



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2023 – 07:47 am GMT

PDB ID : 7PQH
EMDB ID : EMD-13594
Title : Cryo-EM structure of *Saccharomyces cerevisiae* TOROID (TORC1 Organized in Inhibited Domains).
Authors : Felix, J.; Prouteau, M.; Bourgoing, C.; Bonadei, L.; Desfosses, A.; Gabus, C.; Sadian, Y.; Savvides, S.N.; Gutsche, I.; Loewith, R.
Deposited on : 2021-09-17
Resolution : 3.87 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.1

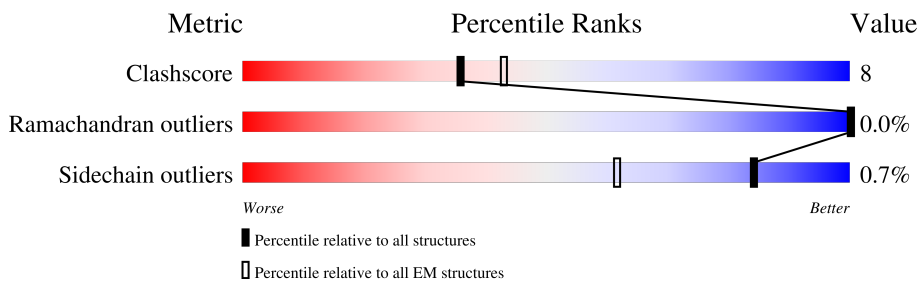
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.87 Å.

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



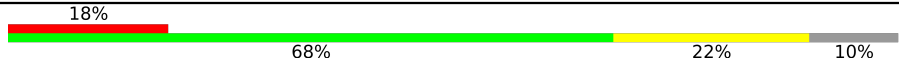



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1608	
1	B	1608	
1	G	1608	
1	J	1608	
2	C	303	
2	D	303	
2	I	303	
2	L	303	

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Mol	Chain	Length	Quality of chain
3	E	2474	
3	F	2474	
3	H	2474	
3	K	2474	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 102671 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 Target of rapamycin complex 1 subunit KOG1, Target of rapamycin complex 1 subunit Kog1.

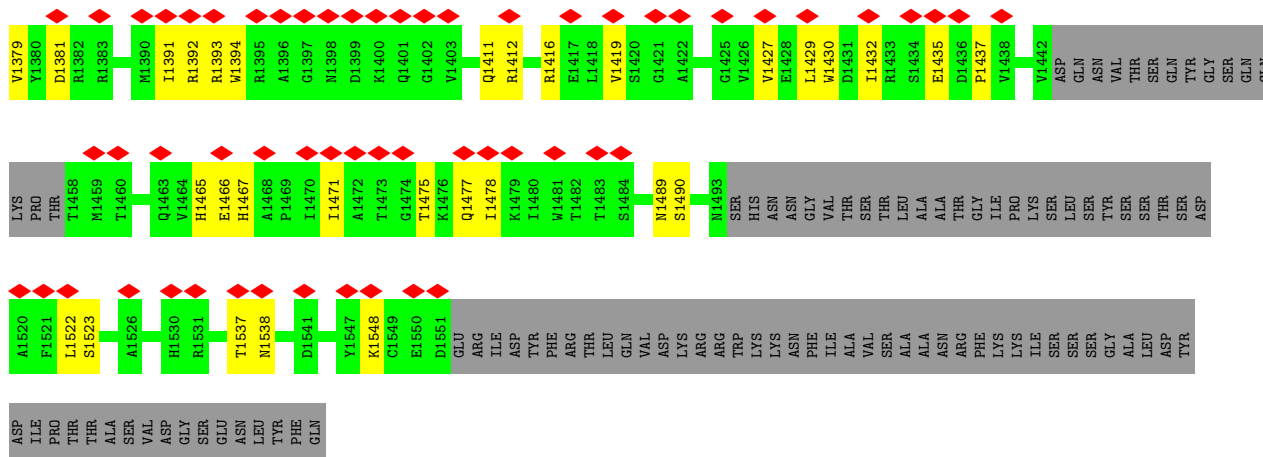
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1209	9693	6225	1638	1784	46	0	0
1	B	1208	9686	6223	1636	1781	46	0	0
1	G	1212	9705	6239	1639	1781	46	0	0
1	J	1213	9711	6242	1641	1782	46	0	0

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

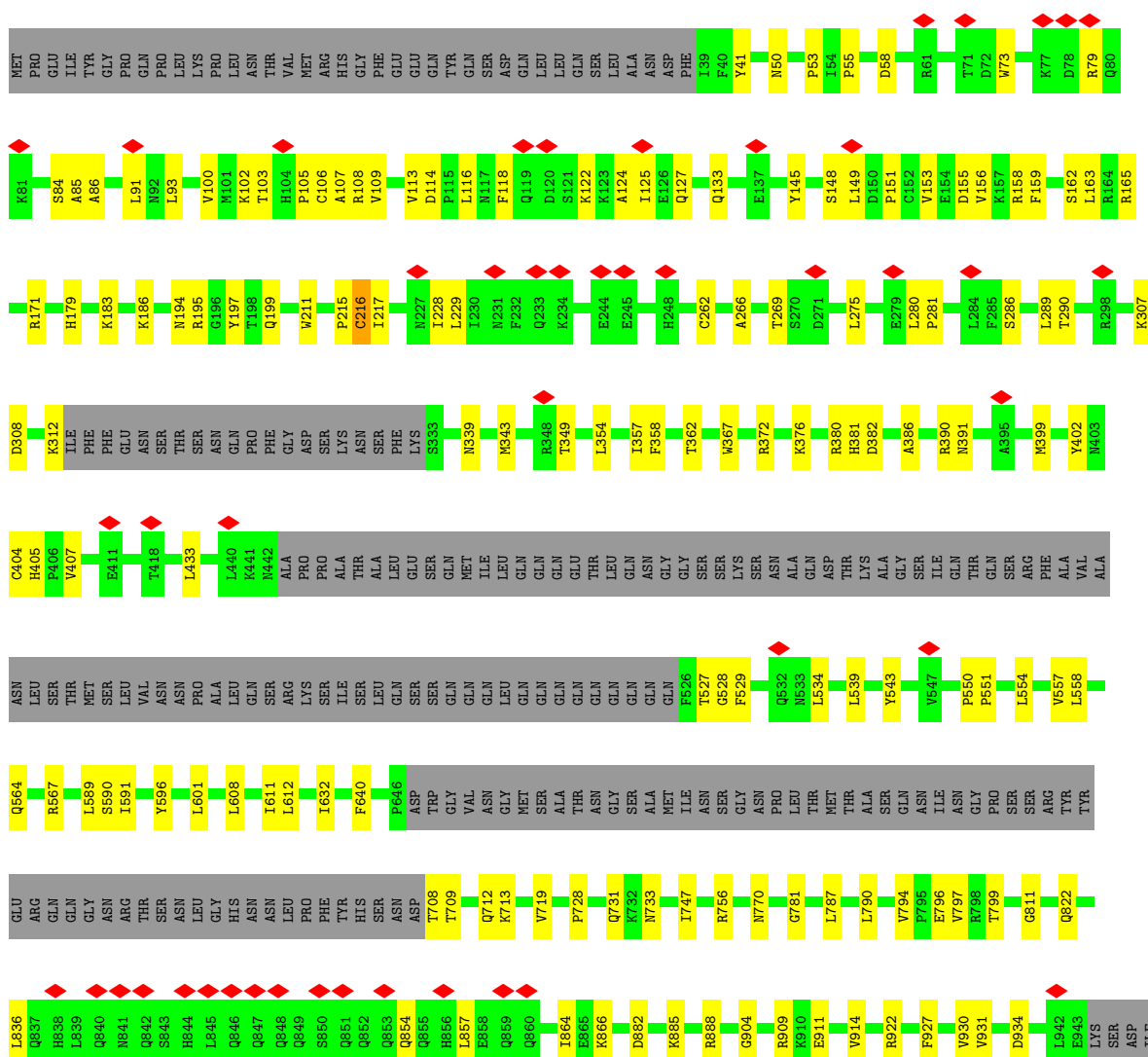
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	300	2366	1465	430	460	11	0	0
2	D	300	2366	1465	430	460	11	0	0
2	I	300	2366	1465	430	460	11	0	0
2	L	300	2366	1465	430	460	11	0	0

- Molecule 3 is a protein called Serine/threonine-protein kinase TOR2.

