



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 08:48 PM UTC

PDB ID : 7X5L / pdb_00007x5l
EMDB ID : EMD-32125
Title : Tir-dsDNA complex, the initial binding state
Authors : Tan, Y.; Xu, C.; Yu, D.; Song, W.; Wu, B.; Schulze-Lefert, P.; Chai, J.
Deposited on : 2022-03-04
Resolution : 3.51 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

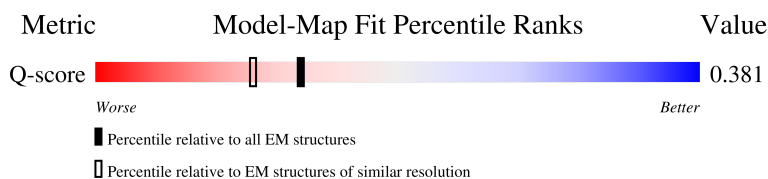
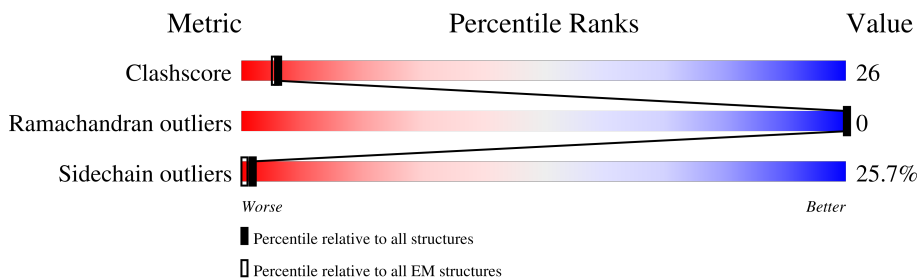
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.51 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	13950 (3.00 - 4.00)

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

Mol	Chain	Length	Quality of chain
1	A	8	25% 12% 88%
2	C	8	38% 38% 62%
3	B	204	11% 42% 30% 11% 17%
3	D	204	10% 35% 34% 14% 17%

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Mol	Chain	Length	Quality of chain
3	E	204	7% 33% 43% 8% 17%
3	F	204	10% 33% 37% 13% 17%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5924 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 DNA chain called DNA (5'-D(*AP*TP*AP*AP*AP*TP*TP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	8	Total	C	N	O	P	0	0
			145	70	26	42	7		

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*TP*AP*AP*TP*TP*AP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	8	Total	C	N	O	P	0	0
			144	70	23	44	7		

- Molecule 3 is a protein called Flax rust resistance protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	170	Total	C	N	O	S	0	0
			1411	904	246	256	5		
3	D	169	Total	C	N	O	S	0	0
			1402	899	245	253	5		
3	E	170	Total	C	N	O	S	0	0
			1411	904	246	256	5		
3	F	170	Total	C	N	O	S	0	0
			1411	904	246	256	5		

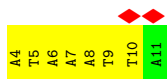
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	197	GLY	GLU	engineered mutation	UNP Q9XEH4
D	197	GLY	GLU	engineered mutation	UNP Q9XEH4
E	197	GLY	GLU	engineered mutation	UNP Q9XEH4
F	197	GLY	GLU	engineered mutation	UNP Q9XEH4

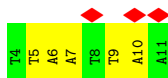
3 Residue-property plots

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.

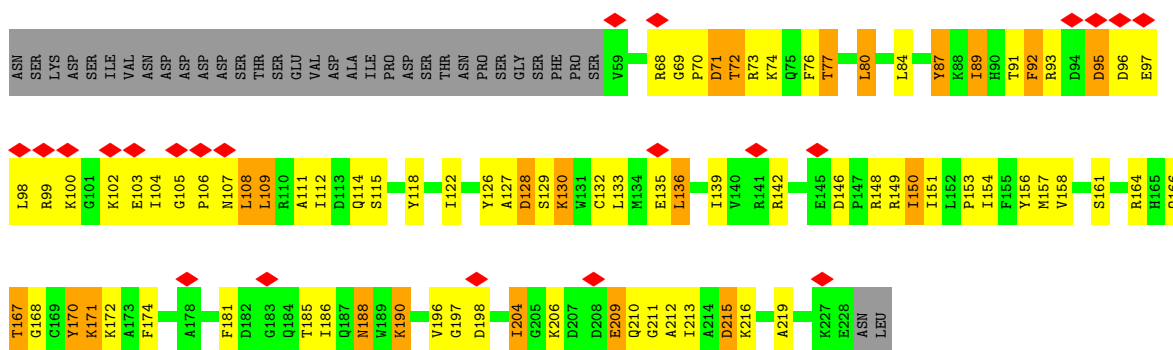
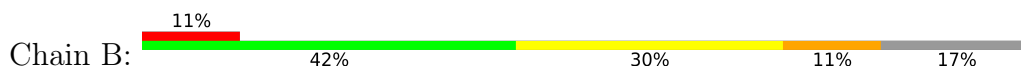
- Molecule 1: DNA (5'-D(*AP*TP*AP*AP*AP*TP*TP*A)-3')



- Molecule 2: DNA (5'-D(*TP*TP*AP*AP*TP*TP*AP*A)-3')

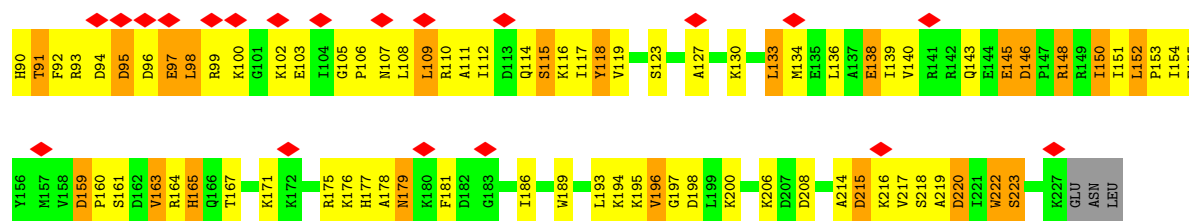


- Molecule 3: Flax rust resistance protein

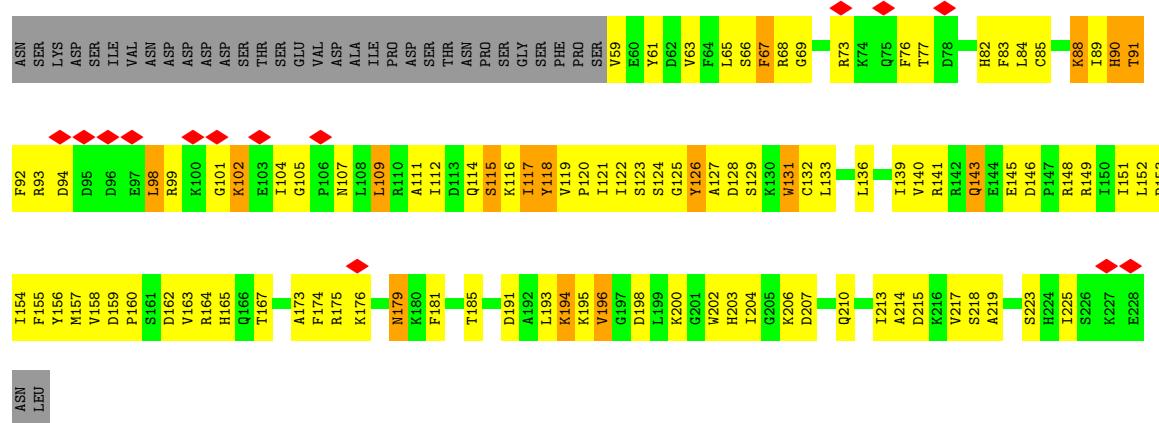


- Molecule 3: Flax rust resistance protein

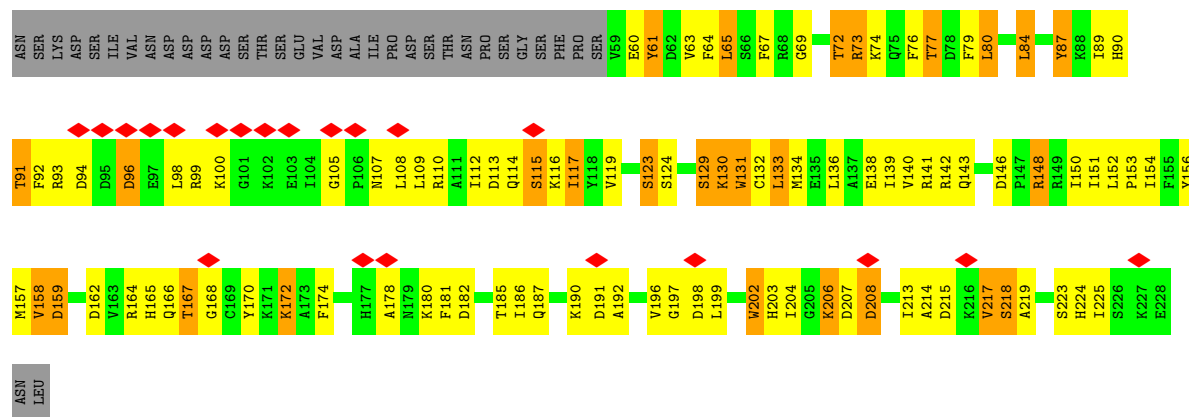




• Molecule 3: Flax rust resistance protein



• Molecule 3: Flax rust resistance protein



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-48.6°, rise=33.51 Å, axial sym=C1	Depositor
Number of segments used	211043	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.117	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	219.648, 219.648, 219.648	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.858, 0.858, 0.858	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	0/162	0.53	0/249
2	C	0.33	0/160	0.54	0/246
3	B	0.38	0/1447	0.62	0/1948
3	D	0.55	0/1438	0.77	0/1936
3	E	0.53	0/1447	0.78	0/1948
3	F	0.43	0/1447	0.61	0/1948
All	All	0.47	0/6101	0.69	0/8275

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	145	0	81	12	0
2	C	144	0	82	15	0
3	B	1411	0	1386	71	0
3	D	1402	0	1380	76	0
3	E	1411	0	1386	69	0
3	F	1411	0	1386	82	0
All	All	5924	0	5701	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 26.

