



Full wwPDB EM Validation Report ⓘ

Jul 27, 2026 – 06:05 PM EDT

PDB ID : 10SJ / pdb_000010sj
EMDB ID : EMD-75436
Title : 20S Alpha 3 Deletion proteasome core particle in complex with Blm10
Authors : Walsh Jr, R.M.; Rawson, S.; Fermin Perez, E.; Venclovaite, U.; Hanna, J.
Deposited on : 2026-02-05
Resolution : 3.70 Å(reported)
Based on initial model : 10QT

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:

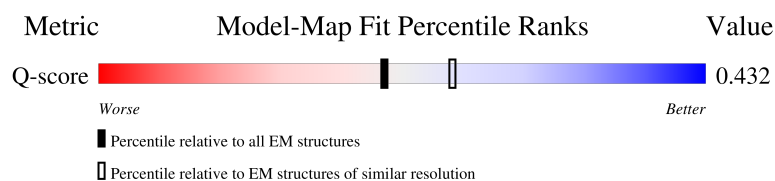
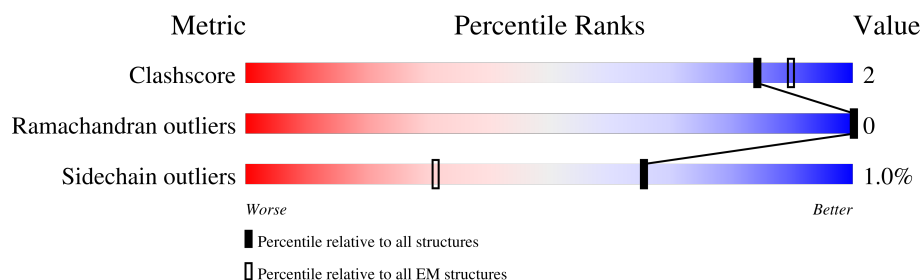
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



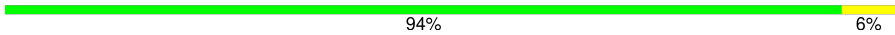
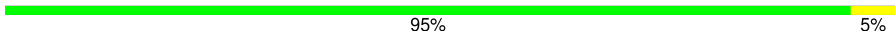
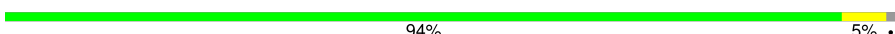
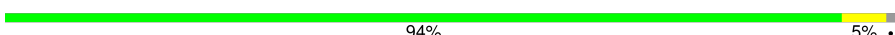
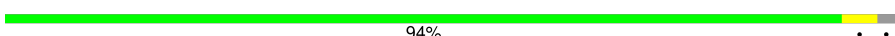
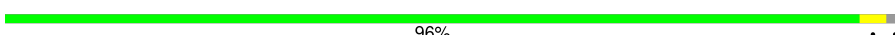
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	1	241	
1	M	241	
2	2	266	
2	N	266	

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Mol	Chain	Length	Quality of chain
3	A	252	
3	O	252	
4	B	250	
4	P	250	
5	C	254	
5	D	254	
5	Q	254	
5	R	254	
6	E	260	
6	S	260	
7	F	234	
7	T	234	
8	G	288	
8	U	288	
9	H	215	
9	V	215	
10	I	261	
10	W	261	
11	J	205	
11	X	205	
12	K	198	
12	Y	198	
13	L	287	
13	Z	287	
14	CA	2167	

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Mol	Chain	Length	Quality of chain
14	DA	2167	78% 7% 15%

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 158332 atoms, of which 79134 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 Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		
1	M	221	Total	C	H	N	O	S	0	0
			3449	1110	1701	301	333	4		

- Molecule 2 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	2	233	Total	C	H	N	O	S	0	0
			3654	1154	1830	312	351	7		
2	N	233	Total	C	H	N	O	S	0	0
			3654	1154	1830	312	351	7		

- Molecule 3 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A	238	Total	C	H	N	O	S	0	0
			3764	1198	1882	316	360	8		
3	O	238	Total	C	H	N	O	S	0	0
			3764	1198	1882	316	360	8		

- Molecule 4 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	249	Total	C	H	N	O	S	0	0
			3826	1214	1919	314	376	3		
4	P	249	Total	C	H	N	O	S	0	0
			3826	1214	1919	314	376	3		

- Molecule 5 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	235	Total	C	H	N	O	S	0	0
			3698	1151	1856	322	365	4		
5	D	234	Total	C	H	N	O	S	0	0
			3687	1148	1851	321	363	4		
5	Q	235	Total	C	H	N	O	S	0	0
			3698	1151	1856	322	365	4		
5	R	234	Total	C	H	N	O	S	0	0
			3687	1148	1851	321	363	4		

- Molecule 6 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	E	241	Total	C	H	N	O	S	0	0
			3694	1163	1835	313	376	7		
6	S	241	Total	C	H	N	O	S	0	0
			3694	1163	1835	313	376	7		

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	F	234	Total	C	H	N	O	S	0	0
			3614	1134	1811	313	351	5		
7	T	234	Total	C	H	N	O	S	0	0
			3613	1134	1810	313	351	5		

- Molecule 8 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	G	242	Total	C	H	N	O	S	0	0
			3763	1199	1878	328	354	4		
8	U	242	Total	C	H	N	O	S	0	0
			3762	1199	1877	328	354	4		

- Molecule 9 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	H	195	Total	C	H	N	O	S	0	0
			2971	949	1468	249	298	7		
9	V	195	Total	C	H	N	O	S	0	0
			2971	949	1468	249	298	7		

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	I	220	Total	C	H	N	O	S	0	0
			3348	1054	1678	291	319	6		
10	W	220	Total	C	H	N	O	S	0	0
			3348	1054	1678	291	319	6		

- Molecule 11 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	J	203	Total	C	H	N	O	S	0	0
			3142	1007	1567	257	303	8		
11	X	203	Total	C	H	N	O	S	0	0
			3142	1007	1567	257	303	8		

- Molecule 12 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	K	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
12	Y	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		

- Molecule 13 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	L	211	Total	C	H	N	O	S	0	0
			3229	1043	1590	279	310	7		
13	Z	211	Total	C	H	N	O	S	0	0
			3229	1043	1590	279	310	7		

- Molecule 14 is a protein called Proteasome activator BLM10.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	CA	1849	Total	C	H	N	O	S	0	0
			30198	9727	15133	2501	2768	69		
14	DA	1849	Total	C	H	N	O	S	0	0
			30198	9727	15133	2501	2768	69		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	-23	MET	-	initiating methionine	UNP P43583
CA	-22	HIS	-	expression tag	UNP P43583
CA	-21	HIS	-	expression tag	UNP P43583

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Chain	Residue	Modelled	Actual	Comment	Reference
CA	-20	HIS	-	expression tag	UNP P43583
CA	-19	HIS	-	expression tag	UNP P43583
CA	-18	HIS	-	expression tag	UNP P43583
CA	-17	HIS	-	expression tag	UNP P43583
CA	-16	HIS	-	expression tag	UNP P43583
CA	-15	HIS	-	expression tag	UNP P43583
CA	-14	HIS	-	expression tag	UNP P43583
CA	-13	HIS	-	expression tag	UNP P43583
CA	-12	HIS	-	expression tag	UNP P43583
CA	-11	HIS	-	expression tag	UNP P43583
CA	-10	THR	-	expression tag	UNP P43583
CA	-9	ALA	-	expression tag	UNP P43583
CA	-8	ASN	-	expression tag	UNP P43583
CA	-7	ASN	-	expression tag	UNP P43583
CA	-6	ASP	-	expression tag	UNP P43583
CA	-5	ASP	-	expression tag	UNP P43583
CA	-4	ASP	-	expression tag	UNP P43583
CA	-3	ILE	-	expression tag	UNP P43583
CA	-2	LYS	-	expression tag	UNP P43583
CA	-1	SER	-	expression tag	UNP P43583
CA	0	PRO	-	expression tag	UNP P43583
DA	-23	MET	-	initiating methionine	UNP P43583
DA	-22	HIS	-	expression tag	UNP P43583
DA	-21	HIS	-	expression tag	UNP P43583
DA	-20	HIS	-	expression tag	UNP P43583
DA	-19	HIS	-	expression tag	UNP P43583
DA	-18	HIS	-	expression tag	UNP P43583
DA	-17	HIS	-	expression tag	UNP P43583
DA	-16	HIS	-	expression tag	UNP P43583
DA	-15	HIS	-	expression tag	UNP P43583
DA	-14	HIS	-	expression tag	UNP P43583
DA	-13	HIS	-	expression tag	UNP P43583
DA	-12	HIS	-	expression tag	UNP P43583
DA	-11	HIS	-	expression tag	UNP P43583
DA	-10	THR	-	expression tag	UNP P43583
DA	-9	ALA	-	expression tag	UNP P43583
DA	-8	ASN	-	expression tag	UNP P43583
DA	-7	ASN	-	expression tag	UNP P43583
DA	-6	ASP	-	expression tag	UNP P43583
DA	-5	ASP	-	expression tag	UNP P43583
DA	-4	ASP	-	expression tag	UNP P43583
DA	-3	ILE	-	expression tag	UNP P43583

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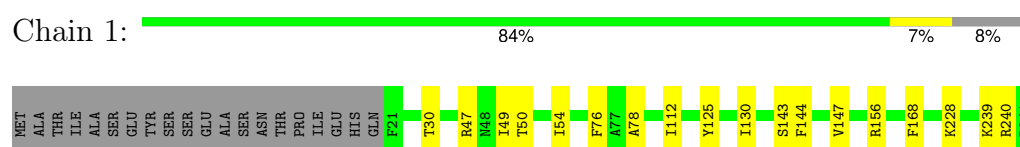
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Chain	Residue	Modelled	Actual	Comment	Reference
DA	-2	LYS	-	expression tag	UNP P43583
DA	-1	SER	-	expression tag	UNP P43583
DA	0	PRO	-	expression tag	UNP P43583

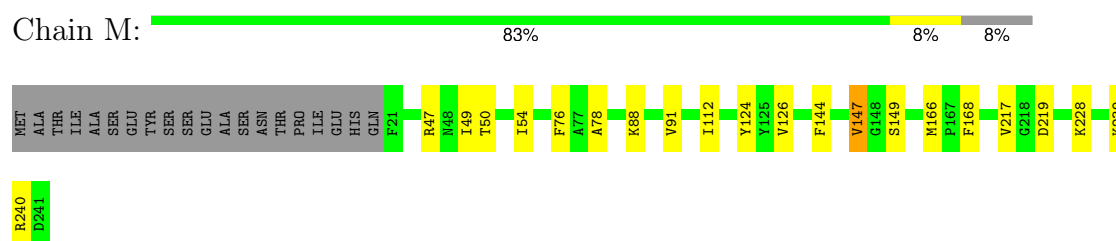
3 Residue-property plots

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.

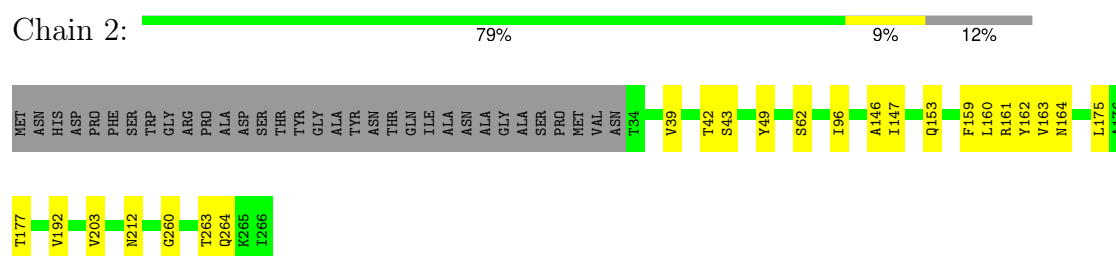
• Molecule 1: Proteasome subunit beta type-6



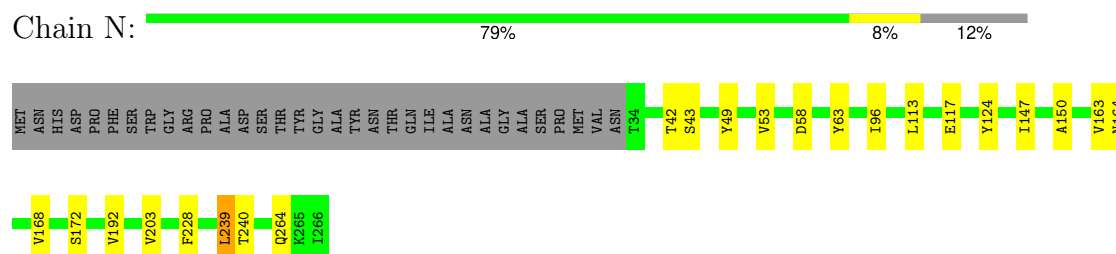
• Molecule 1: Proteasome subunit beta type-6



• Molecule 2: Proteasome subunit beta type-7



• Molecule 2: Proteasome subunit beta type-7



- Molecule 3: Proteasome subunit alpha type-1

Chain A:  88% 6% 6%

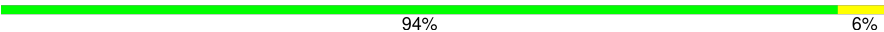


- Molecule 3: Proteasome subunit alpha type-1

Chain O:  92% 6%

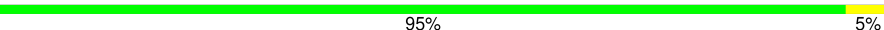


- Molecule 4: Proteasome subunit alpha type-2

Chain B:  94% 6%



- Molecule 4: Proteasome subunit alpha type-2

Chain P:  95% 5%



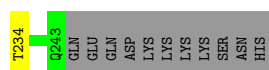
- Molecule 5: Proteasome subunit alpha type-4

