



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:45 AM UTC

PDB ID : 6NYB / pdb_00006nyb
EMDB ID : EMD-0541
Title : Structure of a MAPK pathway complex
Authors : Park, E.; Rawson, S.; Li, K.; Jeon, H.; Eck, M.J.
Deposited on : 2019-02-11
Resolution : 4.10 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

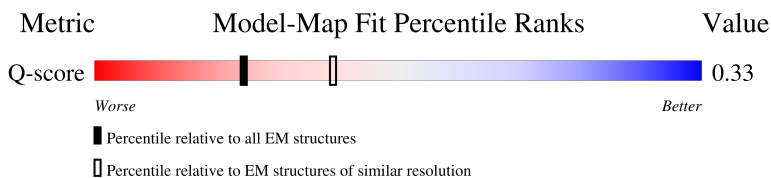
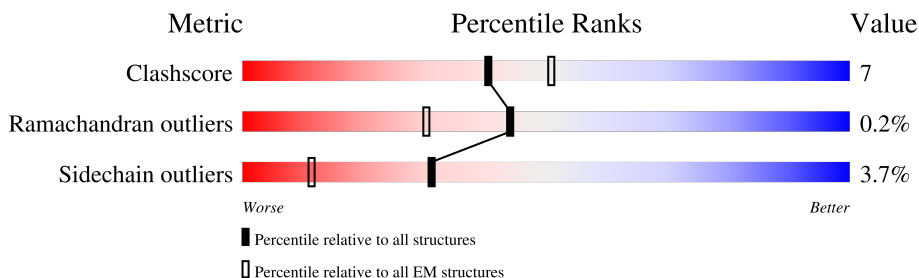
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	805	
2	B	415	
3	C	247	
3	D	247	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8842 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 Serine/threonine-protein kinase B-raf.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	350	Total	C	N	O	P	S	0	0
			2819	1794	502	501	2	20		

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	MET	-	expression tag	UNP P15056
A	-25	SER	-	expression tag	UNP P15056
A	-24	TYR	-	expression tag	UNP P15056
A	-23	TYR	-	expression tag	UNP P15056
A	-22	HIS	-	expression tag	UNP P15056
A	-21	HIS	-	expression tag	UNP P15056
A	-20	HIS	-	expression tag	UNP P15056
A	-19	HIS	-	expression tag	UNP P15056
A	-18	HIS	-	expression tag	UNP P15056
A	-17	HIS	-	expression tag	UNP P15056
A	-16	HIS	-	expression tag	UNP P15056
A	-15	HIS	-	expression tag	UNP P15056
A	-14	ASP	-	expression tag	UNP P15056
A	-13	ILE	-	expression tag	UNP P15056
A	-12	PRO	-	expression tag	UNP P15056
A	-11	THR	-	expression tag	UNP P15056
A	-10	THR	-	expression tag	UNP P15056
A	-9	GLU	-	expression tag	UNP P15056
A	-8	ASN	-	expression tag	UNP P15056
A	-7	LEU	-	expression tag	UNP P15056
A	-6	TYR	-	expression tag	UNP P15056
A	-5	PHE	-	expression tag	UNP P15056
A	-4	GLN	-	expression tag	UNP P15056
A	-3	GLY	-	expression tag	UNP P15056
A	-2	ALA	-	expression tag	UNP P15056
A	-1	MET	-	expression tag	UNP P15056
A	0	ASP	-	expression tag	UNP P15056

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Chain	Residue	Modelled	Actual	Comment	Reference
A	767	GLY	-	expression tag	UNP P15056
A	768	THR	-	expression tag	UNP P15056
A	769	SER	-	expression tag	UNP P15056
A	770	ALA	-	expression tag	UNP P15056
A	771	TRP	-	expression tag	UNP P15056
A	772	SER	-	expression tag	UNP P15056
A	773	HIS	-	expression tag	UNP P15056
A	774	PRO	-	expression tag	UNP P15056
A	775	GLN	-	expression tag	UNP P15056
A	776	PHE	-	expression tag	UNP P15056
A	777	GLU	-	expression tag	UNP P15056
A	778	LYS	-	expression tag	UNP P15056

- Molecule 2 is a protein called Dual specificity mitogen-activated protein kinase kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	289	Total	C	N	O	S	0	0
			2258	1443	386	414	15		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-21	MET	-	expression tag	UNP Q02750
B	-20	GLY	-	expression tag	UNP Q02750
B	-19	SER	-	expression tag	UNP Q02750
B	-18	SER	-	expression tag	UNP Q02750
B	-17	HIS	-	expression tag	UNP Q02750
B	-16	HIS	-	expression tag	UNP Q02750
B	-15	HIS	-	expression tag	UNP Q02750
B	-14	HIS	-	expression tag	UNP Q02750
B	-13	HIS	-	expression tag	UNP Q02750
B	-12	HIS	-	expression tag	UNP Q02750
B	-11	SER	-	expression tag	UNP Q02750
B	-10	ALA	-	expression tag	UNP Q02750
B	-9	VAL	-	expression tag	UNP Q02750
B	-8	ASP	-	expression tag	UNP Q02750
B	-7	GLU	-	expression tag	UNP Q02750
B	-6	ASN	-	expression tag	UNP Q02750
B	-5	LEU	-	expression tag	UNP Q02750
B	-4	TYR	-	expression tag	UNP Q02750
B	-3	PHE	-	expression tag	UNP Q02750
B	-2	GLN	-	expression tag	UNP Q02750

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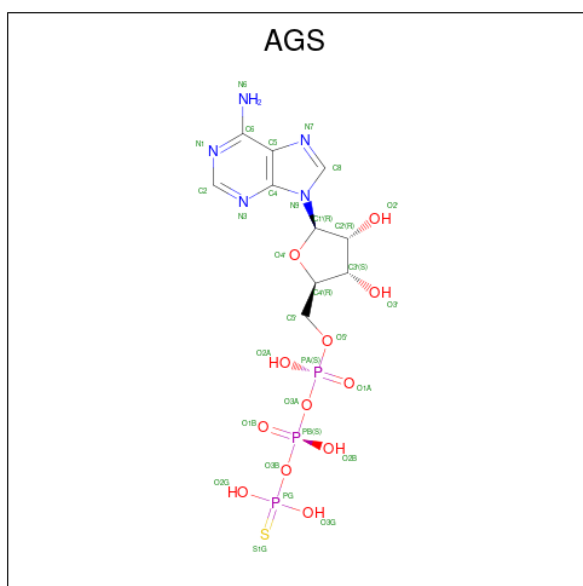
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP Q02750
B	0	GLY	-	expression tag	UNP Q02750
B	218	ALA	SER	engineered mutation	UNP Q02750
B	222	ALA	SER	engineered mutation	UNP Q02750

- Molecule 3 is a protein called 14-3-3 protein zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	229	Total	C	N	O	S	0	0
			1846	1158	314	366	8		
3	D	229	Total	C	N	O	S	0	0
			1833	1152	311	362	8		

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).

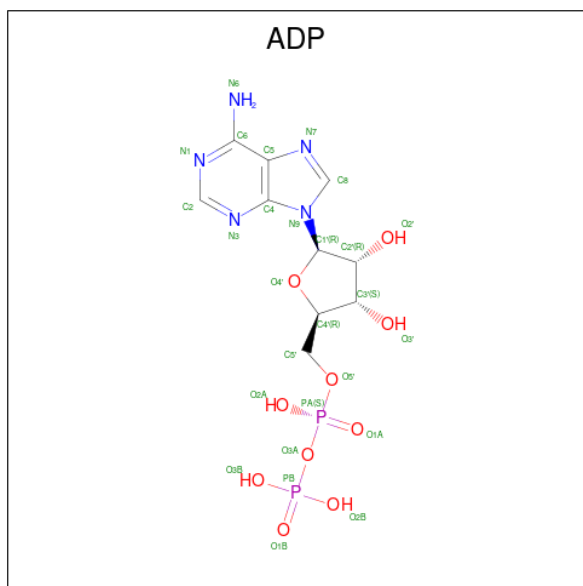


Mol	Chain	Residues	Atoms					AltConf	
4	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
5	A	2	Total	Zn	0
			2	2	

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

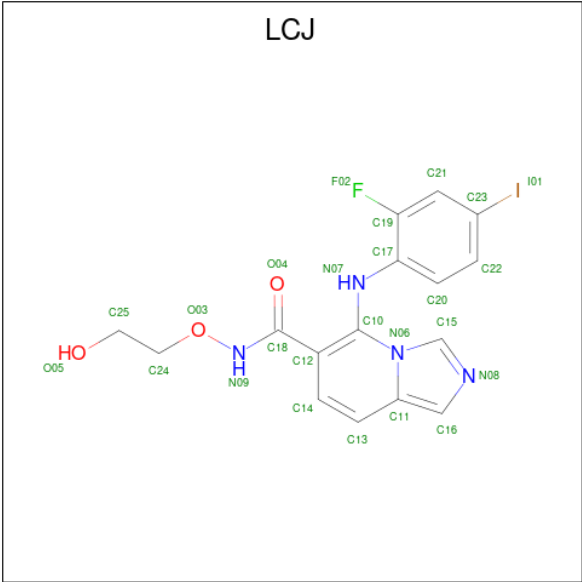


Mol	Chain	Residues	Atoms					AltConf
6	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
7	B	1	Total	Mg	0
			1	1	

- Molecule 8 is 5-[(2-fluoro-4-iodophenyl)amino]-N-(2-hydroxyethoxy)imidazo[1,5-a]pyridine-6-carboxamide (CCD ID: LCJ) (formula: $C_{16}H_{14}FIN_4O_3$).

