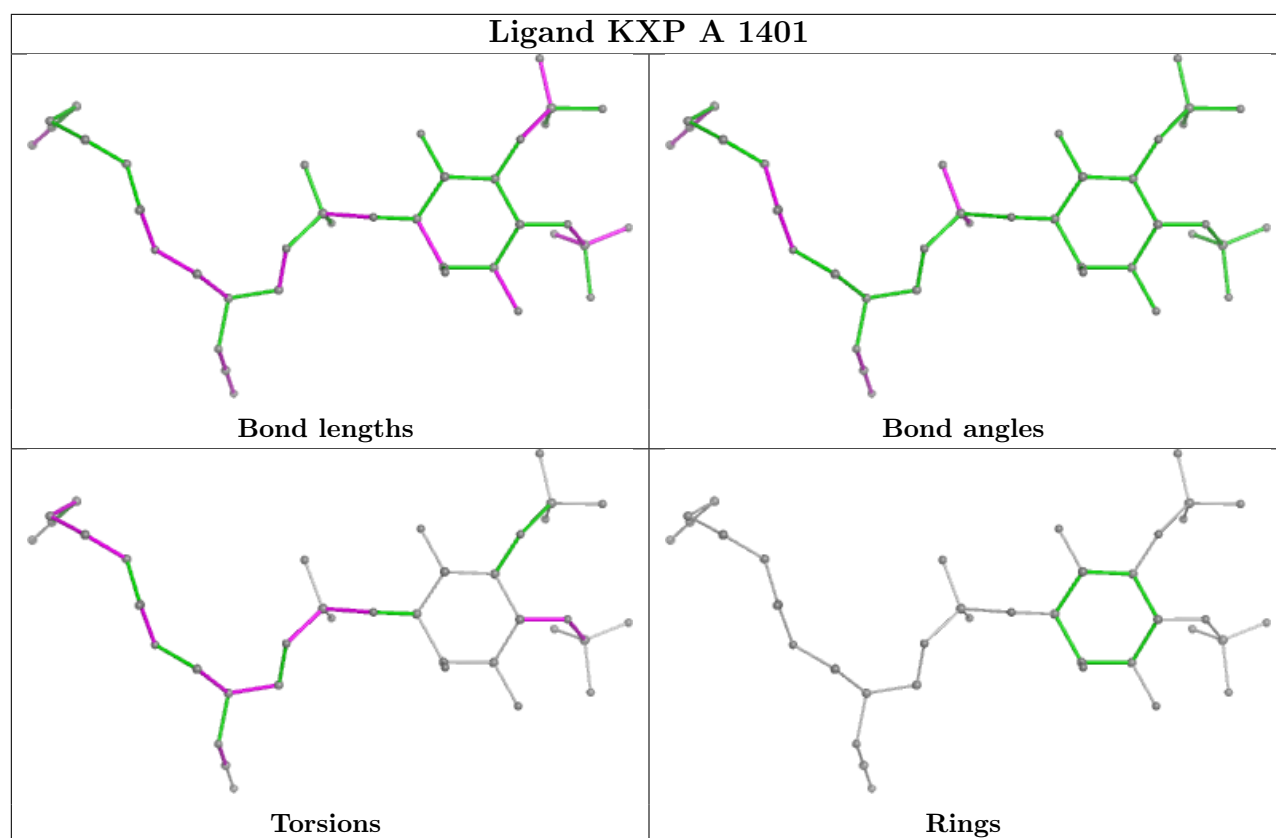
Mol	Chain	Res	Type	Atoms
3	A	1401	KXP	C1-C18-O20-C21
3	A	1401	KXP	C2-C4-C5-C3
3	A	1401	KXP	O1-C18-O20-C21
4	B	502	NAG	O5-C5-C6-O6
3	A	1401	KXP	C23-O24-P25-O28
3	A	1401	KXP	O20-C21-C22-C23
4	B	501	NAG	O5-C5-C6-O6
4	B	505	NAG	O5-C5-C6-O6
3	A	1401	KXP	C29-O28-P25-O26
3	A	1401	KXP	C32-O41-P42-O44
3	A	1401	KXP	O20-C21-C22-O48
3	A	1401	KXP	C21-C22-C23-O24
3	A	1401	KXP	O48-C22-C23-O24
3	A	1401	KXP	C32-O41-P42-O43
3	A	1401	KXP	C23-O24-P25-O27

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	502	NAG	1	0

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.

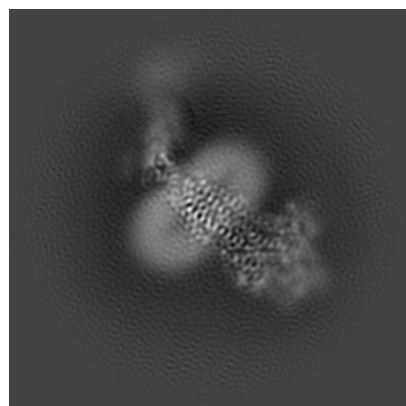
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51545. These allow visual inspection of the internal detail of the map and identification of artifacts.

