



## Full wwPDB EM Validation Report ⓘ

Jun 24, 2023 – 01:15 PM EDT

PDB ID : 8D42  
EMDB ID : EMD-27172  
Title : Human mitochondrial DNA polymerase gamma ternary complex with GT basepair in editing conformer (composite)  
Authors : Park, J.; Yin, Y.W.  
Deposited on : 2022-06-01  
Resolution : 2.91 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev50  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.33

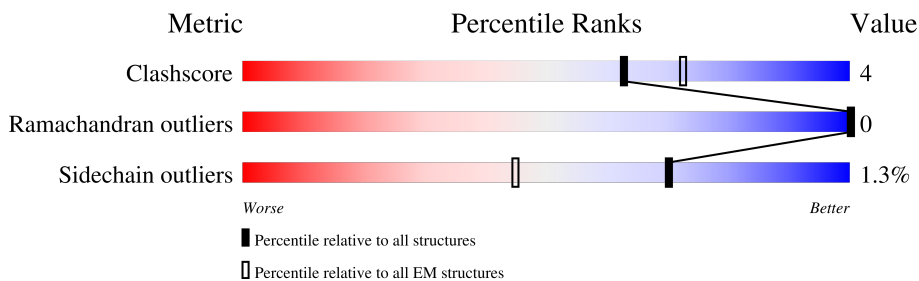
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.91 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1239	 5% 71% 8% 16%
2	B	485	 9% 73% 12% 6%
2	C	485	 8% 74% 7% 11%
3	P	23	 1% 52% 39% 8%
4	T	28	 25% 50% 25%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 29815 atoms, of which 14622 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 DNA polymerase subunit gamma-1.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	974	15393	4951	7615	1364	1413	50	0	0

- Molecule 2 is a protein called DNA polymerase subunit gamma-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	411	6613	2119	3305	578	595	16	0	0
2	C	399	6431	2058	3217	562	578	16	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(P\*AP\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*CP\*AP\*GP\*TP\*GP\*CP\*CP\*AP\*TP\*AP\*T)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
3	P	21	666	204	235	84	122	21	0	0

- Molecule 4 is a DNA chain called DNA (5'-D(P\*GP\*GP\*TP\*AP\*TP\*GP\*GP\*CP\*AP\*CP\*TP\*GP\*GP\*CP\*CP\*GP\*TP\*CP\*GP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
4	T	21	669	205	238	74	131	21	0	0

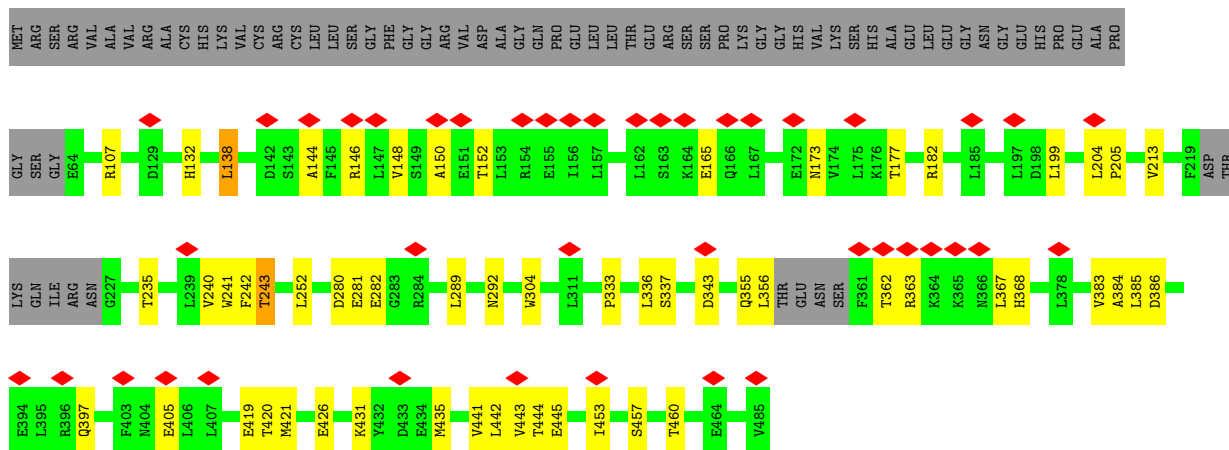
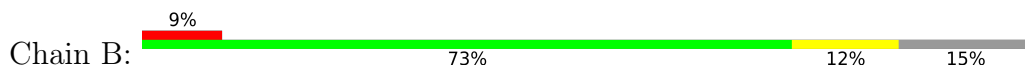
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	3	Total	Ca	0
			3	3	

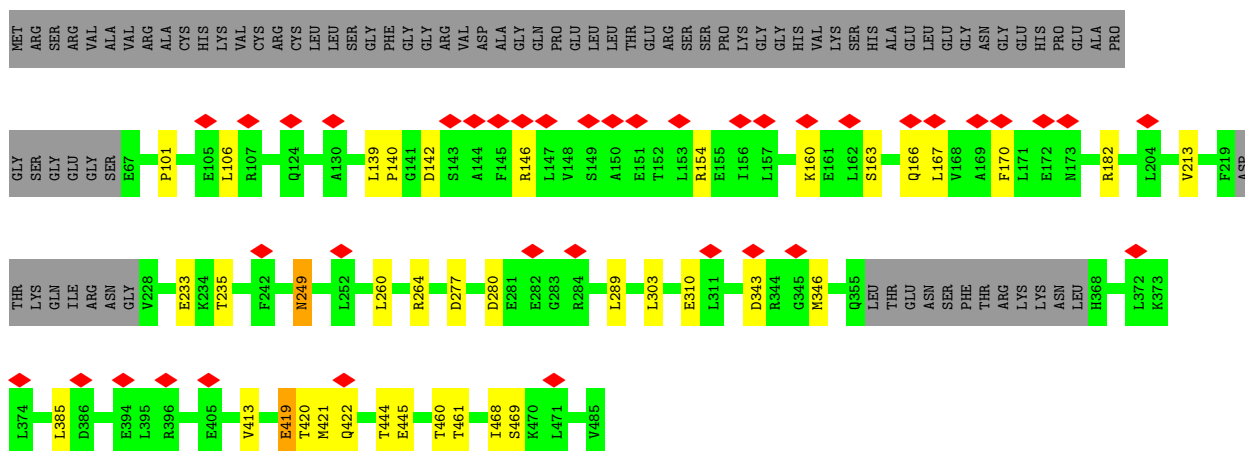
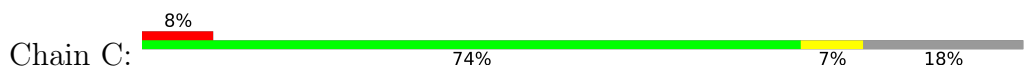
- Molecule 6 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP)







