



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 10:22 PM UTC

PDB ID : 9K07 / pdb_00009k07
EMDB ID : EMD-61941
Title : Cryo-EM structure of the DSO-5a-bound human BRS3-Gq complex
Authors : Li, J.; Li, C.; Zhou, Q.; Han, W.; Fang, M.; Xu, Y.; Mai, Y.; Cui, J.; Xu, H.;
Zhang, Y.; Yin, W.; Wang, M.
Deposited on : 2024-10-15
Resolution : 2.83 Å(reported)

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:

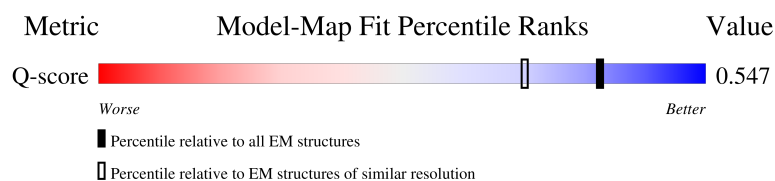
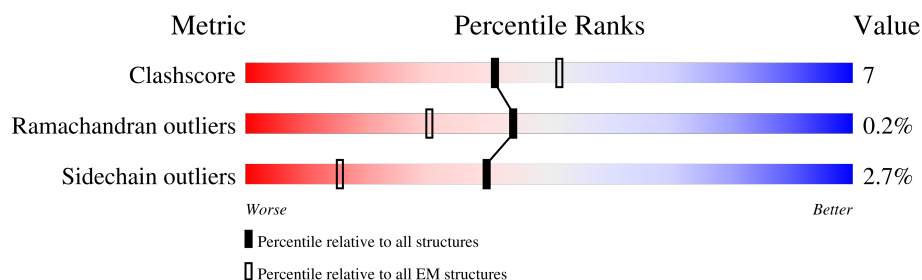
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.83 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	11847 (2.33 - 3.33)

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	R	612	
2	A	246	
3	E	267	
4	B	345	

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Mol	Chain	Length	Quality of chain
5	G	70	
6	N	140	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9618 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 Bombesin receptor subtype-3, Oplophorus-luciferin 2-monooxygenase catalytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	273	Total	C	N	O	S	0	0
			2165	1445	349	361	10		

There are 85 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-15	MET	-	initiating methionine	UNP P32247
R	-14	LYS	-	expression tag	UNP P32247
R	-13	THR	-	expression tag	UNP P32247
R	-12	ILE	-	expression tag	UNP P32247
R	-11	ILE	-	expression tag	UNP P32247
R	-10	ALA	-	expression tag	UNP P32247
R	-9	LEU	-	expression tag	UNP P32247
R	-8	SER	-	expression tag	UNP P32247
R	-7	TYR	-	expression tag	UNP P32247
R	-6	ILE	-	expression tag	UNP P32247
R	-5	PHE	-	expression tag	UNP P32247
R	-4	CYS	-	expression tag	UNP P32247
R	-3	LEU	-	expression tag	UNP P32247
R	-2	VAL	-	expression tag	UNP P32247
R	-1	PHE	-	expression tag	UNP P32247
R	0	ALA	-	expression tag	UNP P32247
R	400	GLY	-	linker	UNP P32247
R	401	SER	-	linker	UNP P32247
R	402	SER	-	linker	UNP P32247
R	403	GLY	-	linker	UNP P32247
R	404	GLY	-	linker	UNP P32247
R	405	GLY	-	linker	UNP P32247
R	406	GLY	-	linker	UNP P32247
R	407	SER	-	linker	UNP P32247
R	408	GLY	-	linker	UNP P32247
R	409	GLY	-	linker	UNP P32247
R	410	GLY	-	linker	UNP P32247

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Chain	Residue	Modelled	Actual	Comment	Reference
R	411	GLY	-	linker	UNP P32247
R	412	SER	-	linker	UNP P32247
R	413	SER	-	linker	UNP P32247
R	414	GLY	-	linker	UNP P32247
R	415	VAL	-	linker	UNP P32247
R	419	GLU	ALA	conflict	UNP Q9GV45
R	426	GLU	GLN	conflict	UNP Q9GV45
R	430	ALA	GLY	conflict	UNP Q9GV45
R	433	LEU	GLN	conflict	UNP Q9GV45
R	442	VAL	LEU	conflict	UNP Q9GV45
R	446	LEU	PHE	conflict	UNP Q9GV45
R	448	ASN	ALA	conflict	UNP Q9GV45
R	450	ALA	GLY	conflict	UNP Q9GV45
R	458	ARG	LYS	conflict	UNP Q9GV45
R	459	ILE	VAL	conflict	UNP Q9GV45
R	461	ARG	LEU	conflict	UNP Q9GV45
R	466	ALA	GLY	conflict	UNP Q9GV45
R	469	ILE	ALA	conflict	UNP Q9GV45
R	482	ALA	GLY	conflict	UNP Q9GV45
R	483	ASP	PHE	conflict	UNP Q9GV45
R	486	ALA	GLY	conflict	UNP Q9GV45
R	487	GLN	LEU	conflict	UNP Q9GV45
R	490	GLU	MET	conflict	UNP Q9GV45
R	491	VAL	ILE	conflict	UNP Q9GV45
R	505	VAL	ILE	conflict	UNP Q9GV45
R	508	PRO	HIS	conflict	UNP Q9GV45
R	522	LEU	ILE	conflict	UNP Q9GV45
R	523	ASN	ASP	conflict	UNP Q9GV45
R	530	GLU	PRO	conflict	UNP Q9GV45
R	539	LYS	GLN	conflict	UNP Q9GV45
R	553	ILE	TYR	conflict	UNP Q9GV45
R	559	THR	ASN	conflict	UNP Q9GV45
R	564	MET	LEU	conflict	UNP Q9GV45
R	572	SER	-	expression tag	UNP Q9GV45
R	573	GLY	-	expression tag	UNP Q9GV45
R	574	GLY	-	expression tag	UNP Q9GV45
R	575	SER	-	expression tag	UNP Q9GV45
R	576	GLU	-	expression tag	UNP Q9GV45
R	577	ASN	-	expression tag	UNP Q9GV45
R	578	LEU	-	expression tag	UNP Q9GV45
R	579	TYR	-	expression tag	UNP Q9GV45
R	580	PHE	-	expression tag	UNP Q9GV45

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Chain	Residue	Modelled	Actual	Comment	Reference
R	581	GLN	-	expression tag	UNP Q9GV45
R	582	GLY	-	expression tag	UNP Q9GV45
R	583	GLY	-	expression tag	UNP Q9GV45
R	584	SER	-	expression tag	UNP Q9GV45
R	585	ALA	-	expression tag	UNP Q9GV45
R	586	GLY	-	expression tag	UNP Q9GV45
R	587	SER	-	expression tag	UNP Q9GV45
R	588	ALA	-	expression tag	UNP Q9GV45
R	589	HIS	-	expression tag	UNP Q9GV45
R	590	HIS	-	expression tag	UNP Q9GV45
R	591	HIS	-	expression tag	UNP Q9GV45
R	592	HIS	-	expression tag	UNP Q9GV45
R	593	HIS	-	expression tag	UNP Q9GV45
R	594	HIS	-	expression tag	UNP Q9GV45
R	595	HIS	-	expression tag	UNP Q9GV45
R	596	HIS	-	expression tag	UNP Q9GV45

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(i) subunit alpha-2, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	212	Total	C	N	O	S	0	0
			1655	1053	292	303	7		