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)
2:C:9:DT:H73	3:B:99:ARG:HB3	1.42	1.01
3:F:204:ILE:HD11	3:F:213:ILE:HG21	1.43	0.98
1:A:6:DA:C2	2:C:9:DT:H4'	2.02	0.94
3:B:129:SER:HB2	3:B:132:CYS:HB2	1.51	0.92
3:B:151:ILE:HG22	3:B:153:PRO:HD3	1.56	0.86
2:C:6:DA:O3'	3:E:175:ARG:NH2	2.12	0.82
2:C:10:DA:OP1	3:B:130:LYS:HD2	1.79	0.81
2:C:9:DT:C7	3:B:99:ARG:HB3	2.10	0.81
3:E:91:THR:OG1	3:E:92:PHE:N	2.13	0.79
3:B:105:GLY:HA2	3:B:109:LEU:HB2	1.64	0.79
3:B:128:ASP:OD1	3:B:128:ASP:N	2.16	0.76
3:D:91:THR:OG1	3:D:92:PHE:N	2.11	0.76
3:F:159:ASP:N	3:F:159:ASP:OD1	2.18	0.76
3:F:202:TRP:HE1	3:F:217:VAL:HG23	1.49	0.76
2:C:10:DA:OP1	3:B:130:LYS:NZ	2.16	0.75
3:B:95:ASP:N	3:B:95:ASP:OD1	2.20	0.75
3:D:164:ARG:O	3:D:165:HIS:ND1	2.20	0.74
3:B:112:ILE:O	3:B:115:SER:OG	2.03	0.74
3:D:159:ASP:OD1	3:D:159:ASP:N	2.20	0.73
3:B:204:ILE:HD11	3:B:213:ILE:HG21	1.71	0.73
3:D:160:PRO:O	3:D:164:ARG:NH2	2.22	0.72
1:A:7:DA:OP1	3:D:175:ARG:NH2	2.22	0.71
3:D:110:ARG:O	3:D:114:GLN:HB2	1.88	0.71
3:F:136:LEU:HA	3:F:139:ILE:HD12	1.72	0.71
3:E:136:LEU:HA	3:E:139:ILE:HD12	1.72	0.71
2:C:5:DT:H72	3:F:172:LYS:HD2	1.75	0.69
3:D:116:LYS:HB3	3:D:117:ILE:HD12	1.74	0.69
3:F:129:SER:OG	3:F:133:LEU:N	2.25	0.69
3:B:136:LEU:HA	3:B:139:ILE:HD12	1.75	0.69
3:B:196:VAL:O	3:B:198:ASP:N	2.25	0.69
1:A:4:DA:H8	3:D:176:LYS:HE3	1.58	0.67
3:D:106:PRO:O	3:D:110:ARG:NH2	2.26	0.67
1:A:6:DA:H2''	1:A:7:DA:H8	1.58	0.67
2:C:7:DA:P	3:E:175:ARG:HH22	2.18	0.67
3:F:187:GLN:NE2	3:F:191:ASP:OD2	2.28	0.67
2:C:10:DA:C8	3:B:70:PRO:HD3	2.29	0.66
3:B:146:ASP:OD2	3:B:148:ARG:NH1	2.28	0.66
3:E:156:TYR:O	3:E:158:VAL:N	2.28	0.65
3:B:164:ARG:NH2	3:B:197:GLY:O	2.29	0.65
3:F:129:SER:HG	3:F:132:CYS:N	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:151:ILE:HG22	3:D:152:LEU:H	1.62	0.65
3:B:98:LEU:HG	3:B:100:LYS:HG2	1.80	0.64
3:B:185:THR:O	3:B:188:ASN:ND2	2.30	0.64
3:D:105:GLY:O	3:D:109:LEU:HB2	1.96	0.64
3:F:115:SER:OG	3:F:116:LYS:N	2.30	0.64
3:D:145:GLU:OE1	3:D:146:ASP:N	2.30	0.64
3:B:68:ARG:HH12	3:B:128:ASP:HB2	1.63	0.63
3:B:129:SER:OG	3:B:133:LEU:N	2.31	0.63
3:B:72:THR:OG1	3:B:77:THR:OG1	2.16	0.63
3:D:92:PHE:CZ	3:D:108:LEU:HD21	2.33	0.63
3:F:91:THR:HG22	3:F:92:PHE:H	1.64	0.63
3:E:116:LYS:HG2	3:E:117:ILE:HG23	1.81	0.62
3:F:105:GLY:HA2	3:F:109:LEU:HD12	1.80	0.62
1:A:6:DA:N6	2:C:10:DA:OP2	2.33	0.62
3:B:209:GLU:H	3:B:209:GLU:CD	2.05	0.62
2:C:10:DA:OP1	3:B:130:LYS:CD	2.47	0.62
3:E:73:ARG:O	3:E:77:THR:HG23	2.00	0.62
3:D:171:LYS:O	3:D:175:ARG:HB3	1.99	0.62
1:A:8:DA:H2''	1:A:9:DT:H2'	1.81	0.62
3:E:118:TYR:HD2	3:E:139:ILE:HG23	1.65	0.62
3:B:107:ASN:OD1	3:B:108:LEU:N	2.31	0.61
3:E:118:TYR:CD2	3:E:139:ILE:HG23	2.36	0.61
3:B:209:GLU:OE1	3:B:209:GLU:N	2.29	0.61
3:D:110:ARG:O	3:D:114:GLN:CB	2.48	0.61
3:F:172:LYS:O	3:F:172:LYS:NZ	2.23	0.61
3:D:130:LYS:HB3	3:D:177:HIS:HE1	1.66	0.60
3:E:160:PRO:O	3:E:164:ARG:NH1	2.34	0.60
3:B:126:TYR:O	3:B:170:TYR:OH	2.19	0.60
3:D:68:ARG:HH11	3:D:69:GLY:H	1.49	0.60
1:A:6:DA:H2	2:C:9:DT:H4'	1.66	0.60
3:E:122:ILE:HG13	3:E:126:TYR:HD2	1.66	0.60
3:D:95:ASP:OD1	3:D:95:ASP:N	2.35	0.59
3:E:173:ALA:HA	3:E:176:LYS:HE2	1.84	0.59
3:B:204:ILE:HD11	3:B:213:ILE:HG13	1.85	0.59
1:A:5:DT:H2'	1:A:5:DT:O2	2.01	0.59
3:D:73:ARG:HH12	3:D:93:ARG:HD2	1.68	0.58
3:E:179:ASN:O	3:E:179:ASN:ND2	2.35	0.58
3:D:171:LYS:O	3:D:175:ARG:CB	2.52	0.58
3:F:166:GLN:N	3:F:166:GLN:OE1	2.37	0.58
3:B:72:THR:OG1	3:B:72:THR:O	2.22	0.57
3:B:129:SER:OG	3:B:129:SER:O	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:67:PHE:HE2	3:D:93:ARG:HG3	1.69	0.57
3:D:118:TYR:HD1	3:D:118:TYR:N	2.02	0.57
3:E:146:ASP:O	3:E:148:ARG:N	2.32	0.57
3:F:156:TYR:O	3:F:158:VAL:N	2.33	0.57
3:B:72:THR:HG1	3:B:77:THR:HG1	1.53	0.57
3:D:165:HIS:O	3:D:167:THR:OG1	2.22	0.57
3:E:101:GLY:O	3:E:102:LYS:NZ	2.27	0.56
3:D:118:TYR:N	3:D:118:TYR:CD1	2.72	0.56
3:F:167:THR:OG1	3:F:168:GLY:N	2.36	0.56
3:B:166:GLN:HG2	3:B:174:PHE:CE2	2.41	0.56
3:F:96:ASP:OD1	3:F:96:ASP:N	2.22	0.56
3:B:210:GLN:OE1	3:B:210:GLN:N	2.38	0.56
3:D:134:MET:HE2	3:D:189:TRP:HZ2	1.70	0.56
3:F:174:PHE:CE2	3:F:190:LYS:HG2	2.41	0.56
1:A:4:DA:C8	3:D:176:LYS:HE3	2.40	0.56
3:D:136:LEU:O	3:D:139:ILE:HB	2.04	0.56
3:F:196:VAL:O	3:F:198:ASP:N	2.37	0.56
3:F:164:ARG:NH1	3:F:197:GLY:O	2.37	0.56
3:F:141:ARG:HE	3:F:142:ARG:HD2	1.71	0.55
3:E:155:PHE:CD2	3:E:160:PRO:HB3	2.41	0.55
3:B:122:ILE:HG13	3:B:126:TYR:HD2	1.71	0.55
3:F:164:ARG:O	3:F:165:HIS:ND1	2.40	0.55
3:E:118:TYR:CD1	3:E:118:TYR:N	2.74	0.55
3:E:126:TYR:CE1	3:E:132:CYS:HB3	2.42	0.55
3:E:202:TRP:H	3:E:202:TRP:HE3	1.53	0.55
3:E:136:LEU:O	3:E:139:ILE:HB	2.07	0.55
3:E:98:LEU:HD11	3:E:104:ILE:HG13	1.88	0.55
3:D:218:SER:OG	3:D:219:ALA:N	2.40	0.54
3:F:129:SER:HG	3:F:131:TRP:H	1.55	0.54
3:B:215:ASP:OD1	3:B:216:LYS:N	2.40	0.54
3:B:129:SER:CB	3:B:132:CYS:HB2	2.31	0.54
3:F:214:ALA:O	3:F:217:VAL:HG12	2.08	0.54
3:E:155:PHE:HD2	3:E:160:PRO:HB3	1.72	0.54
3:B:104:ILE:HD12	3:B:106:PRO:HD2	1.90	0.54
3:B:142:ARG:O	3:B:149:ARG:NH2	2.30	0.54
3:E:67:PHE:HE2	3:E:93:ARG:HD2	1.72	0.54
3:F:151:ILE:HD11	3:F:199:LEU:HD13	1.89	0.54
3:B:157:MET:HE1	3:B:206:LYS:HB3	1.88	0.54
3:B:91:THR:OG1	3:B:92:PHE:N	2.39	0.54
3:D:159:ASP:C	3:D:161:SER:H	2.16	0.53
2:C:10:DA:OP1	3:B:130:LYS:CE	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:216:LYS:O	3:B:219:ALA:N	2.42	0.53
3:F:67:PHE:CE2	3:F:94:ASP:HB3	2.43	0.53
3:B:111:ALA:O	3:B:115:SER:N	2.41	0.53
3:F:153:PRO:HG3	3:F:196:VAL:HG13	1.91	0.53
3:E:128:ASP:OD1	3:E:129:SER:N	2.41	0.53
3:B:161:SER:HA	3:B:164:ARG:HH11	1.73	0.52
3:F:199:LEU:HD12	3:F:199:LEU:H	1.74	0.52
3:E:61:TYR:HD1	3:E:63:VAL:H	1.57	0.52
3:B:132:CYS:HA	3:B:135:GLU:CD	2.35	0.52
3:B:186:ILE:O	3:B:190:LYS:HD2	2.09	0.52
3:F:182:ASP:OD1	3:F:185:THR:N	2.43	0.52
3:D:146:ASP:CG	3:D:148:ARG:H	2.17	0.51
3:E:206:LYS:NZ	3:E:207:ASP:OD1	2.39	0.51
3:D:159:ASP:OD2	3:D:161:SER:OG	2.28	0.51
3:F:69:GLY:O	3:F:73:ARG:HB2	2.11	0.51
3:F:164:ARG:HD3	3:F:197:GLY:HA3	1.93	0.51
3:F:98:LEU:H	3:F:98:LEU:HD23	1.75	0.51
3:B:156:TYR:O	3:B:158:VAL:N	2.40	0.51
3:B:97:GLU:CD	3:B:97:GLU:H	2.19	0.51
3:F:146:ASP:O	3:F:148:ARG:N	2.43	0.51
3:B:104:ILE:HD11	3:B:107:ASN:ND2	2.25	0.51
3:F:164:ARG:HD3	3:F:197:GLY:O	2.12	0.50
3:F:92:PHE:CG	3:F:93:ARG:N	2.78	0.50
3:B:146:ASP:OD2	3:B:148:ARG:HB2	2.10	0.50
3:D:92:PHE:CG	3:D:93:ARG:N	2.79	0.50
3:B:167:THR:HG22	3:B:168:GLY:H	1.76	0.50
3:E:105:GLY:O	3:E:107:ASN:N	2.34	0.50
3:F:130:LYS:HZ1	3:F:131:TRP:CD1	2.29	0.50
3:D:164:ARG:HG3	3:D:197:GLY:HA3	1.93	0.49
3:E:111:ALA:O	3:E:115:SER:OG	2.12	0.49
3:D:61:TYR:HD1	3:D:90:HIS:CE1	2.30	0.49
3:D:87:TYR:CD2	3:D:222:TRP:HD1	2.30	0.49
3:E:151:ILE:HG22	3:E:153:PRO:HD3	1.95	0.49
3:F:98:LEU:C	3:F:100:LYS:H	2.19	0.49
3:E:143:GLN:O	3:E:145:GLU:N	2.44	0.49
3:F:218:SER:OG	3:F:219:ALA:N	2.44	0.49
3:E:118:TYR:N	3:E:118:TYR:HD1	2.10	0.49
