



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:35 PM UTC

PDB ID : 8YZ5 / pdb_00008yz5
EMDB ID : EMD-39685
Title : SARS-CoV-2 Delta Spike in complex with Fab of JE-5C
Authors : Chen, X.; Wu, Y.-M.
Deposited on : 2024-04-06
Resolution : 3.93 Å(reported)

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

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

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

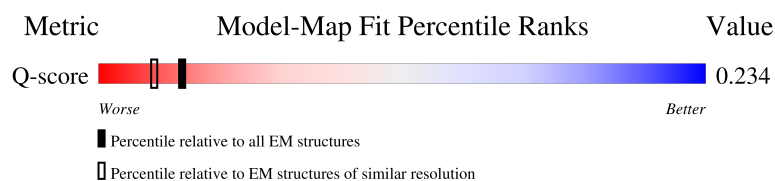
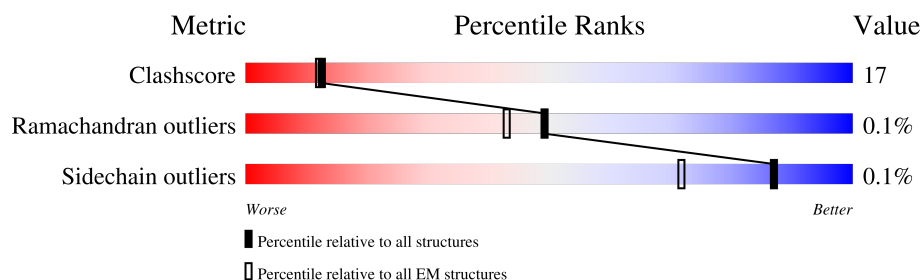
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.93 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	7811 (3.43 - 4.43)

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	1259	24% 52% 31% 17%
1	C	1259	21% 55% 26% 18%
1	D	1259	23% 54% 28% 18%
2	G	119	79% 64% 36%

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Mol	Chain	Length	Quality of chain
2	I	119	82% 60% 39%
3	J	107	68% 65% 35%
3	K	107	77% 78% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27677 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	C	1027	Total	C	N	O	S	0	0
			8023	5124	1339	1526	34		
1	A	1042	Total	C	N	O	S	0	0
			8138	5190	1366	1546	36		
1	D	1037	Total	C	N	O	S	0	0
			8102	5173	1353	1540	36		

There are 243 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	MET	-	expression tag	UNP P0DTC2
C	-4	LYS	-	expression tag	UNP P0DTC2
C	-3	VAL	-	expression tag	UNP P0DTC2
C	-2	LYS	-	expression tag	UNP P0DTC2
C	-1	LEU	-	expression tag	UNP P0DTC2
C	0	LEU	-	expression tag	UNP P0DTC2
C	1	VAL	-	expression tag	UNP P0DTC2
C	2	LEU	-	expression tag	UNP P0DTC2
C	3	LEU	-	expression tag	UNP P0DTC2
C	4	CYS	-	expression tag	UNP P0DTC2
C	5	THR	-	expression tag	UNP P0DTC2
C	6	PHE	-	expression tag	UNP P0DTC2
C	7	THR	-	expression tag	UNP P0DTC2
C	8	ALA	-	expression tag	UNP P0DTC2
C	9	THR	-	expression tag	UNP P0DTC2
C	10	TYR	-	expression tag	UNP P0DTC2
C	11	ALA	-	expression tag	UNP P0DTC2
C	12	GLY	-	expression tag	UNP P0DTC2
C	13	THR	-	expression tag	UNP P0DTC2
C	19	ARG	THR	variant	UNP P0DTC2
C	142	ASP	GLY	variant	UNP P0DTC2
C	?	-	GLU	deletion	UNP P0DTC2
C	?	-	PHE	deletion	UNP P0DTC2
C	158	GLY	ARG	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	452	ARG	LEU	variant	UNP P0DTC2
C	478	LYS	THR	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	681	ARG	PRO	variant	UNP P0DTC2
C	682	GLY	ARG	variant	UNP P0DTC2
C	683	SER	ARG	variant	UNP P0DTC2
C	685	GLY	ARG	variant	UNP P0DTC2
C	950	ASN	ASP	variant	UNP P0DTC2
C	986	PRO	LYS	variant	UNP P0DTC2
C	987	PRO	VAL	variant	UNP P0DTC2
C	1209	ASP	-	expression tag	UNP P0DTC2
C	1210	ILE	-	expression tag	UNP P0DTC2
C	1211	ARG	-	expression tag	UNP P0DTC2
C	1212	SER	-	expression tag	UNP P0DTC2
C	1213	LEU	-	expression tag	UNP P0DTC2
C	1214	VAL	-	expression tag	UNP P0DTC2
C	1215	PRO	-	expression tag	UNP P0DTC2
C	1216	ARG	-	expression tag	UNP P0DTC2
C	1217	GLY	-	expression tag	UNP P0DTC2
C	1218	SER	-	expression tag	UNP P0DTC2
C	1219	PRO	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	SER	-	expression tag	UNP P0DTC2
C	1222	GLY	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	ILE	-	expression tag	UNP P0DTC2
C	1225	PRO	-	expression tag	UNP P0DTC2
C	1226	GLU	-	expression tag	UNP P0DTC2
C	1227	ALA	-	expression tag	UNP P0DTC2
C	1228	PRO	-	expression tag	UNP P0DTC2
C	1229	ARG	-	expression tag	UNP P0DTC2
C	1230	ASP	-	expression tag	UNP P0DTC2
C	1231	GLY	-	expression tag	UNP P0DTC2
C	1232	GLN	-	expression tag	UNP P0DTC2
C	1233	ALA	-	expression tag	UNP P0DTC2
C	1234	TYR	-	expression tag	UNP P0DTC2
C	1235	VAL	-	expression tag	UNP P0DTC2
C	1236	ARG	-	expression tag	UNP P0DTC2
C	1237	LYS	-	expression tag	UNP P0DTC2
C	1238	ASP	-	expression tag	UNP P0DTC2
C	1239	GLY	-	expression tag	UNP P0DTC2
C	1240	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1241	TRP	-	expression tag	UNP P0DTC2
C	1242	VAL	-	expression tag	UNP P0DTC2
C	1243	LEU	-	expression tag	UNP P0DTC2
C	1244	LEU	-	expression tag	UNP P0DTC2
C	1245	SER	-	expression tag	UNP P0DTC2
C	1246	THR	-	expression tag	UNP P0DTC2
C	1247	PHE	-	expression tag	UNP P0DTC2
C	1248	LEU	-	expression tag	UNP P0DTC2
C	1249	GLY	-	expression tag	UNP P0DTC2
C	1250	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	HIS	-	expression tag	UNP P0DTC2
A	-5	MET	-	expression tag	UNP P0DTC2
A	-4	LYS	-	expression tag	UNP P0DTC2
A	-3	VAL	-	expression tag	UNP P0DTC2
A	-2	LYS	-	expression tag	UNP P0DTC2
A	-1	LEU	-	expression tag	UNP P0DTC2
A	0	LEU	-	expression tag	UNP P0DTC2
A	1	VAL	-	expression tag	UNP P0DTC2
A	2	LEU	-	expression tag	UNP P0DTC2
A	3	LEU	-	expression tag	UNP P0DTC2
A	4	CYS	-	expression tag	UNP P0DTC2
A	5	THR	-	expression tag	UNP P0DTC2
A	6	PHE	-	expression tag	UNP P0DTC2
A	7	THR	-	expression tag	UNP P0DTC2
A	8	ALA	-	expression tag	UNP P0DTC2
A	9	THR	-	expression tag	UNP P0DTC2
A	10	TYR	-	expression tag	UNP P0DTC2
A	11	ALA	-	expression tag	UNP P0DTC2
A	12	GLY	-	expression tag	UNP P0DTC2
A	13	THR	-	expression tag	UNP P0DTC2
A	19	ARG	THR	variant	UNP P0DTC2
A	142	ASP	GLY	variant	UNP P0DTC2
A	?	-	GLU	deletion	UNP P0DTC2
A	?	-	PHE	deletion	UNP P0DTC2
A	158	GLY	ARG	variant	UNP P0DTC2
A	452	ARG	LEU	variant	UNP P0DTC2
A	478	LYS	THR	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	681	ARG	PRO	variant	UNP P0DTC2
A	682	GLY	ARG	variant	UNP P0DTC2
A	683	SER	ARG	variant	UNP P0DTC2
A	685	GLY	ARG	variant	UNP P0DTC2
A	950	ASN	ASP	variant	UNP P0DTC2
A	986	PRO	LYS	variant	UNP P0DTC2
A	987	PRO	VAL	variant	UNP P0DTC2
A	1209	ASP	-	expression tag	UNP P0DTC2
A	1210	ILE	-	expression tag	UNP P0DTC2
A	1211	ARG	-	expression tag	UNP P0DTC2
A	1212	SER	-	expression tag	UNP P0DTC2
A	1213	LEU	-	expression tag	UNP P0DTC2
A	1214	VAL	-	expression tag	UNP P0DTC2
A	1215	PRO	-	expression tag	UNP P0DTC2
A	1216	ARG	-	expression tag	UNP P0DTC2
A	1217	GLY	-	expression tag	UNP P0DTC2
A	1218	SER	-	expression tag	UNP P0DTC2
A	1219	PRO	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	SER	-	expression tag	UNP P0DTC2
A	1222	GLY	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	ILE	-	expression tag	UNP P0DTC2
A	1225	PRO	-	expression tag	UNP P0DTC2
A	1226	GLU	-	expression tag	UNP P0DTC2
A	1227	ALA	-	expression tag	UNP P0DTC2
A	1228	PRO	-	expression tag	UNP P0DTC2
A	1229	ARG	-	expression tag	UNP P0DTC2
A	1230	ASP	-	expression tag	UNP P0DTC2
A	1231	GLY	-	expression tag	UNP P0DTC2
A	1232	GLN	-	expression tag	UNP P0DTC2
A	1233	ALA	-	expression tag	UNP P0DTC2
A	1234	TYR	-	expression tag	UNP P0DTC2
A	1235	VAL	-	expression tag	UNP P0DTC2
A	1236	ARG	-	expression tag	UNP P0DTC2
A	1237	LYS	-	expression tag	UNP P0DTC2
A	1238	ASP	-	expression tag	UNP P0DTC2
A	1239	GLY	-	expression tag	UNP P0DTC2
A	1240	GLU	-	expression tag	UNP P0DTC2
A	1241	TRP	-	expression tag	UNP P0DTC2
A	1242	VAL	-	expression tag	UNP P0DTC2
A	1243	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1244	LEU	-	expression tag	UNP P0DTC2
A	1245	SER	-	expression tag	UNP P0DTC2
A	1246	THR	-	expression tag	UNP P0DTC2
A	1247	PHE	-	expression tag	UNP P0DTC2
A	1248	LEU	-	expression tag	UNP P0DTC2
A	1249	GLY	-	expression tag	UNP P0DTC2
A	1250	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2
A	1255	HIS	-	expression tag	UNP P0DTC2
D	-5	MET	-	expression tag	UNP P0DTC2
D	-4	LYS	-	expression tag	UNP P0DTC2
D	-3	VAL	-	expression tag	UNP P0DTC2
D	-2	LYS	-	expression tag	UNP P0DTC2
D	-1	LEU	-	expression tag	UNP P0DTC2
D	0	LEU	-	expression tag	UNP P0DTC2
D	1	VAL	-	expression tag	UNP P0DTC2
D	2	LEU	-	expression tag	UNP P0DTC2
D	3	LEU	-	expression tag	UNP P0DTC2
D	4	CYS	-	expression tag	UNP P0DTC2
D	5	THR	-	expression tag	UNP P0DTC2
D	6	PHE	-	expression tag	UNP P0DTC2
D	7	THR	-	expression tag	UNP P0DTC2
D	8	ALA	-	expression tag	UNP P0DTC2
D	9	THR	-	expression tag	UNP P0DTC2
D	10	TYR	-	expression tag	UNP P0DTC2
D	11	ALA	-	expression tag	UNP P0DTC2
D	12	GLY	-	expression tag	UNP P0DTC2
D	13	THR	-	expression tag	UNP P0DTC2
D	19	ARG	THR	variant	UNP P0DTC2
D	142	ASP	GLY	variant	UNP P0DTC2
D	?	-	GLU	deletion	UNP P0DTC2
D	?	-	PHE	deletion	UNP P0DTC2
D	158	GLY	ARG	variant	UNP P0DTC2
D	452	ARG	LEU	variant	UNP P0DTC2
D	478	LYS	THR	variant	UNP P0DTC2
D	614	GLY	ASP	variant	UNP P0DTC2
D	681	ARG	PRO	variant	UNP P0DTC2
D	682	GLY	ARG	variant	UNP P0DTC2
D	683	SER	ARG	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	685	GLY	ARG	variant	UNP P0DTC2
D	950	ASN	ASP	variant	UNP P0DTC2
D	986	PRO	LYS	variant	UNP P0DTC2
D	987	PRO	VAL	variant	UNP P0DTC2
D	1209	ASP	-	expression tag	UNP P0DTC2
D	1210	ILE	-	expression tag	UNP P0DTC2
D	1211	ARG	-	expression tag	UNP P0DTC2
D	1212	SER	-	expression tag	UNP P0DTC2
D	1213	LEU	-	expression tag	UNP P0DTC2
D	1214	VAL	-	expression tag	UNP P0DTC2
D	1215	PRO	-	expression tag	UNP P0DTC2
D	1216	ARG	-	expression tag	UNP P0DTC2
D	1217	GLY	-	expression tag	UNP P0DTC2
D	1218	SER	-	expression tag	UNP P0DTC2
D	1219	PRO	-	expression tag	UNP P0DTC2
D	1220	GLY	-	expression tag	UNP P0DTC2
D	1221	SER	-	expression tag	UNP P0DTC2
D	1222	GLY	-	expression tag	UNP P0DTC2
D	1223	TYR	-	expression tag	UNP P0DTC2
D	1224	ILE	-	expression tag	UNP P0DTC2
D	1225	PRO	-	expression tag	UNP P0DTC2
D	1226	GLU	-	expression tag	UNP P0DTC2
D	1227	ALA	-	expression tag	UNP P0DTC2
D	1228	PRO	-	expression tag	UNP P0DTC2
D	1229	ARG	-	expression tag	UNP P0DTC2
D	1230	ASP	-	expression tag	UNP P0DTC2
D	1231	GLY	-	expression tag	UNP P0DTC2
D	1232	GLN	-	expression tag	UNP P0DTC2
D	1233	ALA	-	expression tag	UNP P0DTC2
D	1234	TYR	-	expression tag	UNP P0DTC2
D	1235	VAL	-	expression tag	UNP P0DTC2
D	1236	ARG	-	expression tag	UNP P0DTC2
D	1237	LYS	-	expression tag	UNP P0DTC2
D	1238	ASP	-	expression tag	UNP P0DTC2
D	1239	GLY	-	expression tag	UNP P0DTC2
D	1240	GLU	-	expression tag	UNP P0DTC2
D	1241	TRP	-	expression tag	UNP P0DTC2
D	1242	VAL	-	expression tag	UNP P0DTC2
D	1243	LEU	-	expression tag	UNP P0DTC2
D	1244	LEU	-	expression tag	UNP P0DTC2
D	1245	SER	-	expression tag	UNP P0DTC2
D	1246	THR	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1247	PHE	-	expression tag	UNP P0DTC2
D	1248	LEU	-	expression tag	UNP P0DTC2
D	1249	GLY	-	expression tag	UNP P0DTC2
D	1250	HIS	-	expression tag	UNP P0DTC2
D	1251	HIS	-	expression tag	UNP P0DTC2
D	1252	HIS	-	expression tag	UNP P0DTC2
D	1253	HIS	-	expression tag	UNP P0DTC2
D	1254	HIS	-	expression tag	UNP P0DTC2
D	1255	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Fab heavy chain of JE-5C.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	119	Total	C	N	O	S	0	0
			889	551	156	177	5		
2	I	118	Total	C	N	O	S	0	0
			884	548	155	176	5		

