



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:37 AM UTC

PDB ID : 8RDE / pdb_00008rde
EMDB ID : EMD-19070
Title : STRUCTURE OF THE MOUSE FCGBP DIMER PROTEIN IN ITS COMPACT CONFORMATION
Authors : Gallego, P.; Hansson, G.C.; Johansson, M.E.V.
Deposited on : 2023-12-08
Resolution : 3.70 Å(reported)

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<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
Mogul : 2022.3.0, CSD as543be (2022)
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

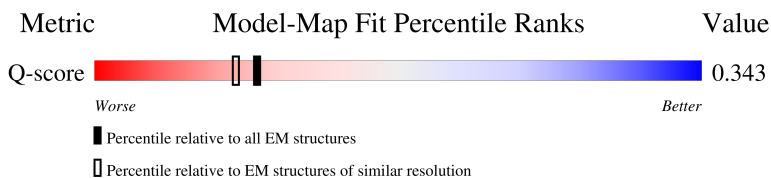
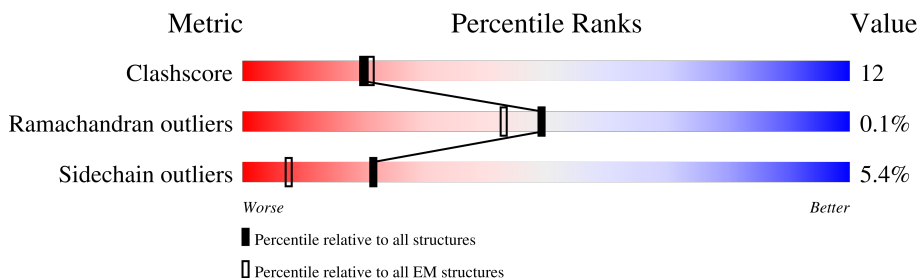
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2587	
1	D	2587	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20050 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.

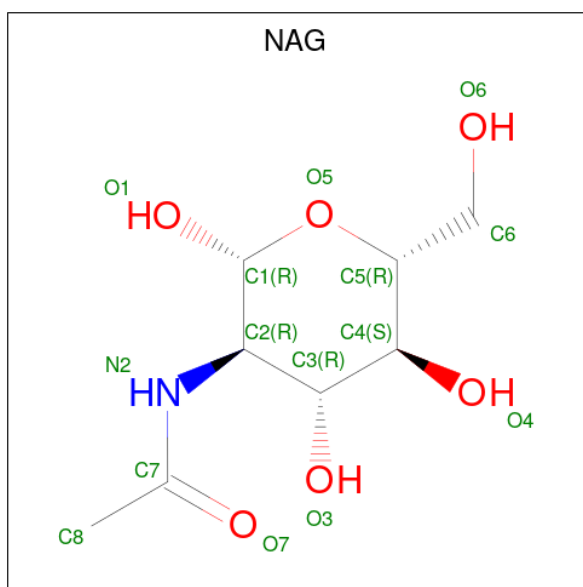
- Molecule 1 is a protein called Fc fragment of IgG binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1342	Total	C	N	O	S	1	0
			9937	6174	1721	1921	121		
1	D	1342	Total	C	N	O	S	1	0
			9937	6174	1721	1921	121		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2584	THR	-	expression tag	UNP E9Q0B5
A	2585	ARG	-	expression tag	UNP E9Q0B5
A	2586	THR	-	expression tag	UNP E9Q0B5
A	2587	ARG	-	expression tag	UNP E9Q0B5
D	2584	THR	-	expression tag	UNP E9Q0B5
D	2585	ARG	-	expression tag	UNP E9Q0B5
D	2586	THR	-	expression tag	UNP E9Q0B5
D	2587	ARG	-	expression tag	UNP E9Q0B5

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



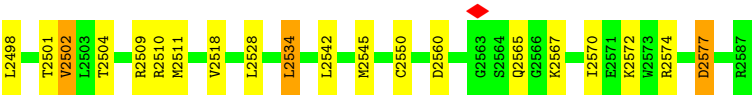
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	
2	D	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
3	A	4	Total 4	Ca 4	0
3	D	4	Total 4	Ca 4	0

S2293	L2180	L2060	L1937	E1826	T1689	G1540	D1374	L1283	ASP	GLY	LEU	ASP	THR	ASN	ASP	ASP	THR	PRO	ASP
R2310	C2161	V2063	V1941	P1827	E1690	P1548	R1378	L1285	HIS	CYS	CYS	HIS	ILE	TYR	ASN	THR	THR	THR	PRO
A2316	L2163	K2067	E1944	P1829	V1694	A1551	V1379	P1285	CYS	GLY	ILE	ASP	GLY	LEU	ASN	THR	ARG	VAL	CYS
A2317	G2165	P2068	T1945	C1832	R1701	T1587	V1381	A1289	PRO	CYS	HIS	GLY	THR	LEU	ASN	THR	THR	THR	THR
A2318	N2166	G2069	I1946	T1833	R1710	V1558	L1382	T1293	GLN	GLY	ALA	CYS	TYR	GLN	GLN	ASP	PHE	ASP	ASP
S2319	F2167	D2070	C1947	T1834	R1717	V1563	L1383	F1293	VAL	CYS	VAL	PRO	GLN	SER	GLN	SER	GLY	ASP	GLY
S2320	N2168	F2073	R1948	E1835	R1719	C1569	P1394	F1295	CYS	SER	VAL	GLY	GLN	GLN	GLN	GLN	ARG	ARG	ARG
L2322	G2169	L2077	L1959	F1840	L1714	E1565	Y1387	V1297	GLY	PHE	GLY	PRO	GLY	GLY	GLY	GLY	PHE	PHE	PHE
T2323	N2170	E2078	S1960	F1843	Y1717	G1566	V1391	V1298	SER	LEU	ALA	SER	LEU	VAL	VAL	VAL	VAL	ASP	ASP
G2324	D2173	K2079	G1961	P1843	G1718	G1569	C1392	T1299	GLY	TYR	ALA	GLY	CYS	LYS	LYS	LYS	ASP	ASP	ASP
C2325	V2176	D2080	D1962	G1847	L1719	D1570	G1393	K1300	VAL	ASN	ALA	GLY	GLY	VAL	ASN	GLY	GLY	MET	MET
T2326	L2177	S2081	C1964	E1848	L1726	D1570	L1394	K1300	VAL	GLY	ALA	GLY	TYR	GLN	ASN	GLY	THR	THR	THR
F2330	V2182	G2082	V1965	I1849	Q1726	S1576	C1395	S1306	THR	LYS	GLN	GLY	GLY	VAL	GLY	GLY	CYS	CYS	CYS
C2335	G2183	K2083	G1968	T1850	R1729	Y1596	V1407	V1309	CYS	ALA	GLN	VAL	GLY	ASP	VAL	ASP	VAL	VAL	VAL
D2336	T2191	D2084	Q1969	A1851	K1730	V1581	M1413	Q1314	VAL	VAL	GLU	VAL	PHE	THR	THR	THR	THR	THR	THR
D2337	P2085	P2085	C1970	P1852	K1736	V1582	M1413	Q1314	THR	THR	PRO	PRO	CYS	ASP	ASP	ASP	ASP	ASP	ASP
H2338	Q2086	Q2086	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
F2339	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2340	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2341	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2342	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2343	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2344	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
L2345	A2195	R2087	G1971	E1853	F1737	G1588	I1417	V1315	ASP	GLY	TRP	TRP	LYS	LYS	LYS	LYS	LYS	LYS	LYS
Q2350	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
D2351	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
C2352	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
V2355	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Q2359	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Y2360	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
M2361	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
P2362	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
V2363	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
N2364	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
S2365	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
S2369	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
S2373	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
E2374	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
R2375	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
C2376	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
C2386	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
C2397	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
E2398	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
I2399	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
V2403	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
Q2406	A2240	C2241	H2242	C2243	G2244	L2245	C2259	A2273	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

