



Full wwPDB EM Validation Report ⓘ

Feb 21, 2022 – 07:32 pm GMT

PDB ID : 7ORI
EMDB ID : EMD-13038
Title : La Crosse virus polymerase at replication late-elongation stage
Authors : Arragain, B.; Durieux Trouillette, Q.; Baudin, F.; Cusack, S.; Schoehn, G.;
Malet, H.
Deposited on : 2021-06-06
Resolution : 3.90 Å (reported)
Based on initial model : 6Z8K

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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

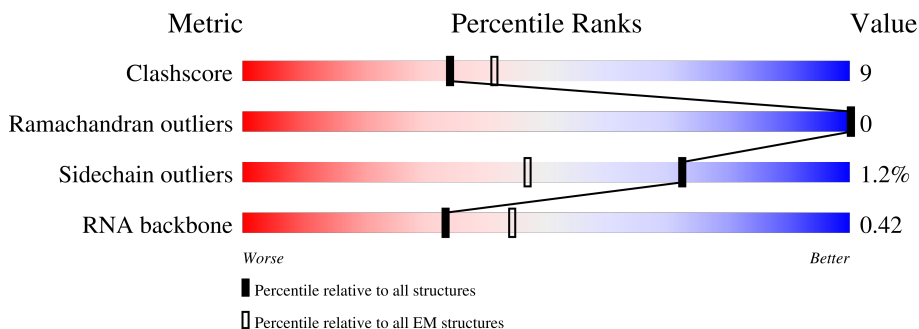
EMDB validation analysis : 0.0.0.dev97
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

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 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	H	17	18% (green), 35% (yellow), 12% (orange), 35% (grey)
2	T	30	13% (green), 47% (yellow), 10% (orange), 30% (grey)
3	P	30	10% (green), 27% (yellow), 60% (grey)
4	A	2276	69% (green), 19% (yellow), 12% (grey)

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 17326 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 RNA chain called RNA (5'-R(P*AP*CP*GP*AP*GP*UP*GP*UP*CP*GP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	H	11	237	105	42	79	11	0	0

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*CP*GP*UP*UP*AP*UP*CP*UP*AP*UP*AP*AP*CP*AP*CP*UP*AP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	T	21	439	198	74	146	21	0	0

- Molecule 3 is a RNA chain called RNA (5'-R(P*AP*UP*AP*GP*AP*UP*AP*AP*CP*GP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	P	12	256	115	46	83	12	0	0

- Molecule 4 is a protein called La Crosse virus polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	2007	16383	10499	2717	3059	108	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	LYS	HIS	engineered mutation	UNP A5HC98
A	1028G	SER	-	insertion	UNP A5HC98
A	1028H	GLY	-	insertion	UNP A5HC98
A	1028I	TRP	-	insertion	UNP A5HC98
A	1028J	SER	-	insertion	UNP A5HC98
A	1028K	HIS	-	insertion	UNP A5HC98

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1028L	PRO	-	insertion	UNP A5HC98
A	1028M	GLN	-	insertion	UNP A5HC98
A	1028N	PHE	-	insertion	UNP A5HC98
A	1028O	GLU	-	insertion	UNP A5HC98
A	1028P	LYS	-	insertion	UNP A5HC98
A	1028Q	GLY	-	insertion	UNP A5HC98
A	1028R	SER	-	insertion	UNP A5HC98
A	1028S	GLY	-	insertion	UNP A5HC98

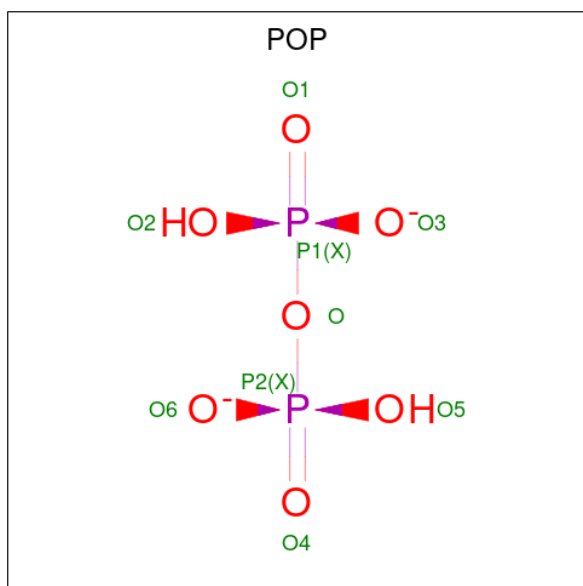
- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
5	A	1	Total Zn 1 1	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
6	A	1	Total Mg 1 1	0

- Molecule 7 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: H₂O₇P₂).

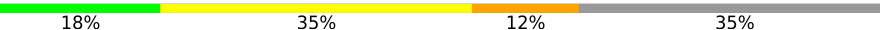


Mol	Chain	Residues	Atoms	AltConf
7	A	1	Total O P 9 7 2	0

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: RNA (5'-R(P*AP*CP*GP*AP*GP*UP*GP*UP*CP*GP*U)-3')

Chain H: 



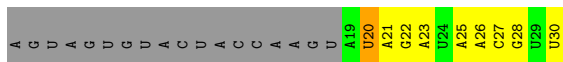
- Molecule 2: RNA (5'-R(P*AP*AP*CP*GP*UP*UP*AP*UP*CP*UP*AP*UP*AP*AP*CP*A P*CP*UP*AP*CP*U)-3')

Chain T: 



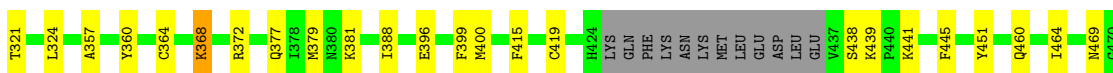
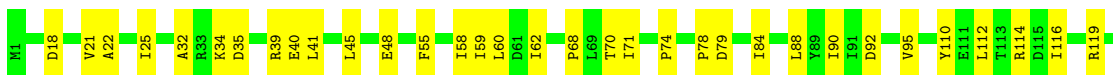
- Molecule 3: RNA (5'-R(P*AP*UP*AP*GP*AP*UP*AP*AP*CP*GP*UP*U)-3')

Chain P: 



- Molecule 4: La Crosse virus polymerase

Chain A: 



