



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 03:15 AM UTC

PDB ID : 5VOT / pdb_00005vot
EMDB ID : EMD-8721
Title : Structure of AMPA receptor-TARP complex
Authors : Chen, S.; Zhao, Y.; Wang, Y.S.; Shekhar, M.; Tajkhorshid, E.; Gouaux, E.
Deposited on : 2017-05-03
Resolution : 4.90 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:

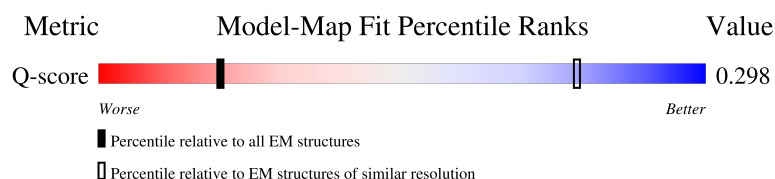
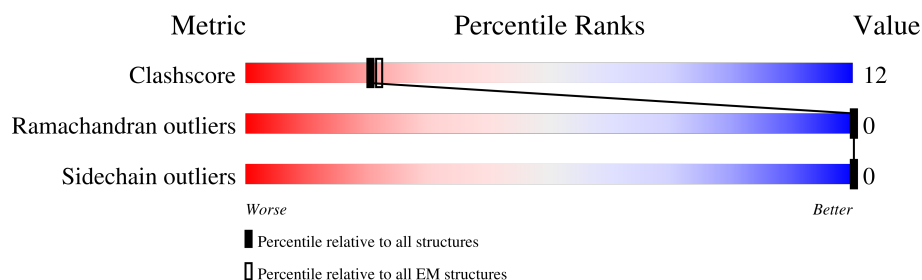
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.90 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	1274 (4.40 - 5.40)

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	889	 33% 13% 54%
1	B	889	 33% 13% 54%
1	C	889	 33% 13% 54%
1	D	889	 34% 12% 54%

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Mol	Chain	Length	Quality of chain
2	E	323	45%7%48%
2	F	323	42%12%46%
2	G	323	46%6%48%
2	H	323	42%12%46%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16463 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 Glutamate receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	408	Total	C	N	O	S	0	0
			3049	1976	487	565	21		
1	C	408	Total	C	N	O	S	0	0
			3046	1974	487	565	20		
1	D	409	Total	C	N	O	S	0	0
			3028	1961	490	560	17		
1	B	409	Total	C	N	O	S	0	0
			3028	1961	490	560	17		

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	586	ARG	GLN	conflict	UNP P19491
A	848	ASP	-	insertion	UNP P19491
A	849	TYR	-	insertion	UNP P19491
A	850	LYS	-	insertion	UNP P19491
A	851	ASP	-	insertion	UNP P19491
A	852	ASP	-	insertion	UNP P19491
A	853	ASP	-	insertion	UNP P19491
A	854	ASP	TYR	conflict	UNP P19491
C	586	ARG	GLN	conflict	UNP P19491
C	848	ASP	-	insertion	UNP P19491
C	849	TYR	-	insertion	UNP P19491
C	850	LYS	-	insertion	UNP P19491
C	851	ASP	-	insertion	UNP P19491
C	852	ASP	-	insertion	UNP P19491
C	853	ASP	-	insertion	UNP P19491
C	854	ASP	TYR	conflict	UNP P19491
D	586	ARG	GLN	conflict	UNP P19491
D	848	ASP	-	insertion	UNP P19491
D	849	TYR	-	insertion	UNP P19491
D	850	LYS	-	insertion	UNP P19491
D	851	ASP	-	insertion	UNP P19491
D	852	ASP	-	insertion	UNP P19491

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Chain	Residue	Modelled	Actual	Comment	Reference
D	853	ASP	-	insertion	UNP P19491
D	854	ASP	TYR	conflict	UNP P19491
B	586	ARG	GLN	conflict	UNP P19491
B	848	ASP	-	insertion	UNP P19491
B	849	TYR	-	insertion	UNP P19491
B	850	LYS	-	insertion	UNP P19491
B	851	ASP	-	insertion	UNP P19491
B	852	ASP	-	insertion	UNP P19491
B	853	ASP	-	insertion	UNP P19491
B	854	ASP	TYR	conflict	UNP P19491

- Molecule 2 is a protein called Voltage-dependent calcium channel gamma-2 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	169	Total	C	N	O	S	0	0
			1007	645	173	186	3		
2	F	175	Total	C	N	O	S	0	0
			1149	750	183	209	7		
2	G	169	Total	C	N	O	S	0	0
			1007	645	173	186	3		
2	H	175	Total	C	N	O	S	0	0
			1149	750	183	209	7		

R824	M825	LYS	VAL	ALA	LYS	ASN	PRO	GLN	ASN	ILE	ASN	PRO	SER	SER	SER	GLN	GLY	ASN	SER	GLN	ASN	PHE	ALA	SER	THR	ASP	TYR	LYS	ASP	ASP	ASP	LYS	GLU	GLY	TYR	ASN	GLY	VAL	TYR	GLY	ILE	GLU	SER	SER	VAL	LYS	ILE
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• Molecule 1: Glutamate receptor 2

Chain C:



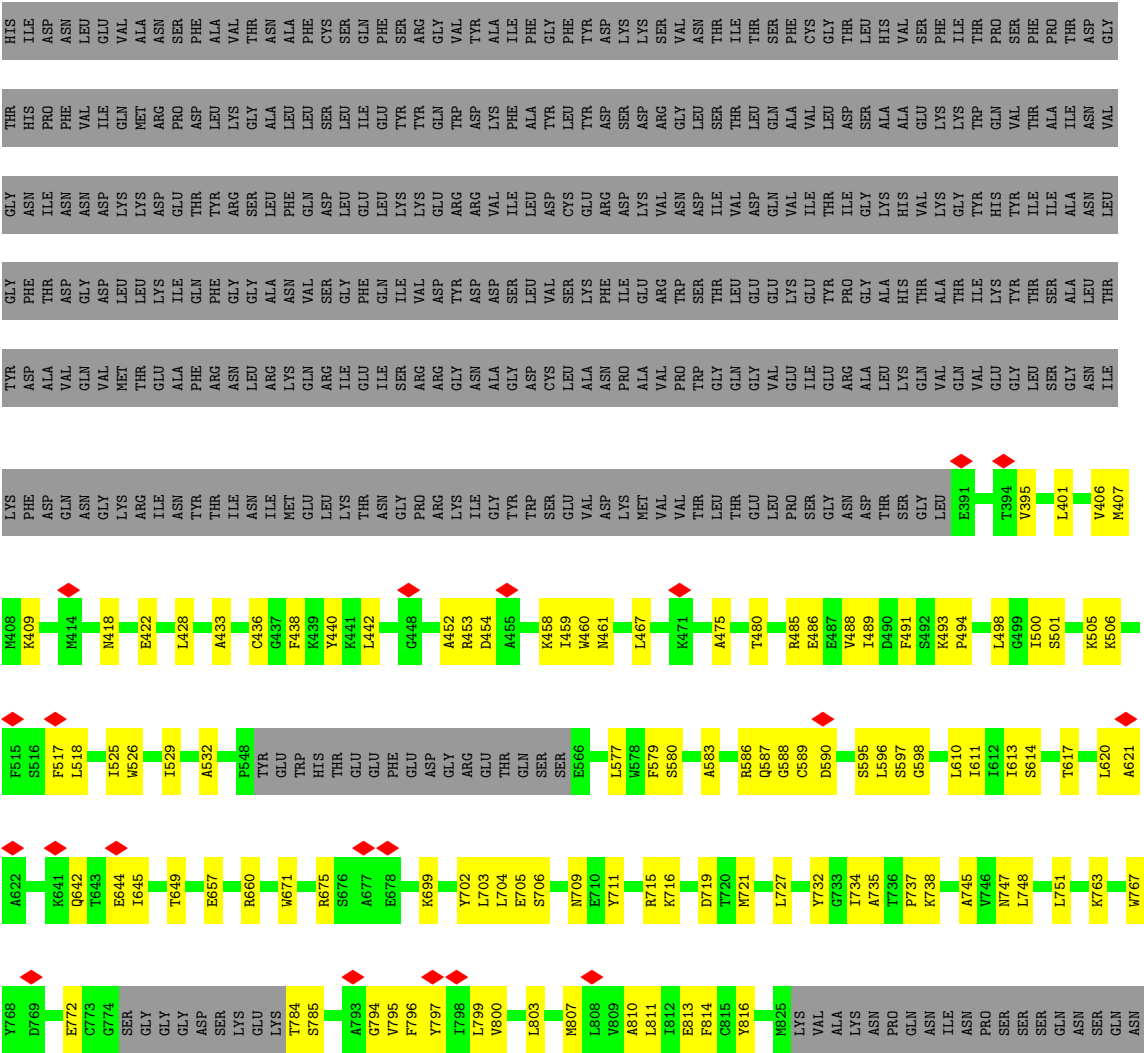
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HIS	ILE	ASP	ASN	VAL	GLY	GLY	VAL	ALA	ALA	SER	PHE	LEU	LEU	VAL	THR	ALA	ASN	ALA	PHE	GLY	CYS	SER	GLN	PHE	VAL	SER	THR	TYR	VAL	ALA	ALA	LYS	LYS	ASP	ASP	GLY	VAL	ASP	ASP	GLY	VAL	GLN	SER	SER	THR	PRO	THR	GLY
THR	HIS	PRO	PHE	VAL	ASN	ILE	GLY	MET	GLN	LYS	ASP	ARG	LEU	GLY	THR	ALA	LEU	ALA	VAL	GLY	GLY	THR	ILE	GLY	VAL	THR	TRP	ASP	TRP	GLY	VAL	ASP	ASP	GLY	VAL	ASP	GLY	VAL	ASP	GLY	VAL	GLN	GLY	THR	THR	ALA	VAL	
GLY	ASN	ILE	THR	ASN	GLY	LYS	LYS	LEU	LEU	LYS	LYS	THR	PHE	GLY	GLY	ALA	ASN	VAL	VAL	SER	SER	PHE	GLY	THR	VAL	THR	ASP	ARG	GLY	VAL	ASP	ASP	GLY	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
GLY	PHE	THR	ASP	GLY	ASP	GLY	VAL	LEU	LEU	LYS	LYS	THR	PHE	GLY	GLY	ALA	ASN	VAL	VAL	SER	SER	PHE	GLY	THR	VAL	THR	ASP	ARG	GLY	VAL	ASP	ASP	GLY	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
TYR	ASP	ALA	VAL	GLN	GLY	VAL	MET	THR	THR	GLY	ALA	PHE	ARG	ASN	ASN	LEU	GLY	ILE	ILE	ARG	GLY	GLY	THR	VAL	THR	ASP	GLY	GLY	ASN	GLY	ALA	PRO	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
LYS	PHE	ASP	GLN	ASN	GLY	LYS	ARG	THR	THR	ILE	ASN	ILE	ASN	ASN	ASN	GLY	GLY	THR	THR	ASN	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
S403	P404	Y405	Y406	Y407	Y408	Y409	Y410	Y411	Y412	Y413	Y414	Y415	Y416	Y417	Y418	Y419	Y420	Y421	Y422	Y423	Y424	Y425	Y426	Y427	Y428	Y429	Y430	Y431	Y432	Y433	Y434	Y435	Y436	Y437	Y438	Y439	Y440	Y441	Y442	Y443	Y444	Y445	Y446	Y447	Y448	Y449	Y450	
1500	F517	A522	Y523	E524	Y525	Y526	Y527	Y528	Y529	Y530	Y531	Y532	Y533	Y534	Y535	Y536	Y537	Y538	Y539	Y540	Y541	Y542	Y543	Y544	Y545	Y546	Y547	Y548	Y549	Y550	Y551	Y552	Y553	Y554	Y555	Y556	Y557	Y558	Y559	Y560	Y561	Y562	Y563	Y564	Y565	Y566	Y567	
F608	T609	I612	F613	S614	S615	A618	N619	A622	F623	L624	T625	V626	E627	R628	H629	V630	S631	E634	S635	S640	R641	Q642	T643	I645	G648	T649	E657	R660	S676	A677	E678	V681	R692	S696	L703	L704	E705	Y711	R715	K716	L727							
K730	G731	Y732	Y733	Y734	A735	Y736	Y737	Y738	Y739	Y740	A745	Y746	N747	L748	L751	Y752	L753	Q756	K763	Y767	E772	G773	G774	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
I812	E813	F814	C815	Y816	R817	S818	A822	R825	LYS	VAL	ALA	LYS	ASN	PRO	GLN	ASN	ILE	ASN	PRO	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER

