



## Full wwPDB EM Validation Report ⓘ

May 24, 2025 – 12:20 PM EDT

PDB ID : 9DN5 / pdb\_00009dn5  
EMDB ID : EMD-47026  
Title : CryoEM structures of yeast cytoplasmic dynein in the presence of ATP and Lis1.  
Authors : Kendrick, A.A.; Leschziner, A.E.  
Deposited on : 2024-09-16  
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](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.dev118  
Mogul : 2022.3.0, CSD as543be (2022)  
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) : 2.43.1

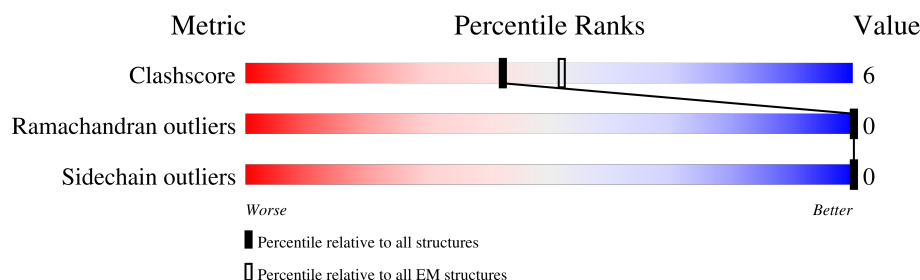
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

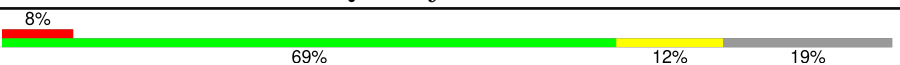

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	2875	 <p>8% 69% 12% 19%</p>
2	C	495	 <p>20% 56% 14% 30%</p>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21000 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 Dynein heavy chain, cytoplasmic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2333	Total	C	N	O	S	0	0
			18190	11681	3056	3374	79		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1220	GLY	-	expression tag	UNP P36022
A	1575	PHE	LEU	conflict	UNP P36022
A	1578	SER	PHE	conflict	UNP P36022
A	1668	GLU	GLN	conflict	UNP P36022
A	1777	VAL	ILE	conflict	UNP P36022
A	1984	VAL	ILE	conflict	UNP P36022
A	2936	VAL	ILE	conflict	UNP P36022
A	3266	GLN	ARG	conflict	UNP P36022
A	3343	GLY	ALA	conflict	UNP P36022
A	3444	VAL	ILE	conflict	UNP P36022
A	3556	ARG	LYS	conflict	UNP P36022
A	3742	ASP	ASN	conflict	UNP P36022
A	3895	VAL	PHE	conflict	UNP P36022
A	4072	ASP	ASN	conflict	UNP P36022

- Molecule 2 is a protein called Nuclear distribution protein PAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	346	Total	C	N	O	S	0	0
			2697	1731	474	477	15		

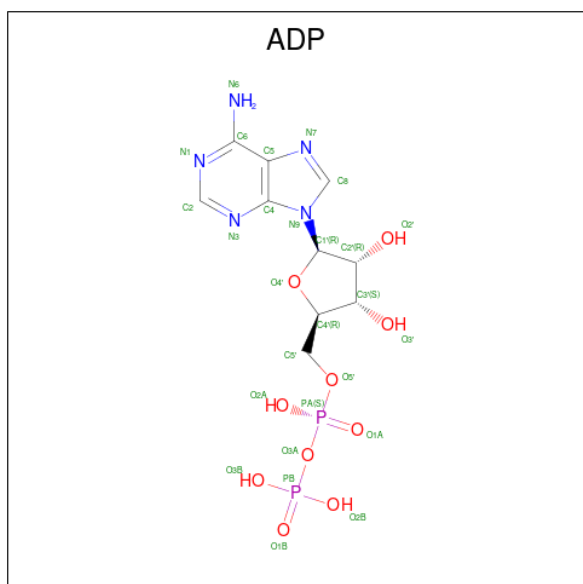
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	GLY	-	expression tag	UNP P39946

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ )

# ATP

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$ ) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Mg	0
			1	1	







• Molecule 2: Nuclear distribution protein PAC1



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

SER VAL ASP ARG GLN PHE ILE SER ASN THR ASP THR SER GLN SER MET VAL ASP ILE LYS SER ASP VAL LEU ARG TYR LEU ASN TRP LYS ASN TYR LYS GLN THR VAL ARG LEU ARG HIS GLU HIS ILE ALA GLN ASP TYR GLU SER VAL ARG THR ALA ILE VAL THR SER GLN ILE SER LYS PHE LEU ASP THR GLN

VAL SER GLU ALA GLN PHE LYS PRO THR THR SER ASN THR GLY THR SER ALA HIS ASN V139 R145 N146 I152 S156 S157 V158 T159 K162 L163 H164 P165 N166 L167 P168 A173 T174 D175 H176 F182 F185 T188 I189 P190 L191 A192 S193 L194 Q195 S196 H197 I201

L207 F208 T209 N210 Y211 T212 N213 SER SER LYS N218 V223 T224 A225 S226 K227 D228 L229 Q230 I231 H232 V233 S238 E239 E240 K241 K242 F243 S248 G251 H252 E253 T255 V256 K260 K264 N265 N266 D267 V268 H269 I270 A271 S274 R275 K280 I281 W282 D283

N286 G287 W288 V299 V300 I303 D304 V305 L306 G307 D308 Y309 I310 S312 G313 S314 H315 D316 R320 L321 T322 H323 W324 P325 S326 G327 N328 G329 G333 T334 G335 F338 I346 H347 E350 D351 SER PRO E354 I355 R356 F357 F360 S361 T362 D363 R364 N367 W368

Q371 V374 S377 R378 D379 R380 T381 E386 I387 P388 L389 P390 T391 L392 MET ALA HIS ARG A397 P398 T399 P400 N401 P402 T403 D404 S405 N406 C409 K414 L417 D422 I423 R426 L430 D436 R440 N445 T446 G447 H451 K455 V461

L464 D465 L466 D467 V468 D469 F470 D471 S472 N473 V474 T475 P476 R477 Q478 N479 N480 V481 G484 L485 S489 N490 V491 F492 N493 R494



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35055	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)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	54	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.039	Depositor
Minimum map value	-0.542	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	312.928, 312.928, 312.928	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.889, 0.889, 0.889	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: ATP, ADP, MG

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	0.14	0/18549	0.34	0/25133
2	C	0.12	0/2770	0.33	0/3771
All	All	0.14	0/21319	0.34	0/28904

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	18190	0	17724	219	0
2	C	2697	0	2575	51	0
3	A	31	0	12	2	0
4	A	81	0	36	5	0
5	A	1	0	0	0	0
All	All	21000	0	20347	267	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 6.