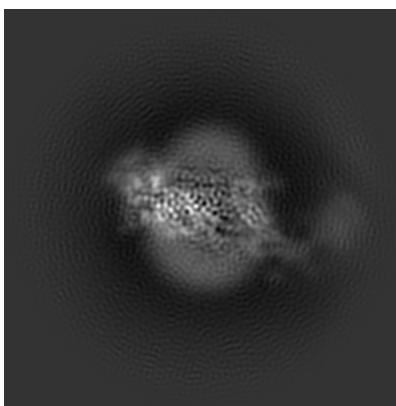
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

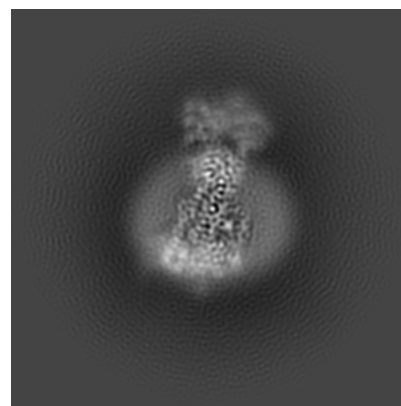
6.1.1 Primary map



X

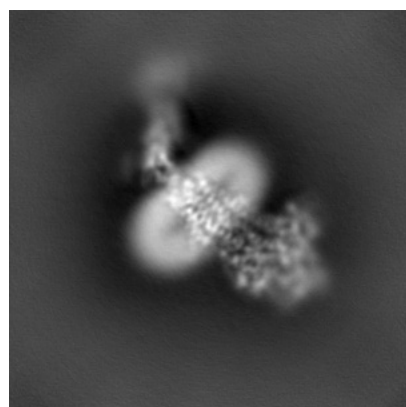


Y

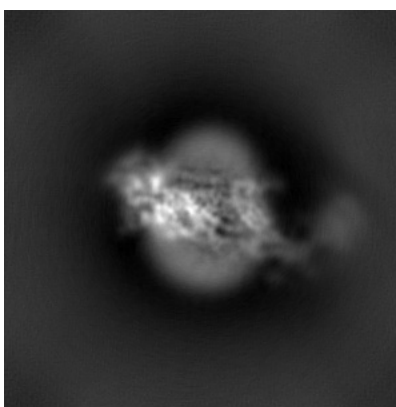


Z

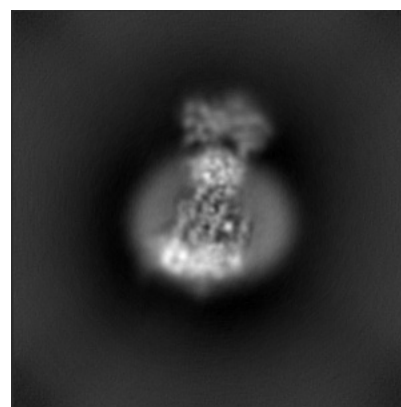
6.1.2 Raw map



X



Y

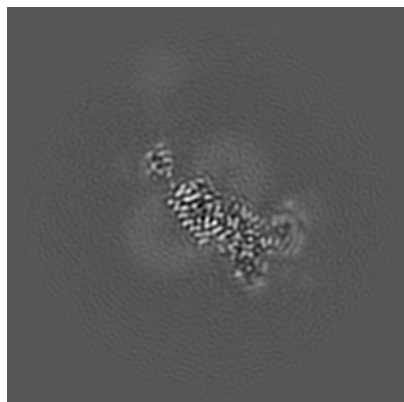


Z

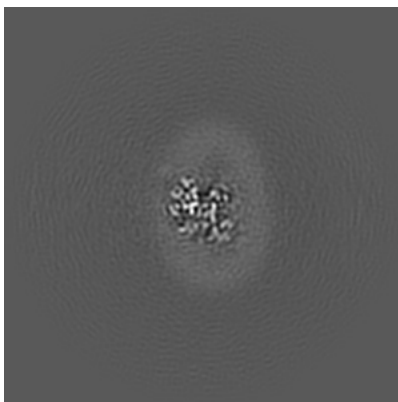
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

