



Full wwPDB EM Validation Report ⓘ

Jul 19, 2026 – 12:36 PM EDT

PDB ID : 9Y9G / pdb_00009y9g
EMDB ID : EMD-72697
Title : Cryo-EM structure of human CNNM4(K113A/R140A/R141A) tetramer with Magnesium and MgATP in outward-facing state
Authors : Bai, Z.; Zhou, E.; Lu, W.; Du, J.
Deposited on : 2025-09-14
Resolution : 3.89 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:

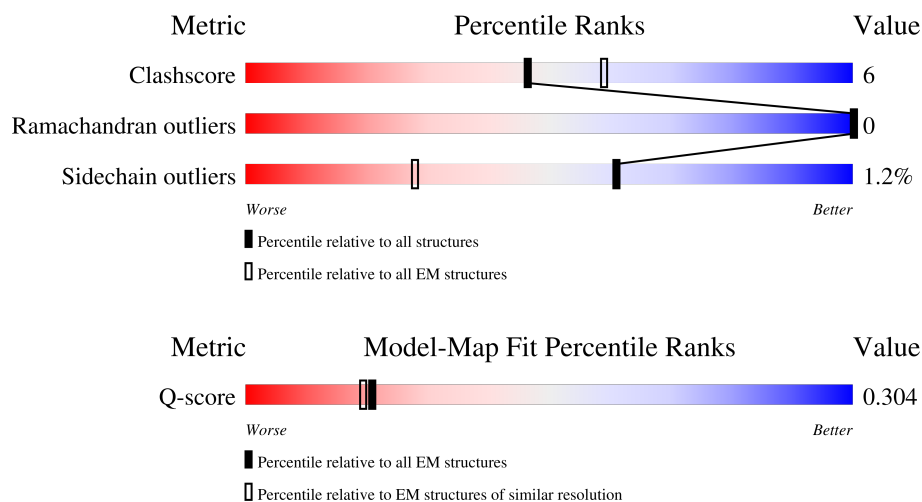
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 3.89 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	8712 (3.39 - 4.39)

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	844	19% 64% 12% 24%
1	B	844	21% 64% 11% 25%
1	C	844	20% 63% 12% 24%
1	D	844	21% 63% 12% 25%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20362 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 Metal transporter CNNM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	639	Total	C	N	O	S	0	0
			5081	3262	837	954	28		
1	B	637	Total	C	N	O	S	0	0
			5030	3232	820	950	28		
1	C	639	Total	C	N	O	S	0	0
			5081	3262	837	954	28		
1	D	637	Total	C	N	O	S	0	0
			5030	3232	820	950	28		

There are 288 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	ALA	LYS	engineered mutation	UNP Q6P4Q7
A	140	ALA	ARG	engineered mutation	UNP Q6P4Q7
A	141	ALA	ARG	engineered mutation	UNP Q6P4Q7
A	776	VAL	-	expression tag	UNP Q6P4Q7
A	777	ASP	-	expression tag	UNP Q6P4Q7
A	778	GLY	-	expression tag	UNP Q6P4Q7
A	779	SER	-	expression tag	UNP Q6P4Q7
A	780	LEU	-	expression tag	UNP Q6P4Q7
A	781	GLU	-	expression tag	UNP Q6P4Q7
A	782	VAL	-	expression tag	UNP Q6P4Q7
A	783	LEU	-	expression tag	UNP Q6P4Q7
A	784	PHE	-	expression tag	UNP Q6P4Q7
A	785	GLN	-	expression tag	UNP Q6P4Q7
A	786	GLY	-	expression tag	UNP Q6P4Q7
A	787	PRO	-	expression tag	UNP Q6P4Q7
A	788	SER	-	expression tag	UNP Q6P4Q7
A	789	GLY	-	expression tag	UNP Q6P4Q7
A	790	GLY	-	expression tag	UNP Q6P4Q7
A	791	SER	-	expression tag	UNP Q6P4Q7
A	792	ARG	-	expression tag	UNP Q6P4Q7
A	793	LEU	-	expression tag	UNP Q6P4Q7
A	794	GLU	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	795	GLU	-	expression tag	UNP Q6P4Q7
A	796	GLU	-	expression tag	UNP Q6P4Q7
A	797	LEU	-	expression tag	UNP Q6P4Q7
A	798	ARG	-	expression tag	UNP Q6P4Q7
A	799	ARG	-	expression tag	UNP Q6P4Q7
A	800	ARG	-	expression tag	UNP Q6P4Q7
A	801	LEU	-	expression tag	UNP Q6P4Q7
A	802	THR	-	expression tag	UNP Q6P4Q7
A	803	GLU	-	expression tag	UNP Q6P4Q7
A	804	GLY	-	expression tag	UNP Q6P4Q7
A	805	GLY	-	expression tag	UNP Q6P4Q7
A	806	SER	-	expression tag	UNP Q6P4Q7
A	807	TRP	-	expression tag	UNP Q6P4Q7
A	808	SER	-	expression tag	UNP Q6P4Q7
A	809	HIS	-	expression tag	UNP Q6P4Q7
A	810	PRO	-	expression tag	UNP Q6P4Q7
A	811	GLN	-	expression tag	UNP Q6P4Q7
A	812	PHE	-	expression tag	UNP Q6P4Q7
A	813	GLU	-	expression tag	UNP Q6P4Q7
A	814	LYS	-	expression tag	UNP Q6P4Q7
A	815	GLY	-	expression tag	UNP Q6P4Q7
A	816	GLY	-	expression tag	UNP Q6P4Q7
A	817	GLY	-	expression tag	UNP Q6P4Q7
A	818	SER	-	expression tag	UNP Q6P4Q7
A	819	GLY	-	expression tag	UNP Q6P4Q7
A	820	GLY	-	expression tag	UNP Q6P4Q7
A	821	GLY	-	expression tag	UNP Q6P4Q7
A	822	SER	-	expression tag	UNP Q6P4Q7
A	823	GLY	-	expression tag	UNP Q6P4Q7
A	824	GLY	-	expression tag	UNP Q6P4Q7
A	825	SER	-	expression tag	UNP Q6P4Q7
A	826	ALA	-	expression tag	UNP Q6P4Q7
A	827	TRP	-	expression tag	UNP Q6P4Q7
A	828	SER	-	expression tag	UNP Q6P4Q7
A	829	HIS	-	expression tag	UNP Q6P4Q7
A	830	PRO	-	expression tag	UNP Q6P4Q7
A	831	GLN	-	expression tag	UNP Q6P4Q7
A	832	PHE	-	expression tag	UNP Q6P4Q7
A	833	GLU	-	expression tag	UNP Q6P4Q7
A	834	LYS	-	expression tag	UNP Q6P4Q7
A	835	GLY	-	expression tag	UNP Q6P4Q7
A	836	SER	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	837	HIS	-	expression tag	UNP Q6P4Q7
A	838	HIS	-	expression tag	UNP Q6P4Q7
A	839	HIS	-	expression tag	UNP Q6P4Q7
A	840	HIS	-	expression tag	UNP Q6P4Q7
A	841	HIS	-	expression tag	UNP Q6P4Q7
A	842	HIS	-	expression tag	UNP Q6P4Q7
A	843	HIS	-	expression tag	UNP Q6P4Q7
A	844	HIS	-	expression tag	UNP Q6P4Q7
B	113	ALA	LYS	engineered mutation	UNP Q6P4Q7
B	140	ALA	ARG	engineered mutation	UNP Q6P4Q7
B	141	ALA	ARG	engineered mutation	UNP Q6P4Q7
B	776	VAL	-	expression tag	UNP Q6P4Q7
B	777	ASP	-	expression tag	UNP Q6P4Q7
B	778	GLY	-	expression tag	UNP Q6P4Q7
B	779	SER	-	expression tag	UNP Q6P4Q7
B	780	LEU	-	expression tag	UNP Q6P4Q7
B	781	GLU	-	expression tag	UNP Q6P4Q7
B	782	VAL	-	expression tag	UNP Q6P4Q7
B	783	LEU	-	expression tag	UNP Q6P4Q7
B	784	PHE	-	expression tag	UNP Q6P4Q7
B	785	GLN	-	expression tag	UNP Q6P4Q7
B	786	GLY	-	expression tag	UNP Q6P4Q7
B	787	PRO	-	expression tag	UNP Q6P4Q7
B	788	SER	-	expression tag	UNP Q6P4Q7
B	789	GLY	-	expression tag	UNP Q6P4Q7
B	790	GLY	-	expression tag	UNP Q6P4Q7
B	791	SER	-	expression tag	UNP Q6P4Q7
B	792	ARG	-	expression tag	UNP Q6P4Q7
B	793	LEU	-	expression tag	UNP Q6P4Q7
B	794	GLU	-	expression tag	UNP Q6P4Q7
B	795	GLU	-	expression tag	UNP Q6P4Q7
B	796	GLU	-	expression tag	UNP Q6P4Q7
B	797	LEU	-	expression tag	UNP Q6P4Q7
B	798	ARG	-	expression tag	UNP Q6P4Q7
B	799	ARG	-	expression tag	UNP Q6P4Q7
B	800	ARG	-	expression tag	UNP Q6P4Q7
B	801	LEU	-	expression tag	UNP Q6P4Q7
B	802	THR	-	expression tag	UNP Q6P4Q7
B	803	GLU	-	expression tag	UNP Q6P4Q7
B	804	GLY	-	expression tag	UNP Q6P4Q7
B	805	GLY	-	expression tag	UNP Q6P4Q7
B	806	SER	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	807	TRP	-	expression tag	UNP Q6P4Q7
B	808	SER	-	expression tag	UNP Q6P4Q7
B	809	HIS	-	expression tag	UNP Q6P4Q7
B	810	PRO	-	expression tag	UNP Q6P4Q7
B	811	GLN	-	expression tag	UNP Q6P4Q7
B	812	PHE	-	expression tag	UNP Q6P4Q7
B	813	GLU	-	expression tag	UNP Q6P4Q7
B	814	LYS	-	expression tag	UNP Q6P4Q7
B	815	GLY	-	expression tag	UNP Q6P4Q7
B	816	GLY	-	expression tag	UNP Q6P4Q7
B	817	GLY	-	expression tag	UNP Q6P4Q7
B	818	SER	-	expression tag	UNP Q6P4Q7
B	819	GLY	-	expression tag	UNP Q6P4Q7
B	820	GLY	-	expression tag	UNP Q6P4Q7
B	821	GLY	-	expression tag	UNP Q6P4Q7
B	822	SER	-	expression tag	UNP Q6P4Q7
B	823	GLY	-	expression tag	UNP Q6P4Q7
B	824	GLY	-	expression tag	UNP Q6P4Q7
B	825	SER	-	expression tag	UNP Q6P4Q7
B	826	ALA	-	expression tag	UNP Q6P4Q7
B	827	TRP	-	expression tag	UNP Q6P4Q7
B	828	SER	-	expression tag	UNP Q6P4Q7
B	829	HIS	-	expression tag	UNP Q6P4Q7
B	830	PRO	-	expression tag	UNP Q6P4Q7
B	831	GLN	-	expression tag	UNP Q6P4Q7
B	832	PHE	-	expression tag	UNP Q6P4Q7
B	833	GLU	-	expression tag	UNP Q6P4Q7
B	834	LYS	-	expression tag	UNP Q6P4Q7
B	835	GLY	-	expression tag	UNP Q6P4Q7
B	836	SER	-	expression tag	UNP Q6P4Q7
B	837	HIS	-	expression tag	UNP Q6P4Q7
B	838	HIS	-	expression tag	UNP Q6P4Q7
B	839	HIS	-	expression tag	UNP Q6P4Q7
B	840	HIS	-	expression tag	UNP Q6P4Q7
B	841	HIS	-	expression tag	UNP Q6P4Q7
B	842	HIS	-	expression tag	UNP Q6P4Q7
B	843	HIS	-	expression tag	UNP Q6P4Q7
B	844	HIS	-	expression tag	UNP Q6P4Q7
C	113	ALA	LYS	engineered mutation	UNP Q6P4Q7
C	140	ALA	ARG	engineered mutation	UNP Q6P4Q7
C	141	ALA	ARG	engineered mutation	UNP Q6P4Q7
C	776	VAL	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	777	ASP	-	expression tag	UNP Q6P4Q7
C	778	GLY	-	expression tag	UNP Q6P4Q7
C	779	SER	-	expression tag	UNP Q6P4Q7
C	780	LEU	-	expression tag	UNP Q6P4Q7
C	781	GLU	-	expression tag	UNP Q6P4Q7
C	782	VAL	-	expression tag	UNP Q6P4Q7
C	783	LEU	-	expression tag	UNP Q6P4Q7
C	784	PHE	-	expression tag	UNP Q6P4Q7
C	785	GLN	-	expression tag	UNP Q6P4Q7
C	786	GLY	-	expression tag	UNP Q6P4Q7
C	787	PRO	-	expression tag	UNP Q6P4Q7
C	788	SER	-	expression tag	UNP Q6P4Q7
C	789	GLY	-	expression tag	UNP Q6P4Q7
C	790	GLY	-	expression tag	UNP Q6P4Q7
C	791	SER	-	expression tag	UNP Q6P4Q7
C	792	ARG	-	expression tag	UNP Q6P4Q7
C	793	LEU	-	expression tag	UNP Q6P4Q7
C	794	GLU	-	expression tag	UNP Q6P4Q7
C	795	GLU	-	expression tag	UNP Q6P4Q7
C	796	GLU	-	expression tag	UNP Q6P4Q7
C	797	LEU	-	expression tag	UNP Q6P4Q7
C	798	ARG	-	expression tag	UNP Q6P4Q7
C	799	ARG	-	expression tag	UNP Q6P4Q7
C	800	ARG	-	expression tag	UNP Q6P4Q7
C	801	LEU	-	expression tag	UNP Q6P4Q7
C	802	THR	-	expression tag	UNP Q6P4Q7
C	803	GLU	-	expression tag	UNP Q6P4Q7
C	804	GLY	-	expression tag	UNP Q6P4Q7
C	805	GLY	-	expression tag	UNP Q6P4Q7
C	806	SER	-	expression tag	UNP Q6P4Q7
C	807	TRP	-	expression tag	UNP Q6P4Q7
C	808	SER	-	expression tag	UNP Q6P4Q7
C	809	HIS	-	expression tag	UNP Q6P4Q7
C	810	PRO	-	expression tag	UNP Q6P4Q7
C	811	GLN	-	expression tag	UNP Q6P4Q7
C	812	PHE	-	expression tag	UNP Q6P4Q7
C	813	GLU	-	expression tag	UNP Q6P4Q7
C	814	LYS	-	expression tag	UNP Q6P4Q7
C	815	GLY	-	expression tag	UNP Q6P4Q7
C	816	GLY	-	expression tag	UNP Q6P4Q7
C	817	GLY	-	expression tag	UNP Q6P4Q7
C	818	SER	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	819	GLY	-	expression tag	UNP Q6P4Q7
C	820	GLY	-	expression tag	UNP Q6P4Q7
C	821	GLY	-	expression tag	UNP Q6P4Q7
C	822	SER	-	expression tag	UNP Q6P4Q7
C	823	GLY	-	expression tag	UNP Q6P4Q7
C	824	GLY	-	expression tag	UNP Q6P4Q7
C	825	SER	-	expression tag	UNP Q6P4Q7
C	826	ALA	-	expression tag	UNP Q6P4Q7
C	827	TRP	-	expression tag	UNP Q6P4Q7
C	828	SER	-	expression tag	UNP Q6P4Q7
C	829	HIS	-	expression tag	UNP Q6P4Q7
C	830	PRO	-	expression tag	UNP Q6P4Q7
C	831	GLN	-	expression tag	UNP Q6P4Q7
C	832	PHE	-	expression tag	UNP Q6P4Q7
C	833	GLU	-	expression tag	UNP Q6P4Q7
C	834	LYS	-	expression tag	UNP Q6P4Q7
C	835	GLY	-	expression tag	UNP Q6P4Q7
C	836	SER	-	expression tag	UNP Q6P4Q7
C	837	HIS	-	expression tag	UNP Q6P4Q7
C	838	HIS	-	expression tag	UNP Q6P4Q7
C	839	HIS	-	expression tag	UNP Q6P4Q7
C	840	HIS	-	expression tag	UNP Q6P4Q7
C	841	HIS	-	expression tag	UNP Q6P4Q7
C	842	HIS	-	expression tag	UNP Q6P4Q7
C	843	HIS	-	expression tag	UNP Q6P4Q7
C	844	HIS	-	expression tag	UNP Q6P4Q7
D	113	ALA	LYS	engineered mutation	UNP Q6P4Q7
D	140	ALA	ARG	engineered mutation	UNP Q6P4Q7
D	141	ALA	ARG	engineered mutation	UNP Q6P4Q7
D	776	VAL	-	expression tag	UNP Q6P4Q7
D	777	ASP	-	expression tag	UNP Q6P4Q7
D	778	GLY	-	expression tag	UNP Q6P4Q7
D	779	SER	-	expression tag	UNP Q6P4Q7
D	780	LEU	-	expression tag	UNP Q6P4Q7
D	781	GLU	-	expression tag	UNP Q6P4Q7
D	782	VAL	-	expression tag	UNP Q6P4Q7
D	783	LEU	-	expression tag	UNP Q6P4Q7
D	784	PHE	-	expression tag	UNP Q6P4Q7
D	785	GLN	-	expression tag	UNP Q6P4Q7
D	786	GLY	-	expression tag	UNP Q6P4Q7
D	787	PRO	-	expression tag	UNP Q6P4Q7
D	788	SER	-	expression tag	UNP Q6P4Q7