• Molecule 1: Glutamate receptor 2

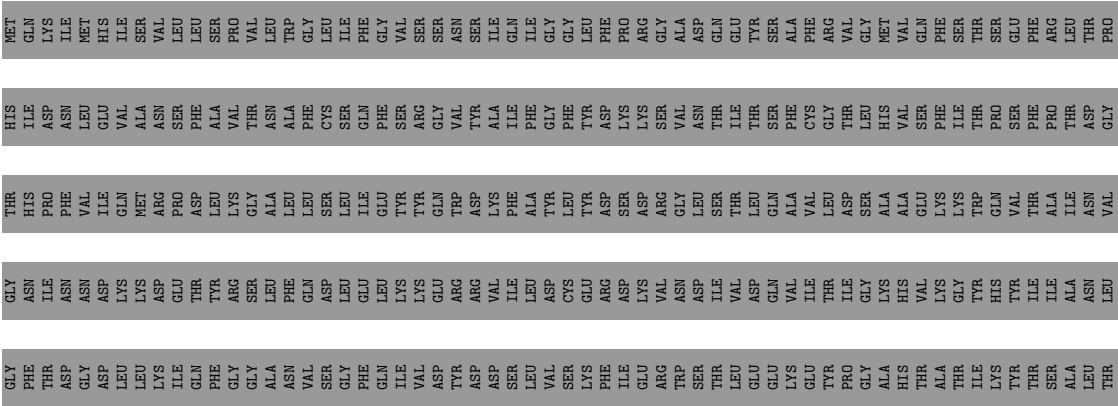
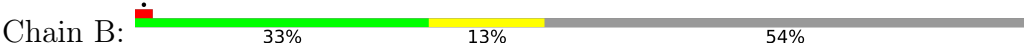
Chain D:

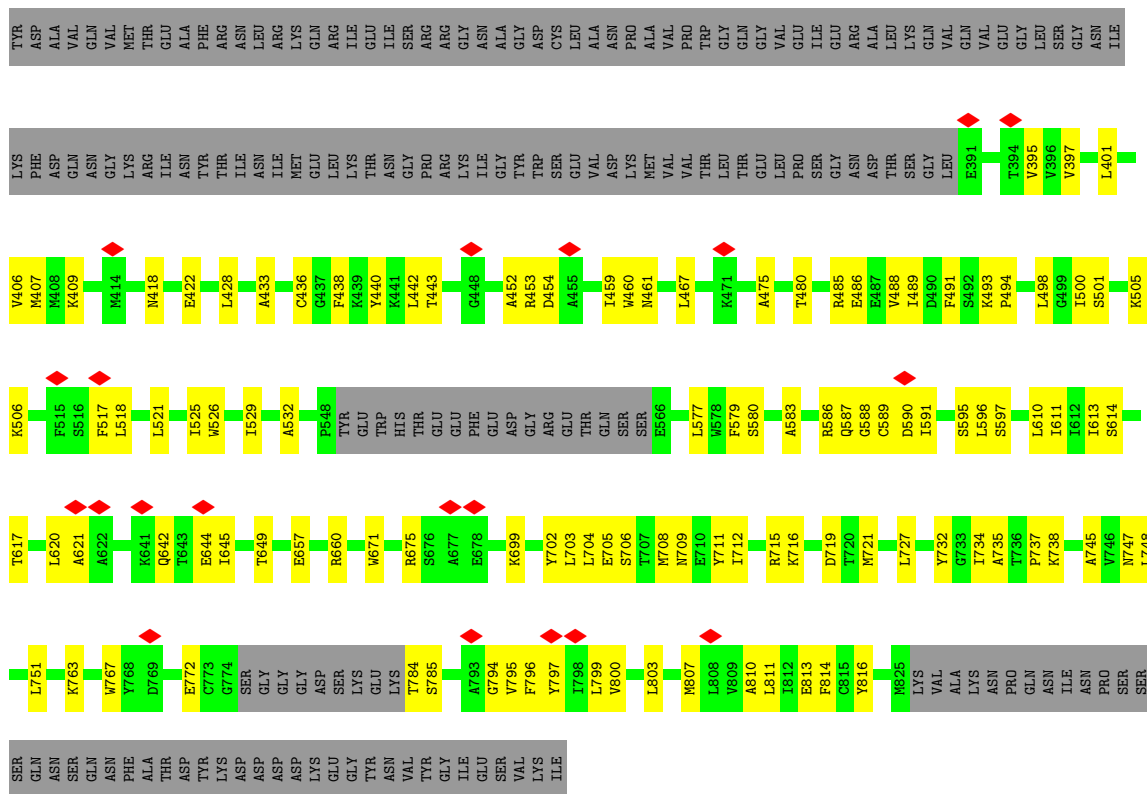


MET	GLN	LYS	ILE	MET	GLY	HIS	ILE	SER	VAL	VAL	GLY	THR	PRO	SER	SER	GLN	GLY	ILE	ASN	SER	GLN	PHE	GLY	VAL	SER	THR	ASP	TYR	LYS	ASP	ASP	LYS	GLU	GLY	TYR	ASN	GLY	VAL	TYR	GLY	ILE	GLU	SER	SER	VAL	LYS	ILE
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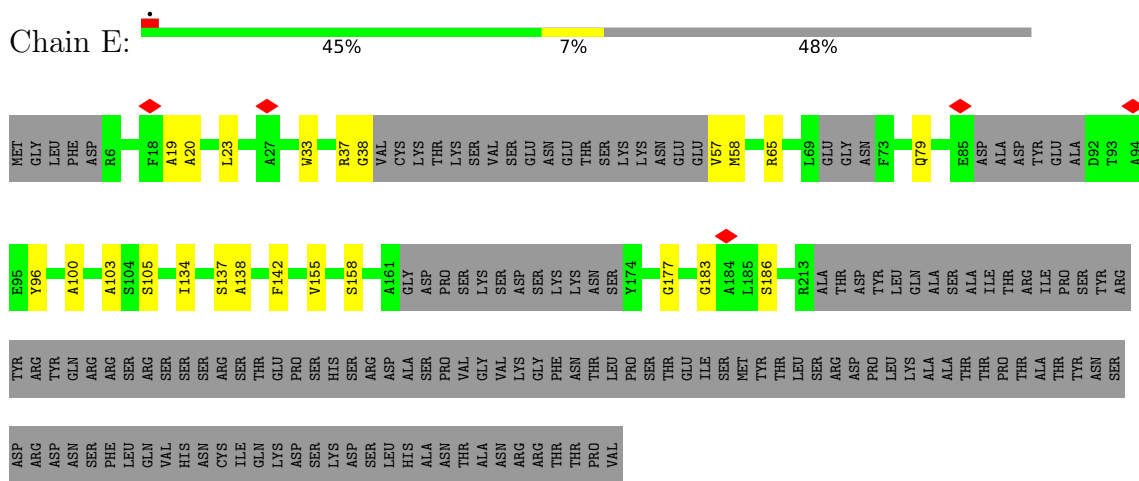