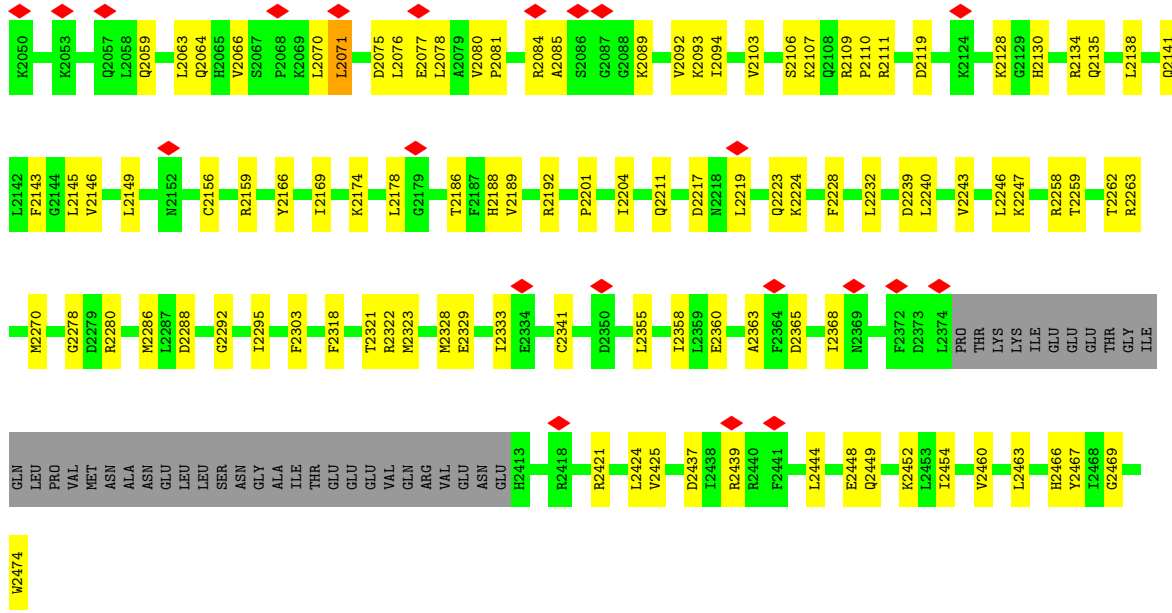
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	2238	17910	11494	3058	3275	83	0	0
3	F	2238	17904	11491	3055	3275	83	0	0
3	H	1157	9299	5981	1588	1684	46	0	0
3	K	1157	9299	5981	1588	1684	46	0	0



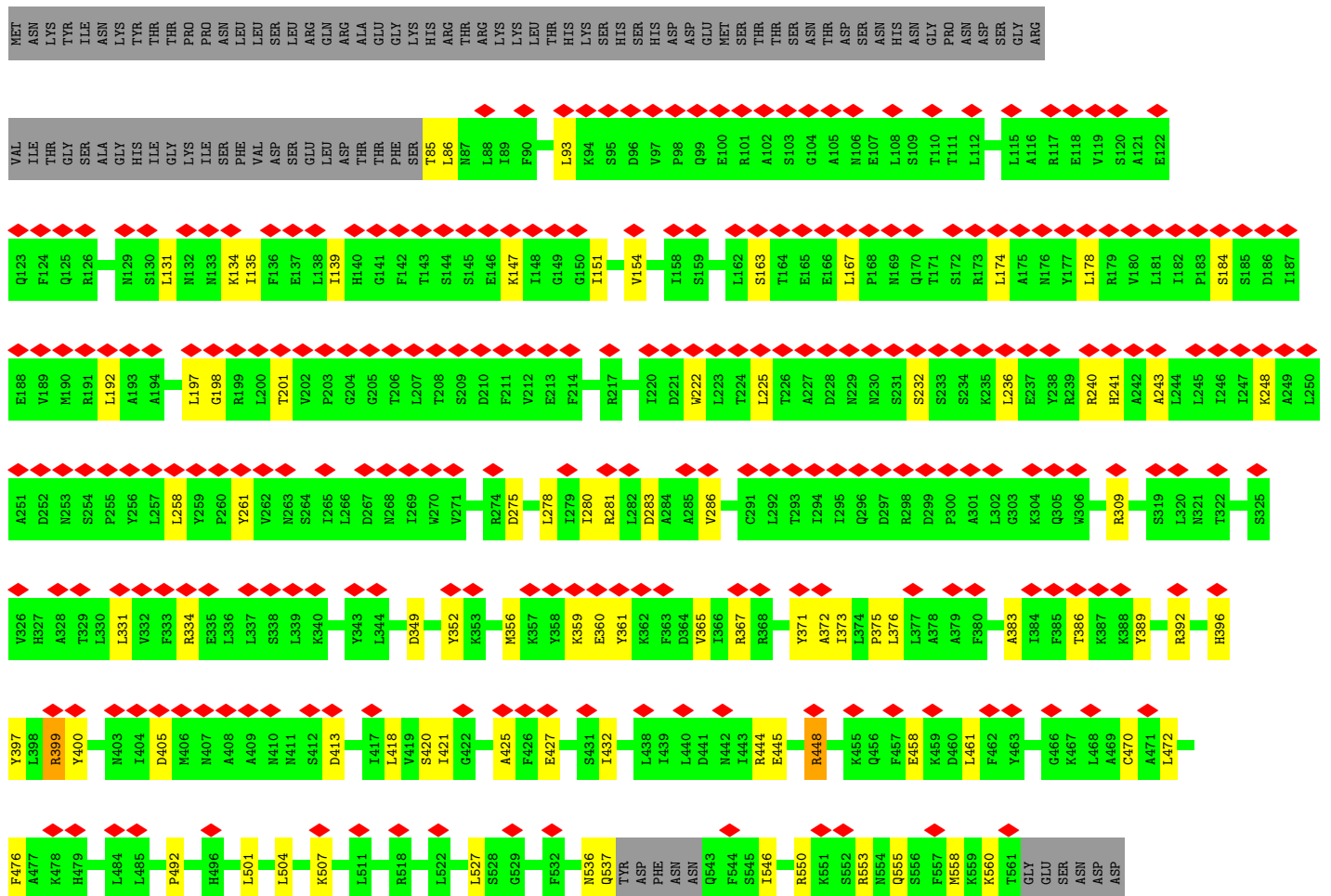
- Molecule 1: Target of rapamycin complex 1 subunit KOG1, Target of rapamycin complex 1 subunit Kog1

