



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 06:33 PM UTC

PDB ID : 9HXW / pdb_00009hwx
EMDB ID : EMD-52490
Title : Cryo-EM structure of the human UBR4/KCMF1/CALM1 complex (composite map)
Authors : Grabarczyk, D.B.; Clausen, T.
Deposited on : 2025-01-08
Resolution : 3.10 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:

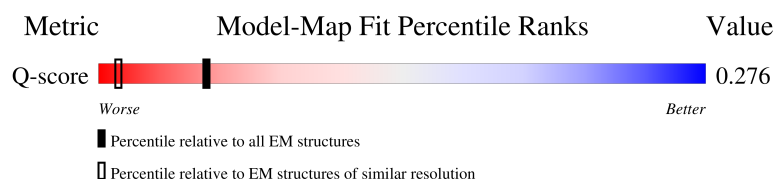
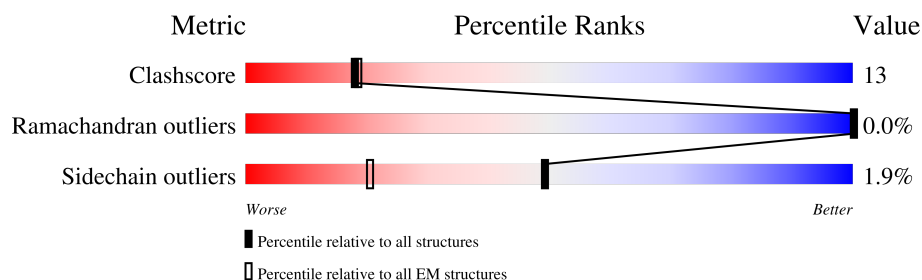
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	C	331	
1	D	331	
2	E	158	
2	F	158	

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Mol	Chain	Length	Quality of chain
3	A	4781	<div><div>16%</div><div><div></div><div>60%</div><div>24%</div><div>•</div><div>15%</div></div></div>
3	B	4781	<div><div>16%</div><div><div></div><div>60%</div><div>24%</div><div>•</div><div>15%</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 68636 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 E3 ubiquitin-protein ligase KCMF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	181	Total	C	N	O	S	0	0
			1423	875	247	285	16		
1	C	181	Total	C	N	O	S	0	0
			1423	875	247	285	16		

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		
2	F	149	Total	C	N	O	S	0	0
			1174	719	189	256	10		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	MET	-	initiating methionine	UNP P0DP23
E	-7	ASP	-	expression tag	UNP P0DP23
E	-6	TYR	-	expression tag	UNP P0DP23
E	-5	LYS	-	expression tag	UNP P0DP23
E	-4	ASP	-	expression tag	UNP P0DP23
E	-3	ASP	-	expression tag	UNP P0DP23
E	-2	ASP	-	expression tag	UNP P0DP23
E	-1	ASP	-	expression tag	UNP P0DP23
E	0	LYS	-	expression tag	UNP P0DP23
F	-8	MET	-	initiating methionine	UNP P0DP23
F	-7	ASP	-	expression tag	UNP P0DP23
F	-6	TYR	-	expression tag	UNP P0DP23
F	-5	LYS	-	expression tag	UNP P0DP23
F	-4	ASP	-	expression tag	UNP P0DP23
F	-3	ASP	-	expression tag	UNP P0DP23
F	-2	ASP	-	expression tag	UNP P0DP23
F	-1	ASP	-	expression tag	UNP P0DP23

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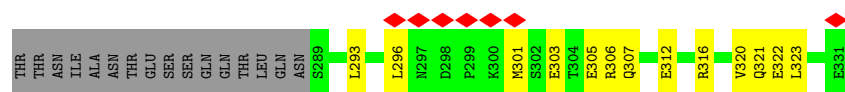
Chain	Residue	Modelled	Actual	Comment	Reference
F	0	LYS	-	expression tag	UNP P0DP23

- Molecule 3 is a protein called E3 ubiquitin-protein ligase UBR4.

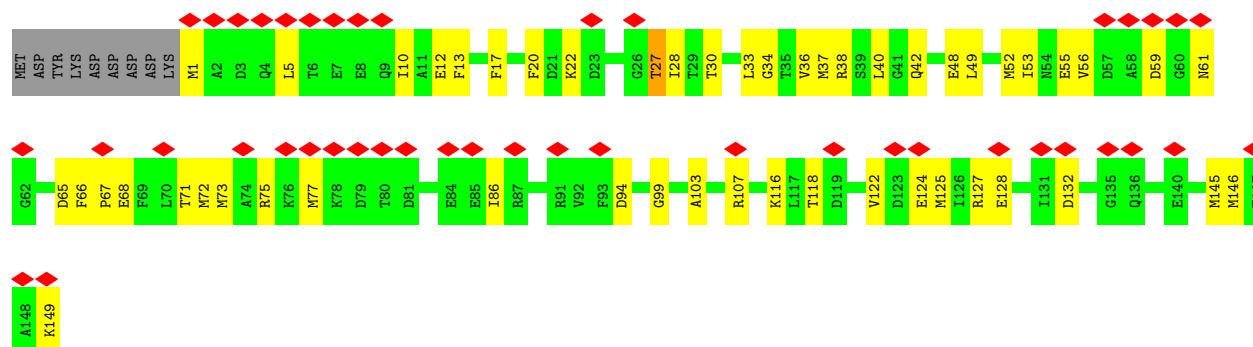
Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	4045	Total	C	N	O	S	0	0
			31711	20123	5410	5969	209		
3	B	4045	Total	C	N	O	S	0	0
			31711	20123	5410	5969	209		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

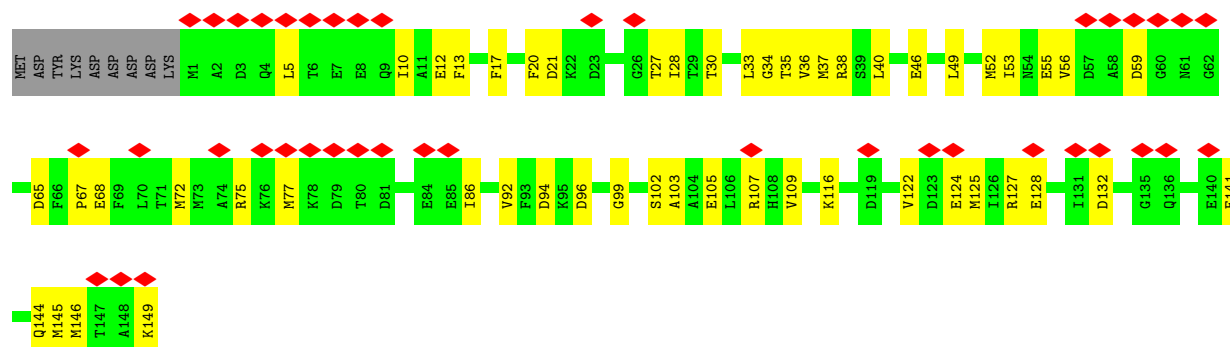
Mol	Chain	Residues	Atoms		AltConf
4	D	4	Total	Zn	0
			4	4	
4	A	6	Total	Zn	0
			6	6	
4	C	4	Total	Zn	0
			4	4	
4	B	6	Total	Zn	0
			6	6	



