



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:16 AM UTC

PDB ID : 6EMK / pdb_00006emk
EMDB ID : EMD-3896
Title : Cryo-EM Structure of Saccharomyces cerevisiae Target of Rapamycin Complex 2
Authors : Karuppasamy, M.; Kusmider, B.; Oliveira, T.M.; Gaubitz, C.; Prouteau, M.; Loewith, R.; Schaffitzel, C.
Deposited on : 2017-10-02
Resolution : 7.90 Å (reported)
Based on initial model : 5FVM

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

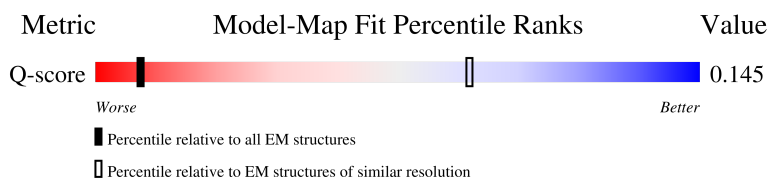
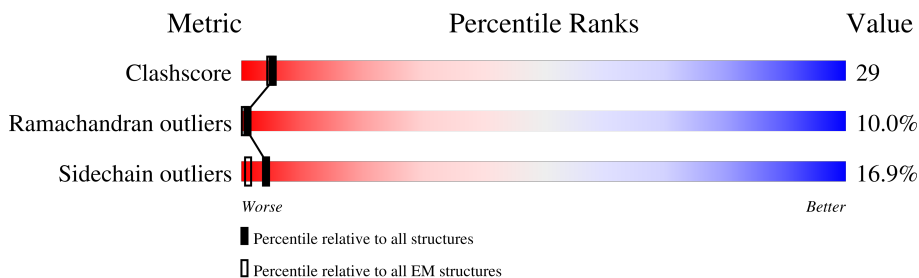
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.90 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	366 (7.40 - 8.40)

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	2474	
1	C	2474	
2	B	303	
2	D	303	

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Mol	Chain	Length	Quality of chain
3	E	303	91% 9%
3	F	303	88% 12%
4	G	426	33% 64%
4	H	426	29% 6% 64%
5	I	1176	6% 5% 88%
5	J	1176	6% 88%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 48012 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 Serine/threonine-protein kinase TOR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2262	Total	C	N	O	S	0	0
			18186	11650	3110	3345	81		
1	C	2262	Total	C	N	O	S	0	0
			18186	11650	3110	3345	81		

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	300	Total	C	N	O	S	0	0
			2372	1468	433	460	11		
2	D	300	Total	C	N	O	S	0	0
			2372	1468	433	460	11		

- Molecule 3 is a protein called Target of rapamycin complex 2 subunit TSC11.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	303	Total	C	N	O	0	0
			1515	909	303	303		
3	F	303	Total	C	N	O	0	0
			1515	909	303	303		

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit AVO2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	155	Total	C	N	O	0	0
			762	452	155	155		
4	H	155	Total	C	N	O	0	0
			762	452	155	155		

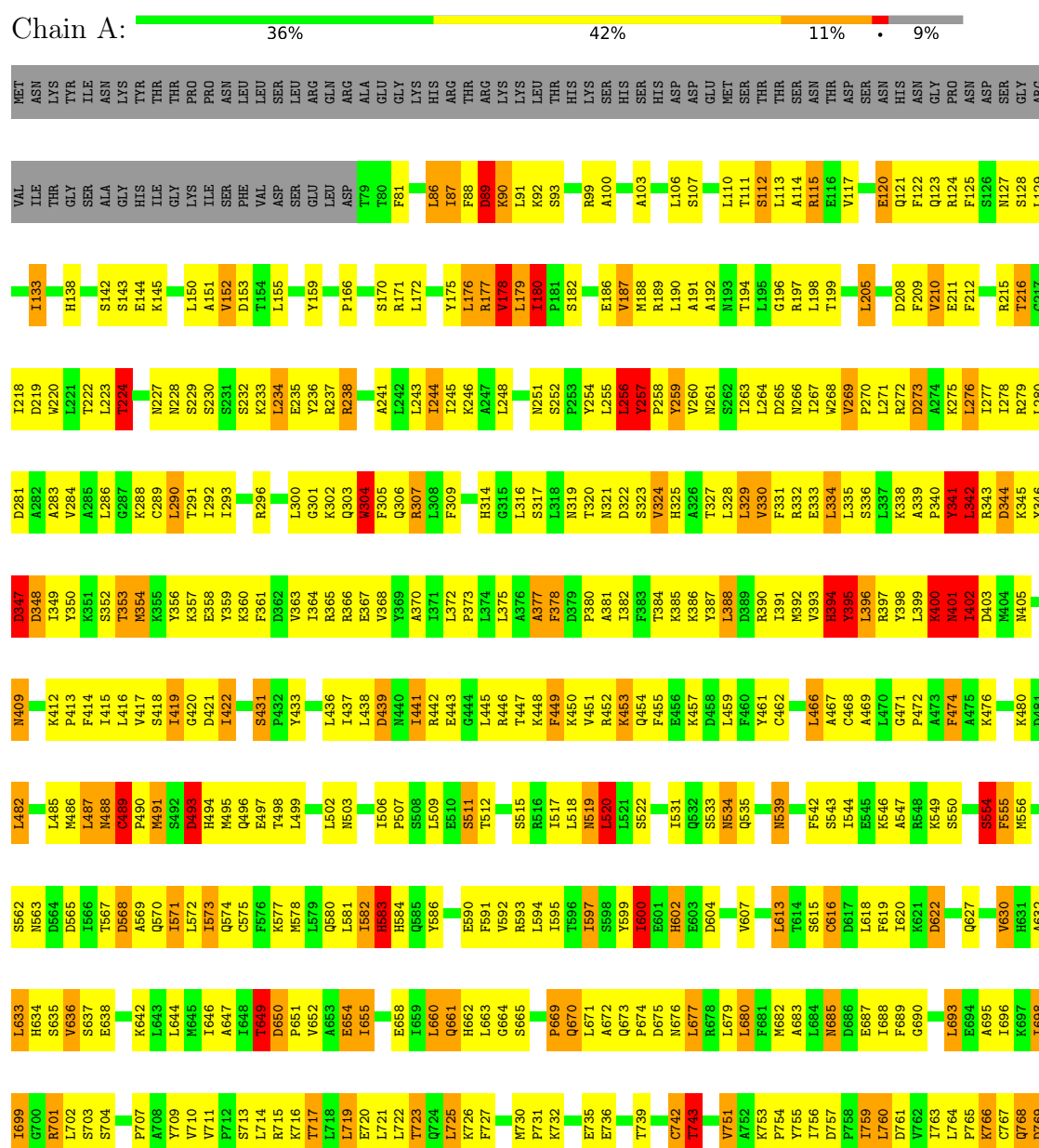
- Molecule 5 is a protein called Target of rapamycin complex 2 subunit AVO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	S	0	0
			1171	739	187	242	3		
5	J	146	Total	C	N	O	S	0	0
			1171	739	187	242	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: Serine/threonine-protein kinase TOR2

