



## wwPDB EM Validation Summary Report ⓘ

Oct 15, 2024 – 12:46 PM JST

PDB ID : 8XL0  
EMDB ID : EMD-38433  
Title : Citrate-induced filament of human acetyl-coenzyme A carboxylase 1 (ACC1-citrate)  
Authors : Zhou, F.Y.; Zhang, Y.Y.; Zhou, Q.; Hu, Q.  
Deposited on : 2023-12-25  
Resolution : 4.14 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

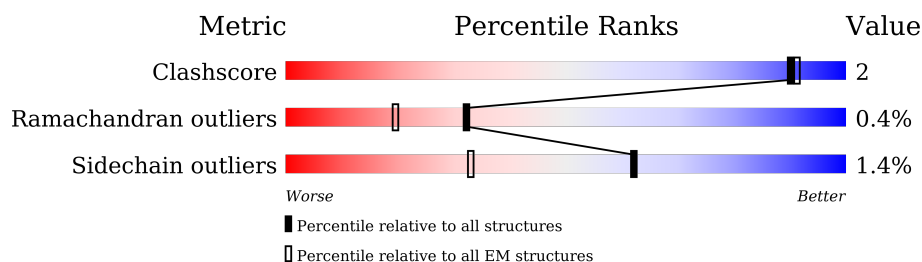
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.14 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	2346	<div> <div>11%</div> <div>88%</div> <div>9%</div> </div>
1	B	2346	<div> <div>5%</div> <div>88%</div> <div>9%</div> </div>
1	C	2346	<div> <div>88%</div> <div>9%</div> </div>
1	D	2346	<div> <div>88%</div> <div>9%</div> </div>
1	E	2346	<div> <div>38%</div> <div>74%</div> <div>22%</div> </div>
1	F	2346	<div> <div>38%</div> <div>53%</div> <div>45%</div> </div>

## 2 Entry composition [i](#)

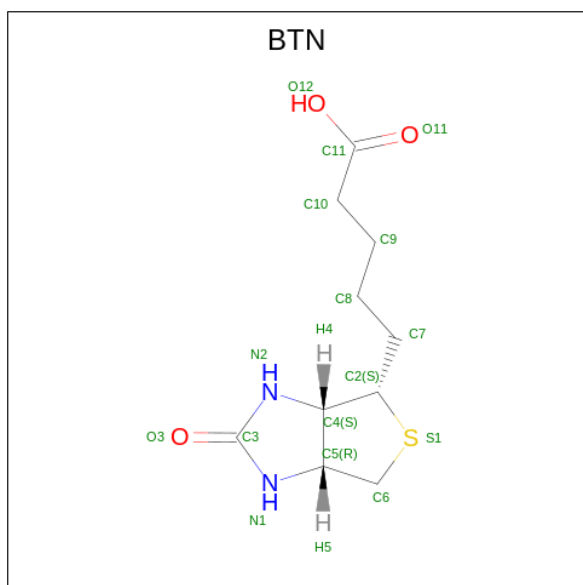
There are 2 unique types of molecules in this entry. The entry contains 93175 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Acetyl-CoA carboxylase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2146	Total	C	N	O	S	0	0
			17120	10879	2976	3166	99		
1	B	2146	Total	C	N	O	S	0	0
			17120	10879	2976	3166	99		
1	C	2146	Total	C	N	O	S	0	0
			17120	10879	2976	3166	99		
1	D	2146	Total	C	N	O	S	0	0
			17120	10879	2976	3166	99		
1	E	1819	Total	C	N	O	S	0	0
			14435	9170	2503	2676	86		
1	F	1289	Total	C	N	O	S	0	0
			10185	6478	1764	1890	53		

- Molecule 2 is BIOTIN (three-letter code: BTN) (formula:  $C_{10}H_{16}N_2O_3S$ ) (labeled as "Ligand of Interest" by depositor).

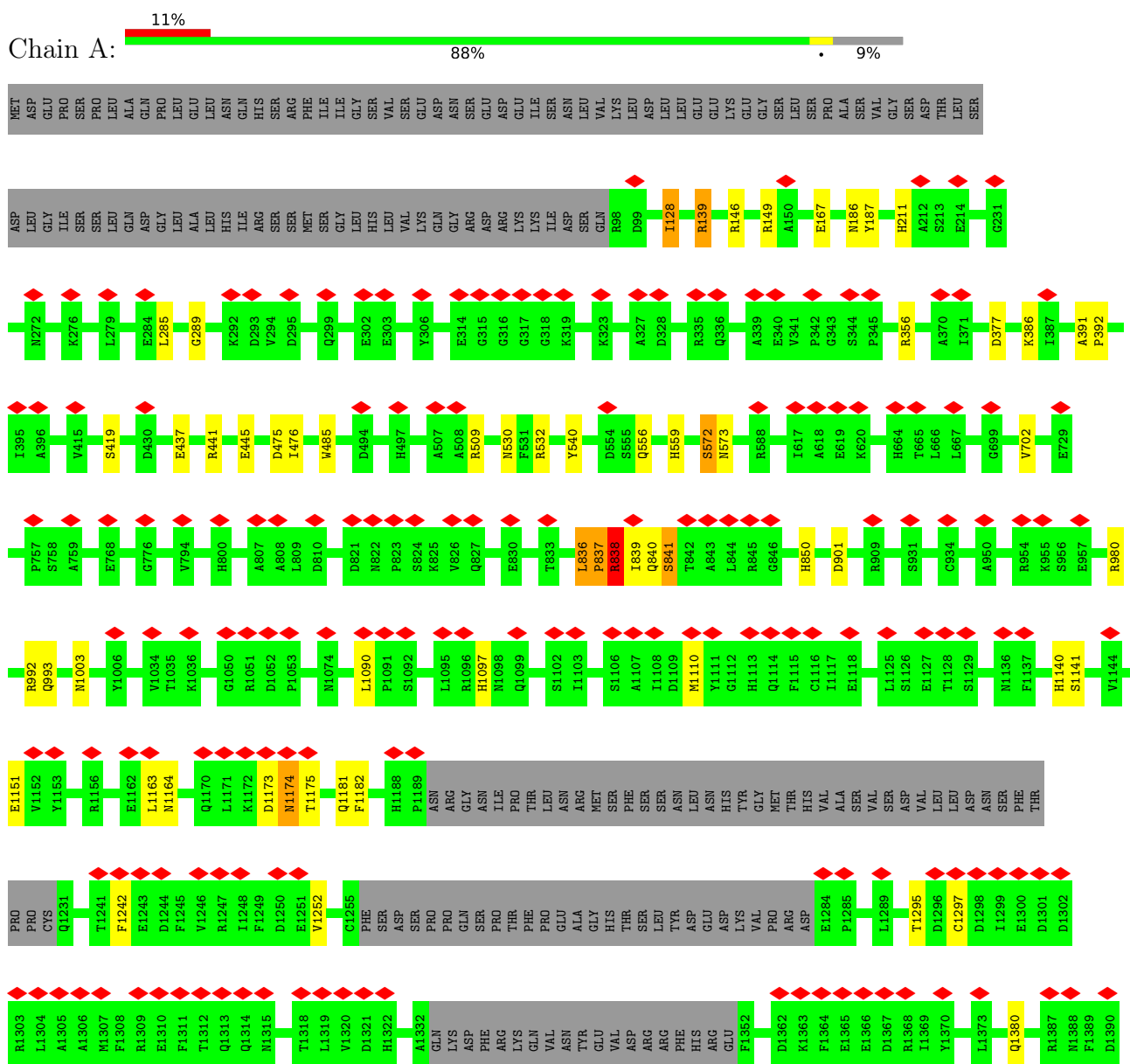


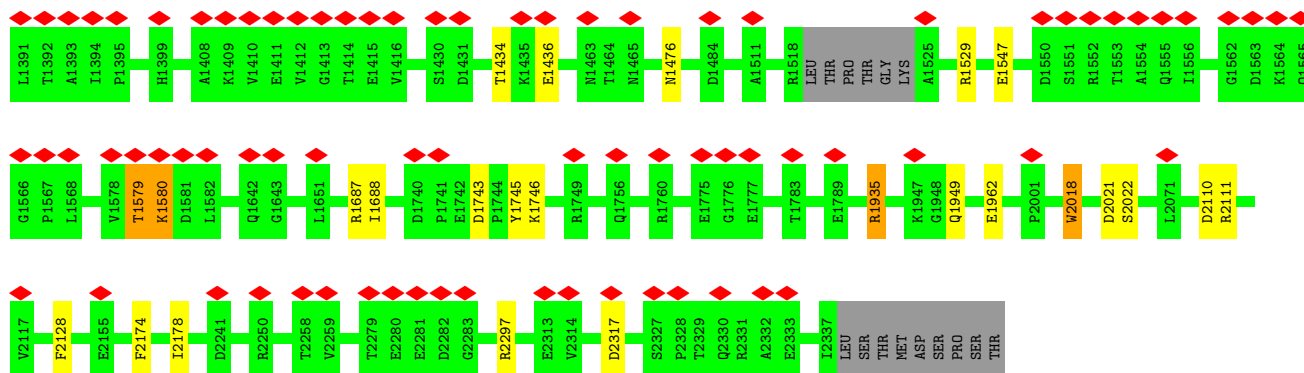
Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total 15	C 10	N 2	O 2	S 1	0
2	B	1	Total 15	C 10	N 2	O 2	S 1	0
2	C	1	Total 15	C 10	N 2	O 2	S 1	0
2	D	1	Total 15	C 10	N 2	O 2	S 1	0
2	E	1	Total 15	C 10	N 2	O 2	S 1	0

