



Full wwPDB EM Validation Report ⓘ

Oct 12, 2024 – 01:14 PM EDT

PDB ID : 6B3R
EMDB ID : EMD-7042
Title : Structure of the mechanosensitive channel Piezo1
Authors : Guo, Y.R.; MacKinnon, R.
Deposited on : 2017-09-22
Resolution : 3.80 Å(reported)
Based on initial model : 4RAX

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.dev113
MolProbity : 4.02b-467
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

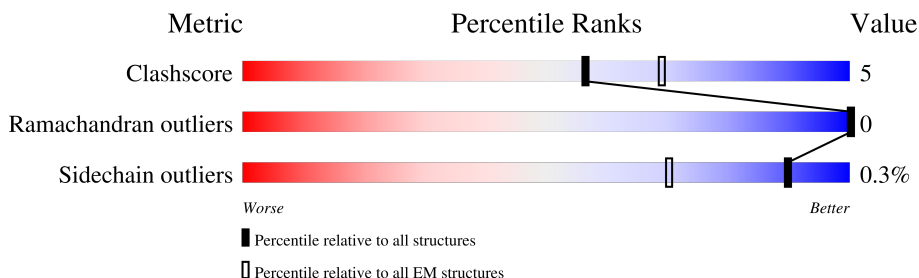
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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 ≥ 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	2547	<div> <div>17%</div> <div>51%</div> <div>8%</div> <div>41%</div> </div>
1	C	2547	<div> <div>50%</div> <div>51%</div> <div>7%</div> <div>41%</div> </div>
1	E	2547	<div> <div>49%</div> <div>51%</div> <div>8%</div> <div>41%</div> </div>
2	B	16	<div> <div>6%</div> <div>100%</div> </div>
2	D	16	<div> <div>6%</div> <div>100%</div> </div>
2	F	16	<div> <div>25%</div> <div>100%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 35718 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 Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		
1	C	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		
1	E	1502	Total	C	N	O	S	0	0
			11826	7739	2004	2013	70		

- Molecule 2 is a protein called Piezo-type mechanosensitive ion channel component 1, unknown fragment.

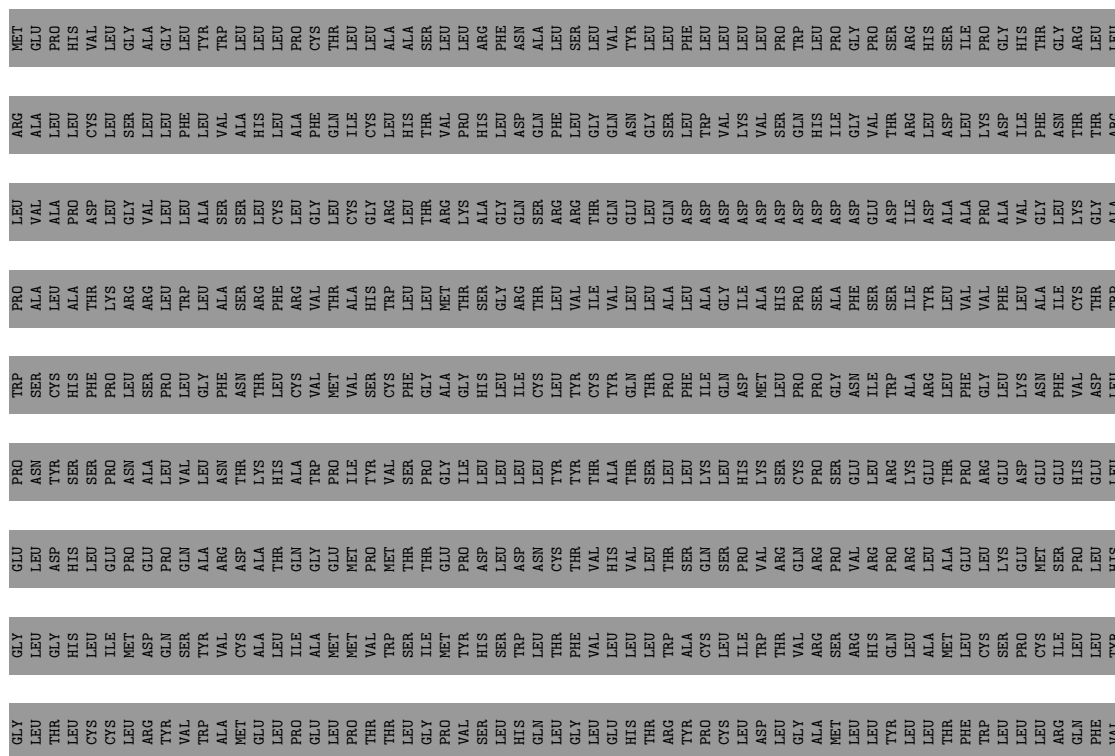
Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	16	Total	C	N	O	0	0
			80	48	16	16		
2	D	16	Total	C	N	O	0	0
			80	48	16	16		
2	F	16	Total	C	N	O	0	0
			80	48	16	16		