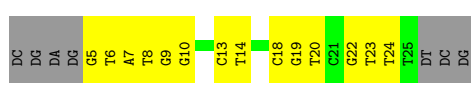
• Molecule 2: DNA polymerase subunit gamma-2, mitochondrial



• Molecule 3: DNA (5'-D(P\*AP\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*CP\*AP\*GP\*TP\*GP\*C P\*CP\*AP\*TP\*AP\*T)-3')



• Molecule 4: DNA (5'-D(P\*GP\*GP\*TP\*AP\*TP\*GP\*GP\*CP\*AP\*CP\*TP\*GP\*GP\*CP\*CP\*G P\*TP\*CP\*GP\*TP\*TP\*T)-3')



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1076466	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 ( $e^-/\text{\AA}^2$ )	44	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	14.037	Depositor
Minimum map value	-1.432	Depositor
Average map value	-0.121	Depositor
Map value standard deviation	0.790	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	272.0, 272.0, 272.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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: DCP, CA

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	0/7987	0.48	0/10843
2	B	0.25	0/3387	0.47	0/4579
2	C	0.25	0/3291	0.46	0/4450
3	P	0.57	0/484	0.87	0/744
4	T	0.55	0/481	1.00	0/741
All	All	0.28	0/15630	0.52	0/21357

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	7778	7615	7615	56	0
2	B	3308	3305	3305	41	0
2	C	3214	3217	3213	28	0
3	P	431	235	235	7	0
4	T	431	238	239	11	0
5	A	3	0	0	0	0
6	A	28	12	12	0	0
All	All	15193	14622	14619	132	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 4.