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	SER	CYS	conflict	UNP P04899
A	31	ARG	ALA	conflict	UNP P04899
A	33	THR	GLU	conflict	UNP P04899
A	34	LEU	VAL	conflict	UNP P04899
A	35	ARG	LYS	conflict	UNP P04899
A	42	ASP	GLY	conflict	UNP P63092
A	43	ASN	GLU	conflict	UNP P63092
A	58	GLY	-	linker	UNP P63092
A	59	GLY	-	linker	UNP P63092
A	60	SER	-	linker	UNP P63092
A	61	GLY	-	linker	UNP P63092
A	62	GLY	-	linker	UNP P63092
A	63	SER	-	linker	UNP P63092
A	64	GLY	-	linker	UNP P63092
A	65	GLY	-	linker	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
A	111	ASP	ALA	conflict	UNP P63092
A	114	ASP	SER	conflict	UNP P63092
A	124	ASP	LEU	conflict	UNP P63092
A	195	LYS	ASP	conflict	UNP P63092
A	198	VAL	LEU	conflict	UNP P63092
A	199	ASP	ARG	conflict	UNP P63092
A	210	ILE	TYR	conflict	UNP P63092
A	224	ALA	ILE	conflict	UNP P63092
A	227	ILE	VAL	conflict	UNP P63092
A	232	LYS	ARG	conflict	UNP P63092
A	236	LEU	GLN	conflict	UNP P63092
A	237	GLN	ARG	conflict	UNP P63092
A	239	ASN	HIS	conflict	UNP P63092
A	242	GLU	GLN	conflict	UNP P63092
A	244	ASN	GLU	conflict	UNP P63092
A	246	VAL	LEU	conflict	UNP P63092

- Molecule 3 is a protein called scFv16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	231	Total	C	N	O	S	0	0
			1776	1128	294	344	10		

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	338	Total	C	N	O	S	0	0
			2600	1604	467	508	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P54311
B	-3	GLY	-	expression tag	UNP P54311
B	-2	SER	-	expression tag	UNP P54311
B	-1	LEU	-	expression tag	UNP P54311
B	0	LEU	-	expression tag	UNP P54311
B	1	GLN	-	expression tag	UNP P54311

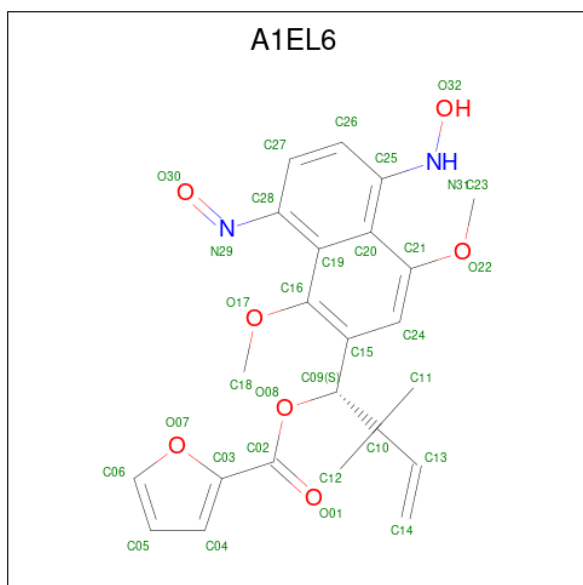
- Molecule 5 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	56	Total	C	N	O	S	0	0
			429	269	76	81	3		

- Molecule 6 is a protein called Nanobody-35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	126	Total	C	N	O	S	0	0
			961	599	168	188	6		

- Molecule 7 is [(1 {S})-1-[1,4-dimethoxy-8-nitroso-5-(oxidanylamino)naphthalen-2-yl]-2,2-dimethyl-but-3-enyl] furan-2-carboxylate (CCD ID: A1EL6) (formula: C₂₃H₂₄N₂O₇) (labeled as "Ligand of Interest" by depositor).

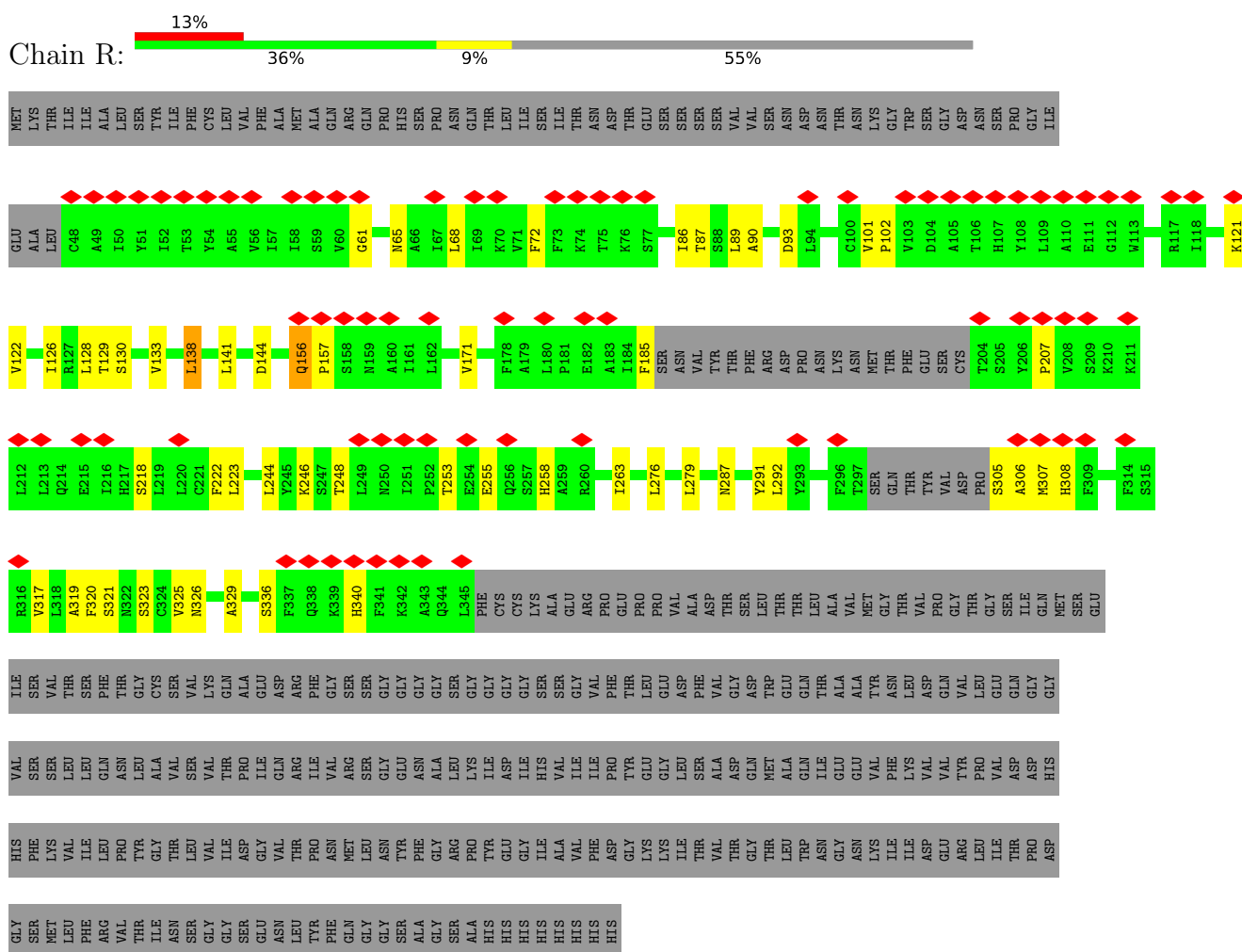


Mol	Chain	Residues	Atoms				AltConf
7	R	1	Total	C	N	O	0
			32	23	2	7	

3 Residue-property plots

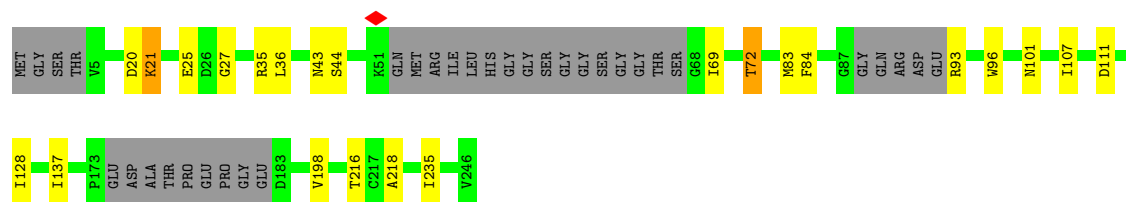
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Bombesin receptor subtype-3,Oplophorus-luciferin 2-monooxygenase catalytic subunit

