



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:59 AM UTC

PDB ID : 8W41 / pdb_00008w41
EMDB ID : EMD-37260
Title : Cryo-EM structure of Myosin VI in the autoinhibited state
Authors : Niu, F.; Wei, Z.
Deposited on : 2023-08-23
Resolution : 3.54 Å(reported)
Based on initial models : 2V26, 2N12, 2KIA, 3GN4, 6OBI

This is a wwPDB EM Validation Summary 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

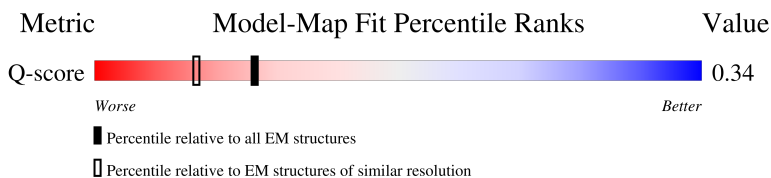
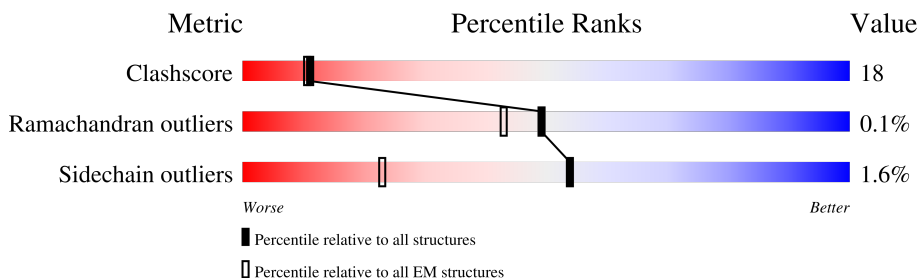
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 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	12891 (3.04 - 4.04)

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	B	149	15% 56% 42% .
1	I	149	19% 51% 46% ..
2	A	1285	10% 56% 33% 10%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11859 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 Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	147	Total	C	N	O	S	0	0
			1156	708	186	253	9		
1	I	146	Total	C	N	O	S	0	0
			1151	705	185	252	9		

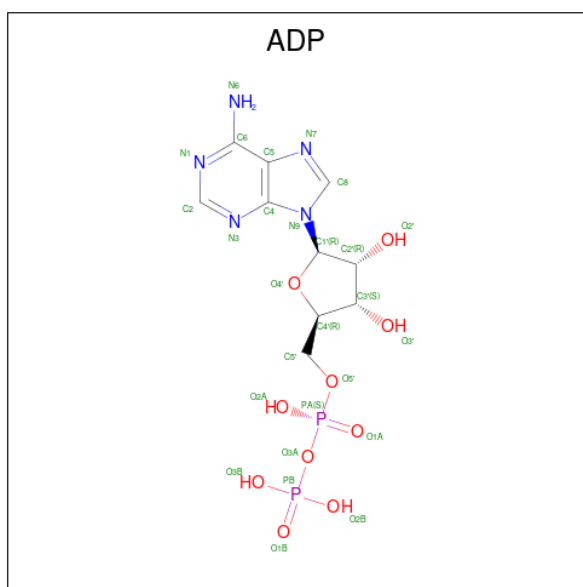
- Molecule 2 is a protein called Unconventional myosin-VI.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1162	Total	C	N	O	S	0	0
			9515	5994	1695	1776	50		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	B	4	Total	Ca	0
			4	4	

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

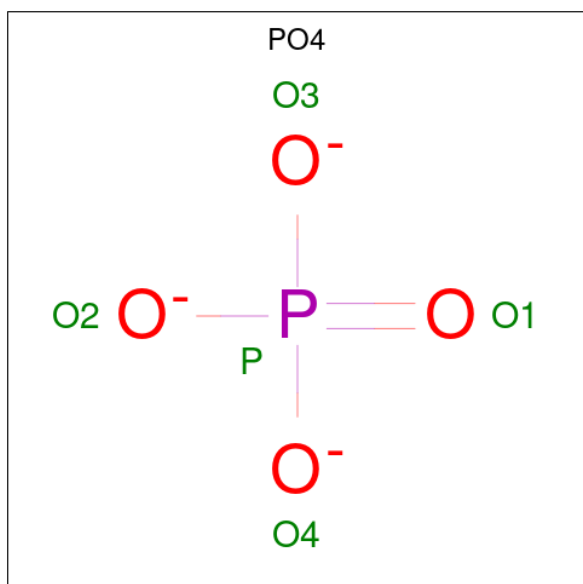


Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- 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 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P) (labeled as "Ligand of Interest" by depositor).