● Molecule 1: Glutamate receptor 2

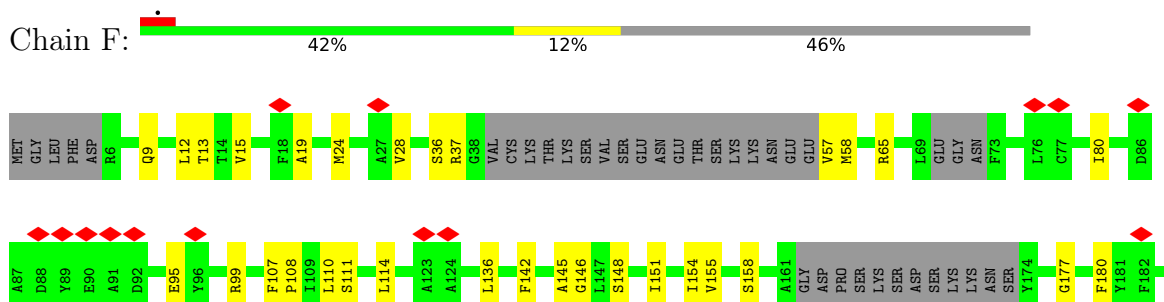


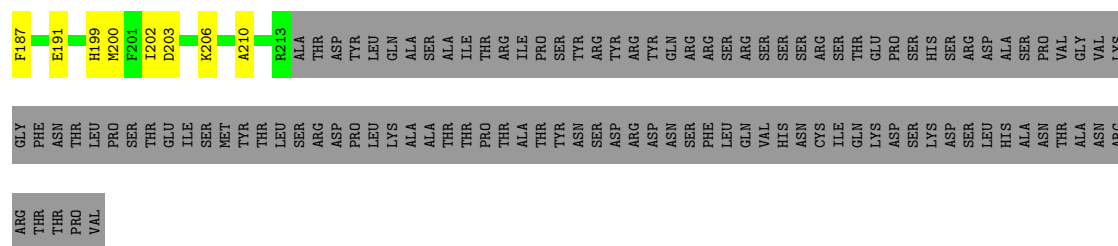


- Molecule 2: Voltage-dependent calcium channel gamma-2 subunit

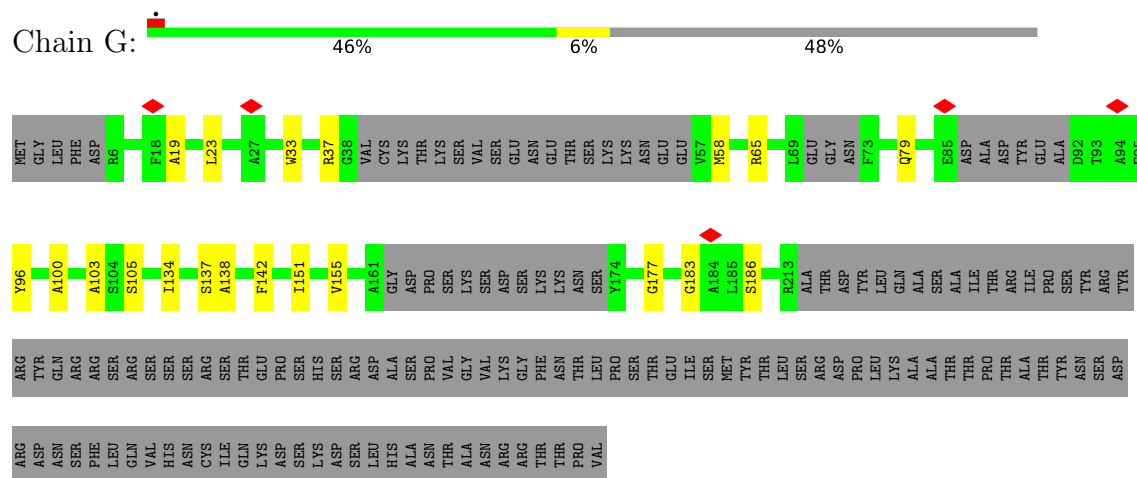


- Molecule 2: Voltage-dependent calcium channel gamma-2 subunit

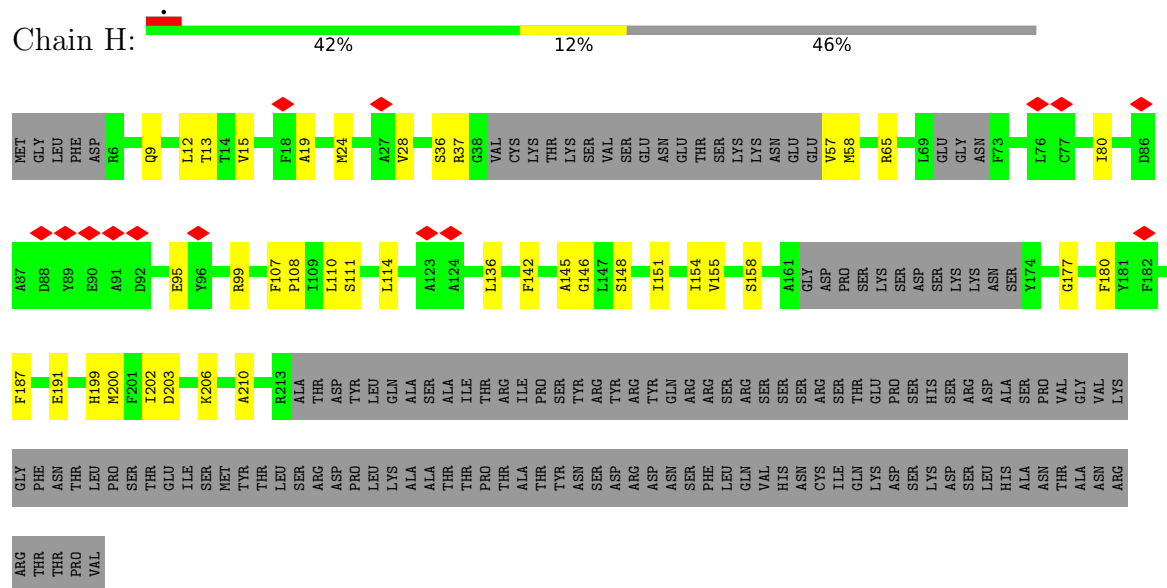




• Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



• Molecule 2: Voltage-dependent calcium channel gamma-2 subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	144150	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 ($e^-/\text{\AA}^2$)	54	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	0.356	Depositor
Minimum map value	-0.201	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	430.0, 430.0, 430.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.72, 1.72, 1.72	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	1/3115 (0.0%)	0.45	3/4223 (0.1%)
1	B	0.19	0/3092	0.40	0/4195
1	C	0.19	0/3112	0.40	1/4220 (0.0%)
1	D	0.19	0/3092	0.40	0/4195
2	E	0.15	0/1021	0.29	0/1401
2	F	0.15	0/1169	0.32	0/1601
2	G	0.14	0/1021	0.29	0/1401
2	H	0.15	0/1169	0.32	0/1601
All	All	0.21	1/16791 (0.0%)	0.39	4/22837 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	588	GLY	C-N	15.02	1.53	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	588	GLY	O-C-N	8.21	139.27	123.02
1	A	588	GLY	CA-C-N	-8.03	104.45	121.32
1	A	588	GLY	C-N-CA	-8.03	104.45	121.32
1	C	795	VAL	N-CA-C	-5.55	108.09	113.53

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	3049	0	2942	82	0
1	B	3028	0	2916	86	0
1	C	3046	0	2935	86	0
1	D	3028	0	2916	84	0
2	E	1007	0	718	13	0
2	F	1149	0	981	26	0
2	G	1007	0	718	11	0
2	H	1149	0	981	26	0
All	All	16463	0	15107	382	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 12.