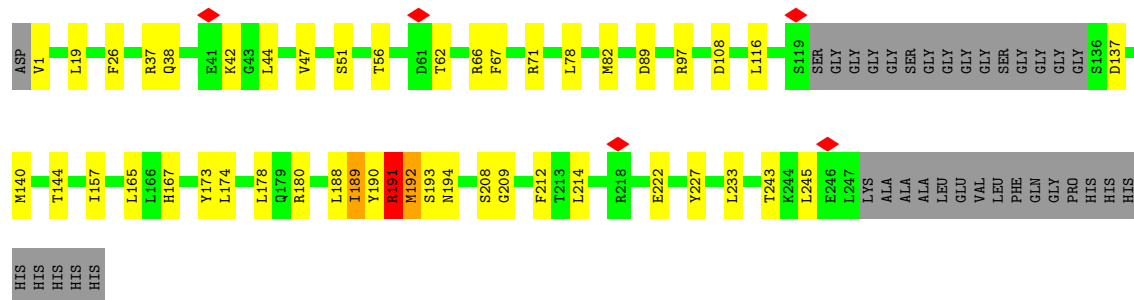


- Molecule 2: Guanine nucleotide-binding protein G(i) subunit alpha-2,Guanine nucleotide-binding protein G(s) subunit alpha isoforms short

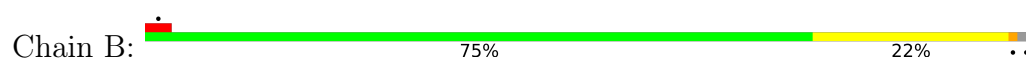




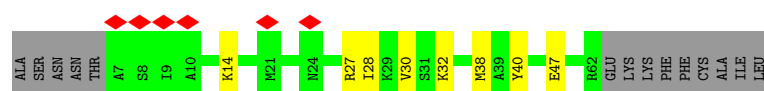
• Molecule 3: scFv16



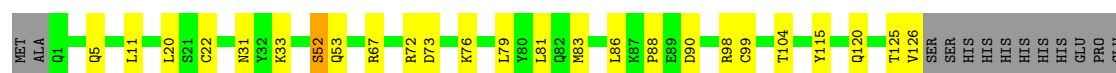
• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



• Molecule 5: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



• Molecule 6: Nanobody-35



ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	311433	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI 10	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	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	3.544	Depositor
Minimum map value	-2.456	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	274.176, 274.176, 274.176	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.071, 1.071, 1.071	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1EL6

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	R	0.16	0/2219	0.36	1/3019 (0.0%)
2	A	0.16	0/1683	0.27	0/2274
3	E	0.34	2/1820 (0.1%)	0.48	3/2468 (0.1%)
4	B	0.17	0/2647	0.29	0/3589
5	G	0.11	0/435	0.21	0/587
6	N	0.15	0/981	0.27	0/1329
All	All	0.20	2/9785 (0.0%)	0.34	4/13266 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	E	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	193	SER	CA-CB	-6.16	1.45	1.54
3	E	189	ILE	C-O	-5.35	1.18	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	121	LYS	N-CA-C	-7.09	104.49	113.43
3	E	194	ASN	CB-CA-C	6.73	120.80	109.84
3	E	191	ARG	CB-CA-C	5.67	121.70	110.42
3	E	190	TYR	CA-CB-CG	5.31	123.46	113.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	191	ARG	Sidechain

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	R	2165	0	2258	33	0
2	A	1655	0	1591	14	0
3	E	1776	0	1716	25	0
4	B	2600	0	2505	51	0
5	G	429	0	441	7	0
6	N	961	0	928	12	0
7	R	32	0	0	1	0
All	All	9618	0	9439	131	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.

The worst 5 of 131 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:R:255:GLU:HB3	2:A:198:VAL:HG11	1.61	0.82
4:B:294:CYS:HB2	4:B:308:LEU:HB2	1.67	0.77
4:B:160:SER:HB3	4:B:190:LEU:HD23	1.69	0.75
4:B:271:CYS:HB2	4:B:290:ASP:HB2	1.68	0.74
2:A:101:ASN:OD1	4:B:57:LYS:NZ	2.23	0.71

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	R	267/612 (44%)	247 (92%)	18 (7%)	2 (1%)	18	35
2	A	204/246 (83%)	201 (98%)	3 (2%)	0	100	100
3	E	227/267 (85%)	216 (95%)	11 (5%)	0	100	100
4	B	336/345 (97%)	327 (97%)	9 (3%)	0	100	100
5	G	54/70 (77%)	53 (98%)	1 (2%)	0	100	100
6	N	124/140 (89%)	120 (97%)	4 (3%)	0	100	100
All	All	1212/1680 (72%)	1164 (96%)	46 (4%)	2 (0%)	44	62

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	156	GLN
1	R	253	THR

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	R	240/531 (45%)	235 (98%)	5 (2%)	47	70
2	A	169/213 (79%)	164 (97%)	5 (3%)	36	60
3	E	195/216 (90%)	191 (98%)	4 (2%)	47	70
4	B	281/287 (98%)	272 (97%)	9 (3%)	34	59
5	G	45/57 (79%)	44 (98%)	1 (2%)	45	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	N	104/116 (90%)	100 (96%)	4 (4%)	29 54
All	All	1034/1420 (73%)	1006 (97%)	28 (3%)	40 63

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	27	ASP
6	N	104	THR
4	B	175	GLN
6	N	5	GLN
4	B	118	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
6	N	82	GLN
4	B	175	GLN
3	E	2	GLN
2	A	244	ASN
3	E	81	GLN

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](#)

1 ligand is 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
7	A1EL6	R	601	-	32,34,34	1.68	3 (9%)	39,49,49	2.63	14 (35%)

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
7	A1EL6	R	601	-	-	16/28/29/29	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	R	601	A1EL6	C15-C09	6.84	1.59	1.51
7	R	601	A1EL6	C16-C15	3.72	1.40	1.37
7	R	601	A1EL6	C25-C20	2.64	1.46	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	R	601	A1EL6	O08-C02-C03	9.92	127.71	110.99
7	R	601	A1EL6	C16-C15-C09	6.07	128.42	119.82
7	R	601	A1EL6	C24-C15-C16	-5.36	113.56	118.68
7	R	601	A1EL6	O08-C02-O01	-3.43	117.00	123.40
7	R	601	A1EL6	C19-C28-N29	3.15	127.47	119.15

