



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:31 PM UTC

PDB ID : 5H64 / pdb_00005h64
EMDB ID : EMD-6668
Title : Cryo-EM structure of mTORC1
Authors : Yang, H.; Wang, J.; Liu, M.; Chen, X.; Huang, M.; Tan, D.; Dong, M.; Wong, C.C.L.; Wang, J.; Xu, Y.; Wang, H.
Deposited on : 2016-11-10
Resolution : 4.40 Å(reported)

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

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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

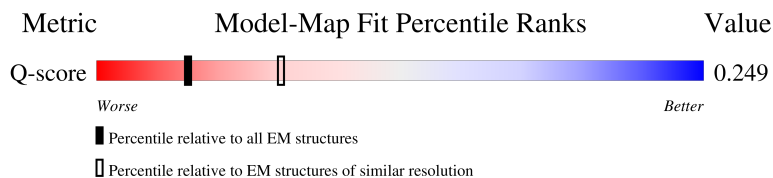
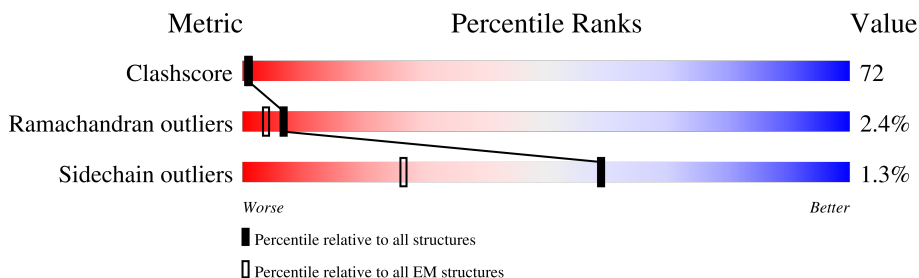
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	2549	
1	a	2549	
2	B	1335	
2	b	1335	

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Mol	Chain	Length	Quality of chain
3	C	326	6%13%83%..
3	c	326	7%13%83%..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 45252 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 mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2101	Total	C	N	O	S	0	0
			15617	9886	2788	2849	94		
1	a	2101	Total	C	N	O	S	0	0
			15617	9886	2788	2849	94		

- Molecule 2 is a protein called Regulatory-associated protein of mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	797	Total	C	N	O	S	0	0
			4553	2817	832	894	10		
2	b	797	Total	C	N	O	S	0	0
			4553	2817	832	894	10		

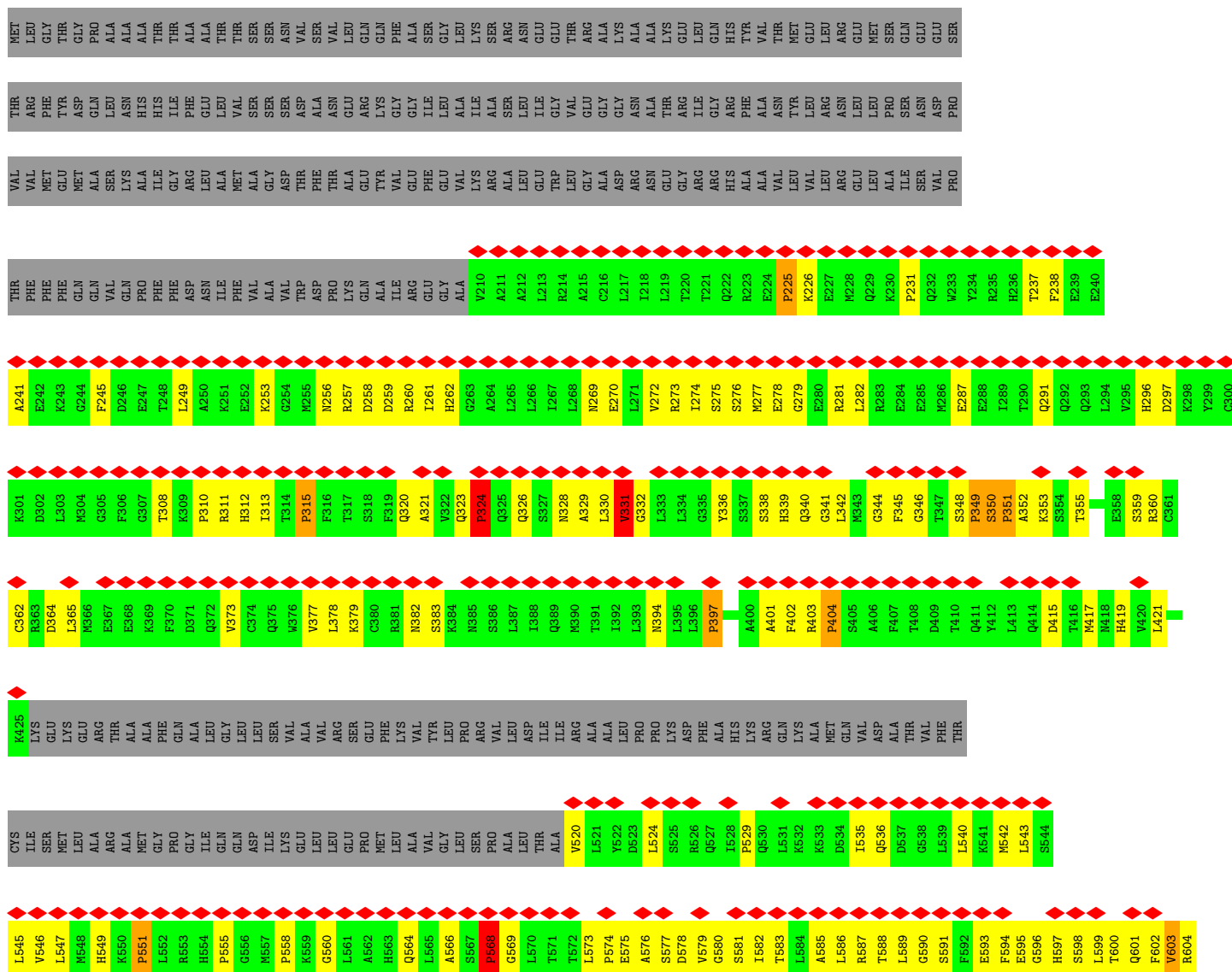
- Molecule 3 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	317	Total	C	N	O	S	0	0
			2456	1526	436	476	18		
3	c	317	Total	C	N	O	S	0	0
			2456	1526	436	476	18		