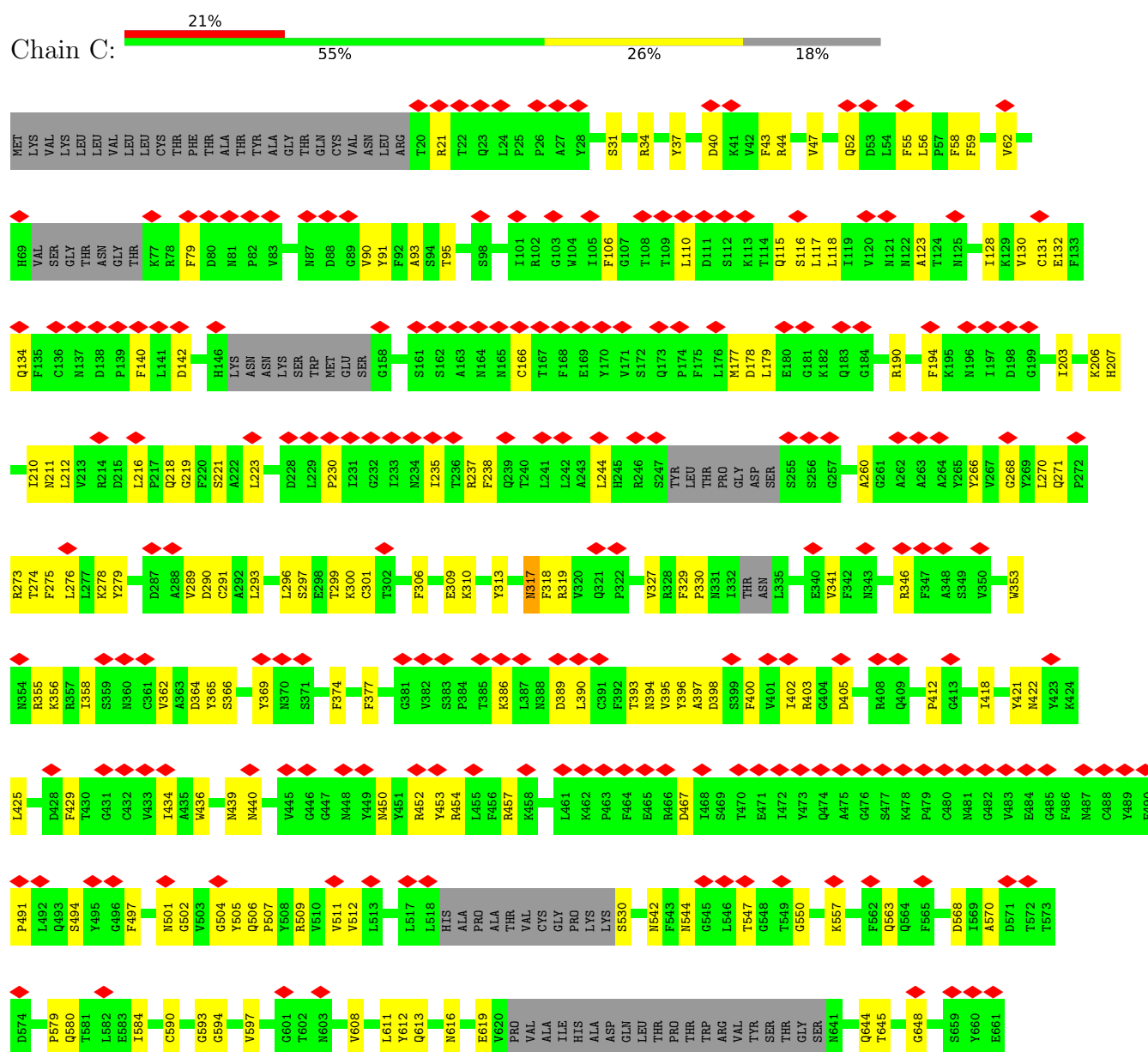
- Molecule 3 is a protein called Fab light chain of JE-5C.