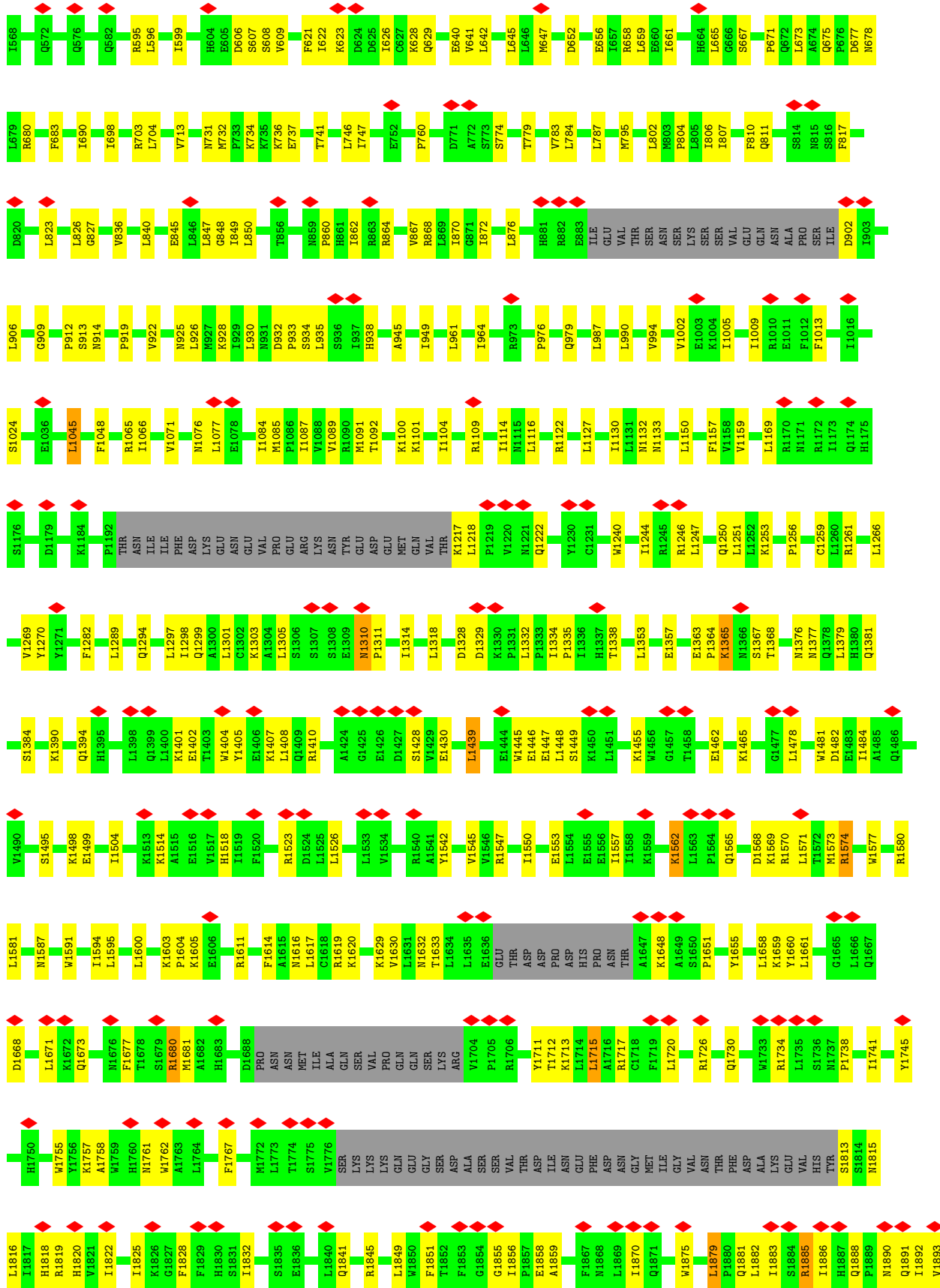


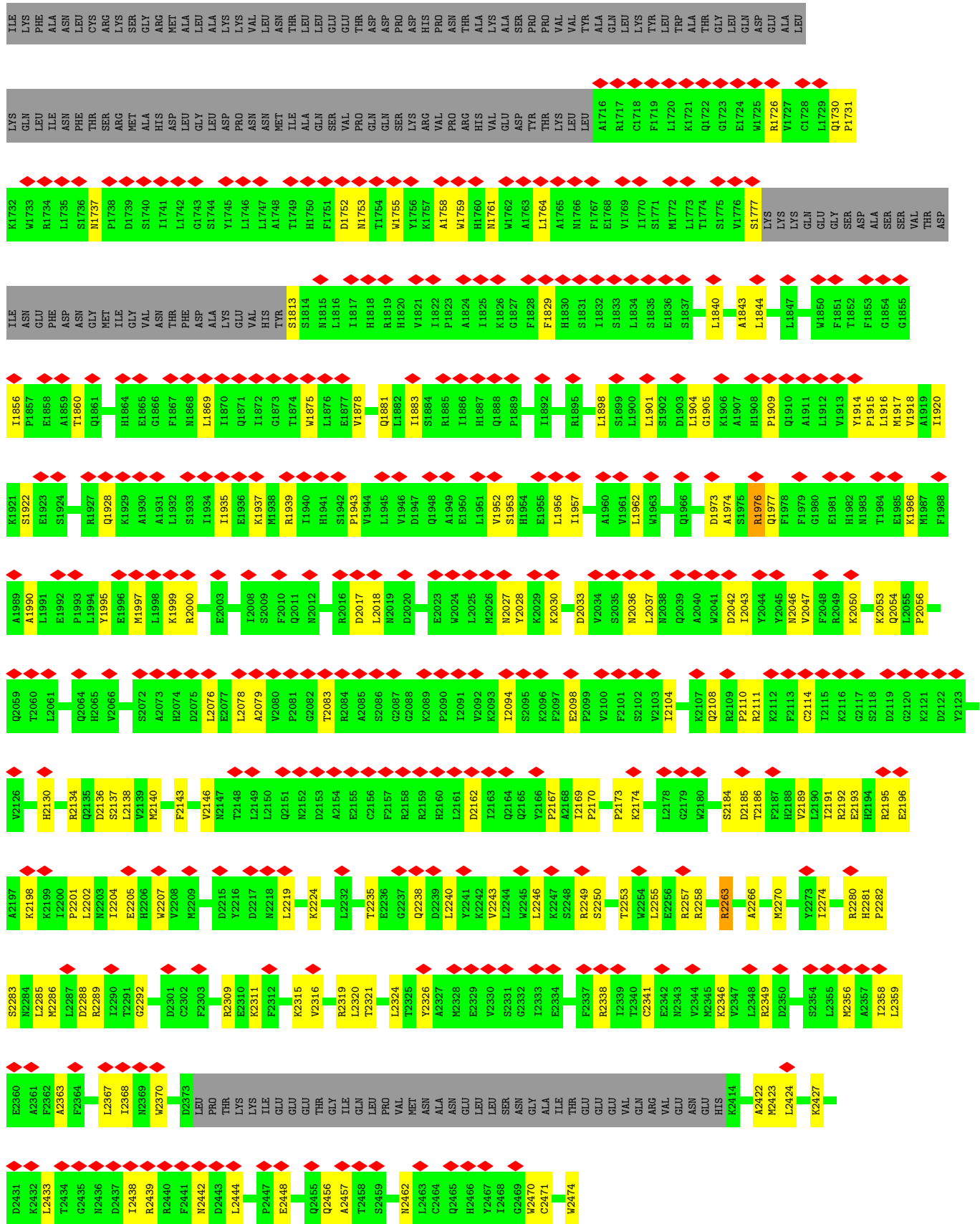
S1975	R1976	E1981	H1982	M1983	K1986	M1987	F1988	L1991	E1992	P1993	L1994	Y1995	E1996	K1999	T2004	R2005	R2006	E2007	I2008	N2012	S2013	F2014	G2015	R2016	D2017	L2018	N2019	D2020	E2023	W2024	L2025	M2026	N2027	K2030	D2033	V2034	L2037	N2038	Q2039	A2040	W2041	D2042	I2043	Y2044	Y2045	N2046	V2047	F2048	R2049		
H1879	P1880	Q1881	L1882	I1883	S1884	R1885	I1886	H1887	M1890	Q1891	H1892	V1893	S1894	R1895	L1898	D1903	K1906	P1909	V1913	Y1914	P1915	L1916	M1917	D1920	K1921	R1927	A1930	I1934	I1935	I1940	L1945	Q1948	R1958	W1963	Q1966	W1967	A2040	E1969	G1970	L1971	D1972	D1973	A1974								
THR	PHE	ASP	ALA	LYS	GLU	VAL	HIS	TYR	S1813	S1814	M1815	L1816	L1817	R1818	R1819	H1820	K1826	G1827	F1828	F1829	I1832	S1835	E1836	S1839	L1840	Q1841	D1842	L1843	L1844	R1845	L1846	L1847	F1851	T1852	F1853	G1854	G1855	E1858	A1859	T1860	H1864	E1865	F1867	N1868	L1869	I1870	Q1871	W1875	L1876		
W1725	R1726	Q1730	W1733	R1734	L1735	S1736	Y1745	H1750	F1751	D1752	K1757	A1758	W1759	H1760	M1761	A1763	A1765	M1766	F1767	E1768	M1769	T1774	S1775	V1776	SER	LYS	LYS	GLN	GLY	SER	ASP	ALA	SER	SER	VAL	THR	ASP	I1704	P1705	R1706	H1707	A1716	L1720	R1721	Q1722						
M1566	S1567	D1568	K1569	R1570	L1571	L1572	W1577	G1577	L1578	T1579	E1579	R1580	W1581	K1586	I1587	D1588	V1589	W1591	I1594	L1595	R1596	V1597	S1599	L1600	V1601	I1602	K1603	K1604	A1605	E1606	V1610	R1611	L1612	K1613	M1616	L1617	C1618	R1619	K1620	K1629	T1633	E1636	GLU	THR	ASP	ASP	PRO	ASP	HIS	PRO	ASN
K1455	W1456	G1457	T1458	K1464	W1476	G1477	L1478	E1479	Q1480	W1481	I1484	Y1487	V1490	S1493	K1498	R1509	M1510	M1511	F1512	K1513	K1514	A1515	E1516	V1517	H1518	I1519	F1520	E1420	K1421	A1424	G1425	E1426	D1427	S1428	V1431	L1436	L1439	E1444	W1445	E1446	E1447	L1448	S1449	K1450	L1451	A1452					
K1366	M1366	S1367	T1368	I1369	E1370	L1379	H1380	Q1381	T1382	D1383	I1386	H1391	H1395	L1398	Q1399	L1400	K1401	W1404	Y1405	E1406	R1410	D1413	A1416	M1419	E1420	K1421	A1424	G1425	E1426	D1427	S1428	V1431	L1436	L1439	E1444	W1445	E1446	E1447	L1448	S1449	K1450	L1451	A1452								
K1237	Q1241	R1245	R1246	L1247	S1248	L1249	Q1250	L1251	L1252	K1253	R1261	L1266	V1269	Y1271	F1282	W1286	T1291	Q1294	L1297	I1298	Q1299	K1303	S1307	M1310	L1321	V1322	E1323	H1327	D1328	D1329	K1330	P1331	I1334	P1335	I1336	H1337	T1338	L1339	Y1355												
F1013	I1016	T1021	S1024	E1036	E1043	T1046	L1049	D1050	M1054	P1063	R1065	I1066	L1067	L1070	L1077	I1087	V1088	G1089	G1097	I1098	P1099	M1099	T1099	S1095	K1100	K1101	I1102	Y983	L987	L990	I991	I998	V1002	E1003	K1004	I1005	W1008	I1009	R1010	E1011	F1012										
G827	Q828	L829	Y835	W836	P839	E845	L846	G848	L849	L850	R851	N852	T856	E857	N858	N859	I862	R863	R864	G865	T866	V867	R868	L869	I870	G871	I872	L873	G874	H881	R882	E883	I1100	GLU	VAL	GLN	ASN	ALA	PRO	SER	ILE	D902	I903								