K643	K782	CYS	ASN	GLU	GLY	L1144	L1298	R1424	P1599	I1730	LYS	ASP	LYS	ASP	V2100	R2205
R653	V794	ASN	GLN	GLY	GLY	Q1145	I1317	R1439	P1602	K1731	ILE	MET	ILE	GLY	S2101	I2216
M655	N795	TRP	TRP	SER	SER	M1147	P1317	L1441	R1602	Y1736	THR	SER	THR	GLN	R2102	P2217
I656	L796	HIS	PRO	HIS	SER	N1149	A1323	E1466	M1605	Q1743	PRO	ASN	GLY	LEU	I1982	P2218
D688	L799	GLN	GLN	PRO	GLN	Y1150	R1326	K1467	S1606	L1744	ASN	THR	ASN	THR	L1987	L2116
Y669	K805	PHE	GLN	GLN	PHE	T1151	D1328	L1498	S1608	L1745	THR	THR	THR	THR	L2117	L2118
K673	R813	GLU	GLU	GLY	GLY	E1164	K1164	E1760	P1611	E1760	ILE	GLY	ILE	ILE	E2119	E2119
V684	L817	LYS	LYS	LYS	LYS	E1165	L1341	A1504	P1611	A1764	THR	TYR	THR	THR	E2120	E2121
R688	L817	SER	SER	SER	SER	K1168	S1342	F1507	K1617	C1767	ARG	ARG	ARG	ARG	T2122	T2122
L689	I821	TRR	TRR	TRR	TRR	E1169	M1343	I1508	L1616	F1768	THR	SER	THR	THR	T2009	E2126
F695	S842	SER	SER	SER	SER	I1170	T1346	I1511	H1621	F1768	LYS	LYS	LYS	LYS	L2010	E2127
Y710	C943	ASN	ASN	ASN	ASN	T1172	T1347	K1546	L1625	L1770	ASP	THR	THR	THR	K2011	A2128
L711	L844	LEU	LEU	LEU	LEU	L1173	G1348	V1625	L1627	L1771	ILE	ILE	ILE	ILE	K2012	F2129
I716	R850	VAL	VAL	VAL	VAL	L1174	L1349	V1517	L1627	T1772	GLY	GLY	GLY	GLY	G2023	T2130
T717	E854	LYS	LYS	LYS	LYS	I1178	L1354	F1518	D1641	H1773	GLU	GLU	GLU	GLU	L2030	N2134
Q718	LEU	GLN	GLN	GLN	GLN	D1188	L1357	Y1528	P1642	L1790	ASN	ASN	ASN	ASN	L2034	F2136
K719	GLN	SER	SER	SER	SER	I1195	I1358	M1530	T1643	I1791	LYS	LYS	LYS	LYS	T2034	N2141
G720	SER	VAL	VAL	VAL	VAL	T1198	K1358	LEU	E1644	E1794	THR	THR	THR	THR	E2035	L2145
I721	R952	VAL	VAL	VAL	VAL	D1198	L1360	HIS	M1645	F1796	TYR	TYR	TYR	TYR	K2038	V2148
N724	R952	ARG	ARG	ARG	ARG	T1232	L1365	ASP	R1647	S1796	ALA	ALA	ALA	ALA	S2039	V2149
I730	R968	LYS	LYS	LYS	LYS	T1235	T1365	SER	H1651	Y1797	LEU	LEU	LEU	LEU	N2046	L2152
W731	N969	LYS	LYS	LYS	LYS	K1236	R1371	ALA	K1666	L1805	THR	THR	THR	THR	N2049	I2160
F732	C970	ILE	ILE	ILE	ILE	K1236	S1372	LEU	V1667	Y1813	THR	THR	THR	THR	F2050	W2160
W736	LYS	LEU	LEU	LEU	LEU	L1241	E1373	GLU	R1668	P1820	ARG	ARG	ARG	ARG	R2051	F2051
V736	VAL	VAL	VAL	VAL	VAL	F1242	Q1377	PRO	M1671	P1820	LYS	LYS	LYS	LYS	L2055	K2166
T737	GLN	VAL	VAL	VAL	VAL	N1243	I1378	ASP	L1671	L1828	THR	THR	THR	THR	L2062	H2169
L738	SER	VAL	VAL	VAL	VAL	L1244	K1382	ILE	K1686	R1829	GLU	GLU	GLU	GLU	I2062	L2172
Y746	ARG	ARG	ARG	ARG	ARG	I1251	T1390	LEU	L1686	L1833	ASN	ASN	ASN	ASN	C2063	L2172
L747	LYS	LYS	LYS	LYS	LYS	R1254	E1393	L1560	R1690	L1837	ILE	ILE	ILE	ILE	N2071	M2177
P748	ARG	ARG	ARG	ARG	ARG	F1255	E1393	L1571	Q1693	D1837	THR	THR	THR	THR	D2072	D2178
F751	ALA	ALA	ALA	ALA	ALA	L1256	K1398	Q1571	Y1696	K1840	GLY	GLY	GLY	GLY	P2081	H2179
K754	ASN	ASN	ASN	ASN	ASN	D1271	R1401	I1573	E1697	SER	ARG	ARG	ARG	ARG	F2081	Y2181
M763	MET	MET	MET	MET	MET	L1272	Y1402	Y1574	Y1698	HIS	LYS	LYS	LYS	LYS	T2085	M2180
L766	VAL	VAL	VAL	VAL	VAL	A1273	L1403	S1575	V1699	THR	THR	THR	THR	THR	E2086	F2184
A767	THR	THR	THR	THR	THR	S1274	L1403	I1577	K1700	THR	THR	THR	THR	THR	G2087	D2185
K768	ASP	ASP	ASP	ASP	ASP	R1275	D1406	L1578	T1702	TRP	TRP	TRP	TRP	TRP	I2090	F2190
L771	GLN	GLN	GLN	GLN	GLN	I1277	E1407	M1580	F1709	ASN	HIS	HIS	HIS	HIS	H2091	GLY
E772	VAL	VAL	VAL	VAL	VAL	S1277	M1409	D1581	S1715	ASN	VAL	VAL	VAL	VAL	S2092	GLY
I773	CYS	CYS	CYS	CYS	CYS	K1284	T1418	M1584	S1715	THR	THR	THR	THR	THR	T2093	ASN
E774	LEU	LEU	LEU	LEU	LEU	P1289	S1419	I1585	T1718	GLN	GLN	GLN	GLN	GLN	P2094	THR
N780	VAL	VAL	VAL	VAL	VAL	M1421	M1421	I1587	L1724	SER	SER	SER	SER	SER	F2096	ARG
I781	HIS	HIS	HIS	HIS	HIS	S1293	G1423	I1587	L1729	LEU	LEU	LEU	LEU	LEU	H2097	ASP
		THR	THR	THR	THR	S1295		T1590							Y2099	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24151	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	297.69998, 297.69998, 297.69998	wwPDB
Map dimensions	260, 260, 260	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.145, 1.145, 1.145	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: POP, ZN, MG

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	H	0.69	1/264 (0.4%)	0.67	0/408
2	T	0.22	0/488	0.79	0/753
3	P	0.23	0/286	0.72	0/443
4	A	0.27	0/16721	0.45	0/22547
All	All	0.28	1/17759 (0.0%)	0.48	0/24151

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	1	A	OP3-P	-10.66	1.48	1.61

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	H	237	0	119	4	0
2	T	439	0	226	14	0
3	P	256	0	129	10	0
4	A	16383	0	16426	289	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	9	0	0	0	0
All	All	17326	0	16900	305	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 9.

