wwPDB EM Validation Summary Report (i)

Apr 5, 2026 – 03:06 PM UTC

PDB ID	:	9H2L / pdb_00009h2l
EMDB ID	:	EMD-51810
Title	:	Cryo-EM structure of an octameric G10-resistosome from wheat
Authors	:	Guo, G.H.; Zhao, H.; Lukoyanova, N.; Selvaraj, M.; Jones, J.
Deposited on	:	2024-10-11
Resolution	:	3.95 Å(reported)
Based on initial model	:	.

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 (i) 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 (i)) were used in the production of this report:

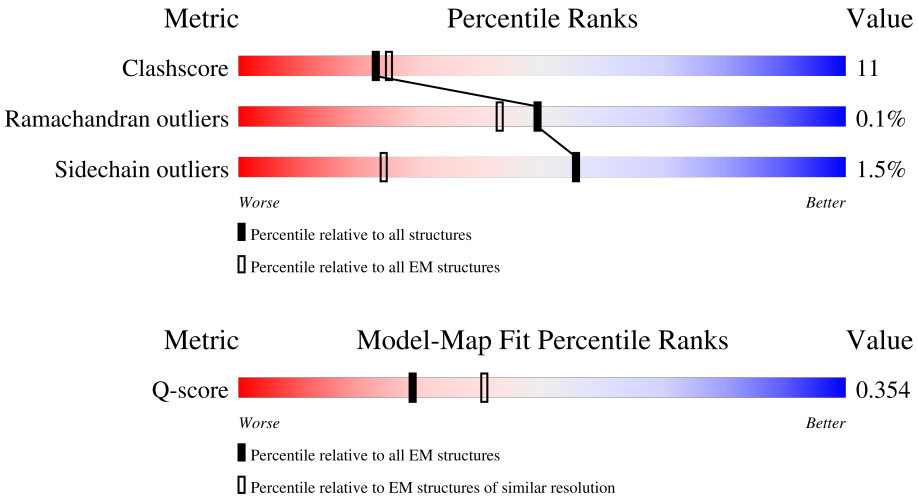
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data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

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.95 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	7707 (3.45 - 4.45)

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 <=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	948	9% 67% 22% • 10%
1	B	948	9% 68% 22% • 10%
1	C	948	9% 66% 23% • 10%
1	D	948	10% 65% 24% • 10%

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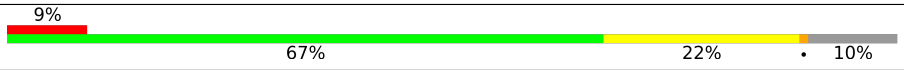
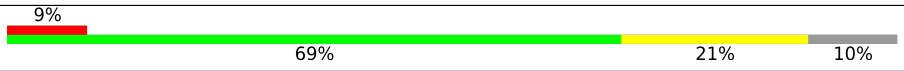
Mol	Chain	Length	Quality of chain
1	E	948	
1	F	948	
1	G	948	
1	H	948	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 54832 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 NB-ARC domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	B	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	C	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	D	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	E	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	F	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	G	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		
1	H	854	Total	C	N	O	S	0	0
			6823	4341	1177	1264	41		

There are 256 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLU	LEU	conflict	UNP A0A3B6DHR8
A	15	GLU	LEU	conflict	UNP A0A3B6DHR8
A	619	PHE	LEU	conflict	UNP A0A3B6DHR8
A	920	GLY	-	expression tag	UNP A0A3B6DHR8
A	921	SER	-	expression tag	UNP A0A3B6DHR8
A	922	ASP	-	expression tag	UNP A0A3B6DHR8
A	923	TYR	-	expression tag	UNP A0A3B6DHR8
A	924	LYS	-	expression tag	UNP A0A3B6DHR8
A	925	ASP	-	expression tag	UNP A0A3B6DHR8
A	926	HIS	-	expression tag	UNP A0A3B6DHR8
A	927	ASP	-	expression tag	UNP A0A3B6DHR8
A	928	GLY	-	expression tag	UNP A0A3B6DHR8
A	929	ASP	-	expression tag	UNP A0A3B6DHR8
A	930	TYR	-	expression tag	UNP A0A3B6DHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	931	LYS	-	expression tag	UNP A0A3B6DHR8
A	932	ASP	-	expression tag	UNP A0A3B6DHR8
A	933	HIS	-	expression tag	UNP A0A3B6DHR8
A	934	ASP	-	expression tag	UNP A0A3B6DHR8
A	935	LEU	-	expression tag	UNP A0A3B6DHR8
A	936	ASP	-	expression tag	UNP A0A3B6DHR8
A	937	ALA	-	expression tag	UNP A0A3B6DHR8
A	938	ALA	-	expression tag	UNP A0A3B6DHR8
A	939	ALA	-	expression tag	UNP A0A3B6DHR8
A	940	ALA	-	expression tag	UNP A0A3B6DHR8
A	941	ASP	-	expression tag	UNP A0A3B6DHR8
A	942	TYR	-	expression tag	UNP A0A3B6DHR8
A	943	LYS	-	expression tag	UNP A0A3B6DHR8
A	944	ASP	-	expression tag	UNP A0A3B6DHR8
A	945	ASP	-	expression tag	UNP A0A3B6DHR8
A	946	ASP	-	expression tag	UNP A0A3B6DHR8
A	947	ASP	-	expression tag	UNP A0A3B6DHR8
A	948	LYS	-	expression tag	UNP A0A3B6DHR8
B	12	GLU	LEU	conflict	UNP A0A3B6DHR8
B	15	GLU	LEU	conflict	UNP A0A3B6DHR8
B	619	PHE	LEU	conflict	UNP A0A3B6DHR8
B	920	GLY	-	expression tag	UNP A0A3B6DHR8
B	921	SER	-	expression tag	UNP A0A3B6DHR8
B	922	ASP	-	expression tag	UNP A0A3B6DHR8
B	923	TYR	-	expression tag	UNP A0A3B6DHR8
B	924	LYS	-	expression tag	UNP A0A3B6DHR8
B	925	ASP	-	expression tag	UNP A0A3B6DHR8
B	926	HIS	-	expression tag	UNP A0A3B6DHR8
B	927	ASP	-	expression tag	UNP A0A3B6DHR8
B	928	GLY	-	expression tag	UNP A0A3B6DHR8
B	929	ASP	-	expression tag	UNP A0A3B6DHR8
B	930	TYR	-	expression tag	UNP A0A3B6DHR8
B	931	LYS	-	expression tag	UNP A0A3B6DHR8
B	932	ASP	-	expression tag	UNP A0A3B6DHR8
B	933	HIS	-	expression tag	UNP A0A3B6DHR8
B	934	ASP	-	expression tag	UNP A0A3B6DHR8
B	935	LEU	-	expression tag	UNP A0A3B6DHR8
B	936	ASP	-	expression tag	UNP A0A3B6DHR8
B	937	ALA	-	expression tag	UNP A0A3B6DHR8
B	938	ALA	-	expression tag	UNP A0A3B6DHR8
B	939	ALA	-	expression tag	UNP A0A3B6DHR8
B	940	ALA	-	expression tag	UNP A0A3B6DHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	941	ASP	-	expression tag	UNP A0A3B6DHR8
B	942	TYR	-	expression tag	UNP A0A3B6DHR8
B	943	LYS	-	expression tag	UNP A0A3B6DHR8
B	944	ASP	-	expression tag	UNP A0A3B6DHR8
B	945	ASP	-	expression tag	UNP A0A3B6DHR8
B	946	ASP	-	expression tag	UNP A0A3B6DHR8
B	947	ASP	-	expression tag	UNP A0A3B6DHR8
B	948	LYS	-	expression tag	UNP A0A3B6DHR8
C	12	GLU	LEU	conflict	UNP A0A3B6DHR8
C	15	GLU	LEU	conflict	UNP A0A3B6DHR8
C	619	PHE	LEU	conflict	UNP A0A3B6DHR8
C	920	GLY	-	expression tag	UNP A0A3B6DHR8
C	921	SER	-	expression tag	UNP A0A3B6DHR8
C	922	ASP	-	expression tag	UNP A0A3B6DHR8
C	923	TYR	-	expression tag	UNP A0A3B6DHR8
C	924	LYS	-	expression tag	UNP A0A3B6DHR8
C	925	ASP	-	expression tag	UNP A0A3B6DHR8
C	926	HIS	-	expression tag	UNP A0A3B6DHR8
C	927	ASP	-	expression tag	UNP A0A3B6DHR8
C	928	GLY	-	expression tag	UNP A0A3B6DHR8
C	929	ASP	-	expression tag	UNP A0A3B6DHR8
C	930	TYR	-	expression tag	UNP A0A3B6DHR8
C	931	LYS	-	expression tag	UNP A0A3B6DHR8
C	932	ASP	-	expression tag	UNP A0A3B6DHR8
C	933	HIS	-	expression tag	UNP A0A3B6DHR8
C	934	ASP	-	expression tag	UNP A0A3B6DHR8
C	935	LEU	-	expression tag	UNP A0A3B6DHR8
C	936	ASP	-	expression tag	UNP A0A3B6DHR8
C	937	ALA	-	expression tag	UNP A0A3B6DHR8
C	938	ALA	-	expression tag	UNP A0A3B6DHR8
C	939	ALA	-	expression tag	UNP A0A3B6DHR8
C	940	ALA	-	expression tag	UNP A0A3B6DHR8
C	941	ASP	-	expression tag	UNP A0A3B6DHR8
C	942	TYR	-	expression tag	UNP A0A3B6DHR8
C	943	LYS	-	expression tag	UNP A0A3B6DHR8
C	944	ASP	-	expression tag	UNP A0A3B6DHR8
C	945	ASP	-	expression tag	UNP A0A3B6DHR8
C	946	ASP	-	expression tag	UNP A0A3B6DHR8
C	947	ASP	-	expression tag	UNP A0A3B6DHR8
C	948	LYS	-	expression tag	UNP A0A3B6DHR8
D	12	GLU	LEU	conflict	UNP A0A3B6DHR8
D	15	GLU	LEU	conflict	UNP A0A3B6DHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	619	PHE	LEU	conflict	UNP A0A3B6DHR8
D	920	GLY	-	expression tag	UNP A0A3B6DHR8
D	921	SER	-	expression tag	UNP A0A3B6DHR8
D	922	ASP	-	expression tag	UNP A0A3B6DHR8
D	923	TYR	-	expression tag	UNP A0A3B6DHR8
D	924	LYS	-	expression tag	UNP A0A3B6DHR8
D	925	ASP	-	expression tag	UNP A0A3B6DHR8
D	926	HIS	-	expression tag	UNP A0A3B6DHR8
D	927	ASP	-	expression tag	UNP A0A3B6DHR8
D	928	GLY	-	expression tag	UNP A0A3B6DHR8
D	929	ASP	-	expression tag	UNP A0A3B6DHR8
D	930	TYR	-	expression tag	UNP A0A3B6DHR8
D	931	LYS	-	expression tag	UNP A0A3B6DHR8
D	932	ASP	-	expression tag	UNP A0A3B6DHR8
D	933	HIS	-	expression tag	UNP A0A3B6DHR8
D	934	ASP	-	expression tag	UNP A0A3B6DHR8
D	935	LEU	-	expression tag	UNP A0A3B6DHR8
D	936	ASP	-	expression tag	UNP A0A3B6DHR8
D	937	ALA	-	expression tag	UNP A0A3B6DHR8
D	938	ALA	-	expression tag	UNP A0A3B6DHR8
D	939	ALA	-	expression tag	UNP A0A3B6DHR8
D	940	ALA	-	expression tag	UNP A0A3B6DHR8
D	941	ASP	-	expression tag	UNP A0A3B6DHR8
D	942	TYR	-	expression tag	UNP A0A3B6DHR8
D	943	LYS	-	expression tag	UNP A0A3B6DHR8
D	944	ASP	-	expression tag	UNP A0A3B6DHR8
D	945	ASP	-	expression tag	UNP A0A3B6DHR8
D	946	ASP	-	expression tag	UNP A0A3B6DHR8
D	947	ASP	-	expression tag	UNP A0A3B6DHR8
D	948	LYS	-	expression tag	UNP A0A3B6DHR8
E	12	GLU	LEU	conflict	UNP A0A3B6DHR8
E	15	GLU	LEU	conflict	UNP A0A3B6DHR8
E	619	PHE	LEU	conflict	UNP A0A3B6DHR8
E	920	GLY	-	expression tag	UNP A0A3B6DHR8
E	921	SER	-	expression tag	UNP A0A3B6DHR8
E	922	ASP	-	expression tag	UNP A0A3B6DHR8
E	923	TYR	-	expression tag	UNP A0A3B6DHR8
E	924	LYS	-	expression tag	UNP A0A3B6DHR8
E	925	ASP	-	expression tag	UNP A0A3B6DHR8
E	926	HIS	-	expression tag	UNP A0A3B6DHR8
E	927	ASP	-	expression tag	UNP A0A3B6DHR8
E	928	GLY	-	expression tag	UNP A0A3B6DHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	929	ASP	-	expression tag	UNP A0A3B6DHR8
E	930	TYR	-	expression tag	UNP A0A3B6DHR8
E	931	LYS	-	expression tag	UNP A0A3B6DHR8
E	932	ASP	-	expression tag	UNP A0A3B6DHR8
E	933	HIS	-	expression tag	UNP A0A3B6DHR8
E	934	ASP	-	expression tag	UNP A0A3B6DHR8
E	935	LEU	-	expression tag	UNP A0A3B6DHR8
E	936	ASP	-	expression tag	UNP A0A3B6DHR8
E	937	ALA	-	expression tag	UNP A0A3B6DHR8
E	938	ALA	-	expression tag	UNP A0A3B6DHR8
E	939	ALA	-	expression tag	UNP A0A3B6DHR8
E	940	ALA	-	expression tag	UNP A0A3B6DHR8
E	941	ASP	-	expression tag	UNP A0A3B6DHR8
E	942	TYR	-	expression tag	UNP A0A3B6DHR8
E	943	LYS	-	expression tag	UNP A0A3B6DHR8
E	944	ASP	-	expression tag	UNP A0A3B6DHR8
E	945	ASP	-	expression tag	UNP A0A3B6DHR8
E	946	ASP	-	expression tag	UNP A0A3B6DHR8
E	947	ASP	-	expression tag	UNP A0A3B6DHR8
E	948	LYS	-	expression tag	UNP A0A3B6DHR8
F	12	GLU	LEU	conflict	UNP A0A3B6DHR8
F	15	GLU	LEU	conflict	UNP A0A3B6DHR8
F	619	PHE	LEU	conflict	UNP A0A3B6DHR8
F	920	GLY	-	expression tag	UNP A0A3B6DHR8
F	921	SER	-	expression tag	UNP A0A3B6DHR8
F	922	ASP	-	expression tag	UNP A0A3B6DHR8
F	923	TYR	-	expression tag	UNP A0A3B6DHR8
F	924	LYS	-	expression tag	UNP A0A3B6DHR8
F	925	ASP	-	expression tag	UNP A0A3B6DHR8
F	926	HIS	-	expression tag	UNP A0A3B6DHR8
F	927	ASP	-	expression tag	UNP A0A3B6DHR8
F	928	GLY	-	expression tag	UNP A0A3B6DHR8
F	929	ASP	-	expression tag	UNP A0A3B6DHR8
F	930	TYR	-	expression tag	UNP A0A3B6DHR8
F	931	LYS	-	expression tag	UNP A0A3B6DHR8
F	932	ASP	-	expression tag	UNP A0A3B6DHR8
F	933	HIS	-	expression tag	UNP A0A3B6DHR8
F	934	ASP	-	expression tag	UNP A0A3B6DHR8
F	935	LEU	-	expression tag	UNP A0A3B6DHR8
F	936	ASP	-	expression tag	UNP A0A3B6DHR8
F	937	ALA	-	expression tag	UNP A0A3B6DHR8
F	938	ALA	-	expression tag	UNP A0A3B6DHR8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	939	ALA	-	expression tag	UNP A0A3B6DHR8
F	940	ALA	-	expression tag	UNP A0A3B6DHR8
F	941	ASP	-	expression tag	UNP A0A3B6DHR8
F	942	TYR	-	expression tag	UNP A0A3B6DHR8
F	943	LYS	-	expression tag	UNP A0A3B6DHR8
F	944	ASP	-	expression tag	UNP A0A3B6DHR8
F	945	ASP	-	expression tag	UNP A0A3B6DHR8
F	946	ASP	-	expression tag	UNP A0A3B6DHR8
F	947	ASP	-	expression tag	UNP A0A3B6DHR8
F	948	LYS	-	expression tag	UNP A0A3B6DHR8
G	12	GLU	LEU	conflict	UNP A0A3B6DHR8
G	15	GLU	LEU	conflict	UNP A0A3B6DHR8
G	619	PHE	LEU	conflict	UNP A0A3B6DHR8
G	920	GLY	-	expression tag	UNP A0A3B6DHR8
G	921	SER	-	expression tag	UNP A0A3B6DHR8
G	922	ASP	-	expression tag	UNP A0A3B6DHR8
G	923	TYR	-	expression tag	UNP A0A3B6DHR8
G	924	LYS	-	expression tag	UNP A0A3B6DHR8
G	925	ASP	-	expression tag	UNP A0A3B6DHR8
G	926	HIS	-	expression tag	UNP A0A3B6DHR8
G	927	ASP	-	expression tag	UNP A0A3B6DHR8
G	928	GLY	-	expression tag	UNP A0A3B6DHR8
G	929	ASP	-	expression tag	UNP A0A3B6DHR8
G	930	TYR	-	expression tag	UNP A0A3B6DHR8
G	931	LYS	-	expression tag	UNP A0A3B6DHR8
G	932	ASP	-	expression tag	UNP A0A3B6DHR8
G	933	HIS	-	expression tag	UNP A0A3B6DHR8
G	934	ASP	-	expression tag	UNP A0A3B6DHR8
G	935	LEU	-	expression tag	UNP A0A3B6DHR8
G	936	ASP	-	expression tag	UNP A0A3B6DHR8
G	937	ALA	-	expression tag	UNP A0A3B6DHR8
G	938	ALA	-	expression tag	UNP A0A3B6DHR8
G	939	ALA	-	expression tag	UNP A0A3B6DHR8
G	940	ALA	-	expression tag	UNP A0A3B6DHR8
G	941	ASP	-	expression tag	UNP A0A3B6DHR8
G	942	TYR	-	expression tag	UNP A0A3B6DHR8
G	943	LYS	-	expression tag	UNP A0A3B6DHR8
G	944	ASP	-	expression tag	UNP A0A3B6DHR8
G	945	ASP	-	expression tag	UNP A0A3B6DHR8
G	946	ASP	-	expression tag	UNP A0A3B6DHR8
G	947	ASP	-	expression tag	UNP A0A3B6DHR8
G	948	LYS	-	expression tag	UNP A0A3B6DHR8