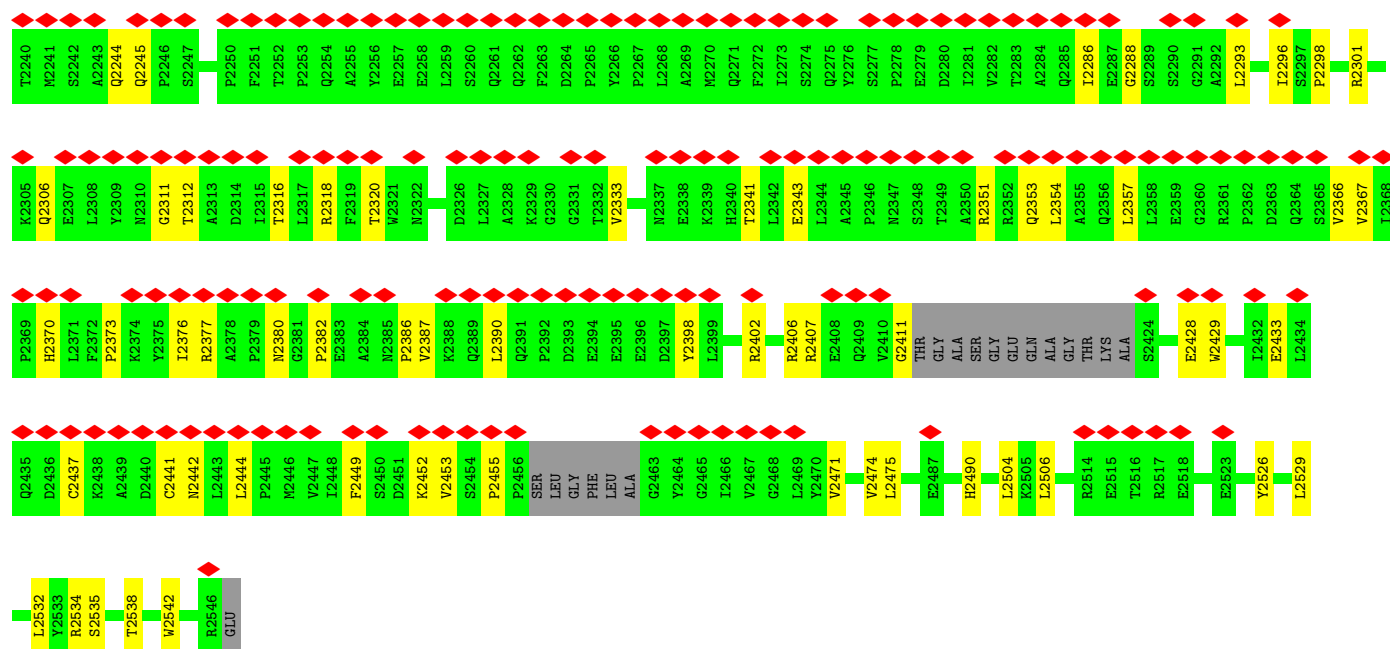


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H2116	V2054	I1992	SER	VAL	GLU	G1750	L1690	GLY	G1570	GLN	SER	A1321
L2117	V2055	F1993	LYS	ILE	ASP	F1751	C1691	SER	P1571	THR	PRO	L1322
N2118	A2056	G1994	ARG	GLN	ARG	F1752	Y1692	GLN	V1572	VAL	PRO	Y1323
L2119	I2057	F1995	GLU	PRO	TYR	P1753	F1693	GLU	E1573	LEU	ARG	N1324
F2120	H2058	W1996	ARG	PRO	LYS	W1754	I1694	LEU	T1574	GLN	GLN	A1325
L2127	I2059	A1997	MET	GLU	ASP	N1755	I1695	ALA	D1575	ARG	TRP	A1326
F2130	W2060	PHE	LYS	LEU	HIS	S1756	I1696	ASN	R1576	ARG	TRP	A1327
L2131	M2061	GLY	ALA	CYS	ASP	Y1757	L1697	LEU	D1578	GLU	ARG	L1328
W2132	F2062	ARG	LYS	PRO	ARG	W1758	N1698	ALA	G1577	ALA	TRP	K1329
E2133	F2063	HIS	ARG	ARG	SER	V1759	L1699	THR	SER	ARG	ASP	S1330
L2064	I2064	VAL	HIS	THR	VAL	L1760	M1700	MET	THR	GLN	ASP	I1331
L2065	W2065	ALA	GLN	ARG	LYS	L1761	V1701	ARG	ALA	GLU	HIS	I1332
PRO	ALA	THR	ASP	ASP	ASP	R1762	T1702	THR	SER	ALA	THR	N1332
VAL	VAL	ILE	SER	ILE	GLU	Y1763	A1703	GLU	GLY	GLN	VAL	F1333
THR	THR	ILE	VAL	THR	LYS	E1764	S1704	LEU	GLY	LEU	ILE	H1334
GLU	GLU	ARG	SER	ARG	GLU	N1765	A1705	LEU	ALA	ALA	HIS	R1335
MET	ARG	PHE	THR	PHE	GLU	K1766	A1706	LEU	GLU	SER	SER	Q1336
PHE	ALA	ARG	ALA	ARG	PRO	P1767	S1707	ASP	GLU	GLY	ASP	I1337
SER	SER	Q1952	Q1953	Q1954	LYS	Y1768	L1708	ARG	PRO	GLY	PHE	E1338
Q2075	N2076	F1954	F1955	Y1956	GLU	F1769	V1709	LEU	SER	LEU	LEU	E1339
A2077	A2077	Y1956	Y1957	Q1957	THR	P1770	L1710	THR	SER	ASN	PHE	K1340
W2078	Q2017	Q1957	Q1958	L1958	GLY	R1772	P1711	MET	THR	PRO	PHE	S1341
A2079	Q2018	L1958	L1959	L1960	SER	I1773	V1712	GLY	ASP	ASP	GLU	L1342
Q2080	A2019	L1959	L1960	R1960	LYS	I1774	L1713	ASP	THR	VAL	ASP	A1343
L2081	F2020	GLY	GLY	GLY	THR	G1775	V1714	E1658	THR	PRO	GLU	Q1344
W2082	L2021	THR	ALA	VAL	GLY	L1776	F1715	E1660	SER	VAL	GLU	L1345
Y2083	F2022	VAL	GLY	GLY	THR	E1777	L1716	E1661	PRO	ASP	GLU	K1346
F2084	N2023	GLY	GLY	GLY	GLY	T1778	W1717	E1662	LEU	GLY	GLU	R1347
V2085	L2024	THR	THR	THR	LYS	T1779	A1718	E1663	THR	ASP	ALA	E1357
K2086	L2025	GLU	GLU	GLU	GLU	D1780	M1719	R1664	TYR	GLY	PRO	L1357
C2087	V2026	GLY	GLY	GLY	VAL	S1781	L1720	F1665	ASN	ALA	GLU	Q1360
L2088	Q2027	GLY	GLY	GLY	LEU	Y1782	T1721	A1667	THR	GLY	ASP	R1361
Y2089	F2028	GLY	GLY	GLY	ALA	I1783	P1722	Q1668	SER	ARG	PRO	S1362
F2090	T2030	GLY	GLY	GLY	THR	K1784	I1723	Q1669	GLY	ALA	PRO	Q1363
A2091	M2031	THR	LYS	LYS	PRO	Y1785	R1724	G1670	SER	ALA	ALA	A1364
L2092	Y2032	THR	THR	THR	ARG	D1786	P1725	R1671	GLU	GLN	GLN	S1365
S2093	D2033	THR	THR	THR	ASP	L1787	S1726	T1672	GLU	ALA	SER	ARG
A2094	D2034	GLU	GLU	GLU	ILE	L1788	K1727	L1673	ILE	PHE	GLY	GLY
Y2095	R2035	ARG	ARG	ARG	GLN	Q1789	R1728	R1674	THR	GLN	LEU	GLN
Q2096	A2036	LYS	LYS	LYS	GLY	L1790	F1729	L1675	ASP	MET	GLN	GLN
L2097	L2037	ARG	ARG	ARG	LYS	M1791	W1730	L1676	ALA	ALA	LYS	LYS
R2098	R2040	PRO	PRO	PRO	PRO	A1792	T1732	R1677	GLY	TYR	ASP	ASP
C2099	K2041	THR	THR	THR	GLY	L1793	I1733	A1678	ASP	GLN	GLN	PRO
G2100	T2042	HIS	HIS	HIS	ARG	F1794	A1733	G1679	GLN	ASP	ALA	TRP
Y2101	V2043	GLN	GLN	GLN	SER	W1795	I1734	Y1680	ALA	THR	VAL	VAL
R2104	L2044	LYS	LYS	LYS	ASP	H1796	V1735	Q1681	THR	ASN	THR	THR
I2105	L2047	L1979	L1979	L1980	LYS	R1797	F1736	C1682	SER	GLN	ALA	ALA
L2106	A2048	D1984	D1984	D1985	THR	Q1798	T1737	V1683	LEU	GLY	GLY	GLY
G2107	F2049	I1985	I1985	I1986	GLY	S1799	E1738	A1684	THR	PRO	PRO	PRO
N2108	Q2050	V1986	V1986	V1987	ARG	L1800	M1740	A1685	GLY	ASP	ASP	ASP
F2109	W2051	D1987	D1987	D1988	LYS	L1801	V1741	H1686	THR	GLY	GLY	GLY
K2112	V2052	I1989	I1989	I1990	GLY	L1802	T1742	S1687	SER	LEU	LEU	LEU
N2115	L2053	I1991	I1991	I1992	LYS	G1804	K1744	E1688	HIS	GLY	GLY	GLY
F2239	F2239	F1747	F1747	F1748	GLU	W1806	L1746	L1689				



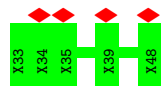
- Molecule 2: Piezo-type mechanosensitive ion channel component 1, unknown fragment



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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	277548	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.334	Depositor
Minimum map value	-0.238	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.35	0/12117	0.59	0/16473
1	C	0.35	0/12117	0.59	0/16473
1	E	0.34	0/12117	0.59	0/16473
All	All	0.35	0/36351	0.59	0/49419

There are no bond length outliers.

There are no bond angle outliers.

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	A	11826	0	11563	118	0
1	C	11826	0	11563	119	0
1	E	11826	0	11563	122	0
2	B	80	0	19	0	0
2	D	80	0	19	0	0
2	F	80	0	19	0	0
All	All	35718	0	34746	333	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 5.

