



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 06:54 AM UTC

PDB ID : 7WCP / pdb_00007wcp
EMDB ID : EMD-32427
Title : CryoEM structure of the SARS-CoV-2 S6P(B.1.617.2) in complex with SWC11 Fab
Authors : Du, S.; Xiao, J.Y.
Deposited on : 2021-12-20
Resolution : 3.01 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

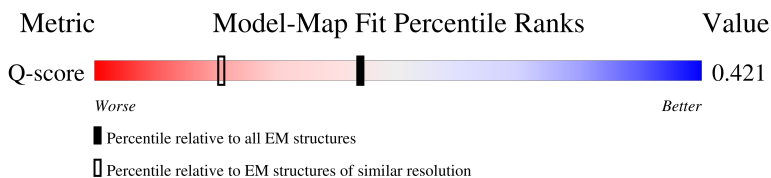
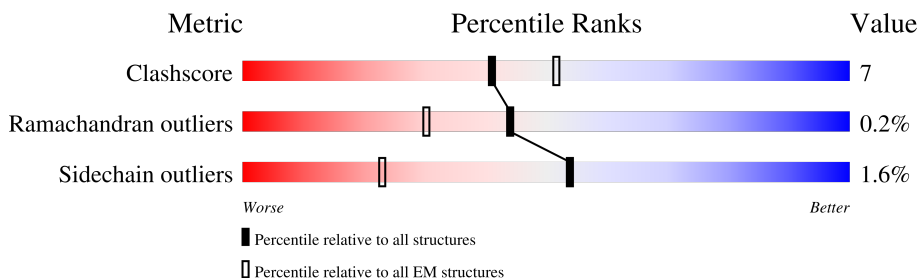
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.01 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13882 (2.51 - 3.51)

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	1286	 66% 11% 22%
1	B	1286	 66% 11% 23%
1	C	1286	 11% 64% 12% 22%
2	D	222	 11% 40% 14% 46%

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Mol	Chain	Length	Quality of chain
2	H	222	6%40%13%46%
2	M	222	52%40%14%46%
3	E	109	27%69%30%
3	L	109	8%67%32%
3	N	109	90%67%32%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28328 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 Surface glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1002	Total	C	N	O	S	0	0
			7736	4933	1295	1473	35		
1	B	991	Total	C	N	O	S	0	0
			7653	4881	1271	1466	35		
1	C	999	Total	C	N	O	S	0	0
			7683	4902	1276	1470	35		

There are 267 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP A0A8B1VBI1
A	683	SER	ARG	conflict	UNP A0A8B1VBI1
A	685	SER	ARG	conflict	UNP A0A8B1VBI1
A	817	PRO	PHE	conflict	UNP A0A8B1VBI1
A	892	PRO	ALA	conflict	UNP A0A8B1VBI1
A	899	PRO	ALA	conflict	UNP A0A8B1VBI1
A	942	PRO	ALA	conflict	UNP A0A8B1VBI1
A	986	PRO	LYS	conflict	UNP A0A8B1VBI1
A	987	PRO	VAL	conflict	UNP A0A8B1VBI1
A	1209	GLY	-	expression tag	UNP A0A8B1VBI1
A	1210	SER	-	expression tag	UNP A0A8B1VBI1
A	1211	GLY	-	expression tag	UNP A0A8B1VBI1
A	1212	TYR	-	expression tag	UNP A0A8B1VBI1
A	1213	ILE	-	expression tag	UNP A0A8B1VBI1
A	1214	PRO	-	expression tag	UNP A0A8B1VBI1
A	1215	GLU	-	expression tag	UNP A0A8B1VBI1
A	1216	ALA	-	expression tag	UNP A0A8B1VBI1
A	1217	PRO	-	expression tag	UNP A0A8B1VBI1
A	1218	ARG	-	expression tag	UNP A0A8B1VBI1
A	1219	ASP	-	expression tag	UNP A0A8B1VBI1
A	1220	GLY	-	expression tag	UNP A0A8B1VBI1
A	1221	GLN	-	expression tag	UNP A0A8B1VBI1
A	1222	ALA	-	expression tag	UNP A0A8B1VBI1
A	1223	TYR	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1224	VAL	-	expression tag	UNP A0A8B1VBI1
A	1225	ARG	-	expression tag	UNP A0A8B1VBI1
A	1226	LYS	-	expression tag	UNP A0A8B1VBI1
A	1227	ASP	-	expression tag	UNP A0A8B1VBI1
A	1228	GLY	-	expression tag	UNP A0A8B1VBI1
A	1229	GLU	-	expression tag	UNP A0A8B1VBI1
A	1230	TRP	-	expression tag	UNP A0A8B1VBI1
A	1231	VAL	-	expression tag	UNP A0A8B1VBI1
A	1232	LEU	-	expression tag	UNP A0A8B1VBI1
A	1233	LEU	-	expression tag	UNP A0A8B1VBI1
A	1234	SER	-	expression tag	UNP A0A8B1VBI1
A	1235	THR	-	expression tag	UNP A0A8B1VBI1
A	1236	PHE	-	expression tag	UNP A0A8B1VBI1
A	1237	LEU	-	expression tag	UNP A0A8B1VBI1
A	1238	GLY	-	expression tag	UNP A0A8B1VBI1
A	1239	ARG	-	expression tag	UNP A0A8B1VBI1
A	1240	SER	-	expression tag	UNP A0A8B1VBI1
A	1241	LEU	-	expression tag	UNP A0A8B1VBI1
A	1242	GLU	-	expression tag	UNP A0A8B1VBI1
A	1243	VAL	-	expression tag	UNP A0A8B1VBI1
A	1244	LEU	-	expression tag	UNP A0A8B1VBI1
A	1245	PHE	-	expression tag	UNP A0A8B1VBI1
A	1246	GLN	-	expression tag	UNP A0A8B1VBI1
A	1247	GLY	-	expression tag	UNP A0A8B1VBI1
A	1248	PRO	-	expression tag	UNP A0A8B1VBI1
A	1249	GLY	-	expression tag	UNP A0A8B1VBI1
A	1250	HIS	-	expression tag	UNP A0A8B1VBI1
A	1251	HIS	-	expression tag	UNP A0A8B1VBI1
A	1252	HIS	-	expression tag	UNP A0A8B1VBI1
A	1253	HIS	-	expression tag	UNP A0A8B1VBI1
A	1254	HIS	-	expression tag	UNP A0A8B1VBI1
A	1255	HIS	-	expression tag	UNP A0A8B1VBI1
A	1256	HIS	-	expression tag	UNP A0A8B1VBI1
A	1257	HIS	-	expression tag	UNP A0A8B1VBI1
A	1258	SER	-	expression tag	UNP A0A8B1VBI1
A	1259	ALA	-	expression tag	UNP A0A8B1VBI1
A	1260	TRP	-	expression tag	UNP A0A8B1VBI1
A	1261	SER	-	expression tag	UNP A0A8B1VBI1
A	1262	HIS	-	expression tag	UNP A0A8B1VBI1
A	1263	PRO	-	expression tag	UNP A0A8B1VBI1
A	1264	GLN	-	expression tag	UNP A0A8B1VBI1
A	1265	PHE	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1266	GLU	-	expression tag	UNP A0A8B1VBI1
A	1267	LYS	-	expression tag	UNP A0A8B1VBI1
A	1268	GLY	-	expression tag	UNP A0A8B1VBI1
A	1269	GLY	-	expression tag	UNP A0A8B1VBI1
A	1270	GLY	-	expression tag	UNP A0A8B1VBI1
A	1271	SER	-	expression tag	UNP A0A8B1VBI1
A	1272	GLY	-	expression tag	UNP A0A8B1VBI1
A	1273	GLY	-	expression tag	UNP A0A8B1VBI1
A	1274	GLY	-	expression tag	UNP A0A8B1VBI1
A	1275	GLY	-	expression tag	UNP A0A8B1VBI1
A	1276	SER	-	expression tag	UNP A0A8B1VBI1
A	1277	GLY	-	expression tag	UNP A0A8B1VBI1
A	1278	GLY	-	expression tag	UNP A0A8B1VBI1
A	1279	SER	-	expression tag	UNP A0A8B1VBI1
A	1280	ALA	-	expression tag	UNP A0A8B1VBI1
A	1281	TRP	-	expression tag	UNP A0A8B1VBI1
A	1282	SER	-	expression tag	UNP A0A8B1VBI1
A	1283	HIS	-	expression tag	UNP A0A8B1VBI1
A	1284	PRO	-	expression tag	UNP A0A8B1VBI1
A	1285	GLN	-	expression tag	UNP A0A8B1VBI1
A	1286	PHE	-	expression tag	UNP A0A8B1VBI1
A	1287	GLU	-	expression tag	UNP A0A8B1VBI1
A	1288	LYS	-	expression tag	UNP A0A8B1VBI1
B	682	GLY	ARG	conflict	UNP A0A8B1VBI1
B	683	SER	ARG	conflict	UNP A0A8B1VBI1
B	685	SER	ARG	conflict	UNP A0A8B1VBI1
B	817	PRO	PHE	conflict	UNP A0A8B1VBI1
B	892	PRO	ALA	conflict	UNP A0A8B1VBI1
B	899	PRO	ALA	conflict	UNP A0A8B1VBI1
B	942	PRO	ALA	conflict	UNP A0A8B1VBI1
B	986	PRO	LYS	conflict	UNP A0A8B1VBI1
B	987	PRO	VAL	conflict	UNP A0A8B1VBI1
B	1209	GLY	-	expression tag	UNP A0A8B1VBI1
B	1210	SER	-	expression tag	UNP A0A8B1VBI1
B	1211	GLY	-	expression tag	UNP A0A8B1VBI1
B	1212	TYR	-	expression tag	UNP A0A8B1VBI1
B	1213	ILE	-	expression tag	UNP A0A8B1VBI1
B	1214	PRO	-	expression tag	UNP A0A8B1VBI1
B	1215	GLU	-	expression tag	UNP A0A8B1VBI1
B	1216	ALA	-	expression tag	UNP A0A8B1VBI1
B	1217	PRO	-	expression tag	UNP A0A8B1VBI1
B	1218	ARG	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1219	ASP	-	expression tag	UNP A0A8B1VBI1
B	1220	GLY	-	expression tag	UNP A0A8B1VBI1
B	1221	GLN	-	expression tag	UNP A0A8B1VBI1
B	1222	ALA	-	expression tag	UNP A0A8B1VBI1
B	1223	TYR	-	expression tag	UNP A0A8B1VBI1
B	1224	VAL	-	expression tag	UNP A0A8B1VBI1
B	1225	ARG	-	expression tag	UNP A0A8B1VBI1
B	1226	LYS	-	expression tag	UNP A0A8B1VBI1
B	1227	ASP	-	expression tag	UNP A0A8B1VBI1
B	1228	GLY	-	expression tag	UNP A0A8B1VBI1
B	1229	GLU	-	expression tag	UNP A0A8B1VBI1
B	1230	TRP	-	expression tag	UNP A0A8B1VBI1
B	1231	VAL	-	expression tag	UNP A0A8B1VBI1
B	1232	LEU	-	expression tag	UNP A0A8B1VBI1
B	1233	LEU	-	expression tag	UNP A0A8B1VBI1
B	1234	SER	-	expression tag	UNP A0A8B1VBI1
B	1235	THR	-	expression tag	UNP A0A8B1VBI1
B	1236	PHE	-	expression tag	UNP A0A8B1VBI1
B	1237	LEU	-	expression tag	UNP A0A8B1VBI1
B	1238	GLY	-	expression tag	UNP A0A8B1VBI1
B	1239	ARG	-	expression tag	UNP A0A8B1VBI1
B	1240	SER	-	expression tag	UNP A0A8B1VBI1
B	1241	LEU	-	expression tag	UNP A0A8B1VBI1
B	1242	GLU	-	expression tag	UNP A0A8B1VBI1
B	1243	VAL	-	expression tag	UNP A0A8B1VBI1
B	1244	LEU	-	expression tag	UNP A0A8B1VBI1
B	1245	PHE	-	expression tag	UNP A0A8B1VBI1
B	1246	GLN	-	expression tag	UNP A0A8B1VBI1
B	1247	GLY	-	expression tag	UNP A0A8B1VBI1
B	1248	PRO	-	expression tag	UNP A0A8B1VBI1
B	1249	GLY	-	expression tag	UNP A0A8B1VBI1
B	1250	HIS	-	expression tag	UNP A0A8B1VBI1
B	1251	HIS	-	expression tag	UNP A0A8B1VBI1
B	1252	HIS	-	expression tag	UNP A0A8B1VBI1
B	1253	HIS	-	expression tag	UNP A0A8B1VBI1
B	1254	HIS	-	expression tag	UNP A0A8B1VBI1
B	1255	HIS	-	expression tag	UNP A0A8B1VBI1
B	1256	HIS	-	expression tag	UNP A0A8B1VBI1
B	1257	HIS	-	expression tag	UNP A0A8B1VBI1
B	1258	SER	-	expression tag	UNP A0A8B1VBI1
B	1259	ALA	-	expression tag	UNP A0A8B1VBI1
B	1260	TRP	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1261	SER	-	expression tag	UNP A0A8B1VBI1
B	1262	HIS	-	expression tag	UNP A0A8B1VBI1
B	1263	PRO	-	expression tag	UNP A0A8B1VBI1
B	1264	GLN	-	expression tag	UNP A0A8B1VBI1
B	1265	PHE	-	expression tag	UNP A0A8B1VBI1
B	1266	GLU	-	expression tag	UNP A0A8B1VBI1
B	1267	LYS	-	expression tag	UNP A0A8B1VBI1
B	1268	GLY	-	expression tag	UNP A0A8B1VBI1
B	1269	GLY	-	expression tag	UNP A0A8B1VBI1
B	1270	GLY	-	expression tag	UNP A0A8B1VBI1
B	1271	SER	-	expression tag	UNP A0A8B1VBI1
B	1272	GLY	-	expression tag	UNP A0A8B1VBI1
B	1273	GLY	-	expression tag	UNP A0A8B1VBI1
B	1274	GLY	-	expression tag	UNP A0A8B1VBI1
B	1275	GLY	-	expression tag	UNP A0A8B1VBI1
B	1276	SER	-	expression tag	UNP A0A8B1VBI1
B	1277	GLY	-	expression tag	UNP A0A8B1VBI1
B	1278	GLY	-	expression tag	UNP A0A8B1VBI1
B	1279	SER	-	expression tag	UNP A0A8B1VBI1
B	1280	ALA	-	expression tag	UNP A0A8B1VBI1
B	1281	TRP	-	expression tag	UNP A0A8B1VBI1
B	1282	SER	-	expression tag	UNP A0A8B1VBI1
B	1283	HIS	-	expression tag	UNP A0A8B1VBI1
B	1284	PRO	-	expression tag	UNP A0A8B1VBI1
B	1285	GLN	-	expression tag	UNP A0A8B1VBI1
B	1286	PHE	-	expression tag	UNP A0A8B1VBI1
B	1287	GLU	-	expression tag	UNP A0A8B1VBI1
B	1288	LYS	-	expression tag	UNP A0A8B1VBI1
C	682	GLY	ARG	conflict	UNP A0A8B1VBI1
C	683	SER	ARG	conflict	UNP A0A8B1VBI1
C	685	SER	ARG	conflict	UNP A0A8B1VBI1
C	817	PRO	PHE	conflict	UNP A0A8B1VBI1
C	892	PRO	ALA	conflict	UNP A0A8B1VBI1
C	899	PRO	ALA	conflict	UNP A0A8B1VBI1
C	942	PRO	ALA	conflict	UNP A0A8B1VBI1
C	986	PRO	LYS	conflict	UNP A0A8B1VBI1
C	987	PRO	VAL	conflict	UNP A0A8B1VBI1
C	1209	GLY	-	expression tag	UNP A0A8B1VBI1
C	1210	SER	-	expression tag	UNP A0A8B1VBI1
C	1211	GLY	-	expression tag	UNP A0A8B1VBI1
C	1212	TYR	-	expression tag	UNP A0A8B1VBI1
C	1213	ILE	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1214	PRO	-	expression tag	UNP A0A8B1VBI1
C	1215	GLU	-	expression tag	UNP A0A8B1VBI1
C	1216	ALA	-	expression tag	UNP A0A8B1VBI1
C	1217	PRO	-	expression tag	UNP A0A8B1VBI1
C	1218	ARG	-	expression tag	UNP A0A8B1VBI1
C	1219	ASP	-	expression tag	UNP A0A8B1VBI1
C	1220	GLY	-	expression tag	UNP A0A8B1VBI1
C	1221	GLN	-	expression tag	UNP A0A8B1VBI1
C	1222	ALA	-	expression tag	UNP A0A8B1VBI1
C	1223	TYR	-	expression tag	UNP A0A8B1VBI1
C	1224	VAL	-	expression tag	UNP A0A8B1VBI1
C	1225	ARG	-	expression tag	UNP A0A8B1VBI1
C	1226	LYS	-	expression tag	UNP A0A8B1VBI1
C	1227	ASP	-	expression tag	UNP A0A8B1VBI1
C	1228	GLY	-	expression tag	UNP A0A8B1VBI1
C	1229	GLU	-	expression tag	UNP A0A8B1VBI1
C	1230	TRP	-	expression tag	UNP A0A8B1VBI1
C	1231	VAL	-	expression tag	UNP A0A8B1VBI1
C	1232	LEU	-	expression tag	UNP A0A8B1VBI1
C	1233	LEU	-	expression tag	UNP A0A8B1VBI1
C	1234	SER	-	expression tag	UNP A0A8B1VBI1
C	1235	THR	-	expression tag	UNP A0A8B1VBI1
C	1236	PHE	-	expression tag	UNP A0A8B1VBI1
C	1237	LEU	-	expression tag	UNP A0A8B1VBI1
C	1238	GLY	-	expression tag	UNP A0A8B1VBI1
C	1239	ARG	-	expression tag	UNP A0A8B1VBI1
C	1240	SER	-	expression tag	UNP A0A8B1VBI1
C	1241	LEU	-	expression tag	UNP A0A8B1VBI1
C	1242	GLU	-	expression tag	UNP A0A8B1VBI1
C	1243	VAL	-	expression tag	UNP A0A8B1VBI1
C	1244	LEU	-	expression tag	UNP A0A8B1VBI1
C	1245	PHE	-	expression tag	UNP A0A8B1VBI1
C	1246	GLN	-	expression tag	UNP A0A8B1VBI1
C	1247	GLY	-	expression tag	UNP A0A8B1VBI1
C	1248	PRO	-	expression tag	UNP A0A8B1VBI1
C	1249	GLY	-	expression tag	UNP A0A8B1VBI1
C	1250	HIS	-	expression tag	UNP A0A8B1VBI1
C	1251	HIS	-	expression tag	UNP A0A8B1VBI1
C	1252	HIS	-	expression tag	UNP A0A8B1VBI1
C	1253	HIS	-	expression tag	UNP A0A8B1VBI1
C	1254	HIS	-	expression tag	UNP A0A8B1VBI1
C	1255	HIS	-	expression tag	UNP A0A8B1VBI1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1256	HIS	-	expression tag	UNP A0A8B1VBI1
C	1257	HIS	-	expression tag	UNP A0A8B1VBI1
C	1258	SER	-	expression tag	UNP A0A8B1VBI1
C	1259	ALA	-	expression tag	UNP A0A8B1VBI1
C	1260	TRP	-	expression tag	UNP A0A8B1VBI1
C	1261	SER	-	expression tag	UNP A0A8B1VBI1
C	1262	HIS	-	expression tag	UNP A0A8B1VBI1
C	1263	PRO	-	expression tag	UNP A0A8B1VBI1
C	1264	GLN	-	expression tag	UNP A0A8B1VBI1
C	1265	PHE	-	expression tag	UNP A0A8B1VBI1
C	1266	GLU	-	expression tag	UNP A0A8B1VBI1
C	1267	LYS	-	expression tag	UNP A0A8B1VBI1
C	1268	GLY	-	expression tag	UNP A0A8B1VBI1
C	1269	GLY	-	expression tag	UNP A0A8B1VBI1
C	1270	GLY	-	expression tag	UNP A0A8B1VBI1
C	1271	SER	-	expression tag	UNP A0A8B1VBI1
C	1272	GLY	-	expression tag	UNP A0A8B1VBI1
C	1273	GLY	-	expression tag	UNP A0A8B1VBI1
C	1274	GLY	-	expression tag	UNP A0A8B1VBI1
C	1275	GLY	-	expression tag	UNP A0A8B1VBI1
C	1276	SER	-	expression tag	UNP A0A8B1VBI1
C	1277	GLY	-	expression tag	UNP A0A8B1VBI1
C	1278	GLY	-	expression tag	UNP A0A8B1VBI1
C	1279	SER	-	expression tag	UNP A0A8B1VBI1
C	1280	ALA	-	expression tag	UNP A0A8B1VBI1
C	1281	TRP	-	expression tag	UNP A0A8B1VBI1
C	1282	SER	-	expression tag	UNP A0A8B1VBI1
C	1283	HIS	-	expression tag	UNP A0A8B1VBI1
C	1284	PRO	-	expression tag	UNP A0A8B1VBI1
C	1285	GLN	-	expression tag	UNP A0A8B1VBI1
C	1286	PHE	-	expression tag	UNP A0A8B1VBI1
C	1287	GLU	-	expression tag	UNP A0A8B1VBI1
C	1288	LYS	-	expression tag	UNP A0A8B1VBI1