C2376	C2386	C2397	E2398	I2399	V2403	C2406	Q2407	I2415	S2416	V2417	G2418	A2419	N2420	T2423	I2431	Y2437	E2438	L2439	S2440	S2441	R2442	L2446	V2450	Y2453	R2454	V2455	D2458	Q2459	Y2459	Q2460	P2461	C2462	K2471	V2472	H2473	I2474	F2475	L2480	P2485	V2490	V2491	R2495				
C2259	T2276	A2277	Q2280	W2289	R2290	T2291	D2292	S2293	R2310	C2316	A2317	A2318	L2319	S2320	G2321	L2322	T2323	G2324	C2325	T2326	F2330	C2335	D2336	H2338	F2339	L2340	L2341	S2342	G2343	G2344	V2345	Q2350	D2351	C2352	C2353	C2354	V2355	Q2359	Y2360	P2362	V2363	N2364	S2369	S2373	E2374	R2375
V2140	D2145	P2153	S2154	S2155	F2156	R2157	G2158	R2159	L2160	C2161	G2162	L2163	C2164	G2165	N2166	F2167	N2168	G2169	N2170	D2173	V2176	L2177	V2182	A2188	T2191	R2194	A2195	L2200	G2201	C2202	C2211	P2212	V2213	C2214	L2215	Y2222	N2225	P2234	A2240	C2241	H2242	K2243	L2244	L2245		
L2045	D2046	G2047	L2052	H2053	G2054	S2057	L2060	V2063	K2067	P2068	G2069	D2070	F2073	L2077	E2078	K2079	W2080	S2081	A2082	G2083	D2084	P2085	Q2086	R2087	V2090	T2091	V2096	G2097	L2099	A2100	R2101	Q2104	V2105	T2106	D2108	G2109	E2110	V2111	V2112	E2126	G2127	R2128	L2132			
P1914	C1917	P1918	S1929	P1935	S1936	L1937	V1941	E1944	T1945	I1946	P1947	R1948	L1959	S1960	G1961	D1962	T1963	C1964	G1968	Q1969	C1970	G1971	V1980	F1985	Y1986	P1987	C1991	G1998	P1999	D2000	G2001	Q2002	C2011	E2012	P2013	Y2014	C2017	R2018	I2019	G2022	V2023	Q2024	C2031			
K1808	P1809	E1810	C1820	D1821	Q1822	C1823	E1826	P1827	C1828	P1829	C1832	T1833	P1834	E1835	F1840	P1843	G1847	I1848	T1849	R1850	A1851	P1852	E1853	A1857	P1858	T1866	Q1867	F1869	A1876	Q1880	G1885	P1888	A1889	T1892	Y1893	L1904	G1905	E1906	K1909	P1910						
H1666	C1674	L1678	P1685	T1689	E1690	V1694	R1701	Y1708	T1709	R1710	L1714	Y1717	G1718	L1719	Q1726	R1729	K1730	E1736	F1737	L1740	P1741	F1742	H1743	L1744	K1747	L1748	S1749	V1750	Y1751	I1752	D1756	V1759	F1774	V1775	G1792	N1793	Y1794	N1795	K1796	N1799						
H1533	S1534	H1535	Y1536	E1537	L1538	G1539	G1540	P1548	A1551	T1557	V1558	C1563	V1564	E1565	G1566	C1569	D1570	L1576	V1581	P1582	G1588	C1589	W1590	Y1596	E1601	K1610	R1611	C1612	L1621	V1622	C1623	A1626	L1636	I1642	A1654	W1655	G1656	D1657	T1662	L1663	D1664	G1665				
D1366	F1367	L1368	L1369	Q1370	T1372	D1374		R1378	V1379	D1380	V1381	L1383	P1384	T1396	Y1387	V1391	C1392	G1393	L1394	C1395	K1400	N1401	H1402	V1407	M1413	I1417	P1418	W1424	N1428	E1430	C1441	C1458	L1461	F1469	G1493	L1499	C1510	T1517	E1518	D1519	D1532					
C1275	N1276	Y1277	A1280	L1283	C1284	P1285	G1286	V1287	N1288	A1289	T1293	P1294	F1295	T1296	V1297	T1298	K1300	S1306	V1309	Q1314	V1315	T1316	V1317	T1318	T1319	I1324	H1327	N1329	E1330	I1331	G1332	K1333	V1334	L1340	L1343	P1344	Y1345	L1347	A1348	G1349	V1354	V1362	L1363			
ASP	HIS	CYS	GLY	ASP	GLN	VAL	CYS	PRO	GLY	SER	GLY	VAL	THR	CYS	VAL	THR	LYS	THR	HIS	GLY	THR	PHE	PRO	GLY	THR	CYS	PRO	GLN	GLU	THR	PRO	GLY	ASP	GLN	CYS	VAL	ASP	ASP	VAL	THR	LYS	GLY	ASN	PRO	GLY	ILE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	184178	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.340	Depositor
Minimum map value	-0.132	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0495	Depositor
Map size (Å)	302.72, 302.72, 302.72	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.36	2/10201 (0.0%)	0.63	20/13926 (0.1%)
1	D	0.36	2/10201 (0.0%)	0.63	20/13926 (0.1%)
All	All	0.36	4/20402 (0.0%)	0.63	40/27852 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1582	PRO	N-CD	9.17	1.60	1.47
1	D	1582	PRO	N-CD	9.14	1.60	1.47
1	A	2234	PRO	N-CD	-7.90	1.36	1.47
1	D	2234	PRO	N-CD	-7.89	1.36	1.47

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2292	ASP	CB-CA-C	-9.86	105.21	116.54
1	D	2292	ASP	CB-CA-C	-9.84	105.22	116.54
1	A	2107	VAL	N-CA-C	-8.01	99.24	109.58
1	D	2107	VAL	N-CA-C	-8.01	99.25	109.58
1	A	1743	HIS	N-CA-C	7.09	120.08	108.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9937	0	9279	236	0
1	D	9937	0	9279	244	0
2	A	84	0	78	8	0
2	D	84	0	78	7	0
3	A	4	0	0	0	0
3	D	4	0	0	0	0
All	All	20050	0	18714	480	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 12.