● Molecule 3: Serine/threonine-protein kinase TOR2







• Molecule 3: Serine/threonine-protein kinase TOR2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	218872	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 ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	37000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.344	Depositor
Minimum map value	-0.057	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	0.29	0/9911	0.58	2/13437 (0.0%)
1	B	0.29	0/9904	0.58	1/13427 (0.0%)
1	G	0.28	0/9923	0.56	2/13455 (0.0%)
1	J	0.28	0/9929	0.55	0/13463
2	C	0.26	0/2422	0.60	0/3302
2	D	0.26	0/2422	0.60	2/3302 (0.1%)
2	I	0.25	0/2422	0.59	2/3302 (0.1%)
2	L	0.25	0/2422	0.61	3/3302 (0.1%)
3	E	0.28	0/18271	0.59	2/24746 (0.0%)
3	F	0.27	0/18265	0.59	6/24739 (0.0%)
3	H	0.26	0/9509	0.58	0/12893
3	K	0.26	0/9509	0.56	0/12893
All	All	0.28	0/104909	0.58	20/142261 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	J	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	120	ASP	CB-CG-OD1	9.13	126.51	118.30
3	F	1715	LEU	CA-CB-CG	8.74	135.41	115.30
3	E	2071	LEU	CA-CB-CG	6.60	130.48	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	137	ASP	CB-CG-OD1	6.47	124.13	118.30
2	I	239	ASP	CB-CG-OD1	6.34	124.01	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	216	CYS	Peptide
1	B	216	CYS	Peptide
1	J	216	CYS	Peptide

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	9693	0	9655	137	0
1	B	9686	0	9656	128	0
1	G	9705	0	9676	153	0
1	J	9711	0	9683	149	0
2	C	2366	0	2251	46	0
2	D	2366	0	2251	42	0
2	I	2366	0	2251	37	0
2	L	2366	0	2251	37	0
3	E	17910	0	18236	351	0
3	F	17904	0	18225	331	0
3	H	9299	0	9374	177	0
3	K	9299	0	9374	168	0
All	All	102671	0	102883	1741	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 8.

The worst 5 of 1741 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:J:632:ILE:HD11	1:J:733:ASN:HD22	1.26	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1105:LYS:HZ1	1:J:1306:LEU:HD11	1.36	0.90
1:G:630:GLU:N	1:G:630:GLU:OE1	2.08	0.85
3:H:971:VAL:O	3:H:975:CYS:HB3	1.80	0.82
3:E:2286:MET:HB2	3:E:2295:ILE:HB	1.62	0.82

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	1189/1608 (74%)	1121 (94%)	68 (6%)	0	100	100
1	B	1188/1608 (74%)	1128 (95%)	60 (5%)	0	100	100
1	G	1192/1608 (74%)	1131 (95%)	59 (5%)	2 (0%)	47	79
1	J	1193/1608 (74%)	1126 (94%)	65 (5%)	2 (0%)	47	79
2	C	298/303 (98%)	267 (90%)	31 (10%)	0	100	100
2	D	298/303 (98%)	267 (90%)	31 (10%)	0	100	100
2	I	298/303 (98%)	266 (89%)	32 (11%)	0	100	100
2	L	298/303 (98%)	268 (90%)	30 (10%)	0	100	100
3	E	2220/2474 (90%)	2072 (93%)	148 (7%)	0	100	100
3	F	2220/2474 (90%)	2069 (93%)	151 (7%)	0	100	100
3	H	1147/2474 (46%)	1097 (96%)	50 (4%)	0	100	100
3	K	1147/2474 (46%)	1091 (95%)	56 (5%)	0	100	100
All	All	12688/17540 (72%)	11903 (94%)	781 (6%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	1099	MET
1	G	1099	MET
1	J	1108	PRO
1	G	1108	PRO

5.3.2 Protein sidechains [i](#)

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	1080/1458 (74%)	1072 (99%)	8 (1%)	84	90
1	B	1079/1458 (74%)	1076 (100%)	3 (0%)	92	95
1	G	1079/1458 (74%)	1068 (99%)	11 (1%)	76	86
1	J	1080/1458 (74%)	1073 (99%)	7 (1%)	86	91
2	C	263/267 (98%)	262 (100%)	1 (0%)	91	94
2	D	263/267 (98%)	262 (100%)	1 (0%)	91	94
2	I	263/267 (98%)	260 (99%)	3 (1%)	73	84
2	L	263/267 (98%)	262 (100%)	1 (0%)	91	94
3	E	1991/2219 (90%)	1977 (99%)	14 (1%)	84	90
3	F	1990/2219 (90%)	1973 (99%)	17 (1%)	78	87
3	H	1037/2219 (47%)	1031 (99%)	6 (1%)	86	91
3	K	1037/2219 (47%)	1033 (100%)	4 (0%)	91	94
All	All	11425/15776 (72%)	11349 (99%)	76 (1%)	84	90

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	1937	LYS
3	K	1245	ARG
3	H	2263	ARG
1	J	822	GLN
2	L	61	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38

such sidechains are listed below:

Mol	Chain	Res	Type
1	J	1102	HIS
3	K	1977	GLN
1	J	1171	ASN
3	K	1250	GLN
2	L	29	GLN

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 monosaccharides 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.

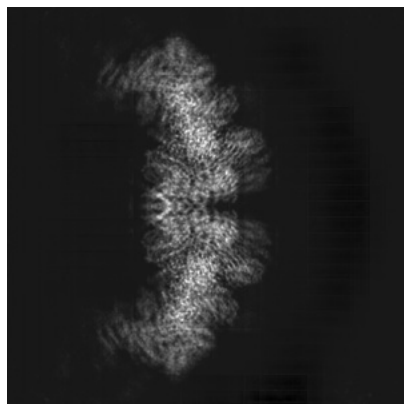
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13594. These allow visual inspection of the internal detail of the map and identification of artifacts.

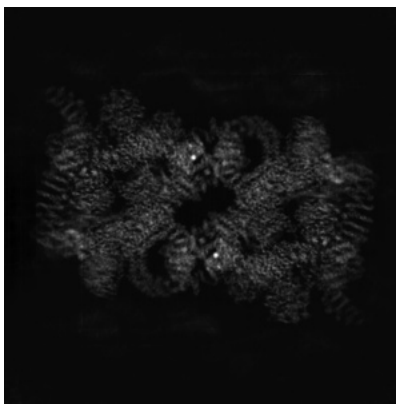
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