All (305) 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)
4:A:813:ARG:NH1	4:A:986:PRO:HD3	1.67	1.09
4:A:2064:CYS:HB2	4:A:2169:HIS:HE1	1.15	1.03
4:A:2064:CYS:CB	4:A:2169:HIS:HE1	1.76	0.98
4:A:2064:CYS:HB2	4:A:2169:HIS:CE1	1.97	0.98
4:A:813:ARG:HH12	4:A:986:PRO:HD3	1.35	0.89
4:A:2064:CYS:CB	4:A:2169:HIS:CE1	2.55	0.89
4:A:70:THR:HG23	4:A:71:ILE:HD12	1.57	0.85
4:A:1424:ARG:HG3	4:A:1424:ARG:HH11	1.41	0.84
4:A:1743:GLN:HE22	4:A:1745:LEU:HB2	1.42	0.83
4:A:2051:ARG:HG2	4:A:2051:ARG:HH11	1.41	0.83
4:A:1360:LEU:HD21	4:A:1393:GLU:HG2	1.62	0.81
4:A:2051:ARG:HG2	4:A:2051:ARG:NH1	1.98	0.77
4:A:1617:LYS:HE3	4:A:1702:THR:N	2.02	0.74
4:A:982:CYS:HB3	4:A:988:GLU:HG2	1.70	0.71
4:A:1401:ARG:HB2	4:A:1573:ILE:HD11	1.73	0.71
2:T:1:A:H2'	2:T:2:A:H8	1.55	0.70
4:A:1027:ILE:HG22	4:A:1028:GLU:HG2	1.74	0.69
4:A:773:ILE:HG21	4:A:1066:ALA:HB1	1.74	0.69
4:A:1064:TRP:HE1	4:A:1152:SER:HG	1.39	0.69
4:A:218:GLU:OE2	4:A:797:LYS:HE3	1.92	0.68
4:A:612:LEU:HD23	4:A:1298:ILE:HD11	1.75	0.68
4:A:950:LYS:HD3	4:A:952:GLN:HB3	1.77	0.66
4:A:1354:LEU:O	4:A:1358:ILE:HG12	1.95	0.66
4:A:1617:LYS:HE3	4:A:1702:THR:H	1.58	0.65
4:A:1837:ASP:HA	4:A:1840:LYS:HE3	1.79	0.65
4:A:1340:PRO:HD2	4:A:1343:MET:HG3	1.79	0.65
4:A:110:TYR:O	4:A:114:ARG:HG2	1.97	0.64
4:A:2092:SER:OG	4:A:2094:PRO:HD2	1.97	0.64
4:A:1715:SER:HB3	4:A:1724:LEU:HD12	1.79	0.64
4:A:295:SER:HB2	4:A:441:LYS:HE3	1.80	0.64
4:A:1398:LYS:HB3	4:A:1560:LEU:HD12	1.78	0.63
4:A:2216:ILE:HG22	4:A:2218:PRO:HD2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1627:LEU:HD11	4:A:1696:TYR:HB2	1.82	0.62
4:A:1421:MET:HG2	4:A:1697:GLU:HB2	1.82	0.61
2:T:1:A:H2'	2:T:2:A:C8	2.35	0.61
4:A:400:MET:HA	4:A:529:THR:HG22	1.82	0.61
4:A:1378:ILE:HG21	4:A:1579:LEU:HD21	1.83	0.61
4:A:2205:ARG:HH11	4:A:2234:ILE:HG13	1.66	0.61
4:A:689:LEU:HD13	4:A:731:TRP:HA	1.84	0.60
4:A:1579:LEU:HA	4:A:1585:ILE:HD11	1.84	0.60
4:A:2064:CYS:HB3	4:A:2169:HIS:CE1	2.34	0.60
4:A:2091:HIS:O	4:A:2091:HIS:ND1	2.35	0.60
4:A:18:ASP:HB3	4:A:21:VAL:HG22	1.85	0.59
4:A:519:LEU:HD13	4:A:1508:ILE:HD11	1.84	0.59
4:A:721:ILE:HD12	4:A:1244:LEU:HD12	1.83	0.58
4:A:175:ASP:HB3	4:A:178:PHE:HB3	1.85	0.58
4:A:656:ILE:HD13	4:A:730:ILE:HD13	1.85	0.58
4:A:78:PRO:HB3	4:A:90:ILE:HG23	1.86	0.58
4:A:84:ILE:HD11	4:A:148:LEU:HD13	1.85	0.58
4:A:79:ASP:HB2	4:A:92:ASP:HA	1.85	0.58
4:A:1346:THR:HG21	4:A:1587:ILE:HD11	1.84	0.58
4:A:961:PHE:CG	4:A:1144:LEU:HD12	2.40	0.57
4:A:1424:ARG:HH11	4:A:1424:ARG:CG	2.14	0.57
4:A:1050:ALA:HA	4:A:1198:ASP:HB3	1.86	0.57
4:A:844:LEU:HD11	4:A:906:TYR:HB2	1.87	0.57
4:A:469:ASN:HB3	4:A:471:LEU:HG	1.86	0.56
4:A:766:LEU:HD22	4:A:959:GLU:HB3	1.86	0.56
4:A:710:TYR:HB2	4:A:718:GLN:HB3	1.87	0.56
4:A:947:PHE:HD1	4:A:1103:LEU:HD11	1.71	0.56
4:A:1357:LEU:HD12	4:A:1578:ILE:HD11	1.87	0.56
4:A:1060:ASP:OD1	4:A:1188:ASP:HA	2.06	0.56
4:A:2064:CYS:SG	4:A:2178:ASP:OD2	2.64	0.56
4:A:324:LEU:HD21	4:A:399:PHE:HZ	1.71	0.55
4:A:74:PRO:HB3	4:A:112:LEU:HD12	1.88	0.55
4:A:933:ILE:HD12	4:A:969:MET:HB2	1.88	0.55
4:A:2128:ALA:HA	4:A:2216:ILE:HG13	1.89	0.55
4:A:1293:TRP:NE1	4:A:1341:LEU:HD21	2.22	0.55
4:A:1578:ILE:HG22	4:A:1585:ILE:HD13	1.89	0.55
4:A:944:TYR:HB3	4:A:1104:ILE:HD11	1.89	0.54
4:A:2087:GLY:HA2	4:A:2098:ILE:O	2.08	0.54
2:T:23:A:H62	4:A:381:LYS:HB3	1.72	0.54
4:A:2055:LEU:HB2	4:A:2121:GLU:HB3	1.87	0.54
4:A:1424:ARG:HG3	4:A:1424:ARG:NH1	2.16	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:7:A:H2'	2:T:8:U:H6	1.72	0.54
4:A:813:ARG:HH12	4:A:986:PRO:CD	2.14	0.54
4:A:2051:ARG:HH11	4:A:2051:ARG:CG	2.14	0.54
4:A:771:LEU:HD12	4:A:1128:MET:HG3	1.90	0.54
4:A:774:GLU:OE1	4:A:774:GLU:HA	2.09	0.53
4:A:1439:ARG:CZ	4:A:1439:ARG:HA	2.37	0.53
2:T:25:A:OP2	4:A:368:LYS:HD2	2.08	0.53
4:A:1602:ARG:HB3	4:A:1605:MET:HE1	1.90	0.53
4:A:780:ASN:O	4:A:782:LYS:HG3	2.08	0.52
4:A:1625:LEU:HB3	4:A:1645:MET:HE1	1.91	0.52
4:A:2034:THR:HG22	4:A:2038:LYS:HE2	1.89	0.52
4:A:364:CYS:HB2	4:A:396:GLU:HB2	1.90	0.52
4:A:1581:ASP:HB3	4:A:1584:MET:HG2	1.92	0.52
4:A:502:THR:HG23	4:A:504:TYR:H	1.74	0.52
4:A:519:LEU:HD11	4:A:601:CYS:HB3	1.92	0.52
4:A:805:LYS:NZ	4:A:1165:GLU:OE2	2.39	0.52
4:A:813:ARG:HH11	4:A:986:PRO:HD3	1.67	0.52
4:A:88:LEU:HD22	4:A:124:ILE:HD12	1.91	0.52
4:A:519:LEU:HB3	4:A:1508:ILE:HD12	1.92	0.52
4:A:1791:ILE:HG13	4:A:1795:PHE:CD2	2.45	0.52
4:A:1017:ARG:O	4:A:1021:ARG:HG3	2.09	0.51
4:A:1466:GLU:OE1	4:A:1467:LYS:HG3	2.10	0.51
4:A:1171:ILE:HD11	4:A:1195:ILE:HD13	1.93	0.51
4:A:261:ASN:ND2	4:A:261:ASN:O	2.43	0.51
4:A:1371:ARG:HB3	4:A:1371:ARG:NH1	2.25	0.51
4:A:2096:PHE:HE2	4:A:2098:ILE:HD11	1.76	0.51
3:P:27:C:H2'	3:P:28:G:H8	1.76	0.51
4:A:41:LEU:HD11	4:A:129:ILE:HG21	1.92	0.50
4:A:1403:LEU:HD21	4:A:1560:LEU:HD21	1.93	0.50
4:A:998:LEU:HD13	4:A:1241:LEU:HB3	1.93	0.50
4:A:1144:LEU:HB2	4:A:1147:ASN:ND2	2.26	0.50
4:A:1516:LYS:O	4:A:1518:VAL:HG13	2.12	0.50
4:A:2090:ILE:HG22	4:A:2092:SER:HB3	1.94	0.50
4:A:1294:VAL:O	4:A:1298:ILE:HG12	2.12	0.50
4:A:1341:LEU:HB3	4:A:1729:LEU:HD13	1.93	0.50
4:A:1424:ARG:CG	4:A:1424:ARG:NH1	2.73	0.50
3:P:20:U:H2'	3:P:21:A:C8	2.47	0.50
4:A:445:PHE:HA	4:A:684:VAL:HG13	1.94	0.49
4:A:1373:SER:O	4:A:1377:GLN:HG3	2.12	0.49
4:A:1409:MET:SD	4:A:1576:TYR:CE1	3.05	0.49
4:A:796:LEU:HD23	4:A:797:LYS:HD3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2085:THR:HA	4:A:2101:SER:HA	1.95	0.49
4:A:2093:THR:HB	4:A:2094:PRO:HD3	1.95	0.49
3:P:22:G:H2'	3:P:23:A:C8	2.47	0.49
4:A:116:ILE:HG13	4:A:119:ARG:HH21	1.77	0.49
4:A:1769:LYS:HG2	4:A:2010:ILE:HG22	1.95	0.49
4:A:576:CYS:HA	4:A:592:ARG:HH21	1.78	0.48
4:A:1507:PHE:CZ	4:A:1511:ILE:HD11	2.48	0.48
4:A:32:ALA:HA	4:A:35:ASP:OD1	2.13	0.48
4:A:625:LEU:HD13	4:A:732:PHE:HE2	1.78	0.48
4:A:937:MET:HG3	4:A:970:CYS:SG	2.53	0.48
4:A:1317:PRO:HD2	4:A:1326:ARG:HH12	1.78	0.48
4:A:1611:PRO:HG3	4:A:1718:THR:HA	1.95	0.48
4:A:763:MET:HE1	4:A:1106:PRO:HG2	1.95	0.48
4:A:48:GLU:HG3	4:A:1813:TYR:CD1	2.48	0.48
4:A:1643:THR:O	4:A:1647:ARG:HG2	2.13	0.48
4:A:132:ASP:HB3	4:A:137:ASP:OD1	2.14	0.48
3:P:21:A:H2'	3:P:22:G:C8	2.49	0.48
4:A:850:ARG:NH2	4:A:897:ARG:HG2	2.29	0.47
4:A:1795:PHE:CD1	4:A:2023:GLY:HA3	2.50	0.47
2:T:4:G:H2'	2:T:5:U:O4'	2.14	0.47
3:P:30:U:H2'	4:A:1145:GLN:HG2	1.97	0.47
4:A:274:LYS:HG2	4:A:695:PHE:HD1	1.80	0.47
4:A:496:MET:HE1	4:A:1294:VAL:HG22	1.95	0.47
4:A:40:GLU:HG3	4:A:156:ILE:HG21	1.96	0.47
4:A:668:ASP:O	4:A:669:TYR:C	2.53	0.47
4:A:1168:LYS:O	4:A:1172:THR:HG23	2.15	0.47
4:A:1365:THR:HG21	4:A:1377:GLN:HB3	1.97	0.47
4:A:2071:ASN:OD1	4:A:2072:ASP:N	2.47	0.47
4:A:289:GLN:HG2	4:A:294:ILE:HG13	1.95	0.47
4:A:1693:GLN:O	4:A:1697:GLU:HG2	2.15	0.47
4:A:2062:ILE:HB	4:A:2166:LYS:HD2	1.97	0.47
4:A:1343:MET:O	4:A:1347:VAL:HG22	2.14	0.47
4:A:1232:THR:HG21	4:A:1235:ILE:HB	1.96	0.47
4:A:1767:CYS:HB2	4:A:1797:TYR:CD2	2.50	0.47
2:T:7:A:H2'	2:T:8:U:C6	2.50	0.46
1:H:2:C:OP1	4:A:592:ARG:NH1	2.48	0.46
4:A:1289:PRO:HG3	4:A:1729:LEU:HA	1.96	0.46
4:A:377:GLN:HG3	4:A:379:MET:SD	2.56	0.46
4:A:748:PRO:HA	4:A:751:PHE:CD2	2.51	0.46
