



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:27 PM UTC

PDB ID : 8F5O / pdb_00008f5o
EMDB ID : EMD-28866
Title : Structure of Leishmania tarentolae IFT-A (state 1)
Authors : Zhou, H.; Brown, A.
Deposited on : 2022-11-14
Resolution : 3.50 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:

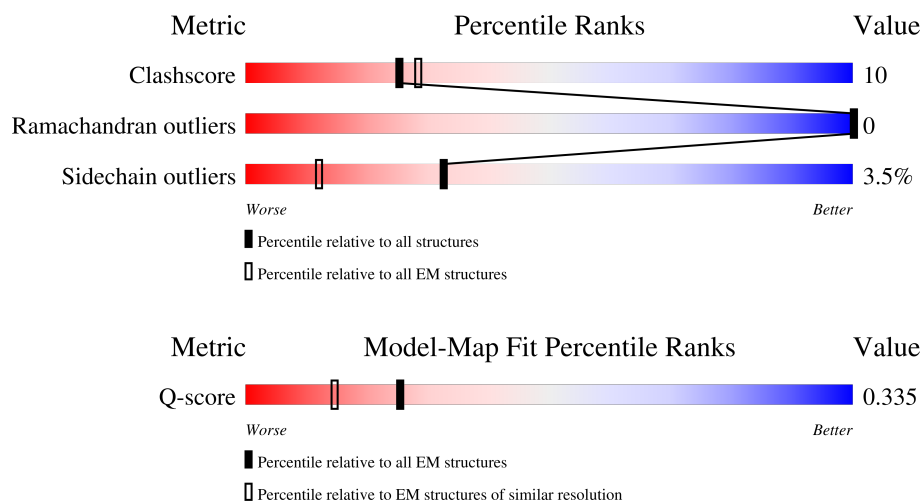
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	B	1247	
2	C	1292	
3	E	1654	
4	A	368	

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Mol	Chain	Length	Quality of chain
5	F	1376	31% 54% 12% 34%
6	D	1642	47% 23% 28%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 43398 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 Intraflagellar transport protein 122B, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1134	Total	C	N	O	S	0	0
			8965	5674	1570	1658	63		

- Molecule 2 is a protein called Intraflagellar transport protein 122 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1179	Total	C	N	O	S	0	0
			9354	5929	1622	1735	68		

- Molecule 3 is a protein called WD_REPEATS_REGION domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	1076	Total	C	N	O	S	0	0
			8380	5291	1451	1588	50		

- Molecule 4 is a protein called NET domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	53	Total	C	N	O	S	0	0
			427	264	69	87	7		

- Molecule 5 is a protein called WD_REPEATS_REGION domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	911	Total	C	N	O	S	0	0
			7045	4431	1231	1349	34		

- Molecule 6 is a protein called TPR_REGION domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	1180	Total	C	N	O	S	0	0
			9223	5796	1638	1738	51		

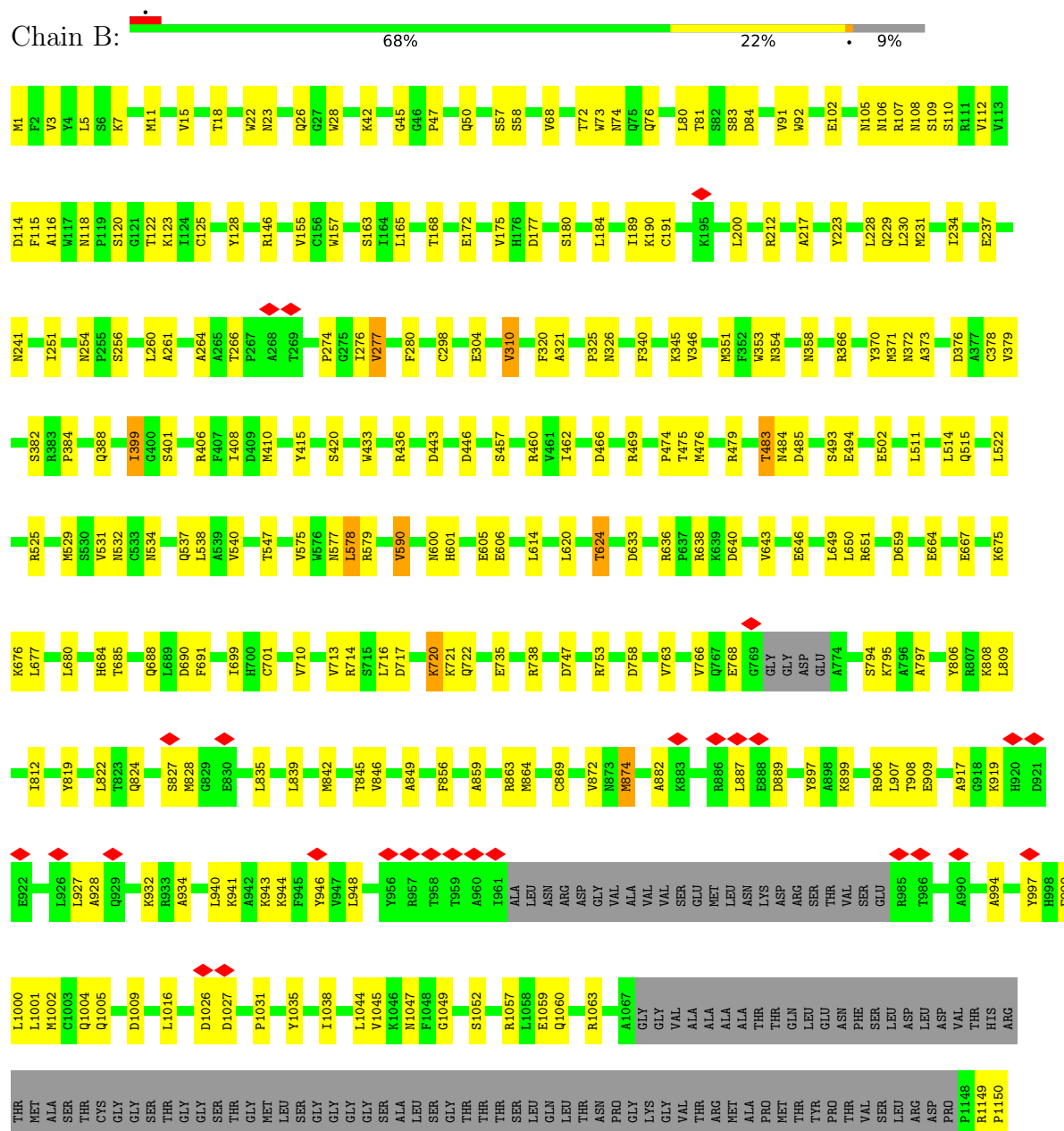
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

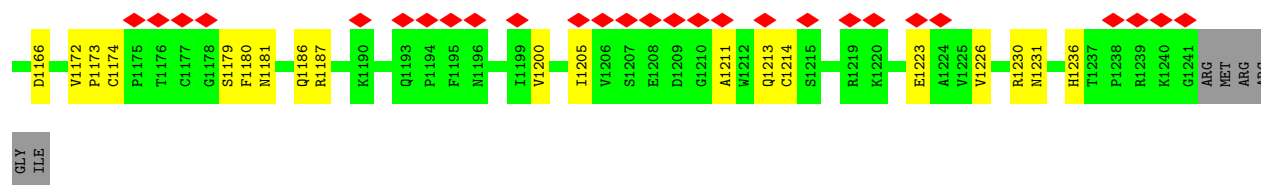
Mol	Chain	Residues	Atoms		AltConf
7	B	2	Total 2	Zn 2	0
7	C	2	Total 2	Zn 2	0

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.

