



## wwPDB EM Validation Summary Report ⓘ

Jan 13, 2024 – 12:33 PM EST

PDB ID : 8U7I  
EMDB ID : EMD-41983  
Title : Structure of the phage immune evasion protein Gad1 bound to the Gabija GajAB complex  
Authors : Antine, S.P.; Johnson, A.G.; Mooney, S.E.; Mayer, M.L.; Kranzsuch, P.J.  
Deposited on : 2023-09-15  
Resolution : 2.57 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

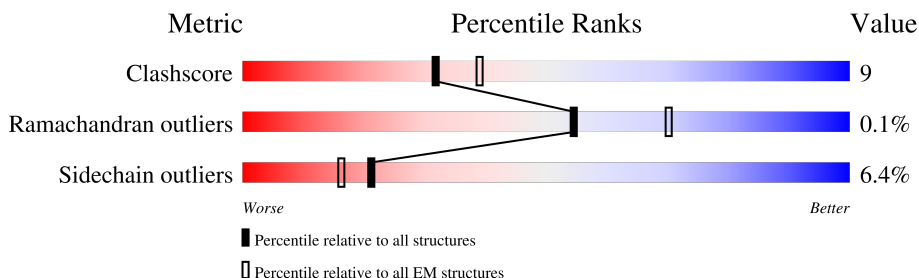
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.57 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.






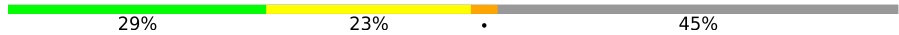




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	675	
1	B	675	
1	C	675	
1	D	675	
2	E	494	
2	F	494	
2	G	494	
2	H	494	

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Mol	Chain	Length	Quality of chain
3	I	295	 32% 19% . 45%
3	J	295	 33% 20% . 45%
3	K	295	 34% 19% . 45%
3	L	295	 29% 23% . 45%
3	M	295	 27% 11% . 61%
3	N	295	 25% 12% . 61%
3	O	295	 25% 12% . 61%
3	P	295	 23% 14% . 61%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 38864 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 Endonuclease GajA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	626	5111	3268	849	977	17	0	0
1	B	626	5111	3268	849	977	17	0	0
1	C	626	5111	3268	849	977	17	0	0
1	D	626	5111	3268	849	977	17	0	0