Chain C:  90% 7%



- Molecule 5: Proteasome subunit alpha type-4

Chain D:  81% 11% 8%

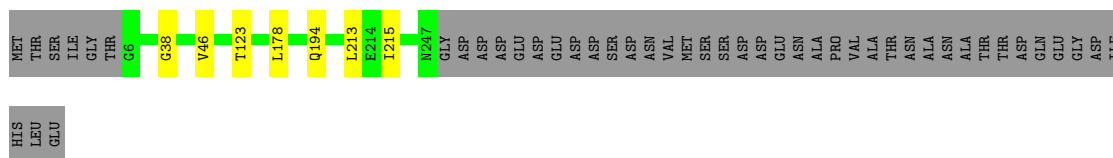


- Molecule 5: Proteasome subunit alpha type-4

Chain Q:  86% 6% 7%

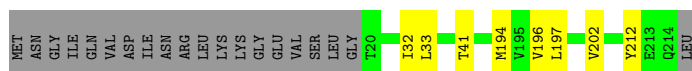


Chain U:  82% 16%



- Molecule 9: Proteasome subunit beta type-1

Chain H:  87% 9%



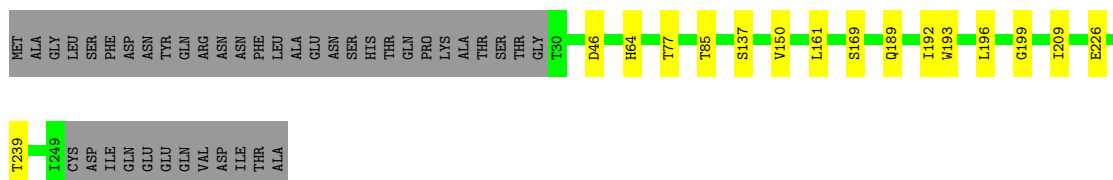
- Molecule 9: Proteasome subunit beta type-1

Chain V:  87% 9%



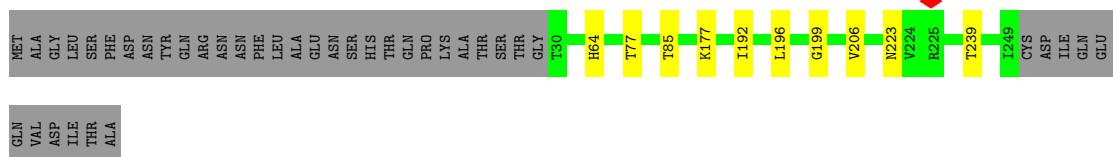
- Molecule 10: Proteasome subunit beta type-2

Chain I:  78% 6% 16%



- Molecule 10: Proteasome subunit beta type-2

Chain W:  80% 16%



- Molecule 11: Proteasome subunit beta type-3

Chain J:  94% 5%



- Molecule 11: Proteasome subunit beta type-3

MET
SER
D3
I11
T88
F124
E132
T141 A142
L146
M149
S168
Q169
A170
D205

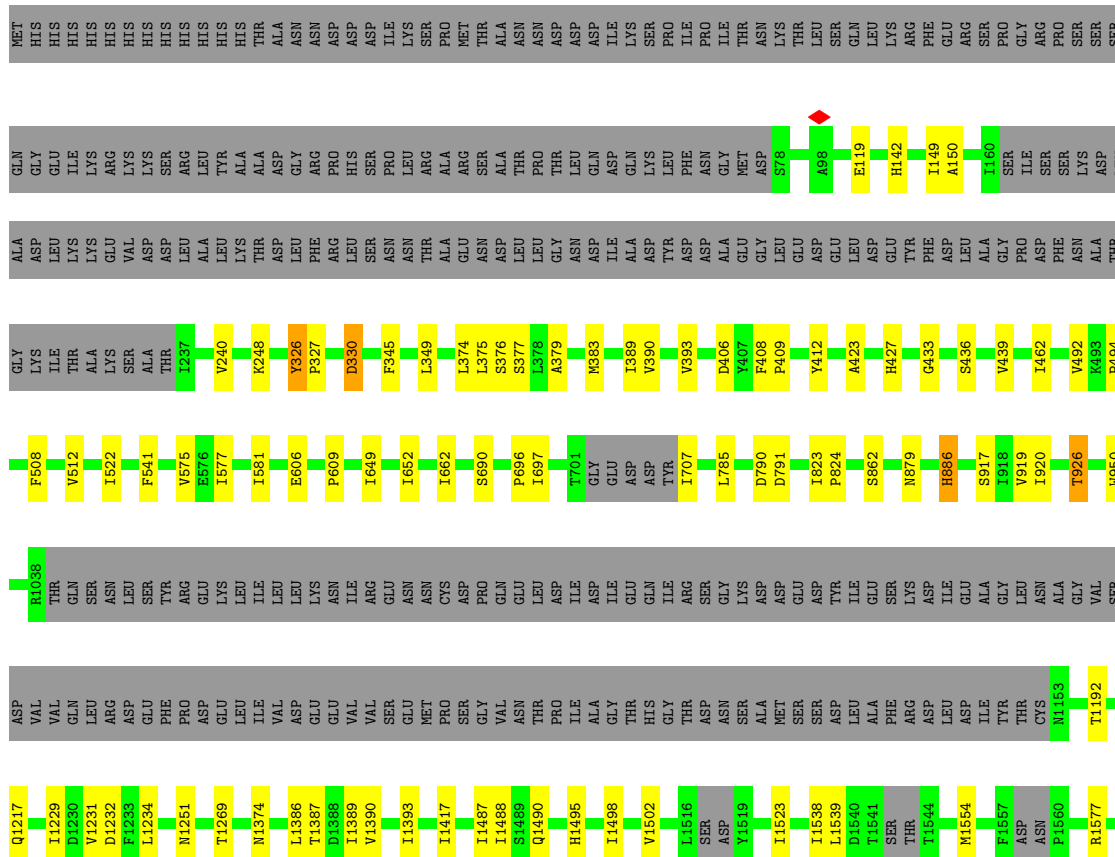
- | | | | | | | | | | | | | | |
|----|----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|
| M1 | V9 | Q10 | A50 | L88 | S91 | I119 | T124 | K125 | V126 | F195 | GLN | ALA | GLN |
|----|----|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-----|

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- | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|
| ASP | ASP | ASP | ASP | ASN | ASN | CYS | ASP | LYS | LYS | ILE | ALA | ARG | HIS | T76 | T77 | T78 | V91 | L116 | A125 | W130 | V151 | A152 | L161 | K182 | T195 | I286 | GLY | |
| MET | GLN | ALA | ILE | ASP | SER | PHE | SER | VAL | LEU | ASN | ARG | LEU | VAL | LYS | GLU | LEU | GLN | TYR | ASN | GLU | LEU | ASP | PHE | VAL | THR | GLY | ALA | SER | GLN | PHE | LEU | ARG | ALA | PRO | SER | LEU | THR | VAL | PRO | PRO | ILE | ALA | SER | PRO | GLN | GLN | THR | THR | HIS | THR |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ASP | ASP | ASP | SER | ARG | ASN | PRO | ASP | CYS | LYS | ILE | ALA | HIS | GLY | T76 | N113 | P114 | T119 | H141 | E145 | A153 | M172 | G173 | T174 | K182 | D191 | I286 | GLY | | | | | | | | | | | | | | | | |
| MET | GLN | ALA | ILE | ASP | SER | PHE | SER | VAL | ASN | ARG | LEU | VAL | GUJ | LEU | GLN | TTR | ASP | ASN | GLJ | ASN | LEU | GLJ | PHE | VAL | THR | GLY | SER | GLN | PHE | ARG | LEU | PRO | SER | VAL | PRO | ILE | ALA | SER | GLN | PHE | ARG | HIS | TTR |

- [illegible]



V1581	R1752	A1958
A1602	GLU	Q1972
L1606	SER	T1983
F1610	ASP	V1995
V1619	ALA	R2009
L1638	A1757	I2013
C1648	S1762	I2017
GLU	P1779	R2033
L1650	D1780	G2066
N1664	V1781	V2075
K1665	V1789	A2093
ASP	H1792	A2103
ASP	P1793	T2106
K1668	Y1794	K2111
M1671	V1797	D2132
I1672	I1817	L2137
M1673	S1818	Y2141
S1674	D1819	Y2142
V1675	M1829	A2143
L1693	ASP	
ASP	PRO	
LYS	ASP	
R1696	GLY	
F1699	L1834	
F1703	I1856	
L1708	V1863	
H1714	P1868	
D1715	F1871	
A1716	I1872	
F1717	K1873	
E1718	T1874	
I1719	D1875	
W1720	Y1876	
L1723	F1877	
A1724	Y1878	
W1725	I1883	
W1726	M1890	
L1727	L1911	
F1740	K1918	
W1745	D1919	
ALA	L1935	
ASP	V1957	
GLY		
W1749		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46626	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.253	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00238	Depositor
Map size (Å)	571.2, 571.2, 571.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.19, 1.19, 1.19	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	1	0.24	0/1786	0.45	0/2408
1	M	0.21	0/1786	0.34	0/2408
2	2	0.22	0/1855	0.35	0/2514
2	N	0.21	0/1855	0.34	0/2514
3	A	0.19	0/1919	0.33	0/2599
3	O	0.19	0/1919	0.31	0/2599
4	B	0.20	0/1944	0.35	0/2632
4	P	0.19	0/1944	0.31	0/2632
5	C	0.15	0/1870	0.43	0/2532
5	D	0.16	0/1864	0.40	0/2524
5	Q	0.16	0/1870	0.43	0/2532
5	R	0.17	0/1864	0.43	0/2524
6	E	0.19	0/1885	0.39	0/2540
6	S	0.19	0/1885	0.39	0/2540
7	F	0.20	0/1831	0.36	0/2473
7	T	0.19	0/1831	0.32	0/2473
8	G	0.20	0/1925	0.37	0/2599
8	U	0.20	0/1925	0.30	0/2599
9	H	0.23	0/1532	0.31	0/2076
9	V	0.22	0/1532	0.30	0/2076
10	I	0.23	0/1701	0.41	0/2307
10	W	0.21	0/1701	0.32	0/2307
11	J	0.23	0/1605	0.37	0/2166
11	X	0.22	0/1605	0.32	0/2166
12	K	0.19	0/1589	0.32	0/2142
12	Y	0.19	0/1589	0.30	0/2142
13	L	0.21	0/1676	0.31	0/2269
13	Z	0.20	0/1676	0.31	0/2269
14	CA	0.16	0/15398	0.34	0/20843
14	DA	0.16	0/15398	0.36	0/20843
All	All	0.19	0/80760	0.36	0/109248

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	D	0	2
6	E	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	D	127	ARG	Sidechain
5	D	197	ARG	Sidechain
6	E	72	ARG	Sidechain

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	1	1748	1701	1700	10	0
1	M	1748	1701	1700	13	0
2	2	1824	1830	1829	14	0
2	N	1824	1830	1829	12	0
3	A	1882	1882	1881	9	0
3	O	1882	1882	1881	3	0
4	B	1907	1919	1917	11	0
4	P	1907	1919	1917	8	0
5	C	1842	1856	1855	7	0
5	D	1836	1851	1850	16	0
5	Q	1842	1856	1855	9	0
5	R	1836	1851	1850	14	0
6	E	1859	1835	1834	9	0
6	S	1859	1835	1834	8	0
7	F	1803	1811	1809	10	0
7	T	1803	1810	1809	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	G	1885	1878	1876	3	0
8	U	1885	1877	1876	4	0
9	H	1503	1468	1467	7	0
9	V	1503	1468	1467	6	0
10	I	1670	1678	1676	10	0
10	W	1670	1678	1676	6	0
11	J	1575	1567	1566	6	0
11	X	1575	1567	1566	6	0
12	K	1561	1569	1569	6	0
12	Y	1561	1569	1569	2	0
13	L	1639	1590	1589	7	0
13	Z	1639	1590	1589	5	0
14	CA	15065	15133	15118	70	0
14	DA	15065	15133	15118	93	0
All	All	79198	79134	79072	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 2.