All (132) 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:355:SER:OG	3:P:22:DT:OP2	1.92	0.87
1:A:544:MET:SD	2:B:397:GLN:NE2	2.49	0.84
1:A:1186:ASP:OD1	1:A:1187:ARG:N	2.16	0.79
2:C:419:GLU:OE1	2:C:420:THR:N	2.16	0.79
1:A:950:ASN:OD1	1:A:953:ARG:NH2	2.18	0.75
2:B:282:GLU:N	2:B:282:GLU:OE1	2.20	0.74
2:C:163:SER:O	2:C:166:GLN:NE2	2.19	0.74
1:A:933:SER:OG	1:A:943:ARG:NH1	2.21	0.74
1:A:784:GLY:O	1:A:787:SER:OG	2.04	0.72
1:A:944:GLU:N	1:A:944:GLU:OE1	2.22	0.72
1:A:484:TRP:O	1:A:601:LYS:NZ	2.16	0.70
1:A:868:ASP:OD2	1:A:869:ARG:NH1	2.24	0.69
2:B:144:ALA:O	2:B:146:ARG:NH1	2.26	0.69
2:C:310:GLU:OE1	2:C:310:GLU:N	2.24	0.69
1:A:201:VAL:N	3:P:24:DT:O3'	2.27	0.67
1:A:1144:GLU:OE1	1:A:1144:GLU:N	2.28	0.65
2:B:457:SER:OG	2:B:460:THR:OG1	2.15	0.64
1:A:358:GLU:OE1	1:A:358:GLU:N	2.30	0.64
1:A:1056:GLU:N	1:A:1056:GLU:OE1	2.31	0.63
1:A:359:VAL:CG1	1:A:406:VAL:HG21	2.29	0.63
2:B:182:ARG:NH1	2:B:213:VAL:O	2.32	0.62
2:B:419:GLU:OE1	2:B:420:THR:N	2.33	0.61
2:B:150:ALA:HB3	2:C:142:ASP:O	2.00	0.61
1:A:758:ASN:O	1:A:759:SER:OG	2.18	0.61
1:A:359:VAL:HG12	1:A:406:VAL:HG21	1.83	0.60
2:B:252:LEU:HD12	2:B:336:LEU:HD21	1.84	0.60
1:A:1098:ASN:ND2	1:A:1102:GLN:OE1	2.33	0.60
1:A:231:GLU:N	1:A:231:GLU:OE1	2.32	0.60
1:A:966:LEU:HD11	1:A:978:ALA:HB1	1.83	0.59
2:B:280:ASP:OD1	2:B:281:GLU:N	2.37	0.58
3:P:21:DA:H4'	3:P:22:DT:H71	1.84	0.58
2:B:148:VAL:O	2:C:146:ARG:N	2.35	0.58
2:B:252:LEU:CD1	2:B:336:LEU:HD21	2.33	0.58
2:C:106:LEU:HD22	2:C:346:MET:HG2	1.86	0.58
4:T:7:DA:H2''	4:T:8:DT:H71	1.88	0.56
1:A:472:GLN:N	1:A:472:GLN:OE1	2.38	0.56
1:A:377:PHE:CE2	1:A:392:LEU:HD22	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:199:LEU:HD11	2:C:101:PRO:HG3	1.88	0.55
2:B:204:LEU:HD11	2:B:333:PRO:HB3	1.89	0.55
1:A:562:ARG:NH2	4:T:24:DT:O4'	2.40	0.54
2:B:426:GLU:N	2:B:426:GLU:OE1	2.40	0.53
1:A:417:ARG:NH2	1:A:1084:GLU:OE2	2.42	0.52
2:B:421:MET:SD	2:B:421:MET:N	2.82	0.52
1:A:263:GLU:OE1	1:A:263:GLU:N	2.38	0.51
2:B:304:TRP:O	2:B:336:LEU:HD22	2.10	0.51
1:A:821:LEU:HB2	1:A:826:ILE:HD11	1.92	0.51
2:C:419:GLU:OE2	2:C:422:GLN:NE2	2.44	0.50
3:P:21:DA:C4'	3:P:22:DT:H71	2.41	0.50
2:C:106:LEU:HD23	2:C:106:LEU:O	2.11	0.50
2:B:152:THR:HG22	2:B:152:THR:O	2.11	0.50
1:A:1066:THR:HG22	1:A:1066:THR:O	2.12	0.50
2:B:235:THR:HG22	2:B:343:ASP:CG	2.31	0.50
1:A:302:SER:HG	1:A:363:TYR:HH	1.58	0.49
1:A:1102:GLN:O	1:A:1106:VAL:HG23	2.11	0.49
2:B:362:THR:HG23	2:B:363:ARG:N	2.26	0.49
1:A:986:TYR:O	1:A:990:LYS:N	2.40	0.49
2:B:453:ILE:HD12	2:B:453:ILE:O	2.12	0.49
1:A:439:GLN:NE2	1:A:440:ASN:OD1	2.44	0.49
2:B:444:THR:HG22	2:B:445:GLU:N	2.28	0.49
3:P:10:DC:H2''	3:P:11:DG:N7	2.27	0.49
2:B:241:TRP:CD1	2:B:243:THR:HG22	2.47	0.49
1:A:799:SER:O	1:A:803:ASN:ND2	2.46	0.48
1:A:1071:ARG:NH1	1:A:1078:CYS:SG	2.85	0.48
4:T:22:DG:H2'	4:T:23:DT:H72	1.96	0.48
1:A:382:MET:SD	1:A:386:ARG:NE	2.81	0.47
1:A:280:GLU:N	1:A:280:GLU:OE1	2.48	0.47
2:B:431:LYS:NZ	2:B:435:MET:SD	2.85	0.47
2:C:444:THR:HG22	2:C:445:GLU:N	2.29	0.47
1:A:1151:LEU:HD23	1:A:1231:LEU:HD12	1.96	0.47
2:B:107:ARG:HD2	2:B:235:THR:HG21	1.96	0.47
1:A:142:LEU:HD21	1:A:1118:TRP:CD2	2.50	0.47
1:A:618:HIS:CG	1:A:619:GLY:N	2.83	0.46
1:A:886:LEU:HD23	1:A:1189:LEU:CD2	2.45	0.46
2:C:289:LEU:HD22	2:C:289:LEU:N	2.30	0.46
2:C:460:THR:O	2:C:461:THR:OG1	2.26	0.46
2:B:132:HIS:N	2:C:233:GLU:OE2	2.48	0.46
1:A:646:VAL:O	1:A:646:VAL:HG12	2.15	0.46
2:B:165:GLU:OE2	2:C:160:LYS:NZ	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:355:GLN:OE1	2:B:356:LEU:N	2.49	0.46
3:P:7:DC:H2''	3:P:8:DG:C8	2.51	0.46
4:T:23:DT:H2'	4:T:24:DT:H72	1.98	0.45
4:T:7:DA:C2'	4:T:8:DT:H71	2.47	0.45
2:B:368:HIS:O	2:B:368:HIS:ND1	2.48	0.45
1:A:549:LEU:HD21	2:B:405:GLU:OE1	2.17	0.45
4:T:5:DG:H4'	4:T:6:DT:OP1	2.16	0.44
1:A:1064:ILE:HD11	1:A:1071:ARG:O	2.17	0.44
1:A:362:LEU:HD13	1:A:362:LEU:C	2.38	0.44
2:B:453:ILE:HD12	2:B:453:ILE:C	2.38	0.44
2:B:205:PRO:HA	2:B:242:PHE:O	2.18	0.44
2:C:139:LEU:HD12	2:C:140:PRO:HD2	1.99	0.44
2:B:240:VAL:O	2:B:240:VAL:HG23	2.18	0.44
2:C:235:THR:O	2:C:235:THR:HG23	2.18	0.44
2:C:420:THR:HG22	2:C:421:MET:N	2.33	0.44
1:A:623:LEU:HB3	1:A:747:CYS:SG	2.58	0.43
1:A:1115:ALA:HB3	1:A:1156:THR:HG23	2.00	0.43
4:T:23:DT:C6	4:T:24:DT:H72	2.53	0.43
2:C:277:ASP:OD1	2:C:277:ASP:N	2.47	0.43
2:B:173:ASN:OD1	2:B:177:THR:OG1	2.37	0.43
1:A:271:VAL:HG12	1:A:293:ASP:HB2	2.01	0.43
1:A:631:LEU:HD23	1:A:747:CYS:O	2.19	0.43
1:A:949:PHE:HE2	1:A:962:ALA:HB1	1.84	0.43
1:A:852:ARG:NH1	1:A:1103:SER:OG	2.52	0.42
2:B:150:ALA:HB2	2:C:146:ARG:HD2	2.01	0.42
2:C:385:LEU:HD13	2:C:413:VAL:CG1	2.49	0.42
1:A:84:HIS:NE2	1:A:1172:ASP:OD1	2.50	0.42
1:A:210:THR:HB	1:A:228:LEU:HD11	2.00	0.42
1:A:892:ASP:OD2	1:A:1181:SER:OG	2.25	0.42
2:B:367:LEU:HD22	2:B:367:LEU:N	2.35	0.42
2:C:385:LEU:HD13	2:C:413:VAL:HG13	2.01	0.42
1:A:897:TRP:CE2	1:A:901:VAL:HG11	2.55	0.42
1:A:1186:ASP:OD1	1:A:1188:CYS:N	2.53	0.42
2:C:167:LEU:O	2:C:170:PHE:HB3	2.20	0.42
1:A:631:LEU:HD21	1:A:748:TRP:CD1	2.55	0.42
2:C:260:LEU:HD21	2:C:264:ARG:HH21	1.84	0.42
4:T:19:DG:C2'	4:T:20:DT:H72	2.50	0.42
4:T:13:DC:C6	4:T:14:DT:H72	2.55	0.41
1:A:966:LEU:HD11	1:A:978:ALA:CB	2.50	0.41
2:C:289:LEU:HD21	2:C:303:LEU:HD11	2.02	0.41
2:B:289:LEU:HD12	2:B:289:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:383:VAL:HG22	2:B:384:ALA:N	2.36	0.41
4:T:18:DC:C2'	4:T:19:DG:C8	3.03	0.41
2:C:235:THR:HG22	2:C:343:ASP:OD1	2.20	0.41
3:P:16:DG:H2'	3:P:17:DT:H71	2.02	0.41
2:B:441:VAL:HG23	2:B:453:ILE:HD13	2.03	0.41
2:B:138:LEU:HD12	2:B:138:LEU:N	2.36	0.41
2:B:336:LEU:HD13	2:B:337:SER:N	2.36	0.41
4:T:9:DG:H2'	4:T:10:DG:C8	2.56	0.40
1:A:484:TRP:CH2	1:A:655:LEU:HD21	2.56	0.40
2:C:249:ASN:OD1	2:C:249:ASN:N	2.52	0.40
2:C:468:ILE:HG23	2:C:469:SER:N	2.35	0.40
2:B:442:LEU:HD23	2:B:443:VAL:N	2.36	0.40
2:C:182:ARG:NH2	2:C:213:VAL:O	2.42	0.40

There are no symmetry-related clashes.