All (382) 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:C:792:VAL:O	1:C:796:PHE:HB2	1.70	0.90
1:A:792:VAL:O	1:A:796:PHE:HB2	1.73	0.88
1:B:586:ARG:NH2	1:B:613:ILE:HD11	1.95	0.81
1:A:475:ALA:HB3	1:A:735:ALA:HB3	1.63	0.79
1:D:586:ARG:NH2	1:D:613:ILE:HD11	1.97	0.79
1:C:475:ALA:HB3	1:C:735:ALA:HB3	1.63	0.78
1:B:813:GLU:O	1:B:816:TYR:HB3	1.84	0.78
1:D:813:GLU:O	1:D:816:TYR:HB3	1.83	0.77
1:B:475:ALA:HB3	1:B:735:ALA:HB3	1.70	0.74
1:A:493:LYS:HG2	1:A:747:ASN:HD21	1.52	0.74
1:D:475:ALA:HB3	1:D:735:ALA:HB3	1.70	0.74
1:B:586:ARG:NH2	1:B:613:ILE:CD1	2.53	0.72
1:A:606:TRP:HA	1:A:609:THR:HG22	1.71	0.72
1:C:493:LYS:HG2	1:C:747:ASN:HD21	1.53	0.72
1:C:480:THR:O	1:C:485:ARG:NH1	2.23	0.71
1:D:586:ARG:NH2	1:D:613:ILE:CD1	2.54	0.71
1:C:586:ARG:HD2	1:D:586:ARG:HG2	1.73	0.70
1:C:606:TRP:HA	1:C:609:THR:HG22	1.71	0.70
1:A:792:VAL:O	1:A:796:PHE:CB	2.40	0.69
1:A:586:ARG:HD2	1:B:586:ARG:HG2	1.74	0.69
1:A:500:ILE:HB	1:A:727:LEU:HB2	1.74	0.69
1:C:792:VAL:O	1:C:796:PHE:CB	2.41	0.69
1:C:500:ILE:HB	1:C:727:LEU:HB2	1.74	0.68
1:A:480:THR:O	1:A:485:ARG:NH1	2.23	0.68
2:H:206:LYS:O	2:H:210:ALA:HB2	1.94	0.67
1:A:489:ILE:HA	1:A:738:LYS:HB2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:642:GLN:NE2	1:A:645:ILE:O	2.27	0.67
1:C:489:ILE:HA	1:C:738:LYS:HB2	1.76	0.66
1:C:476:ILE:HG12	1:C:734:ILE:HD12	1.77	0.66
1:C:763:LYS:O	1:C:767:TRP:HB2	1.95	0.66
1:D:501:SER:HB2	1:D:709:ASN:HD22	1.60	0.66
1:D:811:LEU:HA	1:D:814:PHE:HD2	1.60	0.66
2:E:138:ALA:O	2:E:142:PHE:HB2	1.96	0.65
2:G:138:ALA:O	2:G:142:PHE:HB2	1.96	0.65
1:B:501:SER:HB2	1:B:709:ASN:HD22	1.60	0.65
1:B:811:LEU:HA	1:B:814:PHE:HD2	1.61	0.65
1:A:476:ILE:HG12	1:A:734:ILE:HD12	1.77	0.65
1:C:642:GLN:NE2	1:C:645:ILE:O	2.27	0.65
1:C:812:ILE:O	1:C:816:TYR:HB2	1.97	0.65
1:A:763:LYS:O	1:A:767:TRP:HB2	1.97	0.65
1:D:657:GLU:OE1	1:D:660:ARG:NH2	2.31	0.64
2:F:206:LYS:O	2:F:210:ALA:HB2	1.97	0.64
1:B:657:GLU:OE1	1:B:660:ARG:NH2	2.31	0.63
1:A:812:ILE:O	1:A:816:TYR:HB2	1.98	0.63
1:A:402:GLU:O	1:A:406:VAL:N	2.32	0.63
1:C:657:GLU:OE1	1:C:660:ARG:NH2	2.32	0.63
2:H:108:PRO:O	2:H:111:SER:OG	2.13	0.63
1:A:657:GLU:OE1	1:A:660:ARG:NH2	2.32	0.62
2:H:199:HIS:HD2	2:H:202:ILE:HD11	1.64	0.62
1:B:642:GLN:NE2	1:B:645:ILE:O	2.30	0.62
1:C:452:ALA:N	1:C:461:ASN:OD1	2.32	0.62
1:C:412:HIS:HA	1:C:415:LEU:HD12	1.82	0.61
2:F:199:HIS:HD2	2:F:202:ILE:HD11	1.65	0.61
2:H:36:SER:HA	2:H:58:MET:HA	1.82	0.61
1:D:763:LYS:O	1:D:767:TRP:HB2	2.01	0.61
1:B:480:THR:O	1:B:485:ARG:NH1	2.30	0.60
1:C:402:GLU:O	1:C:406:VAL:N	2.32	0.60
2:F:108:PRO:O	2:F:111:SER:OG	2.13	0.60
2:F:36:SER:HA	2:F:58:MET:HA	1.83	0.60
2:H:206:LYS:O	2:H:210:ALA:CB	2.50	0.60
2:H:15:VAL:O	2:H:19:ALA:HB2	2.02	0.60
2:H:15:VAL:O	2:H:19:ALA:CB	2.50	0.60
1:B:763:LYS:O	1:B:767:TRP:HB2	2.02	0.60
1:C:546:PHE:HE1	2:H:136:LEU:HD13	1.66	0.60
1:D:500:ILE:HB	1:D:727:LEU:HB2	1.83	0.60
2:G:37:ARG:H	2:G:58:MET:HA	1.66	0.60
1:A:412:HIS:HA	1:A:415:LEU:HD12	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:15:VAL:O	2:F:19:ALA:CB	2.50	0.60
1:D:579:PHE:O	1:D:583:ALA:HB2	2.02	0.60
1:D:642:GLN:NE2	1:D:645:ILE:O	2.31	0.60
1:A:796:PHE:HE1	1:D:532:ALA:HB2	1.66	0.59
1:A:546:PHE:HE1	2:F:136:LEU:HD13	1.66	0.59
1:C:793:ALA:HA	1:C:796:PHE:HB3	1.84	0.59
2:F:206:LYS:O	2:F:210:ALA:CB	2.49	0.59
1:B:395:VAL:O	1:B:440:TYR:HA	2.01	0.59
2:E:138:ALA:O	2:E:142:PHE:CB	2.51	0.59
1:B:579:PHE:O	1:B:583:ALA:HB2	2.02	0.59
1:D:800:VAL:O	1:D:803:LEU:HB2	2.03	0.59
2:E:33:TRP:HA	2:E:177:GLY:H	1.67	0.59
2:G:138:ALA:O	2:G:142:PHE:CB	2.51	0.59
1:B:500:ILE:HB	1:B:727:LEU:HB2	1.83	0.59
2:F:15:VAL:O	2:F:19:ALA:HB2	2.01	0.59
1:D:644:GLU:OE2	1:D:699:LYS:NZ	2.28	0.59
1:D:480:THR:O	1:D:485:ARG:NH1	2.30	0.59
1:B:407:MET:N	1:B:422:GLU:O	2.28	0.59
1:D:702:TYR:CE2	1:D:704:LEU:HB3	2.38	0.58
1:D:395:VAL:O	1:D:440:TYR:HA	2.04	0.58
2:G:33:TRP:HA	2:G:177:GLY:H	1.68	0.58
1:B:702:TYR:CE2	1:B:704:LEU:HB3	2.38	0.58
1:A:402:GLU:HB2	1:A:405:TYR:HB2	1.86	0.58
1:A:649:THR:HG22	1:A:703:LEU:HB2	1.85	0.58
2:E:37:ARG:H	2:E:58:MET:HA	1.69	0.58
1:A:452:ALA:N	1:A:461:ASN:OD1	2.32	0.58
1:C:402:GLU:HB2	1:C:405:TYR:HB2	1.86	0.58
1:B:401:LEU:HD23	1:B:406:VAL:HG12	1.86	0.58
1:B:800:VAL:O	1:B:803:LEU:HB2	2.03	0.58
1:D:407:MET:N	1:D:422:GLU:O	2.28	0.57
1:D:401:LEU:HD23	1:D:406:VAL:HG12	1.86	0.57
1:C:649:THR:HG22	1:C:703:LEU:HB2	1.84	0.57
1:D:526:TRP:HA	1:D:529:ILE:HD12	1.86	0.57
1:A:586:ARG:CD	1:B:586:ARG:HG2	2.34	0.56
2:F:9:GLN:O	2:F:13:THR:OG1	2.14	0.56
1:A:486:GLU:HG3	1:D:751:LEU:HD13	1.87	0.56
1:C:818:SER:O	1:C:822:ALA:CB	2.54	0.56
1:A:793:ALA:HA	1:A:796:PHE:HB3	1.87	0.56
1:C:486:GLU:HG3	1:B:751:LEU:HD13	1.88	0.56
2:H:151:ILE:HA	2:H:154:ILE:HD12	1.87	0.56
1:C:586:ARG:CD	1:D:586:ARG:HG2	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:145:ALA:O	2:H:148:SER:OG	2.20	0.55
1:B:526:TRP:HA	1:B:529:ILE:HD12	1.86	0.55
1:A:395:VAL:N	1:A:439:LYS:O	2.32	0.55
1:C:796:PHE:HE1	1:B:532:ALA:HB2	1.71	0.55
1:D:452:ALA:N	1:D:461:ASN:OD1	2.29	0.55
2:F:151:ILE:HA	2:F:154:ILE:HD12	1.87	0.55
1:C:615:SER:HA	1:D:620:LEU:HD22	1.89	0.55
1:B:610:LEU:O	1:B:614:SER:HB3	2.07	0.54
1:A:399:THR:HG23	1:A:444:ILE:HD13	1.89	0.54
1:A:438:PHE:HE2	1:A:440:TYR:HB3	1.71	0.54
1:B:595:SER:C	1:B:597:SER:H	2.15	0.54
1:B:610:LEU:O	1:B:614:SER:CB	2.56	0.54
1:B:644:GLU:OE2	1:B:699:LYS:NZ	2.28	0.54
1:A:608:PHE:CE1	1:B:796:PHE:HE1	2.26	0.54
1:C:395:VAL:N	1:C:439:LYS:O	2.33	0.54
1:A:603:GLY:HA2	1:A:606:TRP:CE3	2.42	0.54
2:E:38:GLY:O	2:E:57:VAL:N	2.41	0.54
2:F:187:PHE:O	2:F:191:GLU:HG2	2.08	0.54
1:C:818:SER:O	1:C:822:ALA:HB2	2.08	0.54
1:D:610:LEU:O	1:D:614:SER:CB	2.56	0.54
1:D:810:ALA:O	1:D:813:GLU:HB3	2.08	0.54
1:B:810:ALA:O	1:B:813:GLU:HB3	2.08	0.54
1:A:397:VAL:HB	1:A:441:LYS:O	2.07	0.54
1:A:615:SER:HA	1:B:620:LEU:HD22	1.89	0.54
1:C:438:PHE:HE2	1:C:440:TYR:HB3	1.71	0.54
2:F:37:ARG:N	2:F:57:VAL:O	2.41	0.54
2:F:65:ARG:HA	2:F:80:ILE:H	1.73	0.54
2:H:37:ARG:N	2:H:57:VAL:O	2.41	0.54
1:C:603:GLY:HA2	1:C:606:TRP:CE3	2.43	0.54
2:H:9:GLN:O	2:H:13:THR:OG1	2.14	0.54
2:H:65:ARG:HA	2:H:80:ILE:H	1.72	0.54
1:A:812:ILE:O	1:A:816:TYR:CB	2.56	0.54
1:C:397:VAL:HB	1:C:441:LYS:O	2.08	0.54
2:E:96:TYR:O	2:E:100:ALA:HB2	2.08	0.54
1:B:489:ILE:HD12	1:B:735:ALA:HB1	1.90	0.53
1:C:705:GLU:OE1	1:C:732:TYR:OH	2.15	0.53
1:C:812:ILE:O	1:C:816:TYR:CB	2.57	0.53
1:B:811:LEU:O	1:B:814:PHE:HB2	2.08	0.53
1:D:595:SER:C	1:D:597:SER:H	2.15	0.53
2:H:187:PHE:O	2:H:191:GLU:HG2	2.08	0.53
1:D:489:ILE:HD12	1:D:735:ALA:HB1	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:498:LEU:HD13	1:C:705:GLU:HB3	1.90	0.53
1:C:608:PHE:CE1	1:D:796:PHE:HE1	2.26	0.53
1:D:610:LEU:O	1:D:614:SER:HB3	2.08	0.53
2:F:155:VAL:O	2:F:158:SER:OG	2.22	0.53
1:A:498:LEU:HD13	1:A:705:GLU:HB3	1.90	0.53
1:B:489:ILE:HA	1:B:738:LYS:HB2	1.90	0.53
1:A:753:LEU:HA	1:A:756:GLN:HB2	1.90	0.53
1:C:399:THR:HG23	1:C:444:ILE:HD13	1.91	0.53
1:C:692:ARG:O	1:C:696:SER:OG	2.22	0.53
2:G:96:TYR:O	2:G:100:ALA:HB2	2.09	0.53
1:C:753:LEU:HA	1:C:756:GLN:HB2	1.91	0.53
1:D:811:LEU:O	1:D:814:PHE:HB2	2.09	0.53
1:B:642:GLN:OE1	1:B:644:GLU:N	2.42	0.53
1:D:489:ILE:HA	1:D:738:LYS:HB2	1.90	0.52
1:A:819:ARG:O	1:A:823:LYS:CB	2.57	0.52
1:B:452:ALA:N	1:B:461:ASN:OD1	2.29	0.52
1:A:745:ALA:HA	1:A:748:LEU:HD12	1.92	0.52
1:D:517:PHE:HD2	1:D:518:LEU:HG	1.75	0.52
1:D:642:GLN:OE1	1:D:644:GLU:N	2.42	0.52
2:F:95:GLU:O	2:F:99:ARG:CB	2.58	0.52
2:F:146:GLY:HA3	2:F:191:GLU:OE2	2.10	0.52
2:H:95:GLU:O	2:H:99:ARG:CB	2.58	0.52
1:D:595:SER:O	1:D:596:LEU:HG	2.10	0.52
2:E:183:GLY:O	2:E:186:SER:OG	2.22	0.51
2:H:146:GLY:HA3	2:H:191:GLU:OE2	2.10	0.51
2:F:145:ALA:O	2:F:148:SER:OG	2.19	0.51
1:C:574:PHE:CZ	1:B:596:LEU:HA	2.46	0.51
1:B:517:PHE:HD2	1:B:518:LEU:HG	1.75	0.51
1:D:705:GLU:OE1	1:D:732:TYR:OH	2.27	0.51
2:H:155:VAL:O	2:H:158:SER:OG	2.22	0.51
1:B:418:ASN:HA	1:B:442:LEU:HD12	1.93	0.51
1:B:595:SER:O	1:B:596:LEU:HG	2.11	0.51
1:D:418:ASN:HA	1:D:442:LEU:HD12	1.93	0.51
1:C:619:ASN:O	1:C:623:PHE:HB2	2.11	0.50
1:C:745:ALA:HA	1:C:748:LEU:HD12	1.92	0.50
1:B:498:LEU:HB2	1:B:706:SER:OG	2.12	0.50
1:A:574:PHE:CZ	1:D:596:LEU:HA	2.47	0.50
1:A:619:ASN:O	1:A:623:PHE:HB2	2.12	0.50
2:G:65:ARG:HA	2:G:79:GLN:HA	1.94	0.50
1:A:711:TYR:O	1:A:715:ARG:HG2	2.12	0.50
1:A:569:ASN:OD1	1:A:594:ARG:NH2	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:818:SER:O	1:A:822:ALA:HB3	2.12	0.49
1:A:526:TRP:HA	1:A:529:ILE:HD12	1.94	0.49
1:C:711:TYR:O	1:C:715:ARG:HG2	2.12	0.49
1:D:506:LYS:HG2	1:D:721:MET:HB2	1.94	0.49
1:D:702:TYR:HE2	1:D:704:LEU:HB3	1.77	0.49
1:D:498:LEU:HB2	1:D:706:SER:OG	2.12	0.49
1:B:579:PHE:O	1:B:583:ALA:CB	2.61	0.49
1:B:800:VAL:HG13	1:B:803:LEU:HD12	1.95	0.49
1:A:795:VAL:HG11	1:D:611:ILE:HG21	1.95	0.49
1:D:671:TRP:HE1	1:D:675:ARG:HH11	1.61	0.49
1:D:525:ILE:O	1:D:529:ILE:HG13	2.13	0.49
1:D:579:PHE:O	1:D:583:ALA:CB	2.60	0.49
1:A:642:GLN:OE1	1:A:644:GLU:N	2.46	0.48
1:A:800:VAL:HA	1:A:803:LEU:HD12	1.95	0.48
