



## Full wwPDB EM Validation Report ⓘ

Nov 4, 2024 – 04:40 AM JST

PDB ID : 7EOY  
EMDB ID : EMD-31233  
Title : Engineered Hepatitis B virus core antigen T=3  
Authors : Jeong, H.; Heo, Y.; Yoo, Y.; Ryu, B.; Yun, J.; Cho, H.; Lee, W.  
Deposited on : 2021-04-24  
Resolution : 3.60 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

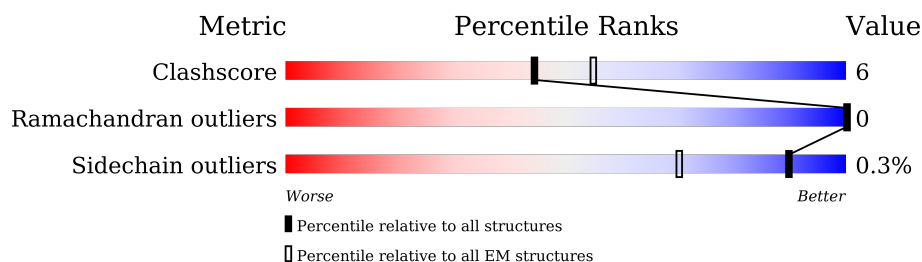
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	337	 35% 7% 58%
1	B	337	 33% 9% 58%
1	C	337	 36% 6% 58%

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3402 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 Capsid protein,Immunoglobulin G-binding protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	141	Total	C	N	O	S	0	0
			1134	738	186	205	5		
1	C	141	Total	C	N	O	S	0	0
			1134	738	186	205	5		
1	A	141	Total	C	N	O	S	0	0
			1134	738	186	205	5		

There are 315 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P69706
B	2	HIS	-	expression tag	UNP P69706
B	3	HIS	-	expression tag	UNP P69706
B	4	HIS	-	expression tag	UNP P69706
B	5	HIS	-	expression tag	UNP P69706
B	6	HIS	-	expression tag	UNP P69706
B	7	HIS	-	expression tag	UNP P69706
B	8	MET	-	expression tag	UNP P69706
B	9	ALA	-	expression tag	UNP P69706
B	10	SER	-	expression tag	UNP P69706
B	11	SER	-	expression tag	UNP P69706
B	12	LEU	-	expression tag	UNP P69706
B	13	ARG	-	expression tag	UNP P69706
B	14	GLN	-	expression tag	UNP P69706
B	15	ILE	-	expression tag	UNP P69706
B	16	LEU	-	expression tag	UNP P69706
B	17	ASP	-	expression tag	UNP P69706
B	18	SER	-	expression tag	UNP P69706
B	19	GLN	-	expression tag	UNP P69706
B	20	LYS	-	expression tag	UNP P69706
B	21	MET	-	expression tag	UNP P69706
B	22	GLU	-	expression tag	UNP P69706
B	23	TRP	-	expression tag	UNP P69706
B	24	ARG	-	expression tag	UNP P69706

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Chain	Residue	Modelled	Actual	Comment	Reference
B	25	SER	-	expression tag	UNP P69706
B	26	ASN	-	expression tag	UNP P69706
B	27	ALA	-	expression tag	UNP P69706
B	28	GLY	-	expression tag	UNP P69706
B	29	GLY	-	expression tag	UNP P69706
B	30	SER	-	expression tag	UNP P69706
B	31	GLY	-	expression tag	UNP P69706
B	32	GLY	-	expression tag	UNP P69706
B	33	GLY	-	expression tag	UNP P69706
B	34	SER	-	expression tag	UNP P69706
B	35	GLY	-	expression tag	UNP P69706
B	36	GLY	-	expression tag	UNP P69706
B	37	GLY	-	expression tag	UNP P69706
B	38	THR	-	expression tag	UNP P69706
B	39	GLY	-	expression tag	UNP P69706
B	40	GLY	-	expression tag	UNP P69706
B	41	GLY	-	expression tag	UNP P69706
B	42	GLY	-	expression tag	UNP P69706
B	43	GLY	-	expression tag	UNP P69706
B	44	GLY	-	expression tag	UNP P69706
B	45	TYR	-	expression tag	UNP P69706
B	46	TYR	-	expression tag	UNP P69706
B	47	TYR	-	expression tag	UNP P69706
B	48	TYR	-	expression tag	UNP P69706
B	49	TYR	-	expression tag	UNP P69706
B	50	TYR	-	expression tag	UNP P69706
B	138	GLY	-	linker	UNP P69706
B	139	GLY	-	linker	UNP P69706
B	140	GLY	-	linker	UNP P69706
B	141	GLY	-	linker	UNP P69706
B	142	SER	-	linker	UNP P69706
B	143	GLY	-	linker	UNP P69706
B	144	GLY	-	linker	UNP P69706
B	145	GLY	-	linker	UNP P69706
B	146	GLY	-	linker	UNP P69706
B	147	THR	-	linker	UNP P69706
B	148	LEU	-	linker	UNP P69706
B	149	GLU	-	linker	UNP P69706
B	150	VAL	ALA	engineered mutation	UNP P38507
B	158	MET	GLN	engineered mutation	UNP P38507
B	159	TRP	GLN	engineered mutation	UNP P38507
B	160	ALA	ASN	engineered mutation	UNP P38507

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Chain	Residue	Modelled	Actual	Comment	Reference
B	162	TRP	PHE	engineered mutation	UNP P38507
B	163	GLU	TYR	engineered mutation	UNP P38507
B	166	ARG	LEU	engineered mutation	UNP P38507
B	167	ASN	HIS	engineered mutation	UNP P38507
B	173	GLY	GLU	engineered mutation	UNP P38507
B	174	TRP	GLU	engineered mutation	UNP P38507
B	176	MET	ARG	engineered mutation	UNP P38507
B	177	THR	ASN	engineered mutation	UNP P38507
B	178	ALA	GLY	engineered mutation	UNP P38507
B	181	ALA	GLN	engineered mutation	UNP P38507
B	184	VAL	LYS	engineered mutation	UNP P38507
B	208	GLU	-	linker	UNP P38507
B	209	PHE	-	linker	UNP P38507
B	210	VAL	ALA	engineered mutation	UNP P38507
B	218	MET	GLN	engineered mutation	UNP P38507
B	219	TRP	GLN	engineered mutation	UNP P38507
B	220	ALA	ASN	engineered mutation	UNP P38507
B	222	TRP	PHE	engineered mutation	UNP P38507
B	223	GLU	TYR	engineered mutation	UNP P38507
B	226	ARG	LEU	engineered mutation	UNP P38507
B	227	ASN	HIS	engineered mutation	UNP P38507
B	233	GLY	GLU	engineered mutation	UNP P38507
B	234	TRP	GLU	engineered mutation	UNP P38507
B	236	MET	ARG	engineered mutation	UNP P38507
B	237	THR	ASN	engineered mutation	UNP P38507
B	238	ALA	GLY	engineered mutation	UNP P38507
B	241	ALA	GLN	engineered mutation	UNP P38507
B	244	VAL	LYS	engineered mutation	UNP P38507
B	268	GLY	-	linker	UNP P38507
B	269	SER	-	linker	UNP P38507
B	270	GLY	-	linker	UNP P38507
B	271	GLY	-	linker	UNP P38507
B	272	GLY	-	linker	UNP P38507
B	273	GLY	-	linker	UNP P38507
B	274	SER	-	linker	UNP P38507
B	275	GLY	-	linker	UNP P38507
B	276	GLY	-	linker	UNP P38507
B	277	GLY	-	linker	UNP P38507
B	278	GLY	-	linker	UNP P38507
C	1	MET	-	initiating methionine	UNP P69706
C	2	HIS	-	expression tag	UNP P69706
C	3	HIS	-	expression tag	UNP P69706

