



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 03:12 PM UTC

PDB ID : 7KXY / pdb_00007kxy
EMDB ID : EMD-23067
Title : Cryo-EM structure of human Factor Va at 4.4 Angstrom resolution
Authors : Ruben, E.A.; Di Cera, E.
Deposited on : 2020-12-05
Resolution : 4.40 Å(reported)

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

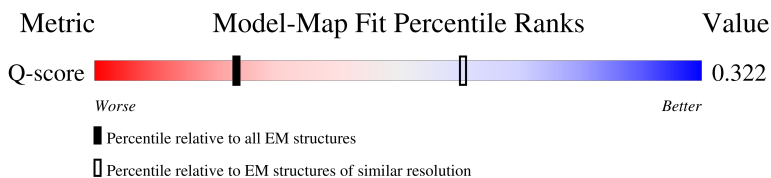
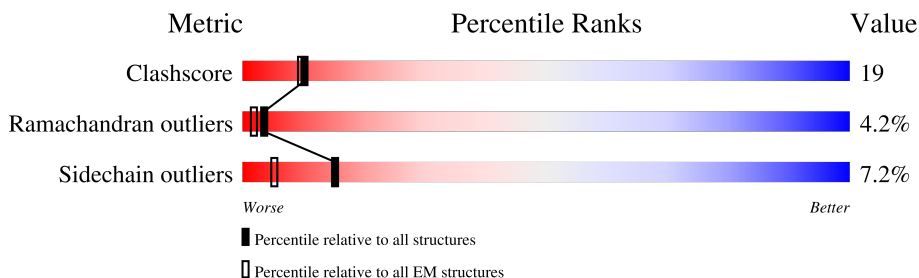
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	709	
2	B	651	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9510 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 Coagulation factor Va.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	588	Total	C	N	O	S	0	0
			4704	2991	793	895	25		

- Molecule 2 is a protein called Coagulation factor Va.

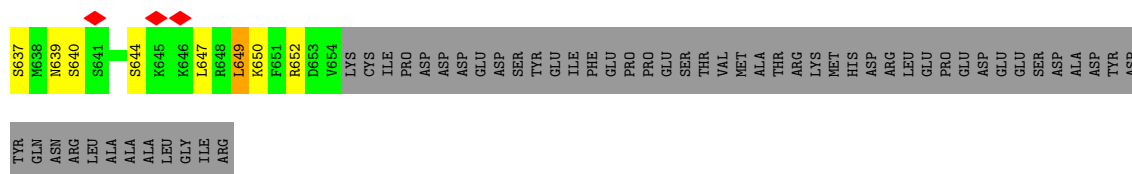
Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	593	Total	C	N	O	S	0	0
			4806	3057	837	889	23		

3 Residue-property plots

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.

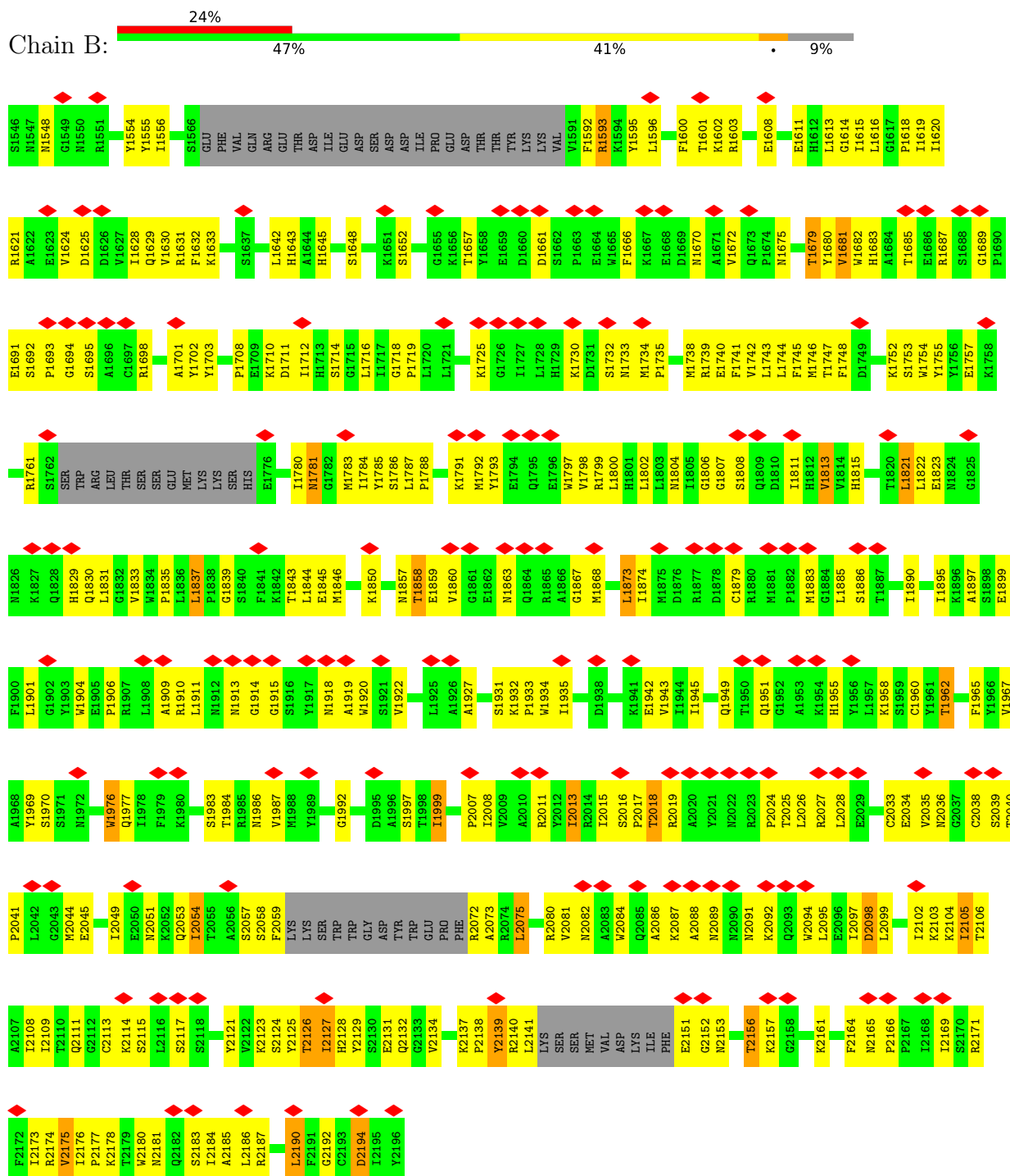
• Molecule 1: Coagulation factor Va





• Molecule 2: Coagulation factor Va

Chain B:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	63745	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.65	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	22.370	Depositor
Minimum map value	-14.862	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.7	Depositor
Map size ($\text{\AA}$)	275.0, 275.0, 275.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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	0.18	0/4817	0.48	0/6519
2	B	0.19	0/4929	0.50	0/6663
All	All	0.19	0/9746	0.49	0/13182

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

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	4704	0	4581	161	0
2	B	4806	0	4682	206	0
All	All	9510	0	9263	361	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 19.