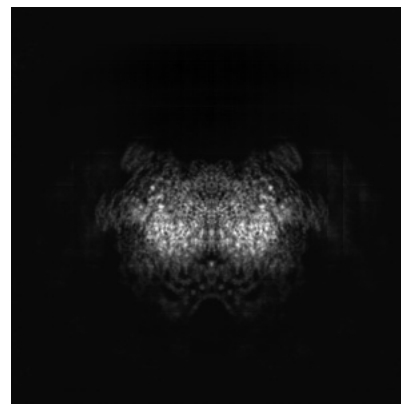
6.1.1 Primary map



X

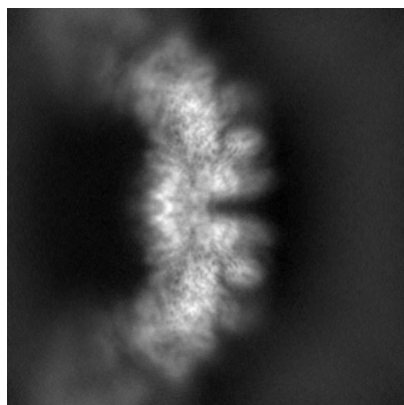


Y

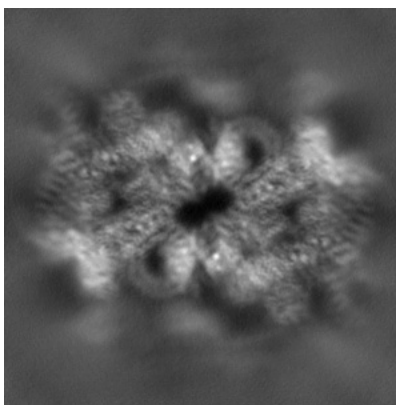


Z

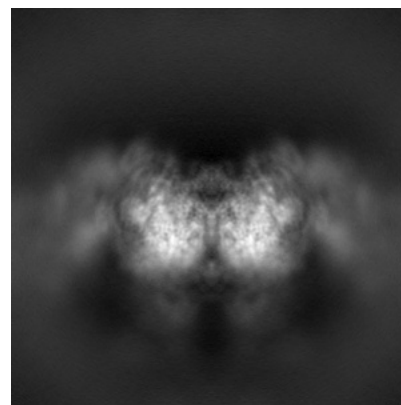
6.1.2 Raw map



X



Y

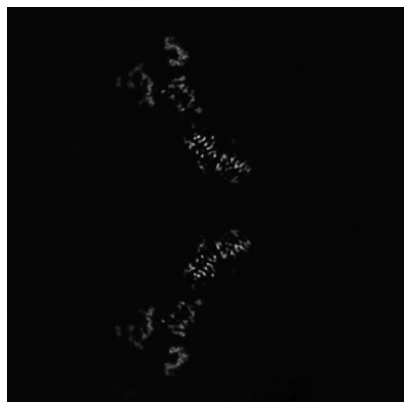


Z

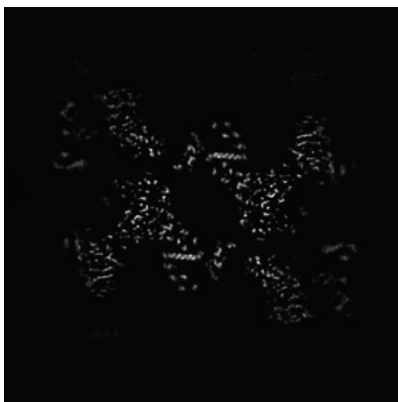
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150

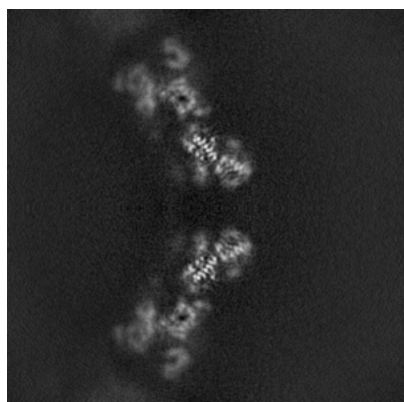


Y Index: 150

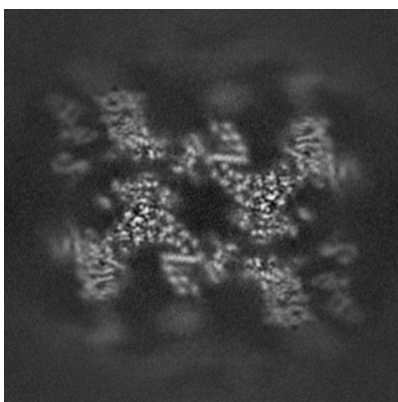


Z Index: 150

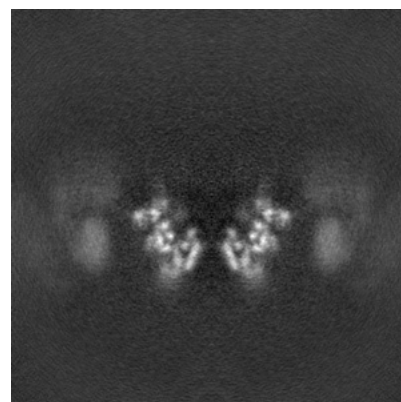
6.2.2 Raw map



X Index: 150



Y Index: 150

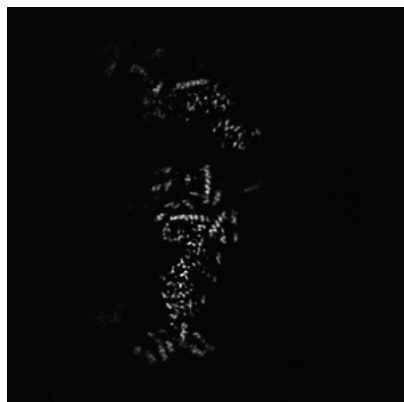


Z Index: 150

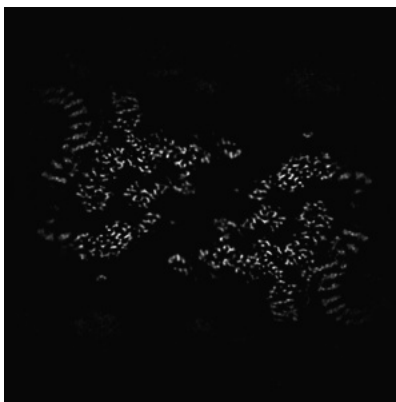
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 187

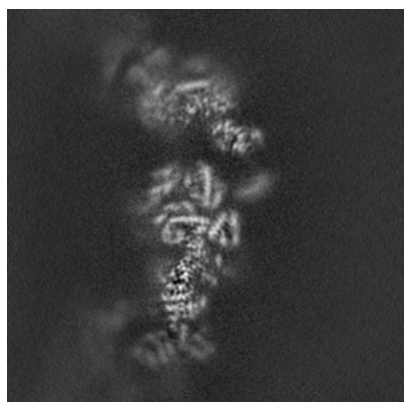


Y Index: 136

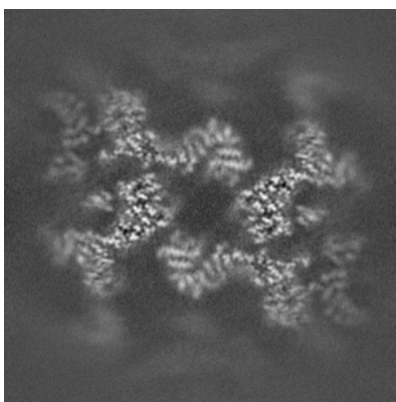


Z Index: 195

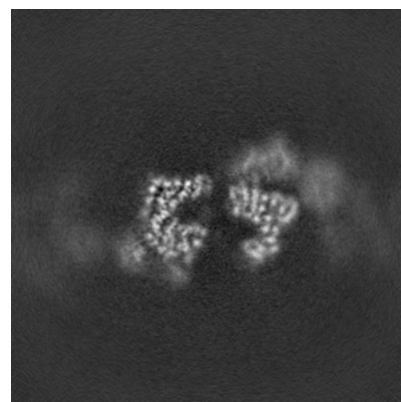
6.3.2 Raw map



X Index: 187



Y Index: 143

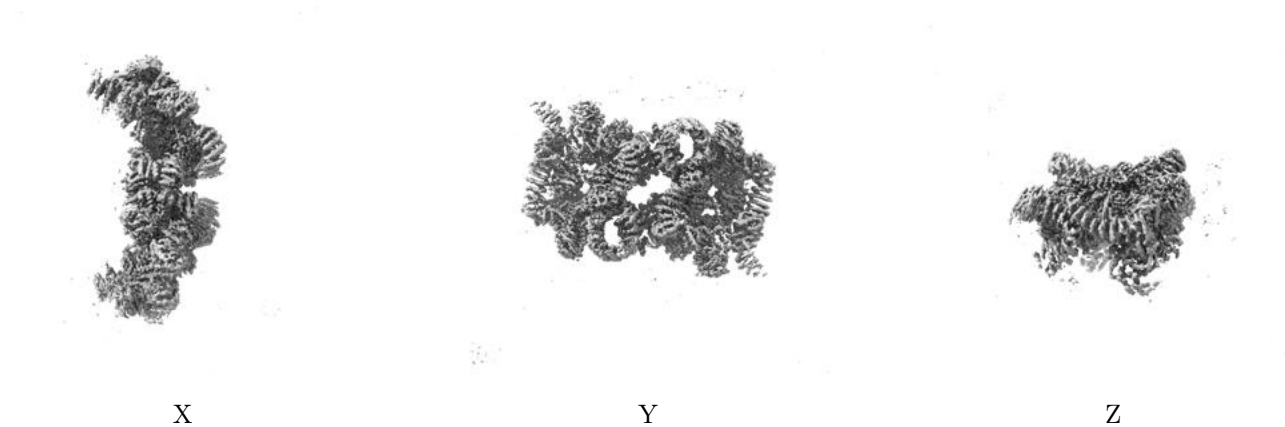


Z Index: 166

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

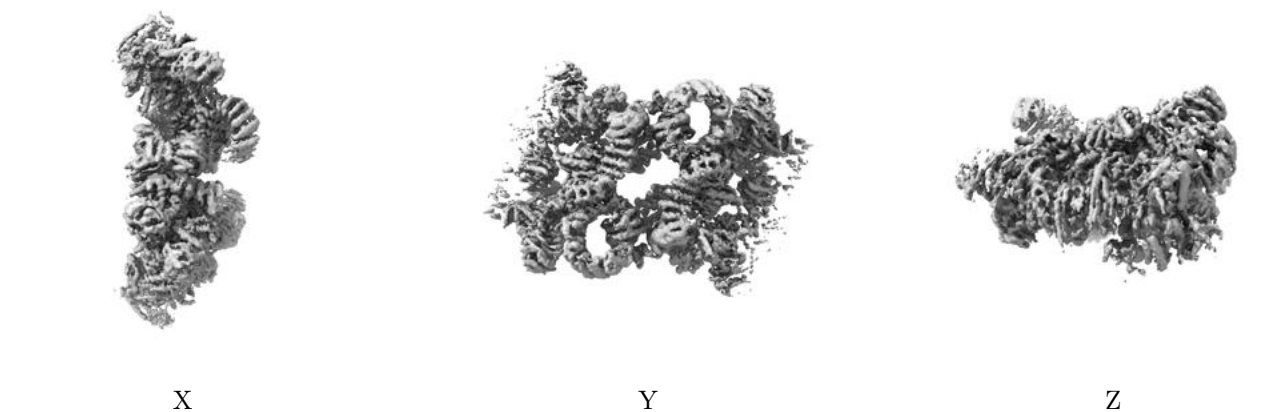
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