All (333) 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:C:2050:GLN:HE22	1:C:2094:ALA:HB2	1.57	0.69
1:E:2050:GLN:HE22	1:E:2094:ALA:HB2	1.57	0.69
1:A:2050:GLN:HE22	1:A:2094:ALA:HB2	1.57	0.69
1:A:1161:LEU:O	1:A:1293:GLN:NE2	2.29	0.66
1:E:1161:LEU:O	1:E:1293:GLN:NE2	2.29	0.65
1:C:2406:ARG:HB3	1:C:2429:TRP:HB2	1.78	0.65
1:C:1161:LEU:O	1:C:1293:GLN:NE2	2.29	0.65
1:E:2406:ARG:HB3	1:E:2429:TRP:HB2	1.78	0.65
1:A:2367:VAL:HG22	1:A:2402:ARG:HG2	1.80	0.64
1:A:2406:ARG:HB3	1:A:2429:TRP:HB2	1.78	0.64
1:E:2229:THR:HG1	1:E:2320:THR:HG1	1.44	0.63
1:E:2367:VAL:HG22	1:E:2402:ARG:HG2	1.80	0.63
1:A:1698:ASN:ND2	1:A:1789:GLN:OE1	2.32	0.63
1:C:2367:VAL:HG22	1:C:2402:ARG:HG2	1.80	0.63
1:A:2286:ILE:HB	1:A:2444:LEU:HB2	1.81	0.62
1:A:2229:THR:HG1	1:A:2320:THR:HG1	1.47	0.62
1:C:1698:ASN:ND2	1:C:1789:GLN:OE1	2.32	0.62
1:C:2188:LYS:NZ	1:E:2143:THR:O	2.30	0.62
1:C:2296:ILE:O	1:E:2429:TRP:NE1	2.33	0.62
1:A:2296:ILE:HD12	1:A:2301:ARG:HE	1.65	0.62
1:C:2286:ILE:HB	1:C:2444:LEU:HB2	1.81	0.61
1:E:2047:LEU:HD12	1:E:2097:ILE:HD12	1.82	0.61
1:E:1698:ASN:ND2	1:E:1789:GLN:OE1	2.32	0.61
1:E:2286:ILE:HB	1:E:2444:LEU:HB2	1.81	0.61
1:C:1698:ASN:HB3	1:C:1785:TYR:HB2	1.82	0.61
1:A:2178:PRO:HD2	1:A:2182:LYS:HD2	1.83	0.61
1:C:2295:ARG:NH1	1:E:2293:LEU:O	2.33	0.61
1:C:2296:ILE:HD12	1:C:2301:ARG:HE	1.65	0.61
1:A:1698:ASN:HB3	1:A:1785:TYR:HB2	1.82	0.60
1:E:2296:ILE:HD12	1:E:2301:ARG:HE	1.65	0.60
1:C:2178:PRO:HD2	1:C:2182:LYS:HD2	1.83	0.60
1:C:1543:GLN:O	1:C:1547:ARG:NH1	2.35	0.60
1:A:2295:ARG:NH1	1:C:2293:LEU:O	2.35	0.60
1:C:1666:GLU:HA	1:C:1669:GLN:HE21	1.66	0.60
1:E:1698:ASN:HB3	1:E:1785:TYR:HB2	1.82	0.60
1:E:1543:GLN:O	1:E:1547:ARG:NH1	2.35	0.59
1:E:1666:GLU:HA	1:E:1669:GLN:HE21	1.66	0.59
1:C:2047:LEU:HD12	1:C:2097:ILE:HD12	1.82	0.59
1:A:1543:GLN:O	1:A:1547:ARG:NH1	2.35	0.59
1:E:2178:PRO:HD2	1:E:2182:LYS:HD2	1.83	0.59
1:A:2047:LEU:HD12	1:A:2097:ILE:HD12	1.83	0.59
1:E:2377:ARG:HA	1:E:2449:PHE:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2206:PRO:HA	1:E:2209:PHE:HB3	1.84	0.59
1:A:2206:PRO:HA	1:A:2209:PHE:HB3	1.84	0.59
1:A:2377:ARG:HA	1:A:2449:PHE:HB2	1.85	0.59
1:E:2370:HIS:ND1	1:E:2398:TYR:O	2.35	0.59
1:C:1146:CYS:SG	1:C:1147:ARG:N	2.76	0.59
1:C:2229:THR:HG1	1:C:2320:THR:HG1	1.49	0.59
1:C:1051:CYS:SG	1:C:1081:TYR:OH	2.60	0.58
1:A:1146:CYS:SG	1:A:1147:ARG:N	2.76	0.58
1:C:2370:HIS:ND1	1:C:2398:TYR:O	2.35	0.58
1:E:2377:ARG:HG3	1:E:2387:VAL:HG22	1.85	0.58
1:C:2206:PRO:HA	1:C:2209:PHE:HB3	1.84	0.58
1:C:1547:ARG:HG2	1:C:1548:VAL:HG13	1.86	0.58
1:E:1524:THR:HG21	1:E:1682:CYS:HA	1.86	0.58
1:A:1666:GLU:HA	1:A:1669:GLN:HE21	1.66	0.58
1:E:1146:CYS:SG	1:E:1147:ARG:N	2.76	0.58
1:A:1722:ILE:HD11	1:A:1966:LEU:HD23	1.86	0.58
1:C:2377:ARG:HG3	1:C:2387:VAL:HG22	1.85	0.58
1:E:1722:ILE:HD11	1:E:1966:LEU:HD23	1.86	0.57
1:A:2377:ARG:HG3	1:A:2387:VAL:HG22	1.85	0.57
1:C:2377:ARG:HA	1:C:2449:PHE:HB2	1.84	0.57
1:A:1524:THR:HG21	1:A:1682:CYS:HA	1.86	0.57
1:E:907:ASP:HB3	1:E:910:ASN:HB2	1.86	0.57
1:E:948:ARG:HE	1:E:953:GLN:HB2	1.70	0.57
1:A:2370:HIS:ND1	1:A:2398:TYR:O	2.35	0.57
1:C:948:ARG:HE	1:C:953:GLN:HB2	1.70	0.57
1:C:1722:ILE:HD11	1:C:1966:LEU:HD23	1.86	0.57
1:E:2316:THR:HG22	1:E:2343:GLU:HG2	1.87	0.57
1:A:1719:MET:O	1:A:2098:ARG:NH1	2.38	0.57
1:A:948:ARG:HE	1:A:953:GLN:HB2	1.70	0.56
1:A:1547:ARG:HG2	1:A:1548:VAL:HG13	1.86	0.56
1:C:1524:THR:HG21	1:C:1682:CYS:HA	1.86	0.56
1:A:2032:VAL:HA	1:A:2138:MET:HE1	1.87	0.56
1:A:1664:ARG:O	1:A:1668:GLN:NE2	2.39	0.56
1:A:907:ASP:HB3	1:A:910:ASN:HB2	1.86	0.56
1:A:1966:LEU:HD13	1:A:2047:LEU:HD21	1.87	0.56
1:C:1719:MET:O	1:C:2098:ARG:NH1	2.38	0.56
1:E:2032:VAL:HA	1:E:2138:MET:HE1	1.88	0.56
1:E:1719:MET:O	1:E:2098:ARG:NH1	2.38	0.56
1:E:1547:ARG:HG2	1:E:1548:VAL:HG13	1.86	0.56
1:E:1664:ARG:O	1:E:1668:GLN:NE2	2.39	0.56
1:A:2437:CYS:HB3	1:A:2441:CYS:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1664:ARG:O	1:C:1668:GLN:NE2	2.39	0.55
1:C:2316:THR:HG22	1:C:2343:GLU:HG2	1.87	0.55
1:A:2316:THR:HG22	1:A:2343:GLU:HG2	1.87	0.55
1:C:907:ASP:HB3	1:C:910:ASN:HB2	1.86	0.55
1:E:2437:CYS:HB3	1:E:2441:CYS:HA	1.87	0.55
1:C:2424:SER:HB2	1:E:2411:GLY:HA3	1.88	0.55
1:E:1966:LEU:HD13	1:E:2047:LEU:HD21	1.87	0.55
1:C:1966:LEU:HD13	1:C:2047:LEU:HD21	1.87	0.55
1:C:803:ARG:HE	1:C:955:PRO:HG2	1.72	0.55
1:C:2032:VAL:HA	1:C:2138:MET:HE1	1.86	0.55
1:C:2437:CYS:HB3	1:C:2441:CYS:HA	1.88	0.55
1:E:1051:CYS:SG	1:E:1081:TYR:OH	2.60	0.55
1:A:956:LEU:HD22	1:A:1122:MET:HG3	1.89	0.54
1:E:1051:CYS:HG	1:E:1081:TYR:HH	1.52	0.54
1:E:956:LEU:HD22	1:E:1122:MET:HG3	1.89	0.54
1:A:2357:LEU:O	1:A:2407:ARG:NH2	2.41	0.54
1:A:803:ARG:HE	1:A:955:PRO:HG2	1.72	0.54
1:E:2357:LEU:O	1:E:2407:ARG:NH2	2.41	0.54
1:A:813:VAL:HG22	1:A:933:LEU:HB3	1.90	0.53
1:C:813:VAL:HG22	1:C:933:LEU:HB3	1.90	0.53
1:C:2199:LEU:HD21	1:E:2130:PHE:HB3	1.90	0.53
1:E:803:ARG:HE	1:E:955:PRO:HG2	1.72	0.53
1:C:956:LEU:HD22	1:C:1122:MET:HG3	1.89	0.53
1:C:1090:ASN:ND2	1:C:1093:ASN:OD1	2.42	0.53
1:A:2221:ASN:ND2	1:A:2380:ASN:OD1	2.42	0.53
1:C:2221:ASN:ND2	1:C:2380:ASN:OD1	2.42	0.53
1:C:2301:ARG:NH2	1:E:2411:GLY:O	2.42	0.53
1:C:2306:GLN:O	1:C:2311:GLY:N	2.39	0.53
1:C:2298:PRO:HG2	1:E:2406:ARG:HD3	1.89	0.53
1:E:813:VAL:HG22	1:E:933:LEU:HB3	1.90	0.53
1:C:2357:LEU:O	1:C:2407:ARG:NH2	2.41	0.52
1:E:1090:ASN:ND2	1:E:1093:ASN:OD1	2.42	0.52
