



## Full wwPDB EM Validation Report ⓘ

Nov 11, 2024 – 07:16 AM EST

PDB ID : 8D37  
EMDB ID : EMD-27155  
Title : Human mitochondrial DNA polymerase gamma ternary complex with GT basepair in replication conformer  
Authors : Park, J.; Yin, Y.W.  
Deposited on : 2022-05-31  
Resolution : 2.65 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.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
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) : 2.39

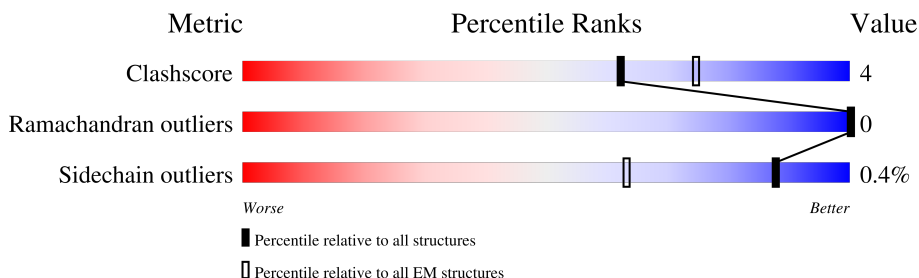
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.65 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  $\geq 3$ , 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	1245	<div> <div>7%</div> <div>70%</div> <div>8%</div> <div>22%</div> </div>
2	B	491	<div> <div>9%</div> <div>75%</div> <div>8%</div> <div>16%</div> </div>
2	C	491	<div> <div>9%</div> <div>71%</div> <div>10%</div> <div>19%</div> </div>
3	P	24	<div> <div>75%</div> <div>17%</div> <div>8%</div> </div>
4	T	28	<div> <div>57%</div> <div>36%</div> <div>7%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15314 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 DNA polymerase subunit gamma-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	974	Total	C	N	O	S	0	0
			7778	4951	1364	1413	50		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1240	HIS	-	expression tag	UNP P54098
A	1241	HIS	-	expression tag	UNP P54098
A	1242	HIS	-	expression tag	UNP P54098
A	1243	HIS	-	expression tag	UNP P54098
A	1244	HIS	-	expression tag	UNP P54098
A	1245	HIS	-	expression tag	UNP P54098

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	411	Total	C	N	O	S	0	0
			3307	2119	578	594	16		
2	C	399	Total	C	N	O	S	0	0
			3213	2058	562	577	16		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	486	HIS	-	expression tag	UNP Q9UHN1
B	487	HIS	-	expression tag	UNP Q9UHN1
B	488	HIS	-	expression tag	UNP Q9UHN1
B	489	HIS	-	expression tag	UNP Q9UHN1
B	490	HIS	-	expression tag	UNP Q9UHN1
B	491	HIS	-	expression tag	UNP Q9UHN1
C	486	HIS	-	expression tag	UNP Q9UHN1
C	487	HIS	-	expression tag	UNP Q9UHN1
C	488	HIS	-	expression tag	UNP Q9UHN1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	489	HIS	-	expression tag	UNP Q9UHN1
C	490	HIS	-	expression tag	UNP Q9UHN1
C	491	HIS	-	expression tag	UNP Q9UHN1

- Molecule 3 is a DNA chain called DNA (5'-D(P\*AP\*AP\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*CP\*AP\*GP\*TP\*GP\*CP\*CP\*AP\*TP\*AP\*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	22	Total	C	N	O	P	0	0
			452	214	89	127	22		

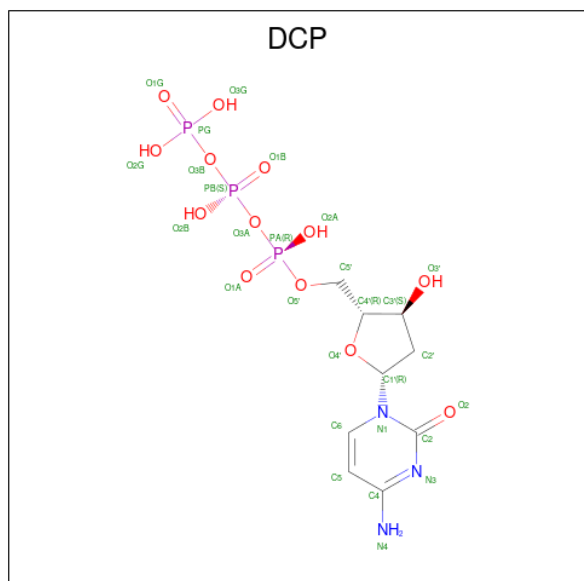
- Molecule 4 is a DNA chain called DNA (25-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	26	Total	C	N	O	P	0	0
			535	254	94	161	26		

- 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	1	Total	Ca	0
			1	1	

- Molecule 6 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C<sub>9</sub>H<sub>16</sub>N<sub>3</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).




Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
6	A	1	28	9	3	13	3	0



HIS  
HIS  
HIS

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

Chain B: 

MET ARG SER ARG VAL VAL ARG ALA CYS HIS LYS VAL CYS ARG CYS LEU LEU SER GLY PHE GLY GLY ARG VAL ASP ALA GLN PRO GLU LEU LEU THR GLU ARG SER SER PRO LYS GLY GLY HIS VAL LYS SER HIS ALA GLU LEU LEU GLY GLY GLY GLU PRO GLU PRO

GLY SER E64 E67 A69 L69 L86 E123 Y128 D129 A130 K134 D142 S143 A144 F145 R146 L147 V148 S149 A150 L153 I156 L157 Q158 L162 S163 K164 E165 Q166 L167 V168 A169 F170 L171 E172 S176 R182 H187 G188 A189 H192 Y193 N195 C196

L197 L204 V213 F219 ASP THR LYS GLN ILE ARG ASN G227 V228 T235 T243 R257 R264 K265 P270 L289 D308 H309 E310 L311 L322 H323 G324 R325 P333 L336 D343 L347 Q355 L356 THR ASN SER F361 T362 R363 H368

P376 K382 V387 E394 L395 R396 Q400 M404 E405 Y417 E426 V443 T447 T453 H454 L455 R456 S457 T460 T461 K470 K477 K483 M484 V485 HIS HIS HIS HIS HIS

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

Chain C: 

MET ARG SER ARG VAL VAL ARG ALA CYS HIS LYS VAL CYS ARG CYS LEU LEU SER GLY PHE GLY GLY ARG VAL ASP ALA GLN PRO GLU LEU LEU THR GLU ARG SER SER PRO LYS GLY GLY HIS VAL LYS SER HIS ALA GLU LEU LEU GLY GLY GLY GLU PRO GLU ALA PRO

GLY SER E67 A68 L69 I72 R76 Q84 Q85 L86 L92 L106 R107 D129 L138 D142 S143 A144 F145 R146 L147 V148 S149 A150 E151 T152 L153 R154 E155 I156 L157 Q158 D159 K160 E161 L162 S163 K164 E165 Q166 L167 F170 L171 E172 T177 S178

N195 R203 L204 G207 F219 ASP THR LYS GLN ILE ARG ASN G228 K229 S230 I231 K234 T235 T243 D253 E263 R264 P270 D277 D280 E281 N287 E310 G324 R325 P333 D343 M346 Q355 LEU THR ASN SER PHE THR

ARG LYS ASN LEU H368 L374 L378 D386 R396 Q400 F403 M404 E405 L406 L407 F408 M409 T420 M421 Q422 S423 Q427 E434 M435 S436 F439 T444 E445 L455 T460 T461 L471 I479 V485 HIS HIS HIS HIS HIS

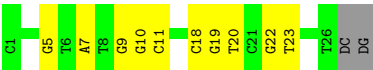
• Molecule 3: DNA (5'-D(P\*AP\*AP\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*CP\*AP\*GP\*TP\*G P\*CP\*CP\*AP\*TP\*AP\*C)-3')

Chain P: 

DC DG A3 C14 A15 T22 A23 T24

• Molecule 4: DNA (25-MER)

Chain T: 





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	1179973	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	12.970	Depositor
Minimum map value	0.000	Depositor
Average map value	0.339	Depositor
Map value standard deviation	0.592	Depositor
Recommended contour level	3	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: CA, DCP

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	0.24	0/7987	0.47	0/10843
2	B	0.24	0/3386	0.47	0/4579
2	C	0.24	0/3290	0.45	0/4450
3	P	0.54	0/508	0.81	0/781
4	T	0.51	0/598	0.97	0/922
All	All	0.27	0/15769	0.51	0/21575