The worst 5 of 480 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:A:2316:CYS:SG	1:A:2360:TYR:CE1	2.29	1.26
1:D:2316:CYS:SG	1:D:2360:TYR:CE1	2.28	1.26
1:A:1621:LEU:HD12	1:A:1621:LEU:O	1.50	1.11
1:D:1621:LEU:HD12	1:D:1621:LEU:O	1.50	1.10
1:D:2352:CYS:SG	1:D:2360:TYR:OH	2.27	0.92

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	1337/2587 (52%)	1253 (94%)	83 (6%)	1 (0%)	48	78
1	D	1337/2587 (52%)	1253 (94%)	83 (6%)	1 (0%)	48	78
All	All	2674/5174 (52%)	2506 (94%)	166 (6%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2109	GLY
1	D	2109	GLY

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	1085/2113 (51%)	1025 (94%)	60 (6%)	19	46
1	D	1085/2113 (51%)	1025 (94%)	60 (6%)	19	46
All	All	2170/4226 (51%)	2050 (94%)	120 (6%)	21	46

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2560	ASP
1	D	2462	CYS
1	D	1557	THR
1	D	2399	ILE
1	D	2567	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1924	GLN
1	D	2065	HIS
1	D	2350	GLN
1	A	2350	GLN
1	A	2465	ASN

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, 8 are monoatomic - leaving 12 for Mogul analysis.

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	NAG	A	5609	1	14,14,15	0.28	0	17,19,21	0.44	0
2	NAG	A	5610	1	14,14,15	0.32	0	17,19,21	0.44	0
2	NAG	D	5607	1	14,14,15	0.86	1 (7%)	17,19,21	1.27	1 (5%)
2	NAG	A	5601	1	14,14,15	0.80	1 (7%)	17,19,21	0.96	1 (5%)
2	NAG	A	5603	1	14,14,15	0.35	0	17,19,21	0.66	0
2	NAG	D	5608	1	14,14,15	0.67	1 (7%)	17,19,21	0.88	0
2	NAG	A	5607	1	14,14,15	0.85	1 (7%)	17,19,21	1.26	1 (5%)
2	NAG	D	5601	1	14,14,15	0.81	1 (7%)	17,19,21	0.97	1 (5%)
2	NAG	D	5610	1	14,14,15	0.32	0	17,19,21	0.45	0
2	NAG	A	5608	1	14,14,15	0.67	1 (7%)	17,19,21	0.88	0
2	NAG	D	5603	1	14,14,15	0.35	0	17,19,21	0.66	0
2	NAG	D	5609	1	14,14,15	0.28	0	17,19,21	0.44	0

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	NAG	A	5609	1	-	1/6/23/26	0/1/1/1
2	NAG	A	5610	1	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	5607	1	-	2/6/23/26	0/1/1/1
2	NAG	A	5601	1	-	2/6/23/26	0/1/1/1
2	NAG	A	5603	1	-	0/6/23/26	0/1/1/1
2	NAG	D	5608	1	-	3/6/23/26	0/1/1/1
2	NAG	A	5607	1	-	2/6/23/26	0/1/1/1
2	NAG	D	5601	1	-	2/6/23/26	0/1/1/1
2	NAG	D	5610	1	-	1/6/23/26	0/1/1/1
2	NAG	A	5608	1	-	3/6/23/26	0/1/1/1
2	NAG	D	5603	1	-	0/6/23/26	0/1/1/1
2	NAG	D	5609	1	-	1/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5607	NAG	O5-C1	3.03	1.48	1.43
2	A	5607	NAG	O5-C1	3.00	1.48	1.43
2	D	5601	NAG	O5-C1	2.46	1.47	1.43
2	A	5601	NAG	O5-C1	2.46	1.47	1.43
2	D	5608	NAG	O5-C1	-2.26	1.39	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	5607	NAG	C1-O5-C5	5.01	118.90	112.19
2	A	5607	NAG	C1-O5-C5	4.98	118.86	112.19
2	D	5601	NAG	C1-O5-C5	3.72	117.18	112.19
2	A	5601	NAG	C1-O5-C5	3.71	117.15	112.19

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5608	NAG	C1-C2-N2-C7
2	D	5608	NAG	C1-C2-N2-C7
2	A	5601	NAG	C4-C5-C6-O6
2	D	5601	NAG	C4-C5-C6-O6
2	A	5601	NAG	O5-C5-C6-O6

There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5609	NAG	1	0
2	D	5607	NAG	3	0
2	A	5601	NAG	1	0
2	D	5608	NAG	3	0
2	A	5607	NAG	3	0
2	A	5608	NAG	3	0
2	D	5609	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	D	2
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	1657:ASP	C	1658:PRO	N	7.71
1	A	1657:ASP	C	1658:PRO	N	7.58
1	A	1258:ASP	C	1259:PRO	N	5.18
1	D	1258:ASP	C	1259:PRO	N	5.03

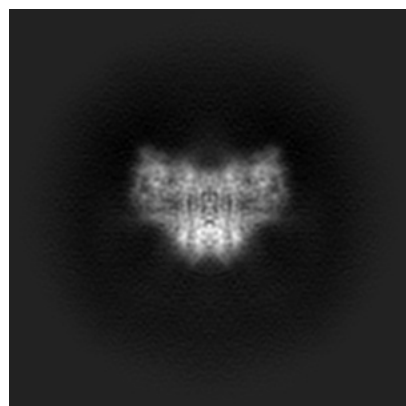
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19070. These allow visual inspection of the internal detail of the map and identification of artifacts.