There are 392 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-96	MET	-	expression tag	UNP J8H9C1
A	-95	GLY	-	expression tag	UNP J8H9C1
A	-94	SER	-	expression tag	UNP J8H9C1
A	-93	SER	-	expression tag	UNP J8H9C1
A	-92	HIS	-	expression tag	UNP J8H9C1
A	-91	HIS	-	expression tag	UNP J8H9C1
A	-90	HIS	-	expression tag	UNP J8H9C1
A	-89	HIS	-	expression tag	UNP J8H9C1
A	-88	HIS	-	expression tag	UNP J8H9C1
A	-87	HIS	-	expression tag	UNP J8H9C1
A	-86	GLY	-	expression tag	UNP J8H9C1
A	-85	SER	-	expression tag	UNP J8H9C1
A	-84	GLY	-	expression tag	UNP J8H9C1
A	-83	VAL	-	expression tag	UNP J8H9C1
A	-82	LYS	-	expression tag	UNP J8H9C1
A	-81	THR	-	expression tag	UNP J8H9C1
A	-80	GLU	-	expression tag	UNP J8H9C1
A	-79	ASN	-	expression tag	UNP J8H9C1
A	-78	ASN	-	expression tag	UNP J8H9C1
A	-77	ASP	-	expression tag	UNP J8H9C1
A	-76	HIS	-	expression tag	UNP J8H9C1
A	-75	ILE	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-74	ASN	-	expression tag	UNP J8H9C1
A	-73	LEU	-	expression tag	UNP J8H9C1
A	-72	LYS	-	expression tag	UNP J8H9C1
A	-71	VAL	-	expression tag	UNP J8H9C1
A	-70	ALA	-	expression tag	UNP J8H9C1
A	-69	GLY	-	expression tag	UNP J8H9C1
A	-68	GLN	-	expression tag	UNP J8H9C1
A	-67	ASP	-	expression tag	UNP J8H9C1
A	-66	GLY	-	expression tag	UNP J8H9C1
A	-65	SER	-	expression tag	UNP J8H9C1
A	-64	VAL	-	expression tag	UNP J8H9C1
A	-63	VAL	-	expression tag	UNP J8H9C1
A	-62	GLN	-	expression tag	UNP J8H9C1
A	-61	PHE	-	expression tag	UNP J8H9C1
A	-60	LYS	-	expression tag	UNP J8H9C1
A	-59	ILE	-	expression tag	UNP J8H9C1
A	-58	LYS	-	expression tag	UNP J8H9C1
A	-57	ARG	-	expression tag	UNP J8H9C1
A	-56	HIS	-	expression tag	UNP J8H9C1
A	-55	THR	-	expression tag	UNP J8H9C1
A	-54	PRO	-	expression tag	UNP J8H9C1
A	-53	LEU	-	expression tag	UNP J8H9C1
A	-52	SER	-	expression tag	UNP J8H9C1
A	-51	LYS	-	expression tag	UNP J8H9C1
A	-50	LEU	-	expression tag	UNP J8H9C1
A	-49	MET	-	expression tag	UNP J8H9C1
A	-48	LYS	-	expression tag	UNP J8H9C1
A	-47	ALA	-	expression tag	UNP J8H9C1
A	-46	TYR	-	expression tag	UNP J8H9C1
A	-45	CYS	-	expression tag	UNP J8H9C1
A	-44	GLU	-	expression tag	UNP J8H9C1
A	-43	ARG	-	expression tag	UNP J8H9C1
A	-42	GLN	-	expression tag	UNP J8H9C1
A	-41	GLY	-	expression tag	UNP J8H9C1
A	-40	LEU	-	expression tag	UNP J8H9C1
A	-39	SER	-	expression tag	UNP J8H9C1
A	-38	MET	-	expression tag	UNP J8H9C1
A	-37	ARG	-	expression tag	UNP J8H9C1
A	-36	GLN	-	expression tag	UNP J8H9C1
A	-35	ILE	-	expression tag	UNP J8H9C1
A	-34	ARG	-	expression tag	UNP J8H9C1
A	-33	PHE	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	ARG	-	expression tag	UNP J8H9C1
A	-31	PHE	-	expression tag	UNP J8H9C1
A	-30	ASP	-	expression tag	UNP J8H9C1
A	-29	GLY	-	expression tag	UNP J8H9C1
A	-28	GLN	-	expression tag	UNP J8H9C1
A	-27	PRO	-	expression tag	UNP J8H9C1
A	-26	ILE	-	expression tag	UNP J8H9C1
A	-25	ASN	-	expression tag	UNP J8H9C1
A	-24	GLU	-	expression tag	UNP J8H9C1
A	-23	THR	-	expression tag	UNP J8H9C1
A	-22	ASP	-	expression tag	UNP J8H9C1
A	-21	THR	-	expression tag	UNP J8H9C1
A	-20	PRO	-	expression tag	UNP J8H9C1
A	-19	ALA	-	expression tag	UNP J8H9C1
A	-18	GLN	-	expression tag	UNP J8H9C1
A	-17	LEU	-	expression tag	UNP J8H9C1
A	-16	GLU	-	expression tag	UNP J8H9C1
A	-15	MET	-	expression tag	UNP J8H9C1
A	-14	GLU	-	expression tag	UNP J8H9C1
A	-13	ASP	-	expression tag	UNP J8H9C1
A	-12	GLU	-	expression tag	UNP J8H9C1
A	-11	ASP	-	expression tag	UNP J8H9C1
A	-10	THR	-	expression tag	UNP J8H9C1
A	-9	ILE	-	expression tag	UNP J8H9C1
A	-8	ASP	-	expression tag	UNP J8H9C1
A	-7	VAL	-	expression tag	UNP J8H9C1
A	-6	PHE	-	expression tag	UNP J8H9C1
A	-5	GLN	-	expression tag	UNP J8H9C1
A	-4	GLN	-	expression tag	UNP J8H9C1
A	-3	GLN	-	expression tag	UNP J8H9C1
A	-2	THR	-	expression tag	UNP J8H9C1
A	-1	GLY	-	expression tag	UNP J8H9C1
A	0	GLY	-	expression tag	UNP J8H9C1
A	1	SER	-	expression tag	UNP J8H9C1
B	-96	MET	-	expression tag	UNP J8H9C1
B	-95	GLY	-	expression tag	UNP J8H9C1
B	-94	SER	-	expression tag	UNP J8H9C1
B	-93	SER	-	expression tag	UNP J8H9C1
B	-92	HIS	-	expression tag	UNP J8H9C1
B	-91	HIS	-	expression tag	UNP J8H9C1
B	-90	HIS	-	expression tag	UNP J8H9C1
B	-89	HIS	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-88	HIS	-	expression tag	UNP J8H9C1
B	-87	HIS	-	expression tag	UNP J8H9C1
B	-86	GLY	-	expression tag	UNP J8H9C1
B	-85	SER	-	expression tag	UNP J8H9C1
B	-84	GLY	-	expression tag	UNP J8H9C1
B	-83	VAL	-	expression tag	UNP J8H9C1
B	-82	LYS	-	expression tag	UNP J8H9C1
B	-81	THR	-	expression tag	UNP J8H9C1
B	-80	GLU	-	expression tag	UNP J8H9C1
B	-79	ASN	-	expression tag	UNP J8H9C1
B	-78	ASN	-	expression tag	UNP J8H9C1
B	-77	ASP	-	expression tag	UNP J8H9C1
B	-76	HIS	-	expression tag	UNP J8H9C1
B	-75	ILE	-	expression tag	UNP J8H9C1
B	-74	ASN	-	expression tag	UNP J8H9C1
B	-73	LEU	-	expression tag	UNP J8H9C1
B	-72	LYS	-	expression tag	UNP J8H9C1
B	-71	VAL	-	expression tag	UNP J8H9C1
B	-70	ALA	-	expression tag	UNP J8H9C1
B	-69	GLY	-	expression tag	UNP J8H9C1
B	-68	GLN	-	expression tag	UNP J8H9C1
B	-67	ASP	-	expression tag	UNP J8H9C1
B	-66	GLY	-	expression tag	UNP J8H9C1
B	-65	SER	-	expression tag	UNP J8H9C1
B	-64	VAL	-	expression tag	UNP J8H9C1
B	-63	VAL	-	expression tag	UNP J8H9C1
B	-62	GLN	-	expression tag	UNP J8H9C1
B	-61	PHE	-	expression tag	UNP J8H9C1
B	-60	LYS	-	expression tag	UNP J8H9C1
B	-59	ILE	-	expression tag	UNP J8H9C1
B	-58	LYS	-	expression tag	UNP J8H9C1
B	-57	ARG	-	expression tag	UNP J8H9C1
B	-56	HIS	-	expression tag	UNP J8H9C1
B	-55	THR	-	expression tag	UNP J8H9C1
B	-54	PRO	-	expression tag	UNP J8H9C1
B	-53	LEU	-	expression tag	UNP J8H9C1
B	-52	SER	-	expression tag	UNP J8H9C1
B	-51	LYS	-	expression tag	UNP J8H9C1
B	-50	LEU	-	expression tag	UNP J8H9C1
B	-49	MET	-	expression tag	UNP J8H9C1
B	-48	LYS	-	expression tag	UNP J8H9C1
B	-47	ALA	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-46	TYR	-	expression tag	UNP J8H9C1
B	-45	CYS	-	expression tag	UNP J8H9C1
B	-44	GLU	-	expression tag	UNP J8H9C1
B	-43	ARG	-	expression tag	UNP J8H9C1
B	-42	GLN	-	expression tag	UNP J8H9C1
B	-41	GLY	-	expression tag	UNP J8H9C1
B	-40	LEU	-	expression tag	UNP J8H9C1
B	-39	SER	-	expression tag	UNP J8H9C1
B	-38	MET	-	expression tag	UNP J8H9C1
B	-37	ARG	-	expression tag	UNP J8H9C1
B	-36	GLN	-	expression tag	UNP J8H9C1
B	-35	ILE	-	expression tag	UNP J8H9C1
B	-34	ARG	-	expression tag	UNP J8H9C1
B	-33	PHE	-	expression tag	UNP J8H9C1
B	-32	ARG	-	expression tag	UNP J8H9C1
B	-31	PHE	-	expression tag	UNP J8H9C1
B	-30	ASP	-	expression tag	UNP J8H9C1
B	-29	GLY	-	expression tag	UNP J8H9C1
B	-28	GLN	-	expression tag	UNP J8H9C1
B	-27	PRO	-	expression tag	UNP J8H9C1
B	-26	ILE	-	expression tag	UNP J8H9C1
B	-25	ASN	-	expression tag	UNP J8H9C1
B	-24	GLU	-	expression tag	UNP J8H9C1
B	-23	THR	-	expression tag	UNP J8H9C1
B	-22	ASP	-	expression tag	UNP J8H9C1
B	-21	THR	-	expression tag	UNP J8H9C1
B	-20	PRO	-	expression tag	UNP J8H9C1
B	-19	ALA	-	expression tag	UNP J8H9C1
B	-18	GLN	-	expression tag	UNP J8H9C1
B	-17	LEU	-	expression tag	UNP J8H9C1
B	-16	GLU	-	expression tag	UNP J8H9C1
B	-15	MET	-	expression tag	UNP J8H9C1
B	-14	GLU	-	expression tag	UNP J8H9C1
B	-13	ASP	-	expression tag	UNP J8H9C1
B	-12	GLU	-	expression tag	UNP J8H9C1
B	-11	ASP	-	expression tag	UNP J8H9C1
B	-10	THR	-	expression tag	UNP J8H9C1
B	-9	ILE	-	expression tag	UNP J8H9C1
B	-8	ASP	-	expression tag	UNP J8H9C1
B	-7	VAL	-	expression tag	UNP J8H9C1
B	-6	PHE	-	expression tag	UNP J8H9C1
B	-5	GLN	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLN	-	expression tag	UNP J8H9C1
B	-3	GLN	-	expression tag	UNP J8H9C1
B	-2	THR	-	expression tag	UNP J8H9C1
B	-1	GLY	-	expression tag	UNP J8H9C1
B	0	GLY	-	expression tag	UNP J8H9C1
B	1	SER	-	expression tag	UNP J8H9C1
C	-96	MET	-	expression tag	UNP J8H9C1
C	-95	GLY	-	expression tag	UNP J8H9C1
C	-94	SER	-	expression tag	UNP J8H9C1
C	-93	SER	-	expression tag	UNP J8H9C1
C	-92	HIS	-	expression tag	UNP J8H9C1
C	-91	HIS	-	expression tag	UNP J8H9C1
C	-90	HIS	-	expression tag	UNP J8H9C1
C	-89	HIS	-	expression tag	UNP J8H9C1
C	-88	HIS	-	expression tag	UNP J8H9C1
C	-87	HIS	-	expression tag	UNP J8H9C1
C	-86	GLY	-	expression tag	UNP J8H9C1
C	-85	SER	-	expression tag	UNP J8H9C1
C	-84	GLY	-	expression tag	UNP J8H9C1
C	-83	VAL	-	expression tag	UNP J8H9C1
C	-82	LYS	-	expression tag	UNP J8H9C1
C	-81	THR	-	expression tag	UNP J8H9C1
C	-80	GLU	-	expression tag	UNP J8H9C1
C	-79	ASN	-	expression tag	UNP J8H9C1
C	-78	ASN	-	expression tag	UNP J8H9C1
C	-77	ASP	-	expression tag	UNP J8H9C1
C	-76	HIS	-	expression tag	UNP J8H9C1
C	-75	ILE	-	expression tag	UNP J8H9C1
C	-74	ASN	-	expression tag	UNP J8H9C1
C	-73	LEU	-	expression tag	UNP J8H9C1
C	-72	LYS	-	expression tag	UNP J8H9C1
C	-71	VAL	-	expression tag	UNP J8H9C1
C	-70	ALA	-	expression tag	UNP J8H9C1
C	-69	GLY	-	expression tag	UNP J8H9C1
C	-68	GLN	-	expression tag	UNP J8H9C1
C	-67	ASP	-	expression tag	UNP J8H9C1
C	-66	GLY	-	expression tag	UNP J8H9C1
C	-65	SER	-	expression tag	UNP J8H9C1
C	-64	VAL	-	expression tag	UNP J8H9C1
C	-63	VAL	-	expression tag	UNP J8H9C1
C	-62	GLN	-	expression tag	UNP J8H9C1
C	-61	PHE	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-60	LYS	-	expression tag	UNP J8H9C1
C	-59	ILE	-	expression tag	UNP J8H9C1
C	-58	LYS	-	expression tag	UNP J8H9C1
C	-57	ARG	-	expression tag	UNP J8H9C1
C	-56	HIS	-	expression tag	UNP J8H9C1
C	-55	THR	-	expression tag	UNP J8H9C1
C	-54	PRO	-	expression tag	UNP J8H9C1
C	-53	LEU	-	expression tag	UNP J8H9C1
C	-52	SER	-	expression tag	UNP J8H9C1
C	-51	LYS	-	expression tag	UNP J8H9C1
C	-50	LEU	-	expression tag	UNP J8H9C1
C	-49	MET	-	expression tag	UNP J8H9C1
C	-48	LYS	-	expression tag	UNP J8H9C1
C	-47	ALA	-	expression tag	UNP J8H9C1
C	-46	TYR	-	expression tag	UNP J8H9C1
C	-45	CYS	-	expression tag	UNP J8H9C1
C	-44	GLU	-	expression tag	UNP J8H9C1
C	-43	ARG	-	expression tag	UNP J8H9C1
C	-42	GLN	-	expression tag	UNP J8H9C1
C	-41	GLY	-	expression tag	UNP J8H9C1
C	-40	LEU	-	expression tag	UNP J8H9C1
C	-39	SER	-	expression tag	UNP J8H9C1
C	-38	MET	-	expression tag	UNP J8H9C1
C	-37	ARG	-	expression tag	UNP J8H9C1
C	-36	GLN	-	expression tag	UNP J8H9C1
C	-35	ILE	-	expression tag	UNP J8H9C1
C	-34	ARG	-	expression tag	UNP J8H9C1
C	-33	PHE	-	expression tag	UNP J8H9C1
C	-32	ARG	-	expression tag	UNP J8H9C1
C	-31	PHE	-	expression tag	UNP J8H9C1
C	-30	ASP	-	expression tag	UNP J8H9C1
C	-29	GLY	-	expression tag	UNP J8H9C1
C	-28	GLN	-	expression tag	UNP J8H9C1
C	-27	PRO	-	expression tag	UNP J8H9C1
C	-26	ILE	-	expression tag	UNP J8H9C1
C	-25	ASN	-	expression tag	UNP J8H9C1
C	-24	GLU	-	expression tag	UNP J8H9C1
C	-23	THR	-	expression tag	UNP J8H9C1
C	-22	ASP	-	expression tag	UNP J8H9C1
C	-21	THR	-	expression tag	UNP J8H9C1
C	-20	PRO	-	expression tag	UNP J8H9C1
C	-19	ALA	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	GLN	-	expression tag	UNP J8H9C1
C	-17	LEU	-	expression tag	UNP J8H9C1
C	-16	GLU	-	expression tag	UNP J8H9C1
C	-15	MET	-	expression tag	UNP J8H9C1
C	-14	GLU	-	expression tag	UNP J8H9C1
C	-13	ASP	-	expression tag	UNP J8H9C1
C	-12	GLU	-	expression tag	UNP J8H9C1
C	-11	ASP	-	expression tag	UNP J8H9C1
C	-10	THR	-	expression tag	UNP J8H9C1
C	-9	ILE	-	expression tag	UNP J8H9C1
C	-8	ASP	-	expression tag	UNP J8H9C1
C	-7	VAL	-	expression tag	UNP J8H9C1
C	-6	PHE	-	expression tag	UNP J8H9C1
C	-5	GLN	-	expression tag	UNP J8H9C1
C	-4	GLN	-	expression tag	UNP J8H9C1
C	-3	GLN	-	expression tag	UNP J8H9C1
C	-2	THR	-	expression tag	UNP J8H9C1
C	-1	GLY	-	expression tag	UNP J8H9C1
C	0	GLY	-	expression tag	UNP J8H9C1
C	1	SER	-	expression tag	UNP J8H9C1
D	-96	MET	-	expression tag	UNP J8H9C1
D	-95	GLY	-	expression tag	UNP J8H9C1
D	-94	SER	-	expression tag	UNP J8H9C1
D	-93	SER	-	expression tag	UNP J8H9C1
D	-92	HIS	-	expression tag	UNP J8H9C1
D	-91	HIS	-	expression tag	UNP J8H9C1
D	-90	HIS	-	expression tag	UNP J8H9C1
D	-89	HIS	-	expression tag	UNP J8H9C1
D	-88	HIS	-	expression tag	UNP J8H9C1
D	-87	HIS	-	expression tag	UNP J8H9C1
D	-86	GLY	-	expression tag	UNP J8H9C1
D	-85	SER	-	expression tag	UNP J8H9C1
D	-84	GLY	-	expression tag	UNP J8H9C1
D	-83	VAL	-	expression tag	UNP J8H9C1
D	-82	LYS	-	expression tag	UNP J8H9C1
D	-81	THR	-	expression tag	UNP J8H9C1
D	-80	GLU	-	expression tag	UNP J8H9C1
D	-79	ASN	-	expression tag	UNP J8H9C1
D	-78	ASN	-	expression tag	UNP J8H9C1
D	-77	ASP	-	expression tag	UNP J8H9C1
D	-76	HIS	-	expression tag	UNP J8H9C1
D	-75	ILE	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-74	ASN	-	expression tag	UNP J8H9C1
D	-73	LEU	-	expression tag	UNP J8H9C1
D	-72	LYS	-	expression tag	UNP J8H9C1
D	-71	VAL	-	expression tag	UNP J8H9C1
D	-70	ALA	-	expression tag	UNP J8H9C1
D	-69	GLY	-	expression tag	UNP J8H9C1
D	-68	GLN	-	expression tag	UNP J8H9C1
D	-67	ASP	-	expression tag	UNP J8H9C1
D	-66	GLY	-	expression tag	UNP J8H9C1
D	-65	SER	-	expression tag	UNP J8H9C1
D	-64	VAL	-	expression tag	UNP J8H9C1
D	-63	VAL	-	expression tag	UNP J8H9C1
D	-62	GLN	-	expression tag	UNP J8H9C1
D	-61	PHE	-	expression tag	UNP J8H9C1
D	-60	LYS	-	expression tag	UNP J8H9C1
D	-59	ILE	-	expression tag	UNP J8H9C1
D	-58	LYS	-	expression tag	UNP J8H9C1
D	-57	ARG	-	expression tag	UNP J8H9C1
D	-56	HIS	-	expression tag	UNP J8H9C1
D	-55	THR	-	expression tag	UNP J8H9C1
D	-54	PRO	-	expression tag	UNP J8H9C1
D	-53	LEU	-	expression tag	UNP J8H9C1
D	-52	SER	-	expression tag	UNP J8H9C1
D	-51	LYS	-	expression tag	UNP J8H9C1
D	-50	LEU	-	expression tag	UNP J8H9C1
D	-49	MET	-	expression tag	UNP J8H9C1
D	-48	LYS	-	expression tag	UNP J8H9C1
D	-47	ALA	-	expression tag	UNP J8H9C1
D	-46	TYR	-	expression tag	UNP J8H9C1
D	-45	CYS	-	expression tag	UNP J8H9C1
D	-44	GLU	-	expression tag	UNP J8H9C1
D	-43	ARG	-	expression tag	UNP J8H9C1
D	-42	GLN	-	expression tag	UNP J8H9C1
D	-41	GLY	-	expression tag	UNP J8H9C1
D	-40	LEU	-	expression tag	UNP J8H9C1
D	-39	SER	-	expression tag	UNP J8H9C1
D	-38	MET	-	expression tag	UNP J8H9C1
D	-37	ARG	-	expression tag	UNP J8H9C1
D	-36	GLN	-	expression tag	UNP J8H9C1
D	-35	ILE	-	expression tag	UNP J8H9C1
D	-34	ARG	-	expression tag	UNP J8H9C1
D	-33	PHE	-	expression tag	UNP J8H9C1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-32	ARG	-	expression tag	UNP J8H9C1
D	-31	PHE	-	expression tag	UNP J8H9C1
D	-30	ASP	-	expression tag	UNP J8H9C1
D	-29	GLY	-	expression tag	UNP J8H9C1
D	-28	GLN	-	expression tag	UNP J8H9C1
D	-27	PRO	-	expression tag	UNP J8H9C1
D	-26	ILE	-	expression tag	UNP J8H9C1
D	-25	ASN	-	expression tag	UNP J8H9C1
D	-24	GLU	-	expression tag	UNP J8H9C1
D	-23	THR	-	expression tag	UNP J8H9C1
D	-22	ASP	-	expression tag	UNP J8H9C1
D	-21	THR	-	expression tag	UNP J8H9C1
D	-20	PRO	-	expression tag	UNP J8H9C1
D	-19	ALA	-	expression tag	UNP J8H9C1
D	-18	GLN	-	expression tag	UNP J8H9C1
D	-17	LEU	-	expression tag	UNP J8H9C1
D	-16	GLU	-	expression tag	UNP J8H9C1
D	-15	MET	-	expression tag	UNP J8H9C1
D	-14	GLU	-	expression tag	UNP J8H9C1
D	-13	ASP	-	expression tag	UNP J8H9C1
D	-12	GLU	-	expression tag	UNP J8H9C1
D	-11	ASP	-	expression tag	UNP J8H9C1
D	-10	THR	-	expression tag	UNP J8H9C1
D	-9	ILE	-	expression tag	UNP J8H9C1
D	-8	ASP	-	expression tag	UNP J8H9C1
D	-7	VAL	-	expression tag	UNP J8H9C1
D	-6	PHE	-	expression tag	UNP J8H9C1
D	-5	GLN	-	expression tag	UNP J8H9C1
D	-4	GLN	-	expression tag	UNP J8H9C1
D	-3	GLN	-	expression tag	UNP J8H9C1
D	-2	THR	-	expression tag	UNP J8H9C1
D	-1	GLY	-	expression tag	UNP J8H9C1
D	0	GLY	-	expression tag	UNP J8H9C1
D	1	SER	-	expression tag	UNP J8H9C1