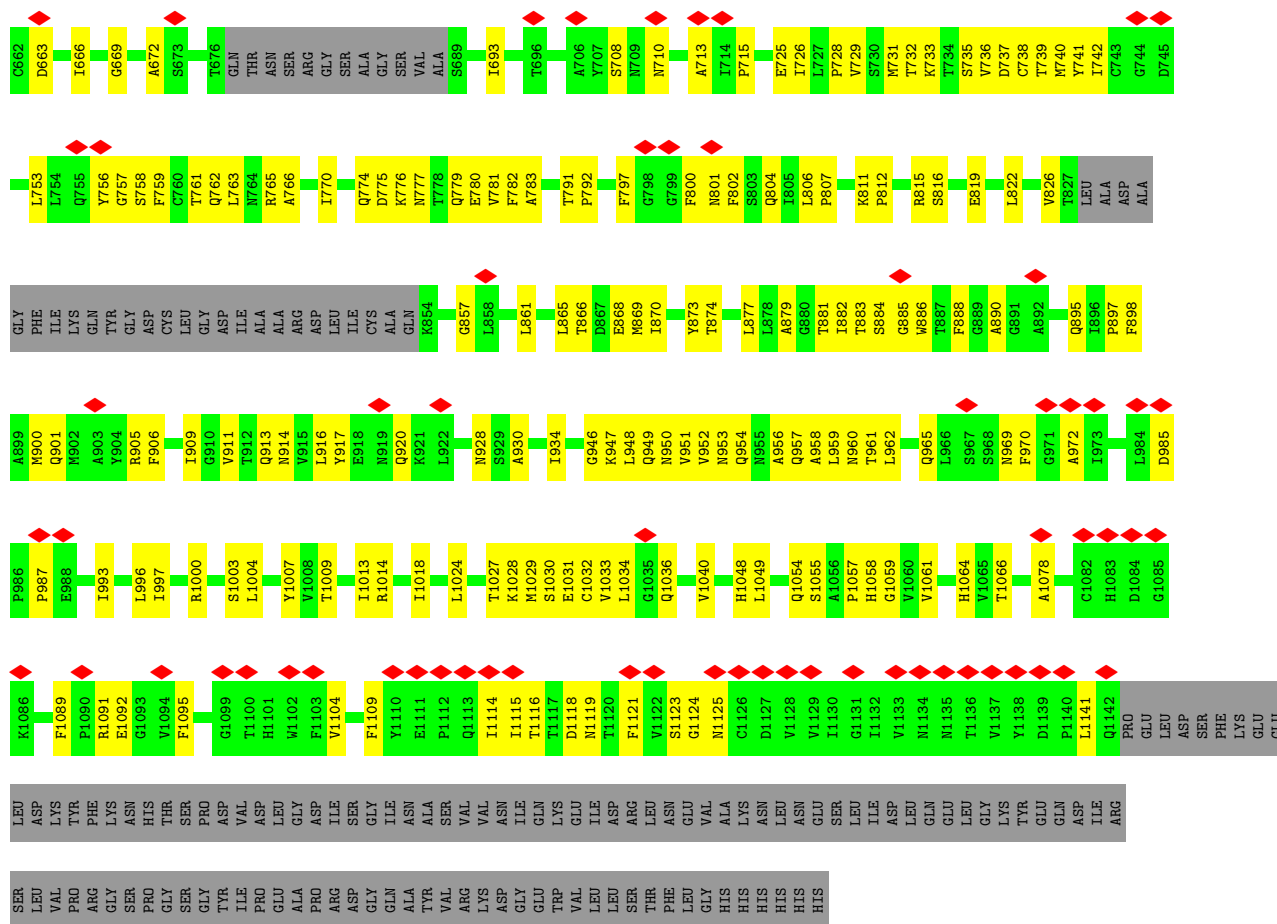
Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	106	Total	C	N	O	S	0	0
			815	514	131	167	3		
3	J	107	Total	C	N	O	S	0	0
			826	520	135	168	3		

3 Residue-property plots

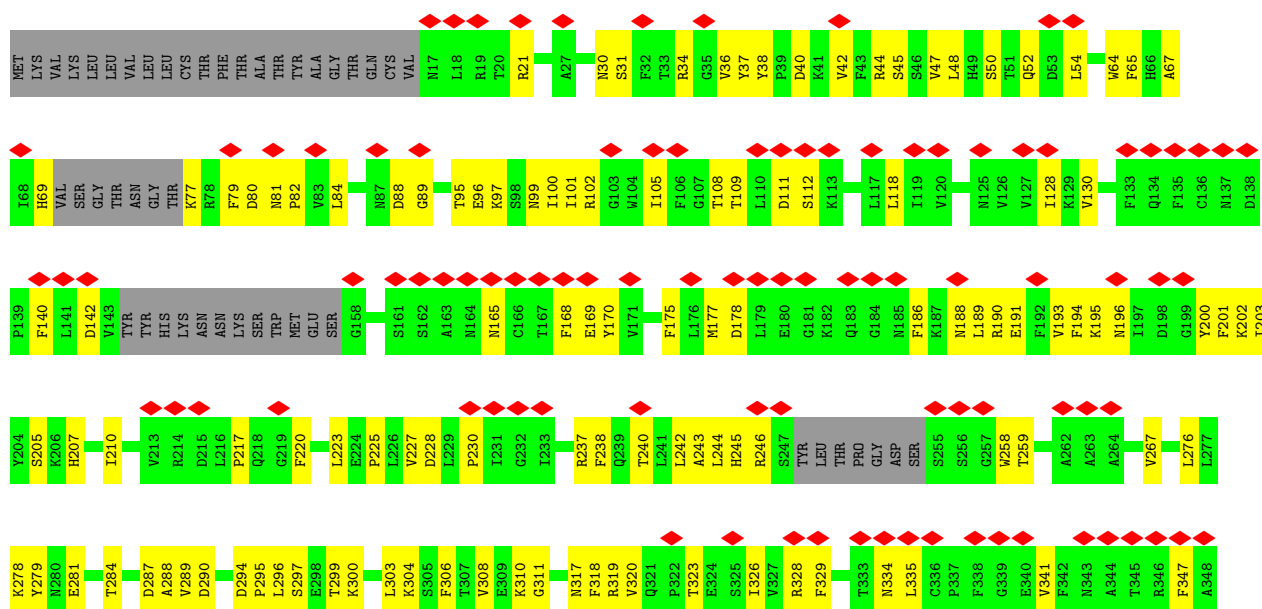
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