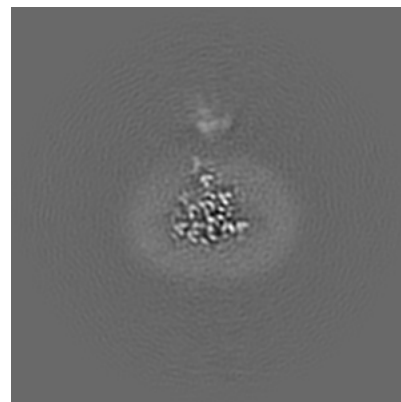
6.2.1 Primary map



X Index: 150

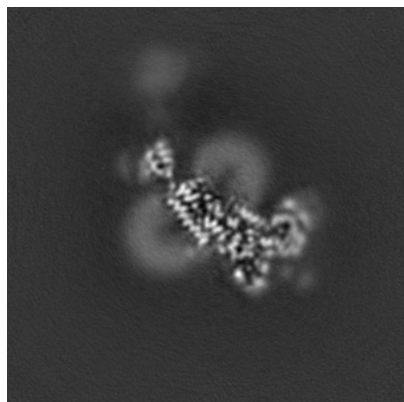


Y Index: 150

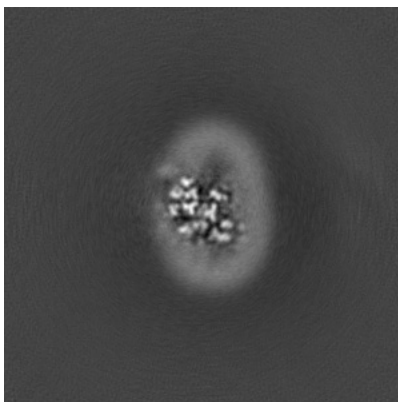


Z Index: 150

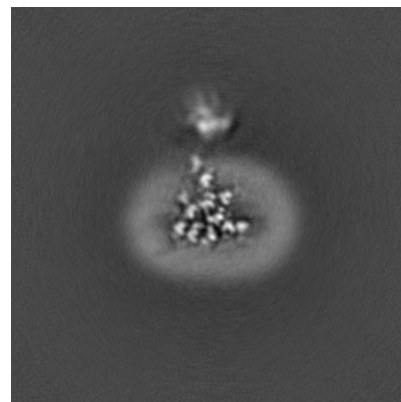
6.2.2 Raw map



X Index: 150



Y Index: 150

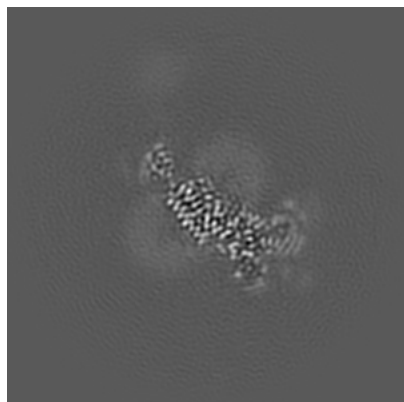


Z Index: 150

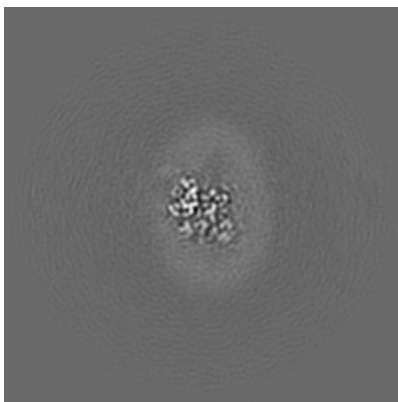
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

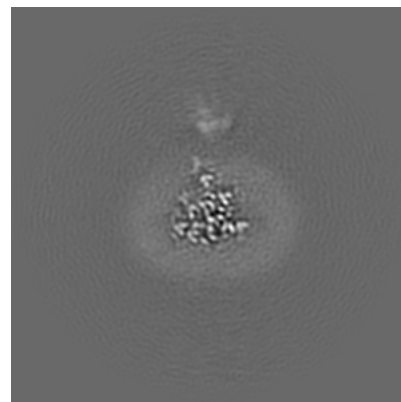
6.3.1 Primary map



X Index: 151

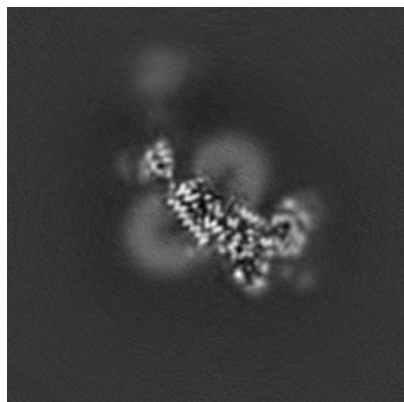


Y Index: 149

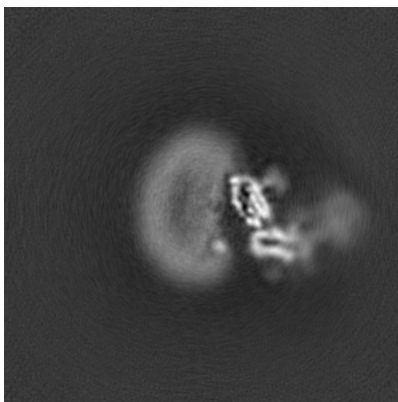


Z Index: 150

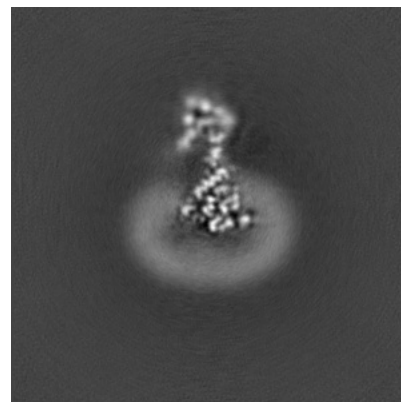
6.3.2 Raw map



X Index: 150



Y Index: 115

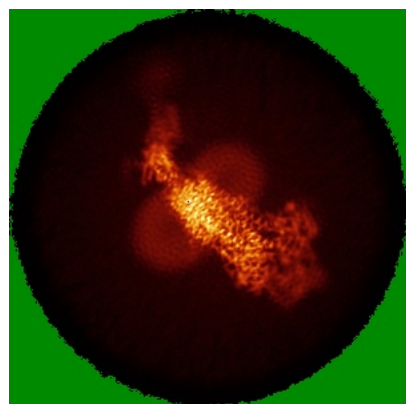


Z Index: 138

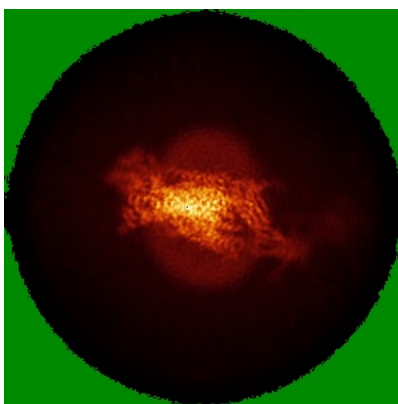
The images above show the largest variance slices of the map in three orthogonal directions.