- Molecule 2 is a protein called Gabija protein GajB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	288	Total	C	N	O	S	0	0
			2326	1502	381	441	2		
2	F	288	Total	C	N	O	S	0	0
			2326	1502	381	441	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	288	Total	C	N	O	S	0	0
			2326	1502	381	441	2		
2	H	288	Total	C	N	O	S	0	0
			2326	1502	381	441	2		

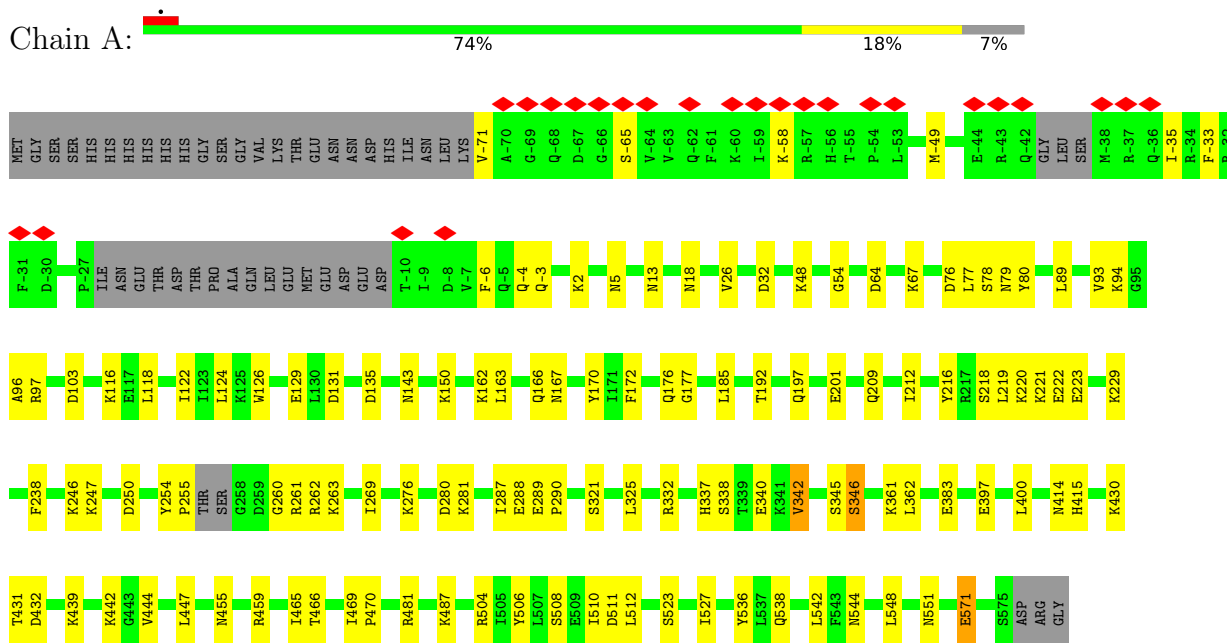
- Molecule 3 is a protein called Gabija Anti-Defense 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	162	Total	C	N	O	S	0	0
			1346	867	231	240	8		
3	J	162	Total	C	N	O	S	0	0
			1346	867	231	240	8		
3	K	162	Total	C	N	O	S	0	0
			1346	867	231	240	8		
3	L	162	Total	C	N	O	S	0	0
			1346	867	231	240	8		
3	M	114	Total	C	N	O	S	0	0
			933	602	152	172	7		
3	N	114	Total	C	N	O	S	0	0
			933	602	152	172	7		
3	O	114	Total	C	N	O	S	0	0
			933	602	152	172	7		
3	P	114	Total	C	N	O	S	0	0
			933	602	152	172	7		

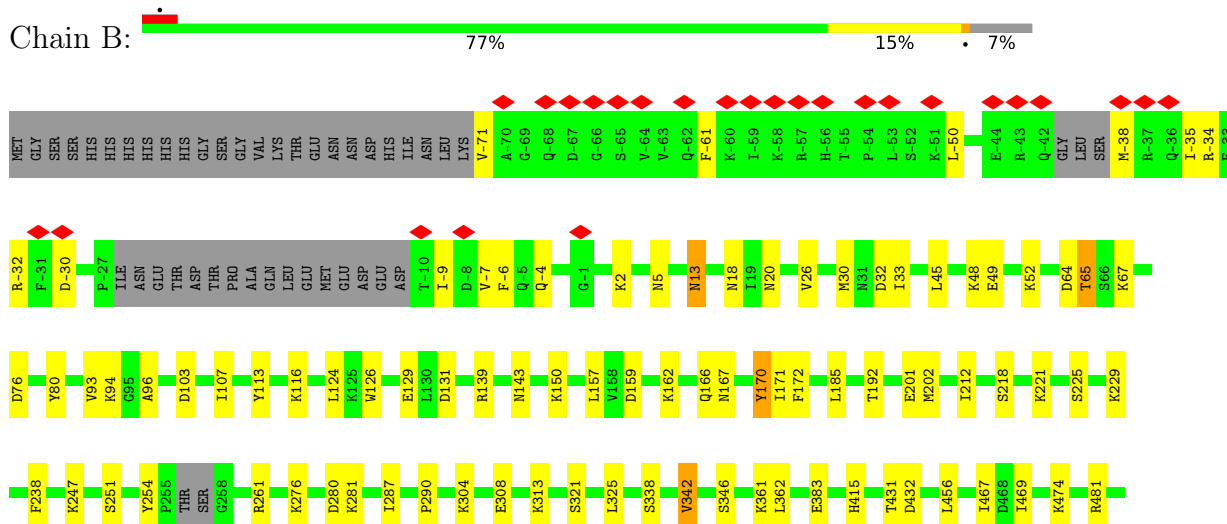
### 3 Residue-property plots

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

#### • Molecule 1: Endonuclease GajA

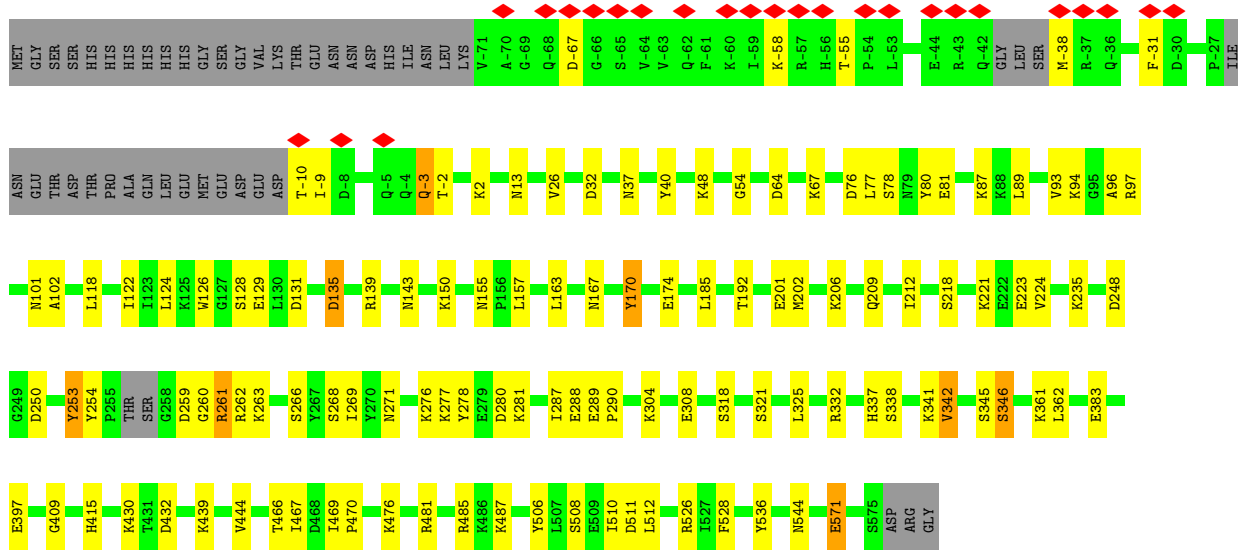
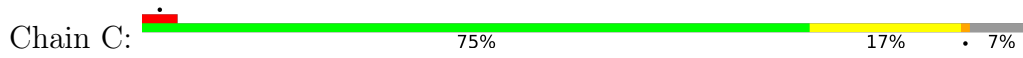


#### • Molecule 1: Endonuclease GajA

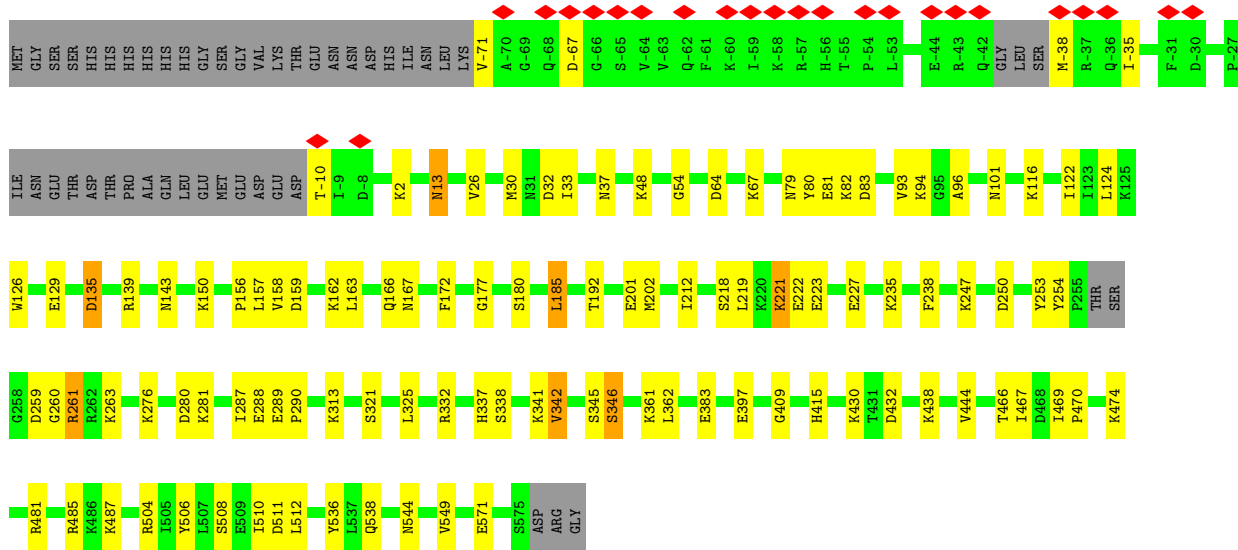
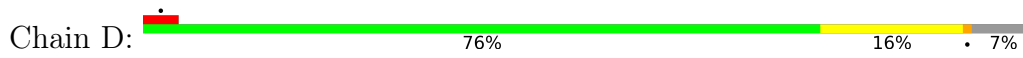




