



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 10:15 AM UTC

PDB ID : 6Z6G / pdb_00006z6g
EMDB ID : EMD-11093
Title : Cryo-EM structure of La Crosse virus polymerase at pre-initiation stage
Authors : Arragain, B.; Effantin, G.; Gerlach, P.; Reguera, J.; Schoehn, G.; Cusack, S.; Malet, H.
Deposited on : 2020-05-28
Resolution : 3.06 Å(reported)
Based on initial model : 5AMQ

This is a Full wwPDB EM Validation 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

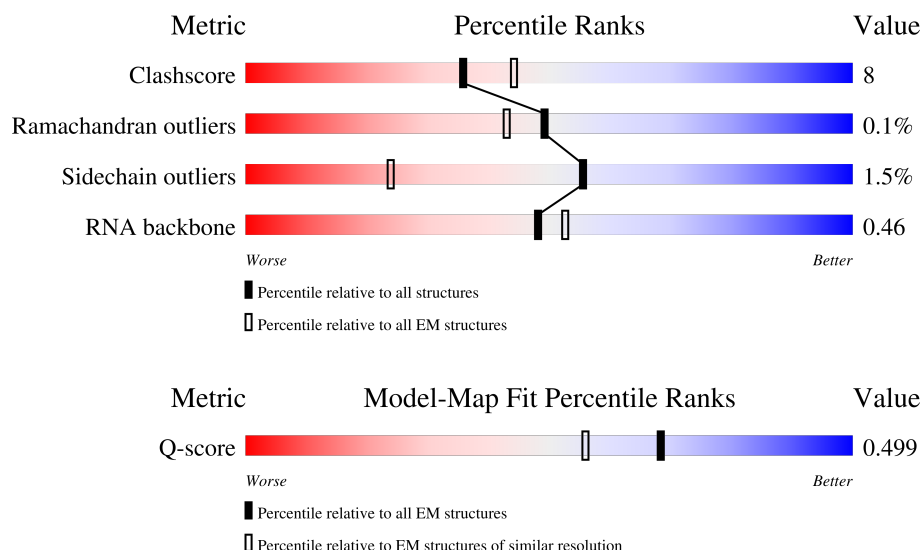
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.06 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13976 (2.56 - 3.56)

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	U	10	
2	X	8	
3	H	16	

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Mol	Chain	Length	Quality of chain
4	A	2285	7% 79% 13% • 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18068 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 RNA chain called 5'vRNA 1-10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	10	Total	C	N	O	P	0	0
			216	96	39	71	10		

- Molecule 2 is a RNA chain called 5'vRNA 9-16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	5	Total	C	N	O	P	0	0
			101	47	18	32	4		

- Molecule 3 is a RNA chain called 3'vRNA 1-16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	13	Total	C	N	O	P	0	0
			274	123	47	91	13		

- Molecule 4 is a protein called RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2142	Total	C	N	O	S	0	0
			17475	11184	2924	3256	111		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP A5HC98
A	-20	GLY	-	expression tag	UNP A5HC98
A	-19	HIS	-	expression tag	UNP A5HC98
A	-18	HIS	-	expression tag	UNP A5HC98
A	-17	HIS	-	expression tag	UNP A5HC98
A	-16	HIS	-	expression tag	UNP A5HC98
A	-15	HIS	-	expression tag	UNP A5HC98
A	-14	HIS	-	expression tag	UNP A5HC98
A	-13	ASP	-	expression tag	UNP A5HC98

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	TYR	-	expression tag	UNP A5HC98
A	-11	ASP	-	expression tag	UNP A5HC98
A	-10	ILE	-	expression tag	UNP A5HC98
A	-9	PRO	-	expression tag	UNP A5HC98
A	-8	THR	-	expression tag	UNP A5HC98
A	-7	THR	-	expression tag	UNP A5HC98
A	-6	GLU	-	expression tag	UNP A5HC98
A	-5	ASN	-	expression tag	UNP A5HC98
A	-4	LEU	-	expression tag	UNP A5HC98
A	-3	TYR	-	expression tag	UNP A5HC98
A	-2	PHE	-	expression tag	UNP A5HC98
A	-1	GLN	-	expression tag	UNP A5HC98
A	0	GLY	-	expression tag	UNP A5HC98

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

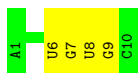
Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Mg	0
			1	1	

3 Residue-property plots [i](#)

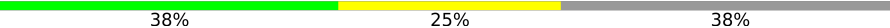
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

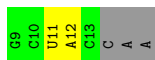
- Molecule 1: 5'vRNA 1-10

Chain U: 



- Molecule 2: 5'vRNA 9-16

Chain X: 



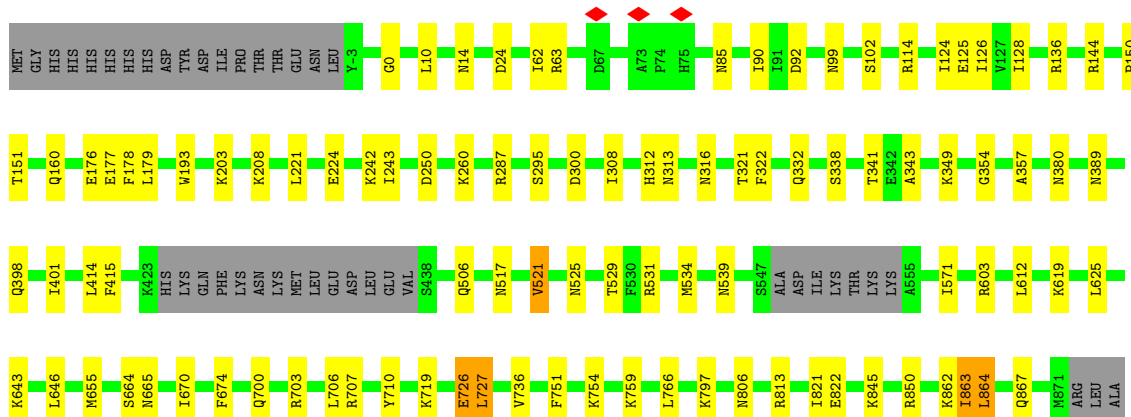
- Molecule 3: 3'vRNA 1-16

Chain H: 



- Molecule 4: RNA-directed RNA polymerase L

Chain A: 



ASN	PRO	MET	PHE	VAL	THR	ASP	GLU	GLN	VAL	CYS	LEU	GLU	VAL	GLY	HIS	CYS	ASN	
R1017	D1328	L1357	L1360	Q1369	E1380	N1383	D1391	M1392	L1400	R1401	V1404	L1405	M1409	ASP	PRO	SER	ASP	
D1024	L1025	A1026	I1027	E1028	A1029	L1030	A1031	THR	GLU	GLY	TYR	GLU	SER	ASN	L1039	I1042	K1054	
E1056	Q1067	K1072	D1080	K953	N1133	L1144	V1155	C1158	I1171	I1178	H1185	S1186	I1206	Q1223	M1226	F1487	R1488	
E1067	K1072	D1080	N1133	L1144	V1155	C1158	I1171	I1178	H1185	S1186	I1206	Q1223	M1226	F1487	R1488	E1509	D1526	
E959	I960	F961	E964	A973	E980	R981	L984	N985	E988	H989	I990	S991	E992	L998	E1006	Q1007	E1008	
I1529	ASN	LEU	HIS	ASP	SER	ARG	ALA	LEU	GLU	LYS	GLU	PRO	ASP	ILE	LEU	G1545	M1557	
V1650	K1653	I1669	E1684	S1701	THR	GLU	HIS	K1705	I1710	S1715	L1724	L1729	Y1736	Q1743	I1744	L1745	S1746	
D1827	L1828	R1829	Q1830	A1831	D1832	L1833	D1834	K1835	Y1836	T1837	A1838	M1839	K1840	S1841	H1842	E1843	R1844	
T1889	R1890	P1893	E1894	N1895	I1896	T1897	I1898	R1901	K1902	L1903	L1904	G1905	S1906	R1907	H1908	G1909	L1910	
R1950	N1951	E1952	E1953	H1954	M1955	A1956	I1957	R1958	T1959	R1960	I1961	Y1962	N1963	E1964	N2083	I1965	T1966	
L2045	N2046	I2050	L2055	I2062	C2063	C2064	S2067	D2068	L2077	P2081	M2082	N2083	F2084	G2087	E2088	P2094	I2098	
S2150	L2151	T2152	K2153	L2154	L2155	K2156	T2157	N2158	E2159	K2160	S2161	D2165	K2166	Y2181	V2186	P2187	K2188	
G2192	N2193	P2194	I2195	T2196	R2197	D2198	I2199	V2202	M2203	F2204	R2205	E2206	F2207	I2208	M2209	P2212	G2213	
T2214	D2215	N2220	V2221	M2222	F2226	C2230	I2231	A2232	L2233	K2237	F2238	GLU	THR					
GLN	ARG	ASP	PHE	S2245	E2246	F2247	T2248	K2249	L2250	M2251	LYS	LYS	GLU	GLY	GLY	ARG	SER	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	57660	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 ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	-3500	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.089	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	247.79999, 247.79999, 247.79999	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	U	0.49	0/241	0.41	0/374
2	X	0.22	0/112	0.37	0/173
3	H	0.46	0/305	0.41	0/472
4	A	0.42	0/17824	0.59	4/24023 (0.0%)
All	All	0.42	0/18482	0.58	4/25042 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	85	ASN	CA-C-N	5.68	132.39	121.54
4	A	85	ASN	C-N-CA	5.68	132.39	121.54
4	A	759	LYS	CA-C-N	5.19	128.61	120.82
4	A	759	LYS	C-N-CA	5.19	128.61	120.82

There are no chirality outliers.