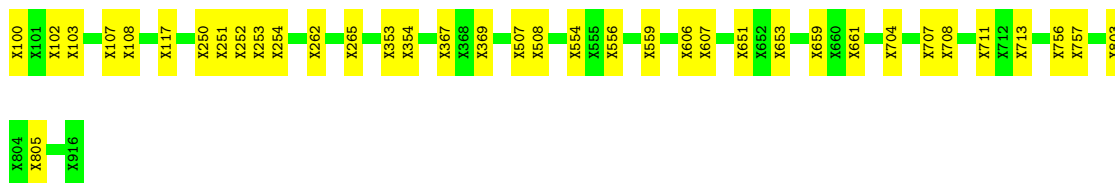


GLU	Q1728	Y1653	T1577	L1502	A1415	I1332	S1266	I1193	V1126	Q1054	F982	VAL
PHE	P1729	A1654	R1578	L1503	A1418	P1333	V1267	I1199	V1127	K1057	F983	SER
ASN	K1730	Q1655	L1579	C1504	E1418	I1334	Y1268	E1200	I1128	R1058	Q984	PRO
GLY	R1732	K1657	L1580	F1510	K1419	K1339	A1272	V1201	L1129	V1060	N850	ASN
MET	L1733	G1581	G1582	K1511	G1423	Y1340	R1273	F1202	N1130	I1062	I851	ASP
ILE	Q1583	Q1583	K1512	K1512	E1424	A1341	E1274	E1203	R1134	E914	E852	E914
GLY	W1660	K1658	A1513	A1513	D1425	Q1342	L1275	R1204	E1135	R1063	K853	Y915
VAL	P1736	W1660	E1514	E1514	F1426	K1343	L1276	K1205	E1136	I1064	T854	Y916
THR	D1666	D1667	V1515	V1515	V1427	H1345	A1278	N1206	L1137	L1065	E855	T918
PHE	A1668	A1668	I1517	I1517	E1428	H1348	S1279	Y1207	K1138	K1066	N856	Y919
ASP	L1669	L1669	F1518	F1518	V1429	A1348	F1280	E1208	A1139	S1067	P988	V920
ALA	K1670	K1670	N1519	N1519	M1430	A1348	S1281	D1209	T1140	L1068	I860	V920
LYS	Q1671	Q1671	A1520	A1520	K1433	L1351	C1282	M1141	M1141	V1069	R861	I921
VAL	L1672	L1672	L1523	L1523	L1434	H1352	C1283	N1142	T1070	E1001	R862	I921
THR	F1675	F1675	L1524	L1524	R1435	Y1353	W1284	T1143	K1003	F1071	G863	N923
TYR	M1679	M1679	V1525	V1525	S1436	K1354	E1285	L1144	I1003	G1072	V865	I927
S1811	D1682	D1682	T1526	T1526	L1437	V1356	L1287	K1215	Y1004	P1073	R866	I928
N1813	L1683	L1683	E1527	E1527	T1438	E1357	Q1288	P1217	L1146	E1076	L867	R929
I1815	GLY	GLY	L1528	L1528	A1439	F1358	T1289	N1219	L1148	D1077	G869	D930
H1816	LEU	LEU	E1534	E1534	L1440	L1359	S1290	Q1220	Q1150	S1079	I1007	S932
V1819	ASP	ASP	S1535	S1535	S1447	P1362	Q1292	N1221	L1151	E1009	L933	L933
I1820	PRO	PRO	A1539	A1539	R1448	T1366	E1293	L1222	G1152	L1082	H837	H837
P1821	ASN	ASN	Y1540	Y1540	L1449	I1367	L1294	L1223	T1153	M1083	T938	T938
I1822	ASN	ASN	V1544	V1544	A1450	E1368	ILE	K1224	D1154	P1084	L800	L800
I1823	ILE	ILE	R1545	R1545	S1481	A1450	GLN	F1155	K1015	I1014	PRO	PRO
K1824	ALA	ALA	A1546	A1546	E1452	L1370	ALA	V1156	L1016	I1016	TYR	I804
G1825	GLN	GLN	Q1547	Q1547	K1453	I1371	LEU	V1157	Q1017	A943	LYS	I805
F1826	SER	SER	I1548	I1548	T1456	S1372	CYS	C1229	Q1017	I944	HIS	I806
F1827	VAL	VAL	F1549	F1549	A1457	I1373	LYS	S1230	I1018	P945	ARG	T807
H1828	PRO	PRO	A1550	A1550	P1458	L1377	LEU	Q1231	T1019	H946	GLU	F808
S1829	GLN	GLN	E1551	E1551	P1459	H1378	SER	K1233	S1022	E1091	ILE	Q809
I1830	GLN	GLN	L1552	L1552	L1468	Q1379	SER	E1236	V1023	I951	GLU	D810
S1831	SER	SER	E1553	E1553	M1465	T1380	SER	A1165	I1024	S812	VAL	G811
L1832	LYS	LYS	E1554	E1554	E1468	I1383	GLU	L1166	E1025	S813	THR	S812
S1835	VAL	VAL	I1555	I1555	L1468	A1383	ASN	L1167	S1026	C955	SER	S813
S1836	VAL	VAL	K1557	K1557	L1476	I1384	PRO	R1170	I1027	R954	ASN	S814
L1838	SER	SER	Y1558	Y1558	E1477	G1385	PRO	Q1171	S1028	C955	LYS	F815
Q1839	ARG	ARG	K1559	K1559	E1477	I1386	GLU	Q1172	S1028	V956	SER	K316
D1840	HIS	HIS	P1562	P1562	D1480	L1387	ILE	H1173	I1027	S957	SER	R817
A1841	VAL	VAL	Q1563	Q1563	V1488	K1388	TYR	S1174	K1029	P959	SER	D818
L1842	GLN	GLN	D1566	D1566	M1489	H1389	GLN	Y1176	G1033	D960	VAL	L821
R1843	GLY	GLY	K1567	K1567	K1489	Q1391	MET	Q1248	E1034	I963	GLN	L821
L1844	SER	SER	L1569	L1569	S1491	A1390	LEU	L1249	F1035	P964	ASN	L824
F1849	ALA	ALA	T1570	T1570	Q1492	Q1391	LEU	E1252	V1039	I966	PRO	L827
W1848	ASP	ASP	E1571	E1571	E1496	W1401	ASN	S1253	P1040	I967	SER	L827
G1852	SER	SER	R1572	R1572	K1497	W1402	LEU	E1253	E1041	Q961	GLN	V835
G1853	VAL	VAL	E1573	E1573	F1498	Y1403	LEU	L1258	T1042	I962	ASP	V835
G1853	THR	THR	W1574	W1574	F1499	K1405	LEU	R1259	L1043	I963	ILE	L838
P1854	ASP	ASP	W1575	W1575	D1500	K1406	LEU	L1189	T1044	P964	ILE	L838
P1855	ILE	ILE	W1576	W1576	D1501	Q1407	LEU	P1190	F1045	R970	ALA	Y841
E1856	ASN	ASN	L1576	L1576	A1501	R1408	LEU	T1191	F1046	R971	LEU	Y841
						A1412	LEU	S1262	I1049	Q977	LEU	P842
								S1263	L1050	L1121	GLY	E843
								L1264		L1122	MET	L844
								V1265		D979	GLY	L845