### 5.3 Torsion angles [i](#)

#### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	960/1239 (78%)	925 (96%)	35 (4%)	0	100	100
2	B	405/485 (84%)	389 (96%)	16 (4%)	0	100	100
2	C	393/485 (81%)	379 (96%)	14 (4%)	0	100	100
All	All	1758/2209 (80%)	1693 (96%)	65 (4%)	0	100	100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	828/1044 (79%)	817 (99%)	11 (1%)	69	89
2	B	365/426 (86%)	360 (99%)	5 (1%)	67	88
2	C	355/426 (83%)	351 (99%)	4 (1%)	73	91
All	All	1548/1896 (82%)	1528 (99%)	20 (1%)	70	89

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	361	ARG
1	A	553	LYS
1	A	564	GLN
1	A	779	LEU
1	A	1049	TRP
1	A	1093	MET
1	A	1096	ARG
1	A	1142	ARG
1	A	1164	PHE
1	A	1202	ASN
1	A	1219	ASP
2	B	138	LEU
2	B	243	THR
2	B	292	ASN
2	B	385	LEU
2	B	386	ASP
2	C	154	ARG
2	C	249	ASN
2	C	280	ASP
2	C	419	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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
6	DCP	A	1304	5	25,29,29	1.61	4 (16%)	37,45,45	1.44	6 (16%)

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
6	DCP	A	1304	5	-	0/22/34/34	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1304	DCP	PA-O5'	5.35	1.80	1.59
6	A	1304	DCP	O5'-C5'	-3.14	1.32	1.44
6	A	1304	DCP	C2-N3	2.51	1.41	1.36
6	A	1304	DCP	C4-N4	2.28	1.39	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1304	DCP	C1'-N1-C2	3.98	124.72	117.74
6	A	1304	DCP	C1'-N1-C6	-3.67	114.29	121.55
6	A	1304	DCP	C5-C4-N3	2.39	125.39	121.33
6	A	1304	DCP	O3B-PG-O1G	-2.37	98.05	111.19
6	A	1304	DCP	C2'-C1'-N1	2.22	118.88	113.77
6	A	1304	DCP	O3G-PG-O2G	2.05	115.49	107.64

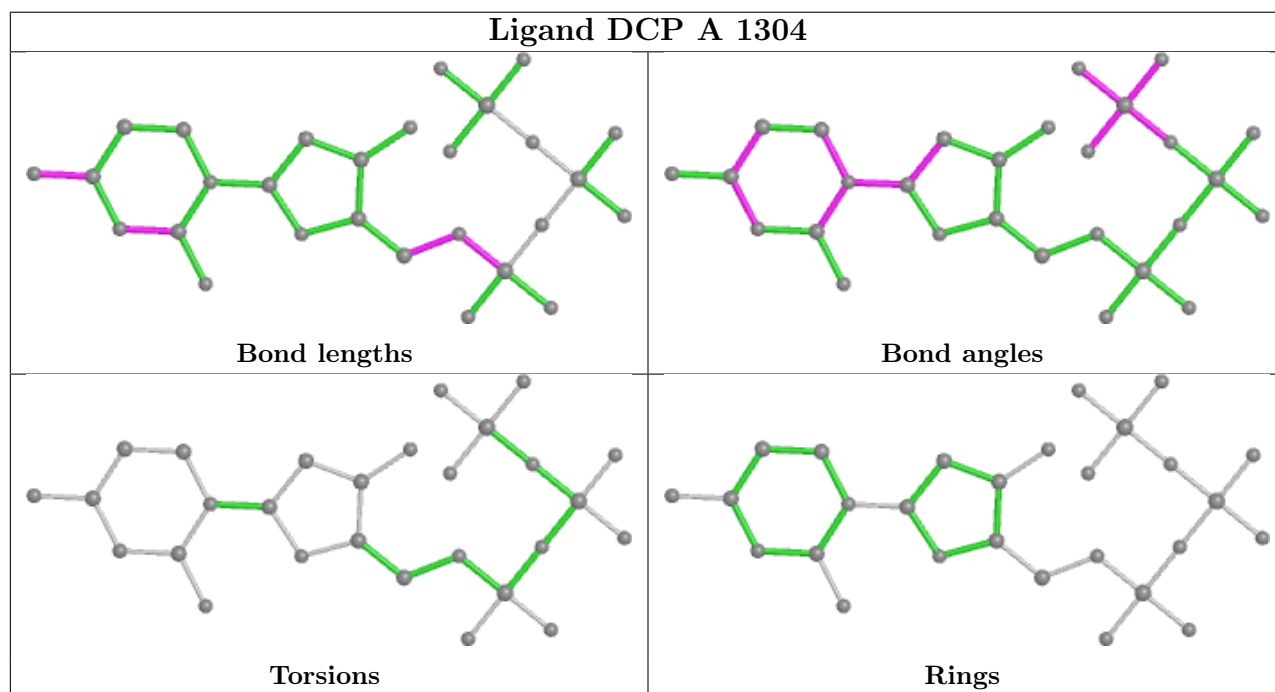
There are no chirality outliers.

There are no torsion outliers.

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



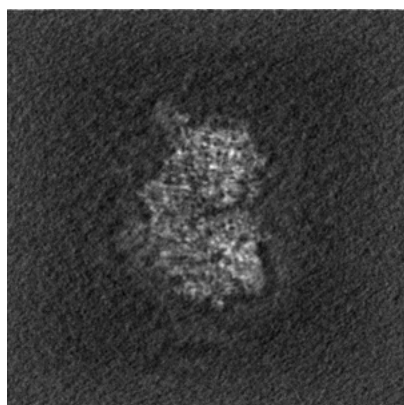
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27172. These allow visual inspection of the internal detail of the map and identification of artifacts.

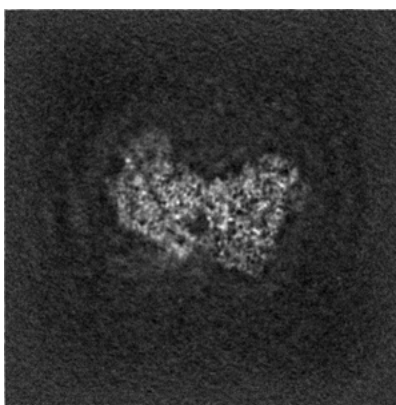
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

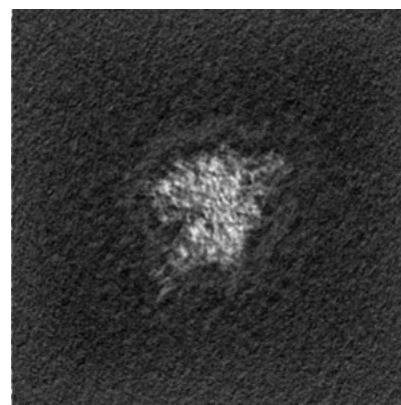
#### 6.1.1 Primary map



X



Y

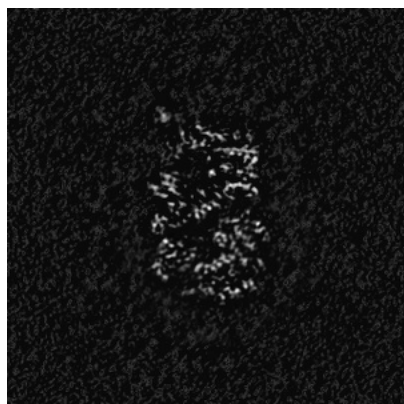


Z

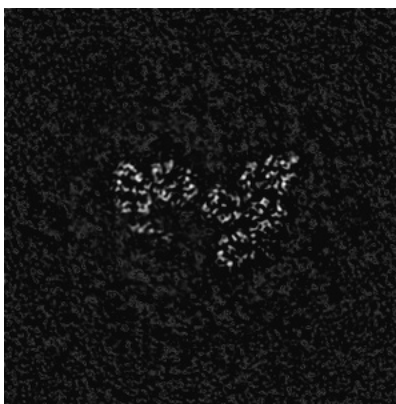
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