3:B:122:ILE:HG13	3:B:126:TYR:CD2	2.48	0.48
3:F:116:LYS:HG2	3:F:117:ILE:HD12	1.94	0.48
3:F:87:TYR:HE2	3:F:218:SER:HG	1.60	0.48
3:F:186:ILE:HG22	3:F:190:LYS:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:112:ILE:O	3:F:115:SER:HB3	2.13	0.48
1:A:7:DA:N3	1:A:7:DA:H2'	2.28	0.48
3:B:171:LYS:O	3:B:174:PHE:N	2.47	0.48
3:F:61:TYR:CD2	3:F:92:PHE:HB2	2.49	0.48
3:B:69:GLY:O	3:B:71:ASP:N	2.45	0.48
2:C:9:DT:H5''	3:B:99:ARG:NH2	2.29	0.48
3:B:132:CYS:O	3:B:135:GLU:HB2	2.14	0.48
3:D:130:LYS:HB3	3:D:177:HIS:CE1	2.47	0.48
3:E:129:SER:HB3	3:E:132:CYS:HB2	1.96	0.47
3:F:168:GLY:C	3:F:170:TYR:H	2.22	0.47
3:D:220:ASP:O	3:D:223:SER:N	2.47	0.47
3:D:98:LEU:HD13	3:D:100:LYS:H	1.78	0.47
3:F:72:THR:O	3:F:72:THR:OG1	2.32	0.47
3:D:151:ILE:HG22	3:D:152:LEU:N	2.27	0.47
3:D:154:ILE:HD11	3:D:217:VAL:HG21	1.97	0.47
3:F:123:SER:OG	3:F:124:SER:N	2.47	0.47
3:D:76:PHE:O	3:D:77:THR:C	2.57	0.46
3:D:178:ALA:O	3:D:181:PHE:N	2.46	0.46
3:F:117:ILE:HD13	3:F:225:ILE:HD11	1.96	0.46
3:E:143:GLN:NE2	3:E:149:ARG:O	2.43	0.46
3:F:129:SER:OG	3:F:132:CYS:N	2.47	0.46
3:D:64:PHE:HE2	3:D:139:ILE:HD11	1.81	0.46
3:F:146:ASP:OD1	3:F:148:ARG:HB2	2.15	0.46
3:E:200:LYS:HA	3:E:200:LYS:HD3	1.65	0.46
3:E:206:LYS:HG2	3:E:206:LYS:O	2.14	0.46
3:E:68:ARG:HG3	3:E:69:GLY:H	1.81	0.46
3:F:84:LEU:HD12	3:F:84:LEU:HA	1.78	0.46
3:D:60:GLU:HG2	3:D:61:TYR:O	2.15	0.46
3:D:98:LEU:C	3:D:100:LYS:H	2.23	0.46
3:F:89:ILE:O	3:F:91:THR:OG1	2.33	0.46
3:F:157:MET:HE1	3:F:206:LYS:HG2	1.98	0.46
3:B:76:PHE:HE1	3:B:80:LEU:HD23	1.81	0.46
3:D:111:ALA:HA	3:D:114:GLN:HB3	1.99	0.45
3:D:96:ASP:HA	3:D:97:GLU:OE2	2.16	0.45
3:F:130:LYS:NZ	3:F:131:TRP:HB2	2.30	0.45
3:F:61:TYR:CE2	3:F:92:PHE:HB2	2.52	0.45
3:E:88:LYS:HE3	3:E:88:LYS:HB2	1.71	0.45
3:B:136:LEU:O	3:B:139:ILE:HB	2.17	0.45
3:E:61:TYR:HB2	3:E:90:HIS:O	2.17	0.45
3:F:138:GLU:OE2	3:F:142:ARG:HD3	2.17	0.45
3:D:72:THR:O	3:D:72:THR:OG1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:152:LEU:N	3:D:153:PRO:HD3	2.32	0.45
3:D:179:ASN:C	3:D:179:ASN:HD22	2.24	0.45
3:F:181:PHE:HB3	3:F:182:ASP:H	1.60	0.45
3:D:214:ALA:O	3:D:217:VAL:HG12	2.17	0.44
3:B:209:GLU:C	3:B:211:GLY:H	2.25	0.44
3:E:204:ILE:HD11	3:E:213:ILE:HG21	2.00	0.44
3:D:215:ASP:OD1	3:D:216:LYS:N	2.51	0.44
3:D:98:LEU:HB3	3:D:99:ARG:H	1.65	0.44
3:E:196:VAL:O	3:E:198:ASP:N	2.51	0.44
3:B:118:TYR:HE2	3:B:139:ILE:HG12	1.83	0.44
3:D:196:VAL:O	3:D:198:ASP:N	2.51	0.44
3:F:63:VAL:HB	3:F:91:THR:HG23	1.99	0.44
3:F:196:VAL:C	3:F:198:ASP:H	2.26	0.44
3:F:129:SER:HG	3:F:132:CYS:H	1.64	0.44
1:A:10:DT:O4'	3:F:99:ARG:NH1	2.51	0.44
3:D:127:ALA:HA	3:D:133:LEU:HD23	2.00	0.44
3:E:119:VAL:N	3:E:120:PRO:HD3	2.32	0.44
3:B:108:LEU:HD12	3:B:108:LEU:HA	1.85	0.43
3:E:101:GLY:C	3:E:102:LYS:HD2	2.43	0.43
3:F:174:PHE:O	3:F:178:ALA:N	2.51	0.43
3:D:67:PHE:CE2	3:D:93:ARG:HG3	2.50	0.43
3:D:108:LEU:O	3:D:112:ILE:HG12	2.18	0.43
3:B:118:TYR:CE2	3:B:139:ILE:HG23	2.53	0.43
3:D:80:LEU:HD22	3:D:80:LEU:HA	1.84	0.43
3:E:82:HIS:O	3:E:85:CYS:N	2.51	0.43
3:E:223:SER:C	3:E:225:ILE:H	2.27	0.43
3:F:80:LEU:HD11	3:F:217:VAL:HG11	2.00	0.43
3:D:139:ILE:HD13	3:D:139:ILE:HA	1.82	0.43
3:E:109:LEU:HD13	3:E:109:LEU:HA	1.81	0.43
3:F:76:PHE:O	3:F:77:THR:C	2.60	0.43
3:B:87:TYR:HB3	3:B:89:ILE:HD11	2.00	0.43
3:D:118:TYR:CD2	3:D:139:ILE:HG23	2.54	0.43
3:E:66:SER:OG	3:E:67:PHE:N	2.51	0.43
3:F:105:GLY:O	3:F:107:ASN:N	2.47	0.43
3:F:64:PHE:CG	3:F:65:LEU:N	2.87	0.43
3:B:68:ARG:HD2	3:B:68:ARG:HA	1.81	0.43
3:B:112:ILE:HD13	3:B:112:ILE:HA	1.85	0.42
3:B:150:ILE:HD13	3:B:150:ILE:H	1.83	0.42
3:E:156:TYR:CD1	3:E:156:TYR:C	2.97	0.42
3:E:191:ASP:O	3:E:194:LYS:HB3	2.20	0.42
3:F:151:ILE:HG13	3:F:153:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:64:PHE:CE2	3:D:139:ILE:HD11	2.54	0.42
3:D:155:PHE:CD1	3:D:160:PRO:HG3	2.54	0.42
3:E:105:GLY:HA2	3:E:109:LEU:HD23	2.01	0.42
3:E:207:ASP:OD1	3:E:207:ASP:N	2.52	0.42
3:F:146:ASP:C	3:F:148:ARG:H	2.27	0.42
3:F:180:LYS:HD2	3:F:180:LYS:HA	1.83	0.42
3:E:139:ILE:HG22	3:E:140:VAL:N	2.34	0.42
3:E:146:ASP:OD1	3:E:146:ASP:N	2.50	0.42
3:F:116:LYS:C	3:F:117:ILE:HD12	2.45	0.42
3:F:157:MET:HE1	3:F:206:LYS:HA	2.02	0.42
3:D:159:ASP:C	3:D:161:SER:N	2.76	0.42
3:E:159:ASP:HB2	3:E:162:ASP:OD1	2.18	0.42
3:E:193:LEU:HD12	3:E:193:LEU:HA	1.83	0.42
3:D:196:VAL:C	3:D:198:ASP:H	2.27	0.42
3:E:124:SER:HB2	3:E:158:VAL:HB	2.01	0.42
3:F:74:LYS:HE3	3:F:74:LYS:HB2	1.83	0.42
3:D:150:ILE:H	3:D:150:ILE:HG12	1.66	0.42
3:E:82:HIS:O	3:E:83:PHE:C	2.62	0.42
3:E:196:VAL:C	3:E:198:ASP:H	2.27	0.42
3:D:98:LEU:HD22	3:D:98:LEU:HA	1.83	0.42
3:D:155:PHE:CE1	3:D:160:PRO:HG3	2.54	0.42
3:E:143:GLN:OE1	3:E:151:ILE:HG12	2.20	0.42
3:B:127:ALA:C	3:B:129:SER:H	2.29	0.41
3:D:163:VAL:C	3:D:165:HIS:H	2.27	0.41
3:E:218:SER:OG	3:E:219:ALA:N	2.52	0.41
3:B:212:ALA:O	3:B:215:ASP:N	2.53	0.41
3:D:94:ASP:OD1	3:D:95:ASP:N	2.52	0.41
3:D:138:GLU:N	3:D:138:GLU:OE1	2.53	0.41
3:F:105:GLY:HA2	3:F:109:LEU:HB2	2.02	0.41
3:D:115:SER:HB2	3:D:116:LYS:H	1.52	0.41
3:F:131:TRP:O	3:F:134:MET:HG2	2.20	0.41
3:B:112:ILE:HG23	3:B:118:TYR:OH	2.21	0.41
3:E:210:GLN:HE21	3:E:210:GLN:HB2	1.59	0.41
3:F:60:GLU:CD	3:F:114:GLN:HG2	2.45	0.41
3:F:76:PHE:HE1	3:F:80:LEU:HD23	1.86	0.41
3:F:182:ASP:O	3:F:185:THR:HG22	2.20	0.41
3:B:130:LYS:HE3	3:B:130:LYS:HB2	1.95	0.41
3:E:68:ARG:HD2	3:E:68:ARG:HA	1.88	0.41
3:E:125:GLY:C	3:E:127:ALA:H	2.28	0.41
3:E:126:TYR:HE1	3:E:132:CYS:HB3	1.83	0.41
1:A:10:DT:O5'	3:F:130:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:193:LEU:HD12	3:D:193:LEU:HA	1.71	0.41
3:D:200:LYS:HD3	3:D:200:LYS:HA	1.65	0.41
3:E:68:ARG:HG3	3:E:69:GLY:N	2.36	0.41
3:E:214:ALA:O	3:E:217:VAL:HG12	2.21	0.41
3:F:140:VAL:HG11	3:F:192:ALA:HB1	2.03	0.41
3:F:162:ASP:OD1	3:F:162:ASP:N	2.54	0.41
3:F:202:TRP:NE1	3:F:217:VAL:HG23	2.26	0.41
3:E:121:ILE:HD13	3:E:154:ILE:HB	2.02	0.41
3:E:125:GLY:O	3:E:127:ALA:N	2.47	0.41
3:B:132:CYS:HA	3:B:135:GLU:CG	2.51	0.40
3:D:105:GLY:O	3:D:107:ASN:N	2.47	0.40
3:E:98:LEU:HD12	3:E:131:TRP:HZ2	1.87	0.40
3:F:207:ASP:O	3:F:208:ASP:C	2.64	0.40
3:F:174:PHE:HE2	3:F:190:LYS:HG2	1.84	0.40
2:C:9:DT:H2'	3:B:130:LYS:NZ	2.37	0.40
3:D:64:PHE:CZ	3:D:65:LEU:O	2.75	0.40
3:D:76:PHE:O	3:D:79:PHE:N	2.55	0.40
3:E:156:TYR:CD1	3:E:157:MET:HB2	2.56	0.40
3:F:130:LYS:HZ2	3:F:131:TRP:HB2	1.87	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	
3	B	168/204 (82%)	121 (72%)	47 (28%)	0	100	100
3	D	167/204 (82%)	126 (75%)	41 (25%)	0	100	100
3	E	168/204 (82%)	124 (74%)	44 (26%)	0	100	100
3	F	168/204 (82%)	120 (71%)	48 (29%)	0	100	100
All	All	671/816 (82%)	491 (73%)	180 (27%)	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	
3	B	151/183 (82%)	118 (78%)	33 (22%)	1	6
3	D	150/183 (82%)	107 (71%)	43 (29%)	0	3
3	E	151/183 (82%)	113 (75%)	38 (25%)	0	4
3	F	151/183 (82%)	110 (73%)	41 (27%)	0	3
All	All	603/732 (82%)	448 (74%)	155 (26%)	2	3