1:B:702:TYR:HE2	1:B:704:LEU:HB3	1.77	0.48
1:B:506:LYS:HG2	1:B:721:MET:HB2	1.94	0.48
1:B:525:ILE:O	1:B:529:ILE:HG13	2.13	0.48
1:B:705:GLU:OE1	1:B:732:TYR:OH	2.26	0.48
1:C:642:GLN:OE1	1:C:644:GLU:N	2.46	0.48
1:D:784:THR:OG1	1:D:785:SER:N	2.46	0.48
1:C:526:TRP:HA	1:C:529:ILE:HD12	1.95	0.48
2:E:134:ILE:O	2:E:137:SER:OG	2.27	0.48
2:F:142:PHE:O	2:F:145:ALA:HB3	2.14	0.48
2:H:142:PHE:O	2:H:145:ALA:HB3	2.14	0.48
1:D:453:ARG:HB2	1:D:460:TRP:CE2	2.50	0.47
1:C:418:ASN:OD1	1:C:442:LEU:N	2.29	0.47
1:C:569:ASN:OD1	1:C:594:ARG:NH2	2.39	0.47
1:D:649:THR:HG22	1:D:703:LEU:HB2	1.97	0.47
1:D:763:LYS:HA	1:D:767:TRP:CE3	2.50	0.47
1:B:467:LEU:HD22	1:B:737:PRO:HD3	1.97	0.47
1:A:436:CYS:HB2	1:A:438:PHE:HE1	1.80	0.47
1:A:483:LEU:HD13	1:D:751:LEU:HB2	1.97	0.47
1:B:671:TRP:HE1	1:B:675:ARG:HH11	1.61	0.47
1:B:784:THR:OG1	1:B:785:SER:N	2.46	0.47
1:B:795:VAL:O	1:B:799:LEU:HB2	2.15	0.47
1:C:433:ALA:HA	1:C:438:PHE:CE1	2.50	0.47
1:C:496:MET:HE2	1:C:763:LYS:HD2	1.97	0.47
1:D:800:VAL:HG13	1:D:803:LEU:HD12	1.95	0.47
1:D:807:MET:O	1:D:810:ALA:HB3	2.15	0.47
1:B:763:LYS:HA	1:B:767:TRP:CE3	2.50	0.47
1:B:807:MET:O	1:B:810:ALA:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:496:MET:HE2	1:A:763:LYS:HD2	1.97	0.46
1:C:800:VAL:HA	1:C:803:LEU:HD12	1.96	0.46
1:D:795:VAL:O	1:D:799:LEU:HB2	2.15	0.46
1:A:433:ALA:HA	1:A:438:PHE:CE1	2.50	0.46
1:D:433:ALA:HA	1:D:438:PHE:CE1	2.50	0.46
1:A:483:LEU:O	1:A:487:GLU:HG3	2.15	0.46
1:D:467:LEU:HD22	1:D:737:PRO:HD3	1.97	0.46
1:B:671:TRP:NE1	1:B:675:ARG:HD2	2.30	0.46
1:D:716:LYS:HG3	1:D:772:GLU:HB3	1.97	0.46
1:B:649:THR:HG22	1:B:703:LEU:HB2	1.97	0.46
2:F:177:GLY:O	2:F:180:PHE:HB3	2.15	0.46
1:C:483:LEU:HD13	1:B:751:LEU:HB2	1.97	0.46
1:B:433:ALA:HA	1:B:438:PHE:CE1	2.50	0.46
2:H:114:LEU:HB3	2:H:145:ALA:HB2	1.98	0.46
2:H:177:GLY:O	2:H:180:PHE:HB3	2.15	0.46
1:C:546:PHE:CG	1:C:547:SER:N	2.84	0.46
1:D:671:TRP:NE1	1:D:675:ARG:HD2	2.30	0.46
1:C:483:LEU:O	1:C:487:GLU:HG3	2.15	0.46
1:B:577:LEU:O	1:B:580:SER:HB2	2.16	0.46
1:A:603:GLY:HA2	1:A:606:TRP:HE3	1.81	0.46
1:C:795:VAL:HG11	1:B:611:ILE:HG21	1.98	0.45
1:B:453:ARG:HB2	1:B:460:TRP:CE2	2.50	0.45
1:C:436:CYS:HB2	1:C:438:PHE:HE1	1.81	0.45
2:H:107:PHE:HD1	2:H:110:LEU:HD12	1.81	0.45
1:B:589:CYS:HG	1:B:591:ILE:HG22	1.82	0.45
1:A:438:PHE:CE2	1:A:440:TYR:HB3	2.51	0.45
1:A:477:ALA:O	1:A:479:LEU:N	2.49	0.45
1:A:517:PHE:HE1	1:D:611:ILE:HB	1.81	0.45
2:F:107:PHE:HD1	2:F:110:LEU:HD12	1.81	0.45
1:C:634:GLU:O	1:C:635:SER:OG	2.32	0.45
1:C:477:ALA:O	1:C:479:LEU:N	2.49	0.45
1:D:493:LYS:HG2	1:D:747:ASN:HD21	1.81	0.45
1:D:577:LEU:O	1:D:580:SER:HB2	2.16	0.45
1:D:711:TYR:O	1:D:715:ARG:HG2	2.16	0.45
2:F:114:LEU:HB3	2:F:145:ALA:HB2	1.98	0.45
1:B:711:TYR:O	1:B:715:ARG:HG2	2.16	0.45
1:B:745:ALA:HA	1:B:748:LEU:HD12	1.99	0.45
1:A:546:PHE:CG	1:A:547:SER:N	2.84	0.44
1:A:648:GLY:HA3	1:A:681:VAL:HB	1.99	0.44
2:G:183:GLY:O	2:G:186:SER:OG	2.22	0.44
1:B:716:LYS:HG3	1:B:772:GLU:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:453:ARG:HB2	1:C:460:TRP:CZ2	2.52	0.44
1:C:609:THR:HA	1:C:612:ILE:HG22	1.99	0.44
1:D:409:LYS:HG2	1:D:422:GLU:CD	2.42	0.44
1:A:453:ARG:HB2	1:A:460:TRP:CZ2	2.52	0.44
1:B:409:LYS:HG2	1:B:422:GLU:CD	2.41	0.44
1:C:438:PHE:CE2	1:C:440:TYR:HB3	2.51	0.44
2:E:20:ALA:HA	2:E:23:LEU:HD12	1.99	0.44
1:B:498:LEU:HD21	1:B:732:TYR:CZ	2.53	0.44
1:D:505:LYS:NZ	1:D:719:ASP:HB2	2.33	0.44
1:A:493:LYS:HD2	1:D:494:PRO:HD3	1.99	0.44
1:D:428:LEU:HD21	1:D:734:ILE:HD11	1.99	0.44
1:D:745:ALA:HA	1:D:748:LEU:HD12	1.99	0.43
1:B:493:LYS:HG2	1:B:747:ASN:HD21	1.84	0.43
1:B:505:LYS:NZ	1:B:719:ASP:HB2	2.33	0.43
1:C:517:PHE:HE1	1:B:611:ILE:HB	1.82	0.43
1:A:418:ASN:OD1	1:A:442:LEU:N	2.29	0.43
1:A:586:ARG:HD2	1:B:586:ARG:CG	2.44	0.43
1:A:609:THR:HA	1:A:612:ILE:HG22	1.99	0.43
1:A:716:LYS:HG3	1:A:772:GLU:HB3	2.01	0.43
1:C:603:GLY:HA2	1:C:606:TRP:HE3	1.82	0.43
1:B:428:LEU:HD21	1:B:734:ILE:HD11	2.01	0.43
1:A:692:ARG:O	1:A:696:SER:OG	2.21	0.43
1:C:648:GLY:HA3	1:C:681:VAL:HB	1.99	0.43
1:C:788:SER:OG	1:C:789:LEU:N	2.52	0.43
1:C:453:ARG:HB2	1:C:460:TRP:CE2	2.53	0.43
2:F:37:ARG:H	2:F:58:MET:HA	1.83	0.43
1:D:498:LEU:HD21	1:D:732:TYR:CZ	2.53	0.43
1:A:493:LYS:HG2	1:A:747:ASN:ND2	2.26	0.43
1:C:493:LYS:HG2	1:C:747:ASN:ND2	2.27	0.43
1:C:586:ARG:HD2	1:D:586:ARG:CG	2.45	0.43
2:F:199:HIS:CD2	2:F:202:ILE:HD11	2.51	0.43
1:D:491:PHE:CE1	1:D:735:ALA:HB2	2.54	0.43
1:A:453:ARG:HB2	1:A:460:TRP:CE2	2.54	0.42
1:C:498:LEU:HG	1:C:730:LYS:O	2.19	0.42
2:F:12:LEU:HA	2:F:15:VAL:HG22	2.01	0.42
2:H:199:HIS:CD2	2:H:202:ILE:HD11	2.51	0.42
1:B:587:GLN:HG3	1:B:588:GLY:O	2.19	0.42
1:C:716:LYS:HG3	1:C:772:GLU:HB3	2.00	0.42
1:D:453:ARG:HB2	1:D:460:TRP:CZ2	2.54	0.42
2:E:155:VAL:O	2:E:158:SER:OG	2.29	0.42
1:B:436:CYS:HB2	1:B:438:PHE:HE1	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:586:ARG:CZ	1:B:613:ILE:HD11	2.47	0.42
1:C:737:PRO:HD2	1:C:740:SER:HB2	2.01	0.42
1:D:436:CYS:HB2	1:D:438:PHE:HE1	1.84	0.42
1:A:614:SER:HB3	1:B:617:THR:HG23	2.02	0.42
1:A:395:VAL:O	1:A:440:TYR:HA	2.19	0.42
1:A:737:PRO:HD2	1:A:740:SER:HB2	2.01	0.42
1:C:493:LYS:HD2	1:B:494:PRO:HD3	2.00	0.42
1:C:793:ALA:HB1	1:C:797:TYR:CZ	2.55	0.42
1:D:454:ASP:N	1:D:459:ILE:O	2.43	0.42
1:D:587:GLN:HG3	1:D:588:GLY:O	2.19	0.42
2:H:37:ARG:H	2:H:58:MET:HA	1.84	0.42
1:B:794:GLY:HA2	1:B:797:TYR:CE1	2.55	0.42
1:C:395:VAL:O	1:C:440:TYR:HA	2.19	0.42
2:E:19:ALA:O	2:E:23:LEU:HG	2.19	0.42
2:F:24:MET:O	2:F:28:VAL:HG23	2.20	0.42
1:A:498:LEU:HG	1:A:730:LYS:O	2.20	0.42
1:A:796:PHE:CE1	1:A:799:LEU:HD23	2.55	0.42
1:A:805:LEU:O	1:A:809:VAL:HG23	2.20	0.42
1:C:409:LYS:HG2	1:C:422:GLU:OE1	2.20	0.42
1:C:618:ALA:HB1	1:D:621:ALA:HB2	2.02	0.42
2:F:200:MET:O	2:F:203:ASP:HB2	2.20	0.42
2:H:24:MET:O	2:H:28:VAL:HG23	2.20	0.42
1:B:491:PHE:CE1	1:B:735:ALA:HB2	2.54	0.42
1:D:488:VAL:C	1:D:738:LYS:HE3	2.45	0.42
1:D:794:GLY:HA2	1:D:797:TYR:CE1	2.55	0.42
2:G:19:ALA:O	2:G:23:LEU:HG	2.20	0.41
1:B:486:GLU:OE2	1:B:491:PHE:HB2	2.19	0.41
1:B:488:VAL:C	1:B:738:LYS:HE3	2.45	0.41
1:A:589:CYS:SG	1:A:590:ASP:N	2.94	0.41
1:D:486:GLU:OE2	1:D:491:PHE:HB2	2.19	0.41
2:H:12:LEU:HA	2:H:15:VAL:HG22	2.01	0.41
2:H:200:MET:O	2:H:203:ASP:HB2	2.20	0.41
1:A:409:LYS:HG2	1:A:422:GLU:OE1	2.21	0.41
1:D:595:SER:C	1:D:597:SER:N	2.79	0.41
1:B:397:VAL:O	1:B:443:THR:OG1	2.23	0.41
1:B:453:ARG:HB2	1:B:460:TRP:CZ2	2.54	0.41
1:C:681:VAL:HA	1:C:692:ARG:HH22	1.86	0.41
1:B:454:ASP:N	1:B:459:ILE:O	2.39	0.41
2:G:134:ILE:O	2:G:137:SER:OG	2.28	0.41
1:C:751:LEU:HD13	1:B:486:GLU:HG3	2.02	0.41
1:C:813:GLU:O	1:C:816:TYR:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:540:LEU:O	1:C:543:VAL:HB	2.20	0.41
1:D:586:ARG:CZ	1:D:613:ILE:HD11	2.49	0.41
2:E:65:ARG:HA	2:E:79:GLN:HA	2.02	0.41
1:A:405:TYR:CE1	1:A:478:PRO:HB3	2.56	0.41
1:A:793:ALA:HB1	1:A:797:TYR:CZ	2.56	0.41
1:C:787:LEU:CB	1:B:521:LEU:HA	2.51	0.41
2:G:103:ALA:C	2:G:105:SER:H	2.29	0.41
1:A:436:CYS:HB2	1:A:438:PHE:CE1	2.56	0.41
1:A:528:CYS:HA	1:A:531:PHE:CD2	2.56	0.41
1:A:540:LEU:O	1:A:543:VAL:HB	2.20	0.41
1:A:681:VAL:HA	1:A:692:ARG:HH22	1.86	0.41
1:C:404:PRO:HD3	1:C:711:TYR:CG	2.56	0.41
1:D:453:ARG:HE	1:D:458:LYS:CA	2.34	0.41
1:A:534:ILE:HD12	1:A:535:GLY:N	2.36	0.41
1:A:618:ALA:HB1	1:B:621:ALA:HB2	2.01	0.41
1:C:436:CYS:HB2	1:C:438:PHE:CE1	2.56	0.41
1:C:614:SER:HB3	1:D:617:THR:HG23	2.02	0.41
1:C:534:ILE:HD12	1:C:535:GLY:N	2.36	0.40
2:E:103:ALA:C	2:E:105:SER:H	2.29	0.40
1:B:708:MET:O	1:B:712:ILE:HG12	2.21	0.40
1:C:597:SER:HA	1:C:600:ILE:HG22	2.04	0.40
1:D:589:CYS:SG	1:D:590:ASP:N	2.95	0.40
2:G:151:ILE:O	2:G:155:VAL:HG23	2.21	0.40
1:B:589:CYS:SG	1:B:590:ASP:N	2.95	0.40
1:A:813:GLU:O	1:A:816:TYR:HB3	2.22	0.40
1:C:522:ALA:HB1	1:C:524:GLU:CD	2.47	0.40
1:C:805:LEU:O	1:C:809:VAL:HG23	2.20	0.40
1:D:595:SER:OG	1:D:598:GLY:N	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	402/889 (45%)	376 (94%)	26 (6%)	0	100	100
1	B	403/889 (45%)	372 (92%)	31 (8%)	0	100	100
1	C	402/889 (45%)	374 (93%)	28 (7%)	0	100	100
1	D	403/889 (45%)	371 (92%)	32 (8%)	0	100	100
2	E	159/323 (49%)	143 (90%)	16 (10%)	0	100	100
2	F	167/323 (52%)	144 (86%)	23 (14%)	0	100	100
2	G	159/323 (49%)	146 (92%)	13 (8%)	0	100	100
2	H	167/323 (52%)	143 (86%)	24 (14%)	0	100	100
All	All	2262/4848 (47%)	2069 (92%)	193 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	308/761 (40%)	308 (100%)	0	100	100
1	B	301/761 (40%)	301 (100%)	0	100	100
1	C	307/761 (40%)	307 (100%)	0	100	100
1	D	301/761 (40%)	301 (100%)	0	100	100
2	E	50/275 (18%)	50 (100%)	0	100	100
2	F	87/275 (32%)	87 (100%)	0	100	100
2	G	50/275 (18%)	50 (100%)	0	100	100
2	H	87/275 (32%)	87 (100%)	0	100	100
All	All	1491/4144 (36%)	1491 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	412	HIS
1	A	747	ASN
1	A	791	ASN
1	C	412	HIS
1	C	747	ASN
1	C	791	ASN
1	D	709	ASN
1	D	747	ASN
1	D	791	ASN
2	F	199	HIS
2	H	199	HIS
1	B	709	ASN
1	B	747	ASN
1	B	791	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](#)