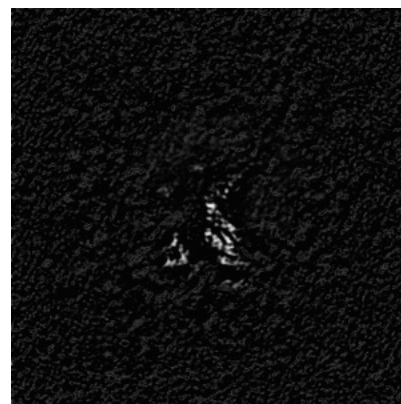
#### 6.2.1 Primary map



X Index: 160



Y Index: 160



Z Index: 160

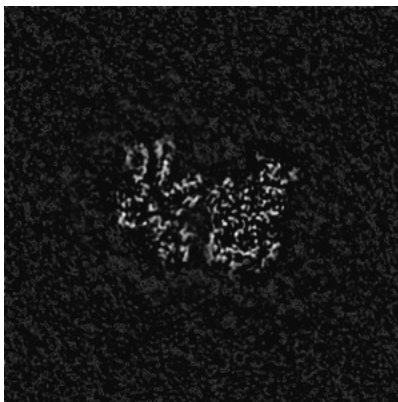
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 0



Y Index: 176

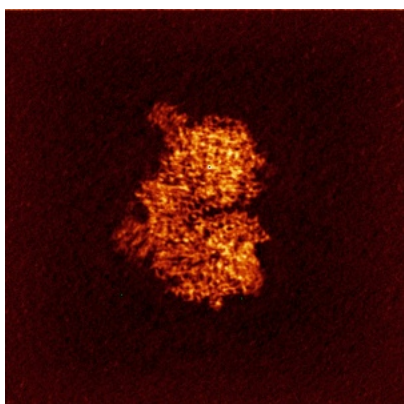


Z Index: 319

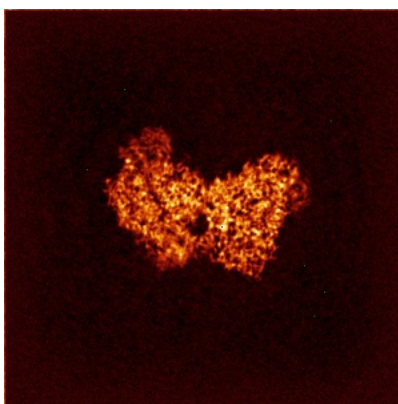
The images above show the largest variance slices of the map in three orthogonal directions.