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

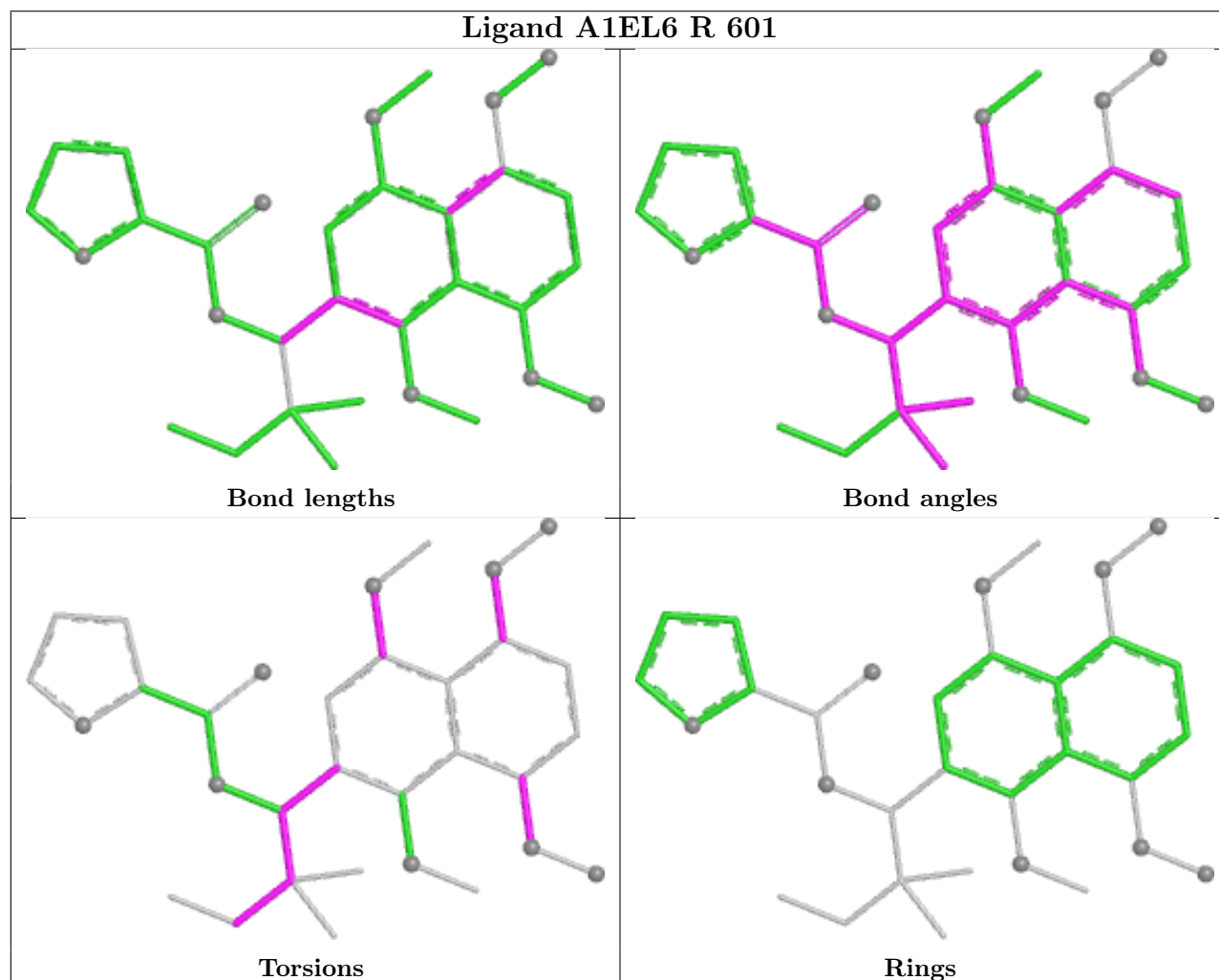
Mol	Chain	Res	Type	Atoms
7	R	601	A1EL6	C09-C10-C13-C14
7	R	601	A1EL6	C15-C09-C10-C11
7	R	601	A1EL6	O08-C09-C10-C11
7	R	601	A1EL6	C15-C09-C10-C12
7	R	601	A1EL6	O08-C09-C10-C12

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	R	601	A1EL6	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.

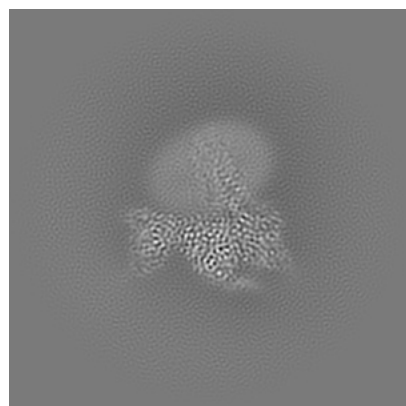
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61941. These allow visual inspection of the internal detail of the map and identification of artifacts.

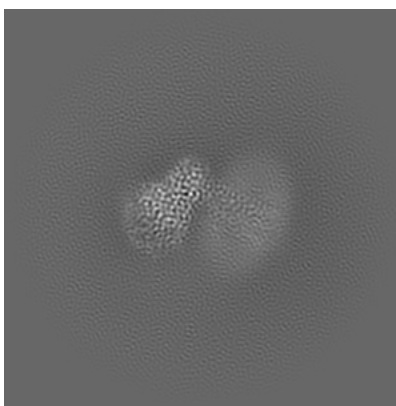
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

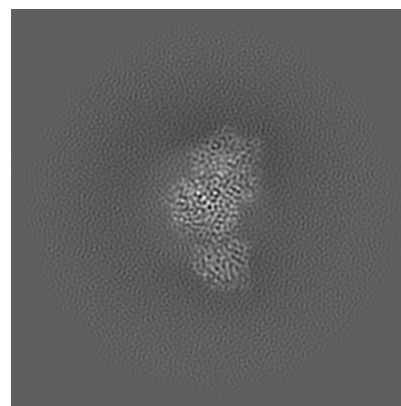
6.1.1 Primary map



X

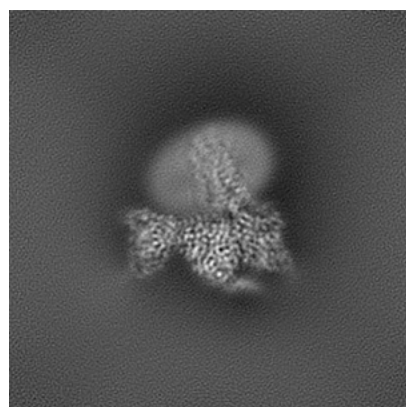


Y

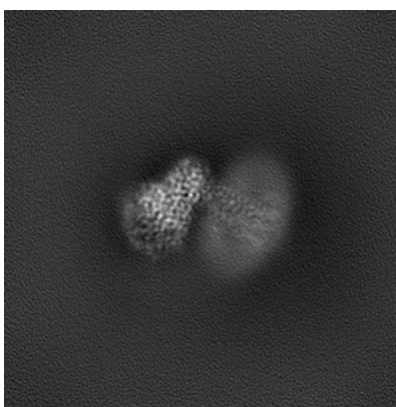


Z

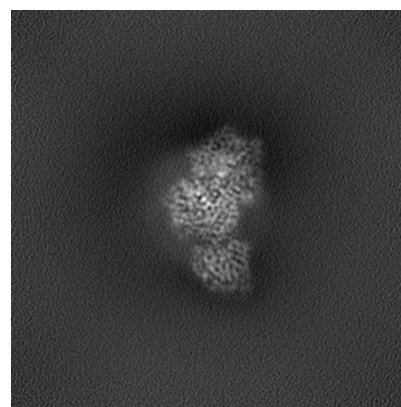
6.1.2 Raw map



X



Y

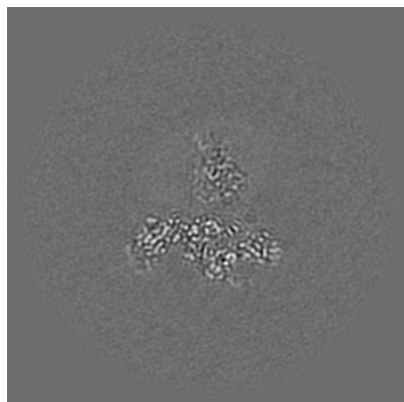


Z

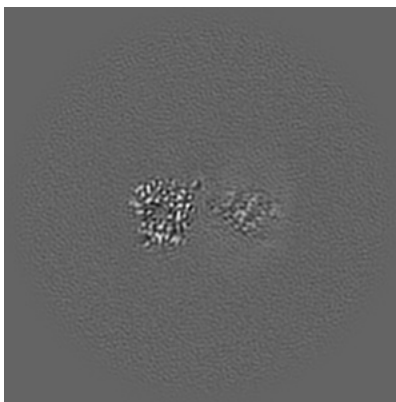
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