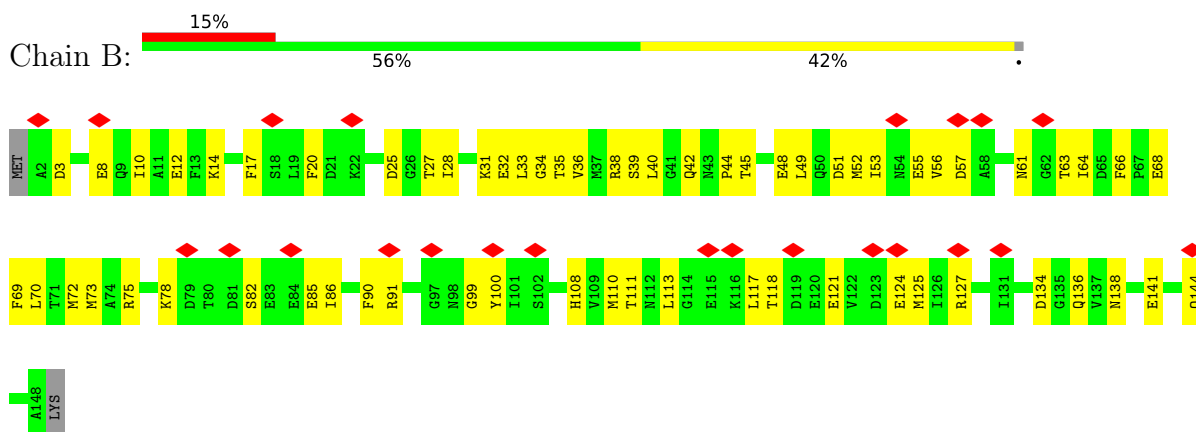


Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	O	P	0
			5	4	1	

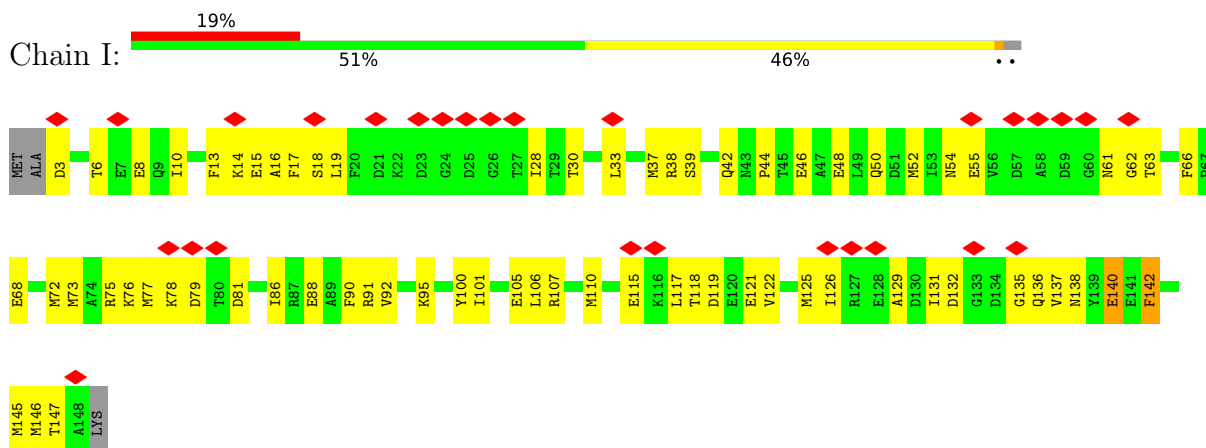
3 Residue-property plots

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

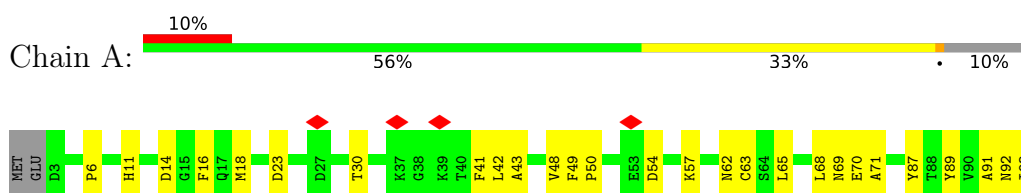
• Molecule 1: Calmodulin-1



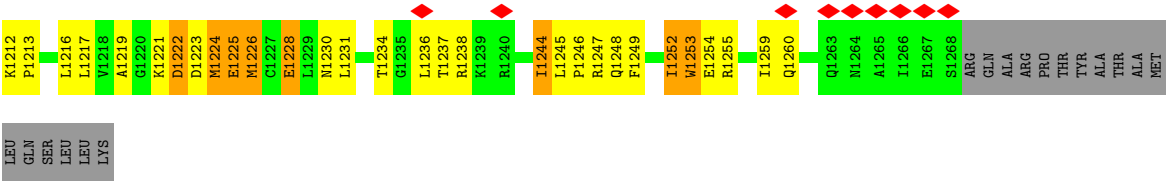
• Molecule 1: Calmodulin-1



• Molecule 2: Unconventional myosin-VI



N1140	A1140	ALA	VAL	LEU	ALA	THR	LYS	ALA	ALA	GLN	GLY	ASN	THR	PRO	GLN	GLY	ASN	THR	LYS	K1074	Y1075	D1076	L1077	S1078	K1079	E1084	L1085	O1086	D1087	T1088	I1089	N1090	T1091	I1095	S1096	L1097	L1098	A1099	A1100	C1101	R1102	E1103	E1104	F1105	H1106	K1110	V1115	K1116	S1117	K1118	N1119	K1120	K1121	R1122	N1123	Q1128	M1206	E1207	L1208	H1209	F1210	D1211	N1165	R1166	Q1167	F1170	I1173	P1174	F1175	D1180	Q1181	Y1182	K1183	D1184	A1185	Q1186	K1190	W1193	Y1194	A1196	H1196	W1201	Q1205	M1206	L1208	H1209	F1210	D1211	R123	D132	R136	I147	I148	V149	E152	K157	T161	K162	L165	Y172	D179	D180	E184	A185	N186	P187	E190	M194	A195	K196	T197	V198	R199	N200	N201	S204	R205	F206	G207	K208	I212	E216	E231	K232	R234	I235	Q238	N244	Y245	F248	R250	L251	C252	A253	G254	A255	D258	L263	S267	P268	D269	F271	R272	Y273	L274	N275	T279	R280	Y281	F282	A283	N284	K285	E286	T287	D288	K289	R295	K296	P298	Y299	A303	M306	K307	L311	D312	D316	F317	I318	R319	M320	C321	A323	I327	E333	K334	L335	D336	L337	F338	R339	V341	G342	G343	L347	G348	R349	I350	E354	A355	G356	S357	T358	S359	G360	G361	G362	N363	L364	K365	N366	K367	S368	L378	L379	D384	D385	L386	R387	R393	VAL	THR	THR	ALA	GLY	THR	LYS	GLY	THR	VAL	ILE	K408	L411	K412	Q415	R420	L423	Y428	S429	H430	V454	Y462	E469	Q470	C472	I473	N474	Y475	C476	N477	K478	K479	L480	G481	Q482	Q493	L495	Y496	Q497	G500	L501	V506	N511	Q512	D513	C514	I515	T518	E519	K521	L522	V523	G524	I525	I528	L529	D530	E531	N533	R534	L535	P538	S539	F543	K550	H551	F555	R556	L557	R561	K562	S563	K564	R569	R572	D573	D574	E575	G576	F577	I578	I579	R580	H581	F582	A585	V586	C587	Y588	E589	T590	F593	V594	N597	L605	L608	I609	D614	K615	F616	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L689	Q690	C691	S692	G693	M694	L700	W701	Q702	Q707	Y705	P706	F711	L714	Y715	M716	N717	K720	Y721	M722	P723	D724	A727	R728	L729	D730	P731	R732	L733	F734	L738	F739	K740	A741	D742	G743	L744	R745	N746	E746	N747	K750	F751	F757	F758	R759	D767	Q768	M770	D773	P774	D775	H776	R783	Y784	R792	V796	Q797	F621	E622	S623	SER	THR	ASN	ASN	LYS	ASP	THR	LYS	GLN	LYS	ALA	GLY	LEU	S639	V643	K646	Q650	L653	L654	L655	K656	G657	L658	R659	S660	T661	S664	I669	V670	P671	M675	E681	Q684	L685	L6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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	173658	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.185	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.1	Depositor
Map size ($\text{\AA}$)	363.88, 363.88, 363.88	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.827, 0.827, 0.827	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, MG, ADP, PO4

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	B	0.26	0/1168	0.46	0/1569
1	I	0.49	1/1163 (0.1%)	0.63	1/1562 (0.1%)
2	A	0.48	11/9691 (0.1%)	0.60	13/13002 (0.1%)
All	All	0.46	12/12022 (0.1%)	0.59	14/16133 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1244	ILE	CA-C	-9.54	1.42	1.53
2	A	1224	MET	CA-C	-6.97	1.43	1.52
2	A	152	GLU	CA-C	-6.95	1.44	1.53
2	A	1221	LYS	CA-C	-6.64	1.47	1.53
2	A	1104	GLU	CA-C	-6.45	1.44	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1089	ILE	N-CA-C	-19.51	94.41	113.53
2	A	1221	LYS	N-CA-C	-16.09	89.98	108.49
2	A	1102	ARG	N-CA-C	-9.04	101.33	111.82
1	I	105	GLU	N-CA-C	-8.23	102.39	111.36
2	A	1249	PHE	N-CA-C	-7.63	102.90	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1156	0	1079	62	0
1	I	1151	0	1075	70	0
2	A	9515	0	9503	328	0
3	B	4	0	0	0	0
4	A	27	0	12	0	0
5	A	1	0	0	0	0
6	A	5	0	0	0	0
All	All	11859	0	11669	429	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 18.