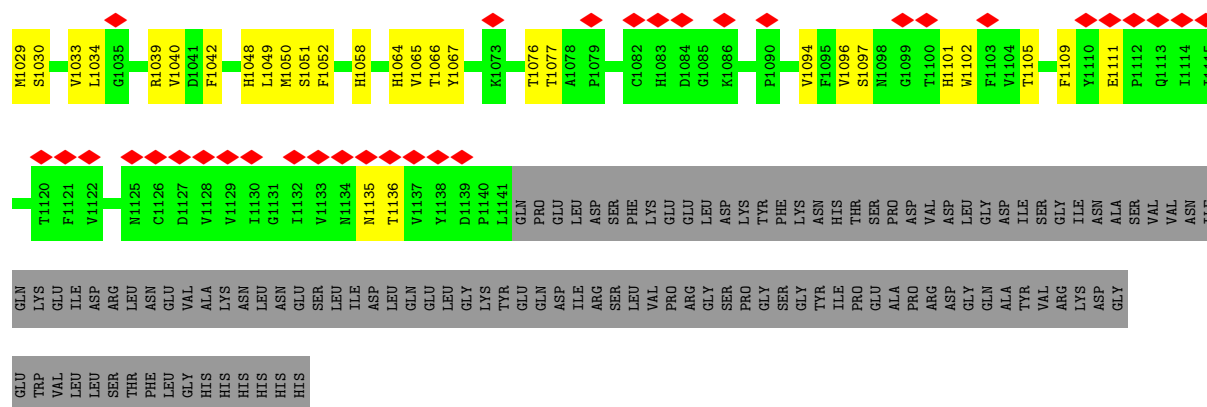


• Molecule 1: Spike glycoprotein

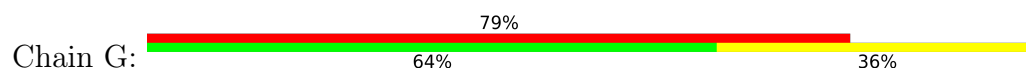




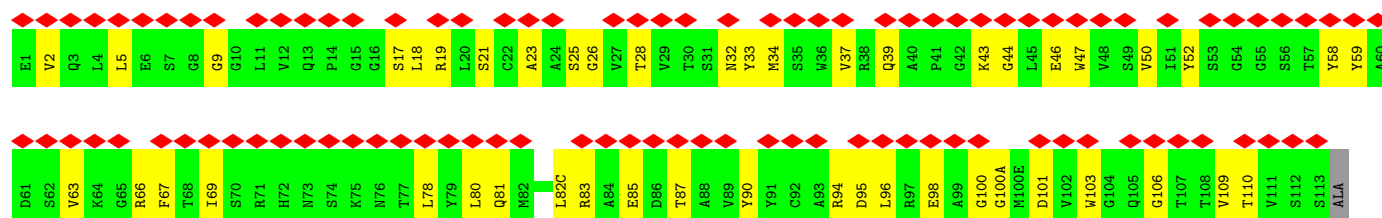
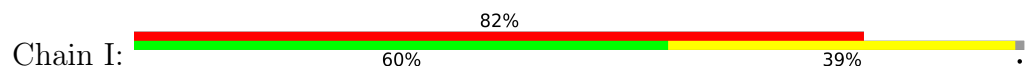
V952	A879	K811	P728	SER	H641	S555	F491	Y421	E340	V267	G199	Q134	A67	MET
N953	G880	R815	M731	H641	S555	L492	L492	N422	E340	V267	Y200	F135	I68	LYS
N954	I881	S816	T732	F643	L560	Q493	Q493	Y423	T345	Y269	K201	C136	H69	VAL
N955	I882	F817	K733	F643	F561	S494	S494	Q431	A348	R273	I203	N137	SER	LEU
Q957	S864	F818	T734	F643	F562	Y495	Y495	C432	S349	T274	Y204	D138	THR	LEU
A958	G885	I818				Q496	Q496	C433	V350	F275	S205	P139	GLY	VAL
L959	F888	F819				F497	F497	L434	V351	L277	K206	F140	LEU	LEU
N960		L822	C738	H655	F565	Q498	Q498	L435	A352	K278	H207	L141	GLY	LEU
N961		K825	T739	G566	R567	T500	T500	W436	K353		I210	D142	THR	CYS
L962	A893	H826	M740	D568	R567	N501	N501	N437	S359	E281	L216	Y143	PHE	THR
N963	Q895	T827	I742	I569	I569	G502	G502	N438	N360	D287	P217	Y144	THR	ALA
Q965	I896	D663	C743	A570	D571	V503	V503	N439	C361	A288	Q218	Y145	THR	ALA
L966	F897	D663	G744	A570	D571	G504	G504	N440	C362	V289	G219	H146	THR	THR
Q967	F898	D663	D745	A570	D571	V505	V505	N440	C363	D290	F220	K147	THR	THR
S968		D663	E748	A575		V506	V506	N440	C364	C291	P225	N148	ALA	ALA
N969	Q901	I670				G507	G507	N440	D364	A292	L226	N149	GLY	GLY
N970	M902	C671				V508	V508	N440	V367	L293	V227	M153	THR	THR
Q971	A903	A672	L752	L582	F583	V511	V511	N440	N360	D294	D228	E154	GLN	GLN
N972	Y904	S673	L753	F583	I584	V513	V513	N440	C361	A292	V227	M153	VAL	VAL
Q973	R905	G674	L754	I584		V515	V515	N440	C362	D294	D228	E154	ASN	ASN
L977	F906	Q675	Q755	T588		V517	V517	N440	V367	L293	V227	M153	LEU	LEU
N978	N907	T676	Y756	P589		V518	V518	N440	N360	D294	D228	E154	ARG	ARG
N979	G908	T676	Y756	C590		V519	V519	N440	N360	D294	D228	E154	T20	T20
N980	Q909	T676	Y756	C590		V521	V521	N440	N360	D294	D228	E154	R21	R21
L981	G910	T676	Y756	C590		V523	V523	N440	N360	D294	D228	E154	T22	T22
Q982	V911	T676	Y756	C590		V525	V525	N440	N360	D294	D228	E154	Q23	Q23
N983	Q913	T676	Y756	C590		V527	V527	N440	N360	D294	D228	E154	L24	L24
L984	N914	T676	Y756	C590		V529	V529	N440	N360	D294	D228	E154	P25	P25
N985	V915	T676	Y756	C590		V531	V531	N440	N360	D294	D228	E154	P26	P26
P986	L916	T676	Y756	C590		V533	V533	N440	N360	D294	D228	E154	A27	A27
N987	E917	T676	Y756	C590		V535	V535	N440	N360	D294	D228	E154	Y28	Y28
Q992	N919	T676	Y756	C590		V537	V537	N440	N360	D294	D228	E154	T29	T29
N993	Q920	T676	Y756	C590		V539	V539	N440	N360	D294	D228	E154	G35	G35
N994	A924	T676	Y756	C590		V541	V541	N440	N360	D294	D228	E154	V36	V36
L995	N928	T676	Y756	C590		V543	V543	N440	N360	D294	D228	E154	D40	D40
L996	S929	T676	Y756	C590		V545	V545	N440	N360	D294	D228	E154	K41	K41
N997	N930	T676	Y756	C590		V547	V547	N440	N360	D294	D228	E154	V42	V42
N998	Q930	T676	Y756	C590		V549	V549	N440	N360	D294	D228	E154	F43	F43
L1000	I934	T676	Y756	C590		V551	V551	N440	N360	D294	D228	E154	R44	R44
L1004	L338	T676	Y756	C590		V553	V553	N440	N360	D294	D228	E154	S46	S46
Q1005	S939	T676	Y756	C590		V555	V555	N440	N360	D294	D228	E154	V47	V47
L1006	E868	T676	Y756	C590		V557	V557	N440	N360	D294	D228	E154	S50	S50
Y1007	M869	T676	Y756	C590		V559	V559	N440	N360	D294	D228	E154	T51	T51
V1008	T941	T676	Y756	C590		V561	V561	N440	N360	D294	D228	E154	Q52	Q52
L1014	A942	T676	Y756	C590		V563	V563	N440	N360	D294	D228	E154	D53	D53
L1018	S943	T676	Y756	C590		V565	V565	N440	N360	D294	D228	E154	L54	L54
L1019	Q944	T676	Y756	C590		V567	V567	N440	N360	D294	D228	E154	F55	F55
L1020	G946	T676	Y756	C590		V569	V569	N440	N360	D294	D228	E154	L56	L56
L1024	Q947	T676	Y756	C590		V571	V571	N440	N360	D294	D228	E154	P57	P57
L1028	N950	T676	Y756	C590		V573	V573	N440	N360	D294	D228	E154	N61	N61
	V951	L878	L878	L878	L878	L878	L878	L878	L878	L878	L878	L878	H66	H66



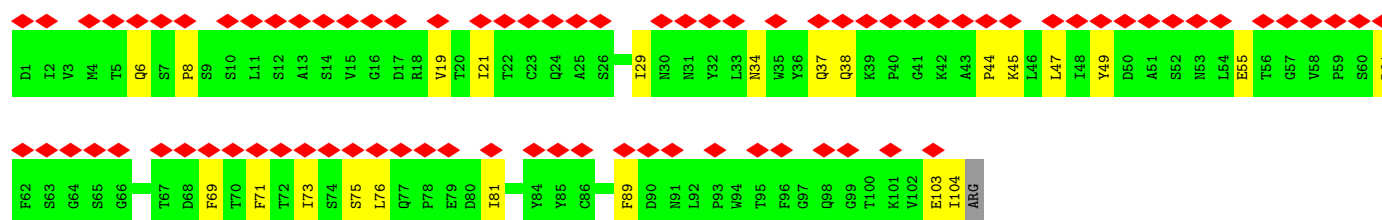
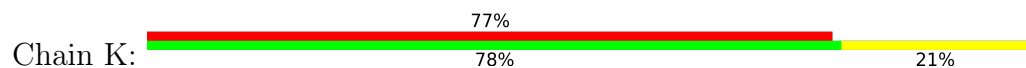
• Molecule 2: Fab heavy chain of JE-5C



• Molecule 2: Fab heavy chain of JE-5C

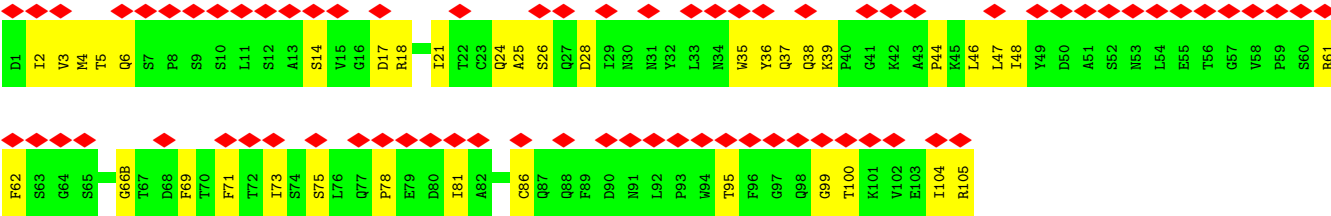


• Molecule 3: Fab light chain of JE-5C



• Molecule 3: Fab light chain of JE-5C





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	180312	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 ($e^-/\text{\AA}^2$)	1.1	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.053	Depositor
Minimum map value	-0.034	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0034	Depositor
Map size (Å)	318.72, 318.72, 318.72	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	0.15	0/8323	0.37	0/11321
1	C	0.15	0/8205	0.37	0/11160
1	D	0.17	0/8287	0.39	0/11271
2	G	0.13	0/905	0.37	0/1228
2	I	0.12	0/900	0.36	0/1221
3	J	0.10	0/845	0.34	0/1151
3	K	0.12	0/834	0.38	0/1137
All	All	0.15	0/28299	0.38	0/38489

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	8138	0	7957	304	0
1	C	8023	0	7814	265	0
1	D	8102	0	7896	297	0
2	G	889	0	857	36	0
2	I	884	0	852	40	0
3	J	826	0	787	28	0
3	K	815	0	774	17	0
All	All	27677	0	26937	918	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 17.

The worst 5 of 918 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:GLY:HA3	1:A:613:GLN:O	1.37	1.24
1:A:142:ASP:HB2	1:A:258:TRP:CZ3	1.86	1.09
1:D:332:ILE:HG22	1:D:333:THR:H	1.13	1.07
1:A:142:ASP:OD2	1:A:258:TRP:CZ2	2.12	1.02
1:C:140:PHE:CE1	1:C:142:ASP:HB3	1.96	1.00

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1028/1259 (82%)	964 (94%)	64 (6%)	0	100	100
1	C	1009/1259 (80%)	950 (94%)	59 (6%)	0	100	100
1	D	1019/1259 (81%)	962 (94%)	54 (5%)	3 (0%)	36	70
2	G	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
2	I	116/119 (98%)	105 (90%)	11 (10%)	0	100	100
3	J	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
3	K	104/107 (97%)	94 (90%)	10 (10%)	0	100	100
All	All	3498/4229 (83%)	3287 (94%)	208 (6%)	3 (0%)	49	81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	332	ILE
1	D	337	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	330	PRO

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	908/1091 (83%)	907 (100%)	1 (0%)	88	90
1	C	892/1091 (82%)	891 (100%)	1 (0%)	88	90
1	D	902/1091 (83%)	902 (100%)	0	100	100
2	G	94/95 (99%)	94 (100%)	0	100	100
2	I	94/95 (99%)	94 (100%)	0	100	100
3	J	93/94 (99%)	93 (100%)	0	100	100
3	K	92/94 (98%)	92 (100%)	0	100	100
All	All	3075/3651 (84%)	3073 (100%)	2 (0%)	87	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	317	ASN
1	A	52	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1054	GLN
3	K	34	ASN
3	J	27	GLN
1	A	544	ASN
1	A	501	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

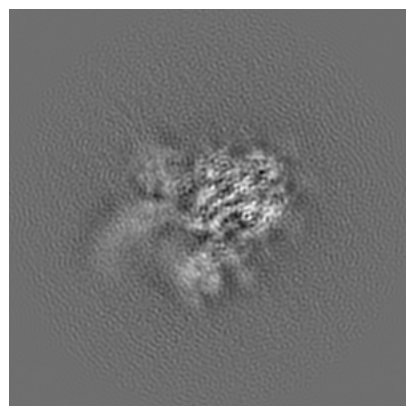
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39685. These allow visual inspection of the internal detail of the map and identification of artifacts.