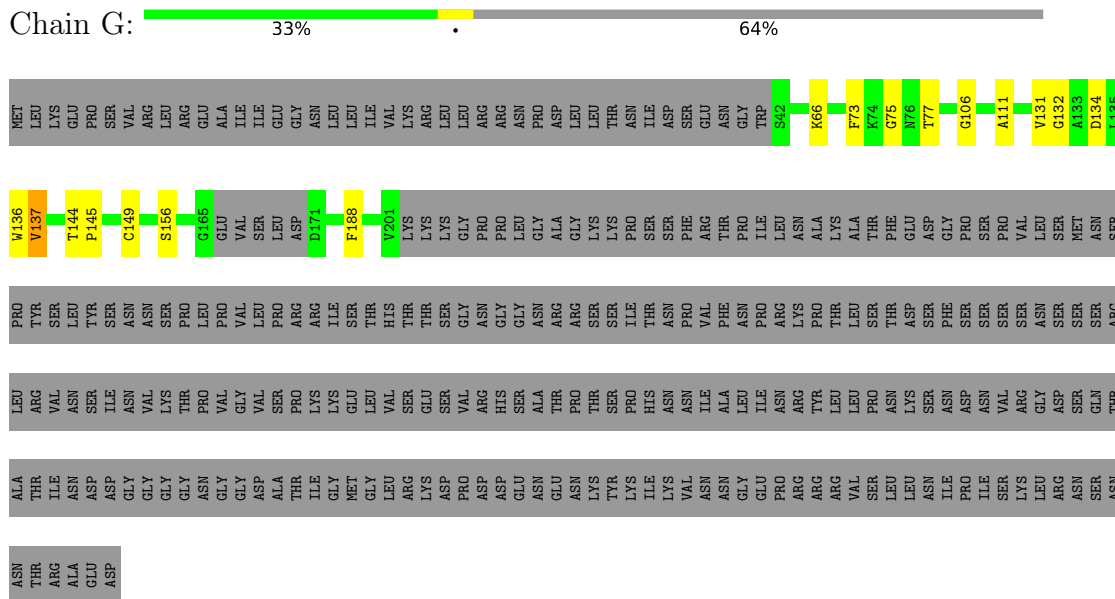
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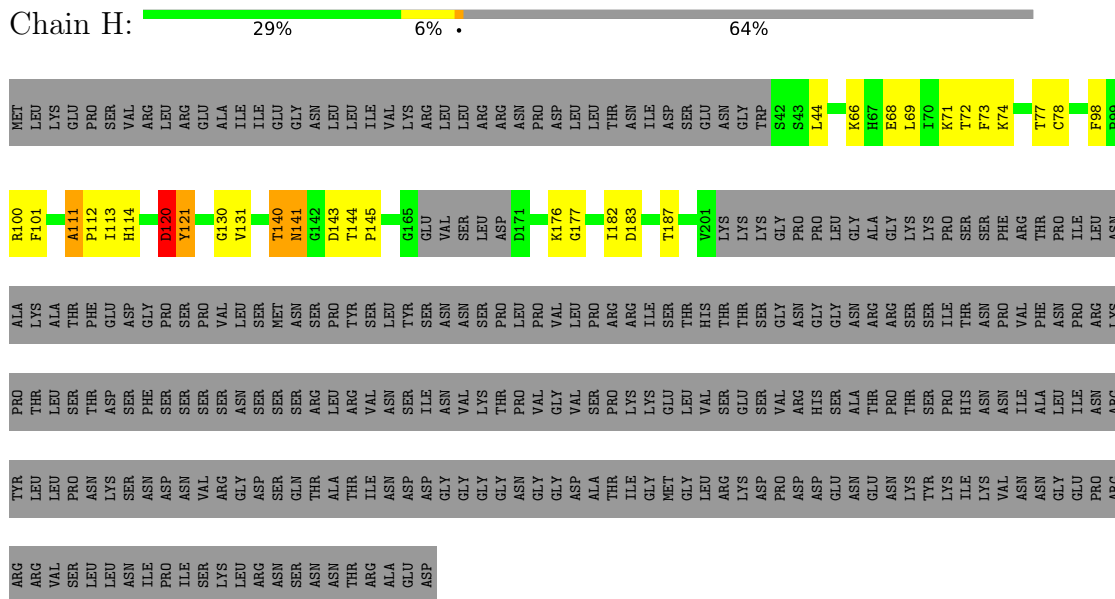
WORLDWIDE
PDB
PROTEIN DATA BANK