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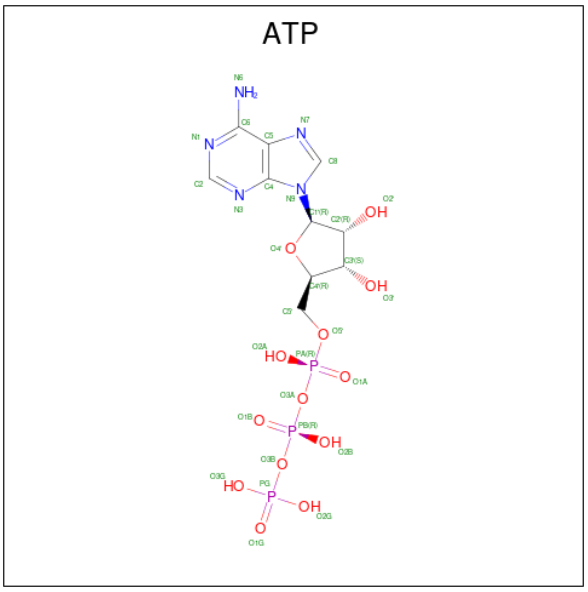
Chain	Residue	Modelled	Actual	Comment	Reference
H	12	GLU	LEU	conflict	UNP A0A3B6DHR8
H	15	GLU	LEU	conflict	UNP A0A3B6DHR8
H	619	PHE	LEU	conflict	UNP A0A3B6DHR8
H	920	GLY	-	expression tag	UNP A0A3B6DHR8
H	921	SER	-	expression tag	UNP A0A3B6DHR8
H	922	ASP	-	expression tag	UNP A0A3B6DHR8
H	923	TYR	-	expression tag	UNP A0A3B6DHR8
H	924	LYS	-	expression tag	UNP A0A3B6DHR8
H	925	ASP	-	expression tag	UNP A0A3B6DHR8
H	926	HIS	-	expression tag	UNP A0A3B6DHR8
H	927	ASP	-	expression tag	UNP A0A3B6DHR8
H	928	GLY	-	expression tag	UNP A0A3B6DHR8
H	929	ASP	-	expression tag	UNP A0A3B6DHR8
H	930	TYR	-	expression tag	UNP A0A3B6DHR8
H	931	LYS	-	expression tag	UNP A0A3B6DHR8
H	932	ASP	-	expression tag	UNP A0A3B6DHR8
H	933	HIS	-	expression tag	UNP A0A3B6DHR8
H	934	ASP	-	expression tag	UNP A0A3B6DHR8
H	935	LEU	-	expression tag	UNP A0A3B6DHR8
H	936	ASP	-	expression tag	UNP A0A3B6DHR8
H	937	ALA	-	expression tag	UNP A0A3B6DHR8
H	938	ALA	-	expression tag	UNP A0A3B6DHR8
H	939	ALA	-	expression tag	UNP A0A3B6DHR8
H	940	ALA	-	expression tag	UNP A0A3B6DHR8
H	941	ASP	-	expression tag	UNP A0A3B6DHR8
H	942	TYR	-	expression tag	UNP A0A3B6DHR8
H	943	LYS	-	expression tag	UNP A0A3B6DHR8
H	944	ASP	-	expression tag	UNP A0A3B6DHR8
H	945	ASP	-	expression tag	UNP A0A3B6DHR8
H	946	ASP	-	expression tag	UNP A0A3B6DHR8
H	947	ASP	-	expression tag	UNP A0A3B6DHR8
H	948	LYS	-	expression tag	UNP A0A3B6DHR8

- 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).

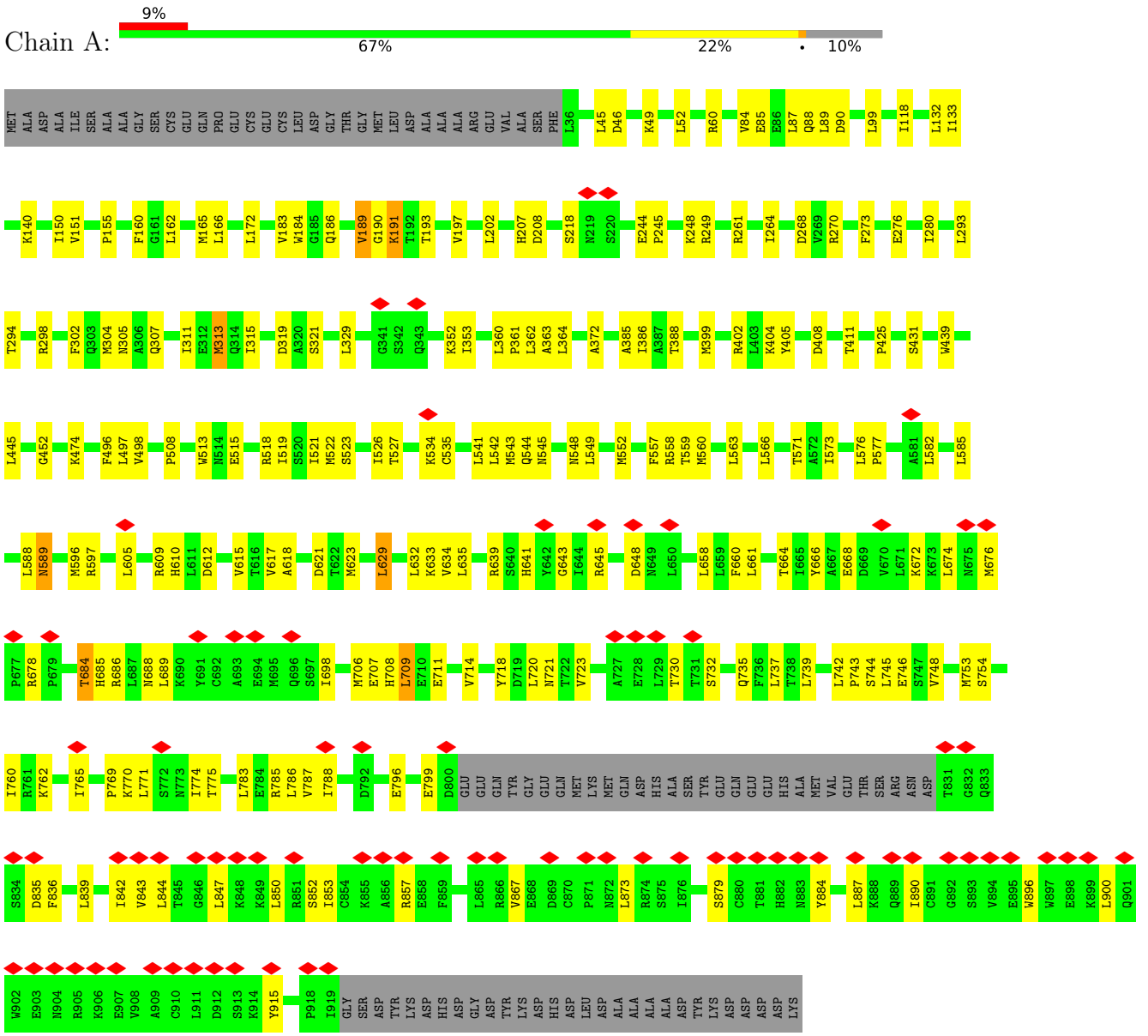


Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	F	1	Total	C	N	O	P	0
			31	10	5	13	3	
2	G	1	Total	C	N	O	P	0
			31	10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

3 Residue-property plots (i)

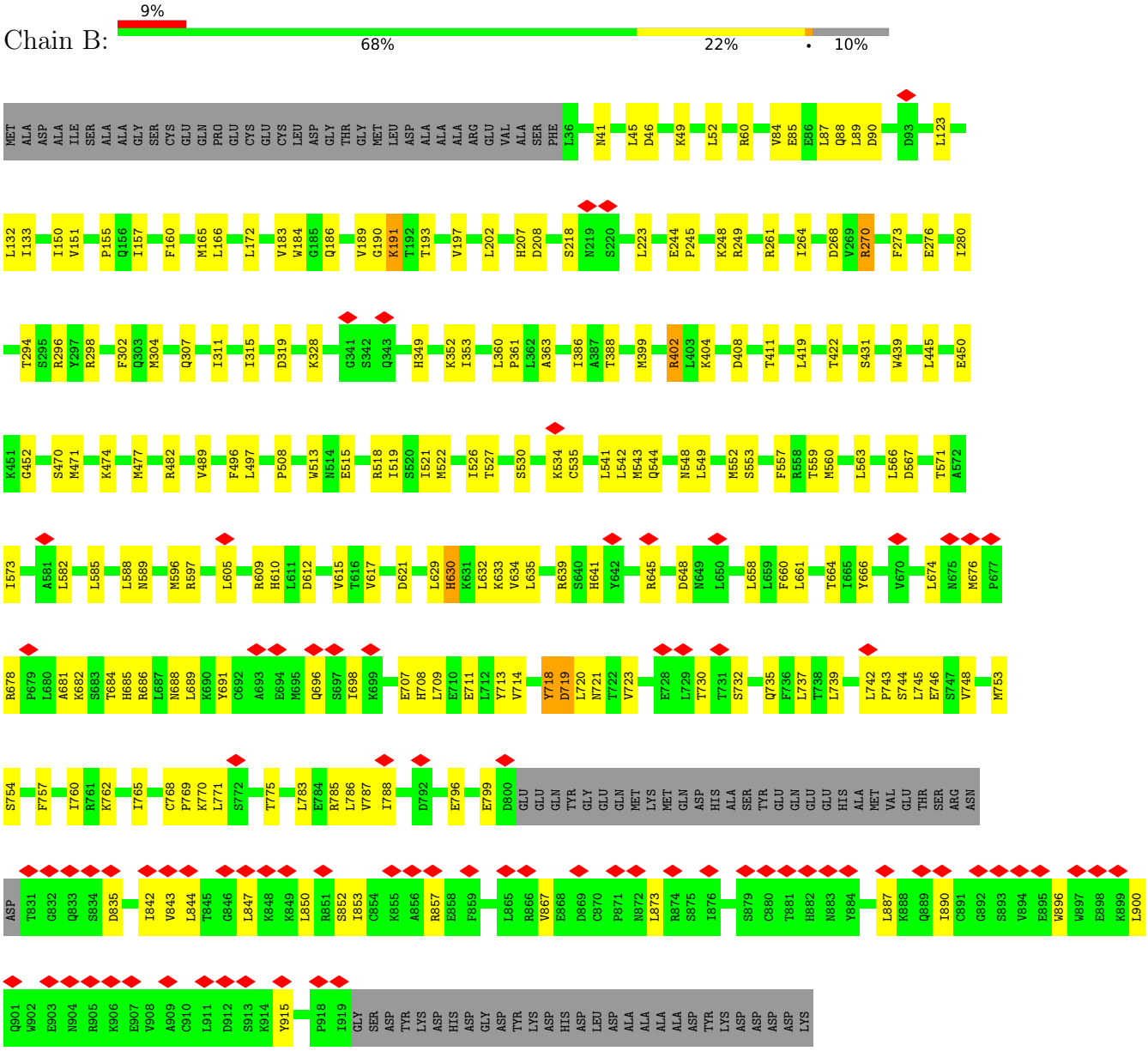
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



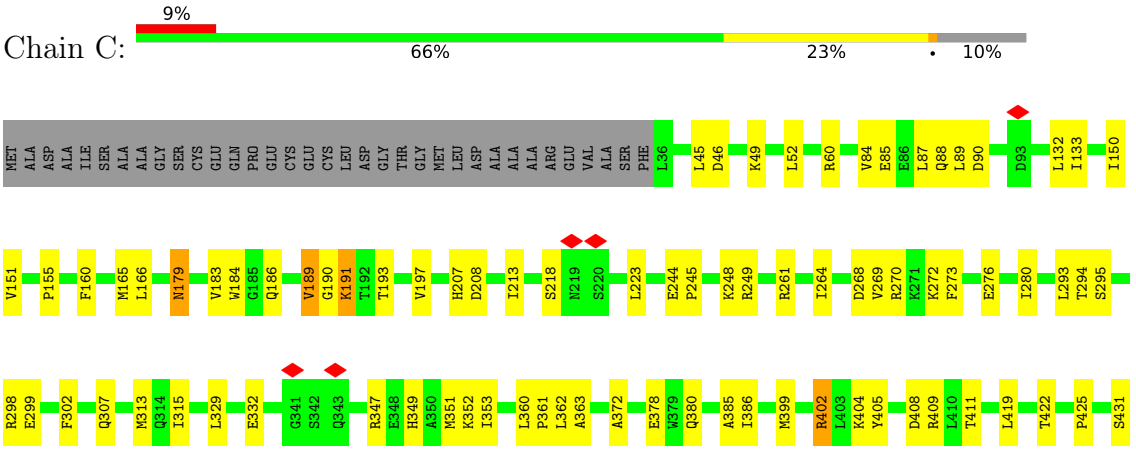
• Molecule 1: NB-ARC domain-containing protein