### 3 Residue-property plots [i](#)

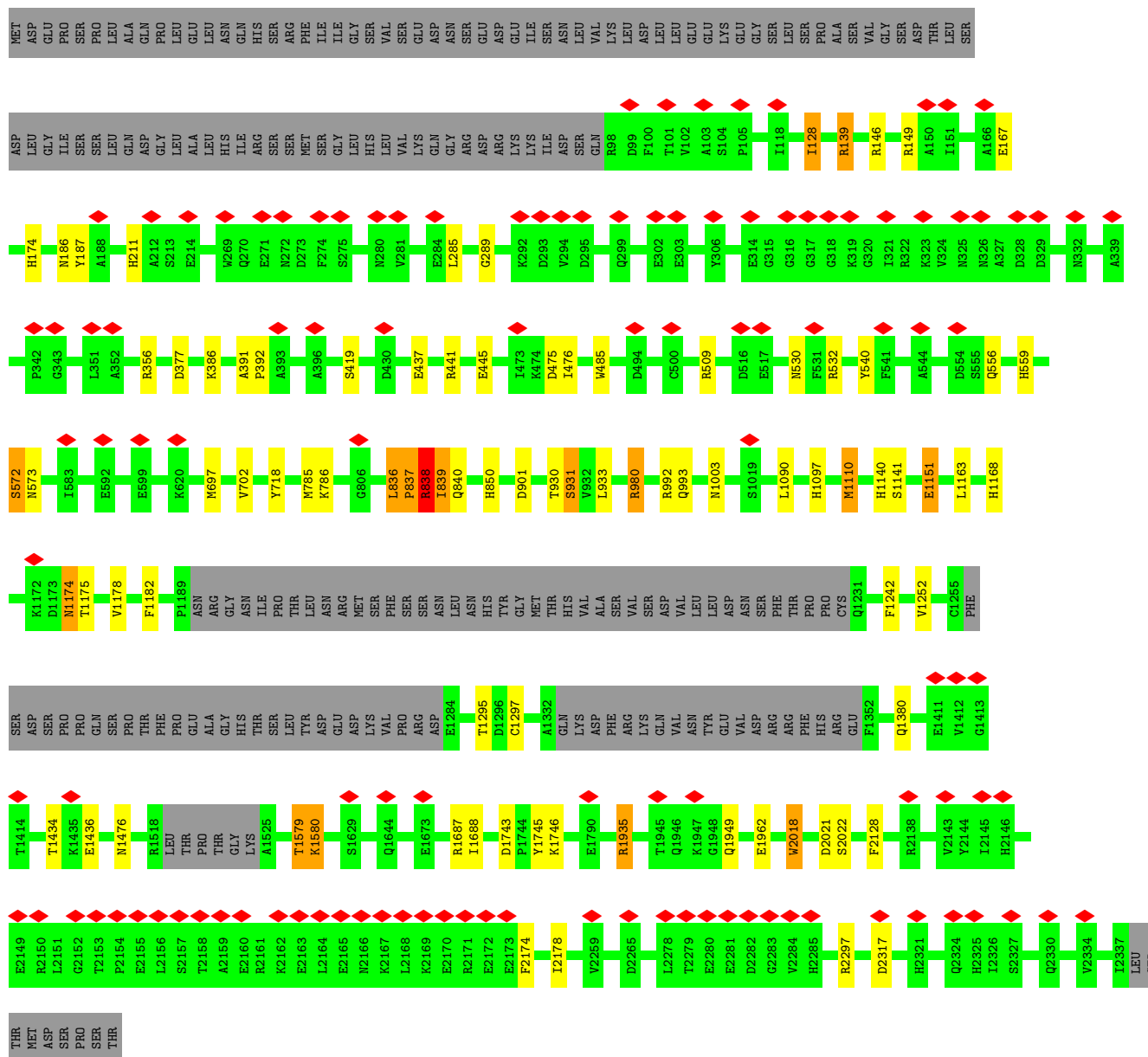
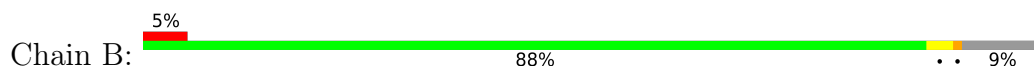
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Acetyl-CoA carboxylase 1

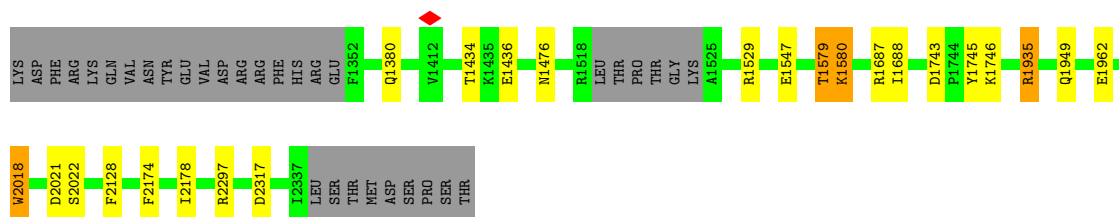




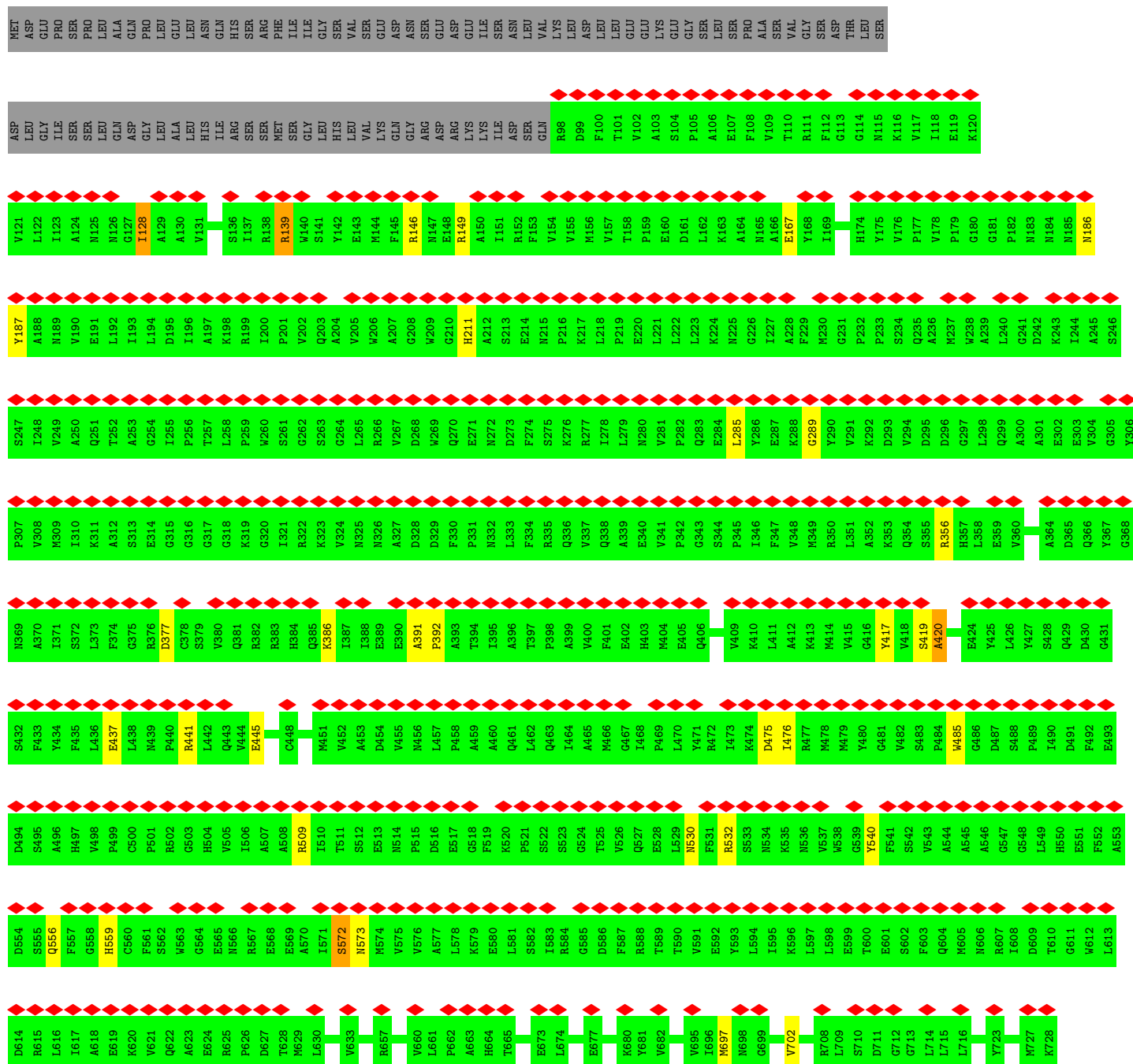
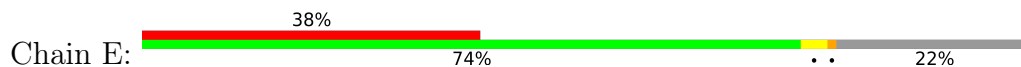
• Molecule 1: Acetyl-CoA carboxylase 1







• Molecule 1: Acetyl-CoA carboxylase 1











GLN	LEU	K2209	I2126	T1990	F1893	K1788	E1728
ARG	ALA	T2210	K2127	R1991	K1904	E1789	E1729
ALA	GLU	S2211	F2128	N2003		E1790	I1730
GLU	LEU		R2129	L2004	H1907	G1791	H1731
ILE	GLU	F2214	R2130	L2005		I1792	H1732
ARG	LYS	P2215	K2131	S2006	S1908	G1793	M1733
LEU	LEU	Y2216	D2132	E2007		P1794	F1734
LEU	THR	W2217	L2133	A2008		H1798	H1735
THR	GLU	R2218	L2134	K2009	S1915	G1799	H1736
LEU	GLU	L2219	V2134	I2010	K1916		A1737
ASP	ASP	R2220	K2135				M1738
SER	GLY	R2221		T2011	D1917	A1810	V1739
PRO	VAL	L2222	P2142	Q2012	P1918	E1813	D1740
SER	HIS	L2223	V2143	Q2013	I1919		P1741
THR	SER	L2224	Y2144	A2014	D1920		E1742
	VAL	E2225	I2145	G2015	R1921	L1819	D1743
	ILE	D2226	H2146	Q2016	I1922	V1820	
	GLU	L2227	L2147	W2017	I1923	T1821	P1744
	GLU	V2228	A2148	W2018	E1924	C1822	Y1745
	ASN	K2229	E2149			R1823	
	LYS			D2021	F1925	A1824	K1746
	ILE	K2230	R2150	S2022	V1926		
	ILE	K2231	L2151		P1927	Q1840	G1747
	SER	K2232	G2152	E2036		V1841	Y1748
	ARG	I2232	T2153	W2041	K1929	E1842	R1749
	ASP	H2233	P2154	A2044	T1930	S1843	Y1750
	TYR	L2234	E2155		P1931	Y1752	L1751
	VAL	A2235	L2156		Y1932	S1844	Y1753
	LEU	N2236	S2157	K2054	D1933	H1845	L1754
	GLN	P2237	T2158				P1755
ILE	ILE	GLU	W2159	Q2059	A1935	A1851	P1756
ARG	ARG	LEU	E2160	V2068	M1937	G1852	Q1756
SER	THR	LEU	K2161	D2069	L1938	D1757	D1757
LEU	ASP	VAL	R2162	G2070	A1939	N1854	Y1758
LEU	GLN	GLN	E2163		G1940	N1855	K1759
ALA	ASN	ASN			R1941	K1856	R1760
GLU	PRO	ALA	L2168	G2075		V1857	V1761
GLU	GLU	VAL	K2169	I2082	P1942	L1858	V1762
VAL	LEU	VAL	E2170	P2083	H1943	G1859	S1762
ALA	ARG	ALA		P2084	P1944	R1860	A1763
MET	MET	ASP		Q2085	T1945	L1764	A1763
ASP	ASP	THR	F2174	A2086	Q1946	M1765	M1765
SER	SER	VAL	P2177	S2092	K1947	S1766	S1766
ILE	ILE	GLU	I2178			V1767	
ILE	VAL	VAL			Q1949	H1768	
THR	GLU	GLY	Q2181	N2101	W1950	N1866	H1768
GLN	THR	THR		P2102	L1951	N1867	C1769
HIS	VAL	LYS	T2192	R2103	G1953	Q1868	E1770
VAL	SER	ALA	P2193	D2110	F1954	L1872	H1771
ALA	ALA	TYR	G2194	R2111		Q1873	V1772
PRO	VAL	VAL		V2117		T1884	E1773
THR	THR	THR	Q2197	L2118	Y1957	V1885	D1774
	ASP	ASP	E2198			C1886	E1775
ASN	ASN	ASN	K2199		E1962	D1887	G1776
LYS	LYS	LYS		E2121		F1889	S1778
ASP	ASP	ASP	S2203	G2122	L1978	D1888	R1779
			D2204	T2123	G1979	F1889	Y1780
			I2205			E1890	I1782
			L2206		G1984	G1891	T1783
			D2207			V1892	D1784
							I1785
							I1786
							G1787