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

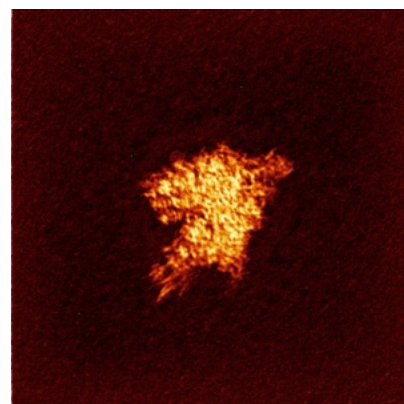
### 6.4.1 Primary map



X



Y

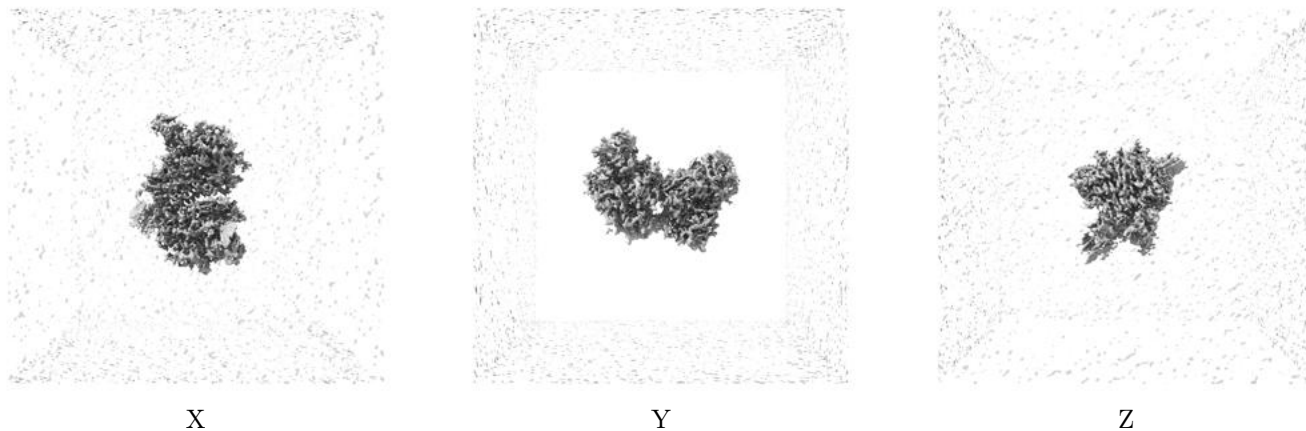


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

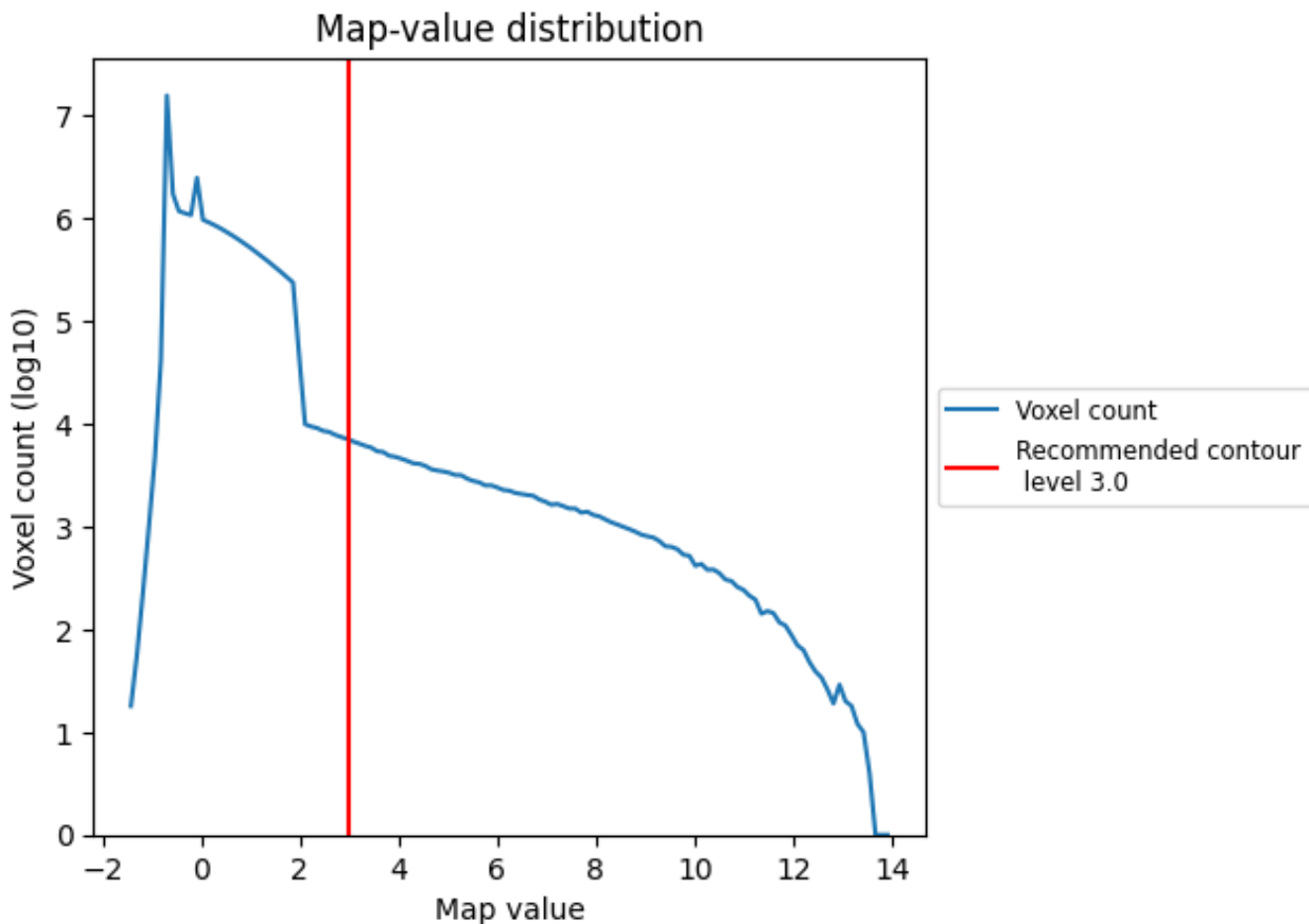
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

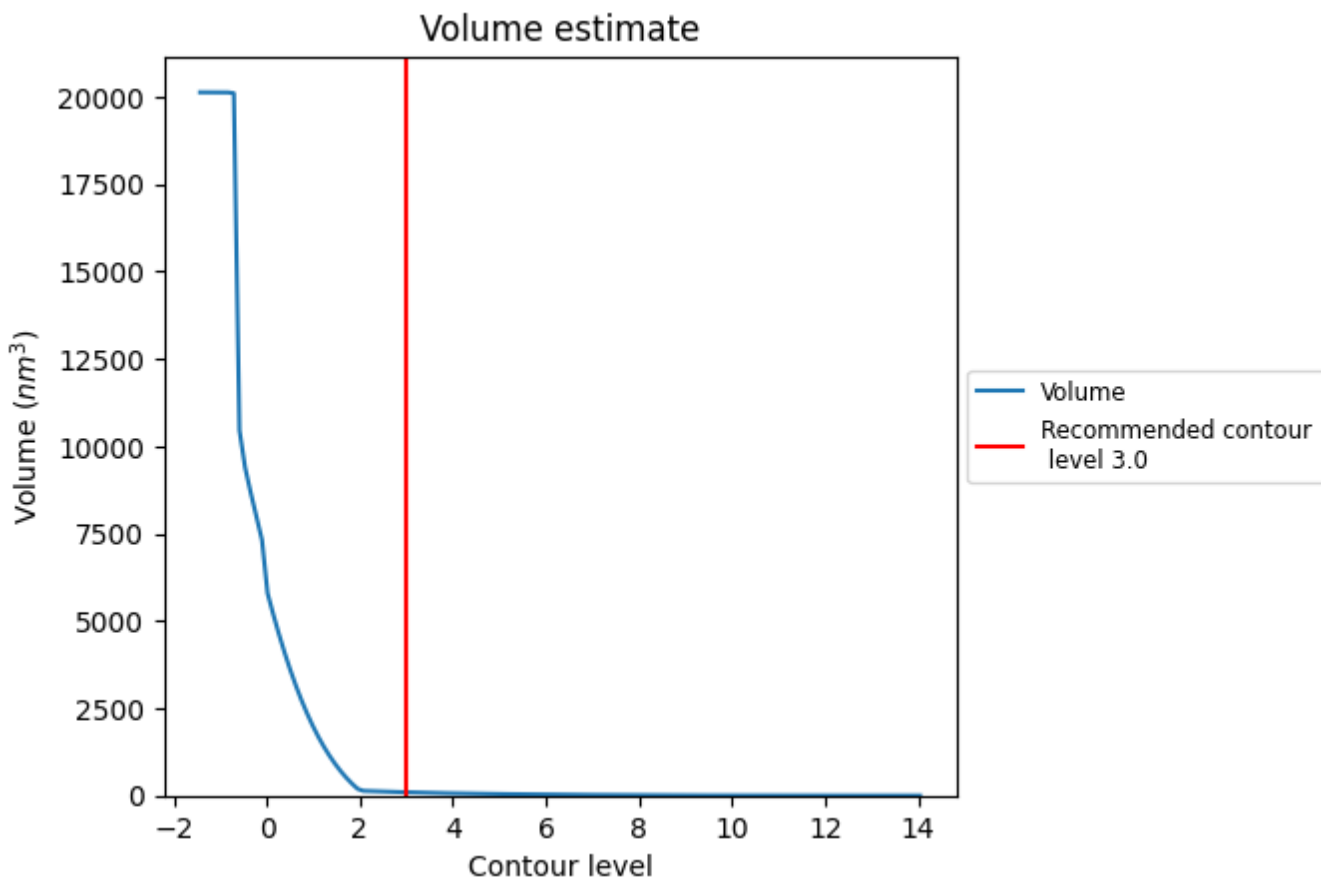
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