- Molecule 1: Serine/threonine-protein kinase mTOR

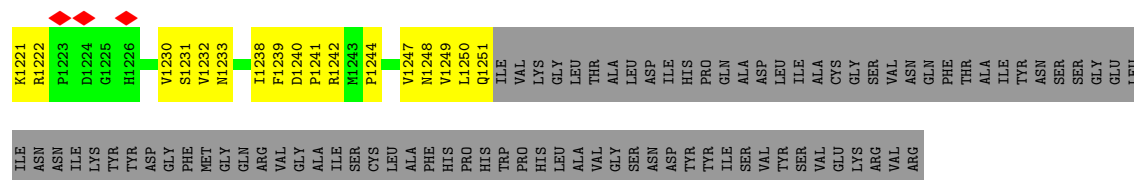


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M1359	L1360	F1363	L1285	L1286	L1287	L1291	S1295	L1302	C1303	L1304	L1305	L1306	L1307	Q1308	L1380	V1381	L1382	L1383	L1384	G1385	E1386	F1387	L1388	L1389	C1390	R1391	A1392	L1393	A1394	K1395	A1396	L1397	H1398	L1399	L1337	L1338	E1400	L1401	L1402	F1404	Q1405	T1409	P1410	A1411	L1412	L1413	E1414	S1415	L1416	L1417	S1418	L1419	M1481	R1482	C1483	L1484													
V1217	K1218	G1219	Y1220	L1221	L1222	ALA	ASP	GLU	GLY	GLU	GLY	ASP	PRO	LEU	ILE	TYR	GLN	HIS	ARG	MET	LEU	ALA	LEU	ALA	SER	GLY	GLN	ASP	ALA	LEU	SER	GLY	VAL	GLU	GLY	THR	PRO	M1255	K1256	K1257	L1258	H1259	T1262	I1263	H1264	L1265	Q1266	K1267	A1268	V1276	K1277	D1278	D1279	W1280	L1281	E1282													
W1283	L1284	R1285	L1286	L1287	L1291	S1295	L1302	C1303	L1304	L1305	L1306	L1307	Q1308	L1380	V1381	L1382	L1383	L1384	G1385	E1386	F1387	L1388	L1389	C1390	R1391	A1392	L1393	A1394	K1395	A1396	L1397	H1398	L1399	L1337	L1338	E1400	L1401	L1402	F1404	Q1405	T1409	P1410	A1411	L1412	L1413	E1414	S1415	L1416	L1417	S1418	L1419	M1481	R1482	C1483	L1484														
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V1217	K1218	G1219	Y1220	L1221	L1222	ALA	ASP	GLU	GLY	GLU	GLY	ASP	PRO	LEU	ILE	TYR	GLN	HIS	ARG	MET	LEU	ALA	LEU	ALA	SER	GLY	GLN	ASP	ALA	LEU	SER	GLY	VAL	GLU	GLY	THR	PRO	M1255	K1256	K1257	L1258	H1259	T1262	I1263	H1264	L1265	Q1266	K1267	A1268	V1276	K1277	D1278	D1279	W1280	L1281	E1282													
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L1422	L1423	Q1424	Q1425	P1426	E1427	A1428	A1429	A1430	G1431	G1432	L1433	E1434	Y1435	A1436	M1437	K1438	H1439	F1440	G1441	E1442	L1443	E1444	I1445	E1446	M1447	T1448	Y1449	C1450	E1451	K1452	L1453	L1454	E1455	W1456	A1459	L1460	V1461	A1462	Y1463	D1464	K1465	M1466	M1467	D1468	D1472	P1473	P1474	E1475	L1476	M1477	L1478	L1479	S1418	L1419	M1481	R1482	C1483	L1484											
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H605	C606	A607	D608	H609	Y673	F610	L611	N612	S613	E614	H615	K616	E617	I618	R619	M620	A623	R624	S627	R628	L629	T631	P632	S633	I634	H635	L636	I637	S638	G639	H640	A641	H642	V643	V644	T647	A648	V649	Q650	V651	V652	A653	D654	V655	L656	S657	K658	L659	A724	D785	F725	V726	G663	I664	T665	D666	P667												
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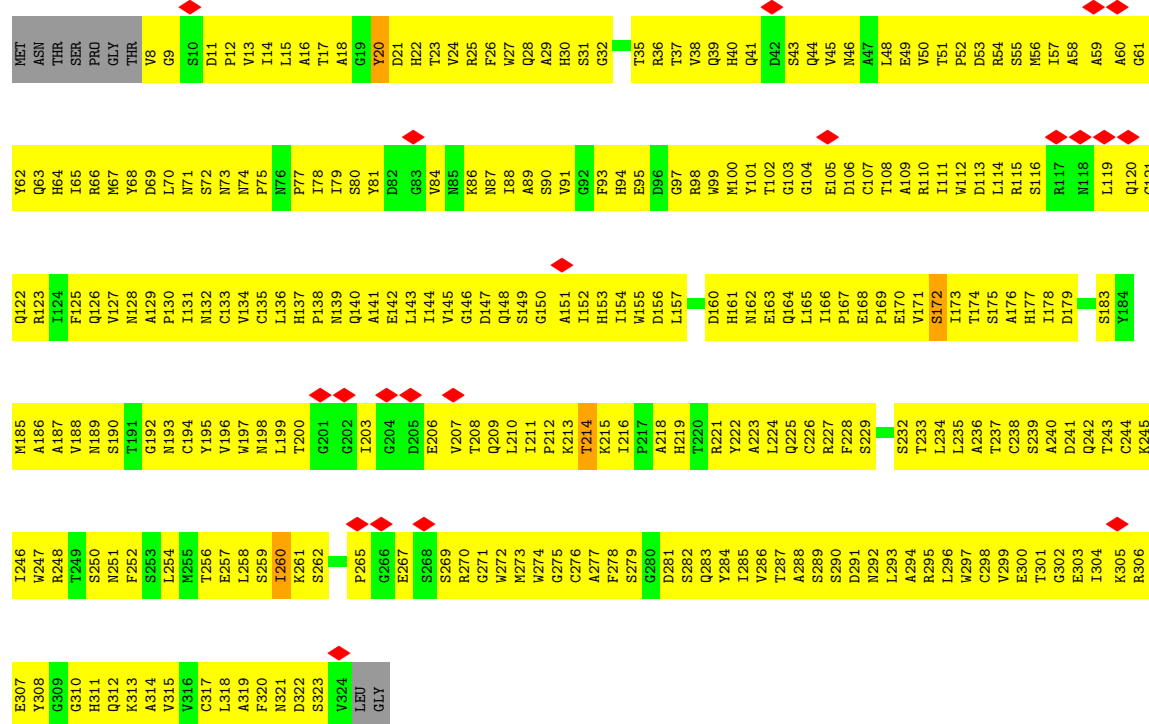
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L2097	T2098	Q2099	A2100	W2101	D2102	L2103	Y2104	Y2105	H2106	V2107	L2108	R2109	R2110	I2111	Q2114	L2115	Q2116	Q2117	L2118	T2119	S2120	L2121	E2122	L2123	Q2124	Y2125	F2126	S2127	P2128	K2129	L2130	L2131	M2132	C2133	R2134	D2135	L2136	E2137	L2138	A2139	V2140	P2141	G2142	T2143	P2146	N2147	I2151	R2152	L2153	R2154	Q2154	S2155	P2156	P2158	Q2161	V2162					
E2032	E2033	A2034	S2035	P2036	L2037	V2038	F2039	G2040	E2041	R2042	N2043	V2044	W2047	F2048	E2049	V2050	L2051	E2052	P2053	L2054	H2055	A2056	M2057	N2058	E2059	R2060	G2061	P2062	Q2063	L2064	L2065	R2066	E2067	N2071	G2075	R2076	D2077	L2078	M2079	E2080	A2081	Q2082	E2083	W2084	C2085	R2086	K2087	W2088	M2089	R2090	L2091	G2092	L2093	V2094	K2095	D2096					
L1972	I1973	Y1974	P1975	A1976	L1977	V1978	A1979	S1980	K1981	S1982	T1983	L1984	T1985	A1986	R1987	H1988	N1989	A1990	A1991	N1992	K1993	L1994	L1995	K1996	N1997	N1998	C1999	E2000	H2001	S2002	N2003	T2004	L2005	V2006	Q2007	Q2008	A2009	M2010	V2012	S2013	E2014	E2015	L2016	L2017	R2018	V2019	A2020	L2021	L2022	W2023	H2024	E2025	M2026	V2027	H2028	E2029	G2030	L2031			
L1909	W1910	F1911	D1912	Y1913	G1914	H1915	W1916	P1917	D1918	V1919	N1920	A1921	A1922	L1923	L1924	E1925	G1926	V1927	K1928	A1929	Q1931	I1932	D1933	T1934	W1935	L1936	Q1937	V1938	T1939	P1940	Q1941	L1942	I1943	A1944	R1945	I1946	D1947	T1948	P1949	R1950	P1951	L1952	G1953	R1954	L1955	L1956	Q1959	L1960	D1963	I1964	Y1967	H1968	P1969	Q1970	A1971						
SER	GLU	SER	GLU	ALA	GLU	SER	THR	GLU	ASN	SER	PRO	THR	PRO	SER	PRO	LEU	GLN	K1867	K1868	V1869	T1870	E1871	D1872	L1873	S1874	K1875	L1876	L1877	L1878	M1879	Y1880	V1882	P1883	A1884	V1885	Q1886	G1887	F1888	F1889	R1890	S1891	I1892	S1893	L1894	S1895	R1896	G1897	N1898	N1899	L1900	Q1901	D1902	T1903	L1904	R1905	V1906	L1907	T1908			
A1789	W1790	H1791	A1792	W1793	A1794	V1795	M1796	N1797	F1798	F1799	A1800	L1801	L1802	H1803	L1804	K1805	H1806	N1807	Q1808	N1809	A1810	R1811	D1812	E1813	K1814	L1815	LVS	LEU	ARG	HIS	ALA	GLY	SER	ASN	ILE	THR	ASN	THR	ALA	THR	ALA	THR	ALA	ALA	THR	ALA	THR	THR	THR	THR	THR	GLU	GLY	SER	ASN						
A1728	Q1729	H1730	A1731	I1732	A1733	T1734	E1735	D1736	Q1737	Q1738	H1739	K1740	Q1741	E1742	L1743	H1744	K1745	L1746	M1747	A1748	R1749	C1750	F1751	L1752	K1753	L1754	G1755	E1756	W1757	Q1758	L1759	M1760	L1761	Q1762	G1763	I1764	E1765	E1766	S1767	T1768	I1769	P1770	K1771	W1772	L1773	Q1774	Y1775	Y1776	S1777	T1780	E1781	H1782	D1783	R1784	S1785	W1786	Y1787	K1788			
R1547	A1548	V1549	L1550	A1551	L1552	H1553	Q1554	D1555	L1556	F1557	Q1558	L1559	A1560	Q1561	Q1562	C1563	I1564	D1565	K1566	A1567	D1568	D1569	L1570	L1571	D1572	A1573	E1574	L1575	T1576	A1577	M1578	A1579	G1580	E1581	S1582	Y1583	S1584	R1585	A1586	Y1587	G1588	A1589	M1590	V1591	S1592	C1593	L1594	H1594	M1595	L1596	P1597	S1597	E1598	L1599	E1600	E1601	V1602	G1603	A1604	Y1605	K1606
E1485	A1486	L1487	G1488	E1489	W1490	G1491	Q1492	L1493	L1494	Q1495	Q1496	C1497	G1498	E1499	K1500	T1501	T1502	L1503	V1504	R1505	D1506	E1507	T1508	L1509	M1512	A1513	R1514	L1515	T1516	A1516	A1517	A1518	A1519	A1520	W1521	G1524	Q1525	W1526	D1527	S1528	M1529	E1530	E1531	Y1532	T1533	C1534	M1535	L1536	P1537	R1538	D1539	T1540	E1541	D1542	G1543	A1544	F1545	Y1546			