1:A:1090:ASN:ND2	1:A:1093:ASN:OD1	2.42	0.52
1:A:1003:GLY:HA2	1:A:1280:ILE:HD13	1.92	0.52
1:C:2402:ARG:N	1:C:2433:GLU:O	2.42	0.52
1:E:2221:ASN:ND2	1:E:2380:ASN:OD1	2.42	0.52
1:E:2306:GLN:O	1:E:2311:GLY:N	2.39	0.52
1:E:1003:GLY:HA2	1:E:1280:ILE:HD13	1.92	0.52
1:C:1003:GLY:HA2	1:C:1280:ILE:HD13	1.92	0.51
1:A:1723:PRO:HD3	1:A:1969:LYS:HE3	1.93	0.51
1:A:2306:GLN:O	1:A:2311:GLY:N	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1723:PRO:HD3	1:C:1969:LYS:HE3	1.93	0.51
1:A:1058:LEU:HB3	1:A:1060:ILE:HG22	1.93	0.51
1:E:1723:PRO:HD3	1:E:1969:LYS:HE3	1.93	0.51
1:C:1058:LEU:HB3	1:C:1060:ILE:HG22	1.93	0.50
1:E:1058:LEU:HB3	1:E:1060:ILE:HG22	1.93	0.50
1:E:1136:GLU:HB3	1:E:1546:LEU:HD21	1.94	0.50
1:A:824:GLU:HG3	1:A:826:SER:HB3	1.93	0.50
1:A:2402:ARG:N	1:A:2433:GLU:O	2.42	0.50
1:C:824:GLU:HG3	1:C:826:SER:HB3	1.93	0.50
1:E:824:GLU:HG3	1:E:826:SER:HB3	1.93	0.50
1:A:1130:LEU:HD12	1:A:1203:THR:HG21	1.93	0.50
1:C:1136:GLU:HB3	1:C:1546:LEU:HD21	1.94	0.50
1:A:2411:GLY:O	1:E:2301:ARG:NH2	2.44	0.49
1:C:1130:LEU:HD12	1:C:1203:THR:HG21	1.93	0.49
1:E:2373:PRO:HG2	1:E:2376:ILE:HD11	1.94	0.49
1:A:2373:PRO:HG2	1:A:2376:ILE:HD11	1.94	0.49
1:E:1754:TRP:HB2	1:E:1769:PHE:HZ	1.77	0.49
1:A:1136:GLU:HB3	1:A:1546:LEU:HD21	1.94	0.49
1:E:2017:PRO:HA	1:E:2020:PHE:HD2	1.78	0.49
1:A:2376:ILE:HA	1:A:2386:PRO:HA	1.95	0.49
1:E:942:ARG:O	1:E:946:HIS:ND1	2.45	0.49
1:E:1009:MET:HB3	1:E:1043:PHE:HZ	1.78	0.49
1:E:2376:ILE:HA	1:E:2386:PRO:HA	1.95	0.49
1:E:1130:LEU:HD12	1:E:1203:THR:HG21	1.93	0.48
1:C:2376:ILE:HA	1:C:2386:PRO:HA	1.95	0.48
1:E:893:PRO:HD2	1:E:896:ILE:HD13	1.95	0.48
1:A:1754:TRP:HB2	1:A:1769:PHE:HZ	1.77	0.48
1:C:2373:PRO:HG2	1:C:2376:ILE:HD11	1.94	0.48
1:C:2387:VAL:HG12	1:C:2390:LEU:H	1.78	0.48
1:C:893:PRO:HD2	1:C:896:ILE:HD13	1.95	0.48
1:A:2506:LEU:HD22	1:A:2529:LEU:HG	1.96	0.48
1:C:2218:GLY:HA2	1:C:2452:LYS:HD3	1.96	0.48
1:E:2402:ARG:N	1:E:2433:GLU:O	2.42	0.48
1:A:2017:PRO:HA	1:A:2020:PHE:HD2	1.78	0.48
1:A:2199:LEU:HD21	1:C:2130:PHE:HB3	1.96	0.48
1:A:2218:GLY:HA2	1:A:2452:LYS:HD3	1.96	0.48
1:C:1754:TRP:HB2	1:C:1769:PHE:HZ	1.78	0.48
1:E:1246:ILE:HA	1:E:1251:LEU:HD12	1.96	0.48
1:C:2506:LEU:HD22	1:C:2529:LEU:HG	1.96	0.48
1:A:893:PRO:HD2	1:A:896:ILE:HD13	1.95	0.47
1:A:1009:MET:HB3	1:A:1043:PHE:HZ	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1139:PRO:HG2	1:A:1140:ILE:HD12	1.96	0.47
1:C:974:LEU:HD23	1:C:1150:LEU:HD23	1.96	0.47
1:C:1139:PRO:HG2	1:C:1140:ILE:HD12	1.96	0.47
1:A:974:LEU:HD23	1:A:1150:LEU:HD23	1.96	0.47
1:E:2387:VAL:HG12	1:E:2390:LEU:H	1.78	0.47
1:A:1246:ILE:HA	1:A:1251:LEU:HD12	1.96	0.47
1:A:2387:VAL:HG12	1:A:2390:LEU:H	1.78	0.47
1:A:2295:ARG:HD3	1:C:2292:ALA:HA	1.97	0.47
1:E:2532:LEU:HD11	1:E:2542:TRP:CD1	2.50	0.47
1:A:2532:LEU:HD11	1:A:2542:TRP:CD1	2.50	0.47
1:C:1009:MET:HB3	1:C:1043:PHE:HZ	1.78	0.47
1:C:2017:PRO:HA	1:C:2020:PHE:HD2	1.78	0.47
1:E:1271:CYS:SG	1:E:1272:LEU:N	2.88	0.47
1:A:1051:CYS:SG	1:A:1081:TYR:OH	2.60	0.47
1:E:974:LEU:HD23	1:E:1150:LEU:HD23	1.96	0.47
1:C:1246:ILE:HA	1:C:1251:LEU:HD12	1.96	0.47
1:E:2298:PRO:HA	1:E:2301:ARG:HB2	1.97	0.47
1:E:1139:PRO:HG2	1:E:1140:ILE:HD12	1.96	0.47
1:E:2506:LEU:HD22	1:E:2529:LEU:HG	1.96	0.47
1:C:1271:CYS:SG	1:C:1272:LEU:N	2.88	0.46
1:E:2218:GLY:HA2	1:E:2452:LYS:HD3	1.96	0.46
1:A:1271:CYS:SG	1:A:1272:LEU:N	2.88	0.46
1:A:2298:PRO:HA	1:A:2301:ARG:HB2	1.97	0.46
1:E:1712:VAL:HG22	1:E:2058:HIS:HD1	1.81	0.46
1:A:1712:VAL:HG22	1:A:2058:HIS:HD1	1.81	0.46
1:E:1181:GLY:HA2	1:E:1184:TYR:HD2	1.81	0.46
1:A:1181:GLY:HA2	1:A:1184:TYR:HD2	1.81	0.46
1:A:2318:ARG:NH2	1:C:2245:GLN:O	2.49	0.46
1:C:1181:GLY:HA2	1:C:1184:TYR:HD2	1.81	0.46
1:C:2532:LEU:HD11	1:C:2542:TRP:CD1	2.50	0.46
1:A:2145:THR:HG21	1:A:2152:TRP:HZ3	1.81	0.46
1:C:2453:VAL:HG12	1:C:2455:PRO:HD3	1.98	0.46
1:A:947:TYR:HD2	1:A:953:GLN:HE21	1.64	0.46
1:C:807:LEU:HD13	1:C:959:GLN:HG3	1.98	0.46
1:E:947:TYR:HD2	1:E:953:GLN:HE21	1.64	0.46
1:A:807:LEU:HD13	1:A:959:GLN:HG3	1.98	0.45
1:C:1179:ILE:HD11	1:C:1248:LEU:HD12	1.98	0.45
1:A:942:ARG:O	1:A:946:HIS:ND1	2.45	0.45
1:C:2145:THR:HG21	1:C:2152:TRP:HZ3	1.81	0.45
1:C:2540:ILE:HD11	1:E:2535:SER:HB3	1.99	0.45
1:C:1747:PHE:HB2	1:C:1776:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2298:PRO:HA	1:C:2301:ARG:HB2	1.97	0.45
1:A:1747:PHE:HB2	1:A:1776:LEU:HD12	1.99	0.45
1:C:811:LYS:HD2	1:C:1102:LEU:HD21	1.99	0.45
1:E:1747:PHE:HB2	1:E:1776:LEU:HD12	1.99	0.45
1:C:947:TYR:HD2	1:C:953:GLN:HE21	1.64	0.45
1:C:1246:ILE:HG23	1:C:1251:LEU:HB2	1.99	0.45
1:A:1176:ARG:HH22	1:A:1281:ILE:HD12	1.82	0.45
1:C:1232:CYS:SG	1:C:1233:VAL:N	2.90	0.45
1:E:2318:ARG:HG2	1:E:2341:THR:HG22	1.98	0.45
1:A:1246:ILE:HG23	1:A:1251:LEU:HB2	1.99	0.45
1:A:2318:ARG:HG2	1:A:2341:THR:HG22	1.98	0.45
1:C:1712:VAL:HG22	1:C:2058:HIS:HD1	1.81	0.45
1:A:1232:CYS:SG	1:A:1233:VAL:N	2.90	0.45
1:E:811:LYS:HD2	1:E:1102:LEU:HD21	1.99	0.44
1:E:1246:ILE:HG23	1:E:1251:LEU:HB2	1.99	0.44
1:A:1771:PRO:HB3	1:A:1776:LEU:HB2	1.99	0.44
1:E:807:LEU:HD13	1:E:959:GLN:HG3	1.98	0.44
1:E:1179:ILE:HD11	1:E:1248:LEU:HD12	1.98	0.44
1:A:2520:GLU:HG3	1:E:2181:GLN:HG3	1.99	0.44
1:C:2312:THR:HA	1:C:2351:ARG:HH12	1.82	0.44
1:E:2145:THR:HG21	1:E:2152:TRP:HZ3	1.81	0.44
1:A:1079:TRP:HE3	1:A:1080:LEU:HD12	1.83	0.44
1:A:1179:ILE:HD11	1:A:1248:LEU:HD12	1.98	0.44
1:E:2453:VAL:HG12	1:E:2455:PRO:HD3	1.98	0.44