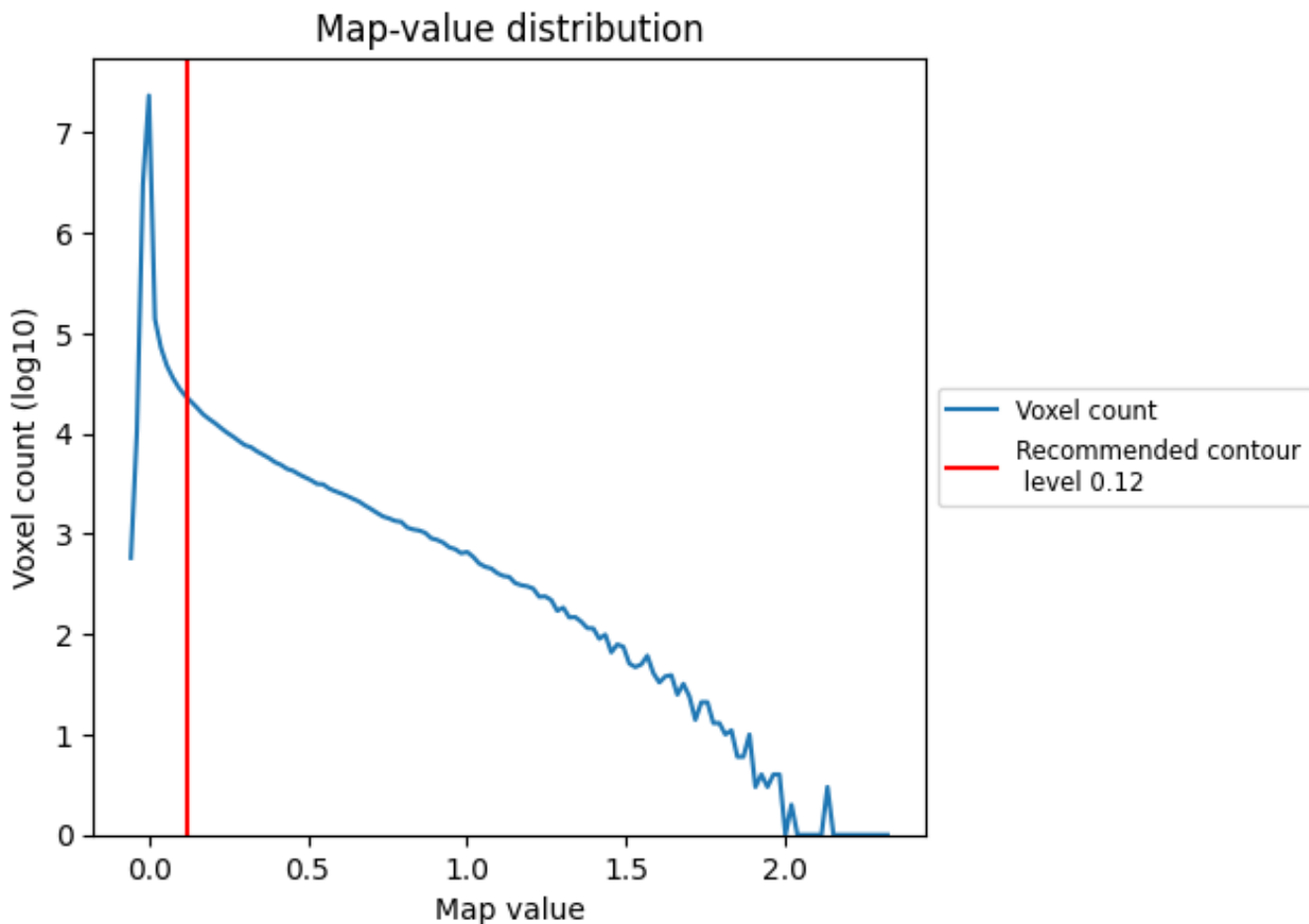
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

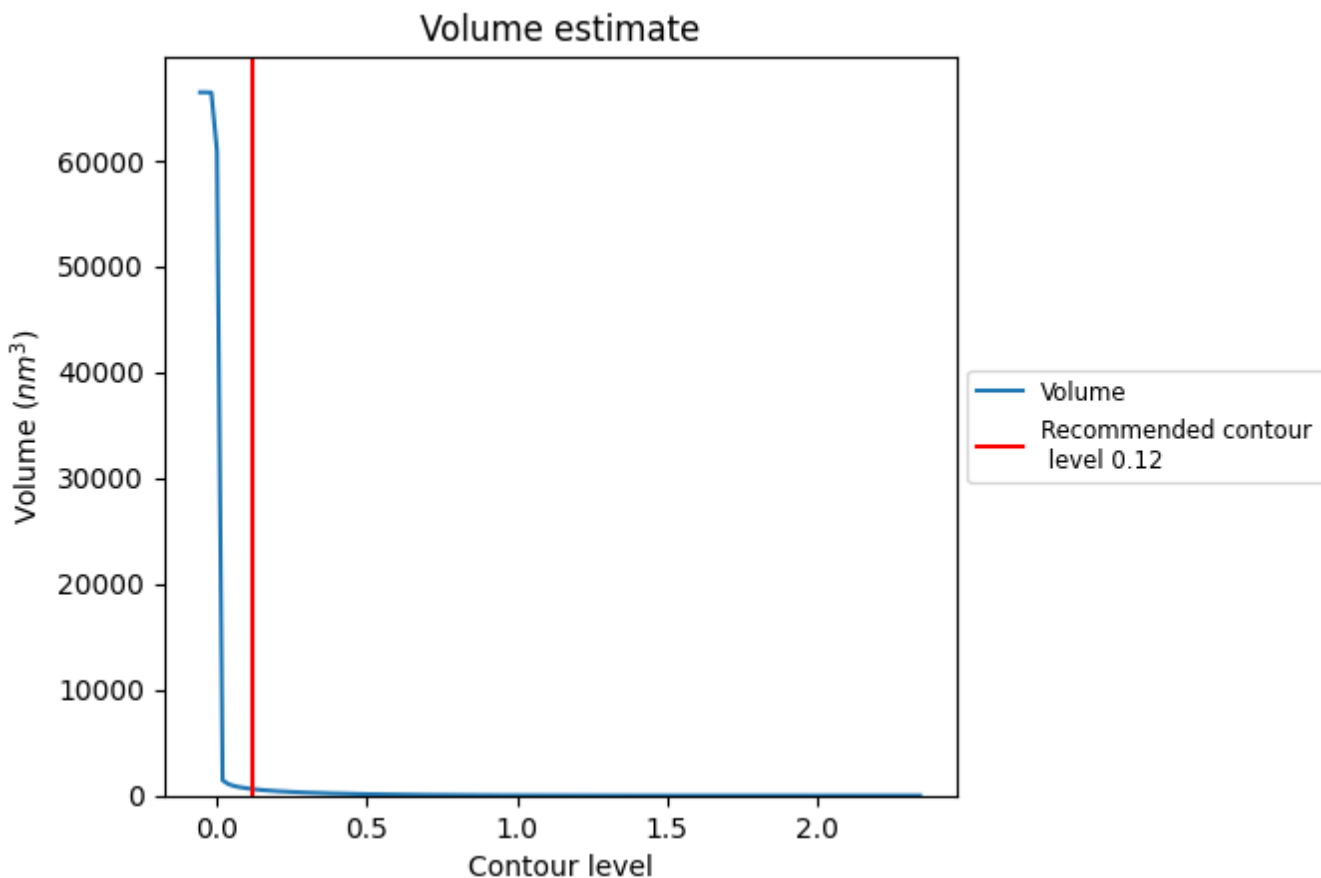
This section contains the results of statistical analysis of the map.

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.