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36041	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.719	Depositor
Minimum map value	-0.669	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	525.72235, 525.72235, 525.72235	wwPDB
Map dimensions	488, 488, 488	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0773, 1.0773, 1.0773	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

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	0.49	1/17490 (0.0%)	0.59	0/23691
1	B	0.49	1/17490 (0.0%)	0.58	0/23691
1	C	0.49	1/17490 (0.0%)	0.59	0/23691
1	D	0.49	1/17490 (0.0%)	0.58	0/23691
1	E	0.49	0/14745	0.59	0/19979
1	F	0.55	1/10423 (0.0%)	0.60	0/14139
All	All	0.50	5/95128 (0.0%)	0.59	0/128882

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	4
1	B	0	4
1	C	0	4
1	D	0	4
1	E	0	4
1	F	0	2
All	All	0	22

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	2018	TRP	C-N	-5.87	1.20	1.34
1	F	2018	TRP	C-N	-5.87	1.20	1.34
1	B	2018	TRP	C-N	-5.83	1.20	1.34
1	A	2018	TRP	C-N	-5.42	1.21	1.34
1	C	2018	TRP	C-N	-5.41	1.21	1.34

There are no bond angle outliers.

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1140	HIS	Peptide
1	A	1579	THR	Mainchain
1	A	1687	ARG	Peptide
1	A	419	SER	Mainchain
1	B	419	SER	Mainchain

## 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	17120	0	17047	48	0
1	B	17120	0	17046	83	0
1	C	17120	0	17047	71	0
1	D	17120	0	17046	73	0
1	E	14435	0	14365	79	0
1	F	10185	0	10085	20	0
2	A	15	0	15	0	0
2	B	15	0	15	1	0
2	C	15	0	15	0	0
2	D	15	0	15	0	0
2	E	15	0	15	0	0
All	All	93175	0	92711	290	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 2.

The worst 5 of 290 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:D:930:THR:HG22	1:E:1168:HIS:HB2	1.23	1.10
1:D:1168:HIS:HB2	1:E:930:THR:HG22	1.44	0.99
1:B:1168:HIS:HB2	1:C:930:THR:HG22	1.51	0.92
1:B:930:THR:HG22	1:C:1168:HIS:HB2	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:933:LEU:HG	1:C:1151:GLU:OE1	1.72	0.89

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	2136/2346 (91%)	2005 (94%)	122 (6%)	9 (0%)	30	67
1	B	2136/2346 (91%)	1998 (94%)	130 (6%)	8 (0%)	30	67
1	C	2136/2346 (91%)	2004 (94%)	123 (6%)	9 (0%)	30	67
1	D	2136/2346 (91%)	2000 (94%)	129 (6%)	7 (0%)	37	71
1	E	1809/2346 (77%)	1691 (94%)	110 (6%)	8 (0%)	30	67
1	F	1285/2346 (55%)	1226 (95%)	57 (4%)	2 (0%)	44	77
All	All	11638/14076 (83%)	10924 (94%)	671 (6%)	43 (0%)	32	67

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	841	SER
1	A	1580	LYS
1	B	837	PRO
1	B	1580	LYS
1	C	837	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	1873/2057 (91%)	1846 (99%)	27 (1%)	62	75
1	B	1873/2057 (91%)	1845 (98%)	28 (2%)	60	75
1	C	1873/2057 (91%)	1847 (99%)	26 (1%)	62	75
1	D	1873/2057 (91%)	1847 (99%)	26 (1%)	62	75
1	E	1581/2057 (77%)	1560 (99%)	21 (1%)	65	77
1	F	1101/2057 (54%)	1085 (98%)	16 (2%)	60	75
All	All	10174/12342 (82%)	10030 (99%)	144 (1%)	62	75

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

Mol	Chain	Res	Type
1	E	530	ASN
1	F	2178	ILE
1	E	980	ARG
1	F	146	ARG
1	B	1110	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1398	ASN
1	D	2285	HIS
1	E	1398	ASN
1	E	1164	ASN
1	B	2285	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	BTN	C	2401	1	16,16,17	1.16	1 (6%)	21,21,23	1.78	4 (19%)
2	BTN	B	2401	1	16,16,17	1.15	1 (6%)	21,21,23	1.77	5 (23%)
2	BTN	E	2401	1	16,16,17	1.17	1 (6%)	21,21,23	1.78	4 (19%)
2	BTN	D	2401	1	16,16,17	1.16	1 (6%)	21,21,23	1.77	5 (23%)
2	BTN	A	2401	1	16,16,17	1.16	1 (6%)	21,21,23	1.78	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BTN	C	2401	1	-	0/5/27/28	0/2/2/2
2	BTN	B	2401	1	-	0/5/27/28	0/2/2/2
2	BTN	E	2401	1	-	0/5/27/28	0/2/2/2
2	BTN	D	2401	1	-	0/5/27/28	0/2/2/2
2	BTN	A	2401	1	-	0/5/27/28	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2401	BTN	C2-S1	-3.61	1.76	1.82
2	A	2401	BTN	C2-S1	-3.60	1.76	1.82
2	C	2401	BTN	C2-S1	-3.56	1.76	1.82
2	B	2401	BTN	C2-S1	-3.53	1.77	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2401	BTN	C2-S1	-3.53	1.77	1.82

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2401	BTN	C4-C2-S1	3.64	108.67	105.20
2	C	2401	BTN	C4-C2-S1	3.64	108.67	105.20
2	E	2401	BTN	C4-C2-S1	3.63	108.66	105.20
2	B	2401	BTN	C4-C2-S1	3.55	108.58	105.20
2	D	2401	BTN	C4-C2-S1	3.54	108.58	105.20

There are no chirality outliers.

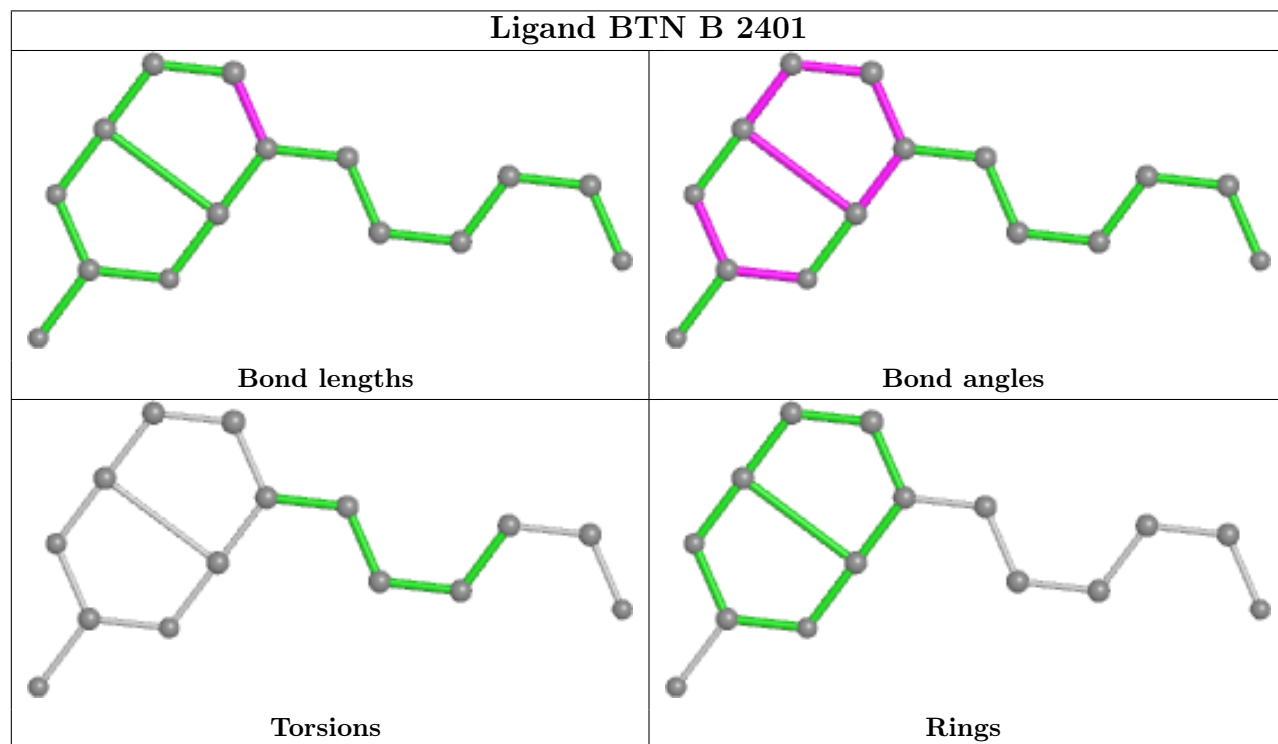
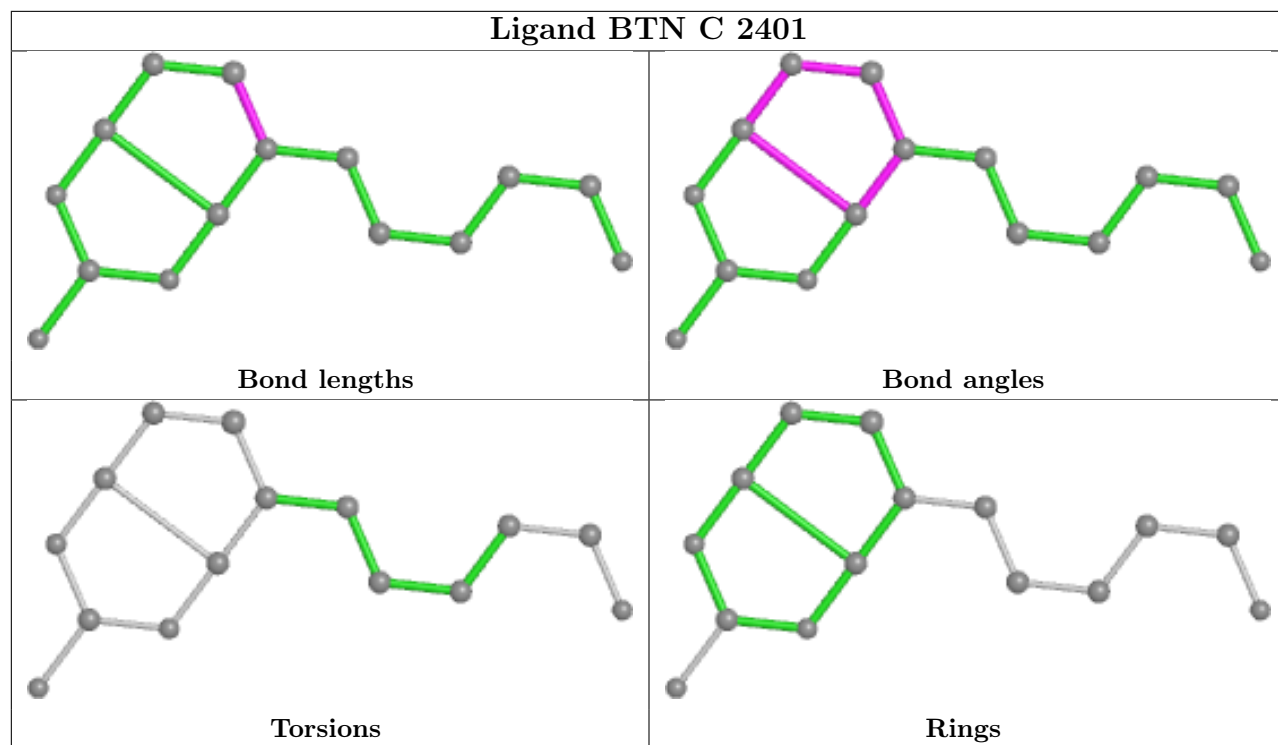
There are no torsion outliers.