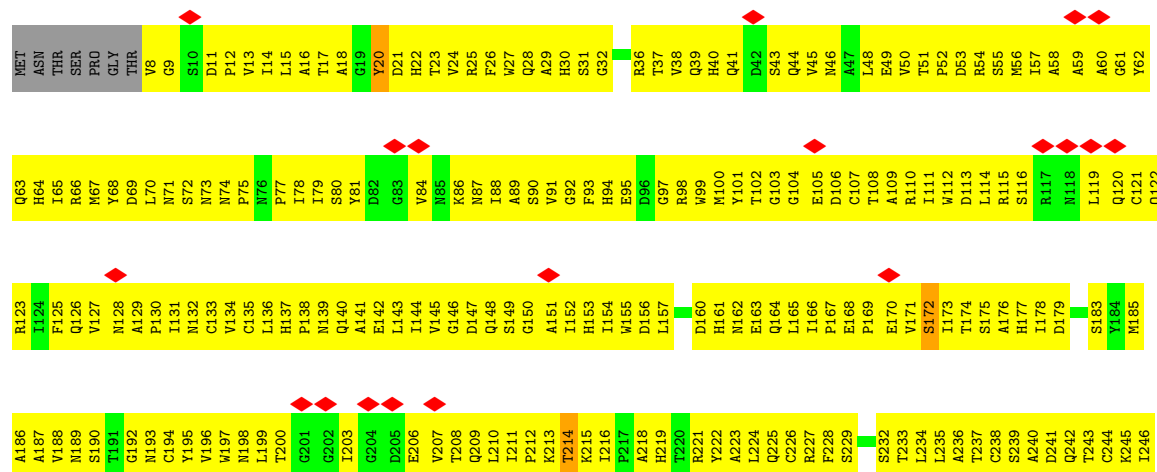




• Molecule 3: Target of rapamycin complex subunit LST8



• Molecule 3: Target of rapamycin complex subunit LST8





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	115039	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 ($e^-/\text{\AA}^2$)	8.25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0142	Depositor
Map size ($\text{\AA}$)	391.962, 391.962, 391.962	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.30654, 1.30654, 1.30654	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	0.59	1/15910 (0.0%)	0.95	58/21634 (0.3%)
1	a	0.59	1/15910 (0.0%)	0.95	58/21634 (0.3%)
2	B	0.44	1/4567 (0.0%)	1.00	32/6217 (0.5%)
2	b	0.44	1/4567 (0.0%)	1.00	32/6217 (0.5%)
3	C	0.43	0/2514	0.77	0/3426
3	c	0.43	0/2514	0.77	0/3426
All	All	0.55	4/45982 (0.0%)	0.95	180/62554 (0.3%)