The worst 5 of 429 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)
2:A:917:LYS:HG3	2:A:926:LEU:HD13	1.44	0.99
2:A:1100:ALA:HA	2:A:1103:GLU:HG3	1.50	0.91
2:A:6:PRO:HB2	2:A:18:MET:HE3	1.48	0.91
2:A:1212:LYS:HD3	2:A:1213:PRO:HD2	1.54	0.88
2:A:863:GLY:HA3	2:A:916:LYS:HZ1	1.46	0.80

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	B	145/149 (97%)	139 (96%)	6 (4%)	0	100	100
1	I	144/149 (97%)	133 (92%)	11 (8%)	0	100	100
2	A	1152/1285 (90%)	1095 (95%)	55 (5%)	2 (0%)	43	73
All	All	1441/1583 (91%)	1367 (95%)	72 (5%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	1095	ILE
2	A	1222	ASP

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	B	125/127 (98%)	125 (100%)	0	100	100
1	I	125/127 (98%)	124 (99%)	1 (1%)	73	77
2	A	1040/1139 (91%)	1020 (98%)	20 (2%)	50	67
All	All	1290/1393 (93%)	1269 (98%)	21 (2%)	54	70

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	1222	ASP
2	A	1247	ARG
2	A	1255	ARG
2	A	1248	GLN
2	A	1226	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	533	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A	870	GLN
2	A	1248	GLN
2	A	868	ASN
2	A	873	ASN

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 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 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	$\# Z > 2$
4	ADP	A	2001	5	28,29,29	1.37	5 (17%)	43,45,45	1.84	8 (18%)
6	PO4	A	2003	5	4,4,4	1.13	0	6,6,6	0.47	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	A	2001	5	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2001	ADP	C5-C4	4.29	1.46	1.39
4	A	2001	ADP	C5-C6	2.68	1.48	1.41
4	A	2001	ADP	C5-N7	-2.62	1.34	1.39
4	A	2001	ADP	C8-N7	2.11	1.35	1.31
4	A	2001	ADP	C4-N9	-2.06	1.33	1.37

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2001	ADP	C5-C4-N3	-6.00	118.45	126.72
4	A	2001	ADP	N3-C4-N9	4.59	134.98	127.17
4	A	2001	ADP	C2-N3-C4	3.76	121.01	111.83
4	A	2001	ADP	C4-C5-N7	-3.59	106.48	110.58
4	A	2001	ADP	N3-C2-N1	-3.23	123.69	128.58

There are no chirality outliers.

All (4) torsion outliers are listed below:

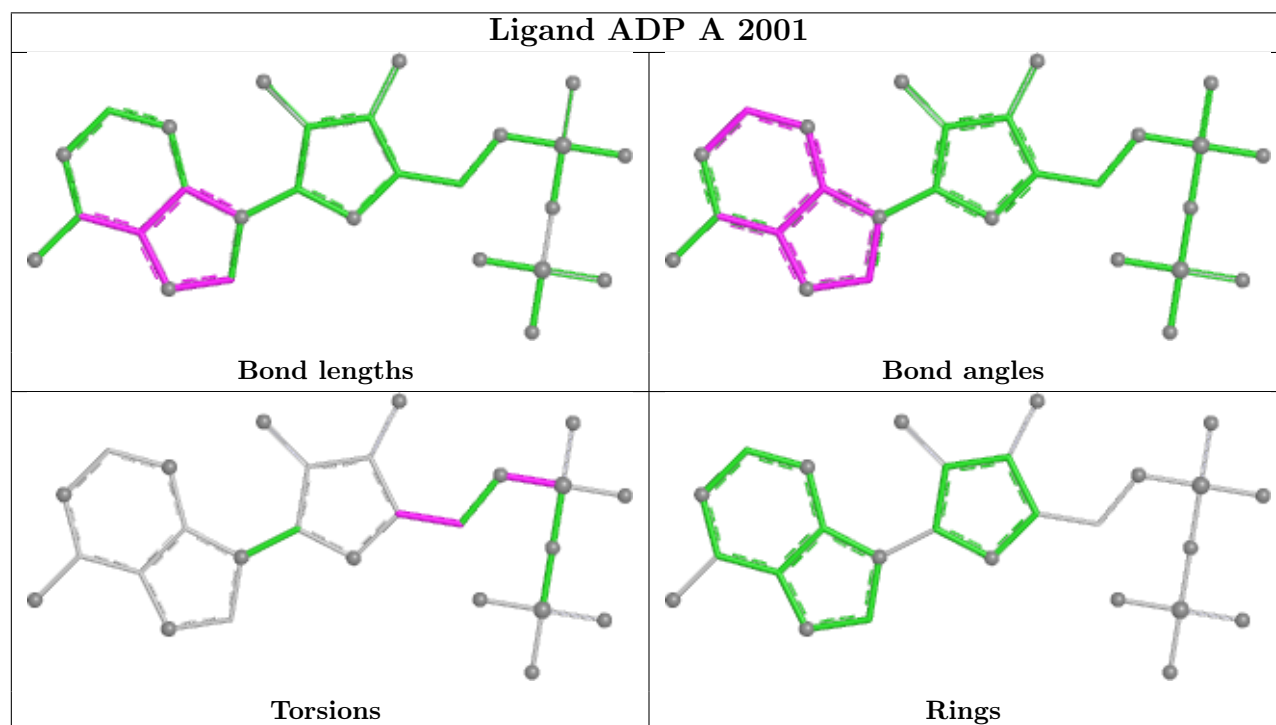
Mol	Chain	Res	Type	Atoms
4	A	2001	ADP	C5'-O5'-PA-O2A
4	A	2001	ADP	C5'-O5'-PA-O3A
4	A	2001	ADP	C3'-C4'-C5'-O5'
4	A	2001	ADP	O4'-C4'-C5'-O5'

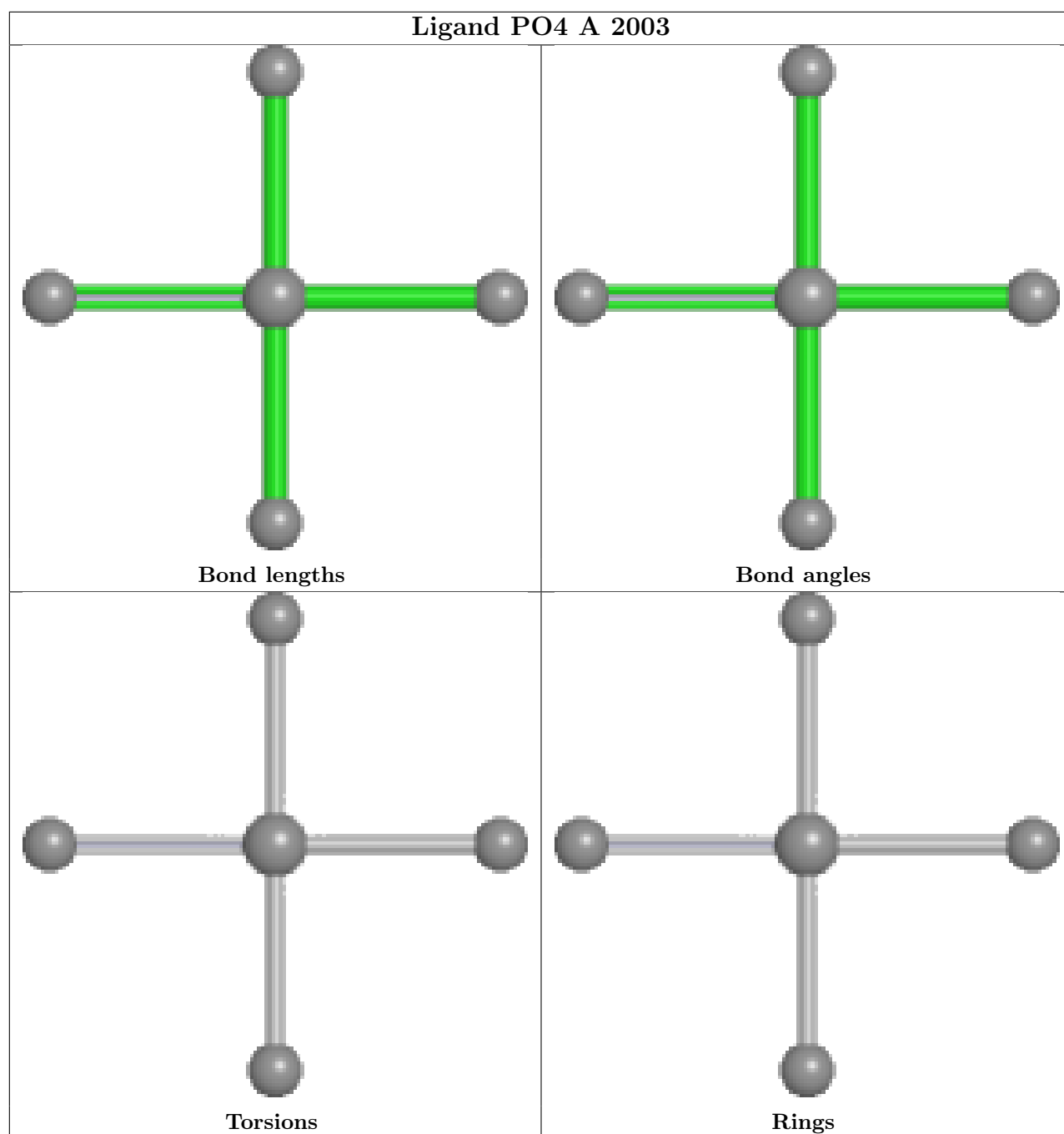
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