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	0	7615	65	0
2	B	3307	0	3305	29	0
2	C	3213	0	3213	31	0
3	P	452	0	246	4	0
4	T	535	0	295	7	0
5	A	1	0	0	0	0
6	A	28	0	12	1	0
All	All	15314	0	14686	124	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 (124) 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)
3:P:24:DT:H3	4:T:5:DG:H1	1.24	0.85
1:A:461:LYS:NZ	2:B:265:LYS:O	2.13	0.81
1:A:904:ASP:OD1	1:A:914:THR:OG1	1.96	0.81
1:A:918:TRP:O	1:A:922:GLN:NE2	2.17	0.78
2:B:144:ALA:O	2:B:146:ARG:NH1	2.20	0.75
1:A:895:GLU:OE1	1:A:955:TYR:OH	2.04	0.75
1:A:439:GLN:NE2	1:A:440:ASN:OD1	2.20	0.74
2:C:277:ASP:OD1	2:C:287:ASN:ND2	2.21	0.73
1:A:372:GLU:OE1	1:A:375:GLU:N	2.22	0.72
2:B:165:GLU:OE2	2:C:160:LYS:NZ	2.19	0.72
1:A:1232:GLU:N	1:A:1232:GLU:OE1	2.24	0.70
1:A:1224:ILE:O	1:A:1228:LYS:N	2.25	0.70
1:A:766:PHE:O	1:A:795:ASN:ND2	2.25	0.69
2:C:405:GLU:O	2:C:409:ASN:ND2	2.26	0.69
1:A:537:GLU:N	1:A:537:GLU:OE1	2.27	0.67
1:A:1186:ASP:OD1	1:A:1187:ARG:N	2.28	0.67
1:A:299:MET:SD	1:A:309:ARG:NH2	2.68	0.66
2:C:204:LEU:HD11	2:C:333:PRO:HB3	1.77	0.66
2:C:435:MET:O	2:C:436:SER:OG	2.14	0.66
1:A:158:LEU:HD11	1:A:411:LEU:HD23	1.77	0.66
1:A:70:ARG:NH1	1:A:122:ASP:OD2	2.27	0.66
1:A:215:ILE:HD11	1:A:404:HIS:HB2	1.78	0.66
1:A:911:HIS:NE2	1:A:1172:ASP:O	2.28	0.65
2:B:376:PRO:O	2:B:382:LYS:NZ	2.29	0.65
1:A:863:SER:OG	1:A:869:ARG:NH1	2.28	0.64
2:C:310:GLU:OE1	2:C:310:GLU:N	2.30	0.64
2:B:400:GLN:O	2:B:404:ASN:ND2	2.32	0.63
2:C:163:SER:O	2:C:166:GLN:NE2	2.32	0.62
1:A:1060:LYS:HE3	1:A:1064:ILE:HD11	1.84	0.60
2:B:67:GLU:OE1	2:B:67:GLU:N	2.35	0.60
2:C:76:ARG:NE	2:C:434:GLU:OE1	2.33	0.60
2:B:130:ALA:O	2:B:182:ARG:NH2	2.35	0.59
2:C:107:ARG:HD2	2:C:235:THR:HG21	1.84	0.59
1:A:377:PHE:CE2	1:A:392:LEU:HD22	2.36	0.59
2:B:460:THR:O	2:B:461:THR:OG1	2.17	0.59
1:A:861:THR:HG23	3:P:22:DT:O2	2.03	0.59
2:C:460:THR:O	2:C:461:THR:OG1	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:ASN:ND2	1:A:1102:GLN:OE1	2.37	0.57
1:A:533:CYS:SG	1:A:534:SER:N	2.77	0.57
2:B:193:TYR:OH	2:B:322:LEU:O	2.24	0.56
2:C:423:SER:OG	2:C:427:GLN:OE1	2.23	0.56
2:C:403:PHE:CE2	2:C:407:LEU:HD11	2.41	0.56
1:A:947:LYS:NZ	6:A:1302:DCP:O1G	2.25	0.55
1:A:1072:THR:OG1	1:A:1076:GLY:N	2.41	0.54
2:C:204:LEU:HD13	2:C:324:GLY:HA3	1.90	0.54
1:A:768:LYS:NZ	3:P:22:DT:OP2	2.30	0.53
2:B:310:GLU:OE1	2:B:310:GLU:N	2.41	0.52
1:A:861:THR:HG22	1:A:861:THR:O	2.10	0.52
1:A:90:GLN:N	1:A:90:GLN:OE1	2.41	0.52
2:B:123:GLU:N	2:B:123:GLU:OE1	2.41	0.51
1:A:1115:ALA:HB3	1:A:1156:THR:HG23	1.93	0.51
1:A:1142:ARG:NH2	1:A:1144:GLU:OE2	2.44	0.51
2:C:444:THR:HG22	2:C:445:GLU:H	1.76	0.51
1:A:890:ASP:OD1	1:A:891:VAL:N	2.44	0.51
2:B:368:HIS:O	2:B:368:HIS:ND1	2.42	0.51
1:A:70:ARG:O	1:A:71:HIS:ND1	2.44	0.50
1:A:438:ASN:ND2	1:A:879:GLN:OE1	2.41	0.50
4:T:10:DG:H2'	4:T:11:DC:C6	2.46	0.50
1:A:594:LEU:HD23	1:A:599:THR:HG21	1.94	0.50
2:B:168:VAL:HG11	2:C:160:LYS:HE2	1.94	0.49
1:A:202:CYS:N	1:A:210:THR:OG1	2.43	0.49
2:B:182:ARG:NH1	2:B:213:VAL:O	2.46	0.48
2:B:394:GLU:OE1	2:B:394:GLU:N	2.43	0.48
1:A:112:LEU:HD23	1:A:918:TRP:CD1	2.48	0.48
1:A:929:THR:HG22	1:A:929:THR:O	2.14	0.47
1:A:87:ILE:HD13	1:A:1162:CYS:SG	2.54	0.47
1:A:198:ASP:OD1	1:A:199:VAL:N	2.47	0.47
1:A:453:GLU:O	1:A:457:ARG:N	2.46	0.47
1:A:275:ARG:NE	1:A:281:GLN:OE1	2.47	0.47
1:A:594:LEU:HA	1:A:599:THR:HG21	1.97	0.47
2:C:264:ARG:NH1	2:C:270:PRO:O	2.47	0.47
2:C:92:LEU:O	2:C:234:LYS:NZ	2.42	0.46
1:A:870:VAL:HG22	1:A:1200:PRO:HG2	1.97	0.46
2:B:387:VAL:HG23	2:B:417:TYR:HB2	1.98	0.46
1:A:593:SER:O	1:A:599:THR:OG1	2.24	0.46
1:A:736:ASN:ND2	1:A:751:LYS:O	2.48	0.45
1:A:929:THR:HG22	1:A:934:LYS:HE3	1.98	0.45
1:A:1066:THR:HG22	1:A:1066:THR:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1068:ASP:OD1	1:A:1069:ILE:N	2.50	0.45
1:A:594:LEU:HD22	1:A:766:PHE:CE2	2.52	0.45
1:A:455:LEU:HD22	1:A:794:ILE:CD1	2.47	0.44
2:C:106:LEU:HD13	2:C:374:LEU:HD23	1.98	0.44
4:T:22:DG:H2''	4:T:23:DT:H72	1.99	0.44
1:A:79:LEU:CD2	1:A:87:ILE:HD12	2.48	0.44
2:B:204:LEU:HD11	2:B:333:PRO:HB3	1.99	0.44
2:B:213:VAL:HG22	2:B:235:THR:HG22	2.00	0.44
2:B:235:THR:OG1	2:B:343:ASP:OD1	2.33	0.44
4:T:19:DG:C2'	4:T:20:DT:H72	2.48	0.44
1:A:1146:ARG:NH2	1:A:1147:TYR:OH	2.49	0.44
2:C:204:LEU:HD11	2:C:333:PRO:CB	2.45	0.44
1:A:552:LEU:HD21	2:B:447:THR:O	2.18	0.44
2:C:444:THR:HG22	2:C:445:GLU:N	2.33	0.44
1:A:1116:MET:SD	1:A:1153:LEU:HD23	2.58	0.43
2:B:150:ALA:HB3	2:C:142:ASP:O	2.17	0.43
1:A:151:LEU:O	1:A:155:ASN:ND2	2.51	0.43
1:A:217:PRO:O	1:A:218:SER:OG	2.22	0.43
1:A:850:ILE:HD13	1:A:1083:LEU:HD11	2.01	0.43
1:A:79:LEU:HD21	1:A:87:ILE:HD12	2.01	0.43
2:B:289:LEU:HD12	2:B:289:LEU:N	2.33	0.43
2:B:264:ARG:NH1	2:B:270:PRO:O	2.52	0.43
2:B:129:ASP:N	2:B:129:ASP:OD1	2.52	0.43
2:B:164:LYS:O	2:C:164:LYS:N	2.52	0.42
1:A:849:THR:HG22	4:T:7:DA:O5'	2.19	0.42
2:C:153:LEU:O	2:C:157:LEU:HD13	2.19	0.42
2:B:153:LEU:O	2:C:171:LEU:HD13	2.20	0.42
2:C:253:ASP:N	2:C:253:ASP:OD1	2.53	0.42
2:B:162:LEU:N	2:B:162:LEU:HD12	2.34	0.42
2:C:280:ASP:OD1	2:C:281:GLU:N	2.53	0.42
4:T:9:DG:H2'	4:T:10:DG:C8	2.54	0.42
4:T:18:DC:H2''	4:T:19:DG:C8	2.54	0.42
1:A:97:GLU:OE2	1:A:101:ARG:NH2	2.48	0.42
1:A:580:LEU:O	2:B:477:LYS:NZ	2.54	0.41
2:C:157:LEU:N	2:C:157:LEU:HD12	2.35	0.41
2:C:161:GLU:O	2:C:166:GLN:NE2	2.52	0.41
1:A:313:ILE:O	1:A:314:ALA:HB3	2.20	0.41
2:C:68:ALA:O	2:C:72:ILE:HD13	2.21	0.41
3:P:14:DC:H2''	3:P:15:DA:C8	2.55	0.41
2:B:362:THR:HG23	2:B:363:ARG:N	2.36	0.41
2:C:439:PHE:CD1	2:C:455:LEU:HD21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:167:LEU:O	2:C:170:PHE:HB3	2.22	0.40
1:A:79:LEU:HD23	1:A:84:HIS:HA	2.03	0.40
1:A:826:ILE:O	1:A:826:ILE:HG22	2.21	0.40
1:A:995:TYR:O	1:A:995:TYR:CG	2.75	0.40
1:A:1064:ILE:HD13	1:A:1073:PRO:HG3	2.03	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	960/1245 (77%)	926 (96%)	34 (4%)	0	100	100
2	B	405/491 (82%)	388 (96%)	17 (4%)	0	100	100
2	C	393/491 (80%)	379 (96%)	14 (4%)	0	100	100
All	All	1758/2227 (79%)	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	828/1050 (79%)	826 (100%)	2 (0%)	92	97
2	B	365/432 (84%)	363 (100%)	2 (0%)	86	94