4:A:961:PHE:CD2	4:A:1144:LEU:HD12	2.49	0.46
4:A:2087:GLY:HA3	4:A:2099:TYR:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:934:MET:HB3	4:A:1090:ARG:HD3	1.98	0.46
4:A:1516:LYS:HB3	4:A:1516:LYS:HE3	1.70	0.46
4:A:321:THR:HG21	4:A:357:ALA:HB1	1.97	0.46
4:A:2172:LEU:HD12	4:A:2181:TYR:HB2	1.97	0.46
4:A:2126:GLU:OE2	4:A:2136:PHE:HB2	2.15	0.46
4:A:2136:PHE:HA	4:A:2141:ASN:HD22	1.81	0.46
4:A:1401:ARG:HH12	4:A:1407:ALA:HA	1.81	0.46
4:A:568:GLU:O	4:A:569:GLU:HG3	2.17	0.45
4:A:269:TYR:CE2	4:A:271:GLN:HB3	2.52	0.45
4:A:817:LEU:HD13	4:A:984:LEU:HD11	1.97	0.45
4:A:1273:ALA:HA	4:A:1349:LEU:HD11	1.98	0.45
3:P:30:U:OP2	4:A:958:ARG:NH2	2.49	0.45
4:A:1256:LEU:HD22	4:A:1295:SER:HB3	1.97	0.45
4:A:1794:GLU:HG3	4:A:2024:PRO:HD2	1.98	0.45
4:A:1504:ALA:O	4:A:1508:ILE:HG12	2.16	0.45
4:A:220:ARG:O	4:A:223:GLU:HG3	2.17	0.45
4:A:622:ASN:HD21	4:A:736:VAL:HG12	1.82	0.45
4:A:794:VAL:HG11	4:A:799:LEU:HD22	1.99	0.45
4:A:2149:VAL:HA	4:A:2152:ILE:HG12	1.98	0.45
4:A:600:ARG:HB3	4:A:641:ILE:HD12	1.99	0.45
4:A:643:LYS:HB3	4:A:643:LYS:HE2	1.73	0.45
4:A:22:ALA:HA	4:A:25:ILE:HG12	1.98	0.45
4:A:222:PHE:HB2	4:A:1075:TRP:CH2	2.51	0.45
4:A:21:VAL:O	4:A:25:ILE:HG23	2.17	0.45
4:A:215:PRO:O	4:A:219:ARG:HG3	2.17	0.45
4:A:305:ILE:HD13	4:A:639:LEU:HD12	1.99	0.45
4:A:813:ARG:HH12	4:A:985:ASN:HA	1.82	0.45
1:H:7:G:N7	4:A:768:LYS:HD2	2.32	0.45
4:A:201:PHE:HB2	4:A:1093:TYR:HB2	2.00	0.44
4:A:721:ILE:HG21	4:A:738:LEU:HD23	1.99	0.44
4:A:817:LEU:O	4:A:821:ILE:HG13	2.18	0.44
4:A:1419:SER:HA	4:A:1422:ARG:NH1	2.32	0.44
4:A:1599:PRO:HG3	4:A:1736:TYR:CE2	2.53	0.44
4:A:460:GLN:O	4:A:464:ILE:HG22	2.16	0.44
4:A:653:ARG:HH21	4:A:746:TYR:HE2	1.65	0.44
4:A:2030:LEU:HD23	4:A:2030:LEU:H	1.82	0.44
4:A:1171:ILE:HG13	4:A:1178:ILE:HB	1.98	0.44
4:A:1174:LEU:HD23	4:A:1174:LEU:HA	1.79	0.44
4:A:1696:TYR:HA	4:A:1699:VAL:HG12	1.99	0.44
2:T:23:A:N6	4:A:381:LYS:HB3	2.33	0.44
2:T:30:U:O2	2:T:30:U:O2'	2.24	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:34:LYS:HZ3	4:A:95:VAL:H	1.65	0.44
4:A:1418:THR:H	4:A:1421:MET:HE3	1.83	0.44
4:A:55:PHE:CE2	4:A:59:ILE:HD11	2.53	0.44
4:A:368:LYS:HE3	4:A:372:ARG:NH2	2.33	0.44
4:A:711:LEU:HD22	4:A:2098:ILE:HG23	1.98	0.44
4:A:1371:ARG:CB	4:A:1371:ARG:CZ	2.95	0.44
4:A:1409:MET:SD	4:A:1576:TYR:CZ	3.11	0.44
4:A:1686:LYS:HA	4:A:1686:LYS:HD3	1.76	0.44
4:A:1700:LYS:HD2	4:A:1700:LYS:HA	1.78	0.44
4:A:1833:LEU:HD21	4:A:1987:LEU:HD11	2.00	0.44
4:A:1764:ALA:HB2	4:A:1805:LEU:HD22	2.00	0.44
2:T:30:U:O4	4:A:536:ALA:HB1	2.18	0.44
4:A:596:LEU:HD23	4:A:596:LEU:HA	1.84	0.44
4:A:929:VAL:O	4:A:933:ILE:HG12	2.18	0.44
4:A:999:LYS:HA	4:A:1607:CYS:SG	2.58	0.44
4:A:41:LEU:HD23	4:A:45:LEU:HD13	1.99	0.43
4:A:1773:HIS:CE1	4:A:2012:LYS:HG2	2.53	0.43
4:A:1343:MET:HE1	4:A:1354:LEU:HG	1.99	0.43
4:A:502:THR:HG23	4:A:504:TYR:N	2.33	0.43
4:A:303:PRO:HB3	4:A:576:CYS:HB2	1.99	0.43
4:A:565:HIS:CE1	4:A:568:GLU:HA	2.54	0.43
4:A:724:ASN:OD1	4:A:724:ASN:N	2.51	0.43
4:A:1608:SER:HG	4:A:1715:SER:HG	1.67	0.43
4:A:211:LYS:HE2	4:A:211:LYS:HB3	1.68	0.43
4:A:307:PHE:HB2	4:A:511:PHE:CZ	2.53	0.43
4:A:950:LYS:HB2	4:A:960:ILE:HG12	2.00	0.43
4:A:1143:TRP:HZ3	4:A:1148:PHE:H	1.67	0.43
4:A:1759:SER:OG	4:A:1760:GLU:N	2.52	0.43
4:A:821:ILE:HG12	4:A:980:GLU:CB	2.48	0.43
4:A:1790:LEU:HG	4:A:1794:GLU:OE2	2.19	0.43
4:A:2185:ASP:OD1	4:A:2185:ASP:N	2.51	0.43
3:P:25:A:H2'	3:P:26:A:C8	2.54	0.42
4:A:2145:LEU:O	4:A:2148:VAL:HG12	2.19	0.42
4:A:360:TYR:HB2	4:A:388:ILE:HD13	2.00	0.42
4:A:58:ILE:O	4:A:62:ILE:HG12	2.20	0.42
4:A:438:SER:OG	4:A:439:LYS:N	2.53	0.42
4:A:1730:ILE:HG12	4:A:1731:LYS:HG2	2.01	0.42
4:A:2145:LEU:HA	4:A:2148:VAL:HG12	2.01	0.42
4:A:218:GLU:OE1	4:A:218:GLU:N	2.45	0.42
4:A:2116:LEU:O	4:A:2119:GLU:HG3	2.18	0.42
4:A:499:ILE:HA	4:A:631:MET:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1164:LYS:HB3	4:A:1168:LYS:HZ1	1.84	0.42
4:A:2091:HIS:O	4:A:2091:HIS:CG	2.70	0.42
4:A:235:ARG:HD2	4:A:235:ARG:HA	1.87	0.42
4:A:1999:ARG:HA	4:A:2009:THR:HG22	2.01	0.42
4:A:2160:TRP:CZ3	4:A:2225:ASN:HB3	2.55	0.42
4:A:1378:ILE:HD11	4:A:1574:TYR:HB3	2.02	0.42
4:A:1641:ASP:O	4:A:1645:MET:HB2	2.20	0.42
4:A:2035:GLU:O	4:A:2039:SER:N	2.53	0.42
4:A:2177:MET:HE2	4:A:2177:MET:HA	2.01	0.42
4:A:499:ILE:O	4:A:502:THR:HG22	2.19	0.42
4:A:616:LEU:HD23	4:A:616:LEU:HA	1.90	0.42
4:A:979:LYS:HB2	4:A:1150:TYR:CD2	2.55	0.42
4:A:1317:PRO:HD2	4:A:1326:ARG:NH1	2.34	0.42
4:A:2145:LEU:O	4:A:2149:VAL:HG13	2.20	0.42
4:A:415:PHE:HA	4:A:419:CYS:HB3	2.01	0.42
4:A:716:ILE:HG22	4:A:719:LYS:HD3	2.01	0.42
4:A:1046:SER:HA	4:A:1049:LYS:HD2	2.02	0.42
4:A:1284:LYS:HG2	4:A:1709:PHE:CE2	2.54	0.42
4:A:1828:LEU:O	4:A:1829:ARG:HG2	2.20	0.42
4:A:2046:ASN:HB2	4:A:2049:ASN:HB2	2.02	0.42
4:A:2081:PRO:HG2	4:A:2103:ARG:HH22	1.83	0.42
2:T:25:A:OP2	4:A:368:LYS:CD	2.68	0.41
4:A:514:LEU:HB2	4:A:535:CYS:HB3	2.02	0.41
4:A:1019:LYS:HA	4:A:1019:LYS:HD2	1.90	0.41
4:A:1169:GLU:OE1	4:A:1169:GLU:HA	2.20	0.41
4:A:754:LYS:HE3	4:A:754:LYS:HB2	1.80	0.41
4:A:2228:LYS:HE3	4:A:2228:LYS:HB3	1.87	0.41
3:P:21:A:H2'	3:P:22:G:H8	1.85	0.41
3:P:22:G:H2'	3:P:23:A:H8	1.85	0.41
4:A:251:TYR:O	4:A:255:ILE:HG12	2.19	0.41
4:A:1441:LEU:HD21	4:A:1498:LEU:HD21	2.01	0.41
4:A:1668:ARG:O	4:A:1671:MET:HG3	2.20	0.41
4:A:2231:ILE:HA	4:A:2234:ILE:HG22	2.02	0.41
4:A:1126:ALA:HB1	4:A:1131:GLN:HA	2.03	0.41
2:T:6:U:H2'	2:T:7:A:C8	2.55	0.41
4:A:1382:LYS:HB3	4:A:1571:GLN:NE2	2.36	0.41
4:A:1771:ILE:HD12	4:A:1791:ILE:HD13	2.02	0.41
4:A:2126:GLU:O	4:A:2130:THR:HG23	2.21	0.41
1:H:4:A:H2'	1:H:5:G:H8	1.86	0.41
4:A:35:ASP:OD2	4:A:39:ARG:NH1	2.54	0.41
4:A:451:TYR:CZ	4:A:688:ARG:HG2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1059:ALA:O	4:A:1060:ASP:OD1	2.39	0.41
4:A:1120:TYR:HB3	4:A:1123:ASP:HB2	2.02	0.41
4:A:1618:LEU:HD11	4:A:1651:HIS:CD2	2.56	0.41
4:A:821:ILE:HG12	4:A:980:GLU:HB2	2.02	0.41
4:A:1323:ALA:HB1	4:A:1328:ASP:HB2	2.03	0.41
4:A:1406:ASP:H	4:A:1409:MET:CE	2.34	0.41
4:A:1696:TYR:CZ	4:A:1700:LYS:HD3	2.56	0.41
3:P:27:C:H2'	3:P:28:G:C8	2.54	0.41
2:T:11:A:OP2	4:A:1690:ARG:NH2	2.43	0.40
4:A:547:SER:OG	4:A:548:ALA:N	2.54	0.40
4:A:1576:TYR:O	4:A:1580:ASN:ND2	2.54	0.40
4:A:576:CYS:O	4:A:576:CYS:SG	2.79	0.40
4:A:968:LYS:HE2	4:A:968:LYS:HB2	1.73	0.40
4:A:1587:ILE:O	4:A:1590:THR:HG22	2.21	0.40
4:A:1621:HIS:HE1	4:A:1644:GLU:HB3	1.86	0.40
4:A:60:LEU:HD21	4:A:68:PRO:HG3	2.03	0.40
4:A:934:MET:HB3	4:A:1090:ARG:HH11	1.86	0.40
4:A:1271:ASP:HB3	4:A:1275:ARG:NH1	2.36	0.40
4:A:1772:THR:HB	4:A:1998:SER:HB3	2.02	0.40
4:A:1820:PRO:HG3	4:A:2000:ILE:HG22	2.03	0.40
4:A:2090:ILE:HG21	4:A:2096:PHE:CE1	2.57	0.40
4:A:2180:MET:HG2	4:A:2184:PHE:CE1	2.56	0.40
1:H:6:U:P	4:A:292:ARG:HH12	2.45	0.40
2:T:1:A:H5'	4:A:842:SER:HB2	2.02	0.40
4:A:1251:ILE:O	4:A:1254:ARG:HG2	2.21	0.40
4:A:1666:LYS:HE3	4:A:1666:LYS:HB3	1.89	0.40
4:A:2118:ILE:O	4:A:2122:THR:OG1	2.30	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	
4	A	1991/2276 (88%)	1923 (97%)	68 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	1852/2097 (88%)	1829 (99%)	23 (1%)	71	83