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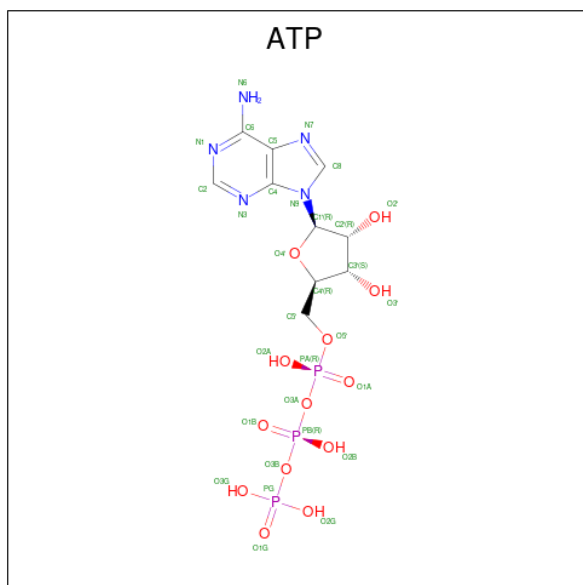
Chain	Residue	Modelled	Actual	Comment	Reference
D	789	GLY	-	expression tag	UNP Q6P4Q7
D	790	GLY	-	expression tag	UNP Q6P4Q7
D	791	SER	-	expression tag	UNP Q6P4Q7
D	792	ARG	-	expression tag	UNP Q6P4Q7
D	793	LEU	-	expression tag	UNP Q6P4Q7
D	794	GLU	-	expression tag	UNP Q6P4Q7
D	795	GLU	-	expression tag	UNP Q6P4Q7
D	796	GLU	-	expression tag	UNP Q6P4Q7
D	797	LEU	-	expression tag	UNP Q6P4Q7
D	798	ARG	-	expression tag	UNP Q6P4Q7
D	799	ARG	-	expression tag	UNP Q6P4Q7
D	800	ARG	-	expression tag	UNP Q6P4Q7
D	801	LEU	-	expression tag	UNP Q6P4Q7
D	802	THR	-	expression tag	UNP Q6P4Q7
D	803	GLU	-	expression tag	UNP Q6P4Q7
D	804	GLY	-	expression tag	UNP Q6P4Q7
D	805	GLY	-	expression tag	UNP Q6P4Q7
D	806	SER	-	expression tag	UNP Q6P4Q7
D	807	TRP	-	expression tag	UNP Q6P4Q7
D	808	SER	-	expression tag	UNP Q6P4Q7
D	809	HIS	-	expression tag	UNP Q6P4Q7
D	810	PRO	-	expression tag	UNP Q6P4Q7
D	811	GLN	-	expression tag	UNP Q6P4Q7
D	812	PHE	-	expression tag	UNP Q6P4Q7
D	813	GLU	-	expression tag	UNP Q6P4Q7
D	814	LYS	-	expression tag	UNP Q6P4Q7
D	815	GLY	-	expression tag	UNP Q6P4Q7
D	816	GLY	-	expression tag	UNP Q6P4Q7
D	817	GLY	-	expression tag	UNP Q6P4Q7
D	818	SER	-	expression tag	UNP Q6P4Q7
D	819	GLY	-	expression tag	UNP Q6P4Q7
D	820	GLY	-	expression tag	UNP Q6P4Q7
D	821	GLY	-	expression tag	UNP Q6P4Q7
D	822	SER	-	expression tag	UNP Q6P4Q7
D	823	GLY	-	expression tag	UNP Q6P4Q7
D	824	GLY	-	expression tag	UNP Q6P4Q7
D	825	SER	-	expression tag	UNP Q6P4Q7
D	826	ALA	-	expression tag	UNP Q6P4Q7
D	827	TRP	-	expression tag	UNP Q6P4Q7
D	828	SER	-	expression tag	UNP Q6P4Q7
D	829	HIS	-	expression tag	UNP Q6P4Q7
D	830	PRO	-	expression tag	UNP Q6P4Q7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	831	GLN	-	expression tag	UNP Q6P4Q7
D	832	PHE	-	expression tag	UNP Q6P4Q7
D	833	GLU	-	expression tag	UNP Q6P4Q7
D	834	LYS	-	expression tag	UNP Q6P4Q7
D	835	GLY	-	expression tag	UNP Q6P4Q7
D	836	SER	-	expression tag	UNP Q6P4Q7
D	837	HIS	-	expression tag	UNP Q6P4Q7
D	838	HIS	-	expression tag	UNP Q6P4Q7
D	839	HIS	-	expression tag	UNP Q6P4Q7
D	840	HIS	-	expression tag	UNP Q6P4Q7
D	841	HIS	-	expression tag	UNP Q6P4Q7
D	842	HIS	-	expression tag	UNP Q6P4Q7
D	843	HIS	-	expression tag	UNP Q6P4Q7
D	844	HIS	-	expression tag	UNP Q6P4Q7

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

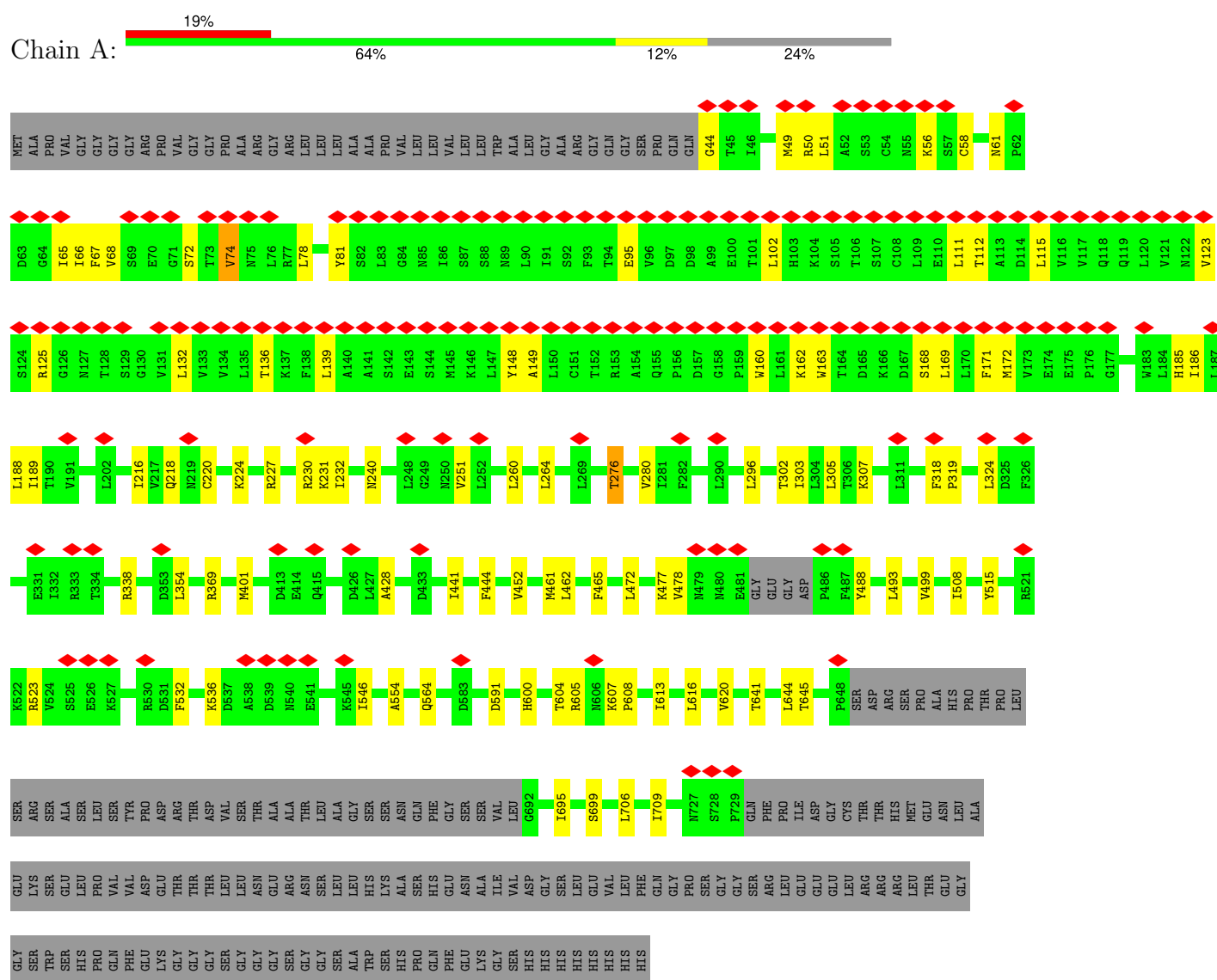
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	4	Total 4	Mg 4	0
3	B	4	Total 4	Mg 4	0
3	C	4	Total 4	Mg 4	0
3	D	4	Total 4	Mg 4	0

3 Residue-property plots

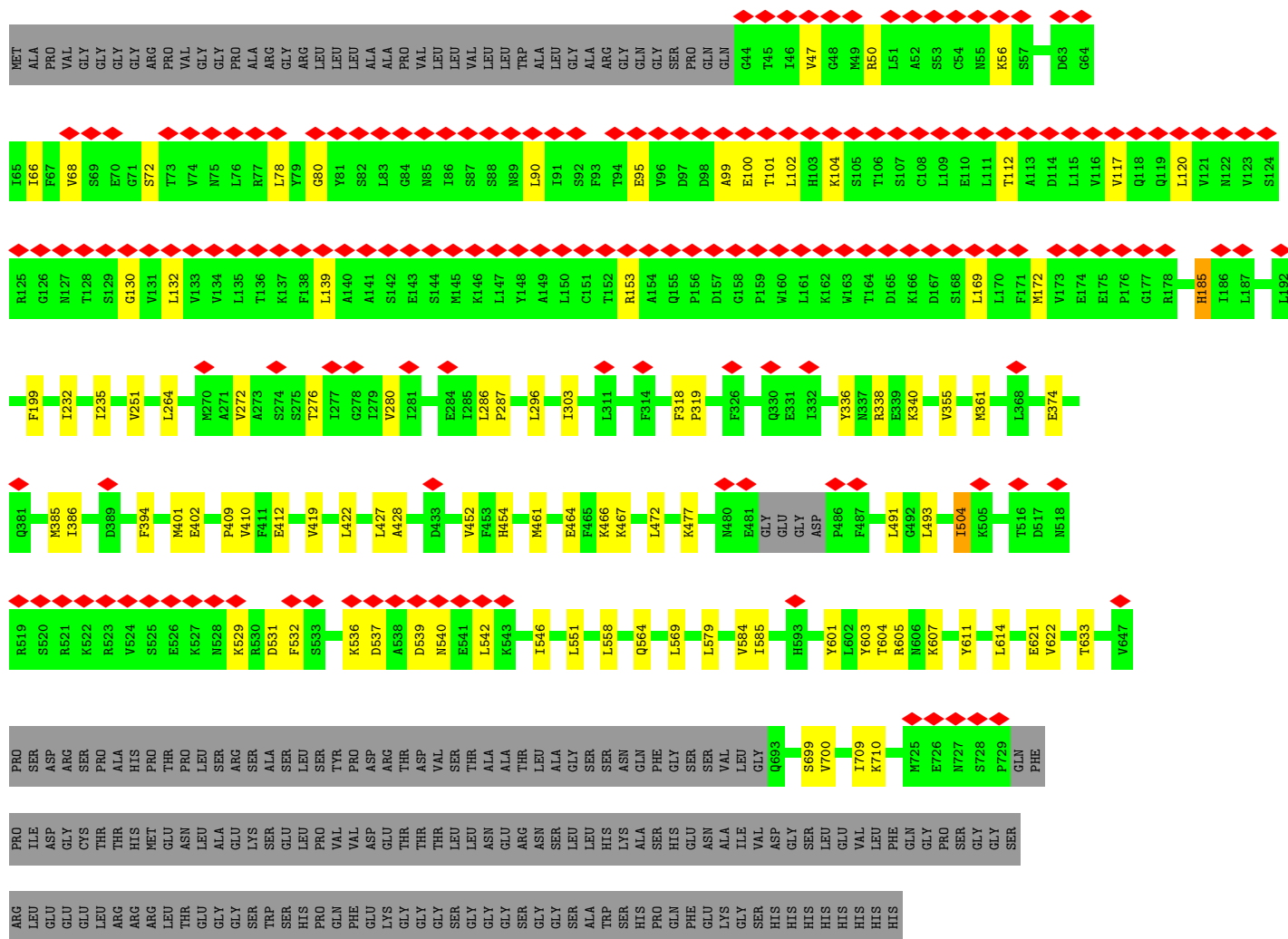
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Metal transporter CNNM4