All (267) 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:2600:TYR:HB2	1:A:2622:LEU:HD11	1.68	0.75
1:A:2392:ILE:HD13	1:A:2570:ILE:HG23	1.71	0.70
1:A:2716:ILE:HG22	1:A:2734:ILE:HD13	1.75	0.69
1:A:1653:GLN:HG2	1:A:1708:PHE:HZ	1.59	0.68
1:A:2494:LEU:HD13	1:A:2544:ILE:HD12	1.75	0.68
1:A:1974:LYS:HG3	4:A:4104:ADP:H1'	1.76	0.68
1:A:3522:LYS:HE3	1:A:3626:VAL:HG21	1.75	0.67
1:A:2732:MET:HE1	1:A:2768:ILE:HG21	1.76	0.67
1:A:2971:HIS:HB3	1:A:3352:LEU:HD11	1.77	0.67
1:A:3829:ILE:HG12	1:A:3873:MET:HE1	1.78	0.66
1:A:2175:ILE:HD11	1:A:2183:ARG:HB3	1.77	0.65
1:A:2323:LEU:HD22	1:A:2339:ILE:HD13	1.78	0.65
1:A:2929:ALA:HA	1:A:2996:LEU:HD21	1.78	0.65
1:A:2974:ARG:HD2	1:A:2987:ARG:HH22	1.62	0.64
2:C:426:ARG:HH21	2:C:467:ASP:H	1.47	0.63
1:A:2392:ILE:O	4:A:4102:ADP:N6	2.32	0.63
2:C:156:SER:HB3	2:C:175:ASP:HB3	1.81	0.62
1:A:2488:GLU:HB3	1:A:2491:LEU:HD23	1.82	0.62
1:A:1831:LEU:HD23	1:A:1861:VAL:HG11	1.82	0.62
2:C:201:ILE:HA	2:C:226:SER:HA	1.82	0.62
1:A:1607:TRP:HA	1:A:1610:ILE:HG12	1.82	0.61
1:A:2279:ARG:NH2	1:A:2282:ASN:OD1	2.33	0.61
1:A:2294:LEU:HB3	1:A:2317:LEU:HD21	1.81	0.61
1:A:1802:LYS:NZ	1:A:1899:ASN:OD1	2.33	0.61
1:A:2976:PHE:HA	1:A:3345:MET:HE1	1.81	0.61
1:A:2761:ALA:O	1:A:2766:LYS:NZ	2.34	0.61
1:A:2229:LEU:HB3	1:A:2288:VAL:HG11	1.83	0.60
1:A:2968:ILE:HD13	1:A:3353:LEU:HD12	1.84	0.60
1:A:1902:TYR:HB2	1:A:1905:ARG:HD2	1.84	0.59
1:A:1823:ASP:OD1	1:A:1852:ARG:NH1	2.34	0.59
1:A:2494:LEU:HD12	1:A:2500:GLN:HG3	1.83	0.59
2:C:275:ARG:HA	2:C:299:TRP:HB2	1.84	0.59
1:A:2738:MET:HG3	1:A:2769:LEU:HD21	1.85	0.59
1:A:3928:CYS:HB3	1:A:3968:LEU:HD13	1.85	0.59
1:A:2148:SER:O	1:A:2189:ASN:ND2	2.33	0.58
1:A:2777:ASN:O	1:A:2812:ARG:NH2	2.31	0.58
1:A:3389:TYR:O	1:A:3393:ASN:ND2	2.38	0.57
1:A:2504:LEU:HA	1:A:2507:ARG:HG2	1.87	0.57
2:C:254:HIS:HB3	2:C:275:ARG:HB3	1.87	0.57
1:A:1627:LEU:HD11	1:A:1655:MET:HE3	1.87	0.57
1:A:2253:ILE:HD11	1:A:2295:ILE:HG21	1.87	0.57
1:A:2095:ASP:OD2	1:A:2149:ARG:NH2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2073:VAL:HG21	1:A:2199:LEU:HD11	1.87	0.56
1:A:3383:GLY:O	1:A:3413:HIS:NE2	2.36	0.56
2:C:254:HIS:HD2	2:C:275:ARG:HD2	1.70	0.56
2:C:422:ASP:OD2	2:C:464:LEU:N	2.38	0.56
1:A:2225:LYS:NZ	1:A:2285:GLU:OE1	2.37	0.56
1:A:2844:PHE:HD1	1:A:2852:LEU:HD22	1.70	0.56
1:A:3700:MET:HE3	1:A:4085:THR:HG21	1.86	0.56
1:A:2861:ARG:NH2	1:A:2865:LEU:O	2.39	0.56
2:C:356:ARG:NH2	2:C:445:ASN:O	2.39	0.56
2:C:381:THR:HG22	2:C:414:LYS:HG3	1.88	0.56
1:A:1847:PHE:HB2	1:A:1896:ILE:HG22	1.87	0.56
1:A:2965:VAL:HG22	1:A:3325:ILE:HD11	1.87	0.56
1:A:1855:GLU:HG3	1:A:1906:SER:HB2	1.88	0.55
2:C:461:VAL:HA	2:C:484:GLY:HA2	1.88	0.55
1:A:2774:ALA:HB1	1:A:2779:LEU:HB2	1.89	0.55
1:A:3419:SER:HA	1:A:3426:THR:HG21	1.89	0.55
1:A:3774:ILE:HG12	1:A:3895:VAL:HG11	1.89	0.55
1:A:3342:ARG:NH1	1:A:3392:GLU:OE1	2.40	0.55
1:A:1460:ILE:HG13	1:A:1461:LEU:HG	1.87	0.55
1:A:1949:ILE:HD11	1:A:1994:VAL:HG21	1.89	0.55
1:A:2726:GLU:OE2	2:C:378:ARG:NH2	2.30	0.54
2:C:274:SER:OG	2:C:275:ARG:N	2.40	0.54
1:A:1774:LEU:HD11	1:A:1921:MET:HG2	1.88	0.54
1:A:1769:LEU:HD21	1:A:1804:GLU:HB3	1.89	0.54
1:A:1849:GLU:HG3	1:A:2167:ASN:HD22	1.73	0.54
2:C:231:ILE:HD11	2:C:256:VAL:HG21	1.90	0.54
1:A:2427:ILE:HD13	1:A:2559:LEU:HD21	1.88	0.54
1:A:2594:ARG:HB3	1:A:2680:TYR:HE2	1.73	0.54
2:C:314:SER:OG	2:C:315:HIS:N	2.41	0.53
1:A:3473:ALA:N	1:A:3476:ARG:O	2.41	0.53
1:A:2552:ARG:NH1	3:A:4101:ATP:O3G	2.42	0.53
1:A:1683:LEU:HB3	1:A:1702:LEU:HD21	1.91	0.53
1:A:2171:ASP:OD2	1:A:2209:ARG:NH1	2.42	0.52
1:A:2838:ALA:HB3	1:A:2878:VAL:HB	1.91	0.52
1:A:2932:MET:HE2	1:A:2996:LEU:HD23	1.91	0.52
1:A:1945:LEU:HD11	1:A:1994:VAL:HG11	1.92	0.52
1:A:2112:GLU:N	1:A:2112:GLU:OE1	2.43	0.52
1:A:2701:SER:HA	2:C:417:LEU:HD22	1.91	0.52
1:A:1820:PHE:O	1:A:1848:ASP:N	2.42	0.52
1:A:2294:LEU:HD23	1:A:2317:LEU:HD11	1.92	0.52
1:A:1797:PRO:O	1:A:1802:LYS:NZ	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2973:ASP:OD1	1:A:3333:TYR:OH	2.27	0.52
1:A:2063:MET:HE1	1:A:2213:LEU:HB2	1.91	0.52
1:A:1637:GLU:O	1:A:1686:LYS:NZ	2.43	0.52
1:A:2149:ARG:HD3	1:A:2191:ARG:HH12	1.75	0.52
1:A:4060:SER:HB3	1:A:4070:ILE:HG13	1.92	0.52
1:A:2081:THR:OG1	1:A:2195:GLU:OE2	2.27	0.51
1:A:2386:MET:HE1	1:A:2627:ARG:HB3	1.91	0.51
1:A:2508:GLN:HG3	1:A:2512:LYS:HD2	1.92	0.51
1:A:2905:SER:HB3	1:A:2908:LEU:HB2	1.92	0.51
1:A:2733:VAL:HG21	1:A:2931:ASN:HB3	1.91	0.51
1:A:2115:TYR:OH	1:A:2162:TYR:O	2.26	0.51
1:A:1749:ILE:HD12	1:A:1813:LEU:HD13	1.91	0.51
1:A:2549:ARG:NH2	3:A:4101:ATP:O2G	2.42	0.51
1:A:3406:PHE:HB3	1:A:3515:LEU:HA	1.92	0.50
1:A:2401:GLU:OE1	1:A:2430:ASN:ND2	2.44	0.50
1:A:3844:ILE:HD13	1:A:3875:MET:HB3	1.92	0.50
2:C:260:LYS:HG3	2:C:304:ASP:HA	1.94	0.50
1:A:1742:ASP:OD2	1:A:1745:ASN:ND2	2.44	0.50
1:A:3377:MET:HE1	1:A:3557:LEU:HB2	1.92	0.50
1:A:2429:ASN:O	1:A:2433:ARG:HG2	2.11	0.50
1:A:1851:ASN:O	1:A:1906:SER:OG	2.29	0.50
2:C:260:LYS:HB2	2:C:271:ALA:HB3	1.93	0.50
1:A:2338:PHE:HA	1:A:2341:THR:HG22	1.92	0.50
1:A:3635:PHE:HE2	1:A:3698:MET:HB2	1.77	0.50
2:C:303:ILE:HD12	2:C:310:ILE:HD11	1.94	0.50
1:A:1848:ASP:OD1	1:A:1897:THR:OG1	2.29	0.49
1:A:4091:GLU:OE2	1:A:4091:GLU:N	2.45	0.49
1:A:2571:TYR:OH	4:A:4102:ADP:O2'	2.30	0.49
2:C:157:SER:HB2	2:C:485:LEU:HA	1.95	0.49
2:C:191:LEU:O	2:C:242:LYS:NZ	2.39	0.49
1:A:2941:THR:OG1	1:A:3318:GLN:OE1	2.31	0.49
1:A:2341:THR:HA	1:A:2344:THR:HG22	1.94	0.49
1:A:2832:ASN:ND2	1:A:2905:SER:OG	2.44	0.49
1:A:2906:PRO:O	1:A:2910:ASN:ND2	2.37	0.49
1:A:1872:LEU:HD11	1:A:1892:THR:HG23	1.95	0.48
1:A:2178:LEU:HD12	1:A:2182:GLU:HB2	1.95	0.48
1:A:4003:ASP:HA	1:A:4006:VAL:HG22	1.95	0.48
2:C:164:HIS:O	2:C:477:ARG:NH2	2.46	0.48
1:A:2489:ILE:HG21	1:A:2550:PHE:HE1	1.78	0.48
1:A:3533:THR:O	1:A:3537:GLU:HB2	2.12	0.48
2:C:165:PRO:HB3	2:C:474:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:374:VAL:HG13	2:C:423:ILE:HD12	1.96	0.48
1:A:2594:ARG:HB3	1:A:2680:TYR:CE2	2.49	0.48
1:A:2038:LEU:HD13	1:A:2057:CYS:HB3	1.96	0.48
1:A:4071:LEU:O	1:A:4075:ARG:HB2	2.13	0.48
2:C:146:ASN:OD1	2:C:451:HIS:NE2	2.45	0.48
2:C:338:PHE:HB3	2:C:378:ARG:HB2	1.94	0.48
1:A:1793:CYS:HB2	1:A:1916:PHE:HB3	1.95	0.48
1:A:2076:ALA:O	1:A:2279:ARG:NH2	2.46	0.48
1:A:2773:VAL:O	1:A:2777:ASN:ND2	2.38	0.48
1:A:1734:PHE:CD1	1:A:1749:ILE:HG12	2.48	0.47
1:A:2657:ALA:HA	1:A:2660:LEU:HG	1.95	0.47
2:C:481:VAL:HG23	2:C:491:VAL:HG22	1.95	0.47
1:A:3655:ARG:HA	1:A:3658:ILE:HB	1.96	0.47
1:A:2252:LEU:HD23	1:A:2314:ILE:HD12	1.97	0.47
1:A:2835:LEU:O	1:A:2911:ARG:NH1	2.46	0.47
1:A:2921:ASP:OD1	1:A:2921:ASP:N	2.47	0.47
1:A:3365:ARG:NH1	1:A:3368:ASP:OD1	2.48	0.47
1:A:3816:LEU:HD12	1:A:3844:ILE:HA	1.95	0.47
2:C:303:ILE:HG22	2:C:312:SER:HA	1.97	0.47
1:A:2428:MET:HE1	1:A:2485:PHE:HB2	1.97	0.47
1:A:2919:ASP:OD1	1:A:2920:TRP:N	2.48	0.47
2:C:174:THR:HG22	2:C:176:HIS:H	1.78	0.47
1:A:1583:ARG:HG2	1:A:1589:VAL:HG22	1.96	0.47
1:A:1851:ASN:HB2	1:A:1905:ARG:HH11	1.80	0.46
1:A:1732:GLN:OE1	1:A:1812:ASN:ND2	2.49	0.46
1:A:3743:ASP:OD1	1:A:3743:ASP:N	2.48	0.46
1:A:4067:ARG:O	1:A:4067:ARG:HD3	2.16	0.46
2:C:159:THR:H	2:C:173:ALA:HB3	1.80	0.46
1:A:1516:LEU:O	1:A:1520:LYS:HG2	2.15	0.46
1:A:2507:ARG:NH2	1:A:2511:GLU:OE1	2.48	0.46
1:A:4082:ALA:HA	1:A:4085:THR:HG22	1.96	0.46
2:C:377:SER:OG	2:C:379:ASP:OD1	2.33	0.46
1:A:2099:ASN:HD21	1:A:2151:TRP:NE1	2.14	0.46
2:C:300:VAL:HA	2:C:314:SER:HA	1.98	0.46
1:A:1653:GLN:HG2	1:A:1708:PHE:CZ	2.46	0.46
1:A:1822:CYS:HB3	1:A:1853:LEU:HG	1.98	0.46
1:A:2421:GLY:HA3	1:A:2618:SER:HB3	1.98	0.46
1:A:2099:ASN:HD21	1:A:2151:TRP:HE1	1.63	0.46
4:A:4102:ADP:H8	4:A:4102:ADP:H2'	1.69	0.46
1:A:2831:MET:HE2	1:A:2831:MET:HA	1.98	0.46
1:A:2329:ASP:OD1	1:A:2329:ASP:N	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1691:SER:O	1:A:1695:LYS:N	2.45	0.45
2:C:223:VAL:HG22	2:C:233:VAL:HG13	1.97	0.45
1:A:1925:GLN:N	1:A:1925:GLN:OE1	2.49	0.45
1:A:3645:SER:HB3	1:A:3890:GLN:HB3	1.99	0.45
1:A:1988:GLY:O	1:A:1993:THR:OG1	2.30	0.45
1:A:2787:HIS:ND1	1:A:2788:ARG:O	2.48	0.45
2:C:374:VAL:HG21	2:C:430:LEU:HD11	1.99	0.45
1:A:2107:LYS:HD3	1:A:2159:ASP:HB2	1.98	0.45
1:A:3844:ILE:HG21	1:A:3875:MET:HG2	1.99	0.45
2:C:168:PRO:HA	2:C:477:ARG:HH12	1.82	0.45
2:C:223:VAL:HG13	2:C:233:VAL:HG22	1.99	0.45
1:A:2844:PHE:HE1	1:A:2852:LEU:HD13	1.82	0.45
1:A:2459:HIS:ND1	1:A:2845:GLN:OE1	2.49	0.44
1:A:2536:ASN:OD1	1:A:2543:ARG:NH2	2.46	0.44
1:A:2658:ASP:OD2	1:A:2659:ARG:N	2.51	0.44
1:A:2745:ILE:HG22	1:A:2773:VAL:HG11	2.00	0.44
1:A:1562:MET:HE2	1:A:1562:MET:HA	1.99	0.44
2:C:152:ILE:HB	2:C:489:SER:HB3	2.00	0.44
1:A:1636:ILE:HA	1:A:1639:VAL:HG22	2.00	0.44
1:A:1832:SER:OG	1:A:1864:ASN:OD1	2.25	0.44
2:C:304:ASP:OD1	2:C:305:VAL:N	2.50	0.44
1:A:3924:TRP:HZ3	1:A:3982:TRP:HZ2	1.65	0.44
1:A:2868:ASP:OD1	1:A:2868:ASP:N	2.49	0.44
1:A:2107:LYS:HB2	1:A:2504:LEU:HD12	2.00	0.44
1:A:1687:LEU:HD12	1:A:1698:ILE:HG22	2.00	0.43
1:A:3334:PHE:HB3	1:A:3342:ARG:HG2	1.99	0.43
1:A:3548:LEU:HD11	1:A:3604:SER:HB3	1.99	0.43
1:A:3676:TRP:O	1:A:3680:GLN:HG2	2.18	0.43
1:A:3873:MET:HE2	1:A:3873:MET:HB2	1.81	0.43
2:C:195:GLN:NE2	2:C:197:HIS:O	2.51	0.43
2:C:260:LYS:HD3	2:C:260:LYS:HA	1.86	0.43
1:A:1547:LYS:HB3	1:A:1557:GLN:HG2	2.00	0.43
1:A:1768:ARG:NH1	1:A:1812:ASN:OD1	2.43	0.43
1:A:3851:VAL:HG22	1:A:3855:LEU:HD12	1.99	0.43
2:C:225:ALA:HB1	2:C:256:VAL:HG13	1.98	0.43
1:A:3373:LEU:HG	1:A:3377:MET:HE3	1.99	0.43
2:C:254:HIS:CG	2:C:255:ILE:H	2.35	0.43
1:A:3812:LYS:HG3	1:A:3814:ILE:HD11	1.99	0.43
1:A:3635:PHE:CE2	1:A:3698:MET:HB2	2.54	0.43
1:A:2370:SER:OG	1:A:2371:PHE:N	2.51	0.43
1:A:2756:MET:HE2	1:A:2756:MET:HB2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2756:MET:HB3	1:A:2888:VAL:HG13	2.00	0.43
1:A:2758:LEU:HD22	1:A:2917:MET:HE2	2.01	0.43
1:A:3313:PHE:HA	1:A:3316:THR:HG22	2.01	0.43
1:A:2735:HIS:CE1	1:A:2738:MET:HB2	2.54	0.43
1:A:1545:LEU:HA	1:A:1548:ILE:HG22	2.01	0.42
1:A:2174:LYS:HB3	1:A:2186:ILE:HB	2.01	0.42
1:A:3642:TYR:OH	1:A:3691:ASP:OD1	2.29	0.42
1:A:3760:LEU:HD11	1:A:4078:ALA:HA	2.01	0.42
2:C:417:LEU:HB2	2:C:436:ASP:HB3	2.01	0.42
1:A:2275:ILE:HD12	1:A:2275:ILE:HA	1.88	0.42
1:A:1459:GLY:HA3	1:A:1550:GLY:HA2	2.01	0.42
2:C:197:HIS:HD1	2:C:201:ILE:HG22	1.85	0.42
1:A:1853:LEU:O	1:A:1906:SER:OG	2.37	0.42
1:A:2536:ASN:HB2	1:A:2543:ARG:HE	1.84	0.42
2:C:465:ASP:OD1	2:C:465:ASP:N	2.51	0.42
1:A:2030:ASN:HB2	1:A:2032:LYS:HE2	2.01	0.42
1:A:2702:LEU:HD23	2:C:417:LEU:HD23	2.02	0.42
1:A:3474:GLY:HA3	2:C:229:LEU:HD11	2.02	0.42
1:A:1626:CYS:SG	1:A:1648:ILE:HD13	2.60	0.42
1:A:1797:PRO:HD2	1:A:1922:LYS:HA	2.02	0.42
1:A:2489:ILE:O	1:A:2492:PRO:HD2	2.19	0.42
1:A:1815:ARG:HD2	1:A:1844:TRP:CE2	2.55	0.42
1:A:2071:ILE:HG12	1:A:2194:PHE:HB2	2.00	0.42
1:A:2426:MET:HE2	1:A:2426:MET:HB3	1.79	0.42
1:A:2929:ALA:O	1:A:2933:VAL:HG22	2.19	0.42
1:A:3676:TRP:HE3	1:A:3677:LEU:HD22	1.85	0.42
1:A:3812:LYS:HG2	1:A:3828:GLU:HG2	2.01	0.42
1:A:1558:VAL:HG21	1:A:1608:LEU:HD21	2.02	0.41
1:A:2720:PHE:CE2	1:A:2732:MET:HB3	2.54	0.41
1:A:1635:ASP:OD1	1:A:1635:ASP:N	2.50	0.41
1:A:4049:LEU:HD23	1:A:4049:LEU:HA	1.92	0.41
1:A:2081:THR:HA	1:A:2084:TRP:NE1	2.35	0.41
1:A:3795:ASP:OD1	1:A:3796:GLY:N	2.54	0.41
1:A:3822:LEU:HD22	1:A:3850:TRP:CD2	2.55	0.41
1:A:1532:ARG:HA	1:A:1840:GLN:HE22	1.86	0.41
1:A:1604:ALA:HA	1:A:1607:TRP:NE1	2.36	0.41
1:A:2578:ILE:HG12	1:A:2630:TYR:HB2	2.03	0.41
1:A:3006:LYS:HD3	1:A:3006:LYS:HA	1.85	0.41
1:A:3622:GLY:O	1:A:3626:VAL:HG13	2.21	0.41
1:A:3743:ASP:HB2	1:A:3762:TRP:CH2	2.56	0.41
2:C:323:HIS:CE1	2:C:325:PRO:HD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1821:ASN:HD21	1:A:2165:ALA:HA	1.86	0.41
1:A:1630:LEU:HD23	1:A:1630:LEU:HA	1.92	0.41
1:A:1795:PHE:CD1	1:A:1918:GLU:HB2	2.56	0.41
1:A:1983:LEU:HD23	1:A:1987:PHE:HB2	2.02	0.41
1:A:2623:THR:HG1	4:A:4102:ADP:HO2'	1.63	0.41
1:A:2998:ALA:HA	1:A:3001:LYS:HE3	2.02	0.41
1:A:3438:LYS:HE2	1:A:3438:LYS:HB2	1.95	0.41
1:A:3848:LEU:HD23	1:A:3848:LEU:HA	1.89	0.41
1:A:2078:CYS:SG	1:A:2080:LYS:NZ	2.91	0.41
1:A:1810:GLY:HA3	1:A:1817:VAL:HG23	2.04	0.40
1:A:2949:ASN:OD1	1:A:2950:LYS:N	2.54	0.40
2:C:491:VAL:HG12	2:C:493:MET:HE2	2.03	0.40
2:C:162:LYS:HD3	2:C:162:LYS:HA	1.95	0.40
1:A:2137:VAL:HA	1:A:2145:PHE:HD2	1.86	0.40
1:A:2196:THR:OG1	1:A:2197:ASP:N	2.54	0.40
1:A:2877:PHE:CZ	1:A:2881:ILE:HD11	2.57	0.40
2:C:254:HIS:CD2	2:C:275:ARG:HD2	2.52	0.40
1:A:3836:GLY:HA2	1:A:3871:PHE:HB2	2.02	0.40
1:A:1786:LEU:HD11	1:A:1895:PHE:HZ	1.86	0.40
2:C:440:ARG:HD3	2:C:440:ARG:HA	1.91	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	2305/2875 (80%)	2275 (99%)	30 (1%)	0	100	100
2	C	338/495 (68%)	328 (97%)	10 (3%)	0	100	100
All	All	2643/3370 (78%)	2603 (98%)	40 (2%)	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	1934/2631 (74%)	1934 (100%)	0	100	100
2	C	288/461 (62%)	288 (100%)	0	100	100
All	All	2222/3092 (72%)	2222 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	1464	ASN
1	A	1468	GLN
1	A	1530	GLN
1	A	1557	GLN
1	A	1609	ASN
1	A	1745	ASN
1	A	1757	GLN
1	A	1840	GLN
1	A	1866	GLN
1	A	2167	ASN
1	A	2351	GLN
1	A	2429	ASN
1	A	2508	GLN
1	A	2513	GLN
1	A	2553	HIS
1	A	2855	ASN
1	A	3363	ASN
1	A	3970	ASN
2	C	166	ASN
2	C	254	HIS
2	C	315	HIS