- Molecule 2 is a protein called SWC11H.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	119	Total 926	C 587	N 153	O 182	S 4	0	0
2	H	119	Total 926	C 587	N 153	O 182	S 4	0	0
2	M	119	Total 926	C 587	N 153	O 182	S 4	0	0

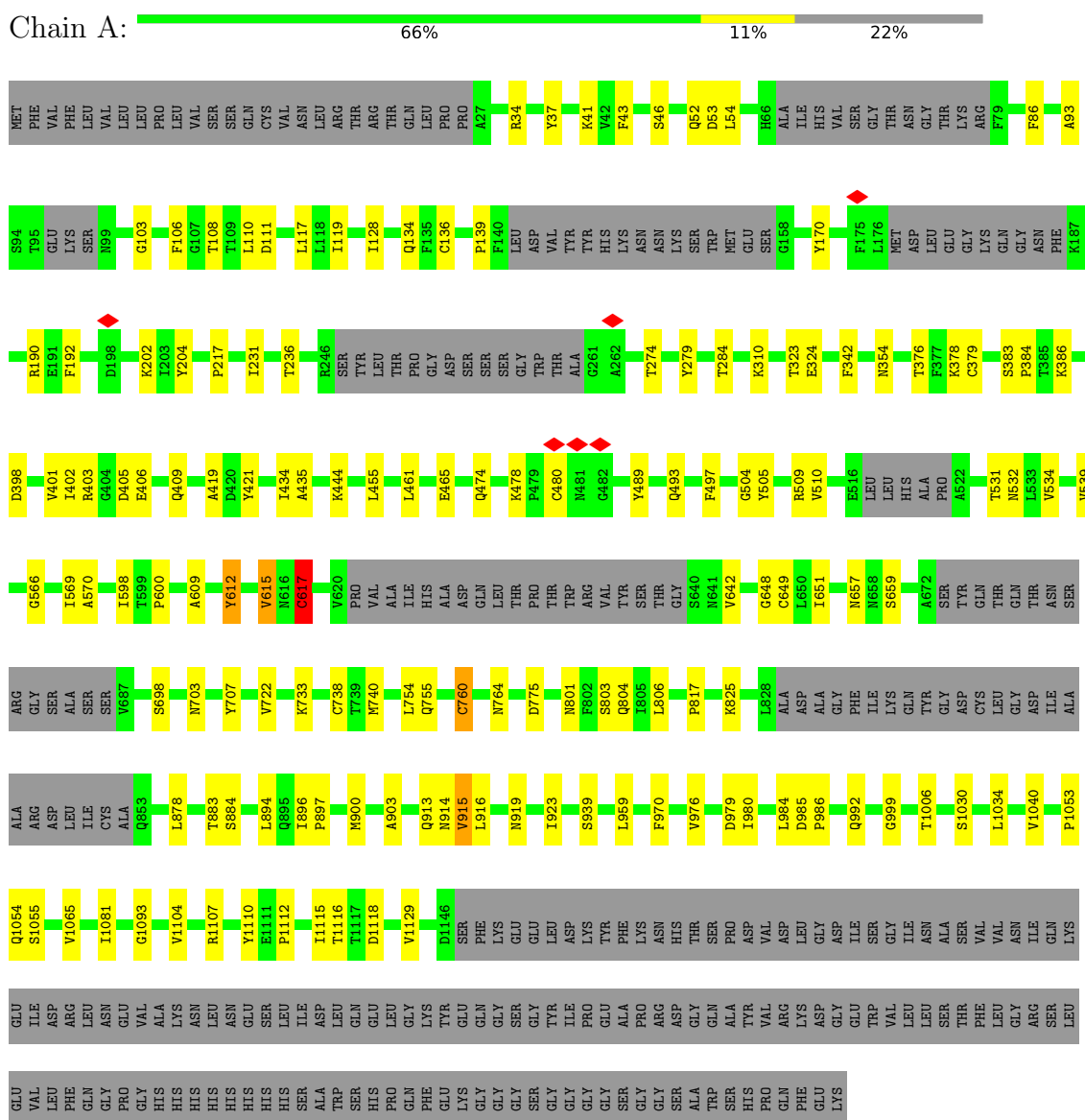
- Molecule 3 is a protein called SWC11L.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	109	Total	C	N	O	S	0	0
			826	510	148	165	3		
3	L	109	Total	C	N	O	S	0	0
			826	510	148	165	3		
3	N	109	Total	C	N	O	S	0	0
			826	510	148	165	3		