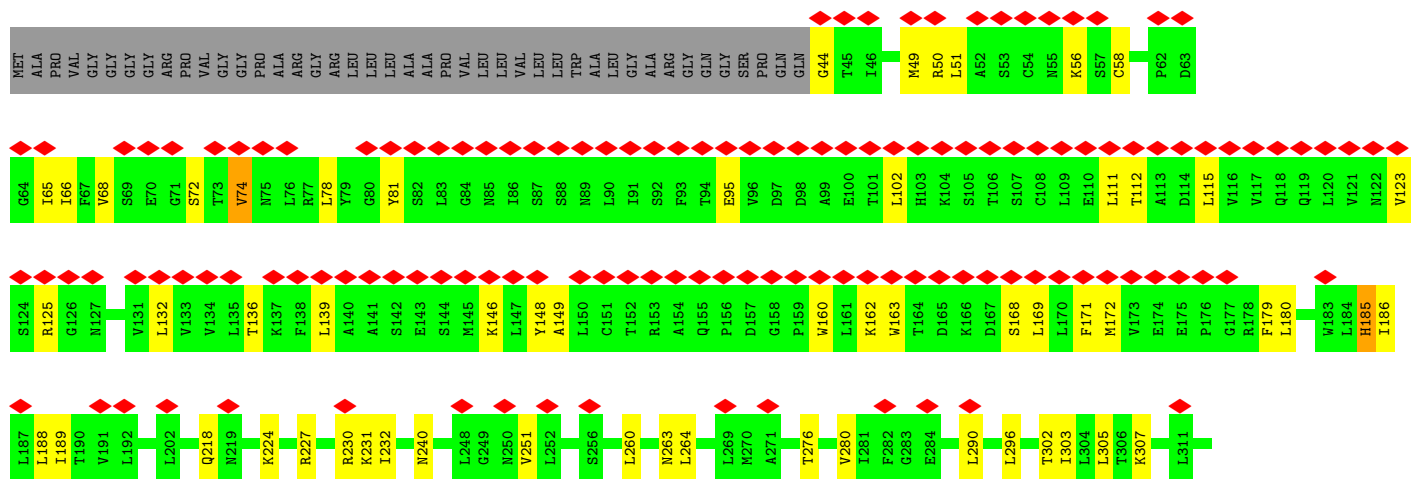


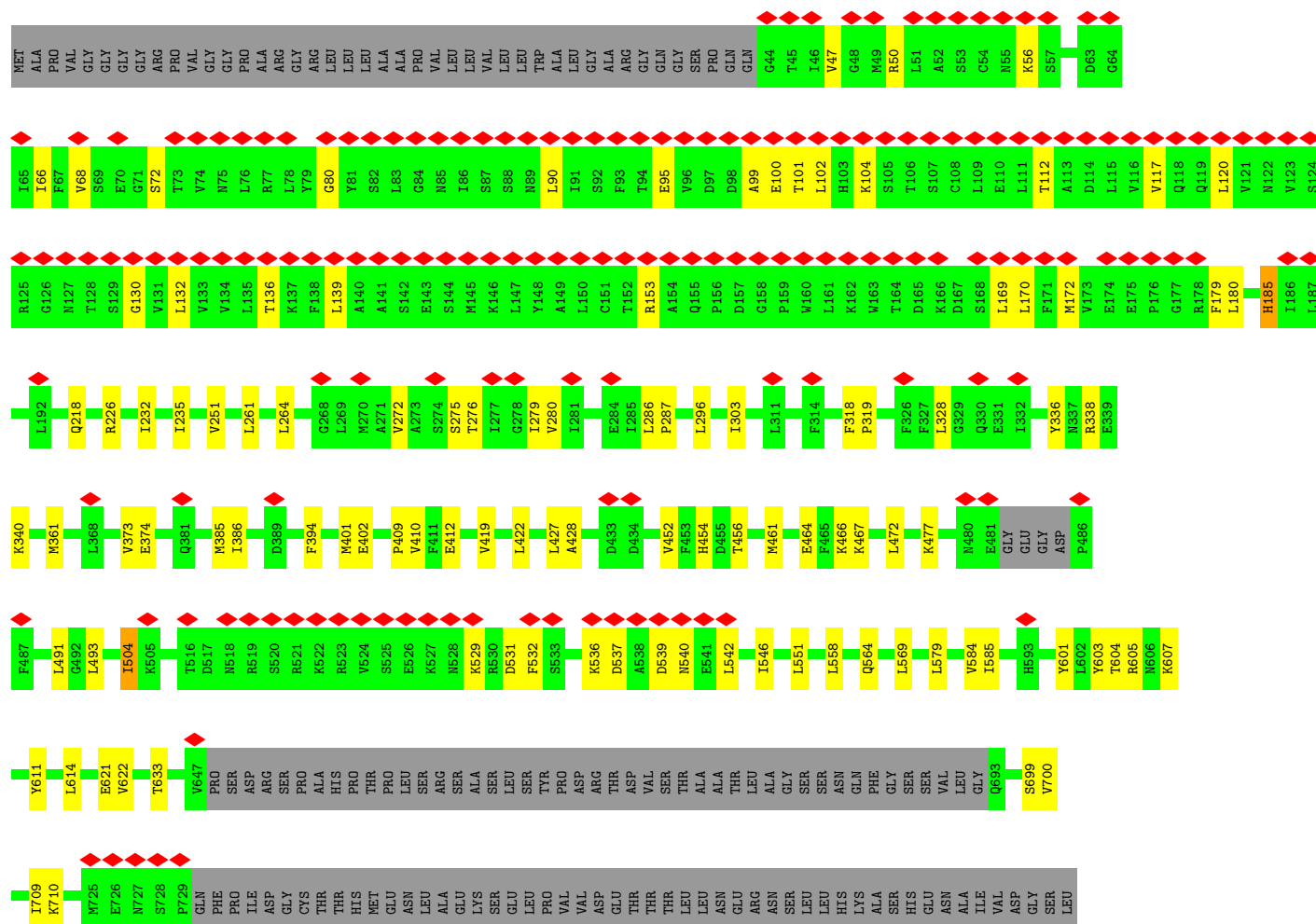
• Molecule 1: Metal transporter CNNM4





• Molecule 1: Metal transporter CNNM4





GLU VAL LEU PHE GLN PRO SER GLY GLY SER ARG LEU GLU GLU GLU LEU ARG ARG ARG LEU THR GLU GLY GLY SER TRP SER HIS PRO GLN PHE GLU LYS GLY GLY SER GLY GLY GLY GLY GLY GLY SER ALA TRP SER HIS PRO GLN PHE GLU LYS GLY SER HIS HIS HIS HIS

HIS
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	537678	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.013	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00283	Depositor
Map size (Å)	361.504, 361.504, 361.504	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.869, 0.869, 0.869	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.19	0/5170	0.30	0/6990
1	B	0.19	0/5118	0.31	0/6928
1	C	0.19	0/5170	0.30	0/6990
1	D	0.21	0/5118	0.33	0/6928
All	All	0.20	0/20576	0.31	0/27836