### 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 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z  > 2$
3	ATP	A	4101	-	28,33,33	0.69	0	34,52,52	0.69	1 (2%)
4	ADP	A	4104	5	24,29,29	0.85	0	29,45,45	1.26	3 (10%)
4	ADP	A	4103	-	24,29,29	0.87	0	29,45,45	1.19	2 (6%)
4	ADP	A	4102	-	24,29,29	0.88	0	29,45,45	1.19	3 (10%)

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
3	ATP	A	4101	-	-	4/18/38/38	0/3/3/3
4	ADP	A	4104	5	-	3/12/32/32	0/3/3/3
4	ADP	A	4103	-	-	2/12/32/32	0/3/3/3
4	ADP	A	4102	-	-	2/12/32/32	0/3/3/3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	4103	ADP	N3-C2-N1	-3.81	123.50	128.67
4	A	4104	ADP	N3-C2-N1	-3.73	123.61	128.67
4	A	4102	ADP	N3-C2-N1	-3.66	123.70	128.67
4	A	4104	ADP	C4-C5-N7	-2.44	106.76	109.34
4	A	4103	ADP	C4-C5-N7	-2.31	106.89	109.34
3	A	4101	ATP	C5-C6-N6	2.31	123.83	120.31
4	A	4102	ADP	C4-C5-N7	-2.30	106.91	109.34
4	A	4102	ADP	O4'-C1'-N9	2.11	111.54	108.75
4	A	4104	ADP	O4'-C1'-N9	2.04	111.45	108.75