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	136	ARG
4	A	261	ASN
4	A	312	HIS
4	A	313	ASN
4	A	368	LYS
4	A	577	LEU
4	A	655	MET
4	A	673	LYS
4	A	782	LYS
4	A	1198	ASP
4	A	1236	LYS
4	A	1243	ASN
4	A	1277	SER
4	A	1371	ARG
4	A	1390	THR
4	A	1528	TYR
4	A	1602	ARG
4	A	2051	ARG
4	A	2072	ASP
4	A	2090	ILE
4	A	2092	SER
4	A	2134	ASN
4	A	2227	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	622	ASN
4	A	760	HIS
4	A	1580	ASN
4	A	1704	HIS
4	A	1743	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	H	10/17 (58%)	4 (40%)	0
2	T	19/30 (63%)	9 (47%)	0
3	P	11/30 (36%)	1 (9%)	0
All	All	40/77 (51%)	14 (35%)	0

All (14) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	H	6	U
1	H	7	G
1	H	8	U
1	H	9	C
2	T	2	A
2	T	3	C
2	T	9	C
2	T	10	U
2	T	11	A
2	T	12	U
2	T	24	C
2	T	28	A
2	T	30	U
3	P	20	U

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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
7	POP	A	2303	-	6,8,8	0.80	0	13,13,13	0.74	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	POP	A	2303	-	-	0/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

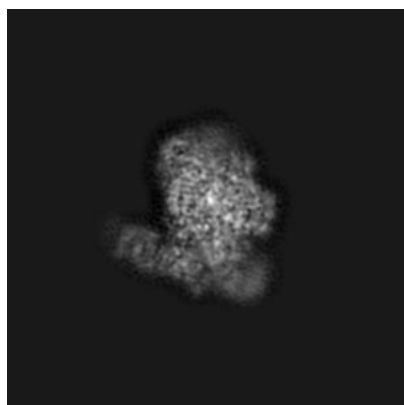
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13038. These allow visual inspection of the internal detail of the map and identification of artifacts.