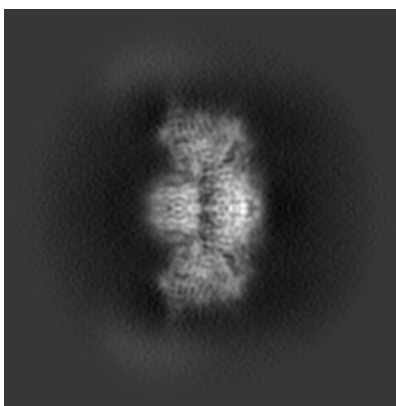
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

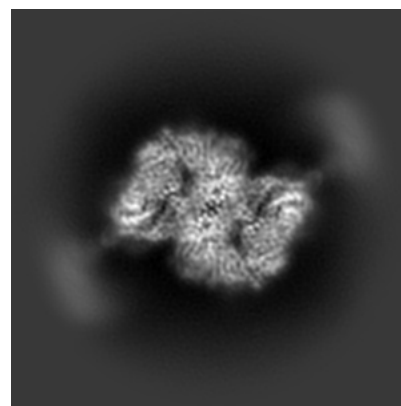
6.1.1 Primary map



X

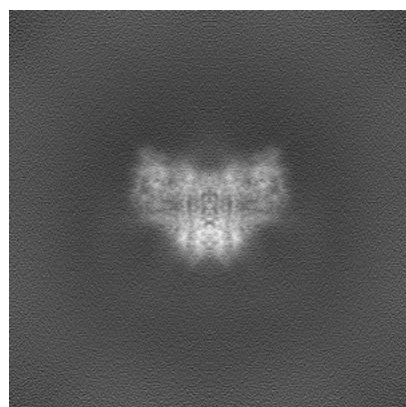


Y

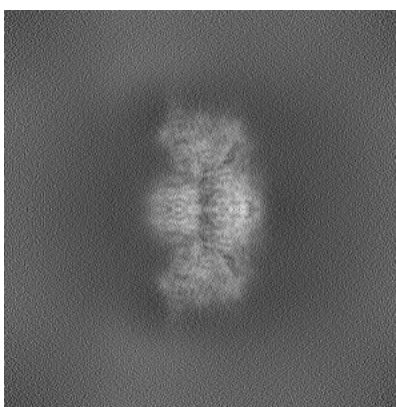


Z

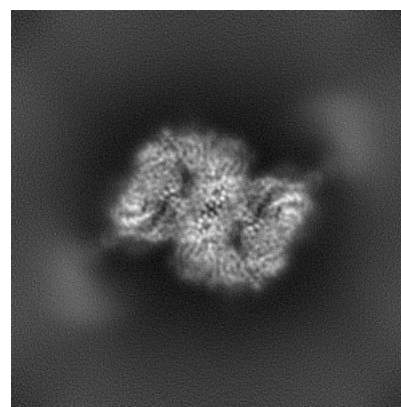
6.1.2 Raw map



X



Y



Z

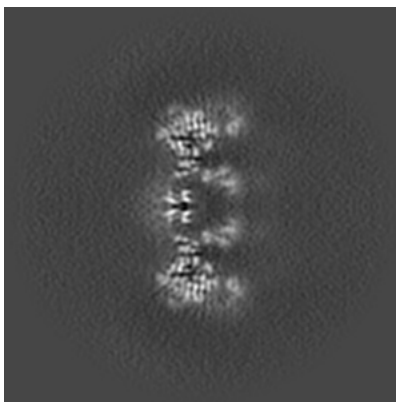
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

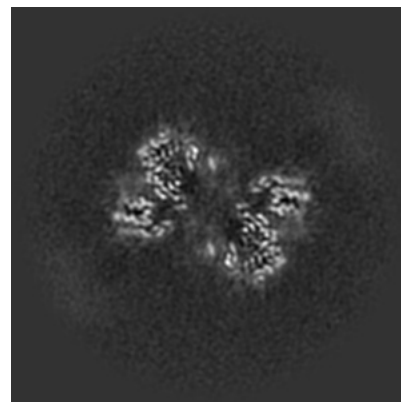
6.2.1 Primary map



X Index: 176

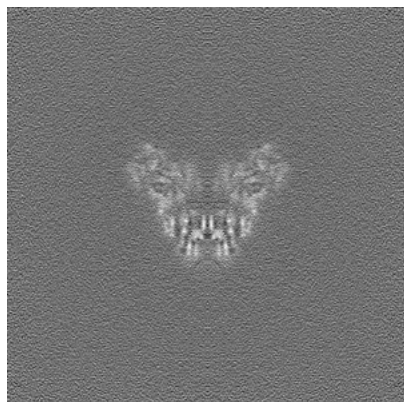


Y Index: 176

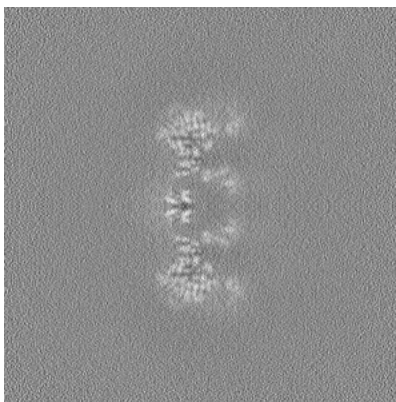


Z Index: 176

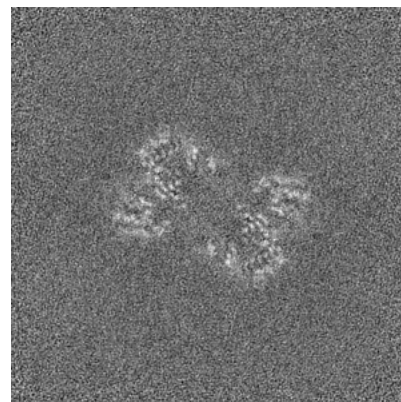
6.2.2 Raw map



X Index: 176



Y Index: 176



Z Index: 176

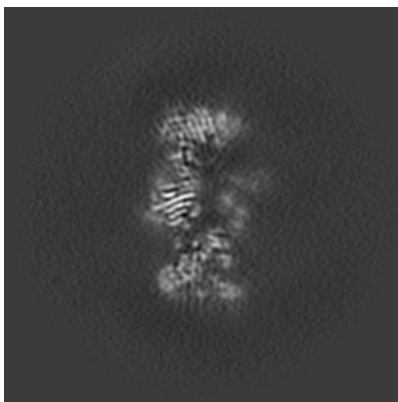
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

