



Full wwPDB EM Validation Report ⓘ

Nov 10, 2024 – 01:18 pm GMT

PDB ID : 7P40
EMDB ID : EMD-13190
Title : P5C3 is a potent fab neutralizer
Authors : perez, L.
Deposited on : 2021-07-09
Resolution : 3.50 Å(reported)
Based on initial model : 7K4N

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

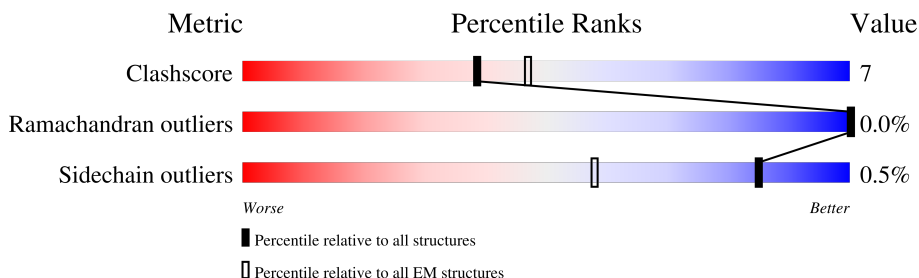
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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 ≥ 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	1281	68% 9% 22%
1	E	1281	69% 9% 22%
1	G	1281	68% 10% 22%
2	B	215	33% 34% 15% 50%
2	D	215	31% 34% 15% 50%
2	H	215	30% 35% 14% 50%
3	C	221	20% 35% 20% 44%
3	F	221	15% 35% 20% 44%

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Mol	Chain	Length	Quality of chain
3	I	221	<div><div></div><div></div><div></div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 26466 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	998	Total	C	N	O	S	0	0
			7064	4529	1209	1292	34		
1	E	998	Total	C	N	O	S	0	0
			7064	4529	1209	1292	34		
1	G	998	Total	C	N	O	S	0	0
			7064	4529	1209	1292	34		

There are 267 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP A0A6N1BWN9
A	-17	GLY	-	expression tag	UNP A0A6N1BWN9
A	-16	ILE	-	expression tag	UNP A0A6N1BWN9
A	-15	LEU	-	expression tag	UNP A0A6N1BWN9
A	-14	PRO	-	expression tag	UNP A0A6N1BWN9
A	-13	SER	-	expression tag	UNP A0A6N1BWN9
A	-12	PRO	-	expression tag	UNP A0A6N1BWN9
A	-11	GLY	-	expression tag	UNP A0A6N1BWN9
A	-10	MET	-	expression tag	UNP A0A6N1BWN9
A	-9	PRO	-	expression tag	UNP A0A6N1BWN9
A	-8	ALA	-	expression tag	UNP A0A6N1BWN9
A	-7	LEU	-	expression tag	UNP A0A6N1BWN9
A	-6	LEU	-	expression tag	UNP A0A6N1BWN9
A	-5	SER	-	expression tag	UNP A0A6N1BWN9
A	-4	LEU	-	expression tag	UNP A0A6N1BWN9
A	-3	VAL	-	expression tag	UNP A0A6N1BWN9
A	-2	SER	-	expression tag	UNP A0A6N1BWN9
A	-1	LEU	-	expression tag	UNP A0A6N1BWN9
A	0	LEU	-	expression tag	UNP A0A6N1BWN9
A	1	SER	-	expression tag	UNP A0A6N1BWN9
A	2	VAL	-	expression tag	UNP A0A6N1BWN9
A	3	LEU	-	expression tag	UNP A0A6N1BWN9
A	4	LEU	-	expression tag	UNP A0A6N1BWN9
A	5	MET	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	6	GLY	-	expression tag	UNP A0A6N1BWN9
A	7	CYS	-	expression tag	UNP A0A6N1BWN9
A	8	VAL	-	expression tag	UNP A0A6N1BWN9
A	9	ALA	-	expression tag	UNP A0A6N1BWN9
A	10	GLU	-	expression tag	UNP A0A6N1BWN9
A	11	THR	-	expression tag	UNP A0A6N1BWN9
A	12	GLY	-	expression tag	UNP A0A6N1BWN9
A	13	THR	SER	conflict	UNP A0A6N1BWN9
A	682	SER	ARG	conflict	UNP A0A6N1BWN9
A	683	GLY	ARG	conflict	UNP A0A6N1BWN9
A	685	GLY	ARG	conflict	UNP A0A6N1BWN9
A	817	PRO	PHE	conflict	UNP A0A6N1BWN9
A	892	PRO	ALA	conflict	UNP A0A6N1BWN9
A	899	PRO	ALA	conflict	UNP A0A6N1BWN9
A	942	PRO	ALA	conflict	UNP A0A6N1BWN9
A	986	PRO	LYS	conflict	UNP A0A6N1BWN9
A	987	PRO	VAL	conflict	UNP A0A6N1BWN9
A	1212	GLY	TRP	conflict	UNP A0A6N1BWN9
A	1213	SER	PRO	conflict	UNP A0A6N1BWN9
A	1214	GLY	TRP	conflict	UNP A0A6N1BWN9
A	1215	ARG	TYR	conflict	UNP A0A6N1BWN9
A	1216	GLU	ILE	conflict	UNP A0A6N1BWN9
A	1217	ASN	TRP	conflict	UNP A0A6N1BWN9
A	1219	TYR	VAL	conflict	UNP A0A6N1BWN9
A	1221	GLN	ILE	conflict	UNP A0A6N1BWN9
A	1222	GLY	ALA	conflict	UNP A0A6N1BWN9
A	1224	GLY	-	expression tag	UNP A0A6N1BWN9
A	1225	GLY	-	expression tag	UNP A0A6N1BWN9
A	1226	SER	-	expression tag	UNP A0A6N1BWN9
A	1227	GLY	-	expression tag	UNP A0A6N1BWN9
A	1228	TYR	-	expression tag	UNP A0A6N1BWN9
A	1229	ILE	-	expression tag	UNP A0A6N1BWN9
A	1230	PRO	-	expression tag	UNP A0A6N1BWN9
A	1231	GLU	-	expression tag	UNP A0A6N1BWN9
A	1232	ALA	-	expression tag	UNP A0A6N1BWN9
A	1233	PRO	-	expression tag	UNP A0A6N1BWN9
A	1234	ARG	-	expression tag	UNP A0A6N1BWN9
A	1235	ASP	-	expression tag	UNP A0A6N1BWN9
A	1236	GLY	-	expression tag	UNP A0A6N1BWN9
A	1237	GLN	-	expression tag	UNP A0A6N1BWN9
A	1238	ALA	-	expression tag	UNP A0A6N1BWN9
A	1239	TYR	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1240	VAL	-	expression tag	UNP A0A6N1BWN9
A	1241	ARG	-	expression tag	UNP A0A6N1BWN9
A	1242	LYS	-	expression tag	UNP A0A6N1BWN9
A	1243	ASP	-	expression tag	UNP A0A6N1BWN9
A	1244	GLY	-	expression tag	UNP A0A6N1BWN9
A	1245	GLU	-	expression tag	UNP A0A6N1BWN9
A	1246	TRP	-	expression tag	UNP A0A6N1BWN9
A	1247	VAL	-	expression tag	UNP A0A6N1BWN9
A	1248	LEU	-	expression tag	UNP A0A6N1BWN9
A	1249	LEU	-	expression tag	UNP A0A6N1BWN9
A	1250	SER	-	expression tag	UNP A0A6N1BWN9
A	1251	THR	-	expression tag	UNP A0A6N1BWN9
A	1252	PHE	-	expression tag	UNP A0A6N1BWN9
A	1253	LEU	-	expression tag	UNP A0A6N1BWN9
A	1254	GLY	-	expression tag	UNP A0A6N1BWN9
A	1255	HIS	-	expression tag	UNP A0A6N1BWN9
A	1256	HIS	-	expression tag	UNP A0A6N1BWN9
A	1257	HIS	-	expression tag	UNP A0A6N1BWN9
A	1258	HIS	-	expression tag	UNP A0A6N1BWN9
A	1259	HIS	-	expression tag	UNP A0A6N1BWN9
A	1260	HIS	-	expression tag	UNP A0A6N1BWN9
A	1261	HIS	-	expression tag	UNP A0A6N1BWN9
A	1262	HIS	-	expression tag	UNP A0A6N1BWN9
E	-18	MET	-	initiating methionine	UNP A0A6N1BWN9
E	-17	GLY	-	expression tag	UNP A0A6N1BWN9
E	-16	ILE	-	expression tag	UNP A0A6N1BWN9
E	-15	LEU	-	expression tag	UNP A0A6N1BWN9
E	-14	PRO	-	expression tag	UNP A0A6N1BWN9
E	-13	SER	-	expression tag	UNP A0A6N1BWN9
E	-12	PRO	-	expression tag	UNP A0A6N1BWN9
E	-11	GLY	-	expression tag	UNP A0A6N1BWN9
E	-10	MET	-	expression tag	UNP A0A6N1BWN9
E	-9	PRO	-	expression tag	UNP A0A6N1BWN9
E	-8	ALA	-	expression tag	UNP A0A6N1BWN9
E	-7	LEU	-	expression tag	UNP A0A6N1BWN9
E	-6	LEU	-	expression tag	UNP A0A6N1BWN9
E	-5	SER	-	expression tag	UNP A0A6N1BWN9
E	-4	LEU	-	expression tag	UNP A0A6N1BWN9
E	-3	VAL	-	expression tag	UNP A0A6N1BWN9
E	-2	SER	-	expression tag	UNP A0A6N1BWN9
E	-1	LEU	-	expression tag	UNP A0A6N1BWN9
E	0	LEU	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1	SER	-	expression tag	UNP A0A6N1BWN9
E	2	VAL	-	expression tag	UNP A0A6N1BWN9
E	3	LEU	-	expression tag	UNP A0A6N1BWN9
E	4	LEU	-	expression tag	UNP A0A6N1BWN9
E	5	MET	-	expression tag	UNP A0A6N1BWN9
E	6	GLY	-	expression tag	UNP A0A6N1BWN9
E	7	CYS	-	expression tag	UNP A0A6N1BWN9
E	8	VAL	-	expression tag	UNP A0A6N1BWN9
E	9	ALA	-	expression tag	UNP A0A6N1BWN9
E	10	GLU	-	expression tag	UNP A0A6N1BWN9
E	11	THR	-	expression tag	UNP A0A6N1BWN9
E	12	GLY	-	expression tag	UNP A0A6N1BWN9
E	13	THR	SER	conflict	UNP A0A6N1BWN9
E	682	SER	ARG	conflict	UNP A0A6N1BWN9
E	683	GLY	ARG	conflict	UNP A0A6N1BWN9
E	685	GLY	ARG	conflict	UNP A0A6N1BWN9
E	817	PRO	PHE	conflict	UNP A0A6N1BWN9
E	892	PRO	ALA	conflict	UNP A0A6N1BWN9
E	899	PRO	ALA	conflict	UNP A0A6N1BWN9
E	942	PRO	ALA	conflict	UNP A0A6N1BWN9
E	986	PRO	LYS	conflict	UNP A0A6N1BWN9
E	987	PRO	VAL	conflict	UNP A0A6N1BWN9
E	1212	GLY	TRP	conflict	UNP A0A6N1BWN9
E	1213	SER	PRO	conflict	UNP A0A6N1BWN9
E	1214	GLY	TRP	conflict	UNP A0A6N1BWN9
E	1215	ARG	TYR	conflict	UNP A0A6N1BWN9
E	1216	GLU	ILE	conflict	UNP A0A6N1BWN9
E	1217	ASN	TRP	conflict	UNP A0A6N1BWN9
E	1219	TYR	VAL	conflict	UNP A0A6N1BWN9
E	1221	GLN	ILE	conflict	UNP A0A6N1BWN9
E	1222	GLY	ALA	conflict	UNP A0A6N1BWN9
E	1224	GLY	-	expression tag	UNP A0A6N1BWN9
E	1225	GLY	-	expression tag	UNP A0A6N1BWN9
E	1226	SER	-	expression tag	UNP A0A6N1BWN9
E	1227	GLY	-	expression tag	UNP A0A6N1BWN9
E	1228	TYR	-	expression tag	UNP A0A6N1BWN9
E	1229	ILE	-	expression tag	UNP A0A6N1BWN9
E	1230	PRO	-	expression tag	UNP A0A6N1BWN9
E	1231	GLU	-	expression tag	UNP A0A6N1BWN9
E	1232	ALA	-	expression tag	UNP A0A6N1BWN9
E	1233	PRO	-	expression tag	UNP A0A6N1BWN9
E	1234	ARG	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1235	ASP	-	expression tag	UNP A0A6N1BWN9
E	1236	GLY	-	expression tag	UNP A0A6N1BWN9
E	1237	GLN	-	expression tag	UNP A0A6N1BWN9
E	1238	ALA	-	expression tag	UNP A0A6N1BWN9
E	1239	TYR	-	expression tag	UNP A0A6N1BWN9
E	1240	VAL	-	expression tag	UNP A0A6N1BWN9
E	1241	ARG	-	expression tag	UNP A0A6N1BWN9
E	1242	LYS	-	expression tag	UNP A0A6N1BWN9
E	1243	ASP	-	expression tag	UNP A0A6N1BWN9
E	1244	GLY	-	expression tag	UNP A0A6N1BWN9
E	1245	GLU	-	expression tag	UNP A0A6N1BWN9
E	1246	TRP	-	expression tag	UNP A0A6N1BWN9
E	1247	VAL	-	expression tag	UNP A0A6N1BWN9
E	1248	LEU	-	expression tag	UNP A0A6N1BWN9
E	1249	LEU	-	expression tag	UNP A0A6N1BWN9
E	1250	SER	-	expression tag	UNP A0A6N1BWN9
E	1251	THR	-	expression tag	UNP A0A6N1BWN9
E	1252	PHE	-	expression tag	UNP A0A6N1BWN9
E	1253	LEU	-	expression tag	UNP A0A6N1BWN9
E	1254	GLY	-	expression tag	UNP A0A6N1BWN9
E	1255	HIS	-	expression tag	UNP A0A6N1BWN9
E	1256	HIS	-	expression tag	UNP A0A6N1BWN9
E	1257	HIS	-	expression tag	UNP A0A6N1BWN9
E	1258	HIS	-	expression tag	UNP A0A6N1BWN9
E	1259	HIS	-	expression tag	UNP A0A6N1BWN9
E	1260	HIS	-	expression tag	UNP A0A6N1BWN9
E	1261	HIS	-	expression tag	UNP A0A6N1BWN9
E	1262	HIS	-	expression tag	UNP A0A6N1BWN9
G	-18	MET	-	initiating methionine	UNP A0A6N1BWN9
G	-17	GLY	-	expression tag	UNP A0A6N1BWN9
G	-16	ILE	-	expression tag	UNP A0A6N1BWN9
G	-15	LEU	-	expression tag	UNP A0A6N1BWN9
G	-14	PRO	-	expression tag	UNP A0A6N1BWN9
G	-13	SER	-	expression tag	UNP A0A6N1BWN9
G	-12	PRO	-	expression tag	UNP A0A6N1BWN9
G	-11	GLY	-	expression tag	UNP A0A6N1BWN9
G	-10	MET	-	expression tag	UNP A0A6N1BWN9
G	-9	PRO	-	expression tag	UNP A0A6N1BWN9
G	-8	ALA	-	expression tag	UNP A0A6N1BWN9
G	-7	LEU	-	expression tag	UNP A0A6N1BWN9
G	-6	LEU	-	expression tag	UNP A0A6N1BWN9
G	-5	SER	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-4	LEU	-	expression tag	UNP A0A6N1BWN9
G	-3	VAL	-	expression tag	UNP A0A6N1BWN9
G	-2	SER	-	expression tag	UNP A0A6N1BWN9
G	-1	LEU	-	expression tag	UNP A0A6N1BWN9
G	0	LEU	-	expression tag	UNP A0A6N1BWN9
G	1	SER	-	expression tag	UNP A0A6N1BWN9
G	2	VAL	-	expression tag	UNP A0A6N1BWN9
G	3	LEU	-	expression tag	UNP A0A6N1BWN9
G	4	LEU	-	expression tag	UNP A0A6N1BWN9
G	5	MET	-	expression tag	UNP A0A6N1BWN9
G	6	GLY	-	expression tag	UNP A0A6N1BWN9
G	7	CYS	-	expression tag	UNP A0A6N1BWN9
G	8	VAL	-	expression tag	UNP A0A6N1BWN9
G	9	ALA	-	expression tag	UNP A0A6N1BWN9
G	10	GLU	-	expression tag	UNP A0A6N1BWN9
G	11	THR	-	expression tag	UNP A0A6N1BWN9
G	12	GLY	-	expression tag	UNP A0A6N1BWN9
G	13	THR	SER	conflict	UNP A0A6N1BWN9
G	682	SER	ARG	conflict	UNP A0A6N1BWN9
G	683	GLY	ARG	conflict	UNP A0A6N1BWN9
G	685	GLY	ARG	conflict	UNP A0A6N1BWN9
G	817	PRO	PHE	conflict	UNP A0A6N1BWN9
G	892	PRO	ALA	conflict	UNP A0A6N1BWN9
G	899	PRO	ALA	conflict	UNP A0A6N1BWN9
G	942	PRO	ALA	conflict	UNP A0A6N1BWN9
G	986	PRO	LYS	conflict	UNP A0A6N1BWN9
G	987	PRO	VAL	conflict	UNP A0A6N1BWN9
G	1212	GLY	TRP	conflict	UNP A0A6N1BWN9
G	1213	SER	PRO	conflict	UNP A0A6N1BWN9
G	1214	GLY	TRP	conflict	UNP A0A6N1BWN9
G	1215	ARG	TYR	conflict	UNP A0A6N1BWN9
G	1216	GLU	ILE	conflict	UNP A0A6N1BWN9
G	1217	ASN	TRP	conflict	UNP A0A6N1BWN9
G	1219	TYR	VAL	conflict	UNP A0A6N1BWN9
G	1221	GLN	ILE	conflict	UNP A0A6N1BWN9
G	1222	GLY	ALA	conflict	UNP A0A6N1BWN9
G	1224	GLY	-	expression tag	UNP A0A6N1BWN9
G	1225	GLY	-	expression tag	UNP A0A6N1BWN9
G	1226	SER	-	expression tag	UNP A0A6N1BWN9
G	1227	GLY	-	expression tag	UNP A0A6N1BWN9
G	1228	TYR	-	expression tag	UNP A0A6N1BWN9
G	1229	ILE	-	expression tag	UNP A0A6N1BWN9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1230	PRO	-	expression tag	UNP A0A6N1BWN9
G	1231	GLU	-	expression tag	UNP A0A6N1BWN9
G	1232	ALA	-	expression tag	UNP A0A6N1BWN9
G	1233	PRO	-	expression tag	UNP A0A6N1BWN9
G	1234	ARG	-	expression tag	UNP A0A6N1BWN9
G	1235	ASP	-	expression tag	UNP A0A6N1BWN9
G	1236	GLY	-	expression tag	UNP A0A6N1BWN9
G	1237	GLN	-	expression tag	UNP A0A6N1BWN9
G	1238	ALA	-	expression tag	UNP A0A6N1BWN9
G	1239	TYR	-	expression tag	UNP A0A6N1BWN9
G	1240	VAL	-	expression tag	UNP A0A6N1BWN9
G	1241	ARG	-	expression tag	UNP A0A6N1BWN9
G	1242	LYS	-	expression tag	UNP A0A6N1BWN9
G	1243	ASP	-	expression tag	UNP A0A6N1BWN9
G	1244	GLY	-	expression tag	UNP A0A6N1BWN9
G	1245	GLU	-	expression tag	UNP A0A6N1BWN9
G	1246	TRP	-	expression tag	UNP A0A6N1BWN9
G	1247	VAL	-	expression tag	UNP A0A6N1BWN9
G	1248	LEU	-	expression tag	UNP A0A6N1BWN9
G	1249	LEU	-	expression tag	UNP A0A6N1BWN9
G	1250	SER	-	expression tag	UNP A0A6N1BWN9
G	1251	THR	-	expression tag	UNP A0A6N1BWN9
G	1252	PHE	-	expression tag	UNP A0A6N1BWN9
G	1253	LEU	-	expression tag	UNP A0A6N1BWN9
G	1254	GLY	-	expression tag	UNP A0A6N1BWN9
G	1255	HIS	-	expression tag	UNP A0A6N1BWN9
G	1256	HIS	-	expression tag	UNP A0A6N1BWN9
G	1257	HIS	-	expression tag	UNP A0A6N1BWN9
G	1258	HIS	-	expression tag	UNP A0A6N1BWN9
G	1259	HIS	-	expression tag	UNP A0A6N1BWN9
G	1260	HIS	-	expression tag	UNP A0A6N1BWN9
G	1261	HIS	-	expression tag	UNP A0A6N1BWN9
G	1262	HIS	-	expression tag	UNP A0A6N1BWN9