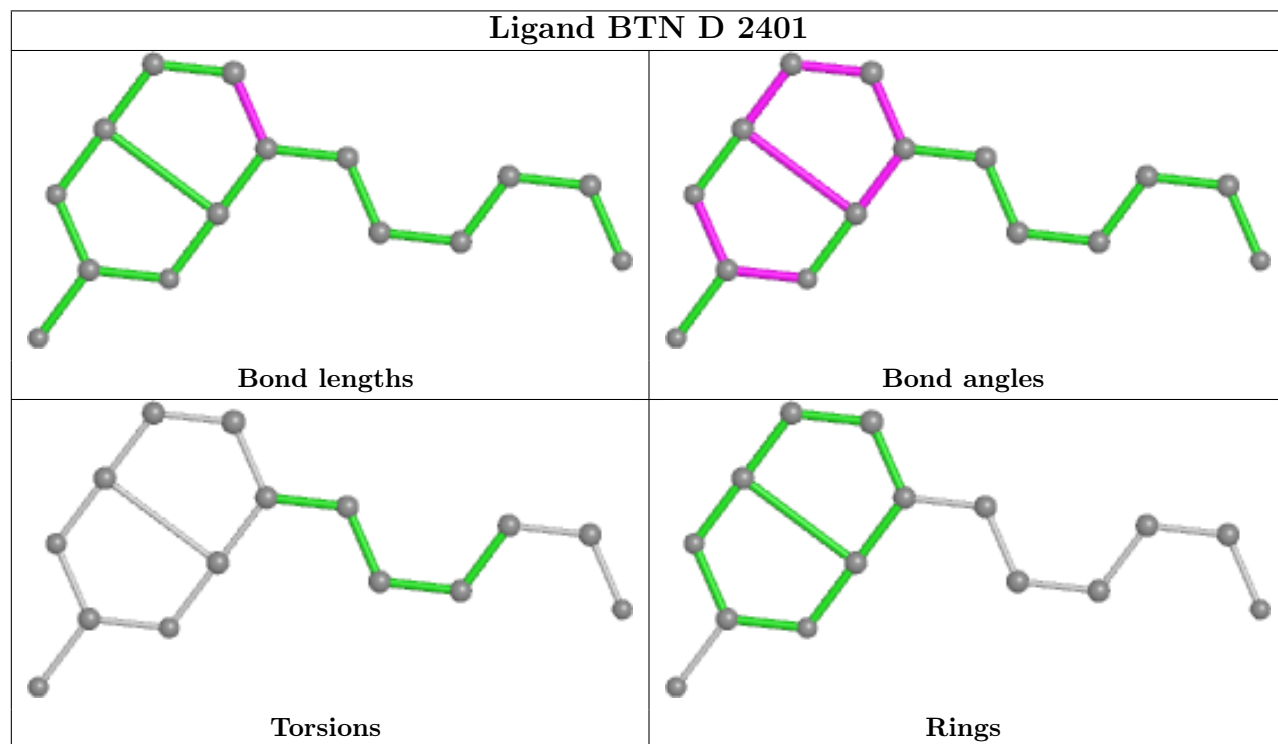
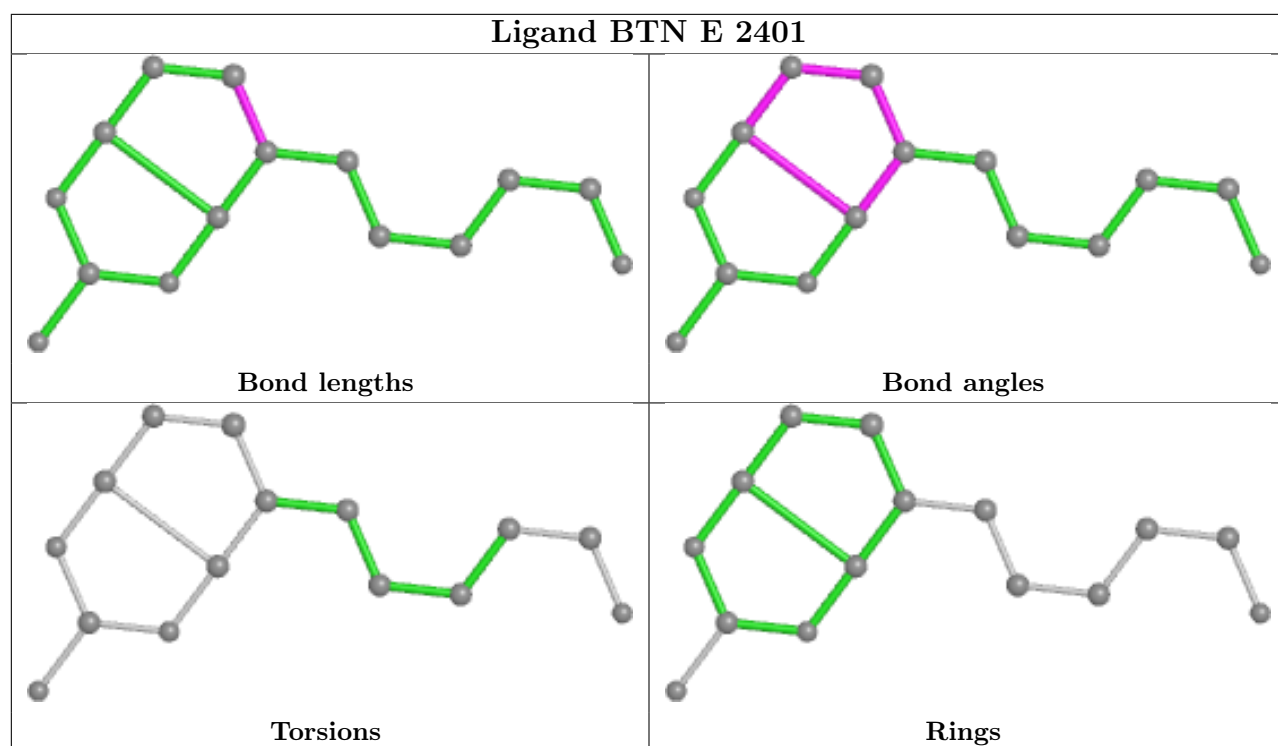
There are no ring outliers.

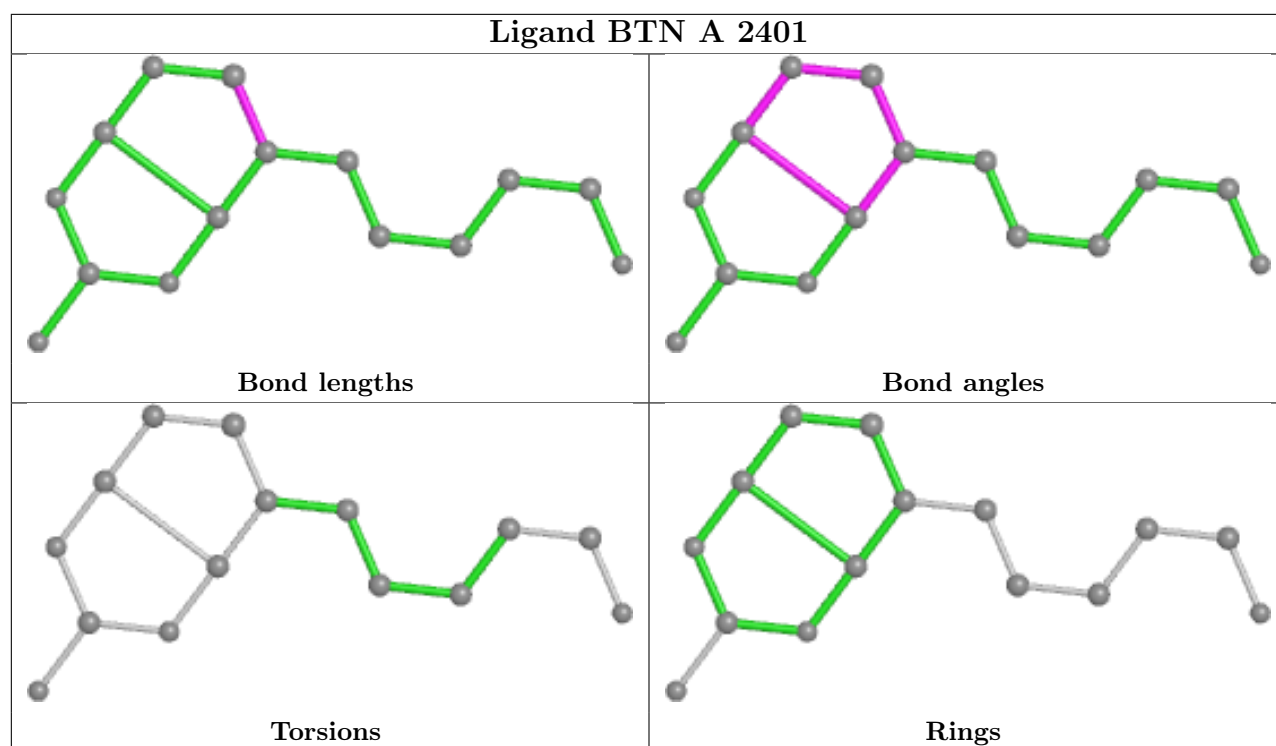
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2401	BTN	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 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.