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)
14:DA:1957:VAL:HG12	14:DA:1958:ALA:N	1.96	0.78
1:1:49:ILE:HD12	10:I:196:LEU:HD11	1.65	0.77
5:R:110:THR:HG22	5:R:135:ILE:HD12	1.73	0.69
1:1:47:ARG:HD3	1:1:49:ILE:HD11	1.75	0.68
14:DA:1957:VAL:CG1	14:DA:1958:ALA:N	2.58	0.66
6:S:163:THR:HG21	14:DA:2141:TYR:HA	1.79	0.64
14:CA:1915:VAL:HG21	14:CA:1966:LEU:CD2	2.27	0.64
5:R:110:THR:HG21	5:R:148:TYR:HB2	1.80	0.62
1:M:166:MET:HE3	1:M:166:MET:HA	1.82	0.61
2:2:49:TYR:CE2	2:2:203:VAL:HG22	2.35	0.61
6:S:20:ARG:HD3	14:DA:2137:LEU:HD22	1.83	0.61
5:R:177:LYS:NZ	14:DA:1794:TYR:HA	2.15	0.61
7:T:155:GLU:C	7:T:156:LEU:HD12	2.26	0.60
7:T:37:GLY:C	7:T:38:LEU:HD12	2.27	0.59
9:V:20:THR:HG23	9:V:52:LYS:HZ2	1.68	0.59
14:DA:436:SER:HA	14:DA:462:ILE:HD12	1.84	0.59
2:N:49:TYR:CE2	2:N:203:VAL:HG22	2.38	0.58
2:2:192:VAL:HG13	2:2:192:VAL:O	2.03	0.58
5:R:42:VAL:HG11	5:R:136:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:CA:1488:ILE:HG23	14:CA:1610:PHE:CE1	2.39	0.57
9:H:32:ILE:HD13	9:H:196:VAL:HG13	1.86	0.57
5:Q:110:THR:HG21	5:Q:148:TYR:HB2	1.86	0.56
1:M:168:PHE:HA	11:X:149:MET:HE1	1.88	0.56
7:F:144:LEU:C	7:F:145:LEU:HD12	2.31	0.56
14:CA:1446:LEU:HG	14:CA:1464:ILE:HG23	1.87	0.55
14:DA:649:ILE:HG21	14:DA:690:SER:HB3	1.89	0.55
1:M:49:ILE:HD12	10:W:196:LEU:HD11	1.88	0.55
14:DA:1619:VAL:HG13	14:DA:1673:MET:SD	2.47	0.55
14:DA:1789:VAL:O	14:DA:1789:VAL:HG13	2.05	0.55
14:CA:1781:VAL:HG22	14:CA:1781:VAL:O	2.06	0.55
5:R:110:THR:HG21	5:R:148:TYR:CB	2.36	0.55
14:DA:1675:VAL:HG11	14:DA:1719:ILE:HG22	1.89	0.55
7:F:74:LEU:HD22	7:F:81:ALA:HB1	1.89	0.55
14:CA:649:ILE:CD1	14:CA:662:ILE:HD12	2.37	0.55
6:S:46:VAL:HG11	6:S:145:ALA:HB1	1.90	0.54
9:H:32:ILE:HD12	9:H:196:VAL:HG22	1.89	0.54
2:2:96:ILE:HD13	2:2:147:ILE:HD11	1.89	0.54
14:DA:508:PHE:O	14:DA:512:VAL:HG23	2.07	0.54
2:N:192:VAL:O	2:N:192:VAL:HG13	2.07	0.54
6:E:209:GLU:HB3	14:CA:1918:LYS:HD2	1.90	0.54
3:A:129:THR:HG22	3:A:129:THR:O	2.08	0.54
5:D:34:VAL:HG12	5:D:199:LEU:HD21	1.89	0.54
7:F:155:GLU:C	7:F:156:LEU:HD12	2.33	0.54
14:CA:1781:VAL:HG22	14:CA:1784:LEU:HB3	1.89	0.53
14:DA:2017:ILE:HD12	14:DA:2017:ILE:H	1.72	0.53
5:D:42:VAL:HG11	5:D:136:ALA:HB1	1.90	0.53
14:DA:1856:ILE:HD11	14:DA:1883:ILE:HG13	1.89	0.53
7:T:74:LEU:HD22	7:T:81:ALA:HB1	1.91	0.53
13:L:125:ALA:HB2	1:M:147:VAL:HG23	1.90	0.52
11:X:11:ILE:CG2	11:X:146:LEU:HD11	2.39	0.52
14:CA:879:ASN:OD1	14:CA:919:VAL:HG22	2.10	0.52
2:N:53:VAL:HG21	2:N:150:ALA:HB1	1.92	0.52
1:I:112:ILE:HG21	1:I:144:PHE:CE2	2.44	0.52
4:P:74:VAL:HG22	4:P:75:TYR:H	1.75	0.52
14:CA:492:VAL:HG11	14:CA:541:PHE:HA	1.91	0.52
14:DA:1872:ILE:HD12	14:DA:1872:ILE:H	1.73	0.52
14:DA:1972:GLN:HB2	14:DA:2013:ILE:HD12	1.91	0.52
5:R:106:VAL:O	5:R:110:THR:HG23	2.09	0.52
7:T:144:LEU:C	7:T:145:LEU:HD12	2.35	0.52
14:CA:910:PRO:HA	14:CA:913:ASP:HB2	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:41:THR:O	9:H:41:THR:HG23	2.10	0.51
9:H:32:ILE:CD1	9:H:196:VAL:HG13	2.40	0.51
6:E:210:GLU:OE1	14:CA:1919:ASP:CB	2.59	0.51
3:A:204:GLU:O	3:A:208:THR:HG23	2.11	0.51
3:O:129:THR:HG22	3:O:129:THR:O	2.11	0.51
14:DA:149:ILE:CG1	14:DA:1417:ILE:HD11	2.40	0.51
5:D:106:VAL:O	5:D:110:THR:HG23	2.11	0.51
6:E:210:GLU:HA	14:CA:1919:ASP:HB3	1.92	0.50
14:CA:1692:ASP:HB2	14:CA:1696:ARG:HB3	1.94	0.50
12:K:50:ALA:HB1	13:L:195:THR:HG22	1.92	0.50
13:L:116:LEU:HD11	13:L:151:VAL:HG23	1.92	0.50
14:CA:1575:TRP:O	14:CA:1820:PRO:HD3	2.11	0.50
2:N:42:THR:HG23	2:N:43:SER:N	2.26	0.50
9:V:32:ILE:HD12	9:V:196:VAL:HG22	1.94	0.50
14:CA:2017:ILE:HD12	14:CA:2017:ILE:H	1.76	0.50
14:CA:1450:LEU:HA	14:CA:1456:MET:HE1	1.94	0.50
1:M:47:ARG:HD3	1:M:49:ILE:HD11	1.93	0.50
5:C:25:GLU:CD	5:C:25:GLU:C	2.80	0.50
5:C:110:THR:HG21	5:C:148:TYR:CB	2.41	0.50
5:D:59:ILE:HG22	5:D:59:ILE:O	2.12	0.50
13:L:78:THR:HG22	13:L:91:VAL:HG12	1.94	0.49
13:L:130:TRP:CZ3	13:L:161:LEU:HD11	2.47	0.49
4:P:122:THR:HG22	4:P:123:GLN:N	2.27	0.49
14:CA:1453:GLU:O	14:CA:1456:MET:HE2	2.12	0.49
14:CA:1499:ILE:HD13	14:CA:1617:ASN:CB	2.42	0.49
14:DA:150:ALA:HB1	14:DA:240:VAL:HG22	1.94	0.49
4:P:14:PRO:HA	5:Q:22:TYR:HE1	1.76	0.49
3:A:51:THR:OG1	3:A:228:ALA:HB3	2.13	0.49
8:G:49:VAL:HG21	8:G:65:LYS:HD2	1.94	0.49
14:CA:1591:LEU:CD1	14:CA:1599:LEU:HD12	2.43	0.49
14:DA:1863:VAL:HG21	14:DA:1876:TYR:CE2	2.47	0.49
2:2:146:ALA:HB3	2:2:177:THR:CG2	2.43	0.49
6:E:204:LEU:O	6:E:208:MET:HG3	2.13	0.49
14:CA:1764:ILE:HD11	14:CA:1804:LEU:HD22	1.93	0.49
14:DA:375:LEU:O	14:DA:376:SER:CB	2.60	0.49
5:D:196:VAL:HG22	5:D:212:ILE:CD1	2.43	0.49
14:DA:1538:ILE:C	14:DA:1539:LEU:HD12	2.38	0.49
4:B:74:VAL:HG22	4:B:75:TYR:H	1.78	0.49
12:K:9:VAL:HG12	12:K:10:GLN:N	2.27	0.49
5:R:17:ILE:HD12	5:R:17:ILE:H	1.78	0.49
14:CA:1972:GLN:HB2	14:CA:2013:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:DA:1873:LYS:HA	14:DA:1878:TYR:OH	2.13	0.49
8:U:123:THR:HG22	8:U:123:THR:O	2.13	0.49
11:J:63:LEU:CD2	11:J:105:VAL:HG21	2.43	0.48
14:CA:623:LEU:HD22	14:CA:645:PHE:CD1	2.49	0.48
14:CA:829:VAL:HG21	14:CA:881:VAL:HG13	1.95	0.48
14:CA:1792:HIS:CD2	14:CA:1797:VAL:HG11	2.48	0.48
1:1:143:SER:HB3	1:1:156:ARG:HG2	1.94	0.48
3:A:228:ALA:HB2	3:A:233:PHE:HD1	1.79	0.48
5:D:33:ALA:O	5:D:163:THR:HG23	2.13	0.48
2:2:146:ALA:HB3	2:2:177:THR:HG23	1.96	0.48
14:CA:1708:LEU:HD23	14:CA:1712:LEU:HD13	1.96	0.48
1:M:239:LYS:O	1:M:240:ARG:HG2	2.13	0.48
14:CA:150:ALA:HB1	14:CA:240:VAL:HG22	1.95	0.48
6:S:18:GLU:OE2	14:DA:2111:LYS:HB3	2.13	0.48
7:T:179:PHE:CD1	7:T:179:PHE:C	2.91	0.48
14:DA:649:ILE:HG21	14:DA:690:SER:CB	2.44	0.48
14:CA:1491:ILE:HD13	14:CA:1614:VAL:HG22	1.96	0.47
14:DA:2066:GLY:HA2	14:DA:2106:THR:HG21	1.96	0.47
2:2:39:VAL:HG13	2:2:62:SER:O	2.14	0.47
14:DA:1498:ILE:O	14:DA:1502:VAL:HG23	2.13	0.47
1:M:76:PHE:CZ	1:M:78:ALA:HB3	2.50	0.47
2:2:263:THR:HG23	2:2:263:THR:O	2.15	0.47
7:F:176:LEU:HD23	7:F:176:LEU:C	2.39	0.47
14:CA:1724:ALA:HB1	14:CA:1770:ILE:HG13	1.96	0.47
14:CA:1789:VAL:O	14:CA:1789:VAL:HG13	2.14	0.47
14:CA:1915:VAL:HG21	14:CA:1966:LEU:HD22	1.96	0.47
7:F:72:LEU:HA	7:F:133:LEU:O	2.15	0.47
12:K:50:ALA:HB1	13:L:195:THR:CG2	2.44	0.47
13:Z:119:THR:O	13:Z:174:THR:HA	2.15	0.47
14:DA:512:VAL:HG22	14:DA:577:ILE:HG12	1.97	0.47
14:DA:1539:LEU:HD13	14:DA:1581:VAL:HG22	1.96	0.47
11:X:149:MET:HG2	11:X:170:ALA:HA	1.96	0.47
4:B:174:PHE:HD2	4:B:195:THR:HG1	1.63	0.47
3:O:87:ILE:N	3:O:88:PRO:HD2	2.29	0.47
14:CA:1538:ILE:C	14:CA:1539:LEU:HD12	2.40	0.47
14:DA:1792:HIS:CD2	14:DA:1797:VAL:HG11	2.49	0.47
10:W:239:THR:HG21	11:X:168:SER:OG	2.16	0.46
12:Y:9:VAL:HG12	12:Y:10:GLN:N	2.30	0.46
14:CA:492:VAL:HG12	14:CA:492:VAL:O	2.15	0.46
14:DA:1817:ILE:HD12	14:DA:1817:ILE:N	2.31	0.46
1:1:239:LYS:O	1:1:240:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:243:GLU:O	3:A:246:VAL:HG22	2.16	0.46
14:DA:492:VAL:HG12	14:DA:492:VAL:O	2.16	0.46
14:DA:1602:ALA:O	14:DA:1606:LEU:HD13	2.16	0.46
2:2:159:PHE:CZ	2:2:161:ARG:HG3	2.51	0.46
12:K:88:LEU:O	12:K:91:SER:HB3	2.16	0.46
14:CA:1539:LEU:HD13	14:CA:1581:VAL:HG22	1.98	0.46
14:DA:1725:TRP:CD1	14:DA:1725:TRP:C	2.94	0.46
14:CA:2079:PRO:HD2	14:CA:2082:ILE:HD12	1.98	0.46
14:DA:1957:VAL:CG1	14:DA:1958:ALA:H	2.29	0.46
8:U:178:LEU:HD11	8:U:194:GLN:HB3	1.98	0.46
14:CA:1723:LEU:HG	14:CA:1727:LEU:HD12	1.97	0.46
14:CA:2007:ARG:HE	14:CA:2059:HIS:CD2	2.34	0.46
5:Q:135:ILE:O	5:Q:147:LEU:HD12	2.17	0.45
13:Z:141:HIS:CE1	13:Z:145:GLU:HG3	2.51	0.45
14:DA:423:ALA:O	14:DA:427:HIS:CD2	2.69	0.45
14:DA:492:VAL:HG11	14:DA:541:PHE:HA	1.98	0.45
6:S:159:GLU:CG	6:S:160:PRO:HD2	2.46	0.45
11:X:141:THR:O	11:X:142:ALA:HB3	2.15	0.45
14:CA:1690:VAL:HG12	14:CA:1690:VAL:O	2.16	0.45
14:DA:652:ILE:CG2	14:DA:662:ILE:HD11	2.46	0.45
14:DA:1393:ILE:HG23	14:DA:1393:ILE:O	2.16	0.45
5:D:121:THR:HG22	5:D:128:PRO:HB3	1.99	0.45
14:DA:575:VAL:HG21	14:DA:609:PRO:HG3	1.97	0.45
9:H:33:LEU:O	9:H:194:MET:HA	2.17	0.45
9:V:41:THR:HG23	9:V:41:THR:O	2.15	0.45
14:DA:1699:PHE:O	14:DA:1703:PHE:N	2.48	0.45
1:1:112:ILE:CD1	1:1:130:ILE:HG21	2.47	0.45
4:B:160:LYS:HD3	4:B:179:TRP:CH2	2.51	0.45
5:D:101:GLU:HG2	13:L:152:ALA:HB1	1.98	0.45
10:I:192:ILE:HG23	10:I:199:GLY:HA2	1.97	0.45
2:N:113:LEU:O	2:N:117:GLU:O	2.34	0.45
1:1:168:PHE:HA	11:J:149:MET:HE1	1.98	0.45
13:Z:113:ASN:HB2	13:Z:114:PRO:CD	2.47	0.45
14:DA:389:ILE:O	14:DA:393:VAL:HG22	2.17	0.45
14:DA:1863:VAL:HG11	14:DA:1876:TYR:CD2	2.52	0.45
14:DA:2075:VAL:O	14:DA:2075:VAL:HG13	2.16	0.45
2:2:160:LEU:HG	2:2:175:LEU:HD12	1.99	0.45
10:I:226:GLU:HA	10:I:226:GLU:OE1	2.17	0.45
4:P:75:TYR:HB3	4:P:82:TYR:CD1	2.51	0.45
4:P:48:GLU:O	4:P:63:LYS:HE2	2.16	0.45
14:CA:619:ILE:HD13	14:CA:648:VAL:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:V:20:THR:HG23	9:V:52:LYS:NZ	2.31	0.45
14:DA:879:ASN:OD1	14:DA:919:VAL:HG22	2.17	0.45
2:N:96:ILE:HD13	2:N:147:ILE:HD11	1.99	0.44
14:CA:1673:MET:CE	14:CA:1677:ILE:HD11	2.47	0.44
14:DA:326:TYR:CG	14:DA:327:PRO:HD2	2.52	0.44
5:D:27:VAL:HG21	5:D:152:PRO:CG	2.47	0.44
6:E:210:GLU:OE1	14:CA:1919:ASP:HB3	2.16	0.44
14:DA:1664:ASN:O	14:DA:1671:MET:HG2	2.17	0.44
14:DA:1780:ASP:O	14:DA:1781:VAL:HG12	2.17	0.44
2:N:58:ASP:HA	2:N:228:PHE:HA	1.98	0.44
3:A:59:VAL:HG13	3:A:59:VAL:O	2.18	0.44
7:T:74:LEU:CD2	7:T:81:ALA:HB1	2.47	0.44
12:Y:130:TYR:HB2	12:Y:144:LEU:HD13	2.00	0.44
14:CA:442:LYS:HB2	14:CA:452:VAL:HG11	1.98	0.44
14:DA:790:ASP:OD1	14:DA:791:ASP:N	2.51	0.44
14:DA:2009:ARG:O	14:DA:2013:ILE:HG12	2.17	0.44
1:1:76:PHE:CZ	1:1:78:ALA:HB3	2.53	0.44
11:J:51:LEU:HD11	11:J:107:PRO:HB3	2.00	0.44
14:DA:1229:ILE:HD12	14:DA:1229:ILE:H	1.82	0.44
1:1:54:ILE:HD11	10:I:196:LEU:HD21	1.99	0.44
4:B:74:VAL:HG22	4:B:75:TYR:N	2.33	0.44
5:D:44:LEU:HD21	5:D:74:SER:HB2	2.00	0.44
5:R:204:GLN:CD	14:DA:1714:HIS:ND1	2.76	0.44
5:R:204:GLN:NE2	14:DA:1714:HIS:ND1	2.65	0.44
6:S:20:ARG:HA	14:DA:2142:TYR:OH	2.18	0.44
14:CA:1499:ILE:HD13	14:CA:1617:ASN:HB2	1.99	0.44
14:CA:1565:ASP:OD1	14:CA:1731:VAL:HG23	2.18	0.44
1:M:112:ILE:HG21	1:M:144:PHE:CE2	2.52	0.44
5:R:203:VAL:HG11	5:R:210:ILE:HG13	2.00	0.44