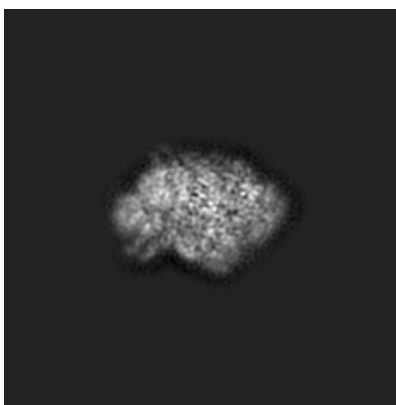
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

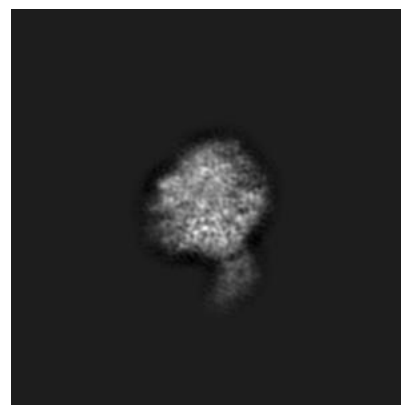
6.1.1 Primary map



X



Y

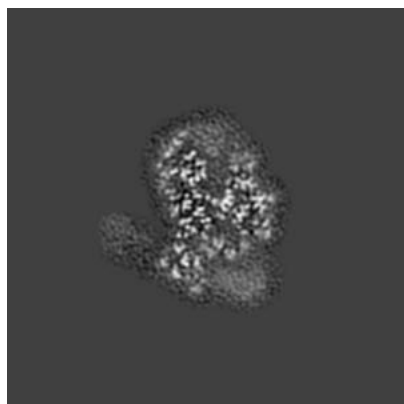


Z

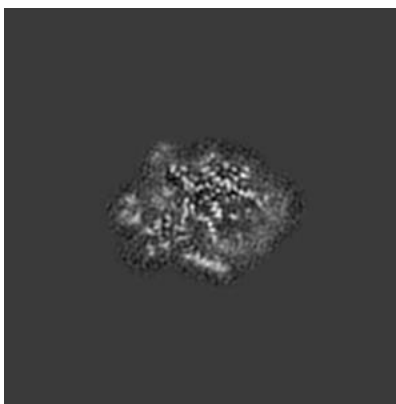
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

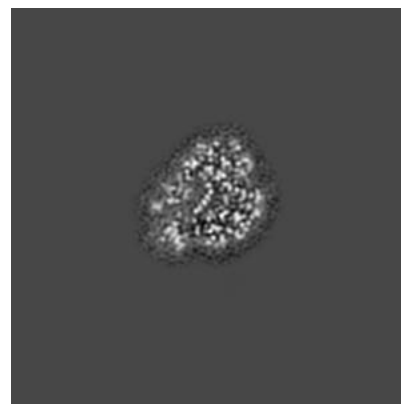
6.2.1 Primary map



X Index: 130



Y Index: 130

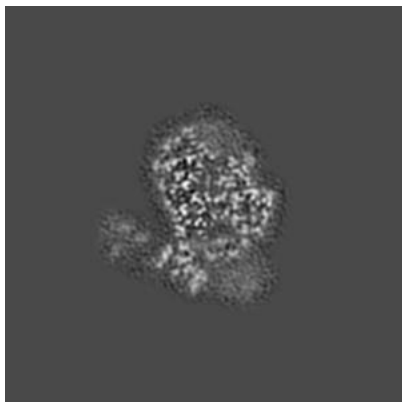


Z Index: 130

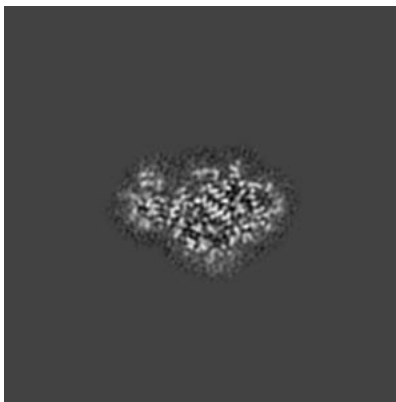
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

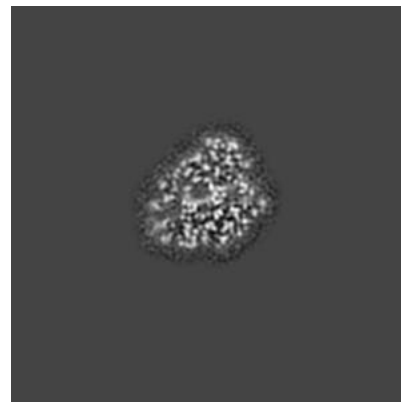
6.3.1 Primary map



X Index: 133



Y Index: 116



Z Index: 134

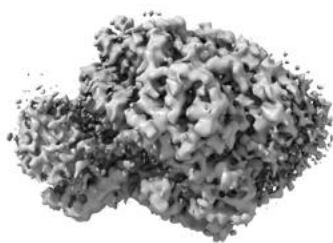
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

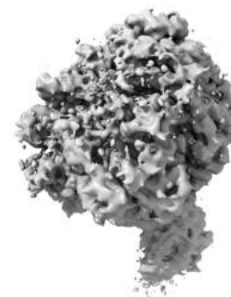
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