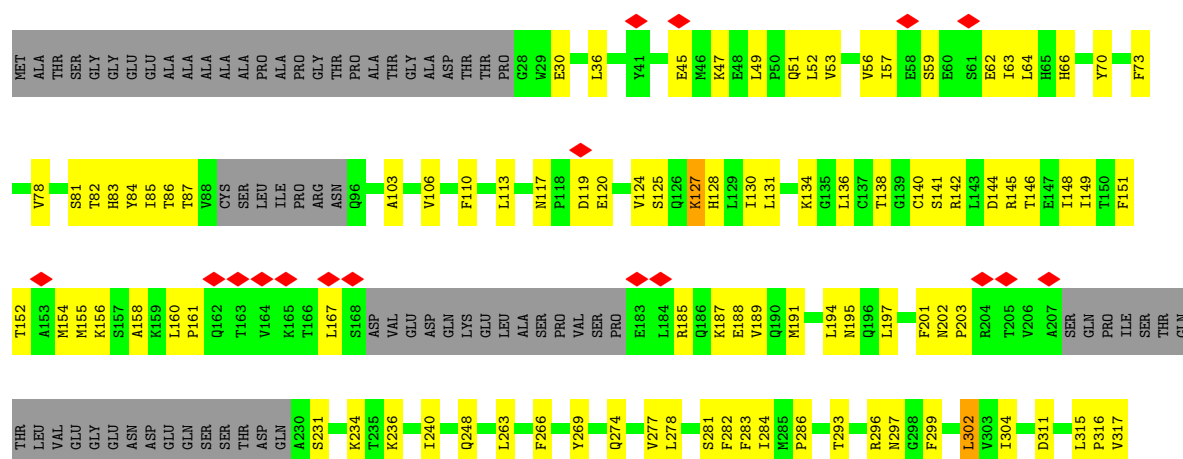
• Molecule 2: Calmodulin-1



• Molecule 2: Calmodulin-1



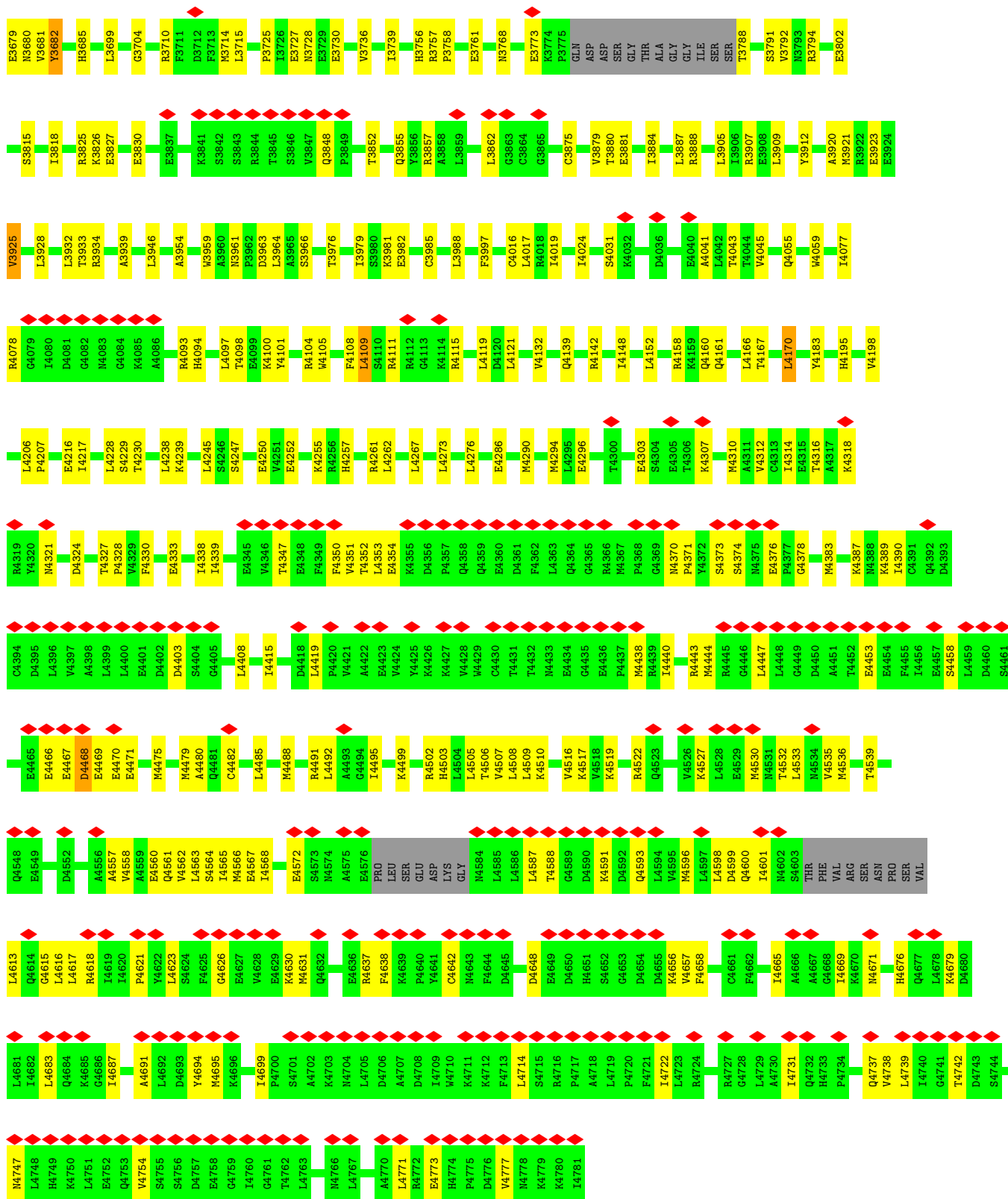
• Molecule 3: E3 ubiquitin-protein ligase UBR4