- Molecule 2 is a protein called Variable Light Chain P5C3 (VL).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	108	Total	C	N	O	S	0	0
			826	519	142	163	2		
2	D	108	Total	C	N	O	S	0	0
			826	519	142	163	2		
2	H	108	Total	C	N	O	S	0	0
			826	519	142	163	2		

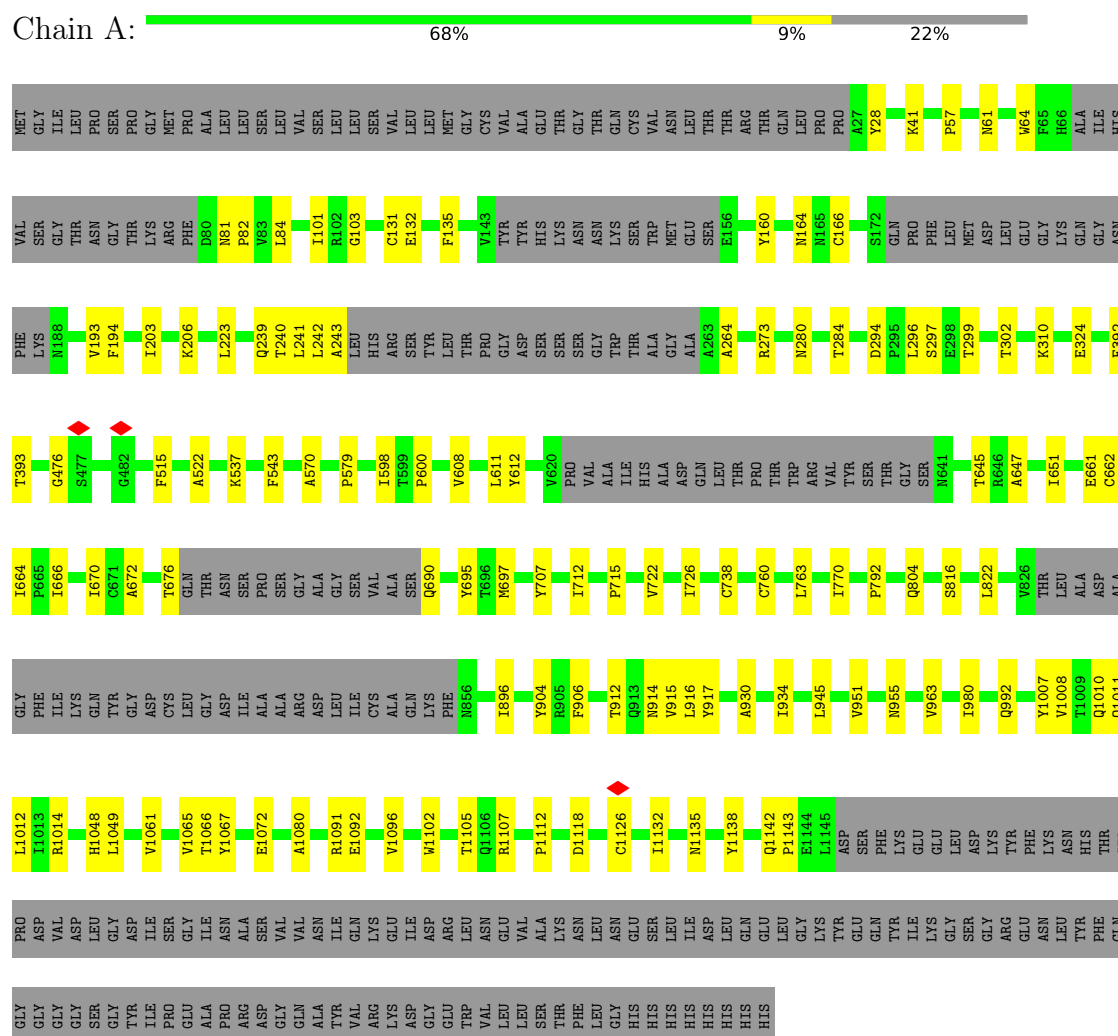
- Molecule 3 is a protein called Variable Heavy Chain P5C3 (VH).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	123	Total	C	N	O	S	0	0
			932	579	158	187	8		
3	F	123	Total	C	N	O	S	0	0
			932	579	158	187	8		
3	I	123	Total	C	N	O	S	0	0
			932	579	158	187	8		