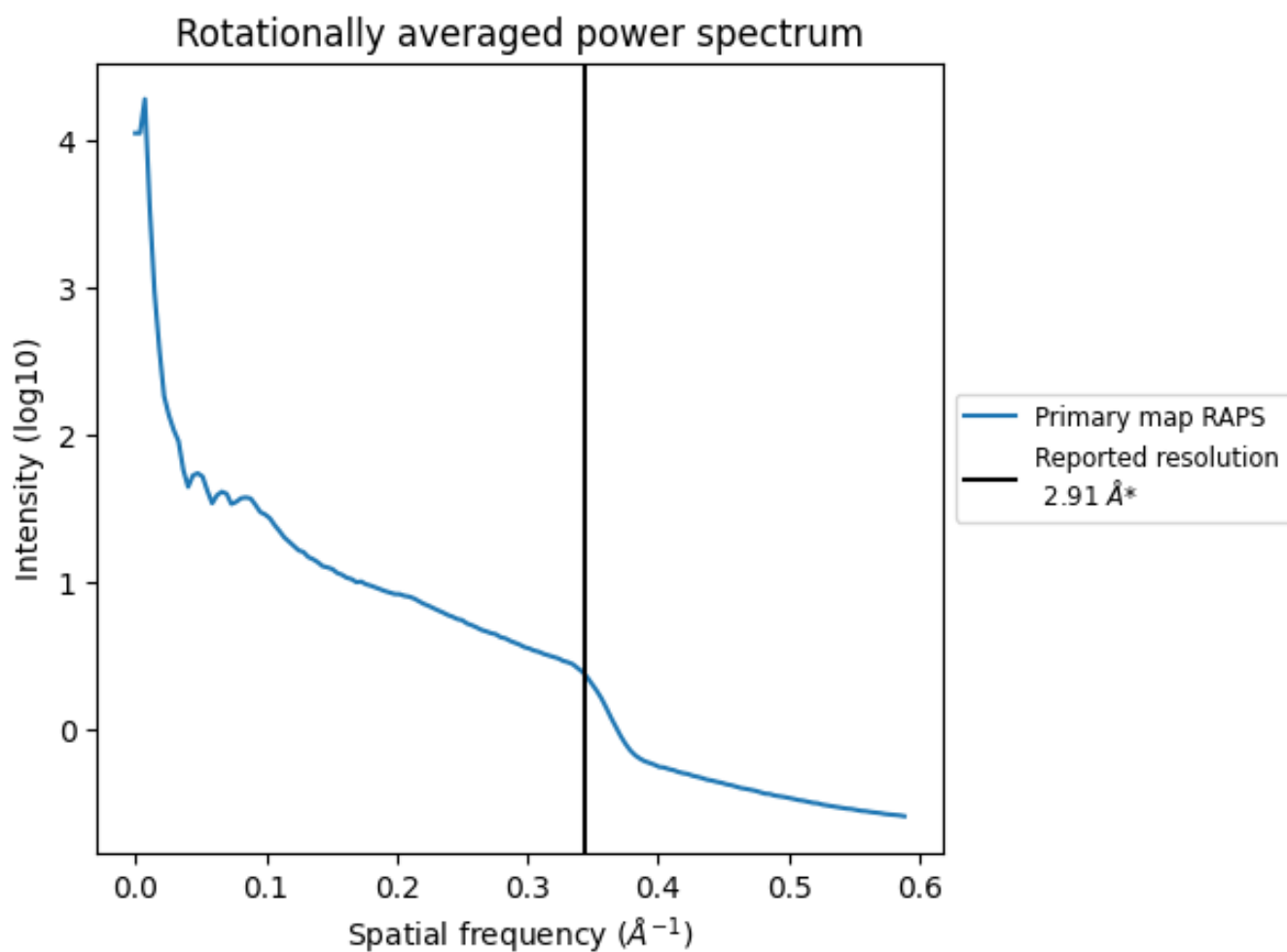
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 95 nm<sup>3</sup>; this corresponds to an approximate mass of 85 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum i



\*Reported resolution corresponds to spatial frequency of 0.344 Å<sup>-1</sup>

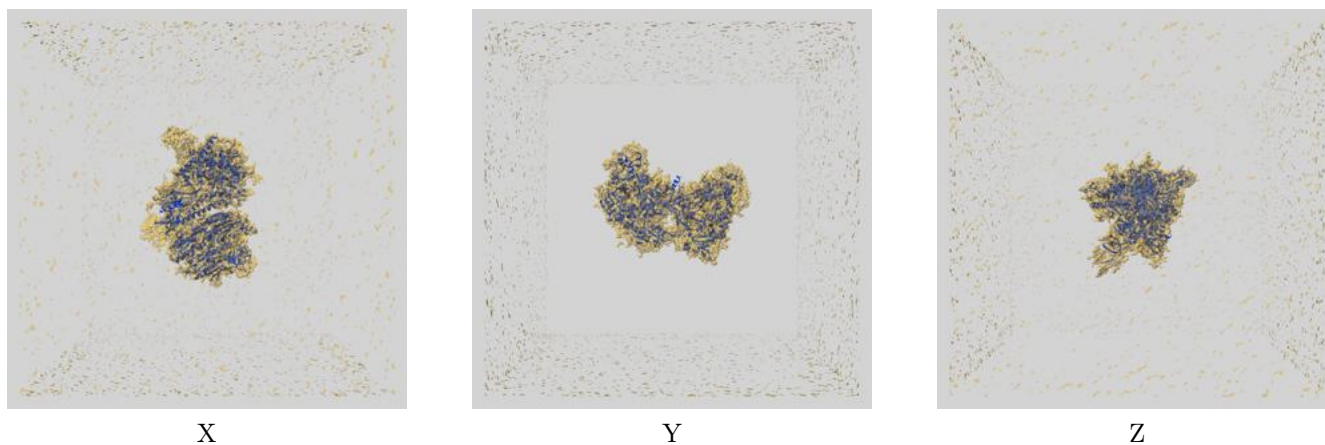
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27172 and PDB model 8D42. Per-residue inclusion information can be found in section [3](#) on page [5](#).