- Molecule 4: Target of rapamycin complex 2 subunit AVO2



- Molecule 4: Target of rapamycin complex 2 subunit AVO2



- Molecule 5: Target of rapamycin complex 2 subunit AVO1





MET
ASN
HIS
LYS

● Molecule 5: Target of rapamycin complex 2 subunit AVO1

Chain J: 6% . . . 88%

MET ASP THR VAL LEU ASN GLU SER LEU PHE MET ASN VAL ASP THR LEU MET LEU

PRO GLU LEU GLU VAL PRO VAL SER GLY LEU MET ASN TYR ASP VAL SER LEU GLY

LYS ASN THR LEU ASP ILE VAL GLU ASN GLY THR ASP MET TYR ASN VAL ASP ARG

SER SER LEU PRO PHE ASP ILE ARG ASP HIS ASN THR SER GLY ASP HIS ASP ASN

LEU GLU GLU GLU ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP

SER ILE LEU ASP VAL ASP SER SER SER SER SER SER SER SER SER SER SER SER

GLY ASN GLY SER VAL SER ASP GLY THR GLU ASN ASN ILE ARG LEU SER LYS

VAL MET ASN ARG ASP LYS ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP

SER ASP MET GLN THR ASN THR ASN ILE PRO MET MET MET MET MET MET MET MET

PRO THR SER LEU THR SER ASN ARG THR THR THR THR THR THR THR THR THR THR

LYS GLN ASP HIS SER PRO VAL VAL HIS VAL VAL VAL VAL VAL VAL VAL VAL VAL

S675 S676 S677 S678 S679 S680 S681 S682 S683 S684 S685 S686 S687 S688

K742 K743 K744 K745 K746 K747 K748 K749 K750 K751 K752 K753 K754 K755

THR ILE ASN GLN LEU PHE TYR LYS PRO SER GLY ILE GLY ASN GLU ASP ASP ASP

TYR CYS LYS MET ASN MET ASP PRO ASN GLU THR PRO LEU THR LYS VAL VAL VAL

PRO VAL LEU PRO THR ILE GLN SER ASN VAL SER THR THR THR THR THR THR THR

SER SER VAL ALA SER GLY SER THR THR THR THR THR THR THR THR THR THR THR

SER SER VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL VAL

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	16190, 10663	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50, 47	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON II (4k x 4k), GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0147	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	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	0.83	14/18019 (0.1%)	1.21	142/23495 (0.6%)
1	C	0.82	19/17986 (0.1%)	1.20	158/23389 (0.7%)
2	B	0.85	1/2362 (0.0%)	1.21	19/3108 (0.6%)
2	D	0.83	2/2353 (0.1%)	1.14	23/3080 (0.7%)
4	G	0.69	0/715	1.23	6/918 (0.7%)
4	H	0.72	0/718	1.46	18/927 (1.9%)
5	I	1.48	12/1165 (1.0%)	1.43	12/1526 (0.8%)
5	J	1.23	8/1160 (0.7%)	1.29	12/1509 (0.8%)
All	All	0.86	56/44478 (0.1%)	1.22	390/57952 (0.7%)

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	1	28
1	C	0	25
2	B	0	4
2	D	0	2
5	I	0	2
5	J	0	2
All	All	1	63

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2389	ASN	CA-C	12.01	1.58	1.52
1	A	768	GLN	CA-C	9.03	1.58	1.53
1	C	1205	ARG	CA-C	8.96	1.60	1.52
5	I	713	LEU	CA-C	8.78	1.64	1.52
1	C	1205	ARG	N-CA	8.66	1.54	1.46

The worst 5 of 390 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	104	VAL	N-CA-C	-20.80	93.95	113.71
1	A	2335	PHE	N-CA-C	-14.30	95.79	113.38
1	A	768	GLN	N-CA-C	-13.76	97.50	108.78
1	C	2077	GLU	N-CA-C	13.26	125.75	111.03
1	C	1996	GLU	N-CA-C	11.32	128.43	113.72

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	257	TYR	CA

5 of 63 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	178	VAL	Peptide
1	A	180	ILE	Peptide
1	A	256	LEU	Peptide
1	A	257	TYR	Peptide
1	A	347	ASP	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	18186	0	18002	1109	0
1	C	18186	0	17976	1109	0
2	B	2372	0	2199	141	0
2	D	2372	0	2191	151	0
3	E	1515	0	491	15	0
3	F	1515	0	490	24	0
4	G	762	0	290	6	0
4	H	762	0	293	11	0
5	I	1171	0	1119	62	0
5	J	1171	0	1116	55	0
All	All	48012	0	44167	2653	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 29.

The worst 5 of 2653 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:2060:GLU:HB3	1:A:2062:GLN:HG2	1.25	1.18
1:A:841:TYR:HB2	1:A:843:GLU:HG2	1.16	1.13
1:C:983:PHE:HB3	1:C:1022:ILE:HG12	1.31	1.10
1:A:179:LEU:HD22	1:A:233:LYS:HG3	1.31	1.10
2:D:297:CYS:HA	2:D:298:VAL:HB	1.25	1.09

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	1309/2474 (53%)	872 (67%)	313 (24%)	124 (10%)	0	8
1	C	1267/2474 (51%)	849 (67%)	290 (23%)	128 (10%)	0	7
2	B	178/303 (59%)	122 (68%)	45 (25%)	11 (6%)	1	13
2	D	173/303 (57%)	113 (65%)	44 (25%)	16 (9%)	0	8
4	G	75/426 (18%)	57 (76%)	12 (16%)	6 (8%)	1	9
4	H	80/426 (19%)	43 (54%)	22 (28%)	15 (19%)	0	2
5	I	95/1176 (8%)	52 (55%)	29 (30%)	14 (15%)	0	3
5	J	88/1176 (8%)	52 (59%)	23 (26%)	13 (15%)	0	3
All	All	3265/8758 (37%)	2160 (66%)	778 (24%)	327 (10%)	1	7

5 of 327 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	ASP
1	A	112	SER

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Mol	Chain	Res	Type
1	A	224	THR
1	A	257	TYR
1	A	342	LEU

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	2029/2219 (91%)	1689 (83%)	340 (17%)	2	10
1	C	2029/2219 (91%)	1675 (83%)	354 (17%)	2	9
2	B	264/267 (99%)	223 (84%)	41 (16%)	2	12
2	D	264/267 (99%)	230 (87%)	34 (13%)	4	15
5	I	137/1066 (13%)	113 (82%)	24 (18%)	2	9
5	J	137/1066 (13%)	109 (80%)	28 (20%)	1	7
All	All	4860/7104 (68%)	4039 (83%)	821 (17%)	4	10

5 of 821 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	566	ASP
1	C	1359	GLU
5	J	697	VAL
1	C	651	ASP
1	C	545	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 162 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1249	GLN
1	C	2343	ASN
1	C	1399	GLN
1	C	1871	GLN
2	D	36	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	567
1	A	534
3	E	90
3	F	87
2	D	75
2	B	66
4	G	45
4	H	42
5	J	31
5	I	26

The worst 5 of 1563 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	416:UNK	C	450:UNK	N	40.12
1	F	416:UNK	C	450:UNK	N	39.07

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	512:UNK	C	550:UNK	N	33.98
1	F	717:UNK	C	750:UNK	N	33.97
1	E	717:UNK	C	750:UNK	N	33.43

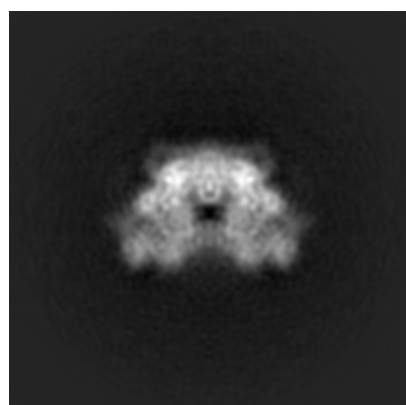
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3896. These allow visual inspection of the internal detail of the map and identification of artifacts.