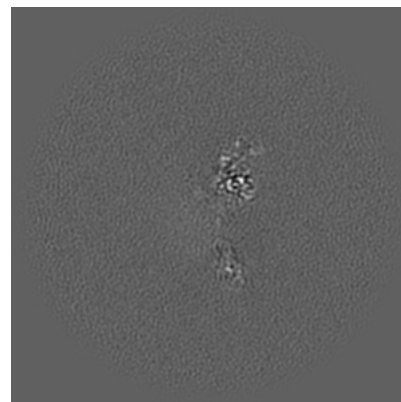
6.2.1 Primary map



X Index: 128

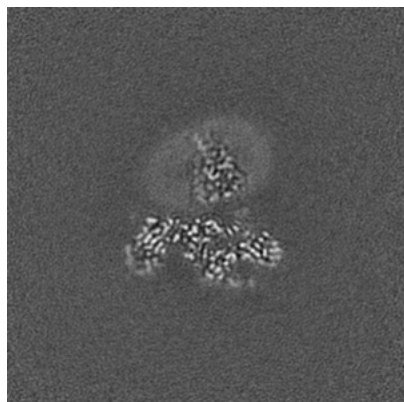


Y Index: 128

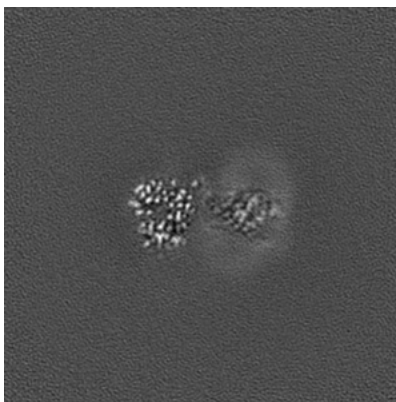


Z Index: 128

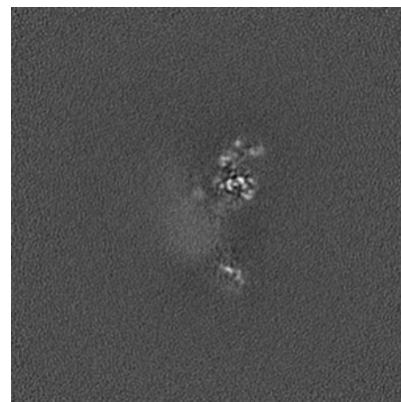
6.2.2 Raw map



X Index: 128



Y Index: 128

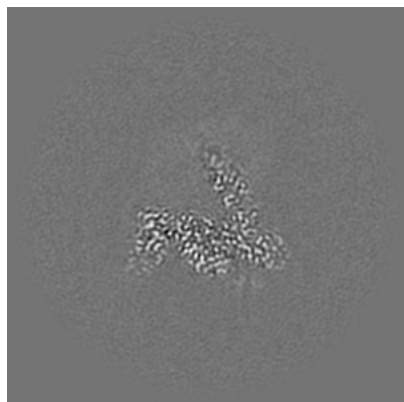


Z Index: 128

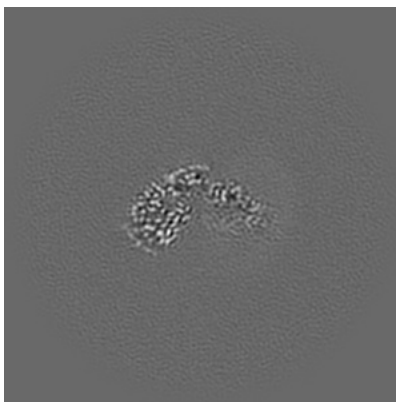
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

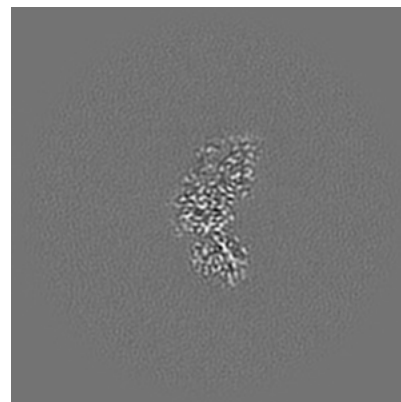
6.3.1 Primary map



X Index: 134

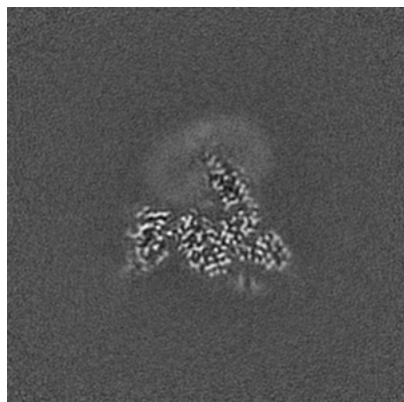


Y Index: 137

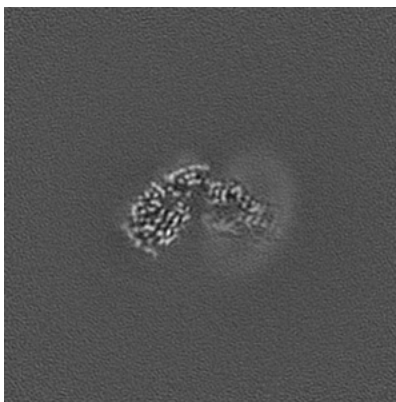


Z Index: 111

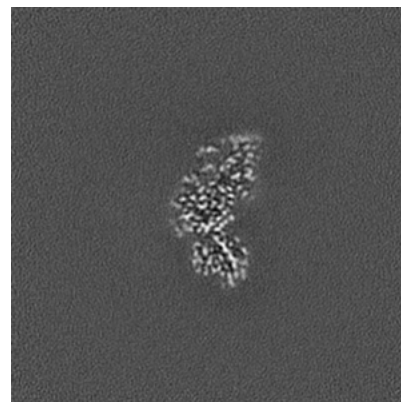
6.3.2 Raw map



X Index: 135



Y Index: 137

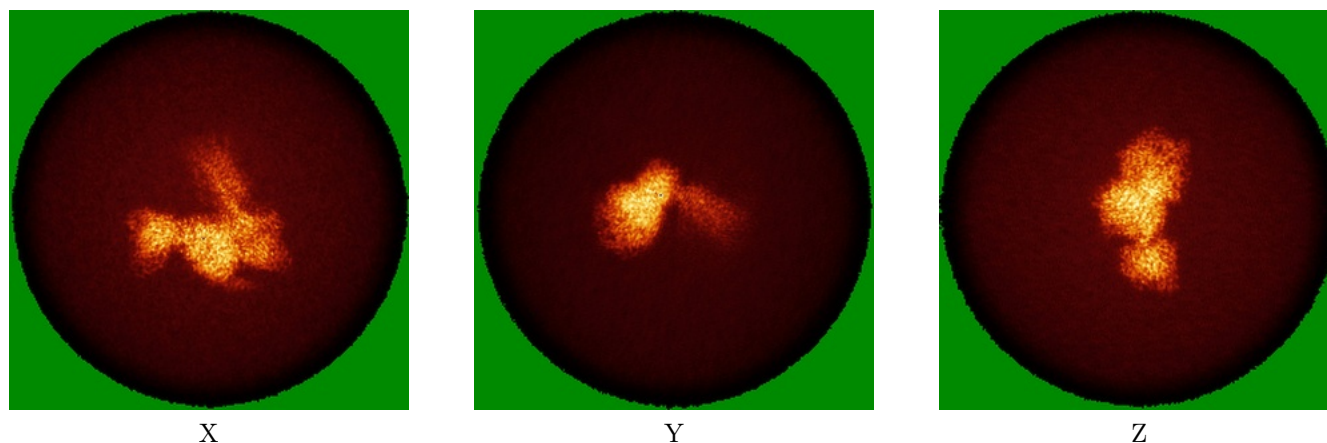


Z Index: 111

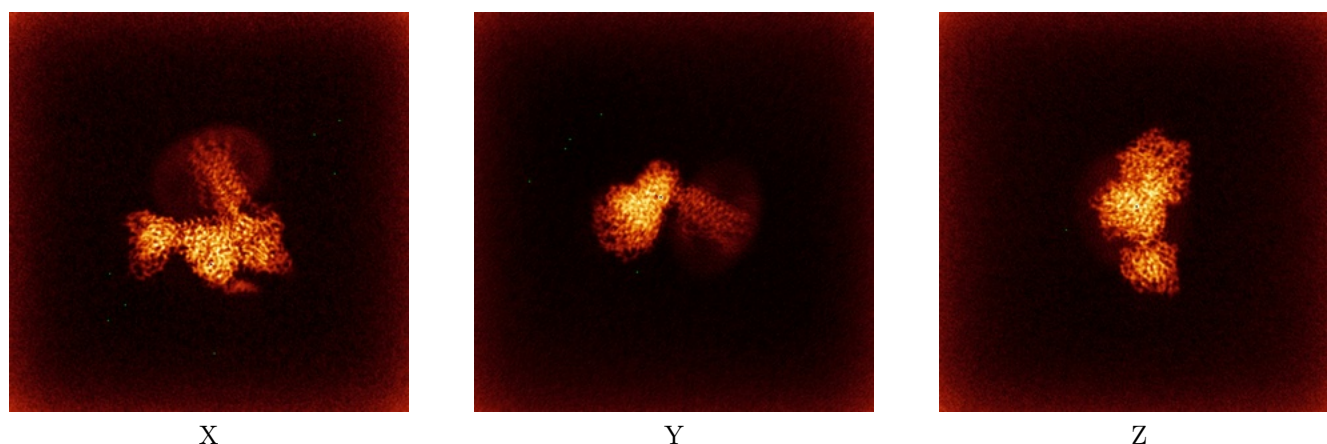
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