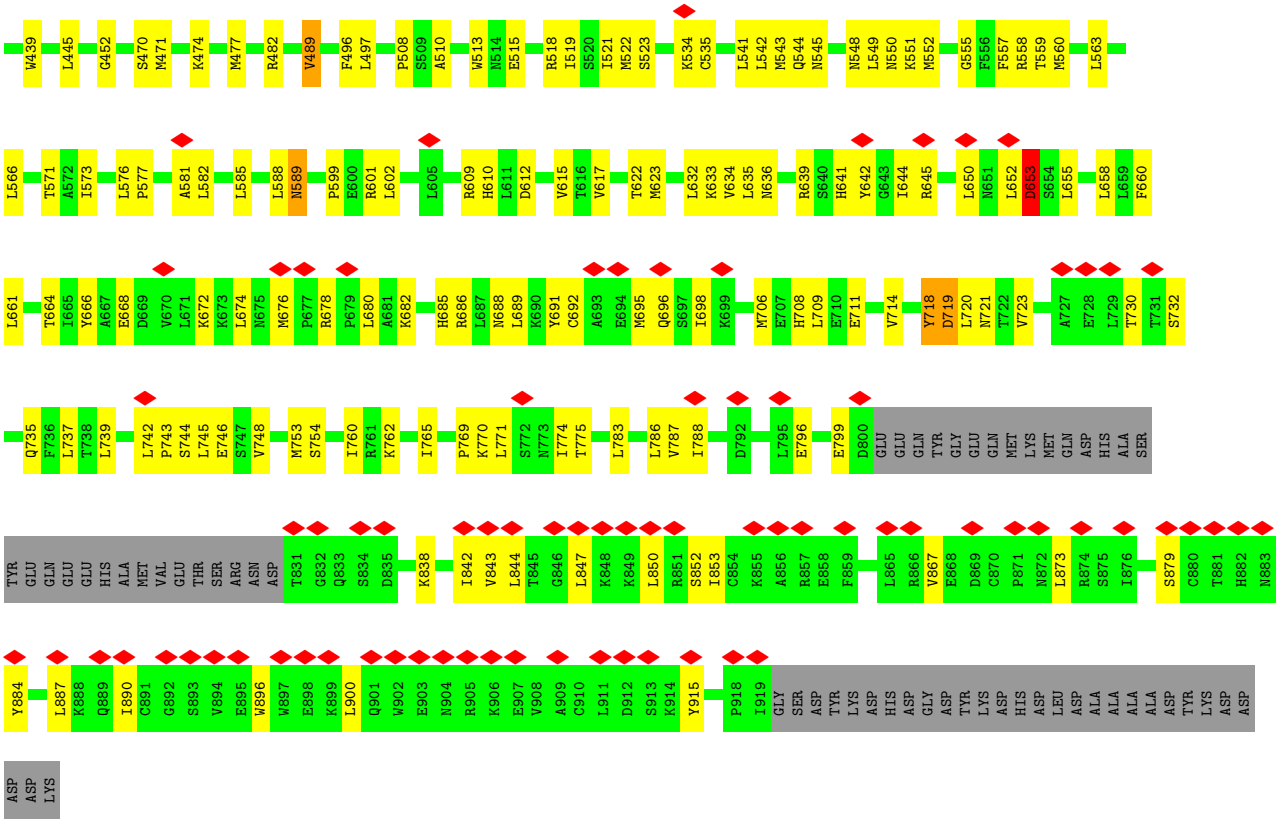
Chain B:



• Molecule 1: NB-ARC domain-containing protein

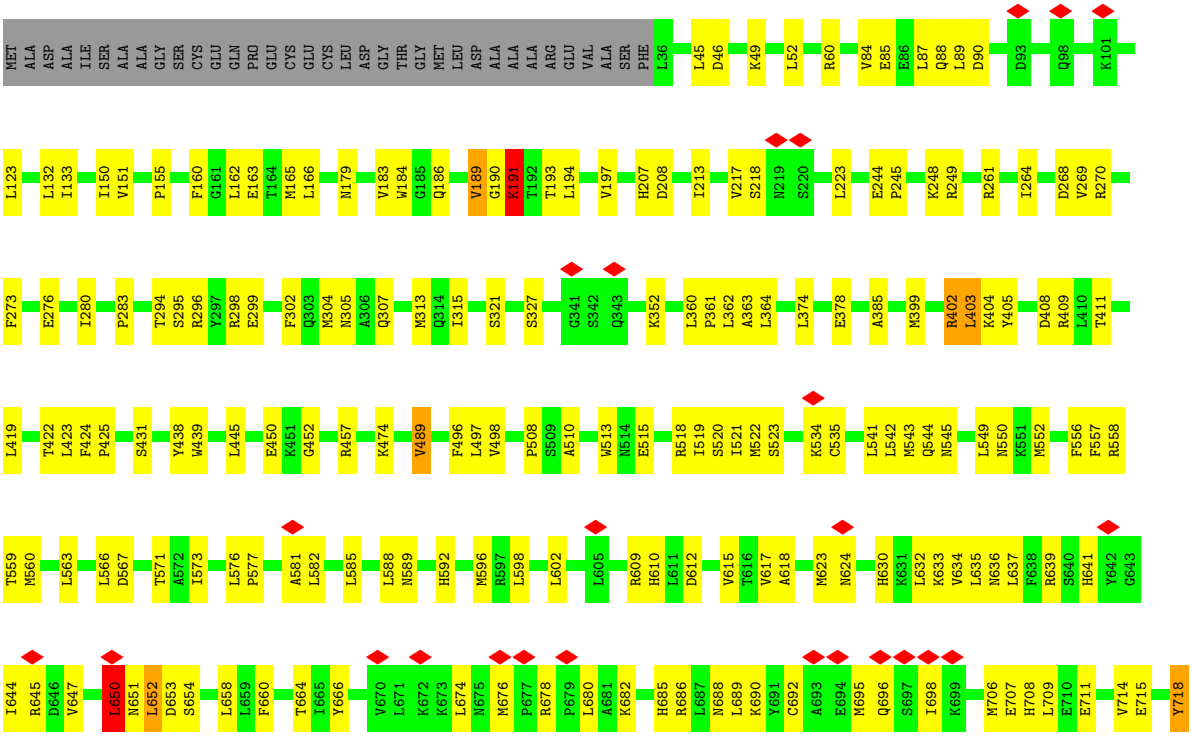
Chain C:

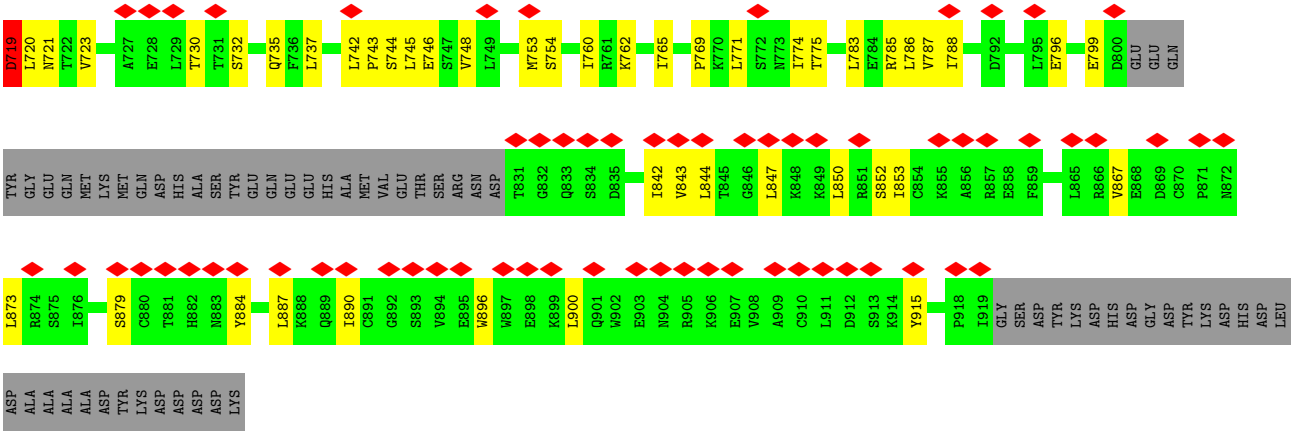




• Molecule 1: NB-ARC domain-containing protein

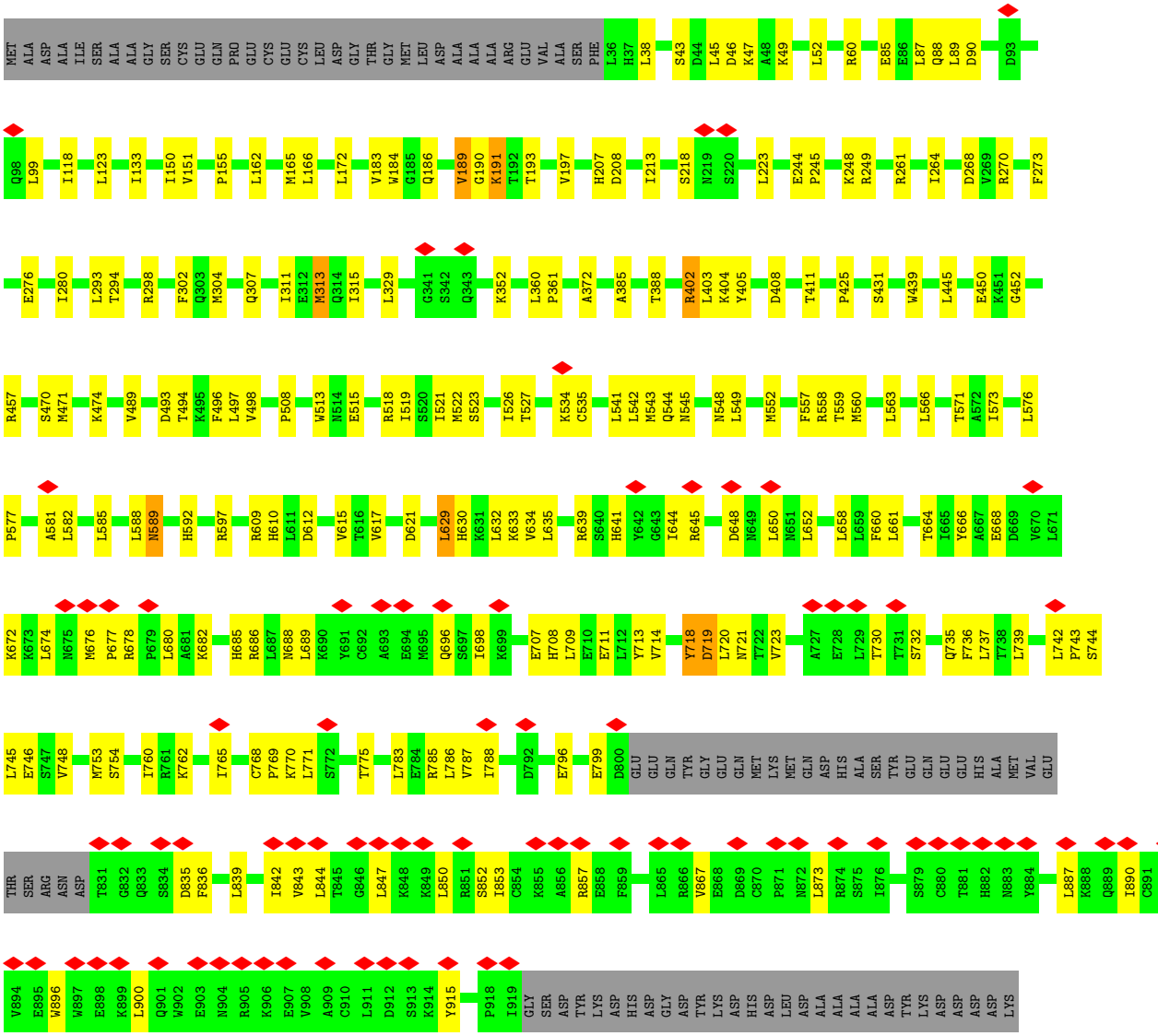
Chain D:





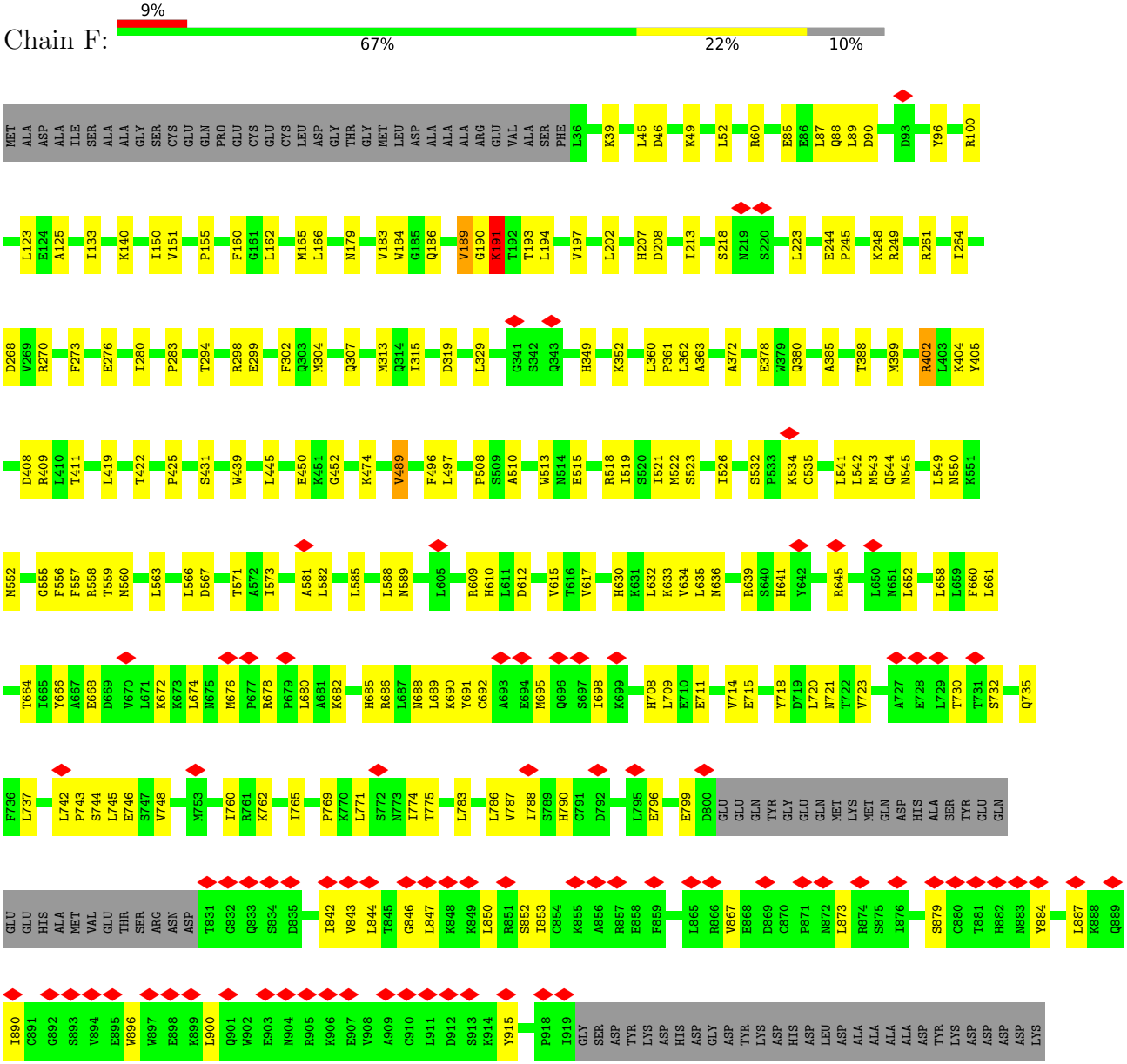
• Molecule 1: NB-ARC domain-containing protein

Chain E:



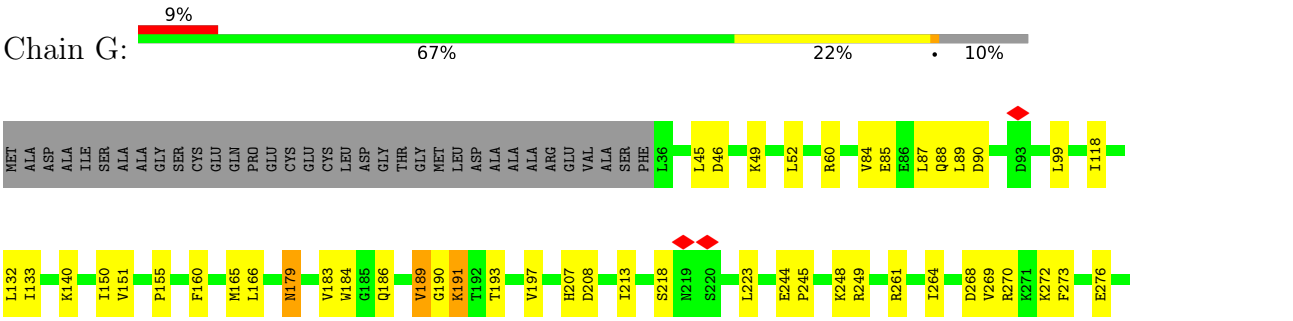
• Molecule 1: NB-ARC domain-containing protein

