



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 08:05 PM UTC

PDB ID : 6SKY / pdb_00006sky
EMDB ID : EMD-10231
Title : FAT and kinase domain of CtTel1
Authors : Jansma, M.; Eustermann, S.E.; Kostrewa, D.; Lammens, K.; Hopfner, K.P.
Deposited on : 2019-08-16
Resolution : 2.80 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

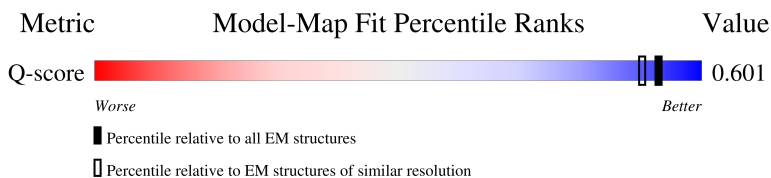
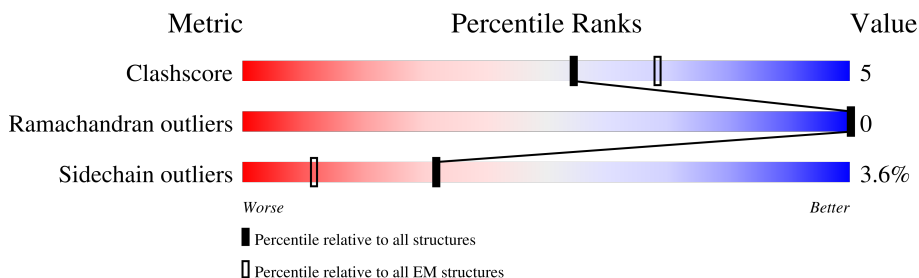
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	2944	
1	B	2944	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22348 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 Serine/threonine-protein kinase Tel1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1412	Total 11142	C 7022	N 1966	O 2109	S 45	0	0
1	B	1412	Total 11142	C 7022	N 1966	O 2109	S 45	0	0

There are 40 discrepancies between the modelled and reference sequences:

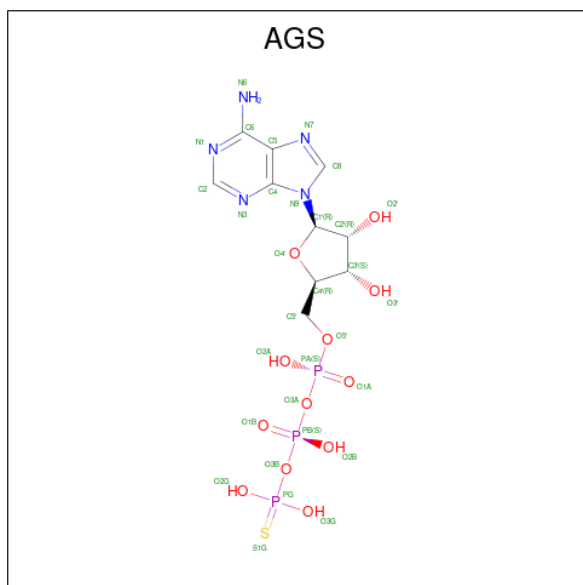
Chain	Residue	Modelled	Actual	Comment	Reference
A	2847	LEU	PHE	conflict	UNP G0S4S9
A	2848	TYR	-	insertion	UNP G0S4S9
A	2849	GLN	-	insertion	UNP G0S4S9
A	2850	TRP	-	insertion	UNP G0S4S9
A	2851	SER	-	insertion	UNP G0S4S9
A	2852	ILE	-	insertion	UNP G0S4S9
A	2853	SER	-	insertion	UNP G0S4S9
A	2854	PRO	-	insertion	UNP G0S4S9
A	2855	VAL	-	insertion	UNP G0S4S9
A	2856	ARG	-	insertion	UNP G0S4S9
A	2857	MET	-	insertion	UNP G0S4S9
A	2858	ALA	-	insertion	UNP G0S4S9
A	2859	LYS	-	insertion	UNP G0S4S9
A	2860	LEU	-	insertion	UNP G0S4S9
A	2861	GLN	-	insertion	UNP G0S4S9
A	2862	ASN	-	insertion	UNP G0S4S9
A	2863	ALA	-	insertion	UNP G0S4S9
A	2864	ARG	-	insertion	UNP G0S4S9
A	2865	GLU	-	insertion	UNP G0S4S9
A	2866	VAL	-	insertion	UNP G0S4S9
B	2847	LEU	PHE	conflict	UNP G0S4S9
B	2848	TYR	-	insertion	UNP G0S4S9
B	2849	GLN	-	insertion	UNP G0S4S9
B	2850	TRP	-	insertion	UNP G0S4S9
B	2851	SER	-	insertion	UNP G0S4S9
B	2852	ILE	-	insertion	UNP G0S4S9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2853	SER	-	insertion	UNP G0S4S9
B	2854	PRO	-	insertion	UNP G0S4S9
B	2855	VAL	-	insertion	UNP G0S4S9
B	2856	ARG	-	insertion	UNP G0S4S9
B	2857	MET	-	insertion	UNP G0S4S9
B	2858	ALA	-	insertion	UNP G0S4S9
B	2859	LYS	-	insertion	UNP G0S4S9
B	2860	LEU	-	insertion	UNP G0S4S9
B	2861	GLN	-	insertion	UNP G0S4S9
B	2862	ASN	-	insertion	UNP G0S4S9
B	2863	ALA	-	insertion	UNP G0S4S9
B	2864	ARG	-	insertion	UNP G0S4S9
B	2865	GLU	-	insertion	UNP G0S4S9
B	2866	VAL	-	insertion	UNP G0S4S9

- Molecule 2 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$).



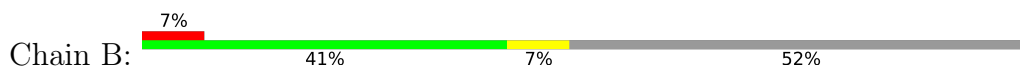
Mol	Chain	Residues	Atoms						AltConf
2	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
2	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

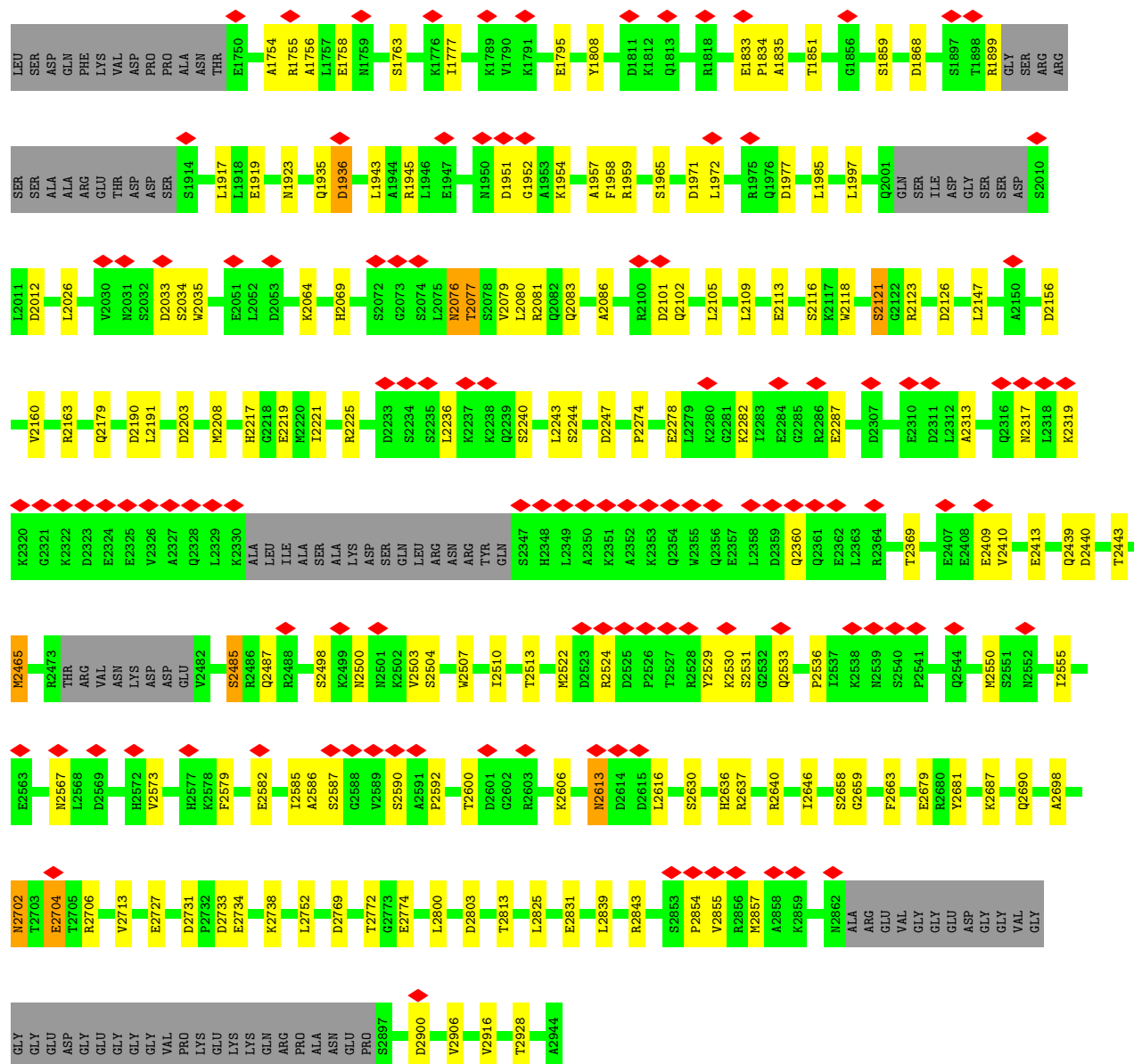
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Mg 1	0
3	B	1	Total 1	Mg 1	0