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	4101	ATP	PB-O3B-PG-O2G
4	A	4102	ADP	O4'-C4'-C5'-O5'
4	A	4102	ADP	C3'-C4'-C5'-O5'
4	A	4103	ADP	C5'-O5'-PA-O1A
4	A	4103	ADP	C5'-O5'-PA-O3A
4	A	4104	ADP	C5'-O5'-PA-O1A
4	A	4104	ADP	O4'-C4'-C5'-O5'
3	A	4101	ATP	PB-O3B-PG-O3G
3	A	4101	ATP	PB-O3B-PG-O1G
4	A	4104	ADP	C3'-C4'-C5'-O5'
3	A	4101	ATP	C4'-C5'-O5'-PA

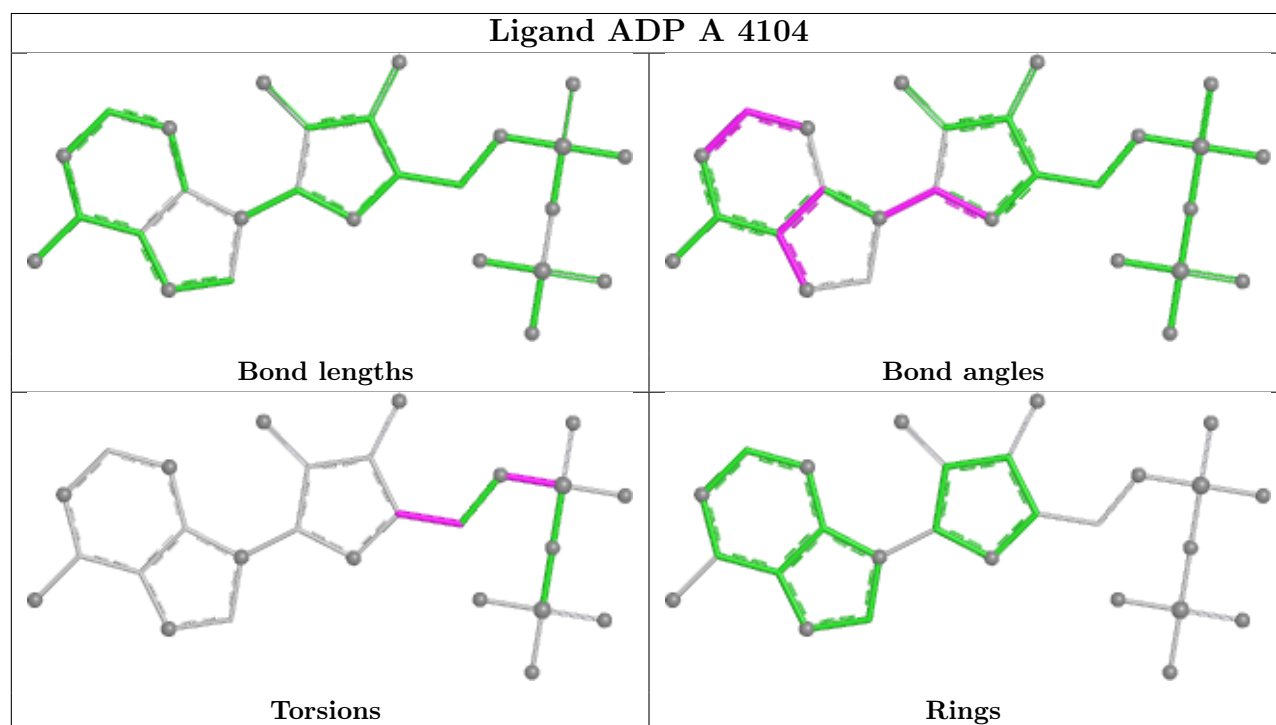
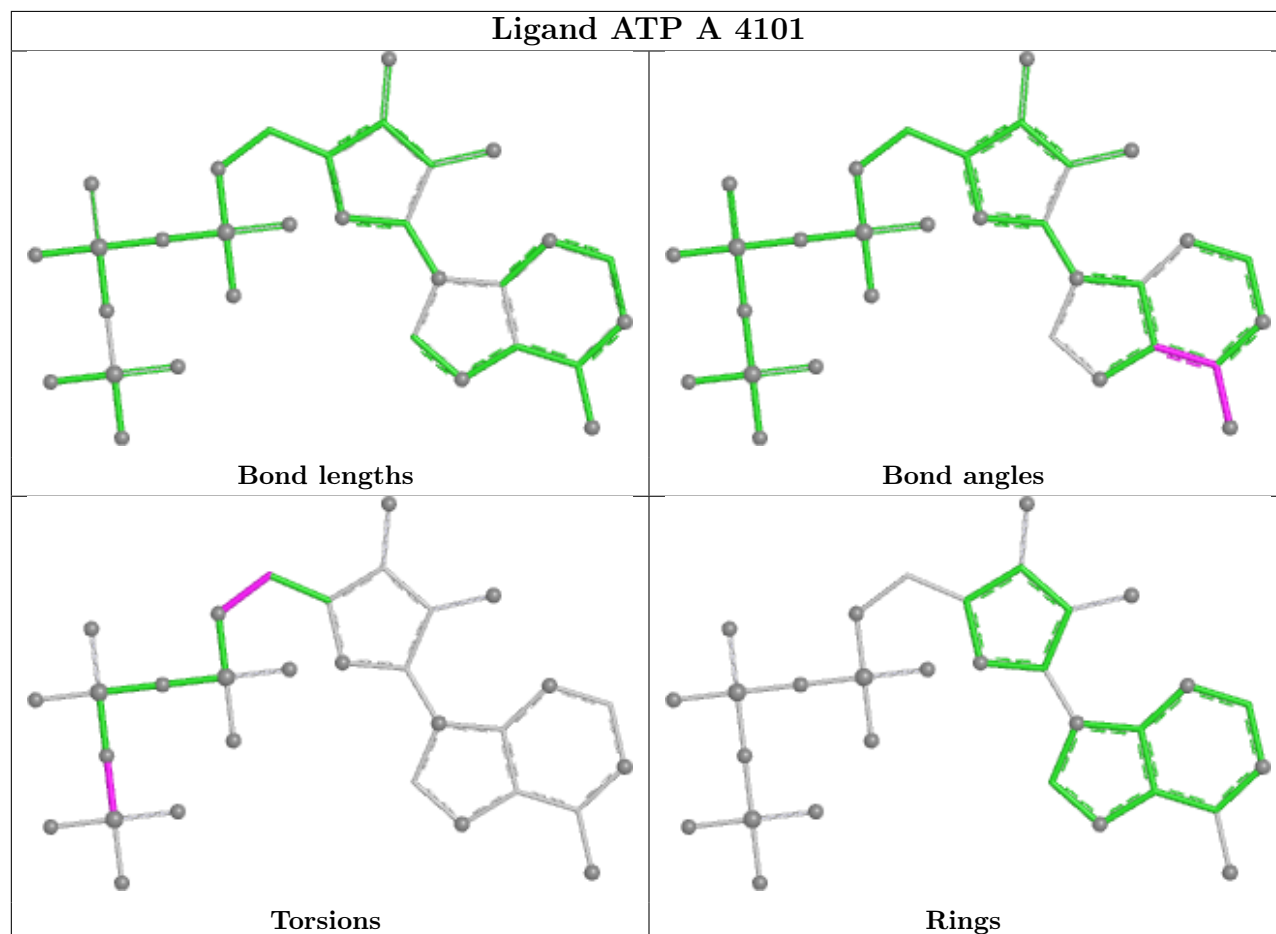
There are no ring outliers.

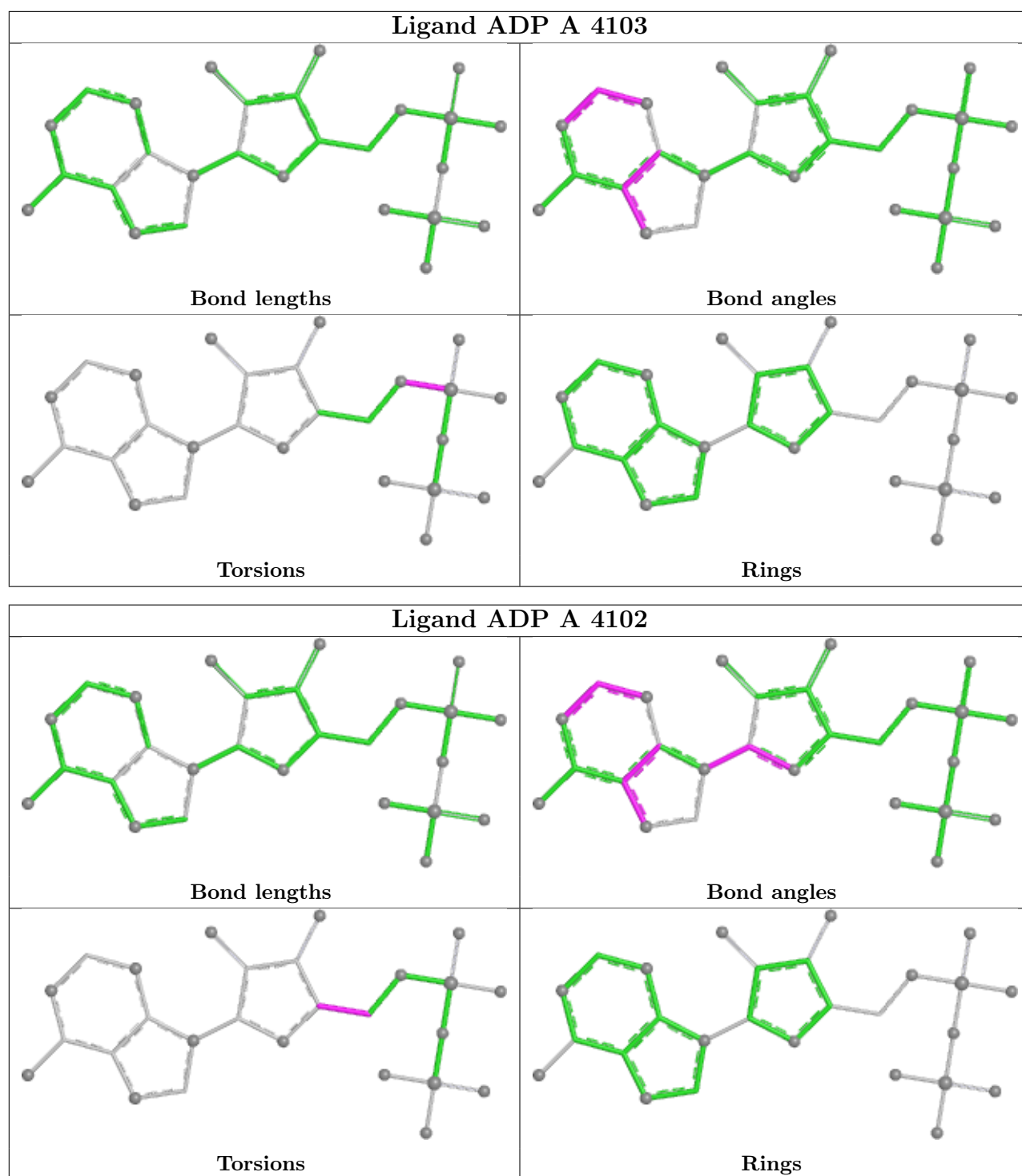
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	4101	ATP	2	0
4	A	4104	ADP	1	0
4	A	4102	ADP	4	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.