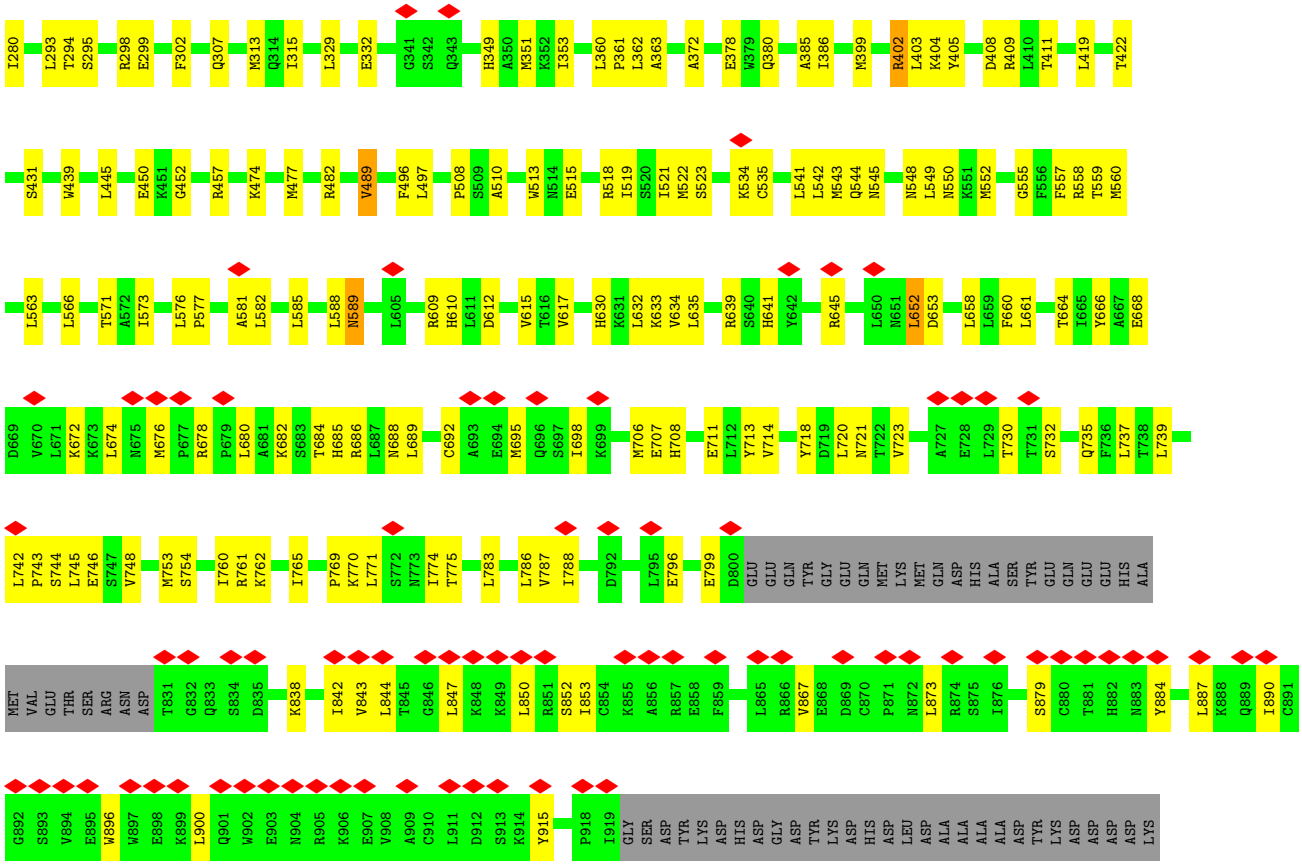
Chain F:



• Molecule 1: NB-ARC domain-containing protein

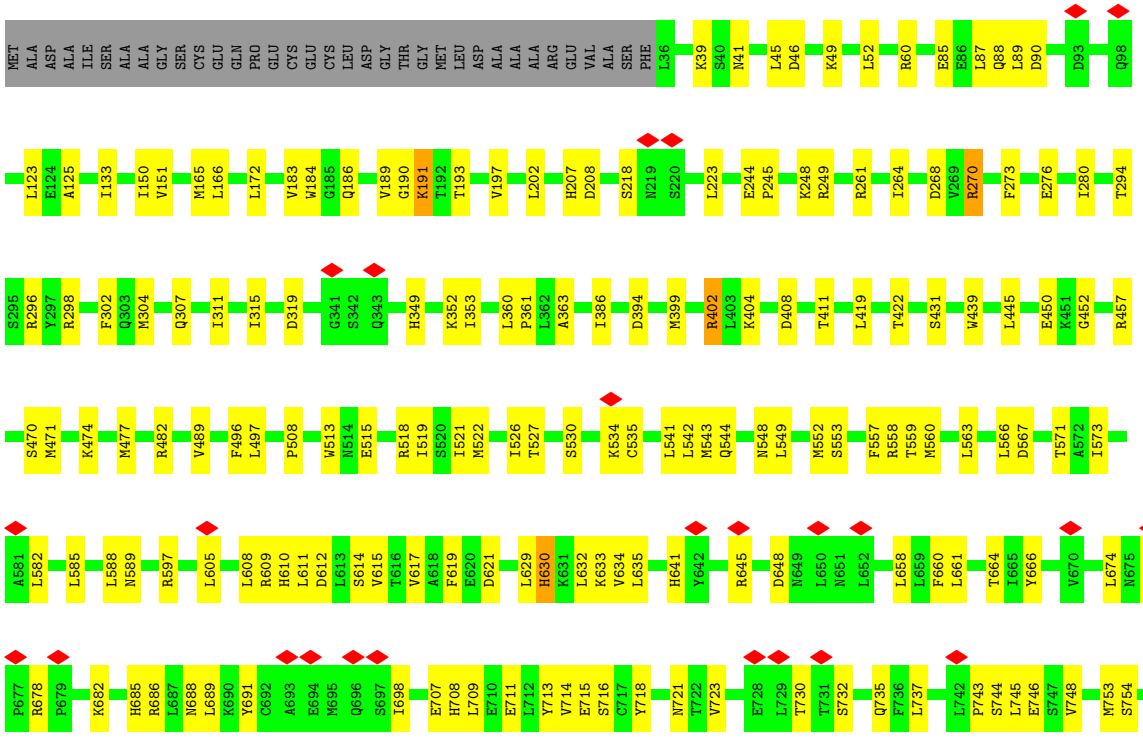
Chain G:

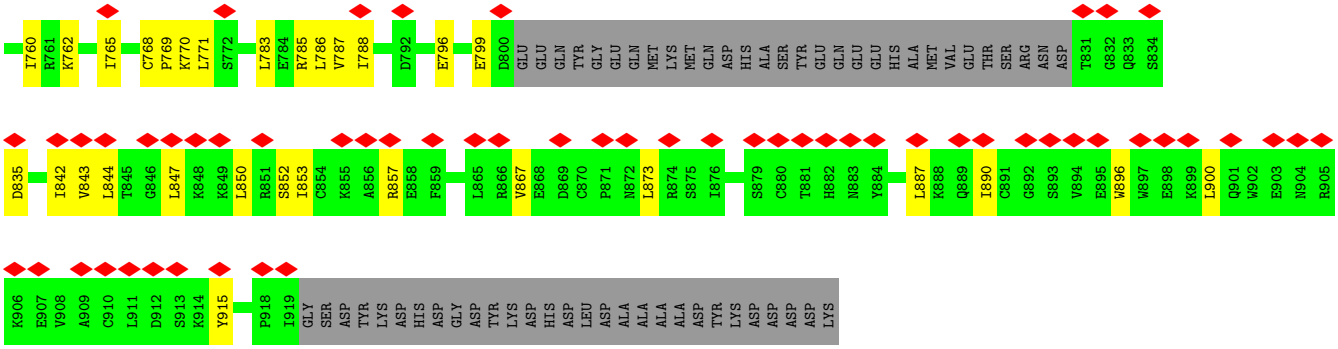




• Molecule 1: NB-ARC domain-containing protein

Chain H:




I760 R761 K762 I765 C768 P769 K770 L771 S772 L783 E784 R785 L786 V787 I788 D792 E796 E799 D800 GLU GLU GLN TYR GLY GLU GLN MET LYS MET GLN ASP HIS ALA SER TYR GLU GLN GLU GLU HIS ALA MET VAL GLU THR SER ARG ASN ASP T831 G832 Q833 S834
D835 I842 V843 L844 T845 G846 L847 K848 K849 L850 R851 S852 I853 C854 K855 A856 R857 E858 F859 L865 R866 V867 E868 D869 C870 P871 N872 L873 R874 S875 I876 S879 C880 T881 H882 N883 Y884 L887 K888 Q889 I890 C891 G892 S893 V894 E895 W896 W897 E898 K899 L900 Q901 W902 E903 N904 R905
K906 E907 V908 A909 C910 L911 D912 S913 K914 Y915 P918 I919 GLY SER ASP TYR LYS ASP HIS ASP GLY ASP TYR LYS ASP HIS ASP LEU ASP ALA ALA ALA ALA ASP TYR LYS ASP ASP ASP ASP LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of particles used	12203	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.053	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	422.912, 422.912, 422.912	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.16	0/6949	0.34	1/9401 (0.0%)
1	B	0.17	0/6949	0.34	0/9401
1	C	0.16	0/6949	0.34	1/9401 (0.0%)
1	D	0.18	0/6949	0.35	1/9401 (0.0%)
1	E	0.15	0/6949	0.33	0/9401
1	F	0.16	0/6949	0.34	1/9401 (0.0%)
1	G	0.16	0/6949	0.34	1/9401 (0.0%)
1	H	0.16	0/6949	0.33	0/9401
All	All	0.16	0/55592	0.34	5/75208 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	774	ILE	N-CA-C	-6.62	106.84	113.20
1	C	774	ILE	N-CA-C	-6.51	106.95	113.20
1	G	774	ILE	N-CA-C	-6.51	106.95	113.20
1	D	774	ILE	N-CA-C	-6.46	107.00	113.20
1	F	774	ILE	N-CA-C	-6.45	107.01	113.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6823	0	6954	152	0
1	B	6823	0	6954	151	0
1	C	6823	0	6954	167	0
1	D	6823	0	6954	181	0
1	E	6823	0	6954	163	0
1	F	6823	0	6954	161	0
1	G	6823	0	6954	163	0
1	H	6823	0	6954	137	0
2	A	31	0	12	4	0
2	B	31	0	12	5	0
2	C	31	0	12	4	0
2	D	31	0	12	7	0
2	E	31	0	12	4	0
2	F	31	0	12	7	0
2	G	31	0	12	4	0
2	H	31	0	12	5	0
All	All	54832	0	55728	1251	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 11.

The worst 5 of 1251 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:G:652:LEU:HB3	1:G:680:LEU:HD11	1.35	1.05
1:C:362:LEU:HD22	1:C:402:ARG:HH11	1.40	0.84
1:H:745:LEU:HG	1:H:771:LEU:HD21	1.59	0.84
1:B:557:PHE:HB3	1:B:582:LEU:HD21	1.59	0.83
1:D:692:CYS:HB3	1:D:695:MET:HG3	1.61	0.82

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	850/948 (90%)	823 (97%)	27 (3%)	0	100	100
1	B	850/948 (90%)	822 (97%)	27 (3%)	1 (0%)	48	81
1	C	850/948 (90%)	821 (97%)	27 (3%)	2 (0%)	43	75
1	D	850/948 (90%)	820 (96%)	27 (3%)	3 (0%)	30	65
1	E	850/948 (90%)	820 (96%)	29 (3%)	1 (0%)	48	81
1	F	850/948 (90%)	824 (97%)	25 (3%)	1 (0%)	48	81
1	G	850/948 (90%)	824 (97%)	26 (3%)	0	100	100
1	H	850/948 (90%)	822 (97%)	28 (3%)	0	100	100
All	All	6800/7584 (90%)	6576 (97%)	216 (3%)	8 (0%)	49	81

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	719	ASP
1	D	719	ASP
1	E	719	ASP
1	C	719	ASP
1	D	650	LEU

5.3.2 Protein sidechains (i)

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	771/845 (91%)	759 (98%)	12 (2%)	55	69
1	B	771/845 (91%)	761 (99%)	10 (1%)	61	72
1	C	771/845 (91%)	757 (98%)	14 (2%)	51	67
1	D	771/845 (91%)	759 (98%)	12 (2%)	55	69
1	E	771/845 (91%)	759 (98%)	12 (2%)	55	69
1	F	771/845 (91%)	760 (99%)	11 (1%)	59	71
1	G	771/845 (91%)	759 (98%)	12 (2%)	55	69
1	H	771/845 (91%)	761 (99%)	10 (1%)	61	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	6168/6760 (91%)	6075 (98%)	93 (2%)	55 70

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	629	LEU
1	G	179	ASN
1	E	718	TYR
1	F	388	THR
1	G	332	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	651	ASN
1	H	545	ASN
1	G	186	GLN
1	G	790	HIS
1	H	790	HIS

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)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	ATP	E	1001	-	32,33,33	0.40	0	48,52,52	0.38	0
2	ATP	B	1001	-	32,33,33	0.39	0	48,52,52	0.37	0
2	ATP	A	1001	-	32,33,33	0.39	0	48,52,52	0.38	0
2	ATP	G	1001	-	32,33,33	0.40	0	48,52,52	0.38	0
2	ATP	F	1001	-	32,33,33	0.39	0	48,52,52	0.38	0
2	ATP	C	1001	-	32,33,33	0.40	0	48,52,52	0.39	0
2	ATP	H	1001	-	32,33,33	0.39	0	48,52,52	0.39	0
2	ATP	D	1001	-	32,33,33	0.40	0	48,52,52	0.38	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	E	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	B	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	A	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	G	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	F	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	C	1001	-	-	1/22/38/38	0/3/3/3
2	ATP	H	1001	-	-	0/22/38/38	0/3/3/3
2	ATP	D	1001	-	-	1/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1001	ATP	C4'-C5'-O5'-PA
2	D	1001	ATP	C4'-C5'-O5'-PA
2	F	1001	ATP	C4'-C5'-O5'-PA
2	E	1001	ATP	C4'-C5'-O5'-PA
2	A	1001	ATP	C4'-C5'-O5'-PA

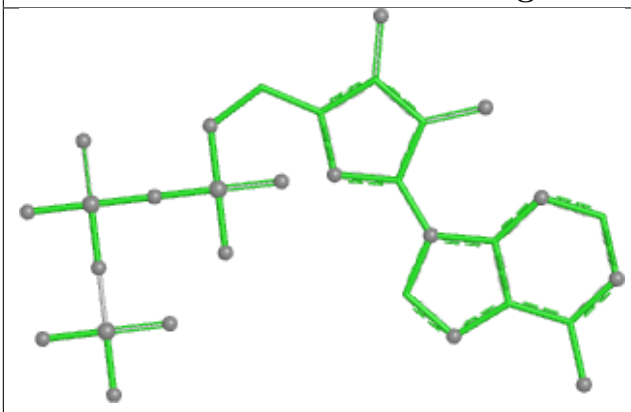
There are no ring outliers.

8 monomers are involved in 40 short contacts:

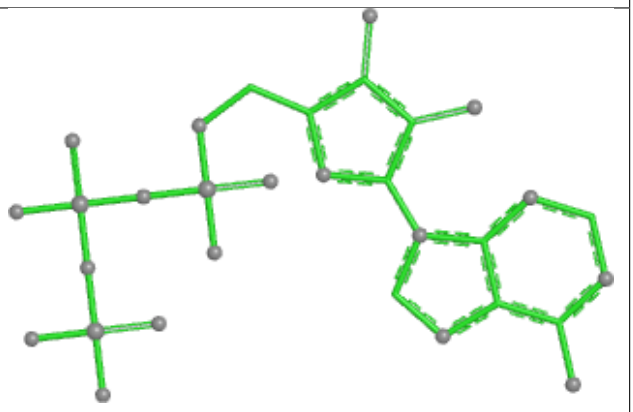
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1001	ATP	4	0
2	B	1001	ATP	5	0
2	A	1001	ATP	4	0
2	G	1001	ATP	4	0
2	F	1001	ATP	7	0
2	C	1001	ATP	4	0
2	H	1001	ATP	5	0
2	D	1001	ATP	7	0

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 then 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.