*Continued on next page...*

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	355/432 (82%)	353 (99%)	2 (1%)	84	92
All	All	1548/1914 (81%)	1542 (100%)	6 (0%)	88	95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	1164	PHE
2	B	243	THR
2	B	361	PHE
2	C	154	ARG
2	C	243	THR

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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	1302	5	28,29,29	2.86	7 (25%)	41,45,45	1.82	10 (24%)

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	1302	5	-	8/22/34/34	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1302	DCP	PB-O3A	10.73	1.71	1.59
6	A	1302	DCP	PA-O3A	-5.80	1.53	1.59
6	A	1302	DCP	PA-O5'	5.36	1.80	1.59
6	A	1302	DCP	PB-O3B	-3.99	1.55	1.59
6	A	1302	DCP	O5'-C5'	-2.98	1.33	1.44
6	A	1302	DCP	C2-N3	2.44	1.41	1.36
6	A	1302	DCP	C4-N4	2.24	1.39	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1302	DCP	O3A-PA-O1A	4.47	124.15	110.70
6	A	1302	DCP	O3B-PB-O1B	4.40	123.95	110.70
6	A	1302	DCP	C1'-N1-C2	3.88	124.49	117.83
6	A	1302	DCP	O2A-PA-O3A	3.56	116.91	107.27
6	A	1302	DCP	C1'-N1-C6	-3.25	115.14	121.53
6	A	1302	DCP	O2B-PB-O3A	-2.68	100.02	107.27
6	A	1302	DCP	O3A-PB-O1B	-2.44	103.37	110.70
6	A	1302	DCP	C5-C4-N3	2.27	125.14	121.32
6	A	1302	DCP	O2-C2-N3	-2.13	118.97	122.33
6	A	1302	DCP	O2G-PG-O3B	-2.01	97.88	104.64

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1302	DCP	C5'-O5'-PA-O1A
6	A	1302	DCP	C5'-O5'-PA-O2A

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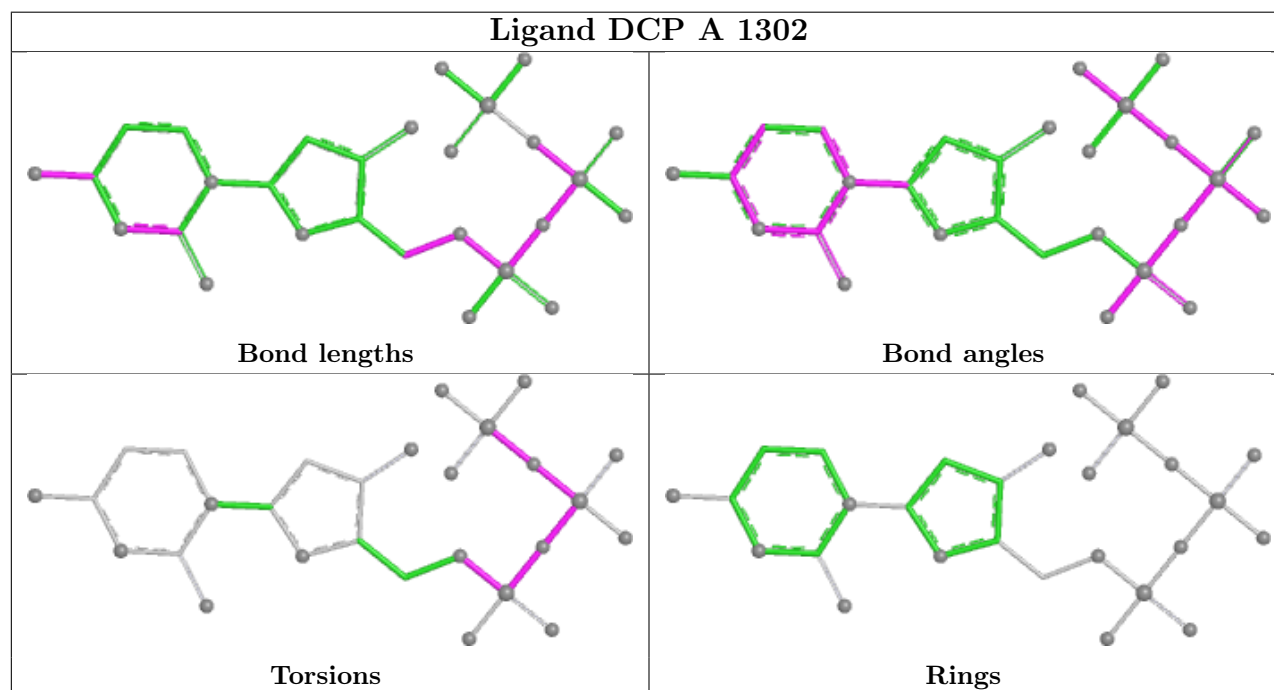
Mol	Chain	Res	Type	Atoms
6	A	1302	DCP	C5'-O5'-PA-O3A
6	A	1302	DCP	PB-O3B-PG-O2G
6	A	1302	DCP	PB-O3A-PA-O2A
6	A	1302	DCP	PB-O3B-PG-O1G
6	A	1302	DCP	PA-O3A-PB-O2B
6	A	1302	DCP	PG-O3B-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1302	DCP	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

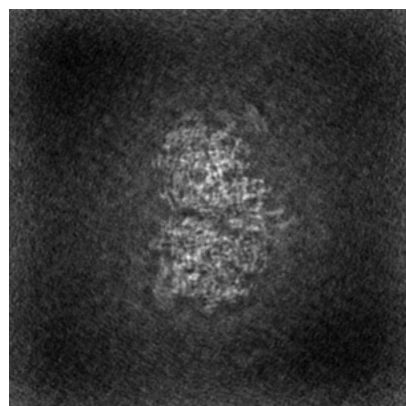
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27155. These allow visual inspection of the internal detail of the map and identification of artifacts.