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	47
1	a	0	46
2	B	0	14
2	b	0	14
3	C	0	4
3	c	0	4
All	All	0	129

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	886	ARG	CA-C	-6.56	1.43	1.52
1	a	886	ARG	CA-C	-6.56	1.43	1.52
2	b	115	PRO	N-CD	5.20	1.55	1.47
2	B	115	PRO	N-CD	5.19	1.55	1.47

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1087	SER	CA-C-N	16.64	140.64	119.84
1	A	1087	SER	C-N-CA	16.64	140.64	119.84
1	a	1087	SER	CA-C-N	16.60	140.59	119.84
1	a	1087	SER	C-N-CA	16.60	140.59	119.84
2	b	363	THR	CA-C-N	15.85	139.66	119.84

There are no chirality outliers.

5 of 129 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	226	LYS	Peptide
1	A	257	ARG	Peptide
1	A	260	ARG	Peptide
1	A	261	ILE	Peptide
1	A	275	SER	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	15617	0	14621	2342	0
1	a	15617	0	14621	2337	0
2	B	4553	0	2926	344	0
2	b	4553	0	2926	344	0
3	C	2456	0	2341	432	0
3	c	2456	0	2341	428	0
All	All	45252	0	39776	6158	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 72.

The worst 5 of 6158 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)
2:B:89:ASP:HB3	2:B:153:HIS:CB	1.53	1.38
2:B:82:ALA:O	2:B:115:PRO:HB2	1.24	1.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:89:ASP:HB3	2:b:153:HIS:CB	1.53	1.35
2:b:82:ALA:O	2:b:115:PRO:HB2	1.24	1.26
2:b:111:GLU:HA	2:b:114:GLN:HA	1.27	1.14

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	2089/2549 (82%)	1654 (79%)	386 (18%)	49 (2%)	5	28
1	a	2089/2549 (82%)	1656 (79%)	384 (18%)	49 (2%)	5	28
2	B	767/1335 (58%)	608 (79%)	132 (17%)	27 (4%)	3	20
2	b	767/1335 (58%)	609 (79%)	131 (17%)	27 (4%)	3	20
3	C	315/326 (97%)	281 (89%)	33 (10%)	1 (0%)	36	71
3	c	315/326 (97%)	281 (89%)	33 (10%)	1 (0%)	36	71
All	All	6342/8420 (75%)	5089 (80%)	1099 (17%)	154 (2%)	7	27

5 of 154 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	PRO
1	A	351	PRO
1	A	404	PRO
1	A	568	PRO
1	A	664	ILE

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	1487/2220 (67%)	1482 (100%)	5 (0%)	86	84
1	a	1487/2220 (67%)	1482 (100%)	5 (0%)	86	84
2	B	185/1163 (16%)	164 (89%)	21 (11%)	5	20
2	b	177/1163 (15%)	159 (90%)	18 (10%)	7	23
3	C	269/276 (98%)	269 (100%)	0	100	100
3	c	269/276 (98%)	269 (100%)	0	100	100
All	All	3874/7318 (53%)	3825 (99%)	49 (1%)	59	72

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	895	ASP
2	b	146	VAL
1	a	1075	ILE
2	b	92	SER
2	b	421	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	311	HIS
3	c	251	ASN
1	a	1112	HIS
3	c	242	GLN
1	a	2535	HIS

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](#)

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.

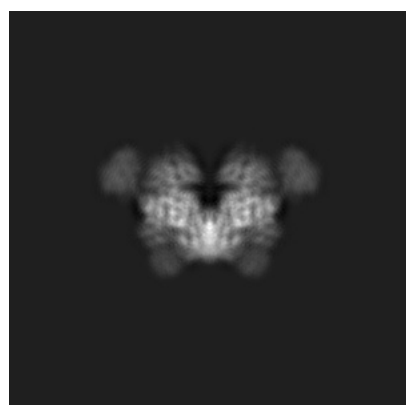
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6668. These allow visual inspection of the internal detail of the map and identification of artifacts.

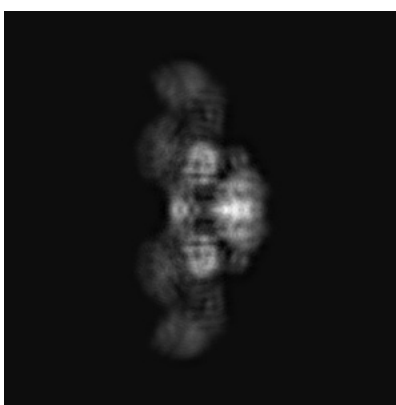
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

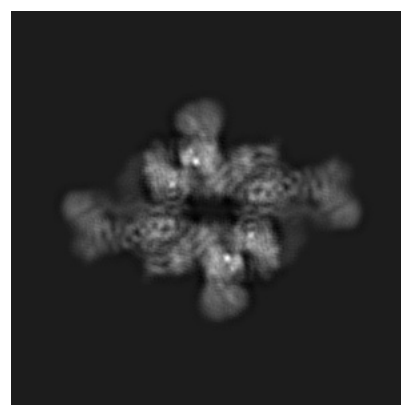
6.1.1 Primary map



X



Y

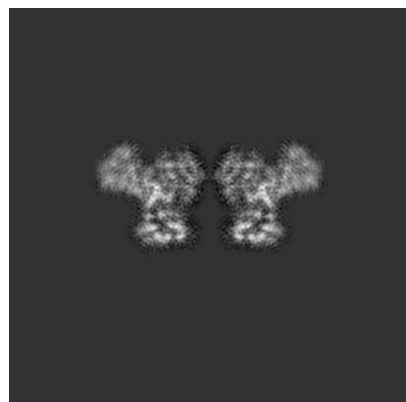


Z

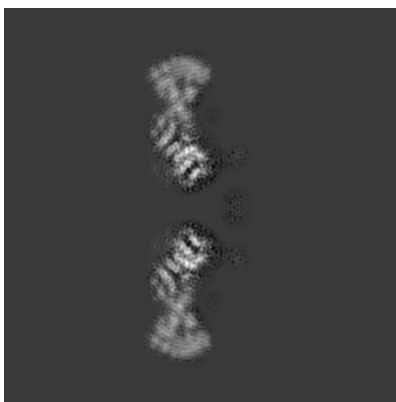
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