There are no planarity outliers.

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	U	216	0	108	0	0
2	X	101	0	53	2	0
3	H	274	0	140	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	17475	0	17524	277	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
All	All	18068	0	17825	279	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.

All (279) 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)
4:A:2151:LEU:HD13	4:A:2204:PHE:CE2	1.35	1.57
4:A:1838:ALA:HA	4:A:1868:TYR:CE1	1.47	1.50
4:A:2151:LEU:HD13	4:A:2204:PHE:CZ	1.50	1.46
4:A:2151:LEU:CD1	4:A:2204:PHE:CE2	1.99	1.44
4:A:1838:ALA:HA	4:A:1868:TYR:CZ	1.60	1.33
4:A:1829:ARG:O	4:A:1832:ASP:OD2	1.61	1.18
4:A:2151:LEU:CD2	4:A:2204:PHE:HE2	1.57	1.17
4:A:1829:ARG:HH11	4:A:1829:ARG:HB2	1.13	1.06
4:A:1838:ALA:CA	4:A:1868:TYR:CZ	2.40	1.05
4:A:1838:ALA:CA	4:A:1868:TYR:CE1	2.41	1.04
4:A:2151:LEU:CD2	4:A:2204:PHE:CE2	2.46	0.99
4:A:710:TYR:CD1	4:A:2099:TYR:HB2	1.97	0.98
4:A:2151:LEU:HD22	4:A:2204:PHE:CE2	1.99	0.97
4:A:1791:ILE:HD11	4:A:2037:MET:HE1	1.50	0.93
4:A:1185:HIS:O	4:A:1186:SER:OG	1.87	0.92
4:A:1833:LEU:O	4:A:1836:TYR:HB3	1.71	0.91
4:A:2084:PHE:CD1	4:A:2108:MET:HE1	2.05	0.91
4:A:710:TYR:CE1	4:A:2099:TYR:HB2	2.07	0.89
4:A:1838:ALA:HB1	4:A:1868:TYR:OH	1.72	0.89
4:A:1985:ARG:HG2	4:A:1985:ARG:HH11	1.36	0.89
4:A:1838:ALA:CB	4:A:1868:TYR:OH	2.22	0.88
4:A:2151:LEU:HD11	4:A:2204:PHE:CE2	2.10	0.85
4:A:2151:LEU:CG	4:A:2204:PHE:HE2	1.89	0.85
4:A:2084:PHE:HB3	4:A:2108:MET:CE	2.08	0.84
4:A:1983:LEU:HD12	4:A:1983:LEU:H	1.43	0.83
4:A:1743:GLN:NE2	4:A:1745:LEU:HB2	1.92	0.83
4:A:1829:ARG:C	4:A:1832:ASP:OD2	2.22	0.82
4:A:2151:LEU:CG	4:A:2204:PHE:CE2	2.62	0.82
4:A:1841:SER:O	4:A:1842:HIS:CD2	2.32	0.82
4:A:2084:PHE:CG	4:A:2108:MET:HE1	2.14	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1837:ASP:O	4:A:1868:TYR:CD1	2.32	0.82
4:A:1838:ALA:CA	4:A:1868:TYR:OH	2.30	0.79
4:A:2084:PHE:HB3	4:A:2108:MET:HE1	1.64	0.79
4:A:2151:LEU:CD1	4:A:2204:PHE:CZ	2.44	0.79
4:A:1743:GLN:HE22	4:A:1745:LEU:HB2	1.45	0.79
4:A:1838:ALA:O	4:A:1868:TYR:CE2	2.35	0.79
4:A:1829:ARG:HH11	4:A:1829:ARG:CB	1.96	0.77
4:A:2084:PHE:CB	4:A:2108:MET:HE1	2.14	0.77
4:A:1829:ARG:HB2	4:A:1829:ARG:NH1	1.98	0.77
4:A:1833:LEU:HG	4:A:1982:ILE:HG22	1.65	0.77
4:A:1842:HIS:HB2	4:A:2006:GLU:OE2	1.84	0.77
4:A:2084:PHE:CE1	4:A:2104:GLY:HA2	2.19	0.77
4:A:1833:LEU:HG	4:A:1982:ILE:CG2	2.15	0.77
4:A:1838:ALA:HA	4:A:1868:TYR:HE1	1.44	0.76
4:A:2084:PHE:HE1	4:A:2104:GLY:HA2	1.51	0.75
4:A:1791:ILE:CD1	4:A:2037:MET:HE1	2.16	0.75
4:A:710:TYR:HD1	4:A:2099:TYR:HB2	1.50	0.75
4:A:710:TYR:CE1	4:A:2099:TYR:CB	2.70	0.74
4:A:1838:ALA:HA	4:A:1868:TYR:OH	1.84	0.74
4:A:177:GLU:OE2	4:A:1954:HIS:CE1	2.41	0.74
4:A:1983:LEU:HD12	4:A:1983:LEU:N	2.02	0.74
4:A:176:GLU:HB2	4:A:1958:ARG:NH2	2.04	0.71
4:A:1838:ALA:O	4:A:1868:TYR:CZ	2.43	0.71
4:A:1832:ASP:OD2	4:A:1832:ASP:N	2.24	0.69
4:A:1185:HIS:C	4:A:1186:SER:HG	1.90	0.69
4:A:2152:ILE:HG22	4:A:2153:LYS:N	2.08	0.69
4:A:338:SER:HG	4:A:341:THR:HG1	1.38	0.69
4:A:1017:ARG:NE	4:A:2088:GLU:OE2	2.26	0.68
4:A:176:GLU:HB2	4:A:1958:ARG:HH22	1.59	0.67
4:A:1841:SER:O	4:A:1842:HIS:CG	2.47	0.67
4:A:2103:ARG:O	4:A:2103:ARG:HG3	1.94	0.67
4:A:1828:LEU:HD21	4:A:1833:LEU:HD22	1.78	0.66
4:A:1830:GLN:O	4:A:1830:GLN:NE2	2.30	0.65
4:A:1030:LEU:HD12	4:A:1042:ILE:HG13	1.78	0.64
4:A:1927:ILE:HG23	4:A:1968:VAL:HG23	1.79	0.64
4:A:1983:LEU:H	4:A:1983:LEU:CD1	2.11	0.64
4:A:1833:LEU:HD21	4:A:1987:LEU:HD11	1.80	0.63
4:A:312:HIS:HD2	4:A:506:GLN:HE22	1.45	0.63
4:A:1833:LEU:HD23	4:A:1984:ILE:CD1	2.28	0.63
4:A:710:TYR:HE1	4:A:2099:TYR:CB	2.12	0.63
4:A:2151:LEU:CD1	4:A:2204:PHE:HE2	1.71	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1837:ASP:O	4:A:1868:TYR:CE1	2.52	0.62
4:A:707:ARG:NH1	4:A:1603:MET:O	2.33	0.62
4:A:517:ASN:ND2	4:A:534:MET:O	2.32	0.61
4:A:1985:ARG:HG2	4:A:1985:ARG:NH1	2.08	0.61
4:A:1328:ASP:HB3	4:A:1392:ASN:HD21	1.65	0.61
4:A:250:ASP:OD2	4:A:797:LYS:NZ	2.30	0.61
4:A:1838:ALA:C	4:A:1868:TYR:CZ	2.78	0.61
4:A:1784:ARG:NH2	4:A:1995:PHE:O	2.34	0.60
4:A:1824:ARG:HH21	4:A:1996:SER:H	1.50	0.60
4:A:813:ARG:NH2	4:A:984:LEU:O	2.33	0.59
4:A:710:TYR:HE1	4:A:2099:TYR:CG	2.20	0.59
4:A:114:ARG:HH22	4:A:124:ILE:H	1.50	0.59
4:A:2046:ASN:HA	4:A:2083:ASN:O	2.03	0.58
4:A:2062:ILE:HG23	4:A:2166:LYS:HD2	1.85	0.58
4:A:521:VAL:HG22	4:A:531:ARG:HE	1.68	0.58