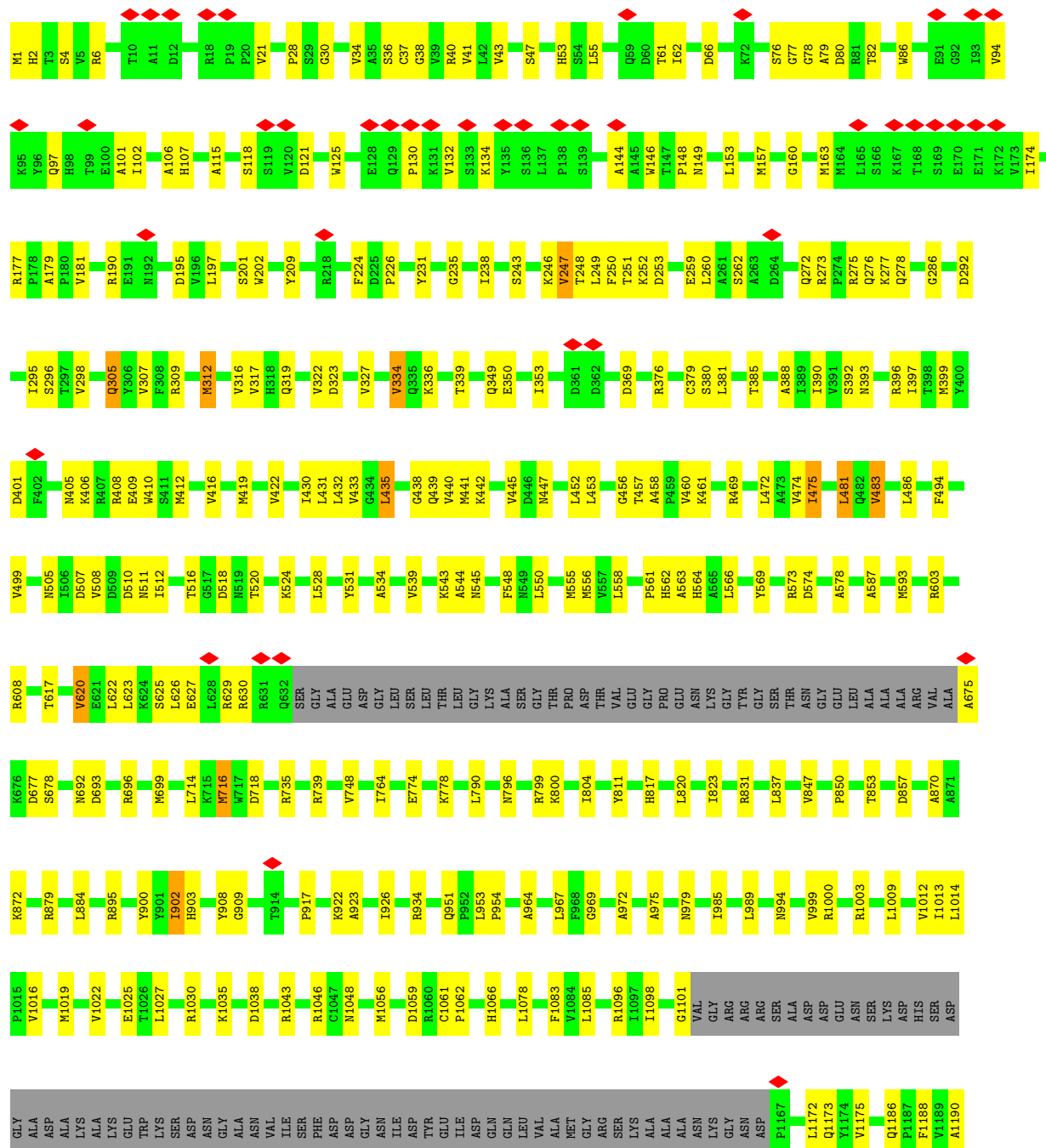
- Molecule 1: Intraflagellar transport protein 122B, putative

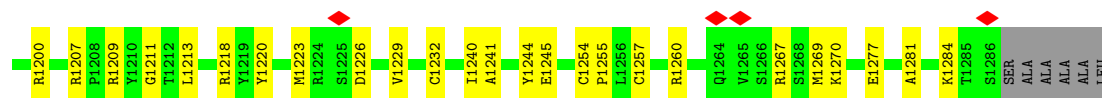




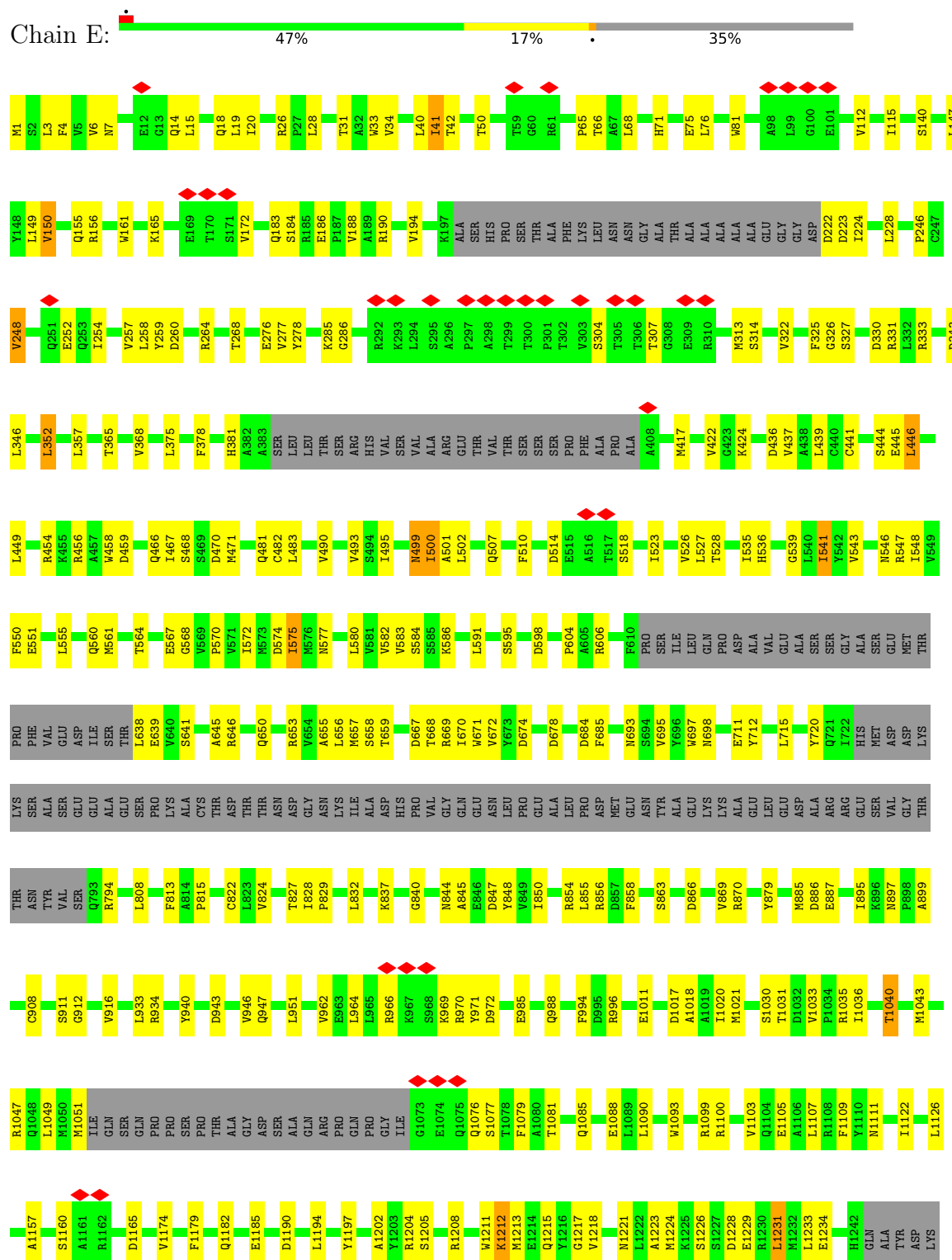
• Molecule 2: Intraflagellar transport protein 122 homolog