ASP	GLY	S2010	L2011	D2012	L2026	V2030	N2031	S2032	D2033	S2034	W2035	E2051	L2052	D2053	K2064	H2069	S2072	D2073	S2074	L2075	N2076	T2077	S2078	V2079	L2080	R2081	G2082	Q2083	A2086	R2100	D2101	Q2102	L2109	E2113	S2116	K2117	W2118	S2121	G2122	R2123	D2126	L2147								
GLY	SER	SER	ARG	ARG	SER	SER	ALA	ALA	ARG	GLU	THR	ASP	ASP	SER	S1914	E1919	N1923	Q1935	D1936	L1943	A1944	R1945	L1946	E1947	N1950	D1951	G1952	A1953	K1954	A1957	F1958	R1959	S1965	D1971	L1972	R1975	Q1976	D1977	L1985	L1997	Q2001	GLN	SER	ILE						
Y1733	R1734	T1735	P1736	LEU	SER	ASP	GLN	PHE	LYS	VAL	ASP	PRO	PRO	ALA	ASN	THR	E1750	A1754	R1755	A1756	L1757	E1758	M1759	S1763	K1776	I1777	L1783	K1789	V1790	K1791	E1795	Y1808	D1811	K1812	Q1813	R1818	E1833	P1834	A1835	L1842	T1851	G1856	S1859	D1868						
D1608	K1611	W1617	S1622	Q1623	R1624	L1637	P1648	E1649	D1650	L1651	Q1656	L1657	Q1658	E1659	Y1660	R1661	Q1665	G1666	V1667	G1668	L1674	L1681	D1686	E1694	D1703	A1704	I1705	S1706	D1707	N1708	D1709	H1710	D1711	L1712	L1713	S1714	A1715	C1716	Q1717	E1718	E1722	I1726	D1731	P1732						
E1530	G1531	Q1532	K1533	Q1534	R1537	S1538	E1541	N1542	H1545	I1546	R1547	A1548	S1549	A1552	E1553	K1554	G1555	T1556	H1557	E1558	S1559	N1560	E1564	K1567	D1568	R1571	E1572	N1573	Q1574	L1575	L1576	N1577	E1578	P1579	D1582	L1585	S1586	M1587	P1595	P1596	S1597	S1598	R1599	L1600	I1603	D1606	E1607			
D1449	D1450	L1454	Y1457	K1460	R1461	G1462	D1463	E1464	K1467	R1468	T1469	P1470	S1471	D1483	L1484	R1485	V1486	F1487	L1488	GLU	SER	GLN	SER	SER	THR	GLN	SER	THR	GLN	F1501	K1502	A1503	T1504	K1505	S1506	K1507	A1508	Q1509	E1510	K1517	A1520	A1521	Y1522	D1523	P1525	E1526	F1527	K1528	D1529	
ILE	TRP	PRO	ALA	VAL	VAL	PHE	VAL	ALA	ARG	LYS	THR	LEU	THR	PRO	ALA	GLY	PRO	HIS	ALA	VAL	VAL	ARG	LYS	ILE	VAL	ILE	ARG	ALA	GLY	ASP	HIS	ALA	ILE	SER	G1428	Y1429	M1433	F1441	V1442	Y1443	D1444	P1445	E1446	C1447	A1448					
GLU	LYS	ALA	PHE	GLU	ARG	ASP	THR	ILE	ASP	GLU	THR	GLU	ILE	LYS	GLY	HIS	LEU	PRO	ARG	GLU	THR	ALA	PRO	ARG	LYS	MET	GLY	LEU	PRO	GLY	LYS	GLU	VAL	HIS	THR	PHE	PHE	ASP	ILE	THR	VAL	GLN	GLU	PRO	ASP	ILE				
HIS	THR	PHE	GLU	ILE	ASP	TRP	ILE	GLY	LYS	THR	ILE	THR	GLY	HIS	THR	HIS	VAL	THR	HIS	VAL	ASP	VAL	PHE	VAL	ASP	VAL	VAL	GLY	GLN	THR	GLY	LYS	GLU	ALA	VAL	ARG	ASP	TRP	GLY	PRO	THR	LEU	LYS	ARG	SER	THR	ASN			
GLY	LEU	LEU	ILE	SER	LYS	PHE	LEU	THR	LYS	THR	LEU	THR	GLY	HIS	THR	HIS	VAL	PHE	VAL	ASP	VAL	ASP	VAL	VAL	ARG	GLY	GLN	THR	GLY	LEU	GLY	ALA	PHE	ARG	ASP	TRP	GLY	PRO	THR	LEU	LYS	ARG	SER	THR	THR	TYR	ILE			
VAL	LYS	PRO	LEU	PRO	ASN	THR	ASN	THR	ILE	ALA	ALA	SER	ASN	SER	GLU	ASN	GLY	LEU	VAL	GLY	HIS	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY		
PRO	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

- Molecule 1: Serine/threonine-protein kinase Tel1







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	613362	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 ($e^-/\text{\AA}^2$)	55.5	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	0.111	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0185	Depositor
Map size (Å)	372.768, 372.768, 372.768	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.39	0/11346	0.39	0/15348
1	B	0.39	0/11346	0.39	0/15348
All	All	0.39	0/22692	0.39	0/30696