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	HIS	-	expression tag	UNP P69706
C	5	HIS	-	expression tag	UNP P69706
C	6	HIS	-	expression tag	UNP P69706
C	7	HIS	-	expression tag	UNP P69706
C	8	MET	-	expression tag	UNP P69706
C	9	ALA	-	expression tag	UNP P69706
C	10	SER	-	expression tag	UNP P69706
C	11	SER	-	expression tag	UNP P69706
C	12	LEU	-	expression tag	UNP P69706
C	13	ARG	-	expression tag	UNP P69706
C	14	GLN	-	expression tag	UNP P69706
C	15	ILE	-	expression tag	UNP P69706
C	16	LEU	-	expression tag	UNP P69706
C	17	ASP	-	expression tag	UNP P69706
C	18	SER	-	expression tag	UNP P69706
C	19	GLN	-	expression tag	UNP P69706
C	20	LYS	-	expression tag	UNP P69706
C	21	MET	-	expression tag	UNP P69706
C	22	GLU	-	expression tag	UNP P69706
C	23	TRP	-	expression tag	UNP P69706
C	24	ARG	-	expression tag	UNP P69706
C	25	SER	-	expression tag	UNP P69706
C	26	ASN	-	expression tag	UNP P69706
C	27	ALA	-	expression tag	UNP P69706
C	28	GLY	-	expression tag	UNP P69706
C	29	GLY	-	expression tag	UNP P69706
C	30	SER	-	expression tag	UNP P69706
C	31	GLY	-	expression tag	UNP P69706
C	32	GLY	-	expression tag	UNP P69706
C	33	GLY	-	expression tag	UNP P69706
C	34	SER	-	expression tag	UNP P69706
C	35	GLY	-	expression tag	UNP P69706
C	36	GLY	-	expression tag	UNP P69706
C	37	GLY	-	expression tag	UNP P69706
C	38	THR	-	expression tag	UNP P69706
C	39	GLY	-	expression tag	UNP P69706
C	40	GLY	-	expression tag	UNP P69706
C	41	GLY	-	expression tag	UNP P69706
C	42	GLY	-	expression tag	UNP P69706
C	43	GLY	-	expression tag	UNP P69706
C	44	GLY	-	expression tag	UNP P69706
C	45	TYR	-	expression tag	UNP P69706

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Chain	Residue	Modelled	Actual	Comment	Reference
C	46	TYR	-	expression tag	UNP P69706
C	47	TYR	-	expression tag	UNP P69706
C	48	TYR	-	expression tag	UNP P69706
C	49	TYR	-	expression tag	UNP P69706
C	50	TYR	-	expression tag	UNP P69706
C	138	GLY	-	linker	UNP P69706
C	139	GLY	-	linker	UNP P69706
C	140	GLY	-	linker	UNP P69706
C	141	GLY	-	linker	UNP P69706
C	142	SER	-	linker	UNP P69706
C	143	GLY	-	linker	UNP P69706
C	144	GLY	-	linker	UNP P69706
C	145	GLY	-	linker	UNP P69706
C	146	GLY	-	linker	UNP P69706
C	147	THR	-	linker	UNP P69706
C	148	LEU	-	linker	UNP P69706
C	149	GLU	-	linker	UNP P69706
C	150	VAL	ALA	engineered mutation	UNP P38507
C	158	MET	GLN	engineered mutation	UNP P38507
C	159	TRP	GLN	engineered mutation	UNP P38507
C	160	ALA	ASN	engineered mutation	UNP P38507
C	162	TRP	PHE	engineered mutation	UNP P38507
C	163	GLU	TYR	engineered mutation	UNP P38507
C	166	ARG	LEU	engineered mutation	UNP P38507
C	167	ASN	HIS	engineered mutation	UNP P38507
C	173	GLY	GLU	engineered mutation	UNP P38507
C	174	TRP	GLU	engineered mutation	UNP P38507
C	176	MET	ARG	engineered mutation	UNP P38507
C	177	THR	ASN	engineered mutation	UNP P38507
C	178	ALA	GLY	engineered mutation	UNP P38507
C	181	ALA	GLN	engineered mutation	UNP P38507
C	184	VAL	LYS	engineered mutation	UNP P38507
C	208	GLU	-	linker	UNP P38507
C	209	PHE	-	linker	UNP P38507
C	210	VAL	ALA	engineered mutation	UNP P38507
C	218	MET	GLN	engineered mutation	UNP P38507
C	219	TRP	GLN	engineered mutation	UNP P38507
C	220	ALA	ASN	engineered mutation	UNP P38507
C	222	TRP	PHE	engineered mutation	UNP P38507
C	223	GLU	TYR	engineered mutation	UNP P38507
C	226	ARG	LEU	engineered mutation	UNP P38507
C	227	ASN	HIS	engineered mutation	UNP P38507

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Chain	Residue	Modelled	Actual	Comment	Reference
C	233	GLY	GLU	engineered mutation	UNP P38507
C	234	TRP	GLU	engineered mutation	UNP P38507
C	236	MET	ARG	engineered mutation	UNP P38507
C	237	THR	ASN	engineered mutation	UNP P38507
C	238	ALA	GLY	engineered mutation	UNP P38507
C	241	ALA	GLN	engineered mutation	UNP P38507
C	244	VAL	LYS	engineered mutation	UNP P38507
C	268	GLY	-	linker	UNP P38507
C	269	SER	-	linker	UNP P38507
C	270	GLY	-	linker	UNP P38507
C	271	GLY	-	linker	UNP P38507
C	272	GLY	-	linker	UNP P38507
C	273	GLY	-	linker	UNP P38507
C	274	SER	-	linker	UNP P38507
C	275	GLY	-	linker	UNP P38507
C	276	GLY	-	linker	UNP P38507
C	277	GLY	-	linker	UNP P38507
C	278	GLY	-	linker	UNP P38507
A	1	MET	-	initiating methionine	UNP P69706
A	2	HIS	-	expression tag	UNP P69706
A	3	HIS	-	expression tag	UNP P69706
A	4	HIS	-	expression tag	UNP P69706
A	5	HIS	-	expression tag	UNP P69706
A	6	HIS	-	expression tag	UNP P69706
A	7	HIS	-	expression tag	UNP P69706
A	8	MET	-	expression tag	UNP P69706
A	9	ALA	-	expression tag	UNP P69706
A	10	SER	-	expression tag	UNP P69706
A	11	SER	-	expression tag	UNP P69706
A	12	LEU	-	expression tag	UNP P69706
A	13	ARG	-	expression tag	UNP P69706
A	14	GLN	-	expression tag	UNP P69706
A	15	ILE	-	expression tag	UNP P69706
A	16	LEU	-	expression tag	UNP P69706
A	17	ASP	-	expression tag	UNP P69706
A	18	SER	-	expression tag	UNP P69706
A	19	GLN	-	expression tag	UNP P69706
A	20	LYS	-	expression tag	UNP P69706
A	21	MET	-	expression tag	UNP P69706
A	22	GLU	-	expression tag	UNP P69706
A	23	TRP	-	expression tag	UNP P69706
A	24	ARG	-	expression tag	UNP P69706