4:A:2055:LEU:HB2	4:A:2121:GLU:HB3	1.86	0.58
4:A:102:SER:HB2	4:A:128:ILE:HD13	1.86	0.58
4:A:703:ARG:HD2	4:A:726:GLU:HB3	1.85	0.57
4:A:981:ARG:NH1	4:A:1080:ASP:OD1	2.36	0.57
4:A:1380:GLU:OE1	4:A:1383:ASN:ND2	2.37	0.57
4:A:2152:ILE:C	4:A:2154:LEU:H	2.12	0.57
4:A:1469:GLU:HG3	4:A:1628:ARG:HG2	1.86	0.57
4:A:1828:LEU:HD21	4:A:1833:LEU:CD2	2.35	0.57
4:A:1838:ALA:CB	4:A:1868:TYR:HH	2.16	0.56
4:A:719:LYS:NZ	4:A:1006:GLU:OE2	2.38	0.56
4:A:221:LEU:HD13	4:A:243:ILE:HG23	1.88	0.56
4:A:2148:VAL:O	4:A:2152:ILE:HD12	2.06	0.56
4:A:1986:SER:O	4:A:1990:LEU:HD12	2.05	0.55
4:A:1815:ARG:NH1	4:A:1827:ASP:O	2.40	0.55
4:A:1575:SER:O	4:A:1580:ASN:ND2	2.40	0.54
4:A:1830:GLN:HA	4:A:1984:ILE:HG12	1.89	0.54
4:A:2152:ILE:HG13	4:A:2161:SER:OG	2.06	0.54
4:A:136:ARG:O	4:A:1615:ASN:ND2	2.39	0.54
4:A:2015:PHE:CE2	4:A:2045:LEU:HD11	2.41	0.54
4:A:1834:ASP:C	4:A:1836:TYR:N	2.61	0.54
4:A:2147:ALA:O	4:A:2151:LEU:HB2	2.08	0.54
4:A:2152:ILE:CG1	4:A:2161:SER:OG	2.56	0.54
4:A:62:ILE:HD12	4:A:63:ARG:HG2	1.90	0.54
4:A:1879:ASN:O	4:A:1914:ASN:ND2	2.41	0.54
4:A:864:LEU:O	4:A:867:GLN:HG3	2.08	0.54
4:A:1834:ASP:C	4:A:1836:TYR:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:92:ASP:HB3	4:A:128:ILE:HG22	1.88	0.54
4:A:2150:SER:O	4:A:2154:LEU:HB2	2.07	0.53
4:A:2120:ARG:NH1	4:A:2121:GLU:OE2	2.41	0.53
4:A:1401:ARG:HB2	4:A:1573:ILE:HD11	1.91	0.53
4:A:177:GLU:CD	4:A:1954:HIS:CE1	2.86	0.53
4:A:603:ARG:NH1	4:A:751:PHE:O	2.42	0.53
4:A:706:LEU:HD11	4:A:2094:PRO:HB2	1.91	0.53
4:A:2087:GLY:HA2	4:A:2098:ILE:O	2.09	0.53
4:A:2151:LEU:CD2	4:A:2208:ILE:HD11	2.39	0.53
4:A:177:GLU:OE1	4:A:1954:HIS:CE1	2.61	0.53
4:A:2151:LEU:HD22	4:A:2208:ILE:HD11	1.89	0.53
4:A:1829:ARG:H	4:A:1832:ASP:CG	2.17	0.53
4:A:2152:ILE:O	4:A:2154:LEU:N	2.41	0.53
4:A:2118:ILE:O	4:A:2122:THR:OG1	2.26	0.52
4:A:2155:LEU:HD13	4:A:2233:LEU:HD23	1.90	0.52
4:A:1590:THR:O	4:A:1594:SER:OG	2.26	0.52
4:A:850:ARG:HD3	4:A:897:ARG:HH21	1.74	0.52
4:A:665:ASN:HD22	4:A:1226:MET:HB3	1.74	0.52
4:A:1008:GLU:OE1	4:A:1054:LYS:NZ	2.42	0.52
4:A:1773:HIS:NE2	4:A:2011:LYS:O	2.42	0.52
4:A:727:LEU:N	4:A:727:LEU:CD2	2.73	0.52
4:A:525:ASN:OD1	4:A:529:THR:OG1	2.27	0.52
4:A:952:GLN:NE2	4:A:954:THR:OG1	2.43	0.51
4:A:1404:VAL:O	4:A:1424:ARG:NH1	2.43	0.51
4:A:2165:ASP:OD1	4:A:2181:TYR:OH	2.27	0.51
3:H:13:U:H5''	3:H:14:A:H5'	1.93	0.51
4:A:2064:CYS:SG	4:A:2067:SER:N	2.81	0.51
4:A:2146:GLU:O	4:A:2150:SER:HB2	2.10	0.51
4:A:24:ASP:CG	4:A:1901:ARG:NH2	2.67	0.51
4:A:2154:LEU:HD11	4:A:2199:ILE:HD13	1.92	0.51
4:A:919:LEU:HD13	4:A:1478:MET:HG3	1.93	0.51
4:A:1833:LEU:HG	4:A:1982:ILE:HG21	1.90	0.51
4:A:1485:VAL:HG23	4:A:1488:ARG:HH21	1.76	0.51
4:A:1791:ILE:HD11	4:A:2037:MET:CE	2.33	0.50
4:A:1985:ARG:NH1	4:A:1985:ARG:CG	2.73	0.50
4:A:1055:MET:HE2	4:A:1206:ILE:HG12	1.94	0.50
4:A:224:GLU:OE2	4:A:242:LYS:NZ	2.42	0.50
4:A:1437:SER:OG	4:A:1438:LEU:N	2.44	0.50
4:A:1912:PHE:HB3	4:A:1968:VAL:HG21	1.94	0.50
4:A:316:ASN:HB3	4:A:322:PHE:HE2	1.77	0.50
4:A:1400:LEU:HD22	4:A:1573:ILE:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1715:SER:HB3	4:A:1724:LEU:HD12	1.94	0.50
4:A:2151:LEU:HB2	4:A:2204:PHE:HZ	1.77	0.49
4:A:2187:PRO:HB3	4:A:2251:MET:HE2	1.94	0.49
4:A:354:GLY:HA3	4:A:389:ASN:HD22	1.77	0.49
4:A:655:MET:HE3	4:A:670:ILE:HG12	1.93	0.49
4:A:2152:ILE:C	4:A:2154:LEU:N	2.70	0.49
4:A:2193:ASN:HB2	4:A:2196:THR:HB	1.94	0.49
4:A:1599:PRO:HB3	4:A:1736:TYR:HE1	1.78	0.49
4:A:177:GLU:OE1	4:A:1954:HIS:HE1	1.95	0.49
4:A:1026:ALA:O	4:A:1030:LEU:HG	2.13	0.48
4:A:619:LYS:NZ	4:A:625:LEU:O	2.47	0.48
4:A:1918:ILE:HG22	4:A:1944:HIS:HD2	1.79	0.48
4:A:2118:ILE:O	4:A:2122:THR:CB	2.62	0.48
4:A:332:GLN:HE21	4:A:349:LYS:HA	1.76	0.48
4:A:1450:ARG:HD3	4:A:1486:ILE:HG21	1.95	0.48
4:A:1837:ASP:HB3	4:A:1982:ILE:HD12	1.95	0.48
4:A:295:SER:OG	4:A:300:ASP:OD2	2.32	0.48
4:A:2160:TRP:HD1	4:A:2222:MET:HG3	1.78	0.48
4:A:150:PRO:HD2	4:A:1754:GLN:HE22	1.79	0.48
4:A:1930:ARG:HG2	4:A:1938:VAL:HG12	1.96	0.48
4:A:90:ILE:HB	4:A:126:ILE:HG22	1.95	0.48
4:A:99:ASN:O	4:A:102:SER:OG	2.31	0.48
4:A:150:PRO:HG2	4:A:1751:ALA:HB2	1.96	0.47
4:A:1743:GLN:HE21	4:A:1745:LEU:H	1.62	0.47
4:A:1834:ASP:O	4:A:1836:TYR:N	2.48	0.47
4:A:1926:TYR:HE1	4:A:1970:VAL:HG22	1.79	0.47
4:A:401:ILE:HD13	4:A:415:PHE:HZ	1.80	0.47
4:A:1056:GLU:HG2	4:A:1236:LYS:HG2	1.96	0.47
4:A:1876:GLY:HA3	4:A:1881:LEU:HA	1.96	0.47
4:A:1650:VAL:HA	4:A:1653:LYS:HG2	1.96	0.47