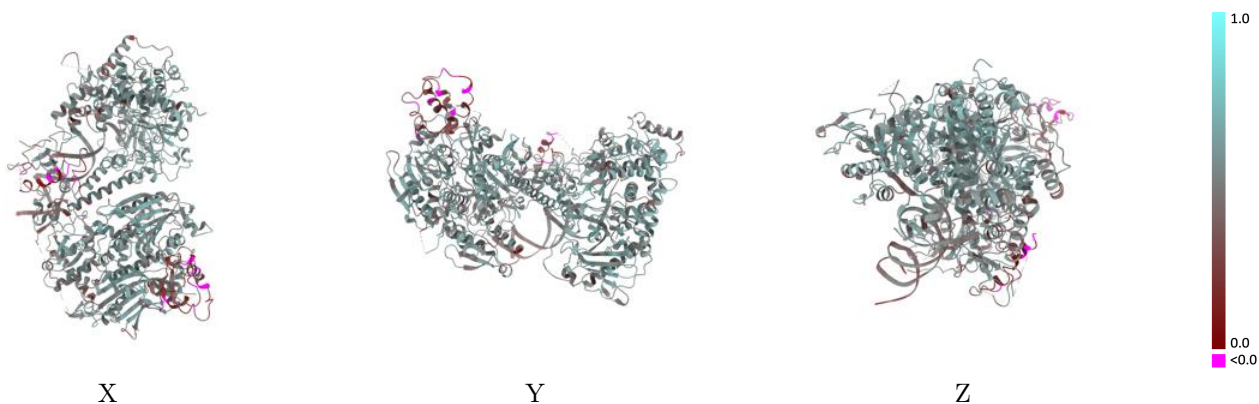
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

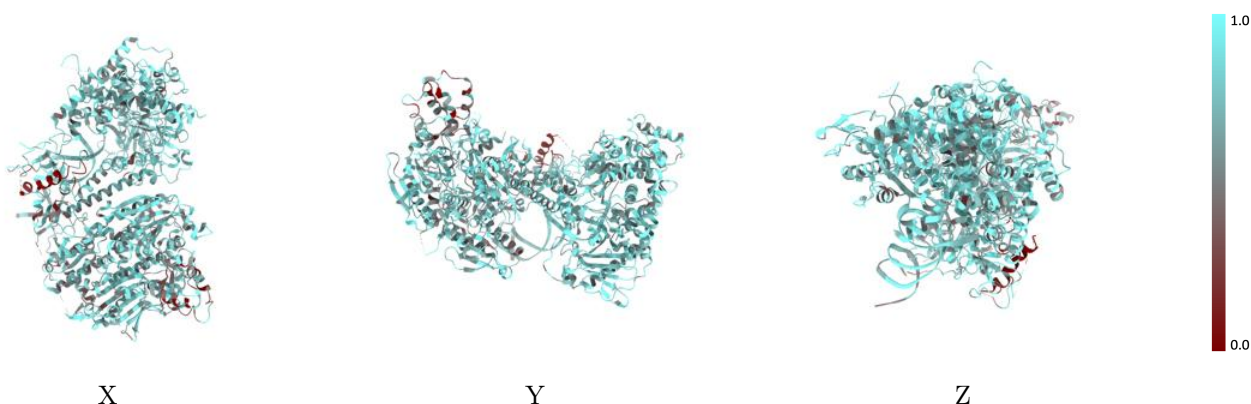


## 9.2 Q-score mapped to coordinate model [i](#)



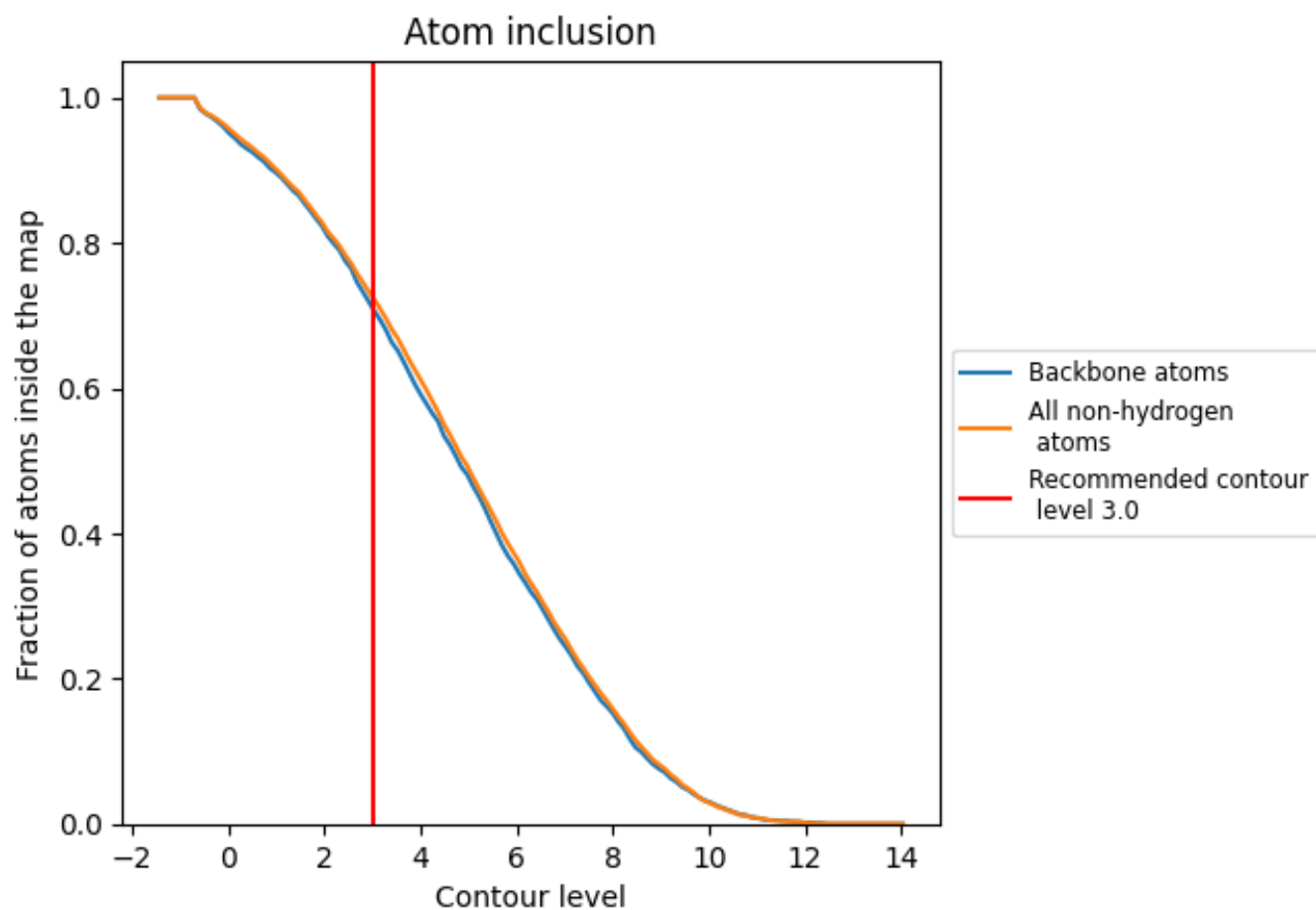
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).













## 9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 72% 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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.5070
A	 0.7480	 0.5190
B	 0.7110	 0.5090
C	 0.7030	 0.5010
P	 0.6980	 0.3940
T	 0.7890	 0.4340