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5081	0	5177	71	0
1	B	5030	0	5086	67	0
1	C	5081	0	5177	71	0
1	D	5030	0	5086	69	0
2	A	31	0	12	0	0
2	B	31	0	12	0	0
2	C	31	0	12	1	0
2	D	31	0	12	0	0
3	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
All	All	20362	0	20574	248	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (248) 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:280:VAL:HG22	1:D:251:VAL:HG21	1.39	1.05
1:A:280:VAL:HG22	1:B:251:VAL:HG21	1.40	1.03
1:C:564:GLN:HE21	1:C:645:THR:HG23	1.45	0.81
1:A:564:GLN:HE21	1:A:645:THR:HG23	1.45	0.81
1:A:276:THR:HG23	1:B:251:VAL:HG11	1.71	0.71
1:C:50:ARG:HG2	1:D:50:ARG:HG2	1.72	0.70
1:B:374:GLU:HB2	1:B:454:HIS:HB2	1.75	0.68
1:D:374:GLU:HB2	1:D:454:HIS:HB2	1.75	0.68
1:C:508:ILE:HG12	1:D:466:LYS:HG2	1.79	0.64
1:D:477:LYS:HE3	1:D:491:LEU:HD11	1.79	0.64
1:A:508:ILE:HG12	1:B:466:LYS:HG2	1.79	0.63
1:B:477:LYS:HE3	1:B:491:LEU:HD11	1.80	0.63
1:B:402:GLU:HG3	1:B:532:PHE:HE2	1.64	0.62
1:D:402:GLU:HG3	1:D:532:PHE:HE2	1.64	0.62
1:B:336:TYR:HA	1:B:340:LYS:HD3	1.81	0.62
1:C:478:VAL:HG22	1:C:488:TYR:HE1	1.65	0.62
1:B:412:GLU:HB2	1:B:419:VAL:HG21	1.82	0.61
1:D:336:TYR:HA	1:D:340:LYS:HD3	1.81	0.61
1:A:478:VAL:HG22	1:A:488:TYR:HE1	1.65	0.61
1:D:68:VAL:HG11	1:D:136:THR:HG21	1.82	0.61
1:B:276:THR:O	1:B:280:VAL:HG23	2.00	0.61
1:D:412:GLU:HB2	1:D:419:VAL:HG21	1.82	0.60
1:C:605:ARG:HG3	1:C:699:SER:HB2	1.84	0.60
1:D:452:VAL:HG11	1:D:461:MET:HE1	1.83	0.60
1:A:50:ARG:HD3	1:A:66:ILE:HD11	1.84	0.59
1:B:235:ILE:HG13	1:B:303:ILE:HD11	1.83	0.59
1:B:452:VAL:HG11	1:B:461:MET:HE1	1.84	0.59
1:A:50:ARG:HG2	1:B:50:ARG:HG2	1.84	0.59
1:C:276:THR:O	1:C:280:VAL:HG23	2.03	0.58
1:C:50:ARG:HD3	1:C:66:ILE:HD11	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:THR:O	1:A:280:VAL:HG23	2.03	0.58
1:C:515:TYR:HE1	1:C:523:ARG:HG2	1.68	0.58
1:C:224:LYS:HG3	1:C:227:ARG:HH21	1.69	0.58
1:A:354:LEU:HD23	1:B:338:ARG:HG2	1.86	0.57
1:D:235:ILE:HG13	1:D:303:ILE:HD11	1.84	0.57
1:A:224:LYS:HG3	1:A:227:ARG:HH21	1.69	0.57
1:A:515:TYR:HE1	1:A:523:ARG:HG2	1.69	0.57
1:D:102:LEU:HD22	1:D:169:LEU:HD21	1.86	0.57
1:B:102:LEU:HD22	1:B:169:LEU:HD21	1.87	0.57
1:C:302:THR:HG22	1:C:305:LEU:HB3	1.87	0.56
1:D:185:HIS:CD2	1:D:264:LEU:HB2	2.40	0.56
1:A:44:GLY:HA2	1:A:81:TYR:O	2.07	0.55
1:B:100:GLU:HG3	1:B:104:LYS:HE3	1.87	0.55
1:C:472:LEU:HD11	1:C:493:LEU:HB2	1.88	0.55
1:A:564:GLN:NE2	1:A:644:LEU:HB2	2.22	0.55
1:A:605:ARG:HG3	1:A:699:SER:HB2	1.87	0.55
1:B:185:HIS:CD2	1:B:264:LEU:HB2	2.41	0.55
1:D:99:ALA:O	1:D:102:LEU:HB3	2.06	0.55
1:A:444:PHE:CZ	1:B:531:ASP:HA	2.42	0.55
1:B:99:ALA:O	1:B:102:LEU:HB3	2.07	0.54
1:C:180:LEU:HD12	1:C:185:HIS:CE1	2.43	0.54
1:C:251:VAL:HG11	1:D:280:VAL:HG21	1.88	0.54
1:A:251:VAL:HG11	1:B:280:VAL:HG21	1.90	0.54
1:C:444:PHE:CZ	1:D:531:ASP:HA	2.42	0.54
1:D:100:GLU:HG3	1:D:104:LYS:HE3	1.88	0.54
1:B:601:TYR:HB3	1:B:603:TYR:O	2.08	0.54
1:C:44:GLY:HA2	1:C:81:TYR:O	2.07	0.54
1:A:188:LEU:HB3	1:A:260:LEU:HD13	1.90	0.54
1:A:276:THR:HG23	1:B:251:VAL:CG1	2.36	0.53
1:C:354:LEU:HD23	1:D:338:ARG:HG2	1.89	0.53
1:A:102:LEU:HD13	1:A:169:LEU:HD21	1.90	0.53
1:A:608:PRO:HA	1:A:695:ILE:HA	1.91	0.53
1:C:95:GLU:HG3	1:C:112:THR:HB	1.90	0.53
1:C:102:LEU:HD13	1:C:169:LEU:HD21	1.90	0.53
1:C:554:ALA:HB2	1:C:616:LEU:HD21	1.89	0.53
1:A:68:VAL:HG11	1:A:74:VAL:HG22	1.91	0.53
1:A:472:LEU:HD11	1:A:493:LEU:HB2	1.90	0.53
1:C:564:GLN:NE2	1:C:644:LEU:HB2	2.23	0.53
1:C:608:PRO:HA	1:C:695:ILE:HA	1.91	0.53
1:D:394:PHE:CE2	1:D:536:LYS:HB2	2.44	0.53
1:D:601:TYR:HB3	1:D:603:TYR:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:PHE:CE2	1:B:536:LYS:HB2	2.44	0.53
1:B:95:GLU:HG3	1:B:112:THR:HB	1.91	0.53
1:C:49:MET:HE3	1:C:66:ILE:HD12	1.91	0.53
1:A:50:ARG:HA	1:A:66:ILE:HD11	1.91	0.52
1:C:68:VAL:HG11	1:C:74:VAL:HG22	1.90	0.52
1:C:515:TYR:CE1	1:C:523:ARG:HG2	2.45	0.52
1:D:401:MET:HB2	1:D:532:PHE:CZ	2.45	0.52
1:A:95:GLU:HG3	1:A:112:THR:HB	1.91	0.51
1:C:188:LEU:HB3	1:C:260:LEU:HD13	1.91	0.51
1:C:303:ILE:HG13	1:C:307:LYS:HE2	1.92	0.51
1:C:461:MET:HE2	1:C:465:PHE:CE1	2.46	0.51
1:D:95:GLU:HG3	1:D:112:THR:HB	1.91	0.51
1:A:515:TYR:CE1	1:A:523:ARG:HG2	2.45	0.51
1:B:394:PHE:CZ	1:B:532:PHE:HB3	2.46	0.51
1:A:78:LEU:HD11	1:A:132:LEU:HD22	1.93	0.51
1:D:394:PHE:CZ	1:D:536:LYS:HB2	2.46	0.51
1:B:558:LEU:HD21	1:B:614:LEU:HD13	1.93	0.50
1:B:611:TYR:CG	1:B:710:LYS:HE3	2.46	0.50
1:C:276:THR:HG23	1:D:251:VAL:HG11	1.93	0.50
1:A:115:LEU:HD23	1:A:136:THR:HG22	1.94	0.50
1:D:385:MET:HE3	1:D:409:PRO:HB2	1.94	0.50
1:D:422:LEU:HD11	1:D:427:LEU:HD21	1.93	0.50
1:A:102:LEU:HD22	1:A:169:LEU:HD11	1.92	0.50
1:A:461:MET:HE2	1:A:465:PHE:CE1	2.46	0.50
1:B:47:VAL:HG23	1:B:80:GLY:HA2	1.94	0.49
1:C:102:LEU:HD22	1:C:169:LEU:HD11	1.93	0.49
1:D:611:TYR:CG	1:D:710:LYS:HE3	2.46	0.49
1:A:49:MET:HE3	1:A:66:ILE:HD12	1.94	0.49
1:B:394:PHE:CZ	1:B:536:LYS:HB2	2.47	0.49
1:C:78:LEU:HD11	1:C:132:LEU:HD22	1.95	0.49
1:D:394:PHE:CZ	1:D:532:PHE:HB3	2.47	0.49
1:A:56:LYS:HD2	1:A:72:SER:HB3	1.94	0.49
1:A:554:ALA:HB2	1:A:616:LEU:HD21	1.95	0.49
1:B:385:MET:HE3	1:B:409:PRO:HB2	1.93	0.49
1:B:422:LEU:HD11	1:B:427:LEU:HD21	1.94	0.49
1:C:115:LEU:HD23	1:C:136:THR:HG22	1.95	0.49
1:A:461:MET:HE3	1:A:461:MET:HA	1.95	0.48
1:B:401:MET:HB2	1:B:532:PHE:CZ	2.48	0.48
1:C:56:LYS:HD2	1:C:72:SER:HB3	1.94	0.48
1:A:303:ILE:HG13	1:A:307:LYS:HE2	1.94	0.48
1:B:564:GLN:HA	1:B:569:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:605:ARG:HG3	1:B:699:SER:HB2	1.95	0.48
1:A:280:VAL:HG22	1:B:251:VAL:CG2	2.30	0.48
1:C:50:ARG:HA	1:C:66:ILE:HD11	1.95	0.48
1:D:276:THR:O	1:D:280:VAL:HG23	2.14	0.48
1:D:564:GLN:HA	1:D:569:LEU:HD12	1.96	0.48
1:C:401:MET:HE3	1:D:428:ALA:HB1	1.96	0.47
1:A:369:ARG:HH21	1:B:355:VAL:HG21	1.79	0.47
1:D:139:LEU:HD11	1:D:172:MET:HG2	1.97	0.47
1:C:461:MET:HE3	1:C:461:MET:HA	1.95	0.47
1:B:579:LEU:HD22	1:B:709:ILE:HD13	1.96	0.47
1:D:579:LEU:HD22	1:D:709:ILE:HD13	1.97	0.47
1:D:605:ARG:HG3	1:D:699:SER:HB2	1.96	0.47
1:D:47:VAL:HG23	1:D:80:GLY:HA2	1.97	0.47
1:D:539:ASP:O	1:D:542:LEU:HG	2.15	0.47
1:D:472:LEU:HD11	1:D:493:LEU:HB2	1.97	0.46
1:A:428:ALA:HB1	1:B:401:MET:HE3	1.96	0.46
1:A:604:THR:HB	1:A:607:LYS:HD3	1.97	0.46
1:A:112:THR:HG21	1:A:148:TYR:CD2	2.51	0.46
1:C:112:THR:HG21	1:C:148:TYR:CD2	2.51	0.46
1:D:558:LEU:HD21	1:D:614:LEU:HD13	1.97	0.46
1:C:163:TRP:HE3	1:C:168:SER:HB3	1.81	0.46
1:D:529:LYS:HA	1:D:532:PHE:CD2	2.51	0.46
1:A:251:VAL:HG11	1:B:280:VAL:CG2	2.46	0.46
1:B:529:LYS:HA	1:B:532:PHE:CD2	2.51	0.46
1:A:532:PHE:O	1:A:536:LYS:HG2	2.16	0.45
1:C:444:PHE:HE2	1:D:531:ASP:CG	2.24	0.45
1:C:51:LEU:HD21	1:C:58:CYS:SG	2.56	0.45
1:C:276:THR:HG23	1:D:251:VAL:CG1	2.46	0.45
1:B:551:LEU:HD11	1:B:579:LEU:HB3	1.97	0.45
1:C:444:PHE:HZ	1:D:531:ASP:HA	1.82	0.45
1:D:56:LYS:HD2	1:D:72:SER:HB3	1.99	0.45
1:D:537:ASP:HA	1:D:540:ASN:HB2	1.97	0.45
1:B:232:ILE:HD12	1:B:296:LEU:HD12	1.99	0.45
1:D:604:THR:HB	1:D:607:LYS:HD2	1.99	0.45
1:A:444:PHE:HE2	1:B:531:ASP:CG	2.25	0.45
1:B:286:LEU:HB3	1:B:287:PRO:HD3	1.99	0.45
1:C:532:PHE:O	1:C:536:LYS:HG2	2.17	0.45
1:A:186:ILE:HD13	1:A:264:LEU:HD21	1.98	0.44
1:B:139:LEU:HD11	1:B:172:MET:HG2	1.98	0.44
1:B:537:ASP:HA	1:B:540:ASN:HB2	2.00	0.44
1:A:401:MET:HE3	1:B:428:ALA:HB1	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:ILE:HG21	1:C:171:PHE:HD2	1.82	0.44
1:A:163:TRP:HE3	1:A:168:SER:HB3	1.82	0.44
1:B:56:LYS:HD2	1:B:72:SER:HB3	1.98	0.44
1:A:111:LEU:HD11	1:A:160:TRP:CE2	2.53	0.44
1:A:444:PHE:HZ	1:B:531:ASP:HA	1.81	0.44
1:C:450:HIS:HB2	1:C:470:SER:HB3	2.00	0.44
1:D:551:LEU:HD11	1:D:579:LEU:HB3	1.99	0.44
1:A:139:LEU:HD11	1:A:172:MET:HG2	1.98	0.44
1:B:604:THR:HB	1:B:607:LYS:HD2	1.99	0.44
1:A:51:LEU:HD21	1:A:58:CYS:SG	2.57	0.44
1:B:472:LEU:HD11	1:B:493:LEU:HB2	1.99	0.44
1:C:604:THR:HB	1:C:607:LYS:HD3	2.00	0.44
1:D:286:LEU:HB3	1:D:287:PRO:HD3	2.00	0.44
1:A:49:MET:HG2	1:A:50:ARG:N	2.33	0.44
1:D:422:LEU:HD21	1:D:427:LEU:HD11	2.00	0.44
1:C:290:LEU:HD23	1:D:328:LEU:HD21	2.00	0.43
1:D:386:ILE:HG23	1:D:410:VAL:HG22	2.00	0.43
1:D:117:VAL:HG13	1:D:132:LEU:HD21	2.00	0.43
1:D:218:GLN:O	1:D:226:ARG:HG3	2.17	0.43
1:B:584:VAL:HG12	1:B:585:ILE:HD12	1.99	0.43
1:C:111:LEU:HD11	1:C:160:TRP:CE2	2.52	0.43
1:B:318:PHE:HB3	1:B:319:PRO:HD3	2.01	0.43
1:A:564:GLN:HE22	1:A:644:LEU:HB2	1.83	0.43
1:B:386:ILE:HG23	1:B:410:VAL:HG22	2.01	0.43
1:A:462:LEU:HB2	1:A:499:VAL:HG11	1.99	0.43
1:B:464:GLU:HA	1:B:467:LYS:HD2	2.01	0.43
1:D:318:PHE:HB3	1:D:319:PRO:HD3	2.00	0.43
1:D:584:VAL:HG12	1:D:585:ILE:HD12	2.00	0.43
1:C:139:LEU:HD11	1:C:172:MET:HG2	2.00	0.43
1:C:564:GLN:HE22	1:C:644:LEU:HB2	1.84	0.43
1:A:591:ASP:H	1:A:600:HIS:CE1	2.37	0.42
1:A:227:ARG:HG2	1:A:231:LYS:HE2	2.01	0.42
1:C:186:ILE:HD13	1:C:264:LEU:HD21	1.99	0.42
1:A:65:ILE:HG21	1:A:171:PHE:HD1	1.85	0.42
1:C:276:THR:CG2	1:D:251:VAL:HG11	2.49	0.42
1:C:409:PRO:HG3	1:C:472:LEU:HD21	2.01	0.42
1:C:179:PHE:HB2	1:C:263:ASN:HD21	1.84	0.42
1:C:591:ASP:H	1:C:600:HIS:CE1	2.37	0.42
1:D:622:VAL:HG22	1:D:700:VAL:HG22	2.00	0.42
1:C:49:MET:HG2	1:C:50:ARG:N	2.34	0.42
1:B:117:VAL:HG13	1:B:132:LEU:HD21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:224:LYS:HG3	1:C:227:ARG:NH2	2.35	0.42
1:C:240:ASN:HD21	1:C:324:LEU:HB3	1.85	0.42
1:D:90:LEU:HA	1:D:153:ARG:HE	1.85	0.42
1:A:149:ALA:HB3	1:A:162:LYS:HD2	2.02	0.42
1:A:232:ILE:HD12	1:A:296:LEU:HD12	2.01	0.42
1:A:620:VAL:HG12	1:A:706:LEU:HD11	2.01	0.42
1:B:120:LEU:HD11	1:B:130:GLY:HA3	2.02	0.42
1:C:227:ARG:HG2	1:C:231:LYS:HE2	2.01	0.42
1:C:428:ALA:HB1	1:D:401:MET:HE3	2.02	0.42
1:C:495:THR:OG1	2:C:901:ATP:H3'	2.19	0.42
1:A:354:LEU:CD2	1:B:338:ARG:HG2	2.50	0.42
1:B:546:ILE:HD11	1:B:551:LEU:HD13	2.02	0.42
1:A:338:ARG:NH2	1:A:369:ARG:HG3	2.35	0.41
1:A:318:PHE:HB3	1:A:319:PRO:HD3	2.03	0.41
1:A:564:GLN:OE1	1:A:641:THR:HB	2.20	0.41
1:B:90:LEU:HA	1:B:153:ARG:HE	1.84	0.41
1:C:452:VAL:HG11	1:C:461:MET:SD	2.60	0.41
1:D:120:LEU:HD11	1:D:130:GLY:HA3	2.02	0.41
1:D:546:ILE:HD11	1:D:551:LEU:HD13	2.02	0.41
1:A:302:THR:HG22	1:A:305:LEU:HB3	2.03	0.41
1:A:452:VAL:HG11	1:A:461:MET:SD	2.60	0.41
1:C:613:ILE:HA	1:C:709:ILE:O	2.19	0.41
1:A:61:ASN:HD21	1:A:67:PHE:HB3	1.85	0.41
1:C:620:VAL:HG12	1:C:706:LEU:HD11	2.03	0.41
1:A:613:ILE:HA	1:A:709:ILE:O	2.21	0.41
1:B:199:PHE:HD1	1:B:199:PHE:HA	1.77	0.41
1:C:139:LEU:HD23	1:C:146:LYS:HG3	2.02	0.41
1:D:179:PHE:HD2	1:D:180:LEU:HG	1.85	0.41
1:B:422:LEU:HD21	1:B:427:LEU:HD11	2.03	0.41
1:C:462:LEU:HB2	1:C:499:VAL:HG11	2.02	0.41
1:D:101:THR:HA	1:D:104:LYS:HD2	2.02	0.41
1:B:50:ARG:HD3	1:B:66:ILE:HD11	2.03	0.41
1:B:622:VAL:HG22	1:B:700:VAL:HG22	2.01	0.41
1:C:149:ALA:HB3	1:C:162:LYS:HD2	2.02	0.41
1:C:218:GLN:NE2	1:C:230:ARG:HG2	2.35	0.41
1:C:338:ARG:NH2	1:C:369:ARG:HG3	2.36	0.41
1:A:224:LYS:HG3	1:A:227:ARG:NH2	2.35	0.41
1:B:539:ASP:O	1:B:542:LEU:HG	2.20	0.41
1:B:361:MET:HG2	1:B:504:ILE:HA	2.03	0.41
1:C:318:PHE:HB3	1:C:319:PRO:HD3	2.02	0.41
1:A:240:ASN:HD21	1:A:324:LEU:HB3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:LEU:HD11	1:B:132:LEU:HD22	2.03	0.40
1:D:66:ILE:O	1:D:170:LEU:HA	2.21	0.40
1:D:261:LEU:HD23	1:D:261:LEU:HA	1.91	0.40
1:A:61:ASN:ND2	1:A:67:PHE:HB3	2.37	0.40
1:A:216:ILE:O	1:A:220:CYS:HB3	2.22	0.40
1:A:218:GLN:NE2	1:A:230:ARG:HG2	2.36	0.40
1:B:101:THR:HA	1:B:104:LYS:HD2	2.02	0.40
1:D:361:MET:HG2	1:D:504:ILE:HA	2.03	0.40
1:D:232:ILE:HD12	1:D:296:LEU:HD12	2.02	0.40
1:C:232:ILE:HD12	1:C:296:LEU:HD12	2.03	0.40
1:D:275:SER:O	1:D:279:ILE:HG12	2.21	0.40
1:D:373:VAL:HG23	1:D:456:THR:O	2.21	0.40
1:D:464:GLU:HA	1:D:467:LYS:HD2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	633/844 (75%)	606 (96%)	27 (4%)	0	100	100
1	B	631/844 (75%)	617 (98%)	14 (2%)	0	100	100
1	C	633/844 (75%)	606 (96%)	27 (4%)	0	100	100
1	D	631/844 (75%)	621 (98%)	10 (2%)	0	100	100
All	All	2528/3376 (75%)	2450 (97%)	78 (3%)	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	574/734 (78%)	565 (98%)	9 (2%)	55	69
1	B	565/734 (77%)	559 (99%)	6 (1%)	65	74
1	C	574/734 (78%)	566 (99%)	8 (1%)	59	71
1	D	565/734 (77%)	560 (99%)	5 (1%)	70	75
All	All	2278/2936 (78%)	2250 (99%)	28 (1%)	61	72