14:CA:100:HIS:CE1	14:CA:104:ILE:HG21	2.53	0.44
1:1:54:ILE:CD1	10:I:196:LEU:HD21	2.48	0.44
10:I:64:HIS:HB2	10:I:85:THR:HG21	2.00	0.44
11:J:56:LEU:HG	11:J:58:THR:HG22	1.98	0.44
14:DA:374:LEU:HD23	14:DA:390:VAL:HG22	2.00	0.44
14:DA:1708:LEU:HD21	14:DA:1720:TRP:CD2	2.52	0.44
5:D:196:VAL:HG22	5:D:212:ILE:HD13	1.99	0.44
2:N:163:VAL:HG22	2:N:164:ASN:N	2.33	0.44
14:CA:408:PHE:HB3	14:CA:412:TYR:CZ	2.53	0.44
5:C:110:THR:HG21	5:C:148:TYR:HB2	1.99	0.43
14:CA:383:MET:HE2	14:CA:424:ILE:HD12	1.99	0.43
14:CA:473:ASN:O	14:CA:476:GLN:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:R:100:LEU:HD22	13:Z:153:ALA:HB1	1.99	0.43
14:CA:436:SER:HA	14:CA:462:ILE:HD12	1.98	0.43
14:DA:1911:LEU:HD12	14:DA:1935:LEU:HD11	1.99	0.43
2:2:42:THR:HG23	2:2:43:SER:N	2.33	0.43
8:G:119:VAL:HG21	8:G:150:LEU:HD21	2.00	0.43
1:M:49:ILE:HD11	1:M:54:ILE:HD13	2.00	0.43
2:N:124:TYR:CD1	2:N:124:TYR:N	2.85	0.43
14:DA:1995:VAL:HG11	14:DA:2033:ARG:CZ	2.49	0.43
2:N:239:LEU:HD23	2:N:240:THR:N	2.34	0.43
14:DA:886:HIS:HA	14:DA:926:THR:HB	2.00	0.43
9:V:212:TYR:CD1	9:V:212:TYR:C	2.97	0.43
10:W:177:LYS:HE3	10:W:206:VAL:HG11	2.01	0.43
14:DA:1554:MET:SD	14:DA:1779:PRO:HA	2.59	0.43
4:B:14:PRO:HA	5:C:22:TYR:HE1	1.84	0.43
8:G:21:PHE:HA	8:G:24:GLU:OE1	2.19	0.43
4:B:122:THR:HG22	4:B:123:GLN:N	2.33	0.43
4:B:196:LEU:O	4:B:200:VAL:HG13	2.19	0.43
5:C:162:GLN:HA	5:C:162:GLN:OE1	2.18	0.43
7:F:78:ALA:N	7:F:79:PRO:HD2	2.33	0.43
1:M:124:TYR:HB3	1:M:126:VAL:HG22	2.01	0.43
14:CA:522:ILE:HD13	14:CA:581:ILE:HG23	1.99	0.43
14:CA:1487:ILE:HG22	14:CA:1502:VAL:HG13	2.01	0.43
14:DA:408:PHE:HB3	14:DA:412:TYR:CZ	2.53	0.43
14:CA:621:ILE:HD11	14:CA:724:ILE:HG22	2.01	0.42
3:A:79:ILE:HA	3:A:145:SER:OG	2.19	0.42
5:Q:205:THR:HG22	14:DA:1374:ASN:O	2.18	0.42
5:R:216:LYS:HG3	5:R:217:PRO:HD2	2.01	0.42
14:CA:532:LYS:HB3	14:CA:533:PRO:HD3	2.02	0.42
14:CA:1905:ASP:HB2	14:CA:1906:TYR:CD2	2.54	0.42
14:DA:433:GLY:HA3	14:DA:494:PRO:HD3	2.00	0.42
14:DA:1234:LEU:HD23	14:DA:1251:ASN:HA	2.01	0.42
11:X:88:THR:HG23	11:X:124:PHE:CZ	2.54	0.42
14:CA:1696:ARG:HD2	14:CA:1696:ARG:O	2.19	0.42
14:DA:917:SER:O	14:DA:920:ILE:HG22	2.19	0.42
14:DA:1386:LEU:HA	14:DA:1389:ILE:HG22	2.00	0.42
4:P:13:SER:HB2	4:P:14:PRO:HD2	2.02	0.42
14:DA:1523:ILE:N	14:DA:1523:ILE:HD12	2.35	0.42
7:T:206:LEU:O	7:T:234:ILE:HD13	2.19	0.42
14:CA:1696:ARG:O	14:CA:1700:ILE:HB	2.20	0.42
14:CA:1815:PRO:HB2	14:CA:1817:ILE:CD1	2.49	0.42
14:DA:1863:VAL:HG12	14:DA:1874:THR:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:15:GLY:HA3	6:E:30:ALA:HB2	2.01	0.42
6:E:70:ILE:HG21	6:E:112:LEU:HD21	2.00	0.42
6:S:68:VAL:HG11	6:S:89:ILE:HG21	2.00	0.42
14:CA:1909:PRO:HA	14:CA:1912:ILE:HG22	2.02	0.42
14:DA:696:PRO:HD2	14:DA:950:TRP:HA	2.01	0.42
14:DA:2093:ALA:HA	14:DA:2103:ALA:HB3	2.01	0.42
2:2:162:TYR:CD1	2:2:162:TYR:C	2.98	0.42
7:F:179:PHE:CD1	7:F:179:PHE:C	2.98	0.42
2:2:163:VAL:HG22	2:2:164:ASN:N	2.35	0.42
6:E:232:ASP:OD1	6:E:232:ASP:N	2.52	0.42
14:CA:1285:ILE:HG21	14:CA:1320:LYS:HG2	2.02	0.42
2:N:63:TYR:O	2:N:63:TYR:CG	2.72	0.42
2:N:163:VAL:HA	2:N:168:VAL:O	2.19	0.42
14:CA:652:ILE:CG2	14:CA:662:ILE:HD11	2.50	0.42
14:DA:522:ILE:HD13	14:DA:581:ILE:HG23	2.02	0.42
4:B:21:ILE:HD11	4:B:122:THR:HG21	2.01	0.41
11:J:82:ILE:O	11:J:82:ILE:HG23	2.20	0.41
1:M:47:ARG:HB2	1:M:219:ASP:HB2	2.02	0.41
14:DA:379:ALA:O	14:DA:383:MET:N	2.53	0.41
14:DA:1868:PRO:HA	14:DA:1871:PHE:CD1	2.55	0.41
1:M:49:ILE:HG22	1:M:50:THR:N	2.35	0.41
5:R:171:VAL:CG2	5:R:202:VAL:HG21	2.50	0.41
6:S:17:PRO:HA	7:T:24:TYR:CD1	2.55	0.41
10:W:64:HIS:CB	10:W:85:THR:HG21	2.50	0.41
7:F:14:SER:HB3	7:F:20:PHE:CE2	2.55	0.41
14:CA:605:LEU:HD21	14:CA:615:ILE:HB	2.01	0.41
14:CA:665:VAL:O	14:CA:669:LEU:HG	2.20	0.41
14:DA:377:SER:OG	14:DA:1577:ARG:HD2	2.20	0.41
10:I:239:THR:HG21	11:J:168:SER:OG	2.21	0.41
5:Q:110:THR:HG21	5:Q:148:TYR:CB	2.49	0.41
14:DA:1495:HIS:HB3	14:DA:1498:ILE:HD12	2.02	0.41
3:A:193:HIS:CD2	3:A:193:HIS:C	2.97	0.41
5:D:34:VAL:CG1	5:D:199:LEU:HD21	2.50	0.41
5:D:230:ASN:O	5:D:234:THR:HG23	2.21	0.41
5:Q:34:VAL:HG23	5:Q:175:LEU:HD11	2.01	0.41
14:DA:406:ASP:O	14:DA:409:PRO:HD2	2.20	0.41
14:DA:1487:ILE:O	14:DA:1490:GLN:HB2	2.20	0.41
14:DA:1723:LEU:HG	14:DA:1727:LEU:HD12	2.02	0.41
5:D:161:ALA:HB1	5:D:175:LEU:HD13	2.02	0.41
7:F:154:THR:OG1	7:F:156:LEU:HD11	2.21	0.41
12:K:126:VAL:O	12:K:126:VAL:HG13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:18:PHE:O	5:Q:22:TYR:HD2	2.03	0.41
8:U:213:LEU:HD21	8:U:215:ILE:HD11	2.03	0.41
14:CA:1424:VAL:O	14:CA:1428:LYS:HG2	2.20	0.41
14:DA:1387:THR:HA	14:DA:1390:VAL:HG22	2.02	0.41
2:2:212:ASN:HD21	10:I:169:SER:HB2	1.86	0.41
7:T:72:LEU:C	7:T:72:LEU:HD12	2.45	0.41
14:CA:326:TYR:CG	14:CA:327:PRO:HD2	2.55	0.41
14:CA:1806:THR:HG21	14:CA:1889:GLU:HG2	2.01	0.41
14:DA:1217:GLN:OE1	14:DA:1269:THR:HG21	2.20	0.41
14:DA:374:LEU:CD2	14:DA:390:VAL:HG22	2.51	0.41
14:DA:1740:PHE:CZ	14:DA:1779:PRO:HG3	2.56	0.41
14:DA:1872:ILE:O	14:DA:1873:LYS:HB2	2.20	0.41
4:P:74:VAL:HG22	4:P:75:TYR:N	2.34	0.41
5:Q:51:THR:HG23	5:Q:51:THR:O	2.21	0.41
13:Z:172:MET:O	13:Z:191:ASP:HA	2.21	0.41
14:CA:1231:VAL:HG13	14:CA:1232:ASP:N	2.36	0.41
14:CA:1872:ILE:O	14:CA:1873:LYS:HB2	2.21	0.41
14:CA:1921:CYS:SG	14:CA:1928:PRO:HG2	2.61	0.41
14:DA:330:ASP:OD1	14:DA:330:ASP:N	2.54	0.41
14:DA:697:ILE:HD11	14:DA:785:LEU:HD23	2.03	0.41
14:DA:823:ILE:HB	14:DA:824:PRO:HD3	2.03	0.41
14:DA:1487:ILE:HG22	14:DA:1502:VAL:HG13	2.02	0.41
5:D:110:THR:HG21	5:D:148:TYR:CB	2.50	0.41
3:O:59:VAL:O	3:O:59:VAL:HG13	2.21	0.41
5:Q:212:ILE:HG21	5:Q:224:LEU:HD12	2.02	0.41
14:CA:1673:MET:HE3	14:CA:1677:ILE:HD11	2.03	0.41
14:DA:1192:THR:O	14:DA:1192:THR:HG22	2.20	0.41
14:DA:1488:ILE:CG2	14:DA:1610:PHE:CE2	3.03	0.41
4:B:123:GLN:HG3	5:C:127:ARG:HB3	2.03	0.40
10:I:189:GLN:O	10:I:193:TRP:CD1	2.74	0.40
10:W:64:HIS:HB2	10:W:85:THR:HG21	2.02	0.40
14:CA:1705:ALA:HA	14:CA:1709:ASP:HB2	2.02	0.40
4:B:92:VAL:HG11	4:B:113:GLU:CG	2.52	0.40
6:E:159:GLU:OE1	14:CA:2140:SER:OG	2.36	0.40
9:H:197:LEU:CD2	9:H:202:VAL:HG22	2.52	0.40
9:H:212:TYR:CD1	9:H:212:TYR:C	2.99	0.40
1:M:88:LYS:HA	1:M:91:VAL:HG12	2.02	0.40
5:R:204:GLN:OE1	14:DA:1715:ASP:OD2	2.39	0.40
7:T:74:LEU:HD13	7:T:81:ALA:CB	2.50	0.40
9:V:33:LEU:O	9:V:194:MET:HA	2.20	0.40
10:W:192:ILE:HG23	10:W:199:GLY:HA2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:DA:345:PHE:CE2	14:DA:349:LEU:HD11	2.56	0.40
14:DA:1781:VAL:O	14:DA:1781:VAL:HG22	2.21	0.40
3:A:50:CYS:SG	3:A:51:THR:N	2.94	0.40
4:B:75:TYR:HB3	4:B:82:TYR:CD1	2.56	0.40
5:C:25:GLU:CD	5:C:25:GLU:O	2.65	0.40
12:K:119:ILE:HA	12:K:124:THR:O	2.21	0.40
4:P:115:ALA:HB1	4:P:154:GLY:O	2.20	0.40
2:2:260:GLY:HA3	2:2:264:GLN:HG3	2.02	0.40
7:F:213:ILE:HG22	7:F:214:ALA:N	2.36	0.40
14:DA:439:VAL:HG21	14:DA:462:ILE:HD11	2.03	0.40
14:DA:1231:VAL:HG13	14:DA:1232:ASP:N	2.37	0.40
10:I:137:SER:HB3	10:I:209:ILE:HD11	2.04	0.40
8:U:38:GLY:HA2	8:U:46:VAL:O	2.21	0.40
14:DA:1717:PHE:CD1	14:DA:1762:SER:HB2	2.56	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	1	219/241 (91%)	213 (97%)	6 (3%)	0	100	100
1	M	219/241 (91%)	211 (96%)	8 (4%)	0	100	100
2	2	231/266 (87%)	220 (95%)	11 (5%)	0	100	100
2	N	231/266 (87%)	224 (97%)	7 (3%)	0	100	100
3	A	236/252 (94%)	232 (98%)	4 (2%)	0	100	100
3	O	236/252 (94%)	232 (98%)	4 (2%)	0	100	100
4	B	247/250 (99%)	245 (99%)	2 (1%)	0	100	100
4	P	247/250 (99%)	244 (99%)	3 (1%)	0	100	100
5	C	233/254 (92%)	218 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	D	232/254 (91%)	224 (97%)	8 (3%)	0	100	100
5	Q	233/254 (92%)	222 (95%)	11 (5%)	0	100	100
5	R	232/254 (91%)	221 (95%)	11 (5%)	0	100	100
6	E	239/260 (92%)	231 (97%)	8 (3%)	0	100	100
6	S	239/260 (92%)	234 (98%)	5 (2%)	0	100	100
7	F	232/234 (99%)	230 (99%)	2 (1%)	0	100	100
7	T	232/234 (99%)	228 (98%)	4 (2%)	0	100	100
8	G	240/288 (83%)	233 (97%)	7 (3%)	0	100	100
8	U	240/288 (83%)	230 (96%)	10 (4%)	0	100	100
9	H	193/215 (90%)	189 (98%)	4 (2%)	0	100	100
9	V	193/215 (90%)	190 (98%)	3 (2%)	0	100	100
10	I	218/261 (84%)	213 (98%)	5 (2%)	0	100	100
10	W	218/261 (84%)	214 (98%)	4 (2%)	0	100	100
11	J	201/205 (98%)	194 (96%)	7 (4%)	0	100	100
11	X	201/205 (98%)	195 (97%)	6 (3%)	0	100	100
12	K	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
12	Y	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
13	L	209/287 (73%)	207 (99%)	2 (1%)	0	100	100
13	Z	209/287 (73%)	207 (99%)	2 (1%)	0	100	100
14	CA	1823/2167 (84%)	1773 (97%)	50 (3%)	0	100	100
14	DA	1823/2167 (84%)	1772 (97%)	51 (3%)	0	100	100
All	All	9892/11264 (88%)	9624 (97%)	268 (3%)	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	1	184/201 (92%)	179 (97%)	5 (3%)	39	59
1	M	184/201 (92%)	180 (98%)	4 (2%)	45	63
2	2	199/224 (89%)	198 (100%)	1 (0%)	81	80
2	N	199/224 (89%)	196 (98%)	3 (2%)	57	68
3	A	204/210 (97%)	202 (99%)	2 (1%)	68	74
3	O	204/210 (97%)	203 (100%)	1 (0%)	81	80
4	B	208/209 (100%)	208 (100%)	0	100	100
4	P	208/209 (100%)	207 (100%)	1 (0%)	81	80
5	C	209/226 (92%)	208 (100%)	1 (0%)	81	80
5	D	208/226 (92%)	207 (100%)	1 (0%)	81	80
5	Q	209/226 (92%)	205 (98%)	4 (2%)	50	65
5	R	208/226 (92%)	208 (100%)	0	100	100
6	E	198/215 (92%)	194 (98%)	4 (2%)	48	64
6	S	198/215 (92%)	194 (98%)	4 (2%)	48	64
7	F	193/193 (100%)	191 (99%)	2 (1%)	68	74
7	T	193/193 (100%)	191 (99%)	2 (1%)	68	74
8	G	200/239 (84%)	199 (100%)	1 (0%)	81	80
8	U	200/239 (84%)	200 (100%)	0	100	100
9	H	161/178 (90%)	161 (100%)	0	100	100
9	V	161/178 (90%)	160 (99%)	1 (1%)	78	79
10	I	179/214 (84%)	175 (98%)	4 (2%)	45	63
10	W	179/214 (84%)	177 (99%)	2 (1%)	65	73
11	J	171/173 (99%)	169 (99%)	2 (1%)	63	72
11	X	171/173 (99%)	169 (99%)	2 (1%)	63	72
12	K	173/175 (99%)	173 (100%)	0	100	100
12	Y	173/175 (99%)	172 (99%)	1 (1%)	78	79
13	L	169/235 (72%)	168 (99%)	1 (1%)	78	79
13	Z	169/235 (72%)	168 (99%)	1 (1%)	78	79
14	CA	1707/1986 (86%)	1691 (99%)	16 (1%)	70	75
14	DA	1707/1986 (86%)	1688 (99%)	19 (1%)	65	73
All	All	8726/9808 (89%)	8641 (99%)	85 (1%)	65	74