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Chain	Residue	Modelled	Actual	Comment	Reference
A	25	SER	-	expression tag	UNP P69706
A	26	ASN	-	expression tag	UNP P69706
A	27	ALA	-	expression tag	UNP P69706
A	28	GLY	-	expression tag	UNP P69706
A	29	GLY	-	expression tag	UNP P69706
A	30	SER	-	expression tag	UNP P69706
A	31	GLY	-	expression tag	UNP P69706
A	32	GLY	-	expression tag	UNP P69706
A	33	GLY	-	expression tag	UNP P69706
A	34	SER	-	expression tag	UNP P69706
A	35	GLY	-	expression tag	UNP P69706
A	36	GLY	-	expression tag	UNP P69706
A	37	GLY	-	expression tag	UNP P69706
A	38	THR	-	expression tag	UNP P69706
A	39	GLY	-	expression tag	UNP P69706
A	40	GLY	-	expression tag	UNP P69706
A	41	GLY	-	expression tag	UNP P69706
A	42	GLY	-	expression tag	UNP P69706
A	43	GLY	-	expression tag	UNP P69706
A	44	GLY	-	expression tag	UNP P69706
A	45	TYR	-	expression tag	UNP P69706
A	46	TYR	-	expression tag	UNP P69706
A	47	TYR	-	expression tag	UNP P69706
A	48	TYR	-	expression tag	UNP P69706
A	49	TYR	-	expression tag	UNP P69706
A	50	TYR	-	expression tag	UNP P69706
A	138	GLY	-	linker	UNP P69706
A	139	GLY	-	linker	UNP P69706
A	140	GLY	-	linker	UNP P69706
A	141	GLY	-	linker	UNP P69706
A	142	SER	-	linker	UNP P69706
A	143	GLY	-	linker	UNP P69706
A	144	GLY	-	linker	UNP P69706
A	145	GLY	-	linker	UNP P69706
A	146	GLY	-	linker	UNP P69706
A	147	THR	-	linker	UNP P69706
A	148	LEU	-	linker	UNP P69706
A	149	GLU	-	linker	UNP P69706
A	150	VAL	ALA	engineered mutation	UNP P38507
A	158	MET	GLN	engineered mutation	UNP P38507
A	159	TRP	GLN	engineered mutation	UNP P38507
A	160	ALA	ASN	engineered mutation	UNP P38507

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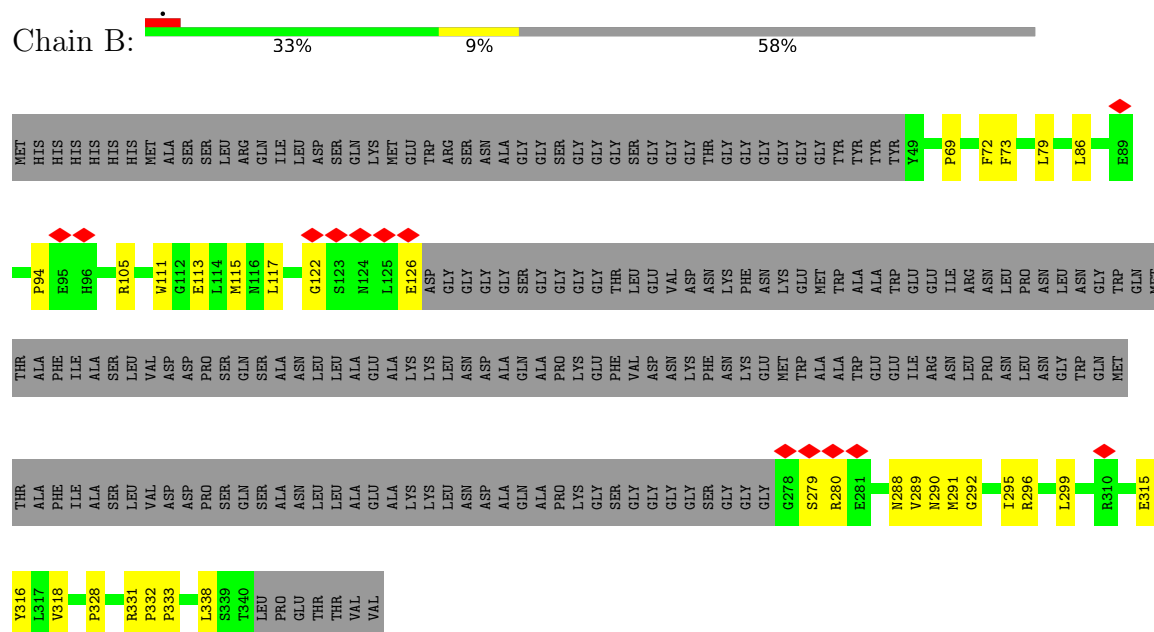
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Chain	Residue	Modelled	Actual	Comment	Reference
A	162	TRP	PHE	engineered mutation	UNP P38507
A	163	GLU	TYR	engineered mutation	UNP P38507
A	166	ARG	LEU	engineered mutation	UNP P38507
A	167	ASN	HIS	engineered mutation	UNP P38507
A	173	GLY	GLU	engineered mutation	UNP P38507
A	174	TRP	GLU	engineered mutation	UNP P38507
A	176	MET	ARG	engineered mutation	UNP P38507
A	177	THR	ASN	engineered mutation	UNP P38507
A	178	ALA	GLY	engineered mutation	UNP P38507
A	181	ALA	GLN	engineered mutation	UNP P38507
A	184	VAL	LYS	engineered mutation	UNP P38507
A	208	GLU	-	linker	UNP P38507
A	209	PHE	-	linker	UNP P38507
A	210	VAL	ALA	engineered mutation	UNP P38507
A	218	MET	GLN	engineered mutation	UNP P38507
A	219	TRP	GLN	engineered mutation	UNP P38507
A	220	ALA	ASN	engineered mutation	UNP P38507
A	222	TRP	PHE	engineered mutation	UNP P38507
A	223	GLU	TYR	engineered mutation	UNP P38507
A	226	ARG	LEU	engineered mutation	UNP P38507
A	227	ASN	HIS	engineered mutation	UNP P38507
A	233	GLY	GLU	engineered mutation	UNP P38507
A	234	TRP	GLU	engineered mutation	UNP P38507
A	236	MET	ARG	engineered mutation	UNP P38507
A	237	THR	ASN	engineered mutation	UNP P38507
A	238	ALA	GLY	engineered mutation	UNP P38507
A	241	ALA	GLN	engineered mutation	UNP P38507
A	244	VAL	LYS	engineered mutation	UNP P38507
A	268	GLY	-	linker	UNP P38507
A	269	SER	-	linker	UNP P38507
A	270	GLY	-	linker	UNP P38507
A	271	GLY	-	linker	UNP P38507
A	272	GLY	-	linker	UNP P38507
A	273	GLY	-	linker	UNP P38507
A	274	SER	-	linker	UNP P38507
A	275	GLY	-	linker	UNP P38507
A	276	GLY	-	linker	UNP P38507
A	277	GLY	-	linker	UNP P38507
A	278	GLY	-	linker	UNP P38507

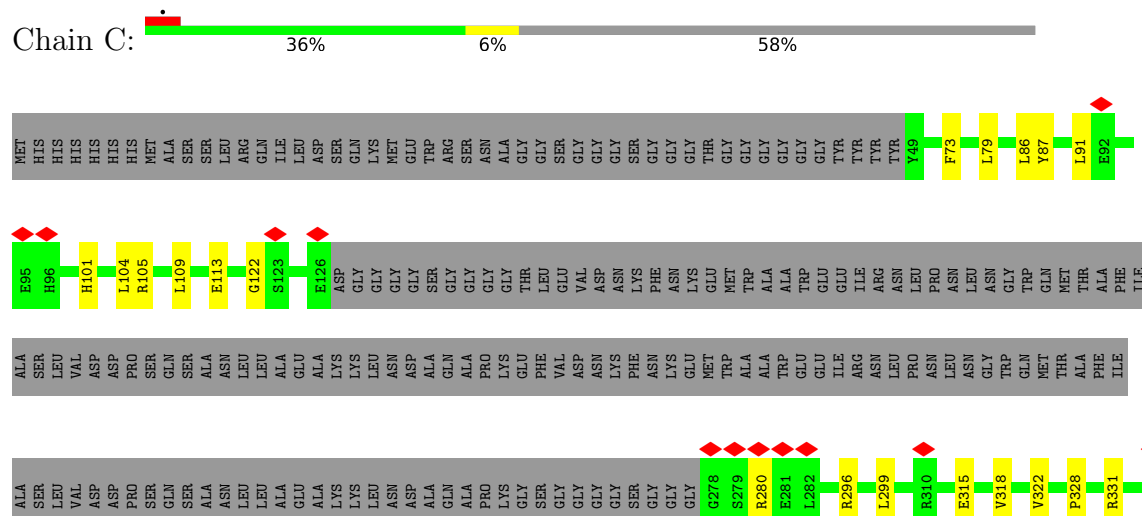
### 3 Residue-property plots

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: Capsid protein,Immunoglobulin G-binding protein A