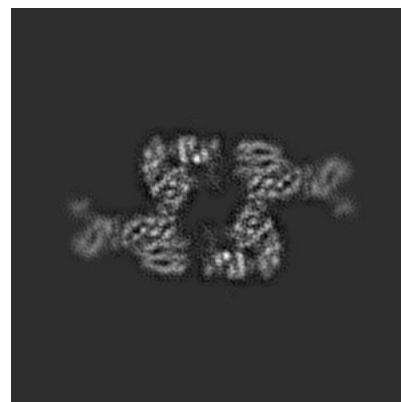
6.2.1 Primary map



X Index: 150



Y Index: 150

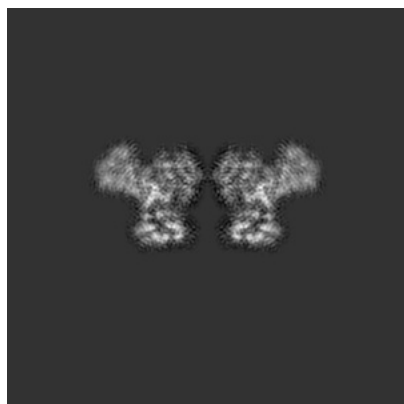


Z Index: 150

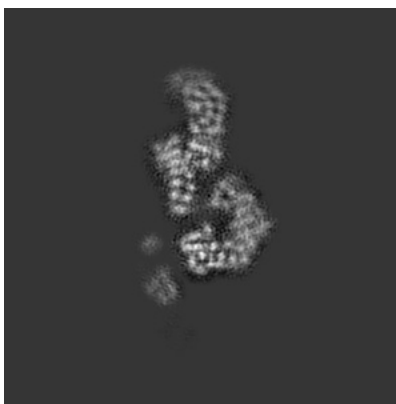
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

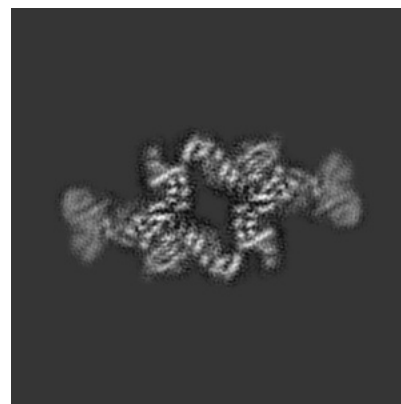
6.3.1 Primary map



X Index: 150



Y Index: 170

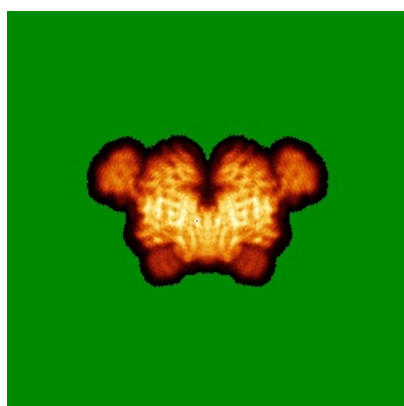


Z Index: 141

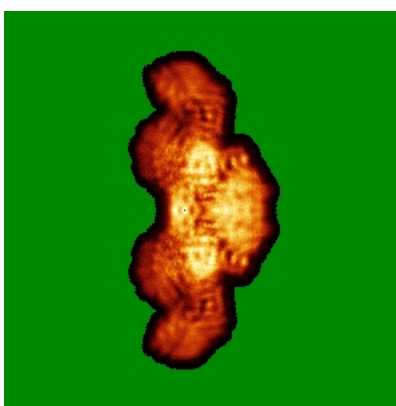
The images above show the largest variance slices of the map in three orthogonal directions.

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

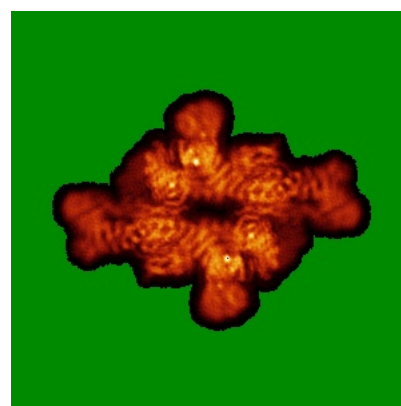
6.4.1 Primary map



X



Y

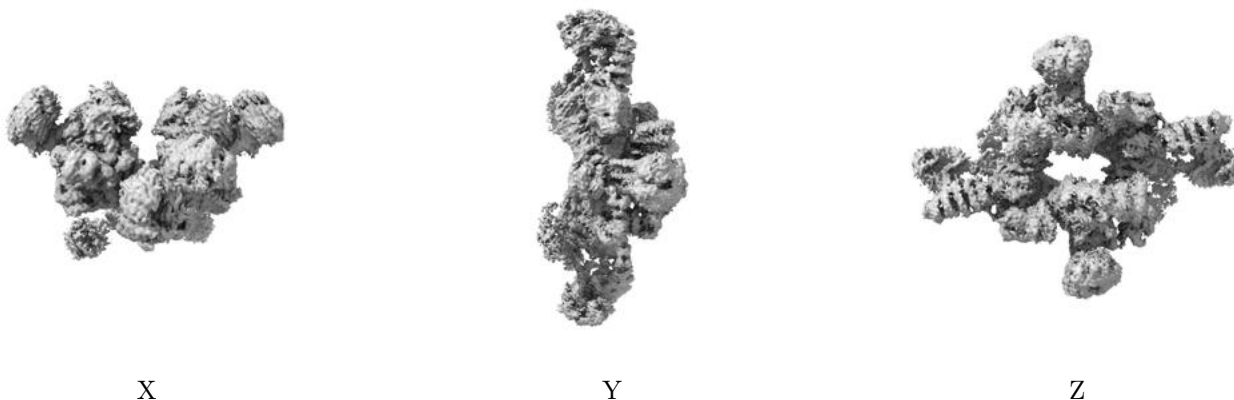


Z

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 0.0142. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