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	30	THR
1	1	50	THR
1	1	125	TYR
1	1	147	VAL
1	1	228	LYS
2	2	153	GLN
3	A	120	ARG
3	A	163	TYR
5	C	25	GLU
5	D	181	ARG
6	E	9	ASP
6	E	18	GLU
6	E	71	ASP
6	E	232	ASP
7	F	3	ARG
7	F	199	GLN
8	G	184	GLU
10	I	46	ASP
10	I	77	THR
10	I	150	VAL
10	I	161	LEU
11	J	34	LEU
11	J	144	ASP
13	L	182	LYS
1	M	147	VAL
1	M	149	SER
1	M	217	VAL
1	M	228	LYS
2	N	172	SER
2	N	239	LEU
2	N	264	GLN
3	O	163	TYR
4	P	198	GLU
5	Q	28	LYS
5	Q	67	ILE
5	Q	85	LEU
5	Q	156	TYR
6	S	25	GLU
6	S	72	ARG
6	S	122	ARG
6	S	207	VAL
7	T	3	ARG
7	T	199	GLN

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Mol	Chain	Res	Type
9	V	55	ARG
10	W	77	THR
10	W	223	ASN
11	X	132	GLU
11	X	205	ASP
12	Y	172	MET
13	Z	182	LYS
14	CA	119	GLU
14	CA	248	LYS
14	CA	326	TYR
14	CA	328	ASP
14	CA	350	LYS
14	CA	441	ASN
14	CA	732	THR
14	CA	1318	ILE
14	CA	1490	GLN
14	CA	1673	MET
14	CA	1819	ASP
14	CA	1874	THR
14	CA	1890	MET
14	CA	1892	ARG
14	CA	1983	THR
14	CA	2006	VAL
14	DA	119	GLU
14	DA	142	HIS
14	DA	248	LYS
14	DA	326	TYR
14	DA	330	ASP
14	DA	606	GLU
14	DA	707	ILE
14	DA	862	SER
14	DA	886	HIS
14	DA	926	THR
14	DA	1638	LEU
14	DA	1693	LEU
14	DA	1725	TRP
14	DA	1819	ASP
14	DA	1890	MET
14	DA	1918	LYS
14	DA	1919	ASP
14	DA	1983	THR
14	DA	2132	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	127	HIS
1	1	177	ASN
2	2	51	ASN
2	2	95	HIS
2	2	212	ASN
2	2	227	ASN
3	A	84	ASN
3	A	175	GLN
3	A	185	HIS
3	A	193	HIS
3	A	209	HIS
3	A	240	ASN
5	C	117	GLN
5	C	178	ASN
5	C	243	GLN
5	D	19	GLN
5	D	79	ASN
5	D	204	GLN
6	E	91	HIS
6	E	99	HIS
7	F	69	HIS
7	F	93	ASN
7	F	166	GLN
8	G	122	HIS
8	G	169	GLN
8	G	203	HIS
9	H	79	GLN
10	I	64	HIS
10	I	95	HIS
10	I	145	HIS
10	I	223	ASN
11	J	32	GLN
11	J	64	ASN
11	J	173	ASN
12	K	146	HIS
13	L	141	HIS
13	L	218	ASN
13	L	284	ASN
1	M	127	HIS
1	M	177	ASN
2	N	212	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	N	227	ASN
2	N	246	GLN
3	O	175	GLN
3	O	221	ASN
3	O	240	ASN
5	Q	19	GLN
5	Q	40	ASN
5	Q	178	ASN
5	R	96	HIS
5	R	204	GLN
5	R	209	ASN
7	T	110	HIS
8	U	86	HIS
8	U	182	HIS
9	V	79	GLN
10	W	59	ASN
11	X	38	ASN
11	X	64	ASN
12	Y	146	HIS
13	Z	141	HIS
13	Z	251	ASN
13	Z	263	HIS
13	Z	265	ASN
13	Z	284	ASN
14	CA	103	ASN
14	CA	136	GLN
14	CA	241	ASN
14	CA	351	HIS
14	CA	427	HIS
14	CA	440	HIS
14	CA	527	ASN
14	CA	546	HIS
14	CA	588	ASN
14	CA	633	ASN
14	CA	664	ASN
14	CA	1168	GLN
14	CA	1181	HIS
14	CA	1405	GLN
14	CA	1664	ASN
14	CA	1944	HIS
14	DA	88	HIS
14	DA	103	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	DA	241	ASN
14	DA	283	HIS
14	DA	313	HIS
14	DA	399	HIS
14	DA	441	ASN
14	DA	633	ASN
14	DA	741	ASN
14	DA	886	HIS
14	DA	1869	GLN
14	DA	1997	ASN
14	DA	2020	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.

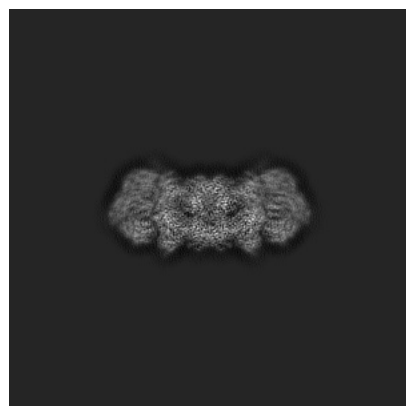
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75436. These allow visual inspection of the internal detail of the map and identification of artifacts.