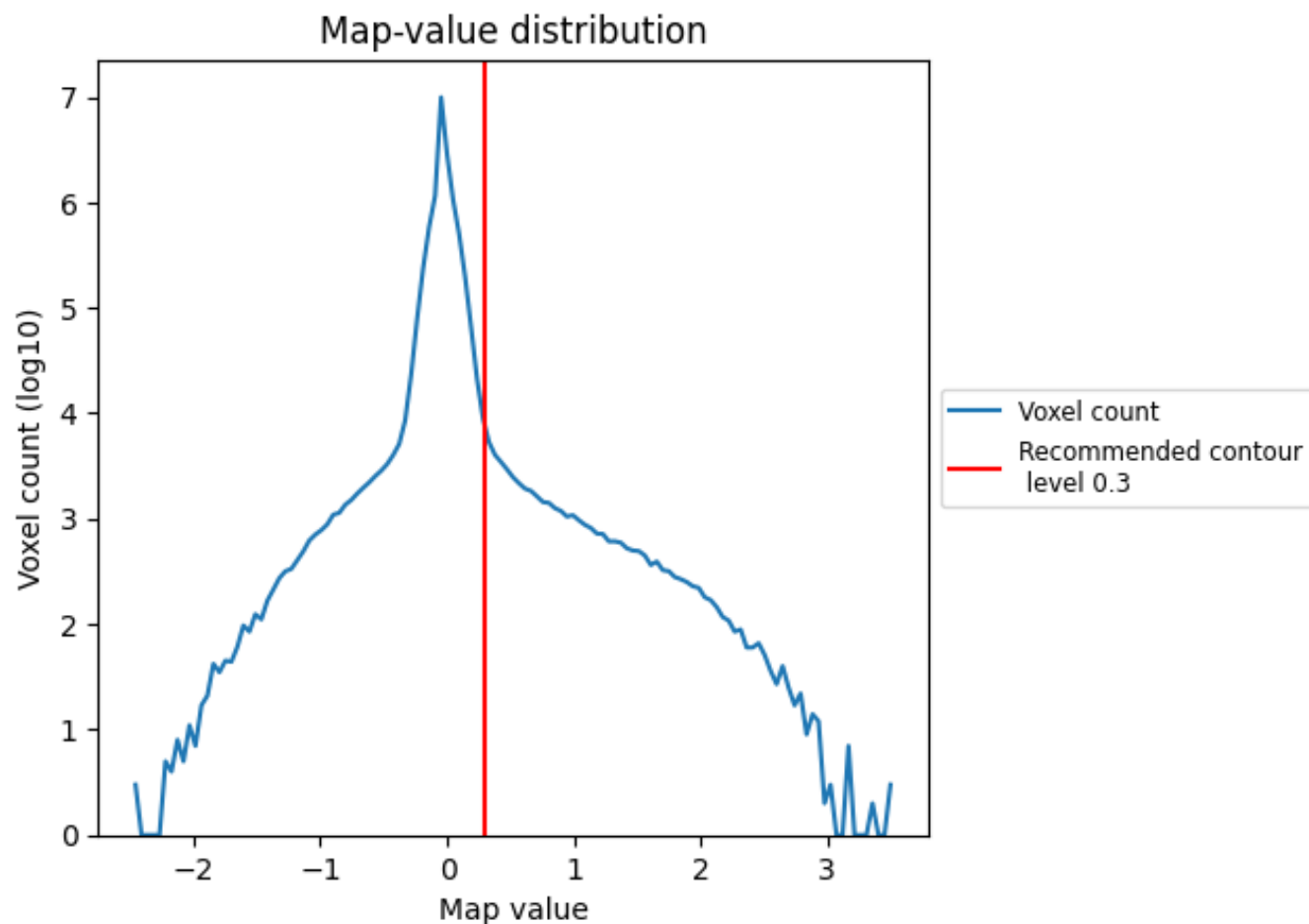
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

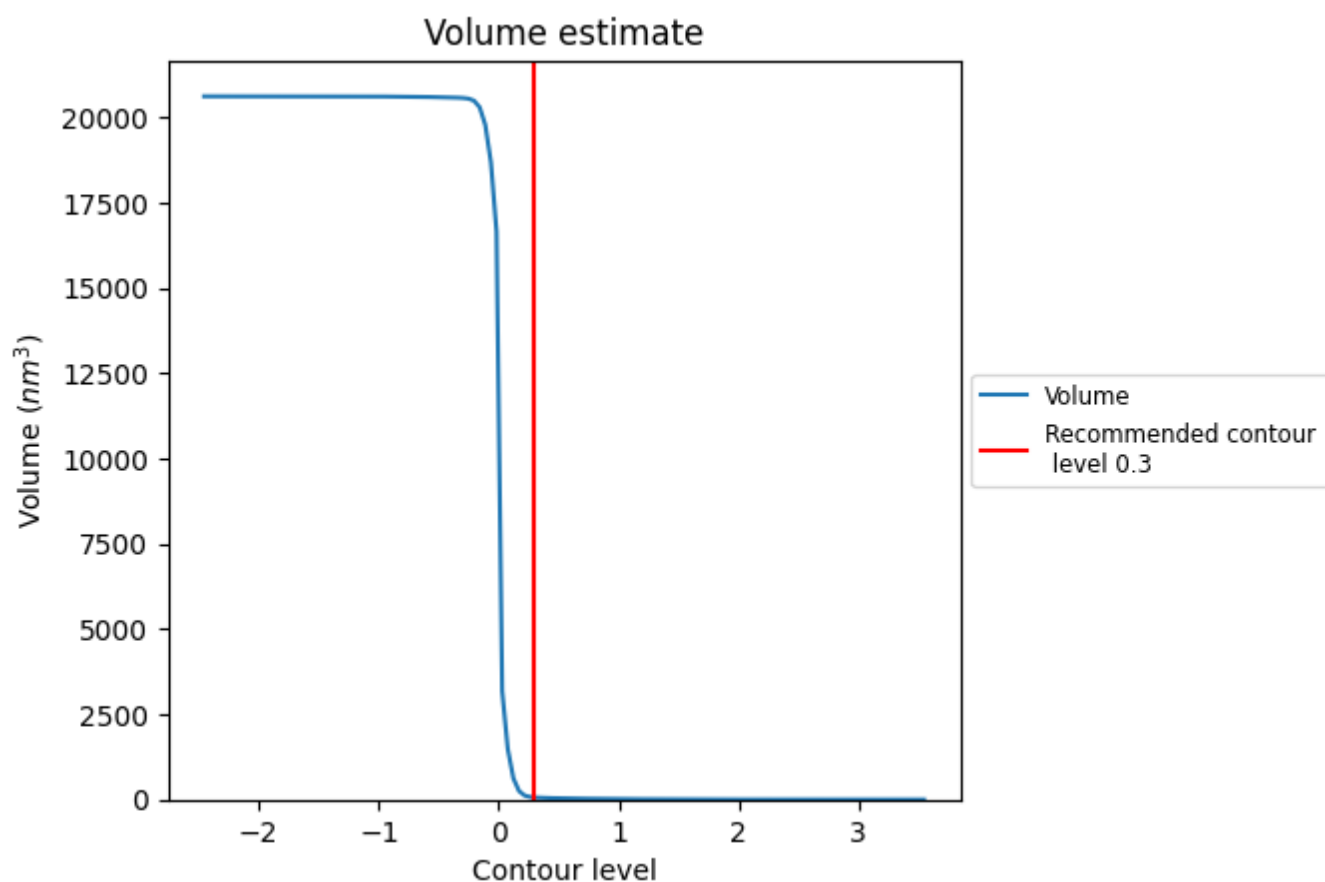
This section contains the results of statistical analysis of the map.