L2417	V2420	K2427	E2428	Q2429	F2430	Q2431	W2432	PRO	ASP	GLU	PRO	M2344	S2345	T2346	M2347	M2352	R2353	I2354	Q2355	I2356	Y2367	I2368	F2371	Q2372	M2375	Q2376	L2377	N2378	L2379	S2380	R2381	W2384	F2385	D2386	R2391	E2392	E2393	A2394	L2395	Q2396	A2397	K2400	L2403	F2404	I2405	V2409	D2410	P2411	A2412	G2413	V2414							
I2417	V2420	K2427	E2428	Q2429	F2430	Q2431	W2432	PRO	ASP	GLU	PRO	M2344	S2345	T2346	M2347	M2352	R2353	I2354	Q2355	I2356	Y2367	I2368	F2371	Q2372	M2375	Q2376	L2377	N2378	L2379	S2380	R2381	W2384	F2385	D2386	R2391	E2392	E2393	A2394	L2395	Q2396	A2397	K2400	L2403	F2404	I2405	V2409	D2410	P2411	A2412	G2413	V2414							
Q2258	P2259	S2260	SER	VAL	ILE	SER	ILE	MET	LYS	PRO	VAL	ARG	LYS	ARG	THR	ALA	THR	THR	ARG	THR	SER	SER	Q2284	P2288	L2289	D2290	F2291	F2292	E2293	H2294	N2295	L2298	D2307	L2308	L2309	Q2310	Y2311	Y2312	N2313	Q2316	T2317	R2320	L2321	W2322	S2323	T2324	G2325	N2326	Y2327	V2328	A2329							
N2330	T2331	K2332	P2333	Q2334	G2335	F2336	E2339	N2344	S2345	T2346	M2347	M2352	R2353	I2354	Q2355	I2356	Y2367	I2368	F2371	Q2372	M2375	Q2376	L2377	N2378	L2379	S2380	R2381	W2384	F2385	D2386	R2391	E2392	E2393	A2394	L2395	Q2396	A2397	K2400	L2403	F2404	I2405	V2409	D2410	P2411	A2412	G2413	V2414											
F2197	L2198	I2199	Q2200	E2201	I2202	K2203	T2204	L2205	F2206	A2207	K2208	A2209	K2210	I2211	Q2212	D2213	M2214	V2215	A2216	I2217	H2218	R2219	T2220	A2221	C2222	N2223	E2224	Q2225	Q2226	E2227	T2228	T2229	L2232	L2233	C2234	E2235	D2236	Q2237	S2238	L2239	R2240	I2241	Y2242	M2243	A2244	N2245	W2246	E2247	N2248	T2249	S2250	Y2251	W2252	L2253	Q2254	P2255	S2256	L2257
N2059	L2060	L2061	Y2062	L2063	A2067	G2068	Y2069	L2070	Y2071	T2072	Q2073	L2074	N2075	E2076	E2077	A2078	S2080	Q2081	Q2082	Q2083	G2084	P2085	F2086	Y2087	Y2088	L2092	E2093	L2094	N2095	H2096	E2097	D2098	L2099	K2100	D2101	S2102	N2103	Q2105	V2106	A2107	G2110	V2111	S2112	V2113	Y2114	Y2115	S2116	H2117	V2118	L2119	Q2120	N2121	L2122	F2123				
Y2126	K2130	S2131	F2132	A2133	A2134	T2135	I2136	T2139	T2140	L2141	E2142	V2143	L2144	Q2145	L2146	F2147	P2148	I2149	N2150	T2151	K2152	S2153	S2154	N2155	G2156	G2157	S2158	K2159	T2160	S2161	P2162	A2163	L2164	C2165	Q2166	W2167	N2172	H2173	P2174	Q2181	Q2182	T2183	T2184	C2185	T2186	P2187	L2188	V2189	Y2192	K2193	P2194	D2195	T2196					
L1992	H1993	P1994	Q1995	L1996	A1997	T1998	G1999	N2000	F2001	I2002	K2004	A2005	V2006	W2007	G2010	E2014	L2015	A2016	I2017	T2018	T2019	V2023	K2024	L2025	Y2026	D2027	L2028	C2029	V2030	D2031	A2032	L2033	S2034	P2035	T2036	F2037	Y2038	F2039	L2040	L2041	P2042	S2043	L2046	R2047	D2048	V2049	T2050	F2051	L2052	F2053	N2054	E2055	K2058					
S1927	A1928	L1929	L1930	K1931	Q1932	D1934	S1935	S1936	K1937	R1938	L1939	T1941	L1942	R1944	L1945	V1950	T1953	V1954	L1955	S1956	L1957	T1958	G1959	N1960	P1961	C1962	K1963	E1964	D1965	Y1966	L1967	A1968	V1969	G1970	G1971	L1972	K1973	D1974	C1975	H1976	V1977	L1978	T1979	F1980	S1981	S1982	S1983	G1984	S1987	D1988	H1989	V1991						
L1863	G1864	S1865	Q1866	E1867	F1870	E1871	N1872	V1873	R1874	M1875	N1876	Y1877	D1880	Q1881	T1884	I1885	R1886	L1888	I1889	S1890	A1891	S1895	V1896	M1899	C1900	V1901	L1902	S1903	S1904	P1905	H1906	G1907	R1908	R1909	Q1910	A1911	L1912	A1913	V1914	S1915	H1916	E1917	K1918	G1919	K1920	T1922	V1923	Q1925	L1926									
LYS	PRO	LYS	LYS	SER	SER	LEU	CYS	ARG	THR	VAL	GLU	G1794	C1795	R1796	M1801	N1804	F1805	S1806	F1807	L1810	V1811	M1814	F1817	L1818	M1819	I1822	F1826	A1829	S1830	A1831	V1832	G1833	R1837	Q1840	L1845	H1846	K1850	A1851	V1852	E1853	M1854	L1858	M1859	V1860	P1861	T1862												
G1722	S1723	C1724	L1725	A1726	L1727	V1728	K1729	R1730	T1731	P1732	S1733	SER	GLY	MET	SER	SER	THR	MET	LYS	GLU	SER	ALA	PHE	GLN	SER	GLU	PRO	ARG	ILE	SER	GLU	SER	LEU	VAL	ARG	ALA	ILE	GLU	VAL	ASP	ASP	ASP	TRP	VAL	GLU	GLU	LEU	ALA	VAL	GLU	ASP	SER						
ASP	GLU	D1655	S1656	L1657	C1658	N1659	I1659	M1660	L1661	C1662	T1663	F1664	T1665	I1666	T1667	Q1668	K1669	E1670	S1671	M1672	N1673	Q1674	H1675	Y1677	H1678	T1681	C1682	K1683	H1684	V1685	D1686	V1690	C1691	T1692	K1696	V1697	C1698	H1699	K1700	D1701	H1702	E1703	I1704	S1705	A1707	K1708	Y1709	G1710	S1711	C1716	K1719	E1720	D1721					