3 Residue-property plots

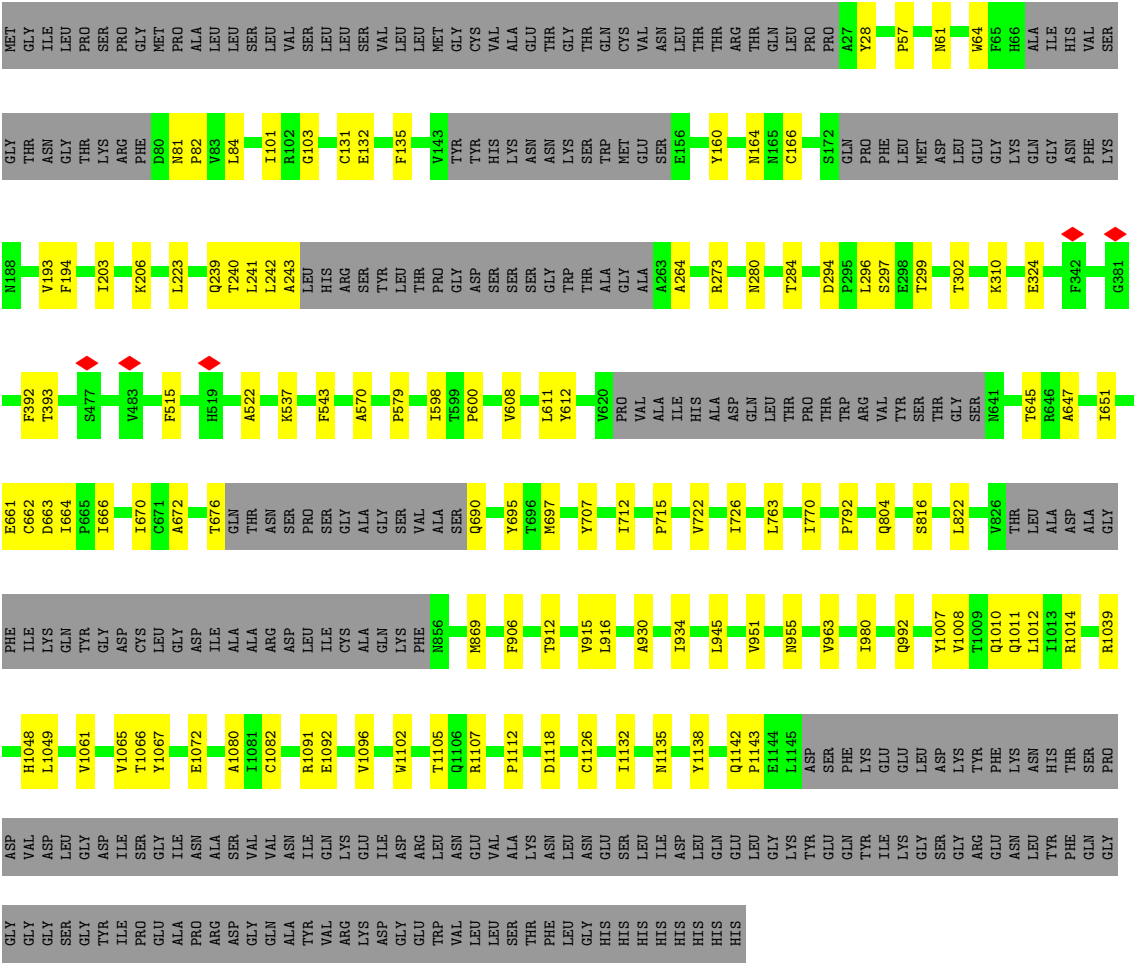
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

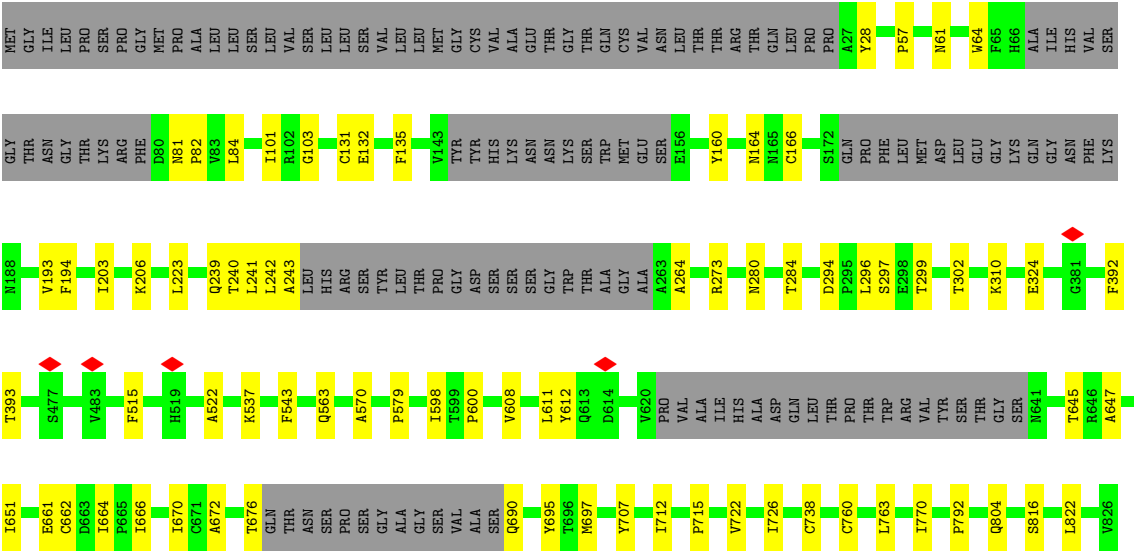


• Molecule 1: Spike glycoprotein

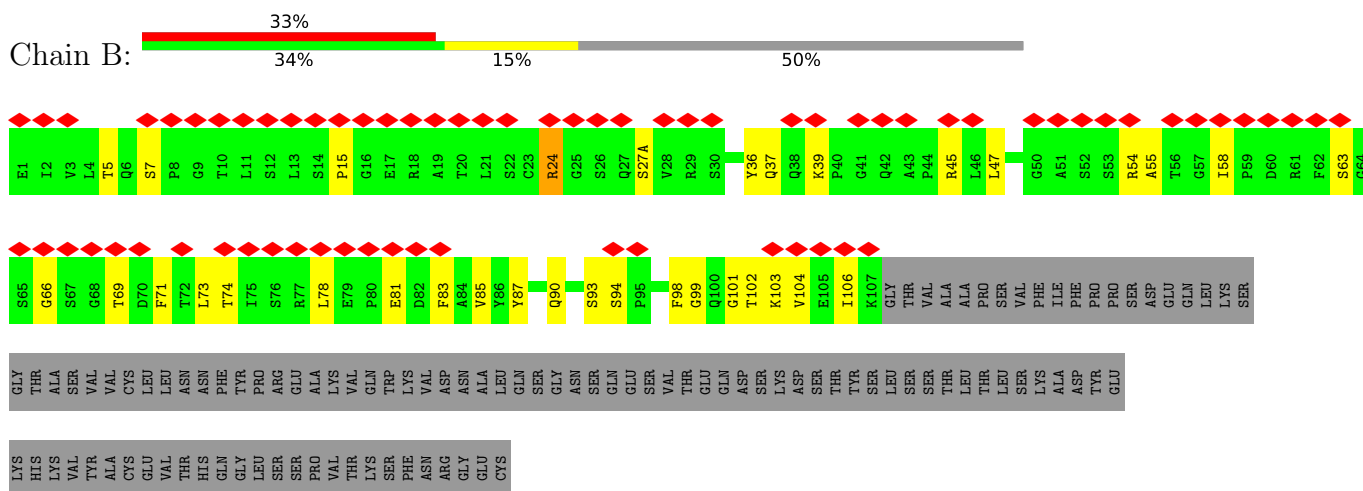




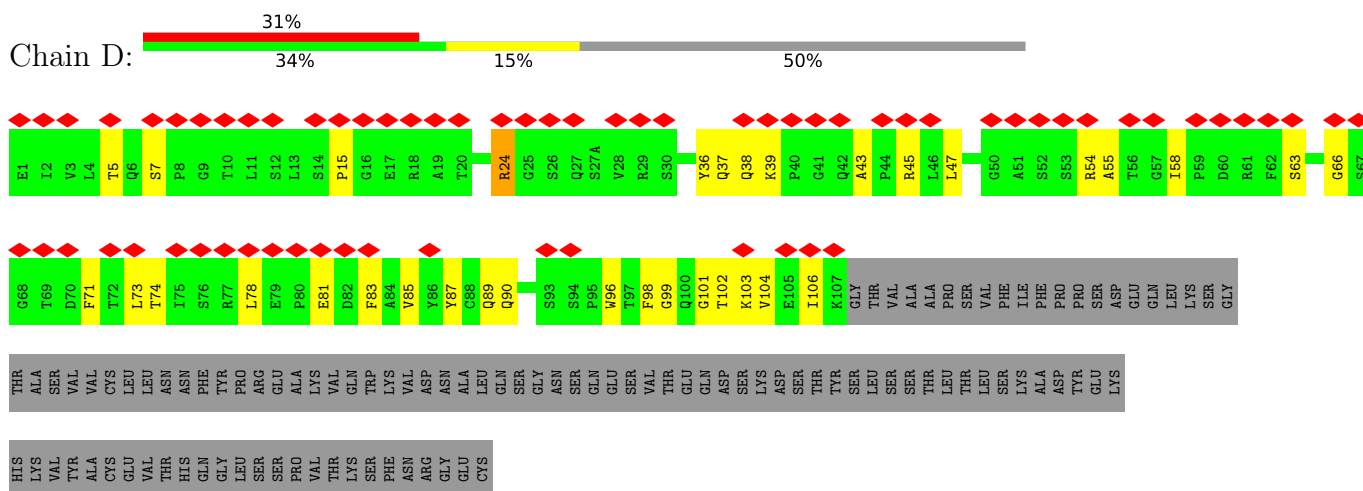
● Molecule 1: Spike glycoprotein



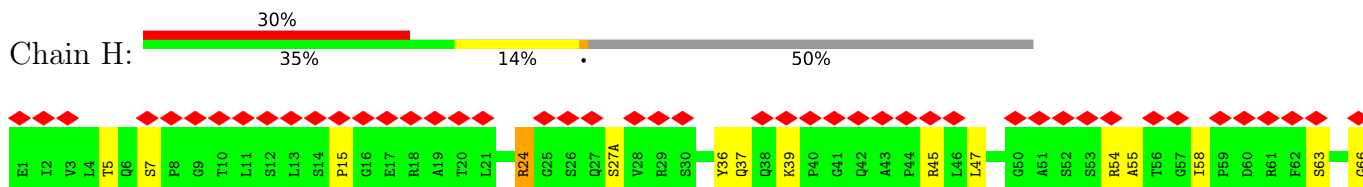
- Molecule 2: Variable Light Chain P5C3 (VL)



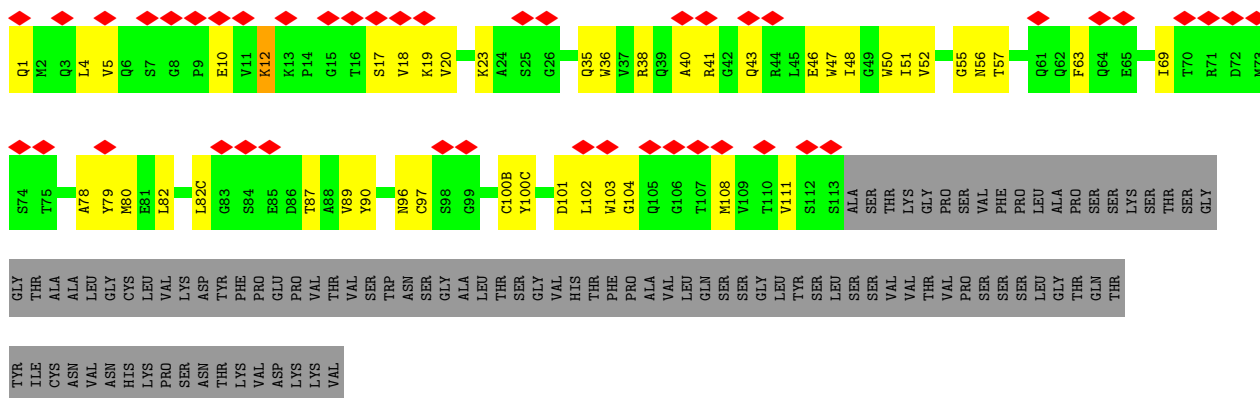
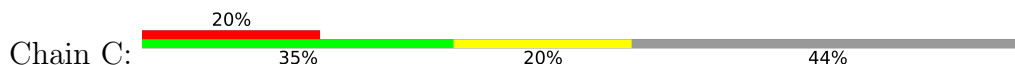
- Molecule 2: Variable Light Chain P5C3 (VL)



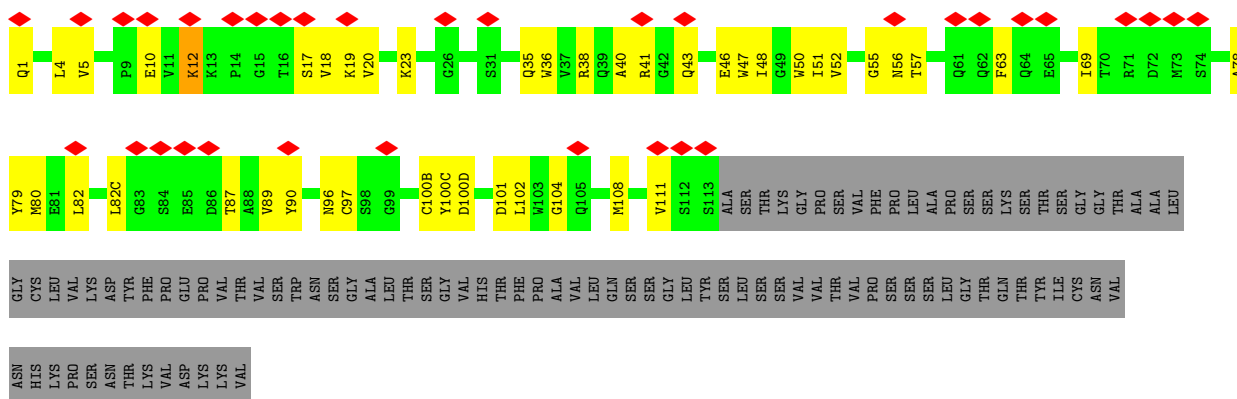
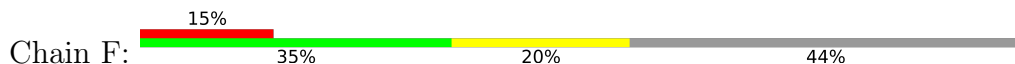
- Molecule 2: Variable Light Chain P5C3 (VL)