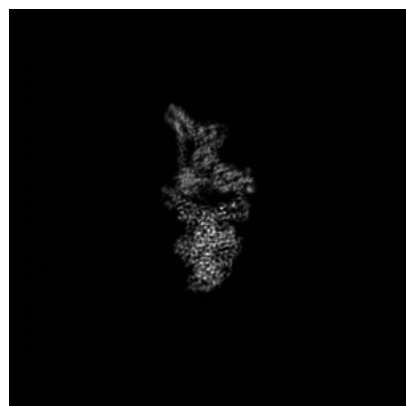
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37260. 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](#)

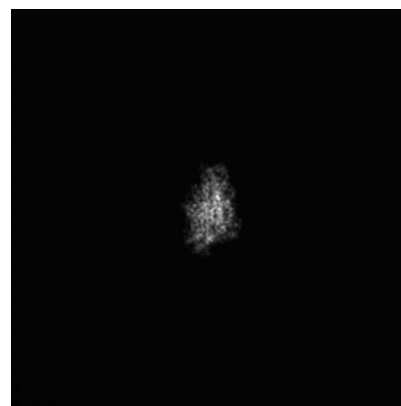
6.1.1 Primary map



X

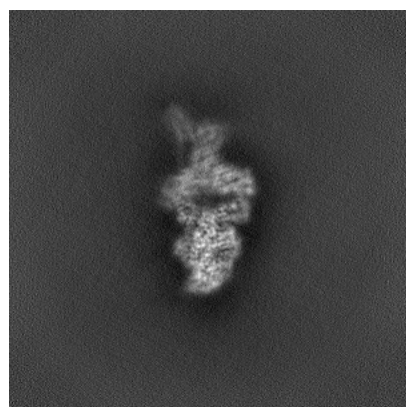


Y

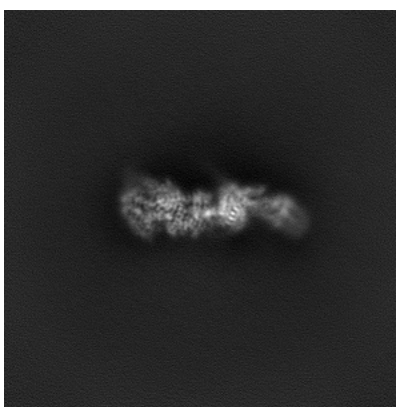


Z

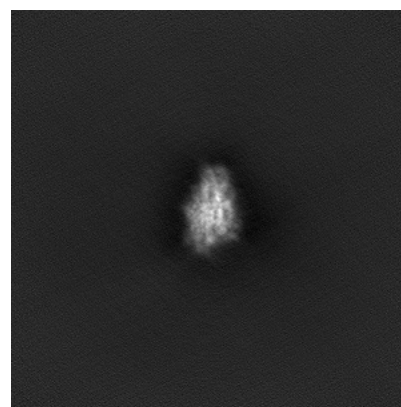
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