All (361) 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:639:ASN:HB2	1:A:647:LEU:HD22	1.62	0.81
2:B:2125:TYR:HA	2:B:2178:LYS:H	1.46	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:ILE:H	1:A:407:PHE:HA	1.46	0.78
2:B:2084:TRP:HB2	2:B:2185:ALA:HA	1.64	0.78
2:B:2108:ILE:HG22	2:B:2190:LEU:HD21	1.67	0.76
2:B:2058:SER:HB2	2:B:2086:ALA:HA	1.68	0.76
1:A:249:GLU:HB2	1:A:269:ASN:HB2	1.69	0.75
2:B:1555:TYR:HB3	2:B:1595:TYR:HB2	1.68	0.74
1:A:87:GLN:HB2	1:A:142:HIS:HB3	1.69	0.73
1:A:232:MET:HA	1:A:263:ALA:H	1.53	0.73
2:B:1739:ARG:HH21	2:B:1793:TYR:HB2	1.53	0.73
2:B:1962:THR:HG21	2:B:2017:PRO:HB2	1.72	0.72
1:A:19:PRO:HG2	1:A:210:VAL:HG23	1.70	0.71
1:A:537:LYS:HG3	1:A:543:ASP:HA	1.71	0.71
2:B:1910:ARG:O	2:B:2027:ARG:NH1	2.24	0.71
1:A:523:PHE:HB2	1:A:558:MET:HB2	1.73	0.71
1:A:36:ILE:HG22	1:A:158:LEU:HD21	1.72	0.71
2:B:2104:LYS:HG3	2:B:2169:ILE:HD11	1.71	0.71
2:B:1815:HIS:HB2	2:B:1859:GLU:HG2	1.75	0.69
2:B:2049:ILE:HB	2:B:2099:LEU:HD22	1.75	0.69
2:B:1791:LYS:HG3	2:B:2007:PRO:HD3	1.76	0.68
1:A:38:TYR:HB3	1:A:60:PRO:HD3	1.76	0.67
1:A:90:ARG:HD2	1:A:126:ILE:HA	1.76	0.67
1:A:277:LYS:HD2	1:A:433:SER:HB2	1.77	0.67
2:B:1698:ARG:HA	2:B:1843:THR:HG21	1.76	0.67
2:B:1619:ILE:HG23	2:B:1719:PRO:HG2	1.78	0.66
2:B:1600:PHE:HD1	2:B:1601:THR:HG23	1.60	0.66
1:A:585:CYS:SG	1:A:586:SER:N	2.69	0.66
2:B:1592:PHE:HB2	2:B:1618:PRO:HD3	1.78	0.66
1:A:115:ALA:H	1:A:118:ARG:HD2	1.60	0.66
1:A:241:ILE:HG13	1:A:282:SER:HB2	1.79	0.65
2:B:2095:LEU:HD12	2:B:2097:ILE:HD11	1.78	0.65
2:B:2129:TYR:HB2	2:B:2137:LYS:HE3	1.78	0.65
2:B:2058:SER:HA	2:B:2087:LYS:HG2	1.78	0.65
1:A:274:PRO:HB2	1:A:426:PRO:HD2	1.78	0.65
1:A:151:ILE:O	1:A:155:ASN:ND2	2.30	0.64
1:A:539:CYS:SG	1:A:540:GLU:N	2.71	0.64
1:A:565:VAL:HB	1:A:566:PRO:HD3	1.80	0.64
1:A:568:SER:O	1:A:650:LYS:NZ	2.30	0.64
2:B:1613:LEU:O	2:B:1781:ASN:ND2	2.30	0.63
2:B:2113:CYS:SG	2:B:2114:LYS:N	2.71	0.63
2:B:2111:GLN:NE2	2:B:2187:ARG:O	2.32	0.62
2:B:1784:ILE:HA	2:B:1868:MET:HE1	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1823:GLU:HB2	2:B:1829:HIS:HB3	1.81	0.62
1:A:602:SER:HB3	1:A:609:HIS:HB3	1.82	0.62
2:B:1624:VAL:O	2:B:1725:LYS:NZ	2.28	0.62
1:A:154:PHE:O	1:A:156:SER:N	2.33	0.61
2:B:1813:VAL:HA	2:B:1835:PRO:HA	1.82	0.61
1:A:359:ILE:HG23	1:A:540:GLU:HB2	1.82	0.61
2:B:1967:VAL:HG23	2:B:2015:ILE:HG12	1.83	0.61
2:B:1895:ILE:HG22	2:B:1906:PRO:HB2	1.82	0.60
2:B:1685:THR:O	2:B:1689:GLY:N	2.32	0.60
2:B:1910:ARG:H	2:B:1913:ASN:HB2	1.65	0.60
2:B:1695:SER:O	2:B:1698:ARG:NH1	2.34	0.60
2:B:1837:LEU:HD23	2:B:1837:LEU:H	1.67	0.60
2:B:1616:LEU:HD11	2:B:1719:PRO:HD3	1.82	0.60
2:B:1743:LEU:HB3	2:B:1780:ILE:HG12	1.83	0.60
1:A:132:PRO:HD3	1:A:140:LEU:HB2	1.85	0.59
2:B:1969:TYR:HA	2:B:2013:ILE:HG22	1.84	0.59
2:B:1648:SER:OG	2:B:1685:THR:OG1	2.20	0.59
2:B:1652:SER:HB2	2:B:1666:PHE:HB3	1.84	0.59
1:A:382:ASN:HB2	1:A:383:PRO:HD3	1.84	0.59
1:A:264:THR:OG1	1:A:265:SER:N	2.37	0.58
1:A:132:PRO:HB3	1:A:136:ASP:HB2	1.84	0.58
1:A:609:HIS:ND1	2:B:1687:ARG:O	2.36	0.58
2:B:1797:TRP:HE3	2:B:1845:GLU:HB3	1.68	0.58
1:A:239:PHE:HD1	1:A:287:HIS:HE1	1.51	0.58
2:B:1692:SER:O	2:B:1694:GLY:N	2.36	0.58
2:B:1919:ALA:HB1	2:B:2025:THR:HG23	1.86	0.58
1:A:11:GLN:HE21	1:A:12:GLY:H	1.52	0.58
1:A:262:SER:HB2	2:B:1813:VAL:HG11	1.84	0.58
1:A:575:CYS:SG	1:A:576:PHE:N	2.74	0.58
1:A:4:ARG:HH12	1:A:63:TYR:HD2	1.51	0.57
2:B:1735:PRO:HB2	2:B:1738:MET:HG3	1.85	0.57
2:B:1951:GLN:O	2:B:2027:ARG:NE	2.36	0.57
2:B:2125:TYR:CE2	2:B:2127:ILE:HG12	2.39	0.57
1:A:585:CYS:HA	1:A:620:GLY:HA3	1.86	0.57
2:B:2034:GLU:HG3	2:B:2035:VAL:H	1.69	0.57
1:A:2:GLN:HE22	1:A:4:ARG:HH11	1.50	0.57
2:B:1615:ILE:HG12	2:B:1781:ASN:HB3	1.86	0.57
2:B:2194:ASP:N	2:B:2194:ASP:OD1	2.38	0.57
1:A:571:THR:HA	1:A:650:LYS:HE3	1.87	0.57
2:B:1739:ARG:HD3	2:B:1791:LYS:HB3	1.87	0.57
1:A:149:ASN:HB3	1:A:153:ASP:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ASN:HB3	1:A:278:TRP:HB3	1.87	0.56
2:B:2128:HIS:HA	2:B:2137:LYS:O	2.05	0.56
1:A:409:ASN:ND2	1:A:413:ARG:O	2.37	0.56
2:B:1965:PHE:HE2	2:B:2015:ILE:HG23	1.71	0.56
1:A:210:VAL:HG12	1:A:292:MET:HG3	1.87	0.56
2:B:1813:VAL:HG12	2:B:1835:PRO:HB3	1.87	0.56
1:A:383:PRO:O	1:A:385:MET:N	2.38	0.56
1:A:203:MET:HE3	1:A:204:TYR:H	1.70	0.55
2:B:1822:LEU:HB2	2:B:1830:GLN:HA	1.87	0.55
2:B:2088:ALA:H	2:B:2092:LYS:HE3	1.71	0.55
2:B:2165:ASN:HB2	2:B:2166:PRO:HD3	1.88	0.55
2:B:1645:HIS:NE2	2:B:1703:TYR:OH	2.35	0.54
2:B:1901:LEU:HD22	2:B:1922:VAL:HA	1.89	0.54
2:B:1901:LEU:HB2	2:B:1922:VAL:HG13	1.89	0.54
2:B:1719:PRO:HG3	2:B:1742:VAL:HG21	1.90	0.54
2:B:1909:ALA:O	2:B:1910:ARG:NE	2.33	0.54
1:A:264:THR:HG21	2:B:1835:PRO:HD3	1.88	0.54
2:B:1983:SER:OG	2:B:1984:THR:N	2.40	0.54
1:A:549:ASP:O	1:A:553:TYR:N	2.32	0.54
2:B:1556:ILE:HD13	2:B:1630:VAL:HG13	1.88	0.54
2:B:2094:TRP:HB2	2:B:2174:ARG:HD3	1.88	0.54
2:B:1746:MET:HE3	2:B:1807:GLY:H	1.71	0.54
2:B:2126:THR:O	2:B:2128:HIS:N	2.40	0.54
2:B:2128:HIS:CE1	2:B:2176:ILE:HG13	2.42	0.54
1:A:594:LEU:HB2	1:A:615:LEU:HD11	1.90	0.54
1:A:11:GLN:O	1:A:37:VAL:N	2.27	0.53
1:A:477:TYR:CD1	1:A:495:LEU:HB2	2.43	0.53
2:B:1628:ILE:HB	2:B:1682:TRP:HB2	1.90	0.53
2:B:1932:LYS:O	2:B:1934:TRP:HD1	1.92	0.53
2:B:1815:HIS:HD2	2:B:1857:ASN:HB2	1.72	0.53
2:B:2099:LEU:HD12	2:B:2173:ILE:HG12	1.89	0.53
2:B:2109:ILE:HG23	2:B:2161:LYS:HB3	1.90	0.53
1:A:607:LYS:O	2:B:1692:SER:OG	2.26	0.53
1:A:58:LEU:HD11	1:A:160:GLY:HA2	1.90	0.53
1:A:138:PRO:HG3	1:A:179:PHE:HE2	1.74	0.53
1:A:482:ASP:HB3	1:A:486:ASP:H	1.73	0.53
1:A:217:ILE:HG12	1:A:219:VAL:HG23	1.91	0.53
1:A:228:HIS:HA	1:A:267:THR:HG22	1.91	0.53
1:A:76:ASN:O	1:A:116:PRO:HA	2.09	0.52
1:A:414:PRO:HB3	1:A:447:VAL:H	1.73	0.52
1:A:652:ARG:NH1	2:B:1661:ASP:OD2	2.35	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2105:ILE:HG22	2:B:2192:GLY:HA3	1.91	0.52
2:B:2131:GLU:HG3	2:B:2132:GLN:H	1.74	0.52
2:B:1752:LYS:HB3	2:B:1754:TRP:CH2	2.44	0.52
2:B:1804:ASN:O	2:B:1839:GLY:N	2.40	0.52
2:B:1631:ARG:HE	2:B:1679:THR:HA	1.74	0.52
2:B:2127:ILE:HB	2:B:2139:TYR:CD1	2.44	0.52
2:B:1548:ASN:ND2	2:B:1625:ASP:OD1	2.43	0.52
1:A:590:GLN:NE2	1:A:592:GLU:O	2.43	0.52
2:B:1945:ILE:HG12	2:B:2008:ILE:HG21	1.91	0.52
2:B:1962:THR:OG1	2:B:2025:THR:O	2.28	0.52
2:B:1702:TYR:CE2	2:B:1718:GLY:HA3	2.45	0.51
2:B:2123:LYS:HD3	2:B:2181:ASN:HD22	1.75	0.51
1:A:597:HIS:HB2	1:A:637:SER:HA	1.91	0.51
1:A:252:HIS:O	1:A:466:THR:HG21	2.11	0.51
1:A:339:ILE:HD12	1:A:566:PRO:HG2	1.93	0.51
2:B:2129:TYR:HB2	2:B:2137:LYS:HB3	1.93	0.51
1:A:595:THR:O	1:A:637:SER:OG	2.28	0.51
2:B:1899:GLU:OE2	2:B:1931:SER:OG	2.28	0.51
2:B:2059:PHE:HB3	2:B:2072:ARG:HE	1.76	0.51
2:B:2108:ILE:HG23	2:B:2164:PHE:HE1	1.76	0.51
1:A:418:TYR:HB3	1:A:480:ASP:HB2	1.93	0.51
1:A:377:THR:OG1	1:A:378:LYS:N	2.43	0.51
2:B:1965:PHE:CZ	2:B:1967:VAL:HB	2.45	0.51
2:B:1621:ARG:HH12	2:B:1735:PRO:HD3	1.76	0.50
1:A:593:ILE:HD13	1:A:616:PHE:HE1	1.75	0.50
1:A:388:ASP:HB3	1:A:517:GLN:HG3	1.93	0.50
1:A:416:SER:OG	1:A:480:ASP:N	2.44	0.50
2:B:2183:SER:OG	2:B:2184:ILE:N	2.45	0.50
2:B:1753:SER:HB3	2:B:1757:GLU:HB2	1.94	0.50
1:A:539:CYS:HB3	1:A:545:VAL:HG21	1.94	0.49
2:B:1608:GLU:HA	2:B:1611:GLU:HB2	1.94	0.49
2:B:1613:LEU:HD22	2:B:1616:LEU:HD23	1.93	0.49
2:B:1798:VAL:HG21	2:B:1846:MET:HE2	1.93	0.49
2:B:2181:ASN:C	2:B:2183:SER:H	2.20	0.49
1:A:227:TRP:N	1:A:268:ALA:O	2.46	0.49
1:A:184:VAL:HG21	1:A:230:LEU:HD13	1.95	0.49
1:A:514:ILE:HB	1:A:580:VAL:HA	1.94	0.49
2:B:2138:PRO:O	2:B:2140:ARG:N	2.45	0.49
1:A:329:GLU:N	1:A:329:GLU:OE1	2.45	0.49
1:A:429:ASP:N	1:A:429:ASP:OD1	2.45	0.49
1:A:520:PHE:CZ	1:A:649:LEU:HD22	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1548:ASN:HD22	2:B:1683:HIS:CD2	2.31	0.49
1:A:63:TYR:CG	1:A:170:LEU:HD13	2.48	0.49
1:A:241:ILE:O	1:A:258:ILE:HB	2.12	0.49
2:B:1897:ALA:HA	2:B:1935:ILE:HG22	1.95	0.49
2:B:1942:GLU:OE1	2:B:2011:ARG:NE	2.42	0.49
2:B:2103:LYS:HB2	2:B:2194:ASP:HA	1.95	0.49
2:B:2132:GLN:HA	2:B:2171:ARG:HE	1.77	0.49
2:B:1613:LEU:HB3	2:B:1616:LEU:HB3	1.94	0.49
1:A:334:ASP:HA	1:A:362:HIS:HA	1.95	0.48
1:A:253:HIS:O	1:A:255:VAL:N	2.46	0.48
2:B:1745:PHE:O	2:B:1804:ASN:ND2	2.47	0.48
2:B:2080:ARG:HG3	2:B:2081:VAL:H	1.78	0.48
1:A:84:ILE:HD11	1:A:144:TYR:CZ	2.48	0.48
1:A:87:GLN:HB2	1:A:143:ILE:H	1.79	0.48
1:A:186:LEU:HD21	1:A:188:ALA:HB3	1.95	0.48