- Molecule 1: Capsid protein,Immunoglobulin G-binding protein A



LEU  
PRO  
GLU  
THR  
VAL  
VAL

● Molecule 1: Capsid protein,Immunoglobulin G-binding protein A



MET  
HIS  
HIS  
HIS  
HIS  
HIS  
MET  
ALA  
SER  
SER  
LEU  
ARG  
GLN  
ILE  
LEU  
ASP  
SER  
GLN  
LYS  
MET  
GLU  
TRP  
ARG  
SER  
ASN  
ALA  
GLY  
GLY  
GLY  
GLY  
GLY  
SER  
GLY  
GLY  
GLY  
GLY  
THR  
GLY  
GLY  
GLY  
GLY  
TYR  
TYR  
TYR  
TYR  
TYR  
Y49  
Y50  
D51  
I52  
D53  
K56  
E57  
F58  
F73

T82  
L86  
P94  
E95  
H96  
R105  
L109  
C110  
E113  
V121  
G122  
S123  
N124  
L125  
E126  
ASP  
GLY  
GLY  
GLY  
GLY  
GLY  
GLY  
THR  
LEU  
GLU  
VAL  
ASP  
ASN  
LYS  
PHE  
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LYS  
MET  
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MET  
TRP  
ALA  
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ILE  
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GLU  
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ARG  
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PRO  
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GLY  
TRP  
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MET  
THR  
ALA  
PHE  
ILE  
ALA  
SER  
LEU  
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ASP  
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PRO  
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LYS  
GLU  
GLY  
G278  
S279  
R280  
E281  
L282  
V283  
M291  
R296  
R310  
I324  
R331  
P332  
P333

H334  
A335  
P336  
T340  
LEU  
PRO  
GLU  
THR  
VAL  
VAL

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	50321	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.758	Depositor
Minimum map value	-1.156	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.714	Depositor
Map size (Å)	630.0, 630.0, 630.0	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	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	0.26	0/1168	0.52	2/1595 (0.1%)
1	B	0.25	0/1168	0.50	0/1595
1	C	0.25	0/1168	0.48	0/1595
All	All	0.25	0/3504	0.50	2/4785 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	51	ASP	CB-CG-OD2	5.02	122.81	118.30

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	1134	0	1108	15	0
1	B	1134	0	1108	19	0
1	C	1134	0	1109	10	0
All	All	3402	0	3325	42	0

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

All (42) 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:A:94:PRO:HB3	1:A:105:ARG:HH22	1.62	0.65
1:C:109:LEU:O	1:C:113:GLU:HG3	2.02	0.60
1:C:91:LEU:HD21	1:C:104:LEU:HD23	1.86	0.57
1:A:121:VAL:HG11	1:A:283:VAL:HG11	1.89	0.54
1:A:324:ILE:HA	1:A:331:ARG:HH12	1.72	0.54
1:B:290:ASN:OD1	1:B:291:MET:N	2.41	0.53
1:B:328:PRO:HA	1:B:331:ARG:HG2	1.90	0.52
1:B:79:LEU:HD13	1:B:299:LEU:HB2	1.92	0.51
1:B:111:TRP:O	1:B:115:MET:HG2	2.10	0.51
1:C:73:PHE:O	1:C:296:ARG:NH2	2.43	0.51
1:C:79:LEU:HD13	1:C:299:LEU:HB2	1.93	0.51
1:B:126:GLU:HG2	1:B:279:SER:HB3	1.92	0.51
1:B:122:GLY:HA2	1:B:280:ARG:HE	1.76	0.50
1:B:94:PRO:HB3	1:B:105:ARG:HH22	1.78	0.49
1:B:113:GLU:OE1	1:A:291:MET:HB2	2.14	0.48
1:A:73:PHE:O	1:A:296:ARG:NH2	2.46	0.48
1:B:288:ASN:OD1	1:B:289:VAL:N	2.47	0.47
1:A:53:ASP:OD2	1:A:56:LYS:HB2	2.14	0.47
1:B:288:ASN:HA	1:B:292:GLY:HA3	1.96	0.47
1:B:73:PHE:O	1:B:296:ARG:NH2	2.48	0.47
1:C:315:GLU:OE2	1:C:315:GLU:N	2.42	0.47
1:A:94:PRO:HB3	1:A:105:ARG:NH2	2.29	0.46
1:A:109:LEU:O	1:A:113:GLU:HG2	2.16	0.45
1:B:315:GLU:OE2	1:B:315:GLU:N	2.48	0.45
1:A:82:THR:O	1:A:86:LEU:HD23	2.16	0.45
1:C:328:PRO:HA	1:C:331:ARG:HG2	1.99	0.45
1:A:51:ASP:O	1:A:51:ASP:OD2	2.35	0.44
1:A:110:CYS:HA	1:A:113:GLU:OE1	2.18	0.43
1:B:332:PRO:HA	1:B:333:PRO:HD3	1.90	0.43
1:C:122:GLY:HA3	1:C:280:ARG:HH11	1.83	0.43
1:A:58:PHE:O	1:A:310:ARG:NH2	2.51	0.43
1:B:69:PRO:HG2	1:B:72:PHE:HB2	2.01	0.43
1:B:315:GLU:HA	1:B:318:VAL:HG22	2.01	0.43
1:B:117:LEU:HD13	1:A:291:MET:HE3	2.01	0.43
1:B:86:LEU:H	1:B:86:LEU:HD23	1.82	0.42
1:C:318:VAL:O	1:C:322:VAL:HG22	2.20	0.42
1:A:335:ALA:N	1:A:336:PRO:HD3	2.34	0.42
1:B:295:ILE:HD12	1:B:295:ILE:H	1.84	0.42
1:B:316:TYR:CD1	1:B:338:LEU:HB3	2.54	0.42
1:A:332:PRO:HA	1:A:333:PRO:HD3	1.87	0.41
1:C:86:LEU:HB2	1:C:87:TYR:CE1	2.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:HIS:O	1:C:105:ARG:HG3	2.21	0.41

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	137/337 (41%)	130 (95%)	7 (5%)	0	100	100
1	B	137/337 (41%)	134 (98%)	3 (2%)	0	100	100
1	C	137/337 (41%)	134 (98%)	3 (2%)	0	100	100
All	All	411/1011 (41%)	398 (97%)	13 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	125/269 (46%)	124 (99%)	1 (1%)	79	88
1	B	125/269 (46%)	125 (100%)	0	100	100
1	C	125/269 (46%)	125 (100%)	0	100	100
All	All	375/807 (46%)	374 (100%)	1 (0%)	90	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	280	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

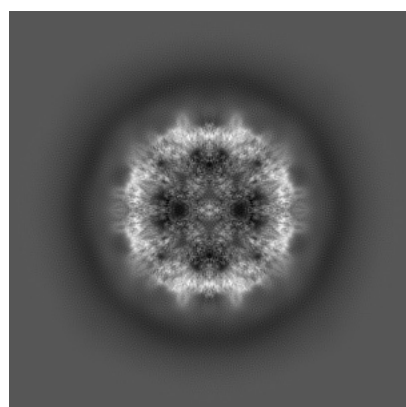
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31233. These allow visual inspection of the internal detail of the map and identification of artifacts.