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	11142	0	11176	121	0
1	B	11142	0	11176	113	0
2	A	31	0	12	1	0
2	B	31	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	22348	0	22376	228	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 (228) 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:1936:ASP:OD1	1:A:1936:ASP:N	2.20	0.75
1:B:2586:ALA:HB3	1:B:2592:PRO:HG2	1.69	0.74
1:A:2586:ALA:HB3	1:A:2592:PRO:HG2	1.69	0.74
1:B:1936:ASP:OD1	1:B:1936:ASP:N	2.20	0.74
1:B:2012:ASP:OD1	1:B:2034:SER:OG	2.08	0.72
1:A:2012:ASP:OD1	1:A:2034:SER:OG	2.08	0.72
1:B:1650:ASP:OD1	1:B:1650:ASP:N	2.26	0.68
1:A:1650:ASP:N	1:A:1650:ASP:OD1	2.26	0.68
1:A:1965:SER:OG	1:B:2190:ASP:OD2	2.13	0.67
1:A:1443:VAL:HG11	1:A:1483:ASP:HB3	1.77	0.67
1:B:1443:VAL:HG11	1:B:1483:ASP:HB3	1.77	0.67
1:B:1777:ILE:HD11	1:B:1808:TYR:HB2	1.77	0.67
1:A:1777:ILE:HD11	1:A:1808:TYR:HB2	1.77	0.66
1:A:2190:ASP:OD2	1:B:1965:SER:OG	2.13	0.66
1:B:2702:ASN:ND2	1:B:2704:GLU:OE1	2.29	0.65
1:B:2313:ALA:O	1:B:2317:ASN:ND2	2.30	0.65
1:A:2313:ALA:O	1:A:2317:ASN:ND2	2.30	0.64
1:A:2702:ASN:ND2	1:A:2704:GLU:OE1	2.29	0.64
1:B:1731:ASP:HB3	1:B:1732:PRO:HD3	1.81	0.63
1:A:1731:ASP:HB3	1:A:1732:PRO:HD3	1.81	0.62
1:B:2498:SER:HB3	1:B:2507:TRP:CD1	2.35	0.62
1:B:2244:SER:OG	1:B:2247:ASP:OD2	2.17	0.62
1:A:2498:SER:HB3	1:A:2507:TRP:CD1	2.35	0.61
1:B:1538:SER:O	1:B:1542:ASN:ND2	2.34	0.60
1:A:2109:LEU:HD21	1:A:2163:ARG:HD2	1.85	0.59
1:A:2244:SER:OG	1:A:2247:ASP:OD2	2.17	0.58
1:A:2636:HIS:NE2	1:A:2831:GLU:OE2	2.36	0.58
1:A:1959:ARG:NH2	1:A:1977:ASP:OD1	2.36	0.58
1:B:1429:TYR:OH	1:B:1694:GLU:OE1	2.20	0.58
1:B:1959:ARG:NH2	1:B:1977:ASP:OD1	2.36	0.58
1:B:1608:ASP:N	1:B:1608:ASP:OD1	2.35	0.58
1:B:2109:LEU:HD21	1:B:2163:ARG:HD2	1.85	0.57
2:B:3001:AGS:O2B	2:B:3001:AGS:O5'	2.22	0.57
1:A:1608:ASP:OD1	1:A:1608:ASP:N	2.35	0.57
1:A:1538:SER:O	1:A:1542:ASN:ND2	2.34	0.57
2:A:3001:AGS:O2B	2:A:3001:AGS:O5'	2.22	0.56
1:B:1449:ASP:OD1	1:B:1449:ASP:N	2.36	0.56
1:A:1444:ASP:O	1:A:1448:ALA:HB2	2.06	0.56
1:A:2550:MET:HG2	1:A:2579:PHE:CE2	2.41	0.56
1:B:2440:ASP:OD1	1:B:2440:ASP:N	2.38	0.56
1:A:2440:ASP:OD1	1:A:2440:ASP:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2636:HIS:NE2	1:B:2831:GLU:OE2	2.36	0.56
1:A:2679:GLU:OE1	1:A:2687:LYS:NZ	2.35	0.56
1:B:2524:ARG:HH11	1:B:2590:SER:HB2	1.71	0.56
1:A:2513:THR:HG23	1:A:2550:MET:HE1	1.88	0.55
1:B:1919:GLU:O	1:B:1923:ASN:ND2	2.36	0.55
1:B:1444:ASP:O	1:B:1448:ALA:HB2	2.06	0.55
1:B:2550:MET:HG2	1:B:2579:PHE:CE2	2.41	0.55
1:A:1919:GLU:O	1:A:1923:ASN:ND2	2.36	0.55
1:A:1449:ASP:OD1	1:A:1449:ASP:N	2.36	0.55
1:A:2522:MET:HE3	1:A:2658:SER:HB3	1.89	0.54
1:B:2550:MET:HG2	1:B:2579:PHE:HE2	1.72	0.54
1:B:2613:ASN:OD1	1:B:2613:ASN:N	2.39	0.54
1:A:2550:MET:HG2	1:A:2579:PHE:HE2	1.72	0.54
1:A:2613:ASN:OD1	1:A:2613:ASN:N	2.39	0.54
1:B:2513:THR:HG23	1:B:2550:MET:HE1	1.88	0.54
1:A:2524:ARG:HH11	1:A:2590:SER:HB2	1.71	0.54
1:A:2439:GLN:HG2	1:A:2485:SER:HB2	1.89	0.54
1:B:2769:ASP:OD2	1:B:2772:THR:OG1	2.26	0.53
1:A:1945:ARG:NH1	1:B:2219:GLU:OE2	2.41	0.53
1:A:2219:GLU:OE2	1:B:1945:ARG:NH1	2.41	0.53
1:B:2439:GLN:HG2	1:B:2485:SER:HB2	1.89	0.53
1:A:2113:GLU:O	1:A:2116:SER:OG	2.21	0.53
1:A:2769:ASP:OD2	1:A:2772:THR:OG1	2.26	0.53
1:B:2522:MET:HE3	1:B:2658:SER:HB3	1.89	0.53
1:A:1429:TYR:OH	1:A:1694:GLU:OE1	2.20	0.53
1:A:2500:ASN:O	1:A:2504:SER:OG	2.21	0.53
1:B:2465:MET:HG2	1:B:2507:TRP:HE3	1.74	0.53
1:A:2465:MET:HG2	1:A:2507:TRP:CE3	2.44	0.52
1:B:2734:GLU:O	1:B:2738:LYS:HG2	2.09	0.52
1:A:2734:GLU:O	1:A:2738:LYS:HG2	2.09	0.52
1:A:2465:MET:HG2	1:A:2507:TRP:HE3	1.74	0.52
1:B:2465:MET:HG2	1:B:2507:TRP:CE3	2.44	0.52
1:B:2616:LEU:HD22	1:B:2659:GLY:HA3	1.92	0.52
1:A:1467:LYS:O	1:A:1524:SER:OG	2.25	0.51
1:A:2616:LEU:HD22	1:A:2659:GLY:HA3	1.92	0.51
1:A:1567:LYS:HE2	1:A:1571:ARG:HH21	1.76	0.51
1:A:2076:ASN:OD1	1:A:2076:ASN:N	2.34	0.51
1:A:2035:TRP:HB2	1:A:2086:ALA:HB2	1.94	0.50
1:B:1686:ASP:OD1	1:B:1686:ASP:N	2.42	0.50
1:B:1859:SER:HB2	1:B:2681:TYR:CE1	2.47	0.50
1:B:1597:SER:OG	1:B:1598:SER:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1597:SER:OG	1:A:1598:SER:N	2.44	0.49
1:A:1859:SER:HB2	1:A:2681:TYR:CE1	2.47	0.49
1:A:2606:LYS:HB2	1:A:2663:PHE:HB3	1.95	0.49
1:B:1567:LYS:HE2	1:B:1571:ARG:HH21	1.76	0.49
1:B:2606:LYS:HB2	1:B:2663:PHE:HB3	1.95	0.49
1:B:1763:SER:OG	1:B:1795:GLU:OE2	2.30	0.49
1:B:2035:TRP:HB2	1:B:2086:ALA:HB2	1.94	0.49
1:B:2203:ASP:OD1	1:B:2203:ASP:N	2.39	0.49
1:A:1617:TRP:HB2	1:A:1637:LEU:HD21	1.95	0.49
1:B:1577:ASN:OD1	1:B:1579:PRO:HD2	2.13	0.49
1:B:1951:ASP:OD1	1:B:1952:GLY:N	2.43	0.49
1:B:2221:ILE:O	1:B:2225:ARG:HG2	2.13	0.49
1:A:1577:ASN:OD1	1:A:1579:PRO:HD2	2.13	0.48
1:B:2102:GLN:NE2	1:B:2156:ASP:OD2	2.36	0.48
1:B:2679:GLU:OE1	1:B:2687:LYS:NZ	2.35	0.48
1:A:2077:THR:O	1:A:2081:ARG:HG3	2.14	0.48
1:B:1552:ALA:HB3	1:B:1595:PRO:HD3	1.95	0.48
1:A:2221:ILE:O	1:A:2225:ARG:HG2	2.13	0.48
1:A:1552:ALA:HB3	1:A:1595:PRO:HD3	1.95	0.48
1:B:2076:ASN:OD1	1:B:2076:ASN:N	2.34	0.48
1:B:2536:PRO:HA	1:B:2582:GLU:HA	1.96	0.47
1:B:2208:MET:HE3	1:B:2208:MET:HB2	1.68	0.47
1:A:2102:GLN:NE2	1:A:2156:ASP:OD2	2.36	0.47
1:B:1617:TRP:HB2	1:B:1637:LEU:HD21	1.95	0.47
1:B:2531:SER:HB3	1:B:2587:SER:HA	1.97	0.47
1:A:1763:SER:OG	1:A:1795:GLU:OE2	2.30	0.47
1:A:2536:PRO:HA	1:A:2582:GLU:HA	1.96	0.47
1:B:2077:THR:O	1:B:2081:ARG:HG3	2.14	0.47
1:A:2531:SER:HB3	1:A:2587:SER:HA	1.97	0.47
1:B:1651:LEU:HD22	1:B:2080:LEU:HD11	1.97	0.47
1:A:1651:LEU:HD22	1:A:2080:LEU:HD11	1.97	0.46
1:A:2236:LEU:HD22	1:A:2243:LEU:HD23	1.97	0.46
1:A:2530:LYS:HB2	1:A:2533:GLN:HG2	1.97	0.46
1:B:2530:LYS:HB2	1:B:2533:GLN:HG2	1.97	0.46
1:A:1622:SER:OG	1:A:1623:GLN:N	2.49	0.46
1:A:1661:ARG:HH12	1:A:2731:ASP:HB2	1.81	0.46
1:B:1959:ARG:HA	1:B:1959:ARG:HD3	1.74	0.46
1:B:2500:ASN:O	1:B:2504:SER:OG	2.21	0.46
1:B:1754:ALA:C	1:B:1756:ALA:H	2.24	0.46
1:B:1661:ARG:HH12	1:B:2731:ASP:HB2	1.81	0.46
1:B:2236:LEU:HD22	1:B:2243:LEU:HD23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1656:GLN:NE2	1:B:1659:GLU:HG3	2.32	0.45
1:B:1758:GLU:HG2	1:B:1835:ALA:HB2	1.99	0.45
1:A:1754:ALA:C	1:A:1756:ALA:H	2.24	0.45
1:B:1603:ILE:HG23	1:B:1608:ASP:HB2	1.99	0.45
1:B:1622:SER:OG	1:B:1623:GLN:N	2.49	0.44
1:B:2319:LYS:HE3	1:B:2360:GLN:HE22	1.81	0.44
1:A:2319:LYS:HE3	1:A:2360:GLN:HE22	1.81	0.44
1:A:2530:LYS:HB2	1:A:2533:GLN:CG	2.47	0.44
1:B:1467:LYS:O	1:B:1524:SER:OG	2.25	0.44
1:B:2698:ALA:O	1:B:2706:ARG:HG2	2.18	0.44
1:A:1758:GLU:HG2	1:A:1835:ALA:HB2	1.99	0.44
1:A:1603:ILE:HG23	1:A:1608:ASP:HB2	1.99	0.44
1:A:1951:ASP:OD1	1:A:1952:GLY:N	2.43	0.44
1:A:1971:ASP:OD1	1:A:1972:LEU:N	2.50	0.44
1:B:1943:LEU:HD13	1:B:1958:PHE:HB2	1.99	0.44
1:B:1971:ASP:OD1	1:B:1972:LEU:N	2.50	0.44
1:A:1661:ARG:HH21	1:A:1851:THR:HG21	1.83	0.44
1:A:1943:LEU:HD13	1:A:1958:PHE:HB2	1.99	0.44
1:A:2800:LEU:HD23	1:A:2928:THR:HG23	2.00	0.44
1:A:2557:PRO:HA	1:A:2558:PRO:HD3	1.94	0.44
1:B:2800:LEU:HD23	1:B:2928:THR:HG23	2.00	0.44
1:A:2274:PRO:O	1:A:2278:GLU:HG2	2.18	0.43
1:A:2698:ALA:O	1:A:2706:ARG:HG2	2.18	0.43
1:B:2274:PRO:O	1:B:2278:GLU:HG2	2.18	0.43
1:A:1686:ASP:OD1	1:A:1686:ASP:N	2.42	0.43
1:A:2614:ASP:OD1	1:A:2614:ASP:N	2.51	0.43
1:A:1656:GLN:NE2	1:A:1659:GLU:HG3	2.32	0.43
1:A:2465:MET:HE2	1:A:2510:ILE:HD12	2.00	0.43
1:B:1661:ARG:HH21	1:B:1851:THR:HG21	1.83	0.43
1:B:2530:LYS:HB2	1:B:2533:GLN:CG	2.47	0.43
1:A:1558:GLU:OE1	1:A:1558:GLU:N	2.35	0.43
1:A:2409:GLU:O	1:A:2413:GLU:HG2	2.19	0.43
1:B:2113:GLU:O	1:B:2116:SER:OG	2.21	0.43
1:A:1755:ARG:HA	1:A:1755:ARG:HD3	1.85	0.43
1:A:1959:ARG:HA	1:A:1959:ARG:HD3	1.74	0.43
1:A:2513:THR:HG21	1:A:2555:ILE:CD1	2.48	0.43
1:A:2208:MET:HE3	1:A:2208:MET:HB2	1.68	0.43
1:A:2825:LEU:HD23	1:A:2916:VAL:HG13	2.01	0.43
1:B:2687:LYS:HB2	1:B:2690:GLN:HG3	2.01	0.43
1:B:2064:LYS:HB2	1:B:2064:LYS:HE3	1.64	0.43
1:B:2513:THR:HG21	1:B:2555:ILE:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1657:LEU:HD23	1:A:1657:LEU:HA	1.83	0.42
1:A:2854:PRO:HA	1:A:2857:MET:HB3	2.01	0.42
1:B:2465:MET:HE2	1:B:2510:ILE:HD12	2.00	0.42
1:A:1783:LEU:HD23	1:A:1783:LEU:HA	1.90	0.42
1:A:2179:GLN:HE22	1:B:1957:ALA:HB1	1.84	0.42
1:B:1713:LEU:HD23	1:B:1713:LEU:HA	1.87	0.42
1:A:2203:ASP:OD1	1:A:2203:ASP:N	2.39	0.42
1:B:2854:PRO:HA	1:B:2857:MET:HB3	2.01	0.42
1:A:1674:LEU:HD23	1:A:1674:LEU:HA	1.80	0.42
1:A:1957:ALA:HB1	1:B:2179:GLN:HE22	1.84	0.42
1:A:2465:MET:SD	1:A:2503:VAL:HG11	2.59	0.42
1:A:2121:SER:HB3	1:A:2640:ARG:HE	1.84	0.42
1:A:2687:LYS:HB2	1:A:2690:GLN:HG3	2.01	0.42
1:A:1842:LEU:HD23	1:A:1842:LEU:HA	1.90	0.42
1:A:1833:GLU:N	1:A:1834:PRO:HD2	2.35	0.42
1:A:2033:ASP:HB3	1:A:2069:HIS:CE1	2.55	0.42
1:B:1575:LEU:HD12	1:B:1575:LEU:HA	1.90	0.42
1:B:2529:TYR:HB3	1:B:2585:ILE:HD13	2.01	0.42
1:A:2624:GLN:HE21	1:A:2624:GLN:HB3	1.60	0.42
1:B:2465:MET:SD	1:B:2503:VAL:HG11	2.59	0.42
1:B:2513:THR:HG21	1:B:2555:ILE:HD11	2.02	0.42
1:B:2681:TYR:OH	1:B:2727:GLU:OE1	2.38	0.42
1:B:2839:LEU:HD11	1:B:2906:VAL:HG11	2.02	0.42
1:B:1985:LEU:HD12	1:B:1997:LEU:HD12	2.02	0.42
1:A:2079:VAL:O	1:A:2083:GLN:HG2	2.20	0.41
1:B:2079:VAL:O	1:B:2083:GLN:HG2	2.20	0.41
1:B:2123:ARG:HE	1:B:2123:ARG:HB2	1.61	0.41
1:A:1954:LYS:NZ	1:B:2217:HIS:O	2.53	0.41
1:A:2843:ARG:NH2	1:A:2900:ASP:OD1	2.53	0.41
1:B:2121:SER:HB3	1:B:2640:ARG:HE	1.84	0.41
1:B:2825:LEU:HD23	1:B:2916:VAL:HG13	2.01	0.41
1:A:2123:ARG:HE	1:A:2123:ARG:HB2	1.61	0.41
1:B:1556:THR:O	1:B:1560:ASN:ND2	2.54	0.41
1:B:1648:PRO:HG2	1:B:1651:LEU:HD12	2.03	0.41
1:A:2839:LEU:HD11	1:A:2906:VAL:HG11	2.02	0.41
1:B:1755:ARG:HA	1:B:1755:ARG:HD3	1.85	0.41
1:B:1833:GLU:N	1:B:1834:PRO:HD2	2.35	0.41
1:A:1648:PRO:HG2	1:A:1651:LEU:HD12	2.03	0.41
1:A:2217:HIS:O	1:B:1954:LYS:NZ	2.53	0.41
1:A:2529:TYR:HB3	1:A:2585:ILE:HD13	2.01	0.41
1:B:2033:ASP:HB3	1:B:2069:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2409:GLU:O	1:B:2413:GLU:HG2	2.19	0.41
1:A:1985:LEU:HD12	1:A:1997:LEU:HD12	2.02	0.41
1:A:2630:SER:OG	1:A:2646:ILE:HG12	2.20	0.41
1:A:2814:GLU:H	1:A:2814:GLU:HG2	1.57	0.41
1:B:1450:ASP:O	1:B:1454:ILE:HG13	2.21	0.41
1:B:2282:LYS:NZ	1:B:2287:GLU:OE1	2.39	0.41
1:B:2636:HIS:HE2	1:B:2831:GLU:CD	2.28	0.41
1:A:2329:LEU:HD11	1:A:2348:HIS:CE1	2.56	0.41
1:B:2630:SER:OG	1:B:2646:ILE:HG12	2.20	0.41
1:A:1542:ASN:O	1:A:1546:ILE:HG23	2.21	0.40
1:A:2064:LYS:HE3	1:A:2064:LYS:HB2	1.64	0.40
1:A:2825:LEU:O	1:A:2829:ARG:HG2	2.21	0.40
1:B:2843:ARG:NH2	1:B:2900:ASP:OD1	2.53	0.40
1:A:1450:ASP:O	1:A:1454:ILE:HG13	2.21	0.40
1:A:1556:THR:O	1:A:1560:ASN:ND2	2.54	0.40
1:A:2513:THR:HG21	1:A:2555:ILE:HD11	2.02	0.40
1:A:2593:LYS:HE3	1:A:2593:LYS:HB3	1.95	0.40
1:A:2358:LEU:HD12	1:A:2358:LEU:HA	1.91	0.40
1:A:2567:ASN:OD1	1:A:2567:ASN:N	2.50	0.40
1:B:1542:ASN:O	1:B:1546:ILE:HG23	2.21	0.40
1:A:2279:LEU:HA	1:A:2279:LEU:HD23	1.83	0.40
1:B:1917:LEU:HD12	1:B:1917:LEU:HA	1.91	0.40
1:B:2105:LEU:HD12	1:B:2105:LEU:HA	1.94	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	1396/2944 (47%)	1337 (96%)	59 (4%)	0	100	100
1	B	1396/2944 (47%)	1337 (96%)	59 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2792/5888 (47%)	2674 (96%)	118 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	1212/2529 (48%)	1168 (96%)	44 (4%)	31	66
1	B	1212/2529 (48%)	1168 (96%)	44 (4%)	31	66
All	All	2424/5058 (48%)	2336 (96%)	88 (4%)	32	66