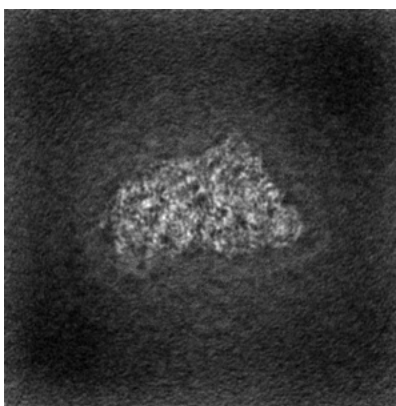
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

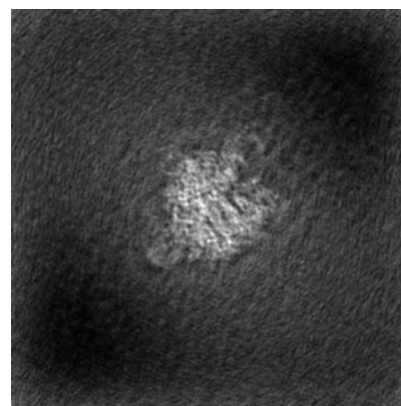
#### 6.1.1 Primary map



X

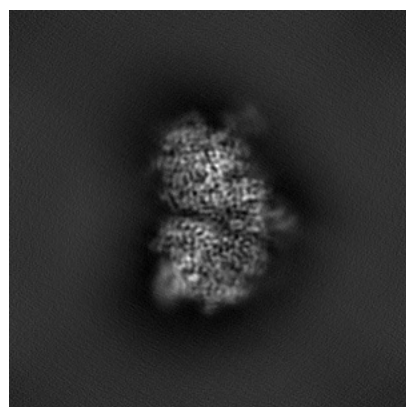


Y

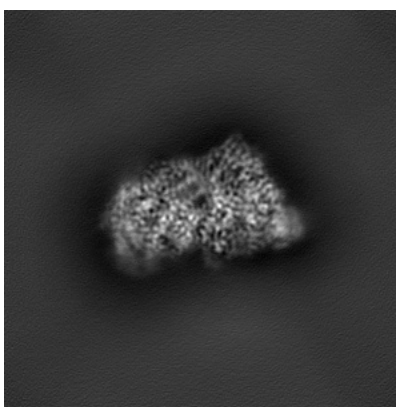


Z

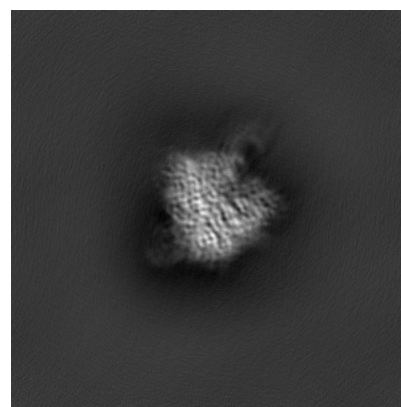
#### 6.1.2 Raw map



X



Y

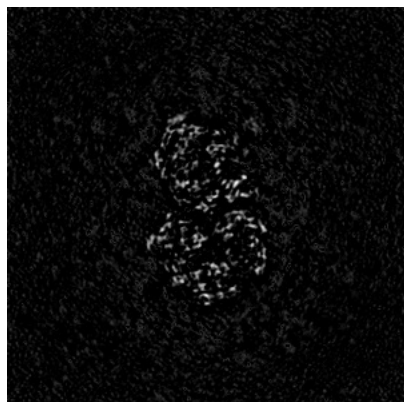


Z

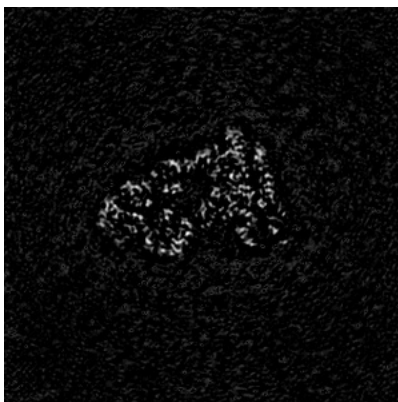
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 160

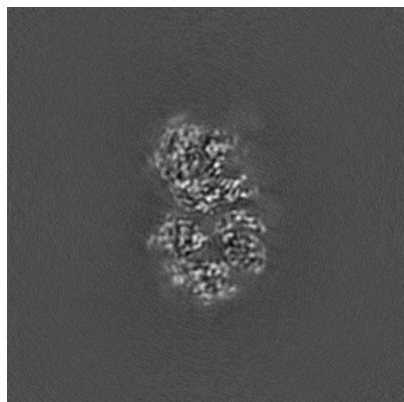


Y Index: 160

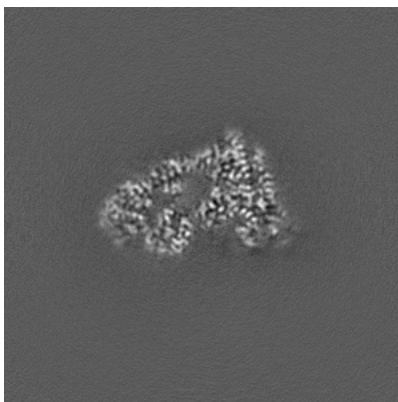


Z Index: 160

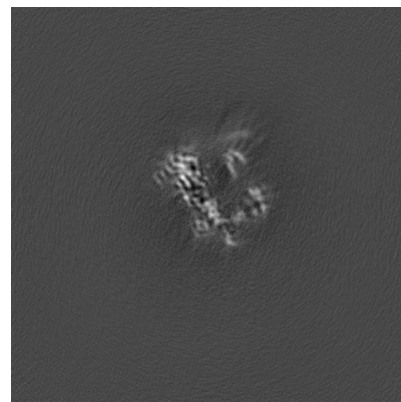
### 6.2.2 Raw map



X Index: 160



Y Index: 160

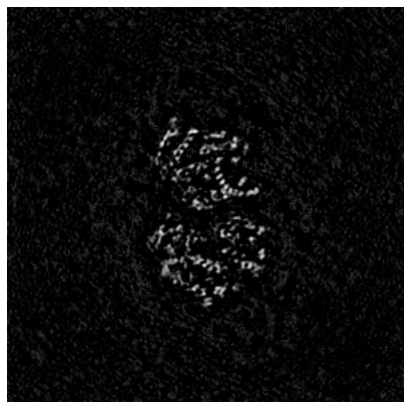


Z Index: 160

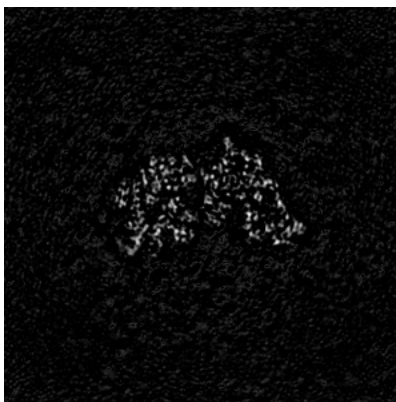
The images above show central slices of the map in three orthogonal directions.