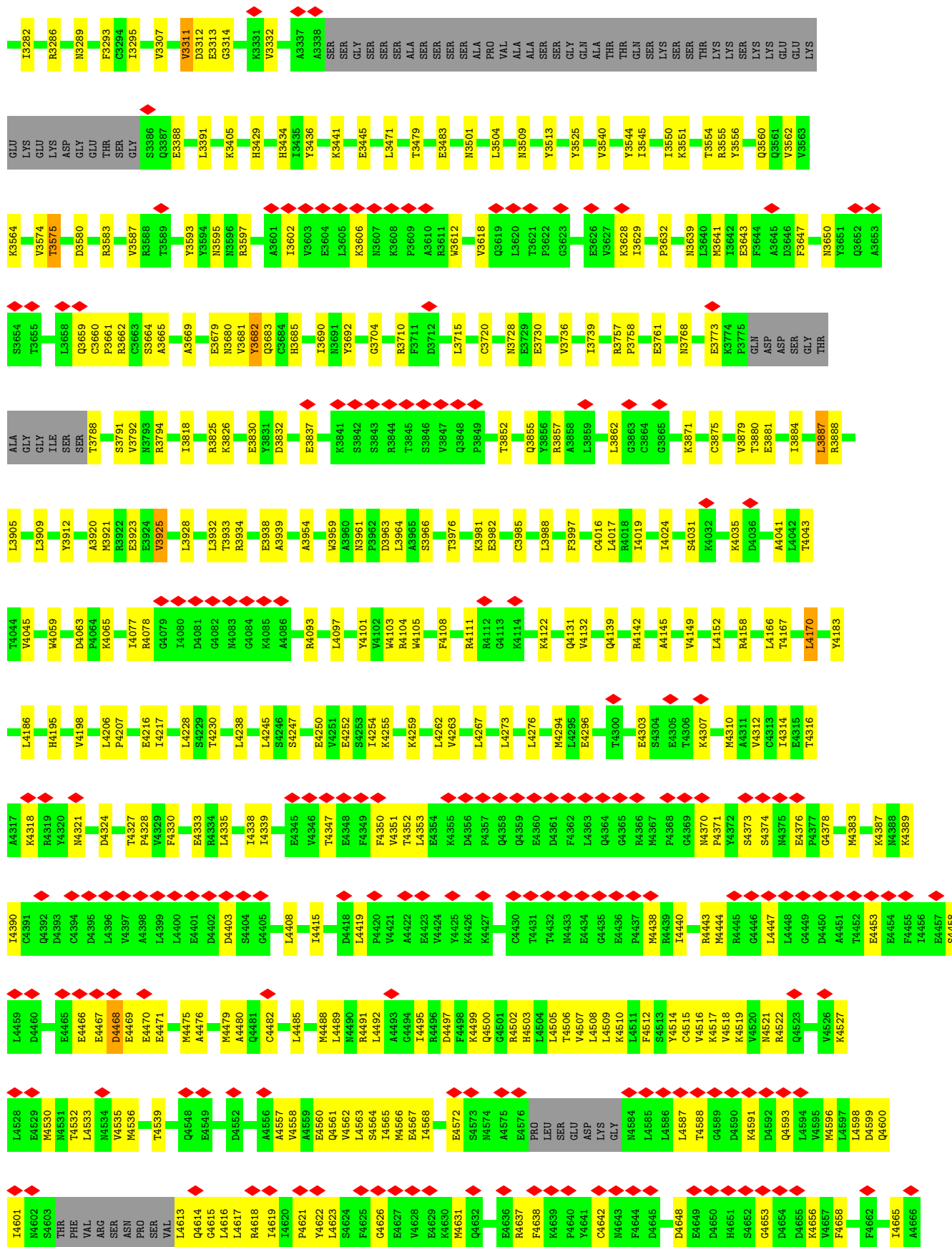


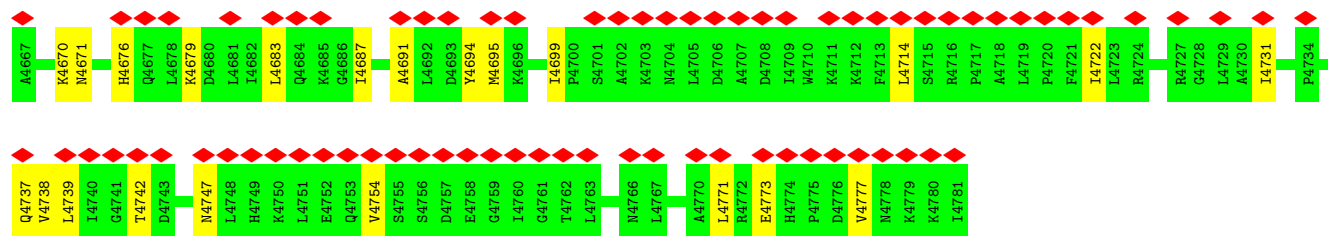












4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1638723	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	0.000	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0089	Depositor
Map size (Å)	486.912, 486.912, 486.912	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.268, 1.268, 1.268	Depositor

5 Model quality

5.1 Standard geometry

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	C	0.10	0/1451	0.26	0/1962
1	D	0.12	0/1451	0.36	0/1962
2	E	0.14	0/1186	0.44	0/1590
2	F	0.14	0/1186	0.39	0/1590
3	A	0.13	0/32281	0.37	4/43722 (0.0%)
3	B	0.13	0/32281	0.38	3/43722 (0.0%)
All	All	0.13	0/69836	0.37	7/94548 (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
3	A	0	2
3	B	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1819	MET	CA-CB-CG	6.21	126.52	114.10
3	B	1599	ILE	CA-C-N	-5.46	111.02	121.94
3	B	1599	ILE	C-N-CA	-5.46	111.02	121.94
3	A	1599	ILE	CA-C-N	-5.34	111.26	121.94
3	A	1599	ILE	C-N-CA	-5.34	111.26	121.94

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	A	117	ASN	Peptide
3	A	4468	ASP	Peptide
3	B	117	ASN	Peptide
3	B	4468	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	C	1423	0	1335	38	0
1	D	1423	0	1335	52	0
2	E	1174	0	1105	46	0
2	F	1174	0	1105	39	0
3	A	31711	0	32086	859	0
3	B	31711	0	32086	860	0
4	A	6	0	0	0	0
4	B	6	0	0	0	0
4	C	4	0	0	0	0
4	D	4	0	0	0	0
All	All	68636	0	69052	1834	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 13.

The worst 5 of 1834 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:B:1020:ILE:O	3:B:1024:SER:HB2	1.66	0.96
3:B:231:SER:HA	3:B:234:LYS:HE3	1.49	0.95
2:E:34:GLY:O	2:E:38:ARG:HB3	1.70	0.91
3:A:1020:ILE:O	3:A:1024:SER:HB2	1.71	0.90
3:B:3233:LEU:HD11	3:B:3282:ILE:HG21	1.57	0.87

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	C	177/331 (54%)	173 (98%)	4 (2%)	0	100	100
1	D	177/331 (54%)	174 (98%)	3 (2%)	0	100	100
2	E	147/158 (93%)	144 (98%)	3 (2%)	0	100	100
2	F	147/158 (93%)	144 (98%)	3 (2%)	0	100	100
3	A	3999/4781 (84%)	3856 (96%)	142 (4%)	1 (0%)	100	100
3	B	3999/4781 (84%)	3862 (97%)	136 (3%)	1 (0%)	100	100
All	All	8646/10540 (82%)	8353 (97%)	291 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	923	SER
3	B	923	SER

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	C	160/287 (56%)	160 (100%)	0	100	100
1	D	160/287 (56%)	156 (98%)	4 (2%)	42	69
2	E	127/136 (93%)	124 (98%)	3 (2%)	43	69
2	F	127/136 (93%)	123 (97%)	4 (3%)	35	64
3	A	3569/4176 (86%)	3505 (98%)	64 (2%)	51	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	B	3569/4176 (86%)	3500 (98%)	69 (2%)	50 73
All	All	7712/9198 (84%)	7568 (98%)	144 (2%)	49 73