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

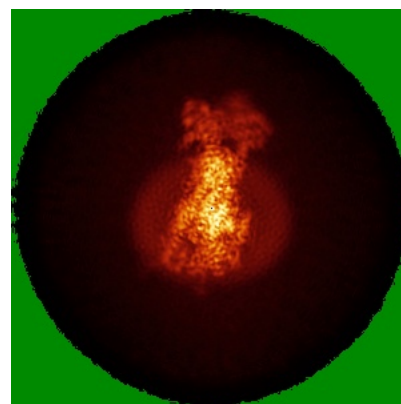
6.4.1 Primary map



X

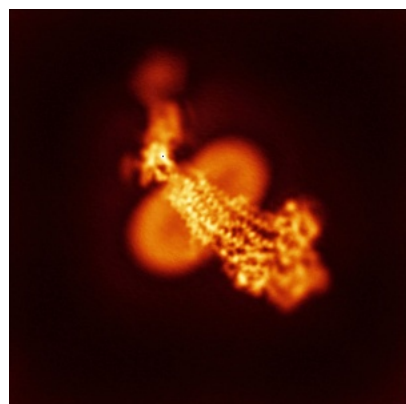


Y

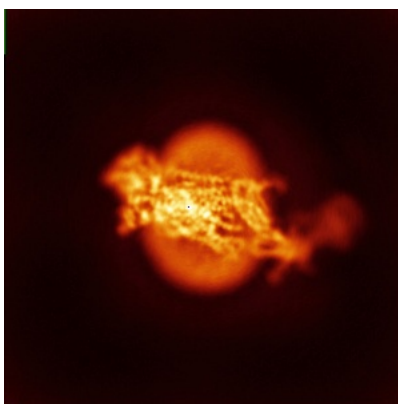


Z

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 0.312. 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.

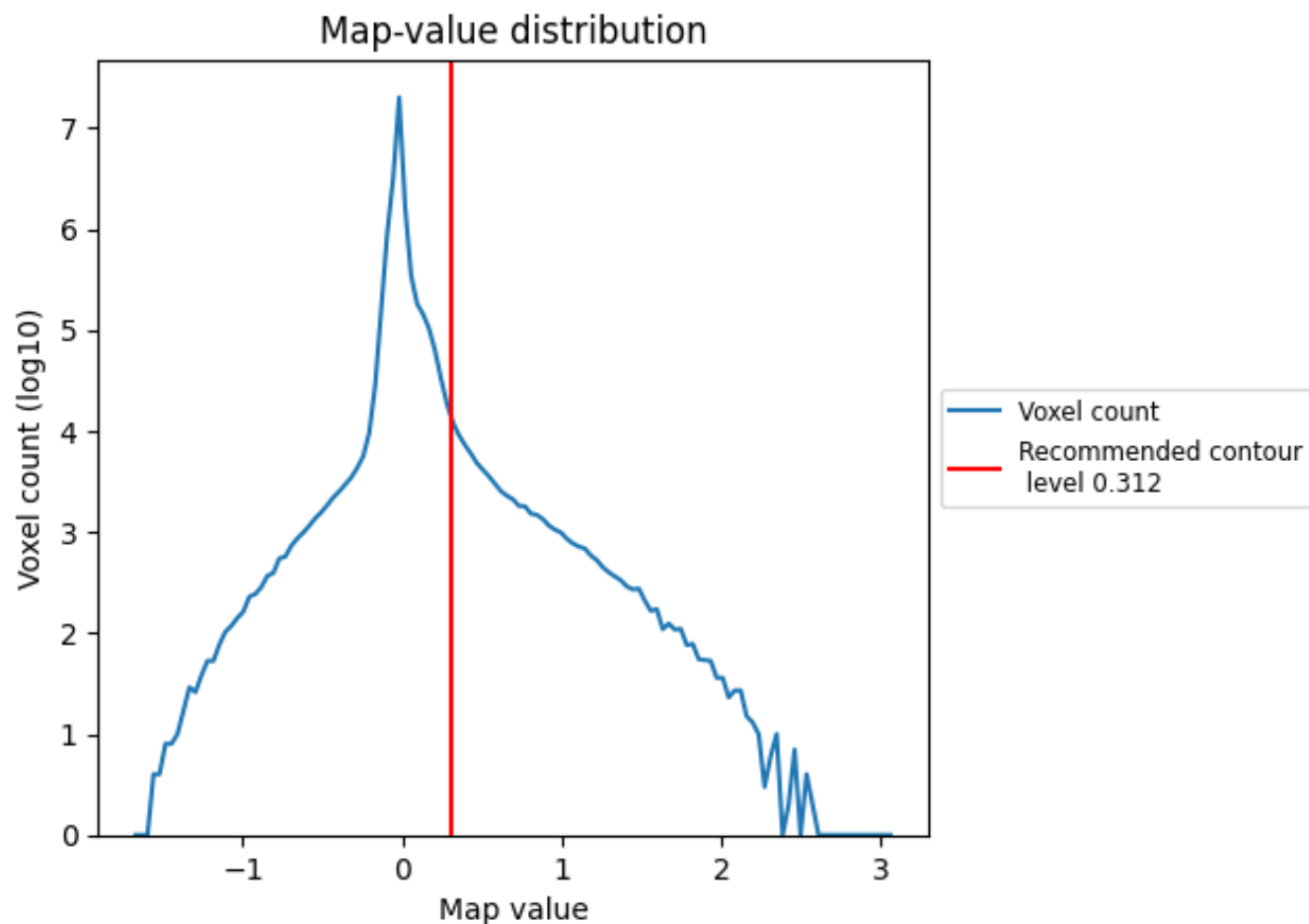
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