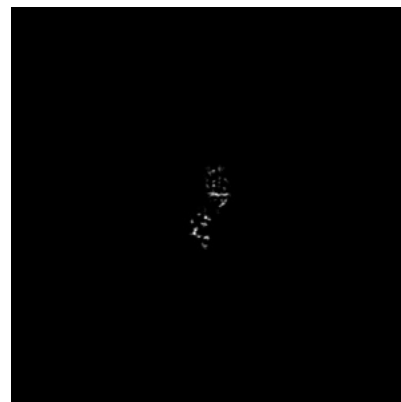
6.2.1 Primary map



X Index: 220

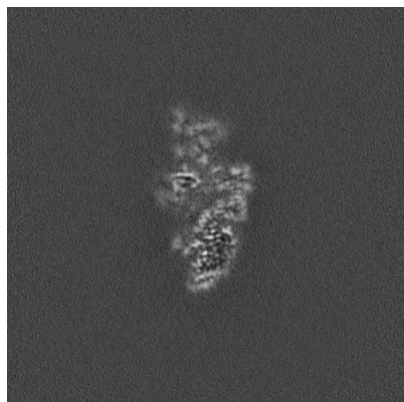


Y Index: 220

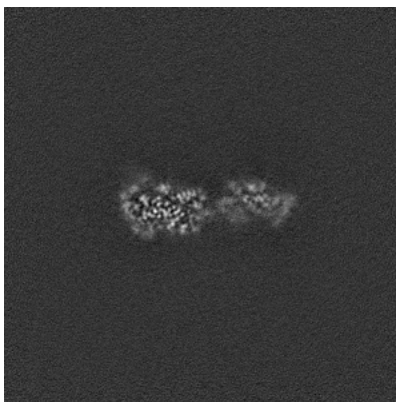


Z Index: 220

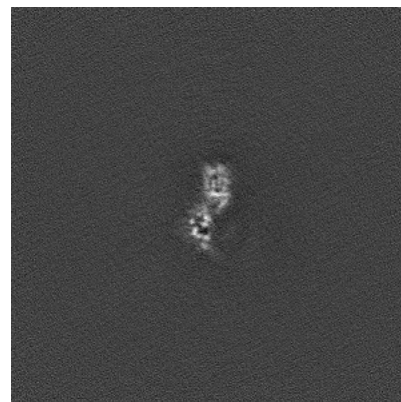
6.2.2 Raw map



X Index: 220



Y Index: 220



Z Index: 220

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

6.3 Largest variance slices [i](#)

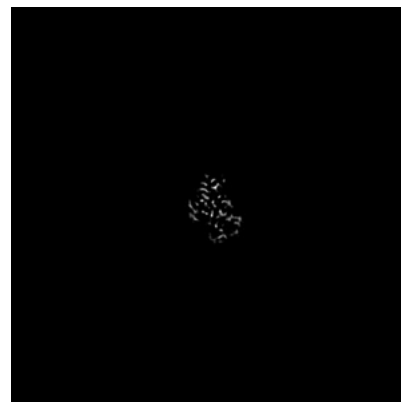
6.3.1 Primary map



X Index: 226



Y Index: 219

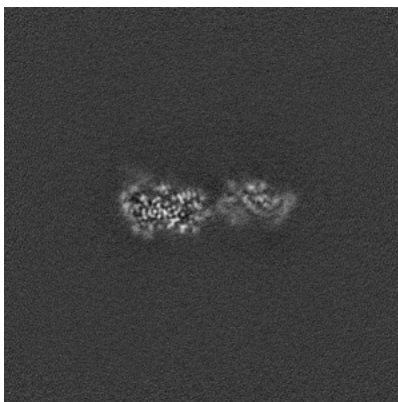


Z Index: 180

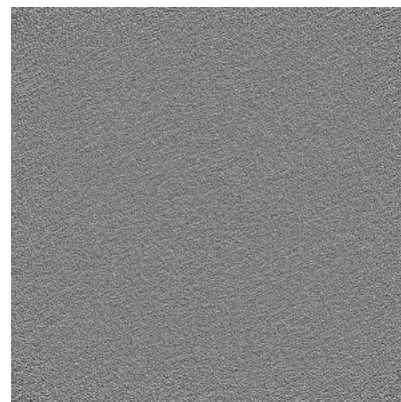
6.3.2 Raw map



X Index: 215



Y Index: 219

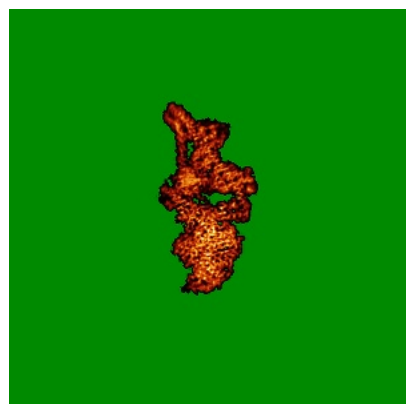


Z Index: 0

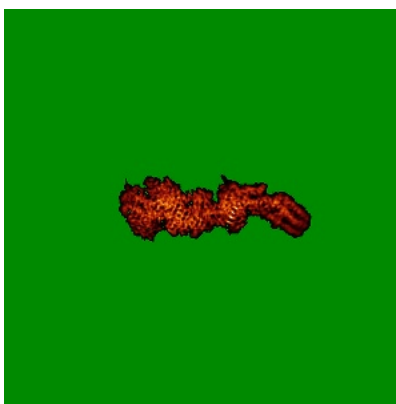
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

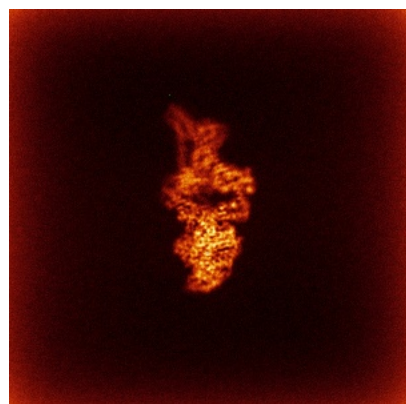


Y

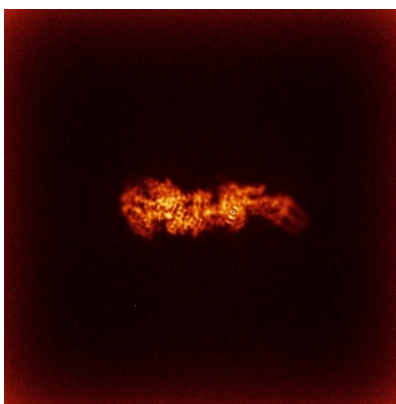


Z

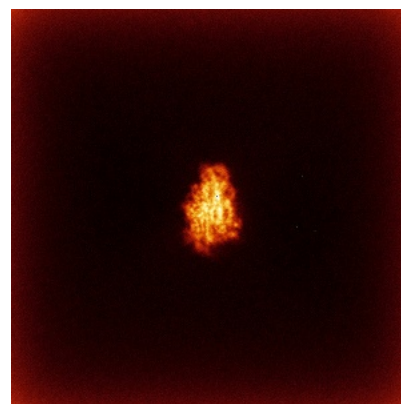
6.4.2 Raw map



X



Y

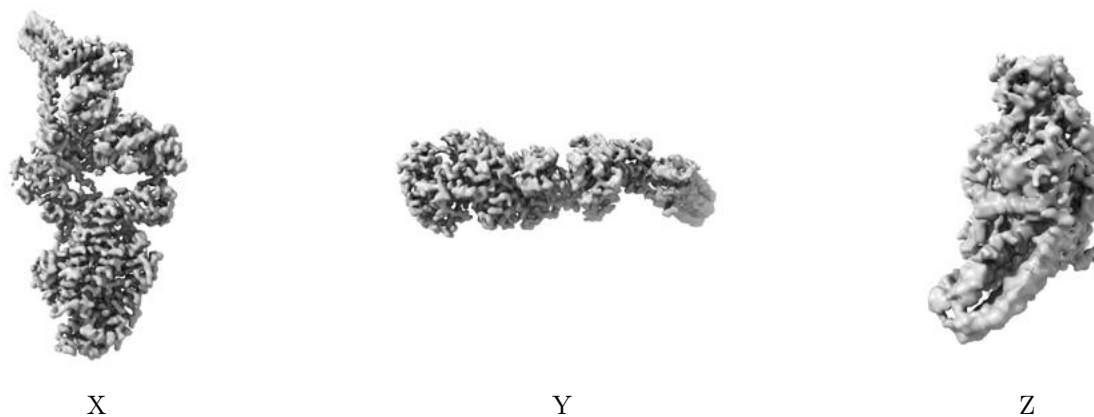


Z

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 0.1. 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.

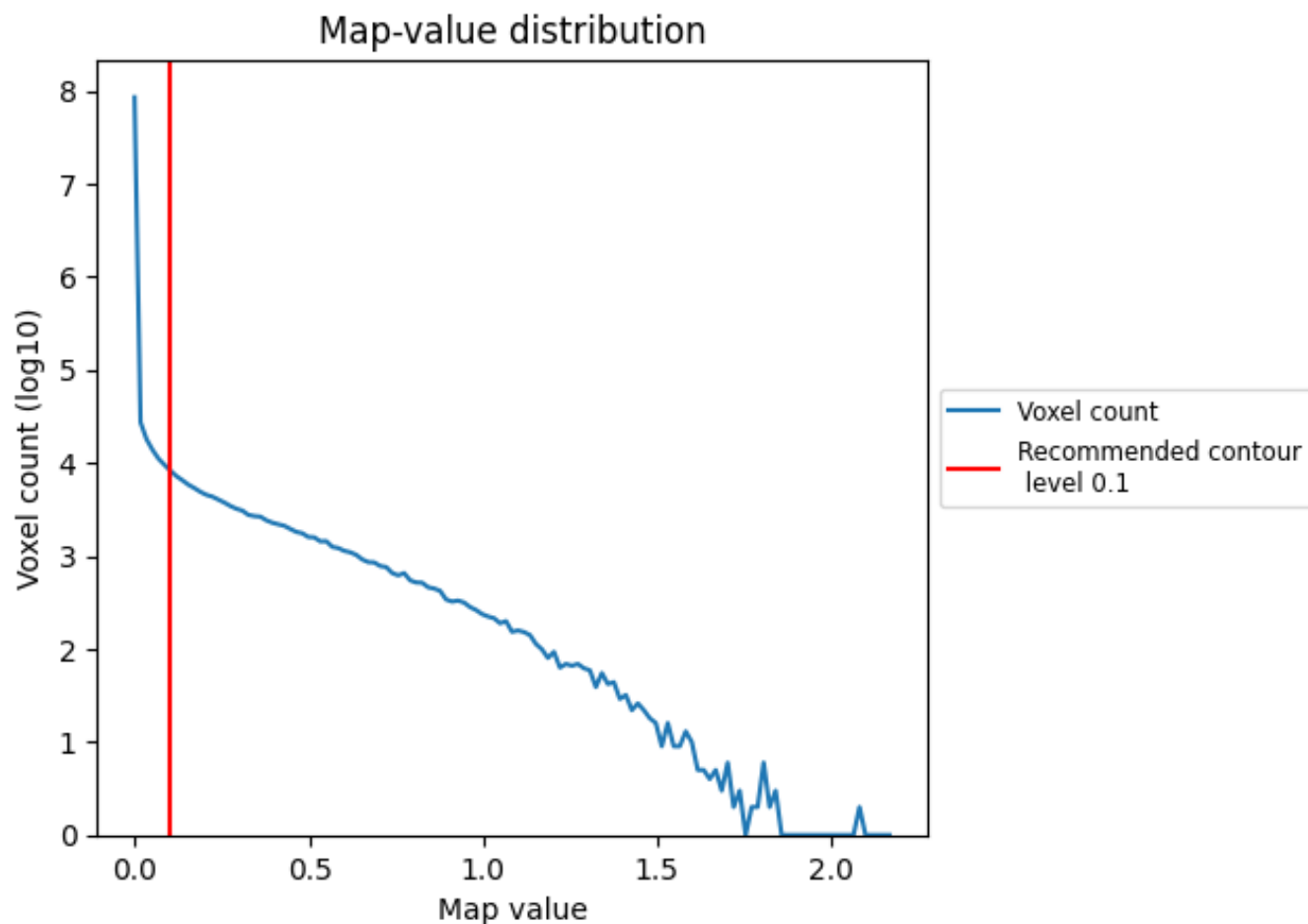
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