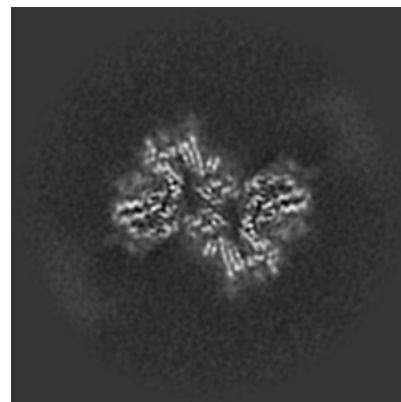
6.3.1 Primary map



X Index: 176

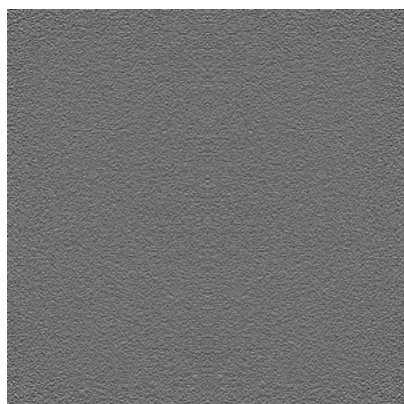


Y Index: 186

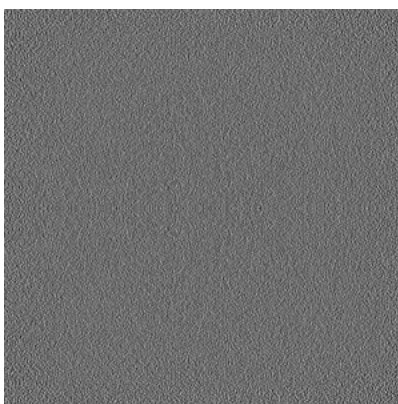


Z Index: 168

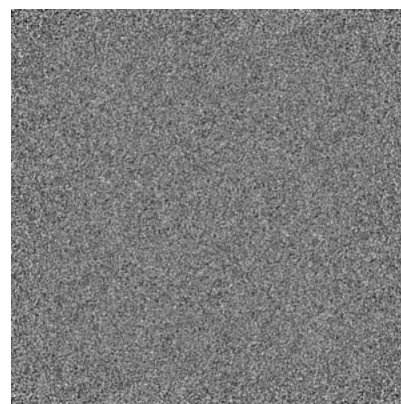
6.3.2 Raw map



X Index: 0



Y Index: 0

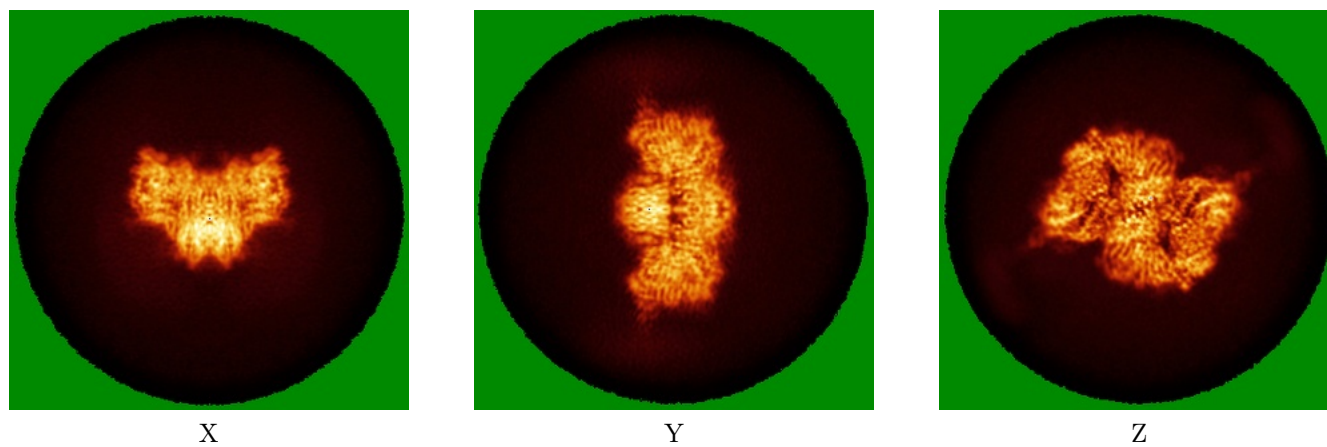


Z Index: 351

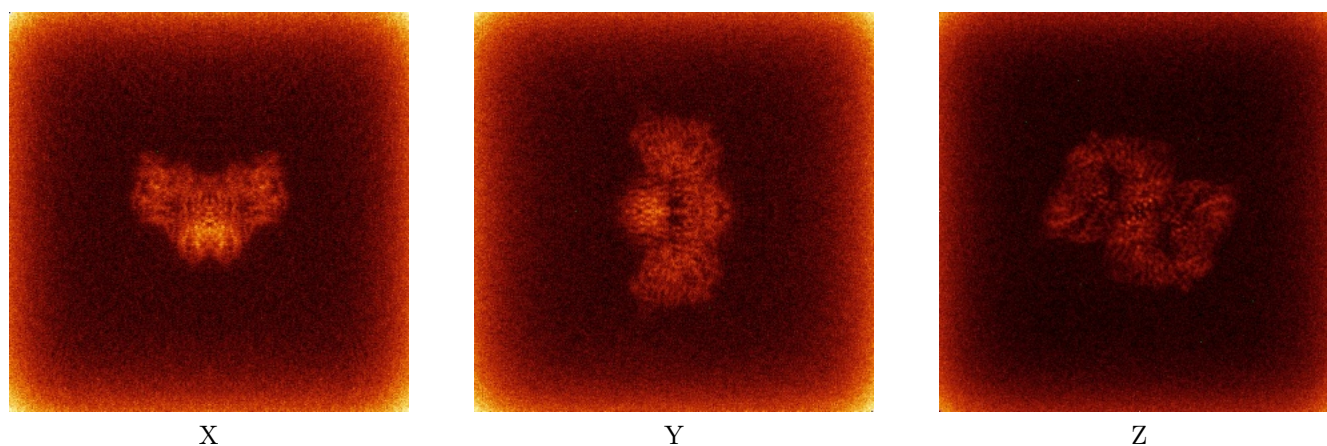
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw 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](#)

This section was not generated.