3 Residue-property plots

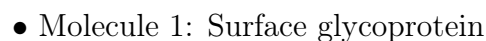
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



- Molecule 1: Surface glycoprotein

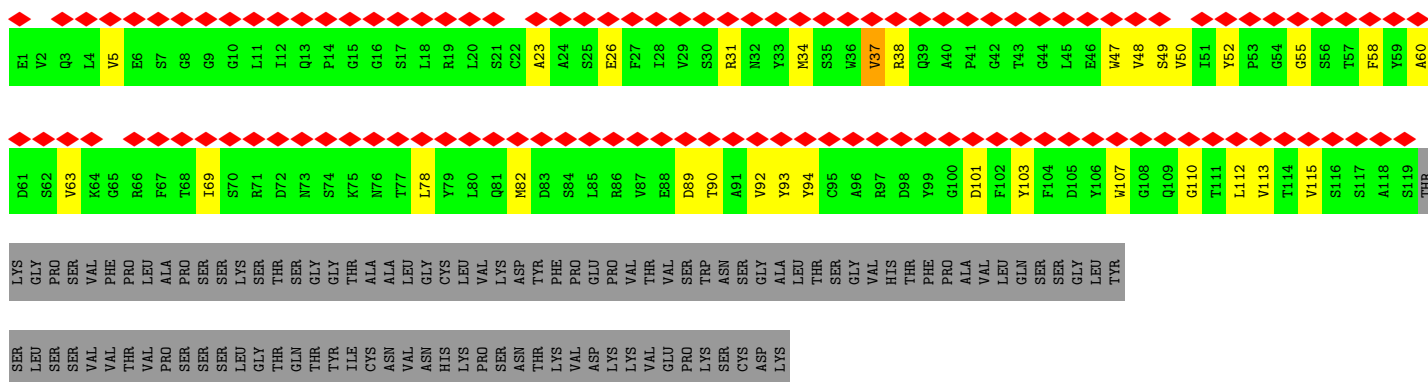
Category	Percentage
Very good	66%
Good	11%
Not good	23%



Frequency	Percentage
Daily	11%
Often	64%
Sometimes	12%
Never	22%



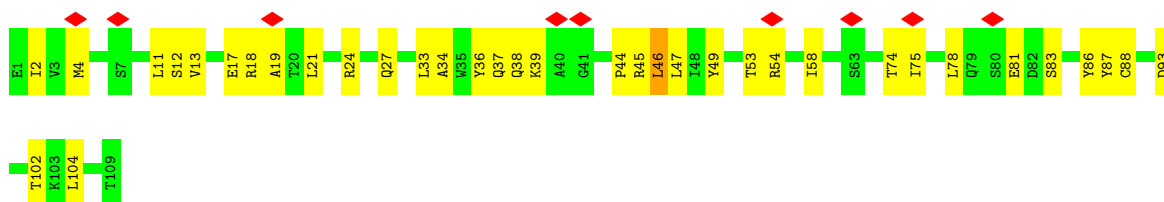
- Molecule 2: SWC11H



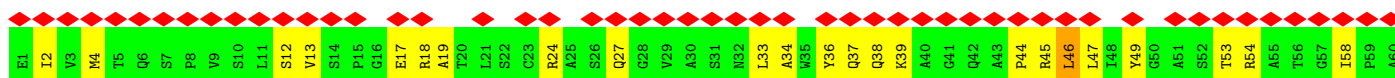
- Molecule 3: SWC11L



- Molecule 3: SWC11L



- Molecule 3: SWC11L



R61	F62	S63	G64	S65	G66	T69	E70	F71	T72	L73	T74	I75	S76	T77	L78	Q79	S80	E81	D82	S83	A84	V85	Y86	Y87	C88	Q89	Q90	Y91	N92	D93	R94	P95	R96	T97	F98	G99	Q100	G101	T102	K103	L104	E105	I106	K107	R108	T109
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	398316	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.462	Depositor
Minimum map value	-1.756	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.072	Depositor
Recommended contour level	0.26	Depositor
Map size (Å)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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	0.65	4/7908 (0.1%)	0.72	9/10767 (0.1%)
1	B	0.65	0/7822	0.72	7/10648 (0.1%)
1	C	0.77	21/7855 (0.3%)	0.81	25/10702 (0.2%)
2	D	0.27	0/948	0.67	0/1287
2	H	0.26	0/948	0.67	0/1287
2	M	0.26	0/948	0.67	0/1287
3	E	0.30	0/840	0.63	0/1136
3	L	0.30	0/840	0.63	0/1136
3	N	0.30	0/840	0.63	0/1136
All	All	0.64	25/28949 (0.1%)	0.73	41/39386 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	5
1	C	0	5
All	All	0	14

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	616	ASN	C-O	-9.29	1.12	1.23
1	C	1072	GLU	C-O	-8.95	1.11	1.23
1	C	1076	THR	C-O	-8.85	1.12	1.24
1	A	615	VAL	C-O	-8.09	1.13	1.24
1	C	1072	GLU	CA-C	-7.68	1.42	1.53
1	C	1076	THR	CA-C	-7.55	1.43	1.52
1	C	1075	PHE	C-O	-7.37	1.13	1.24
1	C	655	HIS	C-O	-7.24	1.15	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1073	LYS	C-O	-7.22	1.14	1.23
1	C	613	GLN	CA-C	-7.15	1.43	1.52
1	C	613	GLN	C-O	-6.70	1.16	1.24
1	C	1072	GLU	CA-CB	-6.48	1.42	1.53
1	C	602	THR	CA-C	-6.22	1.44	1.52
1	C	617	CYS	C-O	-6.01	1.16	1.24
1	C	604	THR	CA-C	-5.95	1.44	1.52
1	C	334	ASN	CA-C	-5.95	1.46	1.53
1	C	615	VAL	C-O	-5.92	1.17	1.24
1	A	615	VAL	N-CA	-5.79	1.39	1.46
1	C	614	GLY	C-O	-5.78	1.16	1.23
1	C	613	GLN	CA-CB	-5.72	1.45	1.53
1	A	914	ASN	CA-C	-5.60	1.45	1.52
1	C	606	ASN	CA-C	-5.56	1.45	1.52
1	A	1055	SER	C-N	-5.50	1.25	1.33
1	C	606	ASN	C-O	-5.23	1.16	1.24
1	C	655	HIS	CA-C	-5.04	1.46	1.52

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	329	PHE	C-N-CD	-14.69	64.78	125.00
1	C	657	ASN	CB-CA-C	-12.44	89.04	109.56
1	C	329	PHE	CA-C-N	10.96	133.54	119.84
1	C	329	PHE	C-N-CA	10.96	133.54	119.84
1	A	915	VAL	N-CA-C	-8.55	104.41	112.96
1	C	334	ASN	CA-C-N	-7.96	109.57	120.87
1	C	334	ASN	C-N-CA	-7.96	109.57	120.87
1	C	613	GLN	N-CA-C	7.84	120.44	109.15
1	C	1072	GLU	CB-CA-C	-7.05	97.18	110.51
1	A	738	CYS	CA-CB-SG	6.74	129.91	114.40
1	B	709	ASN	CA-C-N	6.66	132.33	122.74
1	B	709	ASN	C-N-CA	6.66	132.33	122.74
1	A	570	ALA	N-CA-C	-6.47	104.58	114.16
1	C	330	PRO	N-CA-C	6.44	125.73	112.47
1	A	617	CYS	N-CA-C	6.42	124.47	110.80
1	A	760	CYS	CA-CB-SG	-6.24	100.05	114.40
1	A	617	CYS	CA-CB-SG	-6.13	100.29	114.40
1	C	333	THR	N-CA-C	5.97	122.02	114.31
1	C	41	LYS	CA-CB-CG	5.95	126.01	114.10
1	C	749	CYS	CA-CB-SG	5.70	127.51	114.40
1	C	617	CYS	CA-C-N	5.57	131.55	121.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	617	CYS	C-N-CA	5.57	131.55	121.92
1	C	663	ASP	N-CA-C	-5.54	99.00	110.80
1	B	812	PRO	CA-N-CD	-5.49	104.31	112.00
1	B	760	CYS	CA-CB-SG	-5.27	102.28	114.40
1	C	330	PRO	CA-C-N	5.24	131.56	121.54
1	C	330	PRO	C-N-CA	5.24	131.56	121.54
1	B	1084	ASP	N-CA-C	-5.22	99.69	110.80
1	A	1081	ILE	CA-C-N	-5.21	115.81	123.00
1	A	1081	ILE	C-N-CA	-5.21	115.81	123.00
1	C	1074	ASN	N-CA-C	5.17	116.95	108.52
1	C	215	ASP	CA-C-N	5.16	128.78	121.61
1	C	215	ASP	C-N-CA	5.16	128.78	121.61
1	B	803	SER	N-CA-C	-5.15	107.17	113.50
1	B	710	ASN	CA-CB-CG	5.12	117.72	112.60
1	C	1083	HIS	CA-C-N	5.09	131.26	121.54
1	C	1083	HIS	C-N-CA	5.09	131.26	121.54
1	C	1075	PHE	CB-CA-C	-5.07	105.21	113.37
1	C	334	ASN	N-CA-CB	5.06	118.23	110.60
1	A	738	CYS	CB-CA-C	-5.04	102.94	110.90
1	C	645	THR	CB-CA-C	-5.03	99.89	109.66