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	3166	ARG
3	B	4296	GLU
3	B	3233	LEU
3	B	3575	THR
3	A	3000	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	3400	ASN
3	B	3762	ASN
1	C	122	ASN
3	B	3759	GLN
3	B	3113	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 20 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

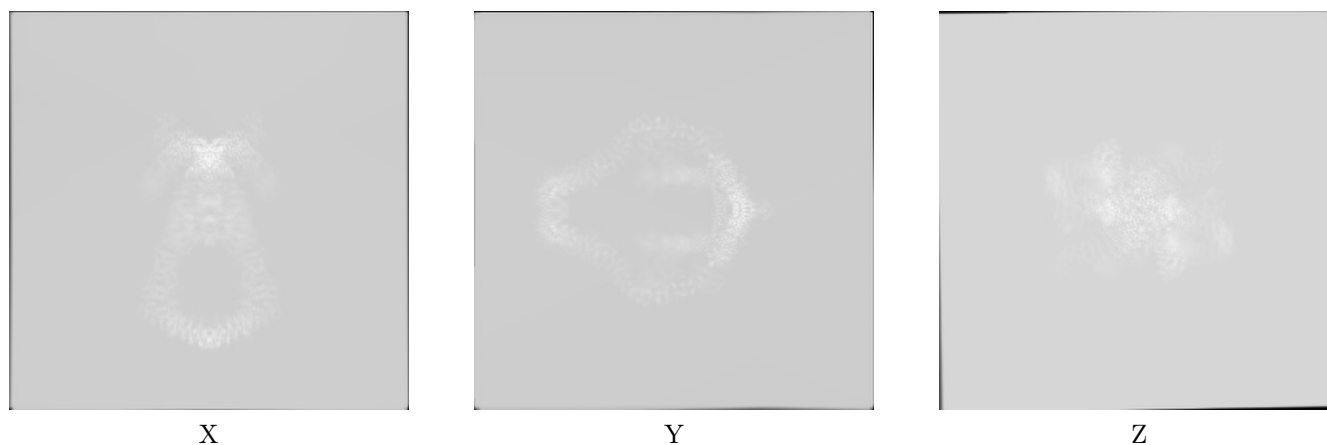
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52490. 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](#)

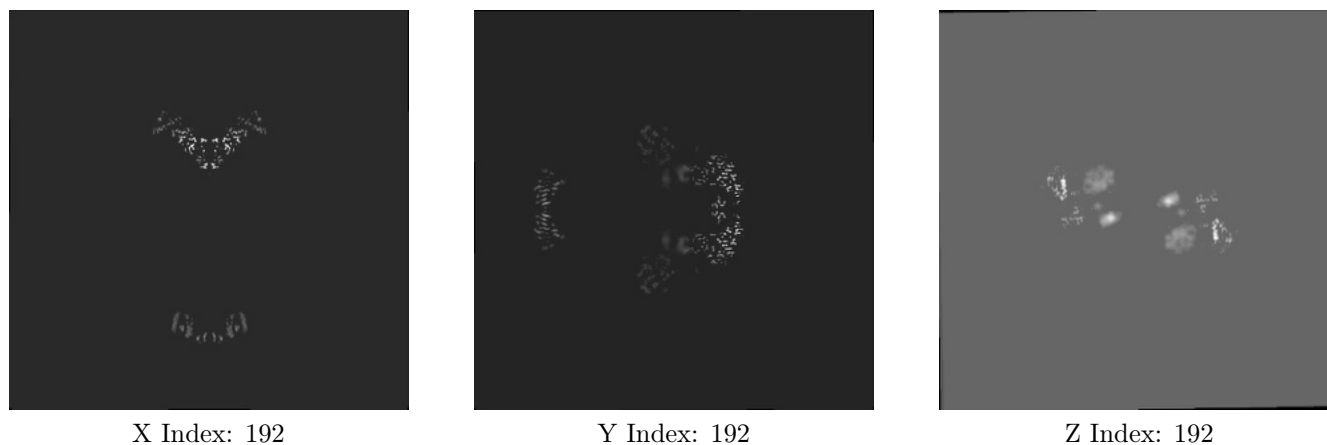
6.1.1 Primary map



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

6.2 Central slices [i](#)

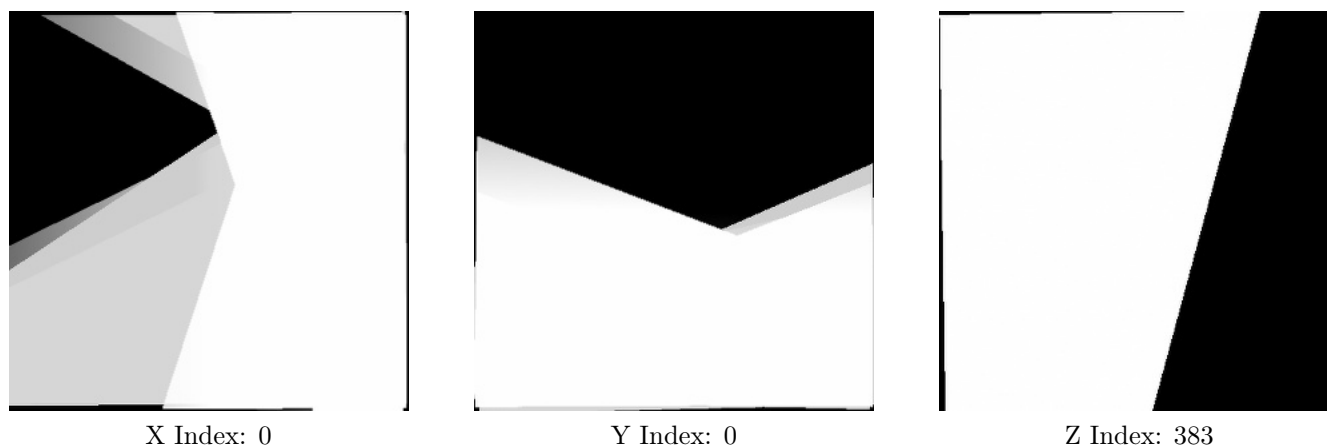
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