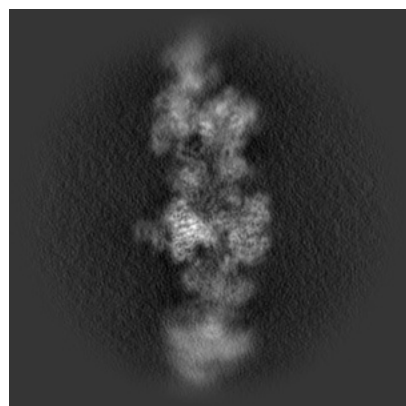
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38433. These allow visual inspection of the internal detail of the map and identification of artifacts.

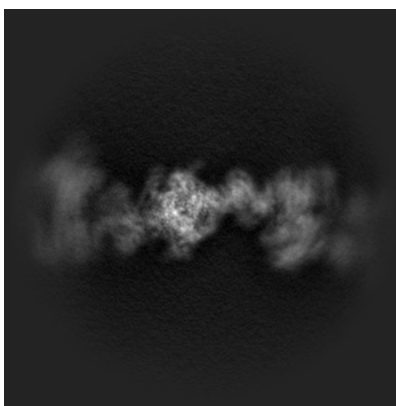
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

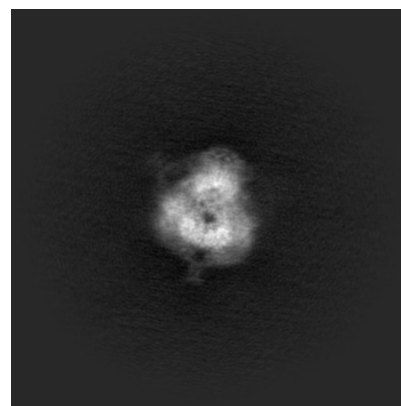
#### 6.1.1 Primary map



X

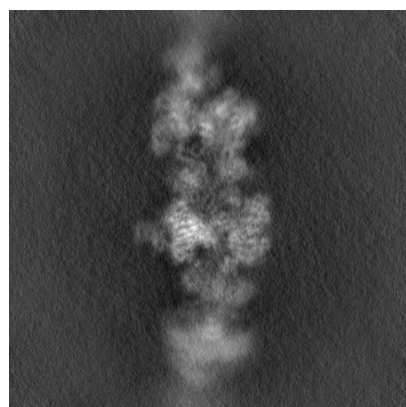


Y

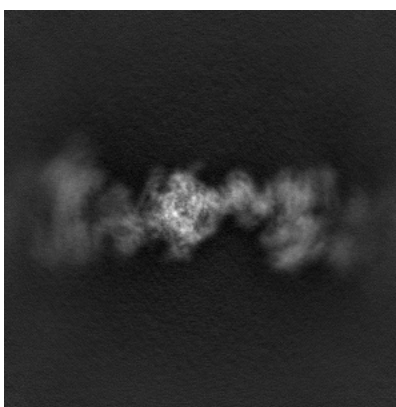


Z

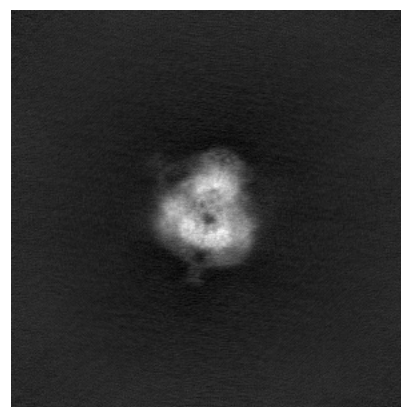
#### 6.1.2 Raw map



X



Y

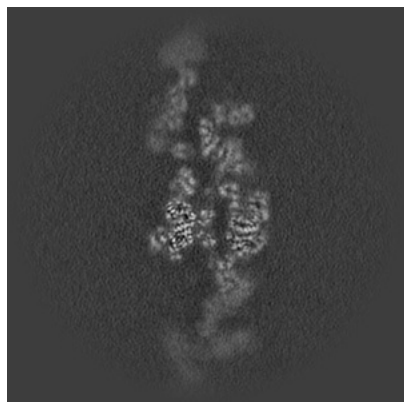


Z

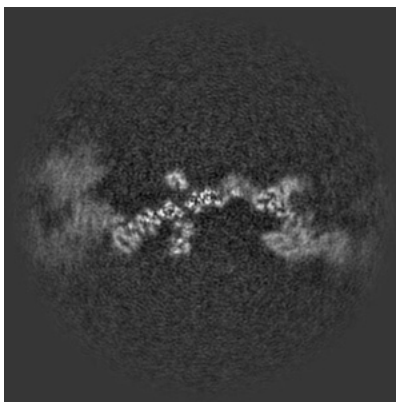
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