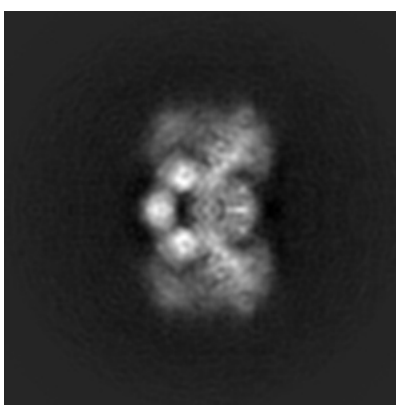
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

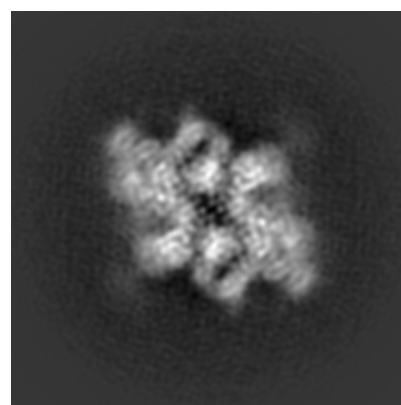
6.1.1 Primary map



X



Y

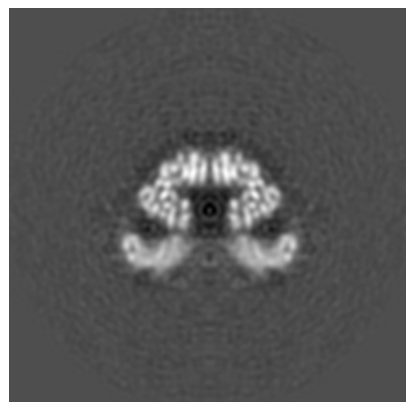


Z

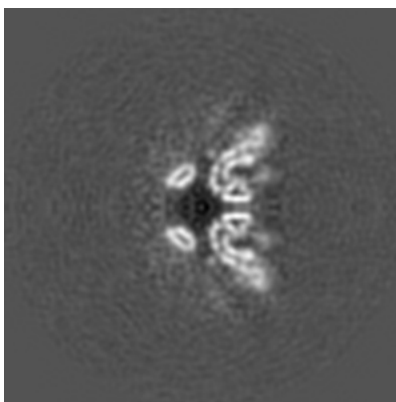
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

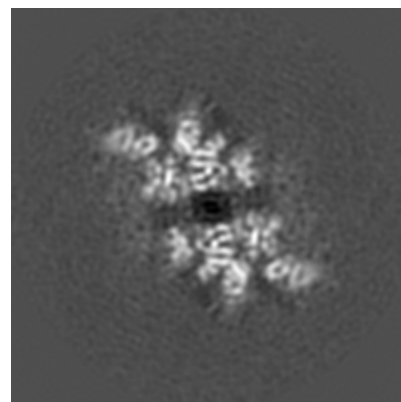
6.2.1 Primary map



X Index: 160



Y Index: 160

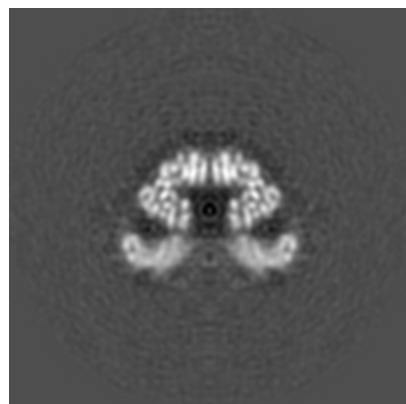


Z Index: 160

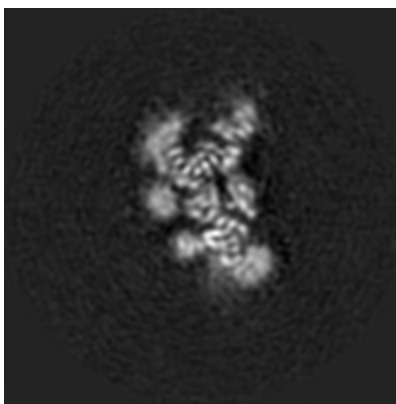
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

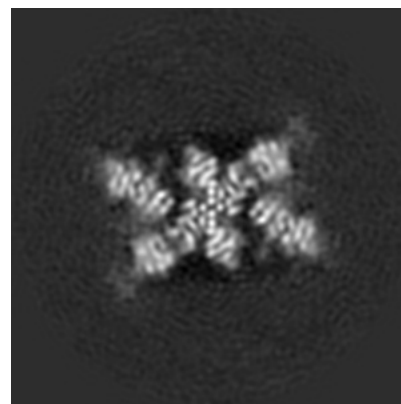
6.3.1 Primary map



X Index: 160



Y Index: 133

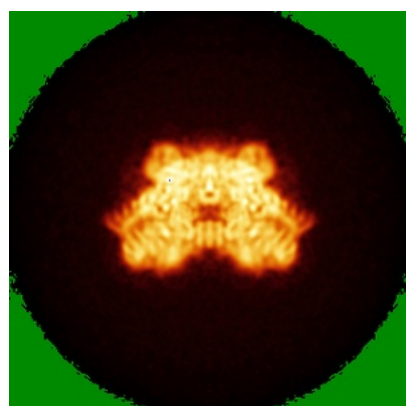


Z Index: 190

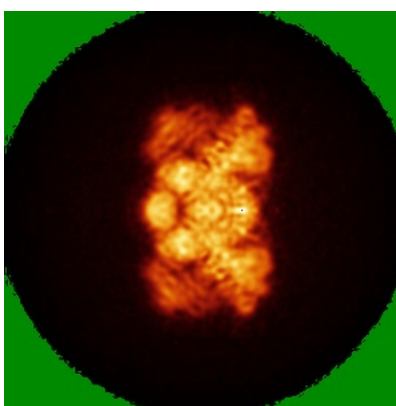
The images above show the largest variance slices of the map in three orthogonal directions.