1:A:72:VAL:O	1:A:74:PHE:N	2.46	0.48
1:A:262:SER:O	1:A:264:THR:HG22	2.12	0.48
1:A:472:CYS:HB3	1:A:499:LYS:HB2	1.94	0.48
1:A:609:HIS:H	2:B:1691:GLU:CD	2.21	0.48
2:B:1752:LYS:HE3	2:B:1754:TRP:CZ2	2.49	0.48
1:A:522:VAL:HG22	1:A:588:GLY:HA3	1.96	0.48
2:B:2121:TYR:HB3	2:B:2186:LEU:HD13	1.96	0.48
1:A:222:HIS:ND1	1:A:303:LYS:O	2.47	0.48
1:A:365:LYS:HD3	1:A:367:MET:HB2	1.95	0.48
1:A:260:LEU:HD21	1:A:264:THR:HG23	1.95	0.48
1:A:324:TYR:HB2	1:A:405:ILE:HA	1.96	0.47
2:B:2097:ILE:O	2:B:2099:LEU:N	2.47	0.47
2:B:1886:SER:HB2	2:B:1911:LEU:HD13	1.96	0.47
2:B:2054:ILE:HD13	2:B:2084:TRP:HZ3	1.79	0.47
1:A:409:ASN:OD1	1:A:410:MET:N	2.48	0.47
1:A:279:ILE:HD11	1:A:434:SER:HB2	1.96	0.47
2:B:2103:LYS:HE2	2:B:2194:ASP:HB3	1.96	0.47
1:A:321:ARG:NH1	1:A:402:THR:HB	2.30	0.47
2:B:2013:ILE:HD12	2:B:2015:ILE:HD11	1.97	0.47
1:A:476:PRO:HA	1:A:495:LEU:HB3	1.97	0.47
2:B:1710:LYS:HA	2:B:1754:TRP:CZ2	2.50	0.47
1:A:488:ALA:O	1:A:490:GLY:N	2.43	0.47
2:B:2089:ASN:HA	2:B:2180:TRP:CD1	2.50	0.47
1:A:209:TYR:CG	1:A:214:MET:HB2	2.50	0.46
2:B:1797:TRP:CE3	2:B:1845:GLU:HB3	2.49	0.46
2:B:2086:ALA:HB2	2:B:2184:ILE:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:GLU:O	1:A:516:GLN:NE2	2.49	0.46
2:B:1784:ILE:C	2:B:1786:SER:H	2.23	0.46
2:B:1823:GLU:OE1	2:B:1823:GLU:N	2.48	0.46
2:B:1711:ASP:OD1	2:B:1712:ILE:HD12	2.15	0.46
2:B:1755:TYR:O	2:B:1761:ARG:NH1	2.49	0.46
1:A:391:LEU:HD11	1:A:494:LEU:HD22	1.98	0.46
2:B:1593:ARG:NH2	2:B:1603:ARG:HB3	2.31	0.46
2:B:1913:ASN:O	2:B:1915:GLY:N	2.48	0.46
2:B:1703:TYR:HB2	2:B:1712:ILE:HD11	1.98	0.46
2:B:2137:LYS:HZ3	2:B:2140:ARG:H	1.64	0.46
1:A:477:TYR:HD1	1:A:495:LEU:HB2	1.80	0.46
2:B:2044:MET:HG3	2:B:2045:GLU:HG3	1.98	0.46
1:A:64:ALA:HB3	1:A:164:ILE:HA	1.98	0.45
1:A:138:PRO:HG3	1:A:179:PHE:CE2	2.50	0.45
1:A:364:LYS:HB3	1:A:538:PHE:HZ	1.81	0.45
2:B:1915:GLY:O	2:B:1918:ASN:ND2	2.49	0.45
2:B:2125:TYR:HB3	2:B:2177:PRO:HA	1.97	0.45
1:A:187:PHE:HB3	1:A:239:PHE:HB3	1.99	0.45
1:A:520:PHE:HE2	1:A:649:LEU:HD13	1.82	0.45
1:A:535:ILE:HA	1:A:547:ARG:HD2	1.97	0.45
2:B:1970:SER:HB3	2:B:1976:TRP:HA	1.97	0.45
1:A:13:ILE:HG21	1:A:39:ARG:HH21	1.81	0.45
1:A:143:ILE:HG21	1:A:232:MET:SD	2.57	0.45
1:A:239:PHE:CD1	1:A:287:HIS:HE1	2.32	0.45
2:B:1850:LYS:HA	2:B:1850:LYS:HD3	1.65	0.45
2:B:2051:ASN:HD22	2:B:2097:ILE:HG23	1.81	0.45
1:A:373:ASP:OD1	1:A:374:GLU:N	2.50	0.45
2:B:2018:THR:OG1	2:B:2019:ARG:N	2.48	0.45
1:A:79:ASP:OD1	1:A:79:ASP:N	2.50	0.45
2:B:2057:SER:O	2:B:2092:LYS:NZ	2.49	0.45
2:B:1920:TRP:CE3	2:B:2026:LEU:HB3	2.52	0.45
2:B:1927:ALA:O	2:B:1932:LYS:HG3	2.17	0.45
2:B:2059:PHE:CE1	2:B:2073:ALA:HB2	2.52	0.45
1:A:536:ASN:OD1	1:A:536:ASN:N	2.50	0.44
1:A:222:HIS:HB3	1:A:303:LYS:HB2	1.99	0.44
1:A:385:MET:O	1:A:387:GLU:N	2.41	0.44
2:B:2151:GLU:HG2	2:B:2152:GLY:N	2.31	0.44
1:A:619:ARG:HD2	1:A:620:GLY:H	1.82	0.44
2:B:1920:TRP:HE1	2:B:1922:VAL:HG23	1.82	0.44
1:A:312:THR:OG1	1:A:316:ARG:O	2.35	0.44
2:B:1596:LEU:HB2	2:B:1602:LYS:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1633:LYS:HB2	2:B:1675:ASN:H	1.82	0.44
2:B:1739:ARG:NH2	2:B:1793:TYR:HB2	2.28	0.44
2:B:2053:GLN:NE2	2:B:2098:ASP:H	2.15	0.44
2:B:1701:ALA:HA	2:B:1719:PRO:HA	1.99	0.44
2:B:1741:PHE:HB2	2:B:1800:LEU:HD12	2.00	0.44
2:B:2099:LEU:HB2	2:B:2173:ILE:HD13	1.99	0.44
1:A:492:ILE:HG21	1:A:587:VAL:HG11	1.99	0.44
2:B:1554:TYR:HE2	2:B:1620:ILE:HD12	1.82	0.44
2:B:1860:VAL:HB	2:B:1863:ASN:HB2	1.98	0.44
2:B:2104:LYS:HG2	2:B:2106:THR:HG22	1.99	0.44
1:A:248:LEU:HD13	1:A:258:ILE:HD11	2.00	0.44
1:A:324:TYR:HE2	1:A:370:GLN:HG3	1.81	0.44
1:A:567:GLU:OE1	1:A:650:LYS:HG2	2.17	0.44
1:A:596:ILE:HG12	1:A:613:LEU:H	1.83	0.44
2:B:1593:ARG:HH21	2:B:1603:ARG:HB3	1.83	0.44
2:B:2115:SER:C	2:B:2117:SER:H	2.26	0.44
2:B:1630:VAL:HB	2:B:1680:TYR:HD2	1.83	0.44
2:B:1904:TRP:HZ3	2:B:1958:LYS:HZ3	1.66	0.44
1:A:256:SER:OG	1:A:475:ARG:HD3	2.18	0.44
1:A:558:MET:SD	1:A:565:VAL:HG22	2.58	0.44
2:B:2113:CYS:O	2:B:2157:LYS:NZ	2.48	0.43
1:A:639:ASN:OD1	1:A:640:SER:N	2.50	0.43
2:B:2141:LEU:HD21	2:B:2166:PRO:HG2	1.99	0.43
1:A:520:PHE:HZ	1:A:649:LEU:HD22	1.81	0.43
2:B:2054:ILE:HD13	2:B:2084:TRP:CZ3	2.54	0.43
1:A:335:TYR:HB3	1:A:564:TYR:HD1	1.83	0.43
1:A:370:GLN:HB2	1:A:393:PRO:HB3	2.00	0.43
2:B:1913:ASN:H	2:B:2027:ARG:HH12	1.66	0.43
1:A:176:GLN:HG3	1:A:177:LYS:H	1.84	0.43
2:B:1685:THR:HG22	2:B:1687:ARG:H	1.84	0.43
2:B:2132:GLN:O	2:B:2171:ARG:NH1	2.39	0.43
1:A:217:ILE:O	1:A:219:VAL:N	2.51	0.43
1:A:468:ASN:O	1:A:606:GLY:HA2	2.18	0.43
1:A:18:ARG:HH22	1:A:290:ALA:HB1	1.84	0.43
1:A:209:TYR:HD1	1:A:209:TYR:HA	1.72	0.43
2:B:1739:ARG:NH1	2:B:1791:LYS:HB3	2.34	0.43
2:B:2051:ASN:O	2:B:2075:LEU:HD21	2.19	0.43
2:B:2125:TYR:CD2	2:B:2127:ILE:HG12	2.54	0.43
2:B:1592:PHE:CE1	2:B:1716:LEU:HD12	2.54	0.43
1:A:132:PRO:CB	1:A:136:ASP:HB2	2.47	0.43
1:A:239:PHE:HD1	1:A:287:HIS:CE1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1615:ILE:H	2:B:1781:ASN:HB3	1.83	0.43
2:B:1714:SER:HB2	2:B:1754:TRP:CE3	2.54	0.43
2:B:2121:TYR:HE1	2:B:2156:THR:HA	1.83	0.43
1:A:62:LEU:HD11	1:A:70:ILE:HD13	2.00	0.42
2:B:1708:PRO:HA	2:B:1712:ILE:HD13	2.01	0.42
2:B:1781:ASN:HB2	2:B:1783:MET:HE3	2.01	0.42
2:B:1815:HIS:CD2	2:B:1857:ASN:HB2	2.53	0.42
2:B:1821:LEU:HD12	2:B:1844:LEU:HG	2.00	0.42
2:B:1965:PHE:CD1	2:B:1992:GLY:HA3	2.54	0.42
2:B:2034:GLU:HG3	2:B:2035:VAL:N	2.34	0.42
1:A:163:LEU:HD12	1:A:163:LEU:HA	1.93	0.42
1:A:256:SER:OG	1:A:475:ARG:NH2	2.38	0.42
1:A:282:SER:HB3	1:A:287:HIS:CG	2.55	0.42
2:B:1625:ASP:C	2:B:1683:HIS:HD2	2.28	0.42
2:B:1691:GLU:O	2:B:1692:SER:OG	2.36	0.42
1:A:74:PHE:HB3	1:A:120:TYR:HB2	2.00	0.42
1:A:499:LYS:HG3	1:A:500:SER:H	1.84	0.42
2:B:1632:PHE:CZ	2:B:1672:VAL:HG21	2.55	0.42
2:B:2180:TRP:CZ3	2:B:2184:ILE:HB	2.54	0.42
2:B:2082:ASN:OD1	2:B:2082:ASN:N	2.53	0.42
2:B:2124:SER:OG	2:B:2178:LYS:NZ	2.50	0.42
2:B:1784:ILE:O	2:B:1786:SER:N	2.53	0.42
1:A:415:TYR:HD1	1:A:481:VAL:HG21	1.84	0.42
1:A:478:TYR:HB2	1:A:487:ILE:HD11	2.01	0.42
2:B:1799:ARG:HD2	2:B:1799:ARG:HA	1.90	0.42
1:A:374:GLU:O	1:A:374:GLU:HG3	2.20	0.41
1:A:465:PRO:HB3	1:A:473:LEU:HD22	2.02	0.41
2:B:1548:ASN:HB2	2:B:1683:HIS:CD2	2.55	0.41
1:A:243:PHE:HD1	1:A:243:PHE:HA	1.77	0.41
2:B:1754:TRP:HD1	2:B:1761:ARG:O	2.04	0.41
2:B:1949:GLN:OE1	2:B:1999:ILE:HB	2.20	0.41
1:A:136:ASP:HB3	1:A:137:PRO:HD2	2.01	0.41
1:A:330:GLU:OE1	1:A:330:GLU:N	2.53	0.41
1:A:443:MET:HE3	1:A:443:MET:HB2	1.88	0.41
1:A:541:ASN:HD22	1:A:545:VAL:HG23	1.86	0.41
2:B:1752:LYS:HA	2:B:1752:LYS:HD2	1.87	0.41
2:B:1792:MET:SD	2:B:1874:ILE:HA	2.60	0.41
1:A:604:ILE:HB	1:A:624:THR:OG1	2.20	0.41
2:B:1548:ASN:HD22	2:B:1683:HIS:CG	2.38	0.41
2:B:1969:TYR:CE1	2:B:1977:GLN:HB3	2.55	0.41
1:A:8:VAL:HB	1:A:72:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:GLN:N	1:A:37:VAL:O	2.54	0.41
2:B:2091:ASN:OD1	2:B:2176:ILE:HG22	2.20	0.41
1:A:209:TYR:CD2	1:A:214:MET:HB2	2.55	0.41
2:B:1554:TYR:HB3	2:B:1629:GLN:O	2.21	0.41
2:B:1600:PHE:HB2	2:B:1601:THR:H	1.66	0.41
2:B:1873:LEU:HD11	2:B:2035:VAL:HA	2.02	0.41
1:A:81:PRO:HB2	1:A:113:ALA:HB1	2.01	0.41
1:A:145:TYR:HB3	1:A:159:ILE:HG22	2.02	0.41
2:B:1746:MET:HE3	2:B:1806:GLY:HA3	2.02	0.41
1:A:166:LYS:HD2	1:A:166:LYS:H	1.86	0.41
1:A:186:LEU:H	1:A:207:ASN:HD22	1.69	0.41
2:B:1621:ARG:HH22	2:B:1740:GLU:CD	2.27	0.41
2:B:1657:THR:OG1	2:B:1670:ASN:ND2	2.31	0.41
2:B:2128:HIS:CE1	2:B:2174:ARG:HB3	2.56	0.41
1:A:7:TYR:CZ	1:A:44:TYR:HA	2.56	0.41
1:A:325:PHE:HB3	1:A:408:LYS:HE2	2.02	0.41
2:B:1739:ARG:HH11	2:B:1791:LYS:HB3	1.84	0.41
2:B:1951:GLN:HG2	2:B:1997:SER:O	2.21	0.41
1:A:143:ILE:HG22	1:A:144:TYR:H	1.86	0.40
2:B:2137:LYS:NZ	2:B:2140:ARG:H	2.19	0.40
1:A:522:VAL:HG12	1:A:559:SER:HA	2.02	0.40
1:A:640:SER:O	1:A:644:SER:N	2.54	0.40
2:B:1643:HIS:N	2:B:1703:TYR:O	2.48	0.40
2:B:1983:SER:HB3	2:B:1986:ASN:HB2	2.04	0.40
2:B:2017:PRO:HG2	2:B:2024:PRO:HB2	2.03	0.40
2:B:2036:ASN:HB3	2:B:2106:THR:HG21	2.03	0.40
1:A:568:SER:OG	1:A:569:ILE:N	2.53	0.40
2:B:1730:LYS:HE2	2:B:1730:LYS:HB2	1.83	0.40
2:B:1732:SER:O	2:B:1734:MET:N	2.54	0.40
2:B:1745:PHE:HZ	2:B:1858:THR:HG22	1.85	0.40
2:B:2123:LYS:HA	2:B:2153:ASN:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	570/709 (80%)	402 (70%)	145 (25%)	23 (4%)	2	18
2	B	583/651 (90%)	403 (69%)	155 (27%)	25 (4%)	2	17
All	All	1153/1360 (85%)	805 (70%)	300 (26%)	48 (4%)	3	17