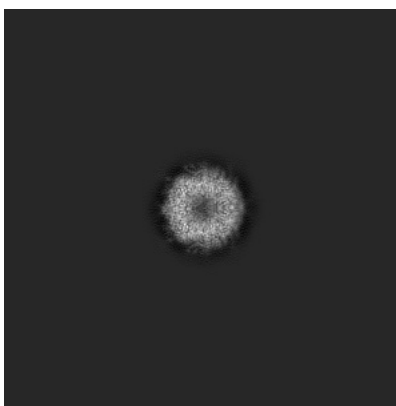
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

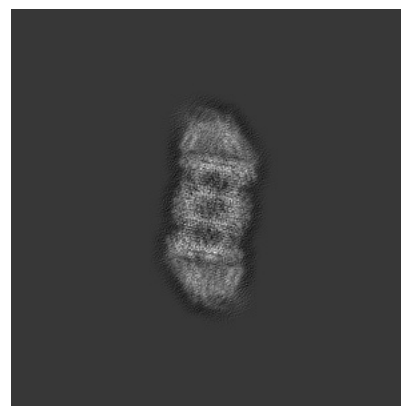
6.1.1 Primary map



X

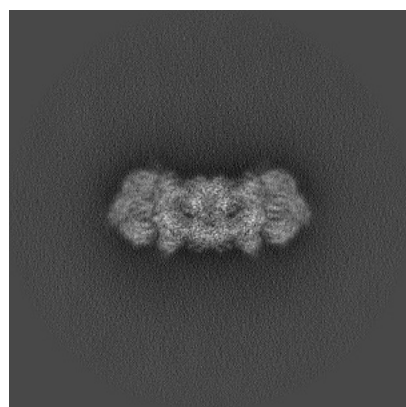


Y

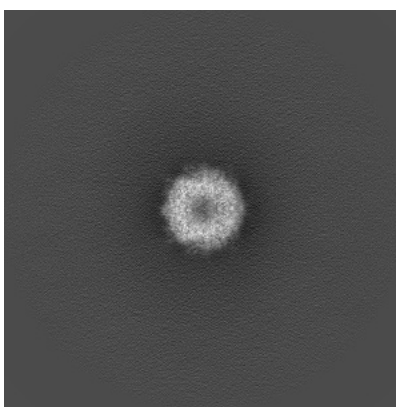


Z

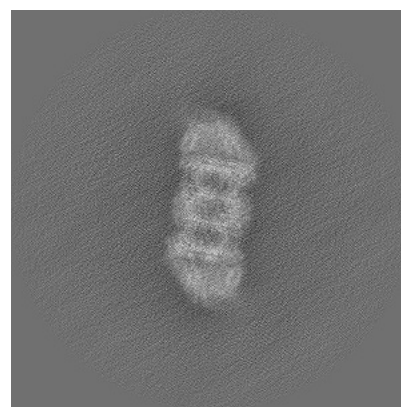
6.1.2 Raw map



X



Y

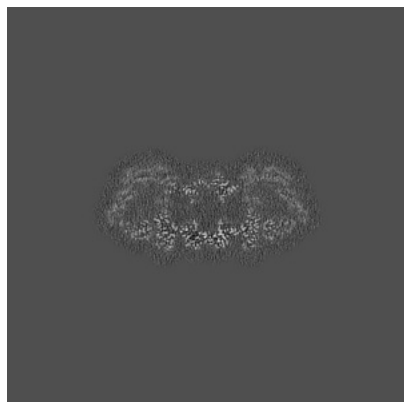


Z

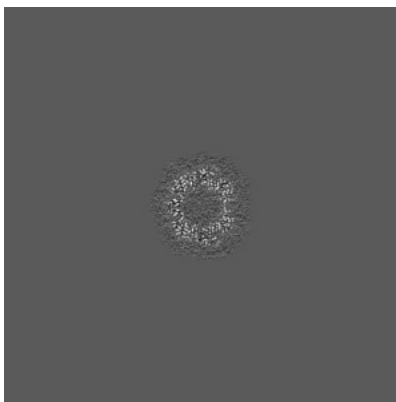
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

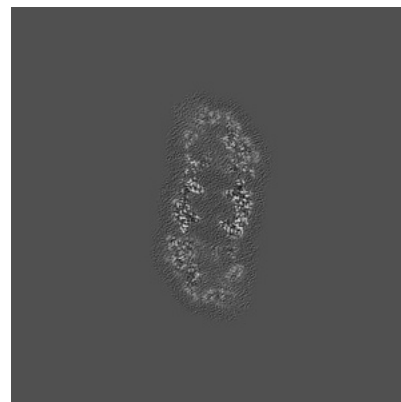
6.2.1 Primary map



X Index: 240

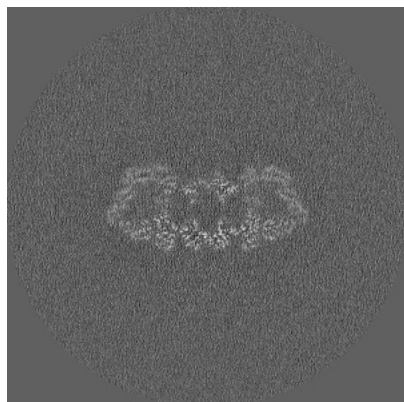


Y Index: 240

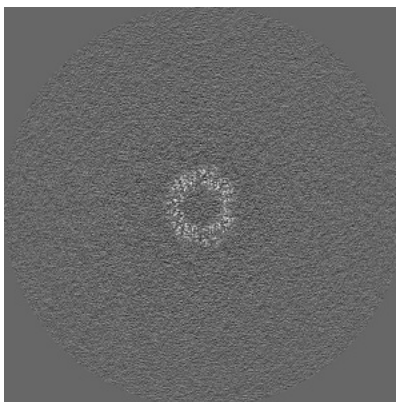


Z Index: 240

6.2.2 Raw map



X Index: 240



Y Index: 240

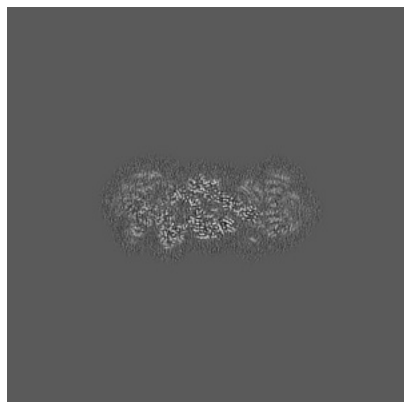


Z Index: 240

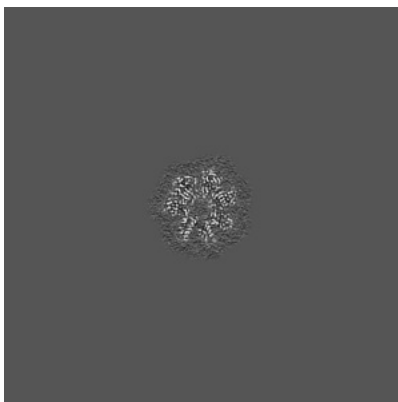
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

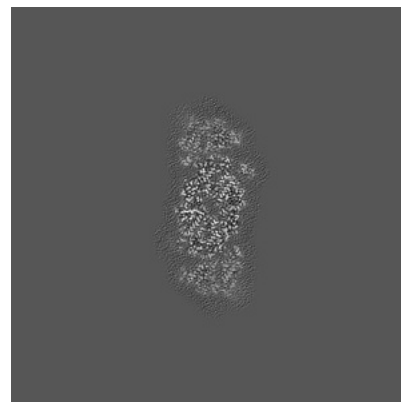
6.3.1 Primary map



X Index: 217

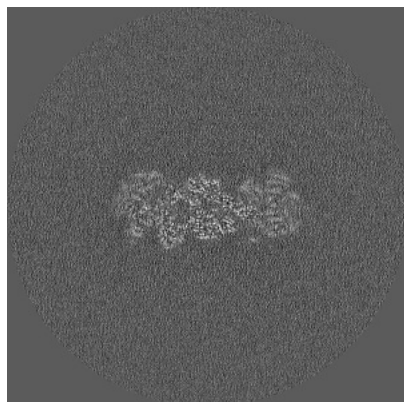


Y Index: 222

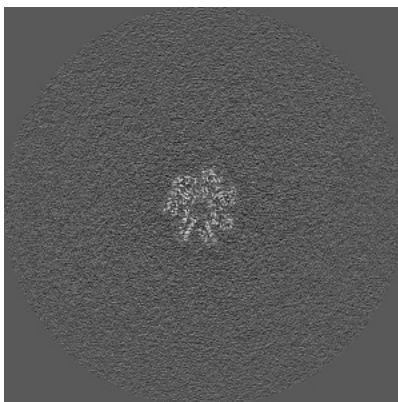


Z Index: 215

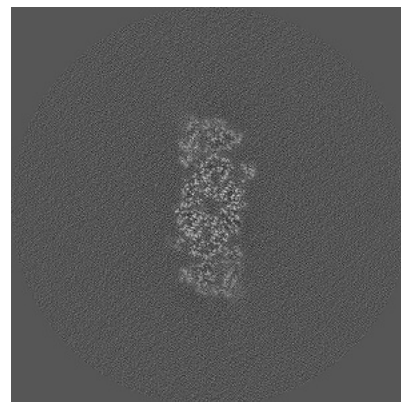
6.3.2 Raw map



X Index: 217



Y Index: 222

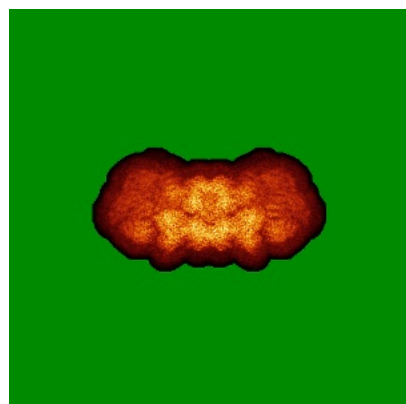


Z Index: 216

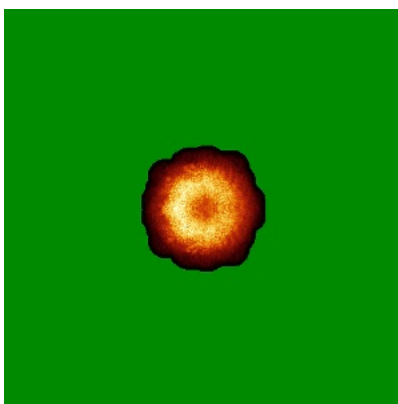
The images above show the largest variance slices of the map in three orthogonal directions.

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

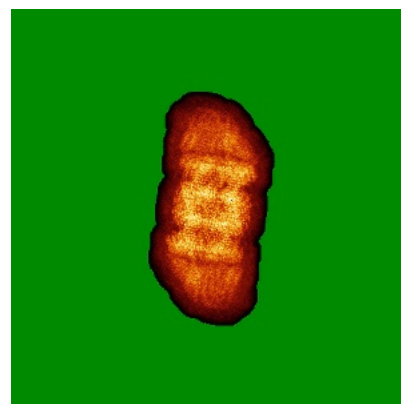
6.4.1 Primary map



X

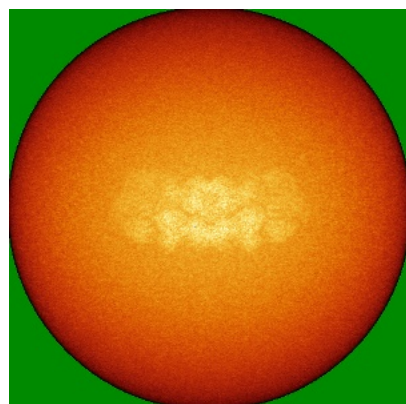


Y

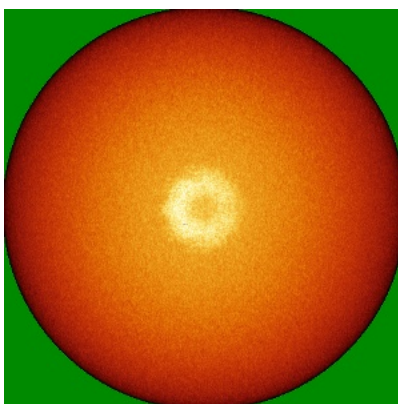


Z

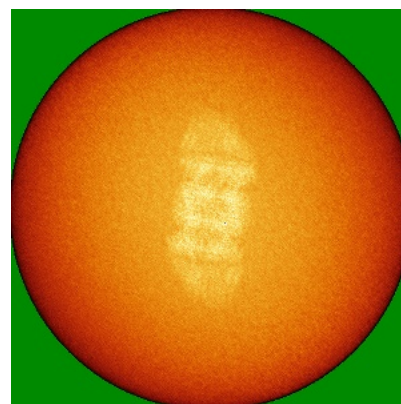
6.4.2 Raw map



X



Y

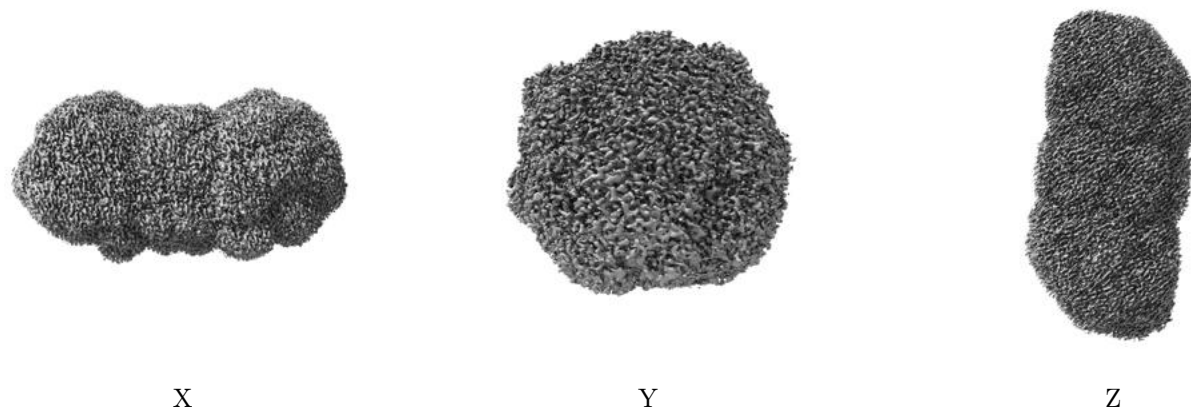


Z

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.