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

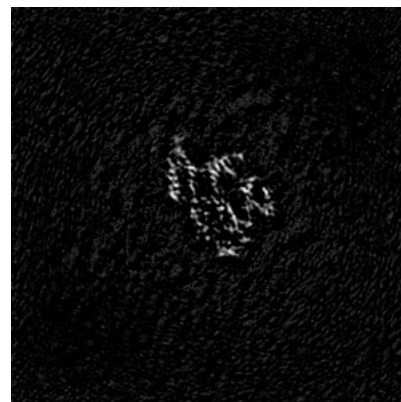
### 6.3.1 Primary map



X Index: 163

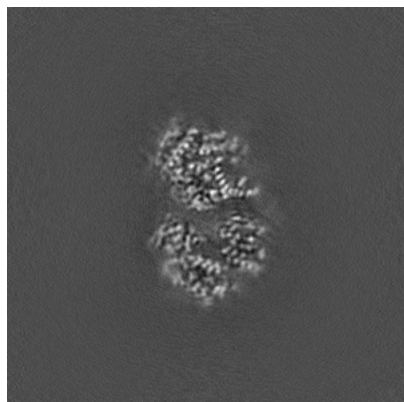


Y Index: 150

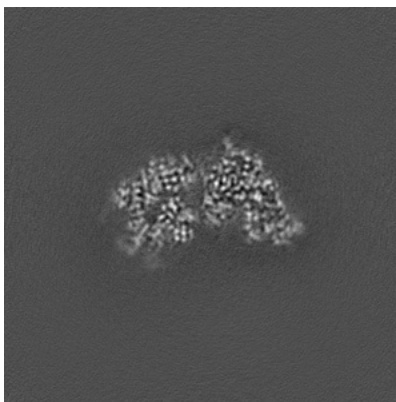


Z Index: 170

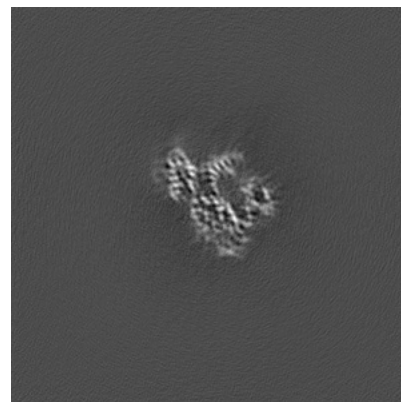
### 6.3.2 Raw map



X Index: 163



Y Index: 150



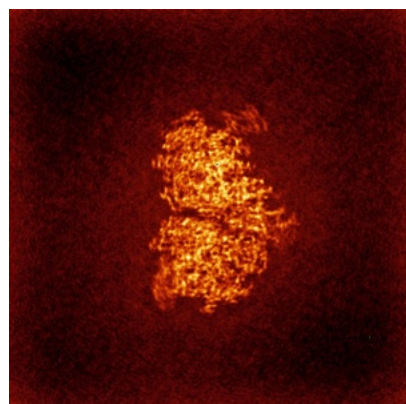
Z Index: 170

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

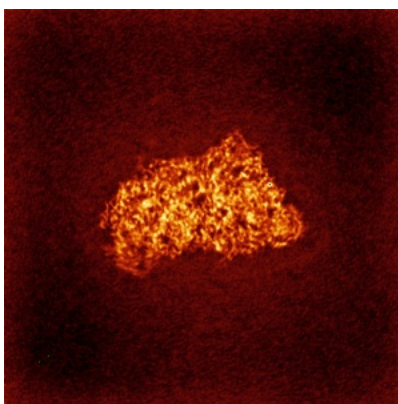


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

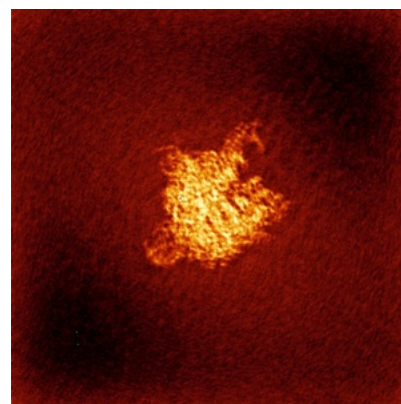
### 6.4.1 Primary map



X

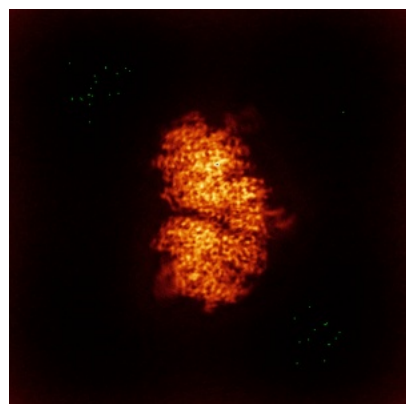


Y

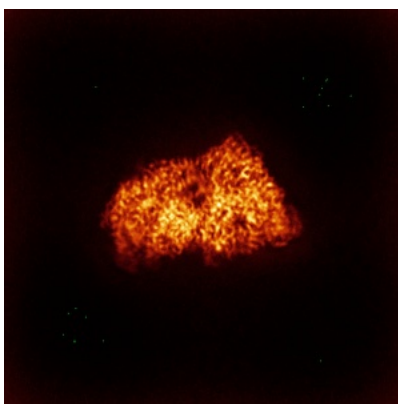


Z

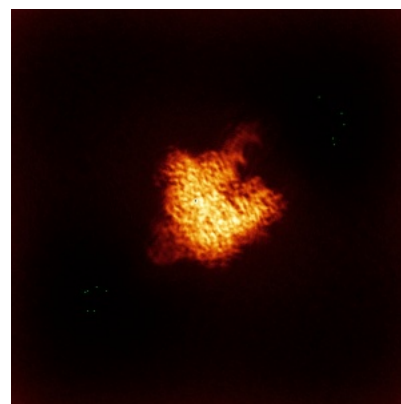
### 6.4.2 Raw map



X



Y

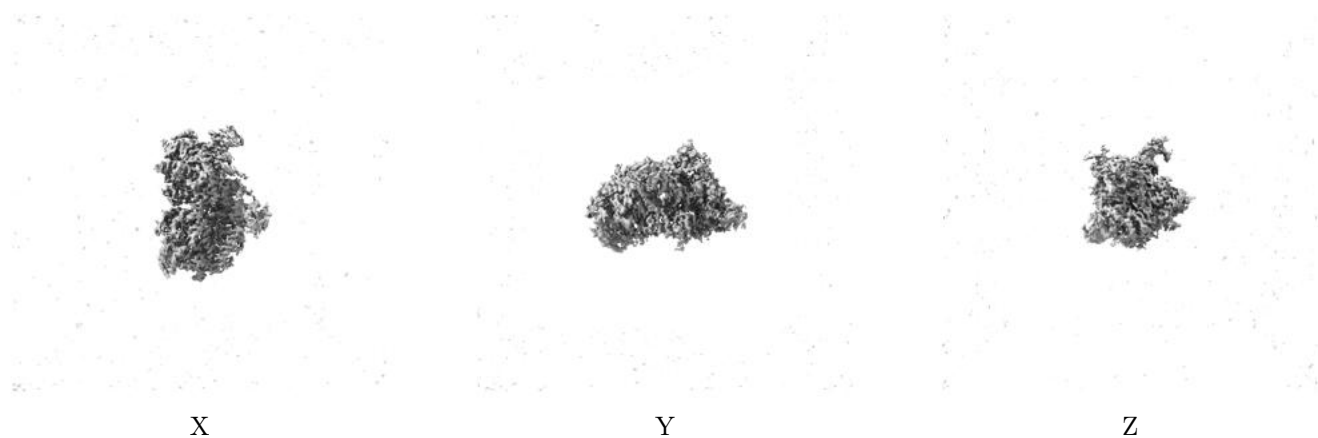


Z

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.

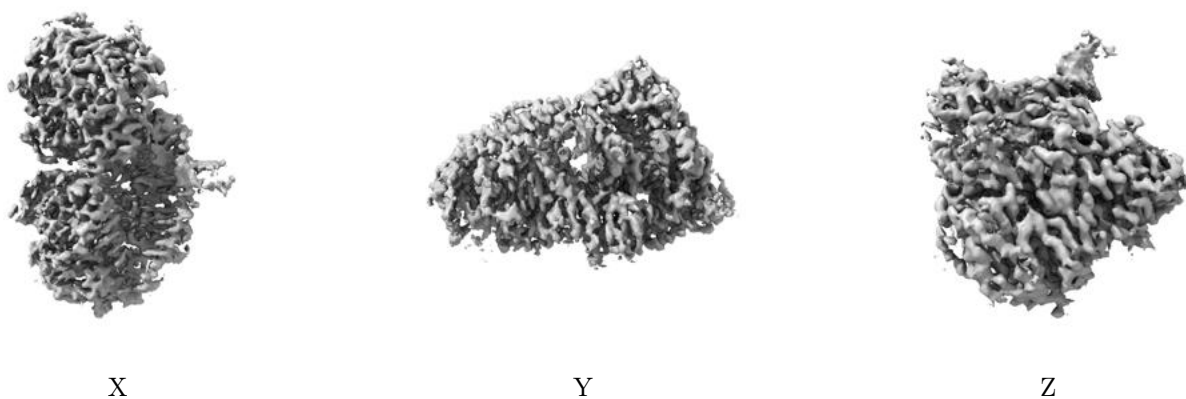
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. 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.