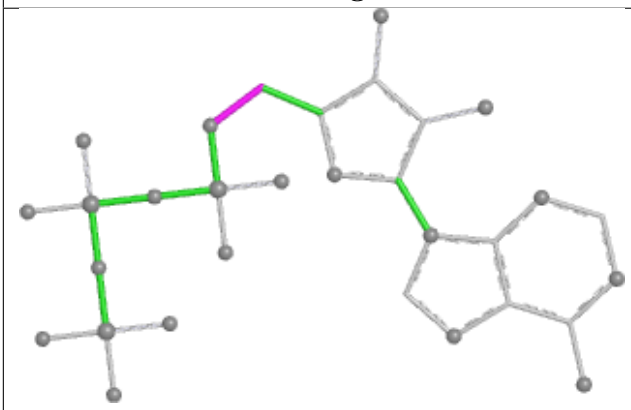
Ligand ATP E 1001



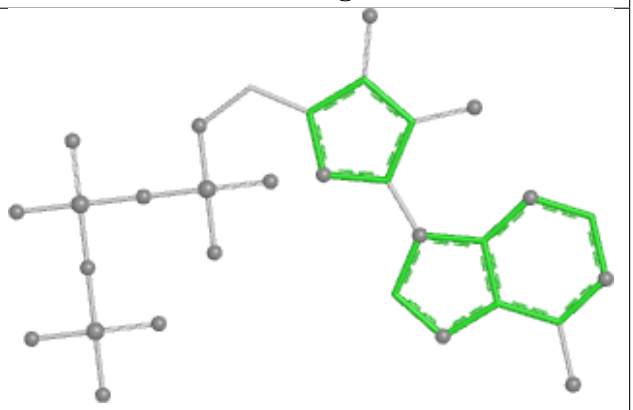
Bond lengths



Bond angles

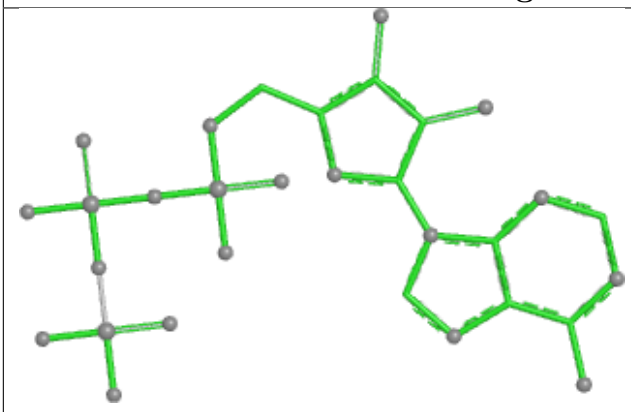


Torsions

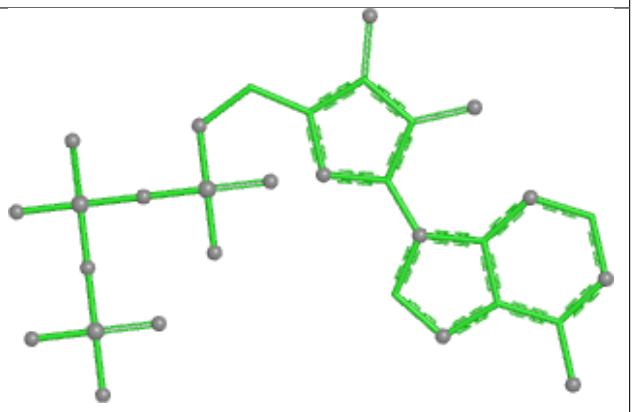


Rings

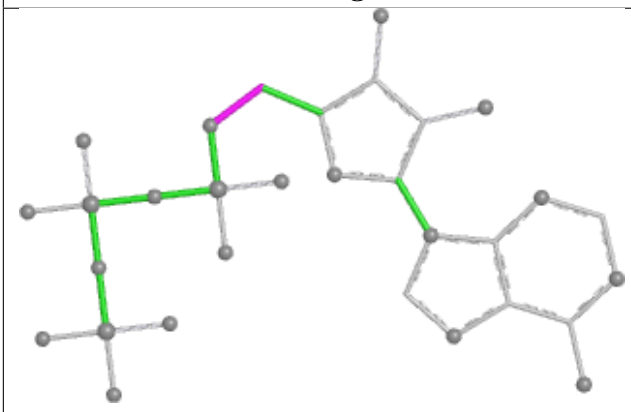
Ligand ATP B 1001



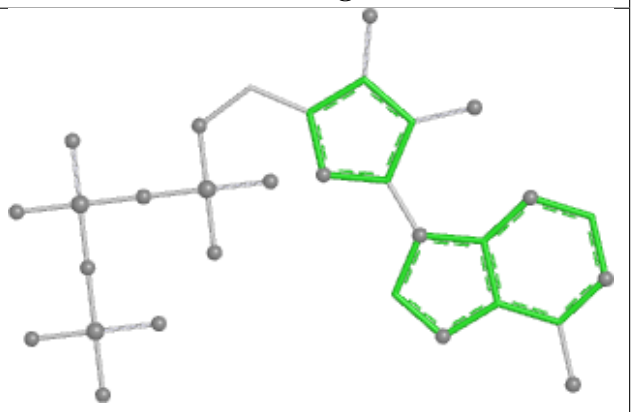
Bond lengths



Bond angles

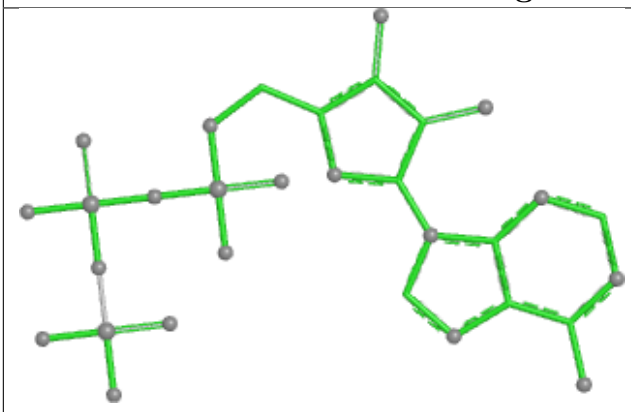


Torsions

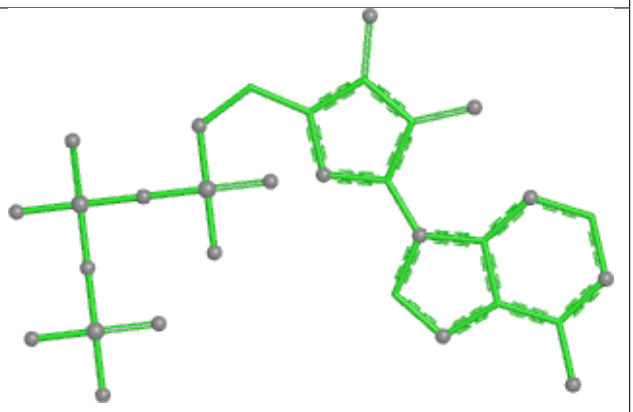


Rings

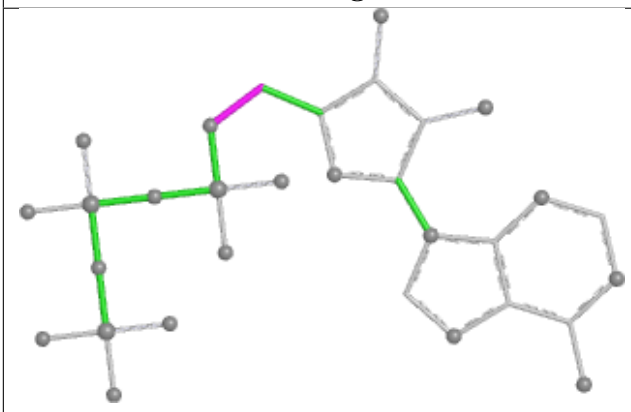
Ligand ATP A 1001



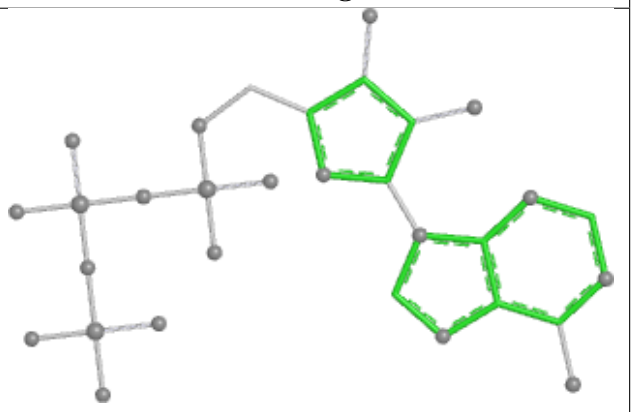
Bond lengths



Bond angles

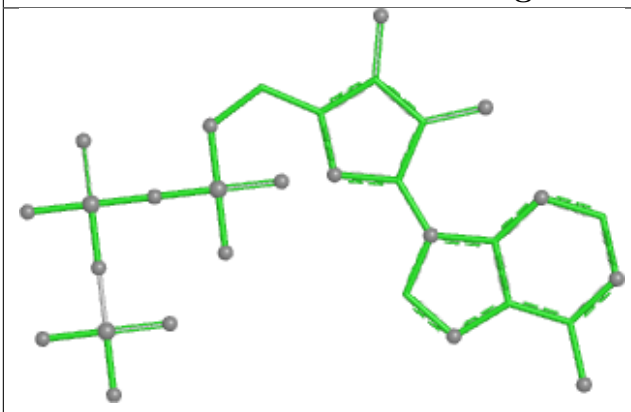


Torsions

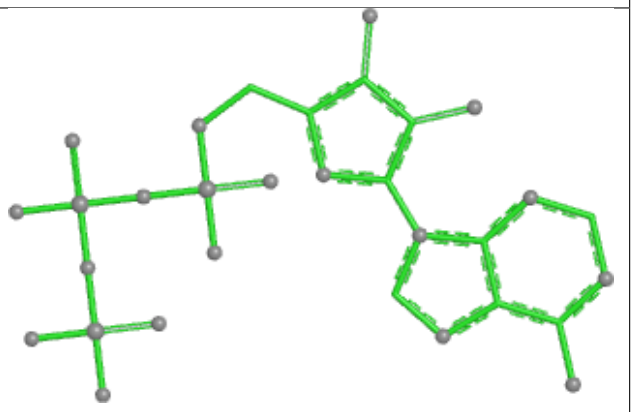


Rings

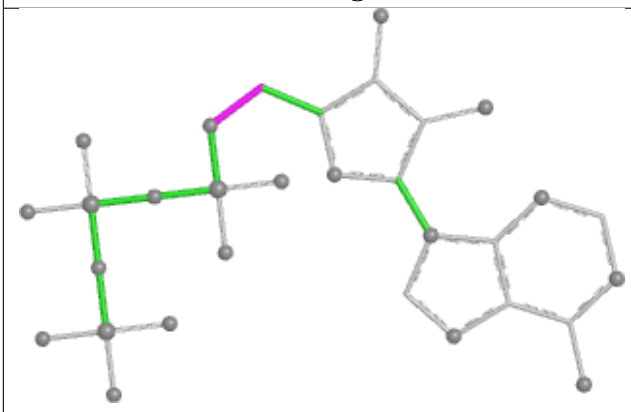
Ligand ATP G 1001



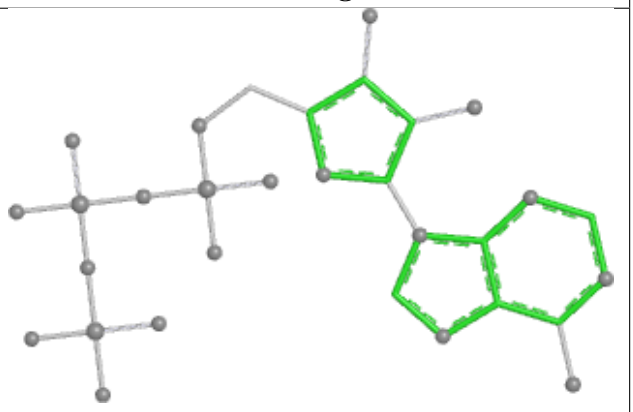
Bond lengths



Bond angles

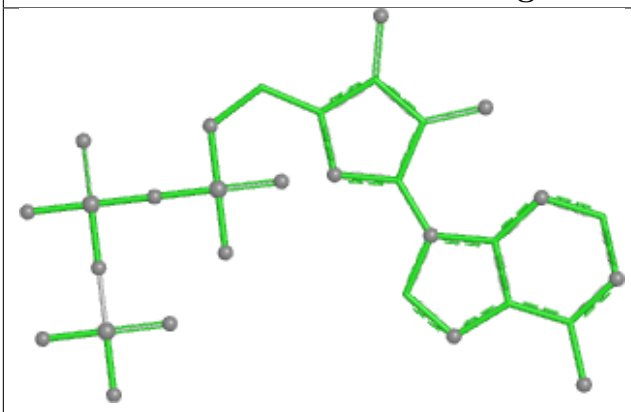


Torsions

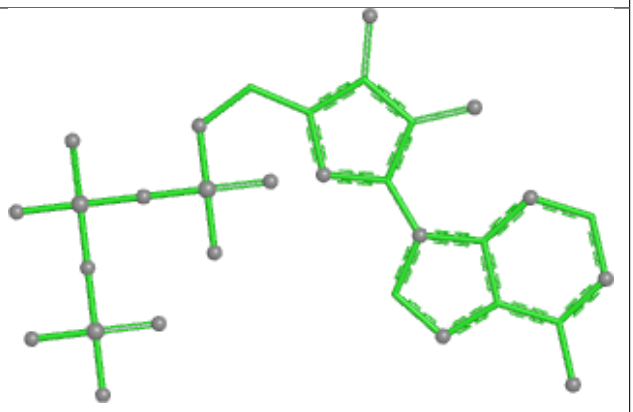


Rings

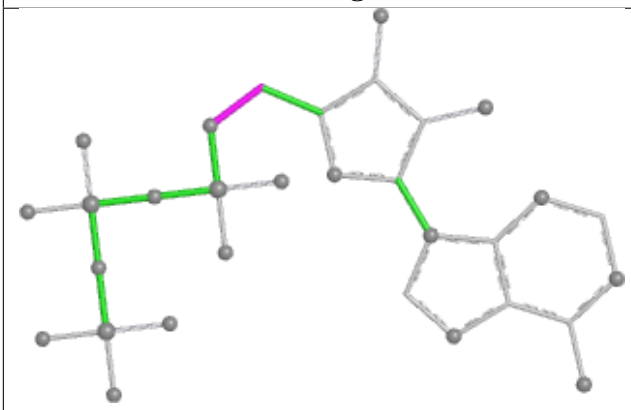
Ligand ATP F 1001



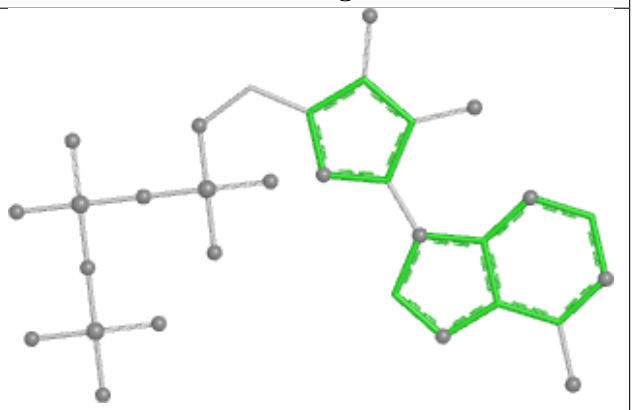
Bond lengths



Bond angles

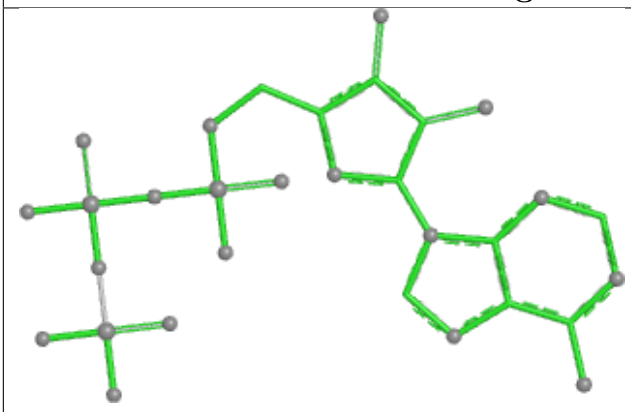


Torsions

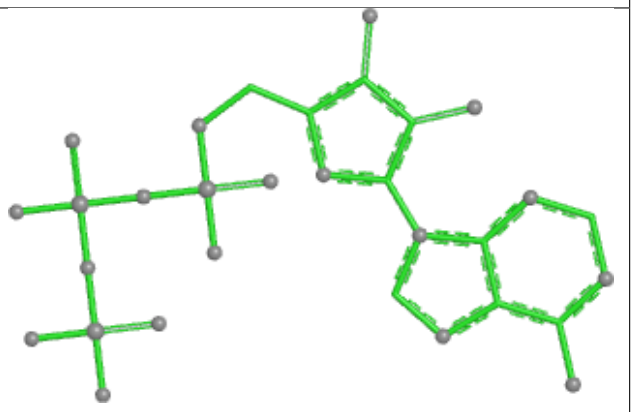


Rings

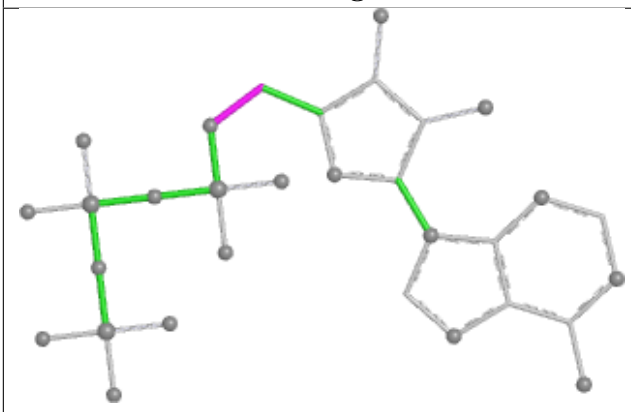
Ligand ATP C 1001



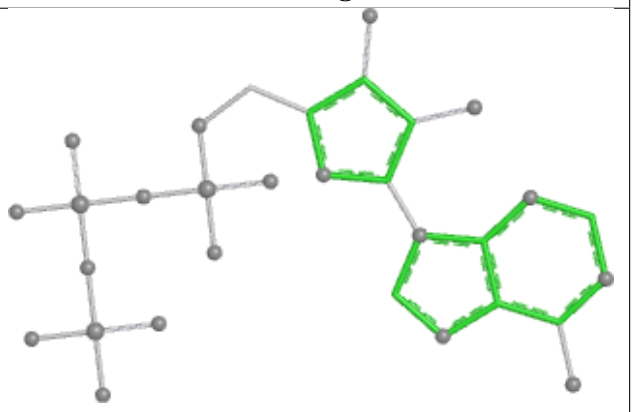
Bond lengths



Bond angles

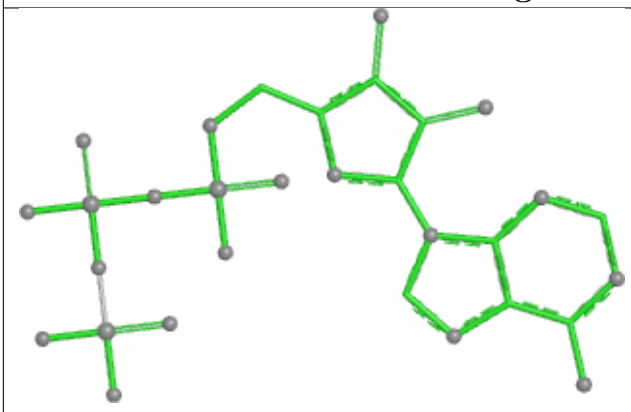


Torsions

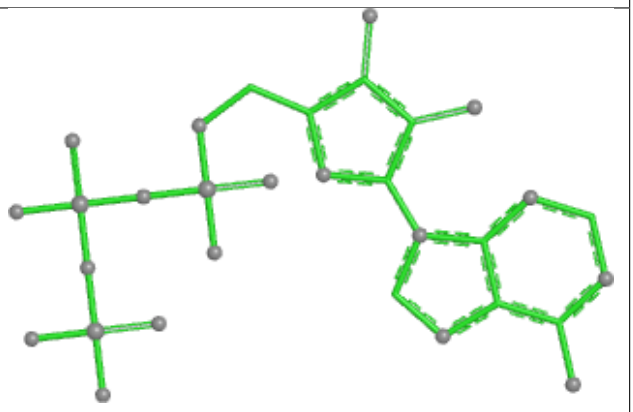