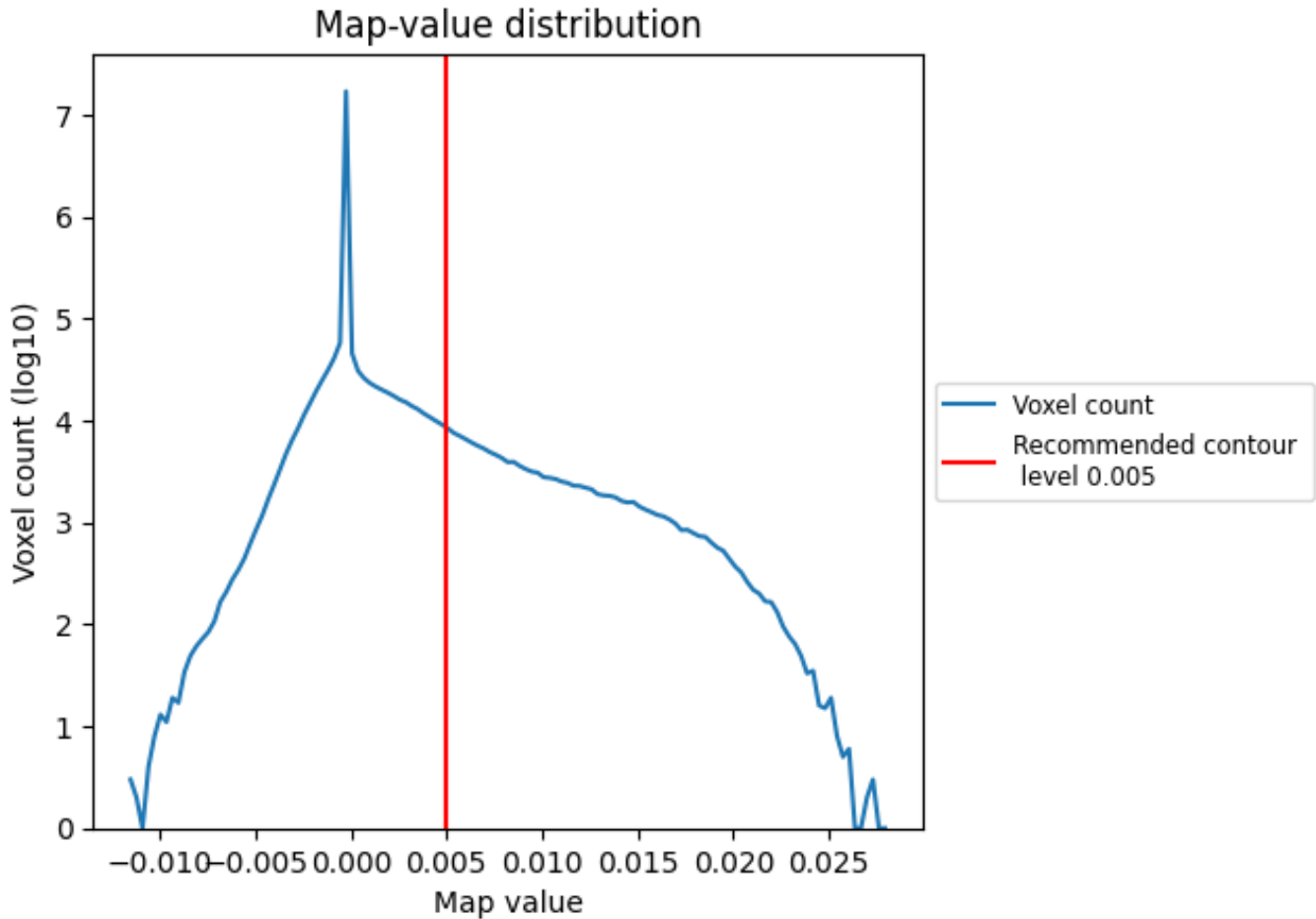
6.5 Mask visualisation

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

7 Map analysis [i](#)

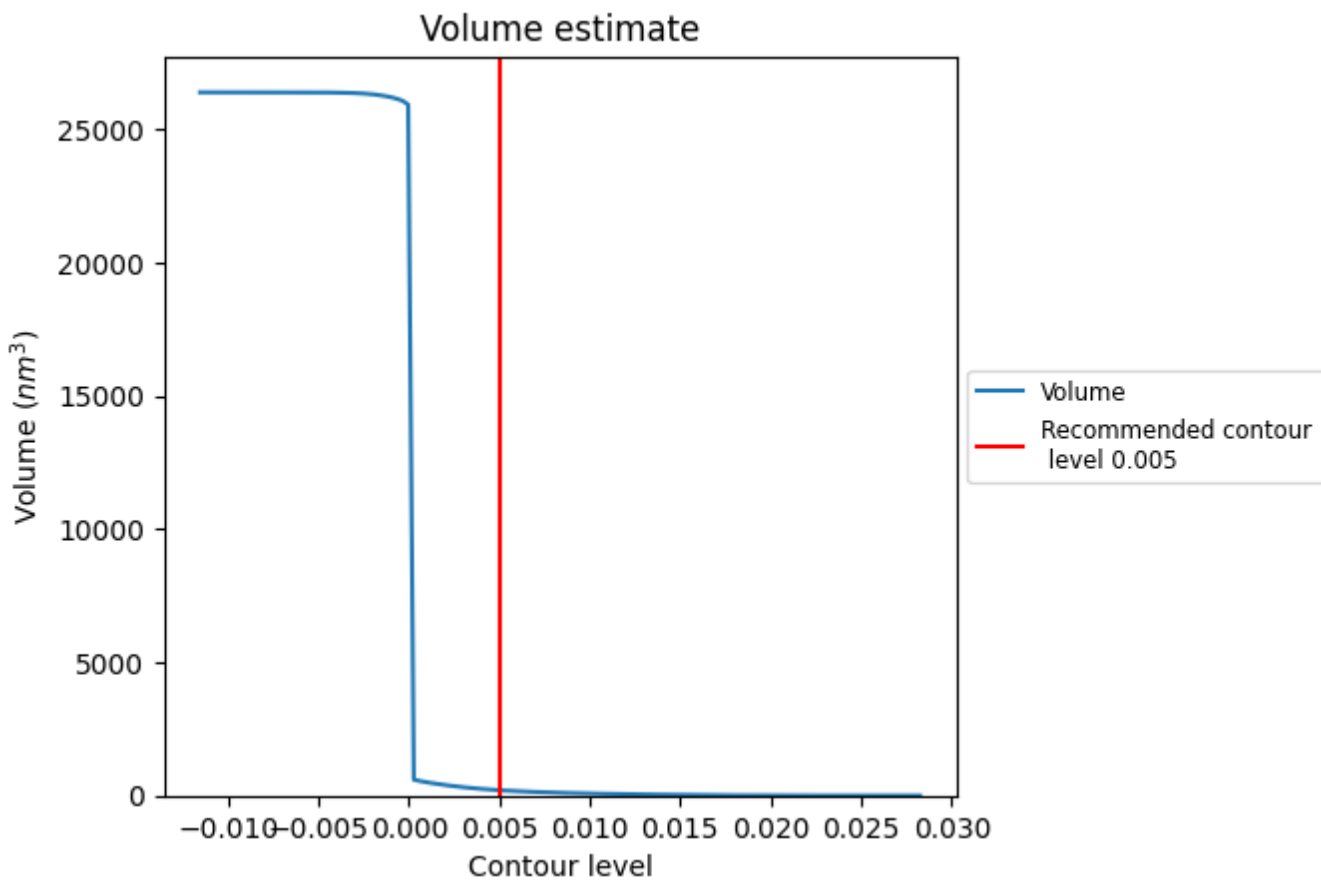
This section contains the results of statistical analysis of the map.

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.

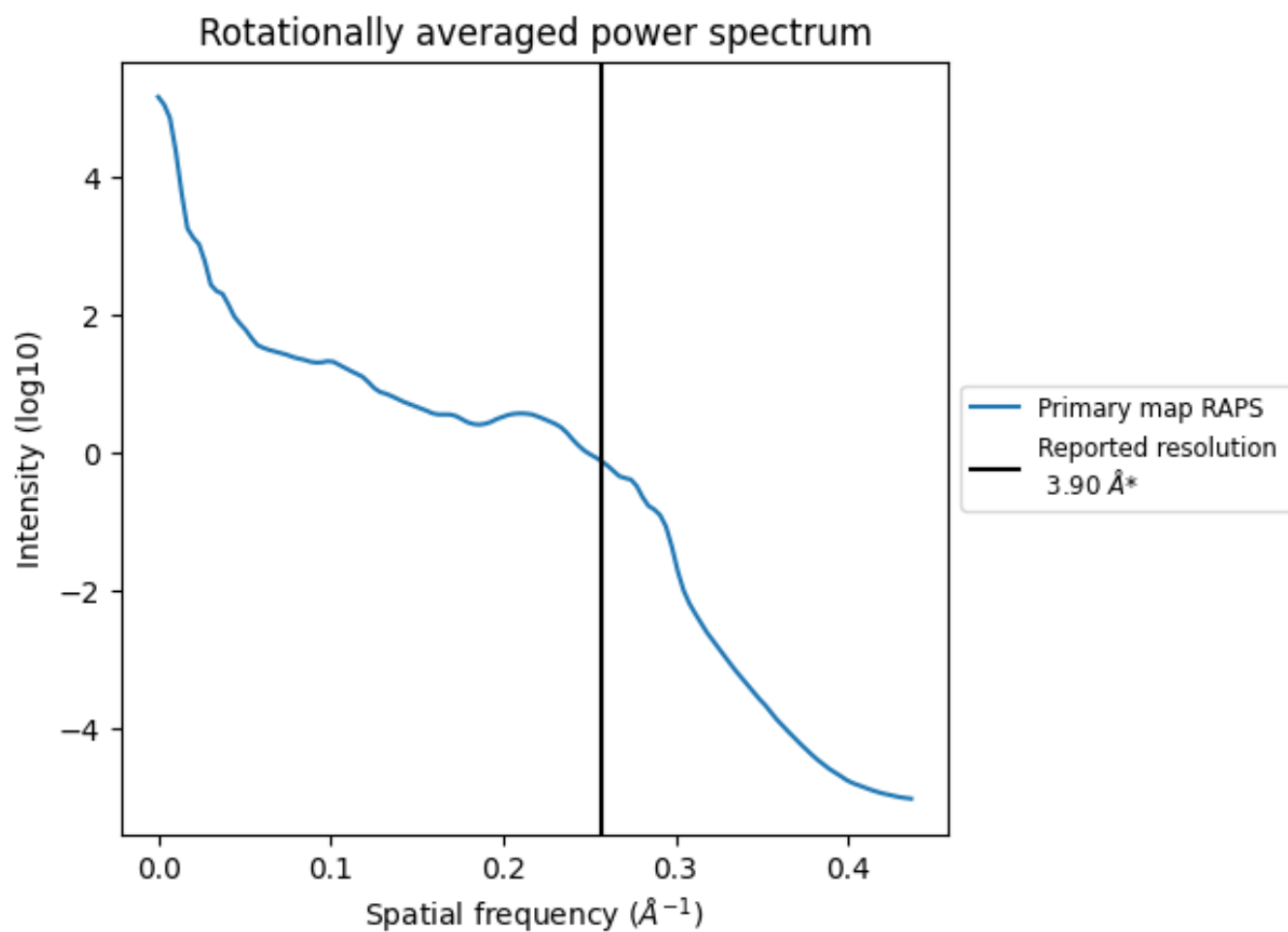
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 201 nm^3 ; this corresponds to an approximate mass of 182 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 [i](#)