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	HIS
1	A	155	ASN
1	A	384	ASN
2	B	1955	HIS
2	B	2054	ILE
2	B	2127	ILE
1	A	273	GLY
1	A	337	PRO
1	A	429	ASP
1	A	575	CYS
2	B	1614	GLY
2	B	1733	ASN
2	B	1748	PHE
2	B	1808	SER
2	B	1867	GLY
2	B	1914	GLY
2	B	1976	TRP
2	B	2098	ASP
2	B	2139	TYR
1	A	134	HIS
1	A	218	THR
1	A	383	PRO
1	A	386	LYS
1	A	469	ASP
2	B	1831	LEU
2	B	2126	THR
1	A	44	TYR
1	A	254	LYS
1	A	483	ILE
1	A	489	SER
1	A	566	PRO
1	A	609	HIS
2	B	1785	TYR

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Mol	Chain	Res	Type
1	A	381	VAL
2	B	1873	LEU
2	B	1933	PRO
2	B	2041	PRO
1	A	156	SER
2	B	1693	PRO
2	B	1811	ILE
1	A	261	VAL
2	B	1681	VAL
2	B	1890	ILE
1	A	481	VAL
2	B	1788	PRO
2	B	1999	ILE
1	A	132	PRO
2	B	2175	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	526/637 (83%)	488 (93%)	38 (7%)	13	35
2	B	519/576 (90%)	482 (93%)	37 (7%)	13	35
All	All	1045/1213 (86%)	970 (93%)	75 (7%)	15	35

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	ASP
1	A	141	THR
1	A	143	ILE
1	A	150	LEU
1	A	159	ILE
1	A	178	THR
1	A	184	VAL
1	A	217	ILE

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Mol	Chain	Res	Type
1	A	218	THR
1	A	224	HIS
1	A	243	PHE
1	A	247	VAL
1	A	256	SER
1	A	261	VAL
1	A	264	THR
1	A	266	THR
1	A	308	LEU
1	A	324	TYR
1	A	366	VAL
1	A	381	VAL
1	A	402	THR
1	A	406	VAL
1	A	417	ILE
1	A	442	THR
1	A	447	VAL
1	A	483	ILE
1	A	519	VAL
1	A	536	ASN
1	A	557	ILE
1	A	561	ILE
1	A	567	GLU
1	A	587	VAL
1	A	593	ILE
1	A	597	HIS
1	A	599	THR
1	A	623	VAL
1	A	636	THR
1	A	649	LEU
2	B	1593	ARG
2	B	1642	LEU
2	B	1679	THR
2	B	1681	VAL
2	B	1744	LEU
2	B	1747	THR
2	B	1781	ASN
2	B	1787	LEU
2	B	1802	LEU
2	B	1813	VAL
2	B	1821	LEU
2	B	1833	VAL

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Mol	Chain	Res	Type
2	B	1837	LEU
2	B	1858	THR
2	B	1879	CYS
2	B	1883	MET
2	B	1885	LEU
2	B	1943	VAL
2	B	1960	CYS
2	B	1962	THR
2	B	1987	VAL
2	B	2013	ILE
2	B	2016	SER
2	B	2018	THR
2	B	2028	LEU
2	B	2033	CYS
2	B	2038	CYS
2	B	2039	SER
2	B	2040	THR
2	B	2075	LEU
2	B	2102	ILE
2	B	2105	ILE
2	B	2134	VAL
2	B	2156	THR
2	B	2175	VAL
2	B	2190	LEU
2	B	2194	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	11	GLN
1	A	147	HIS
1	A	207	ASN
1	A	293	GLN
1	A	362	HIS
1	A	370	GLN
1	A	448	GLN
1	A	468	ASN
1	A	541	ASN
1	A	581	GLN
1	A	591	ASN
1	A	597	HIS

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Mol	Chain	Res	Type
2	B	1547	ASN
2	B	1548	ASN
2	B	1634	ASN
2	B	1670	ASN
2	B	1683	HIS
2	B	1707	ASN
2	B	1819	GLN
2	B	1991	ASN
2	B	2051	ASN
2	B	2128	HIS
2	B	2162	ASN
2	B	2181	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](#)

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.