4:A:1839:MET:SD	4:A:1839:MET:C	2.97	0.47
4:A:2015:PHE:HE2	4:A:2045:LEU:HD11	1.79	0.47
4:A:176:GLU:OE1	4:A:1958:ARG:NH1	2.48	0.47
4:A:1017:ARG:CZ	4:A:2088:GLU:OE2	2.63	0.47
4:A:1322:PRO:HD3	4:A:1557:MET:HE3	1.96	0.47
4:A:0:GLY:H	4:A:160:GLN:HE22	1.61	0.46
4:A:961:PHE:CD2	4:A:1144:LEU:HB3	2.50	0.46
4:A:1830:GLN:NE2	4:A:1830:GLN:C	2.73	0.46
4:A:2152:ILE:HD11	4:A:2226:PHE:CZ	2.50	0.46
4:A:308:ILE:HD12	4:A:571:ILE:HD11	1.96	0.46
4:A:1833:LEU:HD13	4:A:1833:LEU:HA	1.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2084:PHE:CD1	4:A:2108:MET:CE	2.91	0.46
4:A:1865:ILE:HB	4:A:1872:ILE:HG22	1.97	0.46
4:A:2083:ASN:HA	4:A:2102:LYS:O	2.15	0.46
4:A:1171:ILE:HG13	4:A:1178:ILE:HD12	1.97	0.46
4:A:517:ASN:O	4:A:521:VAL:HB	2.15	0.46
4:A:1780:ASP:CA	4:A:2077:LEU:O	2.64	0.46
4:A:2136:PHE:HA	4:A:2141:ASN:HD22	1.80	0.45
4:A:940:HIS:NE2	4:A:964:GLU:OE2	2.41	0.45
4:A:2151:LEU:HD21	4:A:2204:PHE:HE2	1.66	0.45
4:A:1824:ARG:NH2	4:A:1994:ILE:O	2.49	0.45
4:A:2158:ASN:HD21	4:A:2160:TRP:HE3	1.64	0.45
4:A:1072:LYS:HD2	4:A:1155:VAL:HG11	1.98	0.45
4:A:1780:ASP:HA	4:A:2077:LEU:O	2.17	0.45
4:A:1770:LEU:HD21	4:A:2014:HIS:O	2.16	0.45
4:A:178:PHE:HD2	4:A:179:LEU:HD12	1.82	0.45
4:A:845:LYS:HB2	4:A:907:ILE:HG22	1.98	0.45
4:A:151:THR:HG21	4:A:1747:GLY:HA3	1.99	0.45
4:A:998:LEU:HD21	4:A:1710:ILE:HD11	1.98	0.45
4:A:1289:PRO:HG3	4:A:1729:LEU:HA	1.98	0.45
4:A:343:ALA:HB1	4:A:414:LEU:HD22	1.99	0.45
4:A:612:LEU:HD23	4:A:1298:ILE:HD11	1.98	0.45
4:A:988:GLU:HG3	4:A:990:ILE:HG12	1.97	0.45
4:A:1369:GLN:H	4:A:1369:GLN:HG2	1.57	0.45
4:A:664:SER:OG	4:A:665:ASN:N	2.50	0.44
4:A:2088:GLU:O	4:A:2088:GLU:HG3	2.16	0.44
4:A:2014:HIS:CE1	4:A:2016:SER:OG	2.70	0.44
4:A:2084:PHE:CD2	4:A:2084:PHE:C	2.95	0.44
4:A:1391:ASP:OD1	4:A:1391:ASP:N	2.51	0.44
4:A:1830:GLN:N	4:A:1984:ILE:HG12	2.33	0.44
4:A:700:GLN:HB3	4:A:703:ARG:HH21	1.83	0.44
4:A:1881:LEU:HB2	4:A:1969:CYS:HB2	2.00	0.44
4:A:821:ILE:HG12	4:A:980:GLU:HB2	2.00	0.44
4:A:933:ILE:HG21	4:A:973:ALA:HB2	1.99	0.44
4:A:2084:PHE:CD2	4:A:2084:PHE:O	2.70	0.44
4:A:1776:ASP:OD2	4:A:1998:SER:OG	2.27	0.43
4:A:1794:GLU:HG3	4:A:2024:PRO:HG3	2.00	0.43
4:A:1771:ILE:HD13	4:A:1771:ILE:HA	1.82	0.43
4:A:398:GLN:OE1	4:A:531:ARG:NH1	2.51	0.43
4:A:1605:MET:HE3	4:A:1710:ILE:HG22	2.01	0.43
4:A:1669:ILE:HD12	4:A:1684:GLU:HG2	1.99	0.43
4:A:1830:GLN:CA	4:A:1984:ILE:HG12	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:985:ASN:HB3	4:A:988:GLU:HB3	2.01	0.43
4:A:2050:ILE:HD12	4:A:2082:MET:HE1	2.00	0.43
4:A:2081:PRO:HG3	4:A:2106:ARG:HH21	1.84	0.43
4:A:313:ASN:HB2	4:A:539:ASN:HD21	1.84	0.43
4:A:1357:LEU:HD23	4:A:1360:LEU:HD12	2.00	0.43
4:A:10:LEU:O	4:A:14:ASN:ND2	2.51	0.43
4:A:1431:LYS:NZ	4:A:1509:GLU:OE1	2.44	0.43
4:A:1806:TYR:OH	4:A:1825:THR:OG1	2.26	0.42
4:A:754:LYS:HE2	4:A:953:LYS:HE3	2.01	0.42
4:A:766:LEU:HD13	4:A:959:GLU:HB3	2.01	0.42
4:A:125:GLU:HG2	4:A:144:ARG:HB3	2.01	0.42
4:A:1833:LEU:O	4:A:1836:TYR:CB	2.56	0.42
4:A:863:ILE:HG22	4:A:864:LEU:N	2.35	0.42
4:A:2084:PHE:CB	4:A:2108:MET:CE	2.83	0.42
4:A:806:ASN:ND2	4:A:1158:CYS:SG	2.92	0.42
4:A:312:HIS:CD2	4:A:506:GLN:HE22	2.32	0.42
4:A:643:LYS:HD2	4:A:646:LEU:HD22	2.02	0.42
4:A:150:PRO:HD2	4:A:1754:GLN:NE2	2.35	0.41
4:A:203:LYS:HA	4:A:208:LYS:HE3	2.01	0.41
4:A:1526:ASP:HA	4:A:1529:ILE:HG22	2.01	0.41
4:A:193:TRP:NE1	4:A:822:GLU:OE2	2.43	0.41
4:A:1829:ARG:CB	4:A:1829:ARG:NH1	2.73	0.41
4:A:1830:GLN:C	4:A:1830:GLN:HE21	2.28	0.41
4:A:2215:ASP:O	4:A:2220:ASN:ND2	2.53	0.41
4:A:287:ARG:NH2	4:A:674:PHE:O	2.40	0.41
4:A:1816:THR:HG21	4:A:1835:LYS:HG2	2.03	0.41
4:A:1820:PRO:HB3	4:A:2000:ILE:HG23	2.02	0.41
4:A:2136:PHE:HA	4:A:2141:ASN:ND2	2.35	0.41
4:A:321:THR:HG21	4:A:357:ALA:HB1	2.02	0.41
4:A:2245:SER:OG	4:A:2246:GLU:N	2.49	0.41
4:A:1067:GLN:OE1	4:A:1223:GLN:NE2	2.54	0.41
2:X:11:U:H2'	2:X:12:A:C8	2.55	0.41
4:A:521:VAL:HG22	4:A:531:ARG:NE	2.32	0.41
4:A:863:ILE:CG2	4:A:864:LEU:N	2.81	0.41
4:A:901:PRO:HD2	4:A:1133:ASN:HD22	1.86	0.41
4:A:1770:LEU:HD11	4:A:2017:LYS:HB2	2.03	0.41
4:A:2107:HIS:O	4:A:2112:ASN:ND2	2.49	0.41
4:A:260:LYS:HE2	4:A:260:LYS:HB3	1.90	0.40
4:A:1928:THR:HG22	4:A:1967:PRO:HB3	2.03	0.40
4:A:1931:LYS:HE2	4:A:1931:LYS:HB2	1.94	0.40
2:X:11:U:O2	4:A:380:ASN:ND2	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1819:ILE:HG22	4:A:2000:ILE:HD11	2.03	0.40
4:A:1839:MET:SD	4:A:1839:MET:O	2.79	0.40
4:A:2012:LYS:HE3	4:A:2012:LYS:HB2	1.25	0.40