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	VAL
1	A	123	VAL
1	A	125	ARG
1	A	185	HIS
1	A	189	ILE
1	A	276	THR
1	A	441	ILE
1	A	477	LYS
1	A	546	ILE
1	B	68	VAL
1	B	185	HIS
1	B	272	VAL
1	B	504	ILE
1	B	621	GLU
1	B	633	THR
1	C	74	VAL
1	C	123	VAL
1	C	125	ARG
1	C	185	HIS
1	C	189	ILE
1	C	441	ILE
1	C	477	LYS
1	C	546	ILE
1	D	185	HIS

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Mol	Chain	Res	Type
1	D	272	VAL
1	D	504	ILE
1	D	621	GLU
1	D	633	THR

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

Mol	Chain	Res	Type
1	A	61	ASN
1	A	218	GLN
1	A	447	HIS
1	A	479	ASN
1	A	564	GLN
1	B	118	GLN
1	B	127	ASN
1	B	185	HIS
1	B	203	ASN
1	B	263	ASN
1	B	564	GLN
1	C	218	GLN
1	C	263	ASN
1	C	379	GLN
1	C	447	HIS
1	C	479	ASN
1	C	564	GLN
1	D	185	HIS
1	D	263	ASN
1	D	294	HIS
1	D	564	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 20 ligands modelled in this entry, 16 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ATP	C	901	3	32,33,33	0.53	0	48,52,52	0.42	0
2	ATP	B	901	3	32,33,33	0.35	0	48,52,52	0.38	0
2	ATP	D	901	3	32,33,33	0.36	0	48,52,52	0.38	0
2	ATP	A	901	3	32,33,33	0.54	0	48,52,52	0.41	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
2	ATP	C	901	3	-	4/22/38/38	0/3/3/3
2	ATP	B	901	3	-	4/22/38/38	0/3/3/3
2	ATP	D	901	3	-	2/22/38/38	0/3/3/3
2	ATP	A	901	3	-	4/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	901	ATP	PB-O3B-PG-O2G
2	D	901	ATP	PB-O3B-PG-O2G

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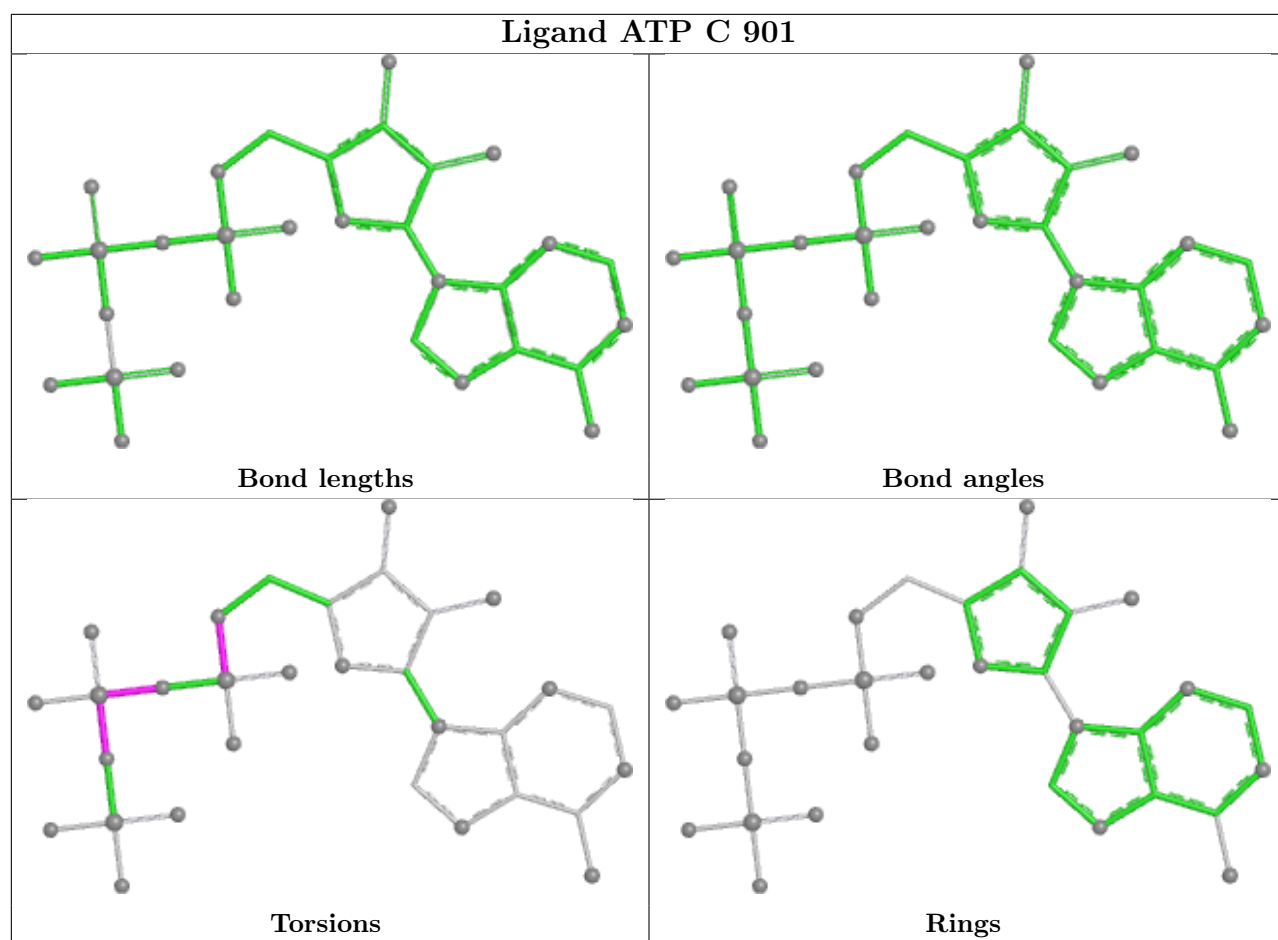
Mol	Chain	Res	Type	Atoms
2	A	901	ATP	PG-O3B-PB-O1B
2	C	901	ATP	PG-O3B-PB-O1B
2	A	901	ATP	C5'-O5'-PA-O1A
2	C	901	ATP	C5'-O5'-PA-O1A
2	B	901	ATP	PG-O3B-PB-O1B
2	B	901	ATP	PB-O3B-PG-O1G
2	D	901	ATP	PB-O3B-PG-O1G
2	C	901	ATP	PG-O3B-PB-O2B
2	A	901	ATP	PG-O3B-PB-O2B
2	A	901	ATP	PA-O3A-PB-O2B
2	B	901	ATP	PG-O3B-PB-O2B
2	C	901	ATP	PA-O3A-PB-O2B

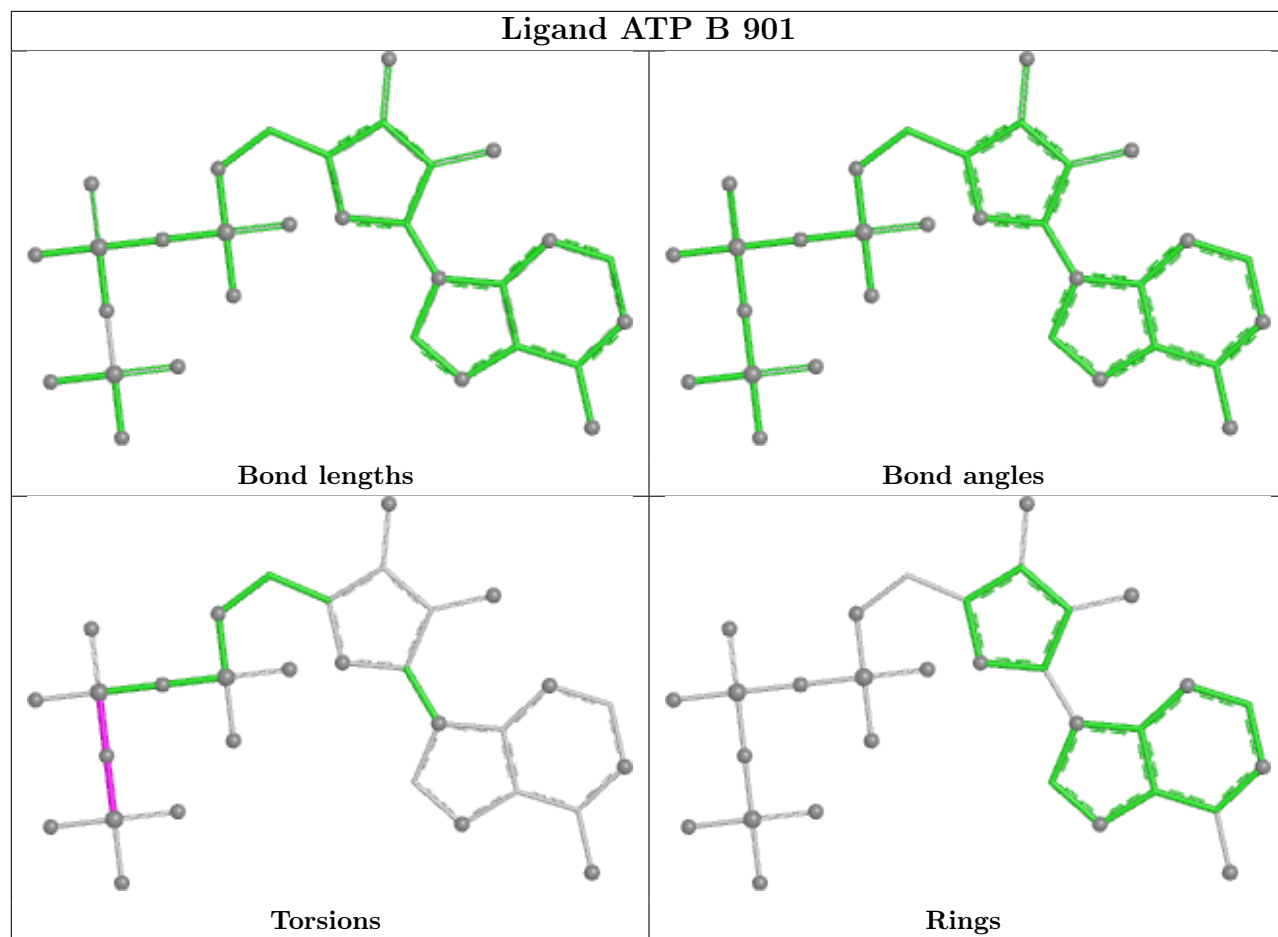
There are no ring outliers.

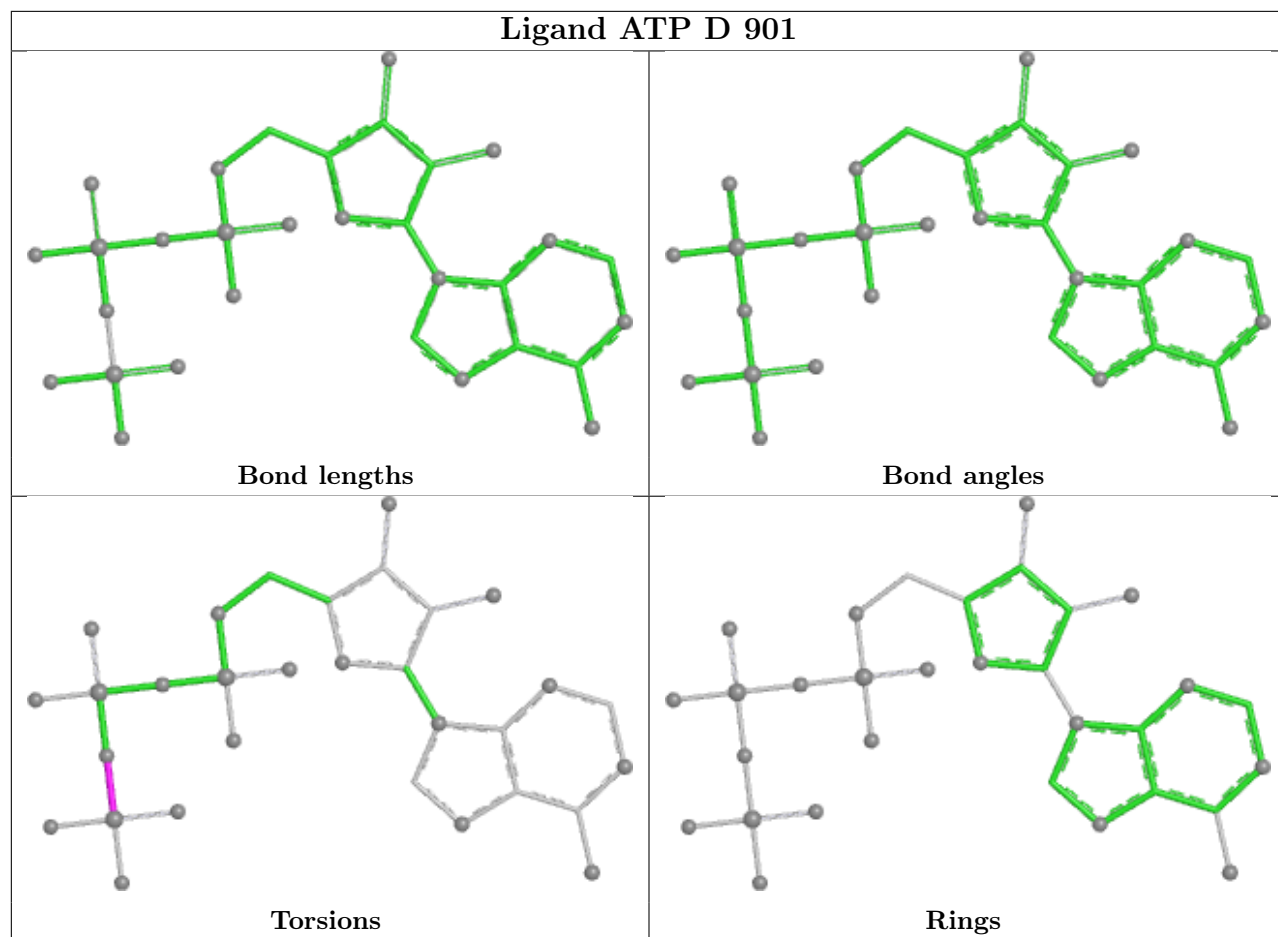
1 monomer is involved in 1 short contact:

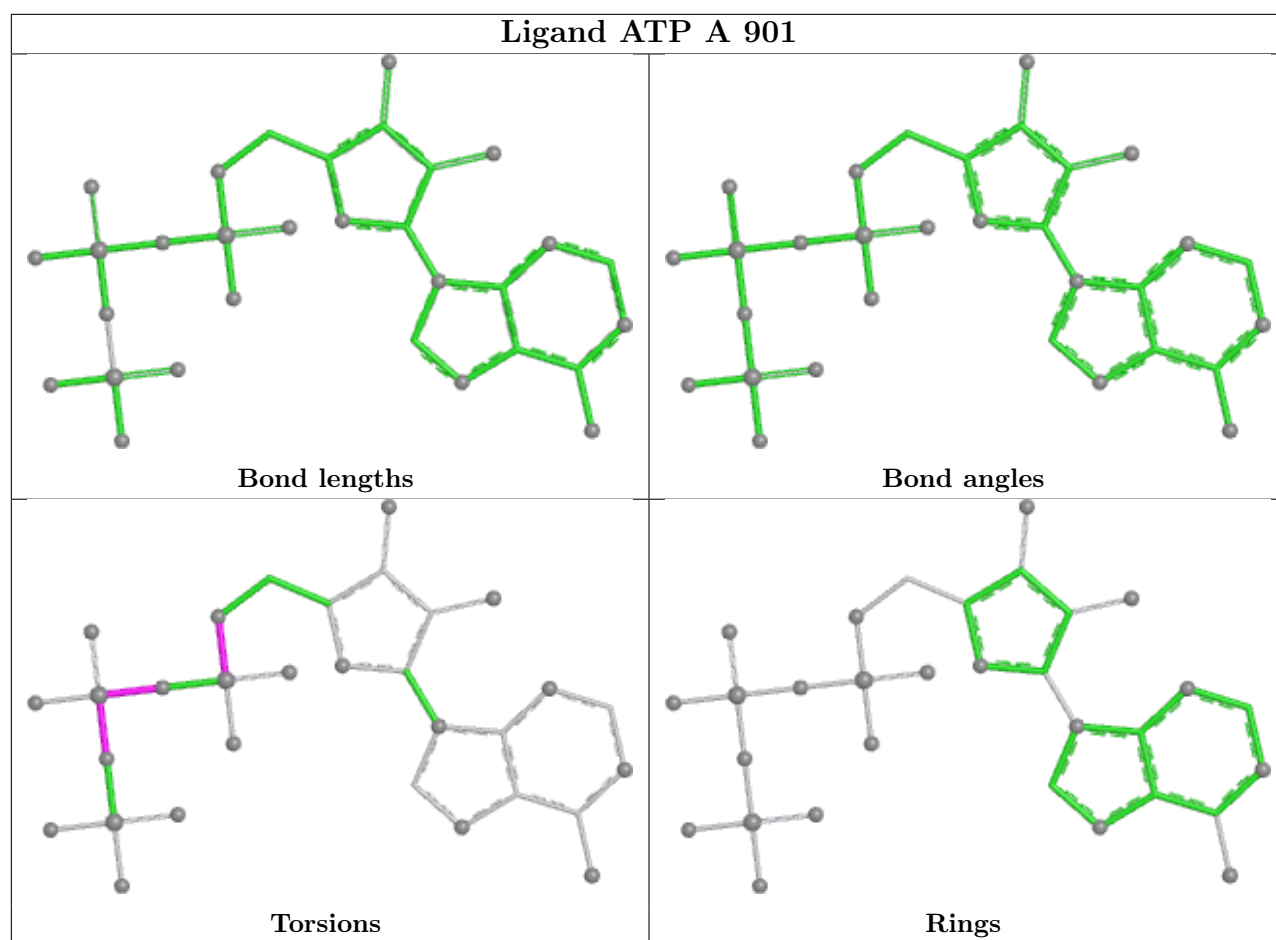
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	901	ATP	1	0

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.

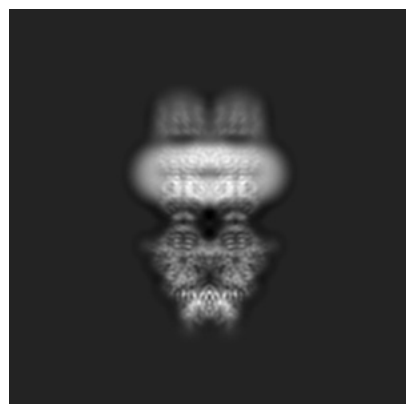
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72697. These allow visual inspection of the internal detail of the map and identification of artifacts.

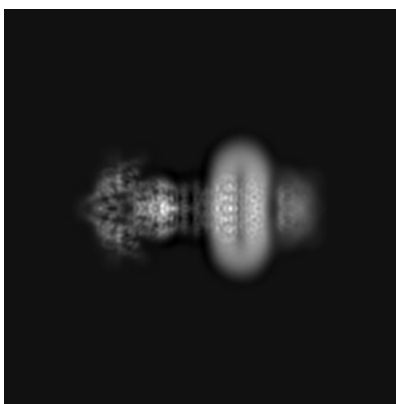
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

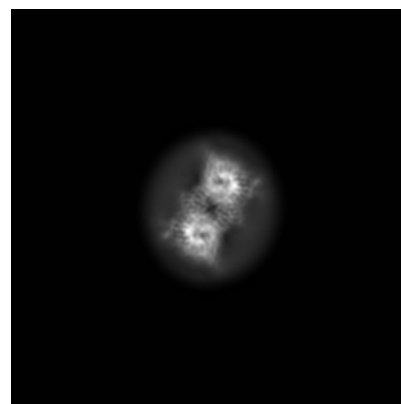
6.1.1 Primary map



X

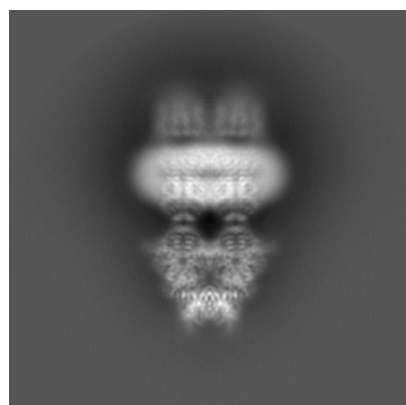


Y

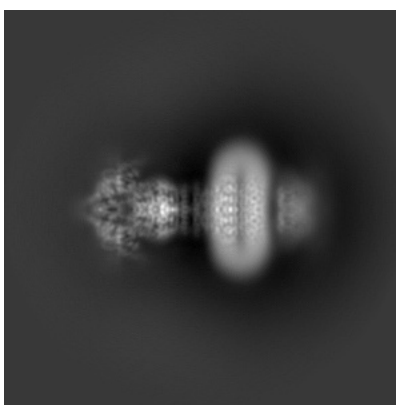


Z

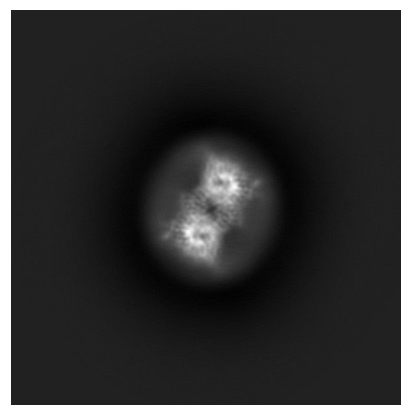
6.1.2 Raw map



X



Y

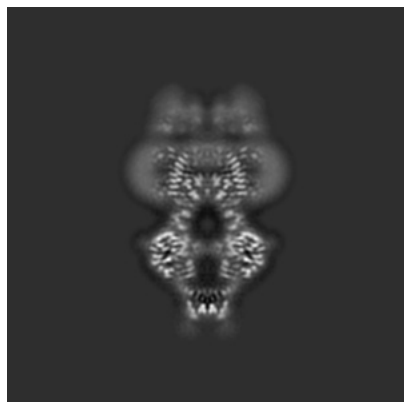


Z

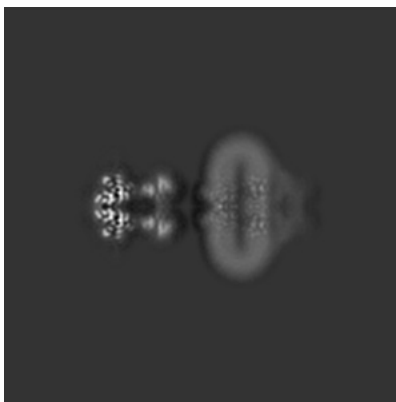
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

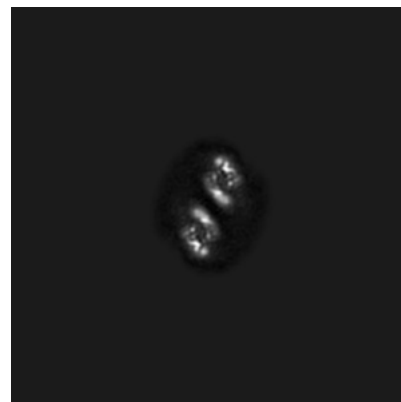
6.2.1 Primary map



X Index: 208

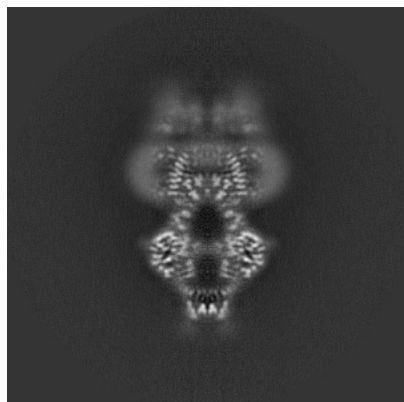


Y Index: 208

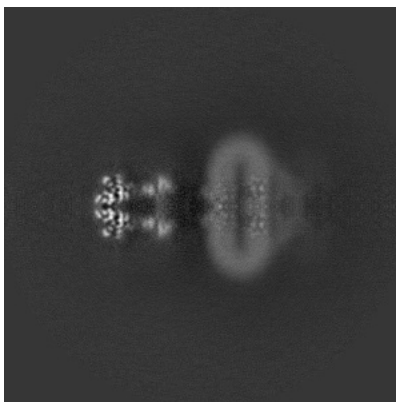


Z Index: 208

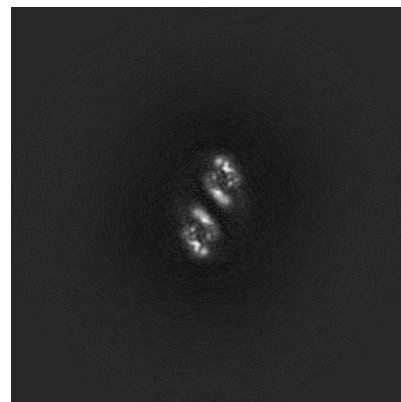
6.2.2 Raw map



X Index: 208



Y Index: 208

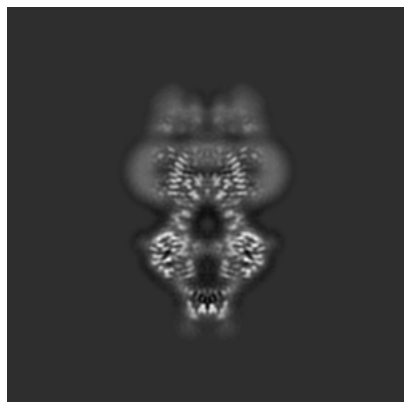


Z Index: 208

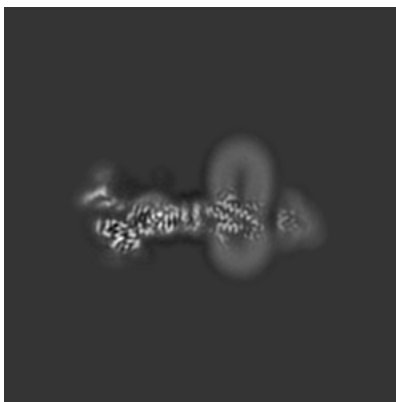
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

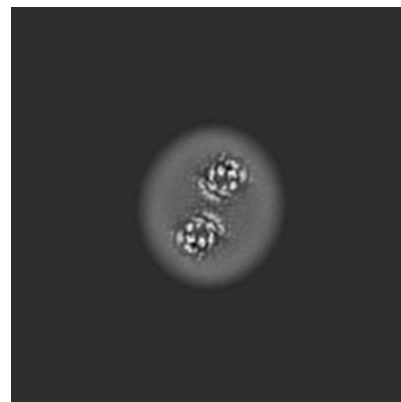
6.3.1 Primary map



X Index: 208

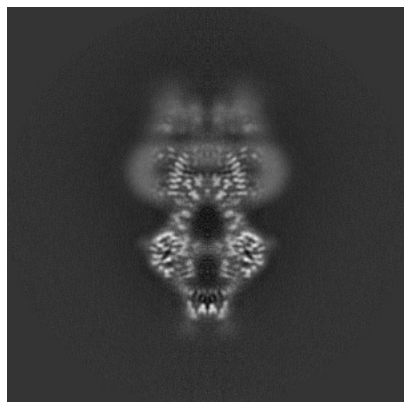


Y Index: 187

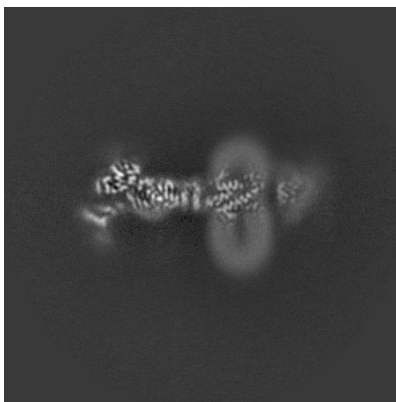


Z Index: 235

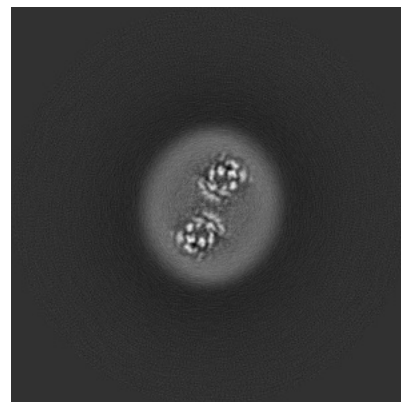
6.3.2 Raw map



X Index: 208



Y Index: 229

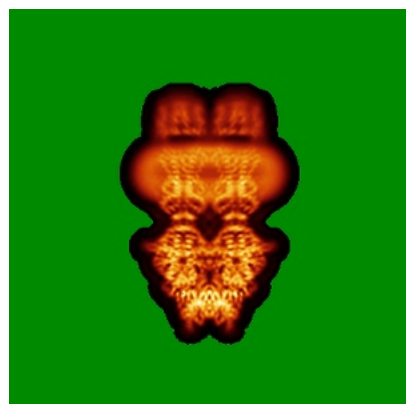


Z Index: 235

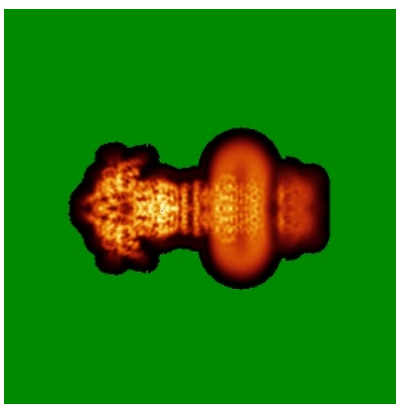
The images above show the largest variance slices of the map in three orthogonal directions.