1:A:811:LYS:HD2	1:A:1102:LEU:HD21	1.99	0.44
1:A:2109:PHE:HA	1:A:2112:LYS:HE2	2.00	0.44
1:C:2318:ARG:HG2	1:C:2341:THR:HG22	1.98	0.44
1:E:1232:CYS:SG	1:E:1233:VAL:N	2.90	0.44
1:A:2453:VAL:HG12	1:A:2455:PRO:HD3	1.98	0.44
1:A:2494:PHE:HE2	1:E:2490:HIS:HA	1.81	0.44
1:E:1079:TRP:HE3	1:E:1080:LEU:HD12	1.83	0.44
1:A:822:LEU:HD22	1:A:1091:SER:HB2	2.00	0.44
1:C:1176:ARG:HH22	1:C:1281:ILE:HD12	1.82	0.44
1:C:1771:PRO:HB3	1:C:1776:LEU:HB2	1.99	0.44
1:A:2312:THR:HA	1:A:2351:ARG:HH12	1.82	0.43
1:A:2494:PHE:CE2	1:E:2490:HIS:HA	2.53	0.43
1:C:2109:PHE:HA	1:C:2112:LYS:HE2	2.00	0.43
1:E:1771:PRO:HB3	1:E:1776:LEU:HB2	1.99	0.43
1:A:2034:ASP:OD2	1:A:2089:TYR:OH	2.33	0.43
1:E:822:LEU:HD22	1:E:1091:SER:HB2	2.00	0.43
1:E:1176:ARG:HH22	1:E:1281:ILE:HD12	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2471:VAL:HA	1:C:2474:VAL:HG12	2.00	0.43
1:A:2204:TRP:CH2	1:C:2021:LEU:HB3	2.53	0.43
1:A:2353:GLN:HB3	1:A:2366:VAL:HG22	2.01	0.43
1:C:2204:TRP:CH2	1:E:2021:LEU:HB3	2.53	0.43
1:E:2471:VAL:HA	1:E:2474:VAL:HG12	2.01	0.43
1:A:2188:LYS:NZ	1:C:2143:THR:O	2.48	0.43
1:C:2064:ILE:HG22	1:C:2065:LEU:HD22	2.01	0.43
1:C:2353:GLN:HB3	1:C:2366:VAL:HG22	2.00	0.43
1:E:996:LEU:HD11	1:E:1288:PHE:HD1	1.84	0.43
1:A:996:LEU:HD11	1:A:1288:PHE:HD1	1.84	0.43
1:A:1521:ARG:HA	1:A:1528:ARG:HH22	1.84	0.43
1:C:996:LEU:HD11	1:C:1288:PHE:HD1	1.84	0.43
1:C:1079:TRP:HE3	1:C:1080:LEU:HD12	1.83	0.43
1:E:1211:ASP:OD1	1:E:1294:ARG:NH1	2.52	0.43
1:C:942:ARG:O	1:C:946:HIS:ND1	2.45	0.43
1:E:2353:GLN:HB3	1:E:2366:VAL:HG22	2.00	0.43
1:E:1964:ASP:O	1:E:1968:THR:OG1	2.32	0.43
1:E:2312:THR:HA	1:E:2351:ARG:HH12	1.82	0.43
1:A:1211:ASP:OD1	1:A:1294:ARG:NH1	2.52	0.43
1:C:1211:ASP:OD1	1:C:1294:ARG:NH1	2.52	0.43
1:E:2286:ILE:O	1:E:2444:LEU:N	2.50	0.43
1:C:822:LEU:HD22	1:C:1091:SER:HB2	2.00	0.42
1:C:1521:ARG:HA	1:C:1528:ARG:HH22	1.84	0.42
1:C:2184:LYS:NZ	1:E:2146:THR:O	2.52	0.42
1:A:2064:ILE:HG22	1:A:2065:LEU:HD22	2.01	0.42
1:A:2471:VAL:HA	1:A:2474:VAL:HG12	2.00	0.42
1:E:2109:PHE:HA	1:E:2112:LYS:HE2	2.00	0.42
1:C:2318:ARG:NH2	1:E:2245:GLN:O	2.52	0.42
1:E:1521:ARG:HA	1:E:1528:ARG:HH22	1.84	0.42
1:C:2286:ILE:O	1:C:2444:LEU:N	2.50	0.42
1:A:2293:LEU:HD22	1:A:2429:TRP:HE1	1.85	0.42
1:E:2151:ASN:ND2	1:E:2526:TYR:OH	2.40	0.42
1:E:2288:GLY:N	1:E:2442:ASN:O	2.51	0.42
1:E:2293:LEU:HD22	1:E:2429:TRP:HE1	1.85	0.42
1:E:2407:ARG:HG2	1:E:2428:GLU:HG2	2.02	0.42
1:E:2535:SER:OG	1:E:2538:THR:OG1	2.25	0.42
1:A:1082:LEU:HD13	1:A:1082:LEU:HA	1.95	0.42
1:A:1963:HIS:HA	1:A:1966:LEU:HD12	2.01	0.42
1:C:2318:ARG:NH1	1:E:2244:GLN:OE1	2.53	0.42
1:C:802:ARG:HG2	1:C:944:GLN:HE22	1.85	0.41
1:E:1963:HIS:HA	1:E:1966:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2288:GLY:N	1:A:2442:ASN:O	2.51	0.41
1:C:2293:LEU:HD22	1:C:2429:TRP:HE1	1.85	0.41
1:E:1082:LEU:HD13	1:E:1082:LEU:HA	1.94	0.41
1:A:802:ARG:HG2	1:A:944:GLN:HE22	1.85	0.41
1:A:2286:ILE:O	1:A:2444:LEU:N	2.50	0.41
1:C:2535:SER:OG	1:C:2538:THR:OG1	2.25	0.41
1:E:2064:ILE:HG22	1:E:2065:LEU:HD22	2.01	0.41
1:E:2354:LEU:HD23	1:E:2357:LEU:HD12	2.03	0.41
1:A:1040:LEU:HD22	1:A:1101:LEU:HD23	2.03	0.41
1:E:802:ARG:HG2	1:E:944:GLN:HE22	1.85	0.41
1:E:1087:ARG:NH2	1:E:1257:GLY:O	2.54	0.41
1:A:2407:ARG:HG2	1:A:2428:GLU:HG2	2.02	0.41
1:C:1769:PHE:HA	1:C:1770:PRO:HD3	1.88	0.41
1:C:1963:HIS:HA	1:C:1966:LEU:HD12	2.01	0.41
1:C:2493:MET:HA	1:E:2534:ARG:HG2	2.03	0.41
1:E:2333:VAL:HG11	1:E:2382:PRO:HA	2.03	0.41
1:A:2151:ASN:ND2	1:A:2526:TYR:OH	2.40	0.41
1:A:2479:LYS:HD3	1:C:2480:PHE:HE1	1.86	0.41
1:C:851:CYS:O	1:C:854:THR:OG1	2.34	0.41
1:E:1253:CYS:SG	1:E:1254:THR:N	2.94	0.41
1:A:2497:LEU:HA	1:A:2498:PRO:HD3	1.92	0.41
1:C:1253:CYS:SG	1:C:1254:THR:N	2.94	0.41
1:C:2354:LEU:HD23	1:C:2357:LEU:HD12	2.03	0.41
1:E:2504:LEU:HD23	1:E:2504:LEU:HA	1.90	0.41
1:A:2378:ALA:HB3	1:A:2450:SER:HA	2.03	0.41
1:C:1087:ARG:NH2	1:C:1257:GLY:O	2.54	0.41
1:E:1040:LEU:HD22	1:E:1101:LEU:HD23	2.03	0.40
1:A:1716:LEU:HD22	1:A:2051:VAL:HG22	2.03	0.40
1:C:2238:LEU:HD22	1:C:2430:TRP:CE2	2.57	0.40
1:E:851:CYS:O	1:E:854:THR:OG1	2.34	0.40
1:A:1087:ARG:NH2	1:A:1257:GLY:O	2.54	0.40
1:A:2204:TRP:HH2	1:C:2021:LEU:HB3	1.86	0.40
1:C:2407:ARG:HG2	1:C:2428:GLU:HG2	2.02	0.40
1:E:822:LEU:HD13	1:E:1094:LEU:HB3	2.04	0.40
1:C:2226:VAL:O	1:C:2243:ALA:N	2.54	0.40
1:A:823:LYS:HA	1:A:1092:THR:HG22	2.04	0.40
1:A:1214:ILE:HG12	1:A:1290:LEU:HB3	2.03	0.40
1:A:1253:CYS:SG	1:A:1254:THR:N	2.94	0.40
1:A:2129:PRO:HG3	1:E:2475:LEU:HD23	2.03	0.40
1:A:2226:VAL:O	1:A:2243:ALA:N	2.54	0.40
1:A:2333:VAL:HG11	1:A:2382:PRO:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2360:GLY:HA2	1:A:2407:ARG:HH12	1.87	0.40
1:A:2535:SER:OG	1:A:2538:THR:OG1	2.25	0.40
1:C:2308:LEU:HB3	1:C:2355:ALA:HB2	2.03	0.40
1:E:1214:ILE:HG12	1:E:1290:LEU:HB3	2.03	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	
1	A	1478/2547 (58%)	1358 (92%)	120 (8%)	0	100	100
1	C	1478/2547 (58%)	1359 (92%)	119 (8%)	0	100	100
1	E	1478/2547 (58%)	1360 (92%)	118 (8%)	0	100	100
All	All	4434/7641 (58%)	4077 (92%)	357 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	1198/2246 (53%)	1195 (100%)	3 (0%)	91	92
1	C	1198/2246 (53%)	1195 (100%)	3 (0%)	91	92
1	E	1198/2246 (53%)	1195 (100%)	3 (0%)	91	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3594/6738 (53%)	3585 (100%)	9 (0%)	90	92