Rings

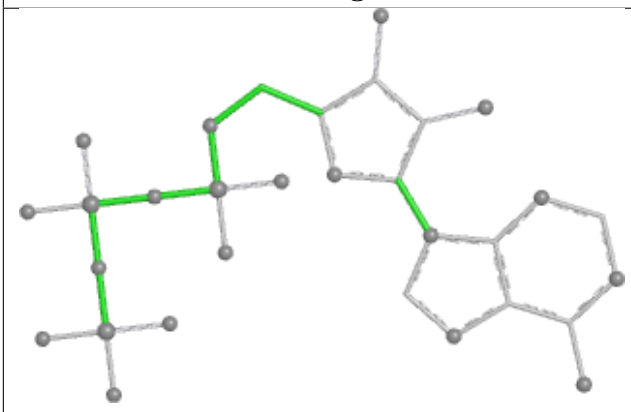
Ligand ATP H 1001



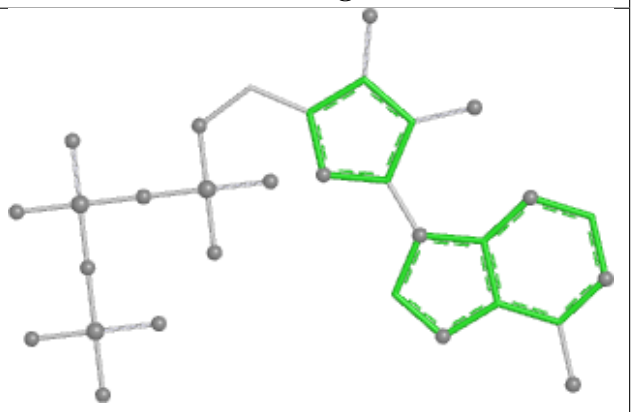
Bond lengths



Bond angles

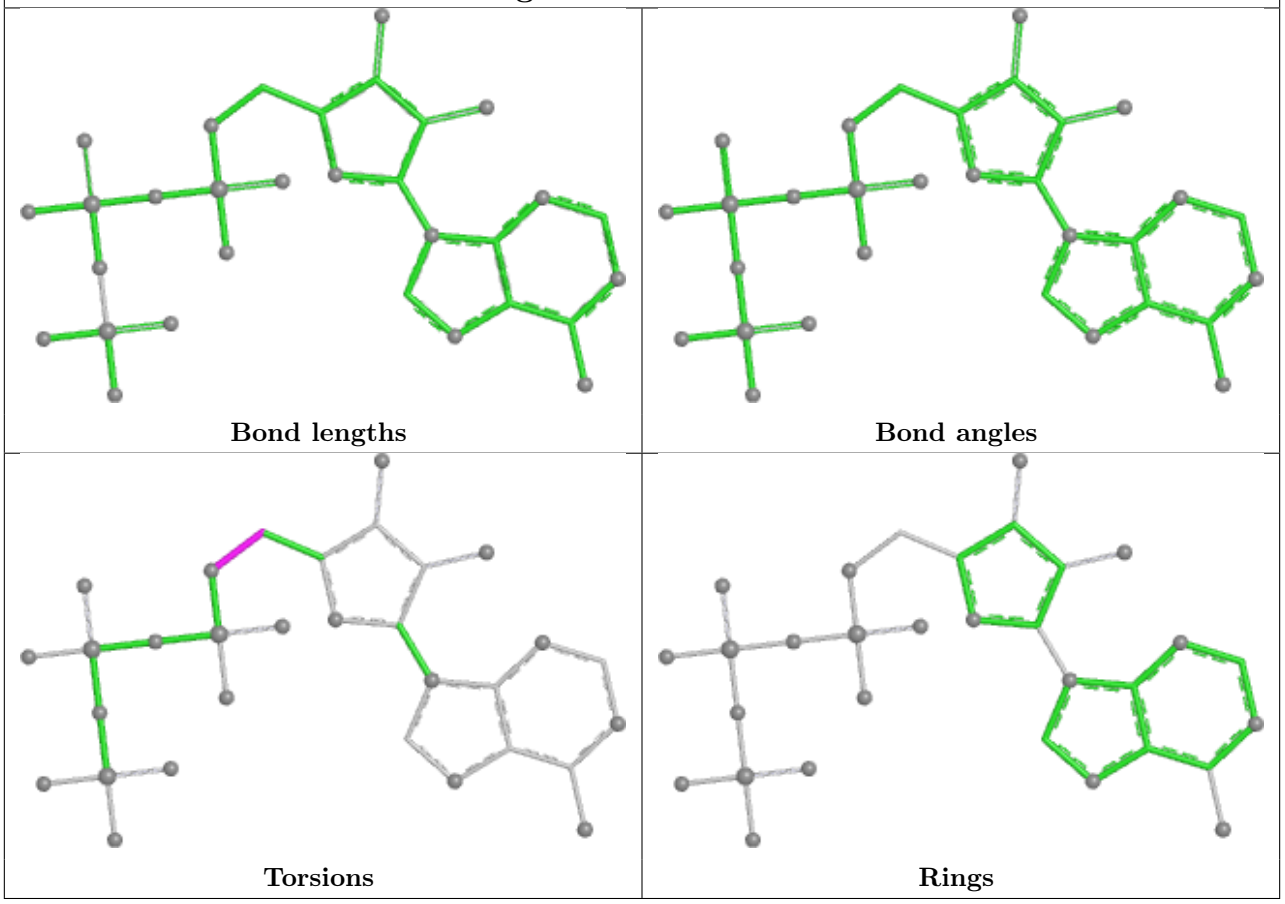


Torsions



Rings

Ligand ATP D 1001



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.

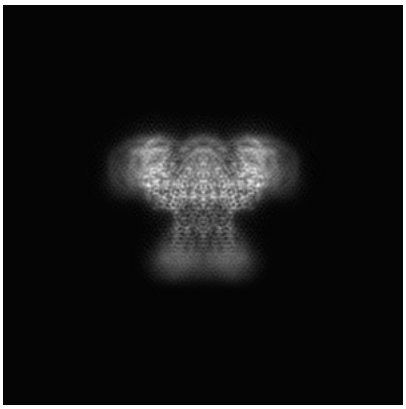
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-51810. These allow visual inspection of the internal detail of the map and identification of artifacts.

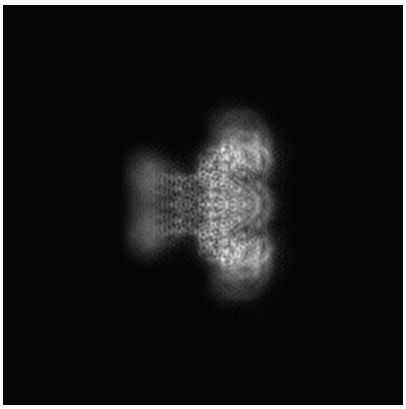
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

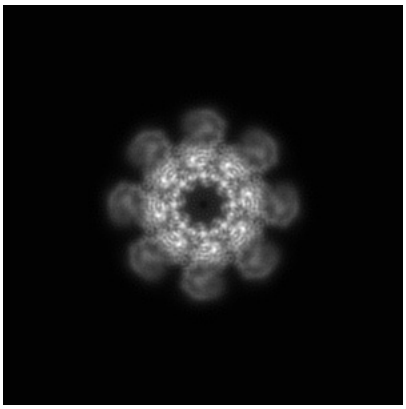
6.1.1 Primary map



X

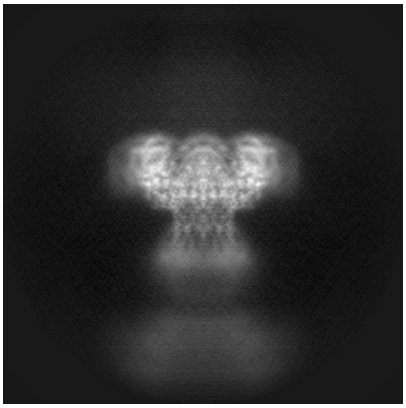


Y

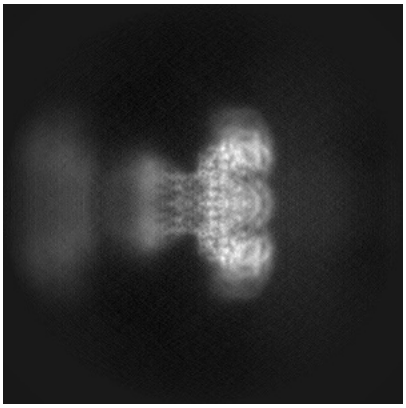


Z

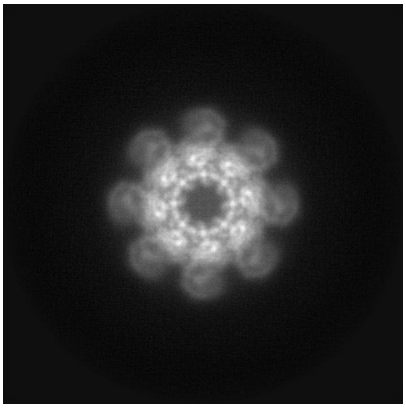
6.1.2 Raw map



X



Y

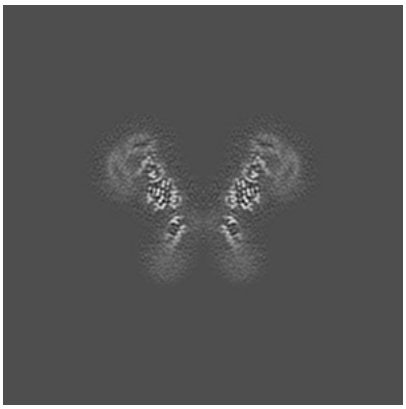


Z

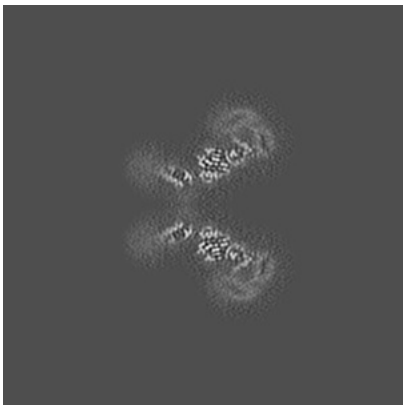
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

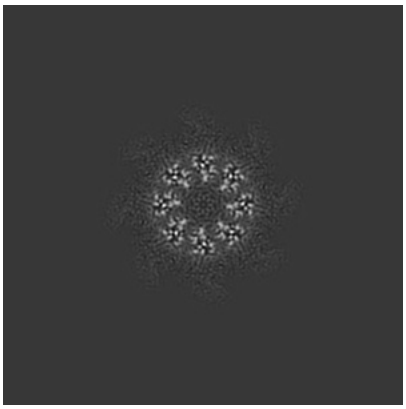
6.2.1 Primary map



X Index: 256

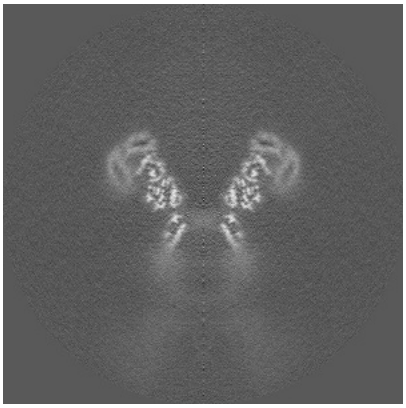


Y Index: 256

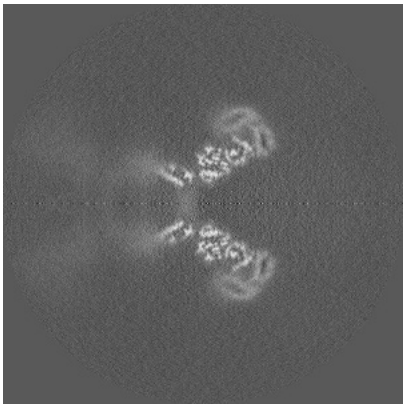


Z Index: 256

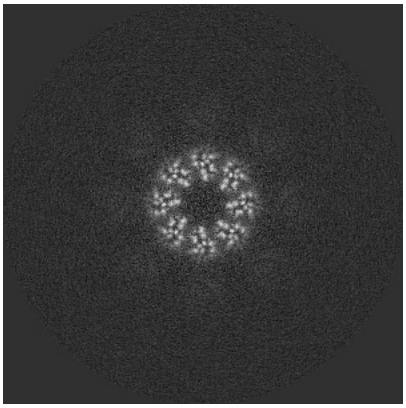
6.2.2 Raw map



X Index: 256



Y Index: 256

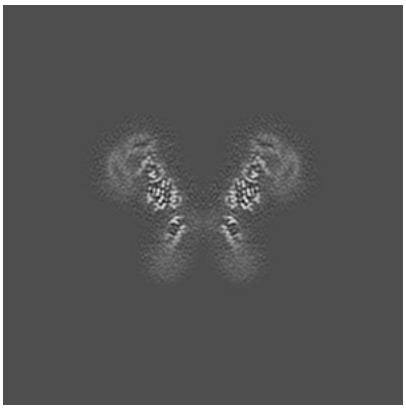


Z Index: 256

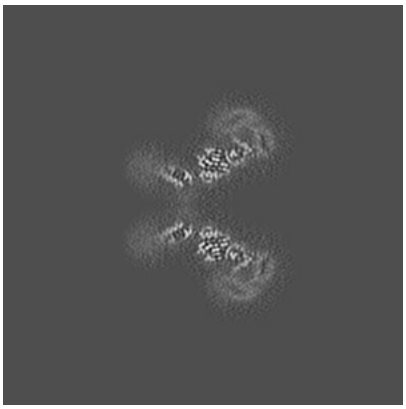
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