• Molecule 1: Endonuclease GajA



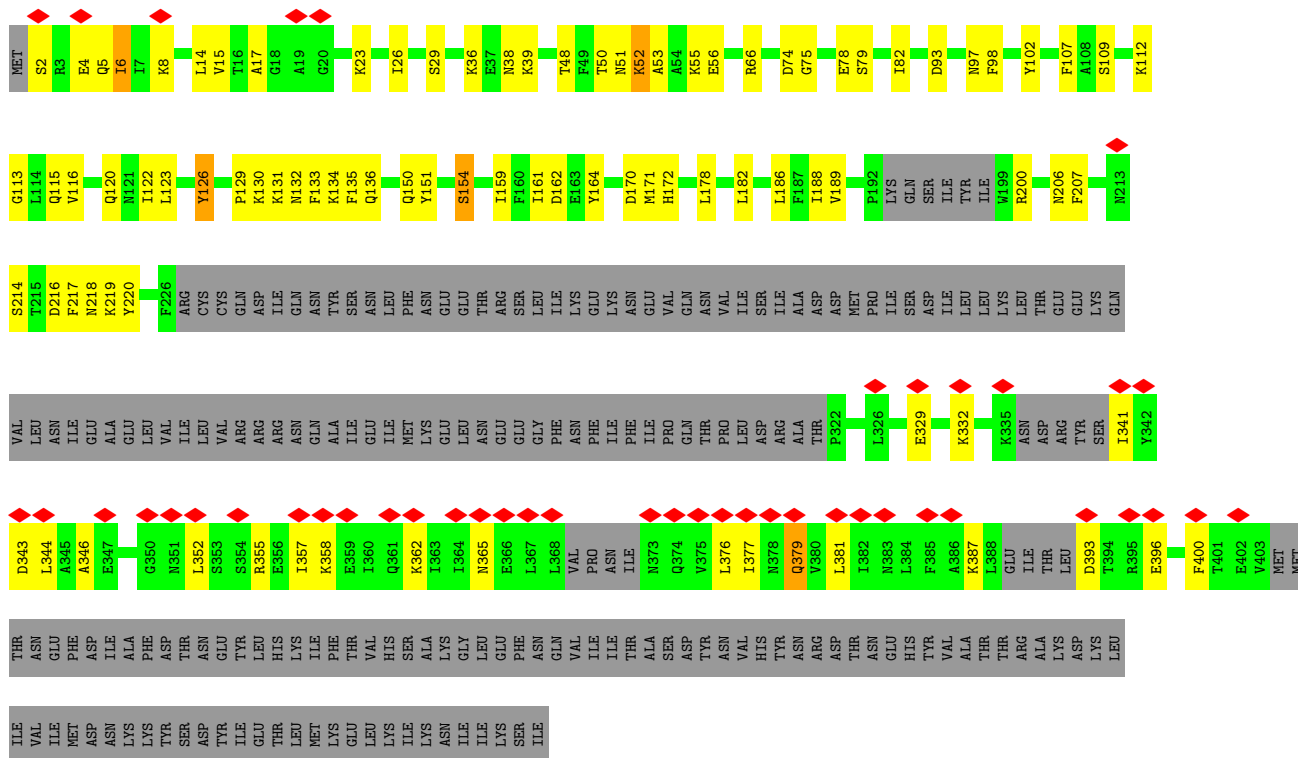
• Molecule 1: Endonuclease GajA



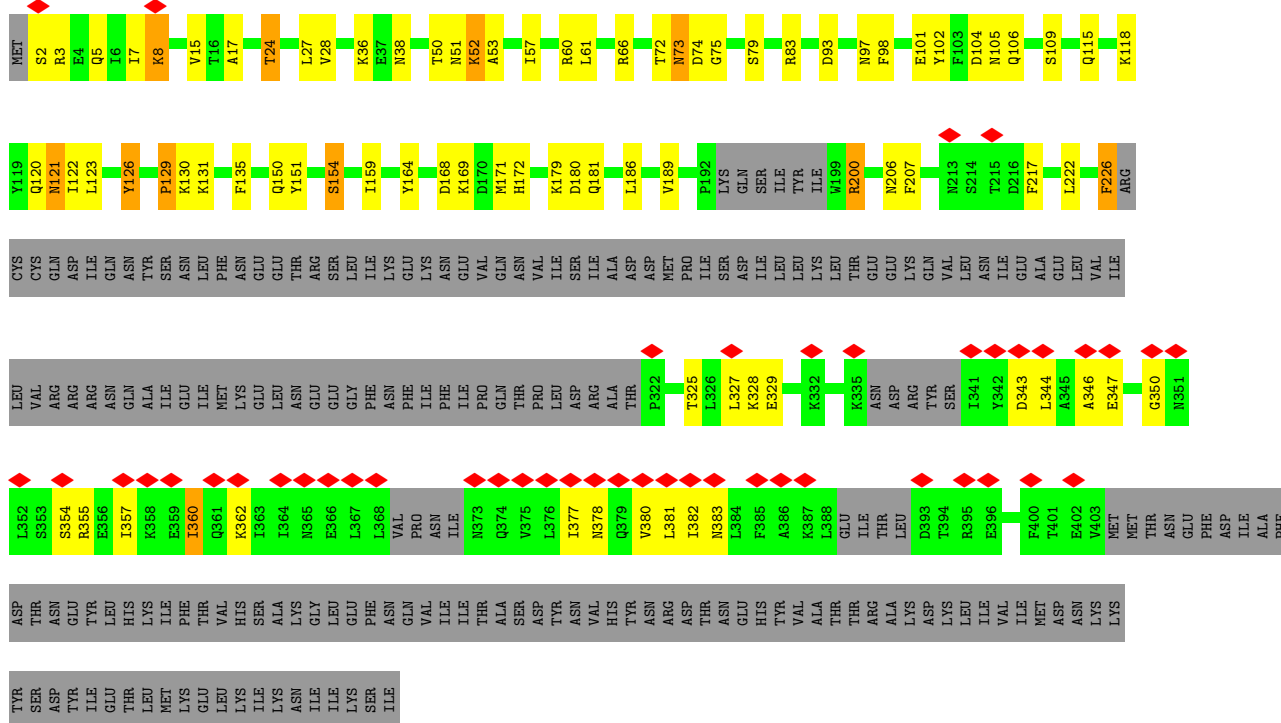
• Molecule 2: Gabija protein GajB







• Molecule 2: Gabija protein GajB

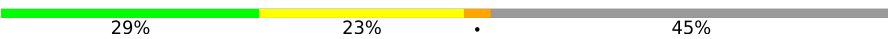


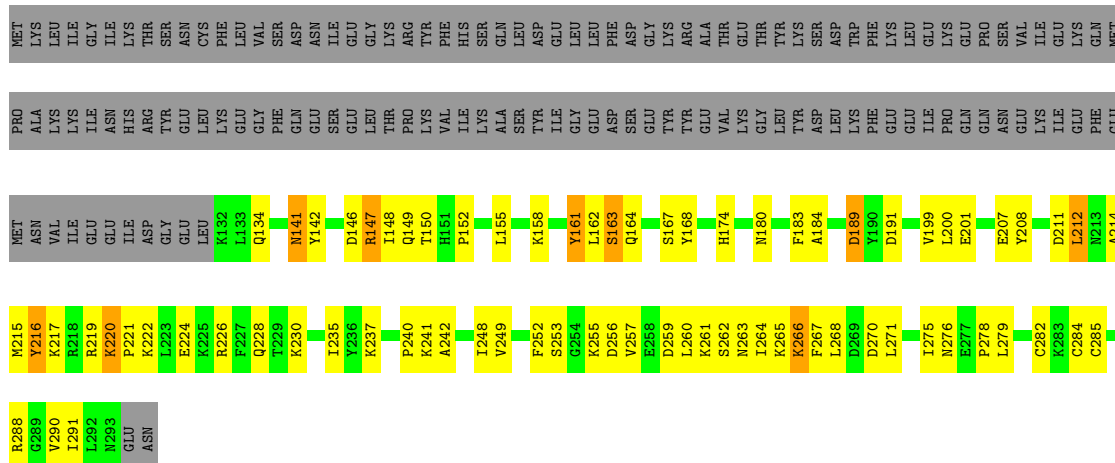
• Molecule 2: Gabija protein GajB





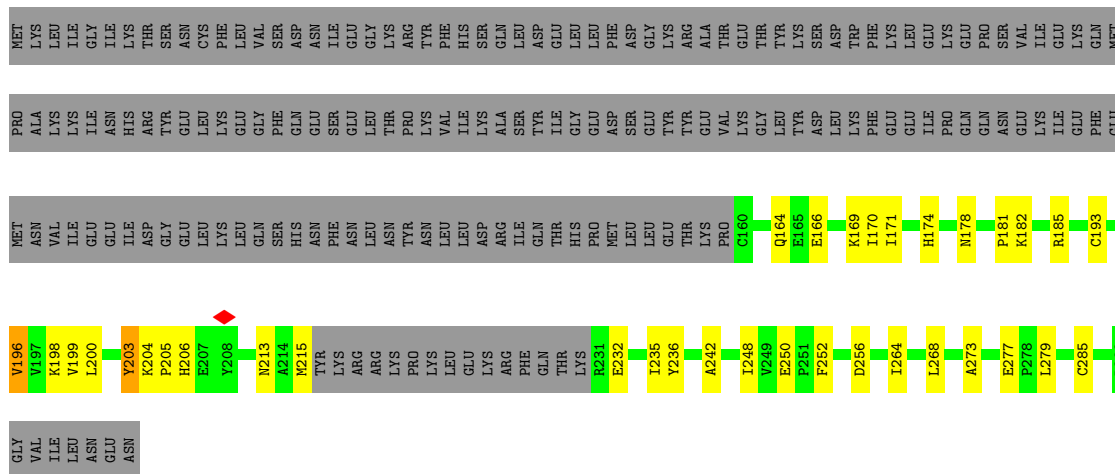
### Molecule 3: Gabija Anti-Defense 1

Chain L:  29% 23% 45%



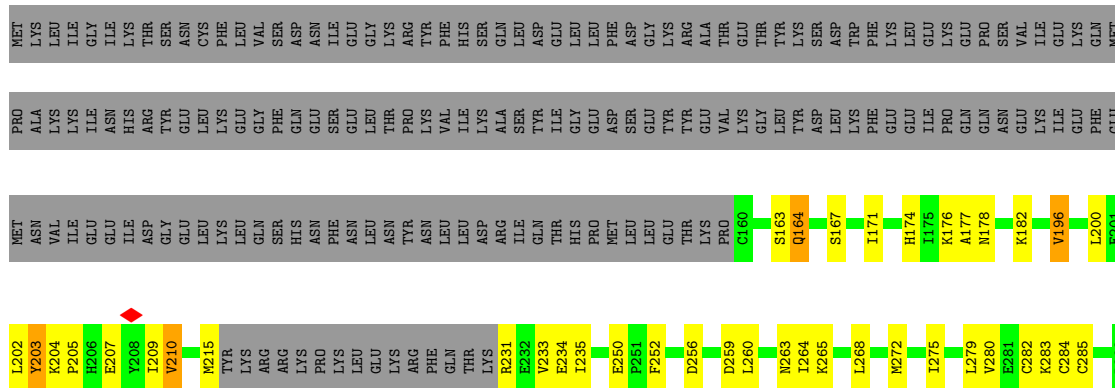
### Molecule 3: Gabija Anti-Defense 1

Chain M:  27% 11% 61%



### Molecule 3: Gabija Anti-Defense 1

Chain N:  25% 12% 61%



GLY  
VAL  
ILE  
LEU  
ASN  
GLU  
ASN

● Molecule 3: Gabija Anti-Defense 1

Chain O:  25% 12% 61%

MET LYS LEU ILE GLY ILE LYS THR SER ASN CYS PHE LEU VAL ASP  
GLN ASN ILE SER LEU GLY PHE ASP GLN LEU GLY LYS THR

PRO ALA LYS ILE GLY ASN ARG TYR LYS THR PRO ARG TYR VAL ILE SER  
ALA LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU

MET ASN VAL GLU GLU ILE ASP GLY GLU LEU LYS LEU GLN SER HIS ASN PHE ASN ARG ASN LYS THR PRO MET LEU LEU TYR ARG LYS THR PRO  
Y160 Y161 L162 S163 Q164 E166 S167 I171 K176 A177 P181 K182 F183 A184 R185 K198

V199 L200 Y203 K204 P205 Y208 I209 V210 D211 L212 N213 A214 M215 TYR LYS ARG ARG LYS PRO TYR LYS LEU LEU LEU LYS ARG PHE GLN THR LYS  
R231 E232 V233 E234 I235 E250 S253 D256 V257 E258 N263 I264 K265 K266 D270 L271 M272 N276 L279 V280 E281 C282 K283