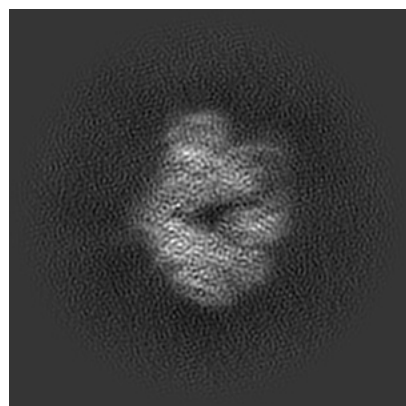
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47026. These allow visual inspection of the internal detail of the map and identification of artifacts.

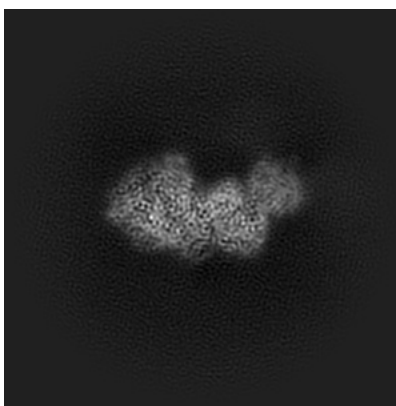
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

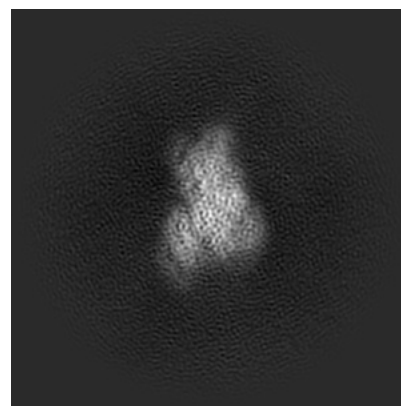
#### 6.1.1 Primary map



X

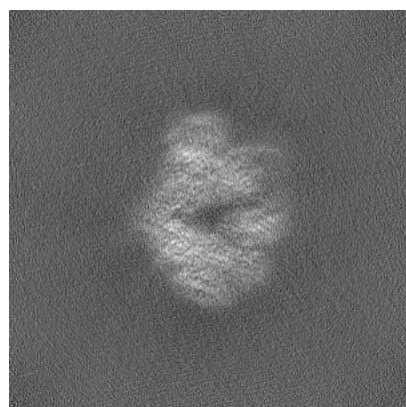


Y

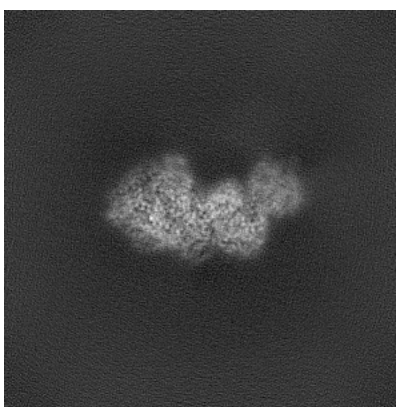


Z

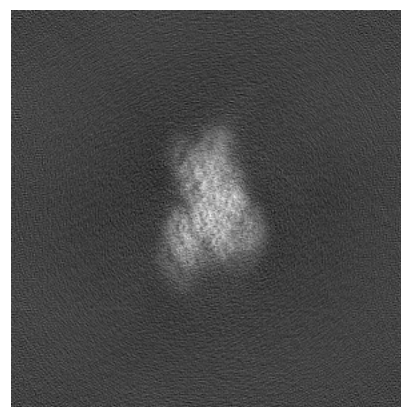
#### 6.1.2 Raw map



X



Y



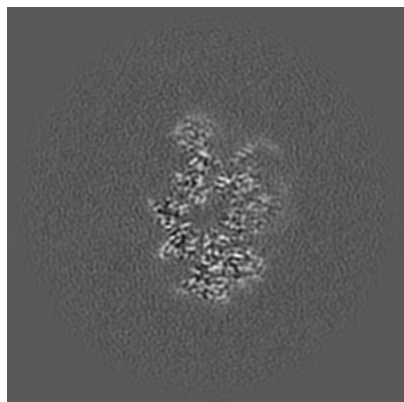
Z

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

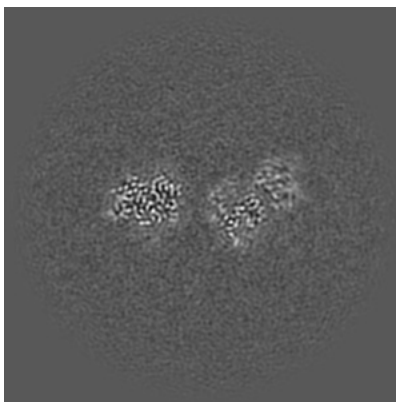


## 6.2 Central slices [i](#)

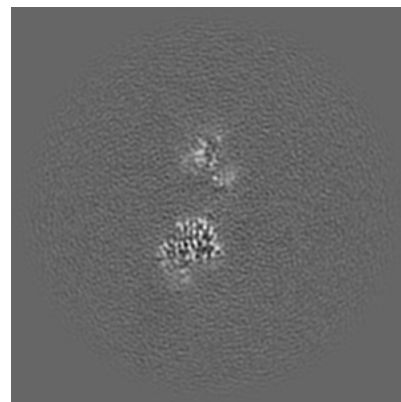
### 6.2.1 Primary map



X Index: 176

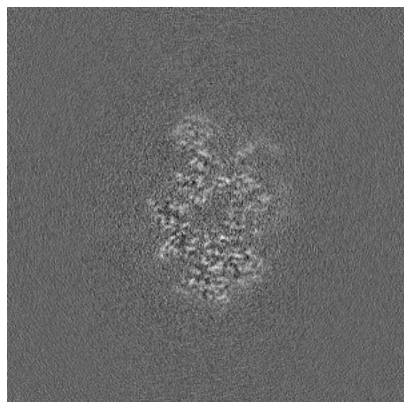


Y Index: 176

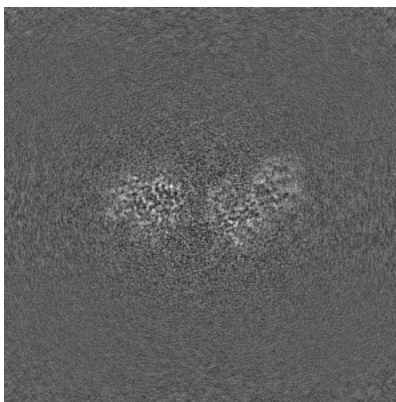


Z Index: 176

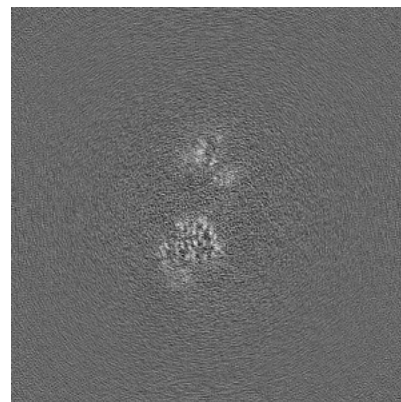
### 6.2.2 Raw map



X Index: 176



Y Index: 176

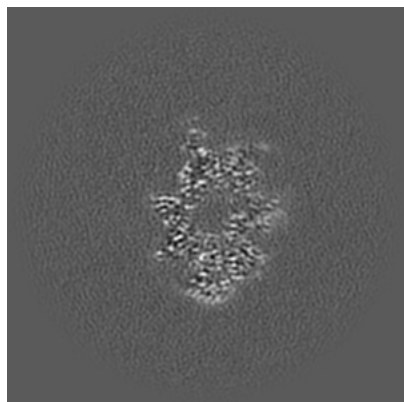


Z Index: 176

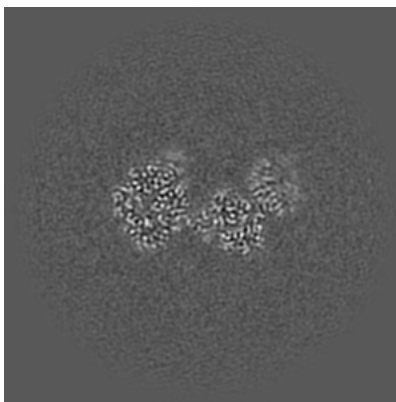
The images above show central slices of the map in three orthogonal directions.