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	903	ARG
1	A	1547	ARG
1	A	1971	ARG
1	C	903	ARG
1	C	1547	ARG
1	C	1971	ARG
1	E	903	ARG
1	E	1547	ARG
1	E	1971	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	944	GLN
1	A	1013	HIS
1	A	1047	GLN
1	A	1669	GLN
1	A	2050	GLN
1	C	944	GLN
1	C	1013	HIS
1	C	1047	GLN
1	C	2050	GLN
1	E	944	GLN
1	E	1047	GLN
1	E	2050	GLN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

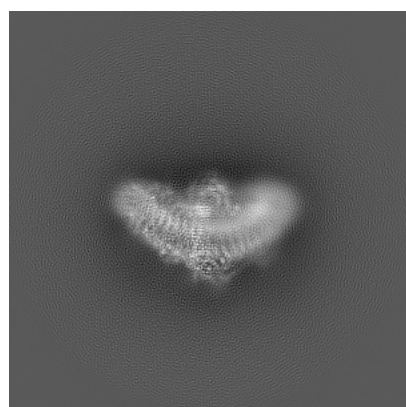
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7042. These allow visual inspection of the internal detail of the map and identification of artifacts.

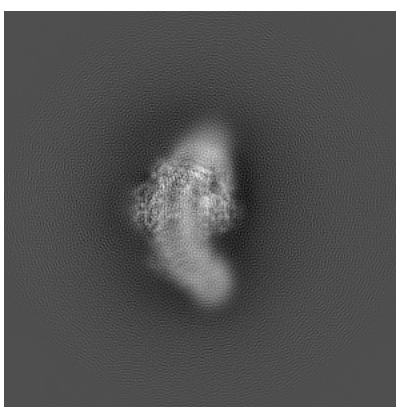
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

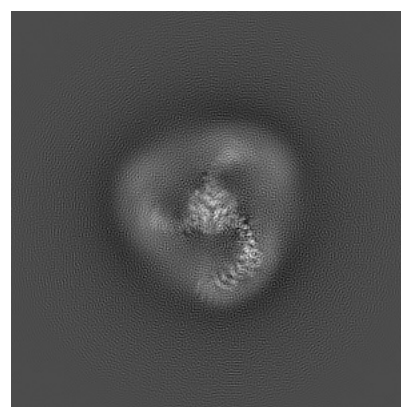
6.1.1 Primary map



X



Y

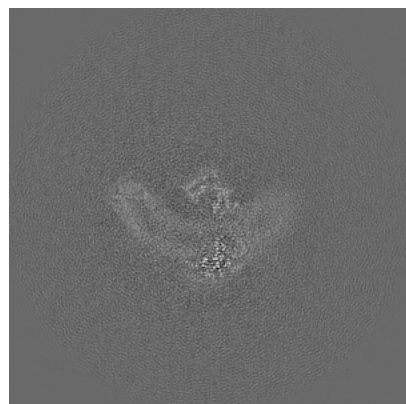


Z

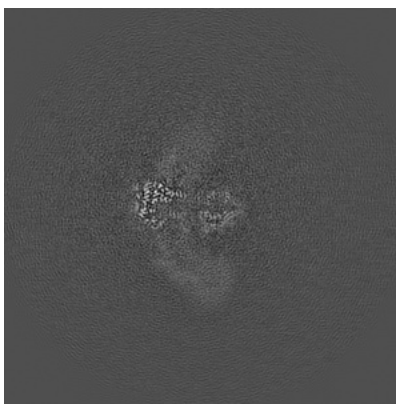
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

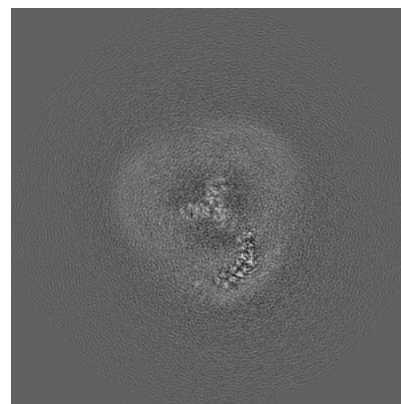
6.2.1 Primary map



X Index: 200



Y Index: 200

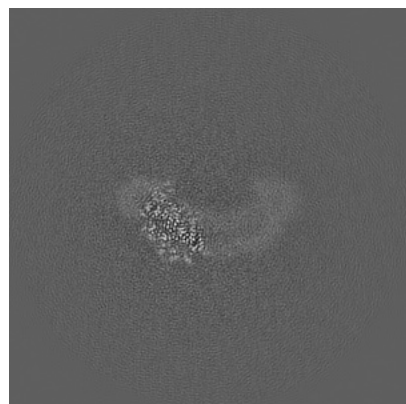


Z Index: 200

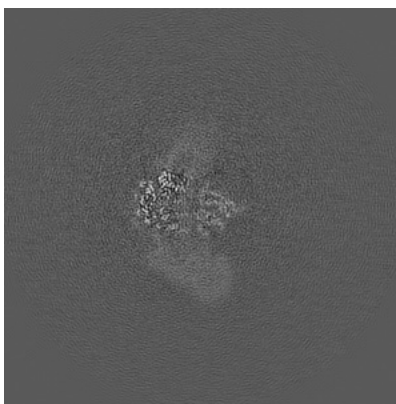
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

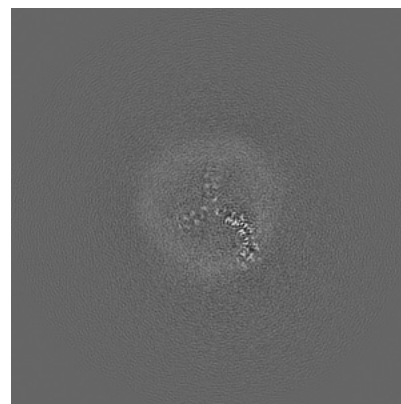
6.3.1 Primary map



X Index: 233



Y Index: 193

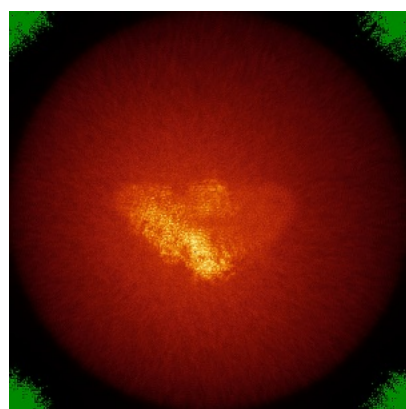


Z Index: 170

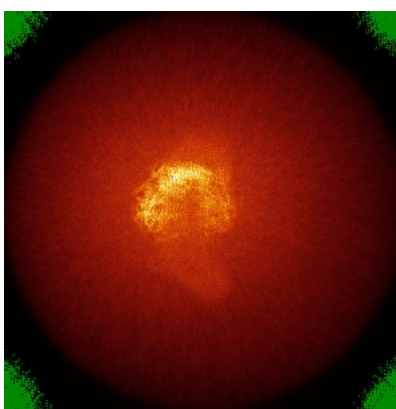
The images above show the largest variance slices of the map in three orthogonal directions.

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

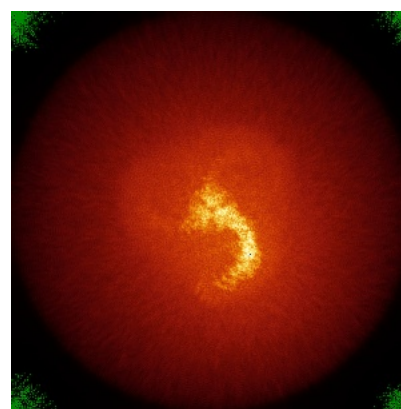
6.4.1 Primary map



X



Y

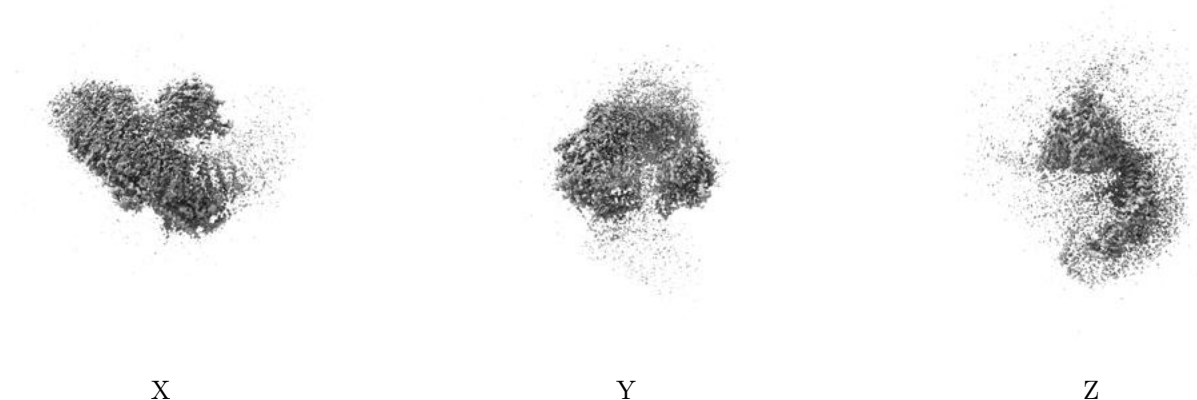


Z

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

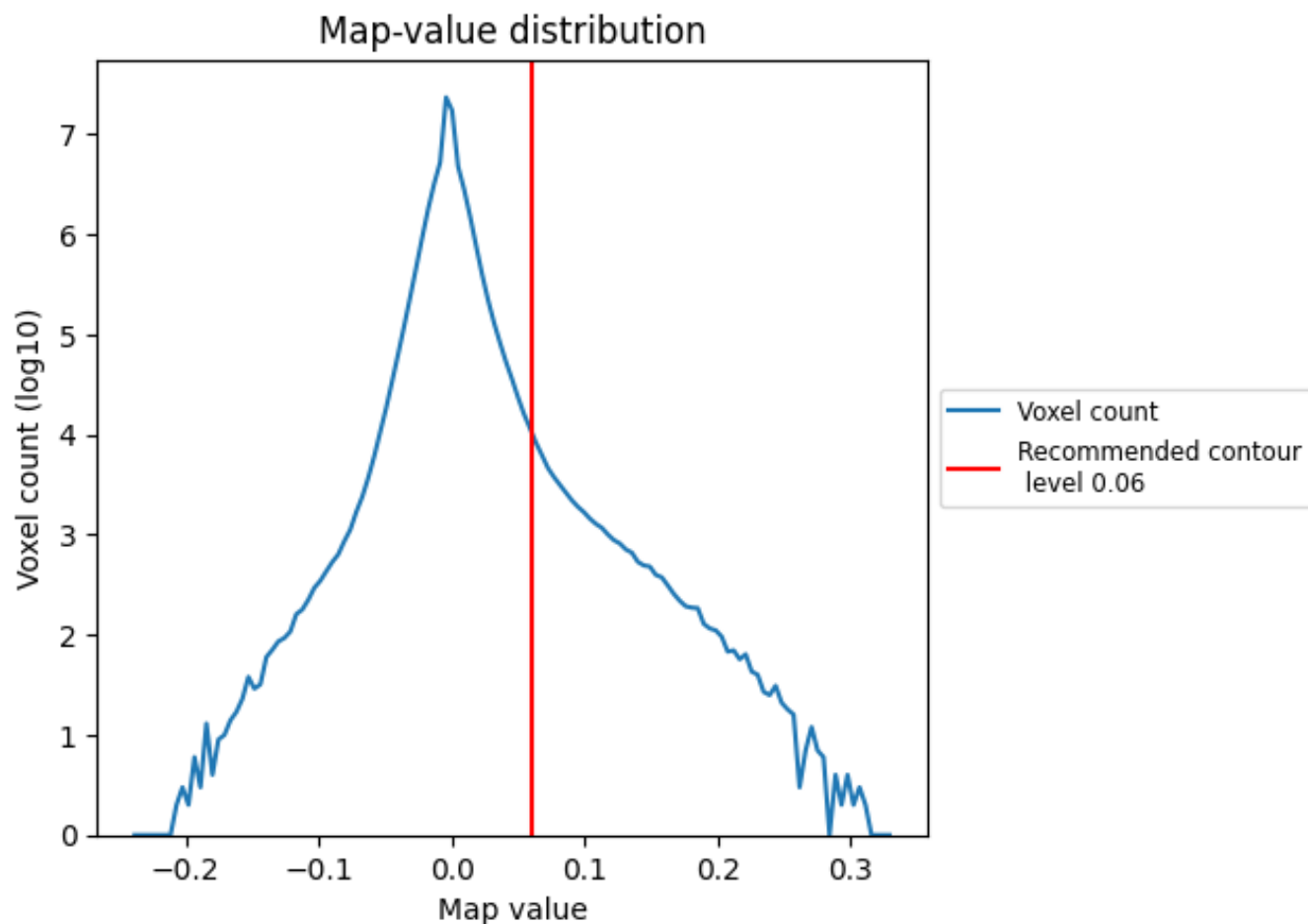
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