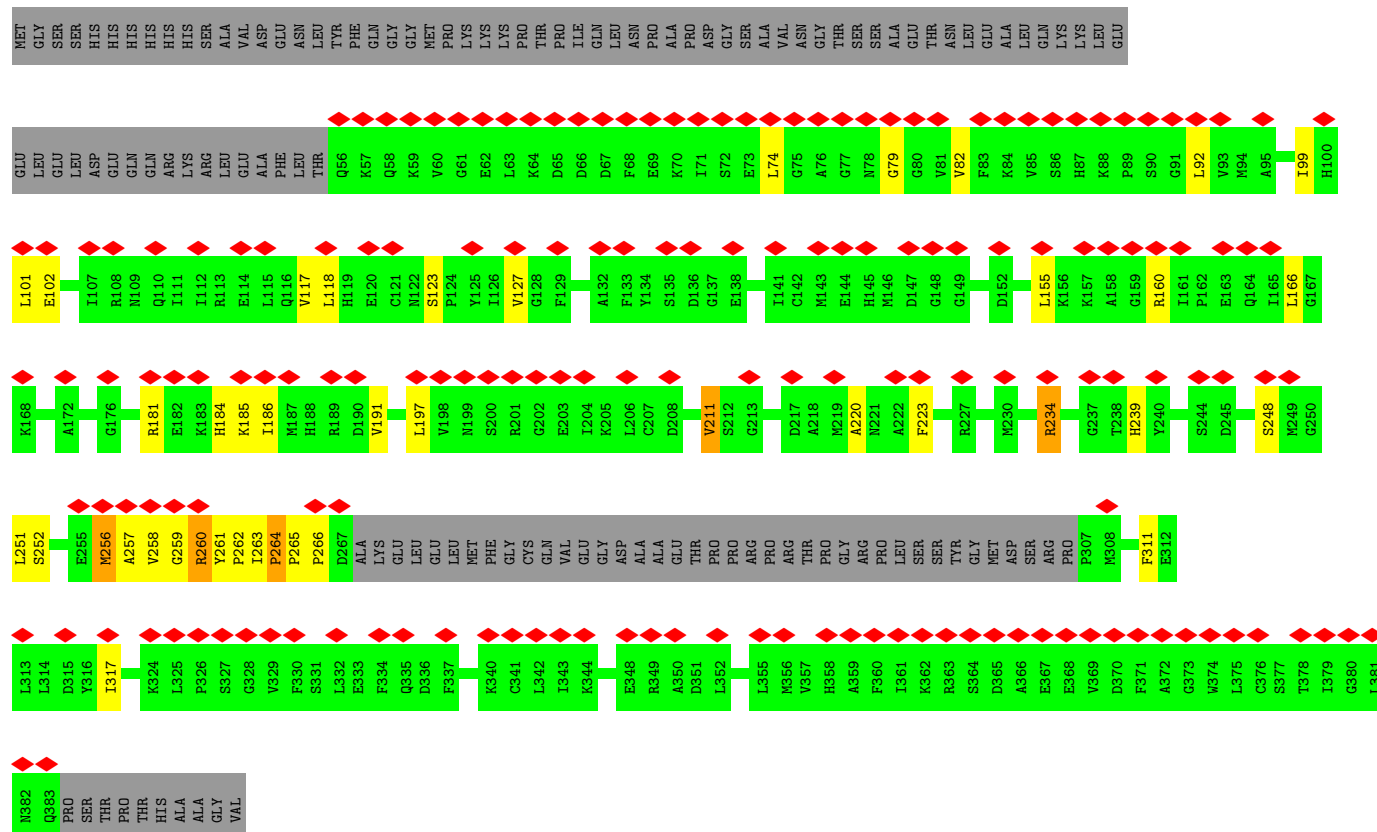


Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	I	N	O	
8	B	1	25	16	1	1	4	3	0

LYS

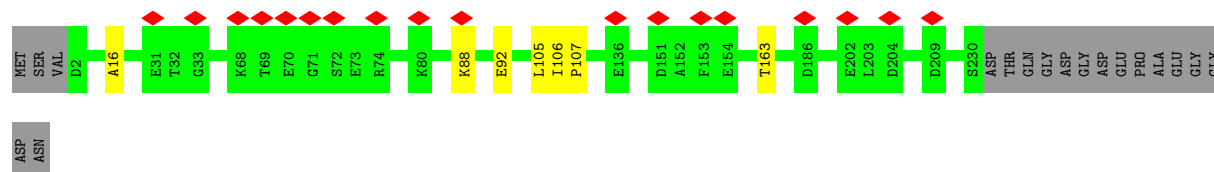
- Molecule 2: Dual specificity mitogen-activated protein kinase kinase 1

Chain B: 



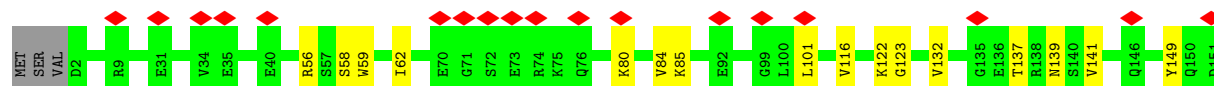
- Molecule 3: 14-3-3 protein zeta

Chain C: 



- Molecule 3: 14-3-3 protein zeta

Chain D: 





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	165298	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.157	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.048	Depositor
Map size ($\text{\AA}$)	211.99998, 211.99998, 211.99998	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	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: ADP, SEP, AGS, MG, ZN, LCJ

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	1.00	0/2862	1.38	2/3854 (0.1%)
2	B	1.03	0/2304	1.46	1/3105 (0.0%)
3	C	0.99	0/1873	1.59	0/2522
3	D	0.99	0/1860	1.54	3/2506 (0.1%)
All	All	1.00	0/8899	1.48	6/11987 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	214	SER	N-CA-C	-6.05	104.37	110.97
1	A	587	ASP	N-CA-C	5.72	120.20	113.23
3	D	139	ASN	N-CA-C	-5.61	105.07	111.07
1	A	602	SER	N-CA-C	5.25	117.05	110.91
2	B	266	PRO	N-CA-C	-5.11	106.42	113.53
3	D	214	SER	CB-CA-C	5.04	118.72	110.96

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	2819	0	2822	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2258	0	2289	27	0
3	C	1846	0	1839	4	0
3	D	1833	0	1822	11	0
4	A	31	0	12	1	0
5	A	2	0	0	2	0
6	B	27	0	12	2	0
7	B	1	0	0	0	0
8	B	25	0	0	0	0
All	All	8842	0	8796	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 7.