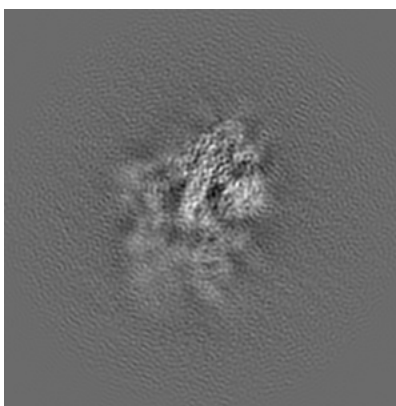
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

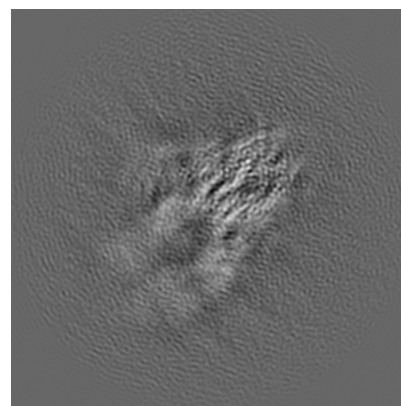
6.1.1 Primary map



X

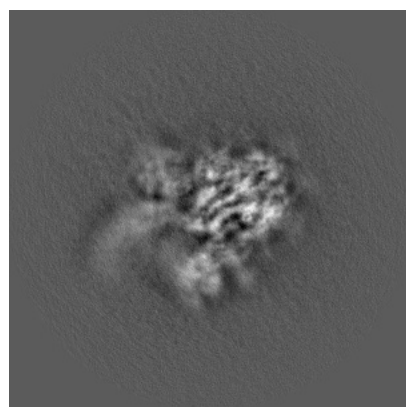


Y

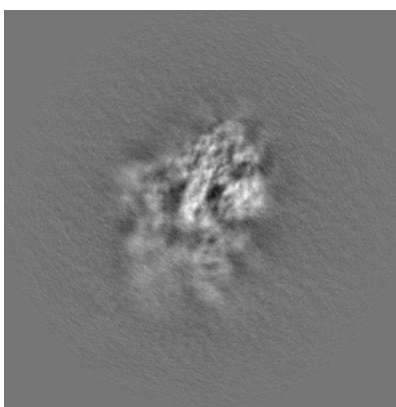


Z

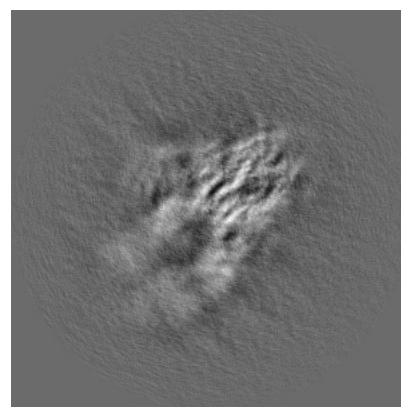
6.1.2 Raw map



X



Y

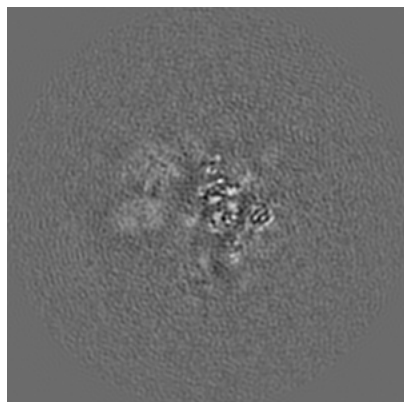


Z

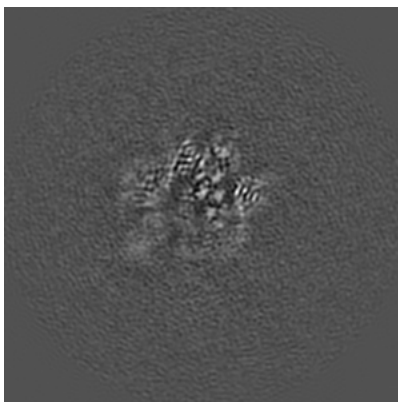
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

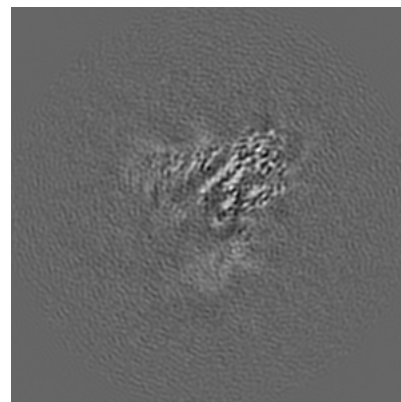
6.2.1 Primary map



X Index: 192

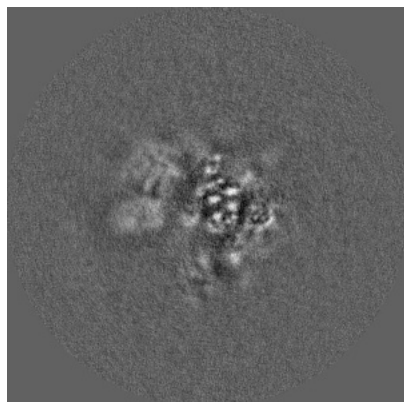


Y Index: 192

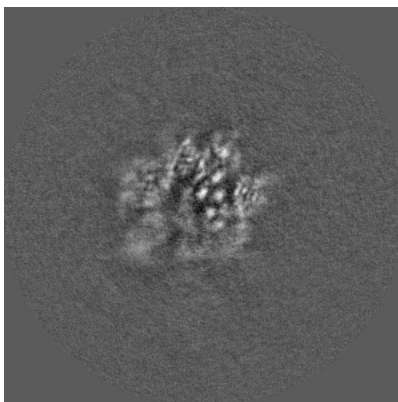


Z Index: 192

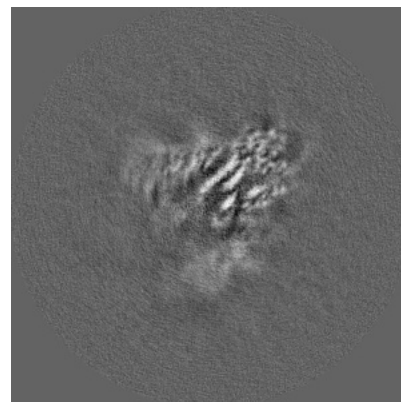
6.2.2 Raw map



X Index: 192



Y Index: 192

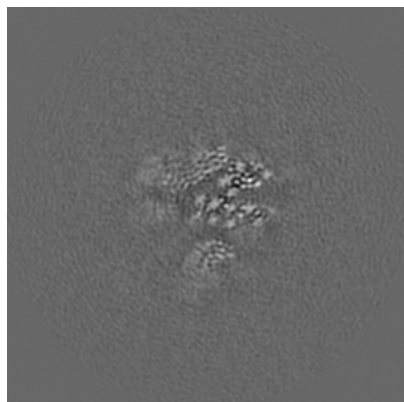


Z Index: 192

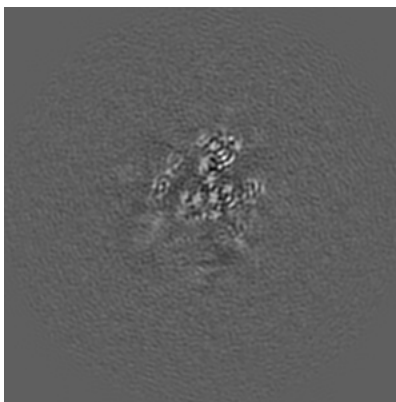
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

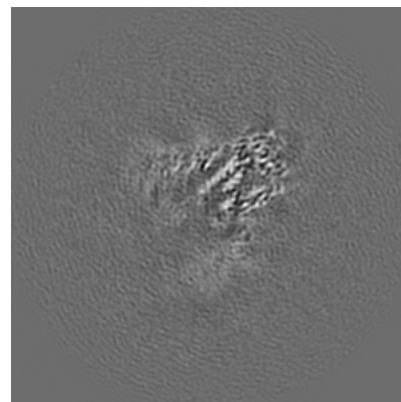
6.3.1 Primary map



X Index: 211

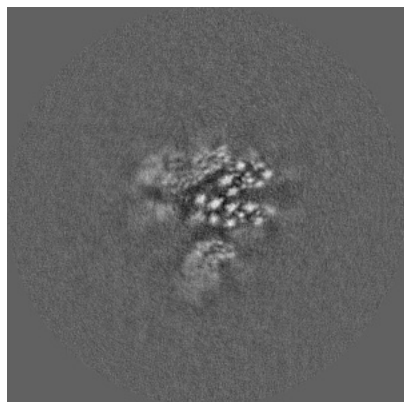


Y Index: 206

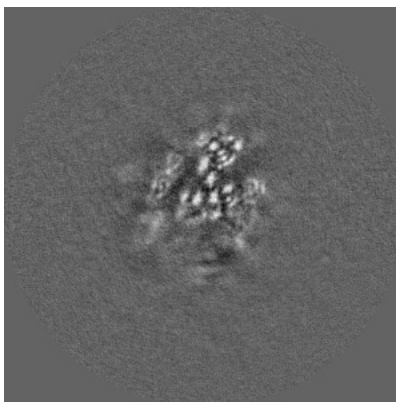


Z Index: 191

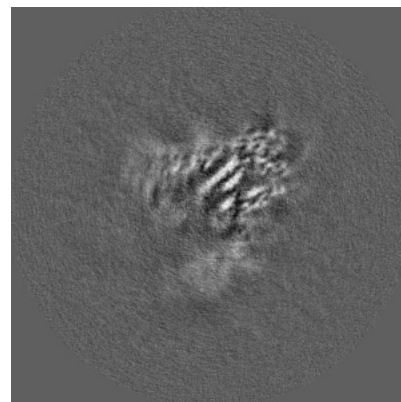
6.3.2 Raw map



X Index: 212



Y Index: 206

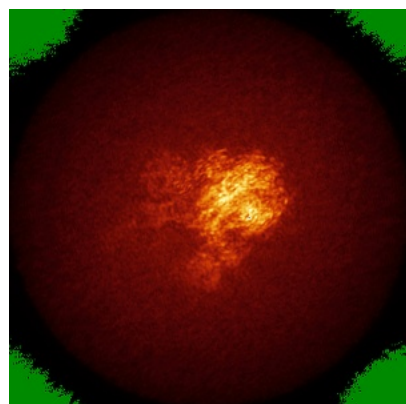


Z Index: 191

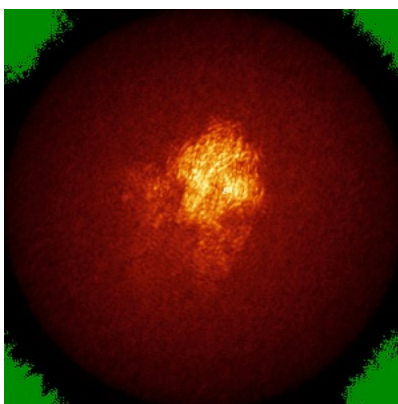
The images above show the largest variance slices of the map in three orthogonal directions.