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	71	ASP
3	B	72	THR
3	B	73	ARG
3	B	74	LYS
3	B	77	THR
3	B	80	LEU
3	B	84	LEU
3	B	87	TYR
3	B	89	ILE
3	B	92	PHE
3	B	93	ARG
3	B	95	ASP
3	B	96	ASP
3	B	102	LYS
3	B	103	GLU
3	B	108	LEU
3	B	109	LEU
3	B	114	GLN
3	B	128	ASP
3	B	130	LYS
3	B	136	LEU
3	B	150	ILE

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Mol	Chain	Res	Type
3	B	154	ILE
3	B	167	THR
3	B	170	TYR
3	B	171	LYS
3	B	172	LYS
3	B	181	PHE
3	B	188	ASN
3	B	190	LYS
3	B	204	ILE
3	B	209	GLU
3	B	215	ASP
3	D	65	LEU
3	D	67	PHE
3	D	72	THR
3	D	80	LEU
3	D	82	HIS
3	D	84	LEU
3	D	86	TYR
3	D	87	TYR
3	D	89	ILE
3	D	91	THR
3	D	95	ASP
3	D	97	GLU
3	D	98	LEU
3	D	102	LYS
3	D	103	GLU
3	D	109	LEU
3	D	115	SER
3	D	118	TYR
3	D	119	VAL
3	D	123	SER
3	D	133	LEU
3	D	138	GLU
3	D	140	VAL
3	D	143	GLN
3	D	145	GLU
3	D	146	ASP
3	D	148	ARG
3	D	150	ILE
3	D	152	LEU
3	D	159	ASP
3	D	163	VAL