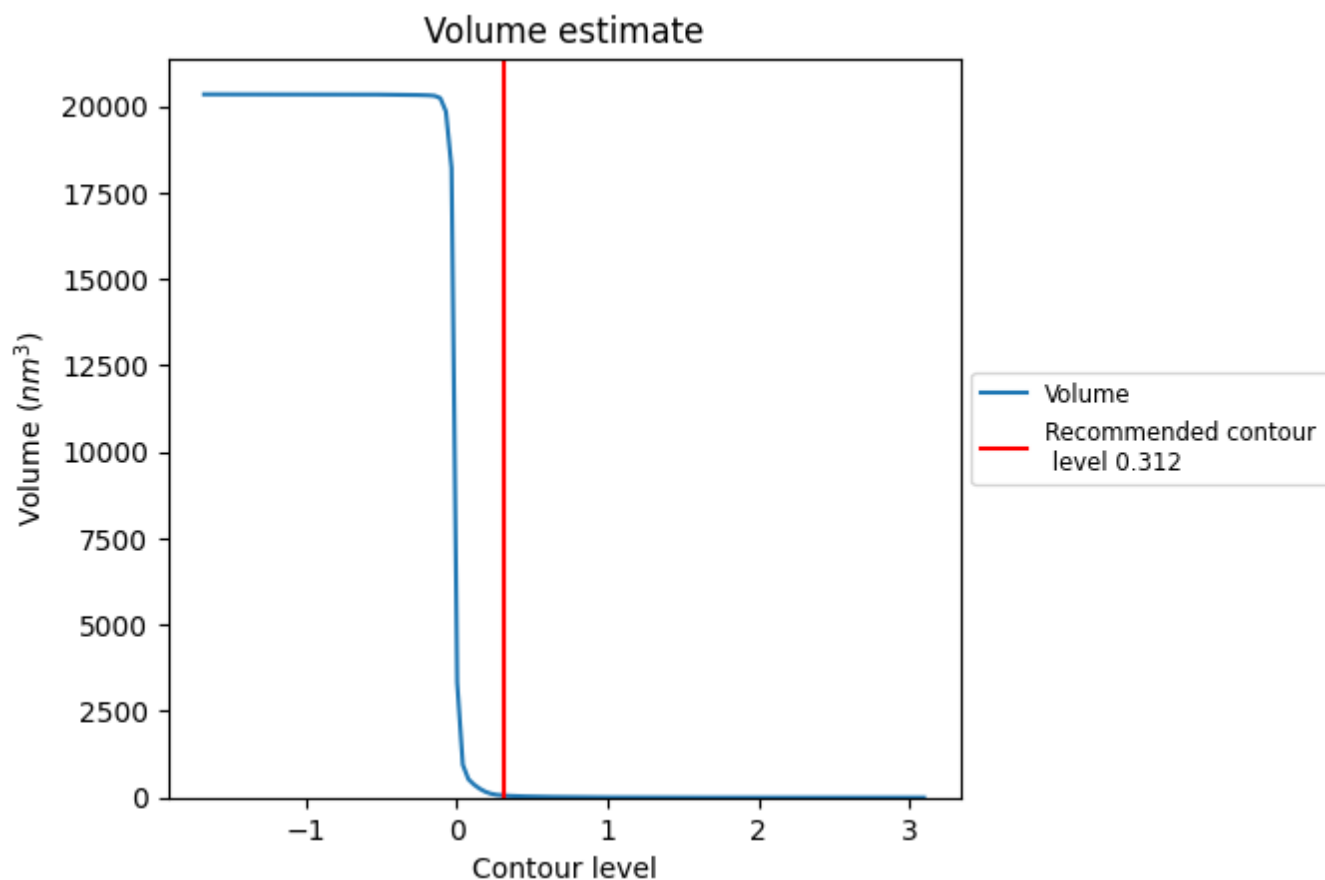
This section contains the results of statistical analysis of the map.

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.