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

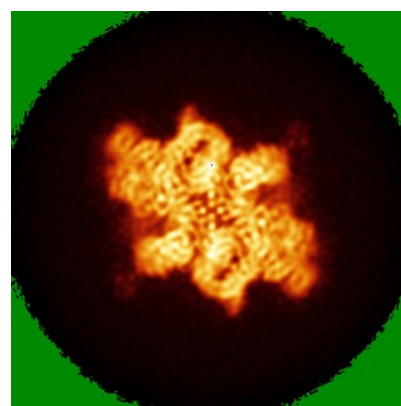
6.4.1 Primary map



X



Y

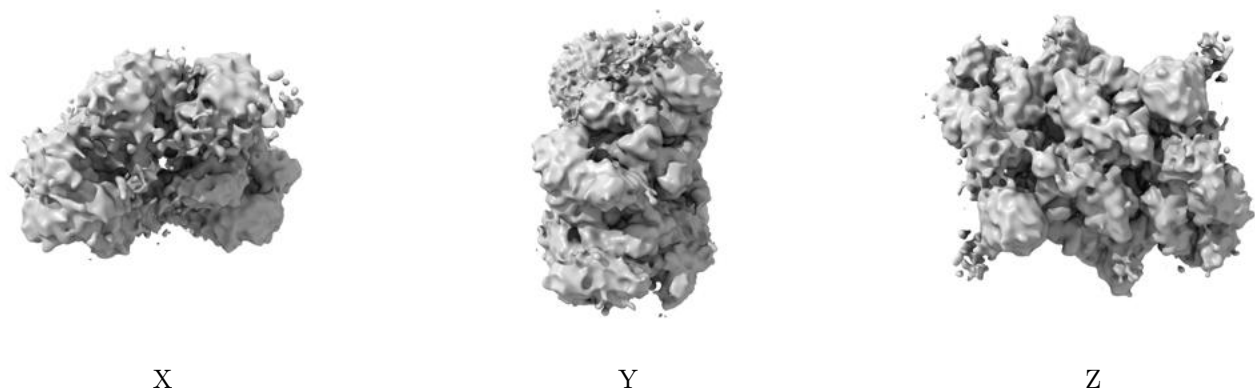


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

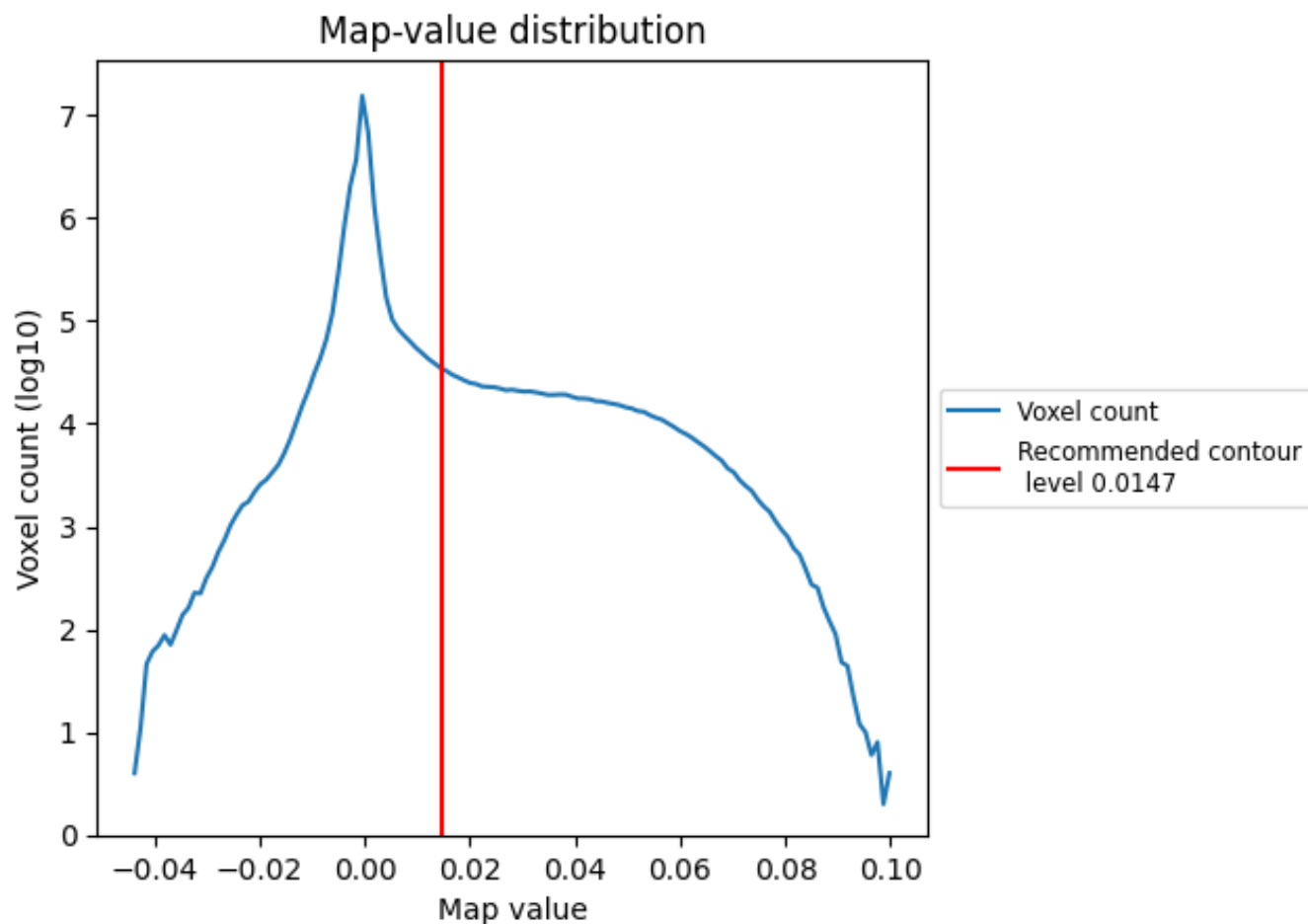
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

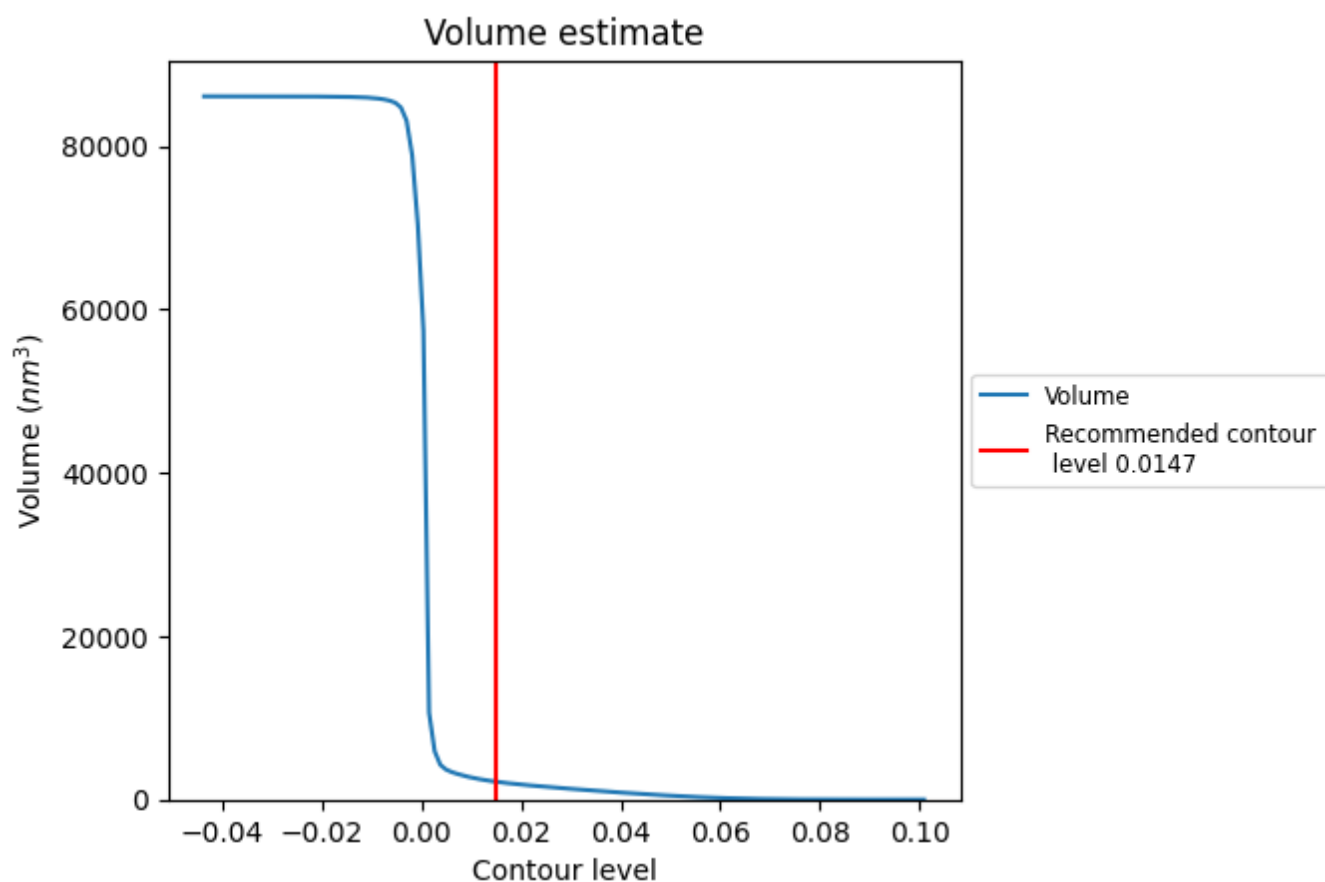
This section contains the results of statistical analysis of the map.