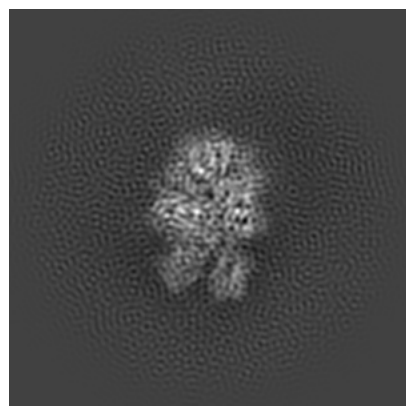
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23067. These allow visual inspection of the internal detail of the map and identification of artifacts.

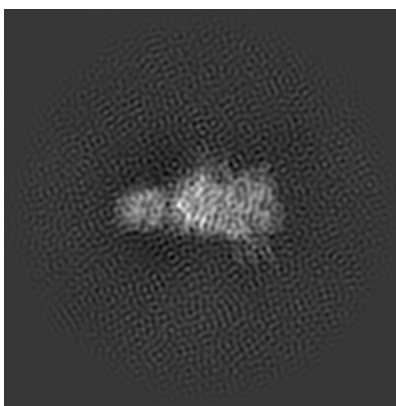
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

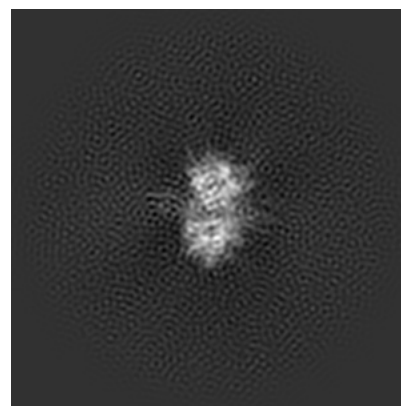
6.1.1 Primary map



X

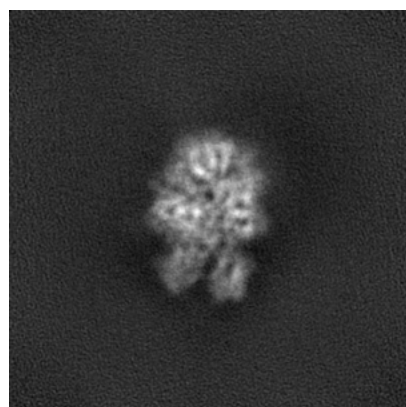


Y

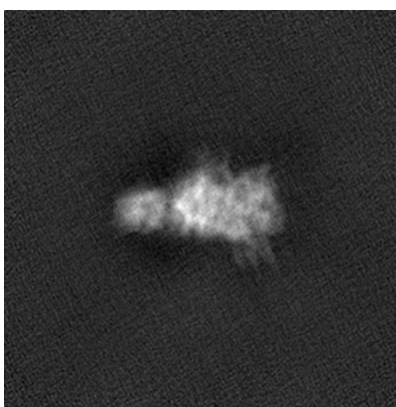


Z

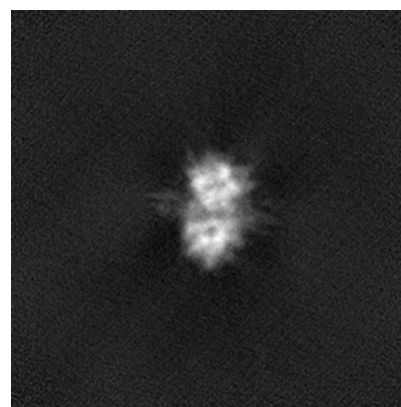
6.1.2 Raw map



X



Y

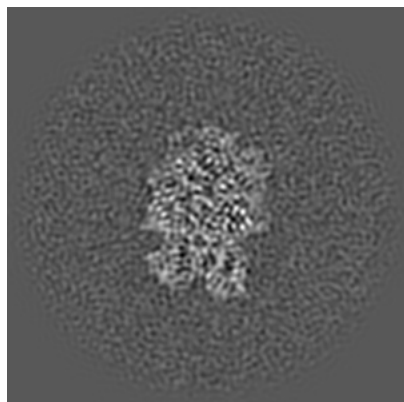


Z

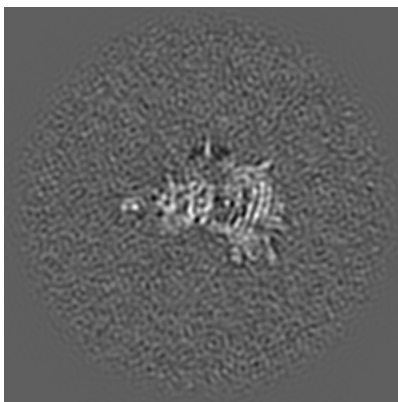
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

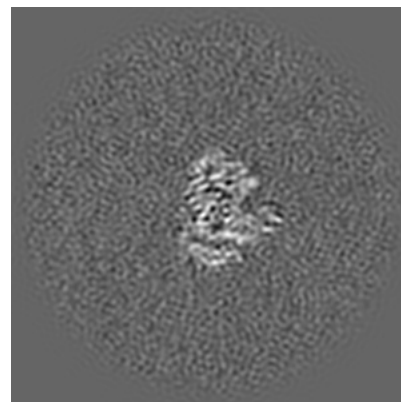
6.2.1 Primary map



X Index: 125

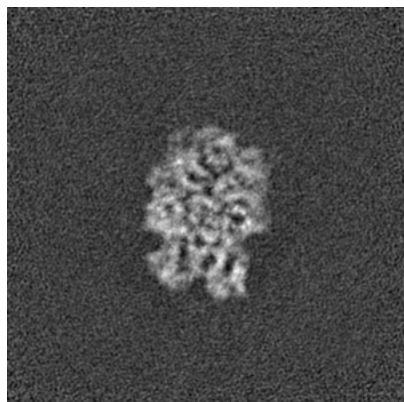


Y Index: 125

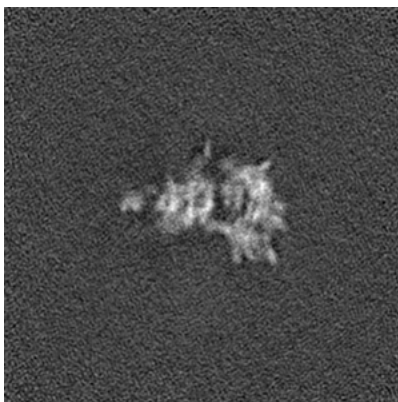


Z Index: 125

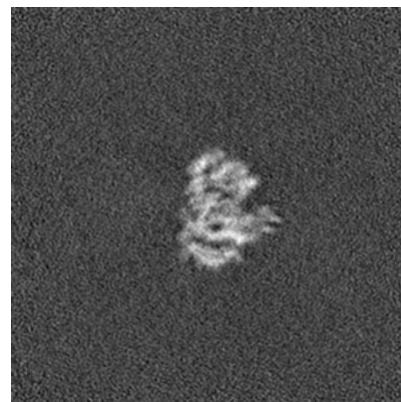
6.2.2 Raw map



X Index: 125



Y Index: 125

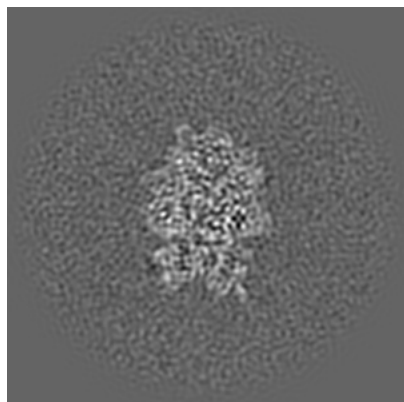


Z Index: 125

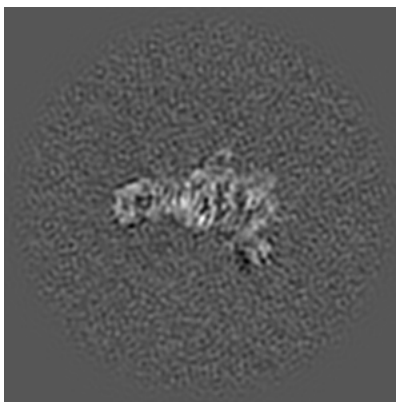
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