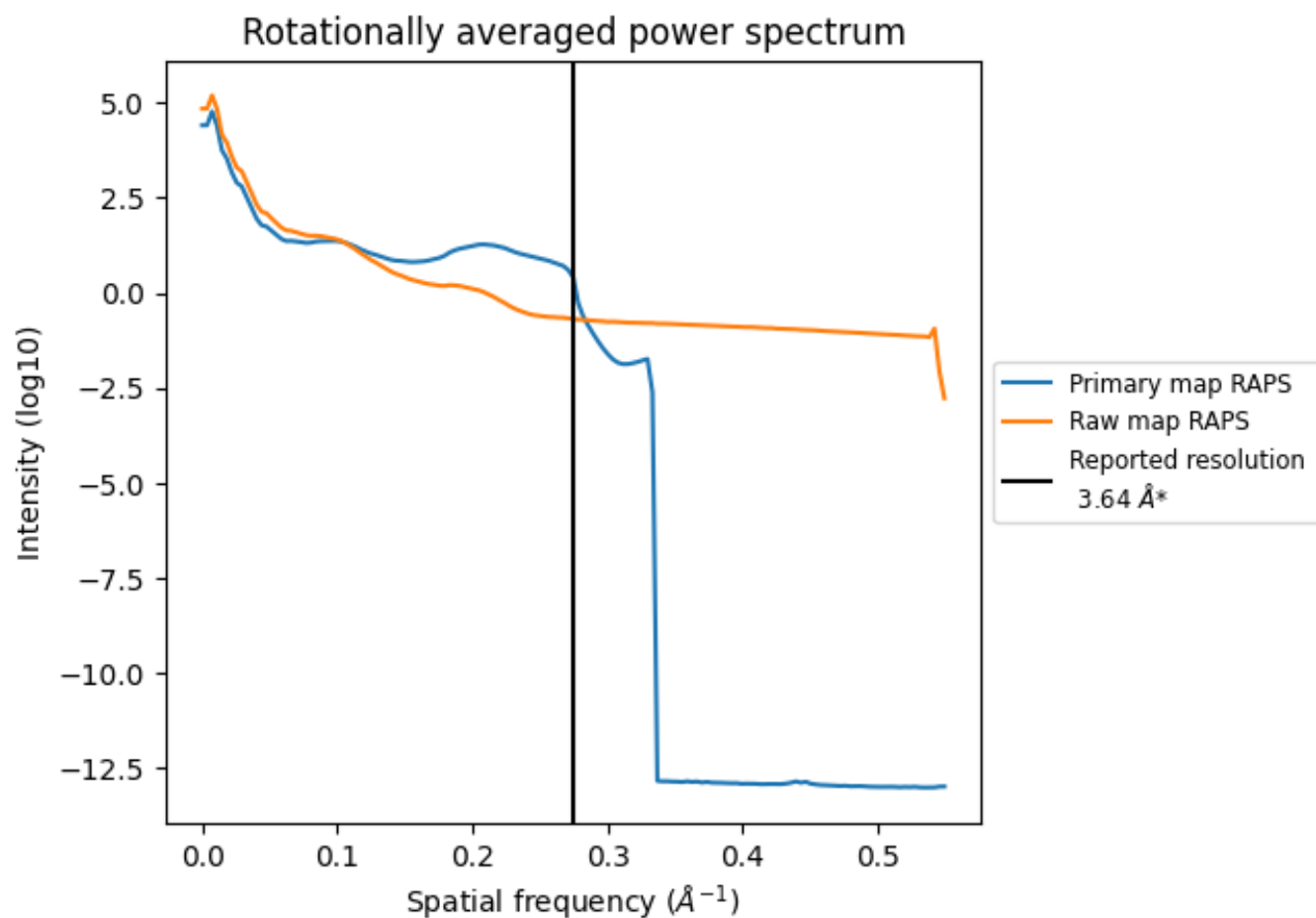
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 60 nm³; this corresponds to an approximate mass of 54 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 ⓘ