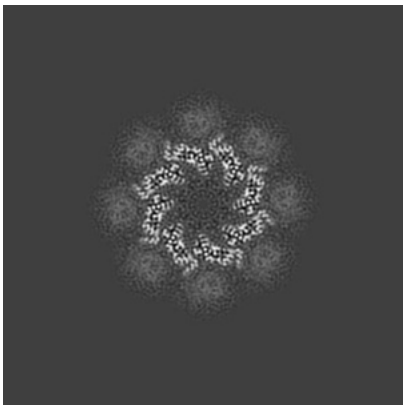
6.3.1 Primary map



X Index: 256

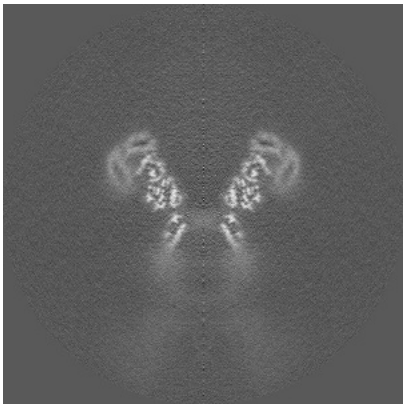


Y Index: 256

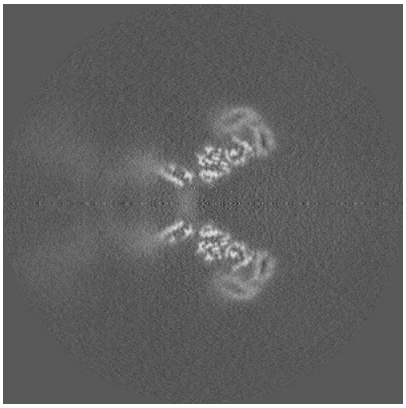


Z Index: 281

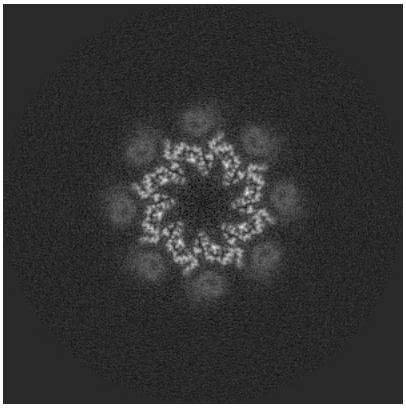
6.3.2 Raw map



X Index: 256



Y Index: 256

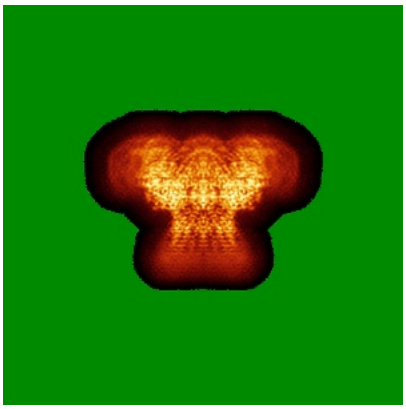


Z Index: 281

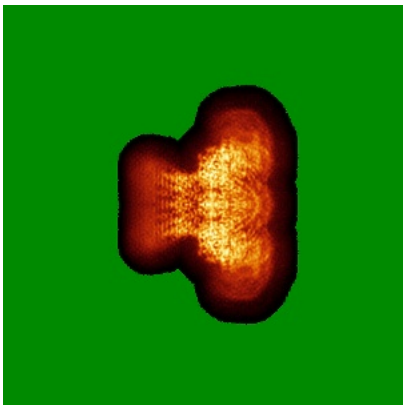
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

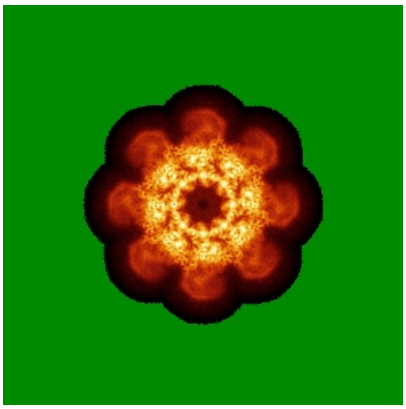
6.4.1 Primary map



X

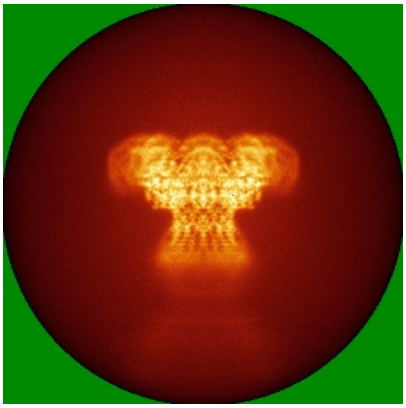


Y

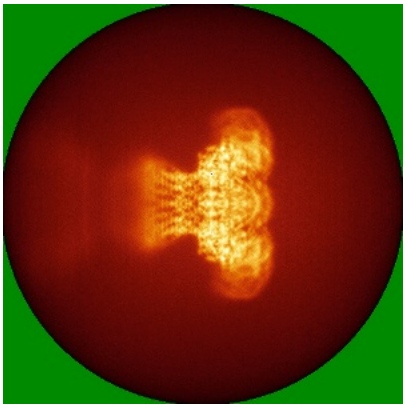


Z

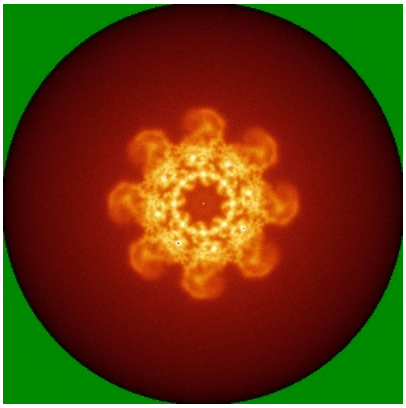
6.4.2 Raw map



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.

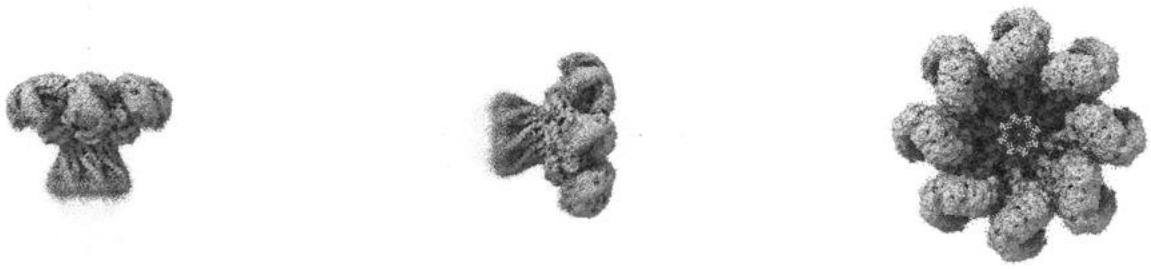
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. 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



X Y Z

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.

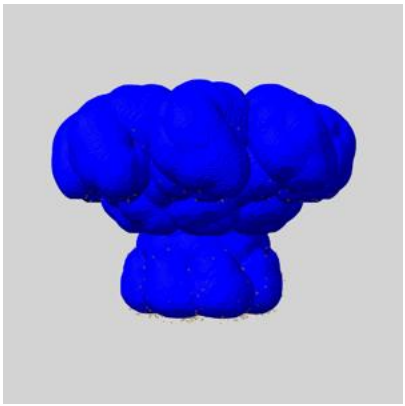
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

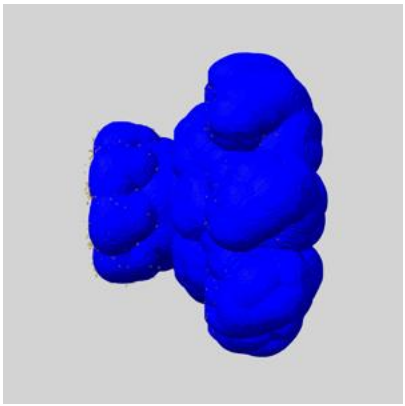
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

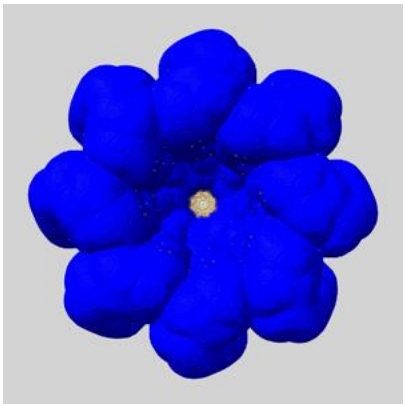
6.6.1 emd_51810_msk_1.map



X



Y

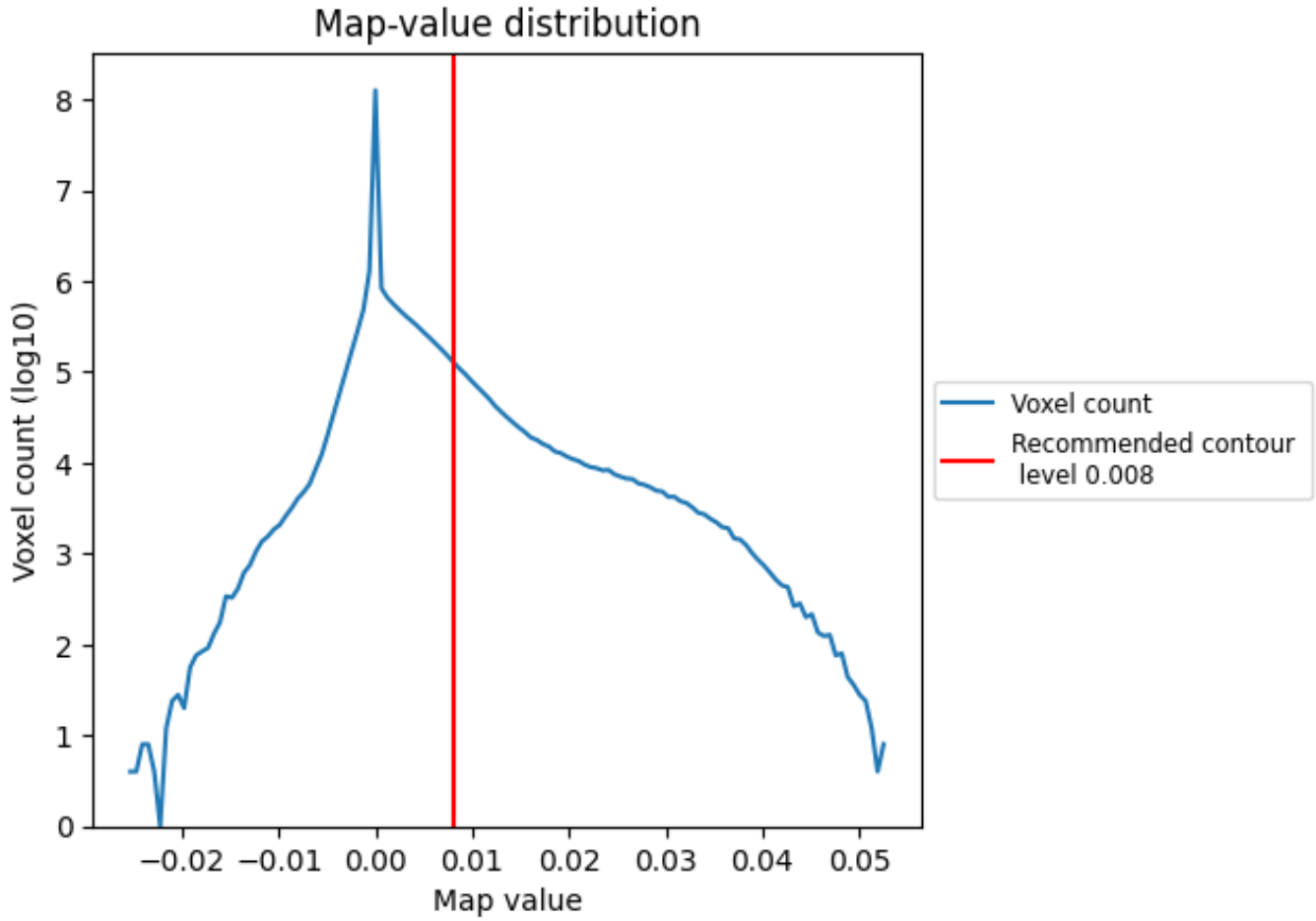


Z

7 Map analysis

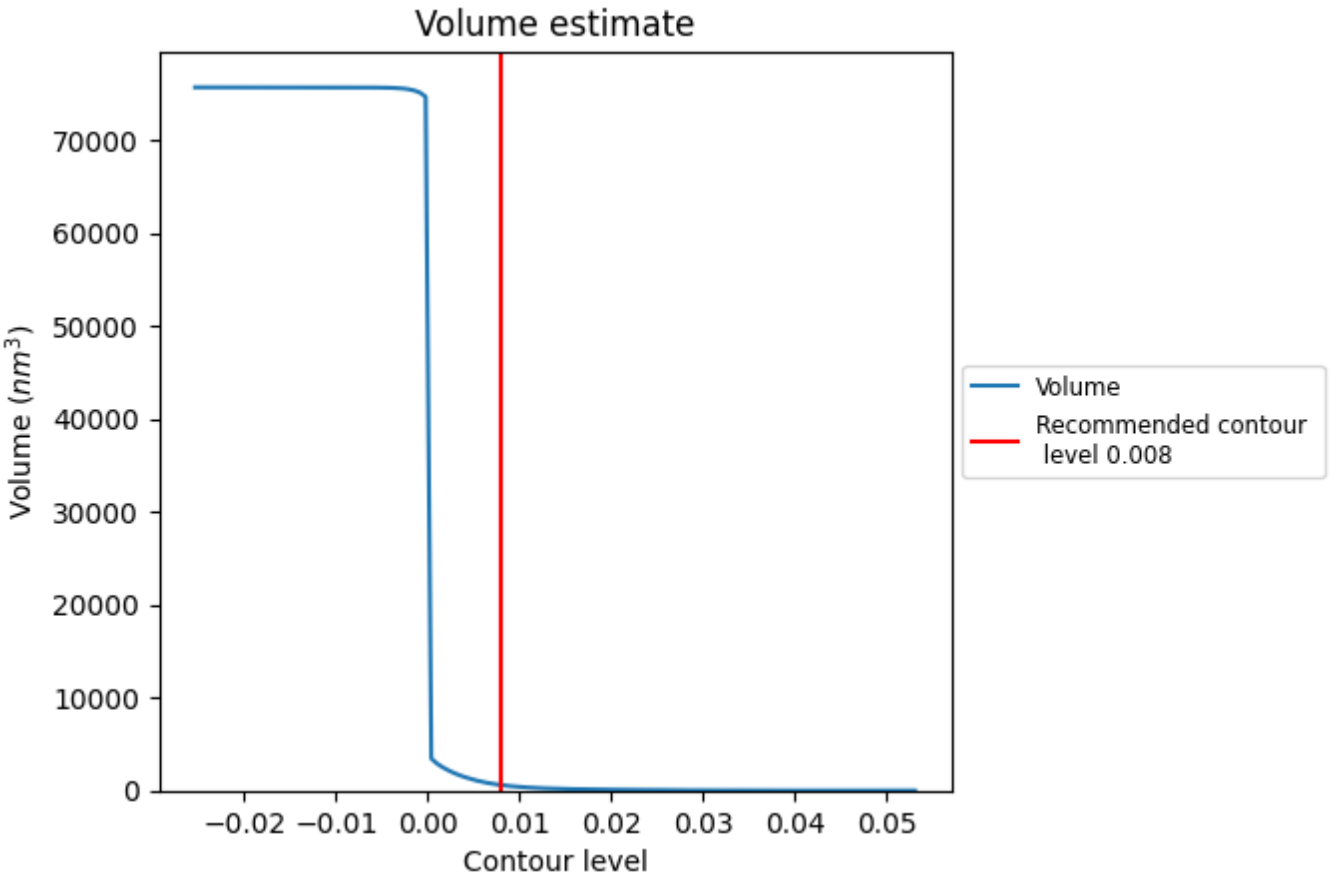
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