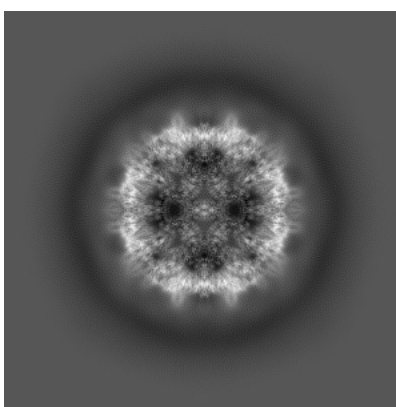
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

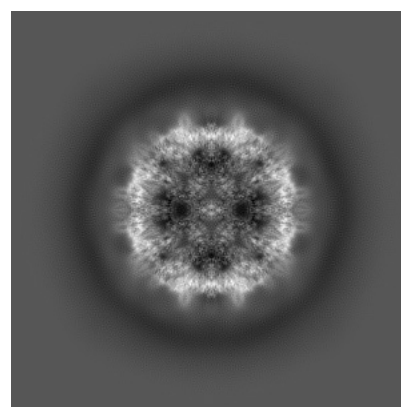
#### 6.1.1 Primary map



X



Y

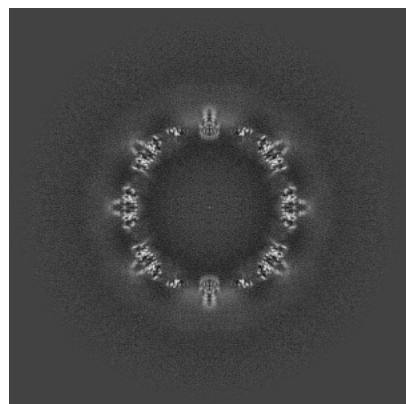


Z

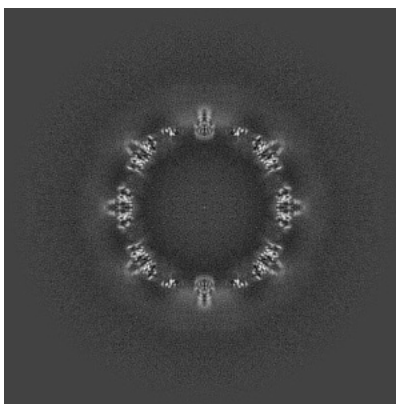
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

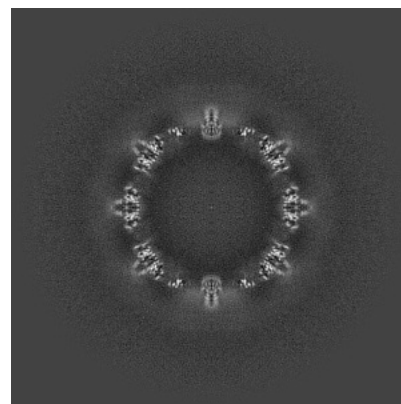
#### 6.2.1 Primary map



X Index: 225



Y Index: 225

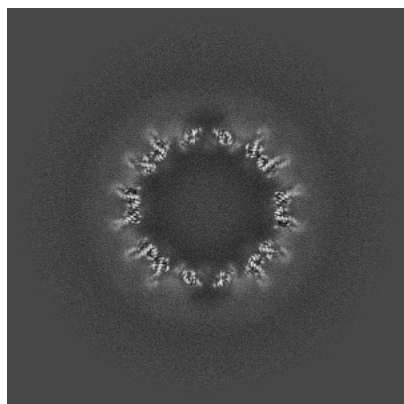


Z Index: 225

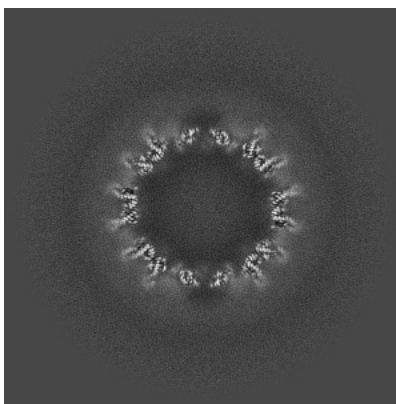
The images above show central slices of the map in three orthogonal directions.

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

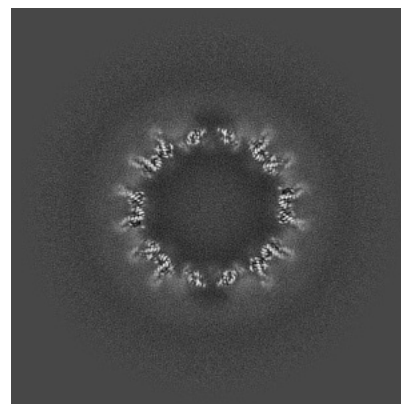
### 6.3.1 Primary map



X Index: 260



Y Index: 260

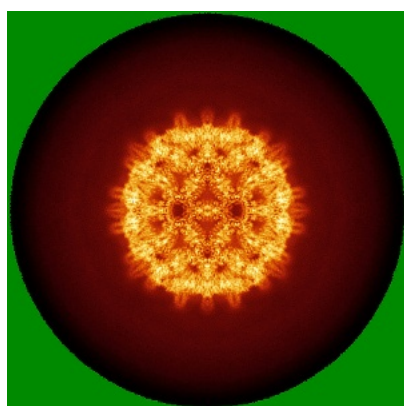


Z Index: 190

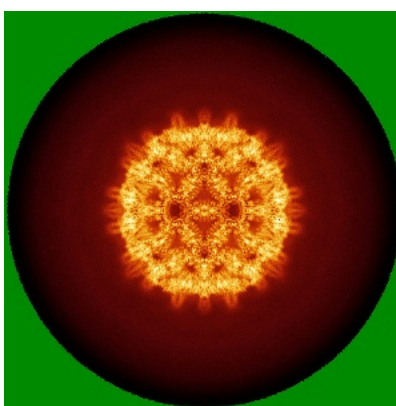
The images above show the largest variance slices of the map in three orthogonal directions.

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

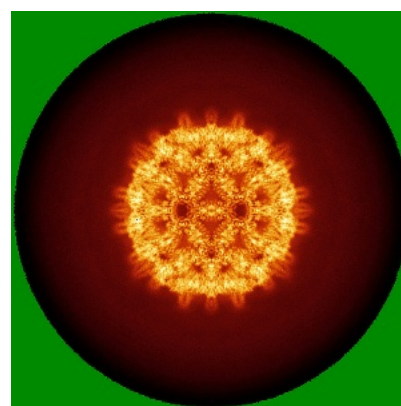
### 6.4.1 Primary map



X



Y

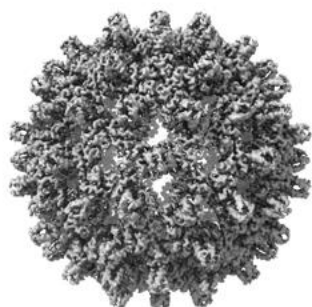


Z

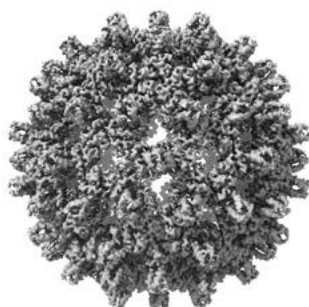
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