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
4	A	2116/2285 (93%)	1974 (93%)	139 (7%)	3 (0%)	48 75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	2153	LYS
4	A	1186	SER
4	A	1969	CYS

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
4	A	1968/2107 (93%)	1939 (98%)	29 (2%)	57 73

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	521	VAL
4	A	726	GLU
4	A	727	LEU
4	A	736	VAL
4	A	862	LYS
4	A	863	ILE
4	A	864	LEU
4	A	1030	LEU
4	A	1405	LEU
4	A	1470	LEU
4	A	1743	GLN
4	A	1829	ARG
4	A	1830	GLN
4	A	1832	ASP
4	A	1833	LEU
4	A	1834	ASP
4	A	1835	LYS
4	A	1839	MET
4	A	1840	LYS
4	A	1918	ILE
4	A	1958	ARG
4	A	1983	LEU
4	A	1984	ILE
4	A	1985	ARG
4	A	2011	LYS
4	A	2012	LYS
4	A	2150	SER
4	A	2152	ILE
4	A	2154	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	4	GLN
4	A	14	ASN
4	A	46	ASN
4	A	160	GLN
4	A	184	HIS
4	A	312	HIS
4	A	313	ASN
4	A	389	ASN
4	A	489	ASN
4	A	565	HIS

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Mol	Chain	Res	Type
4	A	757	HIS
4	A	806	ASN
4	A	823	ASN
4	A	825	ASN
4	A	952	GLN
4	A	1058	ASN
4	A	1112	ASN
4	A	1133	ASN
4	A	1190	GLN
4	A	1223	GLN
4	A	1243	ASN
4	A	1392	ASN
4	A	1571	GLN
4	A	1672	ASN
4	A	1693	GLN
4	A	1743	GLN
4	A	1754	GLN
4	A	1842	HIS
4	A	1914	ASN
4	A	1924	ASN
4	A	1944	HIS
4	A	1954	HIS
4	A	1963	ASN
4	A	2071	ASN
4	A	2141	ASN
4	A	2209	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	U	9/10 (90%)	4 (44%)	0
2	X	4/8 (50%)	0	0
3	H	12/16 (75%)	3 (25%)	0
All	All	25/34 (73%)	7 (28%)	0

All (7) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	U	6	U
1	U	7	G
1	U	8	U

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Mol	Chain	Res	Type
1	U	9	G
3	H	9	A
3	H	10	C
3	H	15	C

There are no RNA pucker outliers to report.

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 2 ligands modelled in this entry, 2 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

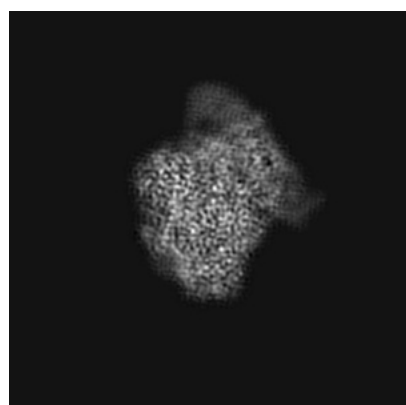
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11093. These allow visual inspection of the internal detail of the map and identification of artifacts.

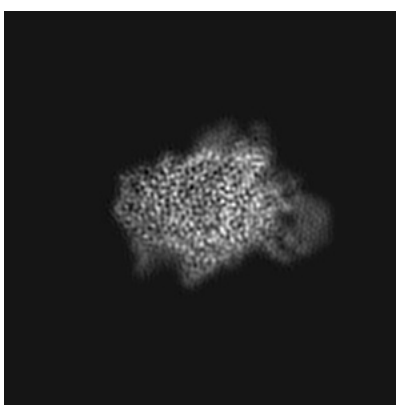
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

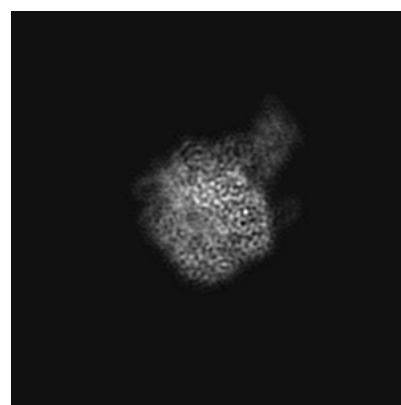
6.1.1 Primary map



X



Y

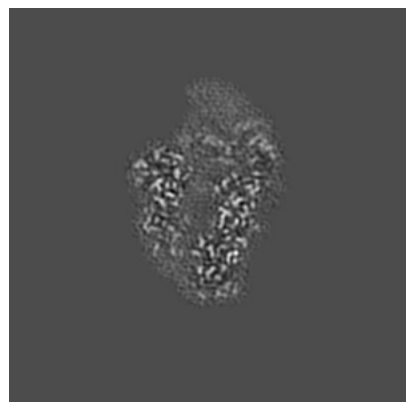


Z

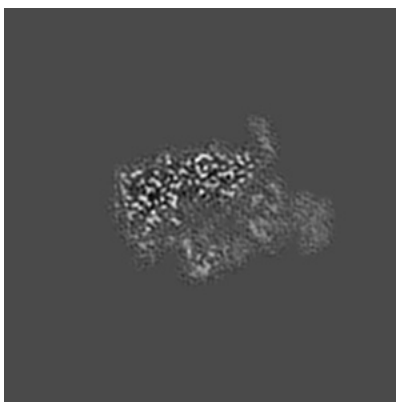
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

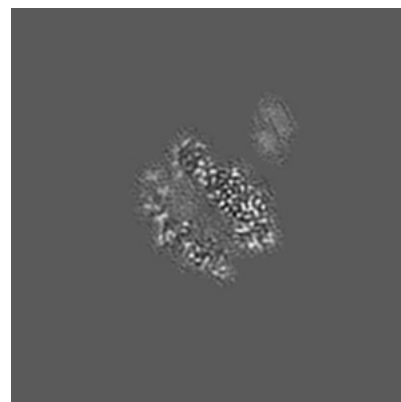
6.2.1 Primary map



X Index: 150



Y Index: 150

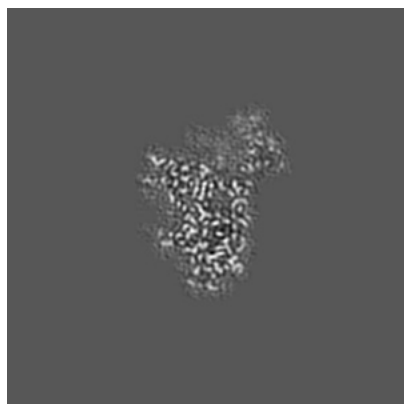


Z Index: 150

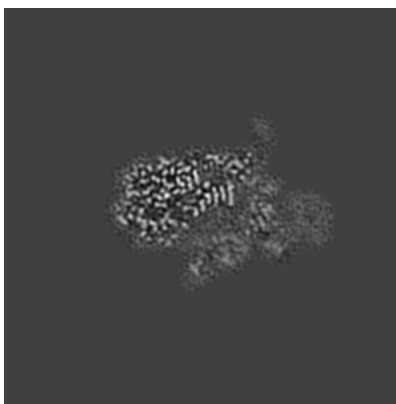
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

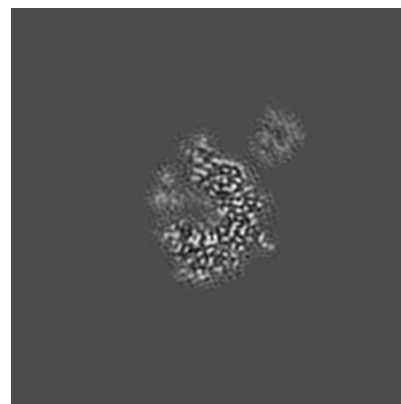
6.3.1 Primary map



X Index: 170



Y Index: 158

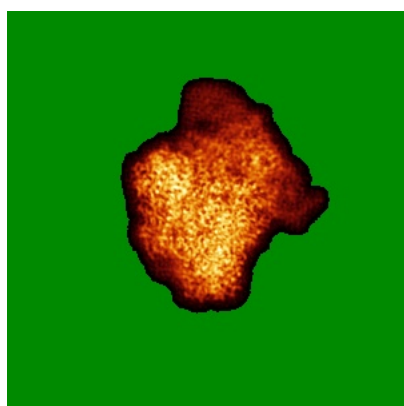


Z Index: 167

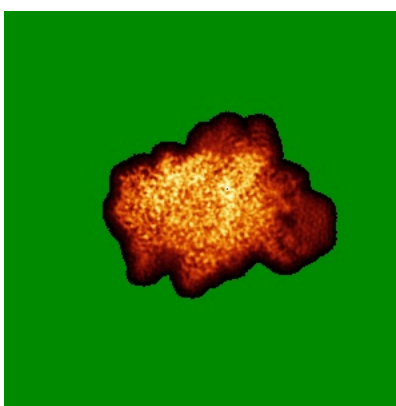
The images above show the largest variance slices of the map in three orthogonal directions.