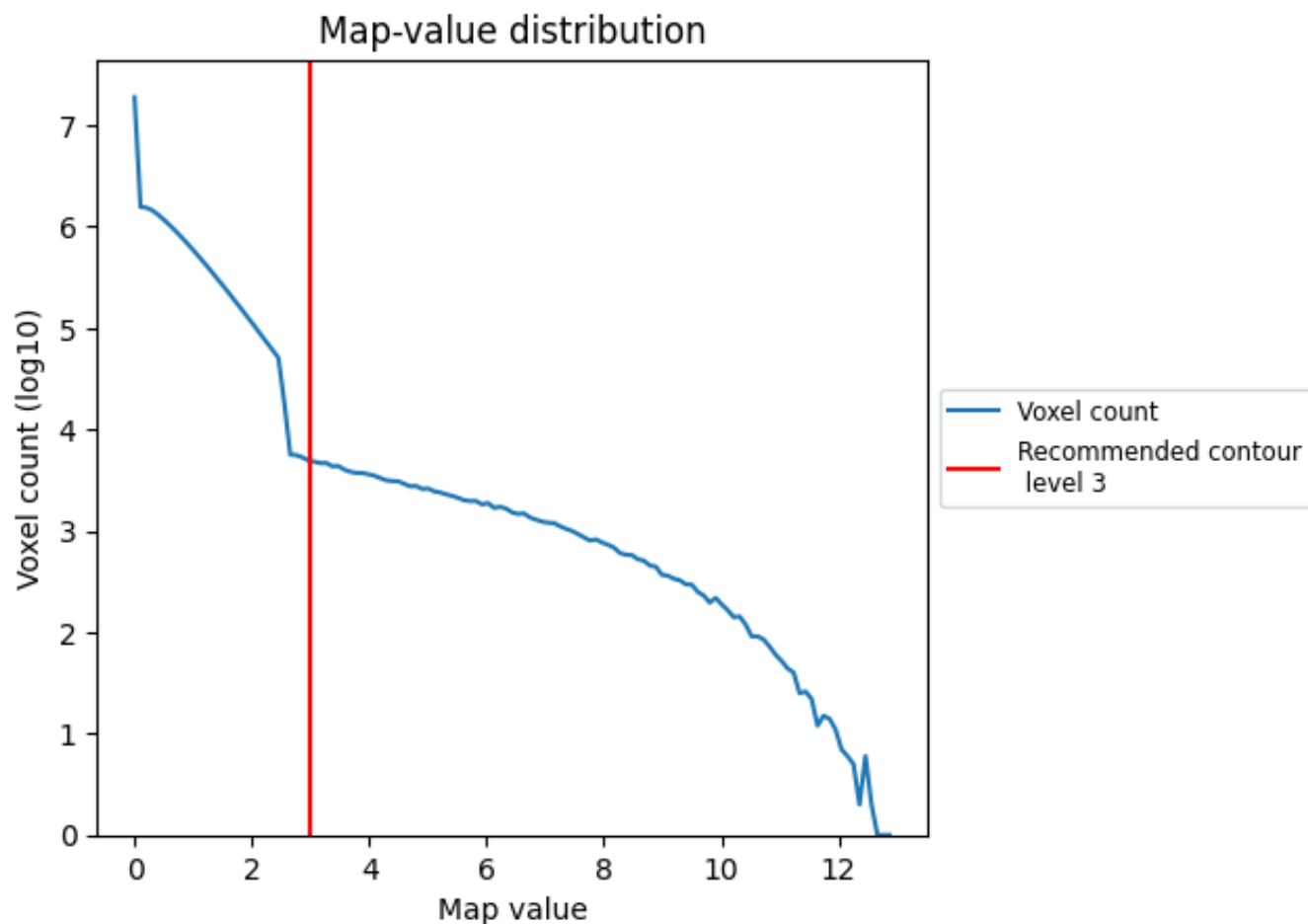
## 6.6 Mask visualisation [i](#)

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.

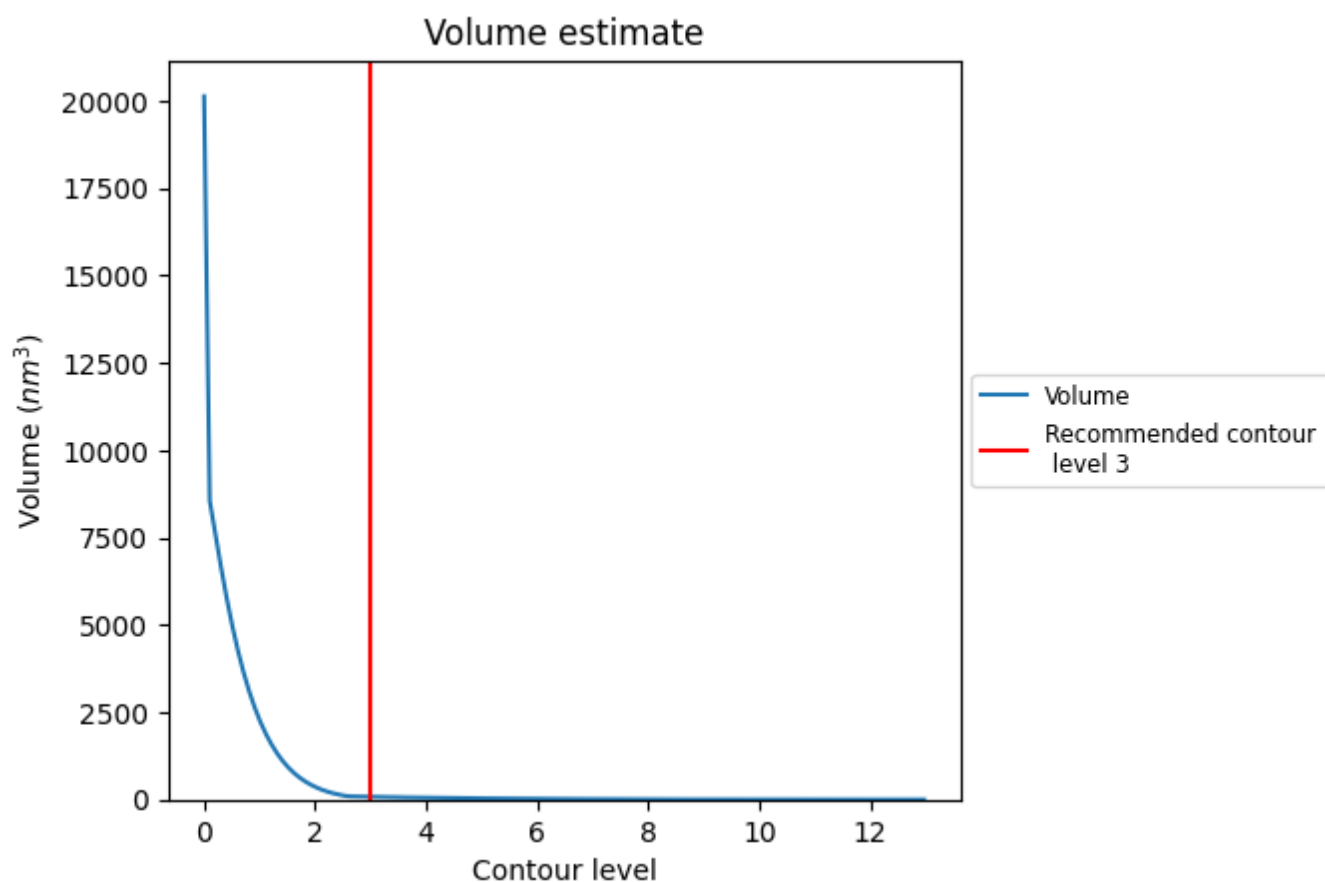
### 7.1 Map-value distribution [i](#)



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.