C284  
R288  
GLY VAL ILE LEU ASN  
GLU ASN

● Molecule 3: Gabija Anti-Defense 1

Chain P:  23% 14% 61%

MET LYS LEU ILE GLY ILE LYS THR SER ASN CYS PHE LEU VAL SER HIS ASN PHE ASN ARG ASN LYS THR PRO MET LEU LEU TYR ARG LYS THR PRO  
ALA LYS ILE GLY ASN HIS ARG TYR TYR LYS LEU LEU LYS LEU

PRO ALA LYS ILE GLY ASN ARG TYR LYS THR PRO ARG TYR VAL ILE SER LYS ARG ALA THR LYS LEU LEU TYR TYR VAL LYS LEU LEU TYR TYR VAL LYS  
C160 Y161 L162 S163 E166 S167 Y168 K169 I170 I171 H174 I175 K176 A177 M178 I179 R185 I186

MET ASN VAL GLU GLU ILE ASP GLY GLU LEU LYS LEU GLN SER HIS ASN PHE ASN ARG ASN LYS THR PRO MET LEU LEU TYR TYR VAL LYS LEU LEU TYR TYR VAL LYS  
T187 S186 C193 T195 V196 V197 K198 V199 L200 E201 K204 Y208 I209 M215 TYR LYS ARG ARG LYS PRO LYS LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU LEU  
R231 E232 V233 E234 I235 Y246 E250 F251 F252 D256 V257 L260 K261 S262 N263 I264 K265 L268 M272

I275  
V280  
K283  
C284  
C285  
R288  
GLY VAL ILE LEU ASN  
GLU ASN

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	351193	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	41.1	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.269	Depositor
Minimum map value	-0.095	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.028	Depositor
Map size ( $\text{\AA}$ )	311.5, 311.5, 311.5	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.89, 0.89, 0.89	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.30	0/5196	0.45	0/6968
1	B	0.30	0/5196	0.46	0/6968
1	C	0.30	0/5196	0.45	0/6968
1	D	0.30	0/5196	0.46	0/6968
2	E	0.27	0/2365	0.47	0/3179
2	F	0.28	0/2365	0.50	1/3179 (0.0%)
2	G	0.26	0/2365	0.45	0/3179
2	H	0.26	0/2365	0.48	1/3179 (0.0%)
3	I	0.28	0/1374	0.57	0/1849
3	J	0.28	0/1374	0.48	0/1849
3	K	0.29	0/1374	0.58	1/1849 (0.1%)
3	L	0.29	0/1374	0.55	0/1849
3	M	0.31	0/951	0.58	0/1280
3	N	0.33	0/951	0.63	0/1280
3	O	0.34	0/951	0.63	0/1280
3	P	0.32	0/951	0.58	0/1280
All	All	0.29	0/39544	0.49	3/53104 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	129	PRO	CA-N-CD	-6.12	102.93	111.50
3	K	270	ASP	CB-CG-OD2	5.67	123.41	118.30
2	H	326	LEU	CA-CB-CG	5.27	127.42	115.30

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	5111	0	5155	78	0
1	B	5111	0	5155	66	0
1	C	5111	0	5155	71	0
1	D	5111	0	5155	75	0
2	E	2326	0	2331	60	0
2	F	2326	0	2331	57	0
2	G	2326	0	2331	54	0
2	H	2326	0	2331	55	0
3	I	1346	0	1388	44	0
3	J	1346	0	1388	38	0
3	K	1346	0	1388	45	0
3	L	1346	0	1388	50	0
3	M	933	0	946	26	0
3	N	933	0	946	34	0
3	O	933	0	946	27	0
3	P	933	0	946	32	0
All	All	38864	0	39280	740	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 9.

The worst 5 of 740 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)
3:O:182:LYS:HD3	3:O:204:LYS:HB3	1.53	0.88
3:L:263:ASN:HA	3:L:266:LYS:HE3	1.57	0.85
3:O:198:LYS:HB2	3:O:235:ILE:HD11	1.63	0.80
3:M:185:ARG:HH22	3:N:177:ALA:HA	1.45	0.80
2:E:112:LYS:HA	2:E:115:GLN:HE22	1.46	0.79

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	618/675 (92%)	602 (97%)	15 (2%)	1 (0%)	47	69
1	B	618/675 (92%)	602 (97%)	15 (2%)	1 (0%)	47	69
1	C	618/675 (92%)	602 (97%)	15 (2%)	1 (0%)	47	69
1	D	618/675 (92%)	600 (97%)	17 (3%)	1 (0%)	47	69
2	E	276/494 (56%)	271 (98%)	5 (2%)	0	100	100
2	F	276/494 (56%)	272 (99%)	4 (1%)	0	100	100
2	G	276/494 (56%)	271 (98%)	5 (2%)	0	100	100
2	H	276/494 (56%)	271 (98%)	5 (2%)	0	100	100
3	I	160/295 (54%)	155 (97%)	5 (3%)	0	100	100
3	J	160/295 (54%)	156 (98%)	4 (2%)	0	100	100
3	K	160/295 (54%)	153 (96%)	7 (4%)	0	100	100
3	L	160/295 (54%)	155 (97%)	5 (3%)	0	100	100
3	M	110/295 (37%)	104 (94%)	6 (6%)	0	100	100
3	N	110/295 (37%)	102 (93%)	8 (7%)	0	100	100
3	O	110/295 (37%)	102 (93%)	8 (7%)	0	100	100
3	P	110/295 (37%)	101 (92%)	9 (8%)	0	100	100
All	All	4656/7036 (66%)	4519 (97%)	133 (3%)	4 (0%)	54	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	VAL
1	B	342	VAL
1	C	342	VAL
1	D	342	VAL

### 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	571/614 (93%)	552 (97%)	19 (3%)	38	61
1	B	571/614 (93%)	550 (96%)	21 (4%)	34	57
1	C	571/614 (93%)	545 (95%)	26 (5%)	27	49
1	D	571/614 (93%)	548 (96%)	23 (4%)	31	55
2	E	253/448 (56%)	241 (95%)	12 (5%)	26	48
2	F	253/448 (56%)	237 (94%)	16 (6%)	18	35
2	G	253/448 (56%)	236 (93%)	17 (7%)	16	31
2	H	253/448 (56%)	238 (94%)	15 (6%)	19	37
3	I	153/276 (55%)	129 (84%)	24 (16%)	2	4
3	J	153/276 (55%)	138 (90%)	15 (10%)	8	14
3	K	153/276 (55%)	138 (90%)	15 (10%)	8	14
3	L	153/276 (55%)	133 (87%)	20 (13%)	4	7
3	M	106/276 (38%)	96 (91%)	10 (9%)	8	16
3	N	106/276 (38%)	94 (89%)	12 (11%)	6	10
3	O	106/276 (38%)	89 (84%)	17 (16%)	2	4
3	P	106/276 (38%)	90 (85%)	16 (15%)	3	4
All	All	4332/6456 (67%)	4054 (94%)	278 (6%)	21	34

5 of 278 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	256	ASP
3	N	210	VAL
3	O	279	LEU
2	E	332	LYS
2	E	102	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	K	178	ASN
3	K	276	ASN
3	N	178	ASN
3	N	174	HIS
3	K	164	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

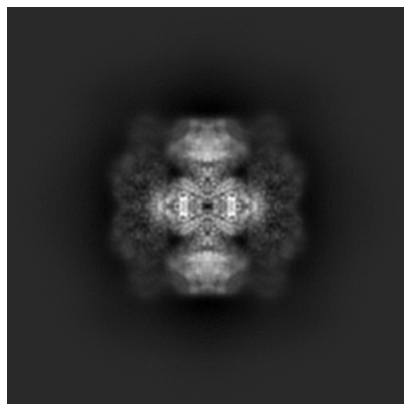
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41983. These allow visual inspection of the internal detail of the map and identification of artifacts.

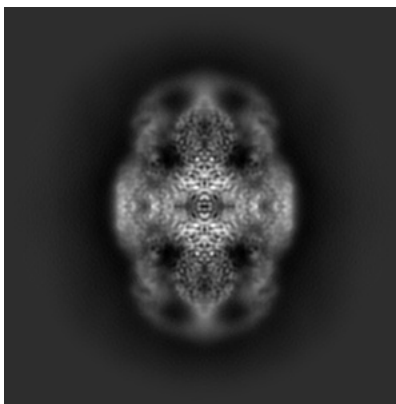
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

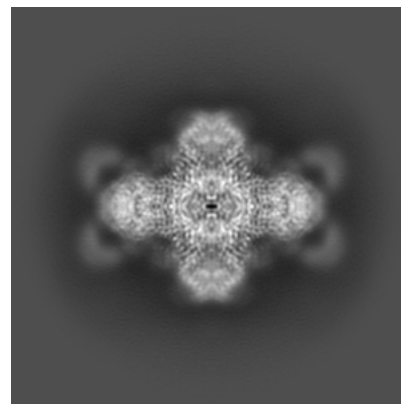
#### 6.1.1 Primary map



X

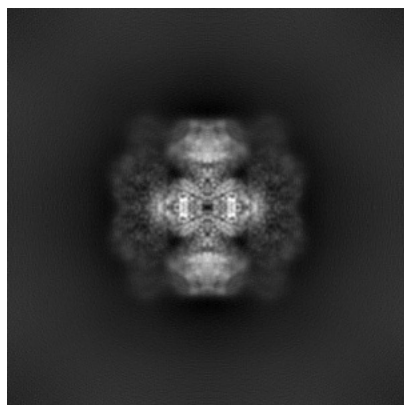


Y

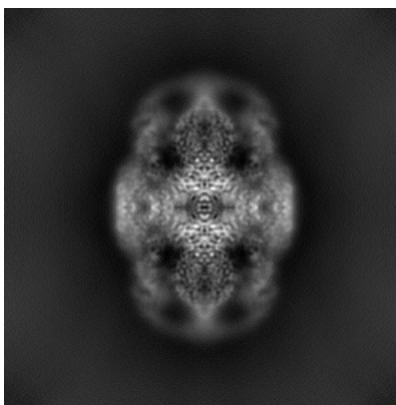


Z

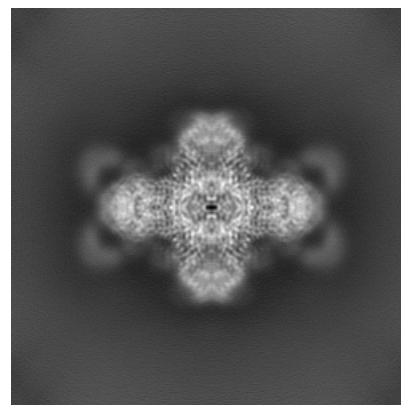
#### 6.1.2 Raw map



X



Y

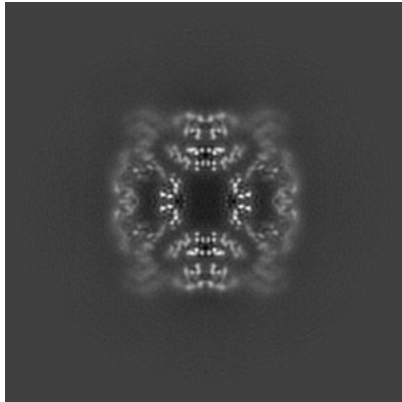


Z

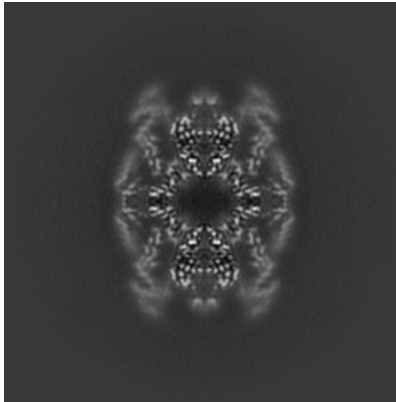
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