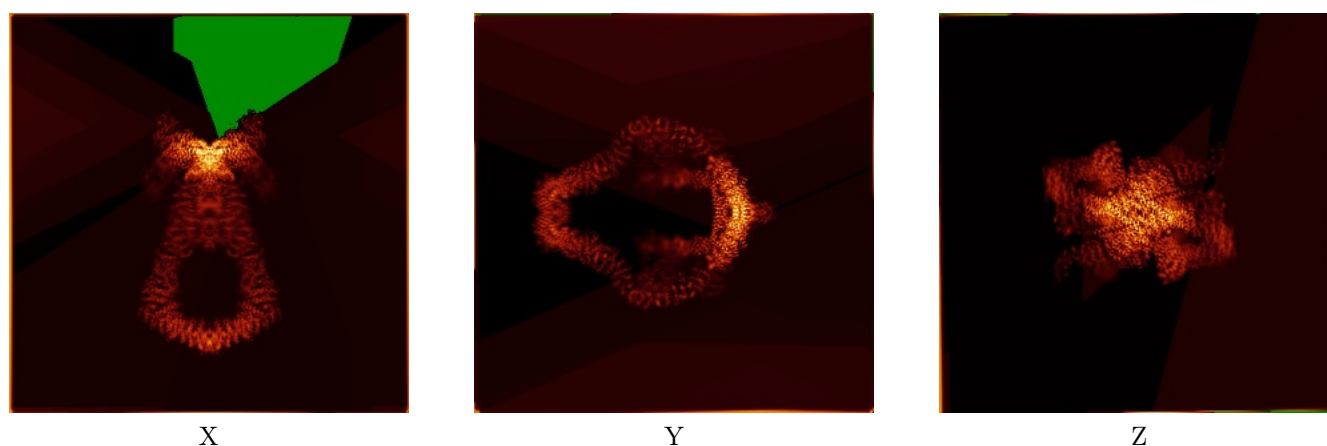
6.3.1 Primary map



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



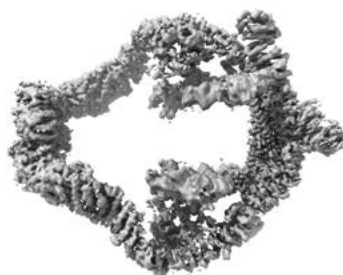
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0089. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

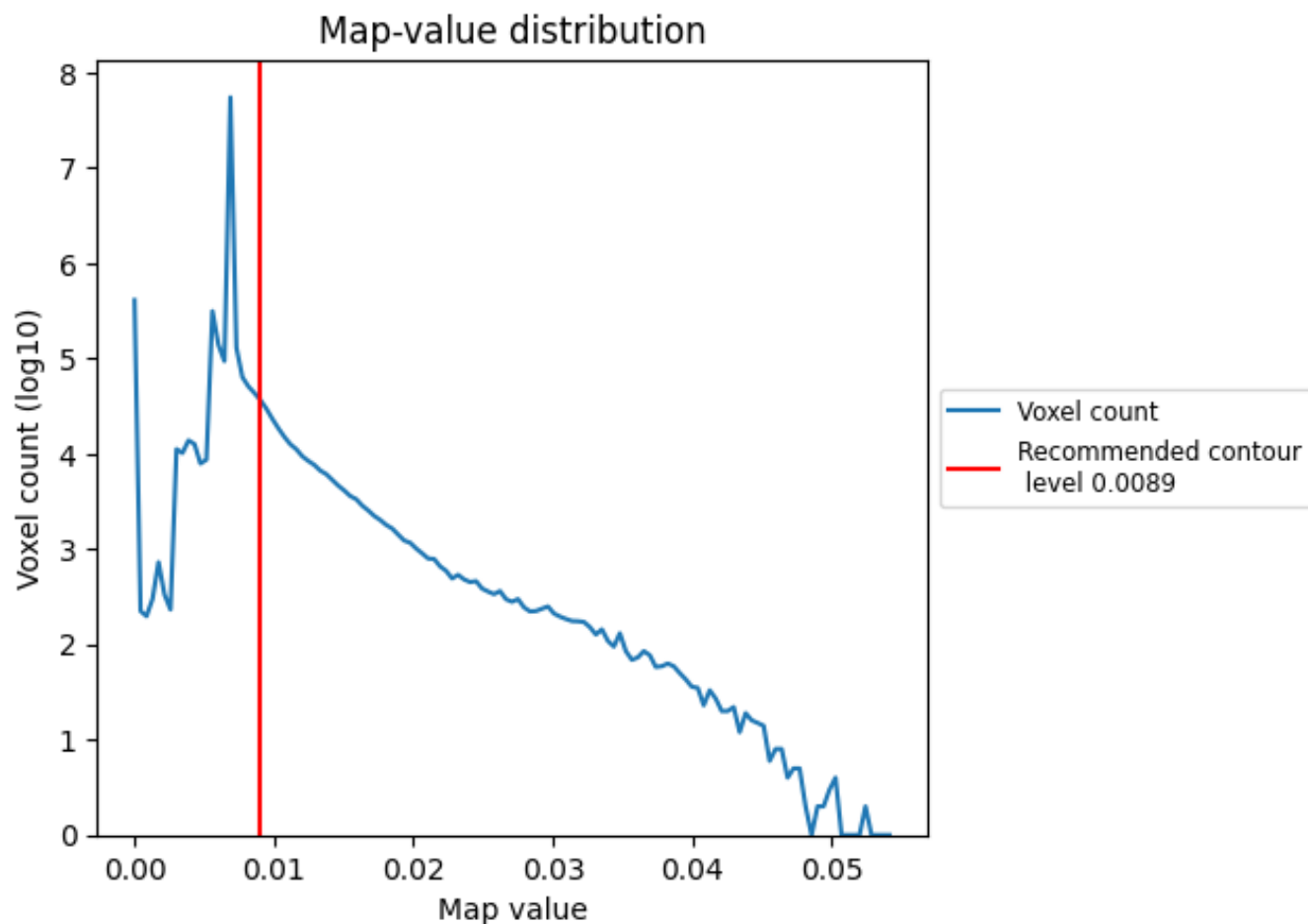
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