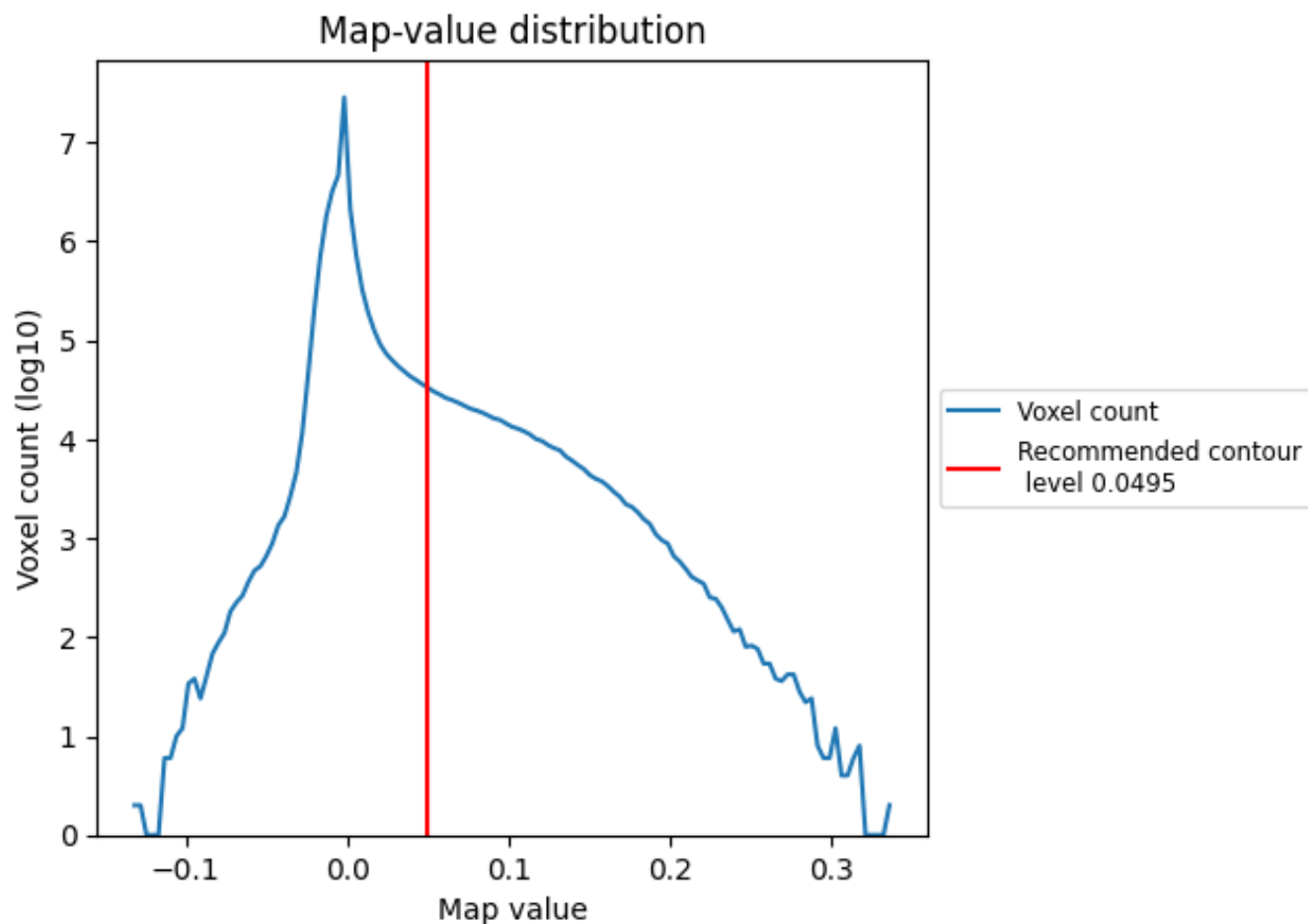
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

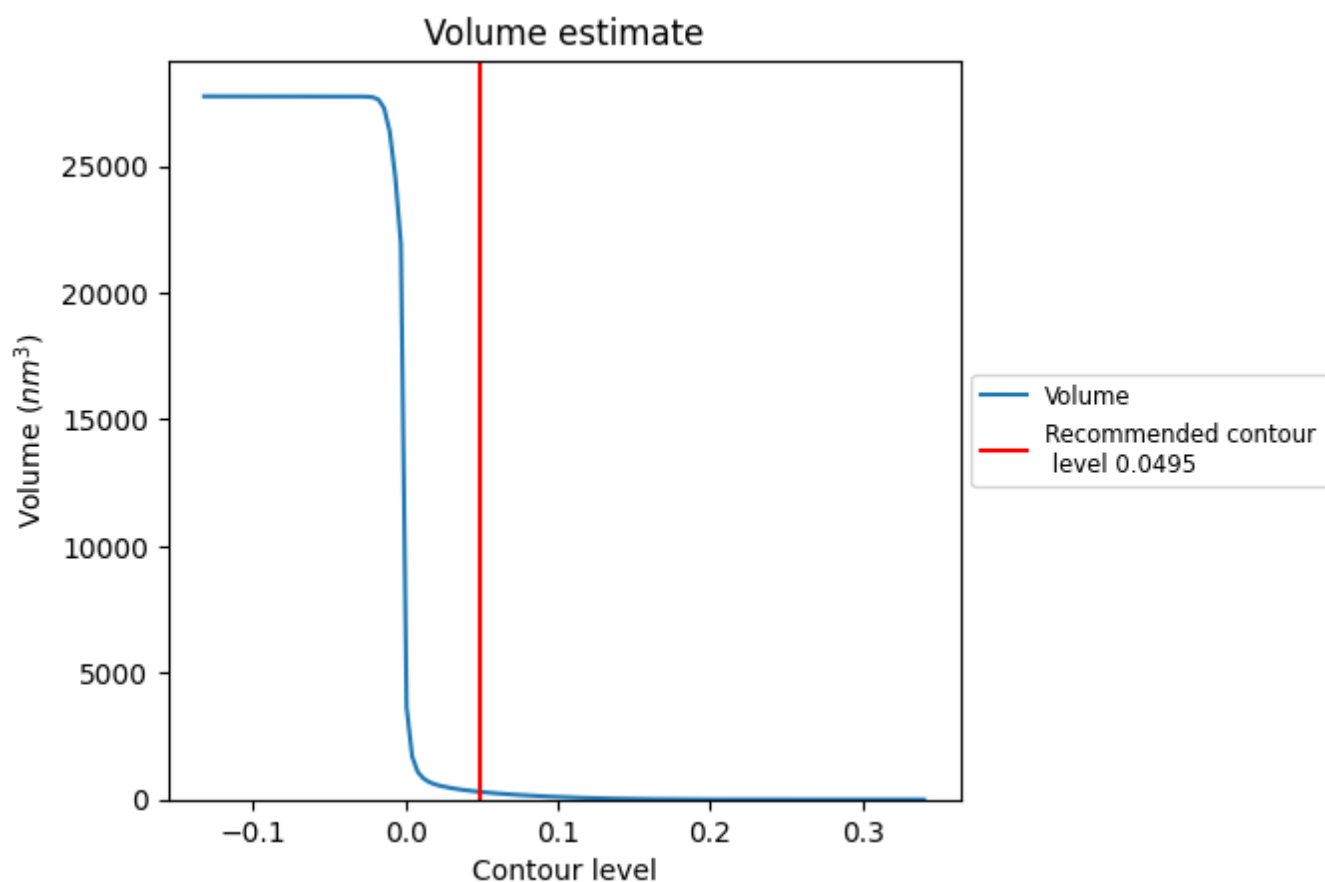
This section contains the results of statistical analysis of the map.

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.