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1433	MET
1	A	1450	ASP
1	A	1585	LEU
1	A	1608	ASP
1	A	1650	ASP
1	A	1658	GLN
1	A	1659	GLU
1	A	1681	LEU
1	A	1686	ASP
1	A	1868	ASP
1	A	1899	ARG
1	A	1935	GLN
1	A	1936	ASP
1	A	2026	LEU
1	A	2076	ASN
1	A	2077	THR
1	A	2101	ASP
1	A	2118	TRP
1	A	2121	SER
1	A	2126	ASP

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Mol	Chain	Res	Type
1	A	2147	LEU
1	A	2160	VAL
1	A	2191	LEU
1	A	2240	SER
1	A	2369	THR
1	A	2410	VAL
1	A	2443	THR
1	A	2465	MET
1	A	2485	SER
1	A	2487	GLN
1	A	2567	ASN
1	A	2573	VAL
1	A	2600	THR
1	A	2613	ASN
1	A	2637	ARG
1	A	2702	ASN
1	A	2704	GLU
1	A	2713	VAL
1	A	2733	ASP
1	A	2752	LEU
1	A	2774	GLU
1	A	2803	ASP
1	A	2813	THR
1	A	2855	VAL
1	B	1433	MET
1	B	1450	ASP
1	B	1585	LEU
1	B	1608	ASP
1	B	1650	ASP
1	B	1658	GLN
1	B	1659	GLU
1	B	1681	LEU
1	B	1686	ASP
1	B	1868	ASP
1	B	1899	ARG
1	B	1935	GLN
1	B	1936	ASP
1	B	2026	LEU
1	B	2076	ASN
1	B	2077	THR
1	B	2101	ASP
1	B	2118	TRP

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Mol	Chain	Res	Type
1	B	2121	SER
1	B	2126	ASP
1	B	2147	LEU
1	B	2160	VAL
1	B	2191	LEU
1	B	2240	SER
1	B	2369	THR
1	B	2410	VAL
1	B	2443	THR
1	B	2465	MET
1	B	2485	SER
1	B	2487	GLN
1	B	2567	ASN
1	B	2573	VAL
1	B	2600	THR
1	B	2613	ASN
1	B	2637	ARG
1	B	2702	ASN
1	B	2704	GLU
1	B	2713	VAL
1	B	2733	ASP
1	B	2752	LEU
1	B	2774	GLU
1	B	2803	ASP
1	B	2813	THR
1	B	2855	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1436	HIS
1	A	1551	ASN
1	A	1560	ASN
1	A	1573	ASN
1	A	1656	GLN
1	A	1765	HIS
1	A	1844	ASN
1	A	1870	ASN
1	A	2031	ASN
1	A	2065	ASN
1	A	2179	GLN
1	A	2255	GLN

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Mol	Chain	Res	Type
1	A	2302	GLN
1	A	2354	GLN
1	A	2360	GLN
1	A	2446	GLN
1	A	2467	HIS
1	A	2487	GLN
1	A	2518	HIS
1	A	2552	ASN
1	A	2553	ASN
1	A	2561	GLN
1	A	2624	GLN
1	A	2641	GLN
1	A	2678	HIS
1	A	2754	HIS
1	A	2770	HIS
1	A	2844	HIS
1	A	2849	GLN
1	A	2925	ASN
1	B	1551	ASN
1	B	1573	ASN
1	B	1656	GLN
1	B	1765	HIS
1	B	2031	ASN
1	B	2065	ASN
1	B	2179	GLN
1	B	2255	GLN
1	B	2290	GLN
1	B	2302	GLN
1	B	2317	ASN
1	B	2354	GLN
1	B	2360	GLN
1	B	2446	GLN
1	B	2467	HIS
1	B	2552	ASN
1	B	2553	ASN
1	B	2624	GLN
1	B	2641	GLN
1	B	2678	HIS
1	B	2754	HIS
1	B	2770	HIS
1	B	2849	GLN
1	B	2925	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	AGS	A	3001	3	32,33,33	0.72	2 (6%)	45,52,52	0.68	1 (2%)
2	AGS	B	3001	3	32,33,33	0.72	2 (6%)	45,52,52	0.68	1 (2%)

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	AGS	A	3001	3	-	5/21/38/38	0/3/3/3
2	AGS	B	3001	3	-	5/21/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3001	AGS	PG-S1G	2.15	1.95	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3001	AGS	PG-S1G	2.15	1.95	1.90
2	A	3001	AGS	PB-O3B	-2.02	1.57	1.59
2	B	3001	AGS	PB-O3B	-2.02	1.57	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3001	AGS	PB-O3B-PG	-3.73	119.52	133.17
2	B	3001	AGS	PB-O3B-PG	-3.73	119.52	133.17

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3001	AGS	O4'-C4'-C5'-O5'
2	B	3001	AGS	O4'-C4'-C5'-O5'
2	A	3001	AGS	C3'-C4'-C5'-O5'
2	B	3001	AGS	C3'-C4'-C5'-O5'
2	A	3001	AGS	PB-O3A-PA-O5'
2	B	3001	AGS	PB-O3A-PA-O5'
2	A	3001	AGS	PA-O3A-PB-O2B
2	B	3001	AGS	PA-O3A-PB-O2B
2	A	3001	AGS	PB-O3A-PA-O2A
2	B	3001	AGS	PB-O3A-PA-O2A