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Mol	Chain	Res	Type
3	D	165	HIS
3	D	179	ASN
3	D	186	ILE
3	D	194	LYS
3	D	195	LYS
3	D	196	VAL
3	D	206	LYS
3	D	208	ASP
3	D	215	ASP
3	D	220	ASP
3	D	222	TRP
3	D	223	SER
3	E	59	VAL
3	E	65	LEU
3	E	67	PHE
3	E	76	PHE
3	E	84	LEU
3	E	88	LYS
3	E	89	ILE
3	E	90	HIS
3	E	91	THR
3	E	94	ASP
3	E	98	LEU
3	E	99	ARG
3	E	102	LYS
3	E	109	LEU
3	E	112	ILE
3	E	114	GLN
3	E	115	SER
3	E	117	ILE
3	E	118	TYR
3	E	123	SER
3	E	126	TYR
3	E	131	TRP
3	E	133	LEU
3	E	141	ARG
3	E	143	GLN
3	E	152	LEU
3	E	163	VAL
3	E	165	HIS
3	E	167	THR
3	E	174	PHE

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Mol	Chain	Res	Type
3	E	179	ASN
3	E	181	PHE
3	E	185	THR
3	E	194	LYS
3	E	195	LYS
3	E	196	VAL
3	E	203	HIS
3	E	215	ASP
3	F	61	TYR
3	F	65	LEU
3	F	72	THR
3	F	73	ARG
3	F	77	THR
3	F	79	PHE
3	F	80	LEU
3	F	84	LEU
3	F	87	TYR
3	F	90	HIS
3	F	91	THR
3	F	96	ASP
3	F	108	LEU
3	F	110	ARG
3	F	113	ASP
3	F	115	SER
3	F	117	ILE
3	F	119	VAL
3	F	123	SER
3	F	129	SER
3	F	130	LYS
3	F	131	TRP
3	F	133	LEU
3	F	143	GLN
3	F	148	ARG
3	F	150	ILE
3	F	152	LEU
3	F	154	ILE
3	F	158	VAL
3	F	159	ASP
3	F	167	THR
3	F	172	LYS
3	F	202	TRP
3	F	203	HIS

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Mol	Chain	Res	Type
3	F	206	LYS
3	F	208	ASP
3	F	215	ASP
3	F	217	VAL
3	F	218	SER
3	F	223	SER
3	F	224	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	90	HIS

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.

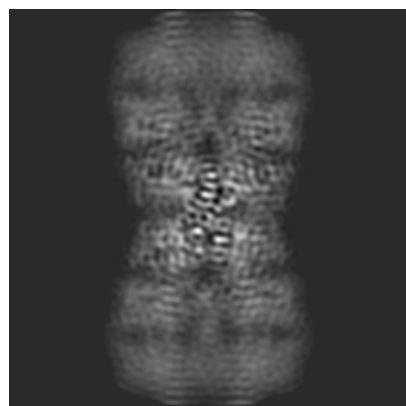
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32125. These allow visual inspection of the internal detail of the map and identification of artifacts.

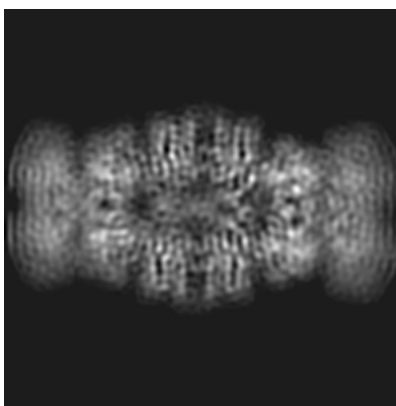
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

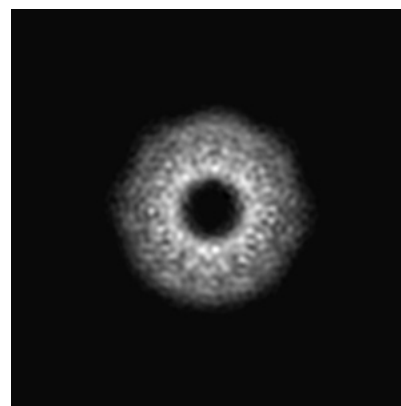
6.1.1 Primary map



X



Y

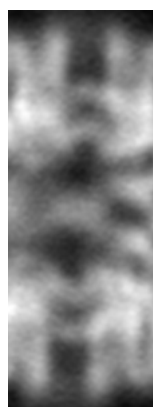


Z

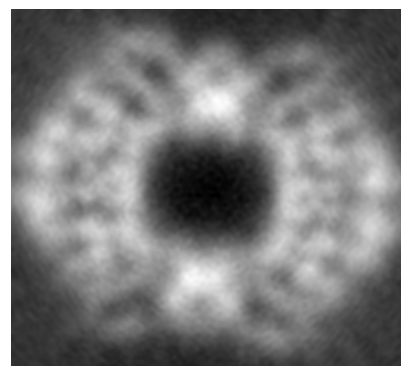
6.1.2 Raw map



X



Y

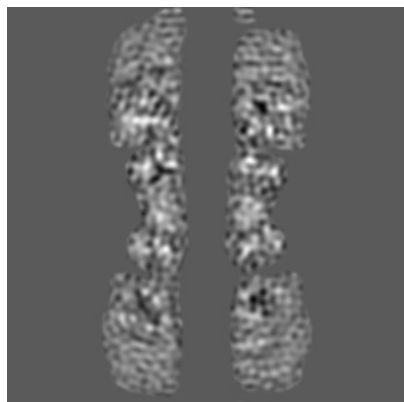


Z

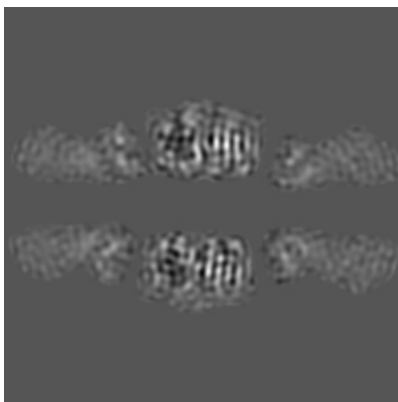
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

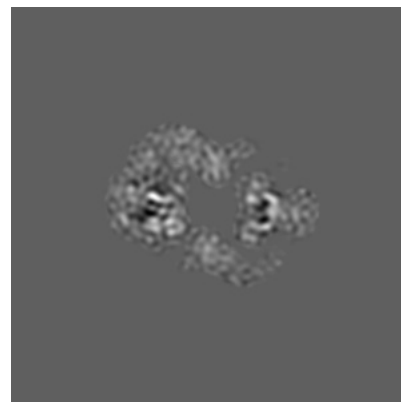
6.2.1 Primary map



X Index: 128

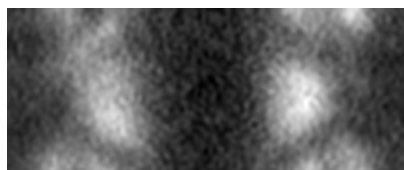


Y Index: 128

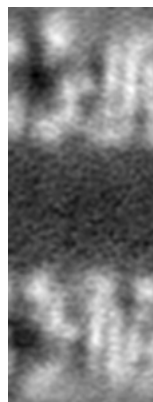


Z Index: 128

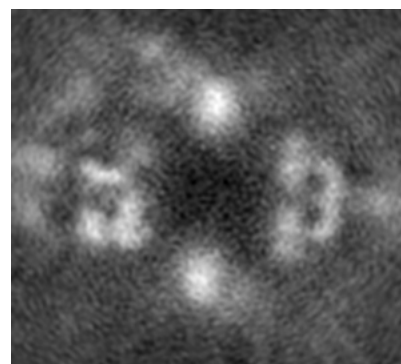
6.2.2 Raw map



X Index: 63



Y Index: 56

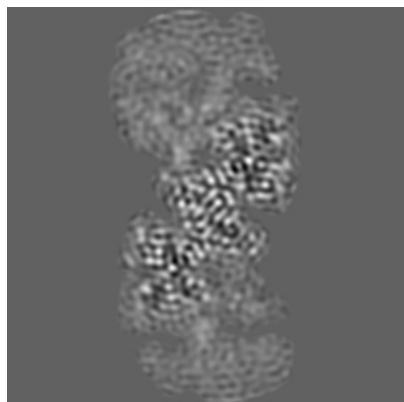


Z Index: 23

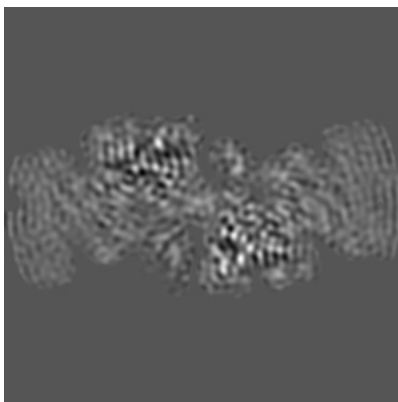
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