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)
1:A:522:LYS:HB3	1:A:523:PRO:HD3	1.38	1.05
1:A:483:LYS:O	1:A:526:ALA:HA	1.65	0.97
1:A:624:VAL:HA	1:A:632:PRO:HB2	1.50	0.92
1:A:280:CYS:HG	5:A:902:ZN:ZN	0.70	0.88
3:D:213:ASP:O	3:D:217:ILE:HG12	1.79	0.83
1:A:721:LEU:HB3	1:A:722:PRO:HD3	1.65	0.78
1:A:721:LEU:C	1:A:721:LEU:HD12	2.15	0.71
1:A:494:GLN:HA	1:A:604:TRP:CZ3	2.26	0.70
1:A:499:LYS:HG2	1:A:519:TYR:OH	1.94	0.68
1:A:723:LYS:O	1:A:726:ARG:HG2	1.94	0.68
1:A:272:CYS:SG	5:A:901:ZN:ZN	1.83	0.67
3:D:58:SER:O	3:D:62:ILE:HG12	1.94	0.67
1:A:729:SEP:O3P	3:D:56:ARG:NH2	2.25	0.66
1:A:539:HIS:O	1:A:543:ILE:HB	1.96	0.66
1:A:485:LEU:HD13	1:A:600:VAL:HG11	1.77	0.66
1:A:516:PHE:CZ	1:A:527:ILE:HD12	2.32	0.65
1:A:522:LYS:HB3	1:A:523:PRO:CD	2.22	0.64
1:A:468:PHE:O	1:A:486:ASN:N	2.26	0.63
1:A:553:LEU:HD11	1:A:649:LEU:O	2.00	0.61
1:A:721:LEU:HD12	1:A:721:LEU:O	2.01	0.61
1:A:485:LEU:HD13	1:A:600:VAL:CG1	2.33	0.59
2:B:258:VAL:HG23	2:B:260:ARG:H	1.68	0.59
1:A:242:PHE:CZ	1:A:267:LYS:HD2	2.38	0.58
1:A:241:THR:HG23	1:A:241:THR:O	2.03	0.58
1:A:248:CYS:HB3	1:A:251:CYS:SG	2.44	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:TRP:CE2	1:A:609:GLN:HB3	2.38	0.57
1:A:242:PHE:HZ	1:A:267:LYS:HB3	1.69	0.56
1:A:506:ARG:NE	1:A:516:PHE:O	2.38	0.56
1:A:511:VAL:O	1:A:591:LYS:NZ	2.38	0.56
2:B:251:LEU:HD11	2:B:262:PRO:HB2	1.86	0.56
2:B:251:LEU:CD1	2:B:262:PRO:HB2	2.36	0.56
1:A:485:LEU:HD12	1:A:525:LEU:HD23	1.88	0.56
1:A:604:TRP:NE1	1:A:609:GLN:HB3	2.20	0.56
1:A:245:LEU:HD23	1:A:245:LEU:H	1.70	0.56
3:D:101:LEU:CD2	3:D:122:LYS:HB2	2.36	0.56
2:B:79:GLY:HA2	2:B:223:PHE:CE1	2.41	0.56
2:B:127:VAL:HG21	2:B:197:LEU:HD12	1.89	0.55
1:A:246:ALA:HB1	1:A:267:LYS:HE2	1.88	0.55
1:A:465:SER:HA	1:A:470:THR:HA	1.88	0.55
1:A:574:HIS:NE2	1:A:592:ILE:CG2	2.70	0.54
1:A:724:ILE:O	1:A:724:ILE:HG23	2.05	0.54
1:A:251:CYS:SG	1:A:269:HIS:CD2	3.00	0.54
1:A:516:PHE:HZ	1:A:527:ILE:HD12	1.71	0.54
2:B:261:TYR:CD1	2:B:262:PRO:HD2	2.42	0.54
1:A:473:LYS:HD2	1:A:531:TRP:CZ2	2.43	0.53
1:A:631:ASN:N	1:A:631:ASN:OD1	2.41	0.53
1:A:721:LEU:CB	1:A:722:PRO:HD3	2.37	0.53
1:A:627:MET:SD	1:A:632:PRO:HG3	2.49	0.52
1:A:604:TRP:CG	1:A:608:HIS:O	2.62	0.52
1:A:463:ILE:HG21	4:A:801:AGS:H1'	1.92	0.52
1:A:602:SER:CB	1:A:611:GLU:HA	2.40	0.52
2:B:191:VAL:O	2:B:248:SER:HB3	2.10	0.52
2:B:234:ARG:O	2:B:234:ARG:NE	2.42	0.52
2:B:251:LEU:O	2:B:262:PRO:HG2	2.10	0.51
1:A:249:ASP:OD2	1:A:691:ARG:NH1	2.42	0.51
3:D:80:LYS:O	3:D:84:VAL:HG23	2.10	0.51
1:A:554:ILE:CD1	1:A:721:LEU:HD22	2.42	0.50
1:A:261:CYS:SG	1:A:263:THR:HB	2.51	0.50
2:B:263:ILE:HD12	2:B:317:ILE:CG1	2.42	0.50
2:B:252:SER:O	2:B:256:MET:HG3	2.12	0.49
1:A:662:ARG:HB3	2:B:220:ALA:O	2.13	0.49
2:B:74:LEU:HD12	2:B:82:VAL:HG12	1.94	0.49
3:D:101:LEU:HD23	3:D:122:LYS:HB2	1.93	0.49
1:A:279:MET:HE3	1:A:279:MET:HA	1.95	0.49
1:A:485:LEU:HB2	1:A:525:LEU:HB3	1.95	0.49
1:A:485:LEU:CD1	1:A:600:VAL:HG11	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:MET:HE2	1:A:577:LEU:HD22	1.94	0.48
1:A:574:HIS:NE2	1:A:592:ILE:HG22	2.28	0.48
2:B:82:VAL:HG21	6:B:601:ADP:C8	2.48	0.48
1:A:235:HIS:CD2	1:A:261:CYS:SG	3.06	0.48
3:D:137:THR:O	3:D:141:VAL:HG23	2.13	0.48
3:D:59:TRP:CE2	3:D:132:VAL:HG12	2.47	0.48
1:A:654:LEU:HD12	1:A:654:LEU:N	2.29	0.47
1:A:539:HIS:HA	1:A:543:ILE:CG1	2.45	0.47
2:B:160:ARG:HG2	2:B:259:GLY:HA3	1.96	0.47
1:A:602:SER:HB3	1:A:611:GLU:HA	1.98	0.46
3:D:123:GLY:HA3	3:D:149:TYR:CE1	2.50	0.46
1:A:630:LYS:HE2	1:A:630:LYS:HB2	1.80	0.46
2:B:251:LEU:HD21	2:B:263:ILE:HD11	1.97	0.46
3:C:88:LYS:O	3:C:92:GLU:HG3	2.16	0.46
1:A:624:VAL:HA	1:A:632:PRO:CB	2.34	0.46
1:A:514:LEU:HD12	1:A:593:GLY:HA3	1.98	0.45
2:B:155:LEU:CD1	2:B:256:MET:HA	2.46	0.45
2:B:118:LEU:HD21	2:B:211:VAL:HG21	1.97	0.45
2:B:166:LEU:CD1	2:B:257:ALA:HB2	2.46	0.45
1:A:576:ASP:O	1:A:578:LYS:HG2	2.16	0.45
1:A:626:ARG:HG2	2:B:311:PHE:CE2	2.52	0.45
3:C:106:ILE:N	3:C:107:PRO:HD2	2.32	0.44
2:B:263:ILE:HD12	2:B:317:ILE:HG12	1.98	0.44
3:D:116:VAL:HG13	3:D:152:ALA:HB1	2.00	0.44
1:A:539:HIS:HA	1:A:543:ILE:HG12	2.00	0.44
2:B:74:LEU:HD13	6:B:601:ADP:C2	2.53	0.44
1:A:485:LEU:HD12	1:A:525:LEU:CD2	2.48	0.44
1:A:604:TRP:NE1	1:A:609:GLN:CB	2.80	0.44
1:A:485:LEU:CD1	1:A:525:LEU:HD23	2.47	0.43
1:A:626:ARG:C	1:A:628:GLN:H	2.26	0.43
3:C:16:ALA:HB2	3:D:62:ILE:HD11	2.00	0.43
1:A:514:LEU:HD21	1:A:532:CYS:SG	2.58	0.43
1:A:520:SER:O	1:A:524:GLN:O	2.37	0.43
1:A:242:PHE:CZ	1:A:267:LYS:CB	3.02	0.43
1:A:491:THR:C	1:A:493:GLN:H	2.27	0.43
1:A:574:HIS:CD2	1:A:595:PHE:HB3	2.54	0.43
2:B:181:ARG:O	2:B:185:LYS:HA	2.19	0.43
1:A:266:TYR:CD2	1:A:266:TYR:O	2.72	0.43
2:B:181:ARG:HD2	2:B:185:LYS:HA	2.00	0.42
2:B:99:ILE:HG22	2:B:101:LEU:HG	2.01	0.42
2:B:102:GLU:HG3	2:B:102:GLU:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:PHE:CE2	1:A:255:LEU:HD23	2.54	0.42
1:A:458:THR:HB	1:A:475:LYS:HB2	2.01	0.42
1:A:498:PHE:CE1	1:A:527:ILE:HD11	2.55	0.42
1:A:266:TYR:OH	1:A:276:VAL:HG21	2.20	0.42
2:B:263:ILE:HB	2:B:264:PRO:HD3	2.02	0.41
1:A:491:THR:C	1:A:493:GLN:N	2.77	0.41
3:C:105:LEU:HD23	3:C:105:LEU:HA	1.94	0.41
1:A:264:CYS:O	1:A:688:ALA:HB2	2.20	0.41
1:A:251:CYS:SG	1:A:269:HIS:NE2	2.94	0.41
1:A:485:LEU:HD12	1:A:525:LEU:CG	2.50	0.41
1:A:574:HIS:NE2	1:A:595:PHE:HB3	2.35	0.41
1:A:488:THR:HG23	1:A:524:GLN:CD	2.46	0.41
1:A:482:VAL:HG12	1:A:526:ALA:HB1	2.02	0.40
1:A:498:PHE:HE1	1:A:527:ILE:HD11	1.86	0.40
1:A:723:LYS:HE3	1:A:723:LYS:HB2	1.87	0.40
1:A:242:PHE:HZ	1:A:267:LYS:CB	2.32	0.40
1:A:515:LEU:HD23	1:A:515:LEU: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	342/805 (42%)	306 (90%)	36 (10%)	0	100	100
2	B	285/415 (69%)	276 (97%)	7 (2%)	2 (1%)	18	55
3	C	227/247 (92%)	220 (97%)	7 (3%)	0	100	100
3	D	227/247 (92%)	219 (96%)	8 (4%)	0	100	100
All	All	1081/1714 (63%)	1021 (94%)	58 (5%)	2 (0%)	44	76