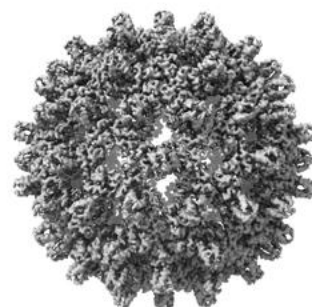
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.714. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

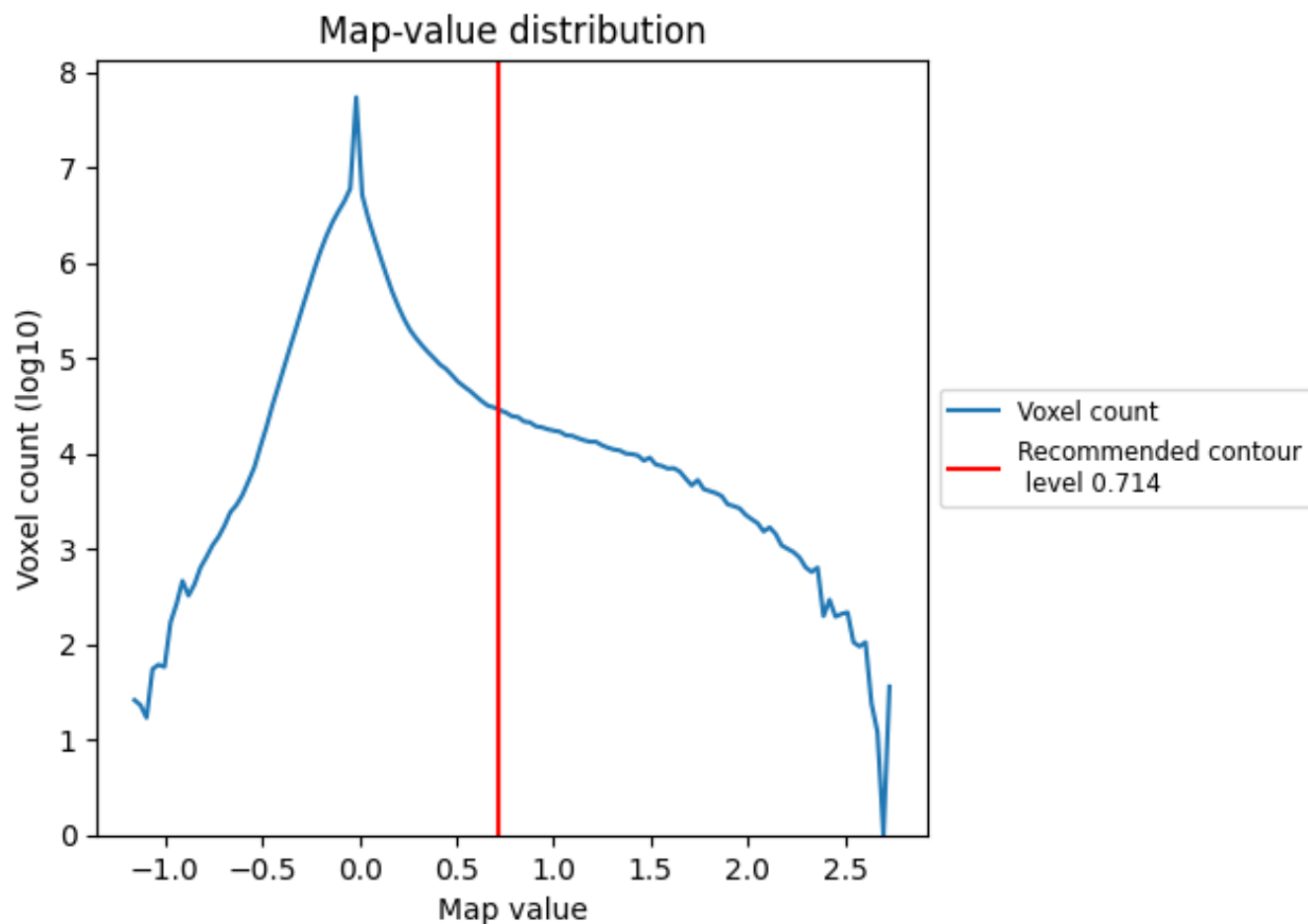
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

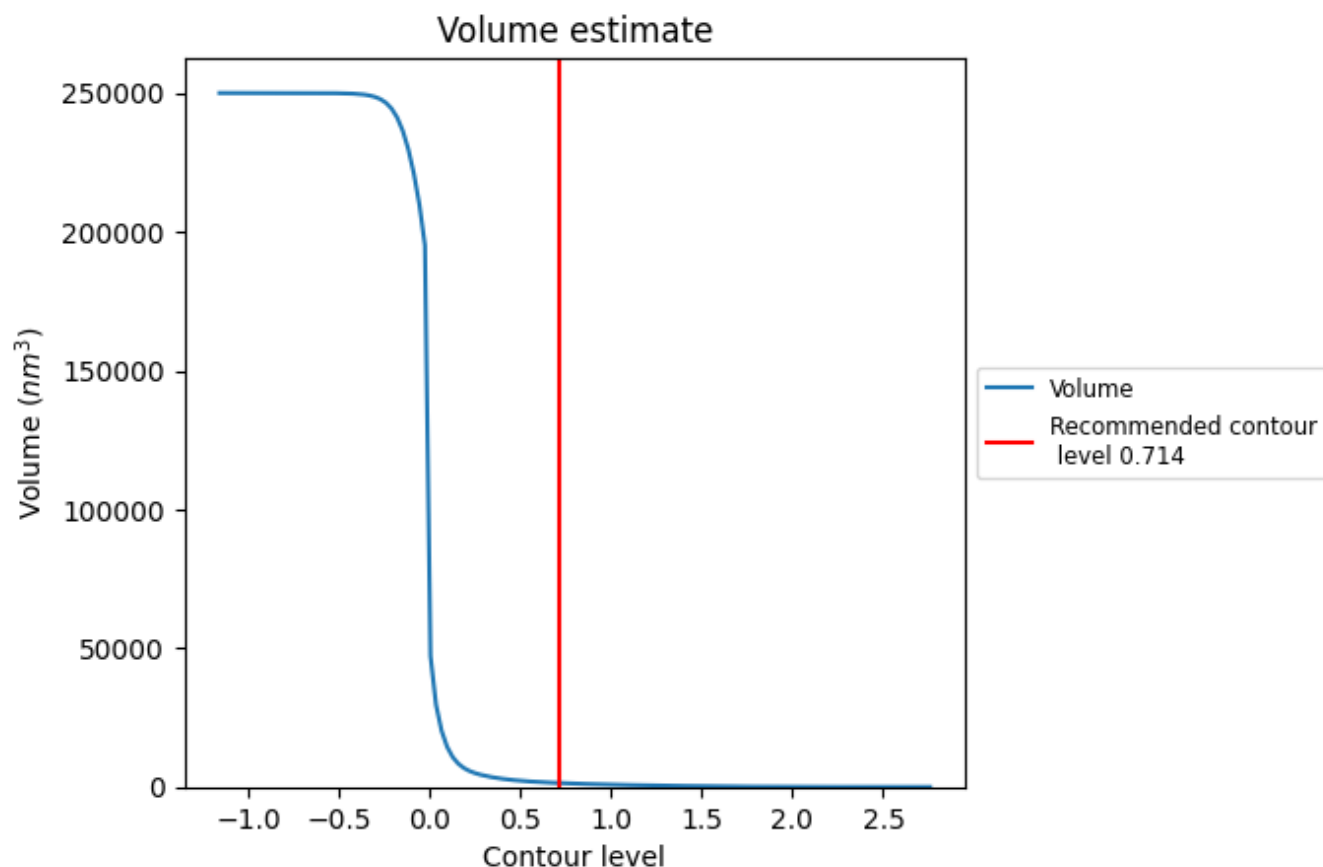
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