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

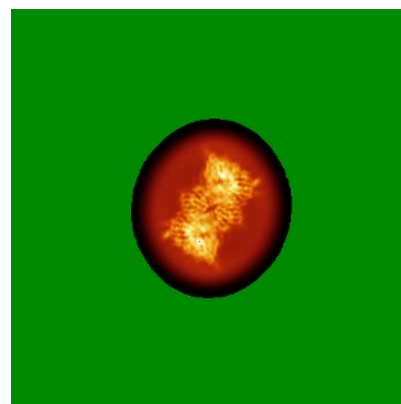
6.4.1 Primary map



X

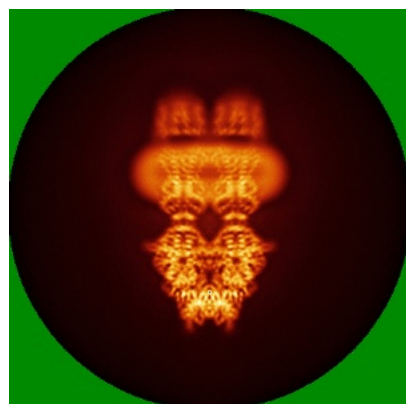


Y

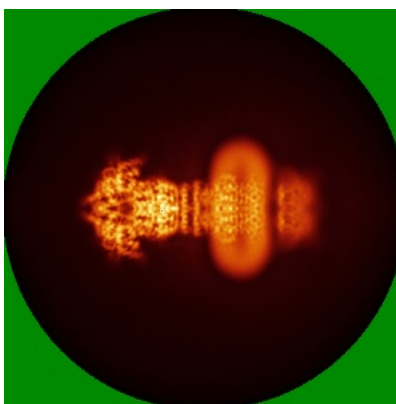


Z

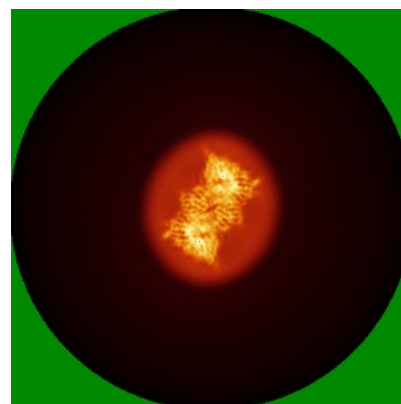
6.4.2 Raw map



X



Y

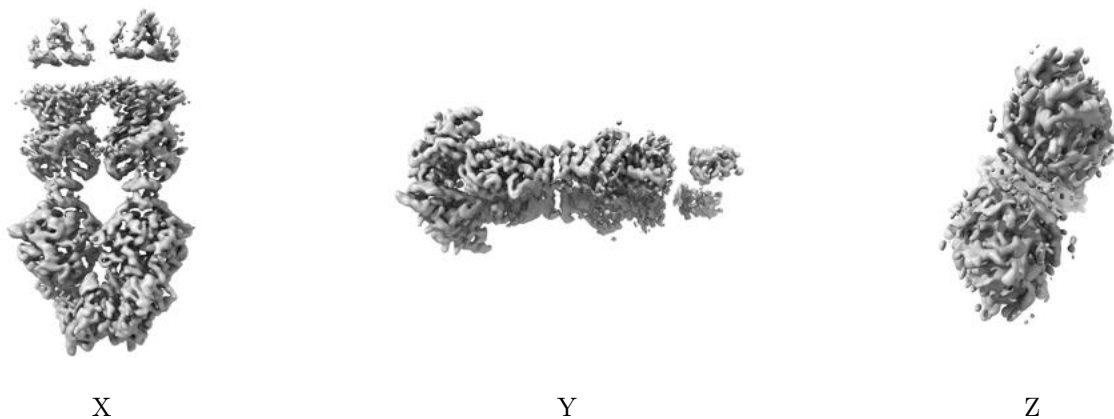


Z

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 0.00283. 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.

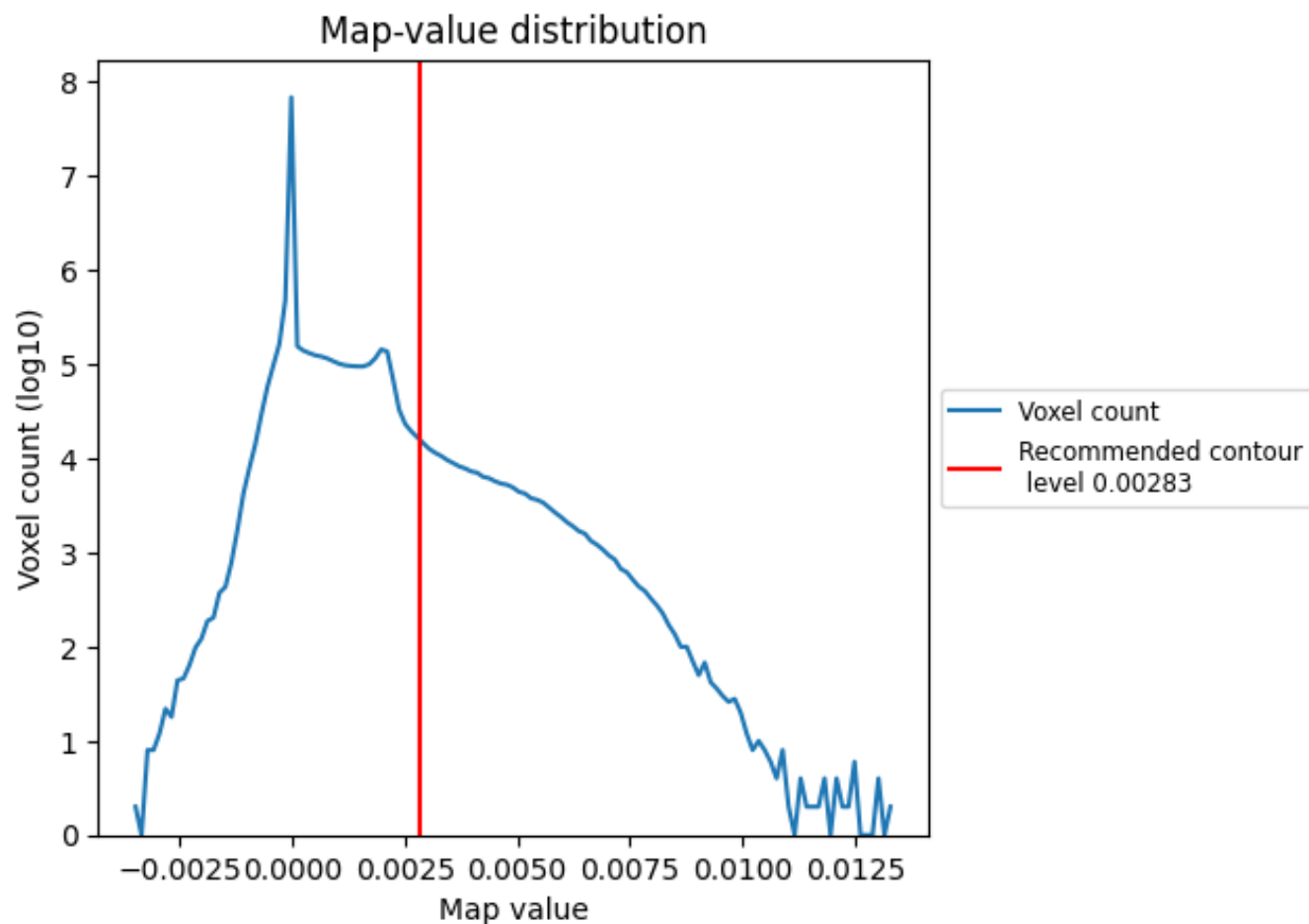
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

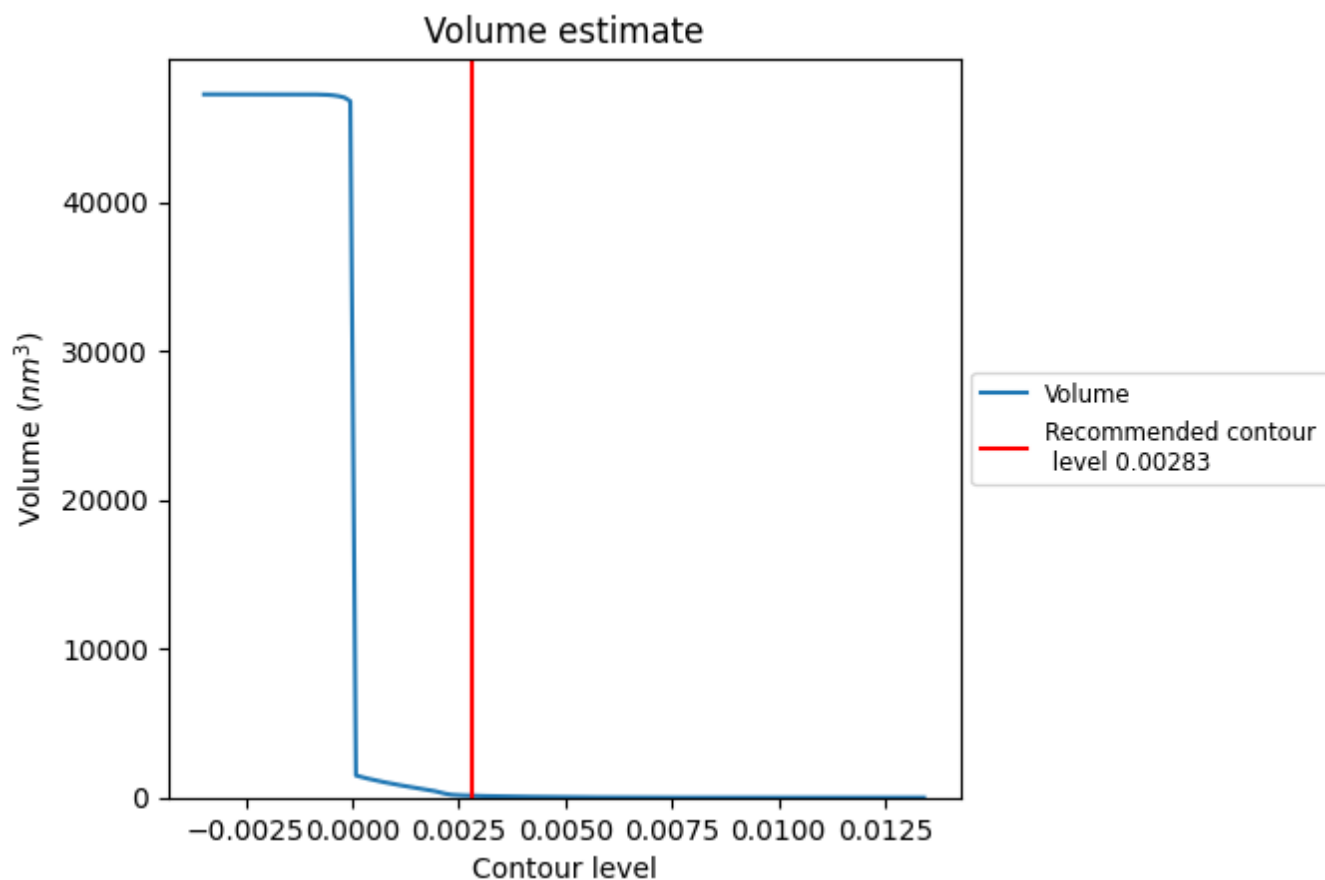
This section contains the results of statistical analysis of the map.

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.

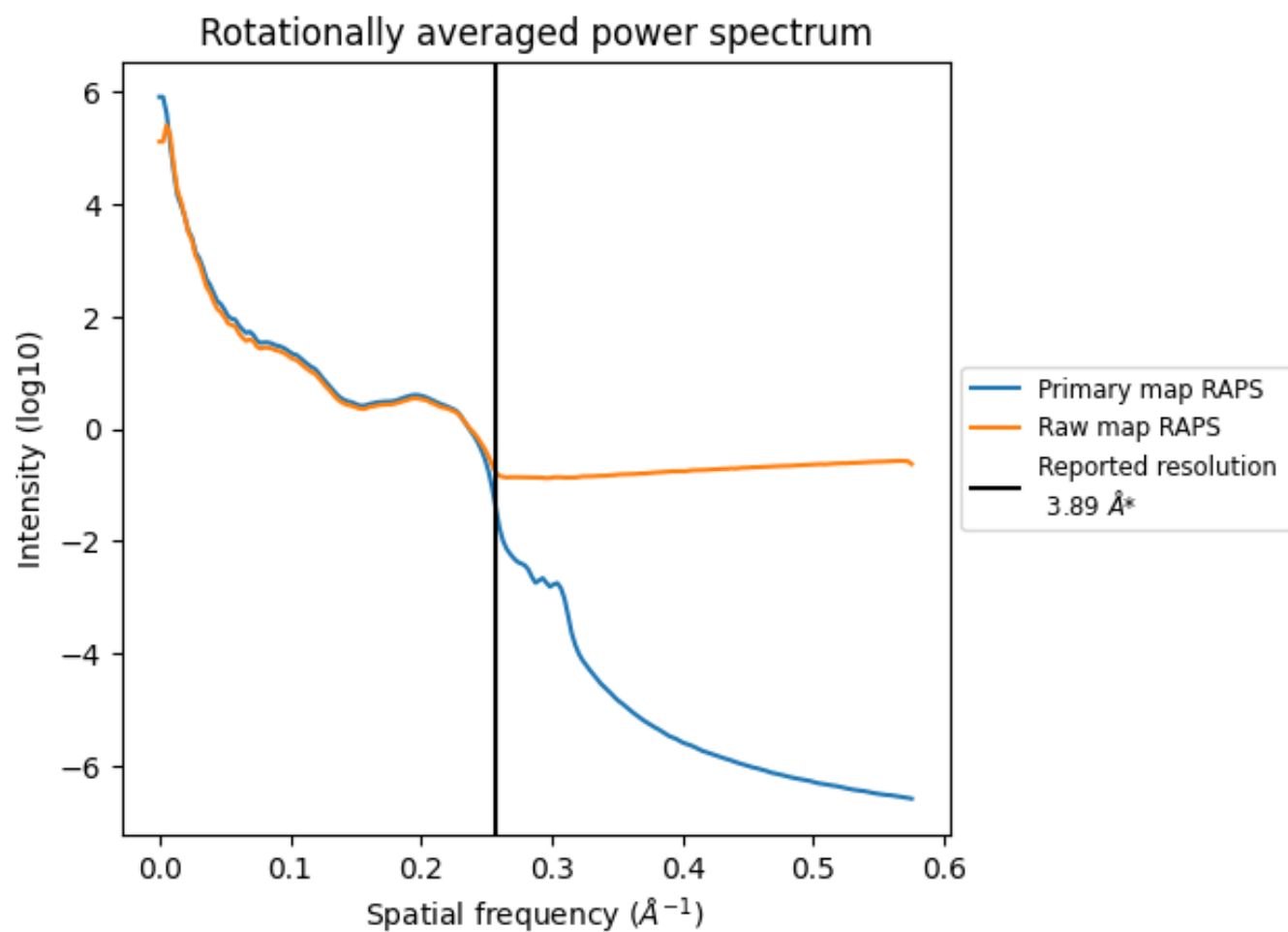
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm^3 ; this corresponds to an approximate mass of 111 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 ⓘ