Chain C: 67% 24% 9%





• Molecule 3: WD_REPEATS_REGION domain-containing protein



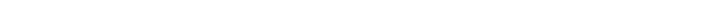
GLN	ASP	GLU	ILE	TRP	VAL	ALA
ALA	HIS	MET	TYR	SER	GLN	VAL
ASN	GLY	GLU	LYS	LEU	MET	GLN
GLY	SER	LYS	SER	ALA	LEU	TYR
LYS	LEU	VAL	ILE	LYS	PHE	ARG
SER	ILE	GLU	VAL	LYS	ALA	ARG
LEU	ASP	GLN	LEU	LYS	LYS	GLY
ALA	ASN	LEU	PHE	TYR	HIS	ALA
ASN	ALA	LYS	THR	THR	PHE	VAL
VAL	LEU	GLN	TYR	GLN	ALA	GLN
LEU	ARG	ARG	LYS	ALA	GLU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

- Molecule 4: NET domain-containing protein

Chain A: 10% 86%

[illegible]

- Molecule 5: WD REPEATS REGION domain-containing protein

Chain F: 

E61	W62	E63	C64	S65	T66	D67	T68	L69	A70	I71	I72	T73	S74	S75	S76	S77	D78	V79	H80	L81	Y82	T83	H84	R85	T86	R87	Q88	T89	D90	T91	I92	D93	T94	K95	L96	K97	D98	C100	F101	I102	C103	W104	S105	Q106	S107	Q108	P109	L110	F111	A112	I113	G114	S115	K116	S117	G118	Q119	Q120	
M1	V2	L3	T4	Q5	Q6	F7	W8	I9	S10	M11	A12	D13	L14	G15	R16	G17	H18	V19	V20	E21	A22	L23	H24	P25	S26	S27	P28	L29	I30	A31	L32	A33	G34	S35	X36	G37	R38	V39	L40	I41	L42	H43	X44	T45	G46	K47	V48	E49	H50	Q51	L52	P53	M54	Q55	M56	V57	M58	A59	W60

ALA	VAL	PRO	THR	ASP	SER	ALA	Q769	V637	L502	F389	D301	F241	V181	V121
VAL	ASP	LYS	LEU	SER	ASN	ALA	W770	L651	T505	L390	G302	L242	P182	L122
PRO	THR	THR	GLU	THR	GLN	VAL	R772	L651	T505	A399	I303	A243	K183	Y123
THR	THR	THR	ALA	ASN	ASP	ALA	E784	N655	V511	A401	A304	G244	S184	N124
PRO	THR	THR	THR	THR	THR	LYS	W785	N656	L514	Q404	P305	F245	V185	R125
MET	MET	VAL	THR	ILE	THR	CYS	I787	R660	T522	E409	T306	A246	C186	R126
THR	THR	THR	THR	THR	THR	THR	F788	T661	T522	Q404	D308	S247	V187	T127
THR	THR	THR	THR	THR	THR	THR	S789	T661	R531	E409	E309	G248	S188	L128
THR	THR	THR	THR	THR	THR	THR	Q794	E665	R531	I412	E309	T249	G189	R129
THR	THR	THR	THR	THR	THR	THR	H795	L673	A532	P80	A310	V250	M190	L130
THR	THR	THR	THR	THR	THR	THR	L796	L673	F533	ASN	S311	A251	A191	V131
THR	THR	THR	THR	THR	THR	THR	E797	R677	A534	SER	L312	L252	N192	P132
THR	THR	THR	THR	THR	THR	THR	R798	W677	N535	LEU	E313	L253	N192	V132
THR	THR	THR	THR	THR	THR	THR	R799	W678	T539	PRO	S314	D254	P194	V133
THR	THR	THR	THR	THR	THR	THR	G800	W679	V556	TYR	E315	L255	K195	A134
THR	THR	THR	THR	THR	THR	THR	W801	N681	Q570	PRO	R316	A256	S196	D135
THR	THR	THR	THR	THR	THR	THR	Y802	Q687	K571	VAL	G317	A257	S197	T136
THR	THR	THR	THR	THR	THR	THR	A805	E690	N572	ASP	V318	S258	S198	H137
THR	THR	THR	THR	THR	THR	THR	F807	W702	L574	ALA	P319	E259	S197	K138
THR	THR	THR	THR	THR	THR	THR	R803	V702	V582	ASN	D320	V260	F199	Q139
THR	THR	THR	THR	THR	THR	THR	R814	W706	T585	VAL	L321	R261	A200	R140
THR	THR	THR	THR	THR	THR	THR	S822	R707	V586	GLN	L322	L262	V202	L141
THR	THR	THR	THR	THR	THR	THR	W826	V718	V595	A434	L322	R263	N203	I142
THR	THR	THR	THR	THR	THR	THR	V827	V718	H599	L439	A323	G264	L204	S143
THR	THR	THR	THR	THR	THR	THR	E833	W721	S600	E443	W324	S265	D205	M145
THR	THR	THR	THR	THR	THR	THR	E837	L723	S608	S446	R326	L266	N206	W146
THR	THR	THR	THR	THR	THR	THR	Q838	R725	V611	S446	Q329	R267	T207	W147
THR	THR	THR	THR	THR	THR	THR	C839	R725	V611	S446	L331	L268	T207	P148
THR	THR	THR	THR	THR	THR	THR	R840	R725	V611	S446	F332	L269	L208	A149
THR	THR	THR	THR	THR	THR	THR	Q841	R725	V611	S446	G334	K270	L209	Q150
THR	THR	THR	THR	THR	THR	THR	G842	R725	V611	S446	T335	N271	I210	D151
THR	THR	THR	THR	THR	THR	THR	A843	R725	V611	S446	T335	E274	D212	S152
THR	THR	THR	THR	THR	THR	THR	A844	R725	V611	S446	N336	M275	D213	R153
THR	THR	THR	THR	THR	THR	THR	R845	R725	V611	S446	Q337	L154	L214	L154
THR	THR	THR	THR	THR	THR	THR	S846	R725	V611	S446	G338	V276	S215	L155
THR	THR	THR	THR	THR	THR	THR	Q847	R725	V611	S446	N339	N277	Y216	I156
THR	THR	THR	THR	THR	THR	THR	T848	R725	V611	S446	V340	F278	I157	I157
THR	THR	THR	THR	THR	THR	THR	R849	R725	V611	S446	T341	G279	A217	S158
THR	THR	THR	THR	THR	THR	THR	T850	R725	V611	S446	V342	E280	T218	E159
THR	THR	THR	THR	THR	THR	THR	Q851	R725	V611	S446	F343	G281	A219	D160
THR	THR	THR	THR	THR	THR	THR	H852	R725	V611	S446	T344	S282	A220	P161
THR	THR	THR	THR	THR	THR	THR	I853	R725	V611	S446	L345	G283	G221	S162
THR	THR	THR	THR	THR	THR	THR	A854	R725	V611	S446	Q346	V284	F223	L163
THR	THR	THR	THR	THR	THR	THR	D855	R725	V611	S446	V347	V285	N224	S164
THR	THR	THR	THR	THR	THR	THR	W857	R725	V611	S446	L348	A286	S225	I165
THR	THR	THR	THR	THR	THR	THR	R858	R725	V611	S446	N349	A287	S226	S166
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	V350	V288	A227	D167
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	V358	G289	L227	A168
THR	THR	THR	THR	THR	THR	THR	T869	R725	V611	S446	N364	E289	G228	E169
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	R365	D290	Q229	E169
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	L372	N291	I230	G170
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	D386	R292	T231	K171
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	P387	G293	C232	V172
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	A388	L294	L233	L173
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	D386	L295	T234	T174
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	P387	L296	A235	T175
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	A388	R297	G236	I176
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	D386	I298	I237	P177
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	A388	T299	N238	L178
THR	THR	THR	THR	THR	THR	THR	W860	R725	V611	S446	D386	E300	G239	P179
THR	THR	THR	THR	THR	THR	THR	R867	R725	V611	S446	A388	E300	E240	S180