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	265	PRO
2	B	264	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	308/691 (45%)	288 (94%)	20 (6%)	15	40
2	B	249/354 (70%)	239 (96%)	10 (4%)	28	50
3	C	201/214 (94%)	200 (100%)	1 (0%)	81	82
3	D	198/214 (92%)	194 (98%)	4 (2%)	48	66
All	All	956/1473 (65%)	921 (96%)	35 (4%)	31	52

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	LYS
1	A	267	LYS
1	A	484	MET
1	A	506	ARG
1	A	521	THR
1	A	522	LYS
1	A	525	LEU
1	A	535	SER
1	A	548	PHE
1	A	562	GLN
1	A	605	SER
1	A	629	ASP
1	A	630	LYS
1	A	631	ASN
1	A	650	MET
1	A	656	TYR
1	A	719	ARG
1	A	721	LEU
1	A	723	LYS
1	A	724	ILE

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Mol	Chain	Res	Type
2	B	92	LEU
2	B	117	VAL
2	B	123	SER
2	B	184	HIS
2	B	186	ILE
2	B	211	VAL
2	B	234	ARG
2	B	239	HIS
2	B	256	MET
2	B	260	ARG
3	C	163	THR
3	D	85	LYS
3	D	203	LEU
3	D	210	SER
3	D	216	LEU

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

Mol	Chain	Res	Type
1	A	235	HIS
1	A	493	GLN
1	A	496	GLN
1	A	530	GLN
1	A	542	HIS
2	B	164	GLN
2	B	188	HIS
3	D	50	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	729	1	8,9,10	0.66	0	7,12,14	0.97	0
1	SEP	A	365	1	8,9,10	0.67	0	7,12,14	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	729	1	-	5/6/8/10	-
1	SEP	A	365	1	-	0/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	729	SEP	N-CA-CB-OG
1	A	729	SEP	C-CA-CB-OG
1	A	729	SEP	CB-OG-P-O1P
1	A	729	SEP	CB-OG-P-O2P
1	A	729	SEP	CB-OG-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	729	SEP	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	ADP	B	601	7	28,29,29	0.48	0	43,45,45	0.54	0
4	AGS	A	801	-	32,33,33	2.05	7 (21%)	45,52,52	1.83	12 (26%)
8	LCJ	B	901	-	26,27,27	2.47	7 (26%)	26,37,37	1.52	6 (23%)

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	ADP	B	601	7	-	4/16/32/32	0/3/3/3
4	AGS	A	801	-	-	5/21/38/38	0/3/3/3
8	LCJ	B	901	-	-	5/13/13/13	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	801	AGS	PG-S1G	7.94	2.07	1.90
8	B	901	LCJ	C18-N09	7.86	1.46	1.34
8	B	901	LCJ	C11-N06	-7.01	1.31	1.40
4	A	801	AGS	C5-C4	4.66	1.47	1.39
8	B	901	LCJ	C10-N07	4.02	1.46	1.37
4	A	801	AGS	C5-C6	2.75	1.48	1.41
8	B	901	LCJ	C17-N07	2.53	1.46	1.41
8	B	901	LCJ	O04-C18	-2.41	1.19	1.23
4	A	801	AGS	C8-N7	2.38	1.36	1.31
8	B	901	LCJ	C12-C10	-2.32	1.40	1.43
4	A	801	AGS	C5-N7	-2.29	1.34	1.39
8	B	901	LCJ	C16-N08	-2.20	1.33	1.37
4	A	801	AGS	C4-N9	-2.18	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	801	AGS	PG-O2G	2.07	1.61	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	801	AGS	C5-C4-N3	-5.28	119.45	126.72
4	A	801	AGS	N3-C4-N9	4.04	134.04	127.17
4	A	801	AGS	C2-N3-C4	3.66	120.78	111.83
4	A	801	AGS	C4-C5-N7	-3.64	106.42	110.58
4	A	801	AGS	N3-C2-N1	-3.55	123.21	128.58
8	B	901	LCJ	C16-C11-N06	3.32	107.89	104.58
4	A	801	AGS	PB-O3B-PG	-3.09	121.85	133.17
4	A	801	AGS	C4-N9-C8	2.79	108.67	105.74
8	B	901	LCJ	C21-C19-C17	-2.72	120.65	123.43
8	B	901	LCJ	O04-C18-N09	-2.62	118.98	122.92
8	B	901	LCJ	C12-C18-N09	2.61	121.33	115.42
4	A	801	AGS	C5-N7-C8	2.56	107.48	103.45
8	B	901	LCJ	C15-N06-C11	2.45	108.38	106.56
4	A	801	AGS	C6-C5-N7	2.35	136.62	132.09
8	B	901	LCJ	C13-C11-C16	-2.33	132.29	137.90
4	A	801	AGS	C3'-C2'-C1'	2.32	105.86	101.46
4	A	801	AGS	N9-C8-N7	-2.12	110.93	113.94
4	A	801	AGS	C2-N1-C6	2.12	122.21	118.73

There are no chirality outliers.

All (14) torsion outliers are listed below:

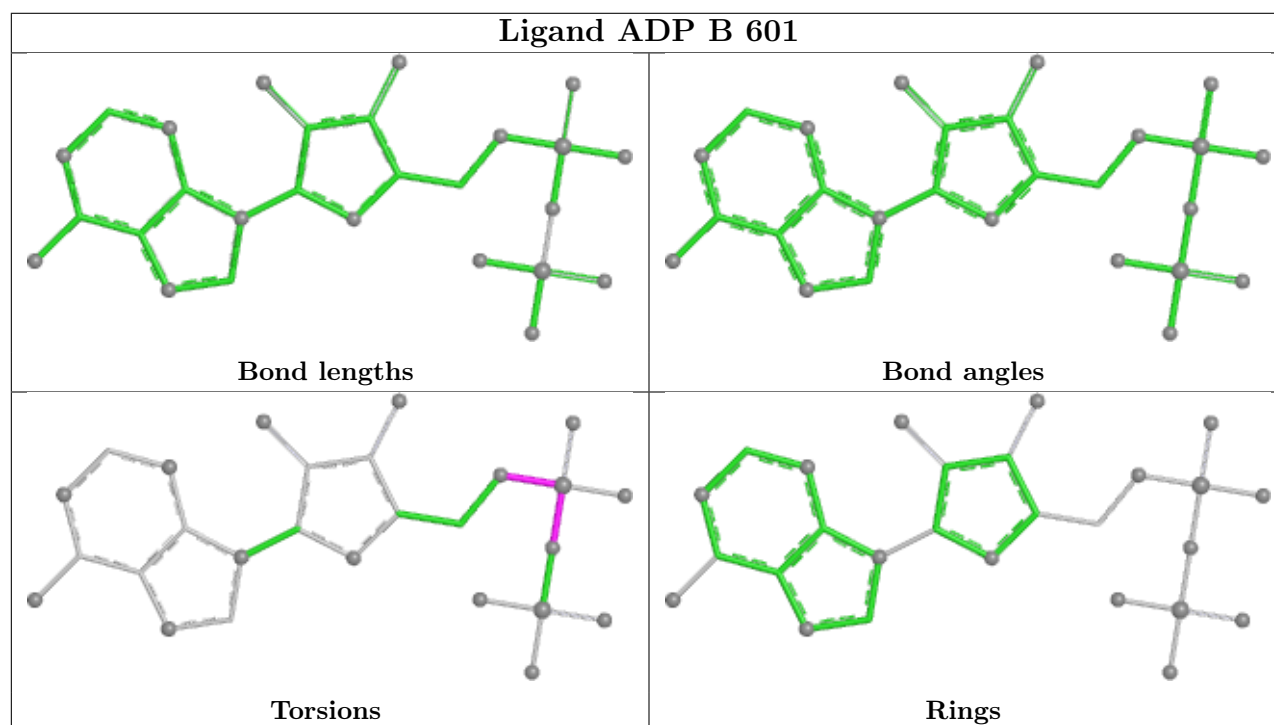
Mol	Chain	Res	Type	Atoms
4	A	801	AGS	C5'-O5'-PA-O2A
4	A	801	AGS	C5'-O5'-PA-O3A
4	A	801	AGS	O4'-C4'-C5'-O5'
6	B	601	ADP	C5'-O5'-PA-O2A
8	B	901	LCJ	C10-C12-C18-N09
4	A	801	AGS	C3'-C4'-C5'-O5'
8	B	901	LCJ	C10-C12-C18-O04
8	B	901	LCJ	C14-C12-C18-N09
8	B	901	LCJ	C14-C12-C18-O04
6	B	601	ADP	PB-O3A-PA-O5'
8	B	901	LCJ	O03-C24-C25-O05
4	A	801	AGS	C5'-O5'-PA-O1A
6	B	601	ADP	C5'-O5'-PA-O1A
6	B	601	ADP	C5'-O5'-PA-O3A