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

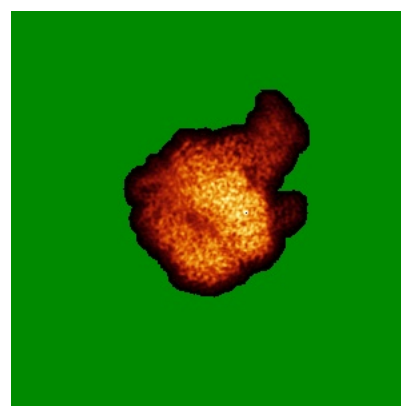
6.4.1 Primary map



X



Y

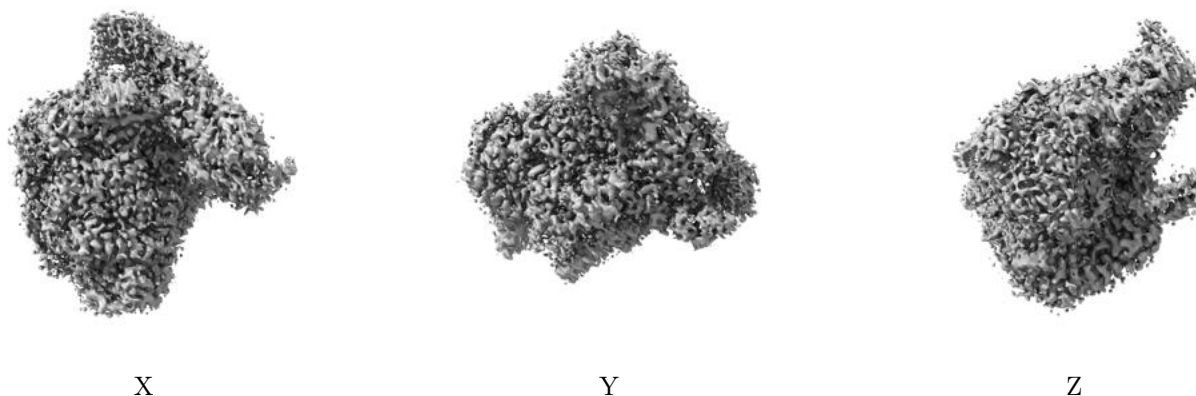


Z

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

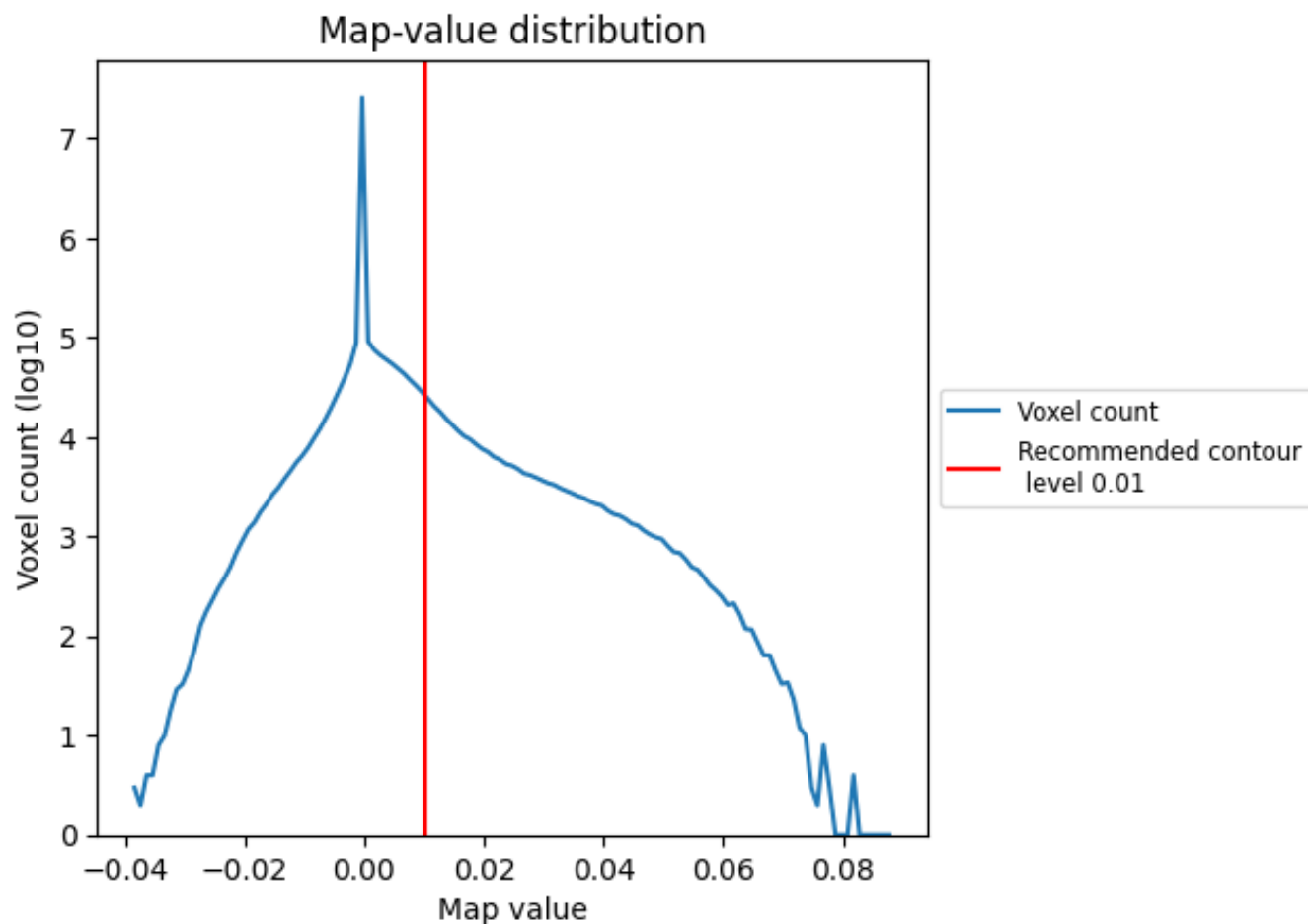
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

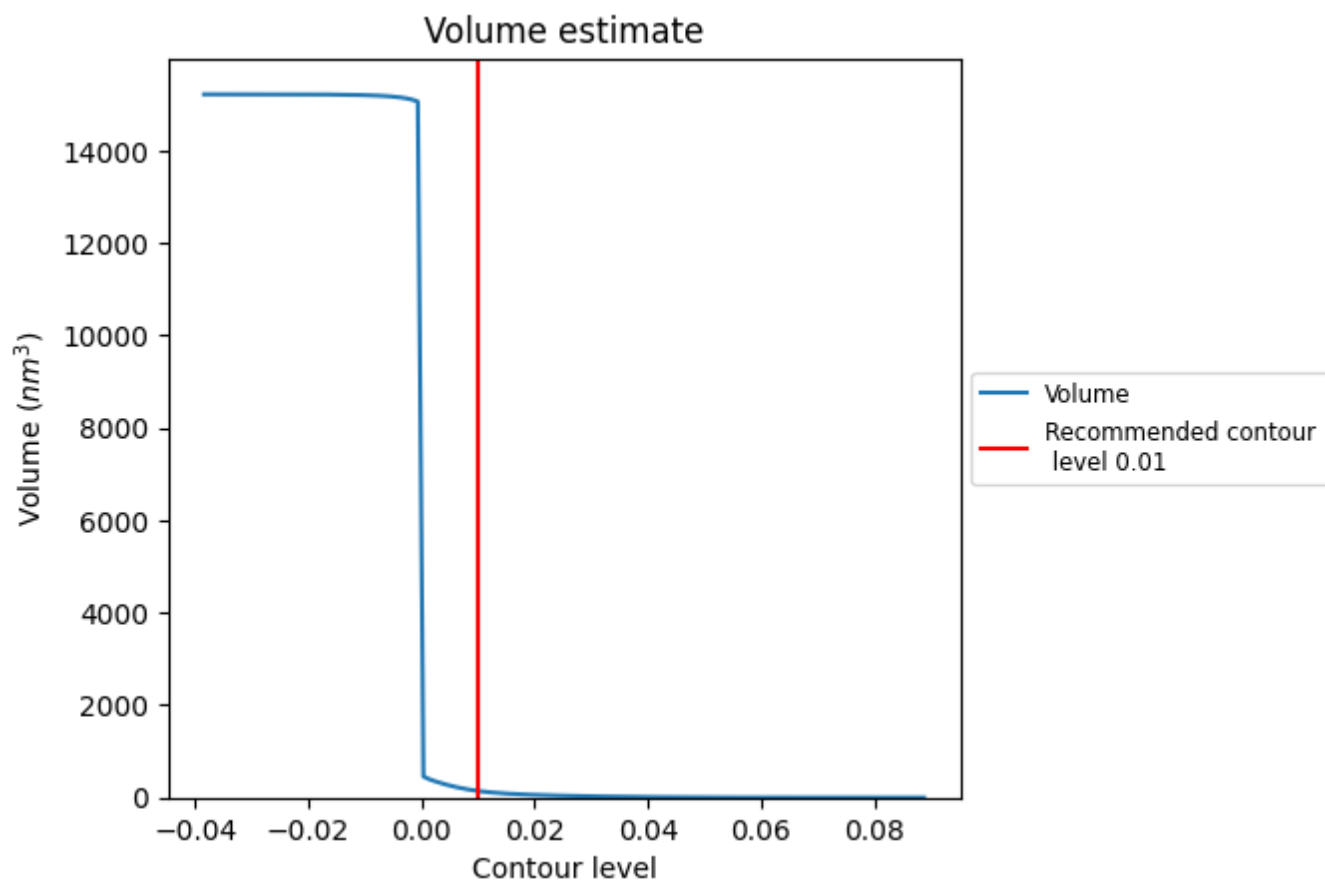
This section contains the results of statistical analysis of the map.