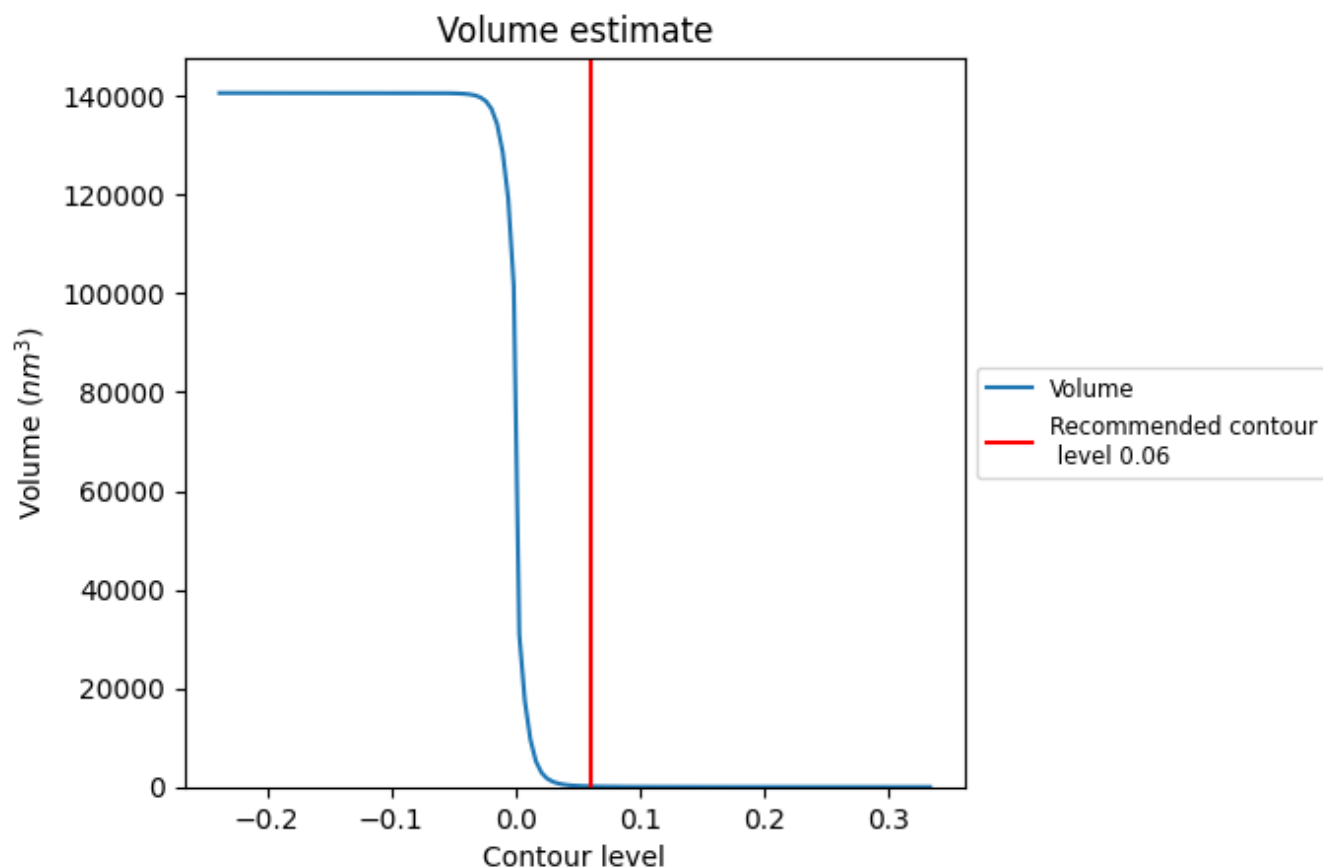
This section contains the results of statistical analysis of the map.

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.

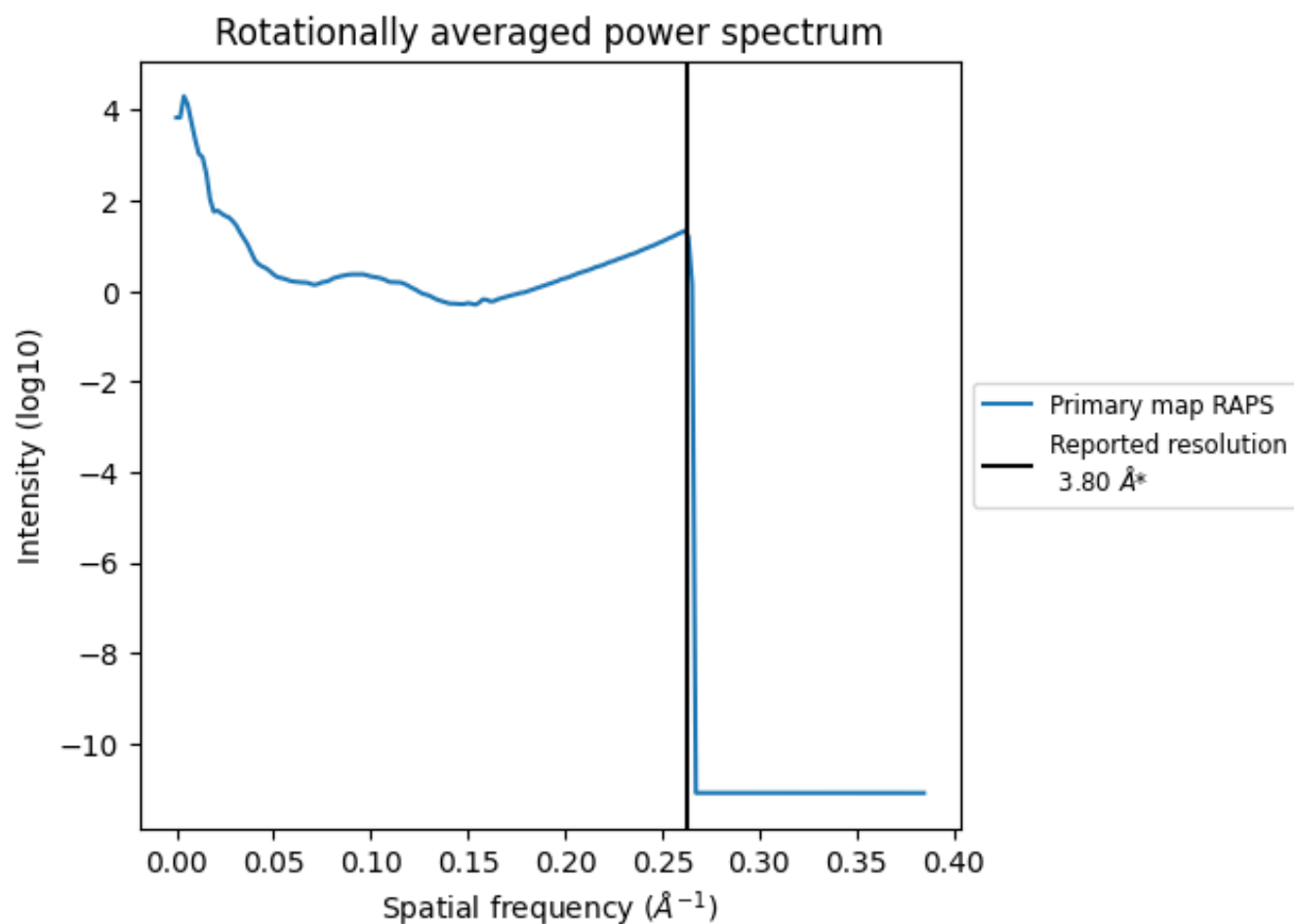
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 123 nm³; this corresponds to an approximate mass of 111 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 0.263 Å⁻¹