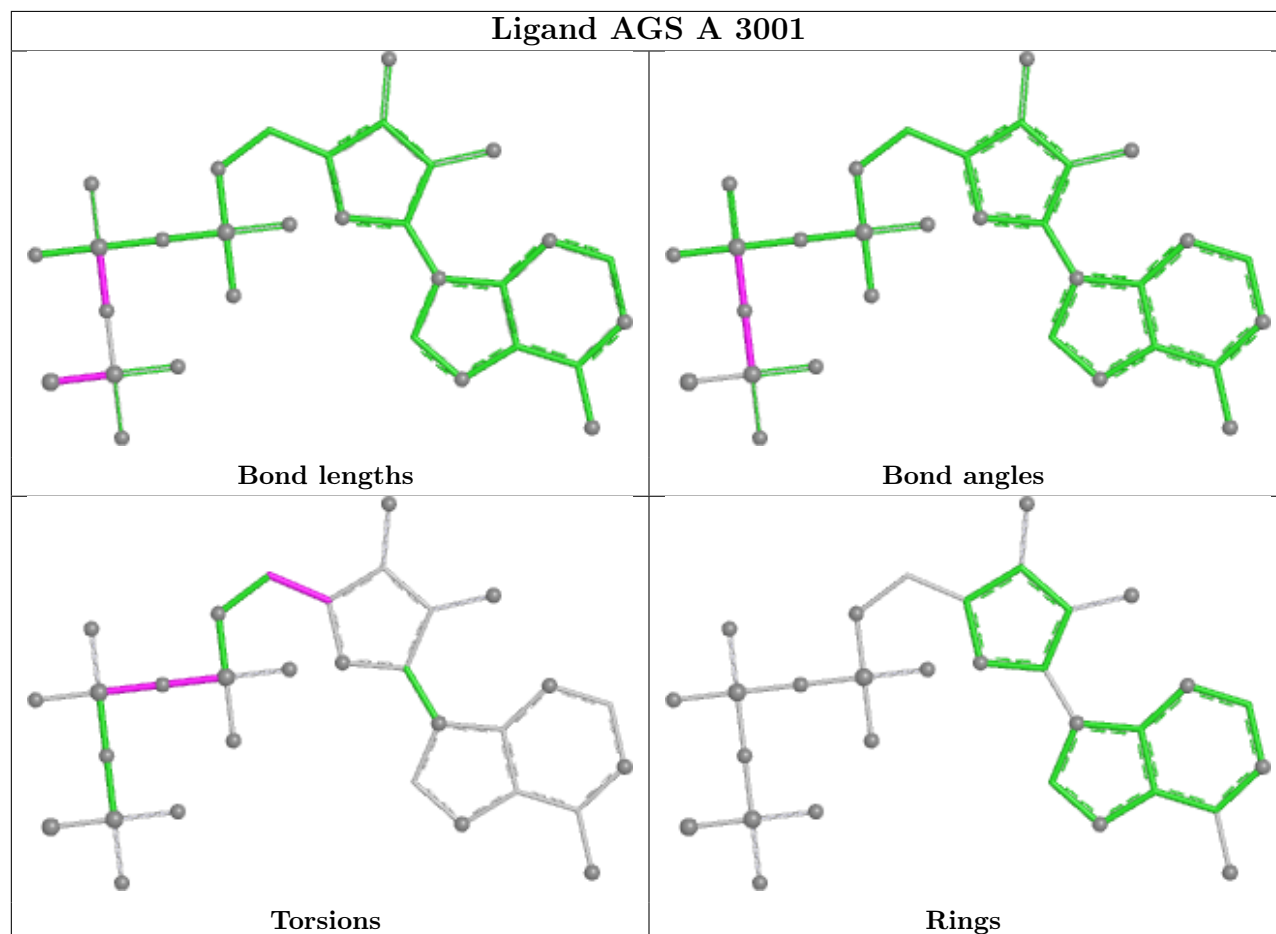
There are no ring outliers.

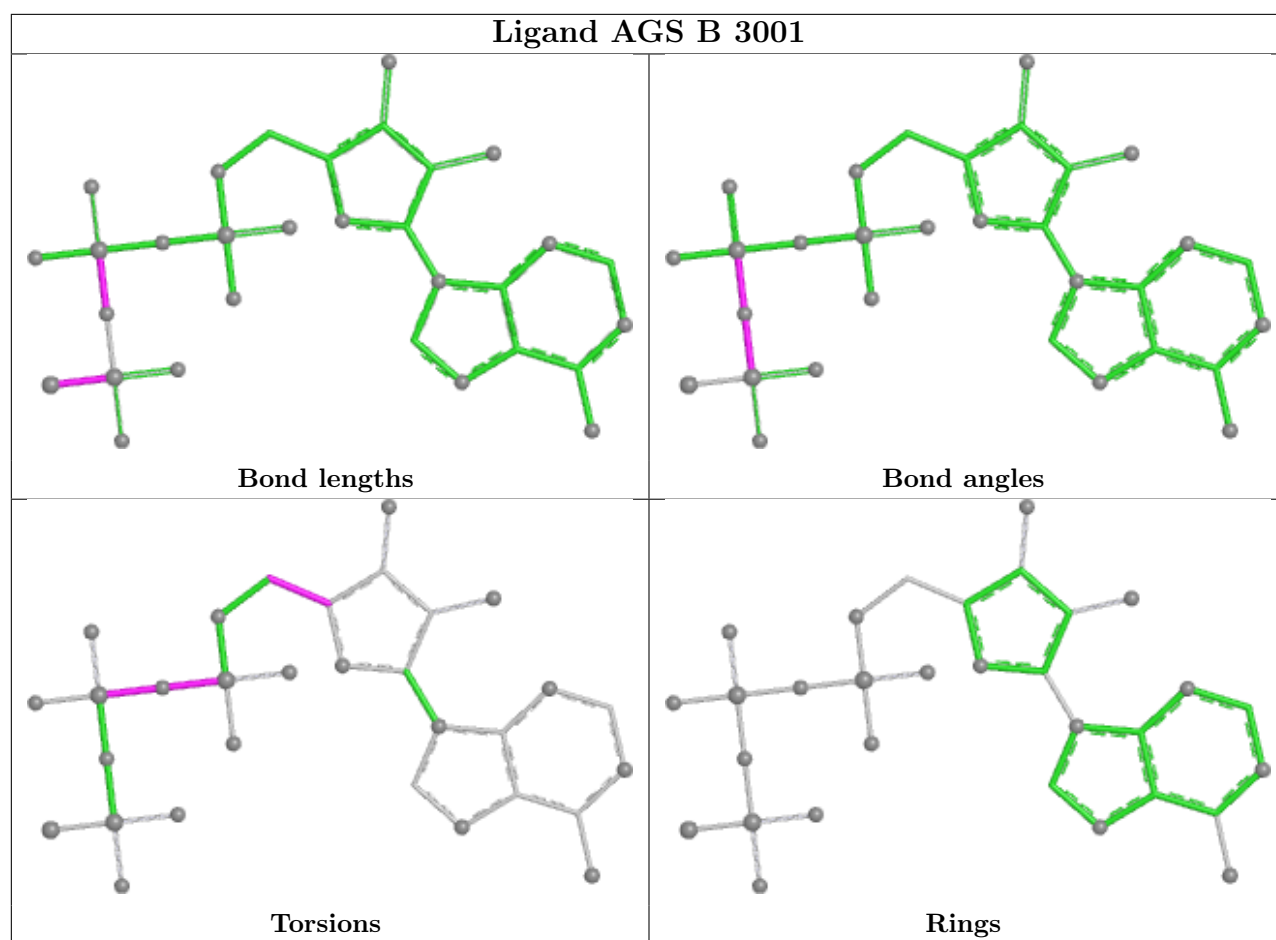
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3001	AGS	1	0
2	B	3001	AGS	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

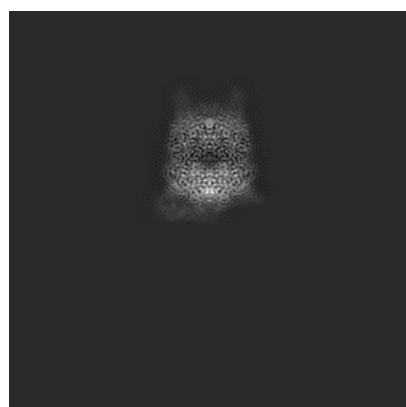
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10231. These allow visual inspection of the internal detail of the map and identification of artifacts.

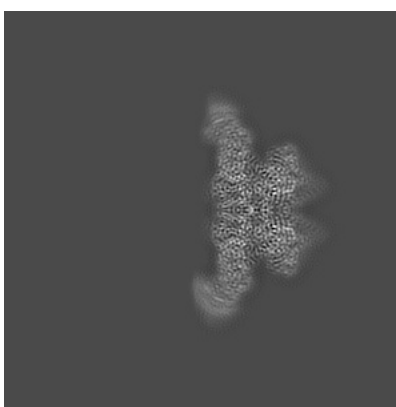
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

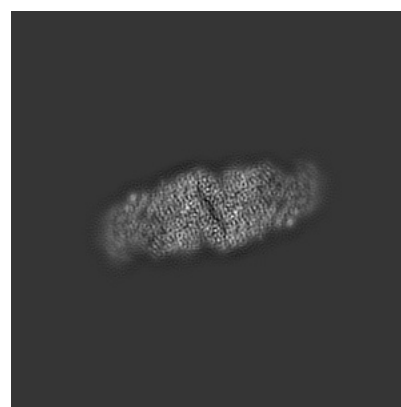
6.1.1 Primary map



X



Y

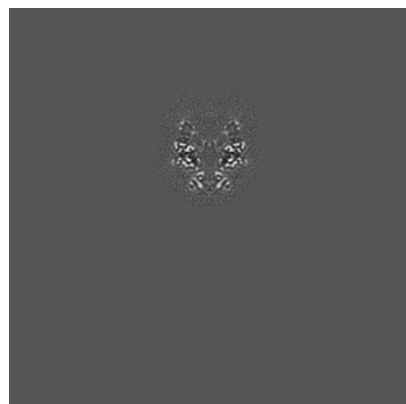


Z

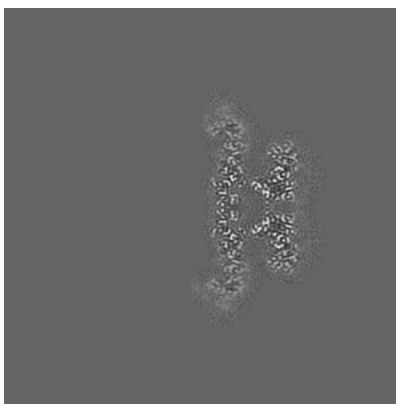
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