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.

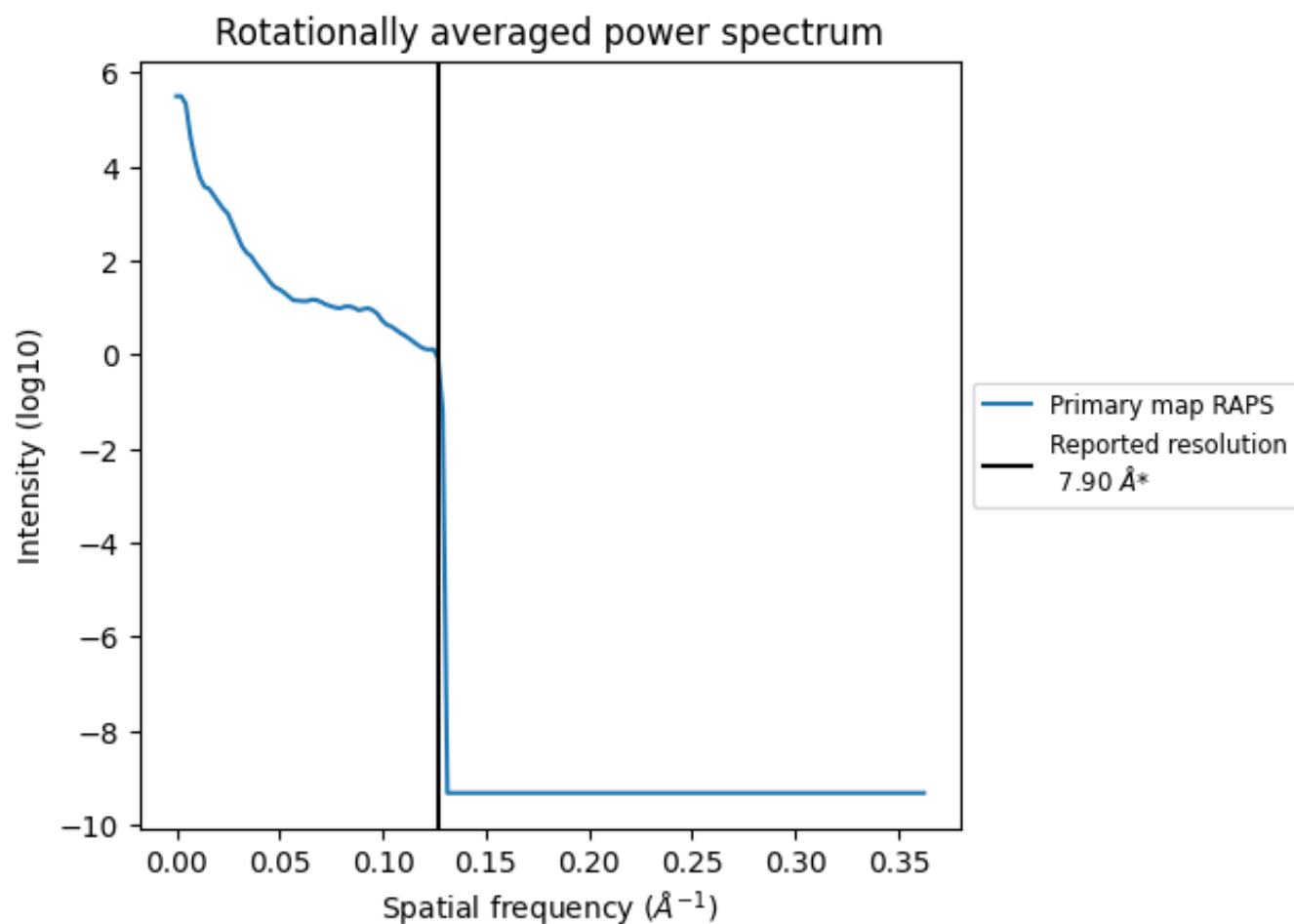
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2205 nm³; this corresponds to an approximate mass of 1992 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 0.127 Å⁻¹

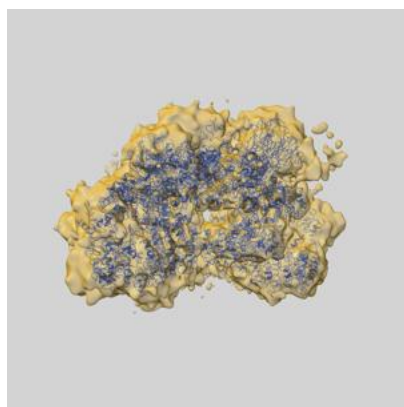
8 Fourier-Shell correlation

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

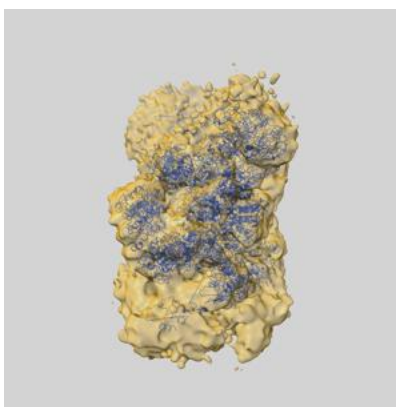
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3896 and PDB model 6EMK. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