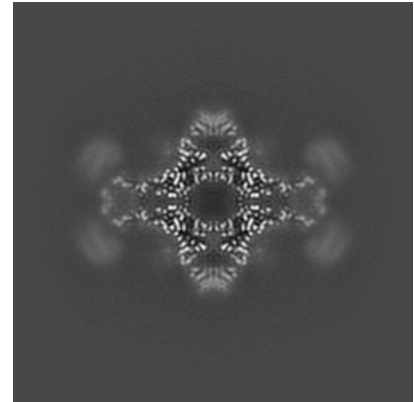
### 6.2.1 Primary map



X Index: 175

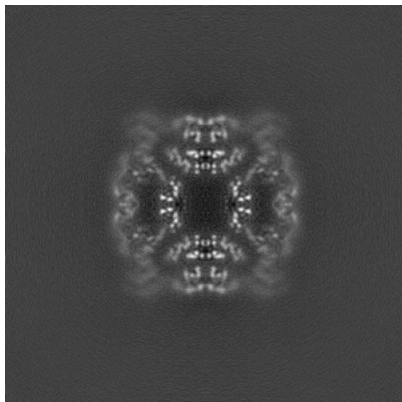


Y Index: 175

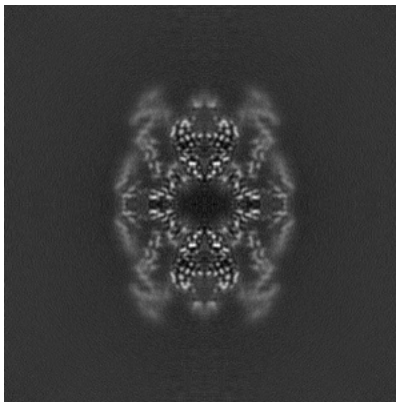


Z Index: 175

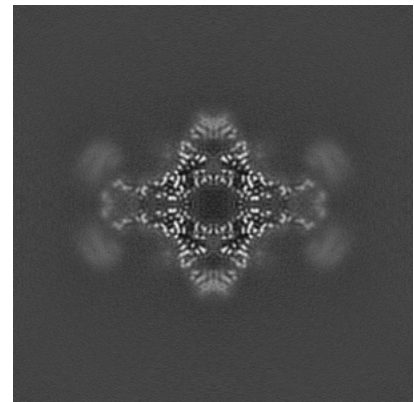
### 6.2.2 Raw map



X Index: 175



Y Index: 175

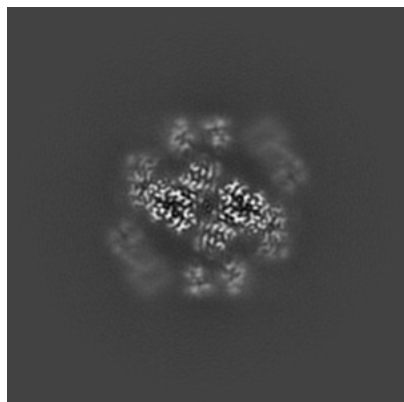


Z Index: 175

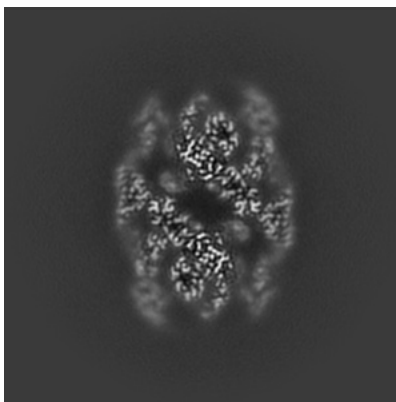
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

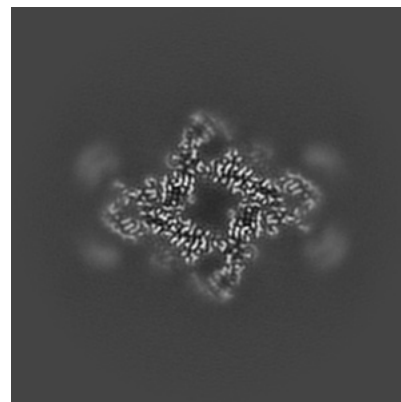
### 6.3.1 Primary map



X Index: 196

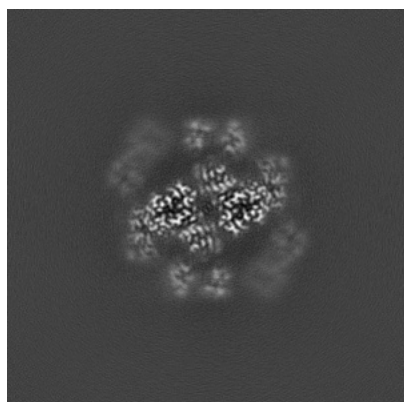


Y Index: 167

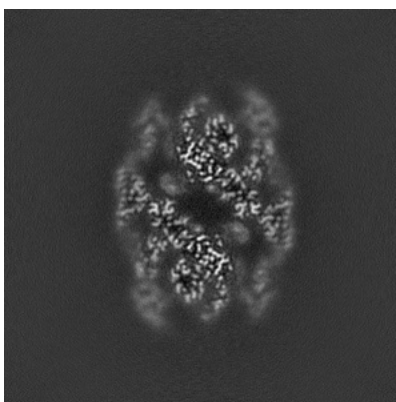


Z Index: 182

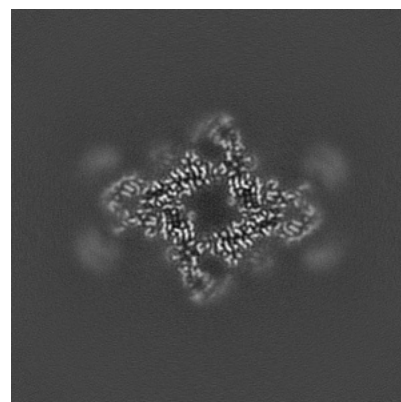
### 6.3.2 Raw map



X Index: 154



Y Index: 167

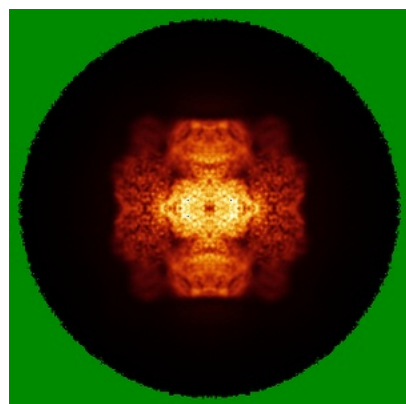


Z Index: 168

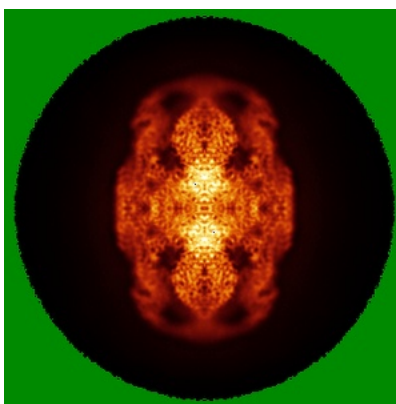
The images above show the largest variance slices of the map in three orthogonal directions.

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

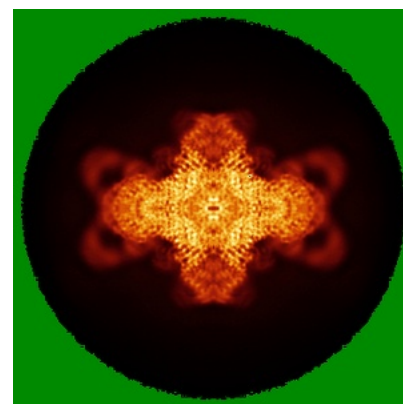
### 6.4.1 Primary map



X

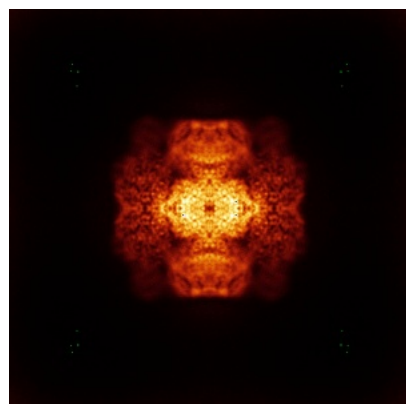


Y

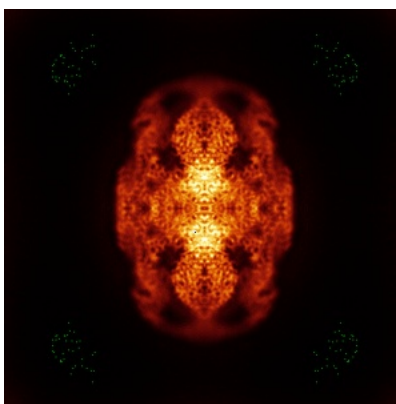


Z

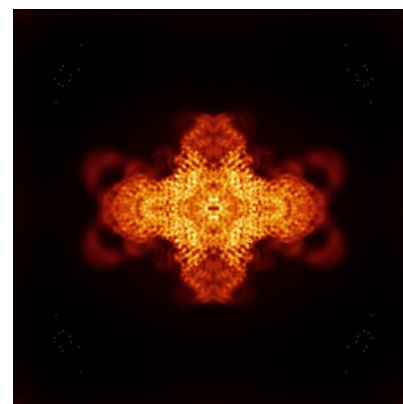
### 6.4.2 Raw map



X



Y

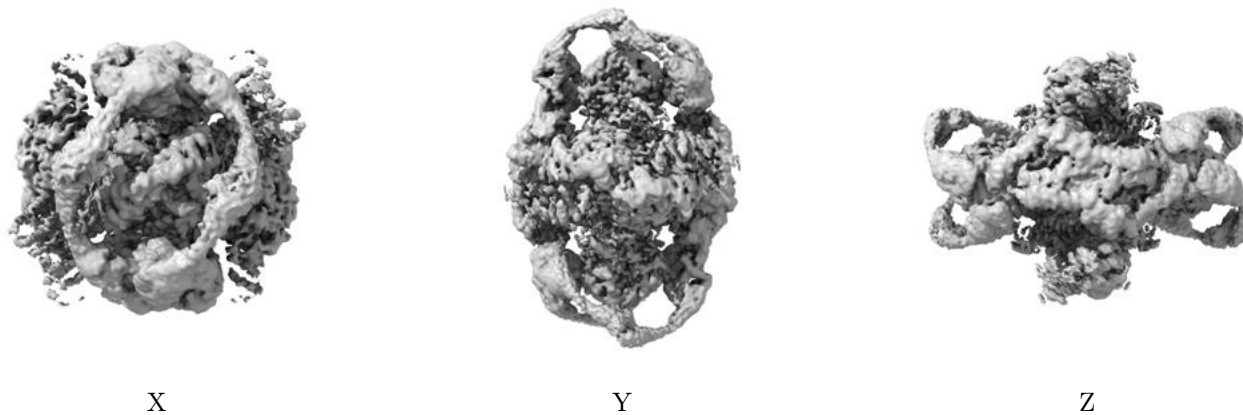


Z

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.

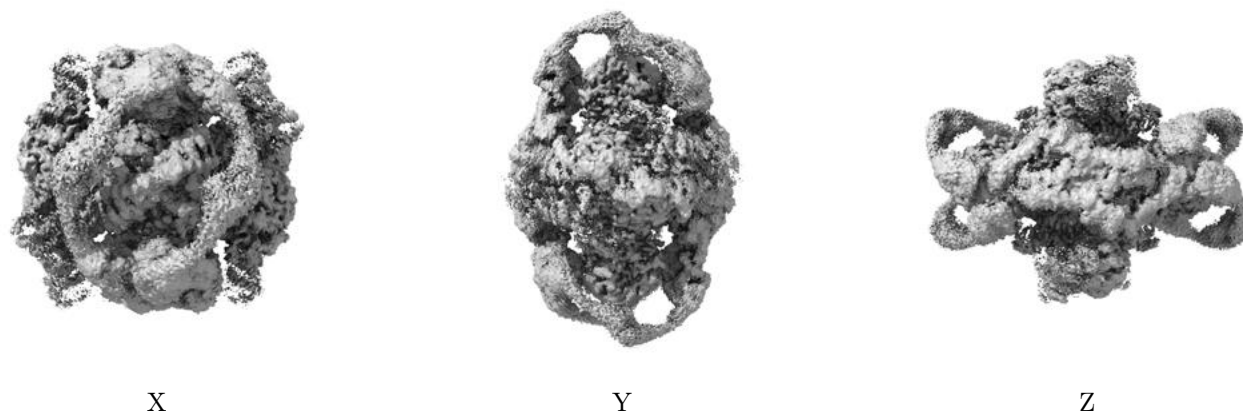
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.028. 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](#)