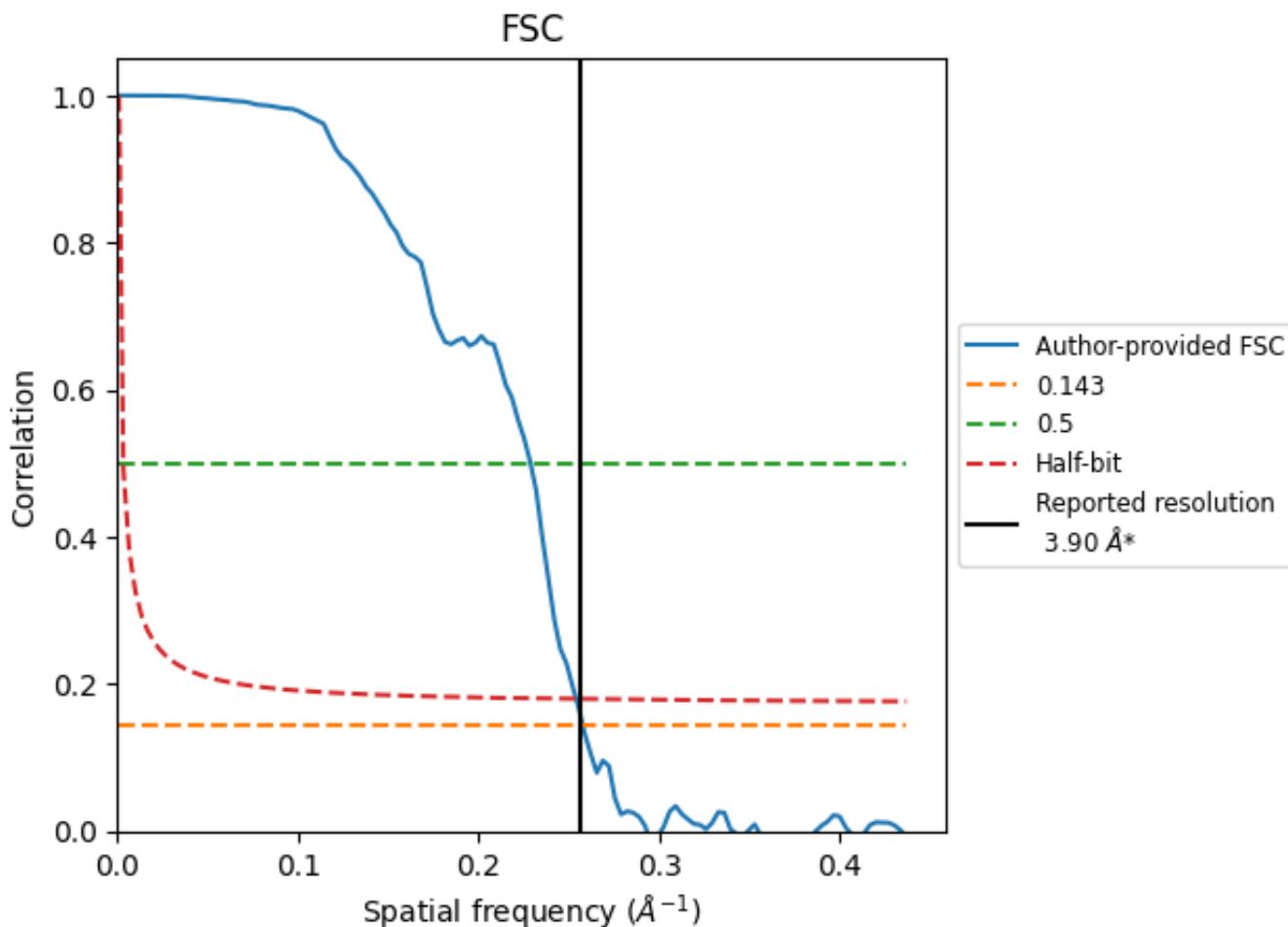


*Reported resolution corresponds to spatial frequency of 0.256\AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

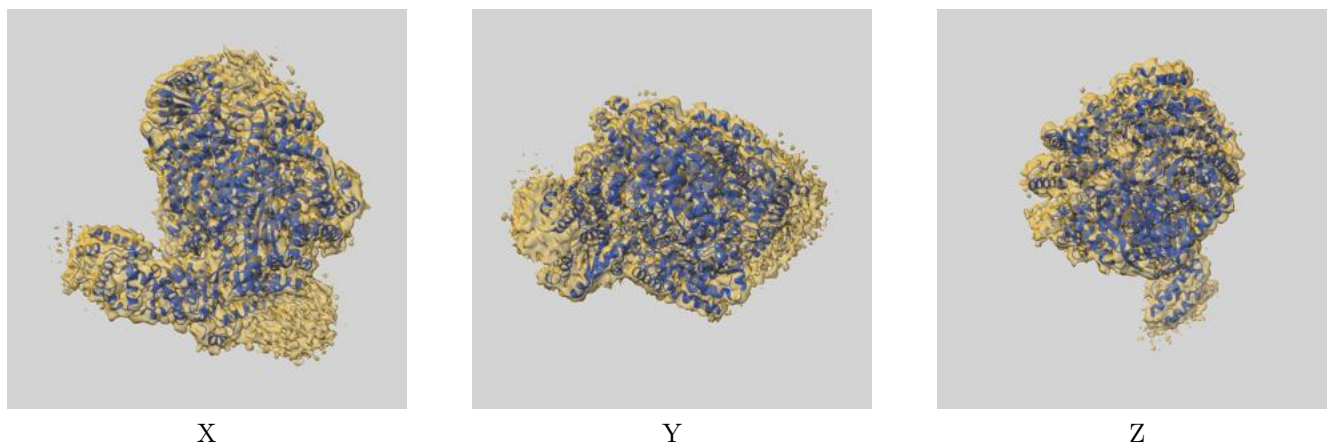
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.88	4.37	3.94
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

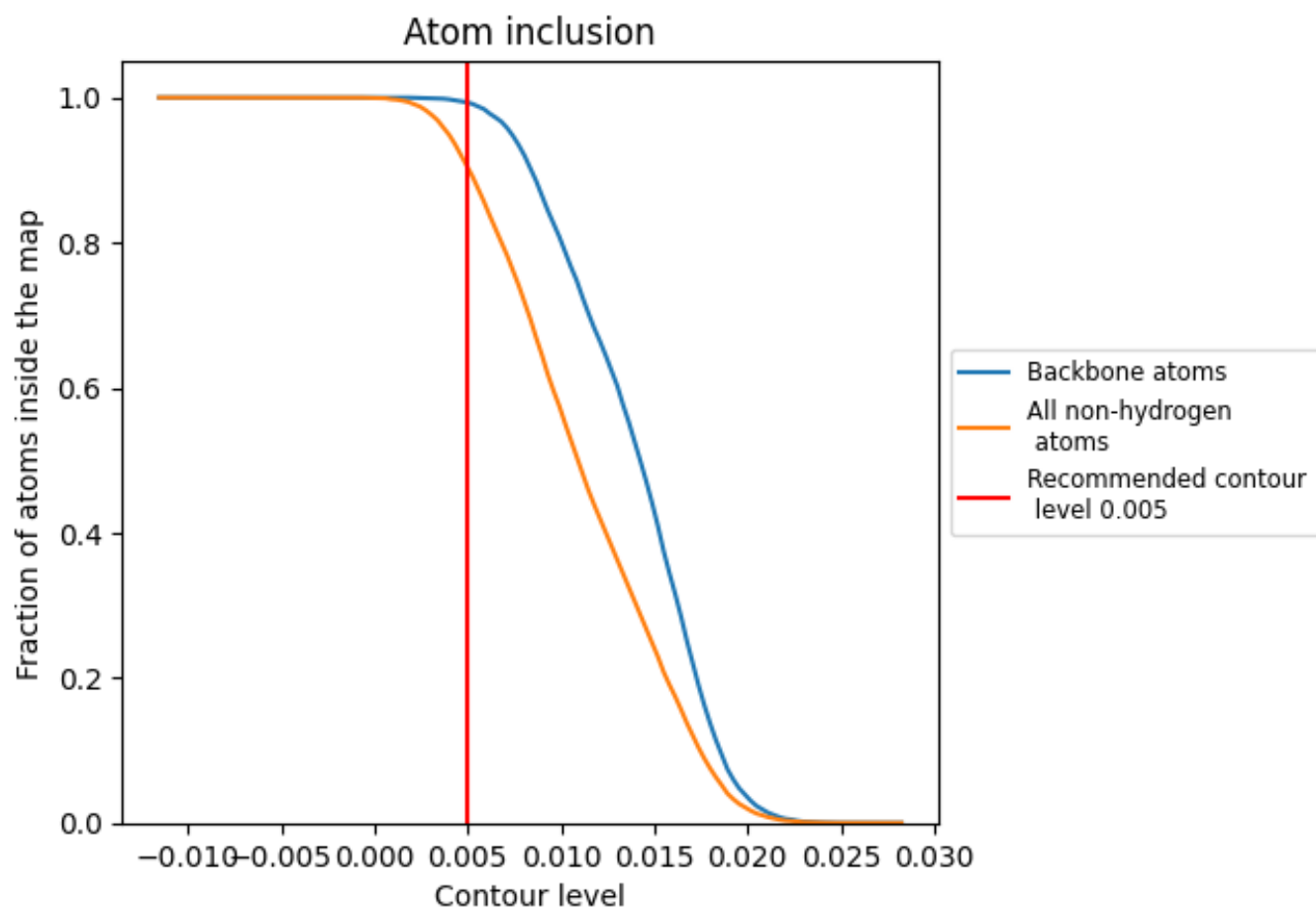
This section contains information regarding the fit between EMDB map EMD-13038 and PDB model 7ORI. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.005 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 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.