There are no ligands in this entry.

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.

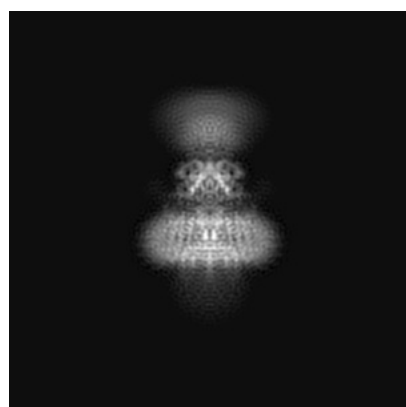
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8721. These allow visual inspection of the internal detail of the map and identification of artifacts.

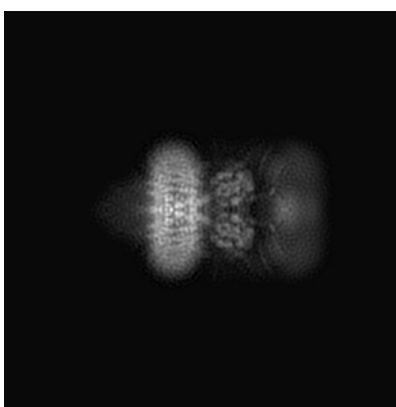
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

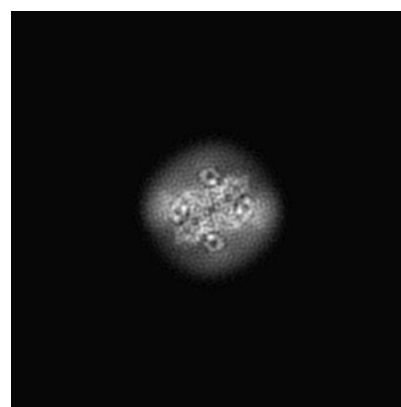
6.1.1 Primary map



X



Y

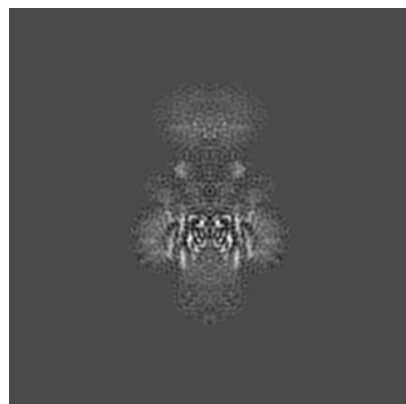


Z

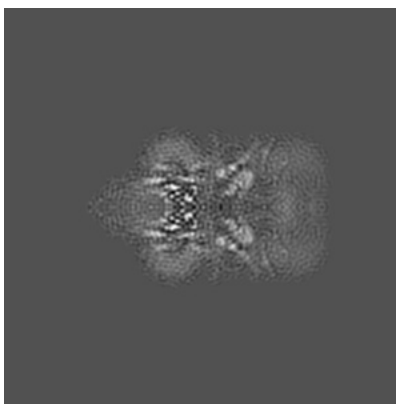
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

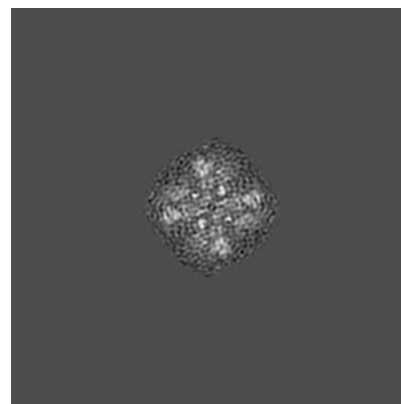
6.2.1 Primary map



X Index: 125



Y Index: 125

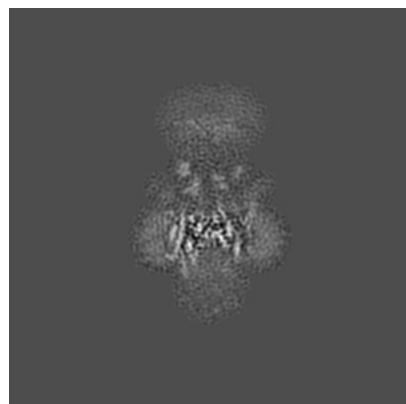


Z Index: 125

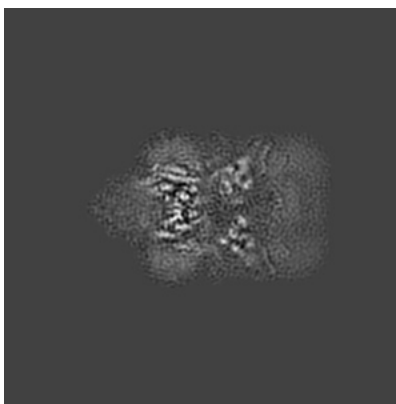
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

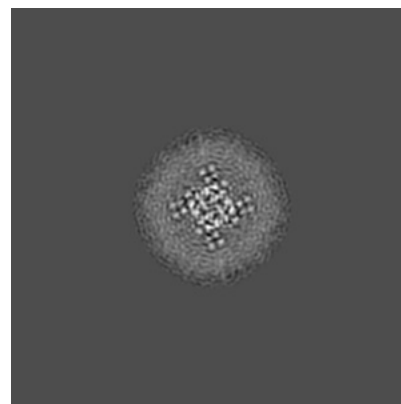
6.3.1 Primary map



X Index: 123



Y Index: 123

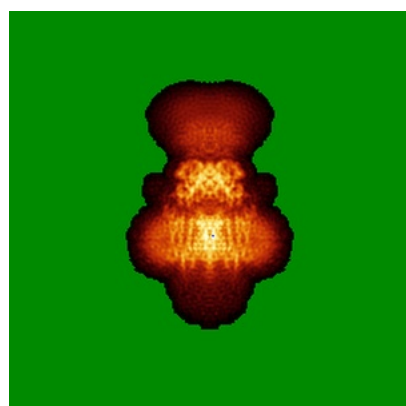


Z Index: 101

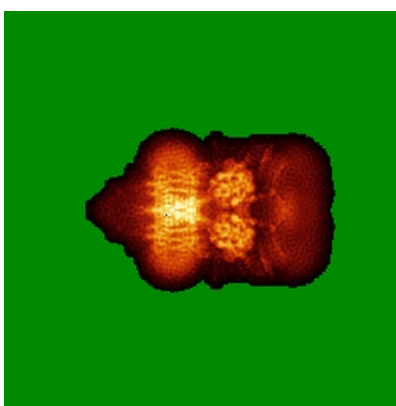
The images above show the largest variance slices of the map in three orthogonal directions.