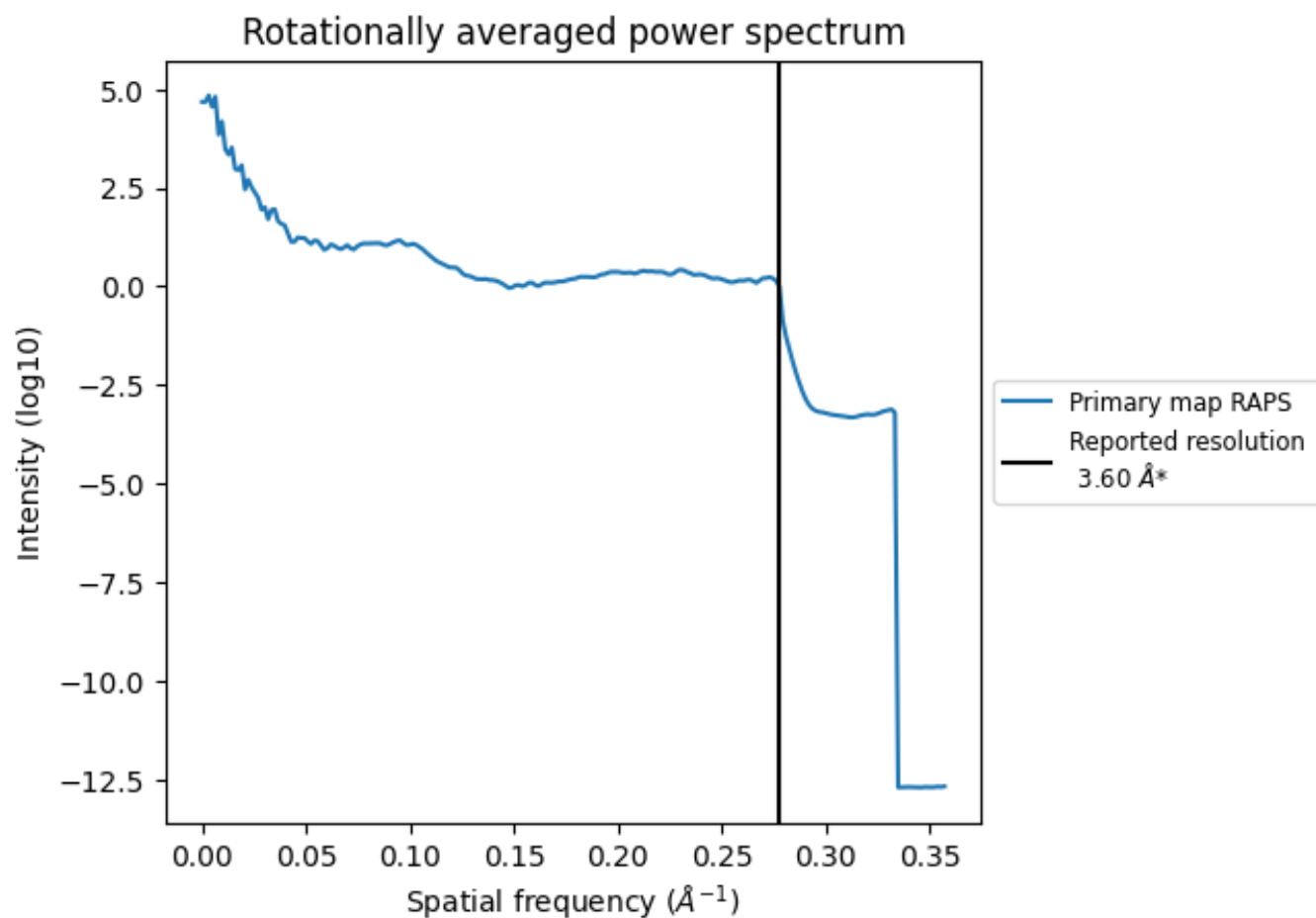
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1425 nm<sup>3</sup>; this corresponds to an approximate mass of 1287 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 8 Fourier-Shell correlation

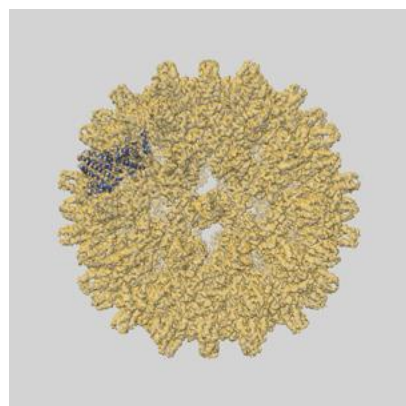
This section was not generated. No FSC curve or half-maps provided.

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

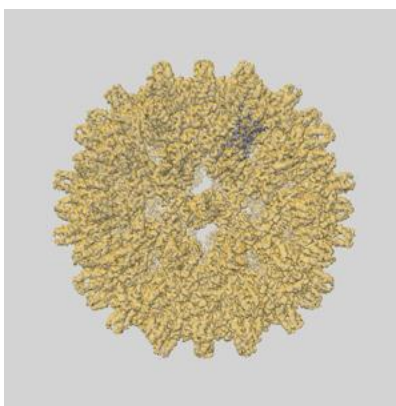
This section contains information regarding the fit between EMDB map EMD-31233 and PDB model 7EOY. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlays

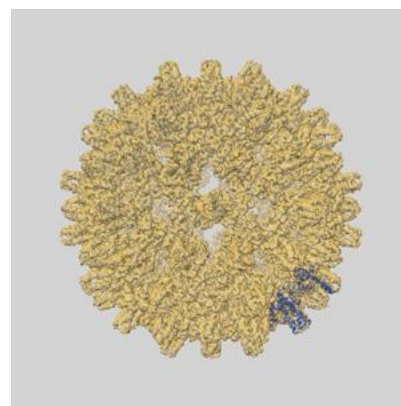
#### 9.1.1 Map-model overlay [i](#)



X

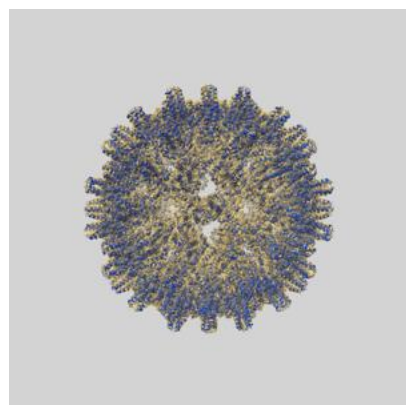


Y

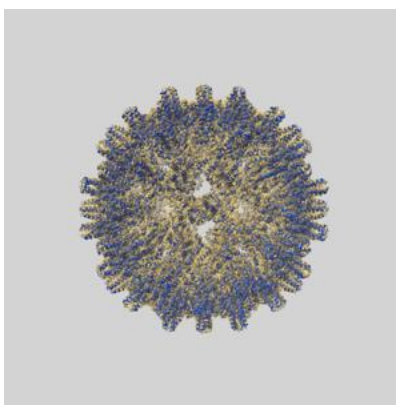


Z

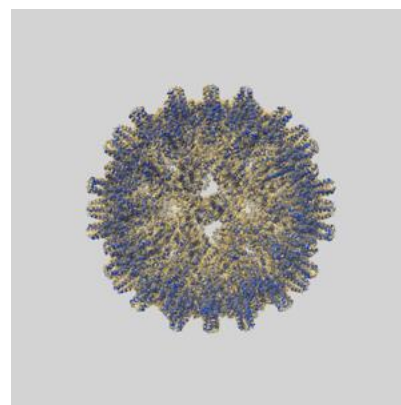
#### 9.1.2 Map-model assembly overlay [i](#)