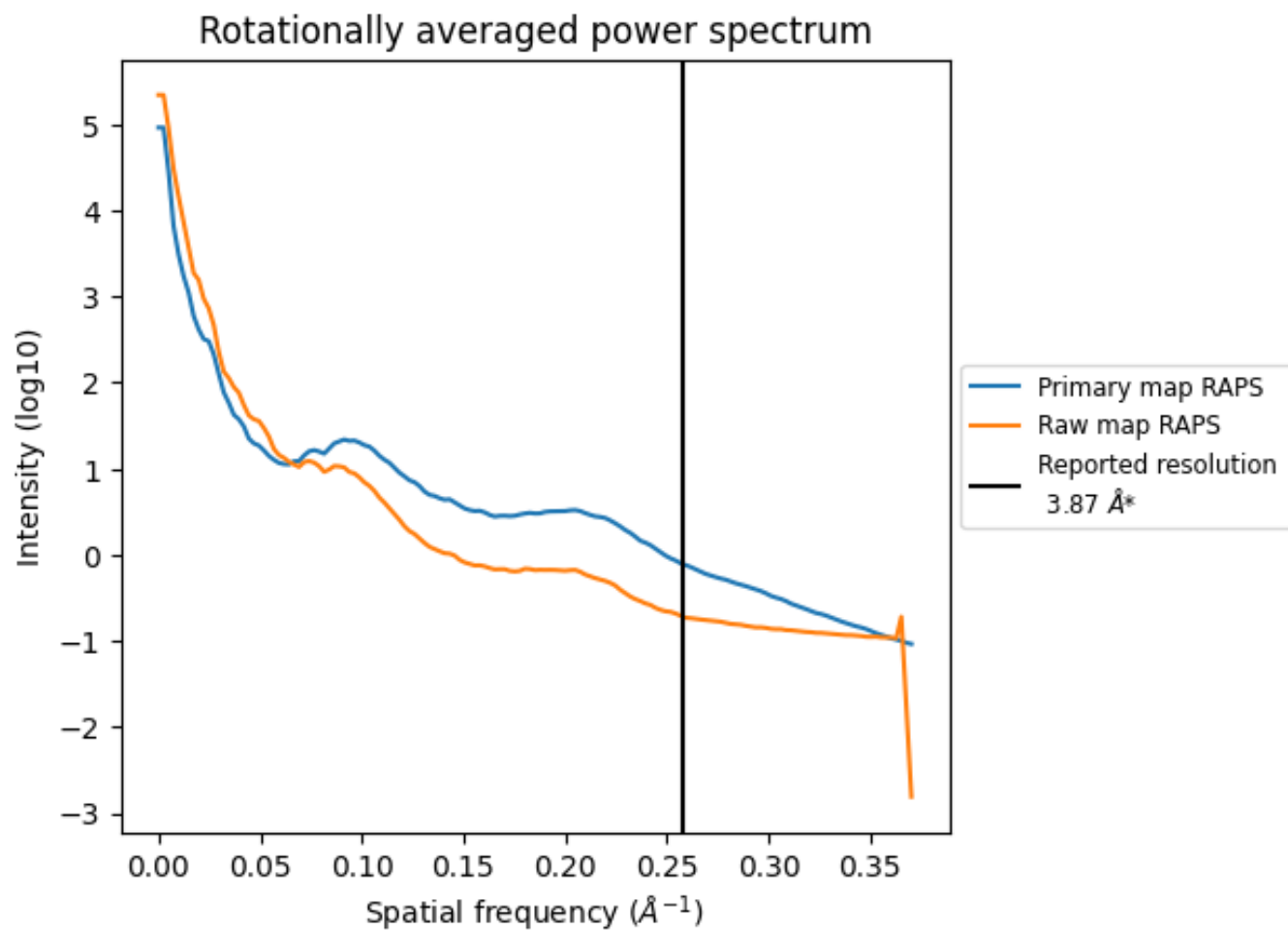
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 609 nm^3 ; this corresponds to an approximate mass of 550 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 i

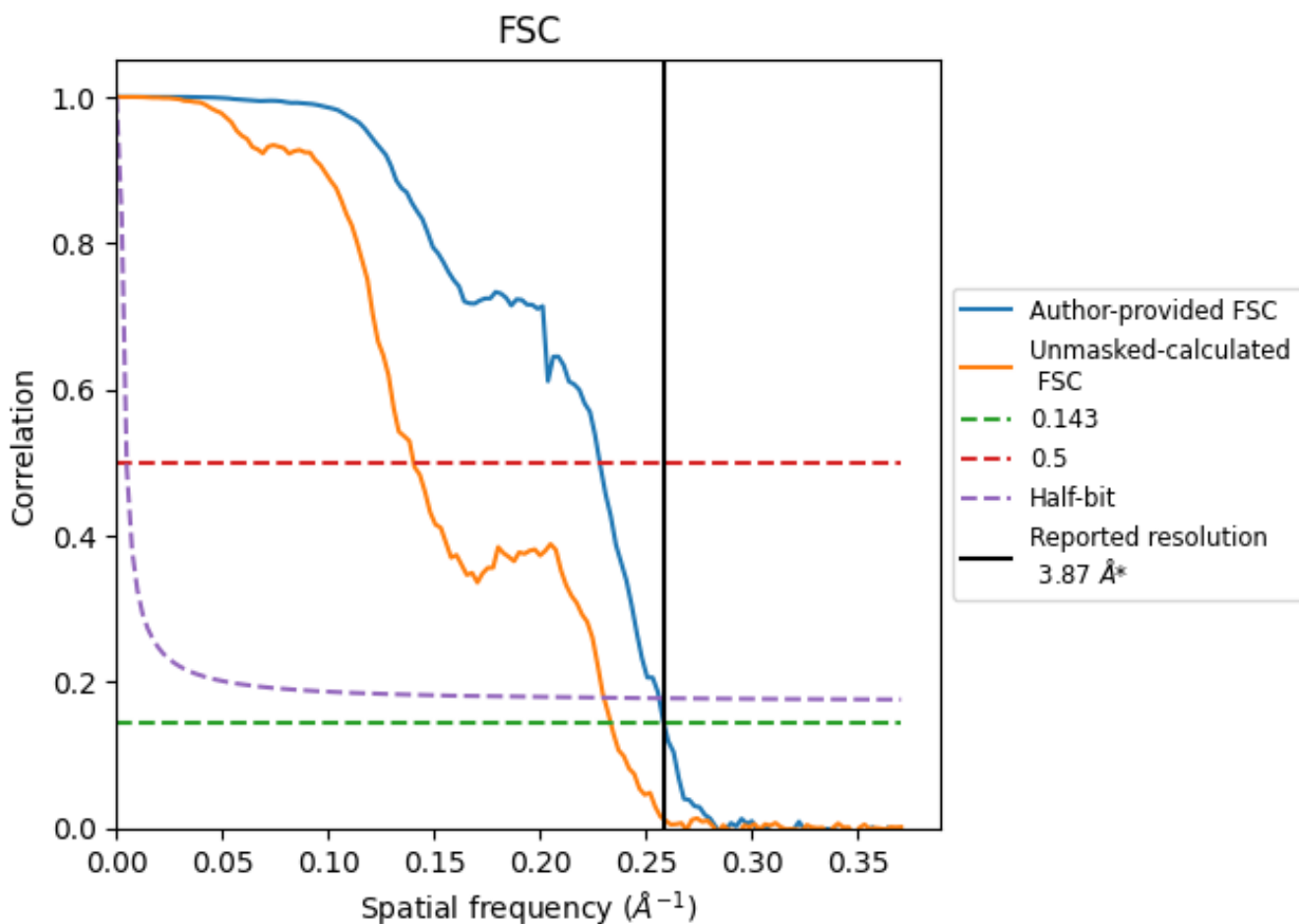


*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

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 0.258 Å⁻¹

8.2 Resolution estimates [i](#)

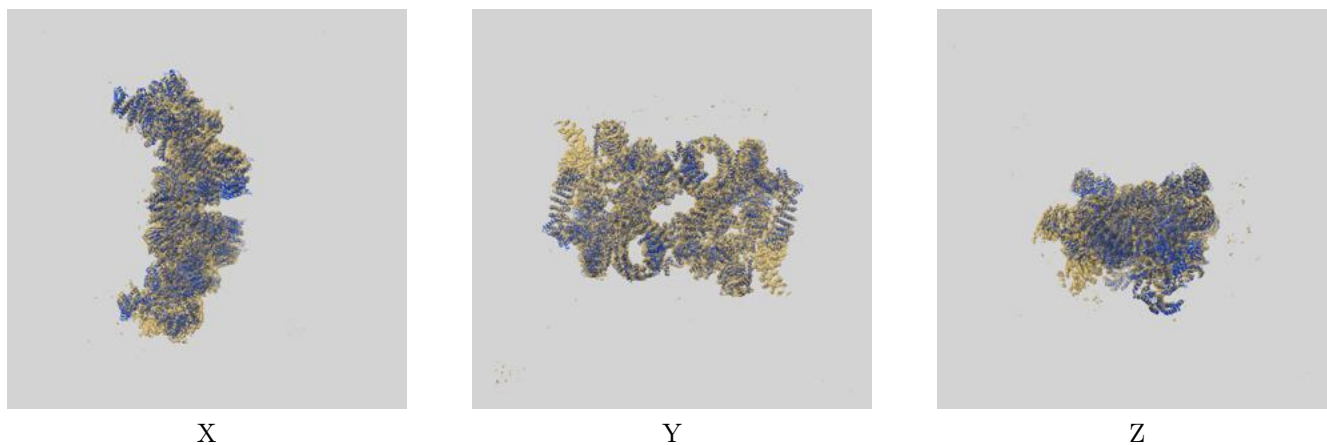
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	3.87	4.38	3.90
Unmasked-calculated*	4.28	7.13	4.35