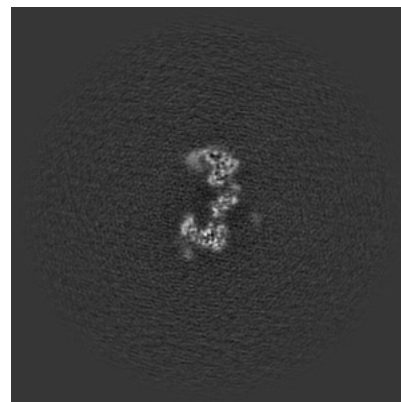
### 6.2.1 Primary map



X Index: 244

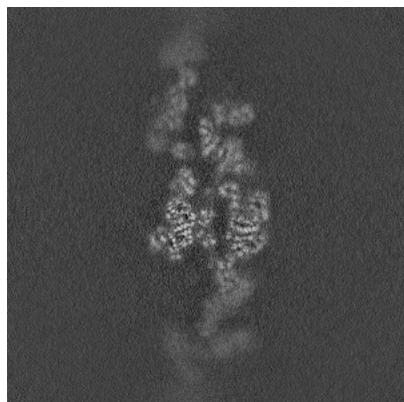


Y Index: 244

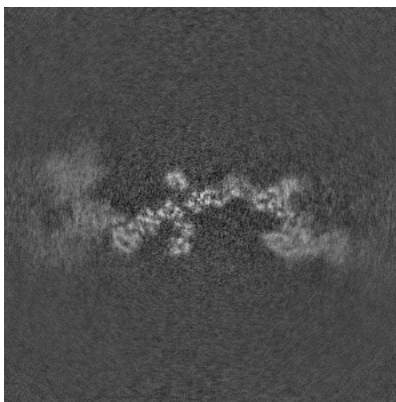


Z Index: 244

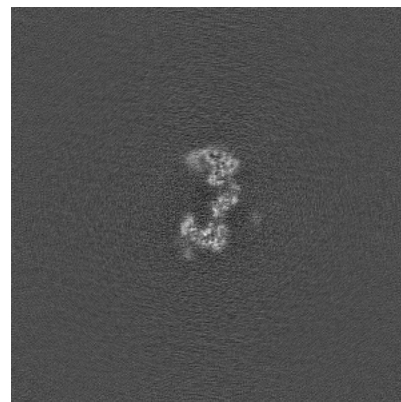
### 6.2.2 Raw map



X Index: 244



Y Index: 244



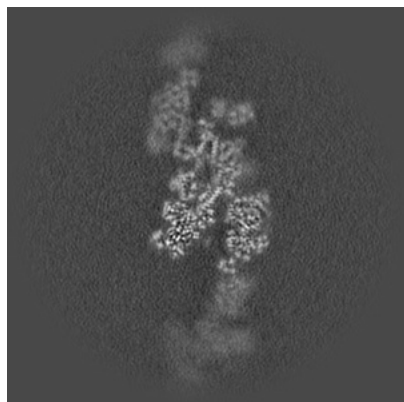
Z Index: 244

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

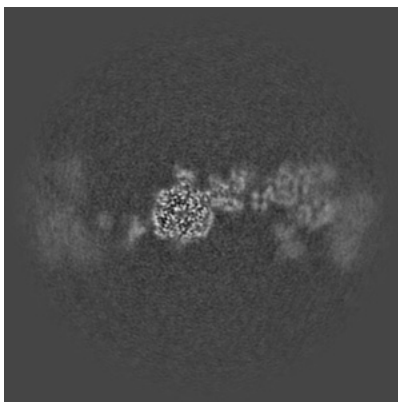


## 6.3 Largest variance slices [i](#)

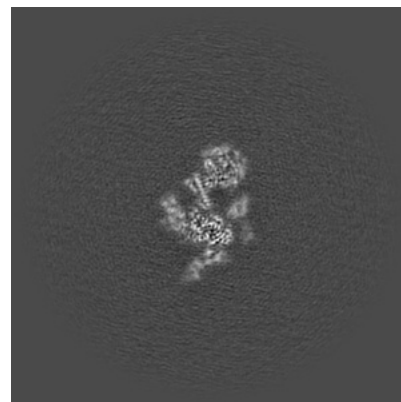
### 6.3.1 Primary map



X Index: 251

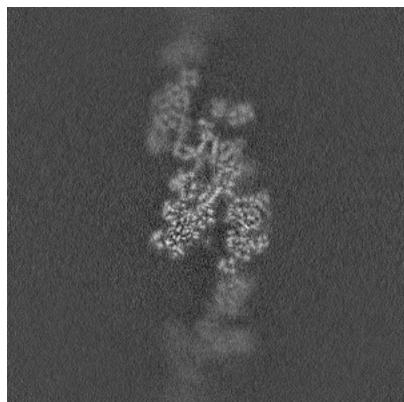


Y Index: 213

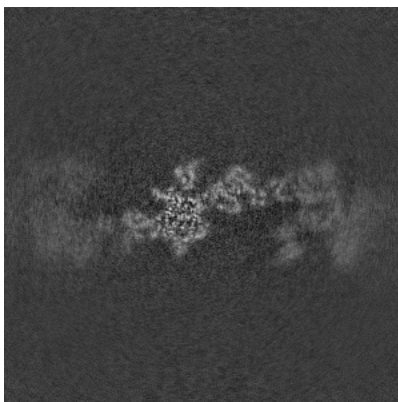


Z Index: 207

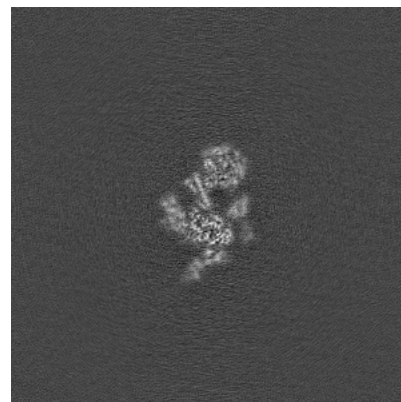
### 6.3.2 Raw map



X Index: 251



Y Index: 220

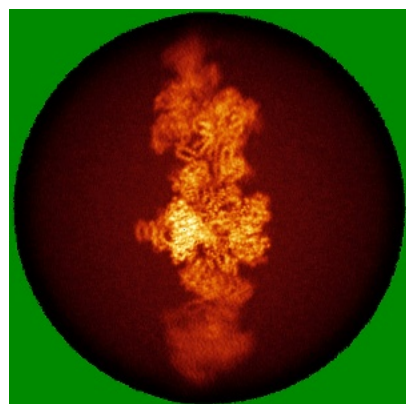


Z Index: 207

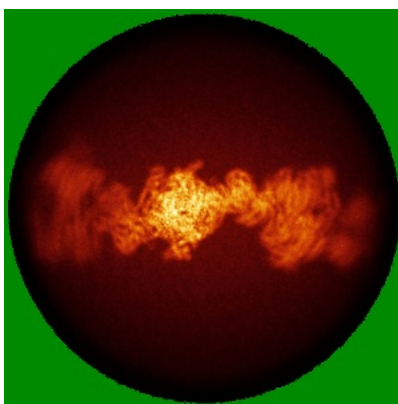
The images above show the largest variance slices of the map in three orthogonal directions.

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

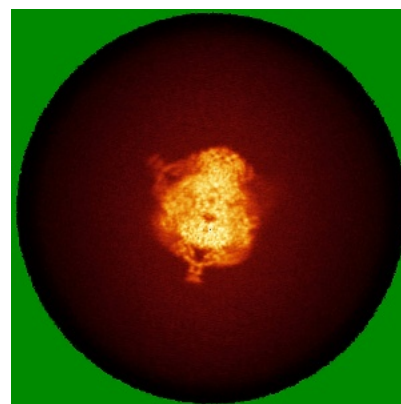
### 6.4.1 Primary map



X

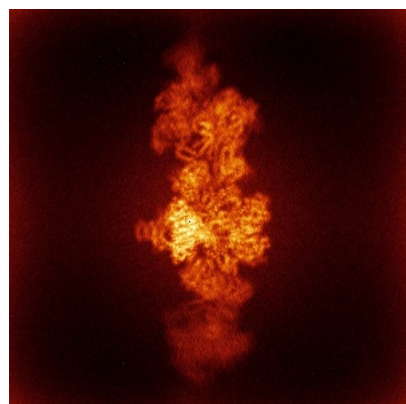


Y

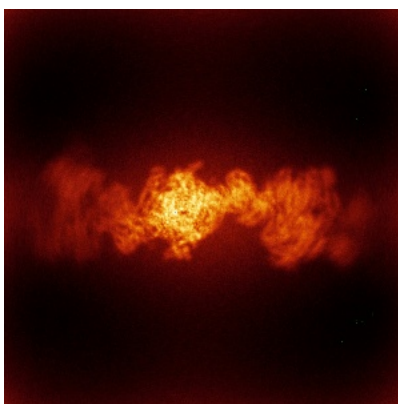


Z

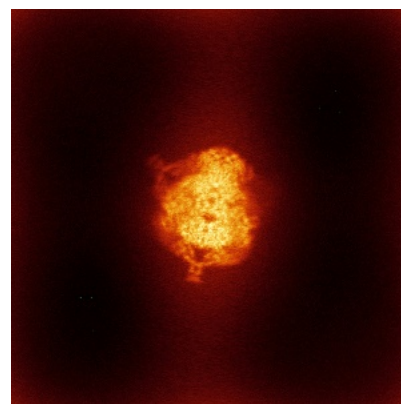
### 6.4.2 Raw map



X



Y

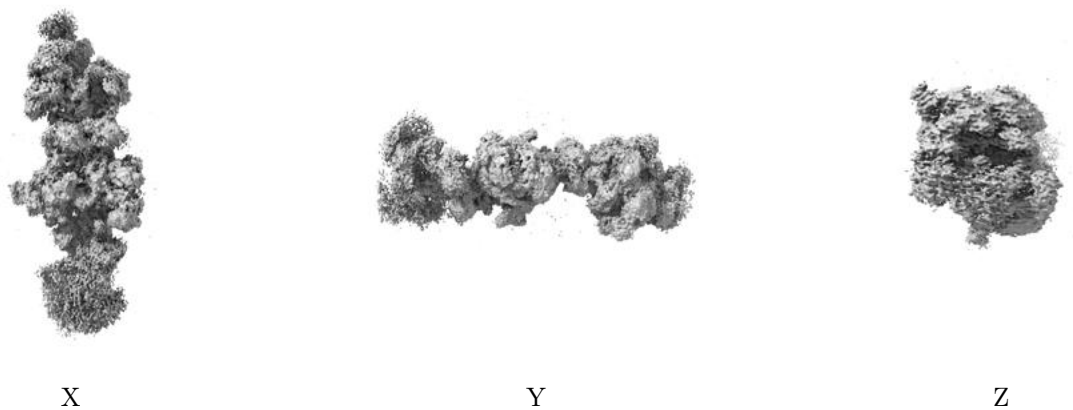


Z

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.

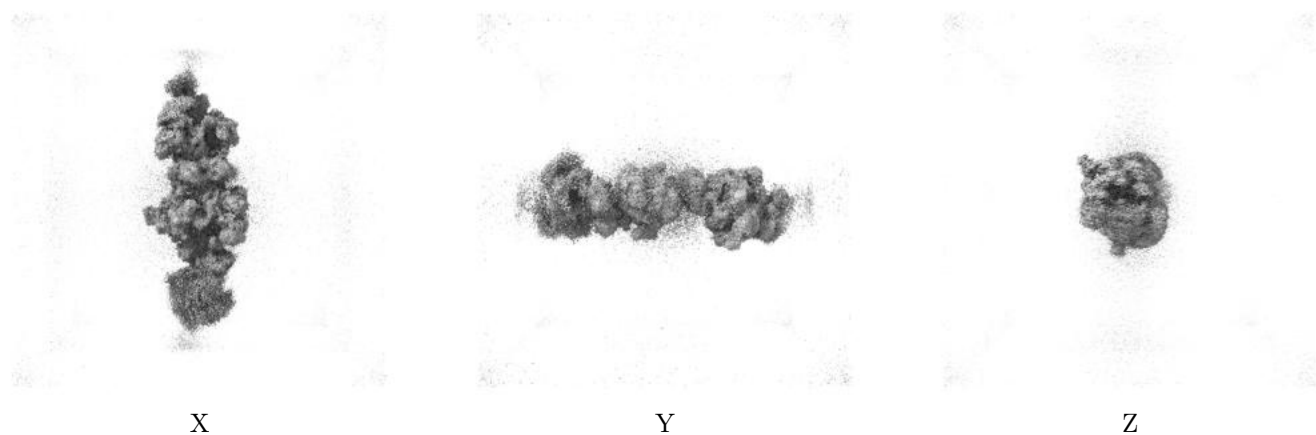
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 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.

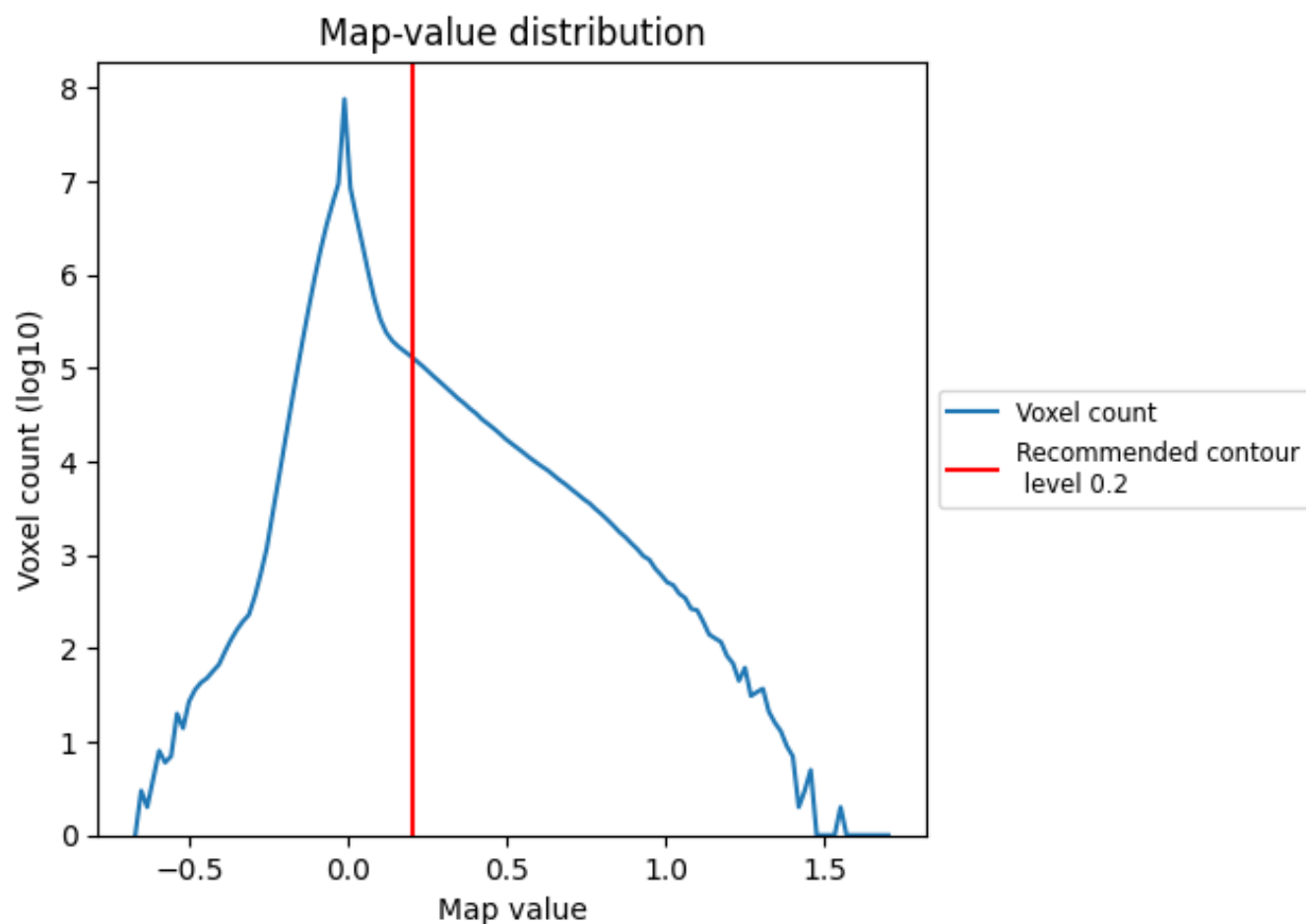
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