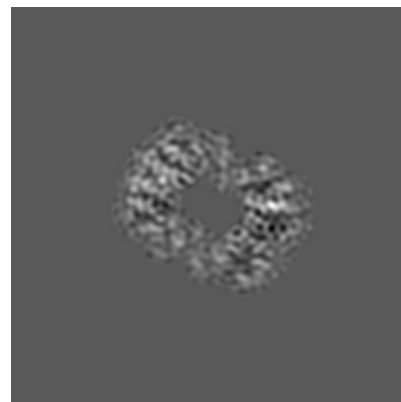
6.3.1 Primary map



X Index: 102



Y Index: 155

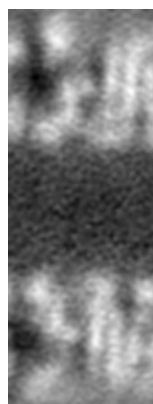


Z Index: 142

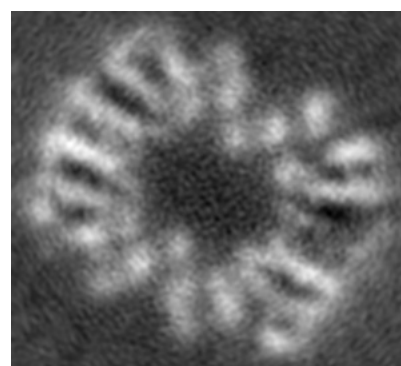
6.3.2 Raw map



X Index: 65



Y Index: 56

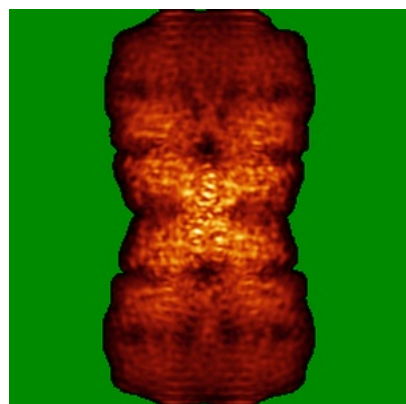


Z Index: 39

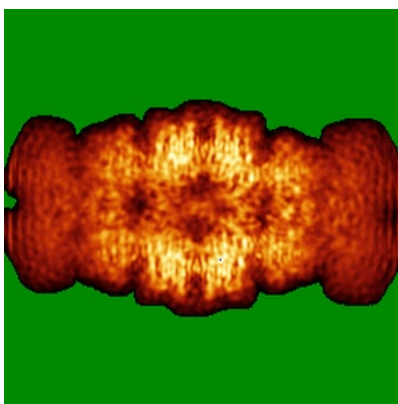
The images above show the largest variance slices of the map in three orthogonal directions.

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

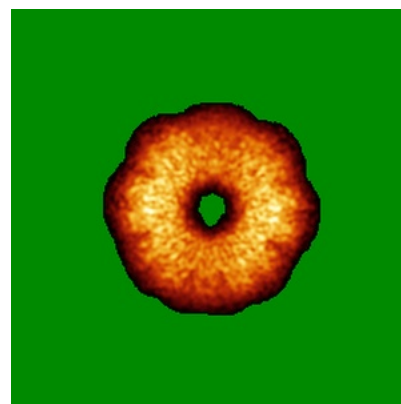
6.4.1 Primary map



X

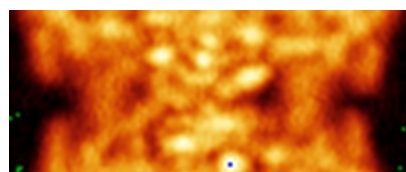


Y

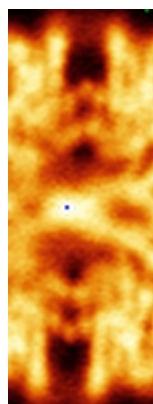


Z

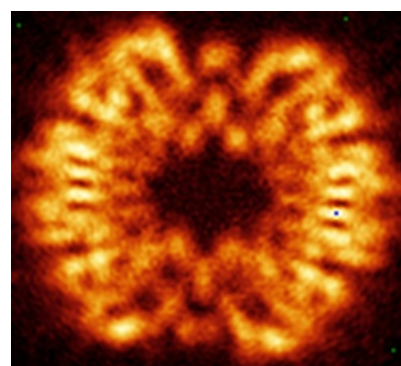
6.4.2 Raw map



X



Y

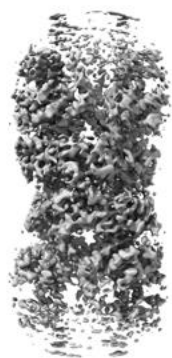


Z

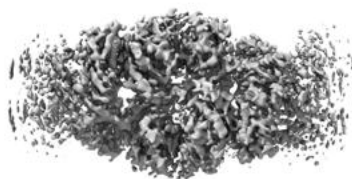
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



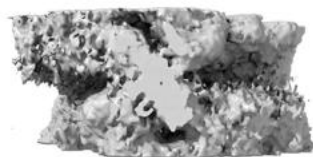
Y



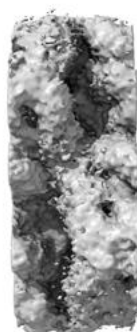
Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

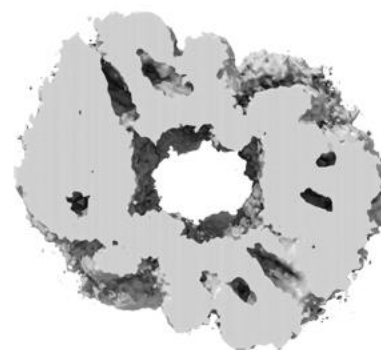
6.5.2 Raw map



X



Y



Z

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.

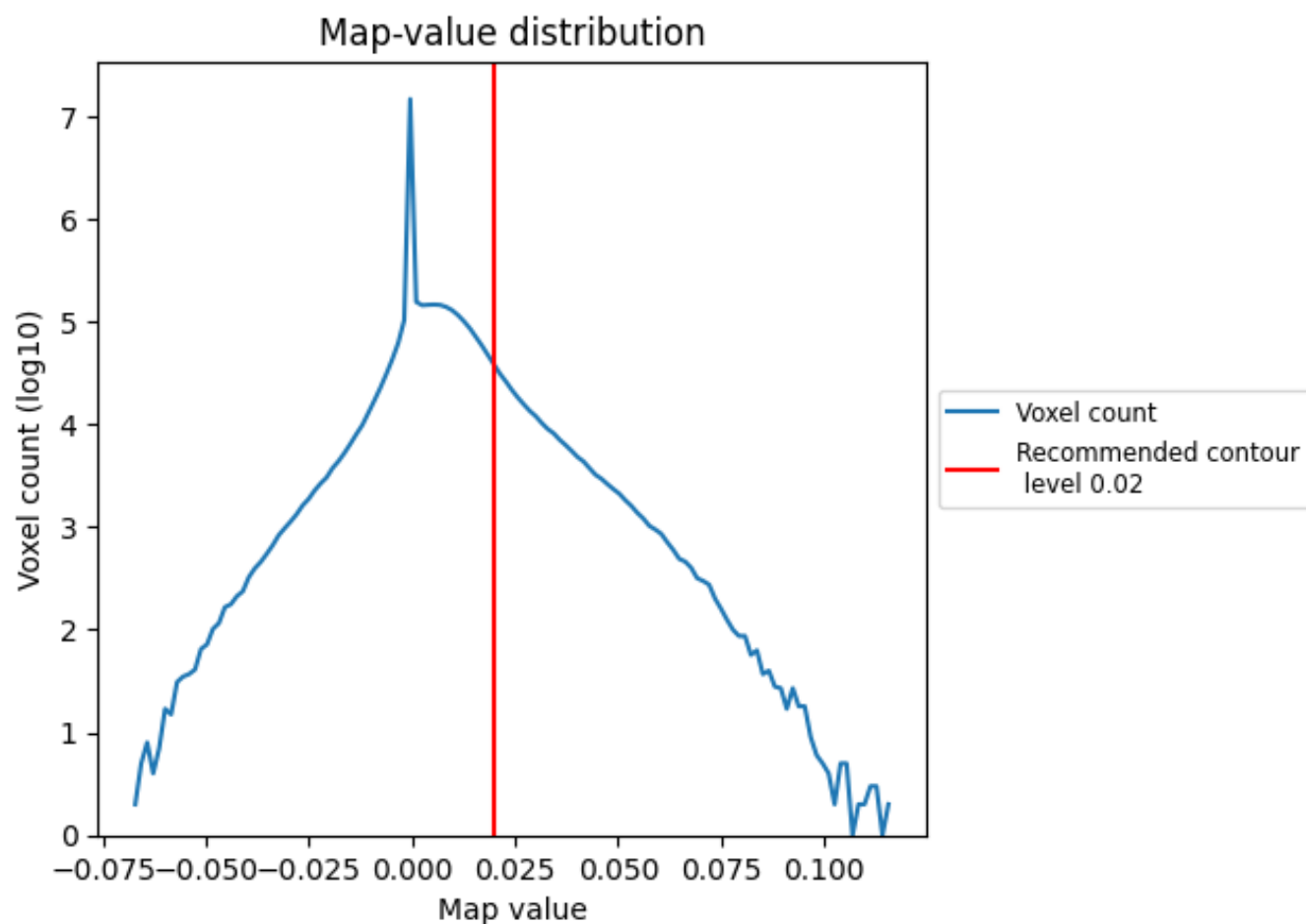
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