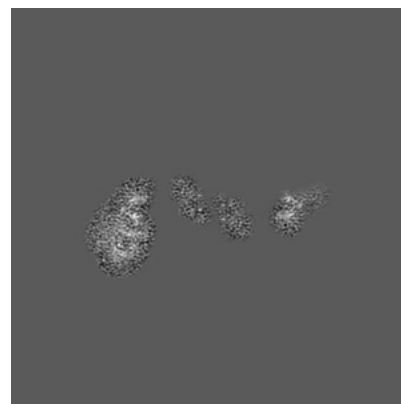
6.2.1 Primary map



X Index: 176



Y Index: 176

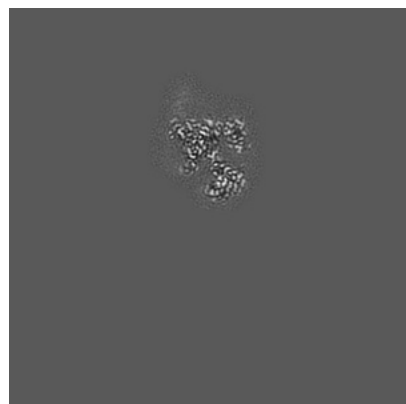


Z Index: 176

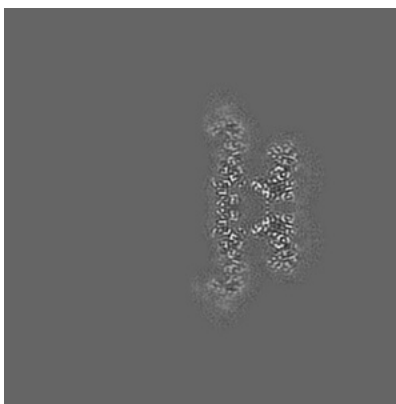
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

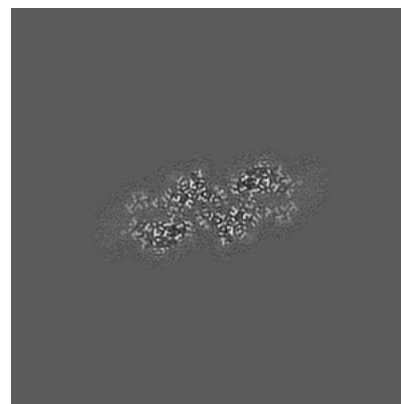
6.3.1 Primary map



X Index: 159



Y Index: 176

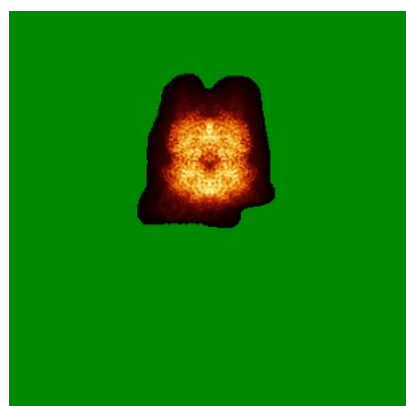


Z Index: 207

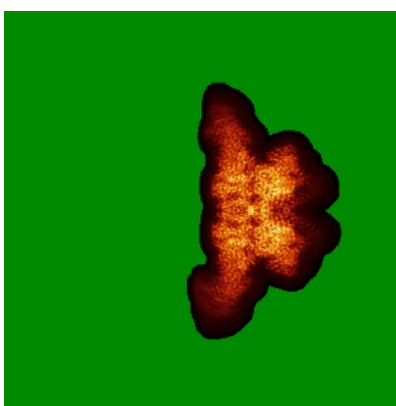
The images above show the largest variance slices of the map in three orthogonal directions.

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

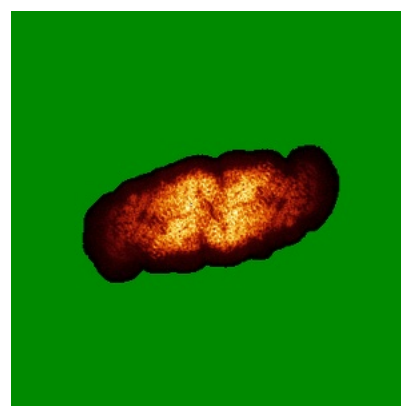
6.4.1 Primary map



X



Y

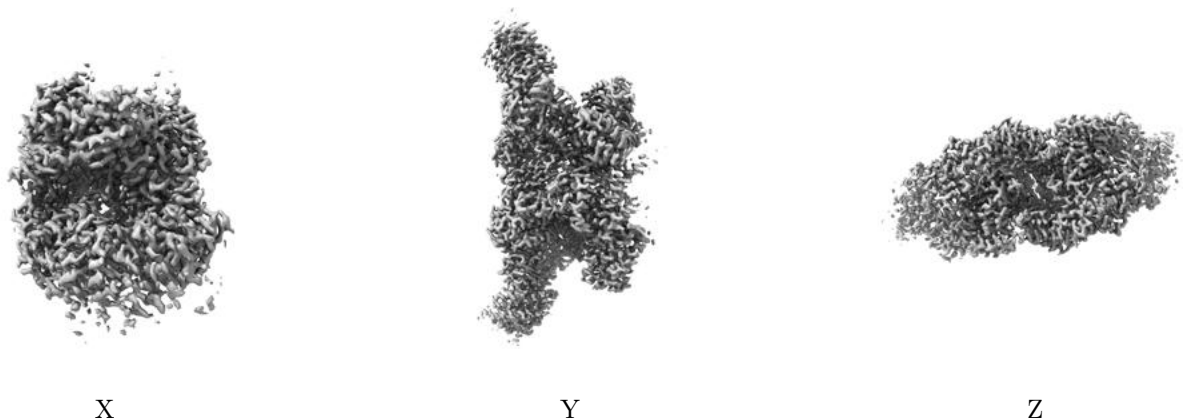


Z

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 0.0185. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

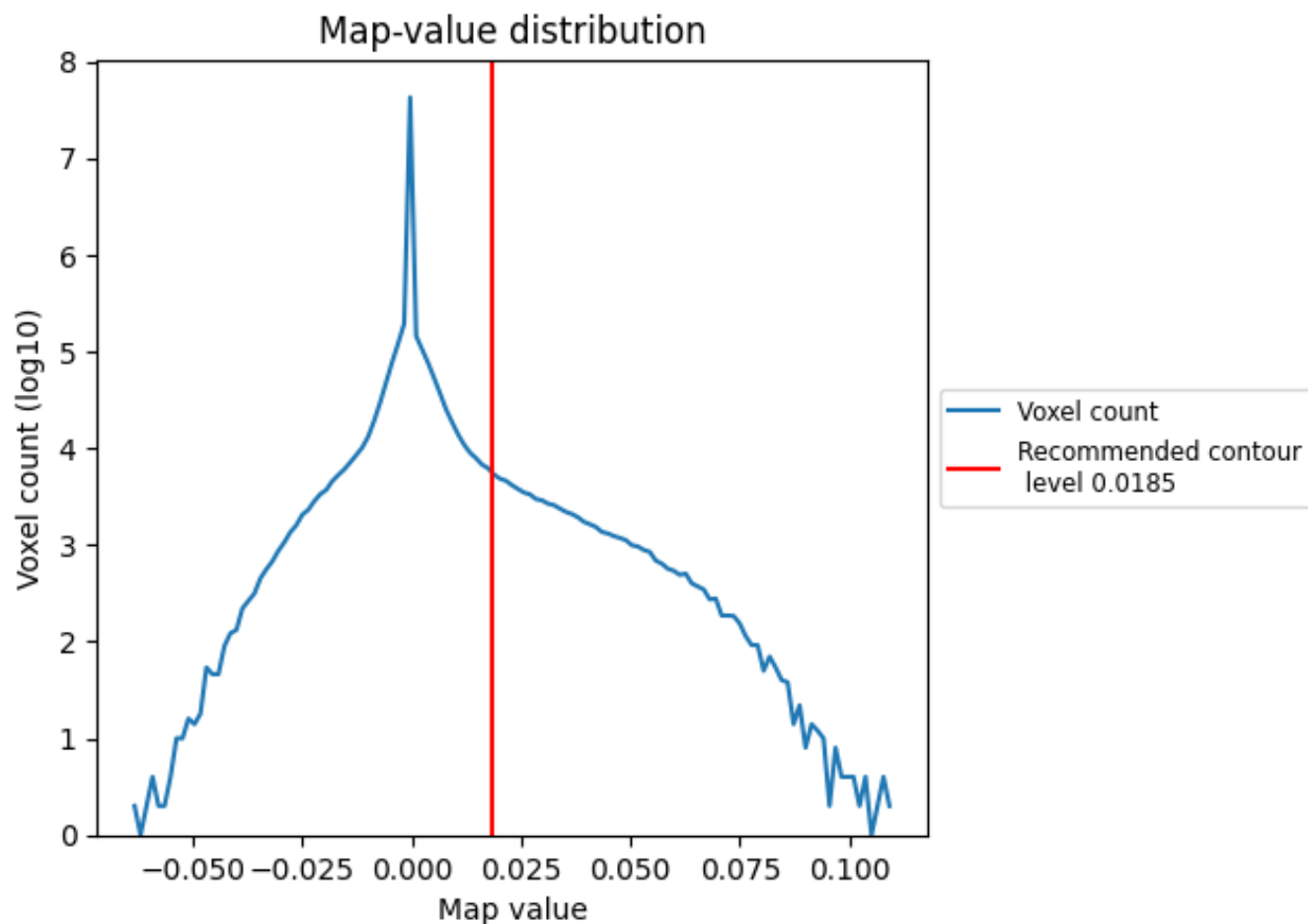
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