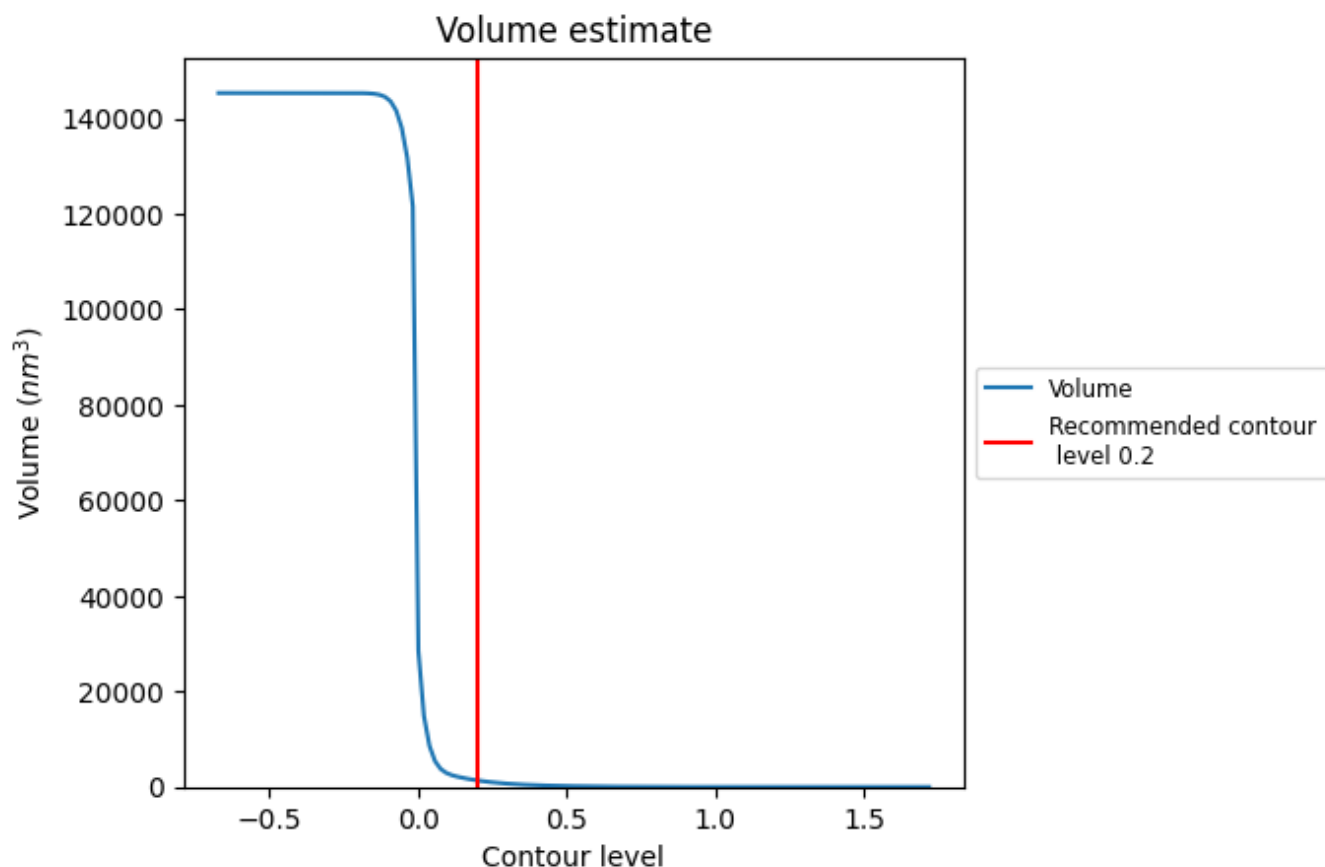
This section contains the results of statistical analysis of the map.

### 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.

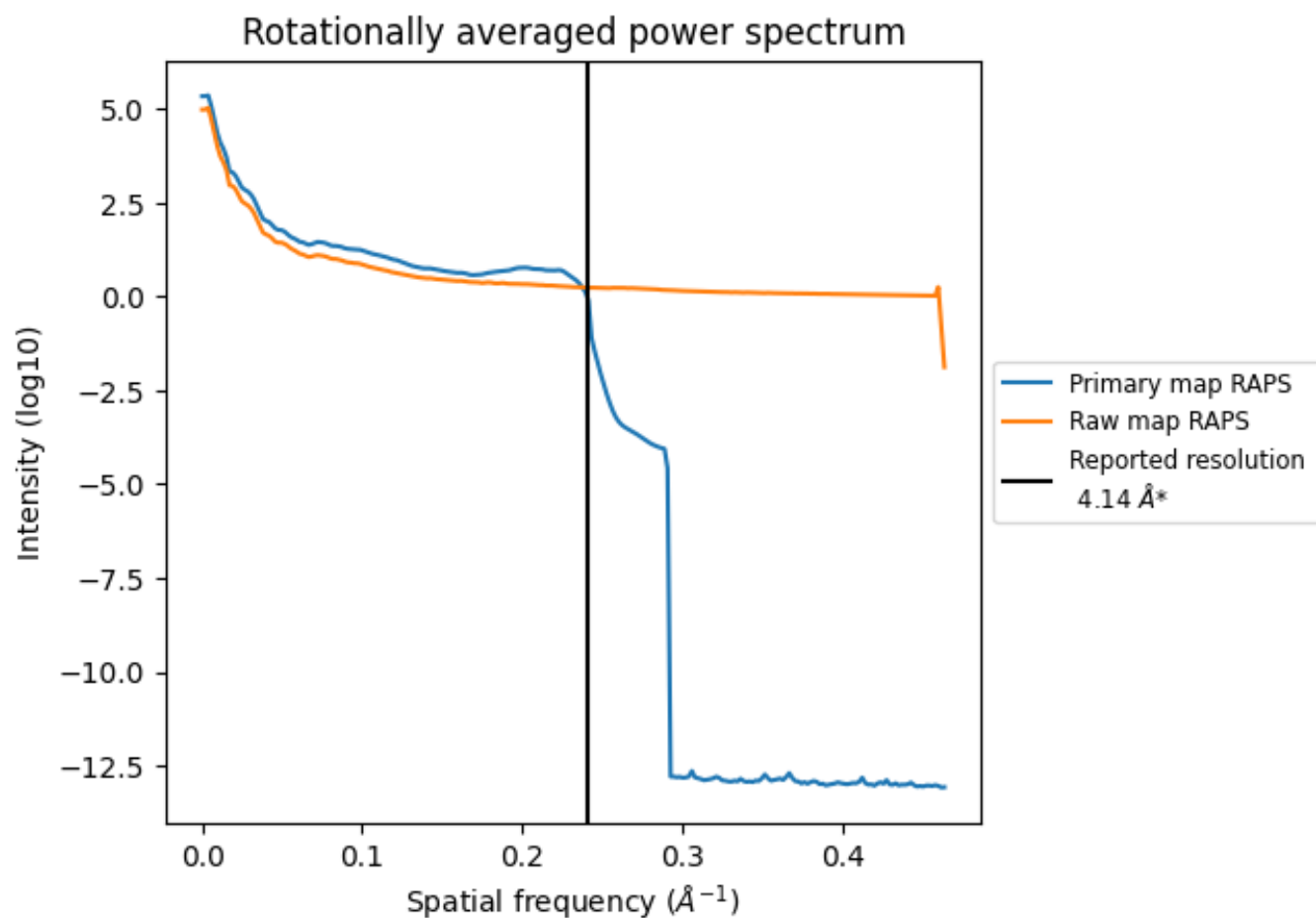
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1379  $\text{nm}^3$ ; this corresponds to an approximate mass of 1246 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 ⓘ

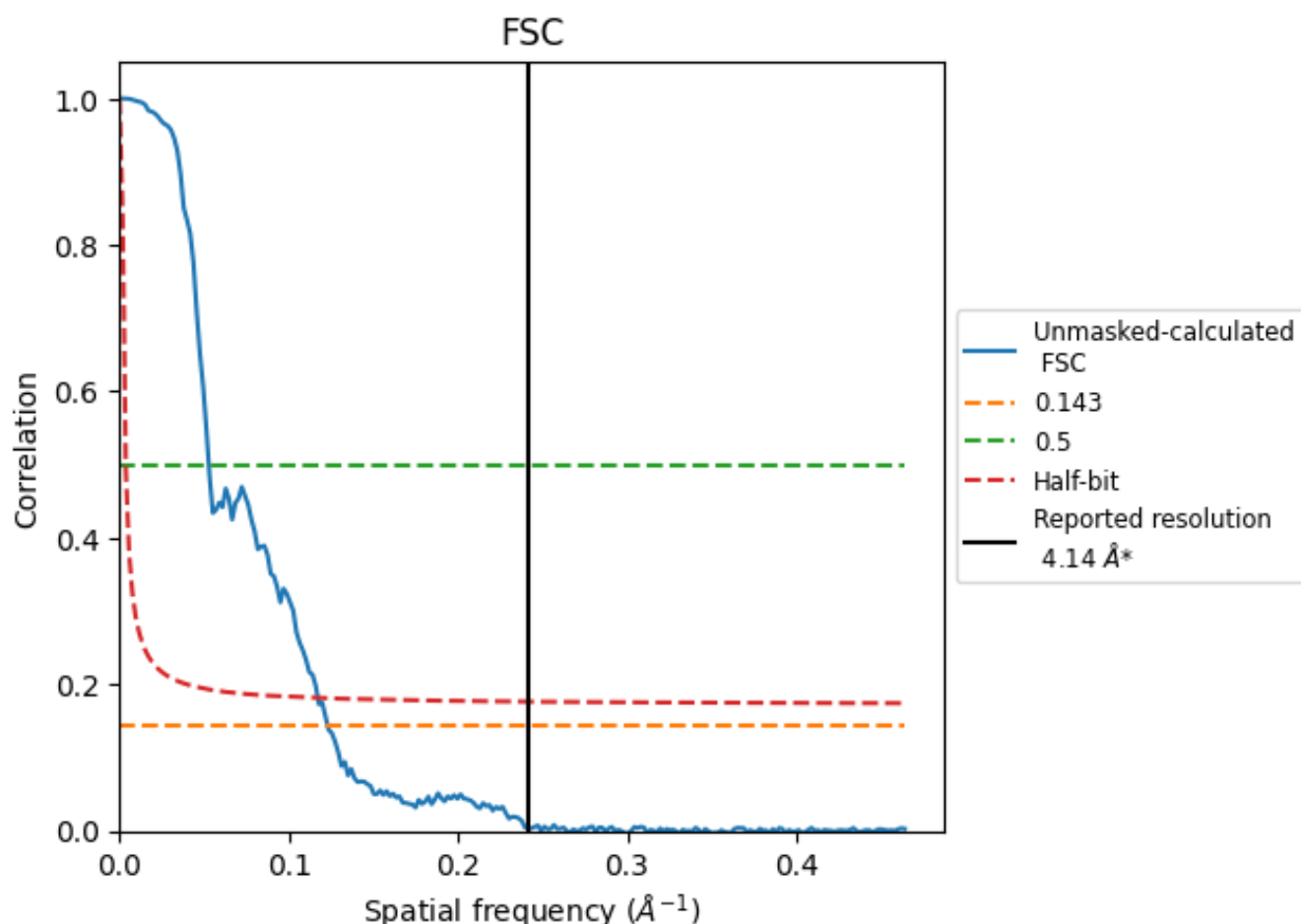


\*Reported resolution corresponds to spatial frequency of 0.242  $\text{\AA}^{-1}$