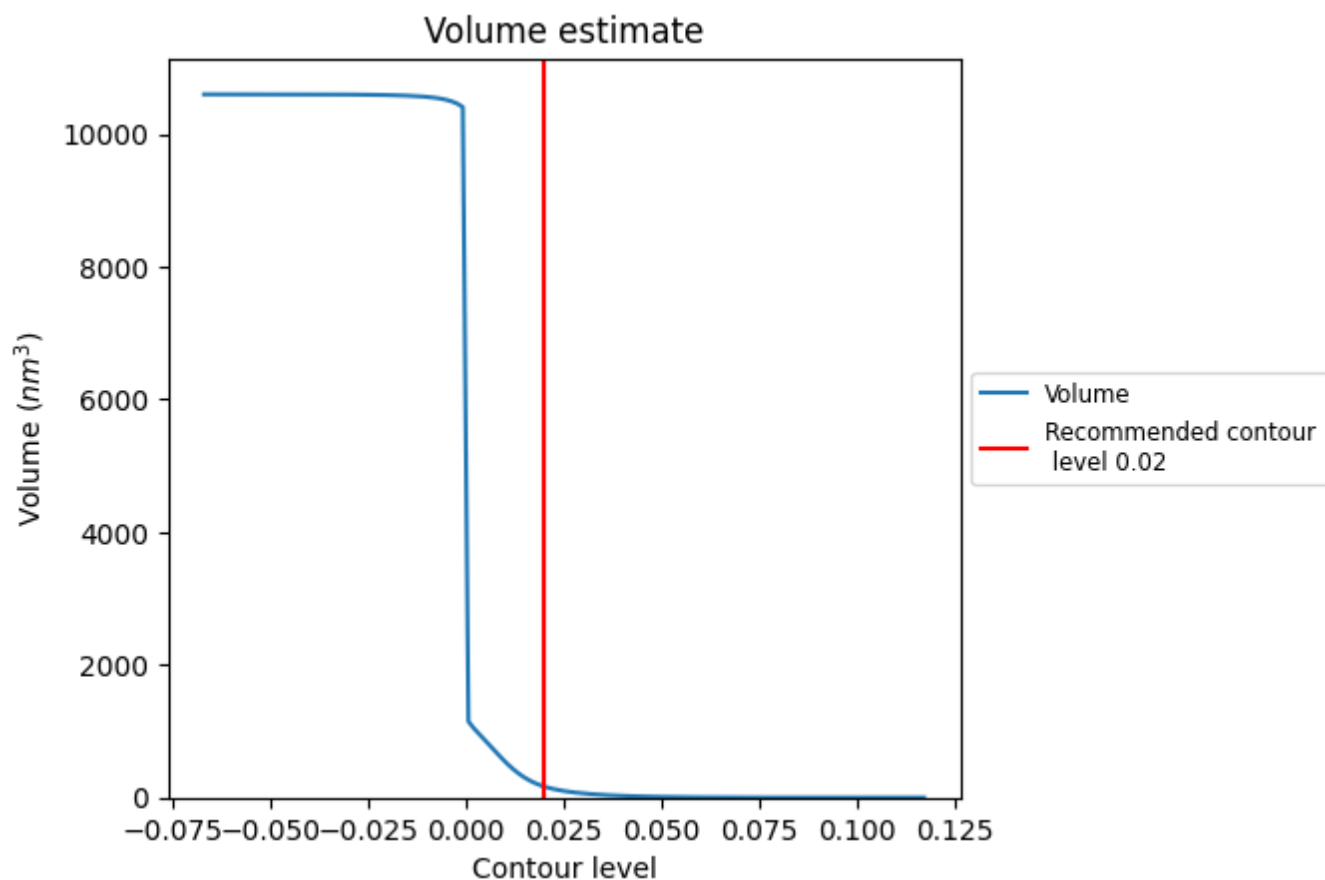
This section contains the results of statistical analysis of the map.

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.

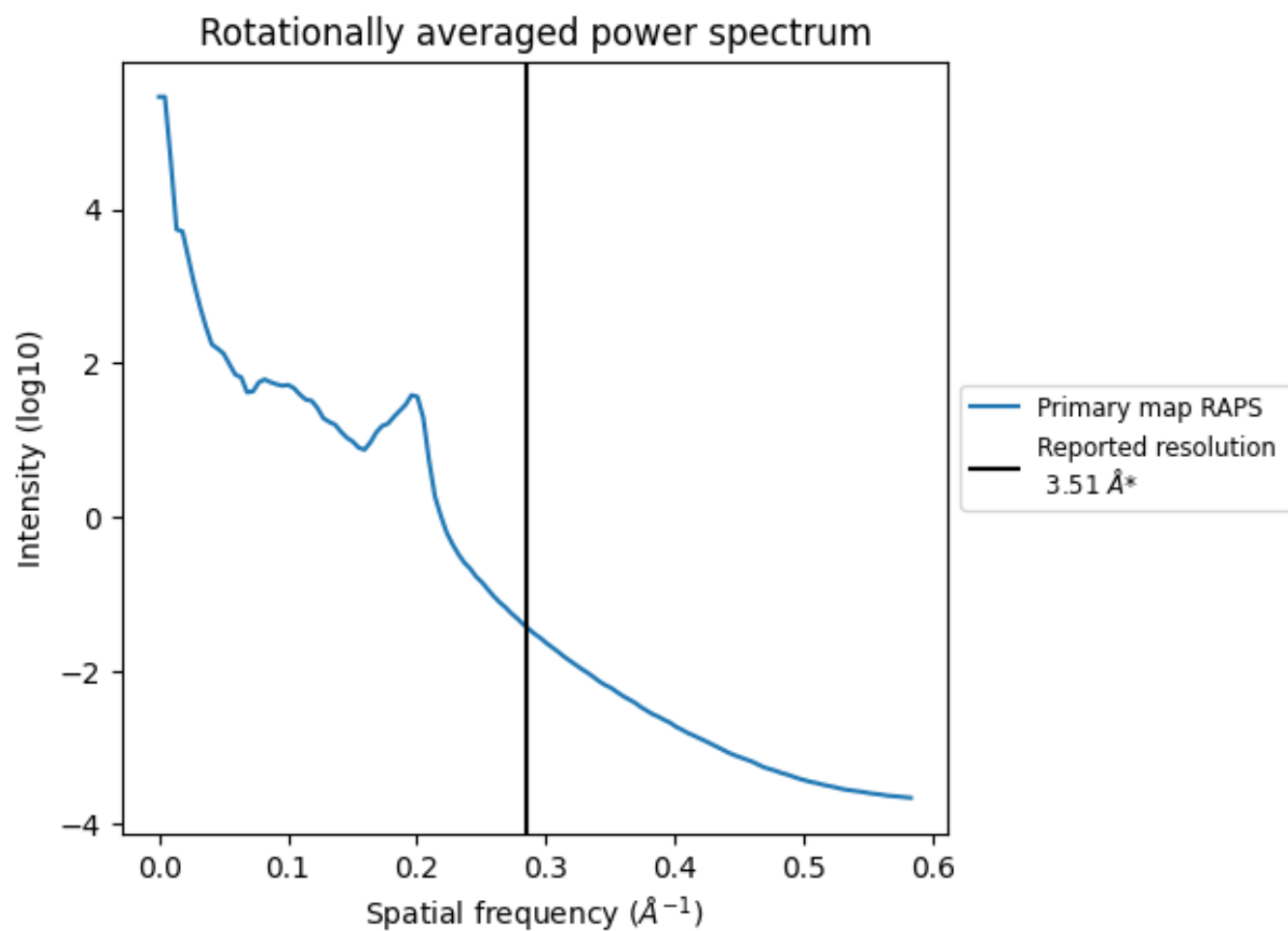
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 165 nm^3 ; this corresponds to an approximate mass of 149 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 0.285 Å⁻¹