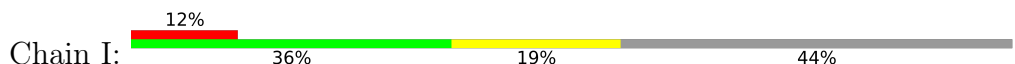
- Molecule 3: Variable Heavy Chain P5C3 (VH)

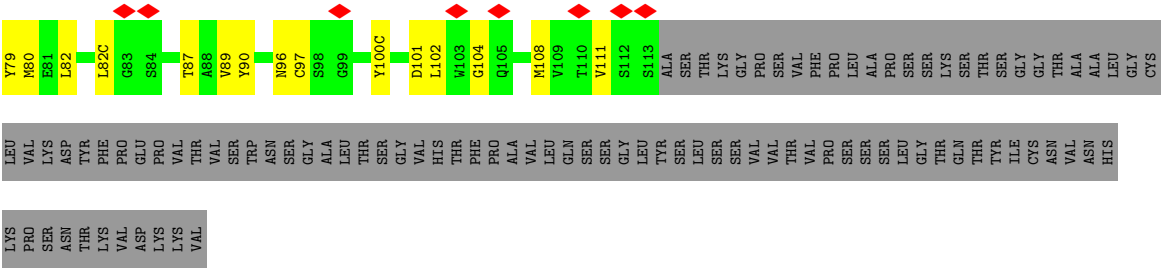


- Molecule 3: Variable Heavy Chain P5C3 (VH)



- Molecule 3: Variable Heavy Chain P5C3 (VH)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	585005	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	10500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	66.413	Depositor
Minimum map value	-37.650	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.9	Depositor
Map size (Å)	492.0, 492.0, 492.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.64, 1.64, 1.64	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	0/7222	0.46	0/9891
1	E	0.26	0/7222	0.46	0/9891
1	G	0.26	0/7222	0.46	0/9891
2	B	0.29	0/846	0.58	0/1147
2	D	0.29	0/846	0.58	0/1147
2	H	0.29	0/846	0.58	0/1147
3	C	0.26	0/951	0.55	0/1289
3	F	0.26	0/951	0.56	0/1289
3	I	0.26	0/951	0.55	0/1289
All	All	0.27	0/27057	0.48	0/36981

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7064	0	6245	71	0
1	E	7064	0	6245	70	0
1	G	7064	0	6245	74	0
2	B	826	0	802	21	0
2	D	826	0	802	23	0
2	H	826	0	802	20	0
3	C	932	0	887	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	932	0	887	33	0
3	I	932	0	887	32	0
All	All	26466	0	23802	357	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 7.