*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 4.28 differs from the reported value 3.87 by more than 10 %

9 Map-model fit [i](#)

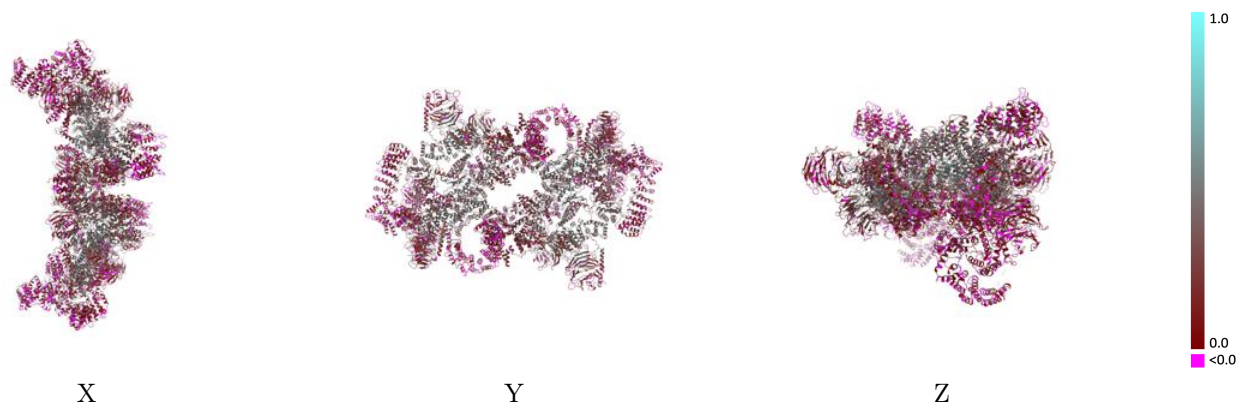
This section contains information regarding the fit between EMDB map EMD-13594 and PDB model 7PQH. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



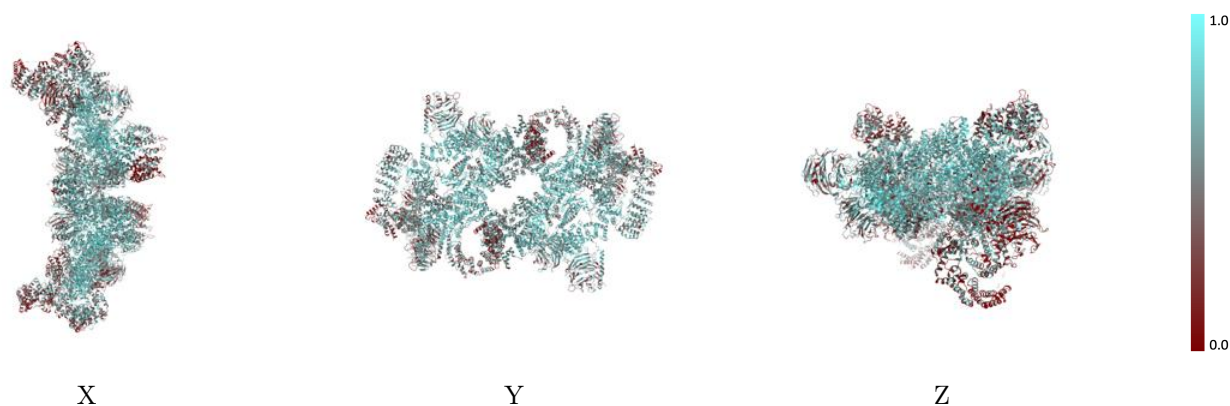
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



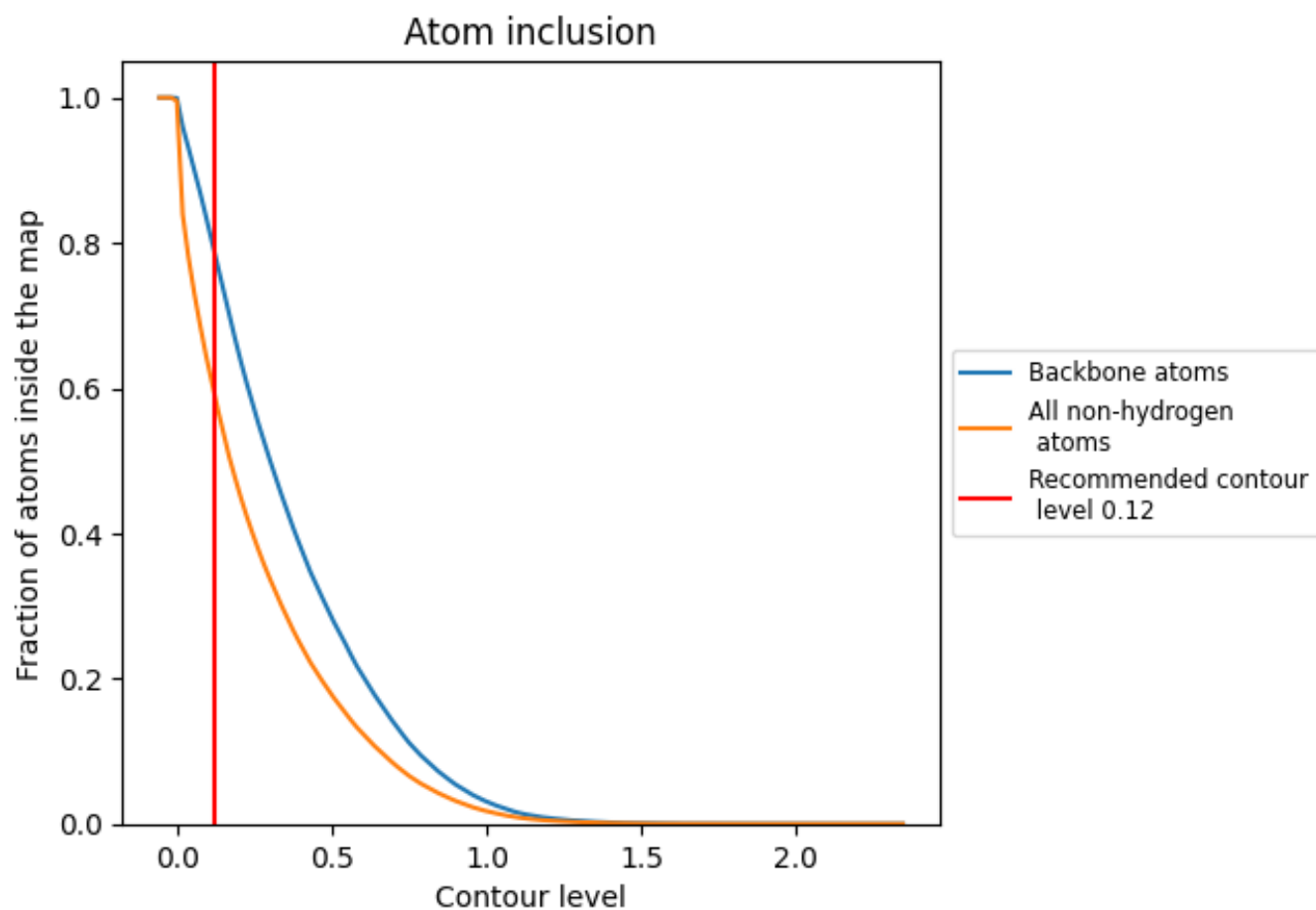
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5920	 0.2410
A	 0.7000	 0.3320
B	 0.7191	 0.3360
C	 0.5663	 0.2680
D	 0.5482	 0.2640
E	 0.6176	 0.2290
F	 0.6111	 0.2270
G	 0.6837	 0.3160
H	 0.4175	 0.1110
I	 0.2017	 0.1100
J	 0.6972	 0.3160
K	 0.4346	 0.1150
L	 0.2449	 0.1250