X



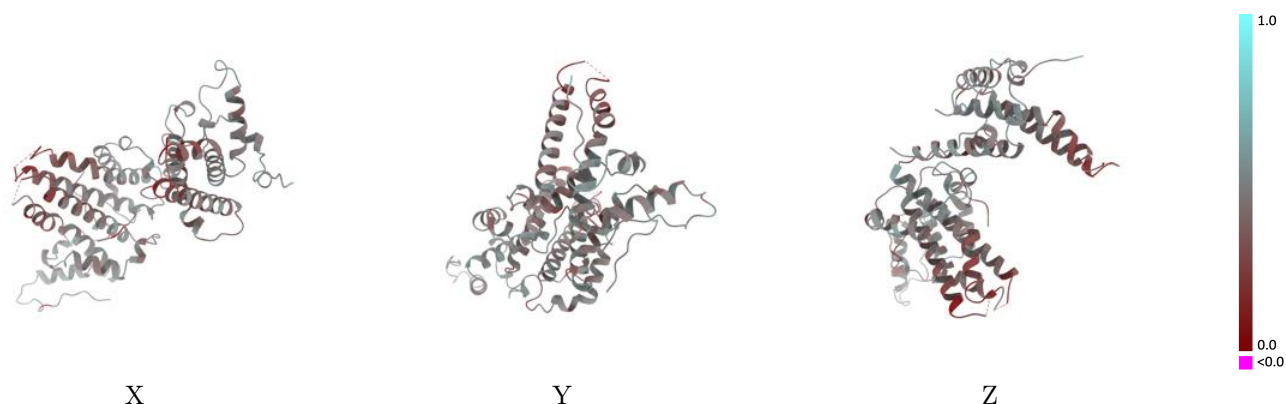
Y



Z

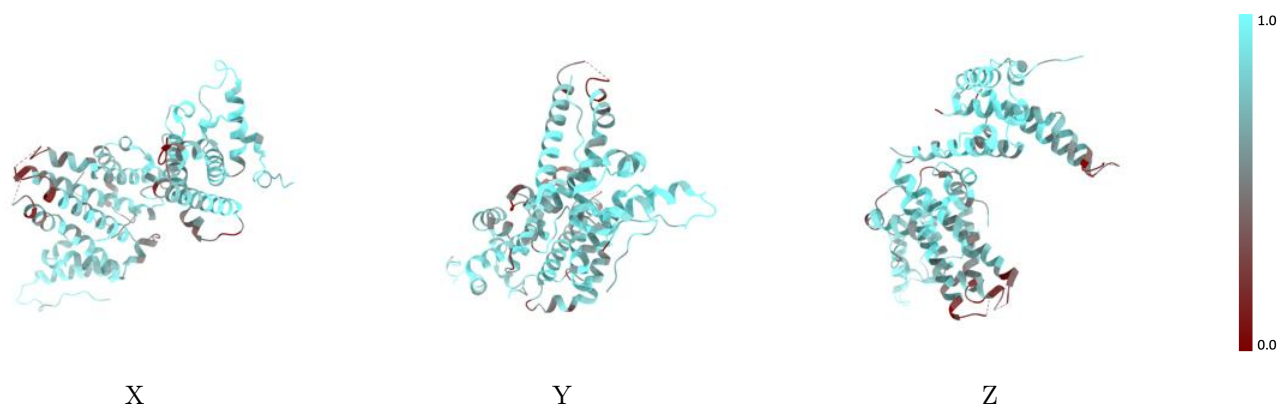
The images above show the 3D surface view of the map at the recommended contour level 0.714 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



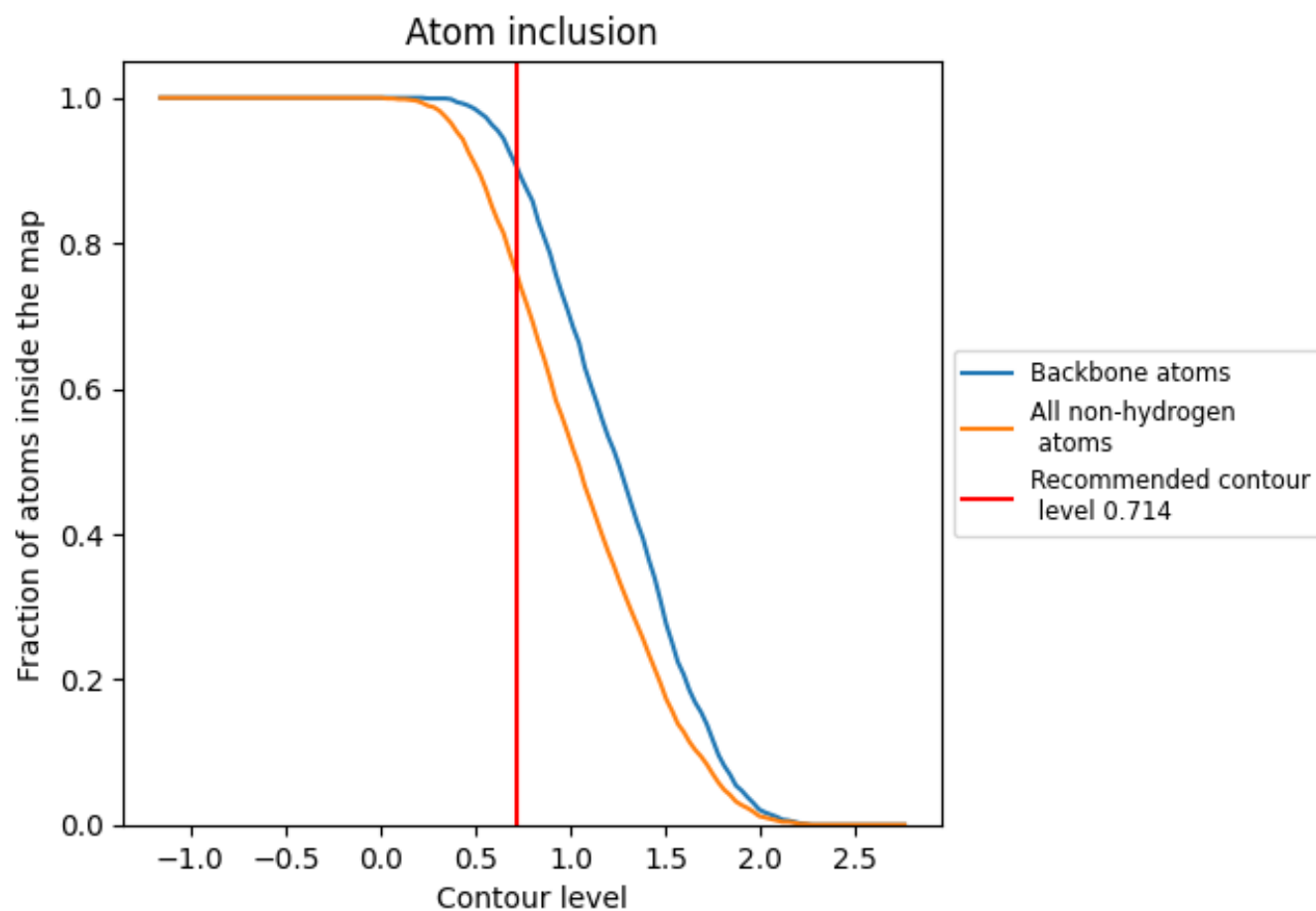
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.714).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 76% 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 (0.714) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7610	<div></div> 0.4320
A	<div></div> 0.7640	<div></div> 0.4400
B	<div></div> 0.7600	<div></div> 0.4220
C	<div></div> 0.7590	<div></div> 0.4330