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.

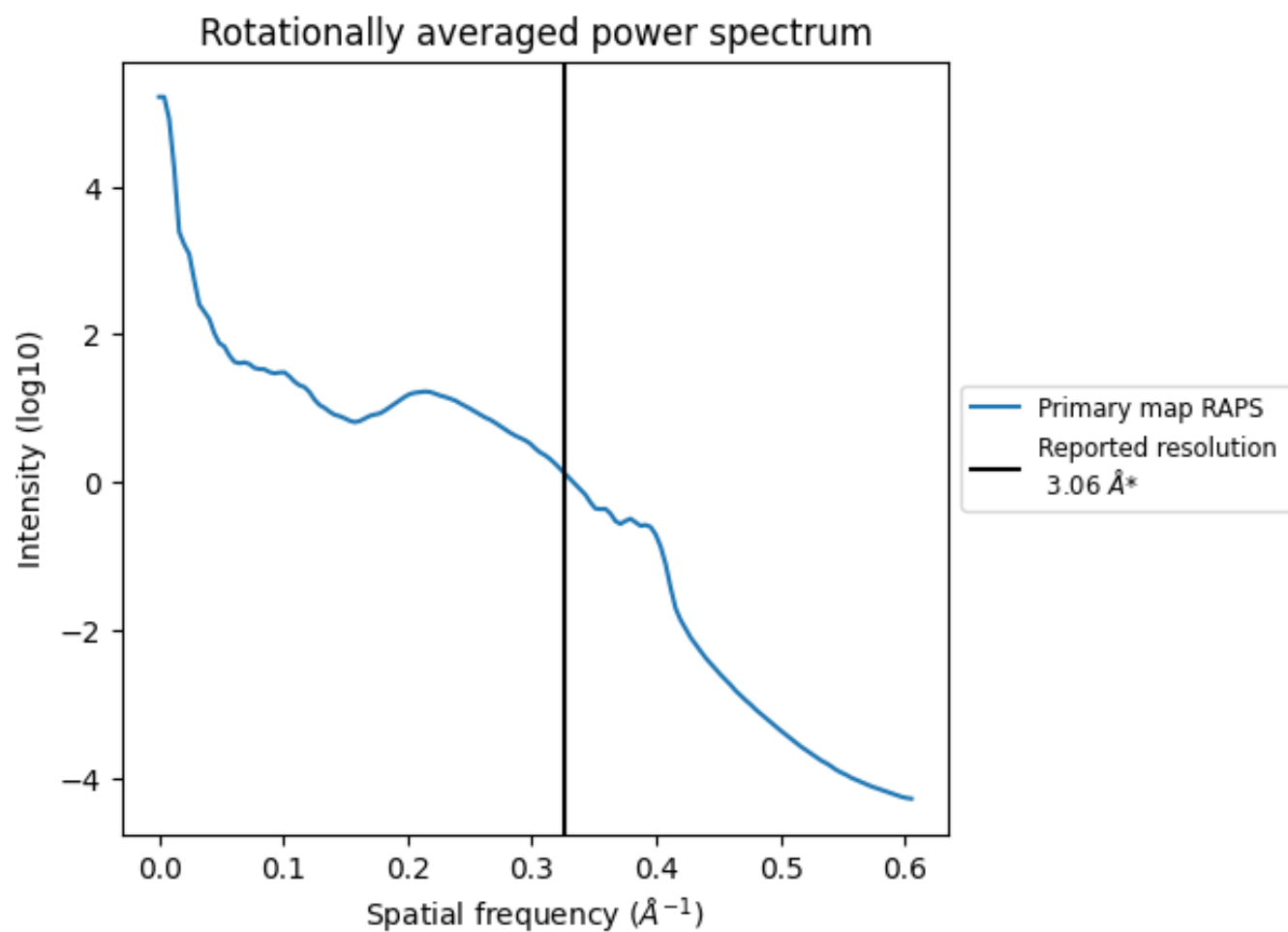
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 143 nm³; this corresponds to an approximate mass of 130 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 ⓘ