All (357) 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:132:GLU:HB2	1:G:164:ASN:O	1.82	0.79
1:E:132:GLU:HB2	1:E:164:ASN:O	1.82	0.79
1:A:132:GLU:HB2	1:A:164:ASN:O	1.82	0.78
3:C:38:ARG:HB3	3:C:48:ILE:HD11	1.68	0.76
3:F:38:ARG:HB3	3:F:48:ILE:HD11	1.68	0.74
3:I:38:ARG:HB3	3:I:48:ILE:HD11	1.68	0.74
3:C:69:ILE:HD11	3:C:78:ALA:HB1	1.71	0.72
3:I:69:ILE:HD11	3:I:78:ALA:HB1	1.71	0.71
3:F:69:ILE:HD11	3:F:78:ALA:HB1	1.71	0.70
1:E:662:CYS:HB2	1:E:697:MET:HG2	1.75	0.69
1:A:662:CYS:HB2	1:A:697:MET:HG2	1.75	0.69
3:I:17:SER:HA	3:I:82:LEU:O	1.94	0.68
3:C:17:SER:HA	3:C:82:LEU:O	1.94	0.67
3:F:17:SER:HA	3:F:82:LEU:O	1.94	0.67
1:E:1092:GLU:O	1:E:1107:ARG:NH1	2.28	0.66
1:G:1092:GLU:O	1:G:1107:ARG:NH1	2.28	0.66
1:A:1092:GLU:O	1:A:1107:ARG:NH1	2.28	0.66
2:H:87:TYR:HB3	2:H:99:GLY:HA3	1.78	0.66
1:G:662:CYS:HB2	1:G:697:MET:HG2	1.75	0.66
2:H:39:LYS:NZ	2:H:81:GLU:O	2.29	0.66
2:D:39:LYS:NZ	2:D:81:GLU:O	2.29	0.65
3:C:5:VAL:HB	3:C:23:LYS:HG2	1.78	0.65
2:D:87:TYR:HB3	2:D:99:GLY:HA3	1.78	0.65
2:B:87:TYR:HB3	2:B:99:GLY:HA3	1.78	0.65
1:G:726:ILE:HG12	1:G:1061:VAL:HG22	1.79	0.64
1:A:726:ILE:HG12	1:A:1061:VAL:HG22	1.79	0.64
2:B:39:LYS:NZ	2:B:81:GLU:O	2.29	0.64
1:E:726:ILE:HG12	1:E:1061:VAL:HG22	1.80	0.64
3:F:5:VAL:HB	3:F:23:LYS:HG2	1.78	0.63
1:E:324:GLU:OE2	1:E:537:LYS:NZ	2.31	0.63
1:G:324:GLU:OE2	1:G:537:LYS:NZ	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:5:VAL:HB	3:I:23:LYS:HG2	1.78	0.62
1:E:763:LEU:HD12	1:E:1008:VAL:HG21	1.81	0.62
1:E:103:GLY:HA3	1:E:241:LEU:HB2	1.82	0.62
1:A:324:GLU:OE2	1:A:537:LYS:NZ	2.31	0.62
1:G:763:LEU:HD12	1:G:1008:VAL:HG21	1.81	0.62
1:A:103:GLY:HA3	1:A:241:LEU:HB2	1.81	0.61
1:A:763:LEU:HD12	1:A:1008:VAL:HG21	1.81	0.61
3:C:35:GLN:HG2	3:C:50:TRP:HB3	1.83	0.61
1:A:1010:GLN:OE1	1:A:1014:ARG:NH1	2.31	0.61
1:A:280:ASN:ND2	1:A:284:THR:OG1	2.34	0.61
3:C:40:ALA:HB3	3:C:43:GLN:HB2	1.83	0.61
3:I:40:ALA:HB3	3:I:43:GLN:HB2	1.83	0.61
3:C:19:LYS:HZ1	3:C:79:TYR:HB3	1.65	0.60
3:I:12:LYS:HE3	3:I:111:VAL:HB	1.83	0.60
2:D:7:SER:HB3	2:D:102:THR:HG21	1.84	0.60
2:H:7:SER:HB3	2:H:102:THR:HG21	1.84	0.60
1:E:280:ASN:ND2	1:E:284:THR:OG1	2.34	0.60
3:F:35:GLN:HG2	3:F:50:TRP:HB3	1.83	0.60
1:G:280:ASN:ND2	1:G:284:THR:OG1	2.34	0.60
1:G:103:GLY:HA3	1:G:241:LEU:HB2	1.82	0.59
1:E:707:TYR:HB3	1:G:792:PRO:HG3	1.85	0.59
3:C:12:LYS:HE3	3:C:111:VAL:HB	1.83	0.59
3:F:12:LYS:HE3	3:F:111:VAL:HB	1.83	0.59
1:A:770:ILE:HD11	1:A:1012:LEU:HD23	1.84	0.59
1:E:770:ILE:HD11	1:E:1012:LEU:HD23	1.84	0.59
3:I:19:LYS:HZ1	3:I:79:TYR:HB3	1.68	0.59
2:B:7:SER:HB3	2:B:102:THR:HG21	1.84	0.59
3:F:40:ALA:HB3	3:F:43:GLN:HB2	1.83	0.59
1:G:770:ILE:HD11	1:G:1012:LEU:HD23	1.84	0.59
3:I:35:GLN:HG2	3:I:50:TRP:HB3	1.83	0.59
1:A:963:VAL:HG11	1:G:570:ALA:HB1	1.85	0.58
1:A:64:TRP:HE1	1:A:264:ALA:HB1	1.69	0.58
1:A:570:ALA:HB1	1:E:963:VAL:HG11	1.84	0.58
1:G:81:ASN:O	1:G:239:GLN:NE2	2.34	0.58
1:A:804:GLN:O	1:A:816:SER:OG	2.22	0.58
3:F:1:GLN:HB2	3:F:102:LEU:HD11	1.86	0.58
3:F:19:LYS:HZ1	3:F:79:TYR:HB3	1.69	0.58
1:A:666:ILE:HD11	1:A:672:ALA:HB2	1.86	0.58
1:E:64:TRP:HE1	1:E:264:ALA:HB1	1.69	0.58
1:E:1010:GLN:OE1	1:E:1014:ARG:NH1	2.31	0.58
1:G:804:GLN:O	1:G:816:SER:OG	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:666:ILE:HD11	1:E:672:ALA:HB2	1.85	0.57
1:G:666:ILE:HD11	1:G:672:ALA:HB2	1.86	0.57
1:G:64:TRP:HE1	1:G:264:ALA:HB1	1.69	0.57
1:G:1010:GLN:OE1	1:G:1014:ARG:NH1	2.31	0.57
1:E:804:GLN:O	1:E:816:SER:OG	2.22	0.57
1:A:81:ASN:O	1:A:239:GLN:NE2	2.34	0.57
3:C:1:GLN:HB2	3:C:102:LEU:HD11	1.86	0.57
3:I:1:GLN:HB2	3:I:102:LEU:HD11	1.86	0.57
2:H:37:GLN:O	2:H:45:ARG:N	2.30	0.55
2:D:45:ARG:NH2	2:D:81:GLU:OE2	2.41	0.54
2:B:98:PHE:CD1	3:F:47:TRP:HB3	2.43	0.54
1:A:393:THR:HA	1:A:522:ALA:HA	1.90	0.54
3:C:87:THR:HB	3:C:111:VAL:HG12	1.90	0.54
1:E:81:ASN:O	1:E:239:GLN:NE2	2.34	0.54
1:G:393:THR:HA	1:G:522:ALA:HA	1.90	0.54
2:B:45:ARG:NH2	2:B:81:GLU:OE2	2.41	0.53
3:C:69:ILE:HD12	3:C:80:MET:HB3	1.90	0.53
2:H:45:ARG:NH2	2:H:81:GLU:OE2	2.41	0.53
2:D:37:GLN:O	2:D:45:ARG:N	2.31	0.53
3:F:69:ILE:HD12	3:F:80:MET:HB3	1.90	0.53
3:F:52:VAL:O	3:F:55:GLY:N	2.42	0.53
3:C:52:VAL:O	3:C:55:GLY:N	2.42	0.53
3:I:69:ILE:HD12	3:I:80:MET:HB3	1.90	0.53
3:I:52:VAL:O	3:I:55:GLY:N	2.42	0.53
1:E:393:THR:HA	1:E:522:ALA:HA	1.90	0.53
3:C:36:TRP:HZ3	3:C:90:TYR:HB3	1.75	0.52
2:B:15:PRO:HA	2:B:78:LEU:HB3	1.92	0.52
2:B:98:PHE:HD1	3:F:47:TRP:HB3	1.74	0.52
3:F:19:LYS:HZ1	3:F:79:TYR:HD1	1.57	0.52
3:I:87:THR:HB	3:I:111:VAL:HG12	1.90	0.52
2:D:15:PRO:HA	2:D:78:LEU:HB3	1.92	0.52
1:E:101:ILE:HD11	1:E:240:THR:HB	1.92	0.52
3:F:87:THR:HB	3:F:111:VAL:HG12	1.90	0.52
1:G:101:ILE:HD11	1:G:240:THR:HB	1.92	0.52
1:G:906:PHE:CD2	1:G:916:LEU:HB2	2.45	0.52
1:E:906:PHE:CD2	1:E:916:LEU:HB2	2.45	0.52
2:H:15:PRO:HA	2:H:78:LEU:HB3	1.92	0.52
2:H:83:PHE:HB2	2:H:106:ILE:HG12	1.92	0.51
2:B:66:GLY:HA3	2:B:71:PHE:HA	1.91	0.51
1:A:476:GLY:HA3	3:F:100(D):ASP:OD1	2.10	0.51
2:D:66:GLY:HA3	2:D:71:PHE:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:19:LYS:HZ1	3:I:79:TYR:HD1	1.57	0.51
1:A:906:PHE:CD2	1:A:916:LEU:HB2	2.45	0.51
2:H:66:GLY:HA3	2:H:71:PHE:HA	1.92	0.51
1:A:392:PHE:CG	1:A:515:PHE:HB3	2.46	0.51
1:E:392:PHE:CG	1:E:515:PHE:HB3	2.46	0.51
3:F:36:TRP:HZ3	3:F:90:TYR:HB3	1.75	0.51
3:I:36:TRP:HZ3	3:I:90:TYR:HB3	1.75	0.51
3:C:20:VAL:HB	3:C:80:MET:SD	2.51	0.50
3:F:20:VAL:HB	3:F:80:MET:SD	2.51	0.50
1:E:294:ASP:OD1	1:E:297:SER:N	2.39	0.50
3:F:41:ARG:HD2	3:F:41:ARG:O	2.12	0.50
1:A:101:ILE:HD11	1:A:240:THR:HB	1.92	0.50
3:F:97:CYS:HB2	3:F:100(C):TYR:H	1.77	0.50
1:E:715:PRO:HA	1:E:1072:GLU:HA	1.94	0.50
2:D:83:PHE:HB2	2:D:106:ILE:HG12	1.92	0.50
1:G:392:PHE:CG	1:G:515:PHE:HB3	2.46	0.50
3:I:20:VAL:HB	3:I:80:MET:SD	2.51	0.50
3:I:41:ARG:HD2	3:I:41:ARG:O	2.11	0.50
1:G:712:ILE:HD11	1:G:1096:VAL:HG12	1.94	0.49
2:B:83:PHE:HB2	2:B:106:ILE:HG12	1.92	0.49
3:C:97:CYS:HB2	3:C:100(C):TYR:H	1.76	0.49
1:G:715:PRO:HA	1:G:1072:GLU:HA	1.93	0.49
2:H:63:SER:OG	2:H:74:THR:OG1	2.31	0.49
3:C:52:VAL:HB	3:C:56:ASN:HB2	1.95	0.49
1:E:1105:THR:HG22	1:E:1112:PRO:HA	1.95	0.49
1:G:310:LYS:HG3	1:G:600:PRO:HA	1.95	0.49
3:I:97:CYS:HB2	3:I:100(C):TYR:H	1.77	0.49
3:C:41:ARG:HD2	3:C:41:ARG:O	2.11	0.49
1:A:715:PRO:HA	1:A:1072:GLU:HA	1.94	0.49
1:A:792:PRO:HG3	1:G:707:TYR:HB3	1.94	0.48
1:A:930:ALA:O	1:A:934:ILE:HG12	2.13	0.48
1:E:310:LYS:HG3	1:E:600:PRO:HA	1.95	0.48
1:A:310:LYS:HG3	1:A:600:PRO:HA	1.95	0.48
1:E:930:ALA:O	1:E:934:ILE:HG12	2.13	0.48
3:C:19:LYS:HZ1	3:C:79:TYR:HD1	1.60	0.48
3:F:97:CYS:HB2	3:F:100(B):CYS:HB2	1.41	0.48
2:H:5:THR:O	2:H:24:ARG:HD3	2.13	0.48
2:B:63:SER:OG	2:B:74:THR:OG1	2.31	0.48
1:G:930:ALA:O	1:G:934:ILE:HG12	2.13	0.48
1:A:1105:THR:HG22	1:A:1112:PRO:HA	1.95	0.48
3:F:52:VAL:HB	3:F:56:ASN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:ILE:HD11	1:A:1096:VAL:HG12	1.94	0.48
3:C:38:ARG:NE	3:C:46:GLU:OE2	2.46	0.48
3:C:97:CYS:HB2	3:C:100(B):CYS:HB2	1.42	0.48
3:I:52:VAL:HB	3:I:56:ASN:HB2	1.95	0.48
1:A:57:PRO:HG3	1:A:273:ARG:HD2	1.96	0.48
3:F:38:ARG:NE	3:F:46:GLU:OE2	2.46	0.48
1:G:1105:THR:HG22	1:G:1112:PRO:HA	1.95	0.48
2:D:63:SER:OG	2:D:74:THR:OG1	2.31	0.47
1:G:57:PRO:HG3	1:G:273:ARG:HD2	1.96	0.47
1:G:294:ASP:OD1	1:G:297:SER:N	2.39	0.47
2:B:5:THR:O	2:B:24:ARG:HD3	2.13	0.47
2:D:5:THR:O	2:D:24:ARG:HD3	2.13	0.47
1:E:712:ILE:HD11	1:E:1096:VAL:HG12	1.94	0.47
3:I:38:ARG:NE	3:I:46:GLU:OE2	2.46	0.47
3:C:97:CYS:HB2	3:C:100(C):TYR:N	2.30	0.47
1:A:707:TYR:HB3	1:E:792:PRO:HG3	1.97	0.47
1:A:1142:GLN:HB2	1:A:1143:PRO:HD3	1.97	0.47
1:E:193:VAL:HG23	1:E:223:LEU:HD22	1.97	0.47
3:I:97:CYS:HB2	3:I:100(C):TYR:N	2.30	0.47
1:A:294:ASP:OD1	1:A:297:SER:N	2.39	0.47
1:A:896:ILE:HD12	1:G:712:ILE:HG22	1.95	0.47
1:E:570:ALA:HB1	1:G:963:VAL:HG11	1.96	0.47
3:I:51:ILE:HD13	3:I:57:THR:HG22	1.97	0.47
2:B:37:GLN:O	2:B:45:ARG:N	2.30	0.46
1:E:57:PRO:HG3	1:E:273:ARG:HD2	1.96	0.46
1:G:1048:HIS:HA	1:G:1066:THR:HG22	1.97	0.46
1:E:543:PHE:HD2	1:E:579:PRO:HD3	1.81	0.46
3:F:97:CYS:HB2	3:F:100(C):TYR:N	2.30	0.46
1:G:543:PHE:HD2	1:G:579:PRO:HD3	1.81	0.46
1:G:1142:GLN:HB2	1:G:1143:PRO:HD3	1.97	0.46
1:A:1091:ARG:NH1	1:A:1118:ASP:O	2.49	0.46
2:B:36:TYR:CE2	2:B:87:TYR:HD2	2.34	0.46
2:D:85:VAL:HG22	2:D:103:LYS:HG2	1.98	0.46
1:A:543:PHE:HD2	1:A:579:PRO:HD3	1.81	0.46
3:F:51:ILE:HD13	3:F:57:THR:HG22	1.97	0.46
1:A:193:VAL:HG23	1:A:223:LEU:HD22	1.97	0.46
1:E:1142:GLN:HB2	1:E:1143:PRO:HD3	1.97	0.46
3:F:10:GLU:HB3	3:F:108:MET:O	2.16	0.46
1:G:1091:ARG:NH1	1:G:1118:ASP:O	2.49	0.46
2:H:36:TYR:CE2	2:H:87:TYR:HD2	2.34	0.46
3:I:10:GLU:HB3	3:I:108:MET:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:10:GLU:HB3	3:C:108:MET:O	2.16	0.46
1:E:1048:HIS:HA	1:E:1066:THR:HG22	1.97	0.46
1:G:193:VAL:HG23	1:G:223:LEU:HD22	1.97	0.46
1:G:738:CYS:HB3	1:G:760:CYS:HB3	1.86	0.46
3:C:51:ILE:HD13	3:C:57:THR:HG22	1.97	0.45
1:E:1091:ARG:NH1	1:E:1118:ASP:O	2.49	0.45
1:A:1048:HIS:HA	1:A:1066:THR:HG22	1.97	0.45
1:G:822:LEU:HD22	1:G:945:LEU:HD21	1.98	0.45
3:I:19:LYS:NZ	3:I:79:TYR:HB3	2.31	0.45
1:A:917:TYR:HB3	1:G:1129:VAL:HG23	1.97	0.45
2:B:54:ARG:HD2	2:B:55:ALA:O	2.17	0.45
2:H:85:VAL:HG22	2:H:103:LYS:HG2	1.98	0.45
1:A:822:LEU:HD22	1:A:945:LEU:HD21	1.98	0.45
3:C:19:LYS:NZ	3:C:79:TYR:HB3	2.31	0.45
2:B:85:VAL:HG22	2:B:103:LYS:HG2	1.98	0.45
1:A:645:THR:HG23	1:A:647:ALA:H	1.82	0.45
1:G:645:THR:HG23	1:G:647:ALA:H	1.82	0.45
2:D:36:TYR:CE2	2:D:87:TYR:HD2	2.34	0.45
2:H:54:ARG:HD2	2:H:55:ALA:O	2.17	0.45
3:F:96:ASN:HB2	3:F:101:ASP:H	1.82	0.44
2:D:54:ARG:HD2	2:D:55:ALA:O	2.17	0.44
1:E:299:THR:HA	1:E:302:THR:HG22	1.99	0.44
1:E:645:THR:HG23	1:E:647:ALA:H	1.82	0.44
3:I:102:LEU:HD23	3:I:102:LEU:HA	1.84	0.44
1:E:135:PHE:HA	1:E:160:TYR:HA	2.00	0.44
1:E:1049:LEU:HD11	1:E:1067:TYR:HB2	2.00	0.44
1:A:82:PRO:HG2	1:A:84:LEU:HD21	2.00	0.44
1:E:822:LEU:HD22	1:E:945:LEU:HD21	1.98	0.44
1:E:912:THR:O	1:E:915:VAL:HG22	2.18	0.44
3:I:96:ASN:HB2	3:I:101:ASP:H	1.82	0.44
1:A:28:TYR:HB3	1:A:61:ASN:OD1	2.18	0.44
1:E:82:PRO:HG2	1:E:84:LEU:HD21	1.99	0.44
3:F:19:LYS:NZ	3:F:79:TYR:HB3	2.31	0.44
1:G:912:THR:O	1:G:915:VAL:HG22	2.18	0.44
1:G:1049:LEU:HD11	1:G:1067:TYR:HB2	2.00	0.44
1:A:206:LYS:HB2	1:A:223:LEU:HA	2.00	0.44
1:A:1049:LEU:HD11	1:A:1067:TYR:HB2	2.00	0.44
3:C:96:ASN:HB2	3:C:101:ASP:H	1.82	0.44
1:E:715:PRO:HD3	1:G:894:LEU:HD13	2.00	0.44
1:E:1082:CYS:HB2	1:E:1126:CYS:HB3	1.73	0.44
1:G:206:LYS:HB2	1:G:223:LEU:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:PHE:HD1	1:A:203:ILE:HG12	1.83	0.44
2:D:63:SER:O	2:D:73:LEU:HD12	2.18	0.44
1:G:296:LEU:HB2	1:G:608:VAL:HG11	2.00	0.44
2:B:63:SER:O	2:B:73:LEU:HD12	2.18	0.44
1:E:206:LYS:HB2	1:E:223:LEU:HA	2.00	0.44
1:G:28:TYR:HB3	1:G:61:ASN:OD1	2.18	0.44
1:A:299:THR:HA	1:A:302:THR:HG22	1.99	0.43
1:G:299:THR:HA	1:G:302:THR:HG22	1.99	0.43
1:G:598:ILE:HG23	1:G:664:ILE:HG21	2.00	0.43
1:A:912:THR:O	1:A:915:VAL:HG22	2.18	0.43
2:D:89:GLN:HE21	2:D:96:TRP:HB3	1.82	0.43
1:G:194:PHE:HD1	1:G:203:ILE:HG12	1.83	0.43
1:A:135:PHE:HA	1:A:160:TYR:HA	2.00	0.43
2:D:47:LEU:HD23	2:D:73:LEU:HD11	2.01	0.43
1:E:194:PHE:HD1	1:E:203:ILE:HG12	1.83	0.43
1:E:296:LEU:HB2	1:E:608:VAL:HG11	2.00	0.43
1:G:661:GLU:O	1:G:695:TYR:OH	2.34	0.43
1:A:661:GLU:O	1:A:695:TYR:OH	2.34	0.43
1:E:28:TYR:HB3	1:E:61:ASN:OD1	2.18	0.43
1:E:676:THR:HA	1:E:690:GLN:HA	1.99	0.43
1:G:82:PRO:HG2	1:G:84:LEU:HD21	2.00	0.43
1:G:135:PHE:HA	1:G:160:TYR:HA	2.00	0.43
1:G:676:THR:HA	1:G:690:GLN:HA	1.99	0.43
1:A:598:ILE:HG23	1:A:664:ILE:HG21	2.00	0.43
3:C:47:TRP:HB3	2:D:98:PHE:CD1	2.53	0.43
2:H:47:LEU:HD23	2:H:73:LEU:HD11	2.01	0.43
1:A:676:THR:HA	1:A:690:GLN:HA	1.99	0.43
1:A:666:ILE:HD12	1:A:670:ILE:HG22	2.01	0.43
1:E:310:LYS:NZ	1:E:663:ASP:OD2	2.37	0.43
3:I:89:VAL:HB	3:I:108:MET:SD	2.59	0.43
1:G:951:VAL:O	1:G:955:ASN:ND2	2.47	0.43
2:H:63:SER:O	2:H:73:LEU:HD12	2.18	0.43
1:E:131:CYS:HA	1:E:166:CYS:HA	2.01	0.42
3:F:51:ILE:HG21	3:F:69:ILE:HD13	2.01	0.42
3:I:51:ILE:HG21	3:I:69:ILE:HD13	2.01	0.42
1:A:131:CYS:HA	1:A:166:CYS:HA	2.01	0.42
1:E:1007:TYR:O	1:E:1010:GLN:HG3	2.19	0.42
1:A:296:LEU:HB2	1:A:608:VAL:HG11	2.00	0.42
1:A:738:CYS:HB3	1:A:760:CYS:HB3	1.87	0.42
3:I:4:LEU:HB2	3:I:104:GLY:HA2	2.02	0.42
1:A:722:VAL:HG22	1:A:1065:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:869:MET:H	1:E:869:MET:HG2	1.72	0.42
1:E:666:ILE:HD12	1:E:670:ILE:HG22	2.01	0.42
1:E:980:ILE:HD13	1:E:992:GLN:HB3	2.02	0.42
1:G:242:LEU:HD23	1:G:243:ALA:N	2.35	0.42
1:G:1007:TYR:O	1:G:1010:GLN:HG3	2.19	0.42
1:G:1102:TRP:HB2	1:G:1135:ASN:ND2	2.35	0.42
1:A:904:TYR:OH	1:G:1094:VAL:HB	2.20	0.42
3:F:4:LEU:HB2	3:F:104:GLY:HA2	2.01	0.42
1:G:1080:ALA:O	1:G:1132:ILE:HG13	2.20	0.42
1:A:612:TYR:HE1	1:A:651:ILE:HD12	1.85	0.42
3:C:18:VAL:HG22	3:C:82(C):LEU:HD11	2.01	0.42
3:C:19:LYS:HZ1	3:C:79:TYR:CB	2.32	0.42
1:E:1102:TRP:HB2	1:E:1135:ASN:ND2	2.35	0.42
1:A:242:LEU:HD23	1:A:243:ALA:N	2.34	0.42
3:F:89:VAL:HB	3:F:108:MET:SD	2.59	0.42
1:G:722:VAL:HG22	1:G:1065:VAL:HG22	2.01	0.42
2:H:98:PHE:CD1	3:I:47:TRP:HB3	2.55	0.42
1:A:41:LYS:HB3	1:G:563:GLN:HA	2.02	0.42
1:E:81:ASN:OD1	1:E:81:ASN:N	2.53	0.42
1:G:1082:CYS:HB2	1:G:1126:CYS:HB3	1.73	0.42
1:A:906:PHE:HD2	1:A:916:LEU:HB2	1.85	0.42
1:A:951:VAL:O	1:A:955:ASN:ND2	2.47	0.42
1:A:1007:TYR:O	1:A:1010:GLN:HG3	2.19	0.42
1:A:1080:ALA:O	1:A:1132:ILE:HG13	2.20	0.42
2:B:47:LEU:HD23	2:B:73:LEU:HD11	2.01	0.42
3:C:89:VAL:HB	3:C:108:MET:SD	2.59	0.42
1:E:242:LEU:HD23	1:E:243:ALA:N	2.34	0.42
1:E:1080:ALA:O	1:E:1132:ILE:HG13	2.20	0.42
1:E:1126:CYS:HB2	1:E:1132:ILE:HG21	2.02	0.42
1:A:1102:TRP:HB2	1:A:1135:ASN:ND2	2.35	0.41
1:E:598:ILE:HG23	1:E:664:ILE:HG21	2.00	0.41
1:G:666:ILE:HD12	1:G:670:ILE:HG22	2.01	0.41
1:G:906:PHE:HD2	1:G:916:LEU:HB2	1.85	0.41
1:G:980:ILE:HD13	1:G:992:GLN:HB3	2.01	0.41
3:I:48:ILE:HA	3:I:63:PHE:CD2	2.55	0.41
1:E:611:LEU:HD22	1:E:666:ILE:HG23	2.02	0.41
3:F:18:VAL:HG22	3:F:82(C):LEU:HD11	2.01	0.41
2:H:47:LEU:HA	2:H:58:ILE:HG13	2.02	0.41
1:E:612:TYR:HE1	1:E:651:ILE:HD12	1.85	0.41
1:G:1126:CYS:HB2	1:G:1132:ILE:HG21	2.02	0.41
3:I:18:VAL:HG22	3:I:82(C):LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:712:ILE:HG22	1:G:896:ILE:HD12	2.03	0.41
1:E:1010:GLN:NE2	1:E:1011:GLN:HG2	2.36	0.41
1:A:980:ILE:HD13	1:A:992:GLN:HB3	2.02	0.41
1:G:869:MET:H	1:G:869:MET:HG2	1.72	0.41
2:B:27(A):SER:HA	2:B:69:THR:HG22	2.02	0.41
2:B:87:TYR:CE1	2:B:101:GLY:HA2	2.56	0.41
3:C:4:LEU:HB2	3:C:104:GLY:HA2	2.02	0.41
3:C:51:ILE:HG21	3:C:69:ILE:HD13	2.01	0.41
1:E:1039:ARG:NE	1:G:1031:GLU:OE2	2.39	0.41
1:A:914:ASN:ND2	1:G:1123:SER:OG	2.54	0.41
1:A:1138:TYR:CE1	1:A:1143:PRO:HG2	2.56	0.41
2:D:36:TYR:HH	2:D:98:PHE:HD2	1.66	0.41
1:E:906:PHE:HD2	1:E:916:LEU:HB2	1.85	0.41
1:G:131:CYS:HA	1:G:166:CYS:HA	2.01	0.41
1:G:612:TYR:HE1	1:G:651:ILE:HD12	1.85	0.41
2:H:87:TYR:CE1	2:H:101:GLY:HA2	2.56	0.41
1:A:611:LEU:HD22	1:A:666:ILE:HG23	2.02	0.41
1:E:722:VAL:HG22	1:E:1065:VAL:HG22	2.01	0.41
1:E:951:VAL:O	1:E:955:ASN:ND2	2.47	0.41
1:A:81:ASN:OD1	1:A:81:ASN:N	2.53	0.41
3:C:48:ILE:HA	3:C:63:PHE:CD2	2.55	0.41
3:C:103:TRP:CE2	2:D:43:ALA:HB3	2.55	0.41
2:D:87:TYR:CE1	2:D:101:GLY:HA2	2.56	0.41
1:E:1138:TYR:CE1	1:E:1143:PRO:HG2	2.56	0.41
3:F:48:ILE:HA	3:F:63:PHE:CD2	2.55	0.41
1:G:81:ASN:N	1:G:81:ASN:OD1	2.53	0.41
1:G:1010:GLN:NE2	1:G:1011:GLN:HG2	2.36	0.41
1:A:1126:CYS:HB2	1:A:1132:ILE:HG21	2.02	0.41
2:H:27(A):SER:HA	2:H:69:THR:HG22	2.02	0.41
1:A:1010:GLN:NE2	1:A:1011:GLN:HG2	2.36	0.40
1:E:661:GLU:O	1:E:695:TYR:OH	2.34	0.40
2:D:83:PHE:HA	2:D:104:VAL:O	2.21	0.40
2:D:47:LEU:HA	2:D:58:ILE:HG13	2.02	0.40
1:G:611:LEU:HD22	1:G:666:ILE:HG23	2.02	0.40
3:I:36:TRP:CZ3	3:I:90:TYR:HB3	2.56	0.40
2:H:83:PHE:HA	2:H:104:VAL:O	2.21	0.40
2:B:47:LEU:HA	2:B:58:ILE:HG13	2.02	0.40
2:B:83:PHE:HA	2:B:104:VAL:O	2.21	0.40
2:D:38:GLN:NE2	2:D:39:LYS:O	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	982/1281 (77%)	957 (98%)	25 (2%)	0	100	100
1	E	982/1281 (77%)	957 (98%)	25 (2%)	0	100	100
1	G	982/1281 (77%)	957 (98%)	25 (2%)	0	100	100
2	B	106/215 (49%)	98 (92%)	8 (8%)	0	100	100
2	D	106/215 (49%)	97 (92%)	9 (8%)	0	100	100
2	H	106/215 (49%)	98 (92%)	7 (7%)	1 (1%)	14	49
3	C	121/221 (55%)	113 (93%)	8 (7%)	0	100	100
3	F	121/221 (55%)	113 (93%)	8 (7%)	0	100	100
3	I	121/221 (55%)	113 (93%)	8 (7%)	0	100	100
All	All	3627/5151 (70%)	3503 (97%)	123 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	93	SER