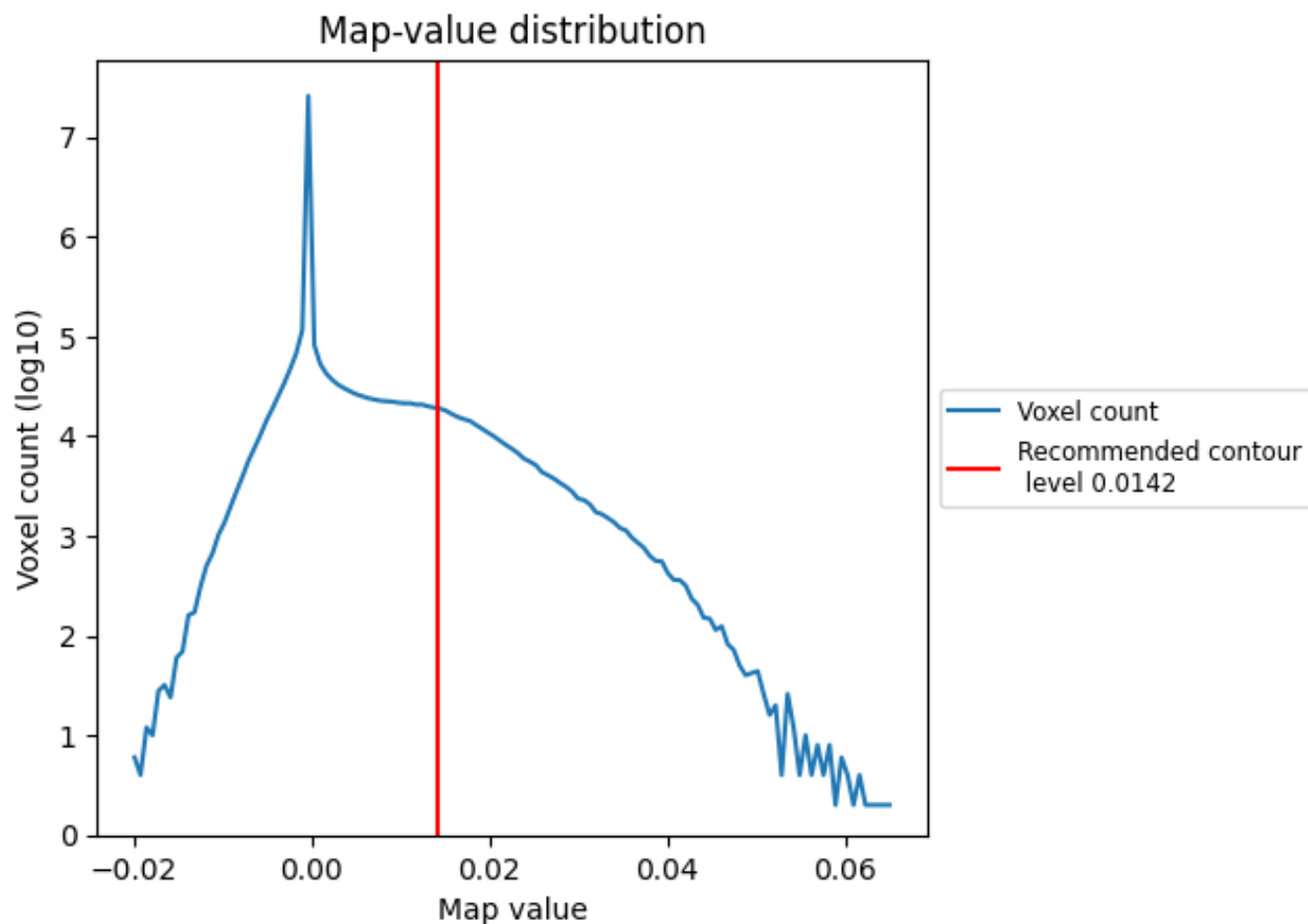
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

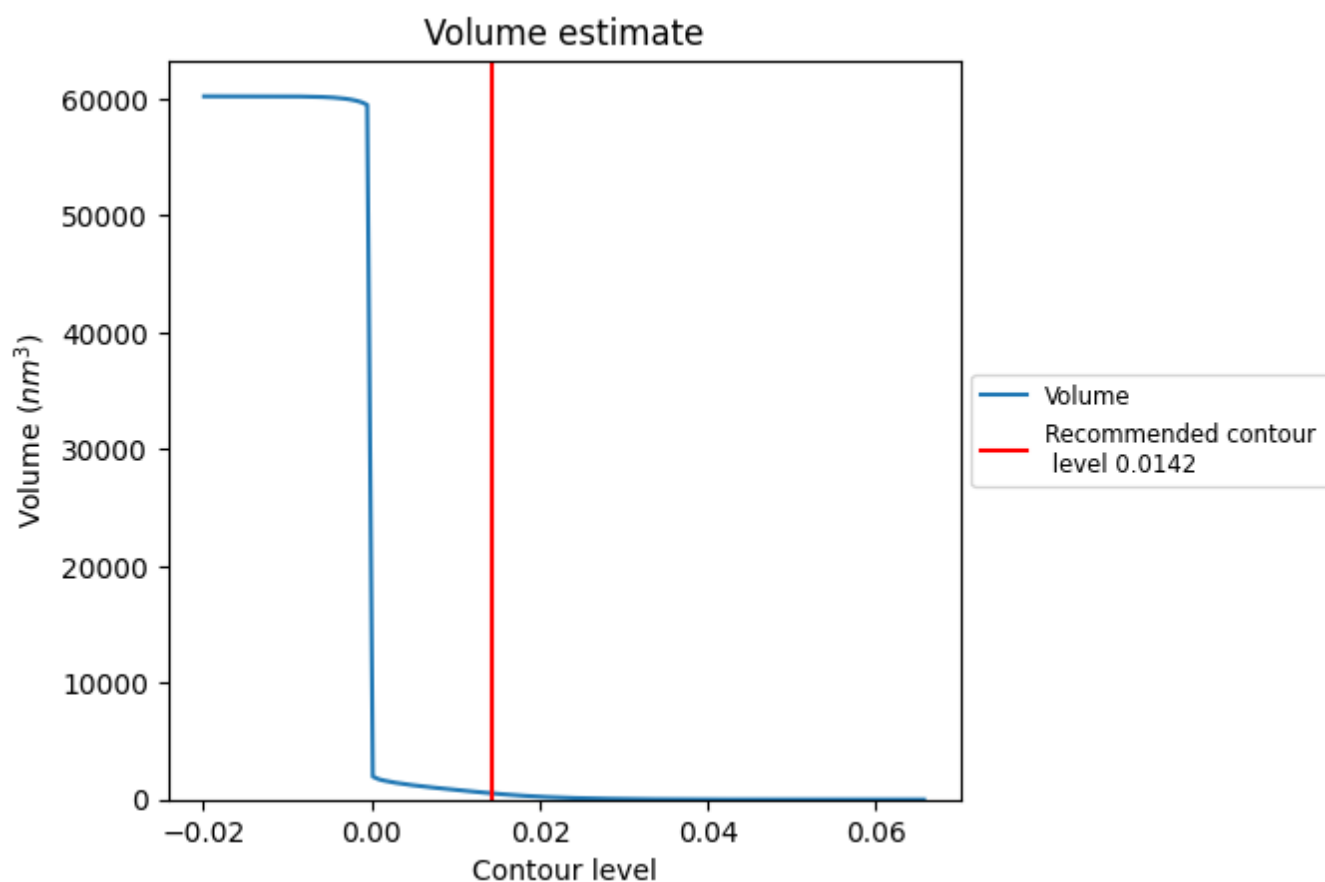
This section contains the results of statistical analysis of the map.

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.