L1087	L1088	E1089	A1090	D1094	E1095	S1096	N1097	E1098	Q1106	Y1109	R1110	E1115	E1118	Q1119	T1122	T1123	R1126	M1127	A1135	I1139	L1140	L1141	L1144	Y1145	T1146	E1147	Q1148	R1149	R1150	A1154	R1155	N1156	M1157	F1158	E1159	D1160	L1161	L1162	R1163	K1164	T1165	H1168	Y1169	L1172	V1173							
H1181	K1189	E1193	R1194	A1197	A1198	Y1211	E1217	N1221	N1222	E1225	A1226	L1227	R1228	L1235	P1236	N1239	C1242	R1248	M1249	I1250	Y1253	T1257	T1258	Q1259	D1260	L1261	W1262	V1263	R1264	G1265	T1266	SER	PRO	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASP	PRO	PRO	ARG							
ALA	LYS	GLN	GLN	LYS	SER	ASN	ALA	THR	GLY	PRO	GLY	LYS	VAL	PRO	LEU	LYS	ALA	ALA	T1301	T1302	L1307	H1308	D1309	N1310	I1311	R1312	L1317	L1318	L1319	P1322	V1323	E1327	A1333	T1336	M1337	A1338	T1339	R1340	R1341	P1342	L1345	F1352	L1353	E1354	C1355	I1356	T1361	GLY	VAL			
SER	ALA	ALA	MET	THR	ALA	GLU	LYS	ASN	GLY	PRO	GLY	SER	GLY	SER	PRO	LYS	THR	ALA	ALA	GLU	GLU	ARG	GLN	PRO	ARG	R1312	GLY	LYS	GLY	GLY	ASP	SER	ASP	ASP	GLU	ASP	GLN	LEU	LEU	ALA	SER	MET	HIS	GLU	ALA	ALA	ALA	GLU	LEU	LYS	GLU	ASN
S1425	T1426	A1427	F1431	A1432	L1433	Q1434	V1437	T1438	H1439	P1440	F1443	L1446	T1452	Q1455	E1456	T1457	R1460	N1461	V1462	R1465	L1466	S1469	I1472	T1473	T1474	K1475	M1476	M1479	K1485	GLU	ASP	ALA	ALA	SER	LYS	ASP	ALA	ALA	ALA	SER	LYS	GLU	ALA	ALA	GLU	ALA	ALA					
PRO	MET	V1506	L1507	S1508	P1509	P1510	I1511	L1514	E1518	E1523	M1526	L1527	Y1531	M1532	D1533	T1534	Q1535	R1538	L1539	K1540	D1541	A1542	R1543	F1544	S1551	A1552	N1553	S1557	W1560	N1561	E1562	L1565	T1566	Y1567	K1572	H1573	K1574	W1575	A1576	S1577	Q1578	C1579	K1582	A1583	W1584	E1589						
A1590	D1591	P1592	D1593	V1594	K1597	N1601	Q1607	P1608	V1609	K1610	A1611	I1612	D1613	K1616	R1617	T1624	Y1625	P1626	R1627	I1628	M1633	D1634	Y1637	S1638	M1639	L1640	R1641	P1642																								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	239280	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 ($e^-/\text{\AA}^2$)	57.8	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	86.420	Depositor
Minimum map value	-36.983	Depositor
Average map value	0.020	Depositor
Map value standard deviation	1.359	Depositor
Recommended contour level	9	Depositor
Map size (Å)	514.6, 514.6, 514.6	wwPDB
Map dimensions	620, 620, 620	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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	B	0.17	0/9156	0.33	0/12403
2	C	0.16	0/9548	0.34	0/12921
3	E	0.19	0/8546	0.35	0/11608
4	A	0.15	0/432	0.40	0/584
5	F	0.16	0/7173	0.31	0/9746
6	D	0.22	0/9377	0.41	0/12718
All	All	0.18	0/44232	0.35	0/59980

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	B	8965	0	8873	178	0
2	C	9354	0	9301	202	0
3	E	8380	0	8309	175	0
4	A	427	0	413	10	0
5	F	7045	0	7054	103	0
6	D	9223	0	9265	259	0
7	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	2	0	0	0	0
All	All	43398	0	43215	903	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 10.