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	LEU	Peptide
1	A	612	TYR	Peptide
1	A	657	ASN	Peptide
1	A	86	PHE	Peptide
1	B	1084	ASP	Peptide
1	B	31	SER	Peptide
1	B	590	CYS	Peptide
1	B	86	PHE	Peptide
1	B	986	PRO	Peptide
1	C	570	ALA	Peptide
1	C	749	CYS	Peptide
1	C	86	PHE	Peptide
1	C	940	SER	Peptide
1	C	986	PRO	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7736	0	7499	92	0
1	B	7653	0	7423	83	0
1	C	7683	0	7409	139	0
2	D	926	0	878	15	0
2	H	926	0	878	15	0
2	M	926	0	878	16	0
3	E	826	0	816	16	0
3	L	826	0	816	18	0
3	N	826	0	816	19	0
All	All	28328	0	27413	382	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 (382) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:332:ILE:CD1	1:C:527:PRO:HA	1.11	1.52
1:C:332:ILE:CD1	1:C:527:PRO:CA	2.00	1.37
1:C:332:ILE:HD12	1:C:527:PRO:CA	1.57	1.27
1:C:330:PRO:HD3	1:C:580:GLN:HG2	1.20	1.15
1:C:332:ILE:HD13	1:C:527:PRO:HA	1.31	1.09
1:C:330:PRO:CD	1:C:580:GLN:HG2	1.58	1.08
1:C:643:PHE:CZ	1:C:655:HIS:CE1	2.43	1.07
1:C:332:ILE:HD11	1:C:527:PRO:HA	1.32	1.03
1:C:332:ILE:HD11	1:C:527:PRO:C	1.85	1.01
1:C:332:ILE:HD11	1:C:528:LYS:N	1.76	1.00
1:A:617:CYS:HA	1:A:649:CYS:SG	2.05	0.97
1:C:334:ASN:OD1	1:C:361:CYS:CB	2.14	0.96
1:C:332:ILE:HD12	1:C:527:PRO:HA	0.98	0.95
1:C:332:ILE:HD12	1:C:527:PRO:CB	1.99	0.91
1:C:334:ASN:OD1	1:C:361:CYS:HA	1.73	0.89
1:C:334:ASN:OD1	1:C:361:CYS:HB3	1.73	0.86
1:C:643:PHE:CZ	1:C:655:HIS:ND1	2.44	0.85
1:C:330:PRO:CD	1:C:580:GLN:CG	2.41	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:PRO:HD3	1:C:580:GLN:CG	2.07	0.81
1:C:334:ASN:OD1	1:C:361:CYS:CA	2.31	0.79
1:C:332:ILE:CD1	1:C:528:LYS:N	2.50	0.74
1:C:296:LEU:HD21	1:C:606:ASN:HD22	1.55	0.71
1:C:643:PHE:CE2	1:C:655:HIS:ND1	2.59	0.71
3:L:36:TYR:HB2	3:L:87:TYR:HB2	1.73	0.70
1:C:332:ILE:HG23	1:C:362:VAL:HG11	1.74	0.70
3:E:36:TYR:HB2	3:E:87:TYR:HB2	1.73	0.69
3:N:36:TYR:HB2	3:N:87:TYR:HB2	1.73	0.69
1:C:328:ARG:HD2	1:C:531:THR:H	1.59	0.68
1:A:612:TYR:O	1:A:648:GLY:HA3	1.93	0.67
1:C:821:LEU:HD11	1:C:939:SER:HB2	1.78	0.66
1:C:643:PHE:CE2	1:C:655:HIS:CE1	2.84	0.66
1:C:327:VAL:HA	1:C:542:ASN:HB3	1.75	0.66
1:B:555:SER:HB2	1:B:586:ASP:HB2	1.78	0.65
1:C:334:ASN:O	1:C:362:VAL:N	2.27	0.65
2:M:90:THR:HG22	2:M:115:VAL:H	1.61	0.65
1:A:617:CYS:HA	1:A:649:CYS:HG	1.61	0.65
2:M:37:VAL:HG12	2:M:94:TYR:HB2	1.79	0.65
1:C:296:LEU:CD2	1:C:606:ASN:HD22	2.09	0.64
2:D:37:VAL:HG12	2:D:94:TYR:HB2	1.79	0.64
2:D:90:THR:HG22	2:D:115:VAL:H	1.61	0.64
1:C:332:ILE:CD1	1:C:527:PRO:C	2.54	0.64
1:C:64:TRP:HE1	1:C:264:ALA:HB1	1.63	0.63
2:H:37:VAL:HG12	2:H:94:TYR:HB2	1.79	0.63
2:H:90:THR:HG22	2:H:115:VAL:H	1.61	0.63
1:A:760:CYS:O	1:A:764:ASN:ND2	2.33	0.62
1:B:1030:SER:HA	1:B:1034:LEU:HD12	1.81	0.62
1:C:724:THR:HB	1:C:934:ILE:HD11	1.81	0.62
1:C:334:ASN:CG	1:C:361:CYS:HA	2.25	0.62
1:C:332:ILE:HD11	1:C:527:PRO:CA	1.92	0.61
1:A:1006:THR:OG1	1:B:1005:GLN:NE2	2.34	0.61
1:A:383:SER:HB3	1:A:386:LYS:HG2	1.83	0.61
1:C:1053:PRO:O	1:C:1054:GLN:NE2	2.34	0.60
3:L:86:TYR:HB2	3:L:102:THR:HB	1.84	0.60
1:A:659:SER:HB3	1:A:698:SER:HB2	1.83	0.60
1:B:326:ILE:O	1:B:531:THR:OG1	2.19	0.60
1:C:332:ILE:CD1	1:C:528:LYS:H	2.14	0.60
1:C:1102:TRP:HB2	1:C:1135:ASN:HD22	1.65	0.60
1:B:811:LYS:NZ	1:B:812:PRO:O	2.31	0.60
1:B:1028:LYS:NZ	1:B:1042:PHE:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:SER:HA	1:B:369:TYR:HD2	1.67	0.59
3:N:18:ARG:HA	3:N:75:ILE:O	2.02	0.59
1:C:916:LEU:HD12	1:C:923:ILE:HD13	1.84	0.59
1:A:117:LEU:HD21	1:A:231:ILE:HG21	1.84	0.59
3:L:18:ARG:HA	3:L:75:ILE:O	2.02	0.59
1:A:43:PHE:HB3	1:C:566:GLY:HA2	1.85	0.59
1:A:976:VAL:HG12	1:A:979:ASP:H	1.68	0.59
3:E:18:ARG:HA	3:E:75:ILE:O	2.02	0.59
2:D:69:ILE:HD11	2:D:78:LEU:HD11	1.84	0.59
3:N:86:TYR:HB2	3:N:102:THR:HB	1.84	0.58
3:E:13:VAL:HG11	3:E:19:ALA:HB2	1.85	0.58
3:E:86:TYR:HB2	3:E:102:THR:HB	1.84	0.58
3:E:54:ARG:HB3	3:E:58:ILE:HB	1.85	0.58
1:C:452:ARG:HE	1:C:492:LEU:HD13	1.67	0.58
2:M:69:ILE:HD11	2:M:78:LEU:HD11	1.85	0.58
3:N:13:VAL:HG11	3:N:19:ALA:HB2	1.85	0.58
1:C:330:PRO:HG2	1:C:579:PRO:O	1.92	0.57
3:L:54:ARG:HB3	3:L:58:ILE:HB	1.85	0.57
1:C:329:PHE:N	1:C:329:PHE:CD1	2.72	0.57
1:C:332:ILE:CG2	1:C:362:VAL:HG11	2.34	0.57
2:H:69:ILE:HD11	2:H:78:LEU:HD11	1.85	0.57
1:C:127:VAL:HG22	1:C:171:VAL:HG22	1.85	0.57
1:A:1116:THR:OG1	1:A:1118:ASP:OD1	2.21	0.57
3:L:83:SER:HA	3:L:104:LEU:O	2.05	0.57
3:L:13:VAL:HG11	3:L:19:ALA:HB2	1.85	0.57
3:N:54:ARG:HB3	3:N:58:ILE:HB	1.85	0.57
1:A:531:THR:OG1	1:A:532:ASN:N	2.34	0.57
1:A:461:LEU:HD12	1:A:465:GLU:HB3	1.87	0.57
3:E:83:SER:HA	3:E:104:LEU:O	2.05	0.56
1:A:41:LYS:NZ	1:C:562:PHE:O	2.37	0.56
1:A:1053:PRO:O	1:A:1054:GLN:NE2	2.36	0.56
3:N:49:TYR:O	3:N:53:THR:OG1	2.23	0.56
1:C:474:GLN:NE2	1:C:480:CYS:SG	2.79	0.56
3:L:49:TYR:O	3:L:53:THR:OG1	2.23	0.56
3:N:83:SER:HA	3:N:104:LEU:O	2.05	0.56
1:C:172:SER:OG	1:C:173:GLN:N	2.39	0.55
2:D:92:VAL:HA	2:D:112:LEU:HA	1.89	0.55
1:A:111:ASP:HA	1:A:134:GLN:HA	1.88	0.55
1:A:474:GLN:NE2	1:A:478:LYS:O	2.39	0.55
1:A:401:VAL:HG22	1:A:509:ARG:HG2	1.87	0.55
1:B:347:PHE:HE1	1:B:399:SER:HB2	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:92:VAL:HA	2:M:112:LEU:HA	1.89	0.55
1:A:376:THR:HB	1:A:435:ALA:HB3	1.87	0.55
1:B:560:LEU:HB3	1:B:563:GLN:HG3	1.88	0.55
1:C:1048:HIS:HA	1:C:1066:THR:HG22	1.89	0.55
2:H:92:VAL:HA	2:H:112:LEU:HA	1.89	0.55
1:A:489:TYR:HE2	2:H:97:ARG:HH22	1.53	0.54
1:C:118:LEU:O	1:C:128:ILE:HA	2.06	0.54
1:C:656:VAL:HG12	1:C:695:TYR:HB3	1.89	0.54
3:E:49:TYR:O	3:E:53:THR:OG1	2.23	0.54
1:B:130:VAL:HB	1:B:168:PHE:HB3	1.88	0.54
1:B:402:ILE:HD12	1:B:406:GLU:HG2	1.90	0.54
1:C:418:ILE:HA	1:C:422:ASN:HD22	1.72	0.54
3:N:17:GLU:H	3:N:78:LEU:HD12	1.73	0.54
1:A:474:GLN:NE2	1:A:480:CYS:SG	2.80	0.54
3:E:46:LEU:HD21	3:E:49:TYR:HB3	1.90	0.54
1:B:376:THR:HB	1:B:435:ALA:HB3	1.90	0.54
1:B:433:VAL:HG23	1:B:512:VAL:HG22	1.90	0.54
1:C:880:GLY:O	1:C:884:SER:OG	2.26	0.54
1:C:946:GLY:O	1:C:950:ASN:HB2	2.08	0.54
3:N:34:ALA:HB1	3:N:46:LEU:HD11	1.90	0.54
1:B:273:ARG:NH2	1:B:290:ASP:OD2	2.40	0.53
1:C:332:ILE:HD11	1:C:528:LYS:H	1.66	0.53
1:C:376:THR:HB	1:C:435:ALA:HB3	1.89	0.53
3:L:46:LEU:HD21	3:L:49:TYR:HB3	1.90	0.53
3:E:17:GLU:H	3:E:78:LEU:HD12	1.73	0.53
3:L:17:GLU:H	3:L:78:LEU:HD12	1.73	0.53
1:C:308:VAL:N	1:C:602:THR:OG1	2.41	0.53
3:N:46:LEU:HD21	3:N:49:TYR:HB3	1.90	0.53
1:B:1053:PRO:O	1:B:1054:GLN:NE2	2.41	0.53
1:C:106:PHE:HB3	1:C:235:ILE:HD11	1.90	0.53
1:A:505:TYR:OH	3:L:93:ASP:OD1	2.26	0.53
1:B:722:VAL:HG22	1:B:1065:VAL:HG22	1.89	0.53
3:N:37:GLN:HB2	3:N:47:LEU:HD11	1.91	0.53
1:A:1030:SER:HA	1:A:1034:LEU:HD12	1.90	0.53
1:C:535:LYS:NZ	1:C:554:GLU:OE2	2.40	0.53
1:A:106:PHE:HB2	1:A:117:LEU:HB2	1.90	0.53
1:B:1106:GLN:HE21	1:B:1111:GLU:HG2	1.73	0.53
3:E:34:ALA:HB1	3:E:46:LEU:HD11	1.90	0.53
2:D:37:VAL:HG11	2:D:107:TRP:HZ3	1.74	0.52
1:B:663:ASP:OD1	1:B:663:ASP:N	2.42	0.52
3:L:34:ALA:HB1	3:L:46:LEU:HD11	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.91	0.52
1:A:37:TYR:OH	1:A:53:ASP:OD2	2.27	0.52
1:C:329:PHE:HD2	1:C:544:ASN:HA	1.73	0.52
3:E:37:GLN:HB2	3:E:47:LEU:HD11	1.91	0.52
1:A:43:PHE:HD1	1:C:563:GLN:HE21	1.56	0.52
2:M:37:VAL:HG11	2:M:107:TRP:HZ3	1.74	0.52
1:C:477:SER:OG	2:M:26:GLU:OE2	2.28	0.52
1:B:347:PHE:HD2	1:B:509:ARG:HH11	1.57	0.52
1:C:294:ASP:OD1	1:C:294:ASP:N	2.43	0.52
1:C:578:ASP:N	1:C:578:ASP:OD1	2.43	0.52
2:D:93:TYR:O	2:D:110:GLY:HA2	2.10	0.52
1:C:126:VAL:HG13	1:C:174:PRO:HA	1.91	0.51
2:M:93:TYR:O	2:M:110:GLY:HA2	2.10	0.51
1:B:712:ILE:HG22	1:C:896:ILE:HA	1.91	0.51
1:C:330:PRO:HG2	1:C:330:PRO:O	2.11	0.51
1:A:894:LEU:HD21	1:C:715:PRO:HD3	1.92	0.51
1:A:1129:VAL:HG13	1:B:917:TYR:HB3	1.93	0.51
2:H:52:TYR:HB2	2:H:55:GLY:HA3	1.92	0.51
1:A:883:THR:HG23	1:C:707:TYR:HB2	1.92	0.51
2:H:37:VAL:HG11	2:H:107:TRP:HZ3	1.74	0.51
1:A:409:GLN:HB3	1:A:419:ALA:HB2	1.93	0.51
2:H:93:TYR:O	2:H:110:GLY:HA2	2.11	0.51
2:M:101:ASP:OD2	3:N:94:ARG:NH1	2.30	0.51
3:N:39:LYS:NZ	3:N:81:GLU:O	2.44	0.51
3:E:39:LYS:NZ	3:E:81:GLU:O	2.44	0.51
1:A:722:VAL:HG22	1:A:1065:VAL:HG22	1.93	0.50
2:D:52:TYR:HB2	2:D:55:GLY:HA3	1.92	0.50
1:B:34:ARG:NH1	1:B:191:GLU:OE2	2.42	0.50
3:L:39:LYS:NZ	3:L:81:GLU:O	2.44	0.50
1:C:565:PHE:HE1	1:C:567:ARG:HH21	1.58	0.50
1:C:439:ASN:O	1:C:443:SER:OG	2.29	0.50
2:M:52:TYR:HB2	2:M:55:GLY:HA3	1.92	0.50
1:B:445:VAL:HG22	1:B:499:PRO:HG3	1.93	0.49
1:A:421:TYR:HA	1:A:461:LEU:HD23	1.95	0.49
1:B:294:ASP:N	1:B:294:ASP:OD1	2.45	0.49
1:C:742:ILE:O	1:C:1000:ARG:NH1	2.45	0.49
1:B:34:ARG:NH2	1:B:218:GLN:O	2.46	0.49
1:B:96:GLU:OE1	1:B:100:ILE:N	2.44	0.49
1:B:108:THR:O	1:B:237:ARG:NE	2.45	0.49
2:M:38:ARG:HH22	2:M:89:ASP:HA	1.77	0.49
1:A:740:MET:HE2	1:C:319:ARG:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:THR:OG1	1:C:219:GLY:O	2.30	0.49
2:H:38:ARG:HH22	2:H:89:ASP:HA	1.77	0.49
2:D:38:ARG:HH22	2:D:89:ASP:HA	1.77	0.48
3:L:38:GLN:HB2	3:L:44:PRO:HB3	1.95	0.48
1:B:703:ASN:ND2	1:C:787:GLN:OE1	2.46	0.48
1:C:643:PHE:CE1	1:C:655:HIS:ND1	2.81	0.48
3:L:33:LEU:HD21	3:L:88:CYS:HB2	1.94	0.48
1:A:1110:TYR:CZ	1:A:1112:PRO:HG3	2.49	0.48