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.

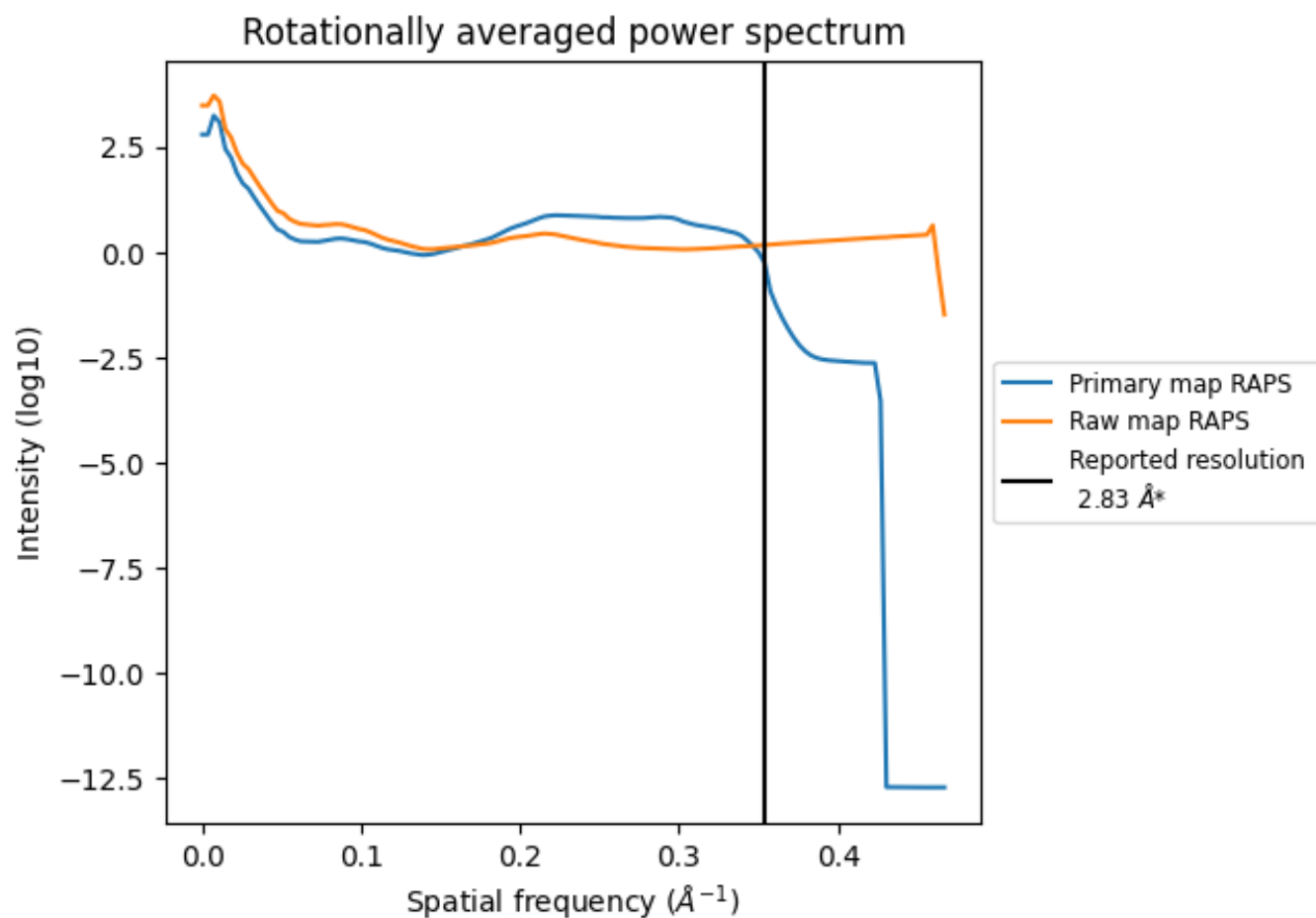
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 63 nm³; this corresponds to an approximate mass of 57 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 ⓘ

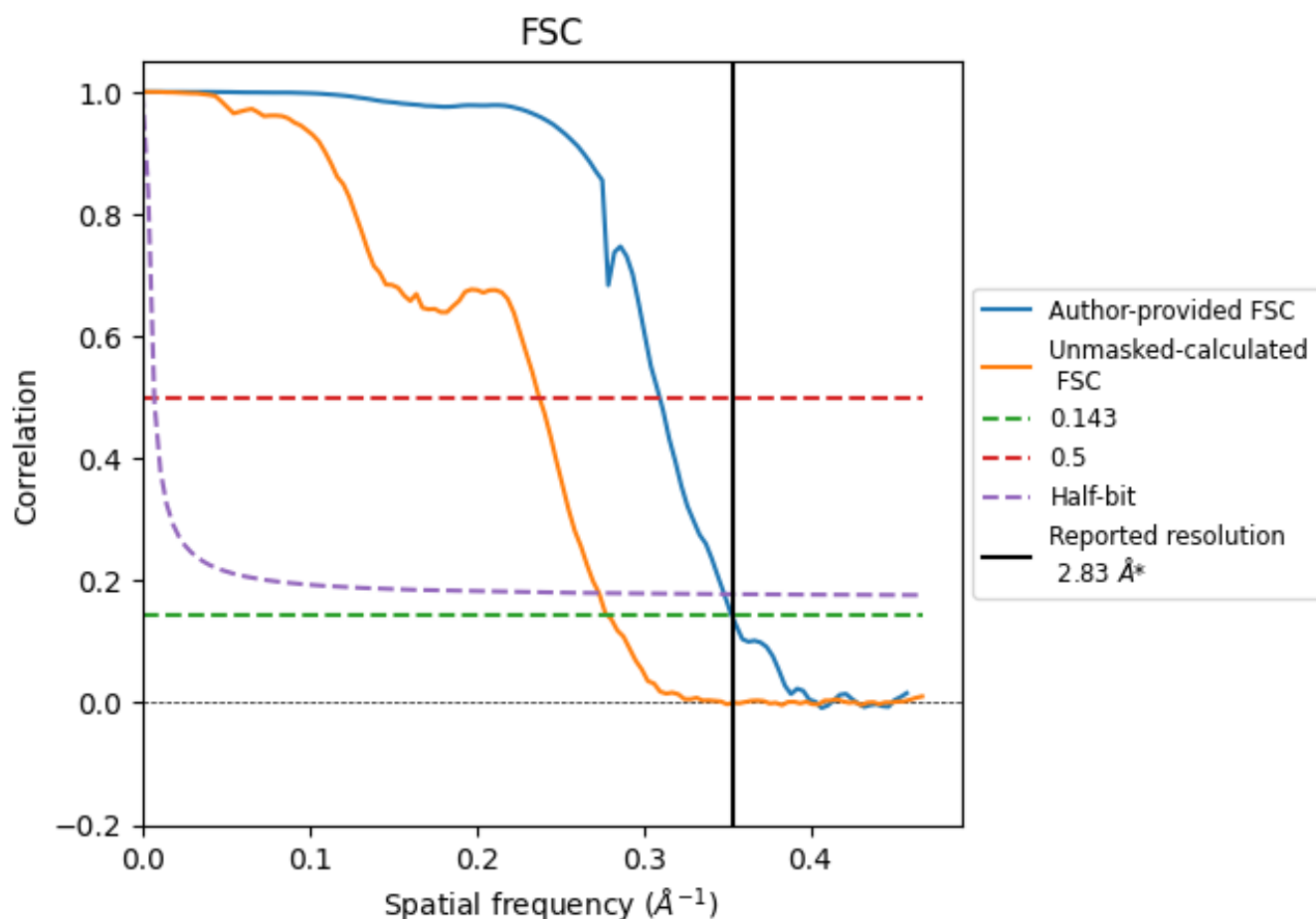


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

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 $0.353 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