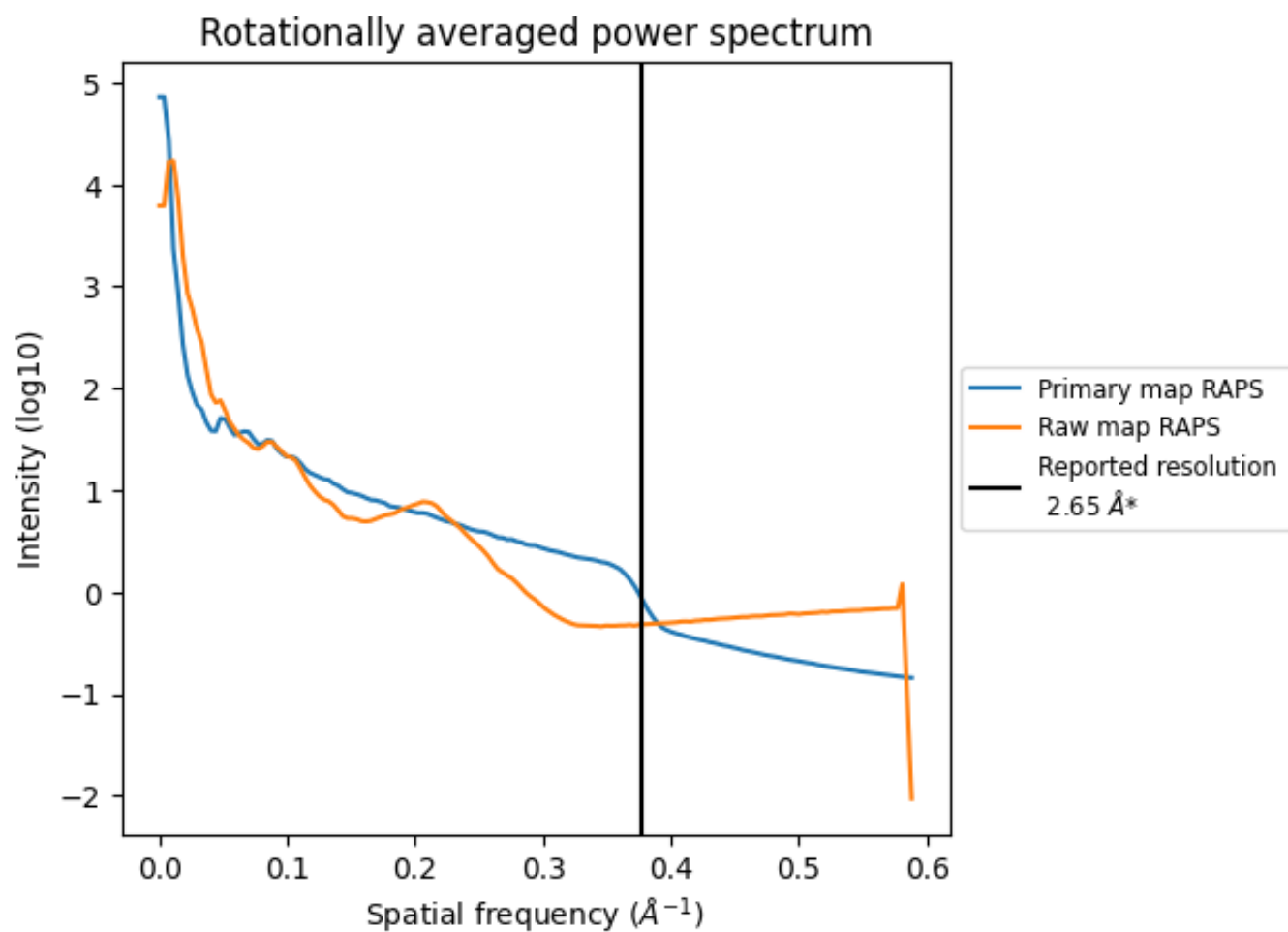
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79  $\text{nm}^3$ ; this corresponds to an approximate mass of 71 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 ⓘ

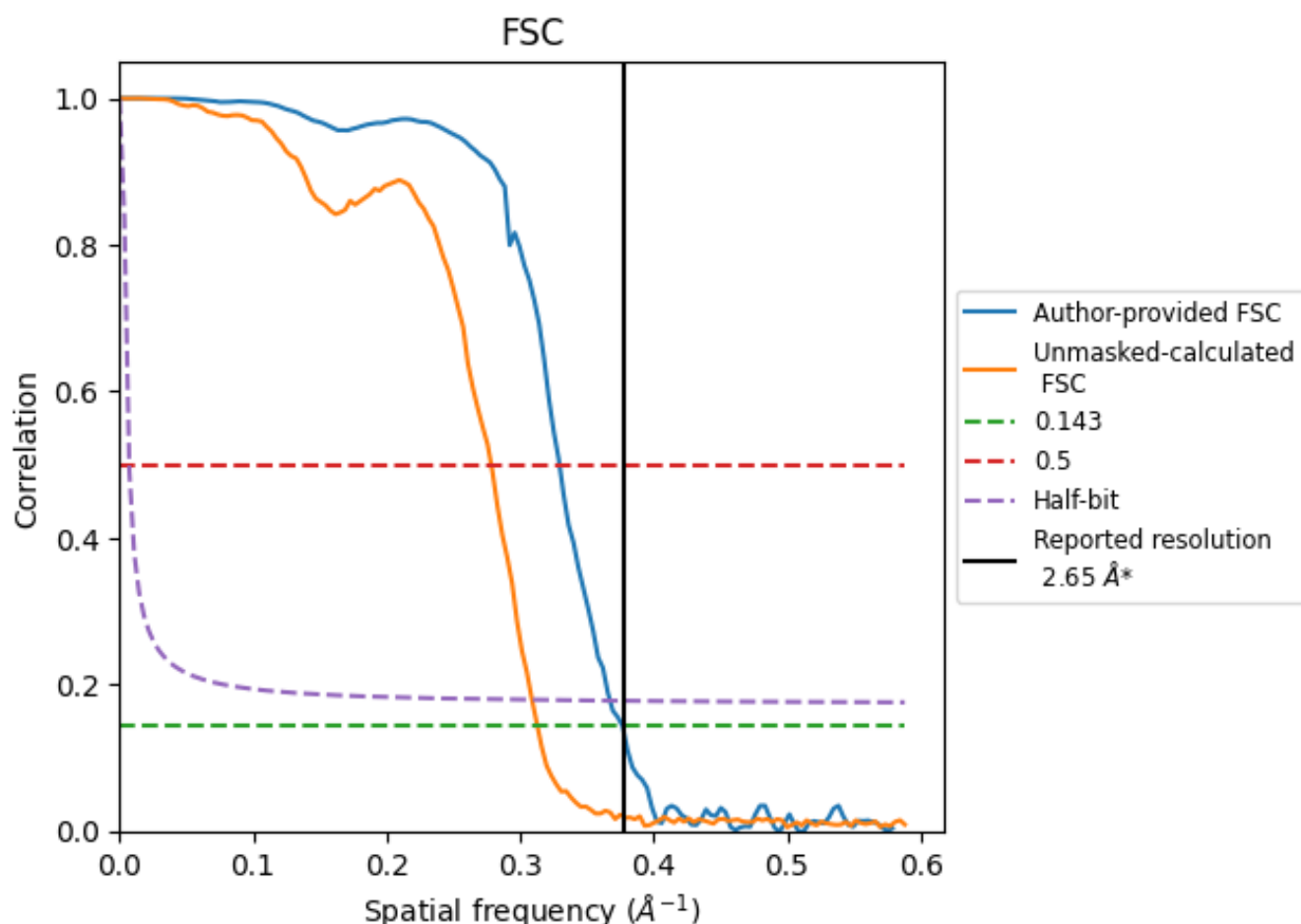


\*Reported resolution corresponds to spatial frequency of  $0.377 \text{\AA}^{-1}$

## 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 0.377  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

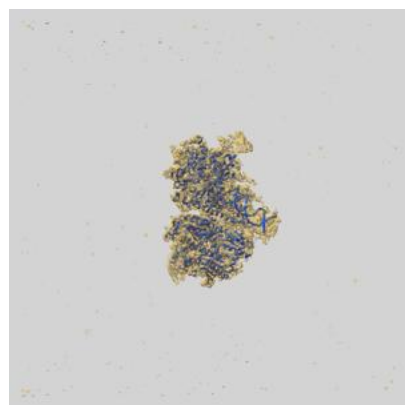
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	2.65	3.03	2.72
Unmasked-calculated*	3.19	3.59	3.24

\*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 3.19 differs from the reported value 2.65 by more than 10 %

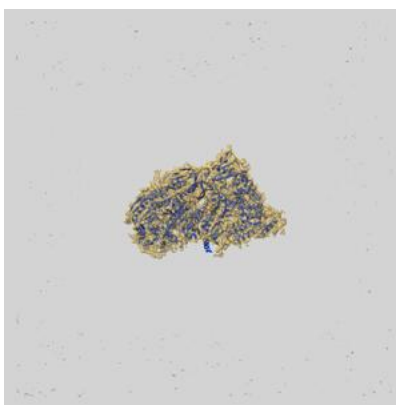
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27155 and PDB model 8D37. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