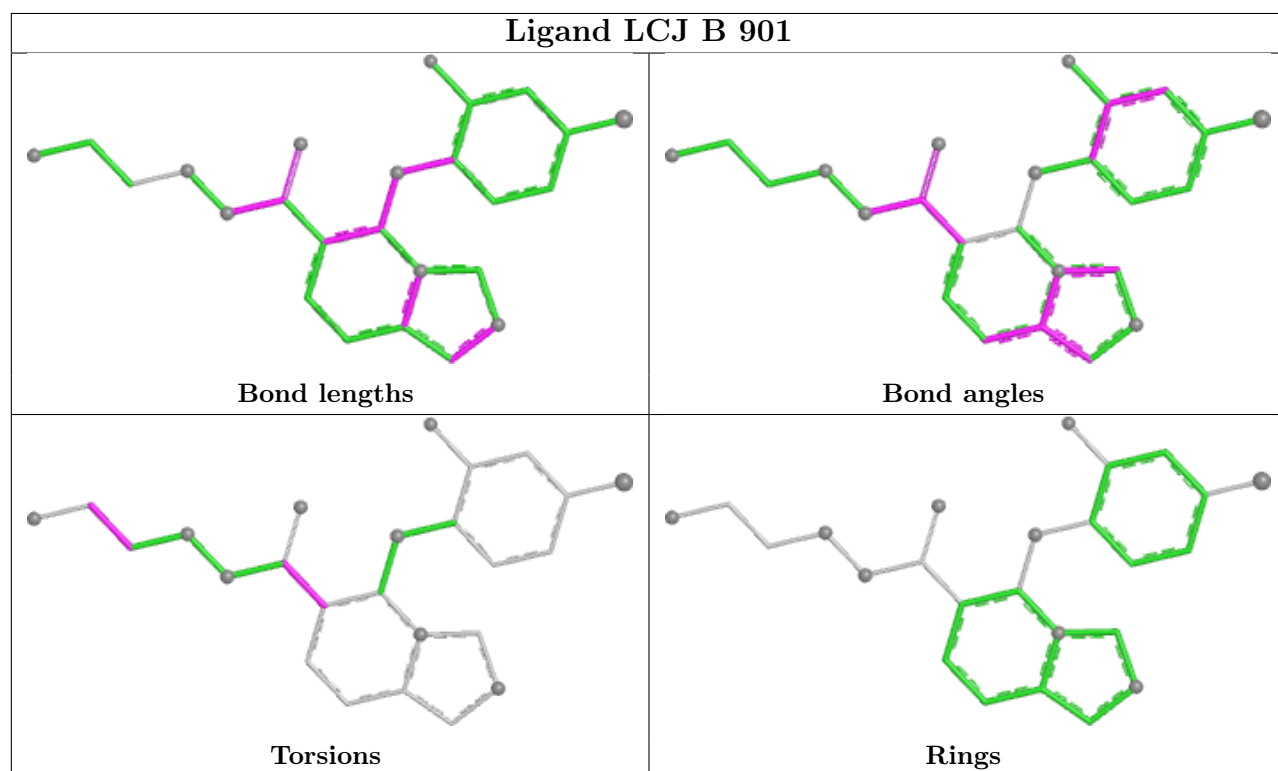
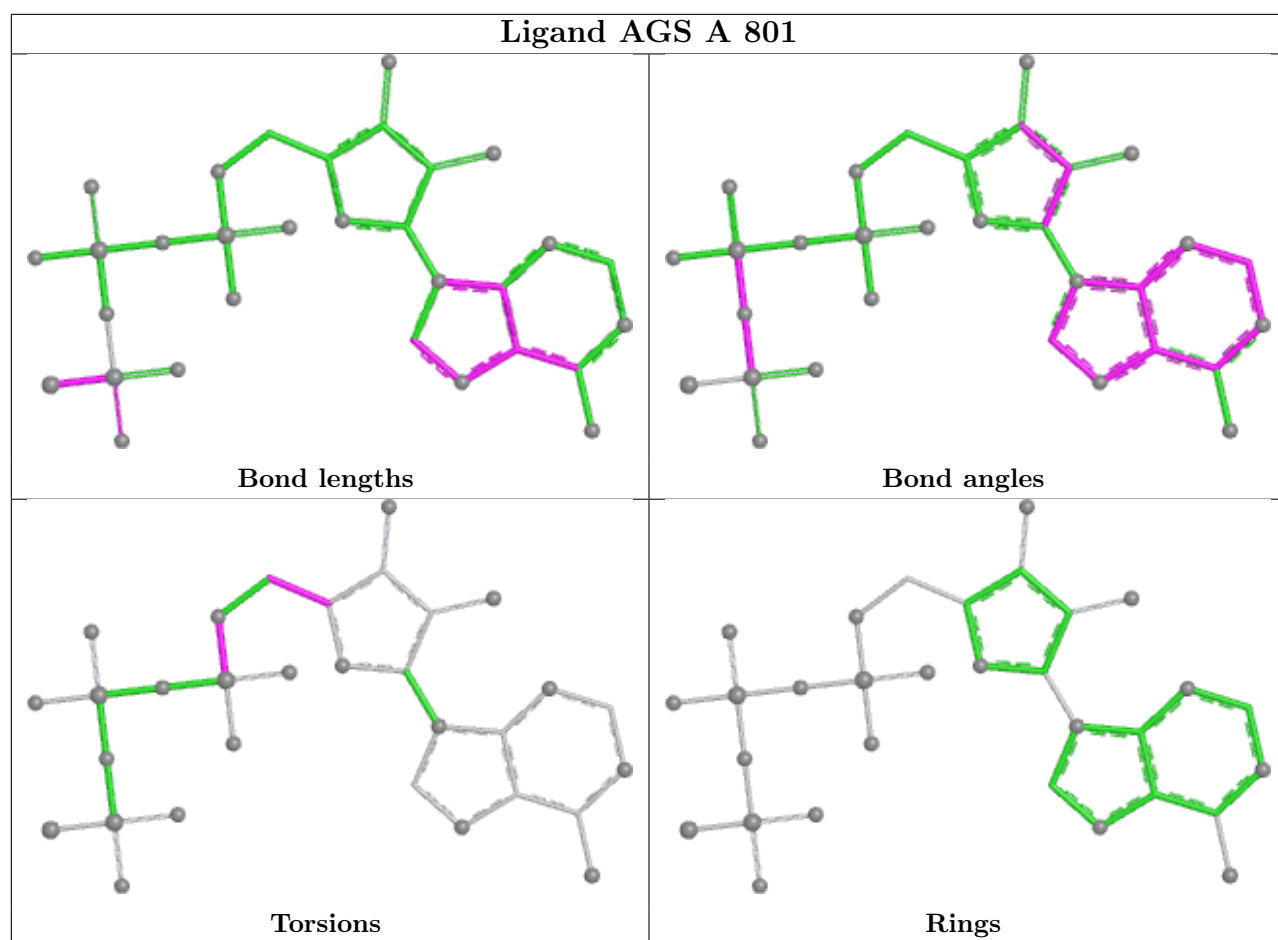
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	601	ADP	2	0
4	A	801	AGS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

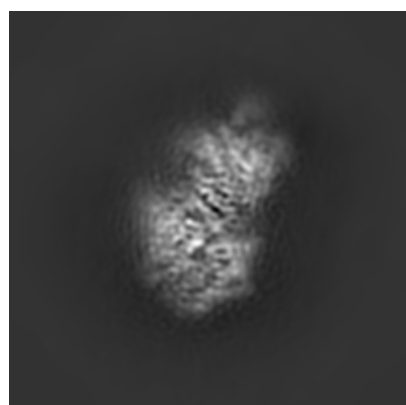
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0541. These allow visual inspection of the internal detail of the map and identification of artifacts.

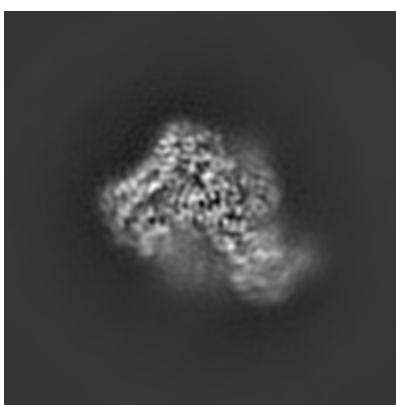
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

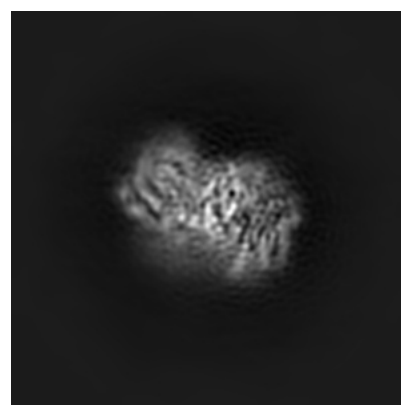
6.1.1 Primary map



X



Y

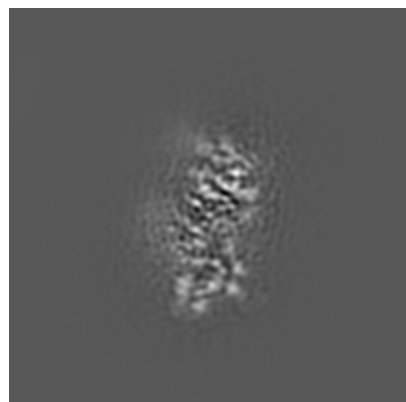


Z

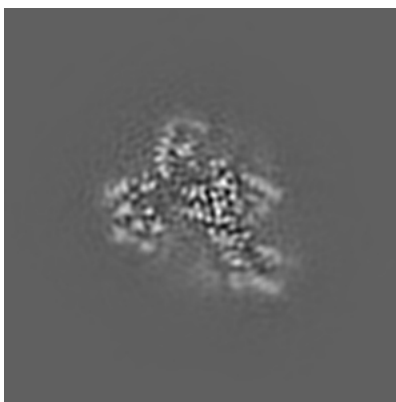
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 100