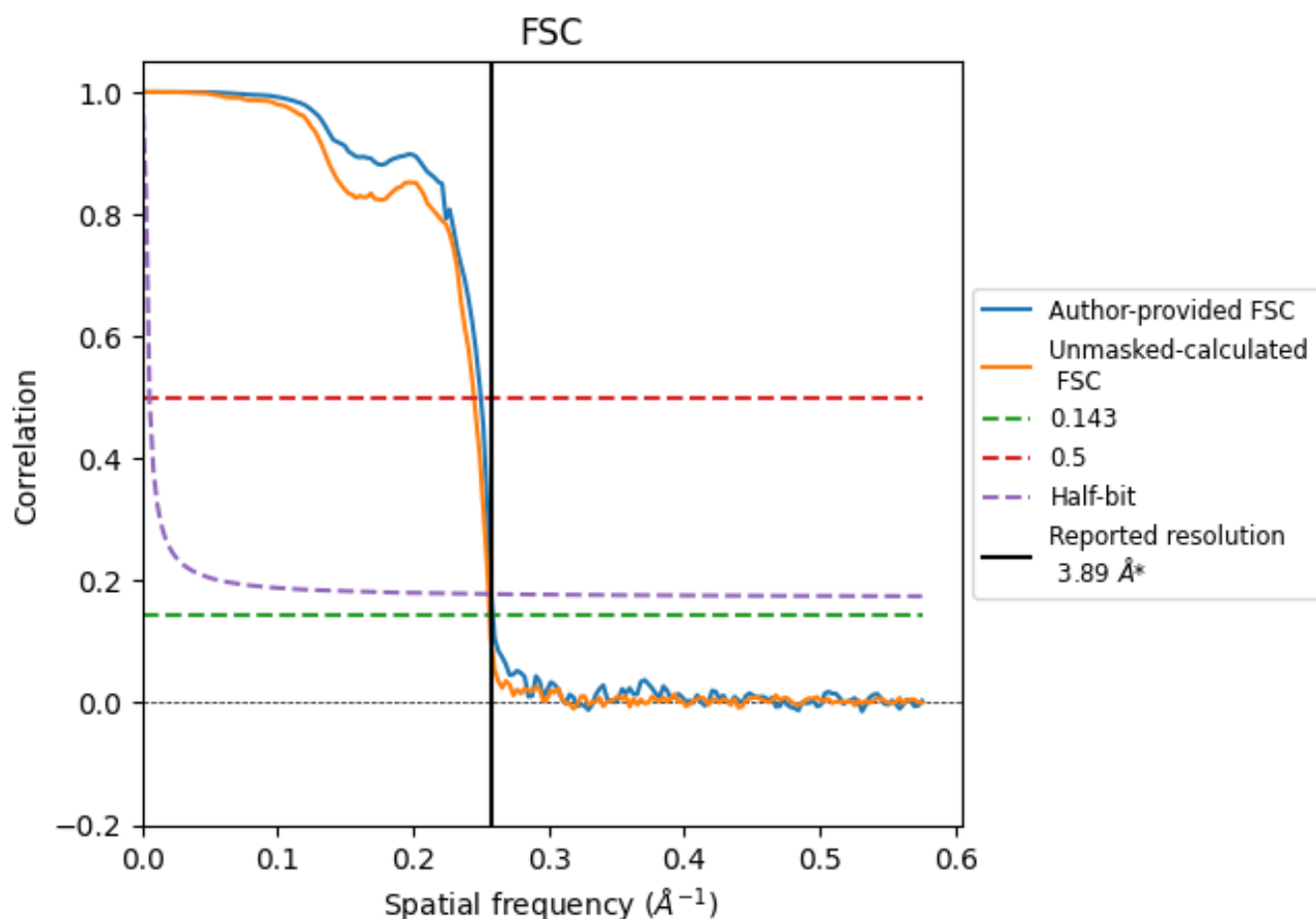


*Reported resolution corresponds to spatial frequency of 0.257 $\text{\AA}^{-1}$

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 0.257 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

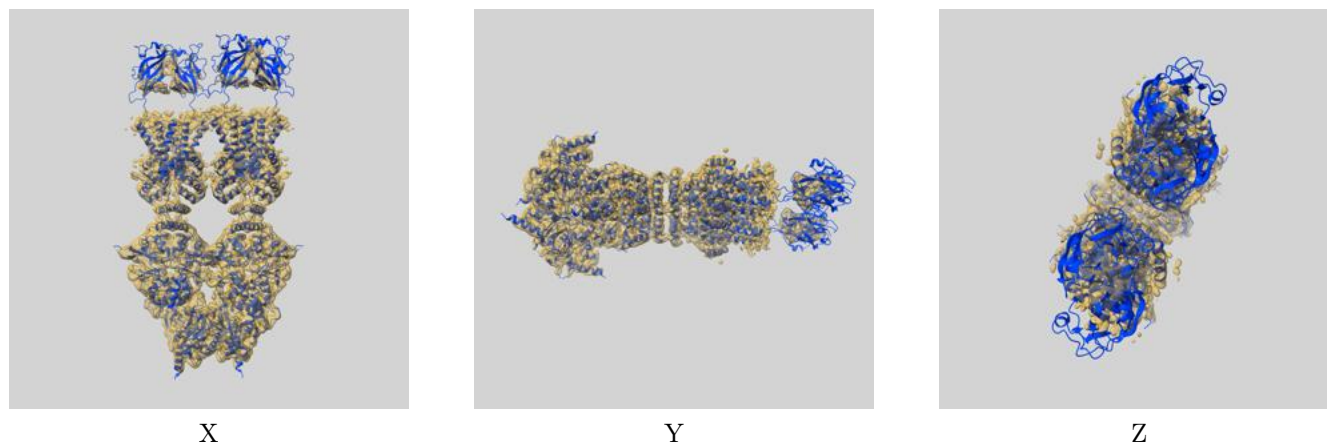
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.89	-	-
Author-provided FSC curve	3.87	4.00	3.89
Unmasked-calculated*	3.90	4.09	3.91

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

9 Map-model fit [i](#)

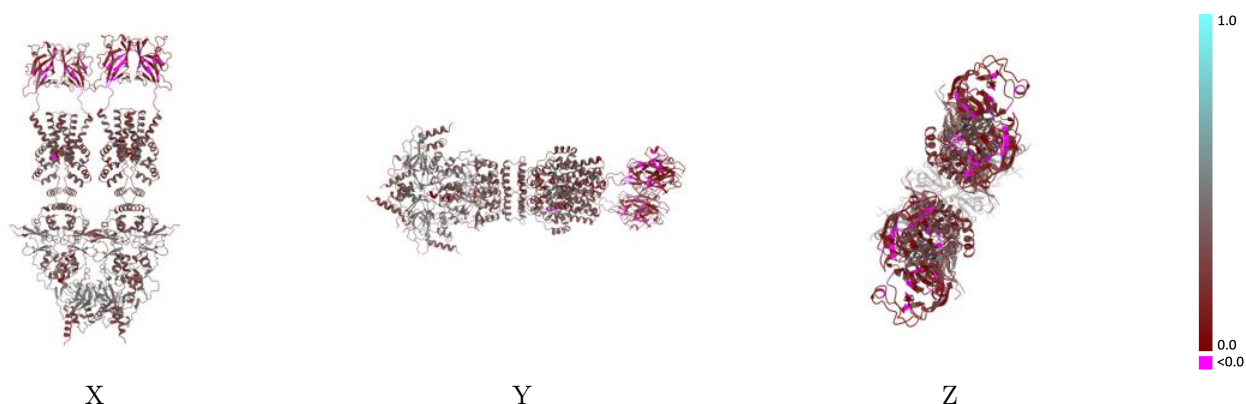
This section contains information regarding the fit between EMDB map EMD-72697 and PDB model 9Y9G. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



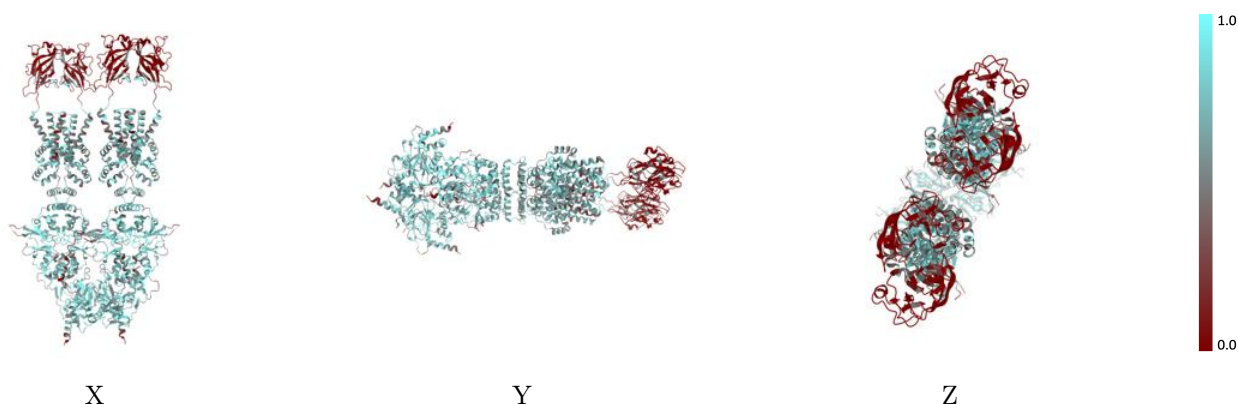
The images above show the 3D surface view of the map at the recommended contour level 0.00283 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



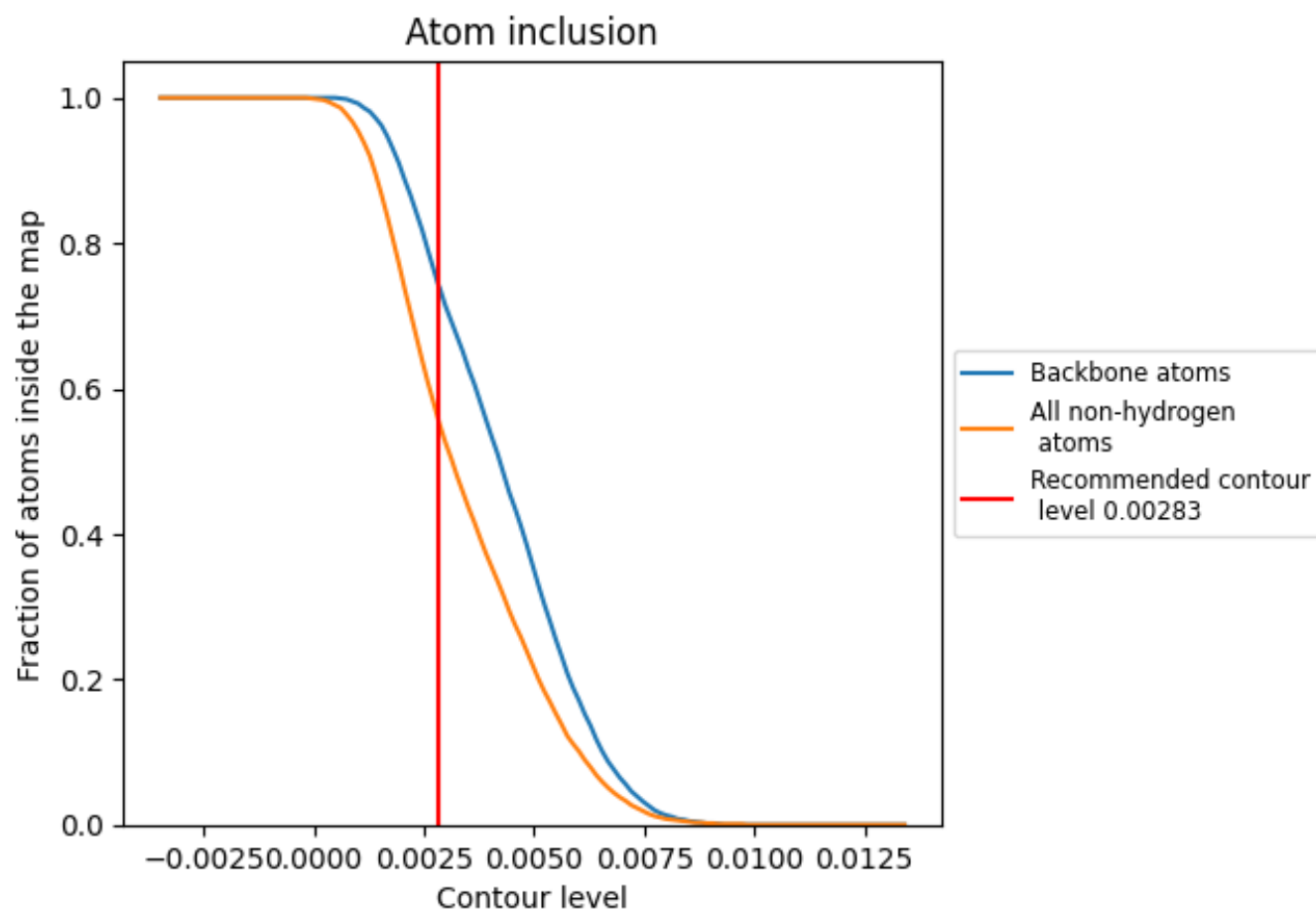
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00283).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.00283) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5560	0.3040
A	0.5630	0.3050
B	0.5490	0.3070
C	0.5610	0.3010
D	0.5490	0.3030