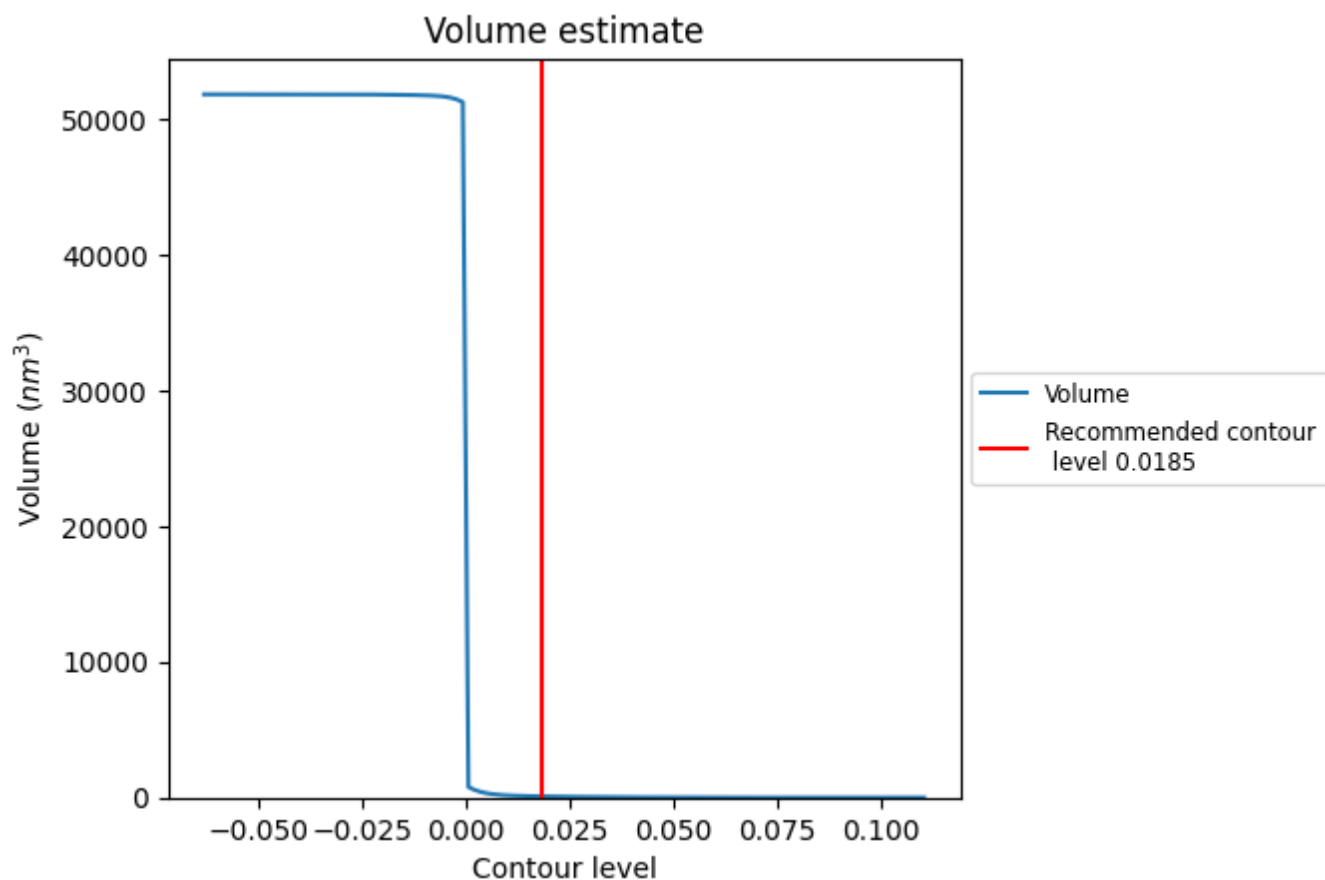
This section contains the results of statistical analysis of the map.

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.

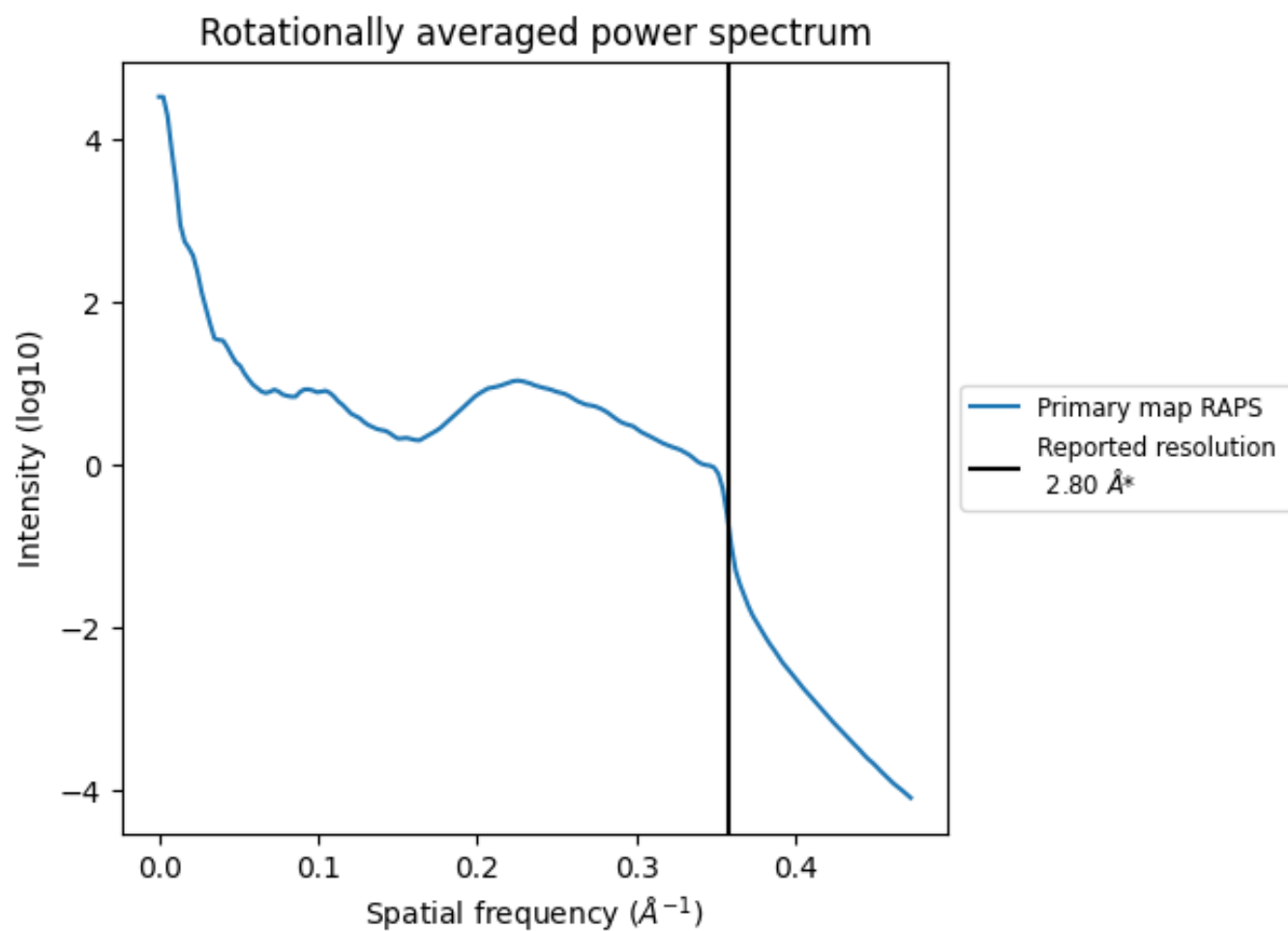
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 86 nm^3 ; this corresponds to an approximate mass of 77 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 ⓘ