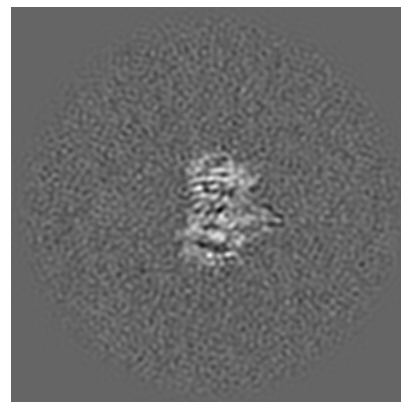
6.3.1 Primary map



X Index: 127

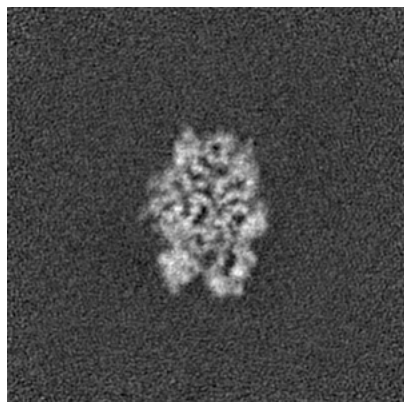


Y Index: 136

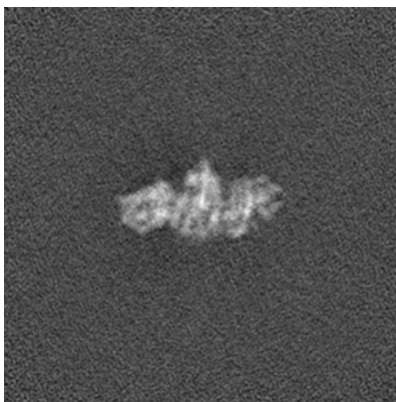


Z Index: 123

6.3.2 Raw map



X Index: 130



Y Index: 106

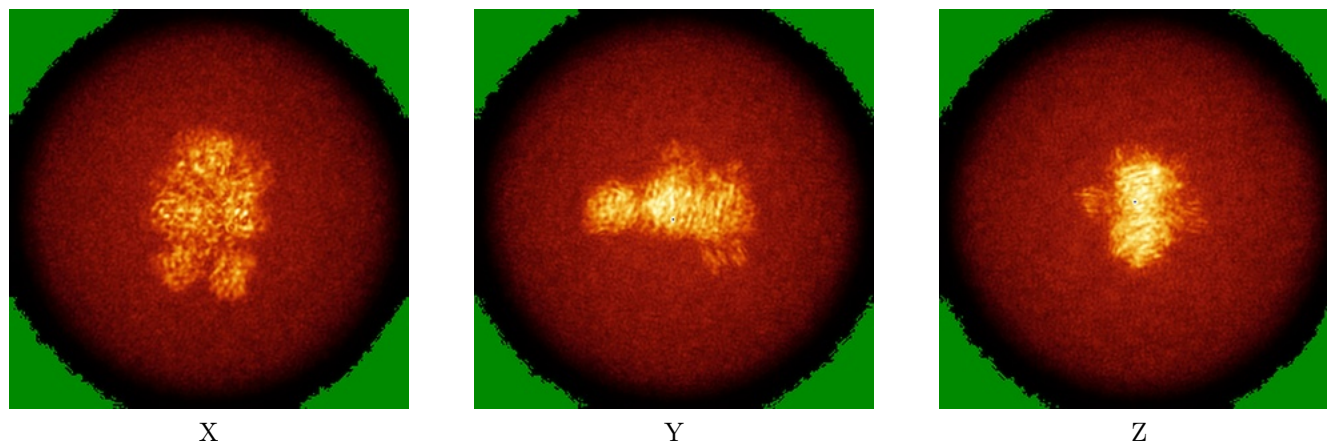


Z Index: 123

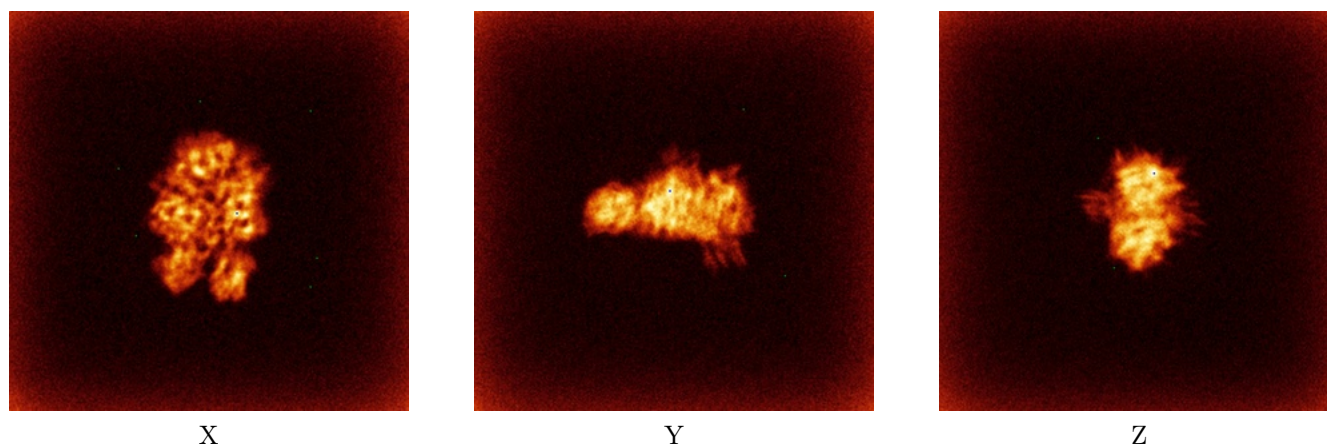
The images above show the largest variance slices of the map in three orthogonal directions.

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.

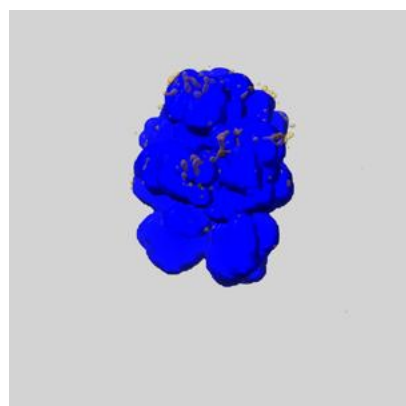
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

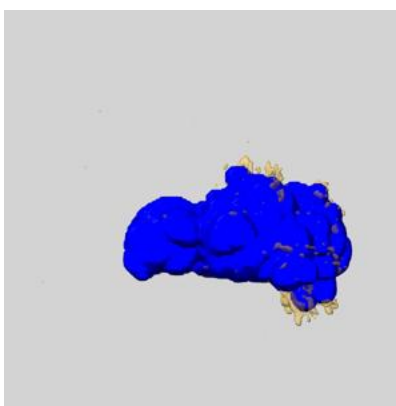
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

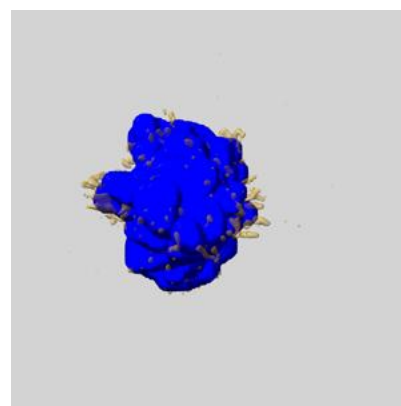
6.6.1 emd_23067_msk_1.map [i](#)