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

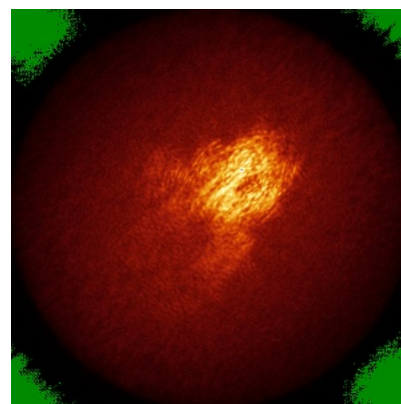
6.4.1 Primary map



X

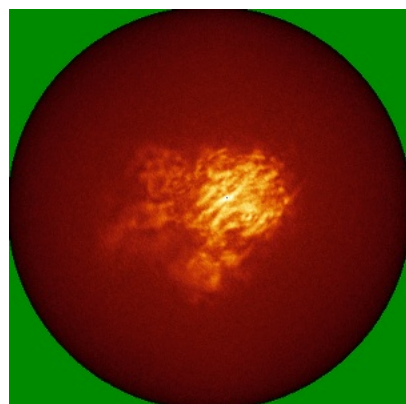


Y

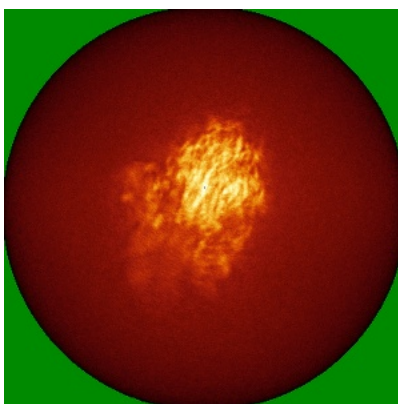


Z

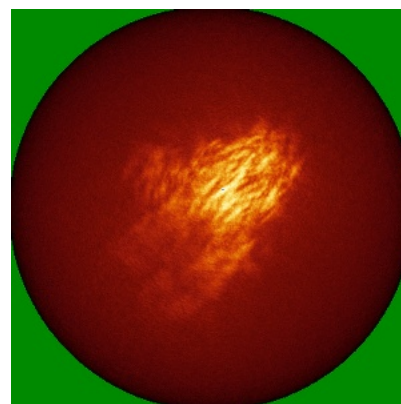
6.4.2 Raw map



X



Y

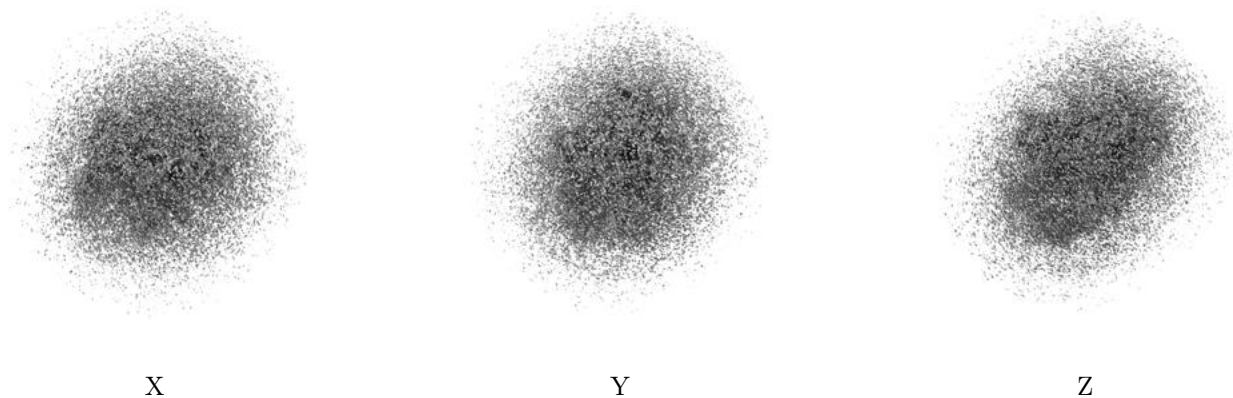


Z

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

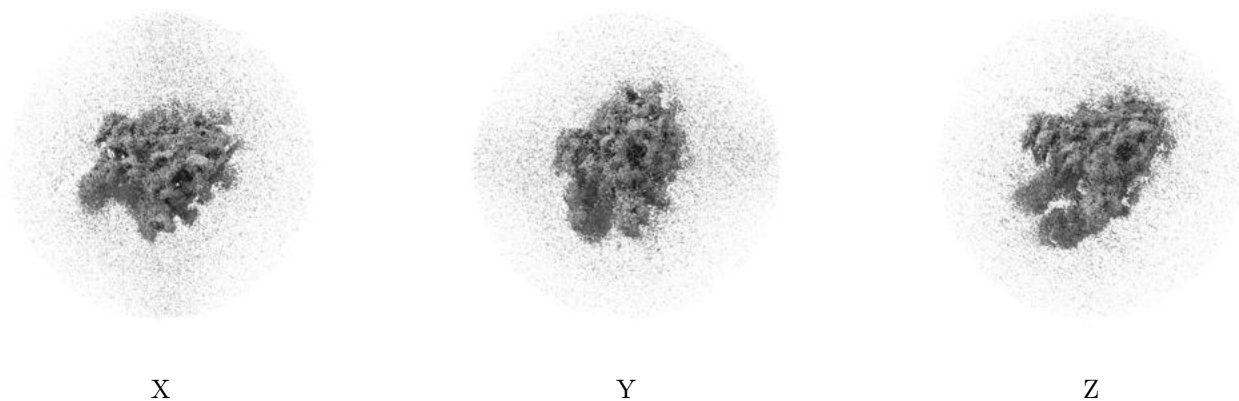
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0034. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

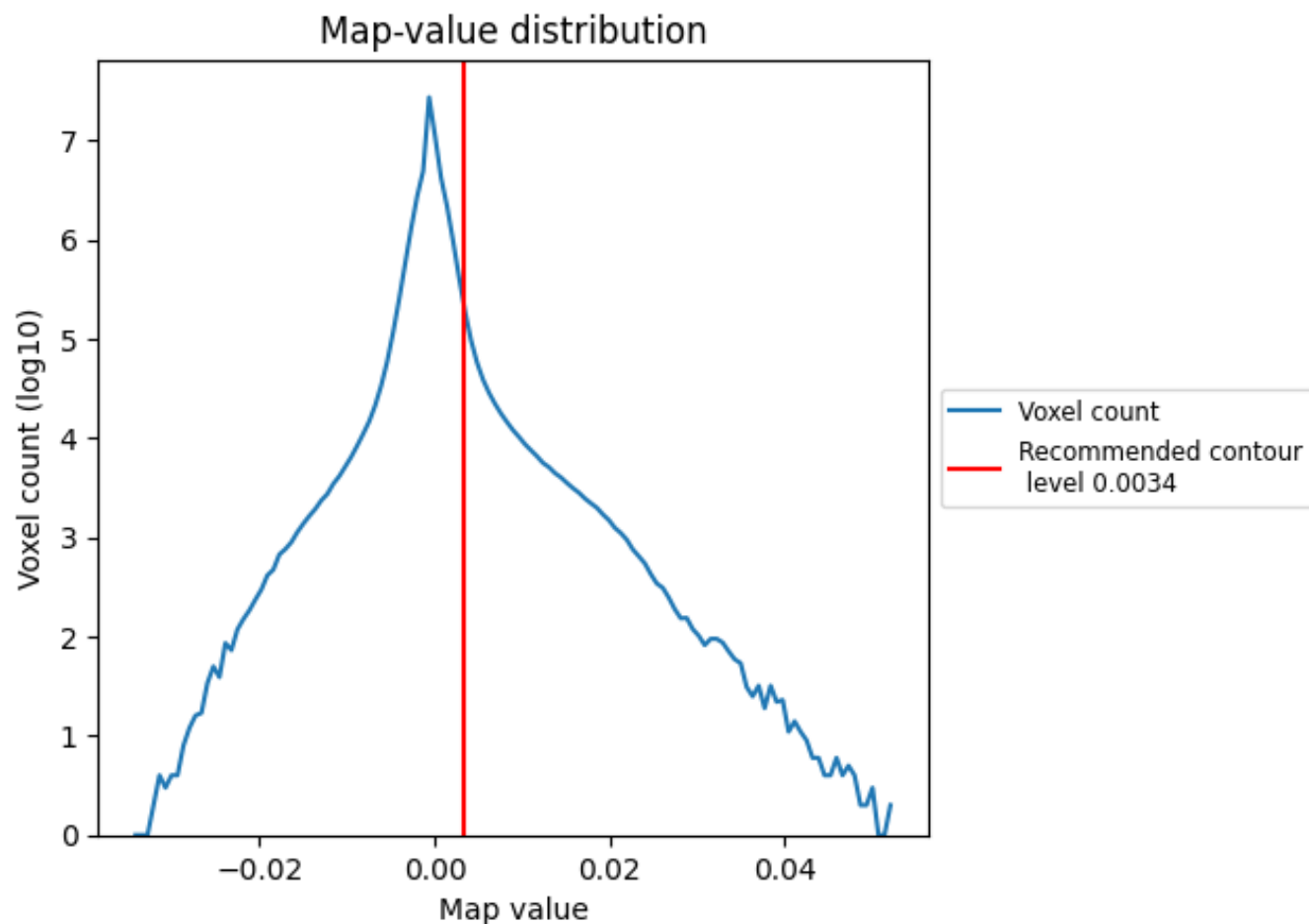
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