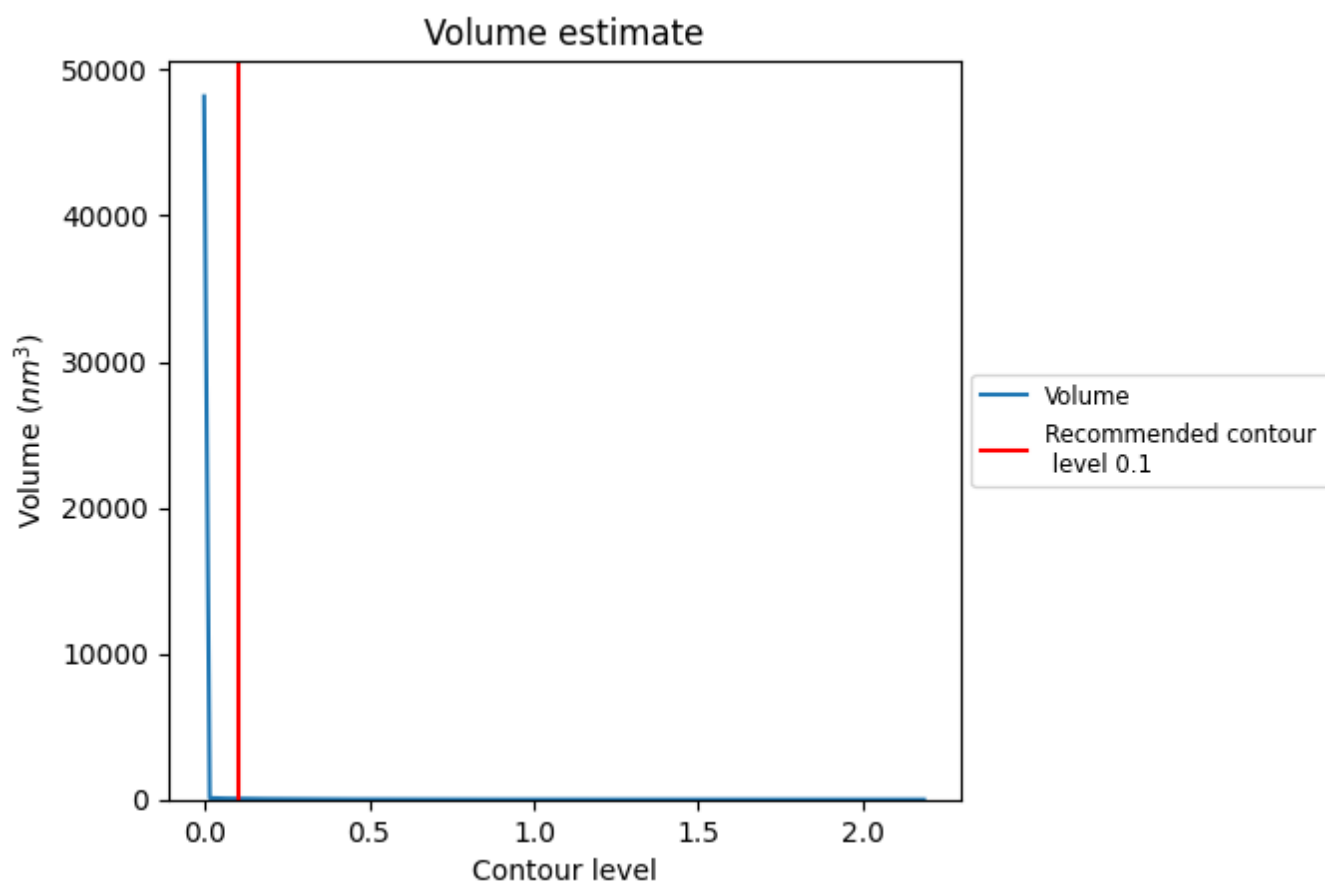
This section contains the results of statistical analysis of the map.

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.