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	631/1110 (57%)	631 (100%)	0	100	100
1	E	631/1110 (57%)	631 (100%)	0	100	100
1	G	631/1110 (57%)	631 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	90/185 (49%)	86 (96%)	4 (4%)	24	53
2	D	90/185 (49%)	88 (98%)	2 (2%)	47	70
2	H	90/185 (49%)	87 (97%)	3 (3%)	33	61
3	C	102/186 (55%)	101 (99%)	1 (1%)	73	84
3	F	102/186 (55%)	101 (99%)	1 (1%)	73	84
3	I	102/186 (55%)	101 (99%)	1 (1%)	73	84
All	All	2469/4443 (56%)	2457 (100%)	12 (0%)	85	93

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	24	ARG
2	B	90	GLN
2	B	93	SER
2	B	94	SER
3	C	12	LYS
2	D	24	ARG
2	D	90	GLN
3	F	12	LYS
2	H	24	ARG
2	H	90	GLN
2	H	93	SER
3	I	12	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	96	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

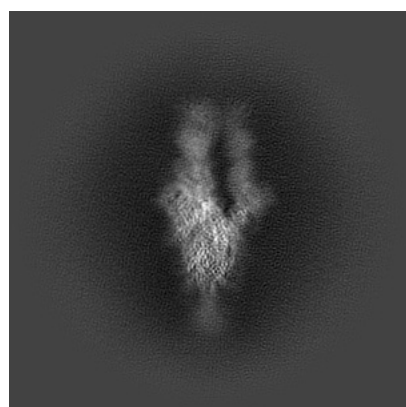
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13190. These allow visual inspection of the internal detail of the map and identification of artifacts.

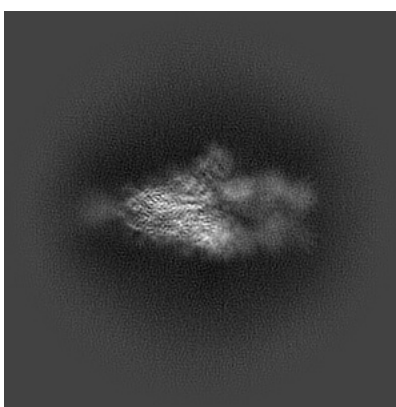
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

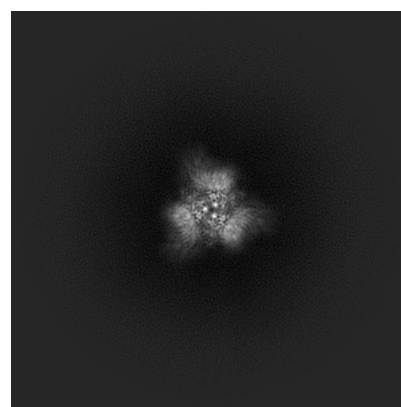
6.1.1 Primary map



X



Y



Z

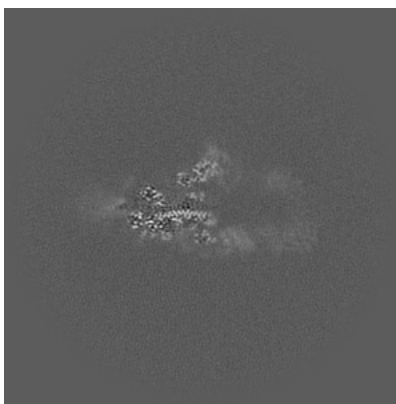
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

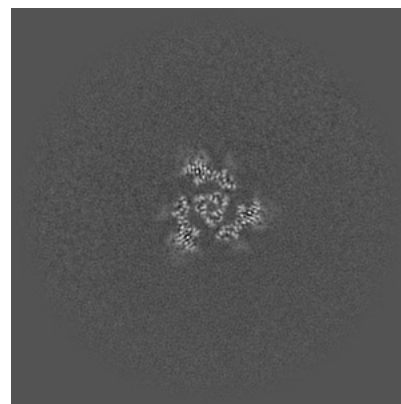
6.2.1 Primary map



X Index: 150



Y Index: 150

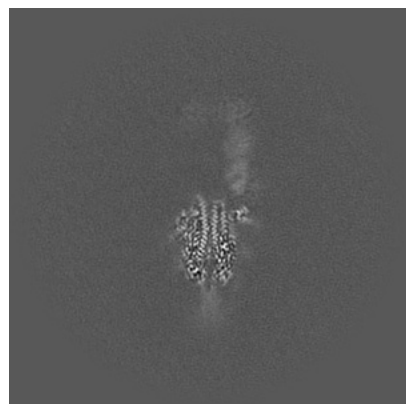


Z Index: 150

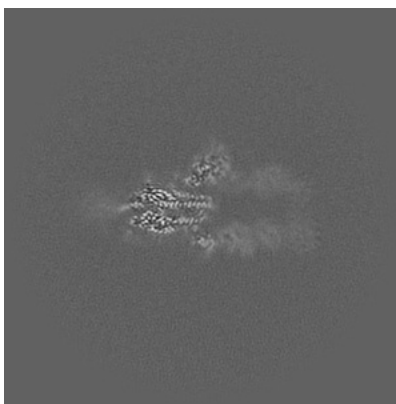
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

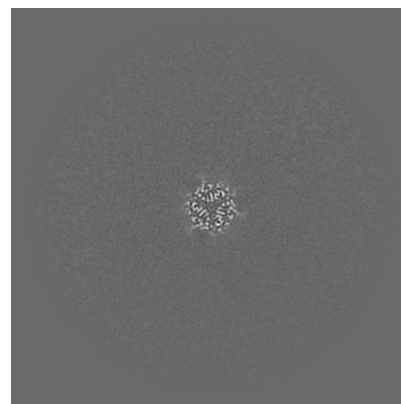
6.3.1 Primary map



X Index: 152



Y Index: 145

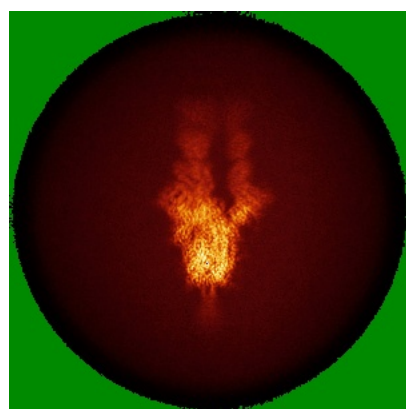


Z Index: 108

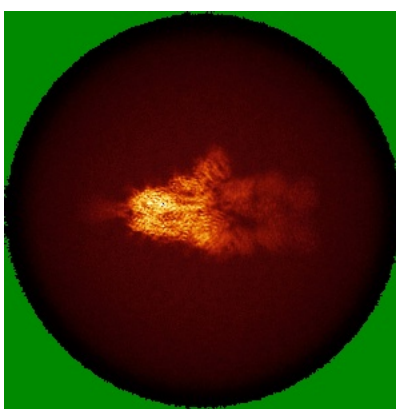
The images above show the largest variance slices of the map in three orthogonal directions.