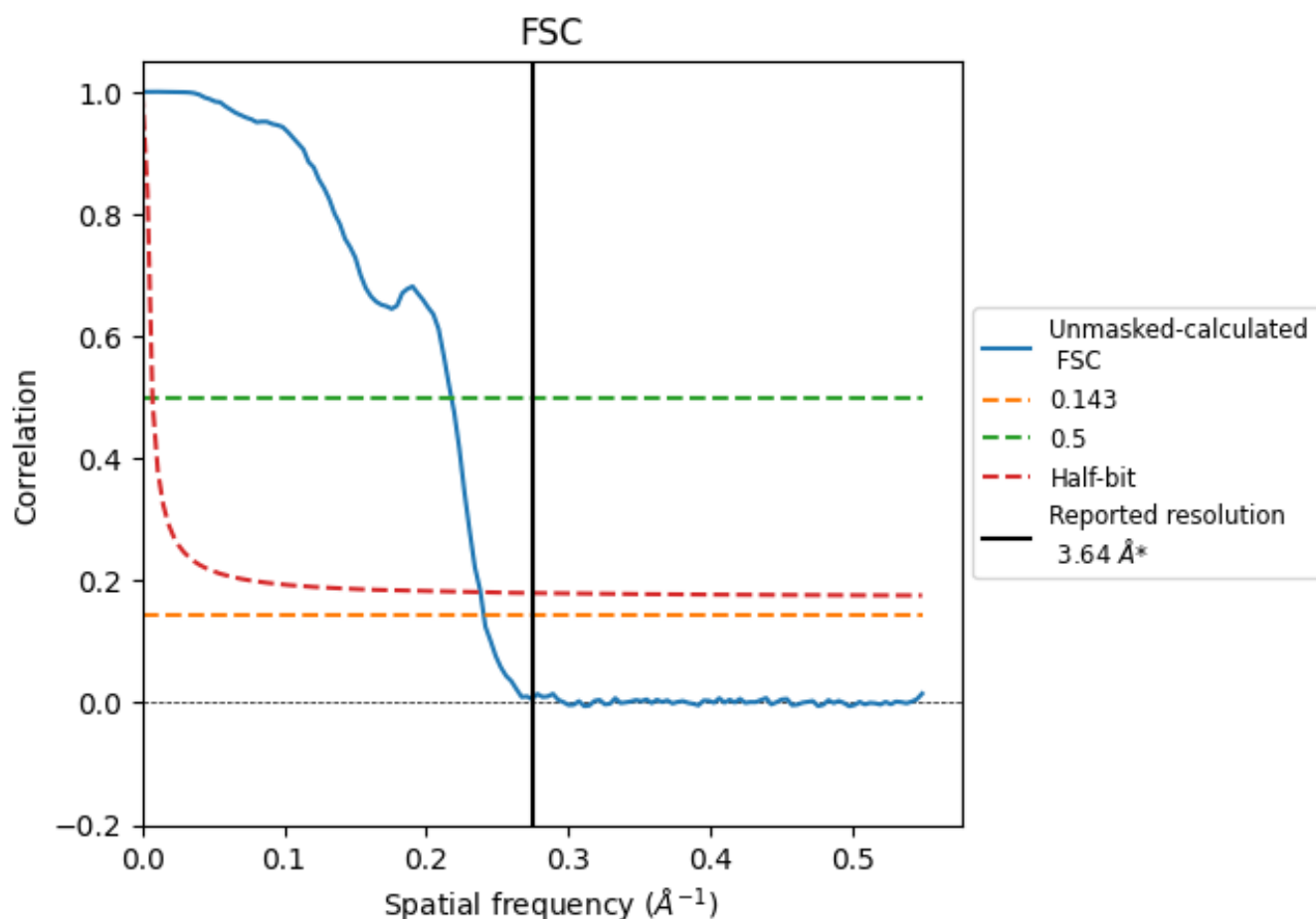


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

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 0.275 \AA^{-1}

8.2 Resolution estimates [i](#)

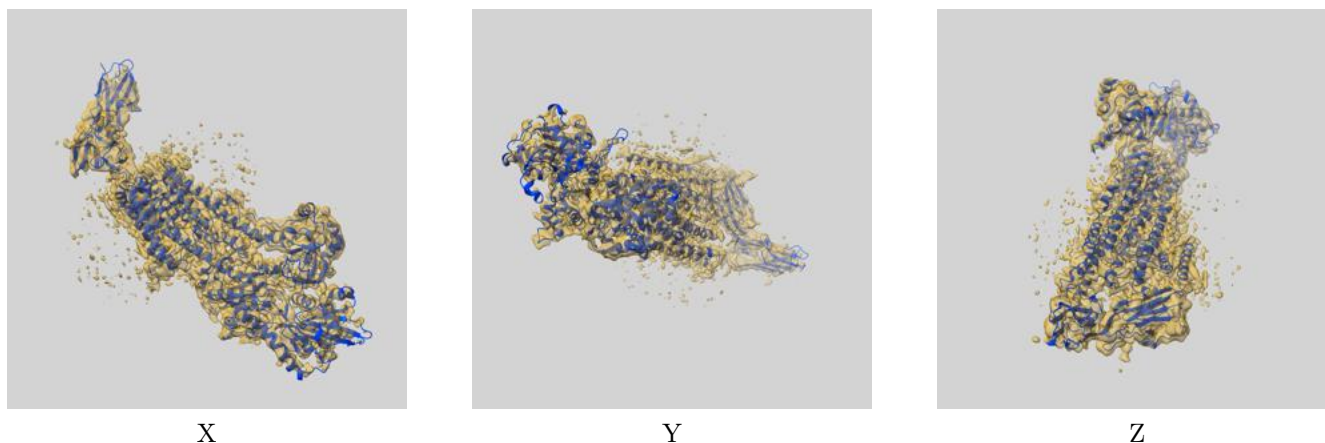
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.16	4.59	4.20

*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 4.16 differs from the reported value 3.64 by more than 10 %

9 Map-model fit [i](#)

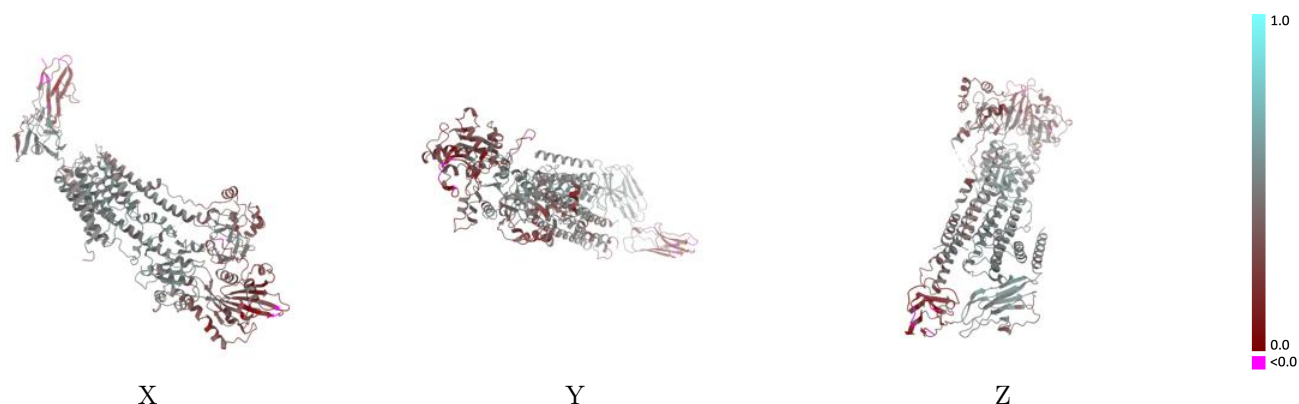
This section contains information regarding the fit between EMDB map EMD-51545 and PDB model 9GSE. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