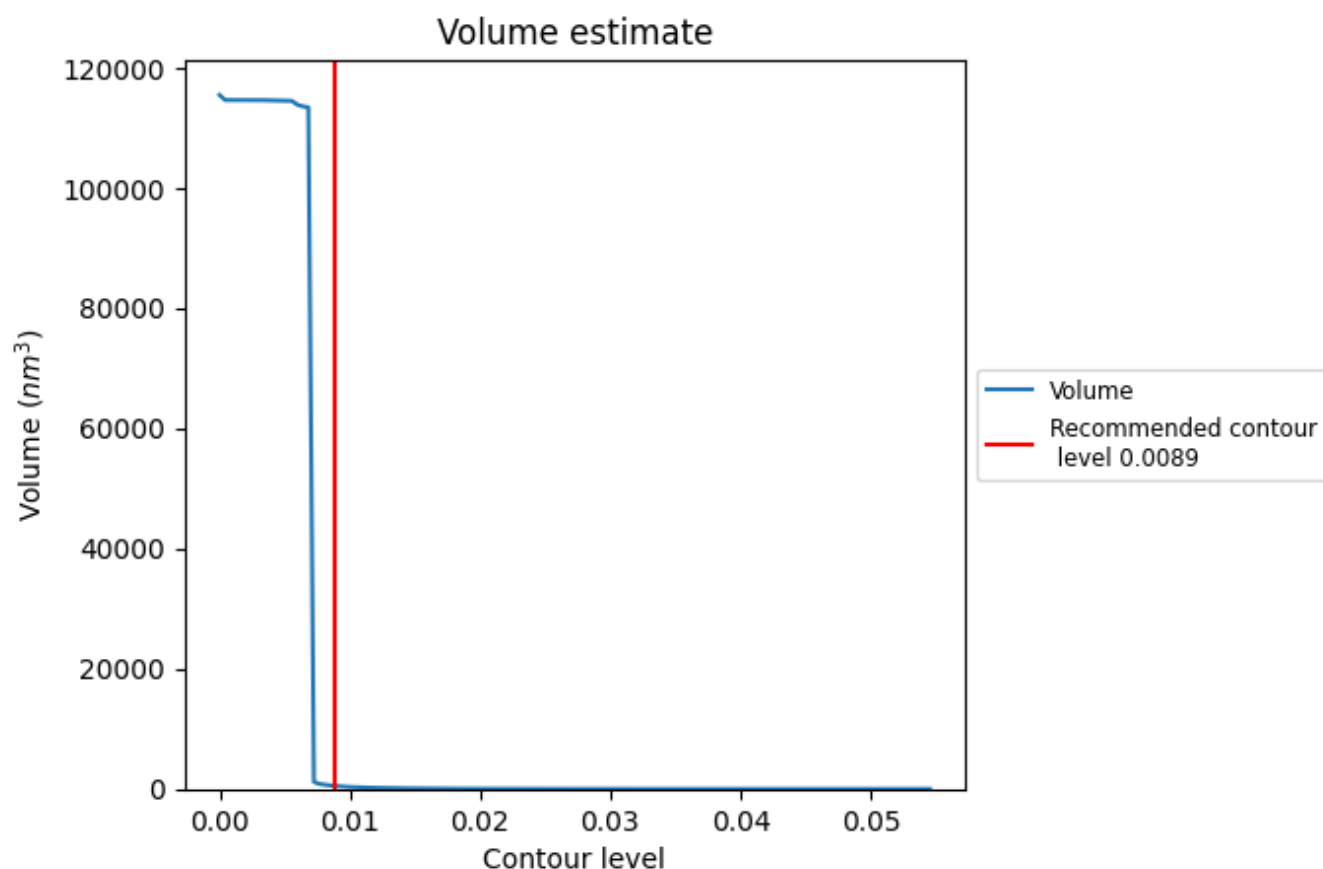
This section contains the results of statistical analysis of the map.

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.

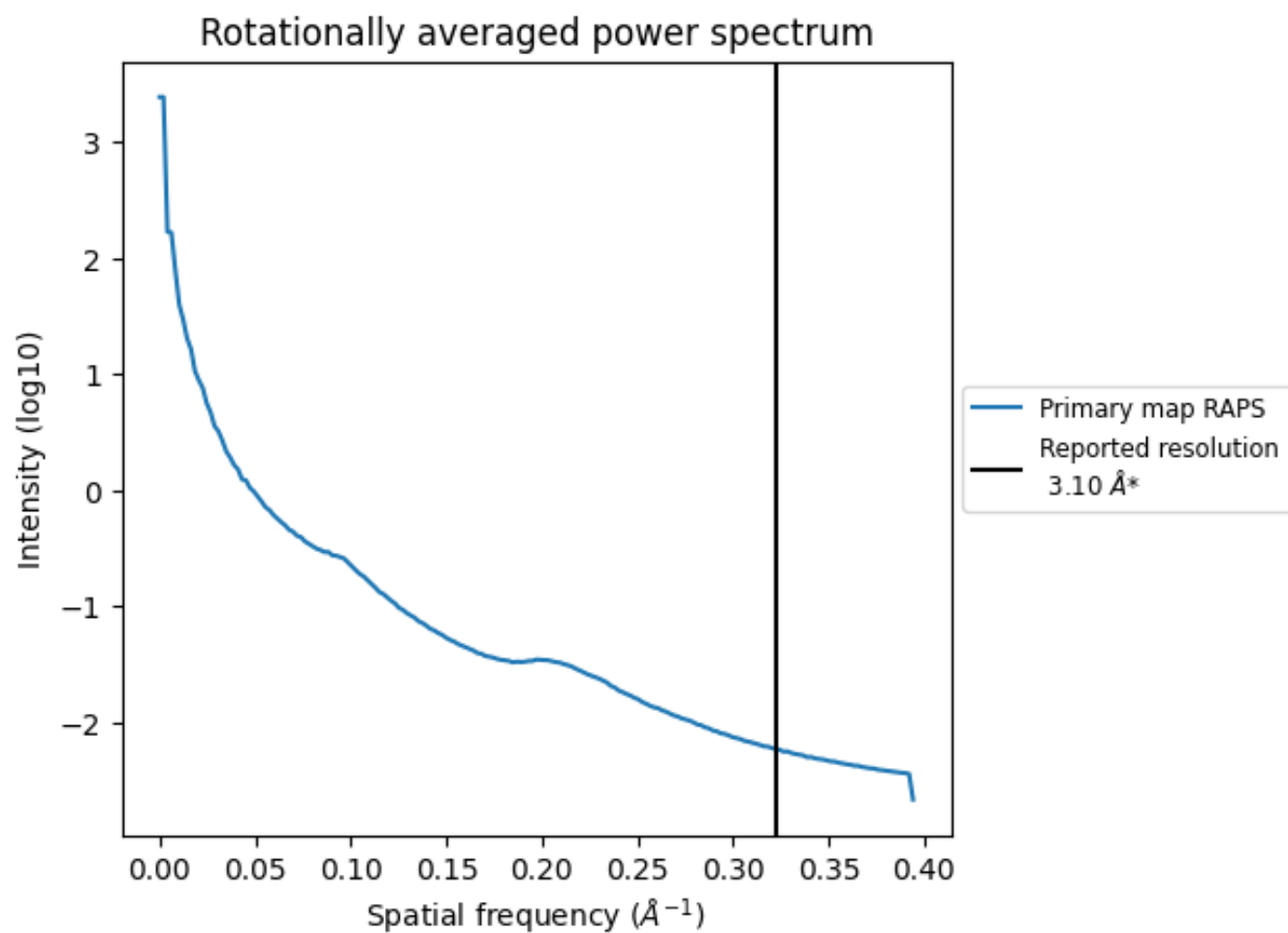
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 507 nm^3 ; this corresponds to an approximate mass of 458 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 0.323 Å⁻¹

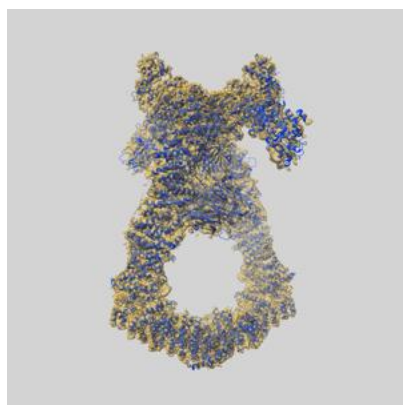
8 Fourier-Shell correlation

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

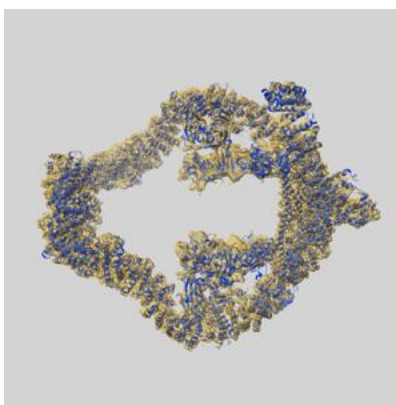
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52490 and PDB model 9HXW. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