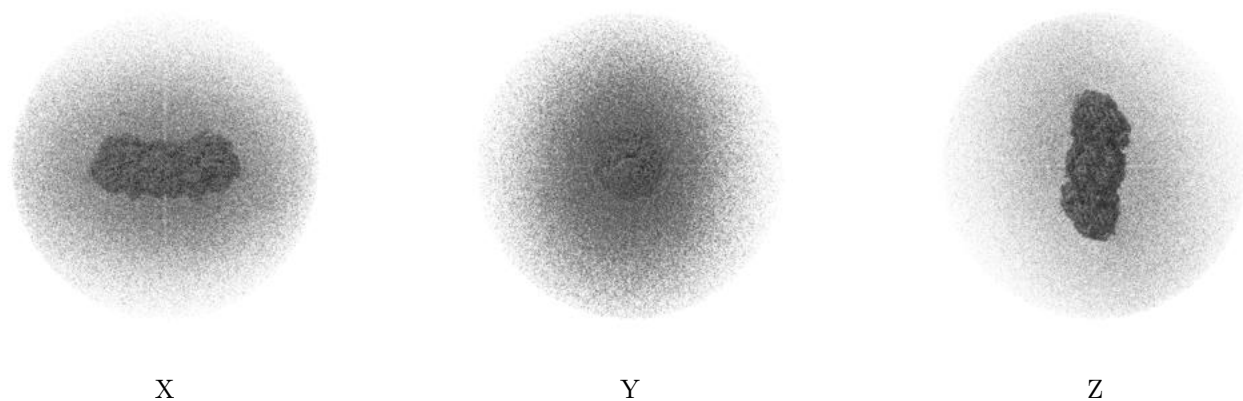
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

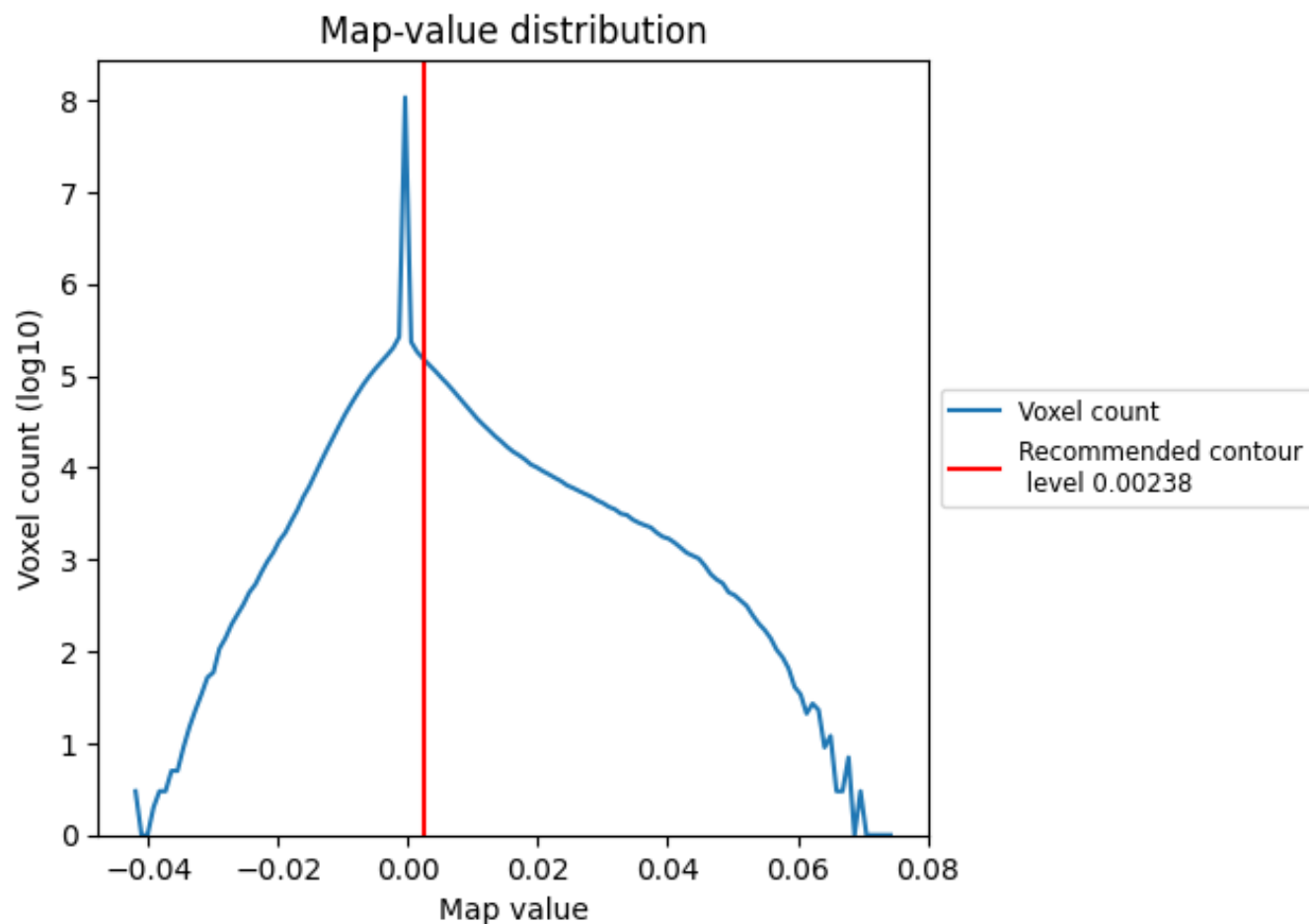
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

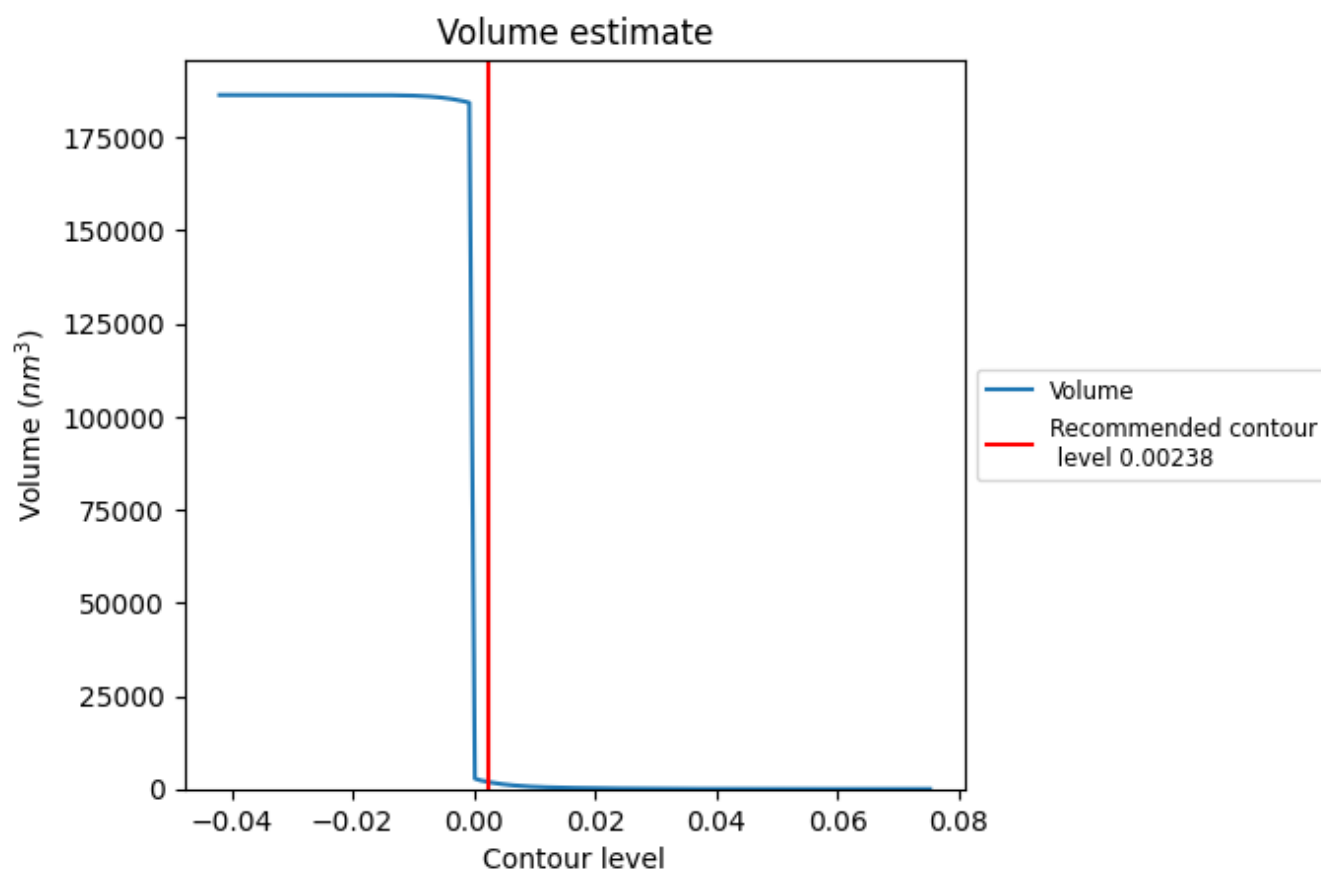
This section contains the results of statistical analysis of the map.

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.

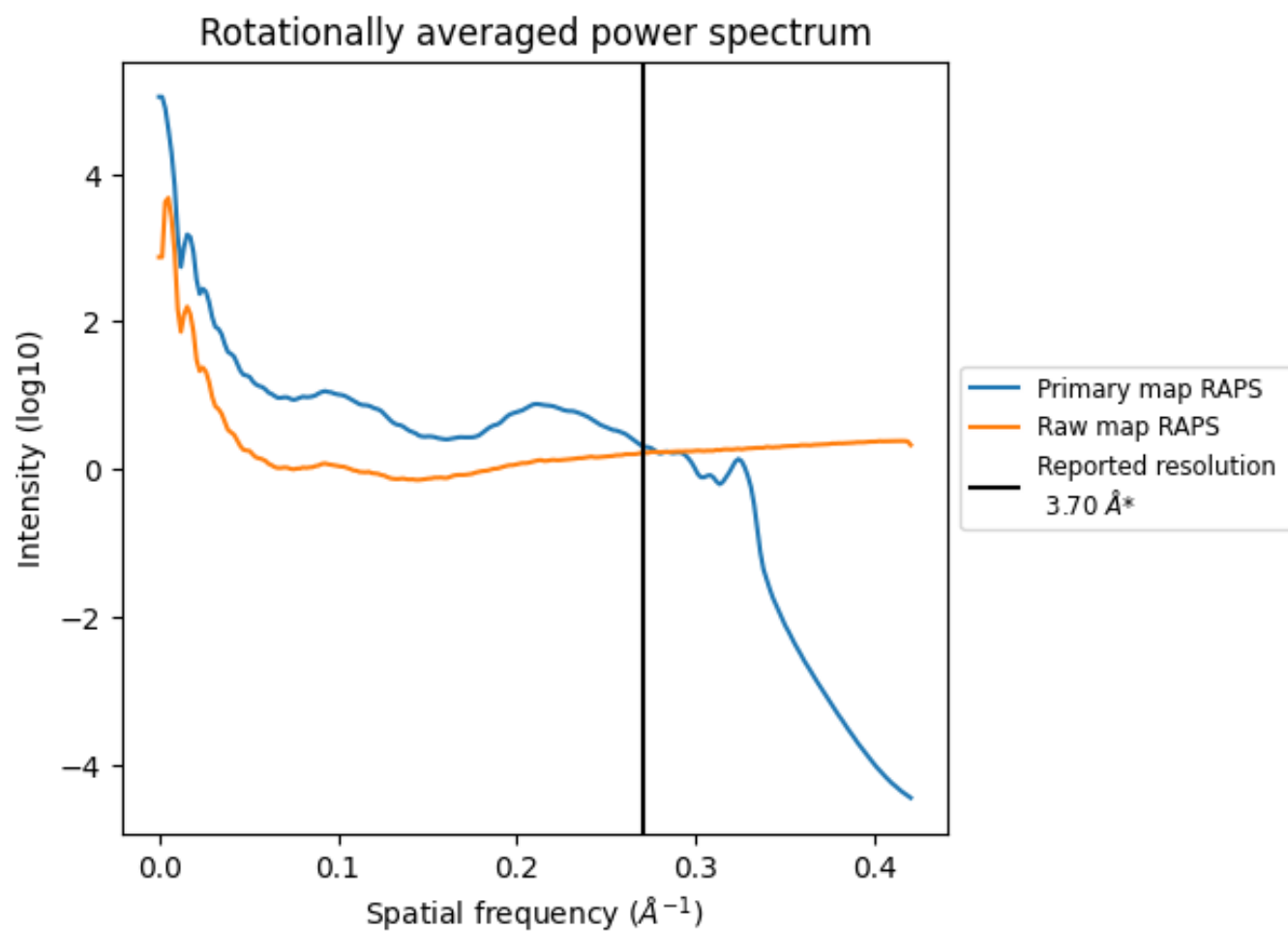
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1866 nm^3 ; this corresponds to an approximate mass of 1686 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