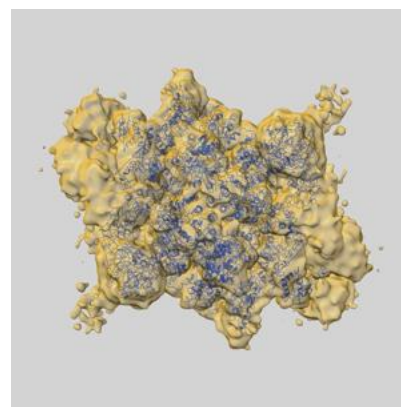
9.1 Map-model overlay [i](#)



X



Y



Z

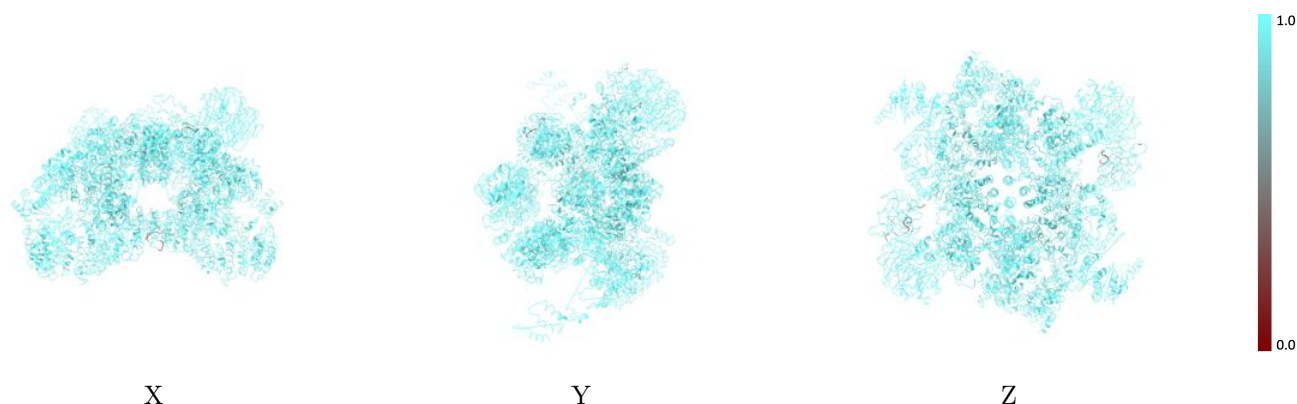
The images above show the 3D surface view of the map at the recommended contour level 0.0147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



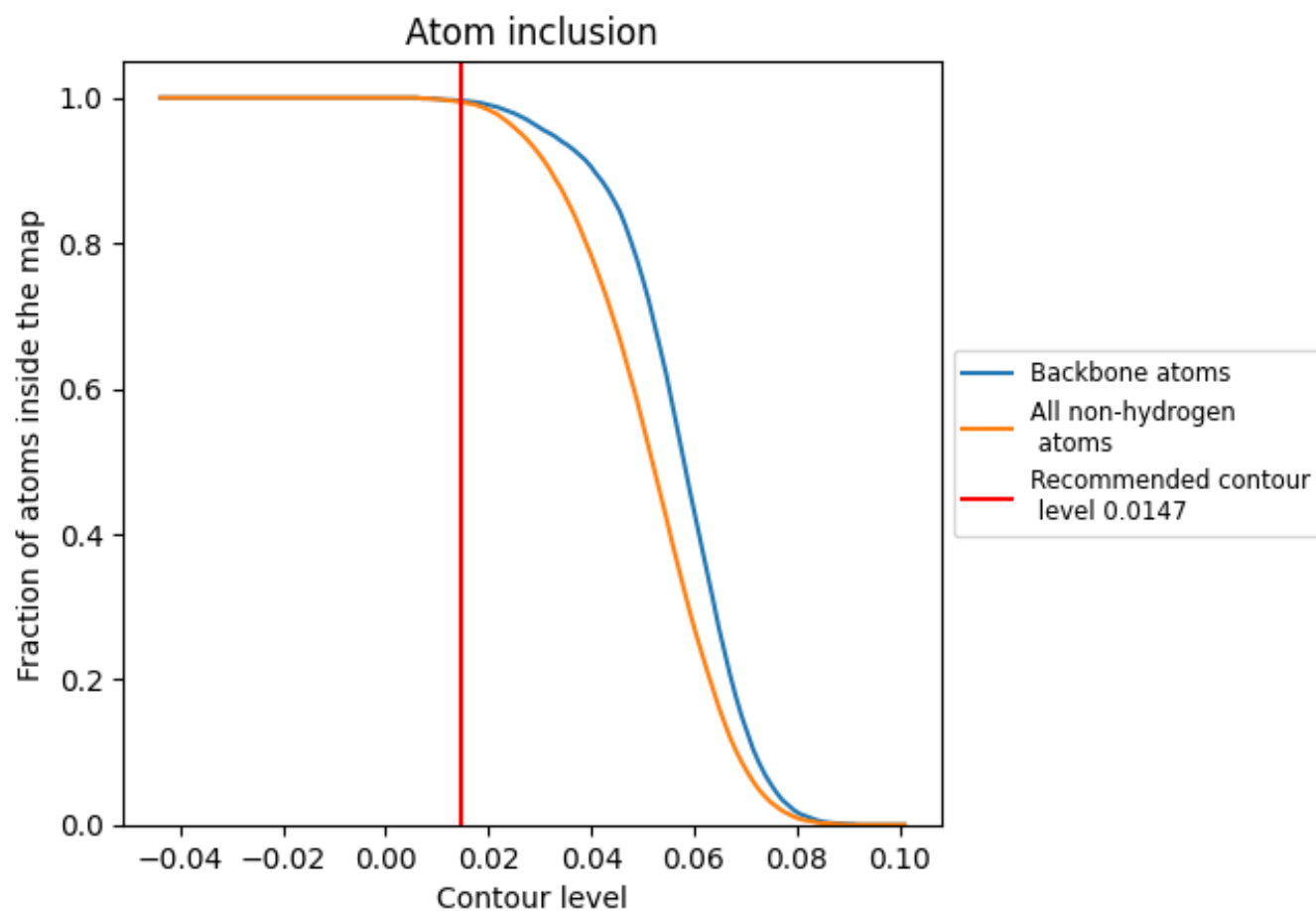
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0147).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9940	0.1450
A	0.9950	0.1430
B	1.0000	0.1080
C	0.9960	0.1410
D	1.0000	0.1070
E	1.0000	0.2680
F	1.0000	0.2690
G	1.0000	0.2330
H	1.0000	0.2340
I	0.9340	0.0480
J	0.9570	0.0550

1.0

0.0

<0.0