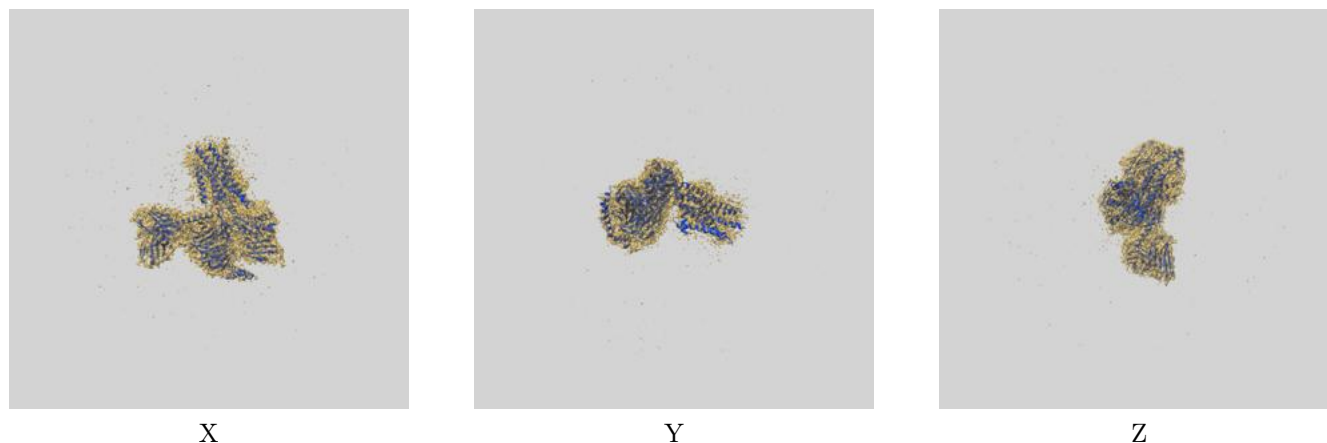
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.83	3.23	2.87
Unmasked-calculated*	3.59	4.21	3.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.59 differs from the reported value 2.83 by more than 10 %

9 Map-model fit [i](#)

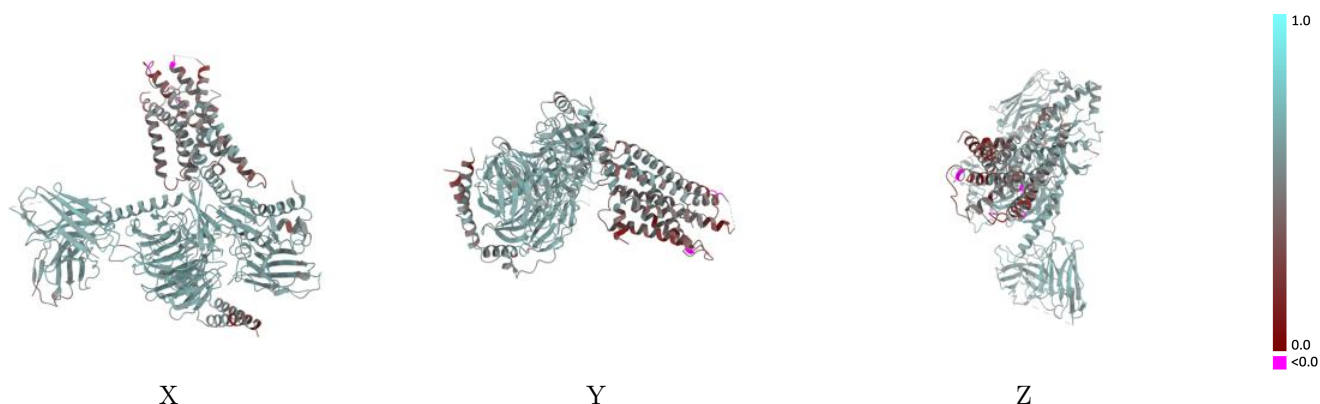
This section contains information regarding the fit between EMDB map EMD-61941 and PDB model 9K07. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.3 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](#)

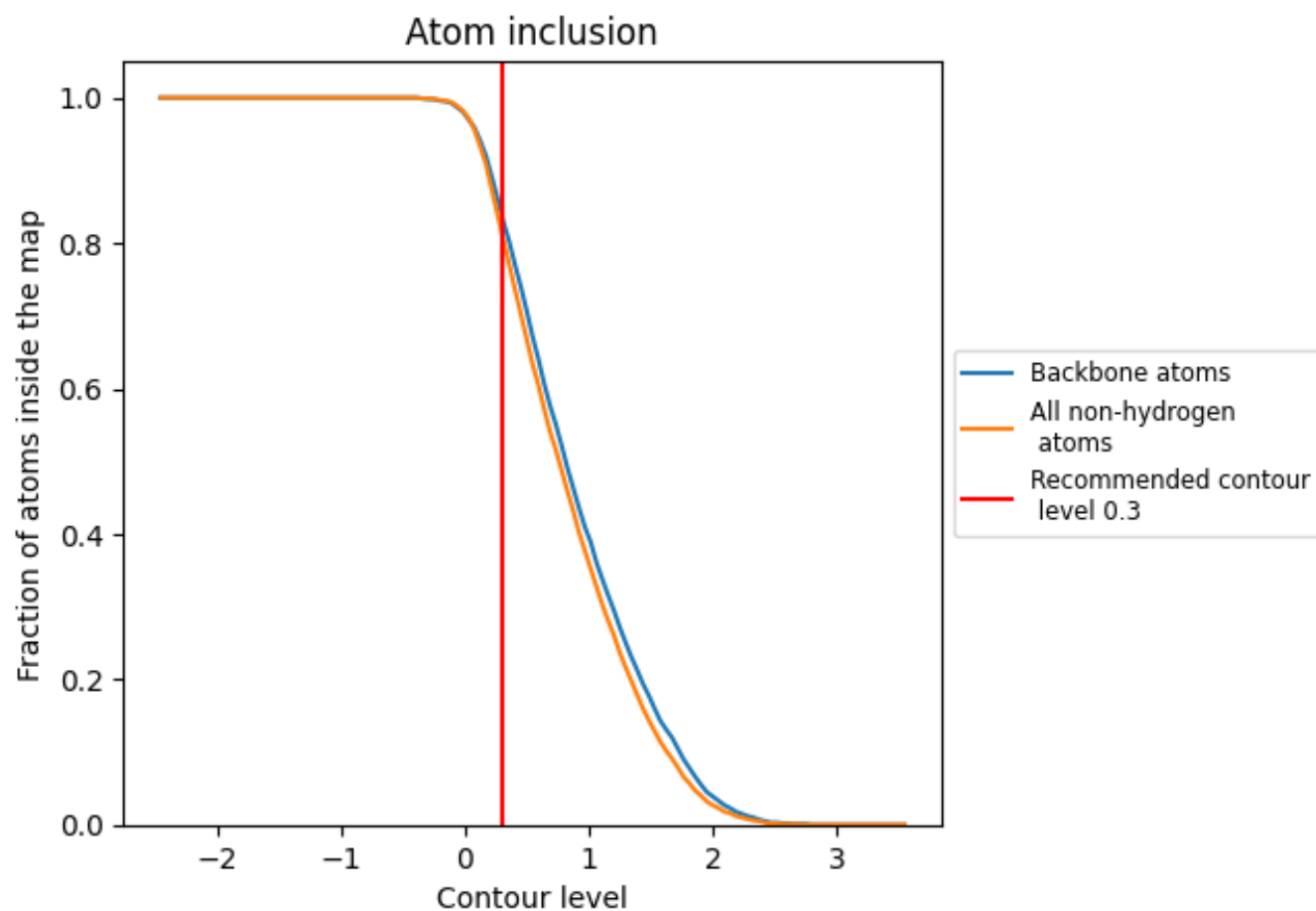


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8110	0.5470
A	0.8980	0.5870
B	0.9040	0.6010
E	0.8760	0.5860
G	0.7090	0.5180
N	0.8990	0.5910
R	0.5670	0.4060