Y Index: 100

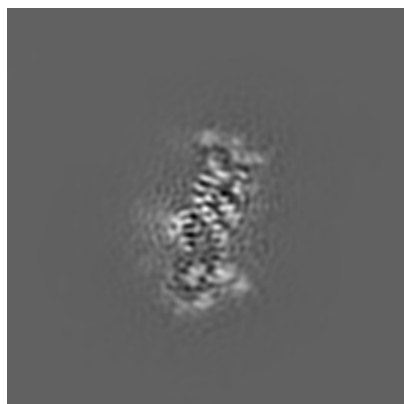


Z Index: 100

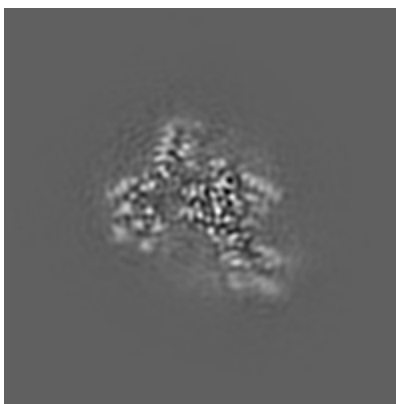
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

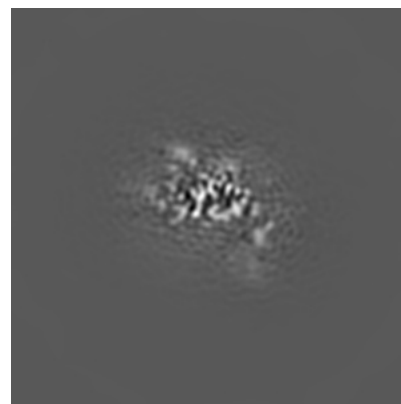
6.3.1 Primary map



X Index: 106



Y Index: 101

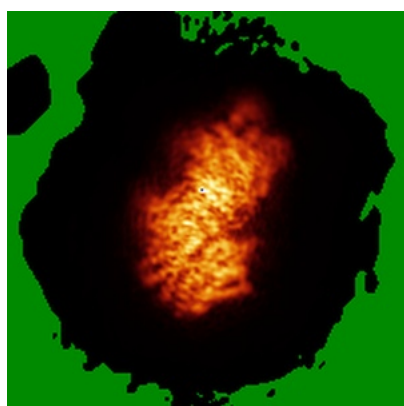


Z Index: 110

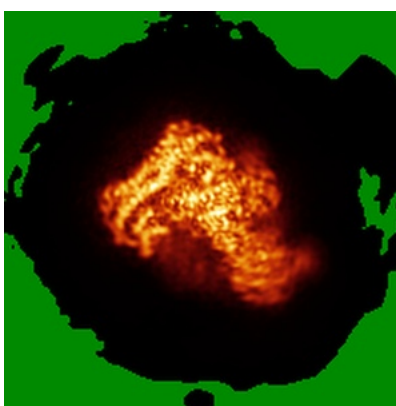
The images above show the largest variance slices of the map in three orthogonal directions.

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

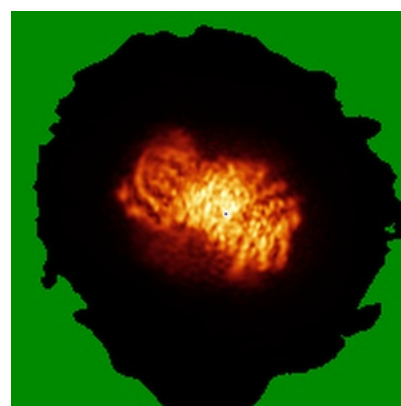
6.4.1 Primary map



X



Y

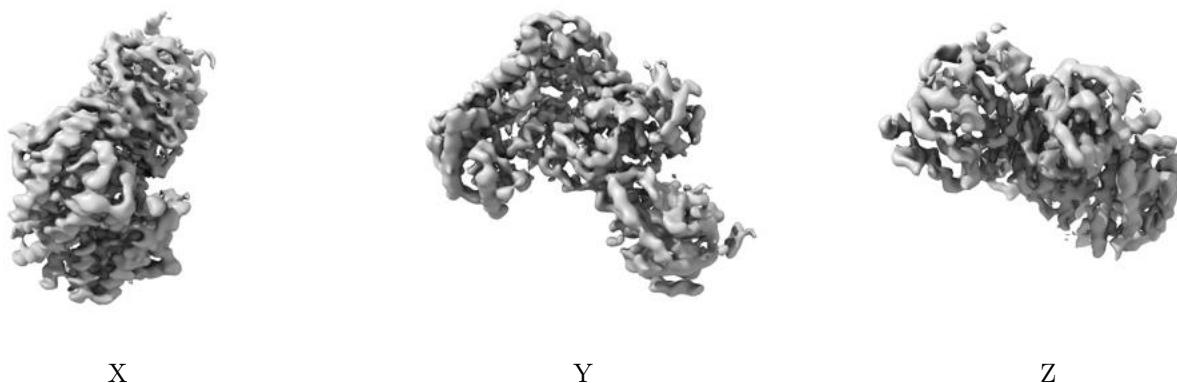


Z

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 0.048. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

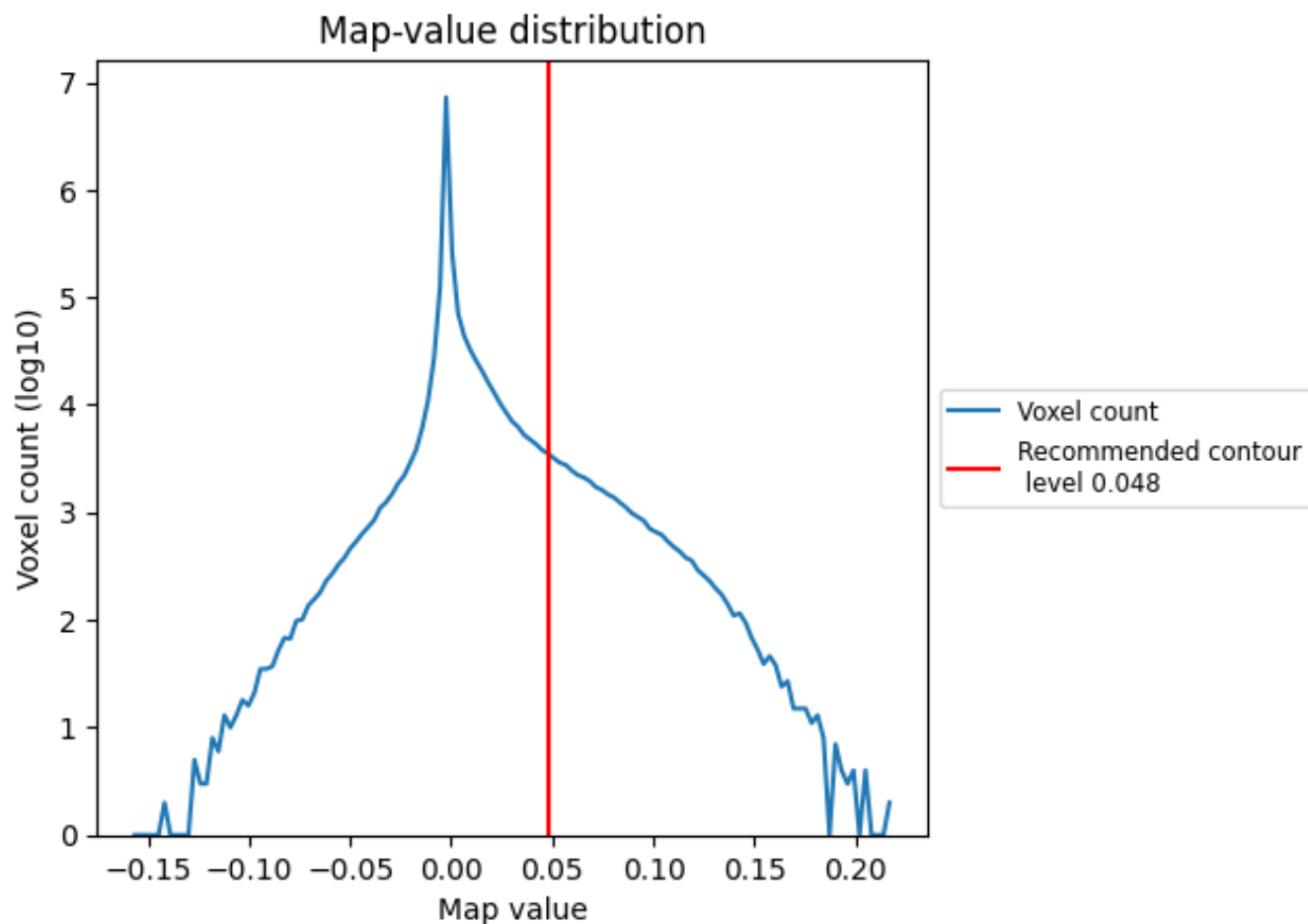
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