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

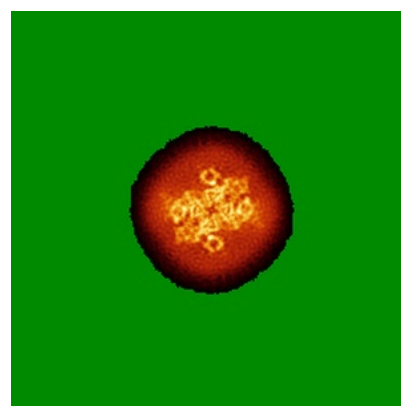
6.4.1 Primary map



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](#)

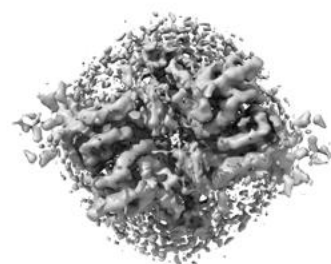
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

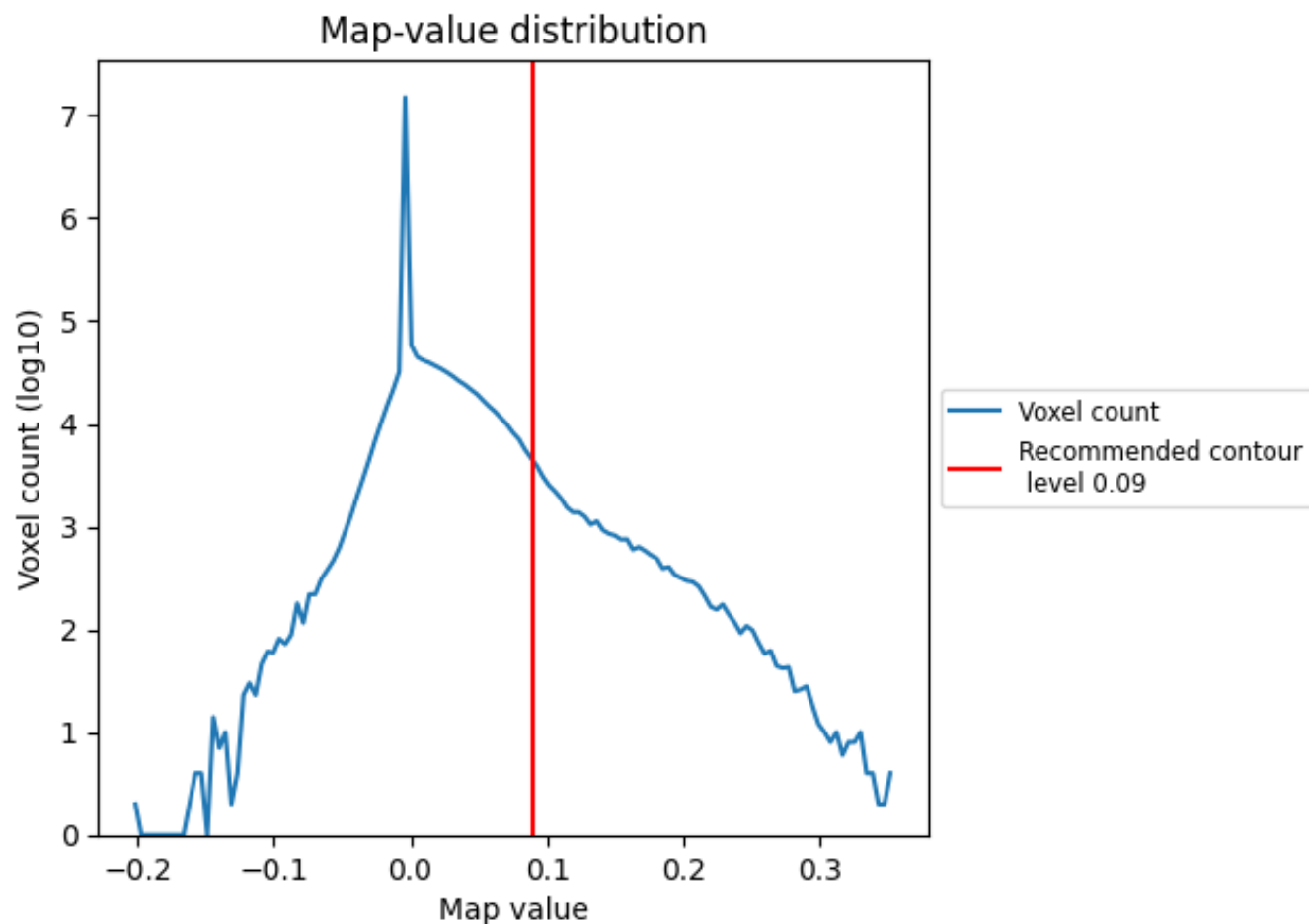
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

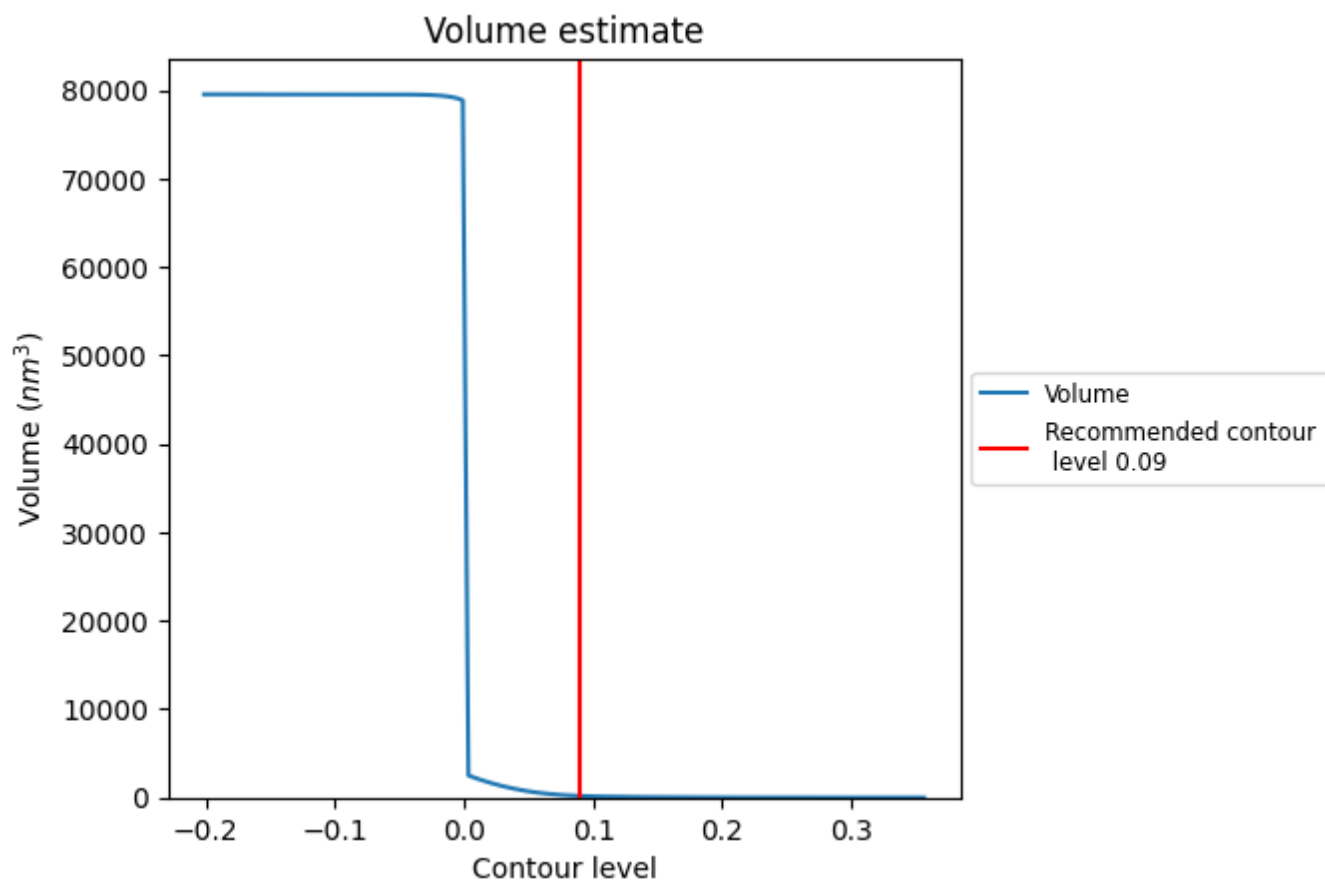
This section contains the results of statistical analysis of the map.

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.

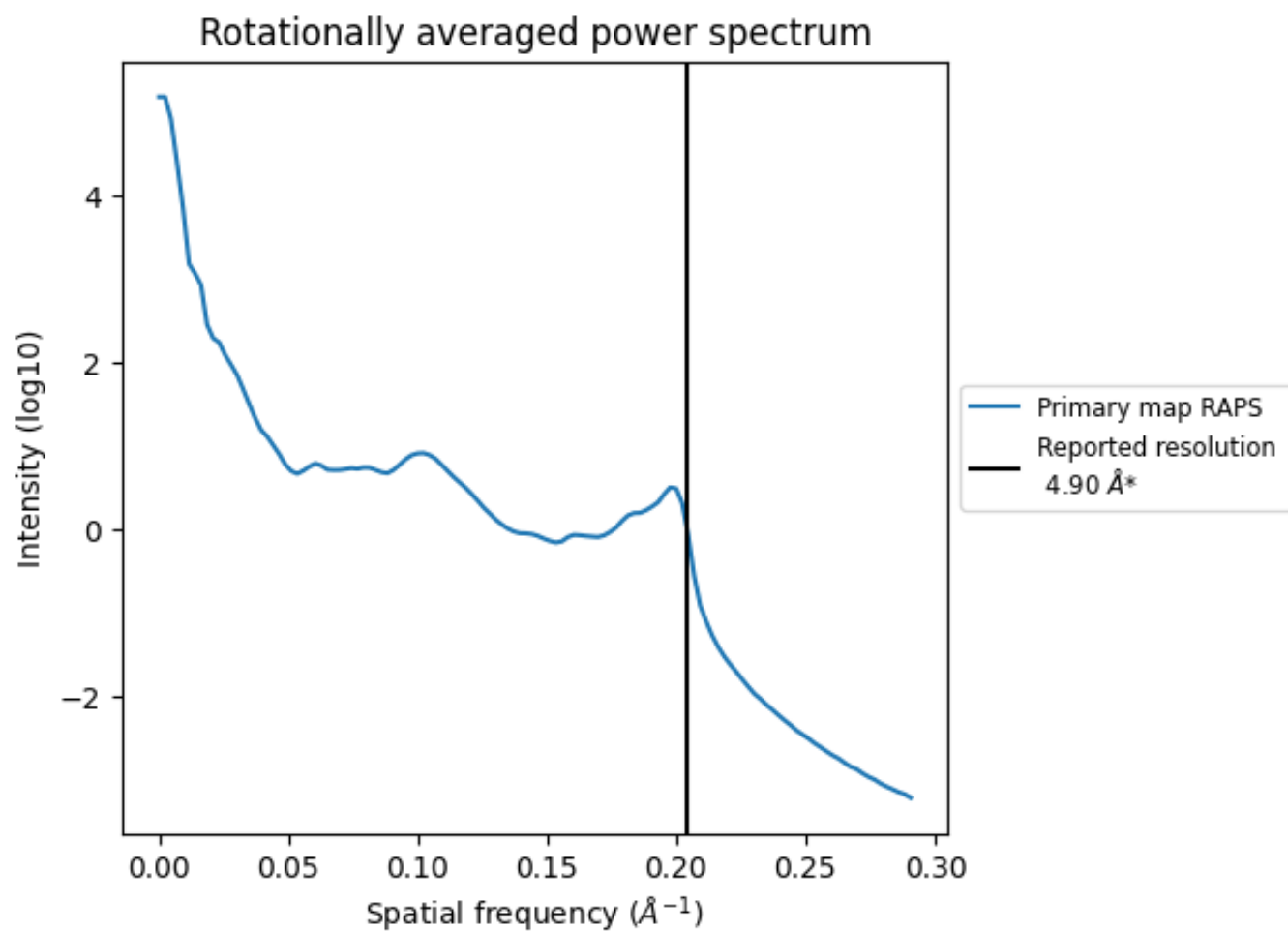
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 162 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 0.204 Å⁻¹