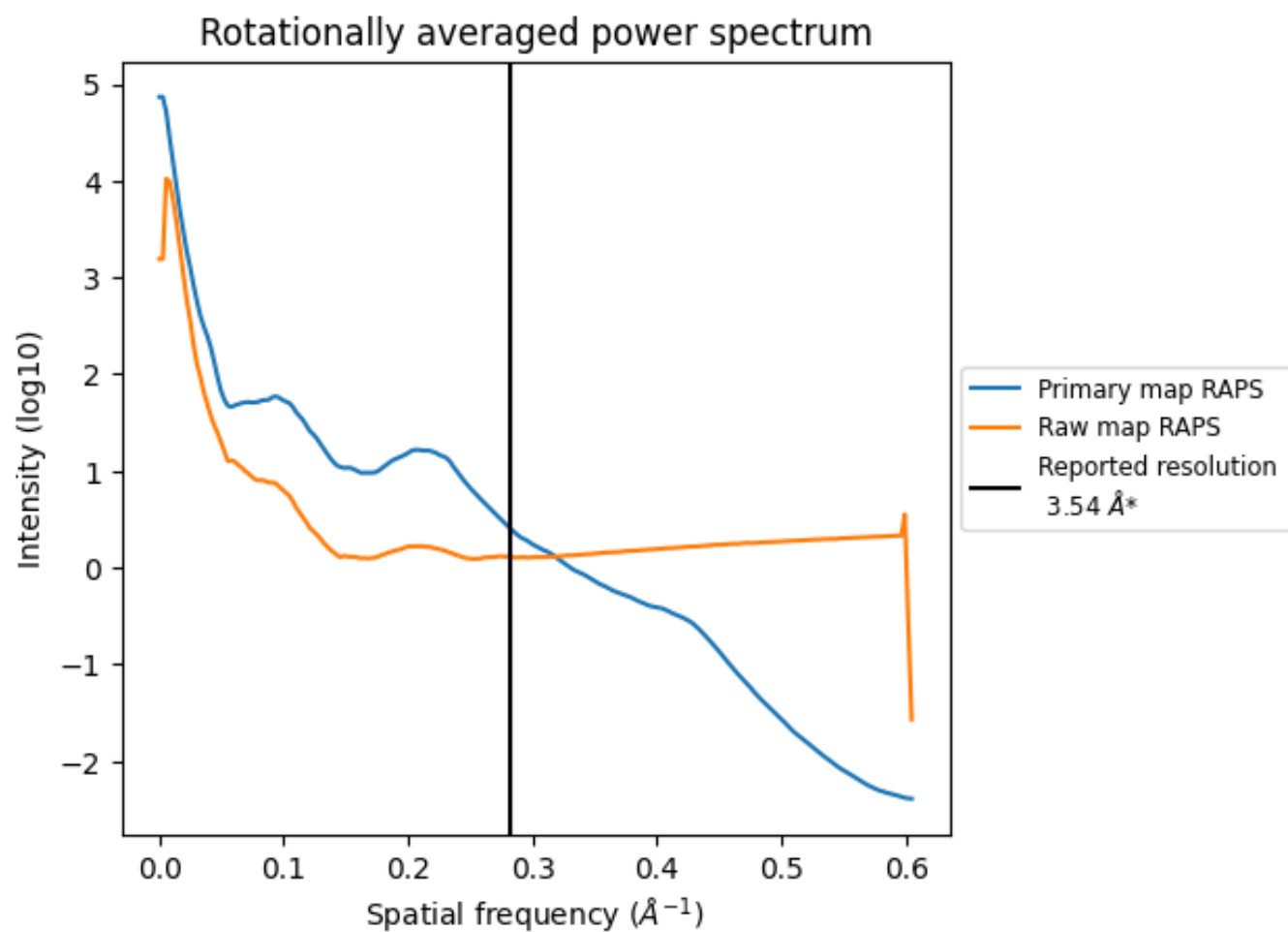
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 64 nm^3 ; this corresponds to an approximate mass of 58 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 ⓘ

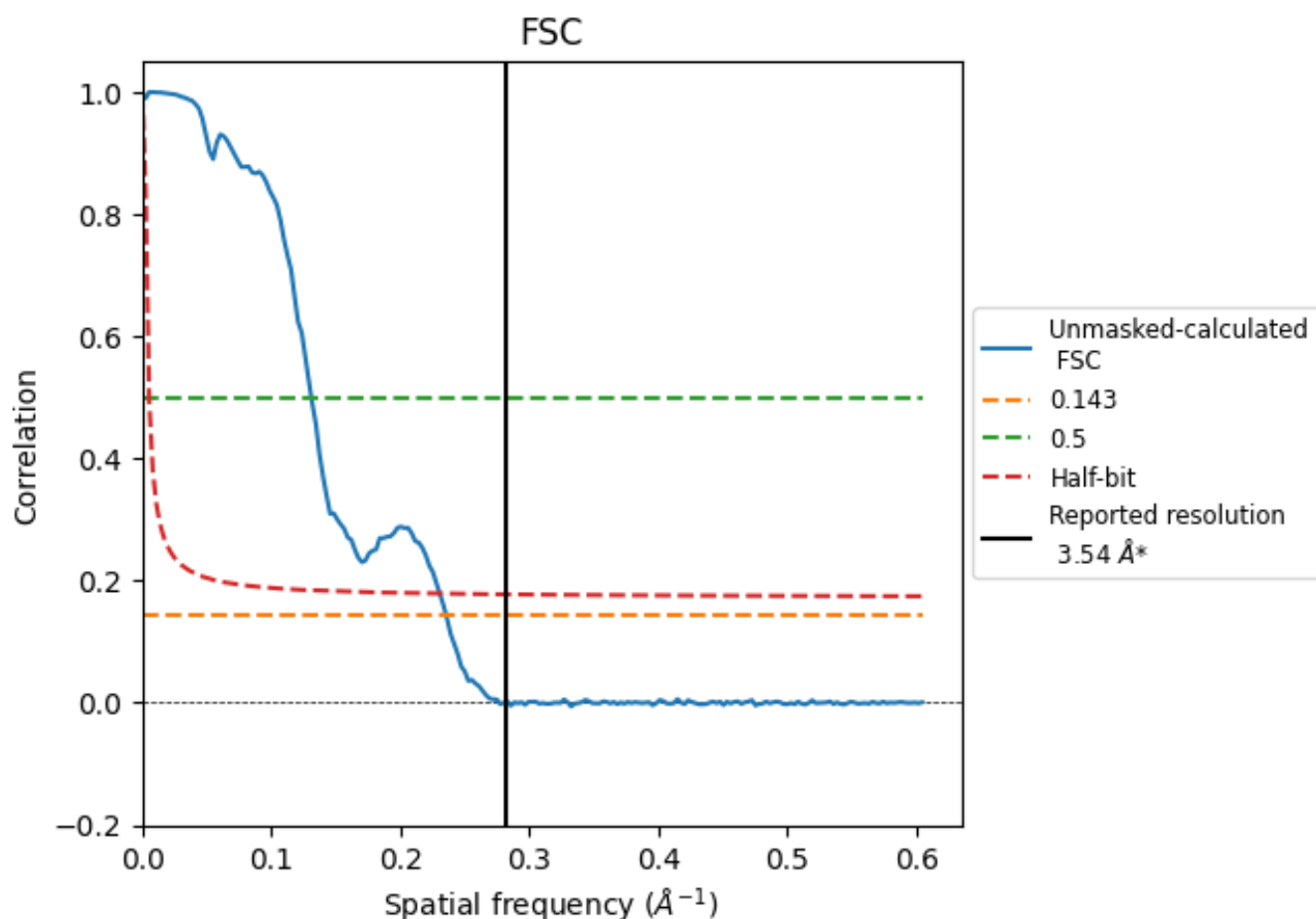


*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

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 0.282 Å⁻¹

8.2 Resolution estimates [i](#)

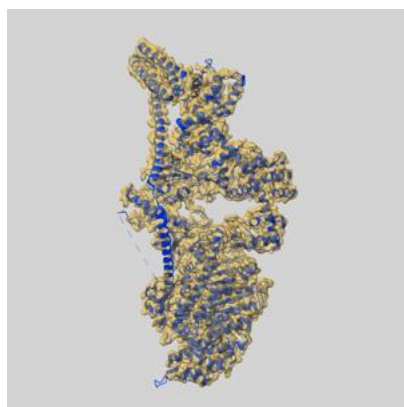
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.24	7.63	4.34

*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 4.24 differs from the reported value 3.54 by more than 10 %

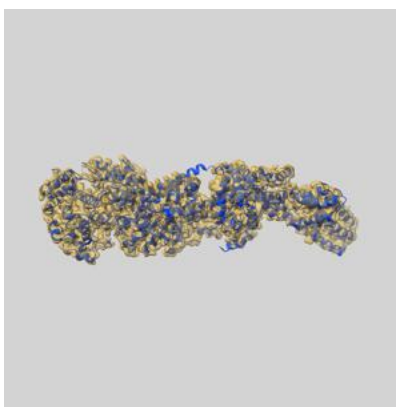
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37260 and PDB model 8W41. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

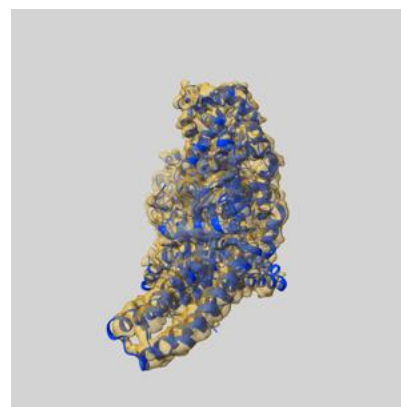
9.1 Map-model overlay [i](#)