3:E:33:LEU:HD21	3:E:88:CYS:HB2	1.94	0.48
3:E:38:GLN:HB2	3:E:44:PRO:HB3	1.96	0.48
2:H:48:VAL:HG13	2:H:63:VAL:HG21	1.94	0.48
3:N:33:LEU:HD21	3:N:88:CYS:HB2	1.94	0.48
3:N:38:GLN:HB2	3:N:44:PRO:HB3	1.96	0.48
1:A:354:ASN:O	1:A:398:ASP:HA	2.13	0.48
1:A:402:ILE:HD12	1:A:406:GLU:HG2	1.96	0.48
1:A:474:GLN:O	2:H:31:ARG:NH1	2.42	0.48
1:B:117:LEU:HG	1:B:130:VAL:HG22	1.96	0.48
1:C:330:PRO:HB3	1:C:580:GLN:HB3	1.11	0.48
1:C:984:LEU:HB3	1:C:989:ALA:HB2	1.96	0.48
2:M:48:VAL:HG13	2:M:63:VAL:HG21	1.94	0.48
1:A:915:VAL:O	1:A:919:ASN:ND2	2.45	0.48
1:C:598:ILE:HG23	1:C:664:ILE:HG21	1.95	0.48
1:C:726:ILE:HG13	1:C:1061:VAL:HG22	1.96	0.48
1:A:883:THR:HG21	1:C:705:VAL:HB	1.95	0.48
1:A:455:LEU:HD22	1:A:493:GLN:HB2	1.96	0.48
1:C:105:ILE:HD11	1:C:241:LEU:HD21	1.94	0.47
1:B:308:VAL:HG22	1:B:602:THR:HG23	1.96	0.47
1:C:445:VAL:HG22	1:C:499:PRO:HG3	1.95	0.47
1:C:1075:PHE:CD1	1:C:1075:PHE:N	2.81	0.47
1:C:614:GLY:H	1:C:648:GLY:HA2	1.79	0.47
1:A:108:THR:HG23	1:A:236:THR:HG22	1.96	0.47
1:B:985:ASP:N	1:B:985:ASP:OD1	2.43	0.47
1:B:88:ASP:OD1	1:B:88:ASP:N	2.48	0.47
1:B:969:ASN:ND2	1:C:755:GLN:OE1	2.43	0.47
1:A:93:ALA:HA	1:A:190:ARG:O	2.15	0.47
1:C:93:ALA:HB1	1:C:189:LEU:HD11	1.97	0.47
1:C:900:MET:HB2	1:C:900:MET:HE3	1.74	0.47
2:D:48:VAL:HG13	2:D:63:VAL:HG21	1.94	0.47
1:A:980:ILE:HD11	1:A:992:GLN:HB3	1.95	0.47
1:B:552:LEU:HD13	1:B:585:LEU:HD13	1.96	0.47
1:C:124:THR:HG22	1:C:174:PRO:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:ASN:ND2	1:B:787:GLN:OE1	2.32	0.47
1:A:740:MET:HE1	1:C:592:PHE:HB2	1.97	0.47
1:B:346:ARG:NH2	1:B:442:ASP:OD1	2.48	0.47
1:B:489:TYR:HE2	2:D:97:ARG:HH22	1.61	0.47
1:B:903:ALA:HB1	1:B:913:GLN:HB2	1.96	0.47
1:C:296:LEU:HD21	1:C:606:ASN:ND2	2.28	0.47
1:C:659:SER:HB3	1:C:698:SER:HB3	1.97	0.47
1:C:722:VAL:HG22	1:C:1065:VAL:HG22	1.97	0.47
1:C:565:PHE:HB3	1:C:576:VAL:HG23	1.97	0.46
1:C:1104:VAL:HG23	1:C:1115:ILE:HG12	1.96	0.46
2:M:47:TRP:CE3	3:N:95:PRO:HB3	2.50	0.46
1:A:310:LYS:HG3	1:A:600:PRO:HA	1.98	0.46
1:B:447:GLY:HA3	1:B:449:TYR:CZ	2.51	0.46
1:A:1040:VAL:HG21	1:B:1035:GLY:HA3	1.97	0.46
1:B:474:GLN:NE2	1:B:480:CYS:SG	2.89	0.46
1:C:560:LEU:HB2	1:C:563:GLN:HE22	1.81	0.46
1:B:1048:HIS:HA	1:B:1066:THR:HG22	1.96	0.46
1:C:1076:THR:HB	1:C:1097:SER:HB3	1.98	0.46
1:A:190:ARG:HB3	1:A:192:PHE:HE1	1.79	0.46
1:A:884:SER:O	1:A:884:SER:OG	2.33	0.46
1:C:865:LEU:HD23	1:C:869:MET:HE3	1.97	0.46
2:D:47:TRP:HE1	2:D:50:VAL:HB	1.81	0.46
2:H:47:TRP:HE1	2:H:50:VAL:HB	1.81	0.46
2:M:47:TRP:HE1	2:M:50:VAL:HB	1.81	0.46
1:A:642:VAL:HG13	1:A:651:ILE:HG12	1.98	0.46
1:B:489:TYR:CG	2:D:99:TYR:HE1	2.34	0.46
1:C:611:LEU:HD23	1:C:613:GLN:HG3	1.98	0.46
1:A:128:ILE:HD12	1:A:170:TYR:HD2	1.81	0.45
1:A:804:GLN:HB2	1:A:817:PRO:HB2	1.98	0.45
1:B:642:VAL:HG12	1:B:651:ILE:HG12	1.97	0.45
1:A:376:THR:HG23	1:A:378:LYS:HE2	1.97	0.45
1:A:405:ASP:N	1:A:504:GLY:O	2.49	0.45
1:A:1104:VAL:HG23	1:A:1115:ILE:HG12	1.97	0.45
1:C:903:ALA:HB1	1:C:913:GLN:HG3	1.99	0.45
2:H:49:SER:HA	2:H:58:PHE:O	2.17	0.45
1:A:52:GLN:OE1	1:A:274:THR:OG1	2.31	0.45
1:A:569:ILE:HD12	1:B:47:VAL:HG23	1.99	0.45
1:A:755:GLN:HB3	1:C:969:ASN:HB3	1.98	0.45
1:B:121:ASN:HD21	1:B:175:PHE:HB2	1.81	0.45
1:A:1107:ARG:HH22	1:B:907:ASN:HD22	1.65	0.45
1:C:103:GLY:HA3	1:C:119:ILE:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:PHE:HE2	1:C:619:GLU:HB3	1.81	0.45
1:A:534:VAL:HG23	1:A:539:VAL:HG11	1.97	0.45
2:D:49:SER:HA	2:D:58:PHE:O	2.17	0.45
2:M:49:SER:HA	2:M:58:PHE:O	2.17	0.45
1:A:939:SER:O	1:A:939:SER:OG	2.28	0.45
1:B:1104:VAL:HG23	1:B:1115:ILE:HG12	1.99	0.45
1:A:1093:GLY:HA2	1:A:1107:ARG:HG3	1.98	0.45
1:A:284:THR:HG22	1:C:560:LEU:HD21	1.99	0.44
1:C:1072:GLU:O	1:C:1072:GLU:HG2	2.17	0.44
1:A:379:CYS:HB2	1:A:384:PRO:HD3	2.00	0.44
1:B:324:GLU:OE2	1:B:537:LYS:NZ	2.51	0.44
1:A:323:THR:OG1	1:A:324:GLU:N	2.50	0.44
1:A:897:PRO:HG2	1:A:900:MET:HB2	1.99	0.44
1:A:192:PHE:HA	1:A:204:TYR:O	2.17	0.44
1:B:176:LEU:HG	1:B:190:ARG:HD3	1.98	0.44
1:A:444:LYS:HA	1:A:444:LYS:HD3	1.80	0.44
1:A:566:GLY:HA2	1:B:43:PHE:HB3	1.99	0.44
3:N:107:LYS:HA	3:N:107:LYS:HD3	1.81	0.44
1:A:403:ARG:HG3	1:A:497:PHE:HE1	1.82	0.44
1:A:598:ILE:HB	1:A:609:ALA:HB3	2.00	0.44
1:B:826:VAL:HB	1:B:1057:PRO:HG2	2.00	0.44
1:A:342:PHE:HE2	1:A:434:ILE:HG21	1.83	0.43
1:C:36:VAL:HG11	1:C:220:PHE:CZ	2.53	0.43
2:H:5:VAL:HG23	2:H:23:ALA:HB3	2.00	0.43
2:D:5:VAL:HG23	2:D:23:ALA:HB3	2.00	0.43
1:C:332:ILE:HD12	1:C:527:PRO:HB3	1.96	0.43
1:A:804:GLN:HA	1:A:817:PRO:HD2	2.01	0.43
1:B:100:ILE:HG22	1:B:242:LEU:HD11	2.00	0.43
1:B:274:THR:HG23	1:B:291:CYS:HB2	1.99	0.43
1:C:330:PRO:O	1:C:580:GLN:HA	2.17	0.43
1:C:996:LEU:HD23	1:C:996:LEU:HA	1.86	0.43
1:A:46:SER:HA	1:A:279:TYR:O	2.19	0.43
1:A:984:LEU:HB3	1:A:985:ASP:H	1.72	0.43
1:C:657:ASN:O	1:C:658:ASN:C	2.61	0.43
1:B:296:LEU:O	1:B:299:THR:OG1	2.34	0.43
1:B:374:PHE:HA	1:B:436:TRP:HB3	2.00	0.43
1:B:702:GLU:HG2	1:C:788:ILE:HB	2.01	0.43
1:B:598:ILE:HB	1:B:609:ALA:HB3	1.99	0.43
1:B:1116:THR:HG22	1:B:1138:TYR:HD2	1.83	0.43
1:C:393:THR:HA	1:C:522:ALA:HA	2.00	0.43
1:C:914:ASN:OD1	1:C:914:ASN:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:566:GLY:HA3	1:C:575:ALA:HB3	2.00	0.43
1:A:34:ARG:HH21	1:A:217:PRO:HG2	1.84	0.43
1:B:878:LEU:HD21	1:B:1052:PHE:HB3	2.00	0.43
1:C:1135:ASN:OD1	1:C:1136:THR:N	2.52	0.42
1:A:136:CYS:HB2	1:A:139:PRO:HG3	2.00	0.42
1:A:733:LYS:NZ	1:A:775:ASP:OD2	2.40	0.42
1:B:1129:VAL:HG13	1:C:917:TYR:HB3	1.99	0.42
1:C:717:ASN:HB3	1:C:1071:GLN:CG	2.49	0.42
2:H:60:ALA:HB3	2:H:63:VAL:HG22	2.01	0.42
1:A:707:TYR:HB3	1:B:792:PRO:HG3	2.01	0.42
1:A:801:ASN:ND2	1:A:803:SER:OG	2.52	0.42
1:A:985:ASP:HA	1:A:986:PRO:HD3	1.94	0.42
3:N:2:ILE:HG12	3:N:27:GLN:HB2	2.01	0.42
1:B:439:ASN:O	1:B:443:SER:OG	2.33	0.42
1:B:959:LEU:HD23	1:B:959:LEU:HA	1.89	0.42
1:B:1084:ASP:HB2	1:B:1086:LYS:HE2	2.00	0.42
3:E:2:ILE:HG12	3:E:27:GLN:HB2	2.01	0.42
1:B:786:LYS:HG3	1:B:787:GLN:HG3	2.00	0.42
1:B:1082:CYS:HB2	1:B:1126:CYS:HB2	1.95	0.42
1:C:945:LEU:HD12	1:C:948:LEU:HD12	2.01	0.42
2:M:5:VAL:HG23	2:M:23:ALA:HB3	2.00	0.42
1:A:103:GLY:HA3	1:A:119:ILE:O	2.20	0.42
1:B:871:ALA:HA	1:B:874:THR:HG22	2.01	0.42
1:C:330:PRO:CD	1:C:579:PRO:HG2	2.50	0.42
1:C:598:ILE:HB	1:C:609:ALA:HB3	2.02	0.42
1:C:643:PHE:HZ	1:C:655:HIS:CE1	2.25	0.42
1:B:109:THR:OG1	1:B:111:ASP:OD1	2.30	0.42
1:C:662:CYS:HB2	1:C:697:MET:HG3	2.00	0.42
3:L:2:ILE:HG12	3:L:27:GLN:HB2	2.01	0.42
1:A:825:LYS:HA	1:A:825:LYS:HD3	1.87	0.42
1:A:916:LEU:HD12	1:A:923:ILE:HD13	2.02	0.42
1:B:406:GLU:O	1:B:409:GLN:HB2	2.19	0.42
1:B:966:LEU:HD23	1:B:966:LEU:HA	1.79	0.42
1:C:738:CYS:HB3	1:C:760:CYS:HB3	1.89	0.42
1:C:650:LEU:HD12	1:C:650:LEU:HA	1.86	0.41
2:D:60:ALA:HB3	2:D:63:VAL:HG22	2.02	0.41
1:B:543:PHE:CG	1:B:576:VAL:HG11	2.55	0.41
1:B:1100:THR:OG1	1:B:1101:HIS:N	2.53	0.41
1:C:490:PHE:CE2	1:C:492:LEU:HB2	2.55	0.41
1:C:1028:LYS:O	1:C:1032:CYS:HB2	2.20	0.41
2:M:60:ALA:HB3	2:M:63:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1083:HIS:HB2	1:B:1135:ASN:O	2.20	0.41
3:N:36:TYR:CE1	3:N:46:LEU:HD12	2.56	0.41
1:B:231:ILE:HD12	1:B:233:ILE:HG22	2.02	0.41
1:B:948:LEU:HD21	1:B:1059:GLY:HA3	2.03	0.41
1:B:1074:ASN:OD1	1:B:1074:ASN:N	2.54	0.41
1:A:806:LEU:HD23	1:A:878:LEU:HD23	2.03	0.41
1:B:204:TYR:HA	1:B:225:PRO:HA	2.03	0.41
1:B:358:ILE:HB	1:B:395:VAL:HB	2.02	0.41
1:C:106:PHE:HB2	1:C:117:LEU:HB3	2.03	0.41
1:C:320:VAL:HG12	1:C:591:SER:HB3	2.01	0.41
3:E:21:LEU:HD22	3:E:102:THR:HG21	2.03	0.41
1:B:34:ARG:HA	1:B:34:ARG:HD3	1.87	0.41
1:B:37:TYR:OH	1:B:54:LEU:O	2.38	0.41
1:B:441:LEU:HB3	1:B:509:ARG:HH21	1.86	0.41
1:C:611:LEU:HD12	1:C:650:LEU:HD13	2.02	0.41
1:C:662:CYS:SG	1:C:663:ASP:N	2.92	0.41
1:C:959:LEU:HD12	1:C:959:LEU:HA	1.91	0.41
1:A:202:LYS:HE2	1:A:202:LYS:HB2	1.91	0.41
3:L:11:LEU:HD12	3:L:11:LEU:HA	1.93	0.40
1:A:37:TYR:OH	1:A:54:LEU:O	2.24	0.40
1:A:903:ALA:HB1	1:A:913:GLN:HG2	2.02	0.40
1:C:310:LYS:HE3	1:C:310:LYS:HB2	1.88	0.40
1:C:1127:ASP:N	1:C:1127:ASP:OD1	2.54	0.40
1:A:434:ILE:O	1:A:510:VAL:HA	2.22	0.40
1:A:959:LEU:HD23	1:A:959:LEU:HA	1.87	0.40
1:A:970:PHE:CG	1:A:999:GLY:HA3	2.56	0.40
1:C:613:GLN:HE21	1:C:613:GLN:HB2	1.63	0.40
1:C:710:ASN:OD1	1:C:710:ASN:N	2.54	0.40
1:A:754:LEU:HD12	1:A:754:LEU:HA	1.92	0.40
1:B:543:PHE:O	1:B:546:LEU:HB3	2.21	0.40
1:C:119:ILE:HG12	1:C:128:ILE:HG13	2.03	0.40
1:C:329:PHE:CD1	1:C:528:LYS:CB	3.04	0.40
1:C:350:VAL:HG22	1:C:422:ASN:HB3	2.04	0.40
1:C:977:LEU:HD12	1:C:977:LEU:HA	1.89	0.40
1:C:1038:LYS:HB3	1:C:1038:LYS:HE3	1.77	0.40
3:L:21:LEU:HD22	3:L:102:THR:HG21	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	982/1286 (76%)	910 (93%)	71 (7%)	1 (0%)	48	79
1	B	969/1286 (75%)	902 (93%)	66 (7%)	1 (0%)	48	79
1	C	979/1286 (76%)	899 (92%)	74 (8%)	6 (1%)	21	54
2	D	117/222 (53%)	109 (93%)	8 (7%)	0	100	100
2	H	117/222 (53%)	109 (93%)	8 (7%)	0	100	100
2	M	117/222 (53%)	109 (93%)	8 (7%)	0	100	100
3	E	107/109 (98%)	94 (88%)	13 (12%)	0	100	100
3	L	107/109 (98%)	94 (88%)	13 (12%)	0	100	100
3	N	107/109 (98%)	94 (88%)	13 (12%)	0	100	100
All	All	3602/4851 (74%)	3320 (92%)	274 (8%)	8 (0%)	44	75