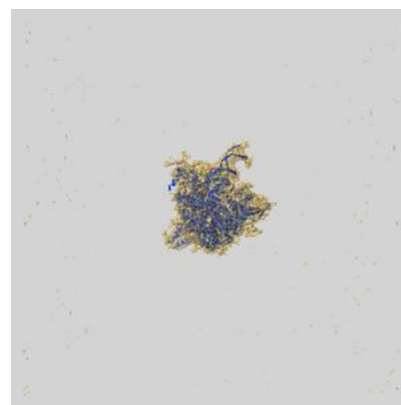
### 9.1 Map-model overlay [i](#)



X



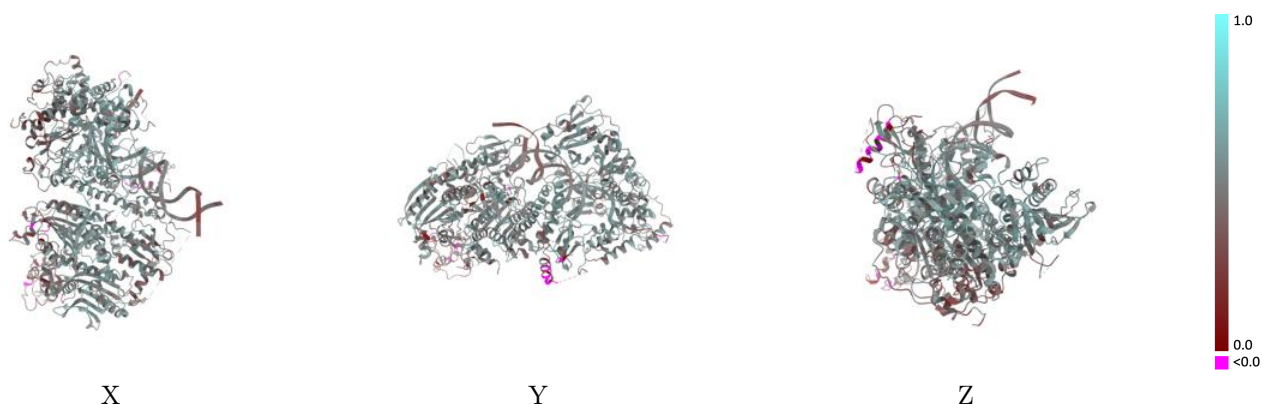
Y



Z

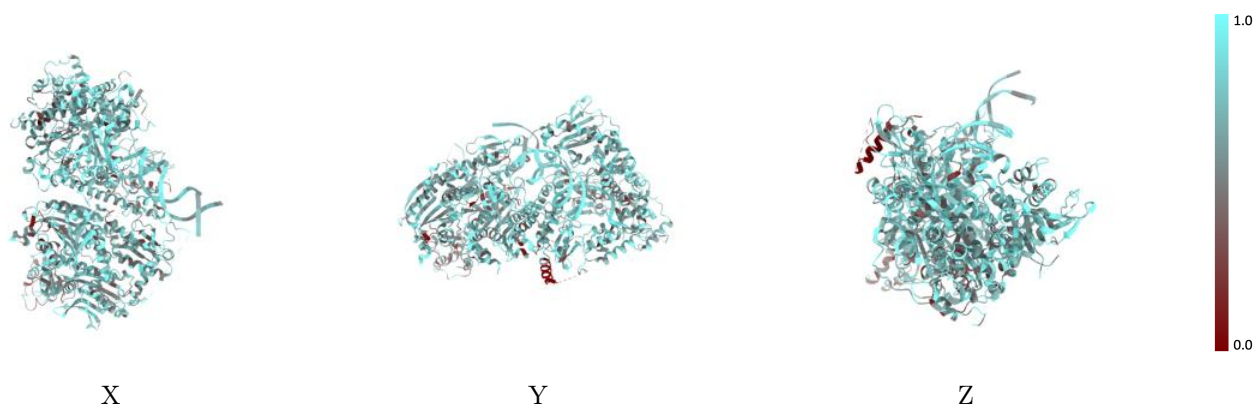
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



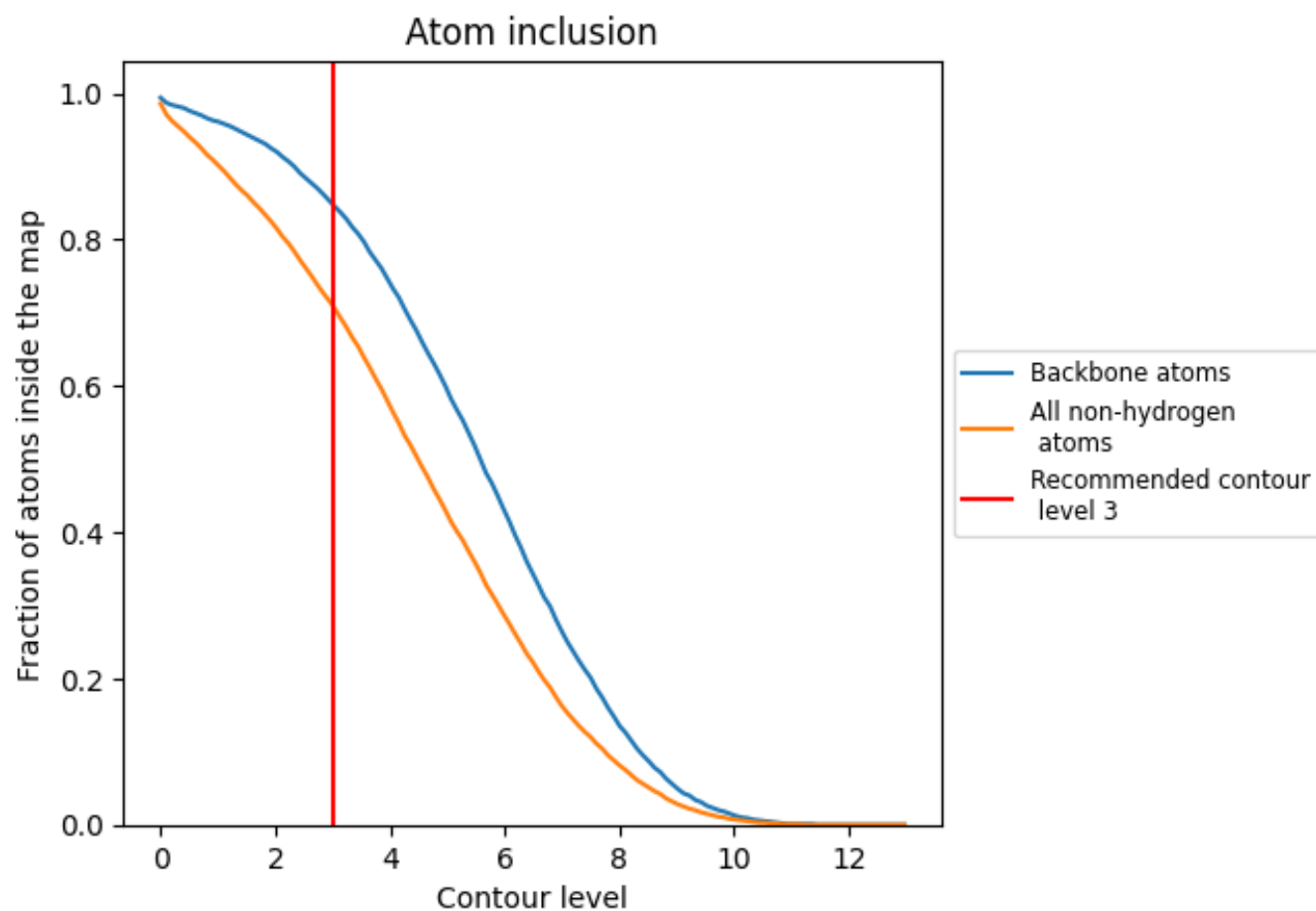
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 71% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7100	<div></div> 0.4900
A	<div></div> 0.7180	<div></div> 0.5010
B	<div></div> 0.6850	<div></div> 0.4730
C	<div></div> 0.6860	<div></div> 0.4810
P	<div></div> 0.8050	<div></div> 0.4670
T	<div></div> 0.7940	<div></div> 0.4970