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

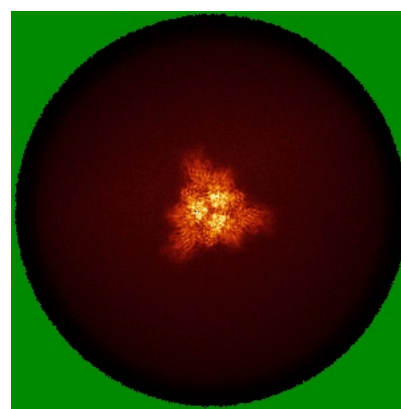
6.4.1 Primary map



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 3.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

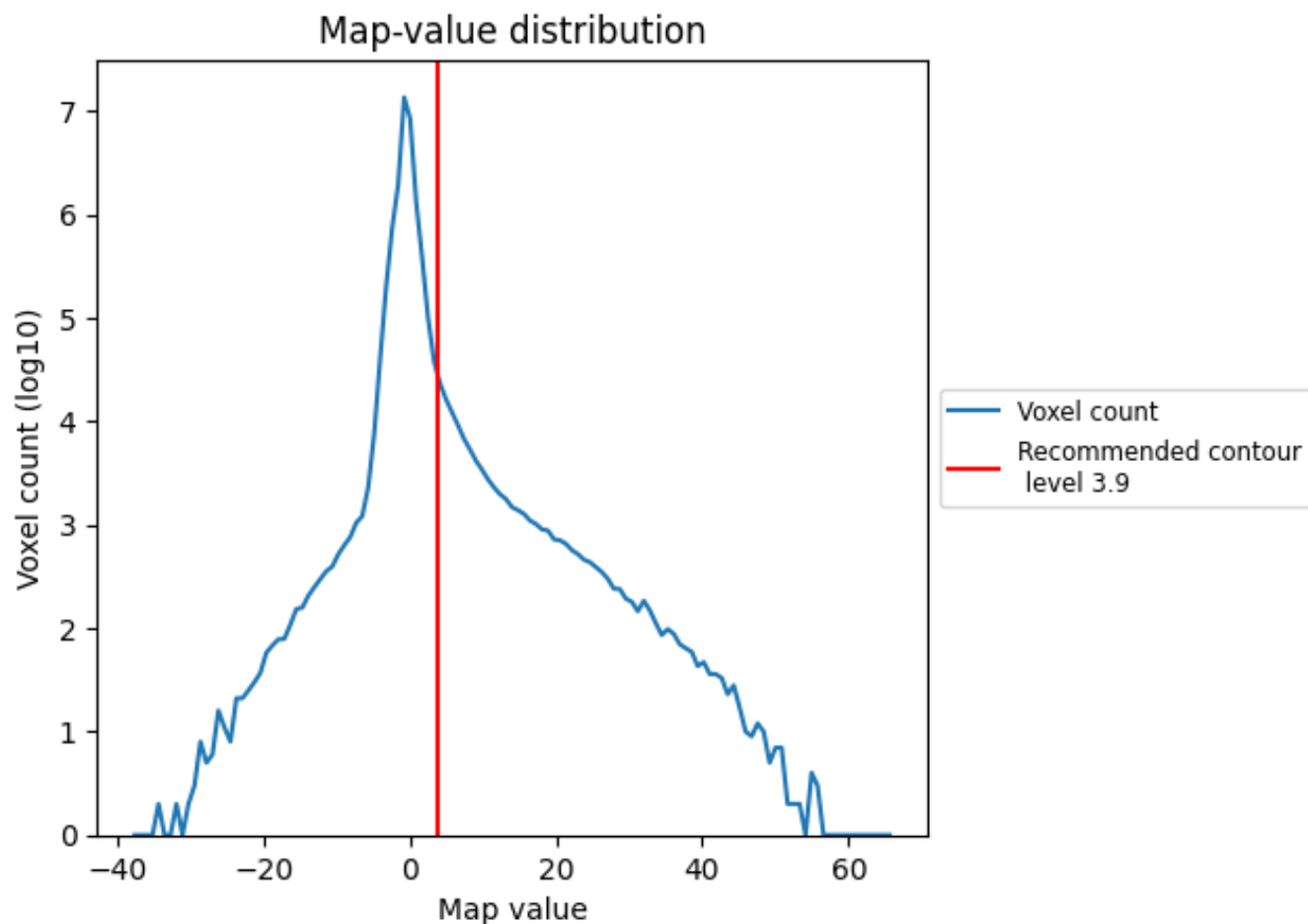
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

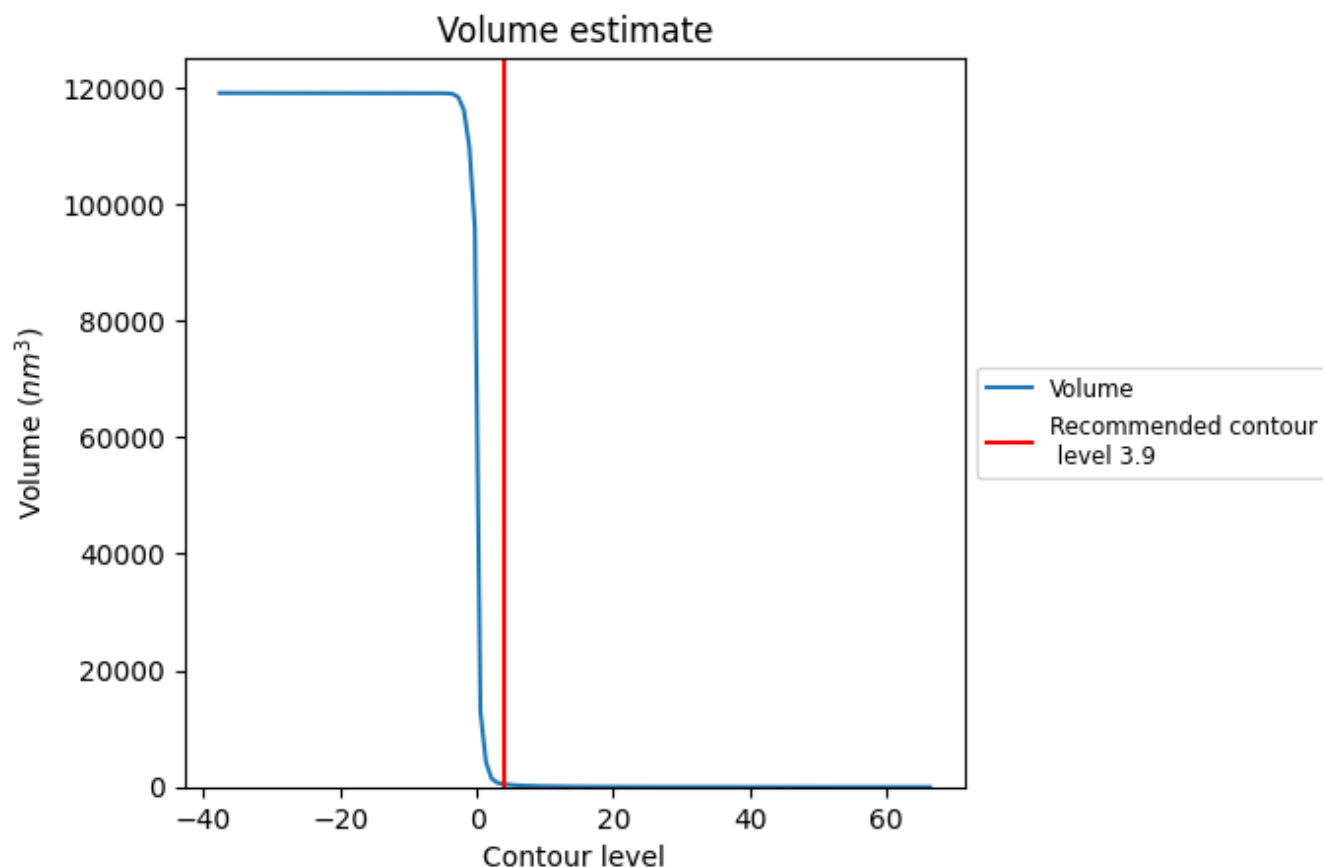
This section contains the results of statistical analysis of the map.

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.

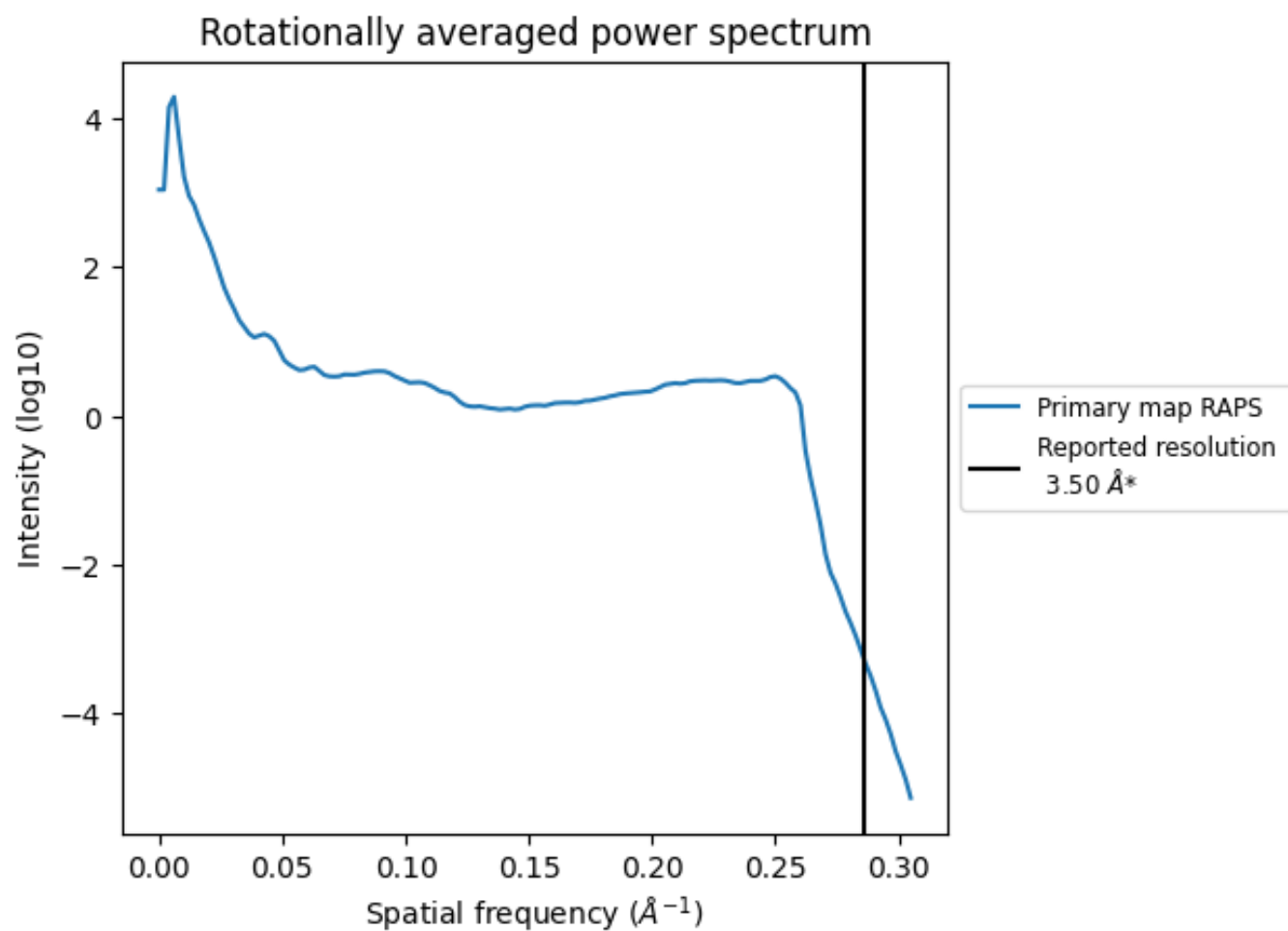
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 502 nm³; this corresponds to an approximate mass of 454 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 ⓘ