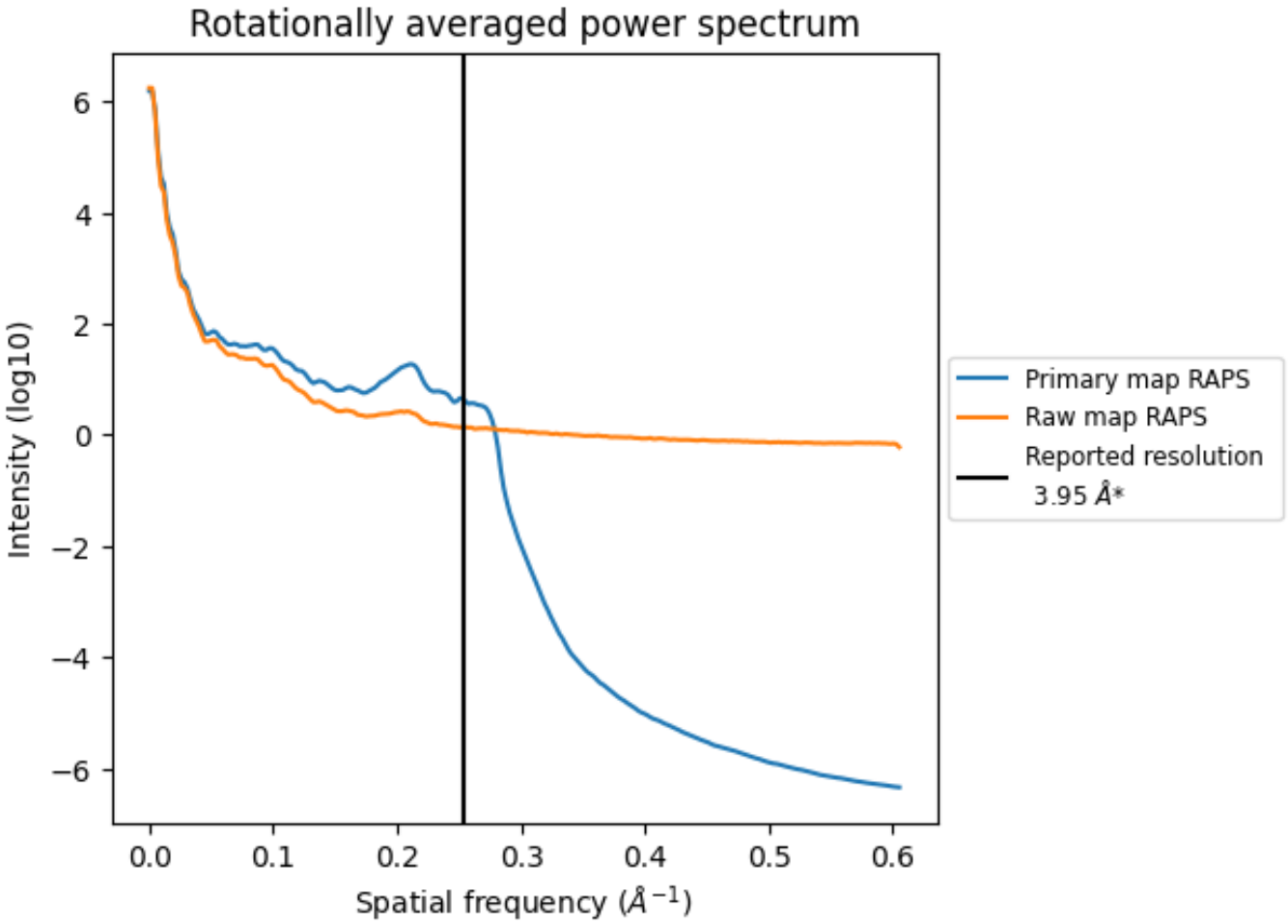
7.2 Volume estimate (i)



The volume at the recommended contour level is 595 nm^3; this corresponds to an approximate mass of 537 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 (i)

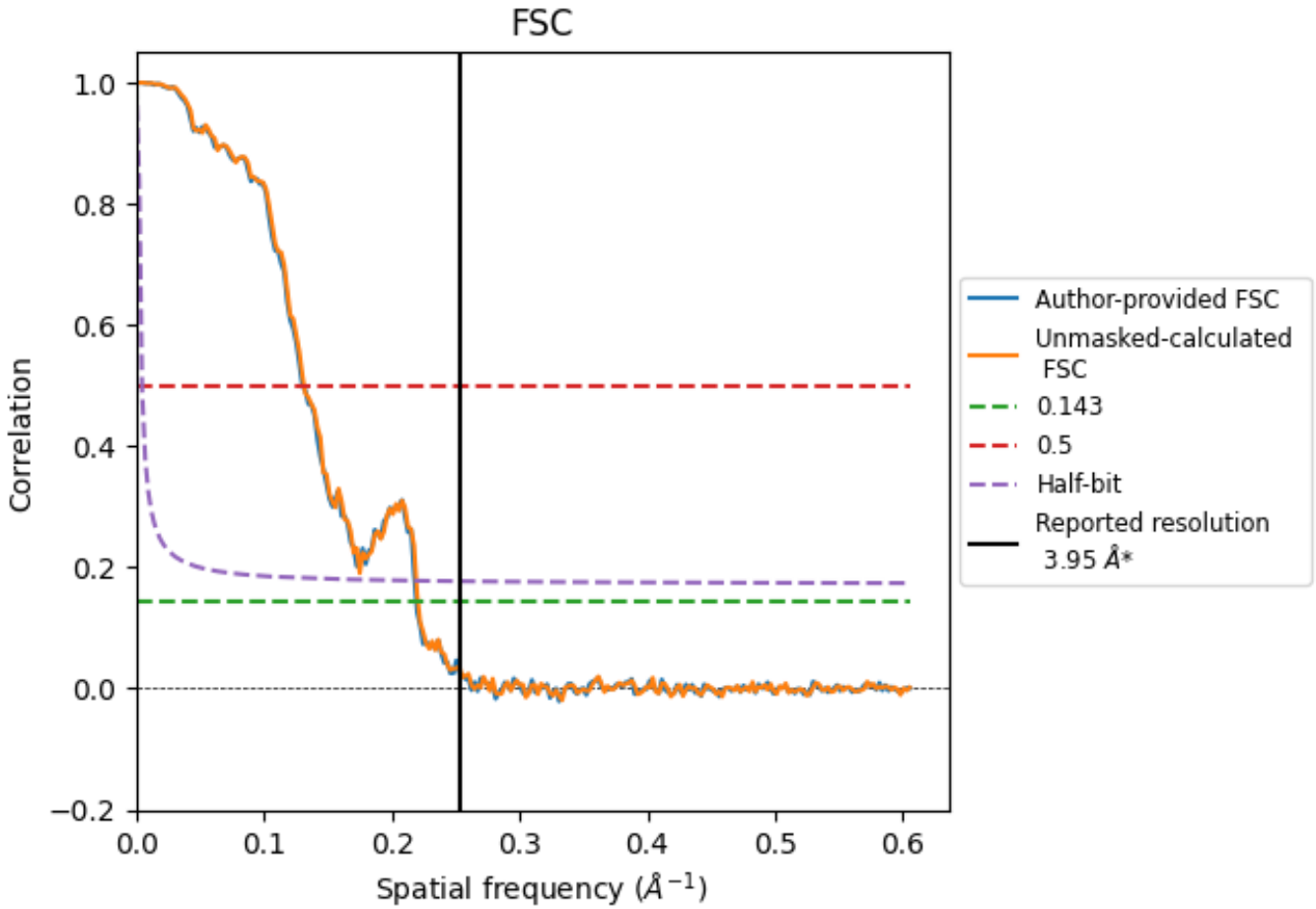


*Reported resolution corresponds to spatial frequency of 0.253 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.253 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.95	-	-
Author-provided FSC curve	4.56	7.69	4.59
Unmasked-calculated*	4.53	7.61	4.56

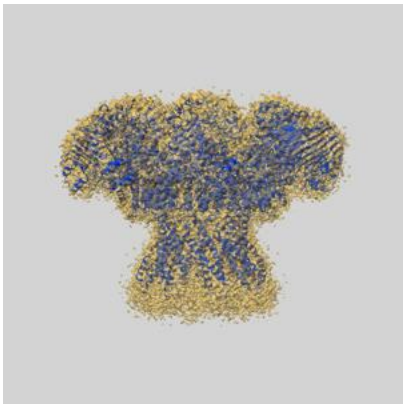
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.56 differs from the reported value 3.95 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.53 differs from the reported value 3.95 by more than 10 %

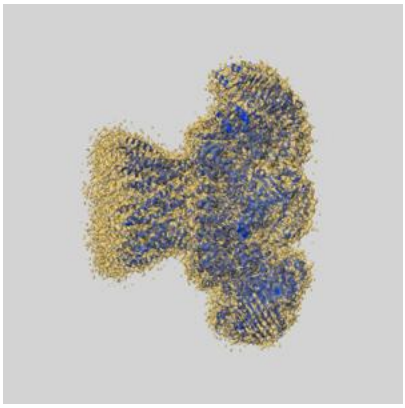
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-51810 and PDB model 9H2L. Per-residue inclusion information can be found in section 3 on page 12.

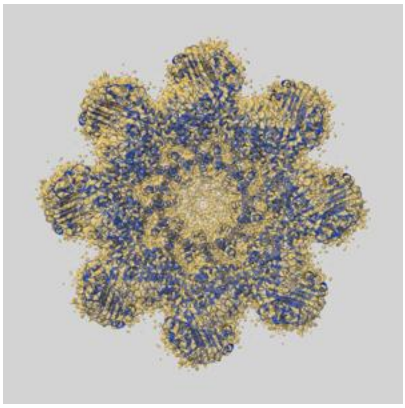
9.1 Map-model overlay



X



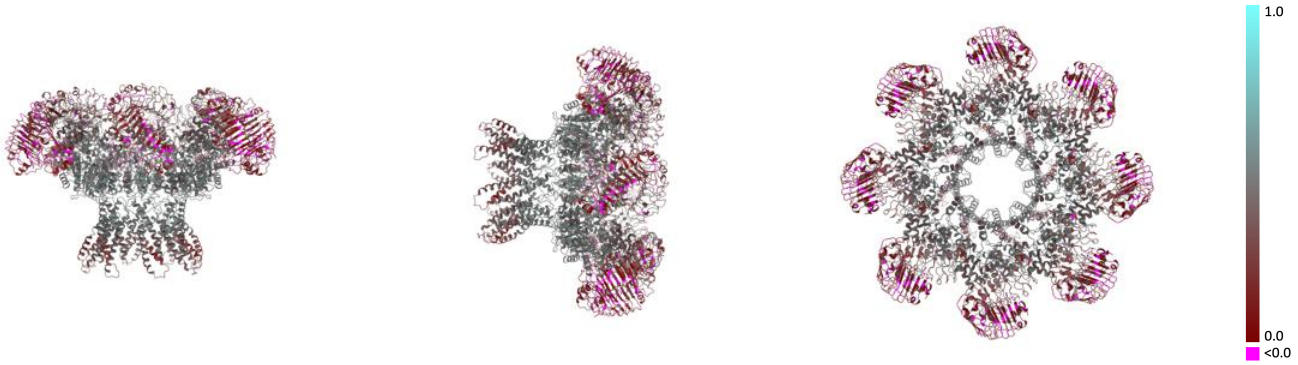
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.008 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.

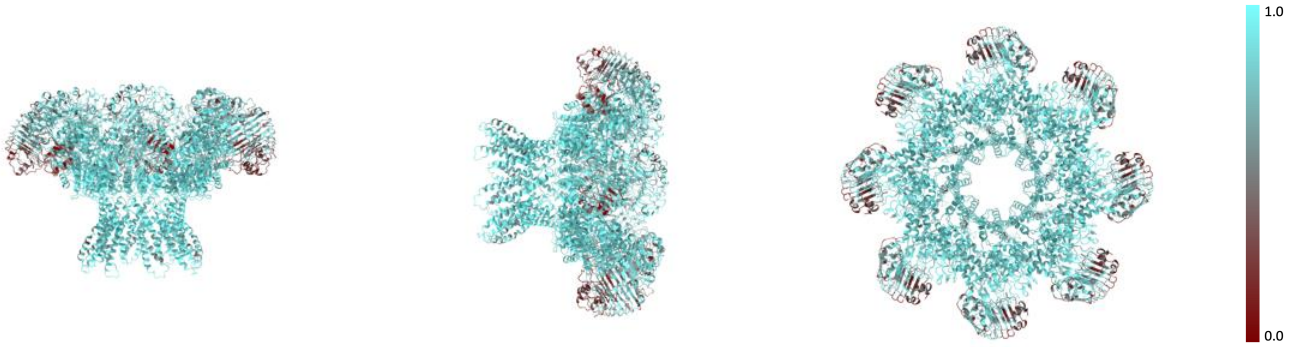
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

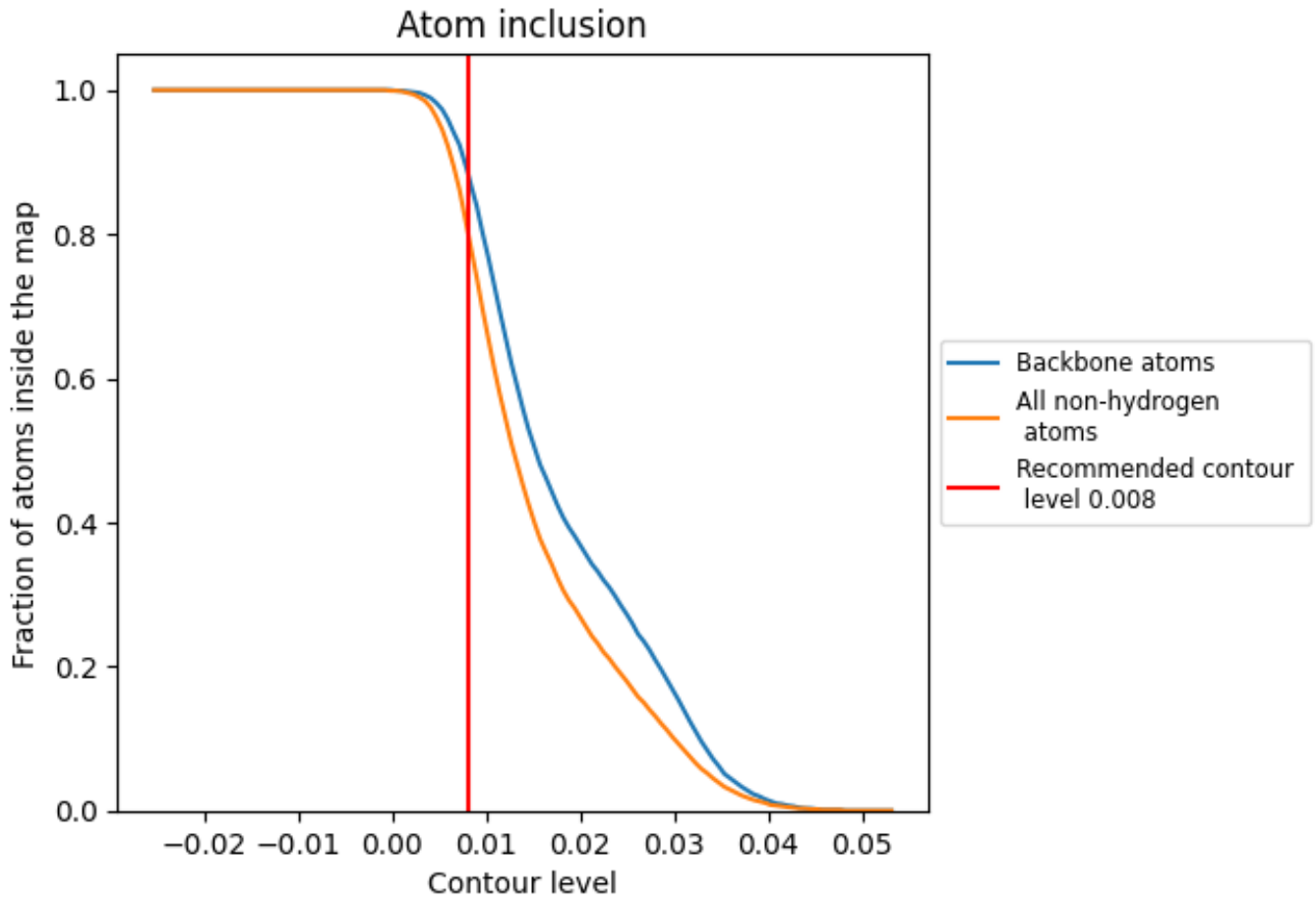
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.008).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8060	0.3540
A	0.8030	0.3540
B	0.8070	0.3540
C	0.8080	0.3540
D	0.8050	0.3530
E	0.8050	0.3540
F	0.8070	0.3550
G	0.8060	0.3530
H	0.8050	0.3530