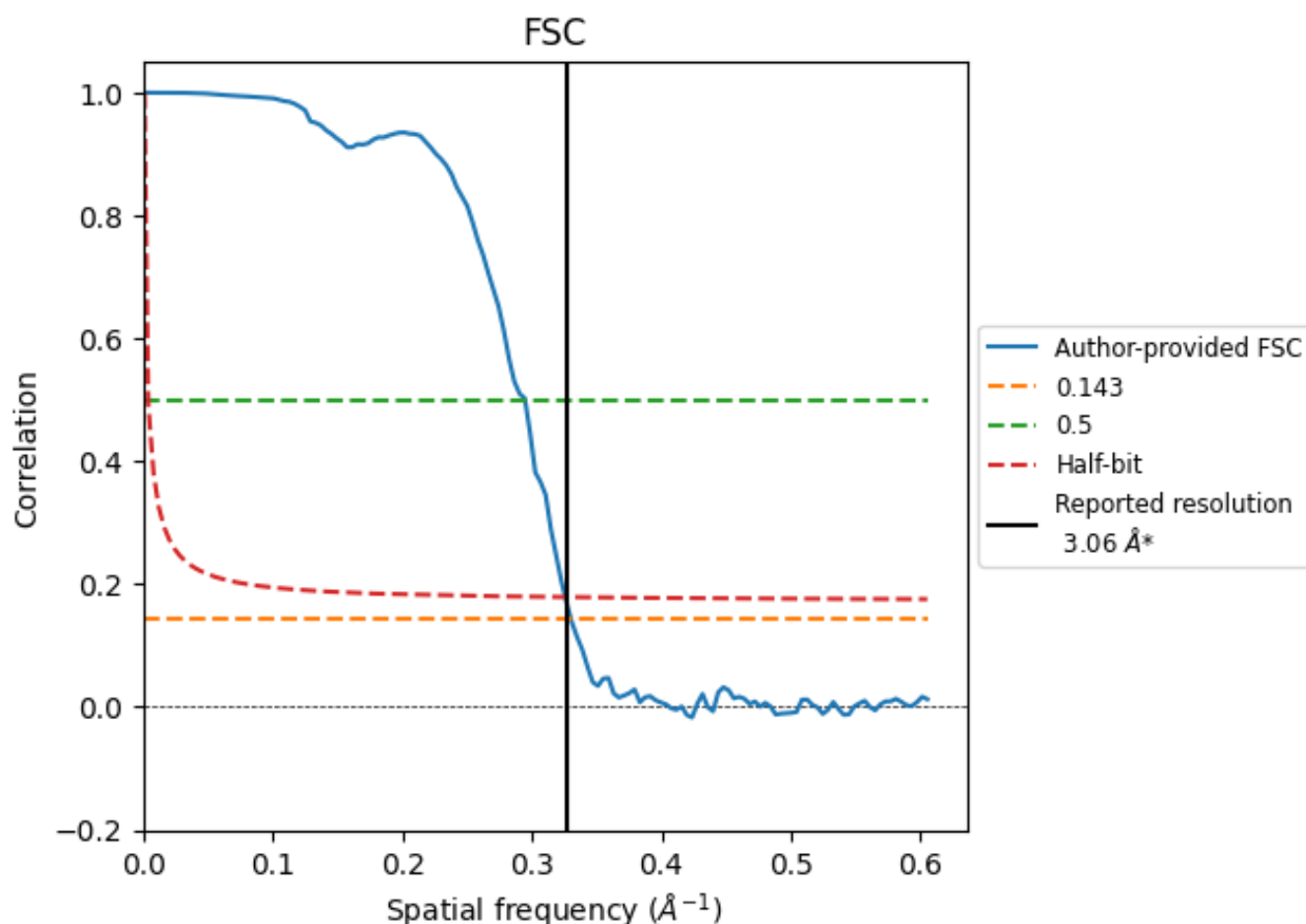


*Reported resolution corresponds to spatial frequency of 0.327 Å⁻¹

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 0.327 Å⁻¹

8.2 Resolution estimates [i](#)

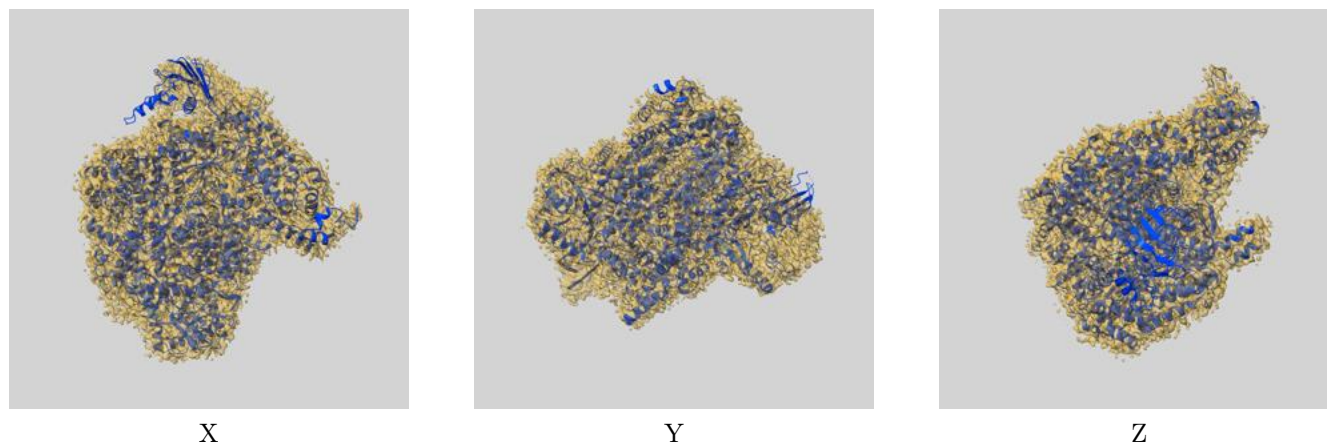
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.06	-	-
Author-provided FSC curve	3.03	3.39	3.07
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

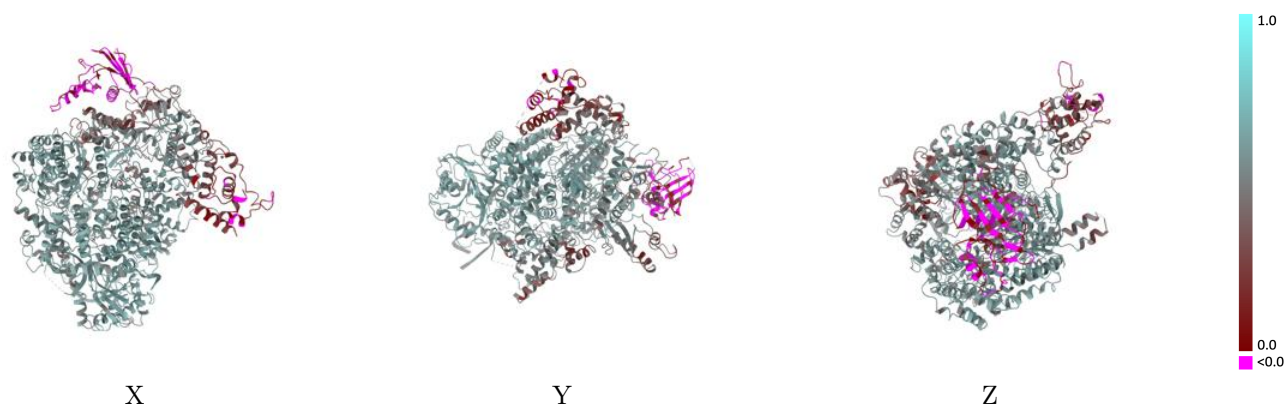
This section contains information regarding the fit between EMDB map EMD-11093 and PDB model 6Z6G. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



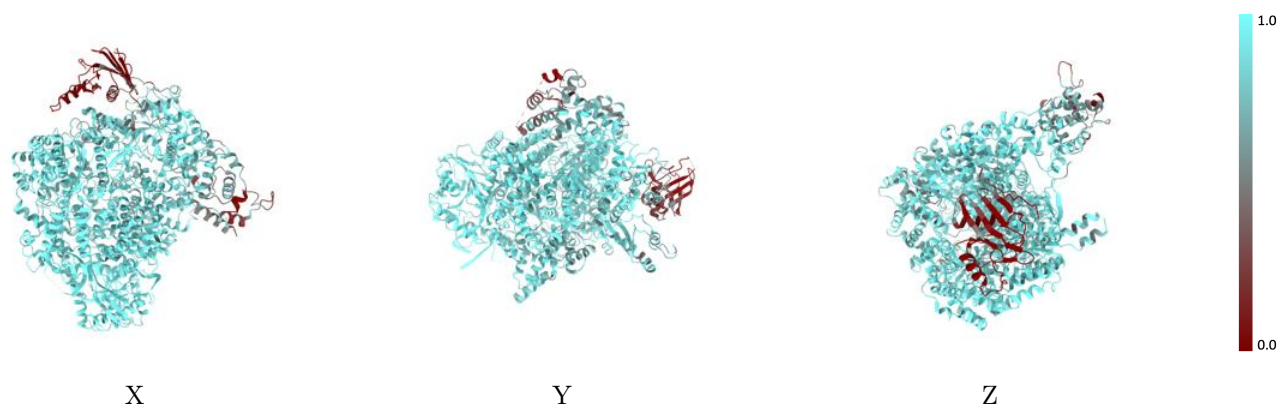
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



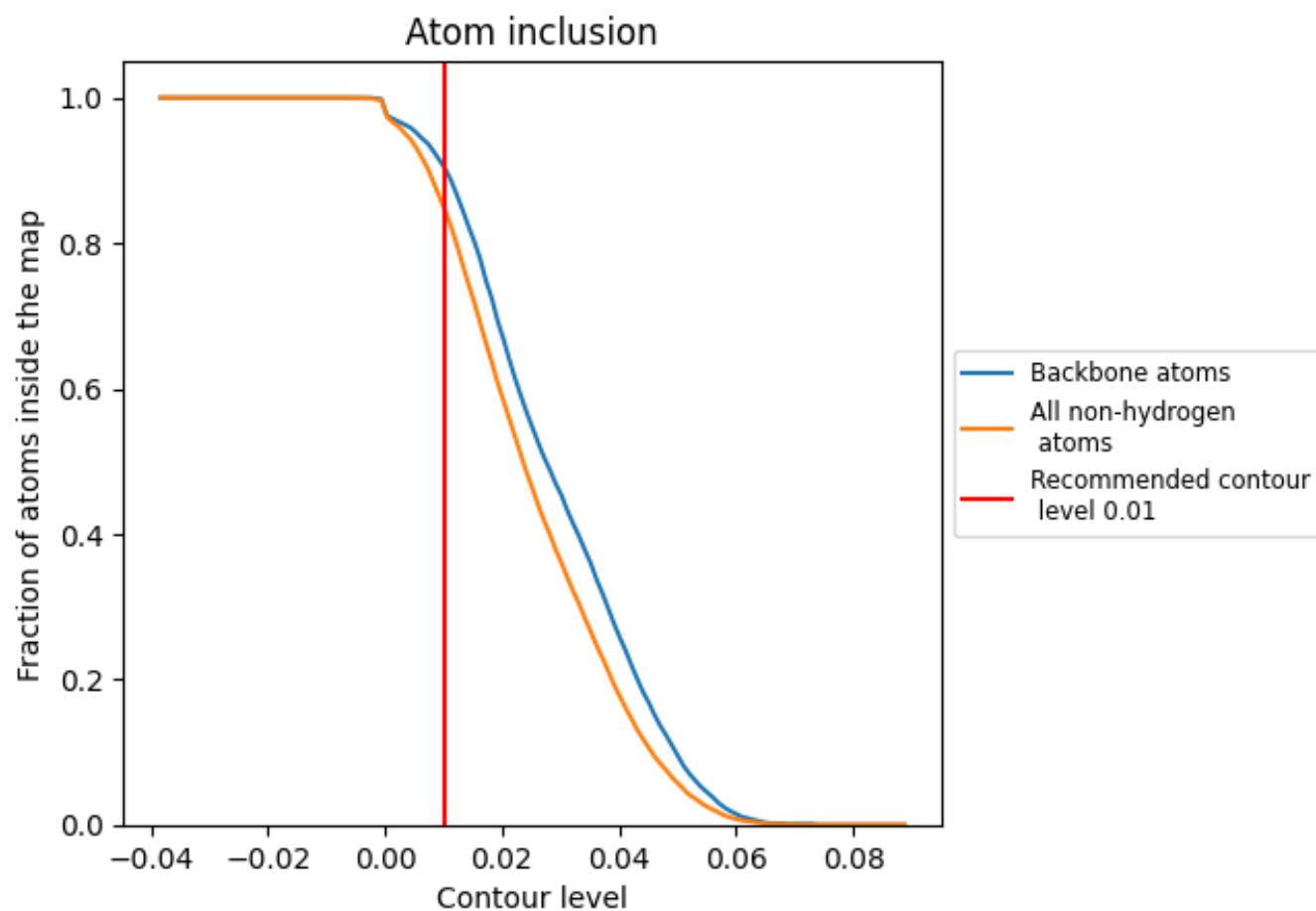
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8500	0.4990
A	0.8460	0.4970
H	0.9820	0.5870
U	0.9860	0.5910
X	0.9800	0.5130