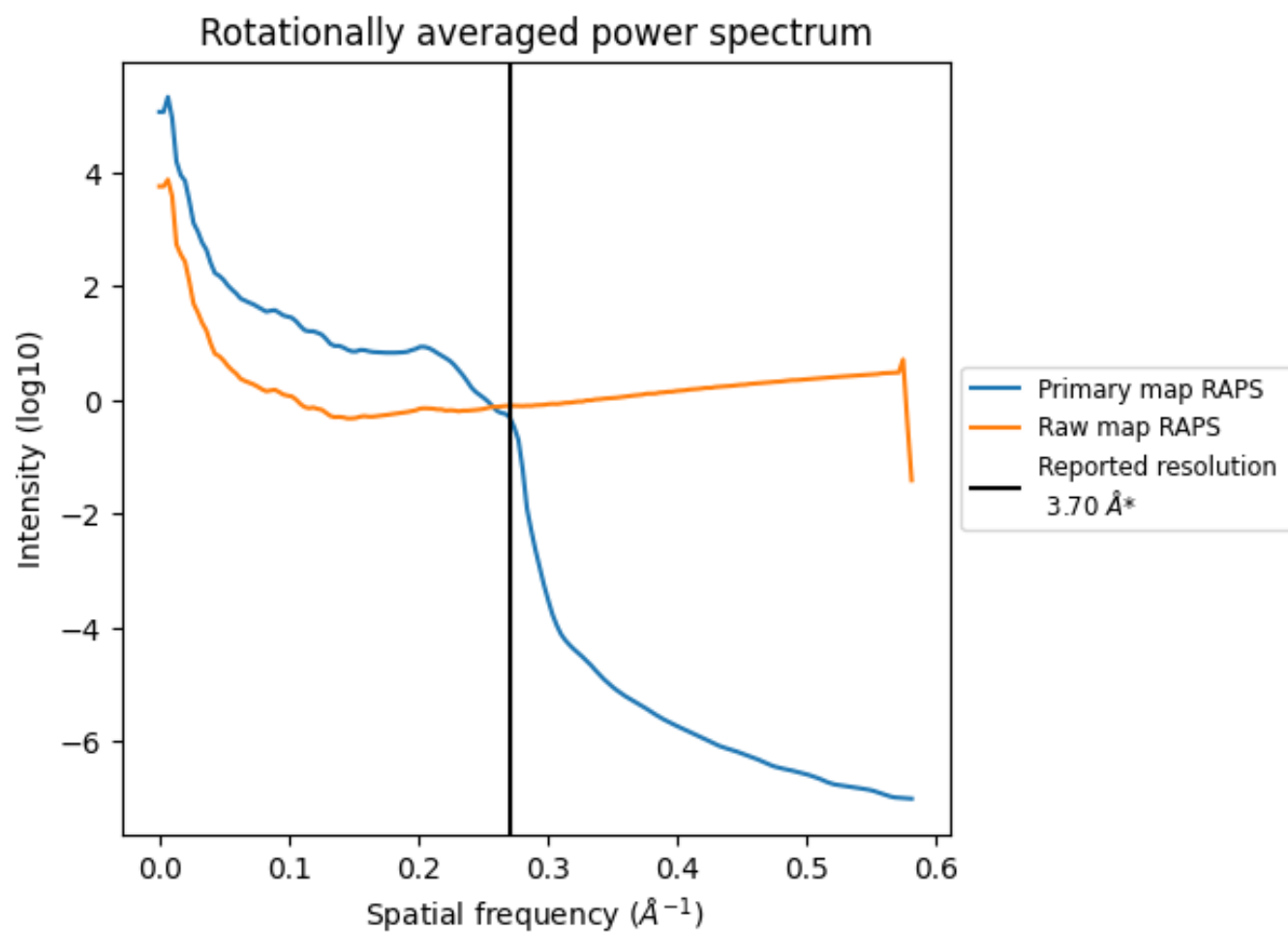
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 300 nm^3 ; this corresponds to an approximate mass of 271 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 ⓘ

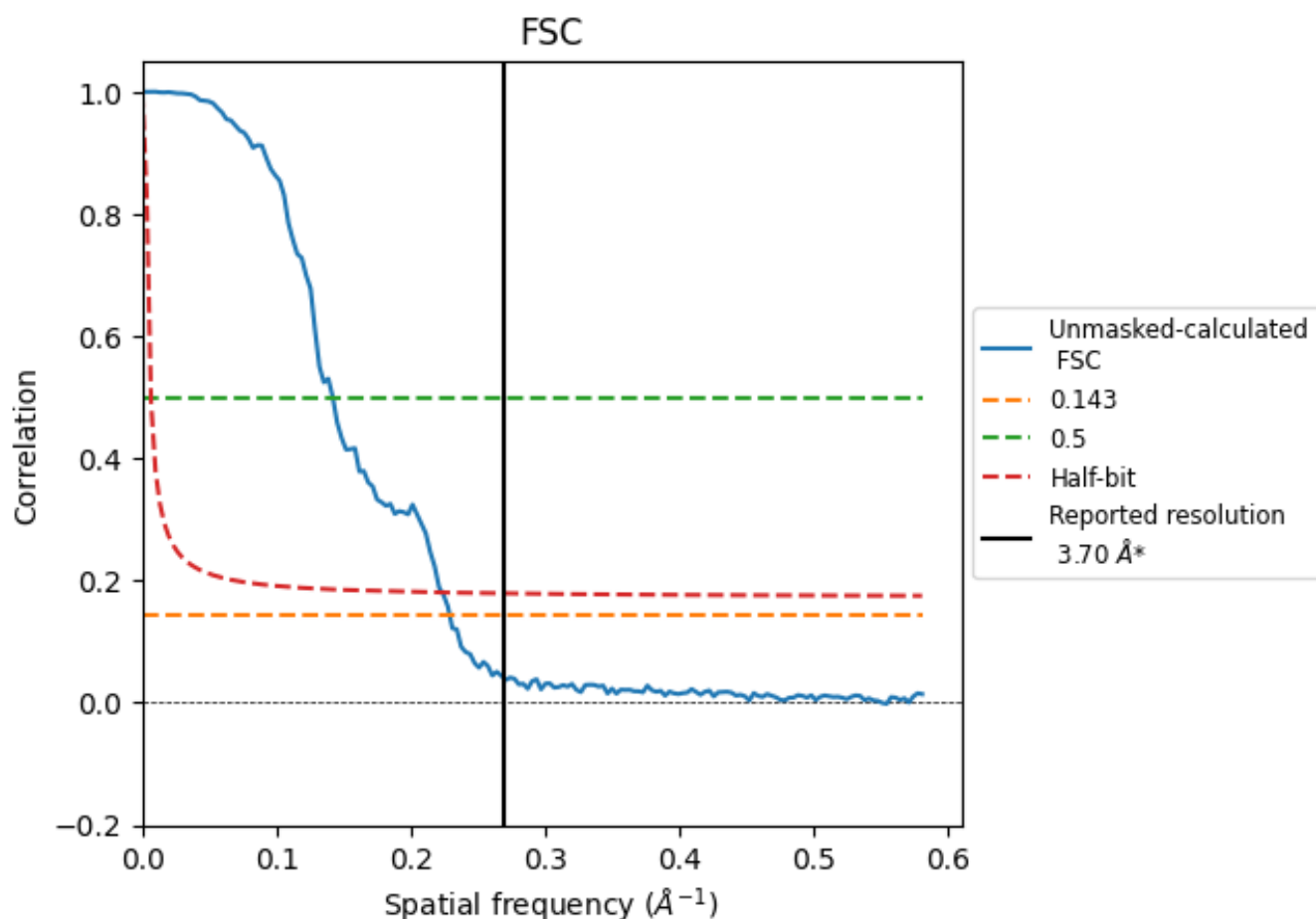


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.36	7.04	4.47

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.36 differs from the reported value 3.7 by more than 10 %