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1084	ASP
1	C	330	PRO
1	C	617	CYS
1	A	896	ILE
1	C	329	PHE
1	C	649	CYS
1	C	650	LEU
1	C	648	GLY

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	854/1113 (77%)	852 (100%)	2 (0%)	87	91
1	B	850/1113 (76%)	850 (100%)	0	100	100
1	C	846/1113 (76%)	835 (99%)	11 (1%)	61	80
2	D	99/189 (52%)	93 (94%)	6 (6%)	17	47
2	H	99/189 (52%)	93 (94%)	6 (6%)	17	47
2	M	99/189 (52%)	93 (94%)	6 (6%)	17	47
3	E	89/89 (100%)	83 (93%)	6 (7%)	15	44
3	L	89/89 (100%)	83 (93%)	6 (7%)	15	44
3	N	89/89 (100%)	83 (93%)	6 (7%)	15	44
All	All	3114/4173 (75%)	3065 (98%)	49 (2%)	54	78

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	615	VAL
1	A	617	CYS
1	C	329	PHE
1	C	330	PRO
1	C	332	ILE
1	C	602	THR
1	C	649	CYS
1	C	651	ILE
1	C	656	VAL
1	C	658	ASN
1	C	1072	GLU
1	C	1073	LYS
1	C	1076	THR
2	D	31	ARG
2	D	34	MET
2	D	37	VAL
2	D	82	MET
2	D	103	TYR
2	D	113	VAL
3	E	4	MET
3	E	12	SER
3	E	24	ARG
3	E	45	ARG
3	E	46	LEU

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Mol	Chain	Res	Type
3	E	74	THR
2	H	31	ARG
2	H	34	MET
2	H	37	VAL
2	H	82	MET
2	H	103	TYR
2	H	113	VAL
3	L	4	MET
3	L	12	SER
3	L	24	ARG
3	L	45	ARG
3	L	46	LEU
3	L	74	THR
2	M	31	ARG
2	M	34	MET
2	M	37	VAL
2	M	82	MET
2	M	103	TYR
2	M	113	VAL
3	N	4	MET
3	N	12	SER
3	N	24	ARG
3	N	45	ARG
3	N	46	LEU
3	N	74	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	196	ASN
1	A	282	ASN
1	A	370	ASN
1	A	474	GLN
1	A	536	ASN
1	A	564	GLN
1	A	580	GLN
1	A	751	ASN
1	A	801	ASN
1	A	856	ASN
1	A	1083	HIS
1	A	1125	ASN
1	B	99	ASN

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Mol	Chain	Res	Type
1	B	125	ASN
1	B	196	ASN
1	B	474	GLN
1	B	556	ASN
1	B	949	GLN
1	B	954	GLN
1	B	1058	HIS
1	B	1064	HIS
1	B	1135	ASN
1	C	343	ASN
1	C	370	ASN
1	C	606	ASN
1	C	613	GLN
1	C	616	ASN
1	C	969	ASN
3	E	27	GLN
3	E	92	ASN
3	L	27	GLN
3	N	27	GLN
3	N	89	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

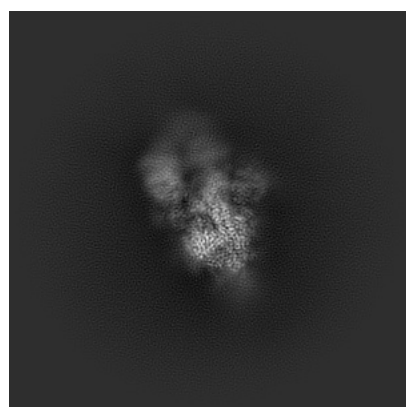
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32427. These allow visual inspection of the internal detail of the map and identification of artifacts.

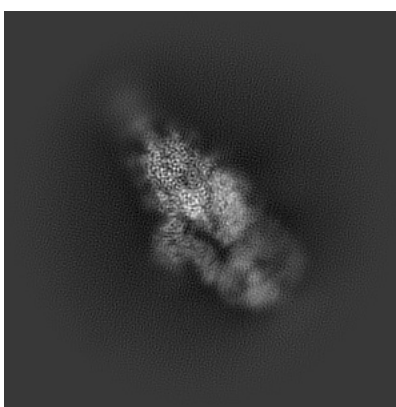
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

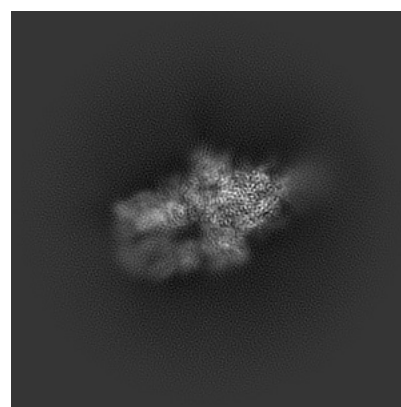
6.1.1 Primary map



X



Y

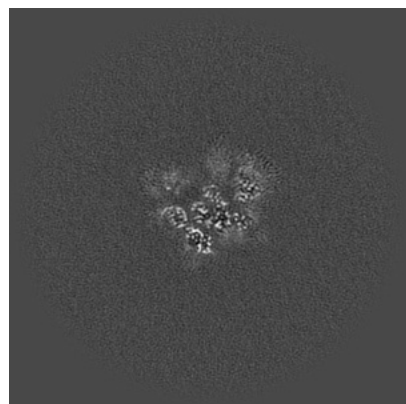


Z

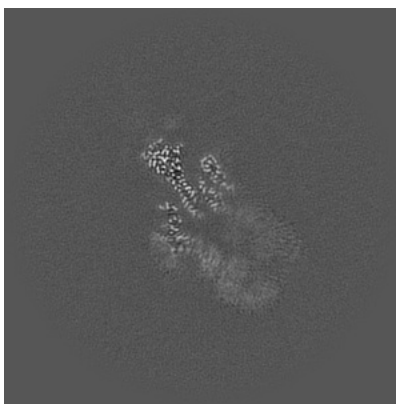
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

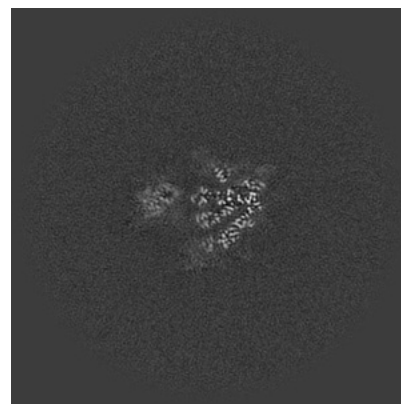
6.2.1 Primary map



X Index: 200



Y Index: 200

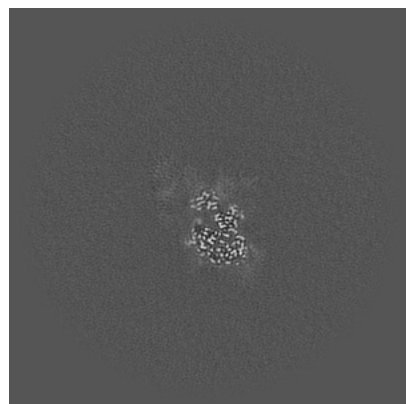


Z Index: 200

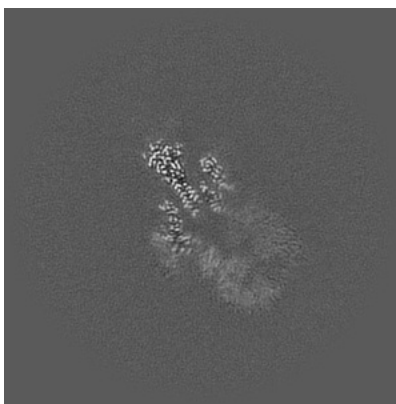
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