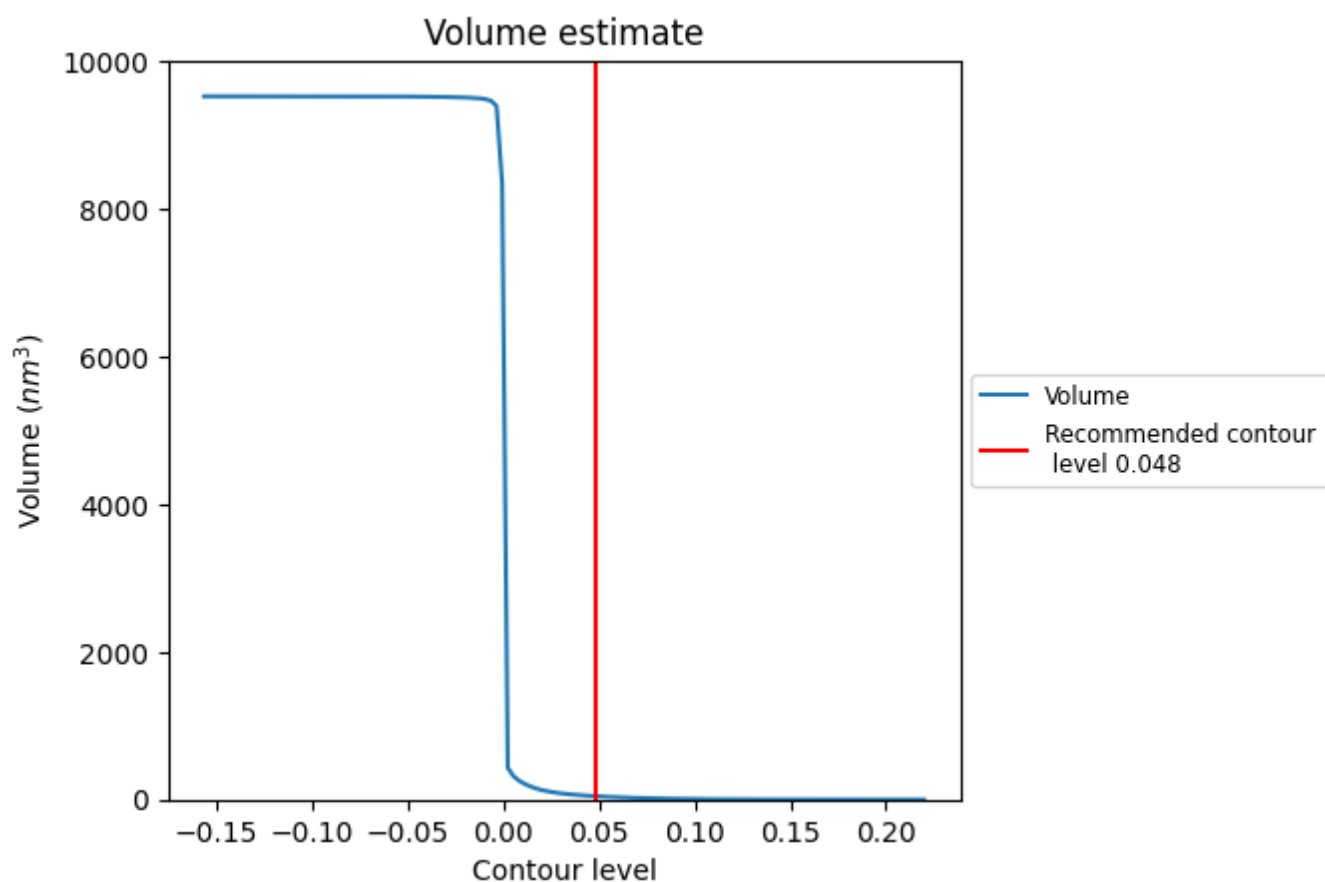
This section contains the results of statistical analysis of the map.

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.

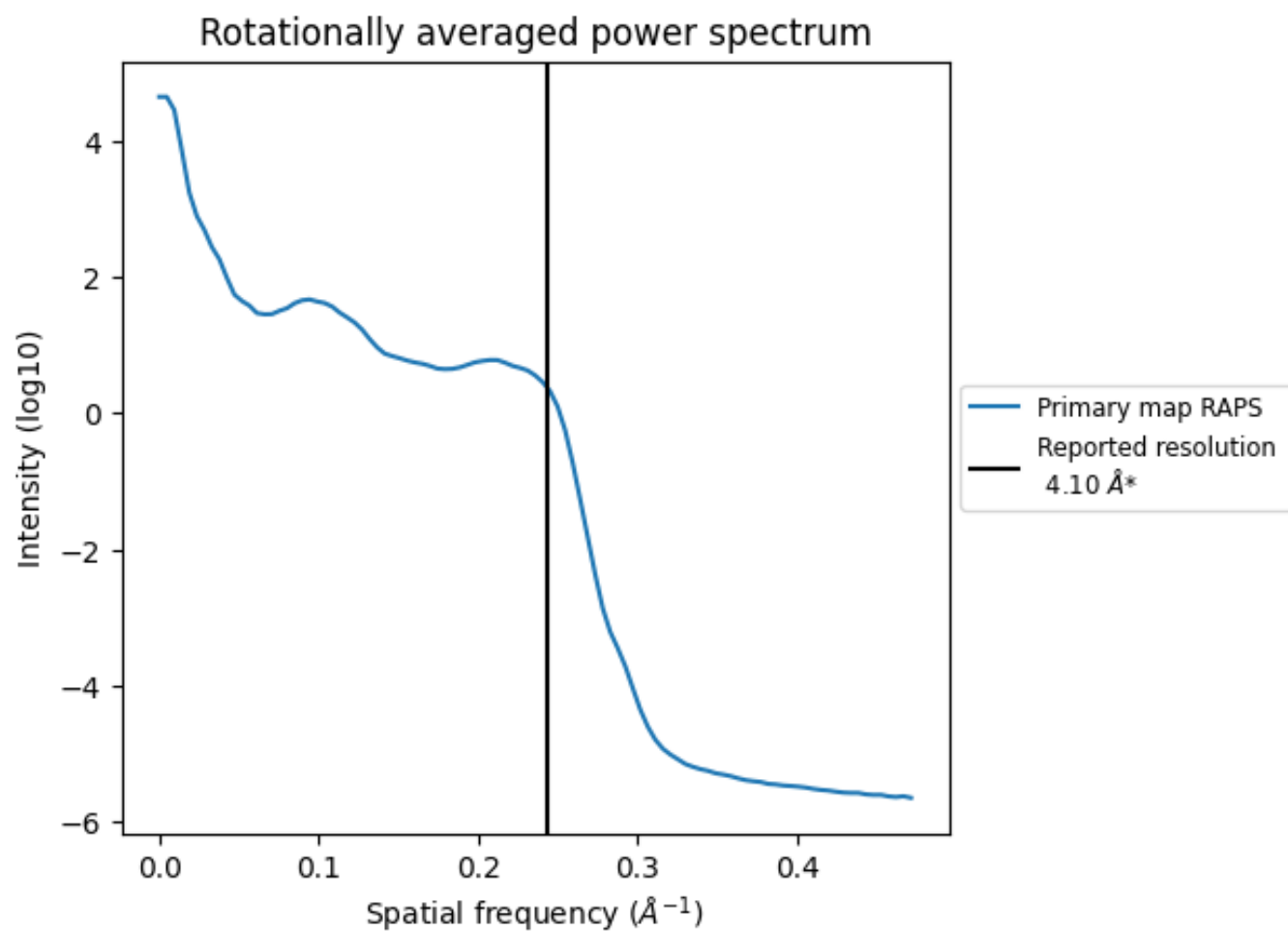
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 46 nm³; this corresponds to an approximate mass of 41 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 ⓘ