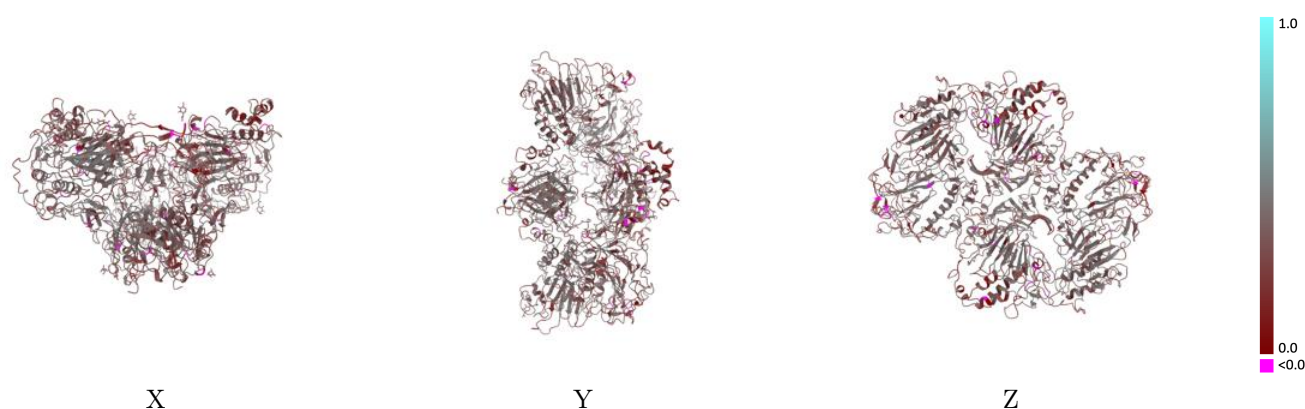
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19070 and PDB model 8RDE. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

This section was not generated.

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

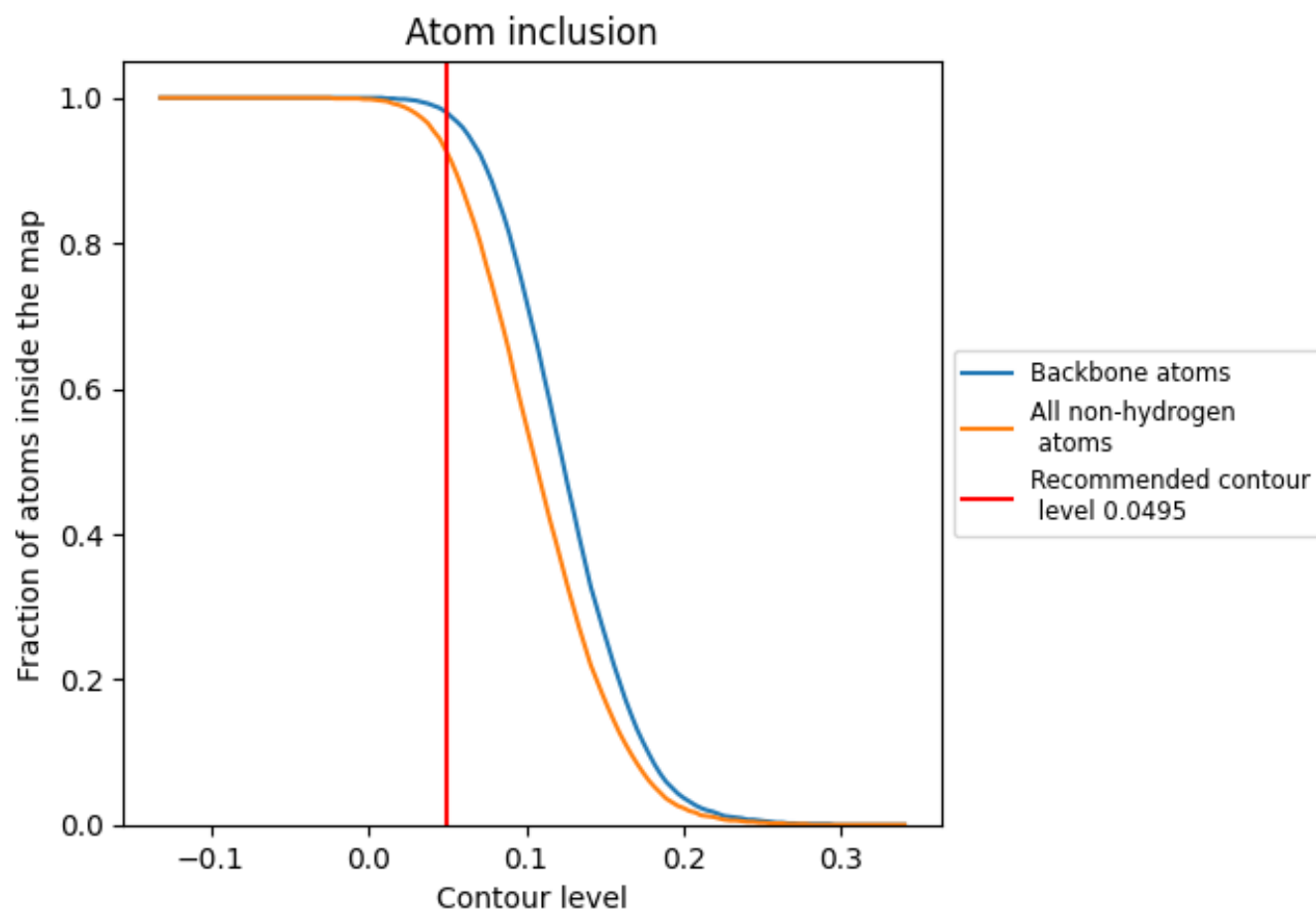


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% 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 (0.0495) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9260	0.3430
A	0.9230	0.3390
D	0.9290	0.3470