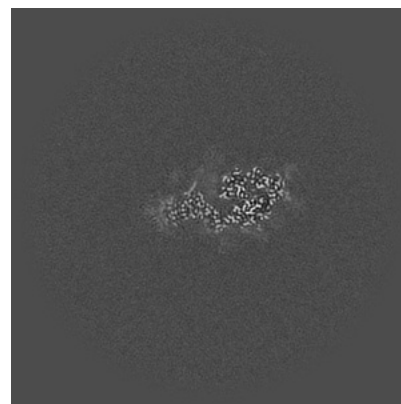
6.3.1 Primary map



X Index: 237



Y Index: 199

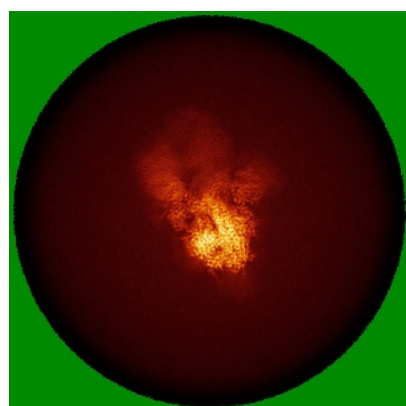


Z Index: 169

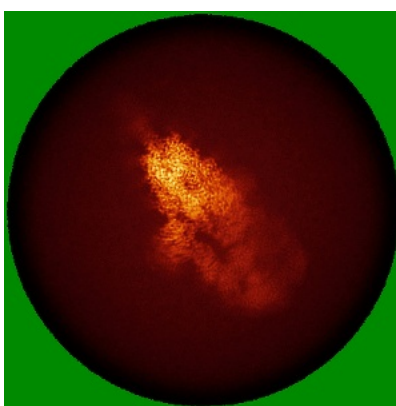
The images above show the largest variance slices of the map in three orthogonal directions.

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

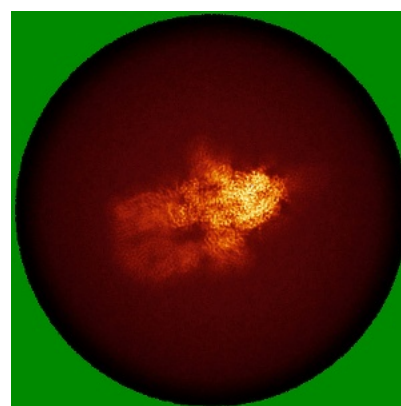
6.4.1 Primary map



X



Y

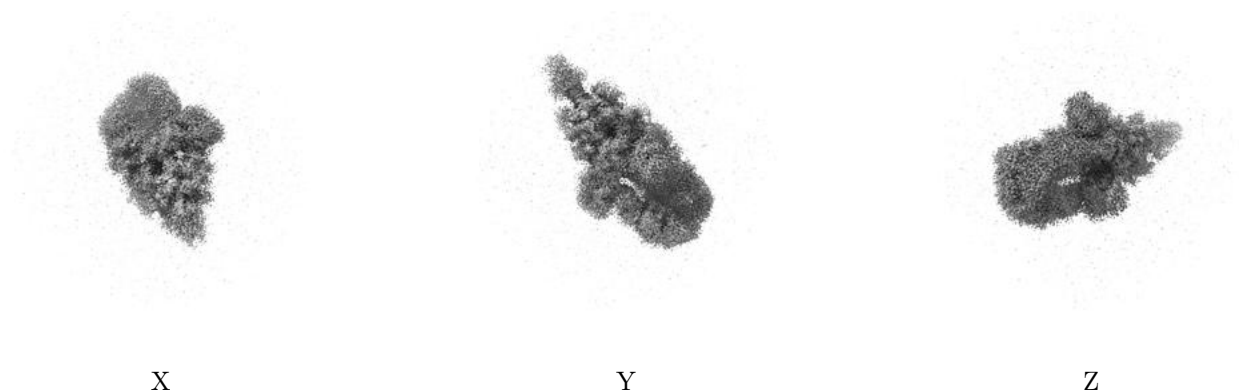


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

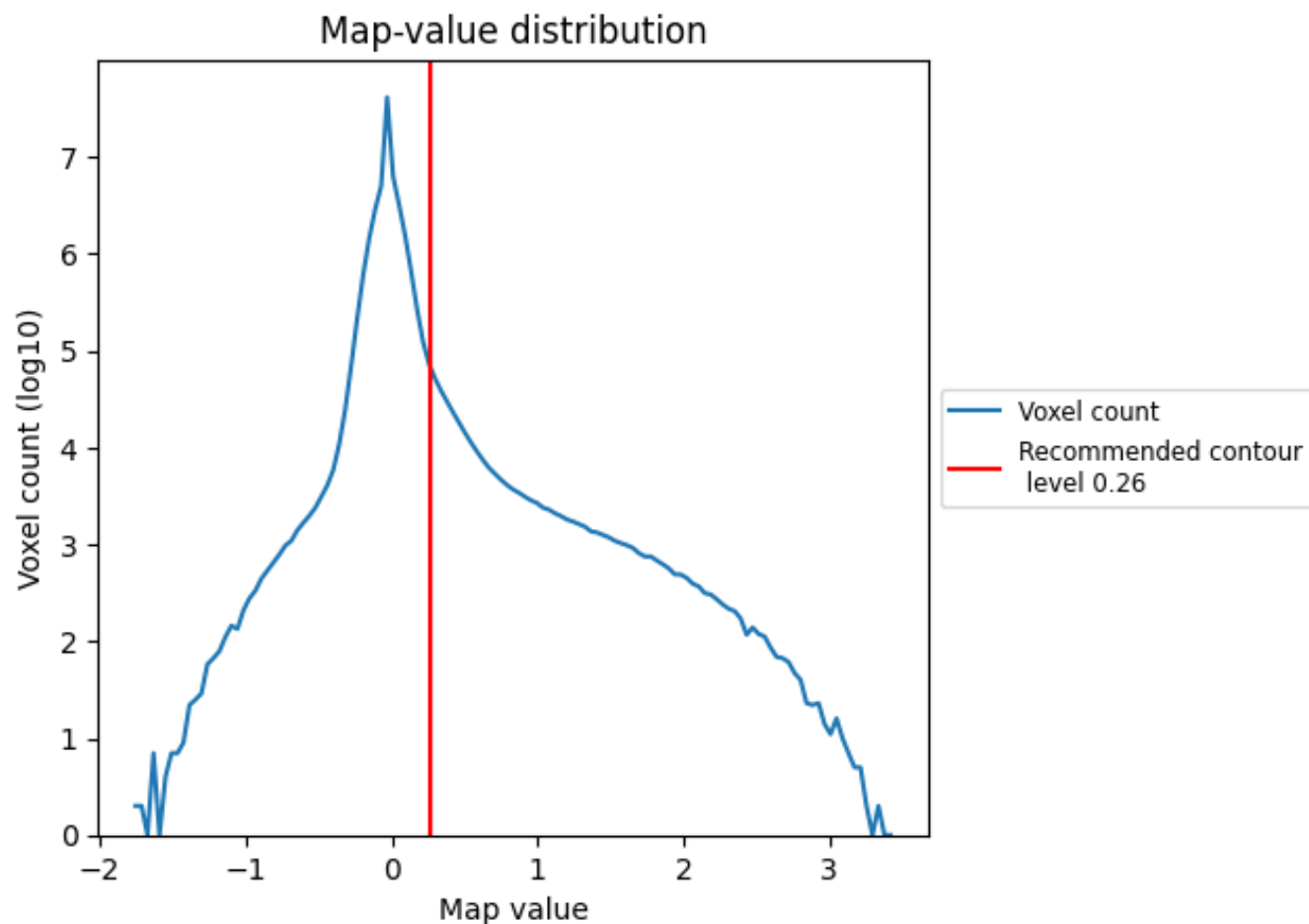
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

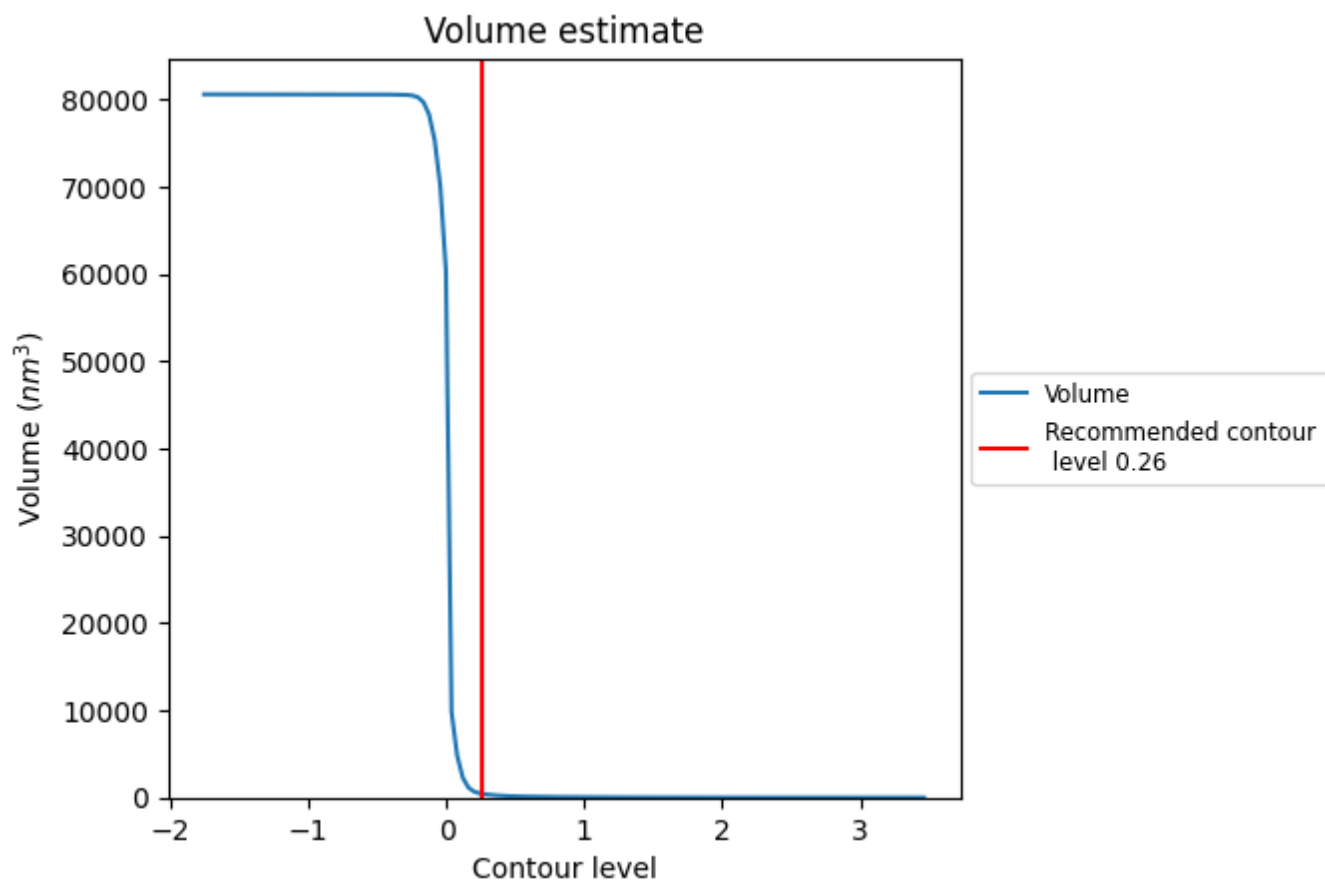
This section contains the results of statistical analysis of the map.

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.