X



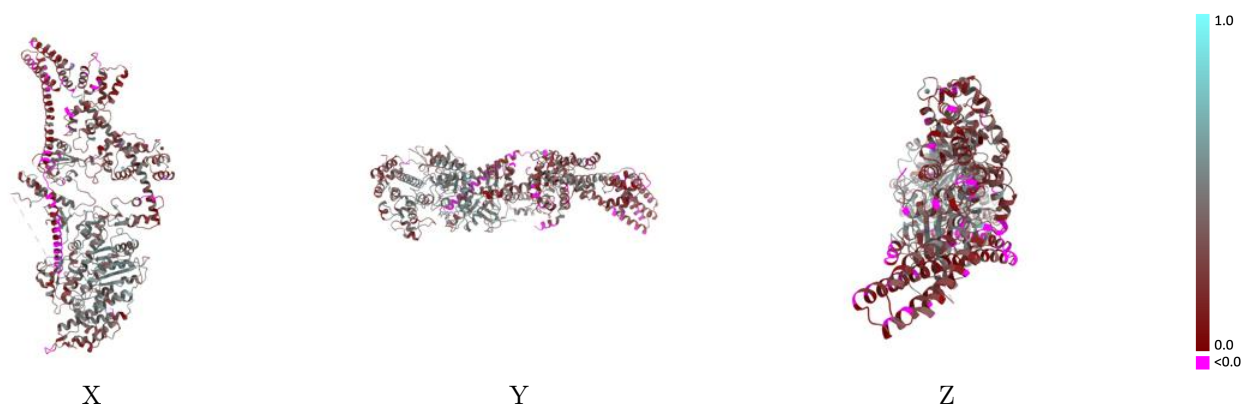
Y



Z

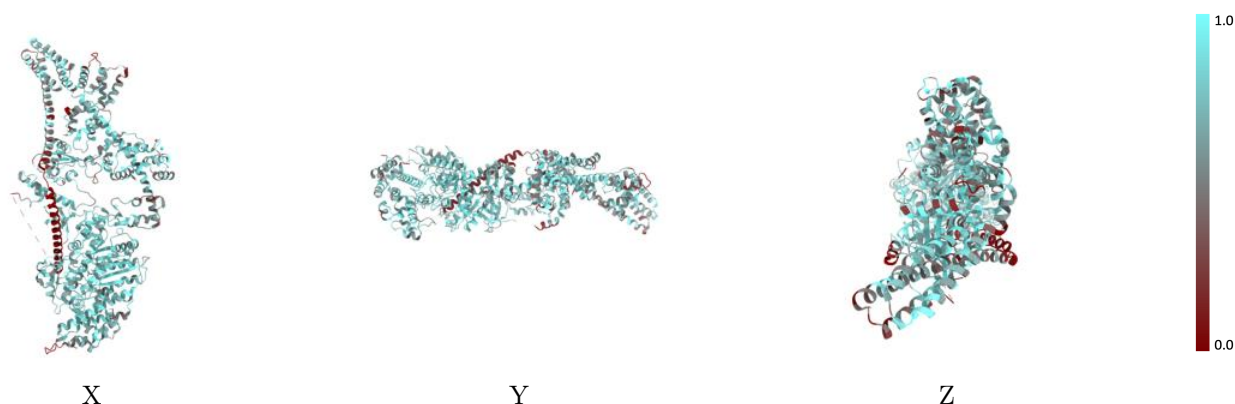
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



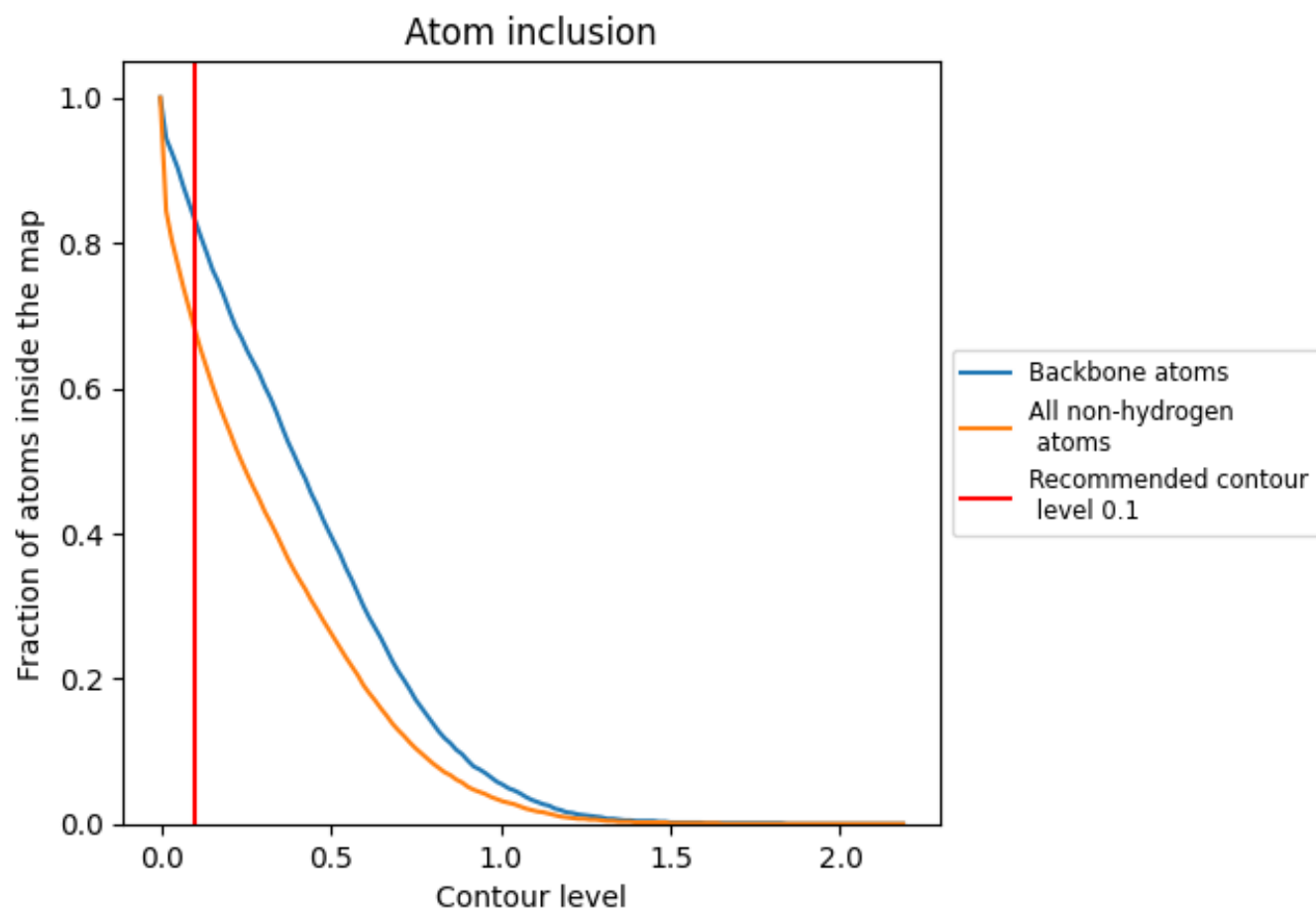
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6810	0.3400
A	0.6920	0.3600
B	0.6540	0.2660
I	0.6190	0.2530