The worst 5 of 903 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:441:CYS:O	3:E:445:GLU:HB3	1.71	0.89
5:F:446:SER:HB3	5:F:462:TYR:HB2	1.66	0.78
2:C:197:LEU:HB3	2:C:209:TYR:O	1.84	0.76
5:F:789:SER:HB3	5:F:808:MET:HB2	1.66	0.76
6:D:567:ALA:HA	6:D:570:MET:HE2	1.70	0.73

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	B	1126/1247 (90%)	1091 (97%)	35 (3%)	0	100	100
2	C	1173/1292 (91%)	1119 (95%)	54 (5%)	0	100	100
3	E	1064/1654 (64%)	1023 (96%)	41 (4%)	0	100	100
4	A	51/368 (14%)	45 (88%)	6 (12%)	0	100	100
5	F	907/1376 (66%)	865 (95%)	42 (5%)	0	100	100
6	D	1164/1642 (71%)	1118 (96%)	46 (4%)	0	100	100
All	All	5485/7579 (72%)	5261 (96%)	224 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	B	960/1046 (92%)	934 (97%)	26 (3%)	39	62
2	C	1014/1094 (93%)	988 (97%)	26 (3%)	40	62
3	E	903/1373 (66%)	864 (96%)	39 (4%)	26	51
4	A	50/288 (17%)	47 (94%)	3 (6%)	17	44
5	F	779/1177 (66%)	762 (98%)	17 (2%)	45	65
6	D	971/1320 (74%)	916 (94%)	55 (6%)	18	45
All	All	4677/6298 (74%)	4511 (96%)	166 (4%)	32	57

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	D	474	THR
6	D	1156	ASN
6	D	622	VAL
6	D	957	THR
6	D	1253	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	519	GLN
6	D	356	ASN
5	F	663	ASN
5	F	794	GLN
6	D	511	ASN

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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-28866. These allow visual inspection of the internal detail of the map and identification of artifacts.

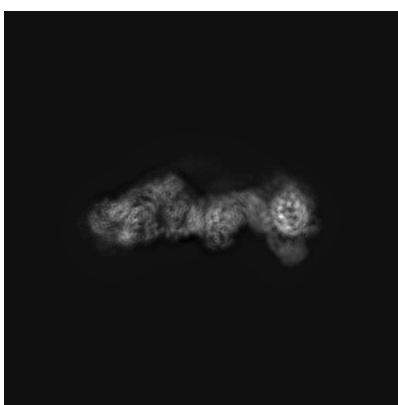
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

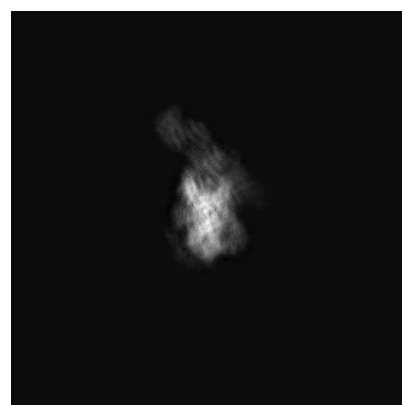
6.1.1 Primary map



X



Y

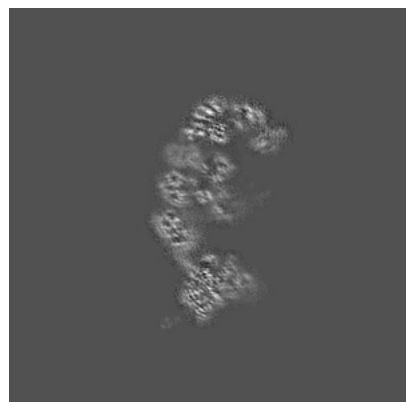


Z

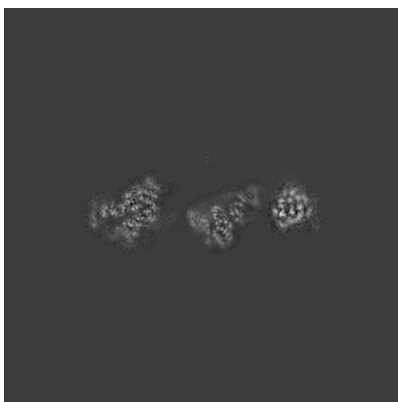
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

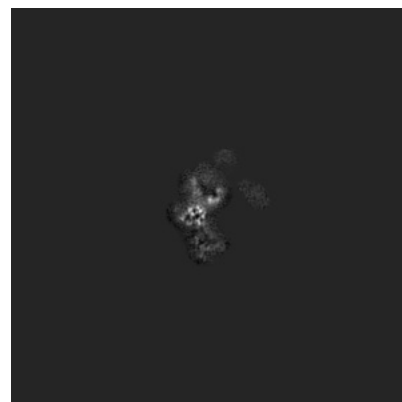
6.2.1 Primary map



X Index: 310



Y Index: 310

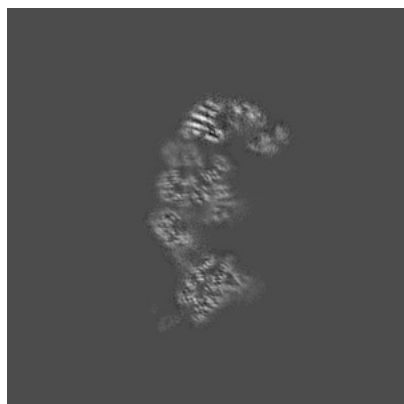


Z Index: 310

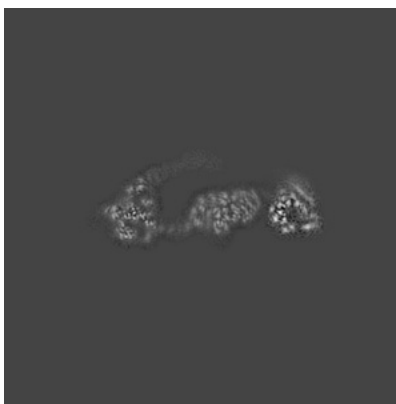
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

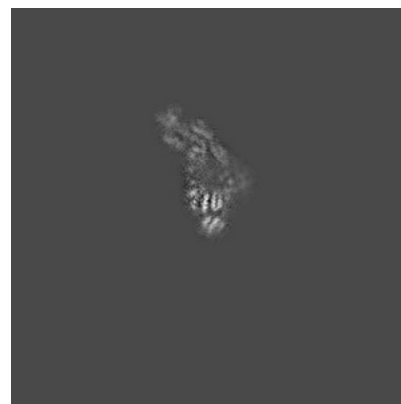
6.3.1 Primary map



X Index: 305



Y Index: 325

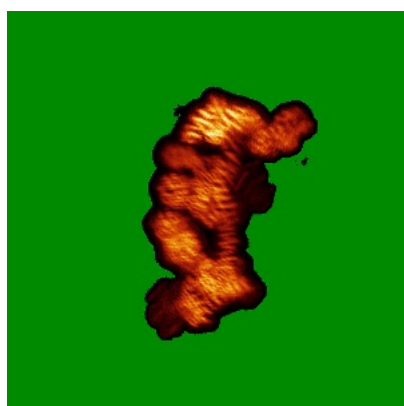


Z Index: 429

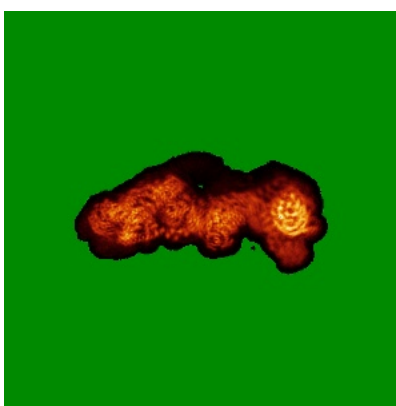
The images above show the largest variance slices of the map in three orthogonal directions.