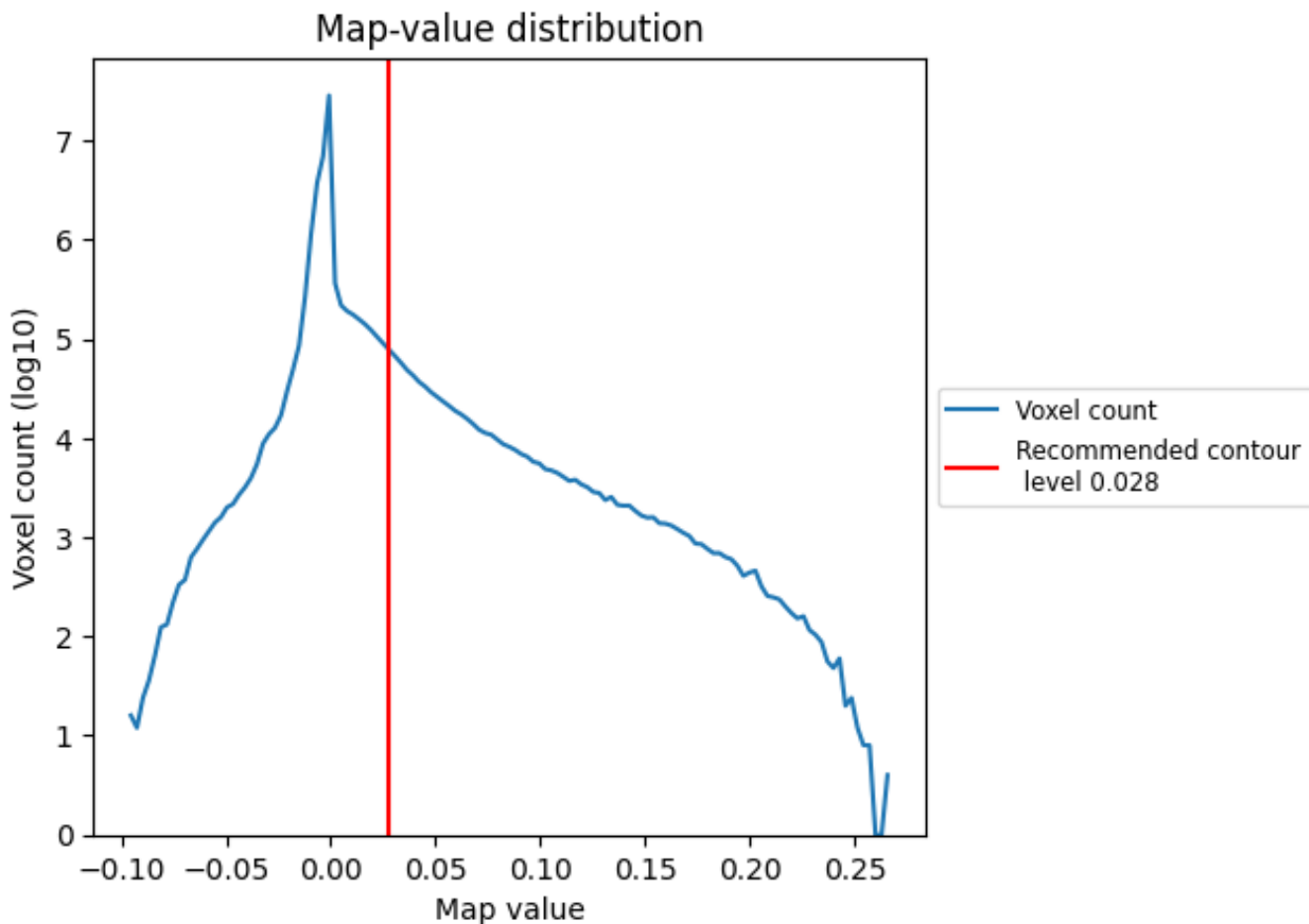
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

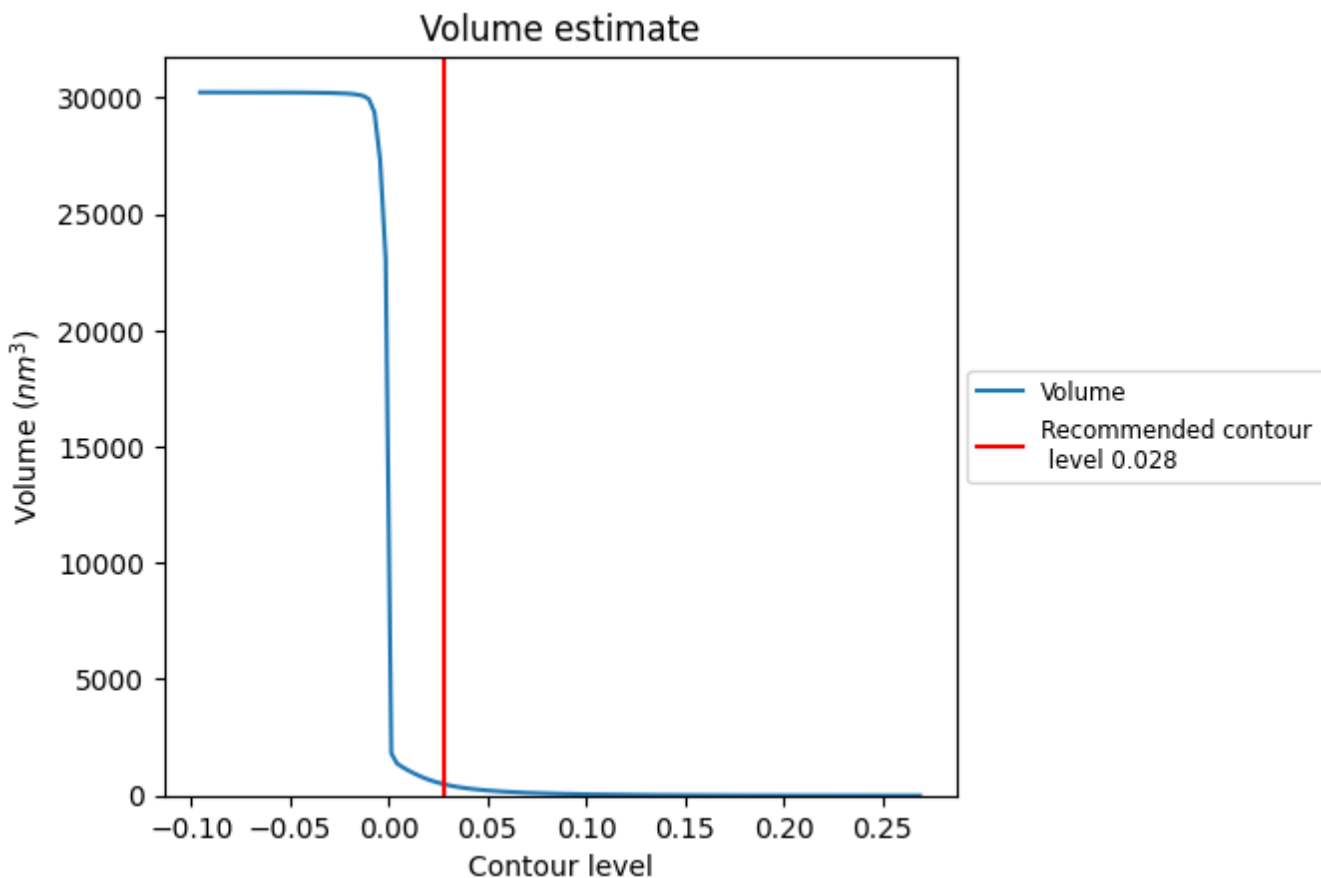
This section contains the results of statistical analysis of the map.

### 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.

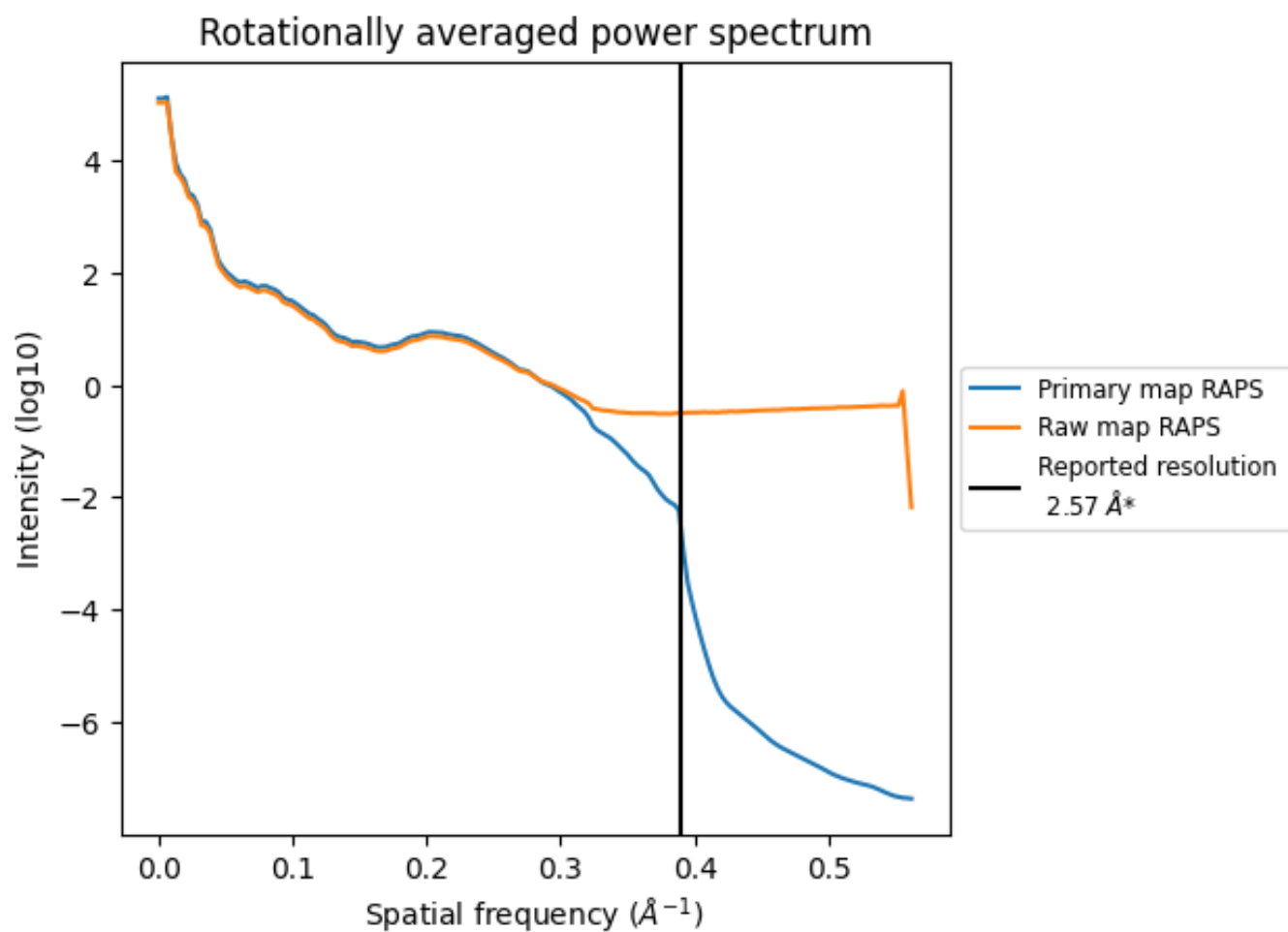
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 487 nm<sup>3</sup>; this corresponds to an approximate mass of 440 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](#)