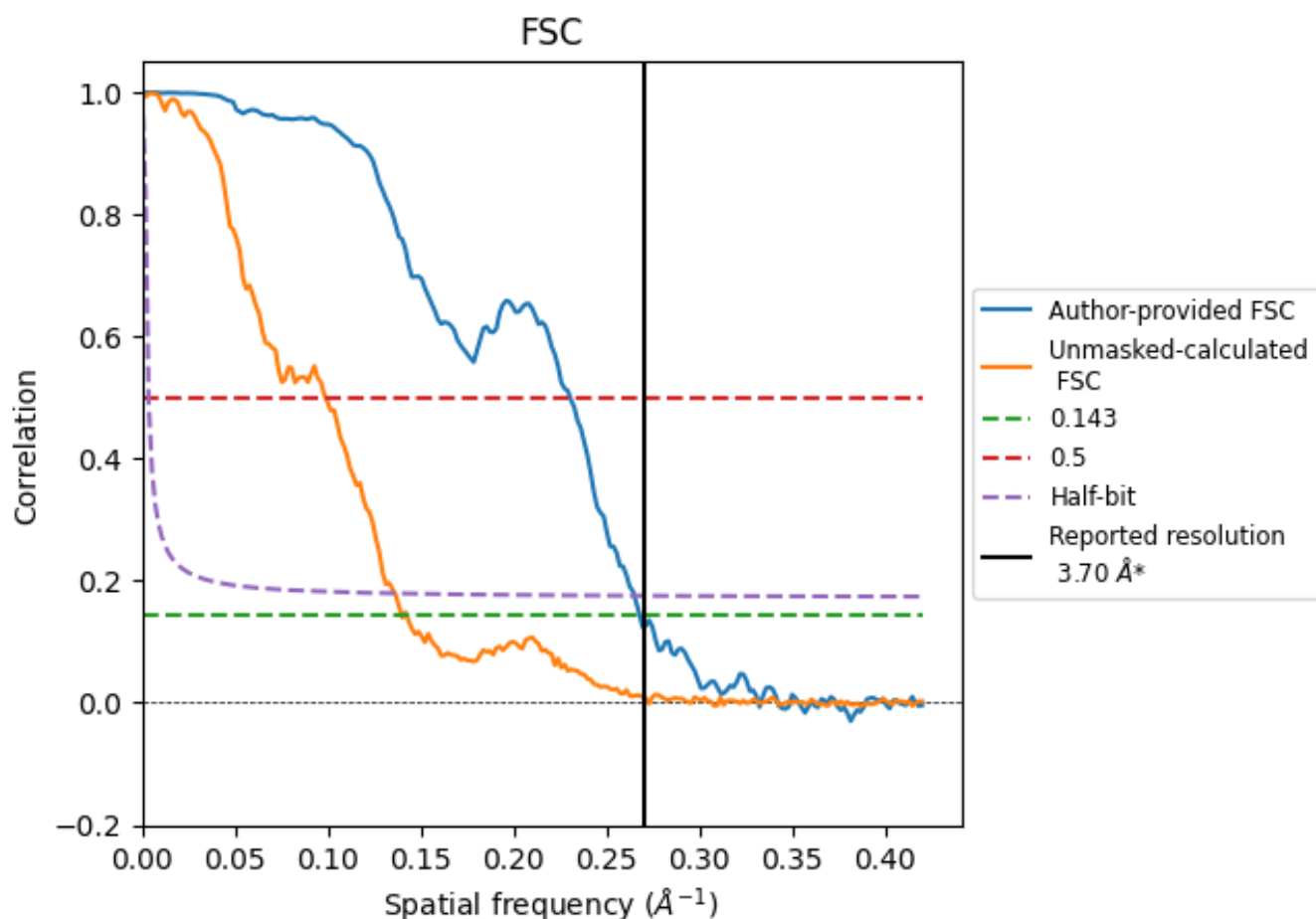


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

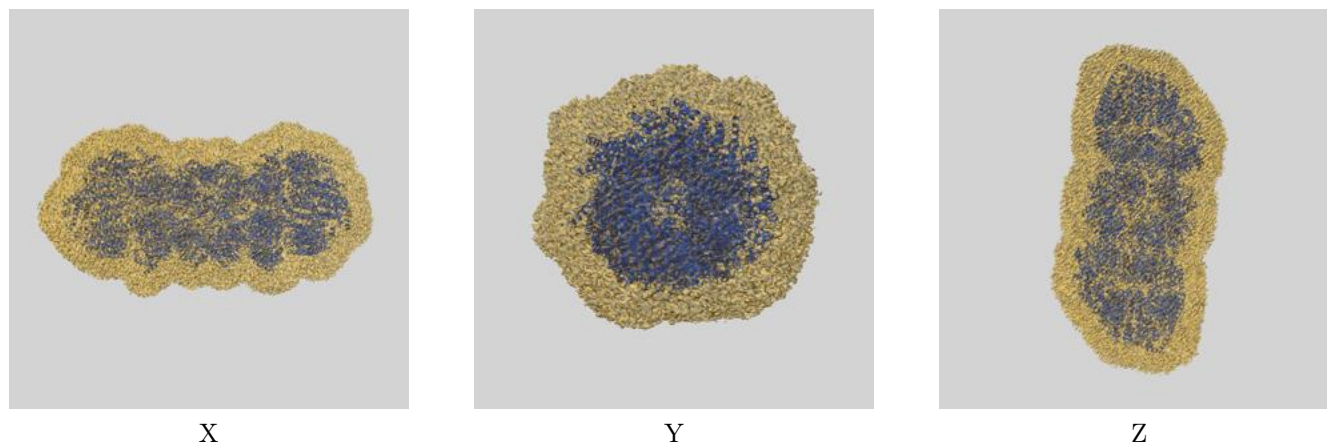
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	4.34	3.77
Unmasked-calculated*	7.16	10.11	7.34

*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 7.16 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

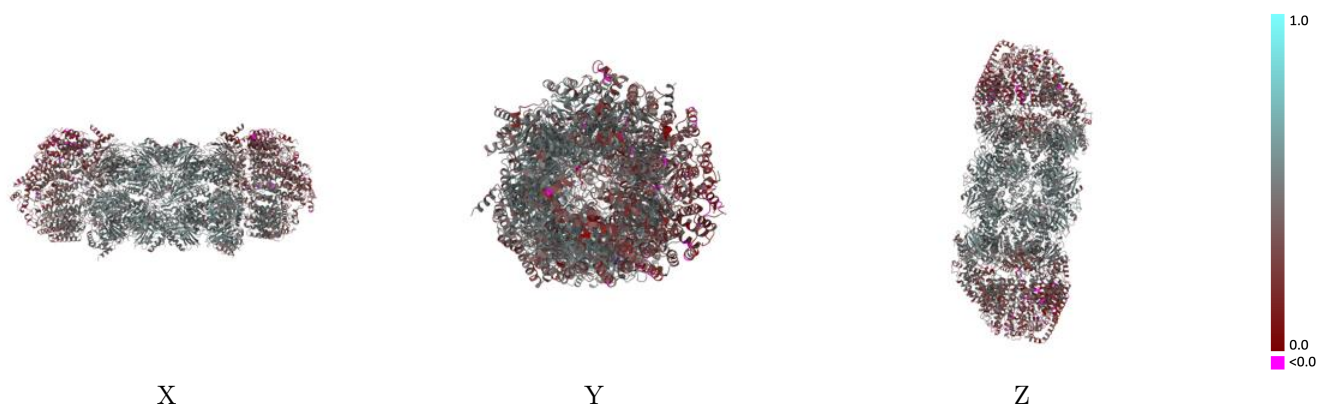
This section contains information regarding the fit between EMDB map EMD-75436 and PDB model 10SJ. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



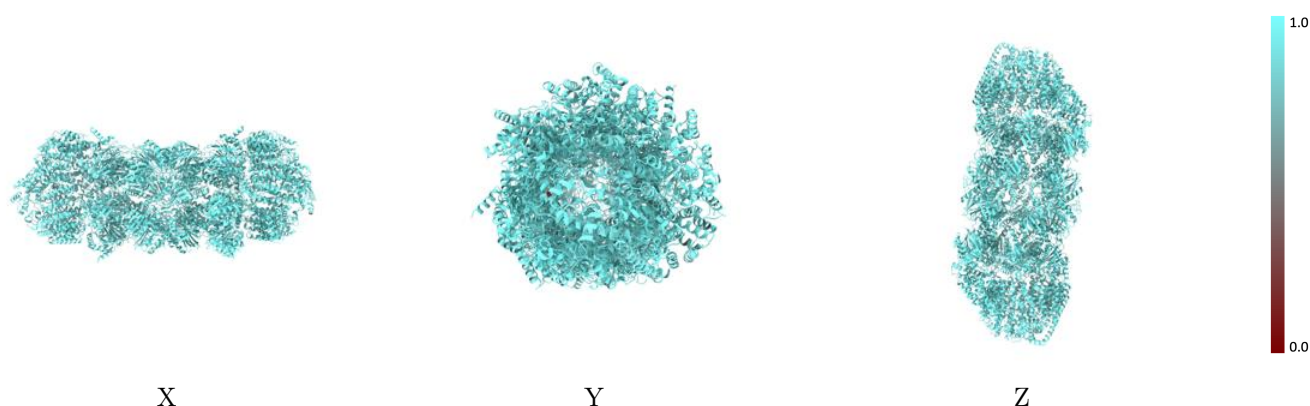
The images above show the 3D surface view of the map at the recommended contour level 0.00238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



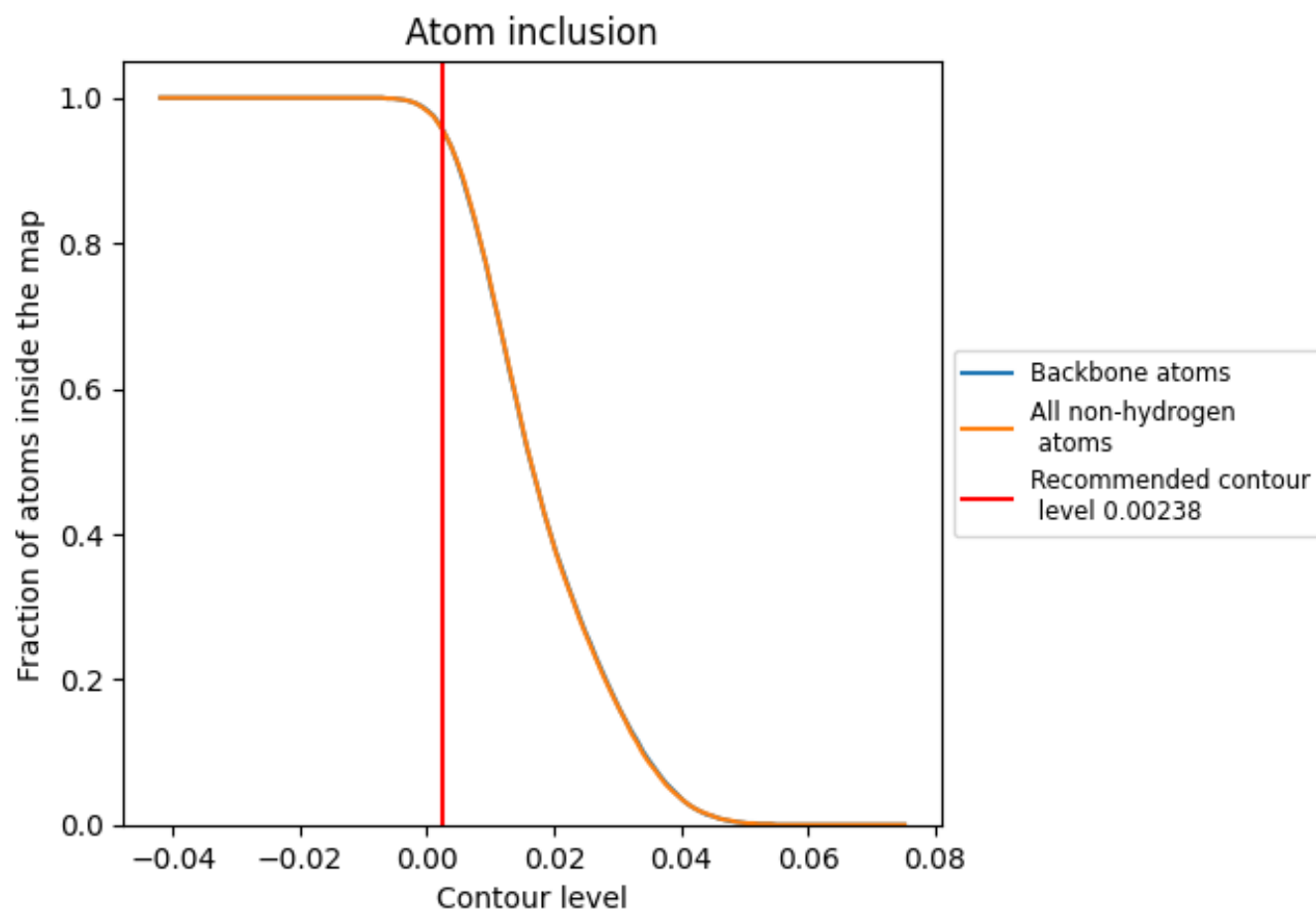
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00238).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.00238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4320
1	 0.9780	 0.5100
2	 0.9740	 0.5180
A	 0.9710	 0.4940
B	 0.9570	 0.4730
C	 0.9510	 0.3890
CA	 0.9410	 0.3510
D	 0.9520	 0.3750
DA	 0.9380	 0.3460
E	 0.9710	 0.4790
F	 0.9690	 0.4950
G	 0.9760	 0.4920
H	 0.9670	 0.5190
I	 0.9790	 0.5040
J	 0.9760	 0.5130
K	 0.9690	 0.4920
L	 0.9760	 0.5110
M	 0.9730	 0.5080
N	 0.9750	 0.5170
O	 0.9770	 0.4980
P	 0.9630	 0.4780
Q	 0.9540	 0.4000
R	 0.9520	 0.3730
S	 0.9650	 0.4740
T	 0.9690	 0.4960
U	 0.9770	 0.4940
V	 0.9780	 0.5210
W	 0.9780	 0.5190
X	 0.9790	 0.5180
Y	 0.9730	 0.4920
Z	 0.9710	 0.5100