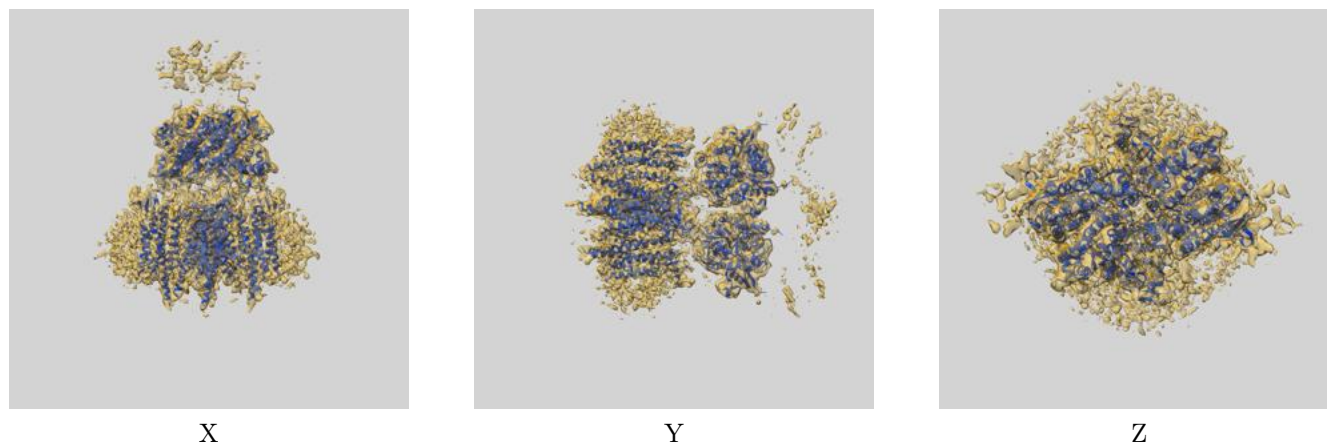
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

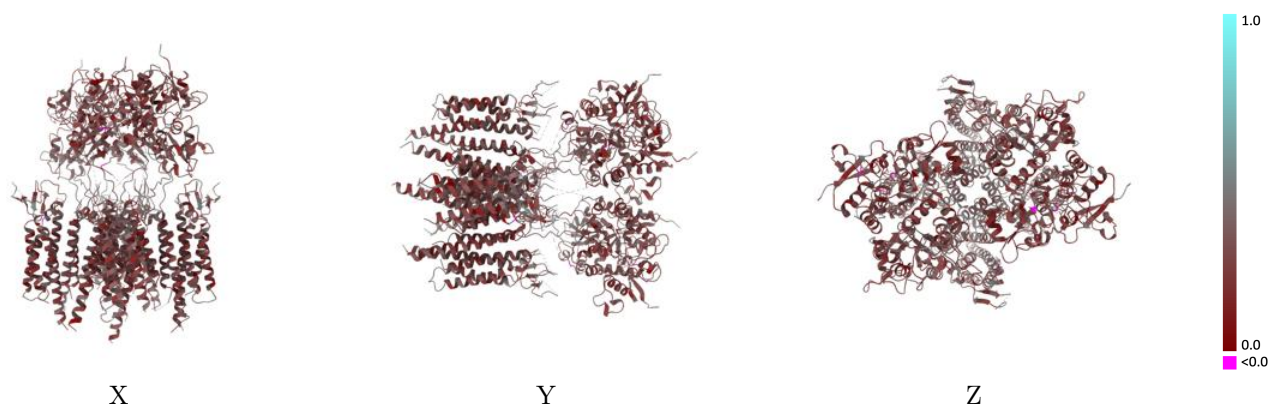
This section contains information regarding the fit between EMDB map EMD-8721 and PDB model 5VOT. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



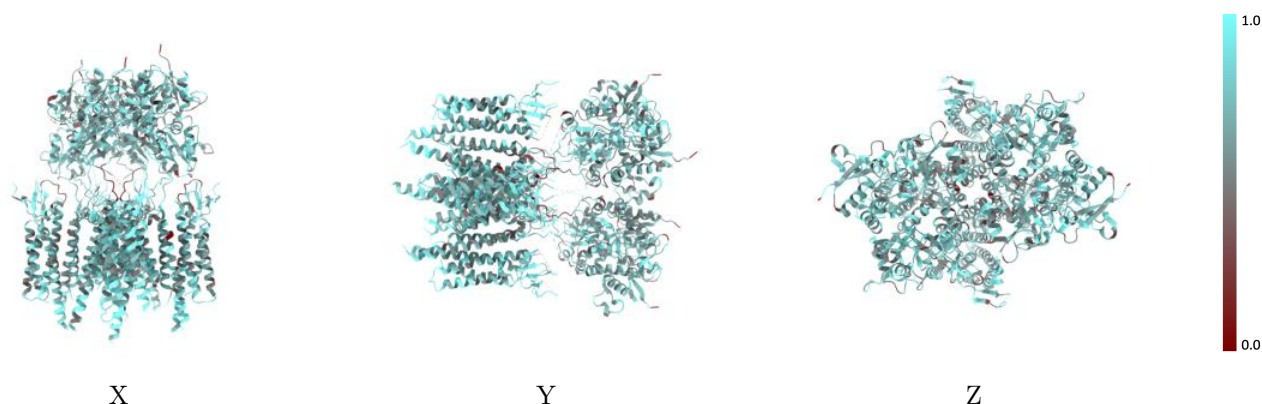
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



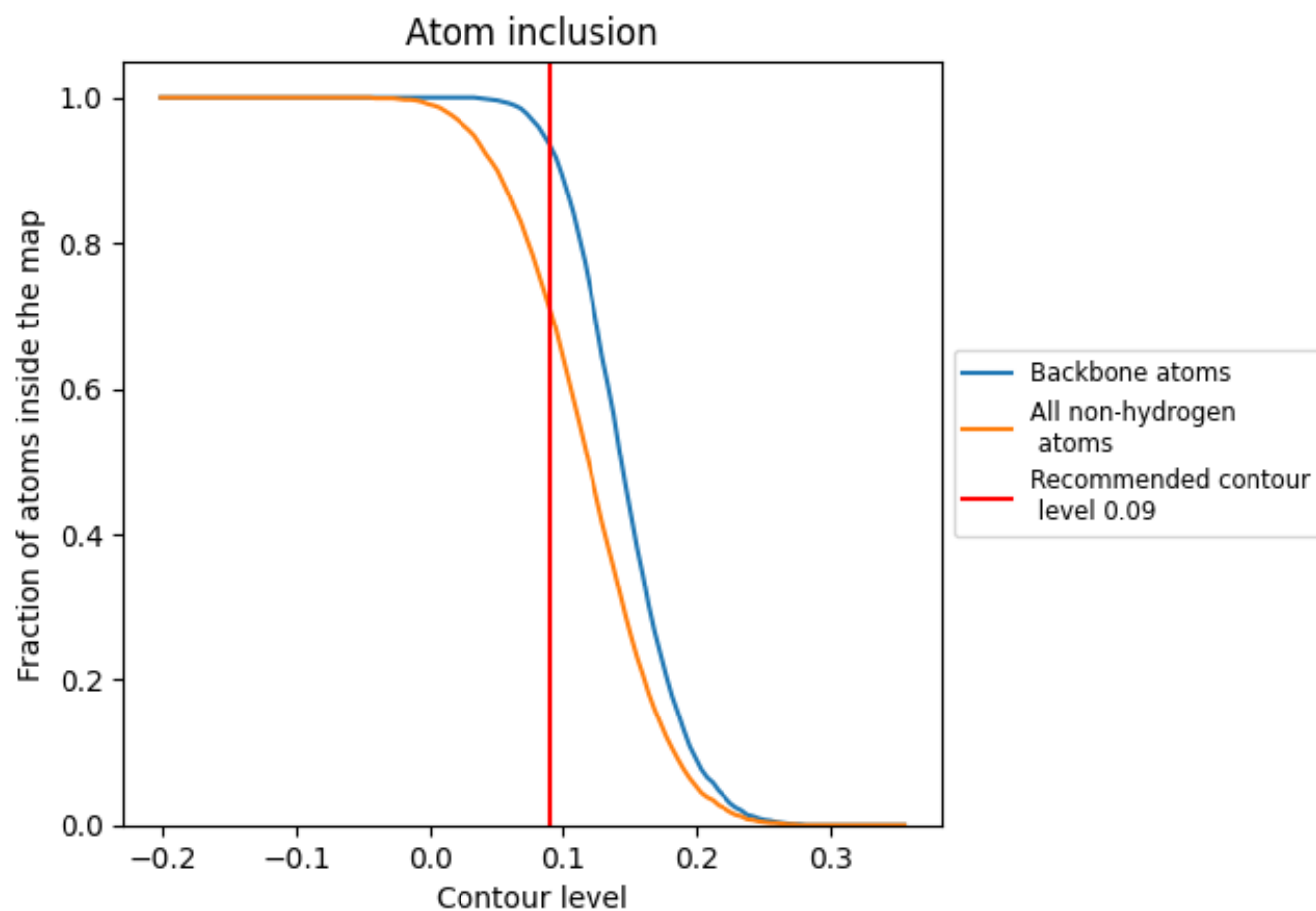
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 71% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7120	0.2980
A	0.6890	0.2860
B	0.7100	0.3080
C	0.6900	0.2860
D	0.7110	0.3080
E	0.7800	0.3110
F	0.7140	0.2970
G	0.7800	0.3090
H	0.7150	0.2950

1.0

0.0

<0.0