X



Y

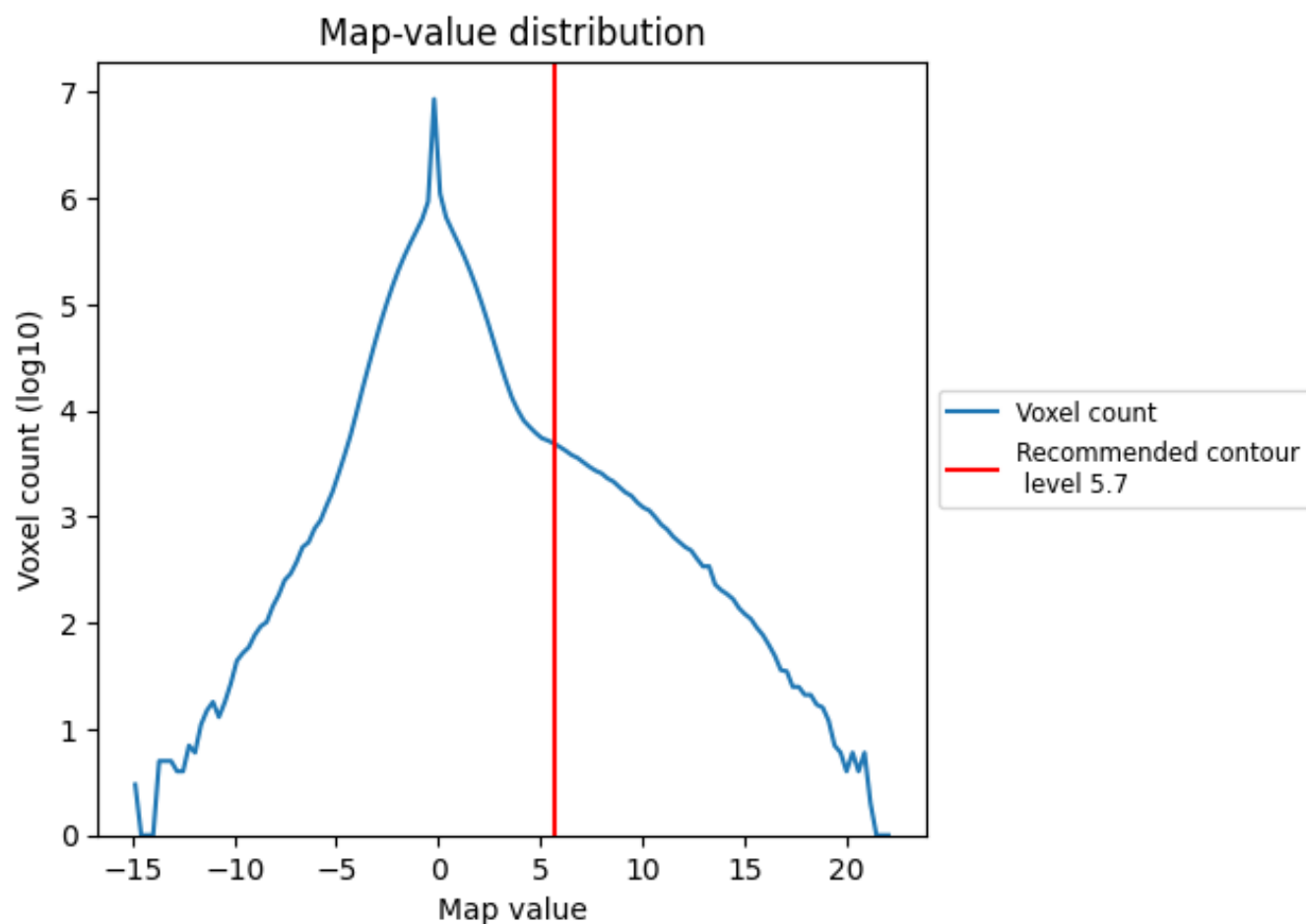


Z

7 Map analysis [i](#)

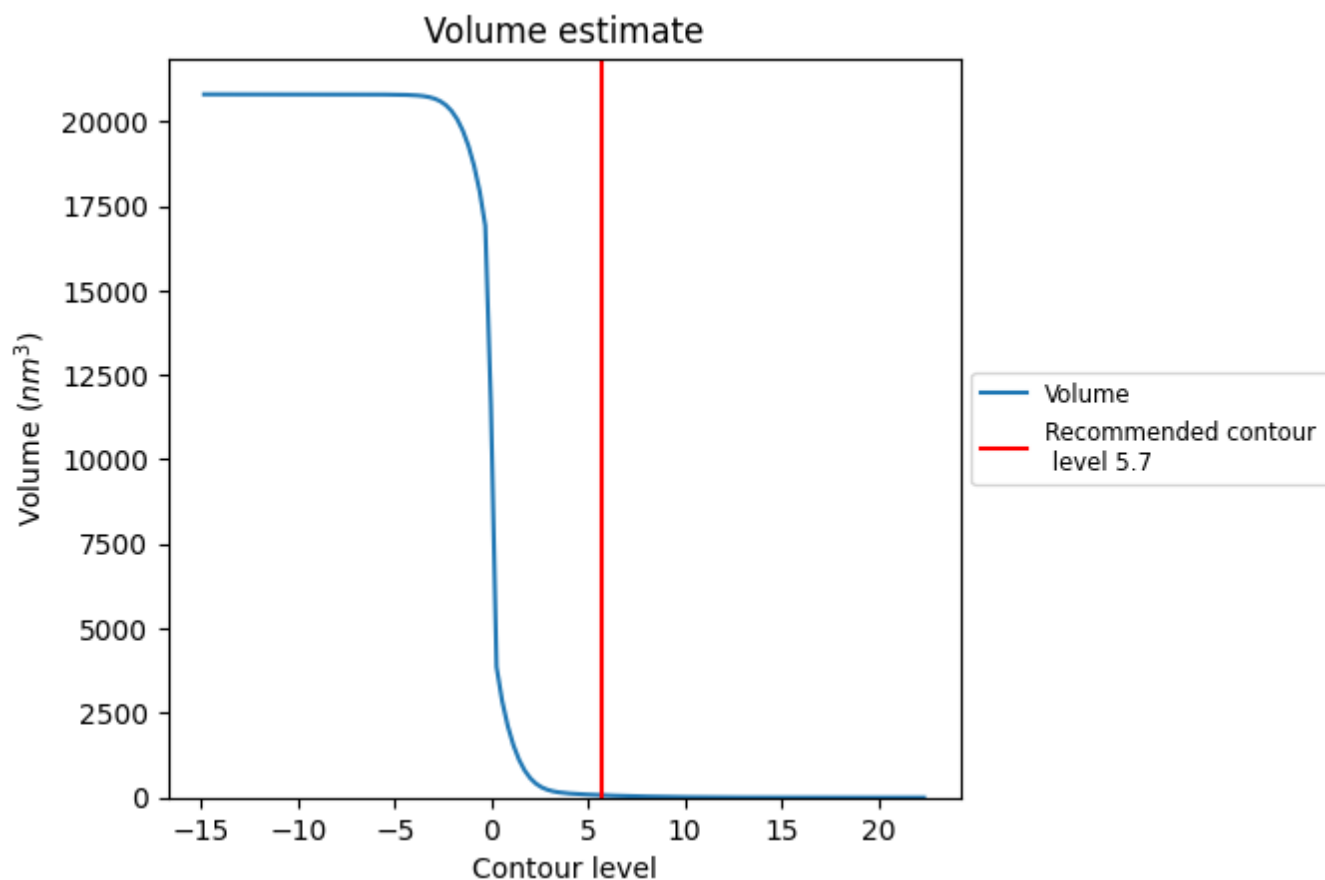
This section contains the results of statistical analysis of the map.

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.

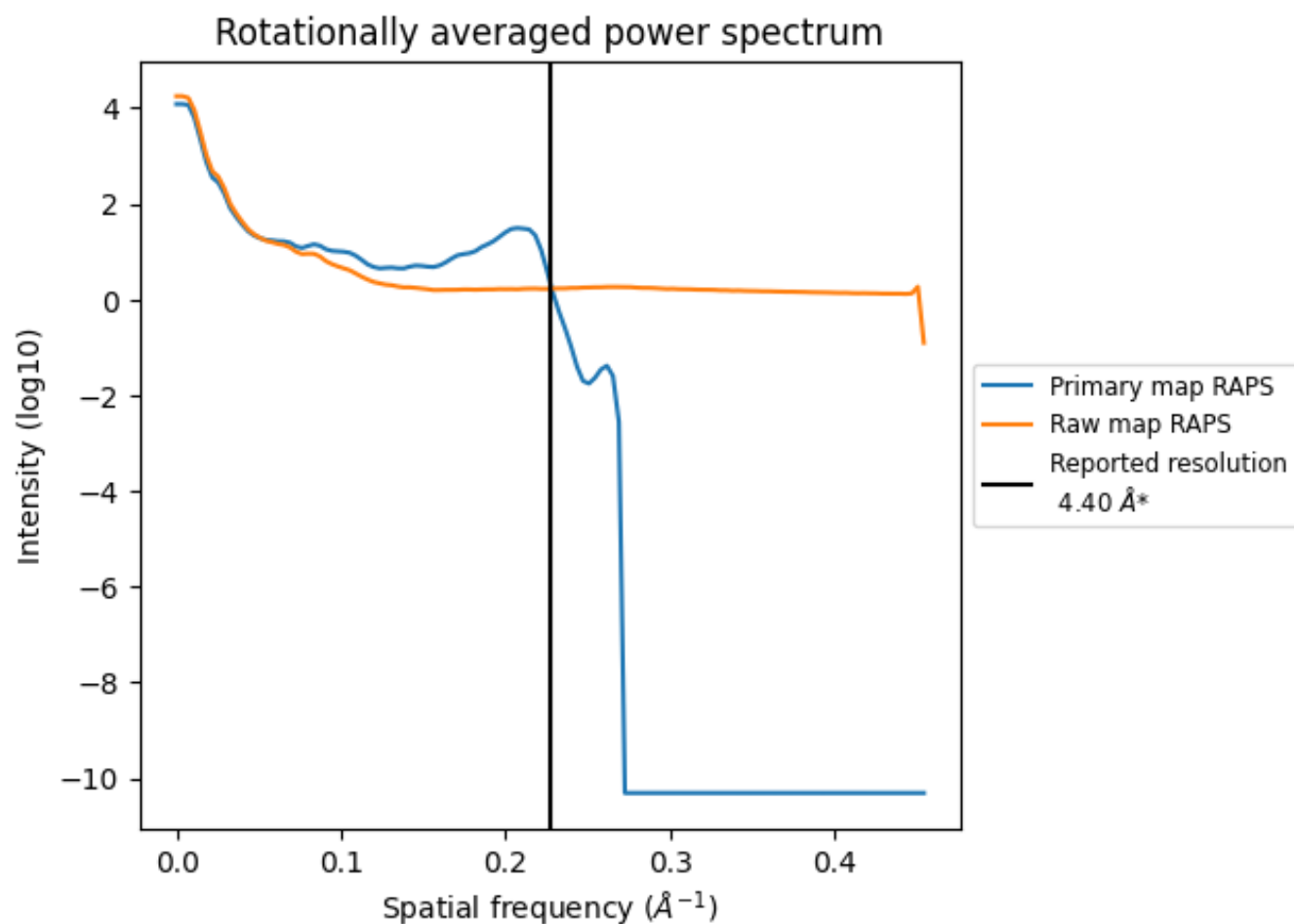
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 70 nm^3 ; this corresponds to an approximate mass of 64 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 ⓘ