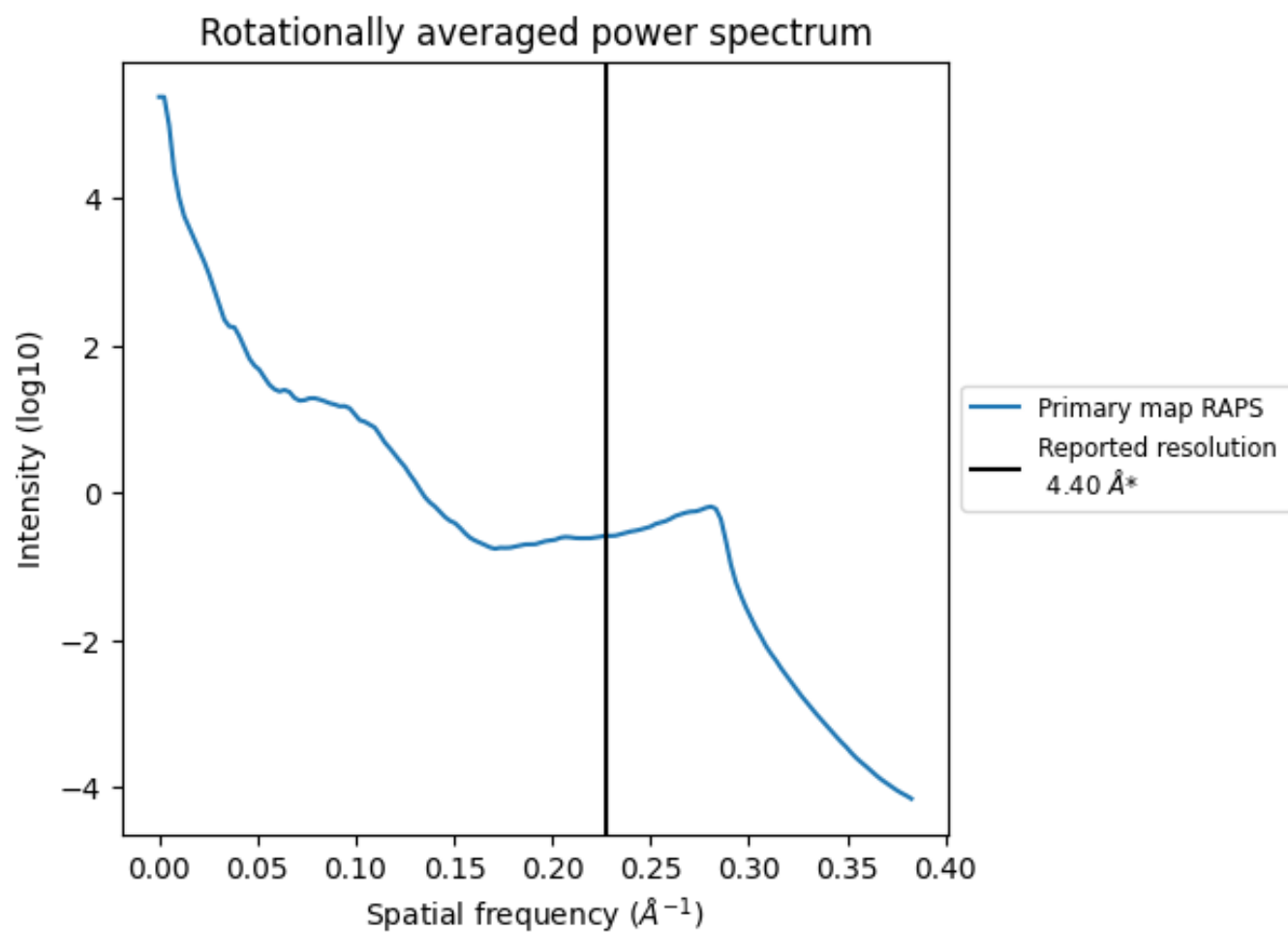
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 541 nm³; this corresponds to an approximate mass of 489 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 0.227 Å⁻¹

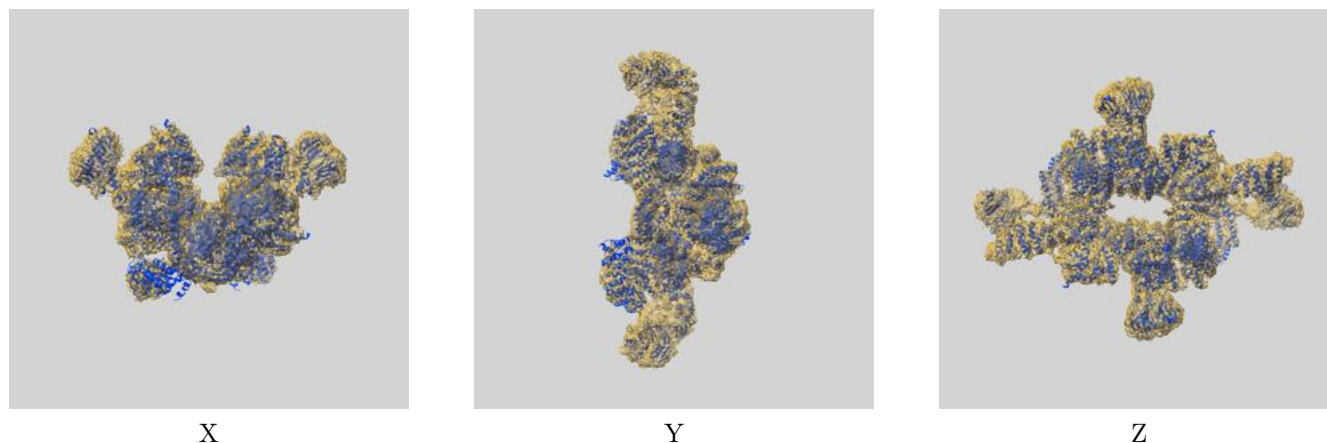
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

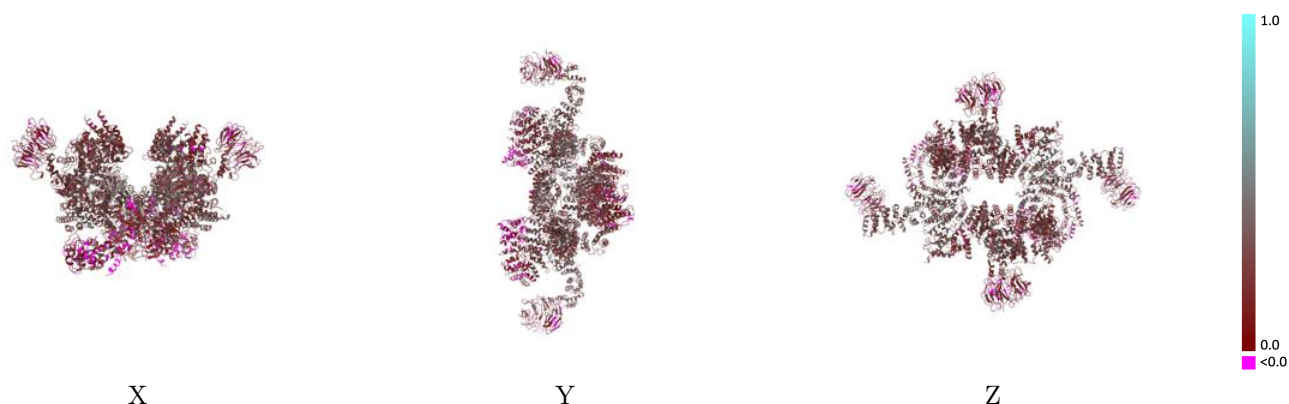
This section contains information regarding the fit between EMDB map EMD-6668 and PDB model 5H64. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