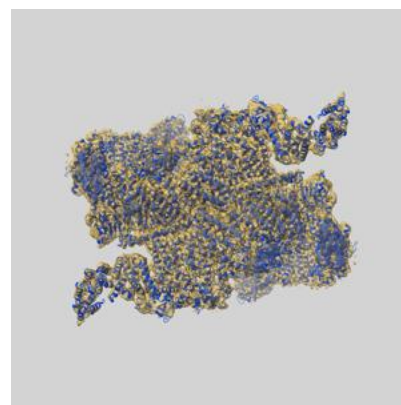
9.1 Map-model overlay [i](#)



X



Y



Z

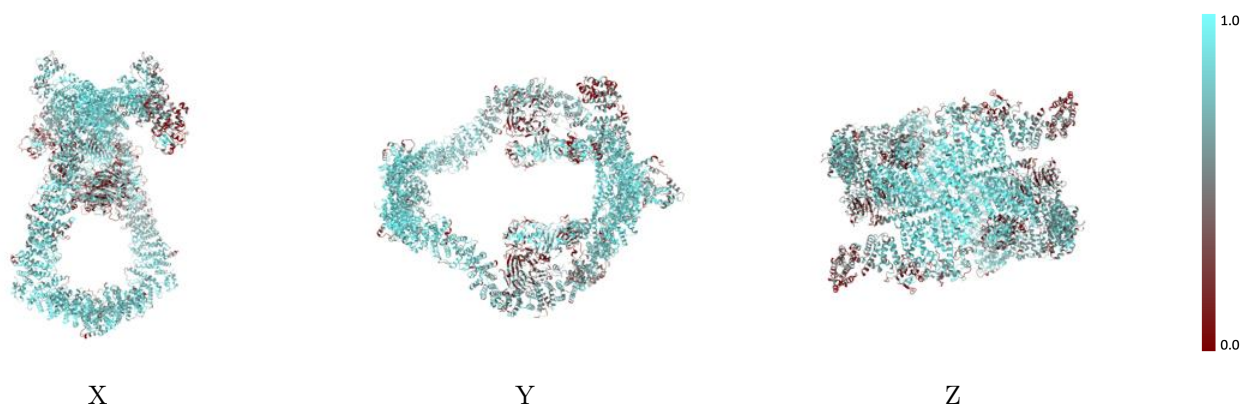
The images above show the 3D surface view of the map at the recommended contour level 0.0089 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



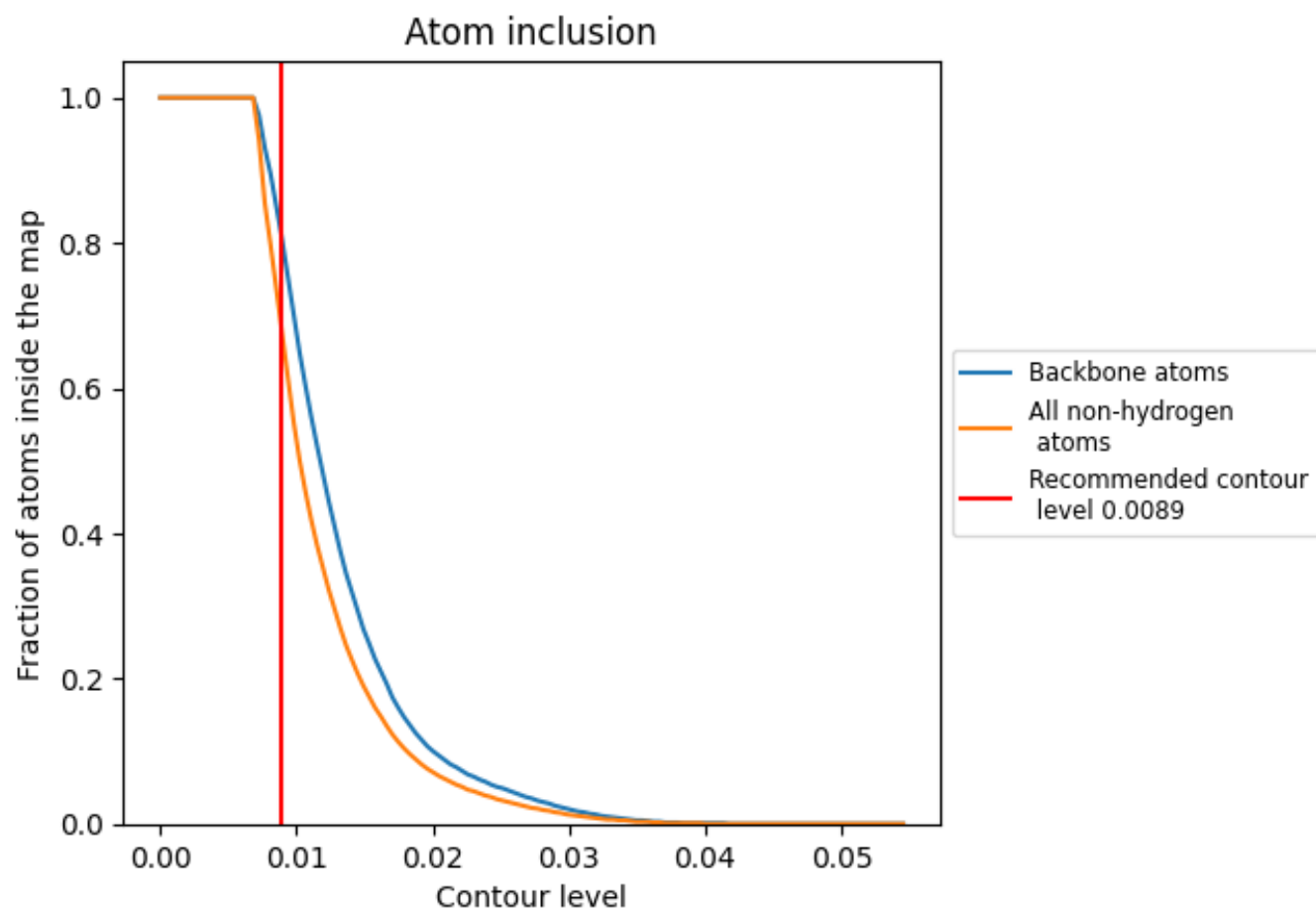
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0089).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 68% 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 (0.0089) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6810	<div></div> 0.2760
A	<div></div> 0.6890	<div></div> 0.2820
B	<div></div> 0.6910	<div></div> 0.2820
C	<div></div> 0.6150	<div></div> 0.1550
D	<div></div> 0.5610	<div></div> 0.1460
E	<div></div> 0.5590	<div></div> 0.2670
F	<div></div> 0.5710	<div></div> 0.2760