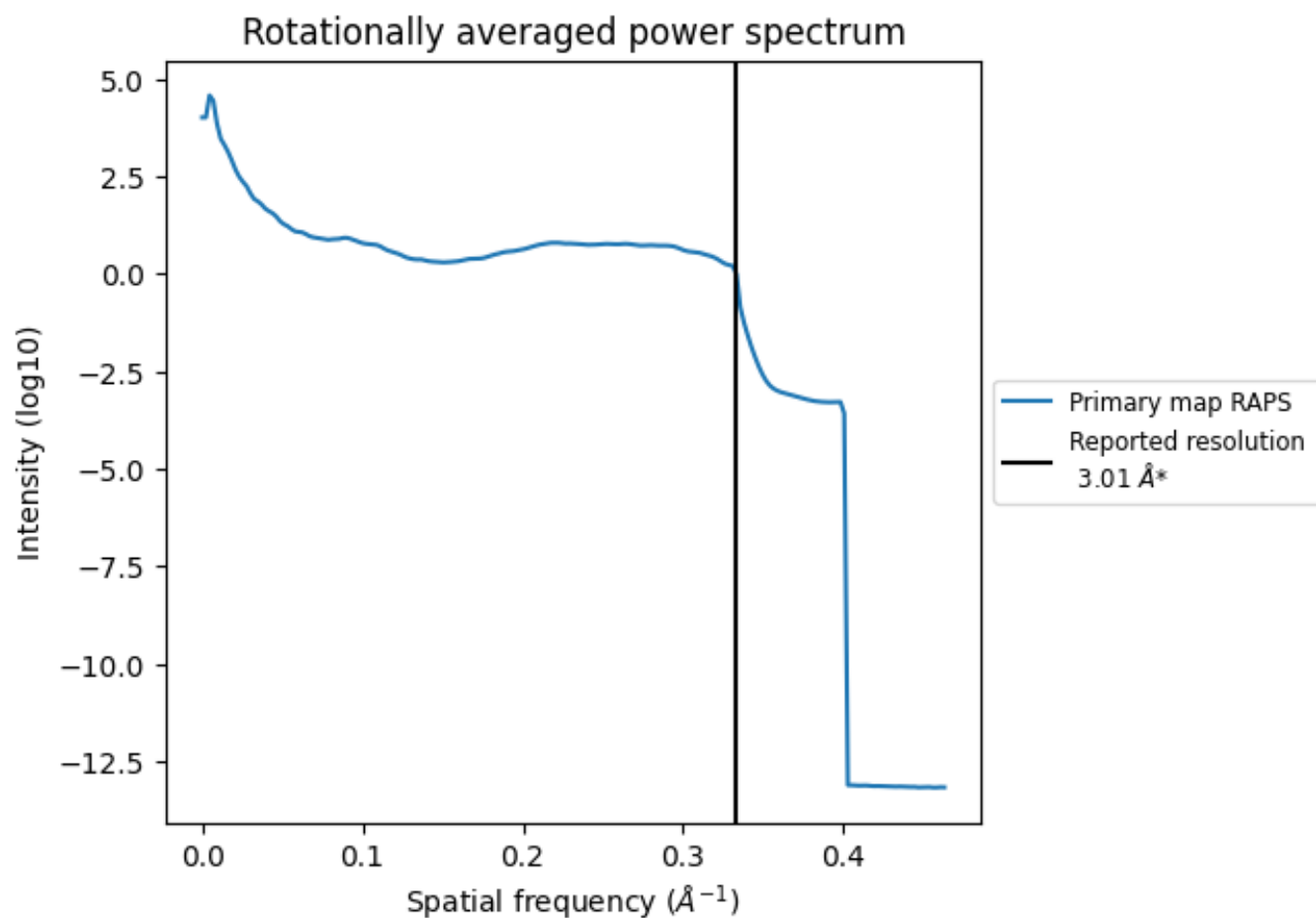
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 433 nm³; this corresponds to an approximate mass of 391 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 0.332 Å⁻¹

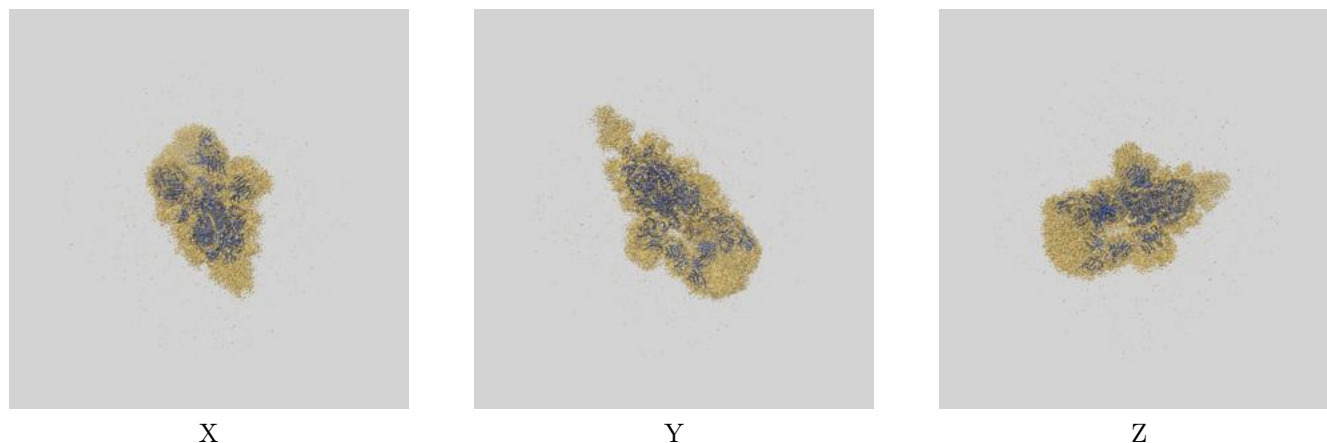
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

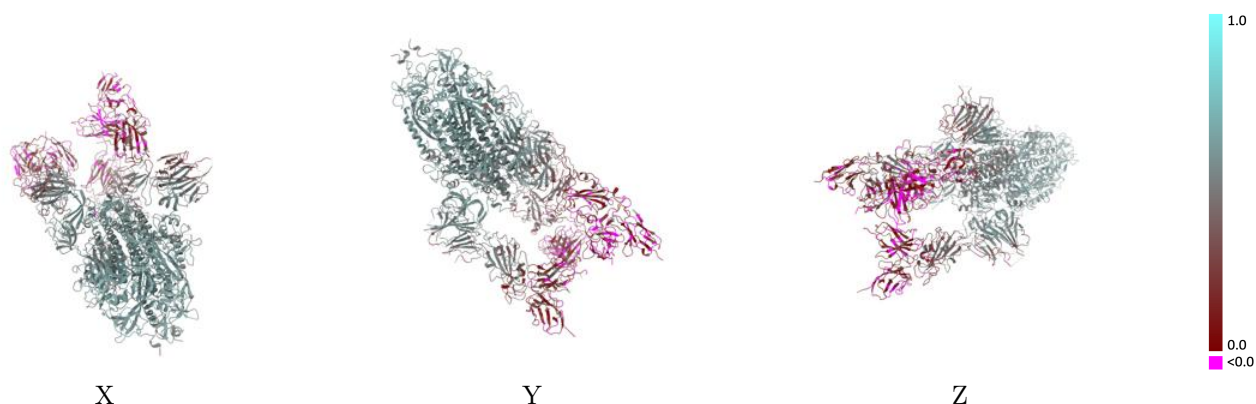
This section contains information regarding the fit between EMDB map EMD-32427 and PDB model 7WCP. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



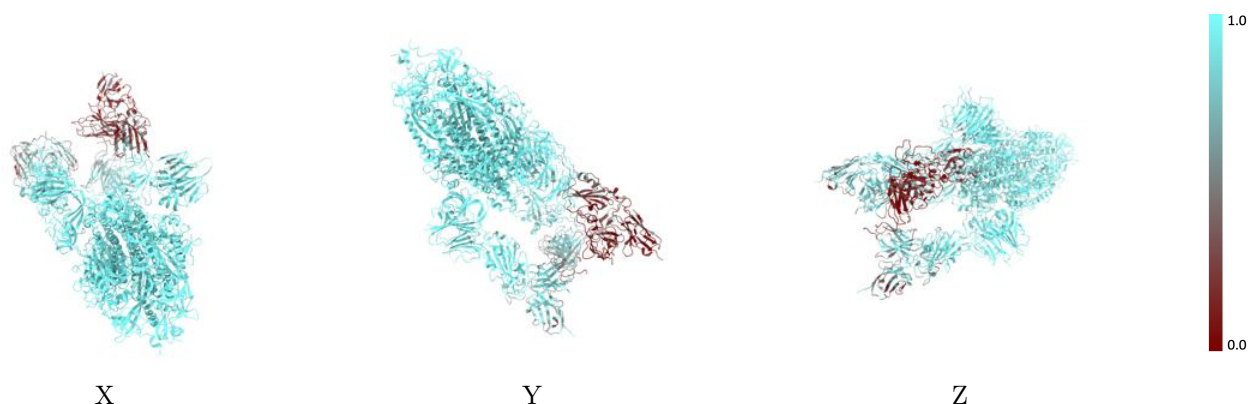
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



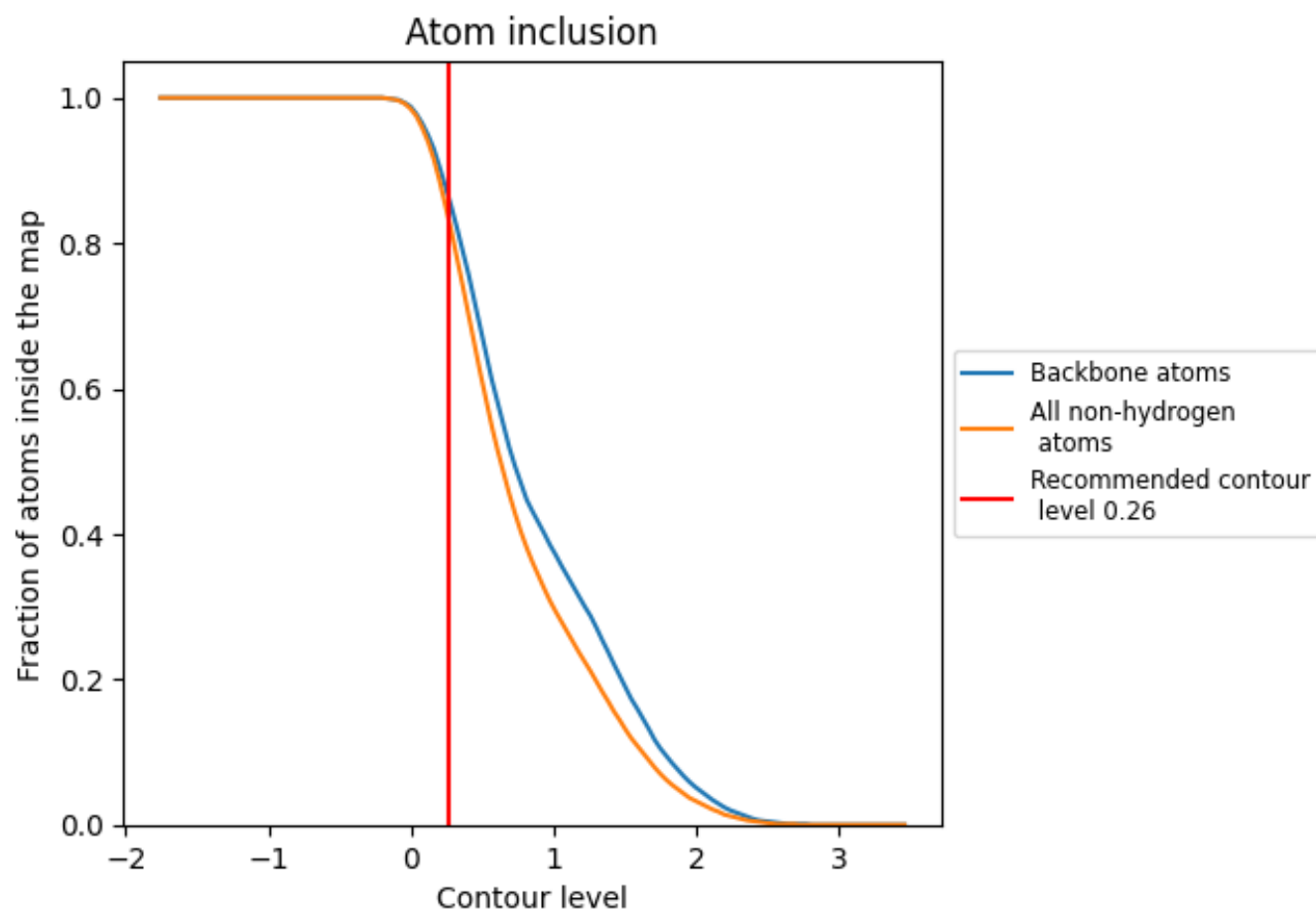
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.26).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8370	0.4210
A	0.9520	0.5030
B	0.9480	0.5050
C	0.8430	0.4580
D	0.6560	0.1350
E	0.5710	0.1160
H	0.7260	0.1960
L	0.7290	0.1830
M	0.1190	0.0370
N	0.1720	0.0890

1.0

0.0

<0.0