## 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 0.242  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.14	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.12	18.94	8.53

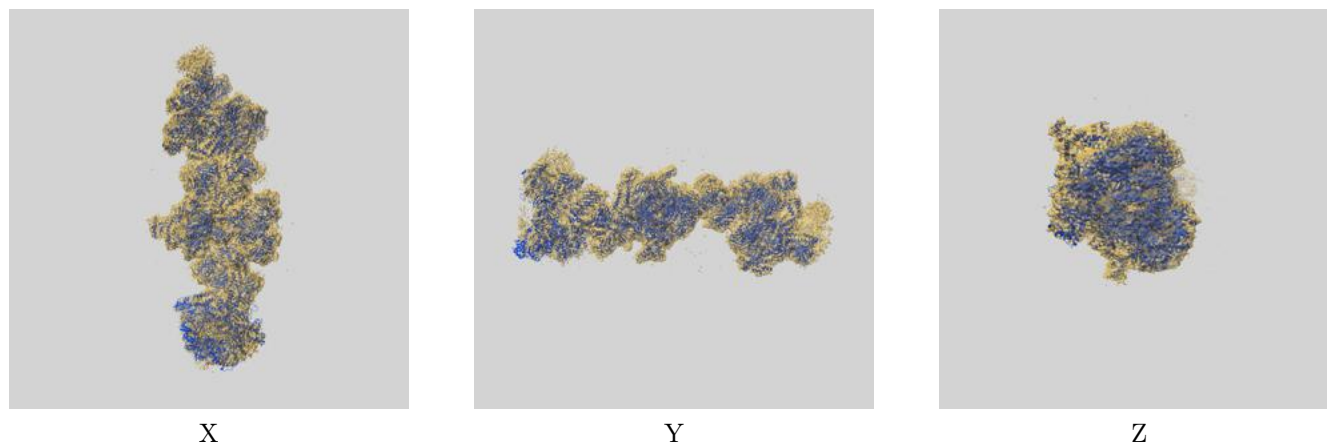
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.12 differs from the reported value 4.14 by more than 10 %



## 9 Map-model fit [i](#)

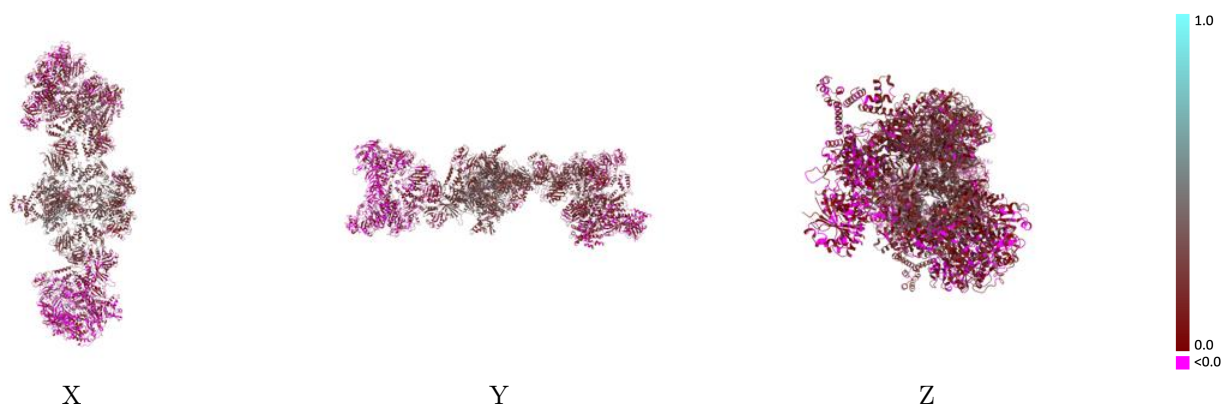
This section contains information regarding the fit between EMDB map EMD-38433 and PDB model 8XL0. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



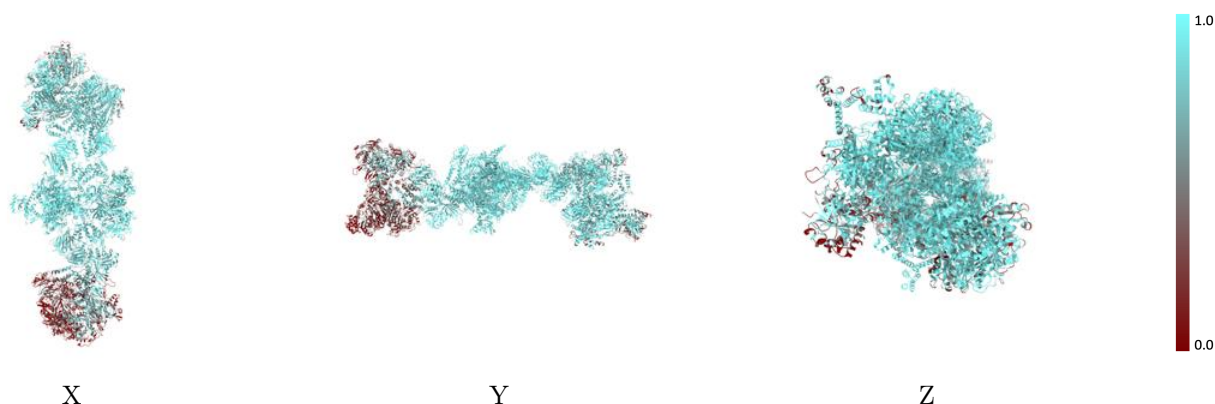
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



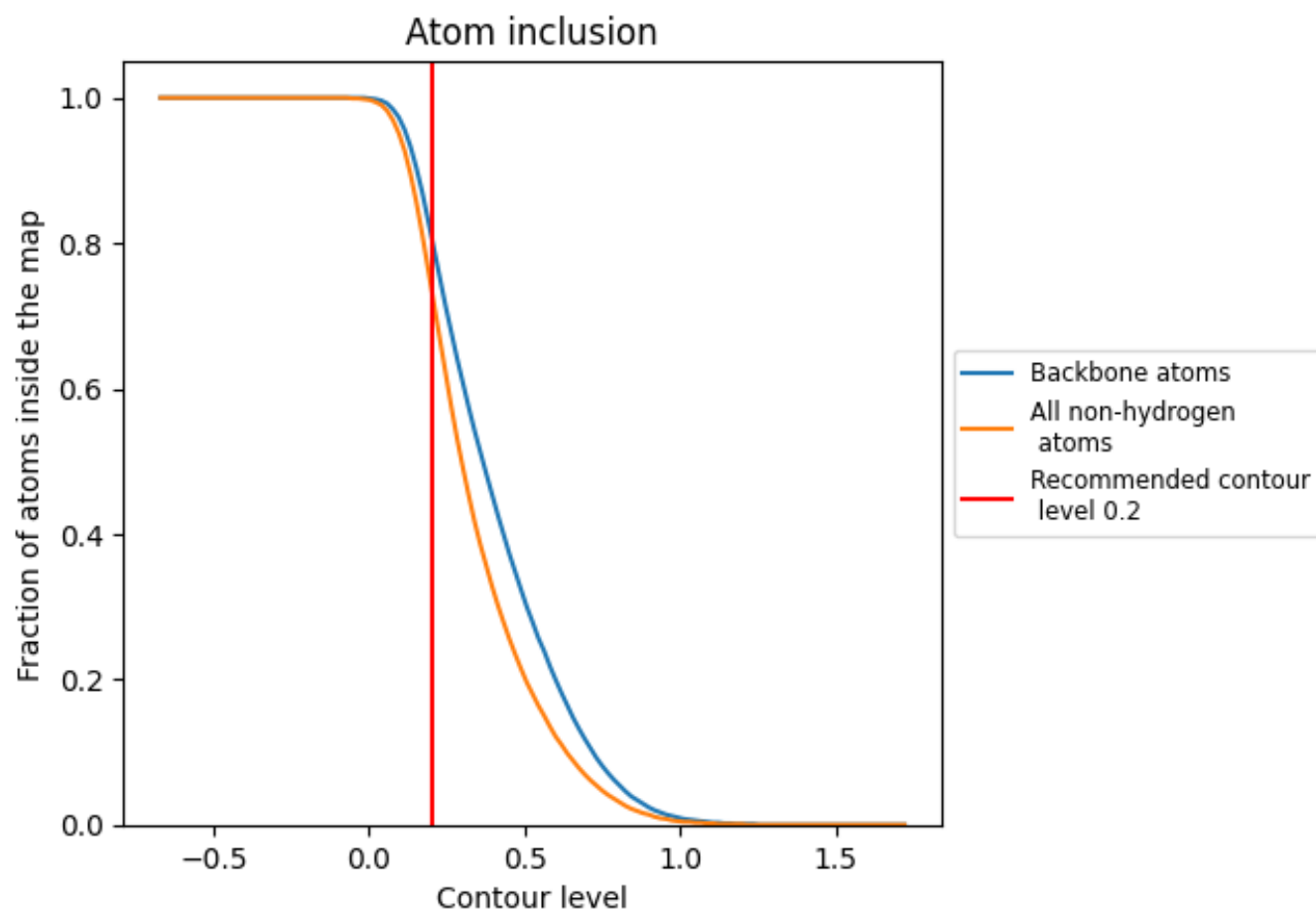
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 74% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7380	<div></div> 0.1620
A	<div></div> 0.7650	<div></div> 0.1060
B	<div></div> 0.8510	<div></div> 0.1530
C	<div></div> 0.9280	<div></div> 0.2830
D	<div></div> 0.9210	<div></div> 0.2770
E	<div></div> 0.4450	<div></div> 0.0520
F	<div></div> 0.2890	<div></div> 0.0270