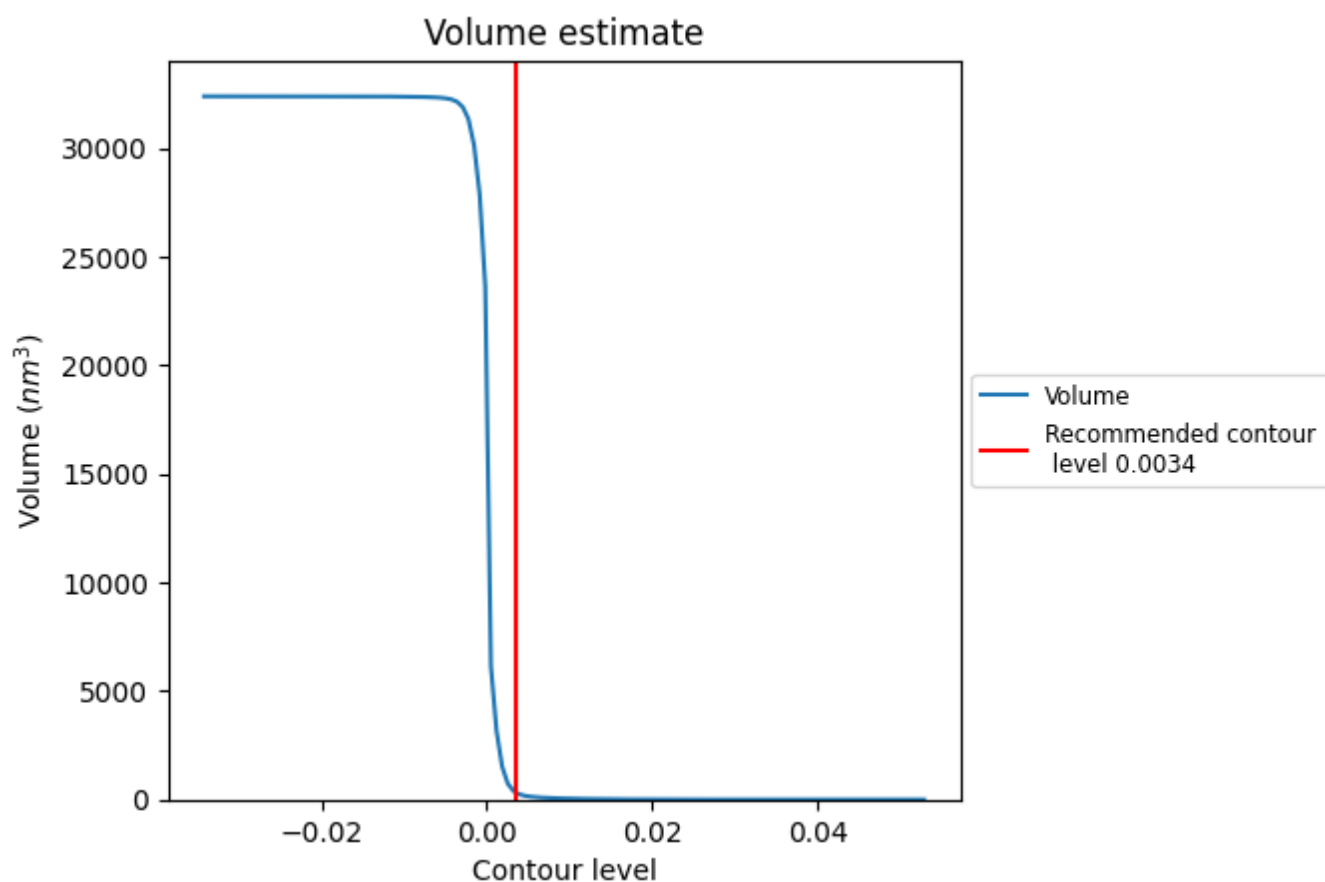
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

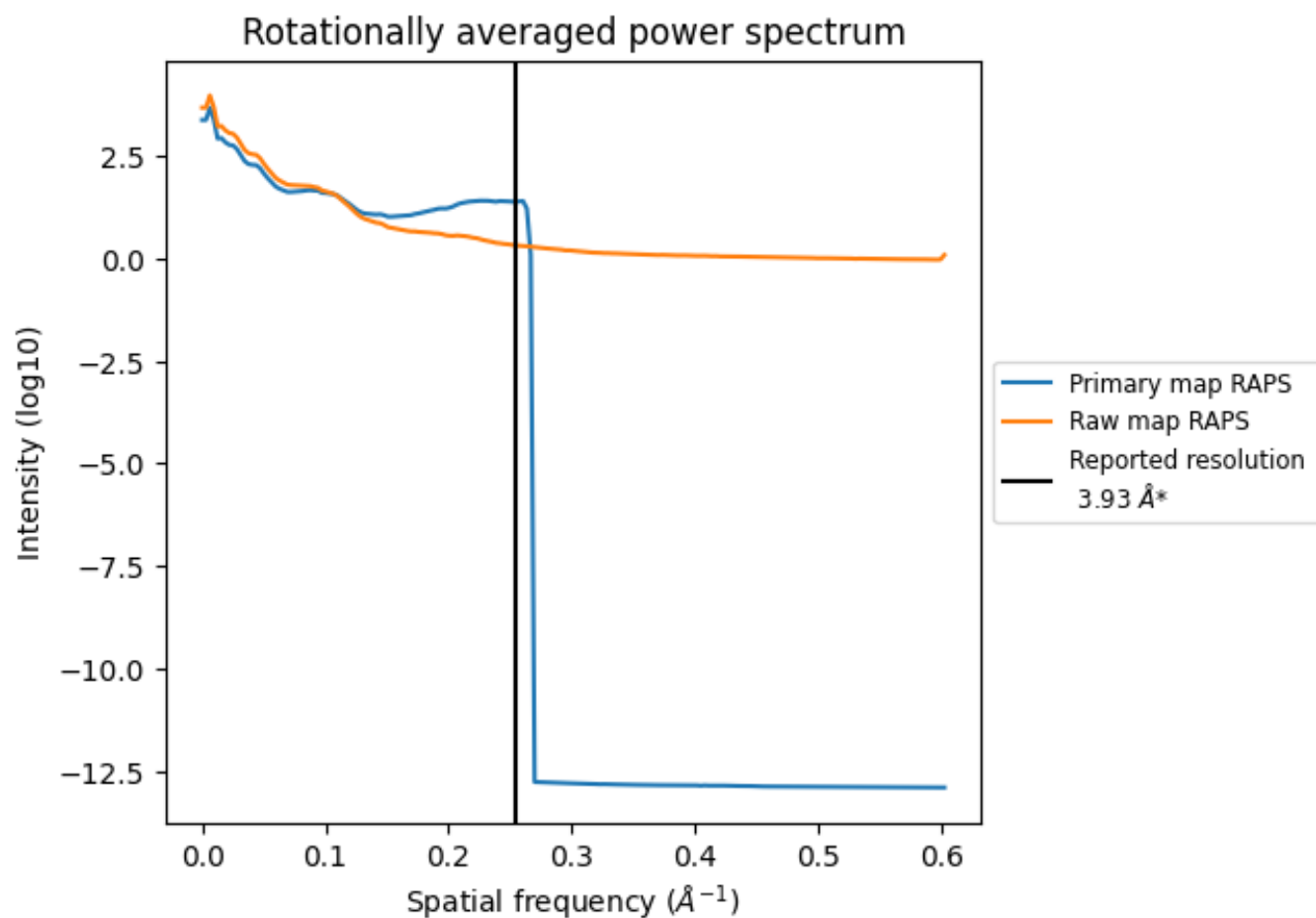
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 356 nm³; this corresponds to an approximate mass of 321 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 ⓘ