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

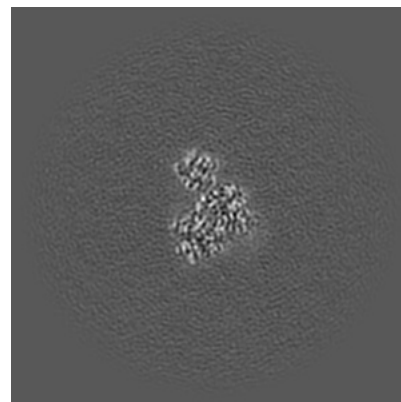
### 6.3.1 Primary map



X Index: 170

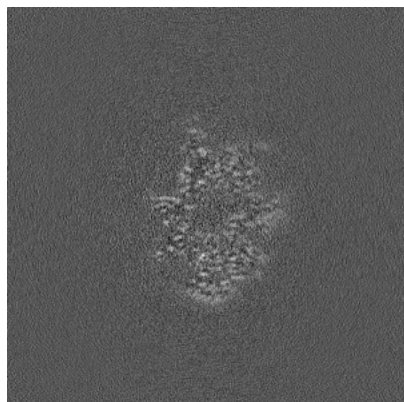


Y Index: 162

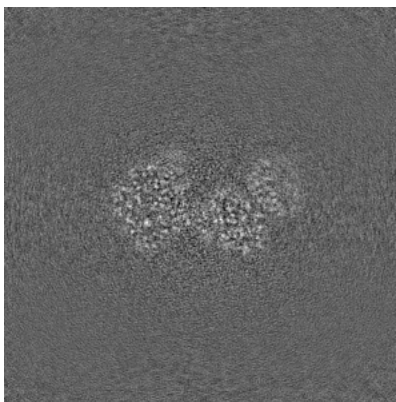


Z Index: 137

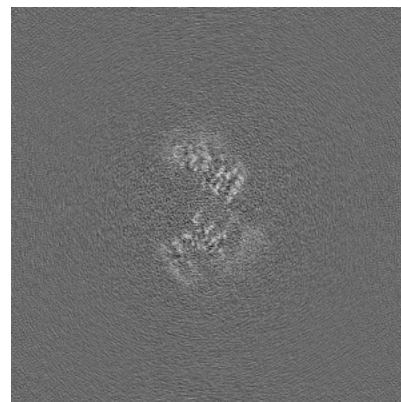
### 6.3.2 Raw map



X Index: 170



Y Index: 162

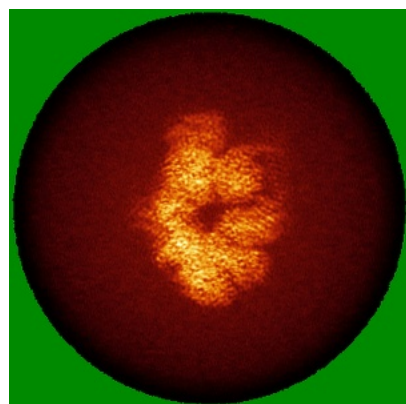


Z Index: 161

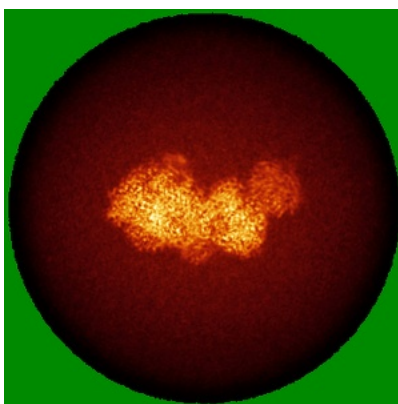
The images above show the largest variance slices of the map in three orthogonal directions.

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

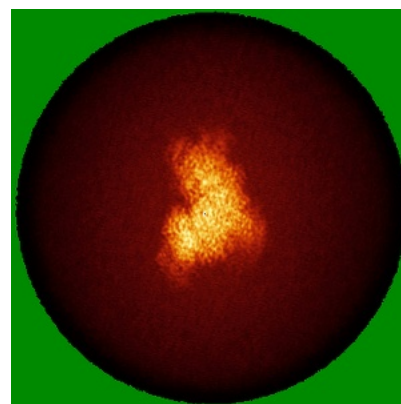
### 6.4.1 Primary map



X

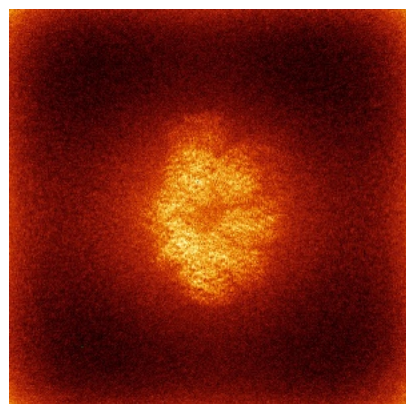


Y

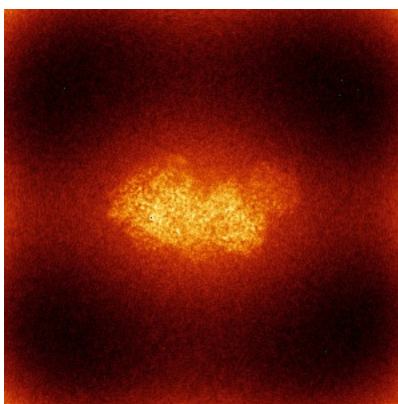


Z

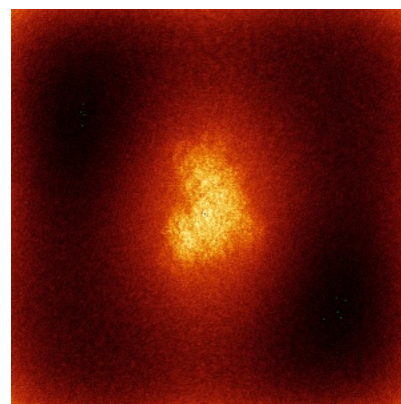
### 6.4.2 Raw map



X



Y

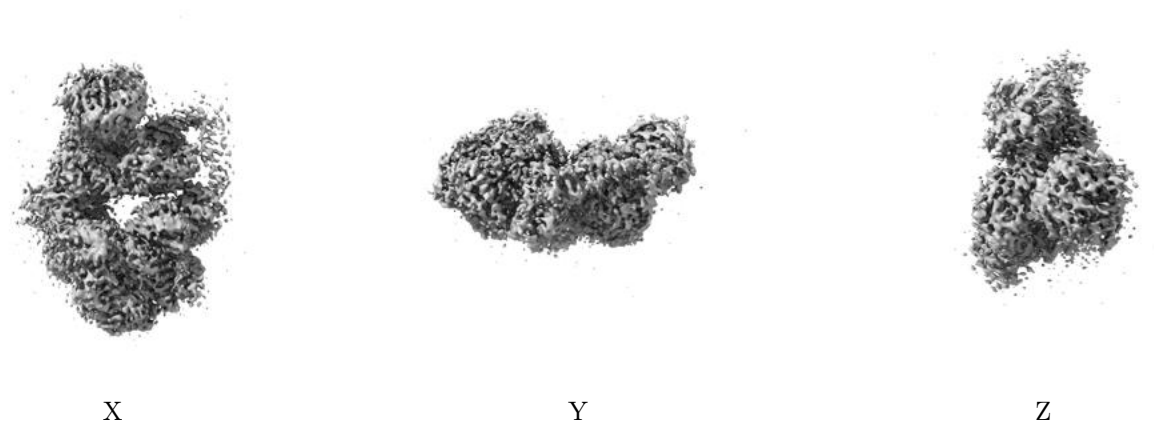


Z

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.

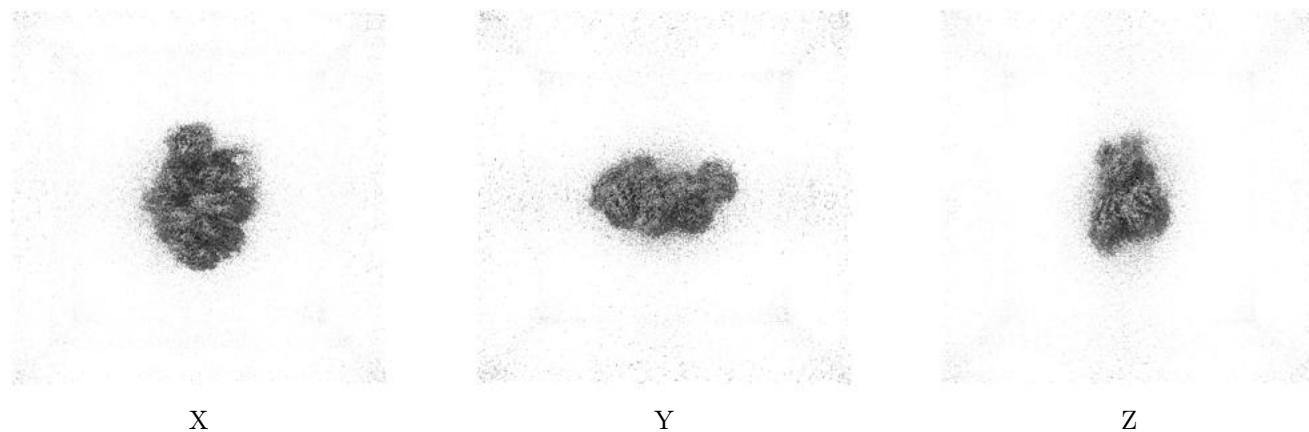
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. 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](#)

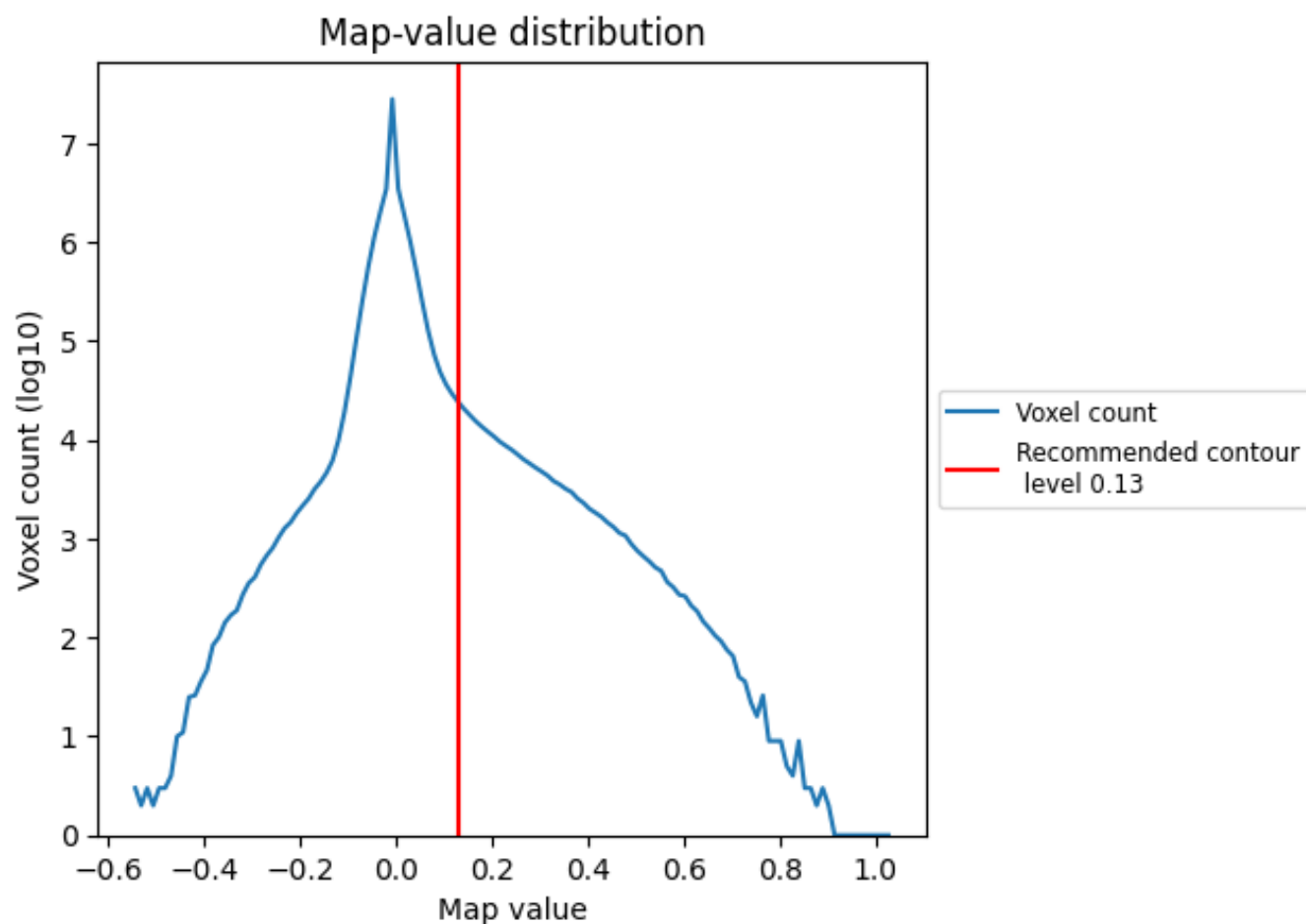
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