9.1 Map-model overlay [i](#)



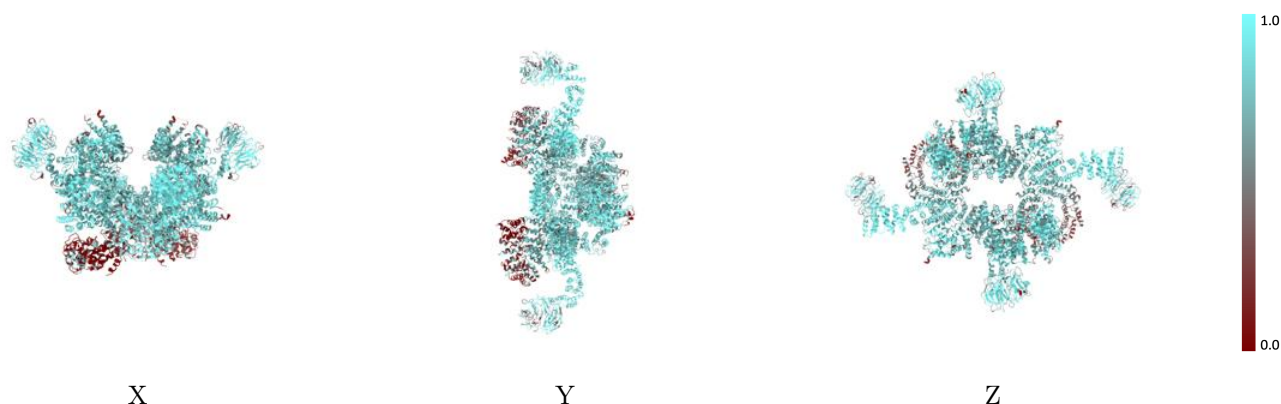
The images above show the 3D surface view of the map at the recommended contour level 0.0142 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



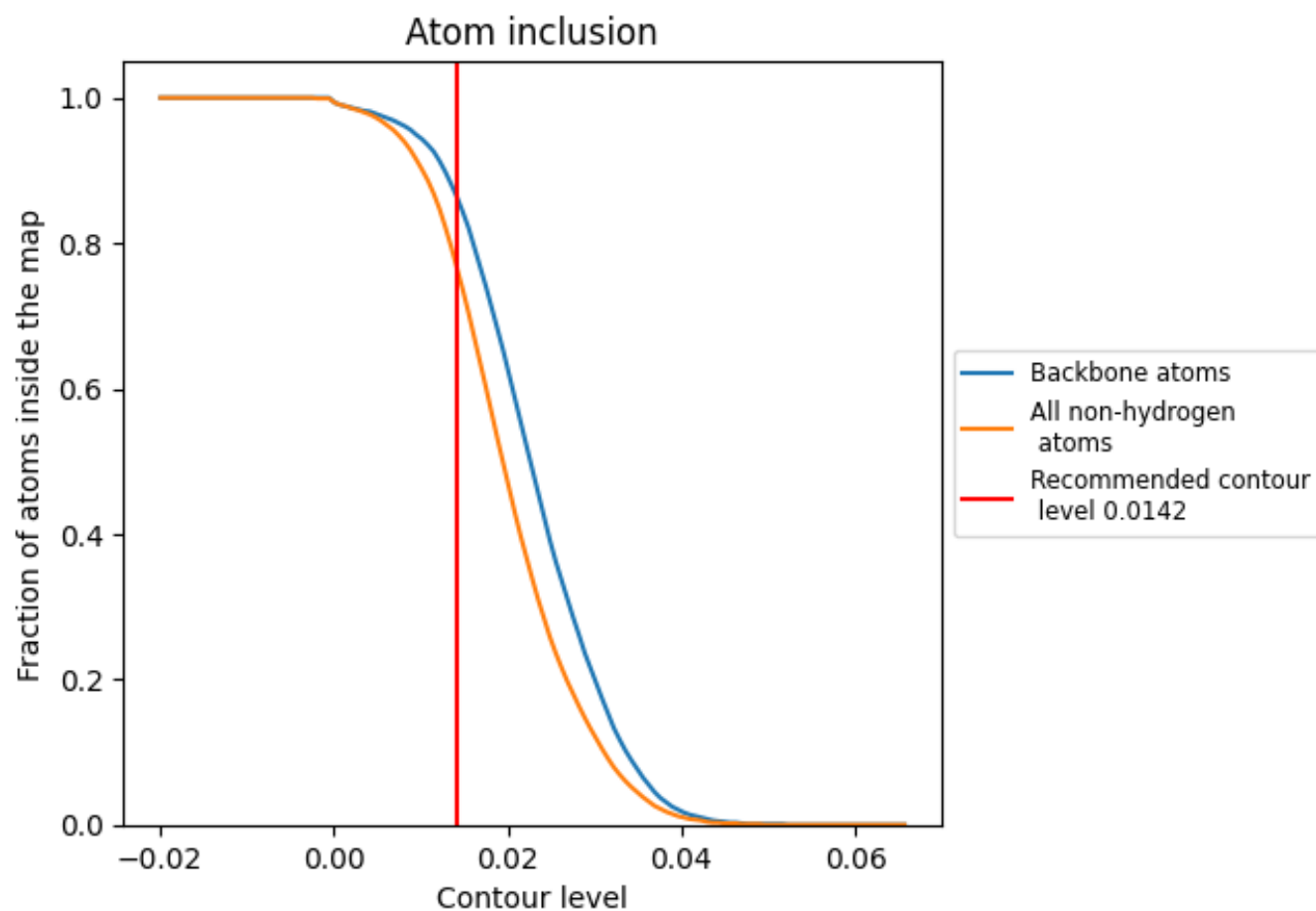
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0142).

9.4 Atom inclusion ⓘ



At the recommended contour level, 86% of all backbone atoms, 76% 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 (0.0142) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7650	0.2490
A	0.7330	0.2560
B	0.8370	0.2700
C	0.8400	0.1710
a	0.7330	0.2550
b	0.8360	0.2700
c	0.8370	0.1680