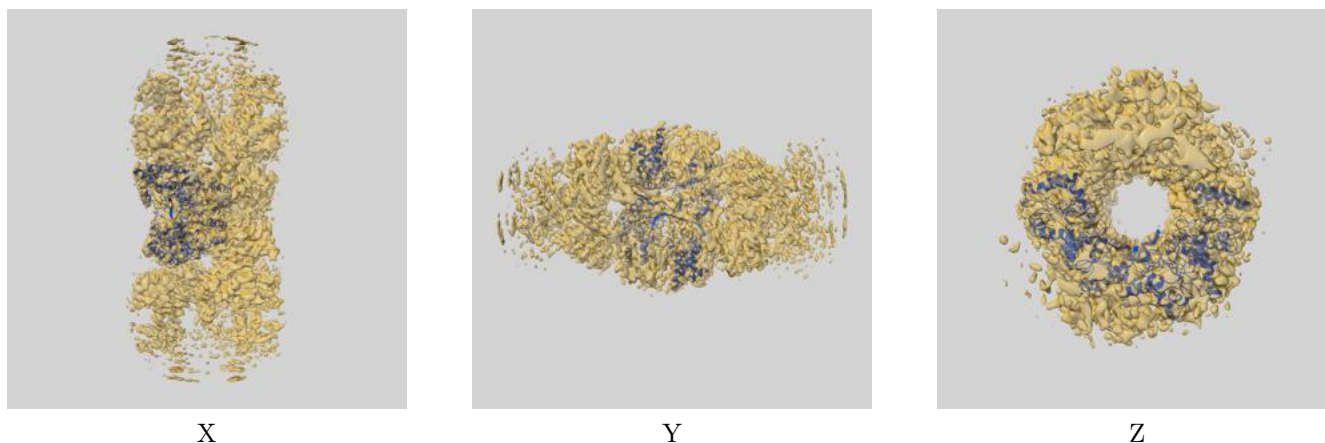
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

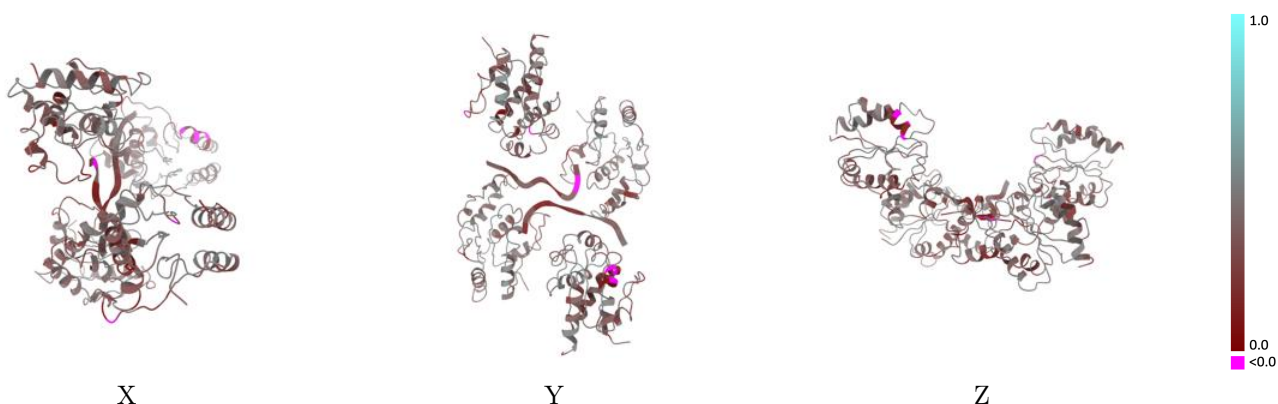
This section contains information regarding the fit between EMDB map EMD-32125 and PDB model 7X5L. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



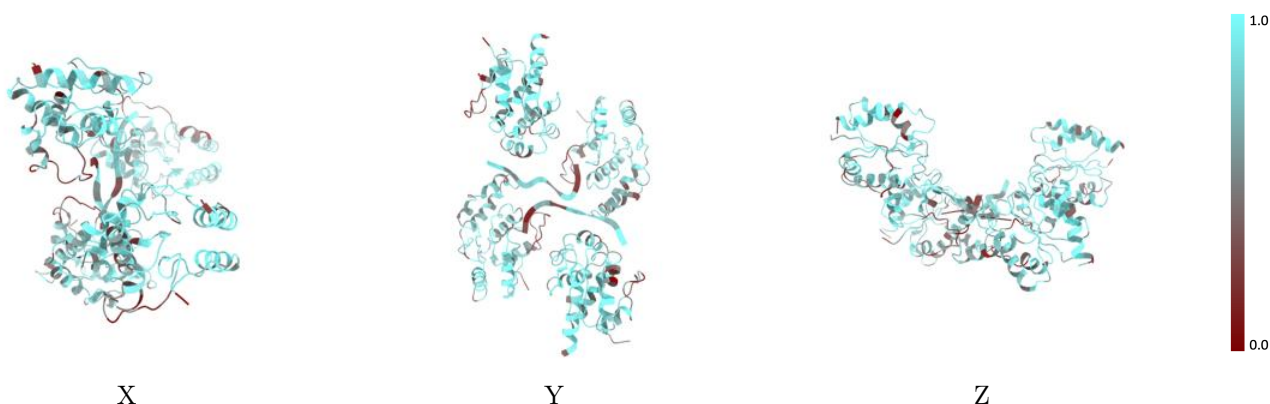
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



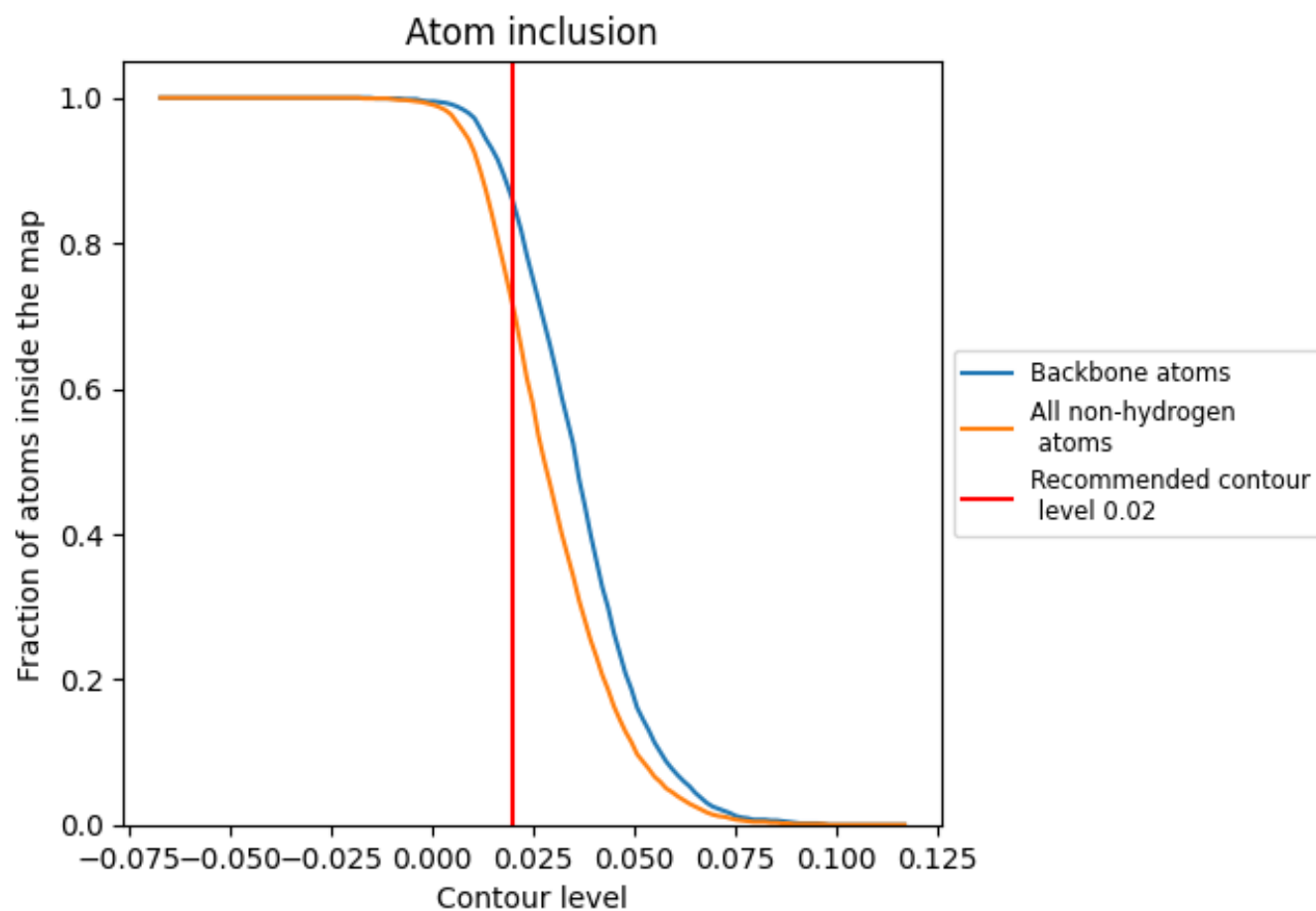
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 72% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7170	0.3810
A	0.6480	0.2470
B	0.7050	0.3910
C	0.5900	0.2770
D	0.7270	0.3810
E	0.7360	0.3820
F	0.7200	0.3940

1.0

0.0

<0.0