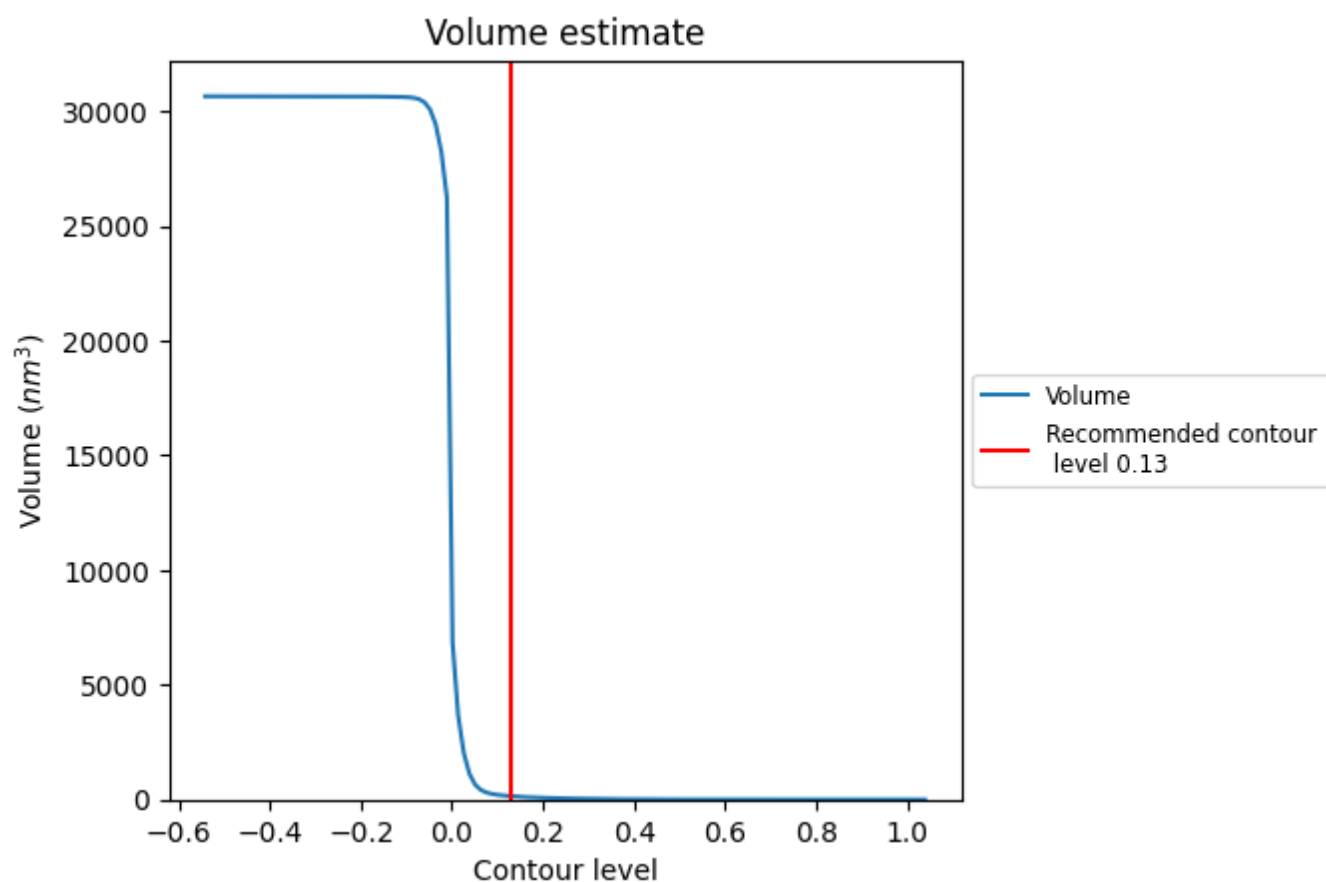
This section contains the results of statistical analysis of the map.

### 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.

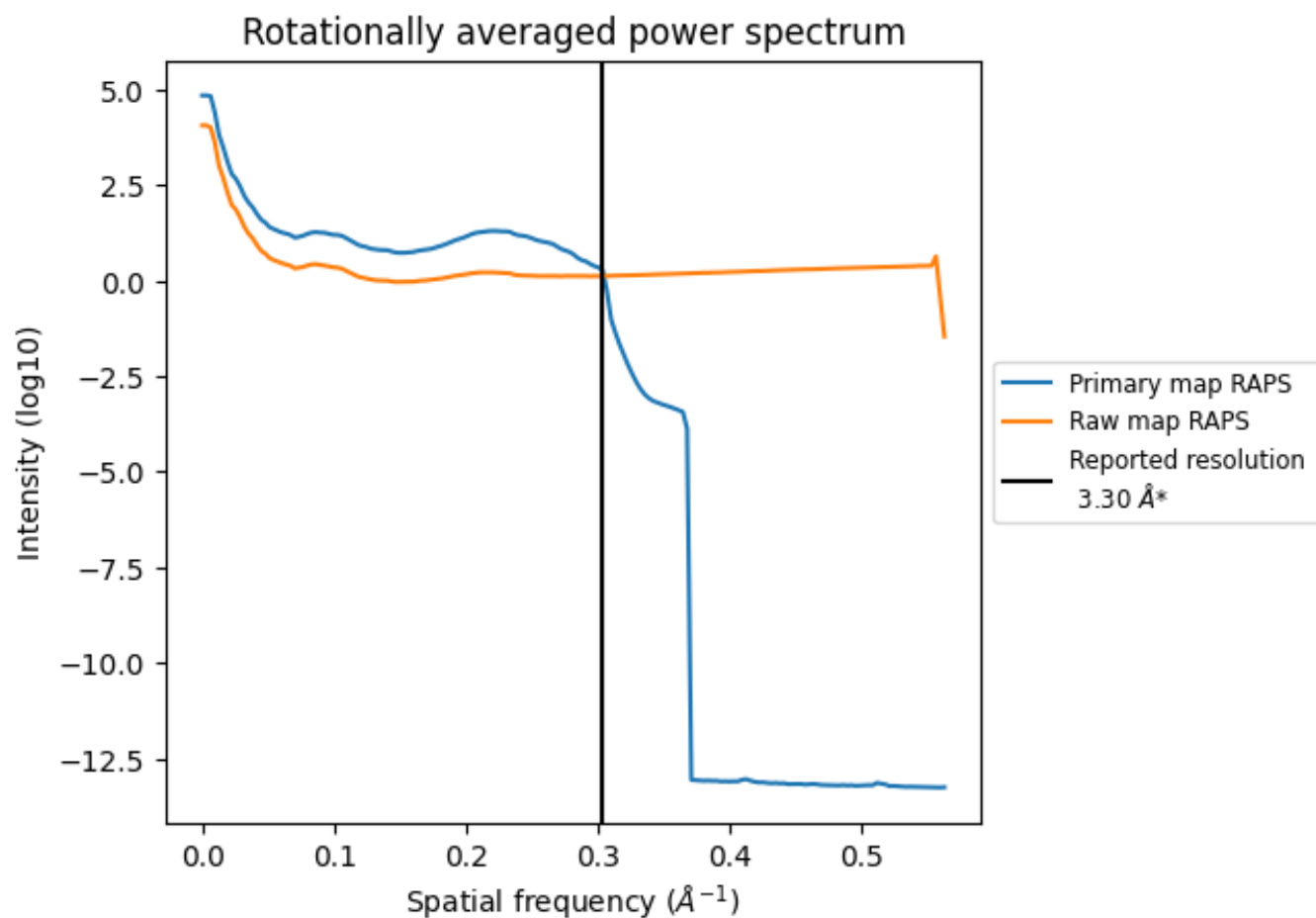
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 148 nm<sup>3</sup>; this corresponds to an approximate mass of 134 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