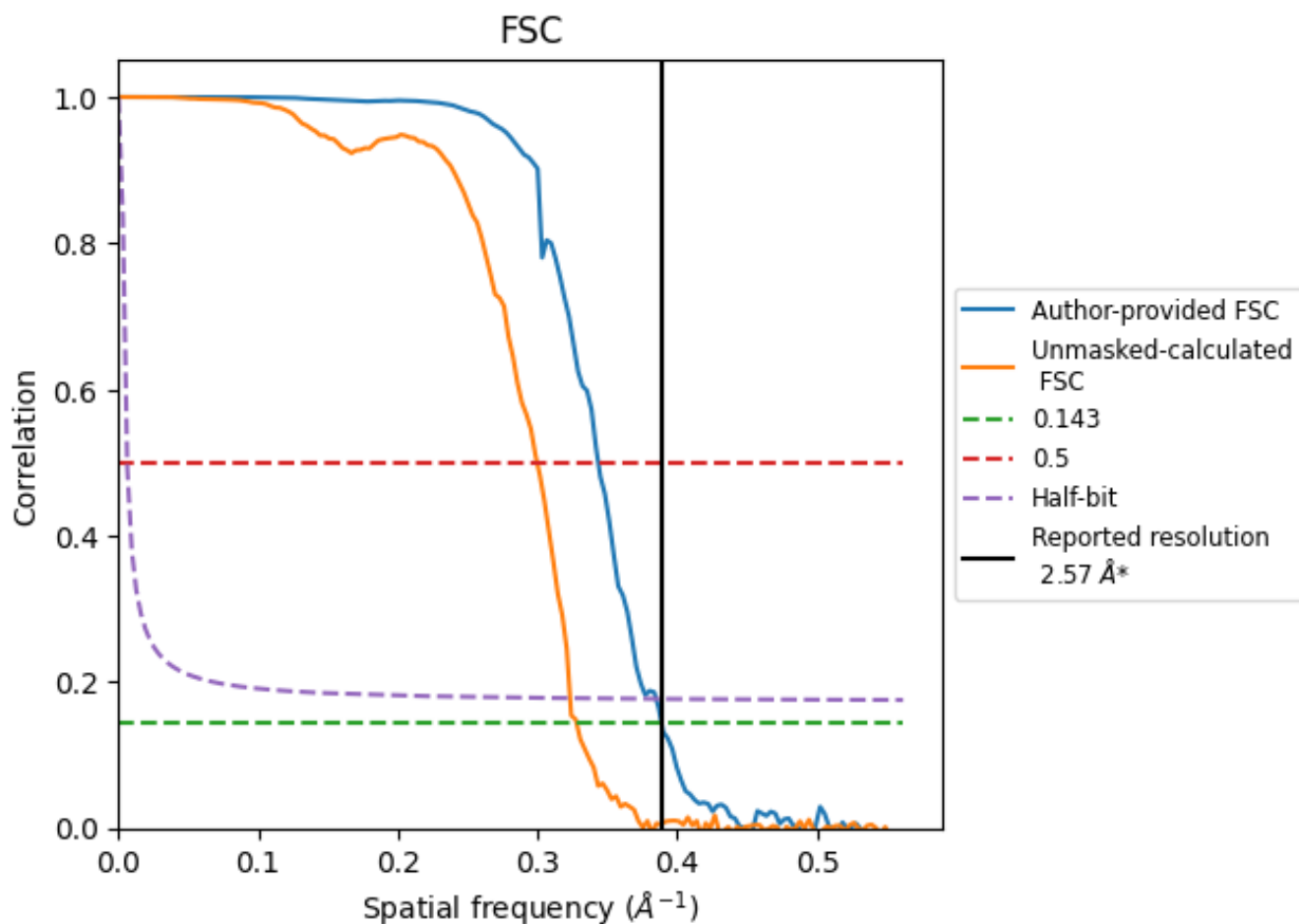


\*Reported resolution corresponds to spatial frequency of 0.389 Å<sup>-1</sup>

## 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 0.389 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

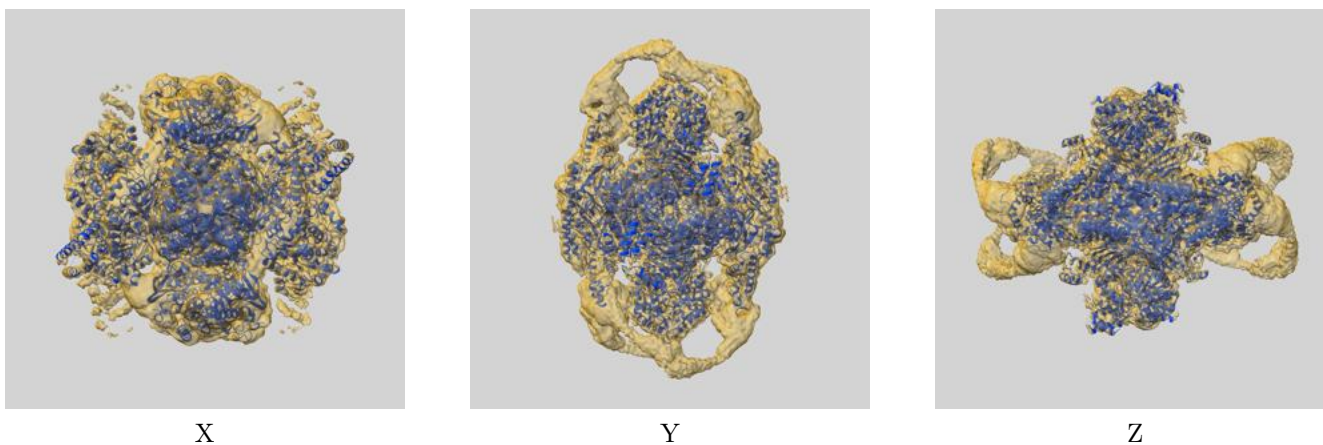
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.57	-	-
Author-provided FSC curve	2.57	2.91	2.60
Unmasked-calculated*	3.05	3.34	3.09

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.05 differs from the reported value 2.57 by more than 10 %

## 9 Map-model fit [i](#)

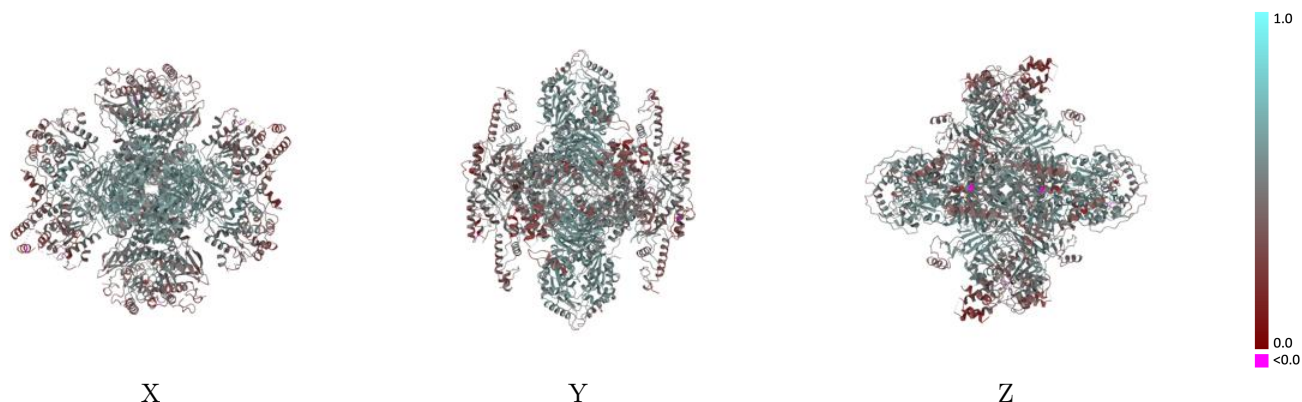
This section contains information regarding the fit between EMDB map EMD-41983 and PDB model 8U7I. Per-residue inclusion information can be found in section 3 on page 15.

### 9.1 Map-model overlay [i](#)



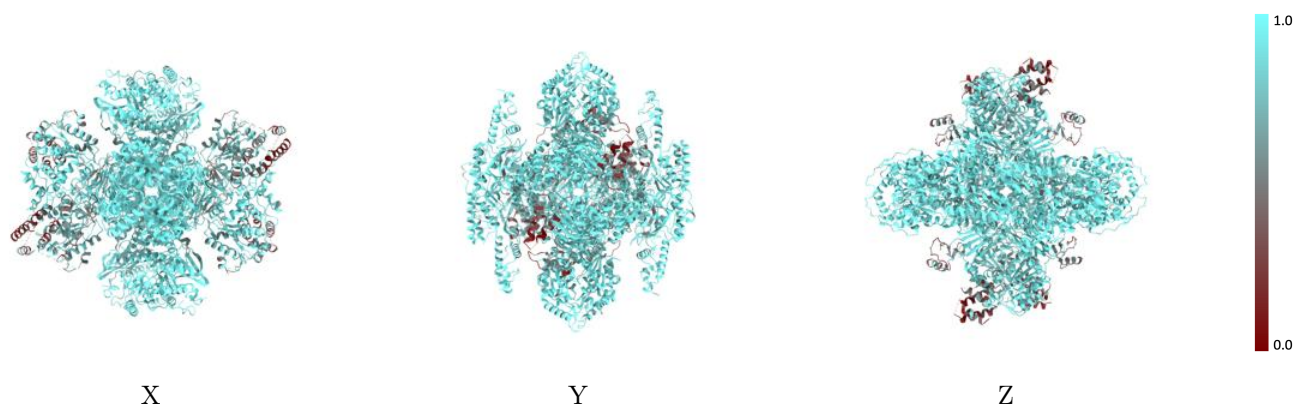
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



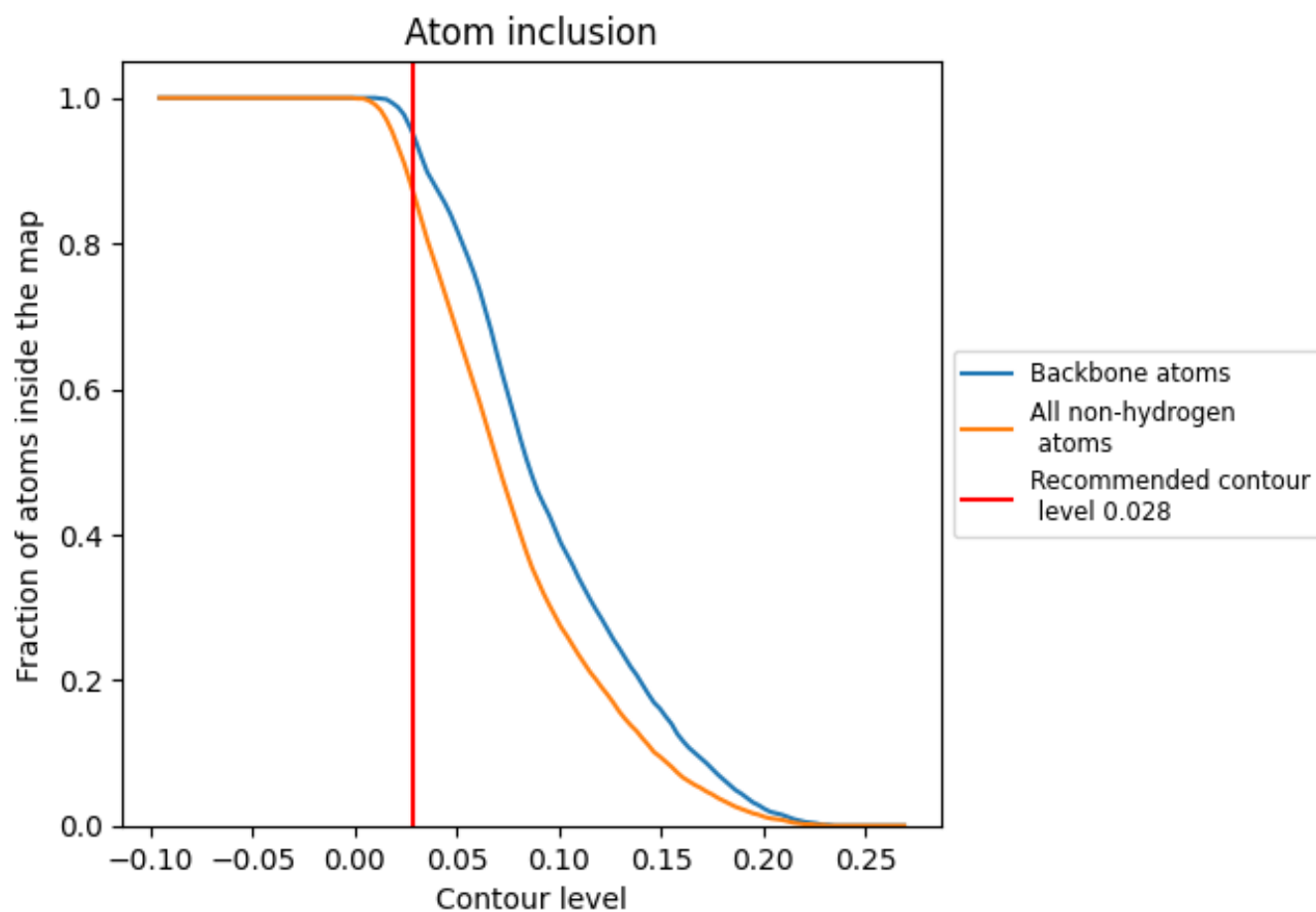
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.028).

## 9.4 Atom inclusion [i](#)





































At the recommended contour level, 95% of all backbone atoms, 88% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8760	 0.4910
A	 0.9100	 0.5540
B	 0.9080	 0.5530
C	 0.9110	 0.5540
D	 0.9100	 0.5550
E	 0.7440	 0.4210
F	 0.7500	 0.4260
G	 0.7460	 0.4240
H	 0.7400	 0.4190
I	 0.9390	 0.4240
J	 0.9390	 0.4250
K	 0.9360	 0.4120
L	 0.9410	 0.4210
M	 0.9280	 0.4080
N	 0.9320	 0.4170
O	 0.9360	 0.4210
P	 0.9350	 0.4190