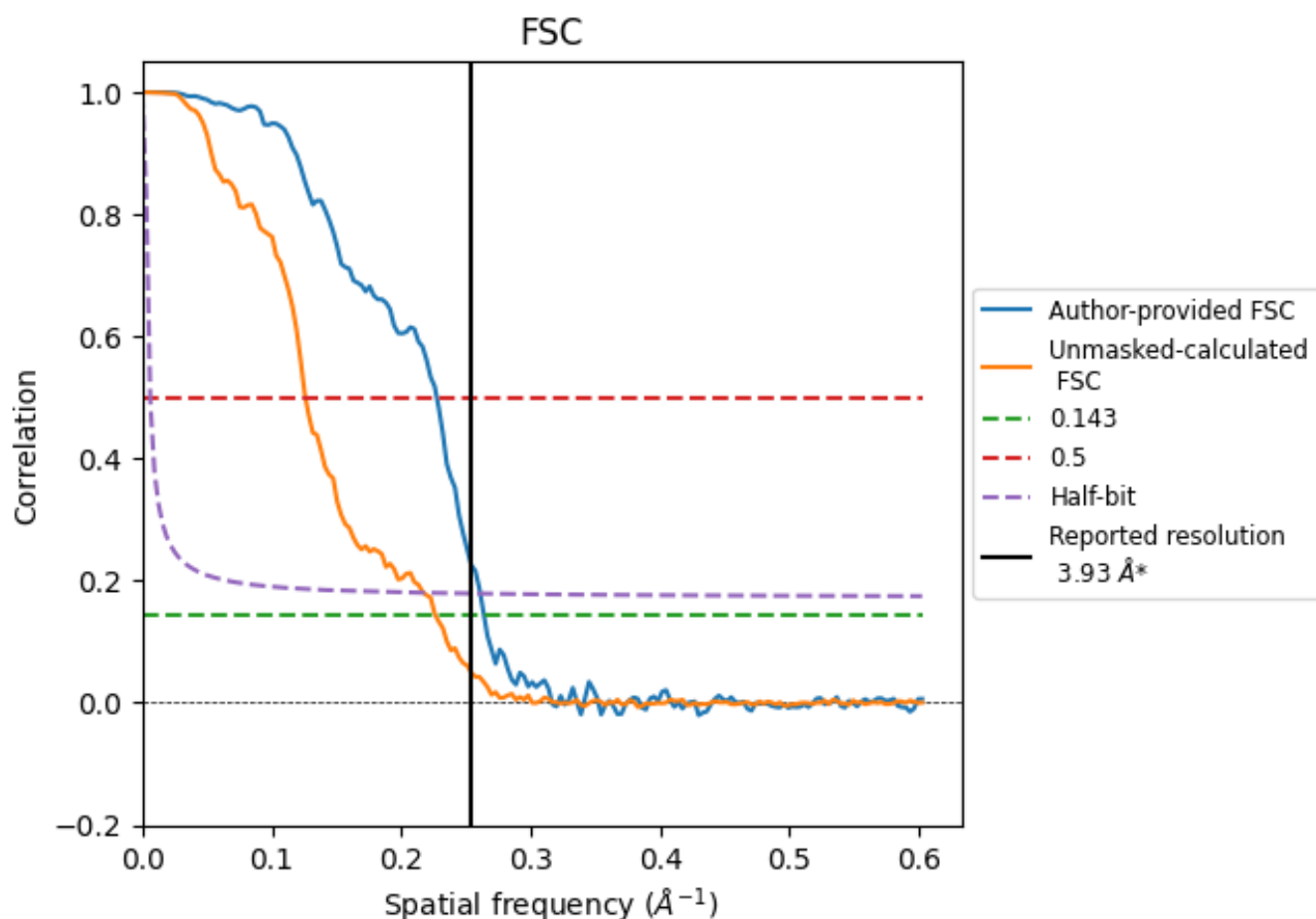


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

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 0.254 Å⁻¹

8.2 Resolution estimates [i](#)

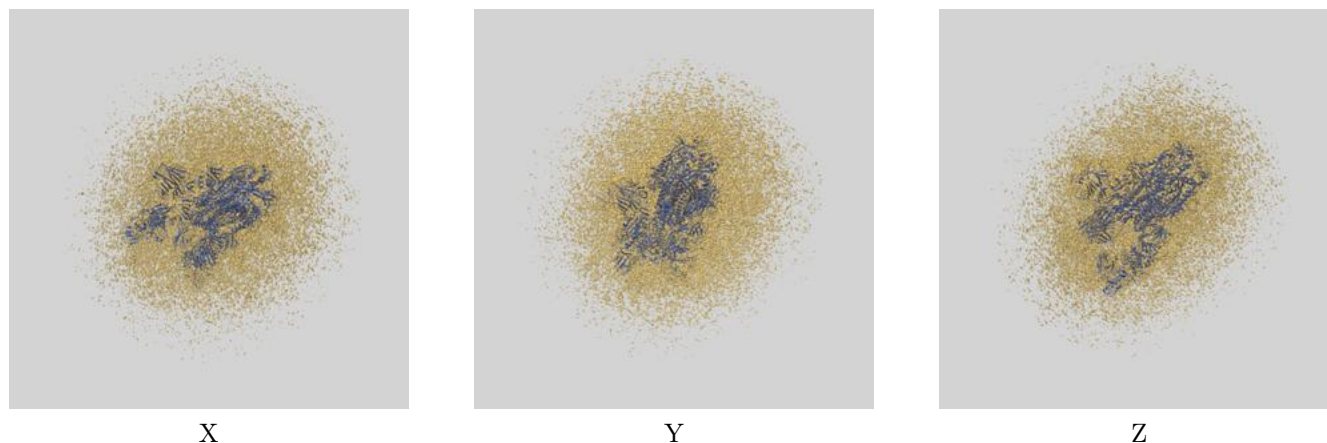
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	3.79	4.40	3.83
Unmasked-calculated*	4.41	7.93	4.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.41 differs from the reported value 3.93 by more than 10 %

9 Map-model fit [i](#)

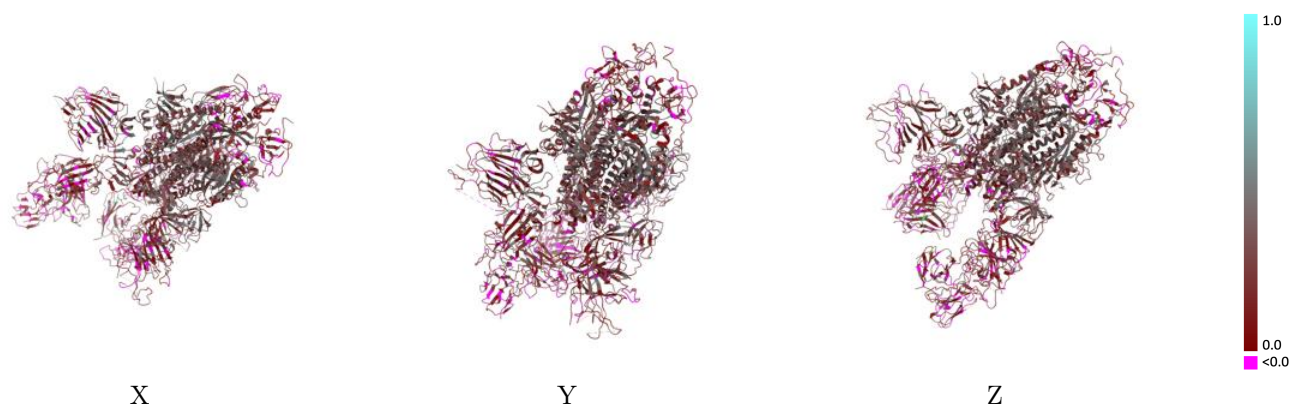
This section contains information regarding the fit between EMDB map EMD-39685 and PDB model 8YZ5. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



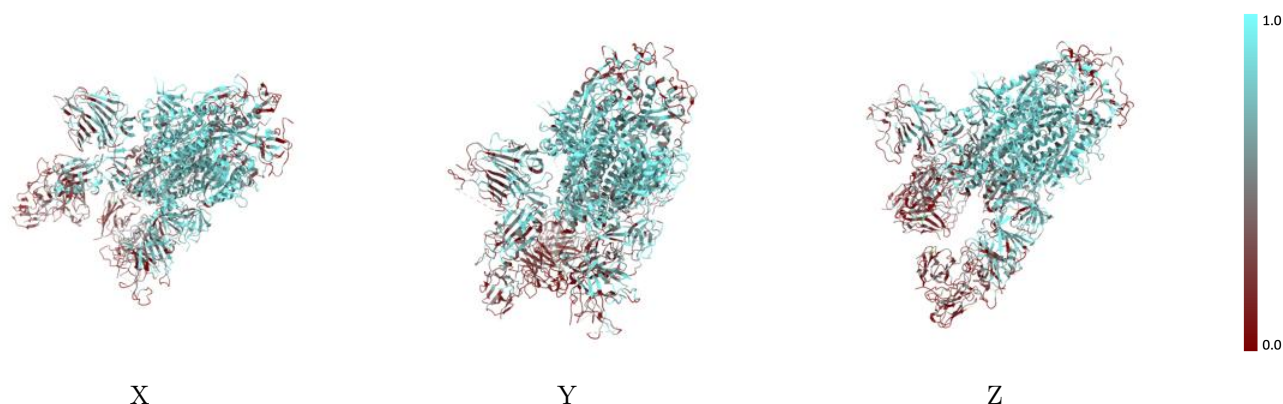
The images above show the 3D surface view of the map at the recommended contour level 0.0034 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



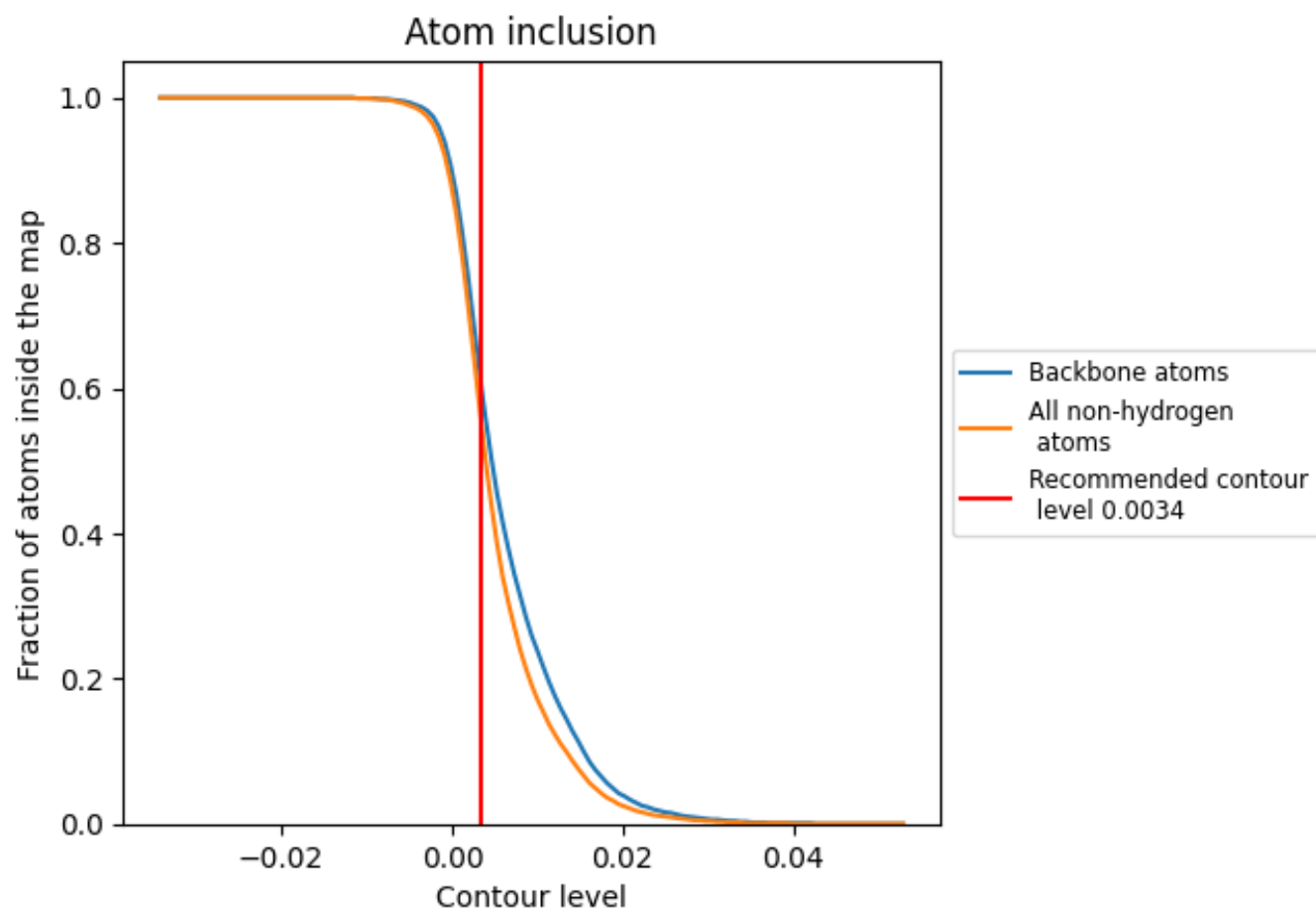
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0034).

9.4 Atom inclusion [i](#)



At the recommended contour level, 60% of all backbone atoms, 55% 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 (0.0034) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5510	0.2340
A	0.5840	0.2450
C	0.6070	0.2490
D	0.5930	0.2450
G	0.2270	0.1510
I	0.1650	0.1590
J	0.3140	0.1480
K	0.2490	0.1370

1.0

0.0

<0.0