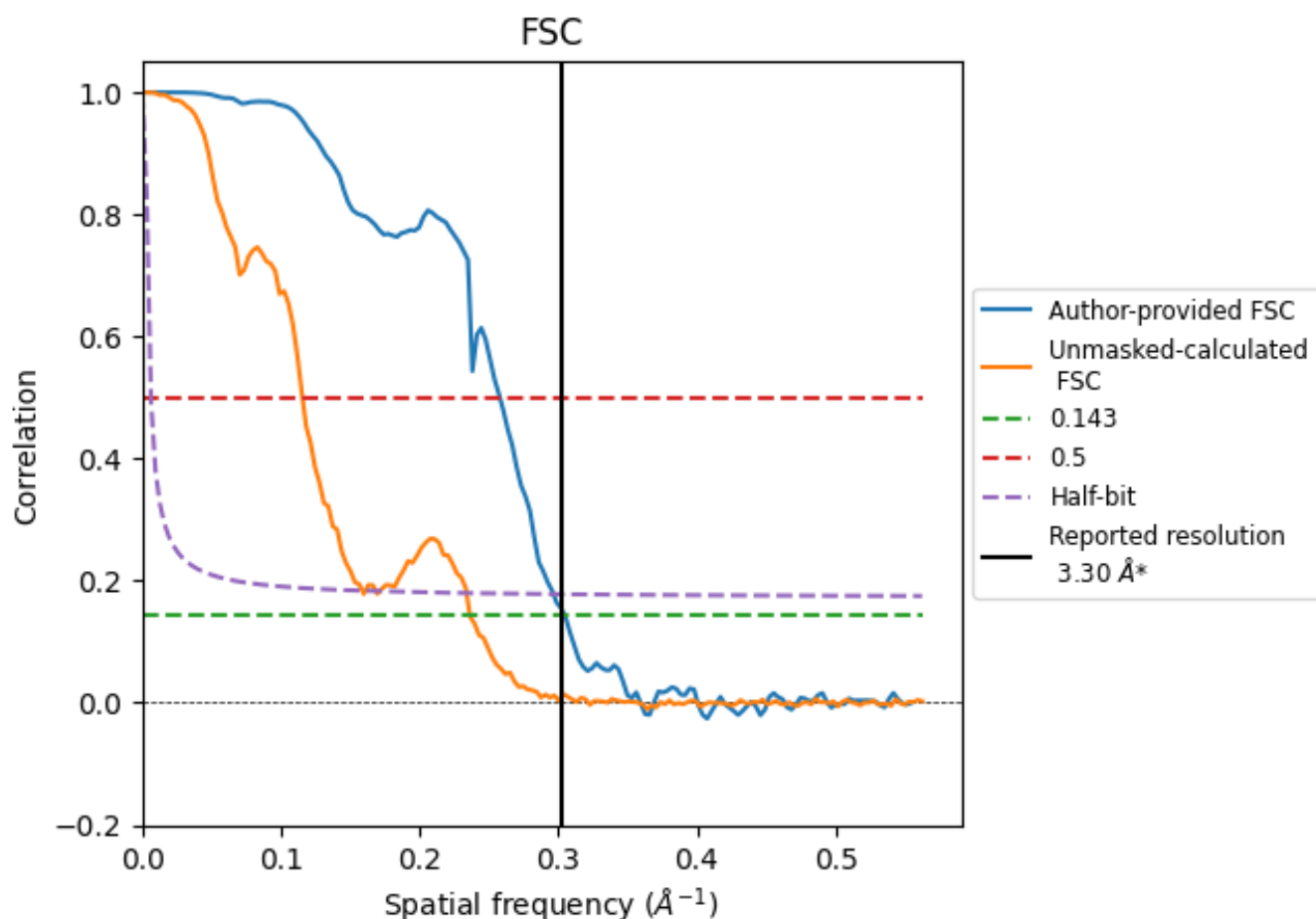


\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

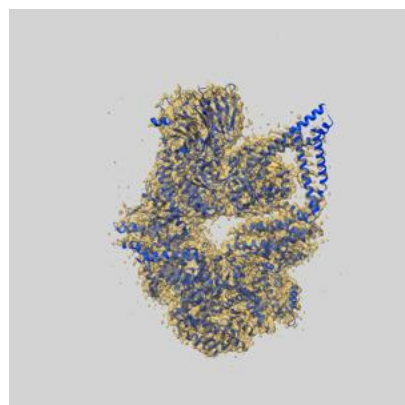
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.28	3.88	3.37
Unmasked-calculated*	4.23	8.65	6.30

\*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 4.23 differs from the reported value 3.3 by more than 10 %

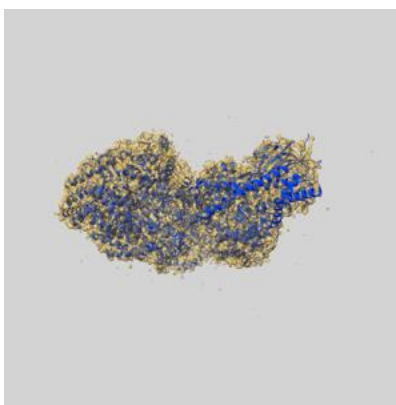
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47026 and PDB model 9DN5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

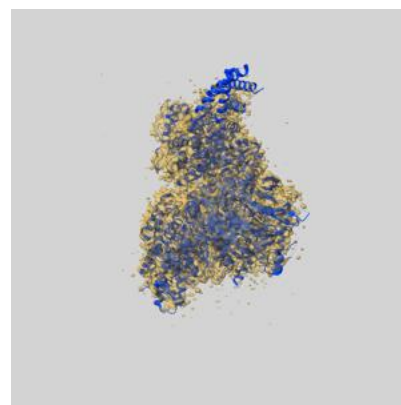
### 9.1 Map-model overlay [i](#)



X



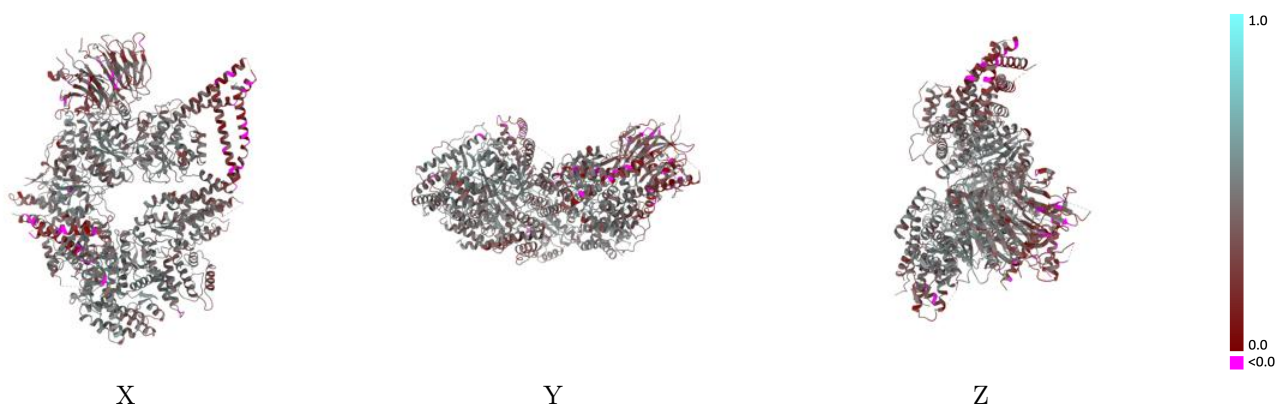
Y



Z

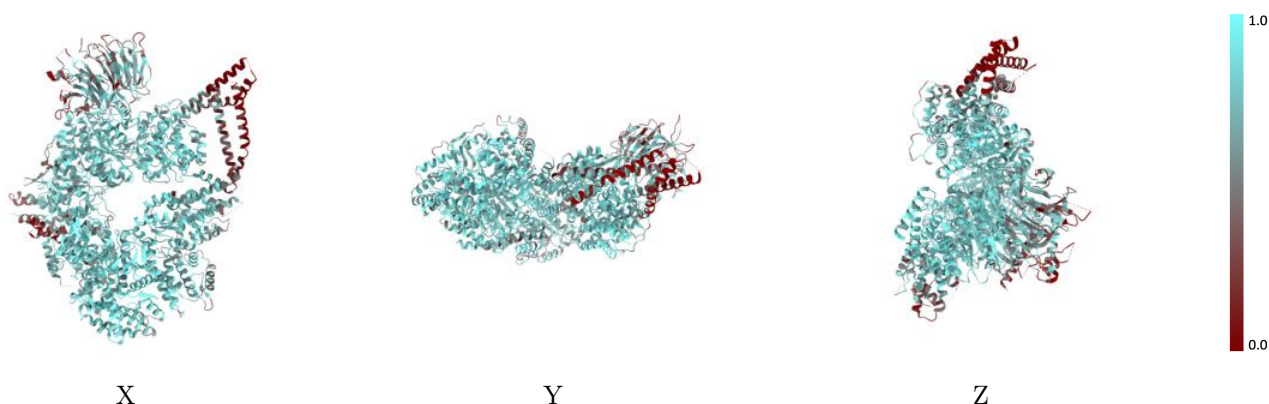
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



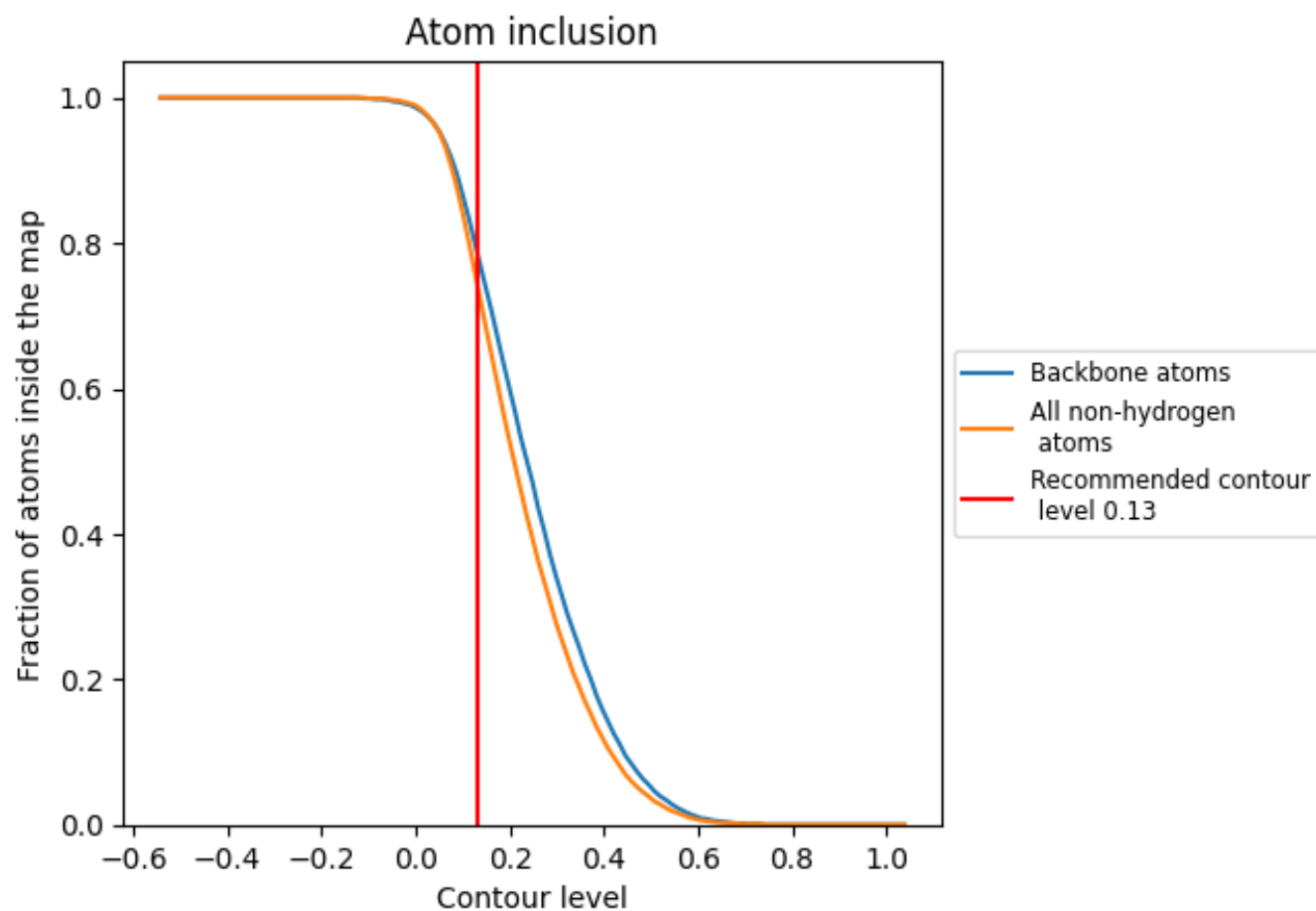
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7460	<div></div> 0.4230
A	<div></div> 0.7700	<div></div> 0.4350
C	<div></div> 0.5830	<div></div> 0.3420