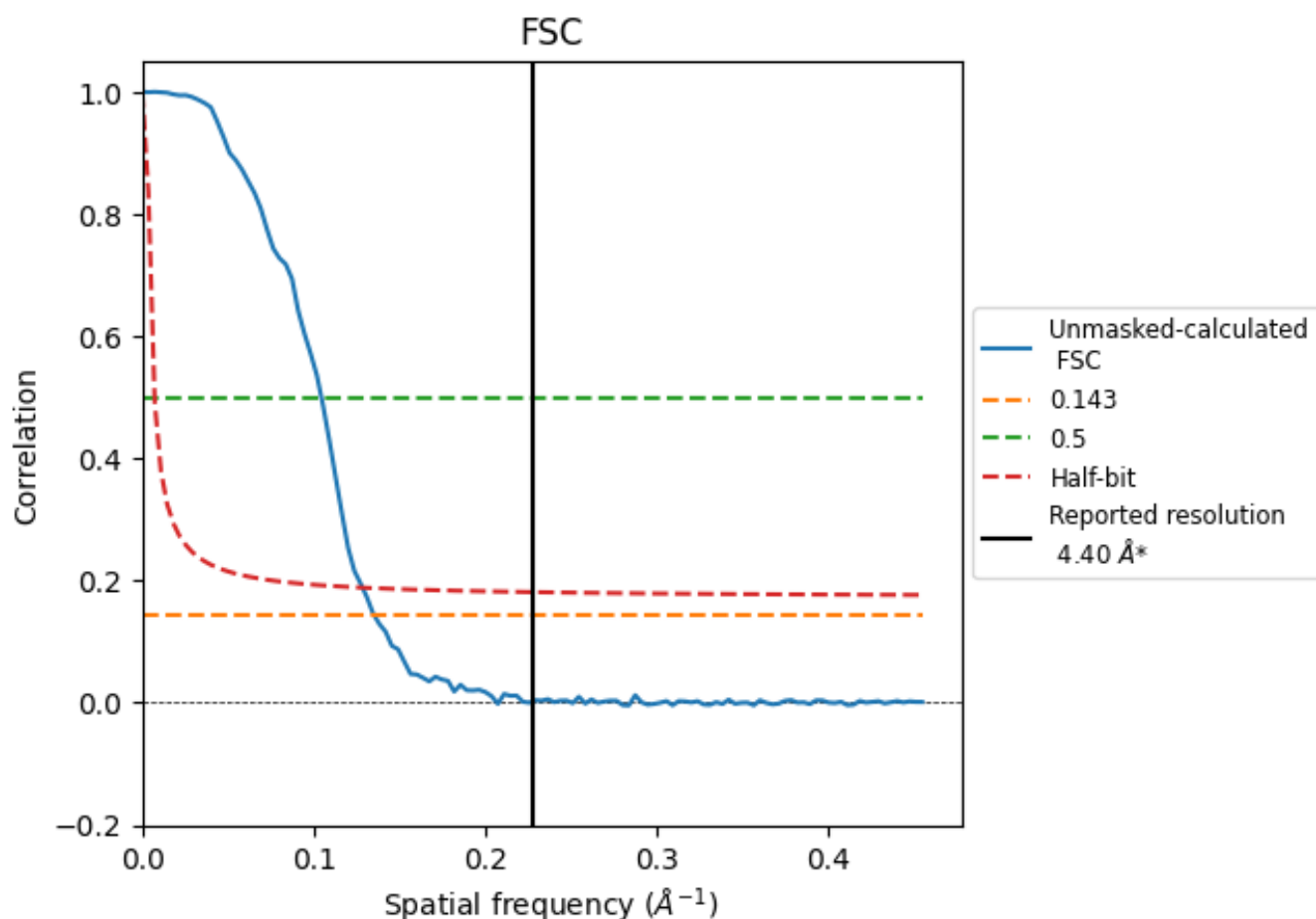


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

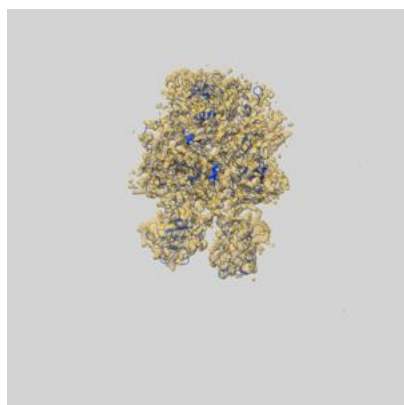
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.40	9.58	7.79

*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 7.40 differs from the reported value 4.4 by more than 10 %

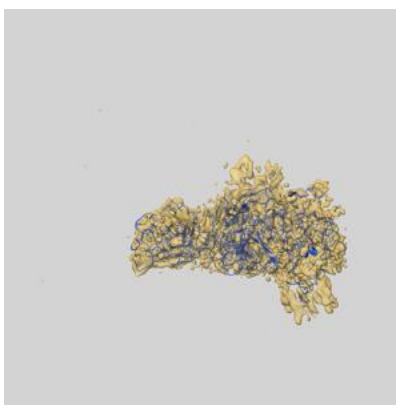
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23067 and PDB model 7KXY. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

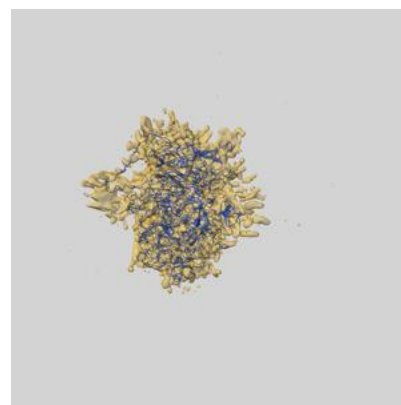
9.1 Map-model overlay [i](#)



X



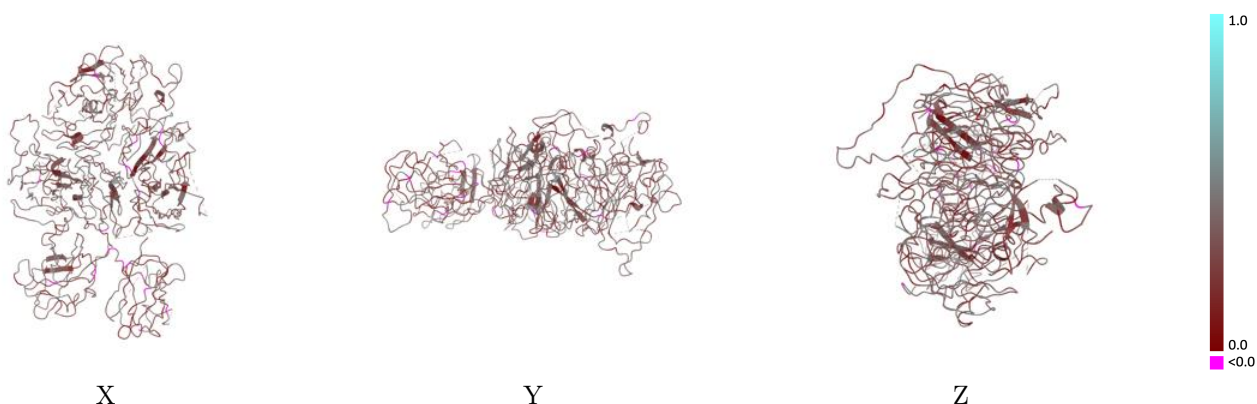
Y



Z

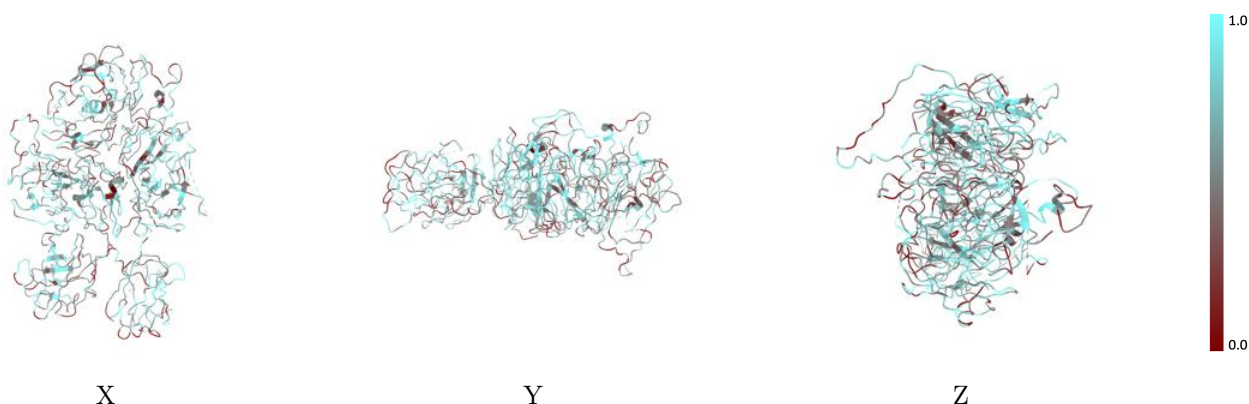
The images above show the 3D surface view of the map at the recommended contour level 5.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



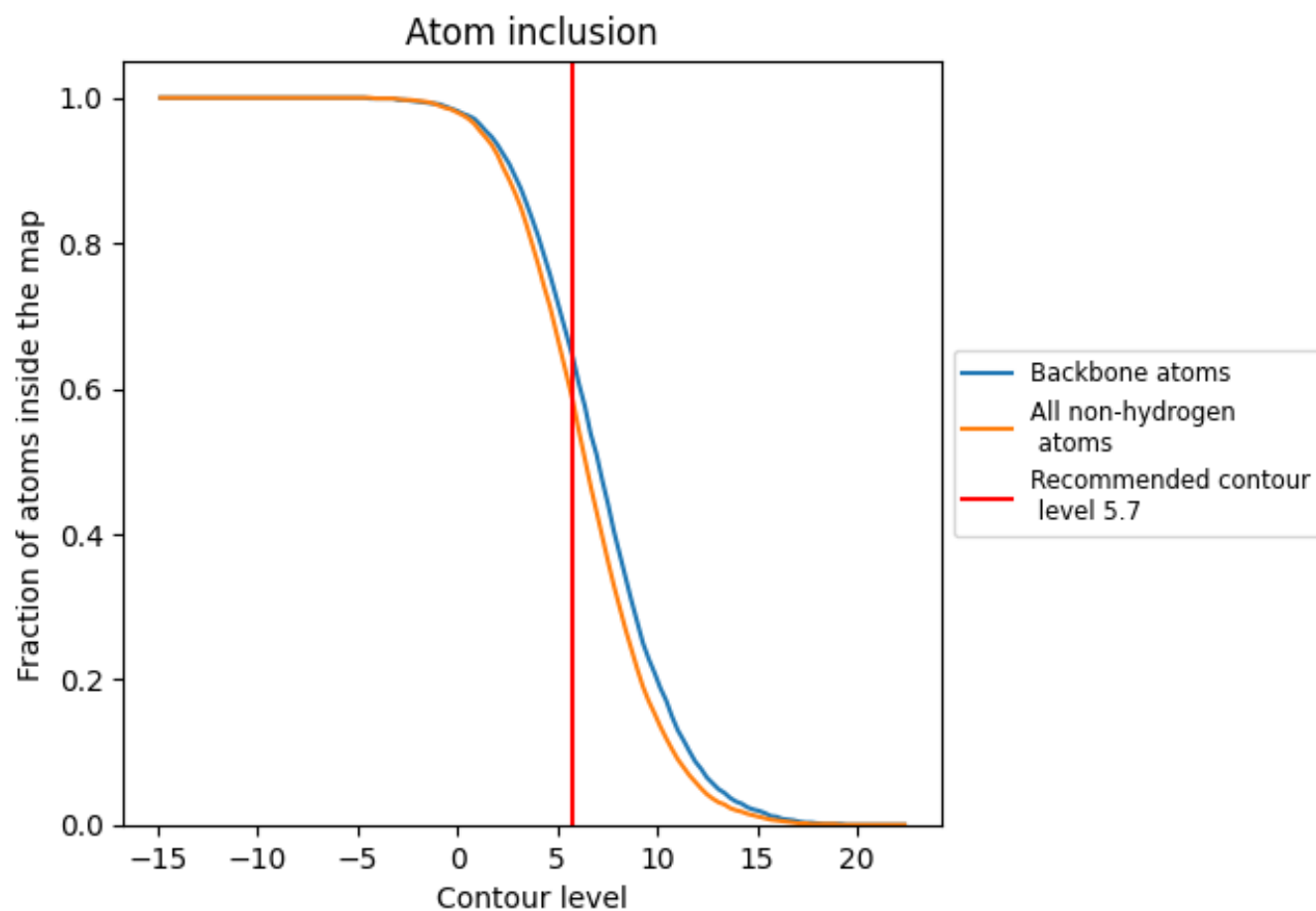
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 59% 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 (5.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5910	0.3220
A	0.5940	0.3270
B	0.5890	0.3180