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

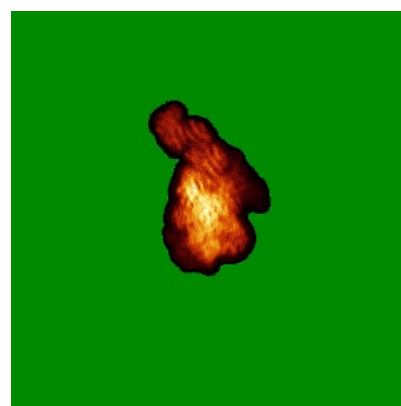
6.4.1 Primary map



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

This section was not generated.

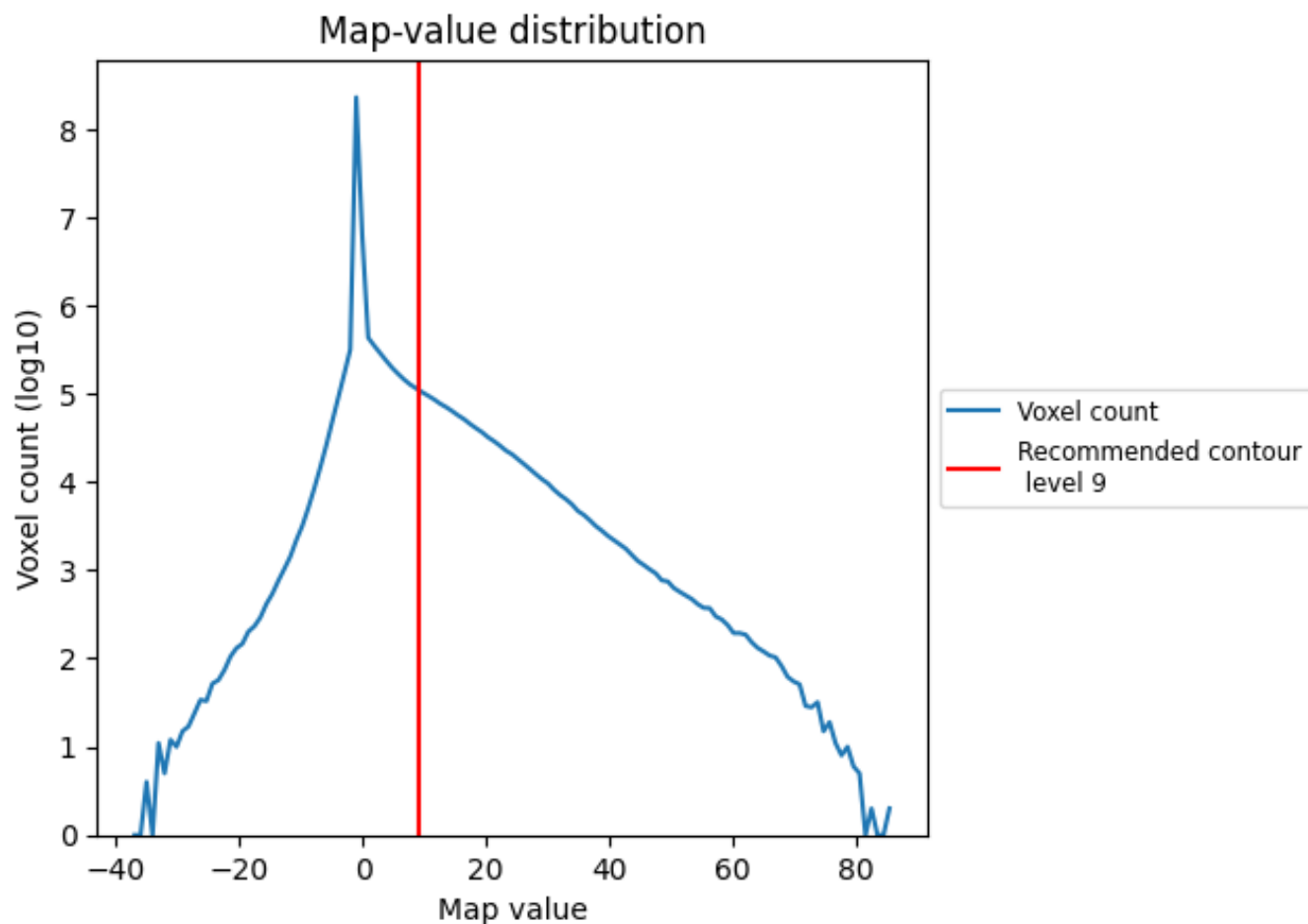
6.6 Mask visualisation

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

7 Map analysis [i](#)

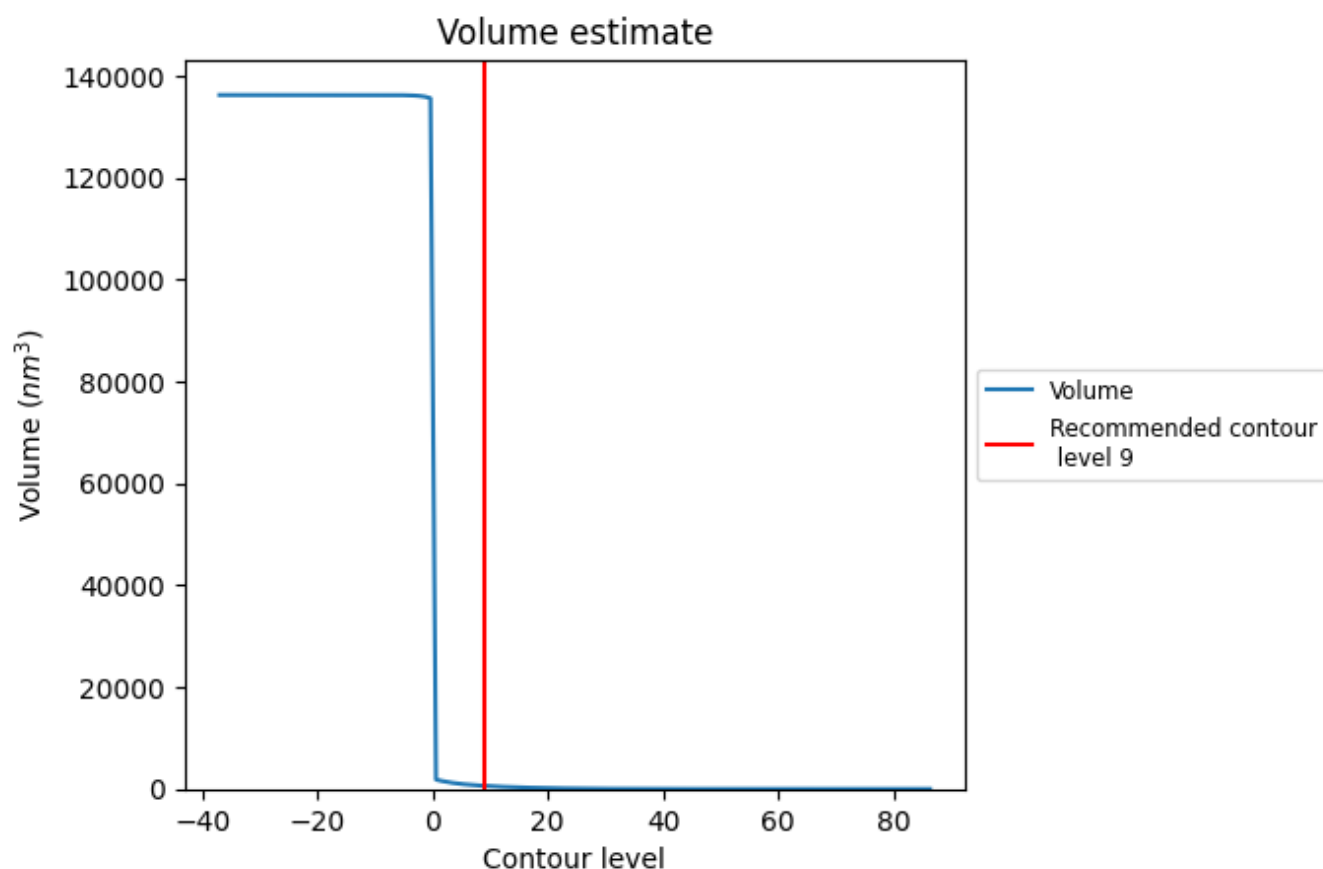
This section contains the results of statistical analysis of the map.