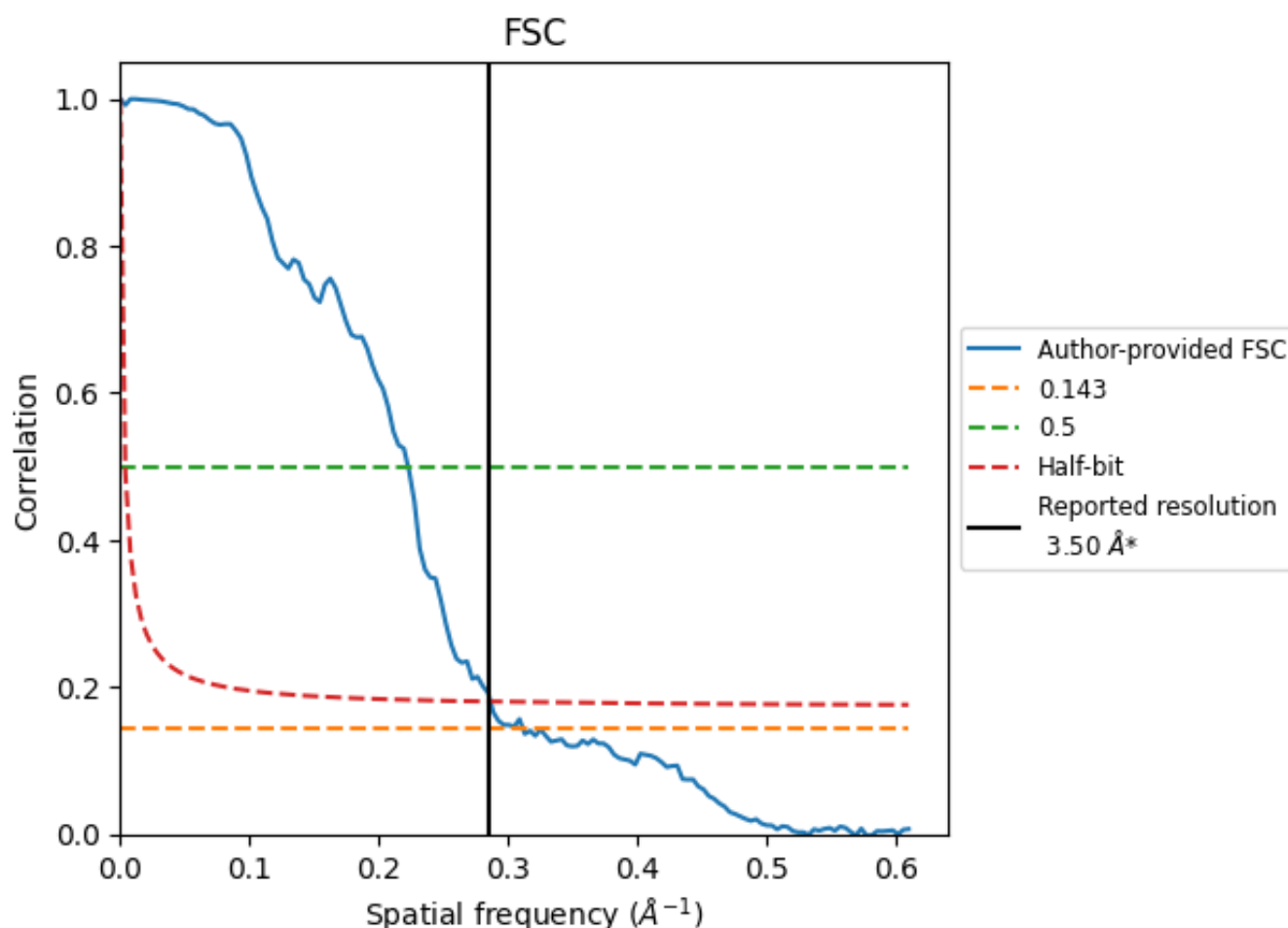


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

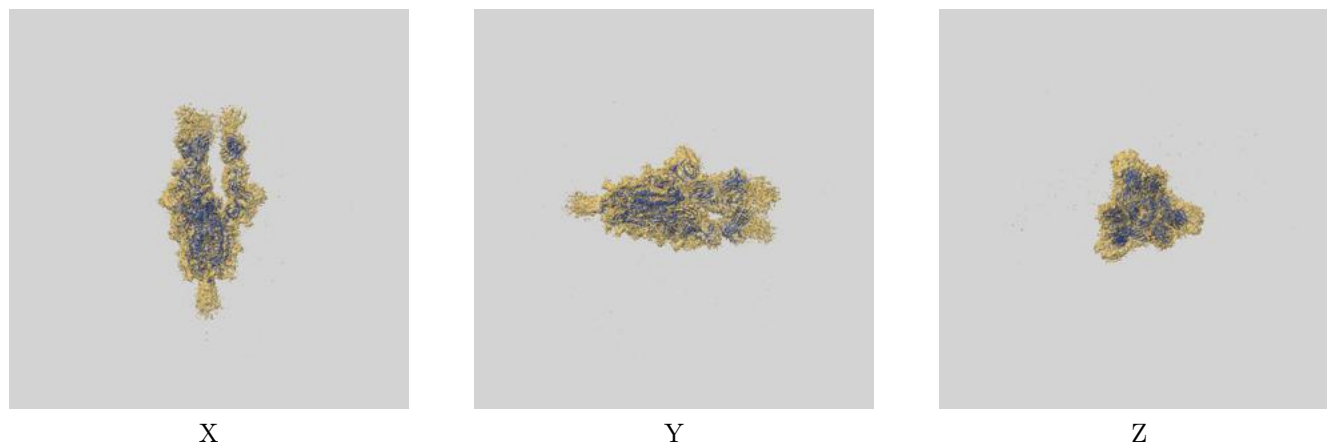
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.21	4.49	3.49
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

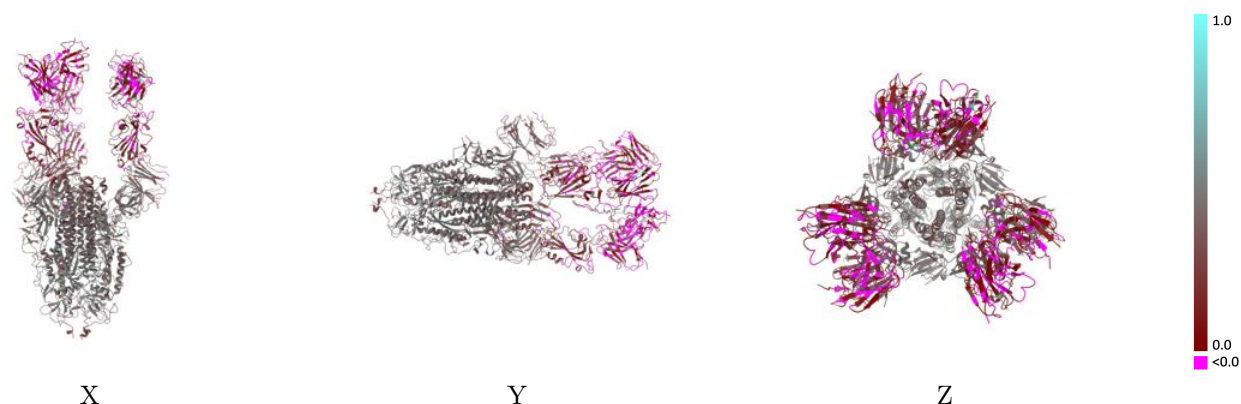
This section contains information regarding the fit between EMDB map EMD-13190 and PDB model 7P40. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



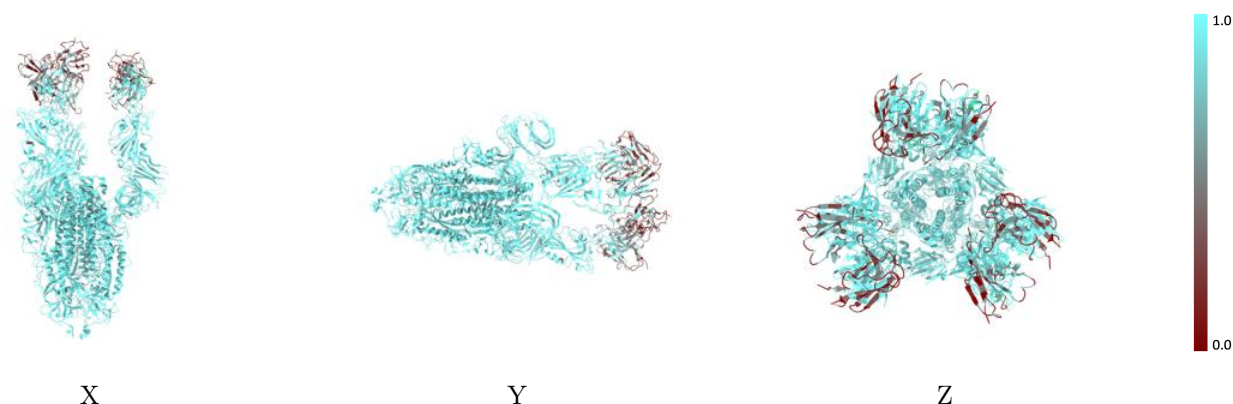
The images above show the 3D surface view of the map at the recommended contour level 3.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



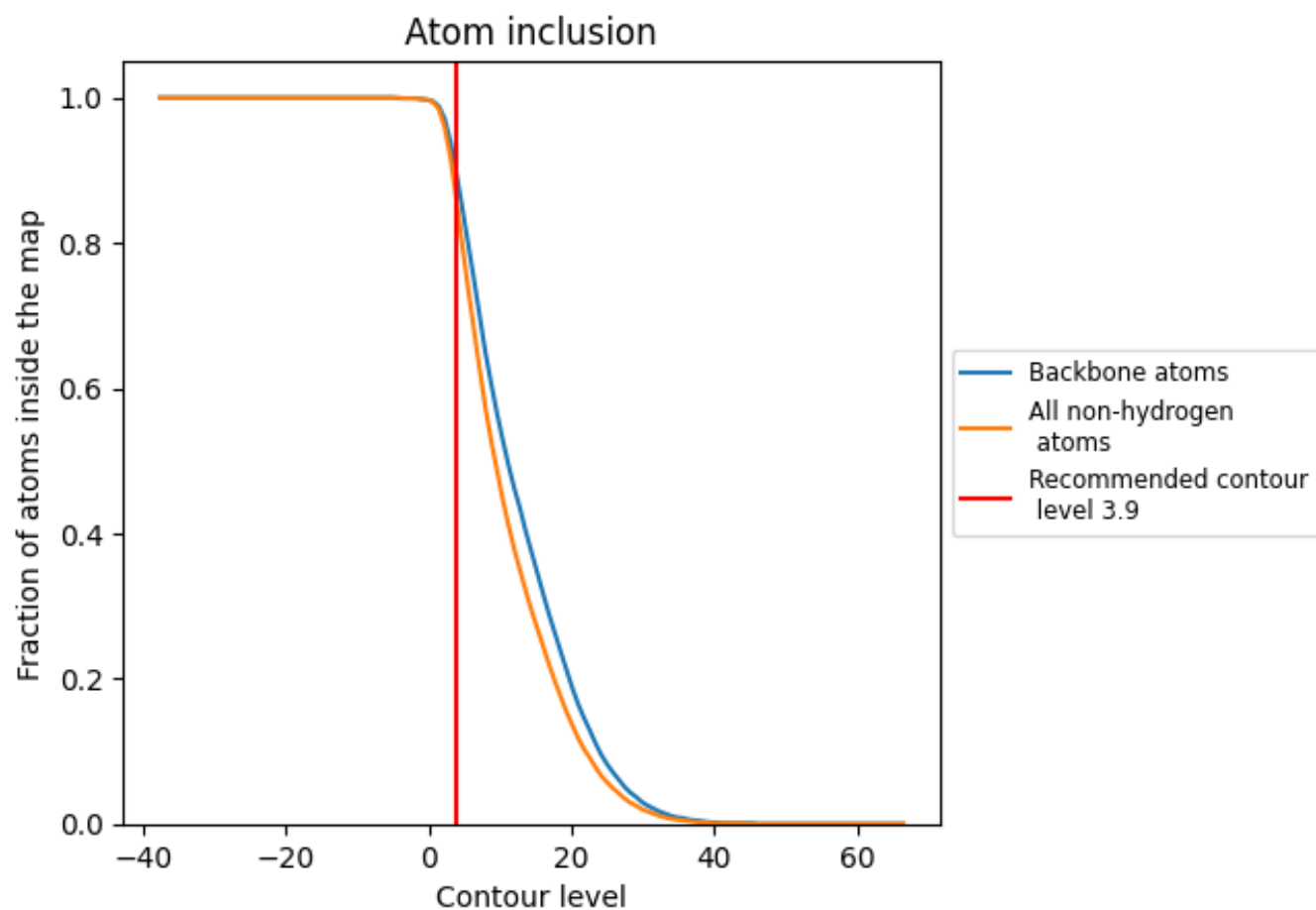
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (3.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8550	<div></div> 0.3080
A	<div></div> 0.9470	<div></div> 0.3720
B	<div></div> 0.3400	<div></div> 0.0210
C	<div></div> 0.5430	<div></div> 0.0260
D	<div></div> 0.3640	<div></div> 0.0490
E	<div></div> 0.9500	<div></div> 0.3740
F	<div></div> 0.5780	<div></div> 0.0580
G	<div></div> 0.9490	<div></div> 0.3730
H	<div></div> 0.3580	<div></div> 0.0330
I	<div></div> 0.6220	<div></div> 0.0960

1.0

0.0

<0.0