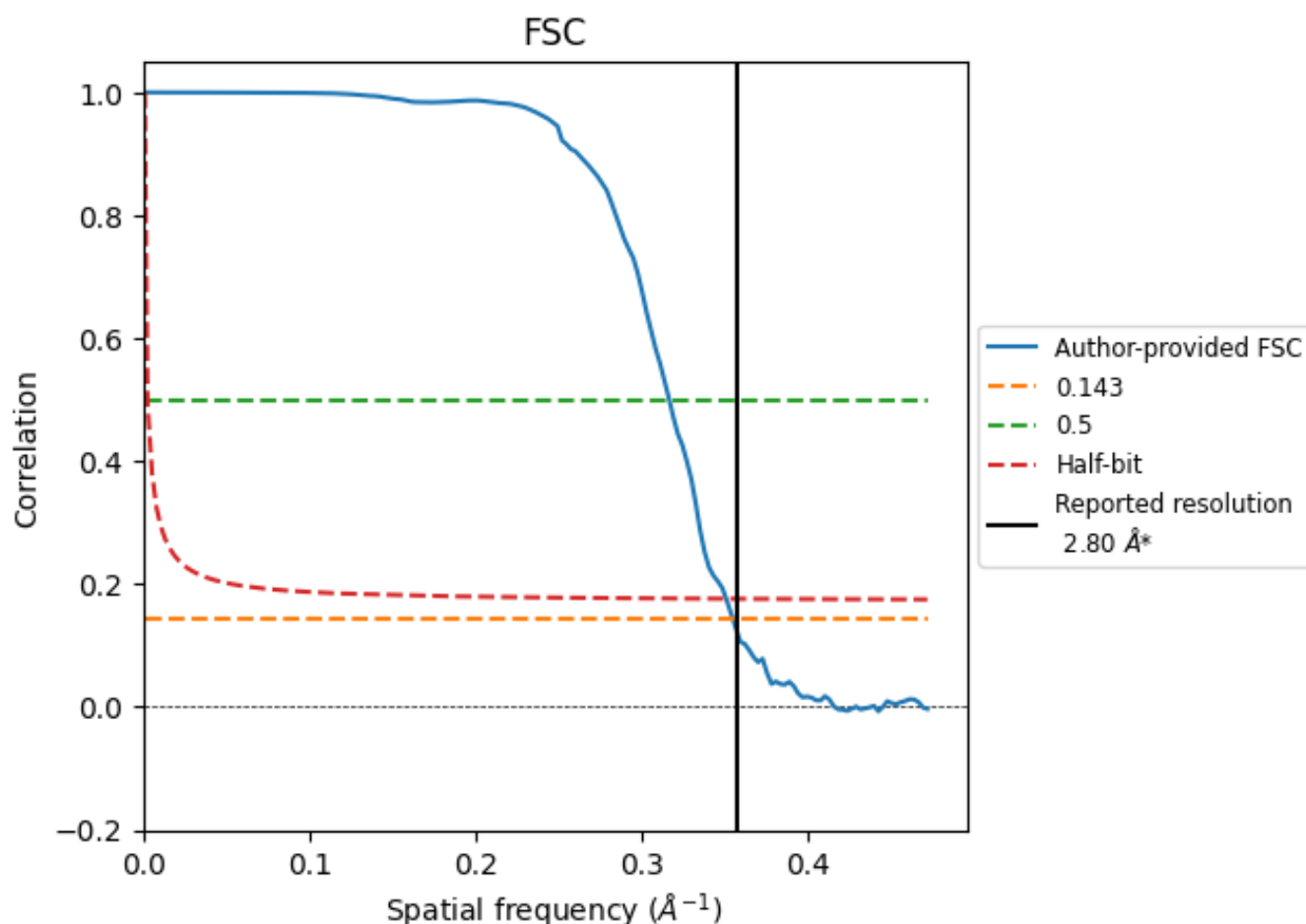


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

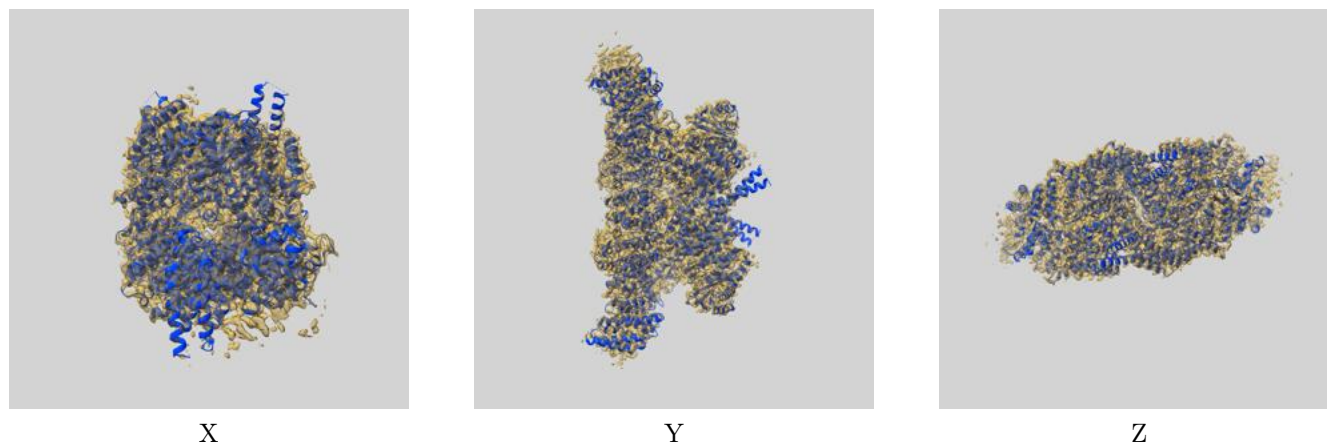
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.82	3.16	2.85
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

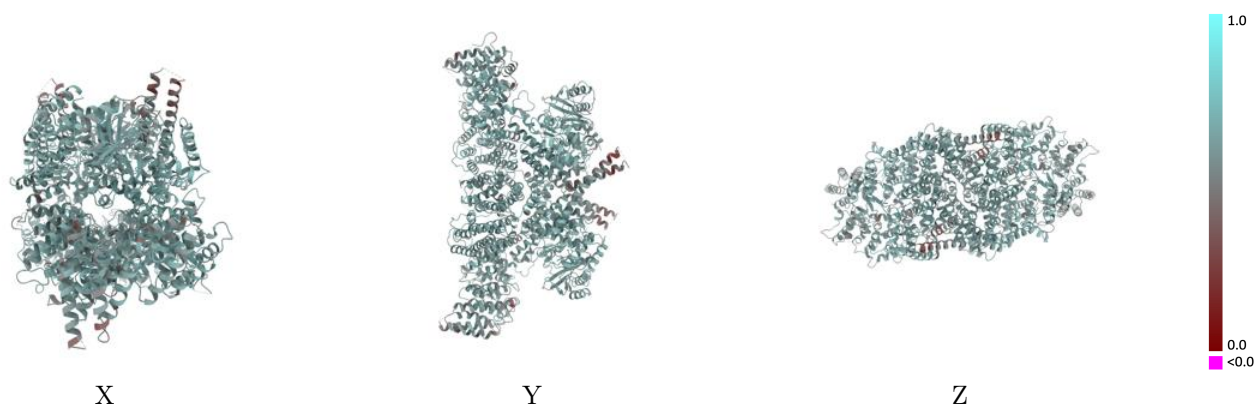
This section contains information regarding the fit between EMDB map EMD-10231 and PDB model 6SKY. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



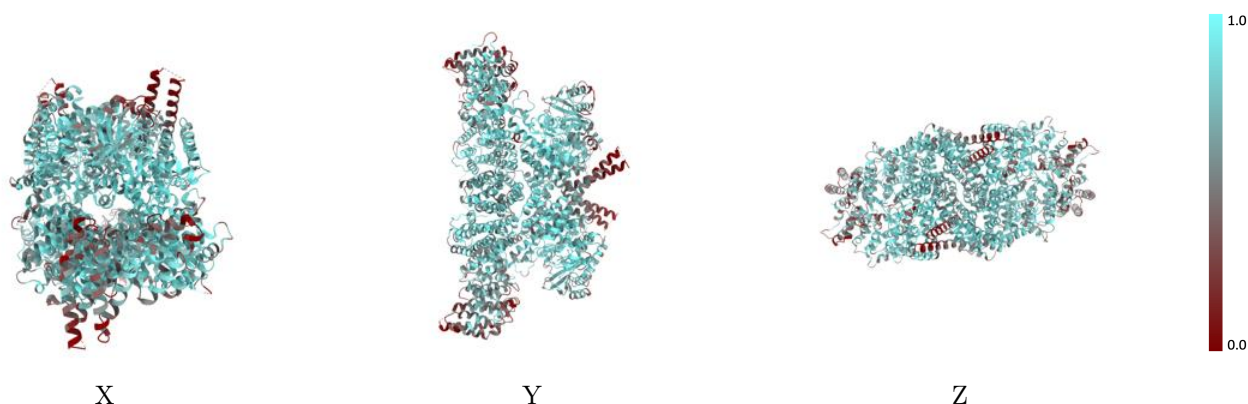
The images above show the 3D surface view of the map at the recommended contour level 0.0185 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



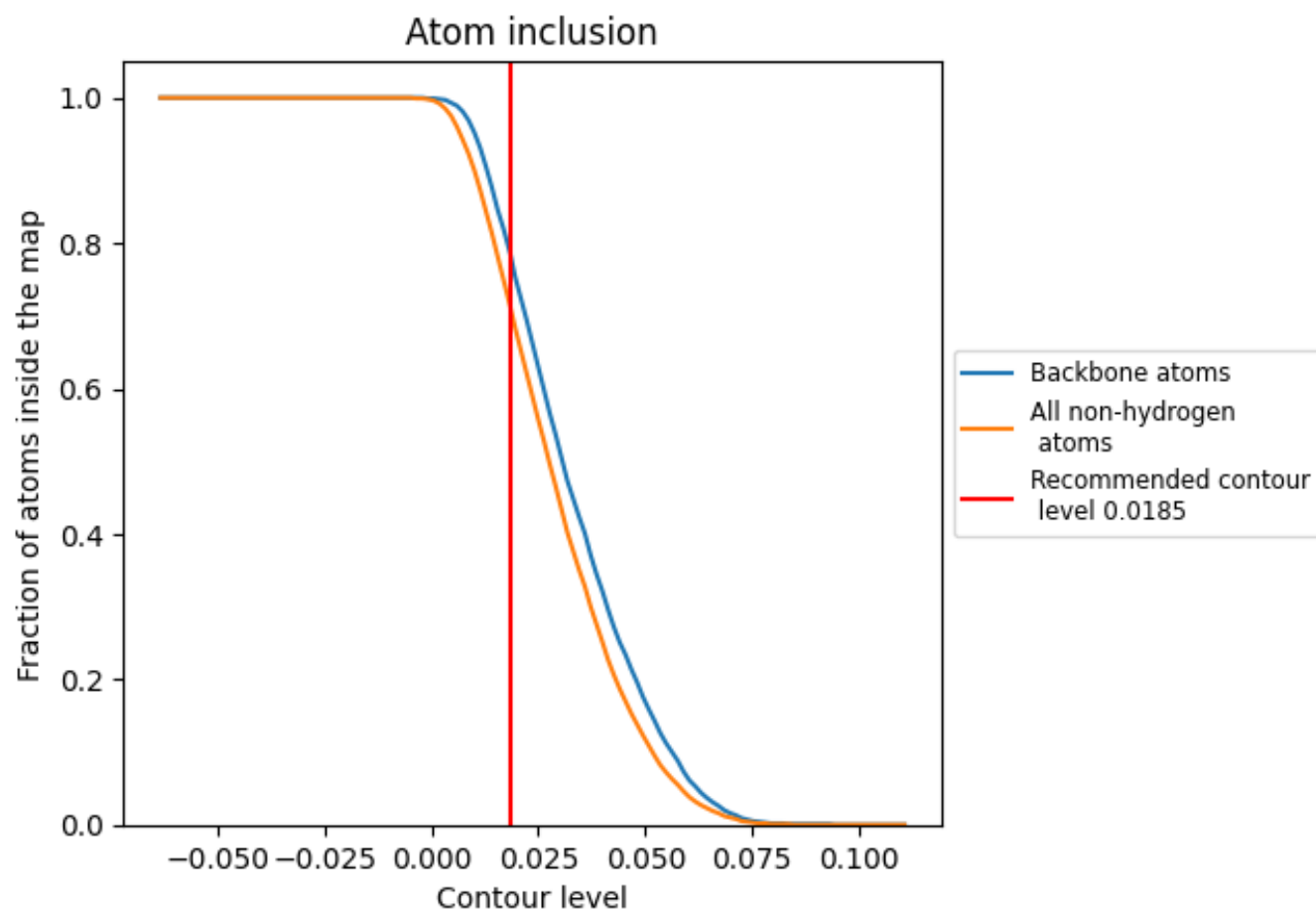
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0185).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 71% 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 (0.0185) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7110	0.6010
A	0.7110	0.6010
B	0.7110	0.6010