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.

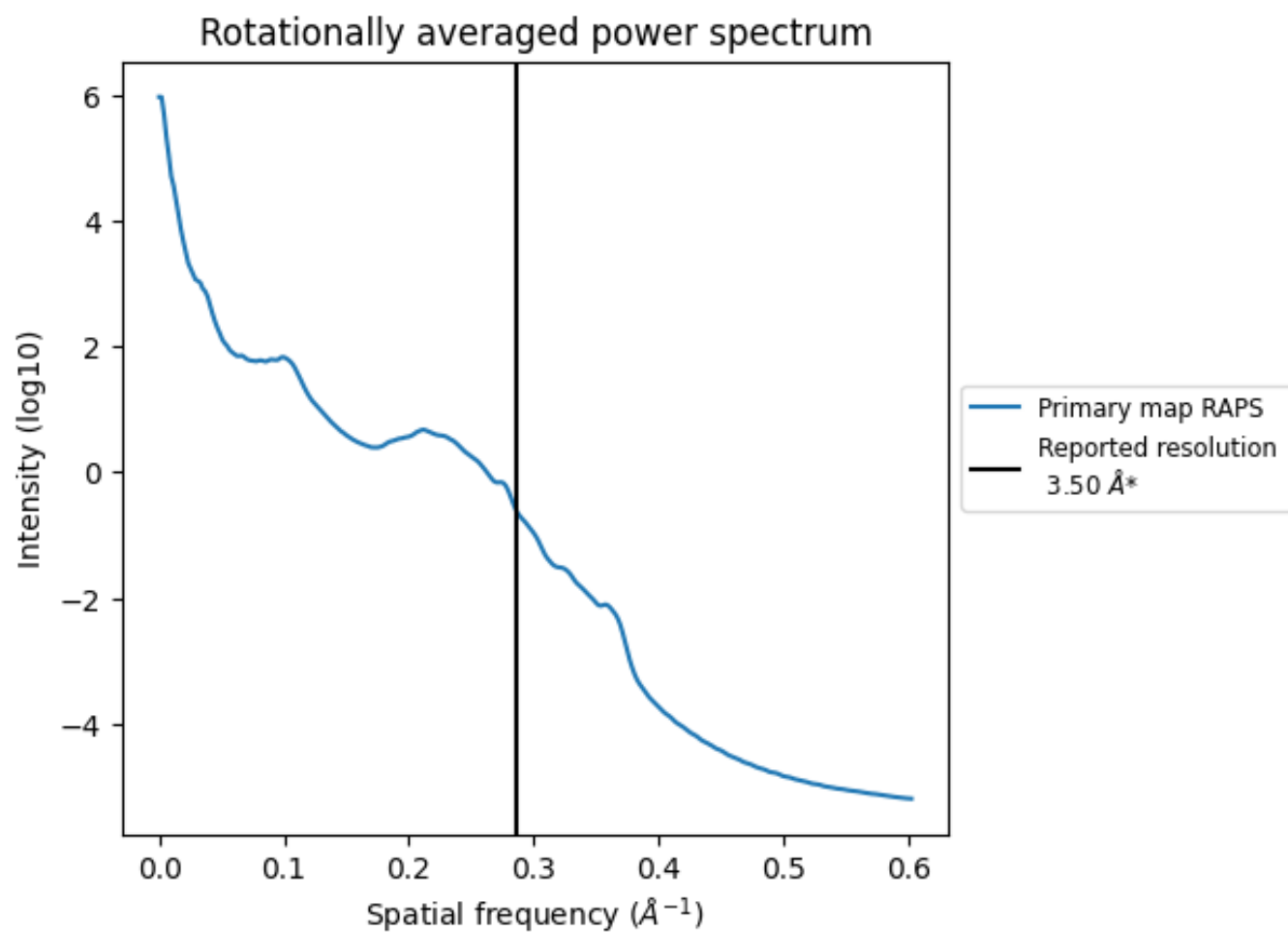
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 619 nm^3 ; this corresponds to an approximate mass of 559 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

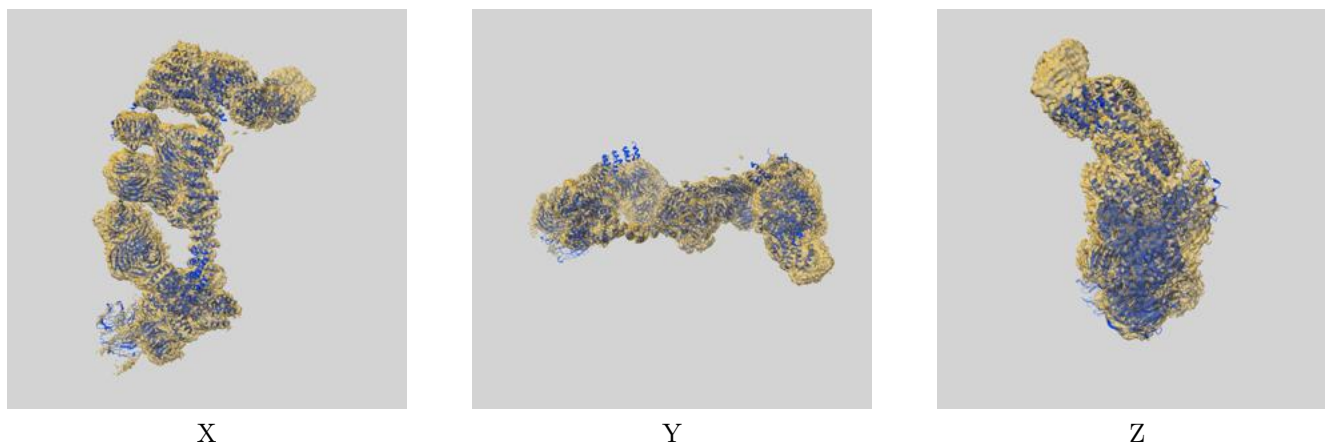
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