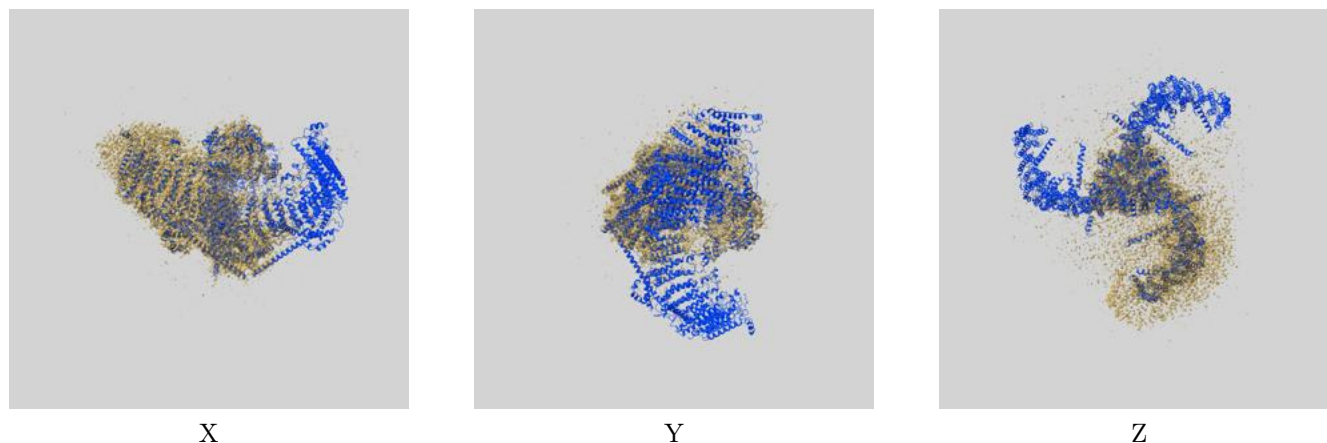
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

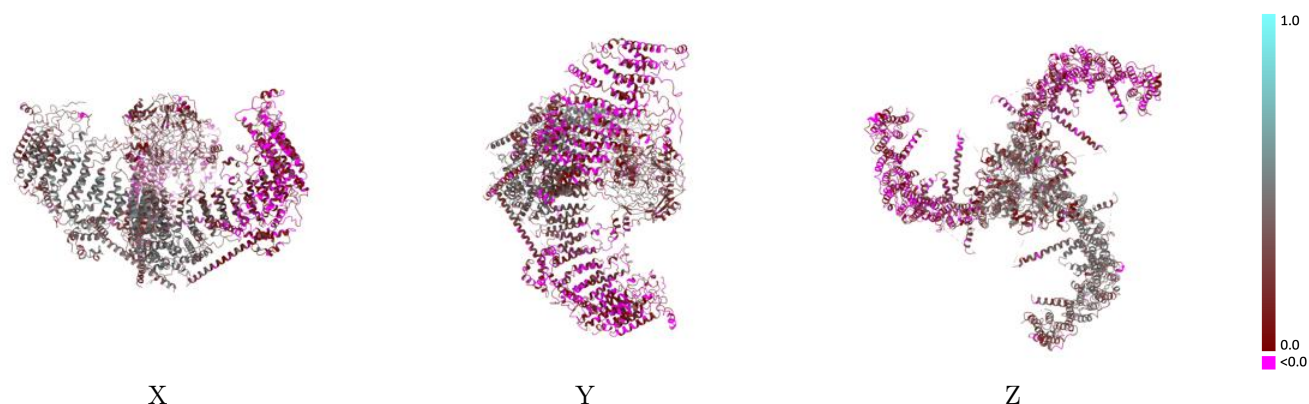
This section contains information regarding the fit between EMDB map EMD-7042 and PDB model 6B3R. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



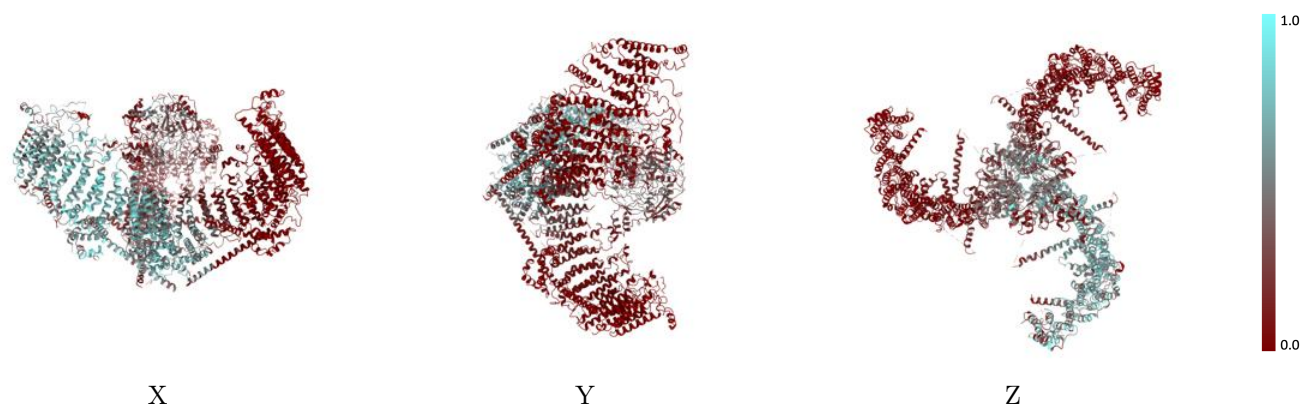
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



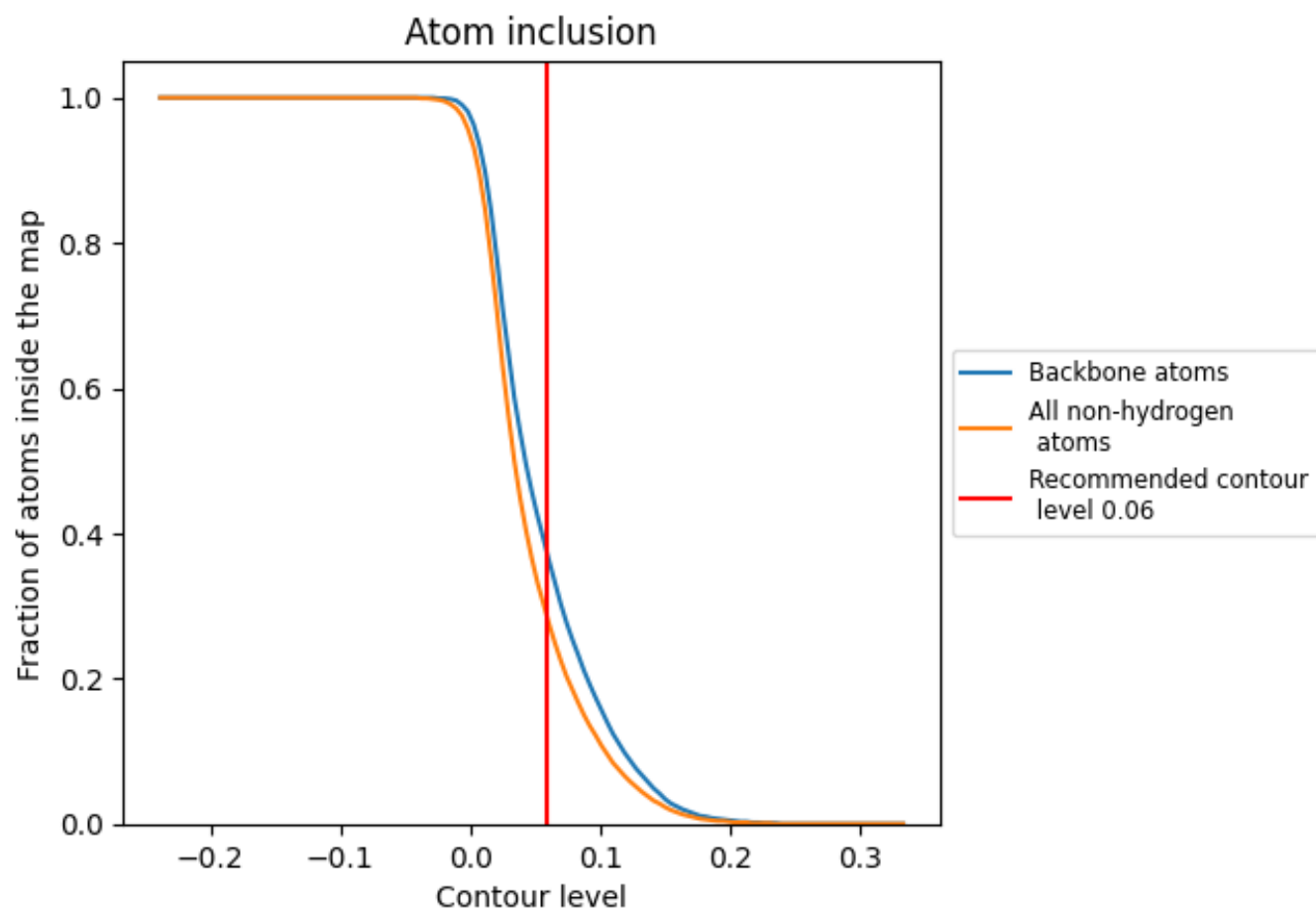
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion ⓘ



At the recommended contour level, 37% of all backbone atoms, 28% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.2810	<div></div> 0.2360
A	<div></div> 0.5390	<div></div> 0.3720
B	<div></div> 0.7250	<div></div> 0.4520
C	<div></div> 0.1470	<div></div> 0.1650
D	<div></div> 0.6880	<div></div> 0.4410
E	<div></div> 0.1470	<div></div> 0.1660
F	<div></div> 0.6250	<div></div> 0.4110

1.0

0.0

<0.0