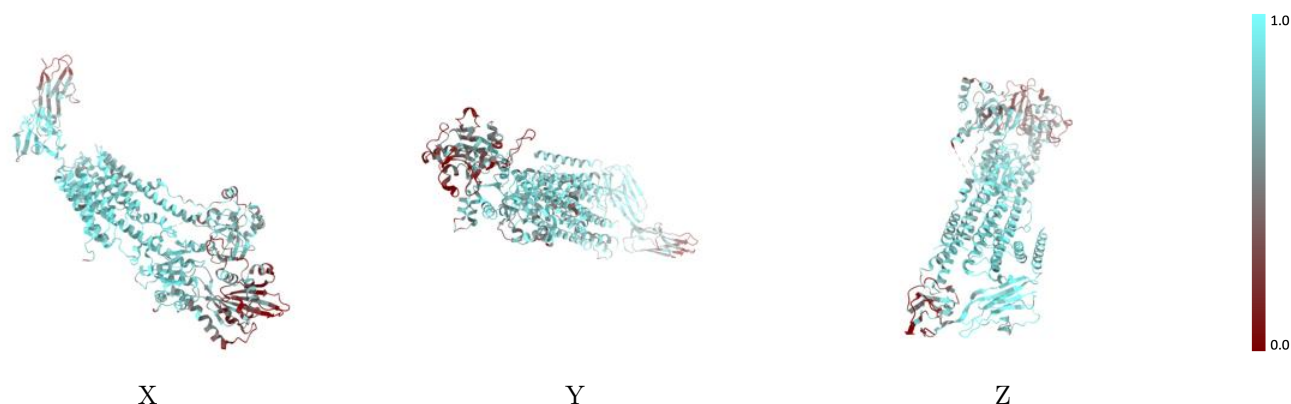
The images above show the 3D surface view of the map at the recommended contour level 0.312 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



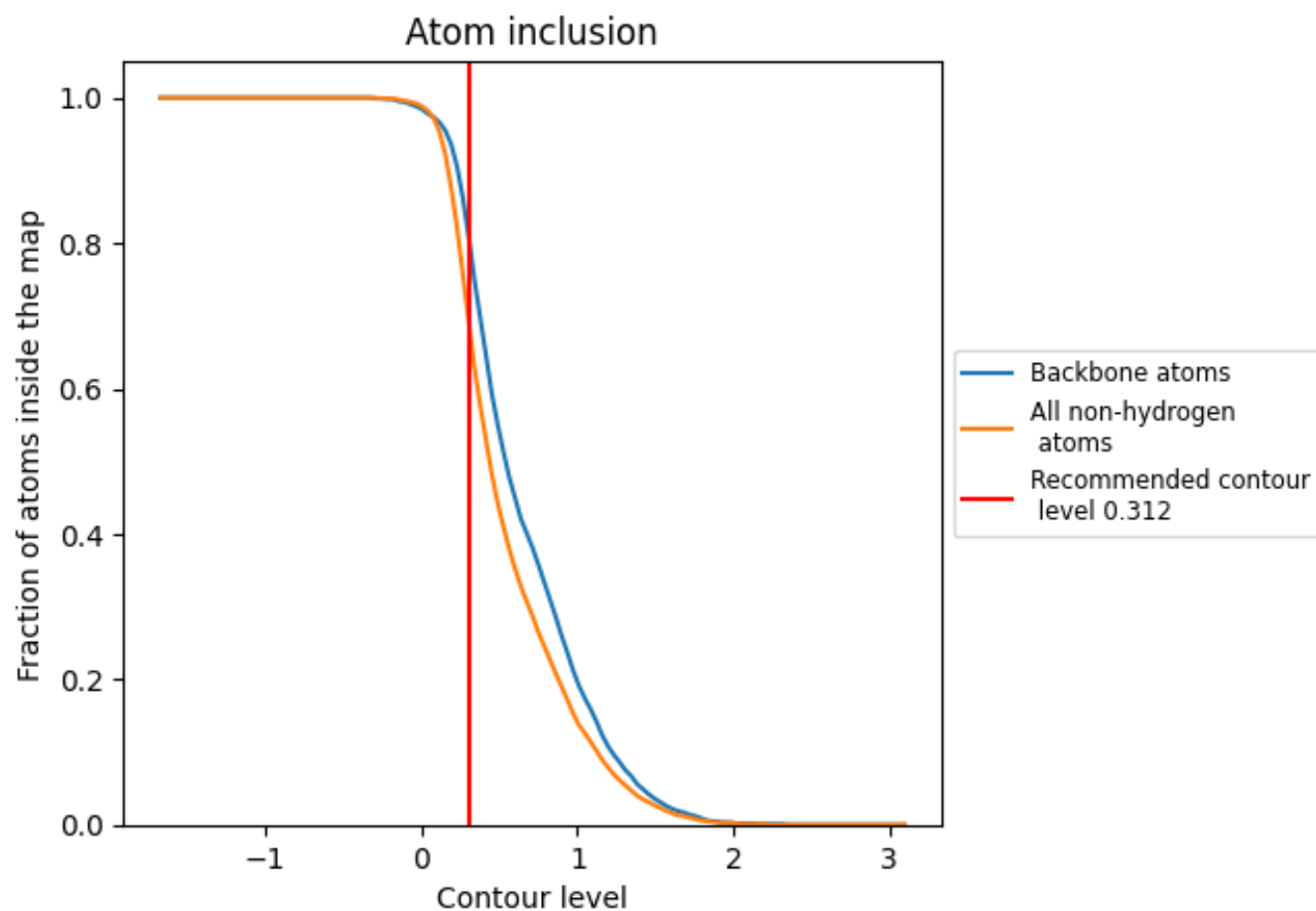
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.312).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 68% 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 (0.312) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6760	<div></div> 0.4110
A	<div></div> 0.6830	<div></div> 0.4210
B	<div></div> 0.6460	<div></div> 0.3710