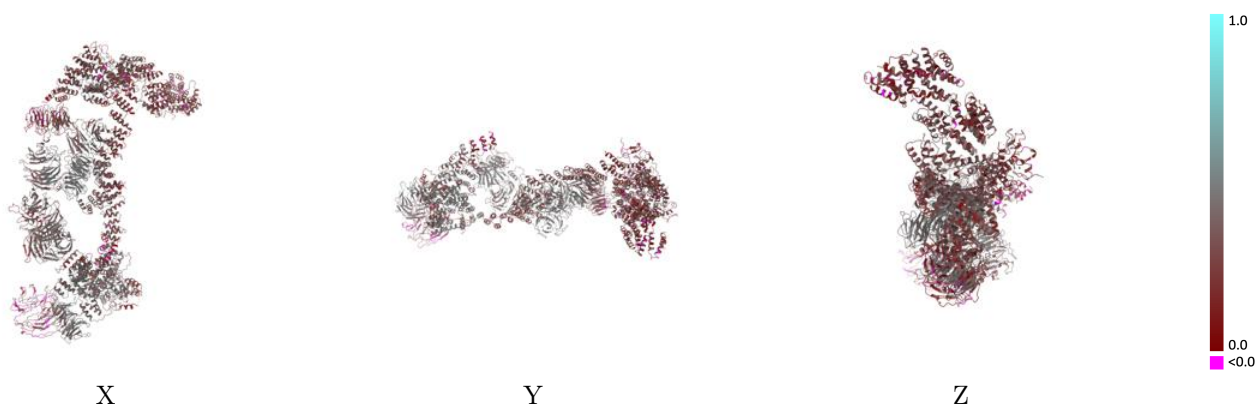
This section contains information regarding the fit between EMDB map EMD-28866 and PDB model 8F5O. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



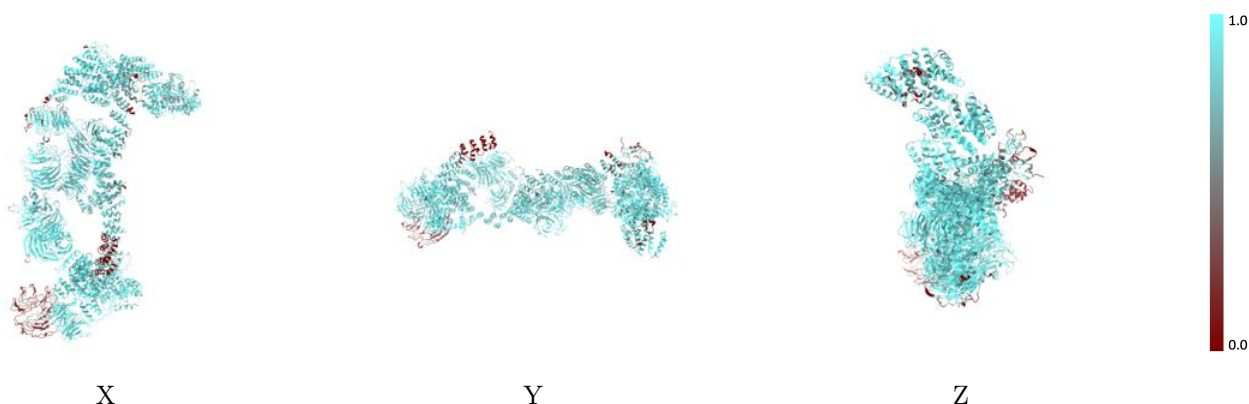
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



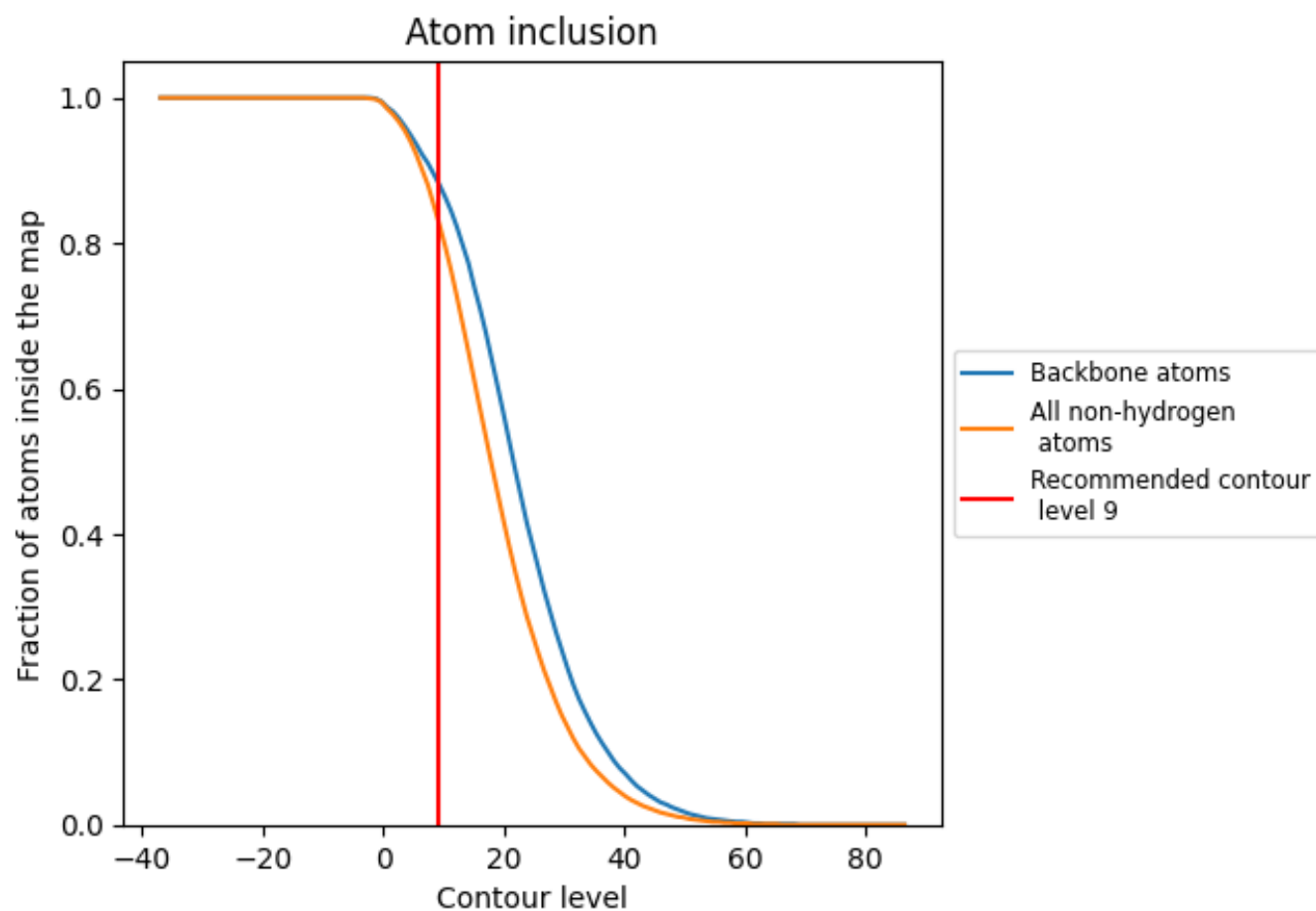
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (9).

9.4 Atom inclusion ⓘ



At the recommended contour level, 88% of all backbone atoms, 83% 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 (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8340	0.3350
A	0.8160	0.2460
B	0.8770	0.3710
C	0.8760	0.3370
D	0.8970	0.2880
E	0.9350	0.3800
F	0.5230	0.2970

1.0

0.0

<0.0