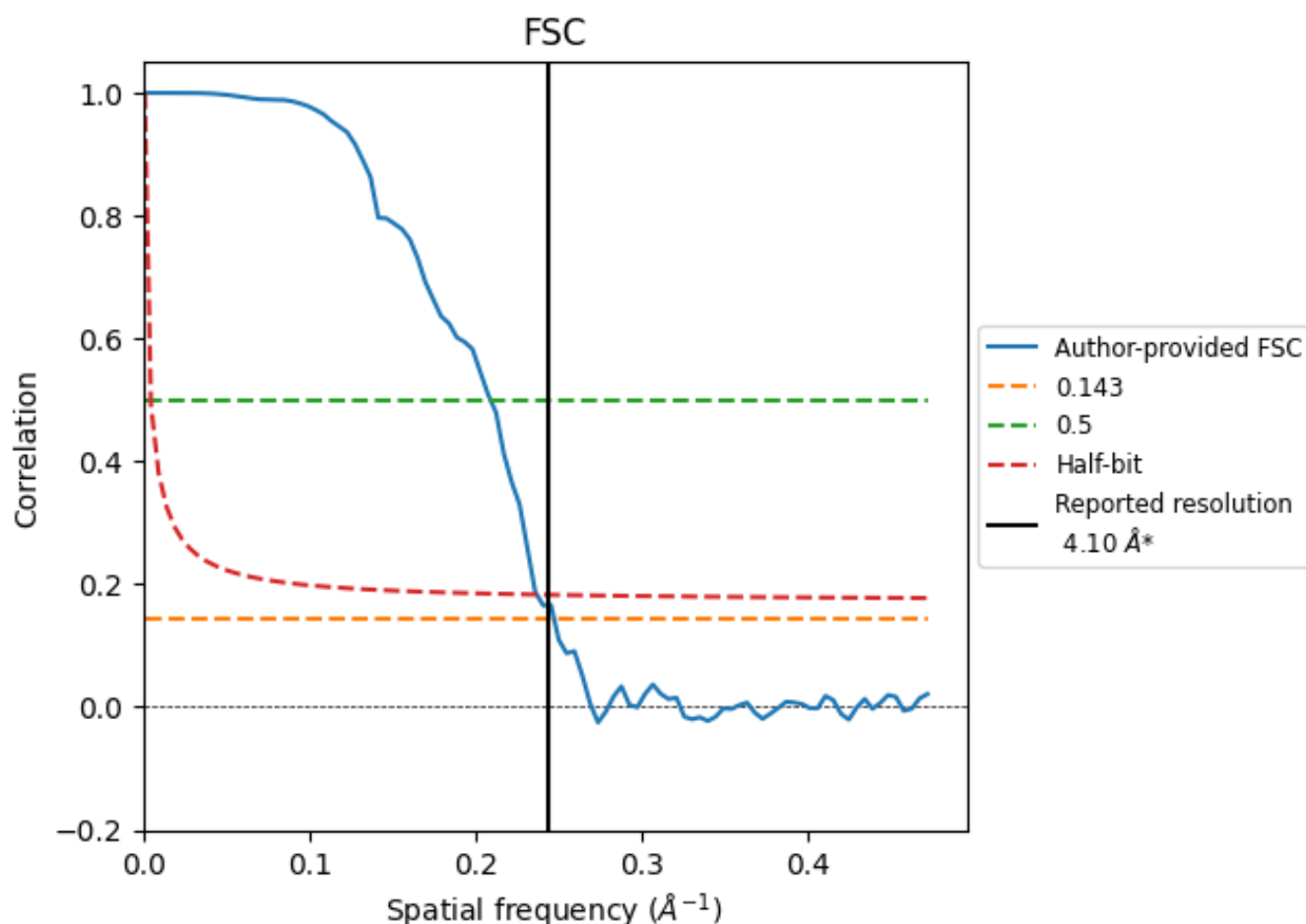


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.05	4.79	4.22
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

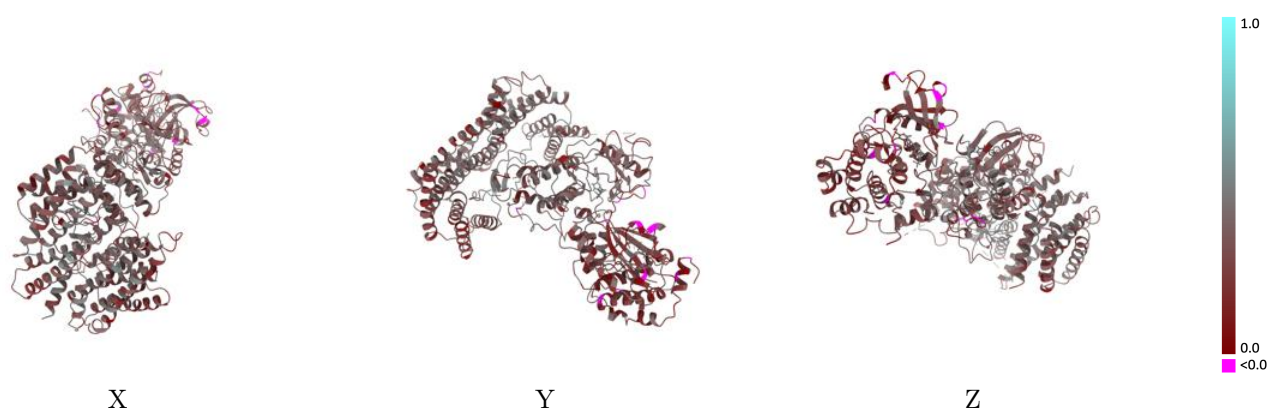
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0541 and PDB model 6NYB. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

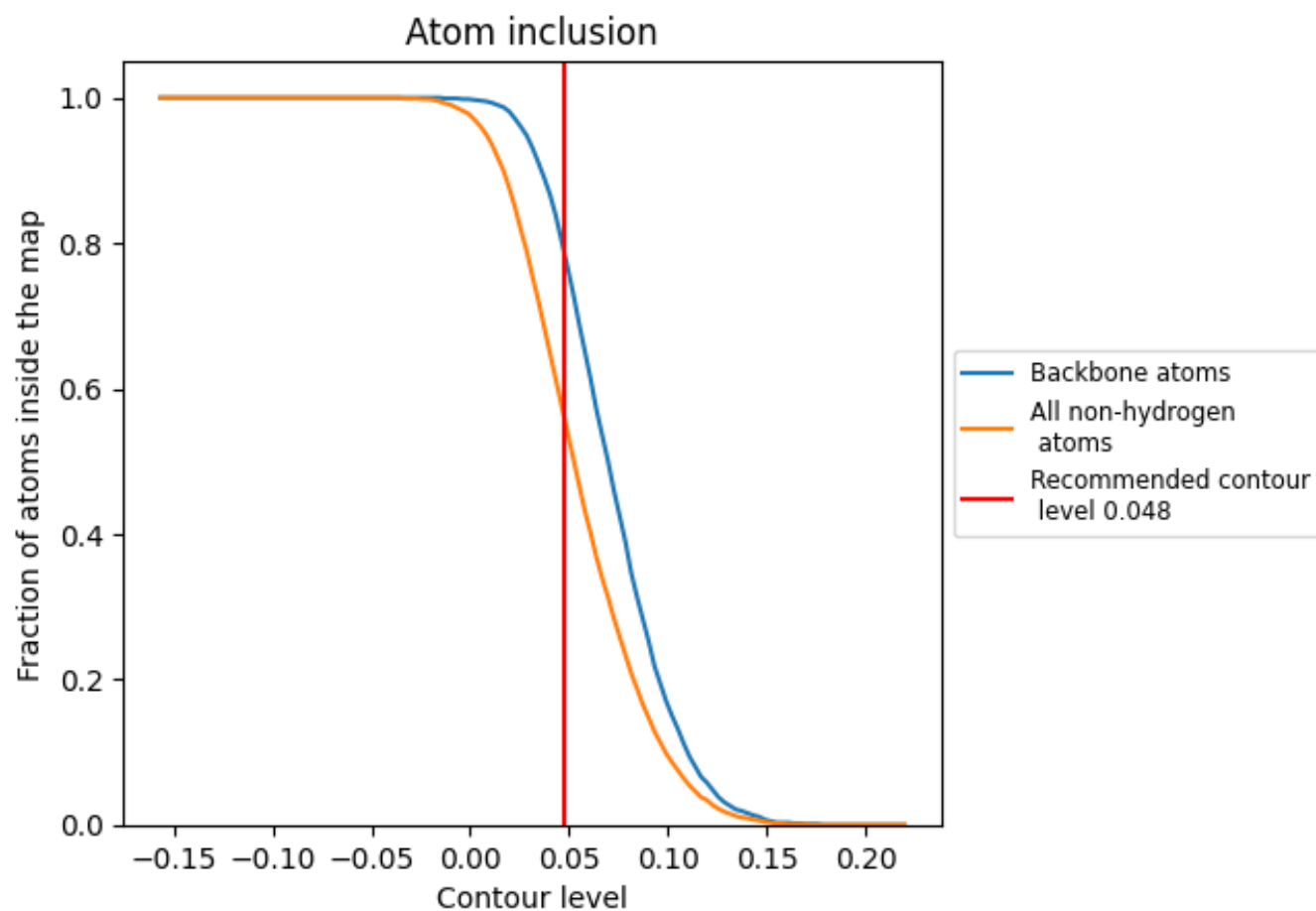


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 56% 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 (0.048) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5560	0.3300
A	0.6130	0.3680
B	0.3610	0.2590
C	0.6570	0.3620
D	0.6130	0.3260

